



**Supplemental Fig. S29.** Overall clustering of twelve samples of BSB, TC, and their reciprocal cross hybrids (BT and TB) based on all normalized count data of allelic expression. The heatmap depicts the relationships of all transcriptomes of liver (L), gonad (G), and muscle (M) tissues. The gene count data in the hybrid relative to the TC and BSB species-specific reads (Ery- and Mam-).