

# Mapping stats

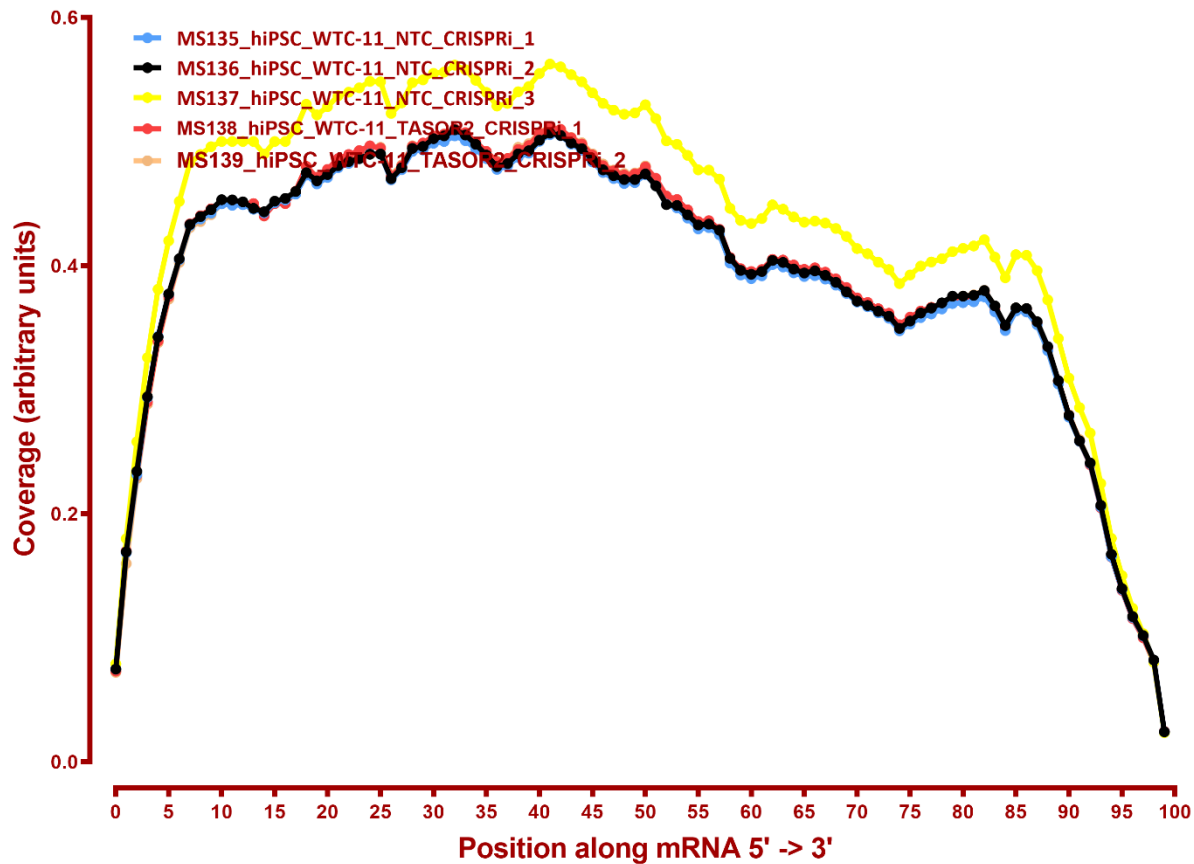
Species	Assay	Read Type + Length	Mapping	#	Complexity	Unique	Unique Splices	Multi	Multi Splices	Mapped fraction	Raw fragments
hg38	RNA-seq	2x150	STAR-2.5.3a	MS135_hiPSC_WTC-11_NTC_CRISPRi_1	0.43	32,371,739	14,439,829	1,873,592	1,046,116	0.91	27,367,066
hg38	RNA-seq	2x150	STAR-2.5.3a	MS136_hiPSC_WTC-11_NTC_CRISPRi_2	0.44	30,861,165	13,928,303	1,717,738	1,133,790	0.91	26,192,271
hg38	RNA-seq	2x150	STAR-2.5.3a	MS137_hiPSC_WTC-11_NTC_CRISPRi_3	0.41	31,602,939	16,542,191	1,854,349	1,317,537	0.91	28,278,981
hg38	RNA-seq	2x150	STAR-2.5.3a	MS138_hiPSC_WTC-11_TASOR2_CRISPRi_1	0.41	34,658,843	15,477,683	1,874,879	1,111,629	0.93	28,704,426
hg38	RNA-seq	2x150	STAR-2.5.3a	MS139_hiPSC_WTC-11_TASOR2_CRISPRi_2	0.41	36,622,201	16,405,023	2,048,559	1,179,431	0.93	30,403,435
hg38	RNA-seq	2x150	STAR-2.5.3a	MS140_hiPSC_WTC-11_TASOR2_CRISPRi_3	0.41	33,907,933	17,108,201	1,996,096	1,354,406	0.91	29,760,415
hg38	RNA-seq	2x150	STAR-2.5.3a	MS141_hiPSC_WTC-11_TASOR_CRISPRi_1	0.42	35,857,339	16,340,217	2,212,003	1,325,435	0.92	30,440,547
hg38	RNA-seq	2x150	STAR-2.5.3a	MS142_hiPSC_WTC-11_TASOR_CRISPRi_2	0.44	32,478,821	14,005,607	1,897,840	1,025,958	0.92	26,829,182
hg38	RNA-seq	2x150	STAR-2.5.3a	MS143_hiPSC_WTC-11_MPP8_CRISPRi_1	0.44	32,980,140	14,480,972	1,980,339	1,029,753	0.91	27,597,766
hg38	RNA-seq	2x150	STAR-2.5.3a	MS144_hiPSC_WTC-11_MPP8_CRISPRi_2	0.41	34,030,492	16,371,054	1,999,094	1,269,202	0.92	29,211,835
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS135_hiPSC_WTC-11_NTC_CRISPRi_1	0.43	32,569,692	14,418,710	1,197,075	872,143	0.90	27,367,066
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS136_hiPSC_WTC-11_NTC_CRISPRi_2	0.43	31,126,311	13,914,753	1,133,424	820,076	0.90	26,192,271
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS137_hiPSC_WTC-11_NTC_CRISPRi_3	0.41	31,853,926	16,517,442	1,216,721	973,743	0.89	28,278,981
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS138_hiPSC_WTC-11_TASOR2_CRISPRi_1	0.41	34,861,379	15,472,217	1,217,815	922,151	0.91	28,704,426
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS139_hiPSC_WTC-11_TASOR2_CRISPRi_2	0.41	36,819,214	16,392,228	1,322,654	972,242	0.91	30,403,435
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS140_hiPSC_WTC-11_TASOR2_CRISPRi_3	0.41	34,146,322	17,084,064	1,272,302	989,354	0.90	29,760,415
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS141_hiPSC_WTC-11_TASOR_CRISPRi_1	0.42	36,086,995	16,319,377	1,427,084	976,520	0.90	30,440,547
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS142_hiPSC_WTC-11_TASOR_CRISPRi_2	0.44	32,627,757	13,982,945	1,223,546	833,276	0.91	26,829,182
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS143_hiPSC_WTC-11_MPP8_CRISPRi_1	0.44	33,133,023	14,460,609	1,268,411	840,869	0.90	27,597,766
hs1-T2T-CHM13v2.0	RNA-seq	2x150	STAR-2.5.3a	MS144_hiPSC_WTC-11_MPP8_CRISPRi_2	0.41	34,272,891	16,348,879	1,328,018	937,696	0.91	29,211,835

## Read distribution

#	Exonic:	Intergenic:	Intronic:
MS135_hiPSC_WTC-11_NTC_CRISPRi_1	0.72	0.10	0.18
MS136_hiPSC_WTC-11_NTC_CRISPRi_2	0.72	0.10	0.18
MS137_hiPSC_WTC-11_NTC_CRISPRi_3	0.78	0.08	0.14
MS138_hiPSC_WTC-11_TASOR2_CRISPRi_1	0.72	0.10	0.18
MS139_hiPSC_WTC-11_TASOR2_CRISPRi_2	0.72	0.10	0.18
MS140_hiPSC_WTC-11_TASOR2_CRISPRi_3	0.77	0.08	0.15
MS141_hiPSC_WTC-11_TASOR_CRISPRi_1	0.73	0.10	0.18
MS142_hiPSC_WTC-11_TASOR_CRISPRi_2	0.71	0.10	0.19
MS143_hiPSC_WTC-11_MPP8_CRISPRi_1	0.71	0.10	0.19
MS144_hiPSC_WTC-11_MPP8_CRISPRi_2	0.75	0.09	0.16

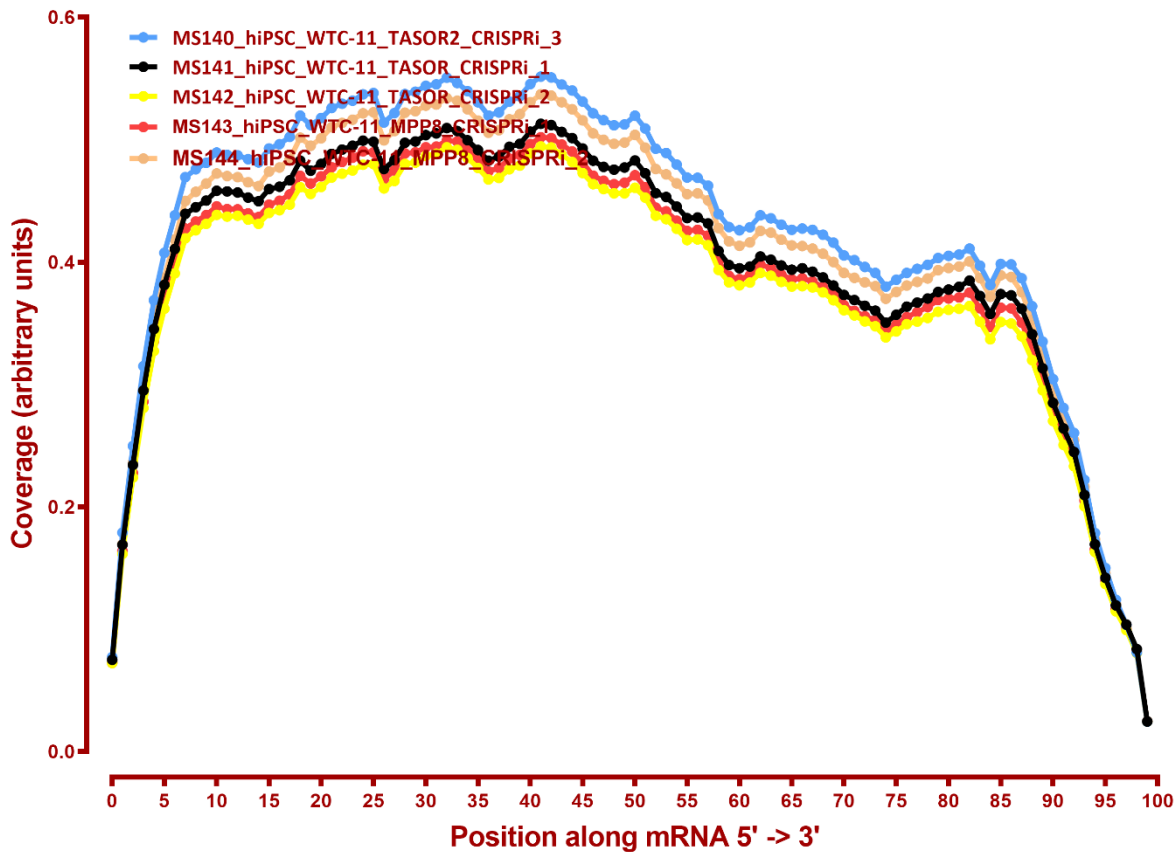
# Read coverage

## Coverage of genes; >1000bp



# Read coverage

## Coverage of genes; >1000bp



# RSEM refSeq T2T

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	NTC	399	696	1,305	1,627
MPP8	TASOR2	333	574	1,177	1,409
MPP8	TASOR	10	26	373	498
NTC	TASOR2	59	8	395	191
NTC	TASOR	254	79	821	658
TASOR2	TASOR	238	90	792	749

# RSEM refSeq hg38

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	NTC	482	706	1,338	1,569
MPP8	TASOR2	406	577	1,182	1,363
MPP8	TASOR	13	21	385	475
NTC	TASOR2	59	7	392	180
NTC	TASOR	209	76	784	625
TASOR2	TASOR	199	99	721	718

# eXpress refSeq T2T

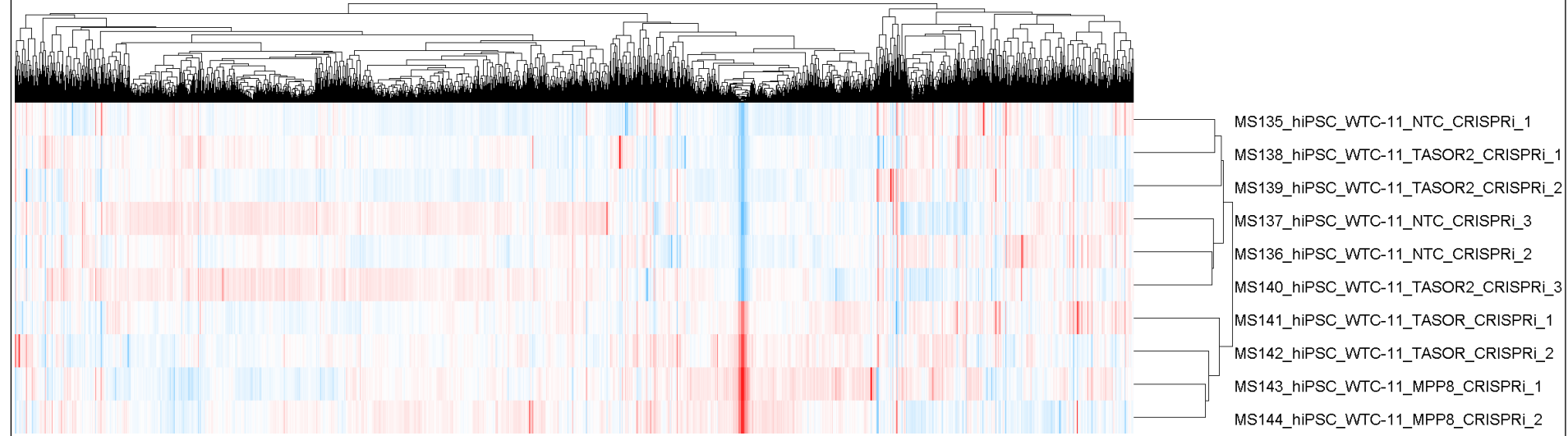
Number differential genes

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	NTC	192	326	1,074	1,192
MPP8	TASOR2	155	285	988	1,079
MPP8	TASOR	6	7	481	551
NTC	TASOR2	22	6	500	346
NTC	TASOR	148	48	779	645
TASOR2	TASOR	149	48	713	723

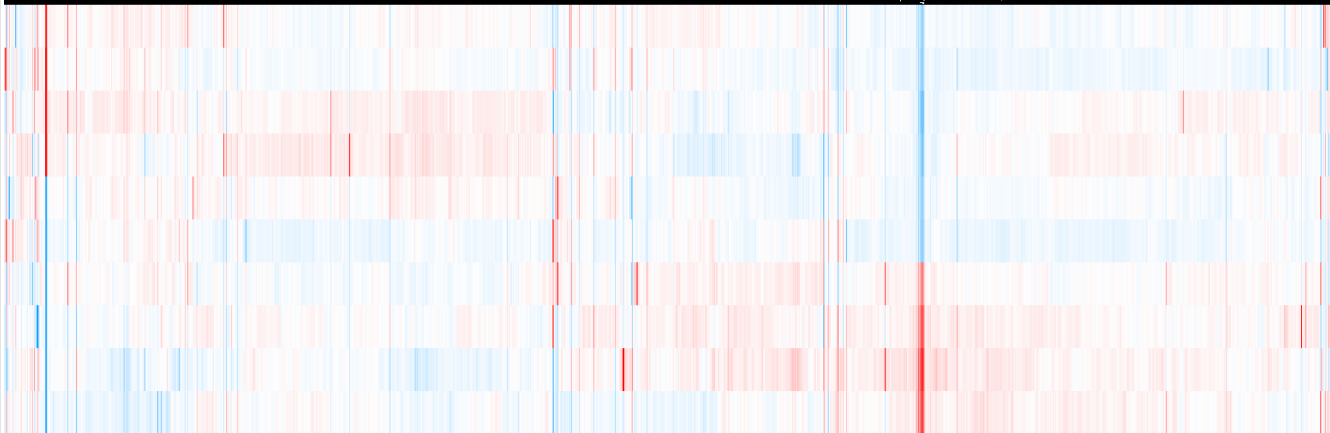
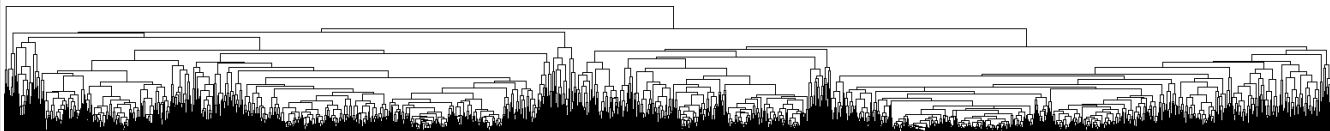
Number differential genes

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	NTC	130	253	803	1,016
MPP8	TASOR2	93	194	735	901
MPP8	TASOR	6	5	340	352
NTC	TASOR2	18	5	312	208
NTC	TASOR	109	26	523	385
TASOR2	TASOR	102	24	521	419

# RSEM refSeq T2T

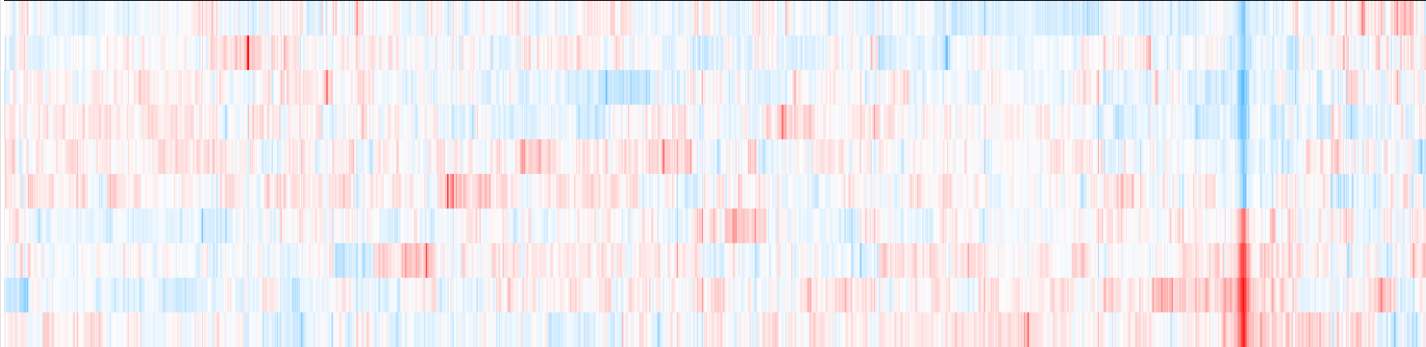
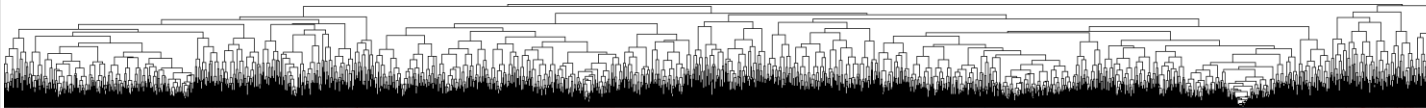


# RSEM refSeq hg38



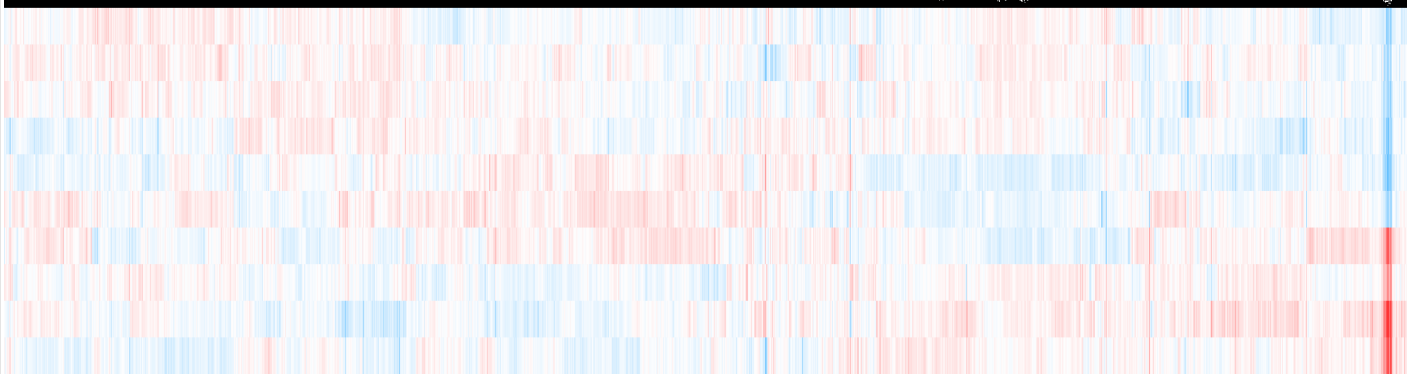
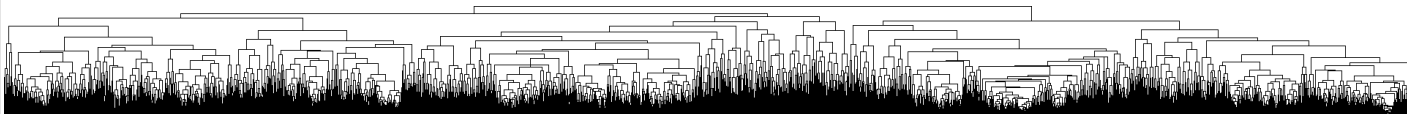
- MS136\_hiPSC\_WTC-11\_NTC\_CRISPRi\_2
- MS135\_hiPSC\_WTC-11\_NTC\_CRISPRi\_1
- MS137\_hiPSC\_WTC-11\_NTC\_CRISPRi\_3
- MS140\_hiPSC\_WTC-11\_TASOR2\_CRISPRi\_3
- MS138\_hiPSC\_WTC-11\_TASOR2\_CRISPRi\_1
- MS139\_hiPSC\_WTC-11\_TASOR2\_CRISPRi\_2
- MS141\_hiPSC\_WTC-11\_TASOR\_CRISPRi\_1
- MS142\_hiPSC\_WTC-11\_TASOR\_CRISPRi\_2
- MS143\_hiPSC\_WTC-11\_MPP8\_CRISPRi\_1
- MS144\_hiPSC\_WTC-11\_MPP8\_CRISPRi\_2

# eXpress refSeq T2T



- MS135\_hiPSC\_WTC-11\_NTC\_CRISPRi\_1
- MS136\_hiPSC\_WTC-11\_NTC\_CRISPRi\_2
- MS137\_hiPSC\_WTC-11\_NTC\_CRISPRi\_3
- MS140\_hiPSC\_WTC-11\_TASOR2\_CRISPRi\_3
- MS138\_hiPSC\_WTC-11\_TASOR2\_CRISPRi\_1
- MS139\_hiPSC\_WTC-11\_TASOR2\_CRISPRi\_2
- MS141\_hiPSC\_WTC-11\_TASOR\_CRISPRi\_1
- MS142\_hiPSC\_WTC-11\_TASOR\_CRISPRi\_2
- MS143\_hiPSC\_WTC-11\_MPP8\_CRISPRi\_1
- MS144\_hiPSC\_WTC-11\_MPP8\_CRISPRi\_2

# eXpress refSeq hg38



- MS135\_hiPSC\_WTC-11\_NTC\_CRISPRi\_1
- MS136\_hiPSC\_WTC-11\_NTC\_CRISPRi\_2
- MS138\_hiPSC\_WTC-11\_TASOR2\_CRISPRi\_1
- MS140\_hiPSC\_WTC-11\_TASOR2\_CRISPRi\_3
- MS137\_hiPSC\_WTC-11\_NTC\_CRISPRi\_3
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- MS143\_hiPSC\_WTC-11\_MPP8\_CRISPRi\_1
- MS144\_hiPSC\_WTC-11\_MPP8\_CRISPRi\_2