

Mapping stats

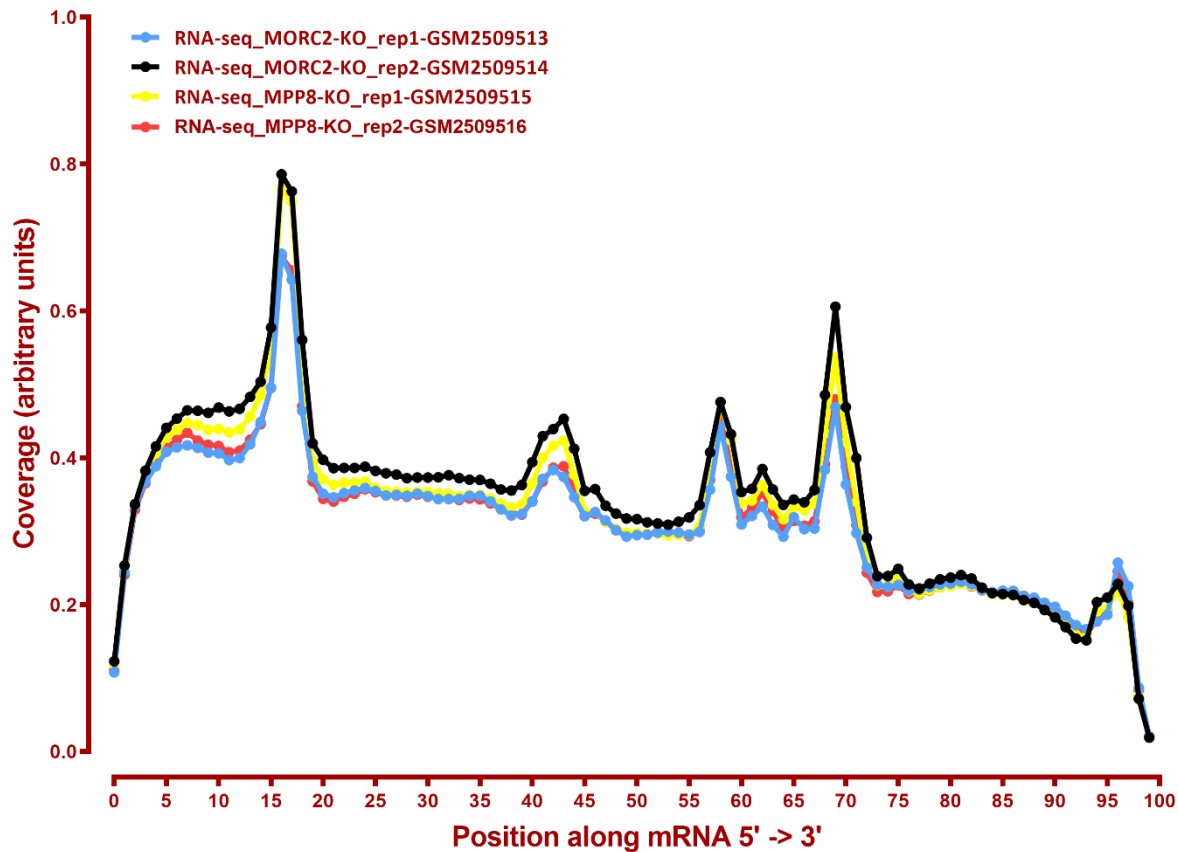
Species	Assay	Read Type + Length	Mapping	#	Complexity	Unique	Unique Splices	Multi	Multi Splices	Mapped fraction	Raw fragments
hs1-T2T-CHM13v2.0	RNA-seq	2x76	STAR-2.5.3a	RNA-seq_MORC2-KO_rep1-GSM2509513	0.46	32,539,404	11,323,636	3,914,316	1,166,860	0.44	56,050,543
hs1-T2T-CHM13v2.0	RNA-seq	2x76	STAR-2.5.3a	RNA-seq_MORC2-KO_rep2-GSM2509514	0.41	28,484,775	11,132,709	3,567,308	1,164,854	0.41	54,183,032
hs1-T2T-CHM13v2.0	RNA-seq	2x76	STAR-2.5.3a	RNA-seq_MPP8-KO_rep1-GSM2509515	0.43	30,186,669	10,597,815	3,526,528	1,143,986	0.44	51,631,436
hs1-T2T-CHM13v2.0	RNA-seq	2x76	STAR-2.5.3a	RNA-seq_MPP8-KO_rep2-GSM2509516	0.44	27,735,527	9,712,503	3,337,848	1,035,350	0.47	44,646,723
hs1-T2T-CHM13v2.0	RNA-seq	2x76	STAR-2.5.3a	RNA-seq_TASOR-KO_rep1-GSM2509517	0.40	30,844,342	11,851,296	3,509,245	1,263,755	0.48	49,732,354
hs1-T2T-CHM13v2.0	RNA-seq	2x76	STAR-2.5.3a	RNA-seq_TASOR-KO_rep2-GSM2509518	0.54	107	3	3,842	6	0.00	18,066,527
hs1-T2T-CHM13v2.0	RNA-seq	2x76	STAR-2.5.3a	RNA-seq_WT_rep1-GSM2509511	0.45	28,498,739	10,285,161	3,401,441	1,025,165	0.41	52,945,813
hs1-T2T-CHM13v2.0	RNA-seq	2x76	STAR-2.5.3a	RNA-seq_WT_rep2-GSM2509512	0.43	22,421,808	8,506,854	3,092,050	857,274	0.37	46,800,903

Read distribution

#	Exonic:	Intergenic:	Intronic:
RNA-seq_MORC2-KO_rep1-GSM2509513	0.83	0.09	0.08
RNA-seq_MORC2-KO_rep2-GSM2509514	0.88	0.07	0.06
RNA-seq_MPP8-KO_rep1-GSM2509515	0.85	0.08	0.06
RNA-seq_MPP8-KO_rep2-GSM2509516	0.83	0.10	0.07
RNA-seq_TASOR-KO_rep1-GSM2509517	0.88	0.07	0.05
RNA-seq_TASOR-KO_rep2-GSM2509518	0.81	0.19	0.00
RNA-seq_WT_rep1-GSM2509511	0.85	0.09	0.06
RNA-seq_WT_rep2-GSM2509512	0.85	0.09	0.06

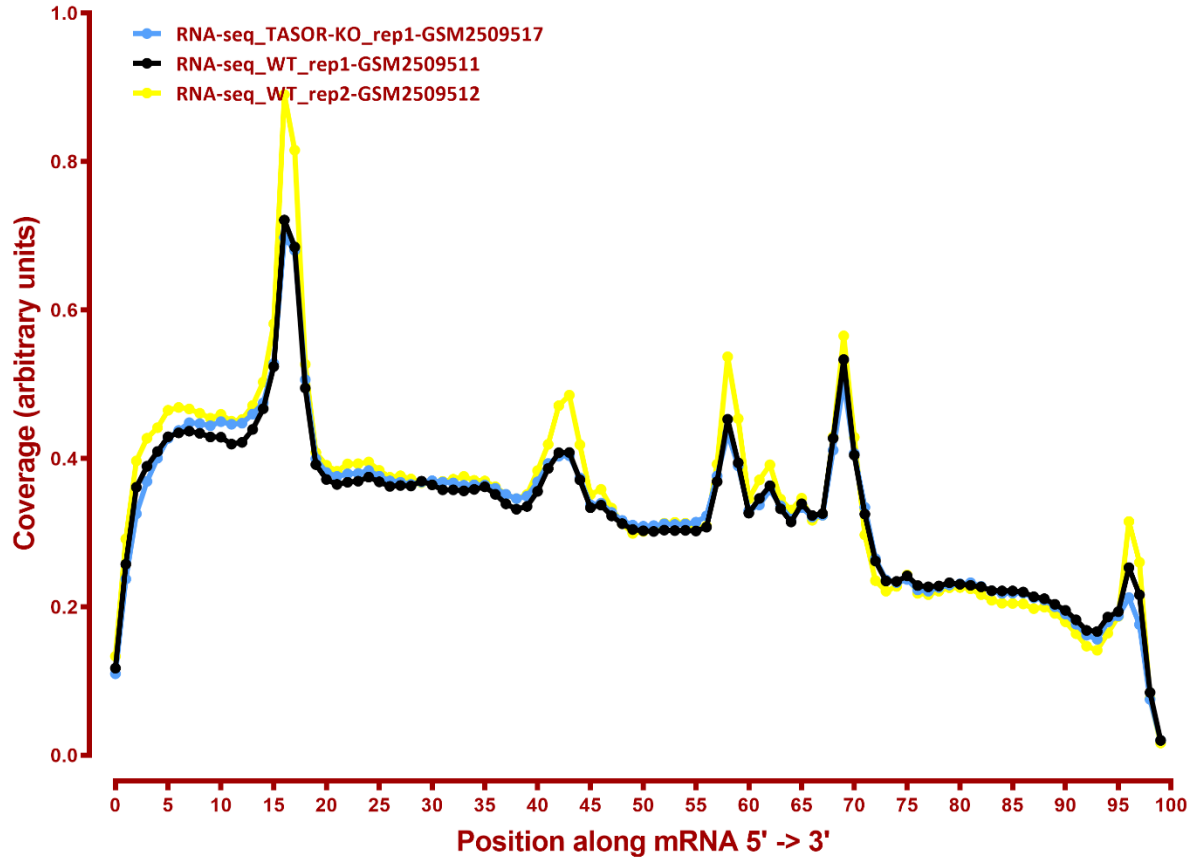
Read coverage

Coverage of genes; >1000bp



Read coverage

Coverage of genes; >1000bp



DESeq

Number differential genes

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
MPP8-KO	MORC2-KO	2	3	15	24
TASOR-KO	MORC2-KO	3	3	29	16
TASOR-KO	MPP8-KO	1	2	31	10
WT	MORC2-KO	1	2	34	33
WT	MPP8-KO	4	2	75	37
WT	TASOR-KO	1	2	24	56

Number differential genes, TASOR rep2 excluded

MPP8-KO	MORC2-KO	8	9	315	358
TASOR-KO	MORC2-KO	20	11	525	223
TASOR-KO	MPP8-KO	18	3	595	213
WT	MORC2-KO	45	18	582	356
WT	MPP8-KO	103	36	850	681
WT	TASOR-KO	24	33	450	592

GO enrichment, WT-vs-MORC2 up, p-val

None

GO enrichment, WT-vs-MORC2 down, p-val

None

GO enrichment, WT-vs-TASOR up, p-val

None

GO enrichment, WT-vs-TASOR down, p-val

None

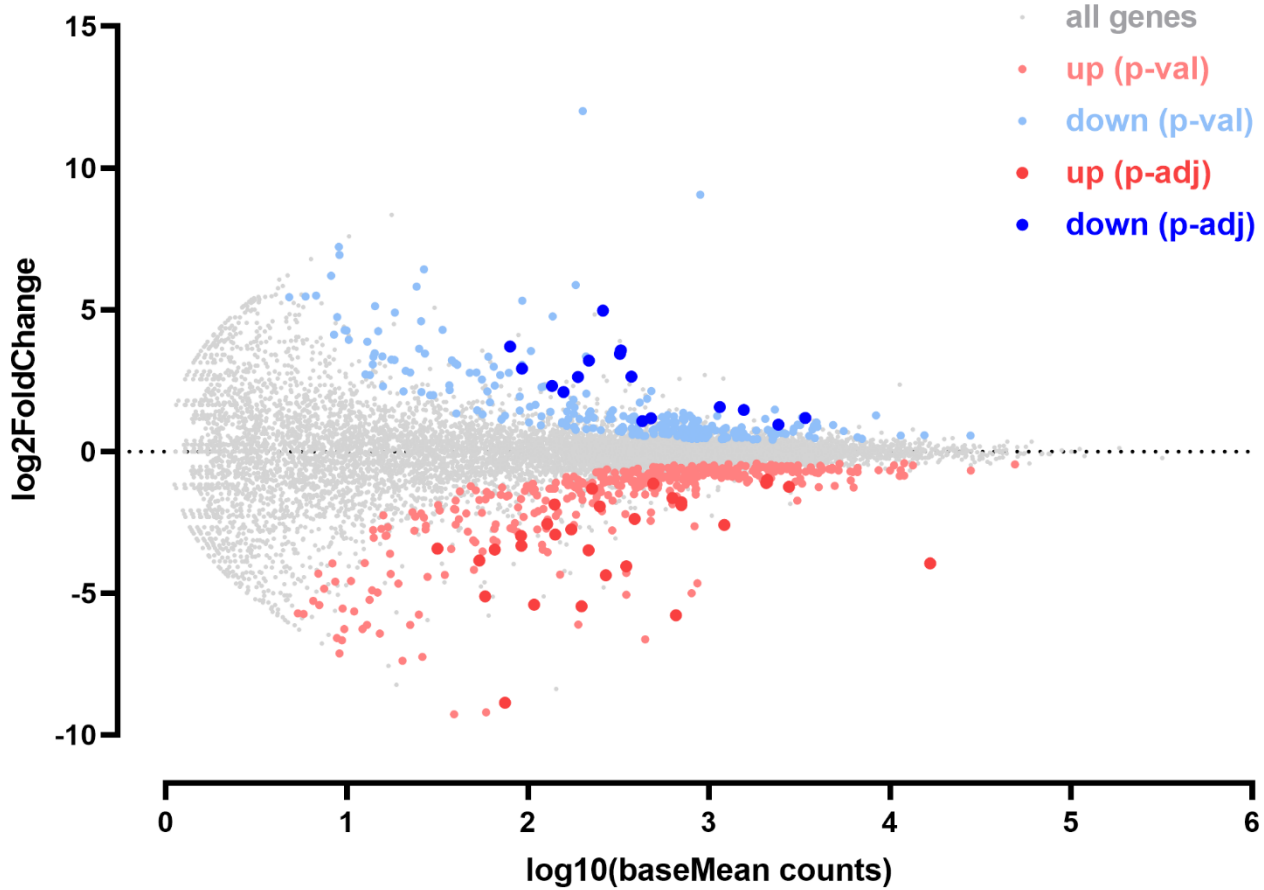
GO enrichment, WT-vs-MPP8 up, p-val

None

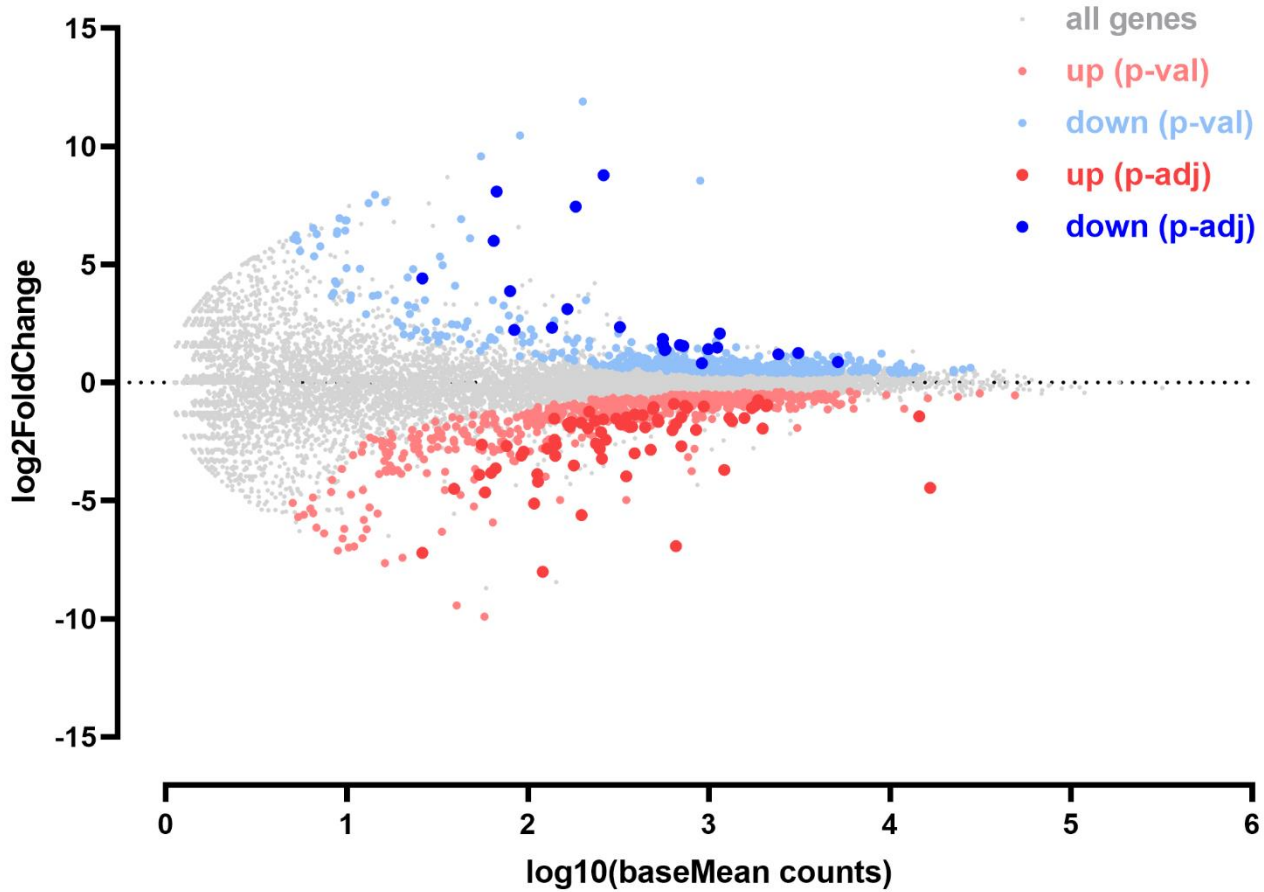
GO enrichment, WT-vs-MPP8 down, p-val

N	X	LOD	P	P_adj	attrib ID	attrib name
4	5	1.895207	8.98E-06	0.032	GO:0010385	double-stranded methylated DNA binding
14	71	0.824878	2.66E-07	0.001	GO:0048024	regulation of mRNA splicing, via spliceosome
17	103	0.730446	2.18E-07	0.001	GO:0006353	DNA-templated transcription, termination
13	81	0.7169	7.95E-06	0.024	GO:0071013	catalytic step 2 spliceosome
21	142	0.674049	6.03E-08	<0.001	GO:0005681	spliceosomal complex
32	223	0.661475	4.76E-11	<0.001	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
32	223	0.661475	4.76E-11	<0.001	GO:0000398	mRNA splicing, via spliceosome
32	229	0.647928	9.62E-11	<0.001	GO:0000375	RNA splicing, via transesterification reactions
15	107	0.647159	9.06E-06	0.032	GO:0050684	regulation of mRNA processing
15	109	0.637819	1.14E-05	0.037	GO:0043484	regulation of RNA splicing
16	127	0.593362	1.83E-05	0.05	GO:1903311	regulation of mRNA metabolic process
41	337	0.581243	2.03E-11	<0.001	GO:0008380	RNA splicing
42	402	0.505785	1.39E-09	<0.001	GO:0006397	mRNA processing
38	371	0.494629	1.47E-08	<0.001	GO:0016607	nuclear speck
50	579	0.414953	2.38E-08	<0.001	GO:0016071	mRNA metabolic process
63	763	0.397599	1.95E-09	<0.001	GO:0006396	RNA processing
109	1534	0.340392	1.76E-11	<0.001	GO:0003723	RNA binding
52	761	0.301542	1.53E-05	0.045	GO:0005730	nucleolus
66	987	0.294997	2.19E-06	0.008	GO:0044451	nucleoplasm part
164	3090	0.20673	4.27E-07	0.001	GO:0005654	nucleoplasm
214	4167	0.204323	4.27E-08	<0.001	GO:0044428	nuclear part

WT vs MORC2



WT vs MPP8



WT vs TASOR

