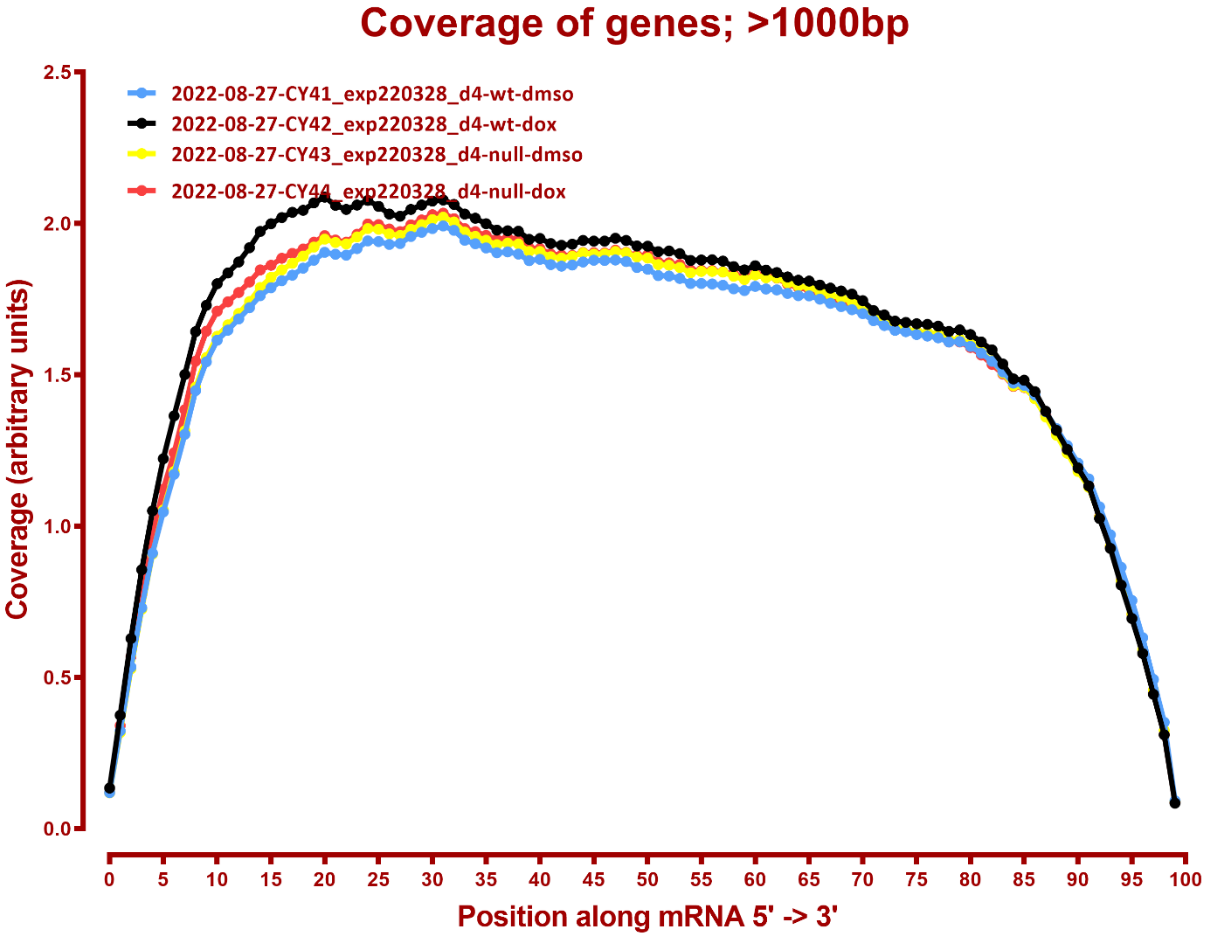
MAPPING STATS

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
2022-08-27-CY41_exp220328_d4-wt-dmso	**2x150**	STAR-2.5.3a	**hg38**	41,007,584	0.33	42,369,273	33,123,385	1,901,013	2,160,759	0.97
2022-08-27-CY42_exp220328_d4-wt-dox	**2x150**	STAR-2.5.3a	**hg38**	38,107,608	0.34	38,307,588	30,756,200	1,783,094	2,005,764	0.96
2022-08-27-CY43_exp220328_d4-null-dmso	**2x150**	STAR-2.5.3a	**hg38**	37,301,730	0.31	38,225,339	30,458,253	1,890,745	1,959,141	0.97
2022-08-27-CY44_exp220328_d4-null-dox	**2x150**	STAR-2.5.3a	**hg38**	32,391,667	0.28	33,094,375	26,811,023	1,498,405	1,687,257	0.97
2022-08-27-CY51_exp220328_d5-wt-dmso	**2x150**	STAR-2.5.3a	**hg38**	36,499,854	0.36	36,656,602	30,218,786	1,866,178	1,973,658	0.97
2022-08-27-CY52_exp220328_d5-wt-dox	**2x150**	STAR-2.5.3a	**hg38**	30,457,589	0.31	30,128,677	23,772,041	2,575,067	1,486,425	0.95
2022-08-27-CY53_exp220328_d5-null-dmso	**2x150**	STAR-2.5.3a	**hg38**	35,423,316	0.23	35,960,572	28,033,576	3,079,744	1,738,716	0.97
2022-08-27-CY54_exp220328_d5-null-dox	**2x150**	STAR-2.5.3a	**hg38**	34,760,581	0.20	35,058,759	27,426,241	3,107,903	1,683,703	0.97

READ DISTRIBUTION

#	Exonic:	Intergenic:	Intronic:
2022-08-27-CY41_exp220328_d4-wt-dmso	0.94	0.01	0.05
2022-08-27-CY42_exp220328_d4-wt-dox	0.94	0.01	0.05
2022-08-27-CY43_exp220328_d4-null-dmso	0.94	0.01	0.05
2022-08-27-CY44_exp220328_d4-null-dox	0.95	0.01	0.04
2022-08-27-CY51_exp220328_d5-wt-dmso	0.95	0.01	0.04
2022-08-27-CY52_exp220328_d5-wt-dox	0.94	0.01	0.05
2022-08-27-CY53_exp220328_d5-null-dmso	0.94	0.01	0.05
2022-08-27-CY54_exp220328_d5-null-dox	0.95	0.01	0.04

COVERAGE QC


Coverage of genes; >1000bp
2022-08-27-CY41_exp220328_d4-wt-dmso
2022-08-27-CY42_exp220328_d4-wt-dox
2022-08-27-CY43_exp220328_d4-null-dmso
2022-08-27-CY44_exp220328_d4-null-dox
Coverage (arbitrary units)
2.5
2.0
1.5
1.0
0.5
0.0
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
Position along mRNA 5' -> 3'

Coverage of genes; >1000bp