

Table S1. Illumina sequencing statistics of OSS/OSC genomes.

Illumina sequencing statistics of PIWI-CLIP-Seq from OSS current cells

Sample	total_read	read_clipped	read_noclippped	read_merged_clipped	read_merged_noclip	virus	mirna	struc	genome_mapped	no_genome_ma	normalization_base
clip-piwi-SiomiAb1-merged	23,476,841	6,682,690	14,653,952	839,534	1,698,342	40,522	383	390,807	1,333,090	581,081	2,537,876
clip-piwi-LauAb1-merged	6,242,340	6,365	6,204,650	2,399	1,733,189	16,280	453	222,496	796,455	699,603	1,735,588
clip-piwi-LauAb2-merged	18,674,490	8,152,133	5,797,240	1,867,114	1,095,822	15,606	625	414,170	1,558,951	533,775	2,962,936
clip-piwi-LauAb3-merged	31,600,452	8,185,739	12,825,412	2,585,416	3,106,201	59,764	746	643,684	2,649,889	1,499,472	5,691,617
clip-piwi-block-merged	21,417,460	4,156,343	15,886,908	281,869	808,714	50,959	52	238,795	201,052	441,072	1,090,583
s_2678_OSSpiRNAs	24,742,206	12,137,524	9,071,006	NA	NA	561,839	3,767,257	6,631,212	2,804,671	8,498,171	21,208,530

Illumina sequencing statistics of transcriptome analysis from OSS current cells

Sample	total_read	read_clipped	read_noclippped	read_merged_clipped	read_merged_noclip	virus	mirna	struc	genome_mapped	no_genome	normalization_base
cytosigfp	10,527,901	537,573	9,671,574	NA	NA	320,496	19	4,368,380	3,048,856	1,990,615	3,048,856
cytosipiwi	20,778,591	1,368,336	18,636,199	NA	NA	1,416,842	44	9,380,971	4,438,336	3,500,146	4,438,336
nucpsigfp	14,837,283	853,516	13,460,845	NA	NA	370,465	110	5,149,984	5,838,133	2,192,292	5,838,133
nucpsipiwi	11,956,880	705,852	10,796,802	NA	NA	725,781	81	3,376,659	4,794,071	1,983,427	4,794,071
nunsigfp	12,825,174	919,402	11,402,711	NA	NA	3,677,831	63	1,777,754	2,088,180	3,954,654	2,088,180
nunsipiwi	15,898,679	973,834	14,351,086	NA	NA	4,427,631	83	2,772,630	2,317,239	4,983,407	2,317,239
Nun-siGFP	8,993,754	202,168	8,666,340	NA	NA	3,305,067	62	1,466,198	1,723,642	2,252,551	1,723,642
Nun-siPiwi	12,263,998	300,343	11,767,991	NA	NA	4,172,796	84	2,433,336	2,029,464	3,270,613	2,029,464
osssigfp	15,411,852	90,209	14,970,932	NA	NA	221,322	163	2,400,857	10,616,075	1,792,092	10,616,075
osssipiwi	16,004,346	161,222	15,409,119	NA	NA	421,131	129	2,095,834	10,392,526	2,555,092	10,392,526
mRNA-siGFP-scriptseq	10,605,545	148,270	10,382,040	NA	NA	9,883	25	6,749,003	2,394,291	1,257,565	2,394,291
mRNA-siPiwi-scriptseq	15,221,965	275,028	14,828,175	NA	NA	29,716	24	10,320,470	2,866,405	1,647,154	2,866,405
mRNA-siGFP-srna	22,206,242	11,310,695	5,949,031	NA	NA	136,257	92	3,607,946	5,189,007	3,118,137	5,189,007
mRNA-siPiwi-srna	23,436,134	10,188,876	6,775,155	NA	NA	502,124	77	3,682,345	4,322,562	3,637,516	4,322,562
siGFP0125	7,669,226	232,096	5,584,328	NA	NA	28,560	122	1,140,946	2,587,308	2,059,610	2,587,308
siPiwi0125	5,743,894	195,892	3,680,964	NA	NA	46,075	132	565,009	1,820,743	1,445,029	1,820,743

Illumina sequencing statistics of OSS/OSC genomes.

	OSS-Early	OSS_E	OSS-Current	OSS_C	OSC-Early	OSC_E	OSC-Current	OSC_C
Unique gSeq reads:	24,006,273		29,031,323		21,970,145		52,124,387	
Genome sequencing total reads	26,568,468		33,718,485		24,627,215		65,749,243	
Rel. 5/Dm3 Reference genome matched	18,242,228	69%	22,661,533	67%	16,205,806	66%	49,469,969	75%
RepeatMasker matched reads	1,763,174	7%	3,095,136	9%	1,494,470	6%	5,854,087	9%
Remaining nonmapping reads	6,563,066	25%	7,961,816	24%	6,926,939	28%	10,425,187	16%
Reads with 1 Genome and 1 TE match	33,729	0.13%	71,255	0.21%	27,382	0.11%	51,654	0.08%
uniqueied reads:	32,383		69,288		26,368		47,019	
Level 1 clusters of TE insertion sites:	1,196		2,847		1,143		1,152	