Supplementary data and figures

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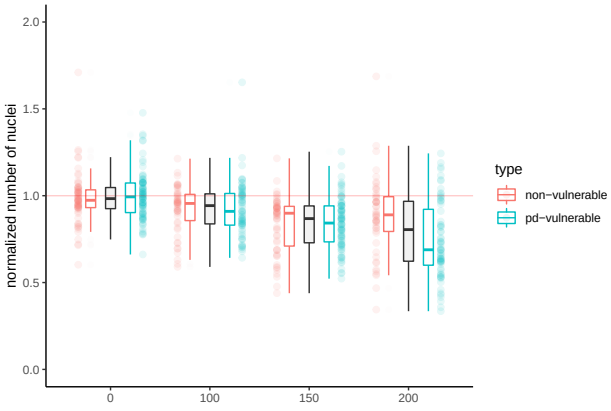
PD-vulnerable neurons are less resilient to cell stress induced by hydrogen peroxide

Figure 1-1

Nuclei (DAPI) count



Kurskal-Wallis

```
    Kruskal-Wallis rank sum test

data:  dapi_normalized by hydrogen_peroxide
Kruskal-Wallis chi-squared = 91.227, df = 3, p-value < 2.2e-16


$method
[1] "Kruskal-Wallis rank sum test"

$var_equal
[1] TRUE

$name
```

```
[1] "dapi_normalized by hydrogen_peroxide"

$statistics
$statistics$statistic
$statistics$statistic$name
[1] "Kruskal-Wallis chi-squared"

$statistics$statistic$value
[1] 91.22654


$statistics$df
[1] 3

$statistics$p
[1] 1.194249e-19


$package
$package$name
[1] "stats"

$package$version
[1] "4.0.3"
```

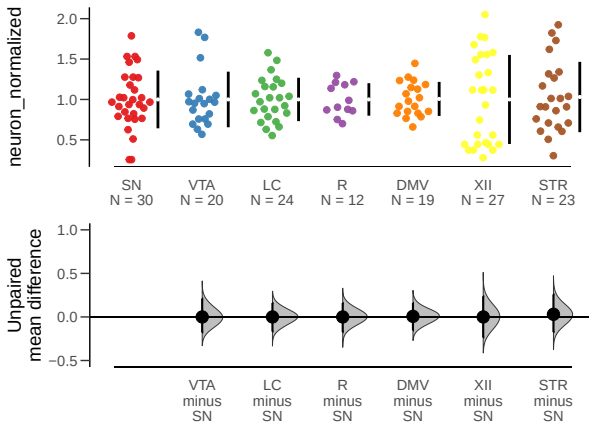
Dunn test

Comparison	Z	P.unadj	P.adj
0 - 100	3.4001879	0.0006734	0.0040404
0 - 150	7.8043915	0.0000000	0.0000000
100 - 150	3.9718484	0.0000713	0.0004279
0 - 200	8.1835348	0.0000000	0.0000000
100 - 200	4.5069337	0.0000066	0.0000395
150 - 200	0.7245953	0.4687004	1.0000000

Comparison	Z	P.unadj	P.adj
0 - 100	3.4001879	0.0006734	0.0040404
0 - 150	7.8043915	0.0000000	0.0000000
100 - 150	3.9718484	0.0000713	0.0004279
0 - 200	8.1835348	0.0000000	0.0000000
100 - 200	4.5069337	0.0000066	0.0000395
150 - 200	0.7245953	0.4687004	1.0000000

Estimation statistics

0 micromollar




```
dabestr (Data Analysis with Bootstrap Estimation in R) v0.3.0
=============================================================

Good morning!
The current time is 11:59 am on Wednesday June 15, 2022.

Dataset    :  .
X Variable :  neuron
Y Variable :  neuron_normalized

Unpaired mean difference of VTA (n = 20) minus SN (n = 30)
 0 [95CI  -0.179; 0.212]

Unpaired mean difference of LC (n = 24) minus SN (n = 30)
 0 [95CI  -0.168; 0.16]

Unpaired mean difference of R (n = 12) minus SN (n = 30)
 -1.11e-16 [95CI  -0.175; 0.16]

Unpaired mean difference of DMV (n = 19) minus SN (n = 30)
 0.00684 [95CI  -0.155; 0.16]

Unpaired mean difference of XII (n = 27) minus SN (n = 30)
 0 [95CI  -0.237; 0.238]

Unpaired mean difference of STR (n = 23) minus SN (n = 30)
 0.0303 [95CI  -0.174; 0.259]


5000 bootstrap resamples.
All confidence intervals are bias-corrected and accelerated.
```

```
output <- shared.control.mean_diff

output
```

```
## dabestr (Data Analysis with Bootstrap Estimation in R) v0.3.0
## =============================================================
##
```

```
## Good morning!
## The current time is 11:59 am on Wednesday June 15, 2022.
##
## Dataset    :  .
## X Variable :  neuron
## Y Variable :  neuron_normalized
##
## Unpaired mean difference of VTA (n = 20) minus SN (n = 30)
##  0 [95CI  -0.179; 0.212]
##
## Unpaired mean difference of LC (n = 24) minus SN (n = 30)
##  0 [95CI  -0.168; 0.16]
##
## Unpaired mean difference of R (n = 12) minus SN (n = 30)
##  -1.11e-16 [95CI  -0.175; 0.16]
##
## Unpaired mean difference of DMV (n = 19) minus SN (n = 30)
##  0.00684 [95CI  -0.155; 0.16]
##
## Unpaired mean difference of XII (n = 27) minus SN (n = 30)
##  0 [95CI  -0.237; 0.238]
##
## Unpaired mean difference of STR (n = 23) minus SN (n = 30)
##  0.0303 [95CI  -0.174; 0.259]
##
##
## 5000 bootstrap resamples.
## All confidence intervals are bias-corrected and accelerated.
```

```
output$result
```

```
## # A tibble: 6 x 15
##   control_group test_group control_size test_size effect_size paired variable
##   <chr>         <chr>             <int>     <int> <chr>       <lgl>  <chr>
## 1 SN            VTA                  30        20 mean_diff   FALSE  neuron_nor~
## 2 SN            LC                   30        24 mean_diff   FALSE  neuron_nor~
## 3 SN            R                    30        12 mean_diff   FALSE  neuron_nor~
## 4 SN            DMV                  30        19 mean_diff   FALSE  neuron_nor~
## 5 SN            XII                  30        27 mean_diff   FALSE  neuron_nor~
## 6 SN            STR                  30        23 mean_diff   FALSE  neuron_nor~
## # ... with 8 more variables: difference <dbl>, ci <dbl>, bca_ci_low <dbl>,
## #   bca_ci_high <dbl>, pct_ci_low <dbl>, pct_ci_high <dbl>, bootstraps <list>,
## #   nboots <int>
```

```
table_out <- output$result %>%
  select(control_group, test_group, difference, bca_ci_low, bca_ci_high)

table_out %>%
  knitr::kable(digits = 3, align = "c")
```

control_group	test_group	difference	bca_ci_low	bca_ci_high
SN	VTA	0.000	-0.179	0.212
SN	LC	0.000	-0.168	0.160
SN	R	0.000	-0.175	0.160
SN	DMV	0.007	-0.155	0.160
SN	XII	0.000	-0.237	0.238
SN	STR	0.030	-0.174	0.259