





(pooled 24 individuals, \log_{10} bins of 0.01)

Additional file 1: Transcriptome size and coverage per contig.

(a) Total transcriptome size in base pairs (red) and number of contigs (blue) as minimum contig size threshold in base pairs (x axis) is varied; and (b) histogram of \log_{10} average coverage for all contigs (purple) versus contigs ≥ 1 kbp (green).