

Additional file 3 Regression model selection results

Regression output from the function `summary.glm` in the statistical software package R

Legend

Fbin: matrix of 96 rows by 2 columns with the number of fed mosquitoes in the first column and the number of unfed mosquitoes in the second column.

Dbin: matrix of 96 rows by 2 columns with the number of dead mosquitoes in the first column and the number of live mosquitoes in the second column.

Verandabin: matrix of 96 rows by 2 columns with the number of mosquitoes collected in the veranda in the first column and the number of mosquitoes collected elsewhere in the second column.

Netbin: matrix of 96 rows by 2 columns with the number of mosquitoes collected under the net in the first column and the number of mosquitoes collected elsewhere in the second column.

Species: mosquito species in the categories 0 (*An. gambiae* KISUMU strain), 1 (*An. gambiae* collected in Akron), and 2 (*Cx. quinquefasciatus* collected in Cotonou).

Type: net type in the categories 0 (untreated net) and 1 (new PermaNet 2.0 LLIN).

Size: hole size in square cm in the categories 0, 3, 30 and 300.

logTHSp1: log of total holed surface area in cm² plus 1.

```
glm(formula = Fbin ~ Population + Type + Species:Type, family = binomial)
```

```
Deviance Residuals:
```

Min	1Q	Median	3Q	Max
-20.8075	-3.0898	0.1389	3.7178	8.9589

```
Coefficients:
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.43758	0.05364	-8.158	3.4e-16 ***
Species1	-0.27392	0.07710	-3.553	0.000381 ***
Species2	0.66044	0.07340	8.998	< 2e-16 ***
Type1	-2.36794	0.12450	-19.019	< 2e-16 ***
Species1:Type1	1.47324	0.14985	9.832	< 2e-16 ***
Species2:Type1	0.84869	0.14728	5.762	8.3e-09 ***

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for binomial family taken to be 1)
```

```
Null deviance: 3720.8 on 95 degrees of freedom
```

Residual deviance: 2435.3 on 90 degrees of freedom

AIC: 2823.8

Number of Fisher Scoring iterations: 5

```
glm(formula = Fbin ~ Species + logTHSp1 + Type + Species:Type +  
     Species:logTHSp1, family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-6.5595	-1.1565	-0.2264	0.8043	4.4321

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-2.90376	0.16397	-17.709	< 2e-16	***
Species1	-1.08711	0.23880	-4.552	5.3e-06	***
Species2	0.42576	0.20945	2.033	0.04208	*
logTHSp1	0.42187	0.02432	17.343	< 2e-16	***
Type1	-2.76852	0.13607	-20.346	< 2e-16	***
Species1:Type1	1.64802	0.16687	9.876	< 2e-16	***
Species2:Type1	0.66696	0.16816	3.966	7.3e-05	***
Species1:logTHSp1	0.10607	0.03397	3.122	0.00179	**
Species2:logTHSp1	0.07642	0.03200	2.388	0.01694	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 3720.78 on 95 degrees of freedom

Residual deviance: 266.99 on 87 degrees of freedom

AIC: 661.44

Number of Fisher Scoring iterations: 5

```
glm(formula = Fbin ~ Species + logTHSp1 + Type + Size + Species:Type +  
     Species:Size + logTHSp1:Size + Species:logTHSp1 + logTHSp1:Type +  
     Species:logTHSp1:Size, family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.04485	-0.51391	0.01078	0.47215	2.21306

Coefficients: (3 not defined because of singularities)

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-1.934e+00	1.921e-01	-10.068	< 2e-16	***
Species1	-2.648e+00	6.120e-01	-4.327	1.51e-05	***
Species2	-1.912e+01	1.333e+03	-0.014	0.988559	
logTHSp1	3.674e-01	9.643e-02	3.809	0.000139	***

Type1	-3.413e+00	2.943e-01	-11.596	< 2e-16	***
Size3	-9.076e-01	5.979e-01	-1.518	0.129027	
Size30	-2.898e+00	7.364e-01	-3.936	8.29e-05	***
Size300	-2.495e-01	8.637e-01	-0.289	0.772700	
Species1>Type1	1.790e+00	1.757e-01	10.187	< 2e-16	***
Species2>Type1	8.881e-01	1.773e-01	5.009	5.48e-07	***
Species1:Size3	-4.171e-02	1.065e+00	-0.039	0.968760	
Species2:Size3	1.806e+01	1.333e+03	0.014	0.989192	
Species1:Size30	2.054e+00	1.120e+00	1.833	0.066767	.
Species2:Size30	2.129e+01	1.333e+03	0.016	0.987259	
Species1:Size300	3.541e-01	1.232e+00	0.287	0.773828	
Species2:Size300	1.868e+01	1.333e+03	0.014	0.988823	
logTHSp1:Size3	-5.955e-03	1.576e-01	-0.038	0.969867	
logTHSp1:Size30	3.143e-01	1.414e-01	2.223	0.026215	*
logTHSp1:Size300		NA	NA	NA	NA
Species1:logTHSp1	1.911e-01	1.215e-01	1.573	0.115785	
Species2:logTHSp1	9.438e-02	1.230e-01	0.767	0.442990	
logTHSp1>Type1	6.690e-02	3.309e-02	2.021	0.043241	*
Species1:logTHSp1:Size3	3.479e-01	2.222e-01	1.565	0.117486	
Species2:logTHSp1:Size3	4.385e-01	2.018e-01	2.173	0.029761	*
Species1:logTHSp1:Size30	-1.057e-01	1.830e-01	-0.577	0.563797	
Species2:logTHSp1:Size30	-2.103e-01	1.791e-01	-1.175	0.240136	
Species1:logTHSp1:Size300		NA	NA	NA	NA
Species2:logTHSp1:Size300		NA	NA	NA	NA

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 3720.776 on 95 degrees of freedom

Residual deviance: 76.934 on 71 degrees of freedom

AIC: 503.38

Number of Fisher Scoring iterations: 16

```
glm(formula = Dbin ~ Species + Type + Species:Type, family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-3.4168	-0.5924	-0.4540	1.1812	2.9188

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.1786	0.2148	-19.451	< 2e-16 ***
Species1	-2.4240	0.7395	-3.278	0.001045 **
Species2	-2.1068	0.6165	-3.417	0.000633 ***

```

Type1          8.8998      0.3518  25.298 < 2e-16 ***
Species1:Type1 -2.7653      0.7917  -3.493 0.000478 ***
Species2:Type1 -5.3622      0.6846  -7.833 4.78e-15 ***

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)

```

```

Null deviance: 6995.17 on 95 degrees of freedom
Residual deviance: 148.04 on 90 degrees of freedom
AIC: 343.87
Number of Fisher Scoring iterations: 6

```

```

glm(formula = Dbin ~ Species + logTHSp1 + Type + Species:Type +
     Species:logTHSp1, family = binomial)

```

Deviance Residuals:

```

      Min       1Q   Median       3Q      Max
-2.9066 -0.6353 -0.4637  1.1636  2.9862

```

Coefficients:

```

              Estimate Std. Error z value Pr(>|z|)
(Intercept)    -4.12126    0.36384 -11.327 < 2e-16 ***
Species1       -2.61915    0.80078  -3.271 0.001073 **
Species2       -1.81343    0.70012  -2.590 0.009593 **
logTHSp1       -0.01075    0.05560  -0.193 0.846637
Type1          8.90092    0.35197  25.289 < 2e-16 ***
Species1:Type1 -2.76342    0.79175  -3.490 0.000483 ***
Species2:Type1 -5.35774    0.68475  -7.824 5.1e-15 ***
Species1:logTHSp1 0.03566    0.05786   0.616 0.537679
Species2:logTHSp1 -0.05794    0.06435  -0.900 0.367952

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)

```

```

Null deviance: 6995.17 on 95 degrees of freedom
Residual deviance: 141.16 on 87 degrees of freedom
AIC: 342.99
Number of Fisher Scoring iterations: 6

```

```

glm(formula = Dbin ~ Species + logTHSp1 + Type + Size + Species:Type +
     Species:logTHSp1 + Species:Size + logTHSp1:Size, family = binomial)

```

Deviance Residuals:

```

      Min       1Q   Median       3Q      Max
-2.3977 -0.6811 -0.3089  0.5885  2.1149

```

Coefficients: (1 not defined because of singularities)

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-5.3494	0.5568	-9.607	< 2e-16 ***
Species1	-1.6118	0.9089	-1.773	0.07617 .
Species2	-0.8858	0.8342	-1.062	0.28826
logTHSp1	-0.3888	0.2066	-1.882	0.05988 .
Type1	9.4394	0.4344	21.730	< 2e-16 ***
Size3	2.2006	1.0513	2.093	0.03633 *
Size30	1.3035	1.4603	0.893	0.37205
Size300	4.0872	1.9208	2.128	0.03335 *
Species1:Type1	-3.2970	0.8316	-3.964	7.36e-05 ***
Species2:Type1	-5.8932	0.7307	-8.065	7.33e-16 ***
Species1:logTHSp1	0.3222	0.1984	1.624	0.10440
Species2:logTHSp1	-0.3269	0.2266	-1.443	0.14912
Species1:Size3	-2.7668	1.0700	-2.586	0.00972 **
Species2:Size3	-0.6664	1.1783	-0.566	0.57168
Species1:Size30	-2.2105	1.4325	-1.543	0.12281
Species2:Size30	1.6778	1.5999	1.049	0.29431
Species1:Size300	-3.2557	1.8585	-1.752	0.07981 .
Species2:Size300	1.5384	2.0744	0.742	0.45832
logTHSp1:Size3	0.3322	0.1175	2.828	0.00469 **
logTHSp1:Size30	0.2644	0.1201	2.201	0.02773 *
logTHSp1:Size300	NA	NA	NA	NA

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 6995.17 on 95 degrees of freedom

Residual deviance: 78.78 on 76 degrees of freedom

AIC: 302.61

Number of Fisher Scoring iterations: 6

```
glm(formula = Verandabin ~ Species + Type + Species:Type, family =
      binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-6.3324	-1.3388	0.0852	0.9334	8.5091

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.14842	0.05252	2.826	0.00472 **
Species1	0.16857	0.07441	2.265	0.02349 *
Species2	-1.28796	0.07832	-16.444	< 2e-16 ***
Type1	0.04636	0.07416	0.625	0.53194

```
Species1:Type1  0.50646    0.10430    4.856  1.2e-06 ***
Species2:Type1  1.58320    0.10729   14.756  < 2e-16 ***
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1310.38 on 95 degrees of freedom

Residual deviance: 456.25 on 90 degrees of freedom

AIC: 931.41

Number of Fisher Scoring iterations: 4

```
glm(formula = Verandabin ~ Species + logTHSp1 + Type + Species:Type +
     Species:logTHSp1, family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-6.3183	-1.1233	0.0976	0.9707	4.3893

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.154966	0.083649	1.853	0.0639 .
Species1	0.305163	0.119094	2.562	0.0104 *
Species2	-0.527844	0.119890	-4.403	1.07e-05 ***
logTHSp1	-0.001217	0.012103	-0.101	0.9199
Type1	0.046360	0.074162	0.625	0.5319
Species1:Type1	0.506418	0.104334	4.854	1.21e-06 ***
Species2:Type1	1.671083	0.109525	15.258	< 2e-16 ***
Species1:logTHSp1	-0.025108	0.017155	-1.464	0.1433
Species2:logTHSp1	-0.149586	0.017820	-8.394	< 2e-16 ***

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1310.38 on 95 degrees of freedom

Residual deviance: 311.82 on 87 degrees of freedom

AIC: 792.99

Number of Fisher Scoring iterations: 4

```
glm(formula = Verandabin ~ Species + logTHSp1 + Type + Size + Species:Type
     + Species:logTHSp1 + Type:Size + logTHSp1:Size + Species:Size +
     Species:Type:Size, family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

-3.7845 -0.6197 0.0044 0.6343 3.3020

Coefficients: (1 not defined because of singularities)

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	0.16990	0.13066	1.300	0.193490	
Species1	0.41918	0.18749	2.236	0.025366	*
Species2	-0.23734	0.17908	-1.325	0.185064	
logTHSp1	0.25193	0.05591	4.506	6.59e-06	***
Type1	-0.10588	0.18190	-0.582	0.560528	
Size3	0.29519	0.28733	1.027	0.304242	
Size30	-0.60067	0.38784	-1.549	0.121439	
Size300	-1.84946	0.51669	-3.579	0.000344	***
Species1:Type1	0.48937	0.26325	1.859	0.063033	.
Species2:Type1	0.99683	0.25749	3.871	0.000108	***
Species1:logTHSp1	-0.09567	0.05919	-1.616	0.106000	
Species2:logTHSp1	-0.27851	0.06264	-4.446	8.73e-06	***
Type1:Size3	0.86204	0.23272	3.704	0.000212	***
Type1:Size30	0.28130	0.22788	1.234	0.217050	
Type1:Size300	-0.62263	0.23468	-2.653	0.007975	**
logTHSp1:Size3	-0.36593	0.06109	-5.990	2.10e-09	***
logTHSp1:Size30	-0.18817	0.06051	-3.110	0.001871	**
logTHSp1:Size300	NA	NA	NA	NA	
Species1:Size3	0.26251	0.34235	0.767	0.443202	
Species2:Size3	0.32706	0.34763	0.941	0.346794	
Species1:Size30	0.55091	0.45040	1.223	0.221274	
Species2:Size30	0.09978	0.47151	0.212	0.832401	
Species1:Size300	0.09215	0.56982	0.162	0.871533	
Species2:Size300	0.79419	0.59838	1.327	0.184433	
Species1:Type1:Size3	-0.67107	0.32895	-2.040	0.041350	*
Species2:Type1:Size3	0.32855	0.33493	0.981	0.326618	
Species1:Type1:Size30	-0.04961	0.32917	-0.151	0.880208	
Species2:Type1:Size30	1.28746	0.33860	3.802	0.000143	***
Species1:Type1:Size300	0.82008	0.33298	2.463	0.013785	*
Species2:Type1:Size300	1.01402	0.33222	3.052	0.002271	**

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1310.38 on 95 degrees of freedom

Residual deviance: 148.58 on 67 degrees of freedom

AIC: 669.75

Number of Fisher Scoring iterations: 4

```
glm(formula = Netbin ~ Species + Type + Species:Type, family = binomial)
```

```
Deviance Residuals:
```

Min	1Q	Median	3Q	Max
-16.4793	-1.8969	0.6938	1.9064	6.3286

```
Coefficients:
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.83318	0.07596	-24.132	< 2e-16 ***
Species1	-0.49577	0.11894	-4.168	3.07e-05 ***
Species2	1.42203	0.09142	15.556	< 2e-16 ***
Type1	0.14081	0.10460	1.346	0.178
Species1:Type1	-0.73879	0.17472	-4.228	2.35e-05 ***
Species2:Type1	-1.23336	0.13304	-9.271	< 2e-16 ***

```
---
```

```
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for binomial family taken to be 1)
```

```
Null deviance: 2038.3 on 95 degrees of freedom
```

```
Residual deviance: 1227.7 on 90 degrees of freedom
```

```
AIC: 1590.9
```

```
Number of Fisher Scoring iterations: 5
```

```
glm(formula = Netbin ~ Species + logTHSp1 + Type + Species:Type +  
logTHSp1:Type + Species:logTHSp1 + Species:logTHSp1:Type, family =  
binomial)
```

```
Deviance Residuals:
```

Min	1Q	Median	3Q	Max
-8.3607	-2.0840	-0.0518	1.4538	5.5201

```
Coefficients:
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.77099	0.19732	-14.043	< 2e-16 ***
Species1	-1.08434	0.34337	-3.158	0.001589 **
Species2	0.80383	0.23899	3.363	0.000770 ***
logTHSp1	0.15942	0.02861	5.572	2.52e-08 ***
Type1	-1.17241	0.32209	-3.640	0.000273 ***
Species1:Type1	-0.52411	0.59618	-0.879	0.379335
Species2:Type1	-0.50409	0.41455	-1.216	0.223985
logTHSp1:Type1	0.19280	0.04428	4.354	1.34e-05 ***
Species1:logTHSp1	0.08412	0.04748	1.772	0.076426 .
Species2:logTHSp1	0.11127	0.03511	3.169	0.001527 **
Species1:logTHSp1:Type1	-0.04361	0.07825	-0.557	0.577278
Species2:logTHSp1:Type1	-0.12771	0.05721	-2.232	0.025595 *

```
---
```

Signif. codes: 0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2038.28 on 95 degrees of freedom

Residual deviance: 532.09 on 84 degrees of freedom

AIC: 907.24

Number of Fisher Scoring iterations: 5

```
glm(formula = Netbin ~ Species + logTHSp1 + Type + Size + logTHSp1:Size +  
     Species:Type + logTHSp1:Type + Species:logTHSp1 + Species:Size +  
     Type:Size + Species:logTHSp1:Size + logTHSp1:Type:Size +  
     Species:Type:Size, family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.7666	-0.8382	-0.1476	0.6012	2.4342

Coefficients: (4 not defined because of singularities)

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-4.76217	0.71012	-6.706	2.00e-11	***
Species1	-0.02114	1.00422	-0.021	0.98320	
Species2	-17.52305	2563.13497	-0.007	0.99455	
logTHSp1	-0.22014	0.10905	-2.019	0.04351	*
Type1	-17.45759	2563.55463	-0.007	0.99457	
Size3	0.63787	1.01587	0.628	0.53007	
Size30	3.10135	0.99153	3.128	0.00176	**
Size300	4.98061	1.18872	4.190	2.79e-05	***
logTHSp1:Size3	0.71765	0.19011	3.775	0.00016	***
logTHSp1:Size30	0.26781	0.15060	1.778	0.07536	.
logTHSp1:Size300	NA	NA	NA	NA	
Species1:Type1	-0.08091	3624.95946	0.000	0.99998	
Species2:Type1	34.18985	3625.11707	0.009	0.99247	
logTHSp1:Type1	-0.09205	0.09877	-0.932	0.35135	
Species1:logTHSp1	-0.06456	0.14079	-0.459	0.64654	
Species2:logTHSp1	0.22038	0.11484	1.919	0.05497	.
Species1:Size3	-4.74850	2.00816	-2.365	0.01805	*
Species2:Size3	18.94224	2563.13511	0.007	0.99410	
Species1:Size30	-6.62859	1.65566	-4.004	6.24e-05	***
Species2:Size30	18.52808	2563.13509	0.007	0.99423	
Species1:Size300	0.37130	1.58727	0.234	0.81504	
Species2:Size300	17.16130	2563.13517	0.007	0.99466	
Type1:Size3	13.75643	2563.55485	0.005	0.99572	
Type1:Size30	15.34029	2563.55475	0.006	0.99523	
Type1:Size300	19.06343	2563.55478	0.007	0.99407	

Species1:logTHSp1:Size3	0.92348	0.37875	2.438	0.01476	*
Species2:logTHSp1:Size3	-0.21112	0.21339	-0.989	0.32248	
Species1:logTHSp1:Size30	0.94240	0.23459	4.017	5.89e-05	***
Species2:logTHSp1:Size30	-0.10696	0.16482	-0.649	0.51637	
Species1:logTHSp1:Size300	NA	NA	NA	NA	
Species2:logTHSp1:Size300	NA	NA	NA	NA	
logTHSp1:Type1:Size3	0.74329	0.23162	3.209	0.00133	**
logTHSp1:Type1:Size30	0.40905	0.14924	2.741	0.00613	**
logTHSp1:Type1:Size300	NA	NA	NA	NA	
Species1:Type1:Size3	-1.81884	3624.95951	-0.001	0.99960	
Species2:Type1:Size3	-35.26199	3625.11708	-0.010	0.99224	
Species1:Type1:Size30	-0.53455	3624.95947	0.000	0.99988	
Species2:Type1:Size30	-35.82615	3625.11708	-0.010	0.99211	
Species1:Type1:Size300	-0.99175	3624.95947	0.000	0.99978	
Species2:Type1:Size300	-35.61632	3625.11708	-0.010	0.99216	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2038.28 on 95 degrees of freedom

Residual deviance: 112.76 on 60 degrees of freedom

AIC: 535.92

Number of Fisher Scoring iterations: 16