Appendix 1. Number of reads and percentage of mapped reads over the nuclear genome of each sample.

Sample Name	Number of reads	Percentage of mapped reads to the nuclear genome
LD ZT0 1	9,446,680	94.09%
LD ZT4 1	9,123,089	84.33%
LD ZT8 1	9,382,983	88.28%
LD ZT12 1	11,090,892	93.81%
LD ZT16 1	10,365,158	91.13%
LD ZT20 1	9,611,641	94.90%
LD ZT0 2	9,911,801	95.07%
LD ZT4 2	10,373,968	92.62%
LD ZT8 2	9,361,305	94.61%
LD ZT12 2	11,531,047	96.77%
LD ZT16 2	10,096,408	91.95%
LD ZT20 2	9,840,739	95.96%
LD ZT0 3	9,271,993	74.71%
LD ZT4 3	12,219,220	73.30%
LD ZT8 3	10,295,962	57.05%
LD ZT12 3	10,776,249	73.88%
LD ZT16 3	9,694,347	71.37%
LD ZT20 3	9,150,451	86.44%
LD ZT0 4	10,040,606	80.48%
LD ZT4 4	13,076,912	98.51%
LD ZT8 4	14,287,019	98.70%
LD ZT12 4	14,578,626	98.48%
LD ZT16 4	12,754,119	98.09%
LD ZT20 4	11,247,222	92.83%
LD ZT0 5	10,652,932	97.36%
LD ZT4 5	10,829,705	97.46%
LD ZT8 5	7,714,090	98.19%
LD ZT12 5	12,194,496	98.34%
LD ZT16 5	10,793,769	98.17%
LD ZT20 5	12,165,205	97.94%
SD ZT0 1	12,493,583	98.05%
SD ZT4 1	13,622,449	98.27%
SD ZT8 1	11,074,612	98.07%

SD ZT12 1	11,907,980	96.64%
SD ZT16 1	10,879,032	97.80%
SD ZT20 1	11,149,175	97.88%
SD ZT0 2	14,740,881	95.05%
SD ZT4 2	12,296,826	97.94%
SD ZT8 2	12,311,981	97.84%
SD ZT12 2	11,499,122	96.45%
SD ZT16 2	10,968,505	97.49%
SD ZT20 2	12,299,619	97.76%
SD ZT0 3	7,072,975	95.81%
SD ZT4 3	11,914,969	84.17%
SD ZT8 3	8,560,034	95.06%
SD ZT12 3	8,898,970	97.89%
SD ZT16 3	9,814,400	97.30%
SD ZT20 3	9,370,821	95.88%
SD ZT0 4	8,980,904	96.01%
SD ZT4 4	9,370,821	95.88%
SD ZT8 4	14,529,619	96.44%
SD ZT12 4	11,373,712	98.13%
SD ZT16 4	13,933,214	92.04%
SD ZT20 4	9,836,745	97.33%
SD ZT0 5	10,287,353	94.11%
SD ZT4 5	9,758,563	97.61%
SD ZT8 5	9,652,648	88.35%
SD ZT12 5	10,409,149	87.66%
SD ZT16 5	9,221,180	97.26%
SD ZT20 5	8,460,013	93.39%