**S1 Table. Assessment of long-read sequence aligners, based on largest average alignment length with respect to Sanger sequence references**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | **LAST** | **BLASR** | **LASTZ** |
|  | Total reads | Pass reads | Mean read length (min-max) | No of mapped reads | Mean Alignt read length (nt) | Mean Alignt Identity | No of mapped reads | Mean Alignt read length (nt) | Mean Alignt Identity | No of mapped reads | Mean Alignt read length (nt) | Mean Alignt Identity |
| **B5584c (6728 nt)** | 7,656 | 1875 | 5,808.4 | 1,670 | 3,388 | 74.6% | 1,357 | 3,202 | 77.25% | 1,374 | 3,416 | 72.45% |
|  |  |  | (226-11,327) | (89.1%)\* |  |  | (72.4%)\* |  |  | (73.3%)\* |  |  |
| **B6260c (6551 nt)** | 25,562 | 4962 | 5,483.1 | 4,372 | 3,273 | 72.8% | 2,908 | 2,923 | 77.75% | 3,262 | 3,253 | 71.4% |
|  |  |  | (391-20,498) | (88.1%)\* |  |  | (58.6%)\* |  |  | (65.7%)\* |  |  |

 \*, Pourcentage calculated with « Pass » reads; No, number.