

Table S1: Sequencing and alignment of PRO-seq libraries.

For each replicate, the total number of reads sequenced, number of reads that passed filter, number of reads after clipping, number of reads that did not align to the ribosomal genes, and number of reads that aligned uniquely to the dm3 reference genome are shown in the table.

Library	Total reads	Passed filter	After clipping	Non-ribosomal	Mapped reads
LacZ_RNAi_NHS_rep1	22002207	20498005	18857033	14282348	9443330
LacZ_RNAi_NHS_rep2	45852143	42614140	37948992	29125104	19052661
LacZ_RNAi_20minHS_rep1	38149191	35411265	32429537	26063433	12372995
LacZ_RNAi_20minHS_rep2	48224407	44752452	39159654	30083167	13759500
GAF_RNAi_NHS_rep1	30007019	27839237	25783567	18298791	11898316
GAF_RNAi_NHS_rep2	29223336	27156681	24128417	18720462	12469522
GAF_RNAi_20minHS_rep1	33083184	30743186	27869887	19884430	9288339
GAF_RNAi_20minHS_rep2	26900768	24906543	20804594	15242537	6899682
HSF_RNAi_NHS_rep1	31620891	29340277	26783955	19754947	12848598
HSF_RNAi_NHS_rep2	20661822	19223633	16847824	13244247	8850116
HSF_RNAi_20minHS_rep1	20303622	18904152	17287939	11342865	5292065
HSF_RNAi_20minHS_rep2	44198627	40832316	33567347	22388032	10971965
NHS_rep1	33326090	27513854	24770885	23263961	12081666
NHS_rep2	40386025	34851525	33127425	31427515	17083774
30secHS_rep1	32103863	26577493	24398076	23568732	13946293
30secHS_rep2	43868016	37825590	35476506	34014449	20066701
2minHS_rep1	29483939	24279233	21513613	20261645	12280319
2minHS_rep2	58929589	52883653	49114894	45522711	25046895
5minHS_rep1	26685698	22026373	20040132	18839288	10202616
5minHS_rep2	49420574	42648406	39527809	34244700	18258123
10minHS_rep1	31518051	26025041	23770378	22787845	10255055
10minHS_rep2	36364173	32508148	30318974	28531182	13973044
20minHS_rep1	53294616	47669950	44625103	42605985	19333234
20minHS_rep2	28918287	25102563	23838584	23118980	9322488