

## Supplementary Data

**Supplementary Dataset 1.** Whole genome DNA methylation and its influence on gene expression at different stages of seed development in JGK 3.

**Supplementary Dataset 2.** Differentially methylated regions in different sequence contexts between successive stages of seed development in JGK 3.

**Supplementary Dataset 3.** Differential methylation in different sequence contexts and genic regions and differential expression of DMR-associated differentially expressed genes between successive stages of seed development.

**Supplementary Dataset 4.** List of genes involved in cell cycle, cell growth, grain filling and QTLs that are associated with DMRs and/or show differential expression between JGK 3 and Himchana 1 chickpea cultivars at S3 and S5 stages.

**Supplementary Dataset 5.** Methylation level within TEs and their flanking regions in different sequence context at different stages of seed development.

**Supplementary Dataset 6.** Small RNAs mediated methylation in TEs during seed development in JGK 3.

**Supplementary Dataset 7.** Frequency of TEs within gene body and flanking regions of protein coding genes that are DMR-associated, not associated with DMRs, differentially expressed genes that are DMR-associated and not associated with DMRs in different sequence contexts.

**Supplementary Dataset 8.** Number of methylcytosines in different sequence contexts in small-seeded (Himchana 1) and large-seeded (JGK 3) cultivars at S3 and S5 stages of seed development.

**Supplementary Dataset 9.** Differentially methylated regions in different sequence contexts between JGK 3 and Himchana 1 at S3 and S5 stages.

**Supplementary Dataset 10.** Differential methylation in different sequence contexts and genic regions and differential expression of DMR-associated differentially expressed genes between chickpea cultivars at S3 and S5 stages.

**Supplementary Dataset 11.** List of genes involved in cell cycle, differentiation, grain filling and desiccation processes that are associated with DMRs and/or show differential expression during successive stages of seed development.