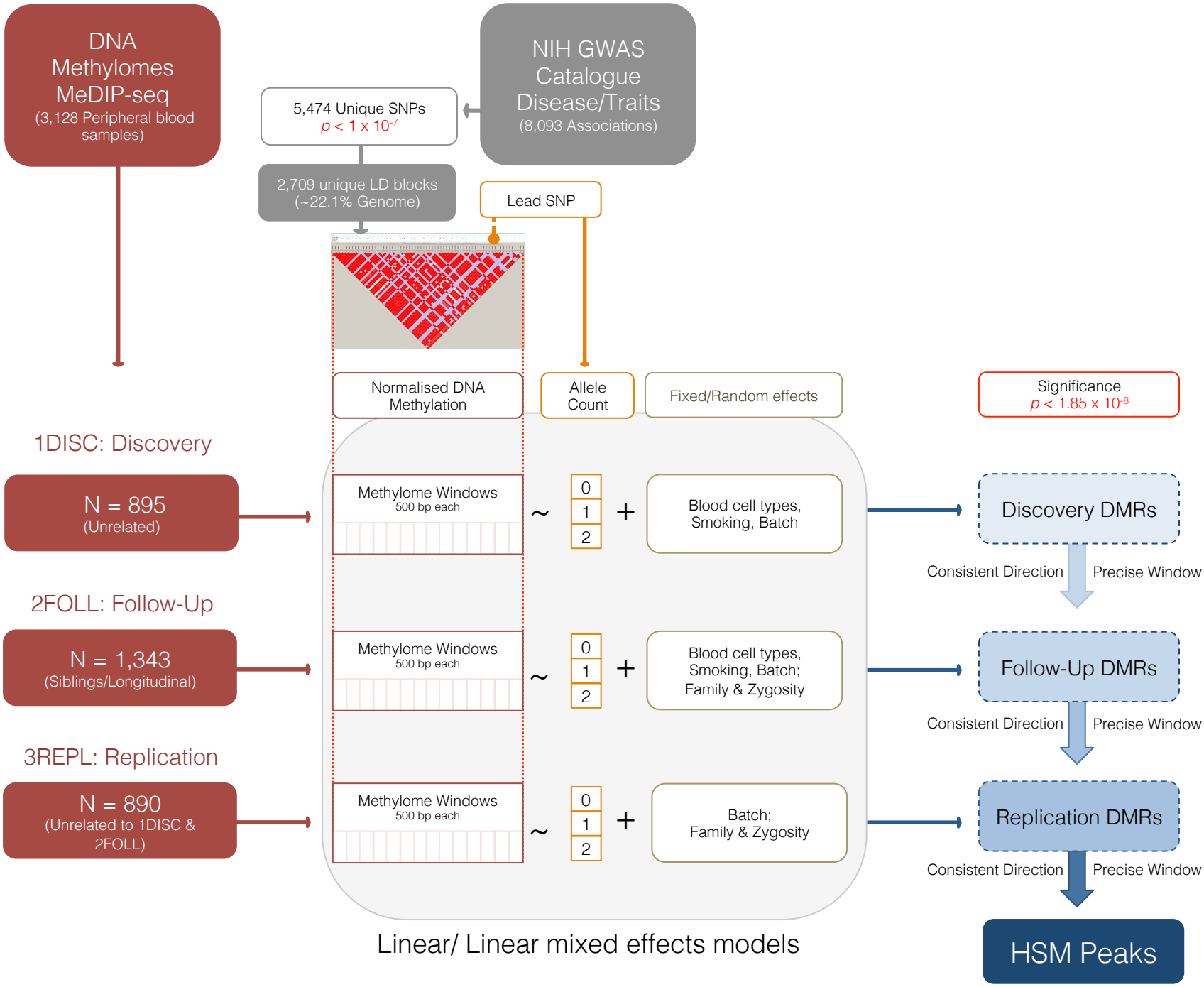
DNA Methylomes MeDIP-seq
(3,128 Peripheral blood samples)
NIH GWAS Catalogue Disease/Traits
(8,093 Associations)
5,474 Unique SNPs
p < 1 x 10-7
2,709 unique LD blocks
(~22.1% Genome)
Lead SNP
Normalised DNA Methylation
Allele Count
Fixed/Random effects
Significance
p < 1.85 x 10-8
1DISC: Discovery
N = 895
(Unrelated)
2FOLL: Follow-Up
N = 1,343
(Siblings/Longitudinal)
3REPL: Replication
N = 890
(Unrelated to 1DISC & 2FOLL)
Methylome Windows
500 bp each
~
0
1
2
+
Blood cell types, Smoking, Batch
Blood cell types, Smoking, Batch; Family & Zygosity
Batch; Family & Zygosity
Discovery DMRs
Follow-Up DMRs
Replication DMRs
Consistent Direction
Precise Window
HSM Peaks
Linear/ Linear mixed effects models