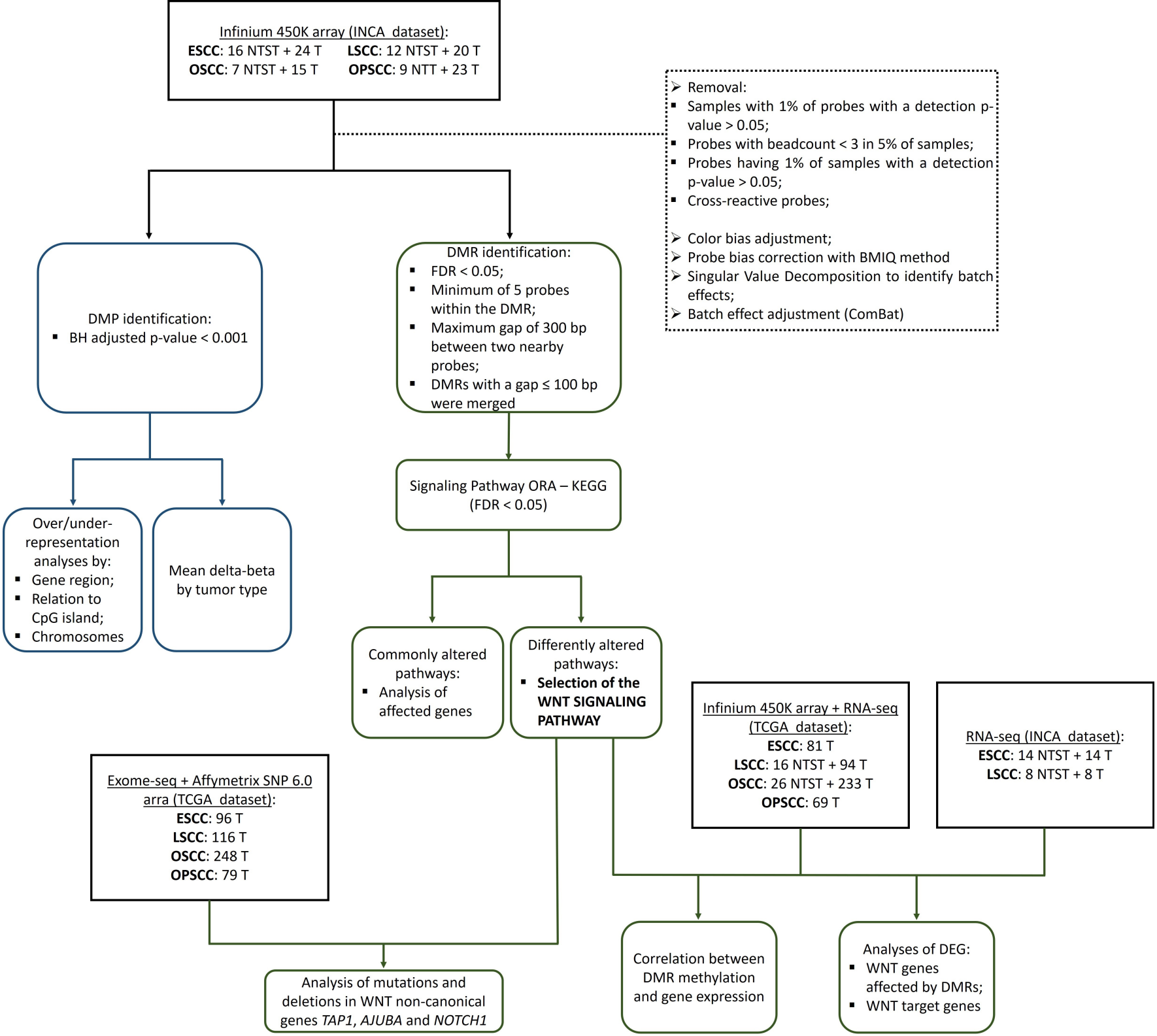
Infinium 450K array (INCA dataset):
ESCC: 16 NTST + 24 T
LSCC: 12 NTST + 20 T
OSCC: 7 NTST + 15 T
OPSCC: 9 NTT + 23 T
Removal:
Samples with 1% of probes with a detection p-value > 0.05;
Probes with beadcount < 3 in 5% of samples;
Probes having 1% of samples with a detection p-value > 0.05;
Cross-reactive probes;
Color bias adjustment;
Probe bias correction with BMIQ method
Singular Value Decomposition to identify batch effects;
Batch effect adjustment (ComBat)
DMP identification:
BH adjusted p-value < 0.001
DMR identification:
FDR < 0.05;
Minimum of 5 probes within the DMR;
Maximum gap of 300 bp between two nearby probes;
DMRs with a gap ≤ 100 bp were merged
Over/under-representation analyses by:
Gene region;
Relation to CpG island;
Chromosomes
Mean delta-beta by tumor type
Signaling Pathway ORA – KEGG (FDR < 0.05)
Commonly altered pathways:
Analysis of affected genes
Differently altered pathways:
Selection of the WNT SIGNALING PATHWAY
Infinium 450K array + RNA-seq (TCGA dataset):
ESCC: 81 T
LSCC: 16 NTST + 94 T
OSCC: 26 NTST + 233 T
OPSCC: 69 T
RNA-seq (INCA dataset):
ESCC: 14 NTST + 14 T
LSCC: 8 NTST + 8 T
Exome-seq + Affymetrix SNP 6.0 arra (TCGA dataset):
ESCC: 96 T
LSCC: 116 T
OSCC: 248 T
OPSCC: 79 T
Analysis of mutations and deletions in WNT non-canonical genes TAP1, AJUBA and NOTCH1
Correlation between DMR methylation and gene expression
Analyses of DEG:
WNT genes affected by DMRs;
WNT target genes