

Supplemental Table S12. Summary of the raw data of transcriptome.

Species	Tissue	Number of libraries	Total number of reads (million)	Total number of bases (Gb)	Average ratio of Q30 bases
BSB (♀)	Liver	Illumina HiSeq™ 2000 ×1	82.42	21.35	92.91%
		Illumina Hiseq™ X Ten ×2			
TC (♂)		Illumina HiSeq™ 2000 ×1	77.57	19.93	93.46%
		Illumina Hiseq™ X Ten ×2			
BTF ₁ (♀)		Illumina HiSeq™ 2000 ×1	83.10	21.51	94.35%
		Illumina Hiseq™ X Ten ×2			
BTF ₂ (♀)		Illumina HiSeq™ 2000 ×1	79.74	20.52	94.28%
		Illumina Hiseq™ X Ten ×2			
BTF ₃ (♀)		Illumina HiSeq™ 4000 ×1	67.38	20.02	91.15%
		Illumina Hiseq™ X Ten ×2			
TBF ₁ (♀)		Illumina HiSeq™ 4000 ×1	77.97	23.16	89.98%
		Illumina Hiseq™ X Ten ×2			
TBF ₂ (♀)		Illumina HiSeq™ 4000 ×1	84.07	24.91	90.59%
		Illumina Hiseq™ X Ten ×2			
TBF ₃ (♀)		Illumina Hiseq™ X Ten ×3	72.08	21.27	94.15%
BTF ₃ (♀)	Gonad	Illumina Hiseq™ X Ten ×3	73.31	21.65	94.15%
TBF ₃ (♀)		Illumina Hiseq™ X Ten ×3	81.60	24.37	91.04%
BTF ₃ (♀)	Muscle	Illumina Hiseq™ X Ten ×3	105.17	31.29	92.03%
TBF ₃ (♀)		Illumina Hiseq™ X Ten ×3	69.96	20.79	91.46%