

Table S1. Sequenced DNA samples

A Sample yield and regulatory enrichment by QPCR

Replicate ID	Flowcell Sample ID	Strain & Stage	DNase I treatment level w/ most enrichment	Highest Fold enrichment vs. background (N5, N6)	DNA yield
A	14140	N2 Embryo	160 U/mL	6.4	19 ng
B	13583	N2 Embryo	80 U/mL	6.3	50 ng
C	13578	N2 Embryo	120 U/mL	3.9	39 ng
D	13577	N2 Embryo	160 U/mL	5.3	3 ng
Z	13576	N2 L1 arrest	80 U/mL	4.7	336 ng
Y	13579	N2 L1 arrest	20 U/mL	5.8	8ng
X	13582	N2 L1 arrest	160 U/mL	5.5	17ng
W	14138	N2 L1 arrest	80 U/mL	1.4	27ng
V	14139	N2 L1 arrest	160 U/mL	5.7	25ng

B Read mapping to C. elegans genome (ce10/WS220) with Bowtie 1.0.0

Replicate ID	Flowcell Sample ID	Strain & Stage	Reads Processed (Q20 filter+trim)	Reads with at least one reported alignment	Reads that failed to align	Reads w/ alignments suppressed due to multimapping
A	14140	N2 Embryo	39,673,047	28040916 (71%)	6059497 (15%)	5572634 (14%)
B	13583	N2 Embryo	21,165,105	16086392 (76%)	657736 (3.1%)	4420977 (21%)
C	13578	N2 Embryo	38,482,313	24084424 (63%)	1021020 (2.7%)	13376869 (35%)
D	13577	N2 Embryo	18,523,832	7096637 (38%)	10334476 (56%)	1092719 (5.9%)
Z	13576	N2 L1 arrest	42,554,211	24045456 (57%)	863912 (2.0%)	17644843 (41%)
Y	13579	N2 L1 arrest	16,074,836	10010938 (62%)	1491568 (9.3%)	4572330 (28%)
X	13582	N2 L1 arrest	11,397,805	7679786 (67%)	699720 (6.1%)	3018299 (26%)
W	14138	N2 L1 arrest	30,376,192	20166440 (66%)	3950146 (13%)	6259606 (21%)
V	14139	N2 L1 arrest	32,487,179	15981175 (49%)	12066750 (37%)	4439254 (14%)