

Number of genome-wide InDel markers revealing 2 to 54-bp *in silico* fragment length polymorphism among *desi* (ICC 4958 and ICC 4951), *kabuli* (ICC 12968) and *wild* (ICC 17160) chickpea accessions developed: **21499**

Selection Criteria

- InDel markers exhibiting 10 to 54-bp *in silico* fragment length polymorphism among four chickpea accessions: **3042**
- InDel markers revealing 2 to 9-bp *in silico* fragment length polymorphism commonly among four chickpea accessions: **648**
- Coding and regulatory InDel markers exhibiting 2 to 9-bp *in silico* fragment length polymorphism among four chickpea accessions: **919**
- Intronic InDel markers exhibiting 2 to 9-bp *in silico* fragment length polymorphism among four chickpea accessions mapped on eight chromosomes: **1412**
- Intronic InDel markers exhibiting 4 to 9-bp *in silico* fragment length polymorphism among four chickpea accessions mapped on scaffolds: **559**

Number of genome-wide InDel markers exhibiting 10 to 54-bp and 2 to 9-bp *in silico* fragment length polymorphism among four chickpea accessions selected for experimental validation: **6580**

Number of *in silico* polymorphic InDel markers showed successful PCR amplification in four chickpea accessions used: **6482** (98% amplification success rate)

Number of amplified *in silico* polymorphic InDel markers revealed polymorphism among 24 chickpea accessions: **6254** (96% polymorphic potential)

InDel markers utilized for understanding the molecular diversity and phylogenetic relationships among 24 *desi*, *kabuli* and *wild* chickpea accessions: **6254**

Number of amplified *in silico* polymorphic InDel markers detected polymorphism experimentally between parental accessions of a mapping population (ICC 4958 x ICC 17160): **6219**

InDel markers showed segregation distortion and could not exhibit goodness-of-fit to the expected Mendelian 1:1 segregation ratio: **57**

Number of amplified *in silico* polymorphic InDel markers used for constructing high-density inter-specific genetic linkage map (ICC 4958 x ICC 17160) and flowering/maturity time QTL mapping: **6197**

Figure S2: Flow chart depicting the strategy adopted to select *in silico* polymorphic InDel markers for their large-scale experimental validation and genotyping applications (molecular diversity analysis, high-density genetic linkage map construction and flowering/maturity time QTL mapping) in chickpea.