Electronic Supplementary Material

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Additional information

1. Methods

1.1 Sperm velocity parameters

Other researchers have occasionally used curvilinear velocity (VCL) as a measure of sperm swimming speed [1,2]. Across all sperm samples tested in this study, VAP at 10 s post-activation in water was strongly correlated with VCL in 50% ($r = 0.95$, $p < 0.0001$, $n = 35$) and 100 % ovarian fluid ($r = 0.95$, $p < 0.0001$, $n = 55$). We focused on VAP as an estimate of sperm

swimming velocity because we feel that it most closely represents the swimming speed of sperm along a trajectory most like to encounter fertilizable ova.

1.2 Genetic analyses

Across the 9 microsatellite loci, the mean levels of observed heterozygosity were close to the values expected (see table S1) indicating the polymorphic nature of each locus and high levels of genetic variation, suggesting that the diversity at these nine loci is likely to be indicative of genome-wide diversity. One locus in the 2010 sample deviated significantly from Hardy-Weinberg (indicated as * in table S1).

Table S1. Mean observed (Ho) and expected heterozygosity (He) and tests for deviation from Hardy-Weinberg compared with chi-square test. Data from 9 microsatellite loci of chinook salmon samples in two different years (2010, n = 19; 2011, n = 19).

Spawning season	Locus	Ho	He
2010	*Ocl*-1	0.749	0.846
2010	*Omy*-325	0.482	0.462
2010	*Ots*-101	0.896	0.962
2010	*Ots*-104*	0.872	0.923
2010	*Ots*-107	0.863	0.923
2010	*Ots*-2	0.730	0.769
2010	*Ots*-3	0.784	0.846
2010	*Ssa*-197	0.871	0.846
2010	*Ssa*-85	0.702	0.808
2011	*Ocl*-1	0.880	0.758
2011	*Omy*-325	0.480	0.577
2011	*Ots*-101	0.920	0.890
2011	*Ots*-104	0.920	0.876
2011	*Ots*-107	0.720	0.832
2011	*Ots*-2	0.760	0.621
2011	*Ots*-3	0.720	0.790
2011	*Ssa*-197	0.880	0.871
2011	*Ssa*-85	0.760	0.698

2. Statistical methods

We constructed generalised linear mixed models (GLMM) using the *lmer* and *glmer* functions in the lme4 package in R [3]. A few *glmer* models failed to converge, so we tested for the effect of this (see Statistical Appendix) and removed interaction terms as we expected that those models may have been overparameterized. Removal of those interaction terms resulted in models that converged and those are the models we report in this paper. On inspection we have no reason to expect that there were significant interactions in those models, but that would need to be verified with larger sample sizes. Removal of those interaction terms does not influence the conclusions of our study.

Because the binomial models were often seriously overdispersed, we applied a correction but that often lead to underdispersion. Thus, to check the validity of conclusions drawn from those models, we also used Markov Chain Monte Carlo (MCMC-GLMM) techniques (using R package *MCMCglmm*) [4,5] with binomial error structure, parameterized to deal with overdispersion. MCMC-GLMMs enabled us to fully correct for the overdispersion of residuals [5], while using the same binary response variables and predictor variables. When results of MCMC-GLMM techniques yielded the same conclusions as underdispersed *glmer* models, we report the glmer models in the main text and MCMC-GLMM models here; when MCMC-GLMM models yielded different conclusions we report the results of those models in the main text.

For the MCMC-GLMM models, we ran the analyses for 800,000 iterations with a burn-in of 100,000 and a thinning interval of 100. This generated 7000 samples from each chain from which model statistics, including the posterior mean and the 95% credible intervals (CI), were calculated. Effects in each model were considered to be statistically significant when 95% CIs did not include 0 and *pMCMC* values were less than 0.05. We initially used an inverse gamma prior (V = 1, *nu* = 0.002), as this prior is often used for random effects models, but finally used an expanded prior (V = 1, *nu* = 1, alpha.mu = 0) due to some variance components being close to 0. We obtained similar results when we ran each chain 3 times using the two different priors. We examined the convergence of models using trace and density plots, along with the Heidelberger-and-Welch diagnostic test for model parameters (using the R package *coda* v 0.16-1)[6]. Autocorrelation was examined and found to be weak (<0.1) between successive iterations, indicating that chains were mixed well with good convergence.

3. Supplementary Figures

3.1 Partial regression plots

Figures 1 and 2 in the main text of this paper are included to illustrate approximately the relations described in the statistical models. We could not construct partial regression plots from the mixed effects models summarized in tables 1 and 2, so to construct figures 1 and 2 we built new linear models using the *lm* function in R, with the excess number of of fertilized by the winning male (figure 1) or the proportion of embryos surviving to day 28 (figure 2) as the response variables, but without controlling for the random effects of male and female identities.

These figures both show reasonably accurately both the distribution of residuals and the partial relations between variables in the actual GLMMs reported in tables 1 and 2.

Figures S1-S3 below show the partial effects of VAP and MLH in the GLMMs reported in tables 1, 2, and S1, plotted using *plotLMER.fnc* function in the *LMERConvenienceFunctions* package [7] in R, and the raw data for each of the variables listed on the axes. The red lines plotted by *plotLMER.fnc* function are the partial effects of each predictor (x-axis) adjusted for the median of the other numerical predictors in the models.

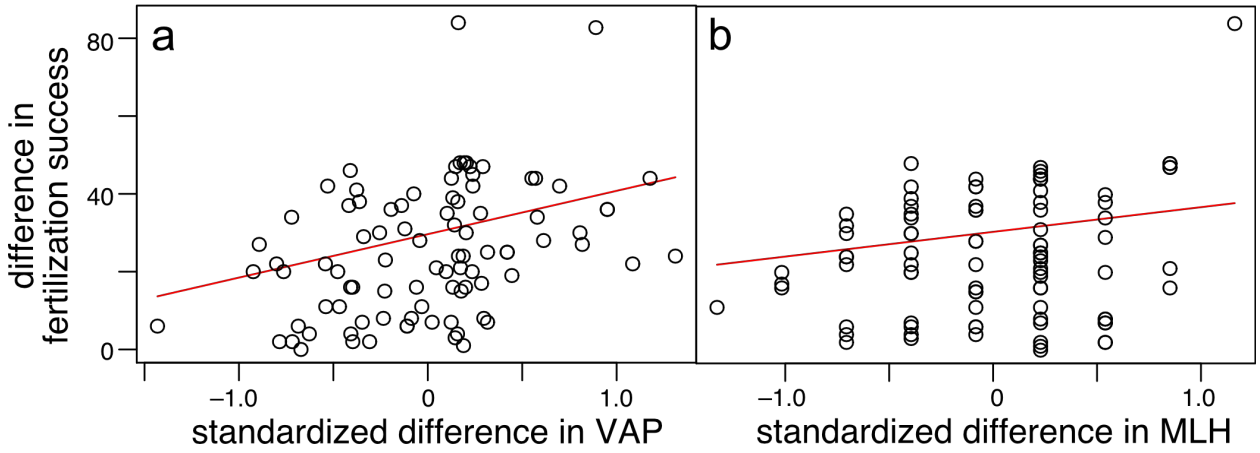


Figure S1. The partial effects of differences between competing males in (a) sperm swimming speed (VAP in $\mu m.s^{-1}$) and (b) multilocus heterozygosity (MLH) on the fertilisation advantage gained by the winning male in competitive fertilization trials, controlling for the effect of ovarian fluid concentration and the random effects of male and female identity. See table 1 in the main text for the model.

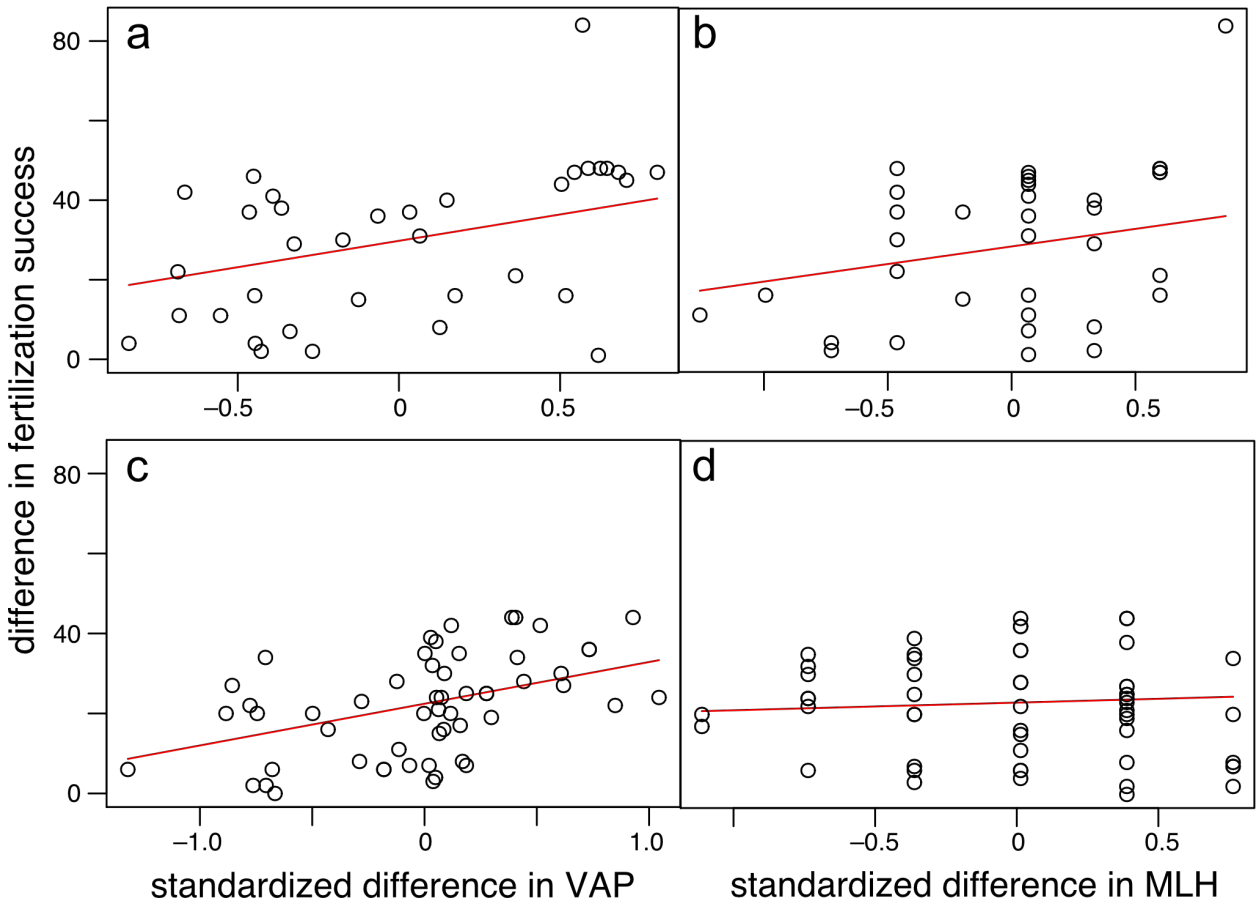


Figure S2. Partial effects of differences between competing males in (a,c) sperm swimming speed (VAP in $\mu m.s^{-1}$) and (b,d) multilocus heterozygosity (MLH) on the fertilisation advantage gained by the winning male in competitive fertilization trials conducted in (a,b) 50% and (c,d) 100% ovarian fluid solutions, controlling for the random effects of male and female identity. See table S3 for models.

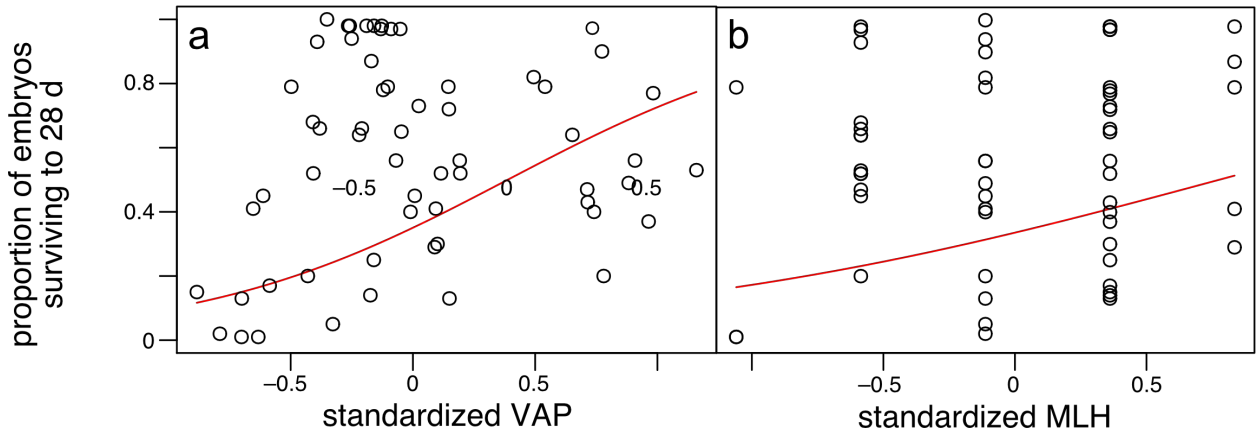


Figure S3. Partial effects of a male's (a) sperm swimming speed (VAP in $\mu m.s^{-1}$) and (b) multilocus heterozygosity (MLH) on embryo survival to 28 days, controlling for spawning season (and thus ovarian fluid concentration) and the random effects of male and female identity. See table 2 in the main text for the model.

4. Supplementary Tables

Table S2. Top models (AICc≤2) to predict the fertilization advantage (additional eggs fertilized) by the winner in competitive fertilization trials. Effects are positive unless noted otherwise; VAP is sperm swimming speed in the female's ovarian fluid, TrioML is genetic relatedness between each male and the female, OF is ovarian fluid concentration, and MLH is individual multilocus heterozygosity. Differences in VAP ($\mu m.s^{-1}$), MLH and TrioML were all standardized (std). This LMEM also included the random effects of male and female identities as individuals were included in more than one trial but never with the same male or female.

Model (fixed effects only)	**df**	**ΔAICc**	**weight**
OF, std ΔVAP, std ΔMLH	8	0	0.26
std ΔVAP, std ΔMLH	7	0.88	0.17
OF, std ΔMLH	7	1.27	0.14
OF, std ΔVAP, std ΔMLH, –std ΔTrioML	9	1.58	0.12

Table S3. LMEMs to predict the fertilization advantage (additional ova fertilized) for the male that fertilized the majority of ova in replicated competitive dyads (n = 35 and 55 in 50% and 100% ovarian fluid, respectively) from differences between the males in their (i) sperm velocities (ΔVAP in $\mu m.s^{-1}$) measured in either 50 and 100% ovarian fluid, and (ii) individual multilocus heterozygosity (MLH). These models included the random effects of female and male identity; differences in VAPs and MHL were standardized in S3a but only ΔMHL was standardized in S3b. Statistics presented as: estimate [95%CL] p. See also figures 1 and S2.

Table S3a

Parameter (fixed effects only)	**50% OF**	**100% OF**
intercept	29.17 [23.58, 34.76]	22.40 [17.54, 27.25]
std ΔVAP in OF ($\mu m.s^{-1}$)	13.25[–0.67, 27.18] 0.20	10.43 [3.97, 16.90] 0.01
std ΔMLH	8.87 [–5.05, 22.80] 0.28	1.92 [–5.49, 9.32] 0.68

Table S3b

Parameter (fixed effects only)	**50% OF**	**100% OF**
intercept	27.22 [21.37, 33.07]	19.33 [14.14, 24.52]
ΔVAP in OF ($\mu m.s^{-1}$)	0.42 [–0.01, 0.85]	0.16 [0.06, 0.26]
std ΔMLH	8.87 [–4.81, 22.56]	1.92 [–5.49, 9.33]

Table S4. Top models (AICc≤2) to predict the fertilisation advantage (additional eggs fertilized) realised by the winner in competitive fertilization trials from the difference in (standardized, std) sperm swimming speed (ΔVAP) measured in fresh water. Note that ΔVAP was not included in any of these top models. Effects are positive unless noted otherwise; OF is ovarian fluid concentration (50 or 100%) and std ΔMHL is the (standardized) difference in individual multilocus heterozygosity. Models also included the random effects of male and female identities as individuals were included in more than one trial but never with the same male or female.

Model (fixed effects only)	**df**	**ΔAICc**	**weight**
std ΔMHL	6	0	0.29
null	5	0.34	0.24
OF, std ΔMHL	7	1.69	0.12
OF	6	1.89	0.11

Table S5. MCMC-GLMM (with binomial error and logit link function) to predict embryo survival (number of eggs survived vs died) in the non-competitive fertilisation trials (n = 59) from the male's mean sperm velocity (VAP in $\mu m.s^{-1}$) measured in ovarian fluid (OF) and individual multilocus heterozygosity (MHL) estimated from 9 polymorphic microsatellite loci. VAP and MHL were standardized (std) in this analysis. We used fish from two different spawning seasons so the model controls for potential differences in embryo survival between years, as well as the random effects of male and female identity.

Parameters (fixed effects only)	**posterior mean [95%CI] p**
Intercept	–0.54 [–1.56, 0.60] 0.28
std MHL	1.00 [0.03, 1.92] 0.03
std VAP in OF ($\mu m.s^{-1}$)	1.44 [0.37, 2.44] 0.009
Spawning season	2.39 [0.62, 4.07] 0.008

5. References

1. Gasparini C., Andreatta G., Pilastro A. 2012 Ovarian fluid of receptive females enhances sperm velocity. *Naturwissenschaften* **99**(5), 417-420. (doi:10.1007/s00114-012-0908-2).
2. Dziewulska K., Rzemieniecki A., Domagała J. 2011 Sperm motility characteristics of wild Atlantic salmon (Salmo salar L.) and sea trout (Salmo trutta m. trutta L.) as a basis for milt selection. *Journal of Applied Ichthyology* **27**(4), 1047-1051. (doi:10.1111/j.1439-0426.20121.01759.x).
3. Bates DMM, Bolker B, Walker S. 2014 lme4: Linear mixed-effects models using Eigen and S4. R package version 1.1-7.
4. Bolker BM, Brooks ME, Clark CJ, Geange SW, Poulsen JR, Stevens MHH, White J-SS. 2009 Generalized linear mixed models: a practical guide for ecology and evolution. *Trends in Ecology & Evolution* **24**, 127-135.
5. Hadfield, J. D. 2010 MCMC Generalised Linear Mixed Models: R package version 2.21.
6. Plummer M. 2015 CODA: Output analysis and diagnostics for MCMC. R package version 0.17-1.
7. Hervé, M. 2014 RVAideMemoire: diverse basic statistical and graphical functions. R package version 0.9–32.

Statistical Appendix

Robert Montgomerie & Patrice Rosengrave

This is a complete set of analyses and output for the both main text and the electronic supplementary material of: *Rosengrave P, Montgomerie R, Gemmell N. 2016. Cryptic female choice enhances fertilization success and embryo survival in chinook salmon. Proceedings of the Royal Society B.*

SA1. Setup for analyses

SA1.1 R details

- File creation date: 2016-02-01
- R version 3.2.3 (2015-12-10)
- *lme4* package version: 1.1.10
- *MCMCglmm* package version: 2.22.1
- *LMERConvenienceFunctions* package version: 2.10
- *RVAideMemoire* package version: 0.9.52
- *arm* package version: 1.8.6
- *MuMIn* package version: 1.15.6
- *Deducer* package version: 0.7.9
- *pbkrtest* package version: 0.4.6
- *Rmisc* package version: 1.5

```
library(lme4)
library(MCMCglmm)
library(LMERConvenienceFunctions)
library(RVAideMemoire)
library(arm)
library(MuMIn)
library(Deducer)
library(pbkrtest)
library(Rmisc)
```

SA1.2 Datasets

Make sure these datasets are all in your working directory if you want to use the code below. The README file that accompanies these data files explains all of the variables.

- Trials.csv: experimental competitive and non-competitive fertilization trials
- Replicates.csv: replicates of competitive fertilization trials

- Esurvival.csv: embryo survival
- TRIOML.csv: relatedness estimates, using TrioML for degree of genetic relatedness between male and female

- Replicates2.csv: same data as v4 but organized for loglinear analysis

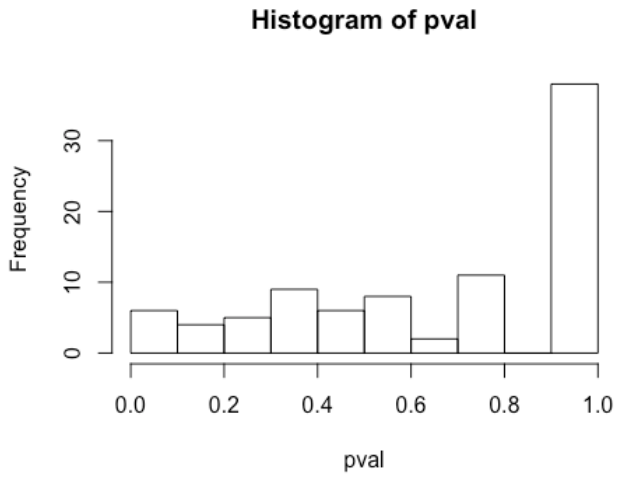
```
Replicates <- read.csv("Replicates.csv", header=TRUE)
Esurvival <- read.csv("Esurvival.csv", header=TRUE)
Trials <- read.csv("Trials.csv", header=TRUE)
Related <- read.csv("TRIOML.csv", header=TRUE)
reps <- read.csv("Replicates2.csv", header=TRUE)
```

SA2. Section 2(b) MATERIALS AND METHODS: competitive fertilization trials

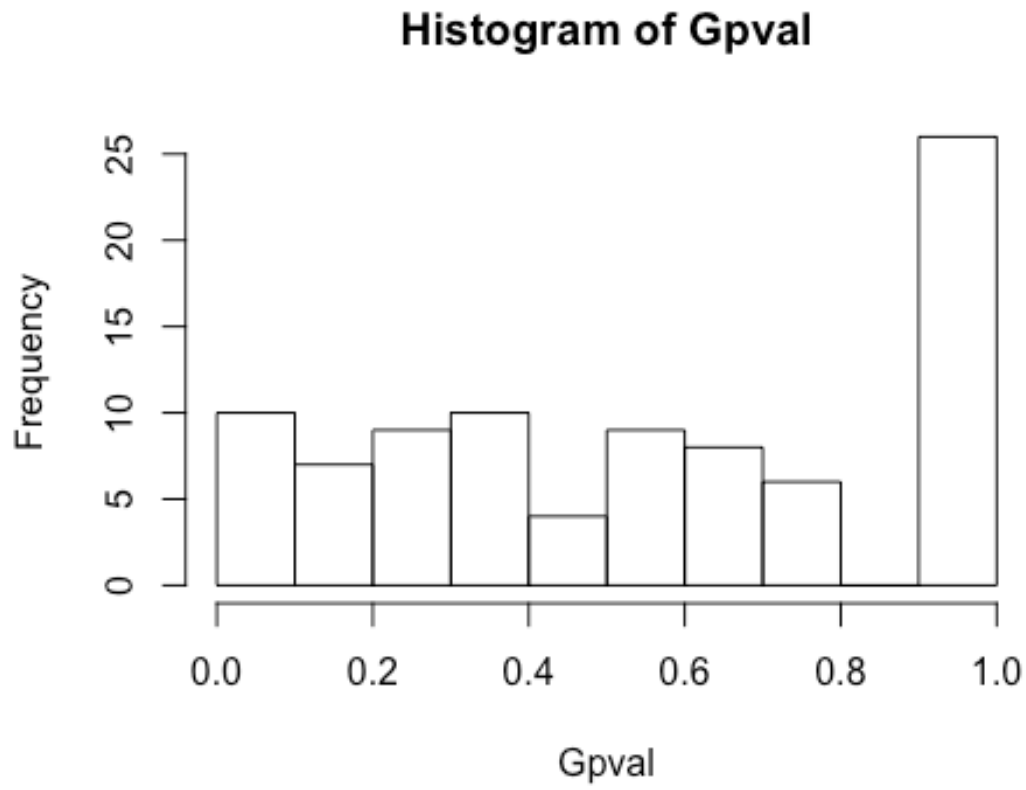
Here we used Fisher exact tests, likelihood ratio tests (G-tests), and a loglinear model to compare the number of ova fertilized by each male in two (replicate) competitive trials with the same triad (one female, two males). We performed this analysis simply to evaluate how repeatable the results from these trials were. We are well aware that the assumptions of these tests have been violated to some extent, but the results indicate that there was some consistency between replicates of the same trial. Whether or not the trials were repeatable has no effect on the conclusions of our study.

```
#Fisher exact and Likelihood ratio (G) tests

pval <- NULL
Gpval <- NULL

count1  <-  0
count2 <- 0
count3  <-  0
count4 <- 0

a <- 1
b <- 2
f1 <- NULL
mat1 <- NULL

for (i in 1:89) {
  mat1 <- Replicates[a:b,5:6]
  #print(mat1) #remove comment if you want to show each 2x2 matrix
  c1 <-  fisher.test(mat1)
  c2 <-  likelihood.test(mat1) #Pete Hurd's Likelihood Ratio (G-test)
for contingency tables
  pval[i] <- c1$p.value #P from the Fisher tests
  Gpval[i] <- c2$p.value #P from the G-tests
  if(pval[i] <0.05) count1 <- count1+1
  if(pval[i] <0.0006) count2 <- count2+1
  if(Gpval[i] <0.05) count3 <- count1+1
  if(Gpval[i] <0.0006) count4 <- count2+1

  a=a+2
```

```
  b=b+2
}

hist(pval) #p from the Fisher tests
```




```
hist(Gpval) #p from the G-tests
```



```r
p.adjust(pval, method = "holm") #adjusted P from the Fisher tests
```

```
##  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [36] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [71] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

```r
p.adjust(pval, method = "bonferroni") #adjusted P from the Fisher tests
```

```
##  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [36] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [71] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

```r
p.adjust(Gpval, method = "holm") #adjusted P from the G-tests
```

```
##  [1] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
##  [8] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [15] 1.000000 1.000000 1.000000 1.000000 1.000000 0.218016 1.000000
## [22] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 0.218016
## [29] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [36] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [43] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [50] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [57] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [64] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [71] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [78] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [85] 1.000000 1.000000 1.000000 1.000000 1.000000
```

```r
p.adjust(Gpval, method = "bonferroni") #adjusted P from the G-tests
```

```
##  [1] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
##  [8] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [15] 1.000000 1.000000 1.000000 1.000000 1.000000 0.218016 1.000000
## [22] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 0.218016
## [29] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [36] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [43] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [50] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [57] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [64] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [71] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [78] 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000
## [85] 1.000000 1.000000 1.000000 1.000000 1.000000
```

```
count1 #number tests with P<0.05 Fisher tests
```

```
## [1] 4
```

```
count2 #number of tests with p<0.006 (Bonferroni corrected alpha) Fish
er tests
```

```
## [1] 0
```

```
count3 #number tests with P<0.05 G-tests
```

```
## [1] 5
```

```
count4 #number of tests with p<0.006 (Bonferroni corrected alpha) G-te
sts
```

```
## [1] 0
```

SUMMARY: Both the Holm and Bonferroni correction methods yield exactly the same results for the Fisher and G-tests, with no P<0.05, and the lowest P = 0.218016 when those corrections were applied to the G-tests

These are the same data on replicate trials but analyzed as a single loglinear model

```
#loglinear model, with male and female IDs as random effects
mod200 <- glmer(fert~as.factor(femtrial)*male+as.factor(rep)+(1|maleID
)+(1|FemaleID), family=poisson, data=reps)
summary(mod200)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula:
## fert ~ as.factor(femtrial) * male + as.factor(rep) + (1 | maleID) +
##     (1 | FemaleID)
##    Data: reps
##
##      AIC      BIC   logLik deviance df.resid
##   2986.6   3114.8  -1460.3   2920.6      327
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.9640 -1.3429 -0.0626  1.2220  5.4826
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  maleID   (Intercept) 2.113e-16 1.453e-08
##  FemaleID (Intercept) 0.000e+00 0.000e+00
## Number of obs: 360, groups:  maleID, 28; FemaleID, 10
```

```
##
## Fixed effects:
##                                Estimate Std. Error z value Pr(>|z|
)
## (Intercept)                     1.87130    0.08934  20.945  < 2e-1
6 ***
## as.factor(femtrial)2            0.19004    0.11900   1.597 0.11027
9
## as.factor(femtrial)3            0.34419    0.11509   2.991 0.00278
5 **
## as.factor(femtrial)4            0.48252    0.11197   4.310 1.64e-0
5 ***
## as.factor(femtrial)5            0.88319    0.10468   8.437  < 2e-1
6 ***
## as.factor(femtrial)6            0.57391    0.11009   5.213 1.85e-0
7 ***
## as.factor(femtrial)7            0.87272    0.10863   8.034 9.44e-1
6 ***
## as.factor(femtrial)8            0.58908    0.11458   5.141 2.73e-0
7 ***
## as.factor(femtrial)9            0.26755    0.12738   2.100 0.03569
9 *
## as.factor(femtrial)10           0.93928    0.15134   6.206 5.42e-1
0 ***
## as.factor(femtrial)11           0.48730    0.23531   2.071 0.03837
2 *
## as.factor(femtrial)12           0.93928    0.19508   4.815 1.47e-0
6 ***
## as.factor(femtrial)13          -0.76547    0.41763  -1.833 0.06682
3 .
## as.factor(femtrial)14           1.24944    0.17313   7.217 5.33e-1
3 ***
## as.factor(femtrial)15           0.87676    0.20002   4.383 1.17e-0
5 ***
## malemaleB                       0.97500    0.10332   9.436  < 2e-1
6 ***
## as.factor(rep)2                -0.01449    0.03058  -0.474 0.63557
1
## as.factor(femtrial)2:malemaleB -0.25341    0.14213  -1.783 0.07459
5 .
## as.factor(femtrial)3:malemaleB -0.47856    0.13970  -3.426 0.00061
3 ***
## as.factor(femtrial)4:malemaleB -0.79587    0.13950  -5.705 1.16e-0
8 ***
## as.factor(femtrial)5:malemaleB -1.60001    0.14096 -11.351  < 2e-1
6 ***
```

```
## as.factor(femtrial)6:malemaleB  -0.89933    0.13817  -6.509 7.57e-1
1 ***
## as.factor(femtrial)7:malemaleB  -1.57173    0.14858 -10.578  < 2e-1
6 ***
## as.factor(femtrial)8:malemaleB  -0.91248    0.14527  -6.281 3.36e-1
0 ***
## as.factor(femtrial)9:malemaleB  -0.36579    0.15414  -2.373 0.01764
0 *
## as.factor(femtrial)10:malemaleB -1.90656    0.25355  -7.519 5.50e-1
4 ***
## as.factor(femtrial)11:malemaleB -0.68732    0.30661  -2.242 0.02498
3 *
## as.factor(femtrial)12:malemaleB -2.52560    0.42876  -5.890 3.85e-0
9 ***
## as.factor(femtrial)13:malemaleB  0.99444    0.44788   2.220 0.02639
7 *
## as.factor(femtrial)14:malemaleB -3.17222    0.48259  -6.573 4.92e-1
1 ***
## as.factor(femtrial)15:malemaleB -1.27349    0.29396  -4.332 1.48e-0
5 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 31 > 20.
## Use print(x, correlation=TRUE)  or
##   vcov(x)     if you need it
```

```
mod201 <- glmer(fert~as.factor(femtrial)*male+(1|maleID)+(1|FemaleID),
family=poisson, data=reps)
anova(mod200, mod201) #no significant effect of replication on model,
P = 0.64
```

```
## Data: reps
## Models:
## mod201: fert ~ as.factor(femtrial) * male + (1 | maleID) + (1 | Fem
aleID)
## mod200: fert ~ as.factor(femtrial) * male + as.factor(rep) + (1 | m
aleID) +
## mod200:     (1 | FemaleID)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mod201 32 2984.8 3109.1 -1460.4   2920.8
## mod200 33 2986.6 3114.8 -1460.3   2920.6 0.2246      1     0.6356
```

SUMMARY: loglinear analysis corroborates previous analysis using both Fisher exact tests and G-tests, showing that there was in general no significant difference in the proportion of ova fertilized by each male in the two replicates for each trial.

SA3. Section 3(a) RESULTS: Genetic analyses

Calculate means and confidence limits from genetic analyses

```
group.CI(Atrioml~year, data=Related) #mean and 95%CL for relatedness b
etween male and female each year

##   year Atrioml.upper Atrioml.mean Atrioml.lower
## 1 2010    0.05671121   0.03164348   0.006575747
## 2 2011    0.03874342   0.02150270   0.004261986

CI(Trials$PfertmaleA) #mean and 95%CL for the proportion of eggs fertl
ized by the winner in each trial

##     upper      mean     lower
## 0.7886339 0.7565246 0.7244152
```

SA4. Section 3(b) RESULTS: Sperm competition trials

SA4.1 Effects of VAP measured in ovarian fluid

SA4.1.1 Tables 1 and S2

These are some models to explore the best analyses to explain male fertilization success ('fitness advantage' = no. of additional offspring assigned to the winner in each trial). Table 1 reports the output from mod2 and the comparison of mod2 with mod2a (without VAP) and mod2b (without MLH), and mod2c without OF concentration; Table S2 reports the results of analysis of mod1a using information theoretic approach

```
##full model to predict fitness advantage from VAP, male heterozygosit
ies and relatedness, including interaction terms

mod1 <- lmer(diffFERT~ rescale(diffVAPof) * rescale(diffTRIOML)* resca
le(diffHmales) + as.factor(ofcon) + (1|female) + (1|maleA) + (1|maleB)
, REML=FALSE,data=Trials)
summary(mod1)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## diffFERT ~ rescale(diffVAPof) * rescale(diffTRIOML) * rescale(diffH
males) +
##     as.factor(ofcon) + (1 | female) + (1 | maleA) + (1 | maleB)
##    Data: Trials
##
##      AIC      BIC   logLik deviance df.resid
##    744.0    776.5   -359.0    718.0       77
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -2.67535 -0.69326  0.08685  0.69223  2.94690
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  maleA    (Intercept)   0.00    0.000
##  maleB    (Intercept)  37.08    6.089
##  female   (Intercept)   0.00    0.000
##  Residual             144.08   12.003
## Number of obs: 90, groups:  maleA, 23; maleB, 22; female, 10
##
## Fixed effects:
##                                                                 Estimate
## (Intercept)                                                      29.1713
## rescale(diffVAPof)                                               10.9640
## rescale(diffTRIOML)                                              -2.7269
## rescale(diffHmales)                                               6.5558
## as.factor(ofcon)100                                              -7.1404
## rescale(diffVAPof):rescale(diffTRIOML)                           -3.7266
## rescale(diffVAPof):rescale(diffHmales)                            5.6350
## rescale(diffTRIOML):rescale(diffHmales)                           6.0901
## rescale(diffVAPof):rescale(diffTRIOML):rescale(diffHmales)  -0.9458
##                                                                Std. Err
or
## (Intercept)                                                         3.10
99
## rescale(diffVAPof)                                                  3.22
81
## rescale(diffTRIOML)                                                 2.93
64
## rescale(diffHmales)                                                 3.52
80
## as.factor(ofcon)100                                                 4.19
60
## rescale(diffVAPof):rescale(diffTRIOML)                             10.69
69
## rescale(diffVAPof):rescale(diffHmales)                              7.51
12
## rescale(diffTRIOML):rescale(diffHmales)                             5.64
08
## rescale(diffVAPof):rescale(diffTRIOML):rescale(diffHmales)    15.65
15
##                                                                t value
## (Intercept)                                                      9.380
## rescale(diffVAPof)                                               3.396
## rescale(diffTRIOML)                                             -0.929
## rescale(diffHmales)                                              1.858
```

```
## as.factor(ofcon)100                                          -1.702
## rescale(diffVAPof):rescale(diffTRIOML)                       -0.348
## rescale(diffVAPof):rescale(diffHmales)                        0.750
## rescale(diffTRIOML):rescale(diffHmales)                       1.080
## rescale(diffVAPof):rescale(diffTRIOML):rescale(diffHmales)  -0.060
##
## Correlation of Fixed Effects:
##                  (Intr) rs(VAP) rs(TRIOML) rsc(H) a.()10 rs(VAP):(T
RIOML)
## rscl(dfVAP)       0.191
## rsc(TRIOML)       0.132  0.086
## rscl(dffHm)      -0.234 -0.056  -0.096
## as.fct()100      -0.790 -0.193  -0.158      0.249
## rs(VAP):(TRIOML)  0.142  0.225   0.008     -0.095 -0.073
## rs(VAP):(H)      -0.175  0.074  -0.180      0.141  0.281 -0.050
## r(TRIOML):(       0.004 -0.094  -0.107      0.169 -0.010 -0.092
## r(VAP):(TRIOML): -0.092  0.007  -0.265      0.281  0.080  0.404
##                  r(VAP):(H r(TRIOML):
## rscl(dfVAP)
## rsc(TRIOML)
## rscl(dffHm)
## as.fct()100
## rs(VAP):(TRIOML)
## rs(VAP):(H)
## r(TRIOML):(       0.229
## r(VAP):(TRIOML):  0.073     0.468
```

```
options(na.action = "na.fail")   #  prevent fitting models to differen
t datasets
dredge(mod1) #evaluate all models using information-theoretic approach
; interaction terms not included in top models so removed to reduce th
e effects of overparameterization
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: lmer(formula = diffFERT ~ rescale(diffVAPof) * r
escale(diffTRIOML) *
##     rescale(diffHmales) + as.factor(ofcon) + (1 | female) + (1 |
##     maleA) + (1 | maleB), data = Trials, REML = FALSE)
## ---
## Model selection table
##     (Int) as.fct(ofc) rsc(dfH) rsc(dTR) rsc(dVA) rsc(dfH):rsc(dTR)
## 12  29.40           +    6.434            11.630
## 11  24.81                7.330             9.757
## 10  30.13           +                     11.390
## 16  29.24           +    6.322   -2.639   11.340
```

```
## 15  24.85                7.223   -2.905    9.606
## 9   24.76                                  9.505
## 44  29.23           +    6.561             11.760
## 14  29.99           +           -2.802    11.160
## 43  24.92                7.576             10.210
## 32  29.75           +    6.076   -2.321   11.100             4.924
## 13  24.86                       -3.126    9.404
## 47  25.00                7.499   -3.333   10.150
## 48  28.96           +    6.513   -2.887   11.520
## 31  24.96                7.092   -2.650    9.320             3.851
## 80  29.34           +    6.225   -2.588   11.460
## 79  24.77                7.381   -2.991    9.471
## 78  30.35           +           -2.585   11.620
## 64  29.41           +    6.332   -2.647   11.340             5.621
## 63  25.17                7.409   -3.113    9.898             5.031
## 96  29.56           +    6.292   -2.414   10.800             5.411
## 77  24.86                       -3.128    9.400
## 95  24.72                7.452   -2.853    8.835             5.052
## 111 24.93                7.624   -3.398   10.030
## 112 29.06           +    6.419   -2.838   11.630
## 3   24.61                6.935
## 1   24.50
## 127 24.93                7.878   -3.311    9.383             6.248
## 128 29.16           +    6.615   -2.774   10.970             6.247
## 7   24.71                6.796   -3.074
## 5   24.66                       -3.282
## 4   27.22           +    6.620
## 2   27.55           +
## 23  24.72                6.526   -2.767                      5.205
## 8   27.22           +    6.457   -3.041
## 6   27.60           +           -3.221
## 255 24.93                7.897   -3.327    9.386             6.299
## 256 29.17           +    6.556   -2.727   10.960             6.090
## 24  27.53           +    6.223   -2.662                      5.795
##     rsc(dfH):rsc(dVA) rsc(dTR):rsc(dVA) rsc(dfH):rsc(dTR):rsc(dVA)
df
## 12
8
## 11
7
## 10
7
## 16
9
## 15
8
```

```
## 9
6
## 44               2.288
9
## 14
8
## 43               5.417
8
## 32
10
## 13
7
## 47               6.765
9
## 48               3.622
10
## 31
9
## 80                             1.14500
10
## 79                            -2.05200
9
## 78                             4.83600
9
## 64               5.445
11
## 63               8.490
10
## 96                            -2.79800
11
## 77                            -0.05136
8
## 95                            -6.24800
10
## 111              6.708        -1.64700
10
## 112              3.613         1.09700
11
## 3
6
## 1
5
## 127              8.660        -6.42500
11
## 128              5.668        -3.45300
12
```

```
## 7
7
## 5
6
## 4
7
## 2
6
## 23
8
## 8
8
## 6
7
## 255             8.672          -6.33900                      0.3025
12
## 256             5.635          -3.72700                     -0.9458
13
## 24
9
##       logLik  AICc delta weight
## 12  -360.325 738.4  0.00  0.171
## 11  -361.973 739.3  0.88  0.110
## 10  -362.164 739.7  1.27  0.091
## 16  -359.881 740.0  1.58  0.078
## 15  -361.438 740.7  2.23  0.056
## 9   -363.867 740.7  2.32  0.054
## 44  -360.276 740.8  2.37  0.052
## 14  -361.676 741.1  2.70  0.044
## 43  -361.692 741.2  2.73  0.044
## 32  -359.315 741.4  2.99  0.038
## 13  -363.288 741.9  3.51  0.030
## 47  -361.003 742.3  3.83  0.025
## 48  -359.761 742.3  3.88  0.025
## 31  -361.092 742.4  4.01  0.023
## 80  -359.874 742.5  4.10  0.022
## 79  -361.415 743.1  4.65  0.017
## 78  -361.543 743.3  4.91  0.015
## 64  -359.050 743.5  5.06  0.014
## 63  -360.435 743.7  5.23  0.013
## 96  -359.277 743.9  5.51  0.011
## 77  -363.288 744.4  5.92  0.009
## 95  -360.919 744.6  6.19  0.008
## 111 -360.988 744.8  6.33  0.007
## 112 -359.754 744.9  6.46  0.007
## 3   -366.042 745.1  6.67  0.006
```

```
## 1   -367.358 745.4  7.00  0.005
## 127 -360.236 745.9  7.43  0.004
## 128 -358.991 746.0  7.61  0.004
## 7   -365.482 746.3  7.90  0.003
## 5   -366.760 746.5  8.10  0.003
## 4   -365.707 746.8  8.35  0.003
## 2   -366.985 747.0  8.55  0.002
## 23  -364.963 747.7  9.28  0.002
## 8   -365.156 748.1  9.66  0.001
## 6   -366.403 748.2  9.74  0.001
## 255 -360.236 748.5 10.10  0.001
## 256 -358.990 748.8 10.34  0.001
## 24  -364.504 749.3 10.83  0.001
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | female', '1 | maleA', '1 | maleB'
```

```
mod1a <- lmer(diffFERT~ rescale(diffVAPof) + rescale(diffTRIOML) + res
cale(diffHmales) + as.factor(ofcon) + (1|female) + (1|maleA) + (1|male
B), REML=FALSE,data=Trials) #same as mod1 without interaction terms
dredge(mod1a) #evaluate all models using information-theoretic approac
h
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: lmer(formula = diffFERT ~ rescale(diffVAPof) + r
escale(diffTRIOML) +
##     rescale(diffHmales) + as.factor(ofcon) + (1 | female) + (1 |
##     maleA) + (1 | maleB), data = Trials, REML = FALSE)
## ---
## Model selection table
##    (Int) as.fct(ofc) rsc(dfH) rsc(dTR) rsc(dVA) df   logLik  AICc d
elta
## 12 29.40           +    6.434           11.630  8 -360.325 738.4
0.00
## 11 24.81                7.330            9.757  7 -361.973 739.3
0.88
## 10 30.13           +                    11.390  7 -362.164 739.7
1.27
## 16 29.24           +    6.322   -2.639   11.340  9 -359.881 740.0
1.58
## 15 24.85                7.223   -2.905    9.606  8 -361.438 740.7
2.23
## 9  24.76                                  9.505  6 -363.867 740.7
2.32
## 14 29.99           +           -2.802   11.160  8 -361.676 741.1
```

```
2.70
## 13 24.86                        -3.126    9.404  7 -363.288 741.9
3.51
## 3  24.61               6.935                   6 -366.042 745.1
6.67
## 1  24.50                                       5 -367.358 745.4
7.00
## 7  24.71               6.796   -3.074          7 -365.482 746.3
7.90
## 5  24.66                       -3.282          6 -366.760 746.5
8.10
## 4  27.22           +   6.620                   7 -365.707 746.8
8.35
## 2  27.55           +                           6 -366.985 747.0
8.55
## 8  27.22           +   6.457   -3.041          8 -365.156 748.1
9.66
## 6  27.60           +           -3.221          7 -366.403 748.2
9.74
##    weight
## 12  0.260
## 11  0.167
## 10  0.138
## 16  0.118
## 15  0.085
## 9   0.082
## 14  0.067
## 13  0.045
## 3   0.009
## 1   0.008
## 7   0.005
## 5   0.005
## 4   0.004
## 2   0.004
## 8   0.002
## 6   0.002
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | female', '1 | maleA', '1 | maleB'

#best-fitting model from information theoretic analysis above
mod2 <- lmer(diffFERT~ rescale(diffVAPof) + rescale(diffHmales)+as.fac
tor(ofcon) + (1|female) + (1|maleA) + (1|maleB), data=Trials)
summary(mod2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + as.factor(ofc
on) +
##     (1 | female) + (1 | maleA) + (1 | maleB)
##    Data: Trials
##
## REML criterion at convergence: 704.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.66756 -0.67341  0.06596  0.73398  2.82023
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  maleA    (Intercept)   0.00    0.000
##  maleB    (Intercept)  47.27    6.875
##  female   (Intercept)   0.00    0.000
##  Residual             152.02   12.330
## Number of obs: 90, groups:  maleA, 23; maleB, 22; female, 10
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           29.166      3.175   9.185
## rescale(diffVAPof)    11.159      3.247   3.436
## rescale(diffHmales)    6.358      3.439   1.849
## as.factor(ofcon)100   -7.498      4.238  -1.769
##
## Correlation of Fixed Effects:
##             (Intr) r(VAP) rsc(H)
## rscl(dfVAP)  0.176
## rscl(dffHm) -0.155 -0.024
## as.fct()100 -0.773 -0.208  0.186
```

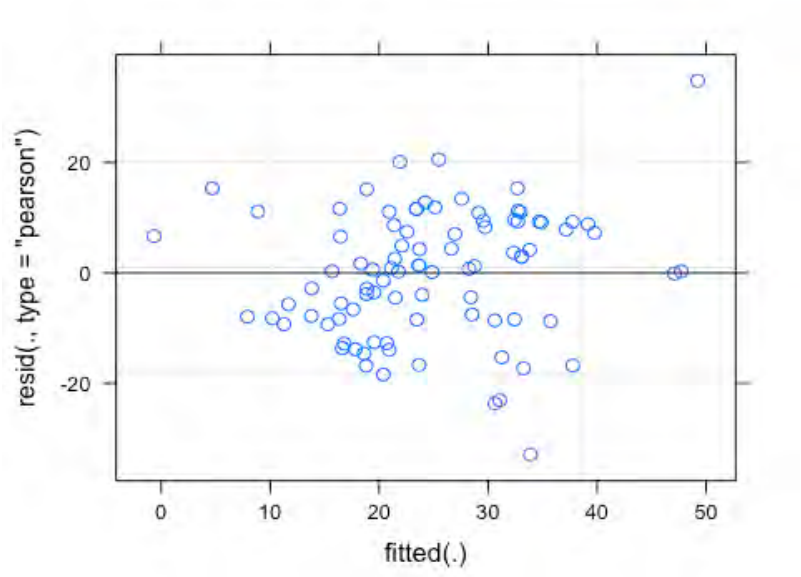
```
confint(mod2, method = "Wald")
```

```
##                             2.5 %     97.5 %
## .sig01                         NA         NA
## .sig02                         NA         NA
## .sig03                         NA         NA
## .sigma                         NA         NA
## (Intercept)          22.9425802 35.3902302
## rescale(diffVAPof)    4.7945388 17.5233706
## rescale(diffHmales)  -0.3823294 13.0976666
## as.factor(ofcon)100 -15.8040219  0.8082567
```

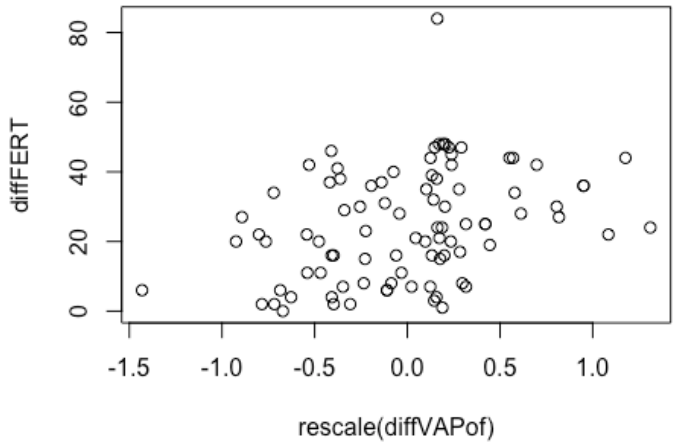
```
shapiro.test(resid(mod2))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  resid(mod2)
## W = 0.98258, p-value = 0.2714
```

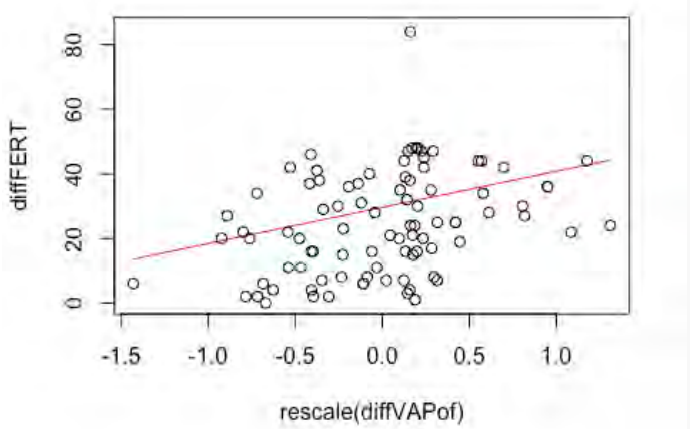
```
plot(mod2)
```



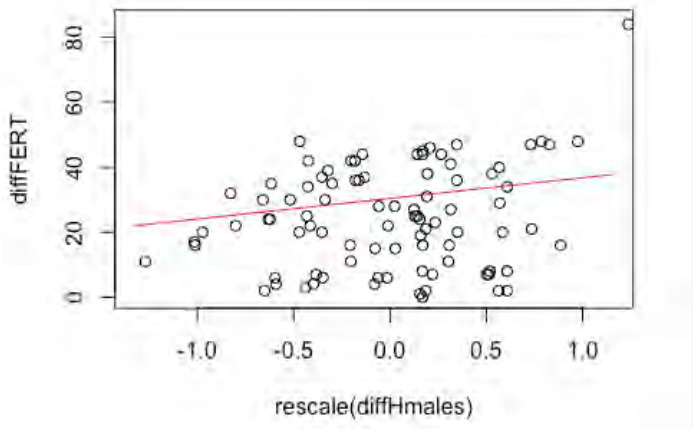

```
with(Trials, plot(diffFERT~rescale(diffVAPof))) #plot to determine yli
mit for plotLMER.fnc
```



```
plotLMER.fnc(mod2, ylimit=c(0,85), pred = "rescale(diffVAPof)",linecol
or = 2) #plot model effect for VAP diff

## effect size (range) for  rescale(diffVAPof) is  30.60411

with(Trials, points(diffFERT~jitter(rescale(diffVAPof),2))) #add data
points to that graph
```




```
plotLMER.fnc(mod2, ylimit=c(0,85), pred = "rescale(diffHmales)",lineco
lor = 2) #plot model effect for MLH diff

## effect size (range) for  rescale(diffHmales) is  15.83314

with(Trials, points(diffFERT~jitter(rescale(diffHmales),2))) #add data
points to that graph
```



```
mod2a <- lmer(diffFERT~ + rescale(diffHmales) + as.factor(ofcon) + (1|
female) + (1|maleA) + (1|maleB), data=Trials) #mod2 without diffVAPof
KRmodcomp(mod2,mod2a) #calculate P for diffVAPof

## F-test with Kenward-Roger approximation; computing time: 0.43 sec.
## large : diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + as.fa
ctor(ofcon) +
##     (1 | female) + (1 | maleA) + (1 | maleB)
## small : diffFERT ~ +rescale(diffHmales) + as.factor(ofcon) + (1 | f
emale) +
##     (1 | maleA) + (1 | maleB)
##          stat     ndf     ddf F.scaling  p.value
## Ftest  9.4467  1.0000 51.2836         1 0.003385 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

mod2b <- lmer(diffFERT~ rescale(diffVAPof) + rescale(diffHmales)  + (1
|female) + (1|maleA) + (1|maleB), data=Trials) #mod2 without ofcon
KRmodcomp(mod2,mod2b) #calculate P for OF concentration (ofcon)

## F-test with Kenward-Roger approximation; computing time: 0.26 sec.
## large : diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + as.fa
ctor(ofcon) +
##     (1 | female) + (1 | maleA) + (1 | maleB)
## small : diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + (1 |
female) +
##     (1 | maleA) + (1 | maleB)
##          stat     ndf     ddf F.scaling p.value
## Ftest  2.9437  1.0000 11.6304         1  0.1127

mod2c <- lmer(diffFERT~ rescale(diffVAPof)  + as.factor(ofcon) + (1|fe
male) + (1|maleA) + (1|maleB), data=Trials) #mod2 without difference i
n heterozygosity between males (diffmales)
KRmodcomp(mod2,mod2c) #calculate P for difference in heterozygosity be
tween males

## F-test with Kenward-Roger approximation; computing time: 0.26 sec.
## large : diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + as.fa
ctor(ofcon) +
##     (1 | female) + (1 | maleA) + (1 | maleB)
## small : diffFERT ~ rescale(diffVAPof) + as.factor(ofcon) + (1 | fem
ale) +
##     (1 | maleA) + (1 | maleB)
##          stat     ndf     ddf F.scaling p.value
## Ftest  2.7932  1.0000 27.9528         1  0.1058
```

```
#evaluate different model with response as fertDIFF relative to the to
tal number of eggs fertilized
Trials$RdiffFERT <- Trials$diffFERT/Trials$TOTALfert
mod3 <- lmer(RdiffFERT~ rescale(diffVAPof) + rescale(diffHmales) + as.
factor(ofcon) + (1|female) + (1|maleA) + (1|maleB), data=Trials)
summary(mod3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## RdiffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + as.factor(of
con) +
##     (1 | female) + (1 | maleA) + (1 | maleB)
##    Data: Trials
##
## REML criterion at convergence: 28.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.6168 -0.7046  0.1969  0.7470  1.5430
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  maleA    (Intercept) 0.000000 0.00000
##  maleB    (Intercept) 0.018538 0.13615
##  female   (Intercept) 0.004039 0.06355
##  Residual             0.056319 0.23732
## Number of obs: 90, groups:  maleA, 23; maleB, 22; female, 10
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)          0.60364    0.07022   8.596
## rescale(diffVAPof)   0.21910    0.06498   3.372
## rescale(diffHmales)  0.09083    0.06761   1.343
## as.factor(ofcon)100 -0.15100    0.09279  -1.627
##
## Correlation of Fixed Effects:
##             (Intr) r(VAP) rsc(H)
## rscl(dfVAP)  0.144
## rscl(dffHm) -0.143 -0.019
## as.fct()100 -0.775 -0.176  0.167
```

```
confint(mod3, method = "Wald") #VAP significant
```

```
##                            2.5 %     97.5 %
## .sig01                        NA         NA
## .sig02                        NA         NA
```

```
## .sig03                       NA         NA
## .sigma                       NA         NA
## (Intercept)          0.46601073 0.74127509
## rescale(diffVAPof)   0.09174274 0.34646086
## rescale(diffHmales) -0.04168001 0.22334298
## as.factor(ofcon)100 -0.33287148 0.03086783
```

```
#evaluate different model with predictors as heterozygosities and VAP
for each male rather than the differences between males
mod4 <- lmer(diffFERT~ rescale(VAPmaleAof) + rescale(VAPmaleBof) +resc
ale(HmaleA) +  rescale(HmaleB)+ as.factor(ofcon) + (1|female) + (1|mal
eA) + (1|maleB), data=Trials)
summary(mod4)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## diffFERT ~ rescale(VAPmaleAof) + rescale(VAPmaleBof) + rescale(Hmal
eA) +
##     rescale(HmaleB) + as.factor(ofcon) + (1 | female) + (1 |
##     maleA) + (1 | maleB)
##    Data: Trials
##
## REML criterion at convergence: 695.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.62494 -0.67587  0.07275  0.67754  2.78598
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  maleA    (Intercept) 5.651e-14 2.377e-07
##  maleB    (Intercept) 4.727e+01 6.875e+00
##  female   (Intercept) 0.000e+00 0.000e+00
##  Residual             1.554e+02 1.247e+01
## Number of obs: 90, groups:  maleA, 23; maleB, 22; female, 10
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           28.561      3.656   7.813
## rescale(VAPmaleAof)    7.593      3.918   1.938
## rescale(VAPmaleBof)   -8.795      3.342  -2.632
## rescale(HmaleA)        2.536      2.849   0.890
## rescale(HmaleB)       -6.215      4.120  -1.508
## as.factor(ofcon)100   -6.533      5.144  -1.270
##
## Correlation of Fixed Effects:
```

```
##             (Intr) r(VAPA r(VAPB rs(HA) rs(HB)
## rscl(VAPmA)  0.459
## rscl(VAPmB)  0.239  0.113
## rescl(HmlA) -0.060 -0.148  0.040
## rescl(HmlB)  0.180 -0.037  0.115  0.184
## as.fct()100 -0.832 -0.528 -0.278  0.074 -0.199
```

```
confint(mod4, method = "Wald") #same result as for mod1a
```

```
##                            2.5 %    97.5 %
## .sig01                        NA        NA
## .sig02                        NA        NA
## .sig03                        NA        NA
## .sigma                        NA        NA
## (Intercept)           21.3956618 35.726017
## rescale(VAPmaleAof)   -0.0854604 15.272311
## rescale(VAPmaleBof) -15.3450577 -2.244891
## rescale(HmaleA)      -3.0469979  8.119588
## rescale(HmaleB)     -14.2902159  1.860416
## as.factor(ofcon)100 -16.6154761  3.550204
```

```
mod4a <- lmer(diffFERT~ rescale(VAPmaleAof) + rescale(VAPmaleBof)+resc
ale(HmaleA) +  rescale(HmaleB)+as.factor(ofcon) + (1|female) + (1|male
A) + (1|maleB), REML=FALSE,data=Trials) #same as mod4 but REML=FALSE s
o that information theoretic approach can be applied
dredge(mod4a)
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: lmer(formula = diffFERT ~ rescale(VAPmaleAof) +
rescale(VAPmaleBof) +
##     rescale(HmaleA) + rescale(HmaleB) + as.factor(ofcon) + (1 |
##     female) + (1 | maleA) + (1 | maleB), data = Trials, REML = FALS
E)
## ---
## Model selection table
##    (Int) as.fct(ofc) rsc(HmA) rsc(HmB) rsc(VAPA) rsc(VAPB) df   log
Lik
## 21 24.56                      -7.045            -11.070  7 -362.
610
## 29 24.66                      -7.978     5.209  -10.610  8 -361.
424
## 30 28.75          +           -6.776     7.966   -9.737  9 -360.
545
## 17 24.56                                         -9.594  6 -364.
369
## 23 24.66               3.443  -6.060            -11.370  8 -361.
```

```
994
## 26 29.97           +                    8.022    -8.420  8 -362.
159
## 19 24.71                4.333                    -10.250  7 -363.
417
## 31 24.71                2.886   -7.127     4.625   -10.750  9 -361.
019
## 25 24.71                                   4.706    -9.236  7 -363.
477
## 22 25.05           +            -6.840              -10.960  8 -362.
592
## 32 28.56           +    2.618   -6.078     7.438    -9.642 10 -360.
111
## 28 29.56           +    3.426              7.307    -8.571  9 -361.
407
## 27 24.79                3.837              3.950    -9.596  8 -362.
753
## 18 26.22           +                                -9.370  7 -364.
185
## 20 26.39           +    4.275                       -9.832  8 -363.
151
## 24 25.37           +    3.453   -5.747             -11.100  9 -361.
945
## 10 32.10           +                    9.491              7 -364.
563
## 14 31.28           +            -6.159  9.818              8 -363.
698
## 1  24.50                                                    5 -367.
358
## 12 31.84           +    3.237              8.893              8 -363.
866
## 9  24.90                                   6.115              6 -366.
265
## 13 24.73                        -7.749     6.586              7 -365.
135
## 5  24.30                        -6.861                        6 -366.
441
## 3  24.76                4.040                                 6 -366.
674
## 11 24.97                3.456              5.963              7 -365.
507
## 16 31.13           +    2.756   -5.402     9.274              9 -363.
198
## 2  27.55           +                                          6 -366.
985
## 15 24.82                2.942   -6.854     6.534              8 -364.
```

```
611
## 7  24.55                3.300   -5.806                      7 -366.
017
## 4  28.02           +    4.035                               7 -366.
176
## 6  26.46           +           -6.120                       7 -366.
250
## 8  27.21           +    3.641   -4.750                      8 -365.
707
##     AICc delta weight
## 21 740.6  0.00  0.121
## 29 740.6  0.04  0.119
## 30 741.3  0.75  0.083
## 17 741.7  1.16  0.068
## 23 741.8  1.18  0.067
## 26 742.1  1.51  0.057
## 19 742.2  1.61  0.054
## 31 742.3  1.70  0.052
## 25 742.3  1.73  0.051
## 22 743.0  2.38  0.037
## 32 743.0  2.42  0.036
## 28 743.1  2.48  0.035
## 27 743.3  2.70  0.032
## 18 743.7  3.15  0.025
## 20 744.1  3.49  0.021
## 24 744.1  3.55  0.021
## 10 744.5  3.91  0.017
## 14 745.2  4.59  0.012
## 1  745.4  4.84  0.011
## 12 745.5  4.92  0.010
## 9  745.5  4.96  0.010
## 13 745.6  5.05  0.010
## 5  745.9  5.31  0.009
## 3  746.4  5.77  0.007
## 11 746.4  5.79  0.007
## 16 746.6  6.06  0.006
## 2  747.0  6.39  0.005
## 15 747.0  6.41  0.005
## 7  747.4  6.81  0.004
## 4  747.7  7.13  0.003
## 6  747.9  7.28  0.003
## 8  749.2  8.61  0.002
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | female', '1 | maleA', '1 | maleB'
```

SA4.1.2 figure 1 and S2, and table S3

In table S3 we report the analyses for the effects of VAP and male heterozygosity on fitness advantage, separately for each ovarian fluid concentration, using the same model structure as in mod2 above

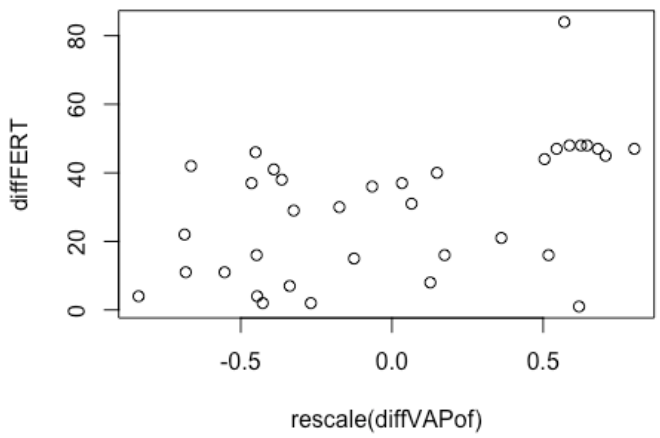
```
Trials50 <- subset(Trials, ofcon==50) #data for trials at 50% ovarian
fluid concentration
Trials100 <- subset(Trials, ofcon==100) #data for trials at 100% ovari
an fluid concentration

#models for trials in 50% ovarian fluid
mod50 <- lmer(diffFERT~rescale(diffVAPof) + rescale(diffHmales) +(1|fe
male)+(1|maleA)+(1|maleB), data=Trials50) #full model based on structu
re of best-fitting model (mod2) above
summary(mod50)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + (1 | female)
+
##     (1 | maleA) + (1 | maleB)
##    Data: Trials50
##
## REML criterion at convergence: 279.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1922 -0.7885  0.2940  0.4380  2.3482
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  maleA    (Intercept)   0.0     0.00
##  maleB    (Intercept)   0.0     0.00
##  female   (Intercept)   0.0     0.00
##  Residual             284.5    16.87
## Number of obs: 35, groups:  maleA, 11; maleB, 10; female, 4
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           29.171      2.851  10.232
## rescale(diffVAPof)    13.254      7.104   1.866
## rescale(diffHmales)    8.873      7.104   1.249
##
## Correlation of Fixed Effects:
##             (Intr) r(VAP)
```

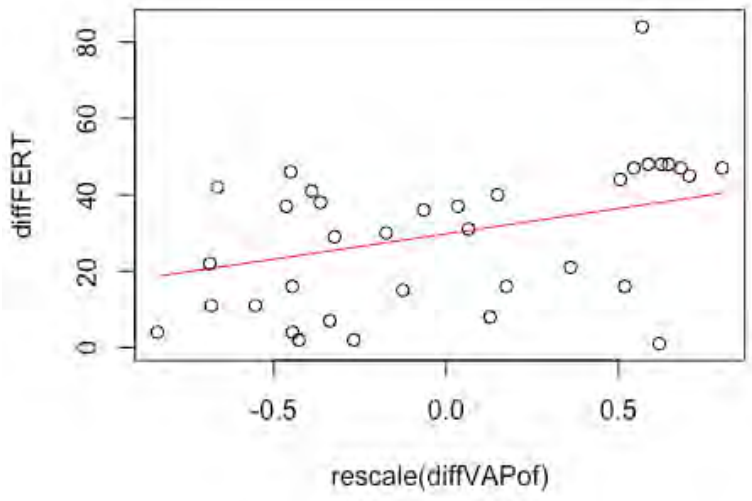
```
## rscl(dfVAP)  0.000
## rscl(dffHm)  0.000 -0.580

confint(mod50, method ="Wald")

##                            2.5 %   97.5 %
## .sig01                        NA       NA
## .sig02                        NA       NA
## .sig03                        NA       NA
## .sigma                        NA       NA
## (Intercept)          23.5833787 34.75948
## rescale(diffVAPof)   -0.6687328 27.17761
## rescale(diffHmales) -5.0497792 22.79656

mod50a <- lmer(diffFERT~rescale(diffHmales) +(1|female)+(1|maleA)+(1|m
aleB), data=Trials50)
mod50b <- lmer(diffFERT ~ rescale(diffVAPof)+(1|female)+(1|maleA)+(1|m
aleB), data=Trials50)
KRmodcomp(mod50,mod50a) #calculate P for difference in VAP between mal
es

## F-test with Kenward-Roger approximation; computing time: 0.27 sec.
## large : diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + (1 |
female) +
##     (1 | maleA) + (1 | maleB)
## small : diffFERT ~ rescale(diffHmales) + (1 | female) + (1 | maleA)
+
##     (1 | maleB)
##         stat    ndf    ddf F.scaling p.value
## Ftest 1.9556 1.0000 8.4829         1  0.1975

KRmodcomp(mod50,mod50b) #calculate P for difference in heterozygosity
between males

## F-test with Kenward-Roger approximation; computing time: 0.27 sec.
## large : diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + (1 |
female) +
##     (1 | maleA) + (1 | maleB)
## small : diffFERT ~ rescale(diffVAPof) + (1 | female) + (1 | maleA)
+
##     (1 | maleB)
##          stat     ndf     ddf F.scaling p.value
## Ftest  1.2121  1.0000 20.4040         1  0.2837

#mod50 without scaling VAP, so that effects of actual values for VAP c
an be assessed
mod51 <- lmer(diffFERT~diffVAPof + rescale(diffHmales) +(1|female)+(1|
```

```
maleA)+(1|maleB), data=Trials50)
summary(mod51)

## Linear mixed model fit by REML ['lmerMod']
## Formula: diffFERT ~ diffVAPof + rescale(diffHmales) + (1 | female)
+ (1 |
##     maleA) + (1 | maleB)
##    Data: Trials50
##
## REML criterion at convergence: 286
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1922 -0.7885  0.2940  0.4380  2.3482
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  maleA    (Intercept) 1.365e-13 3.695e-07
##  maleB    (Intercept) 5.511e-14 2.348e-07
##  female   (Intercept) 2.232e-14 1.494e-07
##  Residual             2.845e+02 1.687e+01
## Number of obs: 35, groups:  maleA, 11; maleB, 10; female, 4
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)          27.2172     3.0374   8.961
## diffVAPof             0.4178     0.2239   1.866
## rescale(diffHmales)   8.8734     7.1038   1.249
##
## Correlation of Fixed Effects:
##             (Intr) dffVAP
## diffVAPof   -0.345
## rscl(dffHm)  0.200 -0.580

confint(mod51)

## Computing profile confidence intervals ...

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows
have
## identical or NA .zeta values: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows
have
## identical or NA .zeta values: using minstep

## Warning in FUN(X[[i]], ...): non-monotonic profile for .sig01
```

```
## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows
have
## identical or NA .zeta values: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows
have
## identical or NA .zeta values: using minstep

## Warning in FUN(X[[i]], ...): non-monotonic profile for .sig02

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows
have
## identical or NA .zeta values: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows
have
## identical or NA .zeta values: using minstep

## Warning in FUN(X[[i]], ...): non-monotonic profile for .sig03

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline
fit
## for .sig01: falling back to linear interpolation

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline
fit
## for .sig02: falling back to linear interpolation

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline
fit
## for .sig03: falling back to linear interpolation

##                            2.5 %     97.5 %
## .sig01                0.00000000 10.3326075
## .sig02                0.00000000 10.0797959
## .sig03                0.00000000  9.7337065
## .sigma               12.97810467 20.7935939
## (Intercept)          21.36507905 33.0693573
## diffVAPof            -0.01363145  0.8492743
## rescale(diffHmales) -4.81347343 22.5602552

#plot effects for ESM fig S2a,b
with(Trials50, plot(diffFERT~rescale(diffVAPof))) #plot to determine y
limit for plotLMER.fnc
```

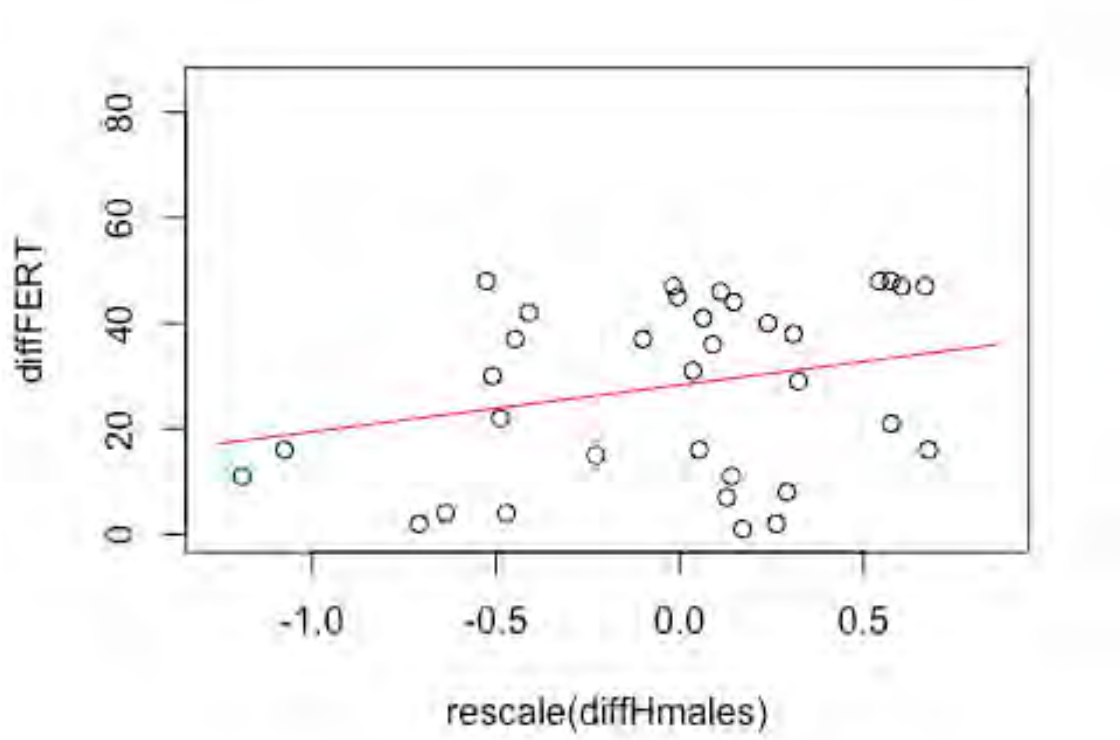



```
plotLMER.fnc(mod50, ylimit=c(0,85), pred = "rescale(diffVAPof)",lineco
lor = 2) #plot model effect for VAP diff

## effect size (range) for  rescale(diffVAPof) is  21.72671

with(Trials50, points(diffFERT~jitter(rescale(diffVAPof),2))) #add dat
a points to that graph
```




```
plotLMER.fnc(mod50, ylimit=c(0,85), pred = "rescale(diffHmales)",linec
olor = 2) #plot model effect for MLH diff

## effect size (range) for  rescale(diffHmales) is  18.83914
```

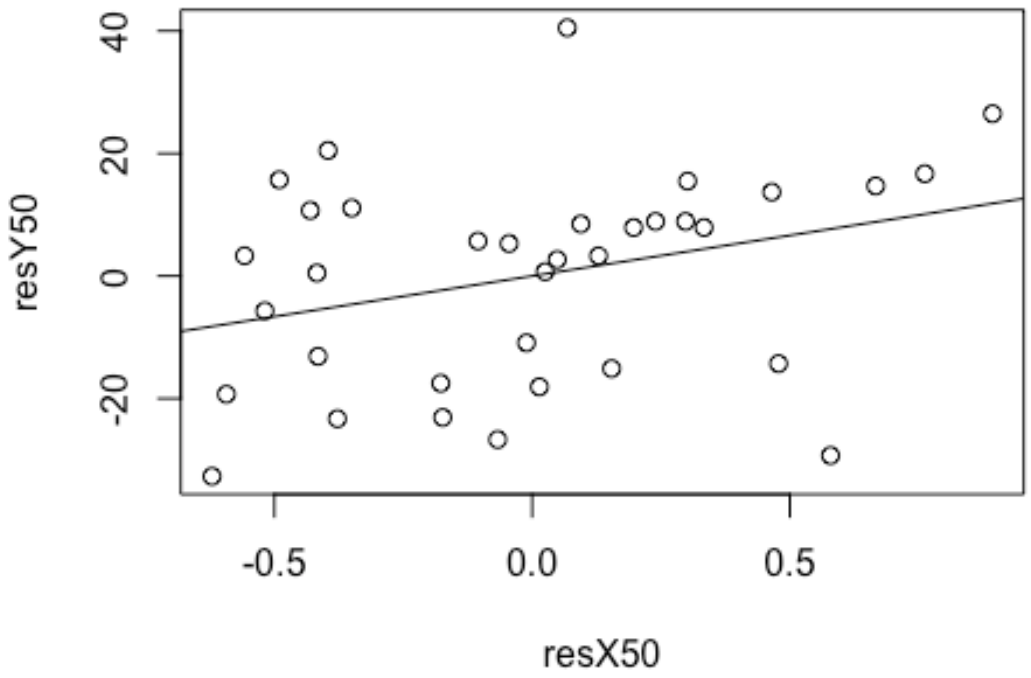
```
with(Trials50, points(diffFERT~jitter(rescale(diffHmales),2))) #add da
ta points to that graph
```




```
#partial regression plot for trials at 50% OF; no random effects in mo
del
resY50 <- residuals(lm(diffFERT~ rescale(diffHmales), data=Trials50))
#calculate partial residual diff in fertilization success
resX50 <- residuals(lm(rescale(diffVAPof)~ rescale(diffHmales), data=T
rials50)) #calculate partial residual diff in VAP in ovarian fluid

mod50c <- lm(resY50~resX50) #partial regression model
summary(mod50c) #slope almost identical to mod50

##
## Call:
## lm(formula = resY50 ~ resX50)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -36.976 -13.301   4.959   7.387  39.607
##
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 9.594e-17  2.808e+00   0.000   1.0000
## resX50      1.325e+01  6.995e+00   1.895   0.0669 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.61 on 33 degrees of freedom
## Multiple R-squared:  0.09812,    Adjusted R-squared:  0.07079
## F-statistic:  3.59 on 1 and 33 DF,  p-value: 0.06691
```

```
plot(resY50~resX50)
abline(mod50c)
```




```
write.csv(cbind(resY50, resX50), file="plot50.csv") #save partial regr
ession data for plotting

#models for trials in 100% ovarian fluid
mod100 <- lmer(diffFERT~rescale(diffVAPof)+ rescale(diffHmales) +(1|fe
male)+(1|maleA)+(1|maleB), data=Trials100) #full model based on struct
ure of best-fitting model (mod2) above
summary(mod100)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + (1 | female)
+
##     (1 | maleA) + (1 | maleB)
##    Data: Trials100
##
## REML criterion at convergence: 398.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.87544 -0.81247 -0.00349  0.72061  1.65645
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  maleB    (Intercept) 48.288   6.949
##  maleA    (Intercept)  3.508   1.873
##  female   (Intercept)  0.000   0.000
##  Residual             80.111   8.950
## Number of obs: 55, groups:  maleB, 12; maleA, 12; female, 6
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           22.398      2.478   9.039
## rescale(diffVAPof)    10.433      3.300   3.162
## rescale(diffHmales)    1.916      3.780   0.507
##
## Correlation of Fixed Effects:
##             (Intr) r(VAP)
## rscl(dfVAP)  0.014
## rscl(dffHm) -0.025  0.161

confint(mod100, method ="Wald")

##                          2.5 %    97.5 %
## .sig01                      NA        NA
## .sig02                      NA        NA
## .sig03                      NA        NA
## .sigma                      NA        NA
## (Intercept)         17.541553 27.254485
## rescale(diffVAPof)   3.965563 16.900045
## rescale(diffHmales) -5.492073  9.324631

mod100a <- lmer(diffFERT~ rescale(diffHmales) +(1|female)+(1|maleA)+(1
|maleB), data=Trials100) #mod100 without difference in VAP
mod100b <- lmer(diffFERT~rescale(diffVAPof)+ (1|female)+(1|maleA)+(1|m
```

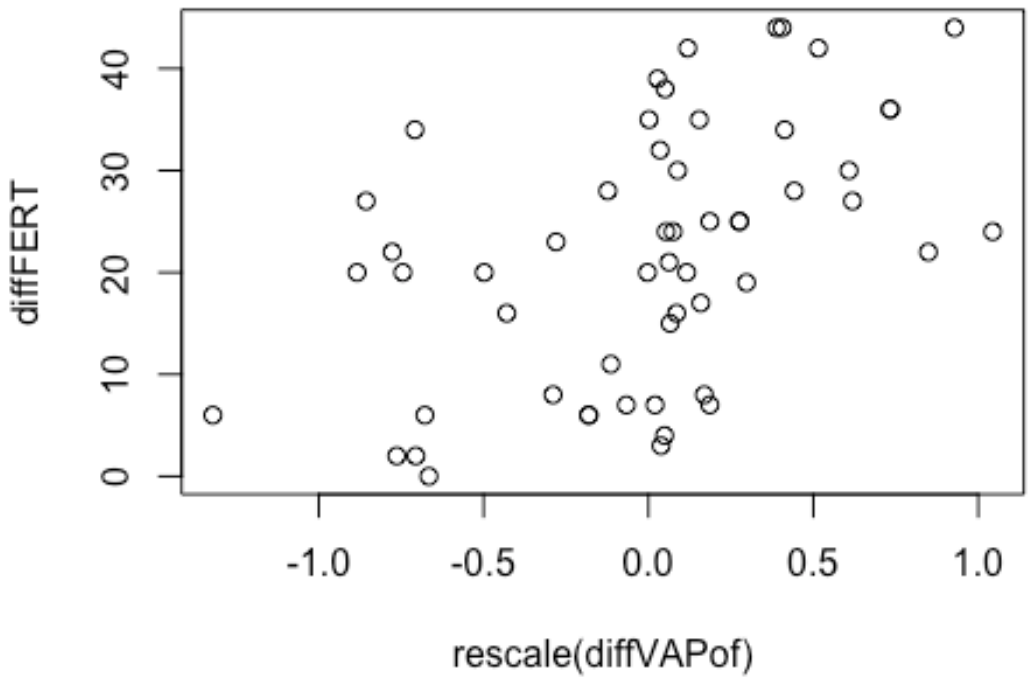
```
aleB), data=Trials100) #mod100 without difference in male heterozygosi
ty
KRmodcomp(mod100,mod100a) #calculate P for difference in VAP between m
ales

## F-test with Kenward-Roger approximation; computing time: 0.25 sec.
## large : diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + (1 |
female) +
##     (1 | maleA) + (1 | maleB)
## small : diffFERT ~ rescale(diffHmales) + (1 | female) + (1 | maleA)
+
##     (1 | maleB)
##          stat     ndf     ddf F.scaling  p.value
## Ftest  7.5195  1.0000 35.0433         1 0.009548 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

KRmodcomp(mod100,mod100b) #calculate P for difference in heterozygosit
y between males

## F-test with Kenward-Roger approximation; computing time: 0.28 sec.
## large : diffFERT ~ rescale(diffVAPof) + rescale(diffHmales) + (1 |
female) +
##     (1 | maleA) + (1 | maleB)
## small : diffFERT ~ rescale(diffVAPof) + (1 | female) + (1 | maleA)
+
##     (1 | maleB)
##          stat     ndf     ddf F.scaling p.value
## Ftest  0.1861  1.0000 10.1102         1  0.6752

# mod100 without scaling VAP so that effects of actual difference in V
AP can be evaluated
mod101 <- lmer(diffFERT~diffVAPof+ rescale(diffHmales) +(1|female)+(1|
maleA)+(1|maleB), data=Trials100)
summary(mod101)

## Linear mixed model fit by REML ['lmerMod']
## Formula: diffFERT ~ diffVAPof + rescale(diffHmales) + (1 | female)
+ (1 |
##     maleA) + (1 | maleB)
##    Data: Trials100
##
## REML criterion at convergence: 407.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.87544 -0.81247 -0.00349  0.72061  1.65645
```

```
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  maleB    (Intercept) 48.288   6.949
##  maleA    (Intercept)  3.508   1.873
##  female   (Intercept)  0.000   0.000
##  Residual             80.111   8.950
## Number of obs: 55, groups:  maleB, 12; maleA, 12; female, 6
##
## Fixed effects:
##                      Estimate Std. Error t value
## (Intercept)         19.33132    2.64857   7.299
## diffVAPof            0.15899    0.05028   3.162
## rescale(diffHmales)  1.91628    3.77984   0.507
##
## Correlation of Fixed Effects:
##             (Intr) dffVAP
## diffVAPof   -0.353
## rscl(dffHm) -0.082  0.161
```

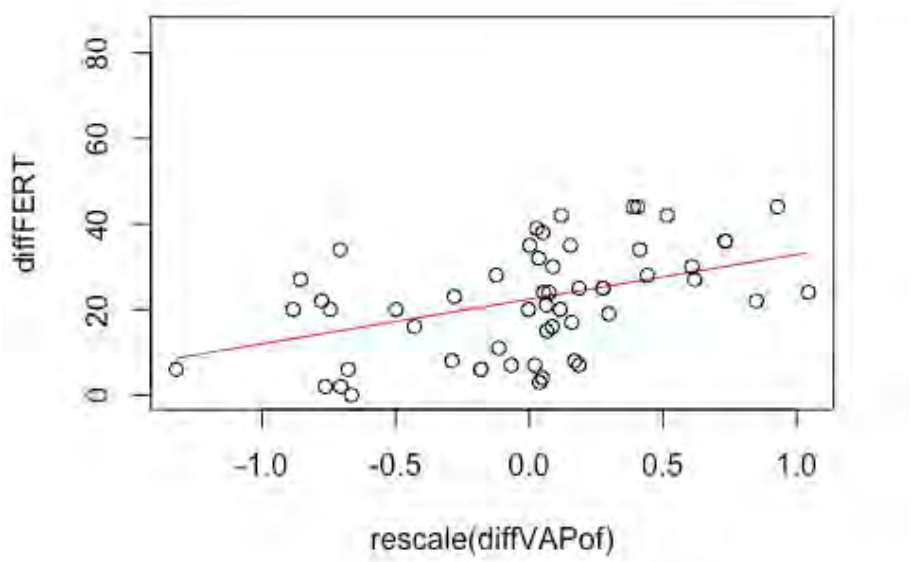
```
confint(mod101, method ="Wald")
```

```
##                             2.5 %     97.5 %
## .sig01                         NA         NA
## .sig02                         NA         NA
## .sig03                         NA         NA
## .sigma                         NA         NA
## (Intercept)         14.14022347 24.5224094
## diffVAPof            0.06043155  0.2575412
## rescale(diffHmales) -5.49207272  9.3246305
```

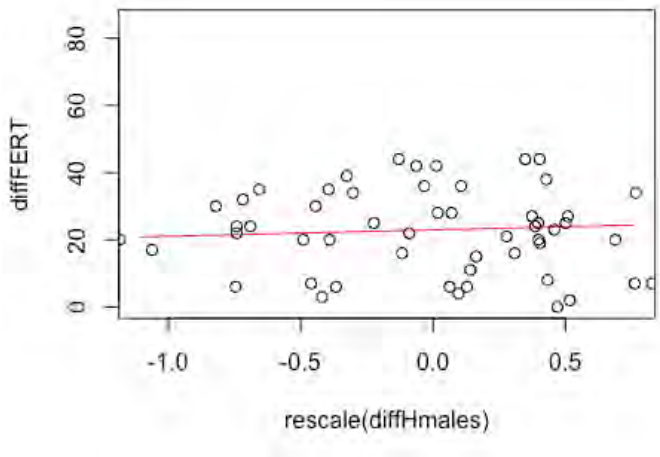
```
#plot effects for ESM fig S2c,d
with(Trials100, plot(diffFERT~rescale(diffVAPof))) #plot to determine
ylimit for plotLMER.fnc
```




```
plotLMER.fnc(mod100, ylimit=c(0,85), pred = "rescale(diffVAPof)",linec
olor = 2) #plot model effect for VAP diff

## effect size (range) for  rescale(diffVAPof) is  24.67469

with(Trials100, points(diffFERT~jitter(rescale(diffVAPof),2))) #add da
ta points to that graph
```




```
plotLMER.fnc(mod100, ylimit=c(0,85), pred = "rescale(diffHmales)",line
color = 2) #plot model effect for MLH diff

## effect size (range) for  rescale(diffHmales) is  3.594385

with(Trials100, points(diffFERT~jitter(rescale(diffHmales),2))) #add d
ata points to that graph
```




```
#partial regression plot for trials at 100% OF; no random effects in m
odel
resY100 <- residuals(lm(diffFERT~ rescale(diffHmales), data=Trials100)
```

```
)
resX100 <- residuals(lm(rescale(diffVAPof)~ rescale(diffHmales), data=
Trials100))

mod100c=lm(resY100~resX100)
summary(mod100c) #estimate for slope very similar to mod100

##
## Call:
## lm(formula = resY100 ~ resX100)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.3531  -9.9299   0.4327   8.3317  20.7456
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 5.411e-17  1.494e+00   0.000 1.000000
## resX100     1.239e+01  3.126e+00   3.962 0.000223 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.08 on 53 degrees of freedom
## Multiple R-squared:  0.2285, Adjusted R-squared:  0.2139
## F-statistic:  15.7 on 1 and 53 DF,  p-value: 0.0002234

write.csv(cbind(resY100, resX100), file="plot100.csv") #save partial r
egression data for plotting
```

4.1.3 Relation between VAP and relatedness

Is the VAP of sperm in ovarian fluid influenced by the genetic relatedness between that male and female?

```
#relatedness between winner male and the female
mod10 <- lmer(VAPmaleAof~ Atrioml+ (1|female) + (1|maleA) + (1|maleB),
data=Trials)
summary(mod10)

## Linear mixed model fit by REML ['lmerMod']
## Formula: VAPmaleAof ~ Atrioml + (1 | female) + (1 | maleA) + (1 | m
aleB)
##    Data: Trials
##
## REML criterion at convergence: 692.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -2.6630 -0.2881  0.0075  0.2869  3.5182
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  maleA    (Intercept) 175.68   13.254
##  maleB    (Intercept)  10.20    3.194
##  female   (Intercept) 325.48   18.041
##  Residual              54.57    7.387
## Number of obs: 90, groups:  maleA, 23; maleB, 22; female, 10
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)   79.506      6.578  12.086
## Atrioml      -11.601     25.812  -0.449
##
## Correlation of Fixed Effects:
##         (Intr)
## Atrioml -0.145
```

```
confint(mod10, method = "Wald")
```

```
##                 2.5 %   97.5 %
## .sig01             NA       NA
## .sig02             NA       NA
## .sig03             NA       NA
## .sigma             NA       NA
## (Intercept)  66.61321 92.39967
## Atrioml     -62.19239 38.99008
```

```
mod10a <- lmer(VAPmaleAof~ (1|female) + (1|maleA) + (1|maleB), data=Tr
ials)
KRmodcomp(mod10,mod10a) #compare models with and without relatedness
```

```
## F-test with Kenward-Roger approximation; computing time: 0.22 sec.
## large : VAPmaleAof ~ Atrioml + (1 | female) + (1 | maleA) + (1 | ma
leB)
## small : VAPmaleAof ~ (1 | female) + (1 | maleA) + (1 | maleB)
##          stat     ndf     ddf F.scaling p.value
## Ftest  0.1918  1.0000 70.8497         1  0.6628
```

```
#relatedness between loser male and the female
mod11 <- lmer(VAPmaleBof~ Btrioml+ (1|female) + (1|maleA) + (1|maleB),
data=Trials)
summary(mod11)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: VAPmaleBof ~ Btrioml + (1 | female) + (1 | maleA) + (1 | m
```

```
aleB)
##    Data: Trials
##
## REML criterion at convergence: 719
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.16429 -0.41462 -0.00371  0.28770  3.15067
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  maleA    (Intercept)  48.19    6.942
##  maleB    (Intercept) 171.85   13.109
##  female   (Intercept) 206.83   14.382
##  Residual              74.80    8.648
## Number of obs: 90, groups:  maleA, 23; maleB, 22; female, 10
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)   65.113      5.707  11.409
## Btrioml       28.118     32.659   0.861
##
## Correlation of Fixed Effects:
##         (Intr)
## Btrioml -0.076
```

```
confint(mod11, method = "Wald")
```

```
##                 2.5 %   97.5 %
## .sig01             NA       NA
## .sig02             NA       NA
## .sig03             NA       NA
## .sigma             NA       NA
## (Intercept)  53.92692 76.29809
## Btrioml     -35.89272 92.12861
```

```
mod11a <- lmer(VAPmaleBof~ (1|female) + (1|maleA) + (1|maleB), data=Tr
ials)
KRmodcomp(mod11,mod11a) #compare models with and without relatedness
```

```
## F-test with Kenward-Roger approximation; computing time: 0.28 sec.
## large : VAPmaleBof ~ Btrioml + (1 | female) + (1 | maleA) + (1 | ma
leB)
## small : VAPmaleBof ~ (1 | female) + (1 | maleA) + (1 | maleB)
##          stat     ndf     ddf F.scaling p.value
## Ftest  0.7121  1.0000 65.4372         1  0.4018
```

SUMMARY: no significant relationships here

SA4.2 Effects of VAP measured in water

This is the same model structure as in mod2 (above), except that VAP was measured in raceway water rather than ovarian fluid. Results from the analysis of mod12b are in Table S4 and the comparison of mod12 and mod12a (with and without VAP) are presented in the text.

```
mod12 <- lmer(diffFERT~ rescale(diffVAPwater) + rescale(diffHmales) +
as.factor(ofcon) + (1|female) + (1|maleA) + (1|maleB), data=Trials)
summary(mod12)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## diffFERT ~ rescale(diffVAPwater) + rescale(diffHmales) + as.factor(
ofcon) +
##     (1 | female) + (1 | maleA) + (1 | maleB)
##    Data: Trials
##
## REML criterion at convergence: 713.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.08469 -0.64125  0.00072  0.63781  2.69722
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  maleA    (Intercept)   2.559   1.600
##  maleB    (Intercept) 118.002  10.863
##  female   (Intercept)  26.909   5.187
##  Residual             133.856  11.570
## Number of obs: 90, groups:  maleA, 23; maleB, 22; female, 10
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)             27.225      4.933   5.519
## rescale(diffVAPwater)   -0.496      3.567  -0.139
## rescale(diffHmales)      6.547      4.103   1.596
## as.factor(ofcon)100     -4.475      6.583  -0.680
##
## Correlation of Fixed Effects:
##             (Intr) r(VAP) rsc(H)
## rscl(dfVAP)  0.117
## rscl(dffHm) -0.135 -0.262
## as.fct()100 -0.764 -0.178  0.163
```

```
confint(mod12, method = "Wald")
```

```
##                              2.5 %    97.5 %
## .sig01                          NA        NA
## .sig02                          NA        NA
## .sig03                          NA        NA
## .sigma                          NA        NA
## (Intercept)             17.556030 36.894269
## rescale(diffVAPwater)   -7.487016  6.495086
## rescale(diffHmales)     -1.493760 14.588489
## as.factor(ofcon)100    -17.377061  8.426565
```

```
mod12a <- lmer(diffFERT~ rescale(diffHmales) + as.factor(ofcon) + (1|female) + (1|maleA) + (1|maleB), data=Trials)
KRmodcomp(mod12,mod12a) #VAPwater is NS
```

```
## F-test with Kenward-Roger approximation; computing time: 0.33 sec.
## large : diffFERT ~ rescale(diffVAPwater) + rescale(diffHmales) + as.factor(ofcon) +
##     (1 | female) + (1 | maleA) + (1 | maleB)
## small : diffFERT ~ rescale(diffHmales) + as.factor(ofcon) + (1 | female) +
##     (1 | maleA) + (1 | maleB)
##         stat    ndf    ddf F.scaling p.value
## Ftest  0.017  1.000 75.701         1  0.8965
```

```
mod12b <- lmer(diffFERT~ rescale(diffVAPwater) + rescale(diffHmales) + as.factor(ofcon) + (1|female) + (1|maleA) + (1|maleB), REML=FALSE, data=Trials)
dredge(mod12b)
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: lmer(formula = diffFERT ~ rescale(diffVAPwater) + rescale(diffHmales) +
##     as.factor(ofcon) + (1 | female) + (1 | maleA) + (1 | maleB),
##     data = Trials, REML = FALSE)
## ---
## Model selection table
##   (Int) as.fct(ofc) rsc(dfH) rsc(dVA) df   logLik  AICc delta weight
## 3 24.61                6.935          6 -366.042 745.1  0.00  0.285
## 1 24.50                               5 -367.358 745.4  0.34  0.241
## 4 27.22           +    6.620          7 -365.707 746.8  1.69  0.123
```

```
## 2 27.55           +                   6 -366.985 747.0  1.89  0.11
1
## 7 24.63                7.080  -0.6092  7 -366.026 747.4  2.32  0.08
9
## 5 24.49                       0.3070  6 -367.354 747.7  2.62  0.07
7
## 8 27.24           +    6.578   0.1339  8 -365.707 749.2  4.10  0.03
7
## 6 27.72           +            1.1050  7 -366.938 749.2  4.15  0.03
6
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | female', '1 | maleA', '1 | maleB'
```

SUMMARY: no significant effect of VAP measured in water

SA5. Section 3(c) RESULTS: Embryo survival

This is the code for the embryo survival analyses in figures 2, S3, as well as tables 2, S5 and the main text, based on results from the noncompetitive fertilization trials

SA5.1 Embryo survival

Models to predict embryo survival from VAP on ovarian fluid, male-female relatedness (TrioML), and both male and female heterozygosities; table 2, figures 2 and S3

```
dispersion <- 1:length(Esurvival$ofcon) #disperion parameter for overd
ispersed models

#GLMM to predict embryo survival from VAP in ovarian fluid and related
ness; table 2
mod12 <- glmer(cbind(Elive, Edead) ~ rescale(VAPof) * rescale(TRIOML)
*rescale(Hmale) + as.factor(ofcon) + (1|female) + (1|male), family="bi
nomial", data=Esurvival) #model failed to converge

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.00402705
(tol =
## 0.001, component 1)

relgrad <- with(mod12@optinfo$derivs,solve(Hessian,gradient)) #Bolker'
s method for checking convergence, see https://github.com/lme4/lme4/is
sues/120
max(abs(relgrad)) #is <0.001 so failure to converge not be a problem

## [1] 0.000657789
```

```
overdisp.glmer(mod12) #calculates overdispersion as 7.29 which is high
and should be corrected

## Residual deviance: 344.928 on 48 degrees of freedom (ratio: 7.186)

mod12a <- glmer(cbind(Elive, Edead) ~ rescale(VAPof) * rescale(TRIOML)
*rescale(Hmale) +as.factor(ofcon) +(1|female) +(1|male) +(1|dispersion
), family="binomial", data=Esurvival) #same as mod12 but corrected for
overdispersion; as with mod12, this also failed to converge

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.00945297
(tol =
## 0.001, component 1)

relgrad <- with(mod12a@optinfo$derivs,solve(Hessian,gradient)) #Bolker
's method for checking convergence, see https://github.com/lme4/lme4/i
ssues/120
max(abs(relgrad)) #value is >0.0001 so failure to converge may be a pr
oblem

## [1] 0.003984148

overdisp.glmer(mod12a) #model is now underdispersed

## Residual deviance: 5.979 on 47 degrees of freedom (ratio: 0.127)

#failure to converge might be due to overparameterization, reduce numb
er of interaction terms
mod12b <- glmer(cbind(Elive, Edead) ~ rescale(VAPof) * rescale(TRIOML)
+ rescale(Hmale) +as.factor(ofcon) +(1|female) +(1|male) +(1|dispersio
n), family="binomial", data=Esurvival) #remove interactions with male
heterozygosity; still fails to converge

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.00134294
(tol =
## 0.001, component 1)

mod12c <- glmer(cbind(Elive, Edead) ~ rescale(VAPof) + rescale(TRIOML)
* rescale(Hmale) +as.factor(ofcon) +(1|female) +(1|male) +(1|dispersio
n), family="binomial", data=Esurvival) #remove interactions with VAP;
model converges OK
dredge(mod12c) #still some failure to converge

## Fixed term is "(Intercept)"

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.00229869
```

```
(tol =
## 0.001, component 1)

## Global model call: glmer(formula = cbind(Elive, Edead) ~ rescale(VA
Pof) + rescale(TRIOML) *
##     rescale(Hmale) + as.factor(ofcon) + (1 | female) + (1 | male) +
##     (1 | dispersion), data = Esurvival, family = "binomial")
## ---
## Model selection table
##      (Int) as.fct(ofc) rsc(Hml) rsc(TRI) rsc(VAP) rsc(Hml):rsc(TRI)
df
## 12 -0.5178           +   0.8848             1.593
7
## 10 -0.4786           +                      1.597
6
## 16 -0.5149           +   0.8849  0.13280    1.603
8
## 32 -0.4838           +   0.9226  0.05822    1.594            -1.026
9
## 14 -0.4758           +           0.12890    1.606
7
## 11  0.4732               0.8028             1.312
6
## 4  -0.2796           +   0.9977
6
## 31  0.4380               0.9185  0.14180    1.294            -1.269
8
## 9   0.4719                                  1.310
5
## 15  0.4742               0.8062  0.18880    1.322
7
## 2  -0.2260           +
5
## 8  -0.2904           +   1.0390  0.29450
7
## 24 -0.2699           +   1.1050  0.26220                     -1.102
8
## 3   0.4074               0.9343
5
## 13  0.4728                       0.17620    1.320
6
## 1   0.4056
4
## 23  0.3800               1.0460  0.30990                     -1.222
7
## 6  -0.2372           +           0.28350
```

```
6
## 7   0.3857               0.9842  0.38820
6
## 5   0.3819                       0.39120
5
##      logLik  AICc delta weight
## 12 -263.865 543.9  0.00  0.472
## 10 -266.230 546.1  2.15  0.161
## 16 -263.813 546.5  2.58  0.130
## 32 -262.627 546.9  3.00  0.105
## 14 -266.184 548.6  4.64  0.046
## 11 -268.387 550.4  6.46  0.019
## 4  -268.767 551.1  7.22  0.013
## 31 -266.422 551.7  7.80  0.010
## 9  -270.297 551.7  7.80  0.010
## 15 -268.284 552.8  8.84  0.006
## 2  -270.900 552.9  9.01  0.005
## 8  -268.588 553.4  9.45  0.004
## 24 -267.294 553.5  9.54  0.004
## 3  -271.269 553.7  9.74  0.004
## 13 -270.214 554.0 10.12  0.003
## 1  -273.027 554.8 10.87  0.002
## 23 -269.316 554.8 10.90  0.002
## 6  -270.756 555.1 11.20  0.002
## 7  -270.937 555.5 11.56  0.001
## 5  -272.716 556.6 12.64  0.001
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | female', '1 | male', '1 | dispersion'

overdisp.glmer(mod12c)

## Residual deviance: 5.983 on 50 degrees of freedom (ratio: 0.12)

#remove all interaction terms to reduce overparameterization
mod12d <- glmer(cbind(Elive, Edead) ~ rescale(VAPof) + rescale(TRIOML)
+ rescale(Hmale) +as.factor(ofcon) +(1|female) +(1|male) +(1|dispersio
n), family="binomial", data=Esurvival)#no failure to converge
dredge(mod12d) #still some failure to converge in some model(s)

## Fixed term is "(Intercept)"

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge with max|grad| = 0.00229869
(tol =
## 0.001, component 1)
```

```
## Global model call: glmer(formula = cbind(Elive, Edead) ~ rescale(VA
Pof) + rescale(TRIOML) +
##     rescale(Hmale) + as.factor(ofcon) + (1 | female) + (1 | male) +
##     (1 | dispersion), data = Esurvival, family = "binomial")
## ---
## Model selection table
##      (Int) as.fct(ofc) rsc(Hml) rsc(TRI) rsc(VAP) df   logLik  AICc
delta
## 12 -0.5178           +   0.8848            1.593  7 -263.865 543.9
0.00
## 10 -0.4786           +                    1.597  6 -266.230 546.1
2.15
## 16 -0.5149           +   0.8849   0.1328   1.603  8 -263.813 546.5
2.58
## 14 -0.4758           +           0.1289   1.606  7 -266.184 548.6
4.64
## 11  0.4732               0.8028           1.312  6 -268.387 550.4
6.46
## 4  -0.2796           +   0.9977                   6 -268.767 551.1
7.22
## 9   0.4719                                1.310  5 -270.297 551.7
7.80
## 15  0.4742               0.8062   0.1888   1.322  7 -268.284 552.8
8.84
## 2  -0.2260           +                          5 -270.900 552.9
9.01
## 8  -0.2904           +   1.0390   0.2945          7 -268.588 553.4
9.45
## 3   0.4074               0.9343                  5 -271.269 553.7
9.74
## 13  0.4728                       0.1762   1.320  6 -270.214 554.0
10.12
## 1   0.4056                                       4 -273.027 554.8
10.87
## 6  -0.2372           +           0.2835          6 -270.756 555.1
11.20
## 7   0.3857               0.9842   0.3882          6 -270.937 555.5
11.56
## 5   0.3819                       0.3912          5 -272.716 556.6
12.64
##    weight
## 12  0.537
## 10  0.183
## 16  0.148
## 14  0.053
## 11  0.021
```

```
## 4   0.015
## 9   0.011
## 15  0.006
## 2   0.006
## 8   0.005
## 3   0.004
## 13  0.003
## 1   0.002
## 6   0.002
## 7   0.002
## 5   0.001
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | female', '1 | male', '1 | dispersion'
```

```
overdisp.glmer(mod12d) #undispersed
```

```
## Residual deviance: 5.906 on 51 degrees of freedom (ratio: 0.116)
```

```
mod12e <- glmer(cbind(Elive, Edead) ~ rescale(VAPof) + rescale(Hmale)
+as.factor(ofcon) +(1|female) +(1|male) +(1|dispersion), family="binom
ial", data=Esurvival) #remove TRIOML from mod12d as it was not in any
of the top models (AICc<2) evaluated using the information-theoretic a
pproach
dredge(mod12e) #no failures to converge here
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: glmer(formula = cbind(Elive, Edead) ~ rescale(VA
Pof) + rescale(Hmale) +
##     as.factor(ofcon) + (1 | female) + (1 | male) + (1 | dispersion)
,
##     data = Esurvival, family = "binomial")
## ---
## Model selection table
##     (Int) as.fct(ofc) rsc(Hml) rsc(VAP) df   logLik  AICc delta wei
ght
## 8 -0.5178           +   0.8848    1.593  7 -263.865 543.9  0.00  0.
689
## 6 -0.4786           +             1.597  6 -266.230 546.1  2.15  0.
235
## 7  0.4732               0.8028    1.312  6 -268.387 550.4  6.46  0.
027
## 4 -0.2796           +   0.9977           6 -268.767 551.1  7.22  0.
019
## 5  0.4719                         1.310  5 -270.297 551.7  7.80  0.
014
```

```
## 2 -0.2260           +                    5 -270.900 552.9  9.01  0.
008
## 3  0.4074               0.9343           5 -271.269 553.7  9.74  0.
005
## 1  0.4056                                4 -273.027 554.8 10.87  0.
003
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | female', '1 | male', '1 | dispersion'
```

```
overdisp.glmer(mod12e) #underdispersed
```

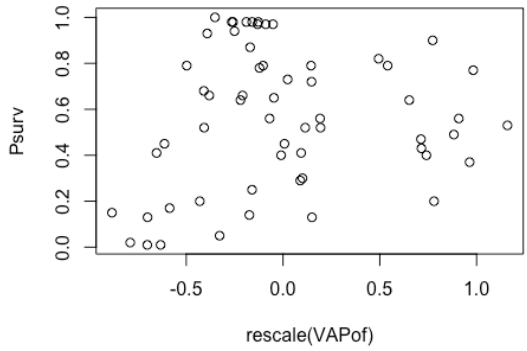
```
## Residual deviance: 5.934 on 52 degrees of freedom (ratio: 0.114)
```

```
summary(mod12e)
```

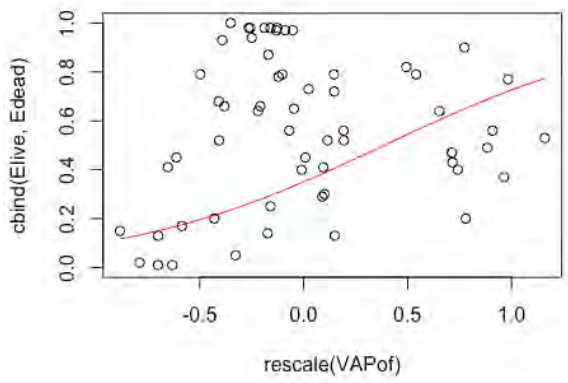
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## cbind(Elive, Edead) ~ rescale(VAPof) + rescale(Hmale) + as.factor(o
fcon) +
##     (1 | female) + (1 | male) + (1 | dispersion)
##    Data: Esurvival
##
##      AIC      BIC   logLik deviance df.resid
##    541.7    556.3   -263.9    527.7       52
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.88656 -0.07781  0.01054  0.13023  0.95325
##
## Random effects:
##  Groups     Name        Variance  Std.Dev.
##  dispersion (Intercept) 2.099e+00 1.4488631
##  male       (Intercept) 2.870e-08 0.0001694
##  female     (Intercept) 5.607e-01 0.7487868
## Number of obs: 59, groups:  dispersion, 59; male, 28; female, 10
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -0.5178     0.4014  -1.290 0.197071
## rescale(VAPof)        1.5931     0.4742   3.359 0.000781 ***
## rescale(Hmale)        0.8848     0.4011   2.206 0.027382 *
## as.factor(ofcon)100   2.5017     0.6686   3.742 0.000183 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation of Fixed Effects:
##             (Intr) r(VAP) rsc(H)
## rescl(VAPf) -0.218
## rescal(Hml) -0.046  0.003
## as.fct()100 -0.647  0.334  0.073
```

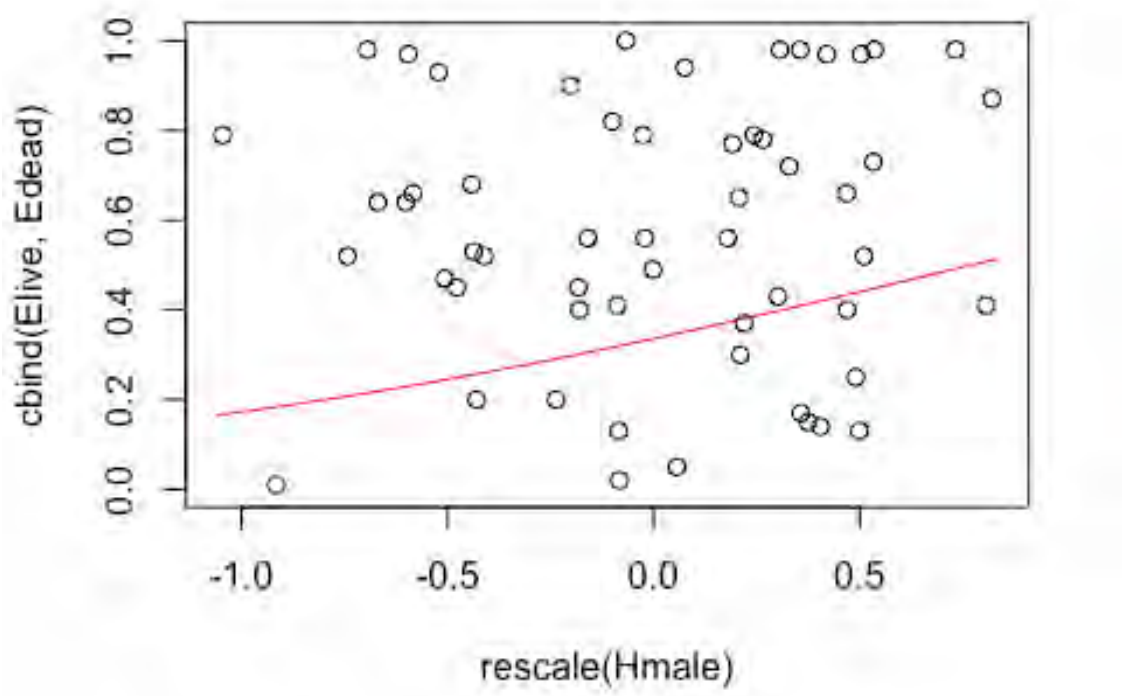
```
#plot effects for fig S3
with(Esurvival, plot(Psurv~rescale(VAPof))) #plot to determine ylimit
for plotLMER.fnc
```




```
plotLMER.fnc(mod12e, ylimit=c(0,1), pred = "rescale(VAPof)",linecolor
= 2) #plot model effect for VAP diff

## log odds are back-transformed to probabilities
## effect size (range) for  rescale(VAPof) is  0.6572549

with(Esurvival, points(Psurv~jitter(rescale(VAPof),2))) #add data poin
ts to that graph
```



```
plotLMER.fnc(mod12e, ylimit=c(0,1), pred = "rescale(Hmale)",linecolor
= 2) #plot model effect for MLH diff

## log odds are back-transformed to probabilities
## effect size (range) for  rescale(Hmale) is  0.3488066

with(Esurvival, points(Psurv~jitter(rescale(Hmale),2))) #add data poin
ts to that graph
```




```
#MCMC-GLMM embryo survival vs VAP in ovarian fluid and TRIOML using sa
me model structure as best-fitting model (mod12e) above; results shown
in table S5
prior2 <- list(R=list(V=1,nu=1),G=list(G1=list(V=1,nu=1),G2=list(V=1,n
u=1)))
mod13 <- MCMCglmm(cbind(Elive,Edead)~rescale(VAPof) + rescale(Hmale) +
as.factor(ofcon), random=~male+female, family="multinomial2", prior=pr
ior2, nitt=800000,thin=100,burnin=100000, verbose = FALSE, data=Esurvi
val)
summary(mod13)

##
##  Iterations = 100001:799901
```

```
##  Thinning interval  = 100
##  Sample size  = 7000
##
##  DIC: 6510.521
##
##  G-structure:  ~male
##
##      post.mean l-95% CI u-95% CI eff.samp
## male    0.5864  0.08182    1.394     6238
##
##                ~female
##
##        post.mean l-95% CI u-95% CI eff.samp
## female     1.076   0.1016    2.657     7000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.999     1.05     3.09     7896
##
##  Location effects: cbind(Elive, Edead) ~ rescale(VAPof) + rescale(H
male) + as.factor(ofcon)
##
##                     post.mean l-95% CI u-95% CI eff.samp   pMCMC
## (Intercept)          -0.53495 -1.57765  0.54182     7091 0.29543
## rescale(VAPof)        1.43738  0.38159  2.42067     7000 0.00771 **
## rescale(Hmale)        0.99562  0.02605  1.99079     7000 0.04657 *
## as.factor(ofcon)100   2.37921  0.61130  4.03663     7000 0.01143 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod12f <- glmer(cbind(Elive, Edead) ~  rescale(Hmale) +as.factor(ofcon
) +(1|female) +(1|male) +(1|dispersion), family="binomial", data=Esurv
ival)
anova(mod12e,mod12f) #LLRTest for VAP
```

```
## Data: Esurvival
## Models:
## mod12f: cbind(Elive, Edead) ~ rescale(Hmale) + as.factor(ofcon) + (
1 |
## mod12f:     female) + (1 | male) + (1 | dispersion)
## mod12e: cbind(Elive, Edead) ~ rescale(VAPof) + rescale(Hmale) + as.
factor(ofcon) +
## mod12e:     (1 | female) + (1 | male) + (1 | dispersion)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mod12f  6 549.53 562.00 -268.77   537.53
```

```
## mod12e  7 541.73 556.27 -263.87   527.73 9.8031      1   0.001742 *
*
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod12g <- glmer(cbind(Elive, Edead) ~ rescale(VAPof) +as.factor(ofcon)
+(1|female) +(1|male) +(1|dispersion), family="binomial", data=Esurviv
al)
anova(mod12e,mod12g) #LLRTest for Hmale
```

```
## Data: Esurvival
## Models:
## mod12g: cbind(Elive, Edead) ~ rescale(VAPof) + as.factor(ofcon) + (
1 |
## mod12g:     female) + (1 | male) + (1 | dispersion)
## mod12e: cbind(Elive, Edead) ~ rescale(VAPof) + rescale(Hmale) + as.
factor(ofcon) +
## mod12e:     (1 | female) + (1 | male) + (1 | dispersion)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mod12g  6 544.46 556.93 -266.23   532.46
## mod12e  7 541.73 556.27 -263.87   527.73 4.7301      1    0.02964 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

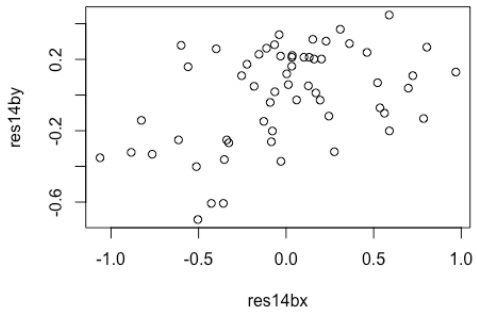
```
mod12h <- glmer(cbind(Elive, Edead) ~ rescale(VAPof) + rescale(Hmale)
+(1|female) +(1|male) +(1|dispersion), family="binomial", data=Esurviv
al)
anova(mod12e,mod12h) #LLRTest for ofcon
```

```
## Data: Esurvival
## Models:
## mod12h: cbind(Elive, Edead) ~ rescale(VAPof) + rescale(Hmale) + (1
|
## mod12h:     female) + (1 | male) + (1 | dispersion)
## mod12e: cbind(Elive, Edead) ~ rescale(VAPof) + rescale(Hmale) + as.
factor(ofcon) +
## mod12e:     (1 | female) + (1 | male) + (1 | dispersion)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mod12h  6 548.77 561.24 -268.39   536.77
## mod12e  7 541.73 556.27 -263.87   527.73 9.0434      1   0.002636 *
*
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

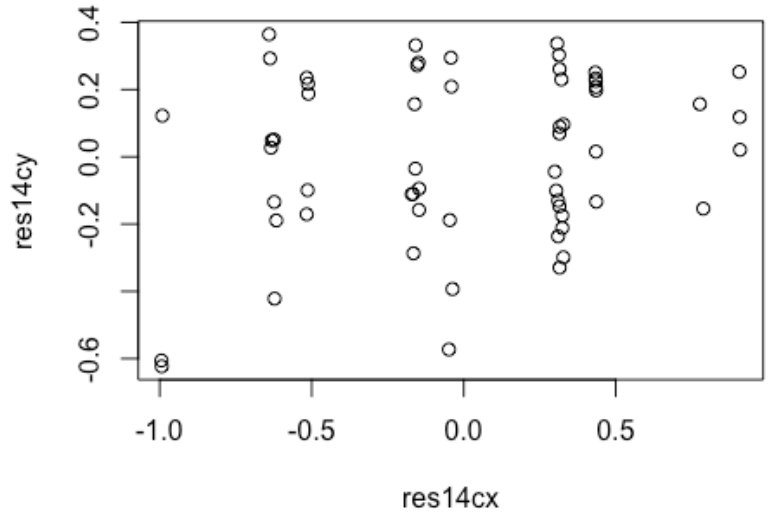
SA5.1.1 Figure 2

```
#Fig 2a proportion of embryos surviving vs VAP in female's ovarian flu
id; no random effects in model
```

```
mod14b <- lm(Psurv ~ rescale(VAPof) + rescale(Hmale) +as.factor(ofcon)
, data=Esurvival)

res14by <- resid(lm(Psurv ~ rescale(Hmale) +as.factor(ofcon), data=Esu
rvival))
res14bx <- resid(lm(rescale(VAPof) ~ rescale(Hmale)+as.factor(ofcon),
data=Esurvival))
plot(res14by~res14bx)
```




```
#fig 2b proportion surviving vs male heterozygosity: no random effects
in model
res14cy <- resid(lm(Psurv ~ rescale(VAPof) +as.factor(ofcon), data=Esu
rvival))
res14cx <- resid(lm(rescale(Hmale) ~ rescale(VAPof) +as.factor(ofcon),
data=Esurvival))
plot(res14cy~res14cx)
```



```
PSURV <- Esurvival$Psurv
OFcon <- Esurvival$ofcon
write.csv(cbind(OFcon, PSURV, res14bx, res14by, res14cx,res14cy),row.n
ames=FALSE, file="F2data.csv")
```

SA6. Electronic supplementary material: Additional information

SA6.1 Table S4

```
#model structure same as in mod2 except with VAP in water instead of o
varian fluid
mod15 <- glmer(cbind(Elive, Edead) ~ rescale(VAPwater) + rescale(Hfema
le) +rescale(Hmale) +as.factor(ofcon) +(1|female) +(1|male), family="b
inomial", data=Esurvival)
summary(mod15)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(Elive, Edead) ~ rescale(VAPwater) + rescale(Hfemale)
+
##     rescale(Hmale) + as.factor(ofcon) + (1 | female) + (1 | male)
##    Data: Esurvival
##
##      AIC      BIC   logLik deviance df.resid
##    866.0    880.6   -426.0    852.0       52
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -14.7448  -1.6369  -0.0296   1.5364   7.3550
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  male   (Intercept) 4.035    2.009
##  female (Intercept) 2.023    1.422
## Number of obs: 59, groups:  male, 28; female, 10
##
## Fixed effects:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -0.59480    0.85916  -0.692    0.489
## rescale(VAPwater)    0.58039    0.09536   6.086 1.15e-09 ***
## rescale(Hfemale)     0.36945    1.28791   0.287    0.774
## rescale(Hmale)       1.17347    0.73299   1.601    0.109
## as.factor(ofcon)100  2.17308    1.50855   1.441    0.150
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Correlation of Fixed Effects:
##             (Intr) r(VAP) rscl(Hf) rscl(Hm)
## rscl(VAPwt) -0.023
## rescl(Hfml) -0.417  0.002
## rescal(Hml) -0.039 -0.008  0.000
## as.fct()100 -0.724  0.036  0.604    0.057
```

```
confint(mod15, method="Wald")
```

```
##                            2.5 %    97.5 %
## .sig01                        NA        NA
## .sig02                        NA        NA
## (Intercept)         -2.2787191 1.0891154
## rescale(VAPwater)    0.3934943 0.7672886
## rescale(Hfemale)    -2.1548051 2.8937061
## rescale(Hmale)      -0.2631602 2.6101053
## as.factor(ofcon)100 -0.7836197 5.1297820
```

```
overdisp.glmer(mod15)  #calculates overdispersion as 7.5 which is seri
ously overdispersed
```

```
## Residual deviance: 386.684 on 52 degrees of freedom (ratio: 7.436)
```

```
mod15a <- glmer(cbind(Elive, Edead) ~ rescale(VAPwater) + rescale(Hfem
ale) +rescale(Hmale) +as.factor(ofcon) +(1|female) +(1|male) +(1|dispe
rsion), family="binomial", data=Esurvival) #same as mod15 but correcte
d for overdispersion
summary(mod15a)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(Elive, Edead) ~ rescale(VAPwater) + rescale(Hfemale)
+
##     rescale(Hmale) + as.factor(ofcon) + (1 | female) + (1 | male) +
##     (1 | dispersion)
##    Data: Esurvival
##
##      AIC      BIC   logLik deviance df.resid
##    549.4    566.0   -266.7    533.4       51
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.96387 -0.04696  0.02773  0.09480  0.93063
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
```

```
##  dispersion (Intercept) 2.3749   1.5411
##  male       (Intercept) 0.1144   0.3383
##  female     (Intercept) 0.3104   0.5571
## Number of obs: 59, groups:  dispersion, 59; male, 28; female, 10
##
## Fixed effects:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -0.8520     0.4497  -1.894 0.058161 .
## rescale(VAPwater)     0.6476     0.5774   1.122 0.262042
## rescale(Hfemale)      1.6572     0.8129   2.038 0.041504 *
## rescale(Hmale)        0.8814     0.4770   1.848 0.064645 .
## as.factor(ofcon)100   3.3294     0.9356   3.558 0.000373 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) r(VAP) rscl(Hf) rscl(Hm)
## rscl(VAPwt) -0.355
## rescl(Hfml) -0.530  0.225
## rescal(Hml)  0.009 -0.254 -0.065
## as.fct()100 -0.766  0.494  0.709   -0.075
```

```
confint(mod15a, method="Wald")
```

```
##                            2.5 %    97.5 %
## .sig01                        NA        NA
## .sig02                        NA        NA
## .sig03                        NA        NA
## (Intercept)         -1.73344933 0.0294471
## rescale(VAPwater)   -0.48410257 1.7793524
## rescale(Hfemale)     0.06380904 3.2505059
## rescale(Hmale)      -0.05355168 1.8164005
## as.factor(ofcon)100  1.49553439 5.1631886
```

```
overdisp.glmer(mod15a)  #calculates overdispersion as 0.1 which is und
erdispersed
```

```
## Residual deviance: 5.722 on 51 degrees of freedom (ratio: 0.112)
```

```
mod15b <- MCMCglmm(cbind(Elive,Edead)~ rescale(VAPwater) +rescale(Hmal
e)+rescale(Hfemale) +as.factor(ofcon), random=~male+female, family="mu
ltinomial2", prior=prior2, nitt=800000,thin=100,burnin=100000, verbose
= FALSE, data=Esurvival) #same as mod15 but evaluated using MCMCglmm
summary(mod15b)
```

```
##
##  Iterations = 100001:799901
```

```
##  Thinning interval  = 100
##  Sample size  = 7000
##
##  DIC: 6510.68
##
##  G-structure:  ~male
##
##      post.mean l-95% CI u-95% CI eff.samp
## male    0.7179  0.08201     1.72     7000
##
##                ~female
##
##        post.mean l-95% CI u-95% CI eff.samp
## female     1.056  0.08244     2.72     7000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     2.236    1.167    3.504     7000
##
##  Location effects: cbind(Elive, Edead) ~ rescale(VAPwater) + rescal
e(Hmale) + rescale(Hfemale) + as.factor(ofcon)
##
##                     post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)           -0.8306  -2.1237   0.4081     7250 0.1851
## rescale(VAPwater)      0.5673  -0.5485   1.7236     7252 0.3257
## rescale(Hmale)         0.9723  -0.1257   1.9576     6260 0.0649 .
## rescale(Hfemale)       1.4607  -0.7523   3.7425     7322 0.1791
## as.factor(ofcon)100    3.1284   0.7490   5.6545     7000 0.0186 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod15c <- MCMCglmm(cbind(Elive,Edead)~ rescale(VAPwater) +rescale(Hmal
e) +as.factor(ofcon), random=~male+female, family="multinomial2", prio
r=prior2, nitt=800000,thin=100,burnin=100000, verbose = FALSE, data=Es
urvival) #same as mod15b but not including Hfemale as a predictor
summary(mod15c)
```

```
##
##  Iterations = 100001:799901
##  Thinning interval  = 100
##  Sample size  = 7000
##
##  DIC: 6510.633
##
##  G-structure:  ~male
```

```
##
##      post.mean l-95% CI u-95% CI eff.samp
## male    0.7972  0.09609    1.893     6762
##
##                ~female
##
##        post.mean l-95% CI u-95% CI eff.samp
## female     1.146   0.0936    2.831     6644
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     2.203    1.078    3.455     7000
##
##  Location effects: cbind(Elive, Edead) ~ rescale(VAPwater) + rescal
e(Hmale) + as.factor(ofcon)
##
##                     post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)          -0.40408 -1.53315  0.73870     6729 0.4511
## rescale(VAPwater)     0.46098 -0.60744  1.66604     7000 0.4137
## rescale(Hmale)        0.97858 -0.08928  2.02439     7000 0.0700 .
## as.factor(ofcon)100   2.00333  0.09159  3.78622     7000 0.0346 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```