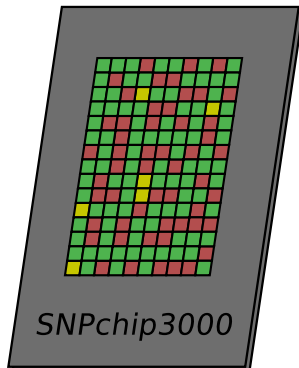


Genotyping



500568 SNPs (Affy 500k)
2000 Cases (T1D)
1500 Controls (NBS)

- 10536 chrX SNPs
- 37 excluded Cases
- 42 excluded Controls

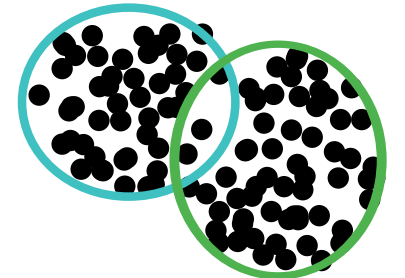
490032 SNPs
1963 Cases (T1D)
1458 Controls (NBS)

Split

Discovery Group
981 Cases (T1D)
729 Controls (NBS)

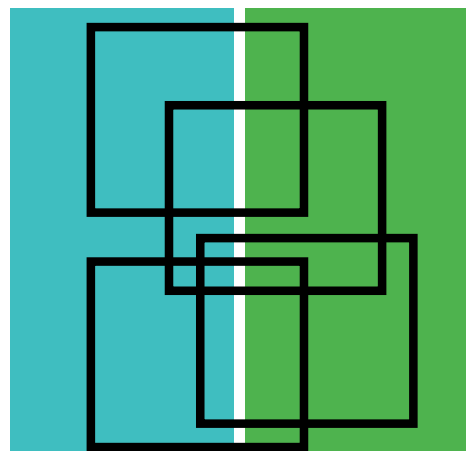
Validation Group
982 Cases (T1D)
729 Controls (NBS)

Validation



982 Cases (T1D)
729 Controls (NBS)
5 SNPs
AUC = 0.8395

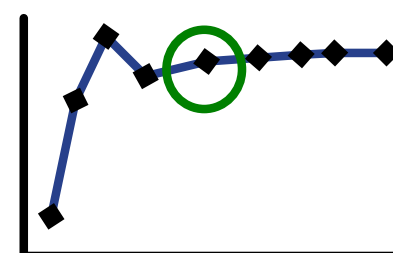
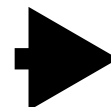
Bootstrap Sub-sampling



100 Replicates:
490 Cases (T1D)
364 Controls (NBS)
24501 SNPs (Top 5%)
[statistic: genotype χ^2]

Consistent Set:
[observed in all 100 replicates]
981 Cases (T1D)
729 Controls (NBS)
458 SNPs

Refinement



- 424 linked SNPs
34 SNPs
Optimal set size = 5 SNPs



SNPs
only