

Supplementary figures and tables

Variation in stress tolerance in the Queensland fruit fly

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20 April 2019

Table S 1: Helper functions and packages in R used in the statistical analyses

| R session information: | | | |
|--------------------------------------|---|--|---|
| Based Packages attached: | | | |
| | grid methods datasets | stats base | graphics grDevices utils |
| Attached Packages: | | | |
| | wesanderson_0.3.6 nortest_1.0-4 Formula_1.2-3 xtable_1.8-3 gridExtra_2.3 purrr_0.3.0 magrittr_1.5 dplyr_0.8.0 ggpubr_0.2 | readr_1.3.1 jtrans_0.2.1 survival_2.43-3 psych_1.8.12 sp_1.3-1 stargazer_5.2.2 ggridges_0.5.1 emmeans_1.3.3.0999901 | boot_1.3-20 Hmisc_4.2-0 lattice_0.20-35 egg_0.4.2 ggalluvial_0.9.1 cowplot_0.9.4 ggplot2_3.1.0 RColorBrewer_1.1-2 |
| Packages loaded via namespace | | | |
| | httr_1.4.0 splines_3.4.4 latticeExtra_0.6-28 pillar_1.3.1 digest_0.6.18 colorspace_1.4-0 htmltools_0.3.6 pkgconfig_2.0.2 scales_1.0.0 TH.data_1.0-10 lazyeval_0.2.1 crayon_1.3.4 fansi_0.4.0 xml2_1.2.0 data.table_1.12.0 stringr_1.4.0 kableExtra_1.0.1 rstudioapi_0.9.0 base64enc_0.1-3 codetools_0.2-15 knitr_1.21 parallel_3.4.4 acepack_1.4.1 coda_0.19-2 | tidyR_0.8.2 assertthat_0.2.0 yaml_2.2.0 backports_1.1.3 checkmate_1.9.1 sandwich_2.5-0 Matrix_1.2-14 mvtnorm_1.0-8 htmlTable_1.13.1 withr_2.1.2 cli_1.0.1 estimability_1.3 nlme_3.1-137 foreign_0.8-70 hms_0.4.2 munsell_0.5.0 compiler_3.4.4 htmlwidgets_1.3 rmarkdown_1.11 R6_2.3.0 utf8_1.1.4 Rcpp_1.0.0 tidyselect_0.2.5 | viridisLite_0.3.0 highr_0.7 sessioninfo_1.1.1 glue_1.3.0 rvest_0.3.2 captioner_2.2.3 plyr_1.8.4 webshot_0.5.1 tibble_2.0.1 nnet_7.3-12 mnormt_1.5-5 evaluate_0.13 MASS_7.3-50 tools_3.4.4 multcomp_1.4-8 cluster_2.0.7-1 rlang_0.3.1 labeling_0.3 gttable_0.2.0 zoo_1.8-4 stringi_1.3.1 rpart_4.1-13 xfun_0.4 |

Table S 2: Methodological differences between the standard desiccation tolerance assay and that used for the resampled 2017/2018 collection

| Difference in protocol | First collection | Resampled collection |
|------------------------|----------------------------------|-----------------------------------|
| Egg collection | Egging device | Baby (vine) capsicum |
| Larvae rearing | Gel diet (Mohadeli et al., 2017) | Gel diet and baby (vine) capsicum |
| Tubes | 5 mL | 10 mL |
| Desiccant | 8 silica gel beads | 0.5g silica gel packet |
| Scoring after 16 hours | Every 2 hours | Every 3 hours |

Table S 3: Individual populations for which the wild (G2/G3) and domesticated (G10-15) bioassay results differed significantly. Contrast are calculated for the estimated mean response variable for each population by looking at the differences of the domesticated over the wild populations. The estimated mean of teh contrast are calculated on the log transformed data for the response variables

| Population | ratio | SE | z.ratio | p.value |
|--------------------|-------|------|---------|---------|
| Heat | | | | |
| Alice Springs | 1.09 | 0.09 | 1.07 | 0.28 |
| Batemans Bay | 1.17 | 0.09 | 2.01 | 0.04 |
| Brisbane | 1.17 | 0.09 | 1.97 | 0.05 |
| Darwin | 1.10 | 0.09 | 1.19 | 0.23 |
| Griffith | 1.21 | 0.10 | 2.42 | 0.02 |
| Mareeba | 1.20 | 0.10 | 2.22 | 0.03 |
| Narrabri | 1.10 | 0.09 | 1.20 | 0.23 |
| Sydney | 1.09 | 0.08 | 1.05 | 0.29 |
| Utchee Creek | 1.14 | 0.09 | 1.66 | 0.10 |
| Desiccation | | | | |
| Alice Springs | 0.68 | 0.05 | -5.74 | 0.00 |
| Batemans Bay | 1.02 | 0.07 | 0.27 | 0.79 |
| Brisbane | 1.07 | 0.07 | 1.05 | 0.29 |
| Griffith | 0.90 | 0.06 | -1.56 | 0.12 |
| Mareeba | 0.94 | 0.06 | -0.93 | 0.35 |
| Narrabri | 1.23 | 0.08 | 3.04 | 0.00 |
| Sydney | 0.54 | 0.04 | -9.37 | 0.00 |
| Utchee Creek | 1.04 | 0.07 | 0.59 | 0.55 |
| Starvation | | | | |
| Alice Springs | 0.79 | 0.07 | -2.70 | 0.01 |
| Batemans Bay | 0.92 | 0.09 | -0.86 | 0.39 |
| Brisbane | 0.94 | 0.09 | -0.71 | 0.48 |
| Griffith | 0.83 | 0.08 | -2.10 | 0.04 |
| Mareeba | 0.95 | 0.09 | -0.59 | 0.56 |
| Narrabri | 0.91 | 0.08 | -1.05 | 0.29 |
| Sydney | 0.57 | 0.05 | -6.37 | 0.00 |
| Utchee Creek | 0.89 | 0.08 | -1.31 | 0.19 |



Figure S 1: Picture of the egging device.

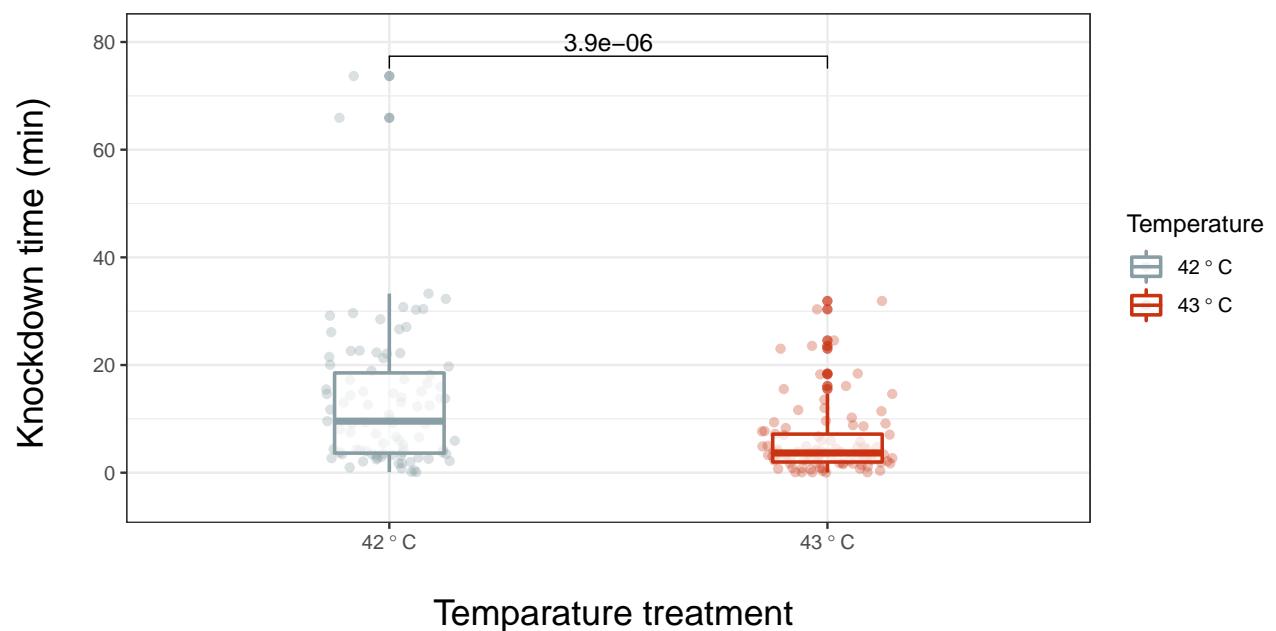


Figure S 2: Results pilot experiment on heat knockdown time. Data are presented as knockdown time in minutes on two different exposure temperature for S06 flies. Significance differences of means between temperatures are reported with Wilcox test P-value.

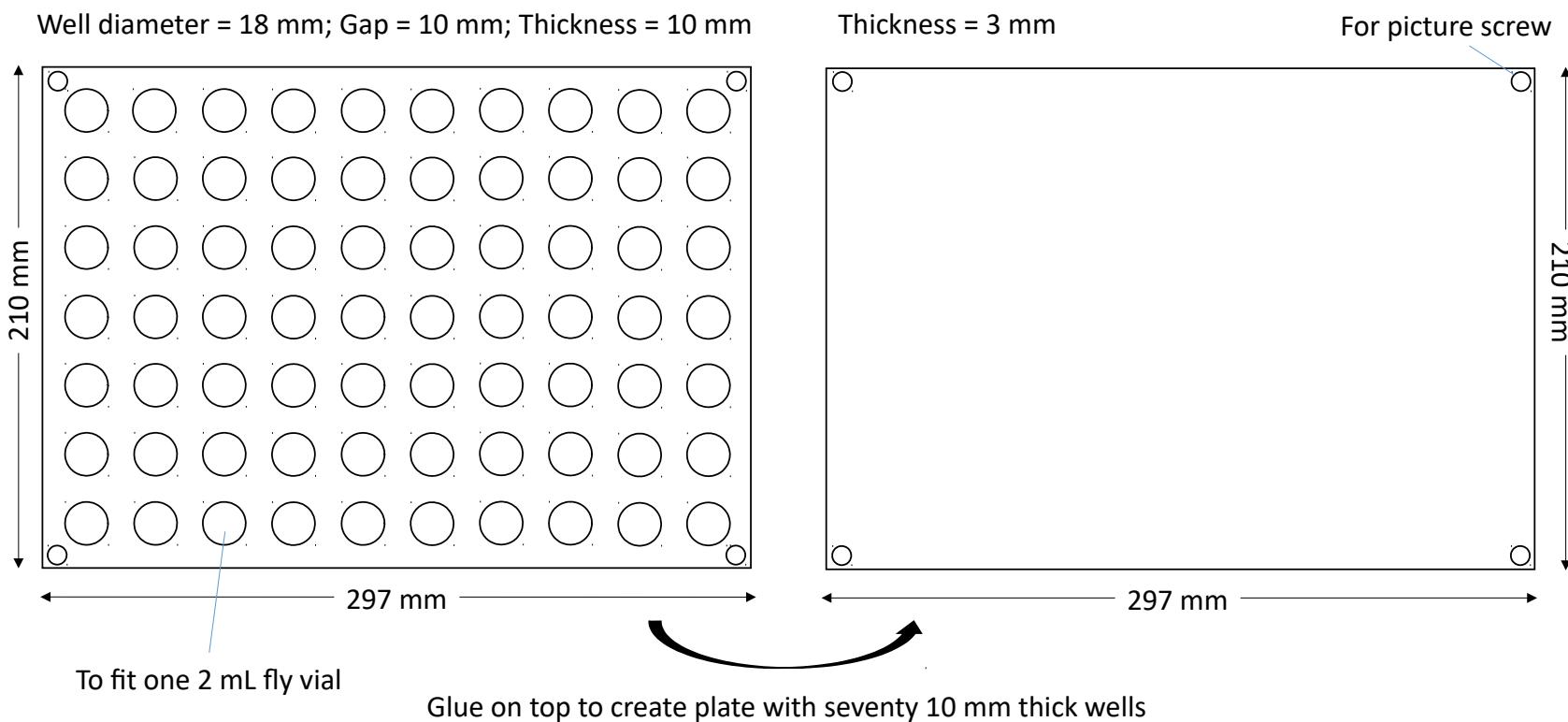


Figure S 3: Units for cold recovery treatment

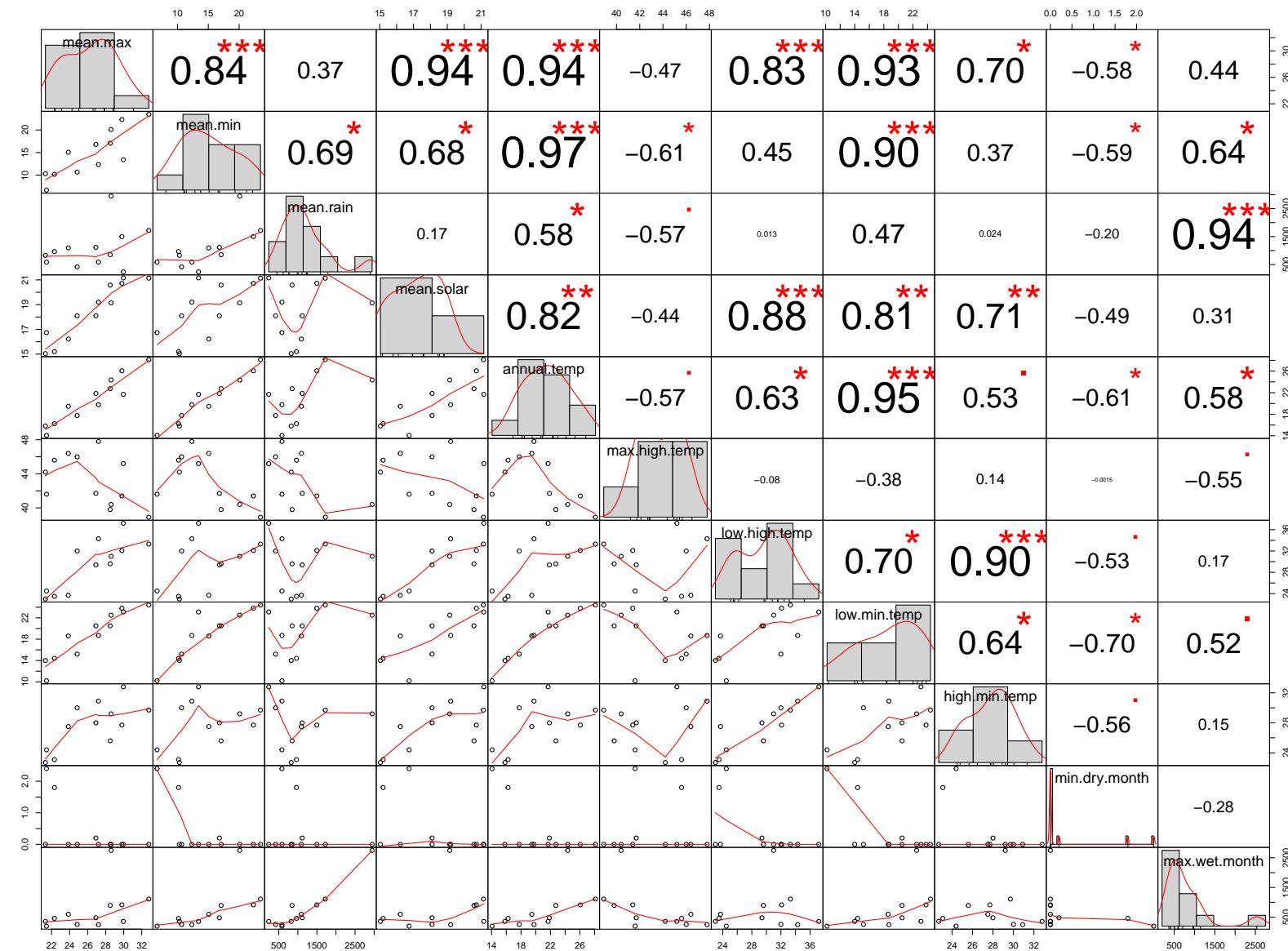


Figure S 4: Correlation among 11 climatic variables. Correlation values are presented together with asterisk indicating significance values for each correlation. Variables names are indicative of the following weather variables: **mean.max**= Annual max temperature; **mean.min** = Annual min temperature; **mean.rain** = Annual rainfall; **mean.solar**= Annual solar exposure; **annual.temp** = Annual temperature; **max.high.temp** = Maximum temperature of the warmest month; **low.high.temp** = Minimum temperature of the warmest month; **low.min.temp** = Minimum temperature of the coldest month; **high.min.temp** = Minimum temperature of the coldest month; **min.dry.month**= Precipitation of the driest month; **max.wet.month** = Precipitation of the wettest month.

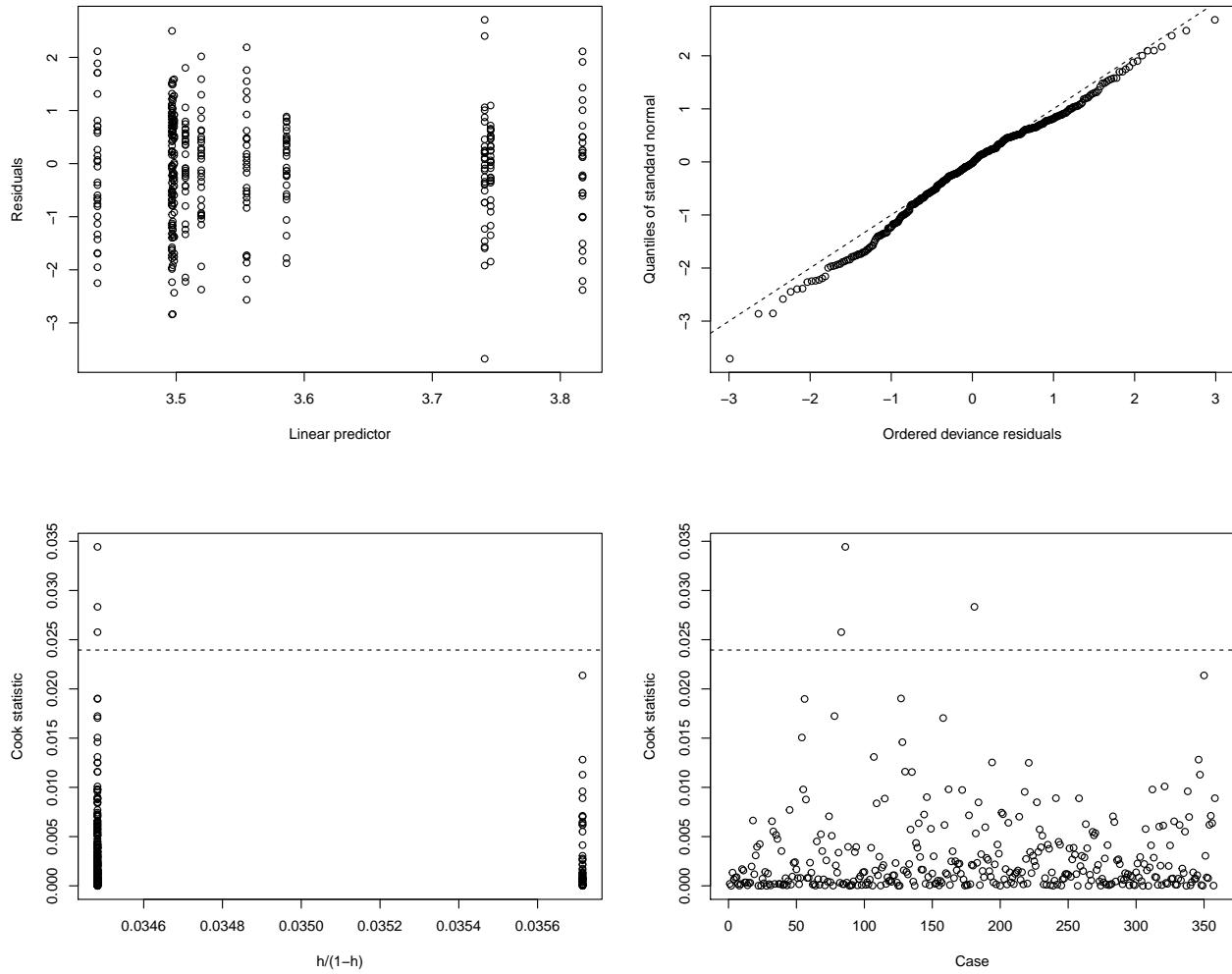


Figure S 5: Diagnostic plots Gamma-GLM heat tolerance in wild populations of the Queensland fruit fly

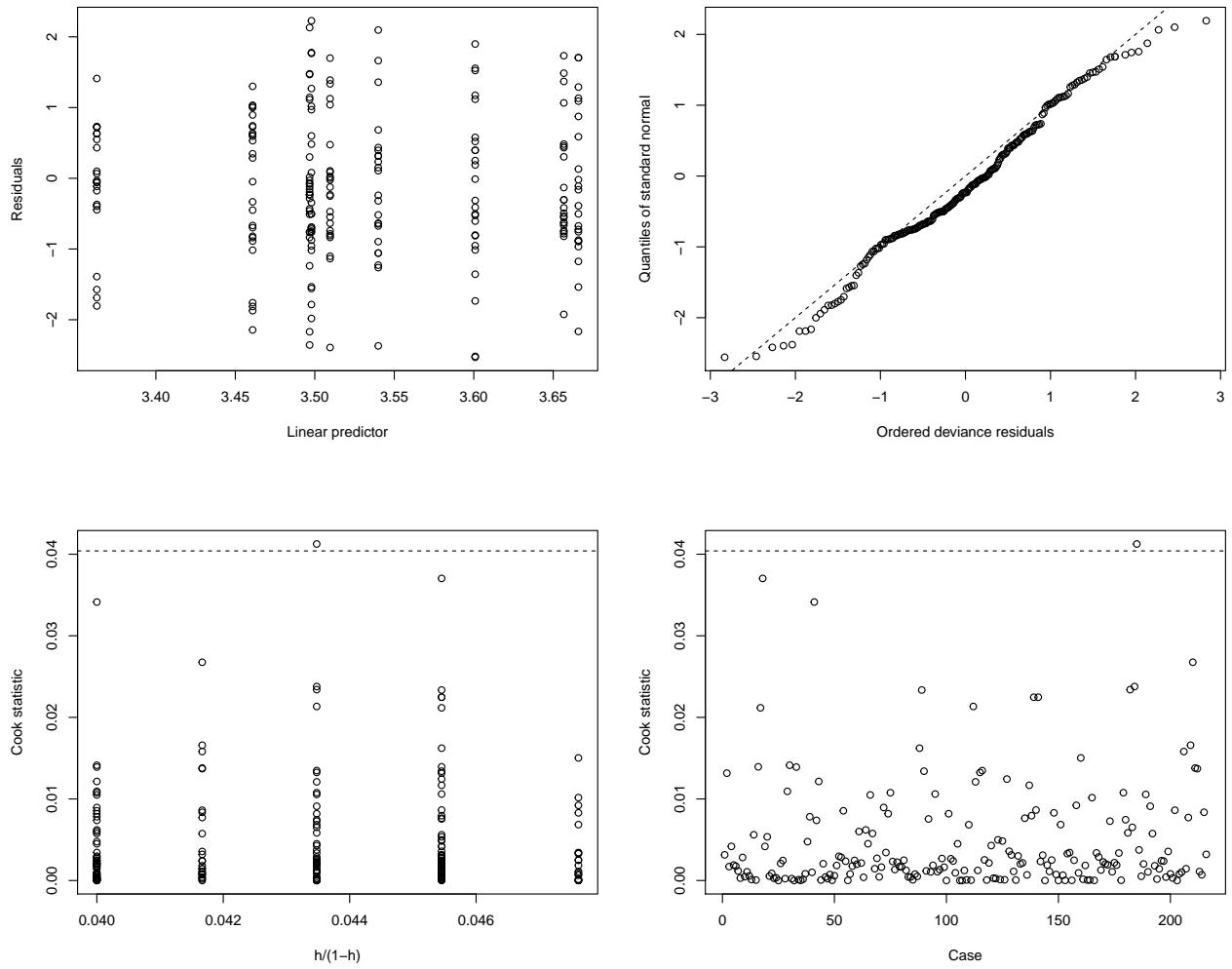


Figure S 6: Diagnostic plots Gamma-GLM heat tolerance in domesticated populations of the Queensland fruit fly

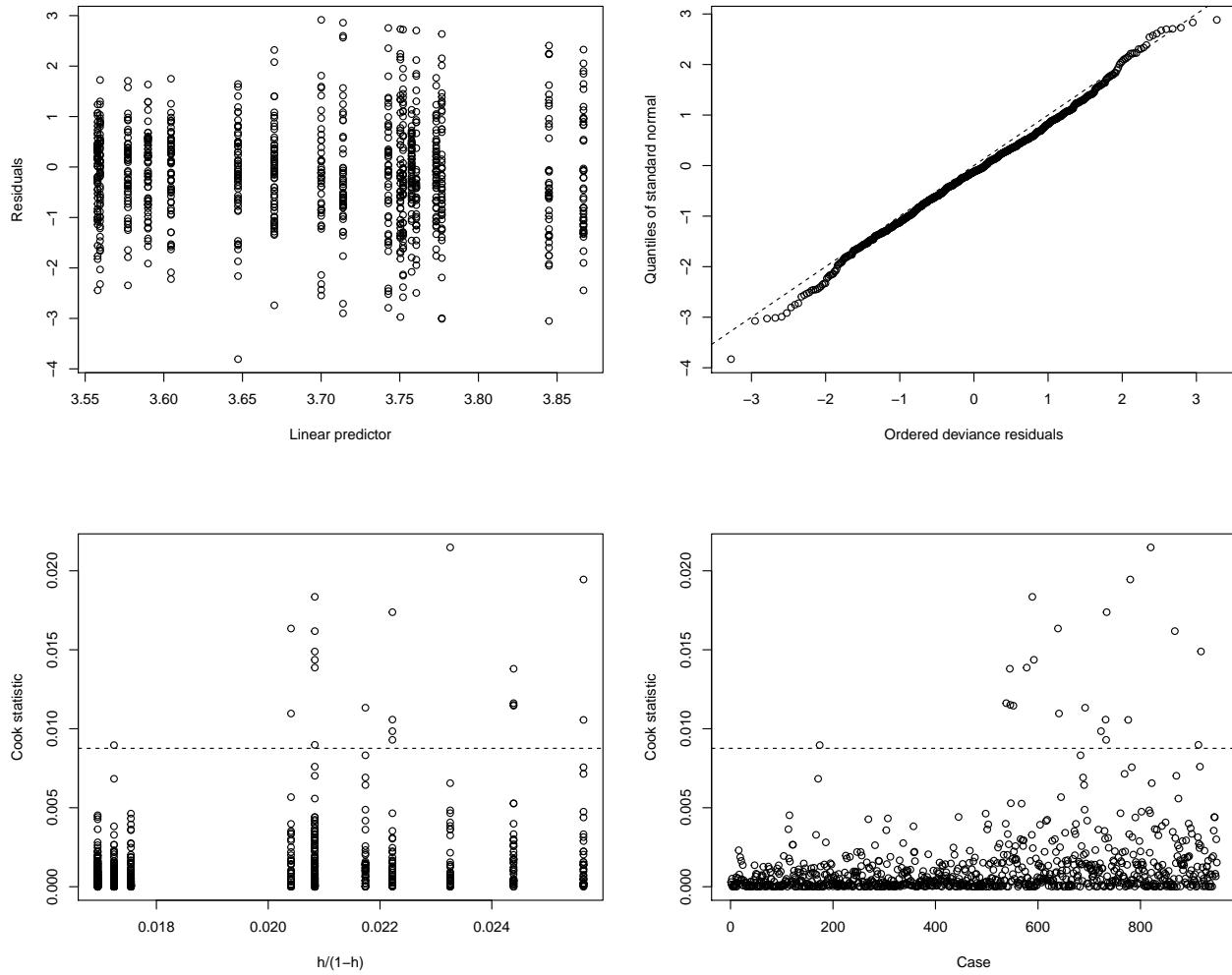


Figure S 7: Diagnostic plots Gamma-GLM heat tolerance change during domestication

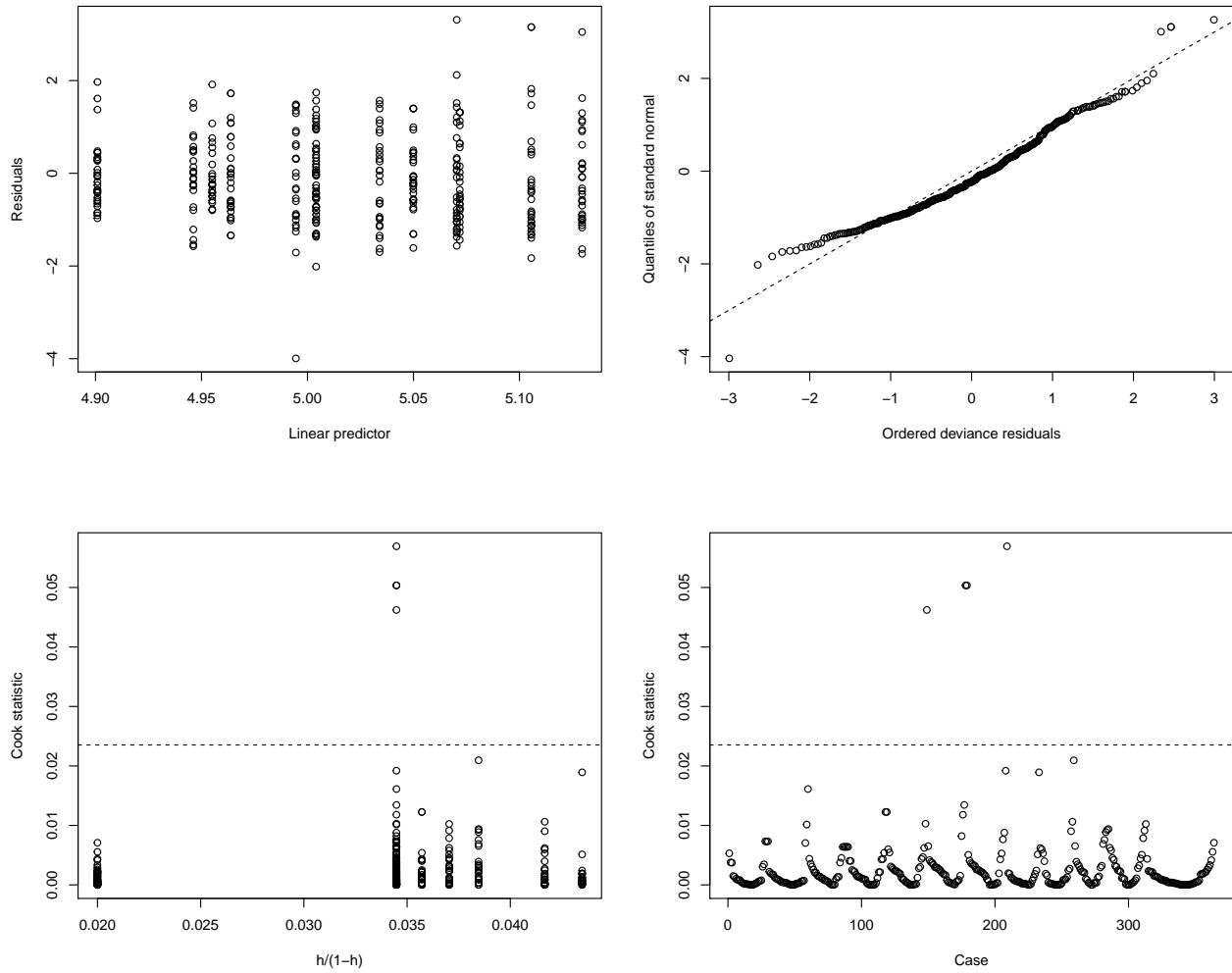


Figure S 8: Diagnostic plots Gamma-GLM cold tolerance in wild populations of the Queensland fruit fly

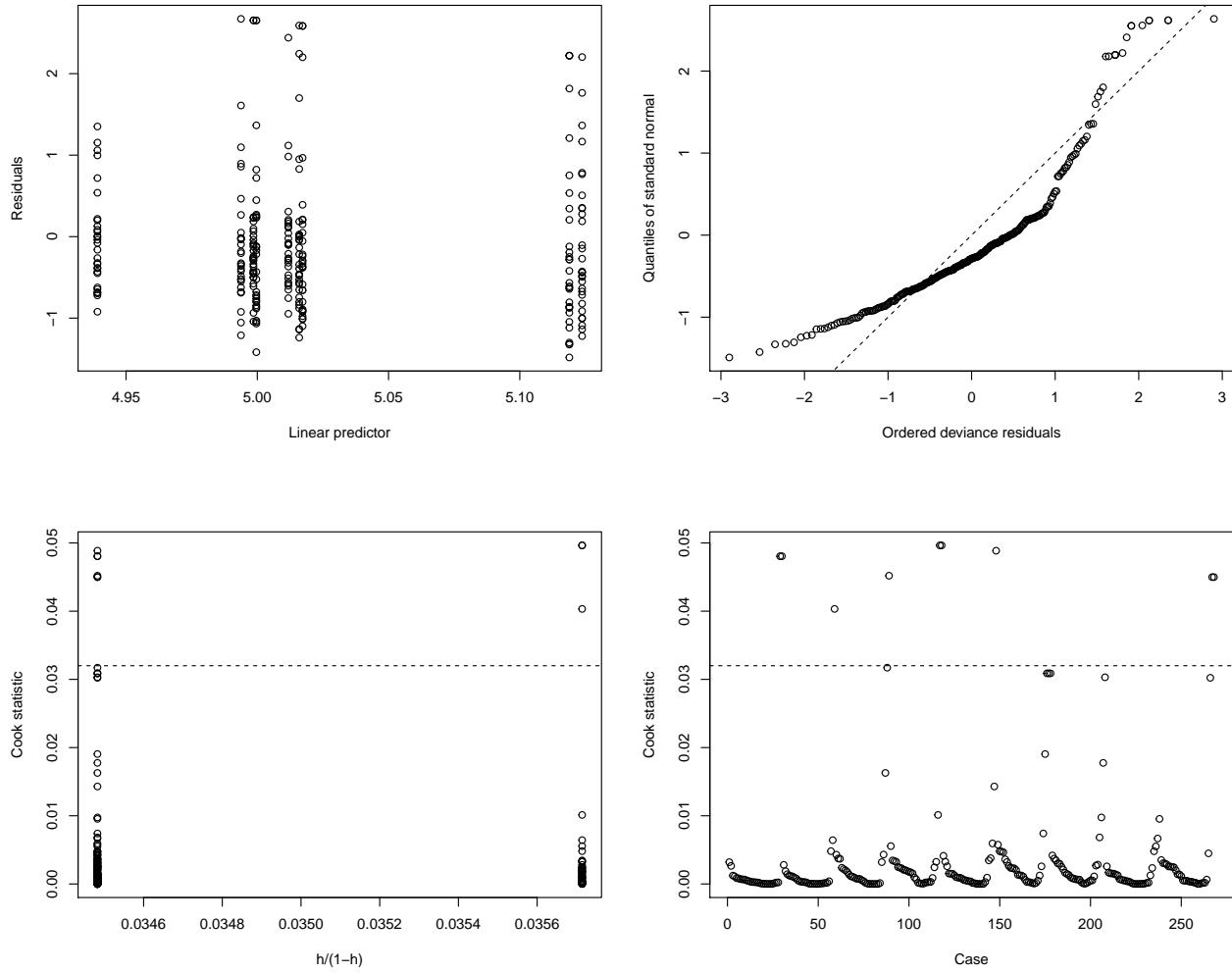


Figure S 9: Diagnostic plots Gamma-GLM heat tolerance in domesticated populations of the Queensland fruit fly

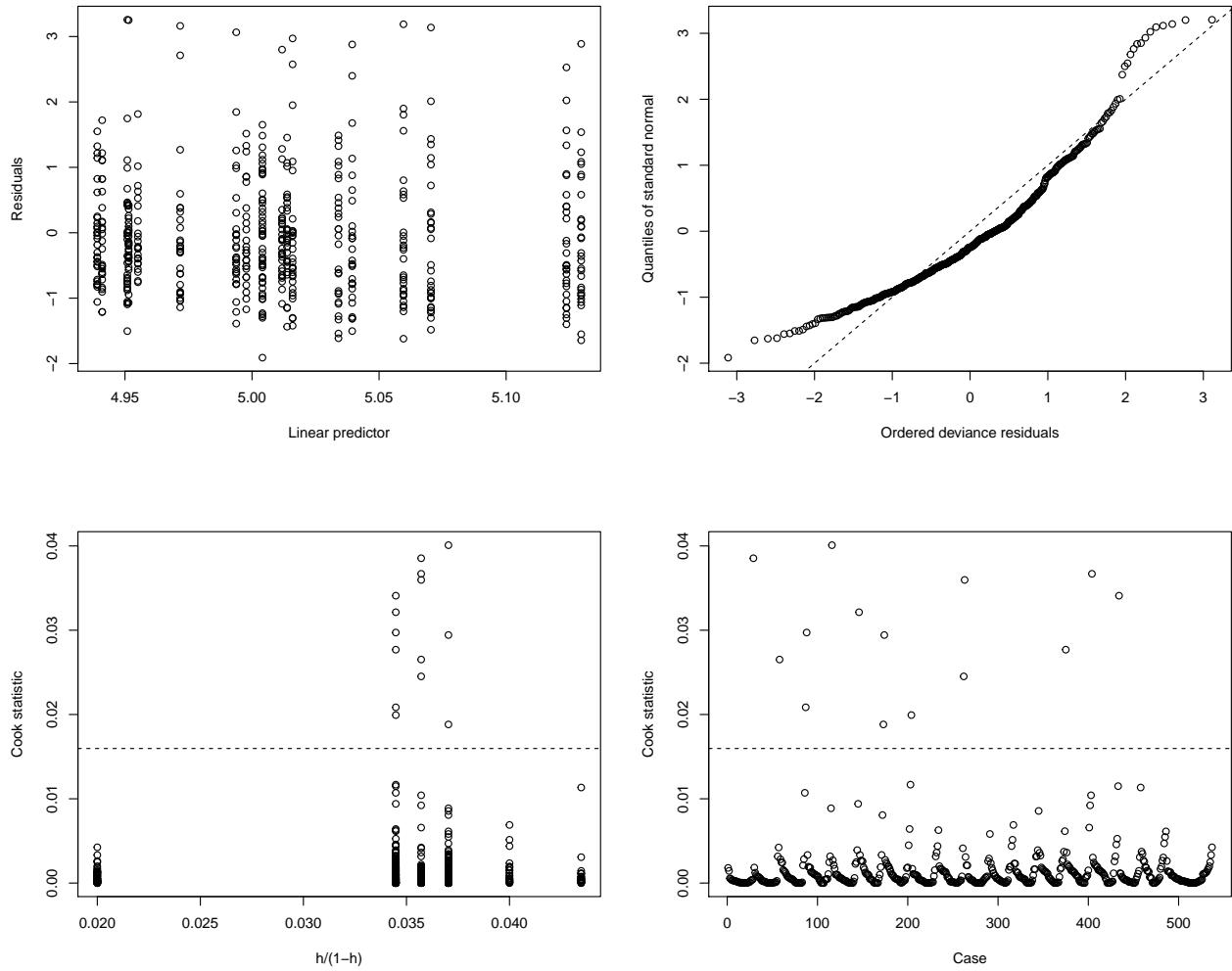


Figure S 10: Diagnostic plots Gamma-GLM cold tolerance change during domestication

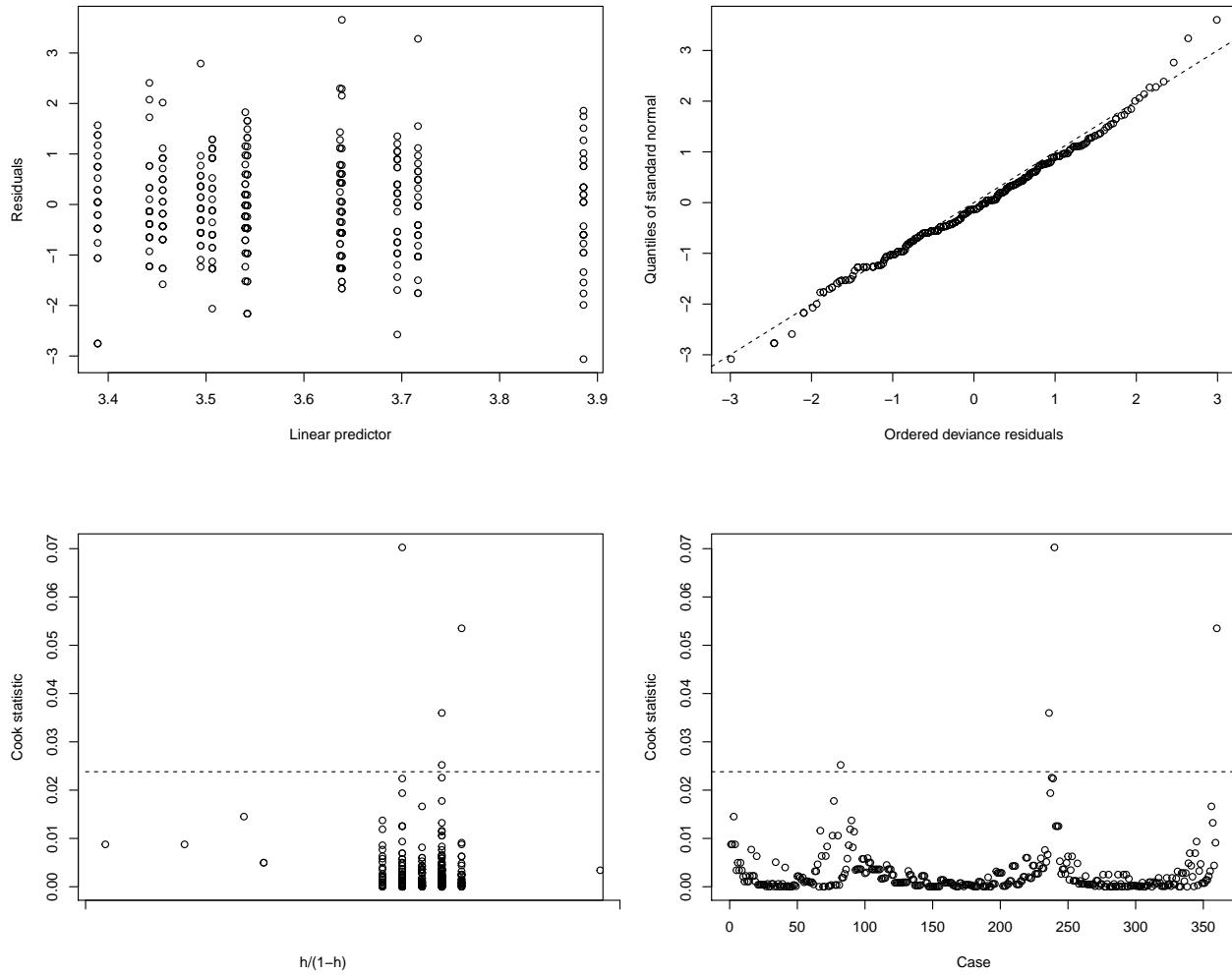


Figure S 11: Diagnostic plots Gamma-GLM desiccation tolerance in wild Qfly populations

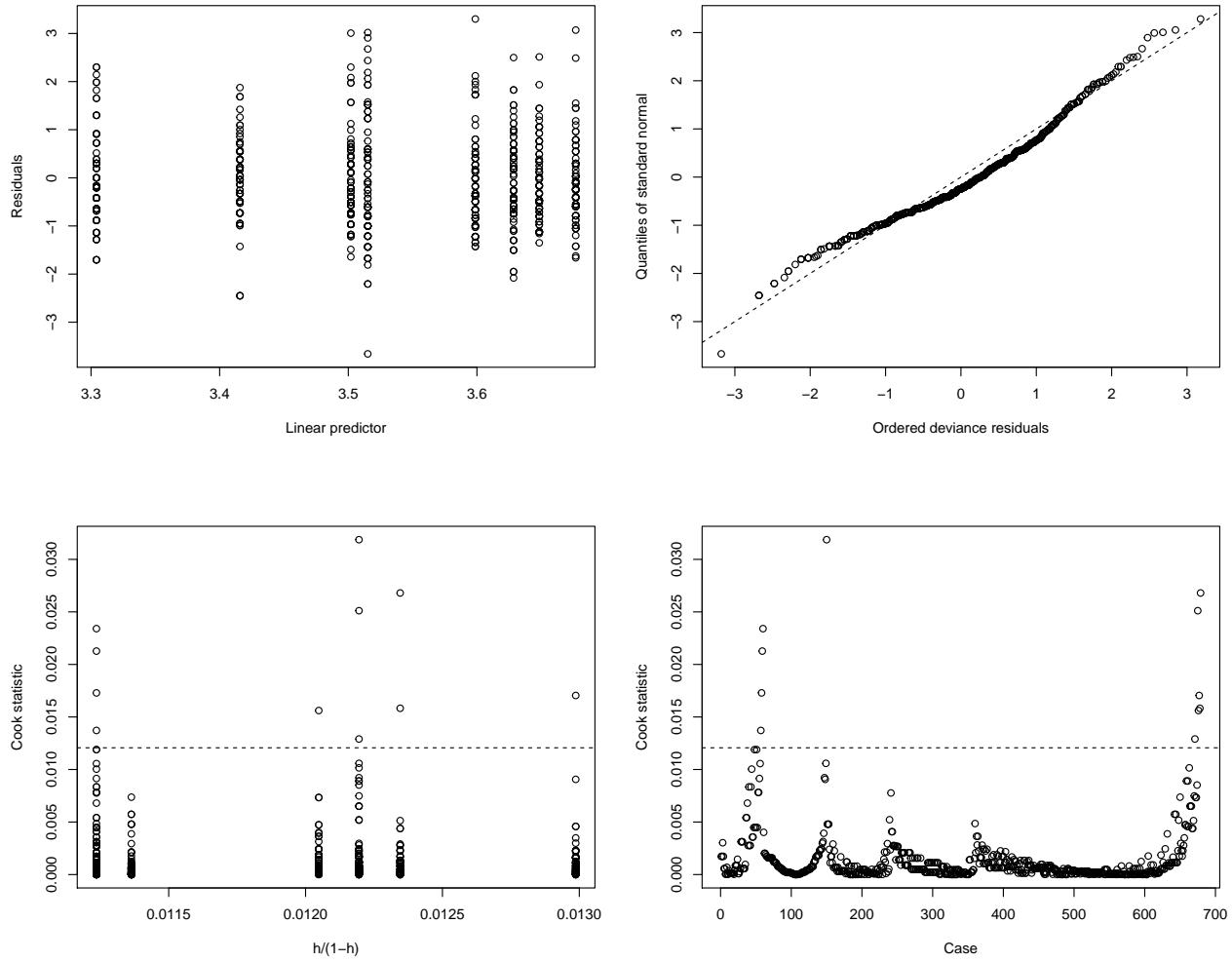


Figure S 12: Diagnostic plots Gamma-GLM desiccation tolerance in domesticated populations of the Queensland fruit fly

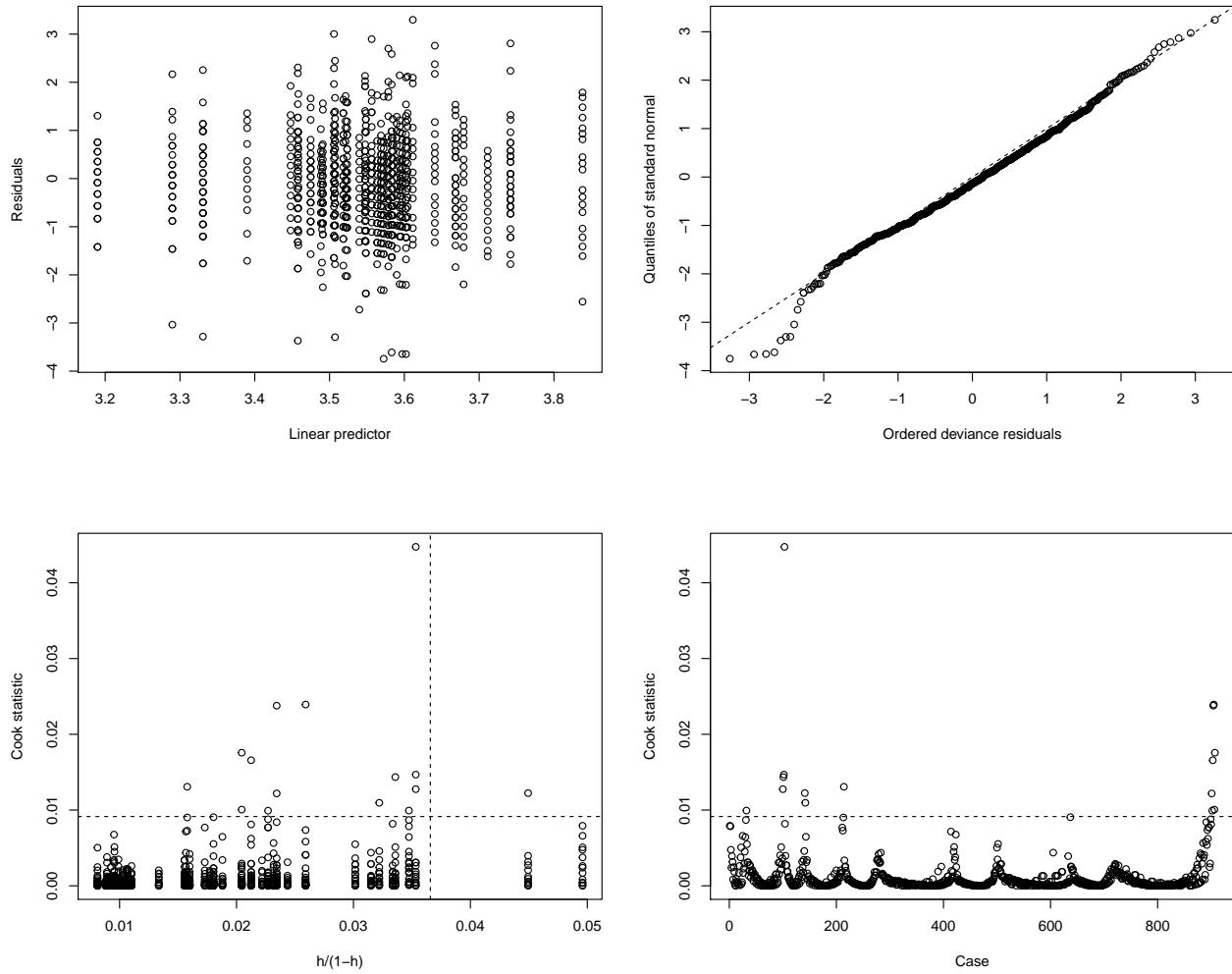


Figure S 13: Diagnostic plots Gamma-GLM desiccation tolerance change during domestication

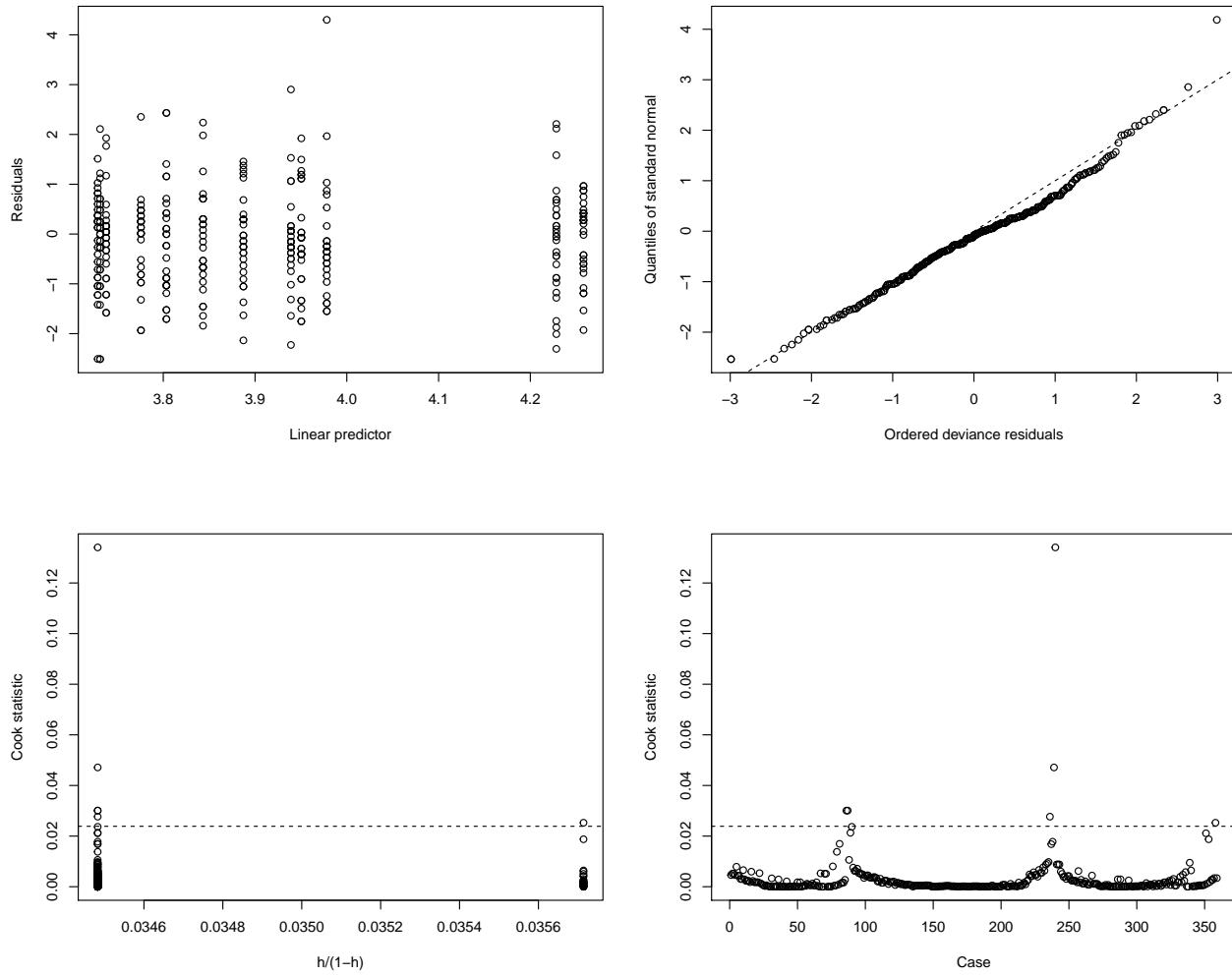


Figure S 14: Diagnostic plots Gamma-GLM starvation tolerance in wild Qfly populations

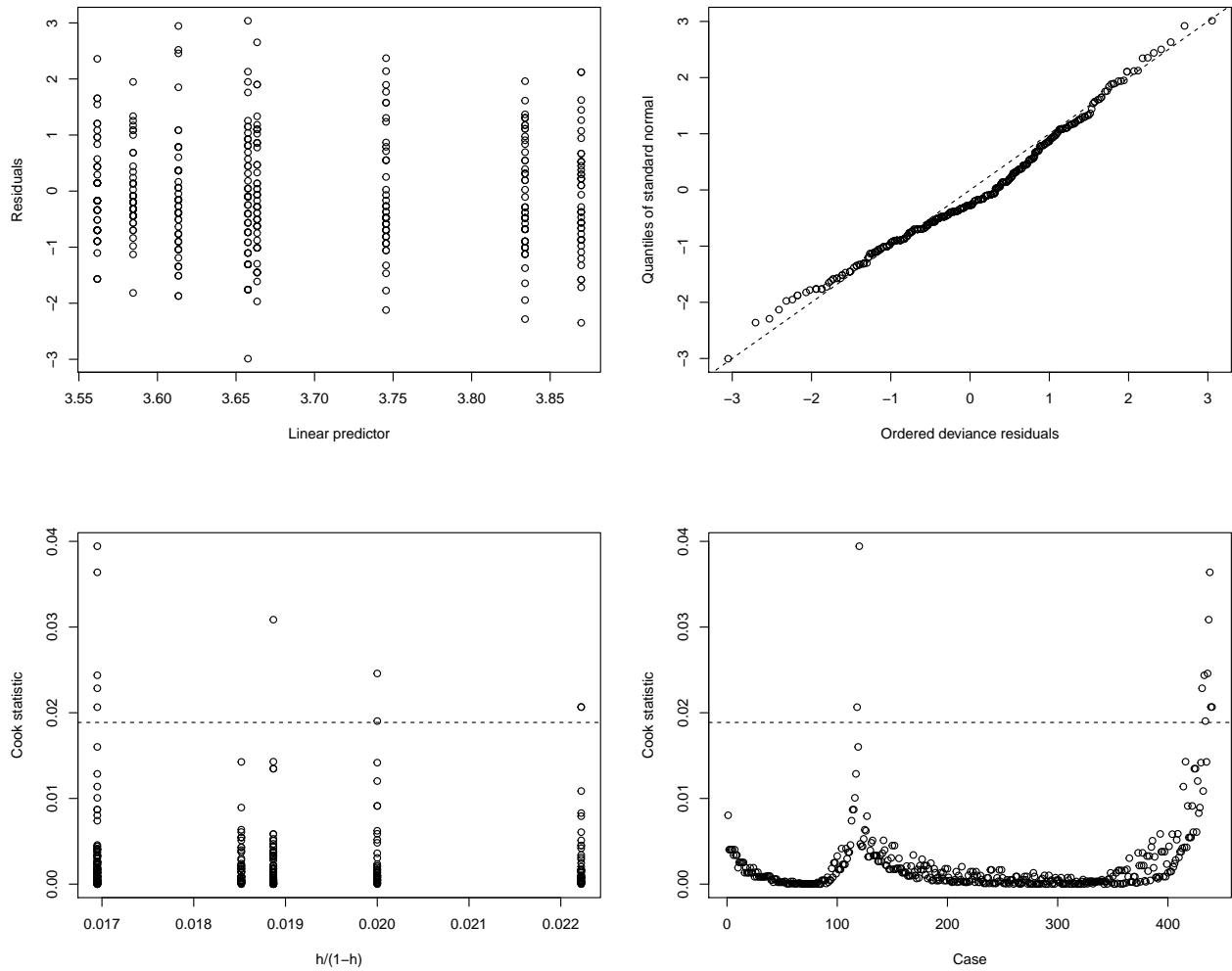


Figure S 15: Diagnostic plots Gamma-GLM starvation tolerance in domesticated populations of the Queensland fruit fly

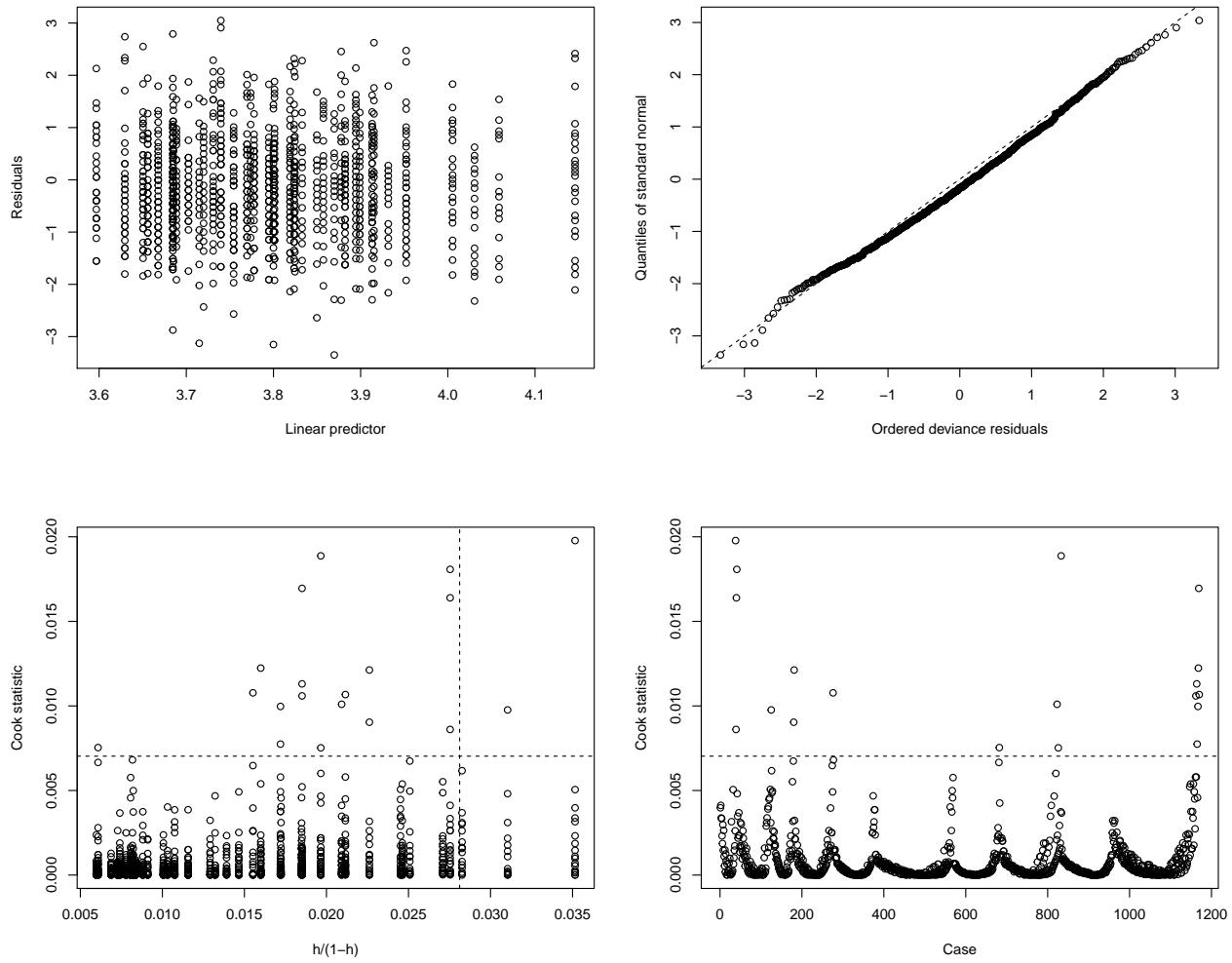


Figure S 16: Diagnostic plots Gamma-GLM starvation tolerance change during domestication

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#### R session information:

## R version 3.4.4 (2018-03-15)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.6 LTS
##
## Matrix products: default
## BLAS: /usr/lib/openblas-base/libblas.so.3
## LAPACK: /usr/lib/libopenblas-r0.2.18.so
##
## locale:
## [1] LC_CTYPE=en_AU.UTF-8      LC_NUMERIC=C
## [3] LC_TIME=en_AU.UTF-8       LC_COLLATE=en_AU.UTF-8
## [5] LC_MONETARY=en_AU.UTF-8   LC_MESSAGES=en_AU.UTF-8
## [7] LC_PAPER=en_AU.UTF-8     LC_NAME=C
## [9] LC_ADDRESS=C              LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_AU.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      stats     graphics grDevices utils     datasets methods
## [8] base
##
## other attached packages:
## [1] PerformanceAnalytics_1.5.2 xts_0.11-2
## [3] zoo_1.8-5                  pander_0.6.3
## [5] emmeans_1.3.3               boot_1.3-20
## [7] nortest_1.0-4              jtrans_0.2.1
## [9] Hmisc_4.2-0                Formula_1.2-3
## [11] survival_2.42-6            lattice_0.20-35
## [13] xtable_1.8-3              psych_1.8.12
## [15] egg_0.4.2                 gridExtra_2.3
## [17] sp_1.3-1                  purrr_0.3.2
## [19] cowplot_0.9.4              ggpubr_0.2
## [21] magrittr_1.5                ggridges_0.5.1
## [23] ggplot2_3.1.0              readr_1.3.1
## [25] dplyr_0.8.0.1              wesanderson_0.3.6
##
## loaded via a namespace (and not attached):
## [1] httr_1.4.0          viridisLite_0.3.0    splines_3.4.4
## [4] assertthat_0.2.1    latticeExtra_0.6-28  yaml_2.2.0
## [7] pillar_1.3.1        backports_1.1.3     quadprog_1.5-5
## [10] glue_1.3.1         digest_0.6.18       RColorBrewer_1.1-2
## [13] ggsignif_0.5.0     checkmate_1.9.1    rvest_0.3.2
## [16] colorspace_1.4-1   htmltools_0.3.6    Matrix_1.2-14
## [19] plyr_1.8.4         pkgconfig_2.0.2    mvtnorm_1.0-8
## [22] scales_1.0.0       webshot_0.5.1     htmlTable_1.13.1
## [25] tibble_2.1.1       withr_2.1.2       nnet_7.3-12
## [28] lazyeval_0.2.2     mnormt_1.5-5     crayon_1.3.4
## [31] estimability_1.3   evaluate_0.13    nlme_3.1-137
## [34] xml2_1.2.0         foreign_0.8-70   tools_3.4.4
## [37] data.table_1.12.0  hms_0.4.2       stringr_1.4.0
## [40] munsell_0.5.0      cluster_2.0.7-1  packrat_0.5.0
## [43] kableExtra_1.1.0   compiler_3.4.4   rlang_0.3.2
## [46] rstudioapi_0.10    htmlwidgets_1.3   base64enc_0.1-3

```

```
## [49] labeling_0.3      rmarkdown_1.12      gtable_0.3.0
## [52] R6_2.4.0          knitr_1.22        stringi_1.4.3
## [55] parallel_3.4.4    Rcpp_1.0.1         rpart_4.1-13
## [58] acepack_1.4.1     tidyselect_0.2.5   xfun_0.5
## [61] coda_0.19-2
```