





Figure S1: Genome scan plots depicting the density of 108170 and 77097 SNPs identified commonly between high and low-pod number-containing parental accessions and homozygous bulks of two mapping population [(A: Pusa 1103 x ILWC 46) and (B: Pusa 256 x ILWC 46)] with respect to their congruent physical positions on *kabuli* reference genome. These SNPs are physically mapped across eight *kabuli* chickpea chromosomes at 100-kb sliding window. The SNP density is defined as number of SNPs mapped within 1-Mb physical interval of chromosomes.