

# MAPPING STATS

Species	Assay	Read Type + Length	Mapping	#	Complexity	Unique	Unique Splices	Multi	Multi Splices	Mapped fraction	Raw fragments
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	ATCC-BXS0114--CGND-HRA-00742--Female--Non-Neurological_Control--Cell_Line_IPS--Unknown	0.47	45,304,822	18,588,646	5,992,451	1,631,047	0.96	37,150,582
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	ATCC-BXS0114--CGND-HRA-00743--Female--Non-Neurological_Control--Cell_Line_Motor_Neuron--Unknown	0.55	61,649,476	17,224,366	4,065,900	1,435,646	0.96	43,748,333
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	ATCC-BYS0112--CGND-HRA-00740--Male--Non-Neurological_Control--Cell_Line_IPS--Unknown	0.58	39,980,734	12,212,976	3,797,696	1,043,362	0.96	29,619,700
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	ATCC-BYS0112--CGND-HRA-00741--Male--Non-Neurological_Control--Cell_Line_Motor_Neuron--Unknown	0.59	51,882,219	12,008,721	2,489,694	990,210	0.94	35,800,577
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	GWF14-01--CGND-HRA-00295--Female--Pre-fALS_FTD--Cerebellum--C9orf72_pos	0.68	112,379,104	12,169,240	3,899,467	1,786,715	0.95	68,581,818
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	GWF14-01--CGND-HRA-00296--Female--Pre-fALS_FTD--Cortex_Motor_Medial--C9orf72_pos	0.75	68,712,442	9,127,072	2,295,543	846,307	0.93	43,705,257
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	GWF14-01--CGND-HRA-00297--Female--Pre-fALS_FTD--Cortex_Motor_Lateral--C9orf72_pos	0.62	83,954,013	13,930,047	3,054,918	1,561,646	0.96	53,634,614
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	GWF14-01--CGND-HRA-00298--Female--Pre-fALS_FTD--Spinal_Cord_Cervical--C9orf72_pos	0.66	66,659,693	13,265,687	3,236,642	1,127,070	0.92	45,564,445
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	GWF14-01--CGND-HRA-00299--Female--Pre-fALS_FTD--Spinal_Cord_Lumbar--C9orf72_pos	0.62	52,868,229	11,343,809	2,065,599	993,215	0.95	35,534,797
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	GWF14-01--CGND-HRA-00300--Female--Pre-fALS_FTD--Cortex_Frontal--C9orf72_pos	0.71	72,962,432	10,048,226	2,517,202	904,162	0.95	45,498,984
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	GWF14-01--CGND-HRA-00301--Female--Pre-fALS_FTD--Cortex_Occipital--C9orf72_pos	0.75	71,058,077	9,232,715	2,368,613	973,313	0.93	45,029,491
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	GWF14-01--CGND-HRA-00302--Female--Pre-fALS_FTD--Spinal_Cord_Thoracic--C9orf72_pos	0.59	78,623,419	16,770,103	2,932,839	1,577,391	0.95	52,743,959
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU10--CGND-HRA-00106--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_OPTN_pos	0.70	95,859,003	9,260,535	2,990,144	1,488,382	0.95	57,466,996
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU12--CGND-HRA-00108--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.66	85,988,079	11,492,263	2,792,424	1,604,552	0.95	53,375,068
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU14--CGND-HRA-00110--Male--ALS--Cerebellum--C9orf72_neg_SOD1_pos	0.69	64,232,468	8,549,192	2,397,934	1,230,036	0.95	40,210,760
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU15--CGND-HRA-00111--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.71	84,471,889	9,126,359	2,803,387	1,316,591	0.96	51,215,158
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU16--CGND-HRA-00112--Female--ALS--Liver--C9orf72_pos_SOD1_neg_NEK1_pos	0.41	84,678,730	32,055,316	4,479,434	3,039,918	0.95	65,161,308
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU22--CGND-HRA-00118--Male--ALS--Cerebellum--C9orf72_pos_SOD1_neg_SPG11_pos	0.75	75,364,300	5,440,340	1,876,442	773,616	0.95	43,732,917
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU25--CGND-HRA-00121--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_OPTN_pos_ANXA11_likely_benign	0.81	41,052,226	2,456,708	1,000,722	373,138	0.96	23,267,125
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU28--CGND-HRA-00124--Male--ALS--Cortex_Sensory--C9orf72_neg_SOD1_neg	0.76	67,244,381	7,040,363	1,844,473	596,989	0.95	40,528,397
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU3--CGND-HRA-00099--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.72	79,120,675	7,182,765	2,597,462	1,304,856	0.95	47,412,154
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU30--CGND-HRA-00126--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.70	79,707,184	8,842,450	2,410,545	1,552,493	0.95	48,484,165
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU32--CGND-HRA-00128--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.65	118,979,005	13,903,477	3,810,170	2,615,610	0.95	72,939,879
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU33--CGND-HRA-00129--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_negMATR3_pos_VUS	0.70	75,631,733	9,771,719	2,048,562	906,912	0.96	46,205,752
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU38--CGND-HRA-00134--Female--ALS--Cortex_Motor_Unspecified--C9orf72_pos_SOD1_neg	0.72	68,423,650	8,243,084	2,080,076	704,274	0.96	41,353,773
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU4--CGND-HRA-00100--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_SETX_pos_likely_benign	0.80	38,041,202	3,340,444	1,082,207	513,253	0.95	22,529,420
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU43--CGND-HRA-00139--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_pos	0.62	104,384,842	17,000,888	4,238,745	1,753,055	0.94	68,030,583
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU47--CGND-HRA-00143--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_ANXA11_pos	0.69	85,382,248	10,204,954	2,759,544	1,705,468	0.95	52,564,880
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU5--CGND-HRA-00101--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_DCTN1_neg	0.74	70,493,932	5,454,256	1,780,857	820,055	0.96	41,042,050
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU52--CGND-HRA-00148--Male--ALS--Cortex_Frontal--C9orf72_pos_SOD1_neg	0.55	78,322,021	16,844,293	4,363,297	1,746,383	0.93	54,382,807
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU53--CGND-HRA-00149--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg_OPTN_pos	0.61	96,767,855	17,030,251	4,201,316	1,426,300	0.95	62,118,601
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU55--CGND-HRA-00151--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.69	127,176,855	8,507,407	2,079,960	1,516,448	0.94	75,035,529
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU56--CGND-HRA-00152--Male--ALS--Liver--C9orf72_neg_SOD1_neg_TARDBP_pos_TBK1_ALS2_likely_benign	0.41	65,008,327	24,847,827	6,504,285	3,385,817	0.95	52,342,165
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU57--CGND-HRA-00153--Male--ALS--Liver--C9orf72_neg_SOD1_neg_FUS_pos_ALS2_likely_benign	0.41	62,551,235	22,218,531	4,683,715	3,925,519	0.90	53,728,518
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU58--CGND-HRA-00154--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.68	84,179,833	10,166,979	2,723,408	1,620,438	0.96	51,523,231
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU59--CGND-HRA-00155--Female--ALS--Liver--C9orf72_neg_SOD1_neg	0.56	62,296,427	12,503,037	4,504,187	1,562,983	0.93	43,378,625
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU60--CGND-HRA-00156--Male--DLB_Peripheral_Neuropathy--Cerebellum--C9orf72_neg_SOD1_neg_NEFH_likely_benign_VAPB	0.72	101,534,465	7,848,901	4,230,113	1,618,385	0.93	62,036,879
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU63--CGND-HRA-00159--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_ALS2_pos	0.74	82,417,646	6,003,778	2,368,484	834,822	0.95	48,219,339
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU64--CGND-HRA-00160--Male--ALS_FTD--Cortex_Frontal--C9orf72_neg_SOD1_neg_NEK1_pos	0.70	109,904,851	12,012,699	5,060,098	1,380,614	0.93	68,781,766
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU7--CGND-HRA-00103--Male--ALS--Liver--C9orf72_neg_SOD1_neg	0.49	90,787,078	23,342,682	5,176,695	3,633,821	0.95	64,396,044
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU70--CGND-HRA-00166--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_OPTN_pos	0.68	85,363,578	8,118,492	2,581,834	1,359,362	0.95	51,368,186
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU72--CGND-HRA-00168--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_CCNF_pos	0.73	88,202,057	5,999,621	2,495,929	854,357	0.94	51,616,394
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU73--CGND-HRA-00169--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_NEFH_likely_benign	0.69	67,635,323	7,641,611	2,476,563	1,732,671	0.95	41,889,048
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU73--CGND-HRA-00523--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_NEF3_pos_likely_benign	0.72	65,349,786	7,367,680	2,186,154	1,458,480	0.96	39,742,983

Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU73-CGND-HRA-00553--Female-ALS-Cortex_Frontal-C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.69	69,040,111	10,737,333	2,339,131	992,533	0.97	42,964,875
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU73-CGND-HRA-00554--Female-ALS-Cortex_Occipital-C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.73	76,561,319	7,394,113	2,385,221	826,955	0.97	45,156,326
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU73-CGND-HRA-00555--Female-ALS-Spinal_Cord_Thoracic-C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.59	66,927,819	16,230,957	2,571,133	1,369,599	0.94	46,136,496
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU73-CGND-HRA-00556--Female-ALS-Cortex_Motor_Medial-C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.68	73,323,031	10,808,511	2,443,154	987,614	0.95	46,115,561
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU73-CGND-HRA-00557--Female-ALS-Cortex_Motor_Lateral-C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.68	89,489,763	12,318,529	2,632,026	1,144,522	0.96	55,273,406
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU73-CGND-HRA-00558--Female-ALS-Spinal_Cord_Lumbar-C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.62	71,517,638	14,801,502	3,066,865	1,368,413	0.94	48,056,147
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU74-CGND-HRA-00170--Male-ALS-Cerebellum-C9orf72_neg_SOD1_pos_ANXA11_likely_benign	0.67	87,510,339	10,121,787	3,425,823	1,869,493	0.94	54,480,447
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU74-CGND-HRA-00559--Male-ALS-Cortex_Frontal-C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.61	56,751,032	12,420,750	3,300,733	1,279,675	0.96	38,549,889
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU74-CGND-HRA-00560--Male-ALS-Cortex_Occipital-C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.68	70,954,134	11,330,902	2,624,429	1,196,645	0.96	44,800,022
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU74-CGND-HRA-00561--Male-ALS-Cortex_Motor_Medial-C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.62	75,928,325	15,619,533	3,232,649	1,533,327	0.95	50,289,183
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU74-CGND-HRA-00562--Male-ALS-Cortex_Motor_Lateral-C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.64	82,917,177	15,255,991	3,507,304	1,408,652	0.94	54,759,689
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU74-CGND-HRA-01217--Male-ALS-Spinal_Cord_Thoracic-C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.62	63,248,855	13,833,883	2,490,459	1,352,125	0.96	42,098,493
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU75-CGND-HRA-00171--Female-ALS-Spinal_Cord_Cervical-C9orf72_pos_SOD1_neg_OPTN_pos_SPG11_likely_benign	0.62	66,926,027	13,228,231	3,420,951	1,545,211	0.95	44,589,623
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU75-CGND-HRA-00631--Female-ALS-Cortex_Motor_Unspecified-C9orf72_pos_SOD1_neg_OPTN_pos_SPG11_likely_benign	0.66	78,375,112	13,369,006	2,688,355	1,156,271	0.94	50,725,306
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU77-CGND-HRA-00633--Male-ALS-Cortex_Motor_Unspecified-C9orf72_neg_SOD1_neg	0.69	71,064,617	9,754,643	3,315,066	935,106	0.97	44,046,052
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU77-CGND-HRA-00634--Male-ALS-Spinal_Cord_Cervical-C9orf72_neg_SOD1_neg	0.56	76,663,115	12,455,573	6,518,504	1,654,648	0.96	50,630,818
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU79-CGND-HRA-00175--Male-ALS-Cerebellum-C9orf72_neg_SOD1_neg	0.70	79,162,632	5,917,664	4,171,655	1,171,291	0.95	47,757,582
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU79-CGND-HRA-00525--Male-ALS-Cerebellum-C9orf72_neg_SOD1_neg	0.62	65,218,957	5,229,021	3,936,508	1,566,202	0.95	39,830,705
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU79-CGND-HRA-00526--Male-ALS-Cortex_Frontal-C9orf72_neg_SOD1_neg	0.59	66,214,050	8,684,918	5,066,518	1,170,310	0.96	42,276,526
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU79-CGND-HRA-00527--Male-ALS-Cortex_Occipital-C9orf72_neg_SOD1_neg	0.52	67,052,340	8,194,982	6,383,181	1,513,719	0.96	43,528,460
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU79-CGND-HRA-00528--Male-ALS-Spinal_Cord_Thoracic-C9orf72_neg_SOD1_neg	0.50	53,350,147	12,481,979	4,559,254	1,490,328	0.96	37,273,626
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU79-CGND-HRA-00563--Male-ALS-Cortex_Motor_Medial-C9orf72_neg_SOD1_neg	0.65	55,758,674	7,433,632	3,026,994	865,550	0.96	34,960,221
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU79-CGND-HRA-00564--Male-ALS-Cortex_Motor_Lateral-C9orf72_neg_SOD1_neg	0.55	43,462,449	7,266,519	3,764,140	882,610	0.96	28,840,603
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU79-CGND-HRA-00565--Male-ALS-Spinal_Cord_Lumbar-C9orf72_neg_SOD1_neg	0.54	40,633,794	7,084,668	9,271,806	982,310	0.96	30,162,523
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU8-CGND-HRA-00104--Male-ALS-Cerebellum-C9orf72_neg_SOD1_pos_ALS2_pos	0.74	76,110,751	6,923,147	2,112,136	1,001,850	0.95	45,336,682
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU80-CGND-HRA-00529--Female-PLS-Cortex_Frontal-C9orf72_neg_SOD1_neg	0.67	70,568,393	11,397,031	2,818,485	1,071,353	0.96	44,668,033
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU80-CGND-HRA-00530--Female-PLS-Spinal_Cord_Thoracic-C9orf72_neg_SOD1_neg	0.65	62,324,482	10,849,618	2,970,730	1,113,942	0.96	40,429,085
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU80-CGND-HRA-00566--Female-PLS-Cerebellum-C9orf72_neg_SOD1_neg	0.74	58,577,290	5,824,454	1,777,803	1,020,031	0.96	34,918,661
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU80-CGND-HRA-00567--Female-PLS-Cortex_Occipital-C9orf72_neg_SOD1_neg	0.67	73,554,264	10,085,416	2,858,322	1,082,982	0.96	45,475,596
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU80-CGND-HRA-00568--Female-PLS-Cortex_Motor_Medial-C9orf72_neg_SOD1_neg	0.71	59,640,629	7,173,197	2,805,350	731,796	0.97	36,426,514
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU80-CGND-HRA-00569--Female-PLS-Cortex_Motor_Lateral-C9orf72_neg_SOD1_neg	0.68	64,298,103	9,482,809	2,807,981	875,171	0.96	40,226,555
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU80-CGND-HRA-00570--Female-PLS-Spinal_Cord_Lumbar-C9orf72_neg_SOD1_neg	0.66	51,834,838	7,581,694	3,413,836	1,010,176	0.96	33,117,838
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU82-CGND-HRA-00178--Male-ALS-Cerebellum-C9orf72_neg_SOD1_neg	0.70	75,117,968	8,210,064	2,788,311	1,400,251	0.94	46,524,278
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU82-CGND-HRA-00531--Male-ALS-Cerebellum-C9orf72_neg_SOD1_neg	0.70	87,562,190	9,394,624	3,084,102	1,864,476	0.94	53,972,320
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU82-CGND-HRA-00571--Male-ALS-Cortex_Frontal-C9orf72_neg_SOD1_neg	0.61	120,835,466	22,465,362	6,264,997	1,944,637	0.94	80,385,953
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU82-CGND-HRA-00572--Male-ALS-Cortex_Occipital-C9orf72_neg_SOD1_neg	0.79	40,418,325	3,866,667	1,945,603	442,673	0.94	24,705,011
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU82-CGND-HRA-00573--Male-ALS-Spinal_Cord_Thoracic-C9orf72_neg_SOD1_neg	0.53	67,772,565	13,335,875	4,474,457	1,415,355	0.96	45,277,753
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU82-CGND-HRA-00574--Male-ALS-Cortex_Motor_Medial-C9orf72_neg_SOD1_neg	0.73	68,209,924	6,617,966	3,911,506	769,030	0.95	42,006,572
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU82-CGND-HRA-00575--Male-ALS-Cortex_Motor_Lateral-C9orf72_neg_SOD1_neg	0.68	65,646,665	10,740,469	3,066,413	963,007	0.94	42,662,326
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU82-CGND-HRA-00576--Male-ALS-Spinal_Cord_Cervical-C9orf72_neg_SOD1_neg	0.67	84,757,102	12,455,992	3,107,957	1,098,081	0.95	53,568,865
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU82-CGND-HRA-00577--Male-ALS-Spinal_Cord_Lumbar-C9orf72_neg_SOD1_neg	0.68	79,614,521	11,733,053	3,973,336	1,148,532	0.94	51,085,720
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU83-CGND-HRA-00179--Male-ALS-Cerebellum-C9orf72_neg_SOD1_pos_SPG11_pos	0.69	93,830,529	9,408,421	3,807,843	1,499,385	0.91	59,376,546
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU83-CGND-HRA-00532--Male-ALS-Cerebellum-C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.71	96,650,059	10,114,501	3,171,070	1,604,722	0.95	58,620,994
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU83-CGND-HRA-00578--Male-ALS-Cortex_Frontal-C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.72	61,603,109	9,491,495	2,194,882	738,514	0.95	39,111,229
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU83-CGND-HRA-00579--Male-ALS-Cortex_Occipital-C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.71	67,681,595	10,482,637	2,353,216	921,742	0.95	42,958,042
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU83-CGND-HRA-00580--Male-ALS-Spinal_Cord_Thoracic-C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.70	44,724,631	7,435,759	2,186,046	648,002	0.95	28,806,936
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU83-CGND-HRA-00581--Male-ALS-Cortex_Motor_Medial-C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.61	161,046,295	25,028,633	5,703,687	2,338,253	0.95	101,749,085
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU83-CGND-HRA-00582--Male-ALS-Cortex_Motor_Lateral-C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.71	61,152,671	10,166,557	2,218,420	801,920	0.95	39,185,134
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU83-CGND-HRA-00583--Male-ALS-Spinal_Cord_Cervical-C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.61	72,637,774	15,806,988	3,130,719	1,446,903	0.96	48,589,227
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	JHU83-CGND-HRA-00584--Male-ALS-Spinal_Cord_Lumbar-C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.63	65,505,092	12,924,560	3,071,795	1,153,341	0.95	43,438,984

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAP156PM4--CGND-HRA-00183--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.69	86,707,117	8,676,939	2,681,670	1,471,886	0.95	52,583,277
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAP156PM4--CGND-HRA-00534--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.70	74,301,280	8,600,512	2,573,762	1,718,634	0.94	46,827,192
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAP156PM4--CGND-HRA-00535--Female--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.63	73,578,539	14,805,077	3,095,171	1,328,765	0.95	48,890,011
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAP156PM4--CGND-HRA-00536--Female--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.69	57,515,489	8,974,651	2,163,501	868,037	0.96	36,684,397
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAP156PM4--CGND-HRA-00537--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.60	48,251,685	10,626,787	3,237,832	1,088,734	0.95	32,933,197
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAP156PM4--CGND-HRA-00603--Female--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg	0.57	76,137,444	17,611,794	2,703,527	1,599,601	0.95	51,358,466
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAP156PM4--CGND-HRA-00604--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg	0.54	72,968,553	18,534,101	3,151,529	1,969,651	0.95	50,915,938
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAP156PM4--CGND-HRA-00605--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.45	120,069,660	34,228,150	6,189,182	3,537,858	0.95	86,314,755
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAP156PM4--CGND-HRA-00606--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.46	69,694,810	18,982,046	4,822,380	1,902,434	0.96	49,906,178
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAT369TG5--CGND-HRA-00333--Female--ALS--Cerebellum--C9orf72_neg	0.69	82,351,328	10,638,148	3,126,234	1,888,358	0.95	51,616,556
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAT369TG5--CGND-HRA-00334--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.68	57,137,312	10,529,686	2,090,575	921,233	0.96	36,964,391
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAT369TG5--CGND-HRA-00335--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.67	65,877,254	11,835,086	2,302,735	1,037,297	0.96	42,936,052
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAT369TG5--CGND-HRA-00336--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.58	55,790,804	13,628,466	2,956,014	1,224,372	0.96	38,533,659
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAT369TG5--CGND-HRA-00337--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.64	56,295,805	10,921,195	2,372,479	967,901	0.93	37,830,381
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAT369TG5--CGND-HRA-00338--Female--ALS--Cortex_Frontal--C9orf72_neg	0.69	68,650,841	10,897,307	2,494,733	1,208,569	0.95	43,819,872
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAT369TG5--CGND-HRA-00339--Female--ALS--Cortex_Occipital--C9orf72_neg	0.68	79,871,213	12,347,129	2,954,561	1,080,149	0.96	50,298,145
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAT369TG5--CGND-HRA-00340--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.63	62,137,428	11,542,730	2,169,925	1,101,577	0.96	39,891,193
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAV667LJK--CGND-HRA-00341--Male--ALS--Cerebellum--C9orf72_neg	0.74	74,573,641	6,501,337	2,401,130	1,582,510	0.95	44,587,197
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAV667LJK--CGND-HRA-00342--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.73	60,915,408	7,048,572	2,521,620	755,450	0.96	37,290,441
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAV667LJK--CGND-HRA-00343--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.66	76,926,282	11,127,430	2,699,040	1,106,288	0.96	48,071,485
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAV667LJK--CGND-HRA-00344--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.60	90,960,245	16,285,225	4,148,524	1,612,268	0.96	59,106,115
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAV667LJK--CGND-HRA-00345--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.54	60,565,123	13,967,565	2,956,218	1,490,478	0.96	41,334,827
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAV667LJK--CGND-HRA-00346--Male--ALS--Cortex_Frontal--C9orf72_neg	0.68	83,006,187	8,848,061	3,465,438	1,196,252	0.96	50,424,646
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAV667LJK--CGND-HRA-00347--Male--ALS--Cortex_Occipital--C9orf72_neg	0.60	69,423,201	9,888,083	2,932,034	1,096,784	0.95	43,818,730
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAV667LJK--CGND-HRA-00348--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.66	68,274,029	13,403,267	2,869,890	1,453,280	0.95	45,029,232
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAY067UTB--CGND-HRA-00746--Female--ALS--Cerebellum--C9orf72_neg	0.62	95,130,733	16,901,009	4,091,549	2,916,663	0.92	64,520,429
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAY067UTB--CGND-HRA-01269--Female--ALS--Cortex_Frontal--C9orf72_neg	0.71	69,511,082	10,587,126	2,277,076	885,706	0.97	43,061,393
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUAY067UTB--CGND-HRA-01270--Female--ALS--Cortex_Occipital--C9orf72_neg	0.64	70,556,263	13,976,843	3,217,349	1,409,115	0.95	46,739,438
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCG551GV1--CGND-HRA-00466--Female--Peripheral_Neuropathy--Cortex_Frontal--Unknown	0.69	55,602,986	8,965,582	3,018,678	824,854	0.96	35,747,845
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCG551GV1--CGND-HRA-00469--Female--Peripheral_Neuropathy--Cerebellum--Unknown	0.60	60,844,930	7,998,436	3,878,138	1,476,486	0.96	38,826,033
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCV649UJK--CGND-HRA-00243--Male--ALS--Cortex_Frontal--Unknown	0.68	46,642,840	8,921,526	1,593,273	636,637	0.95	30,268,722
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCV649UJK--CGND-HRA-00252--Male--ALS--Cortex_Motor_Medial--Unknown	0.62	71,534,212	14,671,462	3,468,696	1,349,340	0.94	48,519,328
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCV649UJK--CGND-HRA-00262--Male--ALS--Spinal_Cord_Cervical--Unknown	0.57	83,761,506	19,692,988	3,757,065	2,080,103	0.91	60,023,006
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCV649UJK--CGND-HRA-00275--Male--ALS--Spinal_Cord_Lumbar--Unknown	0.55	62,503,407	16,580,111	3,717,488	1,704,716	0.91	46,274,854
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCV649UJK--CGND-HRA-00722--Male--ALS--Cerebellum--Unknown	0.71	91,892,415	8,428,535	2,977,001	1,366,789	0.95	55,187,534
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCW292DYJ--CGND-HRA-00247--Female--ALS--Cortex_Frontal--Unknown	0.69	59,133,058	10,454,712	2,433,590	835,594	0.96	37,894,388
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCW292DYJ--CGND-HRA-00256--Female--ALS--Cortex_Motor_Medial--Unknown	0.56	97,301,173	20,072,395	3,544,544	1,737,290	0.96	63,974,038
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCW292DYJ--CGND-HRA-00266--Female--ALS--Spinal_Cord_Cervical--Unknown	0.62	55,755,694	11,758,654	1,648,466	1,065,840	0.97	36,181,220
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCW292DYJ--CGND-HRA-00279--Female--ALS--Spinal_Cord_Lumbar--Unknown	0.58	81,081,803	17,401,857	2,636,213	1,595,441	0.96	53,346,104
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUCW292DYJ--CGND-HRA-00727--Female--ALS--Cerebellum--Unknown	0.65	77,887,357	12,952,823	3,374,226	1,927,208	0.95	50,517,345
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDA151YMK--CGND-HRA-00593--Female--Non-Neurological_Control--Cerebellum--C9orf72_neg	0.74	70,192,869	7,616,237	2,345,846	1,355,694	0.95	42,753,001
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDA151YMK--CGND-HRA-00594--Female--Non-Neurological_Control--Cortex_Motor_Medial--C9orf72_neg	0.72	61,672,182	8,847,130	2,433,566	824,122	0.96	38,482,145
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDA151YMK--CGND-HRA-00595--Female--Non-Neurological_Control--Cortex_Motor_Lateral--C9orf72_neg	0.66	107,283,098	14,391,608	4,267,490	1,452,666	0.96	66,161,456
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDA151YMK--CGND-HRA-01258--Female--Non-Neurological_Control--Cortex_Frontal--C9orf72_neg	0.65	68,305,352	11,495,134	3,491,239	1,170,719	0.96	43,787,996
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDA151YMK--CGND-HRA-01259--Female--Non-Neurological_Control--Spinal_Cord_Thoracic--C9orf72_neg	0.58	51,476,336	10,401,830	3,129,045	1,262,587	0.96	34,448,667
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG361GA9--CGND-HRA-00208--Female--ALS--Cerebellum--C9orf72_neg	0.72	79,549,114	7,741,250	2,364,818	1,163,782	0.95	47,751,494
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG361GA9--CGND-HRA-00214--Female--ALS--Cortex_Frontal--C9orf72_neg	0.68	68,001,137	10,867,779	1,927,123	890,391	0.95	43,080,363
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG361GA9--CGND-HRA-00220--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.67	106,245,639	15,170,993	3,510,559	1,369,875	0.95	66,169,327
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG361GA9--CGND-HRA-00226--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.68	88,999,067	12,467,999	3,482,913	1,139,343	0.95	55,862,286
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG361GA9--CGND-HRA-00232--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.66	64,194,857	11,670,339	2,268,115	1,047,585	0.96	41,319,294

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG361GA9--CGND-HRA-00238--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.68	69,408,767	11,165,223	2,671,354	1,069,326	0.96	43,979,035
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG727NTW--CGND-HRA-00428--Female--ALS--Cerebellum--C9orf72_neg	0.71	50,673,220	6,361,598	1,727,218	1,148,226	0.95	31,596,112
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG727NTW--CGND-HRA-00429--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.61	67,794,085	14,157,045	2,056,044	1,233,128	0.95	44,678,928
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG727NTW--CGND-HRA-00430--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.65	61,563,609	12,055,021	1,838,716	1,015,328	0.95	40,131,427
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG727NTW--CGND-HRA-00431--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.66	36,677,864	8,360,404	1,210,443	699,067	0.95	24,707,323
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG727NTW--CGND-HRA-00431-2--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.60	42,308,165	10,501,295	1,493,570	929,948	0.96	28,726,349
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG727NTW--CGND-HRA-00432--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.54	52,729,070	14,522,794	2,141,031	1,346,505	0.95	37,195,998
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG727NTW--CGND-HRA-00433--Female--ALS--Cortex_Frontal--C9orf72_neg	0.58	98,582,769	19,741,943	3,413,992	1,930,252	0.95	65,122,277
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG727NTW--CGND-HRA-01299--Female--ALS--Cortex_Occipital--C9orf72_neg	0.68	72,702,911	11,949,567	2,867,143	1,194,495	0.95	46,480,861
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDG727NTW--CGND-HRA-01300--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.60	96,526,860	19,937,760	4,483,266	2,000,802	0.95	64,464,131
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDM397JGD--CGND-HRA-00205--Female--ALS--Cerebellum--C9orf72_neg	0.73	61,553,208	7,110,078	2,123,972	1,133,354	0.95	37,698,531
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDM397JGD--CGND-HRA-00211--Female--ALS--Cortex_Frontal--C9orf72_neg	0.63	79,896,968	14,283,556	2,501,067	1,267,353	0.95	51,357,449
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDM397JGD--CGND-HRA-00217--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.66	51,049,657	10,606,345	1,981,871	915,569	0.95	33,907,669
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDM397JGD--CGND-HRA-00223--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.58	99,556,239	19,694,801	3,291,693	1,833,075	0.95	65,207,863
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDM397JGD--CGND-HRA-00229--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.60	74,538,902	14,946,680	2,443,943	1,360,073	0.95	48,965,882
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDM397JGD--CGND-HRA-00235--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.63	94,087,420	16,518,410	3,291,608	1,519,946	0.95	60,502,008
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDR086ZDQ--CGND-HRA-00207--Female--ALS--Cerebellum--Unknown	0.80	32,475,946	3,281,292	949,956	439,630	0.96	19,374,427
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDR086ZDQ--CGND-HRA-00213--Female--ALS--Cortex_Frontal--Unknown	0.65	106,538,804	16,224,768	3,274,424	1,381,240	0.96	66,468,106
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDR086ZDQ--CGND-HRA-00219--Female--ALS--Cortex_Motor_Medial--Unknown	0.76	53,729,671	6,279,563	1,618,305	575,851	0.96	32,486,275
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDR086ZDQ--CGND-HRA-00225--Female--ALS--Cortex_Motor_Lateral--Unknown	0.72	76,938,360	9,840,286	2,487,730	967,042	0.95	47,376,683
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDR086ZDQ--CGND-HRA-00231--Female--ALS--Spinal_Cord_Cervical--Unknown	0.58	110,952,182	21,004,824	4,006,701	2,080,807	0.95	72,320,015
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDR086ZDQ--CGND-HRA-00237--Female--ALS--Spinal_Cord_Lumbar--Unknown	0.65	70,862,243	12,103,319	2,493,292	1,106,760	0.96	45,060,717
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDT233Z1--CGND-HRA-00422--Male--ALS--Cerebellum--C9orf72_neg	0.73	59,453,305	6,737,791	1,787,576	1,068,326	0.95	36,358,347
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDT233Z1--CGND-HRA-00423--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.69	52,037,024	8,834,802	1,493,290	721,384	0.95	33,287,814
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDT233Z1--CGND-HRA-00424--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.68	58,817,445	9,657,063	1,769,828	862,598	0.95	37,392,593
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDT233Z1--CGND-HRA-00425--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.63	51,493,824	10,547,518	1,879,933	954,359	0.96	33,961,544
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDT233Z1--CGND-HRA-00426--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.57	50,834,027	14,049,605	1,865,184	1,233,126	0.96	35,433,082
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDT233Z1--CGND-HRA-00427--Male--ALS--Cortex_Frontal--C9orf72_neg	0.63	57,202,732	11,390,526	1,770,567	1,031,725	0.95	37,436,002
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDT233Z1--CGND-HRA-01297--Male--ALS--Cortex_Occipital--C9orf72_neg	0.70	75,470,322	8,799,862	3,938,261	965,639	0.95	46,741,379
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDT233Z1--CGND-HRA-01298--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.65	81,203,755	14,362,837	3,399,619	1,461,131	0.95	52,646,201
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUDW867L9--CGND-HRA-00271--Male--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.59	65,928,089	14,207,417	2,782,478	1,289,326	0.96	43,913,471
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEA633EN5--CGND-HRA-00671--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.66	150,133,037	11,778,339	5,697,273	2,534,441	0.95	91,605,554
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEA633EN5--CGND-HRA-00672--Female--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg	0.76	44,311,535	6,644,379	1,634,750	582,482	0.94	28,162,807
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEA633EN5--CGND-HRA-00673--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg	0.64	101,753,555	15,427,169	3,917,387	1,455,779	0.96	63,972,664
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEA633EN5--CGND-HRA-00674--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.55	62,640,882	15,691,610	3,868,117	1,552,743	0.96	43,593,721
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEA633EN5--CGND-HRA-00675--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.57	56,335,197	11,088,003	4,856,670	1,178,360	0.95	38,482,881
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEA633EN5--CGND-HRA-01245--Female--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.74	56,408,072	7,247,400	2,375,403	756,157	0.96	34,760,872
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEA633EN5--CGND-HRA-01246--Female--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.68	56,722,821	9,752,481	2,564,197	974,253	0.96	36,375,212
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEA633EN5--CGND-HRA-01247--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.56	64,266,541	14,457,897	4,350,275	1,495,391	0.96	44,001,357
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEC006FND--CGND-HRA-00017--Female--ALS--Cortex_Frontal--C9orf72_neg	0.68	81,923,899	11,215,399	2,262,419	992,695	0.96	50,283,701
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEC006FND--CGND-HRA-00031--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.65	48,586,930	8,275,720	2,837,387	860,237	0.96	31,499,188
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEC006FND--CGND-HRA-00045--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.73	61,881,086	7,384,020	3,193,932	1,713,760	0.96	38,156,702
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEC006FND--CGND-HRA-00059--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.71	72,433,367	8,837,979	2,891,891	859,191	0.96	44,498,097
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEC006FND--CGND-HRA-00073--Female--ALS--Cerebellum--C9orf72_neg	0.69	94,716,761	8,270,567	3,023,523	1,614,047	0.95	56,499,282
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEC006FND--CGND-HRA-00087--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.77	57,896,698	5,489,328	1,763,014	547,398	0.96	34,175,269
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEC006FND--CGND-HRA-01335--Female--ALS--Cortex_Occipital--C9orf72_neg	0.59	43,498,546	10,715,280	3,014,558	1,070,288	0.95	30,614,703
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEE593VY7--CGND-HRA-00404--Male--MSA--Cerebellum--C9orf72_neg	0.67	64,279,986	9,511,152	2,735,510	1,871,040	0.94	41,536,258
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEE593VY7--CGND-HRA-00405--Male--MSA--Cortex_Motor_Medial--C9orf72_neg	0.62	69,277,568	12,507,144	2,217,205	1,341,425	0.95	45,046,571
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEE593VY7--CGND-HRA-00406--Male--MSA--Cortex_Motor_Lateral--C9orf72_neg	0.62	76,400,351	12,612,459	2,308,574	1,256,124	0.95	48,486,175
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEE593VY7--CGND-HRA-00407--Male--MSA--Spinal_Cord_Cervical--C9orf72_neg	0.63	58,405,215	11,086,799	2,363,593	1,122,255	0.96	38,022,234

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUE593VY7--CGND-HRA-00408--Male--MSA--Spinal_Cord_Lumbar--C9orf72_neg	0.53	75,242,081	15,692,985	3,985,920	2,022,214	0.95	50,939,108
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUE593VY7--CGND-HRA-00409--Male--MSA--Cortex_Frontal--C9orf72_neg	0.52	63,863,586	18,006,640	2,621,982	1,691,416	0.95	45,537,776
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUE593VY7--CGND-HRA-01291--Male--MSA--Cortex_Occipital--C9orf72_neg	0.72	70,135,584	8,481,314	3,099,877	1,079,265	0.96	43,288,829
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUE593VY7--CGND-HRA-01292--Male--MSA--Spinal_Cord_Thoracic--C9orf72_neg	0.67	47,350,361	8,419,581	2,575,368	841,864	0.96	30,917,968
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF397VVN--CGND-HRA-00303--Female--ALS_AD--Cerebellum--Unknown	0.68	60,309,790	9,155,708	2,410,884	2,019,736	0.93	39,630,945
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF397VVN--CGND-HRA-00304--Female--ALS_AD--Cortex_Motor_Medial--Unknown	0.62	72,531,452	14,672,626	2,136,547	1,314,455	0.95	47,897,151
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF397VVN--CGND-HRA-00305--Female--ALS_AD--Cortex_Motor_Lateral--Unknown	0.57	135,190,597	26,087,641	4,075,488	2,287,274	0.94	88,858,405
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF397VVN--CGND-HRA-00306--Female--ALS_AD--Spinal_Cord_Cervical--Unknown	0.62	54,414,611	11,280,983	1,947,966	1,078,352	0.95	36,199,873
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF397VVN--CGND-HRA-00307--Female--ALS_AD--Spinal_Cord_Lumbar--Unknown	0.60	60,657,626	14,906,206	3,608,699	1,617,389	0.96	42,212,555
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF397VVN--CGND-HRA-00308--Female--ALS_AD--Cortex_Frontal--Unknown	0.59	70,764,021	15,582,161	2,664,959	1,484,233	0.96	47,329,818
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF397VVN--CGND-HRA-00309--Female--ALS_AD--Cortex_Occipital--Unknown	0.65	46,821,211	8,629,197	2,020,029	905,407	0.96	30,532,991
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF397VVN--CGND-HRA-00310--Female--ALS_AD--Spinal_Cord_Thoracic--Unknown	0.65	64,498,925	13,216,931	2,532,915	1,201,361	0.96	42,369,841
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF856BLV--CGND-HRA-00460--Female--ALS--Cortex_Frontal--C9orf72_pos	0.73	41,885,337	7,222,657	1,479,461	594,501	0.97	26,404,760
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEF856BLV--CGND-HRA-00465--Female--ALS--Cerebellum--C9orf72_pos	0.75	53,659,021	6,328,489	1,523,555	778,785	0.96	32,337,750
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEG442LDR--CGND-HRA-00199--Male--Non-Neurological_Control--Liver--Unknown	0.46	72,278,492	21,872,126	4,173,825	3,055,373	0.96	52,821,597
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEG442LDR--CGND-HRA-00667--Male--Non-Neurological_Control--Cerebellum--Unknown	0.74	61,014,945	7,575,941	2,096,019	1,198,029	0.95	37,961,339
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEG442LDR--CGND-HRA-00668--Male--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.71	62,169,902	9,319,992	2,054,778	823,268	0.95	38,948,432
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEG442LDR--CGND-HRA-00669--Male--Non-Neurological_Control--Cortex_Motor_Lateral--Unknown	0.64	96,263,105	15,750,761	2,940,037	1,255,653	0.96	60,673,578
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEG442LDR--CGND-HRA-00670--Male--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.57	87,881,683	17,783,119	4,554,125	1,881,135	0.96	58,636,200
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEG442LDR--CGND-HRA-01242--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.69	72,087,640	12,117,360	2,249,297	940,097	0.96	45,439,848
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEG442LDR--CGND-HRA-01243--Male--Non-Neurological_Control--Cortex_Occipital--Unknown	0.72	60,727,861	9,291,249	2,006,325	877,065	0.96	37,891,223
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEG442LDR--CGND-HRA-01244--Male--Non-Neurological_Control--Spinal_Cord_Thoracic--Unknown	0.61	81,083,893	14,988,687	3,858,654	1,473,752	0.96	52,581,636
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEH612JPA--CGND-HRA-00542--Female--ALS_AD--Cerebellum--C9orf72_neg_SOD1_neg	0.74	73,426,452	6,338,300	2,180,141	1,178,929	0.95	43,756,205
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEH612JPA--CGND-HRA-00543--Female--ALS_AD--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.73	63,974,062	8,802,734	1,866,008	750,140	0.96	39,403,264
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEH612JPA--CGND-HRA-00544--Female--ALS_AD--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.72	62,711,961	8,717,043	1,962,072	743,210	0.96	38,890,249
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEH612JPA--CGND-HRA-00545--Female--ALS_AD--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.59	60,547,304	14,014,230	2,586,477	1,252,249	0.96	40,910,409
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEH612JPA--CGND-HRA-00611--Female--ALS_AD--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg	0.66	63,849,137	10,530,177	1,884,758	940,838	0.97	40,002,355
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEH612JPA--CGND-HRA-00612--Female--ALS_AD--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg	0.70	106,583,805	12,364,139	3,697,243	1,152,421	0.94	65,572,950
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEH612JPA--CGND-HRA-00613--Female--ALS_AD--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.56	69,490,007	16,696,009	2,784,808	1,626,348	0.96	47,088,529
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEH612JPA--CGND-HRA-00614--Female--ALS_AD--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.58	64,062,604	14,153,906	2,651,710	1,502,496	0.96	42,725,212
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEL133AK6--CGND-HRA-00013--Female--ALS--Cortex_Frontal--C9orf72_neg	0.67	91,056,285	13,131,931	3,004,111	1,197,173	0.96	56,576,541
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEL133AK6--CGND-HRA-00027--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.59	74,487,197	16,734,951	2,611,731	1,548,397	0.96	49,697,789
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEL133AK6--CGND-HRA-00041--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.62	97,450,700	16,611,848	3,812,423	1,622,915	0.96	62,465,250
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEL133AK6--CGND-HRA-00055--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.65	105,716,209	15,696,247	3,476,117	1,434,931	0.96	66,017,702
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEL133AK6--CGND-HRA-00069--Female--ALS--Cerebellum--C9orf72_neg	0.66	78,975,983	10,520,163	2,765,772	1,867,962	0.95	49,401,383
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEL133AK6--CGND-HRA-00083--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.63	85,320,429	15,383,529	2,706,574	1,459,292	0.96	54,829,382
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEL133AK6--CGND-HRA-01327--Female--ALS--Cortex_Occipital--C9orf72_neg	0.67	58,033,664	11,906,866	2,600,906	1,113,182	0.95	43,680,671
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEL133AK6--CGND-HRA-01328--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.54	71,505,872	19,889,692	4,570,137	1,957,513	0.96	51,169,163
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEP010ZFE--CGND-HRA-01178--Male--Non-Neurological_Control--Cerebellum--Unknown	0.72	79,556,699	7,005,531	2,891,087	1,256,329	0.96	47,449,151
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEP010ZFE--CGND-HRA-01179--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.68	54,561,812	9,820,290	2,416,874	859,126	0.93	36,443,371
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEP010ZFE--CGND-HRA-01204--Male--Non-Neurological_Control--Cortex_Occipital--Unknown	0.73	70,891,118	6,206,192	3,179,700	674,306	0.96	42,346,528
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUEP010ZFE--CGND-HRA-01205--Male--Non-Neurological_Control--Spinal_Cord_Thoracic--Unknown	0.53	70,956,950	16,061,940	3,527,204	1,566,530	0.96	48,163,665
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFE255AG2--CGND-HRA-00481--Male--ALS--Cortex_Frontal--Unknown	0.73	48,978,393	7,803,573	1,571,993	638,057	0.97	30,548,606
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFE255AG2--CGND-HRA-00486--Male--ALS--Cerebellum--Unknown	0.66	72,448,710	12,306,026	2,668,815	1,822,171	0.94	47,316,371
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFE255AG2--CGND-HRA-01206--Male--ALS--Cortex_Occipital--Unknown	0.64	84,280,063	14,900,943	2,809,976	1,403,696	0.96	53,945,132
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFE255AG2--CGND-HRA-01207--Male--ALS--Spinal_Cord_Thoracic--Unknown	0.56	47,360,009	13,240,443	3,426,421	1,395,141	0.95	34,269,993
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFF179PPT--CGND-HRA-00487--Male--ALS--Cortex_Frontal--C9orf72_neg	0.69	59,877,523	10,386,685	2,833,145	958,457	0.95	38,947,099
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFF179PPT--CGND-HRA-00492--Male--ALS--Cerebellum--C9orf72_neg	0.70	77,912,336	10,131,036	2,585,516	1,515,070	0.95	48,731,922
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFF179PPT--CGND-HRA-01208--Male--ALS--Cortex_Occipital--C9orf72_neg	0.63	61,753,553	13,865,427	2,953,665	1,250,757	0.96	41,707,488
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFF179PPT--CGND-HRA-01209--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.51	62,015,601	15,643,513	3,043,082	1,597,006	0.96	42,951,788

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFT454ZFP--CGND-HRA-00203--Male--ALS--Cerebellum--C9orf72_neg_ANG_pos	0.74	72,504,834	6,661,350	2,005,557	822,167	0.96	42,912,067
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFT454ZFP--CGND-HRA-00209--Male--ALS--Cortex_Frontal-C9orf72_neg_ANG_pos	0.68	34,977,888	7,218,126	1,129,724	533,420	0.96	22,900,714
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFT454ZFP--CGND-HRA-00215--Male--ALS--Cortex_Motor_Medial-C9orf72_neg_ANG_pos	0.64	54,826,414	10,380,720	2,219,814	906,492	0.95	35,929,933
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFT454ZFP--CGND-HRA-00221--Male--ALS--Cortex_Motor_Lateral-C9orf72_neg_ANG_pos	0.69	65,831,649	9,948,629	2,032,209	872,953	0.95	41,291,996
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFT454ZFP--CGND-HRA-00227--Male--ALS--Spinal_Cord_Cervical-C9orf72_neg_ANG_pos	0.59	69,339,532	14,852,546	2,544,514	1,396,494	0.96	46,933,533
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUFT454ZFP--CGND-HRA-00233--Male--ALS--Spinal_Cord_Lumbar-C9orf72_neg_ANG_pos	0.65	70,141,387	12,736,325	2,517,169	1,199,153	0.95	45,502,970
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGA773REC--CGND-HRA-00025--Male--ALS--Cortex_Frontal-C9orf72_neg	0.71	71,870,036	10,846,812	2,226,786	844,922	0.95	44,979,241
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGA773REC--CGND-HRA-00039--Male--ALS--Spinal_Cord_Lumbar-C9orf72_neg	0.57	80,432,887	17,052,719	3,599,032	1,655,894	0.96	53,753,192
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGA773REC--CGND-HRA-00053--Male--ALS--Spinal_Cord_Cervical-C9orf72_neg	0.61	61,959,008	13,603,914	2,298,646	1,335,826	0.95	41,539,890
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGA773REC--CGND-HRA-00081--Male--ALS--Cerebellum-C9orf72_neg	0.70	90,497,330	8,827,838	2,881,458	1,343,648	0.95	54,405,796
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGA773REC--CGND-HRA-00095--Male--ALS--Cortex_Motor_Lateral-C9orf72_neg	0.70	69,690,118	9,549,258	2,318,804	920,836	0.95	43,447,420
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGJ583BEE--CGND-HRA-01184-2--Male--Non-Neurological_Control--Cerebellum--Unknown	0.57	92,458,268	8,938,562	5,866,348	2,206,664	0.95	57,406,282
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGJ583BEE--CGND-HRA-01185--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.55	87,638,291	13,202,273	7,065,122	2,239,984	0.95	57,833,915
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGJ583BEE--CGND-HRA-01186--Male--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.72	62,063,748	6,207,168	3,771,121	762,555	0.96	38,055,192
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGJ583BEE--CGND-HRA-01187--Male--Non-Neurological_Control--Cortex_Motor_Lateral--Unknown	0.71	77,422,503	7,357,735	4,399,856	978,040	0.96	47,107,187
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGV399KJW--CGND-HRA-00365--Female--ALS--Cerebellum-C9orf72_neg	0.74	76,483,397	5,716,293	2,658,785	1,194,441	0.95	45,199,195
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGV399KJW--CGND-HRA-00366--Female--ALS--Cortex_Motor_Medial-C9orf72_neg	0.65	71,260,194	11,302,594	2,496,193	1,244,185	0.95	45,257,689
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGV399KJW--CGND-HRA-00367--Female--ALS--Cortex_Motor_Lateral-C9orf72_neg	0.72	63,287,168	7,521,544	1,892,685	720,913	0.95	38,468,087
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGV399KJW--CGND-HRA-00368--Female--ALS--Spinal_Cord_Cervical-C9orf72_neg	0.64	41,015,958	8,777,254	1,659,238	867,340	0.96	27,258,414
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGV399KJW--CGND-HRA-00369--Female--ALS--Cortex_Frontal-C9orf72_neg	0.63	70,739,409	10,961,335	4,549,669	1,438,839	0.95	46,290,712
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGV399KJW--CGND-HRA-00370--Female--ALS--Cortex_Occipital-C9orf72_neg	0.70	70,917,800	6,766,506	3,271,594	922,468	0.95	43,518,193
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGV399KJW--CGND-HRA-00371--Female--ALS--Spinal_Cord_Thoracic-C9orf72_neg	0.65	54,205,854	9,610,604	3,258,074	987,108	0.96	35,297,266
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY575NUQ--CGND-HRA-00585--Male--ALS--Cerebellum-C9orf72_neg	0.69	106,448,484	8,141,828	3,124,511	1,601,695	0.94	63,342,524
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY575NUQ--CGND-HRA-00586--Male--ALS--Cortex_Motor_Medial-C9orf72_neg	0.54	81,104,737	12,192,976	4,438,185	1,373,455	0.96	51,768,671
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY575NUQ--CGND-HRA-00587--Male--ALS--Cortex_Motor_Lateral-C9orf72_neg	0.70	36,091,142	5,190,307	1,578,607	511,741	0.96	22,585,736
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY575NUQ--CGND-HRA-00588--Male--ALS--Spinal_Cord_Cervical-C9orf72_neg	0.58	57,254,177	12,213,213	2,948,870	1,204,248	0.96	38,999,082
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY575NUQ--CGND-HRA-00589--Male--ALS--Spinal_Cord_Lumbar-C9orf72_neg	0.44	88,247,128	19,364,982	7,687,212	3,137,844	0.95	62,017,431
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY575NUQ--CGND-HRA-01254--Male--ALS--Cortex_Frontal-C9orf72_neg	0.64	63,662,666	10,842,300	3,841,266	1,246,048	0.96	41,612,549
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY575NUQ--CGND-HRA-01255--Male--ALS--Cortex_Occipital-C9orf72_neg	0.55	57,923,973	9,733,111	4,528,014	1,201,586	0.96	38,363,378
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY575NUQ--CGND-HRA-01256--Male--ALS--Spinal_Cord_Thoracic-C9orf72_neg	0.55	76,133,172	17,639,882	3,725,804	1,849,724	0.97	51,362,762
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY741GH8--CGND-HRA-00476--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.53	86,265,851	13,117,807	7,705,646	1,682,252	0.95	57,245,420
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY741GH8--CGND-HRA-00479--Male--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.61	37,079,156	7,737,870	2,028,132	785,650	0.93	25,584,166
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUGY741GH8--CGND-HRA-00480--Male--Non-Neurological_Control--Cerebellum--Unknown	0.56	64,433,140	7,966,440	5,404,321	1,688,617	0.95	41,823,182
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHA141EEC--CGND-HRA-00590--Male--Non-Neurological_Control--Cortex_Motor_Unspecified-C9orf72_neg	0.71	77,429,507	10,834,217	2,509,405	865,777	0.96	47,873,640
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHA141EEC--CGND-HRA-00592--Male--Non-Neurological_Control--Spinal_Cord_Lumbar-C9orf72_neg	0.54	81,467,174	16,461,284	4,507,095	1,665,899	0.95	54,608,770
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHA141EEC--CGND-HRA-01257--Male--Non-Neurological_Control--Spinal_Cord_Thoracic-C9orf72_neg	0.57	67,700,651	16,032,951	3,240,321	1,759,125	0.96	45,983,073
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHC282LVJ--CGND-HRA-00021--Female--Non-Neurological_Control--Cortex_Frontal-C9orf72_neg	0.71	58,870,199	9,394,009	2,241,380	799,010	0.96	37,243,581
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHC282LVJ--CGND-HRA-00035--Female--Non-Neurological_Control--Spinal_Cord_Lumbar-C9orf72_neg	0.63	72,872,246	13,580,296	3,307,234	1,288,242	0.95	48,168,239
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHC282LVJ--CGND-HRA-00049--Female--Non-Neurological_Control--Spinal_Cord_Cervical-C9orf72_neg	0.58	95,412,073	20,066,121	4,352,534	2,000,104	0.95	63,948,158
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHC282LVJ--CGND-HRA-00063--Female--Non-Neurological_Control--Cortex_Motor_Medial-C9orf72_neg	0.56	74,708,140	17,238,010	7,770,294	2,222,222	0.95	53,678,644
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHC282LVJ--CGND-HRA-00077--Female--Non-Neurological_Control--Cerebellum-C9orf72_neg	0.77	38,224,423	4,512,955	1,360,599	725,375	0.96	23,316,655
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHC282LVJ--CGND-HRA-00091--Female--Non-Neurological_Control--Cortex_Motor_Lateral-C9orf72_neg	0.59	81,344,407	17,596,771	4,051,493	1,880,233	0.95	55,338,595
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHC282LVJ--CGND-HRA-01342--Female--Non-Neurological_Control--Spinal_Cord_Thoracic-C9orf72_neg	0.55	54,839,676	15,284,996	3,035,982	1,418,104	0.95	39,214,154
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHC282LVJ--CGND-HRA-01343--Female--Non-Neurological_Control--Cortex_Occipital-C9orf72_neg	0.52	124,887,861	28,784,375	8,882,578	3,623,162	0.95	87,317,350
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHD481VCL--CGND-HRA-00206--Female--Non-Neurological_Control--Cerebellum--Unknown	0.70	63,581,686	8,069,878	1,963,230	1,169,260	0.96	39,321,320
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHD481VCL--CGND-HRA-00212--Female--Non-Neurological_Control--Cortex_Frontal--Unknown	0.67	77,260,882	12,329,766	2,322,719	966,805	0.95	48,681,670
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHD481VCL--CGND-HRA-00218--Female--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.62	93,089,292	17,364,468	3,834,103	1,599,993	0.95	60,701,366
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHD481VCL--CGND-HRA-00224--Female--Non-Neurological_Control--Cortex_Motor_Lateral--Unknown	0.65	77,383,993	13,237,221	3,073,381	1,306,371	0.95	50,035,088
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHD481VCL--CGND-HRA-00230--Female--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.64	86,612,169	14,092,511	2,995,998	1,407,486	0.95	55,097,473
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHD481VCL--CGND-HRA-00236--Female--Non-Neurological_Control--Spinal_Cord_Lumbar--Unknown	0.58	105,246,653	18,309,731	6,023,370	2,178,798	0.96	68,677,434

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHM340FBZ-CGND-HRA-00706-Male-ALS-Cerebellum-Unknown	0.73	75,951,598	7,199,162	2,604,316	1,108,302	0.95	45,817,779
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHX090PGV-CGND-HRA-00643-Male-Non-Neurological_Control-Cerebellum-Unknown	0.61	101,932,135	8,566,845	5,444,490	2,107,898	0.95	62,029,120
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHX090PGV-CGND-HRA-00644-Male-Non-Neurological_Control-Cortex_Motor_Medial-Unknown	0.63	69,527,654	8,920,562	3,898,871	1,109,625	0.96	43,457,728
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHX090PGV-CGND-HRA-00645-Male-Non-Neurological_Control-Spinal_Cord_Cervical-Unknown	0.60	53,146,333	9,648,667	3,071,496	1,024,024	0.96	34,678,425
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHX090PGV-CGND-HRA-01225-Male-Non-Neurological_Control-Cortex_Frontal-Unknown	0.67	75,246,605	10,112,269	3,641,677	1,313,733	0.96	47,097,276
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUHX090PGV-CGND-HRA-01227-Male-Non-Neurological_Control-Spinal_Cord_Thoracic-Unknown	0.56	57,189,299	10,536,027	2,947,821	1,125,339	0.96	37,475,105
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJB238MJR-CGND-HRA-00596-Male-Non-Neurological_Control-Cortex_Motor_Medial-C9orf72_neg	0.75	67,980,285	7,156,205	2,659,611	668,945	0.96	41,036,767
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJB238MJR-CGND-HRA-01260-Male-Non-Neurological_Control-Cortex_Frontal-C9orf72_neg	0.76	64,874,886	6,259,160	3,202,177	688,203	0.96	38,951,197
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJB238MJR-CGND-HRA-01261-Male-Non-Neurological_Control-Cortex_Occipital-C9orf72_neg	0.76	69,737,212	6,223,700	3,087,658	717,434	0.96	41,508,412
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJL308UBK-CGND-HRA-01348-Female-ALS-Cortex_Occipital-C9orf72_neg	0.65	92,026,163	13,805,797	5,197,349	1,525,339	0.93	60,636,124
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJL308UBK-CGND-HRA-01349-Female-ALS-Cortex_Frontal-C9orf72_neg	0.67	56,339,204	11,381,288	2,521,912	996,172	0.96	37,245,572
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJL308UBK-CGND-HRA-01350-Female-ALS-Cerebellum-C9orf72_neg	0.68	63,467,527	9,168,677	2,860,072	1,402,754	0.96	40,088,336
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJR139GPF-CGND-HRA-00024-Male-ALS-Cortex_Frontal-C9orf72_neg	0.75	67,519,503	7,083,735	2,266,209	650,819	0.95	40,690,250
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJR139GPF-CGND-HRA-00038-Male-ALS-Spinal_Cord_Lumbar-C9orf72_neg	0.49	83,213,311	12,795,339	6,555,147	1,993,225	0.95	55,121,172
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJR139GPF-CGND-HRA-00052-Male-ALS-Spinal_Cord_Cervical-C9orf72_neg	0.54	98,262,369	15,273,645	7,178,208	2,058,410	0.95	64,394,043
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJR139GPF-CGND-HRA-00066-Male-ALS-Cortex_Motor_Medial-C9orf72_neg	0.59	95,126,736	11,112,280	7,740,485	1,631,849	0.94	61,432,405
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJZ255ZC5-CGND-HRA-00020-2-Male-ALS-Cortex_Frontal-C9orf72_neg	0.71	66,249,613	9,121,739	1,778,832	770,560	0.95	41,142,007
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJZ255ZC5-CGND-HRA-00034-Male-ALS-Spinal_Cord_Lumbar-C9orf72_neg	0.57	94,819,558	21,338,310	3,138,338	2,006,494	0.96	63,142,970
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJZ255ZC5-CGND-HRA-00048-Male-ALS-Spinal_Cord_Cervical-C9orf72_neg	0.64	91,307,534	14,841,086	2,993,582	1,335,710	0.96	57,410,318
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJZ255ZC5-CGND-HRA-00062-Male-ALS-Cortex_Motor_Medial-C9orf72_neg	0.63	98,300,926	17,018,494	3,414,135	1,588,631	0.96	62,779,891
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJZ255ZC5-CGND-HRA-00076-Male-ALS-Cerebellum-C9orf72_neg	0.73	82,676,634	6,163,730	2,129,815	835,821	0.96	48,023,610
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJZ255ZC5-CGND-HRA-00090-Male-ALS-Cortex_Motor_Lateral-C9orf72_neg	0.72	74,228,487	9,433,933	2,471,617	787,109	0.96	45,192,610
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJZ255ZC5-CGND-HRA-01340-Male-ALS-Spinal_Cord_Thoracic-C9orf72_neg	0.74	42,992,309	7,115,231	1,728,597	626,143	0.97	27,088,048
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUJZ255ZC5-CGND-HRA-01341-Male-ALS-Cortex_Occipital-C9orf72_neg	0.62	114,473,986	19,693,692	5,004,590	2,036,278	0.96	73,543,128
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKM699KXH-CGND-HRA-00018-Female-ALS_FTD-Cortex_Frontal-C9orf72_pos	0.73	44,119,717	6,778,753	1,538,742	688,676	0.96	27,719,909
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKM699KXH-CGND-HRA-00032-Female-ALS_FTD-Spinal_Cord_Lumbar-C9orf72_pos	0.64	73,895,332	12,325,124	3,249,076	1,252,656	0.96	47,389,996
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKM699KXH-CGND-HRA-00046-Female-ALS_FTD-Spinal_Cord_Cervical-C9orf72_pos	0.56	104,427,397	21,082,945	4,349,508	2,286,228	0.96	69,180,348
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKM699KXH-CGND-HRA-00060-Female-ALS_FTD-Cortex_Motor_Medial-C9orf72_pos	0.68	87,420,730	12,181,926	3,459,263	1,111,355	0.96	54,360,994
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKM699KXH-CGND-HRA-00074-Female-ALS_FTD-Cerebellum-C9orf72_pos	0.69	107,339,840	10,100,424	3,428,215	1,622,751	0.96	63,776,178
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKM699KXH-CGND-HRA-00088-Female-ALS_FTD-Cortex_Motor_Lateral-C9orf72_pos	0.59	76,988,764	15,146,252	2,602,671	1,530,275	0.96	50,307,892
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKM699KXH-CGND-HRA-01336-Female-ALS_FTD-Spinal_Cord_Thoracic-C9orf72_pos	0.64	51,100,236	9,531,352	2,872,413	915,451	0.97	33,344,611
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKM699KXH-CGND-HRA-01337-Female-ALS_FTD-Cortex_Occipital-C9orf72_pos	0.68	91,933,235	12,672,103	3,413,130	1,373,068	0.95	57,788,268
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKN209FNW-CGND-HRA-01360-Male-ALS-Cortex_Occipital-C9orf72_neg_SOD1_pos_AV4	0.68	46,967,011	8,984,681	1,943,839	900,219	0.97	30,403,568
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKN209FNW-CGND-HRA-01361-Male-ALS-Cortex_Frontal-C9orf72_neg_SOD1_pos_AV4	0.57	73,984,658	18,965,142	3,237,352	1,574,586	0.97	50,544,432
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKN209FNW-CGND-HRA-01362-Male-ALS-Cerebellum-C9orf72_neg_SOD1_pos_AV4	0.68	45,444,913	9,333,541	1,869,740	1,365,926	0.96	30,264,386
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKN209FNW-CGND-HRA-01363-Male-ALS-Spinal_Cord_Thoracic-C9orf72_neg_SOD1_pos_AV4	0.65	55,664,658	12,872,266	2,332,649	1,171,857	0.96	37,548,231
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKX037NKA-CGND-HRA-00182-Male-ALS_AD_FTD-Cerebellum-C9orf72_pos_SOD1_neg	0.74	71,994,777	4,928,223	2,443,331	790,935	0.94	42,512,879
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKX037NKA-CGND-HRA-00533-Male-ALS_AD_FTD-Cerebellum-C9orf72_pos_SOD1_neg	0.77	69,220,512	4,967,916	2,184,054	727,168	0.95	40,677,562
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKX037NKA-CGND-HRA-01218-Male-ALS_AD_FTD-Cortex_Frontal-C9orf72_pos_SOD1_neg	0.61	66,750,760	11,735,328	2,442,232	1,146,064	0.96	42,715,752
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKY135CV6-CGND-HRA-00380-Male-ALS_AD-Cerebellum-C9orf72_neg	0.68	65,827,534	9,503,478	2,554,273	2,142,823	0.95	42,007,654
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKY135CV6-CGND-HRA-00381-Male-ALS_AD-Cortex_Motor_Medial-C9orf72_neg	0.67	70,680,442	11,464,114	2,179,460	1,042,252	0.96	44,589,562
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKY135CV6-CGND-HRA-00382-Male-ALS_AD-Cortex_Motor_Lateral-C9orf72_neg	0.55	63,675,218	18,275,096	2,404,173	1,751,287	0.96	44,970,728
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKY135CV6-CGND-HRA-00383-Male-ALS_AD-Spinal_Cord_Cervical-C9orf72_neg	0.56	70,853,531	18,016,911	2,990,789	1,674,087	0.96	48,695,788
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKY135CV6-CGND-HRA-00384-Male-ALS_AD-Spinal_Cord_Lumbar-C9orf72_neg	0.51	88,236,265	21,256,923	3,901,561	2,217,095	0.96	60,462,852
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKY135CV6-CGND-HRA-00385-Male-ALS_AD-Cortex_Frontal-C9orf72_neg	0.63	63,016,145	12,460,025	2,114,437	1,176,473	0.96	41,085,426
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKY135CV6-CGND-HRA-01283-Male-ALS_AD-Cortex_Occipital-C9orf72_neg	0.71	72,348,841	11,315,881	2,922,528	1,132,738	0.96	45,897,045
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKY135CV6-CGND-HRA-01284-Male-ALS_AD-Spinal_Cord_Thoracic-C9orf72_neg	0.59	75,127,074	16,957,078	3,714,665	1,765,917	0.95	51,246,000
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKZ685AR4-CGND-HRA-00738-Female-Non-Neurological_Control-Cell_Line_Motor_Neuron-Unknown	0.63	34,452,765	7,941,787	1,765,098	630,478	0.96	23,336,361
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUKZ685AR4-CGND-HRA-00739-Female-Non-Neurological_Control-Cell_Line_IPS-Unknown	0.51	45,498,955	15,200,111	4,995,062	1,436,112	0.96	34,964,643
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULH901PYF-CGND-HRA-00248-Male-ALS-Cortex_Frontal-C9orf72_pos	0.69	57,762,085	9,546,247	1,712,493	739,933	0.96	36,280,625

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULH901PYF--CGND-HRA-00267--Male--ALS--Spinal_Cord_Cervical--C9orf72_pos	0.60	55,387,782	13,123,712	2,335,177	1,185,857	0.96	37,366,364
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULH901PYF--CGND-HRA-00280--Male--ALS--Spinal_Cord_Lumbar--C9orf72_pos	0.59	67,036,316	14,397,284	4,205,775	1,399,141	0.96	45,462,472
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULH901PYF--CGND-HRA-00287--Male--ALS--Cortex_Motor_Lateral--C9orf72_pos	0.66	71,075,609	11,795,645	2,428,529	1,112,301	0.96	44,985,898
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULH901PYF--CGND-HRA-00726--Male--ALS--Cerebellum--C9orf72_pos	0.71	86,275,705	8,398,893	2,732,409	1,651,459	0.96	52,167,948
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULM733WR7--CGND-HRA-00268--Female--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.49	52,478,470	10,257,684	3,297,618	1,252,974	0.96	34,941,988
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULM733WR7--CGND-HRA-00281--Female--Non-Neurological_Control--Spinal_Cord_Lumbar--Unknown	0.49	77,349,824	15,343,694	4,509,927	1,878,747	0.95	51,969,412
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULN488RD5--CGND-HRA-00731--Male--ALS--Cerebellum--C9orf72_neg_ATXN2_neg	0.70	91,171,208	10,899,368	2,980,946	1,832,924	0.95	55,964,613
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULN488RD5--CGND-HRA-01266--Male--ALS--Cortex_Frontal--C9orf72_neg_ATXN2_neg	0.69	58,444,230	9,317,280	2,202,666	816,652	0.96	36,786,547
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULN488RD5--CGND-HRA-01267--Male--ALS--Cortex_Occipital--C9orf72_neg_ATXN2_neg	0.63	98,933,669	15,434,995	4,387,722	1,753,100	0.96	62,517,388
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULN488RD5--CGND-HRA-01268-2--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_ATXN2_neg	0.68	55,794,717	10,642,699	2,615,265	1,013,287	0.93	37,622,153
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEULT268RM4--CGND-HRA-00719--Male--ALS_FTD--Cerebellum--C9orf72_pos	0.71	99,968,169	9,706,335	3,926,302	1,702,010	0.94	61,024,818
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUME287RK2--CGND-HRA-00016--Female--ALS_FTD--Cortex_Frontal--C9orf72_neg	0.72	77,568,951	8,537,821	3,114,030	825,498	0.95	47,504,301
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUME287RK2--CGND-HRA-00058--Female--ALS_FTD--Cortex_Motor_Medial--C9orf72_neg	0.76	66,887,108	6,316,516	3,092,267	620,951	0.96	40,263,048
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUME287RK2--CGND-HRA-00072--Female--ALS_FTD--Cerebellum--C9orf72_neg	0.70	81,753,241	9,839,499	3,571,612	1,718,320	0.95	50,912,385
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUME287RK2--CGND-HRA-00086--Female--ALS_FTD--Cortex_Motor_Lateral--C9orf72_neg	0.63	85,257,210	13,387,898	3,668,707	1,650,103	0.95	54,633,633
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUME287RK2--CGND-HRA-01333--Female--ALS_FTD--Spinal_Cord_Thoracic--C9orf72_neg	0.72	49,068,941	6,066,609	2,805,318	656,492	0.92	30,754,850
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMK638LUX--CGND-HRA-00188--Male--ALS--Liver--C9orf72_pos_SOD1_neg_ANXA11_likely_benign	0.54	85,504,487	17,340,897	7,089,941	2,638,759	0.92	60,288,134
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMK638LUX--CGND-HRA-00549--Male--ALS--Cerebellum--C9orf72_pos_SOD1_neg_ANXA11_pos_likely_benign	0.78	56,230,017	3,457,205	2,018,635	556,067	0.96	32,524,449
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMK638LUX--CGND-HRA-00550--Male--ALS--Cortex_Frontal--C9orf72_pos_SOD1_neg_ANXA11_pos_likely_benign	0.67	91,363,127	11,356,757	3,855,296	1,156,512	0.94	57,429,297
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMK638LUX--CGND-HRA-00551--Male--ALS--Cortex_Occipital--C9orf72_pos_SOD1_neg_ANXA11_pos_likely_benign	0.73	90,125,331	6,468,471	4,530,831	838,323	0.94	54,188,978
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMK638LUX--CGND-HRA-00552--Male--ALS--Spinal_Cord_Thoracic--C9orf72_pos_SOD1_neg_ANXA11_pos_likely_benign	0.59	57,009,782	13,460,220	3,278,924	1,246,860	0.95	39,318,087
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUML172BXK--CGND-HRA-00197--Female--Non-Neurological_Control--Cerebellum--Unknown	0.72	71,162,817	7,605,139	2,229,931	1,228,981	0.95	43,210,130
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUML172BXK--CGND-HRA-00660--Female--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.64	69,551,102	13,543,998	2,695,436	1,300,382	0.96	45,346,705
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUML172BXK--CGND-HRA-00661--Female--Non-Neurological_Control--Cortex_Motor_Lateral--Unknown	0.61	66,023,268	14,265,346	2,549,635	1,260,865	0.96	43,816,153
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUML172BXK--CGND-HRA-01236--Female--Non-Neurological_Control--Cortex_Frontal--Unknown	0.69	77,226,347	12,191,005	3,540,193	1,141,343	0.95	49,303,427
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUML172BXK--CGND-HRA-01237--Female--Non-Neurological_Control--Cortex_Occipital--Unknown	0.77	42,903,527	5,813,333	1,481,743	526,611	0.96	26,374,821
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUML172BXK--CGND-HRA-01238--Female--Non-Neurological_Control--Spinal_Cord_Thoracic--Unknown	0.58	68,314,055	14,072,909	3,092,366	1,353,986	0.96	45,459,888
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMP035RP4--CGND-HRA-00204--Male--ALS--Cerebellum--C9orf72_neg	0.77	71,280,883	4,752,113	1,926,441	708,719	0.96	41,137,453
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMP035RP4--CGND-HRA-00210--Male--ALS--Cortex_Frontal--C9orf72_neg	0.70	72,368,012	10,567,848	2,147,948	855,028	0.96	44,842,077
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMP035RP4--CGND-HRA-00216--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.71	84,753,566	11,258,256	2,965,880	978,674	0.96	52,162,962
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMP035RP4--CGND-HRA-00222--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.73	73,293,738	8,720,618	3,309,745	1,007,863	0.95	45,300,033
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMP035RP4--CGND-HRA-00228--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.73	85,725,154	5,392,708	1,148,215	494,643	0.95	22,437,725
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMP035RP4--CGND-HRA-00234--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.67	81,053,574	11,338,064	3,164,188	1,176,004	0.96	50,626,179
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMT947ALA--CGND-HRA-00392--Male--ALS--Cerebellum--C9orf72_neg	0.58	67,586,790	15,330,690	3,628,574	2,976,098	0.94	47,424,294
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMT947ALA--CGND-HRA-00393--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.62	83,020,651	15,723,707	2,382,355	1,504,145	0.96	53,632,863
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMT947ALA--CGND-HRA-00394--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.61	46,607,662	10,824,140	1,510,391	1,051,843	0.95	31,608,901
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMT947ALA--CGND-HRA-00395--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.55	83,698,527	20,824,861	2,973,873	1,886,401	0.96	57,095,064
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMT947ALA--CGND-HRA-00396--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.55	56,482,166	15,756,140	2,081,202	1,393,266	0.96	39,392,623
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMT947ALA--CGND-HRA-00397--Male--ALS--Cortex_Frontal--C9orf72_neg	0.57	80,507,869	18,008,739	2,950,582	2,029,786	0.95	54,578,341
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMT947ALA--CGND-HRA-01287--Male--ALS--Cortex_Occipital--C9orf72_neg	0.71	59,991,780	9,566,396	1,883,986	831,072	0.96	37,490,781
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMT947ALA--CGND-HRA-01288-2--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.65	73,886,426	13,425,482	2,472,021	1,148,263	0.96	47,342,228
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMV641VYK--CGND-HRA-00410--Male--AD--Cerebellum--Unknown	0.70	90,306,203	2,935,889	3,116,237	2,058,283	0.95	54,948,365
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMV641VYK--CGND-HRA-00411--Male--AD--Cortex_Motor_Medial--Unknown	0.68	74,959,210	8,926,140	2,822,786	1,349,676	0.96	46,028,894
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMV641VYK--CGND-HRA-00412--Male--AD--Cortex_Motor_Lateral--Unknown	0.63	87,005,518	12,411,556	2,563,853	1,383,883	0.95	54,441,606
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMV641VYK--CGND-HRA-00413--Male--AD--Spinal_Cord_Cervical--Unknown	0.53	68,872,025	17,875,797	3,709,149	1,976,911	0.94	48,976,392
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMV641VYK--CGND-HRA-00414--Male--AD--Spinal_Cord_Lumbar--Unknown	0.65	64,416,661	9,806,523	2,195,332	1,008,066	0.96	40,317,328
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMV641VYK--CGND-HRA-00415--Male--AD--Cortex_Frontal--Unknown	0.67	82,643,659	11,818,749	2,851,521	1,439,083	0.93	52,909,771
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMV641VYK--CGND-HRA-01293--Male--AD--Cortex_Occipital--Unknown	0.74	75,995,259	7,710,401	3,170,375	915,875	0.95	46,064,900
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMV641VYK--CGND-HRA-01294--Male--AD--Spinal_Cord_Thoracic--Unknown	0.75	71,059,389	12,326,853	3,291,830	1,285,908	0.96	45,942,788
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMY028JH4--CGND-HRA-01352--Female--ALS--Cortex_Occipital--C9orf72_neg	0.66	37,346,293	6,140,929	1,616,762	537,168	0.95	23,909,274

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMY028JH4-CGND-HRA-01353-Female-ALS-Cortex_Frontal-C9orf72_neg	0.72	49,238,754	8,498,404	1,833,663	688,785	0.95	31,651,121
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMY028JH4-CGND-HRA-01354-Female-ALS-Cerebellum-C9orf72_neg	0.62	78,729,599	15,354,981	3,219,160	2,482,514	0.95	52,528,470
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUMY028JH4-CGND-HRA-01355-Female-ALS-Spinal_Cord_Thoracic-C9orf72_neg	0.63	77,530,134	15,593,464	2,674,743	1,376,559	0.95	50,884,143
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNE940RZC-CGND-HRA-00398-Male-AD-Cerebellum-Unknown	0.67	60,703,354	9,692,796	2,466,805	1,850,281	0.94	39,612,068
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNE940RZC-CGND-HRA-00399-Male-AD-Cortex_Motor_Medial-Unknown	0.55	71,198,404	18,473,078	2,774,460	1,716,268	0.95	49,394,140
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNE940RZC-CGND-HRA-00400-Male-AD-Cortex_Motor_Lateral-Unknown	0.56	62,235,662	15,793,534	2,274,886	1,559,434	0.95	43,215,255
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNE940RZC-CGND-HRA-00401-Male-AD-Spinal_Cord_Cervical-Unknown	0.54	67,600,215	16,597,073	3,015,453	1,823,803	0.96	46,592,056
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNE940RZC-CGND-HRA-00402-Male-AD-Spinal_Cord_Lumbar-Unknown	0.40	35,064,482	7,425,672	2,377,212	1,131,050	0.95	24,217,096
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNE940RZC-CGND-HRA-00403-Male-AD-Cortex_Frontal-Unknown	0.56	81,179,163	18,749,351	3,258,431	1,874,731	0.95	55,304,238
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNE940RZC-CGND-HRA-01289-Male-AD-Cortex_Occipital-Unknown	0.62	80,874,144	16,253,440	3,713,048	1,801,958	0.96	53,390,676
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNE940RZC-CGND-HRA-01290-2-Male-AD-Spinal_Cord_Thoracic-Unknown	0.45	64,974,822	16,130,754	4,384,210	2,182,238	0.96	45,699,372
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNJ406FRR-CGND-HRA-00270-Female-Non-Neurological_Control-Spinal_Cord_Cervical-Unknown	0.66	89,045,757	11,923,549	3,906,269	1,152,731	0.94	56,624,329
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNJ406FRR-CGND-HRA-00283-Female-Non-Neurological_Control-Spinal_Cord_Lumbar-Unknown	0.61	38,130,823	9,496,845	1,519,701	797,149	0.96	26,007,081
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL548ZBN-CGND-HRA-00244-Male-ALS_FTD-Cortex_Frontal-C9orf72_pos	0.73	50,087,493	7,656,647	1,827,326	610,422	0.96	31,244,475
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL548ZBN-CGND-HRA-00263-Male-ALS_FTD-Spinal_Cord_Cervical-C9orf72_pos	0.61	47,483,448	12,145,256	1,743,075	983,511	0.96	32,523,781
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL548ZBN-CGND-HRA-00276-Male-ALS_FTD-Spinal_Cord_Lumbar-C9orf72_pos	0.59	84,288,995	16,826,109	3,998,036	1,611,788	0.94	56,901,487
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL548ZBN-CGND-HRA-00286-Male-ALS_FTD-Cortex_Motor_Lateral-C9orf72_pos	0.65	61,782,718	11,369,080	2,119,275	1,031,491	0.96	39,812,598
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL548ZBN-CGND-HRA-00730-Male-ALS_FTD-Cerebellum-C9orf72_pos	0.69	63,576,954	8,348,768	2,349,921	1,175,865	0.95	39,726,542
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL974RU6-CGND-HRA-00620-Male-ALS-Cerebellum-C9orf72_neg_SOD1_neg	0.68	74,950,874	11,309,590	2,707,416	1,806,378	0.95	47,631,804
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL974RU6-CGND-HRA-00621-Male-ALS-Cortex_Frontal-C9orf72_neg_SOD1_neg	0.69	64,036,686	11,259,582	2,317,987	857,853	0.96	40,987,591
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL974RU6-CGND-HRA-00622-Male-ALS-Cortex_Occipital-C9orf72_neg_SOD1_neg	0.66	89,108,836	14,931,768	2,712,903	1,175,329	0.96	56,406,069
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL974RU6-CGND-HRA-00623-Male-ALS-Spinal_Cord_Thoracic-C9orf72_neg_SOD1_neg	0.59	64,376,242	14,838,340	3,002,290	1,409,726	0.96	43,723,669
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL974RU6-CGND-HRA-00624-Male-ALS-Cortex_Motor_Unspecified-C9orf72_neg_SOD1_neg	0.55	84,844,190	19,515,798	3,894,826	2,155,264	0.96	57,729,785
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL974RU6-CGND-HRA-00625-Male-ALS-Spinal_Cord_Cervical-C9orf72_neg_SOD1_neg	0.61	67,816,951	14,836,715	3,406,105	1,553,783	0.96	45,636,985
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNL974RU6-CGND-HRA-00626-Male-ALS-Spinal_Cord_Lumbar-C9orf72_neg_SOD1_neg	0.57	67,480,802	15,617,484	3,190,451	1,597,371	0.96	45,878,205
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW210GCW-CGND-HRA-00026-Male-ALS-Cortex_Frontal-C9orf72_neg	0.70	93,647,540	14,396,496	3,214,599	1,229,893	0.93	60,247,076
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW210GCW-CGND-HRA-00040-Male-ALS-Spinal_Cord_Lumbar-C9orf72_neg	0.71	72,118,013	10,597,291	2,740,825	915,733	0.93	46,486,743
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW210GCW-CGND-HRA-00054-Male-ALS-Spinal_Cord_Cervical-C9orf72_neg	0.69	35,173,920	6,025,804	2,034,103	585,301	0.94	23,269,036
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW210GCW-CGND-HRA-00068-Male-ALS-Cortex_Motor_Medial-C9orf72_neg	0.66	77,758,529	12,200,573	3,496,485	1,193,891	0.95	49,562,414
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW210GCW-CGND-HRA-00082-Male-ALS-Cerebellum-C9orf72_neg	0.65	75,787,204	10,732,686	3,218,430	1,667,644	0.96	47,560,568
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW210GCW-CGND-HRA-00096-Male-ALS-Cortex_Motor_Lateral-C9orf72_neg	0.63	83,729,270	13,753,350	3,030,181	1,229,865	0.96	52,907,716
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW244GF0-CGND-HRA-00349-Female-ALS-Cerebellum-C9orf72_neg	0.64	76,837,123	10,988,663	2,889,399	1,909,957	0.96	46,466,931
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW244GF0-CGND-HRA-00350-Female-ALS-Cortex_Motor_Medial-C9orf72_neg	0.59	67,564,639	14,725,459	1,969,209	1,373,655	0.96	44,766,975
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW244GF0-CGND-HRA-00351-Female-ALS-Cortex_Motor_Lateral-C9orf72_neg	0.54	64,211,416	16,272,508	2,036,939	1,460,921	0.96	43,898,508
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW244GF0-CGND-HRA-00352-Female-ALS-Spinal_Cord_Cervical-C9orf72_neg	0.58	68,680,657	16,821,885	2,798,596	1,483,992	0.96	46,606,391
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW244GF0-CGND-HRA-00353-Female-ALS-Spinal_Cord_Lumbar-C9orf72_neg	0.59	77,813,164	17,246,926	3,436,515	1,638,787	0.96	51,938,123
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW244GF0-CGND-HRA-00354-Female-ALS-Cortex_Frontal-C9orf72_neg	0.63	67,644,506	12,873,398	2,082,233	1,244,769	0.96	43,781,149
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW244GF0-CGND-HRA-00355-Female-ALS-Cortex_Occipital-C9orf72_neg	0.58	62,022,710	14,515,668	2,068,285	1,203,357	0.96	41,748,157
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNW244GF0-CGND-HRA-00356-Female-ALS-Spinal_Cord_Thoracic-C9orf72_neg	0.57	65,782,506	16,300,580	2,701,097	1,417,945	0.96	45,108,792
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUNY116EZW-CGND-HRA-00713-Female-ALS_NOS-Cerebellum-C9orf72_pos	0.72	86,354,502	8,441,790	3,003,158	1,258,392	0.95	52,188,030
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUPK732LNT-CGND-HRA-00246-Female-ALS-Cortex_Frontal-Unknown	0.57	74,093,177	17,700,533	2,650,562	1,328,328	0.96	49,829,497
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUPK732LNT-CGND-HRA-00255-Female-ALS-Cortex_Motor_Medial-Unknown	0.62	79,529,951	15,516,817	3,518,189	1,339,265	0.95	51,788,146
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUPK732LNT-CGND-HRA-00285-Female-ALS-Spinal_Cord_Cervical-Unknown	0.55	60,165,121	15,696,069	2,876,420	1,458,528	0.96	41,843,561
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUPK732LNT-CGND-HRA-00725-Female-ALS-Cerebellum-Unknown	0.71	93,183,285	8,350,391	2,693,758	1,383,484	0.95	55,376,723
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUPU334DL1-CGND-HRA-01369-Female-ALS_FTD-Cortex_Frontal-C9orf72_neg	0.64	72,220,397	13,166,885	3,441,460	1,234,954	0.96	46,678,313
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUPU334DL1-CGND-HRA-01370-Female-ALS_FTD-Cerebellum-C9orf72_neg	0.70	54,849,063	6,936,609	2,289,465	1,578,811	0.96	34,201,452
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUPU334DL1-CGND-HRA-01371-Female-ALS_FTD-Spinal_Cord_Thoracic-C9orf72_neg	0.61	43,135,583	7,673,601	2,180,588	784,286	0.96	28,041,329
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURD711XCL-CGND-HRA-00242-Female-Pre-fALS-Cortex_Frontal-ANG_pos	0.68	82,149,711	12,608,749	2,872,657	1,212,227	0.94	52,368,485
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURD711XCL-CGND-HRA-00251-Female-Pre-fALS-Cortex_Motor_Medial-ANG_pos	0.67	68,910,835	11,157,107	2,688,130	1,046,568	0.94	44,802,376
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURD711XCL-CGND-HRA-00261-Female-Pre-fALS-Spinal_Cord_Cervical-ANG_pos	0.58	70,243,954	15,922,600	2,852,237	1,525,735	0.94	48,253,651

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURD711XCL-CGND-HRA-00721-Female-Pre-fALS-Cerebellum-ANG_pos	0.70	78,408,234	8,892,260	2,931,055	1,383,465	0.96	47,842,997
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURJ387PPV-CGND-HRA-00193-Female-ALS-Cortex_Motor_Unspecified-C9orf72_neg_SOD1_neg	0.68	90,499,918	11,784,408	3,087,886	1,253,918	0.95	56,154,814
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURJ387PPV-CGND-HRA-00648-Female-ALS-Spinal_Cord_Cervical-C9orf72_neg_SOD1_neg	0.45	72,871,239	18,619,837	5,916,586	2,286,380	0.95	52,524,542
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURJ387PPV-CGND-HRA-00649-Female-ALS-Spinal_Cord_Lumbar-C9orf72_neg_SOD1_neg	0.57	67,663,977	13,108,911	4,895,078	1,748,060	0.96	46,039,921
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURK749WFB-CGND-HRA-00245-Female-ALS-Cortex_Frontal-C9orf72_pos	0.74	85,890,750	8,263,994	4,013,907	800,943	0.95	51,784,203
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURK749WFB-CGND-HRA-00254-Female-ALS-Cortex_Motor_Medial-C9orf72_pos	0.66	83,639,126	9,369,272	4,000,053	1,064,723	0.91	53,885,980
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURK749WFB-CGND-HRA-00264-Female-ALS-Spinal_Cord_Cervical-C9orf72_pos	0.55	73,673,394	17,172,002	5,302,088	1,771,236	0.90	54,451,142
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURK749WFB-CGND-HRA-00277-Female-ALS-Spinal_Cord_Lumbar-C9orf72_pos	0.58	55,880,027	15,760,337	2,998,760	1,432,730	0.95	39,988,135
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURK749WFB-CGND-HRA-00729-Female-ALS-Cerebellum-C9orf72_pos	0.73	80,715,874	6,895,818	4,020,734	1,089,638	0.95	48,927,714
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURN516YR8-CGND-HRA-00720-Female-ALS-Cerebellum-C9orf72_pos	0.76	76,194,018	7,173,056	2,264,203	1,136,015	0.95	45,684,466
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURX991BWB-CGND-HRA-00546-Female-ALS-Cortex_Frontal-C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.70	68,009,750	10,849,510	1,997,744	874,760	0.96	42,663,153
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURX991BWB-CGND-HRA-00547-Female-ALS-Cortex_Occipital-C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.70	81,592,849	8,960,971	2,583,870	997,694	0.97	48,702,880
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURX991BWB-CGND-HRA-00548-Female-ALS-Spinal_Cord_Thoracic-C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.56	52,793,529	12,558,025	3,678,655	1,250,655	0.96	36,716,219
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURX991BWB-CGND-HRA-00615-Female-ALS-Cortex_Motor_Medial-C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.71	68,690,587	9,083,717	2,853,868	957,860	0.96	42,298,450
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURX991BWB-CGND-HRA-00616-Female-ALS-Cortex_Motor_Lateral-C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.75	67,263,215	7,998,089	2,406,469	735,295	0.97	40,572,904
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURX991BWB-CGND-HRA-00617-2-Female-ALS-Spinal_Cord_Cervical-C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.70	59,866,484	9,568,122	2,770,106	915,556	0.96	38,093,019
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEURX991BWB-CGND-HRA-00618-Female-ALS-Cerebellum-C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.78	44,080,084	4,914,994	1,492,118	861,604	0.95	27,068,378
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTB398FC9-CGND-HRA-00434-Male-ALS-Cerebellum-Unknown	0.71	108,939,117	7,173,891	2,829,902	1,206,830	0.95	63,237,592
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTB398FC9-CGND-HRA-00435-Male-ALS-Cortex_Motor_Medial-Unknown	0.71	56,852,412	7,161,310	2,002,705	709,237	0.94	35,312,699
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTB398FC9-CGND-HRA-00436-Male-ALS-Cortex_Motor_Lateral-Unknown	0.68	53,769,738	8,378,326	1,741,404	786,234	0.93	34,593,732
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTB398FC9-CGND-HRA-00437-Male-ALS-Spinal_Cord_Cervical-Unknown	0.60	66,758,695	12,543,635	3,181,209	1,289,351	0.95	44,319,163
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTB398FC9-CGND-HRA-00438-Male-ALS-Spinal_Cord_Lumbar-Unknown	0.62	47,536,894	8,243,942	3,081,279	1,129,595	0.95	49,412,048
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTB398FC9-CGND-HRA-00439-Male-ALS-Cortex_Frontal-Unknown	0.55	69,694,463	13,128,213	3,031,948	1,633,616	0.94	46,409,389
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTB398FC9-CGND-HRA-01302-Male-ALS-Spinal_Cord_Thoracic-Unknown	0.65	42,560,398	9,196,336	2,738,131	892,297	0.96	28,875,849
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTL441LZ7-CGND-HRA-00319-Male-ALS-Cerebellum-C9orf72_pos	0.76	57,954,316	3,655,852	1,793,077	769,371	0.95	33,708,200
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTL441LZ7-CGND-HRA-00320-Male-ALS-Cortex_Motor_Medial-C9orf72_pos	0.67	59,503,366	5,832,464	3,610,888	780,654	0.95	36,551,089
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTL441LZ7-CGND-HRA-00321-Male-ALS-Cortex_Motor_Lateral-C9orf72_pos	0.76	49,178,411	4,801,409	1,946,398	469,974	0.96	29,476,919
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTL441LZ7-CGND-HRA-00322-Male-ALS-Spinal_Cord_Cervical-C9orf72_pos	0.58	53,318,485	6,863,031	5,148,023	987,337	0.94	35,315,449
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTL441LZ7-CGND-HRA-00323-Male-ALS-Cortex_Frontal-C9orf72_pos	0.68	52,812,978	5,943,842	3,221,668	708,914	0.95	33,166,109
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTL441LZ7-CGND-HRA-00324-Male-ALS-Cortex_Occipital-C9orf72_pos	0.65	48,402,869	5,767,591	3,250,861	749,515	0.95	30,738,368
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTL441LZ7-CGND-HRA-00325-Male-ALS-Spinal_Cord_Thoracic-C9orf72_pos	0.60	69,139,920	9,855,286	4,784,048	1,236,926	0.95	44,954,646
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP019MY9-CGND-HRA-00357-Female-ALS-Cerebellum-C9orf72_pos	0.69	91,217,020	9,114,158	3,181,246	1,729,250	0.95	55,191,168
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP019MY9-CGND-HRA-00358-Female-ALS-Cortex_Motor_Medial-C9orf72_pos	0.70	69,088,393	8,582,801	1,771,897	795,547	0.96	41,844,934
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP019MY9-CGND-HRA-00359-Female-ALS-Cortex_Motor_Lateral-C9orf72_pos	0.64	67,674,793	10,076,273	2,421,833	1,182,401	0.95	42,735,129
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP019MY9-CGND-HRA-00360-Female-ALS-Spinal_Cord_Cervical-C9orf72_pos	0.58	73,574,456	14,290,042	3,375,615	1,362,033	0.95	48,506,975
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP019MY9-CGND-HRA-00361-Female-ALS-Spinal_Cord_Lumbar-C9orf72_pos	0.58	62,583,685	12,975,321	2,935,150	1,258,700	0.95	42,016,188
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP019MY9-CGND-HRA-00362-Female-ALS-Cortex_Frontal-C9orf72_pos	0.62	65,886,277	13,161,589	2,289,744	1,097,946	0.95	43,539,190
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP019MY9-CGND-HRA-00363-Female-ALS-Cortex_Occipital-C9orf72_pos	0.72	87,159,755	6,526,657	2,508,203	782,437	0.95	50,774,198
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP019MY9-CGND-HRA-00364-Female-ALS-Spinal_Cord_Thoracic-C9orf72_pos	0.62	82,035,076	13,153,972	3,653,614	1,263,408	0.94	53,455,838
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP414K22-CGND-HRA-00196-Female-Non-Neurological_Control-Cerebellum-Unknown	0.67	79,304,303	10,445,345	2,814,655	1,658,079	0.94	50,019,311
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP414K22-CGND-HRA-00658-Female-Non-Neurological_Control-Cortex_Motor_Medial-Unknown	0.68	78,899,090	12,069,420	2,784,496	1,056,592	0.96	49,525,414
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP414K22-CGND-HRA-00659-Female-Non-Neurological_Control-Cortex_Motor_Lateral-Unknown	0.57	110,834,972	21,159,910	4,713,123	1,963,323	0.96	72,431,718
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP414K22-CGND-HRA-01234-Female-Non-Neurological_Control-Cortex_Frontal-Unknown	0.70	84,628,655	12,284,353	2,549,395	924,061	0.96	52,260,826
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTP414K22-CGND-HRA-01235-Female-Non-Neurological_Control-Cortex_Occipital-Unknown	0.69	65,396,493	10,721,445	2,217,545	929,412	0.96	41,282,018
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTZ062XC5-CGND-HRA-00195-Male-SBMA-Liver-Unknown	0.47	68,497,958	21,092,314	4,407,749	3,165,265	0.95	51,108,498
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTZ062XC5-CGND-HRA-00653-Male-SBMA-Cerebellum-Unknown	0.68	91,386,333	10,467,633	3,121,323	1,663,149	0.96	55,716,505
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTZ062XC5-CGND-HRA-00654-Male-SBMA-Cortex_Motor_Medial-Unknown	0.69	71,096,899	10,813,517	2,961,978	1,070,476	0.96	44,845,689
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTZ062XC5-CGND-HRA-00655-Male-SBMA-Cortex_Motor_Lateral-Unknown	0.67	72,902,639	11,425,567	2,941,208	1,084,678	0.96	46,073,426
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTZ062XC5-CGND-HRA-00656-Male-SBMA-Spinal_Cord_Cervical-Unknown	0.66	69,099,407	12,447,407	2,544,445	1,068,057	0.96	44,187,820
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUTZ062XC5-CGND-HRA-00657-Male-SBMA-Spinal_Cord_Lumbar-Unknown	0.64	77,122,304	13,987,182	3,270,038	1,260,744	0.96	49,983,125

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUE532LFF--CGND-HRA-00241--Male--ALS--Cortex_Frontal--Unknown	0.72	53,084,735	8,291,847	1,802,528	659,066	0.96	33,188,966
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUE532LFF--CGND-HRA-00250--Male--ALS--Cortex_Motor_Medial--Unknown	0.65	79,327,309	13,885,305	2,702,249	1,180,523	0.94	51,885,485
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUE532LFF--CGND-HRA-00260--Male--ALS--Spinal_Cord_Cervical--Unknown	0.54	69,566,879	15,203,645	3,639,777	1,528,943	0.93	48,170,989
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUE532LFF--CGND-HRA-00273--Male--ALS--Spinal_Cord_Lumbar--Unknown	0.58	62,167,706	14,582,222	2,610,300	1,331,866	0.96	42,122,168
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUE532LFF--CGND-HRA-00285--Male--ALS--Cortex_Motor_Lateral--Unknown	0.66	85,717,445	13,487,189	2,844,800	1,224,426	0.92	56,138,804
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUE532LFF--CGND-HRA-00723--Male--ALS--Cerebellum--Unknown	0.72	79,486,794	7,626,664	2,591,563	1,305,617	0.95	47,892,173
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUF289NRL--CGND-HRA-01364--Male--ALS--Cortex_Occipital-C9orf72_neg	0.61	68,637,569	14,887,903	3,873,013	1,483,551	0.97	45,957,731
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUF289NRL--CGND-HRA-01365--Male--ALS--Cortex_Frontal--C9orf72_neg	0.55	95,819,039	23,386,267	4,555,697	2,159,233	0.97	64,947,916
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUF289NRL--CGND-HRA-01366--Male--ALS--Cerebellum--C9orf72_neg	0.69	59,433,241	8,382,043	2,267,032	1,311,996	0.96	37,005,482
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUF289NRL--CGND-HRA-01367--Male--ALS--Spinal_Cord_Thoracic-C9orf72_neg	0.55	53,969,954	13,322,584	5,947,248	1,460,616	0.95	39,341,449
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUK657CZW--CGND-HRA-01212--Female--ALS_AD--Cortex_Frontal--Unknown	0.62	63,600,777	13,316,671	2,896,614	1,550,588	0.96	42,424,299
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUK657CZW--CGND-HRA-01213--Female--ALS_AD--Cortex_Occipital--Unknown	0.62	61,749,341	13,082,047	2,213,432	1,394,928	0.96	40,664,123
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUT049NND--CGND-HRA-01228--Female--Non-Neurological_Control--Cortex_Frontal--Unknown	0.51	76,635,694	11,690,014	5,123,965	1,576,967	0.96	49,625,808
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUT049NND--CGND-HRA-01230--Female--Non-Neurological_Control--Spinal_Cord_Thoracic--Unknown	0.53	60,037,398	11,728,914	4,221,157	1,381,439	0.95	40,523,397
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUV911LWA--CGND-HRA-00538--Male--ALS_FTD--Cerebellum--C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.73	84,546,764	6,440,214	2,699,093	1,277,749	0.96	49,697,095
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUV911LWA--CGND-HRA-00539--Male--ALS_FTD--Cortex_Frontal-C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.61	63,484,275	7,245,165	4,136,701	1,080,001	0.96	39,753,469
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUV911LWA--CGND-HRA-00540--Male--ALS_FTD--Cortex_Occipital-C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.61	99,152,677	8,474,633	5,398,627	1,545,345	0.96	59,839,290
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUV911LWA--CGND-HRA-00607--Male--ALS_FTD--Cortex_Motor_Medial-C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.65	80,838,949	7,300,601	3,702,842	786,854	0.96	48,245,279
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUV911LWA--CGND-HRA-00608--Male--ALS_FTD--Cortex_Motor_Lateral-C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.57	60,719,005	4,839,443	2,115,500	477,884	0.97	35,263,472
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUV911LWA--CGND-HRA-00609--Male--ALS_FTD--Spinal_Cord_Cervical-C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.78	73,173,687	13,034,855	3,593,942	1,321,972	0.95	47,829,449
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUV911LWA--CGND-HRA-00610--Male--ALS_FTD--Spinal_Cord_Lumbar-C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.74	74,820,662	12,813,442	4,199,086	1,644,842	0.96	48,718,388
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVB305VU7--CGND-HRA-00194--Male--ALS_AD_CTE--Cerebellum--SOD1_neg	0.50	53,647,672	5,559,238	1,839,530	839,548	0.94	32,745,141
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVB305VU7--CGND-HRA-00650--Male--ALS_AD_CTE--Cortex_Motor_Medial--SOD1_neg	0.62	85,388,199	15,767,161	3,421,984	1,474,524	0.96	55,181,513
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVB305VU7--CGND-HRA-00651--Male--ALS_AD_CTE--Cortex_Motor_Lateral--SOD1_neg	0.71	74,584,597	10,366,253	2,887,603	972,815	0.96	46,356,375
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVB305VU7--CGND-HRA-00652--Male--ALS_AD_CTE--Spinal_Cord_Cervical--SOD1_neg	0.62	74,529,224	14,485,296	2,941,012	1,420,478	0.96	48,669,955
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVB305VU7--CGND-HRA-01231--Male--ALS_AD_CTE--Cortex_Frontal--SOD1_neg	0.55	63,544,896	14,467,592	4,680,179	1,692,019	0.95	44,227,870
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVB305VU7--CGND-HRA-01232--Male--ALS_AD_CTE--Cortex_Occipital--SOD1_neg	0.68	60,561,064	10,272,370	2,748,159	1,148,549	0.96	38,916,666
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVB305VU7--CGND-HRA-01233--Male--ALS_AD_CTE--Spinal_Cord_Thoracic--SOD1_neg	0.55	63,300,115	16,881,911	3,058,697	1,782,971	0.96	44,250,940
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUV845ZAB--CGND-HRA-00744--Female--ALS_Cell_Line_iPS--SOD1_neg	0.59	54,723,256	14,458,628	4,397,276	1,221,210	0.96	38,859,961
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUUV845ZAB--CGND-HRA-00745--Female--ALS_Cell_Line_Motor_Neuron--SOD1_pos	0.61	58,690,956	13,357,126	3,140,547	1,057,867	0.96	39,836,054
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVZ387WGH--CGND-HRA-00326--Female--ALS_AD--Cerebellum--C9orf72_neg	0.74	66,503,014	4,804,732	2,999,812	926,520	0.94	39,933,092
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVZ387WGH--CGND-HRA-00328--Female--ALS_AD--Cortex_Motor_Lateral-C9orf72_neg	0.64	76,801,382	10,090,874	4,732,948	1,120,290	0.94	49,151,344
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVZ387WGH--CGND-HRA-00330--Female--ALS_AD--Cortex_Frontal--C9orf72_neg	0.65	71,628,360	8,247,774	3,018,425	887,191	0.95	44,017,121
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUVZ387WGH--CGND-HRA-00331--Female--ALS_AD--Cortex_Occipital--C9orf72_neg	0.57	68,233,271	7,445,867	4,977,992	1,209,870	0.94	43,327,093
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWC334RTZ--CGND-HRA-01372--Male--ALS_CTE--Cerebellum--Unknown	0.75	63,940,918	6,184,996	1,967,793	887,515	0.96	38,042,021
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWC334RTZ--CGND-HRA-01373--Male--ALS_CTE--Cortex_Frontal--Unknown	0.71	80,192,536	9,974,050	4,224,533	1,033,455	0.96	49,618,331
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWD570BTK--CGND-HRA-01378--Male--Non-Neurological_Control--Cerebellum--Unknown	0.65	84,143,691	6,420,721	4,382,419	1,363,965	0.96	50,380,901
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWD570BTK--CGND-HRA-01379--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.69	78,078,469	8,335,497	4,278,643	989,169	0.96	47,670,942
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWG523WRV--CGND-HRA-00640--Male--ALS--Cortex_Motor_Unspecified--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.72	40,856,976	7,152,956	1,281,907	595,005	0.96	25,928,893
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWG523WRV--CGND-HRA-00641--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.62	55,388,409	11,987,049	2,960,532	1,232,662	0.96	37,183,410
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWG523WRV--CGND-HRA-00642--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.51	49,938,944	14,615,400	3,527,842	1,549,596	0.96	36,439,061
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWG523WRV--CGND-HRA-01222--Male--ALS--Cortex_Frontal-C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.66	67,334,699	13,208,455	2,082,631	1,010,737	0.96	43,541,936
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWG523WRV--CGND-HRA-01223--Male--ALS--Cortex_Occipital-C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.66	73,800,385	13,367,685	3,094,607	1,201,327	0.96	47,583,206
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWG523WRV--CGND-HRA-01224--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.55	53,386,020	14,444,400	2,417,766	1,291,558	0.96	37,303,055
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWL993GU2--CGND-HRA-00676--Male--ALS--Cerebellum--SOD1_neg_SETX_likely_benign_FIG4_VUS	0.65	67,808,250	5,592,574	3,661,882	1,636,114	0.96	41,112,464
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWL993GU2--CGND-HRA-01248--Male--ALS--Cortex_Frontal--SOD1_neg_SETX_likely_benign_FIG4_VUS	0.73	55,380,464	7,326,018	2,974,421	802,467	0.96	34,494,612
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWL993GU2--CGND-HRA-01250--Male--ALS--Spinal_Cord_Thoracic--SOD1_neg_SETX_likely_benign_FIG4_VUS	0.53	62,757,128	12,670,026	4,618,684	1,810,886	0.96	42,788,898
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWP285RM6--CGND-HRA-00416--Female--ALS_AD--Cerebellum--Unknown	0.71	80,659,174	6,644,644	2,887,615	1,521,571	0.95	48,125,555
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWP285RM6--CGND-HRA-00417--Female--ALS_AD--Cortex_Motor_Medial--Unknown	0.57	101,721,308	16,715,376	3,665,065	1,776,441	0.95	64,884,323
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWP285RM6--CGND-HRA-00418--Female--ALS_AD--Cortex_Motor_Lateral--Unknown	0.66	108,667,937	12,344,345	3,913,889	1,407,301	0.95	66,648,596



Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWP285RM6-CGND-HRA-00419-Female-ALS_AD-Spinal_Cord_Cervical-Unknown	0.50	87,956,287	22,136,235	3,967,836	2,466,006	0.95	61,497,677
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWP285RM6-CGND-HRA-00420-Female-ALS_AD-Spinal_Cord_Lumbar-Unknown	0.47	84,856,170	23,266,276	3,424,952	2,317,096	0.96	59,590,926
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWP285RM6-CGND-HRA-00421-Female-ALS_AD-Cortex_Frontal-Unknown	0.60	63,059,761	12,971,135	1,871,776	1,111,860	0.95	41,681,922
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWP285RM6-CGND-HRA-01295-Female-ALS_AD-Cortex_Occipital-Unknown	0.68	76,903,596	8,323,290	4,821,753	1,181,155	0.96	47,358,679
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWP285RM6-CGND-HRA-01296-Female-ALS_AD-Spinal_Cord_Thoracic-Unknown	0.65	34,575,995	7,786,795	1,784,362	702,232	0.96	23,320,953
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWX086DGZ-CGND-HRA-00019-Female-ALS-Cortex_Frontal-C9orf72_neg	0.68	70,782,322	10,571,588	2,129,464	878,714	0.96	43,998,322
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWX086DGZ-CGND-HRA-00047-Female-ALS-Spinal_Cord_Cervical-C9orf72_neg	0.53	104,945,932	23,104,332	3,800,379	2,352,043	0.96	69,913,860
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWX086DGZ-CGND-HRA-00061-Female-ALS-Cortex_Motor_Medial-C9orf72_neg	0.64	84,944,004	14,141,722	2,664,304	1,247,818	0.96	53,784,920
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWX086DGZ-CGND-HRA-00075-Female-ALS-Cerebellum-C9orf72_neg	0.67	123,485,891	11,749,841	3,590,746	1,858,162	0.96	73,339,157
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWX086DGZ-CGND-HRA-00089-2-Female-ALS-Cortex_Motor_Lateral-C9orf72_neg	0.64	109,576,850	15,581,434	3,714,716	1,444,820	0.94	69,059,364
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWX086DGZ-CGND-HRA-01338-Female-ALS-Spinal_Cord_Thoracic-C9orf72_neg	0.70	56,804,558	10,137,514	2,479,436	919,384	0.97	36,312,095
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWX086DGZ-CGND-HRA-01339-Female-ALS-Cortex_Occipital-C9orf72_neg	0.69	58,135,507	10,387,387	2,339,246	950,120	0.95	37,802,101
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWZ373ZHA-CGND-HRA-00311-Female-ALS-Cerebellum-C9orf72_neg	0.67	50,750,814	9,268,422	2,136,008	1,543,008	0.94	33,836,815
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWZ373ZHA-CGND-HRA-00312-Female-ALS-Cortex_Motor_Medial-C9orf72_neg	0.62	71,041,992	14,511,912	2,529,738	1,319,804	0.95	47,057,355
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWZ373ZHA-CGND-HRA-00313-Female-ALS-Cortex_Motor_Lateral-C9orf72_neg	0.63	61,243,237	12,993,353	2,045,272	1,132,268	0.95	40,572,140
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWZ373ZHA-CGND-HRA-00314-Female-ALS-Spinal_Cord_Cervical-C9orf72_neg	0.56	68,646,481	17,604,083	3,171,938	1,706,248	0.96	47,569,901
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWZ373ZHA-CGND-HRA-00315-Female-ALS-Spinal_Cord_Lumbar-C9orf72_neg	0.55	63,827,772	16,538,622	3,704,810	1,726,834	0.95	44,937,715
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWZ373ZHA-CGND-HRA-00316-Female-ALS-Cortex_Frontal-C9orf72_neg	0.65	46,639,959	9,641,719	1,745,280	965,728	0.95	30,932,955
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWZ373ZHA-CGND-HRA-00317-Female-ALS-Cortex_Occipital-C9orf72_neg	0.62	61,097,905	13,934,927	2,411,481	1,193,987	0.95	41,251,010
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUWZ373ZHA-CGND-HRA-00318-Female-ALS-Spinal_Cord_Thoracic-C9orf72_neg	0.57	58,212,610	10,903,604	2,984,141	1,380,171	0.95	40,602,493
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXD817GGZ-CGND-HRA-00718-Male-ALS-Cerebellum-C9orf72_pos	0.74	73,899,514	7,133,360	2,252,148	936,448	0.94	44,606,182
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXR099CKK-CGND-HRA-00269-Female-Non-Neurological_Control-Spinal_Cord_Cervical-Unknown	0.64	92,489,063	14,337,881	3,242,061	1,320,903	0.95	58,474,482
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXR099CKK-CGND-HRA-00282-Female-Non-Neurological_Control-Spinal_Cord_Lumbar-Unknown	0.64	107,188,785	14,135,547	4,775,825	1,503,277	0.93	68,611,466
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXR145UBL-CGND-HRA-01356-Male-ALS_FTD-Cortex_Occipital-C9orf72_neg	0.63	48,062,125	11,959,821	2,636,946	1,198,430	0.96	33,117,362
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXR145UBL-CGND-HRA-01357-Male-ALS_FTD-Cortex_Frontal-C9orf72_neg	0.55	95,910,419	22,692,575	4,847,785	2,171,777	0.97	65,005,362
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXR145UBL-CGND-HRA-01358-Male-ALS_FTD-Cerebellum-C9orf72_neg	0.71	45,055,326	7,817,574	1,713,045	1,176,575	0.96	28,988,920
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXR145UBL-CGND-HRA-01359-Male-ALS_FTD-Spinal_Cord_Thoracic-C9orf72_neg	0.57	45,320,551	12,225,525	2,218,516	1,102,102	0.96	31,559,962
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT258BD4-CGND-HRA-00239-Female-ALS-Cortex_Frontal-C9orf72_pos	0.71	66,437,911	9,202,569	2,557,580	762,436	0.96	40,957,926
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT258BD4-CGND-HRA-00258-Female-ALS-Spinal_Cord_Cervical-C9orf72_pos	0.65	38,861,327	9,343,809	1,611,337	774,289	0.97	26,096,002
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT258BD4-CGND-HRA-00288-Female-ALS-Cortex_Motor_Unspecified-C9orf72_pos	0.67	76,745,574	11,661,486	2,841,824	982,562	0.93	49,432,933
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT258BD4-CGND-HRA-00728-Female-ALS-Cerebellum-C9orf72_pos	0.67	83,570,880	10,973,584	3,286,608	1,864,142	0.95	52,425,628
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT979EZV-CGND-HRA-00022-Male-ALS_LB_FTD-Cortex_Frontal-C9orf72_neg	0.64	74,945,761	13,298,769	2,278,260	1,341,786	0.96	47,954,917
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT979EZV-CGND-HRA-00036-Male-ALS_LB_FTD-Spinal_Cord_Lumbar-C9orf72_neg	0.67	82,637,196	12,176,528	3,164,330	1,226,634	0.96	52,161,243
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT979EZV-CGND-HRA-00050-Male-ALS_LB_FTD-Spinal_Cord_Cervical-C9orf72_neg	0.67	65,597,026	10,682,812	2,127,704	1,033,922	0.96	41,534,980
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT979EZV-CGND-HRA-00064-Male-ALS_LB_FTD-Cortex_Motor_Medial-C9orf72_neg	0.69	81,698,575	12,144,283	3,335,295	1,139,377	0.96	51,473,104
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT979EZV-CGND-HRA-00078-Male-ALS_LB_FTD-Cerebellum-C9orf72_neg	0.76	57,065,757	5,003,625	1,636,459	812,013	0.96	33,755,430
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT979EZV-CGND-HRA-00092-Male-ALS_LB_FTD-Spinal_Cord_Lateral-C9orf72_neg	0.67	82,279,620	12,685,408	2,651,457	1,114,875	0.96	51,459,785
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT979EZV-CGND-HRA-01344-Male-ALS_LB_FTD-Spinal_Cord_Thoracic-C9orf72_neg	0.57	45,318,886	12,448,166	2,618,371	1,155,563	0.95	32,296,376
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXT979EZV-CGND-HRA-01345-Male-ALS_LB_FTD-Cortex_Occipital-C9orf72_neg	0.71	39,866,541	8,223,375	2,016,185	746,009	0.94	26,956,580
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXY076JMB-CGND-HRA-00198-Female-ALS-Liver-SOD1_neg_FIG4_pos_SETX	0.39	54,455,043	23,860,521	4,382,980	3,080,866	0.94	45,789,885
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXY076JMB-CGND-HRA-00662-Female-ALS-Cerebellum-SOD1_neg_FIG4_pos_SETX_VUS	0.68	76,915,950	10,908,688	2,736,239	1,846,183	0.96	48,305,016
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXY076JMB-CGND-HRA-00663-Female-ALS-Cortex_Motor_Medial-SOD1_neg_FIG4_pos_SETX_VUS	0.60	87,989,562	18,205,340	3,506,390	1,616,692	0.96	57,980,843
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXY076JMB-CGND-HRA-00664-Female-ALS-Cortex_Motor_Lateral-SOD1_neg_FIG4_pos_SETX_VUS	0.57	97,746,427	19,944,655	3,912,591	1,788,987	0.96	64,047,932
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXY076JMB-CGND-HRA-00665-Female-ALS-Spinal_Cord_Cervical-SOD1_neg_FIG4_pos_SETX_VUS	0.65	68,676,719	13,049,741	2,540,453	1,210,457	0.96	44,701,277
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXY076JMB-CGND-HRA-00666-Female-ALS-Spinal_Cord_Lumbar-SOD1_neg_FIG4_pos_SETX_VUS	0.69	65,791,453	10,724,445	2,671,350	967,786	0.96	41,670,631
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXY076JMB-CGND-HRA-01239-Female-ALS-Cortex_Frontal-SOD1_neg_FIG4_pos_SETX_VUS	0.66	72,552,797	13,493,645	2,518,760	1,059,820	0.96	46,553,733
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXY076JMB-CGND-HRA-01240-Female-ALS-Cortex_Occipital-SOD1_neg_FIG4_pos_SETX_VUS	0.65	78,219,318	14,087,632	2,937,227	1,240,149	0.97	49,991,738
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUXY076JMB-CGND-HRA-01241-Female-ALS-Spinal_Cord_Thoracic-SOD1_neg_FIG4_pos_SETX_VUS	0.57	61,370,406	14,488,852	3,037,778	1,304,406	0.96	41,624,067
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYB686REL-CGND-HRA-00023-Male-ALS-Cortex_Frontal-C9orf72_neg	0.60	104,529,733	12,927,383	4,619,370	1,430,168	0.93	66,455,812
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYB686REL-CGND-HRA-00037-Male-ALS-Spinal_Cord_Lumbar-C9orf72_neg	0.55	59,111,067	9,103,997	3,305,238	1,144,642	0.95	38,231,222
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYB686REL-CGND-HRA-00051-Male-ALS-Spinal_Cord_Cervical-C9orf72_neg	0.57	76,180,134	13,908,022	4,937,036	1,594,682	0.95	50,933,856
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYB686REL-CGND-HRA-00065-Male-ALS-Cortex_Motor_Medial-C9orf72_neg	0.73	88,335,188	8,345,864	3,828,091	919,485	0.95	53,437,701
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYB686REL-CGND-HRA-00079-Male-ALS-Cerebellum-C9orf72_neg	0.76	113,560,310	7,631,492	3,623,720	1,442,478	0.92	68,285,134
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYB686REL-CGND-HRA-00093-Male-ALS-Cortex_Motor_Lateral-C9orf72_neg	0.70	73,908,884	9,263,120	4,524,520	1,106,836	0.94	47,161,814
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYV496XLP-CGND-HRA-00014-2-Male-ALS_FTD_TM-Cortex_Frontal-C9orf72_neg	0.71	82,160,638	10,502,488	2,226,299	891,585	0.95	50,329,905
Homo sapiens hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYV496XLP-CGND-HRA-00028-Male-ALS_FTD_TM-Spinal_Cord_Lumbar-C9orf72_neg	0.66	81,358,162	12,077,182	2,936,167	1,205,105	0.95	51,105,986

<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYV496XLP--CGND-HRA-00042--Male--ALS_FTD_TM--Spinal_Cord_Cervical--C9orf72_neg	0.65	61,499,002	9,663,304	3,350,356	1,057,462	0.96	39,350,571
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYV496XLP--CGND-HRA-00056--Male--ALS_FTD_TM--Cortex_Motor_Medial--C9orf72_neg	0.71	78,110,596	9,455,872	3,176,466	952,640	0.96	47,908,877
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYV496XLP--CGND-HRA-00070--Male--ALS_FTD_TM--Cerebellum--C9orf72_neg	0.78	50,486,309	3,886,317	1,375,590	612,586	0.96	29,477,855
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYV496XLP--CGND-HRA-00084-2--Male--ALS_FTD_TM--Cortex_Motor_Lateral--C9orf72_neg	0.71	87,738,352	9,599,558	3,082,996	909,108	0.95	53,302,663
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYV496XLP--CGND-HRA-01329--Male--ALS_FTD_TM--Cortex_Occipital--C9orf72_neg	0.70	64,713,935	8,166,747	3,616,535	866,677	0.95	40,575,647
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYV496XLP--CGND-HRA-01330--Male--ALS_FTD_TM--Spinal_Cord_Thoracic--C9orf72_neg	0.64	42,648,140	8,678,296	2,730,142	881,730	0.96	28,499,940
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYX020CB0--CGND-HRA-00386--Male--ALS_AD--Cerebellum--C9orf72_neg	0.70	87,782,254	10,013,470	2,883,431	1,933,587	0.95	53,820,139
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYX020CB0--CGND-HRA-00387--Male--ALS_AD--Cortex_Motor_Medial--C9orf72_neg	0.69	50,453,321	7,601,067	1,598,102	815,194	0.95	31,684,509
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYX020CB0--CGND-HRA-00388--Male--ALS_AD--Cortex_Motor_Lateral--C9orf72_neg	0.66	79,539,178	12,940,674	2,430,147	1,310,721	0.96	50,342,440
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYX020CB0--CGND-HRA-00389--Male--ALS_AD--Spinal_Cord_Cervical--C9orf72_neg	0.54	64,069,181	15,938,005	2,638,686	1,598,906	0.96	44,074,153
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYX020CB0--CGND-HRA-00390--Male--ALS_AD--Spinal_Cord_Lumbar--C9orf72_neg	0.45	68,646,249	15,614,573	3,800,812	1,894,812	0.95	47,181,210
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYX020CB0--CGND-HRA-00391--Male--ALS_AD--Cortex_Frontal--C9orf72_neg	0.68	84,309,796	11,420,574	2,448,989	1,111,431	0.96	51,841,241
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYX020CB0--CGND-HRA-01285--Male--ALS_AD--Cortex_Occipital--C9orf72_neg	0.71	80,150,257	7,477,749	4,323,667	992,929	0.96	48,653,298
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYX020CB0--CGND-HRA-01286--Male--ALS_AD--Spinal_Cord_Thoracic--C9orf72_neg	0.52	84,534,139	19,553,189	7,698,532	2,508,590	0.96	59,600,346
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYU221HZA--CGND-HRA-00240--Male--ALS--Cortex_Frontal--Unknown	0.70	68,797,940	8,708,054	2,134,772	787,944	0.96	41,989,419
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYU221HZA--CGND-HRA-00249--Male--ALS--Cortex_Motor_Medial--Unknown	0.56	65,145,946	11,104,506	4,183,492	1,157,980	0.96	42,586,824
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYU221HZA--CGND-HRA-00259--Male--ALS--Spinal_Cord_Cervical--Unknown	0.62	58,241,453	10,948,469	2,869,901	1,179,329	0.86	42,486,416
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYU221HZA--CGND-HRA-00272--Male--ALS--Spinal_Cord_Lumbar--Unknown	0.62	84,191,323	13,207,799	4,936,683	1,345,993	0.94	55,282,745
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYU221HZA--CGND-HRA-00284--Male--ALS--Cortex_Motor_Lateral--Unknown	0.70	78,054,197	8,576,075	2,256,514	852,798	0.94	47,632,461
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUYU221HZA--CGND-HRA-00724--Male--ALS--Cerebellum--Unknown	0.68	67,602,312	8,872,420	4,203,682	1,831,306	0.94	43,789,933
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUB953VCD--CGND-HRA-00598--Female--ALS--Cerebellum--C9orf72_neg	0.73	82,653,624	5,418,552	2,684,549	1,162,401	0.96	47,640,997
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUB953VCD--CGND-HRA-00599--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.71	53,131,006	6,509,726	2,532,205	774,161	0.95	32,987,575
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUB953VCD--CGND-HRA-00600--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.73	67,525,989	7,812,859	2,618,543	779,879	0.95	41,239,474
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUB953VCD--CGND-HRA-00601--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.51	95,065,638	19,888,040	5,444,133	2,292,853	0.93	65,974,321
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUB953VCD--CGND-HRA-01263--Female--ALS--Cortex_Frontal--C9orf72_neg	0.58	64,665,634	11,433,092	5,583,270	1,976,700	0.95	43,864,651
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUB953VCD--CGND-HRA-01264--Female--ALS--Cortex_Occipital--C9orf72_neg	0.71	74,578,996	5,710,724	3,869,924	959,426	0.97	44,091,106
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUB953VCD--CGND-HRA-01265--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.51	59,443,756	13,463,882	4,595,334	1,584,692	0.97	40,967,923
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZK186ZK4--CGND-HRA-00202--Female--ALS--Cerebellum--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.77	61,984,436	4,133,824	1,880,199	747,643	0.96	35,722,818
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZK186ZK4--CGND-HRA-00680--Female--ALS--Cortex_Motor_Medial--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.67	73,304,082	9,689,208	4,231,815	1,016,421	0.95	46,259,366
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZK186ZK4--CGND-HRA-00681--Female--ALS--Cortex_Motor_Lateral--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.64	97,876,522	11,990,788	5,734,283	1,327,795	0.96	60,942,566
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZK186ZK4--CGND-HRA-01251--Female--ALS--Cortex_Frontal--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.68	68,431,094	9,792,466	2,334,794	916,438	0.96	42,305,215
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZK186ZK4--CGND-HRA-01253--Female--ALS--Spinal_Cord_Thoracic--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.59	61,879,593	13,758,241	3,425,035	1,411,809	0.96	41,758,038
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ200WEQ--CGND-HRA-00015--Male--ALS--Cortex_Frontal--C9orf72_neg	0.69	71,547,858	10,049,856	2,167,624	909,694	0.96	44,272,632
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ200WEQ--CGND-HRA-00029--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.69	86,690,944	11,354,066	3,793,001	1,275,629	0.96	53,855,687
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ200WEQ--CGND-HRA-00043--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.70	78,402,657	10,639,307	2,677,596	977,800	0.96	48,388,750
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ200WEQ--CGND-HRA-00057--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.75	71,969,231	8,040,565	2,614,666	724,964	0.96	43,437,849
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ200WEQ--CGND-HRA-00071--Male--ALS--Cerebellum--C9orf72_neg	0.59	201,884,227	20,161,063	7,628,321	3,790,895	0.96	121,773,802
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ200WEQ--CGND-HRA-00085--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.67	110,927,097	13,943,391	3,086,515	1,276,951	0.96	67,568,625
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ200WEQ--CGND-HRA-01331--Male--ALS--Cortex_Occipital--C9orf72_neg	0.73	35,070,837	5,921,663	1,634,194	570,234	0.96	22,609,236
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ200WEQ--CGND-HRA-01332--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.69	69,290,126	10,550,944	2,979,206	1,013,744	0.97	43,321,967
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ622ZHF--CGND-HRA-00636--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_SBMA_neg	0.73	59,954,148	5,204,174	2,738,286	1,009,474	0.97	35,695,581
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ622ZHF--CGND-HRA-00637--Male--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg_SBMA_neg	0.67	60,579,927	8,301,091	3,498,320	920,272	0.96	38,314,244
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ622ZHF--CGND-HRA-00638--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg_SBMA_neg	0.70	72,414,054	8,994,182	3,470,264	924,792	0.96	44,245,321
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ622ZHF--CGND-HRA-01219--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg_SBMA_neg	0.69	67,948,560	9,368,638	2,381,481	855,273	0.96	42,308,772
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZJ622ZHF--CGND-HRA-01220--Male--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg_SBMA_neg	0.61	72,801,431	8,537,905	4,819,666	1,460,286	0.96	45,797,620
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZ073BDK--CGND-HRA-00372--Female--ALS--Cerebellum--C9orf72_neg	0.65	68,893,329	10,737,855	2,739,503	2,200,799	0.95	44,657,899
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZ073BDK--CGND-HRA-00373--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.60	58,660,789	13,288,367	2,341,047	1,182,421	0.95	39,897,526
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZ073BDK--CGND-HRA-00374--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.55	78,566,484	14,936,734	2,788,323	1,946,837	0.95	53,964,437
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZ073BDK--CGND-HRA-00375--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.58	69,240,701	11,133,739	2,630,582	1,331,116	0.96	45,658,691
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZ073BDK--CGND-HRA-00376--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.47	72,826,265	21,305,401	3,496,736	2,184,252	0.95	52,271,931
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZ073BDK--CGND-HRA-00377--Female--ALS--Cortex_Frontal--C9orf72_neg	0.60	58,842,175	13,990,009	1,859,421	1,182,201	0.95	40,025,998
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZ073BDK--CGND-HRA-00378--Female--ALS--Cortex_Occipital--C9orf72_neg	0.57	66,132,146	14,994,528	2,321,287	1,553,673	0.94	45,197,538
<i>Homo sapiens</i> hg38	RNA-seq	2x125	STAR-2.5.3.a	NEUZ073BDK--CGND-HRA-00379--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.58	68,285,582	15,901,580	2,906,077	1,430,463	0.92	47,905,489

# READ DISTRIBUTION

#	Exonic:	Intergenic:	Intronic:
ATCC-BXS0114--CGND-HRA-00742--Female--Non-Neurological_Control--Cell_Line_iPS--Unknown	0.74	0.04	0.21
ATCC-BXS0114--CGND-HRA-00743--Female--Non-Neurological_Control--Cell_Line_Motor_Neuron--Unknown	0.64	0.04	0.32
ATCC-BYS0112--CGND-HRA-00740--Male--Non-Neurological_Control--Cell_Line_iPS--Unknown	0.64	0.04	0.31
ATCC-BYS0112--CGND-HRA-00741--Male--Non-Neurological_Control--Cell_Line_Motor_Neuron--Unknown	0.62	0.05	0.33
GWFF14-01--CGND-HRA-00295--Female--Pre-fALS_FTD--Cerebellum--C9orf72_pos	0.40	0.06	0.54
GWFF14-01--CGND-HRA-00296--Female--Pre-fALS_FTD--Cortex_Motor_Medial--C9orf72_pos	0.47	0.06	0.47
GWFF14-01--CGND-HRA-00297--Female--Pre-fALS_FTD--Cortex_Motor_Lateral--C9orf72_pos	0.49	0.05	0.45
GWFF14-01--CGND-HRA-00298--Female--Pre-fALS_FTD--Spinal_Cord_Cervical--C9orf72_pos	0.60	0.05	0.35
GWFF14-01--CGND-HRA-00299--Female--Pre-fALS_FTD--Spinal_Cord_Lumbar--C9orf72_pos	0.60	0.05	0.36
GWFF14-01--CGND-HRA-00300--Female--Pre-fALS_FTD--Cortex_Frontal--C9orf72_pos	0.46	0.06	0.48
GWFF14-01--CGND-HRA-00301--Female--Pre-fALS_FTD--Cortex_Occipital--C9orf72_pos	0.46	0.06	0.48
GWFF14-01--CGND-HRA-00302--Female--Pre-fALS_FTD--Spinal_Cord_Thoracic--C9orf72_pos	0.58	0.05	0.37
JHU10--CGND-HRA-00106--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_OPTN_pos	0.37	0.06	0.57
JHU12--CGND-HRA-00108--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.48	0.05	0.47
JHU14--CGND-HRA-00110--Male--ALS--Cerebellum--C9orf72_neg_SOD1_pos	0.49	0.06	0.45
JHU15--CGND-HRA-00111--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.41	0.06	0.52
JHU16--CGND-HRA-00112--Female--ALS--Liver--C9orf72_pos_SOD1_neg_NEK1_pos	0.70	0.03	0.27
JHU22--CGND-HRA-00118--Male--ALS--Cerebellum--C9orf72_pos_SOD1_neg_SPG11_pos	0.30	0.06	0.64
JHU25--CGND-HRA-00121--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_OPTN_pos_ANXA11_likely_benign	0.27	0.06	0.67
JHU28--CGND-HRA-00124--Male--ALS--Cortex_Sensory--C9orf72_neg_SOD1_neg	0.38	0.07	0.55
JHU3--CGND-HRA-00099--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.38	0.06	0.56
JHU30--CGND-HRA-00126--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.41	0.05	0.54
JHU32--CGND-HRA-00128--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.42	0.05	0.53
JHU33--CGND-HRA-00129--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_negMATR3_pos_VUS	0.45	0.06	0.49
JHU38--CGND-HRA-00134--Female--ALS--Cortex_Motor_Unspecified--C9orf72_pos_SOD1_neg	0.43	0.06	0.51
JHU4--CGND-HRA-00100--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_SETX_pos_likely_benign	0.35	0.06	0.59
JHU43--CGND-HRA-00139--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_pos	0.53	0.06	0.41
JHU47--CGND-HRA-00143--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_ANXA11_pos	0.43	0.06	0.51
JHU5--CGND-HRA-00101--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_DCTN1_neg	0.32	0.06	0.62
JHU52--CGND-HRA-00148--Male--ALS--Cortex_Frontal--C9orf72_pos_SOD1_neg	0.66	0.05	0.29
JHU53--CGND-HRA-00149--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg_OPTN_pos	0.54	0.05	0.40
JHU55--CGND-HRA-00151--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.31	0.07	0.62
JHU56--CGND-HRA-00152--Male--ALS--Liver--C9orf72_neg_SOD1_neg_TARDBP_pos_TBK1_ALS2_likely_benign	0.69	0.04	0.28
JHU57--CGND-HRA-00153--Male--ALS--Liver--C9orf72_neg_SOD1_neg_FUS_pos_ALS2_likely_benign	0.73	0.03	0.24
JHU58--CGND-HRA-00154--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.44	0.05	0.51
JHU59--CGND-HRA-00155--Female--ALS--Liver--C9orf72_neg_SOD1_neg	0.54	0.04	0.42
JHU60--CGND-HRA-00156--Male--DLB_Peripheral_Neuropathy--Cerebellum--C9orf72_neg_SOD1_neg_NEFH_likely_benign_VAPB	0.33	0.07	0.60
JHU63--CGND-HRA-00159--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_ALS2_pos	0.31	0.08	0.62
JHU64--CGND-HRA-00160--Male--ALS_FTD--Cortex_Frontal--C9orf72_neg_SOD1_neg_NEK1_pos	0.40	0.06	0.54
JHU7--CGND-HRA-00103--Male--ALS--Liver--C9orf72_neg_SOD1_neg	0.61	0.03	0.36
JHU70--CGND-HRA-00166--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_OPTN_pos	0.38	0.05	0.57
JHU72--CGND-HRA-00168--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_CCFN_pos	0.29	0.06	0.66
JHU73--CGND-HRA-00169--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_NEFH_likely_benign	0.44	0.06	0.50
JHU73--CGND-HRA-00523--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.42	0.06	0.52

JHU73--CGND-HRA-00553--Female--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.49	0.06	0.45
JHU73--CGND-HRA-00554--Female--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.37	0.07	0.56
JHU73--CGND-HRA-00555--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.64	0.04	0.32
JHU73--CGND-HRA-00556--Female--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.50	0.06	0.44
JHU73--CGND-HRA-00557--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.46	0.06	0.47
JHU73--CGND-HRA-00558--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg_NEFH_pos_likely_benign	0.58	0.04	0.38
JHU74--CGND-HRA-00170--Male--ALS--Cerebellum--C9orf72_neg_SOD1_pos_ANXA11_likely_benign	0.42	0.06	0.52
JHU74--CGND-HRA-00559--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.60	0.05	0.35
JHU74--CGND-HRA-00560--Male--ALS--Cortex_Occipital--C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.50	0.06	0.44
JHU74--CGND-HRA-00561--Male--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.58	0.05	0.36
JHU74--CGND-HRA-00562--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.56	0.06	0.39
JHU74--CGND-HRA-01217--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_pos_ANXA11_pos_likely_benign	0.57	0.05	0.38
JHU75--CGND-HRA-00171--Female--ALS--Spinal_Cord_Cervical--C9orf72_pos_SOD1_neg_OPTN_pos_SPG11_likely_benign	0.58	0.05	0.38
JHU75--CGND-HRA-00631--Female--ALS--Cortex_Motor_Unspecified--C9orf72_pos_SOD1_neg_OPTN_pos_SPG11_likely_benign	0.54	0.05	0.41
JHU77--CGND-HRA-00633--Male--ALS--Cortex_Motor_Unspecified--C9orf72_neg_SOD1_neg	0.47	0.07	0.47
JHU77--CGND-HRA-00634--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.56	0.05	0.39
JHU79--CGND-HRA-00175--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.35	0.05	0.60
JHU79--CGND-HRA-00525--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.44	0.05	0.51
JHU79--CGND-HRA-00526--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.49	0.06	0.45
JHU79--CGND-HRA-00527--Male--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.57	0.05	0.38
JHU79--CGND-HRA-00528--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.65	0.04	0.32
JHU79--CGND-HRA-00563--Male--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg	0.49	0.06	0.45
JHU79--CGND-HRA-00564--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg	0.60	0.05	0.36
JHU79--CGND-HRA-00565--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.62	0.04	0.34
JHU8--CGND-HRA-00104--Male--ALS--Cerebellum--C9orf72_neg_SOD1_pos_ALS2_pos	0.35	0.06	0.59
JHU80--CGND-HRA-00529--Female--PLS--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.51	0.06	0.43
JHU80--CGND-HRA-00530--Female--PLS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.53	0.05	0.43
JHU80--CGND-HRA-00566--Female--PLS--Cerebellum--C9orf72_neg_SOD1_neg	0.38	0.06	0.56
JHU80--CGND-HRA-00567--Female--PLS--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.47	0.06	0.47
JHU80--CGND-HRA-00568--Female--PLS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg	0.44	0.06	0.50
JHU80--CGND-HRA-00569--Female--PLS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg	0.48	0.06	0.45
JHU80--CGND-HRA-00570--Female--PLS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.52	0.05	0.43
JHU82--CGND-HRA-00178--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.43	0.05	0.52
JHU82--CGND-HRA-00531--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.41	0.06	0.54
JHU82--CGND-HRA-00571--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.54	0.06	0.40
JHU82--CGND-HRA-00572--Male--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.39	0.07	0.54
JHU82--CGND-HRA-00573--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.59	0.05	0.36
JHU82--CGND-HRA-00574--Male--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg	0.40	0.07	0.53
JHU82--CGND-HRA-00575--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg	0.51	0.06	0.42
JHU82--CGND-HRA-00576--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.47	0.06	0.47
JHU82--CGND-HRA-00577--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.48	0.05	0.47
JHU83--CGND-HRA-00179--Male--ALS--Cerebellum--C9orf72_neg_SOD1_pos_SPG11_pos	0.38	0.06	0.56
JHU83--CGND-HRA-00532--Male--ALS--Cerebellum--C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.39	0.06	0.56
JHU83--CGND-HRA-00578--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.48	0.06	0.46
JHU83--CGND-HRA-00579--Male--ALS--Cortex_Occipital--C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.49	0.06	0.45
JHU83--CGND-HRA-00580--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.50	0.05	0.45
JHU83--CGND-HRA-00581--Male--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.49	0.06	0.46
JHU83--CGND-HRA-00582--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.51	0.06	0.44
JHU83--CGND-HRA-00583--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.58	0.05	0.37
JHU83--CGND-HRA-00584--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_pos_N139K_SPG11_pos_VUS	0.54	0.05	0.41

NEUAP156PM4--CGND-HRA-00183--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.40	0.06	0.54
NEUAP156PM4--CGND-HRA-00534--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.45	0.06	0.49
NEUAP156PM4--CGND-HRA-00535--Female--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.58	0.05	0.36
NEUAP156PM4--CGND-HRA-00536--Female--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.52	0.07	0.42
NEUAP156PM4--CGND-HRA-00537--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.60	0.05	0.36
NEUAP156PM4--CGND-HRA-00603--Female--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg	0.65	0.05	0.31
NEUAP156PM4--CGND-HRA-00604--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg	0.69	0.04	0.27
NEUAP156PM4--CGND-HRA-00605--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.69	0.03	0.28
NEUAP156PM4--CGND-HRA-00606--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.70	0.04	0.26
NEUAT369TG5--CGND-HRA-00333--Female--ALS--Cerebellum--C9orf72_neg	0.45	0.07	0.49
NEUAT369TG5--CGND-HRA-00334--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.53	0.06	0.41
NEUAT369TG5--CGND-HRA-00335--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.53	0.07	0.41
NEUAT369TG5--CGND-HRA-00336--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.64	0.04	0.32
NEUAT369TG5--CGND-HRA-00337--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.56	0.05	0.39
NEUAT369TG5--CGND-HRA-00338--Female--ALS--Cortex_Frontal--C9orf72_neg	0.50	0.07	0.43
NEUAT369TG5--CGND-HRA-00339--Female--ALS--Cortex_Occipital--C9orf72_neg	0.48	0.07	0.45
NEUAT369TG5--CGND-HRA-00340--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.56	0.05	0.40
NEUAV667LJK--CGND-HRA-00341--Male--ALS--Cerebellum--C9orf72_neg	0.35	0.06	0.59
NEUAV667LJK--CGND-HRA-00342--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.42	0.06	0.52
NEUAV667LJK--CGND-HRA-00343--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.47	0.06	0.46
NEUAV667LJK--CGND-HRA-00344--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.52	0.05	0.43
NEUAV667LJK--CGND-HRA-00345--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.65	0.04	0.31
NEUAV667LJK--CGND-HRA-00346--Male--ALS--Cortex_Frontal--C9orf72_neg	0.41	0.06	0.53
NEUAV667LJK--CGND-HRA-00347--Male--ALS--Cortex_Occipital--C9orf72_neg	0.51	0.06	0.43
NEUAV667LJK--CGND-HRA-00348--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.59	0.05	0.36
NEUAY067UTB--CGND-HRA-00746--Female--ALS--Cerebellum--C9orf72_neg	0.54	0.05	0.41
NEUAY067UTB--CGND-HRA-01269--Female--ALS--Cortex_Frontal--C9orf72_neg	0.48	0.06	0.45
NEUAY067UTB--CGND-HRA-01270--Female--ALS--Cortex_Occipital--C9orf72_neg	0.57	0.05	0.37
NEUCG551GV1--CGND-HRA-00466--Female--Peripheral_Neuropathy--Cortex_Frontal--Unknown	0.49	0.07	0.44
NEUCG551GV1--CGND-HRA-00469--Female--Peripheral_Neuropathy--Cerebellum--Unknown	0.47	0.07	0.47
NEUCV649UJK--CGND-HRA-00243--Male--ALS--Cortex_Frontal--Unknown	0.57	0.05	0.37
NEUCV649UJK--CGND-HRA-00252--Male--ALS--Cortex_Motor_Medial--Unknown	0.58	0.05	0.36
NEUCV649UJK--CGND-HRA-00262--Male--ALS--Spinal_Cord_Cervical--Unknown	0.63	0.04	0.33
NEUCV649UJK--CGND-HRA-00275--Male--ALS--Spinal_Cord_Lumbar--Unknown	0.68	0.04	0.28
NEUCV649UJK--CGND-HRA-00722--Male--ALS--Cerebellum--Unknown	0.36	0.06	0.58
NEUCW292DYJ--CGND-HRA-00247--Female--ALS--Cortex_Frontal--Unknown	0.53	0.06	0.41
NEUCW292DYJ--CGND-HRA-00256--Female--ALS--Cortex_Motor_Medial--Unknown	0.62	0.05	0.33
NEUCW292DYJ--CGND-HRA-00266--Female--ALS--Spinal_Cord_Cervical--Unknown	0.59	0.05	0.36
NEUCW292DYJ--CGND-HRA-00279--Female--ALS--Spinal_Cord_Lumbar--Unknown	0.59	0.04	0.36
NEUCW292DYJ--CGND-HRA-00727--Female--ALS--Cerebellum--Unknown	0.52	0.05	0.43
NEUDA151YMK--CGND-HRA-00593--Female--Non-Neurological_Control--Cerebellum--C9orf72_neg	0.40	0.05	0.55
NEUDA151YMK--CGND-HRA-00594--Female--Non-Neurological_Control--Cortex_Motor_Medial--C9orf72_neg	0.47	0.06	0.48
NEUDA151YMK--CGND-HRA-00595--Female--Non-Neurological_Control--Cortex_Motor_Lateral--C9orf72_neg	0.46	0.06	0.48
NEUDA151YMK--CGND-HRA-01258--Female--Non-Neurological_Control--Cortex_Frontal--C9orf72_neg	0.53	0.05	0.41
NEUDA151YMK--CGND-HRA-01259--Female--Non-Neurological_Control--Spinal_Cord_Thoracic--C9orf72_neg	0.60	0.04	0.36
NEUDG361GA9--CGND-HRA-00208--Female--ALS--Cerebellum--C9orf72_neg	0.38	0.06	0.56
NEUDG361GA9--CGND-HRA-00214--Female--ALS--Cortex_Frontal--C9orf72_neg	0.52	0.06	0.42
NEUDG361GA9--CGND-HRA-00220--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.48	0.06	0.46
NEUDG361GA9--CGND-HRA-00226--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.48	0.06	0.46
NEUDG361GA9--CGND-HRA-00232--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.56	0.05	0.39

NEUDG361GA9--CGND-HRA-00238--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.51	0.06	0.43
NEUDG727NTW--CGND-HRA-00428--Female--ALS--Cerebellum--C9orf72_neg	0.45	0.05	0.50
NEUDG727NTW--CGND-HRA-00429--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.61	0.05	0.35
NEUDG727NTW--CGND-HRA-00430--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.57	0.05	0.38
NEUDG727NTW--CGND-HRA-00431--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.61	0.04	0.35
NEUDG727NTW--CGND-HRA-00431-2--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.62	0.04	0.34
NEUDG727NTW--CGND-HRA-00432--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.67	0.04	0.29
NEUDG727NTW--CGND-HRA-00433--Female--ALS--Cortex_Frontal--C9orf72_neg	0.59	0.05	0.36
NEUDG727NTW--CGND-HRA-01299--Female--ALS--Cortex_Occipital--C9orf72_neg	0.51	0.06	0.44
NEUDG727NTW--CGND-HRA-01300--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.55	0.05	0.40
NEUDM397JGD--CGND-HRA-00205--Female--ALS--Cerebellum--C9orf72_neg	0.44	0.06	0.50
NEUDM397JGD--CGND-HRA-00211--Female--ALS--Cortex_Frontal--C9orf72_neg	0.57	0.06	0.37
NEUDM397JGD--CGND-HRA-00217--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.61	0.05	0.34
NEUDM397JGD--CGND-HRA-00223--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.61	0.05	0.34
NEUDM397JGD--CGND-HRA-00229--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.60	0.05	0.35
NEUDM397JGD--CGND-HRA-00235--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.54	0.05	0.41
NEUDR086ZDQ--CGND-HRA-00207--Female--ALS--Cerebellum--Unknown	0.40	0.05	0.55
NEUDR086ZDQ--CGND-HRA-00213--Female--ALS--Cortex_Frontal--Unknown	0.50	0.06	0.44
NEUDR086ZDQ--CGND-HRA-00219--Female--ALS--Cortex_Motor_Medial--Unknown	0.42	0.06	0.52
NEUDR086ZDQ--CGND-HRA-00225--Female--ALS--Cortex_Motor_Lateral--Unknown	0.43	0.06	0.51
NEUDR086ZDQ--CGND-HRA-00231--Female--ALS--Spinal_Cord_Cervical--Unknown	0.58	0.05	0.37
NEUDR086ZDQ--CGND-HRA-00237--Female--ALS--Spinal_Cord_Lumbar--Unknown	0.54	0.05	0.41
NEUDT233Z21--CGND-HRA-00422--Male--ALS--Cerebellum--C9orf72_neg	0.42	0.05	0.53
NEUDT233Z21--CGND-HRA-00423--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.52	0.05	0.42
NEUDT233Z21--CGND-HRA-00424--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.52	0.05	0.43
NEUDT233Z21--CGND-HRA-00425--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.59	0.05	0.36
NEUDT233Z21--CGND-HRA-00426--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.69	0.04	0.27
NEUDT233Z21--CGND-HRA-00427--Male--ALS--Cortex_Frontal--C9orf72_neg	0.60	0.05	0.35
NEUDT233Z21--CGND-HRA-01297--Male--ALS--Cortex_Occipital--C9orf72_neg	0.42	0.07	0.51
NEUDT233Z21--CGND-HRA-01298--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.51	0.05	0.44
NEUDW867LF9--CGND-HRA-00271--Male--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.59	0.04	0.37
NEUEA633EN5--CGND-HRA-00671--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.37	0.07	0.56
NEUEA633EN5--CGND-HRA-00672--Female--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg	0.46	0.06	0.47
NEUEA633EN5--CGND-HRA-00673--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg	0.48	0.07	0.45
NEUEA633EN5--CGND-HRA-00674--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.63	0.05	0.32
NEUEA633EN5--CGND-HRA-00675--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.60	0.05	0.35
NEUEA633EN5--CGND-HRA-01245--Female--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.45	0.07	0.49
NEUEA633EN5--CGND-HRA-01246--Female--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.52	0.06	0.41
NEUEA633EN5--CGND-HRA-01247--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.59	0.05	0.36
NEUEC006FND--CGND-HRA-00017--Female--ALS--Cortex_Frontal--C9orf72_neg	0.47	0.06	0.47
NEUEC006FND--CGND-HRA-00031--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.55	0.05	0.40
NEUEC006FND--CGND-HRA-00045--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.43	0.06	0.51
NEUEC006FND--CGND-HRA-00059--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.45	0.06	0.49
NEUEC006FND--CGND-HRA-00073--Female--ALS--Cerebellum--C9orf72_neg	0.38	0.06	0.57
NEUEC006FND--CGND-HRA-00087--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.37	0.06	0.56
NEUEC006FND--CGND-HRA-01335--Female--ALS--Cortex_Occipital--C9orf72_neg	0.64	0.04	0.32
NEUEE593VY7--CGND-HRA-00404--Male--MSA--Cerebellum--C9orf72_neg	0.50	0.05	0.45
NEUEE593VY7--CGND-HRA-00405--Male--MSA--Cortex_Motor_Medial--C9orf72_neg	0.56	0.05	0.39
NEUEE593VY7--CGND-HRA-00406--Male--MSA--Cortex_Motor_Lateral--C9orf72_neg	0.53	0.05	0.42
NEUEE593VY7--CGND-HRA-00407--Male--MSA--Spinal_Cord_Cervical--C9orf72_neg	0.56	0.05	0.39

NEUEE593VY7--CGND-HRA-00408--Male--MSA--Spinal_Cord_Lumbar--C9orf72_neg	0.62	0.04	0.34
NEUEE593VY7--CGND-HRA-00409--Male--MSA--Cortex_Frontal--C9orf72_neg	0.72	0.04	0.24
NEUEE593VY7--CGND-HRA-01291--Male--MSA--Cortex_Occipital--C9orf72_neg	0.43	0.06	0.51
NEUEE593VY7--CGND-HRA-01292--Male--MSA--Spinal_Cord_Thoracic--C9orf72_neg	0.55	0.05	0.40
NEUEF397VVN--CGND-HRA-00303--Female--ALS_AD--Cerebellum--Unknown	0.52	0.05	0.43
NEUEF397VVN--CGND-HRA-00304--Female--ALS_AD--Cortex_Motor_Medial--Unknown	0.60	0.05	0.35
NEUEF397VVN--CGND-HRA-00305--Female--ALS_AD--Cortex_Motor_Lateral--Unknown	0.57	0.05	0.38
NEUEF397VVN--CGND-HRA-00306--Female--ALS_AD--Spinal_Cord_Cervical--Unknown	0.59	0.05	0.37
NEUEF397VVN--CGND-HRA-00307--Female--ALS_AD--Spinal_Cord_Lumbar--Unknown	0.64	0.04	0.32
NEUEF397VVN--CGND-HRA-00308--Female--ALS_AD--Cortex_Frontal--Unknown	0.62	0.05	0.33
NEUEF397VVN--CGND-HRA-00309--Female--ALS_AD--Cortex_Occipital--Unknown	0.55	0.06	0.39
NEUEF397VVN--CGND-HRA-00310--Female--ALS_AD--Spinal_Cord_Thoracic--Unknown	0.55	0.05	0.40
NEUEF856BLV--CGND-HRA-00460--Female--ALS--Cortex_Frontal--C9orf72_pos	0.51	0.06	0.43
NEUEF856BLV--CGND-HRA-00465--Female--ALS--Cerebellum--C9orf72_pos	0.41	0.06	0.54
NEUEG442LDR--CGND-HRA-00199--Male--Non-Neurological_Control--Liver--Unknown	0.66	0.03	0.31
NEUEG442LDR--CGND-HRA-00667--Male--Non-Neurological_Control--Cerebellum--Unknown	0.42	0.05	0.52
NEUEG442LDR--CGND-HRA-00668--Male--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.47	0.06	0.47
NEUEG442LDR--CGND-HRA-00669--Male--Non-Neurological_Control--Cortex_Motor_Lateral--Unknown	0.50	0.06	0.43
NEUEG442LDR--CGND-HRA-00670--Male--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.56	0.05	0.39
NEUEG442LDR--CGND-HRA-01242--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.51	0.06	0.43
NEUEG442LDR--CGND-HRA-01243--Male--Non-Neurological_Control--Cortex_Occipital--Unknown	0.49	0.06	0.44
NEUEG442LDR--CGND-HRA-01244--Male--Non-Neurological_Control--Spinal_Cord_Thoracic--Unknown	0.54	0.05	0.41
NEUEH612JPA--CGND-HRA-00542--Female--ALS_AD--Cerebellum--C9orf72_neg_SOD1_neg	0.34	0.06	0.59
NEUEH612JPA--CGND-HRA-00543--Female--ALS_AD--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.45	0.06	0.48
NEUEH612JPA--CGND-HRA-00544--Female--ALS_AD--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.46	0.07	0.48
NEUEH612JPA--CGND-HRA-00545--Female--ALS_AD--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.61	0.04	0.35
NEUEH612JPA--CGND-HRA-00611--Female--ALS_AD--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg	0.53	0.06	0.41
NEUEH612JPA--CGND-HRA-00612--Female--ALS_AD--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg	0.41	0.07	0.52
NEUEH612JPA--CGND-HRA-00613--Female--ALS_AD--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.64	0.04	0.32
NEUEH612JPA--CGND-HRA-00614--Female--ALS_AD--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.61	0.04	0.35
NEUEL133AK6--CGND-HRA-00013--Female--ALS--Cortex_Frontal--C9orf72_neg	0.48	0.07	0.45
NEUEL133AK6--CGND-HRA-00027--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.62	0.04	0.34
NEUEL133AK6--CGND-HRA-00041--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.53	0.05	0.42
NEUEL133AK6--CGND-HRA-00055--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.50	0.06	0.43
NEUEL133AK6--CGND-HRA-00069--Female--ALS--Cerebellum--C9orf72_neg	0.48	0.06	0.46
NEUEL133AK6--CGND-HRA-00083--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.56	0.06	0.39
NEUEL133AK6--CGND-HRA-01327--Female--ALS--Cortex_Occipital--C9orf72_neg	0.55	0.06	0.38
NEUEL133AK6--CGND-HRA-01328--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.66	0.04	0.30
NEUEP010ZFE--CGND-HRA-01178--Male--Non-Neurological_Control--Cerebellum--Unknown	0.33	0.06	0.61
NEUEP010ZFE--CGND-HRA-01179--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.54	0.06	0.41
NEUEP010ZFE--CGND-HRA-01204--Male--Non-Neurological_Control--Cortex_Occipital--Unknown	0.38	0.07	0.55
NEUEP010ZFE--CGND-HRA-01205--Male--Non-Neurological_Control--Spinal_Cord_Thoracic--Unknown	0.63	0.04	0.33
NEUFE255AG2--CGND-HRA-00481--Male--ALS--Cortex_Frontal--Unknown	0.48	0.06	0.46
NEUFE255AG2--CGND-HRA-00486--Male--ALS--Cerebellum--Unknown	0.53	0.05	0.42
NEUFE255AG2--CGND-HRA-01206--Male--ALS--Cortex_Occipital--Unknown	0.54	0.05	0.40
NEUFE255AG2--CGND-HRA-01207--Male--ALS--Spinal_Cord_Thoracic--Unknown	0.66	0.05	0.30
NEUFF179PPT--CGND-HRA-00487--Male--ALS--Cortex_Frontal--C9orf72_neg	0.51	0.05	0.44
NEUFF179PPT--CGND-HRA-00492--Male--ALS--Cerebellum--C9orf72_neg	0.44	0.05	0.51
NEUFF179PPT--CGND-HRA-01208--Male--ALS--Cortex_Occipital--C9orf72_neg	0.57	0.05	0.38
NEUFF179PPT--CGND-HRA-01209--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.66	0.04	0.30

NEUFT454ZFP--CGND-HRA-00203--Male--ALS--Cerebellum--C9orf72_neg_ANG_pos	0.36	0.07	0.57
NEUFT454ZFP--CGND-HRA-00209--Male--ALS--Cortex_Frontal--C9orf72_neg_ANG_pos	0.62	0.05	0.33
NEUFT454ZFP--CGND-HRA-00215--Male--ALS--Cortex_Motor_Medial--C9orf72_neg_ANG_pos	0.60	0.05	0.35
NEUFT454ZFP--CGND-HRA-00221--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg_ANG_pos	0.51	0.06	0.43
NEUFT454ZFP--CGND-HRA-00227--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg_ANG_pos	0.62	0.05	0.33
NEUFT454ZFP--CGND-HRA-00233--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg_ANG_pos	0.55	0.05	0.40
NEUGA773REC--CGND-HRA-00025--Male--ALS--Cortex_Frontal--C9orf72_neg	0.48	0.06	0.46
NEUGA773REC--CGND-HRA-00039--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.60	0.05	0.36
NEUGA773REC--CGND-HRA-00053--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.61	0.04	0.34
NEUGA773REC--CGND-HRA-00081--Male--ALS--Cerebellum--C9orf72_neg	0.38	0.06	0.56
NEUGA773REC--CGND-HRA-00095--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.47	0.06	0.47
NEUGJ583BEE--CGND-HRA-01184-2--Male--Non-Neurological_Control--Cerebellum--Unknown	0.41	0.06	0.52
NEUGJ583BEE--CGND-HRA-01185--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.54	0.06	0.40
NEUGJ583BEE--CGND-HRA-01186--Male--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.43	0.07	0.50
NEUGJ583BEE--CGND-HRA-01187--Male--Non-Neurological_Control--Cortex_Motor_Lateral--Unknown	0.41	0.07	0.52
NEUGV399KJW--CGND-HRA-00365--Female--ALS--Cerebellum--C9orf72_neg	0.33	0.06	0.61
NEUGV399KJW--CGND-HRA-00366--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.49	0.05	0.46
NEUGV399KJW--CGND-HRA-00367--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.43	0.07	0.50
NEUGV399KJW--CGND-HRA-00368--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.59	0.05	0.36
NEUGV399KJW--CGND-HRA-00369--Female--ALS--Cortex_Frontal--C9orf72_neg	0.52	0.06	0.42
NEUGV399KJW--CGND-HRA-00370--Female--ALS--Cortex_Occipital--C9orf72_neg	0.43	0.07	0.51
NEUGV399KJW--CGND-HRA-00371--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.52	0.05	0.43
NEUGY575NUQ--CGND-HRA-00585--Male--ALS--Cerebellum--C9orf72_neg	0.32	0.06	0.62
NEUGY575NUQ--CGND-HRA-00586--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.53	0.06	0.41
NEUGY575NUQ--CGND-HRA-00587--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.50	0.06	0.44
NEUGY575NUQ--CGND-HRA-00588--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.61	0.05	0.34
NEUGY575NUQ--CGND-HRA-00589--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.70	0.04	0.26
NEUGY575NUQ--CGND-HRA-01254--Male--ALS--Cortex_Frontal--C9orf72_neg	0.53	0.07	0.41
NEUGY575NUQ--CGND-HRA-01255--Male--ALS--Cortex_Occipital--C9orf72_neg	0.56	0.06	0.38
NEUGY575NUQ--CGND-HRA-01256--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.61	0.05	0.34
NEUGY741GH8--CGND-HRA-00476--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.52	0.06	0.42
NEUGY741GH8--CGND-HRA-00479--Male--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.58	0.05	0.37
NEUGY741GH8--CGND-HRA-00480--Male--Non-Neurological_Control--Cerebellum--Unknown	0.52	0.05	0.43
NEUHA141EEC--CGND-HRA-00590--Male--Non-Neurological_Control--Cortex_Motor_Unspecified--C9orf72_neg	0.45	0.07	0.48
NEUHA141EEC--CGND-HRA-00592--Male--Non-Neurological_Control--Spinal_Cord_Lumbar--C9orf72_neg	0.61	0.05	0.34
NEUHA141EEC--CGND-HRA-01257--Male--Non-Neurological_Control--Spinal_Cord_Thoracic--C9orf72_neg	0.61	0.04	0.34
NEUHC282LVJ--CGND-HRA-00021--Female--Non-Neurological_Control--Cortex_Frontal--C9orf72_neg	0.51	0.06	0.42
NEUHC282LVJ--CGND-HRA-00035--Female--Non-Neurological_Control--Spinal_Cord_Lumbar--C9orf72_neg	0.55	0.05	0.41
NEUHC282LVJ--CGND-HRA-00049--Female--Non-Neurological_Control--Spinal_Cord_Cervical--C9orf72_neg	0.59	0.04	0.36
NEUHC282LVJ--CGND-HRA-00063--Female--Non-Neurological_Control--Cortex_Motor_Medial--C9orf72_neg	0.62	0.05	0.33
NEUHC282LVJ--CGND-HRA-00077--Female--Non-Neurological_Control--Cerebellum--C9orf72_neg	0.43	0.07	0.51
NEUHC282LVJ--CGND-HRA-00091--Female--Non-Neurological_Control--Cortex_Motor_Lateral--C9orf72_neg	0.61	0.06	0.33
NEUHC282LVJ--CGND-HRA-01342--Female--Non-Neurological_Control--Spinal_Cord_Thoracic--C9orf72_neg	0.66	0.04	0.30
NEUHC282LVJ--CGND-HRA-01343--Female--Non-Neurological_Control--Cortex_Occipital--C9orf72_neg	0.61	0.05	0.34
NEUHD481VCL--CGND-HRA-00206--Female--Non-Neurological_Control--Cerebellum--Unknown	0.46	0.05	0.49
NEUHD481VCL--CGND-HRA-00212--Female--Non-Neurological_Control--Cortex_Frontal--Unknown	0.51	0.06	0.43
NEUHD481VCL--CGND-HRA-00218--Female--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.56	0.05	0.39
NEUHD481VCL--CGND-HRA-00224--Female--Non-Neurological_Control--Cortex_Motor_Lateral--Unknown	0.54	0.05	0.41
NEUHD481VCL--CGND-HRA-00230--Female--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.52	0.05	0.43
NEUHD481VCL--CGND-HRA-00236--Female--Non-Neurological_Control--Spinal_Cord_Lumbar--Unknown	0.55	0.05	0.40

NEUHM340FBZ--CGND-HRA-00706--Male--ALS--Cerebellum--Unknown	0.38	0.07	0.55
NEUHX090PGV--CGND-HRA-00643--Male--Non-Neurological_Control--Cerebellum--Unknown	0.38	0.06	0.56
NEUHX090PGV--CGND-HRA-00644--Male--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.50	0.06	0.44
NEUHX090PGV--CGND-HRA-00645--Male--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.55	0.05	0.40
NEUHX090PGV--CGND-HRA-01225--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.47	0.06	0.47
NEUHX090PGV--CGND-HRA-01227--Male--Non-Neurological_Control--Spinal_Cord_Thoracic--Unknown	0.57	0.05	0.38
NEUJB238MJR--CGND-HRA-00596--Male--Non-Neurological_Control--Cortex_Motor_Medial--C9orf72_neg	0.39	0.07	0.54
NEUJB238MJR--CGND-HRA-01260--Male--Non-Neurological_Control--Cortex_Frontal--C9orf72_neg	0.38	0.07	0.55
NEUJB238MJR--CGND-HRA-01261--Male--Non-Neurological_Control--Cortex_Occipital--C9orf72_neg	0.36	0.07	0.57
NEUJL308UBK--CGND-HRA-01348--Female--ALS--Cortex_Occipital--C9orf72_neg	0.47	0.07	0.46
NEUJL308UBK--CGND-HRA-01349--Female--ALS--Cortex_Frontal--C9orf72_neg	0.55	0.06	0.39
NEUJL308UBK--CGND-HRA-01350--Female--ALS--Cerebellum--C9orf72_neg	0.46	0.06	0.49
NEUJR139GPF--CGND-HRA-00024--Male--ALS--Cortex_Frontal--C9orf72_neg	0.39	0.07	0.53
NEUJR139GPF--CGND-HRA-00038--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.58	0.04	0.37
NEUJR139GPF--CGND-HRA-00052--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.53	0.05	0.42
NEUJR139GPF--CGND-HRA-00066--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.46	0.06	0.48
NEUJZ255ZC5--CGND-HRA-00020-2--Male--ALS--Cortex_Frontal--C9orf72_neg	0.46	0.06	0.48
NEUJZ255ZC5--CGND-HRA-00034--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.60	0.05	0.35
NEUJZ255ZC5--CGND-HRA-00048--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.51	0.05	0.44
NEUJZ255ZC5--CGND-HRA-00062--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.54	0.06	0.41
NEUJZ255ZC5--CGND-HRA-00076--Male--ALS--Cerebellum--C9orf72_neg	0.31	0.06	0.63
NEUJZ255ZC5--CGND-HRA-00090--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.43	0.06	0.51
NEUJZ255ZC5--CGND-HRA-01340--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.46	0.05	0.48
NEUJZ255ZC5--CGND-HRA-01341--Male--ALS--Cortex_Occipital--C9orf72_neg	0.49	0.06	0.45
NEUKM699KKH--CGND-HRA-00018--Female--ALS_FTD--Cortex_Frontal--C9orf72_pos	0.50	0.06	0.44
NEUKM699KKH--CGND-HRA-00032--Female--ALS_FTD--Spinal_Cord_Lumbar--C9orf72_pos	0.54	0.05	0.42
NEUKM699KKH--CGND-HRA-00046--Female--ALS_FTD--Spinal_Cord_Cervical--C9orf72_pos	0.59	0.04	0.37
NEUKM699KKH--CGND-HRA-00060--Female--ALS_FTD--Cortex_Motor_Medial--C9orf72_pos	0.48	0.07	0.46
NEUKM699KKH--CGND-HRA-00074--Female--ALS_FTD--Cerebellum--C9orf72_pos	0.38	0.06	0.56
NEUKM699KKH--CGND-HRA-00088--Female--ALS_FTD--Cortex_Motor_Lateral--C9orf72_pos	0.61	0.05	0.34
NEUKM699KKH--CGND-HRA-01336--Female--ALS_FTD--Spinal_Cord_Thoracic--C9orf72_pos	0.53	0.05	0.43
NEUKM699KKH--CGND-HRA-01337--Female--ALS_FTD--Cortex_Occipital--C9orf72_pos	0.45	0.07	0.49
NEUKN209FNW--CGND-HRA-01360--Male--ALS--Cortex_Occipital--C9orf72_neg_SOD1_pos_AV4	0.54	0.06	0.40
NEUKN209FNW--CGND-HRA-01361--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_pos_AV4	0.64	0.05	0.31
NEUKN209FNW--CGND-HRA-01362--Male--ALS--Cerebellum--C9orf72_neg_SOD1_pos_AV4	0.58	0.05	0.37
NEUKN209FNW--CGND-HRA-01363--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_pos_AV4	0.59	0.05	0.37
NEUKX037NKA--CGND-HRA-00182--Male--ALS_AD_FTD--Cerebellum--C9orf72_pos_SOD1_neg	0.32	0.06	0.62
NEUKX037NKA--CGND-HRA-00533--Male--ALS_AD_FTD--Cerebellum--C9orf72_pos_SOD1_neg	0.31	0.06	0.62
NEUKX037NKA--CGND-HRA-01218--Male--ALS_AD_FTD--Cortex_Frontal--C9orf72_pos_SOD1_neg	0.56	0.05	0.38
NEUKY135CV6--CGND-HRA-00380--Male--ALS_AD--Cerebellum--C9orf72_neg	0.49	0.05	0.46
NEUKY135CV6--CGND-HRA-00381--Male--ALS_AD--Cortex_Motor_Medial--C9orf72_neg	0.49	0.06	0.46
NEUKY135CV6--CGND-HRA-00382--Male--ALS_AD--Cortex_Motor_Lateral--C9orf72_neg	0.68	0.04	0.28
NEUKY135CV6--CGND-HRA-00383--Male--ALS_AD--Spinal_Cord_Cervical--C9orf72_neg	0.63	0.04	0.33
NEUKY135CV6--CGND-HRA-00384--Male--ALS_AD--Spinal_Cord_Lumbar--C9orf72_neg	0.64	0.04	0.32
NEUKY135CV6--CGND-HRA-00385--Male--ALS_AD--Cortex_Frontal--C9orf72_neg	0.57	0.05	0.38
NEUKY135CV6--CGND-HRA-01283--Male--ALS_AD--Cortex_Occipital--C9orf72_neg	0.47	0.06	0.47
NEUKY135CV6--CGND-HRA-01284--Male--ALS_AD--Spinal_Cord_Thoracic--C9orf72_neg	0.58	0.05	0.37
NEUKZ685AR4--CGND-HRA-00738--Female--Non-Neurological_Control--Cell_Line_Motor_Neuron--Unknown	0.61	0.06	0.33
NEUKZ685AR4--CGND-HRA-00739--Female--Non-Neurological_Control--Cell_Line_iPS--Unknown	0.66	0.07	0.27
NEULH901PYF--CGND-HRA-00248--Male--ALS--Cortex_Frontal--C9orf72_pos	0.52	0.06	0.42

NEULH901PYF--CGND-HRA-00267--Male--ALS--Spinal_Cord_Cervical--C9orf72_pos	0.62	0.04	0.34
NEULH901PYF--CGND-HRA-00280--Male--ALS--Spinal_Cord_Lumbar--C9orf72_pos	0.58	0.04	0.37
NEULH901PYF--CGND-HRA-00287--Male--ALS--Cortex_Motor_Lateral--C9orf72_pos	0.53	0.05	0.42
NEULH901PYF--CGND-HRA-00726--Male--ALS--Cerebellum--C9orf72_pos	0.38	0.06	0.56
NEULM733WR7--CGND-HRA-00268--Female--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.67	0.04	0.30
NEULM733WR7--CGND-HRA-00281--Female--Non-Neurological_Control--Spinal_Cord_Lumbar--Unknown	0.64	0.04	0.32
NEULN488RD5--CGND-HRA-00731--Male--ALS--Cerebellum--C9orf72_neg_ATXN2_neg	0.41	0.06	0.54
NEULN488RD5--CGND-HRA-01266--Male--ALS--Cortex_Frontal--C9orf72_neg_ATXN2_neg	0.52	0.06	0.42
NEULN488RD5--CGND-HRA-01267--Male--ALS--Cortex_Occipital--C9orf72_neg_ATXN2_neg	0.52	0.06	0.42
NEULN488RD5--CGND-HRA-01268-2--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_ATXN2_neg	0.52	0.05	0.43
NEULT268RM4--CGND-HRA-00719--Male--ALS_FTD--Cerebellum--C9orf72_pos	0.38	0.06	0.56
NEUME287RK2--CGND-HRA-00016--Female--ALS_FTD--Cortex_Frontal--C9orf72_neg	0.40	0.07	0.53
NEUME287RK2--CGND-HRA-00058--Female--ALS_FTD--Cortex_Motor_Medial--C9orf72_neg	0.39	0.07	0.54
NEUME287RK2--CGND-HRA-00072--Female--ALS_FTD--Cerebellum--C9orf72_neg	0.44	0.06	0.50
NEUME287RK2--CGND-HRA-00086--Female--ALS_FTD--Cortex_Motor_Lateral--C9orf72_neg	0.51	0.05	0.44
NEUME287RK2--CGND-HRA-01333--Female--ALS_FTD--Spinal_Cord_Thoracic--C9orf72_neg	0.44	0.07	0.49
NEUMK638LUX--CGND-HRA-00188--Male--ALS--Liver--C9orf72_pos_SOD1_neg_ANXA11_likely_benign	0.53	0.03	0.44
NEUMK638LUX--CGND-HRA-00549--Male--ALS--Cerebellum--C9orf72_pos_SOD1_neg_ANXA11_pos_likely_benign	0.29	0.06	0.65
NEUMK638LUX--CGND-HRA-00550--Male--ALS--Cortex_Frontal--C9orf72_pos_SOD1_neg_ANXA11_pos_likely_benign	0.44	0.07	0.49
NEUMK638LUX--CGND-HRA-00551--Male--ALS--Cortex_Occipital--C9orf72_pos_SOD1_neg_ANXA11_pos_likely_benign	0.35	0.07	0.58
NEUMK638LUX--CGND-HRA-00552--Male--ALS--Spinal_Cord_Thoracic--C9orf72_pos_SOD1_neg_ANXA11_pos_likely_benign	0.59	0.04	0.37
NEUMLI172BXX--CGND-HRA-00197--Female--Non-Neurological_Control--Cerebellum--Unknown	0.41	0.06	0.53
NEUMLI172BXX--CGND-HRA-00660--Female--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.55	0.06	0.40
NEUMLI172BXX--CGND-HRA-00661--Female--Non-Neurological_Control--Cortex_Motor_Lateral--Unknown	0.59	0.05	0.36
NEUMLI172BXX--CGND-HRA-01236--Female--Non-Neurological_Control--Cortex_Frontal--Unknown	0.48	0.06	0.45
NEUMLI172BXX--CGND-HRA-01237--Female--Non-Neurological_Control--Cortex_Occipital--Unknown	0.44	0.07	0.49
NEUMLI172BXX--CGND-HRA-01238--Female--Non-Neurological_Control--Spinal_Cord_Thoracic--Unknown	0.59	0.04	0.37
NEUMP035RP4--CGND-HRA-00204--Male--ALS--Cerebellum--C9orf72_neg	0.29	0.06	0.65
NEUMP035RP4--CGND-HRA-00210--Male--ALS--Cortex_Frontal--C9orf72_neg	0.49	0.06	0.45
NEUMP035RP4--CGND-HRA-00216--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.45	0.07	0.48
NEUMP035RP4--CGND-HRA-00222--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.42	0.06	0.51
NEUMP035RP4--CGND-HRA-00228--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.51	0.06	0.43
NEUMP035RP4--CGND-HRA-00234--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.49	0.06	0.45
NEUMT947ALA--CGND-HRA-00392--Male--ALS--Cerebellum--C9orf72_neg	0.61	0.04	0.35
NEUMT947ALA--CGND-HRA-00393--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.56	0.05	0.39
NEUMT947ALA--CGND-HRA-00394--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.67	0.04	0.29
NEUMT947ALA--CGND-HRA-00395--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.65	0.04	0.31
NEUMT947ALA--CGND-HRA-00396--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.70	0.04	0.26
NEUMT947ALA--CGND-HRA-00397--Male--ALS--Cortex_Frontal--C9orf72_neg	0.61	0.05	0.35
NEUMT947ALA--CGND-HRA-01287--Male--ALS--Cortex_Occipital--C9orf72_neg	0.49	0.06	0.45
NEUMT947ALA--CGND-HRA-01288-2--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.50	0.05	0.45
NEUMV641VYK--CGND-HRA-00410--Male--AD--Cerebellum--Unknown	0.39	0.06	0.55
NEUMV641VYK--CGND-HRA-00411--Male--AD--Cortex_Motor_Medial--Unknown	0.42	0.06	0.53
NEUMV641VYK--CGND-HRA-00412--Male--AD--Cortex_Motor_Lateral--Unknown	0.49	0.06	0.45
NEUMV641VYK--CGND-HRA-00413--Male--AD--Spinal_Cord_Cervical--Unknown	0.67	0.04	0.29
NEUMV641VYK--CGND-HRA-00414--Male--AD--Spinal_Cord_Lumbar--Unknown	0.52	0.05	0.43
NEUMV641VYK--CGND-HRA-00415--Male--AD--Cortex_Frontal--Unknown	0.47	0.06	0.47
NEUMV641VYK--CGND-HRA-01293--Male--AD--Cortex_Occipital--Unknown	0.38	0.07	0.55
NEUMV641VYK--CGND-HRA-01294--Male--AD--Spinal_Cord_Thoracic--Unknown	0.53	0.05	0.42
NEUMY028JH4--CGND-HRA-01352--Female--ALS--Cortex_Occipital--C9orf72_neg	0.49	0.06	0.45

NEUMY028JH4--CGND-HRA-01353--Female--ALS--Cortex_Frontal--C9orf72_neg	0.51	0.06	0.43
NEUMY028JH4--CGND-HRA-01354--Female--ALS--Cerebellum--C9orf72_neg	0.55	0.05	0.40
NEUMY028JH4--CGND-HRA-01355--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.53	0.05	0.41
NEUNE940RZC--CGND-HRA-00398--Male--AD--Cerebellum--Unknown	0.51	0.05	0.44
NEUNE940RZC--CGND-HRA-00399--Male--AD--Cortex_Motor_Medial--Unknown	0.67	0.04	0.28
NEUNE940RZC--CGND-HRA-00400--Male--AD--Cortex_Motor_Lateral--Unknown	0.66	0.05	0.29
NEUNE940RZC--CGND-HRA-00401--Male--AD--Spinal_Cord_Cervical--Unknown	0.65	0.04	0.32
NEUNE940RZC--CGND-HRA-00402--Male--AD--Spinal_Cord_Lumbar--Unknown	0.80	0.03	0.17
NEUNE940RZC--CGND-HRA-00403--Male--AD--Cortex_Frontal--Unknown	0.63	0.04	0.32
NEUNE940RZC--CGND-HRA-01289--Male--AD--Cortex_Occipital--Unknown	0.57	0.05	0.38
NEUNE940RZC--CGND-HRA-01290-2--Male--AD--Spinal_Cord_Thoracic--Unknown	0.69	0.04	0.27
NEUNJ406FRR--CGND-HRA-00270--Female--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.47	0.05	0.48
NEUNJ406FRR--CGND-HRA-00283--Female--Non-Neurological_Control--Spinal_Cord_Lumbar--Unknown	0.63	0.04	0.32
NEUNL548ZBN--CGND-HRA-00244--Male--ALS_FTD--Cortex_Frontal--C9orf72_pos	0.49	0.06	0.45
NEUNL548ZBN--CGND-HRA-00263--Male--ALS_FTD--Spinal_Cord_Cervical--C9orf72_pos	0.64	0.04	0.32
NEUNL548ZBN--CGND-HRA-00276--Male--ALS_FTD--Spinal_Cord_Lumbar--C9orf72_pos	0.58	0.05	0.37
NEUNL548ZBN--CGND-HRA-00286--Male--ALS_FTD--Cortex_Motor_Lateral--C9orf72_pos	0.56	0.05	0.39
NEUNL548ZBN--CGND-HRA-00730--Male--ALS_FTD--Cerebellum--C9orf72_pos	0.46	0.05	0.49
NEUNL974RU6--CGND-HRA-00620--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg	0.49	0.05	0.46
NEUNL974RU6--CGND-HRA-00621--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg	0.53	0.06	0.42
NEUNL974RU6--CGND-HRA-00622--Male--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg	0.51	0.06	0.44
NEUNL974RU6--CGND-HRA-00623--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg	0.60	0.05	0.36
NEUNL974RU6--CGND-HRA-00624--Male--ALS--Cortex_Motor_Unspecified--C9orf72_neg_SOD1_neg	0.62	0.05	0.33
NEUNL974RU6--CGND-HRA-00625--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.57	0.05	0.38
NEUNL974RU6--CGND-HRA-00626--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.62	0.05	0.34
NEUNW210GCW--CGND-HRA-00026--Male--ALS--Cortex_Frontal--C9orf72_neg	0.52	0.05	0.43
NEUNW210GCW--CGND-HRA-00040--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.51	0.05	0.44
NEUNW210GCW--CGND-HRA-00054--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.54	0.05	0.42
NEUNW210GCW--CGND-HRA-00068--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.51	0.05	0.44
NEUNW210GCW--CGND-HRA-00082--Male--ALS--Cerebellum--C9orf72_neg	0.49	0.04	0.46
NEUNW210GCW--CGND-HRA-00096--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.51	0.05	0.43
NEUNW244GF0--CGND-HRA-00349--Female--ALS--Cerebellum--C9orf72_neg	0.48	0.05	0.47
NEUNW244GF0--CGND-HRA-00350--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.63	0.05	0.32
NEUNW244GF0--CGND-HRA-00351--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.70	0.04	0.26
NEUNW244GF0--CGND-HRA-00352--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.63	0.05	0.32
NEUNW244GF0--CGND-HRA-00353--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.61	0.04	0.35
NEUNW244GF0--CGND-HRA-00354--Female--ALS--Cortex_Frontal--C9orf72_neg	0.58	0.05	0.37
NEUNW244GF0--CGND-HRA-00355--Female--ALS--Cortex_Occipital--C9orf72_neg	0.67	0.05	0.28
NEUNW244GF0--CGND-HRA-00356--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.64	0.05	0.32
NEUNY116EZW--CGND-HRA-00713--Female--ALS_NOS--Cerebellum--C9orf72_pos	0.38	0.06	0.56
NEUPK732LNT--CGND-HRA-00246--Female--ALS--Cortex_Frontal--Unknown	0.67	0.05	0.29
NEUPK732LNT--CGND-HRA-00255--Female--ALS--Cortex_Motor_Medial--Unknown	0.54	0.06	0.41
NEUPK732LNT--CGND-HRA-00265--Female--ALS--Spinal_Cord_Cervical--Unknown	0.65	0.04	0.31
NEUPK732LNT--CGND-HRA-00725--Female--ALS--Cerebellum--Unknown	0.35	0.05	0.60
NEUPU334DL1--CGND-HRA-01369--Female--ALS_FTD--Cortex_Frontal--C9orf72_neg	0.53	0.07	0.41
NEUPU334DL1--CGND-HRA-01370--Female--ALS_FTD--Cerebellum--C9orf72_neg	0.48	0.07	0.46
NEUPU334DL1--CGND-HRA-01371--Female--ALS_FTD--Spinal_Cord_Thoracic--C9orf72_neg	0.56	0.05	0.39
NEURD711XCL--CGND-HRA-00242--Female--Pre-fALS--Cortex_Frontal--ANG_pos	0.49	0.06	0.45
NEURD711XCL--CGND-HRA-00251--Female--Pre-fALS--Cortex_Motor_Medial--ANG_pos	0.52	0.06	0.42
NEURD711XCL--CGND-HRA-00261--Female--Pre-fALS--Spinal_Cord_Cervical--ANG_pos	0.63	0.04	0.32

NEURD711XCL--CGND-HRA-00721--Female--Pre-fALS--Cerebellum--ANG_pos	0.43	0.06	0.51
NEURJ387PPV--CGND-HRA-00193--Female--ALS--Cortex_Motor_Unspecified--C9orf72_neg_SOD1_neg	0.46	0.06	0.48
NEURJ387PPV--CGND-HRA-00648--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg	0.66	0.04	0.30
NEURJ387PPV--CGND-HRA-00649--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg	0.57	0.05	0.38
NEURK749WFB--CGND-HRA-00245--Female--ALS--Cortex_Frontal--C9orf72_pos	0.36	0.08	0.57
NEURK749WFB--CGND-HRA-00254--Female--ALS--Cortex_Motor_Medial--C9orf72_pos	0.45	0.06	0.49
NEURK749WFB--CGND-HRA-00264--Female--ALS--Spinal_Cord_Cervical--C9orf72_pos	0.62	0.05	0.34
NEURK749WFB--CGND-HRA-00277--Female--ALS--Spinal_Cord_Lumbar--C9orf72_pos	0.67	0.04	0.29
NEURK749WFB--CGND-HRA-00729--Female--ALS--Cerebellum--C9orf72_pos	0.36	0.06	0.59
NEURN516YR8--CGND-HRA-00720--Female--ALS--Cerebellum--C9orf72_pos	0.37	0.06	0.57
NEURX991BWB--CGND-HRA-00546--Female--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.50	0.06	0.45
NEURX991BWB--CGND-HRA-00547--Female--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.42	0.06	0.52
NEURX991BWB--CGND-HRA-00548--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.61	0.05	0.34
NEURX991BWB--CGND-HRA-00615--Female--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.45	0.06	0.49
NEURX991BWB--CGND-HRA-00616--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.42	0.07	0.51
NEURX991BWB--CGND-HRA-00617-2--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.47	0.05	0.47
NEURX991BWB--CGND-HRA-00618--Female--ALS--Cerebellum--C9orf72_neg_SOD1_neg_DCTN1_pos_likely_benign	0.40	0.06	0.54
NEUTB398FC9--CGND-HRA-00434--Male--ALS--Cerebellum--Unknown	0.27	0.06	0.67
NEUTB398FC9--CGND-HRA-00435--Male--ALS--Cortex_Motor_Medial--Unknown	0.43	0.06	0.51
NEUTB398FC9--CGND-HRA-00436--Male--ALS--Cortex_Motor_Lateral--Unknown	0.49	0.06	0.45
NEUTB398FC9--CGND-HRA-00437--Male--ALS--Spinal_Cord_Cervical--Unknown	0.52	0.05	0.43
NEUTB398FC9--CGND-HRA-00438--Male--ALS--Spinal_Cord_Lumbar--Unknown	0.54	0.07	0.39
NEUTB398FC9--CGND-HRA-00439--Male--ALS--Cortex_Frontal--Unknown	0.57	0.05	0.37
NEUTB398FC9--CGND-HRA-01302--Male--ALS--Spinal_Cord_Thoracic--Unknown	0.54	0.05	0.40
NEUTL441LZ7--CGND-HRA-00319--Male--ALS--Cerebellum--C9orf72_pos	0.28	0.07	0.65
NEUTL441LZ7--CGND-HRA-00320--Male--ALS--Cortex_Motor_Medial--C9orf72_pos	0.42	0.08	0.50
NEUTL441LZ7--CGND-HRA-00321--Male--ALS--Cortex_Motor_Lateral--C9orf72_pos	0.39	0.07	0.54
NEUTL441LZ7--CGND-HRA-00322--Male--ALS--Spinal_Cord_Cervical--C9orf72_pos	0.55	0.06	0.39
NEUTL441LZ7--CGND-HRA-00323--Male--ALS--Cortex_Frontal--C9orf72_pos	0.44	0.07	0.48
NEUTL441LZ7--CGND-HRA-00324--Male--ALS--Cortex_Occipital--C9orf72_pos	0.46	0.07	0.46
NEUTL441LZ7--CGND-HRA-00325--Male--ALS--Spinal_Cord_Thoracic--C9orf72_pos	0.48	0.06	0.46
NEUTP019MY9--CGND-HRA-00357--Female--ALS--Cerebellum--C9orf72_pos	0.40	0.06	0.54
NEUTP019MY9--CGND-HRA-00358--Female--ALS--Cortex_Motor_Medial--C9orf72_pos	0.46	0.06	0.48
NEUTP019MY9--CGND-HRA-00359--Female--ALS--Cortex_Motor_Lateral--C9orf72_pos	0.49	0.05	0.46
NEUTP019MY9--CGND-HRA-00360--Female--ALS--Spinal_Cord_Cervical--C9orf72_pos	0.57	0.05	0.38
NEUTP019MY9--CGND-HRA-00361--Female--ALS--Spinal_Cord_Lumbar--C9orf72_pos	0.62	0.04	0.34
NEUTP019MY9--CGND-HRA-00362--Female--ALS--Cortex_Frontal--C9orf72_pos	0.59	0.05	0.36
NEUTP019MY9--CGND-HRA-00363--Female--ALS--Cortex_Occipital--C9orf72_pos	0.36	0.07	0.57
NEUTP019MY9--CGND-HRA-00364--Female--ALS--Spinal_Cord_Thoracic--C9orf72_pos	0.52	0.05	0.43
NEUTP414KZ2--CGND-HRA-00196--Female--Non-Neurological_Control--Cerebellum--Unknown	0.47	0.06	0.47
NEUTP414KZ2--CGND-HRA-00658--Female--Non-Neurological_Control--Cortex_Motor_Medial--Unknown	0.48	0.07	0.45
NEUTP414KZ2--CGND-HRA-00659--Female--Non-Neurological_Control--Cortex_Motor_Lateral--Unknown	0.55	0.07	0.38
NEUTP414KZ2--CGND-HRA-01234--Female--Non-Neurological_Control--Cortex_Frontal--Unknown	0.46	0.08	0.46
NEUTP414KZ2--CGND-HRA-01235--Female--Non-Neurological_Control--Cortex_Occipital--Unknown	0.51	0.07	0.42
NEUTZ062XC5--CGND-HRA-00195--Male--SBMA--Liver--Unknown	0.64	0.03	0.33
NEUTZ062XC5--CGND-HRA-00653--Male--SBMA--Cerebellum--Unknown	0.41	0.06	0.53
NEUTZ062XC5--CGND-HRA-00654--Male--SBMA--Cortex_Motor_Medial--Unknown	0.49	0.06	0.45
NEUTZ062XC5--CGND-HRA-00655--Male--SBMA--Cortex_Motor_Lateral--Unknown	0.52	0.06	0.42
NEUTZ062XC5--CGND-HRA-00656--Male--SBMA--Spinal_Cord_Cervical--Unknown	0.55	0.05	0.40
NEUTZ062XC5--CGND-HRA-00657--Male--SBMA--Spinal_Cord_Lumbar--Unknown	0.55	0.05	0.40

NEUUE532LFF--CGND-HRA-00241--Male--ALS--Cortex_Frontal--Unknown	0.49	0.07	0.45
NEUUE532LFF--CGND-HRA-00250--Male--ALS--Cortex_Motor_Medial--Unknown	0.53	0.06	0.41
NEUUE532LFF--CGND-HRA-00260--Male--ALS--Spinal_Cord_Cervical--Unknown	0.63	0.04	0.33
NEUUE532LFF--CGND-HRA-00273--Male--ALS--Spinal_Cord_Lumbar--Unknown	0.61	0.04	0.35
NEUUE532LFF--CGND-HRA-00285--Male--ALS--Cortex_Motor_Lateral--Unknown	0.51	0.06	0.42
NEUUE532LFF--CGND-HRA-00723--Male--ALS--Cerebellum--Unknown	0.38	0.06	0.56
NEUUF289NRL--CGND-HRA-01364--Male--ALS--Cortex_Occipital--C9orf72_neg	0.60	0.05	0.35
NEUUF289NRL--CGND-HRA-01365--Male--ALS--Cortex_Frontal--C9orf72_neg	0.63	0.05	0.32
NEUUF289NRL--CGND-HRA-01366--Male--ALS--Cerebellum--C9orf72_neg	0.48	0.05	0.47
NEUUF289NRL--CGND-HRA-01367--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.64	0.04	0.32
NEUUK557CZW--CGND-HRA-01212--Female--ALS_AD--Cortex_Frontal--Unknown	0.60	0.05	0.35
NEUUK557CZW--CGND-HRA-01213--Female--ALS_AD--Cortex_Occipital--Unknown	0.62	0.05	0.33
NEUUTO49NND--CGND-HRA-01228--Female--Non-Neurological_Control--Cortex_Frontal--Unknown	0.58	0.05	0.37
NEUUTO49NND--CGND-HRA-01230--Female--Non-Neurological_Control--Spinal_Cord_Thoracic--Unknown	0.59	0.05	0.36
NEUUW911LWA--CGND-HRA-00538--Male--ALS_FTD--Cerebellum--C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.33	0.06	0.60
NEUUW911LWA--CGND-HRA-00539--Male--ALS_FTD--Cortex_Frontal--C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.47	0.06	0.47
NEUUW911LWA--CGND-HRA-00540--Male--ALS_FTD--Cortex_Occipital--C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.45	0.06	0.49
NEUUW911LWA--CGND-HRA-00607--Male--ALS_FTD--Cortex_Motor_Medial--C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.39	0.07	0.55
NEUUW911LWA--CGND-HRA-00608--Male--ALS_FTD--Cortex_Motor_Lateral--C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.35	0.07	0.58
NEUUW911LWA--CGND-HRA-00609--Male--ALS_FTD--Spinal_Cord_Cervical--C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.55	0.05	0.40
NEUUW911LWA--CGND-HRA-00610--Male--ALS_FTD--Spinal_Cord_Lumbar--C9orf72_pos_SOD1_neg_NEFH_pos_VUS	0.61	0.04	0.34
NEUVB305VU7--CGND-HRA-00194--Male--ALS_AD_CTE--Cerebellum--SOD1_neg	0.41	0.07	0.53
NEUVB305VU7--CGND-HRA-00650--Male--ALS_AD_CTE--Cortex_Motor_Medial--SOD1_neg	0.53	0.07	0.40
NEUVB305VU7--CGND-HRA-00651--Male--ALS_AD_CTE--Cortex_Motor_Lateral--SOD1_neg	0.44	0.08	0.48
NEUVB305VU7--CGND-HRA-00652--Male--ALS_AD_CTE--Spinal_Cord_Cervical--SOD1_neg	0.54	0.05	0.41
NEUVB305VU7--CGND-HRA-01231--Male--ALS_AD_CTE--Cortex_Frontal--SOD1_neg	0.61	0.06	0.34
NEUVB305VU7--CGND-HRA-01232--Male--ALS_AD_CTE--Cortex_Occipital--SOD1_neg	0.50	0.07	0.42
NEUVB305VU7--CGND-HRA-01233--Male--ALS_AD_CTE--Spinal_Cord_Thoracic--SOD1_neg	0.63	0.05	0.32
NEUVU845ZAB--CGND-HRA-00744--Female--ALS--Cell_Line_iPS--SOD1_pos	0.57	0.06	0.36
NEUVU845ZAB--CGND-HRA-00745--Female--ALS--Cell_Line_Motor_Neuron--SOD1_pos	0.58	0.04	0.38
NEUVZ387WGH--CGND-HRA-00326--Female--ALS_AD--Cerebellum--C9orf72_neg	0.31	0.08	0.61
NEUVZ387WGH--CGND-HRA-00328--Female--ALS_AD--Cortex_Motor_Lateral--C9orf72_neg	0.47	0.07	0.46
NEUVZ387WGH--CGND-HRA-00330--Female--ALS_AD--Cortex_Frontal--C9orf72_neg	0.44	0.08	0.48
NEUVZ387WGH--CGND-HRA-00331--Female--ALS_AD--Cortex_Occipital--C9orf72_neg	0.49	0.08	0.43
NEUWC334RTZ--CGND-HRA-01372--Male--ALS_CTE--Cerebellum--Unknown	0.36	0.06	0.58
NEUWC334RTZ--CGND-HRA-01373--Male--ALS_CTE--Cortex_Frontal--Unknown	0.41	0.07	0.51
NEUWD570BTK--CGND-HRA-01378--Male--Non-Neurological_Control--Cerebellum--Unknown	0.37	0.06	0.58
NEUWD570BTK--CGND-HRA-01379--Male--Non-Neurological_Control--Cortex_Frontal--Unknown	0.41	0.07	0.52
NEUWG523WRV--CGND-HRA-00640--Male--ALS--Cortex_Motor_Unspecified--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.51	0.05	0.44
NEUWG523WRV--CGND-HRA-00641--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.56	0.05	0.40
NEUWG523WRV--CGND-HRA-00642--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.68	0.04	0.29
NEUWG523WRV--CGND-HRA-01222--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.56	0.05	0.39
NEUWG523WRV--CGND-HRA-01223--Male--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.53	0.05	0.42
NEUWG523WRV--CGND-HRA-01224--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg_SOD1_neg_SETX_pos_CCNF_likely_benign	0.66	0.04	0.30
NEUWL993GU2--CGND-HRA-00676--Male--ALS--Cerebellum--SOD1_neg_SETX_likely_benign_FIG4_VUS	0.42	0.06	0.52
NEUWL993GU2--CGND-HRA-01248--Male--ALS--Cortex_Frontal--SOD1_neg_SETX_likely_benign_FIG4_VUS	0.44	0.07	0.49
NEUWL993GU2--CGND-HRA-01250--Male--ALS--Spinal_Cord_Thoracic--SOD1_neg_SETX_likely_benign_FIG4_VUS	0.60	0.04	0.36
NEUWP285RM6--CGND-HRA-00416--Female--ALS_AD--Cerebellum--Unknown	0.36	0.06	0.59
NEUWP285RM6--CGND-HRA-00417--Female--ALS_AD--Cortex_Motor_Medial--Unknown	0.53	0.06	0.41
NEUWP285RM6--CGND-HRA-00418--Female--ALS_AD--Cortex_Motor_Lateral--Unknown	0.44	0.07	0.49

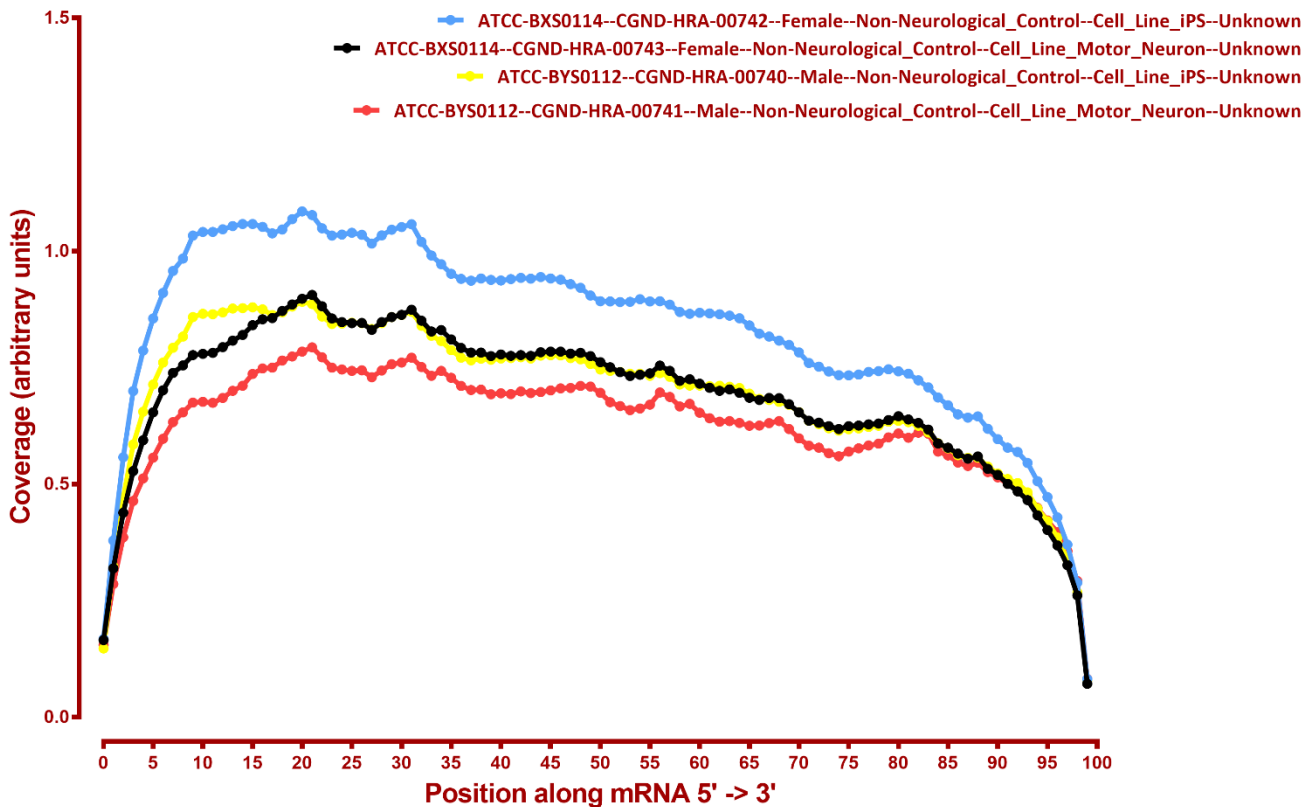
NEUWP285RM6--CGND-HRA-00419--Female--ALS_AD--Spinal_Cord_Cervical--Unknown	0.66	0.04	0.30
NEUWP285RM6--CGND-HRA-00420--Female--ALS_AD--Spinal_Cord_Lumbar--Unknown	0.71	0.04	0.26
NEUWP285RM6--CGND-HRA-00421--Female--ALS_AD--Cortex_Frontal--Unknown	0.59	0.05	0.36
NEUWP285RM6--CGND-HRA-01295--Female--ALS_AD--Cortex_Occipital--Unknown	0.42	0.07	0.51
NEUWP285RM6--CGND-HRA-01296--Female--ALS_AD--Spinal_Cord_Thoracic--Unknown	0.58	0.05	0.37
NEUWX086DGZ--CGND-HRA-00019--Female--ALS--Cortex_Frontal--C9orf72_neg	0.50	0.06	0.44
NEUWX086DGZ--CGND-HRA-00047--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.64	0.04	0.32
NEUWX086DGZ--CGND-HRA-00061--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.54	0.06	0.41
NEUWX086DGZ--CGND-HRA-00075--Female--ALS--Cerebellum--C9orf72_neg	0.37	0.06	0.57
NEUWX086DGZ--CGND-HRA-00089-2--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.46	0.05	0.48
NEUWX086DGZ--CGND-HRA-01338--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.48	0.05	0.46
NEUWX086DGZ--CGND-HRA-01339--Female--ALS--Cortex_Occipital--C9orf72_neg	0.52	0.06	0.43
NEUWZ373ZHA--CGND-HRA-00311--Female--ALS--Cerebellum--C9orf72_neg	0.57	0.05	0.38
NEUWZ373ZHA--CGND-HRA-00312--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.59	0.05	0.36
NEUWZ373ZHA--CGND-HRA-00313--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.61	0.05	0.34
NEUWZ373ZHA--CGND-HRA-00314--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.64	0.04	0.32
NEUWZ373ZHA--CGND-HRA-00315--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.65	0.04	0.31
NEUWZ373ZHA--CGND-HRA-00316--Female--ALS--Cortex_Frontal--C9orf72_neg	0.61	0.05	0.34
NEUWZ373ZHA--CGND-HRA-00317--Female--ALS--Cortex_Occipital--C9orf72_neg	0.62	0.04	0.33
NEUWZ373ZHA--CGND-HRA-00318--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.64	0.04	0.32
NEUXD817GGZ--CGND-HRA-00718--Male--ALS--Cerebellum--C9orf72_pos	0.38	0.06	0.56
NEUXO99CKK--CGND-HRA-00269--Female--Non-Neurological_Control--Spinal_Cord_Cervical--Unknown	0.50	0.06	0.45
NEUXO99CKK--CGND-HRA-00282--Female--Non-Neurological_Control--Spinal_Cord_Lumbar--Unknown	0.48	0.06	0.46
NEUXR145UBL--CGND-HRA-01356--Male--ALS_FTD--Cortex_Occipital--C9orf72_neg	0.64	0.05	0.32
NEUXR145UBL--CGND-HRA-01357--Male--ALS_FTD--Cortex_Frontal--C9orf72_neg	0.60	0.05	0.35
NEUXR145UBL--CGND-HRA-01358--Male--ALS_FTD--Cerebellum--C9orf72_neg	0.53	0.05	0.42
NEUXR145UBL--CGND-HRA-01359--Male--ALS_FTD--Spinal_Cord_Thoracic--C9orf72_neg	0.63	0.04	0.33
NEUXT258BD4--CGND-HRA-00239--Female--ALS--Cortex_Frontal--C9orf72_pos	0.46	0.06	0.48
NEUXT258BD4--CGND-HRA-00258--Female--ALS--Spinal_Cord_Cervical--C9orf72_pos	0.61	0.04	0.35
NEUXT258BD4--CGND-HRA-00288--Female--ALS--Cortex_Motor_Unspecified--C9orf72_pos	0.52	0.06	0.42
NEUXT258BD4--CGND-HRA-00728--Female--ALS--Cerebellum--C9orf72_pos	0.47	0.05	0.47
NEUXT979EZV--CGND-HRA-00022--Male--ALS_LB_FTD--Cortex_Frontal--C9orf72_neg	0.55	0.05	0.39
NEUXT979EZV--CGND-HRA-00036--Male--ALS_LB_FTD--Spinal_Cord_Lumbar--C9orf72_neg	0.50	0.05	0.46
NEUXT979EZV--CGND-HRA-00050--Male--ALS_LB_FTD--Spinal_Cord_Cervical--C9orf72_neg	0.51	0.05	0.44
NEUXT979EZV--CGND-HRA-00064--Male--ALS_LB_FTD--Cortex_Motor_Medial--C9orf72_neg	0.48	0.06	0.46
NEUXT979EZV--CGND-HRA-00078--Male--ALS_LB_FTD--Cerebellum--C9orf72_neg	0.36	0.06	0.58
NEUXT979EZV--CGND-HRA-00092--Male--ALS_LB_FTD--Cortex_Motor_Lateral--C9orf72_neg	0.50	0.06	0.44
NEUXT979EZV--CGND-HRA-01344--Male--ALS_LB_FTD--Spinal_Cord_Thoracic--C9orf72_neg	0.64	0.04	0.32
NEUXT979EZV--CGND-HRA-01345--Male--ALS_LB_FTD--Cortex_Occipital--C9orf72_neg	0.54	0.06	0.40
NEUXY076JMB--CGND-HRA-00198--Female--ALS--Liver--SOD1_neg_FIG4_pos_SETX	0.74	0.03	0.23
NEUXY076JMB--CGND-HRA-00662--Female--ALS--Cerebellum--SOD1_neg_FIG4_pos_SETX_VUS	0.47	0.05	0.48
NEUXY076JMB--CGND-HRA-00663--Female--ALS--Cortex_Motor_Medial--SOD1_neg_FIG4_pos_SETX_VUS	0.56	0.05	0.39
NEUXY076JMB--CGND-HRA-00664--Female--ALS--Cortex_Motor_Lateral--SOD1_neg_FIG4_pos_SETX_VUS	0.56	0.05	0.38
NEUXY076JMB--CGND-HRA-00665--Female--ALS--Spinal_Cord_Cervical--SOD1_neg_FIG4_pos_SETX_VUS	0.52	0.05	0.43
NEUXY076JMB--CGND-HRA-00666--Female--ALS--Spinal_Cord_Lumbar--SOD1_neg_FIG4_pos_SETX_VUS	0.48	0.06	0.47
NEUXY076JMB--CGND-HRA-01239--Female--ALS--Cortex_Frontal--SOD1_neg_FIG4_pos_SETX_VUS	0.55	0.06	0.40
NEUXY076JMB--CGND-HRA-01240--Female--ALS--Cortex_Occipital--SOD1_neg_FIG4_pos_SETX_VUS	0.55	0.06	0.40
NEUXY076JMB--CGND-HRA-01241--Female--ALS--Spinal_Cord_Thoracic--SOD1_neg_FIG4_pos_SETX_VUS	0.60	0.05	0.36
NEUYB686REL--CGND-HRA-00023--Male--ALS--Cortex_Frontal--C9orf72_neg	0.42	0.07	0.51
NEUYB686REL--CGND-HRA-00037--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.60	0.04	0.36

NEUYB686REL--CGND-HRA-00051--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.56	0.05	0.39
NEUYB686REL--CGND-HRA-00065--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.37	0.07	0.55
NEUYB686REL--CGND-HRA-00079--Male--ALS--Cerebellum--C9orf72_neg	0.32	0.07	0.61
NEUYB686REL--CGND-HRA-00093--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.43	0.07	0.50
NEUYV496XLP--CGND-HRA-00014-2--Male--ALS_FTD_TM--Cortex_Frontal--C9orf72_neg	0.44	0.06	0.50
NEUYV496XLP--CGND-HRA-00028--Male--ALS_FTD_TM--Spinal_Cord_Lumbar--C9orf72_neg	0.50	0.05	0.45
NEUYV496XLP--CGND-HRA-00042--Male--ALS_FTD_TM--Spinal_Cord_Cervical--C9orf72_neg	0.53	0.05	0.42
NEUYV496XLP--CGND-HRA-00056--Male--ALS_FTD_TM--Cortex_Motor_Medial--C9orf72_neg	0.44	0.06	0.50
NEUYV496XLP--CGND-HRA-00070--Male--ALS_FTD_TM--Cerebellum--C9orf72_neg	0.32	0.06	0.62
NEUYV496XLP--CGND-HRA-00084-2--Male--ALS_FTD_TM--Cortex_Motor_Lateral--C9orf72_neg	0.43	0.06	0.51
NEUYV496XLP--CGND-HRA-01329--Male--ALS_FTD_TM--Cortex_Occipital--C9orf72_neg	0.44	0.07	0.50
NEUYV496XLP--CGND-HRA-01330--Male--ALS_FTD_TM--Spinal_Cord_Thoracic--C9orf72_neg	0.55	0.05	0.40
NEUYX020CB0--CGND-HRA-00386--Male--ALS_AD--Cerebellum--C9orf72_neg	0.41	0.06	0.54
NEUYX020CB0--CGND-HRA-00387--Male--ALS_AD--Cortex_Motor_Medial--C9orf72_neg	0.49	0.05	0.46
NEUYX020CB0--CGND-HRA-00388--Male--ALS_AD--Cortex_Motor_Lateral--C9orf72_neg	0.49	0.05	0.46
NEUYX020CB0--CGND-HRA-00389--Male--ALS_AD--Spinal_Cord_Cervical--C9orf72_neg	0.63	0.04	0.33
NEUYX020CB0--CGND-HRA-00390--Male--ALS_AD--Spinal_Cord_Lumbar--C9orf72_neg	0.69	0.04	0.28
NEUYX020CB0--CGND-HRA-00391--Male--ALS_AD--Cortex_Frontal--C9orf72_neg	0.45	0.06	0.48
NEUYX020CB0--CGND-HRA-01285--Male--ALS_AD--Cortex_Occipital--C9orf72_neg	0.38	0.08	0.55
NEUYX020CB0--CGND-HRA-01286--Male--ALS_AD--Spinal_Cord_Thoracic--C9orf72_neg	0.59	0.05	0.36
NEUY221HZA--CGND-HRA-00240--Male--ALS--Cortex_Frontal--Unknown	0.45	0.06	0.49
NEUY221HZA--CGND-HRA-00249--Male--ALS--Cortex_Motor_Medial--Unknown	0.56	0.05	0.39
NEUY221HZA--CGND-HRA-00259--Male--ALS--Spinal_Cord_Cervical--Unknown	0.57	0.05	0.38
NEUY221HZA--CGND-HRA-00272--Male--ALS--Spinal_Cord_Lumbar--Unknown	0.50	0.05	0.44
NEUY221HZA--CGND-HRA-00284--Male--ALS--Cortex_Motor_Lateral--Unknown	0.41	0.06	0.53
NEUY221HZA--CGND-HRA-00724--Male--ALS--Cerebellum--Unknown	0.47	0.06	0.47
NEUZB953VCD--CGND-HRA-00598--Female--ALS--Cerebellum--C9orf72_neg	0.30	0.06	0.64
NEUZB953VCD--CGND-HRA-00599--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.45	0.06	0.49
NEUZB953VCD--CGND-HRA-00600--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.41	0.07	0.52
NEUZB953VCD--CGND-HRA-00601--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.62	0.04	0.34
NEUZB953VCD--CGND-HRA-01263--Female--ALS--Cortex_Frontal--C9orf72_neg	0.57	0.04	0.39
NEUZB953VCD--CGND-HRA-01264--Female--ALS--Cortex_Occipital--C9orf72_neg	0.38	0.07	0.56
NEUZB953VCD--CGND-HRA-01265--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.64	0.04	0.32
NEUZK186ZK4--CGND-HRA-00202--Female--ALS--Cerebellum--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.30	0.07	0.63
NEUZK186ZK4--CGND-HRA-00680--Female--ALS--Cortex_Motor_Medial--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.46	0.07	0.47
NEUZK186ZK4--CGND-HRA-00681--Female--ALS--Cortex_Motor_Lateral--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.44	0.07	0.49
NEUZK186ZK4--CGND-HRA-01251--Female--ALS--Cortex_Frontal--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.46	0.07	0.47
NEUZK186ZK4--CGND-HRA-01253--Female--ALS--Spinal_Cord_Thoracic--SOD1_neg_UBQLN2_pos_SPG11_NEK1_ANG	0.59	0.05	0.36
NEUZU200WEQ--CGND-HRA-00015--Male--ALS--Cortex_Frontal--C9orf72_neg	0.47	0.06	0.47
NEUZU200WEQ--CGND-HRA-00029--Male--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.46	0.06	0.48
NEUZU200WEQ--CGND-HRA-00043--Male--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.45	0.06	0.50
NEUZU200WEQ--CGND-HRA-00057--Male--ALS--Cortex_Motor_Medial--C9orf72_neg	0.40	0.07	0.53
NEUZU200WEQ--CGND-HRA-00071--Male--ALS--Cerebellum--C9orf72_neg	0.39	0.06	0.55
NEUZU200WEQ--CGND-HRA-00085--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.44	0.06	0.50
NEUZU200WEQ--CGND-HRA-01331--Male--ALS--Cortex_Occipital--C9orf72_neg	0.52	0.06	0.43
NEUZU200WEQ--CGND-HRA-01332--Male--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.45	0.06	0.49
NEUZV62ZHF--CGND-HRA-00636--Male--ALS--Cerebellum--C9orf72_neg_SOD1_neg_SBMA_neg	0.37	0.06	0.57
NEUZV62ZHF--CGND-HRA-00637--Male--ALS--Cortex_Motor_Medial--C9orf72_neg_SOD1_neg_SBMA_neg	0.46	0.07	0.47
NEUZV62ZHF--CGND-HRA-00638--Male--ALS--Cortex_Motor_Lateral--C9orf72_neg_SOD1_neg_SBMA_neg	0.42	0.07	0.51
NEUZV62ZHF--CGND-HRA-01219--Male--ALS--Cortex_Frontal--C9orf72_neg_SOD1_neg_SBMA_neg	0.47	0.07	0.46

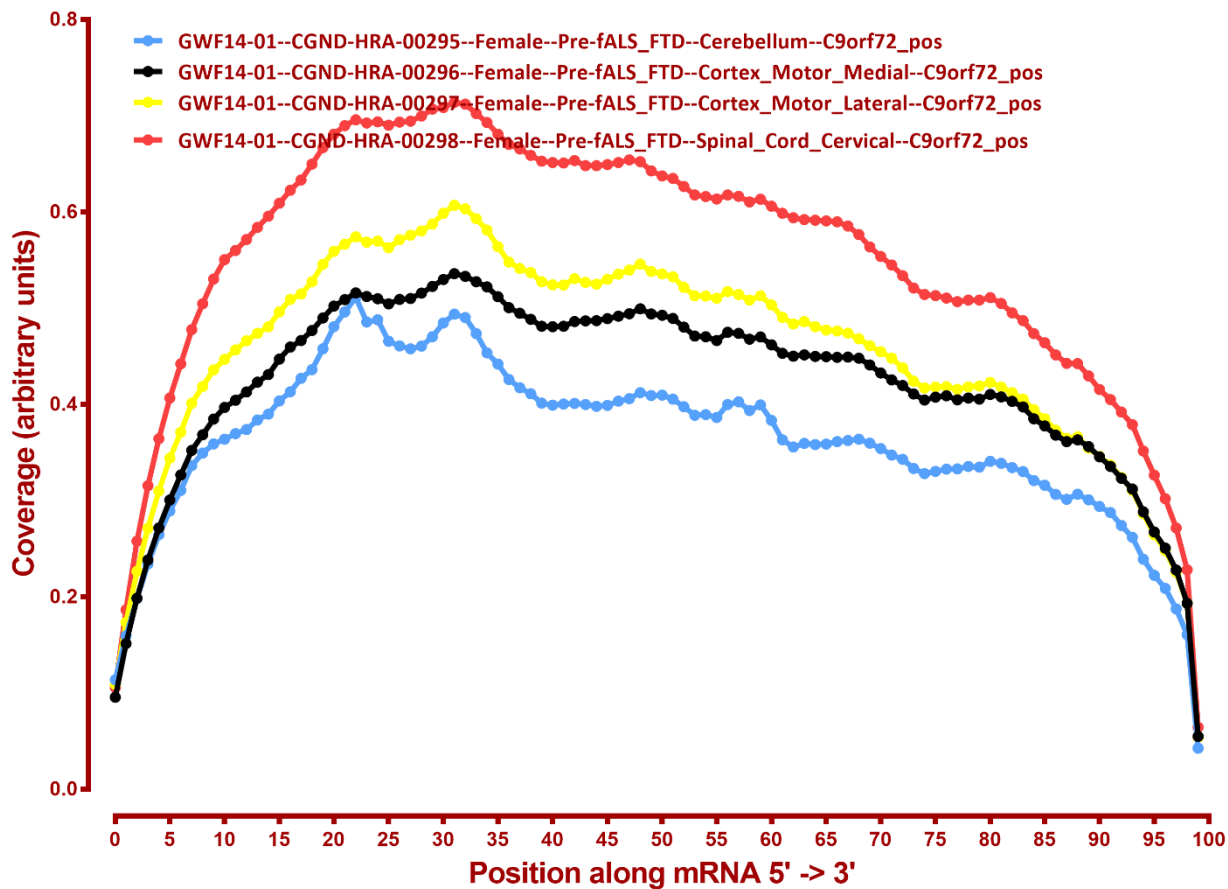
NEUZV622ZHF--CGND-HRA-01220--Male--ALS--Cortex_Occipital--C9orf72_neg_SOD1_neg_SBMA_neg	0.52	0.06	0.42
NEUX073BDK--CGND-HRA-00372--Female--ALS--Cerebellum--C9orf72_neg	0.52	0.05	0.43
NEUX073BDK--CGND-HRA-00373--Female--ALS--Cortex_Motor_Medial--C9orf72_neg	0.61	0.05	0.34
NEUX073BDK--CGND-HRA-00374--Female--ALS--Cortex_Motor_Lateral--C9orf72_neg	0.66	0.05	0.29
NEUX073BDK--CGND-HRA-00375--Female--ALS--Spinal_Cord_Cervical--C9orf72_neg	0.58	0.05	0.37
NEUX073BDK--CGND-HRA-00376--Female--ALS--Spinal_Cord_Lumbar--C9orf72_neg	0.73	0.04	0.24
NEUX073BDK--CGND-HRA-00377--Female--ALS--Cortex_Frontal--C9orf72_neg	0.63	0.05	0.32
NEUX073BDK--CGND-HRA-00378--Female--ALS--Cortex_Occipital--C9orf72_neg	0.61	0.05	0.33
NEUX073BDK--CGND-HRA-00379--Female--ALS--Spinal_Cord_Thoracic--C9orf72_neg	0.61	0.05	0.34

# READ COVERAGE (SOME SAMPLES)

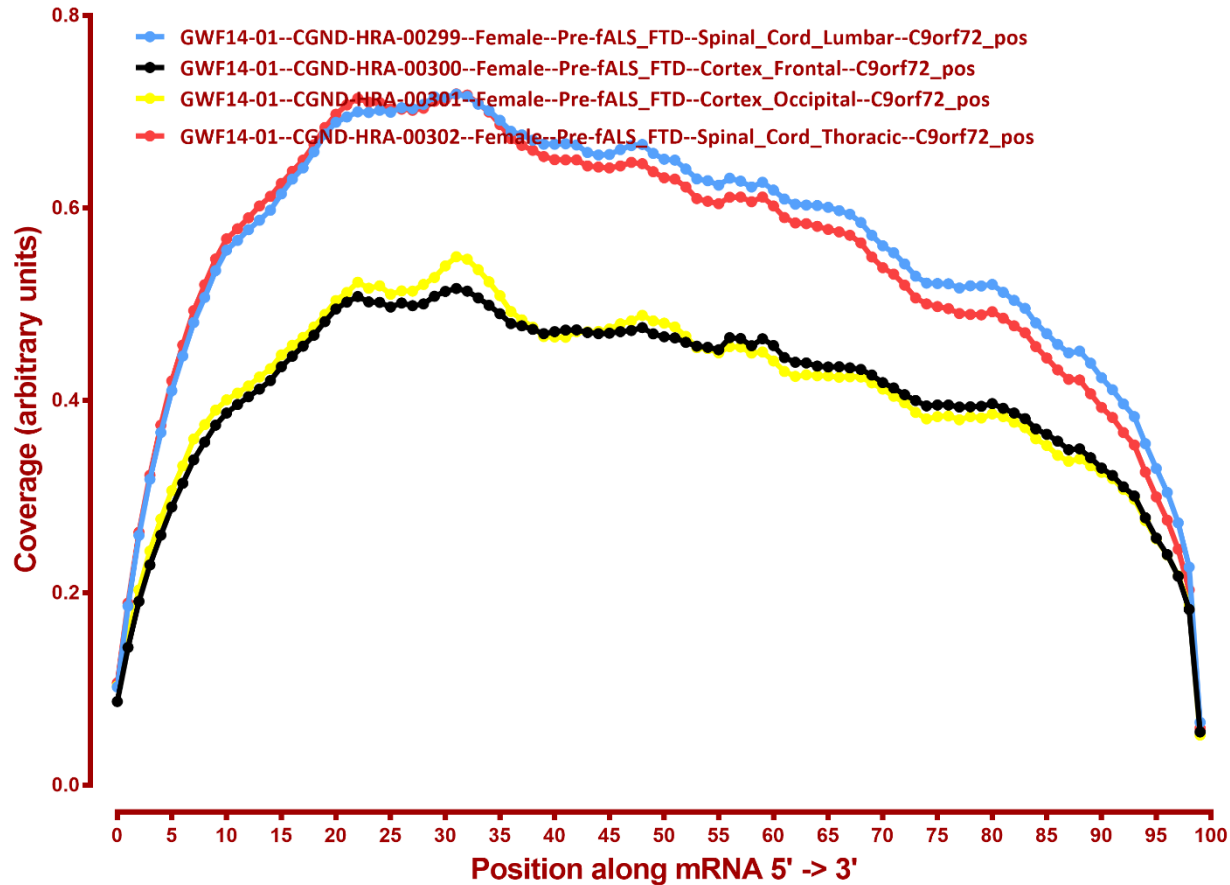
## Coverage of genes; >1000bp



## Coverage of genes; >1000bp

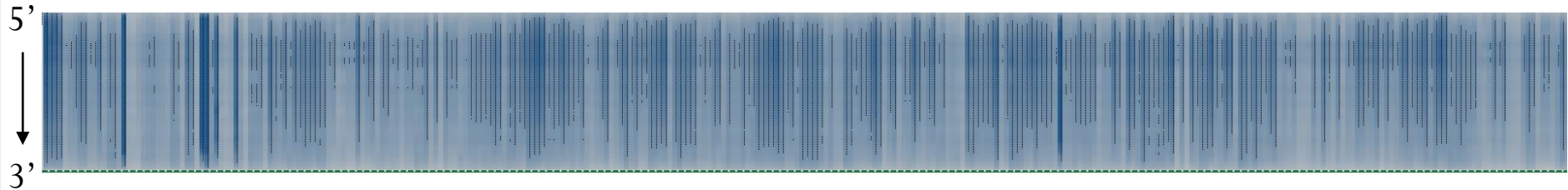


## Coverage of genes; >1000bp

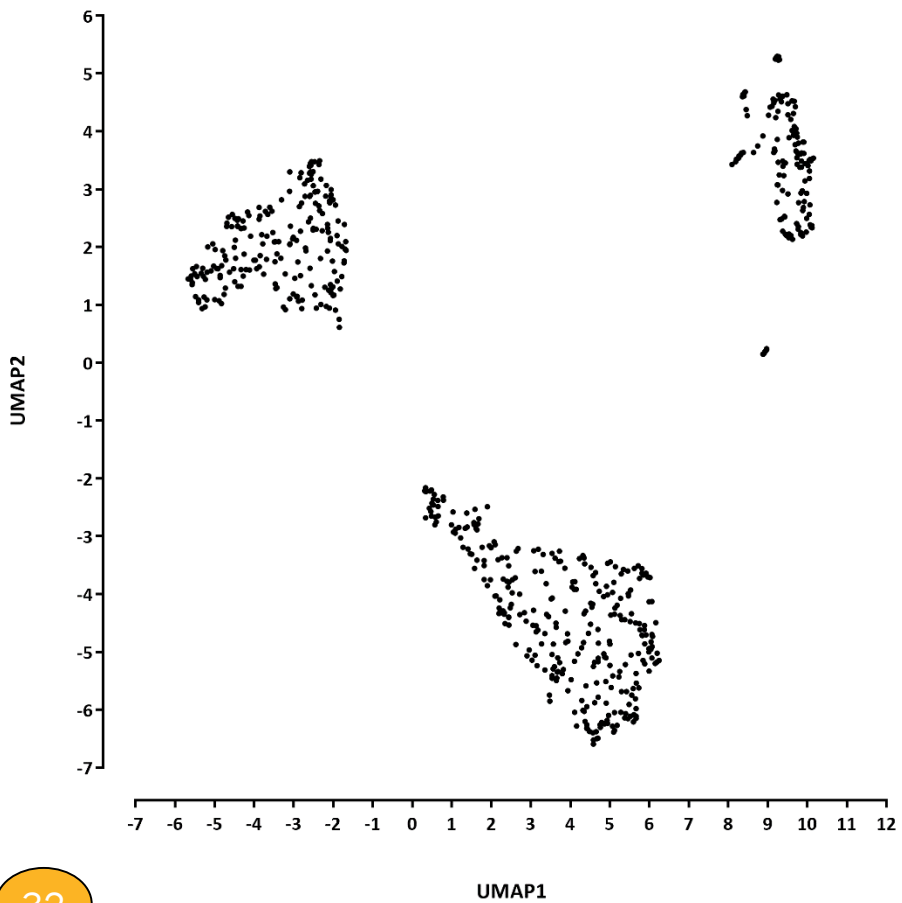


There aren't really any bad samples, which is good

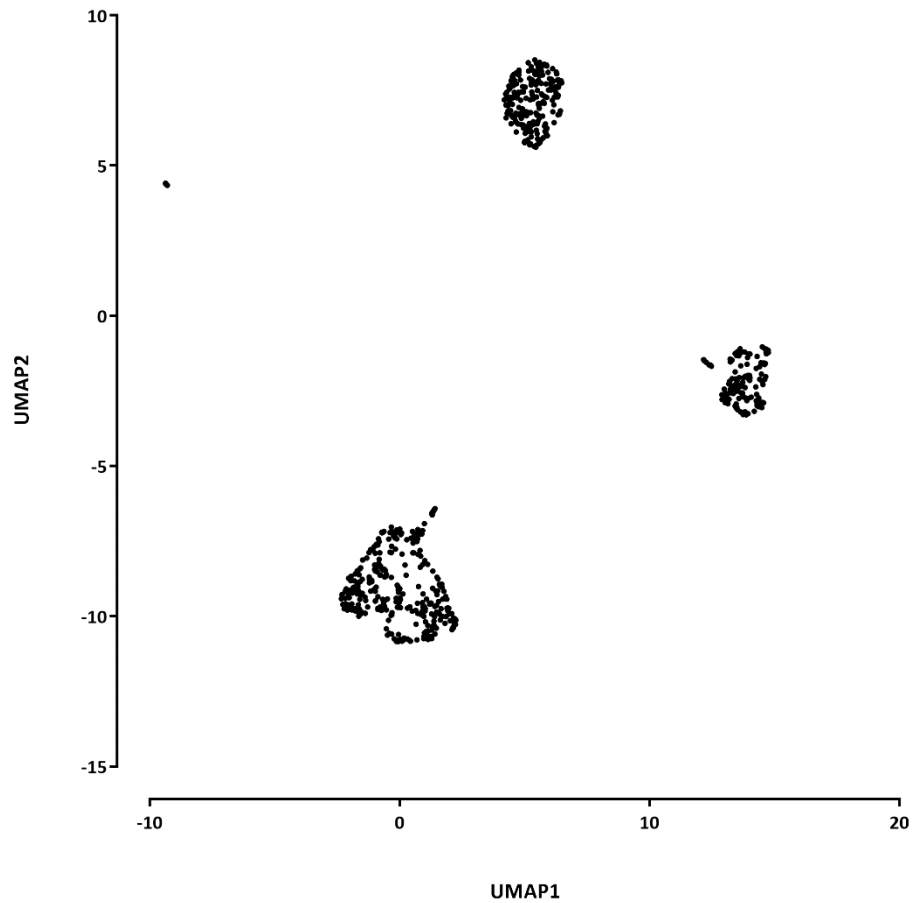
Here is a heatmap of the whole dataset:



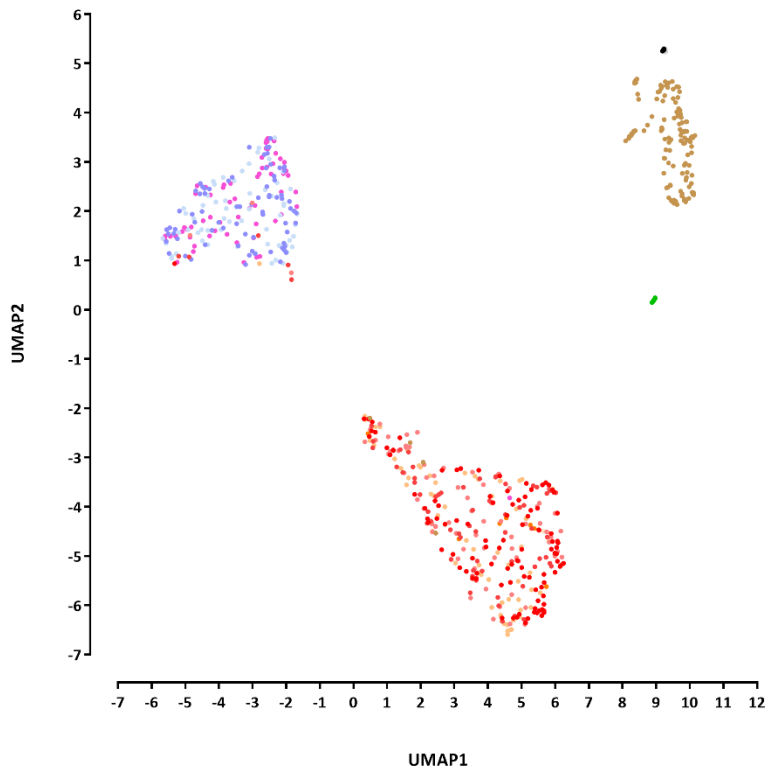
UMAP



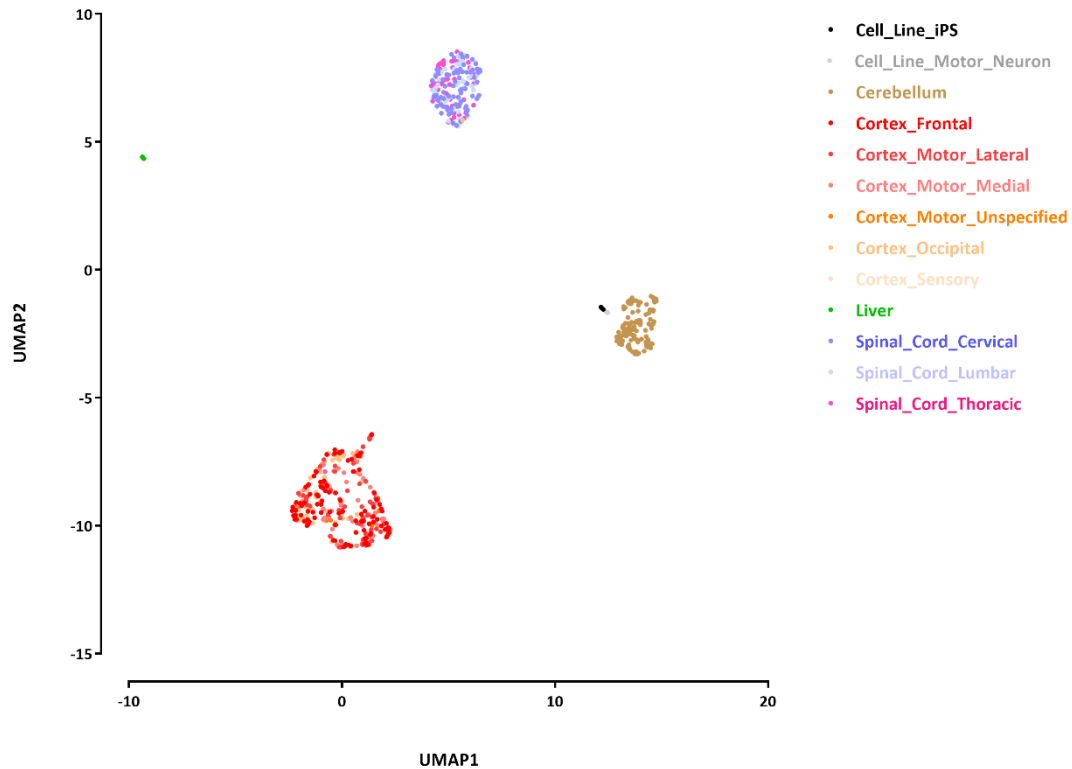
UMAP



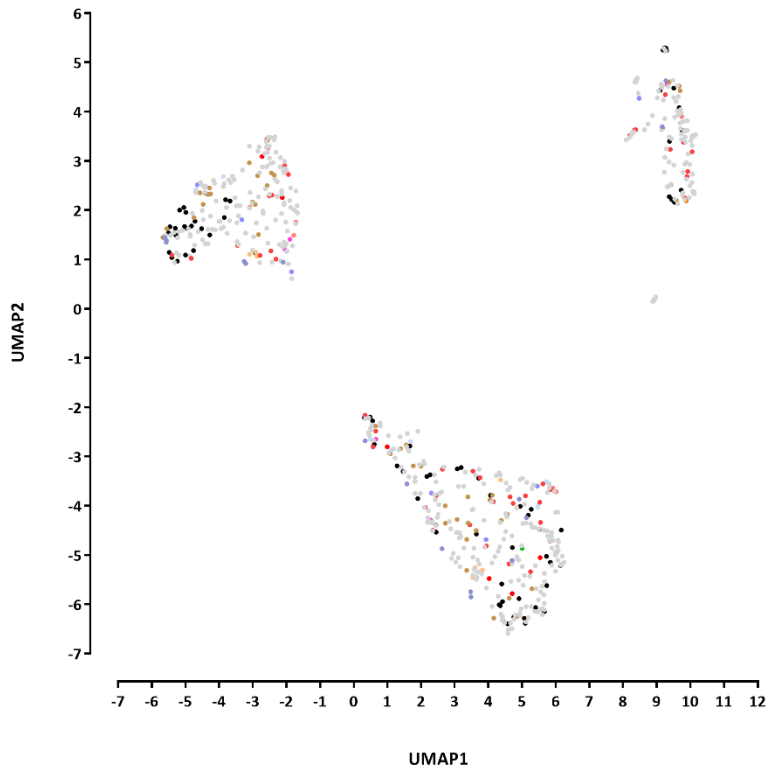
UMAP cell types



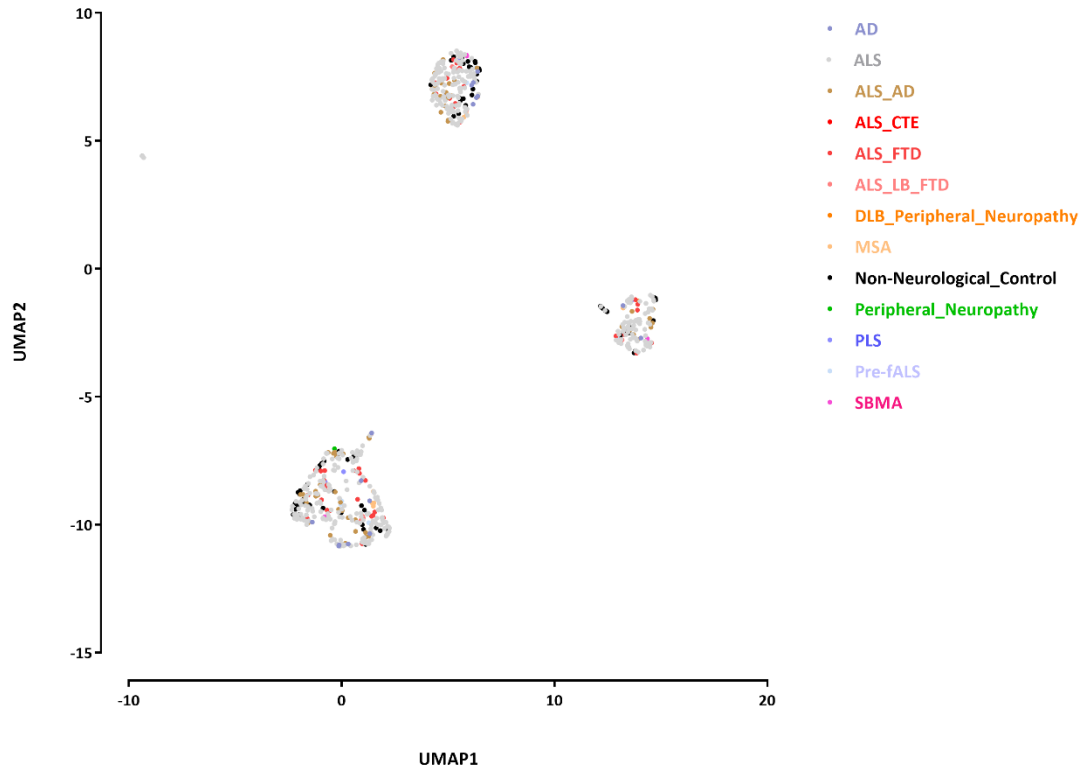
UMAP cell types



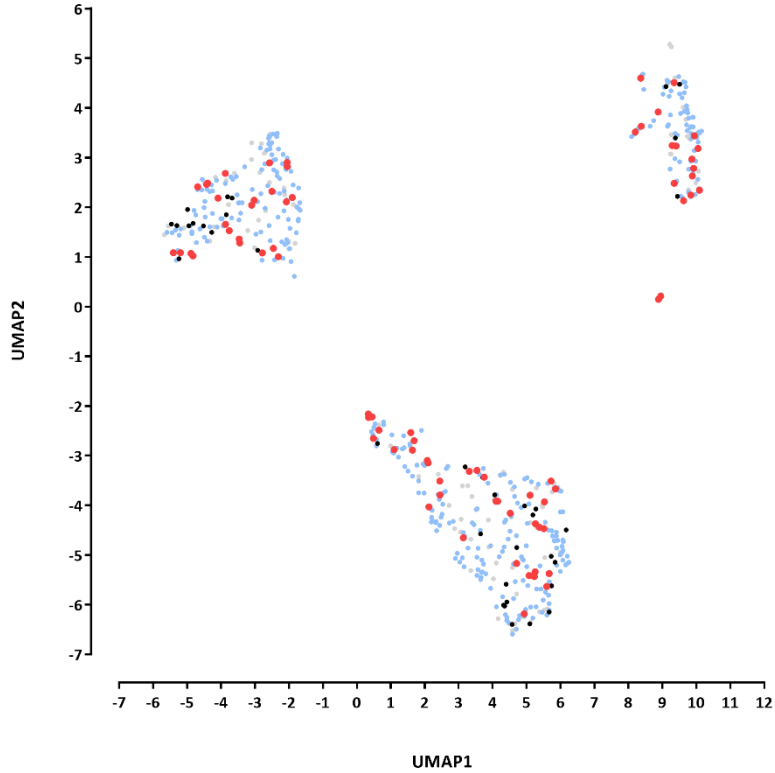
UMAP disease



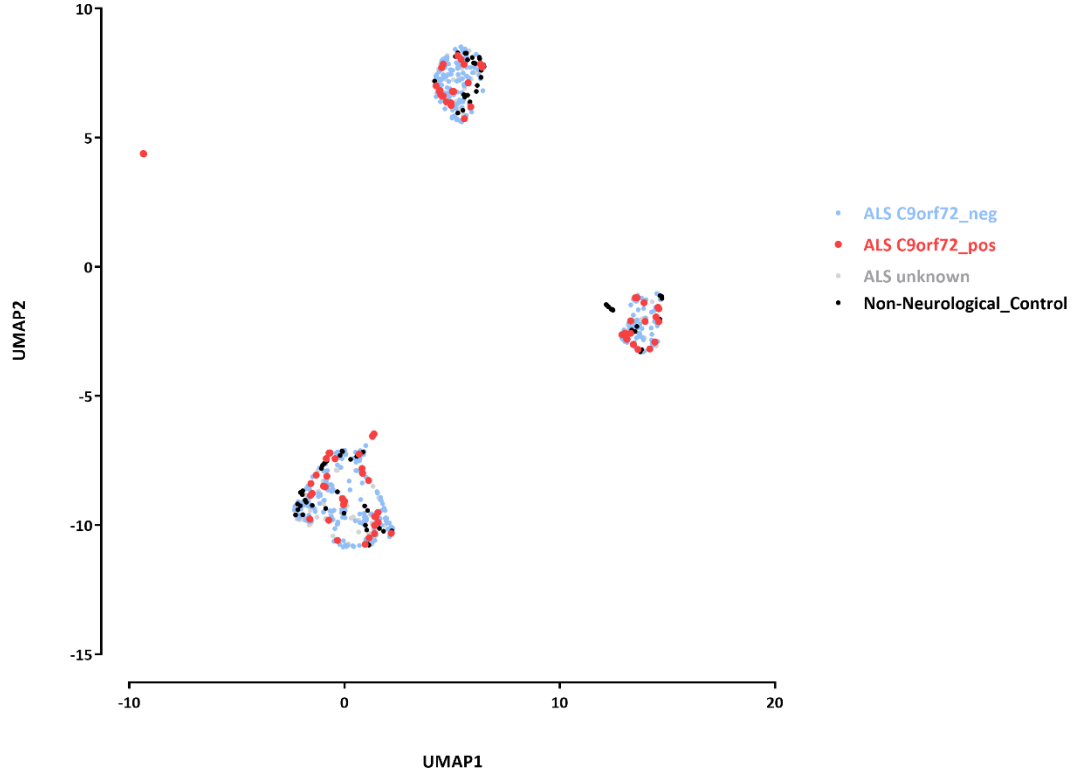
UMAP disease



UMAP C9orf72



UMAP C9orf72



# DESEQ RESULTS

Notes:

1. To narrow the conditions space, I have ignored other additional mutations -- SOD1, etc. – but have kept those separate if there was no C9orf72 mutation but a mutation in a different gene. Will redo with a more complex matrix design if necessary and with the additional samples
2. I have not lumped all ALS variations together, but only ran analysis between the pure ALS samples
3. It takes forever to run on the full 653-sample matrix, so I have run it on individual pairwise matrices

all genes

A	B	p-adj	
		up in B vs A	down in B vs A
ALS--Cerebellum--C9orf72_neg	ALS--Cerebellum--C9orf72_pos	16	1
ALS--Cortex_Frontal--C9orf72_neg	ALS--Cortex_Frontal--C9orf72_pos	5	1
ALS--Cortex_Motor_Lateral--C9orf72_neg	ALS--Cortex_Motor_Lateral--C9orf72_pos	0	0
ALS--Cortex_Motor_Medial--C9orf72_neg	ALS--Cortex_Motor_Medial--C9orf72_pos	89	68
ALS--Cortex_Occipital--C9orf72_neg	ALS--Cortex_Occipital--C9orf72_pos	988	1,180
ALS--Liver--C9orf72_neg	ALS--Liver--C9orf72_pos	1	2
ALS--Spinal_Cord_Cervical--C9orf72_neg	ALS--Spinal_Cord_Cervical--C9orf72_pos	3	0
ALS--Spinal_Cord_Lumbar--C9orf72_neg	ALS--Spinal_Cord_Lumbar--C9orf72_pos	122	33
ALS--Spinal_Cord_Thoracic--C9orf72_neg	ALS--Spinal_Cord_Thoracic--C9orf72_pos	0	0

<b>BBC3</b>						
#	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Cerebellum	148.68	-0.06	0.126746	-0.50678	6.12E-01	0.925915
Cortex_Frontal	118.73	0.03	0.13778	0.223127	8.23E-01	0.982128
Cortex_Motor_Lateral	85.85	0.26	0.183971	1.400862	1.61E-01	0.937896
Cortex_Motor_Medial	88.12	0.30	0.235441	1.273976	2.03E-01	0.482623
Cortex_Occipital	95.96	0.04	0.233426	0.151465	8.80E-01	9.48E-01
Liver	72.34	-0.33	0.331889	-0.9807	3.27E-01	0.999968
Spinal_Cord_Cervical	94.73	-0.05	0.167597	-0.27071	7.87E-01	0.997691
Spinal_Cord_Lumbar	99.38	-0.38	0.272373	-1.40225	1.61E-01	0.619453
Spinal_Cord_Thoracic	113.33	-0.04	0.202335	-0.19584	8.45E-01	0.997226

<b>TP53</b>						
#	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Cerebellum	75.52	-0.21	0.150164	-1.38355	1.66E-01	0.649791
Cortex_Frontal	160.40	0.00	0.167319	0.007656	9.94E-01	0.998027
Cortex_Motor_Lateral	171.36	-0.03	0.22611	-0.14263	8.87E-01	0.99571
Cortex_Motor_Medial	177.16	-0.09	0.273906	-0.3247	7.45E-01	0.884541
Cortex_Occipital	140.33	0.11	0.271219	0.398877	6.90E-01	0.848963
Liver	393.12	0.26	0.314987	0.838385	4.02E-01	0.999968
Spinal_Cord_Cervical	404.30	0.14	0.157239	0.899172	3.69E-01	0.997691
Spinal_Cord_Lumbar	421.47	0.09	0.215076	0.418959	6.75E-01	0.910393
Spinal_Cord_Thoracic	424.04	0.02	0.189932	0.09651	9.23E-01	0.997226

# ALS--Cerebellum

down  
up

#	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
★ C9orf72	1995.43	0.70	0.1261	5.590735	2.26E-08	0.000227
BOK	490.74	-0.54	0.132225	-4.1063	4.02E-05	0.047552
DLX6	0.23	-0.24	0.04845	-4.99983	5.74E-07	0.002308
DPYSL5	666.36	-0.50	0.108765	-4.59446	4.34E-06	0.012463
HOXA4	1.38	-0.75	0.093147	-8.05427	8.00E-16	1.61E-11
IL10	6.36	-0.61	0.139653	-4.34042	1.42E-05	0.021996
LOC100129917	258.38	-0.71	0.156854	-4.54492	5.50E-06	0.013813
LOC100130557	161.74	-0.52	0.12406	-4.15142	3.30E-05	0.044291
LOC154860	2.51	-0.80	0.144473	-5.5047	3.70E-08	0.000248
MTRNR2L3	0.87	-0.39	0.072616	-5.43254	5.56E-08	0.000279
PITX2	0.41	-0.28	0.057847	-4.76413	1.90E-06	0.006356
SHOX2	2.24	-0.53	0.118274	-4.50223	6.72E-06	0.015023
SIM2	7.95	-0.71	0.159667	-4.4598	8.20E-06	0.016495
SLC6A14	1.61	-0.44	0.101297	-4.34139	1.42E-05	0.021996
SPATA18	6.59	-0.69	0.158392	-4.34102	1.42E-05	0.021996
ZNF323	274.87	-0.63	0.151247	-4.13527	3.55E-05	0.044554
ZNF514	431.61	-0.62	0.144061	-4.3155	1.59E-05	0.02287

## ALS--Cortex\_Frontal

down  
up

#	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
★ C9orf72	1031.49	0.55	0.112857	4.912508	8.99E-07	0.003981
LOC100130954	6.96	-0.82	0.167347	-4.89465	9.85E-07	0.003981
NCRUPAR	3.39	-0.81	0.15308	-5.29637	1.18E-07	0.001194
PDE6A	27.58	-0.90	0.17541	-5.10499	3.31E-07	0.002229
TFAP2B	0.76	-0.72	0.116629	-6.18546	6.19E-10	1.25E-05
TRAF3	484.80	-0.37	0.081281	-4.56845	4.91E-06	0.016553

# ALS--Liver

#	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
CLRN3	476.86	1.40	0.307833	4.547495	5.43E-06	0.033885
ITLN1	614.84	1.59	0.341703	4.646913	3.37E-06	0.031546
IL2RA	33.16	-1.82	0.342085	-5.31553	1.06E-07	0.001991

down  
up

# ALS--Spinal\_Cord\_Cervical

#	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
CA9	2.91	-0.58	0.123557	-4.69325	2.69E-06	0.026689
FER1L6	15.29	-0.73	0.155504	-4.69862	2.62E-06	0.026689
LOC100335030	24.01	-0.81	0.17804	-4.52507	6.04E-06	0.039951

down  
up

## ALS--Spinal\_Cord\_Lumbar, down genes: no GO enrichment

## ALS--Spinal\_Cord\_Lumbar, up genes:

N	X	LOD	P	P_adj	attrib ID	attrib name
3	7	2.07125	1.00E-05	0.02	GO:0071499	cellular response to laminar fluid shear stress
4	25	1.50441	2.17E-05	0.041	GO:0017147	Wnt-protein binding
6	38	1.491794	1.84E-07	<0.001	GO:0030199	collagen fibril organization
6	58	1.283038	2.42E-06	0.004	GO:0043010	camera-type eye development
8	115	1.09449	1.04E-06	0.003	GO:0044420	extracellular matrix component
7	111	1.04872	9.66E-06	0.017	GO:0001503	ossification
18	312	1.029719	2.93E-12	<0.001	GO:0030198	extracellular matrix organization
7	116	1.028301	1.29E-05	0.023	GO:0007423	sensory organ development
18	313	1.028223	3.09E-12	<0.001	GO:0043062	extracellular structure organization
9	151	1.023352	7.95E-07	0.002	GO:0030203	glycosaminoglycan metabolic process
7	120	1.012623	1.61E-05	0.036	GO:0048754	branching morphogenesis of an epithelial tube
9	155	1.011233	9.90E-07	0.003	GO:0006022	aminoglycan metabolic process
11	244	0.89737	7.49E-07	0.002	GO:2000146	negative regulation of cell motility
10	228	0.883184	3.12E-06	0.005	GO:0030336	negative regulation of cell migration
11	258	0.871741	1.30E-06	0.003	GO:0051271	negative regulation of cellular component movement
9	214	0.86283	1.39E-05	0.024	GO:0035239	tube morphogenesis
14	355	0.842149	1.12E-07	<0.001	GO:0048729	tissue morphogenesis
11	279	0.835861	2.77E-06	0.004	GO:0040013	negative regulation of locomotion
11	280	0.834223	2.87E-06	0.004	GO:0002009	morphogenesis of an epithelium
11	280	0.834223	2.87E-06	0.004	GO:1901342	regulation of vasculature development
12	397	0.716048	1.45E-05	0.025	GO:0048598	embryonic morphogenesis
20	752	0.67616	1.27E-07	<0.001	GO:2000145	regulation of cell motility
18	700	0.655138	9.45E-07	0.003	GO:0030334	regulation of cell migration
20	801	0.646812	3.48E-07	<0.001	GO:0051270	regulation of cellular component movement
14	550	0.641177	1.89E-05	0.038	GO:0009888	tissue development
16	638	0.638673	5.53E-06	0.008	GO:0030155	regulation of cell adhesion
31	1360	0.637954	9.35E-10	<0.001	GO:0009653	anatomical structure morphogenesis
20	822	0.634769	5.23E-07	<0.001	GO:0040012	regulation of locomotion
31	1714	0.526168	2.06E-07	<0.001	GO:0005576	extracellular region
22	1169	0.519702	9.15E-06	0.017	GO:0048513	organ development
37	2396	0.466484	5.33E-07	<0.001	GO:0032879	regulation of localization
45	3082	0.464321	8.94E-08	<0.001	GO:0044707	single-multicellular organism process
45	3139	0.454601	1.55E-07	<0.001	GO:0032501	multicellular organismal process
49	3563	0.446614	1.16E-07	<0.001	GO:0044421	extracellular region part
38	2706	0.42097	3.76E-06	0.005	GO:0048856	anatomical structure development
53	4303	0.399614	1.01E-06	0.003	GO:0044767	single-organism developmental process
54	4677	0.36557	6.03E-06	0.012	GO:0032502	developmental process

## ALS--Cortex\_Occipital, up genes:

N	X	LOD	P	P_adj	attrib ID	attrib name
224	2219	0.357993	2.94E-22	<0.001	GO:0003677	DNA binding
45	412	0.351605	4.41E-06	0.008	GO:0005813	centrosome
218	2345	0.311299	2.72E-17	<0.001	GO:0006351	transcription, DNA-templated
218	2346	0.311067	2.86E-17	<0.001	GO:0097659	nucleic acid-templated transcription
232	2658	0.280588	3.13E-15	<0.001	GO:0032774	RNA biosynthetic process
305	3648	0.276751	7.66E-18	<0.001	GO:0003676	nucleic acid binding
277	3292	0.272362	2.43E-16	<0.001	GO:0016070	RNA metabolic process
308	3785	0.261707	2.52E-16	<0.001	GO:0090304	nucleic acid metabolic process
234	2827	0.251711	8.04E-13	<0.001	GO:0034645	cellular macromolecule biosynthetic process
241	2943	0.247464	1.01E-12	<0.001	GO:0034654	nucleobase-containing compound biosynthetic process
241	3004	0.235976	8.95E-12	<0.001	GO:0018130	heterocycle biosynthetic process
241	3009	0.235043	1.06E-11	<0.001	GO:0019438	aromatic compound biosynthetic process
250	3140	0.233852	6.95E-12	<0.001	GO:0009059	macromolecule biosynthetic process
318	4216	0.219112	2.40E-12	<0.001	GO:0006139	nucleobase-containing compound metabolic process
244	3166	0.214074	3.76E-10	<0.001	GO:0044271	cellular nitrogen compound biosynthetic process
241	3134	0.212161	6.27E-10	<0.001	GO:1901362	organic cyclic compound biosynthetic process
320	4402	0.197181	2.01E-10	<0.001	GO:0046483	heterocycle metabolic process
320	4415	0.195379	2.87E-10	<0.001	GO:0006725	cellular aromatic compound metabolic process
375	5471	0.172752	4.51E-09	<0.001	GO:1901363	heterocyclic compound binding
277	3942	0.167636	1.79E-07	<0.001	GO:0046872	metal ion binding
376	5538	0.166709	1.40E-08	<0.001	GO:0097159	organic cyclic compound binding
321	4643	0.166531	5.53E-08	<0.001	GO:1901360	organic cyclic compound metabolic process
325	4710	0.166145	5.29E-08	<0.001	GO:0034641	cellular nitrogen compound metabolic process
277	4003	0.158547	7.16E-07	0.001	GO:0043169	cation binding
309	4630	0.142406	3.41E-06	0.007	GO:0005634	nucleus
333	5127	0.129464	1.40E-05	0.049	GO:0006807	nitrogen compound metabolic process

# ALS--Cortex\_Occipital, down genes:

N	X	LOD	P	P_adj	attrib ID	attrib name
7	8	1.863308	3.42E-08	<0.001	GO:0005832	chaperonin-containing T-complex
15	19	1.704352	3.82E-15	<0.001	GO:0005753	mitochondrial proton-transporting ATP synthase complex
15	19	1.704352	3.82E-15	<0.001	GO:0045259	proton-transporting ATP synthase complex
13	17	1.643609	5.78E-13	<0.001	GO:0022624	proteasome accessory complex
7	9	1.641434	1.45E-07	0.002	GO:0046933	proton-transporting ATP synthase activity, rotational mechanism
14	19	1.58784	1.69E-13	<0.001	GO:0005839	proteasome core complex
14	19	1.58784	1.69E-13	<0.001	GO:0042776	mitochondrial ATP synthesis coupled proton transport
6	8	1.578916	1.77E-06	0.008	GO:0005838	proteasome regulatory particle
6	8	1.578916	1.77E-06	0.008	GO:0019773	proteasome core complex, alpha-subunit complex
33	46	1.568475	1.48E-29	<0.001	GO:0005747	mitochondrial respiratory chain complex I
33	46	1.568475	1.48E-29	<0.001	GO:0030964	NADH dehydrogenase complex
33	46	1.568475	1.48E-29	<0.001	GO:0045271	respiratory chain complex I
9	13	1.489513	1.05E-08	<0.001	GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c
33	49	1.481249	4.03E-28	<0.001	GO:0006120	mitochondrial electron transport, NADH to ubiquinone
30	45	1.466547	1.78E-25	<0.001	GO:0003954	NADH dehydrogenase activity
30	45	1.466547	1.78E-25	<0.001	GO:0008137	NADH dehydrogenase (ubiquinone) activity
30	45	1.466547	1.78E-25	<0.001	GO:0050136	NADH dehydrogenase (quinone) activity
22	33	1.461156	5.12E-19	<0.001	GO:0016469	proton-transporting two-sector ATPase complex
14	21	1.453091	1.50E-12	<0.001	GO:0015985	energy coupled proton transport, down electrochemical gradient
14	21	1.453091	1.50E-12	<0.001	GO:0015986	ATP synthesis coupled proton transport
40	61	1.451235	4.03E-33	<0.001	GO:0098803	respiratory chain complex
6	9	1.432762	5.01E-06	0.02	GO:0002199	zona pellucida receptor complex
7	11	1.38611	1.19E-06	0.008	GO:0019774	proteasome core complex, beta-subunit complex
13	21	1.367301	3.88E-11	<0.001	GO:0004298	threonine-type endopeptidase activity
13	21	1.367301	3.88E-11	<0.001	GO:0070003	threonine-type peptidase activity
63	106	1.348792	1.28E-47	<0.001	GO:0098800	inner mitochondrial membrane protein complex
7	12	1.298935	2.69E-06	0.013	GO:0006119	oxidative phosphorylation
7	12	1.298935	2.69E-06	0.013	GO:0034709	methylosome
19	33	1.297138	7.07E-15	<0.001	GO:0005684	U2-type spliceosomal complex
15	26	1.296689	4.95E-12	<0.001	GO:0097525	spliceosomal snRNP complex
54	96	1.289057	3.44E-39	<0.001	GO:0022904	respiratory electron transport chain
16	28	1.287976	1.16E-12	<0.001	GO:0071007	U2-type catalytic step 2 spliceosome
8	14	1.281087	6.14E-07	0.003	GO:0033178	proton-transporting two-sector ATPase complex, catalytic domain
9	16	1.267589	1.41E-07	0.002	GO:0044769	ATPase activity, coupled to transmembrane movement of ions, rotational mechanism
10	18	1.257042	3.23E-08	<0.001	GO:0006123	mitochondrial electron transport, cytochrome c to oxygen
35	64	1.254522	2.91E-25	<0.001	GO:0000502	proteasome complex
35	64	1.254522	2.91E-25	<0.001	GO:0010257	NADH dehydrogenase complex assembly
35	64	1.254522	2.91E-25	<0.001	GO:0032981	mitochondrial respiratory chain complex I assembly
35	64	1.254522	2.91E-25	<0.001	GO:0097031	mitochondrial respiratory chain complex I biogenesis
17	31	1.249395	5.69E-13	<0.001	GO:0042407	cristae formation
31	58	1.23163	4.02E-22	<0.001	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor
8	15	1.218913	1.24E-06	0.008	GO:0005665	DNA-directed RNA polymerase II, core complex
26	50	1.204923	2.27E-18	<0.001	GO:0000315	organellar large ribosomal subunit
26	50	1.204923	2.27E-18	<0.001	GO:0005762	mitochondrial large ribosomal subunit
71	140	1.199287	4.83E-47	<0.001	GO:0098798	mitochondrial protein complex
32	63	1.186501	6.85E-22	<0.001	GO:0006521	regulation of cellular amino acid metabolic process
33	65	1.186443	1.59E-22	<0.001	GO:0038061	NIK/NF-kappaB signaling
43	86	1.176803	1.34E-28	<0.001	GO:0070126	mitochondrial translational termination
42	84	1.176447	5.79E-28	<0.001	GO:0070125	mitochondrial translational elongation

19	38	1.168345	2.24E-13	<0.001	GO:0007007	inner mitochondrial membrane organization
7	14	1.164186	1.04E-05	0.036	GO:0005852	eukaryotic translation initiation factor 3 complex
45	93	1.14971	4.45E-29	<0.001	GO:0006415	translational termination
44	91	1.14875	1.92E-28	<0.001	GO:1990204	oxidoreductase complex
16	33	1.141721	3.28E-11	<0.001	GO:0006754	ATP biosynthetic process
33	69	1.135932	1.82E-21	<0.001	GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
12	25	1.132464	1.15E-08	<0.001	GO:0006099	tricarboxylic acid cycle
10	21	1.125687	2.18E-07	0.002	GO:0032543	mitochondrial translation
17	36	1.120601	1.36E-11	<0.001	GO:0030532	small nuclear ribonucleoprotein complex
77	169	1.111895	1.51E-46	<0.001	GO:0044455	mitochondrial membrane part
34	74	1.103821	2.30E-21	<0.001	GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
37	81	1.100164	5.07E-23	<0.001	GO:0070271	protein complex biogenesis
38	84	1.09283	2.03E-23	<0.001	GO:0033108	mitochondrial respiratory chain complex assembly
34	76	1.082836	6.71E-21	<0.001	GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I
13	29	1.079033	7.94E-09	<0.001	GO:0006101	citrate metabolic process
12	27	1.072415	3.40E-08	<0.001	GO:0000314	organellar small ribosomal subunit
12	27	1.072415	3.40E-08	<0.001	GO:0005763	mitochondrial small ribosomal subunit
11	25	1.064821	1.46E-07	0.002	GO:0000313	organellar ribosome
11	25	1.064821	1.46E-07	0.002	GO:0005761	mitochondrial ribosome
33	76	1.059558	7.94E-20	<0.001	GO:0051437	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transi
34	79	1.053138	3.10E-20	<0.001	GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia
52	122	1.051537	5.22E-30	<0.001	GO:0043624	cellular protein complex disassembly
34	81	1.034405	8.18E-20	<0.001	GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
17	41	1.021343	1.76E-10	<0.001	GO:0009206	purine ribonucleoside triphosphate biosynthetic process
37	90	1.019942	4.59E-21	<0.001	GO:0002474	antigen processing and presentation of peptide antigen via MHC class I
44	108	1.015452	1.32E-24	<0.001	GO:0006414	translational elongation
33	81	1.012178	8.68E-19	<0.001	GO:0010972	negative regulation of G2/M transition of mitotic cell cycle
9	22	1.012164	4.29E-06	0.019	GO:0000715	nucleotide-excision repair, DNA damage recognition
17	42	1.003943	2.77E-10	<0.001	GO:0009145	purine nucleoside triphosphate biosynthetic process
33	83	0.994578	2.13E-18	<0.001	GO:0051436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
33	83	0.994578	2.13E-18	<0.001	GO:0051439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
13	33	0.984662	5.26E-08	<0.001	GO:0072350	tricarboxylic acid metabolic process
39	101	0.975513	5.92E-21	<0.001	GO:0015934	large ribosomal subunit
34	88	0.974524	1.89E-18	<0.001	GO:0033238	regulation of cellular amine metabolic process
37	96	0.973626	6.47E-20	<0.001	GO:0016651	oxidoreductase activity, acting on NAD(P)H
54	144	0.959576	9.04E-28	<0.001	GO:0043241	protein complex disassembly
37	98	0.959217	1.48E-19	<0.001	GO:0060071	Wnt signaling pathway, planar cell polarity pathway
9	24	0.952115	1.00E-05	0.033	GO:0005689	U12-type spliceosomal complex
12	32	0.950866	3.27E-07	0.002	GO:0006734	NADH metabolic process
58	158	0.946107	3.67E-29	<0.001	GO:0022900	electron transport chain
37	100	0.945268	3.31E-19	<0.001	GO:0051443	positive regulation of ubiquitin-protein transferase activity
37	100	0.945268	3.31E-19	<0.001	GO:0090175	regulation of establishment of planar polarity
38	103	0.943559	1.23E-19	<0.001	GO:1902036	regulation of hematopoietic stem cell differentiation
10	27	0.943195	3.64E-06	0.015	GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient
10	27	0.943195	3.64E-06	0.015	GO:0015991	ATP hydrolysis coupled proton transport
33	90	0.938023	3.87E-17	<0.001	GO:2000060	positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic proces
38	105	0.930445	2.67E-19	<0.001	GO:0051351	positive regulation of ligase activity
20	55	0.929838	7.49E-11	<0.001	GO:1990542	mitochondrial transmembrane transport
136	396	0.927622	2.12E-63	<0.001	GO:0005743	mitochondrial inner membrane
17	47	0.926057	2.19E-09	<0.001	GO:0009201	ribonucleoside triphosphate biosynthetic process

9	25	0.924938	1.48E-05	0.05	GO:0006735	NADH regeneration
9	25	0.924938	1.48E-05	0.05	GO:0061621	canonical glycolysis
9	25	0.924938	1.48E-05	0.05	GO:0061718	glucose catabolic process to pyruvate
34	95	0.921867	3.08E-17	<0.001	GO:0051444	negative regulation of ubiquitin-protein transferase activity
33	93	0.915859	1.22E-16	<0.001	GO:1902750	negative regulation of cell cycle G2/M phase transition
34	96	0.914837	4.48E-17	<0.001	GO:0051352	negative regulation of ligase activity
54	155	0.909478	6.17E-26	<0.001	GO:0032984	macromolecular complex disassembly
33	96	0.894765	3.62E-16	<0.001	GO:0070498	interleukin-1-mediated signaling pathway
35	102	0.894074	4.90E-17	<0.001	GO:0046034	ATP metabolic process
55	162	0.892664	9.41E-26	<0.001	GO:0044391	ribosomal subunit
138	434	0.877627	1.40E-59	<0.001	GO:0019866	organelle inner membrane
43	129	0.877182	4.61E-20	<0.001	GO:0044085	cellular component biogenesis
37	111	0.875605	1.88E-17	<0.001	GO:0003735	structural constituent of ribosome
12	36	0.873353	1.43E-06	0.008	GO:0006626	protein targeting to mitochondrion
19	58	0.861275	1.74E-09	<0.001	GO:0009142	nucleoside triphosphate biosynthetic process
18	55	0.860655	4.73E-09	<0.001	GO:0009127	purine nucleoside monophosphate biosynthetic process
18	55	0.860655	4.73E-09	<0.001	GO:0009168	purine ribonucleoside monophosphate biosynthetic process
14	43	0.857772	2.64E-07	0.002	GO:0045851	pH reduction
55	172	0.85378	2.70E-24	<0.001	GO:0002478	antigen processing and presentation of exogenous peptide antigen
55	174	0.846399	5.10E-24	<0.001	GO:0019884	antigen processing and presentation of exogenous antigen
13	41	0.841368	9.96E-07	0.007	GO:0050434	positive regulation of viral transcription
56	179	0.840139	3.49E-24	<0.001	GO:0048002	antigen processing and presentation of peptide antigen
35	111	0.839487	9.88E-16	<0.001	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress
23	73	0.836832	8.34E-11	<0.001	GO:0006283	transcription-coupled nucleotide-excision repair
11	35	0.836769	7.51E-06	0.031	GO:0000387	spliceosomal snRNP assembly
11	35	0.836769	7.51E-06	0.031	GO:0030120	vesicle coat
33	106	0.830997	9.91E-15	<0.001	GO:2000058	regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process
13	42	0.826365	1.36E-06	0.008	GO:0051452	intracellular pH reduction
50	163	0.825997	2.65E-21	<0.001	GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process
37	121	0.82065	4.60E-16	<0.001	GO:1904813	ficolin-1-rich granule lumen
40	131	0.820472	3.13E-17	<0.001	GO:0051340	regulation of ligase activity
11	36	0.819369	1.02E-05	0.033	GO:0006096	glycolytic process
11	36	0.819369	1.02E-05	0.033	GO:0033572	transferrin transport
39	128	0.818882	8.47E-17	<0.001	GO:0051438	regulation of ubiquitin-protein transferase activity
37	123	0.81044	8.32E-16	<0.001	GO:0009205	purine ribonucleoside triphosphate metabolic process
15	50	0.806549	3.32E-07	0.002	GO:0046364	monosaccharide biosynthetic process
35	117	0.806542	6.06E-15	<0.001	GO:0043620	regulation of DNA-templated transcription in response to stress
11	37	0.802638	1.37E-05	0.048	GO:0006757	ATP generation from ADP
11	37	0.802638	1.37E-05	0.048	GO:0015682	ferric iron transport
11	37	0.802638	1.37E-05	0.048	GO:0072512	trivalent inorganic cation transport
24	81	0.798751	1.38E-10	<0.001	GO:0007006	mitochondrial membrane organization
24	81	0.798751	1.38E-10	<0.001	GO:1901800	positive regulation of proteasomal protein catabolic process
15	51	0.794459	4.42E-07	0.002	GO:0070585	protein localization to mitochondrion
38	130	0.792971	9.74E-16	<0.001	GO:0009144	purine nucleoside triphosphate metabolic process
17	58	0.792029	8.03E-08	0.002	GO:0072655	establishment of protein localization to mitochondrion
34	117	0.788496	3.83E-14	<0.001	GO:0006839	mitochondrial transport
58	203	0.784262	8.94E-23	<0.001	GO:0019882	antigen processing and presentation
42	146	0.784142	5.69E-17	<0.001	GO:0043209	myelin sheath
51	178	0.784026	3.08E-20	<0.001	GO:1903364	positive regulation of cellular protein catabolic process
157	581	0.782278	4.67E-57	<0.001	GO:0031966	mitochondrial membrane

37	129	0.781161	4.55E-15	<0.001	GO:0009199	ribonucleoside triphosphate metabolic process
33	115	0.780601	1.35E-13	<0.001	GO:1902600	hydrogen ion transmembrane transport
12	42	0.778066	8.78E-06	0.032	GO:0046031	ADP metabolic process
37	130	0.776466	5.98E-15	<0.001	GO:0035567	non-canonical Wnt signaling pathway
23	81	0.772764	8.50E-10	<0.001	GO:0071013	catalytic step 2 spliceosome
19	67	0.771901	2.54E-08	<0.001	GO:0009156	ribonucleoside monophosphate biosynthetic process
27	96	0.767424	3.74E-11	<0.001	GO:0005840	ribosome
33	118	0.765012	3.03E-13	<0.001	GO:0002223	stimulatory C-type lectin receptor signaling pathway
36	129	0.764348	2.72E-14	<0.001	GO:0090263	positive regulation of canonical Wnt signaling pathway
39	140	0.763934	2.44E-15	<0.001	GO:0009167	purine ribonucleoside monophosphate metabolic process
22	79	0.761017	2.96E-09	<0.001	GO:0042451	purine nucleoside biosynthetic process
22	79	0.761017	2.96E-09	<0.001	GO:0046129	purine ribonucleoside biosynthetic process
39	141	0.75965	3.16E-15	<0.001	GO:0009126	purine nucleoside monophosphate metabolic process
87	322	0.759047	1.23E-31	<0.001	GO:0006091	generation of precursor metabolites and energy
33	121	0.749959	6.58E-13	<0.001	GO:0002220	innate immune response activating cell surface receptor signaling pathway
18	66	0.748665	1.14E-07	0.002	GO:0015078	hydrogen ion transmembrane transporter activity
18	66	0.748665	1.14E-07	0.002	GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process
28	103	0.747198	3.98E-11	<0.001	GO:0006289	nucleotide-excision repair
48	178	0.746631	6.20E-18	<0.001	GO:0031398	positive regulation of protein ubiquitination
40	148	0.74603	3.31E-15	<0.001	GO:0009141	nucleoside triphosphate metabolic process
34	126	0.743811	4.12E-13	<0.001	GO:0015992	proton transport
61	229	0.742818	3.82E-22	<0.001	GO:0000375	RNA splicing, via transesterification reactions
41	153	0.741179	2.06E-15	<0.001	GO:1901532	regulation of hematopoietic progenitor cell differentiation
18	67	0.739776	1.47E-07	0.002	GO:0005758	mitochondrial intermembrane space
34	127	0.739116	5.29E-13	<0.001	GO:0033209	tumor necrosis factor-mediated signaling pathway
59	223	0.738221	2.68E-21	<0.001	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
59	223	0.738221	2.68E-21	<0.001	GO:0000398	mRNA splicing, via spliceosome
20	75	0.735265	3.45E-08	<0.001	GO:0009124	nucleoside monophosphate biosynthetic process
34	128	0.73447	6.76E-13	<0.001	GO:0006818	hydrogen transport
51	194	0.732275	1.88E-18	<0.001	GO:1903322	positive regulation of protein modification by small protein conjugation or removal
40	152	0.730205	8.86E-15	<0.001	GO:0009161	ribonucleoside monophosphate metabolic process
15	57	0.728211	2.12E-06	0.01	GO:0051453	regulation of intracellular pH
38	145	0.727321	4.79E-14	<0.001	GO:0043488	regulation of mRNA stability
26	99	0.726556	4.51E-10	<0.001	GO:0042470	melanosome
26	99	0.726556	4.51E-10	<0.001	GO:0048770	pigment granule
217	924	0.719426	1.27E-67	<0.001	GO:0044429	mitochondrial part
16	62	0.71657	1.30E-06	0.008	GO:0015935	small ribosomal subunit
38	148	0.715291	9.73E-14	<0.001	GO:0043487	regulation of RNA stability
13	51	0.710498	1.47E-05	0.048	GO:0022625	cytosolic large ribosomal subunit
32	126	0.707777	1.19E-11	<0.001	GO:0038095	Fc-epsilon receptor signaling pathway
42	166	0.707578	8.49E-15	<0.001	GO:0009123	nucleoside monophosphate metabolic process
19	75	0.705391	1.84E-07	0.002	GO:0031970	organelle envelope lumen
37	147	0.703482	3.99E-13	<0.001	GO:0031397	negative regulation of protein ubiquitination
20	80	0.697676	1.12E-07	0.002	GO:0006901	vesicle coating
44	179	0.691262	6.06E-15	<0.001	GO:0010389	regulation of G2/M transition of mitotic cell cycle
15	61	0.689045	5.32E-06	0.021	GO:0008135	translation factor activity, RNA binding
15	61	0.689045	5.32E-06	0.021	GO:0030641	regulation of cellular pH
25	103	0.680765	5.72E-09	<0.001	GO:0048524	positive regulation of viral process
16	66	0.68063	3.18E-06	0.014	GO:0033116	endoplasmic reticulum-Golgi intermediate compartment membrane
22	91	0.678395	5.03E-08	<0.001	GO:0042455	ribonucleoside biosynthetic process

39	162	0.678171	4.33E-13	<0.001	GO:0090090	negative regulation of canonical Wnt signaling pathway
33	137	0.677378	2.69E-11	<0.001	GO:0006413	translational initiation
34	142	0.674115	1.61E-11	<0.001	GO:0005681	spliceosomal complex
146	647	0.671794	1.26E-42	<0.001	GO:0030529	intracellular ribonucleoprotein complex
15	63	0.670705	8.15E-06	0.032	GO:0006090	pyruvate metabolic process
15	63	0.670705	8.15E-06	0.032	GO:0048208	COPII vesicle coating
146	650	0.669125	2.26E-42	<0.001	GO:1990904	ribonucleoprotein complex
23	97	0.667357	3.71E-08	<0.001	GO:1903902	positive regulation of viral life cycle
58	248	0.666078	3.54E-18	<0.001	GO:1903050	regulation of proteolysis involved in cellular protein catabolic process
37	157	0.665602	3.44E-12	<0.001	GO:1903321	negative regulation of protein modification by small protein conjugation or removal
58	249	0.663778	4.34E-18	<0.001	GO:0045732	positive regulation of protein catabolic process
15	64	0.661816	1.00E-05	0.033	GO:0045454	cell redox homeostasis
39	167	0.660807	1.22E-12	<0.001	GO:0006412	translation
38	163	0.659627	2.51E-12	<0.001	GO:0030177	positive regulation of Wnt signaling pathway
33	142	0.656952	7.54E-11	<0.001	GO:0050852	T cell receptor signaling pathway
28	121	0.653875	2.26E-09	<0.001	GO:0072522	purine-containing compound biosynthetic process
49	214	0.651796	3.60E-15	<0.001	GO:0046128	purine ribonucleoside metabolic process
16	70	0.647423	7.22E-06	0.03	GO:0006885	regulation of pH
42	185	0.64541	4.60E-13	<0.001	GO:0006457	protein folding
18	79	0.645201	2.06E-06	0.01	GO:0051082	unfolded protein binding
49	217	0.643917	6.45E-15	<0.001	GO:0042278	purine nucleoside metabolic process
42	186	0.642369	5.58E-13	<0.001	GO:0043043	peptide biosynthetic process
44	197	0.636633	2.35E-13	<0.001	GO:1902749	regulation of cell cycle G2/M phase transition
22	98	0.63654	2.06E-07	0.002	GO:0009163	nucleoside biosynthetic process
24	107	0.636071	5.93E-08	<0.001	GO:0006164	purine nucleotide biosynthetic process
22	99	0.630875	2.49E-07	0.002	GO:1901659	glycosyl compound biosynthetic process
31	141	0.625488	1.22E-09	<0.001	GO:0006888	ER to Golgi vesicle-mediated transport
59	272	0.623733	7.97E-17	<0.001	GO:1903362	regulation of cellular protein catabolic process
52	241	0.619077	6.97E-15	<0.001	GO:0010498	proteasomal protein catabolic process
71	333	0.617203	1.47E-19	<0.001	GO:0043623	cellular protein complex assembly
21	97	0.616422	7.36E-07	0.006	GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II
35	162	0.616338	1.76E-10	<0.001	GO:0061136	regulation of proteasomal protein catabolic process
21	98	0.610756	8.81E-07	0.006	GO:0002495	antigen processing and presentation of peptide antigen via MHC class II
21	98	0.610756	8.81E-07	0.006	GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
22	103	0.608917	5.16E-07	0.002	GO:0009152	purine ribonucleotide biosynthetic process
49	231	0.608896	8.42E-14	<0.001	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process
39	184	0.606413	2.97E-11	<0.001	GO:1901991	negative regulation of mitotic cell cycle phase transition
40	190	0.60285	2.08E-11	<0.001	GO:0038093	Fc receptor signaling pathway
19	90	0.602752	3.66E-06	0.015	GO:0043021	ribonucleoprotein complex binding
70	337	0.602372	1.21E-18	<0.001	GO:0008380	RNA splicing
28	134	0.597005	2.49E-08	<0.001	GO:0022618	ribonucleoprotein complex assembly
65	316	0.59567	3.57E-17	<0.001	GO:0022411	cellular component disassembly
49	237	0.594694	2.36E-13	<0.001	GO:0009119	ribonucleoside metabolic process
40	193	0.594202	3.46E-11	<0.001	GO:0030178	negative regulation of Wnt signaling pathway
56	273	0.59194	6.46E-15	<0.001	GO:1901657	glycosyl compound metabolic process
55	270	0.587862	1.54E-14	<0.001	GO:0007005	mitochondrion organization
54	266	0.585745	3.11E-14	<0.001	GO:0031396	regulation of protein ubiquitination
52	257	0.583464	1.08E-13	<0.001	GO:0009116	nucleoside metabolic process
21	104	0.578218	2.44E-06	0.01	GO:0016236	macroautophagy
29	144	0.576897	3.35E-08	<0.001	GO:0071826	ribonucleoprotein complex subunit organization

33	165	0.573563	4.63E-09	<0.001	GO:0050851	antigen receptor-mediated signaling pathway
57	290	0.568707	2.59E-14	<0.001	GO:1903320	regulation of protein modification by small protein conjugation or removal
216	1195	0.568445	1.28E-46	<0.001	GO:0005739	mitochondrion
48	244	0.56719	2.82E-12	<0.001	GO:0043604	amide biosynthetic process
40	204	0.563863	2.05E-10	<0.001	GO:1901988	negative regulation of cell cycle phase transition
52	268	0.560536	6.08E-13	<0.001	GO:0006163	purine nucleotide metabolic process
62	321	0.560338	4.39E-15	<0.001	GO:0030163	protein catabolic process
23	119	0.554425	1.83E-06	0.008	GO:0046390	ribose phosphate biosynthetic process
47	247	0.548904	1.62E-11	<0.001	GO:0009150	purine ribonucleotide metabolic process
46	243	0.545905	3.20E-11	<0.001	GO:0060828	regulation of canonical Wnt signaling pathway
52	276	0.544572	2.00E-12	<0.001	GO:0006518	peptide metabolic process
22	116	0.544312	4.22E-06	0.018	GO:0009260	ribonucleotide biosynthetic process
118	647	0.543749	1.59E-25	<0.001	GO:0034622	cellular macromolecular complex assembly
63	338	0.541224	1.50E-14	<0.001	GO:0005759	mitochondrial matrix
43	229	0.540965	1.84E-10	<0.001	GO:2000027	regulation of organ morphogenesis
36	192	0.539036	5.75E-09	<0.001	GO:0010565	regulation of cellular ketone metabolic process
56	305	0.531507	8.48E-13	<0.001	GO:0072521	purine-containing compound metabolic process
27	146	0.530766	6.01E-07	0.003	GO:2001242	regulation of intrinsic apoptotic signaling pathway
21	114	0.528838	1.11E-05	0.036	GO:0016051	carbohydrate biosynthetic process
23	126	0.523834	5.05E-06	0.02	GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process
72	402	0.521831	1.66E-15	<0.001	GO:0006397	mRNA processing
70	391	0.521122	4.24E-15	<0.001	GO:0042176	regulation of protein catabolic process
50	277	0.521093	2.73E-11	<0.001	GO:0019693	ribose phosphate metabolic process
30	166	0.518666	2.44E-07	0.002	GO:0044445	cytosolic part
45	250	0.518631	2.95E-10	<0.001	GO:0045930	negative regulation of mitotic cell cycle
47	262	0.517187	1.34E-10	<0.001	GO:0009259	ribonucleotide metabolic process
48	270	0.512556	1.18E-10	<0.001	GO:0072594	establishment of protein localization to organelle
41	231	0.510442	2.80E-09	<0.001	GO:2000736	regulation of stem cell differentiation
39	225	0.497548	1.34E-08	<0.001	GO:0006605	protein targeting
62	362	0.495574	1.24E-12	<0.001	GO:0045862	positive regulation of proteolysis
239	1534	0.492762	2.60E-40	<0.001	GO:0003723	RNA binding
57	336	0.489429	1.50E-11	<0.001	GO:0060205	cytoplasmic membrane-bounded vesicle lumen
36	211	0.488787	7.30E-08	0.002	GO:0006364	rRNA processing
57	337	0.487852	1.70E-11	<0.001	GO:0031983	vesicle lumen
96	579	0.486329	5.96E-18	<0.001	GO:0016071	mRNA metabolic process
40	236	0.485846	1.69E-08	<0.001	GO:0002218	activation of innate immune response
30	178	0.481765	1.15E-06	0.008	GO:1901293	nucleoside phosphate biosynthetic process
30	179	0.478825	1.29E-06	0.008	GO:0016241	regulation of macroautophagy
57	344	0.476967	3.94E-11	<0.001	GO:0031331	positive regulation of cellular catabolic process
34	204	0.476236	2.97E-07	0.002	GO:0006914	autophagy
68	413	0.475954	6.76E-13	<0.001	GO:0016068	posttranscriptional regulation of gene expression
29	174	0.47585	2.17E-06	0.01	GO:0009165	nucleotide biosynthetic process
36	218	0.471622	1.70E-07	0.002	GO:0002758	innate immune response-activating signal transduction
64	393	0.469271	5.37E-12	<0.001	GO:0009117	nucleotide metabolic process
121	763	0.468862	9.15E-21	<0.001	GO:0006396	RNA processing
49	300	0.467849	1.53E-09	<0.001	GO:0070646	protein modification by small protein removal
52	319	0.467359	5.20E-10	<0.001	GO:0034774	secretory granule lumen
36	220	0.466838	2.14E-07	0.002	GO:0016072	rRNA metabolic process
57	351	0.466339	8.88E-11	<0.001	GO:1901990	regulation of mitotic cell cycle phase transition
48	296	0.463891	2.87E-09	<0.001	GO:0010948	negative regulation of cell cycle process

52	323	0.46081	8.19E-10	<0.001	GO:0016055	Wnt signaling pathway
28	173	0.460496	5.79E-06	0.024	GO:0043902	positive regulation of multi-organism process
64	400	0.459961	1.18E-11	<0.001	GO:0006753	nucleoside phosphate metabolic process
64	401	0.458646	1.32E-11	<0.001	GO:0009896	positive regulation of catabolic process
51	319	0.456976	1.53E-09	<0.001	GO:0030111	regulation of Wnt signaling pathway
41	256	0.456248	5.81E-08	<0.001	GO:0000209	protein polyubiquitination
30	188	0.453207	3.66E-06	0.015	GO:0050792	regulation of viral process
58	367	0.452251	1.81E-10	<0.001	GO:0006511	ubiquitin-dependent protein catabolic process
821	8480	0.451265	1.42E-62	<0.001	GO:0044446	intracellular organelle part
58	372	0.445162	3.11E-10	<0.001	GO:0019941	modification-dependent protein catabolic process
129	857	0.44302	4.32E-20	<0.001	GO:0055114	oxidation-reduction process
122	813	0.439621	6.38E-19	<0.001	GO:1902494	catalytic complex
58	376	0.43957	4.74E-10	<0.001	GO:0043632	modification-dependent macromolecule catabolic process
71	463	0.439133	6.84E-12	<0.001	GO:0016032	viral process
71	463	0.439133	6.84E-12	<0.001	GO:0044403	symbiosis, encompassing mutualism through parasitism
826	8708	0.437175	1.64E-58	<0.001	GO:0044422	organelle part
63	412	0.435987	1.21E-10	<0.001	GO:0051603	proteolysis involved in cellular protein catabolic process
68	447	0.43431	2.78E-11	<0.001	GO:0055086	nucleobase-containing small molecule metabolic process
44	287	0.433934	7.15E-08	0.002	GO:0016579	protein deubiquitination
31	202	0.433027	5.81E-06	0.024	GO:0032104	regulation of response to extracellular stimulus
31	202	0.433027	5.81E-06	0.024	GO:0032107	regulation of response to nutrient levels
72	478	0.429973	1.15E-11	<0.001	GO:0044764	multi-organism cellular process
51	336	0.429876	9.28E-09	<0.001	GO:0034470	ncRNA processing
42	276	0.429787	1.74E-07	0.002	GO:0002429	immune response-activating cell surface receptor signaling pathway
97	653	0.42823	6.26E-15	<0.001	GO:0016491	oxidoreductase activity
117	797	0.426731	1.98E-17	<0.001	GO:0016482	cytoplasmic transport
58	386	0.425886	1.32E-09	<0.001	GO:1901987	regulation of cell cycle phase transition
62	416	0.422407	4.93E-10	<0.001	GO:0043603	cellular amide metabolic process
32	213	0.422109	6.53E-06	0.029	GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism
72	489	0.418091	3.39E-11	<0.001	GO:0034660	ncRNA metabolic process
349	2721	0.417509	5.15E-41	<0.001	GO:0070062	extracellular exosome
349	2722	0.417297	5.59E-41	<0.001	GO:0065010	extracellular membrane-bounded organelle
164	1167	0.415189	3.03E-22	<0.001	GO:0031974	membrane-enclosed lumen
349	2739	0.413697	2.26E-40	<0.001	GO:1903561	extracellular vesicle
349	2740	0.413486	2.46E-40	<0.001	GO:0043230	extracellular organelle
39	265	0.412132	1.13E-06	0.008	GO:0048193	Golgi vesicle transport
42	286	0.411394	4.68E-07	0.002	GO:0045089	positive regulation of innate immune response
48	329	0.408889	8.83E-08	0.002	GO:0051348	negative regulation of transferase activity
62	427	0.408851	1.42E-09	<0.001	GO:0043687	post-translational protein modification
93	651	0.406826	2.50E-13	<0.001	GO:0044265	cellular macromolecule catabolic process
525	4621	0.406781	3.24E-50	<0.001	GO:0032991	macromolecular complex
36	250	0.400637	4.79E-06	0.019	GO:0016887	ATPase activity
127	914	0.40005	6.71E-17	<0.001	GO:0098796	membrane protein complex
73	514	0.399534	1.35E-10	<0.001	GO:0006886	intracellular protein transport
378	3118	0.393957	3.30E-39	<0.001	GO:0031988	membrane-bounded vesicle
60	425	0.39395	7.69E-09	<0.001	GO:0033365	protein localization to organelle
42	298	0.390277	1.42E-06	0.008	GO:0045296	cadherin binding
1013	13217	0.388092	6.76E-31	<0.001	GO:0044424	intracellular part
818	9048	0.387845	1.51E-46	<0.001	GO:0044444	cytoplasmic part
66	475	0.386841	2.62E-09	<0.001	GO:0043312	neutrophil degranulation

94	687	0.38453	2.37E-12	<0.001	GO:0031329	regulation of cellular catabolic process
146	1093	0.383681	8.64E-18	<0.001	GO:0043233	organelle lumen
144	1078	0.383221	1.49E-17	<0.001	GO:1902582	single-organism intracellular transport
66	479	0.382515	3.70E-09	<0.001	GO:0002283	neutrophil activation involved in immune response
107	790	0.382047	1.26E-13	<0.001	GO:0009057	macromolecule catabolic process
389	3303	0.380377	1.37E-37	<0.001	GO:0031982	vesicle
67	491	0.377699	4.20E-09	<0.001	GO:0036230	granulocyte activation
42	307	0.375068	3.08E-06	0.014	GO:0002768	immune response-regulating cell surface receptor signaling pathway
106	793	0.374944	3.89E-13	<0.001	GO:0009894	regulation of catabolic process
174	1342	0.374535	8.47E-20	<0.001	GO:0065003	macromolecular complex assembly
80	593	0.374309	2.20E-10	<0.001	GO:0044419	interspecies interaction between organisms
192	1494	0.374198	1.97E-21	<0.001	GO:0071822	protein complex subunit organization
66	487	0.373985	7.24E-09	<0.001	GO:0042119	neutrophil activation
166	1281	0.372314	7.29E-19	<0.001	GO:0046907	intracellular transport
73	542	0.3721	1.50E-09	<0.001	GO:0007346	regulation of mitotic cell cycle
66	495	0.365612	1.39E-08	<0.001	GO:0043299	leukocyte degranulation
67	505	0.363243	1.31E-08	<0.001	GO:0002275	myeloid cell activation involved in immune response
355	3064	0.360334	3.53E-32	<0.001	GO:0031090	organelle membrane
67	508	0.360204	1.66E-08	<0.001	GO:0045055	regulated secretory pathway
41	315	0.349636	1.38E-05	0.048	GO:0051186	cofactor metabolic process
96	753	0.348267	7.95E-11	<0.001	GO:1901566	organonitrogen compound biosynthetic process
113	898	0.34496	3.45E-12	<0.001	GO:0070013	intracellular organelle lumen
67	529	0.339476	8.11E-08	0.002	GO:0044437	vacuolar part
144	1184	0.333707	4.17E-14	<0.001	GO:0044248	cellular catabolic process
75	601	0.333294	2.53E-08	<0.001	GO:1903047	mitotic cell cycle process
63	508	0.328096	4.20E-07	0.002	GO:0045786	negative regulation of cell cycle
123	1025	0.322298	9.19E-12	<0.001	GO:0015031	protein transport
244	2143	0.32096	4.10E-20	<0.001	GO:0043933	macromolecular complex subunit organization
414	3973	0.314347	5.89E-28	<0.001	GO:0043234	protein complex
133	1130	0.314224	4.82E-12	<0.001	GO:0006461	protein complex assembly
67	556	0.314132	5.20E-07	0.002	GO:0002274	myeloid leukocyte activation
776	9049	0.312992	9.23E-32	<0.001	GO:0043227	membrane-bounded organelle
129	1101	0.311053	1.43E-11	<0.001	GO:0045184	establishment of protein localization
52	434	0.30908	1.14E-05	0.036	GO:0006281	DNA repair
237	2131	0.306398	3.25E-18	<0.001	GO:0051649	establishment of localization in cell
73	617	0.305779	3.29E-07	0.002	GO:0016023	cytoplasmic membrane-bounded vesicle
168	1474	0.304508	8.33E-14	<0.001	GO:1901564	organonitrogen compound metabolic process
172	1512	0.304325	4.74E-14	<0.001	GO:0009056	catabolic process
158	1391	0.300638	6.88E-13	<0.001	GO:1901575	organic substance catabolic process
369	3563	0.29817	9.09E-24	<0.001	GO:0044421	extracellular region part
67	574	0.297978	1.62E-06	0.008	GO:0002366	leukocyte activation involved in immune response
83	719	0.294902	1.48E-07	0.002	GO:0030162	regulation of proteolysis
67	578	0.294464	2.07E-06	0.01	GO:0002263	cell activation involved in immune response
80	694	0.293681	2.64E-07	0.002	GO:0010564	regulation of cell cycle process
80	698	0.290758	3.35E-07	0.002	GO:0006887	exocytosis
59	515	0.287408	1.20E-05	0.044	GO:1990234	transferase complex
821	10094	0.287115	6.38E-26	<0.001	GO:0043226	organelle
198	1819	0.286193	3.33E-14	<0.001	GO:0022607	cellular component assembly
118	1068	0.27851	4.06E-09	<0.001	GO:0044433	cytoplasmic vesicle part
75	670	0.278003	1.92E-06	0.009	GO:0016462	pyrophosphatase activity

75	670	0.278003	1.92E-06	0.009	GO:0016817	hydrolase activity, acting on acid anhydrides
75	670	0.278003	1.92E-06	0.009	GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
74	661	0.277903	2.24E-06	0.01	GO:0016567	protein ubiquitination
151	1385	0.277679	5.50E-11	<0.001	GO:0033554	cellular response to stress
148	1378	0.269247	2.59E-10	<0.001	GO:0016192	vesicle-mediated transport
86	785	0.268769	8.33E-07	0.006	GO:0031410	cytoplasmic vesicle
397	4074	0.268678	9.74E-21	<0.001	GO:0044710	single-organism metabolic process
81	739	0.268245	1.72E-06	0.008	GO:1901135	carbohydrate derivative metabolic process
657	7582	0.26749	1.33E-24	<0.001	GO:0043231	intracellular membrane-bounded organelle
69	630	0.266114	1.04E-05	0.033	GO:0017111	nucleoside-triphosphatase activity
80	736	0.263862	2.75E-06	0.014	GO:0032446	protein modification by small protein conjugation
402	4167	0.263767	3.14E-20	<0.001	GO:0044428	nuclear part
309	3090	0.263042	4.42E-17	<0.001	GO:0005654	nucleoplasm
85	787	0.261385	1.73E-06	0.008	GO:0019752	carboxylic acid metabolic process
721	8648	0.260909	3.26E-23	<0.001	GO:0043229	intracellular organelle
89	830	0.258333	1.33E-06	0.008	GO:0061024	membrane organization
81	762	0.252728	5.58E-06	0.024	GO:0080135	regulation of cellular response to stress
125	1204	0.24756	5.39E-08	<0.001	GO:0044711	single-organism biosynthetic process
103	987	0.246665	6.87E-07	0.006	GO:0044451	nucleoplasm part
149	1462	0.241962	8.33E-09	<0.001	GO:0033036	macromolecule localization
168	1660	0.241569	1.33E-09	<0.001	GO:0044281	small molecule metabolic process
147	1449	0.239226	1.43E-08	<0.001	GO:0008104	protein localization
435	4767	0.237063	1.55E-17	<0.001	GO:0005829	cytosol
678	8209	0.235917	1.59E-19	<0.001	GO:0044237	cellular metabolic process
97	966	0.226147	7.65E-06	0.031	GO:0022402	cell cycle process
724	9039	0.226104	7.82E-18	<0.001	GO:0008152	metabolic process
103	1028	0.225889	4.36E-06	0.019	GO:0051726	regulation of cell cycle
342	3707	0.222995	8.11E-14	<0.001	GO:0006810	transport
298	3191	0.221331	1.63E-12	<0.001	GO:0044765	single-organism transport
347	3827	0.213652	5.58E-13	<0.001	GO:0051234	establishment of localization
305	3391	0.200888	7.56E-11	<0.001	GO:1902578	single-organism localization
369	4190	0.200352	4.34E-12	<0.001	GO:0051179	localization
397	4559	0.198934	2.00E-12	<0.001	GO:0071840	cellular component organization or biogenesis
395	4539	0.198121	2.61E-12	<0.001	GO:0016043	cellular component organization
160	1733	0.191819	1.42E-06	0.008	GO:0071702	organic substance transport
918	12876	0.180225	1.47E-09	<0.001	GO:0009987	cellular process
807	10883	0.180193	3.09E-11	<0.001	GO:0005515	protein binding
313	3648	0.174639	8.12E-09	<0.001	GO:0003676	nucleic acid binding
205	2391	0.158404	6.99E-06	0.029	GO:0098588	bounding membrane of organelle
209	2445	0.157286	6.80E-06	0.029	GO:0043228	non-membrane-bounded organelle
209	2445	0.157286	6.80E-06	0.029	GO:0043232	intracellular non-membrane-bounded organelle
210	2478	0.152697	1.14E-05	0.036	GO:0051716	cellular response to stimulus
376	4710	0.140493	5.95E-07	0.003	GO:0034641	cellular nitrogen compound metabolic process
402	5127	0.132779	1.39E-06	0.008	GO:0006807	nitrogen compound metabolic process
636	8619	0.127052	6.92E-07	0.006	GO:0071704	organic substance metabolic process
688	9467	0.123948	1.44E-06	0.008	GO:0044763	single-organism cellular process
382	4931	0.122229	1.05E-05	0.036	GO:0003824	catalytic activity
418	5471	0.117948	1.26E-05	0.045	GO:1901363	heterocyclic compound binding

## ALS--Cortex\_Motor\_Medial, down genes

<b>N</b>	<b>X</b>	<b>LOD</b>	<b>P</b>	<b>P_adj</b>	<b>attrib ID</b>	<b>attrib name</b>
12	579	0.836322	1.35E-06	0.003	GO:0016071	mRNA metabolic process
13	647	0.827379	6.53E-07	<0.001	GO:0030529	intracellular ribonucleoprotein complex
13	650	0.825256	6.88E-07	<0.001	GO:1990904	ribonucleoprotein complex
30	3090	0.592124	1.43E-07	<0.001	GO:0005654	nucleoplasm
33	4167	0.505436	3.00E-06	0.004	GO:0044428	nuclear part
50	8480	0.498535	5.37E-06	0.012	GO:0044446	intracellular organelle part
50	8708	0.476652	1.35E-05	0.025	GO:0044422	organelle part
34	4621	0.471212	1.05E-05	0.022	GO:0032991	macromolecular complex

## ALS--Cortex\_Motor\_Medial, no enrichment

## all genes

A	B	p-adj	
		up in B vs A	down in B vs A
ALS--Cerebellum--C9orf72_neg	ALS--Cerebellum--C9orf72_pos	16	1
ALS--Cerebellum--C9orf72_neg	Non-Neurological_Control--Cerebellum	2,841	2,146
ALS--Cerebellum--C9orf72_pos	Non-Neurological_Control--Cerebellum	8	8
ALS--Cortex_Frontal--C9orf72_neg	ALS--Cortex_Frontal--C9orf72_pos	5	1
ALS--Cortex_Frontal--C9orf72_neg	Non-Neurological_Control--Cortex_Frontal	593	639
ALS--Cortex_Frontal--C9orf72_pos	Non-Neurological_Control--Cortex_Frontal	1	0
ALS--Cortex_Motor_Lateral--C9orf72_neg	ALS--Cortex_Motor_Lateral--C9orf72_pos	0	0
ALS--Cortex_Motor_Lateral--C9orf72_neg	Non-Neurological_Control--Cortex_Motor_Lateral	1	0
ALS--Cortex_Motor_Lateral--C9orf72_pos	Non-Neurological_Control--Cortex_Motor_Lateral	11	38
ALS--Cortex_Motor_Medial--C9orf72_neg	ALS--Cortex_Motor_Medial--C9orf72_pos	89	68
ALS--Cortex_Motor_Medial--C9orf72_neg	Non-Neurological_Control--Cortex_Motor_Medial	2	0
ALS--Cortex_Motor_Medial--C9orf72_pos	Non-Neurological_Control--Cortex_Motor_Medial	4	12
ALS--Cortex_Occipital--C9orf72_neg	ALS--Cortex_Occipital--C9orf72_pos	988	1,180
ALS--Cortex_Occipital--C9orf72_neg	Non-Neurological_Control--Cortex_Occipital	1	0
ALS--Cortex_Occipital--C9orf72_pos	Non-Neurological_Control--Cortex_Occipital	268	220
ALS--Liver--C9orf72_neg	ALS--Liver--C9orf72_pos	1	2
ALS--Liver--C9orf72_neg	Non-Neurological_Control--Liver	34	36
ALS--Liver--C9orf72_pos	Non-Neurological_Control--Liver	34	30
ALS--Spinal_Cord_Cervical--C9orf72_neg	ALS--Spinal_Cord_Cervical--C9orf72_pos	3	0
ALS--Spinal_Cord_Cervical--C9orf72_neg	Non-Neurological_Control--Spinal_Cord_Cervical	1,557	1,937
ALS--Spinal_Cord_Cervical--C9orf72_pos	Non-Neurological_Control--Spinal_Cord_Cervical	871	1,201
ALS--Spinal_Cord_Lumbar--C9orf72_neg	ALS--Spinal_Cord_Lumbar--C9orf72_pos	122	33
ALS--Spinal_Cord_Lumbar--C9orf72_neg	Non-Neurological_Control--Spinal_Cord_Lumbar	88	495
ALS--Spinal_Cord_Lumbar--C9orf72_pos	Non-Neurological_Control--Spinal_Cord_Lumbar	454	692
ALS--Spinal_Cord_Thoracic--C9orf72_neg	ALS--Spinal_Cord_Thoracic--C9orf72_pos	0	0
ALS--Spinal_Cord_Thoracic--C9orf72_neg	Non-Neurological_Control--Spinal_Cord_Thoracic	3	32
ALS--Spinal_Cord_Thoracic--C9orf72_pos	Non-Neurological_Control--Spinal_Cord_Thoracic	44	36

# GO enrichment, Cerebellum C9orf72\_neg vs Non-Neurological\_Control down genes

N	X	LOD	P	P_adj	attrib ID	attrib name
16	38	0.748328	1.92E-06	0.005	GO:0008287	protein serine/threonine phosphatase complex
16	38	0.748328	1.92E-06	0.005	GO:1903293	phosphatase complex
24	59	0.723251	1.23E-08	<0.001	GO:0019003	GDP binding
17	47	0.641755	1.09E-05	0.043	GO:0030117	membrane coat
29	84	0.610332	3.17E-08	<0.001	GO:0070125	mitochondrial translational elongation
20	59	0.598545	5.85E-06	0.015	GO:0004722	protein serine/threonine phosphatase activity
28	86	0.572206	2.24E-07	<0.001	GO:0070126	mitochondrial translational termination
23	71	0.569087	2.91E-06	0.011	GO:0031124	mRNA 3'-end processing
26	81	0.563141	8.17E-07	0.002	GO:0071013	catalytic step 2 spliceosome
21	66	0.557859	1.06E-05	0.04	GO:0006369	termination of RNA polymerase II transcription
29	93	0.544824	3.86E-07	0.001	GO:0006415	translational termination
45	146	0.53841	4.08E-10	<0.001	GO:0043209	myelin sheath
25	86	0.501488	9.72E-06	0.037	GO:0031123	RNA 3'-end processing
31	108	0.493633	1.18E-06	0.002	GO:0006414	translational elongation
29	103	0.48196	3.95E-06	0.012	GO:0006353	DNA-templated transcription, termination
34	122	0.475822	7.81E-07	0.001	GO:0043624	cellular protein complex disassembly
66	241	0.467782	1.45E-11	<0.001	GO:0010498	proteasomal protein catabolic process
39	142	0.46723	1.89E-07	<0.001	GO:0005681	spliceosomal complex
63	231	0.464974	5.08E-11	<0.001	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process
60	223	0.456548	2.63E-10	<0.001	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
60	223	0.456548	2.63E-10	<0.001	GO:0000398	mRNA splicing, via spliceosome
61	229	0.450659	2.90E-10	<0.001	GO:0000375	RNA splicing, via transesterification reactions
52	196	0.447451	6.80E-09	<0.001	GO:0000151	ubiquitin ligase complex
38	144	0.443398	8.12E-07	0.002	GO:0043241	protein complex disassembly
40	155	0.43033	7.90E-07	0.002	GO:0032984	macromolecular complex disassembly
37	145	0.423629	2.69E-06	0.008	GO:0043488	regulation of mRNA stability
41	163	0.415388	1.19E-06	0.002	GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process
37	148	0.411703	4.52E-06	0.013	GO:0043487	regulation of RNA stability
92	372	0.41007	1.00E-12	<0.001	GO:0019941	modification-dependent protein catabolic process
48	194	0.406181	2.59E-07	0.001	GO:1903322	positive regulation of protein modification by small protein conjugation or removal
44	178	0.40541	8.25E-07	0.002	GO:0031398	positive regulation of protein ubiquitination
90	367	0.404906	2.94E-12	<0.001	GO:0006511	ubiquitin-dependent protein catabolic process
92	376	0.403812	1.93E-12	<0.001	GO:0043632	modification-dependent macromolecule catabolic process
78	321	0.398285	1.34E-10	<0.001	GO:0030163	protein catabolic process
41	169	0.394459	3.21E-06	0.011	GO:0044455	mitochondrial membrane part
43	178	0.392089	2.11E-06	0.007	GO:1903364	positive regulation of cellular protein catabolic process
43	179	0.388869	2.46E-06	0.007	GO:0016241	regulation of macroautophagy
98	412	0.388024	2.21E-12	<0.001	GO:0051603	proteolysis involved in cellular protein catabolic process
78	337	0.370213	1.51E-09	<0.001	GO:0008380	RNA splicing
59	255	0.368367	1.48E-07	<0.001	GO:0003924	GTPase activity

57	248	0.364431	3.03E-07	0.001	GO:1903050	regulation of proteolysis involved in cellular protein catabolic process
51	224	0.358679	1.68E-06	0.003	GO:0006913	nucleocytoplasmic transport
90	402	0.352369	5.22E-10	<0.001	GO:0006397	mRNA processing
56	249	0.352038	8.07E-07	0.002	GO:0045732	positive regulation of protein catabolic process
57	256	0.346441	9.10E-07	0.002	GO:0000209	protein polyubiquitination
51	229	0.346206	3.32E-06	0.011	GO:0051169	nuclear transport
67	303	0.343273	1.37E-07	<0.001	GO:0004842	ubiquitin-protein transferase activity
60	272	0.341386	6.63E-07	0.001	GO:1903362	regulation of cellular protein catabolic process
112	515	0.338071	2.69E-11	<0.001	GO:1990234	transferase complex
71	326	0.335037	1.10E-07	<0.001	GO:0019787	ubiquitin-like protein transferase activity
92	434	0.321658	6.25E-09	<0.001	GO:0019866	organelle inner membrane
167	813	0.311419	6.19E-14	<0.001	GO:1902494	catalytic complex
75	361	0.308942	3.61E-07	0.001	GO:0005525	GTP binding
81	391	0.307824	1.41E-07	<0.001	GO:0042176	regulation of protein catabolic process
82	396	0.307663	1.21E-07	<0.001	GO:0005743	mitochondrial inner membrane
133	651	0.304847	3.72E-11	<0.001	GO:0044265	cellular macromolecule catabolic process
78	379	0.303925	3.16E-07	0.001	GO:0032561	guanyl ribonucleotide binding
78	380	0.302459	3.54E-07	0.001	GO:0019001	guanyl nucleotide binding
133	661	0.296275	1.10E-10	<0.001	GO:0016567	protein ubiquitination
130	650	0.292602	2.71E-10	<0.001	GO:1990904	ribonucleoprotein complex
129	647	0.290773	3.91E-10	<0.001	GO:0030529	intracellular ribonucleoprotein complex
68	338	0.290612	4.05E-06	0.012	GO:0005759	mitochondrial matrix
116	581	0.290325	2.82E-09	<0.001	GO:0031966	mitochondrial membrane
146	736	0.289559	3.84E-11	<0.001	GO:0032446	protein modification by small protein conjugation
181	924	0.285951	4.81E-13	<0.001	GO:0044429	mitochondrial part
79	401	0.279819	1.64E-06	0.003	GO:0009896	positive regulation of catabolic process
111	579	0.267334	6.08E-08	<0.001	GO:0016071	mRNA metabolic process
89	463	0.267043	1.10E-06	0.002	GO:0016032	viral process
89	463	0.267043	1.10E-06	0.002	GO:0044403	symbiosis, encompassing mutualism through parasitism
179	946	0.266229	1.44E-11	<0.001	GO:0070647	protein modification by small protein conjugation or removal
79	413	0.263626	5.26E-06	0.013	GO:0010608	posttranscriptional regulation of gene expression
90	478	0.255758	2.36E-06	0.007	GO:0044764	multi-organism cellular process
120	647	0.249836	1.18E-07	<0.001	GO:0034622	cellular macromolecular complex assembly
124	670	0.248985	8.19E-08	<0.001	GO:0016462	pyrophosphatase activity
124	670	0.248985	8.19E-08	<0.001	GO:0016817	hydrolase activity, acting on acid anhydrides
124	670	0.248985	8.19E-08	<0.001	GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
145	790	0.246167	1.11E-08	<0.001	GO:0009057	macromolecule catabolic process
270	1534	0.233931	4.08E-13	<0.001	GO:0003723	RNA binding
113	630	0.230935	1.53E-06	0.002	GO:0017111	nucleoside-triphosphatase activity
223	1281	0.223437	1.69E-10	<0.001	GO:0046907	intracellular transport
138	793	0.216284	6.36E-07	0.001	GO:0009894	regulation of catabolic process

177	1025	0.215077	2.74E-08	<0.001	GO:0015031	protein transport
118	687	0.207709	7.84E-06	0.023	GO:0031329	regulation of cellular catabolic process
130	763	0.204154	4.15E-06	0.012	GO:0006396	RNA processing
182	1078	0.202995	9.05E-08	<0.001	GO:1902582	single-organism intracellular transport
201	1195	0.202401	2.46E-08	<0.001	GO:0005739	mitochondrion
129	762	0.200598	6.27E-06	0.016	GO:0080135	regulation of cellular response to stress
184	1101	0.197523	1.59E-07	<0.001	GO:0045184	establishment of protein localization
134	797	0.197202	5.95E-06	0.015	GO:0016482	cytoplasmic transport
219	1342	0.186953	6.83E-08	<0.001	GO:0065003	macromolecular complex assembly
182	1130	0.177039	2.25E-06	0.007	GO:0006461	protein complex assembly
238	1494	0.174896	1.36E-07	<0.001	GO:0071822	protein complex subunit organization
231	1449	0.174801	2.00E-07	<0.001	GO:0008104	protein localization
233	1462	0.174771	1.81E-07	<0.001	GO:0033036	macromolecule localization
465	3064	0.163974	5.20E-11	<0.001	GO:0031090	organelle membrane
468	3090	0.162984	5.99E-11	<0.001	GO:0005654	nucleoplasm
329	2143	0.160468	2.14E-08	<0.001	GO:0043933	macromolecular complex subunit organization
613	4167	0.156607	3.84E-12	<0.001	GO:0044428	nuclear part
1050	7582	0.155958	4.38E-15	<0.001	GO:0043231	intracellular membrane-bounded organelle
1663	13217	0.149883	4.86E-11	<0.001	GO:0044424	intracellular part
1148	8480	0.148057	7.20E-14	<0.001	GO:0044446	intracellular organelle part
684	4767	0.146085	1.71E-11	<0.001	GO:0005829	cytosol
1163	8648	0.143821	3.50E-13	<0.001	GO:0043229	intracellular organelle
1106	8209	0.138718	2.22E-12	<0.001	GO:0044237	cellular metabolic process
654	4621	0.134424	8.46E-10	<0.001	GO:0032991	macromolecular complex
1159	8708	0.133699	1.25E-11	<0.001	GO:0044422	organelle part
1197	9049	0.132347	2.11E-11	<0.001	GO:0043227	membrane-bounded organelle
877	6384	0.131661	8.68E-11	<0.001	GO:0044260	cellular macromolecule metabolic process
409	2867	0.122748	1.77E-06	0.003	GO:0006464	cellular protein modification process
409	2867	0.122748	1.77E-06	0.003	GO:0036211	protein modification process
513	3648	0.12042	3.29E-07	0.001	GO:0003676	nucleic acid binding
446	3159	0.118727	1.67E-06	0.003	GO:0044267	cellular protein metabolic process
1179	9048	0.115799	3.89E-09	<0.001	GO:0044444	cytoplasmic part
550	3973	0.112815	8.52E-07	0.002	GO:0043234	protein complex
634	4630	0.110979	3.85E-07	0.001	GO:0005634	nucleus
1291	10094	0.108904	3.98E-08	<0.001	GO:0043226	organelle
735	5471	0.104421	5.72E-07	0.001	GO:1901363	heterocyclic compound binding
573	4216	0.102359	5.11E-06	0.013	GO:0006139	nucleobase-containing compound metabolic process
740	5538	0.100921	1.22E-06	0.002	GO:0097159	organic cyclic compound binding
595	4402	0.100035	6.22E-06	0.016	GO:0046483	heterocycle metabolic process
1159	9039	0.098311	4.76E-07	0.001	GO:0008152	metabolic process
1051	8239	0.085005	1.17E-05	0.045	GO:0044238	primary metabolic process
1095	8619	0.084449	1.28E-05	0.049	GO:0071704	organic substance metabolic process

# GO enrichment, C9orf72\_neg vs Non-Neurological\_Control up genes

N	X	LOD	P	P_adj	attrib ID	attrib name
9	11	1.327602	1.76E-06	0.007	GO:0017154	semaphorin receptor activity
14	24	0.888545	1.47E-06	0.006	GO:0071526	semaphorin-plexin signaling pathway
13	24	0.817821	1.07E-05	0.029	GO:0035924	cellular response to vascular endothelial growth factor stimulus
18	38	0.704125	2.77E-06	0.009	GO:0004407	histone deacetylase activity
18	40	0.663641	6.89E-06	0.023	GO:0033558	protein deacetylase activity
21	52	0.582995	9.78E-06	0.027	GO:0019213	deacetylase activity
29	72	0.581103	2.24E-07	<0.001	GO:0005089	Rho guanyl-nucleotide exchange factor activity
30	80	0.530741	8.70E-07	0.003	GO:0043535	regulation of blood vessel endothelial cell migration
27	77	0.485311	1.30E-05	0.044	GO:0008013	beta-catenin binding
40	117	0.468691	2.60E-07	<0.001	GO:0035023	regulation of Rho protein signal transduction
43	129	0.452228	2.12E-07	<0.001	GO:0051015	actin filament binding
31	94	0.445067	1.29E-05	0.039	GO:0060560	developmental growth involved in morphogenesis
43	132	0.437338	4.37E-07	0.002	GO:0031589	cell-substrate adhesion
57	191	0.382554	1.93E-07	<0.001	GO:0046578	regulation of Ras protein signal transduction
41	138	0.379185	1.08E-05	0.029	GO:0010594	regulation of endothelial cell migration
70	245	0.356419	5.71E-08	<0.001	GO:0030036	actin cytoskeleton organization
100	352	0.354999	1.25E-10	<0.001	GO:0003779	actin binding
81	289	0.34537	1.38E-08	<0.001	GO:0051056	regulation of small GTPase mediated signal transduction
54	195	0.336588	5.03E-06	0.019	GO:0010632	regulation of epithelial cell migration
83	302	0.33358	2.43E-08	<0.001	GO:0030029	actin filament-based process
60	220	0.327638	2.65E-06	0.009	GO:0031267	small GTPase binding
67	248	0.322298	1.03E-06	0.004	GO:0001525	angiogenesis
67	258	0.298728	4.55E-06	0.015	GO:0045765	regulation of angiogenesis
72	280	0.293137	3.00E-06	0.011	GO:1901342	regulation of vasculature development
64	250	0.290143	1.21E-05	0.03	GO:0051020	GTPase binding
73	292	0.276609	7.59E-06	0.023	GO:0005085	guanyl-nucleotide exchange factor activity
91	378	0.255479	3.36E-06	0.011	GO:0005911	cell-cell junction
102	432	0.244787	2.26E-06	0.008	GO:0050839	cell adhesion molecule binding
93	400	0.23542	1.20E-05	0.03	GO:0043087	regulation of GTPase activity
155	690	0.218915	1.74E-07	<0.001	GO:0005856	cytoskeleton
174	782	0.214487	6.07E-08	<0.001	GO:0008092	cytoskeletal protein binding
109	488	0.213175	1.50E-05	0.047	GO:0070161	anchoring junction
154	703	0.204346	9.44E-07	0.004	GO:0048646	anatomical structure formation involved in morphogenesis
233	1164	0.156467	2.97E-06	0.011	GO:0006928	movement of cell or subcellular component
284	1428	0.15516	4.09E-07	0.002	GO:0005524	ATP binding
288	1463	0.14938	8.47E-07	0.003	GO:0032559	adenyl ribonucleotide binding
288	1471	0.146198	1.37E-06	0.006	GO:0030554	adenyl nucleotide binding

# GO enrichment, Cortex Frontal C9orf72\_neg vs Non-Neurological\_Control down genes

N	X	LOD	P	P_adj	attrib ID	attrib name
6	8	1.859442	4.72E-08	<0.001	GO:0005832	chaperonin-containing T-complex
5	9	1.530885	5.78E-06	0.018	GO:0002199	zona pellucida receptor complex
11	32	1.175701	5.81E-09	<0.001	GO:0003743	translation initiation factor activity
13	45	1.067005	2.71E-09	<0.001	GO:0003954	NADH dehydrogenase activity
13	45	1.067005	2.71E-09	<0.001	GO:0008137	NADH dehydrogenase (ubiquinone) activity
13	45	1.067005	2.71E-09	<0.001	GO:0050136	NADH dehydrogenase (quinone) activity
16	61	1.009791	1.96E-10	<0.001	GO:0098803	respiratory chain complex
12	46	1.006903	3.96E-08	<0.001	GO:0005747	mitochondrial respiratory chain complex I
12	46	1.006903	3.96E-08	<0.001	GO:0030964	NADH dehydrogenase complex
12	46	1.006903	3.96E-08	<0.001	GO:0045271	respiratory chain complex I
12	49	0.970617	8.52E-08	<0.001	GO:0006120	mitochondrial electron transport, NADH to ubiquinone
14	58	0.96196	8.71E-09	<0.001	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor
14	64	0.906881	3.38E-08	<0.001	GO:0010257	NADH dehydrogenase complex assembly
14	64	0.906881	3.38E-08	<0.001	GO:0032981	mitochondrial respiratory chain complex I assembly
14	64	0.906881	3.38E-08	<0.001	GO:0097031	mitochondrial respiratory chain complex I biogenesis
17	81	0.884024	2.27E-09	<0.001	GO:0070271	protein complex biogenesis
20	96	0.88044	1.00E-10	<0.001	GO:0022904	respiratory electron transport chain
22	106	0.878879	1.26E-11	<0.001	GO:0098800	inner mitochondrial membrane protein complex
17	84	0.864206	4.09E-09	<0.001	GO:0033108	mitochondrial respiratory chain complex assembly
12	61	0.849747	1.10E-06	0.002	GO:0008135	translation factor activity, RNA binding
17	91	0.82118	1.46E-08	<0.001	GO:1990204	oxidoreductase complex
12	66	0.807832	2.64E-06	0.008	GO:0006369	termination of RNA polymerase II transcription
15	84	0.797376	1.93E-07	<0.001	GO:0070125	mitochondrial translational elongation
14	79	0.79356	5.42E-07	0.001	GO:0051082	unfolded protein binding
24	140	0.77701	1.04E-10	<0.001	GO:0098798	mitochondrial protein complex
12	71	0.769588	5.86E-06	0.018	GO:0031124	mRNA 3'-end processing
14	86	0.74929	1.58E-06	0.004	GO:0070126	mitochondrial translational termination
21	129	0.749265	4.05E-09	<0.001	GO:0044085	cellular component biogenesis
15	93	0.744269	7.60E-07	0.002	GO:0006415	translational termination
15	96	0.727906	1.15E-06	0.002	GO:0016651	oxidoreductase activity, acting on NAD(P)H
26	169	0.721307	2.08E-10	<0.001	GO:0044455	mitochondrial membrane part
28	185	0.713548	6.21E-11	<0.001	GO:0006457	protein folding
16	108	0.700498	1.07E-06	0.002	GO:0006414	translational elongation
23	158	0.692122	6.89E-09	<0.001	GO:0022900	electron transport chain
17	122	0.669317	1.19E-06	0.002	GO:0043624	cellular protein complex disassembly
14	103	0.657384	1.39E-05	0.035	GO:0006353	DNA-templated transcription, termination
51	434	0.595022	2.98E-14	<0.001	GO:0019866	organelle inner membrane
46	396	0.586901	8.69E-13	<0.001	GO:0005743	mitochondrial inner membrane
17	144	0.586513	1.18E-05	0.033	GO:0043241	protein complex disassembly
38	333	0.574604	1.49E-10	<0.001	GO:0043623	cellular protein complex assembly

32	337	0.482012	3.30E-07	<0.001	GO:0008380	RNA splicing
53	581	0.4701	1.83E-10	<0.001	GO:0031966	mitochondrial membrane
29	322	0.455515	3.40E-06	0.01	GO:0006091	generation of precursor metabolites and energy
79	924	0.449612	1.33E-13	<0.001	GO:0044429	mitochondrial part
56	647	0.44551	3.99E-10	<0.001	GO:0034622	cellular macromolecular complex assembly
34	402	0.426371	2.04E-06	0.005	GO:0006397	mRNA processing
113	1534	0.39062	1.42E-14	<0.001	GO:0003723	RNA binding
86	1195	0.366821	1.10E-10	<0.001	GO:0005739	mitochondrion
59	813	0.360338	8.97E-08	<0.001	GO:1902494	catalytic complex
55	763	0.355633	3.12E-07	<0.001	GO:0006396	RNA processing
45	647	0.335079	9.62E-06	0.028	GO:0030529	intracellular ribonucleoprotein complex
45	650	0.332845	1.08E-05	0.031	GO:1990904	ribonucleoprotein complex
91	1494	0.285284	1.16E-07	<0.001	GO:0071822	protein complex subunit organization
154	2721	0.271155	3.11E-10	<0.001	GO:0070062	extracellular exosome
154	2722	0.270957	3.20E-10	<0.001	GO:0065010	extracellular membrane-bounded organelle
154	2739	0.267601	5.05E-10	<0.001	GO:1903561	extracellular vesicle
154	2740	0.267405	5.18E-10	<0.001	GO:0043230	extracellular organelle
172	3118	0.26456	1.44E-10	<0.001	GO:0031988	membrane-bounded vesicle
78	1342	0.257557	6.05E-06	0.018	GO:0065003	macromolecular complex assembly
178	3303	0.25408	4.03E-10	<0.001	GO:0031982	vesicle
525	13217	0.251815	2.65E-09	<0.001	GO:0044424	intracellular part
385	8480	0.251436	6.44E-13	<0.001	GO:0044446	intracellular organelle part
403	9048	0.248765	1.66E-12	<0.001	GO:0044444	cytoplasmic part
119	2143	0.247935	1.63E-07	<0.001	GO:0043933	macromolecular complex subunit organization
164	3064	0.24476	4.47E-09	<0.001	GO:0031090	organelle membrane
388	8708	0.237677	1.07E-11	<0.001	GO:0044422	organelle part
228	4621	0.223512	1.91E-09	<0.001	GO:0032991	macromolecular complex
208	4167	0.222301	6.01E-09	<0.001	GO:0044428	nuclear part
158	3090	0.217468	2.08E-07	<0.001	GO:0005654	nucleoplasm
195	3973	0.207484	9.00E-08	<0.001	GO:0043234	protein complex
445	10883	0.19817	5.07E-08	<0.001	GO:0005515	protein binding
385	9049	0.195216	1.98E-08	<0.001	GO:0043227	membrane-bounded organelle
170	3563	0.182875	5.44E-06	0.015	GO:0044421	extracellular region part
327	7582	0.175703	3.28E-07	<0.001	GO:0043231	intracellular membrane-bounded organelle
364	8648	0.173959	4.33E-07	0.001	GO:0043229	intracellular organelle
218	4767	0.173348	2.88E-06	0.009	GO:0005829	cytosol
409	10094	0.163582	2.99E-06	0.009	GO:0043226	organelle

## GO enrichment, Cortex Frontal C9orf72\_neg vs Non-Neurological\_Control up genes

<b>N</b>	<b>X</b>	<b>LOD</b>	<b>P</b>	<b>P_adj</b>	<b>attrib ID</b>	<b>attrib name</b>
26	289	0.490954	2.74E-06	0.014	GO:0051056	regulation of small GTPase mediated signal transduction

## GO enrichment, Cortex Occipital C9orf72\_pos vs Non-Neurological\_Control down genes

- no enrichment

## GO enrichment, Cortex Occipital C9orf72\_pos vs Non-Neurological\_Control up genes

N	X	LOD	P	P_adj	attrib ID	attrib name
5	9	1.920906	7.92E-08	<0.001	GO:0046933	proton-transporting ATP synthase activity, rotational mechanism
6	11	1.907933	4.13E-09	<0.001	GO:0019774	proteasome core complex, beta-subunit complex
9	19	1.796788	2.27E-12	<0.001	GO:0005839	proteasome core complex
5	11	1.761156	2.83E-07	<0.001	GO:0046961	proton-transporting ATPase activity, rotational mechanism
7	16	1.734281	1.40E-09	<0.001	GO:0044769	ATPase activity, coupled to transmembrane movement of ions, rotational mechanism
6	14	1.718804	2.59E-08	<0.001	GO:0033178	proton-transporting two-sector ATPase complex, catalytic domain
8	21	1.637596	3.37E-10	<0.001	GO:0004298	threonine-type endopeptidase activity
8	21	1.637596	3.37E-10	<0.001	GO:0070003	threonine-type peptidase activity
7	19	1.615022	5.92E-09	<0.001	GO:0005753	mitochondrial proton-transporting ATP synthase complex
7	19	1.615022	5.92E-09	<0.001	GO:0045259	proton-transporting ATP synthase complex
5	14	1.596274	1.18E-06	0.005	GO:0036442	hydrogen-exporting ATPase activity
16	46	1.58483	2.01E-18	<0.001	GO:0005747	mitochondrial respiratory chain complex I
16	46	1.58483	2.01E-18	<0.001	GO:0030964	NADH dehydrogenase complex
16	46	1.58483	2.01E-18	<0.001	GO:0045271	respiratory chain complex I
15	45	1.555961	5.04E-17	<0.001	GO:0003954	NADH dehydrogenase activity
15	45	1.555961	5.04E-17	<0.001	GO:0008137	NADH dehydrogenase (ubiquinone) activity
15	45	1.555961	5.04E-17	<0.001	GO:0050136	NADH dehydrogenase (quinone) activity
11	33	1.551839	8.16E-13	<0.001	GO:0016469	proton-transporting two-sector ATPase complex
6	18	1.551217	1.52E-07	<0.001	GO:0006123	mitochondrial electron transport, cytochrome c to oxygen
9	27	1.550612	1.04E-10	<0.001	GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient
9	27	1.550612	1.04E-10	<0.001	GO:0015991	ATP hydrolysis coupled proton transport
16	49	1.544012	6.53E-18	<0.001	GO:0006120	mitochondrial electron transport, NADH to ubiquinone
6	19	1.517769	2.20E-07	<0.001	GO:0042776	mitochondrial ATP synthesis coupled proton transport
6	21	1.457722	4.29E-07	<0.001	GO:0015985	energy coupled proton transport, down electrochemical gradient
6	21	1.457722	4.29E-07	<0.001	GO:0015986	ATP synthesis coupled proton transport
17	61	1.447708	1.25E-17	<0.001	GO:0098803	respiratory chain complex
16	58	1.44045	1.39E-16	<0.001	GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor

9	34	1.411074	1.06E-09	<0.001	GO:0090662	ATP hydrolysis coupled transmembrane transport
26	106	1.385434	9.09E-25	<0.001	GO:0098800	inner mitochondrial membrane protein complex
23	96	1.367594	8.89E-22	<0.001	GO:0022904	respiratory electron transport chain
15	64	1.345196	1.82E-14	<0.001	GO:0010257	NADH dehydrogenase complex assembly
15	64	1.345196	1.82E-14	<0.001	GO:0032981	mitochondrial respiratory chain complex I assembly
15	64	1.345196	1.82E-14	<0.001	GO:0097031	mitochondrial respiratory chain complex I biogenesis
7	31	1.322476	2.66E-07	<0.001	GO:0042407	cristae formation
6	27	1.315471	2.17E-06	0.012	GO:0090383	phagosome acidification
7	33	1.288348	4.21E-07	<0.001	GO:0006754	ATP biosynthetic process
8	38	1.283219	6.53E-08	<0.001	GO:0007007	inner mitochondrial membrane organization
7	36	1.241699	7.92E-07	0.003	GO:0033572	transferrin transport
26	140	1.231598	1.94E-21	<0.001	GO:0098798	mitochondrial protein complex
8	42	1.229602	1.50E-07	<0.001	GO:0006094	gluconeogenesis
7	37	1.227197	9.65E-07	0.003	GO:0015682	ferric iron transport
7	37	1.227197	9.65E-07	0.003	GO:0072512	trivalent inorganic cation transport
6	32	1.224542	6.25E-06	0.032	GO:0006734	NADH metabolic process
17	91	1.223185	1.81E-14	<0.001	GO:1990204	oxidoreductase complex
8	43	1.217169	1.82E-07	<0.001	GO:0045851	pH reduction
15	81	1.216567	7.43E-13	<0.001	GO:0070271	protein complex biogenesis
9	50	1.199179	4.13E-08	<0.001	GO:0046364	monosaccharide biosynthetic process
15	84	1.197331	1.30E-12	<0.001	GO:0033108	mitochondrial respiratory chain complex assembly
17	96	1.194852	4.60E-14	<0.001	GO:0016651	oxidoreductase activity, acting on NAD(P)H
29	169	1.194077	8.89E-23	<0.001	GO:0044455	mitochondrial membrane part
8	45	1.193318	2.63E-07	<0.001	GO:0019319	hexose biosynthetic process
11	63	1.183136	1.76E-09	<0.001	GO:0006521	regulation of cellular amino acid metabolic process
11	64	1.174917	2.10E-09	<0.001	GO:0000502	proteasome complex
7	41	1.173581	2.00E-06	0.011	GO:0009206	purine ribonucleoside triphosphate biosynthetic process
11	65	1.16685	2.49E-09	<0.001	GO:0038061	NIK/NF-kappaB signaling
7	42	1.161147	2.38E-06	0.012	GO:0009145	purine nucleoside triphosphate biosynthetic process
7	42	1.161147	2.38E-06	0.012	GO:0051452	intracellular pH reduction
11	66	1.158929	2.95E-09	<0.001	GO:0015078	hydrogen ion transmembrane transporter activity
11	69	1.135994	4.82E-09	<0.001	GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
9	57	1.131316	1.36E-07	<0.001	GO:0051453	regulation of intracellular pH
24	158	1.123548	9.48E-18	<0.001	GO:0022900	electron transport chain
7	46	1.114682	4.48E-06	0.025	GO:0019829	cation-transporting ATPase activity
12	79	1.11153	1.69E-09	<0.001	GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia
7	47	1.1038	5.20E-06	0.029	GO:0009201	ribonucleoside triphosphate biosynthetic process
17	115	1.101322	1.00E-12	<0.001	GO:1902600	hydrogen ion transmembrane transport
11	74	1.100255	1.03E-08	<0.001	GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
9	61	1.096801	2.48E-07	<0.001	GO:0030641	regulation of cellular pH
11	76	1.086739	1.38E-08	<0.001	GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I
11	76	1.086739	1.38E-08	<0.001	GO:0051437	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transi

10	70	1.080154	7.24E-08	<0.001	GO:0006885	regulation of pH
17	126	1.055077	4.60E-12	<0.001	GO:0015992	proton transport
11	81	1.054669	2.74E-08	<0.001	GO:0010972	negative regulation of G2/M transition of mitotic cell cycle
11	81	1.054669	2.74E-08	<0.001	GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
17	128	1.047167	5.97E-12	<0.001	GO:0006818	hydrogen transport
12	90	1.045697	7.84E-09	<0.001	GO:0002474	antigen processing and presentation of peptide antigen via MHC class I
11	83	1.042472	3.55E-08	<0.001	GO:0051436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
11	83	1.042472	3.55E-08	<0.001	GO:0051439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
11	88	1.013387	6.61E-08	<0.001	GO:0033238	regulation of cellular amine metabolic process
16	129	1.01212	7.29E-11	<0.001	GO:0044085	cellular component biogenesis
12	98	1.003356	2.09E-08	<0.001	GO:0060071	Wnt signaling pathway, planar cell polarity pathway
11	90	1.002273	8.37E-08	<0.001	GO:2000060	positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process
12	100	0.99338	2.64E-08	<0.001	GO:0051443	positive regulation of ubiquitin-protein transferase activity
12	100	0.99338	2.64E-08	<0.001	GO:0090175	regulation of establishment of planar polarity
11	93	0.986113	1.18E-07	<0.001	GO:1902750	negative regulation of cell cycle G2/M phase transition
20	172	0.984102	9.85E-13	<0.001	GO:0002478	antigen processing and presentation of exogenous peptide antigen
12	102	0.983627	3.31E-08	<0.001	GO:0046034	ATP metabolic process
13	111	0.981765	9.27E-09	<0.001	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress
9	77	0.980882	1.88E-06	0.011	GO:0030004	cellular monovalent inorganic cation homeostasis
12	103	0.97883	3.69E-08	<0.001	GO:1902036	regulation of hematopoietic stem cell differentiation
20	174	0.978394	1.23E-12	<0.001	GO:0019884	antigen processing and presentation of exogenous antigen
11	95	0.975662	1.47E-07	<0.001	GO:0051444	negative regulation of ubiquitin-protein transferase activity
11	96	0.970528	1.64E-07	<0.001	GO:0051352	negative regulation of ligase activity
11	96	0.970528	1.64E-07	<0.001	GO:0070498	interleukin-1-mediated signaling pathway
12	105	0.969391	4.59E-08	<0.001	GO:0051351	positive regulation of ligase activity
20	179	0.96444	2.09E-12	<0.001	GO:0048002	antigen processing and presentation of peptide antigen
13	117	0.955939	1.77E-08	<0.001	GO:0043620	regulation of DNA-templated transcription in response to stress
14	130	0.941175	7.45E-09	<0.001	GO:0009144	purine nucleoside triphosphate metabolic process
33	322	0.938998	1.33E-18	<0.001	GO:0006091	generation of precursor metabolites and energy
13	123	0.931547	3.24E-08	<0.001	GO:0009205	purine ribonucleoside triphosphate metabolic process
11	106	0.922248	4.54E-07	<0.001	GO:2000058	regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process
13	129	0.908438	5.75E-08	<0.001	GO:0009199	ribonucleoside triphosphate metabolic process
10	100	0.904533	2.15E-06	0.011	GO:0055067	monovalent inorganic cation homeostasis
20	203	0.90298	2.16E-11	<0.001	GO:0019882	antigen processing and presentation
14	148	0.878341	3.96E-08	<0.001	GO:0009141	nucleoside triphosphate metabolic process
12	128	0.873317	4.14E-07	<0.001	GO:0051438	regulation of ubiquitin-protein transferase activity
11	118	0.870552	1.34E-06	0.005	GO:0002223	stimulatory C-type lectin receptor signaling pathway
12	129	0.869581	4.51E-07	<0.001	GO:0090263	positive regulation of canonical Wnt signaling pathway
9	97	0.869144	1.29E-05	0.048	GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II
12	130	0.865876	4.90E-07	0.001	GO:0035567	non-canonical Wnt signaling pathway
12	131	0.862202	5.33E-07	0.001	GO:0051340	regulation of ligase activity
11	121	0.858525	1.72E-06	0.008	GO:0002220	innate immune response activating cell surface receptor signaling pathway
13	146	0.848869	2.48E-07	<0.001	GO:0043209	myelin sheath
13	147	0.845603	2.69E-07	<0.001	GO:0031397	negative regulation of protein ubiquitination
11	126	0.839184	2.56E-06	0.012	GO:0038095	Fc-epsilon receptor signaling pathway

11	127	0.835415	2.77E-06	0.013	GO:0033209	tumor necrosis factor-mediated signaling pathway
12	140	0.830448	1.09E-06	0.003	GO:0009167	purine ribonucleoside monophosphate metabolic process
12	141	0.827057	1.17E-06	0.003	GO:0009126	purine nucleoside monophosphate metabolic process
14	166	0.823355	1.68E-07	<0.001	GO:0009123	nucleoside monophosphate metabolic process
13	157	0.814214	5.75E-07	0.001	GO:1903321	negative regulation of protein modification by small protein conjugation or removal
12	145	0.813748	1.58E-06	0.008	GO:0043488	regulation of mRNA stability
12	148	0.804024	1.96E-06	0.011	GO:0043487	regulation of RNA stability
13	163	0.796399	8.83E-07	0.003	GO:0030177	positive regulation of Wnt signaling pathway
12	152	0.791383	2.60E-06	0.012	GO:0009161	ribonucleoside monophosphate metabolic process
30	396	0.788435	1.87E-13	<0.001	GO:0005743	mitochondrial inner membrane
12	153	0.788278	2.78E-06	0.013	GO:1901532	regulation of hematopoietic progenitor cell differentiation
14	179	0.78751	4.24E-07	<0.001	GO:0010389	regulation of G2/M transition of mitotic cell cycle
11	142	0.782451	8.18E-06	0.035	GO:0050852	T cell receptor signaling pathway
31	434	0.761588	3.46E-13	<0.001	GO:0019866	organelle inner membrane
12	162	0.761279	5.04E-06	0.029	GO:0090090	negative regulation of canonical Wnt signaling pathway
13	178	0.754772	2.38E-06	0.012	GO:0031398	positive regulation of protein ubiquitination
14	197	0.742232	1.35E-06	0.005	GO:1902749	regulation of cell cycle G2/M phase transition
13	184	0.73916	3.44E-06	0.019	GO:1901991	negative regulation of mitotic cell cycle phase transition
13	193	0.716727	5.81E-06	0.032	GO:0030178	negative regulation of Wnt signaling pathway
13	194	0.714303	6.15E-06	0.032	GO:1903322	positive regulation of protein modification by small protein conjugation or removal
14	214	0.703339	3.57E-06	0.021	GO:0046128	purine ribonucleoside metabolic process
14	217	0.696815	4.20E-06	0.024	GO:0042278	purine nucleoside metabolic process
13	204	0.690767	1.06E-05	0.038	GO:1901988	negative regulation of cell cycle phase transition
14	229	0.671639	7.80E-06	0.035	GO:2000027	regulation of organ morphogenesis
14	231	0.667578	8.62E-06	0.035	GO:2000736	regulation of stem cell differentiation
20	333	0.667193	1.15E-07	<0.001	GO:0043623	cellular protein complex assembly
18	300	0.66511	5.12E-07	0.001	GO:0070646	protein modification by small protein removal
14	237	0.655613	1.15E-05	0.04	GO:0009119	ribonucleoside metabolic process
32	581	0.639245	1.34E-10	<0.001	GO:0031966	mitochondrial membrane
15	266	0.634341	9.80E-06	0.037	GO:0031396	regulation of protein ubiquitination
35	653	0.630039	3.58E-11	<0.001	GO:0016491	oxidoreductase activity
46	914	0.614489	1.85E-13	<0.001	GO:0098796	membrane protein complex
41	857	0.583565	2.24E-11	<0.001	GO:0055114	oxidation-reduction process
21	427	0.574513	1.49E-06	0.006	GO:0043687	post-translational protein modification
42	924	0.560386	6.21E-11	<0.001	GO:0044429	mitochondrial part
30	647	0.555637	2.80E-08	<0.001	GO:0034622	cellular macromolecular complex assembly
19	413	0.541924	1.23E-05	0.04	GO:0010608	posttranscriptional regulation of gene expression
92	2739	0.482004	1.99E-15	<0.001	GO:1903561	extracellular vesicle
92	2740	0.481812	2.04E-15	<0.001	GO:0043230	extracellular organelle
91	2721	0.478109	4.01E-15	<0.001	GO:0070062	extracellular exosome
91	2722	0.477915	4.11E-15	<0.001	GO:0065010	extracellular membrane-bounded organelle
101	3118	0.477634	4.45E-16	<0.001	GO:0031988	membrane-bounded vesicle
31	813	0.464476	1.20E-06	0.005	GO:1902494	catalytic complex
102	3303	0.45341	7.62E-15	<0.001	GO:0031982	vesicle
43	1195	0.449566	4.22E-08	<0.001	GO:0005739	mitochondrion

## GO enrichment, liver C9orf72\_pos vs Non-Neurological\_Control down genes

N	X	LOD	P	P_adj	attrib ID	attrib name
2	4	2.805167	1.57E-05	0.039	GO:0033695	oxidoreductase activity, acting on CH or CH2 groups, quinone or similar compound as acceptor
2	4	2.805167	1.57E-05	0.039	GO:0034875	caffeine oxidase activity
3	27	1.975056	1.15E-05	0.026	GO:0016712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,
4	89	1.556027	1.32E-05	0.03	GO:0004497	monooxygenase activity
4	102	1.494245	2.26E-05	0.044	GO:0006805	xenobiotic metabolic process

## GO enrichment, liver C9orf72\_pos vs Non-Neurological\_Control down genes

N	X	LOD	P	P_adj	attrib ID	attrib name
3	18	2.115008	4.75E-06	0.016	GO:0071294	cellular response to zinc ion

# GO enrichment, Spinal Cord Cervical C9orf72\_neg vs Non-Neurological\_Control down genes

N	X	LOD	P	P_adj	attrib ID	attrib name
12	15	1.484266	6.09E-10	<0.001	GO:0042613	MHC class II protein complex
8	10	1.462028	5.55E-07	<0.001	GO:0032395	MHC class II receptor activity
18	23	1.459536	4.78E-14	<0.001	GO:0042611	MHC protein complex
10	14	1.298924	1.11E-07	<0.001	GO:0045730	respiratory burst
9	15	1.095479	4.35E-06	0.015	GO:0050765	negative regulation of phagocytosis
16	28	1.052664	1.92E-09	<0.001	GO:0050853	B cell receptor signaling pathway
16	28	1.052664	1.92E-09	<0.001	GO:0071556	integral component of luminal side of endoplasmic reticulum membrane
11	21	0.970522	2.23E-06	0.009	GO:0042605	peptide antigen binding
17	34	0.932184	9.15E-09	<0.001	GO:0042116	macrophage activation
11	22	0.930987	4.04E-06	0.01	GO:0050858	negative regulation of antigen receptor-mediated signaling pathway
34	70	0.911069	1.09E-15	<0.001	GO:0060333	interferon-gamma-mediated signaling pathway
15	31	0.904606	1.21E-07	<0.001	GO:0031663	lipopolysaccharide-mediated signaling pathway
13	27	0.900325	9.17E-07	0.001	GO:0006911	phagocytosis, engulfment
15	32	0.879025	2.05E-07	<0.001	GO:0002755	MyD88-dependent toll-like receptor signaling pathway
23	50	0.865013	1.88E-10	<0.001	GO:0012507	ER to Golgi transport vesicle membrane
11	24	0.861299	1.17E-05	0.05	GO:2000482	regulation of interleukin-8 secretion
15	33	0.854865	3.40E-07	<0.001	GO:0030669	clathrin-coated endocytic vesicle membrane
15	34	0.831976	5.49E-07	<0.001	GO:0010324	membrane invagination
14	32	0.825676	1.49E-06	0.004	GO:0042098	T cell proliferation
28	66	0.803507	2.24E-11	<0.001	GO:0070661	leukocyte proliferation
25	59	0.802268	2.72E-10	<0.001	GO:0032943	mononuclear cell proliferation
24	57	0.797468	7.23E-10	<0.001	GO:0046651	lymphocyte proliferation
13	31	0.794416	6.28E-06	0.025	GO:0097028	dendritic cell differentiation
23	55	0.79233	1.92E-09	<0.001	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin genes
17	41	0.78587	2.89E-07	<0.001	GO:0043300	regulation of leukocyte degranulation
18	44	0.776098	1.65E-07	<0.001	GO:0002886	regulation of myeloid leukocyte mediated immunity
13	32	0.771526	9.56E-06	0.041	GO:0006734	NADH metabolic process
19	47	0.767535	9.43E-08	<0.001	GO:1903305	regulation of regulated secretory pathway
14	35	0.76033	5.40E-06	0.019	GO:0030593	neutrophil chemotaxis
37	93	0.757681	1.57E-13	<0.001	GO:0002224	toll-like receptor signaling pathway
29	73	0.755653	6.87E-11	<0.001	GO:0070821	tertiary granule membrane
14	36	0.740559	7.98E-06	0.029	GO:0002720	positive regulation of cytokine production involved in immune response
14	36	0.740559	7.98E-06	0.029	GO:0050856	regulation of T cell receptor signaling pathway
21	54	0.74006	4.49E-08	<0.001	GO:1904724	tertiary granule lumen
25	66	0.721854	4.52E-09	<0.001	GO:0003823	antigen binding
25	66	0.721854	4.52E-09	<0.001	GO:0045335	phagocytic vesicle
16	43	0.709844	3.58E-06	0.01	GO:0050663	cytokine secretion
24	65	0.704253	1.65E-08	<0.001	GO:0002718	regulation of cytokine production involved in immune response
21	57	0.702732	1.35E-07	<0.001	GO:0035577	azurophil granule membrane
26	71	0.698717	5.16E-09	<0.001	GO:0030670	phagocytic vesicle membrane

19	52	0.697203	6.15E-07	<0.001	GO:0032722	positive regulation of chemokine production
28	77	0.694071	1.61E-09	<0.001	GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis
28	77	0.694071	1.61E-09	<0.001	GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis
29	80	0.692021	9.01E-10	<0.001	GO:0038094	Fc-gamma receptor signaling pathway
21	58	0.690967	1.90E-07	<0.001	GO:0034121	regulation of toll-like receptor signaling pathway
28	78	0.685358	2.26E-09	<0.001	GO:0002431	Fc receptor mediated stimulatory signaling pathway
19	53	0.684402	8.65E-07	0.001	GO:0050854	regulation of antigen receptor-mediated signaling pathway
24	67	0.683758	3.28E-08	<0.001	GO:0050764	regulation of phagocytosis
169	491	0.680494	2.77E-47	<0.001	GO:0036230	granulocyte activation
190	556	0.679676	1.20E-52	<0.001	GO:0002274	myeloid leukocyte activation
16	45	0.679302	7.11E-06	0.027	GO:0002704	negative regulation of leukocyte mediated immunity
164	479	0.675983	1.55E-45	<0.001	GO:0002283	neutrophil activation involved in immune response
172	505	0.673988	2.12E-47	<0.001	GO:0002275	myeloid cell activation involved in immune response
166	487	0.673378	8.49E-46	<0.001	GO:0042119	neutrophil activation
162	475	0.672997	9.89E-45	<0.001	GO:0043312	neutrophil degranulation
32	91	0.671844	3.04E-10	<0.001	GO:0035578	azurophil granule lumen
168	495	0.670863	4.64E-46	<0.001	GO:0043299	leukocyte degranulation
16	46	0.664798	9.85E-06	0.041	GO:0071621	granulocyte chemotaxis
170	508	0.661834	1.16E-45	<0.001	GO:0045055	regulated secretory pathway
188	574	0.65098	6.19E-49	<0.001	GO:0002366	leukocyte activation involved in immune response
189	578	0.650087	4.46E-49	<0.001	GO:0002263	cell activation involved in immune response
40	118	0.648386	7.20E-12	<0.001	GO:0002221	pattern recognition receptor signaling pathway
30	90	0.63654	4.65E-09	<0.001	GO:0002474	antigen processing and presentation of peptide antigen via MHC class I
28	84	0.636442	1.51E-08	<0.001	GO:0001816	cytokine production
23	69	0.63639	2.87E-07	<0.001	GO:0032642	regulation of chemokine production
29	88	0.629099	1.12E-08	<0.001	GO:0030658	transport vesicle membrane
54	165	0.627262	8.59E-15	<0.001	GO:0050851	antigen receptor-mediated signaling pathway
23	70	0.627123	3.85E-07	<0.001	GO:0050871	positive regulation of B cell activation
21	64	0.62635	1.25E-06	0.001	GO:0045454	cell redox homeostasis
91	281	0.626177	1.20E-23	<0.001	GO:0030667	secretory granule membrane
20	61	0.625933	2.27E-06	0.009	GO:0032729	positive regulation of interferon-gamma production
20	61	0.625933	2.27E-06	0.009	GO:0101003	ficolin-1-rich granule membrane
28	86	0.621282	2.70E-08	<0.001	GO:0042102	positive regulation of T cell proliferation
250	818	0.617616	8.07E-59	<0.001	GO:0045321	leukocyte activation
19	59	0.614607	5.46E-06	0.019	GO:0002449	lymphocyte mediated immunity
24	76	0.60185	4.96E-07	<0.001	GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I
23	73	0.600446	8.93E-07	0.001	GO:0002690	positive regulation of leukocyte chemotaxis
38	121	0.598985	3.08E-10	<0.001	GO:1904813	ficolin-1-rich granule lumen
47	150	0.598495	2.75E-12	<0.001	GO:0030666	endocytic vesicle membrane
35	112	0.595611	1.78E-09	<0.001	GO:0050715	positive regulation of cytokine secretion
19	61	0.59362	9.44E-06	0.041	GO:0035580	specific granule lumen
23	74	0.591903	1.17E-06	0.001	GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
112	368	0.589917	3.00E-26	<0.001	GO:0002757	immune response-activating signal transduction
21	68	0.58804	3.78E-06	0.01	GO:0031295	T cell costimulation
21	68	0.58804	3.78E-06	0.01	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production

37	120	0.587327	9.37E-10	<0.001	GO:0050671	positive regulation of lymphocyte proliferation
257	885	0.586171	1.12E-55	<0.001	GO:0002252	immune effector process
20	65	0.585864	6.81E-06	0.026	GO:0032760	positive regulation of tumor necrosis factor production
24	78	0.585556	8.45E-07	0.001	GO:2000106	regulation of leukocyte apoptotic process
28	91	0.585532	1.06E-07	<0.001	GO:0035579	specific granule membrane
269	931	0.58525	6.88E-58	<0.001	GO:0001775	cell activation
37	121	0.58213	1.21E-09	<0.001	GO:0032946	positive regulation of mononuclear cell proliferation
90	298	0.581477	4.62E-21	<0.001	GO:0050867	positive regulation of cell activation
21	69	0.578966	4.90E-06	0.016	GO:0031294	lymphocyte costimulation
28	92	0.578719	1.37E-07	<0.001	GO:0043202	lysosomal lumen
128	430	0.578617	7.81E-29	<0.001	GO:0002253	activation of immune response
38	125	0.578557	8.78E-10	<0.001	GO:0050777	negative regulation of immune response
203	698	0.577121	7.68E-44	<0.001	GO:0006887	exocytosis
119	400	0.576738	7.63E-27	<0.001	GO:0002764	immune response-regulating signaling pathway
20	66	0.576396	8.81E-06	0.037	GO:1903725	regulation of phospholipid metabolic process
86	288	0.573747	7.91E-20	<0.001	GO:0002696	positive regulation of leukocyte activation
38	126	0.573595	1.13E-09	<0.001	GO:0070665	positive regulation of leukocyte proliferation
82	276	0.569967	8.14E-19	<0.001	GO:0002429	immune response-activating cell surface receptor signaling pathway
54	182	0.565181	7.85E-13	<0.001	GO:0002250	adaptive immune response
36	121	0.565027	4.61E-09	<0.001	GO:0045807	positive regulation of endocytosis
53	179	0.563774	1.40E-12	<0.001	GO:0048002	antigen processing and presentation of peptide antigen
60	203	0.563578	5.10E-14	<0.001	GO:0019882	antigen processing and presentation
50	169	0.56293	6.19E-12	<0.001	GO:0005775	vacuolar lumen
38	129	0.559038	2.37E-09	<0.001	GO:0002819	regulation of adaptive immune response
59	202	0.556108	1.47E-13	<0.001	GO:1903039	positive regulation of leukocyte cell-cell adhesion
89	307	0.555804	1.55E-19	<0.001	GO:0002768	immune response-regulating cell surface receptor signaling pathway
29	99	0.555135	2.06E-07	<0.001	GO:0042470	melanosome
29	99	0.555135	2.06E-07	<0.001	GO:0048770	pigment granule
24	82	0.554694	2.29E-06	0.009	GO:0034341	response to interferon-gamma
31	106	0.554189	8.26E-08	<0.001	GO:0002698	negative regulation of immune effector process
166	586	0.554119	2.76E-34	<0.001	GO:0050778	positive regulation of immune response
73	252	0.552955	3.07E-16	<0.001	GO:0051251	positive regulation of lymphocyte activation
55	190	0.550086	1.46E-12	<0.001	GO:0038093	Fc receptor signaling pathway
31	107	0.548448	1.05E-07	<0.001	GO:0030168	platelet activation
41	142	0.547001	1.09E-09	<0.001	GO:0050852	T cell receptor signaling pathway
58	202	0.545473	5.26E-13	<0.001	GO:0034112	positive regulation of homotypic cell-cell adhesion
240	879	0.5443	1.20E-46	<0.001	GO:0032940	secretion by cell
23	80	0.543884	5.18E-06	0.018	GO:0045621	positive regulation of lymphocyte differentiation
56	196	0.542202	1.65E-12	<0.001	GO:0050870	positive regulation of T cell activation
49	172	0.539608	4.51E-11	<0.001	GO:0002478	antigen processing and presentation of exogenous peptide antigen
29	102	0.536958	4.15E-07	<0.001	GO:0016052	carbohydrate catabolic process
27	95	0.536743	1.04E-06	0.001	GO:0002673	regulation of acute inflammatory response
47	166	0.535642	1.41E-10	<0.001	GO:0002703	regulation of leukocyte mediated immunity
30	106	0.534209	2.94E-07	<0.001	GO:0050864	regulation of B cell activation

226	840	0.532691	1.01E-42	<0.001	GO:0050776	regulation of immune response
49	174	0.532578	7.08E-11	<0.001	GO:0019884	antigen processing and presentation of exogenous antigen
66	236	0.530442	5.27E-14	<0.001	GO:0002218	activation of innate immune response
27	96	0.530422	1.30E-06	0.001	GO:0044724	single-organism carbohydrate catabolic process
61	218	0.530127	4.63E-13	<0.001	GO:0002758	innate immune response-activating signal transduction
32	114	0.529297	1.47E-07	<0.001	GO:0002700	regulation of production of molecular mediator of immune response
32	114	0.529297	1.47E-07	<0.001	GO:0009306	protein secretion
33	118	0.527094	1.04E-07	<0.001	GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built f
70	252	0.52688	1.31E-14	<0.001	GO:000323	lytic vacuole
70	252	0.52688	1.31E-14	<0.001	GO:0005764	lysosome
31	111	0.526207	2.60E-07	<0.001	GO:0032680	regulation of tumor necrosis factor production
36	129	0.525969	2.96E-08	<0.001	GO:0030662	coated vesicle membrane
52	187	0.525261	3.13E-11	<0.001	GO:0050670	regulation of lymphocyte proliferation
32	115	0.524038	1.84E-07	<0.001	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production
25	90	0.523025	4.06E-06	0.01	GO:0032649	regulation of interferon-gamma production
52	188	0.522041	3.90E-11	<0.001	GO:0032944	regulation of mononuclear cell proliferation
48	174	0.520011	2.41E-10	<0.001	GO:0071593	lymphocyte aggregation
30	109	0.517424	5.69E-07	<0.001	GO:0050729	positive regulation of inflammatory response
54	197	0.516833	2.41E-11	<0.001	GO:0070663	regulation of leukocyte proliferation
47	172	0.514207	5.23E-10	<0.001	GO:0042110	T cell activation
47	172	0.514207	5.23E-10	<0.001	GO:0070489	T cell aggregation
29	106	0.513837	1.00E-06	0.001	GO:0032675	regulation of interleukin-6 production
38	139	0.513727	2.28E-08	<0.001	GO:0042129	regulation of T cell proliferation
49	180	0.512136	2.60E-10	<0.001	GO:0070486	leukocyte aggregation
46	169	0.511766	9.15E-10	<0.001	GO:0002699	positive regulation of immune effector process
99	368	0.511685	4.72E-19	<0.001	GO:0045088	regulation of innate immune response
253	984	0.509593	4.19E-44	<0.001	GO:0046903	secretion
33	122	0.507131	2.46E-07	<0.001	GO:0008064	regulation of actin polymerization or depolymerization
85	319	0.503888	2.89E-16	<0.001	GO:0034774	secretory granule lumen
25	93	0.503496	7.69E-06	0.029	GO:0002688	regulation of leukocyte chemotaxis
29	108	0.502719	1.52E-06	0.004	GO:0002687	positive regulation of leukocyte migration
33	123	0.502279	3.03E-07	<0.001	GO:0009205	purine ribonucleoside triphosphate metabolic process
33	123	0.502279	3.03E-07	<0.001	GO:0030832	regulation of actin filament length
26	97	0.501734	5.39E-06	0.019	GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II
28	105	0.498632	2.66E-06	0.009	GO:0030833	regulation of actin filament polymerization
62	234	0.497455	4.08E-12	<0.001	GO:0022409	positive regulation of cell-cell adhesion
463	1959	0.496955	1.97E-71	<0.001	GO:0002376	immune system process
44	166	0.495772	5.16E-09	<0.001	GO:0050707	regulation of cytokine secretion
26	98	0.495675	6.61E-06	0.026	GO:0002495	antigen processing and presentation of peptide antigen via MHC class II
26	98	0.495675	6.61E-06	0.026	GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
36	136	0.494429	1.29E-07	<0.001	GO:0051092	positive regulation of NF-kappaB transcription factor activity
221	875	0.493244	4.08E-37	<0.001	GO:0002684	positive regulation of immune system process
75	286	0.492979	4.10E-14	<0.001	GO:0045089	positive regulation of innate immune response
97	372	0.492671	1.08E-17	<0.001	GO:0002697	regulation of immune effector process
56	213	0.492145	6.16E-11	<0.001	GO:0007159	leukocyte cell-cell adhesion
34	130	0.487243	3.89E-07	<0.001	GO:0009144	purine nucleoside triphosphate metabolic process
54	209	0.481635	2.72E-10	<0.001	GO:0030100	regulation of endocytosis
261	1068	0.480121	3.04E-41	<0.001	GO:0044433	cytoplasmic vesicle part
86	336	0.480079	2.58E-15	<0.001	GO:0060205	cytoplasmic membrane-bounded vesicle lumen
51	198	0.479506	9.53E-10	<0.001	GO:0032535	regulation of cellular component size

## GO enrichment, Spinal Cord Cervical C9orf72\_neg vs Non-Neurological\_Control up genes

N	X	LOD	P	P_adj	attrib ID	attrib name
20	68	0.666222	4.63E-07	0.002	GO:0007272	ensheathment of neurons
20	68	0.666222	4.63E-07	0.002	GO:0008366	axon ensheathment
18	63	0.648883	2.74E-06	0.013	GO:0042552	myelination
34	170	0.444597	1.71E-06	0.009	GO:0048812	neuron projection morphogenesis
31	164	0.413963	1.59E-05	0.043	GO:0045216	cell-cell junction organization
40	224	0.383839	4.37E-06	0.017	GO:0008017	microtubule binding
51	304	0.351574	1.57E-06	0.009	GO:0015631	tubulin binding
55	346	0.323562	3.44E-06	0.014	GO:0005874	microtubule
51	330	0.308492	1.71E-05	0.049	GO:0043547	positive regulation of GTPase activity
60	400	0.293712	8.31E-06	0.026	GO:0043087	regulation of GTPase activity
77	543	0.266168	4.05E-06	0.014	GO:0045664	regulation of neuron differentiation
109	782	0.260784	9.90E-08	<0.001	GO:0008092	cytoskeletal protein binding
76	553	0.249822	1.45E-05	0.042	GO:0031344	regulation of cell projection organization
102	749	0.247793	7.82E-07	0.005	GO:0051960	regulation of nervous system development
89	668	0.235028	9.57E-06	0.033	GO:0050767	regulation of neurogenesis

# GO enrichment, Spinal Cord Cervical C9orf72\_pos vs Non-Neurological\_Control down genes

N	X	LOD	P	P_adj	attrib ID	attrib name
5	5	2.197301	1.20E-06	0.006	GO:0001875	lipopolysaccharide receptor activity
5	5	2.197301	1.20E-06	0.006	GO:2001188	regulation of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell
6	8	1.571194	1.95E-06	0.009	GO:0034135	regulation of toll-like receptor 2 signaling pathway
11	15	1.565475	9.75E-11	<0.001	GO:0042613	MHC class II protein complex
16	23	1.502164	1.65E-14	<0.001	GO:0042611	MHC protein complex
7	10	1.487552	5.12E-07	0.002	GO:0032395	MHC class II receptor activity
7	10	1.487552	5.12E-07	0.002	GO:1902563	regulation of neutrophil activation
6	10	1.315871	1.30E-05	0.04	GO:0002887	negative regulation of myeloid leukocyte mediated immunity
6	10	1.315871	1.30E-05	0.04	GO:0034138	toll-like receptor 3 signaling pathway
7	12	1.291206	3.01E-06	0.012	GO:0032490	detection of molecule of bacterial origin
8	14	1.273352	6.97E-07	0.004	GO:0045730	respiratory burst
15	28	1.219221	2.69E-11	<0.001	GO:0050853	B cell receptor signaling pathway
7	13	1.21863	6.15E-06	0.018	GO:0010885	regulation of cholesterol storage
8	15	1.211178	1.41E-06	0.007	GO:0001911	negative regulation of leukocyte mediated cytotoxicity
8	15	1.211178	1.41E-06	0.007	GO:2000484	positive regulation of interleukin-8 secretion
11	21	1.197346	1.75E-08	<0.001	GO:0042100	B cell proliferation
11	21	1.197346	1.75E-08	<0.001	GO:0042605	peptide antigen binding
14	28	1.158832	4.19E-10	<0.001	GO:0071556	integral component of luminal side of endoplasmic reticulum membrane
7	14	1.156457	1.16E-05	0.033	GO:0016064	immunoglobulin mediated immune response
8	17	1.108465	4.73E-06	0.013	GO:0008329	signaling pattern recognition receptor activity
8	17	1.108465	4.73E-06	0.013	GO:0038187	pattern recognition receptor activity
11	24	1.088126	1.03E-07	<0.001	GO:2000482	regulation of interleukin-8 secretion
9	20	1.074109	1.87E-06	0.009	GO:0034123	positive regulation of toll-like receptor signaling pathway
8	18	1.064974	8.02E-06	0.026	GO:0032928	regulation of superoxide anion generation
19	44	1.04388	8.22E-12	<0.001	GO:0002886	regulation of myeloid leukocyte mediated immunity
9	21	1.037872	3.09E-06	0.012	GO:0001782	B cell homeostasis
9	21	1.037872	3.09E-06	0.012	GO:0022612	gland morphogenesis
8	19	1.02544	1.30E-05	0.04	GO:0031342	negative regulation of cell killing
13	31	1.021527	2.60E-08	<0.001	GO:0031663	lipopolysaccharide-mediated signaling pathway
17	41	1.013549	2.27E-10	<0.001	GO:0043300	regulation of leukocyte degranulation
9	22	1.004423	4.92E-06	0.014	GO:0002888	positive regulation of myeloid leukocyte mediated immunity
9	22	1.004423	4.92E-06	0.014	GO:0009595	detection of biotic stimulus
13	32	0.998639	4.12E-08	<0.001	GO:0002755	MyD88-dependent toll-like receptor signaling pathway
19	47	0.995499	3.37E-11	<0.001	GO:1903305	regulation of regulated secretory pathway
12	31	0.96485	2.60E-07	0.002	GO:0097028	dendritic cell differentiation
10	26	0.961026	2.83E-06	0.012	GO:0043304	regulation of mast cell degranulation
13	34	0.956184	9.74E-08	<0.001	GO:0034122	negative regulation of toll-like receptor signaling pathway
13	34	0.956184	9.74E-08	<0.001	GO:0042116	macrophage activation
25	67	0.940314	2.33E-13	<0.001	GO:0050764	regulation of phagocytosis
22	59	0.939335	6.50E-12	<0.001	GO:0032943	mononuclear cell proliferation

10	27	0.935447	4.23E-06	0.012	GO:0033006	regulation of mast cell activation involved in immune response
21	57	0.930987	2.56E-11	<0.001	GO:0046651	lymphocyte proliferation
24	66	0.922571	1.36E-12	<0.001	GO:0070661	leukocyte proliferation
21	58	0.919223	3.77E-11	<0.001	GO:0034121	regulation of toll-like receptor signaling pathway
25	70	0.910615	7.43E-13	<0.001	GO:0060333	interferon-gamma-mediated signaling pathway
16	45	0.906845	1.10E-08	<0.001	GO:0050766	positive regulation of phagocytosis
23	66	0.893978	1.11E-11	<0.001	GO:0003823	antigen binding
12	35	0.883715	1.20E-06	0.006	GO:0030593	neutrophil chemotaxis
11	33	0.866049	4.61E-06	0.012	GO:0030669	clathrin-coated endocytic vesicle membrane
15	45	0.864824	8.58E-08	<0.001	GO:0002704	negative regulation of leukocyte mediated immunity
14	43	0.849997	3.23E-07	0.002	GO:0032757	positive regulation of interleukin-8 production
13	40	0.849138	8.72E-07	0.004	GO:0033628	regulation of cell adhesion mediated by integrin
30	93	0.845005	8.63E-14	<0.001	GO:0002224	toll-like receptor signaling pathway
16	50	0.838721	6.13E-08	<0.001	GO:0012507	ER to Golgi transport vesicle membrane
11	35	0.829014	8.80E-06	0.027	GO:0002707	negative regulation of lymphocyte mediated immunity
21	68	0.816307	1.13E-09	<0.001	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production
20	65	0.813987	3.01E-09	<0.001	GO:0032760	positive regulation of tumor necrosis factor production
14	46	0.80786	8.20E-07	0.004	GO:0071621	granulocyte chemotaxis
11	37	0.794884	1.60E-05	0.045	GO:0030101	natural killer cell activation
11	37	0.794884	1.60E-05	0.045	GO:0033003	regulation of mast cell activation
17	57	0.794854	7.68E-08	<0.001	GO:0042108	positive regulation of cytokine biosynthetic process
16	55	0.779816	2.71E-07	0.002	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin genes
21	73	0.772714	4.75E-09	<0.001	GO:0070821	tertiary granule membrane
22	78	0.760835	3.09E-09	<0.001	GO:2000106	regulation of leukocyte apoptotic process
16	57	0.758314	4.66E-07	0.002	GO:0035577	azurophil granule membrane
14	50	0.757349	2.50E-06	0.01	GO:0032655	regulation of interleukin-12 production
12	43	0.756269	1.35E-05	0.042	GO:1990266	neutrophil migration
19	68	0.755205	4.31E-08	<0.001	GO:0031295	T cell costimulation
17	61	0.753847	2.30E-07	0.002	GO:0032677	regulation of interleukin-8 production
19	69	0.746494	5.59E-08	<0.001	GO:0031294	lymphocyte costimulation
22	80	0.745677	5.20E-09	<0.001	GO:0045621	positive regulation of lymphocyte differentiation
25	91	0.745271	4.85E-10	<0.001	GO:0035579	specific granule membrane
25	92	0.738763	6.25E-10	<0.001	GO:0043202	lysosomal lumen
32	118	0.738502	2.71E-12	<0.001	GO:0002221	pattern recognition receptor signaling pathway
14	52	0.73413	4.18E-06	0.012	GO:0032722	positive regulation of chemokine production
32	121	0.723619	5.67E-12	<0.001	GO:0045807	positive regulation of endocytosis
14	53	0.722968	5.34E-06	0.014	GO:0050854	regulation of antigen receptor-mediated signaling pathway
19	72	0.721355	1.18E-07	<0.001	GO:0048010	vascular endothelial growth factor receptor signaling pathway
29	111	0.715992	7.67E-11	<0.001	GO:0032680	regulation of tumor necrosis factor production
30	115	0.715252	3.77E-11	<0.001	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production
18	70	0.706345	3.86E-07	0.002	GO:0050871	positive regulation of B cell activation
32	125	0.704528	1.46E-11	<0.001	GO:0050777	negative regulation of immune response
135	556	0.702196	2.40E-42	<0.001	GO:0002274	myeloid leukocyte activation
14	55	0.701466	8.54E-06	0.026	GO:0097530	granulocyte migration

46	182	0.69991	8.68E-16	<0.001	GO:0002250	adaptive immune response
42	166	0.699615	1.50E-14	<0.001	GO:0002703	regulation of leukocyte mediated immunity
14	56	0.6911	1.07E-05	0.029	GO:0001910	regulation of leukocyte mediated cytotoxicity
21	84	0.68982	7.15E-08	<0.001	GO:0001816	cytokine production
69	281	0.689001	2.83E-22	<0.001	GO:0030667	secretory granule membrane
50	202	0.688708	1.22E-16	<0.001	GO:1903039	positive regulation of leukocyte cell-cell adhesion
16	65	0.681554	3.17E-06	0.012	GO:0002718	regulation of cytokine production involved in immune response
15	61	0.681264	6.50E-06	0.018	GO:0032729	positive regulation of interferon-gamma production
14	57	0.680974	1.33E-05	0.042	GO:0030888	regulation of B cell proliferation
117	495	0.680874	1.72E-35	<0.001	GO:0043299	leukocyte degranulation
72	298	0.680437	9.54E-23	<0.001	GO:0050867	positive regulation of cell activation
116	491	0.680295	3.62E-35	<0.001	GO:0036230	granulocyte activation
119	505	0.679715	5.92E-36	<0.001	GO:0002275	myeloid cell activation involved in immune response
115	487	0.679713	7.59E-35	<0.001	GO:0042119	neutrophil activation
113	479	0.678536	3.33E-34	<0.001	GO:0002283	neutrophil activation involved in immune response
49	202	0.676781	5.92E-16	<0.001	GO:0034112	positive regulation of homotypic cell-cell adhesion
21	86	0.676301	1.11E-07	<0.001	GO:0042102	positive regulation of T cell proliferation
119	508	0.676279	1.10E-35	<0.001	GO:0045055	regulated secretory pathway
69	288	0.674746	1.26E-21	<0.001	GO:0002696	positive regulation of leukocyte activation
17	70	0.673624	1.92E-06	0.009	GO:0032755	positive regulation of interleukin-6 production
17	70	0.673624	1.92E-06	0.009	GO:0045582	positive regulation of T cell differentiation
17	70	0.673624	1.92E-06	0.009	GO:0070664	negative regulation of leukocyte proliferation
184	818	0.673475	1.03E-52	<0.001	GO:0045321	leukocyte activation
111	475	0.672446	3.31E-33	<0.001	GO:0043312	neutrophil degranulation
14	58	0.671078	1.65E-05	0.047	GO:0007249	I-kappaB kinase/NF-kappaB signaling
133	578	0.67025	5.54E-39	<0.001	GO:0002263	cell activation involved in immune response
47	196	0.669686	3.75E-15	<0.001	GO:0050870	positive regulation of T cell activation
132	574	0.669591	1.17E-38	<0.001	GO:0002366	leukocyte activation involved in immune response
18	75	0.666709	1.16E-06	0.004	GO:0071260	cellular response to mechanical stimulus
59	252	0.65888	3.75E-18	<0.001	GO:0051251	positive regulation of lymphocyte activation
25	106	0.656553	1.49E-08	<0.001	GO:0032675	regulation of interleukin-6 production
25	106	0.656553	1.49E-08	<0.001	GO:0050864	regulation of B cell activation
17	73	0.649853	3.58E-06	0.012	GO:0002690	positive regulation of leukocyte chemotaxis
30	129	0.649038	7.94E-10	<0.001	GO:0002819	regulation of adaptive immune response
58	252	0.648875	1.70E-17	<0.001	GO:0000323	lytic vacuole
58	252	0.648875	1.70E-17	<0.001	GO:0005764	lysosome
23	99	0.647967	7.53E-08	<0.001	GO:0042470	melanosome
23	99	0.647967	7.53E-08	<0.001	GO:0048770	pigment granule
16	69	0.647704	7.31E-06	0.024	GO:0032642	regulation of chemokine production
25	108	0.645973	2.23E-08	<0.001	GO:0002687	positive regulation of leukocyte migration
15	65	0.645324	1.49E-05	0.045	GO:0032945	negative regulation of mononuclear cell proliferation
15	65	0.645324	1.49E-05	0.045	GO:0048029	monosaccharide binding
15	65	0.645324	1.49E-05	0.045	GO:0050672	negative regulation of lymphocyte proliferation
38	165	0.644774	6.15E-12	<0.001	GO:0050851	antigen receptor-mediated signaling pathway
21	91	0.644226	3.11E-07	0.002	GO:0035578	azurophil granule lumen

27	118	0.639566	8.05E-09	<0.001	GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built f
53	234	0.638554	8.74E-16	<0.001	GO:0022409	positive regulation of cell-cell adhesion
82	368	0.636815	2.84E-23	<0.001	GO:0002757	immune response-activating signal transduction
15	66	0.636783	1.82E-05	0.049	GO:0045335	phagocytic vesicle
195	931	0.635911	7.78E-51	<0.001	GO:0001775	cell activation
16	71	0.631714	1.08E-05	0.029	GO:0030670	phagocytic vesicle membrane
38	169	0.631256	1.33E-11	<0.001	GO:0002699	positive regulation of immune effector process
39	174	0.62965	7.97E-12	<0.001	GO:0071593	lymphocyte aggregation
19	85	0.626556	1.88E-06	0.009	GO:0007229	integrin-mediated signaling pathway
31	139	0.625584	1.25E-09	<0.001	GO:0042129	regulation of T cell proliferation
25	112	0.62555	4.83E-08	<0.001	GO:0050715	positive regulation of cytokine secretion
40	180	0.625017	5.75E-12	<0.001	GO:0070486	leukocyte aggregation
87	400	0.624504	7.27E-24	<0.001	GO:0002764	immune response-regulating signaling pathway
38	172	0.621383	2.34E-11	<0.001	GO:0042110	T cell activation
38	172	0.621383	2.34E-11	<0.001	GO:0070489	T cell aggregation
46	209	0.620834	2.15E-13	<0.001	GO:0030100	regulation of endocytosis
32	145	0.619834	9.01E-10	<0.001	GO:0002695	negative regulation of leukocyte activation
26	118	0.618364	3.47E-08	<0.001	GO:0042113	B cell activation
33	150	0.618223	5.38E-10	<0.001	GO:0030666	endocytic vesicle membrane
41	187	0.617669	4.96E-12	<0.001	GO:0050670	regulation of lymphocyte proliferation
34	155	0.616729	3.21E-10	<0.001	GO:0002685	regulation of leukocyte migration
27	123	0.616333	2.07E-08	<0.001	GO:0051250	negative regulation of lymphocyte activation
16	73	0.616288	1.57E-05	0.045	GO:0046634	regulation of alpha-beta T cell activation
37	169	0.616138	5.66E-11	<0.001	GO:0005775	vacuolar lumen
43	197	0.615564	1.76E-12	<0.001	GO:0070663	regulation of leukocyte proliferation
97	456	0.614764	9.90E-26	<0.001	GO:0002694	regulation of leukocyte activation
41	188	0.614689	5.95E-12	<0.001	GO:0032944	regulation of mononuclear cell proliferation
104	491	0.614338	2.24E-27	<0.001	GO:0050865	regulation of cell activation
20	92	0.610974	1.62E-06	0.008	GO:0042035	regulation of cytokine biosynthetic process
46	213	0.610235	4.43E-13	<0.001	GO:0007159	leukocyte cell-cell adhesion
91	430	0.610204	5.06E-24	<0.001	GO:0002253	activation of immune response
23	106	0.609763	2.84E-07	0.002	GO:0002698	negative regulation of immune effector process
26	120	0.609023	5.00E-08	<0.001	GO:0050671	positive regulation of lymphocyte proliferation
21	97	0.608601	9.63E-07	0.004	GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II
27	125	0.607373	2.97E-08	<0.001	GO:0071219	cellular response to molecule of bacterial origin
20	93	0.604999	1.94E-06	0.009	GO:0050868	negative regulation of T cell activation
26	121	0.604426	5.98E-08	<0.001	GO:0002706	regulation of lymphocyte mediated immunity
26	121	0.604426	5.98E-08	<0.001	GO:0032946	positive regulation of mononuclear cell proliferation
63	297	0.604146	5.06E-17	<0.001	GO:0046649	lymphocyte activation
66	312	0.603357	1.04E-17	<0.001	GO:1903037	regulation of leukocyte cell-cell adhesion
27	126	0.60296	3.55E-08	<0.001	GO:0070665	positive regulation of leukocyte proliferation
21	98	0.602935	1.15E-06	0.004	GO:0002495	antigen processing and presentation of peptide antigen via MHC class II
21	98	0.602935	1.15E-06	0.004	GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
17	80	0.59895	1.33E-05	0.042	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds
17	80	0.59895	1.33E-05	0.042	GO:0038094	Fc-gamma receptor signaling pathway

## GO enrichment, Spinal Cord Cervical C9orf72\_pos vs Non-Neurological\_Control up genes

N	X	LOD	P	P_adj	attrib ID	attrib name
16	38	1.174715	4.88E-12	<0.001	GO:0006695	cholesterol biosynthetic process
16	38	1.174715	4.88E-12	<0.001	GO:1902653	secondary alcohol biosynthetic process
17	42	1.146345	2.27E-12	<0.001	GO:0016126	sterol biosynthetic process
19	53	1.062856	1.53E-12	<0.001	GO:0090181	regulation of cholesterol metabolic process
15	42	1.059781	3.72E-10	<0.001	GO:0045540	regulation of cholesterol biosynthetic process
8	23	1.044633	6.50E-06	0.033	GO:0099738	cell cortex region
14	63	0.77449	1.14E-06	0.004	GO:0042552	myelination
15	68	0.770112	5.25E-07	0.004	GO:0007272	ensheathment of neurons
15	68	0.770112	5.25E-07	0.004	GO:0008366	axon ensheathment
18	82	0.766995	4.21E-08	<0.001	GO:0050810	regulation of steroid biosynthetic process
24	111	0.759031	3.35E-10	<0.001	GO:1902652	secondary alcohol metabolic process
23	107	0.755647	8.82E-10	<0.001	GO:0008203	cholesterol metabolic process
22	107	0.731115	4.94E-09	<0.001	GO:0019218	regulation of steroid metabolic process
24	122	0.707327	2.55E-09	<0.001	GO:0016125	sterol metabolic process
15	78	0.695442	3.32E-06	0.01	GO:1902930	regulation of alcohol biosynthetic process
21	120	0.644653	2.06E-07	<0.001	GO:0046165	alcohol biosynthetic process
19	120	0.592536	3.70E-06	0.013	GO:0006694	steroid biosynthetic process
23	163	0.533425	2.83E-06	0.009	GO:0046890	regulation of lipid biosynthetic process
25	188	0.503504	3.19E-06	0.01	GO:1901617	organic hydroxy compound biosynthetic process
29	223	0.492663	8.51E-07	0.004	GO:0045202	synapse
27	222	0.458891	7.23E-06	0.033	GO:0033267	axon part
38	346	0.409754	1.40E-06	0.006	GO:0005874	microtubule
56	541	0.384386	3.62E-08	<0.001	GO:0008610	lipid biosynthetic process
37	363	0.37272	1.08E-05	0.045	GO:0006066	alcohol metabolic process
63	712	0.30825	1.45E-06	0.006	GO:0043005	neuron projection
99	1246	0.262852	2.55E-07	0.003	GO:0097458	neuron part

# GO enrichment, Spinal Cord Lumbar C9orf72\_neg vs Non-Neurological\_Control down genes

N	X	LOD	P	P_adj	attrib ID	attrib name
4	6	1.81296	7.69E-06	0.019	GO:0043305	negative regulation of mast cell degranulation
9	15	1.72684	3.21E-11	<0.001	GO:0042613	MHC class II protein complex
6	10	1.71911	7.40E-08	0.001	GO:1902563	regulation of neutrophil activation
8	14	1.677644	7.21E-10	<0.001	GO:0045730	respiratory burst
4	7	1.666807	1.75E-05	0.046	GO:0002883	regulation of hypersensitivity
4	7	1.666807	1.75E-05	0.046	GO:0033007	negative regulation of mast cell activation involved in immune response
4	7	1.666807	1.75E-05	0.046	GO:0045359	positive regulation of interferon-beta biosynthetic process
6	12	1.55936	3.11E-07	0.001	GO:0032490	detection of molecule of bacterial origin
5	10	1.558498	3.24E-06	0.01	GO:0002887	negative regulation of myeloid leukocyte mediated immunity
5	10	1.558498	3.24E-06	0.01	GO:0032395	MHC class II receptor activity
5	10	1.558498	3.24E-06	0.01	GO:0043020	NADPH oxidase complex
11	23	1.52746	5.28E-12	<0.001	GO:0042611	MHC protein complex
8	17	1.51276	5.44E-09	<0.001	GO:0001774	microglial cell activation
5	11	1.485923	5.81E-06	0.014	GO:0033004	negative regulation of mast cell activation
5	11	1.485923	5.81E-06	0.014	GO:0043301	negative regulation of leukocyte degranulation
5	11	1.485923	5.81E-06	0.014	GO:1903306	negative regulation of regulated secretory pathway
7	16	1.457512	9.59E-08	0.001	GO:0023026	MHC class II protein complex binding
6	14	1.442806	9.65E-07	0.005	GO:0016064	immunoglobulin mediated immune response
14	34	1.415788	8.25E-14	<0.001	GO:0042116	macrophage activation
7	17	1.414022	1.59E-07	0.001	GO:0002577	regulation of antigen processing and presentation
6	15	1.394476	1.57E-06	0.006	GO:0034162	toll-like receptor 9 signaling pathway
6	15	1.394476	1.57E-06	0.006	GO:2000484	positive regulation of interleukin-8 secretion
11	28	1.381209	7.42E-11	<0.001	GO:0050853	B cell receptor signaling pathway
7	18	1.374489	2.54E-07	0.001	GO:0032928	regulation of superoxide anion generation
17	44	1.372422	6.21E-16	<0.001	GO:0002886	regulation of myeloid leukocyte mediated immunity
10	26	1.366384	7.09E-10	<0.001	GO:0043304	regulation of mast cell degranulation
8	21	1.360052	4.13E-08	0.001	GO:0042605	peptide antigen binding
10	27	1.340805	1.10E-09	<0.001	GO:0006911	phagocytosis, engulfment
10	27	1.340805	1.10E-09	<0.001	GO:0033006	regulation of mast cell activation involved in immune response
7	19	1.338253	3.94E-07	0.003	GO:0023023	MHC protein complex binding
15	41	1.334015	8.53E-14	<0.001	GO:0043300	regulation of leukocyte degranulation
8	22	1.328993	6.34E-08	0.001	GO:0036336	dendritic cell migration
6	17	1.311453	3.71E-06	0.01	GO:0019724	B cell mediated immunity
16	47	1.286885	4.69E-14	<0.001	GO:1903305	regulation of regulated secretory pathway
6	18	1.275217	5.44E-06	0.012	GO:0002407	dendritic cell chemotaxis
7	21	1.273746	8.66E-07	0.005	GO:0042100	B cell proliferation
8	24	1.272828	1.39E-07	0.001	GO:2000482	regulation of interleukin-8 secretion
9	28	1.249401	3.23E-08	0.001	GO:0071556	integral component of luminal side of endoplasmic reticulum membrane
8	25	1.24725	2.00E-07	0.001	GO:0050718	positive regulation of interleukin-1 beta secretion
7	22	1.244757	1.24E-06	0.005	GO:0002888	positive regulation of myeloid leukocyte mediated immunity

7	22	1.244757	1.24E-06	0.005	GO:009595	detection of biotic stimulus
6	19	1.241768	7.77E-06	0.019	GO:0098581	detection of external biotic stimulus
10	32	1.231539	7.44E-09	<0.001	GO:0002755	MyD88-dependent toll-like receptor signaling pathway
6	20	1.21071	1.08E-05	0.025	GO:0019865	immunoglobulin binding
6	20	1.21071	1.08E-05	0.025	GO:0034123	positive regulation of toll-like receptor signaling pathway
6	20	1.21071	1.08E-05	0.025	GO:0050855	regulation of B cell receptor signaling pathway
6	20	1.21071	1.08E-05	0.025	GO:0097300	programmed necrotic cell death
11	37	1.200781	2.37E-09	<0.001	GO:0033003	regulation of mast cell activation
10	34	1.194506	1.44E-08	<0.001	GO:0010324	membrane invagination
6	21	1.181721	1.48E-05	0.031	GO:0002335	mature B cell differentiation
6	21	1.181721	1.48E-05	0.031	GO:0070265	necrotic cell death
8	28	1.17846	5.34E-07	0.003	GO:0050716	positive regulation of interleukin-1 secretion
11	40	1.154132	5.95E-09	<0.001	GO:0030890	positive regulation of B cell proliferation
9	33	1.150147	1.60E-07	0.001	GO:0030669	clathrin-coated endocytic vesicle membrane
15	55	1.149463	1.13E-11	<0.001	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin genes
16	59	1.146412	2.54E-12	<0.001	GO:0032943	mononuclear cell proliferation
7	26	1.144957	4.36E-06	0.011	GO:0042346	positive regulation of NF-kappaB import into nucleus
7	26	1.144957	4.36E-06	0.011	GO:0045577	regulation of B cell differentiation
9	34	1.132748	2.12E-07	0.001	GO:0034122	negative regulation of toll-like receptor signaling pathway
15	57	1.12848	1.99E-11	<0.001	GO:0030888	regulation of B cell proliferation
15	57	1.12848	1.99E-11	<0.001	GO:0046651	lymphocyte proliferation
16	61	1.126841	4.46E-12	<0.001	GO:0032729	positive regulation of interferon-gamma production
8	31	1.119073	1.26E-06	0.005	GO:0031663	lipopolysaccharide-mediated signaling pathway
17	66	1.11661	1.31E-12	<0.001	GO:0003823	antigen binding
17	66	1.11661	1.31E-12	<0.001	GO:0070661	leukocyte proliferation
18	70	1.116025	2.94E-13	<0.001	GO:0060333	interferon-gamma-mediated signaling pathway
11	43	1.111997	1.38E-08	<0.001	GO:0032757	positive regulation of interleukin-8 production
17	67	1.107899	1.72E-12	<0.001	GO:0050764	regulation of phagocytosis
8	32	1.10095	1.64E-06	0.006	GO:0042098	T cell proliferation
23	93	1.096021	3.61E-16	<0.001	GO:0002224	toll-like receptor signaling pathway
18	73	1.091817	6.46E-13	<0.001	GO:0070821	tertiary granule membrane
14	57	1.088489	2.57E-10	<0.001	GO:0042108	positive regulation of cytokine biosynthetic process
11	45	1.086012	2.31E-08	<0.001	GO:0050766	positive regulation of phagocytosis
7	29	1.082735	9.63E-06	0.021	GO:0090322	regulation of superoxide metabolic process
14	58	1.078593	3.31E-10	<0.001	GO:0034121	regulation of toll-like receptor signaling pathway
8	34	1.066821	2.70E-06	0.01	GO:0032731	positive regulation of interleukin-1 beta production
7	30	1.063825	1.23E-05	0.028	GO:0032733	positive regulation of interleukin-10 production
8	35	1.05071	3.42E-06	0.01	GO:0001784	phosphotyrosine binding
8	36	1.035173	4.30E-06	0.011	GO:0032715	negative regulation of interleukin-6 production
8	36	1.035173	4.30E-06	0.011	GO:0050706	regulation of interleukin-1 beta secretion
15	68	1.028246	3.04E-10	<0.001	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production
9	41	1.027233	1.20E-06	0.005	GO:0032732	positive regulation of interleukin-1 production
11	50	1.027111	7.52E-08	0.001	GO:0032655	regulation of interleukin-12 production
8	37	1.020172	5.35E-06	0.011	GO:0030101	natural killer cell activation

14	65	1.014975	1.67E-09	<0.001	GO:0032760	positive regulation of tumor necrosis factor production
15	70	1.012257	4.71E-10	<0.001	GO:0050871	positive regulation of B cell activation
25	118	1.010147	9.48E-16	<0.001	GO:0002221	pattern recognition receptor signaling pathway
13	61	1.009178	7.37E-09	<0.001	GO:0032677	regulation of interleukin-8 production
11	52	1.005611	1.16E-07	0.001	GO:0032722	positive regulation of chemokine production
18	86	1.000101	1.29E-11	<0.001	GO:0042102	positive regulation of T cell proliferation
8	39	0.991634	8.13E-06	0.02	GO:0002312	B cell activation involved in immune response
8	39	0.991634	8.13E-06	0.02	GO:0061515	myeloid cell development
24	120	0.978062	1.41E-14	<0.001	GO:0050671	positive regulation of lymphocyte proliferation
8	40	0.978037	9.93E-06	0.022	GO:0033628	regulation of cell adhesion mediated by integrin
9	45	0.976726	2.75E-06	0.01	GO:0002704	negative regulation of leukocyte mediated immunity
18	90	0.975355	2.91E-11	<0.001	GO:0032649	regulation of interferon-gamma production
16	80	0.974827	3.69E-10	<0.001	GO:0038094	Fc-gamma receptor signaling pathway
25	126	0.974296	4.82E-15	<0.001	GO:0070665	positive regulation of leukocyte proliferation
24	121	0.97356	1.72E-14	<0.001	GO:0032946	positive regulation of mononuclear cell proliferation
21	106	0.971411	7.82E-13	<0.001	GO:0032675	regulation of interleukin-6 production
13	66	0.966444	2.03E-08	<0.001	GO:0045335	phagocytic vesicle
36	187	0.965144	1.17E-20	<0.001	GO:0050670	regulation of lymphocyte proliferation
8	41	0.964851	1.20E-05	0.026	GO:0050704	regulation of interleukin-1 secretion
36	188	0.962263	1.41E-20	<0.001	GO:0032944	regulation of mononuclear cell proliferation
15	77	0.960498	1.93E-09	<0.001	GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis
15	77	0.960498	1.93E-09	<0.001	GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis
15	78	0.95358	2.33E-09	<0.001	GO:0002431	Fc receptor mediated stimulatory signaling pathway
9	47	0.953509	4.03E-06	0.01	GO:0032720	negative regulation of tumor necrosis factor production
37	197	0.952544	8.19E-21	<0.001	GO:0070663	regulation of leukocyte proliferation
8	42	0.952052	1.45E-05	0.031	GO:0045309	protein phosphorylated amino acid binding
13	68	0.950455	2.96E-08	0.001	GO:0031295	T cell costimulation
31	166	0.94533	1.49E-17	<0.001	GO:0002703	regulation of leukocyte mediated immunity
20	106	0.944738	7.15E-12	<0.001	GO:0050864	regulation of B cell activation
13	69	0.942675	3.56E-08	0.001	GO:0031294	lymphocyte costimulation
15	80	0.940063	3.37E-09	<0.001	GO:0045621	positive regulation of lymphocyte differentiation
13	70	0.935031	4.26E-08	0.001	GO:0032755	positive regulation of interleukin-6 production
10	54	0.934822	1.62E-06	0.006	GO:0006909	phagocytosis
64	368	0.93275	2.38E-33	<0.001	GO:0002757	immune response-activating signal transduction
17	92	0.93263	3.84E-10	<0.001	GO:0042035	regulation of cytokine biosynthetic process
9	49	0.931466	5.79E-06	0.012	GO:0046635	positive regulation of alpha-beta T cell activation
9	49	0.931466	5.79E-06	0.012	GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production
11	60	0.928858	5.40E-07	0.004	GO:0071346	cellular response to interferon-gamma
21	115	0.927724	4.12E-12	<0.001	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production
15	82	0.926952	4.82E-09	<0.001	GO:0034341	response to interferon-gamma
126	818	0.926048	1.53E-60	<0.001	GO:0045321	leukocyte activation
9	50	0.920848	6.89E-06	0.014	GO:0012507	ER to Golgi transport vesicle membrane
20	111	0.92021	1.74E-11	<0.001	GO:0032680	regulation of tumor necrosis factor production
13	72	0.920133	6.06E-08	0.001	GO:0048010	vascular endothelial growth factor receptor signaling pathway
72	430	0.919407	2.24E-36	<0.001	GO:0002253	activation of immune response

14	78	0.916903	2.03E-08	<0.001	GO:2000106	regulation of leukocyte apoptotic process
10	56	0.91568	2.29E-06	0.006	GO:0032651	regulation of interleukin-1 beta production
67	400	0.915293	7.35E-34	<0.001	GO:0002764	immune response-regulating signaling pathway
32	182	0.913871	2.82E-17	<0.001	GO:0002250	adaptive immune response
51	298	0.913535	2.42E-26	<0.001	GO:0050867	positive regulation of cell activation
19	107	0.91213	7.29E-11	<0.001	GO:0030168	platelet activation
49	288	0.908851	3.20E-25	<0.001	GO:0002696	positive regulation of leukocyte activation
35	202	0.908139	1.43E-18	<0.001	GO:0034112	positive regulation of homotypic cell-cell adhesion
35	202	0.908139	1.43E-18	<0.001	GO:1903039	positive regulation of leukocyte cell-cell adhesion
34	196	0.908072	4.32E-18	<0.001	GO:0050870	positive regulation of T cell activation
16	91	0.906169	2.71E-09	<0.001	GO:0035579	specific granule membrane
88	556	0.903763	1.52E-42	<0.001	GO:0002274	myeloid leukocyte activation
12	69	0.900709	3.01E-07	0.001	GO:0032642	regulation of chemokine production
24	139	0.899539	4.28E-13	<0.001	GO:0042129	regulation of T cell proliferation
13	75	0.898697	1.01E-07	0.001	GO:0002285	lymphocyte activation involved in immune response
134	931	0.898194	5.68E-61	<0.001	GO:0001775	cell activation
12	70	0.893196	3.54E-07	0.002	GO:0045582	positive regulation of T cell differentiation
12	70	0.893196	3.54E-07	0.002	GO:0070664	negative regulation of leukocyte proliferation
42	252	0.892651	2.15E-21	<0.001	GO:0051251	positive regulation of lymphocyte activation
49	297	0.892607	1.33E-24	<0.001	GO:0046649	lymphocyte activation
9	53	0.890463	1.13E-05	0.026	GO:0001776	leukocyte homeostasis
10	59	0.888454	3.76E-06	0.01	GO:0002449	lymphocyte mediated immunity
11	65	0.886944	1.25E-06	0.005	GO:0032945	negative regulation of mononuclear cell proliferation
11	65	0.886944	1.25E-06	0.005	GO:0050672	negative regulation of lymphocyte proliferation
12	71	0.88581	4.16E-07	0.003	GO:0030670	phagocytic vesicle membrane
87	574	0.880021	1.62E-40	<0.001	GO:0002366	leukocyte activation involved in immune response
87	578	0.876371	2.84E-40	<0.001	GO:0002263	cell activation involved in immune response
20	121	0.874919	8.91E-11	<0.001	GO:0045807	positive regulation of endocytosis
14	85	0.871985	6.34E-08	0.001	GO:0007229	integrin-mediated signaling pathway
9	55	0.871321	1.55E-05	0.036	GO:0015918	sterol transport
10	61	0.871203	5.14E-06	0.011	GO:0101003	ficolin-1-rich granule membrane
73	479	0.870612	4.44E-34	<0.001	GO:0002283	neutrophil activation involved in immune response
74	487	0.86992	1.85E-34	<0.001	GO:0042119	neutrophil activation
75	495	0.869276	7.68E-35	<0.001	GO:0043299	leukocyte degranulation
35	218	0.868122	1.76E-17	<0.001	GO:0002758	innate immune response-activating signal transduction
76	505	0.866602	4.21E-35	<0.001	GO:0002275	myeloid cell activation involved in immune response
74	491	0.865639	3.24E-34	<0.001	GO:0036230	granulocyte activation
37	234	0.861538	3.47E-18	<0.001	GO:0022409	positive regulation of cell-cell adhesion
19	118	0.860979	4.20E-10	<0.001	GO:0042113	B cell activation
71	475	0.858772	1.37E-32	<0.001	GO:0043312	neutrophil degranulation
20	125	0.858034	1.63E-10	<0.001	GO:0071219	cellular response to molecule of bacterial origin
12	75	0.857455	7.69E-07	0.004	GO:0071260	cellular response to mechanical stimulus
37	236	0.857113	4.65E-18	<0.001	GO:0002218	activation of innate immune response
11	69	0.856086	2.31E-06	0.006	GO:0032652	regulation of interleukin-1 production
75	508	0.855727	4.63E-34	<0.001	GO:0045055	regulated secretory pathway

GO enrichment, Spinal Cord Lumbar C9orf72\_neg vs Non-Neurological\_Control up genes

-- no enrichment

# GO enrichment, Spinal Cord Lumbar C9orf72\_pos vs Non-Neurological\_Control down genes

N	X	LOD	P	P_adj	attrib ID	attrib name
5	5	2.449077	7.69E-08	<0.001	GO:2001188	regulation of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen
4	4	2.361296	2.04E-06	0.007	GO:0032010	phagolysosome
12	15	1.964897	3.26E-15	<0.001	GO:0042613	MHC class II protein complex
4	5	1.88415	9.90E-06	0.035	GO:0002730	regulation of dendritic cell cytokine production
4	5	1.88415	9.90E-06	0.035	GO:0032611	interleukin-1 beta production
4	5	1.88415	9.90E-06	0.035	GO:0032612	interleukin-1 production
16	23	1.756939	2.90E-18	<0.001	GO:0042611	MHC protein complex
5	8	1.603905	3.91E-06	0.01	GO:0034135	regulation of toll-like receptor 2 signaling pathway
6	10	1.567919	5.33E-07	0.001	GO:0032395	MHC class II receptor activity
5	9	1.494736	8.53E-06	0.025	GO:0046598	positive regulation of viral entry into host cell
6	12	1.408168	2.20E-06	0.007	GO:0032490	detection of molecule of bacterial origin
5	10	1.407561	1.65E-05	0.05	GO:0043020	NADPH oxidase complex
10	21	1.371074	1.38E-09	<0.001	GO:0042605	peptide antigen binding
8	17	1.361057	7.31E-08	<0.001	GO:0002577	regulation of antigen processing and presentation
13	28	1.352399	6.55E-12	<0.001	GO:0071556	integral component of luminal side of endoplasmic reticulum membrane
6	14	1.291613	6.69E-06	0.016	GO:0045730	respiratory burst
7	17	1.262574	1.51E-06	0.003	GO:0008329	signaling pattern recognition receptor activity
7	17	1.262574	1.51E-06	0.003	GO:0038187	pattern recognition receptor activity
7	17	1.262574	1.51E-06	0.003	GO:0071675	regulation of mononuclear cell migration
9	22	1.257287	4.87E-08	<0.001	GO:0009595	detection of biotic stimulus
13	33	1.230853	8.41E-11	<0.001	GO:0030669	clathrin-coated endocytic vesicle membrane
10	26	1.214164	1.75E-08	<0.001	GO:0043304	regulation of mast cell degranulation
8	21	1.208347	5.34E-07	0.001	GO:0001782	B cell homeostasis
10	27	1.188585	2.68E-08	<0.001	GO:0033006	regulation of mast cell activation involved in immune response
7	19	1.186804	3.67E-06	0.009	GO:0098581	detection of external biotic stimulus
12	34	1.156313	2.02E-09	<0.001	GO:0034122	negative regulation of toll-like receptor signaling pathway
9	28	1.097438	5.51E-07	0.001	GO:0050853	B cell receptor signaling pathway
8	25	1.095544	2.48E-06	0.008	GO:0050718	positive regulation of interleukin-1 beta secretion
22	70	1.083812	5.92E-15	<0.001	GO:0060333	interferon-gamma-mediated signaling pathway
10	32	1.079317	1.73E-07	<0.001	GO:0002755	MyD88-dependent toll-like receptor signaling pathway
7	23	1.066131	1.56E-05	0.044	GO:2000406	positive regulation of T cell migration
10	33	1.060407	2.39E-07	<0.001	GO:2000249	regulation of actin cytoskeleton reorganization
8	27	1.048498	4.76E-06	0.012	GO:0006911	phagocytosis, engulfment
11	37	1.0483	7.40E-08	<0.001	GO:0033003	regulation of mast cell activation
13	44	1.044024	5.19E-09	<0.001	GO:0002886	regulation of myeloid leukocyte mediated immunity
12	41	1.0385	2.28E-08	<0.001	GO:0043300	regulation of leukocyte degranulation
8	28	1.026754	6.45E-06	0.015	GO:0050716	positive regulation of interleukin-1 secretion
14	50	1.011592	2.91E-09	<0.001	GO:0012507	ER to Golgi transport vesicle membrane
8	29	1.006045	8.61E-06	0.026	GO:0008305	integrin complex
13	47	1.004441	1.27E-08	<0.001	GO:1903305	regulation of regulated secretory pathway

9	34	0.980784	3.41E-06	0.009	GO:0010324	membrane invagination
9	34	0.980784	3.41E-06	0.009	GO:0015026	coreceptor activity
9	34	0.980784	3.41E-06	0.009	GO:0042116	macrophage activation
8	31	0.967366	1.48E-05	0.043	GO:0031663	lipopolysaccharide-mediated signaling pathway
8	31	0.967366	1.48E-05	0.043	GO:0097028	dendritic cell differentiation
15	58	0.964827	2.67E-09	<0.001	GO:0034121	regulation of toll-like receptor signaling pathway
17	66	0.962552	2.48E-10	<0.001	GO:0003823	antigen binding
9	36	0.947942	5.72E-06	0.014	GO:0050706	regulation of interleukin-1 beta secretion
13	55	0.913674	9.87E-08	<0.001	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin genes
16	68	0.910727	3.54E-09	<0.001	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production
11	47	0.909006	1.07E-06	0.001	GO:0032720	negative regulation of tumor necrosis factor production
10	43	0.906183	3.52E-06	0.009	GO:0032757	positive regulation of interleukin-8 production
17	73	0.904936	1.36E-09	<0.001	GO:0070821	tertiary granule membrane
12	52	0.900595	4.07E-07	<0.001	GO:0032722	positive regulation of chemokine production
21	92	0.894286	2.37E-11	<0.001	GO:0043202	lysosomal lumen
13	57	0.893653	1.55E-07	<0.001	GO:0035577	azurophil granule membrane
21	93	0.888229	2.95E-11	<0.001	GO:0002224	toll-like receptor signaling pathway
11	49	0.885788	1.67E-06	0.003	GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production
18	80	0.885732	8.15E-10	<0.001	GO:0038094	Fc-gamma receptor signaling pathway
15	67	0.882934	2.26E-08	<0.001	GO:0050764	regulation of phagocytosis
10	45	0.88095	5.47E-06	0.014	GO:0002260	lymphocyte homeostasis
26	118	0.875982	2.40E-13	<0.001	GO:0002221	pattern recognition receptor signaling pathway
15	68	0.874714	2.80E-08	<0.001	GO:0031295	T cell costimulation
13	59	0.87451	2.39E-07	<0.001	GO:0032943	mononuclear cell proliferation
17	78	0.867985	4.05E-09	<0.001	GO:2000106	regulation of leukocyte apoptotic process
15	69	0.866647	3.45E-08	<0.001	GO:0031294	lymphocyte costimulation
13	60	0.865245	2.95E-07	<0.001	GO:0071346	cellular response to interferon-gamma
14	65	0.861706	1.12E-07	<0.001	GO:0032760	positive regulation of tumor necrosis factor production
12	56	0.85959	9.58E-07	0.001	GO:0032651	regulation of interleukin-1 beta production
15	70	0.858725	4.24E-08	<0.001	GO:0070664	negative regulation of leukocyte proliferation
10	47	0.857097	8.28E-06	0.019	GO:0045806	negative regulation of endocytosis
13	61	0.856172	3.62E-07	<0.001	GO:0006027	glycosaminoglycan catabolic process
12	57	0.849914	1.17E-06	0.002	GO:0046651	lymphocyte proliferation
18	86	0.845773	2.83E-09	<0.001	GO:0042102	positive regulation of T cell proliferation
24	115	0.845346	6.95E-12	<0.001	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production
31	150	0.84242	7.80E-15	<0.001	GO:0030666	endocytic vesicle membrane
22	106	0.841804	5.87E-11	<0.001	GO:0032675	regulation of interleukin-6 production
16	77	0.841788	2.40E-08	<0.001	GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis
16	77	0.841788	2.40E-08	<0.001	GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis

# GO enrichment, Spinal Cord Lumbar C9orf72\_pos vs Non-Neurological\_Control up genes

<b>N</b>	<b>X</b>	<b>LOD</b>	<b>P</b>	<b>P_adj</b>	<b>attrib ID</b>	<b>attrib name</b>
12	97	0.76873	4.95E-06	0.011	GO:0005875	microtubule associated complex
12	104	0.734384	1.03E-05	0.024	GO:0003774	motor activity
38	712	0.371925	8.13E-06	0.019	GO:0043005	neuron projection

## GO enrichment, Spinal Cord Thoracic C9orf72\_neg vs Non-Neurological\_Control down genes

<b>N</b>	<b>X</b>	<b>LOD</b>	<b>P</b>	<b>P_adj</b>	<b>attrib ID</b>	<b>attrib name</b>
4	79	1.578519	1.07E-05	0.026	GO:0048259	regulation of receptor-mediated endocytosis
7	330	1.210759	1.37E-06	0.005	GO:0005765	lysosomal membrane
7	330	1.210759	1.37E-06	0.005	GO:0098852	lytic vacuole membrane
7	356	1.176554	2.26E-06	0.007	GO:0005774	vacuolar membrane

## GO enrichment, Spinal Cord Thoracic C9orf72\_neg vs Non-Neurological\_Control up genes

- no enrichment

## GO enrichment, Spinal Cord Thoracic C9orf72\_pos vs Non-Neurological\_Control down genes

- no enrichment

## GO enrichment, Spinal Cord Thoracic C9orf72\_pos vs Non-Neurological\_Control up genes

<b>N</b>	<b>X</b>	<b>LOD</b>	<b>P</b>	<b>P_adj</b>	<b>attrib ID</b>	<b>attrib name</b>
3	10	2.310636	1.55E-06	0.006	GO:0060285	cilium-dependent cell motility
3	11	2.256255	2.13E-06	0.01	GO:0001539	cilium or flagellum-dependent cell motility
3	13	2.164436	3.69E-06	0.011	GO:0036159	inner dynein arm assembly
3	21	1.918263	1.69E-05	0.037	GO:0042384	cilium assembly
3	21	1.918263	1.69E-05	0.037	GO:0044458	motile cilium assembly
4	42	1.719233	3.09E-06	0.011	GO:0003341	cilium movement
5	95	1.444808	3.19E-06	0.011	GO:0031514	motile cilium
5	116	1.353677	8.51E-06	0.027	GO:0010927	cellular component assembly involved in morphogenesis
7	299	1.087721	6.77E-06	0.025	GO:0005929	cilium