**Table S3** Genomic distribution of RNA-Seq PACs that were supported by the PacBio sites.

|  |  |  |
| --- | --- | --- |
| **Genomic region of RNA-Seq PACsa** | **Number of PacBio Sites within 24 nt** | **Percentage of PacBio Sites within 24 nt** |
| 3'-UTR | 21,796 | 63.24% |
| extended | 7,664 | 22.24% |
| intron | 2,064 | 5.99% |
| CDS | 143 | 0.41% |
| 5'-UTR | 136 | 0.39% |
| intergenic | 2,662 | 7.68% |
| Total | 34,465 (of 70,741) | 48.72% |

aGenomic region of PACs was calculated based on Ensembl annotation (details in materials and method section)