

Figure S3

A

ChIP: Set3-9myc

MACS PEAKS	total bases	%	% of region in genome	enrichment (fold)
Coding sequence	1815095	86.69	62.96	1.38
Promoter (-1000bp)	177023	8.45	22.77	0.37
tRNA	5437	0.26	0.09	2.81
Intergenic	96273	4.60	14.18	0.32

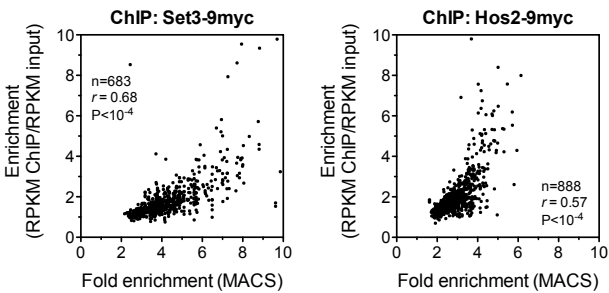
PEAK SUMMITS	# of summits	% of total
Coding sequence	1455	92.92
Promoter (-1000bp)	32	2.04
tRNA	39	2.49
Intergenic	40	2.55

ChIP: Hos2-9myc

MACS PEAKS	total bases	%	% of region in genome	enrichment (fold)
Coding sequence	1983187	84.57	62.96	1.34
Promoter (-1000bp)	252850	10.78	22.77	0.47
tRNA	5317	0.23	0.09	2.46
Intergenic	103578	4.42	14.18	0.31

PEAK SUMMITS	# of summits	% of total
Coding sequence	1270	94.78
Promoter (-1000bp)	29	2.16
tRNA	21	1.57
Intergenic	20	1.49

B



C

