Table S1. Statistical models that were used for differential expression analysis of the RNA-seq data.

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| --- | --- | --- | --- |
| Analysis | Package | Test | Model |
| R vs S due to T vs C  Peanut | edgeR | glmLRT | time16\_effect = (R\_T\_16-R\_C\_16)-(S\_T\_16-S\_C\_16)  time32\_effect = (R\_T\_32-R\_C\_32)-(S\_T\_32-S\_C\_32)  time64\_effect = (R\_T\_64-R\_C\_64)-(S\_T\_64-S\_C\_64) |
| Deseq2 | LRT | full = ~ genotype (R/S)+ afla\_trt16 (T/C) + **genotype:afla\_trt16**)  reduced = ~ genotype (R/S)+ afla\_trt16 (T/C)  full = ~ genotype (R/S)+ afla\_trt32 (T/C) + **genotype:afla\_trt32**)  reduced = ~ genotype (R/S)+ afla\_trt32 (T/C)  full = ~ genotype (R/S)+ afla\_trt64 (T/C) + **genotype:afla\_trt64**)  reduced = ~ genotype (R/S)+ afla\_trt64 (T/C) |
| Next MaSigPro | LLRT | R\_C, R\_T, S\_C, S\_T |
| R vs S  *A. flavus* | edgeR | etLRT | time16\_effect = R\_H\_16-S\_H\_16  time32\_effect = R\_H\_32-S\_H\_32  time64\_effect = R\_H\_64-S\_H\_64 |
| Deseq2 | WT | time16\_effect = ~ genotype (R\_H\_16/S\_H\_16)  time32\_effect = ~ genotype (R\_H\_32/S\_H\_32)  time64\_effect = ~ genotype (R\_H\_64/S\_H\_64) |
| Next MaSigPro | LLRT | time16, time32, time64; R\_H, S\_H |
| Peanut  (R)\* | edgeR | etLRT | time32\_effect = R\_T\_32-R\_C\_32  time64\_effect = R\_T\_64-R\_C\_64 |
| Peanut  (S)\* | etLRT | time32\_effect = S\_T\_32-S\_C\_32  time64\_effect = S\_T\_64-S\_C\_64 |
| *A. flavus*  (R)\* | etLRT | time32\_effect = R\_T\_32-R\_T\_16  time64\_effect = R\_T\_64-R\_T\_16 |
| *A. flavus*  (S)\* | etLRT | time32\_effect = S\_T\_32-S\_T\_16  time64\_effect = S\_T\_64-S\_T\_16 |

\* Design for network analysis; R, Resistant cultivar; S, susceptible cultivar; T, Treatment; C, Control; H, High-level of aflatoxin; 16, 16 hours after infection; 32, 32 hours of infection; 64, 64 hours after infection; LRT, Likelihood Ratio Test; WT, Wald Test; glmLRT, general linear model - Likelihood Ratio Test; etLRT, exact test - Likelihood Ratio Test; LLRT, Log Likelihood Ratio Test.