



Supplemental Fig. S2. Distribution of sequencing libraries insert sizes. Insert sizes were calculated by mapping the paired end or mate-pair reads to the scaffolds using BWA tool for DNA libraries of **(a)** 180 bp, **(b)** 500 bp, **(c)** 2 kb, **(d)** 5kb, **(e)** 6 kb and **(f)** 10kb in length. Both reads in a pair should be uniquely mapped.