

**Supplemental Table S15. Summary of full-length transcriptome.**

Type	TBF <sub>3</sub>	BTF <sub>3</sub>
The sequencing datas (Gb)	21.22	15.49
Insert reads (Gb)	2.02	1.30
Average length of insert reads (bp)	3080.18	2936.23
Average full pass of insert reads	12	13
Number of consensus reads	663,834	479,667
Number of five prime reads	622,119 (93.72%)	459,029 (95.70%)
Number of three prime reads	628,065 (94.61%)	456,107 (95.09%)
Number of full-length reads	586,075 (88.29%)	431,999 (90.06%)