MAPPING STATS RNA

Species	Assay	Read Type + Length	Mapping	#	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Mapped fraction
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_negative_S1-GSM3603	151,210,060	0.85	149,670,505	3,888,797	9,506,476	2,186,848	0.55
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_negative_S2-GSM3603	144,818,443	0.91	157,455,659	4,729,781	6,571,659	996,855	0.59
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_negative_S3-GSM3603	117,780,545	0.84	145,250,869	5,030,569	9,166,210	1,503,518	0.68
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_negative_S4-GSM3603	127,236,303	0.87	158,893,855	5,343,965	8,019,888	784,642	0.68
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_negative_S5-GSM3603	170,786,112	0.90	174,344,389	5,518,383	7,848,408	1,359,320	0.55
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_negative_S6-GSM3603	156,150,613	0.87	168,550,933	5,882,329	8,191,041	1,469,469	0.59
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_negative_S7-GSM3603	133,307,846	0.81	144,821,331	4,676,087	8,452,150	1,984,690	0.60
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_positive_S1-GSM3603	145,718,214	0.83	144,163,694	4,065,614	11,584,182	3,185,402	0.56
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_positive_S2-GSM3603	154,923,320	0.92	166,875,395	5,970,115	8,517,526	1,091,934	0.59
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_positive_S3-GSM3603	120,024,367	0.86	141,406,011	4,955,155	11,875,512	2,051,670	0.67
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_positive_S4-GSM3603	126,356,871	0.87	166,278,018	6,299,450	8,586,871	910,391	0.72
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_positive_S5-GSM3603	137,878,652	0.90	165,989,004	5,548,340	8,172,806	1,354,640	0.66
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_positive_S6-GSM3603	146,966,879	0.88	160,123,274	5,616,678	9,107,092	1,567,540	0.60
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-NeuN_positive_TDP-43_positive_S7-GSM3603	137,913,088	0.81	157,467,840	4,537,002	9,134,924	2,264,168	0.63
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-Unsorted_S3-GSM3603269	24,839,209	0.79	33,511,389	1,021,727	3,148,274	765,256	0.77
Homo sapiens hg38	RNA-seq	2x100	STAR-2.5.3.a	RNA-Unsorted_S4-GSM3603272	35,860,020	0.89	52,296,590	1,698,912	2,905,127	235,863	0.80

Note:

For quantification, which is done in transcriptome space, the number of reads that map is much smaller because of the huge fraction of intronic reads

#	Exonic:	Intergenic:	Intronic:
RNA-NeuN_positive_TDP-43_negative_S1-GSM3603264	0.22	0.08	0.70
RNA-NeuN_positive_TDP-43_negative_S2-GSM3603266	0.17	0.09	0.74
RNA-NeuN_positive_TDP-43_negative_S3-GSM3603268	0.23	0.09	0.68
RNA-NeuN_positive_TDP-43_negative_S4-GSM3603271	0.20	0.09	0.71
RNA-NeuN_positive_TDP-43_negative_S5-GSM3603274	0.18	0.10	0.72
RNA-NeuN_positive_TDP-43_negative_S6-GSM3603276	0.20	0.09	0.70
RNA-NeuN_positive_TDP-43_negative_S7-GSM3603278	0.22	0.10	0.68
RNA-NeuN_positive_TDP-43_positive_S1-GSM3603263	0.24	0.08	0.67
RNA-NeuN_positive_TDP-43_positive_S2-GSM3603265	0.20	0.09	0.71
RNA-NeuN_positive_TDP-43_positive_S3-GSM3603267	0.24	0.09	0.66
RNA-NeuN_positive_TDP-43_positive_S4-GSM3603270	0.22	0.09	0.69
RNA-NeuN_positive_TDP-43_positive_S5-GSM3603273	0.19	0.10	0.71
RNA-NeuN_positive_TDP-43_positive_S6-GSM3603275	0.21	0.10	0.69
RNA-NeuN_positive_TDP-43_positive_S7-GSM3603277	0.22	0.10	0.68
RNA-Unsorted_S3-GSM3603269	0.33	0.08	0.59
RNA-Unsorted_S4-GSM3603272	0.23	0.08	0.69

DESEQ RESULTS

all genes

A	B	p-adj	
		up in B vs A	down in B vs A
negative	**positive**	281	141
negative	**Unsorted**	872	466
positive	**Unsorted**	588	173

MAPPING STATS ATAC

Aligned against	Read Length	Library	Raw fragments	Unique non-chrM reads	Multi reads	Complexity	chrM reads	chrM fraction	Unique non-chrM reads after dedup	TSS ratio	MACS default peaks	FRiP (MACS)
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_negative_S1-GSM3603250		30,669,674		0.91	4,940,765	0.14		3.13	19,615	26,139
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_negative_S2-GSM3603252		34,332,830		0.91	1,501,403	0.04		2.82	24,092	32,816
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_negative_S3-GSM3603254		34,434,015		0.85	6,140,410	0.15		4.26	62,393	66,416
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_negative_S4-GSM3603256		38,446,253		0.89	1,686,774	0.04		4.14	38,967	47,770
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_negative_S5-GSM3603258		38,125,869		0.84	1,718,180	0.04		2.92	30,459	32,620
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_negative_S6-GSM3603260		36,088,813		0.88	1,971,757	0.05		3.69	58,821	67,877
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_negative_S7-GSM3603262		38,414,830		0.90	2,815,076	0.07		1.67	68,911	58,081
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_positive_S1-GSM3603249		33,281,444		0.91	6,222,249	0.16		3.95	40,356	44,726
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_positive_S2-GSM3603251		35,811,259		0.49	2,228,426	0.06		3.45	173,147	101,118
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_positive_S3-GSM3603253		32,665,499		0.92	6,545,348	0.17		3.25	16,024	21,032
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_positive_S4-GSM3603255		34,756,675		0.84	2,960,657	0.08		7.23	93,606	117,387
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_positive_S5-GSM3603257		36,702,056		0.51	2,046,793	0.05		3.77	151,787	92,543
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_positive_S6-GSM3603259		36,276,466		0.87	4,235,949	0.10		3.66	39,230	42,665
hg38-male	**1x36**	ATAC-NeuN_positive_TDP-43_positive_S7-GSM3603261		37,349,692		0.90	3,002,034	0.07		2.10	41,803	35,718

Note:

This is very poor quality ATAC – TSS ratios should be at least 7-8 in mammalian samples