Today is November 26, 2012.

```
> library("vcf2R")
> library("GenomicRanges")


> file = "/home/sgy/jhsph/targeted-sequencing/repo/vcf2R/inst/extdata/snvs.fixed_header.hwe"
> hwe.df <- hwe2R(file = file)
> head(hwe.df)

  chr      pos    chi.sq  p.value homo.major het homo.minor
1   1 18772169  0.000056 1.000000       4494   1          0
2   1 18772190  0.000223 1.000000       4493   2          0
3   1 18772191 15.727310 0.053862       4464  30          1
4   1 18772203  0.000223 1.000000       4493   2          0
5   1 18772218  0.000223 1.000000       4493   2          0
6   1 18772236  0.016134 1.000000       4478  17          0


> file = "/home/sgy/jhsph/targeted-sequencing/repo/vcf2R/inst/extdata/snvs.fixed_header.frq"
> pos.df <- frq2pos(file)
> with(pos.df, table(chr))

chr
    1    10    14    17    20     4     8     9
44713 29857  1559 29486 18740  2444 27639 20751

> pos.gr <- with(pos.df, GRanges(seqnames = paste("chr",
+     chr, sep = ""), ranges = IRanges(start = pos, end = pos),
+     strand = "+"))
> pos.gr

GRanges with 175189 ranges and 0 metadata columns:
          seqnames                 ranges strand
             <Rle>              <IRanges>  <Rle>
      [1]     chr1 [18771811, 18771811]      +
      [2]     chr1 [18771817, 18771817]      +
      [3]     chr1 [18771849, 18771849]      +
      [4]     chr1 [18771875, 18771875]      +
      [5]     chr1 [18771893, 18771893]      +
      [6]     chr1 [18771920, 18771920]      +
      [7]     chr1 [18771931, 18771931]      +
      [8]     chr1 [18772013, 18772013]      +
      [9]     chr1 [18772069, 18772069]      +
      ...      ...                    ...    ...
  [175181]   chr20 [39614777, 39614777]      +
  [175182]   chr20 [39614783, 39614783]      +
  [175183]   chr20 [39614798, 39614798]      +
  [175184]   chr20 [39614826, 39614826]      +
  [175185]   chr20 [39614830, 39614830]      +
  [175186]   chr20 [39614868, 39614868]      +
  [175187]   chr20 [39614885, 39614885]      +
  [175188]   chr20 [39614940, 39614940]      +
```

```
> with(hwe.df, hist(p.value, breaks = 100))
```

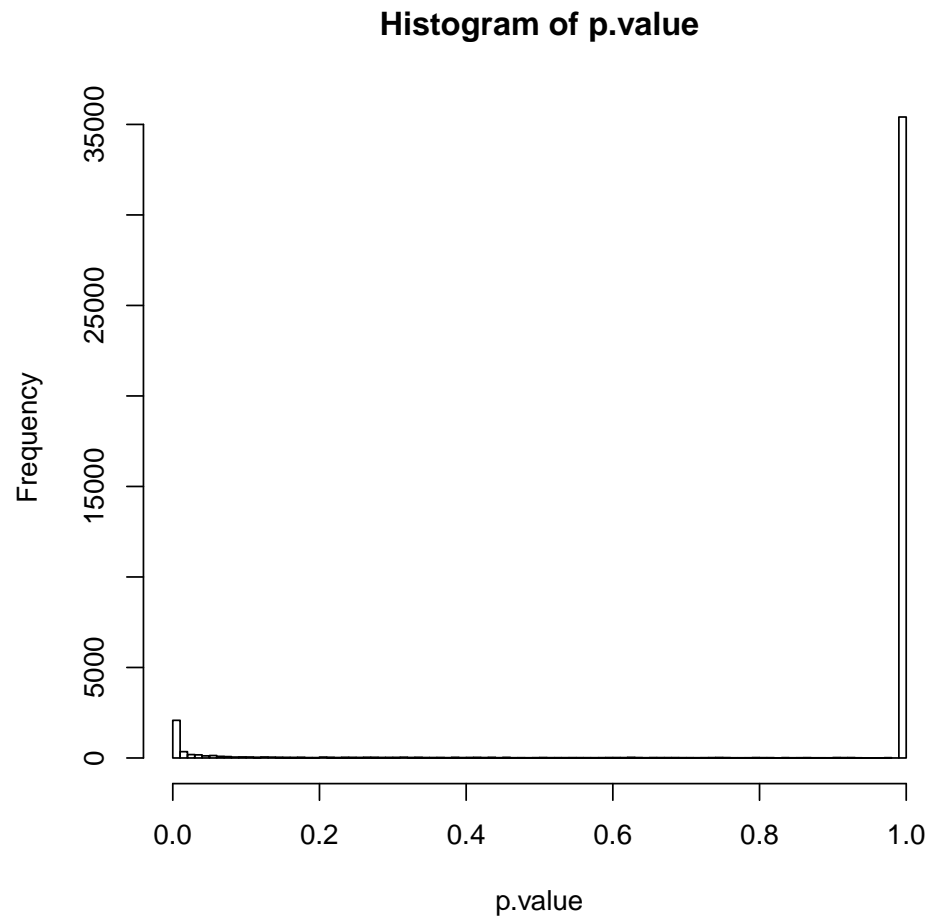**Histogram of p.value**

Figure 1: Histogram of Hardy-Weinberg p-values

```
[175189]     chr20 [39614945, 39614945]        +
---
seqlengths:
  chr1 chr10 chr14 chr17 chr20  chr4  chr8  chr9
    NA    NA    NA    NA    NA    NA    NA    NA
```