**Figure 6 – Source Data 1. Read-wide mapping statistics.**

JunctionSeq was applied to analyse the RNA-seq data. All percentages are relative to the total read pairs and the filtering steps were consecutively applied from left to right. 1Percent reads that are not duplicates of another read pair and passed qorts filter. 2Percent reads that unambiguously aligned to a single gene. 3Percent reads that overlapped a splice junction. 4Percent reads that overlapped a novel splice junction.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Total**  **(106)** | **Aligned (%)** | **Coherent (%)1** | **Unique**  **(%)2** | **Splice events (%)3** | **Novel events (%)4** |
| D0-1 | 80.3 | 93.7 | 83.1 | 67.0 | 47.5 | 1.26 |
| D0-2 | 66.9 | 91.5 | 81.6 | 62.4 | 43.5 | 1.14 |
| D3-1 | 59.3 | 94.0 | 84.4 | 58.0 | 41.6 | 1.27 |
| D3-2 | 69.8 | 89.8 | 79.1 | 54.5 | 39.0 | 1.13 |
| D6-1 | 81.7 | 92.9 | 83.5 | 46.5 | 32.6 | 1.09 |
| D6-2 | 78.0 | 91.8 | 82.0 | 49.0 | 34.8 | 1.09 |
| D9-1 | 76.8 | 92.2 | 80.6 | 47.9 | 33.2 | 1.16 |
| D9-2 | 66.2 | 88.9 | 79.8 | 45.8 | 31.4 | 1.05 |
| D12-1 | 62.4 | 92.4 | 83.6 | 43.5 | 29.7 | 1.12 |
| D12-2 | 76.5 | 92.6 | 83.5 | 47.5 | 32.9 | 1.12 |
| iPSC-1 | 91.3M | 92.8 | 83.3 | 53.0 | 37.9 | 1.26 |
| iPSC-2 | 67.0M | 92.2 | 81.8 | 57.1 | 41.2 | 1.32 |