

FunciSNP: Functional Identification of SNPs with Phenotype by Coincidence with Chromatin Biofeatures Vignette

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Introduction

FunciSNP's aim is to assist in identifying putative functional SNP. Using information from the 1000 genomes database as well as known position of GWAS tagSNP curated for a particular trait or disease, FunciSNP integrates the two data along with sequence information provided by peaks identified from high-throughput sequencing. FunciSNP assumes user will provide processed peaks identified using any available peak algorithm, such as FindPeaks.

This vignette provides a HOW-TO guide to setup and run FunciSNP on your machine. FunciSNP was developed with the idea that a FunciSNP user will have uninterrupted high-speed internet access as well as a desktop machine with more than 4 multiple cores. If user is using a windows machine, multiple cores options will not work and thus total time to complete initial FunciSNP analysis will take longer than expected.

Using a 64bit Linux machine running 11.04 Ubuntu with 24gig RAM and 8 cores and academic high-speed internet access, the amount of time to complete 99 tagSNP across 20 different biofeatures took less than 30 min to complete. We anticipate it would take about 2 hours to complete on a single core.

Load FunciSNP+other useful libraries

```
> #When package is offically posted in Bioconductor, uncomment next 2 lines.
> #source("http://bioconductor.org/biocLite.R")
> #biocLite("FunciSNP");
> ## Following two packages and options() are not required to run 'FunciSNP' but
> #will enhance the analysis experience.
> #library(setwidth); ## Automatically set the value of options("width") when the
> #terminal emulator is resized
> #library(colorout); ## colorize R output on terminal emulators
> options(width=80);
> ##FunciSNP library and other related libraries needed.
> library("org.Hs.eg.db");
> library("gplots");
> library("gtools");
> library("ggplot2");
> library("matlab");
> library(FunciSNP);
> package.version("FunciSNP");

[1] "0.1.7"
```

Identify FuncySNP using published GWAS SNPs and publicly available biological features (ENCODE ChIPseq peaks)

FuncySNP()

This is the main funtion of FunciSNP. It will identify correlated SNPs which are in linkage disequilibrium (LD) to a known disease associated tagSNP. It will also determine if the correlated SNP in LD to the tagSNP overlaps a genomic biological feature. Correlated SNPs are directly imported from the current public release of the 1000 genomes database. 1000 genomes ftp servers available for the 1000 genomes public data: 1) National Center for Biotechnology Information (NCBI) ftp://ftp-trace.ncbi.nih.gov/1000genomes/; 2) European Bioinformatics Institute (EBI) ftp://ftp.1000genomes.ebi.ac.uk/vol1/.

Correlated SNPs in LD to a tagSNP and overlapping genomic biological features are known as putative functional SNPs (also defined as 'FuncySNP' elsewhere in the package.).

As an example, we collected SNPs identified by GWAS for Glioblastoma multiforme (GBM). In this example, GBM includes lower grade glioma, thus we label all objects with 'glioma'.

```
> ## Full path to the example GWAS SNP regions file for Glioblastoma
> # (collected from SNPedia on Jan 2012)
> glioma.snp <- file.path(system.file('extdata', package='FunciSNP'),
+ dir(system.file('extdata',package='FunciSNP'), pattern='.snp$'));
> #glioma.snp;
> ## Full path to the example biological features BED files
```

```

> # derived from the ENCODE project for Glioblastoma U-87 cell lines.
> glioma.bio <- system.file('extdata',package='FunciSNP');
> #glioma.bio;
> ## FunciSNP analysis, extracts correlated SNPs from the
> # 1000 genomes db ("ncbi" or "ebi") and finds overlaps between
> # correlated SNP and biological features and then
> # calculates LD (Rsquare, Dprime, distance, p-value).
> ## Depending on number of CPUs and internet connection, this step may take
> # some time. Please consider using a unix machine to access multiple cores.
> # glioma <- FunciSNP(snp.regions.file=glioma.snp,
> #                   bio.features.loc = glioma.bio,
> #                   bio.features.TSS=FALSE);
> # glioma;
> # summary(glioma);
>
> ## The glioma example set above is called directly by
> data(glioma);
> glioma;

```

TagSNP List with 4 Tag SNPs and

778 nearby, potentially correlated SNPs, that overlap at least one biofeature
 \$`R squared: 0.1`

	Total	R.squared.cuff.0.1	Percent
tagSNPs	4	3	75.00
1kSNPs	778	64	8.23
bio.features	3	3	100.00

\$`R squared: 0.5`

	Total	R.squared.cuff.0.5	Percent
tagSNPs	4	3	75.00
1kSNPs	778	44	5.66
bio.features	2	2	100.00

\$`R squared: 0.9`

	Total	R.squared.cuff.0.9	Percent
tagSNPs	4	1	25.00
1kSNPs	778	13	1.67
bio.features	2	2	100.00

```
> summary(glioma);
```

TagSNP List with 4 Tag SNPs and

778 nearby, potentially correlated SNPs, that overlap at least one biofeature
 Number of potentially correlated SNPs

overlapping at least x biofeatures, per Tag SNP at an R squared of

\$`R squared: 0.1 in 4 Tag SNPs with a total of `

	bio.1	bio.2
rs4977756	3	0
rs498872	9	2
rs6010620	52	9
TOTAL # CORRELATED SNPS	64	11

```
$`R squared: 0.5 in 4 Tag SNPs with a total of `
```

	bio.1	bio.2
rs4977756	2	0
rs498872	2	0
rs6010620	40	6
TOTAL # CORRELATED SNPS	44	6

```
$`R squared: 0.9 in 2 Tag SNPs with a total of `
```

	bio.1
rs6010620	13
TOTAL # CORRELATED SNPS	13

```
> class(glioma);
```

```
[1] "TSList"
attr(,"package")
[1] "FunciSNP"
```

Annotating newly identified FuncySNPs

All known genomic features (exon, intron, 5'UTR, 3'UTR, promoter, lincRNA or in gene desert (intergenic)) are used to annotate each newly identified FuncySNP. Information described in this data.frame() is used for all summary plots, table, and to output results in BED format. This step should be completed after running FuncySNP().

```
> glioma.anno <- FunciSNPAnnotateSummary(glioma);
> class(glioma.anno);
```

```
[1] "data.frame"
```

```
> gl.anno <- glioma.anno;
> ## remove rownames for this example section.
> rownames(gl.anno) <- c(1:length(rownames(gl.anno)))
> dim(gl.anno);
```

```
[1] 862 28
```

```
> head(gl.anno); ##
```

	chromosome	bio.feature.start	bio.feature.end	bio.feature	corr.snp.id
1	5	1200710	1201809	knownGene.TSS.hg19	chr5:1200720
2	5	1200710	1201809	knownGene.TSS.hg19	chr5:1200766
3	5	1200710	1201809	knownGene.TSS.hg19	chr5:1200817
4	5	1200710	1201809	knownGene.TSS.hg19	chr5:1200946
5	5	1200710	1201809	knownGene.TSS.hg19	chr5:1200976
6	5	1200710	1201809	knownGene.TSS.hg19	chr5:1201033

	corr.snp.position	tag.snp.id	tag.snp.position	D.prime	R.squared	p.value
1	1200720	rs2736100	1286516	NA	NA	1
2	1200766	rs2736100	1286516	NA	NA	1
3	1200817	rs2736100	1286516	NA	NA	1

4	1200946	rs2736100	1286516	NA	NA	1
5	1200976	rs2736100	1286516	1.0000000	0.0022585199	1
6	1201033	rs2736100	1286516	0.1795671	0.0004069606	1
	distance.from.tag	population.count	population	nearest.lincRNA.ID		
1	-85796	286	ASN	TCONS_00010241		
2	-85750	286	ASN	TCONS_00010241		
3	-85699	286	ASN	TCONS_00010241		
4	-85570	286	ASN	TCONS_00010241		
5	-85540	286	ASN	TCONS_00010241		
6	-85483	286	ASN	TCONS_00010241		
	nearest.lincRNA.distancetoFeature	nearest.lincRNA.coverage				
1		-39302		upstream		
2		-39348		upstream		
3		-39399		upstream		
4		-39528		upstream		
5		-39558		upstream		
6		-39615		upstream		
	nearest.TSS.GeneSymbol	nearest.TSS.refseq	nearest.TSS.ensembl			
1	SLC6A19	NM_001003841;NP_001003841	ENSG00000174358			
2	SLC6A19	NM_001003841;NP_001003841	ENSG00000174358			
3	SLC6A19	NM_001003841;NP_001003841	ENSG00000174358			
4	SLC6A19	NM_001003841;NP_001003841	ENSG00000174358			
5	SLC6A19	NM_001003841;NP_001003841	ENSG00000174358			
6	SLC6A19	NM_001003841;NP_001003841	ENSG00000174358			
	nearest.TSS.coverage	nearest.TSS.distancetoFeature	Promoter	utr5	Exon	Intron
1	upstream	-990	YES	NO	NO	NO
2	upstream	-944	YES	NO	NO	NO
3	upstream	-893	YES	NO	NO	NO
4	upstream	-764	YES	NO	NO	NO
5	upstream	-734	YES	NO	NO	NO
6	upstream	-677	YES	NO	NO	NO
	utr3	Intergenic				
1	NO	NO				
2	NO	NO				
3	NO	NO				
4	NO	NO				
5	NO	NO				
6	NO	NO				

> names(gl.anno);

[1]	"chromosome"	"bio.feature.start"
[3]	"bio.feature.end"	"bio.feature"
[5]	"corr.snp.id"	"corr.snp.position"
[7]	"tag.snp.id"	"tag.snp.position"
[9]	"D.prime"	"R.squared"
[11]	"p.value"	"distance.from.tag"
[13]	"population.count"	"population"
[15]	"nearest.lincRNA.ID"	"nearest.lincRNA.distancetoFeature"
[17]	"nearest.lincRNA.coverage"	"nearest.TSS.GeneSymbol"

```

[19] "nearest.TSS.refseq"          "nearest.TSS.ensembl"
[21] "nearest.TSS.coverage"       "nearest.TSS.distancetoFeature"
[23] "Promoter"                   "utr5"
[25] "Exon"                       "Intron"
[27] "utr3"                       "Intergenic"

> summary(gl.anno[,c(1:18,20:28)]);

      chromosome      bio.feature.start      bio.feature.end
Length:862      Min.   : 1200710      Min.   : 1201809
Class :character 1st Qu.: 62295044      1st Qu.: 62295926
Mode  :character Median : 62326155      Median : 62337392
                        Mean  : 65165595      Mean   : 65169512
                        3rd Qu.: 62374564      3rd Qu.: 62376020
                        Max.   :118531575      Max.   :118532674

      bio.feature      corr.snp.id      corr.snp.position
knownGene.TSS.hg19:372 chr11:118442863: 2      Min.   : 1200720
TFBS_Nrsf_U87      : 22      chr11:118443036: 2      1st Qu.: 62295889
TFBS_Pol2_U87      :468      chr11:118443046: 2      Median : 62327508
                        chr11:118478342: 2      Mean   : 65167605
                        chr20:62289690 : 2      3rd Qu.: 62375255
                        chr20:62289873 : 2      Max.   :118532636
                        (Other)      :850

      tag.snp.id      tag.snp.position      D.prime      R.squared
rs2736100: 96      Min.   : 1286516      Min.   :7.835e-04      Min.   :9.520e-08
rs4977756: 25      1st Qu.: 62309839      1st Qu.:9.338e-01      1st Qu.:7.765e-04
rs498872 :166      Median : 62309839      Median :1.000e+00      Median :4.501e-03
rs6010620:575      Mean   : 65163135      Mean   :8.995e-01      Mean   :1.258e-01
                        3rd Qu.: 62309839      3rd Qu.:1.000e+00      3rd Qu.:2.804e-02
                        Max.   :118477367      Max.   :1.000e+00      Max.   :9.776e-01
                        NA's      :4.710e+02      NA's      :4.710e+02

      p.value      distance.from.tag      population.count      population
Min.   :2.115e-163      Min.   :-100000      Min.   :286.0      ASN: 96
1st Qu.: 1.000e+00      1st Qu.: -19966      1st Qu.:379.0      EUR:766
Median : 1.000e+00      Median : 13942      Median :379.0
Mean   : 7.989e-01      Mean   : 4470      Mean   :368.6
3rd Qu.: 1.000e+00      3rd Qu.: 25290      3rd Qu.:379.0
Max.   : 1.000e+00      Max.   : 67371      Max.   :379.0

      nearest.lincRNA.ID      nearest.lincRNA.distancetoFeature
TCONS_00010241: 96      Min.   : -265183
TCONS_00015797: 25      1st Qu.: -92280
TCONS_00020001:166      Median : 59111
TCONS_00027984: 26      Mean   : 2073
TCONS_00028269:549      3rd Qu.: 73343
                        Max.   : 246019

nearest.lincRNA.coverage      nearest.TSS.GeneSymbol      nearest.TSS.ensembl
downstream:565      TNFRSF6B      :305      ENSG00000243509:305

```

```

inside      : 9          PHLDB1      : 86          ENSG00000019144: 86
upstream    :288        ZGPAT       : 68          ENSG00000197114: 68
                                   RTTEL1;TNFRSF6B: 37          ENSG00000229299: 59
                                   SLC6A18      : 34          ENSG0000026036: 37
                                   (Other)      :202          ENSG00000244977: 36
                                   NA's         :130          (Other)         :271
nearest.TSS.coverage nearest.TSS.distancetoFeature Promoter   utr5
downstream:103      Min.      :-16454.0      NO :694    NO :825
inside      :311      1st Qu.: -3117.0      YES:168   YES: 37
upstream    :448      Median :   -76.0
                                   Mean      :   890.4
                                   3rd Qu.:  2305.8
                                   Max.      :  28781.0

      Exon      Intron      utr3      Intergenic
NO :776      NO :413      NO :702      NO :810
YES: 86      YES:449      YES:160      YES: 52

```

```
> rm(gl.anno);
```

Summary table used to describe newly identified FuncySNPs

Using a specified Rsquare value (0-1) to subset the data, a table is generated which summarizes the total number of FuncySNPs, associated tagSNPs, and number of overlapping biofeatures. This will provide user a first look at the total number of available FuncySNP at a particular Rsquare cutoff. If geneSum is set to TRUE, a list of gene names is reported instead.

```
> FunciSNPtable(glioma.anno, rsq=0.5);
```

	Total	R.squared.cuff.0.5	Percent
tagSNPs	4	3	75.00
1kSNPs	778	44	5.66
bio.features	2	2	100.00

```
> FunciSNPtable(glioma.anno, rsq=0.5, geneSum=TRUE);
```

	Gene_Names
1	CDKN2B
2	LIME1
3	PHLDB1
4	SLC2A4RG
5	TNFRSF6B
6	TREH
7	ZGPAT
8	RTTEL1;TNFRSF6B

Summary of correlated SNPs overlapping biofeatures

This function helps in determining the number of correlated SNPs overlapping a number of different biofeatures. This is similar to running 'glioma' above. But

now you can specifically call the function and set a pre-determined rsq value to subset the data and thereby obtain a more objective result.

```
> FunciSNPsummaryOverlaps(glioma.anno)
```

	bio.1	bio.2
rs2736100	41	0
rs4977756	12	0
rs498872	59	3
rs6010620	236	40
TOTAL # CORRELATED SNPS	348	43

```
> FunciSNPsummaryOverlaps(glioma.anno, rsq=0.5)
```

	bio.1	bio.2
rs4977756	2	0
rs498872	2	0
rs6010620	40	6
TOTAL # CORRELATED SNPS	44	6

Summary of correlated SNPs for a number of different tagSNPs

After running FunciSNPsummaryOverlaps(), the next question one would like to know is which correlated SNPs overlapping a number of different biofeatures for a number of associated tagSNP. Thus, in the example above, we have determined that we are interested in learning more about the correlated SNPs associated with 'rs6010620' and which overlap at least 2 different biofeatures.

```
> rs6010620 <- FunciSNPidsFromSummary(glioma.anno, tagsnpid="rs6010620",
+ num.features=2, rsq=0.5)
> summary(rs6010620);
```

chromosome	bio.feature.start	bio.feature.end
Length:12	Min. :62326155	Min. :62330994
Class :character	1st Qu.:62329895	1st Qu.:62337392
Mode :character	Median :62354158	Median :62355398
	Mean :62351007	Mean :62353861
	3rd Qu.:62370211	3rd Qu.:62371310
	Max. :62371621	Max. :62372970

bio.feature	corr.snp.id	corr.snp.position	tag.snp.id
knownGene.TSS.hg19:6	rs1056441:2	Min. :62330439	rs2736100: 0
TFBS_Nrsf_U87 :0	rs1291209:2	1st Qu.:62330484	rs4977756: 0
TFBS_Pol2_U87 :6	rs1295810:2	Median :62354704	rs498872 : 0
	rs1741708:2	Mean :62352184	rs6010620:12
	rs6062498:2	3rd Qu.:62370732	
	rs6122159:2	Max. :62372041	
	(Other) :0		
tag.snp.position	D.prime	R.squared	p.value
Min. :62309839	Min. :0.8380	Min. :0.5073	Min. :1.555e-127

1st Qu.:62309839	1st Qu.:0.8979	1st Qu.:0.5365	1st Qu.:1.555e-127
Median :62309839	Median :0.9204	Median :0.7588	Median :1.868e-117
Mean :62309839	Mean :0.9039	Mean :0.6967	Mean :1.046e-81
3rd Qu.:62309839	3rd Qu.:0.9234	3rd Qu.:0.8092	3rd Qu.:2.955e-89
Max. :62309839	Max. :0.9234	Max. :0.8092	Max. :6.274e-81

distance.from.tag	population.count	population	nearest.lincRNA.ID
Min. :20600	Min. :379	ASN: 0	TCONS_00010241: 0
1st Qu.:20645	1st Qu.:379	EUR:12	TCONS_00015797: 0
Median :44865	Median :379		TCONS_00020001: 0
Mean :42345	Mean :379		TCONS_00027984: 0
3rd Qu.:60893	3rd Qu.:379		TCONS_00028269:12
Max. :62202	Max. :379		

nearest.lincRNA.distancetoFeature	nearest.lincRNA.coverage
Min. :71755	downstream:12
1st Qu.:71800	inside :0
Median :96020	upstream :0
Mean :93500	
3rd Qu.:112048	
Max. :113357	

nearest.TSS.GeneSymbol

SLC2A4RG:6

TNFRSF6B:4

ZGPAT :2

ARCN1 :0

ARFRP1 :0

CDKN2B :0

(Other) :0

NM_020062;NP_064446

NM_003823;NP_003814

NM_001083113;NM_001195653;NM_001195654;NM_032527;NM_181485;NP_001076582;NP_001182582;NP_001182583

NM_001003841;NP_001003841

NM_001037335;NM_033405;NP_001032412;NP_208384

NM_001080441;NP_001073910

(Other)

nearest.TSS.ensembl	nearest.TSS.coverage	nearest.TSS.distancetoFeature
ENSG00000125520:6	downstream:4	Min. :265
ENSG00000243509:4	inside :8	1st Qu.:726
ENSG00000197114:2	upstream :0	Median :1764
ENSG00000019144:0		Mean :1566
ENSG00000026036:0		3rd Qu.:2418
ENSG00000049656:0		Max. :2463
(Other) :0		

Promoter	utr5	Exon	Intron	utr3	Intergenic
NO :12	NO :12	NO :12	NO :8	NO :6	NO :10
YES: 0	YES: 0	YES: 0	YES:4	YES:6	YES: 2

```
> dim(rs6010620);  
[1] 12 28  
> class(rs6010620);  
[1] "data.frame"  
> ## See FunciSNPbed to visualize this data in a genome browser.
```

Plot FunciSNP results

FunciSNPplot is a function developed to plot various types of plots to summarize and assist end-user in making informed discoveries of FunciSNP results. Plots can be stored in a folder for future reference. Most plots were created in publication standard.

The following example plots the distribution of the Rsquare values for each correlated SNP. We recommend attempting this plot before subsetting any data by a specified rsq value. The distribution helps to identify a specific Rsquare value that will provide the most informative discovery.

```
> pdf("glioma_dist.pdf")
> FunciSNPplot(glioma.anno)
> dev.off()
```

```
null device
      1
```

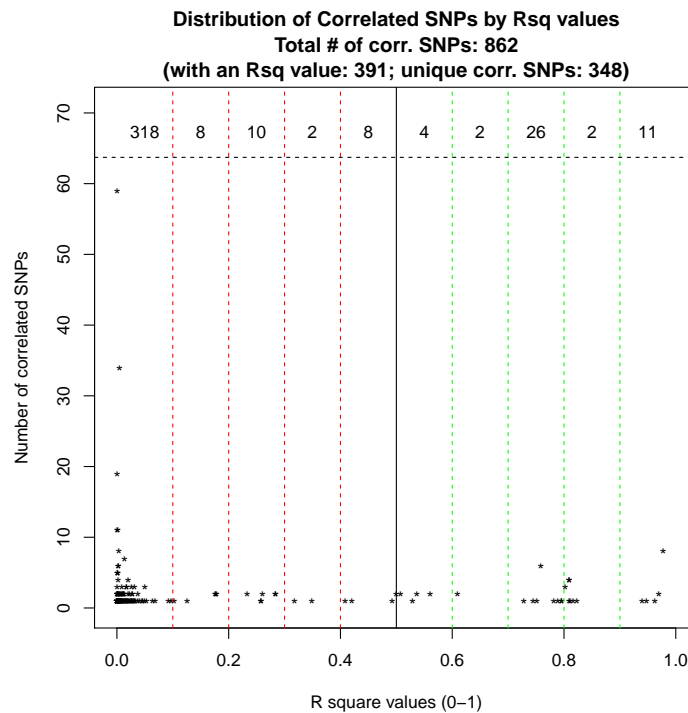


Figure 1: Distribution of Rsquare values of all Correlated SNPs. Each marked bin contains the total number of correlated SNPs. The sum of all the counts would total the number of correlated SNPs.

Using splitbysnp argument, the same type of plot as above is generated, however the total number of correlated SNPs are divided by the associated tagSNP.

```
> FunciSNPplot(glioma.anno, splitbysnp=TRUE)
> ggsave("glioma_dist_bysnp.pdf")
```

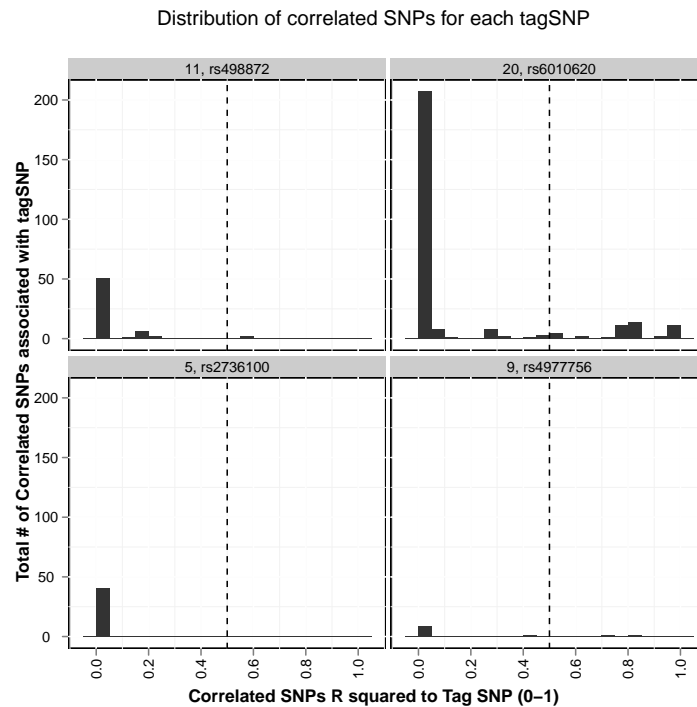


Figure 2: Distribution of Rsquare values of all Correlated SNPs divided by the tagSNP and it's location.

Using genomicSum argument will result the overall genomic distribution of the newly identified correlated SNPs. Using rsq value, the plot is divided into all correlated SNPs vs subset. This type of plot is informs the relative enrichment for genomic features.

```
> pdf("glioma_genomic_sum_rcut.pdf")
> FunciSNPplot(glioma.anno, rsq=0.5, genomicSum=TRUE, save=FALSE)
> dev.off()
```

```
pdf
2
```

tagSummary argument is unique in that it will automatically save the plots in a specific folder. This is done because this function will generate a summary plot for each biofeatures. The first plot is a scatter plot showing the relationship between Rsquare and Distance to tagSNP for each FuncySNP. The second plot is a histogram distribution of number of correlated SNPs at each Rsquare value. Each set of plot is further divided by tagSNP. Best if used with rsq value.

```
> ## Following will output a series of plots for each biofeature at rsq=0.5
> FunciSNPplot(glioma.anno, tagSummary=TRUE, rsq=0.5)
```

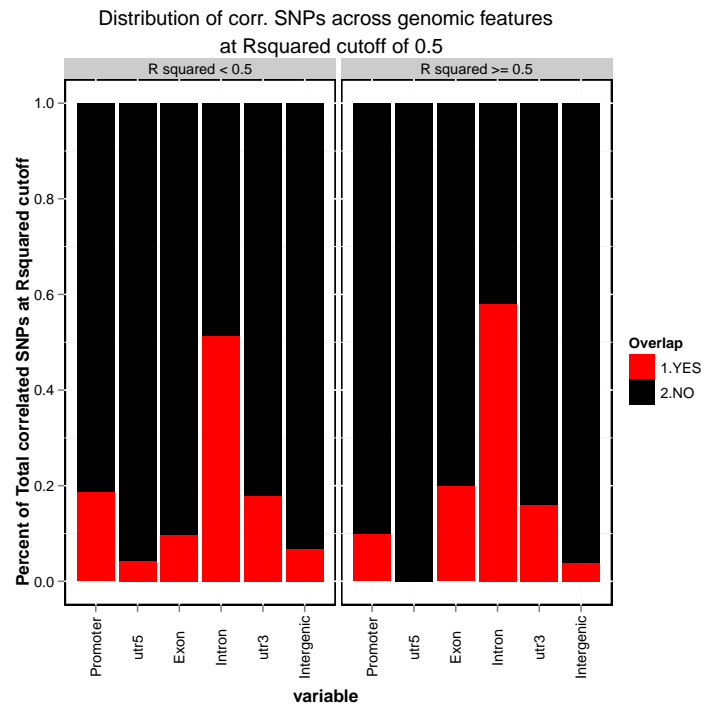


Figure 3: Stacked bar chart summarizing all correlated SNPs for each of the identified genomic features: exon, intron, 5UTR, 3UTR, promoter, lincRNA or in gene desert. Rsquare cutoff at 0.5. This plot is most informative if used with a rsq value.

Finished plotting 1 / 3
 Finished plotting 2 / 3
 Finished plotting 3 / 3

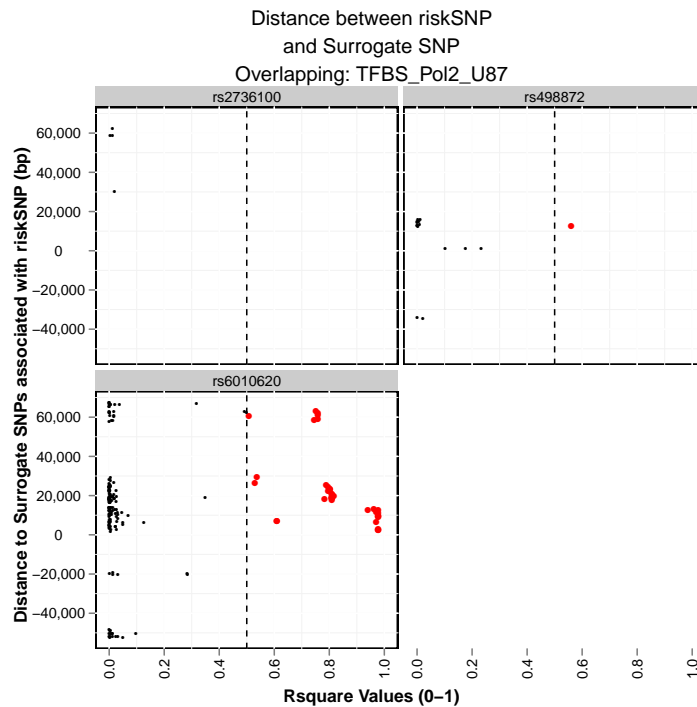


Figure 4: Scatter plot showing the relationship between Rsquare and Distance to tagSNP for each FuncySNP

Output results in BED format - visualize results

FunciSNPbed outputs a unique BED file which can be used to view in any genomic browser compatible with BED formats. To learn more about BED formats, see UCSC Genome Browser FAQ (<http://genome.ucsc.edu/FAQ/FAQformat>). Each tagSNP which is in LD to a corresponding FuncySNP overlapping at least one biofeature is colored black, while the FuncySNP is colored red. The initial position is provided by the first tagSNP and the first linked FuncySNP. We recommend using UCSC genome browser to view your BED files. This is useful so you can view all public and private tracks in relation to FunciSNP results.

```
> ## will output to current working directory.
> FunciSNPbed(glioma.anno, rsq=0.5);
```

```
Total corSNP (RED): 44
Total tagSNP (BLK): 3
```

```
> # FunciSNPbed(rs6010620, rsq=0.5);
```

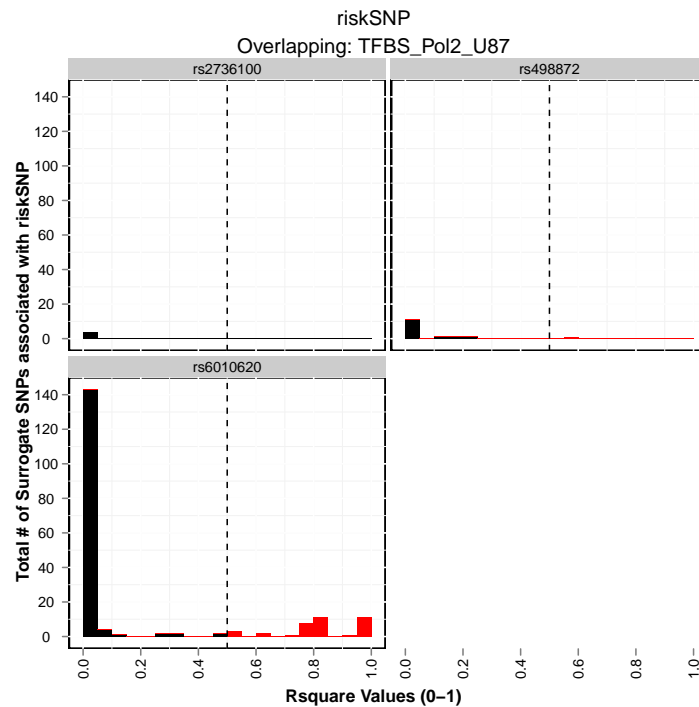


Figure 5: Histogram distribution of number of correlated SNPs at each Rsquare value

```
> sessionInfo()

R version 2.14.1 (2011-12-22)
Platform: x86_64-pc-linux-gnu (64-bit)

locale:
 [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
 [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=C               LC_NAME=C
 [9] LC_ADDRESS=C            LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

attached base packages:
 [1] tools      splines    grid        stats      graphics  grDevices  utils
 [8] datasets  methods    base

other attached packages:
 [1] FunciSNP_0.1.7
 [2] VariantAnnotation_1.0.5
 [3] TxDb.Hsapiens.UCSC.hg19.knownGene_2.6.2
 [4] GenomicFeatures_1.6.7
```

```

[5] ChIPpeakAnno_2.2.0
[6] limma_3.10.2
[7] GO.db_2.6.1
[8] BSgenome.Ecoli.NCBI.20080805_1.3.17
[9] BSgenome_1.22.0
[10] multtest_2.10.0
[11] biomaRt_2.10.0
[12] GGtools_4.0.0
[13] ff_2.2-4
[14] bit_1.1-8
[15] annotate_1.32.1
[16] GGBase_3.14.0
[17] genefilter_1.36.0
[18] snpStats_1.4.1
[19] Matrix_1.0-3
[20] lattice_0.20-0
[21] survival_2.36-12
[22] rtracklayer_1.14.4
[23] RCurl_1.9-5
[24] Rsamtools_1.6.3
[25] Biostrings_2.22.0
[26] GenomicRanges_1.6.4
[27] IRanges_1.12.5
[28] matlab_0.8.9
[29] ggplot2_0.8.9
[30] proto_0.3-9.2
[31] reshape_0.8.4
[32] plyr_1.7.1
[33] gplots_2.10.1
[34] KernSmooth_2.23-7
[35] caTools_1.12
[36] bitops_1.0-4.1
[37] gdata_2.8.2
[38] gtools_2.6.2
[39] org.Hs.eg.db_2.6.4
[40] RSQLite_0.11.1
[41] DBI_0.2-5
[42] AnnotationDbi_1.16.11
[43] Biobase_2.14.0

```

loaded via a namespace (and not attached):

```

[1] digest_0.5.1    MASS_7.3-16     parallel_2.14.1 XML_3.9-2
[5] xtable_1.6-0    zlibbioc_1.0.0

```

Questions or comments, please contact Simon G. Coetzee (scoetzee NEAR gmail POINT com) or Houtan Noushmehr (houtana NEAR gmail POINT com).