Supplementary Table S2. Mapping statistics of DNA sequencing data

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| Origin\* | Accession ID | Mapped Reads | Coverage  (1st quantile, Median, 3rd quantile) | # Insertions/Deletions |
| UNC | SRR2986339 | 47.6M (54.24%) | 36/48/56 | 6.85M/7.70M |
| SRR2986435 | 53.8M (83.95%) | 40/53/62 | 1.84M/2.02 |
| SRR2986451 | 39.2M (85.68%) | 26/37/46 | 2.82M/2.90M |
| Edinburgh | ERR1147177 | 116.0M (77.15%) | 61/98/134 | 3.2M/3.32M |
| ERR1147178 | 99.2M (80.03%) | 22/50/70 | 2.30M/2.37M |
| Keio | DRR055040 | 50.0M (96.91%) | 66/109/153 | 8.59M/8/48 |

UNC = University of North Carolina (Boothby *et al.* 2015); Edinburgh = University of Edinburgh (Koutsovoulos *et al.* 2016); Keio = Keio University (this work and Arakawa *et al.* 2016)