

fraction aligned reads (normalised by # input reads)

Stage	WaGa scr DMSO EV			WaGa scr Dox EV			WaGa sT DMSO EV			WaGa sT Dox EV			WaGa wt cells			WaGa wt EV	
	nf933	nf938	nf973	nf934	nf939	nf974	nf931	nf936	nf971	nf932	nf937	nf972	nf774	nf961	nf962	nf930	nf935
input	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
successfully_clipped	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
failed_quality_filter	5.2%	6.6%	2.8%	13.9%	5.1%	2.4%	7.4%	4.9%	4.5%	6.8%	5.3%	3.0%	8.1%	0.5%	0.5%	6.0%	5.0%
failed_homopolymer_filter	1.0%	1.0%	0.2%	1.2%	1.2%	0.3%	1.1%	1.5%	0.3%	0.9%	1.1%	0.4%	1.4%	0.1%	0.1%	1.8%	0.5%
calibrator	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
UniVec_contaminants	0.1%	0.1%	0.4%	0.1%	0.2%	0.2%	0.1%	0.1%	0.3%	0.0%	0.0%	1.1%	0.0%	0.0%	0.0%	4.0%	0.1%
rRNA	8.3%	9.3%	3.1%	6.4%	8.7%	2.6%	9.3%	9.8%	3.0%	10.9%	9.0%	3.2%	2.7%	2.7%	3.3%	8.1%	2.5%
reads_used_for_alignment	85.4%	83.1%	93.5%	78.5%	84.9%	94.6%	82.1%	83.8%	91.9%	81.4%	84.6%	92.4%	87.8%	96.7%	96.1%	80.1%	92.0%
genome	62.6%	65.8%	84.7%	54.4%	66.4%	84.4%	53.9%	60.2%	84.4%	63.9%	68.8%	84.0%	85.5%	95.7%	95.2%	36.0%	19.6%
miRNA_sense	6.4%	12.7%	72.9%	5.5%	12.5%	67.1%	10.6%	12.2%	74.5%	12.9%	13.7%	73.2%	3.2%	85.7%	83.2%	5.7%	3.2%
miRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
miRNAprecursor_sense	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.1%	0.1%	0.1%	0.0%	0.0%
miRNAprecursor_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
tRNA_sense	44.5%	39.3%	1.2%	38.5%	35.1%	1.6%	33.9%	28.4%	1.2%	39.7%	38.3%	1.3%	0.4%	2.8%	2.9%	20.3%	7.7%
tRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
piRNA_sense	0.4%	0.3%	1.0%	0.4%	0.3%	0.9%	0.3%	0.5%	1.5%	0.4%	0.2%	1.2%	0.0%	0.4%	0.4%	0.3%	0.1%
piRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
gencode_sense	9.5%	10.7%	5.1%	8.5%	14.1%	7.5%	7.0%	15.3%	4.2%	8.8%	13.3%	4.5%	75.4%	5.2%	6.7%	6.9%	6.2%
gencode_antisense	0.2%	0.2%	0.3%	0.1%	0.3%	0.5%	0.2%	0.3%	0.2%	0.2%	0.2%	0.2%	0.1%	0.2%	0.2%	0.2%	0.7%
circularRNA_sense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
circularRNA_antisense	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
not_mapped_to_genome_or_libs	22.8%	17.2%	8.8%	24.2%	18.4%	10.2%	28.2%	23.6%	7.5%	17.5%	15.8%	8.4%	2.3%	0.9%	0.9%	44.1%	72.4%
repetitiveElements	0.2%	0.1%	0.1%	0.2%	0.1%	0.2%	0.2%	0.2%	0.1%	0.1%	0.1%	0.1%	0.0%	0.0%	0.0%	0.2%	0.1%
endogenous_gapped	0.6%	0.2%	0.6%	0.7%	0.3%	0.7%	0.8%	0.5%	0.4%	0.4%	0.2%	0.5%	0.0%	0.1%	0.1%	1.1%	0.2%
input_to_exogenous_miRNA	22.1%	16.9%	8.1%	23.3%	18.1%	9.3%	27.3%	22.9%	6.9%	17.0%	15.5%	7.7%	2.3%	0.9%	0.9%	42.8%	72.0%
exogenous_miRNA	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
input_to_exogenous_rRNA	22.1%	16.9%	8.1%	23.3%	18.1%	9.3%	27.3%	22.9%	6.9%	17.0%	15.5%	7.7%	2.3%	0.9%	0.9%	42.8%	72.0%
exogenous_rRNA	0.7%	0.2%	0.2%	0.6%	0.2%	0.3%	0.7%	0.6%	0.2%	0.4%	0.2%	0.2%	0.0%	0.0%	0.0%	1.2%	0.1%
input_to_exogenous_genomes	21.4%	16.7%	7.9%	22.7%	17.8%	9.1%	26.6%	22.3%	6.8%	16.6%	15.3%	7.5%	2.3%	0.9%	0.9%	41.7%	71.9%
exogenous_genomes	5.9%	2.7%	3.0%	7.4%	2.9%	2.6%	7.7%	4.7%	1.5%	3.6%	2.1%	2.0%	0.0%	0.0%	0.0%	14.2%	3.2%