



Figure S1: Proportionate (%) distribution of 21499 InDel markers (derived from diverse intergenic and gene regions of *desi* chickpea genome) showing 2 to 6 and 7 to 54-bp *in silico* fragment length polymorphism among different possible-pair combination of four chickpea accessions (ICC 4958, ICC 4951, ICC 12968 and ICC 17160). The abundance of InDel markers showing 2 to 6-bp fragment length polymorphism in all possible-pair combination of accessions was evident.