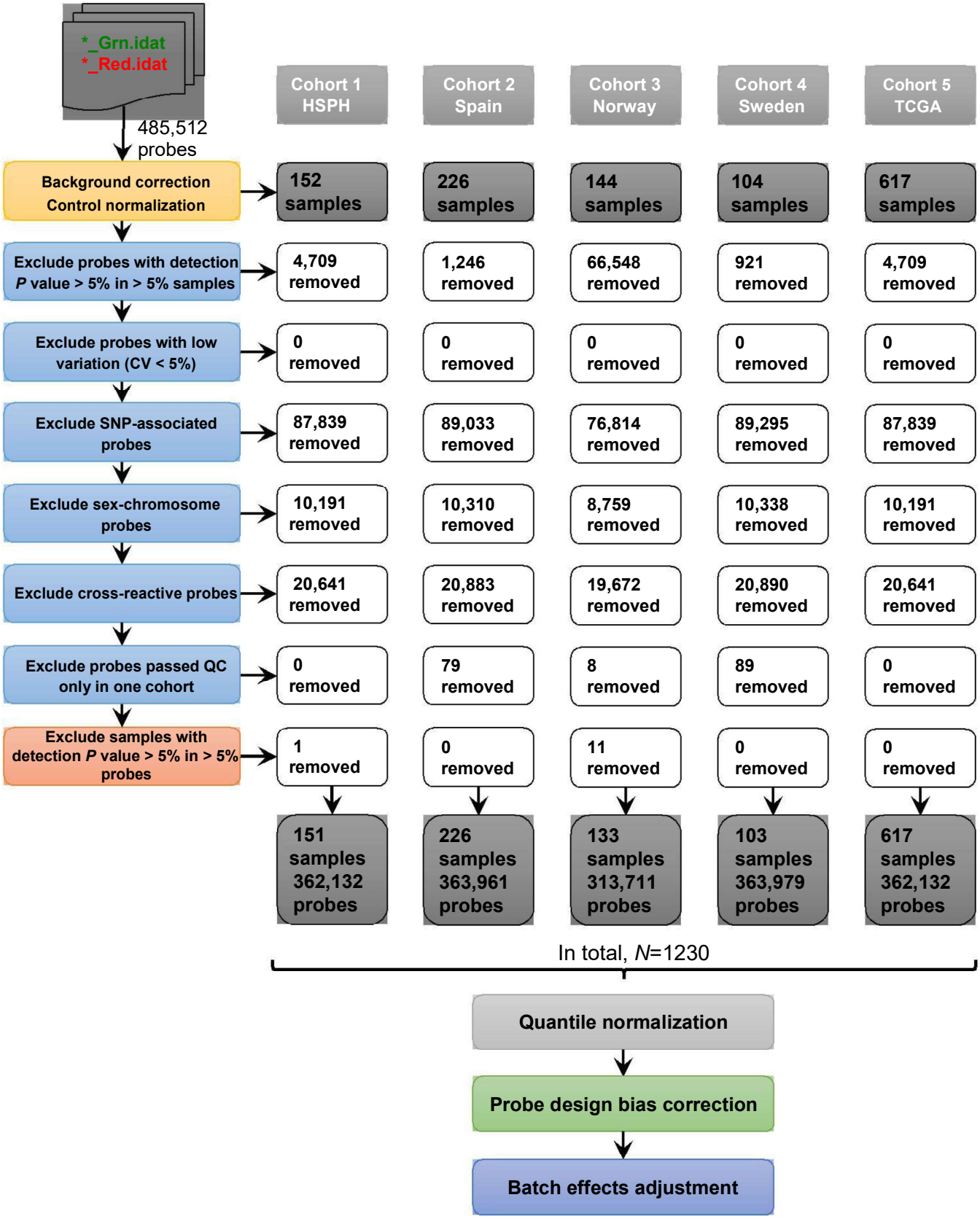
Figure S1


*_Grn.idat
*_Red.idat
485,512 probes
Cohort 1 HSPH
Cohort 2 Spain
Cohort 3 Norway
Cohort 4 Sweden
Cohort 5 TCGA
Background correction Control normalization
152 samples
226 samples
144 samples
104 samples
617 samples
Exclude probes with detection P value > 5% in > 5% samples
4,709 removed
1,246 removed
66,548 removed
921 removed
4,709 removed
Exclude probes with low variation (CV < 5%)
0 removed
0 removed
0 removed
0 removed
0 removed
Exclude SNP-associated probes
87,839 removed
89,033 removed
76,814 removed
89,295 removed
87,839 removed
Exclude sex-chromosome probes
10,191 removed
10,310 removed
8,759 removed
10,338 removed
10,191 removed
Exclude cross-reactive probes
20,641 removed
20,883 removed
19,672 removed
20,890 removed
20,641 removed
Exclude probes passed QC only in one cohort
0 removed
79 removed
8 removed
89 removed
0 removed
Exclude samples with detection P value > 5% in > 5% probes
1 removed
0 removed
11 removed
0 removed
0 removed
151 samples 362,132 probes
226 samples 363,961 probes
133 samples 313,711 probes
103 samples 363,979 probes
617 samples 362,132 probes
In total, N=1230
Quantile normalization
Probe design bias correction
Batch effects adjustment