

Read mapping stats

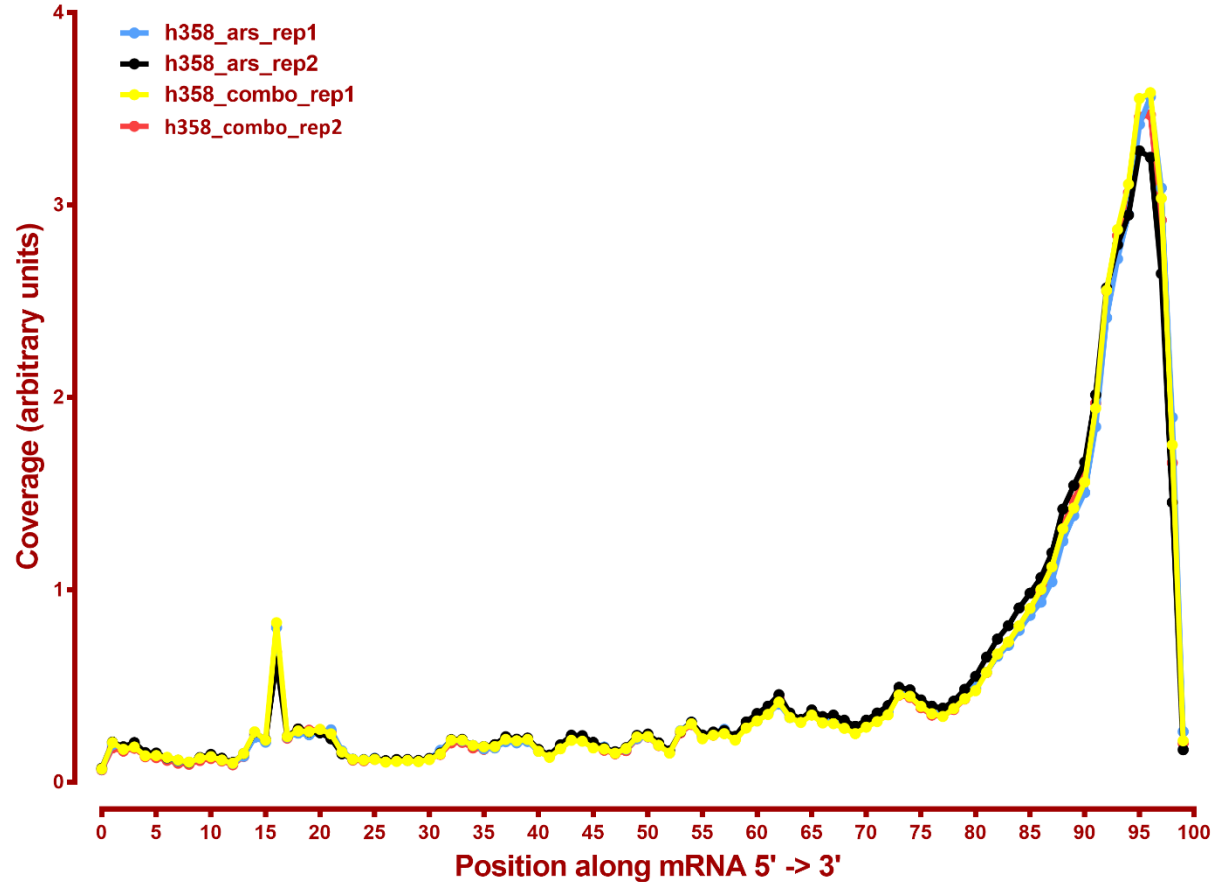
Species	Read Length	Mapping	Library	Raw reads	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped	
hg38	1x50	STAR-2.5.3a	GENCODE25	h358_ars_rep1	11,391,695	0.31	8,311,668	590,788	2,119,361	198,534	0.49
hg38	1x50	STAR-2.5.3a	GENCODE25	h358_ars_rep2	15,897,214	0.27	11,335,611	918,185	3,113,466	307,945	0.49
hg38	1x50	STAR-2.5.3a	GENCODE25	h358_combo_rep1	21,810,762	0.22	15,685,059	1,220,272	4,184,335	437,278	0.49
hg38	1x50	STAR-2.5.3a	GENCODE25	h358_combo_rep2	14,194,775	0.28	10,340,059	742,140	2,671,465	254,459	0.49
hg38	1x50	STAR-2.5.3a	GENCODE25	h358_dmso_rep1	20,049,741	0.25	14,478,866	1,083,740	3,839,586	379,725	0.49
hg38	1x50	STAR-2.5.3a	GENCODE25	h358_dmso_rep2	15,275,833	0.28	11,076,823	840,670	2,866,762	301,569	0.49
hg38	1x50	STAR-2.5.3a	GENCODE25	h358_palbo_rep1	16,992,183	0.24	12,272,643	908,184	3,278,272	316,193	0.49
hg38	1x50	STAR-2.5.3a	GENCODE25	h358_palbo_rep2	14,383,624	0.27	10,353,779	816,546	2,754,187	277,726	0.49

#	Exonic:	Intergenic:	Intronic:
h358_ars_rep1	0.90	0.05	0.05
h358_ars_rep2	0.92	0.04	0.04
h358_combo_rep1	0.91	0.04	0.05
h358_combo_rep2	0.91	0.04	0.05
h358_dmso_rep1	0.90	0.05	0.06
h358_dmso_rep2	0.91	0.04	0.04
h358_palbo_rep1	0.91	0.04	0.05
h358_palbo_rep2	0.92	0.04	0.04

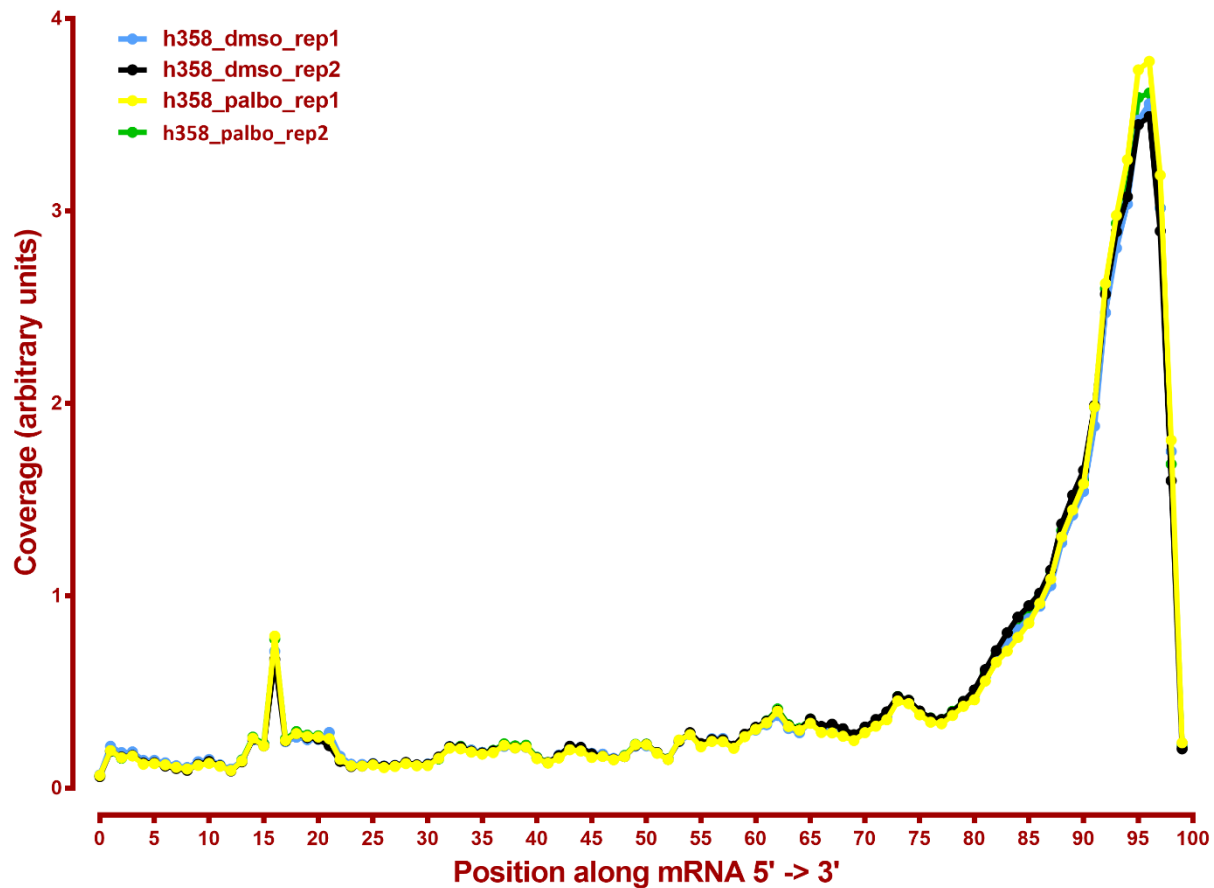
From the methods section on GEO:

“RNA-seq libraries were prepared with the QuantSeq 3’ mRNA-Seq Library Prep Kit FWD for Illumina (Lexogen) and assessed on a BioAnalyzer 2100 (Agilent) for quantification and quality control.”

Coverage of genes; >1000bp



Coverage of genes; >1000bp



Number DE genes, DESeq2, eXpress

all genes

A	B	p-val		p-adj	
		up in B vs A	down in B vs A	up in B vs A	down in B vs A
h358_combo	h358_ars	520	372	42	8
h358_dmso	h358_ars	1,125	1,517	350	651
h358_dmso	h358_combo	1,244	1,703	480	923
h358_dmso	h358_palbo	498	872	39	308
h358_palbo	h358_ars	1,336	1,434	506	592
h358_palbo	h358_combo	969	1,195	225	445