

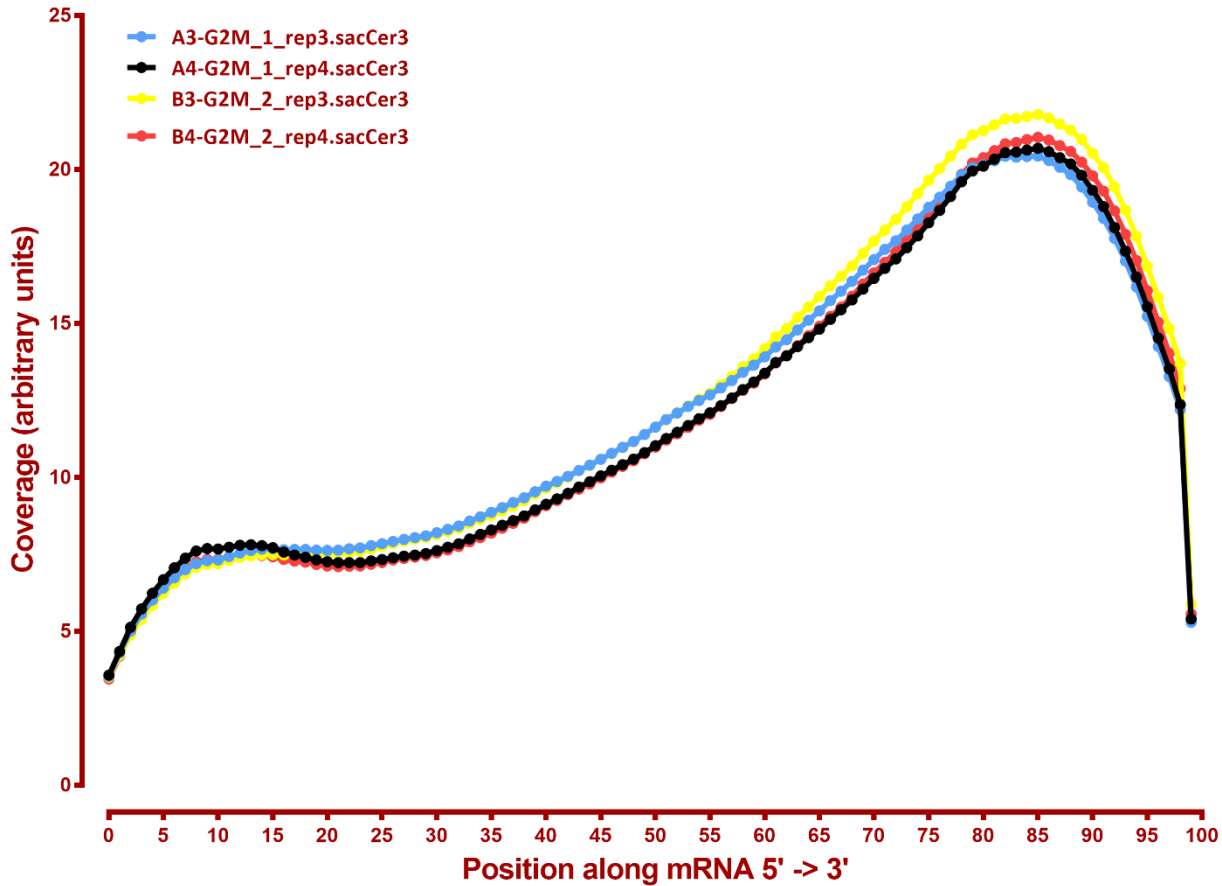
# MAPPING STATS

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
A3-G2M_1_rep3	2x150	STAR-2.5.3a	S_pombe	40,578,753	0.28	36,073,151	3,170,871	645,088	152,292	0.49
A3-G2M_1_rep3	2x150	STAR-2.5.3a	sacCer3	40,578,753	0.27	36,302,910	989,238	1,865,029	80,345	0.48
A4-G2M_1_rep4	2x150	STAR-2.5.3a	S_pombe	42,423,531	0.26	49,316,027	4,417,741	1,047,791	253,495	0.65
A4-G2M_1_rep4	2x150	STAR-2.5.3a	sacCer3	42,423,531	0.27	25,537,086	751,758	1,425,701	65,509	0.33
B3-G2M_2_rep3	2x150	STAR-2.5.3a	S_pombe	41,568,094	0.25	38,251,302	3,372,154	631,962	184,154	0.51
B3-G2M_2_rep3	2x150	STAR-2.5.3a	sacCer3	41,568,094	0.25	35,700,696	812,906	1,847,450	102,548	0.46
B4-G2M_2_rep4	2x150	STAR-2.5.3a	S_pombe	41,614,983	0.25	40,117,813	3,622,171	739,815	189,665	0.54
B4-G2M_2_rep4	2x150	STAR-2.5.3a	sacCer3	41,614,983	0.25	33,525,605	970,979	1,841,606	77,364	0.44
C3-G2M_3_rep3	2x150	STAR-2.5.3a	S_pombe	42,618,137	0.18	32,145,296	2,856,548	523,779	132,239	0.42
C3-G2M_3_rep3	2x150	STAR-2.5.3a	sacCer3	42,618,137	0.17	43,135,910	988,178	2,411,361	94,523	0.55
C4-G2M_3_rep4	2x150	STAR-2.5.3a	S_pombe	46,341,502	0.29	41,983,420	3,868,282	740,299	206,131	0.50
C4-G2M_3_rep4	2x150	STAR-2.5.3a	sacCer3	46,341,502	0.27	40,790,979	1,126,775	2,142,002	98,562	0.48
D3-G2M_4_rep3	2x150	STAR-2.5.3a	S_pombe	41,674,662	0.32	26,683,779	2,419,169	424,890	119,634	0.36
D3-G2M_4_rep3	2x150	STAR-2.5.3a	sacCer3	41,674,662	0.27	47,449,518	1,336,822	2,639,507	120,679	0.62
D4-G2M_4_rep4	2x150	STAR-2.5.3a	S_pombe	40,642,869	0.29	35,842,623	3,345,305	628,582	154,648	0.49
D4-G2M_4_rep4	2x150	STAR-2.5.3a	sacCer3	40,642,869	0.27	36,119,880	1,164,412	2,191,363	90,989	0.49
E3-input_rep3	2x150	STAR-2.5.3a	S_pombe	40,865,855	0.27	17,398,727	1,621,783	303,137	78,791	0.24
E3-input_rep3	2x150	STAR-2.5.3a	sacCer3	40,865,855	0.22	54,937,099	1,384,973	3,409,252	143,840	0.73
E4-input_rep4	2x150	STAR-2.5.3a	S_pombe	39,236,211	0.61	132	16	241	7	0.00
E4-input_rep4	2x150	STAR-2.5.3a	sacCer3	39,236,211	0.22	69,444,592	2,320,210	4,517,134	240,060	0.98
F3-unstained_input_rep3	2x150	STAR-2.5.3a	S_pombe	42,286,018	0.28	21,795,416	2,032,250	397,258	84,650	0.29
F3-unstained_input_rep3	2x150	STAR-2.5.3a	sacCer3	42,286,018	0.23	53,385,142	1,698,254	3,142,950	170,286	0.69
F4-unstained_input_rep4	2x150	STAR-2.5.3a	S_pombe	40,647,301	0.44	3,049	237	270	4	0.00
F4-unstained_input_rep4	2x150	STAR-2.5.3a	sacCer3	40,647,301	0.24	73,176,020	1,934,778	3,983,091	225,773	0.98

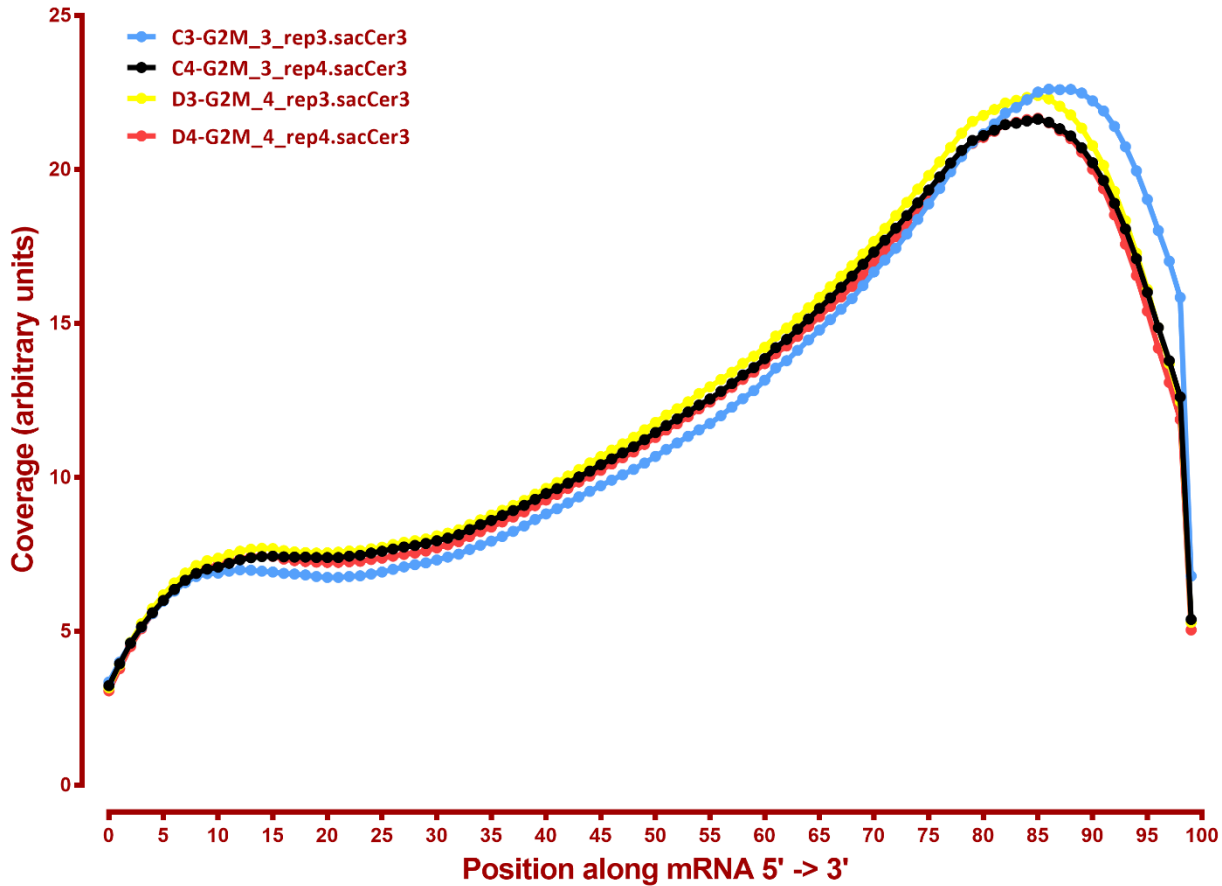
# READ DISTRIBUTION

2019-08-21-A3-G2M_1_rep3.S_pombe	0.97	0.02	0.01
2019-08-21-A3-G2M_1_rep3.sacCer3	0.89	0.10	0.01
2019-08-21-A4-G2M_1_rep4.S_pombe	0.97	0.02	0.01
2019-08-21-A4-G2M_1_rep4.sacCer3	0.89	0.11	0.00
2019-08-21-B3-G2M_2_rep3.S_pombe	0.97	0.03	0.01
2019-08-21-B3-G2M_2_rep3.sacCer3	0.89	0.11	0.01
2019-08-21-B4-G2M_2_rep4.S_pombe	0.97	0.02	0.01
2019-08-21-B4-G2M_2_rep4.sacCer3	0.89	0.11	0.00
2019-08-21-C3-G2M_3_rep3.S_pombe	0.97	0.03	0.01
2019-08-21-C3-G2M_3_rep3.sacCer3	0.88	0.12	0.00
2019-08-21-C4-G2M_3_rep4.S_pombe	0.97	0.02	0.01
2019-08-21-C4-G2M_3_rep4.sacCer3	0.90	0.10	0.00
2019-08-21-D3-G2M_4_rep3.S_pombe	0.97	0.02	0.01
2019-08-21-D3-G2M_4_rep3.sacCer3	0.90	0.09	0.00
2019-08-21-D4-G2M_4_rep4.S_pombe	0.97	0.02	0.01
2019-08-21-D4-G2M_4_rep4.sacCer3	0.90	0.09	0.00
2019-08-21-E3-input_rep3.S_pombe	0.97	0.02	0.01
2019-08-21-E3-input_rep3.sacCer3	0.90	0.10	0.00
2019-08-21-E4-input_rep4.S_pombe	0.99	0.01	0.00
2019-08-21-E4-input_rep4.sacCer3	0.89	0.10	0.00
2019-08-21-F3-unstained_input_rep3.S_pombe	0.97	0.02	0.01
2019-08-21-F3-unstained_input_rep3.sacCer3	0.89	0.11	0.00
2019-08-21-F4-unstained_input_rep4.S_pombe	0.97	0.02	0.01
2019-08-21-F4-unstained_input_rep4.sacCer3	0.89	0.10	0.00

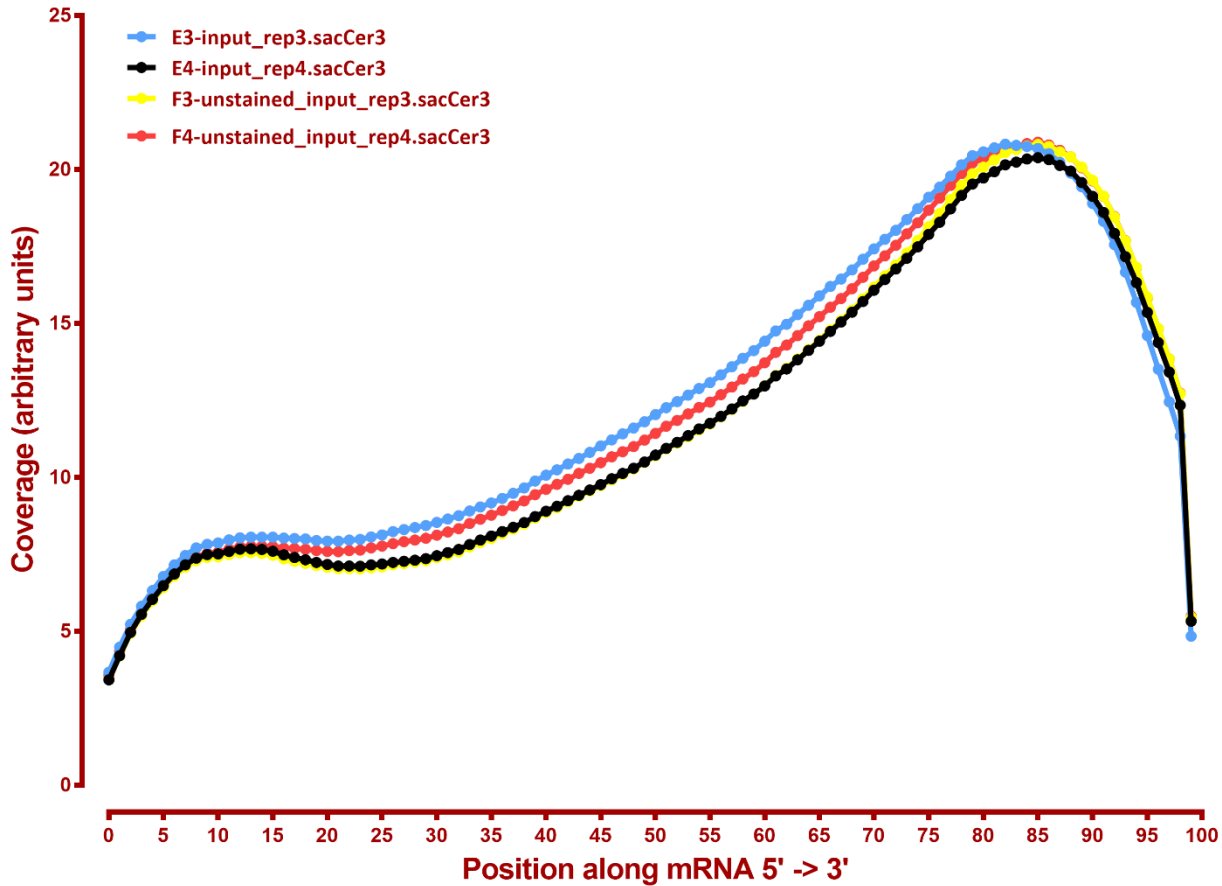
## Coverage of genes; >1000bp, sacCer3



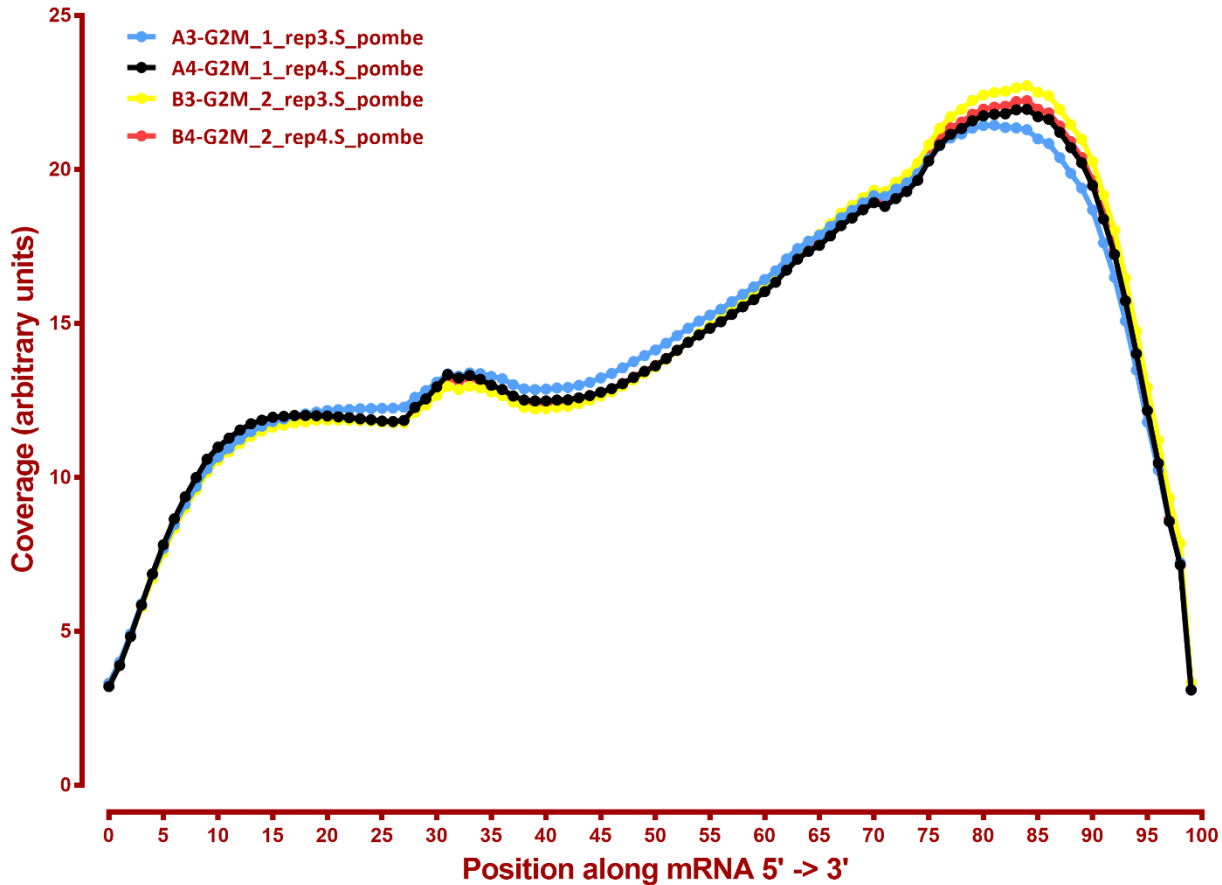
## Coverage of genes; >1000bp, sacCer3



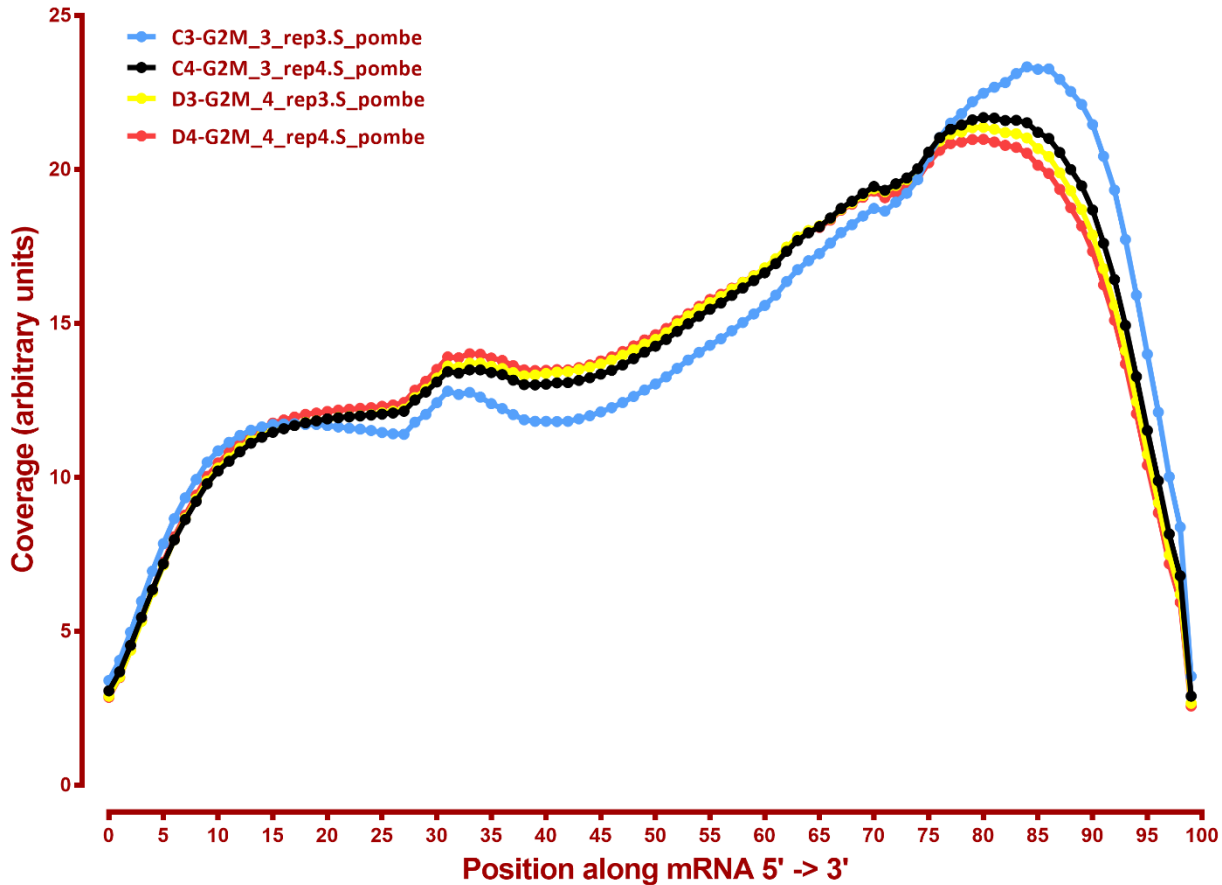
## Coverage of genes; >1000bp, sacCer3



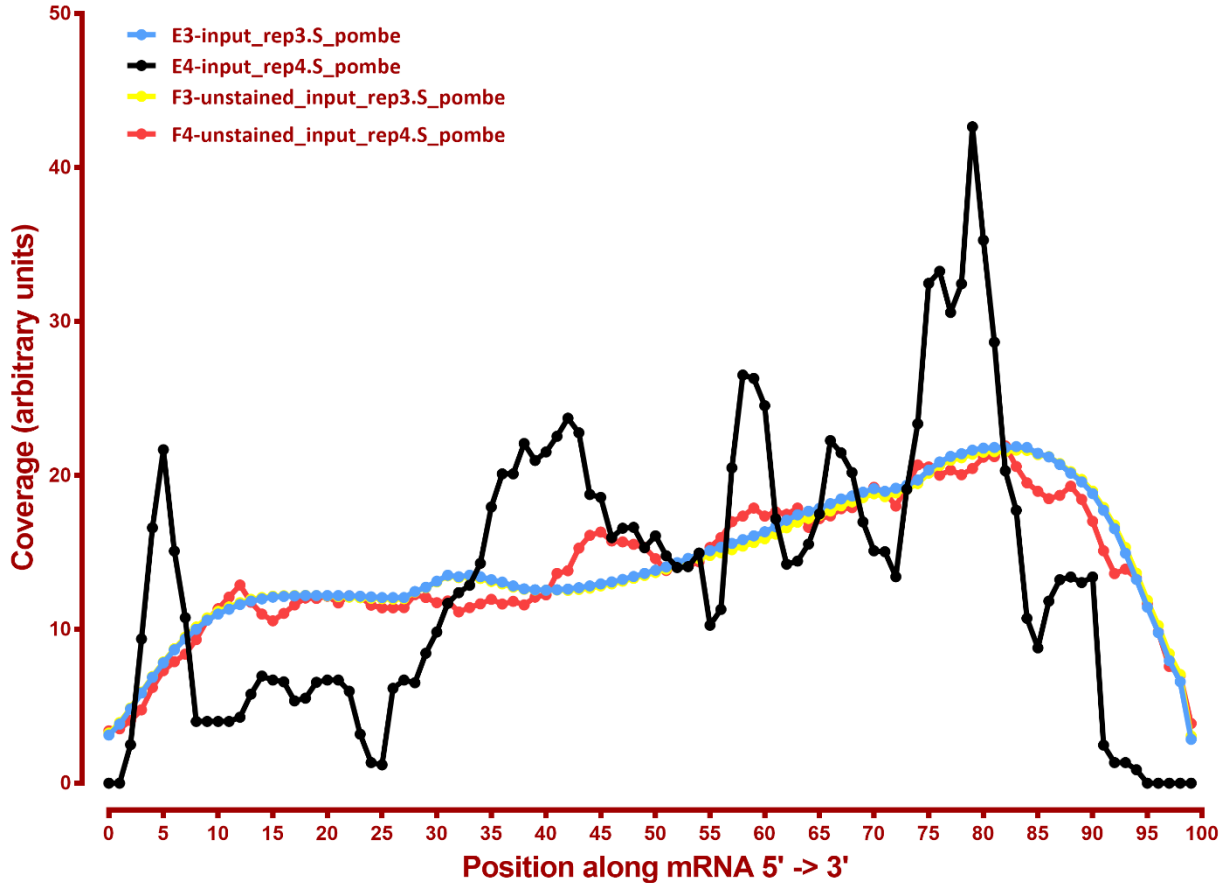
## Coverage of genes; >1000bp, *S.pombe*



## Coverage of genes; >1000bp, *S.pombe*



## Coverage of genes; >1000bp, *S.pombe*



Number differential genes, sacCer3

A	B	p-adj		p-val	
		up in B vs A	down in B vs A	up in B vs A	down in B vs A
G2M_1	G2M_2	78	26	339	221
G2M_1	G2M_3	318	262	645	521
G2M_1	G2M_4	716	558	1,072	869
G2M_1	input	513	281	839	584
G2M_1	unstained_input	331	163	628	419
G2M_2	G2M_3	100	60	295	250
G2M_2	G2M_4	720	472	1,162	870
G2M_2	input	257	119	571	382
G2M_2	unstained_input	176	59	437	273
G2M_3	G2M_4	145	40	689	291
G2M_3	input	183	88	524	372
G2M_3	unstained_input	70	28	253	164
G2M_4	input	362	324	771	810
G2M_4	unstained_input	109	143	394	509
input	unstained_input	0	3	69	124

Number differential genes, *S. pombe*

A	B	p-adj		p-val	
		up in B vs A	down in B vs A	up in B vs A	down in B vs A
G2M_1	G2M_2	0	0	57	1
G2M_1	G2M_3	0	0	110	0
G2M_1	G2M_4	95	0	379	3
G2M_1	input	66	1	1,525	5
G2M_1	unstained_input	0	0	17	1
G2M_2	G2M_3	0	0	7	0
G2M_2	G2M_4	94	0	213	8
G2M_2	input	2	2	173	11
G2M_2	unstained_input	0	0	16	36
G2M_3	G2M_4	46	0	138	6
G2M_3	input	1	1	144	15
G2M_3	unstained_input	0	0	14	59
G2M_4	input	1	37	215	144
G2M_4	unstained_input	1	23	13	181
input	unstained_input	0	0	12	1092

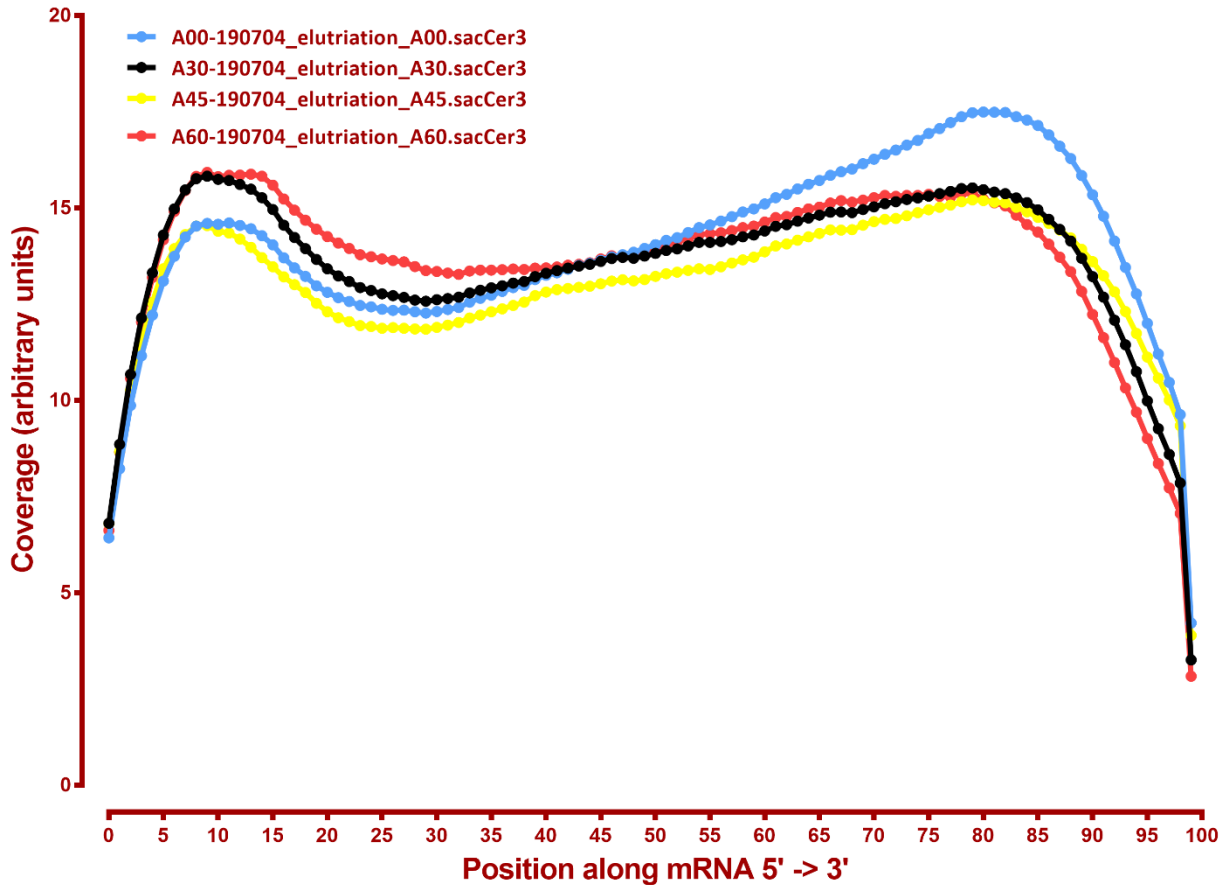
# MAPPING STATS

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
A00-190704_elutriation_A00	2x150	STAR-2.5.3a	S_pombe	39,846,109	0.86	26	4	114	2	0.00
A00-190704_elutriation_A00	2x150	STAR-2.5.3a	sacCer3	39,846,109	0.33	72,066,411	1,574,365	3,944,765	220,529	0.98
A30-190704_elutriation_A30	2x150	STAR-2.5.3a	S_pombe	43,189,364	1.00	10	0	152	0	0.00
A30-190704_elutriation_A30	2x150	STAR-2.5.3a	sacCer3	43,189,364	0.31	77,844,379	2,205,959	4,205,928	259,784	0.98
A45-190704_elutriation_A45	2x150	STAR-2.5.3a	S_pombe	44,758,775	0.95	14	2	112	2	0.00
A45-190704_elutriation_A45	2x150	STAR-2.5.3a	sacCer3	44,758,775	0.30	81,821,569	1,968,153	3,300,510	280,938	0.98
A60-190704_elutriation_A60	2x150	STAR-2.5.3a	S_pombe	45,836,126	1.00	12	6	155	1	0.00
A60-190704_elutriation_A60	2x150	STAR-2.5.3a	sacCer3	45,836,126	0.30	82,336,028	2,780,308	3,912,908	426,062	0.98
A75-190704_elutriation_A75	2x150	STAR-2.5.3a	S_pombe	41,550,192	0.86	33	1	168	2	0.00
A75-190704_elutriation_A75	2x150	STAR-2.5.3a	sacCer3	41,550,192	0.29	75,048,029	2,610,353	3,292,509	274,965	0.98
A90-190704_elutriation_A90	2x150	STAR-2.5.3a	S_pombe	42,909,325	0.88	26	2	128	0	0.00
A90-190704_elutriation_A90	2x150	STAR-2.5.3a	sacCer3	42,909,325	0.30	77,720,317	2,489,269	3,385,377	338,453	0.98
B00-190704_elutriation_A00	2x150	STAR-2.5.3a	S_pombe	41,274,553	0.67	244	14	492	16	0.00
B00-190704_elutriation_A00	2x150	STAR-2.5.3a	sacCer3	41,274,553	0.29	73,975,724	1,718,352	4,674,873	215,117	0.98
B30-190704_elutriation_A30	2x150	STAR-2.5.3a	S_pombe	42,256,973	0.93	118	6	138	4	0.00
B30-190704_elutriation_A30	2x150	STAR-2.5.3a	sacCer3	42,256,973	0.29	76,264,656	2,052,302	4,172,947	253,549	0.98
B45-190704_elutriation_A45	2x150	STAR-2.5.3a	S_pombe	35,380,753	0.75	39	9	429	11	0.00
B45-190704_elutriation_A45	2x150	STAR-2.5.3a	sacCer3	35,380,753	0.23	62,559,451	2,020,459	3,253,726	185,386	0.96
B60-190704_elutriation_A60	2x150	STAR-2.5.3a	S_pombe	42,735,442	0.97	134	10	269	9	0.00
B60-190704_elutriation_A60	2x150	STAR-2.5.3a	sacCer3	42,735,442	0.26	76,180,119	3,103,605	3,900,506	406,710	0.98
B75-190704_elutriation_A75	2x150	STAR-2.5.3a	S_pombe	40,343,672	0.69	31	9	147	3	0.00
B75-190704_elutriation_A75	2x150	STAR-2.5.3a	sacCer3	40,343,672	0.29	72,289,892	2,665,622	3,586,627	303,923	0.98
B90-190704_elutriation_A90	2x150	STAR-2.5.3a	S_pombe	43,118,409	0.91	21	3	137	7	0.00
B90-190704_elutriation_A90	2x150	STAR-2.5.3a	sacCer3	43,118,409	0.28	77,440,846	2,576,438	3,889,538	319,810	0.98
C00-190704_elutriation_A00	2x150	STAR-2.5.3a	S_pombe	44,648,618	0.66	7,556	668	300	26	0.00
C00-190704_elutriation_A00	2x150	STAR-2.5.3a	sacCer3	44,648,618	0.33	80,101,983	1,648,325	4,999,775	266,723	0.97
C30-190704_elutriation_A30	2x150	STAR-2.5.3a	S_pombe	42,051,642	0.79	32	4	147	1	0.00
C30-190704_elutriation_A30	2x150	STAR-2.5.3a	sacCer3	42,051,642	0.31	75,834,525	2,268,851	4,022,691	237,189	0.98
C45-190704_elutriation_A45	2x150	STAR-2.5.3a	S_pombe	40,327,379	0.82	15	1	130	4	0.00
C45-190704_elutriation_A45	2x150	STAR-2.5.3a	sacCer3	40,327,379	0.28	73,216,231	1,873,793	3,479,423	260,709	0.98
C60-190704_elutriation_A60	2x150	STAR-2.5.3a	S_pombe	39,825,985	0.56	19	5	40	2	0.00
C60-190704_elutriation_A60	2x150	STAR-2.5.3a	sacCer3	39,825,985	0.29	71,774,251	2,287,561	3,748,395	347,547	0.98
C75-190704_elutriation_A75	2x150	STAR-2.5.3a	S_pombe	42,239,120	0.86	34	2	396	10	0.00
C75-190704_elutriation_A75	2x150	STAR-2.5.3a	sacCer3	42,239,120	0.28	74,696,600	2,857,434	4,101,693	431,065	0.97
C90-190704_elutriation_A90	2x150	STAR-2.5.3a	S_pombe	40,918,318	0.95	40	4	228	2	0.00
C90-190704_elutriation_A90	2x150	STAR-2.5.3a	sacCer3	40,918,318	0.28	73,212,211	2,356,753	3,723,209	259,029	0.97

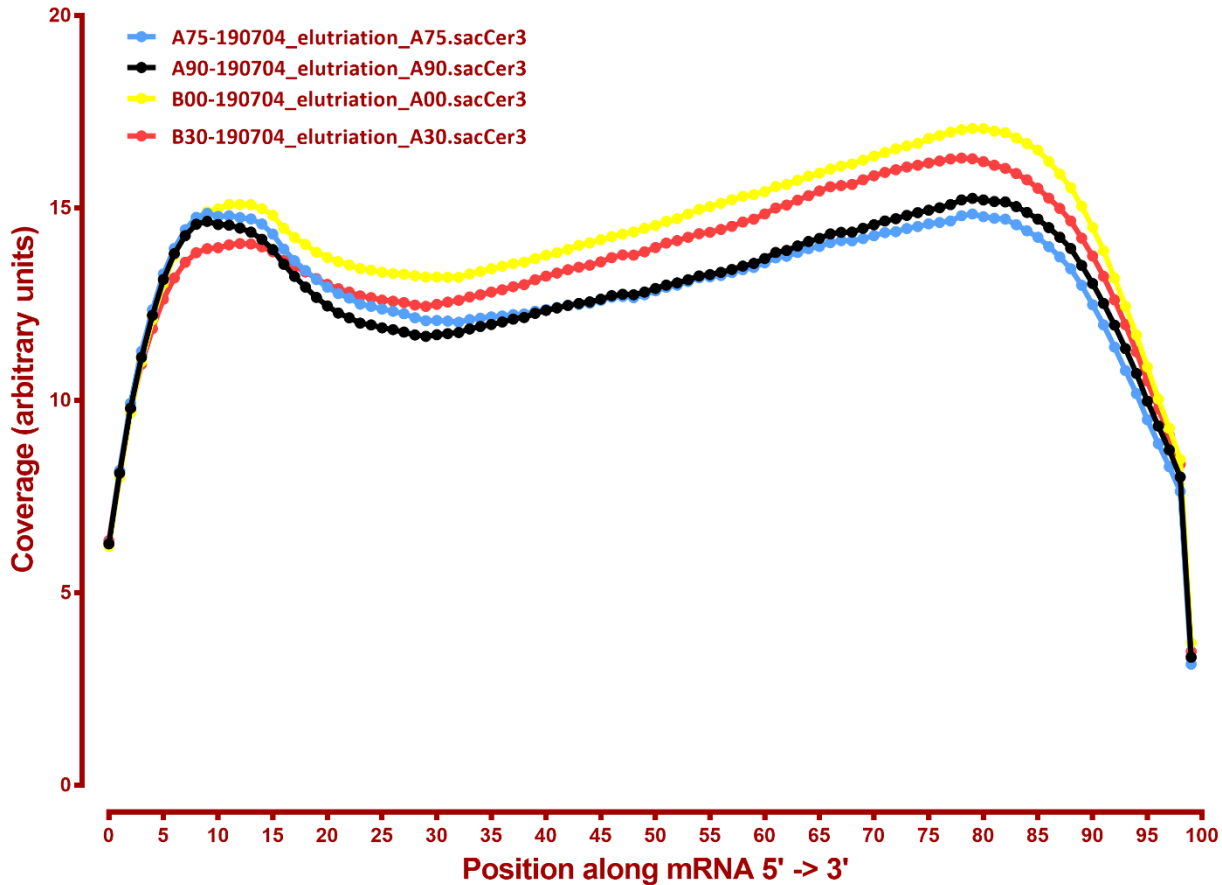
# READ DISTRIBUTION

#	Exonic:	Intergenic:	Intronic:
2019-08-21-A00-190704_elutriation_A00.S_pombe	1.00	0.00	0.00
2019-08-21-A00-190704_elutriation_A00.sacCer3	0.90	0.09	0.00
2019-08-21-A30-190704_elutriation_A30.S_pombe	1.00	0.00	0.00
2019-08-21-A30-190704_elutriation_A30.sacCer3	0.92	0.08	0.00
2019-08-21-A45-190704_elutriation_A45.S_pombe	1.00	0.00	0.00
2019-08-21-A45-190704_elutriation_A45.sacCer3	0.90	0.10	0.00
2019-08-21-A60-190704_elutriation_A60.S_pombe	1.00	0.00	0.00
2019-08-21-A60-190704_elutriation_A60.sacCer3	0.92	0.08	0.00
2019-08-21-A75-190704_elutriation_A75.S_pombe	1.00	0.00	0.00
2019-08-21-A75-190704_elutriation_A75.sacCer3	0.91	0.09	0.01
2019-08-21-A90-190704_elutriation_A90.S_pombe	1.00	0.00	0.00
2019-08-21-A90-190704_elutriation_A90.sacCer3	0.91	0.09	0.01
2019-08-21-B00-190704_elutriation_A00.S_pombe	0.97	0.03	0.00
2019-08-21-B00-190704_elutriation_A00.sacCer3	0.91	0.09	0.00
2019-08-21-B30-190704_elutriation_A30.S_pombe	1.00	0.00	0.00
2019-08-21-B30-190704_elutriation_A30.sacCer3	0.91	0.08	0.00
2019-08-21-B45-190704_elutriation_A45.S_pombe	1.00	0.00	0.00
2019-08-21-B45-190704_elutriation_A45.sacCer3	0.91	0.08	0.00
2019-08-21-B60-190704_elutriation_A60.S_pombe	0.97	0.03	0.00
2019-08-21-B60-190704_elutriation_A60.sacCer3	0.91	0.09	0.00
2019-08-21-B75-190704_elutriation_A75.S_pombe	1.00	0.00	0.00
2019-08-21-B75-190704_elutriation_A75.sacCer3	0.91	0.09	0.00
2019-08-21-B90-190704_elutriation_A90.S_pombe	1.00	0.00	0.00
2019-08-21-B90-190704_elutriation_A90.sacCer3	0.91	0.08	0.00
2019-08-21-C00-190704_elutriation_A00.S_pombe	0.97	0.02	0.01
2019-08-21-C00-190704_elutriation_A00.sacCer3	0.91	0.09	0.00
2019-08-21-C30-190704_elutriation_A30.S_pombe	1.00	0.00	0.00
2019-08-21-C30-190704_elutriation_A30.sacCer3	0.92	0.07	0.00
2019-08-21-C45-190704_elutriation_A45.S_pombe	1.00	0.00	0.00
2019-08-21-C45-190704_elutriation_A45.sacCer3	0.90	0.10	0.00
2019-08-21-C60-190704_elutriation_A60.S_pombe	1.00	0.00	0.00
2019-08-21-C60-190704_elutriation_A60.sacCer3	0.89	0.10	0.00
2019-08-21-C75-190704_elutriation_A75.S_pombe	1.00	0.00	0.00
2019-08-21-C75-190704_elutriation_A75.sacCer3	0.91	0.09	0.00
2019-08-21-C90-190704_elutriation_A90.S_pombe	0.95	0.02	0.02
2019-08-21-C90-190704_elutriation_A90.sacCer3	0.90	0.10	0.00

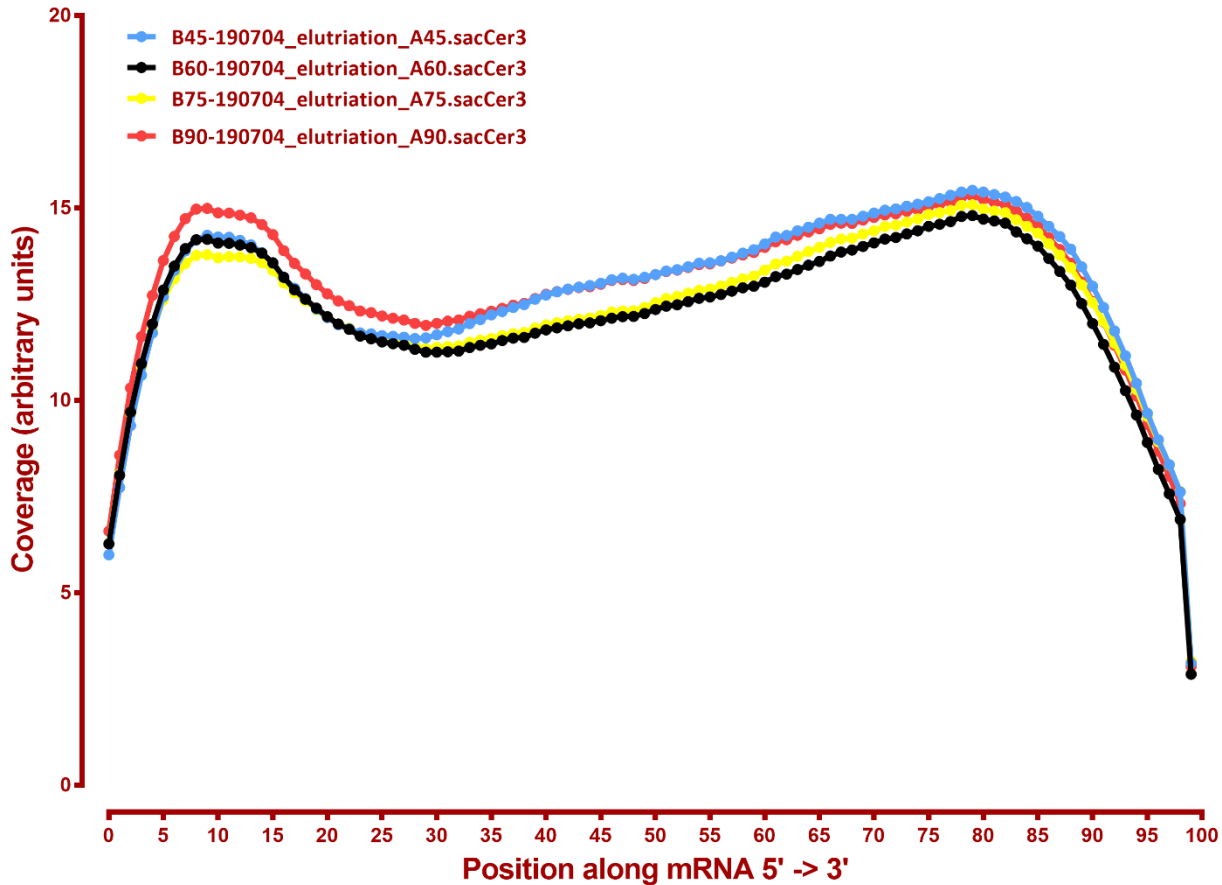
## Coverage of genes; >1000bp, sacCer3



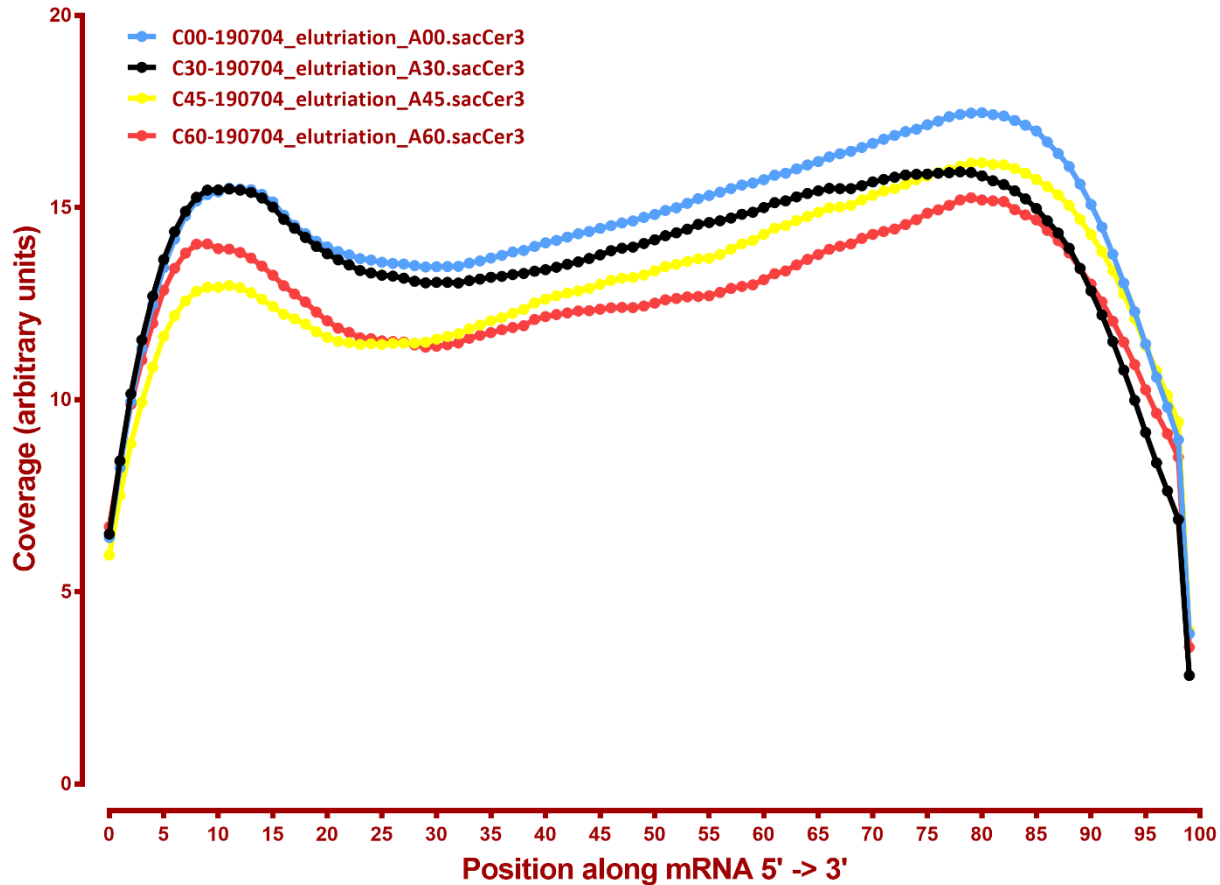
## Coverage of genes; >1000bp, sacCer3



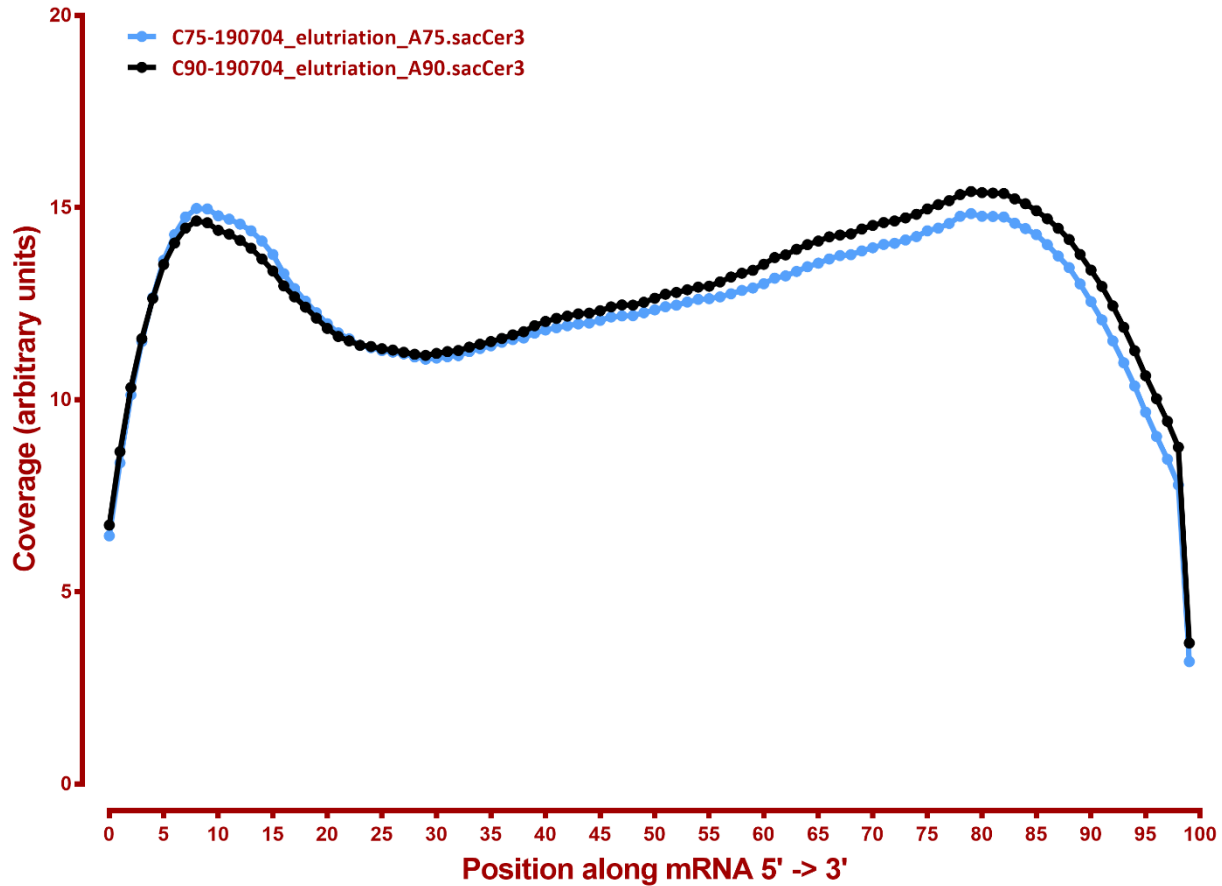
## Coverage of genes; >1000bp, sacCer3



## Coverage of genes; >1000bp, sacCer3



## Coverage of genes; >1000bp, sacCer3



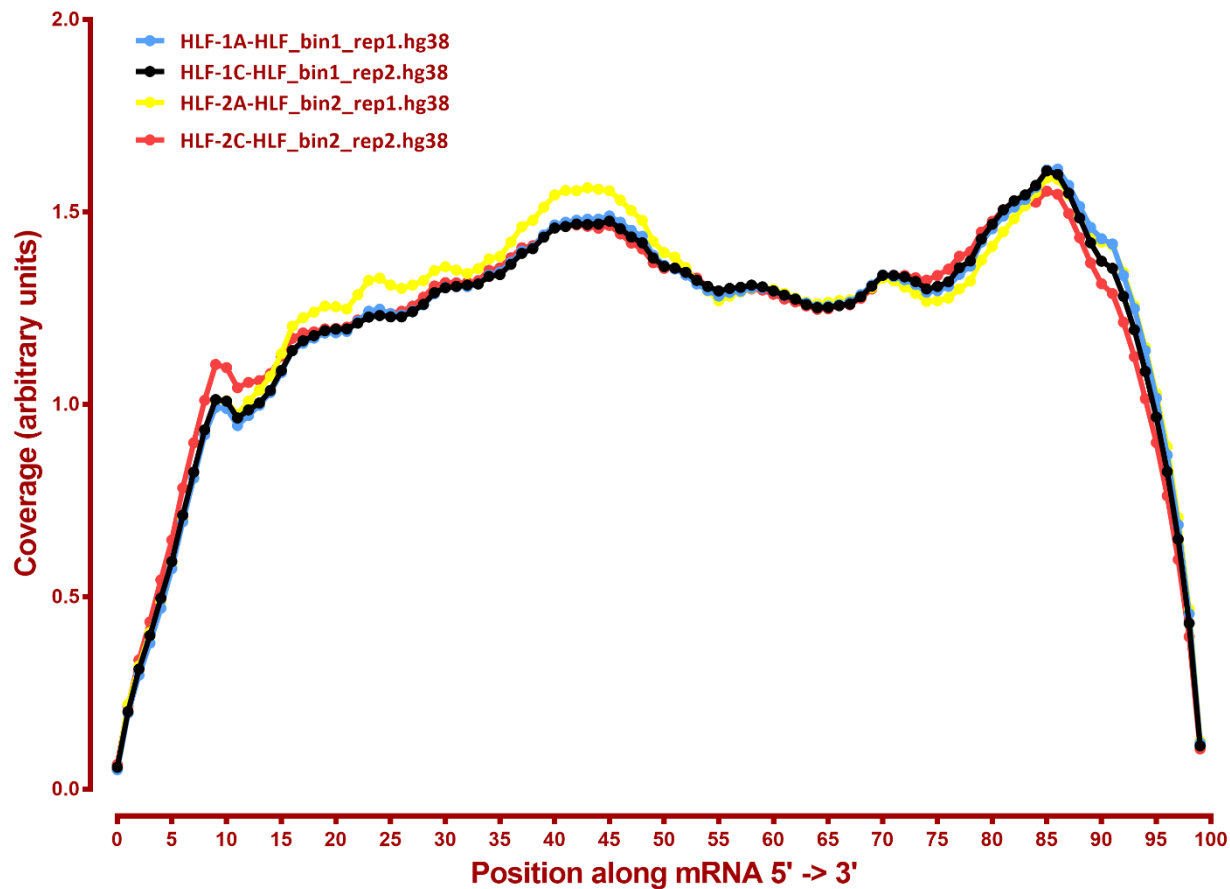
# MAPPING STATS

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
HLF-1A-HLF_bin1_rep1	2x150	STAR-2.5.3a	dm6	40,393,265	0.29	4,961,983	506,887	3,761,415	73,045	0.12
HLF-1A-HLF_bin1_rep1	2x150	STAR-2.5.3a	hg38	40,393,265	0.28	48,760,420	17,971,020	1,577,502	1,473,856	0.86
HLF-1C-HLF_bin1_rep2	2x150	STAR-2.5.3a	dm6	39,224,381	0.29	5,180,394	640,772	4,031,220	81,116	0.13
HLF-1C-HLF_bin1_rep2	2x150	STAR-2.5.3a	hg38	39,224,381	0.28	45,328,240	18,537,868	1,515,623	1,552,243	0.85
HLF-2A-HLF_bin2_rep1	2x150	STAR-2.5.3a	dm6	41,270,859	0.19	4,681,749	398,897	3,933,705	52,785	0.11
HLF-2A-HLF_bin2_rep1	2x150	STAR-2.5.3a	hg38	41,270,859	0.18	51,470,548	17,351,058	1,464,360	1,342,662	0.87
HLF-2C-HLF_bin2_rep2	2x150	STAR-2.5.3a	dm6	38,846,957	0.32	4,137,826	612,338	3,176,618	68,810	0.10
HLF-2C-HLF_bin2_rep2	2x150	STAR-2.5.3a	hg38	38,846,957	0.28	45,272,282	19,729,980	1,546,307	1,684,215	0.88
HLF-3A-HLF_bin3_rep1	2x150	STAR-2.5.3a	dm6	40,410,168	0.24	4,197,930	369,966	3,155,861	58,545	0.10
HLF-3A-HLF_bin3_rep1	2x150	STAR-2.5.3a	hg38	40,410,168	0.23	50,494,747	17,921,663	1,505,246	1,386,656	0.88
HLF-3C-HLF_bin3_rep2	2x150	STAR-2.5.3a	dm6	42,880,443	0.33	4,533,795	424,417	4,072,927	52,471	0.11
HLF-3C-HLF_bin3_rep2	2x150	STAR-2.5.3a	hg38	42,880,443	0.31	53,720,241	18,370,201	1,552,851	1,426,113	0.88
HLF-4A-HLF_bin4_rep1	2x150	STAR-2.5.3a	dm6	41,232,906	0.23	4,378,766	346,846	3,626,266	48,644	0.10
HLF-4A-HLF_bin4_rep1	2x150	STAR-2.5.3a	hg38	41,232,906	0.23	52,331,264	17,326,570	1,470,805	1,357,211	0.88
HLF-4C-HLF_bin4_rep2	2x150	STAR-2.5.3a	dm6	41,001,126	0.33	4,108,941	598,187	2,565,211	54,863	0.09
HLF-4C-HLF_bin4_rep2	2x150	STAR-2.5.3a	hg38	41,001,126	0.31	47,024,951	20,843,459	1,781,206	1,810,088	0.87
HLF-pre-Sort-A-HLF_pre-sort_rep1	2x150	STAR-2.5.3a	dm6	43,770,987	0.27	4,890,588	467,102	4,140,089	67,483	0.11
HLF-pre-Sort-A-HLF_pre-sort_rep1	2x150	STAR-2.5.3a	hg38	43,770,987	0.26	55,282,004	19,662,064	1,677,665	1,544,373	0.89
HLF-pre-Sort-C-HLF_pre-sort_rep2	2x150	STAR-2.5.3a	dm6	42,687,916	0.23	5,089,377	579,409	3,630,409	72,445	0.11
HLF-pre-Sort-C-HLF_pre-sort_rep2	2x150	STAR-2.5.3a	hg38	42,687,916	0.21	50,724,688	22,243,874	1,628,184	1,744,666	0.89
HLF-SortAll-A-HLF_sort-all_rep1	2x150	STAR-2.5.3a	dm6	44,719,272	0.30	2,684,256	298,806	1,925,015	37,491	0.06
HLF-SortAll-A-HLF_sort-all_rep1	2x150	STAR-2.5.3a	hg38	44,719,272	0.32	53,445,081	21,665,897	1,742,972	1,751,596	0.88

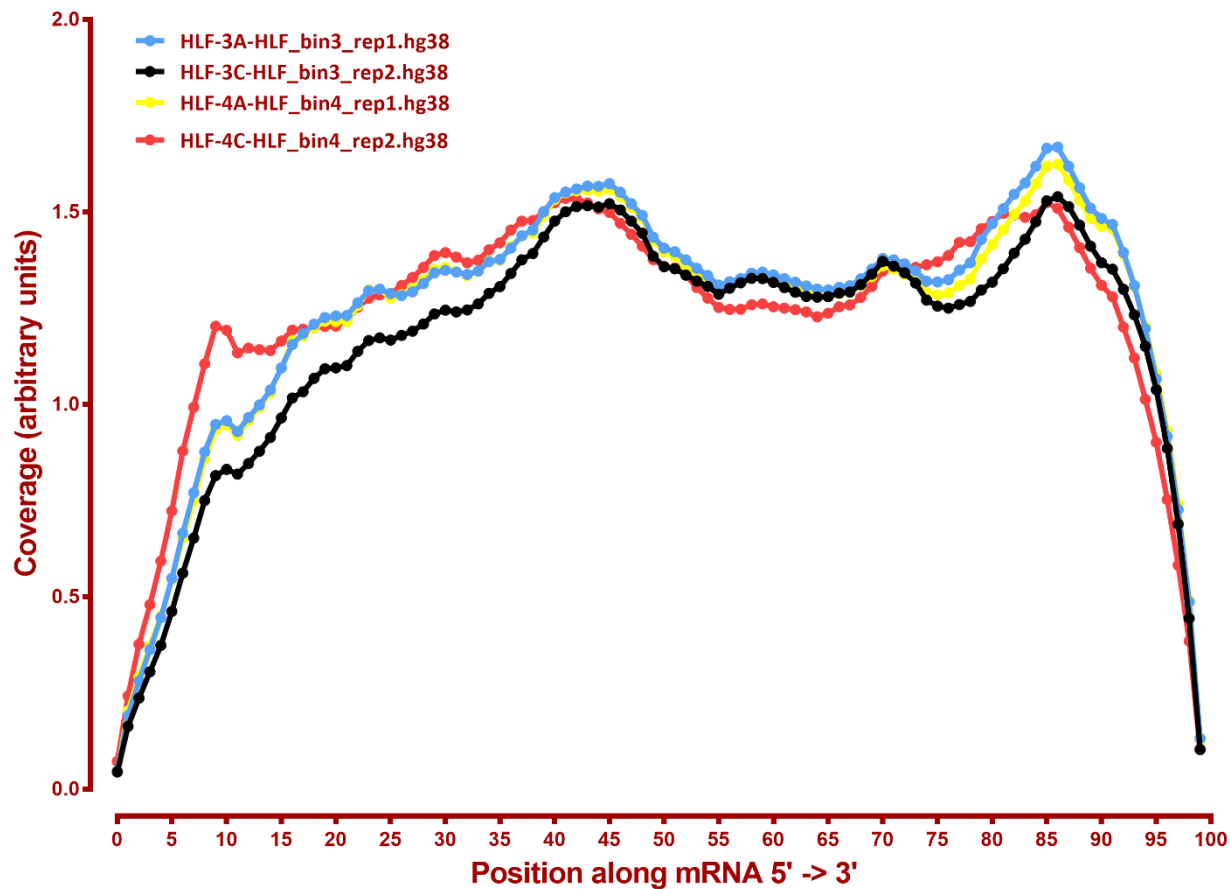
# READ DISTRIBUTION

#	Exonic:	Intergenic:	Intronic:
2019-08-21-HLF-1A-HLF_bin1_rep1.dm6	0.88	0.04	0.09
2019-08-21-HLF-1A-HLF_bin1_rep1.hg38	0.89	0.01	0.10
2019-08-21-HLF-1C-HLF_bin1_rep2.dm6	0.88	0.03	0.08
2019-08-21-HLF-1C-HLF_bin1_rep2.hg38	0.89	0.01	0.09
2019-08-21-HLF-2A-HLF_bin2_rep1.dm6	0.87	0.04	0.09
2019-08-21-HLF-2A-HLF_bin2_rep1.hg38	0.88	0.01	0.10
2019-08-21-HLF-2C-HLF_bin2_rep2.dm6	0.88	0.03	0.09
2019-08-21-HLF-2C-HLF_bin2_rep2.hg38	0.90	0.01	0.09
2019-08-21-HLF-3A-HLF_bin3_rep1.dm6	0.88	0.03	0.09
2019-08-21-HLF-3A-HLF_bin3_rep1.hg38	0.90	0.01	0.09
2019-08-21-HLF-3C-HLF_bin3_rep2.dm6	0.86	0.04	0.10
2019-08-21-HLF-3C-HLF_bin3_rep2.hg38	0.88	0.01	0.10
2019-08-21-HLF-4A-HLF_bin4_rep1.dm6	0.87	0.04	0.09
2019-08-21-HLF-4A-HLF_bin4_rep1.hg38	0.88	0.01	0.10
2019-08-21-HLF-4C-HLF_bin4_rep2.dm6	0.89	0.03	0.08
2019-08-21-HLF-4C-HLF_bin4_rep2.hg38	0.90	0.01	0.09
2019-08-21-HLF-SortAll-A-HLF_sort-all_rep1.dm6	0.87	0.04	0.09
2019-08-21-HLF-SortAll-A-HLF_sort-all_rep1.hg38	0.89	0.01	0.09
2019-08-21-HLF-pre-Sort-A-HLF_pre-sort_rep1.dm6	0.90	0.03	0.07
2019-08-21-HLF-pre-Sort-A-HLF_pre-sort_rep1.hg38	0.93	0.01	0.06
2019-08-21-HLF-pre-Sort-C-HLF_pre-sort_rep2.dm6	0.93	0.02	0.05
2019-08-21-HLF-pre-Sort-C-HLF_pre-sort_rep2.hg38	0.91	0.01	0.08

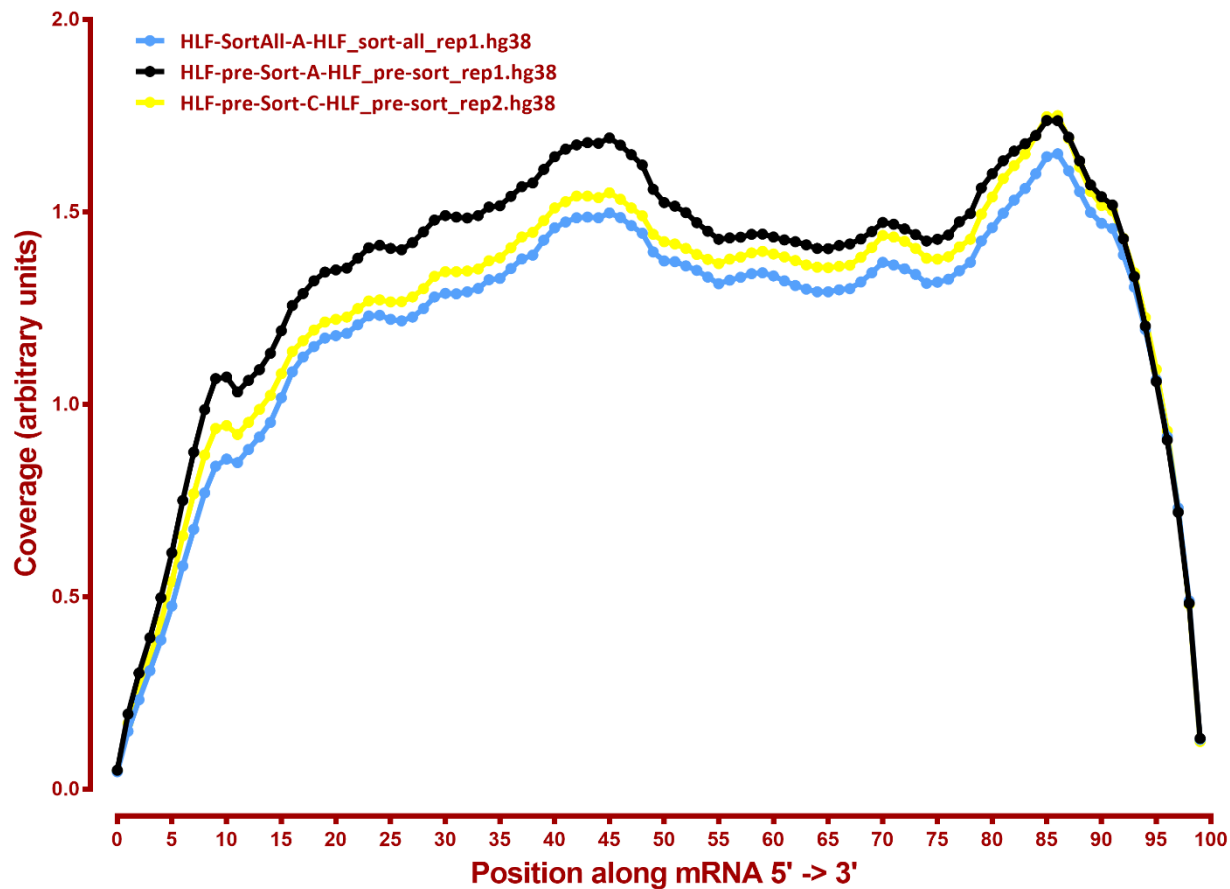
## Coverage of genes; >1000bp, sacCer3



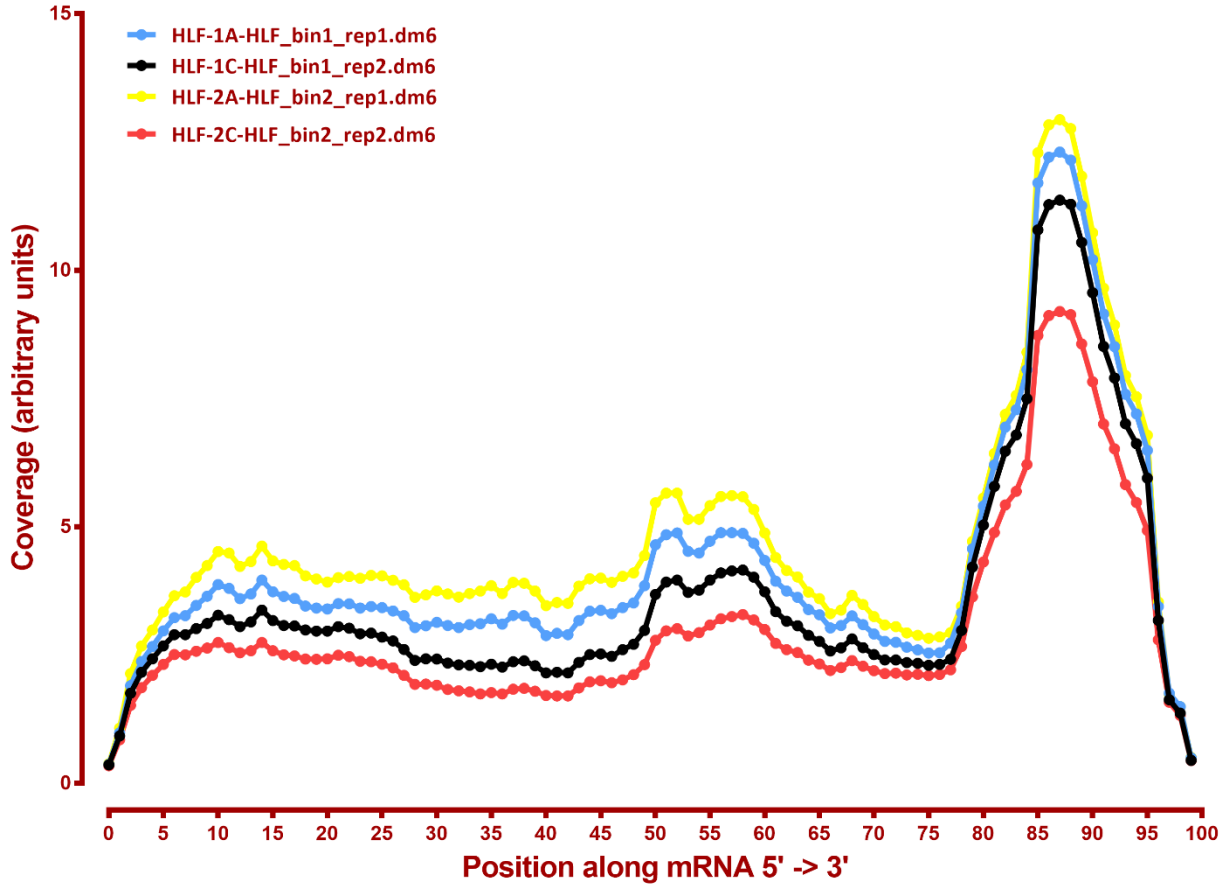
## Coverage of genes; >1000bp, sacCer3



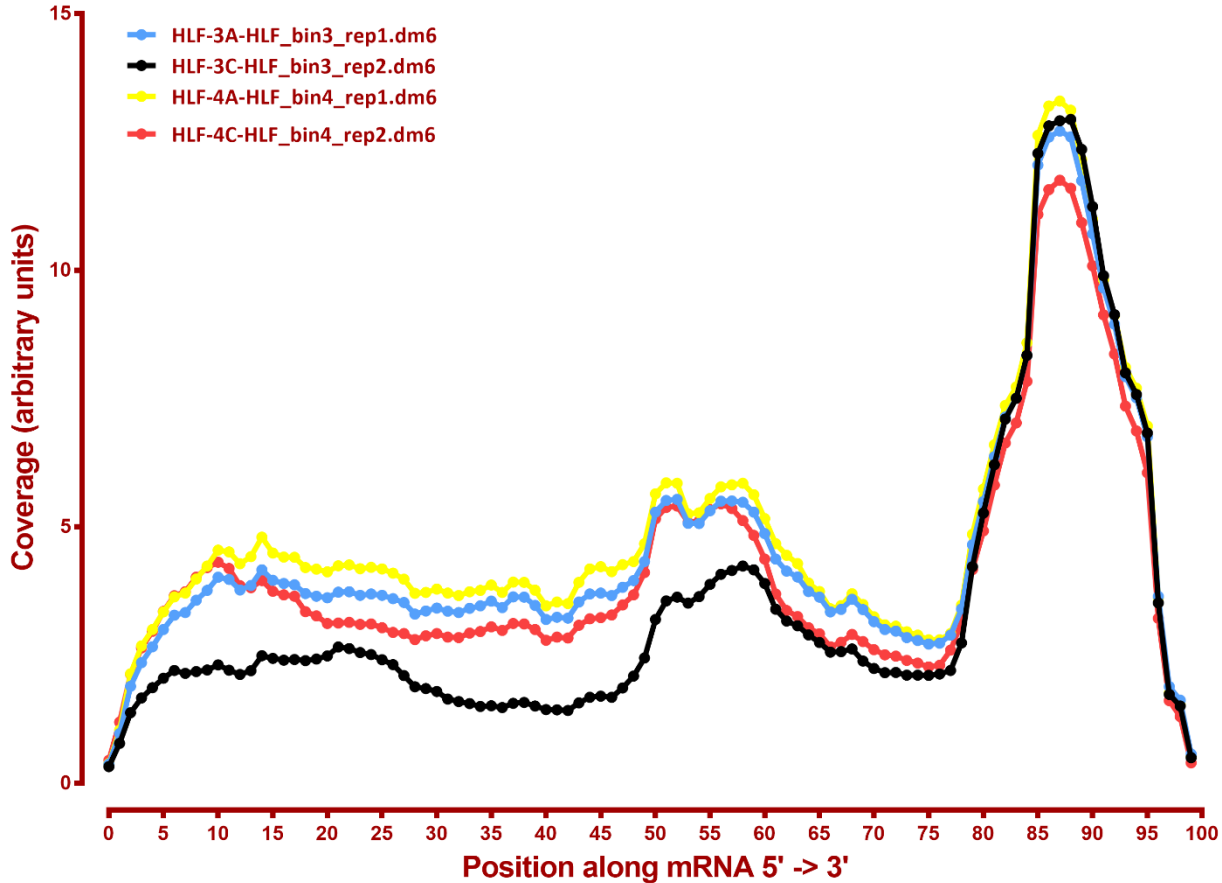
## Coverage of genes; >1000bp, sacCer3



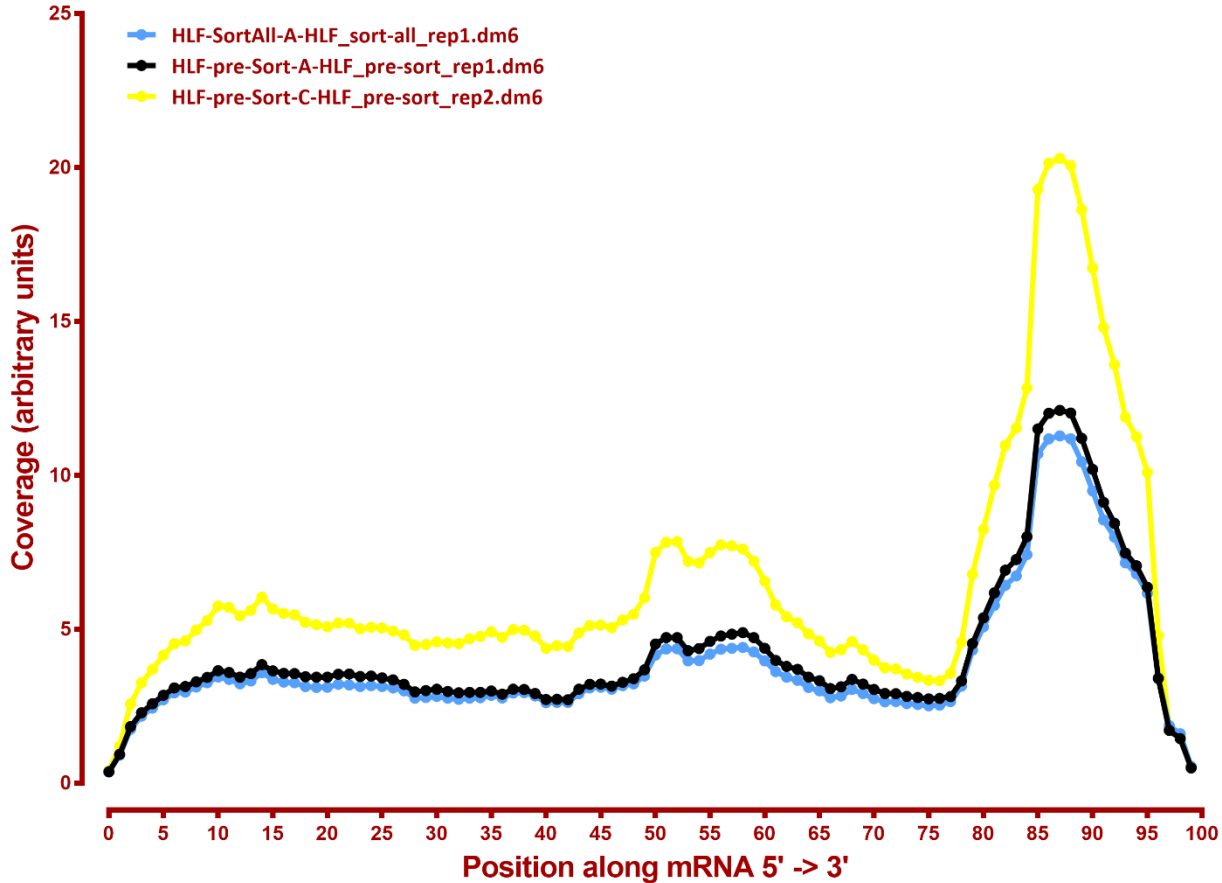
## Coverage of genes; >1000bp, *S.pombe*



## Coverage of genes; >1000bp, *S.pombe*



## Coverage of genes; >1000bp, *S.pombe*



Number differential genes, hg38

A	B	p-adj		p-val	
		up in B vs A	down in B vs A	up in B vs A	down in B vs A
HLF_bin1	HLF_bin2	0	10	150	138
HLF_bin1	HLF_bin3	20	23	421	431
HLF_bin1	HLF_bin4	25	3	548	245
HLF_bin1	HLF_pre-sort	1	2	173	262
HLF_bin1	HLF_sort-all	0	0	187	141
HLF_bin2	HLF_bin3	0	0	164	263
HLF_bin2	HLF_bin4	28	1	356	143
HLF_bin2	HLF_pre-sort	4	4	152	347
HLF_bin2	HLF_sort-all	2	0	165	136
HLF_bin3	HLF_bin4	4	0	709	142
HLF_bin3	HLF_pre-sort	1	2	276	453
HLF_bin3	HLF_sort-all	1	1	151	95
HLF_bin4	HLF_pre-sort	1	1	183	551
HLF_bin4	HLF_sort-all	3	2	179	535
HLF_sort-all	HLF_pre-sort	1	2	85	248

Number differential genes, dm6

A	B	p-adj		p-val	
		up in B vs A	down in B vs A	up in B vs A	down in B vs A
HLF_bin1	HLF_bin2	0	0	33	15
HLF_bin1	HLF_bin3	1	0	53	77
HLF_bin1	HLF_bin4	0	0	61	34
HLF_bin1	HLF_pre-sort	0	0	116	117
HLF_bin1	HLF_sort-all	0	0	35	15
HLF_bin2	HLF_bin3	0	0	77	116
HLF_bin2	HLF_bin4	0	0	86	49
HLF_bin2	HLF_pre-sort	0	1	157	206
HLF_bin2	HLF_sort-all	0	0	53	42
HLF_bin3	HLF_bin4	0	1	245	80
HLF_bin3	HLF_pre-sort	12	18	232	340
HLF_bin3	HLF_sort-all	0	1	48	30
HLF_bin4	HLF_pre-sort	0	0	201	269
HLF_bin4	HLF_sort-all	0	0	57	143
HLF_sort-all	HLF_pre-sort	0	0	100	119