Figure S9  Results of the ultra-deep amplicon bisulfite sequencing of a region spanning the nucleotides 2,212,717-2,213,154 on sorghum chromosome 9 (JGI, v1.4) surrounding the CNS sequence in sorghum B.Tx623 at the V1 and V7 stage. On the y-axis, % of cytosine methylation as estimated by the Kismeth software. Methylation data points (mean values) are represented in different colours, according to cytosine context: red for CG, blue for CHG, green for CHH. The orange dotted lines highlight the CNS sequence.