Numero of scenario	Dataset	Size of training set	Causal SNPs (number and location)	Distribution of effects	Heritability	Simulation model	Methods
1	**All 22 chromosomes**	**6000**	**30 in HLA** **30 in all** **300 in all** **3000 in all**	**Gaussian** Laplace	**0.8** 0.5	**simple** fancy	**PRS** **logit-simple** logit-triple (T-Trees)
2	Chromosome 6 only	-	-	-	-	simple	PRS logit-simple
3	**All 22 chromosomes**	**1000** **2000** **3000** **4000** **5000**	**300 in all**	-	-	-	-