Experiment	Sample	spike In Genome	Ribosomal	Genome	Unmapped	Total Reads	Norm. Factor
PRO-Seq	SC_WTr1	348939	7314357	2113476	1351857	11128629	1
PRO-Seq	SC_WTr2	321265	7097561	1917056	1144824	10480706	0.920691009
PRO-Seq	SC_Spt4KOr1	309441	6780503	3337629	1073766	11501339	0.88680543
PRO-Seq	SC_Spt4KOr2	323311	7680125	3268891	1886762	13159089	0.926554498
mRNA-seq	SC_WTr1	1631698	NA	35165891	6766362	43563951	0.856646354
mRNA-seq	SC_WTr2	1829123	NA	37399417	6702414	45930954	0.960295073
mRNA-seq	SC_Spt4KOr1	1619275	NA	35026042	6040124	42685441	0.850124242
mRNA-seq	SC_Spt4KOr2	1904751	NA	41592838	7227292	50724881	1
PRO-Seq	pombeWTr1	722562	7231534	5535779	1073132	14563007	0.837361789
PRO-Seq	pombeWTr2	540885	4659402	4079360	744834	10024481	0.626820164
PRO-Seq	pombeSpt4KOr1	405405	5511285	3898856	789841	10605387	0.469815263
PRO-Seq	pombeSpt4KOr2	862903	12837838	8960587	2101368	24762696	1
mRNA-seq	pombeWTr1	3546756	NA	34199493	3786757	41533006	0.750287962
mRNA-seq	pombeWTr2	5144621	NA	51375901	5183180	61703702	1.088303566
mRNA-seq	pombeSpt4KOr1	4107511	NA	37414945	4194282	45716738	0.868911212
mRNA-seq	pombeSpt4KOr2	4727193	NA	35433485	3977657	44138335	1
PRO-Cap	SC_CAP+Tap	NA	7930727	1865241	818844	10614812	NA
PRO-Cap	SC_CAP-Tap	NA	15093960	2268916	1148714	18511590	NA
PRO-Cap	SP_CAP+Tap	NA	10428693	11373221	2246184	24048098	NA
PRO-Cap	SP_CAP-Tap	NA	15663591	8337945	1967933	25969469	NA

Table S1: Sequencing alignment statistics for each experiment performed.
Normalization factors refer to the relative amount of reads mapping to the spike in
organism genome within each experiment (set of 4 libraries). In the PRO-cap
experiments reads per million (RPM) was used for normalization between plus-TAP and
minus-TAP samples.