

EGF

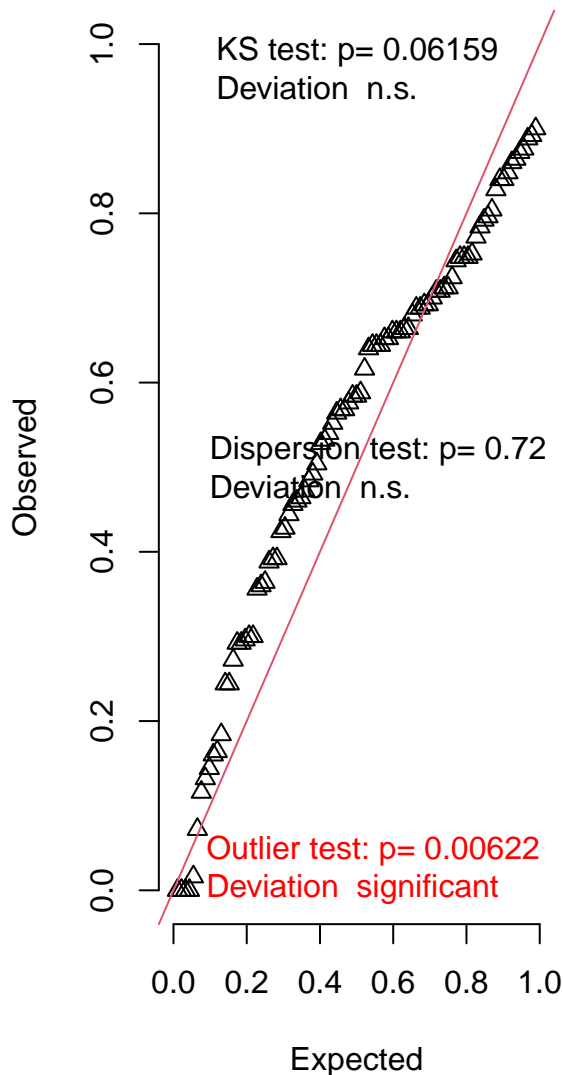
Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 4

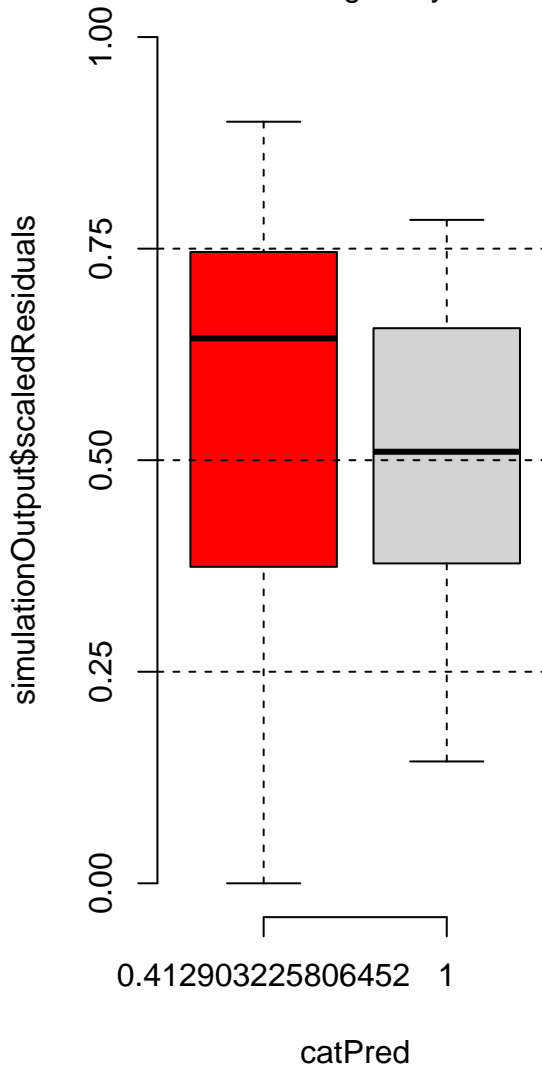
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
37.1	49.7	-13.6	27.1	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.053372	0.23102
day	(Intercept)	0.009268	0.09627
Residual		0.054232	0.23288

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0542

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.71755	0.09008	19.066	<2e-16 ***
inf_statusControl	0.23722	0.14856	1.597	0.11

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

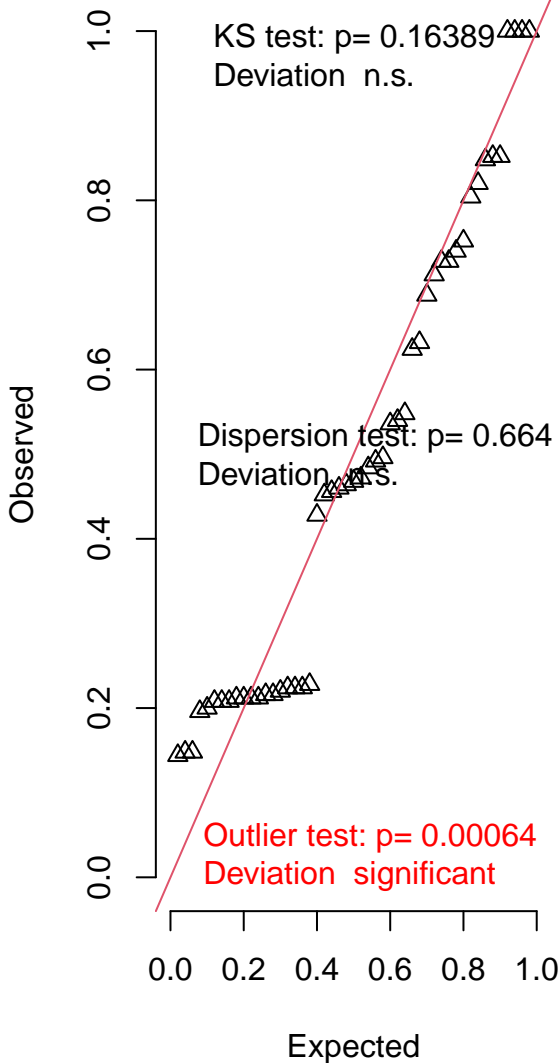
Infection in DENV-squirrel

Nb obs (total) : 49

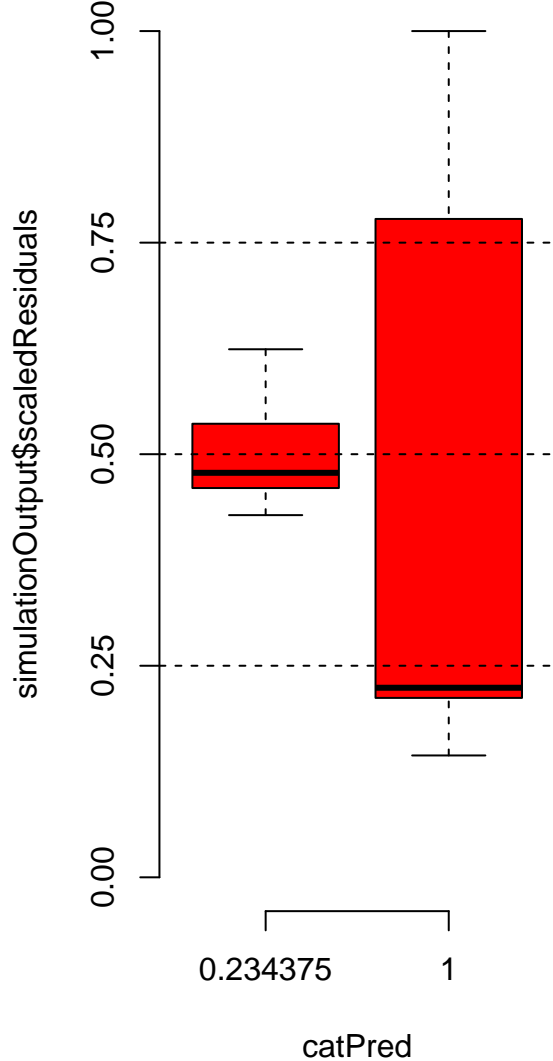
Nb LOD (included) : 31

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant




```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-33.5	-24.0	21.7	-43.5	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.3712150	0.60927
day	(Intercept)	0.0009288	0.03048
Residual		0.0043019	0.06559

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0043

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.0397	0.1933	5.378	7.55e-08 ***
inf_statusControl	-0.5065	0.3611	-1.403	0.161

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

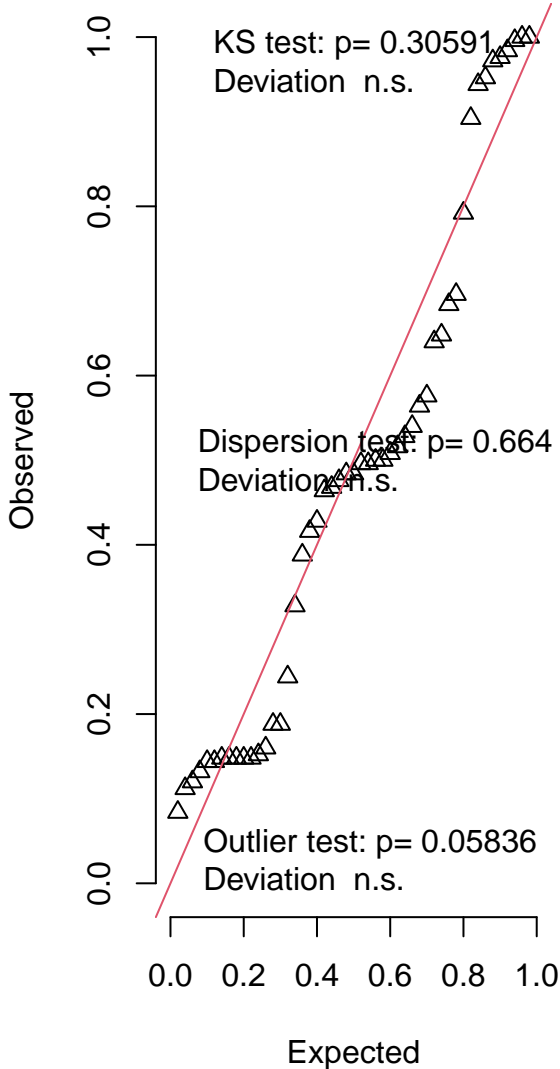
Infection in ZIKV-squirrel

Nb obs (total) : 49

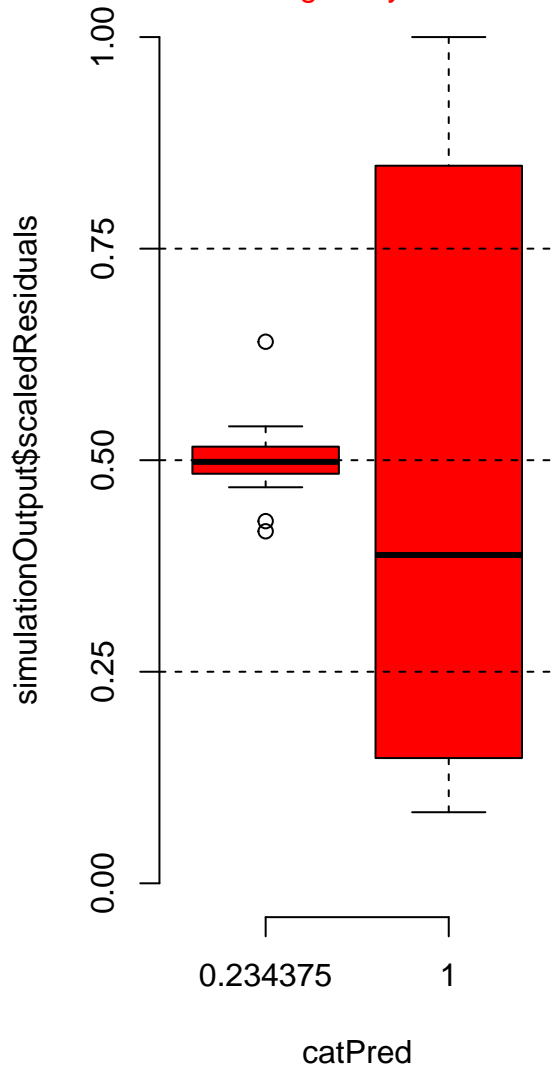
Nb LOD (included) : 27

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
30.5	40.0	-10.3	20.5	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.132e-01	4.617e-01
day	(Intercept)	2.462e-12	1.569e-06
Residual		3.742e-02	1.934e-01

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0374

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.0168	0.1497	6.793	1.1e-11 ***
inf_statusControl	-0.4837	0.2800	-1.727	0.0841 .

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

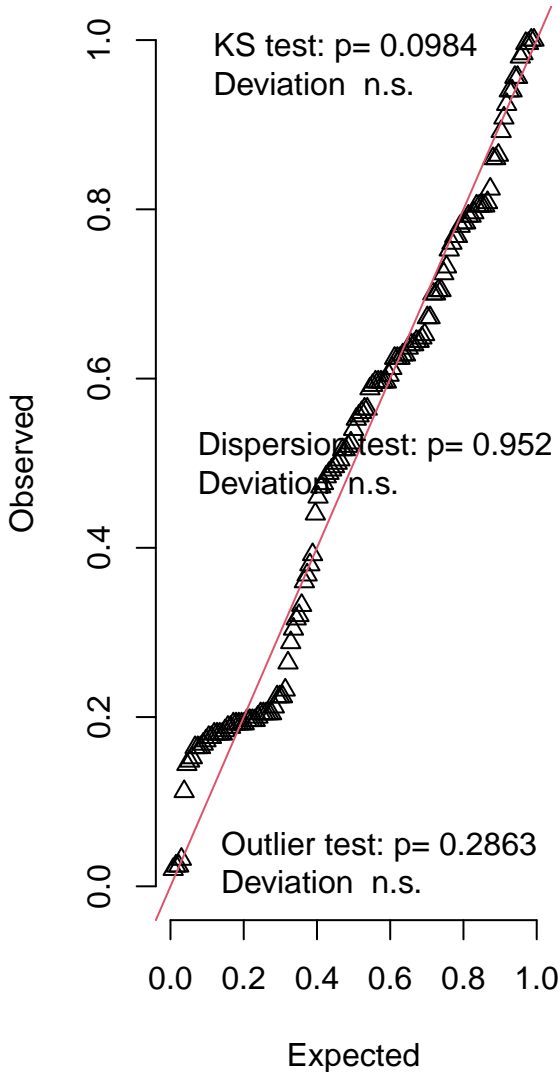
Effect of experiment

Nb obs (total): 133

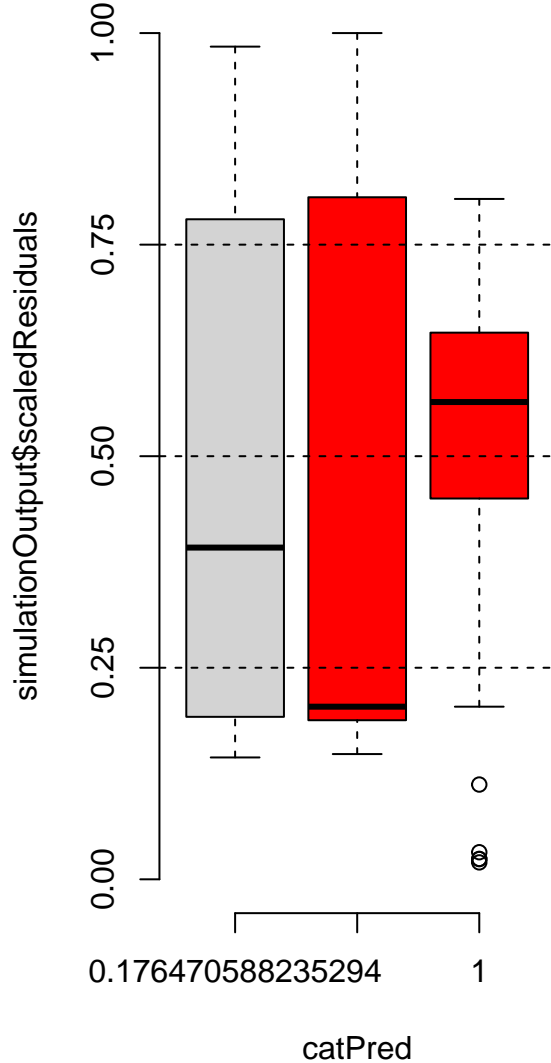
Nb LOD (included): 38

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant




```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
96.3	113.6	-42.1	84.3	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.277498	0.52678
day	(Intercept)	0.005294	0.07276
Residual		0.052768	0.22971

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0528

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.04932	0.17328	6.056	1.4e-09 ***
groupCyno.Dengue virus	0.66518	0.24735	2.689	0.00716 **
groupSquirrel.Zika virus	-0.02618	0.24202	-0.108	0.91385

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

Eotaxin

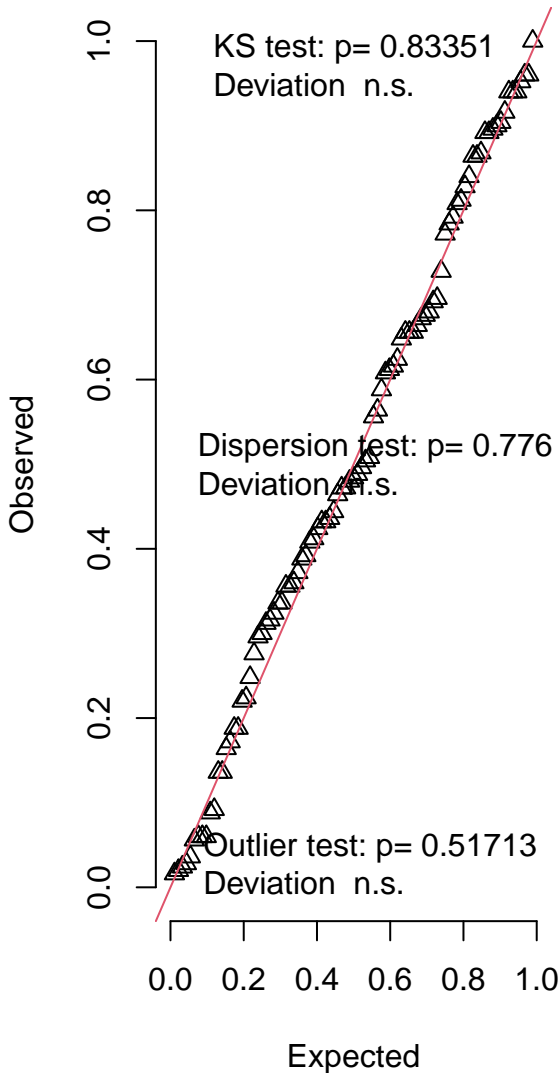
Infection in DENV-cyno

Nb obs (total): 91

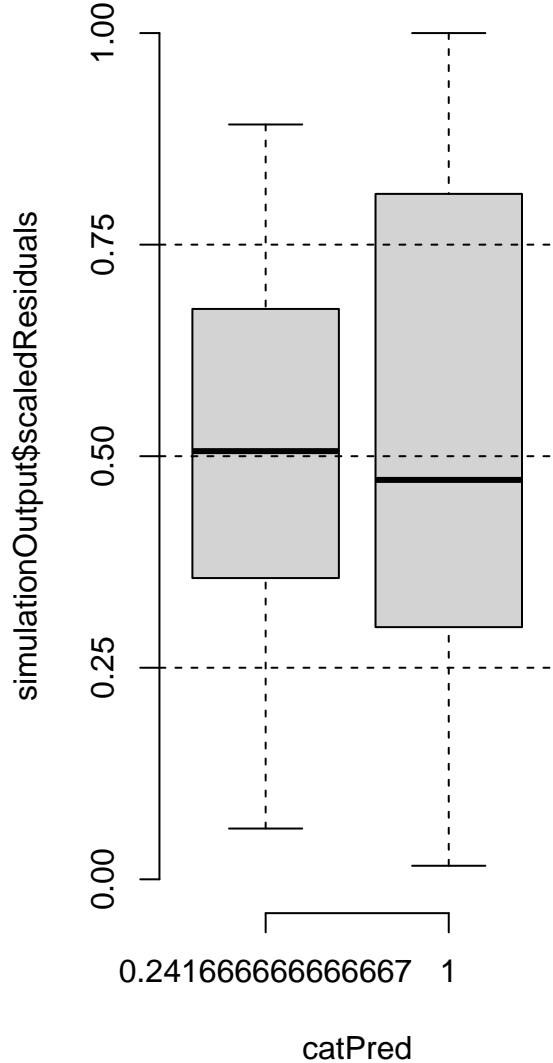
Nb LOD (included): 0

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-73.7	-61.2	41.9	-83.7	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.012398	0.1113
day	(Intercept)	0.002238	0.0473
Residual		0.016794	0.1296

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0168

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.18662	0.04431	49.34	<2e-16 ***
inf_statusControl	-0.08375	0.07310	-1.15	0.252

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

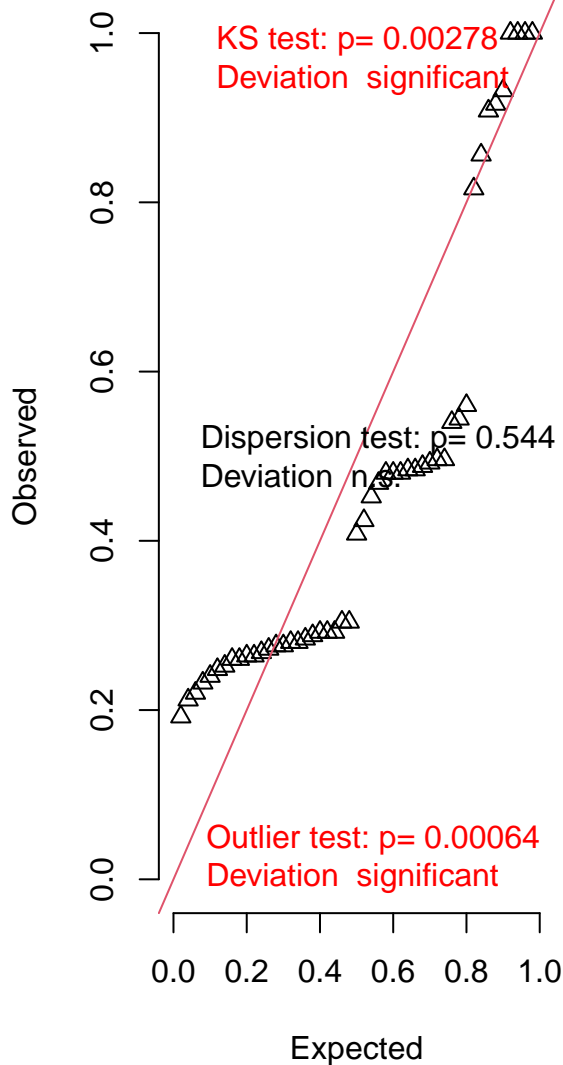
Infection in DENV-squirrel

Nb obs (total) : 49

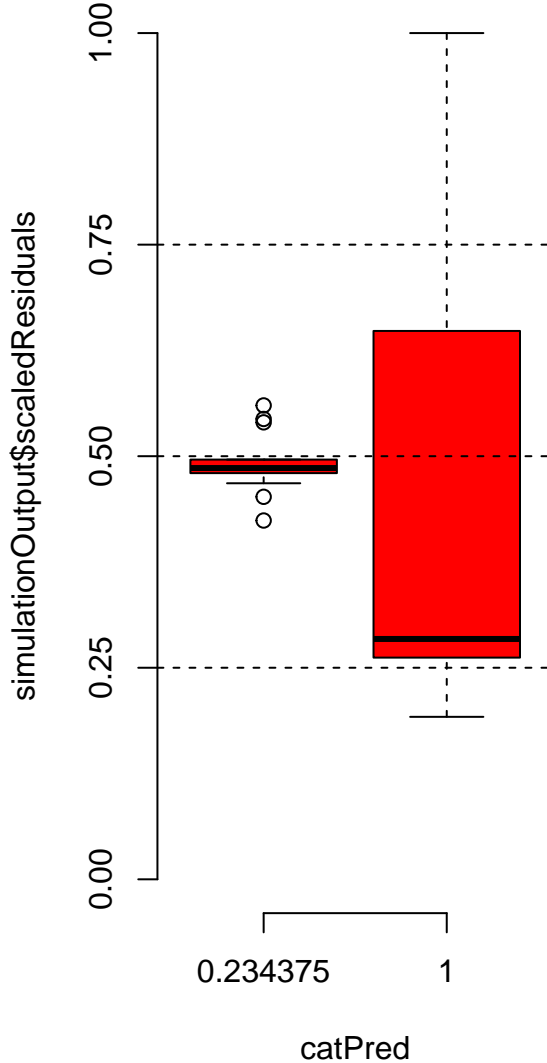
Nb LOD (included) : 38

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-8.0	1.4	9.0	-18.0	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.109496	0.3309
day	(Intercept)	0.002862	0.0535
Residual		0.014357	0.1198

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0144

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.6038	0.1086	5.562	2.67e-08 ***
inf_statusControl	-0.2243	0.1995	-1.125	0.261

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

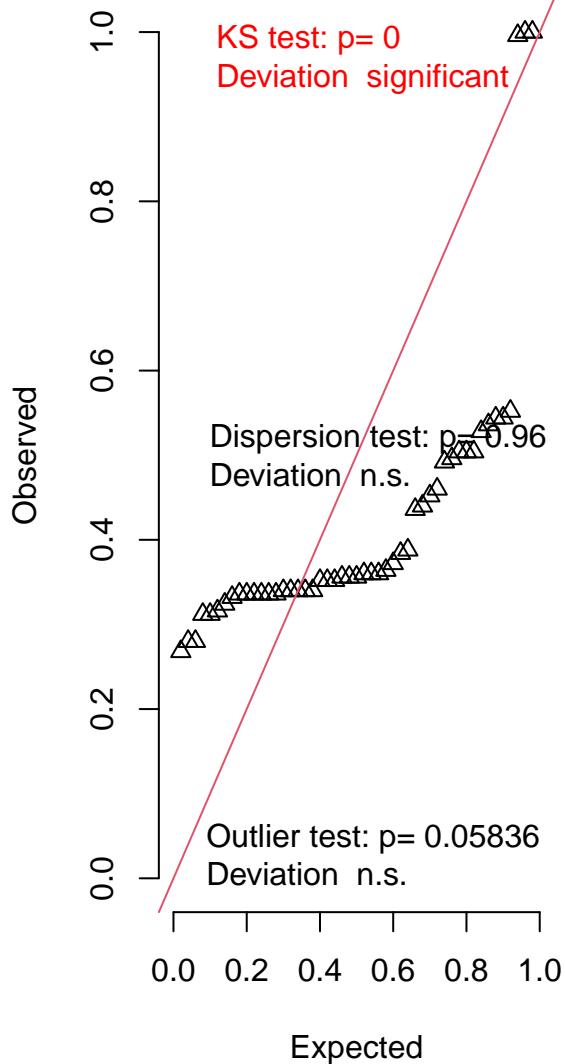
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 46

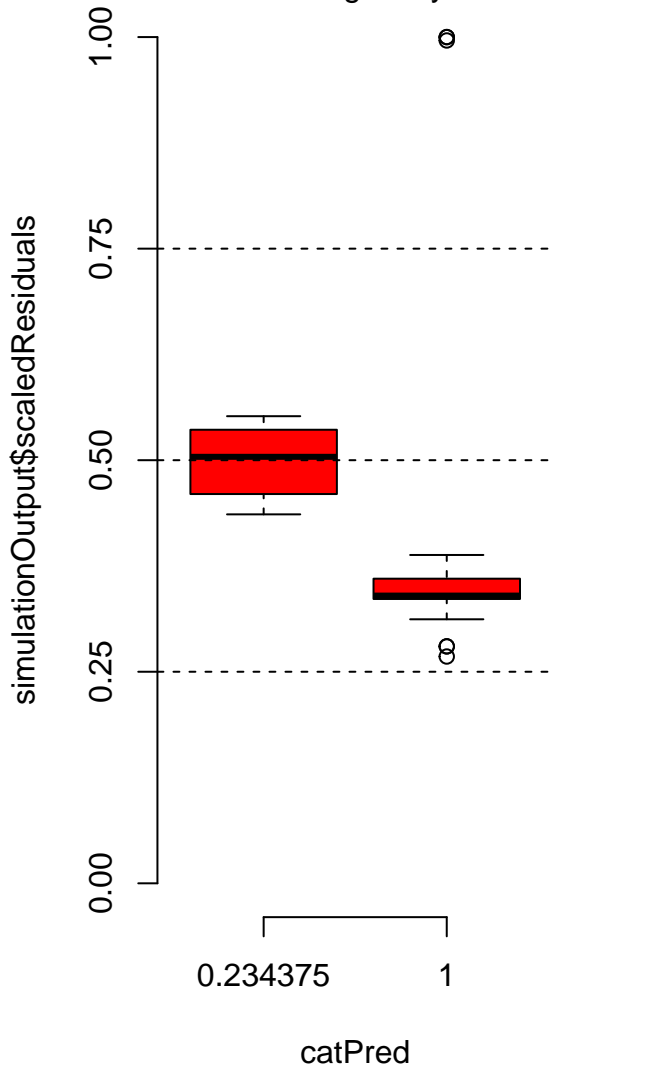
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-136.6	-127.1	73.3	-146.6	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.344e-02	1.531e-01
day	(Intercept)	1.235e-10	1.111e-05
Residual		7.771e-04	2.788e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000777

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.43907	0.04865	9.025	<2e-16 ***
inf_statusControl	-0.06067	0.09102	-0.667	0.505

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

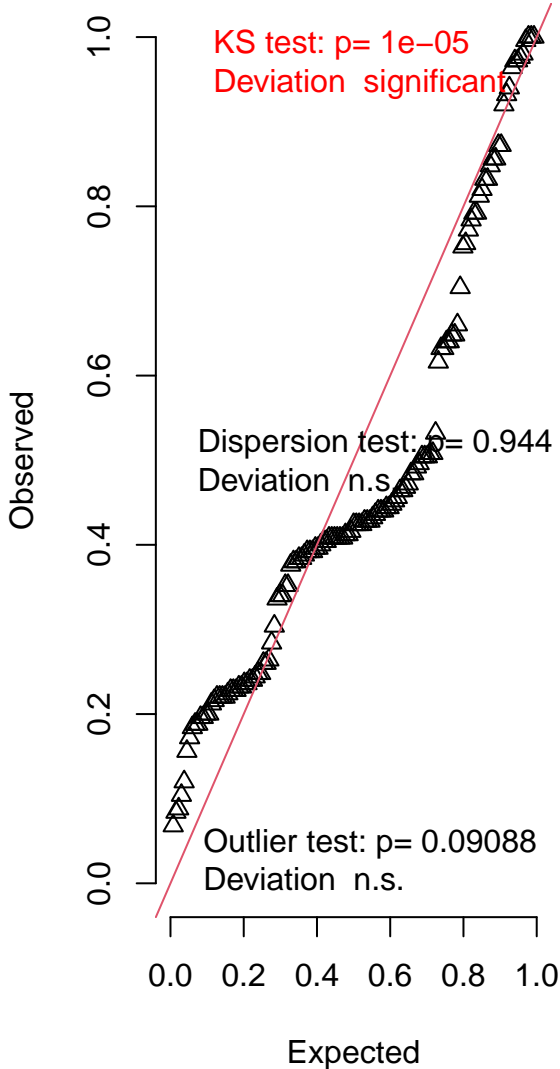
Effect of experiment

Nb obs (total): 133

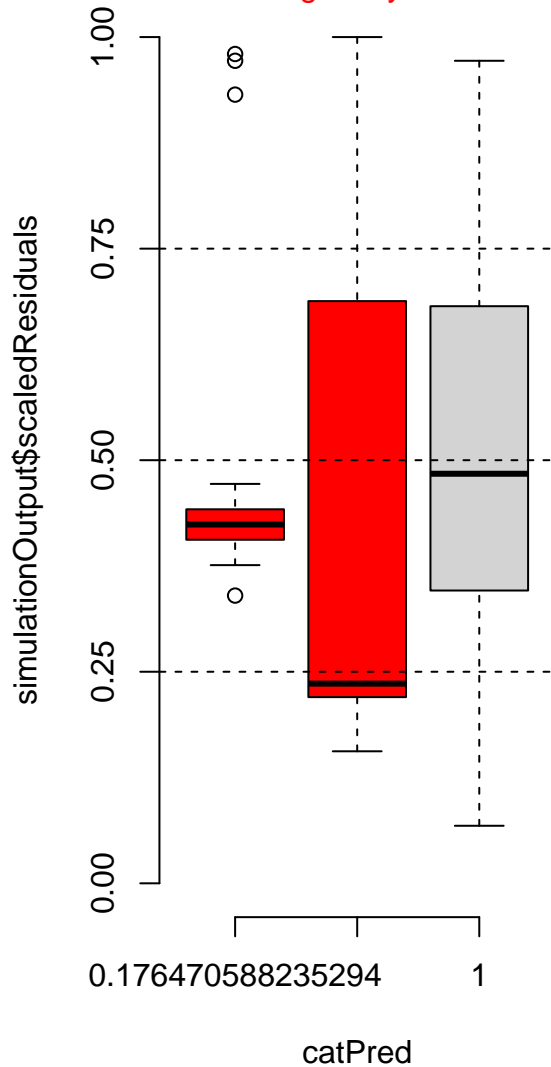
Nb LOD (included): 56

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-70.3	-52.9	41.1	-82.3	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.066700	0.25826
day	(Intercept)	0.001097	0.03312
Residual		0.015999	0.12649

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.016

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.6062	0.0854	7.098	1.26e-12 ***
groupCyno.Dengue virus	1.5795	0.1219	12.959	< 2e-16 ***
groupSquirrel.Zika virus	-0.1651	0.1195	-1.382	0.167

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

G . C S F

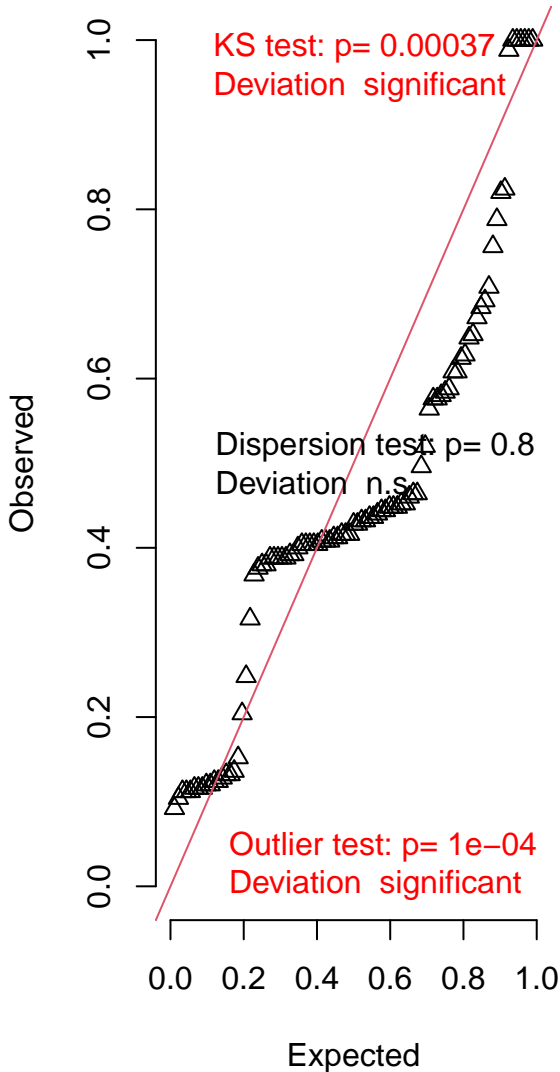
Infection in DENV-cyno

Nb obs (total) : 91

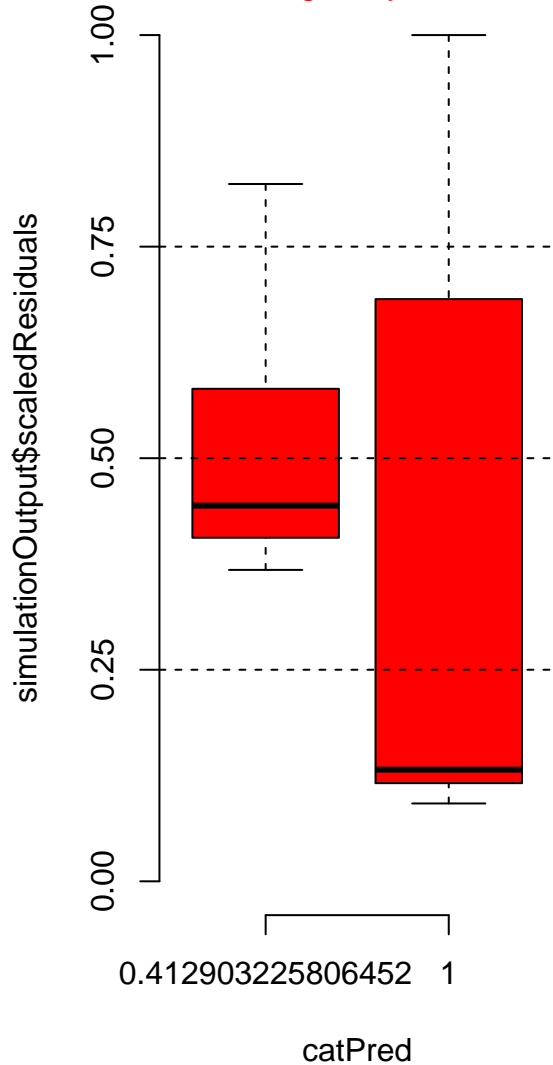
Nb LOD (included) : 53

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-204.2	-191.7	107.1	-214.2	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0615303	0.24805
day	(Intercept)	0.0002639	0.01624
Residual		0.0025175	0.05018

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00252

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.11198	0.08315	25.399	<2e-16 ***
inf_statusControl	0.22210	0.14950	1.486	0.137

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

Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 49

G.CSF ERROR : valeurs infinies ou manquantes dans 'x'

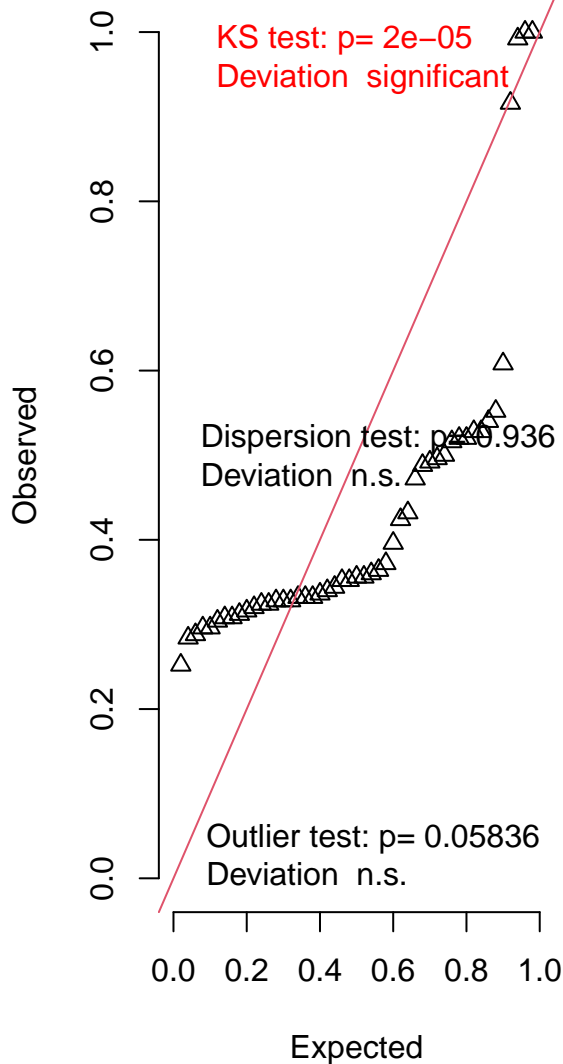
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 44

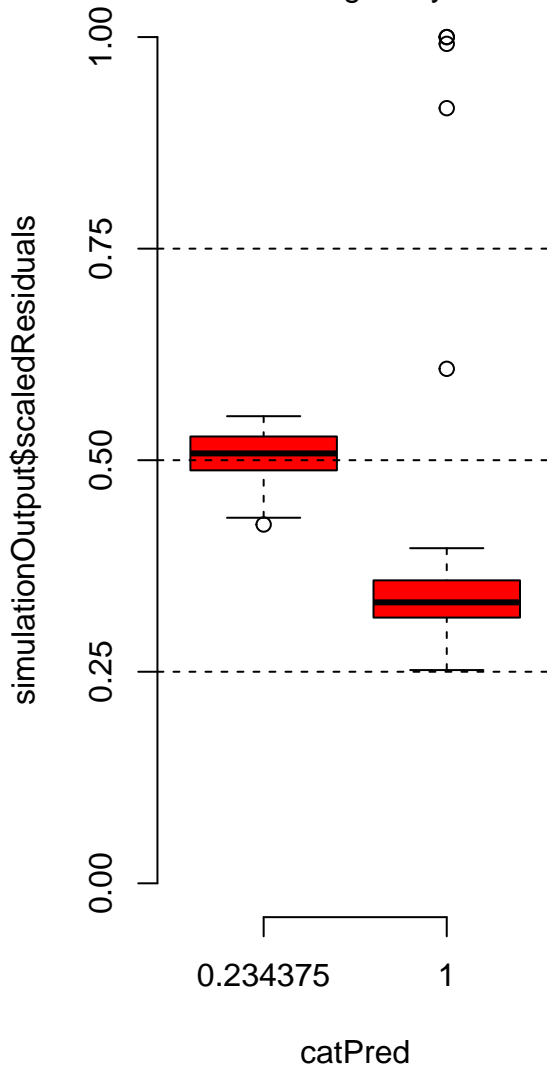
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-207.4	-198.0	108.7	-217.4	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	9.127e-04	0.030211
day	(Intercept)	7.262e-06	0.002695
Residual		3.544e-04	0.018826

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000354

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.07122	0.01013	204.43	<2e-16 ***
inf_statusControl	-0.01590	0.01886	-0.84	0.399

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

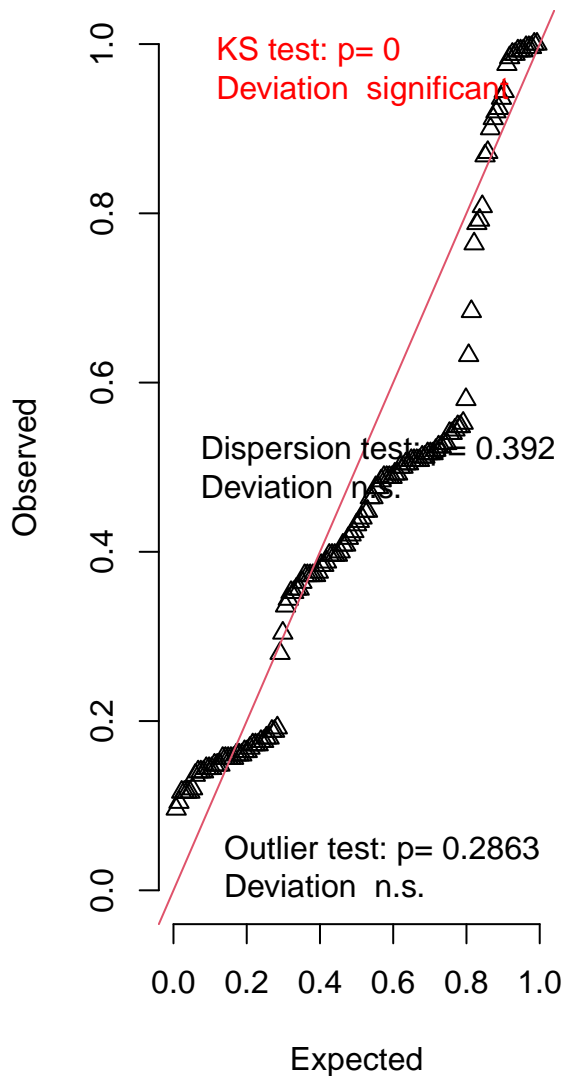
Effect of experiment

Nb obs (total) : 133

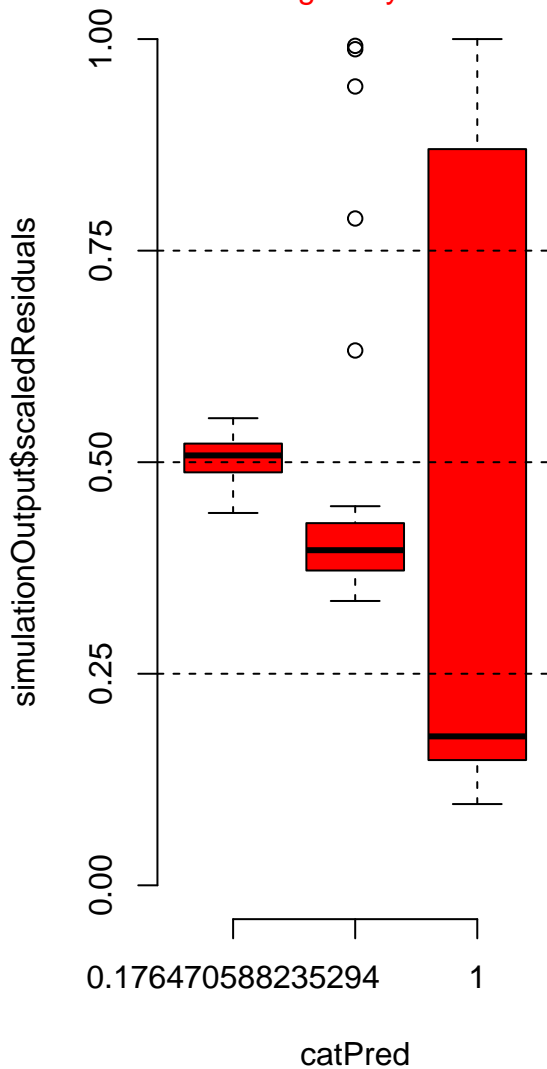
Nb LOD (included) : 103

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-415.3	-397.9	213.6	-427.3	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.523e-03	0.0390293
day	(Intercept)	3.611e-12	0.0000019
Residual		1.659e-03	0.0407351

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00166

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.05534	0.01416	145.16	< 2e-16 ***
groupCyno.Dengue virus	0.05664	0.01990	2.85	0.00442 **
groupSquirrel.Zika virus	0.01567	0.02002	0.78	0.43392

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

GM . CSF

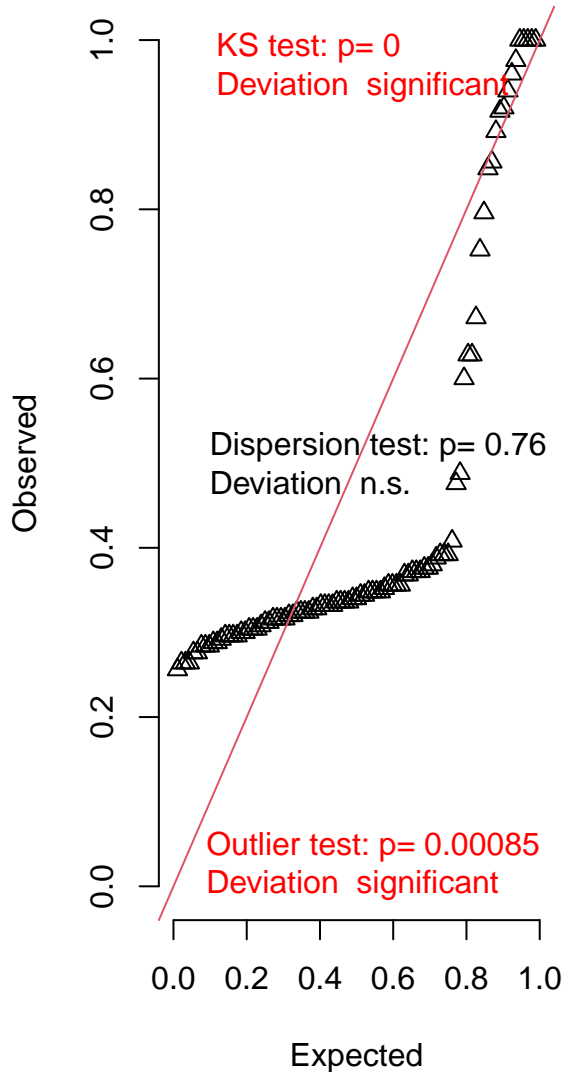
Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 65

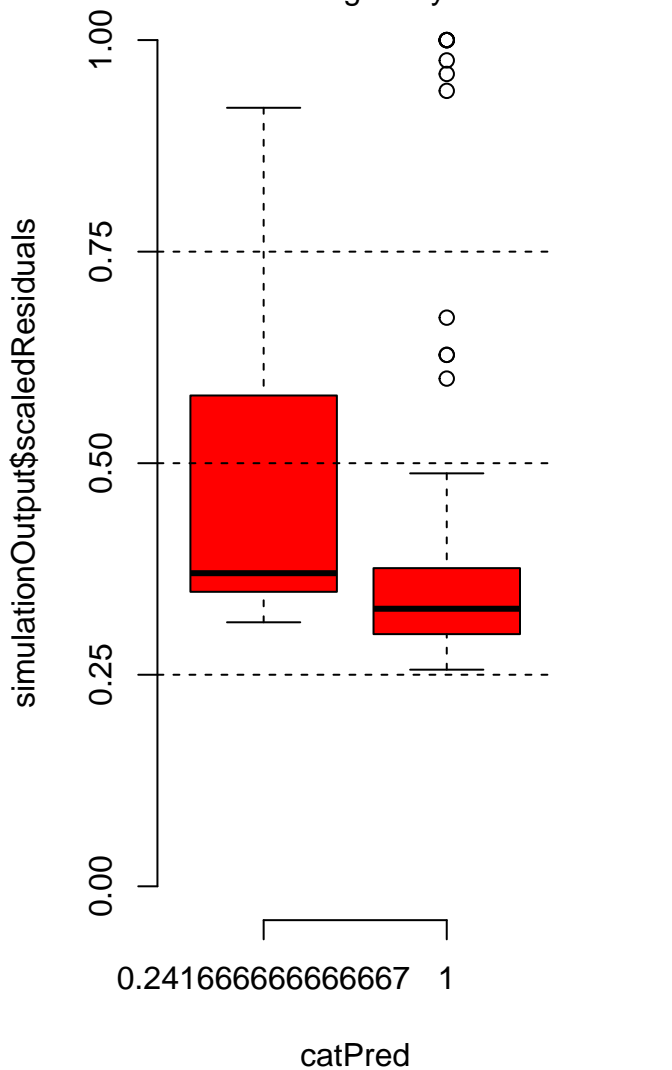
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-146.5	-134.0	78.3	-156.5	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0090121	0.09493
day	(Intercept)	0.0001396	0.01182
Residual		0.0075011	0.08661

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0075

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.17464	0.03377	34.78	<2e-16 ***
inf_statusControl	-0.01984	0.06034	-0.33	0.742

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

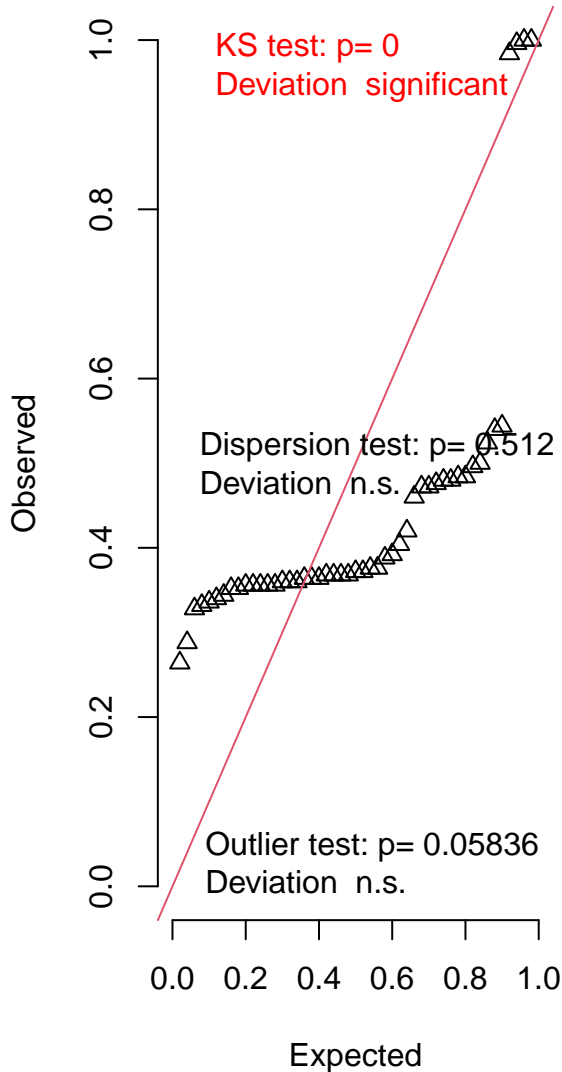
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 45

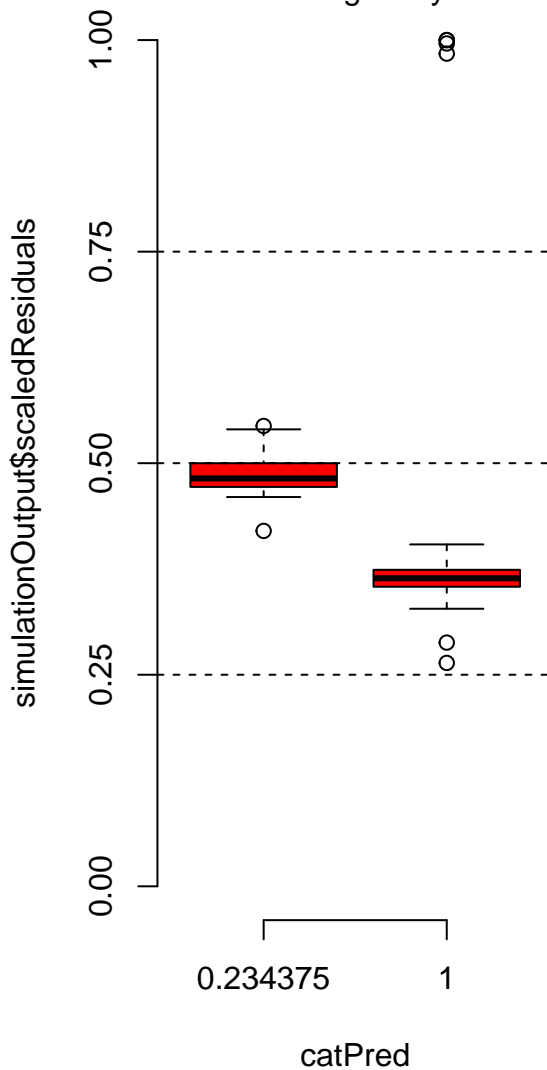
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-233.6	-224.1	121.8	-243.6	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.078e-03	3.283e-02
day	(Intercept)	1.851e-11	4.302e-06
Residual		1.644e-04	1.282e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000164

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.24369	0.01061	117.22	<2e-16 ***
inf_statusControl	-0.01324	0.01985	-0.67	0.505

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

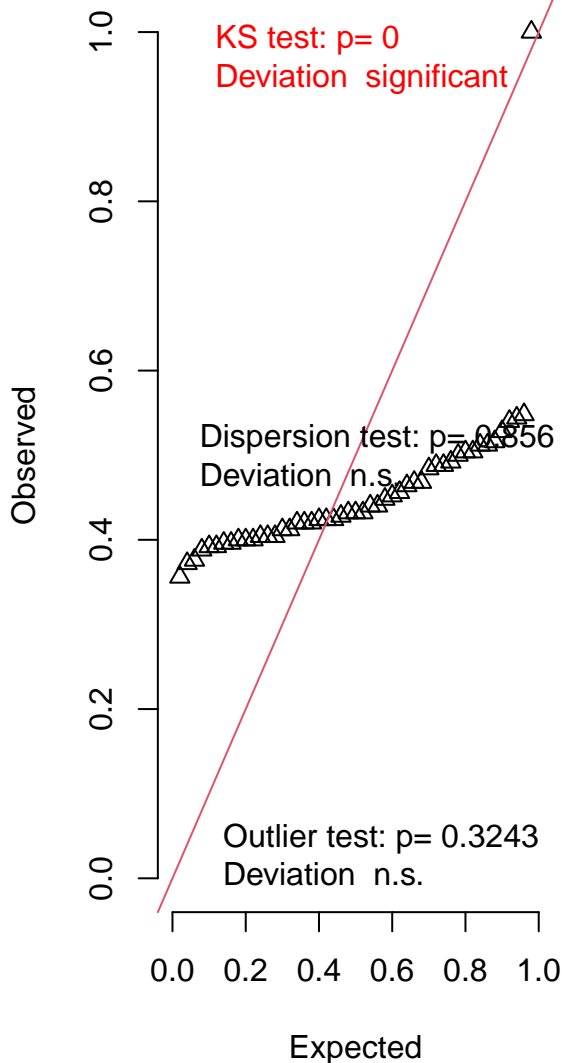
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 48

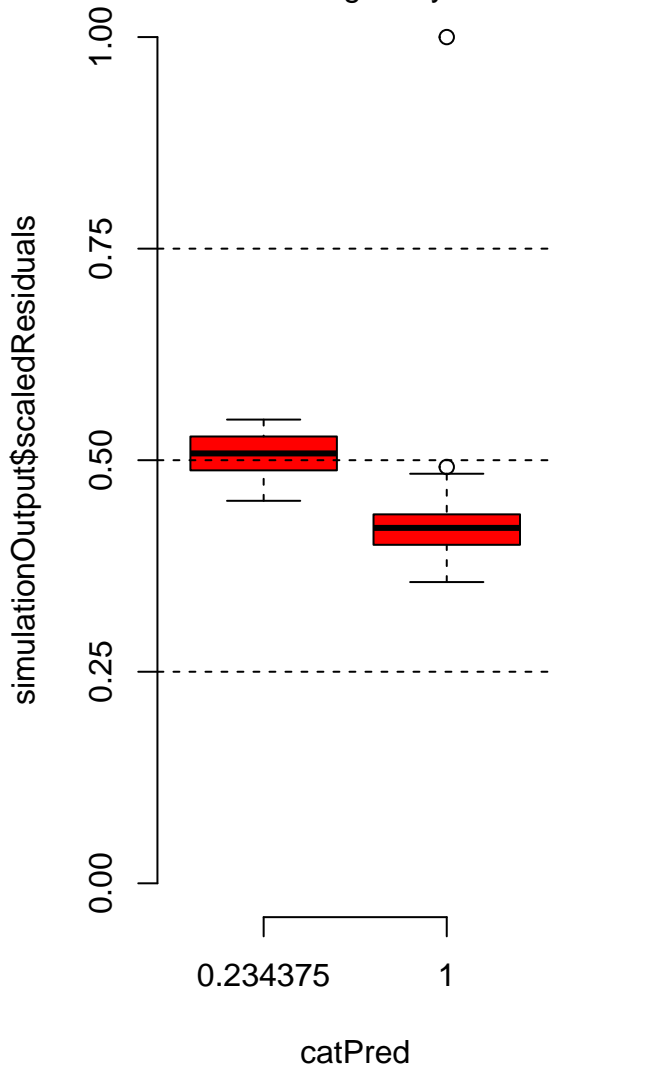
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:          log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-343.8	-334.4	176.9	-353.8	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	3.343e-13	5.782e-07
day	(Intercept)	4.894e-17	6.996e-09
Residual		4.282e-05	6.543e-03

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (σ^2): 4.28e-05

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.231777	NaN	NaN	NaN
inf_statusControl	-0.001328	NaN	NaN	NaN

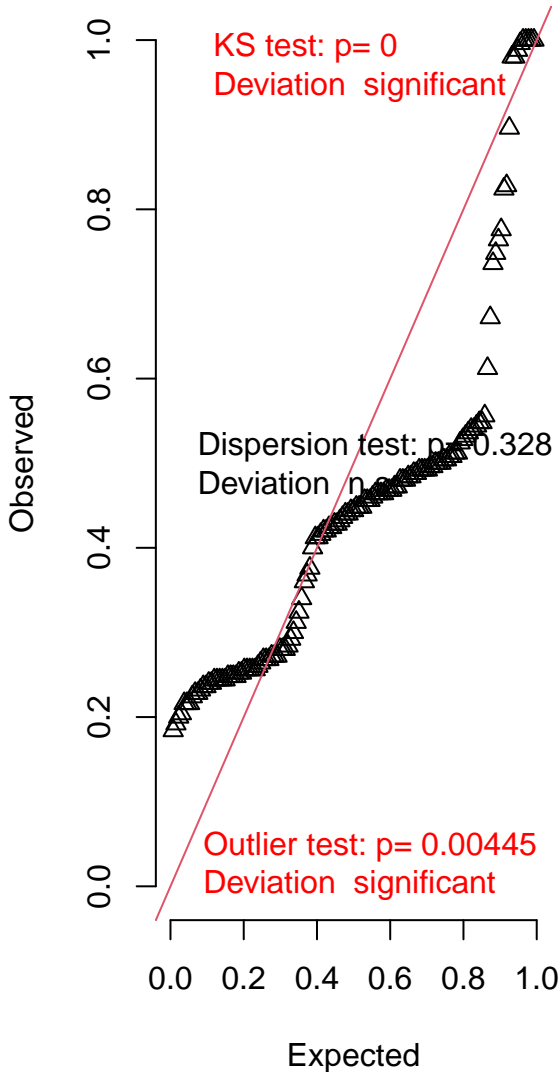
Effect of experiment

Nb obs (total) : 133

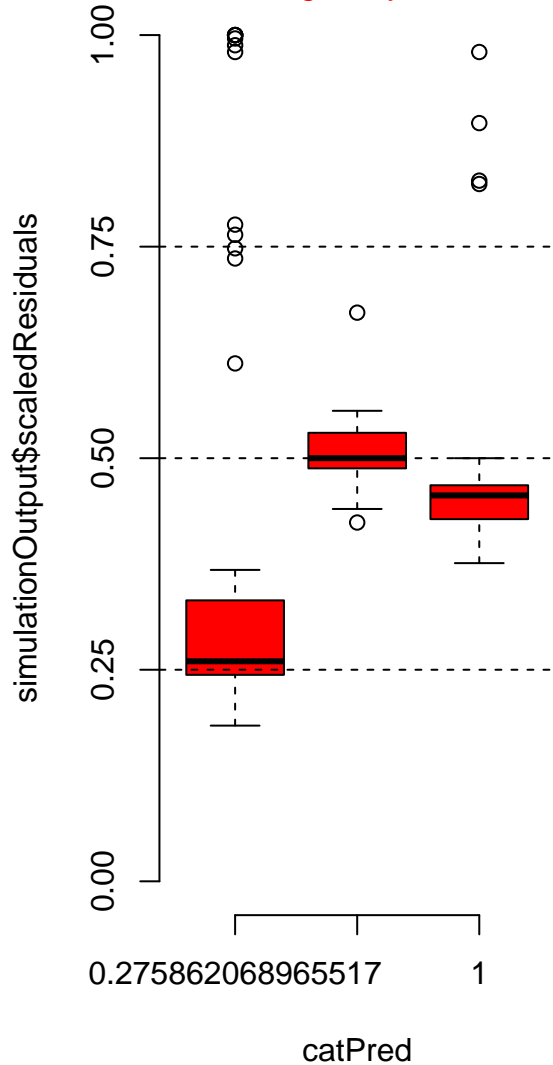
Nb LOD (included) : 109

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-268.2	-250.9	140.1	-280.2	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	4.076e-03	0.0638460
day	(Intercept)	1.393e-10	0.0000118
Residual		5.138e-03	0.0716790

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00514

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.24412	0.02359	52.73	<2e-16 ***
groupCyno.Dengue virus	-0.06948	0.03303	-2.10	0.0354 *
groupSquirrel.Zika virus	-0.01246	0.03337	-0.37	0.7088

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

HGF

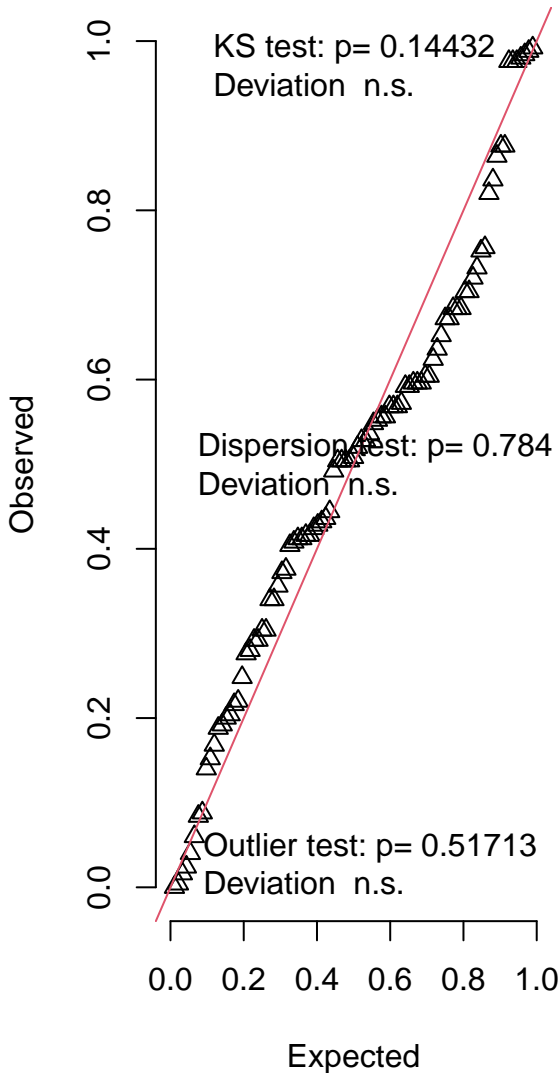
Infection in DENV-cyno

Nb obs (total) : 91

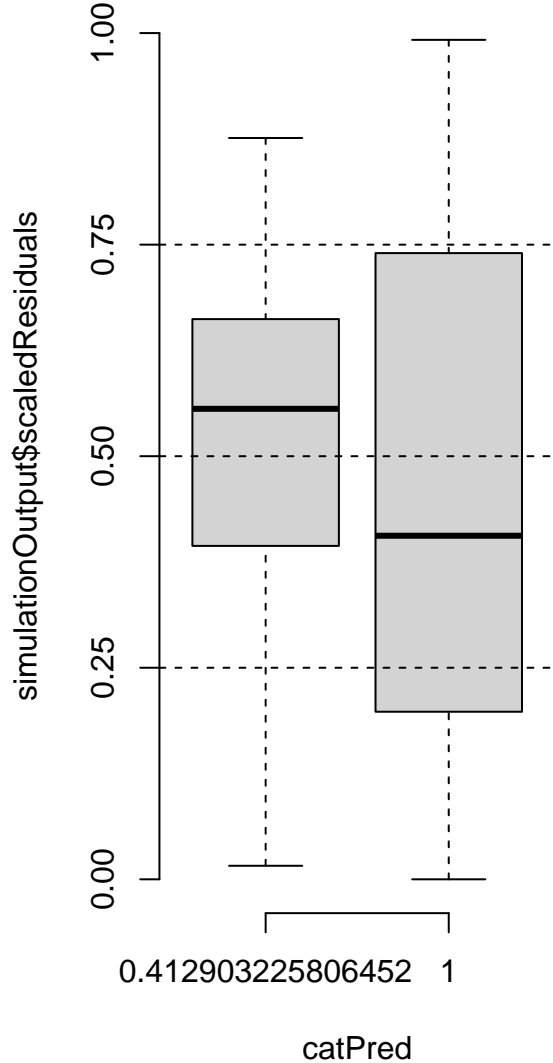
Nb LOD (included) : 4

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
30.4	43.0	-10.2	20.4	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.126421	0.35556
day	(Intercept)	0.001845	0.04296
Residual		0.046440	0.21550

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0464

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.8337	0.1227	23.100	<2e-16 ***
inf_statusControl	0.1895	0.2192	0.864	0.387

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

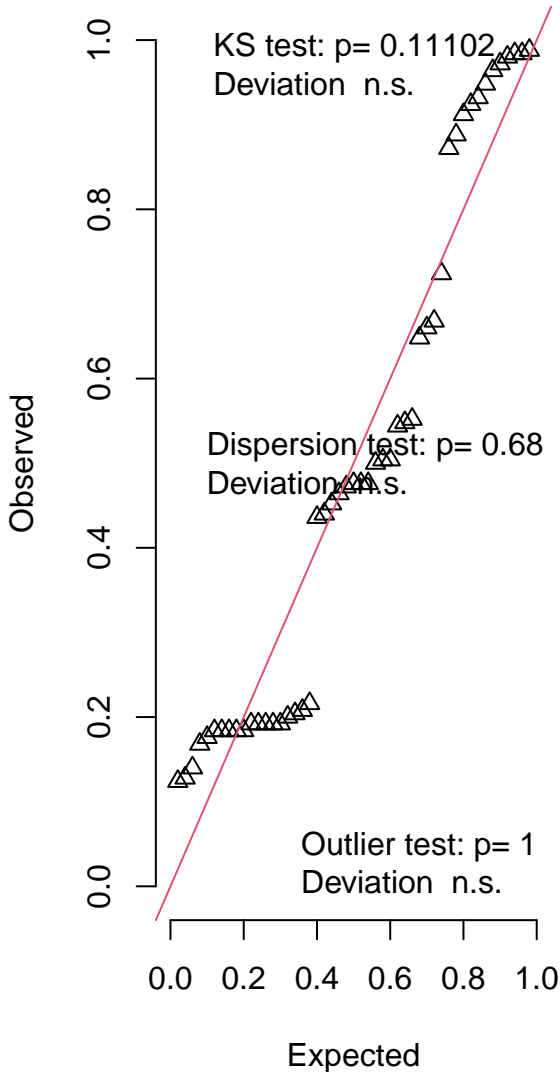
Infection in DENV-squirrel

Nb obs (total) : 49

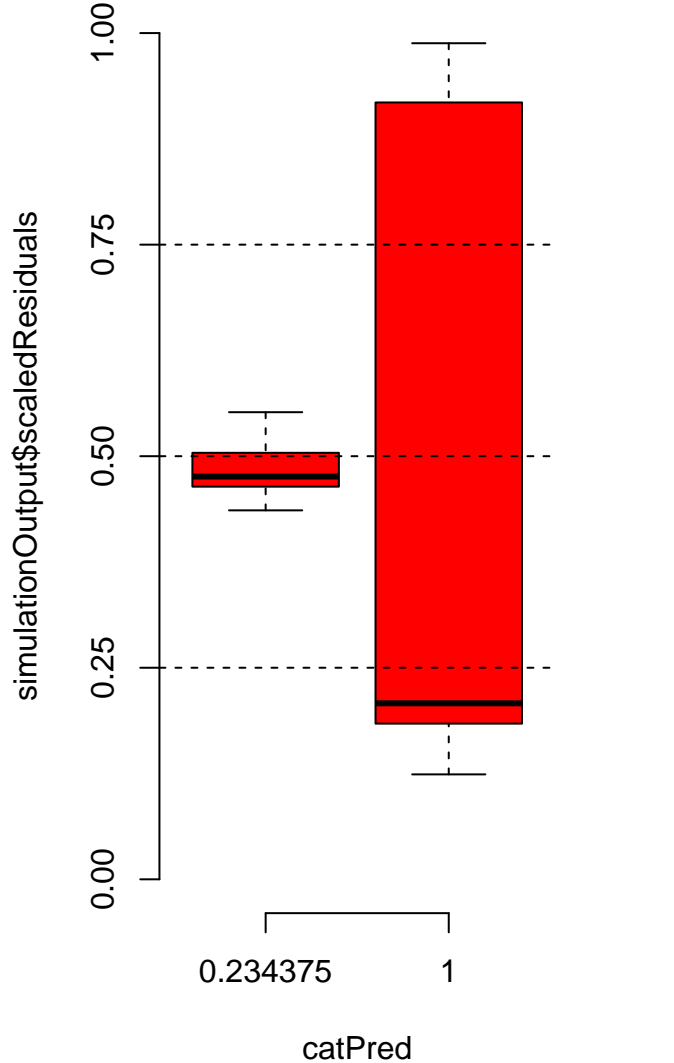
Nb LOD (included) : 33

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-24.4	-14.9	17.2	-34.4	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.390602	0.62498
day	(Intercept)	0.001495	0.03866
Residual		0.005331	0.07301

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00533

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.4251	0.1986	12.212	<2e-16 ***
inf_statusControl	-0.5755	0.3705	-1.553	0.12

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

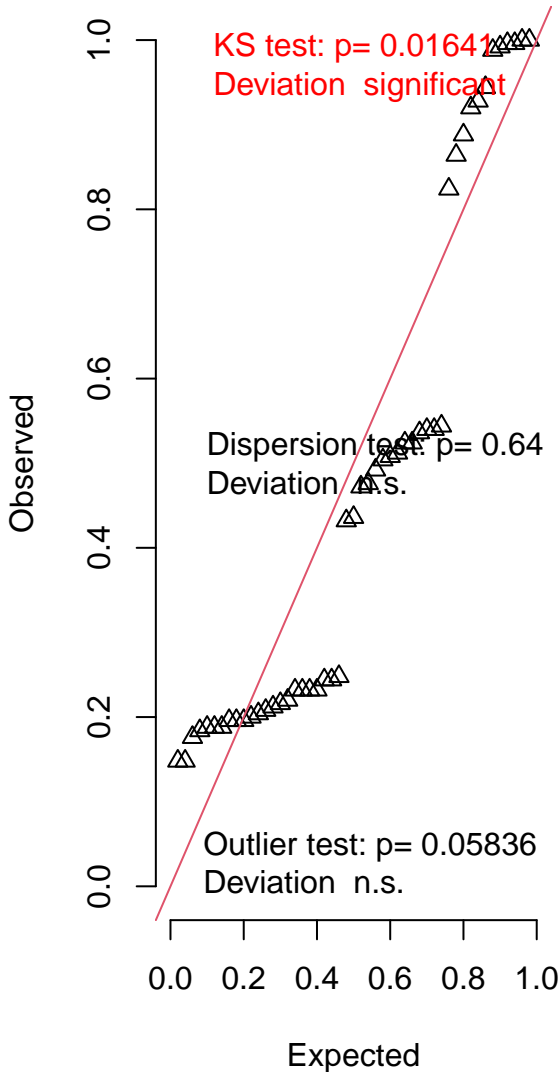
Infection in ZIKV-squirrel

Nb obs (total) : 49

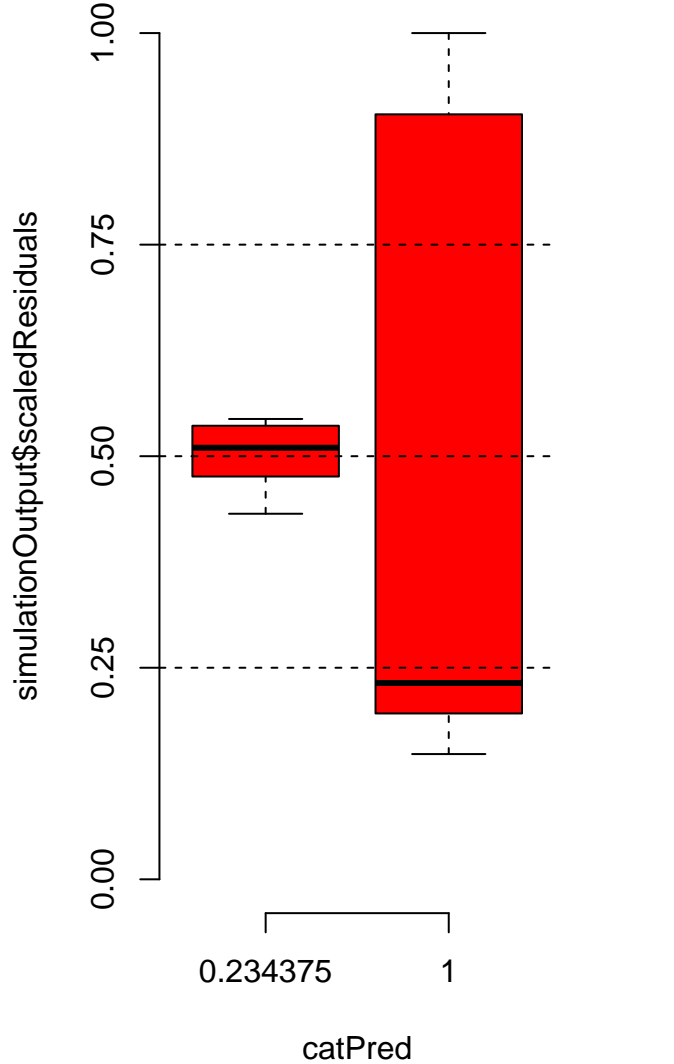
Nb LOD (included) : 37

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
49.7	59.2	-19.9	39.7	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.407269	0.63818
day	(Intercept)	0.006023	0.07761
Residual		0.045784	0.21397

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0458

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.3868	0.2072	11.518	<2e-16 ***
inf_statusControl	-0.5369	0.3837	-1.399	0.162

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

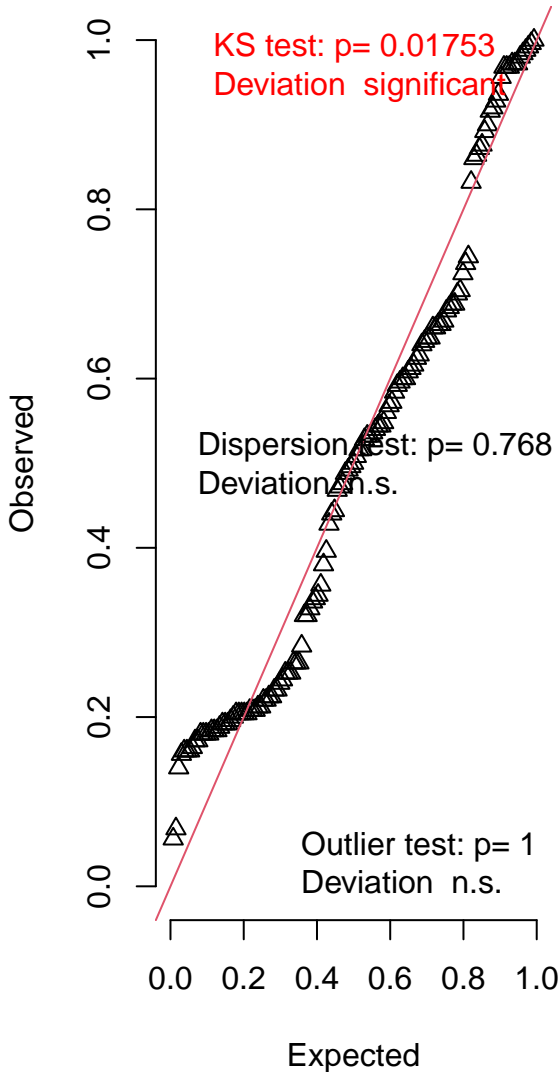
Effect of experiment

Nb obs (total) : 133

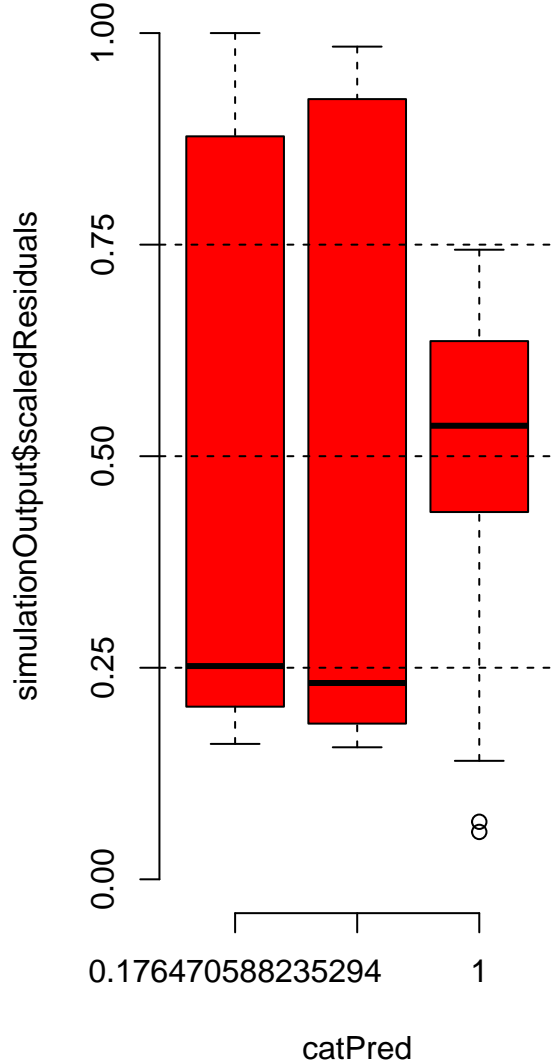
Nb LOD (included) : 44

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
63.9	81.2	-25.9	51.9	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	4.009e-01	6.332e-01
day	(Intercept)	4.222e-12	2.055e-06
Residual		3.728e-02	1.931e-01

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0373

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.42651	0.20293	11.958	<2e-16 ***
groupCyno.Dengue virus	0.40719	0.29380	1.386	0.166
groupSquirrel.Zika virus	-0.04065	0.28698	-0.142	0.887

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

I . TAC

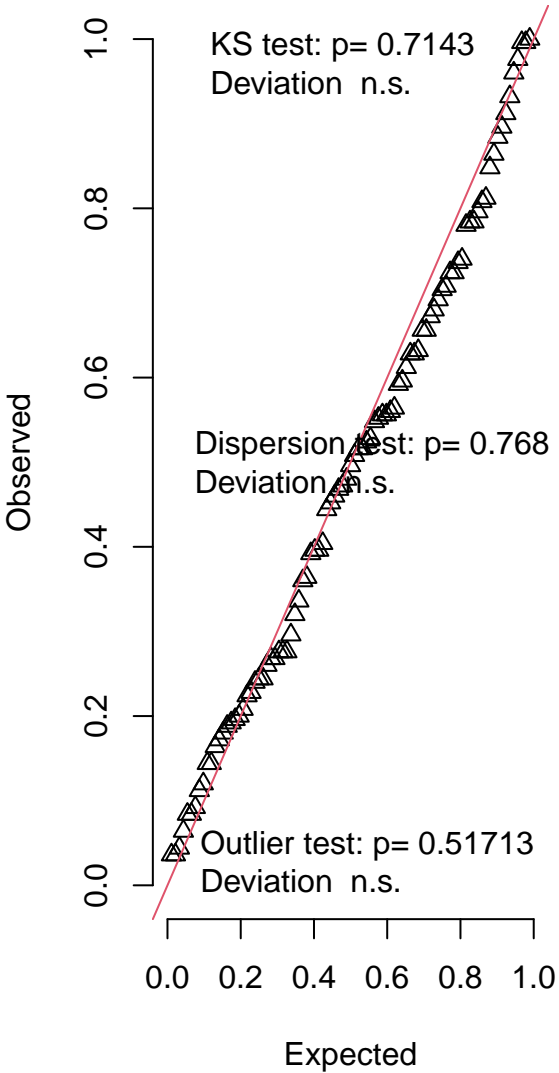
Infection in DENV-cyno

Nb obs (total): 91

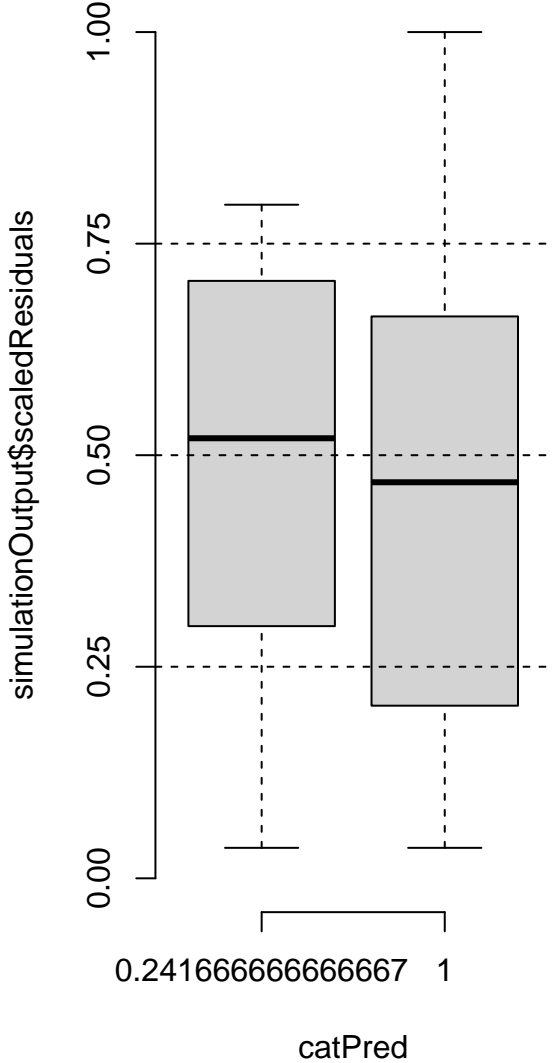
Nb LOD (included): 0

DHARMa residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.




```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-54.6	-42.0	32.3	-64.6	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	8.698e-03	9.326e-02
day	(Intercept)	6.813e-12	2.610e-06
Residual		2.405e-02	1.551e-01

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0241

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.22216	0.03672	60.52	< 2e-16 ***
inf_statusControl	-0.18251	0.06619	-2.76	0.00583 **

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

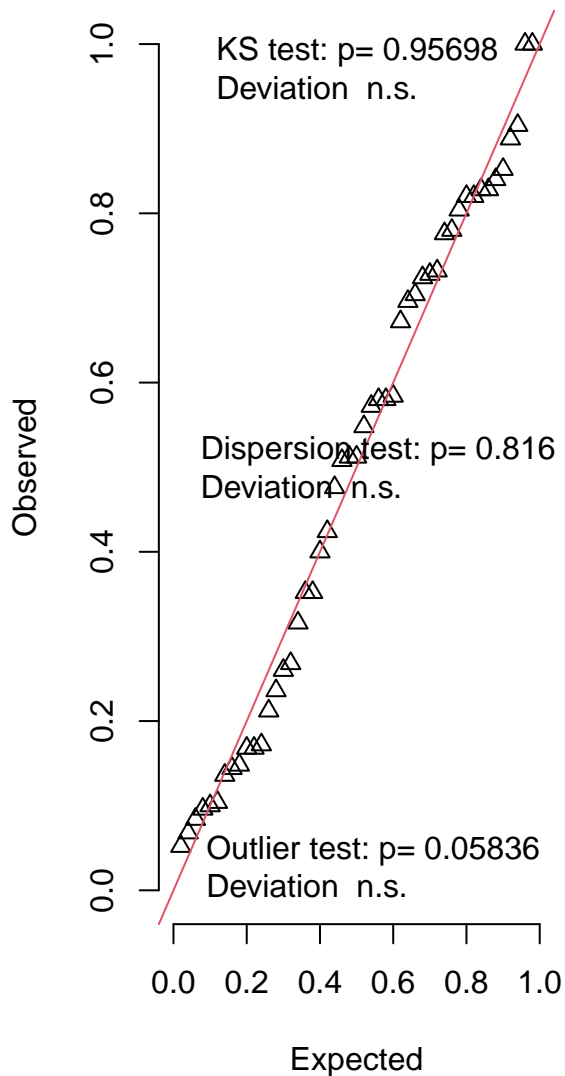
Infection in DENV-squirrel

Nb obs (total) : 49

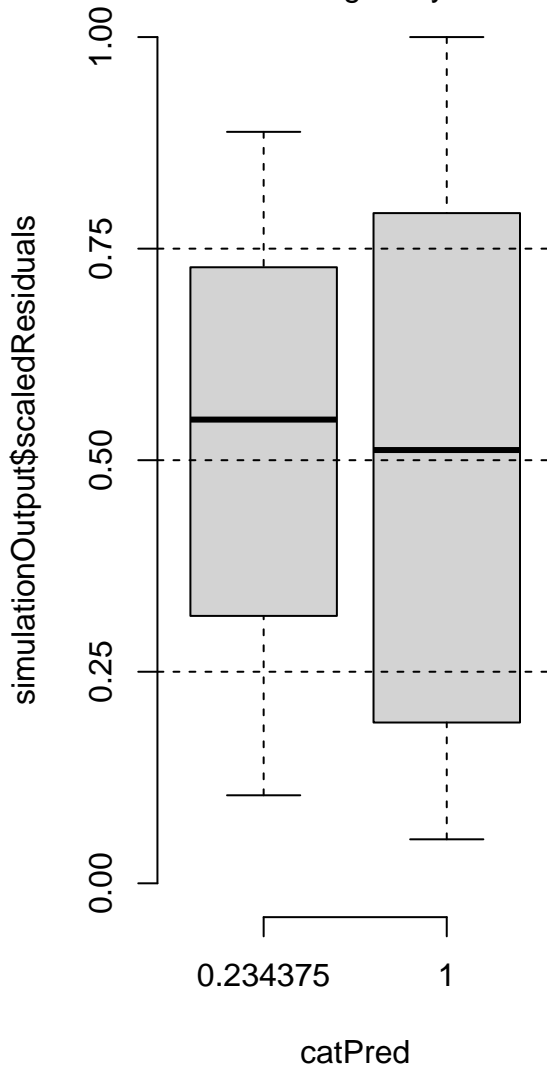
Nb LOD (included) : 7

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-68.3	-58.9	39.2	-78.3	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.005122	0.07157
day	(Intercept)	0.000226	0.01503
Residual		0.008377	0.09153

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00838

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.67176	0.02812	59.45	<2e-16 ***
inf_statusControl	-0.04285	0.05141	-0.83	0.405

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

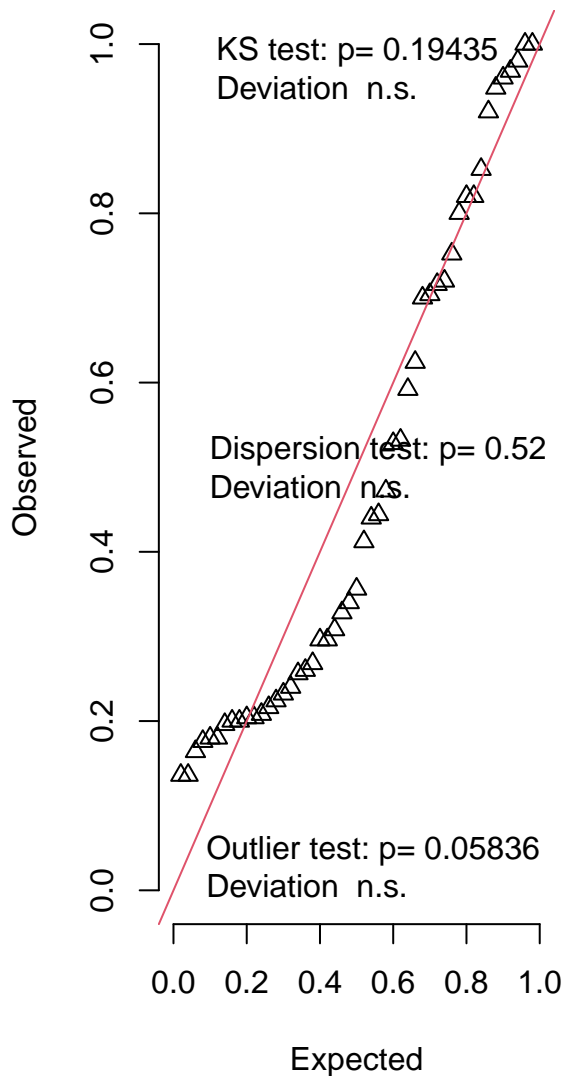
Infection in ZIKV-squirrel

Nb obs (total) : 49

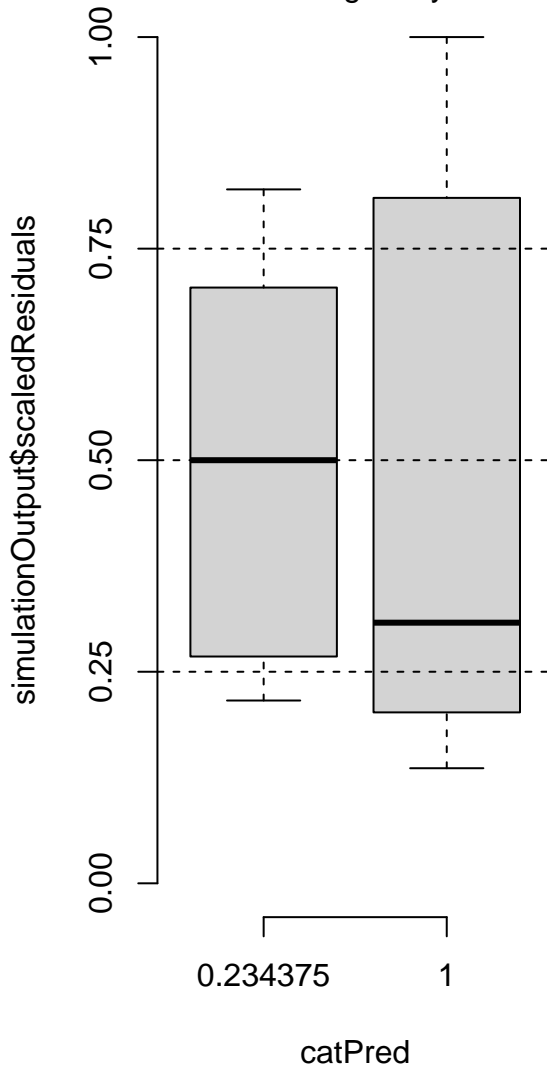
Nb LOD (included) : 15

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.




```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-57.0	-47.5	33.5	-67.0	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.009847	0.09923
day	(Intercept)	0.004683	0.06843
Residual		0.007531	0.08678

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00753

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.639635	0.043448	37.74	<2e-16 ***
inf_statusControl	-0.007063	0.064914	-0.11	0.913

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

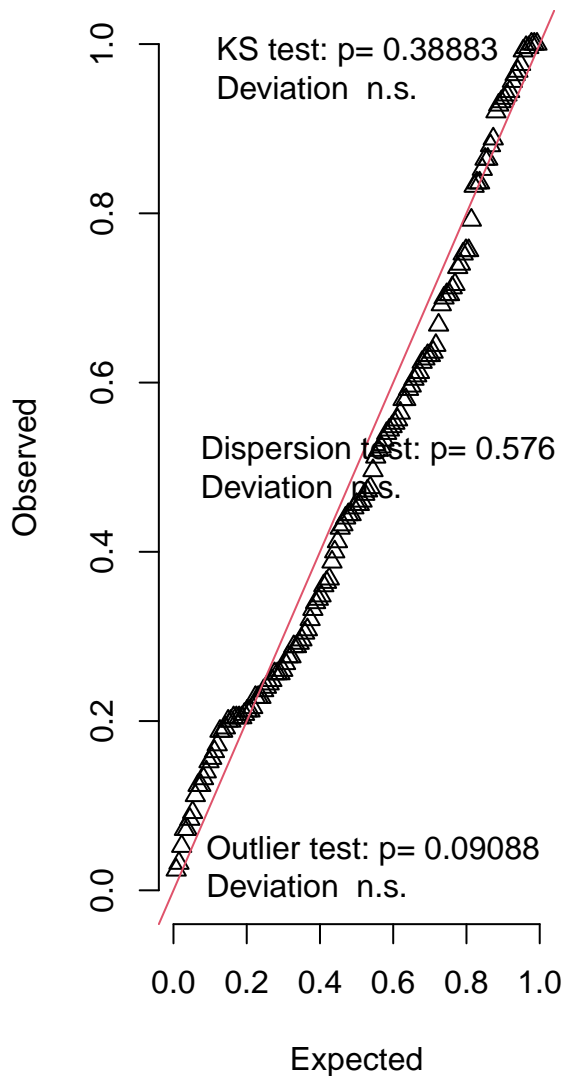
Effect of experiment

Nb obs (total): 133

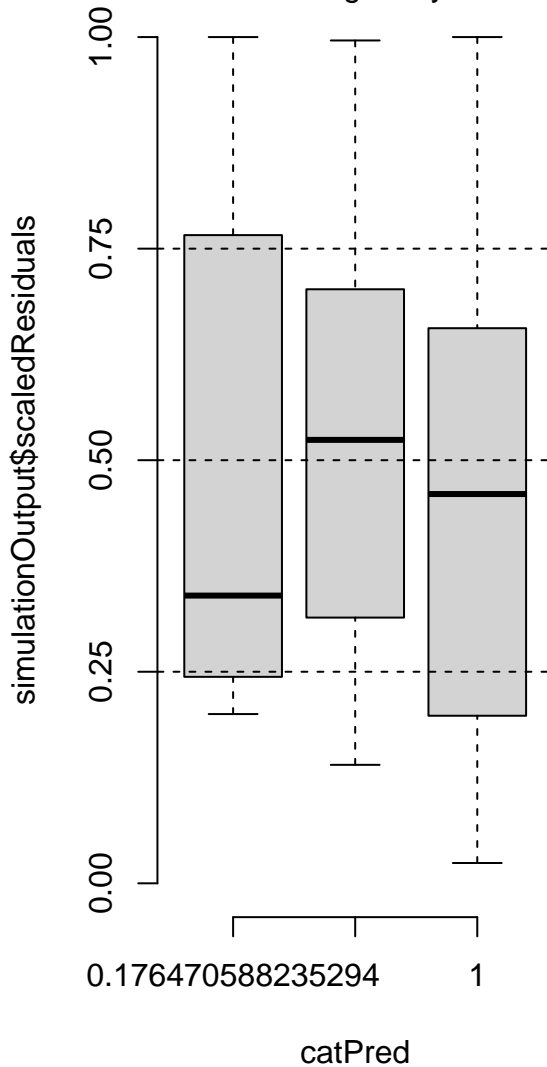
Nb LOD (included): 16

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.



Family: gaussian (identity)
Formula: log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

AIC	BIC	logLik	deviance	df.resid
-90.2	-72.9	51.1	-102.2	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.009405	0.09698
day	(Intercept)	0.001328	0.03644
Residual		0.020554	0.14337

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0206

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.67411	0.04148	40.36	<2e-16 ***
groupCyno.Dengue virus	0.54649	0.05439	10.05	<2e-16 ***
groupSquirrel.Zika virus	-0.03347	0.05542	-0.60	0.546

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

IFN.g

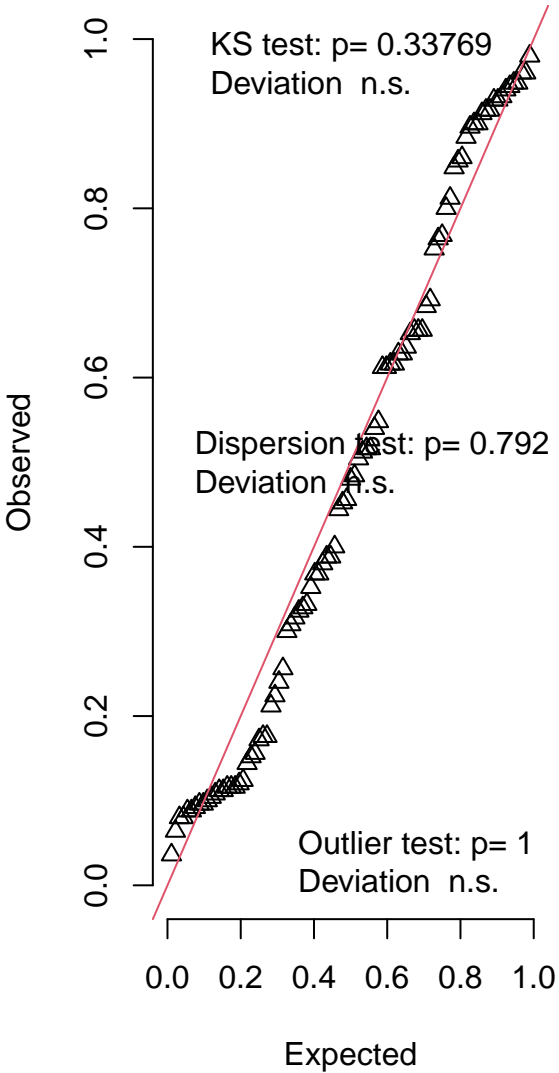
Infection in DENV-cyno

Nb obs (total) : 91

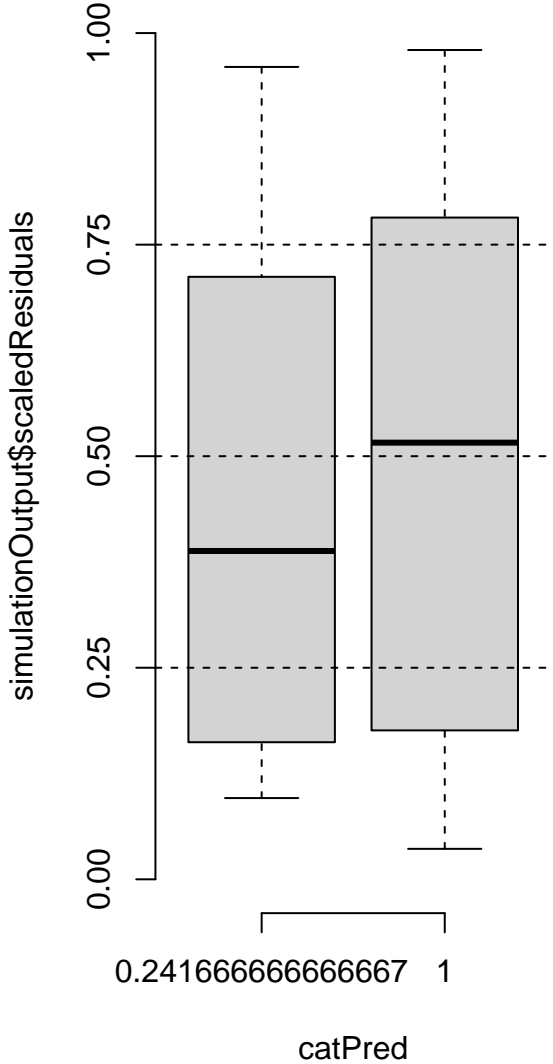
Nb LOD (included) : 20

DHARMa residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
4.8	17.3	2.6	-5.2	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.137901	0.37135
day	(Intercept)	0.005656	0.07521
Residual		0.031066	0.17625

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0311

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.7330	0.1289	13.441	<2e-16 ***
inf_statusControl	-0.1193	0.2267	-0.526	0.599

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

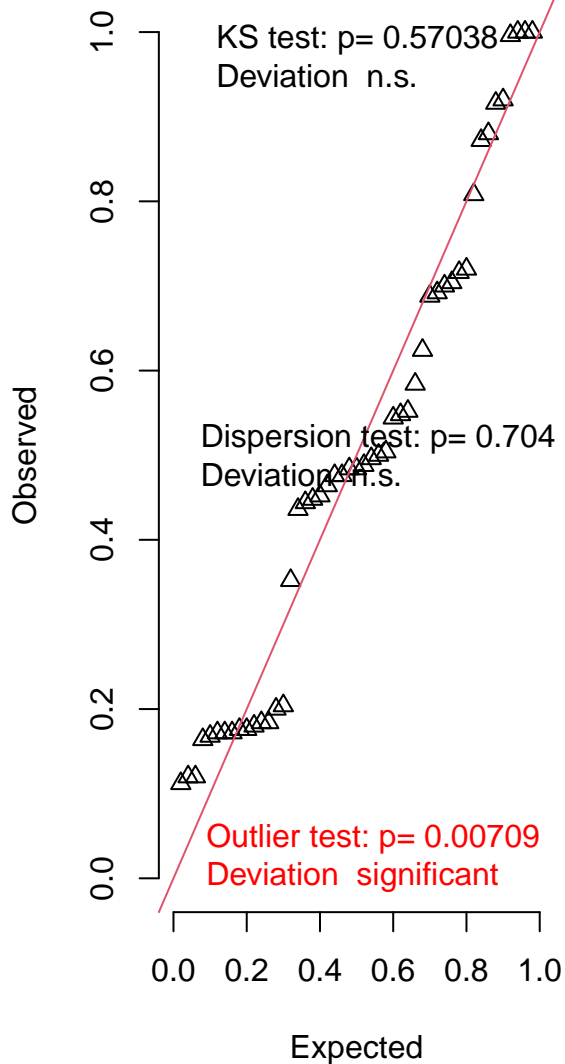
Infection in DENV-squirrel

Nb obs (total) : 49

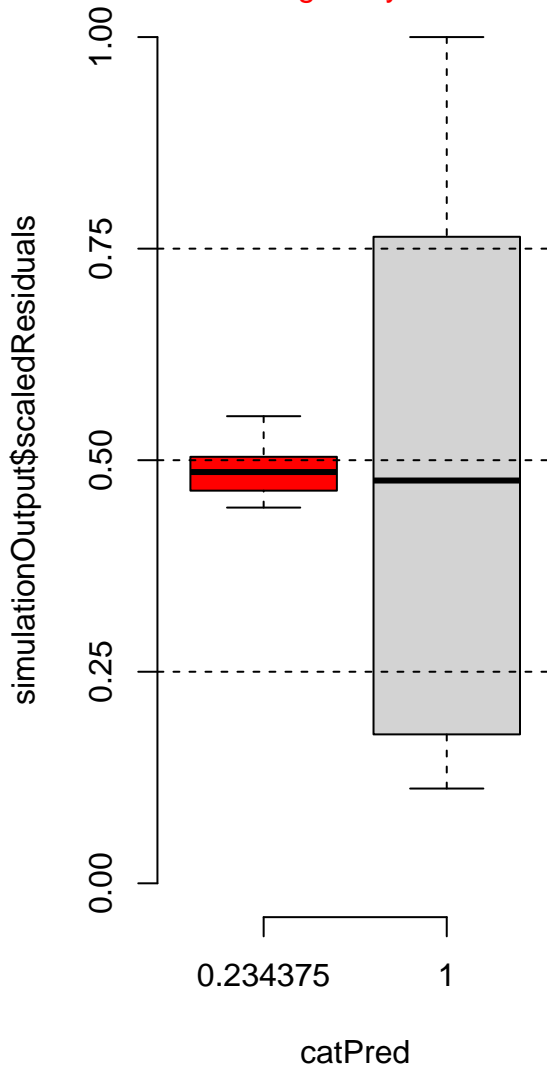
Nb LOD (included) : 29

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-16.7	-7.3	13.4	-26.7	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.5645407	0.75136
day	(Intercept)	0.0001633	0.01278
Residual		0.0065407	0.08087

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00654

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.9394	0.2381	8.147	3.73e-16 ***
inf_statusControl	-0.7510	0.4453	-1.687	0.0917 .

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

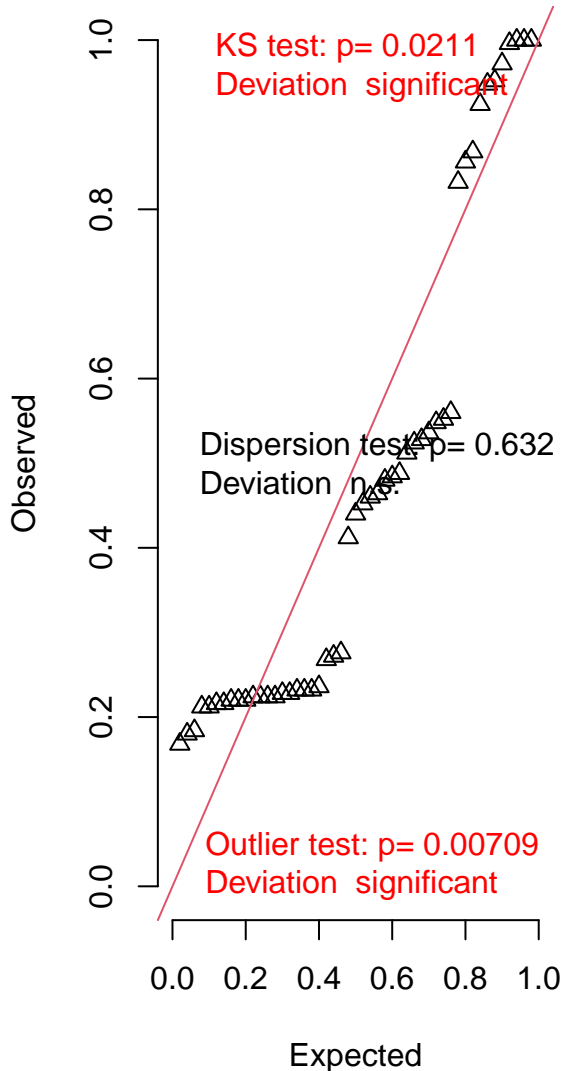
Infection in ZIKV-squirrel

Nb obs (total) : 49

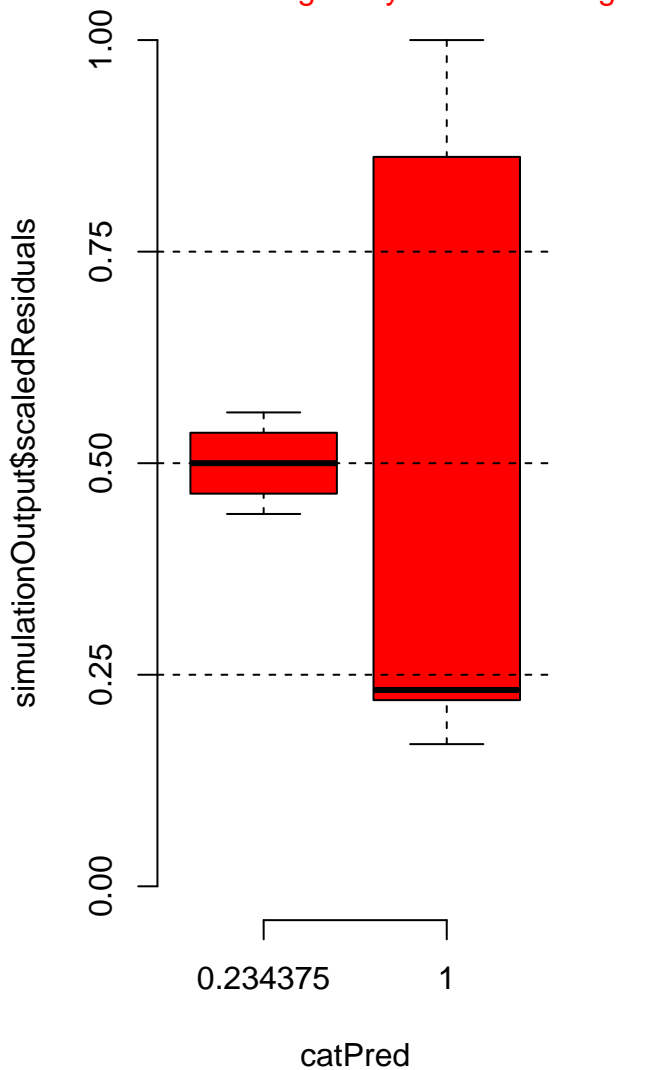
Nb LOD (included) : 37

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-28.4	-18.9	19.2	-38.4	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.480729	0.69335
day	(Intercept)	0.001180	0.03435
Residual		0.004398	0.06631

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0044

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.7122	0.2199	7.785	6.98e-15 ***
inf_statusControl	-0.5237	0.4107	-1.275	0.202

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

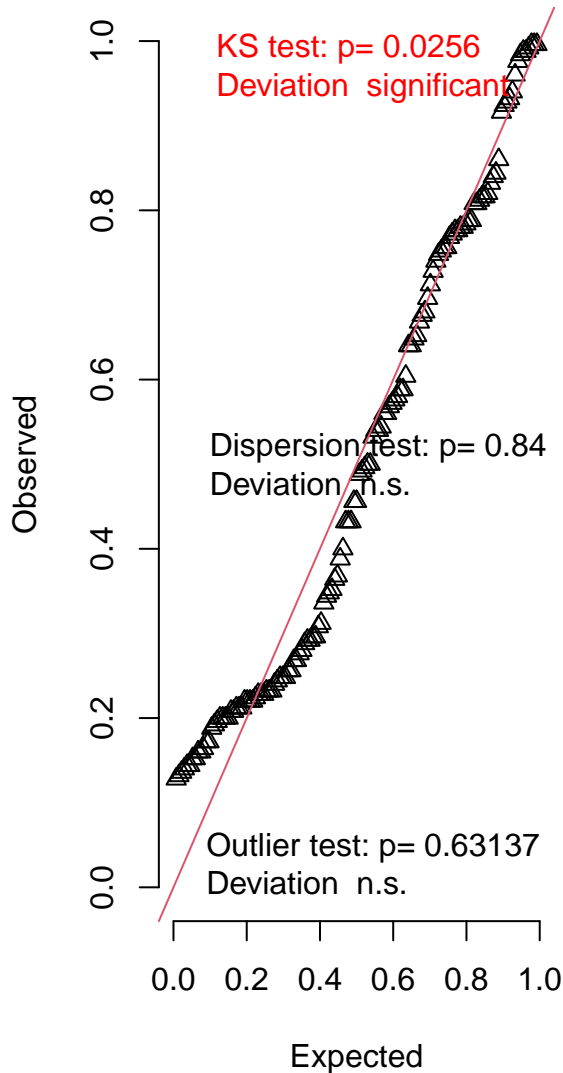
Effect of experiment

Nb obs (total) : 133

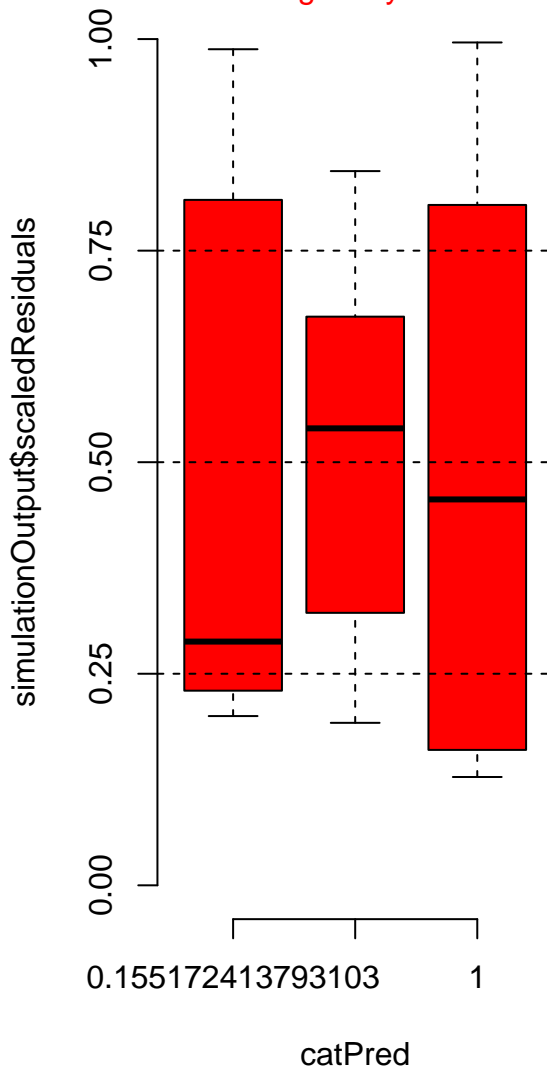
Nb LOD (included) : 52

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
16.9	34.3	-2.5	4.9	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.463e-01	0.739094
day	(Intercept)	7.806e-06	0.002794
Residual		2.185e-02	0.147806

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0218

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.9402	0.2351	8.253	<2e-16 ***
groupCyno.Dengue virus	-0.2073	0.3410	-0.608	0.543
groupSquirrel.Zika virus	-0.2278	0.3325	-0.685	0.493

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

IL.10

Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 91

IL.10 ERROR : valeurs infinies ou manquantes dans 'x'

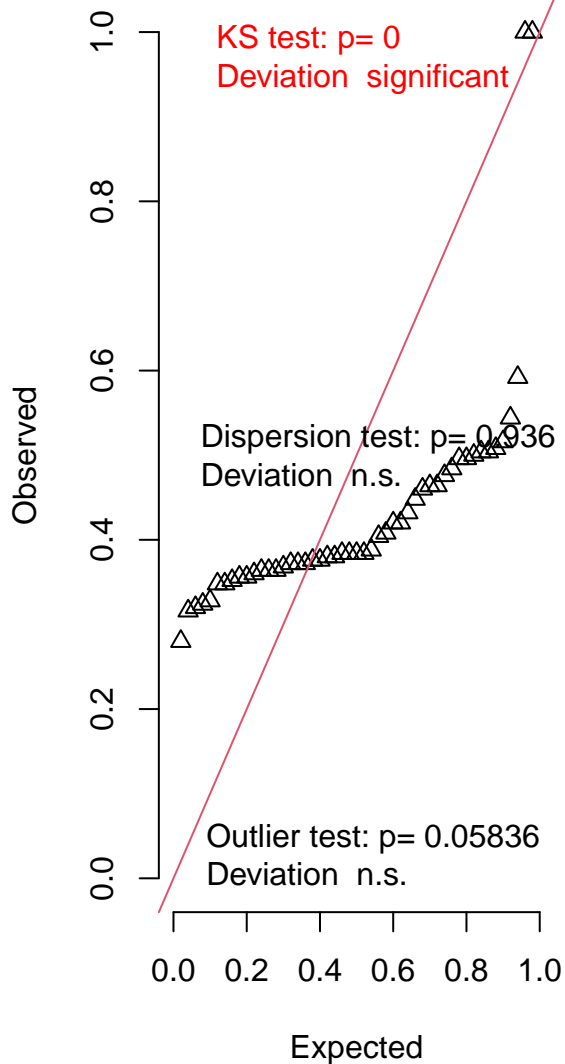
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 46

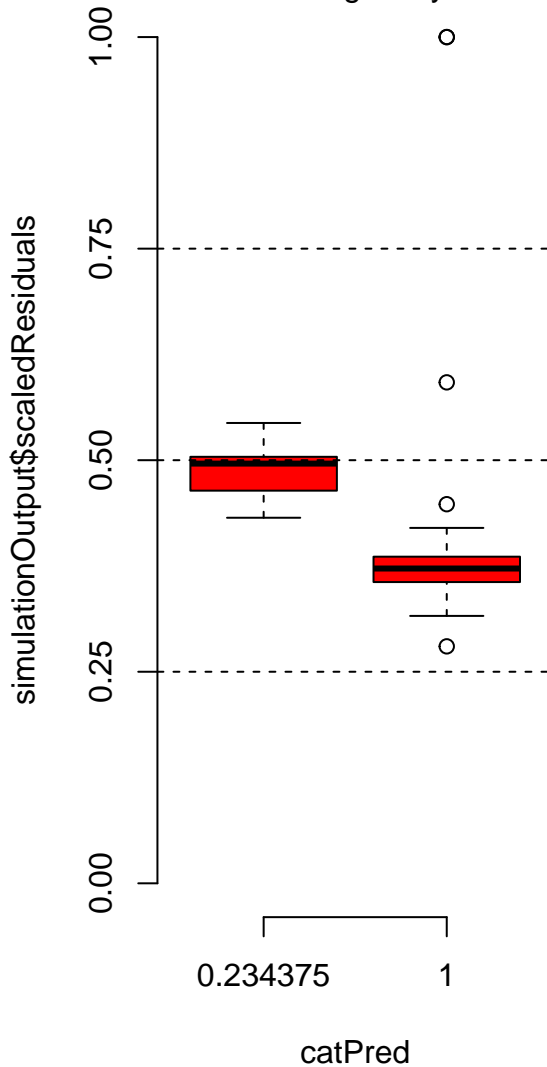
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-204.9	-195.4	107.4	-214.9	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.088e-04	0.022556
day	(Intercept)	3.931e-06	0.001983
Residual		4.626e-04	0.021508

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000463

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.143003	0.008057	141.9	<2e-16 ***
inf_statusControl	-0.010434	0.015004	-0.7	0.487

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

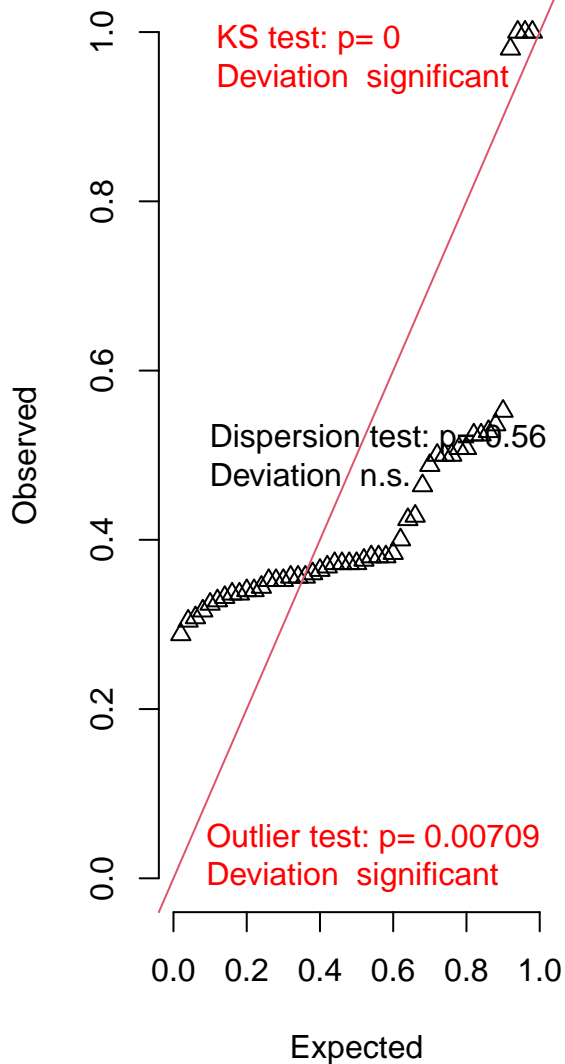
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 45

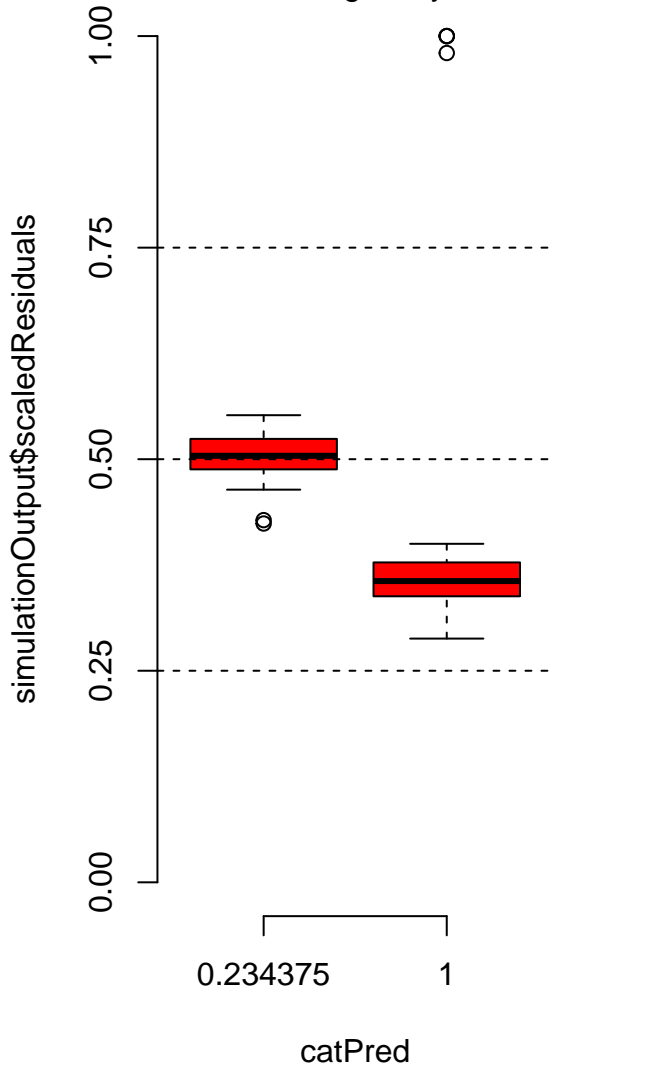
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-33.6	-24.1	21.8	-43.6	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.197e-02	2.280e-01
day	(Intercept)	1.633e-10	1.278e-05
Residual		1.052e-02	1.026e-01

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0105

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.22519	0.07419	16.514	<2e-16 ***
inf_statusControl	-0.09261	0.13879	-0.667	0.505

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

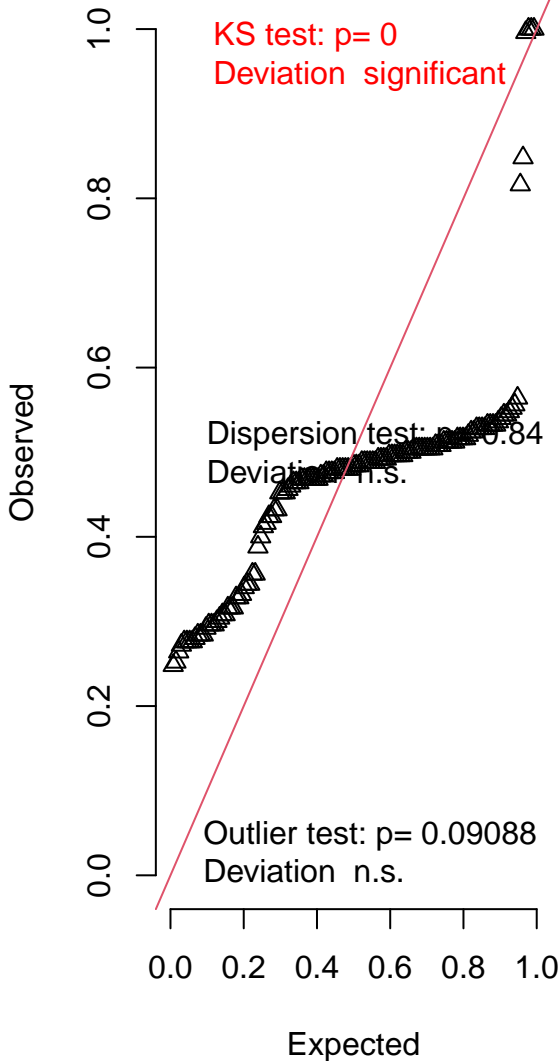
Effect of experiment

Nb obs (total) : 133

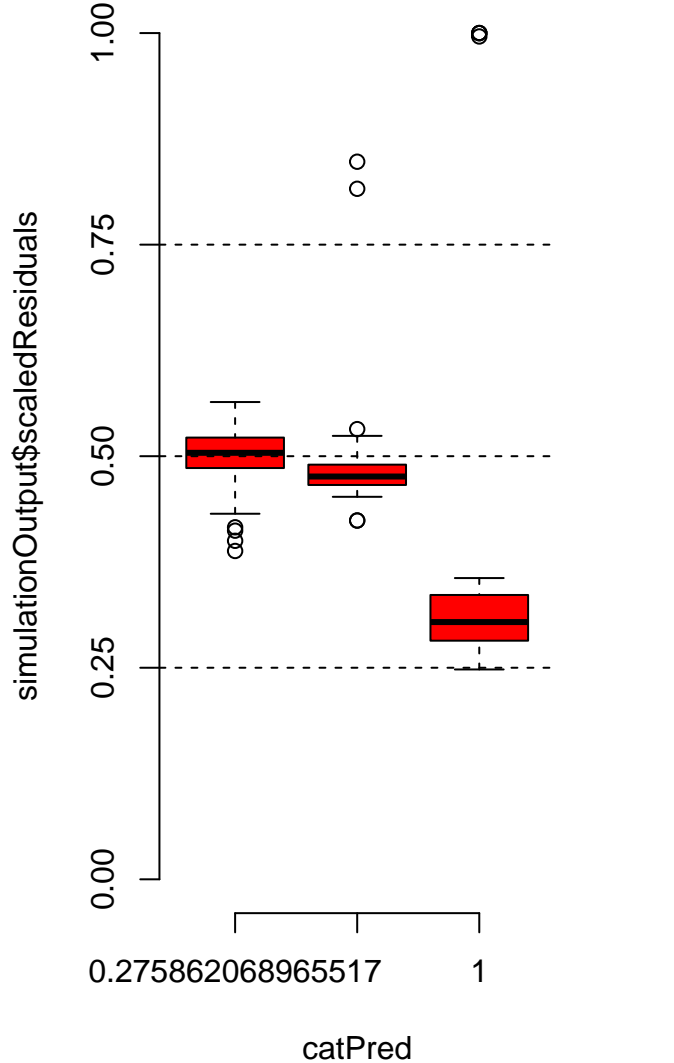
Nb LOD (included) : 126

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-255.7	-238.3	133.8	-267.7	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.554e-02	1.598e-01
day	(Intercept)	8.677e-10	2.946e-05
Residual		3.707e-03	6.089e-02

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00371

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.14327	0.05159	22.159	<2e-16 ***
groupCyno.Dengue virus	-0.01069	0.07456	-0.143	0.886
groupSquirrel.Zika virus	0.08172	0.07297	1.120	0.263

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

IL.12

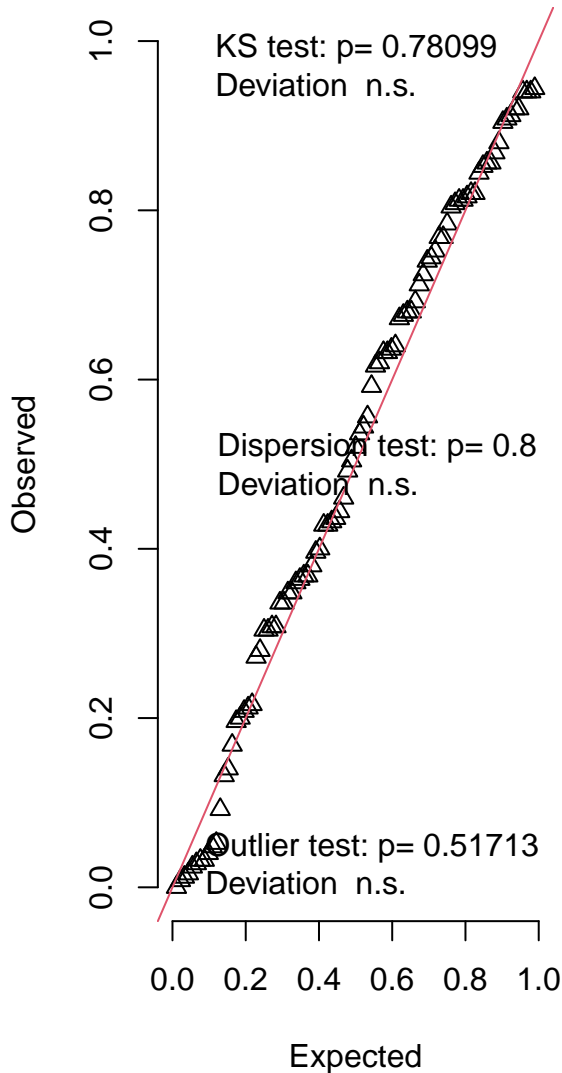
Infection in DENV-cyno

Nb obs (total) : 91

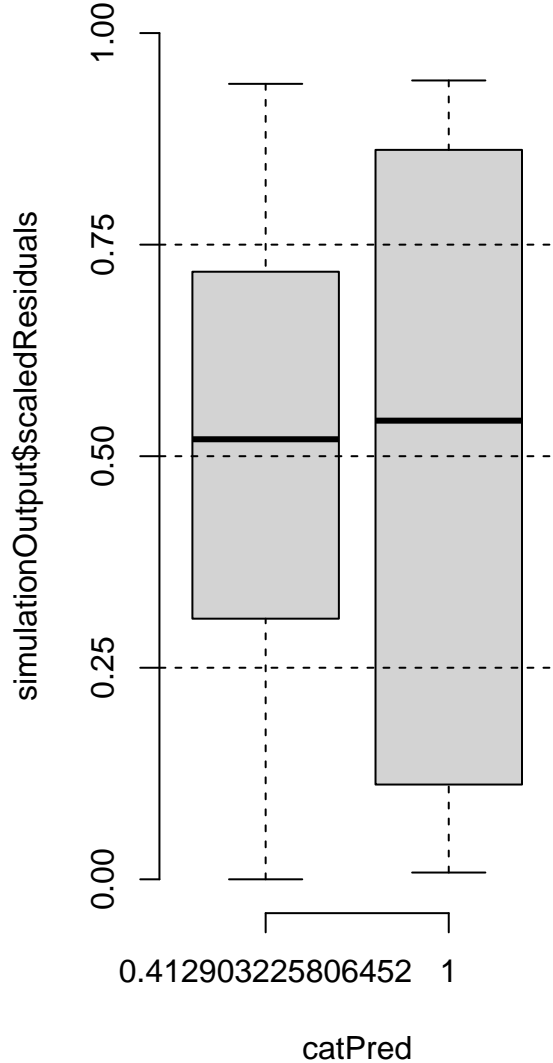
Nb LOD (included) : 1

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-81.8	-69.3	45.9	-91.8	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.079233	0.2815
day	(Intercept)	0.002777	0.0527
Residual		0.011049	0.1051

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.011

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.99122	0.09683	30.892	<2e-16 ***
inf_statusControl	0.14651	0.17083	0.858	0.391

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

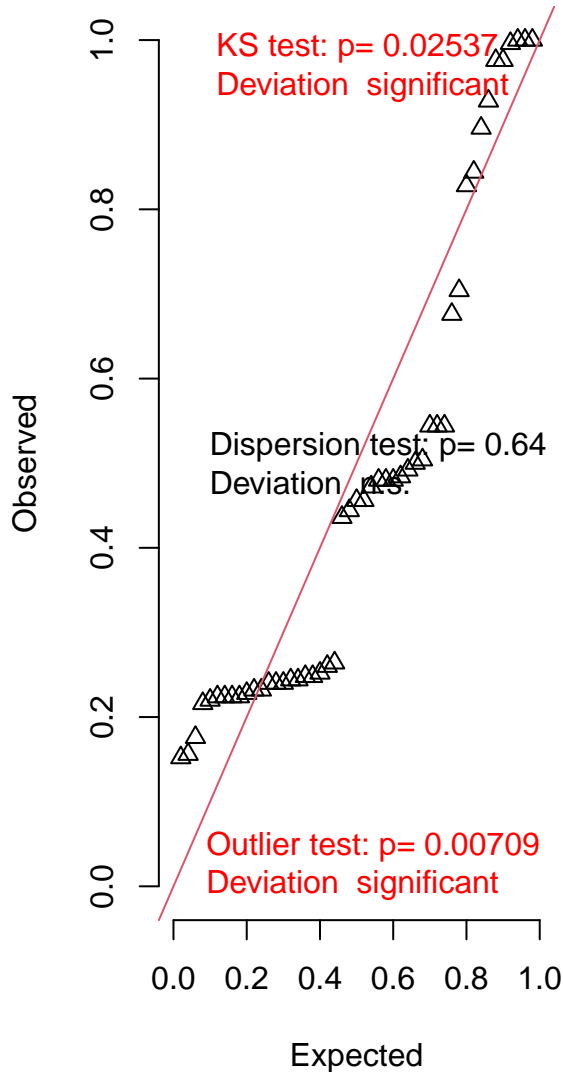
Infection in DENV-squirrel

Nb obs (total) : 49

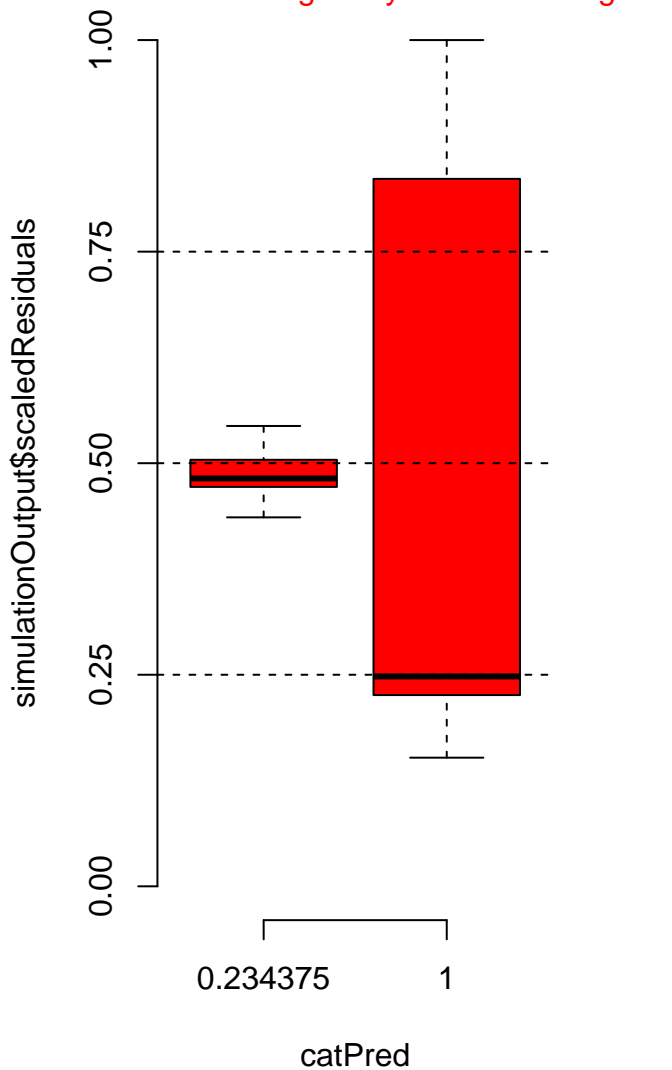
Nb LOD (included) : 36

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-28.5	-19.1	19.3	-38.5	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.783e-01	4.223e-01
day	(Intercept)	8.205e-12	2.864e-06
Residual		7.550e-03	8.689e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00755

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.3655	0.1344	17.61	<2e-16 ***
inf_statusControl	-0.3216	0.2513	-1.28	0.201

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

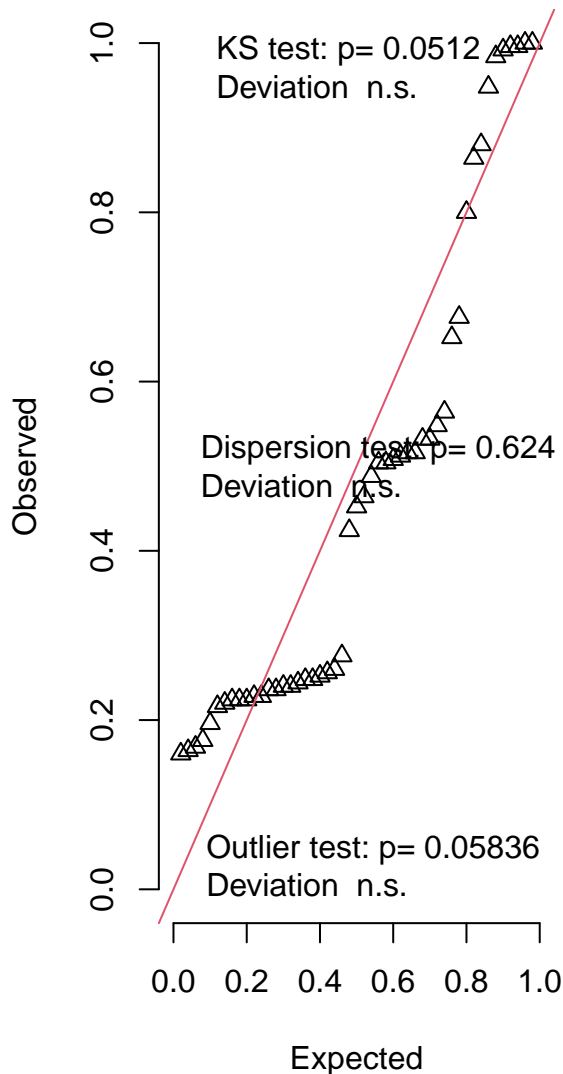
Infection in ZIKV-squirrel

Nb obs (total) : 49

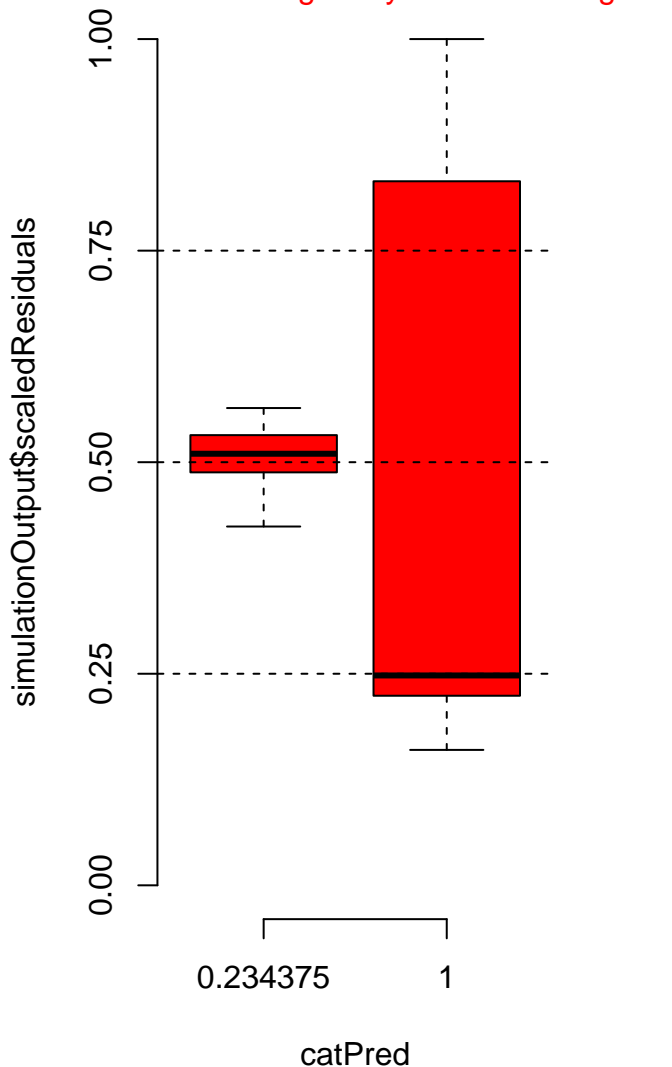
Nb LOD (included) : 37

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-5.5	3.9	7.8	-15.5	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.142950	0.37809
day	(Intercept)	0.002639	0.05137
Residual		0.013988	0.11827

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.014

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.3446	0.1228	19.088	<2e-16 ***
inf_statusControl	-0.3001	0.2268	-1.323	0.186

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

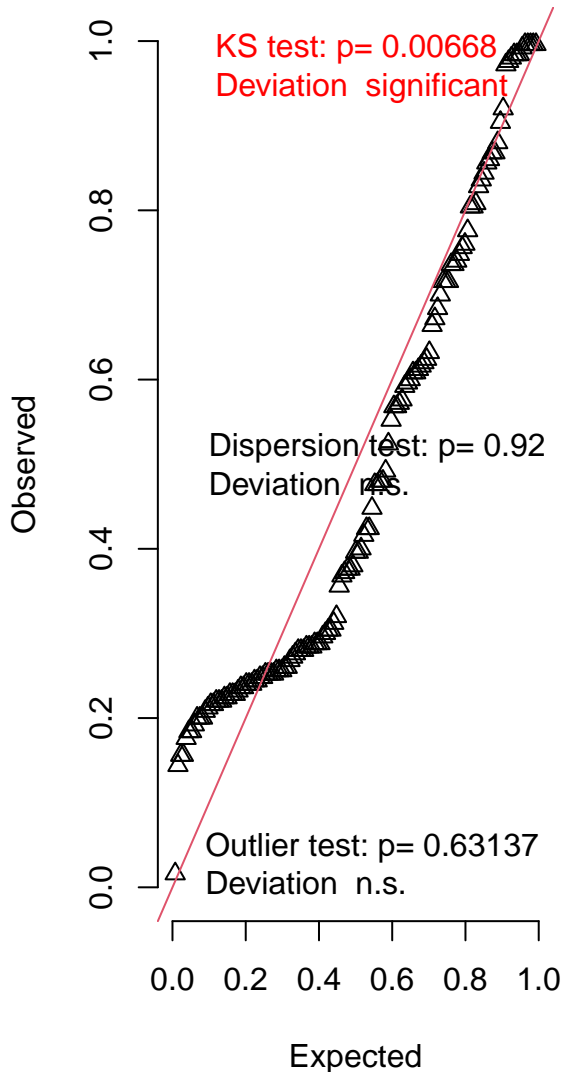
Effect of experiment

Nb obs (total) : 133

Nb LOD (included) : 46

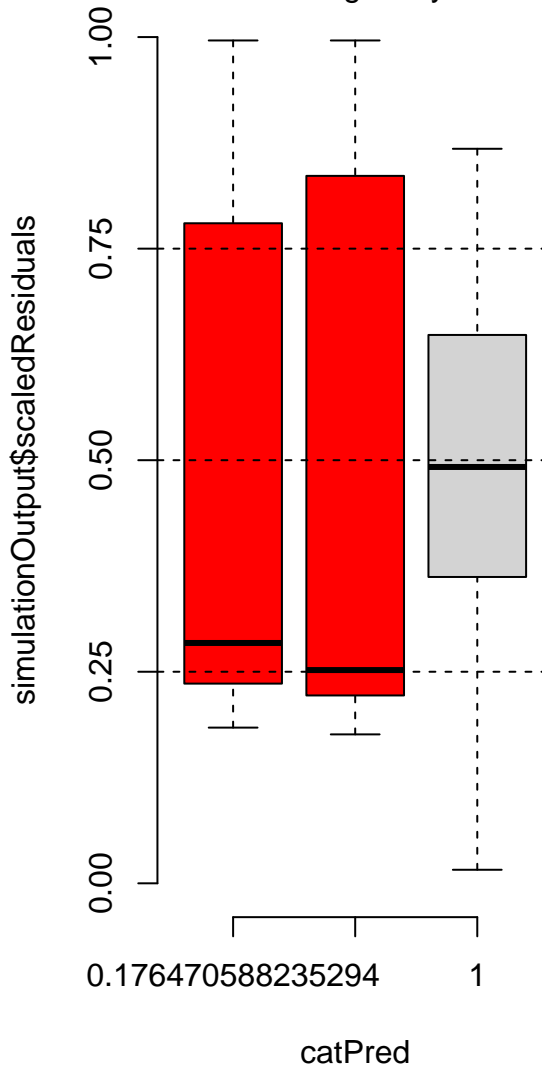
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-46.2	-28.9	29.1	-58.2	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.701e-01	4.125e-01
day	(Intercept)	2.501e-12	1.581e-06
Residual		1.643e-02	1.282e-01

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0164

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.36618	0.13226	17.890	<2e-16 ***
groupCyno.Dengue virus	0.62504	0.19146	3.265	0.0011 **
groupSquirrel.Zika virus	-0.02221	0.18705	-0.119	0.9055

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

IL.15

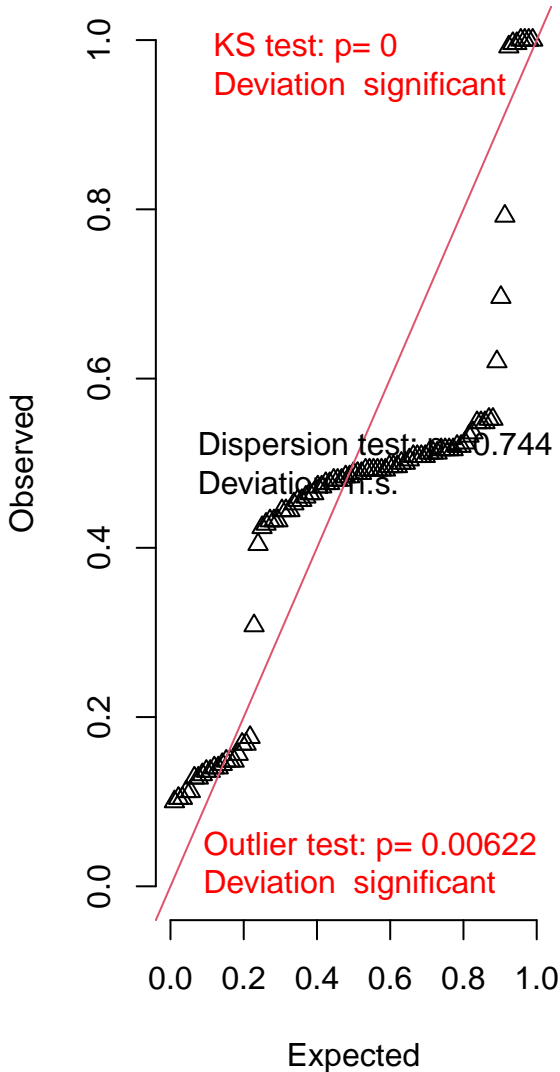
Infection in DENV-cyno

Nb obs (total) : 91

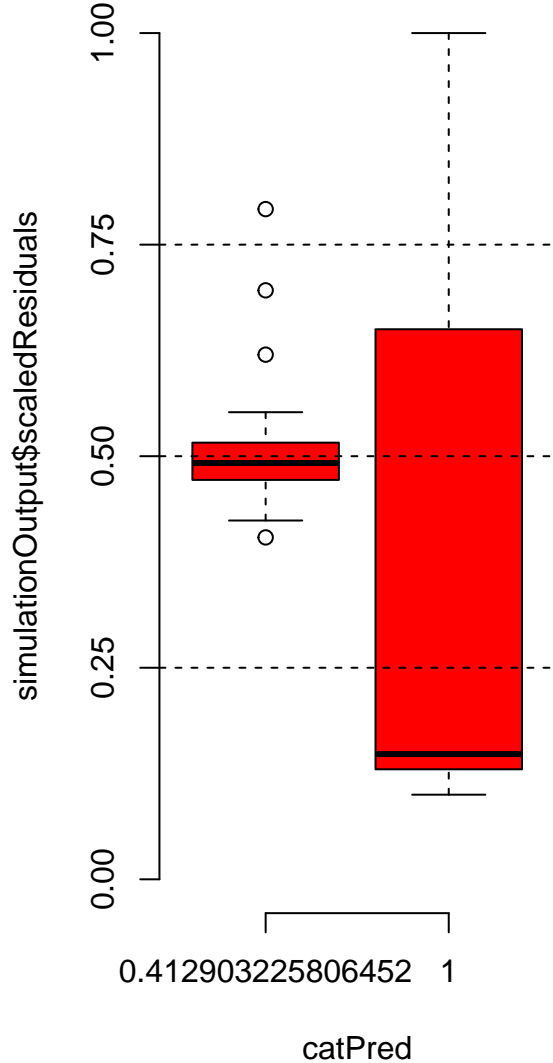
Nb LOD (included) : 80

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-31.6	-19.1	20.8	-41.6	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	4.881e-02	2.209e-01
day	(Intercept)	1.243e-12	1.115e-06
Residual		2.529e-02	1.590e-01

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0253

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.88536	0.07632	24.704	<2e-16 ***
inf_statusControl	0.27961	0.13759	2.032	0.0421 *

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

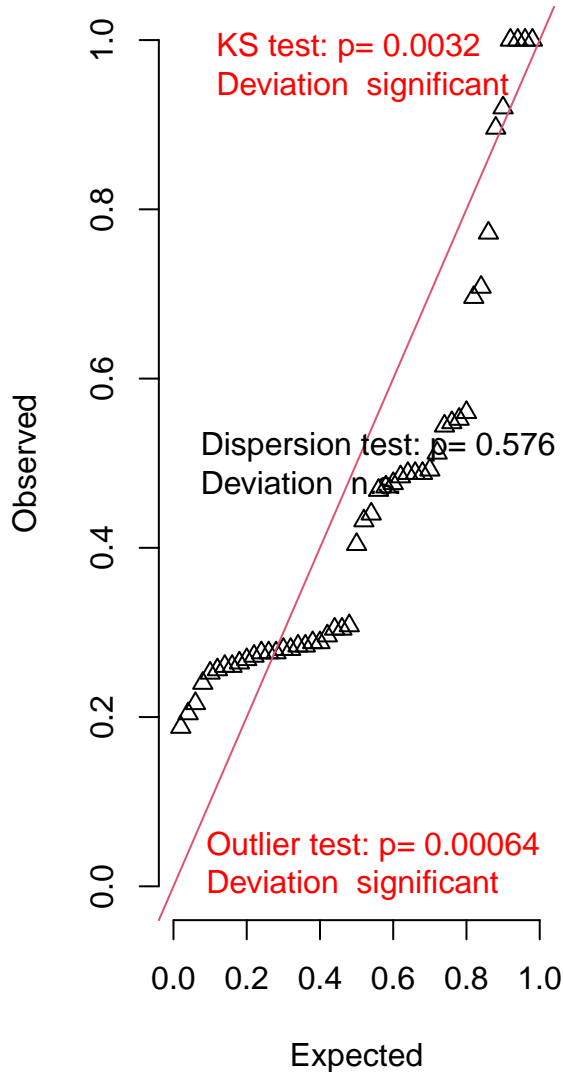
Infection in DENV-squirrel

Nb obs (total) : 49

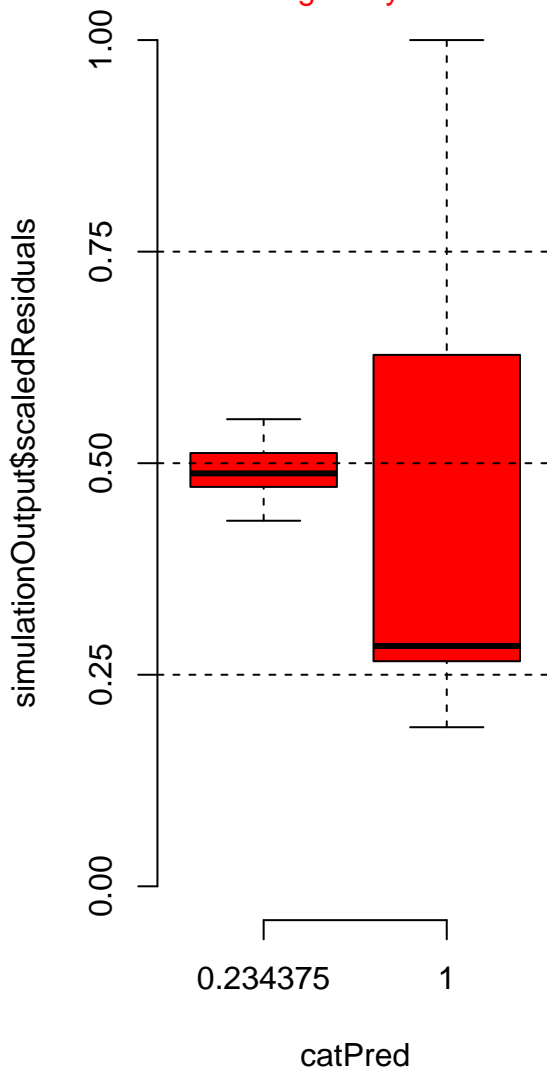
Nb LOD (included) : 38

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
0.4	9.9	4.8	-9.6	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.208886	0.4570
day	(Intercept)	0.000713	0.0267
Residual		0.015505	0.1245

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0155

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.1702	0.1464	14.820	<2e-16 ***
inf_statusControl	-0.2891	0.2733	-1.058	0.29

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

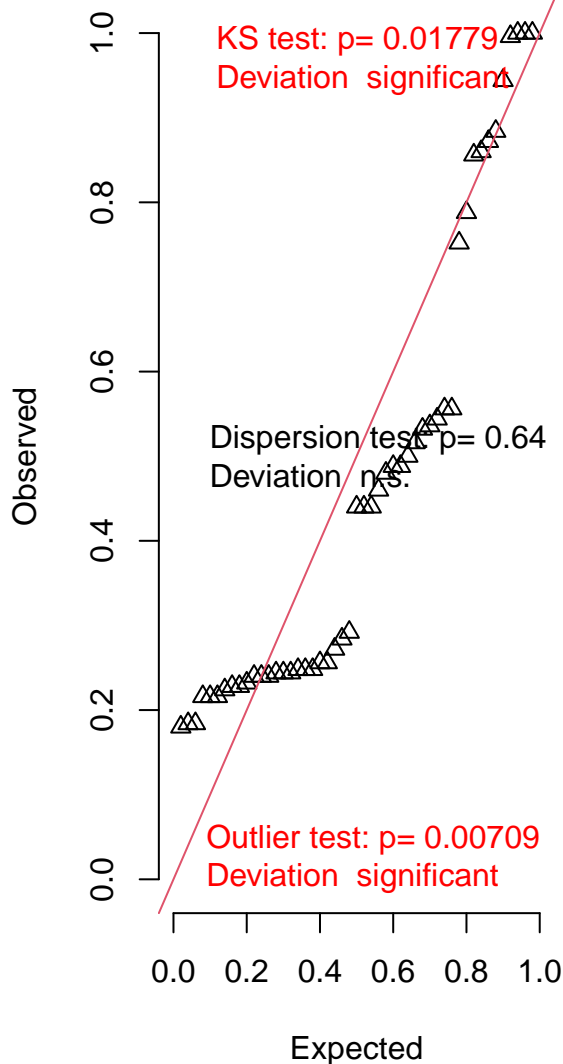
Infection in ZIKV-squirrel

Nb obs (total) : 49

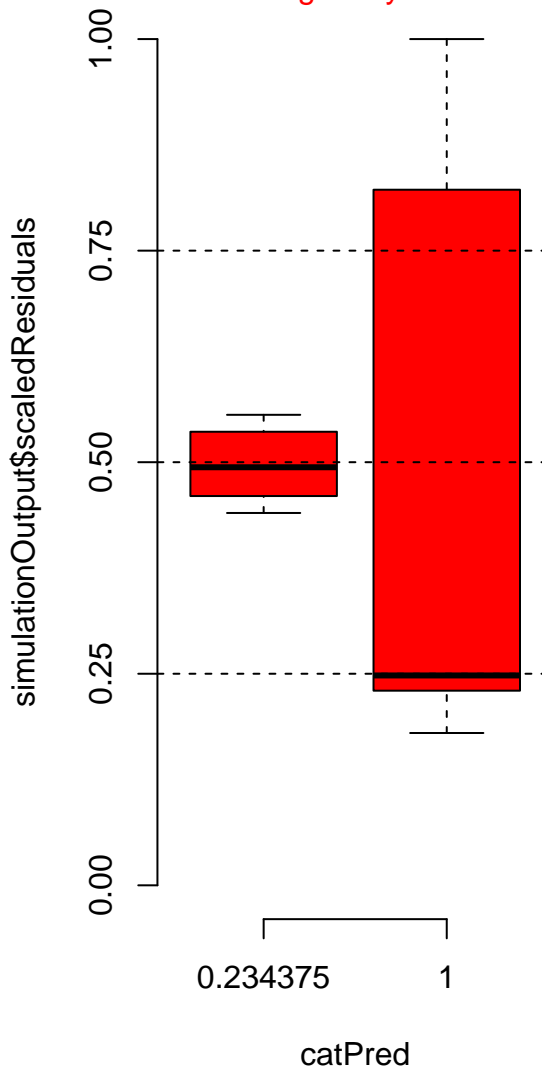
Nb LOD (included) : 38

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-44.0	-34.5	27.0	-54.0	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.1959924	0.44271
day	(Intercept)	0.0003778	0.01944
Residual		0.0043795	0.06618

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00438

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.1971	0.1406	15.621	<2e-16 ***
inf_statusControl	-0.3160	0.2628	-1.203	0.229

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

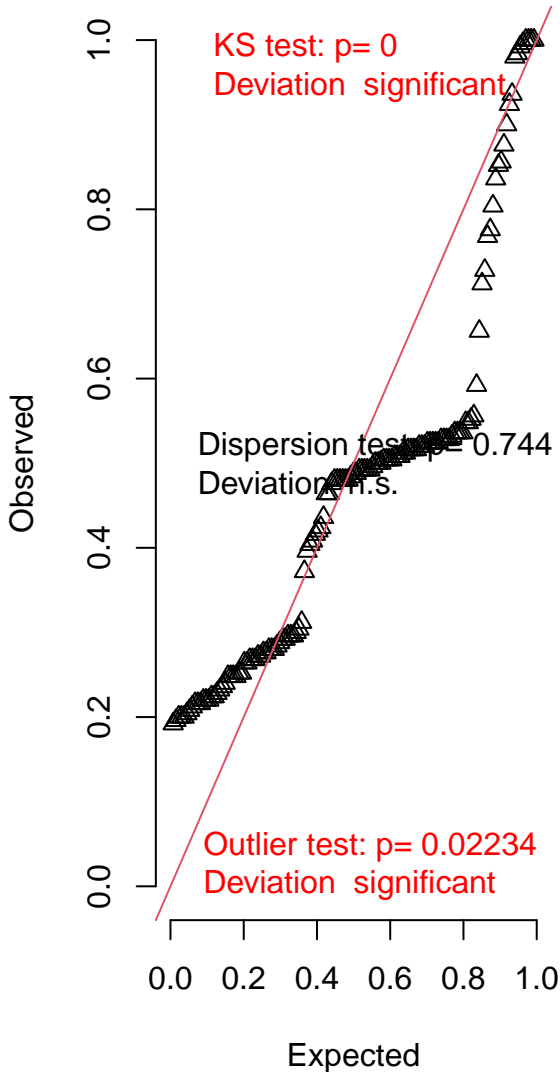
Effect of experiment

Nb obs (total) : 133

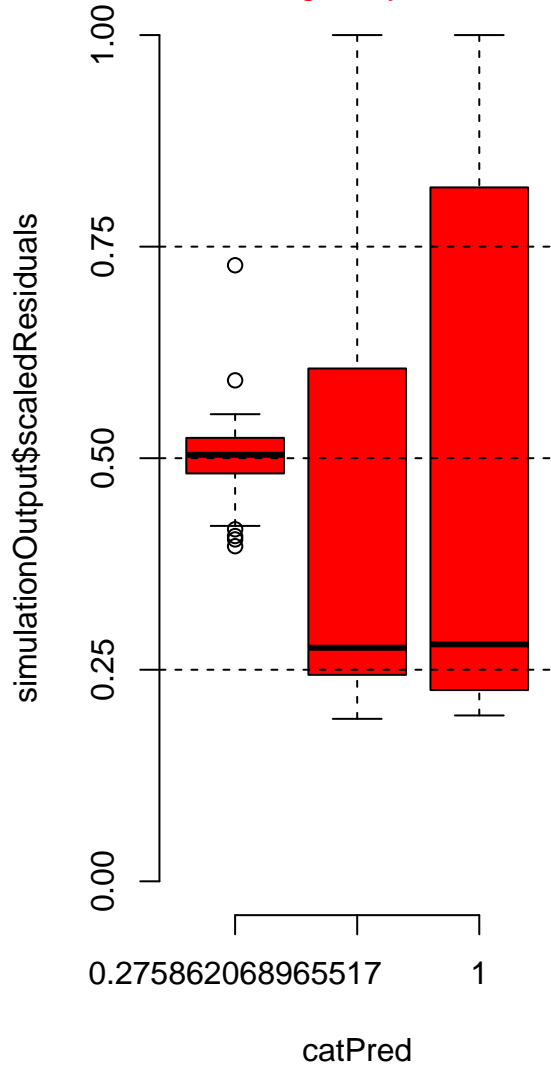
Nb LOD (included) : 108

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-121.7	-104.3	66.8	-133.7	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.957e-01	4.424e-01
day	(Intercept)	2.078e-12	1.442e-06
Residual		7.675e-03	8.761e-02

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00768

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.16983	0.14069	15.423	<2e-16 ***
groupCyno.Dengue virus	-0.28447	0.20410	-1.394	0.163
groupSquirrel.Zika virus	0.02731	0.19896	0.137	0.891

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

IL.17

Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 91

IL.17 ERROR : valeurs infinies ou manquantes dans 'x'

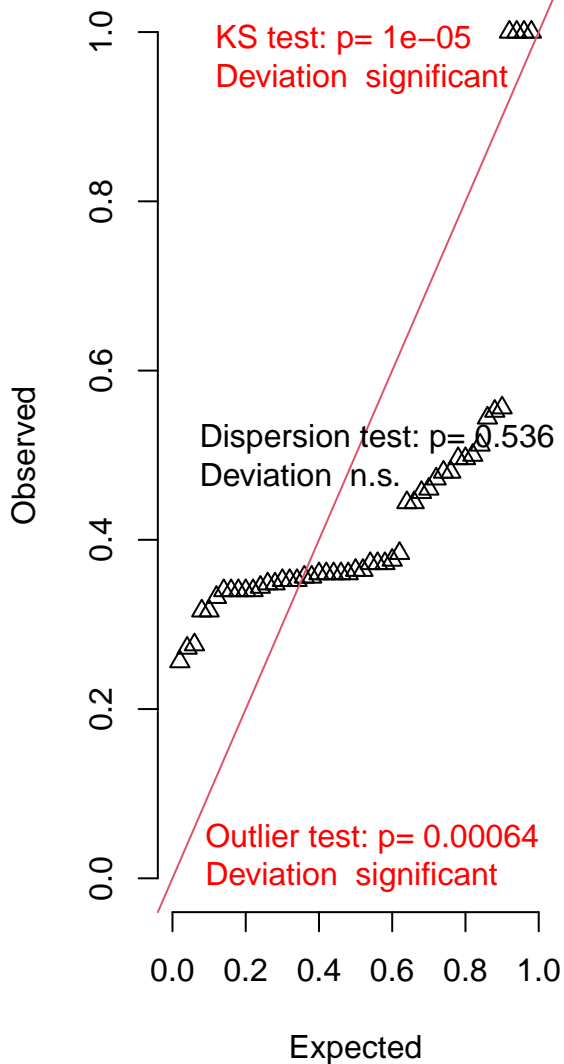
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 45

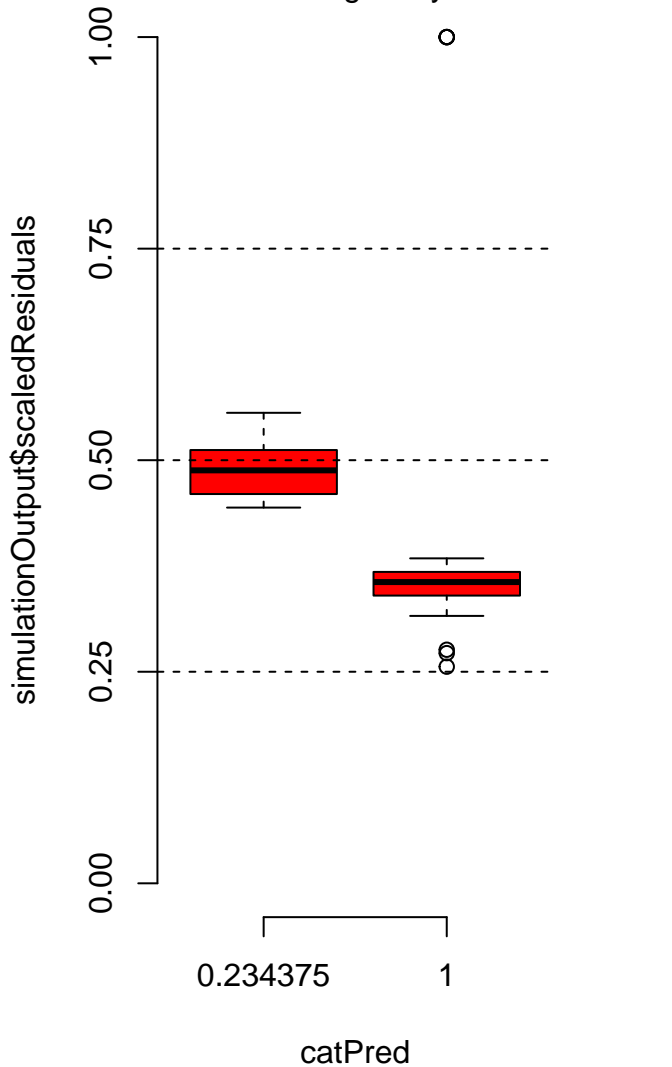
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-204.2	-194.7	107.1	-214.2	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.027e-02	1.013e-01
day	(Intercept)	1.598e-10	1.264e-05
Residual		1.569e-04	1.252e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000157

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.53588	0.03212	47.82	<2e-16 ***
inf_statusControl	-0.04006	0.06009	-0.67	0.505

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

Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 49

IL.17 ERROR : valeurs infinies ou manquantes dans 'x'

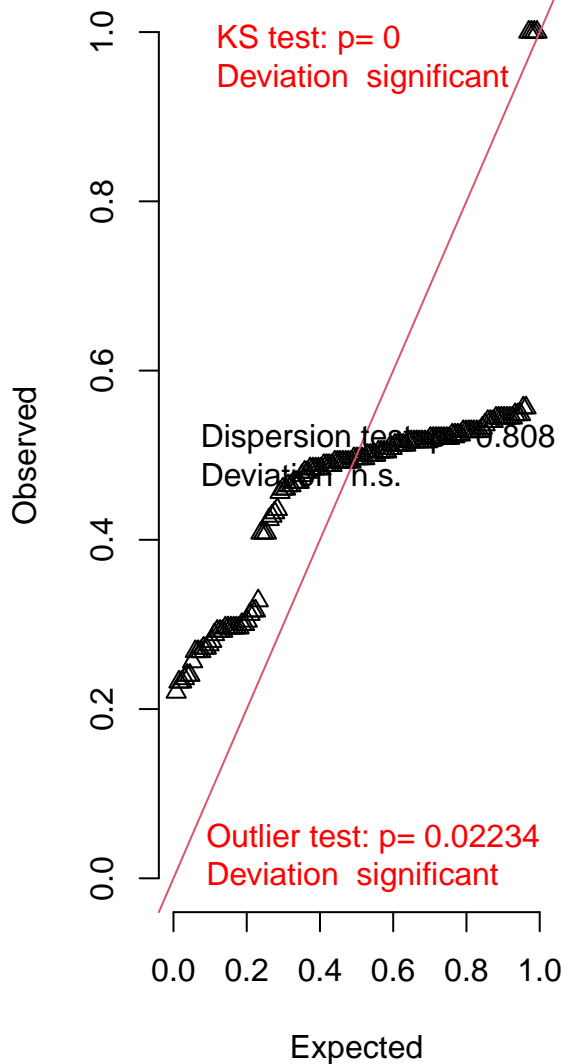
Effect of experiment

Nb obs (total) : 133

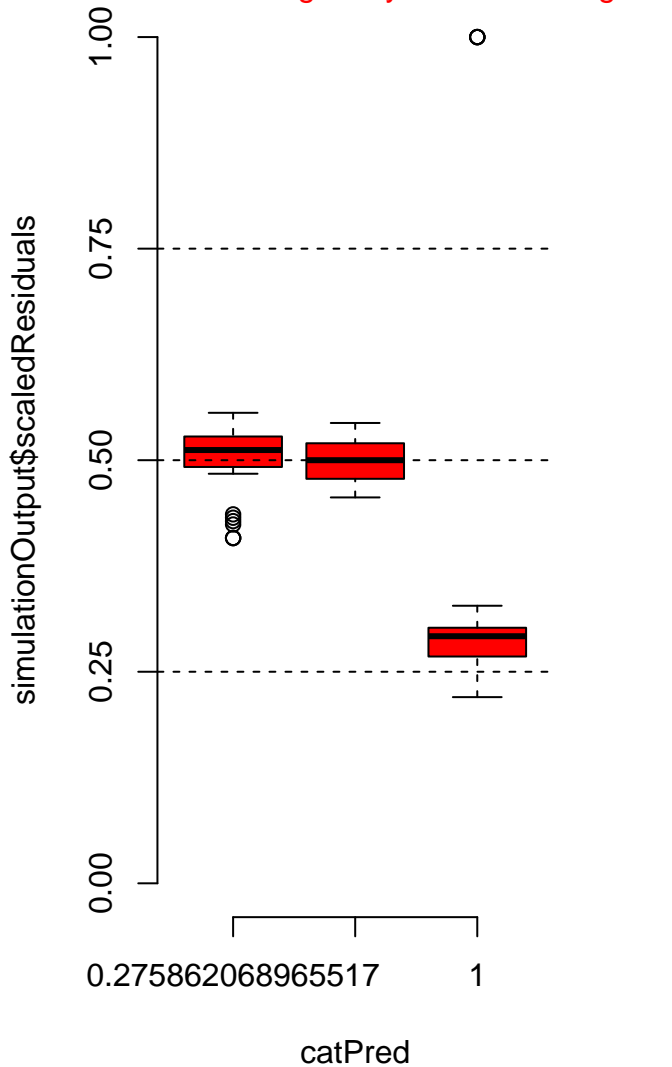
Nb LOD (included) : 129

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-746.3	-729.0	379.2	-758.3	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	4.960e-03	7.043e-02
day	(Intercept)	2.233e-10	1.494e-05
Residual		5.280e-05	7.266e-03

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 5.28e-05

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.53587	0.02231	68.85	<2e-16 ***
groupCyno.Dengue virus	-0.04507	0.03240	-1.39	0.164
groupSquirrel.Zika virus	-0.04005	0.03155	-1.27	0.204

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

IL.1B

Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 91

IL.1B ERROR : valeurs infinies ou manquantes dans 'x'

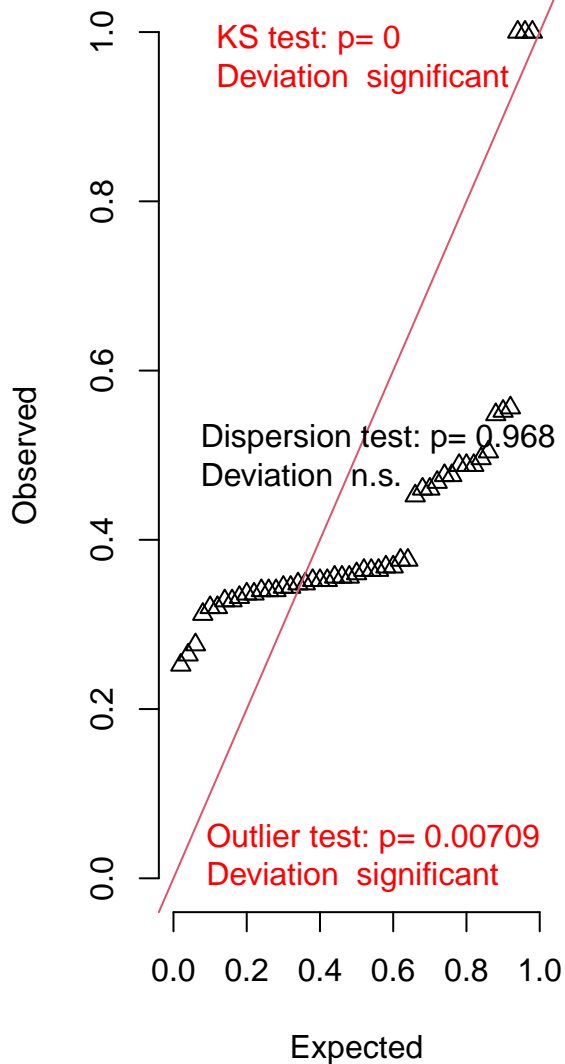
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 45

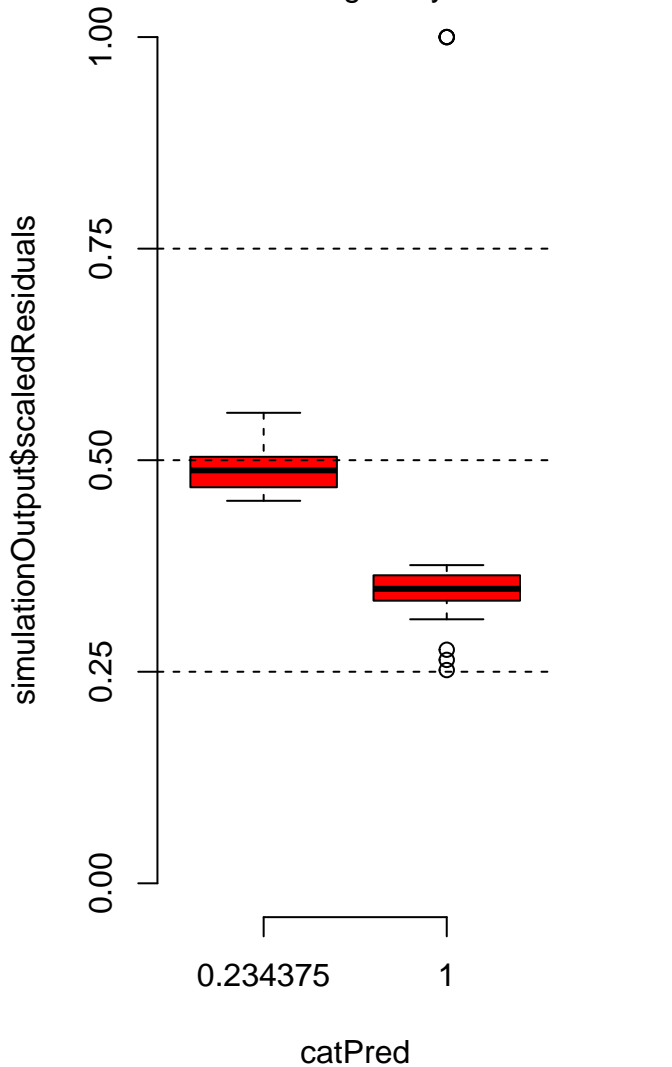
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-118.8	-109.3	64.4	-128.8	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.319e-01	0.363234
day	(Intercept)	4.692e-06	0.002166
Residual		6.443e-04	0.025384

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000644

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.2277	0.1149	10.681	<2e-16 ***
inf_statusControl	-0.1435	0.2150	-0.667	0.505

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

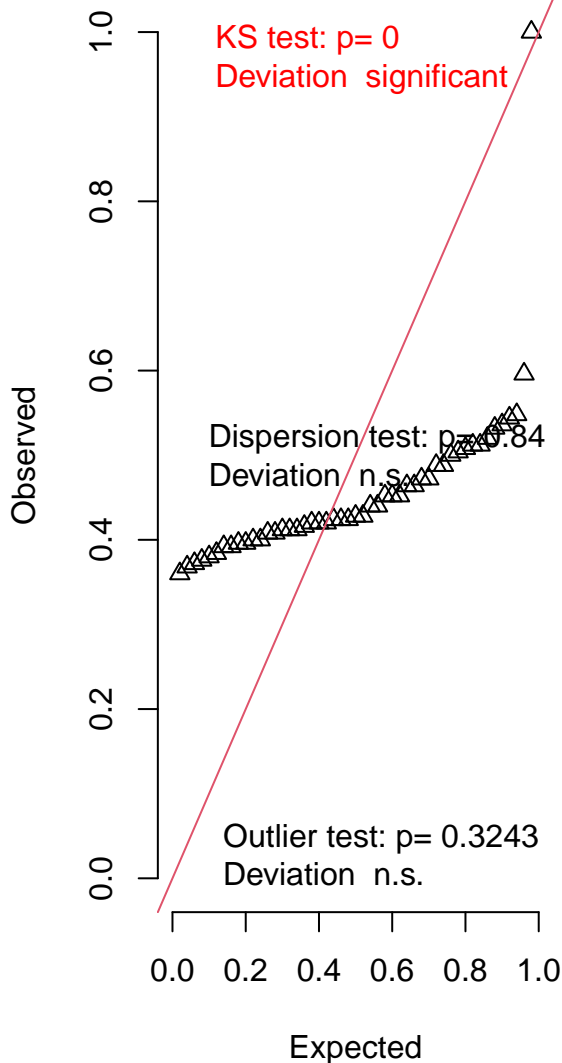
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 47

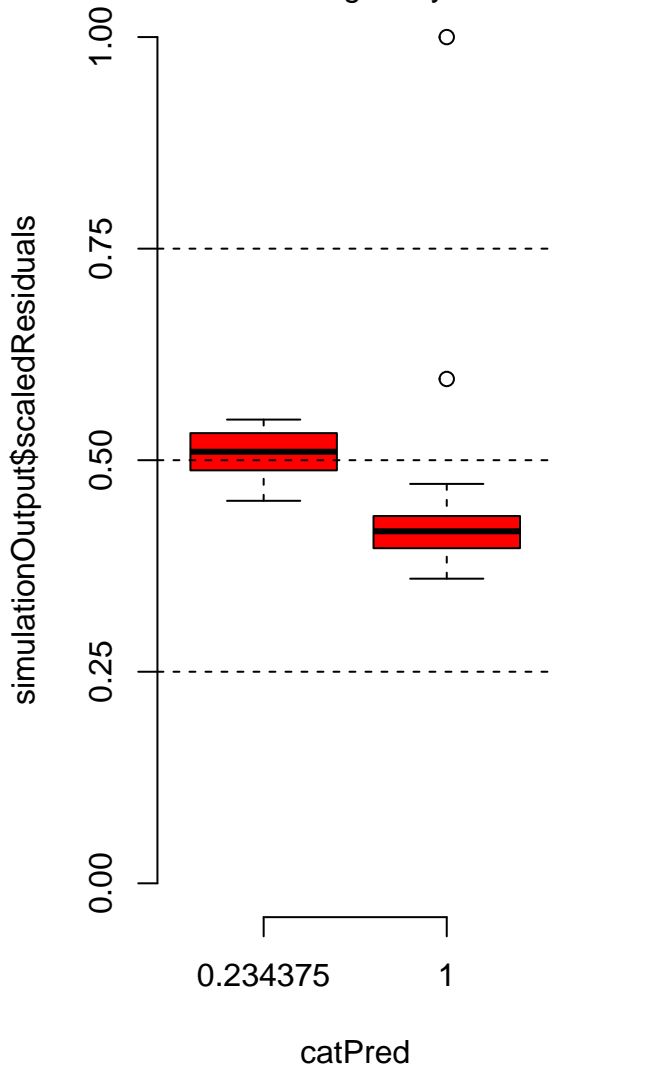
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-113.9	-104.5	62.0	-123.9	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.938e-05	4.402e-03
day	(Intercept)	6.934e-12	2.633e-06
Residual		4.648e-03	6.818e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00465

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.09891	0.01163	94.49	<2e-16 ***
inf_statusControl	-0.01469	0.02173	-0.68	0.499

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

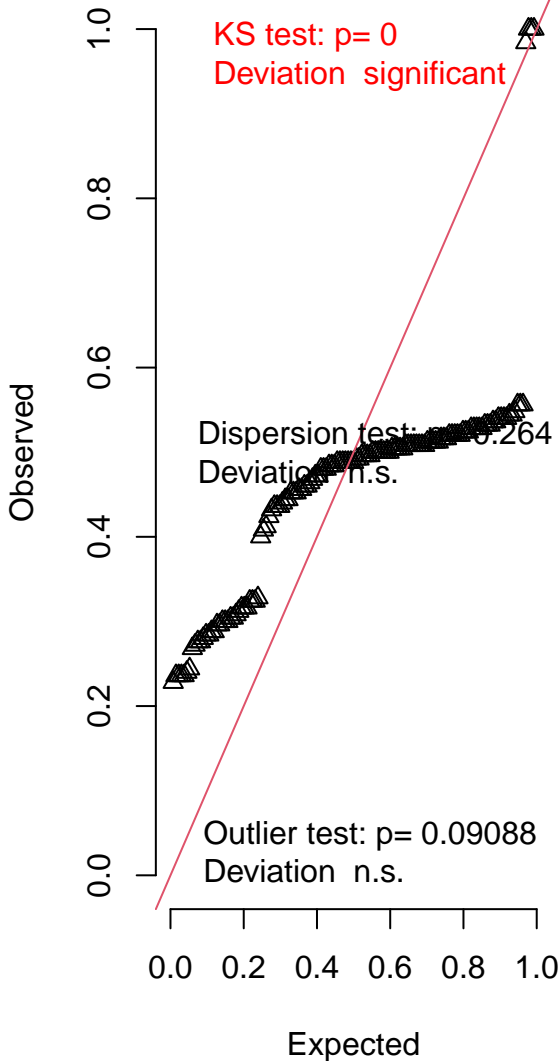
Effect of experiment

Nb obs (total) : 133

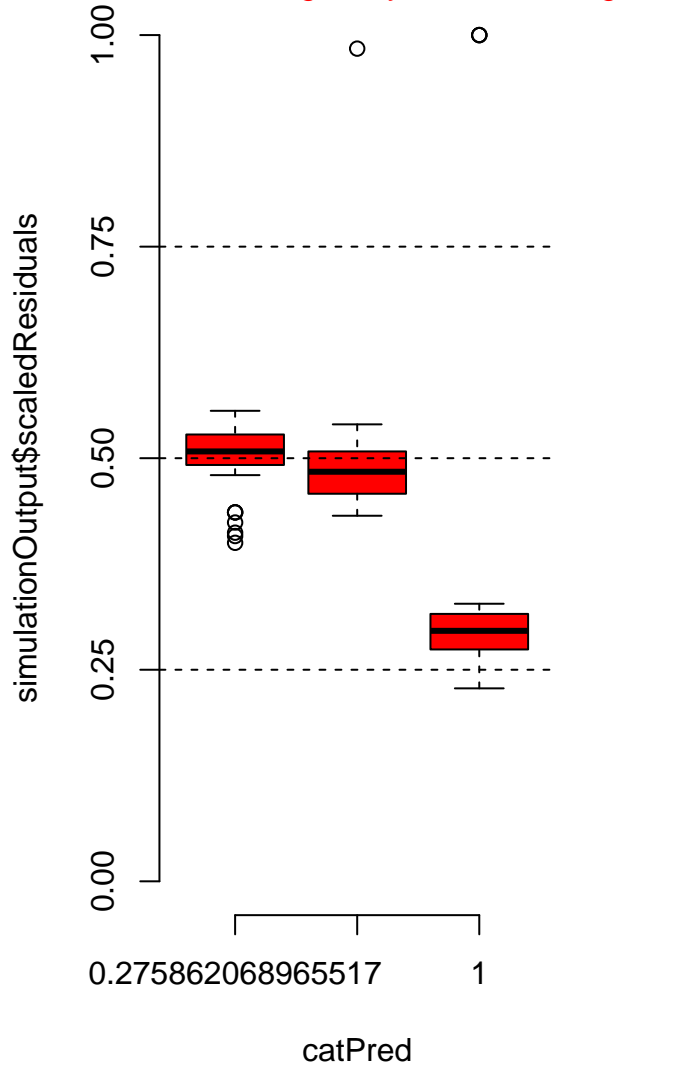
Nb LOD (included) : 127

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-302.1	-284.8	157.1	-314.1	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	6.356e-02	0.2521141
day	(Intercept)	3.585e-07	0.0005987
Residual		1.853e-03	0.0430478

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00185

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.22759	0.08006	15.333	<2e-16 ***
groupCyno.Dengue virus	-0.14696	0.11620	-1.265	0.206
groupSquirrel.Zika virus	-0.13048	0.11323	-1.152	0.249

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

IL . 2

Infection in DENV-cyno

Nb obs (total) : 91

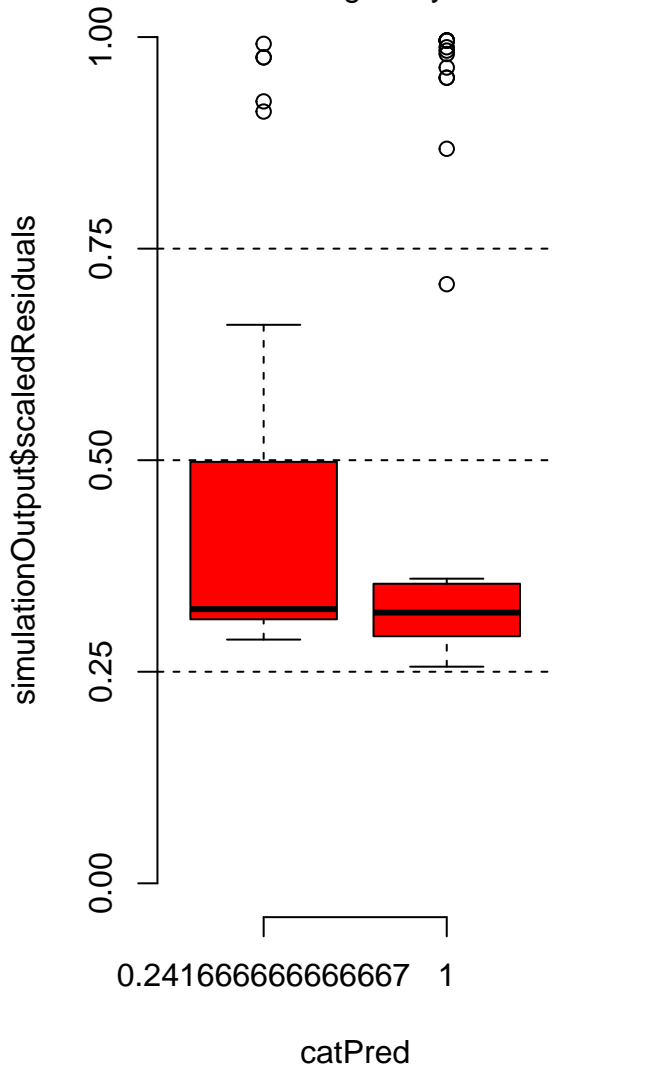
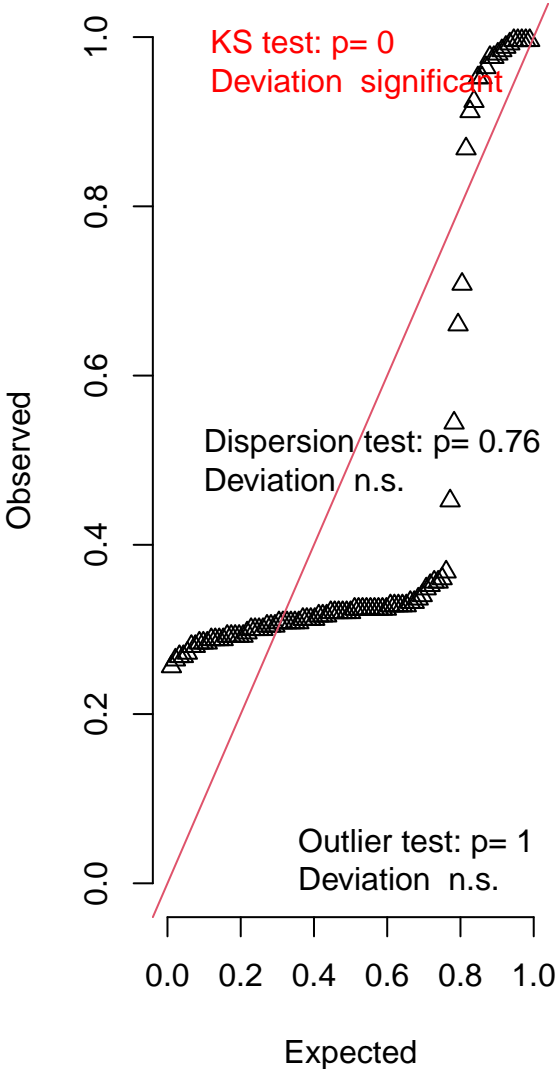
Nb LOD (included) : 68

DHARMa residual

QQ plot residuals

Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
42.0	54.6	-16.0	32.0	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.104719	0.32360
day	(Intercept)	0.002918	0.05402
Residual		0.054955	0.23443

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.055

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.84937	0.11369	16.267	<2e-16 ***
inf_statusControl	-0.02899	0.20162	-0.144	0.886

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

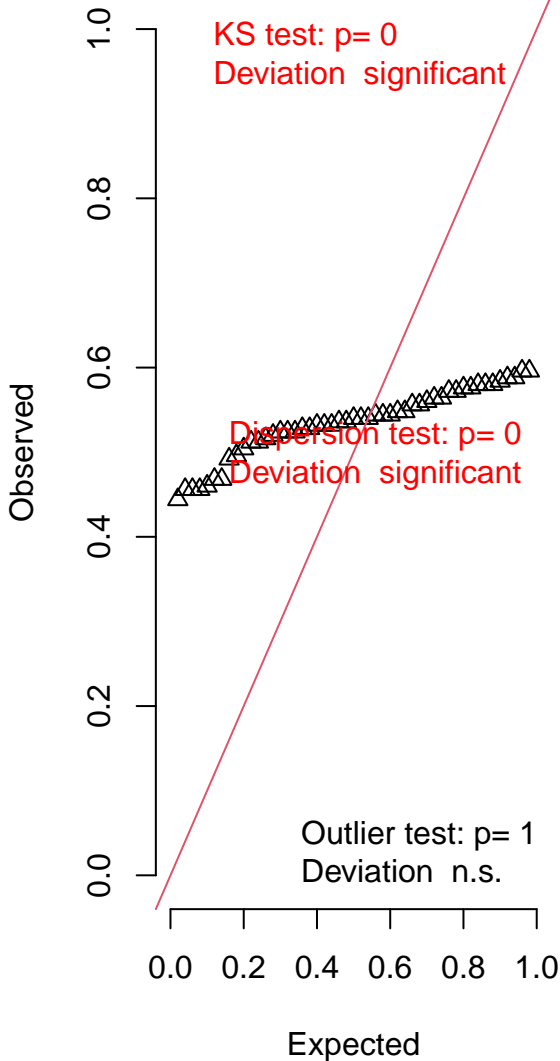
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 49

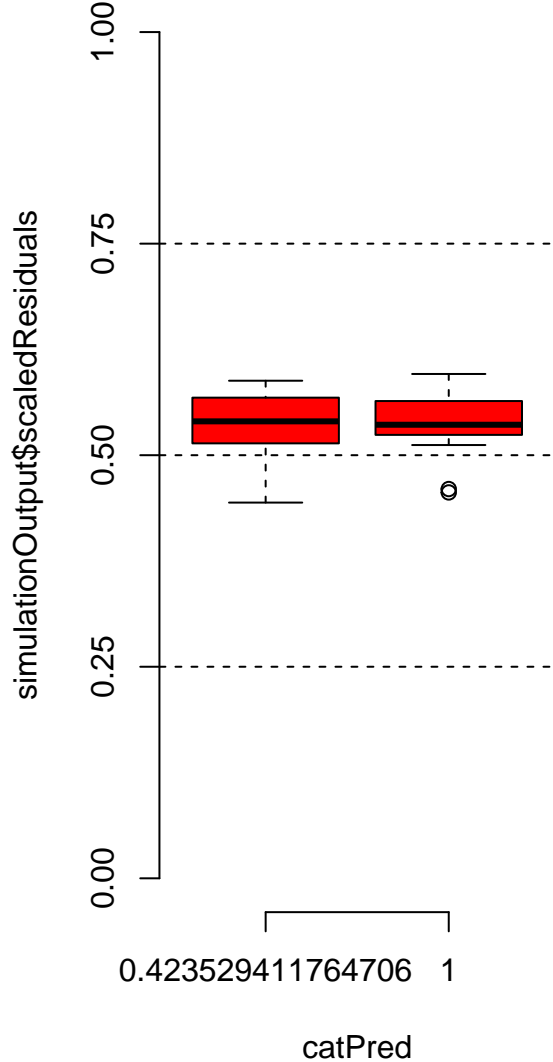
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
NA	NA	NA	NA	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.306e-09	4.802e-05
day	(Intercept)	1.097e-07	3.312e-04
Residual		4.086e-23	6.392e-12

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 4.09e-23

Conditional model:

	Estimate	Std. Error	z	value	Pr(> z)
(Intercept)	1.641e+00	1.276e-03	1286	<2e-16	***
inf_statusControl	1.118e-06	2.843e-05	0	0.969	

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

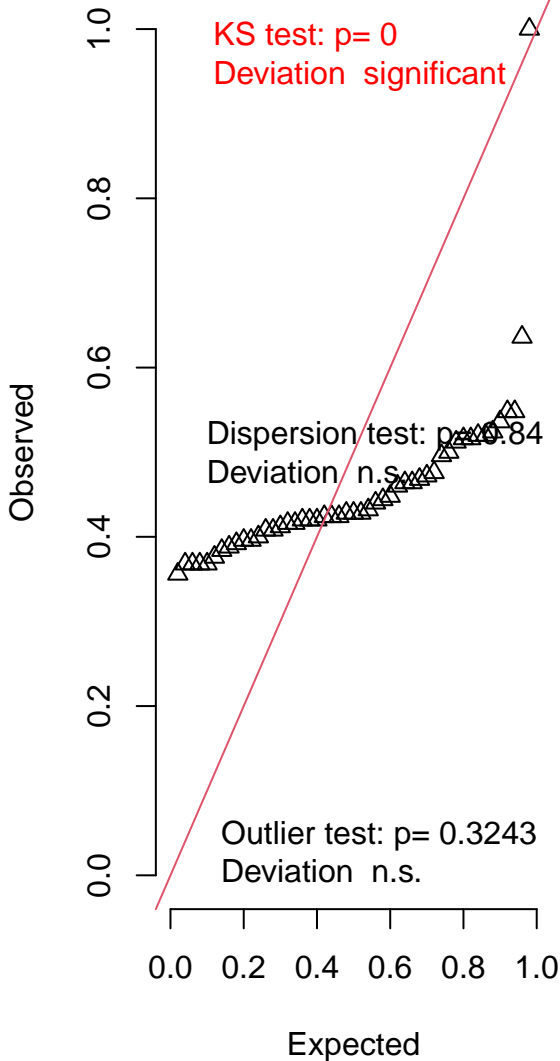
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 47

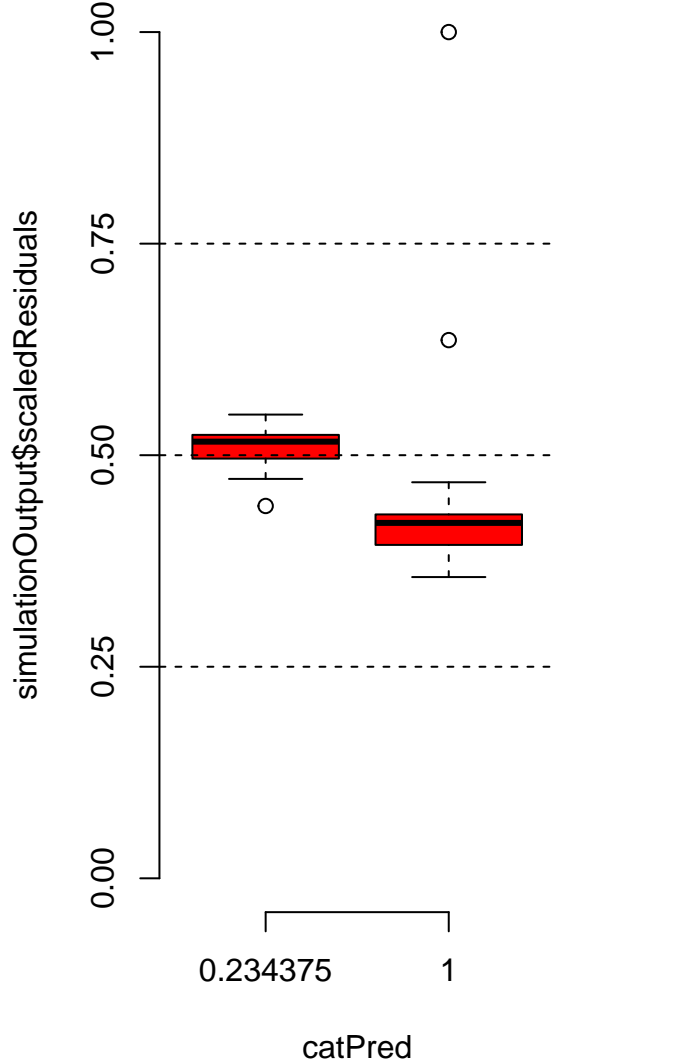
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-73.4	-64.0	41.7	-83.4	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.604e-04	1.267e-02
day	(Intercept)	1.447e-11	3.803e-06
Residual		1.051e-02	1.025e-01

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0105

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.66369	0.01782	93.34	<2e-16 ***
inf_statusControl	-0.02251	0.03330	-0.68	0.499

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

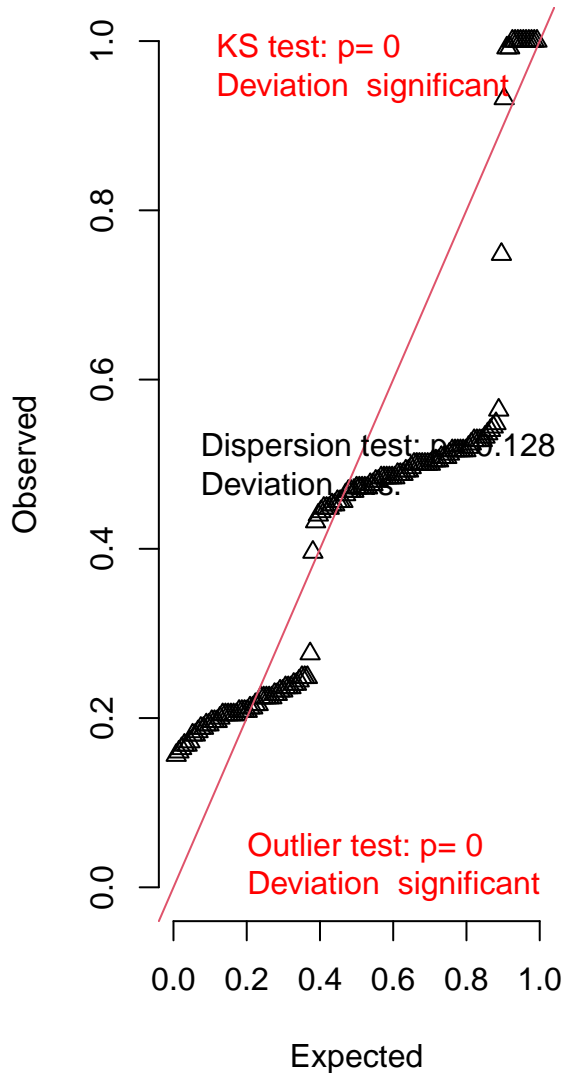
Effect of experiment

Nb obs (total) : 133

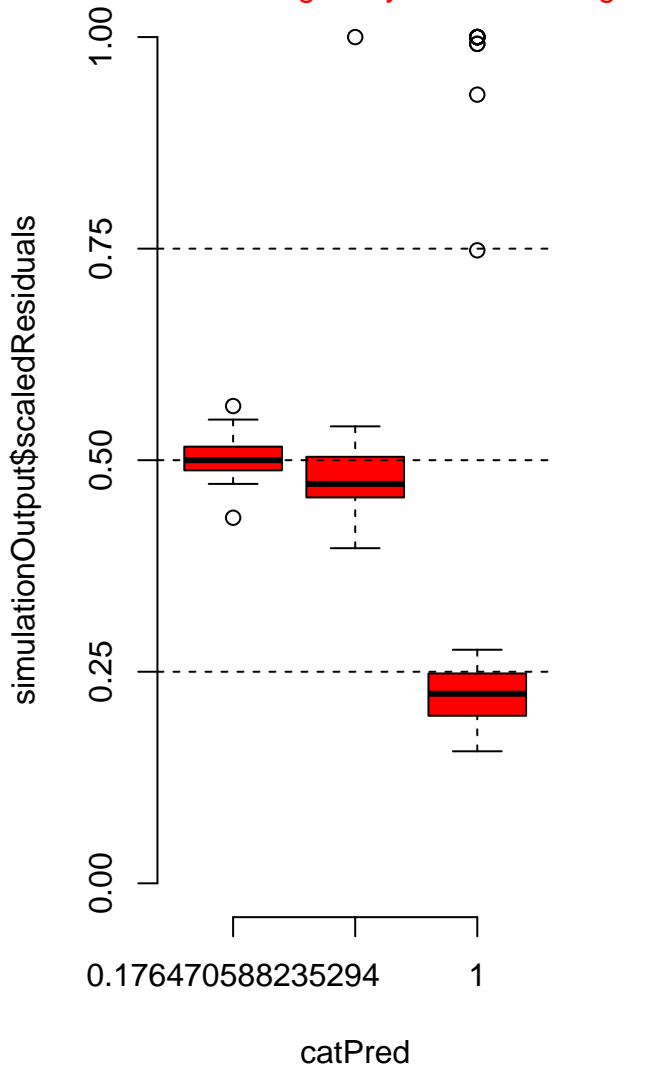
Nb LOD (included) : 116

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-48.2	-30.8	30.1	-60.2	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	4.702e-02	2.168e-01
day	(Intercept)	4.901e-12	2.214e-06
Residual		2.252e-02	1.501e-01

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0225

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.64118	0.07319	22.423	<2e-16 ***
groupCyno.Dengue virus	0.20820	0.10459	1.991	0.0465 *
groupSquirrel.Zika virus	0.02017	0.10351	0.195	0.8455

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

IL . 4₁

Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 91

IL.4 ERROR : valeurs infinies ou manquantes dans 'x'

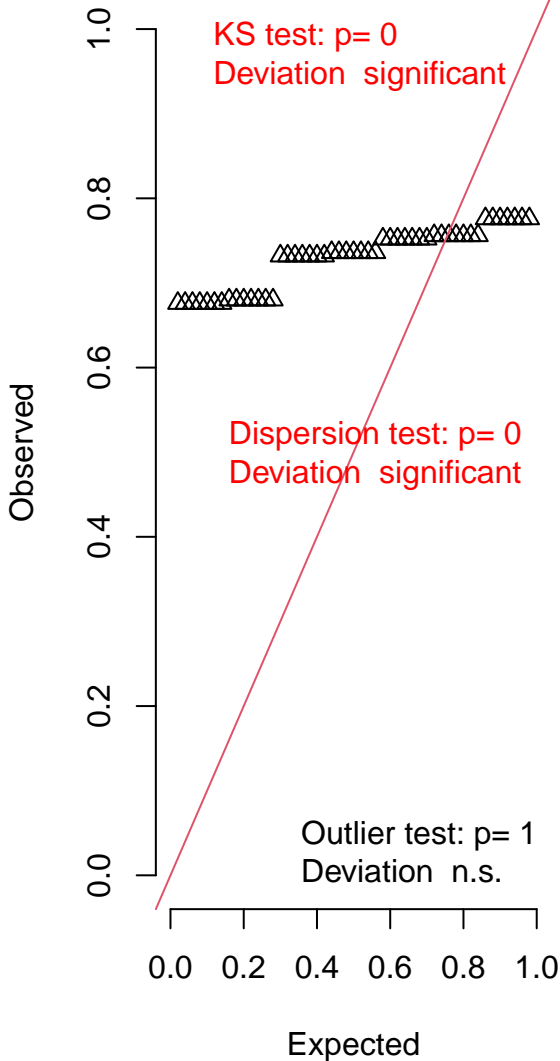
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 49

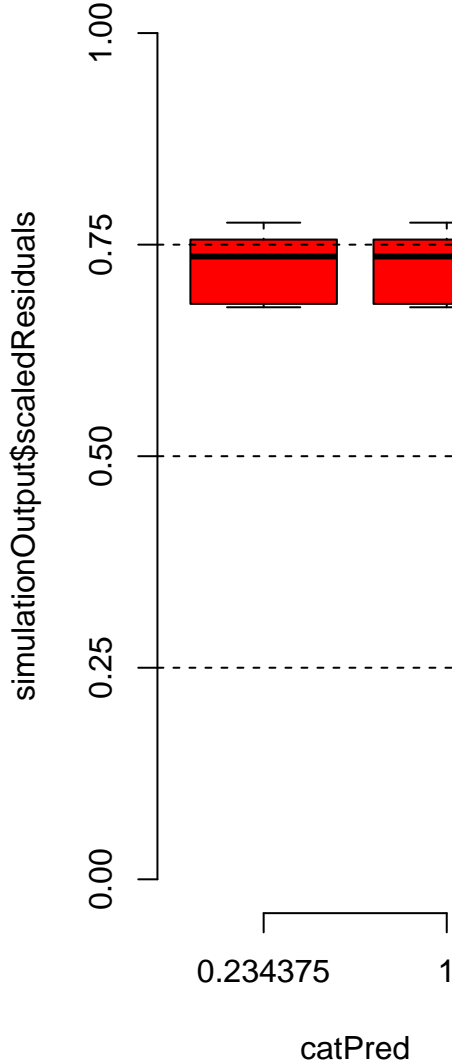
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:          log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
NA	NA	NA	NA	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.034e-10	1.017e-05
day	(Intercept)	3.647e-03	6.039e-02
Residual		1.299e-24	1.140e-12

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (σ^2): 1.3e-24

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.554e+00	NaN	NaN	NaN
inf_statusControl	-4.044e-09	6.016e-06	-0.001	0.999

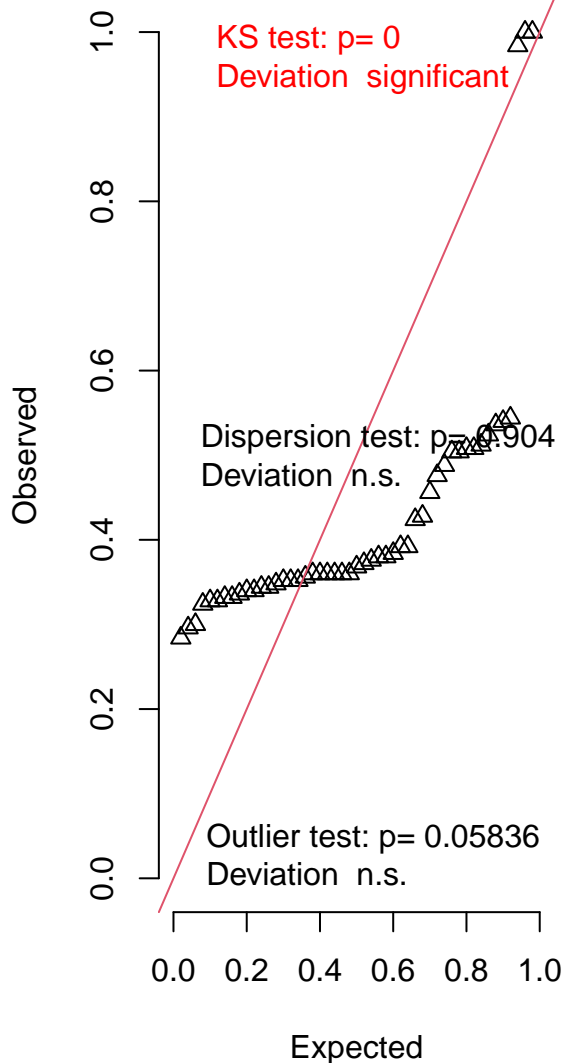
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 46

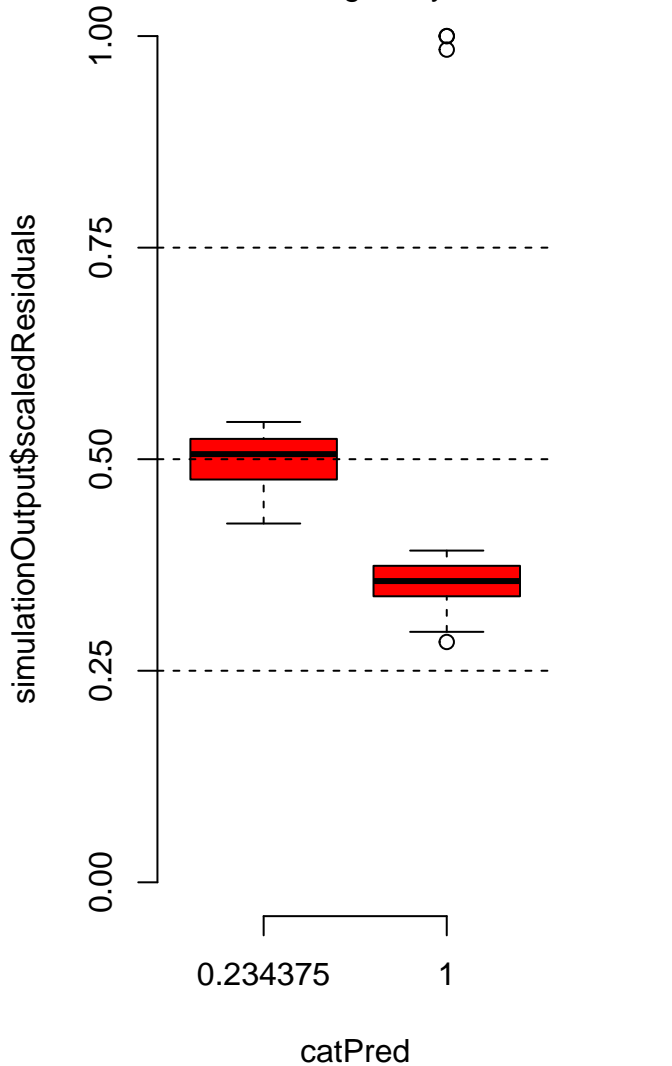
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-163.7	-154.2	86.8	-173.7	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.352e-03	7.316e-02
day	(Intercept)	4.453e-11	6.673e-06
Residual		6.406e-04	2.531e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000641

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.62007	0.02353	68.84	<2e-16 ***
inf_statusControl	-0.02934	0.04403	-0.67	0.505

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

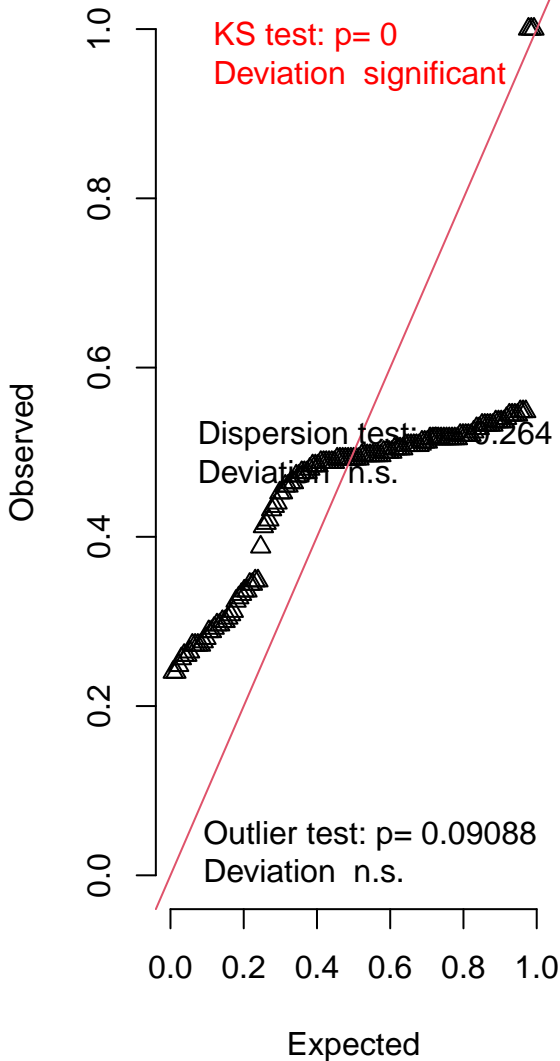
Effect of experiment

Nb obs (total) : 133

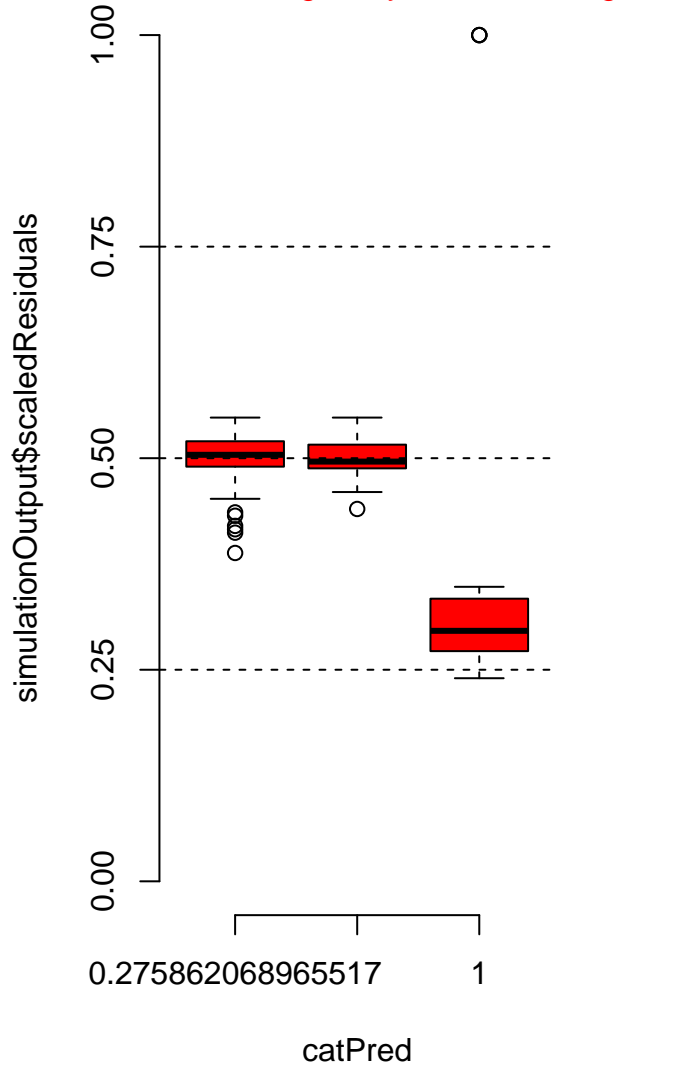
Nb LOD (included) : 130

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-618.1	-600.8	315.1	-630.1	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.608e-03	5.107e-02
day	(Intercept)	5.289e-11	7.272e-06
Residual		2.156e-04	1.468e-02

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.000216

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.5907296	0.0163426	97.34	<2e-16 ***
groupCyno.Dengue virus	-0.0001103	0.0236702	0.00	0.996
groupSquirrel.Zika virus	0.0293810	0.0231120	1.27	0.204

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

IL. 5

Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 91

IL.5 ERROR : valeurs infinies ou manquantes dans 'x'

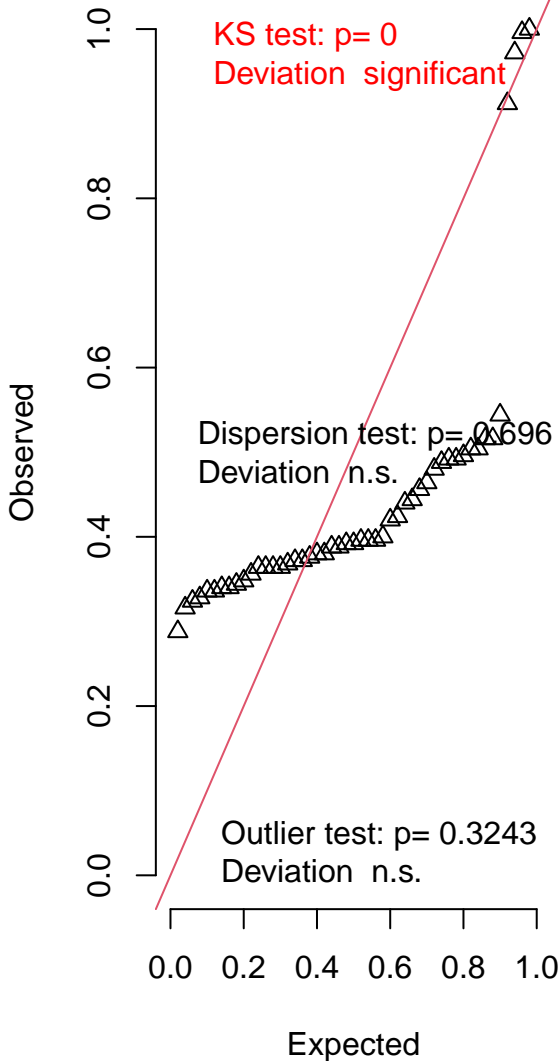
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 45

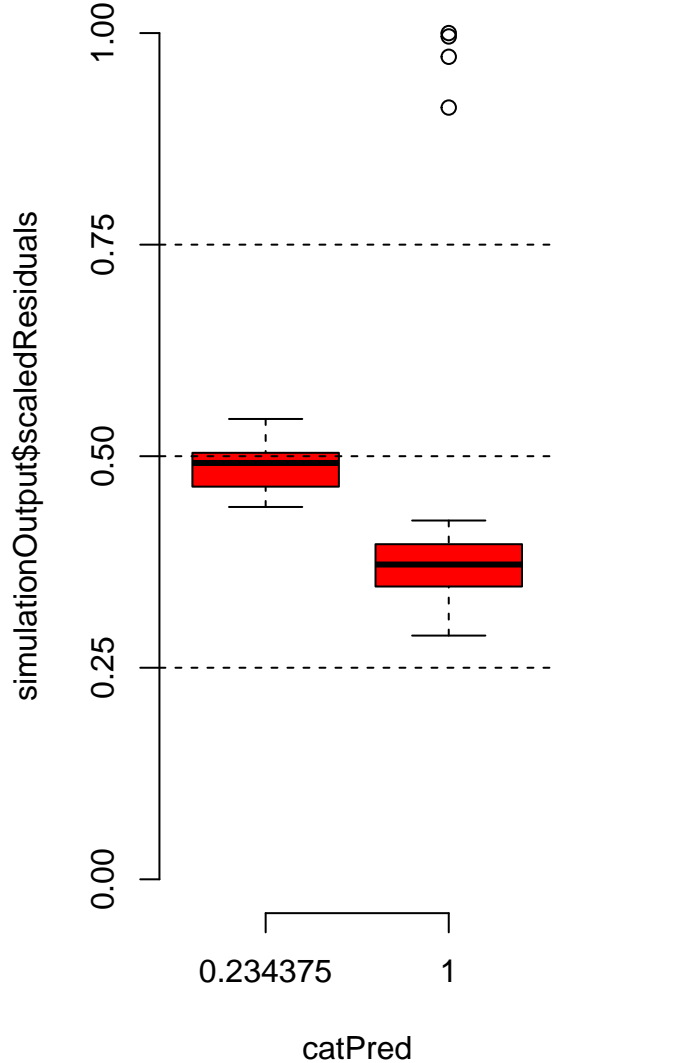
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-201.0	-191.5	105.5	-211.0	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	3.217e-04	1.794e-02
day	(Intercept)	4.387e-12	2.094e-06
Residual		5.811e-04	2.411e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000581

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.815931	0.007002	116.5	<2e-16 ***
inf_statusControl	-0.010430	0.013097	-0.8	0.426

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

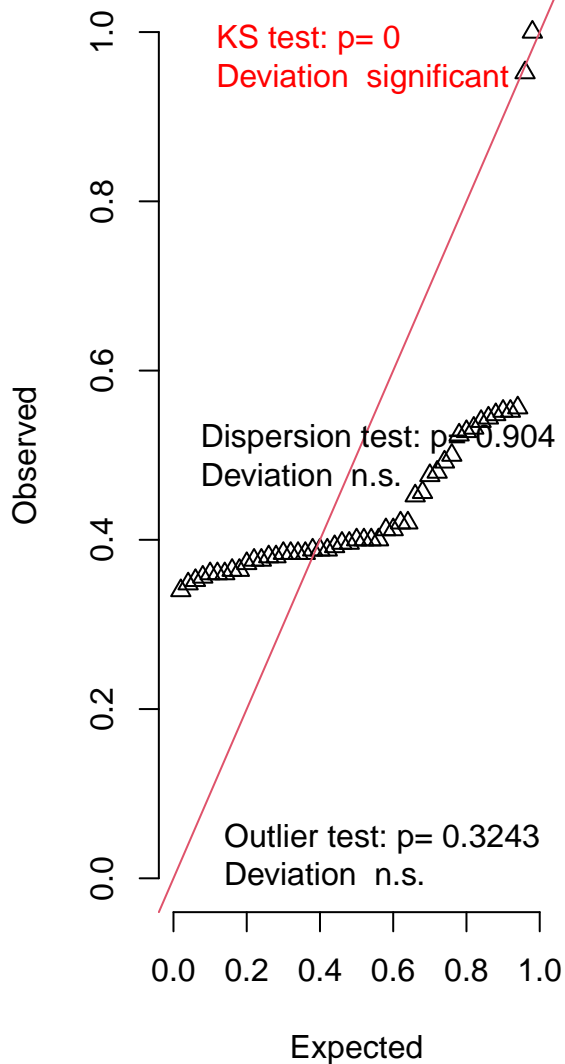
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 46

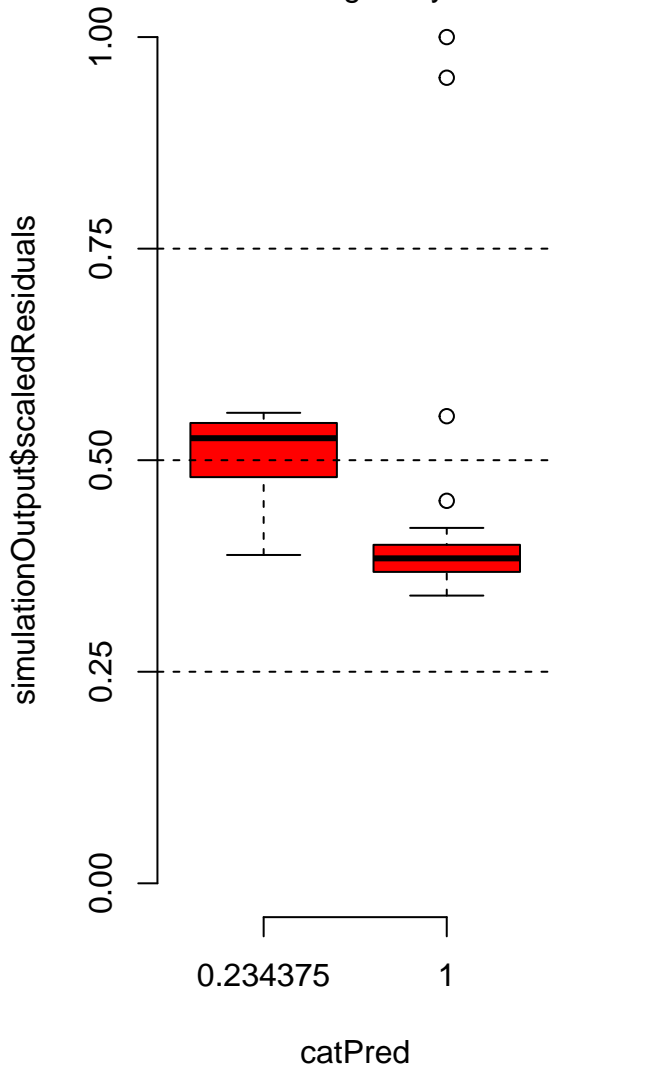
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-386.0	-376.5	198.0	-396.0	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.503e-06	2.346e-03
day	(Intercept)	1.329e-13	3.646e-07
Residual		1.419e-05	3.767e-03

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 1.42e-05

Conditional model:

	Estimate	Std. Error	z	value	Pr(> z)
(Intercept)	0.8067828	0.0009809	822.5	<2e-16	***
inf_statusControl	-0.0012819	0.0018340	-0.7	0.485	

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

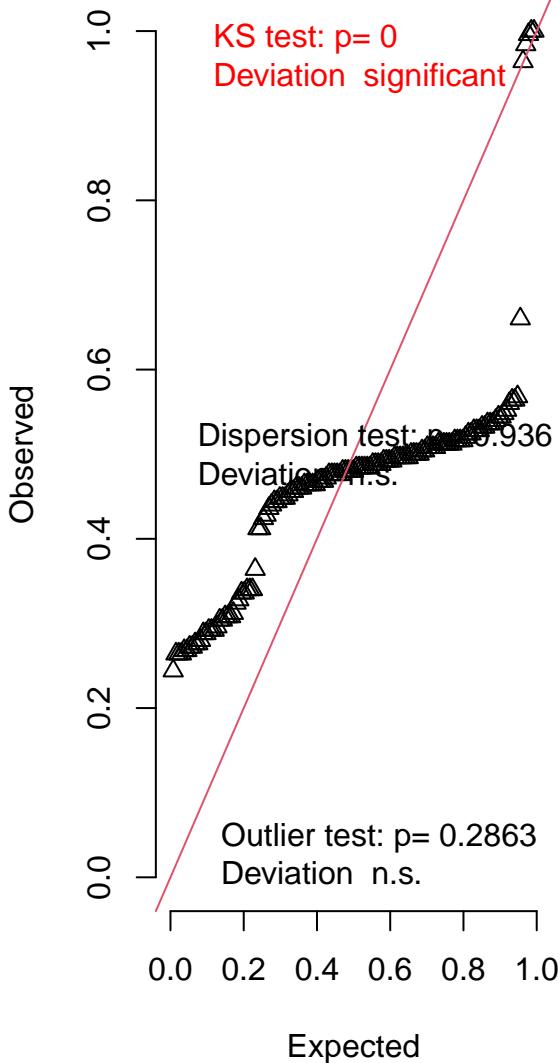
Effect of experiment

Nb obs (total) : 133

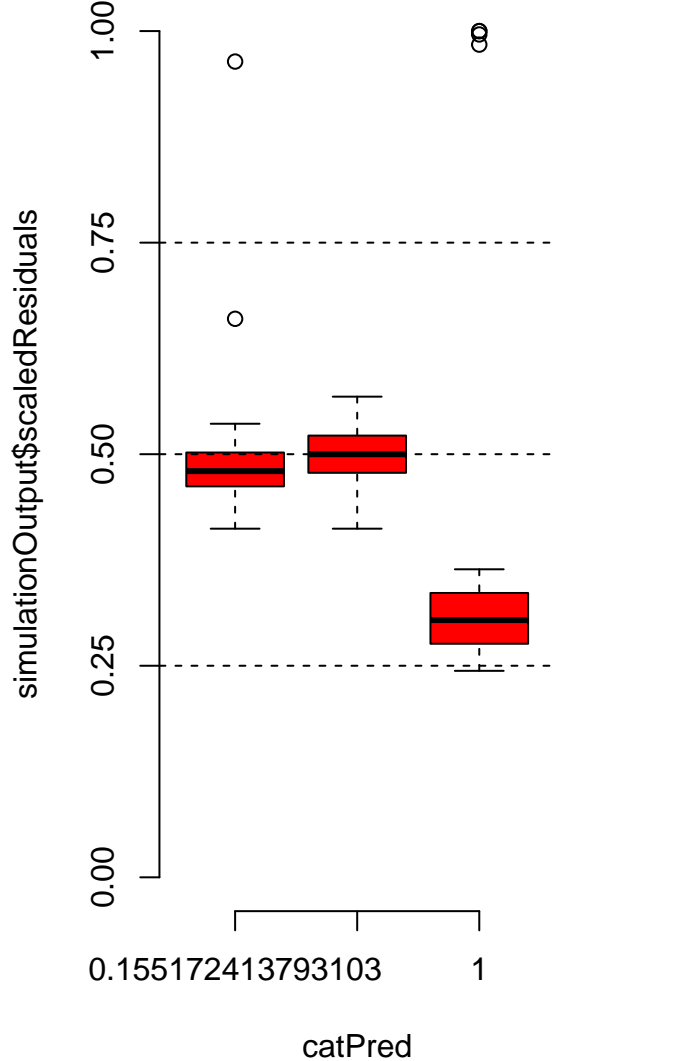
Nb LOD (included) : 126

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-696.5	-679.1	354.2	-708.5	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.668e-04	1.292e-02
day	(Intercept)	2.726e-12	1.651e-06
Residual		2.043e-04	1.429e-02

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.000204

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.815853	0.004756	171.55	<2e-16 ***
groupCyno.Dengue virus	-0.006293	0.006663	-0.94	0.345
groupSquirrel.Zika virus	-0.009038	0.006725	-1.34	0.179

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

IL. 6

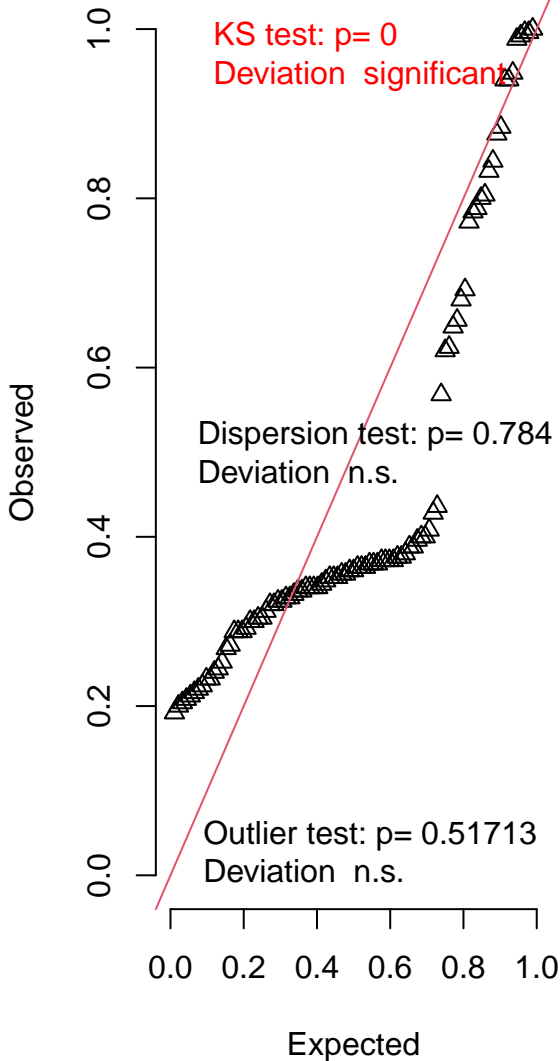
Infection in DENV-cyno

Nb obs (total) : 91

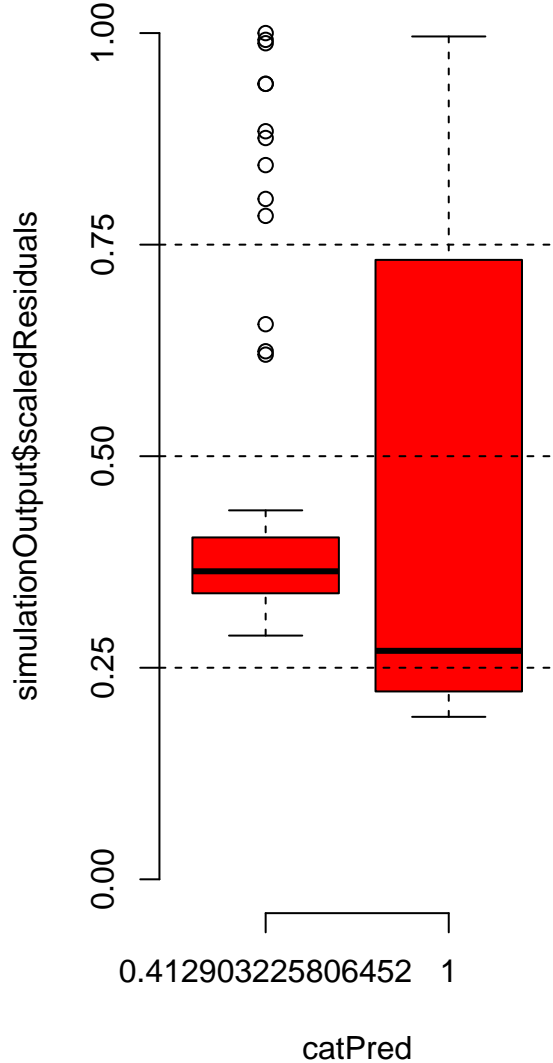
Nb LOD (included) : 66

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-319.1	-306.5	164.5	-329.1	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.372e-04	0.023177
day	(Intercept)	5.748e-05	0.007581
Residual		1.249e-03	0.035345

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00125

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.903906	0.009366	96.51	<2e-16 ***
inf_statusControl	0.013968	0.016076	0.87	0.385

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

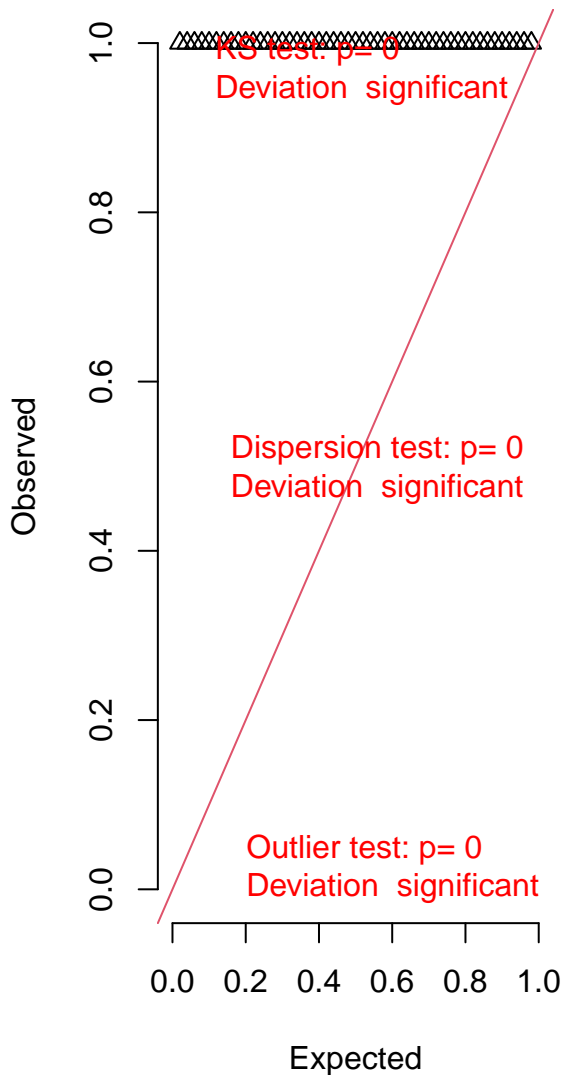
Infection in DENV-squirrel

Nb obs (total) : 49

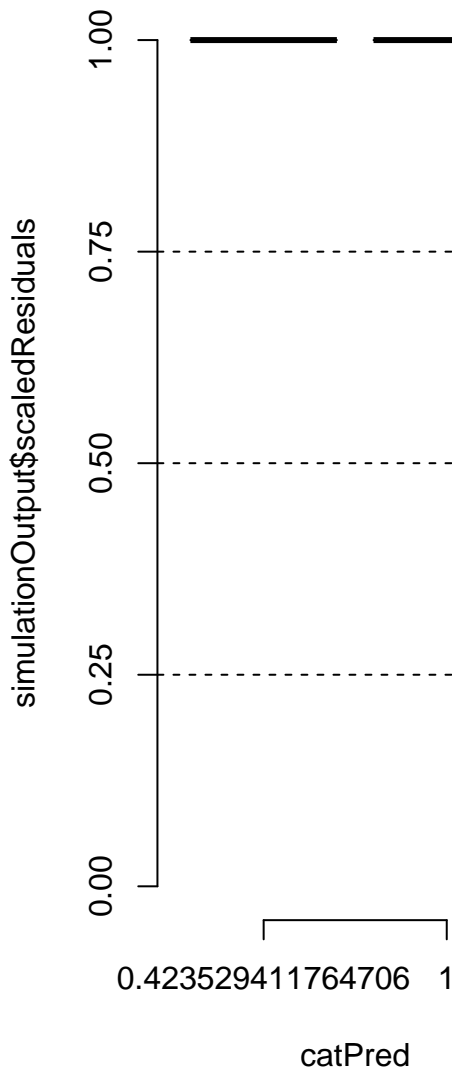
Nb LOD (included) : 49

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant




```

Family: gaussian ( identity )
Formula:          log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
NA	NA	NA	NA	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	3.081e-21	5.551e-11
day	(Intercept)	5.905e-09	7.684e-05
Residual		2.405e-32	1.551e-16

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (σ^2): 2.4e-32

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	8.867e-01	NaN	NaN	NaN
inf_statusControl	1.781e-14	NaN	NaN	NaN

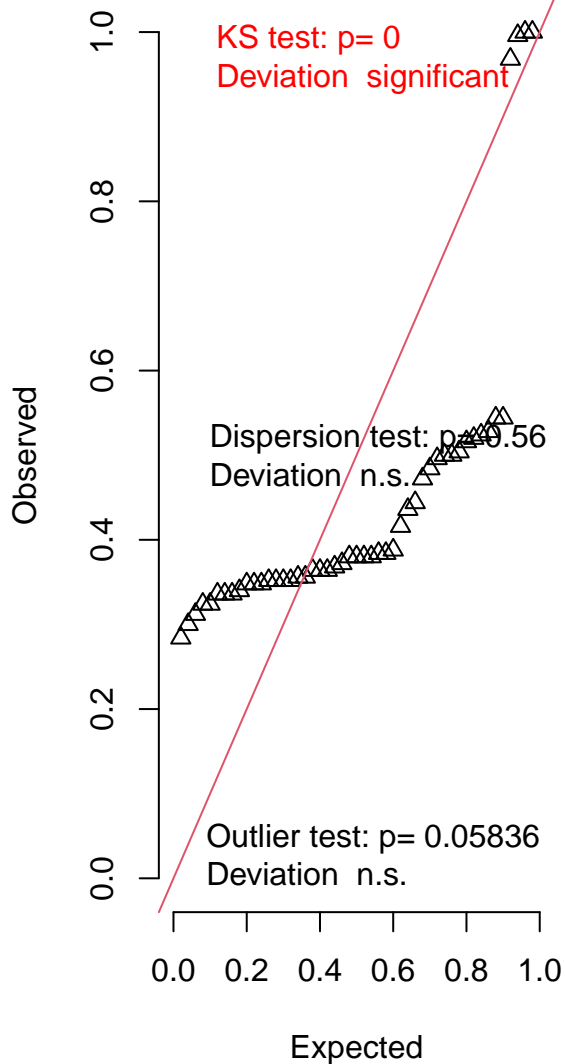
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 45

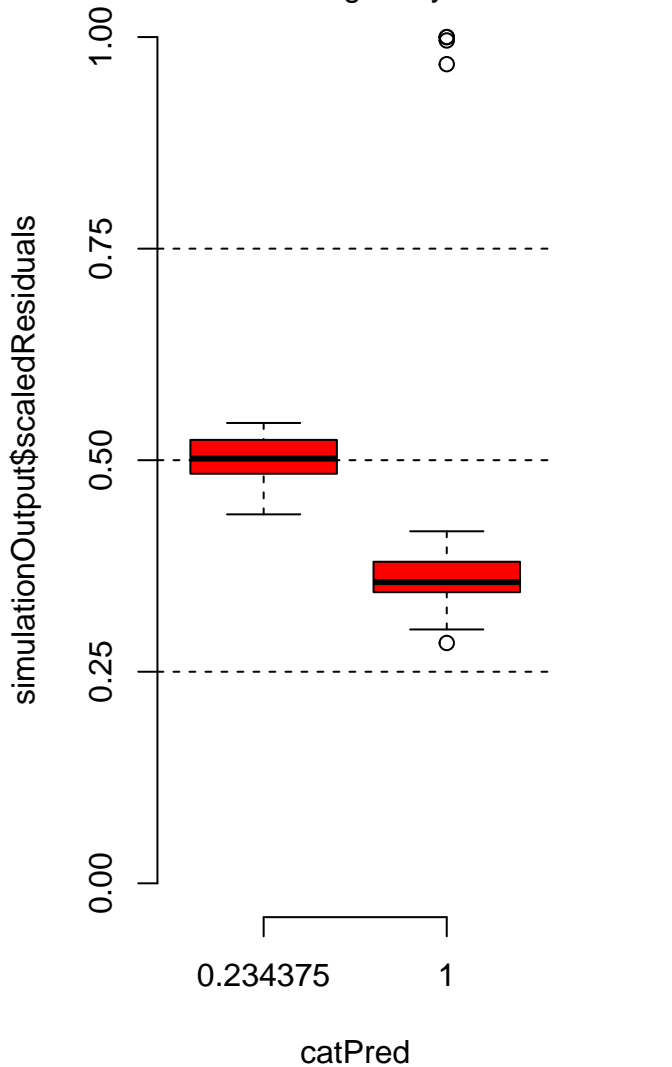
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-47.7	-38.2	28.9	-57.7	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	3.495e-02	1.869e-01
day	(Intercept)	2.318e-10	1.522e-05
Residual		8.201e-03	9.056e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0082

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.96334	0.06110	15.765	<2e-16 ***
inf_statusControl	-0.07629	0.11432	-0.667	0.505

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

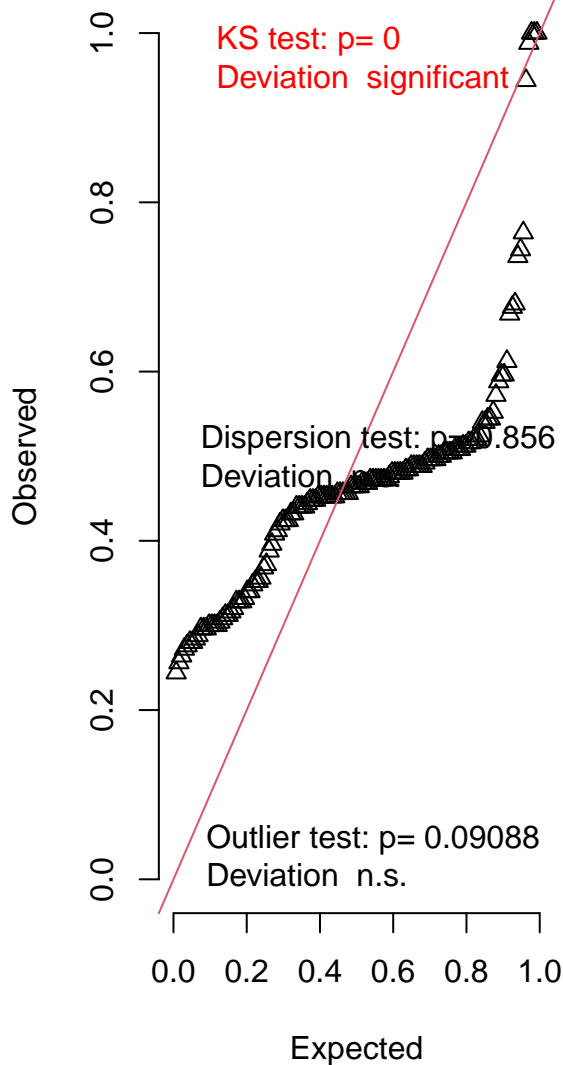
Effect of experiment

Nb obs (total) : 133

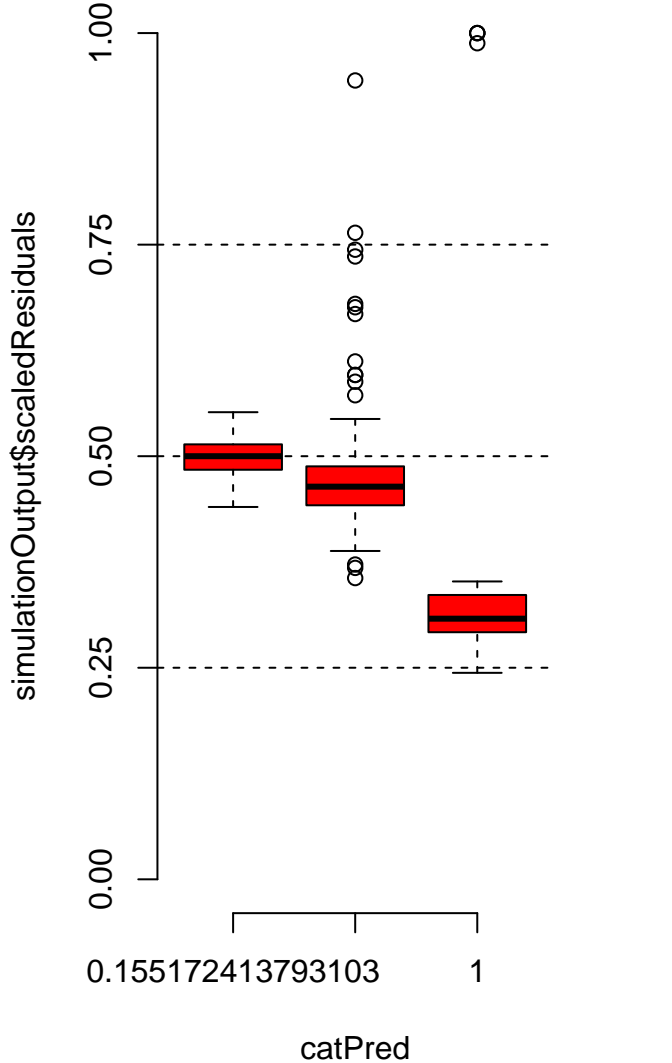
Nb LOD (included) : 116

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant




```

Family: gaussian ( identity )
Formula:      log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-273.2	-255.9	142.6	-285.2	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.700e-02	1.304e-01
day	(Intercept)	2.858e-12	1.691e-06
Residual		3.494e-03	5.911e-02

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00349

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.88705	0.04245	20.896	<2e-16 ***
groupCyno.Dengue virus	0.01685	0.06121	0.275	0.783
groupSquirrel.Zika virus	0.07621	0.06004	1.269	0.204

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

IL.8

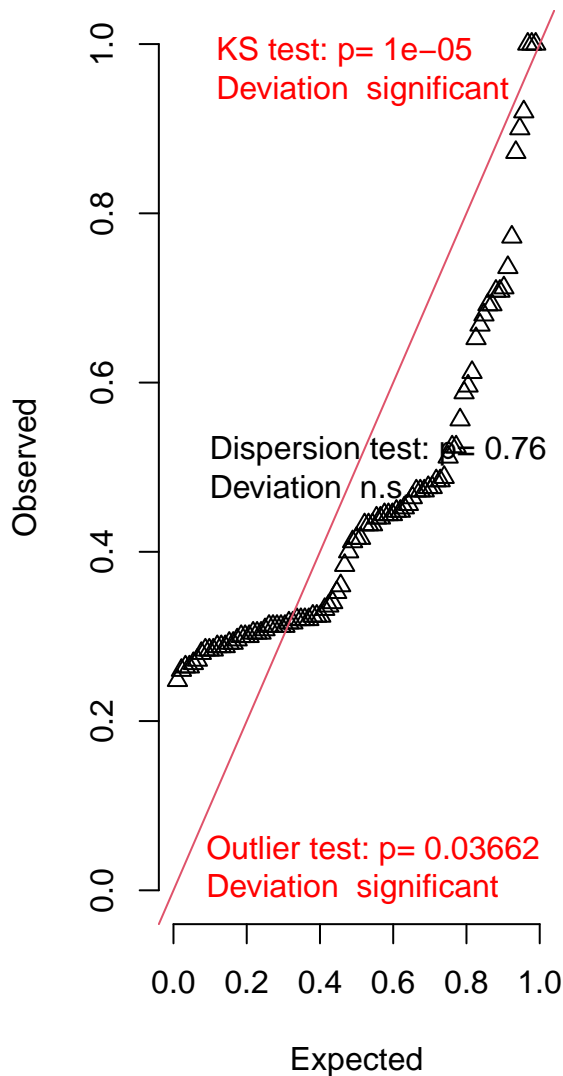
Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 62

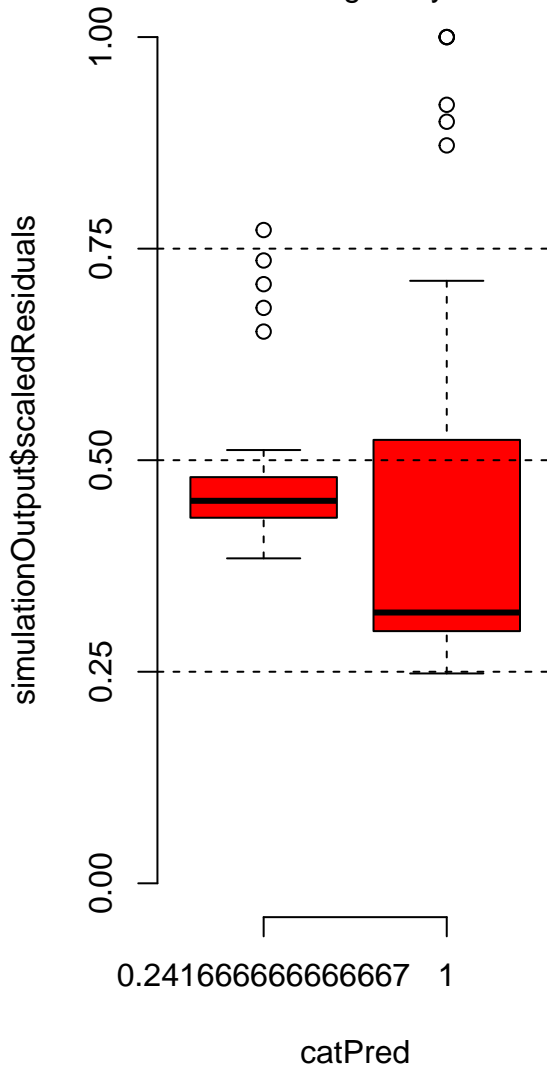
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-95.9	-83.4	53.0	-105.9	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0152009	0.12329
day	(Intercept)	0.0004415	0.02101
Residual		0.0129915	0.11398

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.013

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.15866	0.04425	26.18	<2e-16 ***
inf_statusControl	-0.06984	0.07848	-0.89	0.374

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

Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 49

IL.8 ERROR : valeurs infinies ou manquantes dans 'x'

Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 49

IL.8 ERROR : valeurs infinies ou manquantes dans 'x'

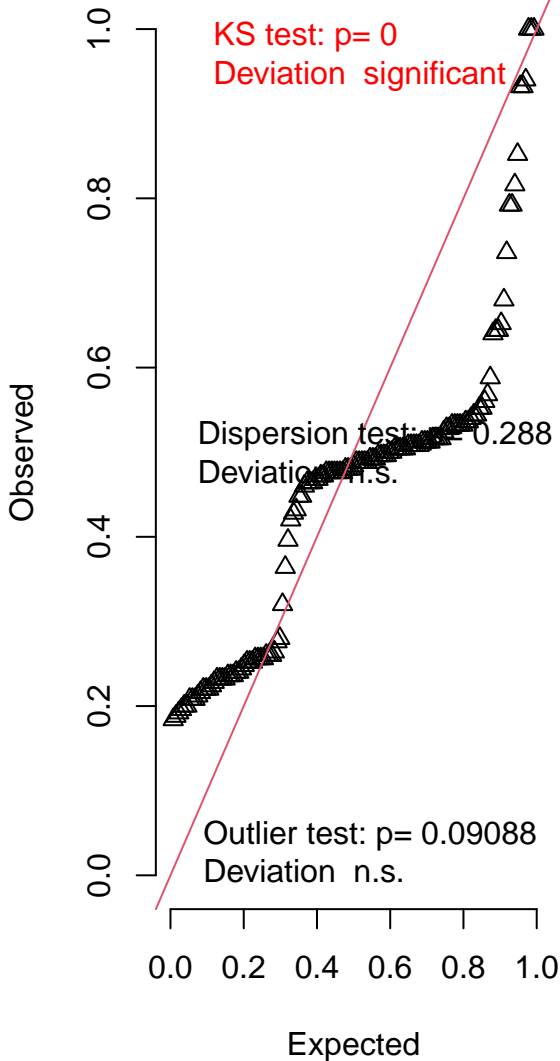
Effect of experiment

Nb obs (total) : 133

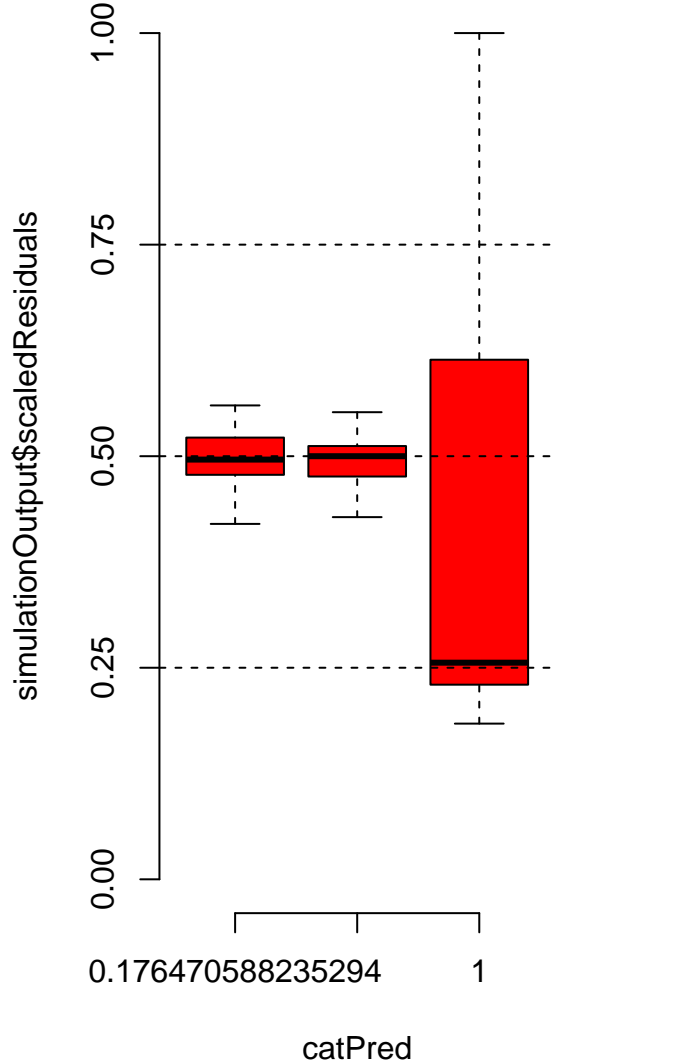
Nb LOD (included) : 110

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-187.3	-170.0	99.7	-199.3	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0069767	0.08353
day	(Intercept)	0.0003114	0.01765
Residual		0.0093213	0.09655

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00932

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.069e+00	3.194e-02	33.47	<2e-16 ***
groupCyno.Dengue virus	8.952e-02	4.376e-02	2.05	0.0408 *
groupSquirrel.Zika virus	-5.598e-08	4.400e-02	0.00	1.0000

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

IL . RA

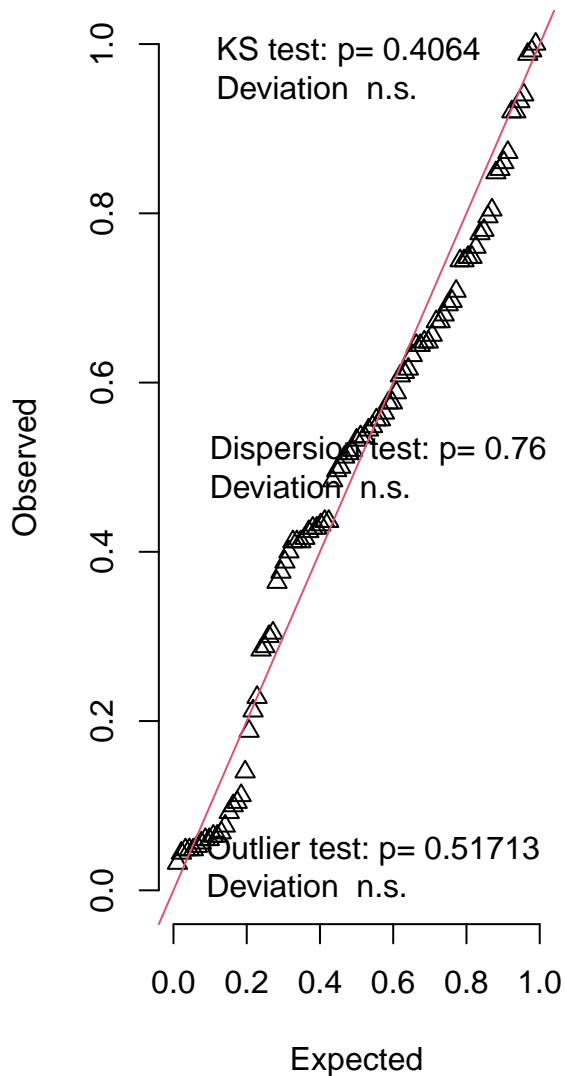
Infection in DENV-cyno

Nb obs (total) : 91

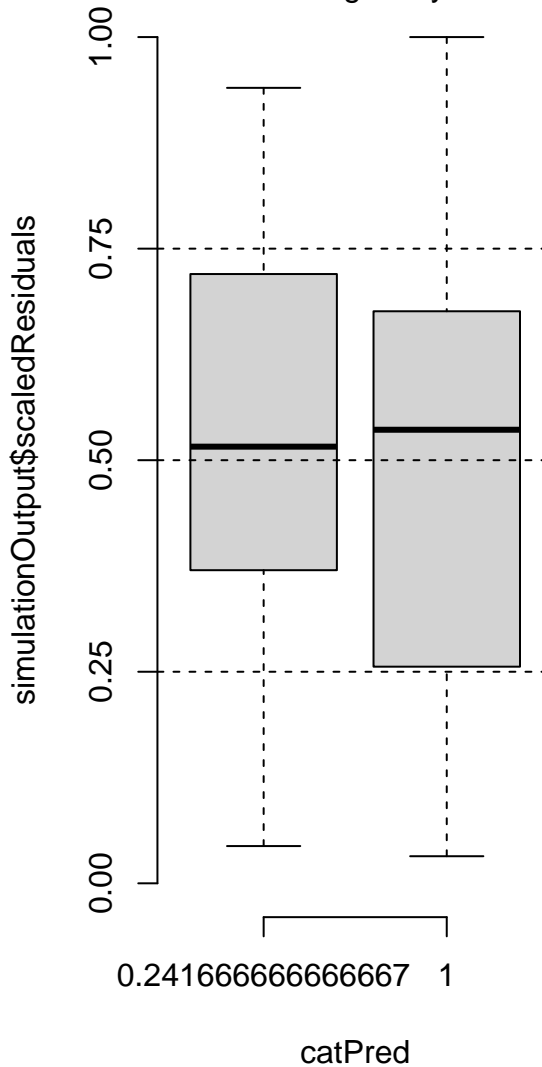
Nb LOD (included) : 12

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
46.1	58.7	-18.1	36.1	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0518091	0.22762
day	(Intercept)	0.0009615	0.03101
Residual		0.0658643	0.25664

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0659

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.26279	0.08330	27.163	<2e-16 ***
inf_statusControl	-0.00266	0.14868	-0.018	0.986

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

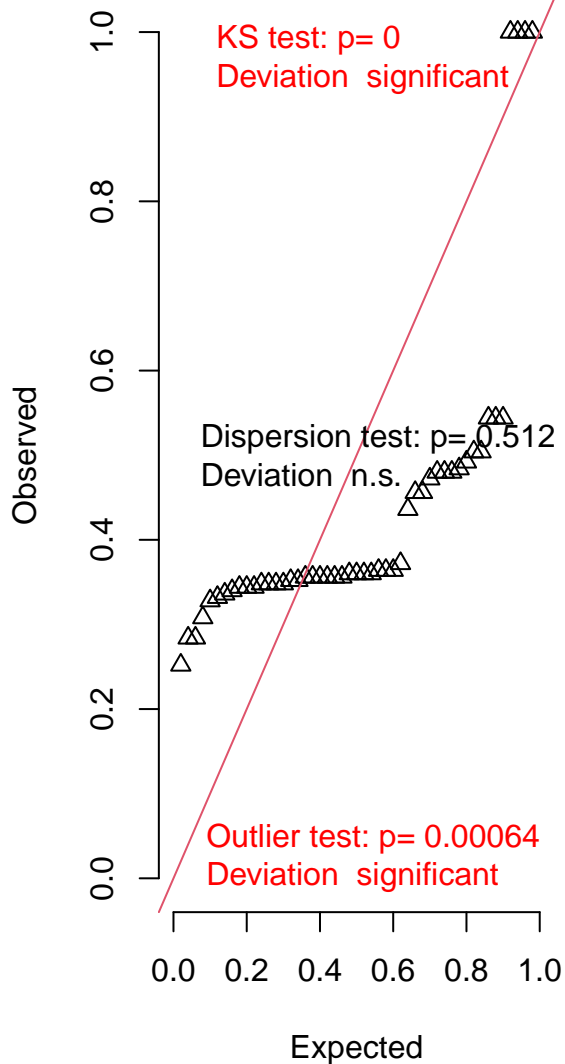
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 45

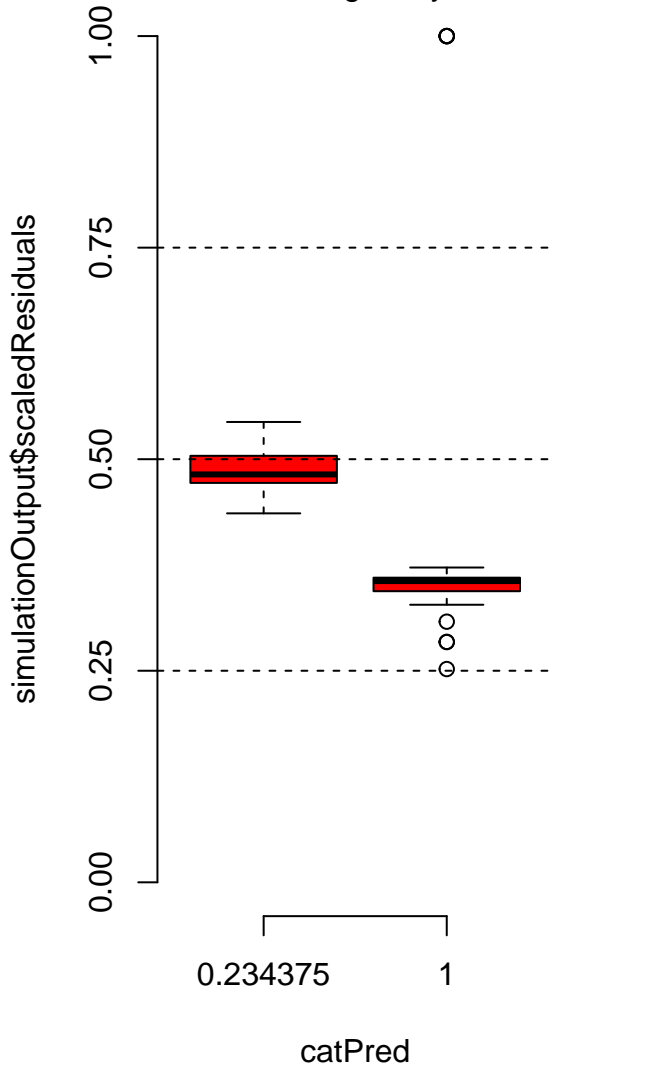
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.




```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-165.4	-155.9	87.7	-175.4	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.106e-02	1.052e-01
day	(Intercept)	1.656e-10	1.287e-05
Residual		4.604e-04	2.146e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00046

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.78595	0.03346	53.38	<2e-16 ***
inf_statusControl	-0.04174	0.06259	-0.67	0.505

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

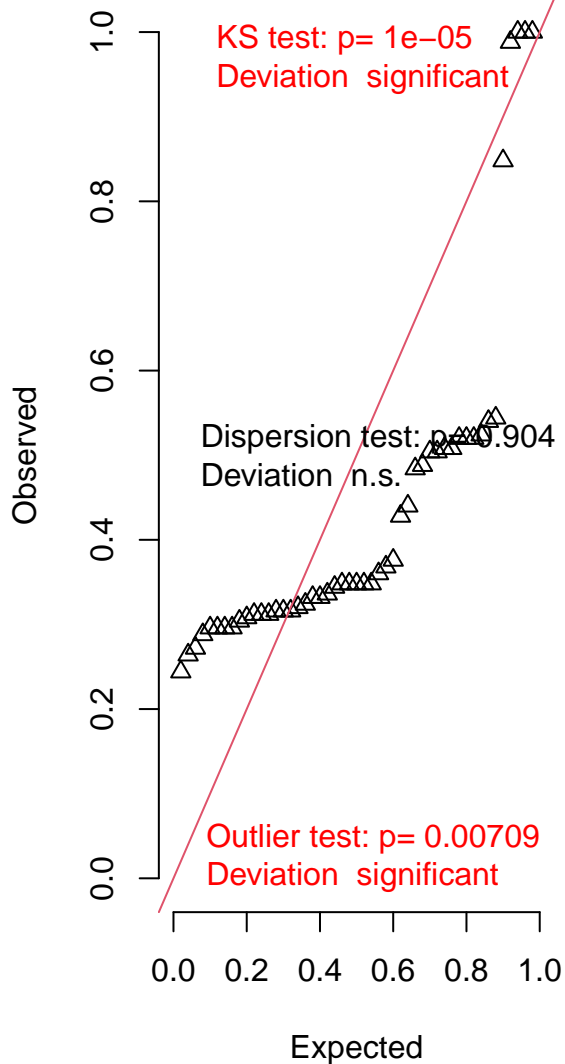
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 43

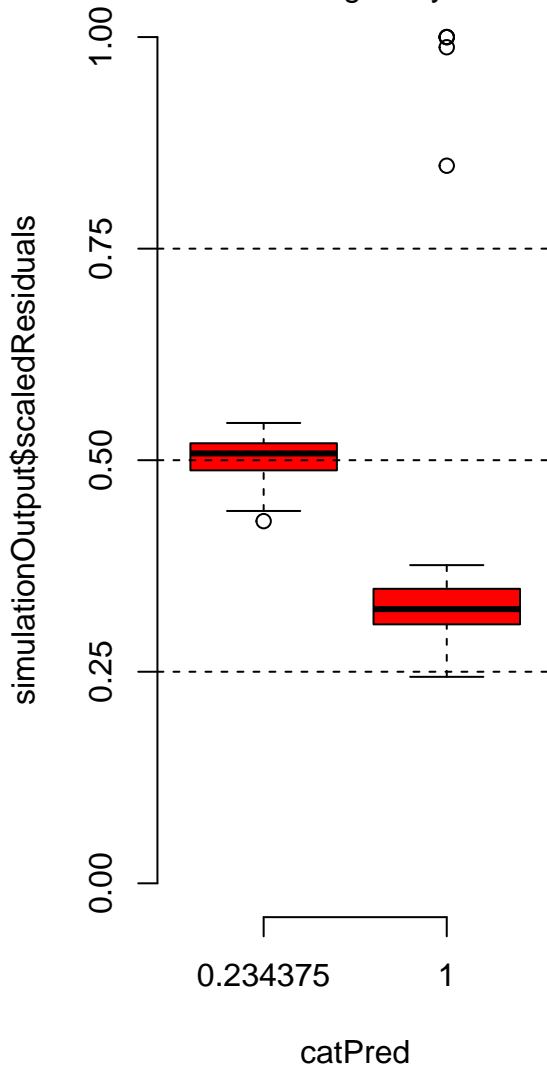
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-100.3	-90.9	55.2	-110.3	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	8.732e-03	9.344e-02
day	(Intercept)	3.910e-11	6.253e-06
Residual		3.134e-03	5.598e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00313

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.79589	0.03106	57.83	<2e-16 ***
inf_statusControl	-0.05167	0.05810	-0.89	0.374

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

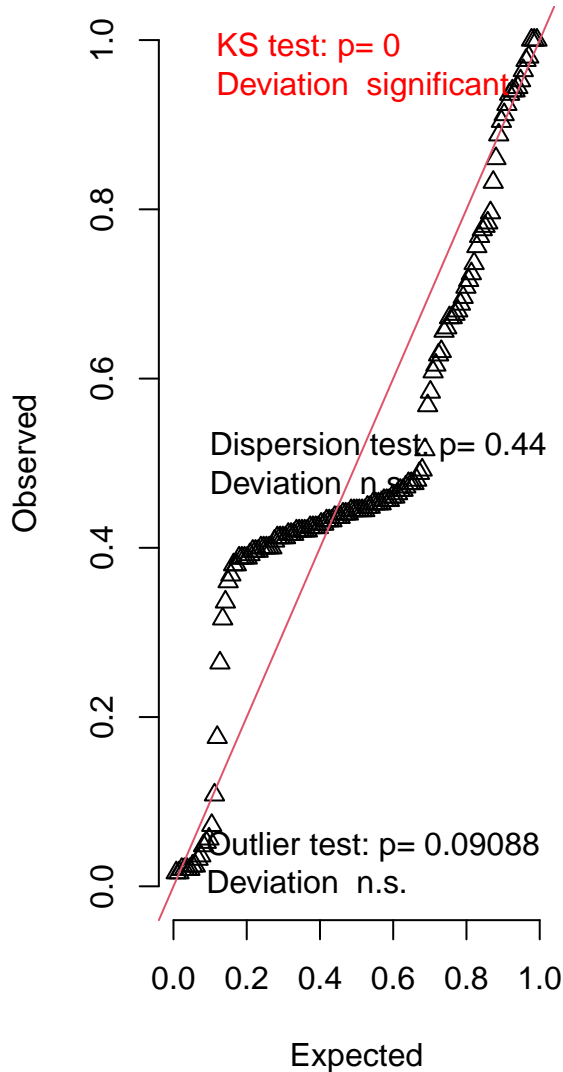
Effect of experiment

Nb obs (total) : 133

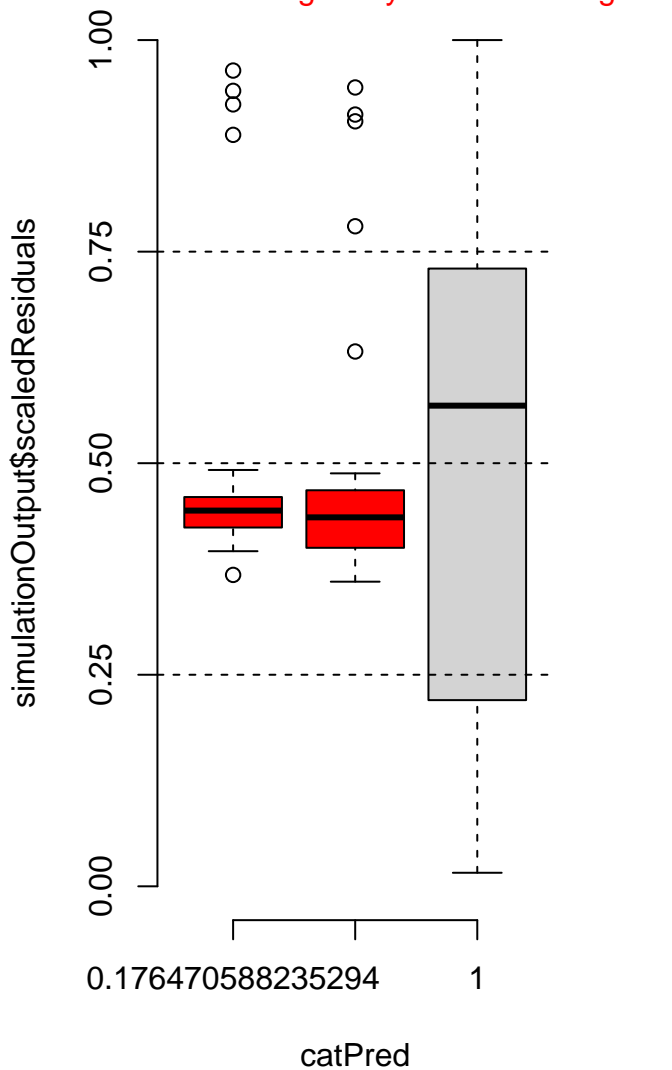
Nb LOD (included) : 69

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant




```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
2.3	19.6	4.9	-9.7	127

Random effects:

```

Conditional model:
Groups   Name             Variance Std.Dev.
ID       (Intercept) 2.790e-02 1.670e-01
day      (Intercept) 3.711e-12 1.926e-06
Residual                    4.014e-02 2.004e-01
Number of obs: 133, groups: ID, 29; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.0401

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.787639   0.062879  28.430 < 2e-16 ***
groupCyno.Dengue virus  0.475155   0.087697   5.418 6.02e-08 ***
groupSquirrel.Zika virus 0.007551   0.088925   0.085  0.932
---

```

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

IP.10

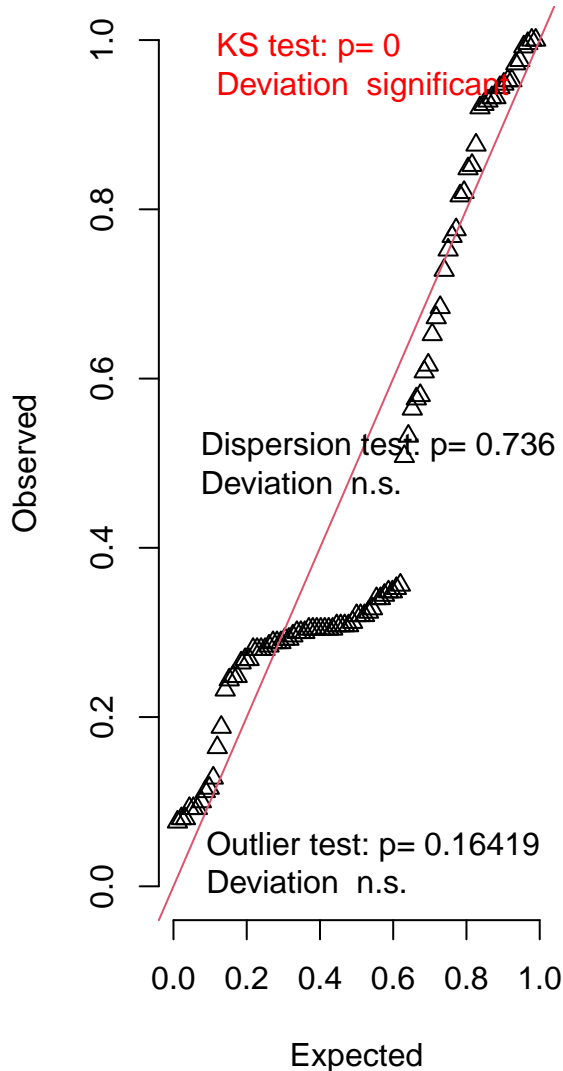
Infection in DENV-cyno

Nb obs (total) : 91

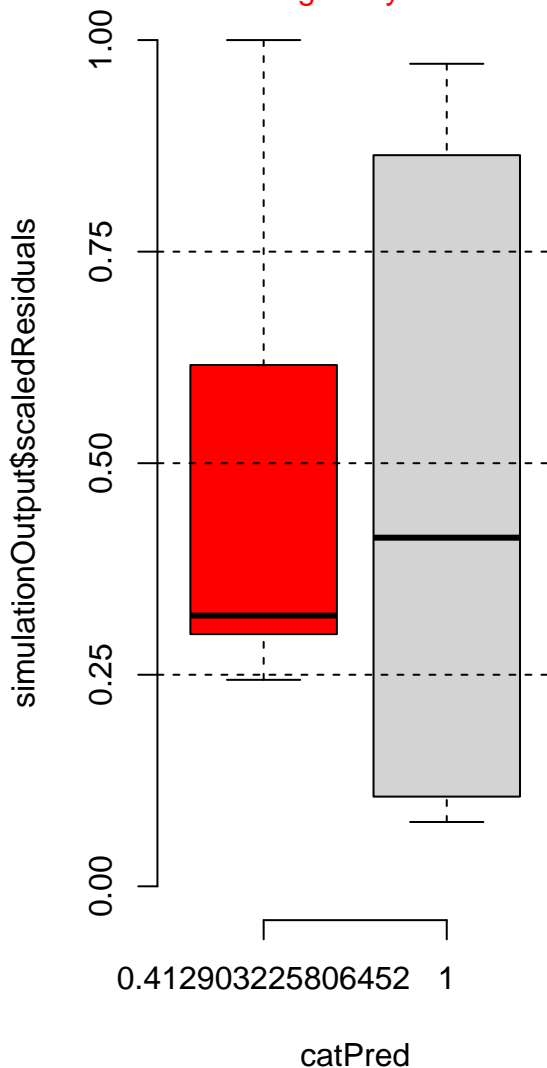
Nb LOD (included) : 51

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-122.0	-109.4	66.0	-132.0	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.587e-02	1.260e-01
day	(Intercept)	6.622e-12	2.573e-06
Residual		9.556e-03	9.776e-02

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00956

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.72508	0.04377	16.567	<2e-16 ***
inf_statusControl	0.11277	0.07890	1.429	0.153

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

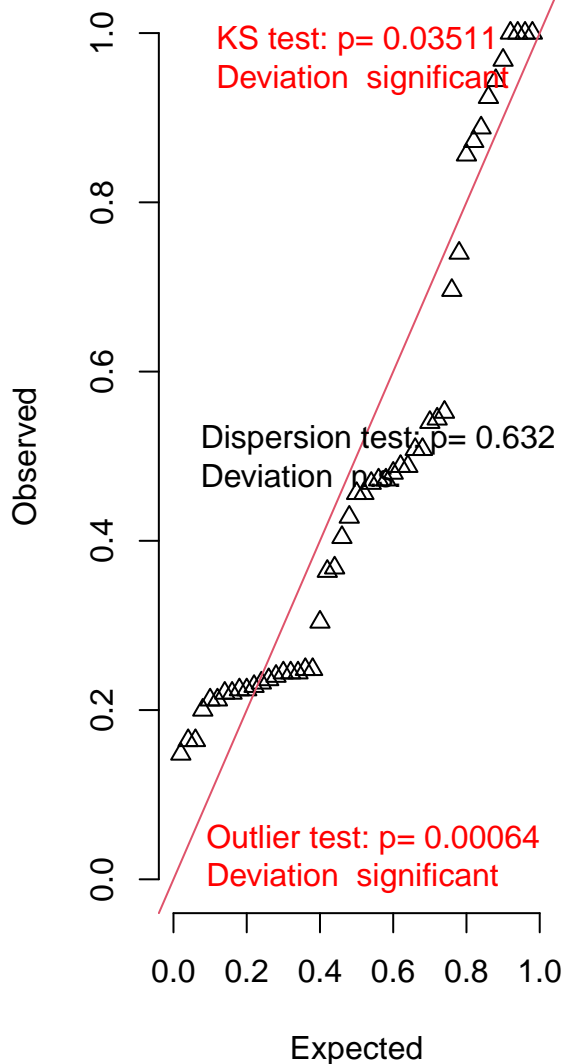
Infection in DENV-squirrel

Nb obs (total) : 49

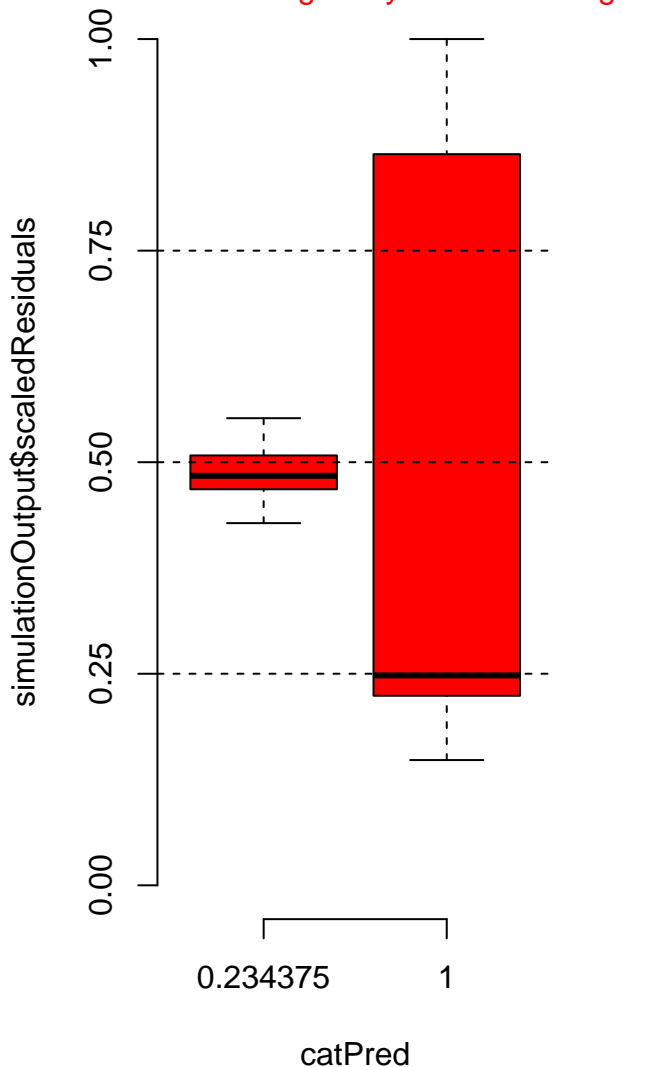
Nb LOD (included) : 33

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-52.1	-42.7	31.1	-62.1	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.1074522	0.32780
day	(Intercept)	0.0006921	0.02631
Residual		0.0042243	0.06499

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00422

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.9005	0.1047	8.598	<2e-16 ***
inf_statusControl	-0.2617	0.1950	-1.342	0.18

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

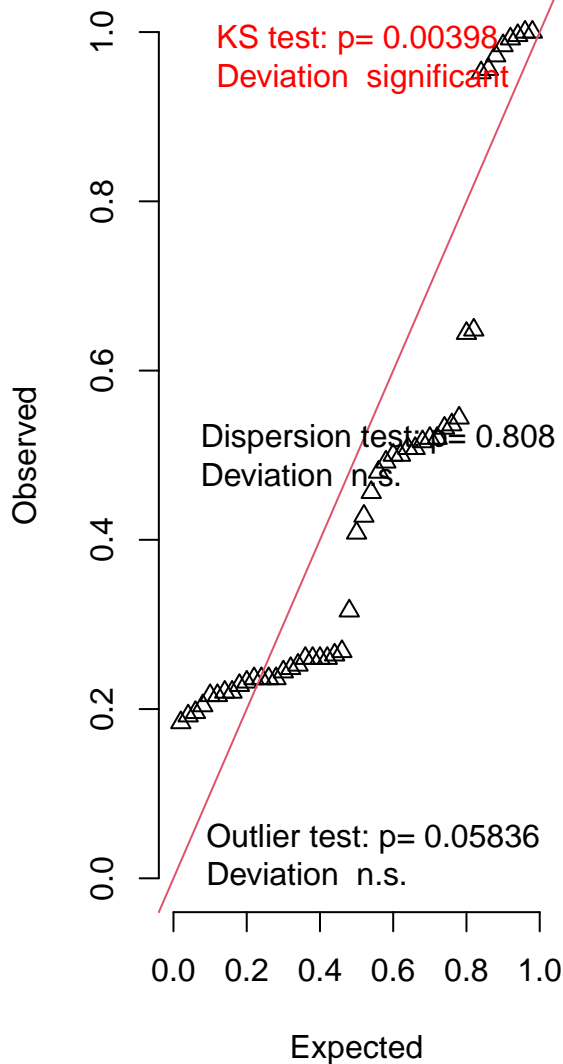
Infection in ZIKV-squirrel

Nb obs (total) : 49

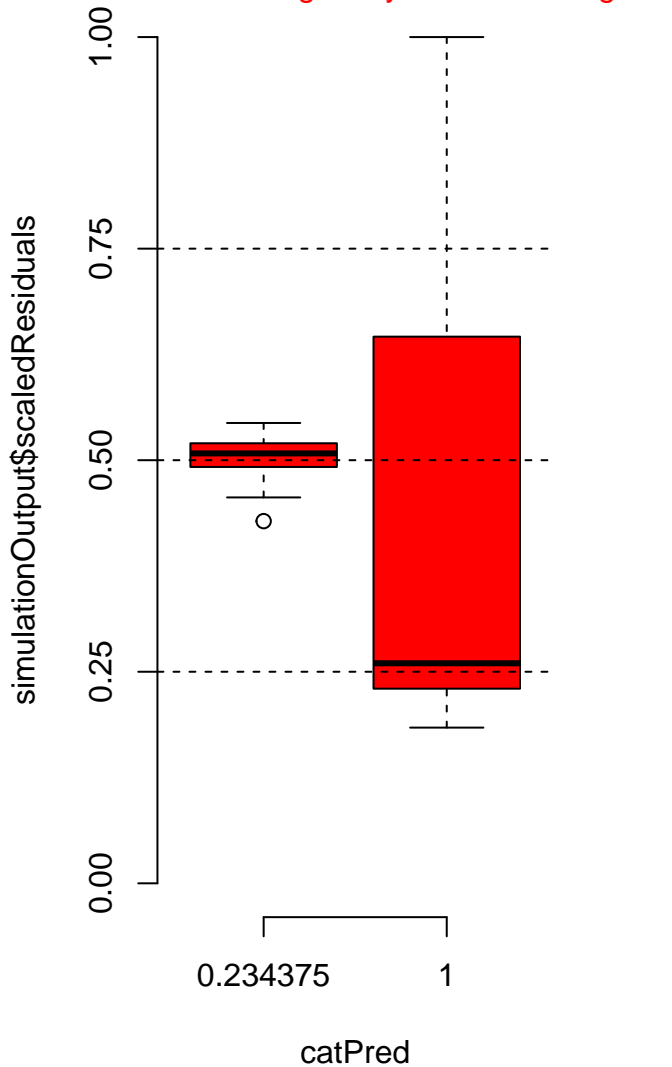
Nb LOD (included) : 37

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-62.7	-53.3	36.4	-72.7	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.035274	0.18781
day	(Intercept)	0.001163	0.03410
Residual		0.004636	0.06809

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00464

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.7811	0.0619	12.619	<2e-16 ***
inf_statusControl	-0.1426	0.1132	-1.259	0.208

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

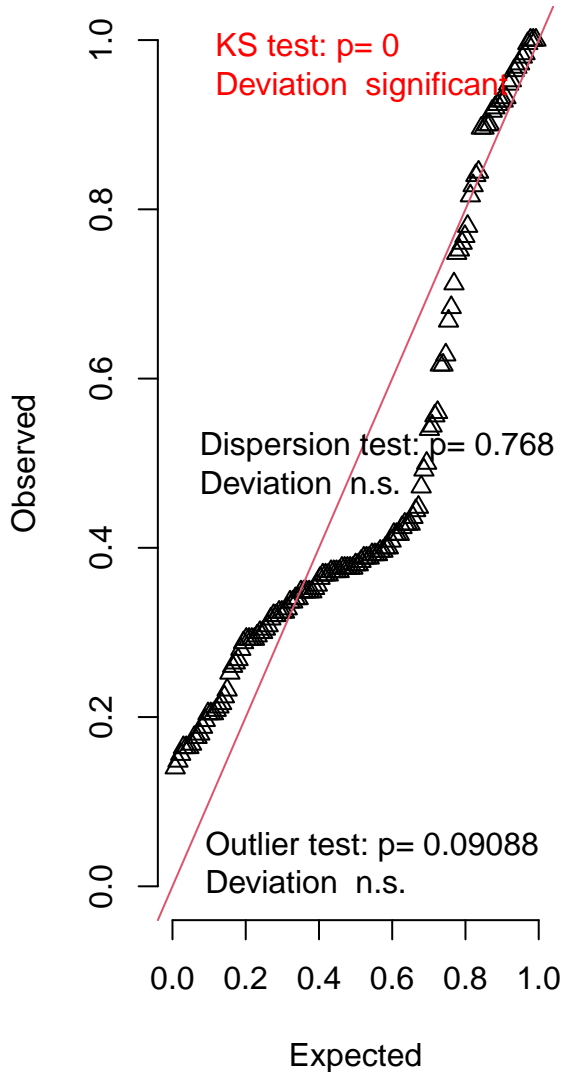
Effect of experiment

Nb obs (total) : 133

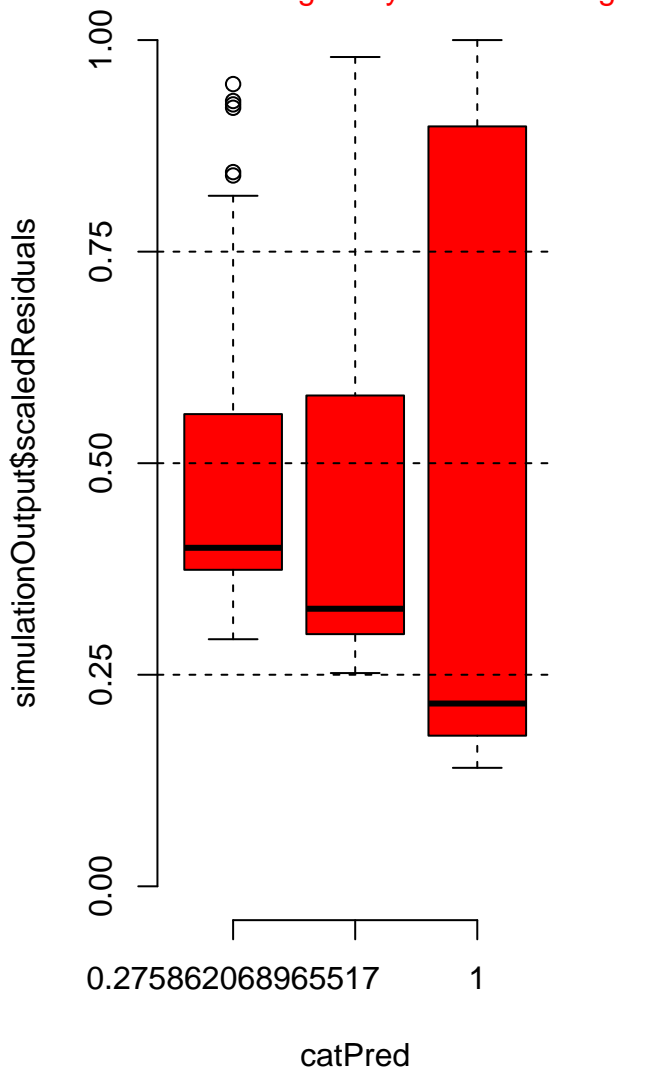
Nb LOD (included) : 83

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-126.9	-109.5	69.4	-138.9	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	7.076e-02	0.266004
day	(Intercept)	5.493e-05	0.007411
Residual		9.581e-03	0.097883

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00958

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.90127	0.08581	10.503	<2e-16 ***
groupCyno.Dengue virus	-0.17615	0.12398	-1.421	0.155
groupSquirrel.Zika virus	-0.12010	0.12129	-0.990	0.322

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

MCP . 1

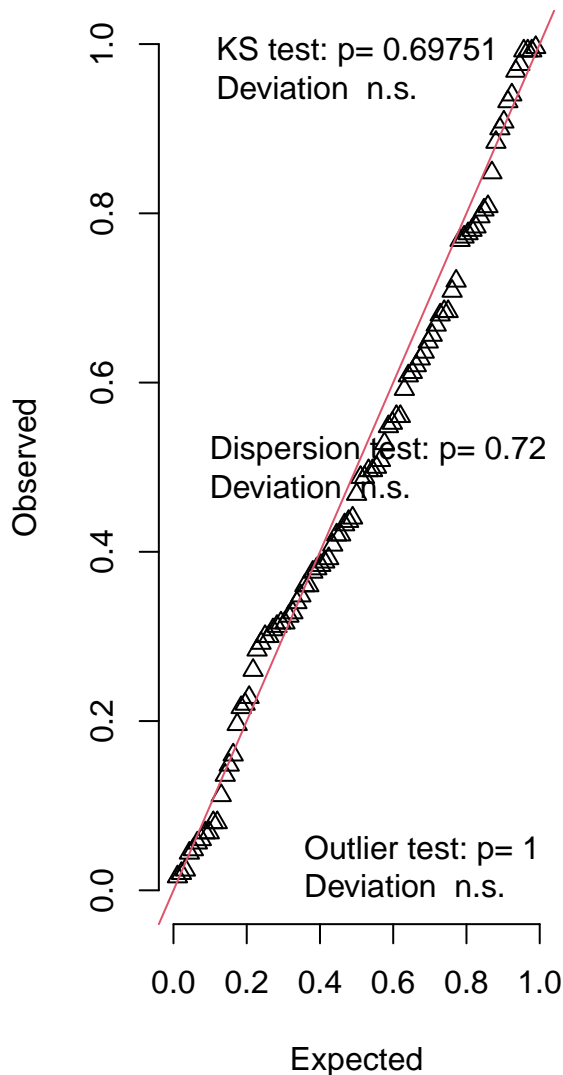
Infection in DENV-cyno

Nb obs (total): 91

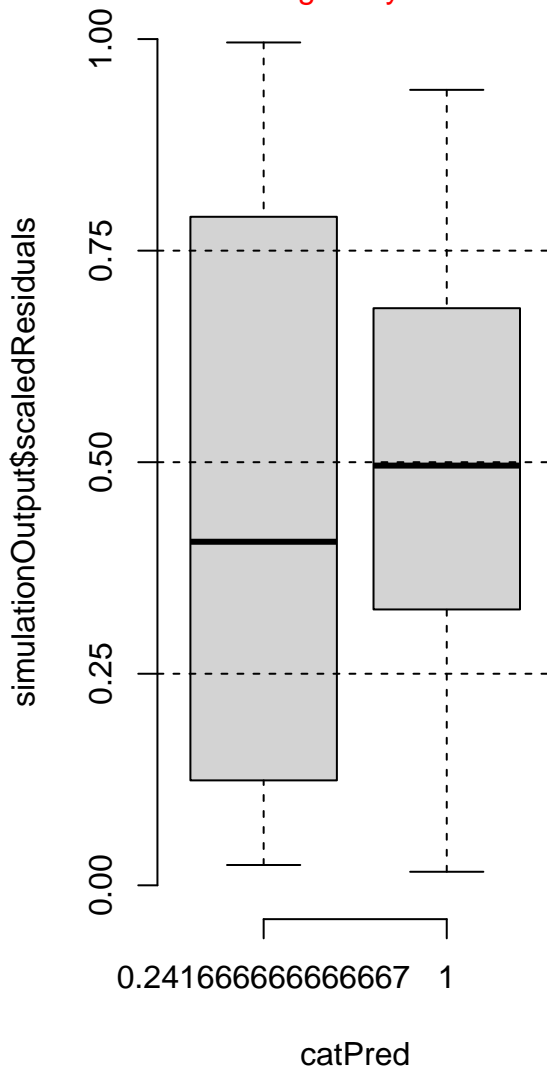
Nb LOD (included): 0

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-77.1	-64.6	43.6	-87.1	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.056e-02	1.434e-01
day	(Intercept)	2.664e-11	5.161e-06
Residual		1.621e-02	1.273e-01

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0162

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.683242	0.050410	53.23	<2e-16 ***
inf_statusControl	-0.001313	0.090878	-0.01	0.988

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

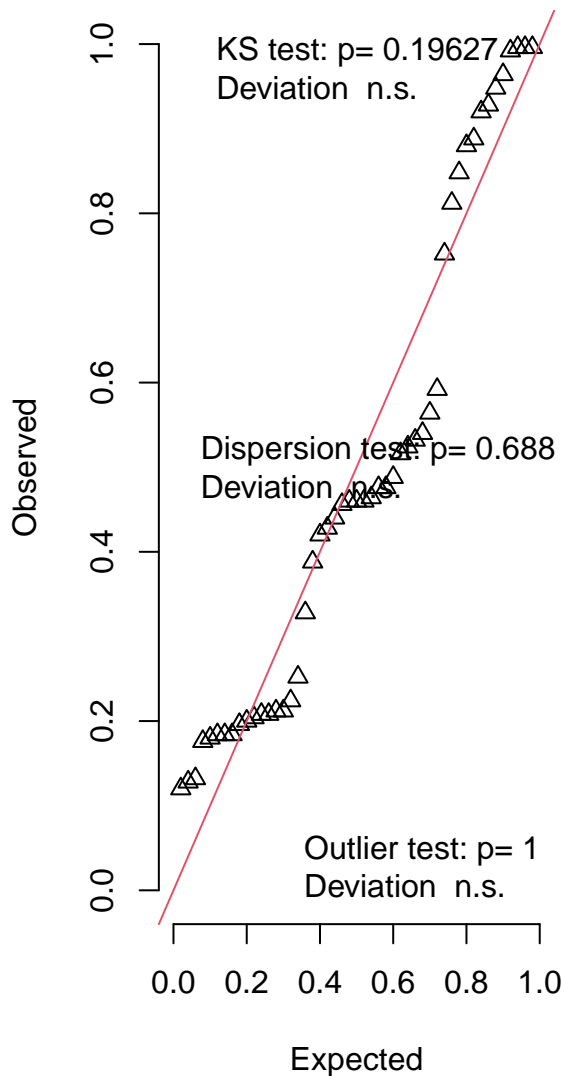
Infection in DENV-squirrel

Nb obs (total) : 49

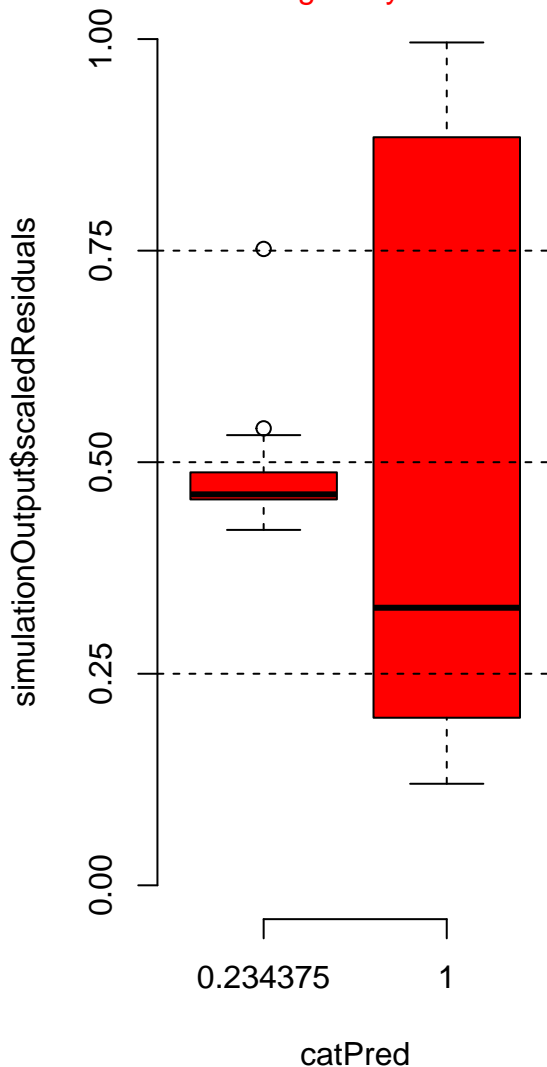
Nb LOD (included) : 28

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
31.4	40.9	-10.7	21.4	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	6.199e-01	7.873e-01
day	(Intercept)	3.744e-12	1.935e-06
Residual		2.543e-02	1.595e-01

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0254

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.0470	0.2505	8.173	3.01e-16 ***
inf_statusControl	-0.7036	0.4686	-1.502	0.133

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

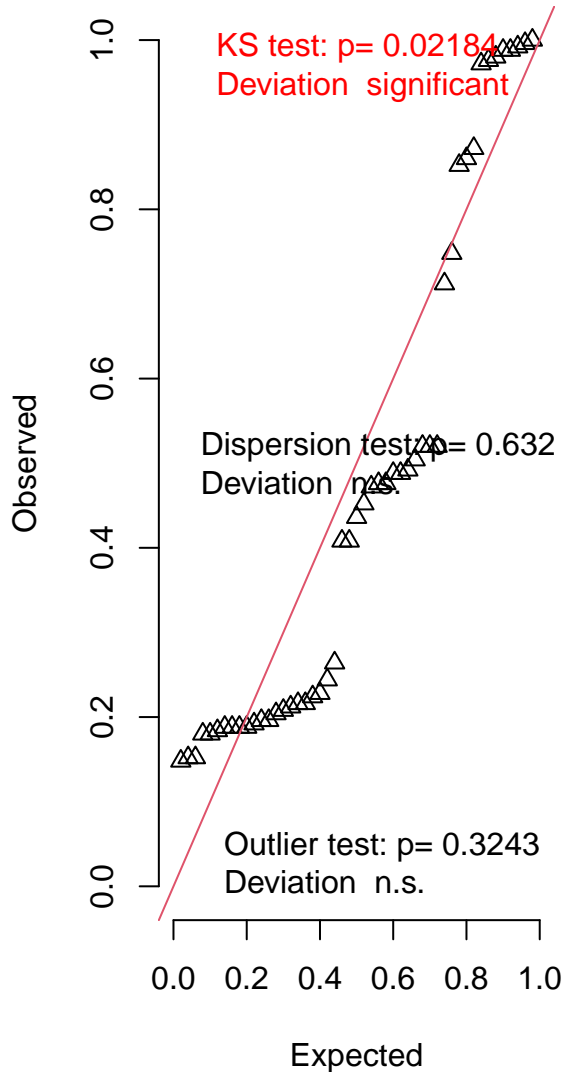
Infection in ZIKV-squirrel

Nb obs (total) : 49

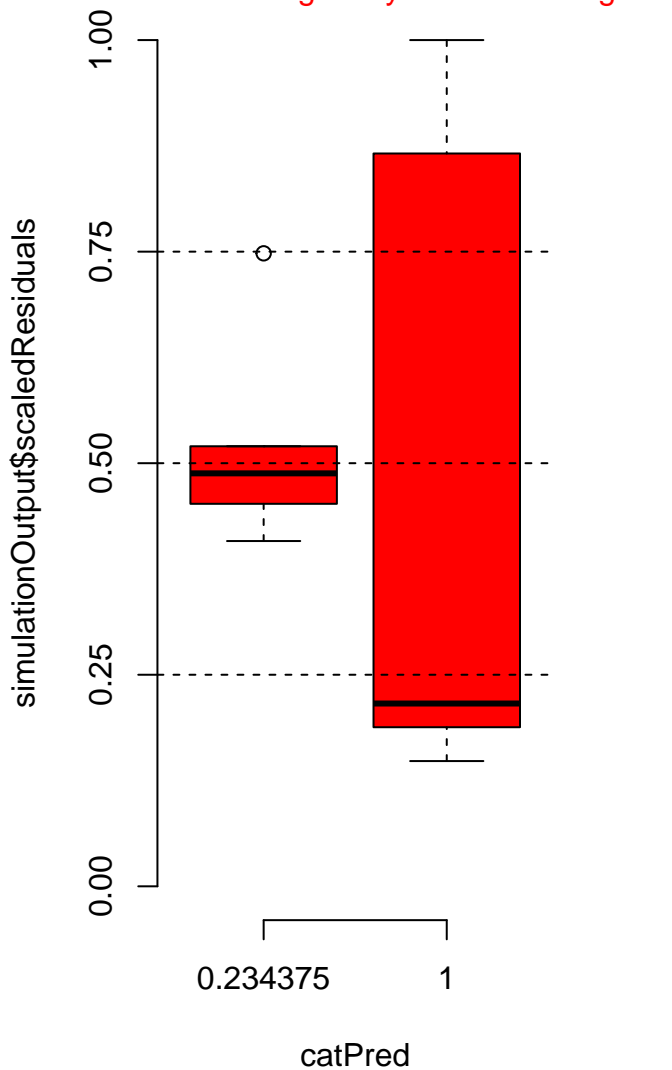
Nb LOD (included) : 35

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
47.9	57.4	-19.0	37.9	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.550461	0.74193
day	(Intercept)	0.001339	0.03659
Residual		0.041348	0.20334

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0413

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.9378	0.2376	8.156	3.46e-16 ***
inf_statusControl	-0.5944	0.4437	-1.339	0.18

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

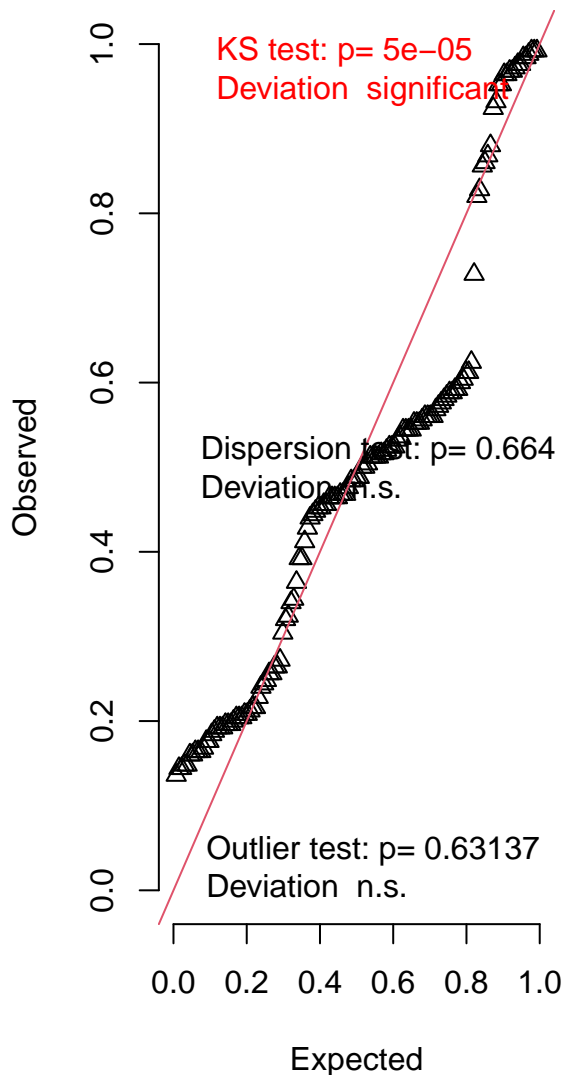
Effect of experiment

Nb obs (total) : 133

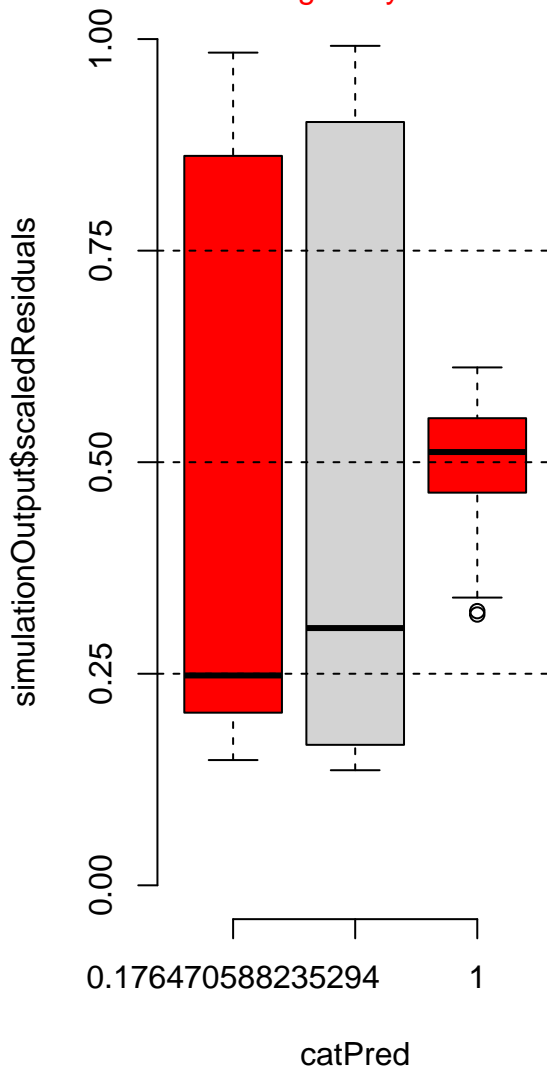
Nb LOD (included) : 37

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
48.4	65.7	-18.2	36.4	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.650e-01	7.517e-01
day	(Intercept)	2.527e-12	1.590e-06
Residual		2.928e-02	1.711e-01

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0293

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.0473	0.2395	8.548	<2e-16 ***
groupCyno.Dengue virus	0.6359	0.3473	1.831	0.0671 .
groupSquirrel.Zika virus	-0.1099	0.3387	-0.325	0.7455

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

MDC

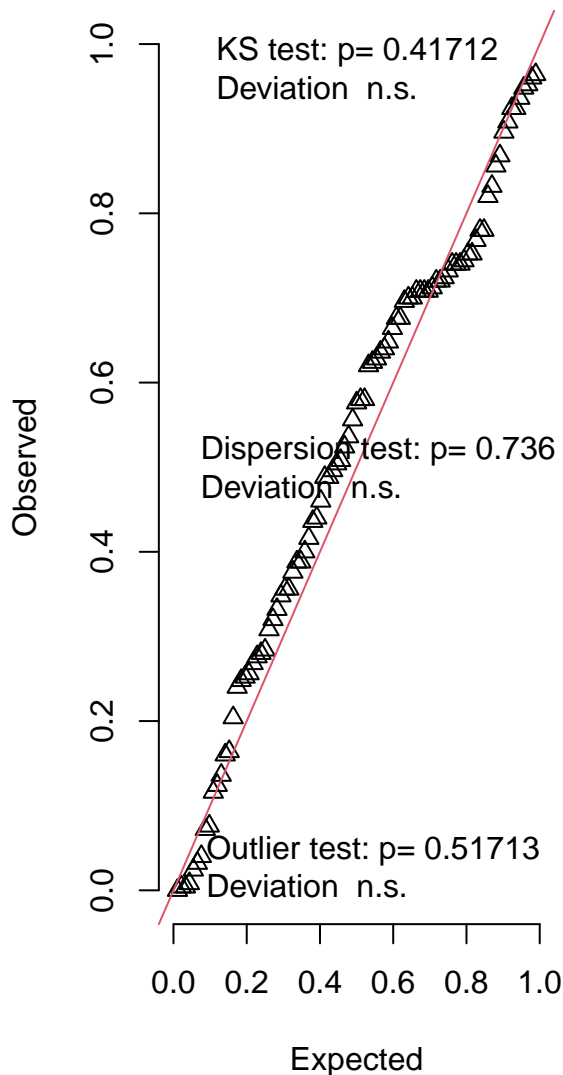
Infection in DENV-cyno

Nb obs (total): 91

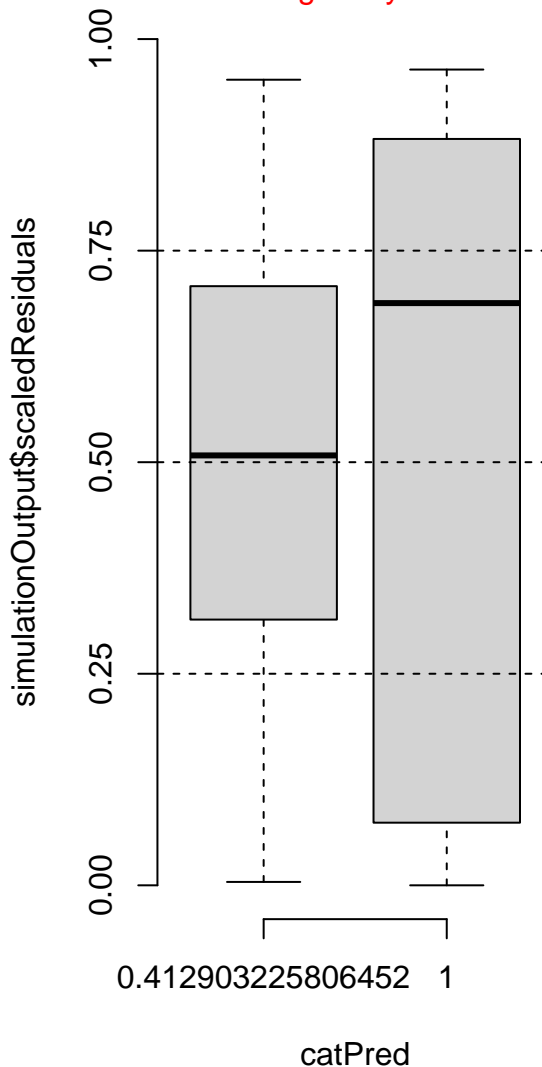
Nb LOD (included): 0

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-151.8	-139.2	80.9	-161.8	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.058e-02	0.102858
day	(Intercept)	2.666e-05	0.005163
Residual		6.942e-03	0.083318

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00694

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.04976	0.03591	84.93	<2e-16 ***
inf_statusControl	0.08367	0.06464	1.29	0.196

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

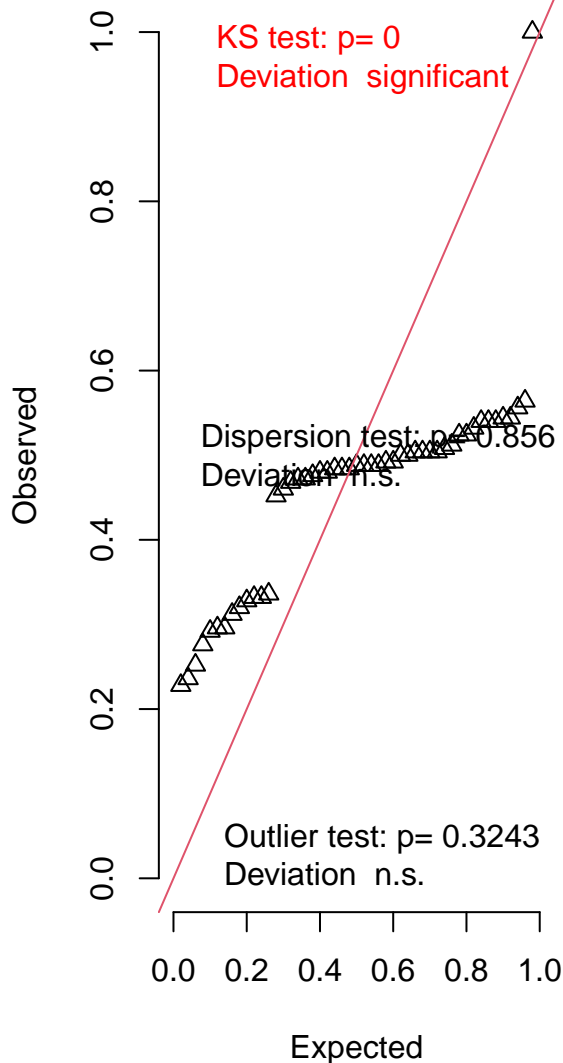
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 48

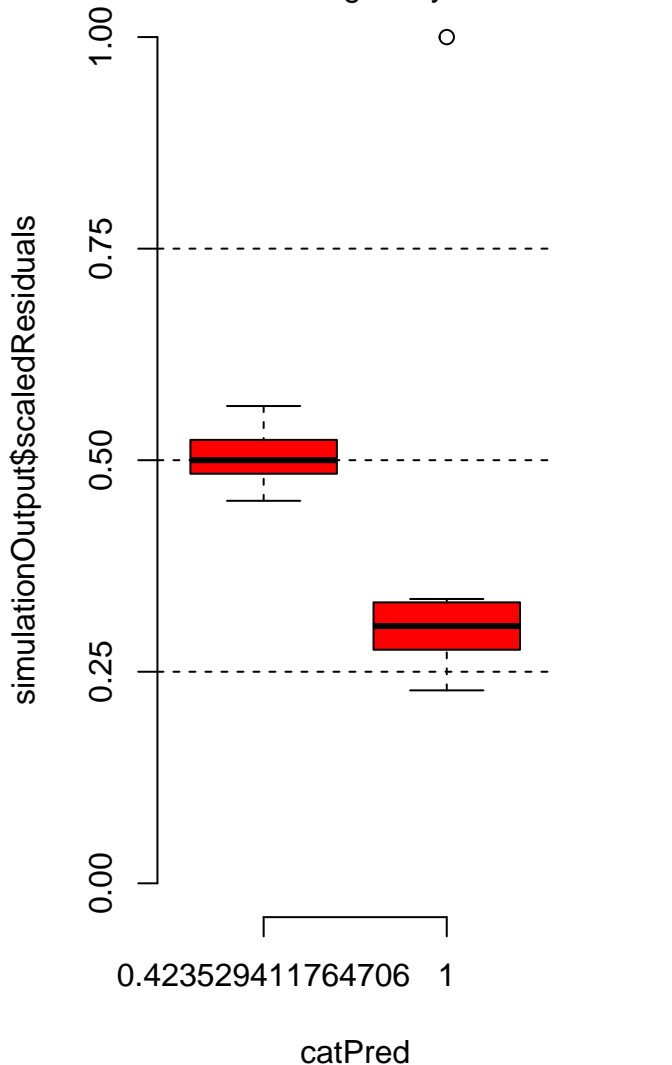
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-245.3	-235.8	127.6	-255.3	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	8.814e-13	9.388e-07
day	(Intercept)	1.251e-12	1.119e-06
Residual		3.200e-04	1.789e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00032

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.470058	0.003024	816.9	<2e-16 ***
inf_statusControl	0.009282	0.005657	1.6	0.101

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

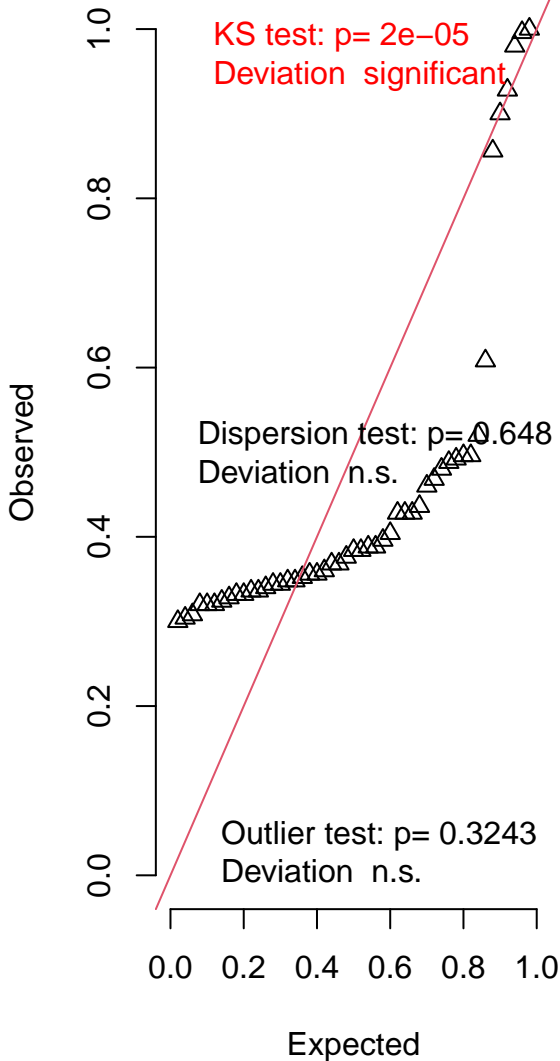
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 42

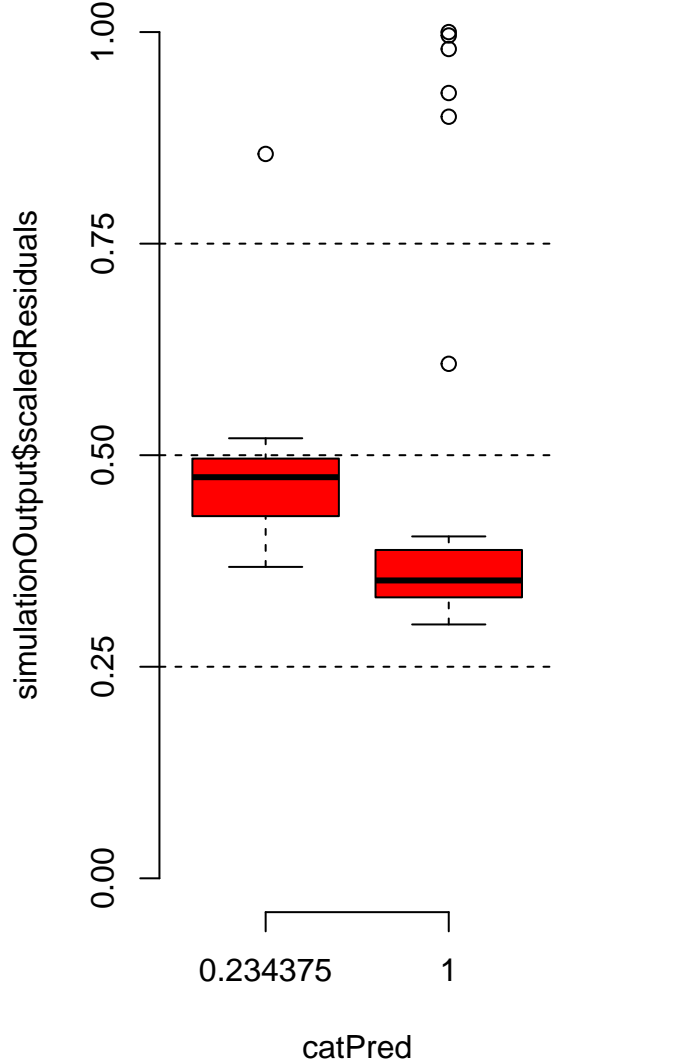
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-79.9	-70.4	44.9	-89.9	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.005311	0.07287
day	(Intercept)	0.001330	0.03647
Residual		0.005468	0.07395

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00547

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.51431	0.02970	84.65	<2e-16 ***
inf_statusControl	-0.03294	0.04914	-0.67	0.503

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

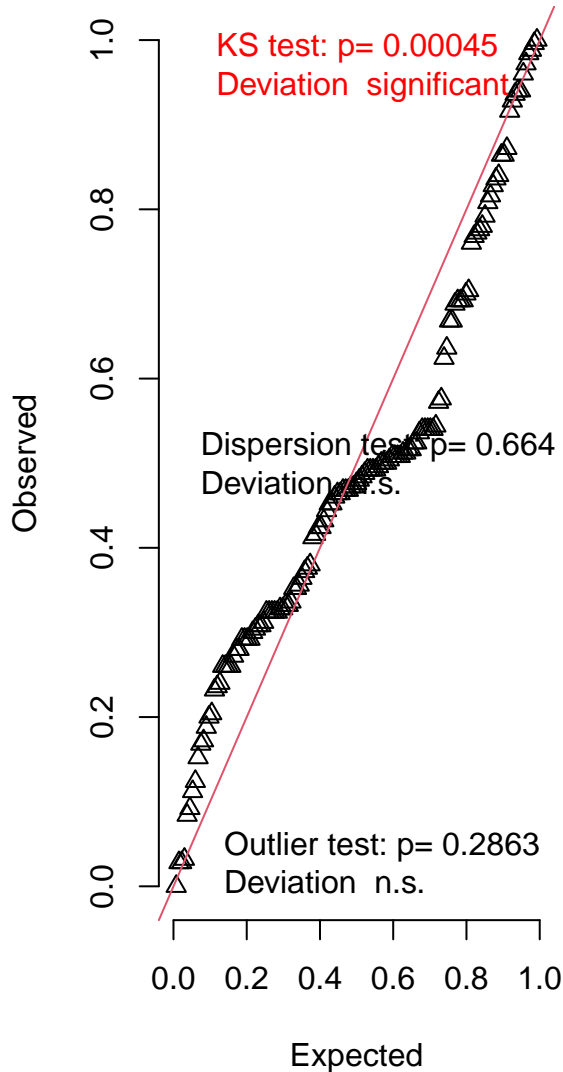
Effect of experiment

Nb obs (total): 133

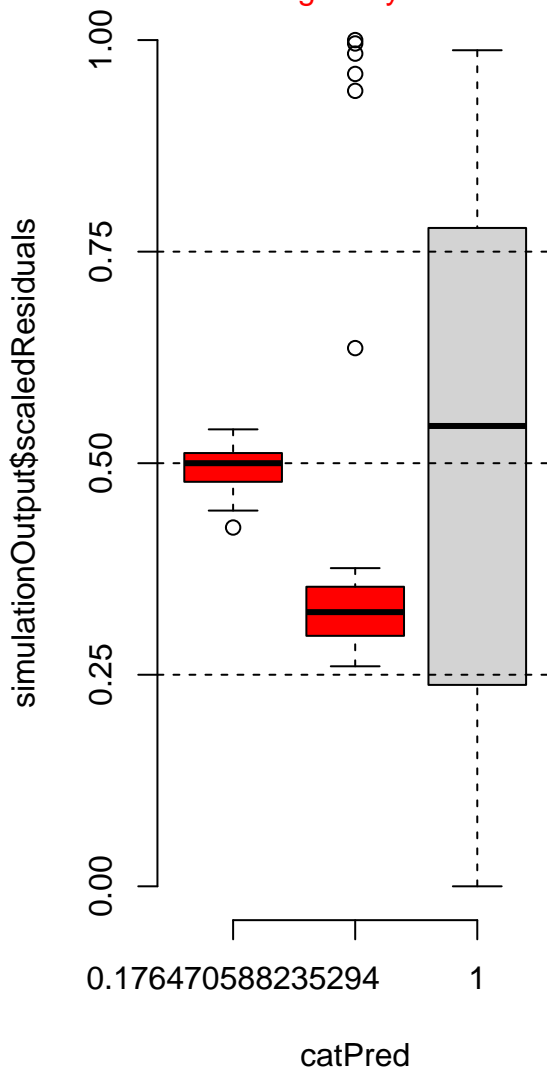
Nb LOD (included): 64

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-276.9	-259.6	144.5	-288.9	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0032840	0.05731
day	(Intercept)	0.0007628	0.02762
Residual		0.0045665	0.06758

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00457

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.47354	0.02374	104.19	<2e-16 ***
groupCyno.Dengue virus	0.57448	0.03031	18.95	<2e-16 ***
groupSquirrel.Zika virus	0.04376	0.03036	1.44	0.15

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

MIF

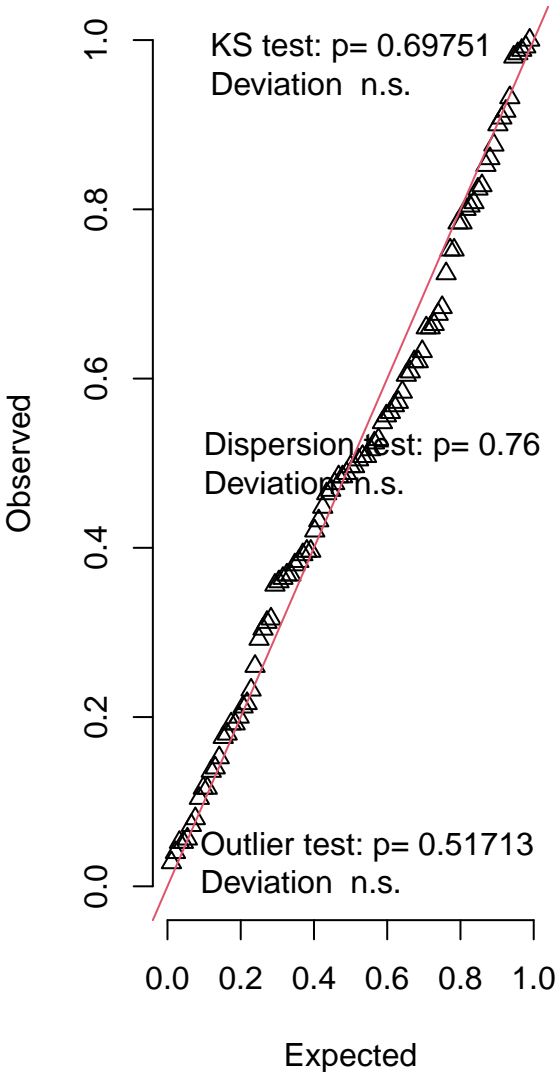
Infection in DENV-cyno

Nb obs (total): 91

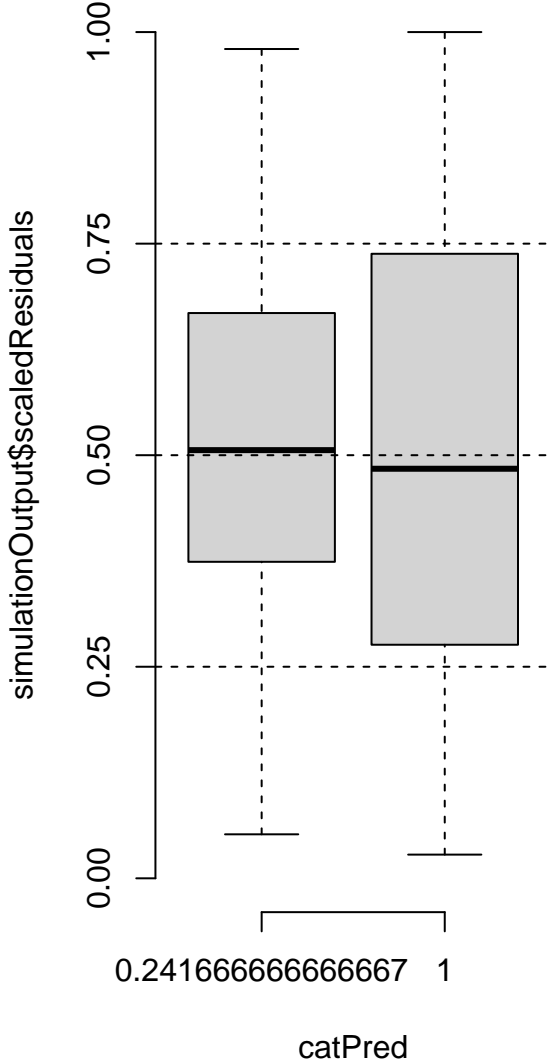
Nb LOD (included): 0

DHARMa residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.




```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
24.5	37.1	-7.3	14.5	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.03126	0.1768
day	(Intercept)	0.03599	0.1897
Residual		0.04491	0.2119

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0449

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.30898	0.09658	23.908	<2e-16 ***
inf_statusControl	-0.01415	0.11664	-0.121	0.903

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

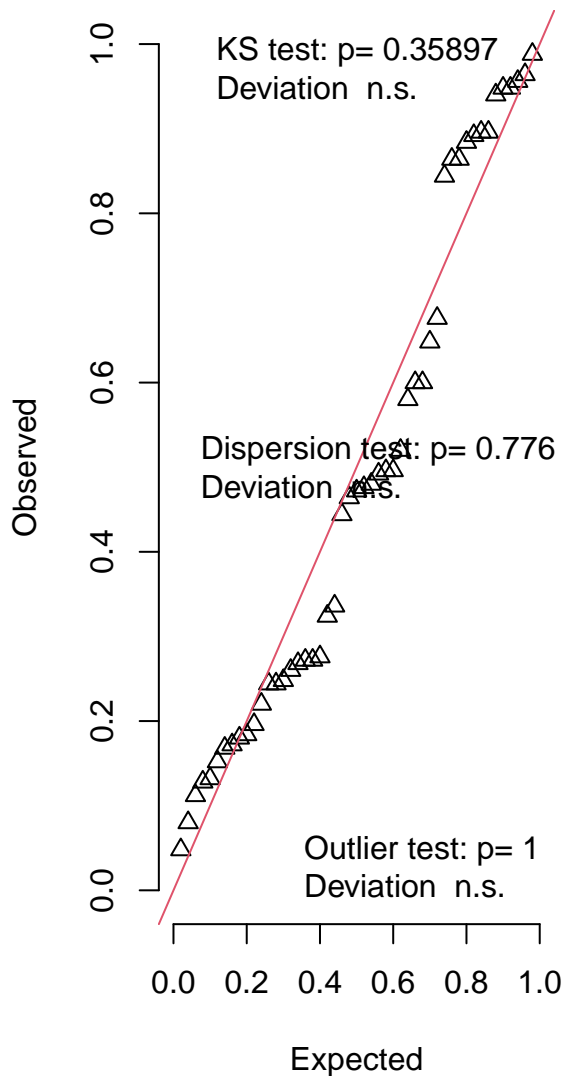
Infection in DENV-squirrel

Nb obs (total) : 49

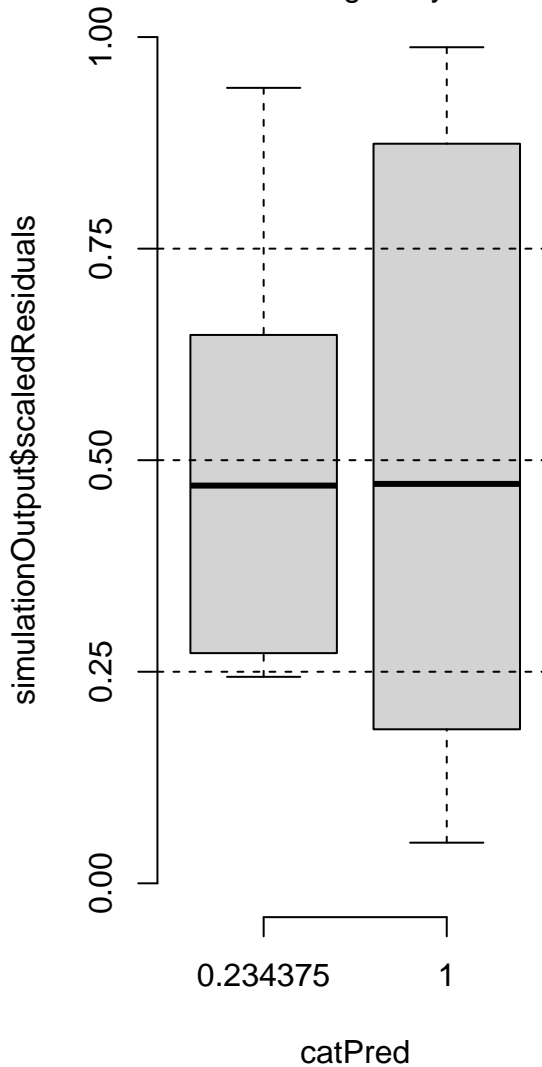
Nb LOD (included) : 0

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
40.9	50.4	-15.5	30.9	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.03433	0.1853
day	(Intercept)	0.03675	0.1917
Residual		0.06769	0.2602

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0677

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.35201	0.10326	22.777	<2e-16 ***
inf_statusControl	-0.01089	0.13739	-0.079	0.937

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

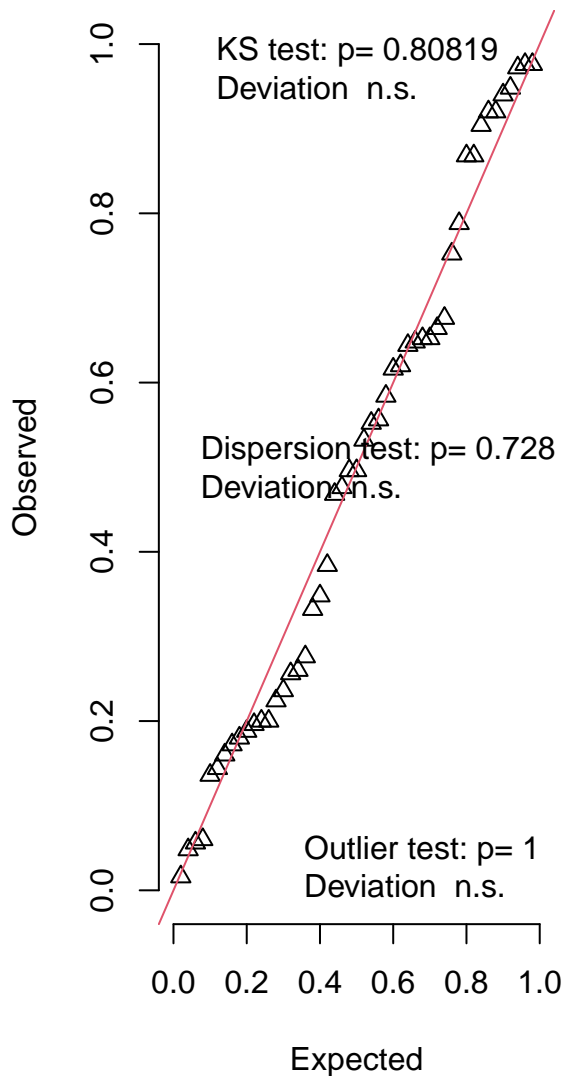
Infection in ZIKV-squirrel

Nb obs (total) : 49

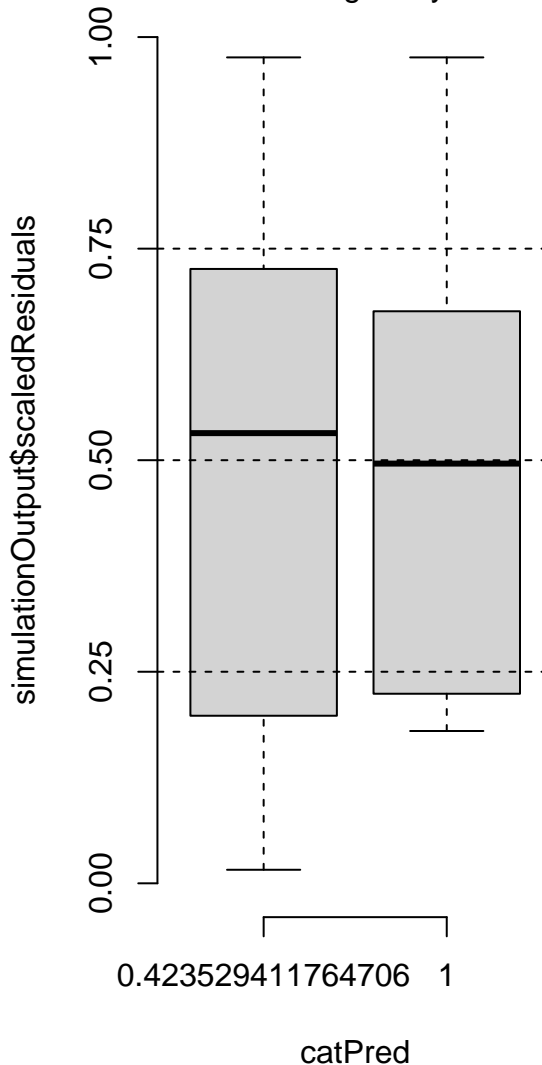
Nb LOD (included) : 0

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.




```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
15.0	24.5	-2.5	5.0	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.01268	0.1126
day	(Intercept)	0.02515	0.1586
Residual		0.04288	0.2071

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0429

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.32508	0.07818	29.740	<2e-16 ***
inf_statusControl	0.01463	0.09373	0.156	0.876

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

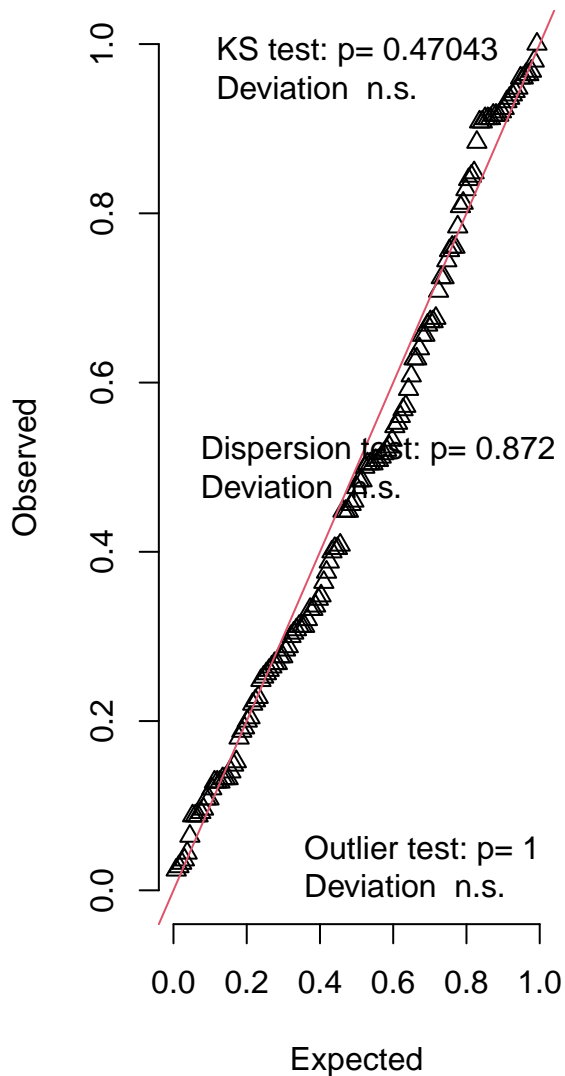
Effect of experiment

Nb obs (total):133

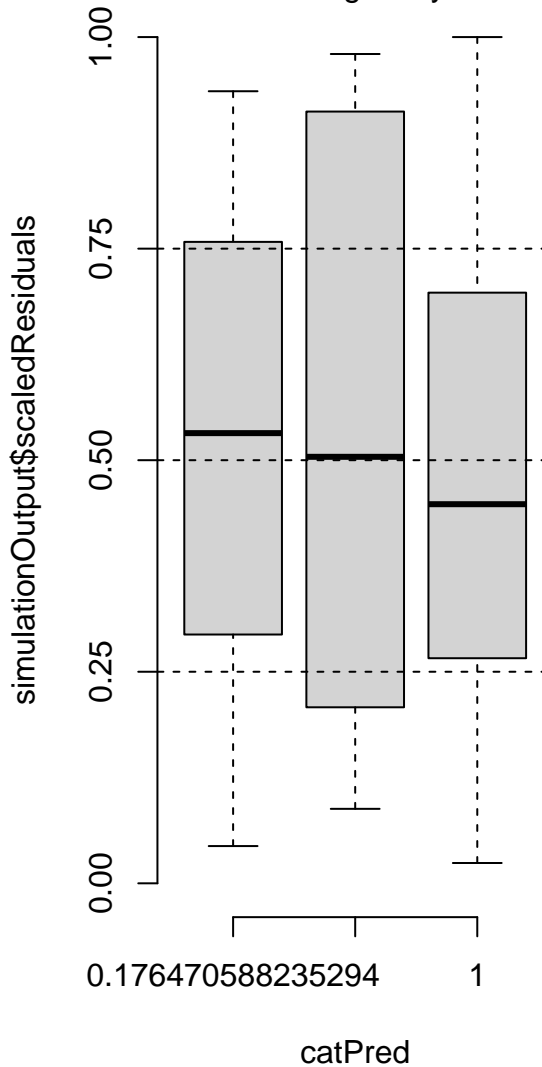
Nb LOD (included): 0

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
91.6	108.9	-39.8	79.6	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.02776	0.1666
day	(Intercept)	0.02394	0.1547
Residual		0.07868	0.2805

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0787

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.32518	0.09061	25.662	<2e-16 ***
groupCyno.Dengue virus	0.01777	0.09964	0.178	0.858
groupSquirrel.Zika virus	-0.02386	0.10050	-0.237	0.812

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

MIG

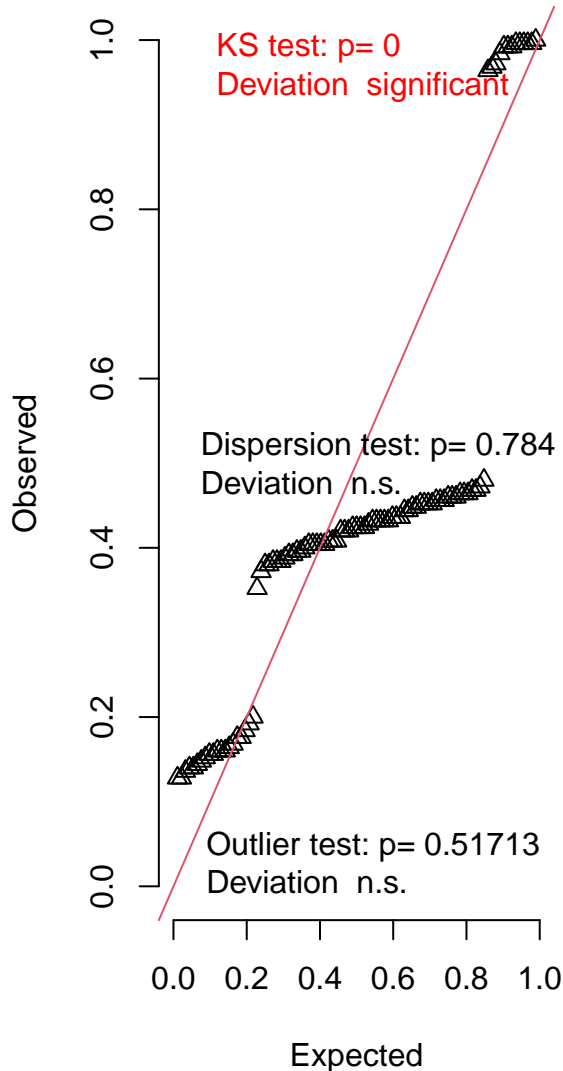
Infection in DENV-cyno

Nb obs (total) : 91

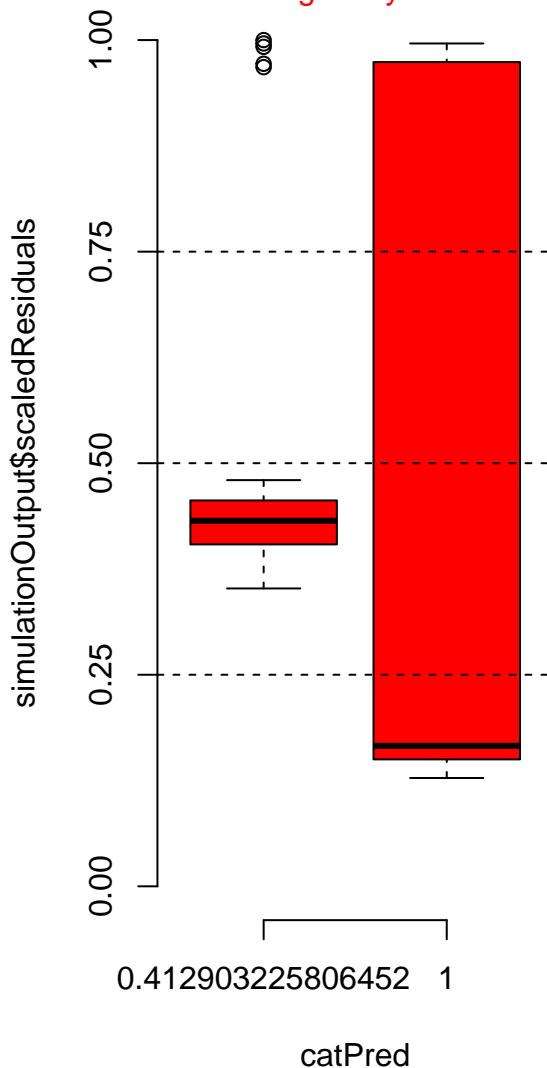
Nb LOD (included) : 77

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-45.2	-32.7	27.6	-55.2	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0753700	0.27454
day	(Intercept)	0.0007275	0.02697
Residual		0.0192722	0.13882

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0193

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.44094	0.09372	15.374	<2e-16 ***
inf_statusControl	0.24237	0.16796	1.443	0.149

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

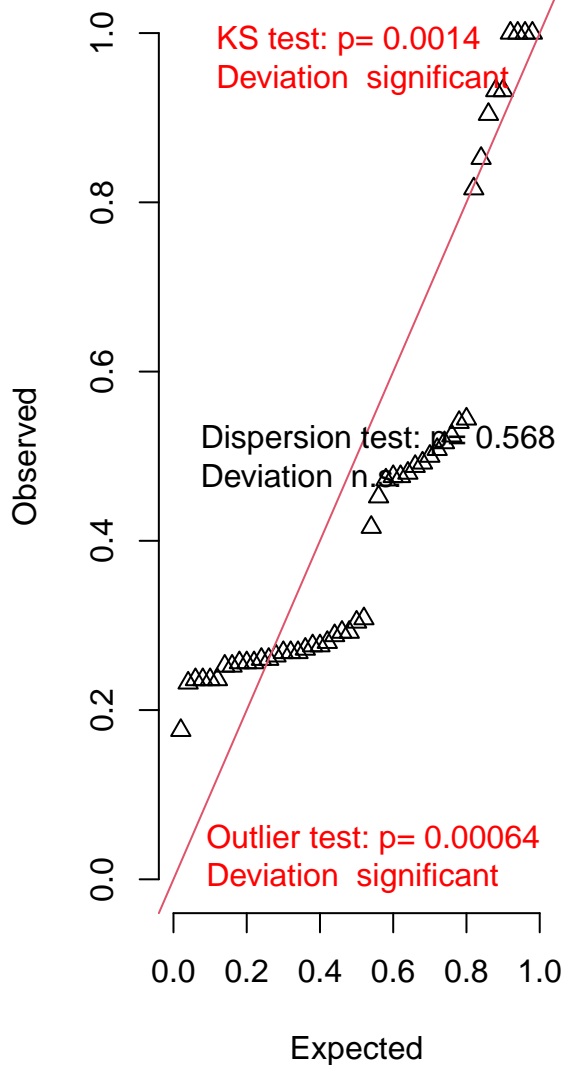
Infection in DENV-squirrel

Nb obs (total) : 49

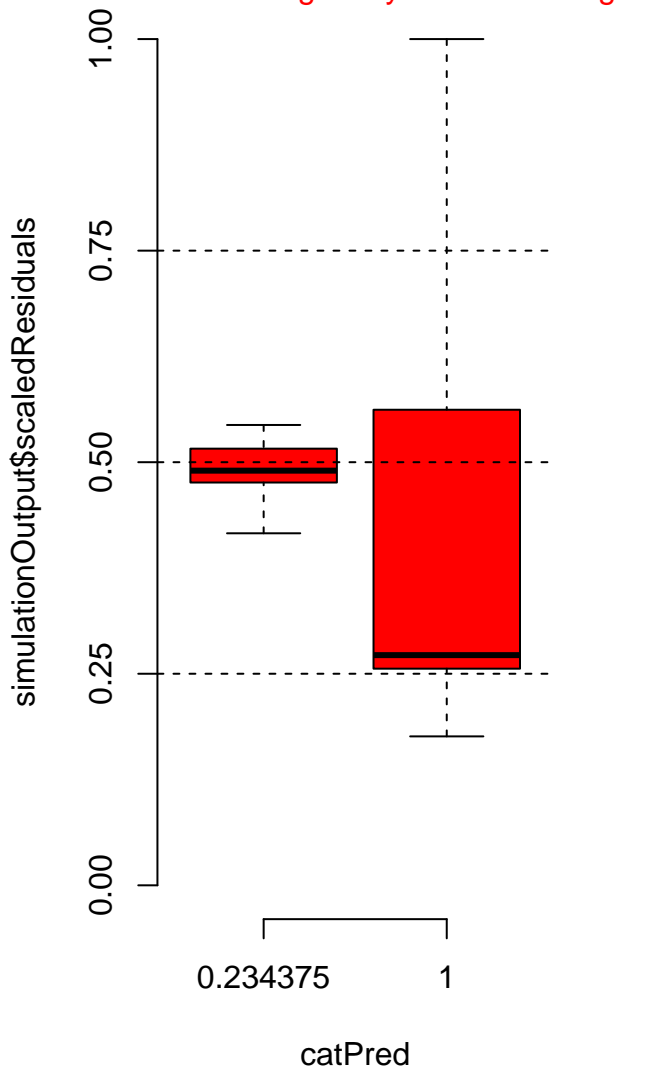
Nb LOD (included) : 40

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
10.8	20.3	-0.4	0.8	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.105427	0.32470
day	(Intercept)	0.001003	0.03166
Residual		0.027067	0.16452

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0271

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.6032	0.1071	14.964	<2e-16 ***
inf_statusControl	-0.2303	0.1991	-1.156	0.248

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

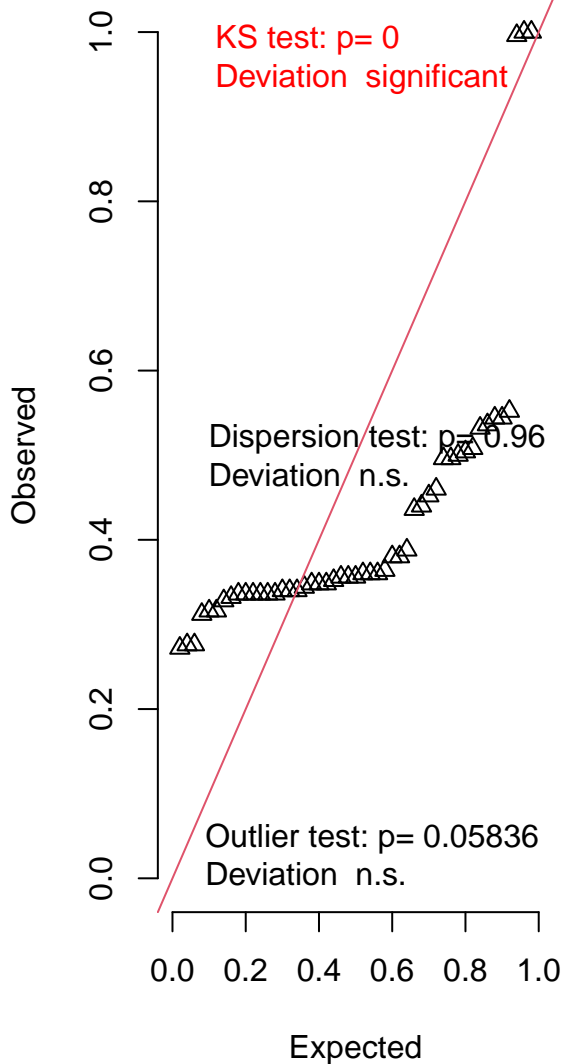
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 46

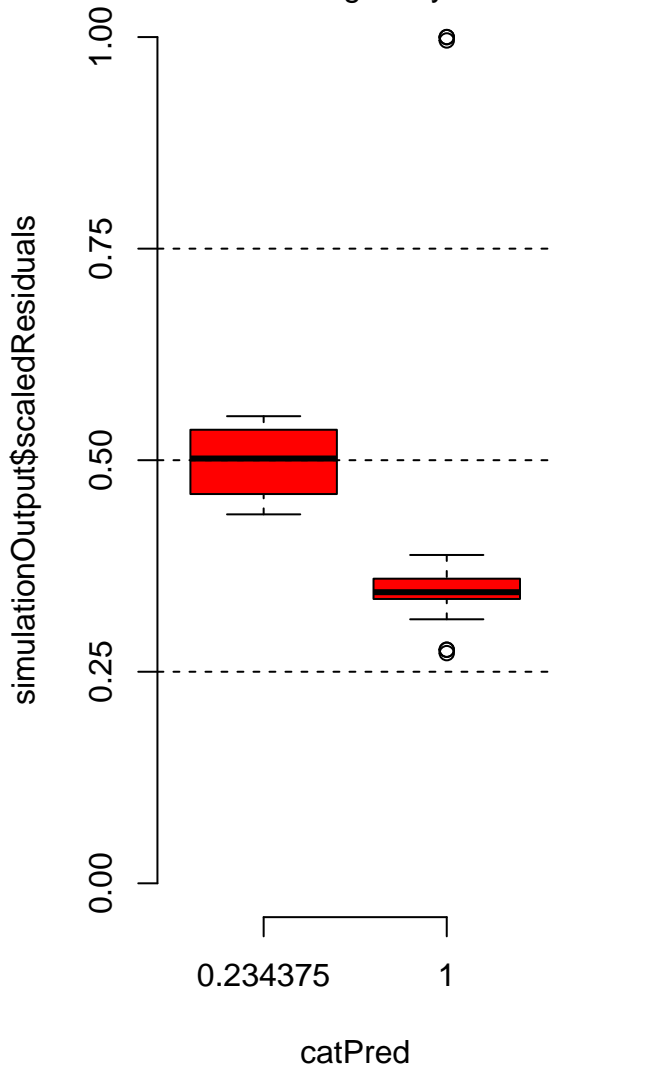
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-150.4	-141.0	80.2	-160.4	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.629e-02	1.276e-01
day	(Intercept)	1.404e-10	1.185e-05
Residual		6.041e-04	2.458e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000604

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.42333	0.04058	35.07	<2e-16 ***
inf_statusControl	-0.05060	0.07592	-0.67	0.505

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

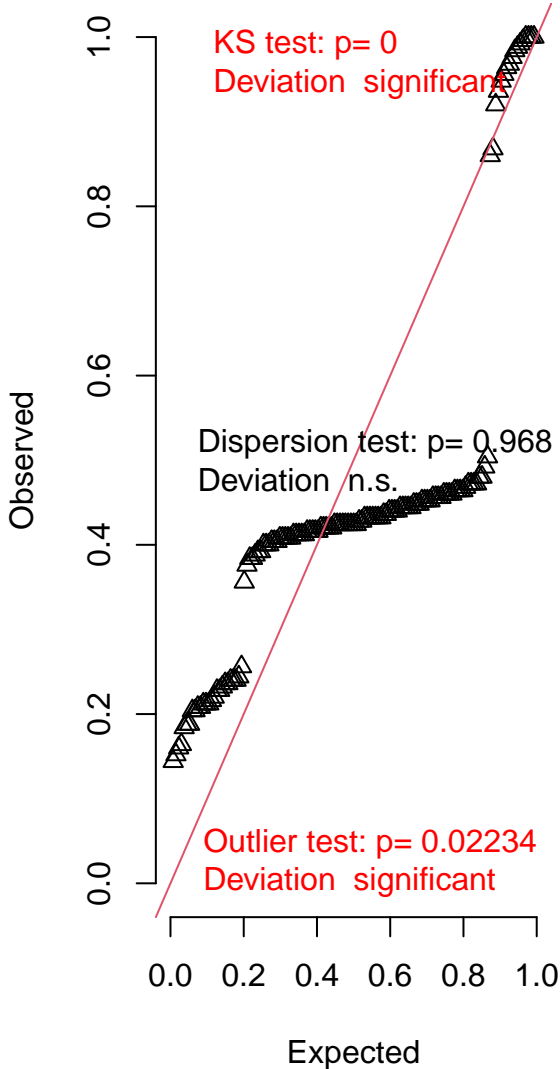
Effect of experiment

Nb obs (total) : 133

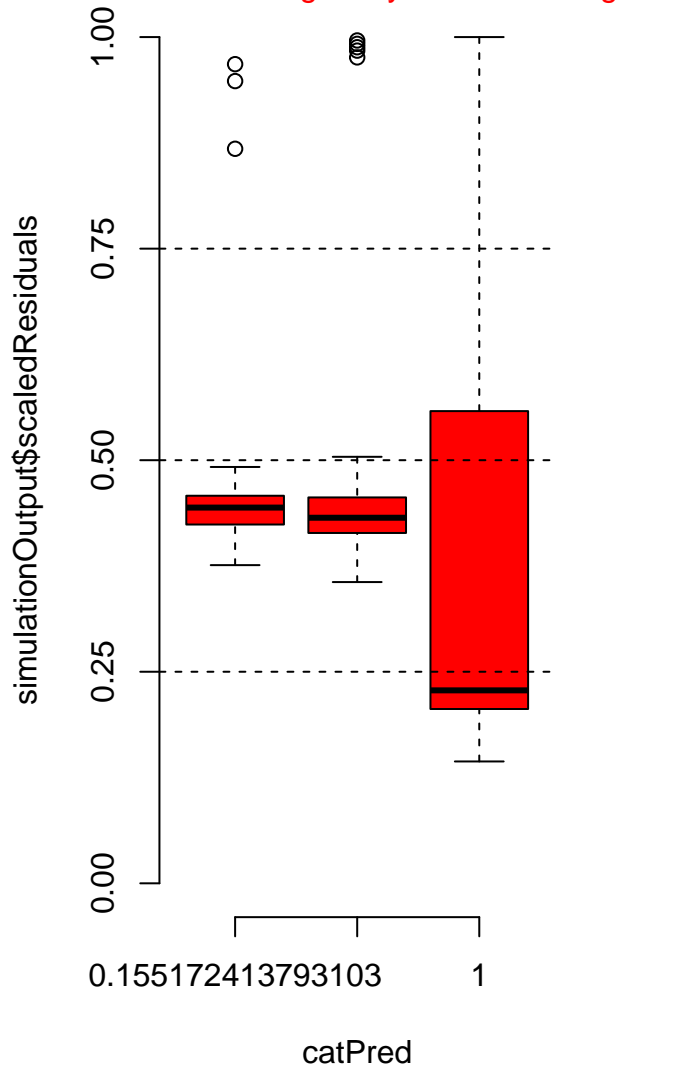
Nb LOD (included) : 115

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-70.4	-53.1	41.2	-82.4	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0654491	0.25583
day	(Intercept)	0.0002512	0.01585
Residual		0.0165843	0.12878

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0166

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.60304	0.08405	19.073	<2e-16 ***
groupCyno.Dengue virus	-0.16314	0.12076	-1.351	0.177
groupSquirrel.Zika virus	-0.18007	0.11856	-1.519	0.129

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

MIP.1a

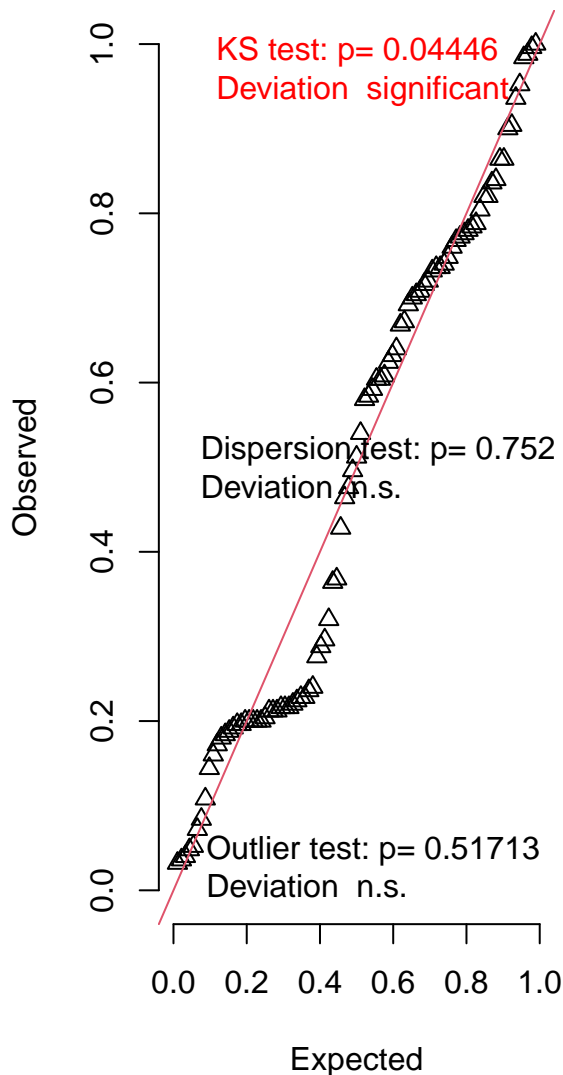
Infection in DENV-cyno

Nb obs (total) : 91

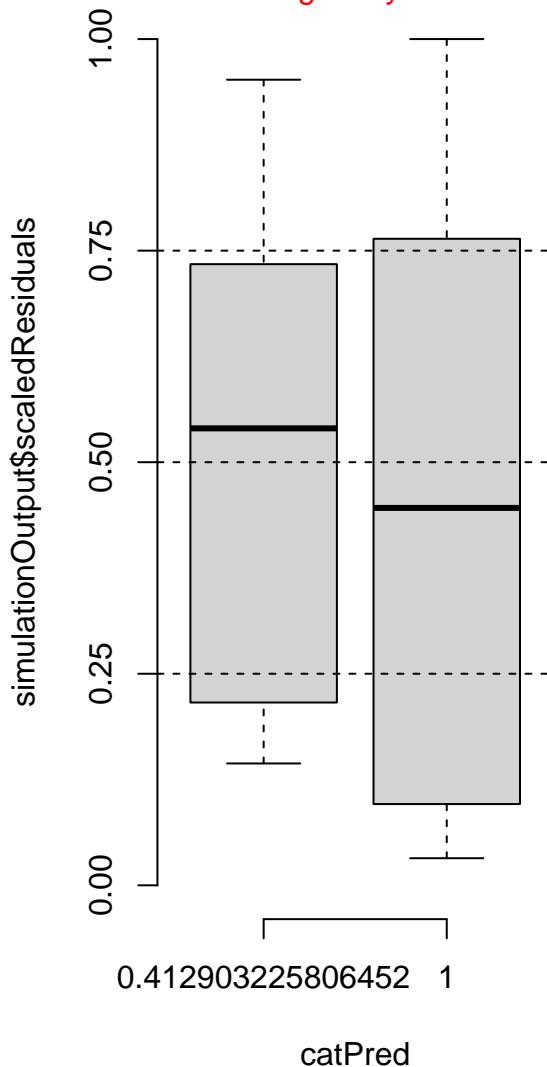
Nb LOD (included) : 29

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-92.6	-80.1	51.3	-102.6	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0252813	0.15900
day	(Intercept)	0.0006409	0.02532
Residual		0.0124070	0.11139

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0124

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.62409	0.05566	29.181	<2e-16 ***
inf_statusControl	0.14247	0.09884	1.441	0.149

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

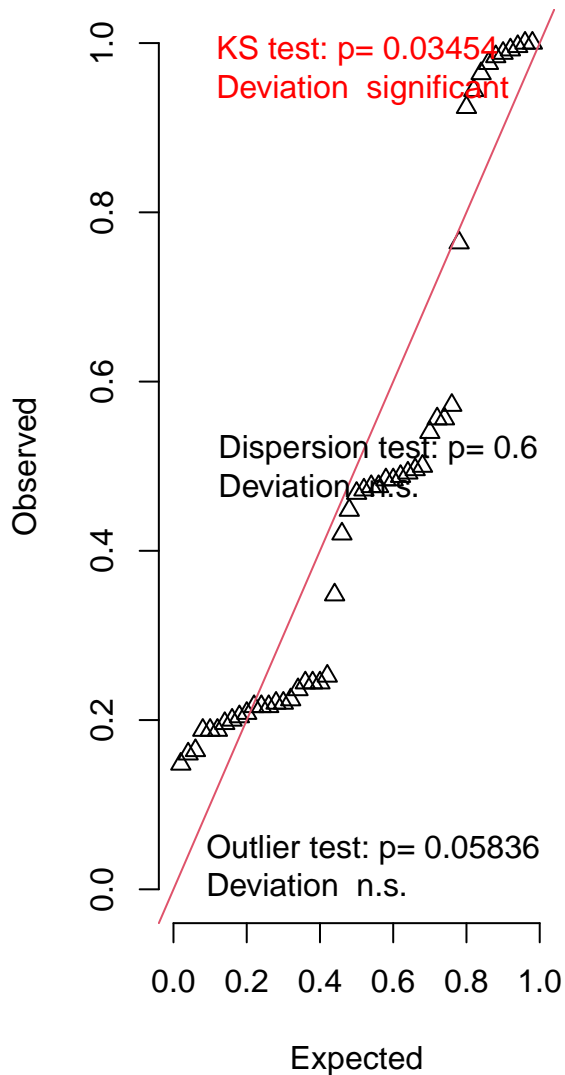
Infection in DENV-squirrel

Nb obs (total) : 49

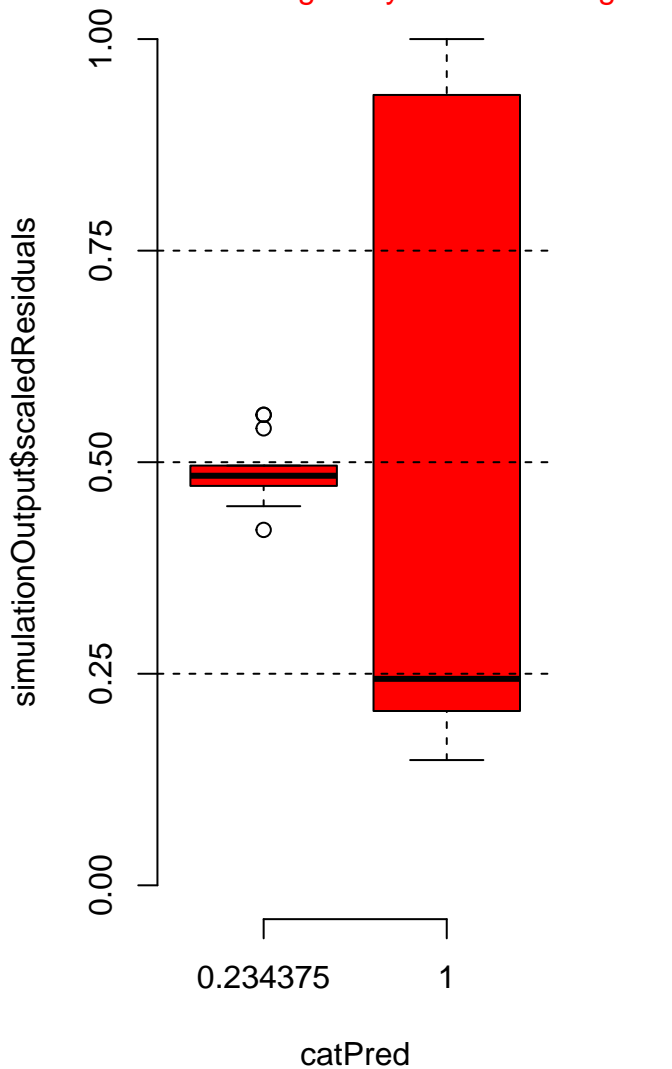
Nb LOD (included) : 33

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-16.1	-6.7	13.1	-26.1	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.108771	0.32980
day	(Intercept)	0.001601	0.04001
Residual		0.011806	0.10865

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0118

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.7325	0.1070	16.187	<2e-16 ***
inf_statusControl	-0.2782	0.1982	-1.404	0.16

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

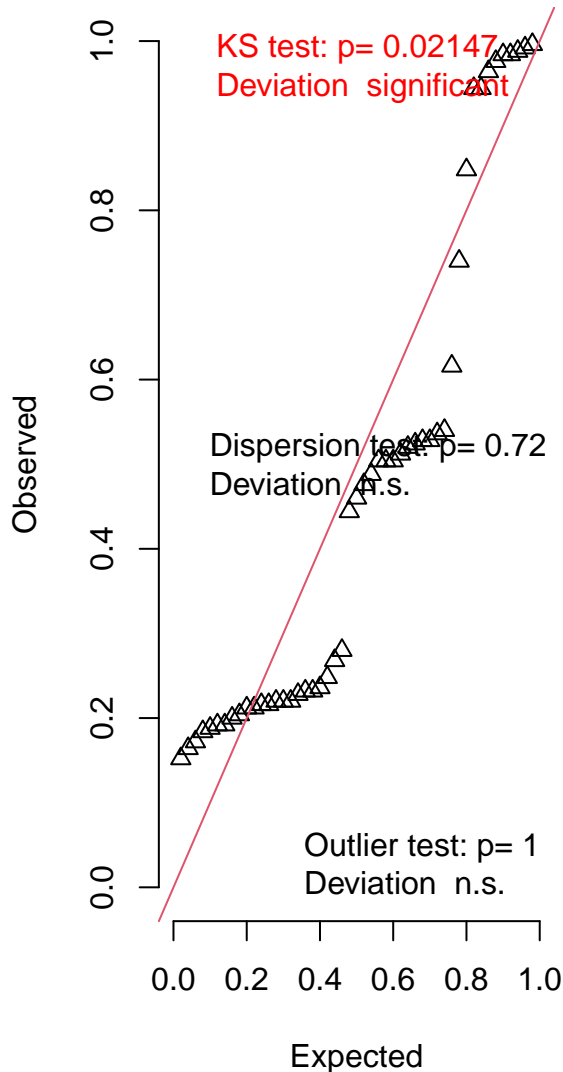
Infection in ZIKV-squirrel

Nb obs (total) : 49

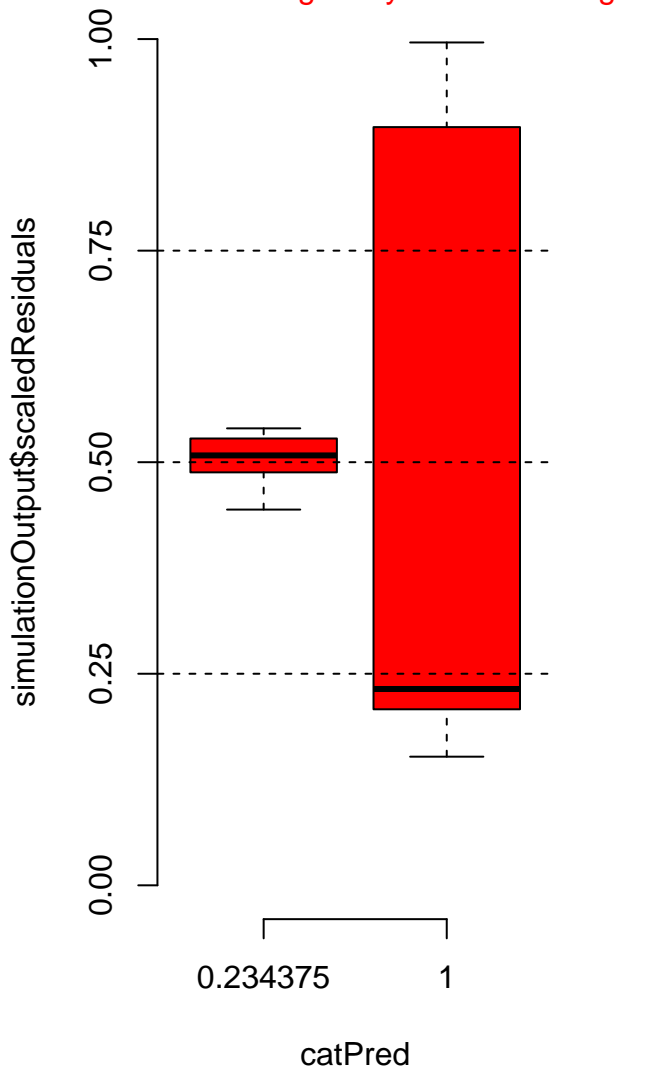
Nb LOD (included) : 36

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-35.9	-26.4	22.9	-45.9	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.058468	0.24180
day	(Intercept)	0.001709	0.04134
Residual		0.008298	0.09109

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0083

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.65707	0.07961	20.816	<2e-16 ***
inf_statusControl	-0.20309	0.14598	-1.391	0.164

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

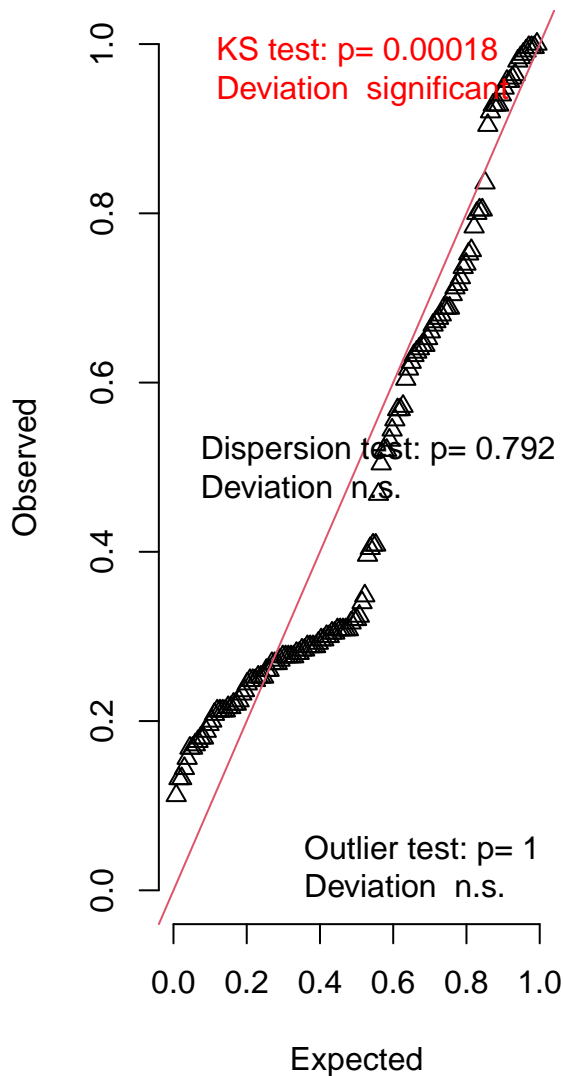
Effect of experiment

Nb obs (total): 133

Nb LOD (included): 66

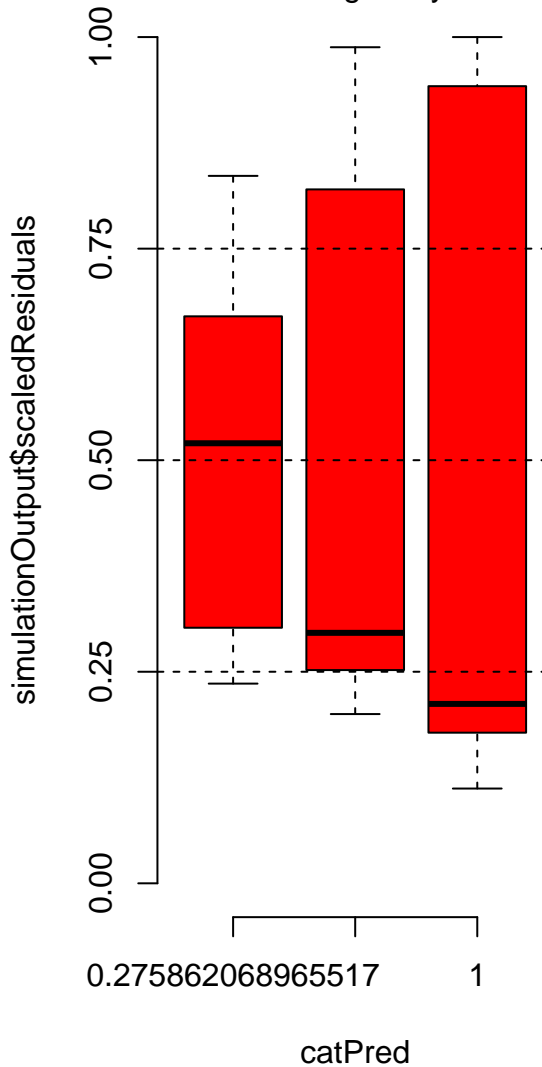
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-90.8	-73.4	51.4	-102.8	127

Random effects:

```

Conditional model:
Groups   Name             Variance Std.Dev.
ID       (Intercept) 8.444e-02 2.906e-01
day      (Intercept) 1.148e-11 3.389e-06
Residual                1.296e-02 1.138e-01
Number of obs: 133, groups:  ID, 29; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.013

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)      1.73221    0.09392   18.443  <2e-16 ***
groupCyno.Dengue virus -0.10812    0.13568   -0.797    0.426
groupSquirrel.Zika virus -0.07545    0.13283   -0.568    0.570
---

```

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

MIP.1B

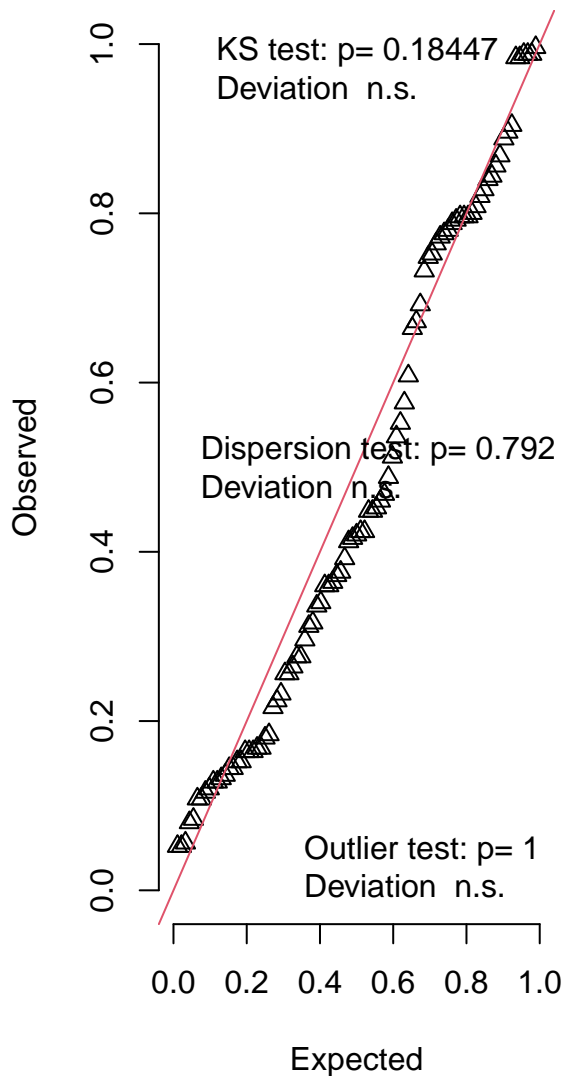
Infection in DENV-cyno

Nb obs (total) : 91

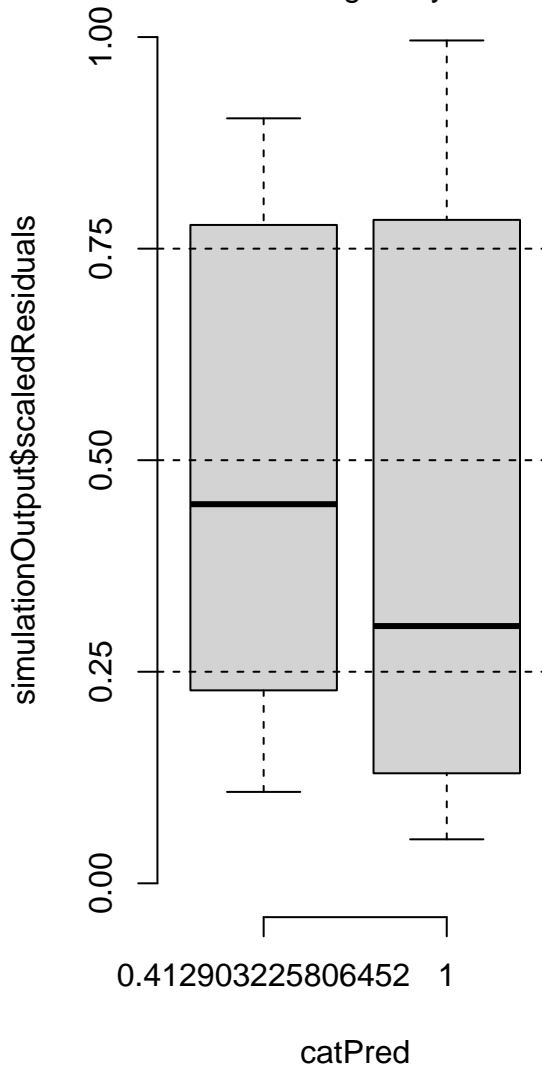
Nb LOD (included) : 18

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-91.3	-78.7	50.6	-101.3	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	7.138e-02	2.672e-01
day	(Intercept)	6.548e-12	2.559e-06
Residual		1.114e-02	1.055e-01

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0111

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.81100	0.09004	20.113	<2e-16 ***
inf_statusControl	0.12597	0.16233	0.776	0.438

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

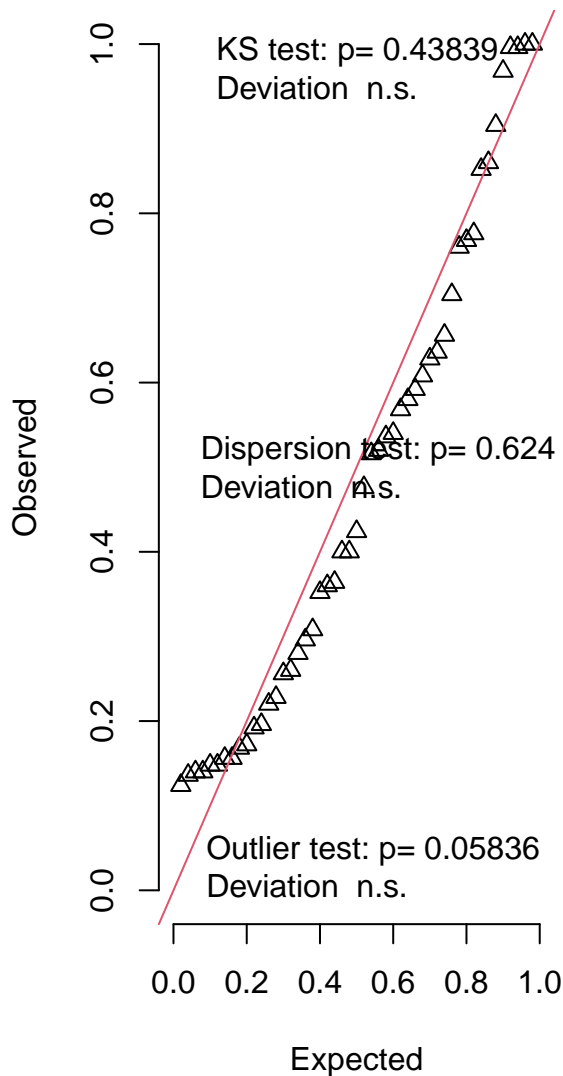
Infection in DENV-squirrel

Nb obs (total) : 49

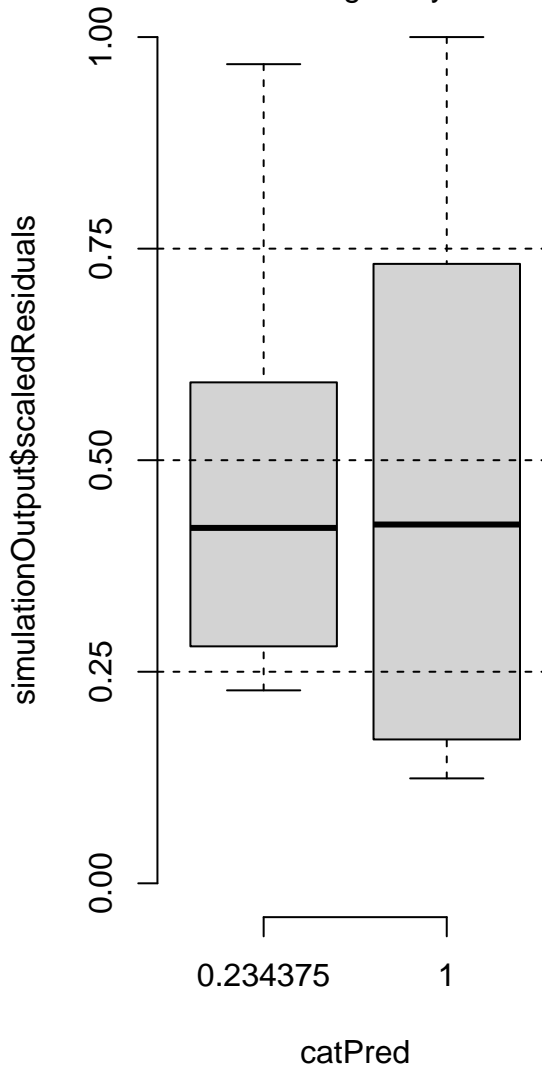
Nb LOD (included) : 13

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
46.8	56.2	-18.4	36.8	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.25757	0.5075
day	(Intercept)	0.04534	0.2129
Residual		0.03978	0.1994

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0398

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.1365	0.1830	11.673	<2e-16 ***
inf_statusControl	-0.2777	0.3069	-0.905	0.366

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

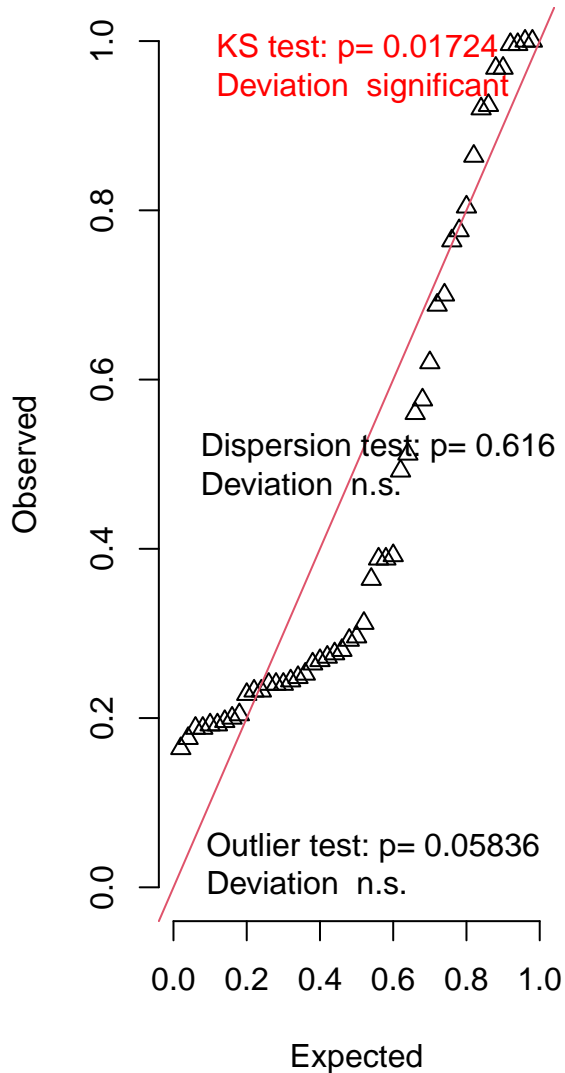
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 20

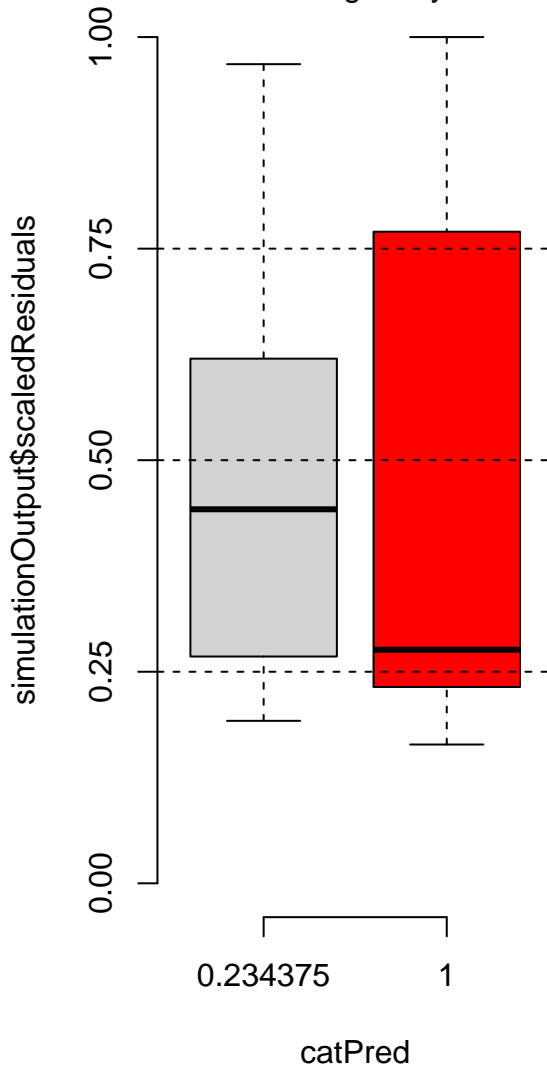
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
41.6	51.1	-15.8	31.6	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.229985	0.47957
day	(Intercept)	0.001064	0.03262
Residual		0.048662	0.22059

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0487

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.91484	0.15675	12.216	<2e-16 ***
inf_statusControl	-0.06202	0.29233	-0.212	0.832

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

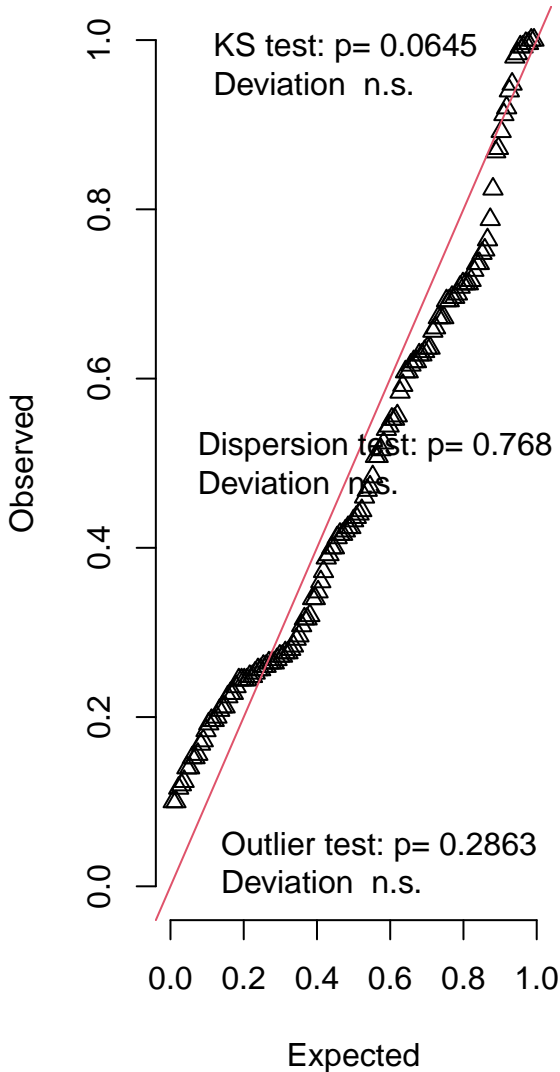
Effect of experiment

Nb obs (total) : 133

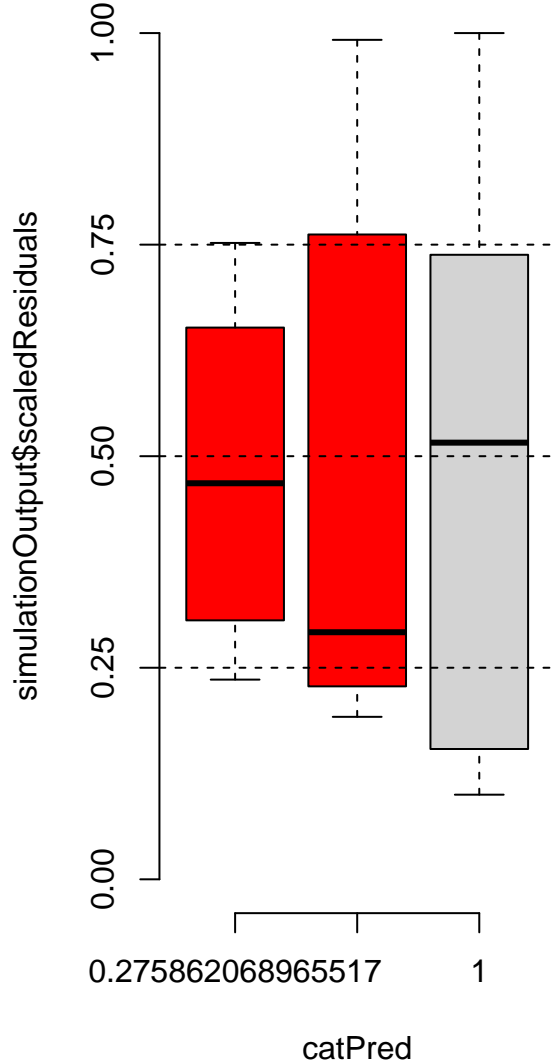
Nb LOD (included) : 37

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-9.2	8.1	10.6	-21.2	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.24718	0.49717
day	(Intercept)	0.00691	0.08313
Residual		0.01871	0.13677

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0187

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.1248	0.1618	13.135	<2e-16 ***
groupCyno.Dengue virus	-0.2887	0.2306	-1.252	0.211
groupSquirrel.Zika virus	-0.2161	0.2248	-0.962	0.336

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

RANTES

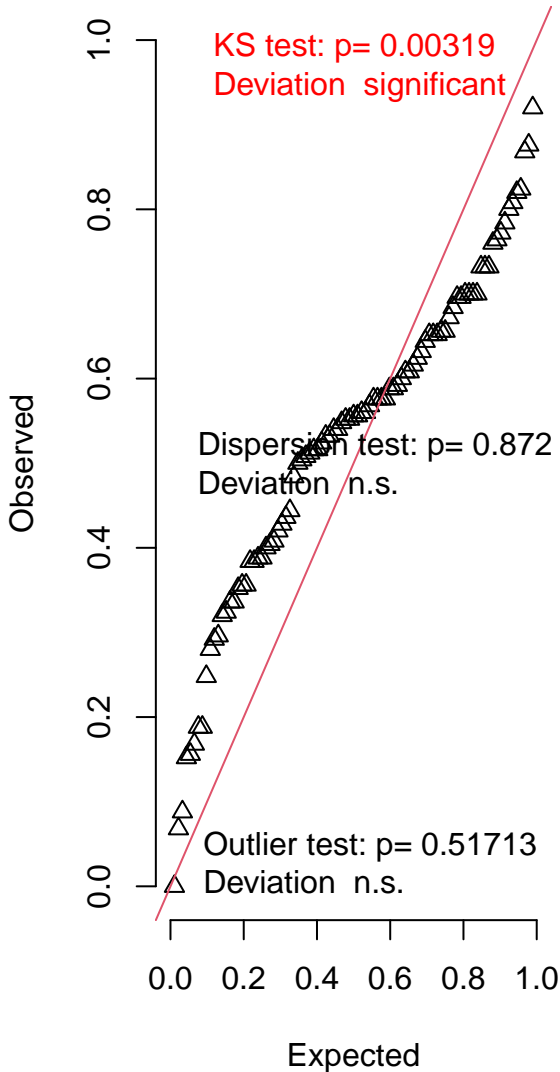
Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 1

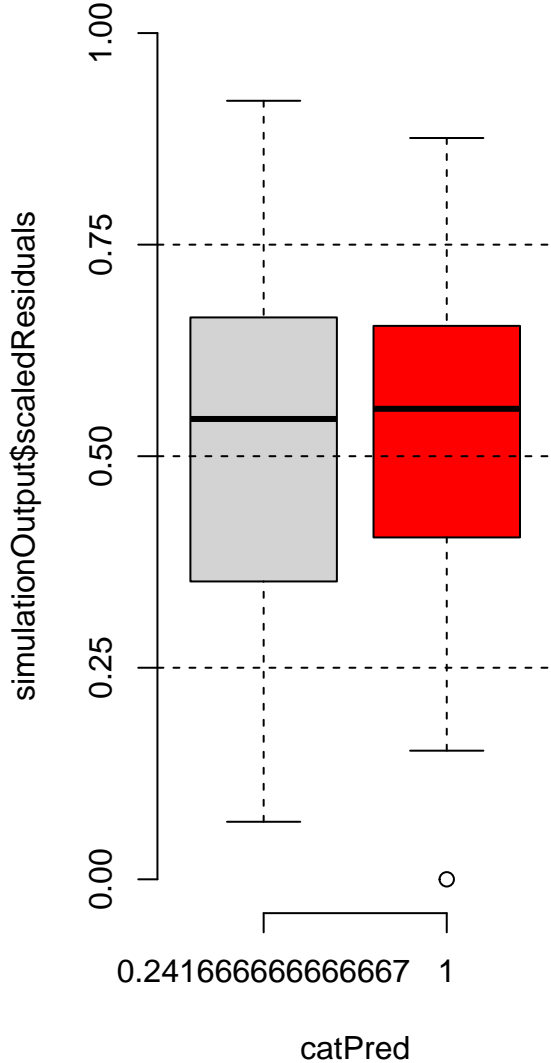
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
62.7	75.3	-26.4	52.7	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.968e-03	7.726e-02
day	(Intercept)	6.206e-11	7.878e-06
Residual		9.938e-02	3.152e-01

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0994

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.51535	0.04734	74.27	<2e-16 ***
inf_statusControl	-0.01824	0.08533	-0.21	0.831

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

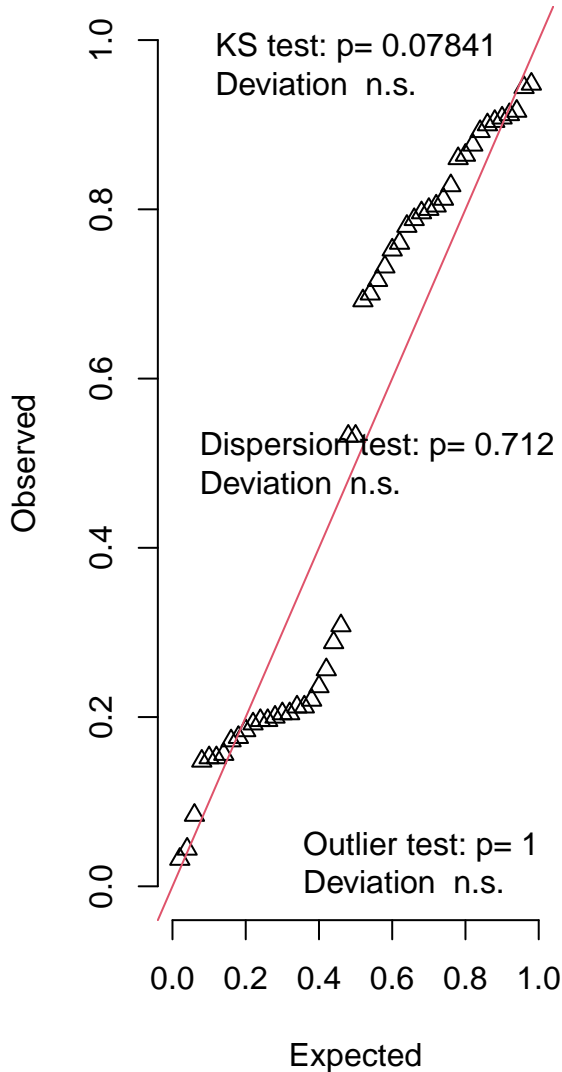
Infection in DENV-squirrel

Nb obs (total) : 49

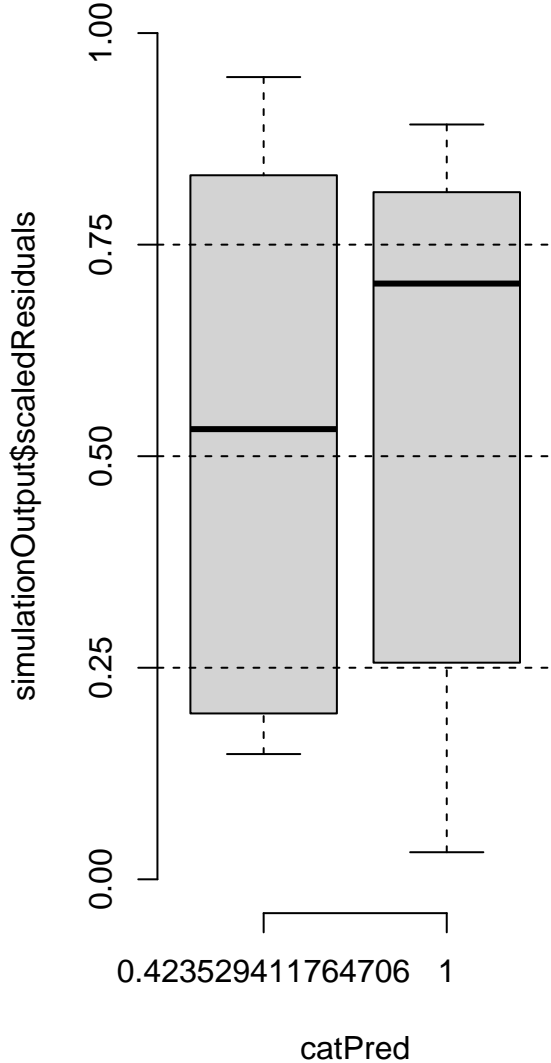
Nb LOD (included) : 20

DHARMA residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.




```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-13.7	-4.2	11.8	-23.7	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.027807	0.16675
day	(Intercept)	0.002233	0.04726
Residual		0.020652	0.14371

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0207

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.14136	0.06092	18.735	<2e-16 ***
inf_statusControl	0.16385	0.10878	1.506	0.132

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

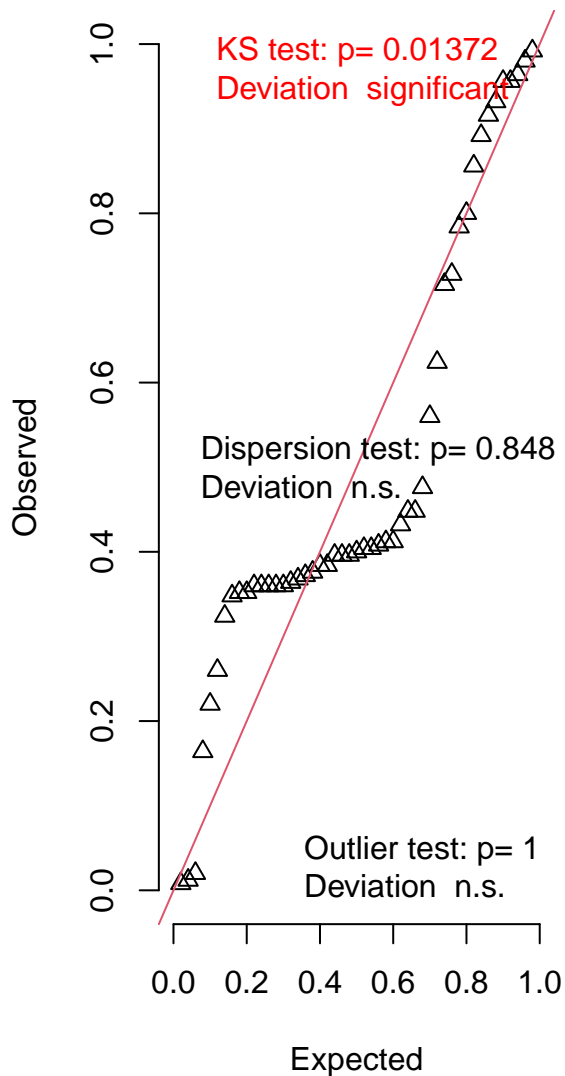
Infection in ZIKV-squirrel

Nb obs (total) : 49

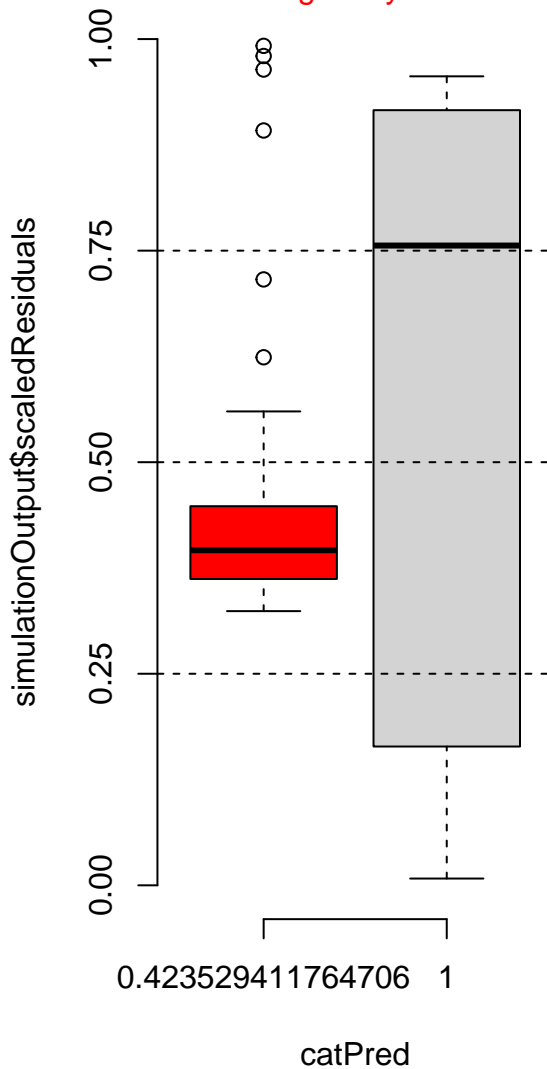
Nb LOD (included) : 29

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-36.1	-26.6	23.0	-46.1	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0055936	0.07479
day	(Intercept)	0.0007737	0.02782
Residual		0.0179381	0.13393

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0179

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.98462	0.03451	28.529	< 2e-16 ***
inf_statusControl	0.32155	0.06141	5.236	1.64e-07 ***

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

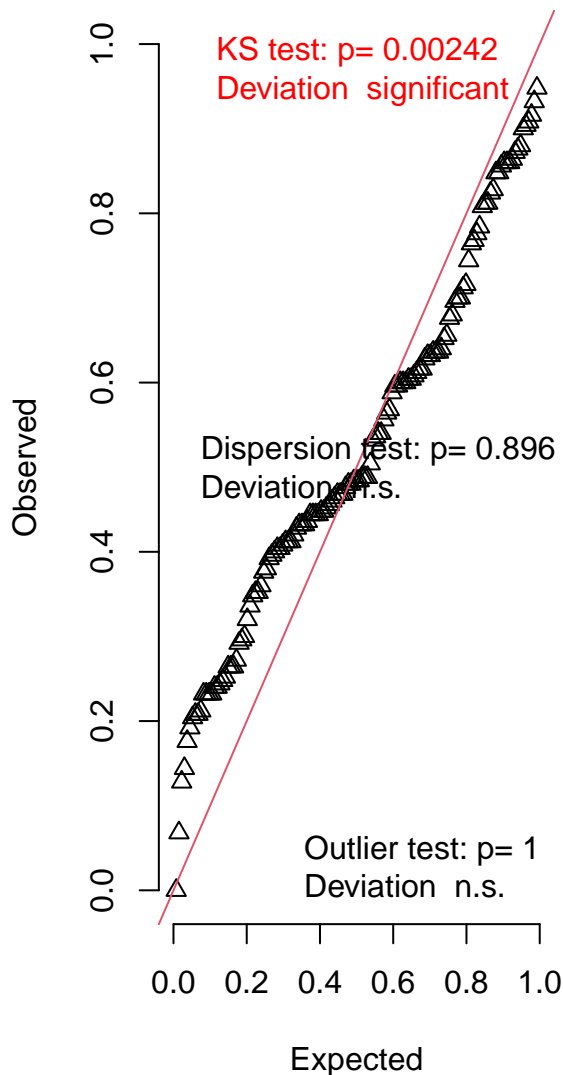
Effect of experiment

Nb obs (total) : 133

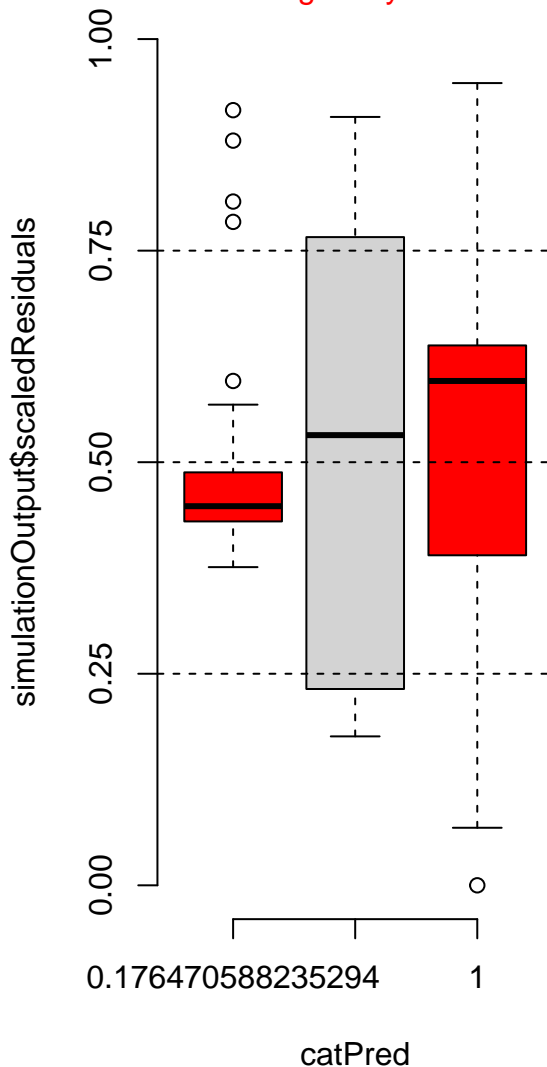
Nb LOD (included) : 44

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant




```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
48.8	66.1	-18.4	36.8	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0070701	0.08408
day	(Intercept)	0.0007404	0.02721
Residual		0.0705565	0.26562

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0706

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.15119	0.05354	21.50	<2e-16 ***
groupCyno.Dengue virus	2.36265	0.06907	34.21	<2e-16 ***
groupSquirrel.Zika virus	-0.16410	0.07397	-2.22	0.0265 *

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

TGFbeta

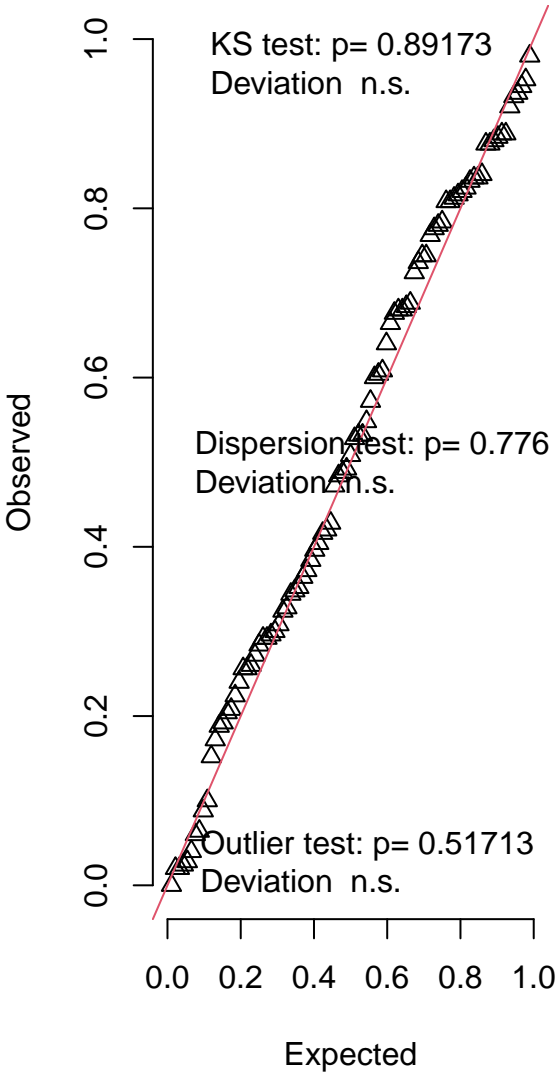
Infection in DENV-cyno

Nb obs (total): 91

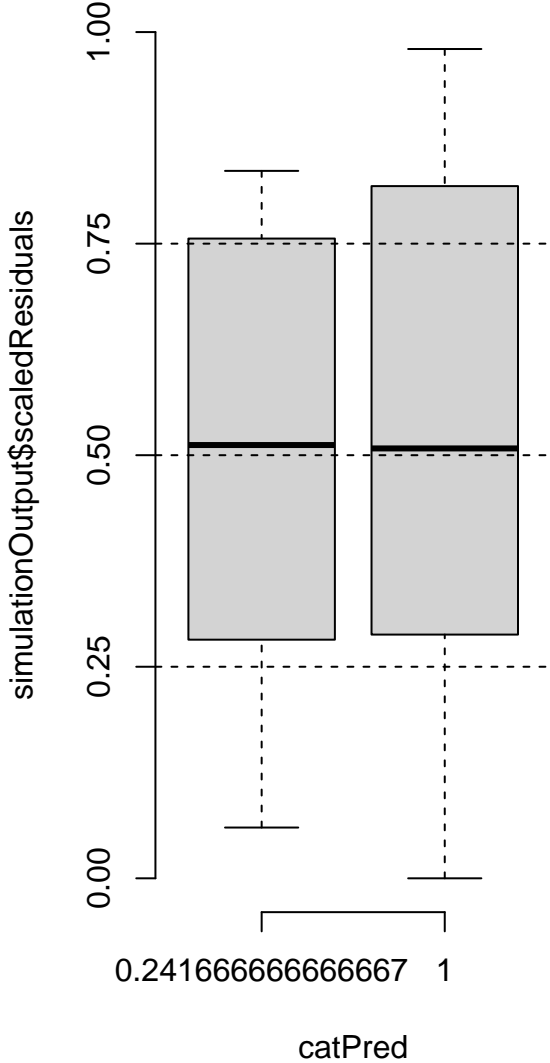
Nb LOD (included): 0

DHARMa residual

QQ plot residuals



Within-group deviation from uniformity n.s.
Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-109.5	-97.0	59.8	-119.5	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0223555	0.14952
day	(Intercept)	0.0005247	0.02291
Residual		0.0102115	0.10105

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0102

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.92891	0.05216	36.98	<2e-16 ***
inf_statusControl	-0.05351	0.09273	-0.58	0.564

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

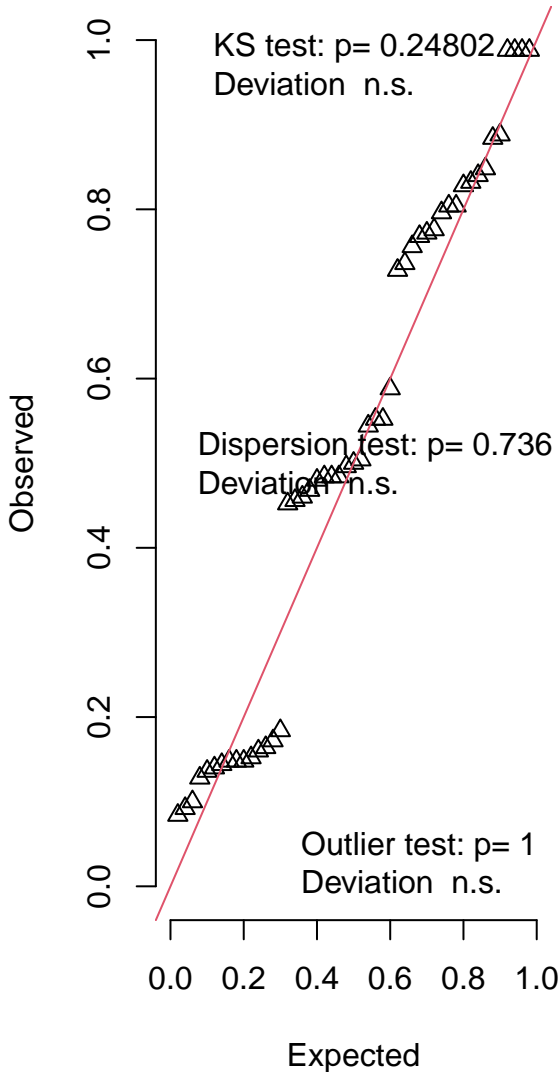
Infection in DENV-squirrel

Nb obs (total) : 49

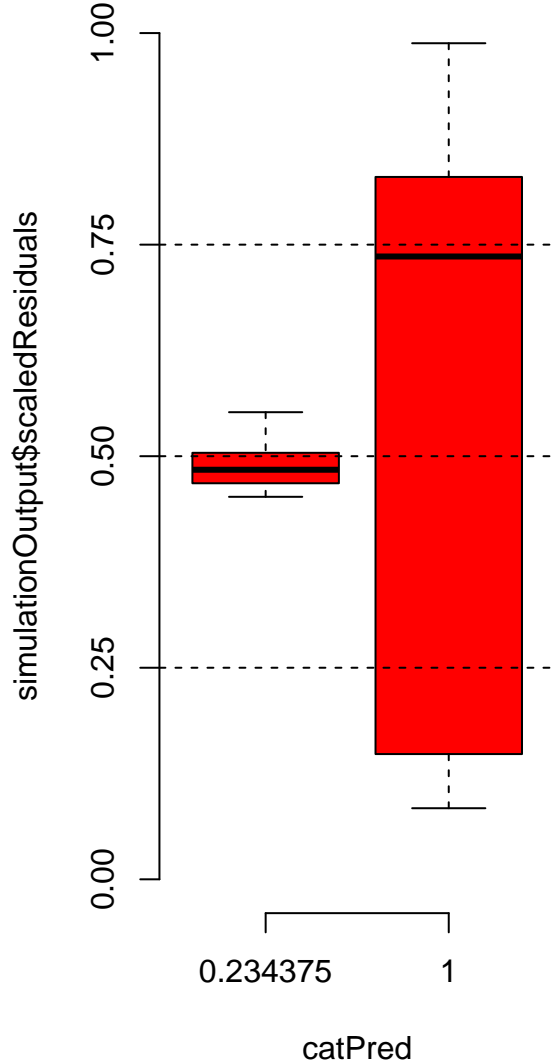
Nb LOD (included) : 29

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-29.7	-20.2	19.9	-39.7	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	6.303e-01	7.939e-01
day	(Intercept)	8.520e-12	2.919e-06
Residual		4.424e-03	6.651e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00442

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.3438	0.2513	5.347	8.94e-08 ***
inf_statusControl	-0.8799	0.4702	-1.871	0.0613 .

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

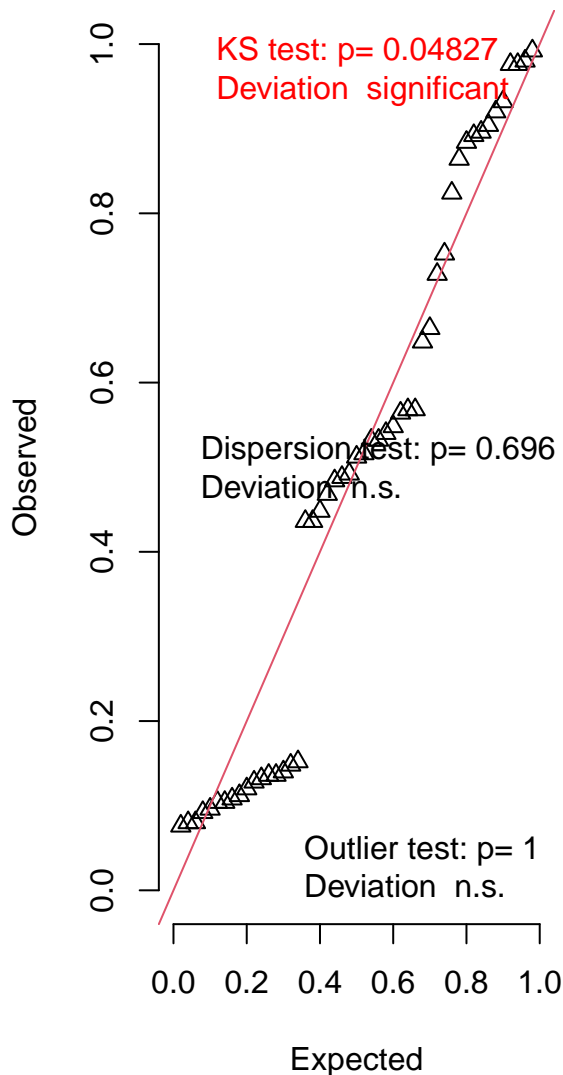
Infection in ZIKV-squirrel

Nb obs (total) : 49

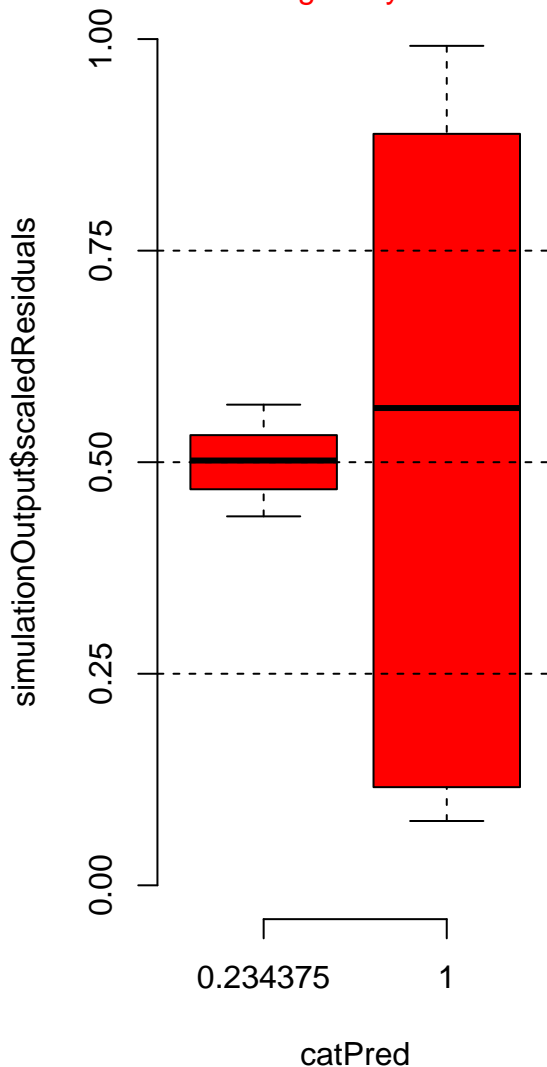
Nb LOD (included) : 31

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-10.0	-0.6	10.0	-20.0	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.4909446	0.70067
day	(Intercept)	0.0006895	0.02626
Residual		0.0080090	0.08949

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00801

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.2517	0.2223	5.630	1.8e-08 ***
inf_statusControl	-0.7877	0.4155	-1.896	0.058 .

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

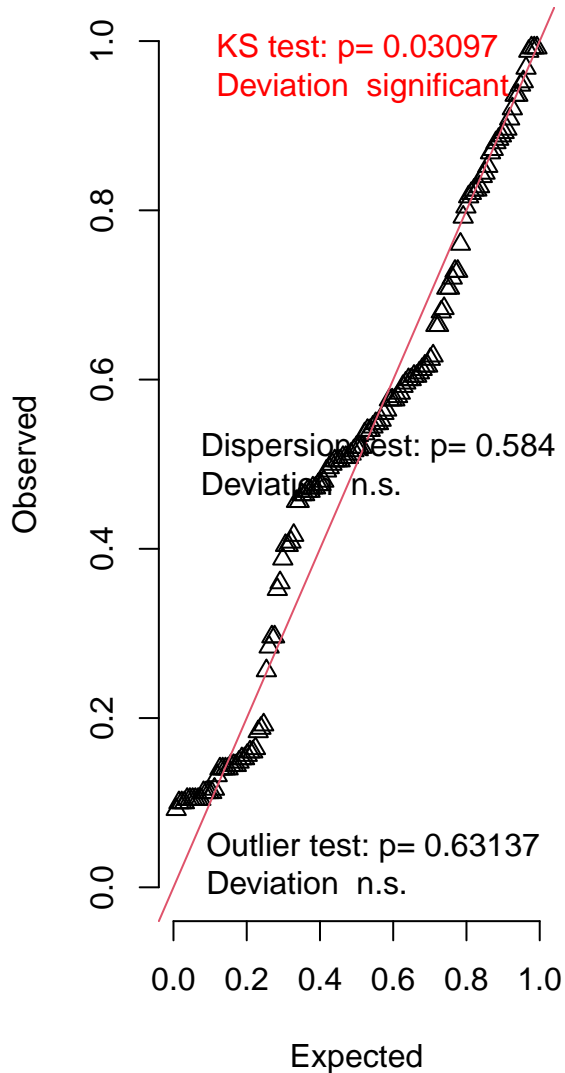
Effect of experiment

Nb obs (total): 133

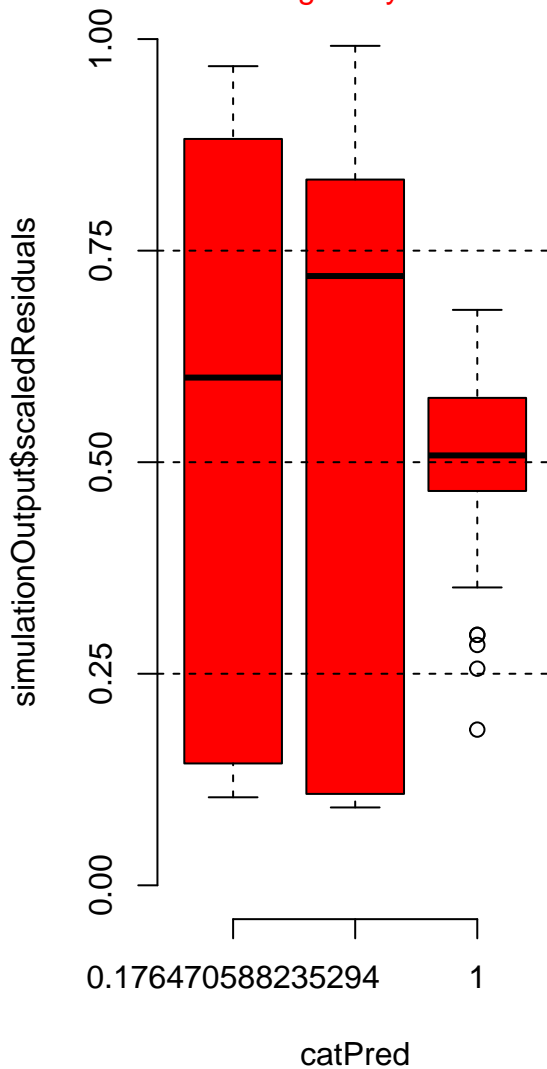
Nb LOD (included): 32

DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant
Levene Test for homogeneity of variance significant



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-71.6	-54.2	41.8	-83.6	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.498e-01	0.7414628
day	(Intercept)	1.439e-12	0.0000012
Residual		9.330e-03	0.0965928

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00933

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.34419	0.23505	5.719	1.07e-08 ***
groupCyno.Dengue virus	0.58472	0.34129	1.713	0.0867 .
groupSquirrel.Zika virus	-0.09259	0.33241	-0.279	0.7806

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

TNF. *alpha*

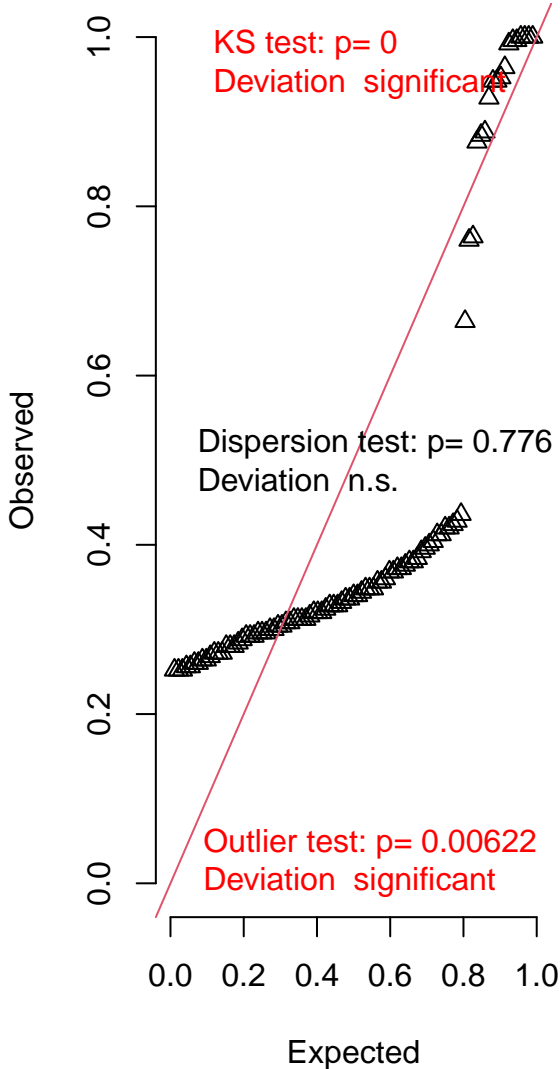
Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 73

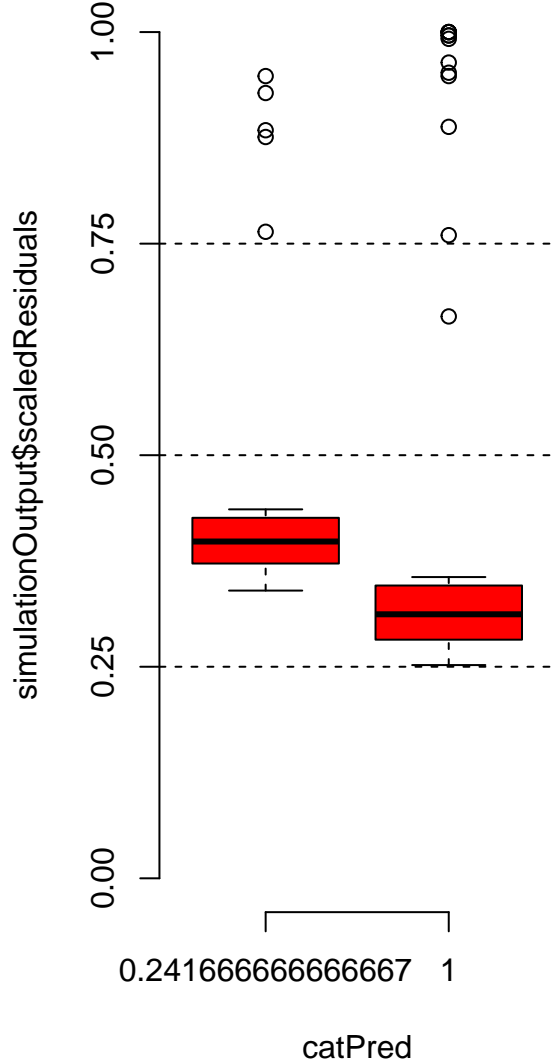
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-377.2	-364.6	193.6	-387.2	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	8.498e-04	0.029152
day	(Intercept)	4.281e-05	0.006543
Residual		5.586e-04	0.023635

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000559

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.17286	0.01046	112.13	<2e-16 ***
inf_statusControl	-0.00992	0.01832	-0.54	0.588

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

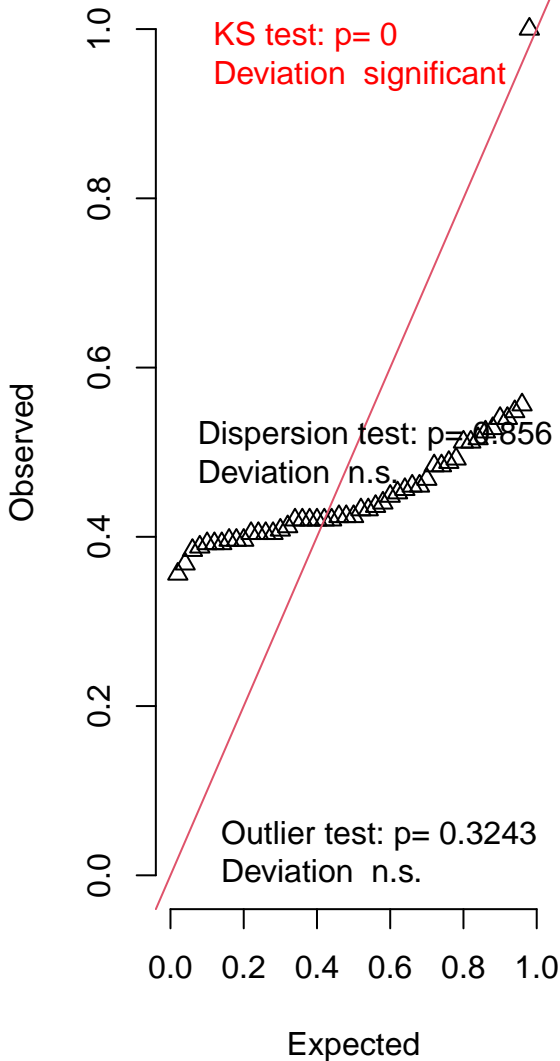
Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 47

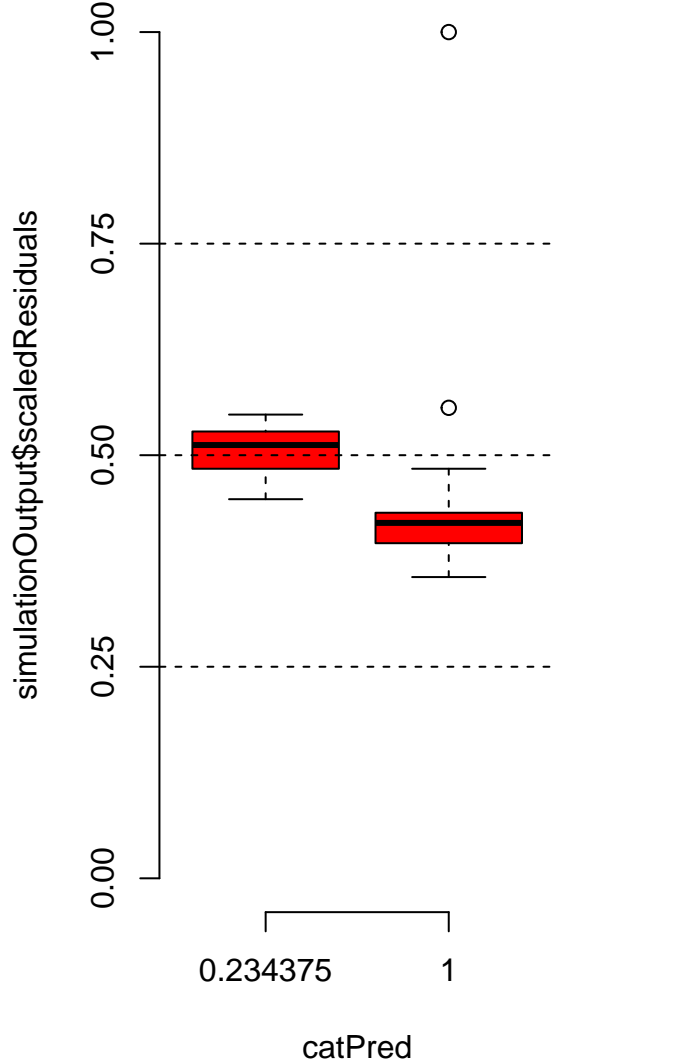
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_sq

```

AIC	BIC	logLik	deviance	df.resid
-298.5	-289.0	154.2	-308.5	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.296e-12	1.515e-06
day	(Intercept)	1.869e-13	4.323e-07
Residual		1.080e-04	1.039e-02

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000108

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.162355	0.001757	661.7	<2e-16 ***
inf_statusControl	-0.002187	0.003287	-0.7	0.506

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

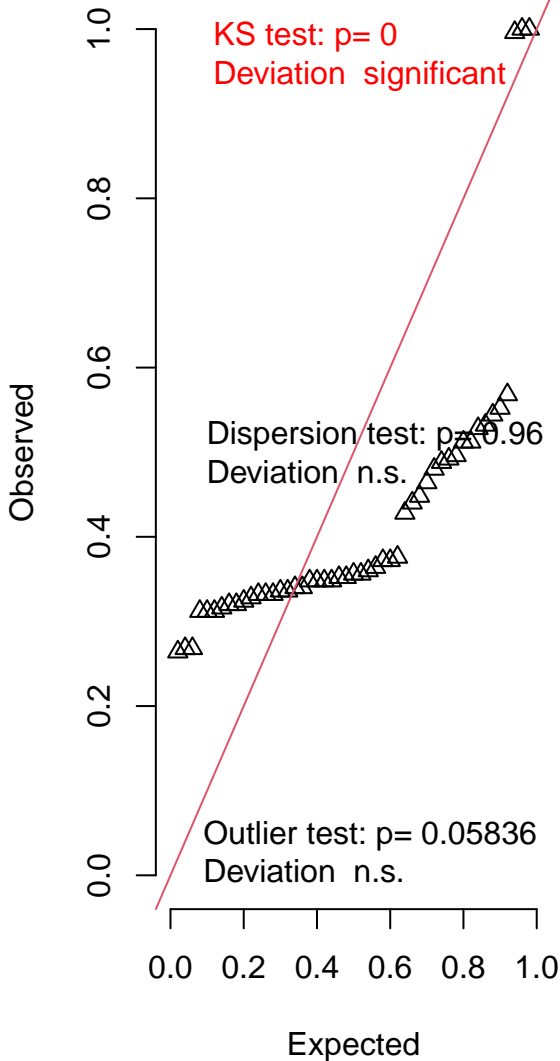
Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 45

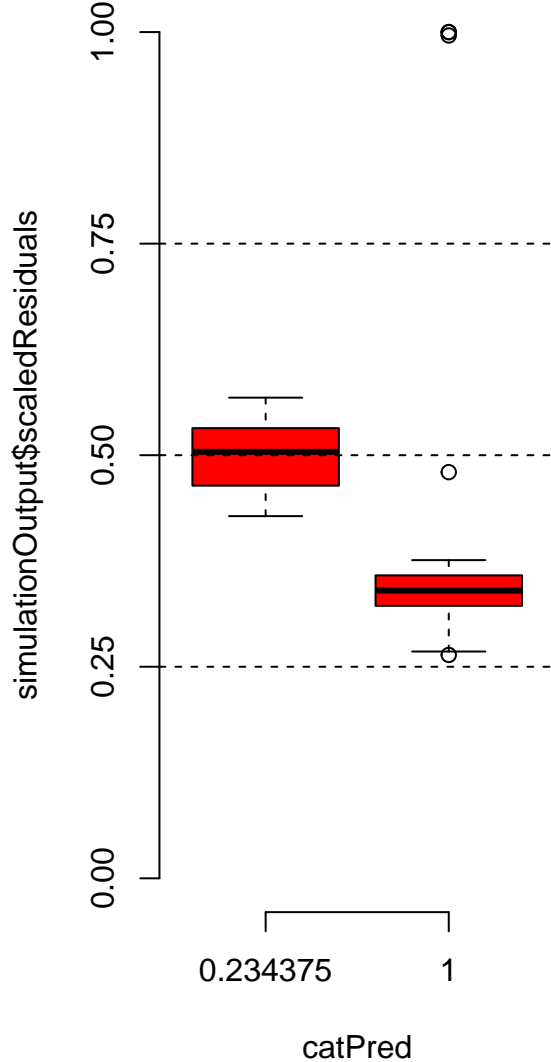
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-155.9	-146.5	83.0	-165.9	44

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.436e-02	0.156065
day	(Intercept)	1.441e-10	0.000012
Residual		4.407e-04	0.020992

Number of obs: 49, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.000441

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.22336	0.04948	24.723	<2e-16 ***
inf_statusControl	-0.06319	0.09257	-0.683	0.495

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

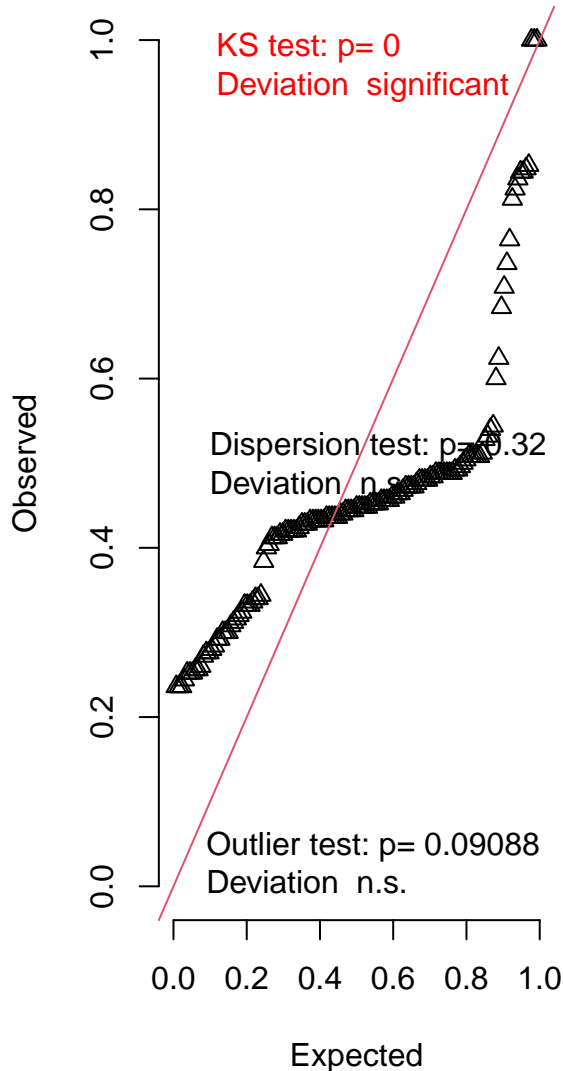
Effect of experiment

Nb obs (total) : 133

Nb LOD (included) : 114

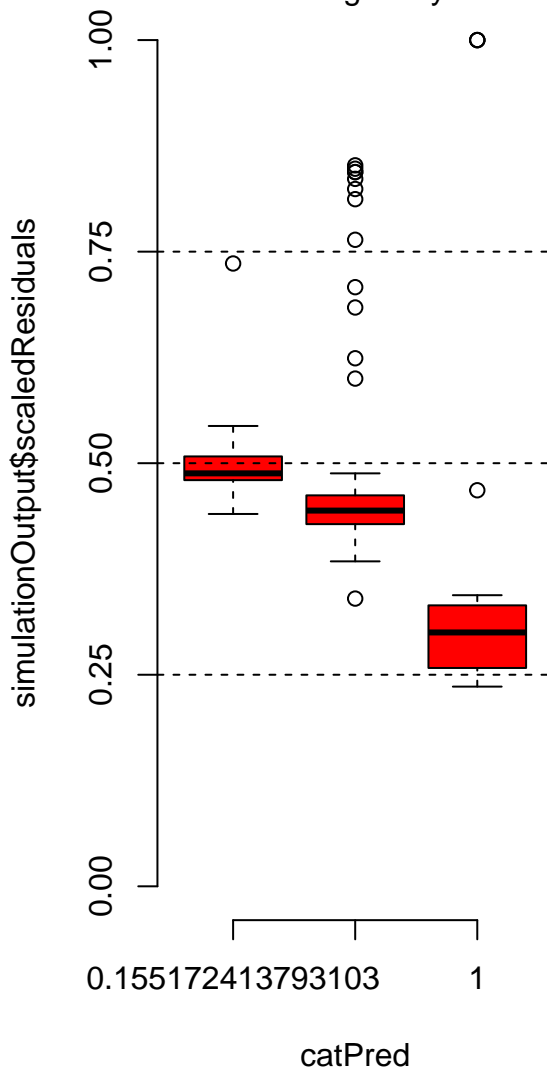
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-476.6	-459.3	244.3	-488.6	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.196e-02	0.109353
day	(Intercept)	2.384e-05	0.004882
Residual		5.330e-04	0.023087

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.000533

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.16197	0.03485	33.34	<2e-16 ***
groupCyno.Dengue virus	0.01125	0.05050	0.22	0.824
groupSquirrel.Zika virus	0.06121	0.04922	1.24	0.214

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

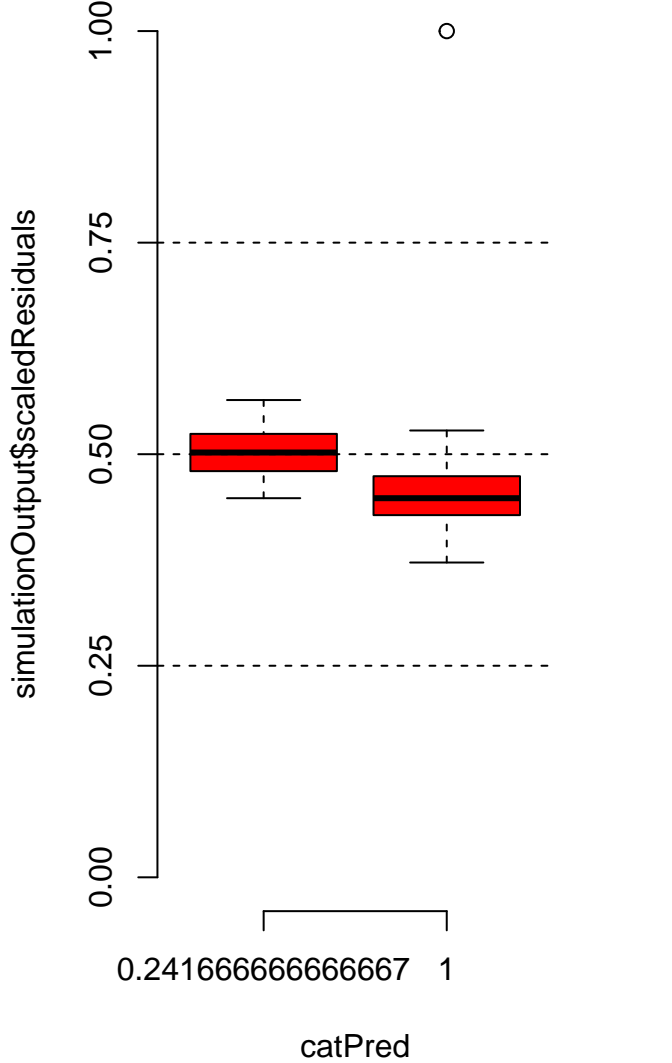
VEGF

Infection in DENV-cyno

Nb obs (total) : 91

Nb LOD (included) : 90

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:      log10(value) ~ inf_status + (1 | ID) + (1 | day)
Data: d_cyno

```

AIC	BIC	logLik	deviance	df.resid
-308.2	-295.7	159.1	-318.2	86

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	8.409e-12	2.900e-06
day	(Intercept)	3.826e-13	6.186e-07
Residual		1.774e-03	4.211e-02

Number of obs: 91, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00177

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.136762	0.005306	25.776	<2e-16 ***
inf_statusControl	-0.006428	0.009565	-0.672	0.502

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

Infection in DENV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 49

VEGF ERROR : valeurs infinies ou manquantes dans 'x'

Infection in ZIKV-squirrel

Nb obs (total) : 49

Nb LOD (included) : 49

VEGF ERROR : valeurs infinies ou manquantes dans 'x'

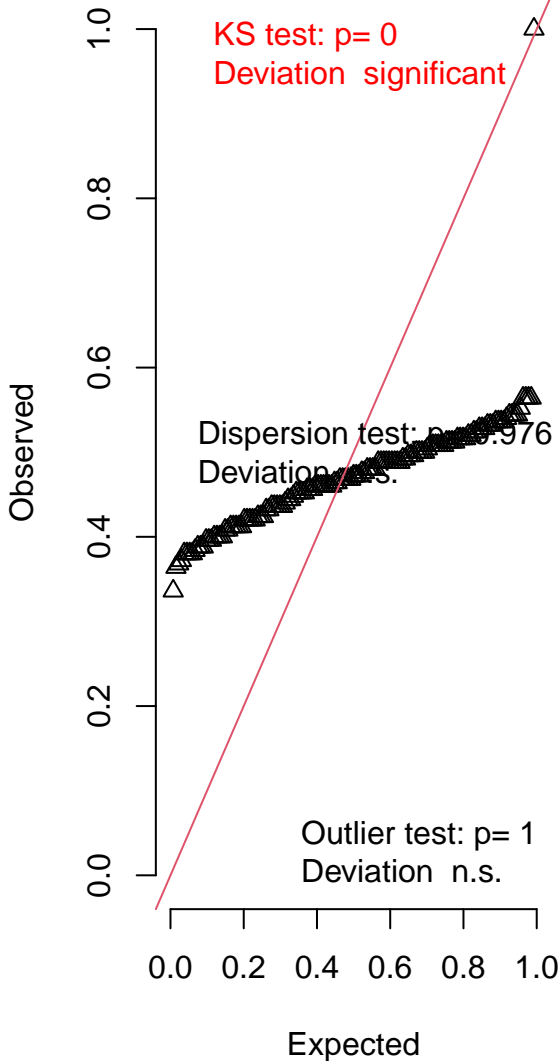
Effect of experiment

Nb obs (total) : 133

Nb LOD (included) : 132

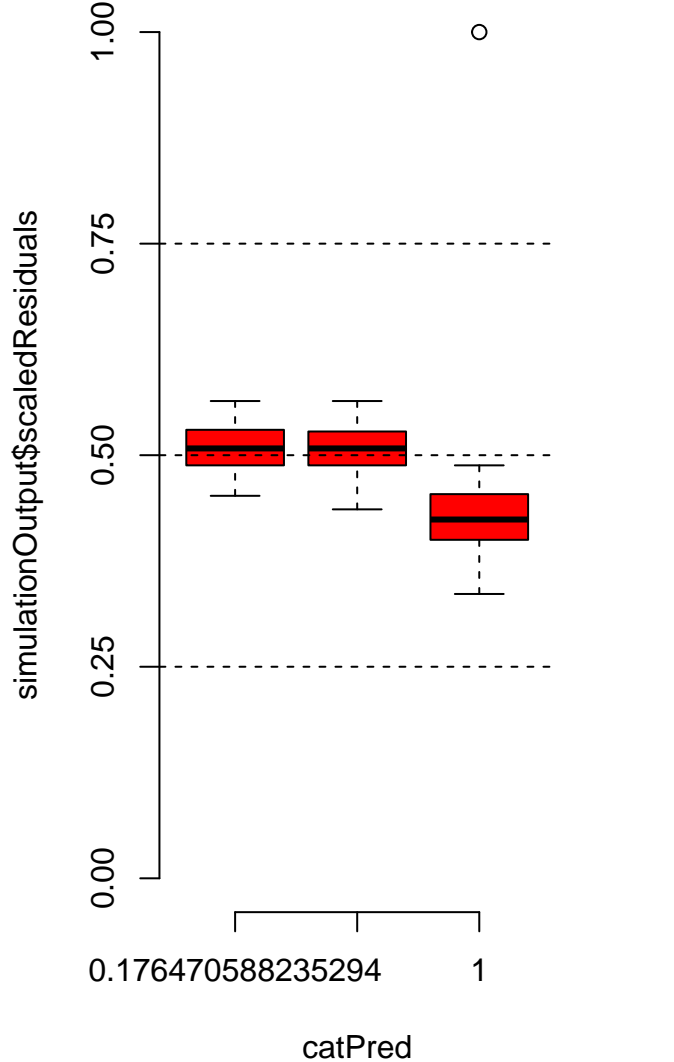
DHARMA residual

QQ plot residuals



Within-group deviations from uniformity significant

Levene Test for homogeneity of variance n.s.



```

Family: gaussian ( identity )
Formula:          log10(value) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-503.6	-486.2	257.8	-515.6	127

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	3.828e-12	1.957e-06
day	(Intercept)	4.990e-16	2.234e-08
Residual		1.213e-03	3.483e-02

Number of obs: 133, groups: ID, 29; day, 8

Dispersion estimate for gaussian family (σ^2): 0.00121

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.773e-02	NaN	NaN	NaN
groupCyno.Dengue virus	1.545e-01	NaN	NaN	NaN
groupSquirrel.Zika virus	-4.071e-14	NaN	NaN	NaN