

# iMKT loading data

## iMKT PopFly and PopHuman data

PopFly and PopHuman are. The package include functions to download all genes statics of all populations located in these genome browsers. Here we will explain how to load this information in your working enviroment and how to access it in order to use it efficiently!

## Loading the row data

Remember you are downloading gene information of 20ypico *Drosophila melanogaster* populations and 26 Human populations. This procces could take a while!

```
library(iMKT)
dataPopfly<-loadPopFly()
#> Loading PopFly data into your workspace.
#> This process may take some seconds to complete, please be patient.
knitr::kable(head(dataPopfly))
```

Pop	Name	Start	End	Chr	p0	pi	d0	di	m0	mi	alpha	fisher_pval	DoS	K
EA	FBgn0000008	18024473	18060339	2R	28	17	36	19	647	2449	-0.1504	0.8348	-0.0323	0.0
EA	FBgn0000014	12632936	12655771	3R	5	0	19	0	155	643	NA	1.0000	0.0000	0.0
EA	FBgn0000015	12752932	12797958	3R	6	1	4	0	150	630	-Inf	1.0000	-0.1429	0.0
EA	FBgn0000017	16608966	16640982	3L	10	5	83	134	867	3263	0.6903	0.0530	0.2842	1.0
EA	FBgn0000018	10973443	10975293	2L	12	8	18	18	233	1019	0.3333	0.5796	0.1000	1.0
EA	FBgn0000022	264064	264980	X	1	0	17	73	63	345	1.0000	0.1978	0.8111	4.0

The data is presented at the most compress form in a simple dataframe. Each gene were analyzed by populations and contains information about segreating, divergent and analyzed sites, in addition to the Standard MKT calculation, Direction of Selection, Ka/Ks, and the Derived Allele Frequency (P0). The same information is provided by selected sites (Pi). If you have some basics R knowledge, you can access manually to the diverse gene information manually, in order to perform the test individually, by recombination information or concatenating them.

As we compress the Derived Allele Frequency in a column field, you will need to create the correct variables forms to pass them properly at the functions. It can be done in a few R basics lines!

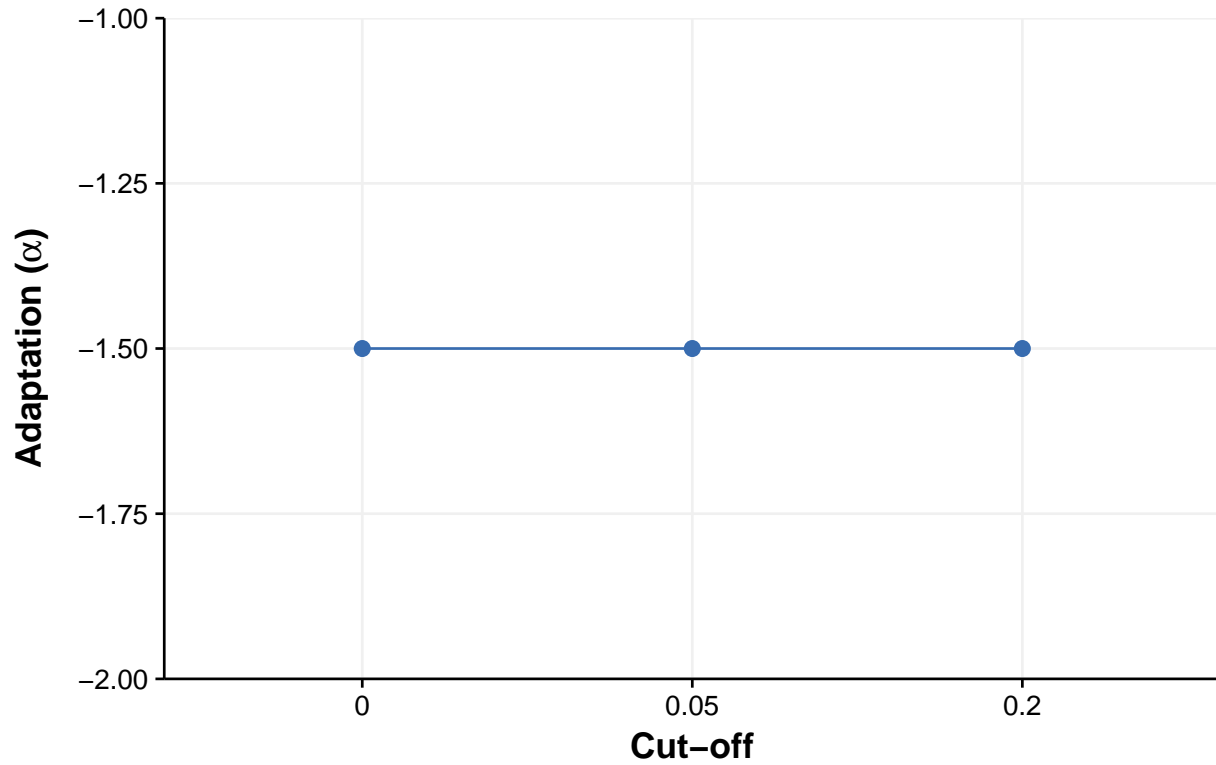
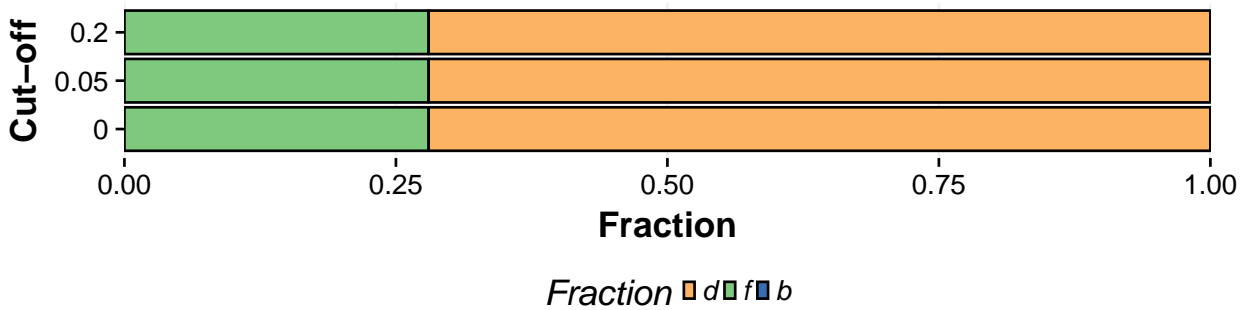
```
## Preparing RAL Adh
adhRAL<-dataPopfly[dataPopfly$Name=='FBgn0000055' & dataPopfly$Pop=='RAL',]

adhRAL$DAF0f <- as.character(adhRAL$DAF0f); adhRAL$DAF4f <- as.character(adhRAL$DAF4f)
adhRAL0f<-unlist(strsplit(adhRAL$DAF0f, split=";"))
adhRAL4f <- unlist(strsplit(adhRAL$DAF4f, split=":"))
adhRAL0f <- as.numeric(adhRAL0f); adhRAL4f <- as.numeric(adhRAL0f)

f <- seq(0.05,0.95,0.1)
mi <- adhRAL$mi; m0 <- adhRAL$m0
Di <- adhRAL$di; D0 <- adhRAL$d0

dafAdhRAL <- cbind(f, adhRAL0f, adhRAL4f); dafAdhRAL <- as.data.frame(dafAdhRAL)
names(dafAdhRAL) <- c("daf","Pi","P0")
divAdhRAL <- cbind(mi, Di, m0, D0); divAdhRAL <- as.data.frame(divAdhRAL)
```



**A****B**

```
#>
#> $`Divergence metrics`
#> $`Divergence metrics`$`Global metrics`
#>      Ka      Ks      omega
#> 1 0.00408998 0.03649635 0.1120654
#>
#> $`Divergence metrics`$`Estimates by cutoff`
#>      omegaA.symbol omegaD.symbol
#> Cutoff = 0      -0.1680982      0.2801636
#> Cutoff = 0.05   -0.1680982      0.2801636
#> Cutoff = 0.2    -0.1680982      0.2801636
#>
#>
#> $`MKT tables`
```

```

#> $MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0`
#>
#>
#> Table: cutoff
#>
#>           DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class              0                4
#> Selected class             0                4
#>
#> $MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.05`
#>
#>
#> Table: cutoff
#>
#>           DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class              3                1
#> Selected class             3                1
#>
#> $MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.2`
#>
#>
#> Table: cutoff
#>
#>           DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class              3                1
#> Selected class             3                1
#>
#> $MKT tables`$`MKT standard table`
#>
#>
#>           Polymorphism  Divergence
#> -----
#> Neutral class          4            5
#> Selected class          4            2
#>
#>
#> $Fractions
#>           0           0.05           0.2
#> d 0.7198364 0.7198364 0.7198364
#> f 0.2801636 0.2801636 0.2801636
#> b 0.0000000 0.0000000 0.0000000
#>
#> standard(daf = dafAdhZI, divergence = divAdhZI)
#> Warning in check_input(daf, divergence, 0, 1): Input daf file contains P0 values = 0.
#> This can bias the function fitting and the estimation of alpha.
#> $alpha.symbol
#> [1] -2
#>
#> $Fishers exact test P-value`
#> [1] 0.3665158
#>

```

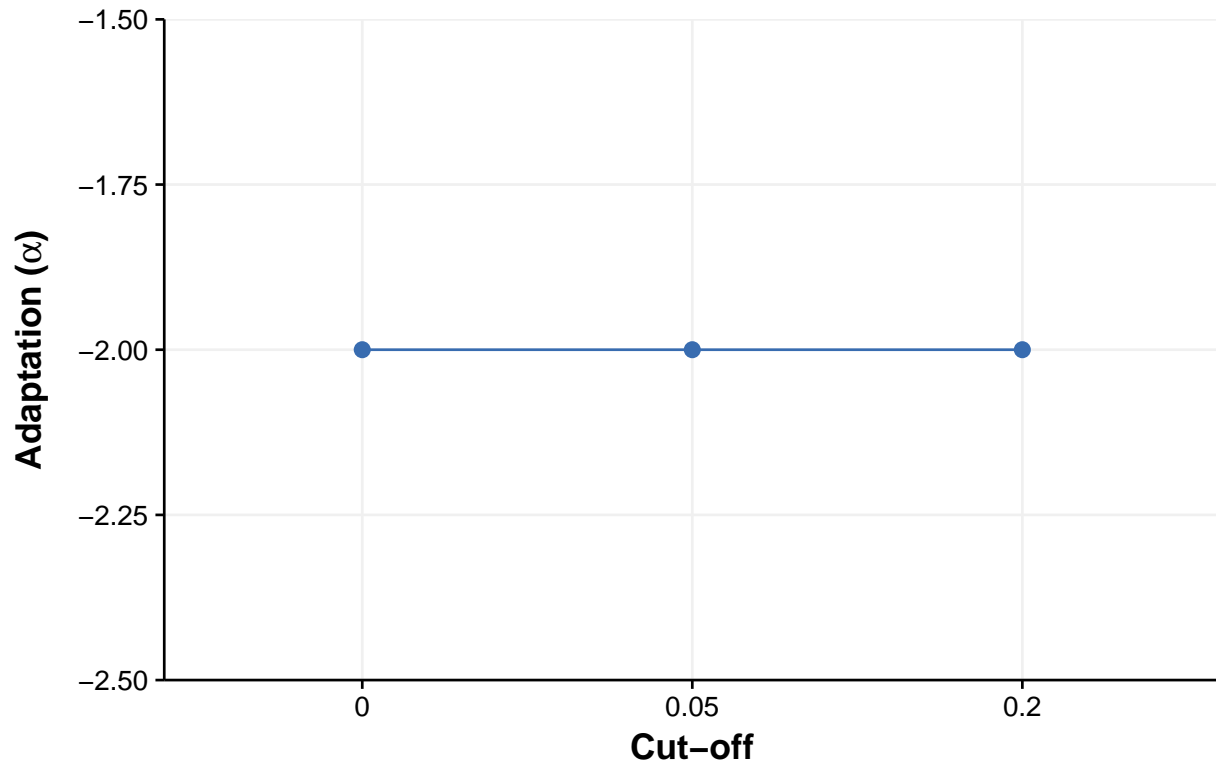
```

#> `$MKT table`
#>
#>
#>
#>      Polymorphism  Divergence
#> -----
#> Neutral class      5          6
#> Selected class     5          2
#>
#> `$Divergence metrics`
#>
#>
#>      Ka      Ks      omega      omegaA      omegaD
#> -----
#> 0.00409 0.0434783 0.0940695 -0.1881391 0.2822086
DGRP(daf = dafAdhZI, divergence = divAdhZI, plot = TRUE)
#> Warning in check_input(daf, divergence, 0, 1): Input daf file contains P0 values = 0.
#> This can bias the function fitting and the estimation of alpha.
#> $Results
#>
#>      alpha.symbol Fishers exact test P-value
#> Cutoff = 0      -2      0.3665158
#> Cutoff = 0.05   -2      0.3665158
#> Cutoff = 0.2    -2      0.3665158
#>
#> $Graph

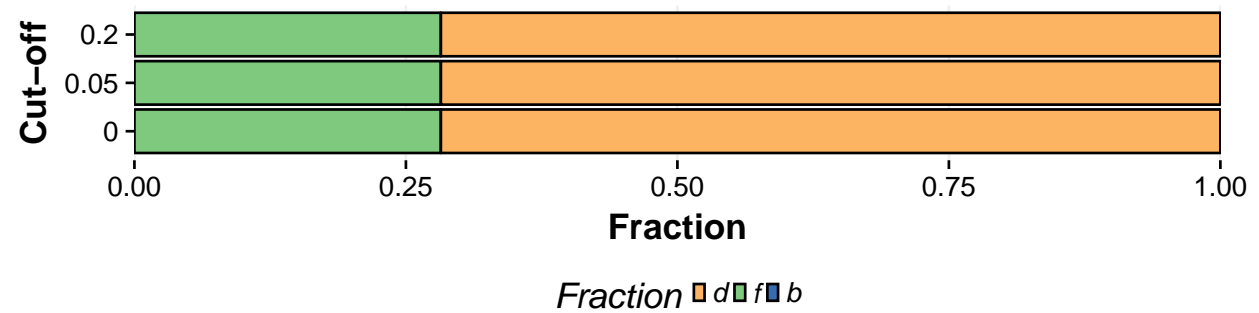
```

data retrieve Adh ZI-1.bb

**A**



**B**



```
#>
#> $`Divergence metrics`
#> $`Divergence metrics`$`Global metrics`
#>      Ka      Ks      omega
#> 1 0.00408998 0.04347826 0.09406953
#>
#> $`Divergence metrics`$`Estimates by cutoff`
#>      omegaA.symbol omegaD.symbol
#> Cutoff = 0      -0.1881391      0.2822086
#> Cutoff = 0.05   -0.1881391      0.2822086
#> Cutoff = 0.2    -0.1881391      0.2822086
#>
#>
#> $`MKT tables`
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0`
```

```

#>
#>
#> Table: cutoff
#>
#>           DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class              0              5
#> Selected class             0              5
#>
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.05`
#>
#>
#> Table: cutoff
#>
#>           DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class              5              0
#> Selected class             5              0
#>
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.2`
#>
#>
#> Table: cutoff
#>
#>           DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class              5              0
#> Selected class             5              0
#>
#> $`MKT tables`$`MKT standard table`
#>
#>
#>           Polymorphism  Divergence
#> -----
#> Neutral class          5           6
#> Selected class          5           2
#>
#>
#> $Fractions
#>           0           0.05           0.2
#> d 0.7177914 0.7177914 0.7177914
#> f 0.2822086 0.2822086 0.2822086
#> b 0.0000000 0.0000000 0.0000000

```

This process could be tedious depending on the number of genes you want to analyze. To solve this, we just add the ***PopFlyAnalysis()*** function to the package. It allows you select a huge amount of genes and/or populations and retrieve the information easily! Remember to save the information in the most appropriate way to yours analysis or results!

```

PopFlyAnalysis(genes = c("FBgn0000055","FBgn0003016"),pops = c("RAL","ZI","FR"),recomb = F)
#> [1] "Population = FR"
#> Warning in check_input(daf, divergence, 0, 1): Input daf file contains P0 values = 0.
#> This can bias the function fitting and the estimation of alpha.
#> [1] "Population = RAL"
#> Warning in check_input(daf, divergence, 0, 1): Input daf file contains P0 values = 0.

```

```
#> This can bias the function fitting and the estimation of alpha.
#> [1] "Population = ZI"
#> $`Population` = FR`
#> $`Population` = FR`$alpha.symbol
#> [1] -0.3675214
#>
#> $`Population` = FR`$`Fishers exact test P-value`
#> [1] 0.5274392
#>
#> $`Population` = FR`$`MKT table`
#>
#>
#>
#> Polymorphism Divergence
#> -----
#> Neutral class 45 50
#> Selected class 16 13
#>
#> $`Population` = FR`$`Divergence metrics`
#>
#>
#> Ka Ks omega omegaA omegaD
#> -----
#> 0.003767 0.058072 0.0648682 -0.0238404 0.0887086
#>
#>
#> $`Population` = RAL`
#> $`Population` = RAL`$alpha.symbol
#> [1] -1.197802
#>
#> $`Population` = RAL`$`Fishers exact test P-value`
#> [1] 0.03712979
#>
#> $`Population` = RAL`$`MKT table`
#>
#>
#>
#> Polymorphism Divergence
#> -----
#> Neutral class 63 45
#> Selected class 40 13
#>
#> $`Population` = RAL`$`Divergence metrics`
#>
#>
#>
#> Ka Ks omega omegaA omegaD
#> -----
#> 0.003767 0.0522648 0.0720757 -0.0863325 0.1584082
#>
#>
#> $`Population` = ZI`
#> $`Population` = ZI`$alpha.symbol
#> [1] -0.5279503
#>
#> $`Population` = ZI`$`Fishers exact test P-value`
#> [1] 0.2545795
```





```

#>
#> Table: cutoff
#>
#>
#>      DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class          0             826
#> Selected class         0            1202
#>
#> $`Population` = RAL`$`Recombination bin = 1`$`MKT tables`$`Number of segregating sites by DAF categ
#>
#>
#> Table: cutoff
#>
#>      DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class        375             451
#> Selected class       707             495
#>
#> $`Population` = RAL`$`Recombination bin = 1`$`MKT tables`$`Number of segregating sites by DAF categ
#>
#>
#> Table: cutoff
#>
#>      DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class        464             362
#> Selected class       815             387
#>
#> $`Population` = RAL`$`Recombination bin = 1`$`MKT tables`$`MKT standard table`
#>
#>
#>
#>      Polymorphism  Divergence
#> -----
#> Neutral class      826         1115
#> Selected class     1202         2371
#>
#>
#> $`Population` = RAL`$`Recombination bin = 1`$`Fractions
#>      0      0.05      0.2
#> d 0.678485 0.67840530 0.67854260
#> f 0.321515 0.27845021 0.28406737
#> b 0.000000 0.04314449 0.03739003
#>
#> $`Population` = RAL`$`Recombination bin = 1`$`Recombination bin Summary`
#>      numGenes minRecomb medianRecomb meanRecomb maxRecomb
#> 1      4 0.6230327      0.9417518 0.9900698 1.453743
#>
#>
#> $`Population` = RAL`$`Recombination bin = 2`
#> $`Population` = RAL`$`Recombination bin = 2`$`Results
#>      alpha.symbol Fishers exact test P-value
#> Cutoff = 0      0.02881113      0.76379938
#> Cutoff = 0.05   0.14129004      0.08157691
#> Cutoff = 0.2    0.13282389      0.10747337

```

```

#>
#> $`Population = RAL`$`Recombination bin = 2`$`Divergence metrics`
#> $`Population = RAL`$`Recombination bin = 2`$`Divergence metrics`$`Global metrics`
#>      Ka      Ks      omega
#> 1 0.05678986 0.09626249 0.589948
#>
#> $`Population = RAL`$`Recombination bin = 2`$`Divergence metrics`$`Estimates by cutoff`
#>      omegaA.symbol omegaD.symbol
#> Cutoff = 0      0.01699707      0.5729509
#> Cutoff = 0.05    0.08335377      0.5065942
#> Cutoff = 0.2     0.07835918      0.5115888
#>
#>
#> $`Population = RAL`$`Recombination bin = 2`$`MKT tables`
#> $`Population = RAL`$`Recombination bin = 2`$`MKT tables`$`Number of segregating sites by DAF categ
#>
#>
#> Table: cutoff
#>
#>      DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class          0                342
#> Selected class         0                803
#>
#> $`Population = RAL`$`Recombination bin = 2`$`MKT tables`$`Number of segregating sites by DAF categ
#>
#>
#> Table: cutoff
#>
#>      DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class          160                182
#> Selected class         469                334
#>
#> $`Population = RAL`$`Recombination bin = 2`$`MKT tables`$`Number of segregating sites by DAF categ
#>
#>
#> Table: cutoff
#>
#>      DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class          185                157
#> Selected class         520                283
#>
#> $`Population = RAL`$`Recombination bin = 2`$`MKT tables`$`MKT standard table`
#>
#>
#>      Polymorphism  Divergence
#> -----
#> Neutral class      342         443
#> Selected class      803        1071
#>
#>
#> $`Population = RAL`$`Recombination bin = 2`$`Fractions

```

```

#>           0           0.05           0.2
#> d 0.4270491 0.42681545 0.42731408
#> f 0.5729509 0.50659418 0.51158877
#> b 0.0000000 0.06659037 0.06109715
#>
#> $`Population = RAL`$`Recombination bin = 2`$`Recombination bin Summary`
#>   numGenes minRecomb medianRecomb meanRecomb maxRecomb
#> 1         4  1.524576    2.018437    2.238379    3.392067
#>
#>
#> $`Population = RAL`$`Recombination bin = 3`
#> $`Population = RAL`$`Recombination bin = 3`$Results
#>           alpha.symbol Fishers exact test P-value
#> Cutoff = 0           0.4812584           2.791715e-59
#> Cutoff = 0.05       0.5573293           2.578578e-86
#> Cutoff = 0.2       0.5472239           3.195443e-82
#>
#> $`Population = RAL`$`Recombination bin = 3`$`Divergence metrics`
#> $`Population = RAL`$`Recombination bin = 3`$`Divergence metrics`$`Global metrics`
#>           Ka           Ks           omega
#> 1 0.0646586 0.1393272 0.4640773
#>
#> $`Population = RAL`$`Recombination bin = 3`$`Divergence metrics`$`Estimates by cutoff`
#>           omegaA.symbol omegaD.symbol
#> Cutoff = 0           0.2233411           0.2407362
#> Cutoff = 0.05       0.2586439           0.2054335
#> Cutoff = 0.2       0.2539542           0.2101231
#>
#>
#> $`Population = RAL`$`Recombination bin = 3`$`MKT tables`
#> $`Population = RAL`$`Recombination bin = 3`$`MKT tables`$`Number of segregating sites by DAF categ
#>
#>
#> Table: cutoff
#>
#>           DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class                0             1851
#> Selected class               0             1848
#>
#> $`Population = RAL`$`Recombination bin = 3`$`MKT tables`$`Number of segregating sites by DAF categ
#>
#>
#> Table: cutoff
#>
#>           DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class             904             947
#> Selected class           1174             674
#>
#>
#> $`Population = RAL`$`Recombination bin = 3`$`MKT tables`$`Number of segregating sites by DAF categ
#>
#>
#> Table: cutoff

```

```

#>
#>
#> ----- DAF.below.cutoff DAF.above.cutoff -----
#> Neutral class 1087 764
#> Selected class 1320 528
#>
#> $`Population = RAL`$`Recombination bin = 3`$`MKT tables`$`MKT standard table`
#>
#>
#> ----- Polymorphism Divergence -----
#> Neutral class 1851 2746
#> Selected class 1848 5285
#>
#>
#> $`Population = RAL`$`Recombination bin = 3`$`Fractions
#> 0 0.05 0.2
#> d 0.7592638 0.75920318 0.75929481
#> f 0.2407362 0.20543346 0.21012312
#> b 0.0000000 0.03536336 0.03058207
#>
#> $`Population = RAL`$`Recombination bin = 3`$`Recombination bin Summary`
#> numGenes minRecomb medianRecomb meanRecomb maxRecomb
#> 1 4 3.518252 3.548785 3.680112 4.104627
#>
#>
#>
#> $`Population = ZI`
#> $`Population = ZI`$`Recombination bin = 1`
#> $`Population = ZI`$`Recombination bin = 1`$`Results
#> alpha.symbol Fishers exact test P-value
#> Cutoff = 0 -0.05192913 0.4064121
#> Cutoff = 0.05 0.07538958 0.1998081
#> Cutoff = 0.2 0.03676480 0.5321975
#>
#> $`Population = ZI`$`Recombination bin = 1`$`Divergence metrics`
#> $`Population = ZI`$`Recombination bin = 1`$`Divergence metrics`$`Global metrics`
#> Ka Ks omega
#> 1 0.02203177 0.07151324 0.3080796
#>
#> $`Population = ZI`$`Recombination bin = 1`$`Divergence metrics`$`Estimates by cutoff`
#> omegaA.symbol omegaD.symbol
#> Cutoff = 0 -0.01599831 0.3240779
#> Cutoff = 0.05 0.02322599 0.2848536
#> Cutoff = 0.2 0.01132649 0.2967531
#>
#>
#> $`Population = ZI`$`Recombination bin = 1`$`MKT tables`
#> $`Population = ZI`$`Recombination bin = 1`$`MKT tables`$`Number of segregating sites by DAF category`
#>
#>
#> Table: cutoff
#>
#> ----- DAF.below.cutoff DAF.above.cutoff -----

```

```

#> -----
#> Neutral class          0          1575
#> Selected class        0          2206
#>
#> $`Population` = ZI`$`Recombination bin = 1`$`MKT tables`$`Number of segregating sites by DAF category`
#>
#>
#> Table: cutoff
#>
#>          DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class          1053          522
#> Selected class          1742          464
#>
#> $`Population` = ZI`$`Recombination bin = 1`$`MKT tables`$`Number of segregating sites by DAF category`
#>
#>
#> Table: cutoff
#>
#>          DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class          1186          389
#> Selected class          1847          359
#>
#> $`Population` = ZI`$`Recombination bin = 1`$`MKT tables`$`MKT standard table`
#>
#>
#>          Polymorphism  Divergence
#> -----
#> Neutral class          1575          724
#> Selected class          2206          964
#>
#>
#> $`Population` = ZI`$`Recombination bin = 1`$`Fractions
#>          0          0.05          0.2
#> d 0.6759221 0.6759028 0.67594459
#> f 0.3240779 0.2848536 0.29675310
#> b 0.0000000 0.0392436 0.02730231
#>
#> $`Population` = ZI`$`Recombination bin = 1`$`Recombination bin Summary`
#> numGenes minRecomb medianRecomb meanRecomb maxRecomb
#> 1          4 0.6230327 0.9417518 0.9900698 1.453743
#>
#>
#> $`Population` = ZI`$`Recombination bin = 2`
#> $`Population` = ZI`$`Recombination bin = 2`$`Results
#>          alpha.symbol Fishers exact test P-value
#> Cutoff = 0          0.1704018          0.014492246
#> Cutoff = 0.05       0.2219296          0.001046664
#> Cutoff = 0.2        0.2110515          0.002012941
#>
#> $`Population` = ZI`$`Recombination bin = 2`$`Divergence metrics`
#> $`Population` = ZI`$`Recombination bin = 2`$`Divergence metrics`$`Global metrics`
#>          Ka          Ks          omega

```

```

#> 1 0.05226333 0.08340555 0.626617
#>
#> $`Population` = ZI`$`Recombination bin = 2`$`Divergence metrics`$`Estimates by cutoff`
#>          omegaA.symbol omegaD.symbol
#> Cutoff = 0          0.1067766      0.5198403
#> Cutoff = 0.05       0.1390649      0.4875521
#> Cutoff = 0.2        0.1322484      0.4943685
#>
#>
#> $`Population` = ZI`$`Recombination bin = 2`$`MKT tables`
#> $`Population` = ZI`$`Recombination bin = 2`$`MKT tables`$`Number of segregating sites by DAF category`
#>
#>
#> Table: cutoff
#>
#>          DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class              0                682
#> Selected class             0                1449
#>
#> $`Population` = ZI`$`Recombination bin = 2`$`MKT tables`$`Number of segregating sites by DAF category`
#>
#>
#> Table: cutoff
#>
#>          DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class             446                236
#> Selected class            1038               411
#>
#> $`Population` = ZI`$`Recombination bin = 2`$`MKT tables`$`Number of segregating sites by DAF category`
#>
#>
#> Table: cutoff
#>
#>          DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class             500                182
#> Selected class            1133               316
#>
#> $`Population` = ZI`$`Recombination bin = 2`$`MKT tables`$`MKT standard table`
#>
#>
#>          Polymorphism  Divergence
#> -----
#> Neutral class         682          385
#> Selected class        1449          986
#>
#>
#> $`Population` = ZI`$`Recombination bin = 2`$`Fractions
#>          0          0.05          0.2
#> d 0.4801597 0.48001131 0.48027328
#> f 0.5198403 0.48755212 0.49436853
#> b 0.0000000 0.03243656 0.02535819

```

```

#>
#> $`Population = ZI`$`Recombination bin = 2`$`Recombination bin Summary`
#>   numGenes minRecomb medianRecomb meanRecomb maxRecomb
#> 1         4  1.524576    2.018437    2.238379    3.392067
#>
#>
#> $`Population = ZI`$`Recombination bin = 3`
#> $`Population = ZI`$`Recombination bin = 3`$`Results
#>      alpha.symbol Fishers exact test P-value
#> Cutoff = 0        0.4217070                3.382690e-61
#> Cutoff = 0.05     0.5070683                7.771059e-98
#> Cutoff = 0.2      0.4848931                5.523986e-87
#>
#> $`Population = ZI`$`Recombination bin = 3`$`Divergence metrics`
#> $`Population = ZI`$`Recombination bin = 3`$`Divergence metrics`$`Global metrics`
#>      Ka      Ks      omega
#> 1 0.06157707 0.1228686 0.501162
#>
#> $`Population = ZI`$`Recombination bin = 3`$`Divergence metrics`$`Estimates by cutoff`
#>      omegaA.symbol omegaD.symbol
#> Cutoff = 0        0.2113435    0.2898185
#> Cutoff = 0.05     0.2541233    0.2470386
#> Cutoff = 0.2      0.2430100    0.2581520
#>
#>
#> $`Population = ZI`$`Recombination bin = 3`$`MKT tables`
#> $`Population = ZI`$`Recombination bin = 3`$`MKT tables`$`Number of segregating sites by DAF category`
#>
#>
#> Table: cutoff
#>
#>      DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class         0                3611
#> Selected class        0                4329
#>
#> $`Population = ZI`$`Recombination bin = 3`$`MKT tables`$`Number of segregating sites by DAF category`
#>
#>
#> Table: cutoff
#>
#>      DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class        2275                1336
#> Selected class        3366                963
#>
#> $`Population = ZI`$`Recombination bin = 3`$`MKT tables`$`Number of segregating sites by DAF category`
#>
#>
#> Table: cutoff
#>
#>      DAF.below.cutoff  DAF.above.cutoff
#> -----
#> Neutral class        2600                1011

```



```

#> Selected class                3590                739
#>
#> $`Population` = ZI`$`Recombination bin` = 3`$`MKT tables`$`MKT standard table`
#>
#>
#>
#> Polymorphism Divergence
#> -----
#> Neutral class      3611      2450
#> Selected class     4329      5079
#>
#>
#> $`Population` = ZI`$`Recombination bin` = 3`$`Fractions
#>      0      0.05      0.2
#> d 0.7101815 0.71020522 0.71017991
#> f 0.2898185 0.24703862 0.25815201
#> b 0.0000000 0.04275616 0.03166808
#>
#> $`Population` = ZI`$`Recombination bin` = 3`$`Recombination bin Summary`
#> numGenes minRecomb medianRecomb meanRecomb maxRecomb
#> 1      4 3.518252 3.548785 3.680112 4.104627

```