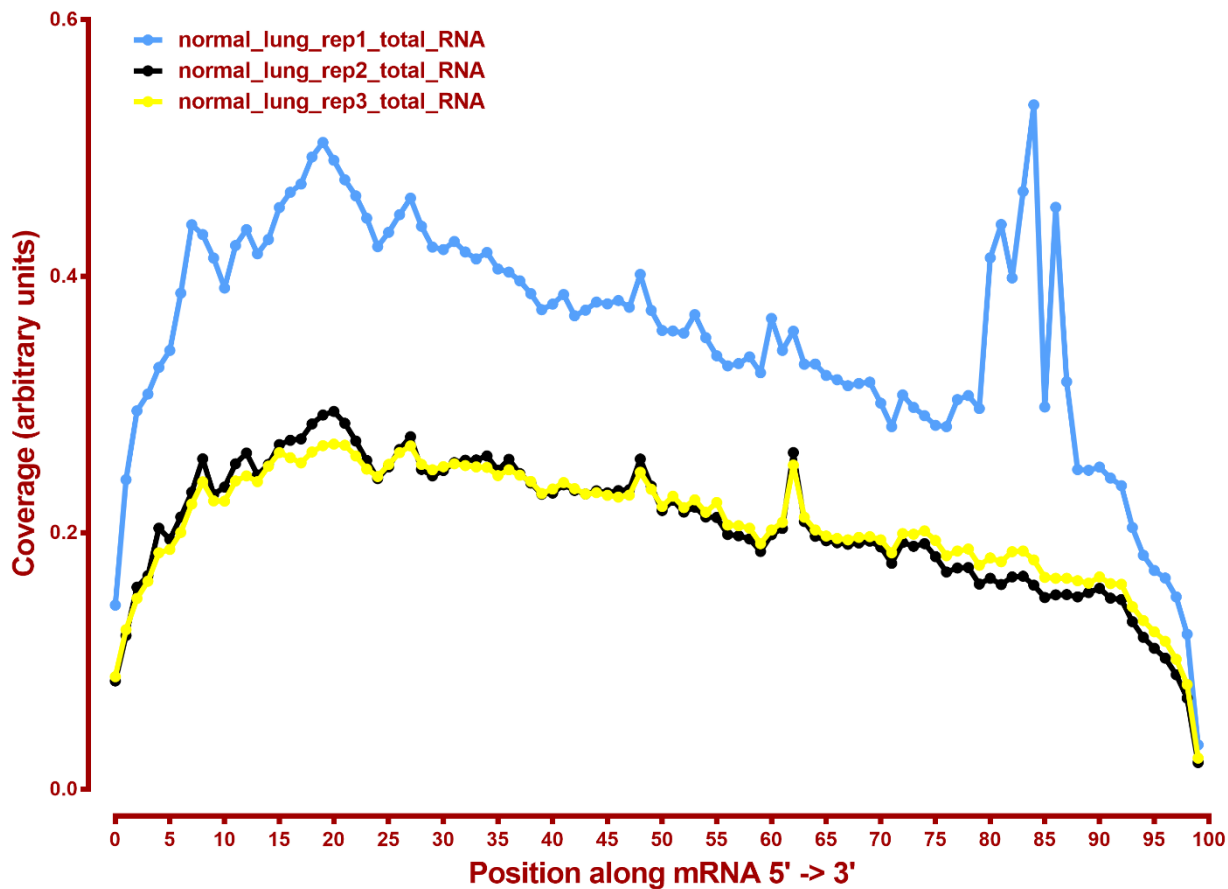


Read mapping stats

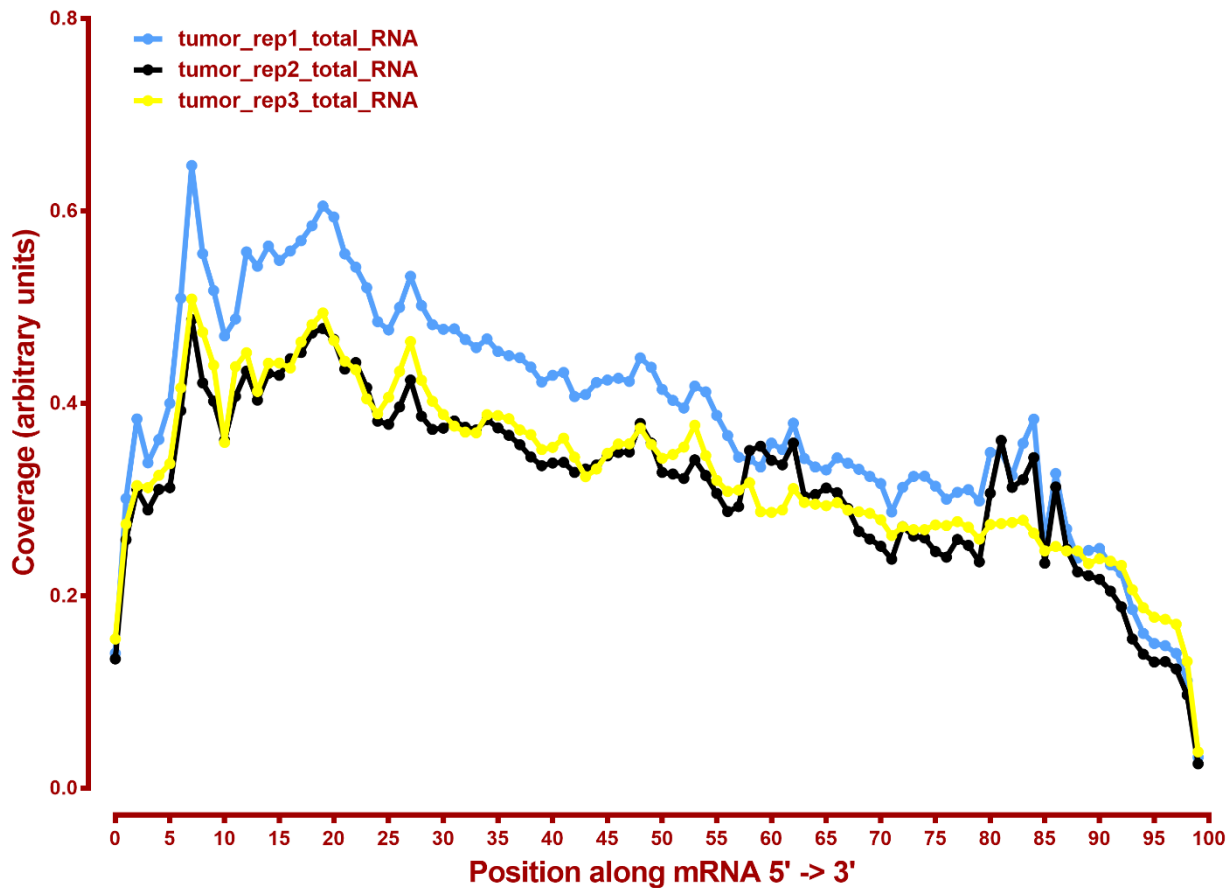
Species	Read Length	Mapping	Library	Raw reads	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
mm10	2x50	STAR-2.5.3 GENCODEv4	normal_lung_rep1_total_RNA	171,553,662	0.39	201,539,293	20,675,233	55,200,098	5,693,986	0.83
mm10	2x50	STAR-2.5.3 GENCODEv4	normal_lung_rep2_total_RNA	171,393,687	0.52	216,013,642	12,771,338	30,304,806	2,442,980	0.76
mm10	2x50	STAR-2.5.3 GENCODEv4	normal_lung_rep3_total_RNA	180,671,287	0.46	236,600,064	13,784,236	33,333,604	2,872,718	0.79
mm10	2x50	STAR-2.5.3 GENCODEv4	tumor_rep1_total_RNA	165,569,498	0.38	197,335,840	22,305,060	48,771,844	5,410,268	0.83
mm10	2x50	STAR-2.5.3 GENCODEv4	tumor_rep2_total_RNA	149,208,283	0.40	170,815,796	15,195,114	33,476,161	3,293,747	0.75
mm10	2x50	STAR-2.5.3 GENCODEv4	tumor_rep3_total_RNA	164,380,205	0.41	197,226,532	17,185,620	44,762,745	4,872,901	0.80

#	Exonic:	Intergenic:	Intronic:
normal_lung_rep1_total_RNA	0.58	0.12	0.29
normal_lung_rep2_total_RNA	0.38	0.15	0.46
normal_lung_rep3_total_RNA	0.40	0.17	0.43
tumor_rep1_total_RNA	0.60	0.12	0.28
tumor_rep2_total_RNA	0.55	0.13	0.33
tumor_rep3_total_RNA	0.54	0.18	0.28

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
normal_lung	tumor	913	1,107	106	223