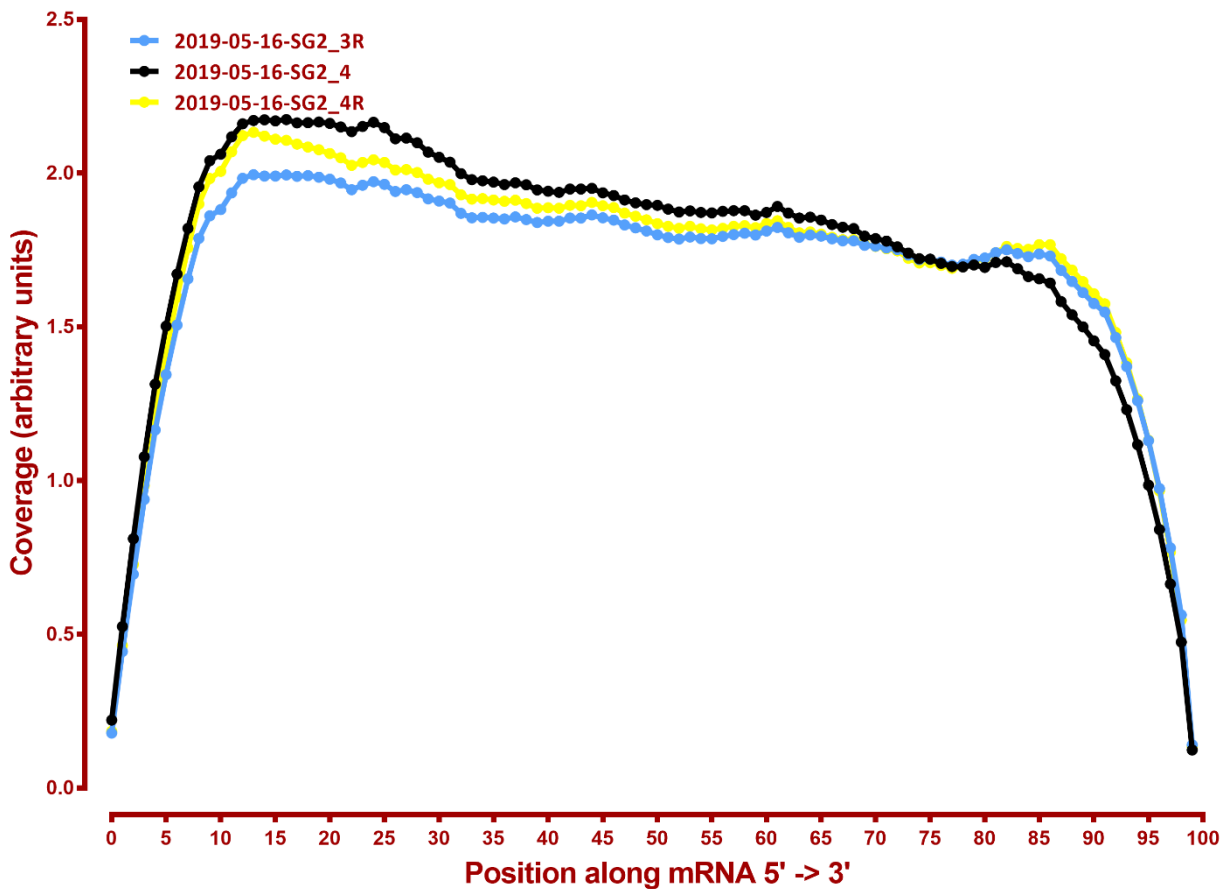


MAPPING STATS

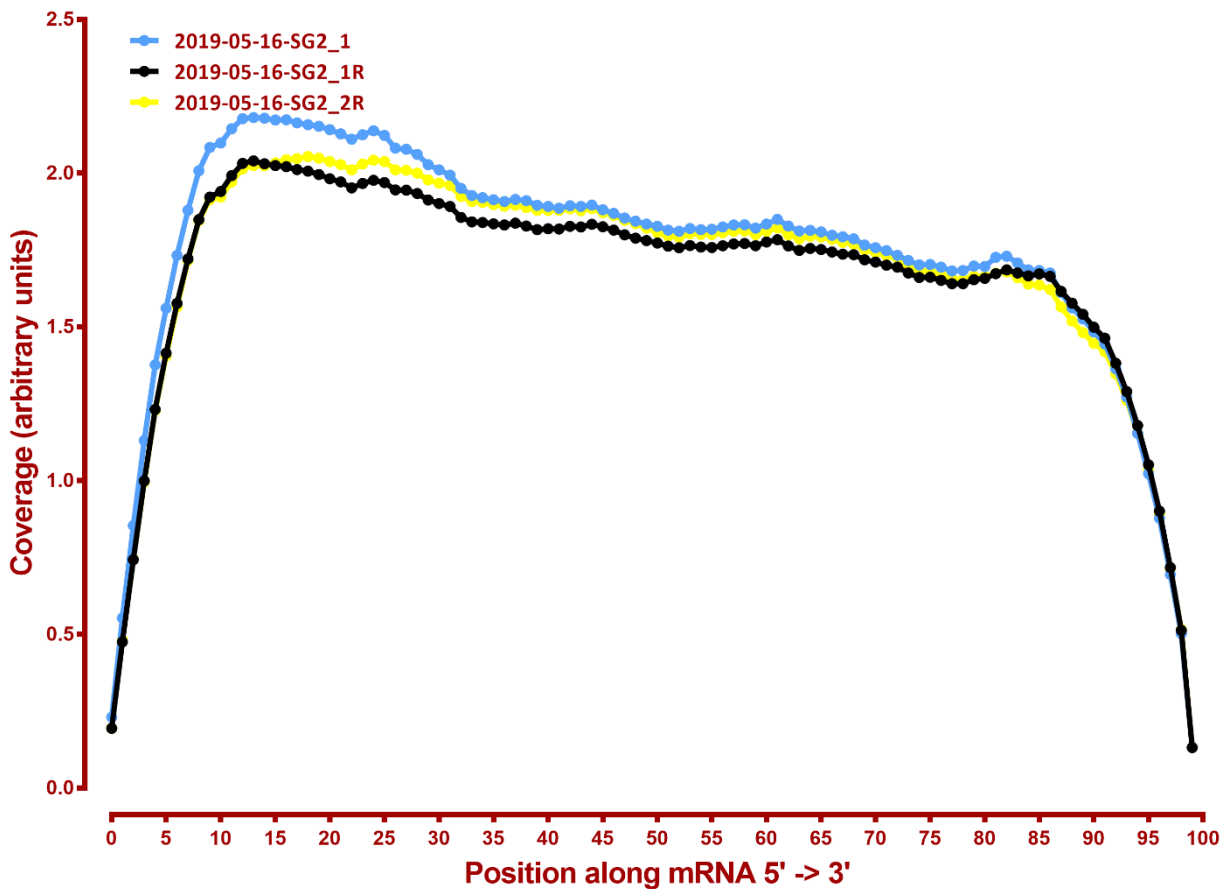
Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
2019-05-16-SG2_1	2x150	STAR-2.5.3a	hg38	50,777,738	0.27	51,192,843	42,319,409	2,574,408	3,426,282	0.98
2019-05-16-SG2_1R	2x150	STAR-2.5.3a	hg38	25,126,115	0.36	26,673,024	19,821,714	1,099,135	1,393,949	0.97
2019-05-16-SG2_2R	2x150	STAR-2.5.3a	hg38	48,472,733	0.25	50,551,498	38,918,858	2,209,399	2,923,625	0.98
2019-05-16-SG2_3R	2x150	STAR-2.5.3a	hg38	48,589,117	0.28	51,447,847	38,507,267	2,151,768	2,894,736	0.98
2019-05-16-SG2_4	2x150	STAR-2.5.3a	hg38	51,428,399	0.27	51,372,568	43,186,766	2,360,903	3,450,769	0.98
2019-05-16-SG2_4R	2x150	STAR-2.5.3a	hg38	54,104,393	0.24	55,005,619	44,870,483	2,514,213	3,435,227	0.98

#	Exonic:	Intergenic:	Intronic:
2019-05-16-SG2_1	0.93	0.01	0.06
2019-05-16-SG2_1R	0.92	0.01	0.06
2019-05-16-SG2_2R	0.93	0.01	0.06
2019-05-16-SG2_3R	0.93	0.01	0.06
2019-05-16-SG2_4	0.94	0.01	0.05
2019-05-16-SG2_4R	0.95	0.01	0.04

Coverage of genes; >1000bp



Coverage of genes; >1000bp

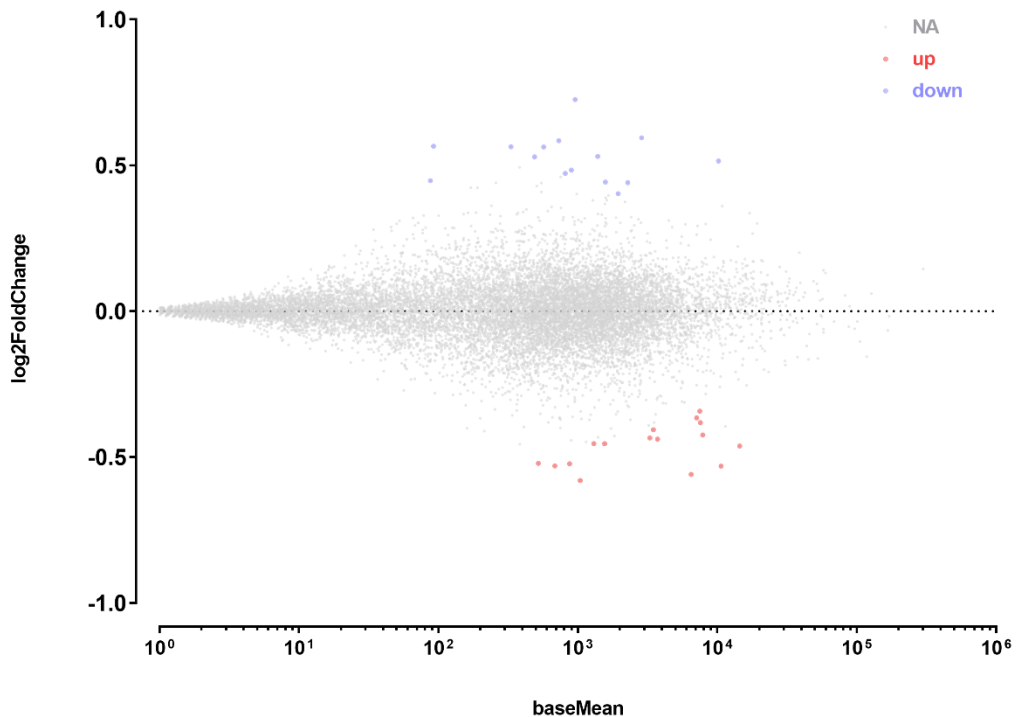


DESEQ SUMMARY

all 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
SG2_1	SG2_4	17	16	240	241

SG2_1 vs SG2_4



UP GENES

#	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ARL6IP1	10670.23332	-0.530646894	0.09257	-5.73238	9.90E-09	6.84E-05
AURKA	7877.482235	-0.424244719	0.087476	-4.84983	1.24E-06	0.002133
CDC25B	7505.1234	-0.342753354	0.088064	-3.89211	9.94E-05	0.044533
CDCA8	3729.195096	-0.437954713	0.095244	-4.59822	4.26E-06	0.005349
DEPDC1	3482.559018	-0.406016689	0.096432	-4.21038	2.55E-05	0.01989
EHF	1301.599627	-0.453793516	0.11303	-4.01479	5.95E-05	0.031596
FAM72B	874.5849134	-0.522606441	0.118365	-4.41521	1.01E-05	0.010659
FAM72D	520.9996032	-0.521169614	0.128123	-4.06774	4.75E-05	0.02731
FAM83D	6506.332365	-0.55916127	0.102415	-5.45978	4.77E-08	0.000132
HYLS1	684.2142564	-0.530089264	0.127528	-4.15666	3.23E-05	0.022294
INCENP	3290.281174	-0.433884573	0.104994	-4.13248	3.59E-05	0.023595
KIF18A	1558.708447	-0.453472381	0.107802	-4.20654	2.59E-05	1.99E-02
KPNA2	14507.47253	-0.461621397	0.098836	-4.67058	3.00E-06	0.004147
PLK1	7580.24696	-0.381311576	0.09128	-4.17739	2.95E-05	0.021428
TNFAIP8L1	1040.553847	-0.579741228	0.115166	-5.03398	4.80E-07	0.000948
UBE2S	7131.874631	-0.365391022	0.092838	-3.93579	8.29E-05	0.040891

UP GENES, GO ENRICHMENT

N	X	LOD	P	P_adj	attrib ID	attrib name
3	46	2.034492	8.24E-06	0.014	GO:0051310	metaphase plate congression
3	60	1.912979	1.84E-05	0.024	GO:0051303	establishment of chromosome localization
3	62	1.898082	2.03E-05	0.033	GO:0050000	chromosome localization
4	116	1.762745	2.67E-06	0.004	GO:0007062	sister chromatid cohesion
4	119	1.751243	2.96E-06	0.005	GO:0000922	spindle pole
4	131	1.708027	4.34E-06	0.008	GO:1903046	meiotic cell cycle process
4	143	1.668674	6.15E-06	0.01	GO:0030496	midbody
7	601	1.369056	3.62E-07	<0.001	GO:1903047	mitotic cell cycle process
5	396	1.33778	1.69E-05	0.024	GO:0051301	cell division
7	966	1.152069	8.63E-06	0.014	GO:0022402	cell cycle process
8	1403	1.080928	8.88E-06	0.014	GO:0044430	cytoskeletal part

DOWN GENES

#	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
BBS5	814.7579418	0.472978277	0.120148	3.936621	8.26E-05	4.09E-02
BLOC1S5- TXNDC5	92.34078793	0.56584155	0.102227	5.535132	3.11E-08	0.000123
CCNE2	332.1070888	0.563513455	0.129493	4.351686	1.35E-05	0.012435
CDCA7	731.5830586	0.584832591	0.1233	4.743156	2.10E-06	0.003228
FAM111B	569.8101441	0.56315923	0.127981	4.400348	1.08E-05	0.010659
MCM3	1947.317109	0.403498533	0.103711	3.890621	1.00E-04	0.044533
MCM6	2289.011529	0.441274634	0.10191	4.330027	1.49E-05	0.012866
MSH6	1389.937637	0.530976016	0.116332	4.564322	5.01E-06	0.005766
NEAT1	10202.45143	0.514934012	0.101617	5.06742	4.03E-07	0.000928
RSRP1	490.5024905	0.529459797	0.128894	4.107709	4.00E-05	0.025079
SLBP	1579.713343	0.44267597	0.113538	3.898933	9.66E-05	0.044533
SNHG19	957.3174482	0.72582046	0.121908	5.953844	2.62E-09	3.62E-05
TSIX	2870.010355	0.594949245	0.107966	5.510549	3.58E-08	0.000123
UNG	900.6557601	0.484285764	0.120294	4.025861	5.68E-05	0.031351
ZNF674-AS1	87.73523446	0.447716423	0.109993	4.070396	4.69E-05	0.02731

DOWN GENES, GO ENRICHMENT

N	X	LOD	P	P_adj	attrib ID	attrib name
2	8	2.714967	1.76E-05	0.03	GO:0016446	somatic hypermutation of immunoglobulin genes
2	8	2.714967	1.76E-05	0.03	GO:0042555	MCM complex
2	9	2.652795	2.27E-05	0.039	GO:0002566	somatic diversification of immune receptors via somatic mutation
3	29	2.283709	1.63E-06	0.002	GO:0006270	DNA replication initiation
6	726	1.220457	1.44E-05	0.025	GO:0006259	DNA metabolic process