Table S4 Power calculation for GWAS with 154 lines

<table>
<thead>
<tr>
<th>Minor Allele Frequency</th>
<th>Effect Size*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.75</td>
</tr>
<tr>
<td>0.01</td>
<td>0.00</td>
</tr>
<tr>
<td>0.05</td>
<td>0.00</td>
</tr>
<tr>
<td>0.1</td>
<td>0.00</td>
</tr>
<tr>
<td>0.2</td>
<td>0.02</td>
</tr>
<tr>
<td>0.3</td>
<td>0.06</td>
</tr>
<tr>
<td>0.4</td>
<td>0.11</td>
</tr>
<tr>
<td>0.5</td>
<td>0.13</td>
</tr>
</tbody>
</table>

* 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:

```R
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)
```