

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 = "+"))
> start(pos.gr) <- start(pos.gr) - 1e+05
> end(pos.gr) <- end(pos.gr) + 1e+05
> reduce(pos.gr)
```

GRanges with 13 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
[1]	chr1	[18671811, 19308536]	+
[2]	chr1	[94224232, 95113570]	+
[3]	chr1	[209736758, 210568863]	+
[4]	chr10	[118321219, 119267920]	+
[5]	chr10	[122995899, 123599252]	+
[6]	chr14	[54282326, 54545461]	+
[7]	chr17	[8654615, 9366552]	+
[8]	chr17	[54302391, 55057844]	+
[9]	chr20	[38802239, 39714945]	+
[10]	chr4	[4724627, 5001842]	+
[11]	chr8	[129195457, 130455340]	+
[12]	chr9	[98033217, 98513595]	+
[13]	chr9	[100257256, 100977263]	+

seqlengths:

chr1	chr10	chr14	chr17	chr20	chr4	chr8	chr9
NA	NA	NA	NA	NA	NA	NA	NA

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

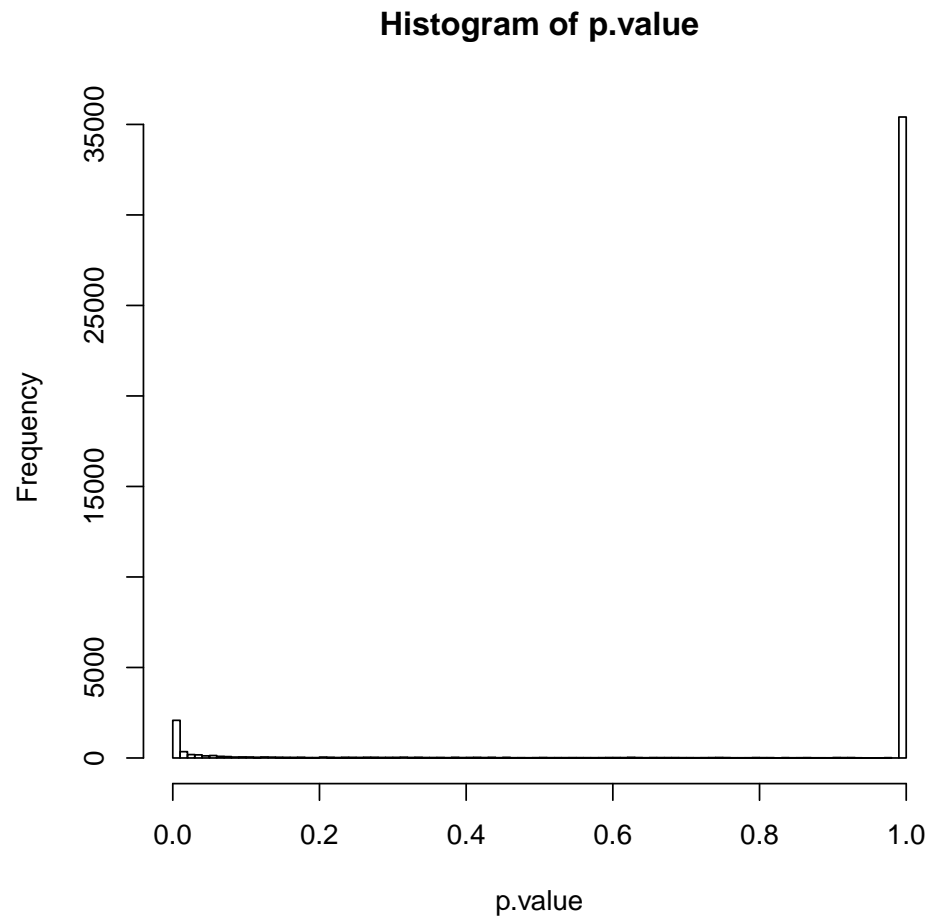


Figure 1: Histogram of Hardy-Weinberg p -values