To identify DMRs, CGmaps from each group of three individual replicates were merged into single CGmaps using the merge2 tool of CGmapTools version 0.1.2 (Guo et al. 2018). Intersected CGmaps for each pair of merged CGmaps were produced using the CGmapTools intersect tool in each sequence context separately (CG, CHG, and CHH). CG and CHG DMRs and control eligible regions (EMRs) were then identified from the separate CG and CHG intersected maps using DMR\_Finder.py, parameters as follows: binSize = 200, minCov = 3 minCountC = 5, minAbsDif = .20, minRelDif = .5. The set of CG DMRs that overlapped CHG DMRs were identified using the BEDTools (version 2.29.2) intersect tool. To finalize the set of DMRs, all DMRs located on scaffolds rather than chromosomes 1 through 10 were discarded. DMR\_METHY\_Finder.py works nearly identically as DMR\_Finder.py but identifies controls regions (methylEMRs) that are methylated in at least one of the two methylomes. See sample data files “sample\_intersected\_CGmap\_CHG.gz” and “sample\_intersected\_CGmap\_CHG.gz” to test scripts.

mCHH regions were identified from the merged endosperm CGmap using MR\_Finder.py, parameters as follows: binSize = 200, minCov = 2, minCountC = 5, minMeth = .2, context1 = 'CHH', context2 = 'CHH'. See sample data file “sample\_CGmap.gz” to test script.

CHG unmethylated regions (UMRs) were identified from the merged embryo CGmap using UMR\_Finder.py, parameters as follows: binSize = 200, minCov = 2, minCountC = 5, maxMeth = .2, context1 = 'CHG', context2 = 'CHG'. See sample data file “sample\_CGmap.gz” to test script.