|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Pool** | **Library** | **Reads** | **Platform** | **Facility** |
| 67 | RBJC37 | 38,713,102 | Novaseq SP PE150 | UC Berkeley |
| 69 | RBJC38 | 38,875,221 |
| 69 | RBJC39 | 43,194,450 |
| 69 | RBJC40 | 39,778,862 |
| 69 | RBJC41 | 38,836,065 |
| 67 | RBJC42 | 39,265,466 |
| 67 | RBJC43 | 47,124,575 |
| 67 | RBJC44 | 39,762,187 |
| 67 | RBJC48 | 91,531,071 | HiSeq4000 PE150 | Novogene |
| 67 | RBJC48\_reseq | 86,892,060 |
| 70 | RBCJ51 | 86,254,426 |
| 70 | RBCJ51\_reseq | 86,130,880 |
| 70 | RBJC52 | 52,108,306 |
| 70 | RBJC52\_reseq | 53,363,169 |
| 71 | RBJC54 | 88,154,532 |
| 71 | RBJC54\_reseq | 86,878,835 |
| 71 | RBJC55 | 90,265,981 |
| 71 | RBJC55\_reseq | 82,130,170 |
| 69 | RBJC57 | 84,296,399 |
| 69 | RBJC57\_reseq | 85,606,080 |

**Supplementary Table 4. Tn-seq sequencing data sets.** Each row reports numbers of reads from the indicated sequencing of insertion positions of barcoded transposons in the *S. cerevisiae* x *S. paradoxus* hybrid, as in Figure 1A, left, of the main text. Experiment identifiers are from PRJNA735401; “reseq” indicates the reads from a technical replicate performed to gather additional reads for the indicated library.