**Supplementary table and figure legends**

**Supplementary Table S1.**

List of selected genes

Genes selected for the study using GO and GeneCard databases and literature search to represent 10 epigenetic sub-pathways, specifically DNA methylation, DNA demethylation, histone acetylation, histone deacetylation, chromatin remodeling, histone methylation, histone demethylation, other histone modification, chromatin modification and histones.

**Supplementary Table S2.**

List of software and databases used for the analysis and functional follow up

**Supplementary Table S3.**

Significant associations of the ASSET meta-analysis

Although the method tests for associations of both directions (preventive and susceptible), here we report only the significant direction.

**Supplementary Table S4.**

Result of the FunciSNP analysis.

Summary of the functional annotation of all significant SNPs based on FunciSNP (SNPs that were annotated as not functional are not listed).

**Supplementary Table S5.**

Summary of candidate genes with identified risk associations and previously in GWAS identified SNPs in the respective regions.

Summary of candidate genes with identified risk associations, chromosomal region, previously through GWAS identified risk associations in these regions and list of additional genes located in the selected regions.

**Supplementary Fig. S1.**

Diagram of SNP selection and functional look-up of hits within epigenetic pathways.

Flow chart of SNP selection and functional follow-up of hits within epigenetic pathways using different databases and software packages.

**Supplementary Fig. S2.**

Venn diagrams showing the number of SNPs associated across all five cancer types, without differentiation for subtypes. A. Including *MORF4L1*, B. Excluding *MORF4L1*\*

\*http://bioinformatics.psb.ugent.be/webtools/Venn/

**Supplementary Fig. S3.**

Locuszoom plots of the regions with pleiotropic association.

(A) *TNP1* (2q35), (B) *RUVBL1* and *GATA2* (3q21), (C) *PHC3* (3q26), (D) *TET2* (4q24), (E) *POU5F1, BAG6* and *EHMT2* (6p21),(F) *L3MBTL3* (6q23), (G) *HDAC9* (7p21), (H) *LOXL2* (8p21), (I) *BRCA2* (13q12), (J) *WDR61* and *MORF4L1* (15q25), (K) *TADA2A* (17q12), (L) *BABAM1* (19p13), (M) *DPF1* (19q13) and (N) *TGFB1* (19q13).