Table S1 Statistics for filtering and mapping reads

| Sample | Total[a] | Unmapped[b] | Unique_ Mapped[c] | Multiple_ Mapped[d] | Total_ Mapped[e] |
|---|---|---|---|---|---|
| H1 | 59964760 | 9066482 | 47380876 | 3517402 | 50898278 |
| H2 | 63533624 | 10671923 | 48784652 | 4077049 | 52861701 |
| H3 | 56794110 | 9534115 | 43462525 | 3797470 | 47259995 |
| H4 | 60582058 | 9378794 | 46859700 | 4343564 | 51203264 |
| L1 | 63935382 | 10529588 | 49131821 | 4273973 | 53405794 |
| L2 | 69215198 | 11304511 | 53523484 | 4387203 | 57910687 |
| L3 | 63074270 | 9600083 | 49311578 | 4162609 | 53474187 |
| L4 | 58074524 | 8705438 | 45735733 | 3633353 | 49369086 |

[a] Total: Total number of clean reads

[b] Unmapped: Reads not aligned to the reference sequence

[c] Unique_ Mapped: Reads aligned to only one position

[d] Multiple_ Mapped: Reads aligned to two or more positions

[e] T Total_ mapped: Reads that completely aligned to the reference sequence