Table S1: Summary of normalized individual sequence reads obtained from low and high pod number-containing parents and bulks of two inter-specific mapping populations mapped on *kabuli* chickpea genome

Characteristics	**Pusa 1103 X ILWC 46**				**Pusa 256 X ILWC 46**				**Total**
	Pusa 1103	**ILWC 46**	**LPNB**	**HPNB**	**Pusa 256**	**ILWC 46**	**LPNB**	**HPNB**	
Sequencing depth of coverage (fold)	12.3	11.8	10.7	12.5	12.7	11.8	11.1	10.3	11.6
Genome coverage (%) by uniquely mapped sequence reads	64.7	63.5	64.1	65.2	65.1	63.5	63.8	62.7	64.1
Genomic regions (Mb) covered (considering estimated chickpea genome size of ~ 740 Mb)	478.8	469.9	474.3	482.5	481.7	469.9	472.1	464.0	474.2