S3 Table. TruSeq® Stranded mRNA Illumina sequencing results and coverage for each condition.

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample ID** | **Total read bases (bp)** | **Total reads a (N)** | **GC (%)** | **AT (%)** | **Q20 (%) b** | **Q30 (%) c** | **Coverage d**  |
| **NP** | 22,467,804,106 | 222,453,506 | 54.59 | 45.41 | 97.96 | 94.54 | 2055x |
| ***ardC +*** | 19,110,456,642 | 189,212,442 | 54.55 | 45.45 | 97.95 | 94.45 | 1743x |
| ***ardC -*** | 23,255,871,352 | 230,256,152 | 56.05 | 43.95 | 97.9 | 94.33 | 2121x |

a Total reads refers to the sum of reads 1 and reads 2 from strand-specific sequencing. b Q20 stands for phred quality score over 20. c Q30 stands for phred quality score over 30. d Coverage was calculated according to the formula C=L·N/G from the length of reads (L = 100), N and the genome size (G) being the sum of all genomes present in the sample.