Generate histograms in Figures 1, S5

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```
## Warning: package 'BiocStyle' was built under R version 3.3.2
```

Load the relevant libraries:

```r
library(readr)
```

```
## Warning: package 'readr' was built under R version 3.3.3
```
```r
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 3.3.3
```
```r
library(fdrtool)
```

```
## Warning: package 'fdrtool' was built under R version 3.3.2
```
```r
library(betareg)
```

```
## Warning: package 'betareg' was built under R version 3.3.3
```
```r
library(splines)
library(Hmisc)
```

```
## Warning: package 'Hmisc' was built under R version 3.3.3
```

```
## Warning: package 'survival' was built under R version 3.3.3
```

```
## Warning: package 'Formula' was built under R version 3.3.2
```

```
## Warning: package 'ggplot2' was built under R version 3.3.3
```
```r
library(ggplot2)
library(IHW)
```

Load the .RData file with the BMI GIANT GWAS meta-analysis data:
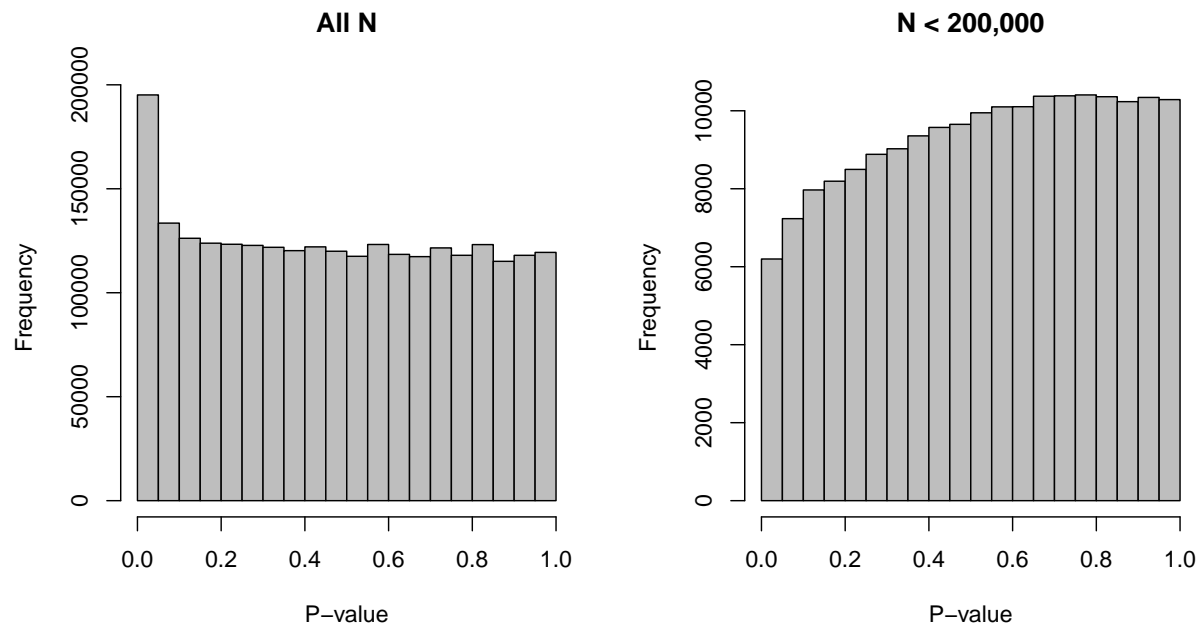
```r
load("BMI_GIANT_GWAS.RData")
```

Generate histogram of p-values for all sample sizes and histogram of p-values for sample sizes < 200,000:

```r
par(mfrow=c(1,2))
hist(BMI_GIANT_GWAS$p, col="grey", main="All N", xlab="P-value")
hist(BMI_GIANT_GWAS$p[BMI_GIANT_GWAS$N < 200000],
     col="grey", main="N < 200,000", xlab="P-value")
```

| All N | N < 200,000 |

Do diagnostic plots as in http://bioconductor.org/packages/release/bioc/vignettes/IHW/inst/doc/introduction_to_ihw.html#diagnostic-plots:

```
BMI_GIANT_GWAS$NGroup <- groups_by_filter(BMI_GIANT_GWAS$N,8)

table(BMI_GIANT_GWAS$NGroup)

##
##      1      2      3      4      5      6      7      8
## 312571 312572 312571 312572 312572 312571 312572 312572
ggplot(BMI_GIANT_GWAS, aes(x=p)) +
  geom_histogram(binwidth = 0.025, boundary = 0) +
  facet_wrap( ~ NGroup, nrow=2)
```
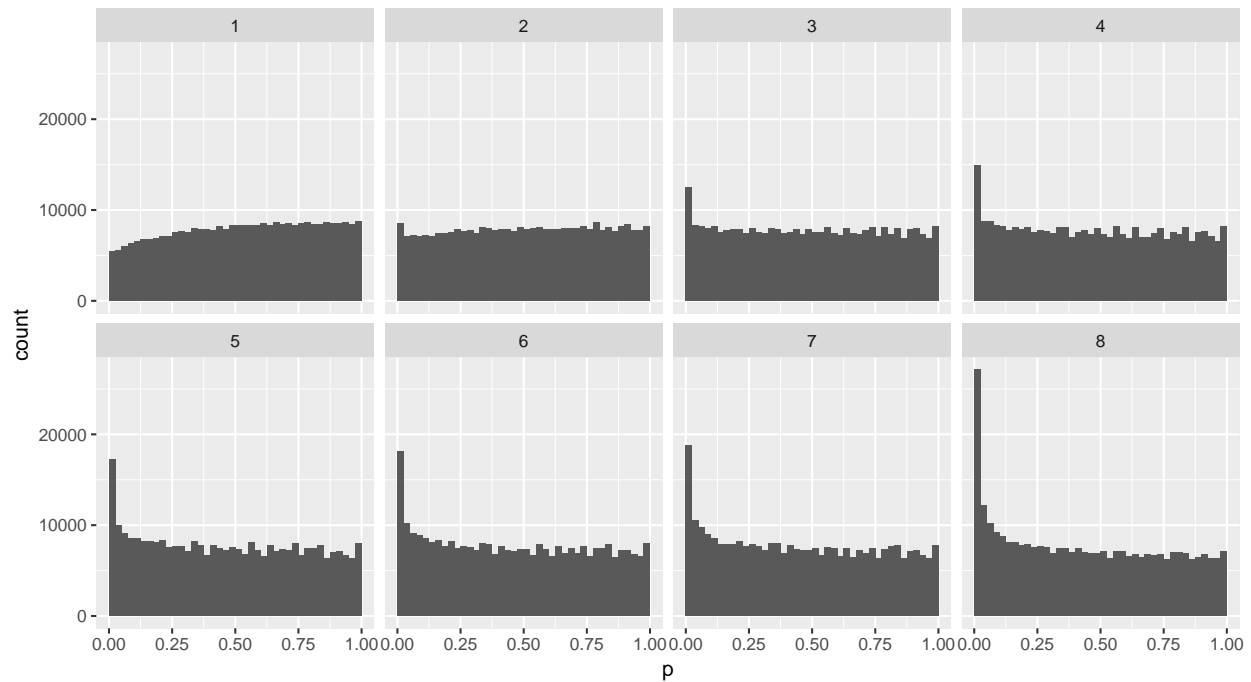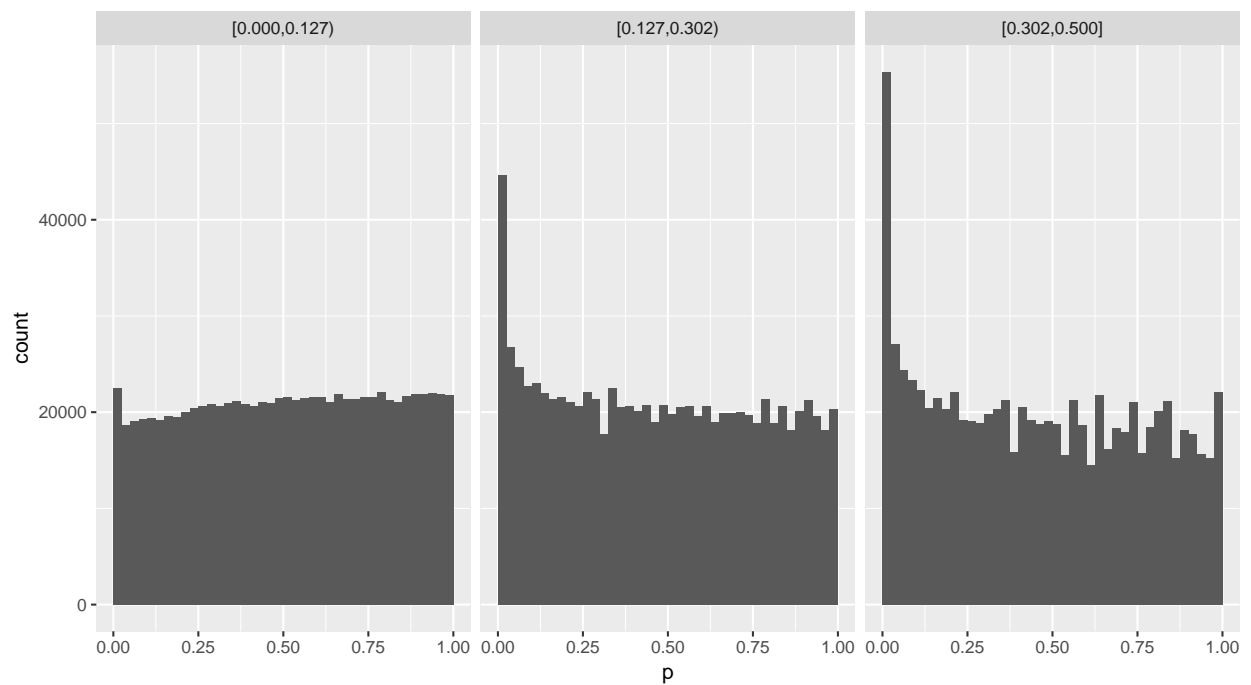
```
ggplot(BMI_GIANT_GWAS, aes(x=p)) +
  geom_histogram(binwidth = 0.025, boundary = 0) +
  facet_wrap( ~ Freq_MAF_Int_Hapmap, nrow=1)
```


Session Information

```
devtools::session_info()
```

```
## Session info -------------------------------------------------------------
##   setting  value
##   version  R version 3.3.1 (2016-06-21)
##   system   x86_64, mingw32
##   ui       RTerm
##   language (EN)
##   collate  English_United States.1252
##   tz       America/New_York
##   date     2017-06-23

## Packages -----------------------------------------------------------------

##   package     * version date       source
##   acepack       1.4.1   2016-10-29 CRAN (R 3.3.3)
##   assertthat    0.1     2013-12-06 CRAN (R 3.3.3)
##   backports     1.0.5   2017-01-18 CRAN (R 3.3.2)
##   base        * 3.3.1   2016-06-21 local
##   base64enc     0.1-3   2015-07-28 CRAN (R 3.3.2)
##   betareg     * 3.1-0   2016-08-06 CRAN (R 3.3.3)
##   BiocGenerics  0.20.0  2016-10-18 Bioconductor
##   BiocStyle   * 2.2.1   2016-11-24 Bioconductor
##   checkmate     1.8.2   2016-11-02 CRAN (R 3.3.3)
##   cluster       2.0.4   2016-04-18 CRAN (R 3.3.1)
##   colorspace    1.3-2   2016-12-14 CRAN (R 3.3.3)
##   data.table    1.10.4  2017-02-01 CRAN (R 3.3.2)
##   datasets    * 3.3.1   2016-06-21 local
##   DBI           0.6     2017-03-09 CRAN (R 3.3.3)
##   devtools      1.13.2  2017-06-02 CRAN (R 3.3.3)
##   digest        0.6.12  2017-01-27 CRAN (R 3.3.3)
##   dplyr       * 0.5.0   2016-06-24 CRAN (R 3.3.3)
##   evaluate      0.10    2016-10-11 CRAN (R 3.3.3)
##   fdrtool     * 1.2.15  2015-07-08 CRAN (R 3.3.2)
##   flexmix       2.3-14  2017-04-28 CRAN (R 3.3.3)
##   foreign       0.8-66  2015-08-19 CRAN (R 3.3.1)
##   Formula     * 1.2-1   2015-04-07 CRAN (R 3.3.2)
##   ggplot2     * 2.2.1   2016-12-30 CRAN (R 3.3.3)
##   graphics    * 3.3.1   2016-06-21 local
##   grDevices   * 3.3.1   2016-06-21 local
##   grid          3.3.1   2016-06-21 local
##   gridExtra     2.2.1   2016-02-29 CRAN (R 3.3.3)
##   gtable        0.2.0   2016-02-26 CRAN (R 3.3.3)
##   Hmisc       * 4.0-3   2017-05-02 CRAN (R 3.3.3)
##   hms           0.3     2016-11-22 CRAN (R 3.3.3)
##   htmlTable     1.9     2017-01-26 CRAN (R 3.3.3)
##   htmltools     0.3.5   2016-03-21 CRAN (R 3.3.3)
##   htmlwidgets   0.8     2016-11-09 CRAN (R 3.3.3)
##   IHW         * 1.2.0   2016-10-18 Bioconductor
##   knitr         1.15.1  2016-11-22 CRAN (R 3.3.1)
##   labeling      0.3     2014-08-23 CRAN (R 3.3.2)
##   lattice     * 0.20-33 2015-07-14 CRAN (R 3.3.1)
##   latticeExtra  0.6-28  2016-02-09 CRAN (R 3.3.3)
##   lazyeval      0.2.0   2016-06-12 CRAN (R 3.3.3)
##   lmtest        0.9-35  2017-02-11 CRAN (R 3.3.3)
##   lpsymphony    1.2.0   2016-10-18 Bioconductor (R 3.3.1)
```

```
##   magrittr     1.5     2014-11-22 CRAN (R 3.3.3)
##   Matrix       1.2-6   2016-05-02 CRAN (R 3.3.1)
##   memoise      1.1.0   2017-04-21 CRAN (R 3.3.3)
##   methods    * 3.3.1   2016-06-21 local
##   modeltools   0.2-21  2013-09-02 CRAN (R 3.3.2)
##   munsell      0.4.3   2016-02-13 CRAN (R 3.3.3)
##   nnet         7.3-12  2016-02-02 CRAN (R 3.3.1)
##   parallel     3.3.1   2016-06-21 local
##   plyr         1.8.4   2016-06-08 CRAN (R 3.3.3)
##   R6           2.2.0   2016-10-05 CRAN (R 3.3.3)
##   RColorBrewer 1.1-2   2014-12-07 CRAN (R 3.3.2)
##   Rcpp         0.12.9  2017-01-14 CRAN (R 3.3.3)
##   readr      * 1.1.1   2017-05-16 CRAN (R 3.3.3)
##   rmarkdown    1.6     2017-06-15 CRAN (R 3.3.1)
##   rpart        4.1-10  2015-06-29 CRAN (R 3.3.1)
##   rprojroot    1.2     2017-01-16 CRAN (R 3.3.3)
##   sandwich     2.3-4   2015-09-24 CRAN (R 3.3.3)
##   scales       0.4.1   2016-11-09 CRAN (R 3.3.3)
##   slam         0.1-40  2016-12-01 CRAN (R 3.3.2)
##   splines    * 3.3.1   2016-06-21 local
##   stats      * 3.3.1   2016-06-21 local
##   stats4       3.3.1   2016-06-21 local
##   stringi      1.1.2   2016-10-01 CRAN (R 3.3.2)
##   stringr      1.2.0   2017-02-18 CRAN (R 3.3.3)
##   survival   * 2.41-3  2017-04-04 CRAN (R 3.3.3)
##   tibble       1.2     2016-08-26 CRAN (R 3.3.3)
##   tools        3.3.1   2016-06-21 local
##   utils      * 3.3.1   2016-06-21 local
##   withr        1.0.2   2016-06-20 CRAN (R 3.3.3)
##   yaml         2.1.14  2016-11-12 CRAN (R 3.3.3)
##   zoo          1.8-0   2017-04-12 CRAN (R 3.3.3)
```