

manhattan_plot.R

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```
library("qqman", lib.loc=~ /R/x86_64-redhat-linux-gnu-library/3.3")
```

```
##
```

```
## For example usage please run: vignette('qqman')
```

```
##
```

```
## Citation appreciated but not required:
```

```
## Turner, S.D. qqman: an R package for visualizing GWAS results using Q-Q and manhattan plots. biorXiv
```

```
##
```

```
# Import pc1 gwas data
```

```
pc1 <- read.table("pc1.assoc.logistic",header=TRUE)
```

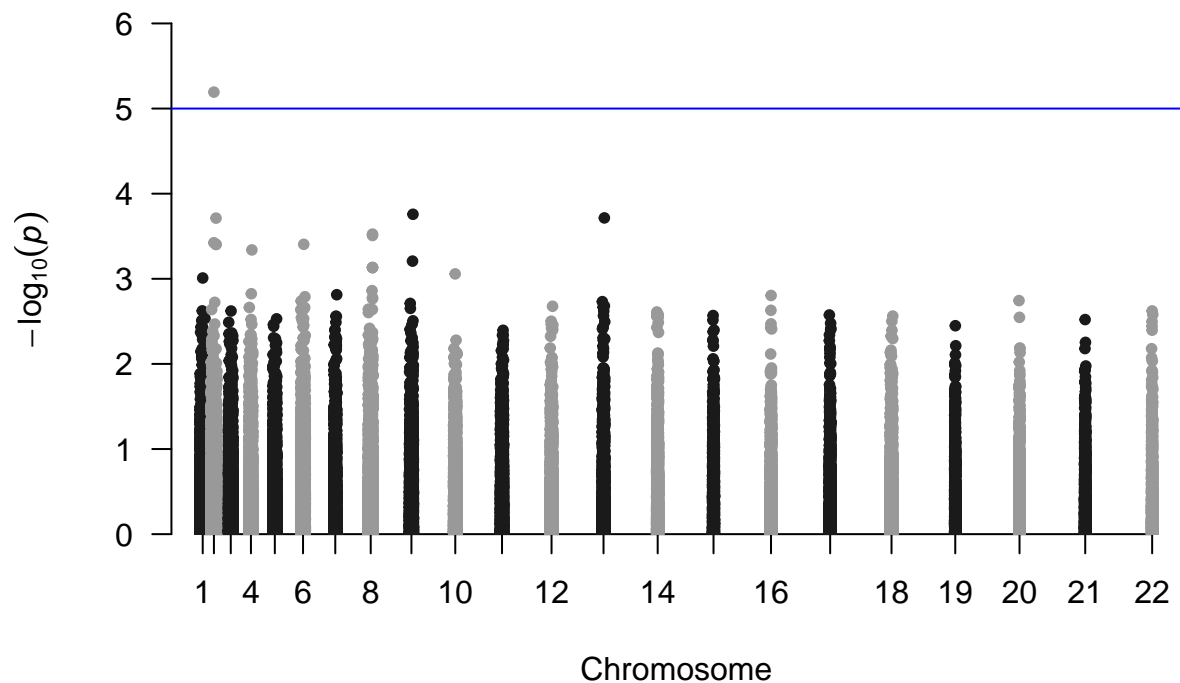
```
# select only tests of SNP
```

```
pc1 <- pc1[pc1$TEST=="ADD",]
```

```
# Plot SNPs P values with suggestive line of significance = -log10(1e-05)
```

```
#png(file="plot.png",width=800,height=600)
```

```
manhattan(pc1[,c("SNP", "CHR", "BP", "P")])
```



```
dev.off()
```

```
## null device
##      1
```

```
# Identify the SNP pass the suggestive line of significance = -log10(1e-05)
head(pc1[order(pc1$P),])
```

##	CHR	SNP	BP	A1	TEST	NMISS	OR	STAT	P	
##	14621	2	rs2222162	10602	1	ADD	89	0.01695	-4.512	6.407e-06
##	70241	9	rs7046471	49725	1	ADD	89	6.16900	3.753	1.747e-04
##	90445	13	rs9585021	64274	1	ADD	88	4.78400	3.728	1.927e-04
##	18119	2	rs4675607	13220	1	ADD	88	0.19870	-3.727	1.938e-04
##	62561	8	rs2395989	44638	1	ADD	89	6.01300	3.617	2.985e-04
##	62573	8	rs10505549	44646	1	ADD	89	6.06300	3.607	3.099e-04

```
# SNP: rs2222162 has a pval of 6.407e-06
```