

Table S4 Power calculation for GWAS with 154 lines

Minor Allele Frequency	Effect Size*				
	0.75	1	1.25	1.5	2
0.01	0.00	0.00	0.00	0.00	0.00
0.05	0.00	0.00	0.01	0.03	0.26
0.1	0.00	0.02	0.12	0.39	0.94
0.2	0.02	0.19	0.63	0.94	1.00
0.3	0.06	0.45	0.90	1.00	1.00
0.4	0.11	0.60	0.96	1.00	1.00
0.5	0.13	0.66	0.97	1.00	1.00

* Effect size is measured as the shift in the phenotype mean in units of s.d. for the trait

The calculation is done using the t-distribution. The R-code is attached below:

```
myPower.t <- function(effect.size=1,alpha=0.05,m,n){
  ## Power for GWAS t test
  ## calculate power for a t test comparing two populations with equal variance but unequal sample sizes
  ## m, n: sample size of each allele class, not to be confused with m above
  df = m+n-2
  A = 1/sqrt(1/m+1/n) ## factor for calculating t statistics
  T = qt(1-alpha/2,m+n-2)
  T1 <- T-effect.size*A
  beta <- pt(T1,m+n-2)
  return(1-beta)
}
## plot power of GWAS t test ##
alpha1=.05/1.37e6
power <- NULL
effect.size <- c(0.75,1,1.25,1.5,2)
freq <- c(0.01,0.05,0.1,0.2,0.3,0.4,0.5)
N = 154 # size of GWAS mapping population
for(p in freq){
  m = as.integer(N*p)
  n = N-m
  power <- rbind(power, sapply(effect.size,function(x) myPower.t(x,alpha1,m,n)))
}
dimnames(power) <- list("freq"=freq,"effect.size"=effect.size)
```