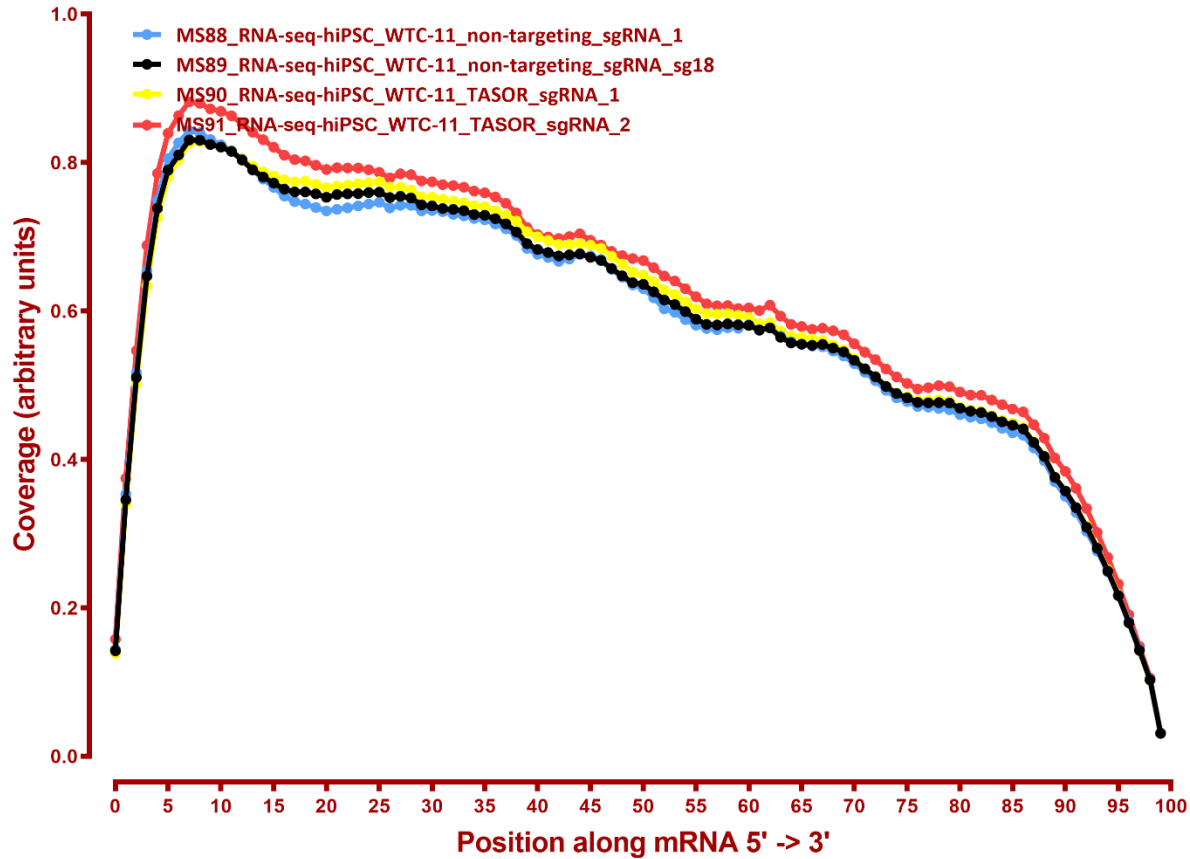


Mapping stats

Species	Assay	Read Type + Length	Mapping	#	Complexity	Unique	Unique Splices	Multi	Multi Splices	Mapped fraction	Raw fragments
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS88_RNA-seq-hiPSC_WTC-11_non-targeting_sgRNA_1	0.46	24,078,212	21,081,212	1,094,919	1,336,815	0.88	26,909,984
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS89_RNA-seq-hiPSC_WTC-11_non-targeting_sgRNA_sg18	0.48	21,665,113	19,213,917	958,441	1,210,979	0.87	24,794,011
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS90_RNA-seq-hiPSC_WTC-11_TASOR_sgRNA_1	0.45	25,071,557	22,711,151	1,201,305	1,449,081	0.88	28,497,620
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS91_RNA-seq-hiPSC_WTC-11_TASOR_sgRNA_2	0.49	21,660,524	19,688,040	1,106,584	1,230,102	0.85	25,783,955
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS92_RNA-seq-hiPSC_WTC-11_TASOR2_sgRNA_1	0.43	31,438,510	28,709,294	1,381,886	1,863,368	0.89	35,733,758
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS93_RNA-seq-hiPSC_WTC-11_TASOR2_sgRNA_2	0.46	21,407,720	19,144,524	908,782	1,217,002	0.90	23,773,802
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS94_RNA-seq-hiPSC_WTC-11_MPP8_sgRNA_1	0.49	21,164,211	18,279,819	1,053,868	1,143,424	0.85	24,364,224
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS95_RNA-seq-hiPSC_WTC-11_MPP8_sgRNA_2	0.47	22,607,211	19,759,883	1,076,832	1,252,398	0.89	25,248,124

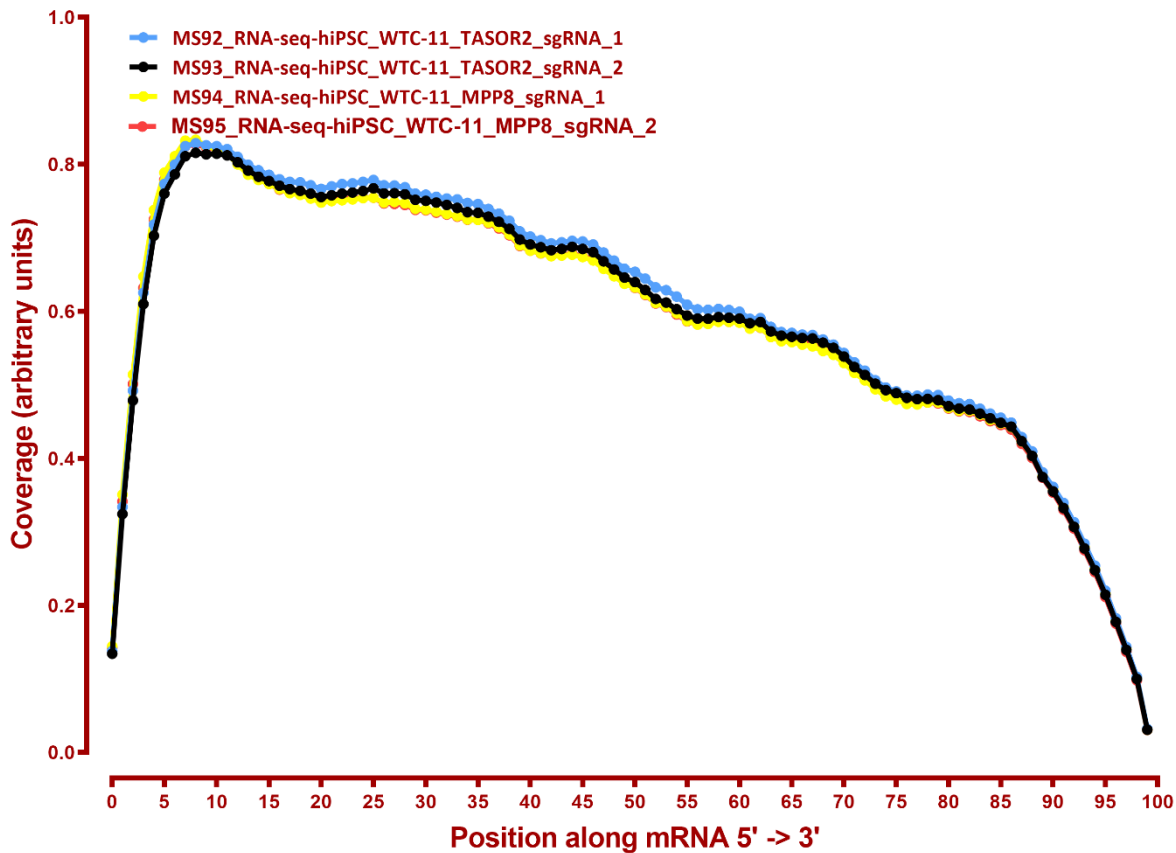
Read distribution

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	TASOR2	5	123	177	422
MPP8	TASOR	2	4	162	220
NTC	MPP8	146	131	1,004	1,349
NTC	TASOR2	10	26	859	1,421
NTC	TASOR	117	147	1,170	1,484
TASOR2	TASOR	91	8	382	186

GO enrichment, NTC-vs-MPP8 down, p-adj

None

GO enrichment, NTC-vs-MPP8 up, p-adj

None

GO enrichment, NTC-vs-TASOR down, p-adj

None

GO enrichment, NTC-vs-TASOR up, p-adj

None

GO enrichment, NTC-vs-TASOR2 down, p-adj

None

GO enrichment, NTC-vs-TASOR2 up, p-adj

None