Figure S6, continued
Figure S6. The putative centromere regions on the *S. fibuligera* KPH12 and KJJ81 genomes. The locations and densities of LTR retrotransposons (green) were analyzed using LTR_FINDER [1] and were plotted for each 25-kb window of the chromosomal coordinates. GC contents (black) and gene density (blue) were analyzed using the codonW program and plotted for each 2.5-kb window of the chromosomal coordinates. The log scale plots of RNA-Seq reads (green) show the transcriptome density for each 2.5-kb window of the chromosomal coordinates. TopHat2 [2] was used to map RNA-Seq reads to the PacBio genome assembly.
Reference