**Table S2: Alignment summaries for four Red Fife (RF) and Stettler (S) STAR aligned RNA-Seq samples.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample name | Geno | Mapping speed, million of reads per hour | Number of input reads | Average input read length | Uniquely mapped reads number | Average mapped length | Uniquely mapped reads % | % of reads mapped to multiple loci | % of reads mapped to too many loci |
| LL2017\_2271 | RF\_1 | 71.28 | 22451643 | 199 | 18605823 | 193.91 | 82.87% | 16.33% | 0.50% |
| LL2017\_2272 | RF\_2 | 44.76 | 22119769 | 199 | 17070644 | 192.89 | 77.17% | 18.48% | 2.27% |
| LL2017\_2273 | RF\_3 | 61.77 | 20693686 | 199 | 17112900 | 193.64 | 82.70% | 16.29% | 0.40% |
| LL2017\_2274 | RF\_4 | 69.33 | 22743795 | 199 | 18945320 | 193.72 | 83.30% | 15.93% | 0.45% |
| LL2017\_2281 | S\_1 | 47.42 | 23223286 | 199 | 19308124 | 193.91 | 83.14% | 16.33% | 0.24% |
| LL2017\_2282 | S\_2 | 53.74 | 25438856 | 199 | 21143836 | 193.94 | 83.12% | 16.09% | 0.37% |
| LL2017\_2283 | S\_3 | 53.22 | 23284657 | 199 | 19152314 | 193.95 | 82.25% | 16.58% | 0.49% |
| LL2017\_2284 | S\_4 | 51.56 | 24721598 | 199 | 20349827 | 193.84 | 82.32% | 16.99% | 0.32% |