

# DIANNmv

This package can be used to process and analyze mass spec data generated by DIANN. It mainly uses the DEP package under the hood, so you can use all DEP functions once you have created the summarizedExperiment object (check out the DEP vignette). Also included are some visualization function that I prefer over the default DEP options.

Install and load the package from github with the following code (you can ignore the warnings):

```
if (!require('BiocManager', quietly = T)){
  install_packages('BiocManager')
}

if (!require('devtools', quietly = T)){
  install_packages('devtools')
}

install_github('DijkJel/DIANNmv')
```

```
library(DIANNmv)
#> Warning in fun(libname, pkgname): mzR has been built against a different Rcpp version (1.0.12)
#> than is installed on your system (1.0.13.1). This might lead to errors
#> when loading mzR. If you encounter such issues, please send a report,
#> including the output of sessionInfo() to the Bioc support forum at
#> https://support.bioconductor.org/. For details see also
#> https://github.com/sneumann/mzR/wiki/mzR-Rcpp-compiler-linker-issue.
#> Warning: replacing previous import 'SummarizedExperiment::start' by
#> 'stats::start' when loading 'DIANNmv'
#> Warning: replacing previous import 'SummarizedExperiment::end' by 'stats::end'
#> when loading 'DIANNmv'
library(SummarizedExperiment)
#> Loading required package: MatrixGenerics
#> Loading required package: matrixStats
#>
#> Attaching package: 'MatrixGenerics'
#> The following objects are masked from 'package:matrixStats':
#>
#> colAlls, colAnyNAs, colAnys, colAugsPerRowSet, colCollapse,
#> colCounts, colCummaxs, colCummins, colCumprods, colCumsums,
#> colDiffs, colIQRDiffs, colIQRs, colLogSumExps, colMadDiffs,
#> colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats,
#> colProds, colQuantiles, colRanges, colRanks, colSdDiffs, colSds,
#> colSums2, colTabulates, colVarDiffs, colVars, colWeightedMads,
#> colWeightedMeans, colWeightedMedians, colWeightedSds,
#> colWeightedVars, rowAlls, rowAnyNAs, rowAnys, rowAugsPerColSet,
#> rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods,
#> rowCumsums, rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,
#> rowMadDiffs, rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,
```

```

#>      rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,
#>      rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars,
#>      rowWeightedMads, rowWeightedMeans, rowWeightedMedians,
#>      rowWeightedSds, rowWeightedVars
#> Loading required package: GenomicRanges
#> Loading required package: stats4
#> Loading required package: BiocGenerics
#>
#> Attaching package: 'BiocGenerics'
#> The following objects are masked from 'package:stats':
#>
#>      IQR, mad, sd, var, xtabs
#> The following objects are masked from 'package:base':
#>
#>      anyDuplicated, aperm, append, as.data.frame, basename, cbind,
#>      colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
#>      get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
#>      match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
#>      Position, rank, rbind, Reduce, rownames, sapply, setdiff, table,
#>      tapply, union, unique, unsplit, which.max, which.min
#> Loading required package: S4Vectors
#>
#> Attaching package: 'S4Vectors'
#> The following object is masked from 'package:utils':
#>
#>      findMatches
#> The following objects are masked from 'package:base':
#>
#>      expand.grid, I, unname
#> Loading required package: IRanges
#>
#> Attaching package: 'IRanges'
#> The following object is masked from 'package:grDevices':
#>
#>      windows
#> Loading required package: GenomeInfoDb
#> Loading required package: Biobase
#> Welcome to Bioconductor
#>
#>      Vignettes contain introductory material; view with
#>      'browseVignettes()'. To cite Bioconductor, see
#>      'citation("Biobase")', and for packages 'citation("pkgname")'.
#>
#> Attaching package: 'Biobase'
#> The following object is masked from 'package:MatrixGenerics':
#>
#>      rowMedians
#> The following objects are masked from 'package:matrixStats':
#>
#>      anyMissing, rowMedians
library(ggplot2)
#> Warning: package 'ggplot2' was built under R version 4.4.2

```

As input files you will need the protein (report.pg\_matrix) and peptide (report.pr\_matrix) DIANN output files. In addition, you need an experimental design table. This package comes with these files from a DNA pull down experiment for demonstration goals. You can inspect the data with 'expDesign', 'report.pg\_matrix', and 'report.pr\_matrix'.

```
head(report.pg_matrix)
#>      Protein.Group      Protein.Names
#> 1 AOA075B6H7;AOAOC4DH55;P01624 KV315_HUMAN;KV37_HUMAN;KVD07_HUMAN
#> 2 AOA0A0MRZ8;P04433 KV311_HUMAN;KVD11_HUMAN
#> 3 AOA0B4J2D5;P0DPI2 GAL3A_HUMAN;GAL3B_HUMAN
#> 4 AOA183 LCE6A_HUMAN
#> 5 AOA1BOGTR4 SPRR5_HUMAN
#> 6 AOA1BOGTU1 ZC11B_HUMAN
#>      Genes
#> 1 IGKV3-15;IGKV3-7;IGKV3D-7
#> 2 IGKV3-11;IGKV3D-11
#> 3 GATD3;GATD3B
#> 4 LCE6A
#> 5 SPRR5
#> 6 ZC3H11B
#>
#>      First.Protein.Description
#> 1 Probable non-functional immunoglobulin kappa variable 3-7
#> 2 Immunoglobulin kappa variable 3D-11
#> 3 Putative glutamine amidotransferase-like class 1 domain-containing protein 3B, mitochondrial
#> 4 Late cornified envelope protein 6A
#> 5 Putative small proline-rich protein 5
#> 6 Zinc finger CCCH domain-containing protein 11B
#> neg_ctrl_1 neg_ctrl_2 neg_ctrl_3 motif1_1 motif1_2 motif1_3 motif2_1 motif2_2
#> 1 35045.4 NA NA 60838.8 56361.50 45830.7 NA 41375.0
#> 2 13531.4 NA NA 26054.8 NA 50914.5 20547.4 NA
#> 3 50098.9 36549.70 43047.0 29253.3 25503.00 47893.5 36321.2 25036.7
#> 4 92060.5 92580.80 NA 49035.6 67543.30 33898.6 NA 33731.9
#> 5 57016.4 58424.50 NA 215301.0 77330.30 NA NA 69601.4
#> 6 10773.4 9745.44 17668.3 16804.8 9534.48 17388.9 16438.0 25568.2
#> motif2_3
#> 1 155669.0
#> 2 66331.5
#> 3 28612.7
#> 4 NA
#> 5 47255.0
#> 6 NA
head(report.pr_matrix)
#> Protein.Group Protein.Ids Protein.Names Genes
#> 1 Q86U42 Q86U42 PABP2_HUMAN PABPN1
#> 2 Q8NFD5 Q8NFD5;Q9Y651 ARI1B_HUMAN ARID1B
#> 3 Q96JP5 Q96JP5 ZFP91_HUMAN ZFP91
#> 4 Q16585 Q16585 SGCB_HUMAN SGCB
#> 5 P36578 P36578 RL4_HUMAN RPL4
#> 6 P36578 P36578 RL4_HUMAN RPL4
#>
#>      First.Protein.Description Proteotypic
#> 1 Polyadenylate-binding protein 2 1
#> 2 AT-rich interactive domain-containing protein 1B 0
#> 3 E3 ubiquitin-protein ligase ZFP91 1
```

```

#> 4                      Beta-sarcoglycan                      1
#> 5                      60S ribosomal protein L4              1
#> 6                      60S ribosomal protein L4              1
#> Stripped.Sequence Modified.Sequence Precursor.Charge Precursor.Id
#> 1 AAAAAAAAAAGGAAGGR AAAAAAAAAAGGAAGGR 2 AAAAAAAAAAGGAAGGR2
#> 2 AAAAAAAAAAAR AAAAAAAAAAAR 2 AAAAAAAAAAAR2
#> 3 AAAAAAAAAVSR AAAAAAAAAVSR 2 AAAAAAAAAVSR2
#> 4 AAAAAAAAEQQSSNGPVKK AAAAAAAAEQQSSNGPVKK 3 AAAAAAAAEQQSSNGPVKK3
#> 5 AAAAAAALQAK AAAAAAALQAK 1 AAAAAAALQAK1
#> 6 AAAAAAALQAK AAAAAAALQAK 2 AAAAAAALQAK2
#> neg_ctrl_1 neg_ctrl_2 neg_ctrl_3 motif1_1 motif1_2 motif1_3
#> 1 14201.4 17402.1 22342.6 9617.31 12355.2 10824.8
#> 2 56500900.0 59560000.0 64613700.0 51690200.00 23066300.0 40866800.0
#> 3 12186100.0 12535000.0 15420900.0 28513800.00 32014600.0 43538700.0
#> 4 NA NA NA 8669.59 NA NA
#> 5 3729720.0 4311790.0 2780390.0 3405560.00 4964600.0 4373450.0
#> 6 71649900.0 31629500.0 43972100.0 67226000.00 48326400.0 47199700.0
#> motif2_1 motif2_2 motif2_3
#> 1 11469.50 11064 9728.03
#> 2 30508900.00 30926500 39211400.00
#> 3 41882400.00 53996100 30695300.00
#> 4 8965.43 NA NA
#> 5 6242340.00 3104850 6942140.00
#> 6 32204200.00 40380400 39495700.00
expDesign
#> label condition replicate
#> 1 neg_ctrl_1 neg_ctrl 1
#> 2 neg_ctrl_2 neg_ctrl 2
#> 3 neg_ctrl_3 neg_ctrl 3
#> 4 motif1_1 motif1 1
#> 5 motif1_2 motif1 2
#> 6 motif1_3 motif1 3
#> 7 motif2_1 motif2 1
#> 8 motif2_2 motif2 2
#> 9 motif2_3 motif2 3

```

As you can see in `expDesign`, there are three conditions with 3 replicates each: Two variations of a TF binding motif and one negative control that can be used for both motifs. The names in the 'label' column correspond to the intensity columns in `report.pg_matrix` and should be in the same order and identically named.

The `report.pr_matrix` file can be used to add peptide number information and the median peptide intensity, which is an alternative to `iBAQ`.

To get the number of razor/unique peptides per proteinGroup per sample and the total number of razor/unique peptides over all samples, and add these to the `report.pg_matrix` file:

```

peptides <- get_nPep_prMatrix(report.pr_matrix)
pg_matrix <- add_peptide_numbers(report.pg_matrix, peptides)

```

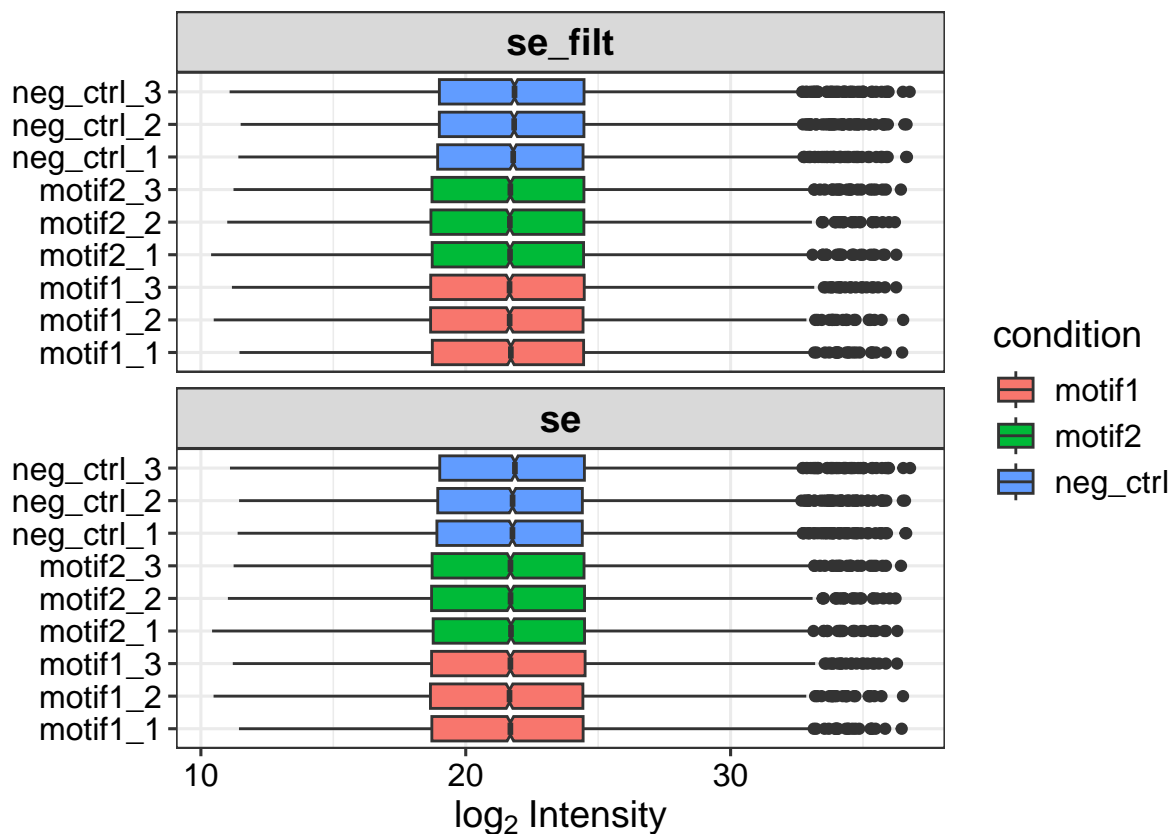
This adds new columns with the suffix 'npep' to the `report.pg_matrix` with the number of identified peptides per sample, and 'n\_total' with the total number of identified razor/unique peptides per proteinGroup.

```
colnames(pg_matrix)
#> [1] "Protein.Group"           "Protein.Names"
#> [3] "Genes"                   "First.Protein.Description"
#> [5] "neg_ctrl_1"              "neg_ctrl_2"
#> [7] "neg_ctrl_3"              "motif1_1"
#> [9] "motif1_2"                "motif1_3"
#> [11] "motif2_1"                "motif2_2"
#> [13] "motif2_3"                "neg_ctrl_1_npep"
#> [15] "neg_ctrl_2_npep"         "neg_ctrl_3_npep"
#> [17] "motif1_1_npep"          "motif1_2_npep"
#> [19] "motif1_3_npep"          "motif2_1_npep"
#> [21] "motif2_2_npep"          "motif2_3_npep"
#> [23] "n_total"
```

Median peptide intensities can be added after the summarizedExperiment object is created.

To create this, you can run the `prepare_se()` function with the `report.pg_matrix` file and associated experimental design. You can specify if and what type of imputation is done. The default is 'knn', which is better for DIA data I think. For DDA data, 'MinProb' would be the good. When 'none' is entered for the `impute` parameter, no imputation is done. Additionally, you can filter on missing values (`missing_thr`), and potential contaminants are removed by default. (Source: `contaminants.txt` file from `maxquant`).

```
se <- prepare_se(report.pg_matrix, expDesign) # without peptide information
```



```
#> Imputing along margin 1 (features/rows).
```

```

#> Warning in knnimp(x, k, maxmiss = rowmax, maxp = maxp): 36 rows with more than 50 % entries missing;
#> mean imputation used for these rows
#> Cluster size 5548 broken into 2022 3526
#> Cluster size 2022 broken into 673 1349
#> Done cluster 673
#> Done cluster 1349
#> Done cluster 2022
#> Cluster size 3526 broken into 1495 2031
#> Done cluster 1495
#> Cluster size 2031 broken into 1030 1001
#> Done cluster 1030
#> Done cluster 1001
#> Done cluster 2031
#> Done cluster 3526
se
#> class: SummarizedExperiment
#> dim: 5584 9
#> metadata(0):
#> assays(1): ''
#> rownames(5584): A2M A2ML1 ... ZYX ZZZ3
#> rowData names(9): Protein.Group Protein.Names ... imputed num_NAs
#> colnames(9): neg_ctrl_1 neg_ctrl_2 ... motif2_2 motif2_3
#> colData names(4): label ID condition replicate

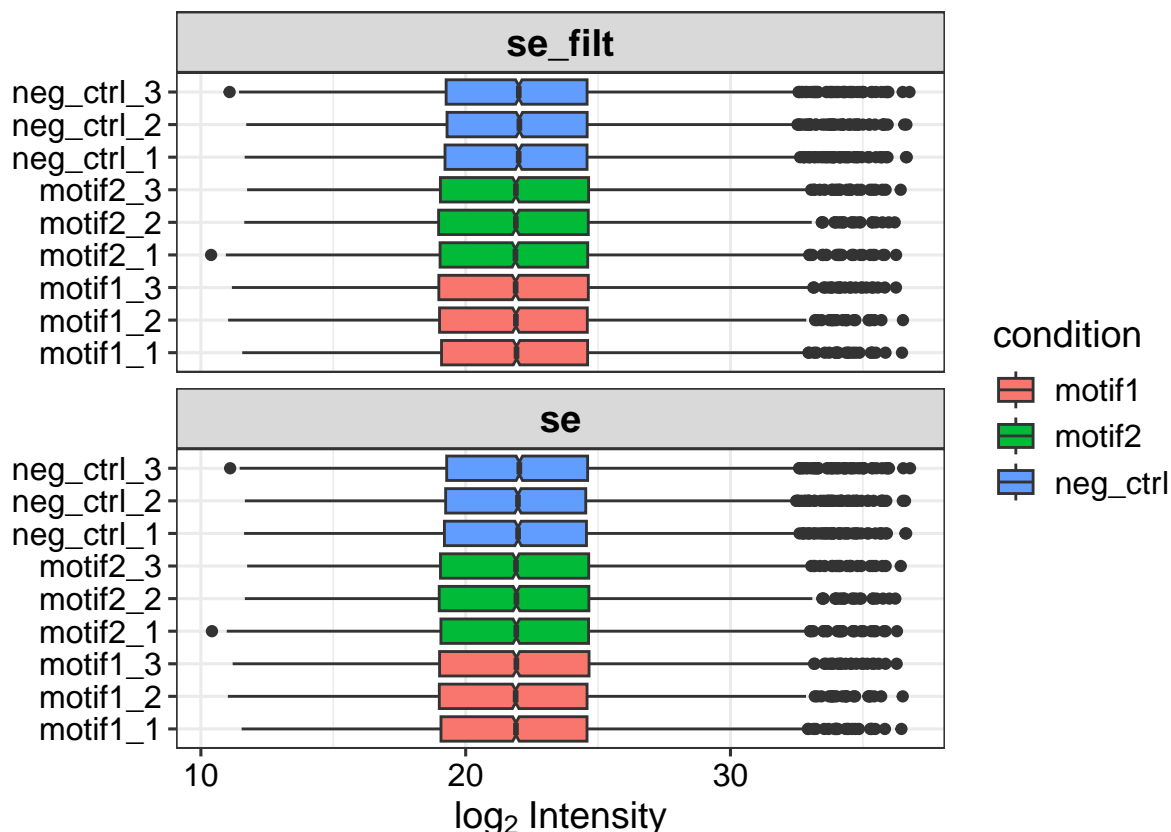
```

If you provide the `report.pr_matrix` alongside the `report.pg_matrix`, peptide information is automatically added and you can filter on a minimal number of razor/unique peptides (`min_pep`, default = 0). Make sure the sample column names are identical and match the label column in the experimental design.

```

# Add peptide information and remove all proteinGroups with <2 total
# razor/unique peptides
se <- prepare_se(report.pg_matrix, expDesign, report.pr_matrix, min_pep = 1)

```



```
#> Imputing along margin 1 (features/rows).
#> Warning in knnimp(x, k, maxmiss = rowmax, maxp = maxp): 19 rows with more than 50 % entries missing;
#> mean imputation used for these rows
#> Cluster size 5237 broken into 2152 3085
#> Cluster size 2152 broken into 1645 507
#> Cluster size 1645 broken into 656 989
#> Done cluster 656
#> Done cluster 989
#> Done cluster 1645
#> Done cluster 507
#> Done cluster 2152
#> Cluster size 3085 broken into 1977 1108
#> Cluster size 1977 broken into 976 1001
#> Done cluster 976
#> Done cluster 1001
#> Done cluster 1977
#> Done cluster 1108
#> Done cluster 3085
se
#> class: SummarizedExperiment
#> dim: 5256 9
#> metadata(0):
#> assays(2): '' peptide_info
#> rownames(5256): A2M A2ML1 ... ZYX ZZZ3
#> rowData names(11): Protein.Group Protein.Names ... imputed num_NAs
#> colnames(9): neg_ctrl1_1 neg_ctrl1_2 ... motif2_2 motif2_3
```

```
#> colData names(4): label ID condition replicate
```

The summarizedExperiment object stores a lot of information. As you can see from the output above, it consists of 5584 proteinGroups (rows) and 9 samples (columns). Furthermore, the experimental design is stored as 'colData', and extra information is stored as 'rowData'. The log2 transformed intensities form the main assay. Furthermore, if the report.pr\_matrix file was provided, a second assay is added. For a detailed description of the structure of summarizedExperiments, check its documentation. In short, to access different parts of data:

```
intensities <- assay(se) # log2 protein intensities
peptides <- assay(se, 'peptide_info') # peptide numbers

rd = as.data.frame(rowData(se))
colnames(rd) # Information for each proteinGroup in the se.
#> [1] "Protein.Group" "Protein.Names"
#> [3] "Genes" "First.Protein.Description"
#> [5] "n_total" "Potential.contaminant"
#> [7] "name" "ID"
#> [9] "npep_total" "imputed"
#> [11] "num_NAs"

cd = as.data.frame(colData(se))
cd # The experimental design
#>          label          ID condition replicate
#> neg_ctrl_1 neg_ctrl_1 neg_ctrl_1 neg_ctrl      1
#> neg_ctrl_2 neg_ctrl_2 neg_ctrl_2 neg_ctrl      2
#> neg_ctrl_3 neg_ctrl_3 neg_ctrl_3 neg_ctrl      3
#> motif1_1 motif1_1 motif1_1 motif1      1
#> motif1_2 motif1_2 motif1_2 motif1      2
#> motif1_3 motif1_3 motif1_3 motif1      3
#> motif2_1 motif2_1 motif2_1 motif2      1
#> motif2_2 motif2_2 motif2_2 motif2      2
#> motif2_3 motif2_3 motif2_3 motif2      3
```

To get and add the median peptide intensities as additional assay:

```
mpi <- get_median_intensities_prMatrix(report.pr_matrix)
se <- add_median_peptide_intensity(se, mpi)
se # an extra assay 'median_peptide_intensities' is added
#> class: SummarizedExperiment
#> dim: 5256 9
#> metadata(0):
#> assays(3): '' peptide_info median_peptide_intensities
#> rownames(5256): A2M A2ML1 ... ZYX ZZZ3
#> rowData names(12): Protein.Group Protein.Names ... num_NAs baseMean_mpi
#> colnames(9): neg_ctrl_1 neg_ctrl_2 ... motif2_2 motif2_3
#> colData names(4): label ID condition replicate

mpi <- assay(se, 'median_peptide_intensities')

rd <- as.data.frame(rowData(se))
head(rd$baseMean_mpi) # shows the average mpi per proteinGroup over all samples
#> [1] 339967.8 366450.2 411634.6 600430.1 307316.9 108054.2
```



To perform differential protein expression analysis, you have to run the `get_DEPresults()` function. There are three main types: 'manual' (1 vs 1), 'control' (all vs 1), and 'all' (all vs all). In addition, you can choose the `p.adj` cutoff and `log2` fold change cutoffs for significant, and the method of FDR correction. The DEP default is 'fdrtool', but this has given some weird results in the past. Therefore, the default here is 'BH' (Benjamini-Hochberg), which is also the default that limma uses (which DEP uses in the background).

`get_DEPresults` returns a data frame with statistics for the specified tests, and can be used for visualization afterwards.

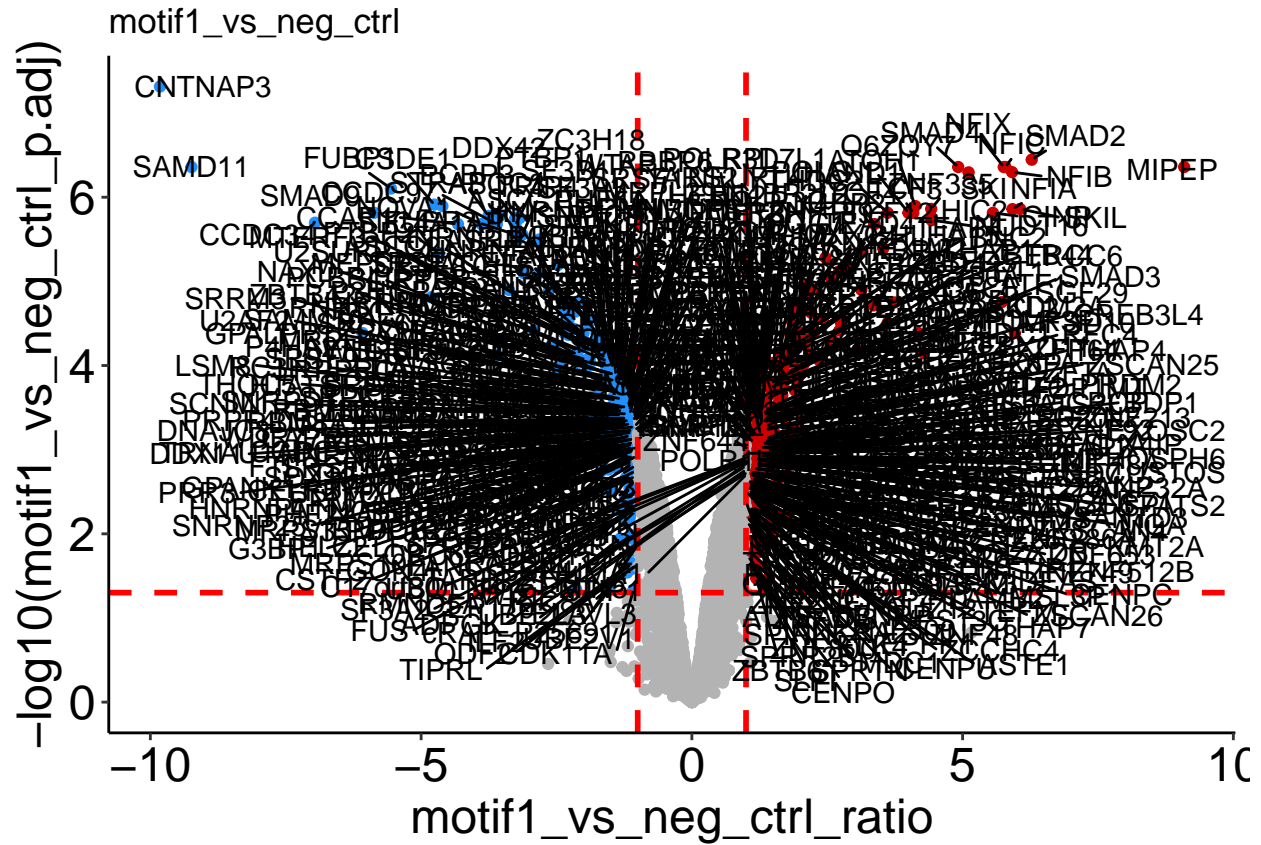
```
# To test a 1 vs 1 comparison
res_man <- get_DEPresults(se, condition1 = 'motif1', condition2 = 'neg_ctrl',
                          type = 'manual')
#> Tested contrasts: motif1_vs_neg_ctrl

# To test all conditions vs 1 reference condition
res_ref <- get_DEPresults(se, ref_condition = 'neg_ctrl', type = 'control')
#> Tested contrasts: motif1_vs_neg_ctrl, motif2_vs_neg_ctrl

# To test all vs all
res <- get_DEPresults(se, type = 'all')
#> Tested contrasts: neg_ctrl_vs_motif1, neg_ctrl_vs_motif2, motif1_vs_motif2
```

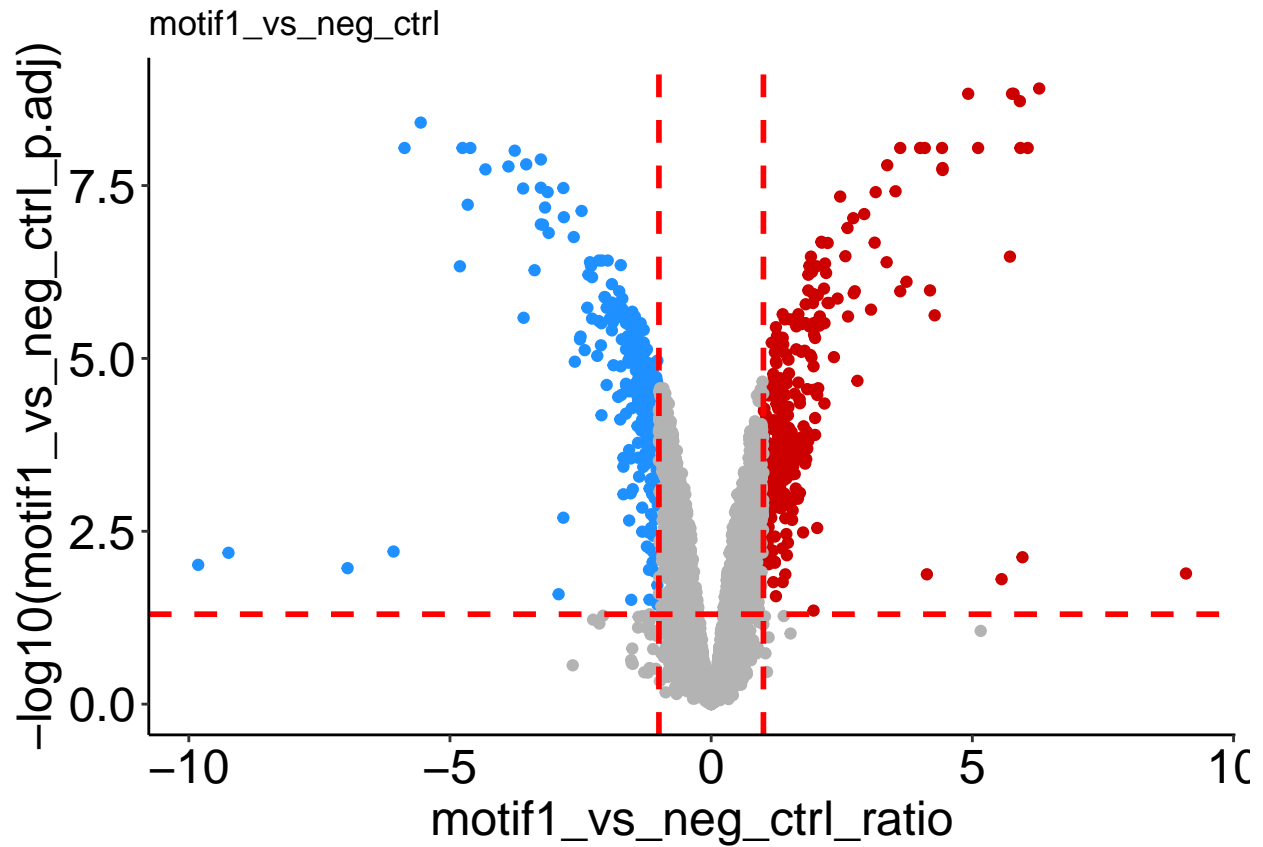
The `plotVolcano()` function returns volcano plots with the specified significance cutoffs. If more than 1 comparison is present in your results data frame, a list of volcano plots will be returned which can be accessed by the '\$' operator. Check the help page for `plotVolcano()` (`?plotVolcano`) to see the different options for labeling specific points in the volcano.

```
plotVolcano(res_man) # Default volcano plot if one comparison is present.
```

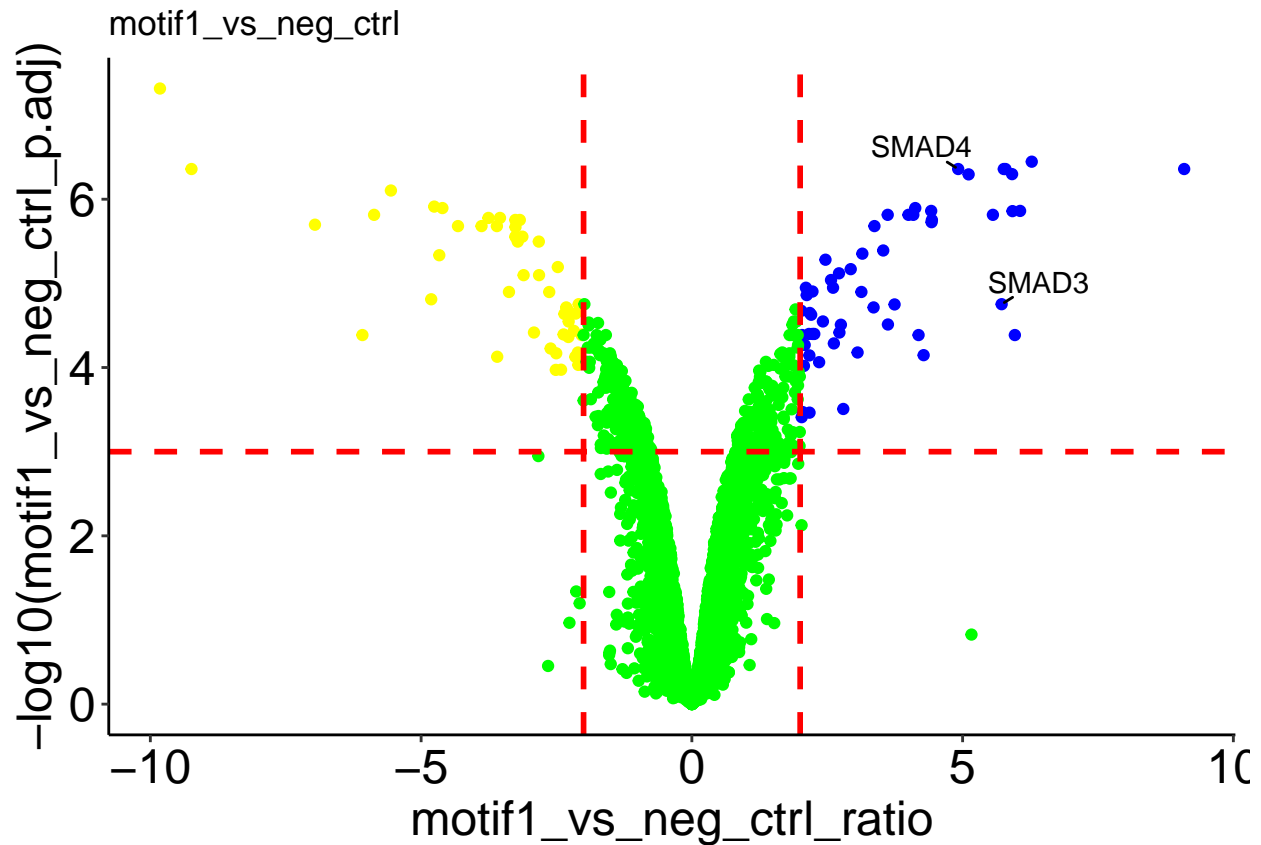


*# labels all significant points (can be a bit much).*

```
volcano_list <- plotVolcano(res_ref, label = '') # returns list of volcano plots
                                                    # Don't label anything.
volcano_list$motif1_vs_neg_ctrl # Select which plot you want to see.
```

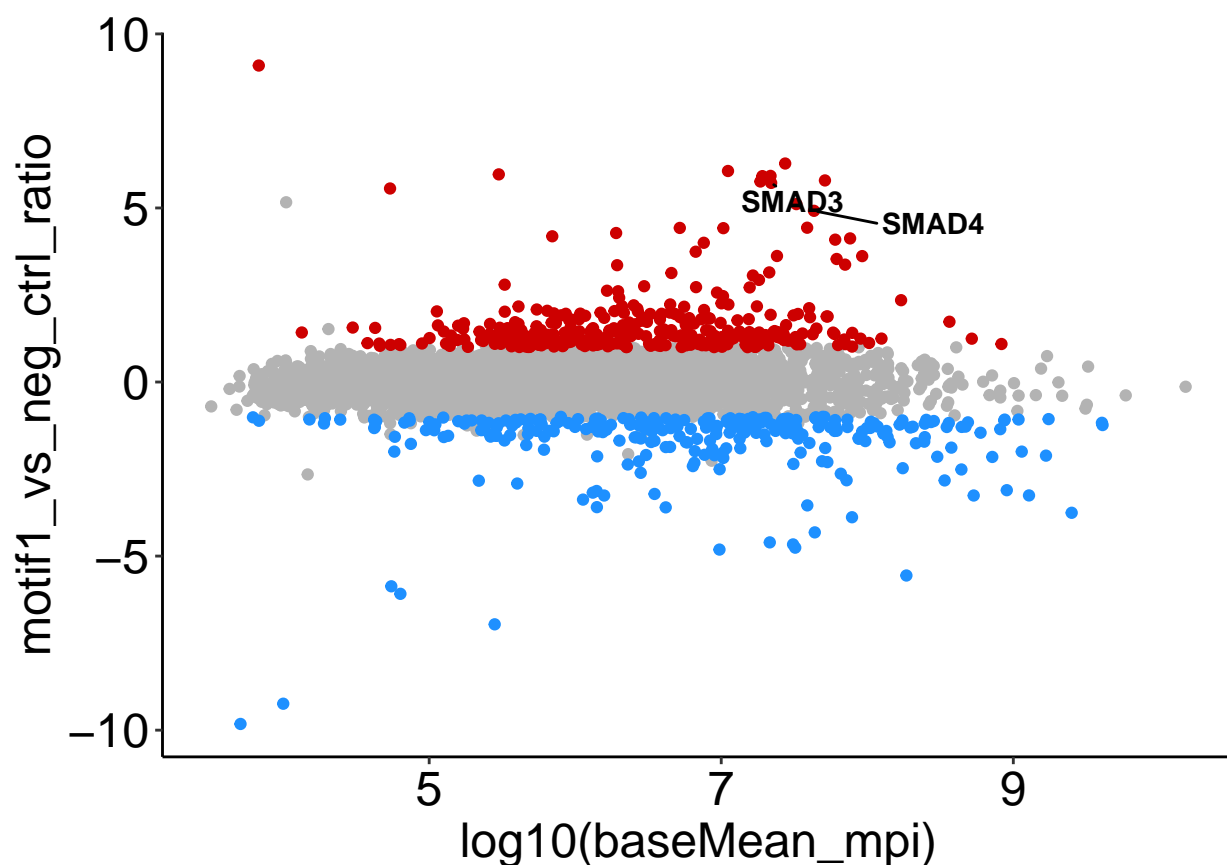


```
# Example of a very ugly volcano plot.
plotVolcano(res_man, pval_cutoff = 0.001, fc_cutoff = 2,
             up_color = 'blue', down_color = 'yellow', ns_color = 'green',
             label = c('SMAD3', 'SMAD4'))
```



If median\_peptide\_intensities are added to the se, you can also plot an MA-plot, with abundances on the x-axis, and fold-changes on the y-axis:

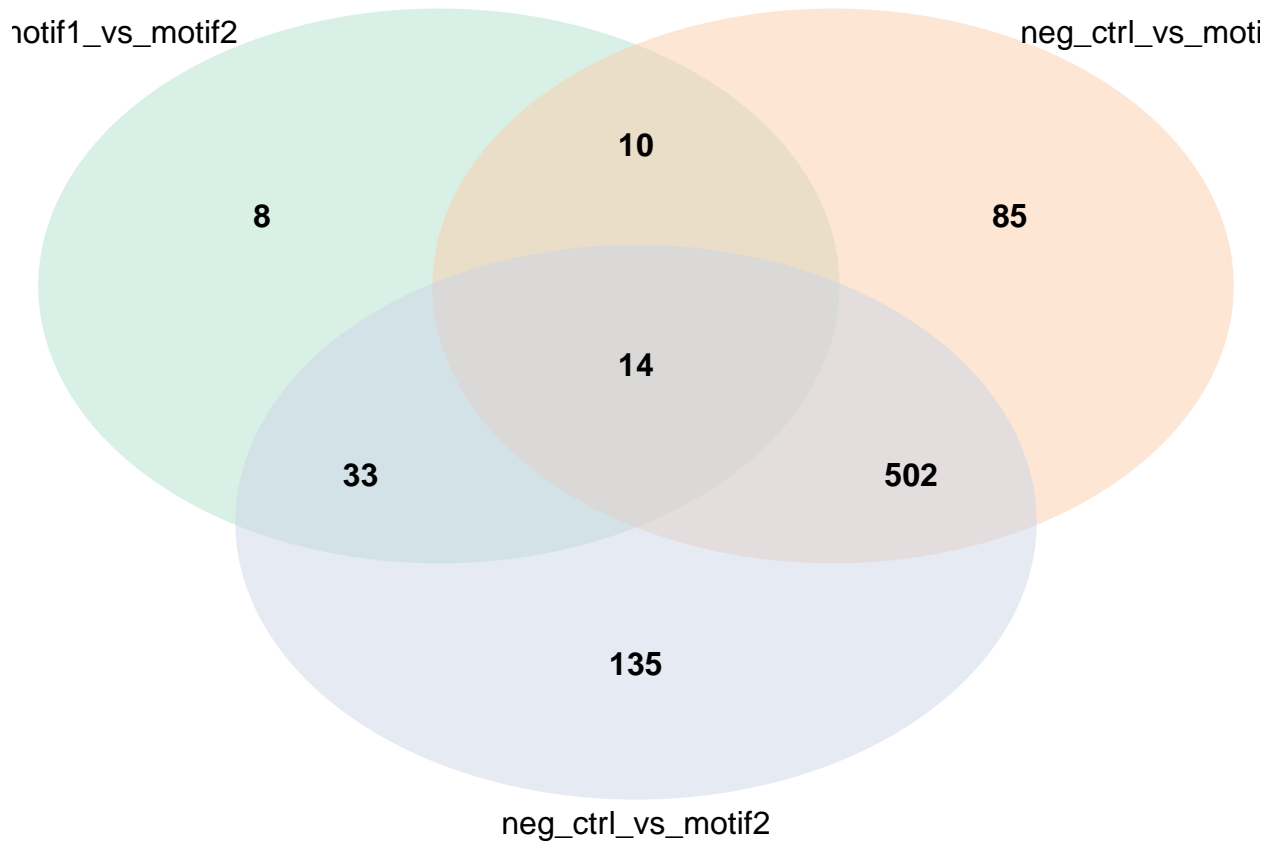
```
plot_MA(res_man, label = c('SMAD3', 'SMAD4'))
#> Warning: Removed 1 row containing missing values or values outside the scale range
#> (`geom_point()`).
#> Warning: Removed 1 row containing missing values or values outside the scale range
#> (`geom_text_repel()`).
```



You can also make a Venn diagram showing overlapping significant proteins. By default, all comparisons present in your results data frame are used, but it can handle five comparisons maximally. You can specify which comparisons to include.

```
plot_venn_diagram(res) # all comparisons
#> INFO [2025-02-24 15:15:17] [[1]]
#> INFO [2025-02-24 15:15:17] venn_list
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $filename
#> INFO [2025-02-24 15:15:17] NULL
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $disable.logging
#> INFO [2025-02-24 15:15:17] T
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $fill
#> INFO [2025-02-24 15:15:17] colors
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $fontfamily
#> INFO [2025-02-24 15:15:17] [1] "sans"
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $fontface
#> INFO [2025-02-24 15:15:17] [1] "bold"
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $cat.fontfamily
#> INFO [2025-02-24 15:15:17] [1] "sans"
#> INFO [2025-02-24 15:15:17]
```

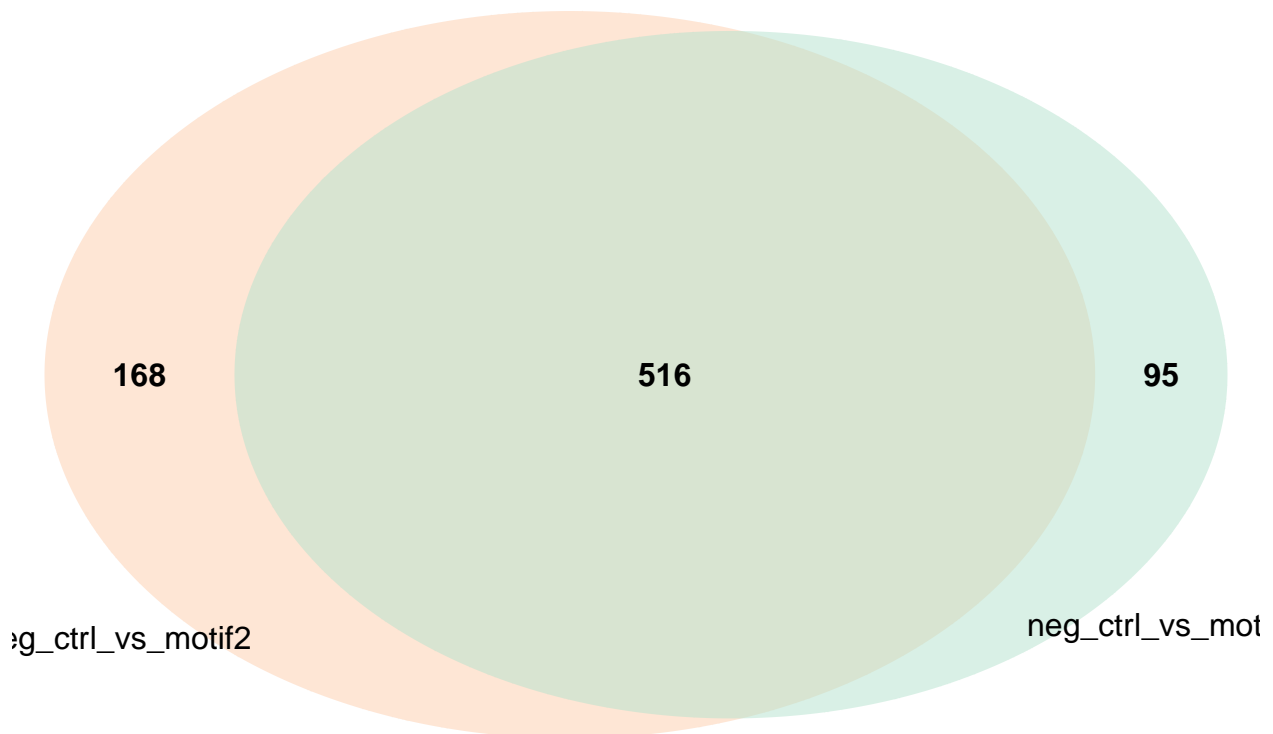
```
#> INFO [2025-02-24 15:15:17] $lty
#> INFO [2025-02-24 15:15:17] [1] 0
#> INFO [2025-02-24 15:15:17]
```



```
plot_venn_diagram(res, comparisons = c('neg_ctrl_vs_motif1',
                                         'neg_ctrl_vs_motif2')) # only two comp.

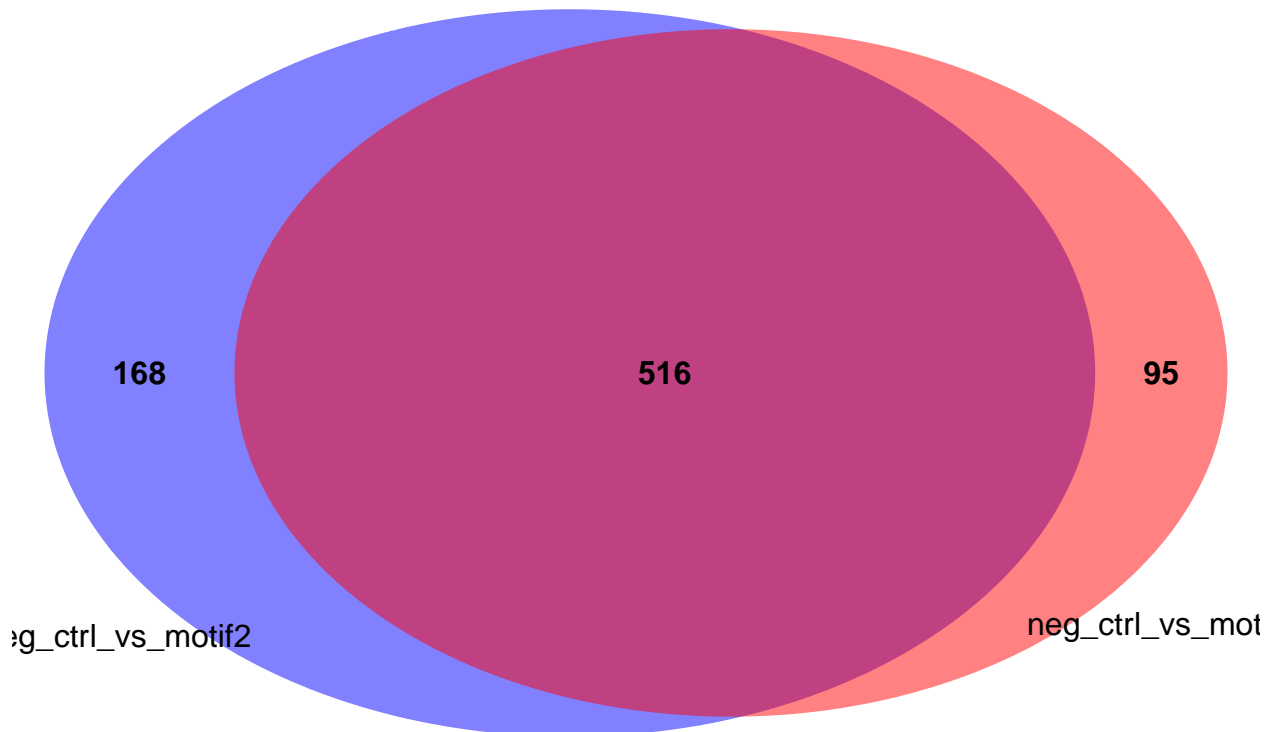
#> INFO [2025-02-24 15:15:17] [[1]]
#> INFO [2025-02-24 15:15:17] venn_list
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $filename
#> INFO [2025-02-24 15:15:17] NULL
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $disable_logging
#> INFO [2025-02-24 15:15:17] T
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $fill
#> INFO [2025-02-24 15:15:17] colors
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $fontfamily
#> INFO [2025-02-24 15:15:17] [1] "sans"
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $fontface
#> INFO [2025-02-24 15:15:17] [1] "bold"
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $cat.fontfamily
```

```
#> INFO [2025-02-24 15:15:17] [1] "sans"
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $lty
#> INFO [2025-02-24 15:15:17] [1] 0
#> INFO [2025-02-24 15:15:17]
```



```
plot_venn_diagram(res, comparisons = c('neg_ctrl_vs_motif1',
                                       'neg_ctrl_vs_motif2'),
                  colors = c('red', 'blue')) # specify colors used
#> INFO [2025-02-24 15:15:17] [[1]]
#> INFO [2025-02-24 15:15:17] venn_list
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $filename
#> INFO [2025-02-24 15:15:17] NULL
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $disable_logging
#> INFO [2025-02-24 15:15:17] T
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $fill
#> INFO [2025-02-24 15:15:17] colors
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $fontfamily
#> INFO [2025-02-24 15:15:17] [1] "sans"
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $fontface
```

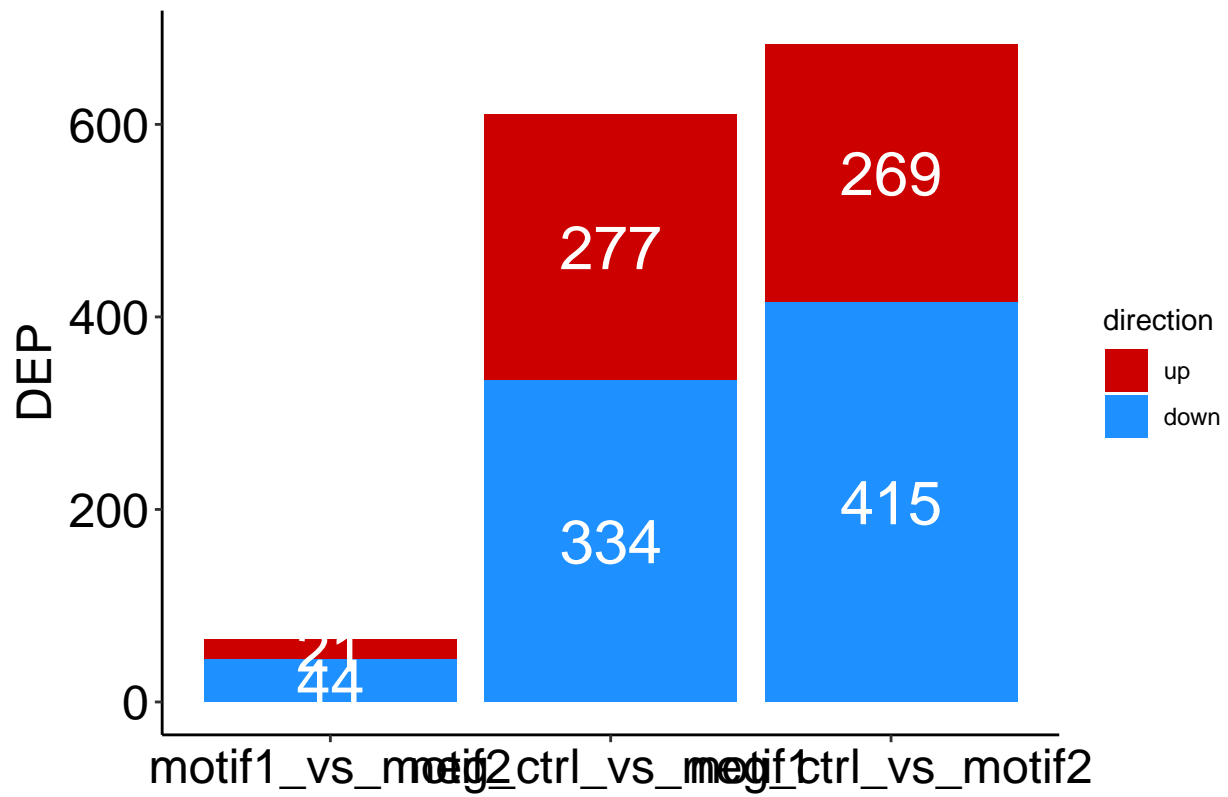
```
#> INFO [2025-02-24 15:15:17] [1] "bold"
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $cat.fontfamily
#> INFO [2025-02-24 15:15:17] [1] "sans"
#> INFO [2025-02-24 15:15:17]
#> INFO [2025-02-24 15:15:17] $lty
#> INFO [2025-02-24 15:15:17] [1] 0
#> INFO [2025-02-24 15:15:17]
```



Finally, to get an overview of the number of identified significant proteins per condition:

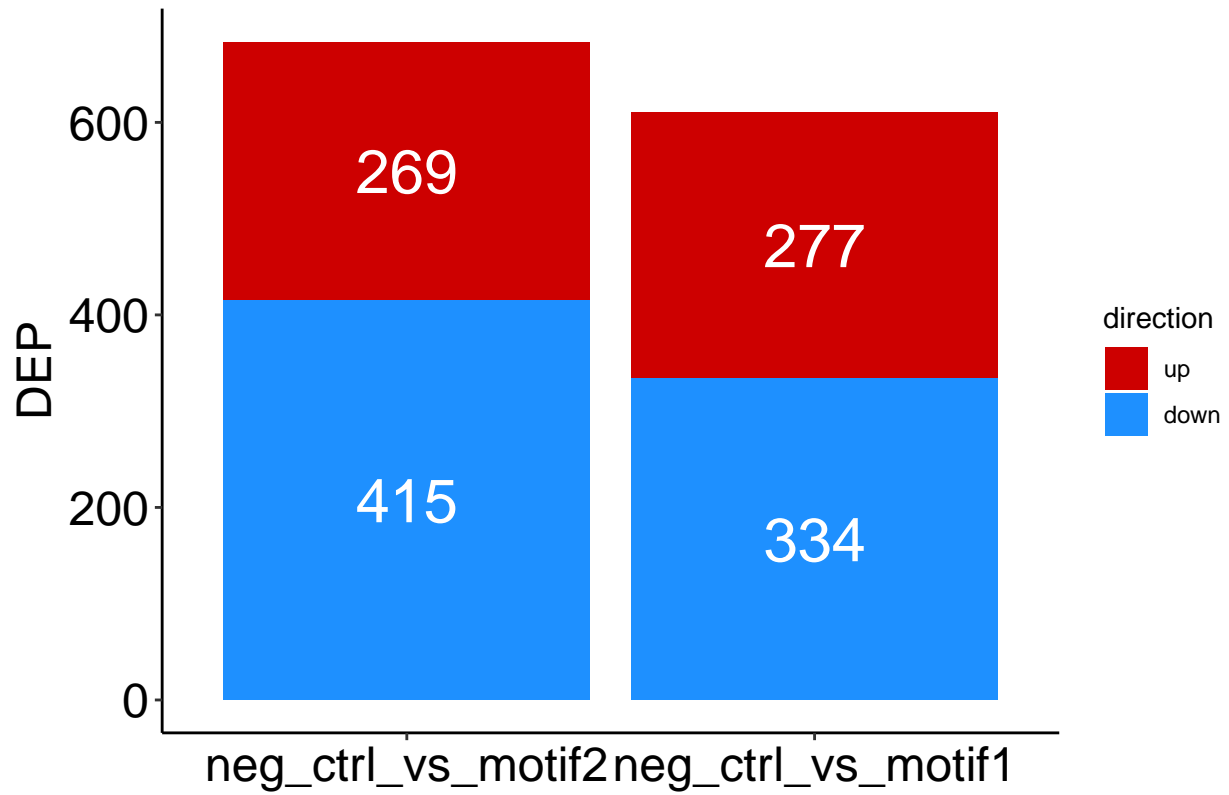
```
plot_DEP_barplot(res)
```





You can change the conditions included, order of columns, and labels:

```
# Include only two comparisons and change the order:
plot_DEP_barplot(res, comparisons = c('neg_ctrl_vs_motif2',
                                     'neg_ctrl_vs_motif1'))
```



```
# Same as above, but axis labels are changed.  
plot_DEP_barplot(res, comparisons = c('neg_ctrl_vs_motif2',  
                                     'neg_ctrl_vs_motif1'),  
                 names = c('motif2', 'motif1'))
```

