**Table S3.** Data of NGS statistics and mapping rate to the genome of Japanese eel for each library.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Name of library | Raw read pairs | Yield (Mbases) | % >= Q30 bases | Mean quality score | Mapping  read pairs (Trimmed) | Mapping rate |
| FPF1 | 11,187,738 | 3,379 | 95.84 | 38.09 | 10,929,449 | 81.22% |
| FPF2 | 11,806,314 | 3,566 | 95.71 | 38.04 | 11,530,527 | 79.55% |
| MPF1 | 11,555,769 | 3,490 | 96.2 | 38.2 | 11,308,110 | 86.05% |
| MPF2 | 11,615,537 | 3,508 | 95.9 | 38.1 | 11,349,480 | 82.77% |