

FARDEEP analysis

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Contents

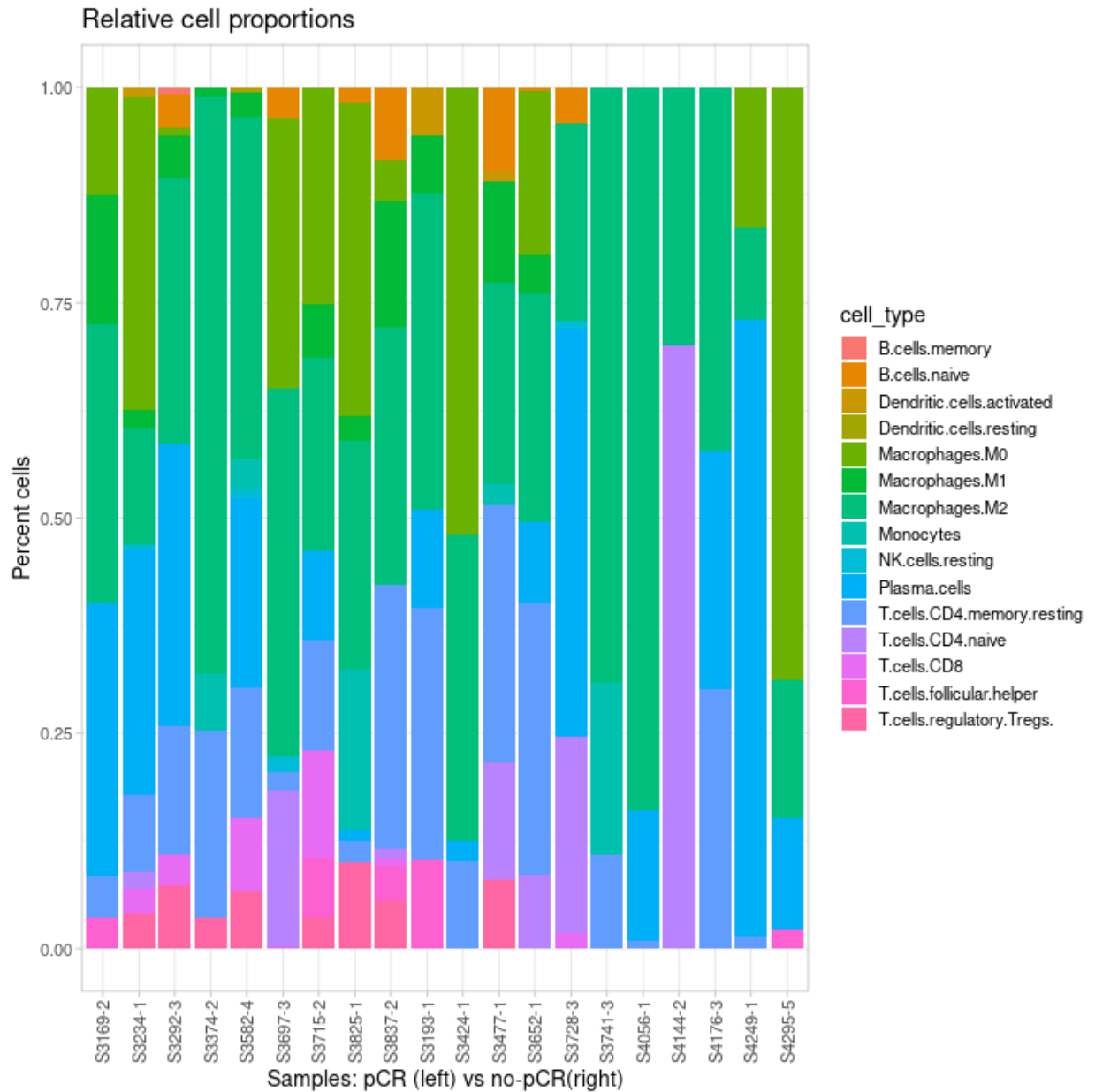
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Overview

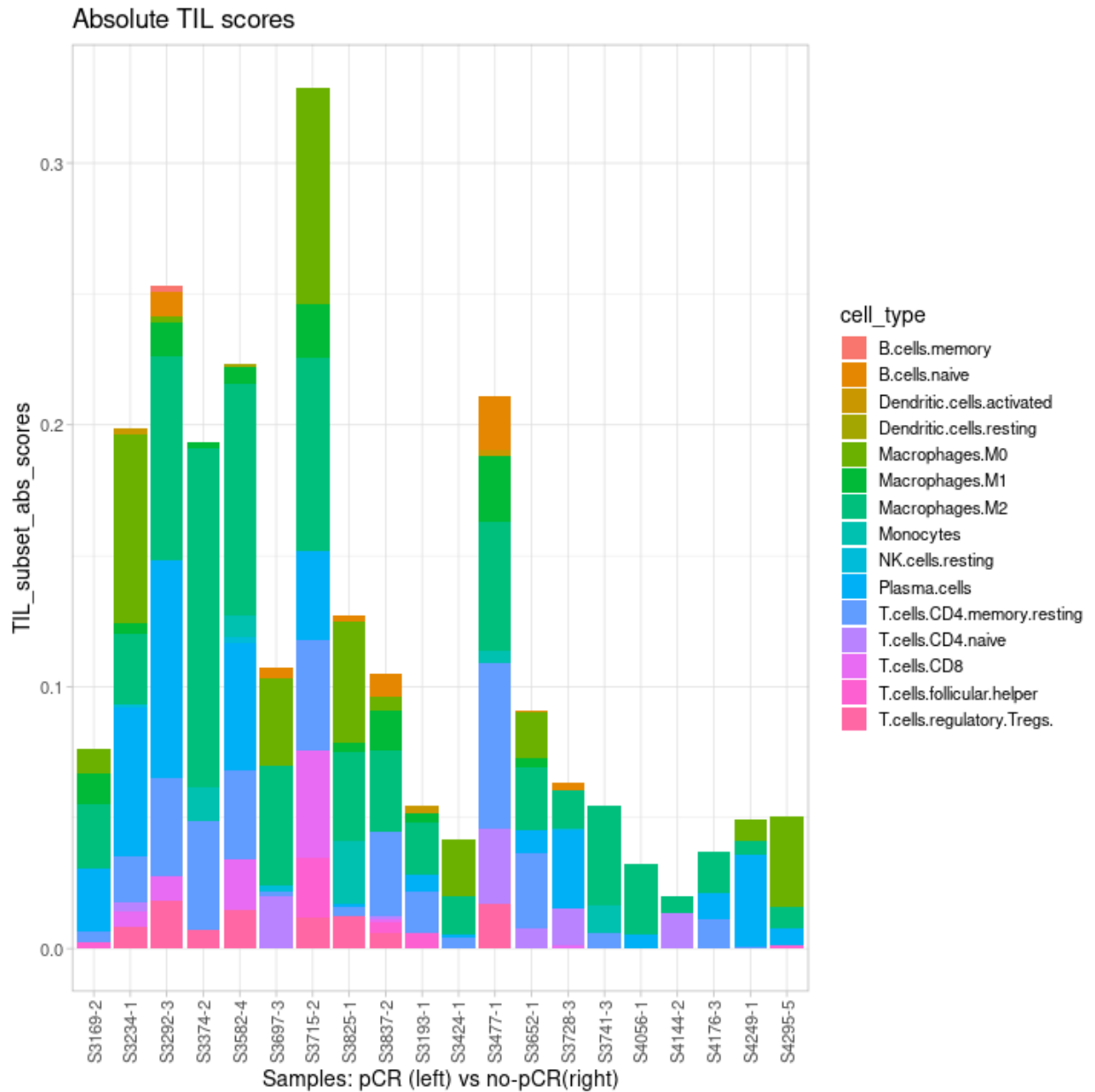
- Principal Investigator: Beth Overmoyer
- Experiment: RNAseq_analysis_of_inflammatory_breast_cancer_hbc04141
- study 6 was excluded because of low read depth in 3373-3
- <https://cran.r-project.org/web/packages/FARDEEP/FARDEEP.pdf>

FARDEEP

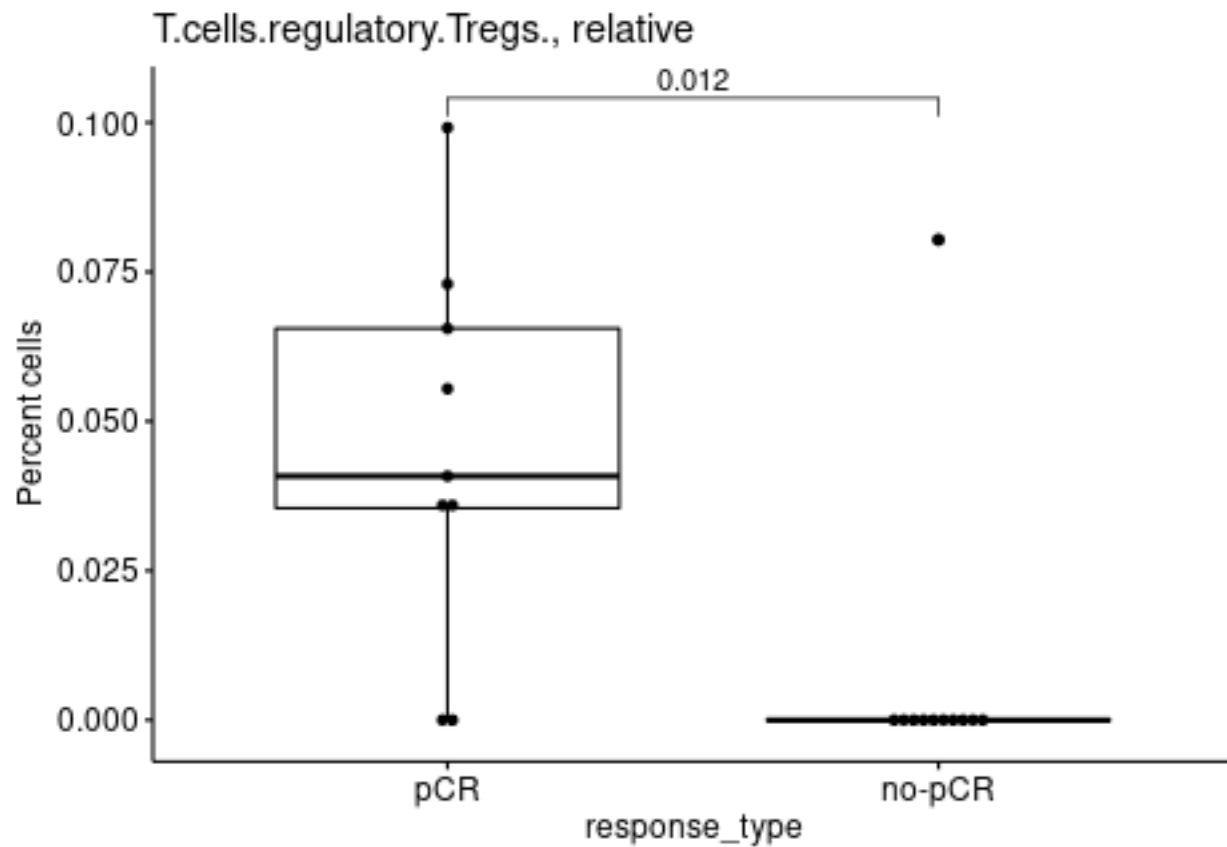
```
df_fardeep_long$response_order <- ifelse(df_fardeep_long$response == "Yes", 0, 1)
df_fardeep_long %>% ggplot(aes(fill = cell_type,
                               y = cell_pct,
                               x = reorder(sample_name, response_order))) +
  geom_bar(position = "stack",
           stat = "identity") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)) +
  xlab("Samples: pCR (left) vs no-pCR(right)") +
  ylab("Percent cells") +
  ggtitle("Relative cell proportions")
```



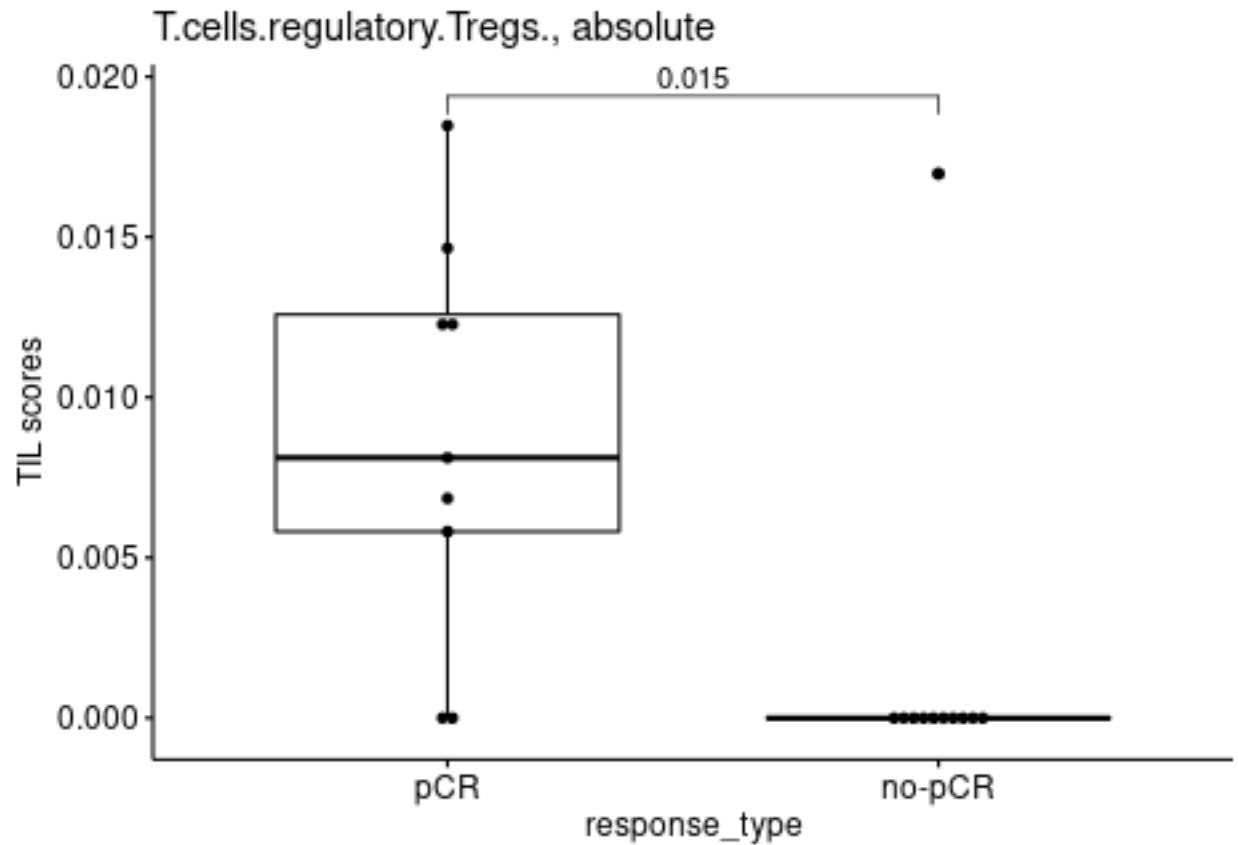
```
df_fardeep_abs_long$response_order <- ifelse(df_fardeep_abs_long$response == "Yes", 0, 1)
df_fardeep_abs_long %>% ggplot(aes(fill = cell_type,
                                   y = TIL_subset_abs_scores,
                                   x = reorder(sample_name, response_order))) +
  geom_bar(position = "stack",
           stat = "identity") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1)) +
  xlab("Samples: pCR (left) vs no-pCR(right)") +
  ggtitle("Absolute TIL scores")
```



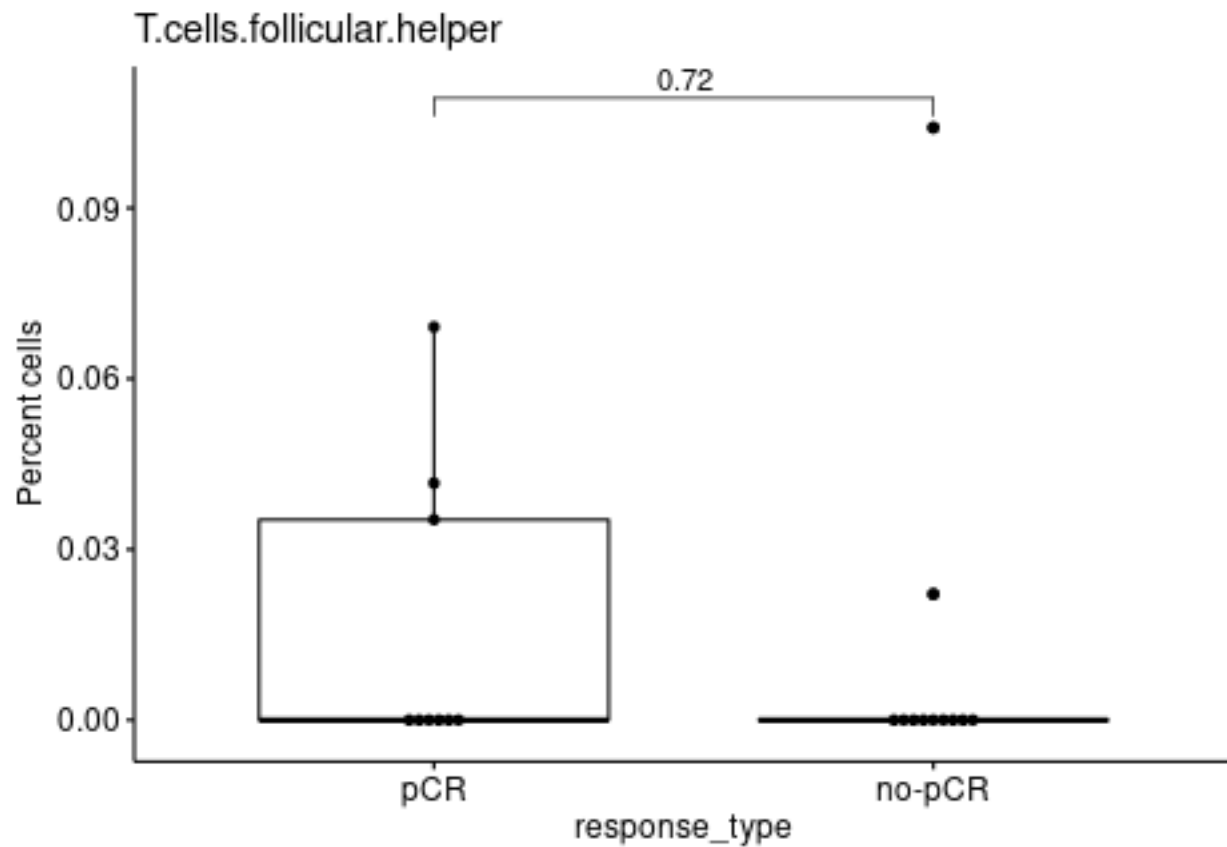
```
library(ggpubr)
cell_type <- "T.cells.regulatory.Tregs."
my_comparisons <- list(c("pCR", "no-pCR"))
ggboxplot(df_fardeep,
  x = "response_type", y = cell_type,
  add = "dotplot", add.params = list(size = 0.5)) +
  stat_compare_means(comparisons = my_comparisons, method = "t.test") +
  ylab("Percent cells") +
  ggtitle(paste0(cell_type, ", relative"))
```



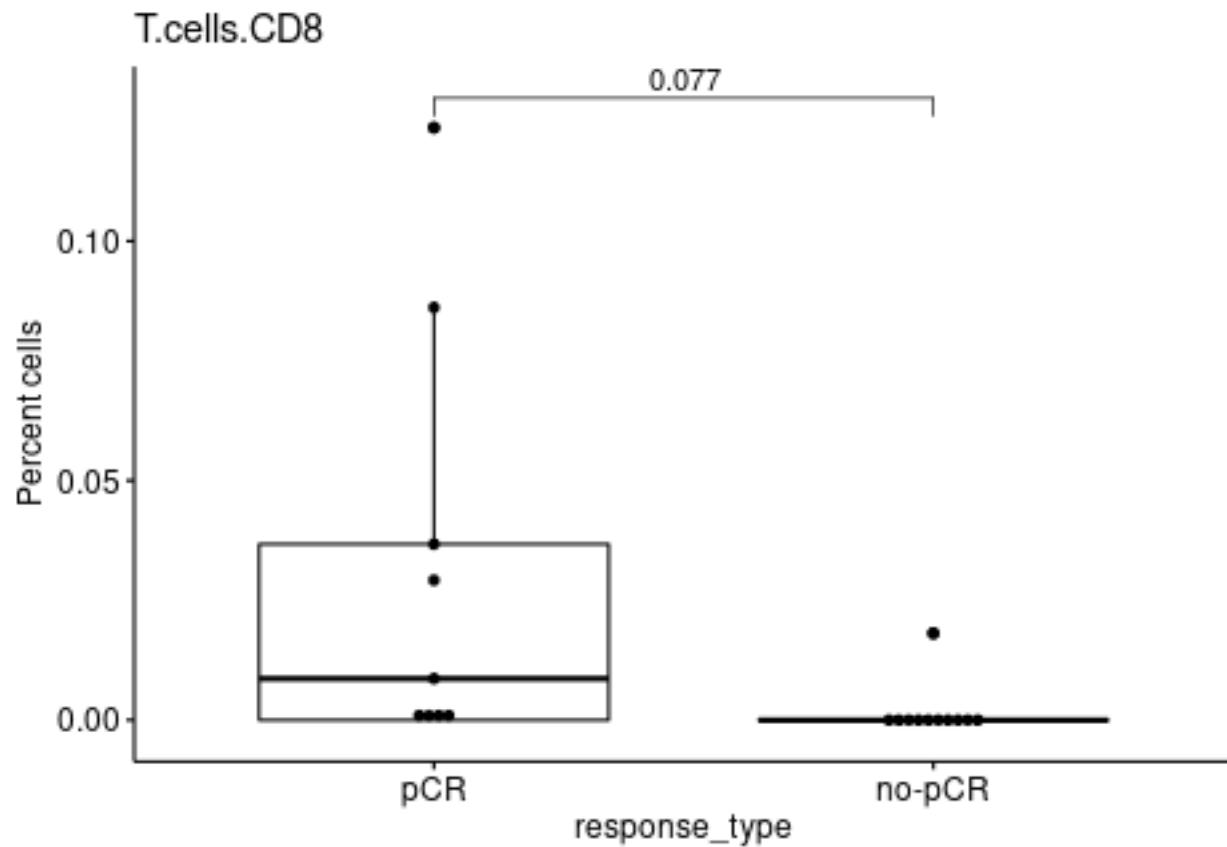
```
library(ggpubr)
cell_type <- "T.cells.regulatory.Tregs."
my_comparisons <- list(c("pCR", "no-pCR"))
ggboxplot(df_fardeep_abs,
  x = "response_type", y = cell_type,
  add = "dotplot", add.params = list(size = 0.5)) +
  stat_compare_means(comparisons = my_comparisons, method = "t.test") +
  ylab("TIL scores") +
  ggtitle(paste0(cell_type, ", absolute"))
```



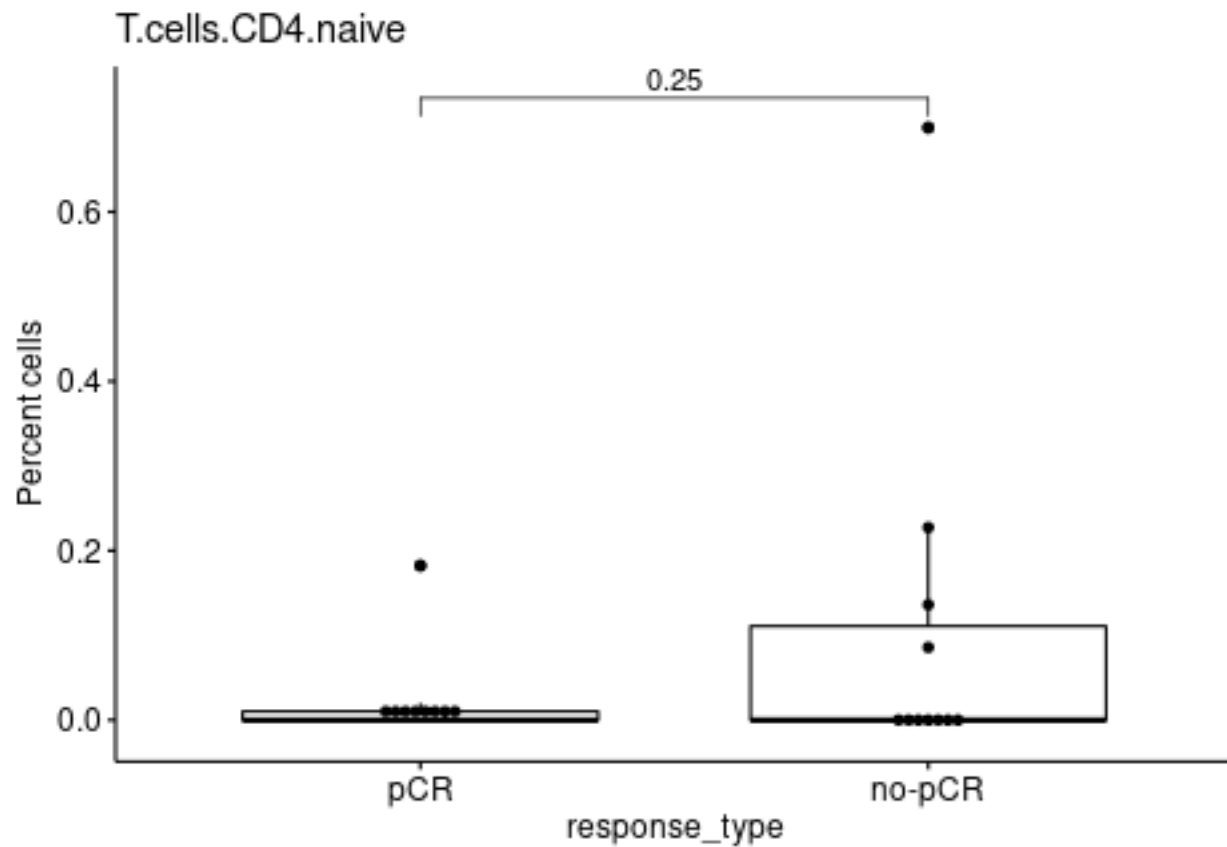
```
cell_type <- "T.cells.follicular.helper"
my_comparisons <- list(c("pCR", "no-pCR"))
ggboxplot(df_fardeep,
  x = "response_type", y = cell_type,
  add = "dotplot", add.params = list(size = 0.5)) +
  stat_compare_means(comparisons = my_comparisons, method = "t.test") +
  ylab("Percent cells") +
  ggtitle(cell_type)
```



```
cell_type <- "T.cells.CD8"
my_comparisons <- list(c("pCR", "no-pCR"))
ggboxplot(df_fardeep,
  x = "response_type", y = cell_type,
  add = "dotplot", add.params = list(size = 0.5)) +
  stat_compare_means(comparisons = my_comparisons, method = "t.test") +
  ylab("Percent cells") +
  ggtitle(cell_type)
```

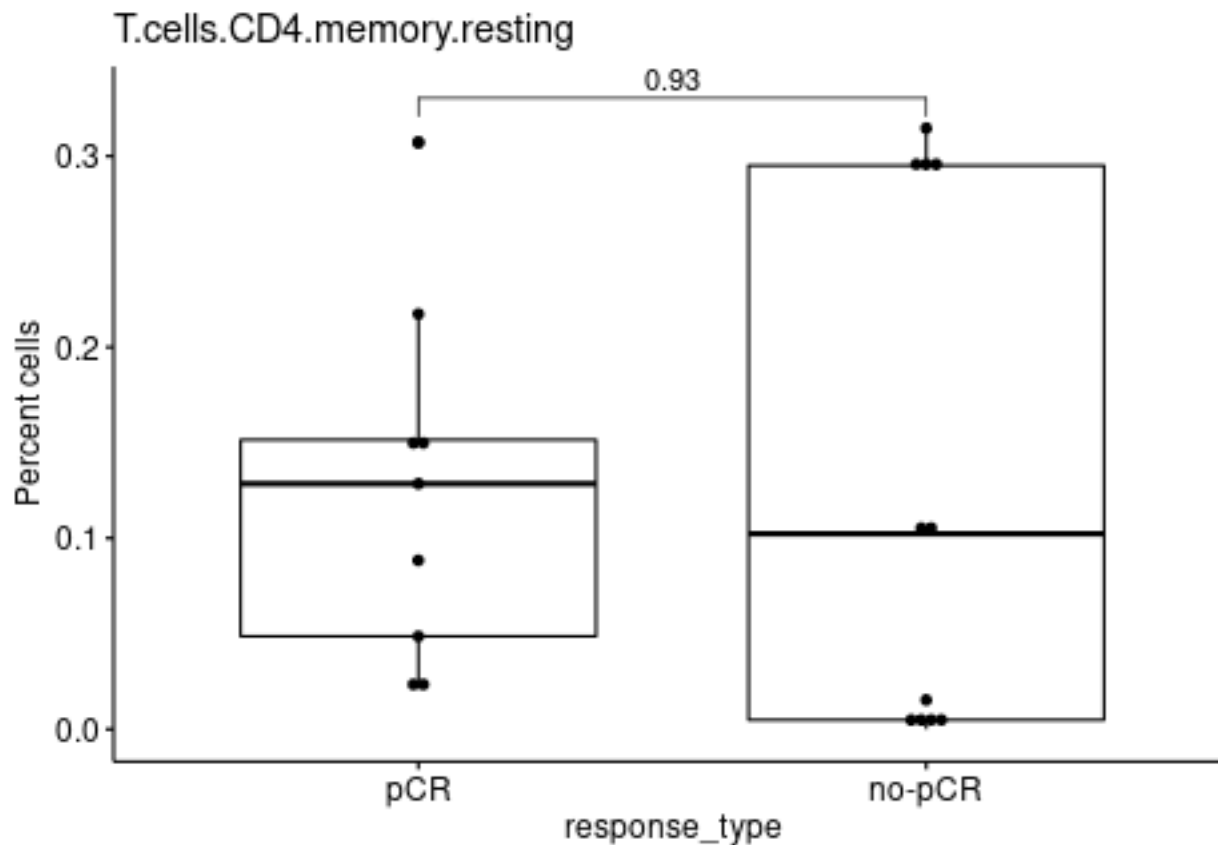


```
cell_type <- "T.cells.CD4.naive"
my_comparisons <- list(c("pCR", "no-pCR"))
ggboxplot(df_fardeep,
  x = "response_type", y = cell_type,
  add = "dotplot", add.params = list(size = 0.5)) +
  stat_compare_means(comparisons = my_comparisons, method = "t.test") +
  ylab("Percent cells") +
  ggtitle(cell_type)
```



```
cell_type <- "T.cells.CD4.memory.resting"

my_comparisons <- list(c("pCR", "no-pCR"))
ggboxplot(df_fardeep,
  x = "response_type", y = cell_type,
  add = "dotplot", add.params = list(size = 0.5)) +
  stat_compare_means(comparisons = my_comparisons, method = "t.test") +
  ylab("Percent cells") +
  ggtitle(cell_type)
```

R session

`sessionInfo()`

```
## R version 4.0.3 (2020-10-10)
## 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] ggpubr_0.4.0             ensemblDb_2.14.1
##  [3] AnnotationFilter_1.14.0   GenomicFeatures_1.42.3
##  [5] AnnotationDbi_1.52.0      AnnotationHub_2.22.1
```

```

## [7] BiocFileCache_1.14.0      dbplyr_2.1.1
## [9] knitr_1.30                 ggrepel_0.9.1
## [11] tximport_1.18.0           DEGreport_1.26.0
## [13] pheatmap_1.0.12           RColorBrewer_1.1-2
## [15] forcats_0.5.1             stringr_1.4.0
## [17] dplyr_1.0.5               purrr_0.3.4
## [19] readr_1.4.0               tidyr_1.1.3
## [21] tibble_3.1.1              ggplot2_3.3.3
## [23] tidyverse_1.3.1           DESeq2_1.30.1
## [25] SummarizedExperiment_1.20.0 Biobase_2.50.0
## [27] MatrixGenerics_1.2.1      matrixStats_0.58.0
## [29] GenomicRanges_1.42.0      GenomeInfoDb_1.26.7
## [31] IRanges_2.24.1            S4Vectors_0.28.1
## [33] BiocGenerics_0.36.1
##
## loaded via a namespace (and not attached):
## [1] readxl_1.3.1               backports_1.2.1
## [3] circlize_0.4.12            plyr_1.8.6
## [5] lazyeval_0.2.2             ConsensusClusterPlus_1.54.0
## [7] splines_4.0.3              BiocParallel_1.24.1
## [9] digest_0.6.27              htmltools_0.5.1.1
## [11] fansi_0.4.2                magrittr_2.0.1
## [13] memoise_2.0.0              cluster_2.1.0
## [15] openxlsx_4.2.3             limma_3.46.0
## [17] ComplexHeatmap_2.6.2       Biostrings_2.58.0
## [19] annotate_1.68.0            Nozzle.R1_1.1-1
## [21] modelr_0.1.8               askpass_1.1
## [23] prettyunits_1.1.1          colorspace_2.0-0
## [25] blob_1.2.1                 rvest_1.0.0
## [27] rappdirs_0.3.3             haven_2.4.1
## [29] xfun_0.19                  crayon_1.4.1
## [31] RCurl_1.98-1.3             jsonlite_1.7.2
## [33] genefilter_1.72.1          survival_3.2-7
## [35] glue_1.4.2                 gtable_0.3.0
## [37] zlibbioc_1.36.0            XVector_0.30.0
## [39] GetoptLong_1.0.5           DelayedArray_0.16.3
## [41] car_3.0-10                 shape_1.4.5
## [43] abind_1.4-5                scales_1.1.1
## [45] DBI_1.1.1                  edgeR_3.32.1
## [47] rstatix_0.7.0              Rcpp_1.0.6
## [49] progress_1.2.2             xtable_1.8-4
## [51] lasso2_1.2-21.1            tmvnsim_1.0-2
## [53] clue_0.3-59                foreign_0.8-80
## [55] bit_4.0.4                  httr_1.4.2
## [57] ellipsis_0.3.1             farver_2.1.0
## [59] pkgconfig_2.0.3            reshape_0.8.8
## [61] XML_3.99-0.6               locfit_1.5-9.4
## [63] utf8_1.2.1                 labeling_0.4.2
## [65] tidyselect_1.1.0           rlang_0.4.10
## [67] later_1.2.0                munsell_0.5.0
## [69] BiocVersion_3.12.0         cellranger_1.1.0
## [71] tools_4.0.3                cachem_1.0.4
## [73] cli_2.5.0                  generics_0.1.0
## [75] RSQLite_2.2.7              broom_0.7.6

```

## [77] evaluate_0.14	fastmap_1.1.0
## [79] ggdendro_0.1.22	yaml_2.2.1
## [81] bit64_4.0.5	fs_1.5.0
## [83] zip_2.1.1	nlme_3.1-149
## [85] mime_0.9	xml2_1.3.2
## [87] biomaRt_2.46.3	compiler_4.0.3
## [89] rstudioapi_0.13	curl_4.3
## [91] png_0.1-7	interactiveDisplayBase_1.28.0
## [93] ggsignif_0.6.1	reprex_2.0.0
## [95] geneplotter_1.68.0	stringi_1.5.3
## [97] lattice_0.20-41	ProtGenerics_1.22.0
## [99] Matrix_1.2-18	psych_2.1.3
## [101] vctrs_0.3.7	pillar_1.6.0
## [103] lifecycle_1.0.0	BiocManager_1.30.12
## [105] GlobalOptions_0.1.2	data.table_1.14.0
## [107] cowplot_1.1.1	bitops_1.0-7
## [109] rtracklayer_1.50.0	httpuv_1.6.0
## [111] R6_2.5.0	promises_1.2.0.1
## [113] rio_0.5.26	MASS_7.3-53
## [115] assertthat_0.2.1	openssl_1.4.3
## [117] rjson_0.2.20	withr_2.4.2
## [119] GenomicAlignments_1.26.0	Rsamtools_2.6.0
## [121] mnormt_2.0.2	GenomeInfoDbData_1.2.4
## [123] hms_1.0.0	grid_4.0.3
## [125] rmarkdown_2.5	carData_3.0-4
## [127] Cairo_1.5-12.2	logging_0.10-108
## [129] shiny_1.6.0	lubridate_1.7.10