**S6 Table.** Mapping sensitivity and precision of simulated RNA-seq paired-end (PE) datasets by picking “best” hits with or without applying AlignerBoost procedures. ⑴ DNA-seq aligner without local alignment ability, so 1DP function of AlingerBoost was enabled; ⑵ DNA-seq aligners; ⑶ RNA-seq aligners; ⑷ Aligners that don’t support reporting multiple-mapped PE-reads, thus filtering was ineffective.

|  |  |  |  |
| --- | --- | --- | --- |
| Dataset | Aligner | AlignerBoost | Default |
| Precision | Sensitivity | F1 score | Precision | Sensitivity | F1 score |
| refGene | Bowtie ⑴ | 98.62% | 77.66% | 0.8689 | 97.05% | 61.61% | 0.7537 |
| Bowtie2 ⑵ | 98.84% | 95.93% | 0.9736 | 96.71% | 86.13% | 0.9111 |
| BWA ⑵ | NA ⑷ | NA ⑷ | NA ⑷ | 97.23% | 97.22% | 0.9723 |
| Tophat2 ⑶ | 99.55% | 94.94% | 0.9719 | 98.15% | 94.71% | 0.9640 |
| STAR ⑶ | 99.88% | 96.14% | 0.9797 | 98.29% | 97.68% | 0.9798 |