



Supplemental Fig. S23. Overall clustering of twelve samples of BSB, TC, and their reciprocal cross hybrids (BT and TB) based on all normalized count data. The heatmap depicts the relationships of all transcriptomes of liver (L), gonad (G), and muscle (M) tissues. The gene count data in the hybrid were mapped to the two parental genomes (Ery-: TC and Mam-: BSB), while the gene count data in BSB and TC were mapped to the respective genomes.