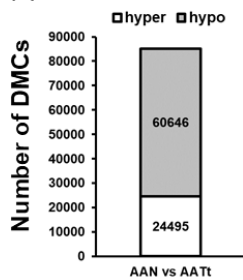
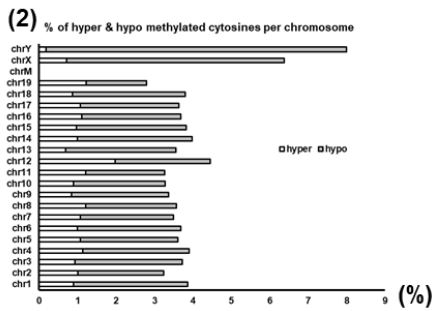


# A) AAN vs AATt

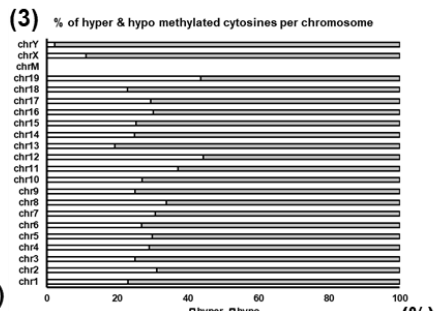
(1)



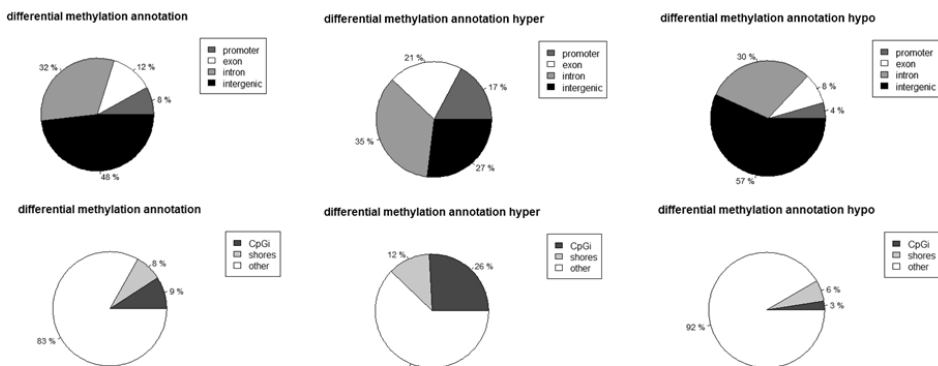
(2)



(3)

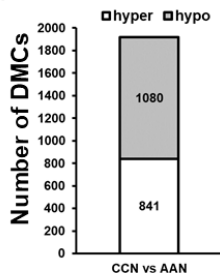


(4)

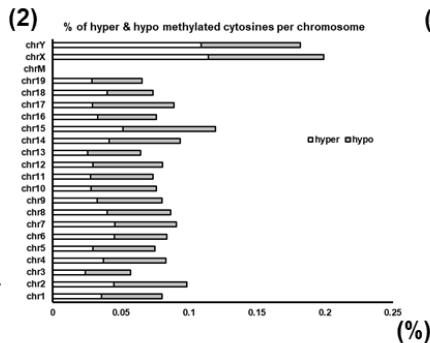


# B) CCN vs AAN

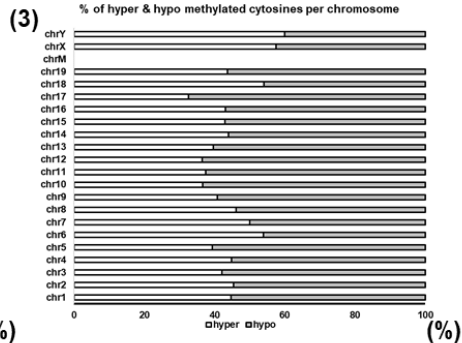
(1)



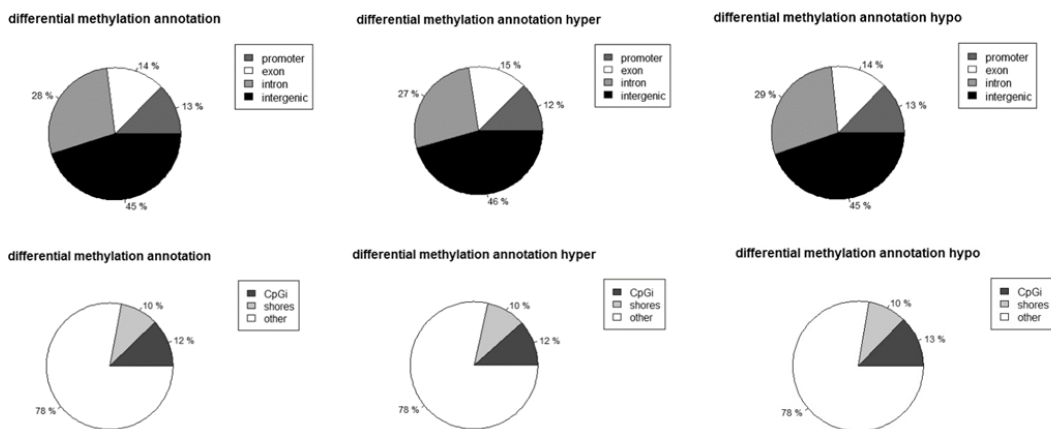
(2)



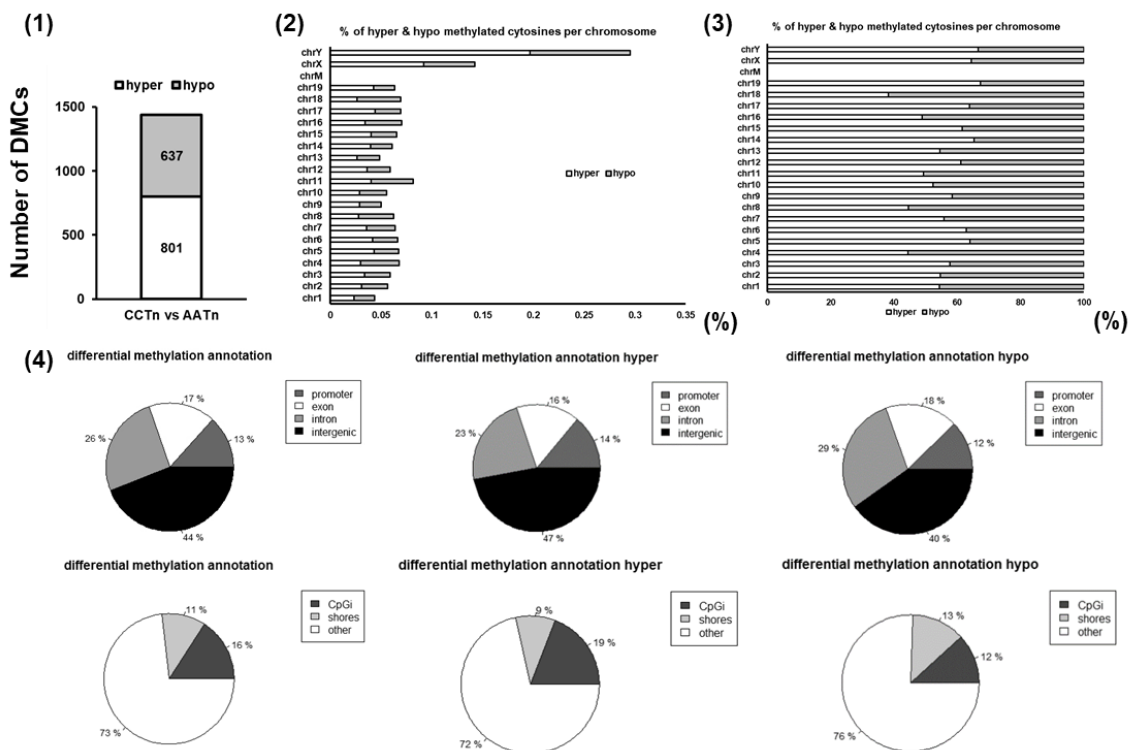
(3)



(4)



### C) CCTn vs AATn



### D) CCTt vs AATt

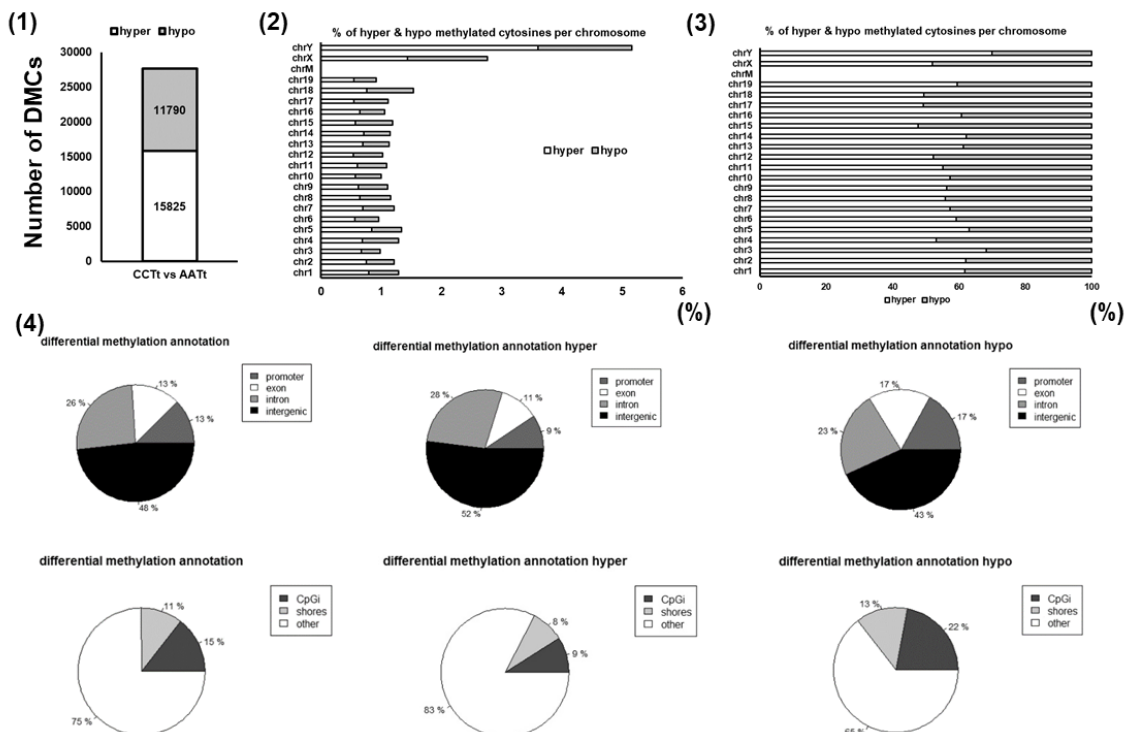


Figure S2

The features of DMCs obtained by analysis of RRBS data using methylKit package. In A) AATt compared to AAN, B) AAN compared to CCN, C) AATn compared to CCTn, and D) AATt compared to CCTt, (1) number of DMCs (white; hypermethylated, gray; hypomethylated), (2) % of hyper and hypo DMCs in detected CpGs per chromosome, (3) % of hyper and hypo DMCs in DMCs per chromosome, (4) annotation data of DMCs, are shown respectively. The analysis was done under the default condition of methylKit.