Table S2 Spo11-oligo sequencing statistics

Sample	Total sequenced	Total mapped[a]	Total filtered[b]	Uniquely mapped[c]
wild type sample 1	4,361,438	4,302,910 (98.6%)	3,762,134 (86.2%)	3,633,091 (83.3%)
wild type sample 2	2,783,885	2,700,065 (97.0%)	2,360,467 (84.8%)	2,280,452 (81.9%)
bas1 sample 1	5,615,623	5,545,624 (98.8%)	4,823,794 (85.9%)	4,665,416 (83.1%)
bas1 sample 2	5,219,925	3,906,560 (74.8%)	3,212,796 (61.5%)	2,983,690 (57.2%)
bas1 sample 3	5,410,693	5,349,120 (98.9%)	4,794,677 (88.6%)	4,542,315 (84.0%)
bas1 sample 4	5,401,936	5,211,575 (96.5%)	4,540,169 (84.0%)	4,413,658 (81.7%)
ino4 sample 1	3,241,998	3,203,647 (98.8%)	2,867,655 (88.4%)	2,664,527 (82.2%)
ino4 sample 2	3,631,197	3,614,320 (99.5%)	3,188,652 (87.8%)	3,117,705 (85.9%)
ino4 sample 3	4,160,807	4,127,194 (99.2%)	3,616,144 (86.9%)	3,480,102 (83.6%)

[a] The fraction of sequences that could not be mapped likely reflect sequencing errors, adaptor dimers, PCR dimers and *bona fide* Spo11-oligos derived from genomic regions that are unique to SK1 (i.e., not found in the S288C reference strain).
[b] Total number of reads that filtered to get rid of reads with poor alignment and/or adaptor clipping.
[c] Total number of reads that mapped to only one position in the genome.