

DE analysis

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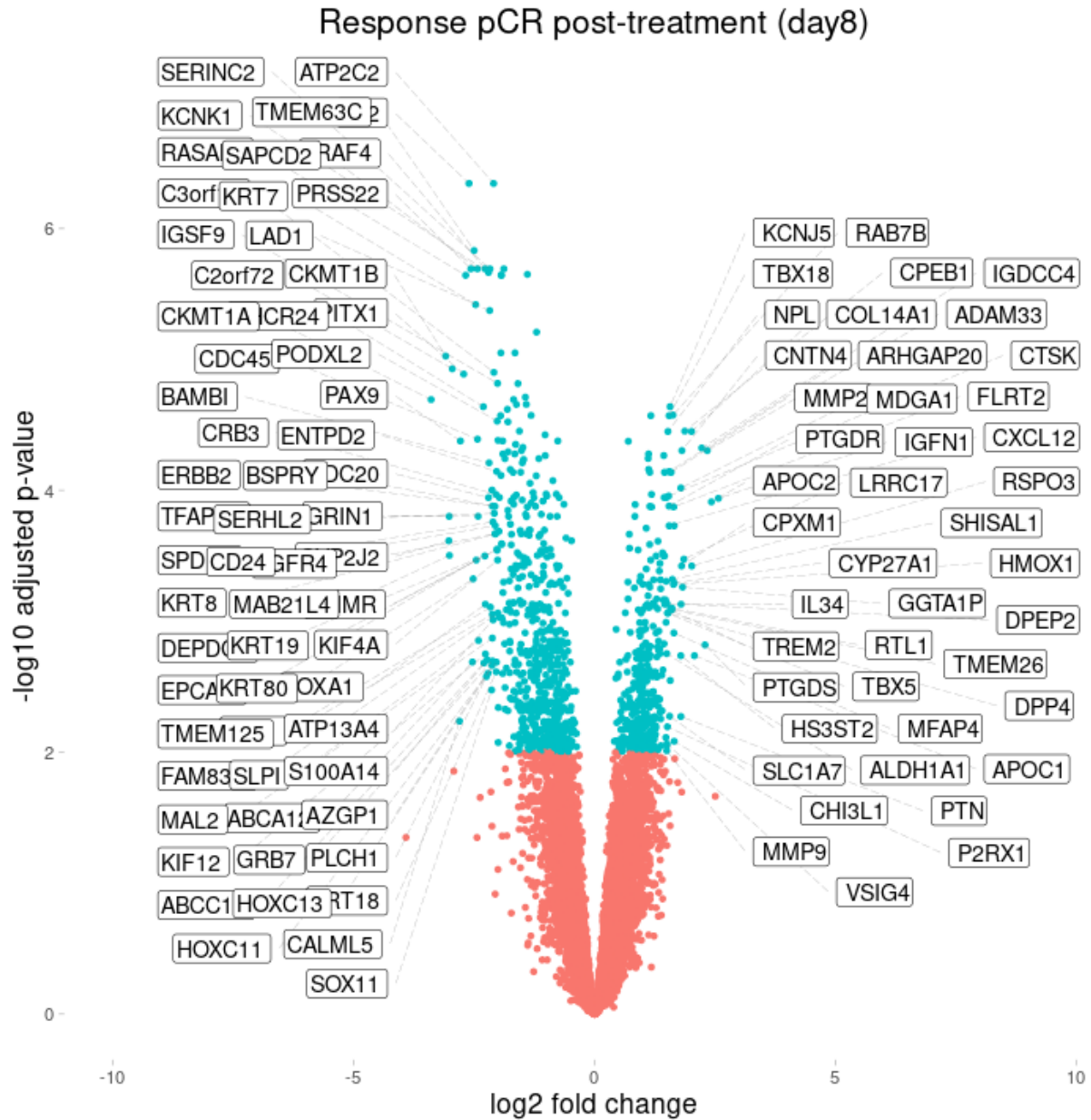
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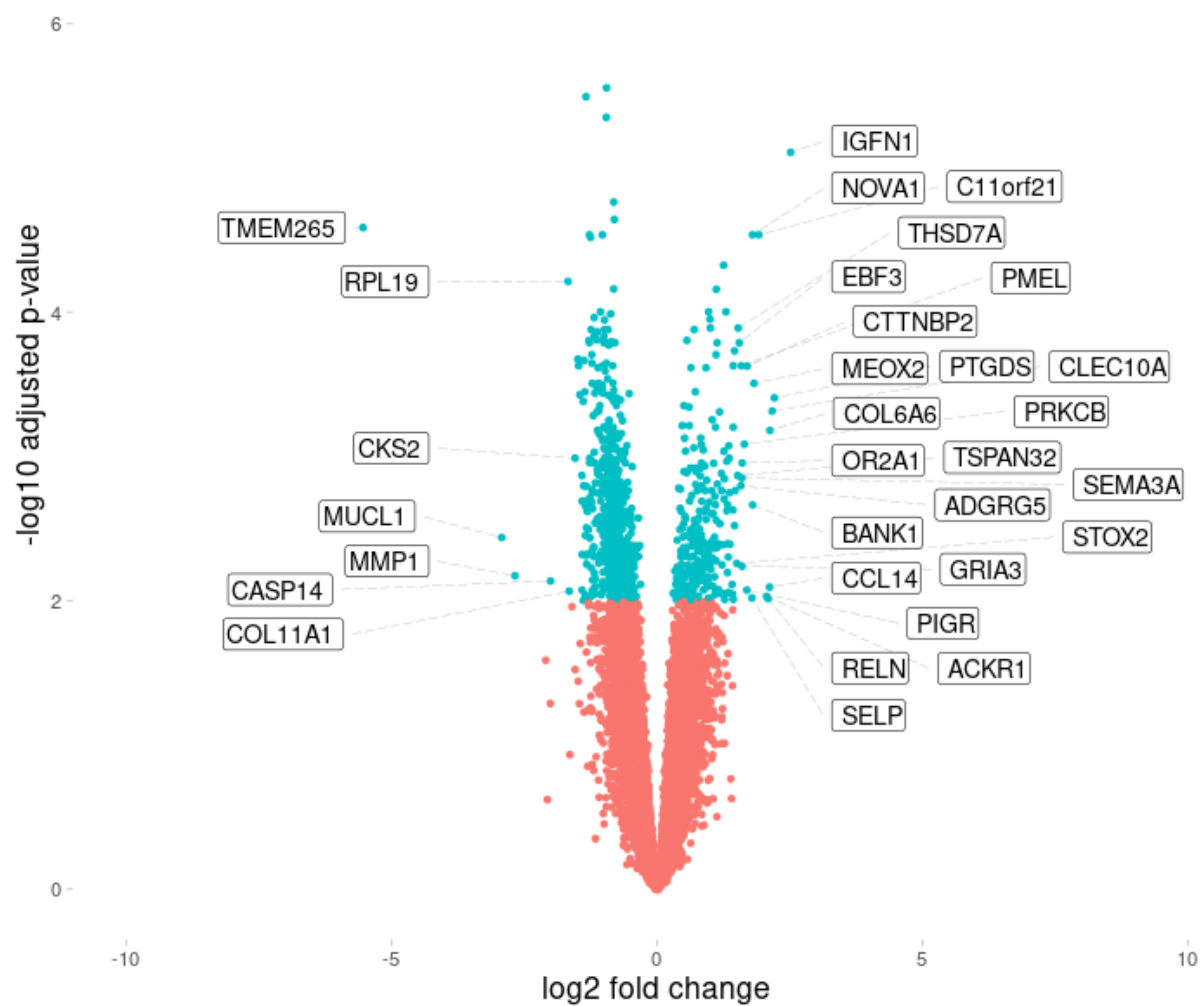
Overview

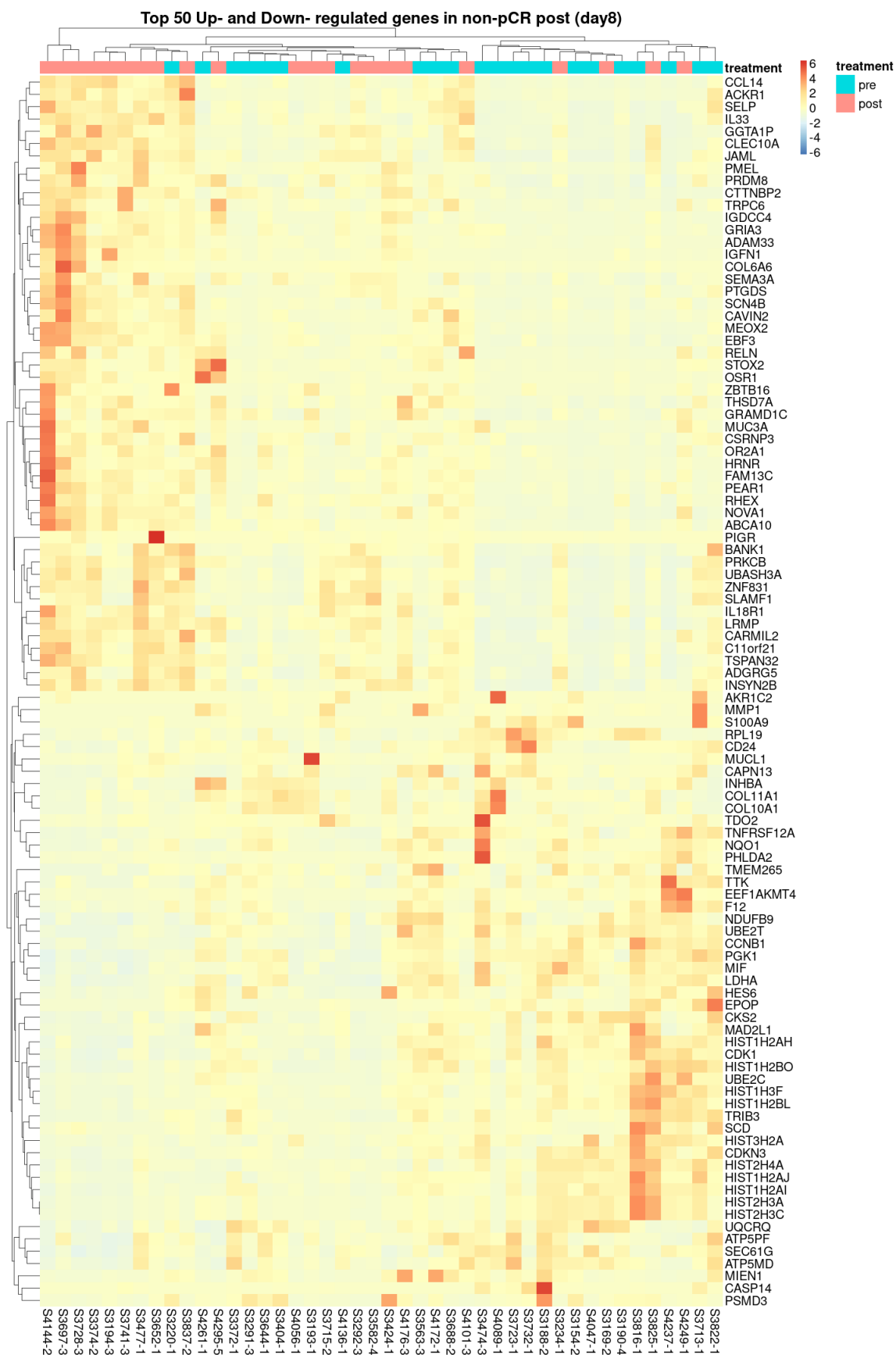
- **paired multifactor test version**
- Principal Investigator: Beth Overmoyer
- Experiment: RNAseq_analysis_of_inflammatory_breast_cancer_hbc04141
- study 6 was excluded because of low read depth in 3373-3
- <https://www.bioconductor.org/packages/release/bioc/vignettes/DEGreport/inst/doc/DEGreport.html>
- AnnotationHub. We use ensembl version matching bcbio pipeline - v94.
- HBC materials
- HBC materials - functional analysis
- <http://bioconductor.org/packages/release/bioc/vignettes/DESeq2/inst/doc/DESeq2.html>
- <https://support.bioconductor.org/p/62357/#62368>
- <https://support.bioconductor.org/p/84241/>
- <https://support.bioconductor.org/p/98628/>

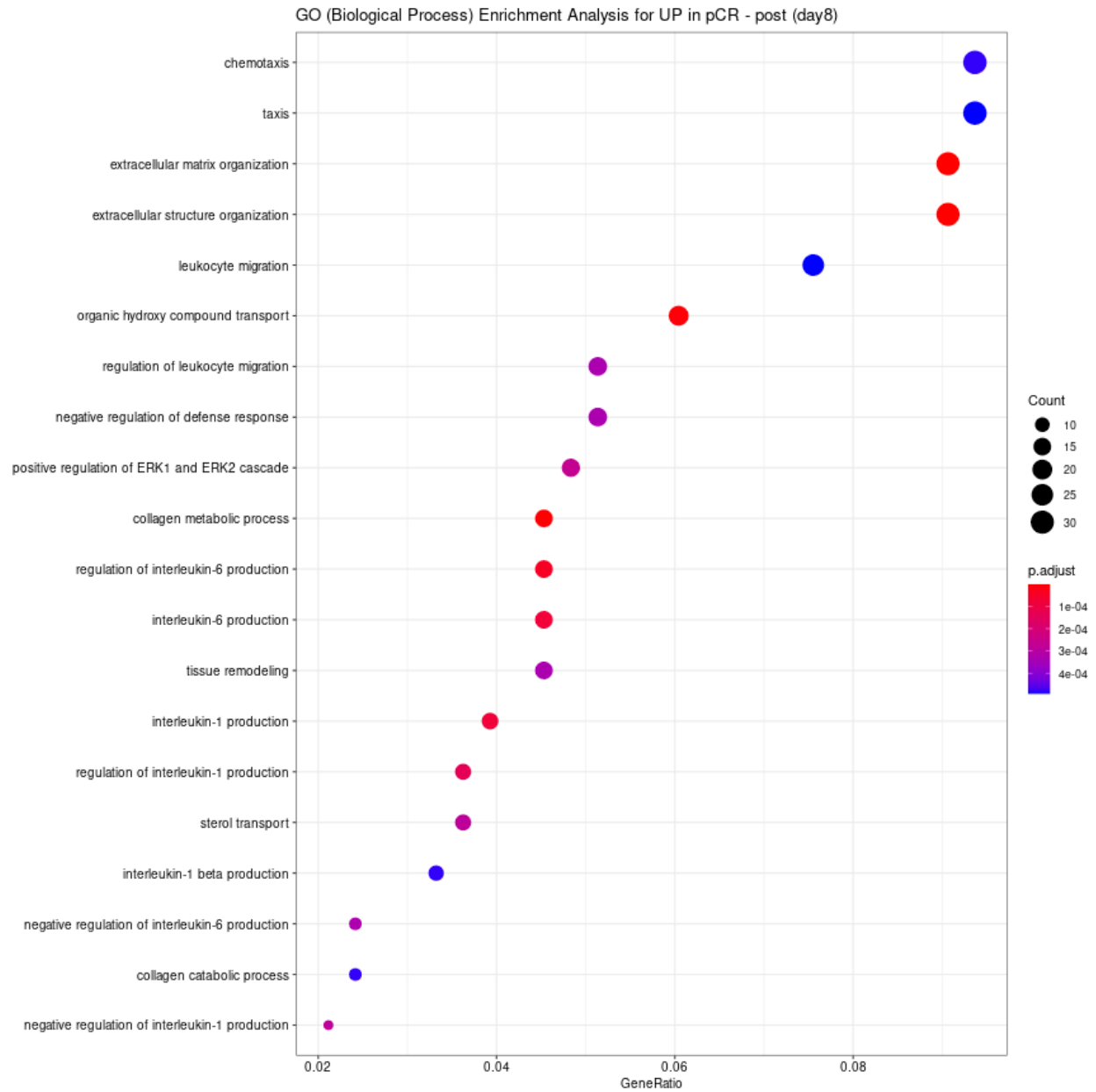
fig5a

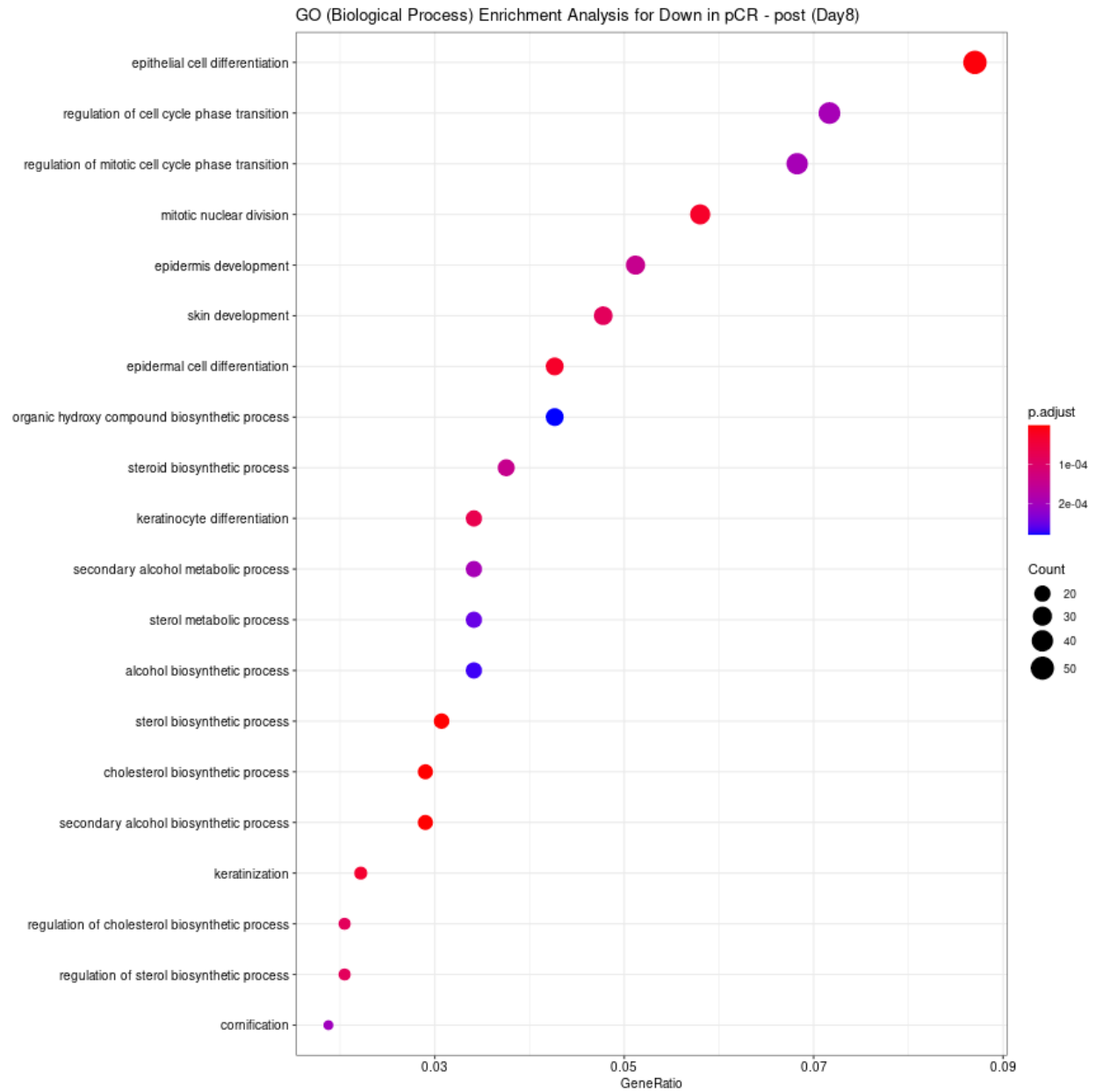


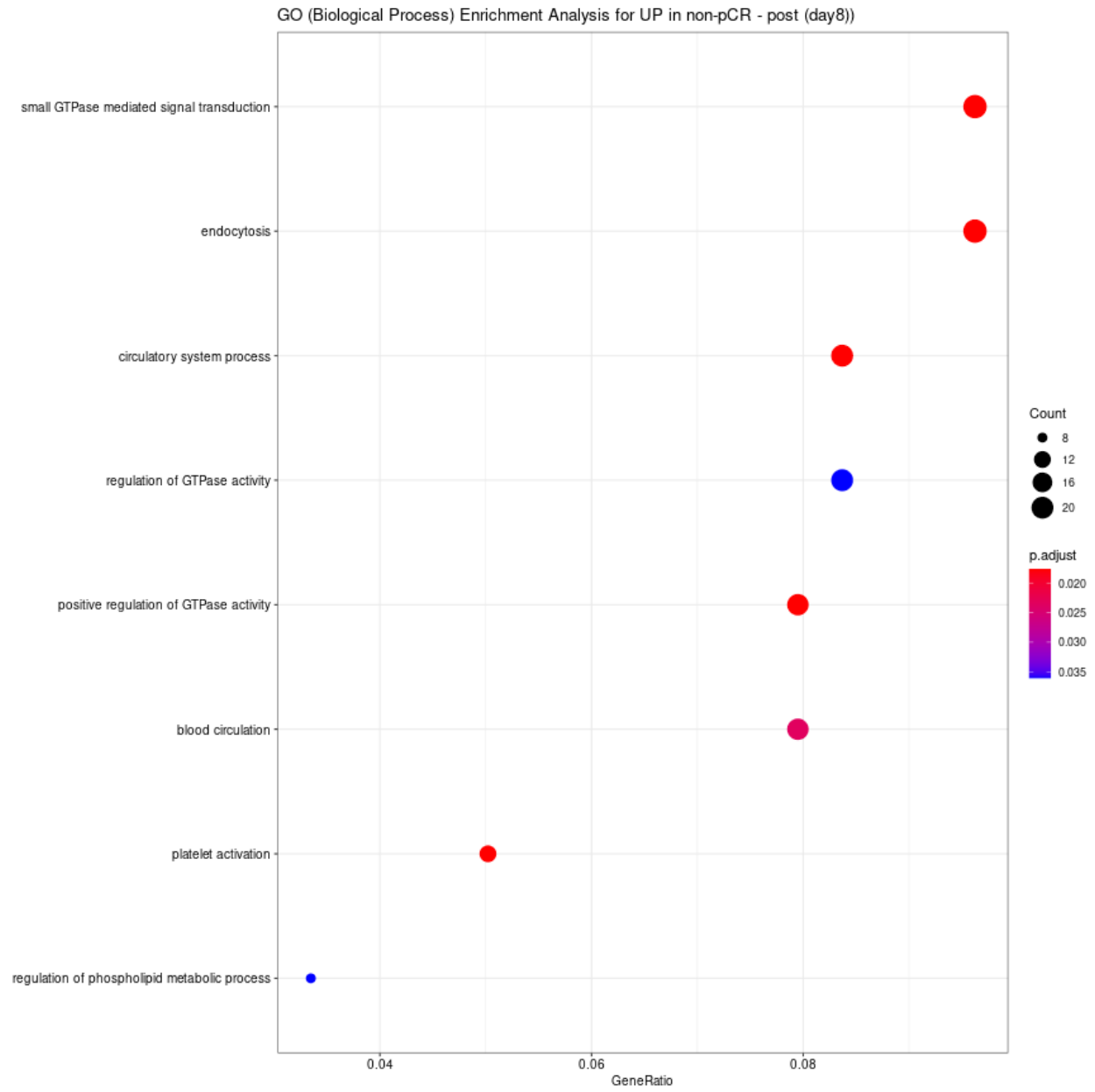
Response non-pCR post treatment (day8)

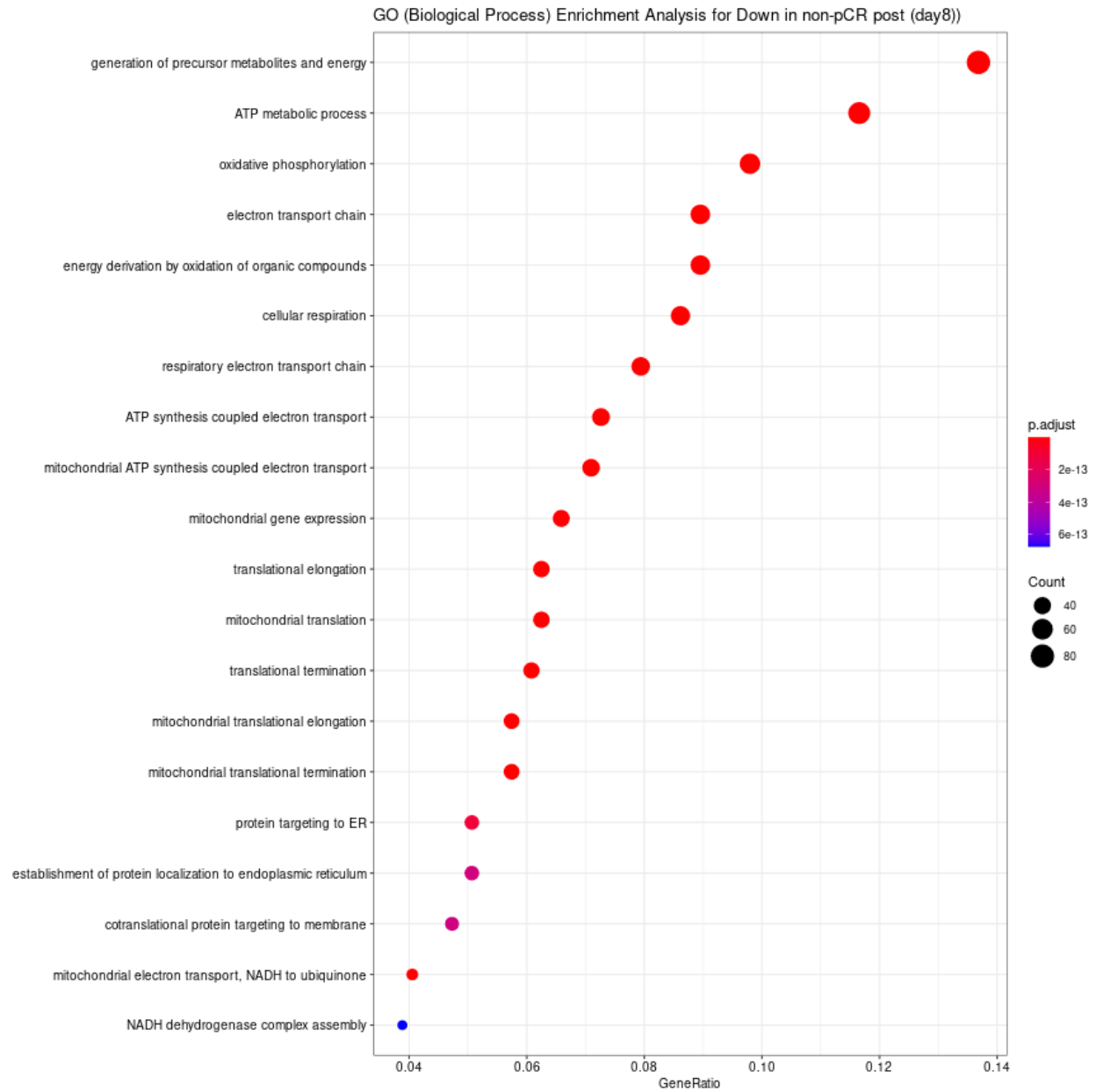












R session

```
sessionInfo()
```

```
## R version 4.0.5 (2021-03-31)
## Platform: x86_64-redhat-linux-gnu (64-bit)
## Running under: Fedora 32 (Workstation Edition)
##
## Matrix products: default
## BLAS/LAPACK: /usr/lib64/libopenblas-r0.3.12.so
##
## locale:
##  [1] LC_CTYPE=en_CA.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_CA.UTF-8      LC_COLLATE=en_CA.UTF-8
##  [5] LC_MONETARY=en_CA.UTF-8  LC_MESSAGES=en_CA.UTF-8
##  [7] LC_PAPER=en_CA.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_CA.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel stats4      stats      graphics  grDevices  utils      datasets
## [8] methods   base
##
## other attached packages:
##  [1] clusterProfiler_3.18.1      writexl_1.4.0
##  [3] ggplotify_0.0.7            ensemblDb_2.14.1
##  [5] AnnotationFilter_1.14.0     GenomicFeatures_1.42.3
##  [7] AnnotationDbi_1.52.0        AnnotationHub_2.22.1
##  [9] BiocFileCache_1.14.0        dbplyr_2.1.1
## [11] knitr_1.33                  ggrepel_0.9.1
## [13] tximport_1.18.0            DESeqReport_1.26.0
## [15] pheatmap_1.0.12            RColorBrewer_1.1-2
## [17] forcats_0.5.1              stringr_1.4.0
## [19] dplyr_1.0.7                purrr_0.3.4
## [21] readr_1.4.0                tidyr_1.1.3
## [23] tibble_3.1.2               ggplot2_3.3.5
## [25] tidyverse_1.3.1            DESeq2_1.30.1
## [27] SummarizedExperiment_1.20.0 Biobase_2.50.0
## [29] MatrixGenerics_1.2.1       matrixStats_0.59.0
## [31] GenomicRanges_1.42.0       GenomeInfoDb_1.26.7
## [33] IRanges_2.24.1             S4Vectors_0.28.1
## [35] BiocGenerics_0.36.1
##
## loaded via a namespace (and not attached):
##  [1] utf8_1.2.1                  tidyselect_1.1.1
##  [3] RSQLite_2.2.7              grid_4.0.5
##  [5] BiocParallel_1.24.1        scatterpie_0.1.6
##  [7] munsell_0.5.0              withr_2.4.2
##  [9] colorspace_2.0-2           GOSemSim_2.16.1
## [11] highr_0.9                  rstudioapi_0.13
## [13] DOSE_3.16.0                labeling_0.4.2
## [15] lasso2_1.2-21.1            GenomeInfoDbData_1.2.4
## [17] polyclip_1.10-0            mnormt_2.0.2
## [19] farver_2.1.0               bit64_4.0.5
```

## [21] downloader_0.4	vctr_0.3.8
## [23] generics_0.1.0	xfun_0.22
## [25] R6_2.5.0	graphlayouts_0.7.1
## [27] clue_0.3-59	locfit_1.5-9.4
## [29] bitops_1.0-7	cachem_1.0.5
## [31] reshape_0.8.8	fgsea_1.16.0
## [33] gridGraphics_0.5-1	DelayedArray_0.16.3
## [35] assertthat_0.2.1	promises_1.2.0.1
## [37] scales_1.1.1	ggraph_2.0.5
## [39] enrichplot_1.10.2	gtable_0.3.0
## [41] Cairo_1.5-12.2	tidygraph_1.2.0
## [43] rlang_0.4.11	genefilter_1.72.1
## [45] GlobalOptions_0.1.2	splines_4.0.5
## [47] rtracklayer_1.50.0	lazyeval_0.2.2
## [49] broom_0.7.8	BiocManager_1.30.16
## [51] yaml_2.2.1	reshape2_1.4.4
## [53] modelr_0.1.8	backports_1.2.1
## [55] httpuv_1.6.1	qvalue_2.22.0
## [57] tools_4.0.5	psych_2.1.6
## [59] logging_0.10-108	ellipsis_0.3.2
## [61] ggdendro_0.1.22	Rcpp_1.0.7
## [63] plyr_1.8.6	progress_1.2.2
## [65] zlibbioc_1.36.0	RCurl_1.98-1.3
## [67] prettyunits_1.1.1	openssl_1.4.4
## [69] viridis_0.6.1	GetoptLong_1.0.5
## [71] cowplot_1.1.1	haven_2.4.1
## [73] cluster_2.1.1	fs_1.5.0
## [75] magrittr_2.0.1	data.table_1.14.0
## [77] DO.db_2.9	circlize_0.4.13
## [79] reprex_2.0.0	tmvnsim_1.0-2
## [81] ProtGenerics_1.22.0	hms_1.1.0
## [83] mime_0.11	evaluate_0.14
## [85] xtable_1.8-4	XML_3.99-0.6
## [87] readxl_1.3.1	gridExtra_2.3
## [89] shape_1.4.6	compiler_4.0.5
## [91] biomaRt_2.46.3	shadowtext_0.0.8
## [93] crayon_1.4.1	htmltools_0.5.1.1
## [95] later_1.2.0	geneplotter_1.68.0
## [97] lubridate_1.7.10	DBI_1.1.1
## [99] tweenr_1.0.2	ComplexHeatmap_2.6.2
## [101] MASS_7.3-53.1	rappdirs_0.3.3
## [103] Matrix_1.3-4	cli_3.0.1
## [105] igraph_1.2.6	pkgconfig_2.0.3
## [107] rvcheck_0.1.8	GenomicAlignments_1.26.0
## [109] xml2_1.3.2	annotate_1.68.0
## [111] XVector_0.30.0	rvest_1.0.0
## [113] digest_0.6.27	ConsensusClusterPlus_1.54.0
## [115] Biostrings_2.58.0	rmarkdown_2.6
## [117] cellranger_1.1.0	fastmatch_1.1-0
## [119] edgeR_3.32.1	curl_4.3.2
## [121] shiny_1.6.0	Rsamtools_2.6.0
## [123] rjson_0.2.20	lifecycle_1.0.0
## [125] nlme_3.1-152	jsonlite_1.7.2
## [127] viridisLite_0.4.0	askpass_1.1

## [129]	limma_3.46.0	fansi_0.5.0
## [131]	pillar_1.6.1	lattice_0.20-41
## [133]	Nozzle.R1_1.1-1	fastmap_1.1.0
## [135]	httr_1.4.2	survival_3.2-10
## [137]	GO.db_3.12.1	interactiveDisplayBase_1.28.0
## [139]	glue_1.4.2	png_0.1-7
## [141]	BiocVersion_3.12.0	bit_4.0.4
## [143]	ggforce_0.3.3	stringi_1.7.3
## [145]	blob_1.2.1	memoise_2.0.0