

EGF

Infection in DENV-cyno

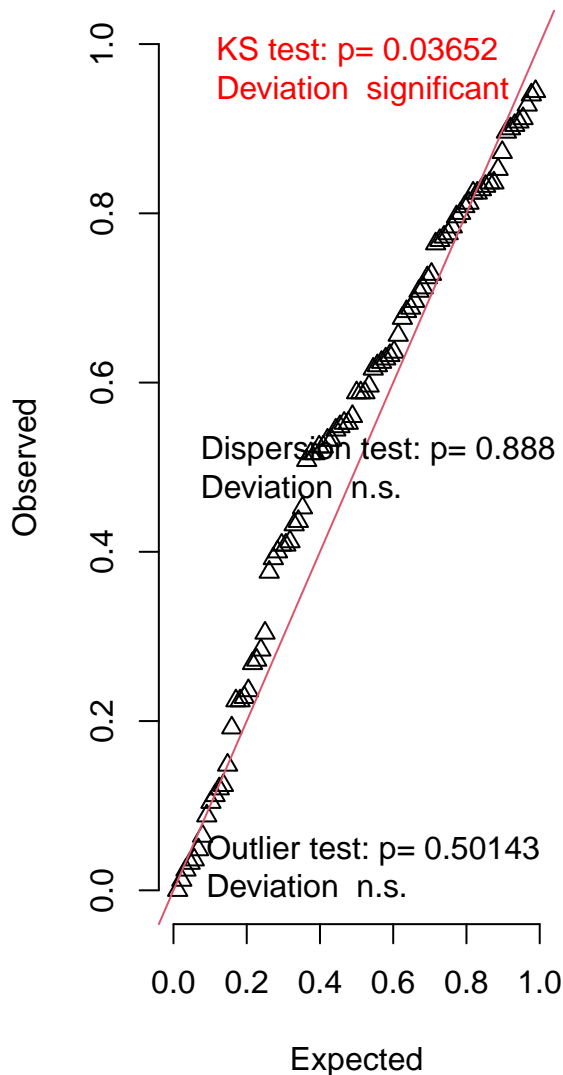
Nb excluded (LOD): 4

Nb obs infection: 59

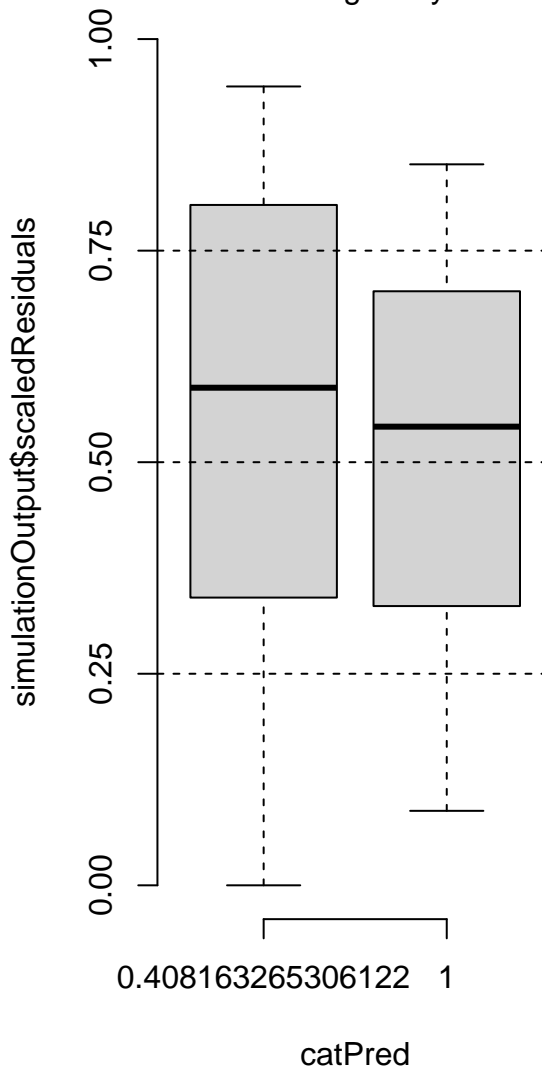
Nb obs control: 28

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
-30.2	-17.8	20.1	-40.2	82

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.025921	0.16100
day	(Intercept)	0.006215	0.07883
Residual		0.024401	0.15621

Number of obs: 87, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0244

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.7802	0.0648	27.474	<2e-16 ***
inf_statusControl	0.1746	0.1033	1.691	0.0909 .

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

Infection in DENV-squirrel

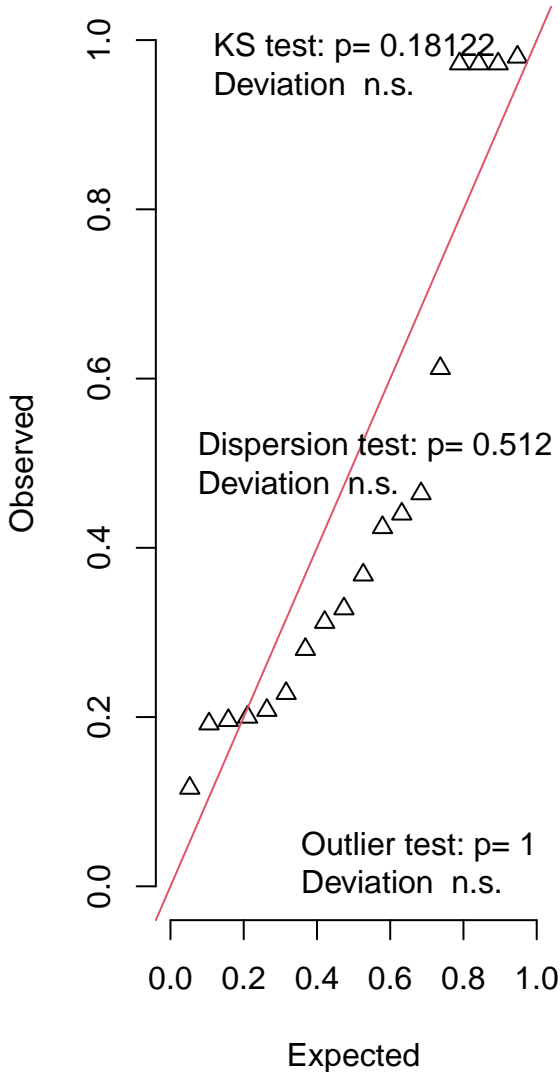
Nb excluded (LOD): 31

Nb obs infection: 16

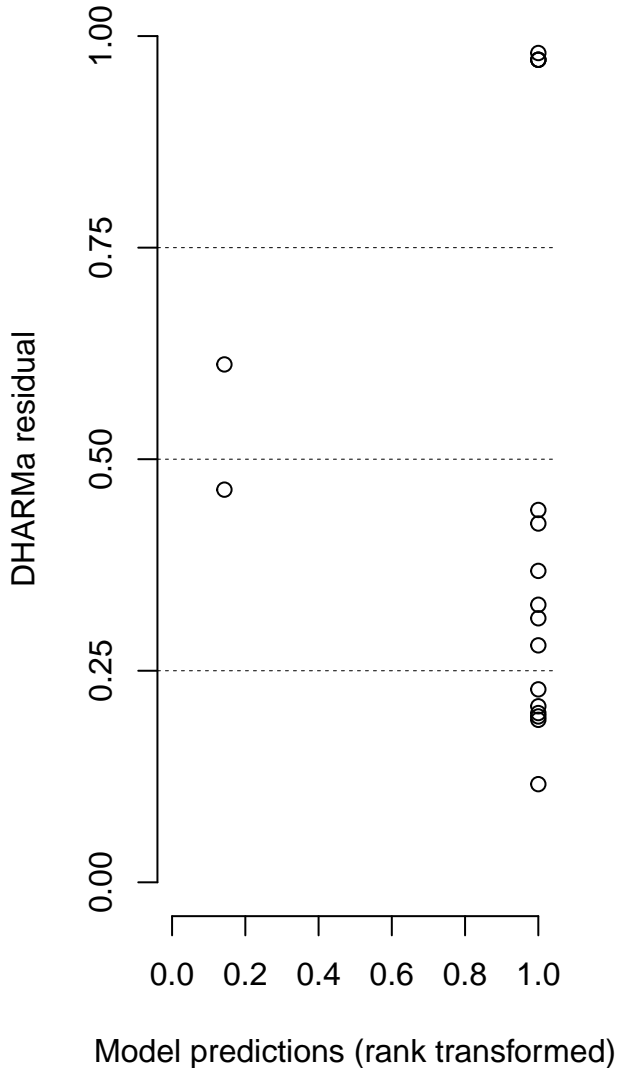
Nb obs control: 2

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected




```

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

```

AIC	BIC	logLik	deviance	df.resid
2.5	7.0	3.7	-7.5	13

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.226460	0.47588
day	(Intercept)	0.003039	0.05512
Residual		0.009896	0.09948

Number of obs: 18, groups: ID, 5; day, 4

Dispersion estimate for gaussian family (sigma^2): 0.0099

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.8222	0.2408	7.567	3.83e-14 ***
inf_statusControl	-1.2021	0.5379	-2.235	0.0254 *

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

Infection in ZIKV-squirrel

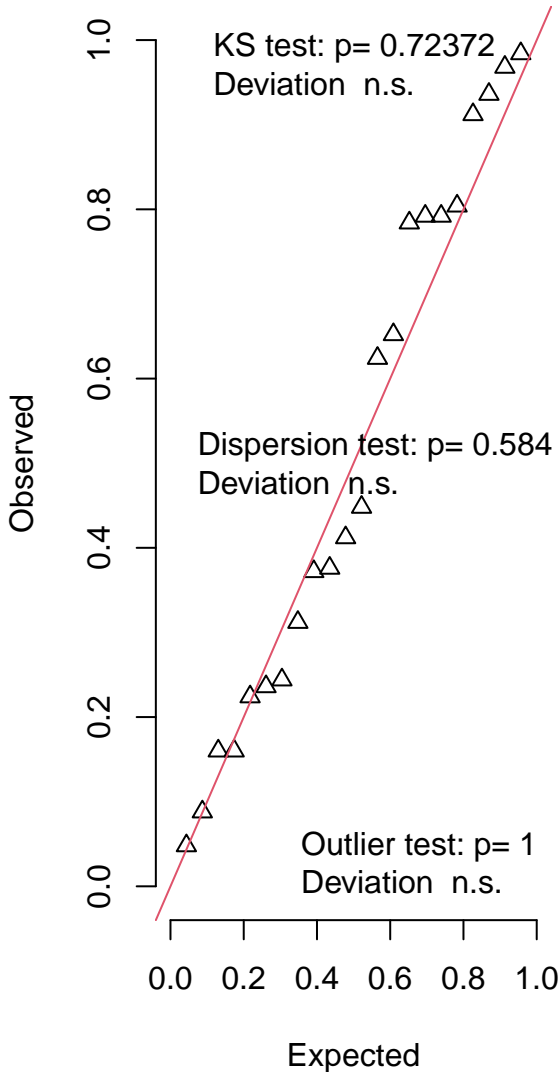
Nb excluded (LOD): 27

Nb obs infection: 20

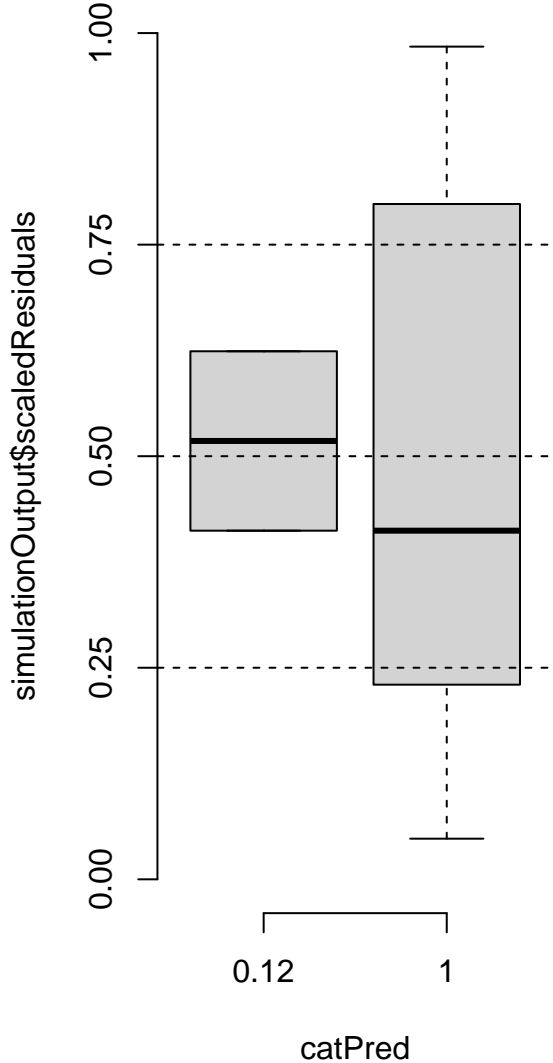
Nb obs control: 2

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
20.0	25.5	-5.0	10.0	17

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.173382	0.41639
day	(Intercept)	0.004365	0.06607
Residual		0.035503	0.18842

Number of obs: 22, groups: ID, 7; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0355

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.4081	0.1771	7.950	1.86e-15 ***
inf_statusControl	-0.7523	0.4727	-1.592	0.111

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

Effect of experiment

Nb excluded (LOD): 38

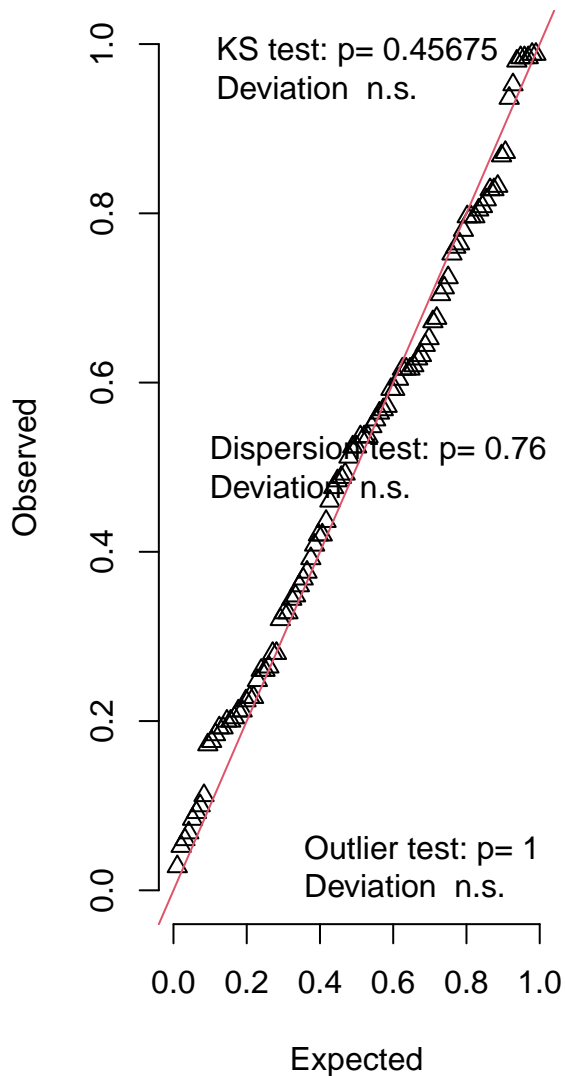
Nb obs DENV-squirrel (infected only): 16

Nb obs DENV-cyno (infected only): 59

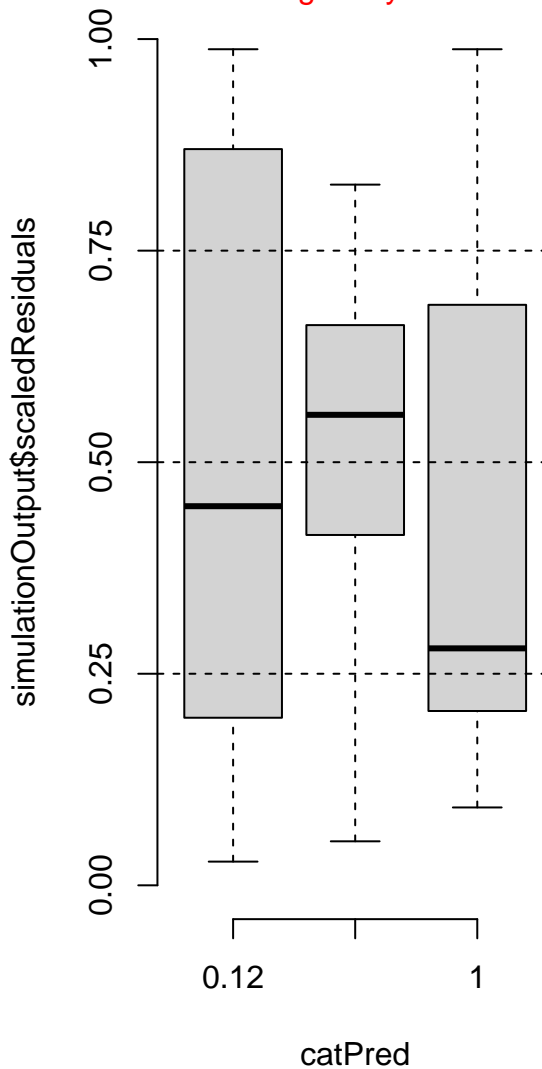
Nb obs ZIKV-squirrel (infected only): 20

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) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
12.1	27.5	-0.1	0.1	89

Random effects:

```

Conditional model:
Groups   Name          Variance Std.Dev.
ID       (Intercept)  0.138172 0.37171
day      (Intercept)  0.002615 0.05113
Residual                0.029887 0.17288
Number of obs: 95, groups: ID, 19; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.0299

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)      1.81392    0.19225   9.435  <2e-16 ***
groupCyno.Dengue virus -0.03307    0.22904  -0.144   0.8852
groupSquirrel.Zika virus -0.41075    0.24715  -1.662   0.0965 .
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```

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

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Infection in DENV-cyno

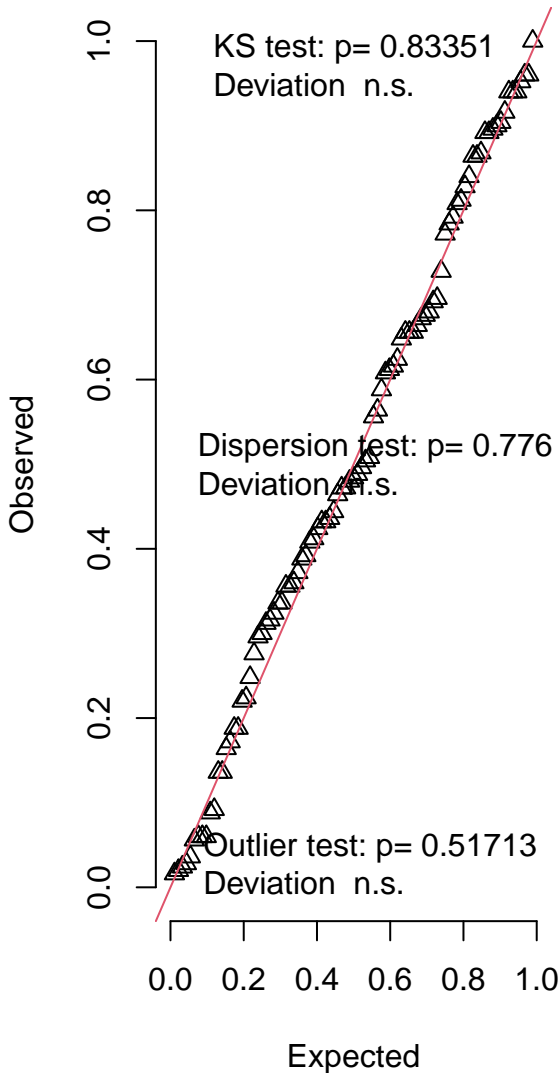
Nb excluded (LOD): 0

Nb obs infection: 63

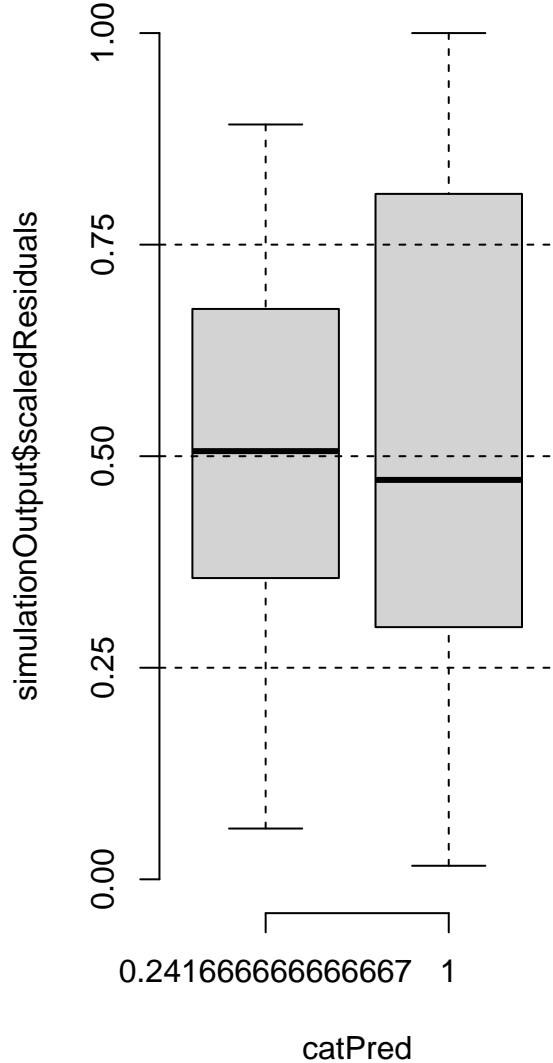
Nb obs control: 28

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 excluded (LOD): 38

Nb obs infection: 11

Nb obs control: 0

Botaxin ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 46

Nb obs infection: 3

Nb obs control: 0

Botaxin ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 56

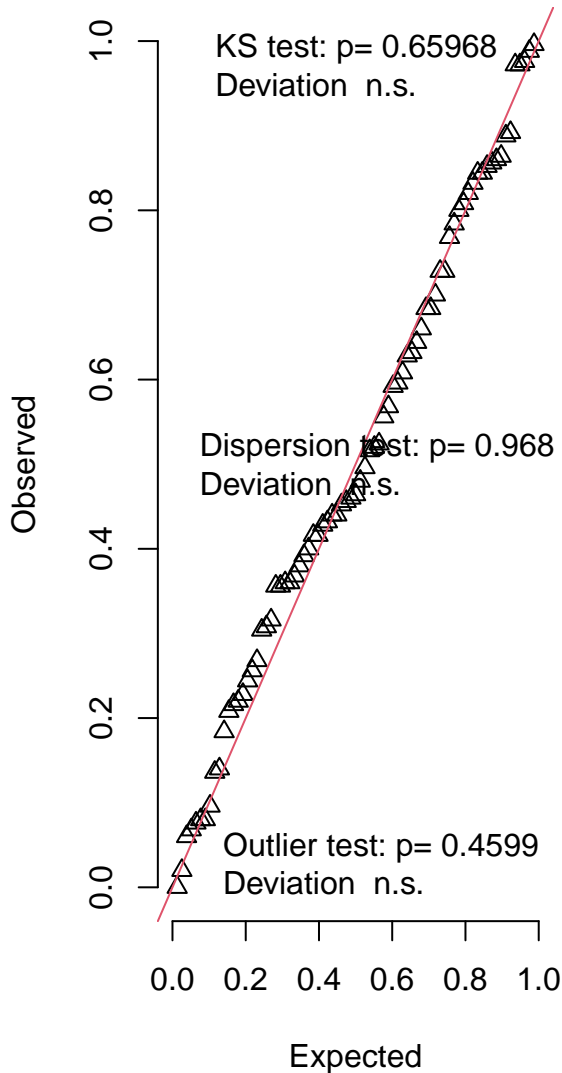
Nb obs DENV-squirrel (infected only): 11

Nb obs DENV-cyno (infected only): 63

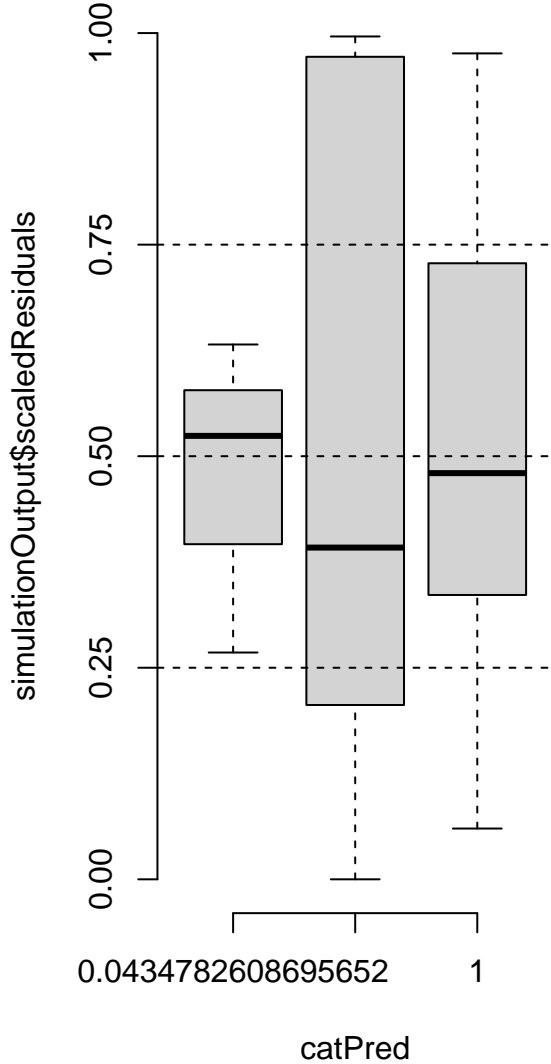
Nb obs ZIKV-squirrel (infected only): 3

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
-28.5	-14.4	20.3	-40.5	71

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.036188	0.19023
day	(Intercept)	0.001304	0.03611
Residual		0.022525	0.15008

Number of obs: 77, groups: ID, 13; day, 8

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

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.1583	0.1210	9.571	< 2e-16 ***
groupCyno.Dengue virus	1.0290	0.1374	7.492	6.81e-14 ***
groupSquirrel.Zika virus	-0.1545	0.2440	-0.633	0.527

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

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Infection in DENV-cyno

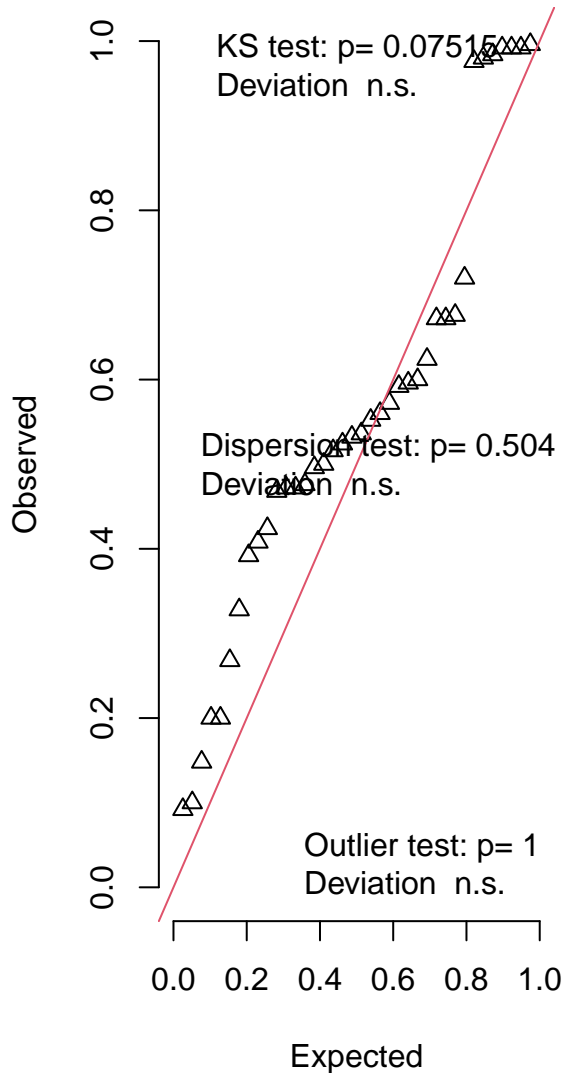
Nb excluded (LOD): 53

Nb obs infection: 25

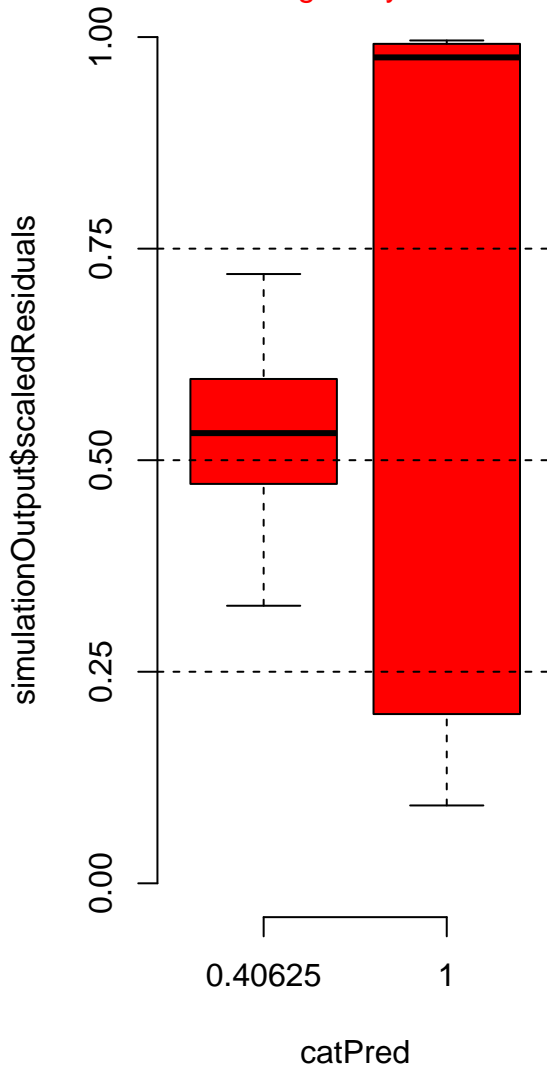
Nb obs control: 13

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
-59.8	-51.6	34.9	-69.8	33

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0750784	0.27400
day	(Intercept)	0.0005856	0.02420
Residual		0.0029446	0.05426

Number of obs: 38, groups: ID, 9; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00294

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.1621	0.1133	19.079	<2e-16 ***
inf_statusControl	0.2761	0.1955	1.413	0.158

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

Infection in DENV-squirrel

Nb excluded (LOD): 49

Nb obs infection: 0

Nb obs control: 0

G.CSF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 44

Nb obs infection: 5

Nb obs control: 0

G.CSF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 103

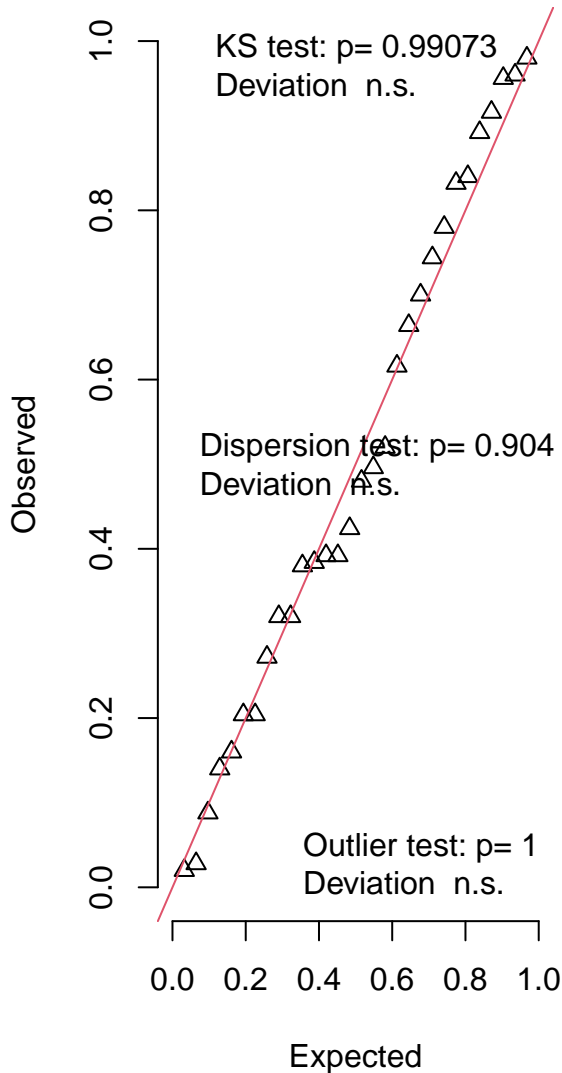
Nb obs DENV-squirrel (infected only): 0

Nb obs DENV-cyno (infected only): 25

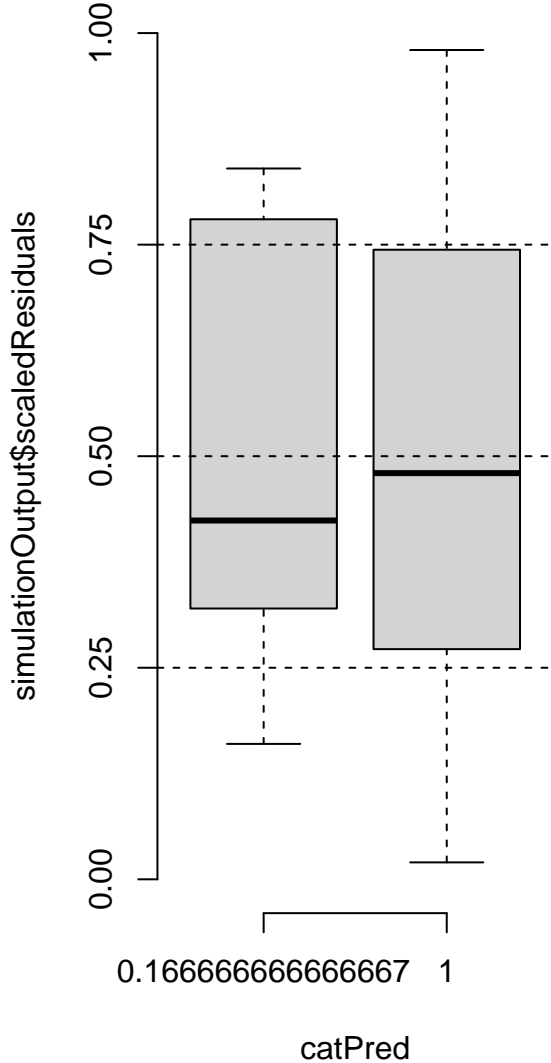
Nb obs ZIKV-squirrel (infected only): 5

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
-70.1	-63.1	40.1	-80.1	25

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.852e-04	1.361e-02
day	(Intercept)	2.401e-12	1.549e-06
Residual		3.882e-03	6.231e-02

Number of obs: 30, groups: ID, 9; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00388

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.19610	0.01667	131.77	<2e-16 ***
groupSquirrel.Zika virus	-0.04121	0.03252	-1.27	0.205

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

GM . CSF

Infection in DENV-cyno

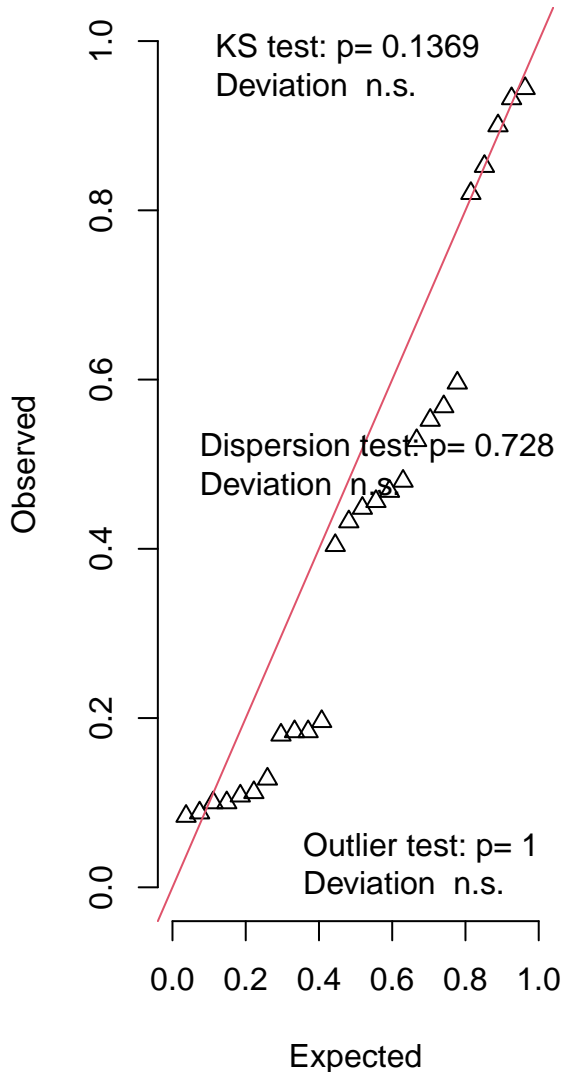
Nb excluded (LOD): 65

Nb obs infection: 19

Nb obs control: 7

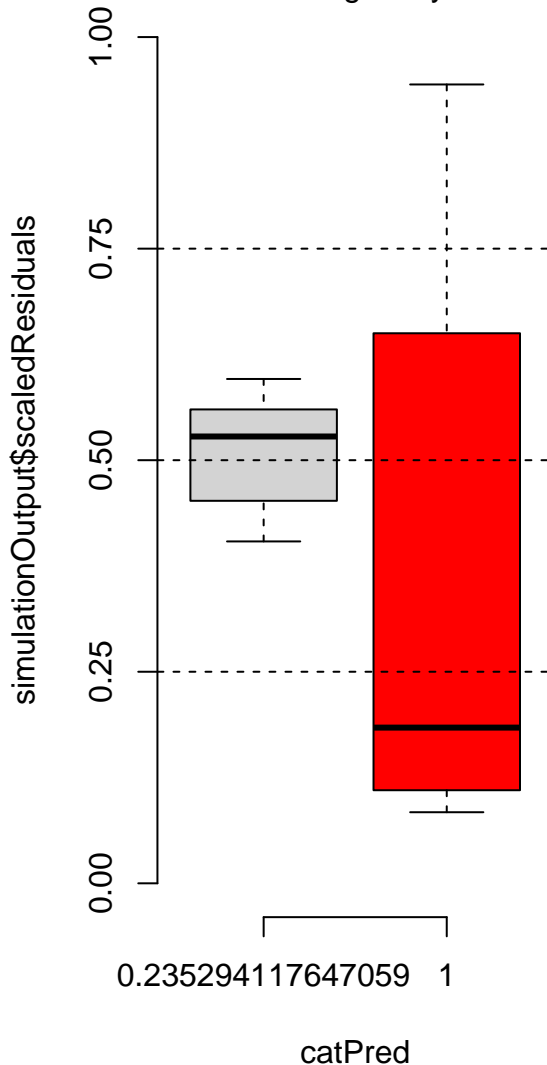
DHARMA residual

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
-35.3	-29.0	22.7	-45.3	21

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.809e-02	1.676e-01
day	(Intercept)	1.976e-11	4.445e-06
Residual		5.172e-03	7.191e-02

Number of obs: 26, groups: ID, 6; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00517

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.38813	0.08668	16.015	<2e-16 ***
inf_statusControl	-0.10549	0.15164	-0.696	0.487

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

Infection in DENV-squirrel

Nb excluded (LOD): 45

Nb obs infection: 4

Nb obs control: 0

GM.CSF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 48

Nb obs infection: 1

Nb obs control: 0

GM.CSF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 109

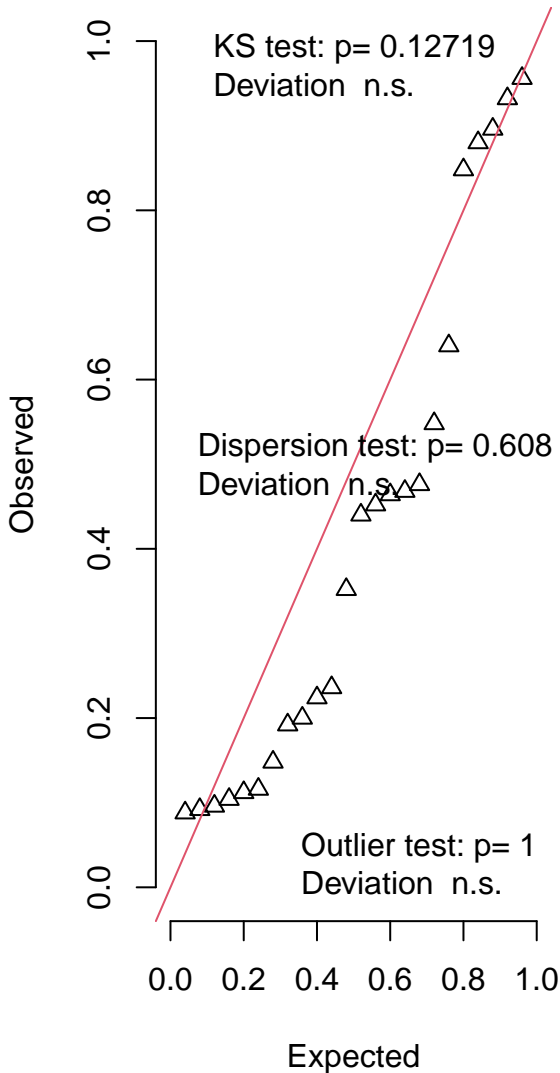
Nb obs DENV-squirrel (infected only): 4

Nb obs DENV-cyno (infected only): 19

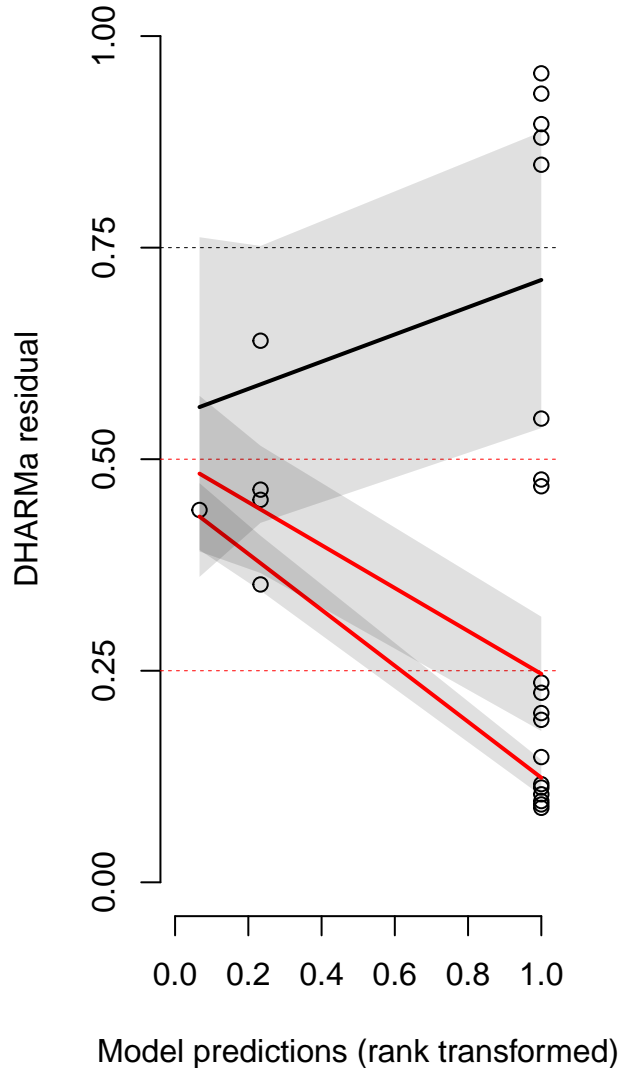
Nb obs ZIKV-squirrel (infected only): 1

DHARMA residual

QQ plot residuals



Residual vs. predicted Quantile deviations detected (red curves) Combined adjusted quantile test significant



```

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

```

AIC	BIC	logLik	deviance	df.resid
-27.0	-20.0	19.5	-39.0	18

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.789e-02	0.166996
day	(Intercept)	5.068e-05	0.007119
Residual		5.668e-03	0.075289

Number of obs: 24, groups: ID, 6; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00567

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.36245	0.17159	7.940	2.02e-15 ***
groupCyno.Dengue virus	0.02463	0.19252	0.128	0.898
groupSquirrel.Zika virus	-0.08401	0.25307	-0.332	0.740

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

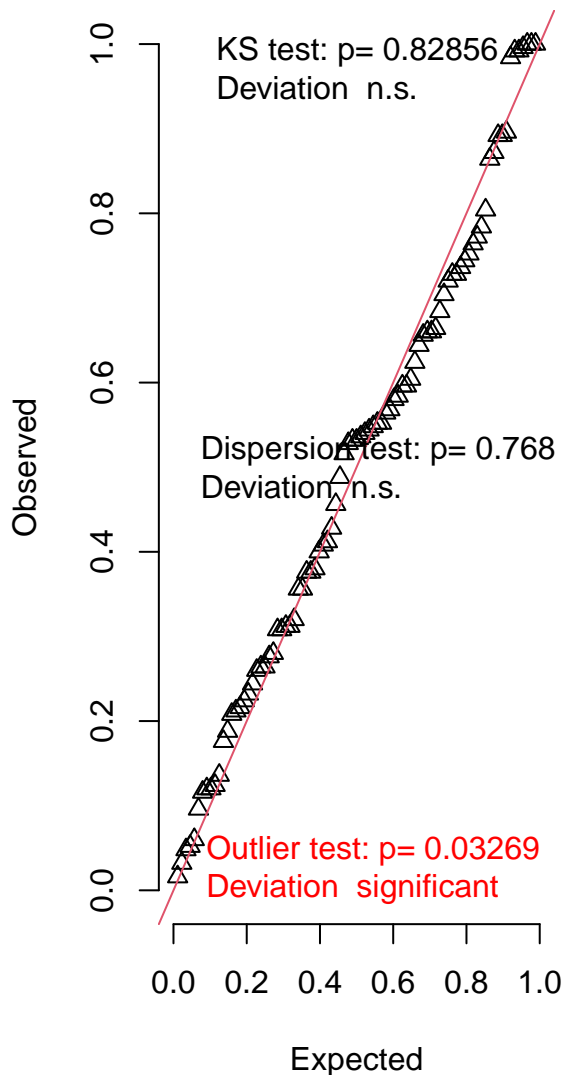
HGF

Infection in DENV-cyno

Nb excluded (LOD): 4
Nb obs infection: 61
Nb obs control: 26

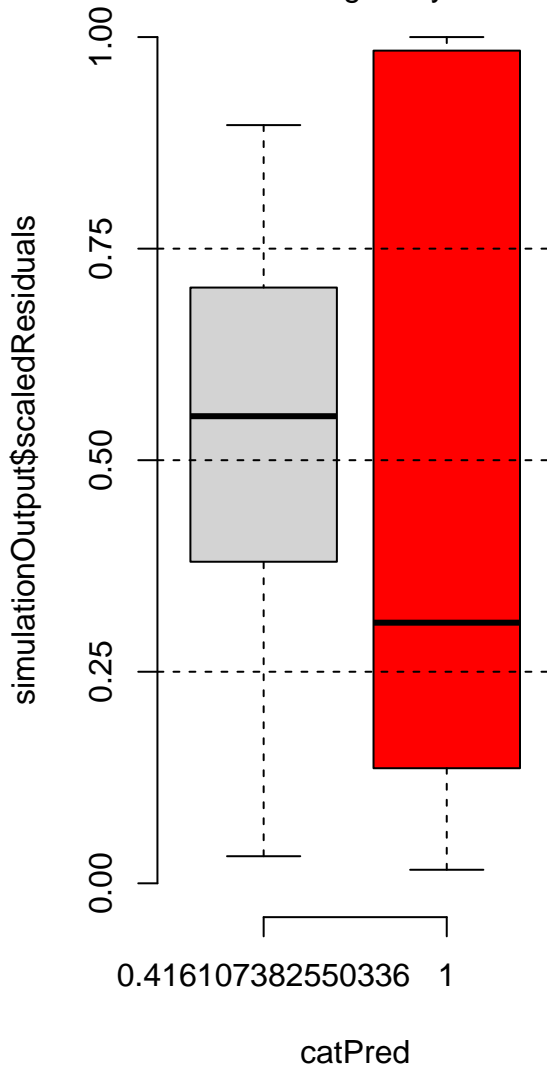
DHARMA residual

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
-17.5	-5.1	13.7	-27.5	82

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.041e-01	0.322649
day	(Intercept)	2.356e-05	0.004854
Residual		2.597e-02	0.161160

Number of obs: 87, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.026

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.8505	0.1096	26.020	<2e-16 ***
inf_statusControl	0.2394	0.1976	1.212	0.226

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

Infection in DENV-squirrel

Nb excluded (LOD): 33

Nb obs infection: 16

Nb obs control: 0

HGF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 37

Nb obs infection: 12

Nb obs control: 0

HGF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 44

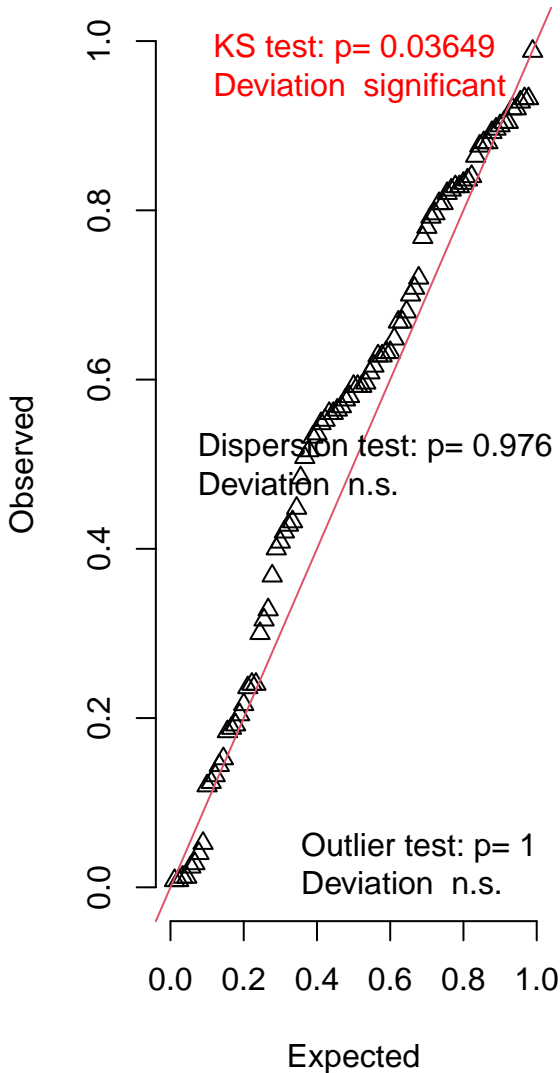
Nb obs DENV-squirrel (infected only): 16

Nb obs DENV-cyno (infected only): 61

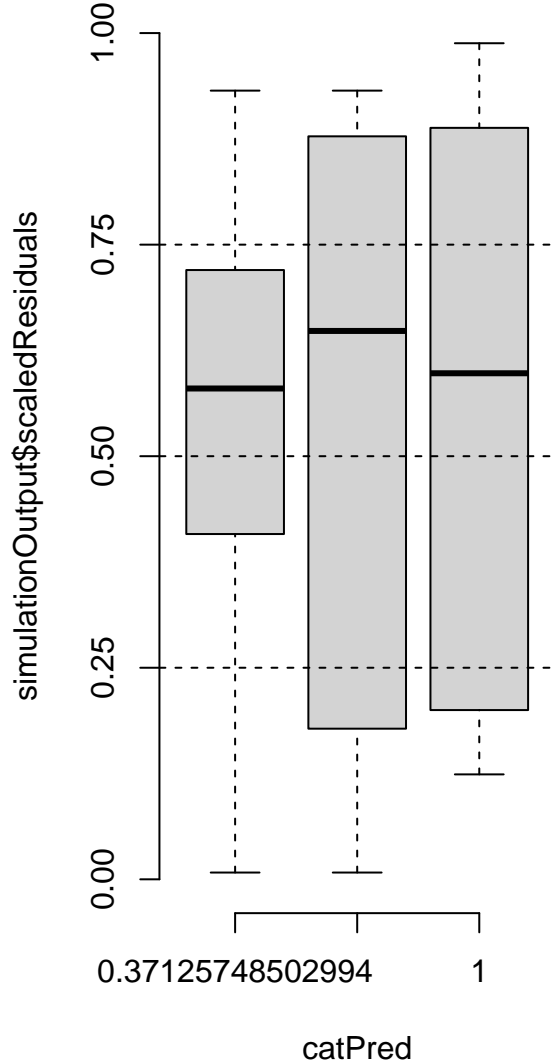
Nb obs ZIKV-squirrel (infected only): 12

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) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-11.9	3.0	12.0	-23.9	83

Random effects:

```

Conditional model:
Groups   Name          Variance Std.Dev.
ID       (Intercept)  6.821e-02 2.612e-01
day      (Intercept)  1.924e-12 1.387e-06
Residual                2.741e-02 1.656e-01
Number of obs: 89, groups: ID, 17; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.0274

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    3.2871    0.1370  23.995 < 2e-16 ***
groupCyno.Dengue virus -0.4362    0.1637  -2.665  0.00771 **
groupSquirrel.Zika virus  0.1822    0.1969   0.925  0.35492
---

```

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

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Infection in DENV-cyno

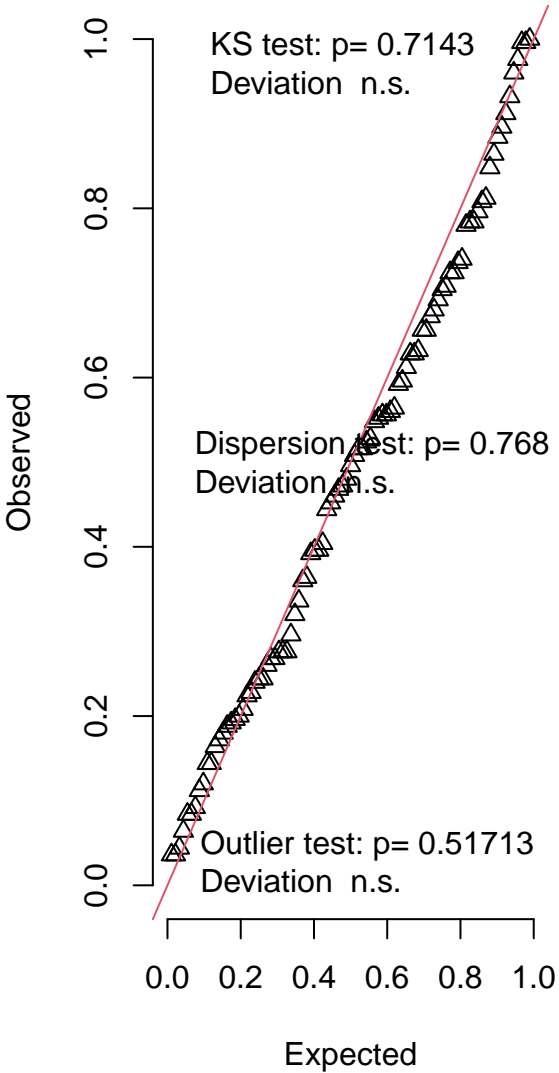
Nb excluded (LOD): 0

Nb obs infection: 63

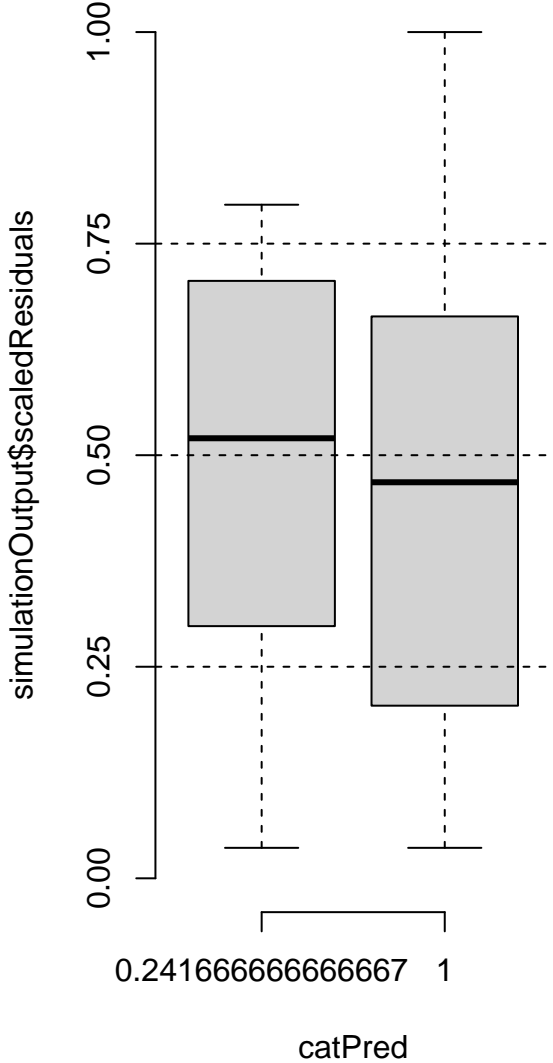
Nb obs control: 28

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

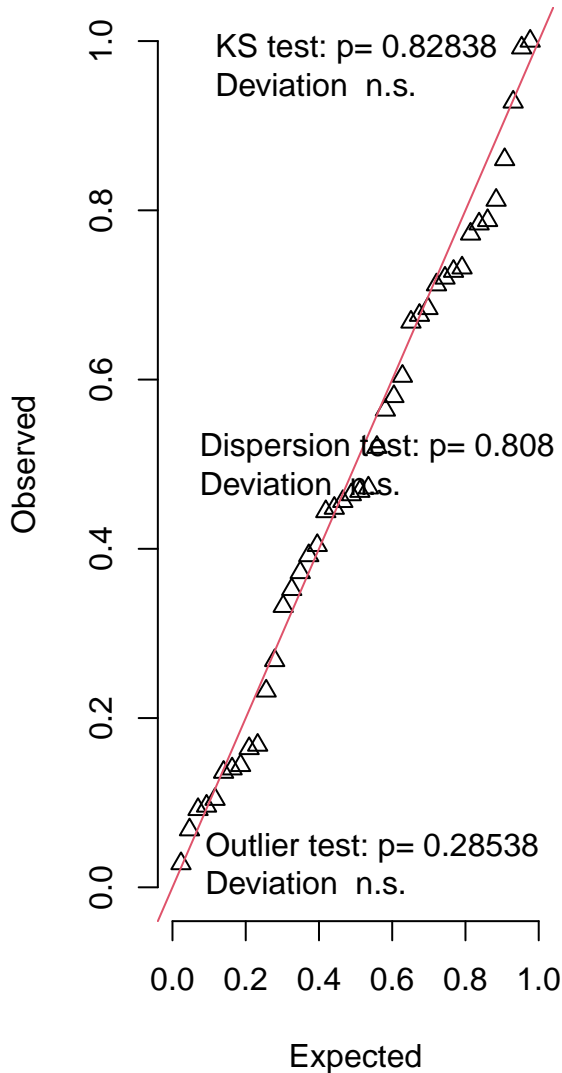
Nb excluded (LOD): 7

Nb obs infection: 31

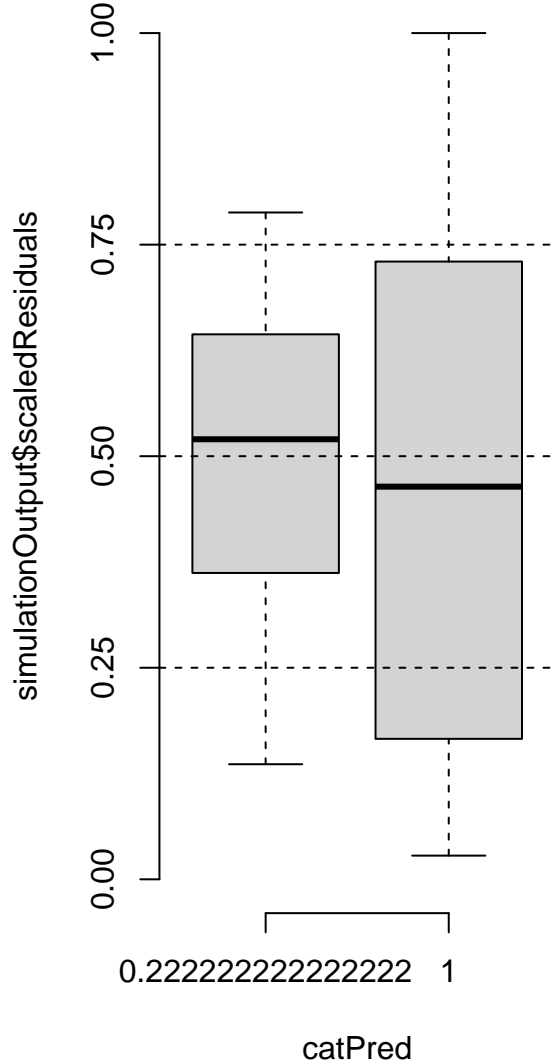
Nb obs control: 11

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
-60.3	-51.7	35.2	-70.3	37

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.083e-03	4.564e-02
day	(Intercept)	5.117e-12	2.262e-06
Residual		9.307e-03	9.647e-02

Number of obs: 42, groups: ID, 12; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00931

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.69662	0.02324	72.99	<2e-16 ***
inf_statusControl	-0.03054	0.04574	-0.67	0.504

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

Infection in ZIKV-squirrel

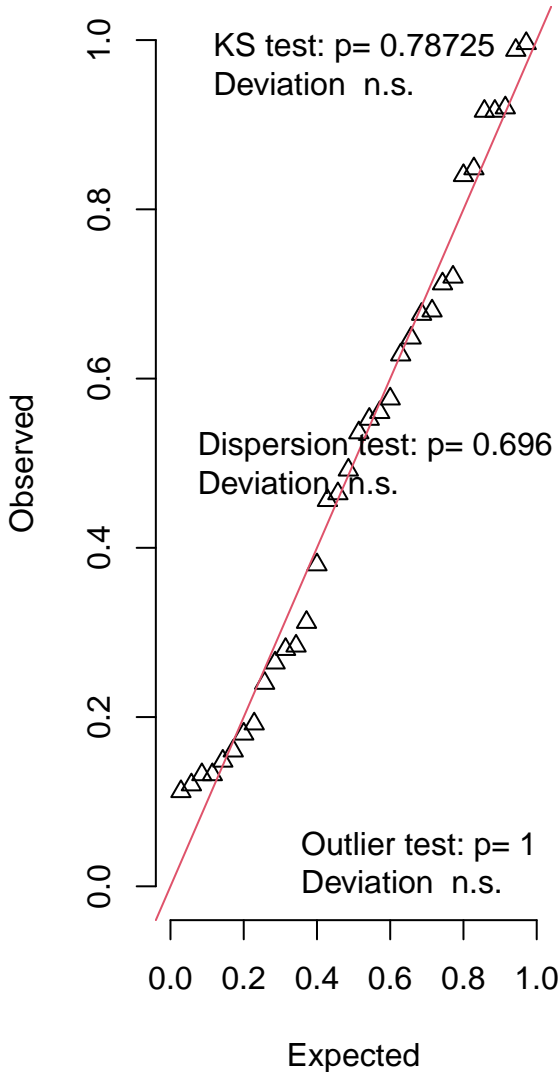
Nb excluded (LOD): 15

Nb obs infection: 23

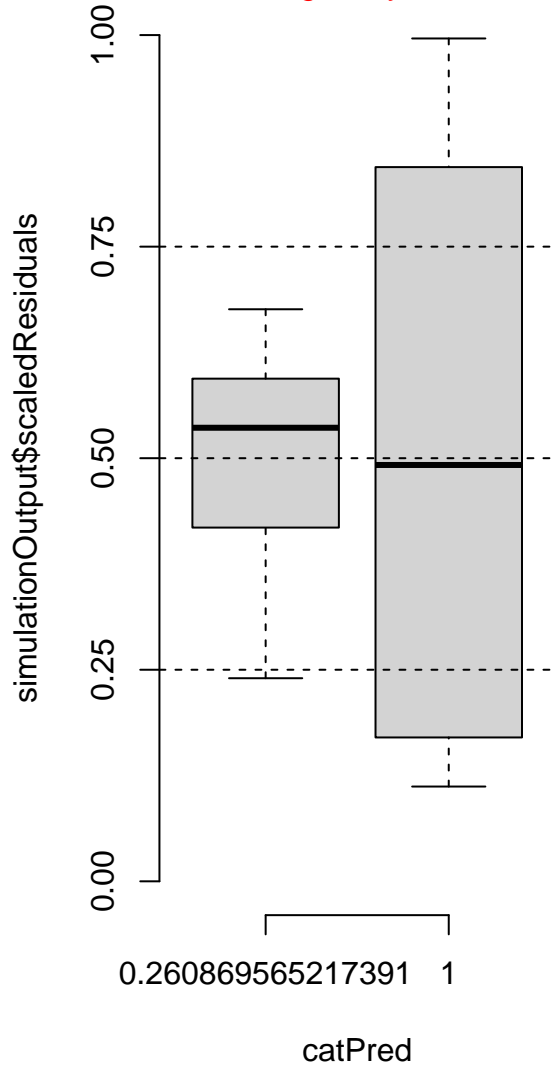
Nb obs control: 11

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: z_sq

```

AIC	BIC	logLik	deviance	df.resid
-30.4	-22.8	20.2	-40.4	29

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.008135	0.09019
day	(Intercept)	0.003341	0.05780
Residual		0.010591	0.10291

Number of obs: 34, groups: ID, 11; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0106

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.70342	0.04687	36.35	<2e-16 ***
inf_statusControl	-0.03800	0.07331	-0.52	0.604

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

Effect of experiment

Nb excluded (LOD): 16

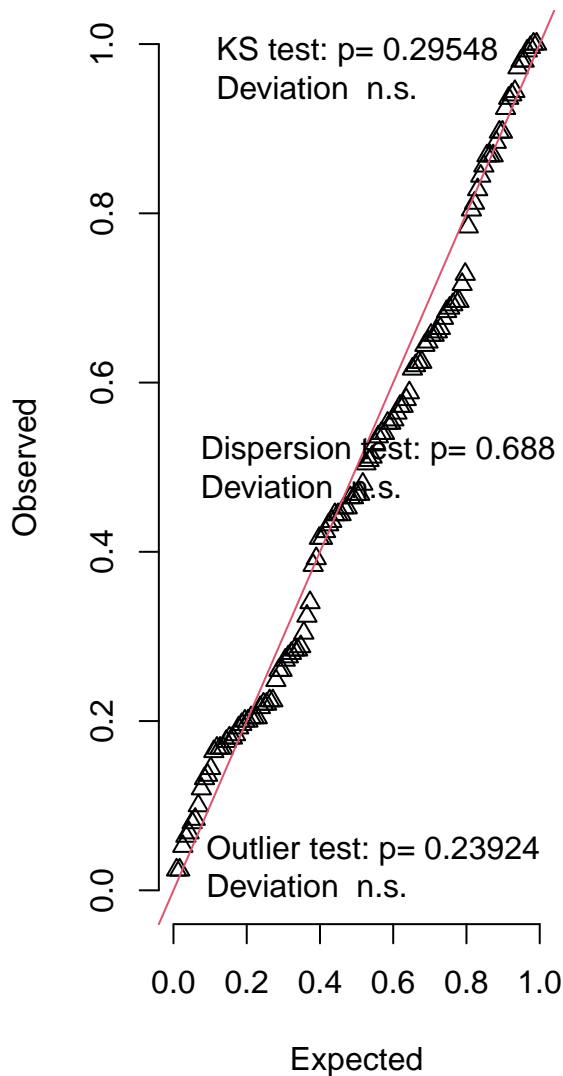
Nb obs DENV-squirrel (infected only): 31

Nb obs DENV-cyno (infected only): 63

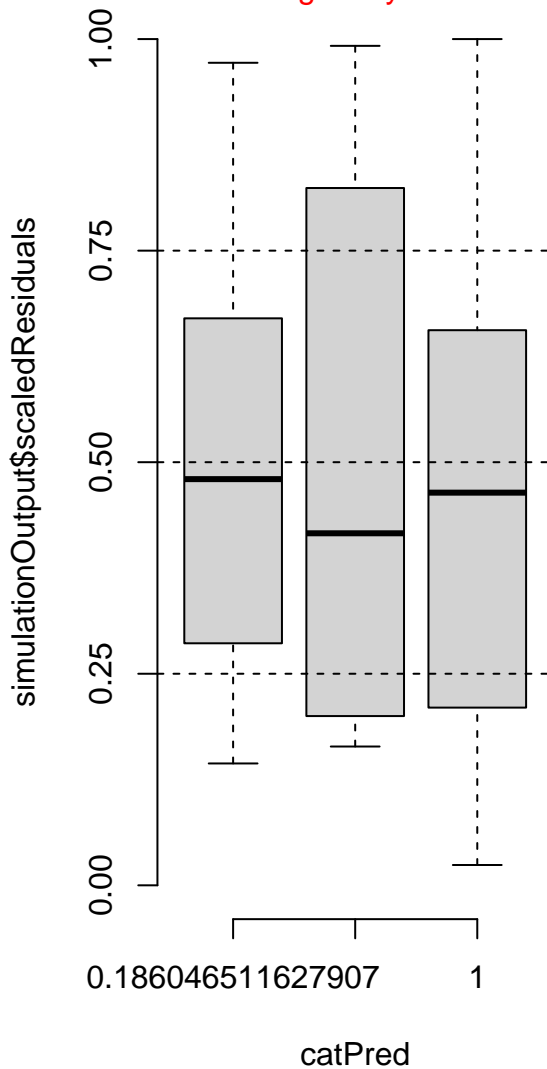
Nb obs ZIKV-squirrel (infected only): 23

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) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-71.9	-55.3	41.9	-83.9	111

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.007862	0.08867
day	(Intercept)	0.001073	0.03275
Residual		0.022703	0.15067

Number of obs: 117, groups: ID, 26; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.0227

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.69607	0.04211	40.28	<2e-16 ***
groupCyno.Dengue virus	0.52586	0.05381	9.77	<2e-16 ***
groupSquirrel.Zika virus	0.01451	0.06162	0.24	0.814

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

IFN.g

Infection in DENV-cyno

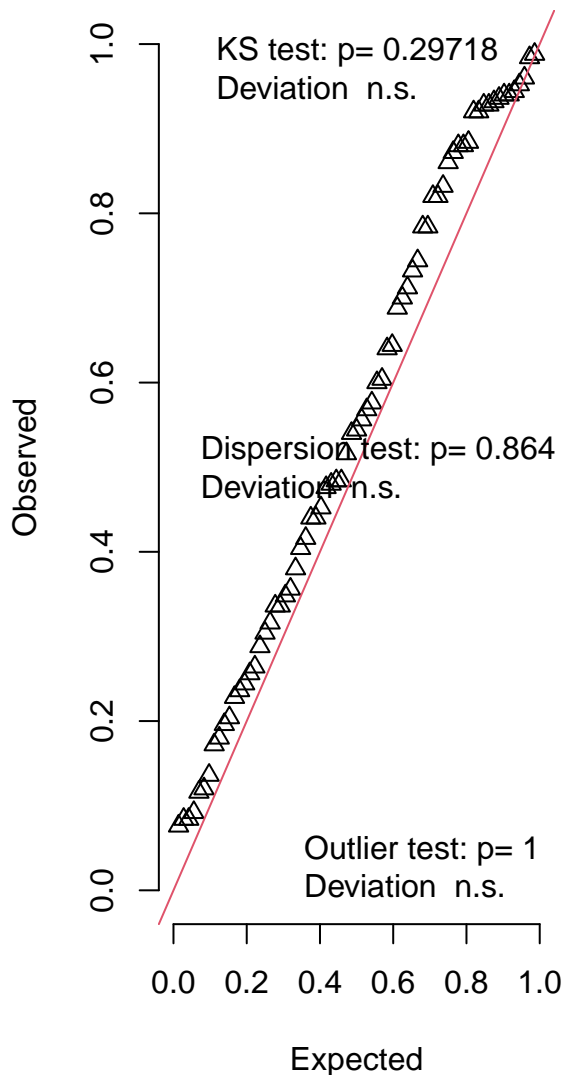
Nb excluded (LOD): 20

Nb obs infection: 49

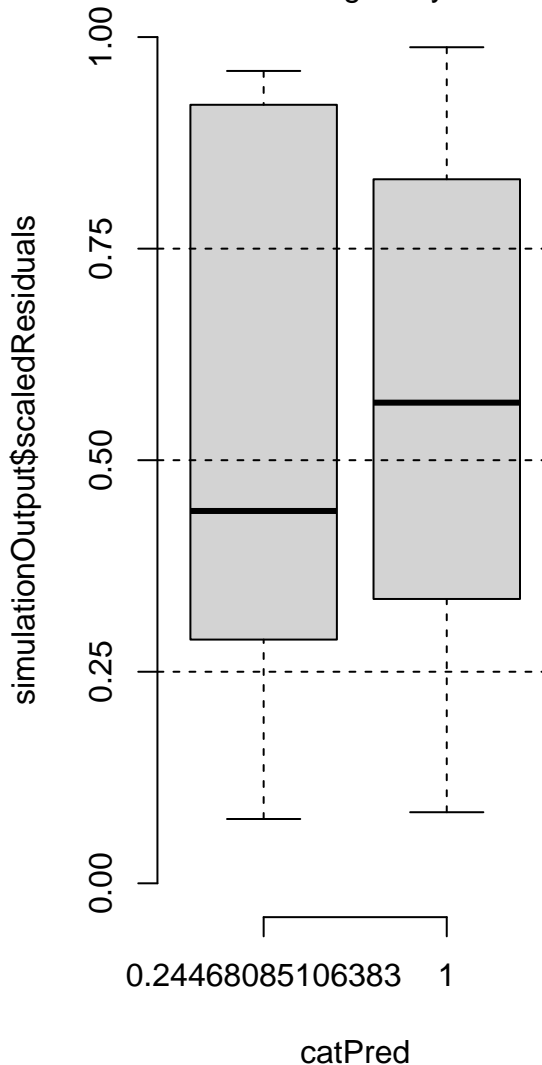
Nb obs control: 22

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
-2.6	8.7	6.3	-12.6	66

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.09779	0.31272
day	(Intercept)	0.00545	0.07382
Residual		0.02577	0.16052

Number of obs: 71, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0258

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.8030	0.1116	16.16	<2e-16 ***
inf_statusControl	-0.1314	0.1932	-0.68	0.497

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

Infection in DENV-squirrel

Nb excluded (LOD): 29

Nb obs infection: 20

Nb obs control: 0

IFN.g ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 37

Nb obs infection: 12

Nb obs control: 0

IFN.g ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 52

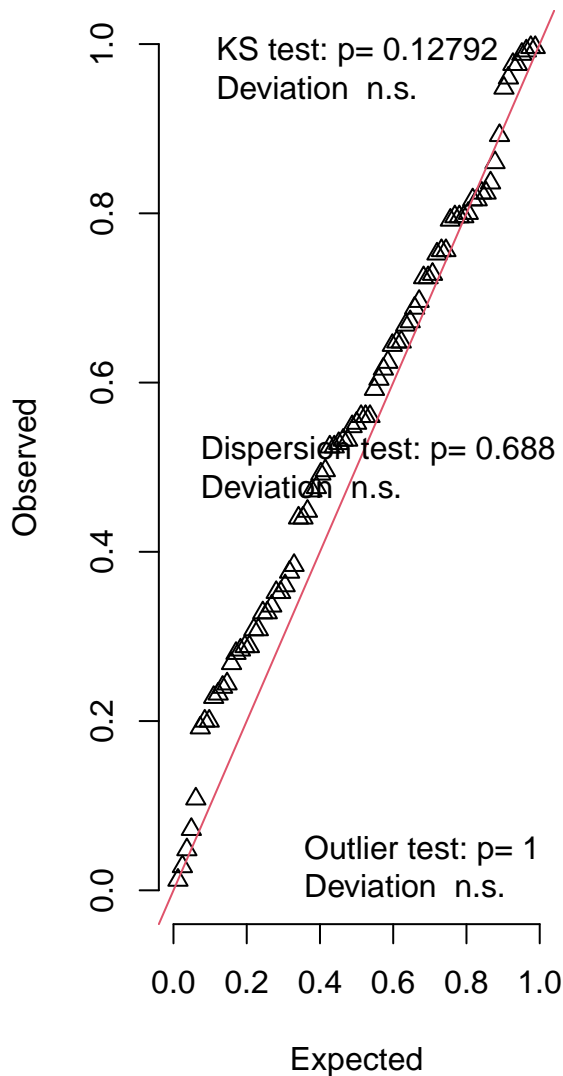
Nb obs DENV-squirrel (infected only): 20

Nb obs DENV-cyno (infected only): 49

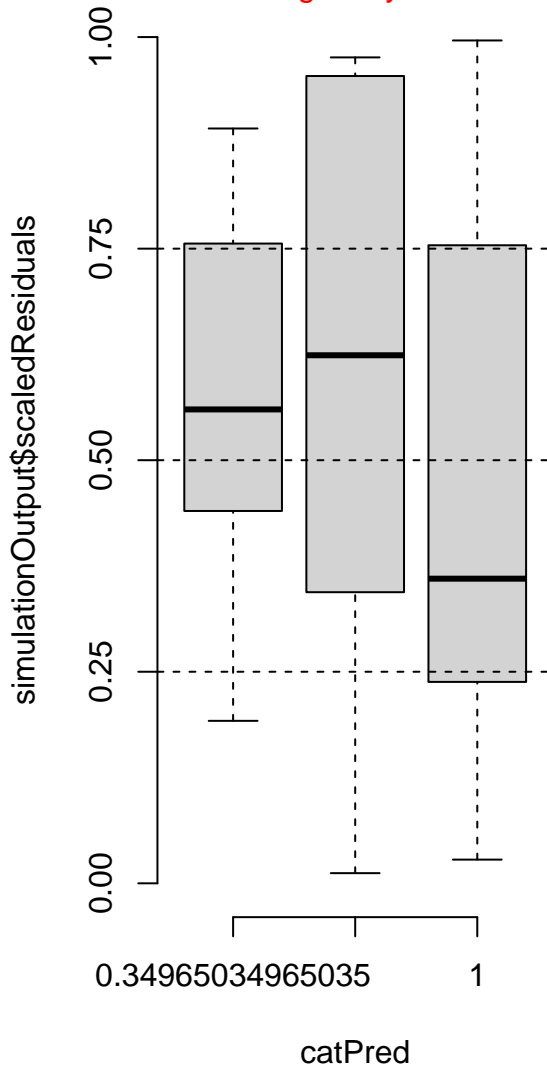
Nb obs ZIKV-squirrel (infected only): 12

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) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
11.1	25.5	0.5	-0.9	75

Random effects:

```

Conditional model:
Groups   Name          Variance Std.Dev.
ID       (Intercept)  0.276095 0.52545
day      (Intercept)  0.001352 0.03678
Residual                0.023730 0.15405
Number of obs: 81, groups:  ID, 18; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.0237

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    2.6934      0.2382  11.309 < 2e-16 ***
groupCyno.Dengue virus -0.8906      0.2965  -3.004  0.00267 **
groupSquirrel.Zika virus -0.1038      0.3581  -0.290  0.77191
---

```

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

IL.10

Infection in DENV-cyno

Nb excluded (LOD): 91

Nb obs infection: 0

Nb obs control: 0

IL.10 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in DENV-squirrel

Nb excluded (LOD): 46

Nb obs infection: 3

Nb obs control: 0

IL.10 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 45

Nb obs infection: 4

Nb obs control: 0

IL.10 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 126

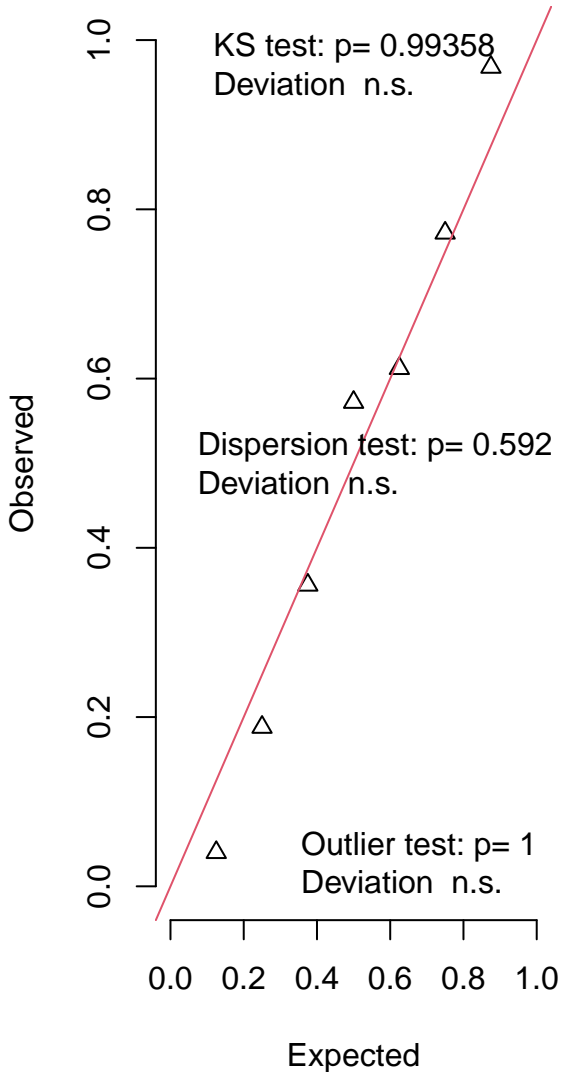
Nb obs DENV-squirrel (infected only): 3

Nb obs DENV-cyno (infected only): 0

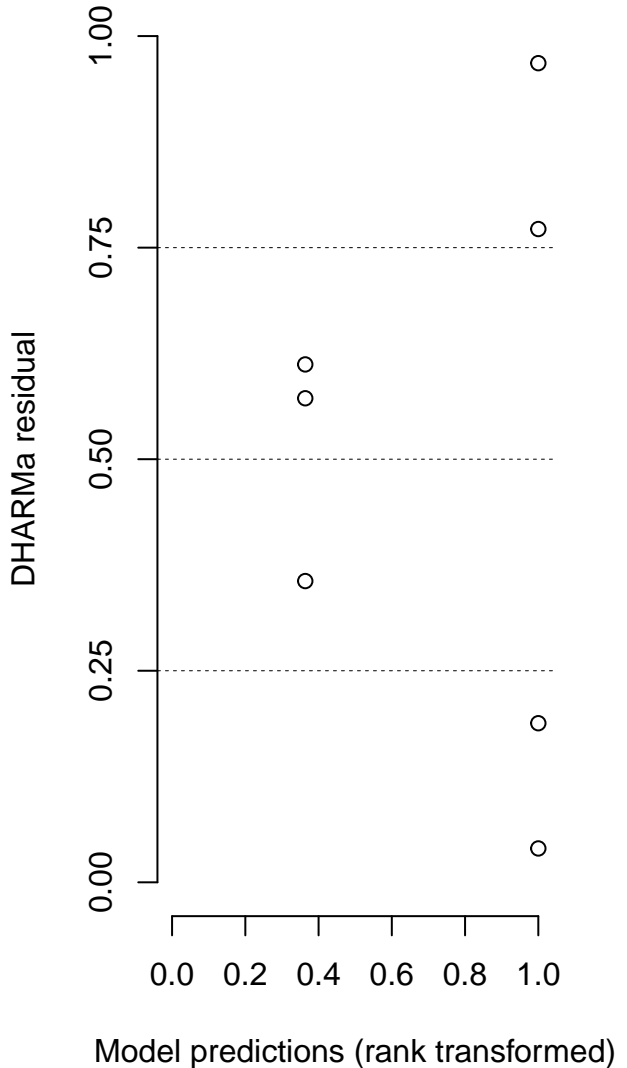
Nb obs ZIKV-squirrel (infected only): 4

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



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

AIC	BIC	logLik	deviance	df.resid
NA	NA	NA	NA	2

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	3.028e-25	5.503e-13
day	(Intercept)	1.212e-11	3.481e-06
Residual		5.467e-02	2.338e-01

Number of obs: 7, groups: ID, 3; day, 6

Dispersion estimate for gaussian family (sigma^2): 0.0547

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.2401	NaN	NaN	NaN
groupSquirrel.Zika virus	0.8112	NaN	NaN	NaN

IL.12

Infection in DENV-cyno

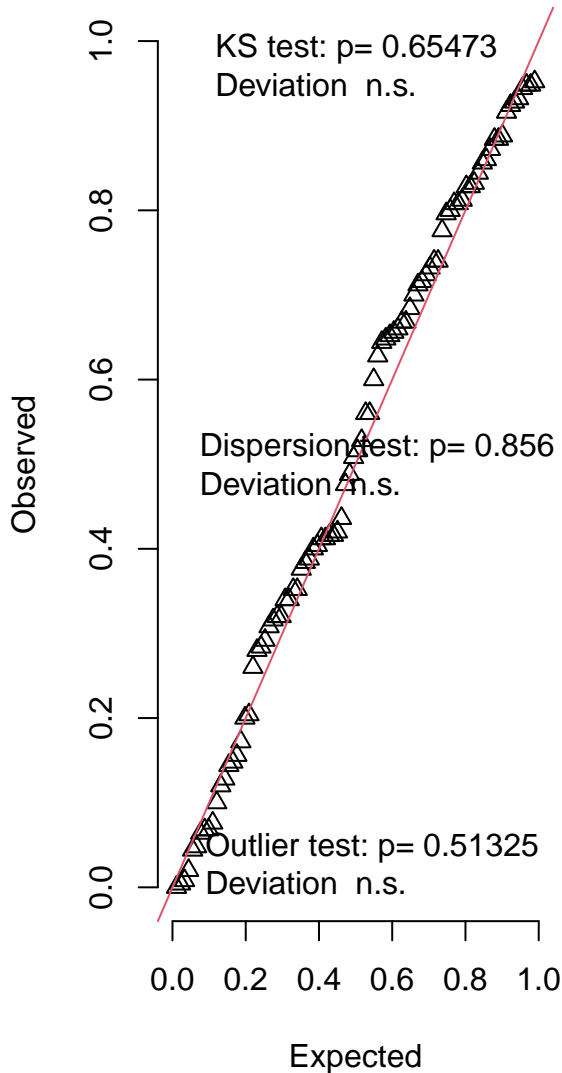
Nb excluded (LOD): 1

Nb obs infection: 62

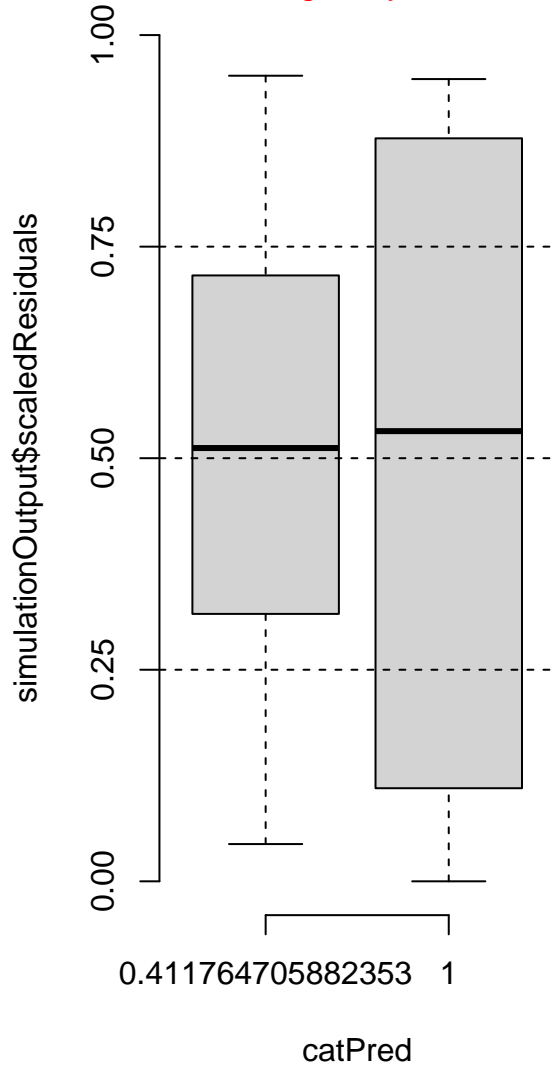
Nb obs control: 28

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
-118.8	-106.3	64.4	-128.8	85

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.073955	0.27195
day	(Intercept)	0.004311	0.06566
Residual		0.006363	0.07977

Number of obs: 90, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00636

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.00159	0.09453	31.75	<2e-16 ***
inf_statusControl	0.13615	0.16443	0.83	0.408

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

Infection in DENV-squirrel

Nb excluded (LOD): 36

Nb obs infection: 13

Nb obs control: 0

IL.12 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 37

Nb obs infection: 12

Nb obs control: 0

IL.12 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 46

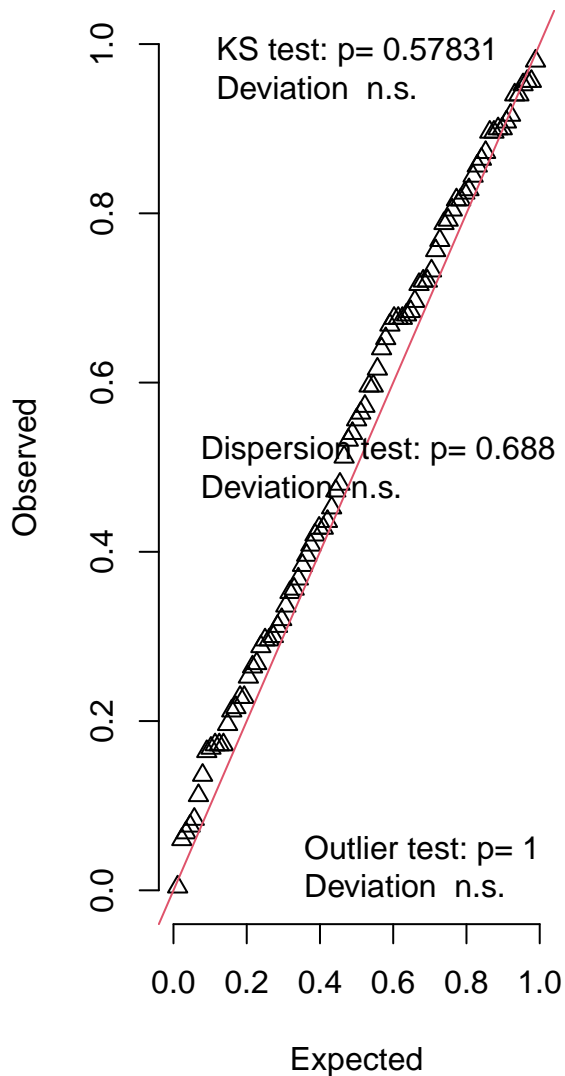
Nb obs DENV-squirrel (infected only): 13

Nb obs DENV-cyno (infected only): 62

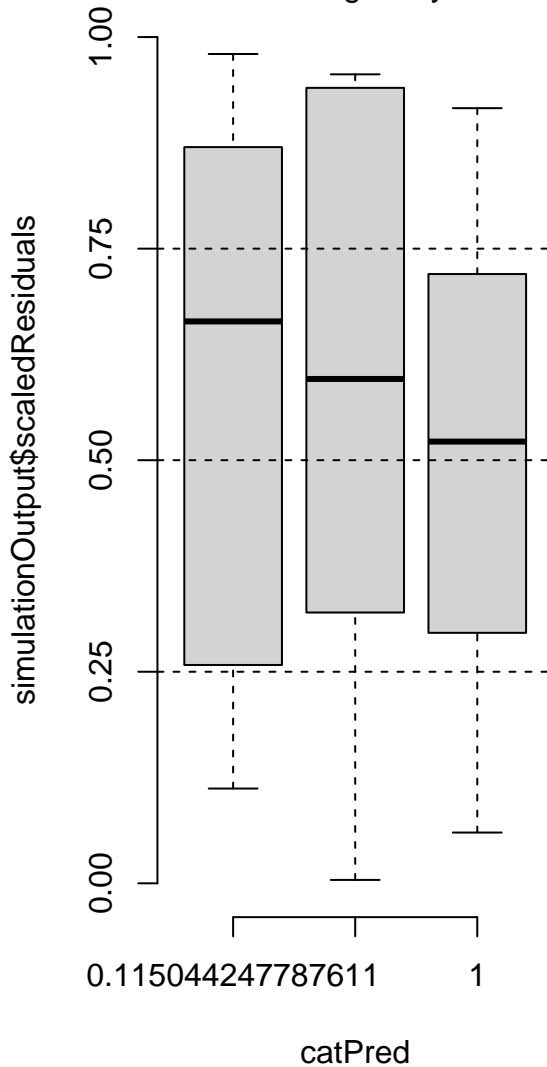
Nb obs ZIKV-squirrel (infected only): 12

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) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-41.7	-26.9	26.8	-53.7	81

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.07591	0.2755
day	(Intercept)	0.00126	0.0355
Residual		0.01657	0.1287

Number of obs: 87, groups: ID, 17; day, 8

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

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.92419	0.14530	20.125	<2e-16 ***
groupCyno.Dengue virus	0.07794	0.17206	0.453	0.651
groupSquirrel.Zika virus	-0.02098	0.20387	-0.103	0.918

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

IL.15

Infection in DENV-cyno

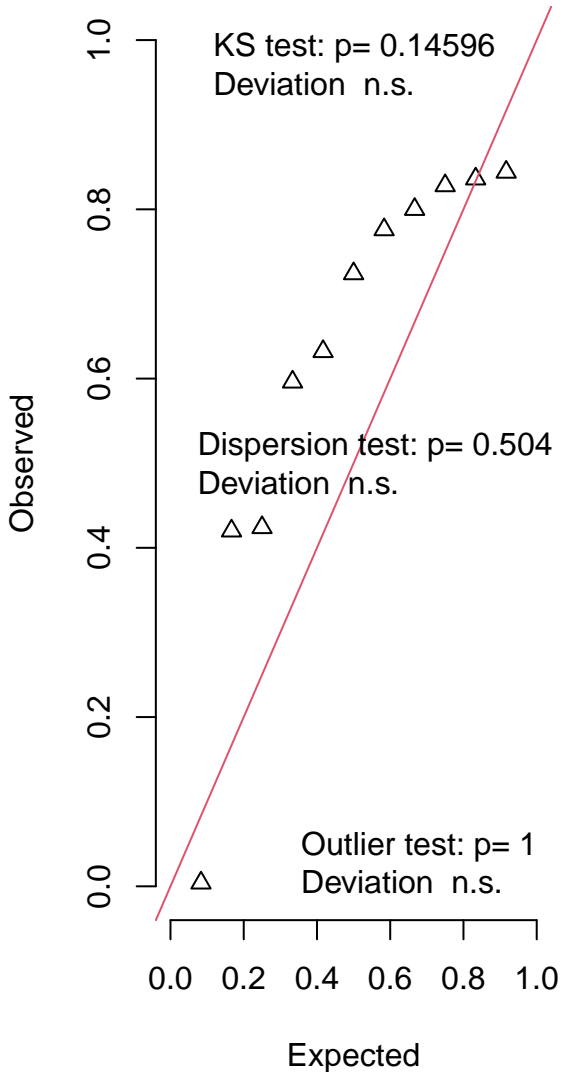
Nb excluded (LOD): 80

Nb obs infection: 3

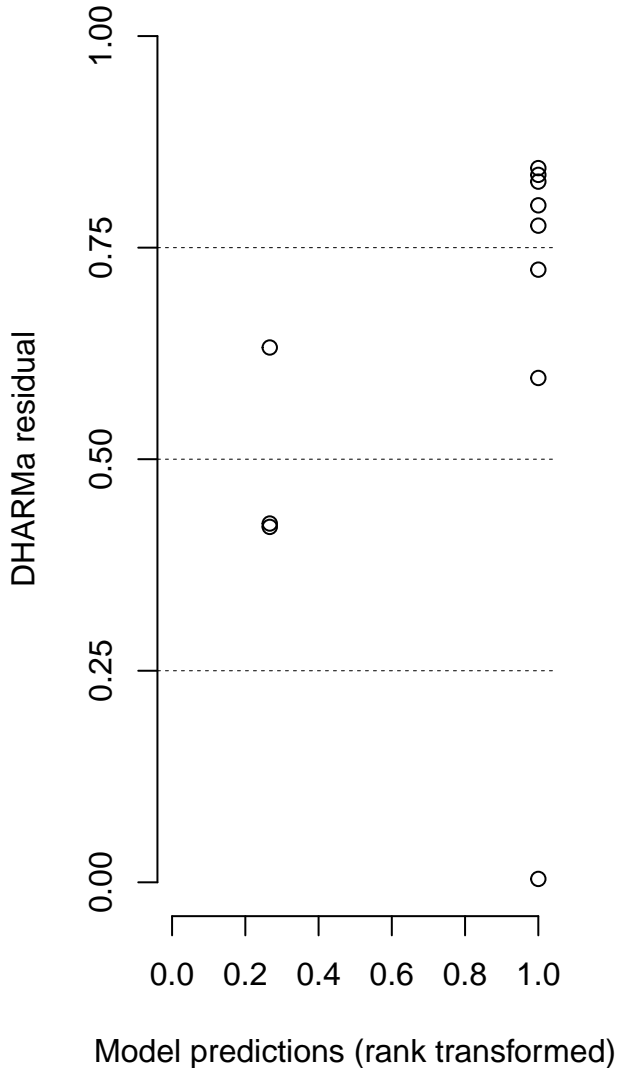
Nb obs control: 8

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
11.2	13.2	-0.6	1.2	6

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.047583	0.21813
day	(Intercept)	0.004035	0.06353
Residual		0.038759	0.19687

Number of obs: 11, groups: ID, 3; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0388

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.0342	0.2501	8.133	4.19e-16 ***
inf_statusControl	0.7369	0.3075	2.397	0.0166 *

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

Infection in DENV-squirrel

Nb excluded (LOD): 38

Nb obs infection: 11

Nb obs control: 0

IL.15 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 38

Nb obs infection: 11

Nb obs control: 0

IL.15 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 108

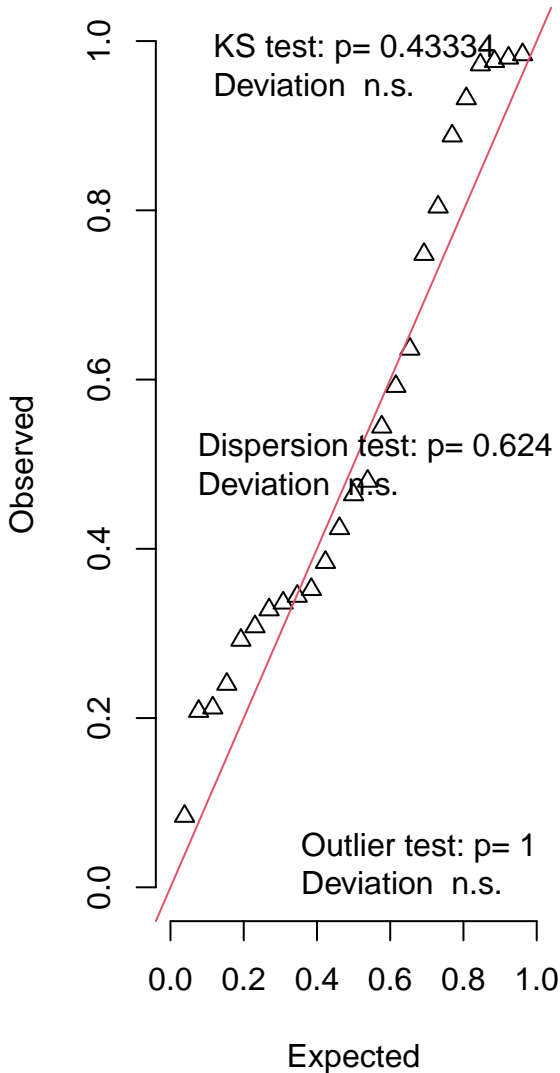
Nb obs DENV-squirrel (infected only): 11

Nb obs DENV-cyno (infected only): 3

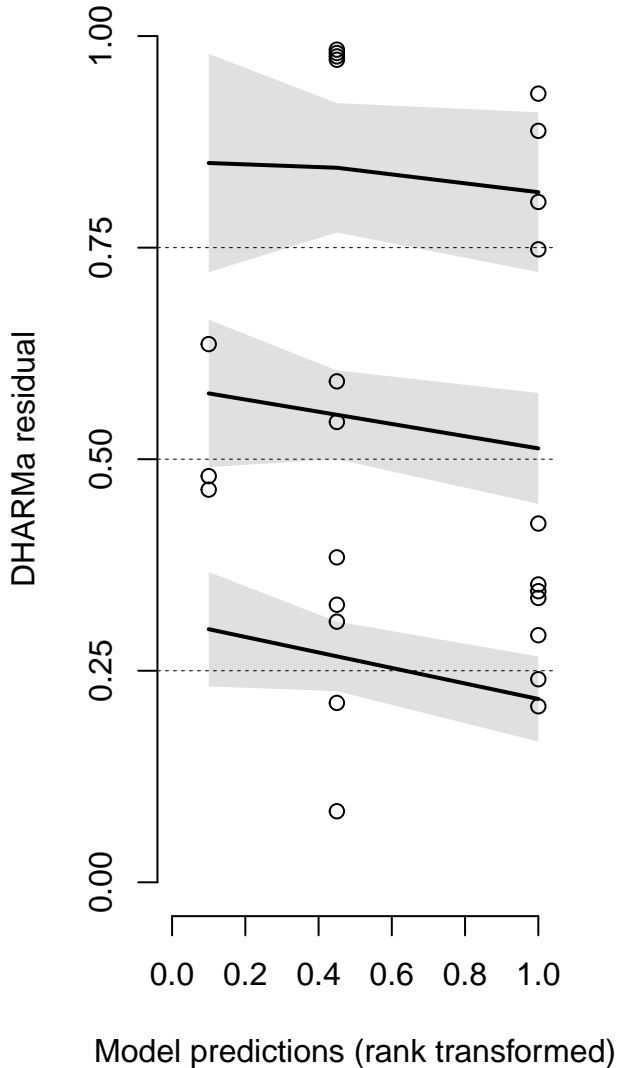
Nb obs ZIKV-squirrel (infected only): 11

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected




```

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

```

AIC	BIC	logLik	deviance	df.resid
12.1	19.5	-0.1	0.1	19

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.395e-01	4.894e-01
day	(Intercept)	6.885e-14	2.624e-07
Residual		1.815e-02	1.347e-01

Number of obs: 25, groups: ID, 8; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0182

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.6852	0.2491	10.779	<2e-16 ***
groupCyno.Dengue virus	-0.6459	0.5547	-1.164	0.244
groupSquirrel.Zika virus	0.2492	0.3789	0.658	0.511

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

IL.17

Infection in DENV-cyno

Nb excluded (LOD): 91

Nb obs infection: 0

Nb obs control: 0

IL.17 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in DENV-squirrel

Nb excluded (LOD): 45

Nb obs infection: 4

Nb obs control: 0

IL.17 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 49

Nb obs infection: 0

Nb obs control: 0

IL.17 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 129

Nb obs DENV-squirrel (infected only): 4

Nb obs DENV-cyno (infected only): 0

Nb obs ZIKV-squirrel (infected only): 0

IL.17 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

IL.1B

Infection in DENV-cyno

Nb excluded (LOD): 91

Nb obs infection: 0

Nb obs control: 0

IL.1B ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in DENV-squirrel

Nb excluded (LOD): 45

Nb obs infection: 4

Nb obs control: 0

IL.1B ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 47

Nb obs infection: 2

Nb obs control: 0

IL.1B ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 127

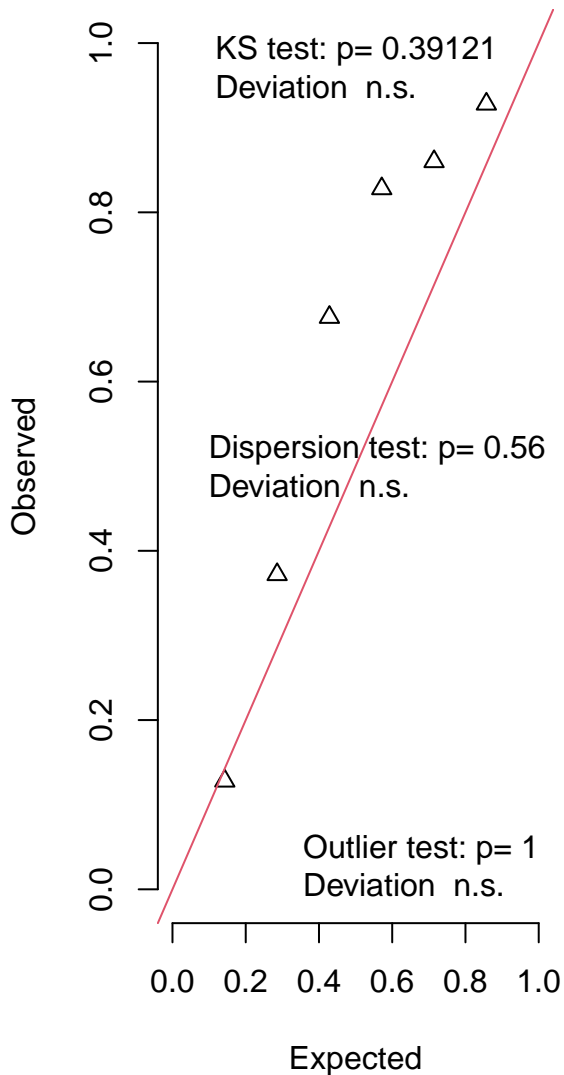
Nb obs DENV-squirrel (infected only): 4

Nb obs DENV-cyno (infected only): 0

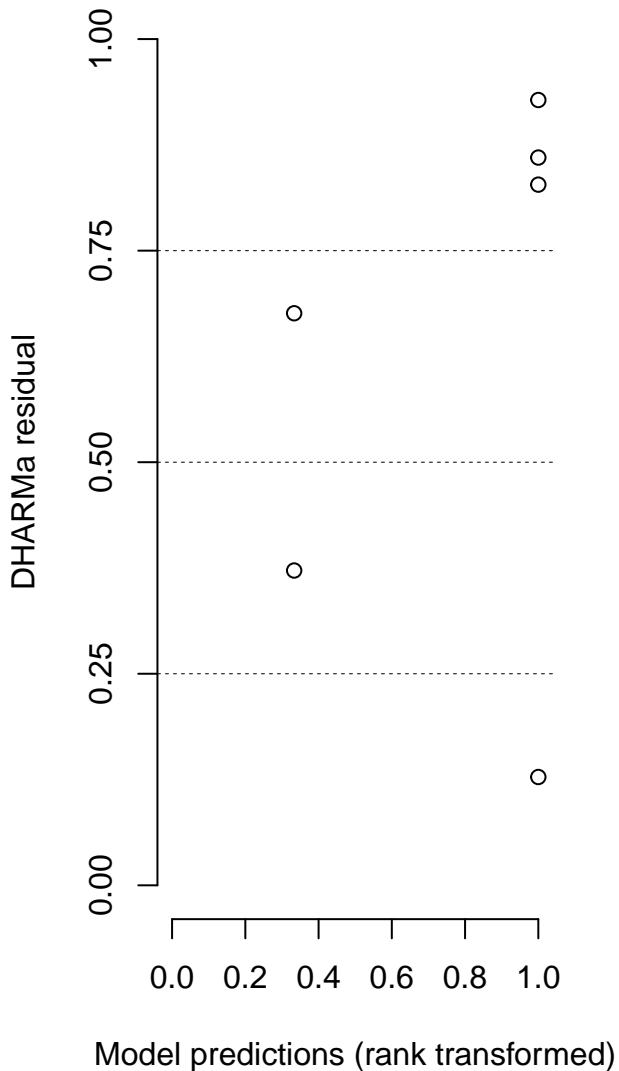
Nb obs ZIKV-squirrel (infected only): 2

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
16.1	15.0	-3.0	6.1	1

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	3.096e-01	5.564e-01
day	(Intercept)	4.593e-11	6.777e-06
Residual		4.244e-02	2.060e-01

Number of obs: 6, groups: ID, 3; day, 5

Dispersion estimate for gaussian family (sigma^2): 0.0424

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.8333	0.4122	4.448	8.67e-06 ***
groupSquirrel.Zika virus	-0.4915	0.7076	-0.695	0.487

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

IL. 2

Infection in DENV-cyno

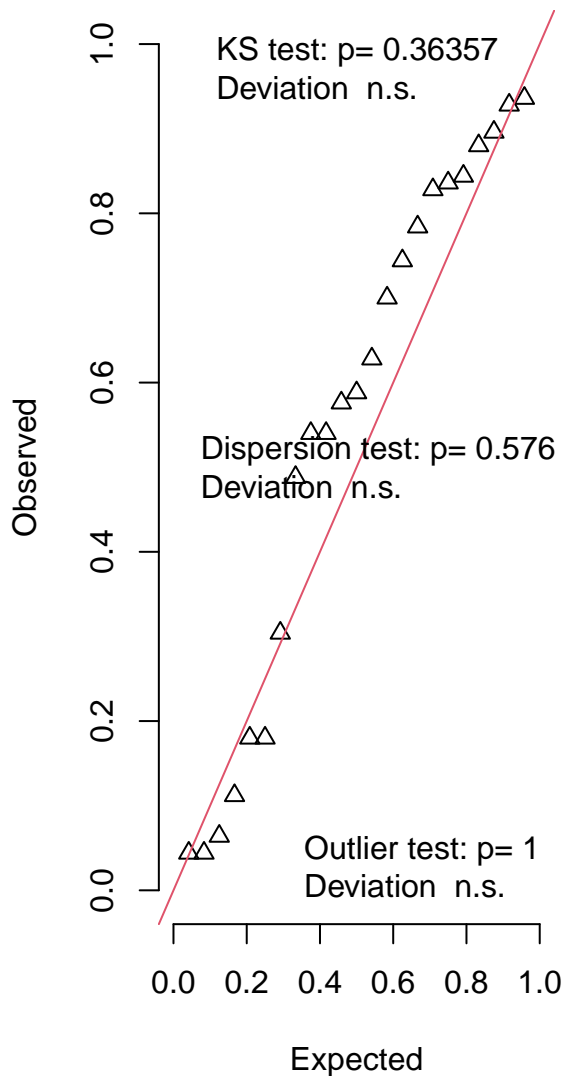
Nb excluded (LOD): 68

Nb obs infection: 15

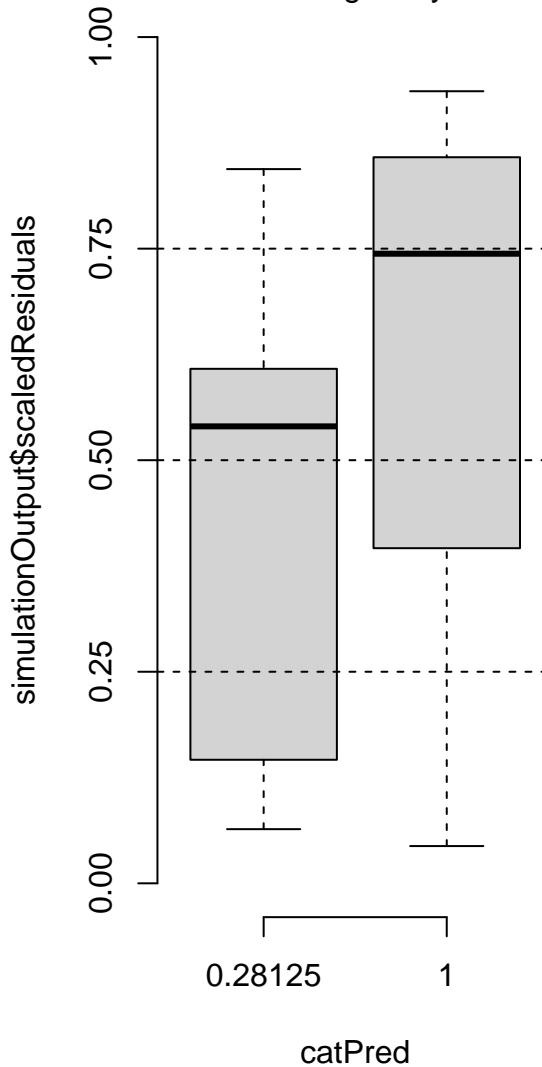
Nb obs control: 8

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
28.8	34.5	-9.4	18.8	18

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.08303	0.2882
day	(Intercept)	0.01527	0.1236
Residual		0.07974	0.2824

Number of obs: 23, groups: ID, 7; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0797

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.391142	0.186608	12.814	<2e-16 ***
inf_statusControl	-0.001741	0.291105	-0.006	0.995

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

Infection in DENV-squirrel

Nb excluded (LOD): 49

Nb obs infection: 0

Nb obs control: 0

IL.2 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 47

Nb obs infection: 2

Nb obs control: 0

IL.2 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 116

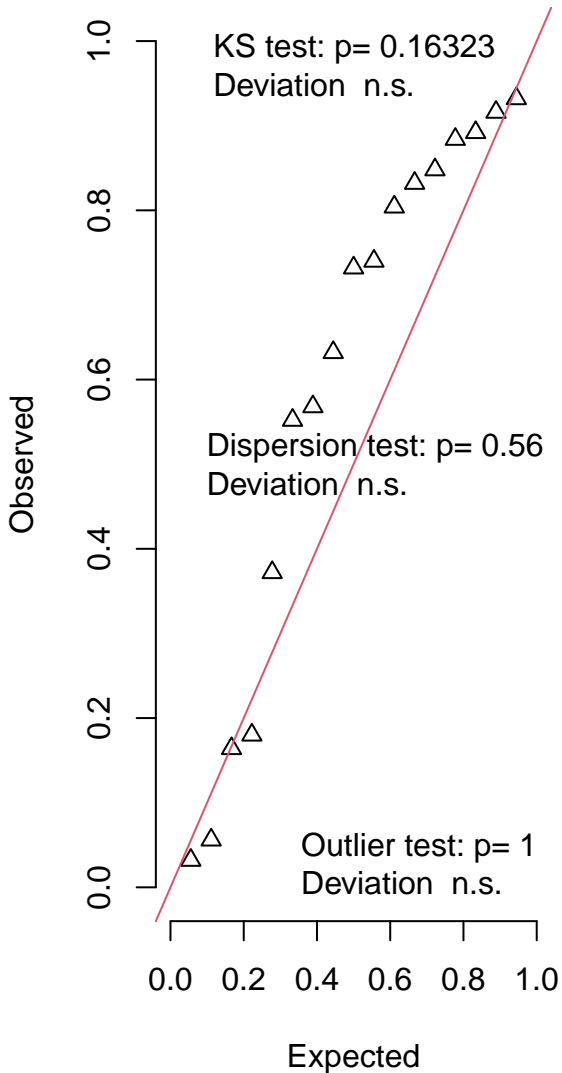
Nb obs DENV-squirrel (infected only): 0

Nb obs DENV-cyno (infected only): 15

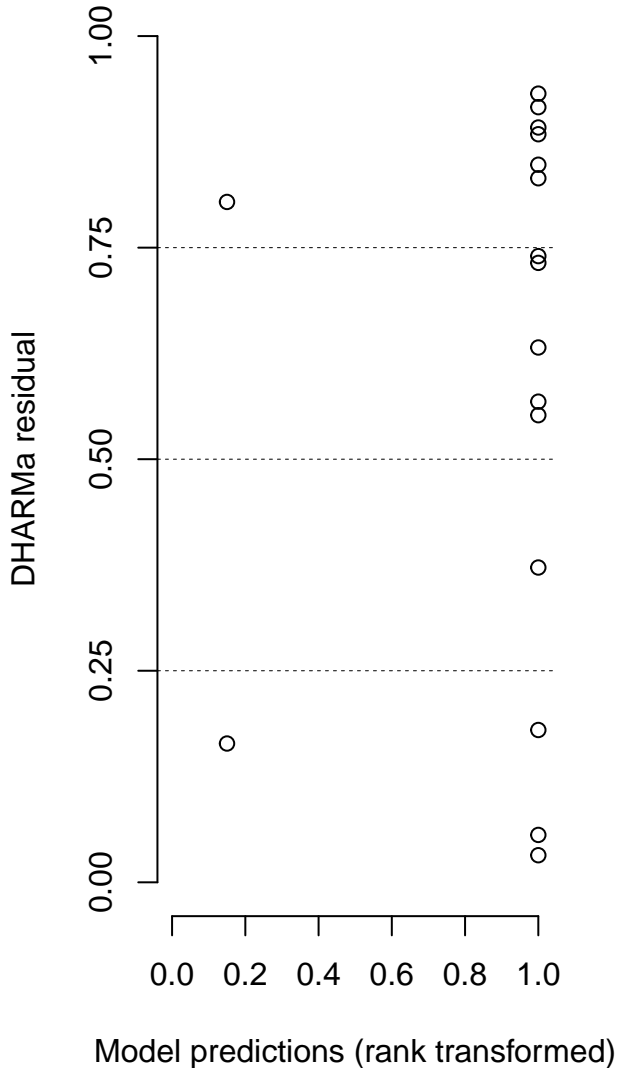
Nb obs ZIKV-squirrel (infected only): 2

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
25.7	29.8	-7.8	15.7	12

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	7.930e-02	2.816e-01
day	(Intercept)	1.004e-10	1.002e-05
Residual		1.060e-01	3.256e-01

Number of obs: 17, groups: ID, 5; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.106

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.3952	0.1871	12.802	<2e-16 ***
groupSquirrel.Zika virus	-0.3576	0.4090	-0.874	0.382

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

IL . 4₁

Infection in DENV-cyno

Nb excluded (LOD): 91

Nb obs infection: 0

Nb obs control: 0

IL.4 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in DENV-squirrel

Nb excluded (LOD): 49

Nb obs infection: 0

Nb obs control: 0

IL.4 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 46

Nb obs infection: 3

Nb obs control: 0

IL.4 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 130

Nb obs DENV-squirrel (infected only): 0

Nb obs DENV-cyno (infected only): 0

Nb obs ZIKV-squirrel (infected only): 3

IL.4 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

IL.5

Infection in DENV-cyno

Nb excluded (LOD): 91

Nb obs infection: 0

Nb obs control: 0

IL.5 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in DENV-squirrel

Nb excluded (LOD): 45

Nb obs infection: 4

Nb obs control: 0

IL.5 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 46

Nb obs infection: 3

Nb obs control: 0

IL.5 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 126

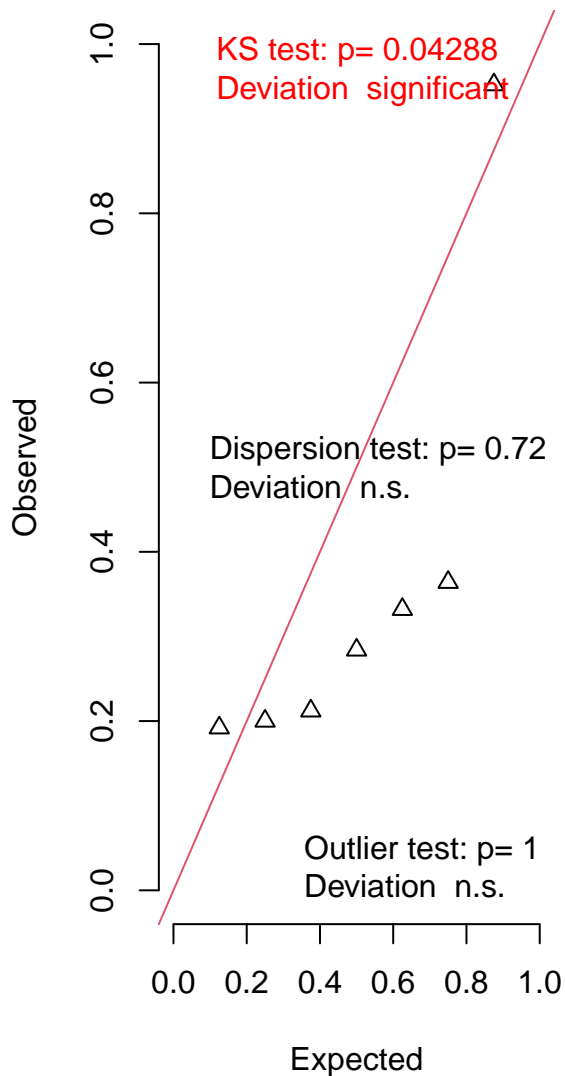
Nb obs DENV-squirrel (infected only): 4

Nb obs DENV-cyno (infected only): 0

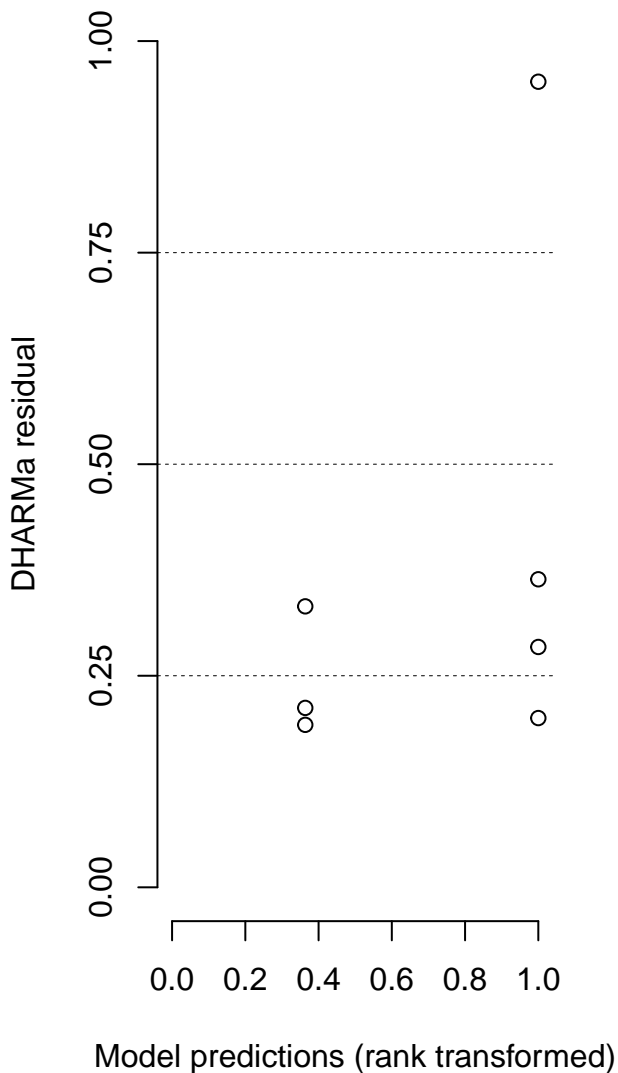
Nb obs ZIKV-squirrel (infected only): 3

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
-21.7	-22.0	15.9	-31.7	2

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.731e-24	1.653e-12
day	(Intercept)	2.510e-03	5.010e-02
Residual		1.130e-05	3.361e-03

Number of obs: 7, groups: ID, 4; day, 5

Dispersion estimate for gaussian family (sigma^2): 1.13e-05

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.89817	NaN	NaN	NaN
groupSquirrel.Zika virus	-0.04613	NaN	NaN	NaN

IL. 6

Infection in DENV-cyno

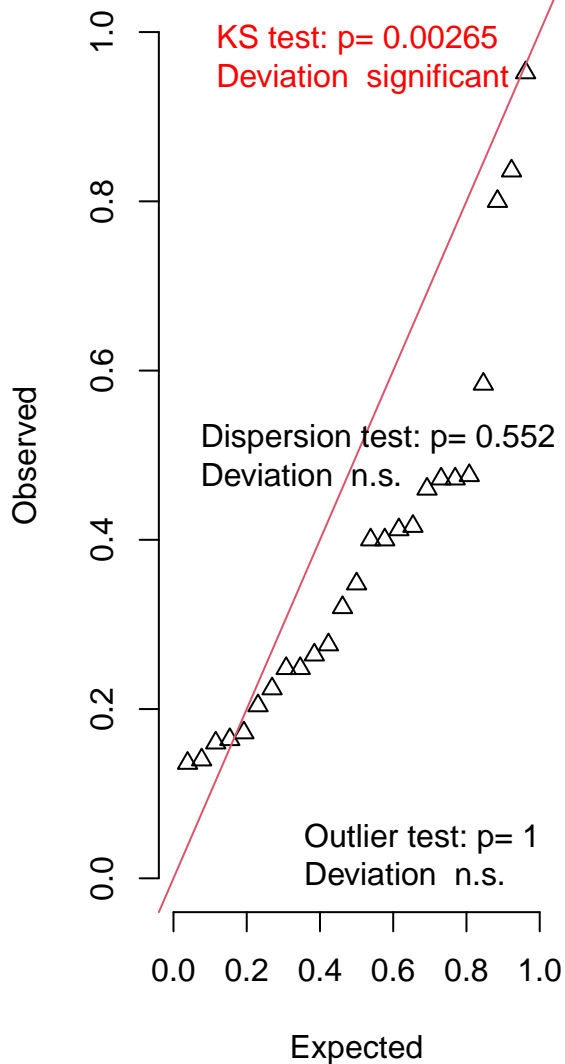
Nb excluded (LOD): 66

Nb obs infection: 13

Nb obs control: 12

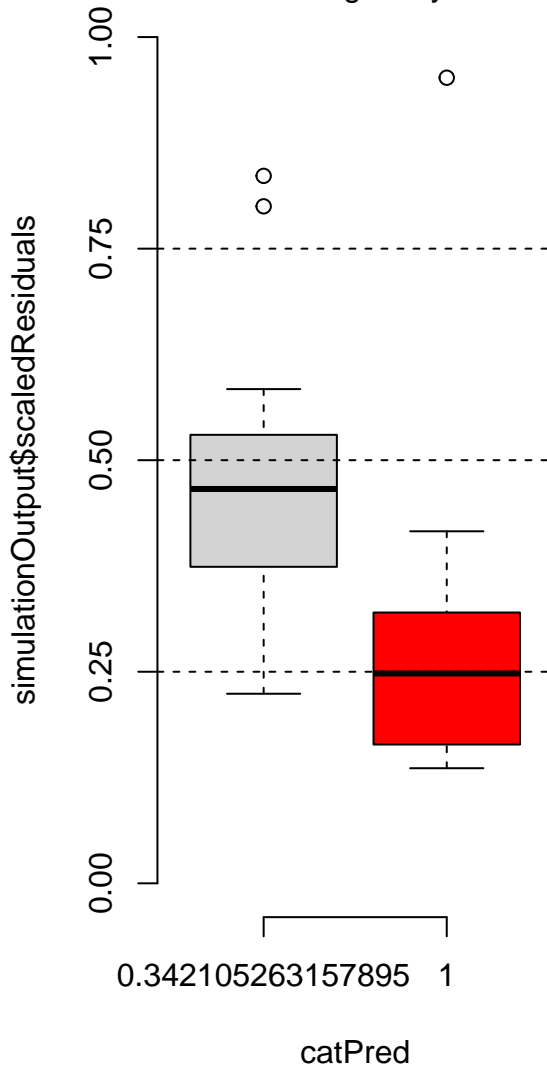
DHARMA residual

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
-73.2	-67.2	41.6	-83.2	20

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0045940	0.06778
day	(Intercept)	0.0004226	0.02056
Residual		0.0009070	0.03012

Number of obs: 25, groups: ID, 5; day, 6

Dispersion estimate for gaussian family (sigma^2): 0.000907

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.01508	0.04218	24.066	<2e-16 ***
inf_statusControl	-0.05611	0.06388	-0.878	0.38

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

Infection in DENV-squirrel

Nb excluded (LOD): 49

Nb obs infection: 0

Nb obs control: 0

IL.6 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 45

Nb obs infection: 4

Nb obs control: 0

IL.6 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 116

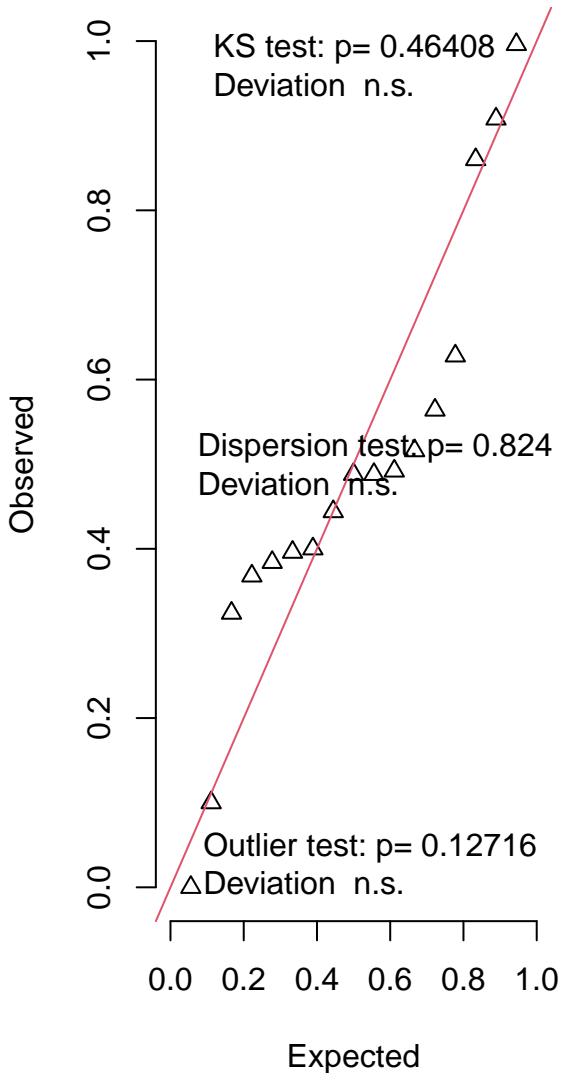
Nb obs DENV-squirrel (infected only): 0

Nb obs DENV-cyno (infected only): 13

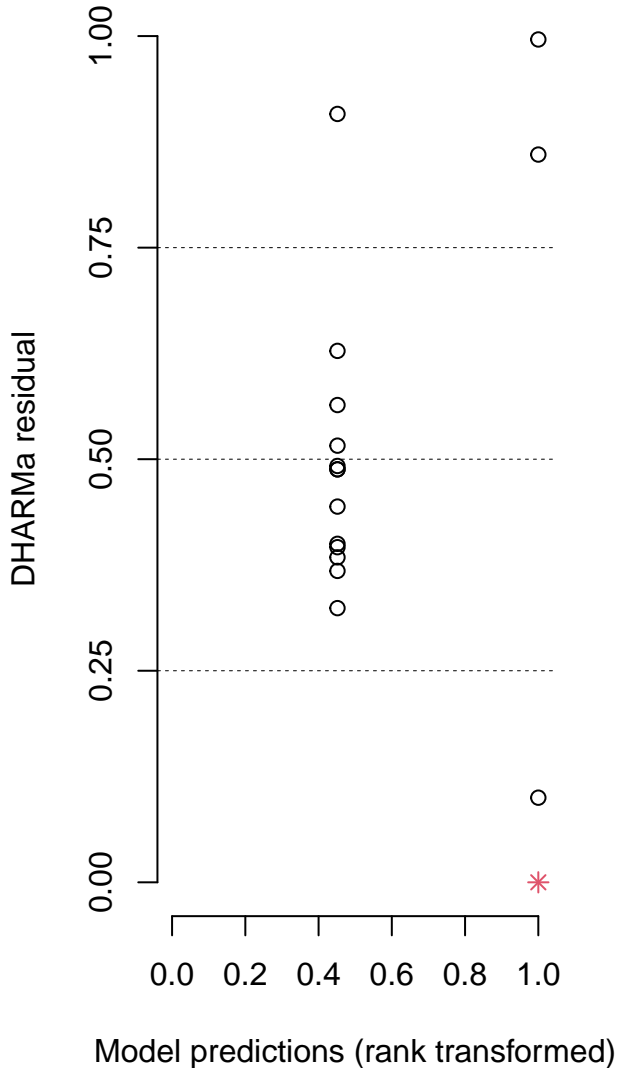
Nb obs ZIKV-squirrel (infected only): 4

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
-8.7	-4.5	9.3	-18.7	12

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.804e-15	5.295e-08
day	(Intercept)	2.021e-11	4.495e-06
Residual		1.953e-02	1.397e-01

Number of obs: 17, groups: ID, 4; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0195

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.96872	0.03876	24.994	<2e-16 ***
groupSquirrel.Zika virus	0.67429	0.07990	8.439	<2e-16 ***

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

IL.8

Infection in DENV-cyno

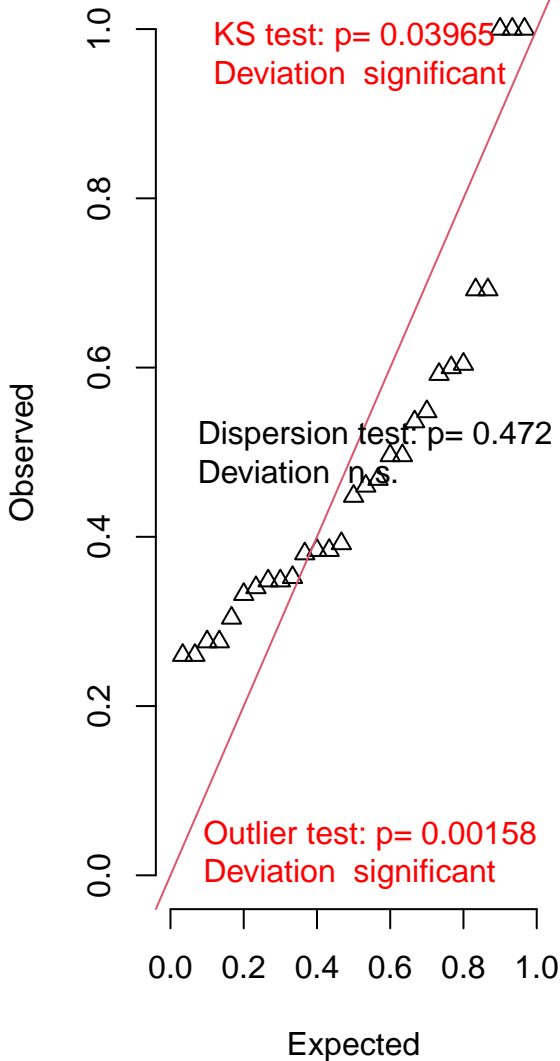
Nb excluded (LOD): 62

Nb obs infection: 23

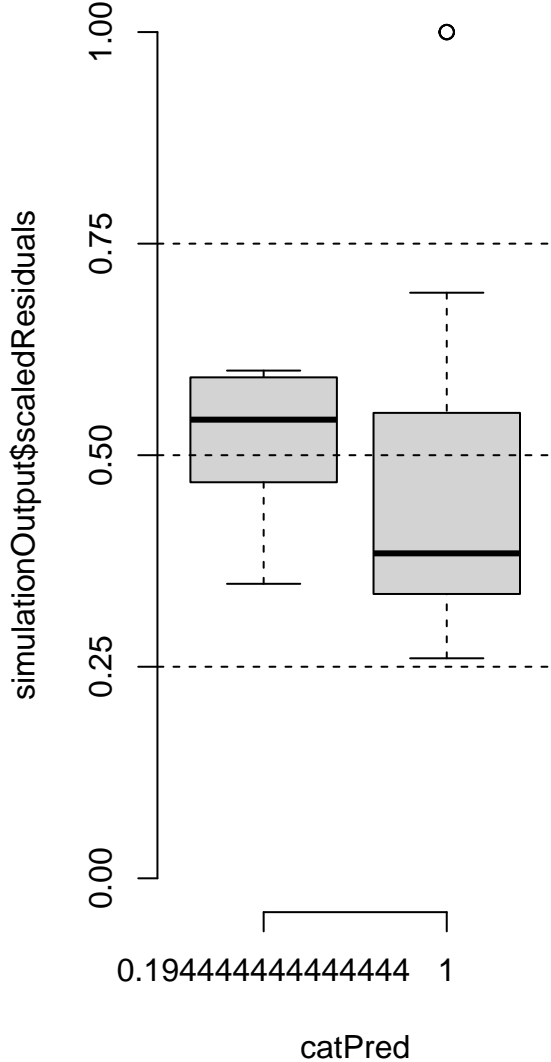
Nb obs control: 6

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
-0.9	5.9	5.5	-10.9	24

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0251498	0.15859
day	(Intercept)	0.0009346	0.03057
Residual		0.0272711	0.16514

Number of obs: 29, groups: ID, 7; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0273

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.27697	0.07793	16.386	<2e-16 ***
inf_statusControl	-0.10929	0.18914	-0.578	0.563

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

Infection in DENV-squirrel

Nb excluded (LOD): 49

Nb obs infection: 0

Nb obs control: 0

IL.8 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 49

Nb obs infection: 0

Nb obs control: 0

IL.8 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 110

Nb obs DENV-squirrel (infected only): 0

Nb obs DENV-cyno (infected only): 23

Nb obs ZIKV-squirrel (infected only): 0

IL.8 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

IL . RA

Infection in DENV-cyno

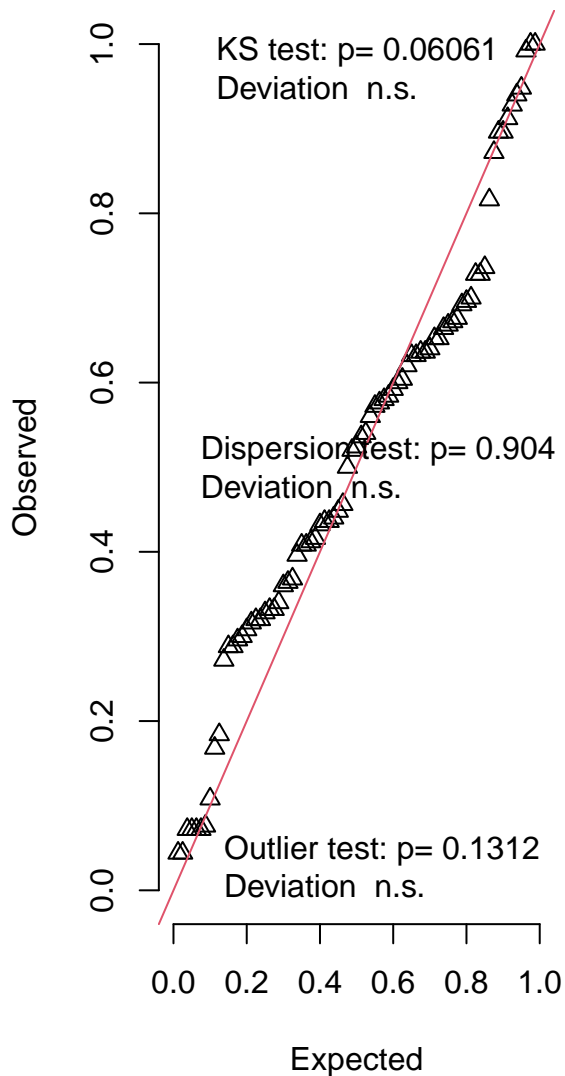
Nb excluded (LOD): 12

Nb obs infection: 54

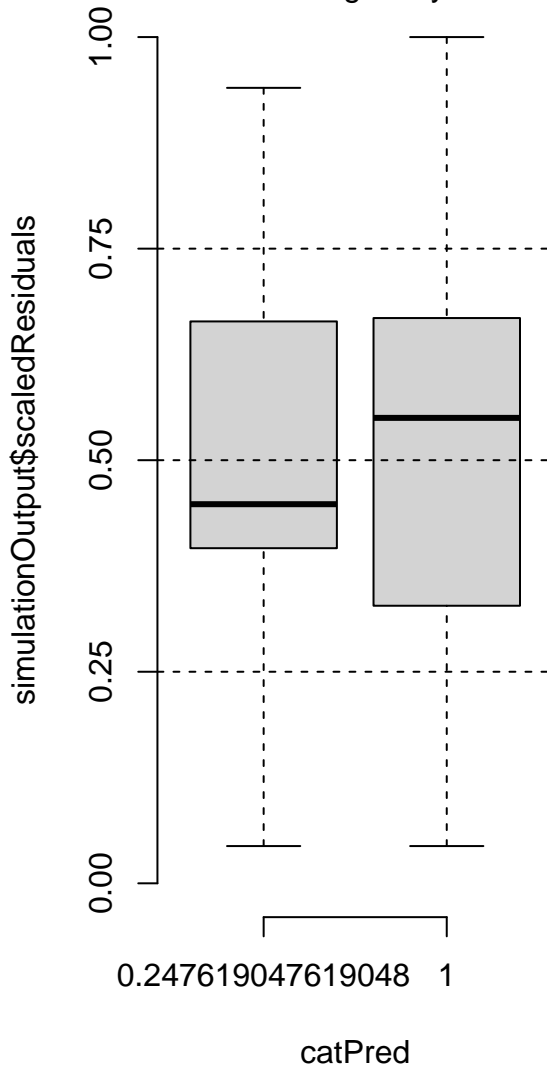
Nb obs control: 25

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
29.0	40.8	-9.5	19.0	74

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.036552	0.19119
day	(Intercept)	0.001996	0.04468
Residual		0.055886	0.23640

Number of obs: 79, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0559

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.3185117	0.0740515	31.309	<2e-16 ***
inf_statusControl	-0.0004848	0.1291759	-0.004	0.997

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

Infection in DENV-squirrel

Nb excluded (LOD): 45

Nb obs infection: 4

Nb obs control: 0

IL.RA ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 43

Nb obs infection: 6

Nb obs control: 0

IL.RA ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 69

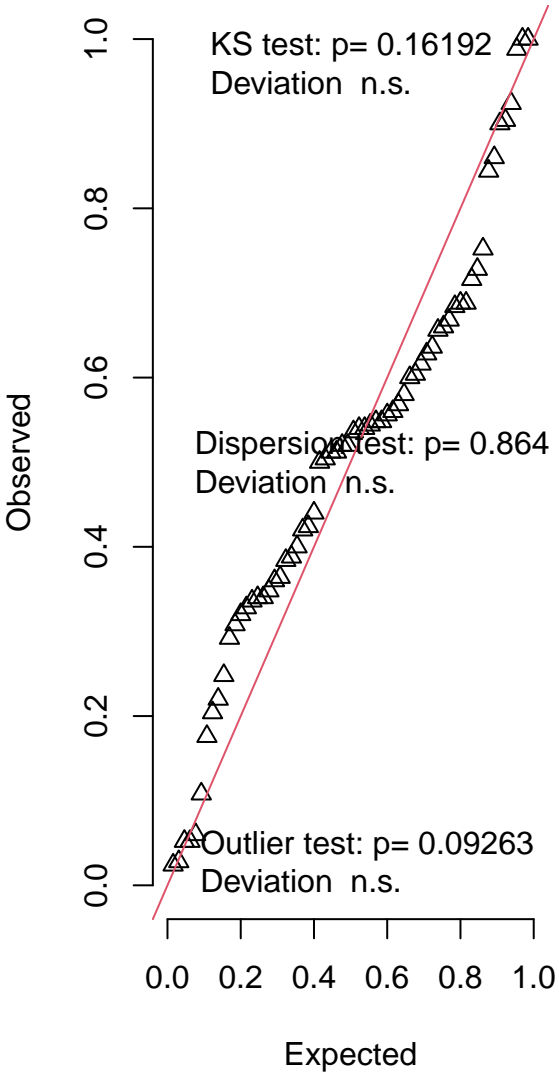
Nb obs DENV-squirrel (infected only): 4

Nb obs DENV-cyno (infected only): 54

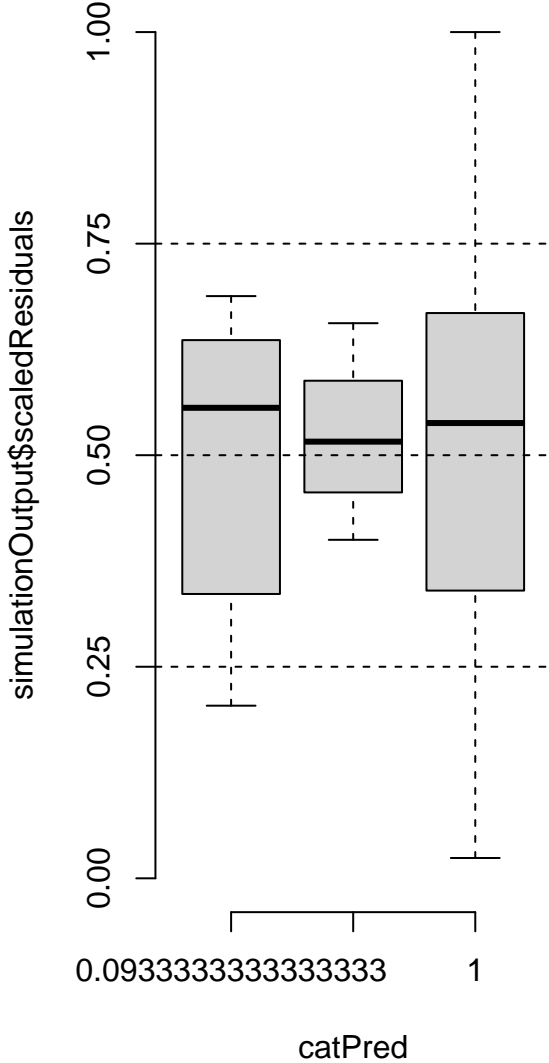
Nb obs ZIKV-squirrel (infected only): 6

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
32.6	45.6	-10.3	20.6	58

Random effects:

```

Conditional model:
Groups   Name          Variance Std.Dev.
ID       (Intercept) 3.472e-02 1.863e-01
day      (Intercept) 8.227e-12 2.868e-06
Residual                6.288e-02 2.508e-01
Number of obs: 64, groups: ID, 12; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.0629

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    2.1609    0.2246    9.621  <2e-16 ***
groupCyno.Dengue virus    0.1594    0.2357    0.676    0.499
groupSquirrel.Zika virus -0.1336    0.2798   -0.477    0.633
---

```

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

IP.10

Infection in DENV-cyno

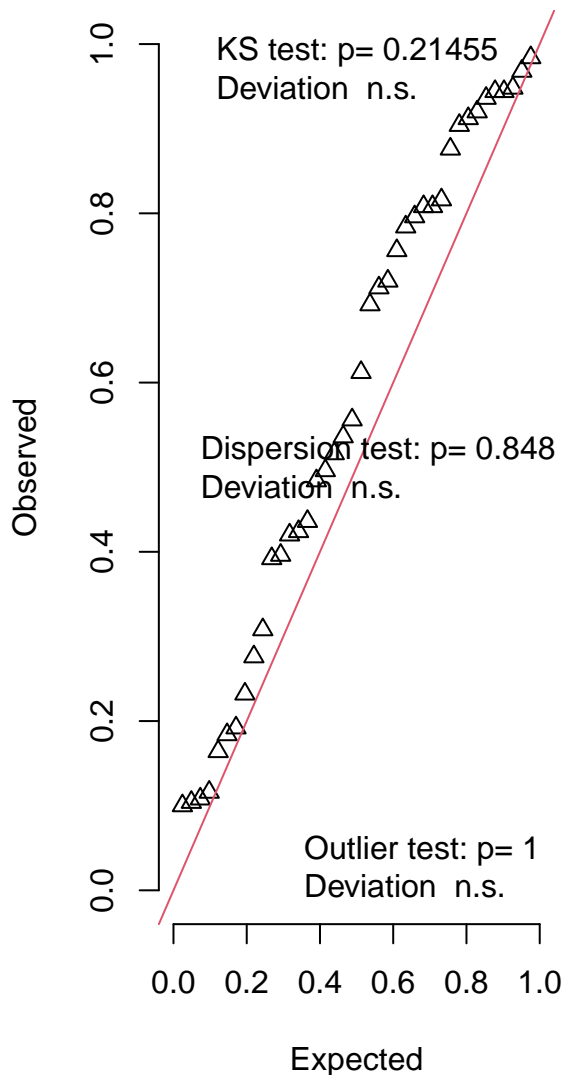
Nb excluded (LOD): 51

Nb obs infection: 22

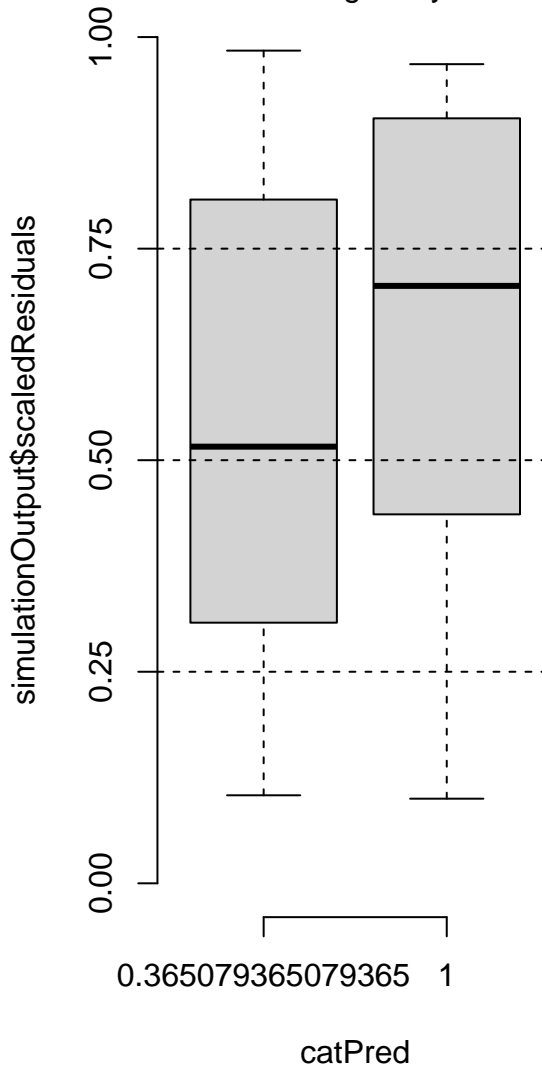
Nb obs control: 18

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
-37.4	-28.9	23.7	-47.4	35

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.584e-02	1.259e-01
day	(Intercept)	3.426e-12	1.851e-06
Residual		1.139e-02	1.067e-01

Number of obs: 40, groups: ID, 12; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0114

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.84447	0.05378	15.703	<2e-16 ***
inf_statusControl	0.04309	0.08843	0.487	0.626

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

Infection in DENV-squirrel

Nb excluded (LOD): 33

Nb obs infection: 16

Nb obs control: 0

IP.10 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 37

Nb obs infection: 12

Nb obs control: 0

IP.10 ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 83

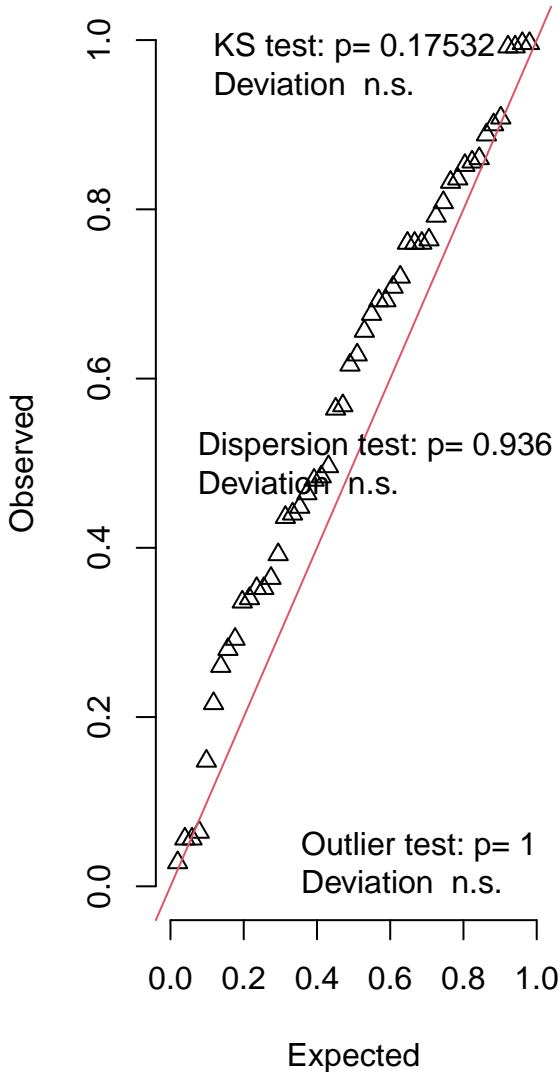
Nb obs DENV-squirrel (infected only): 16

Nb obs DENV-cyno (infected only): 22

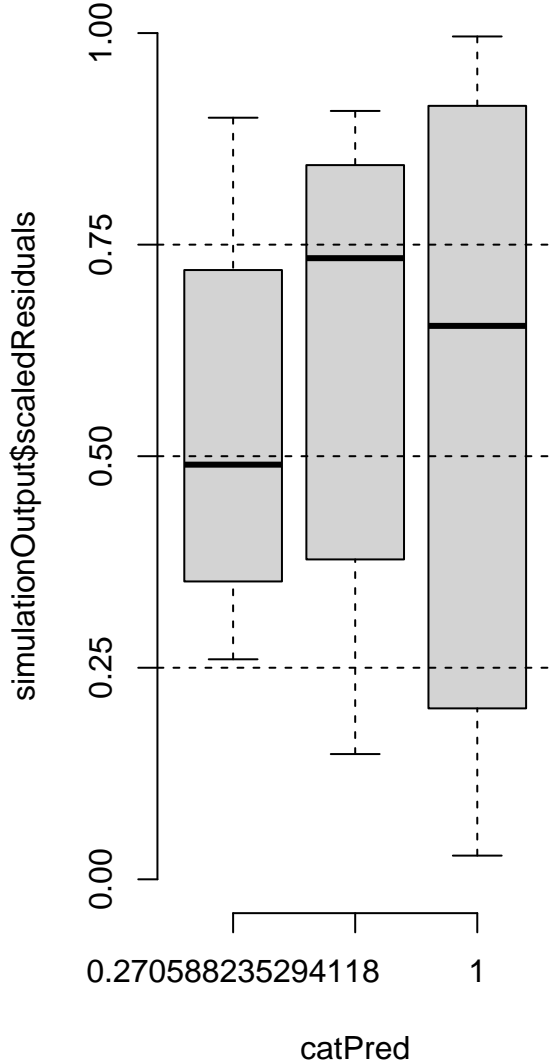
Nb obs ZIKV-squirrel (infected only): 12

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) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-16.8	-5.3	14.4	-28.8	44

Random effects:

```

Conditional model:
Groups   Name          Variance Std.Dev.
ID       (Intercept)  5.989e-02 2.447e-01
day      (Intercept)  1.915e-11 4.376e-06
Residual                1.361e-02 1.167e-01
Number of obs: 50, groups:  ID, 19; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.0136

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.1925     0.1145   10.418  <2e-16 ***
groupCyno.Dengue virus -0.3551     0.1473   -2.411  0.0159 *
groupSquirrel.Zika virus -0.2343     0.1567   -1.495  0.1348
---

```

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

MCP . 1

Infection in DENV-cyno

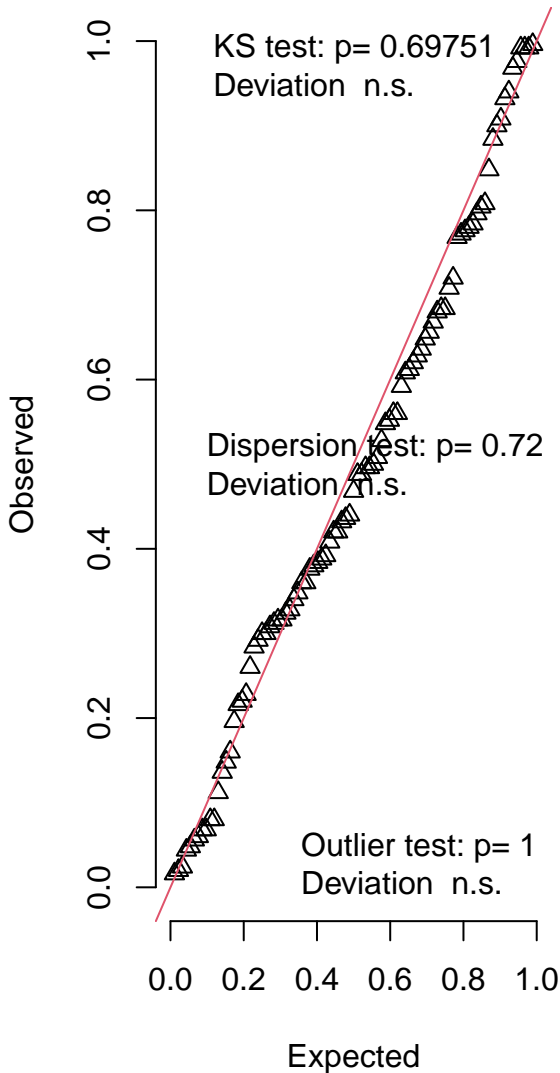
Nb excluded (LOD): 0

Nb obs infection: 63

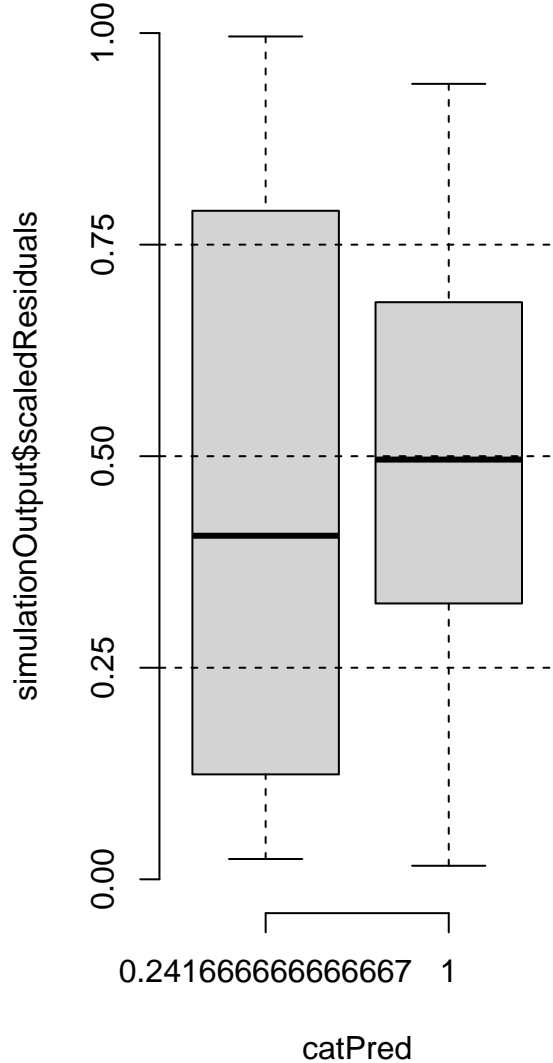
Nb obs control: 28

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

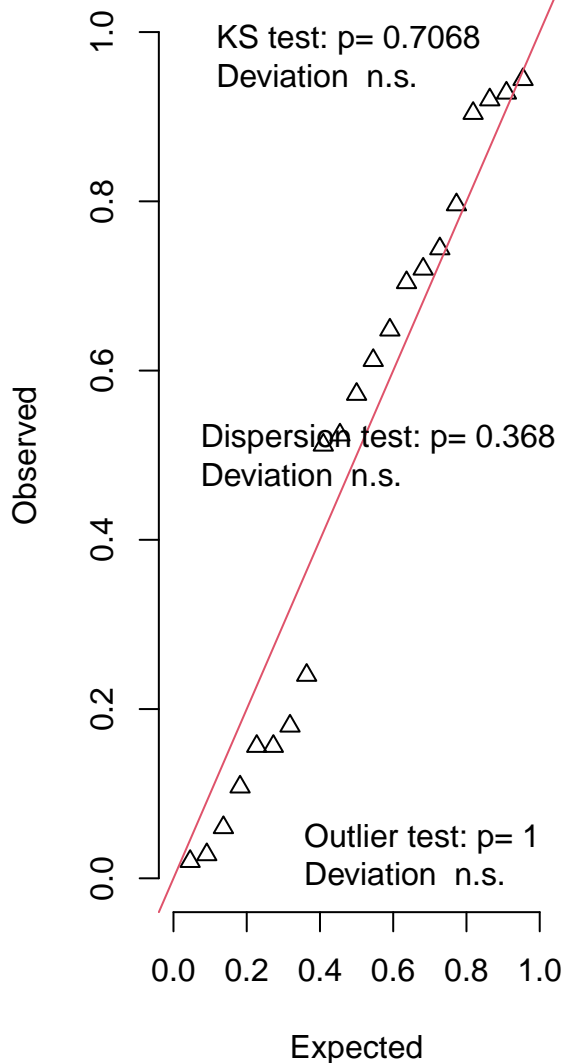
Nb excluded (LOD): 28

Nb obs infection: 20

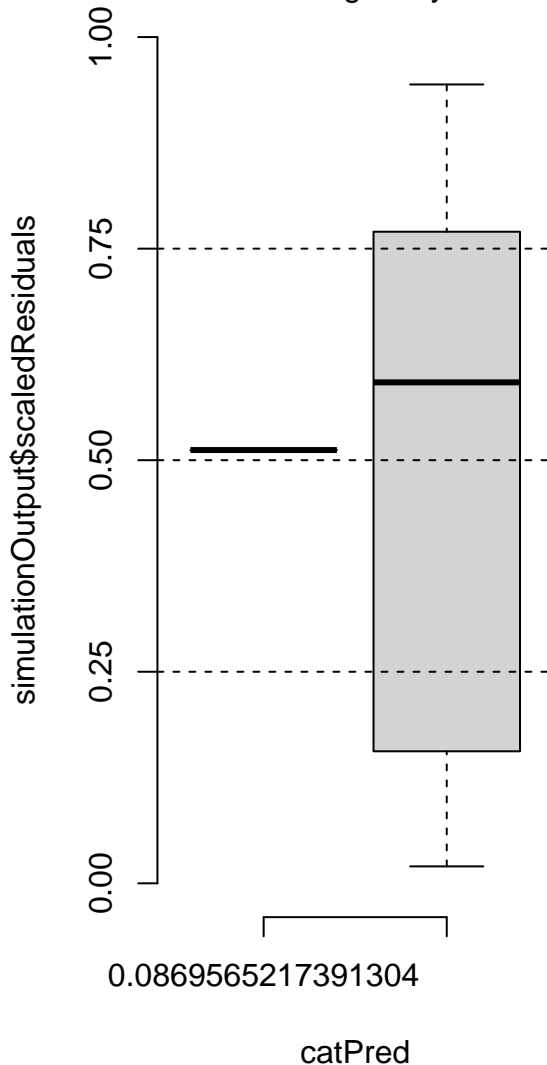
Nb obs control: 1

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
27.7	33.0	-8.9	17.7	16

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	5.343e-01	7.310e-01
day	(Intercept)	9.397e-12	3.066e-06
Residual		4.903e-02	2.214e-01

Number of obs: 21, groups: ID, 6; day, 5

Dispersion estimate for gaussian family (sigma^2): 0.049

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.7878	0.3306	8.432	<2e-16 ***
inf_statusControl	-1.0068	0.8323	-1.210	0.226

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

Infection in ZIKV-squirrel

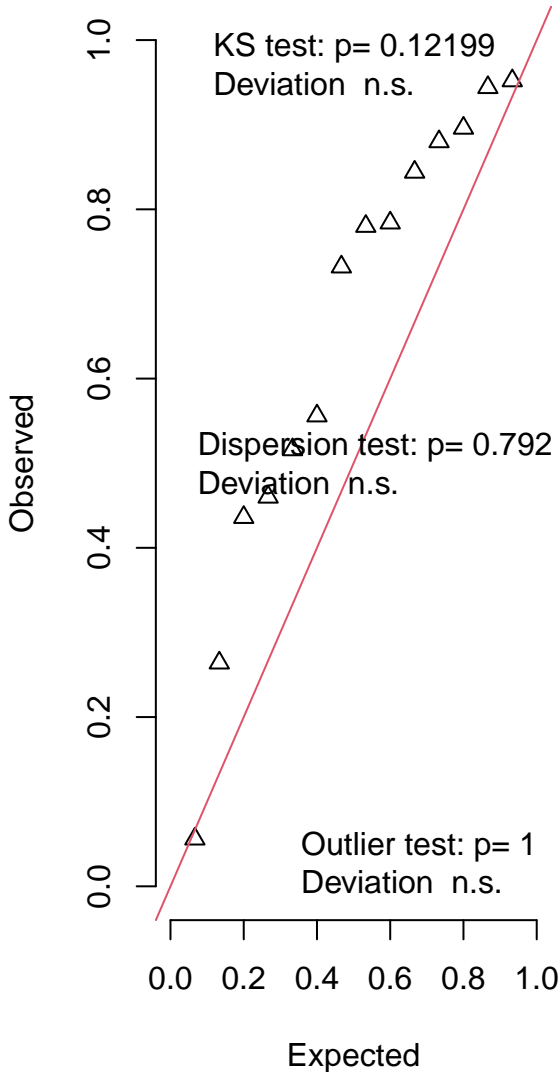
Nb excluded (LOD): 35

Nb obs infection: 13

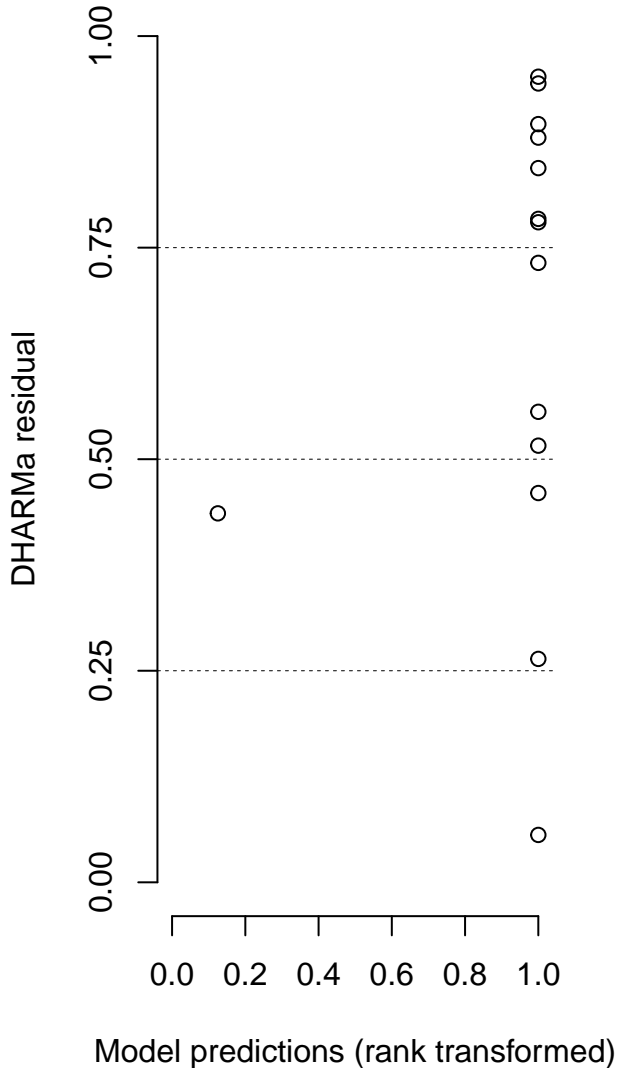
Nb obs control: 1

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
8.0	11.2	1.0	-2.0	9

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.316561	0.56264
day	(Intercept)	0.004227	0.06502
Residual		0.004437	0.06661

Number of obs: 14, groups: ID, 6; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00444

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.8148	0.2542	11.073	<2e-16 ***
inf_statusControl	-0.9999	0.6237	-1.603	0.109

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

Effect of experiment

Nb excluded (LOD): 37

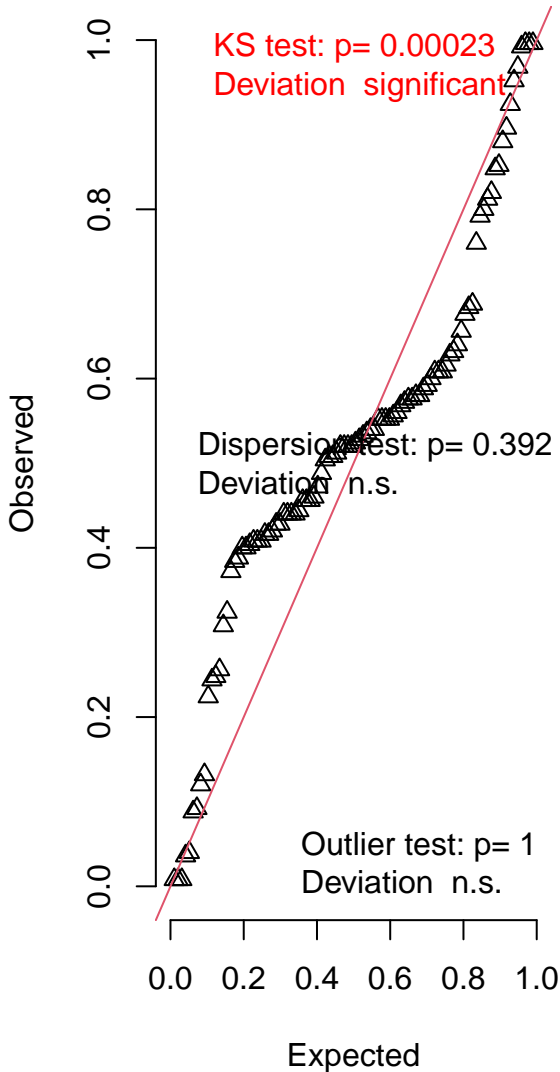
Nb obs DENV-squirrel (infected only): 20

Nb obs DENV-cyno (infected only): 63

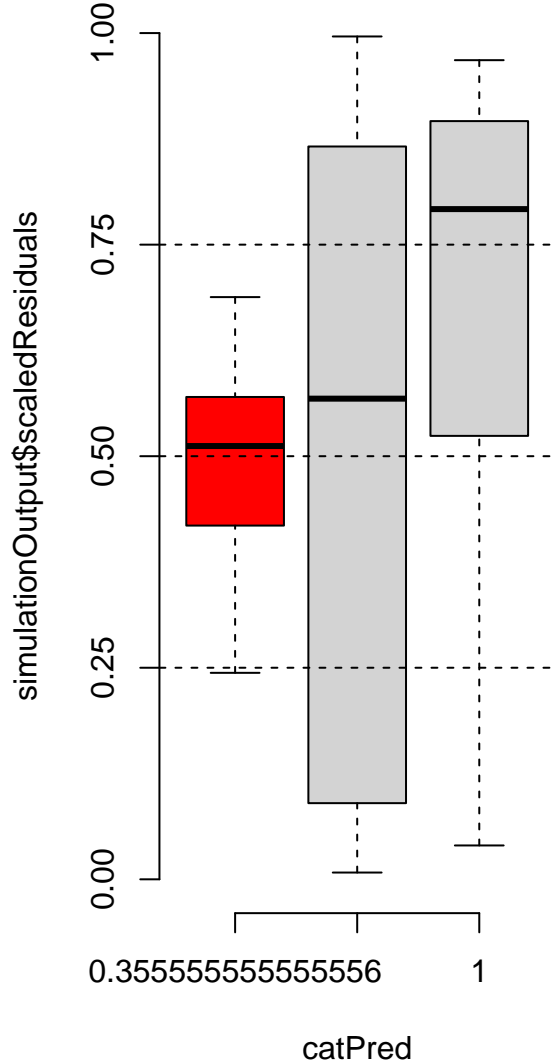
Nb obs ZIKV-squirrel (infected only): 13

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
-2.5	12.8	7.3	-14.5	90

Random effects:

```

Conditional model:
Groups   Name          Variance Std.Dev.
ID       (Intercept)  2.607e-01 5.106e-01
day      (Intercept)  7.176e-13 8.471e-07
Residual                2.307e-02 1.519e-01
Number of obs: 96, groups: ID, 19; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.0231

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    2.78781    0.23087   12.075  <2e-16 ***
groupCyno.Dengue virus -0.10456    0.28747   -0.364    0.716
groupSquirrel.Zika virus 0.05389    0.32870    0.164    0.870
---

```

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

MDC

Infection in DENV-cyno

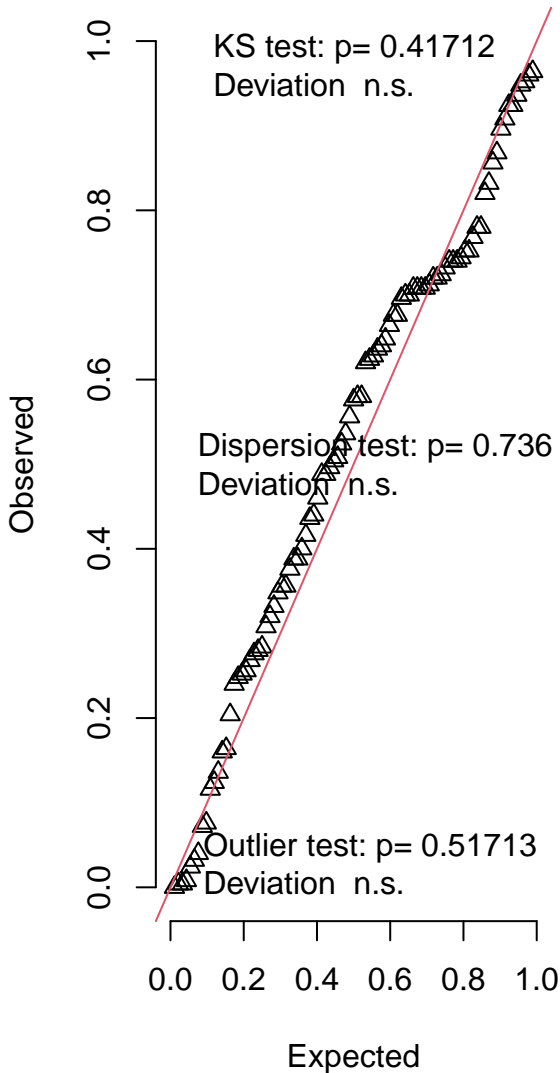
Nb excluded (LOD): 0

Nb obs infection: 63

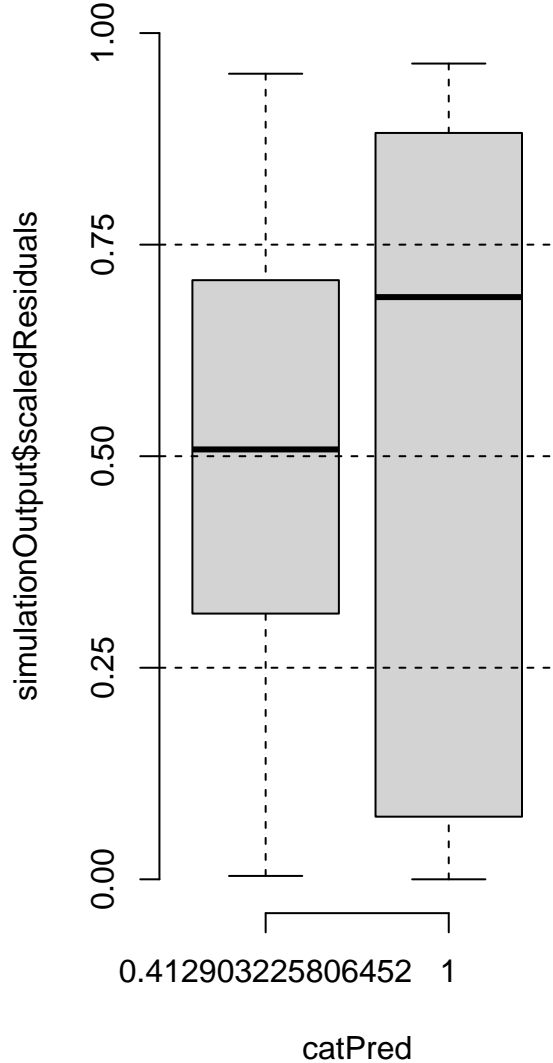
Nb obs control: 28

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 excluded (LOD): 48

Nb obs infection: 0

Nb obs control: 1

MDC ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

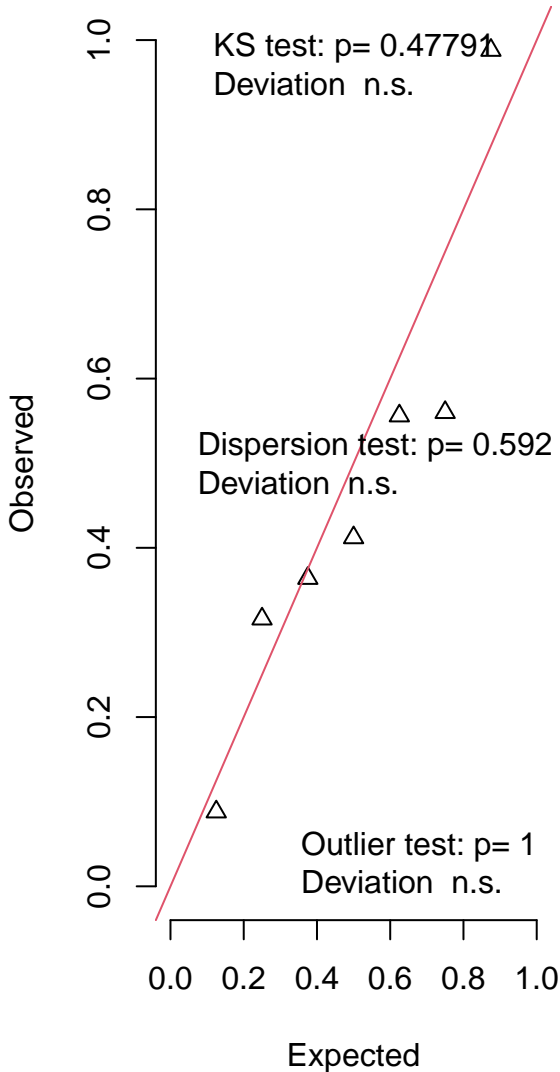
Nb excluded (LOD): 42

Nb obs infection: 6

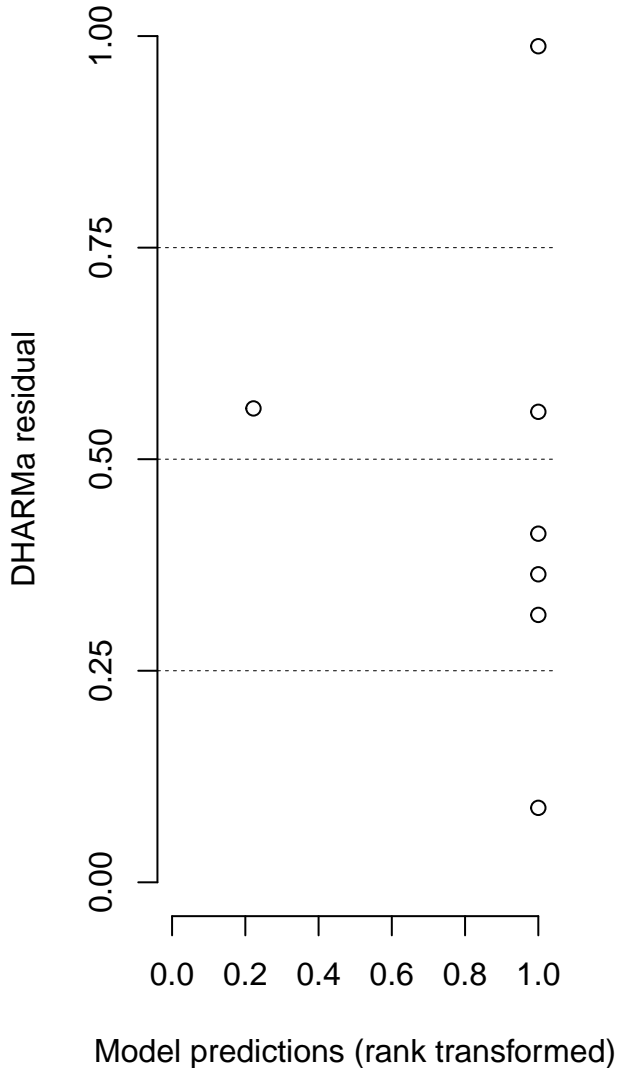
Nb obs control: 1

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
4.9	4.7	2.5	-5.1	2

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.561e-13	3.951e-07
day	(Intercept)	3.238e-12	1.799e-06
Residual		2.844e-02	1.686e-01

Number of obs: 7, groups: ID, 4; day, 5

Dispersion estimate for gaussian family (sigma^2): 0.0284

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.75024	0.06885	39.95	<2e-16 ***
inf_statusControl	-0.15024	0.18215	-0.82	0.409

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

Effect of experiment

Nb excluded (LOD): 64

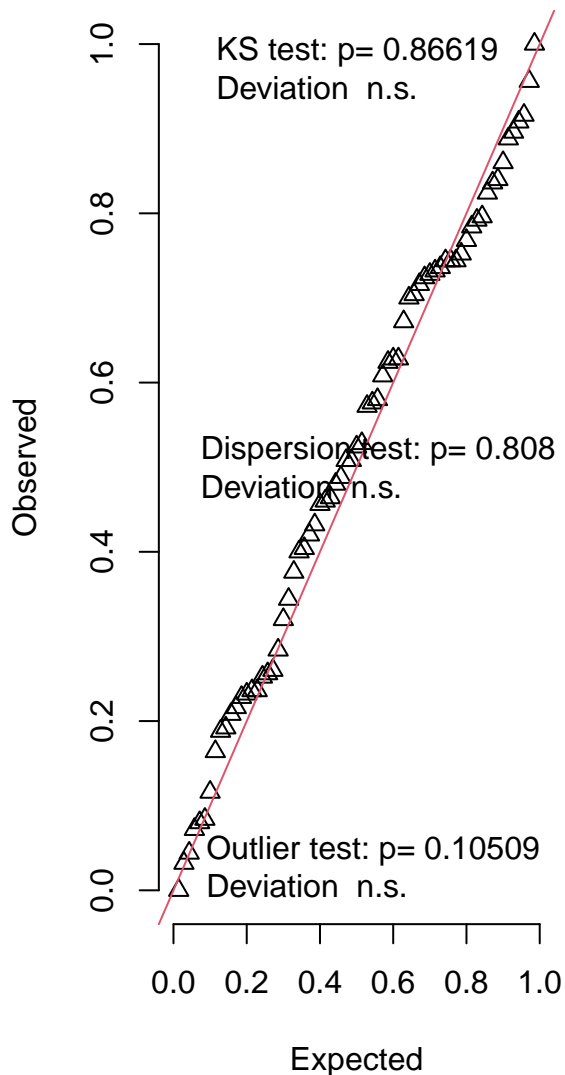
Nb obs DENV-squirrel (infected only): 0

Nb obs DENV-cyno (infected only): 63

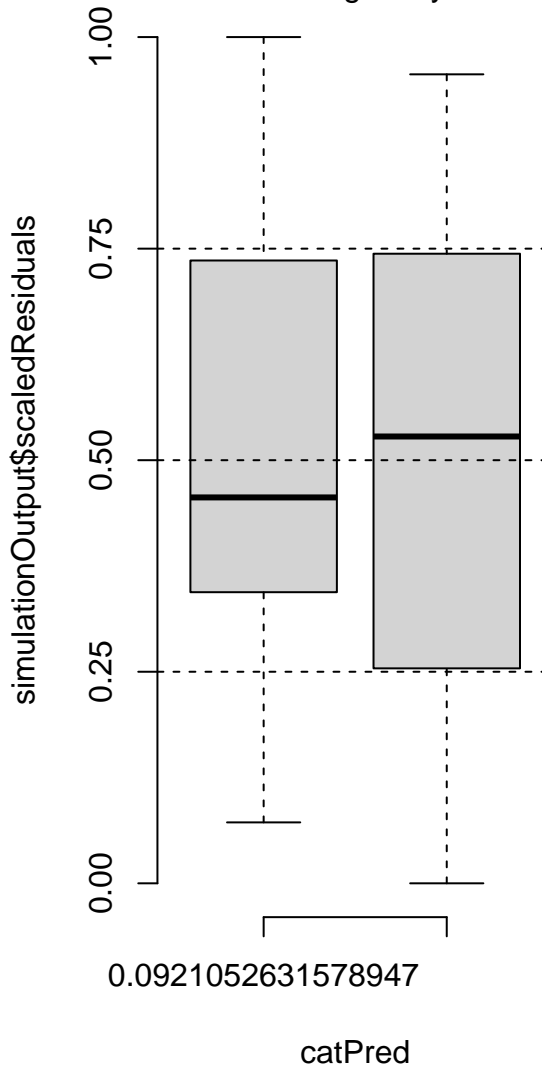
Nb obs ZIKV-squirrel (infected only): 6

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
-112.3	-101.1	61.1	-122.3	64

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0028981	0.05383
day	(Intercept)	0.0008603	0.02933
Residual		0.0076790	0.08763

Number of obs: 69, groups: ID, 12; day, 7

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

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.04976	0.02381	128.10	< 2e-16 ***
groupSquirrel.Zika virus	-0.34030	0.05820	-5.85	5.01e-09 ***

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

MIF

Infection in DENV-cyno

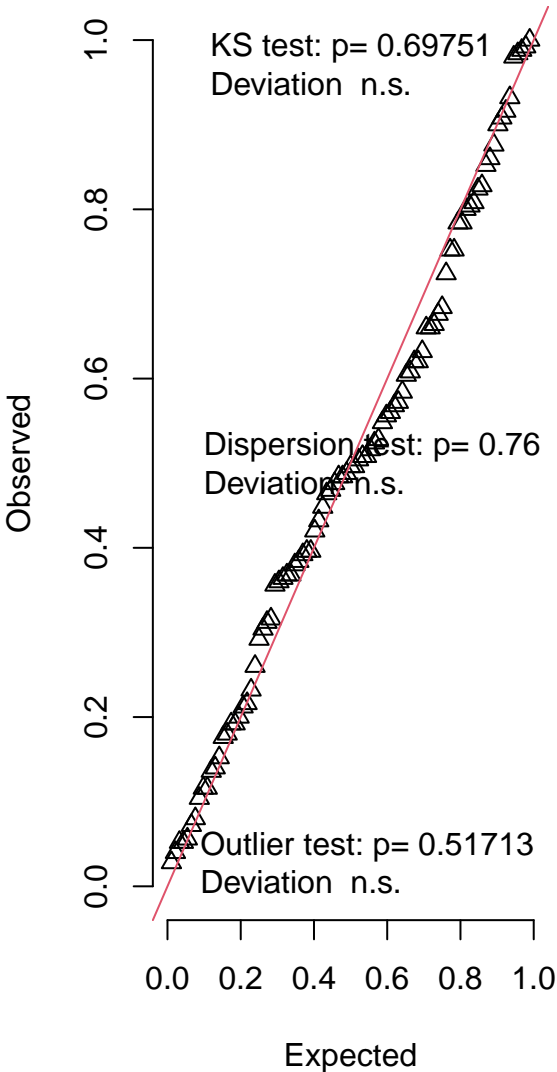
Nb excluded (LOD): 0

Nb obs infection: 63

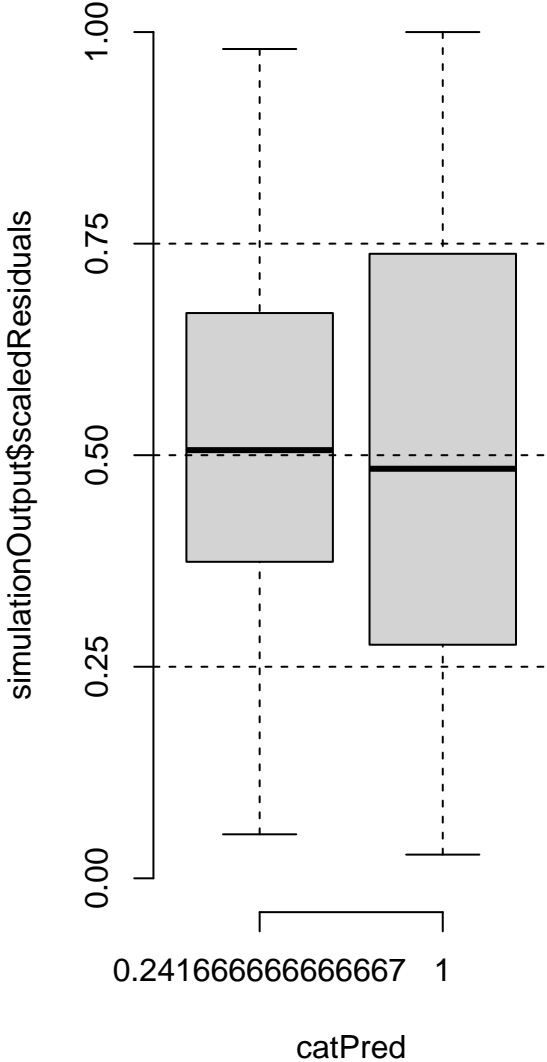
Nb obs control: 28

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

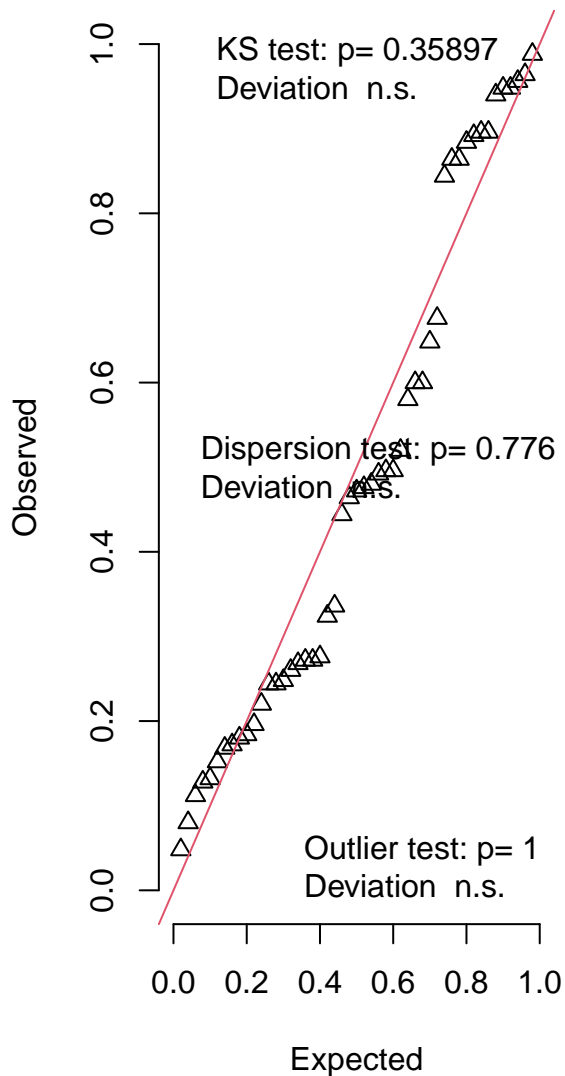
Nb excluded (LOD): 0

Nb obs infection: 35

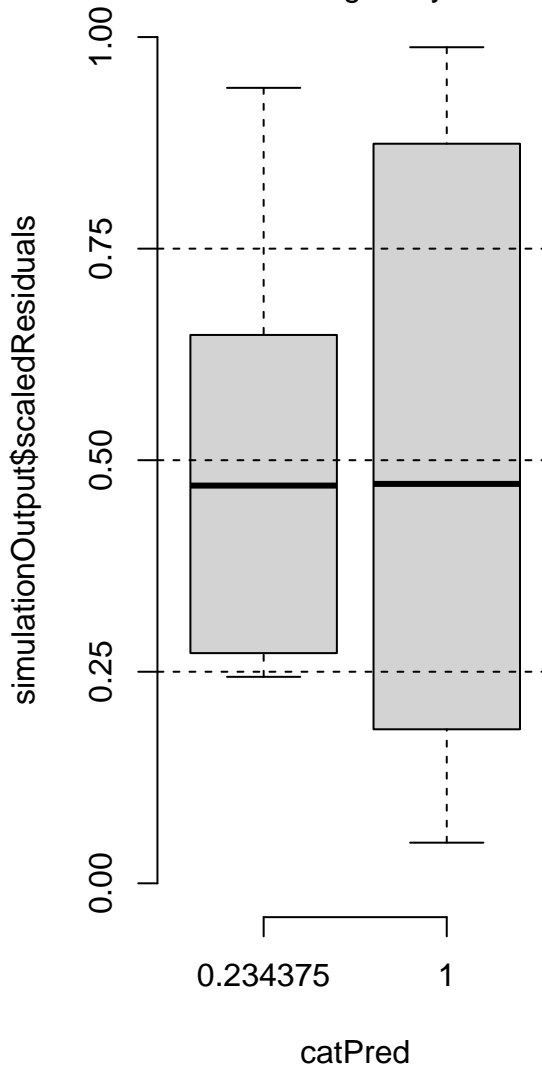
Nb obs control: 14

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

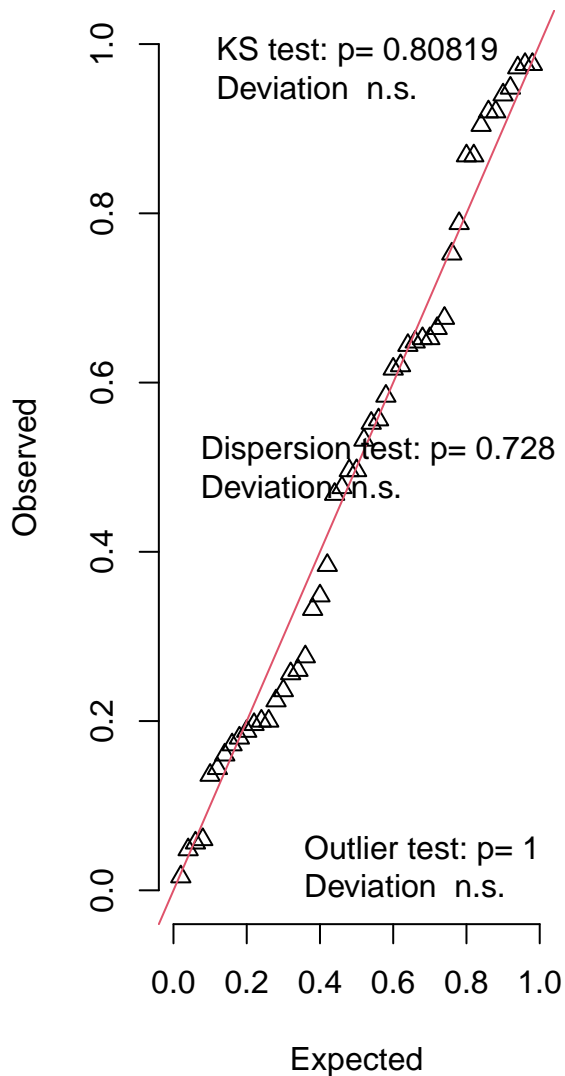
Nb excluded (LOD): 0

Nb obs infection: 35

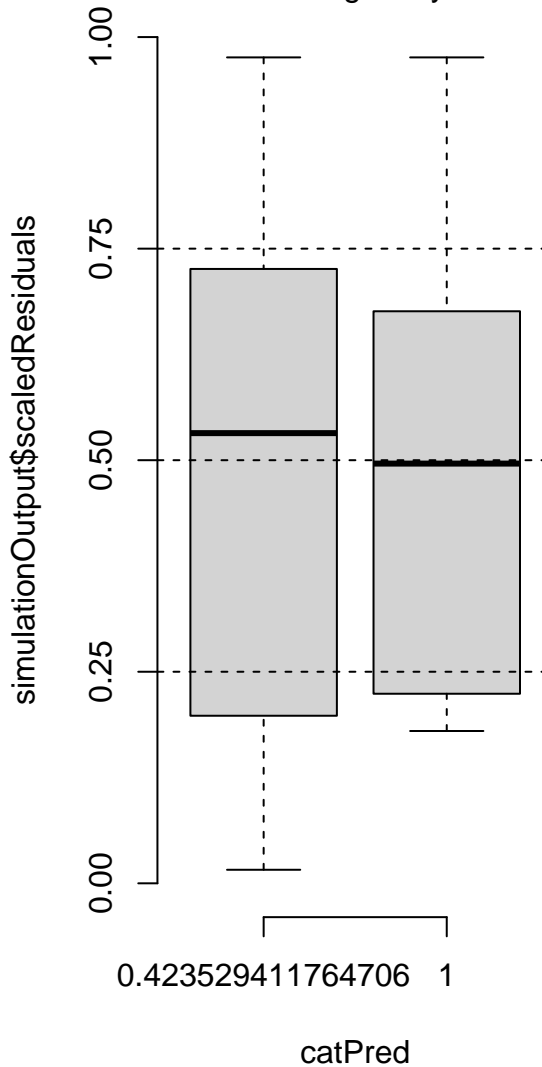
Nb obs control: 14

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 excluded (LOD): 0

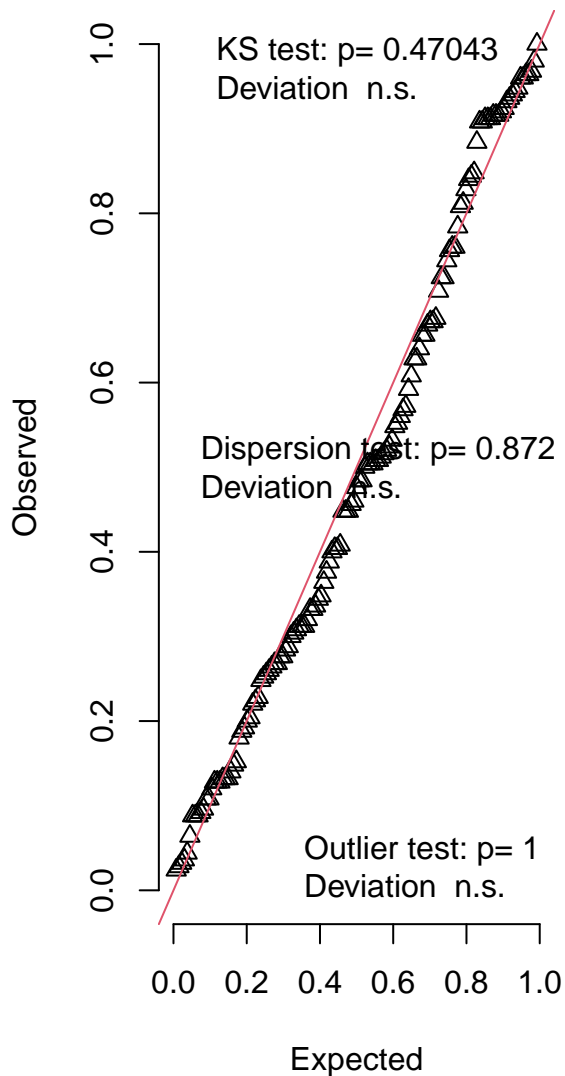
Nb obs DENV-squirrel (infected only): 35

Nb obs DENV-cyno (infected only): 63

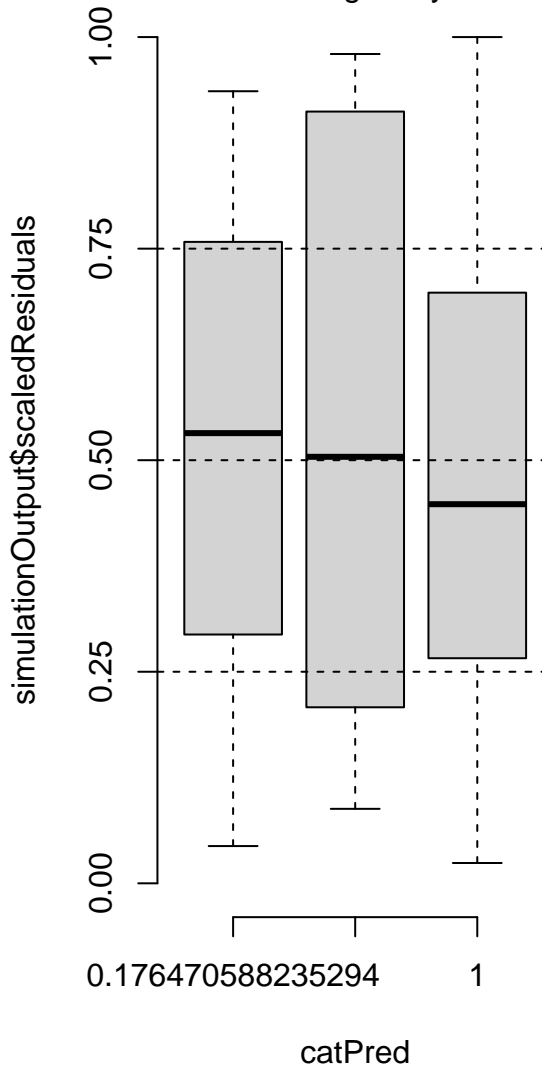
Nb obs ZIKV-squirrel (infected only): 35

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

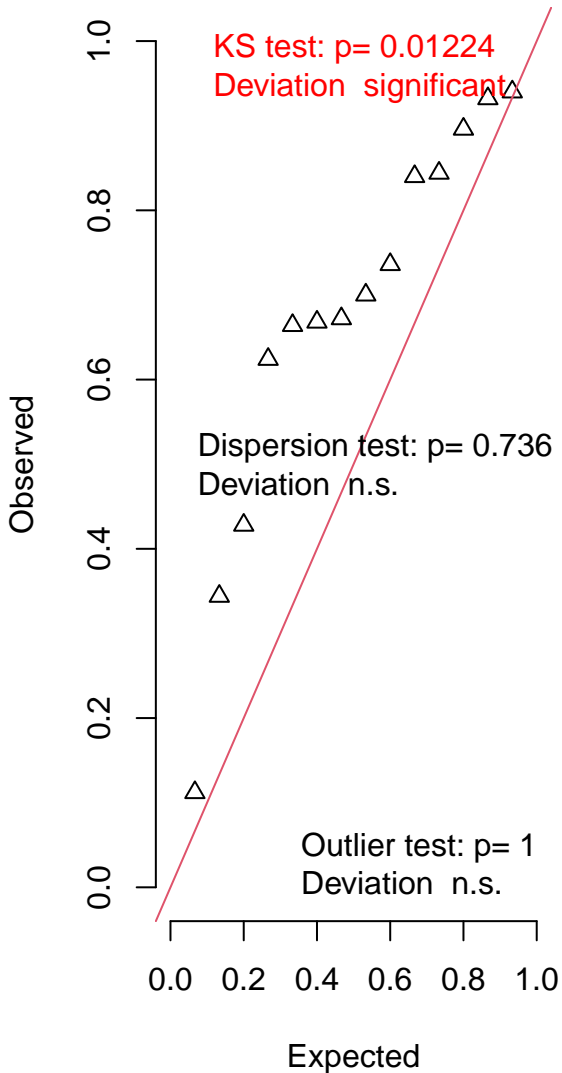
Nb excluded (LOD): 77

Nb obs infection: 6

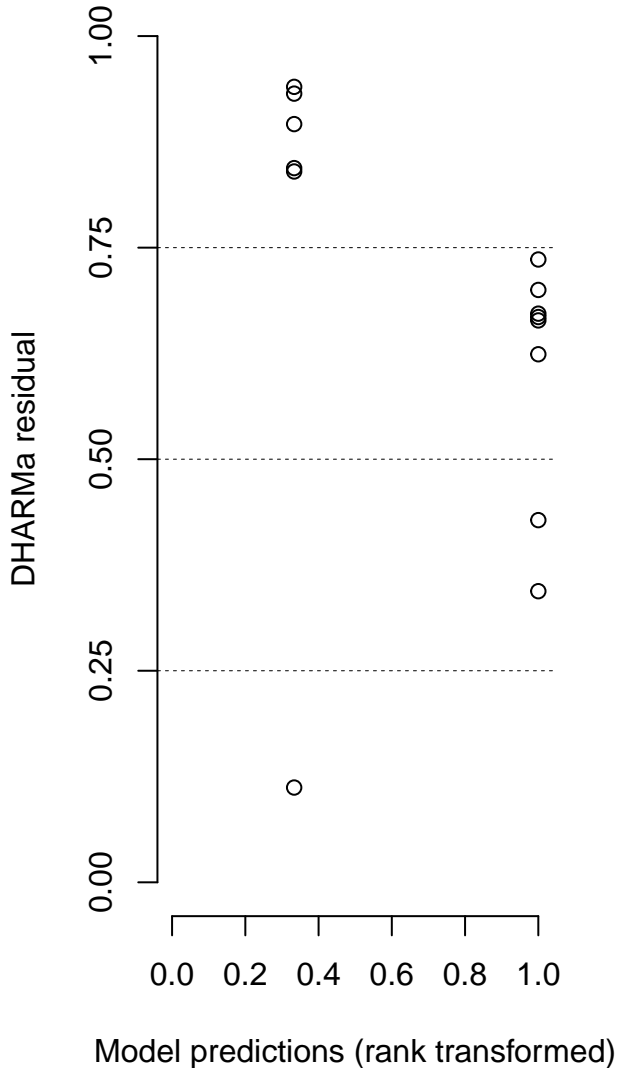
Nb obs control: 8

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
-8.6	-5.4	9.3	-18.6	9

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.068139	0.26104
day	(Intercept)	0.006636	0.08146
Residual		0.001940	0.04405

Number of obs: 14, groups: ID, 4; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00194

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.7241	0.1897	9.089	<2e-16 ***
inf_statusControl	0.6466	0.2633	2.456	0.0141 *

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

Infection in DENV-squirrel

Nb excluded (LOD): 40

Nb obs infection: 9

Nb obs control: 0

MIG ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 46

Nb obs infection: 3

Nb obs control: 0

MIG ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 115

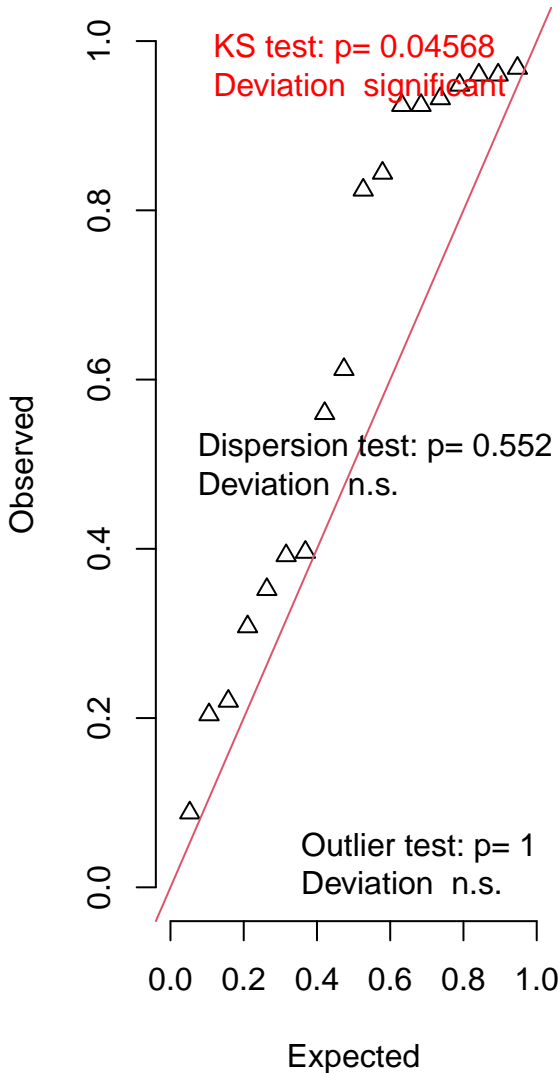
Nb obs DENV-squirrel (infected only): 9

Nb obs DENV-cyno (infected only): 6

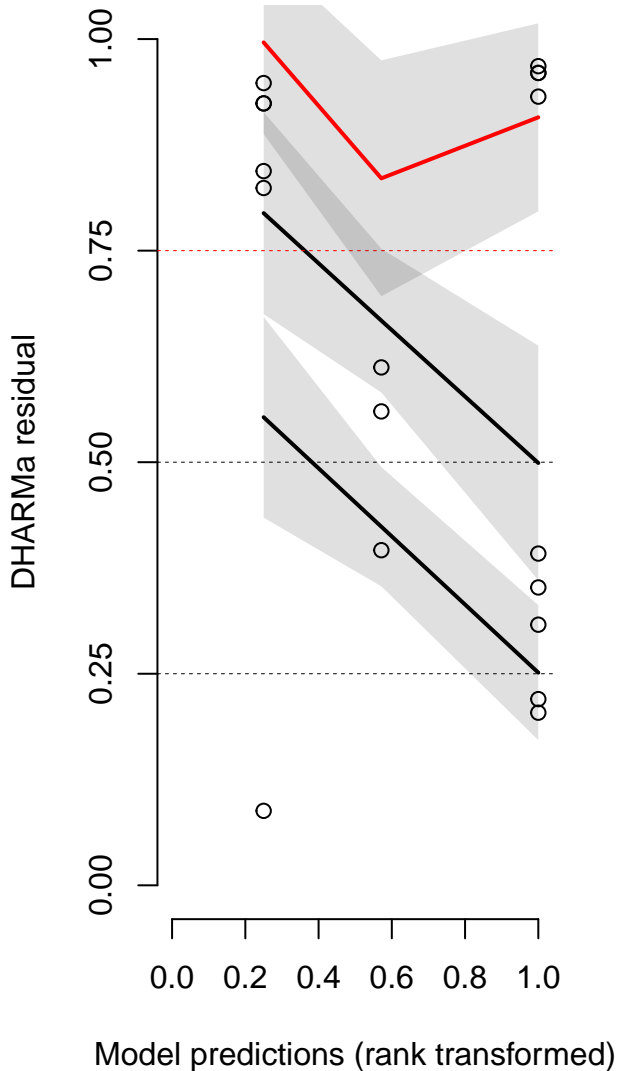
Nb obs ZIKV-squirrel (infected only): 3

DHARMA residual

QQ plot residuals



Residual vs. predicted Quantile deviations detected (red curves) Combined adjusted quantile test n.s.



```

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

```

AIC	BIC	logLik	deviance	df.resid
-6.6	-1.3	9.3	-18.6	12

Random effects:

```

Conditional model:
Groups   Name          Variance Std.Dev.
ID       (Intercept)  0.0812457 0.28504
day      (Intercept)  0.0009677 0.03111
Residual                0.0043221 0.06574
Number of obs: 18, groups:  ID, 7; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.00432

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    2.1855     0.1454  15.035  <2e-16 ***
groupCyno.Dengue virus -0.4207     0.2511  -1.675   0.0939 .
groupSquirrel.Zika virus -0.3082     0.3223  -0.956   0.3390
---

```

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

MIP.1a

Infection in DENV-cyno

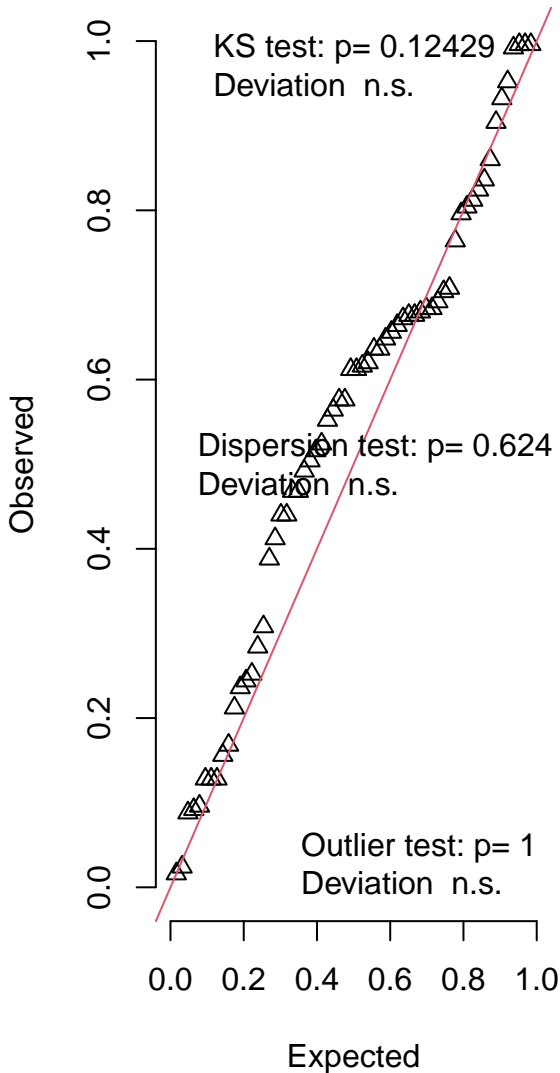
Nb excluded (LOD): 29

Nb obs infection: 40

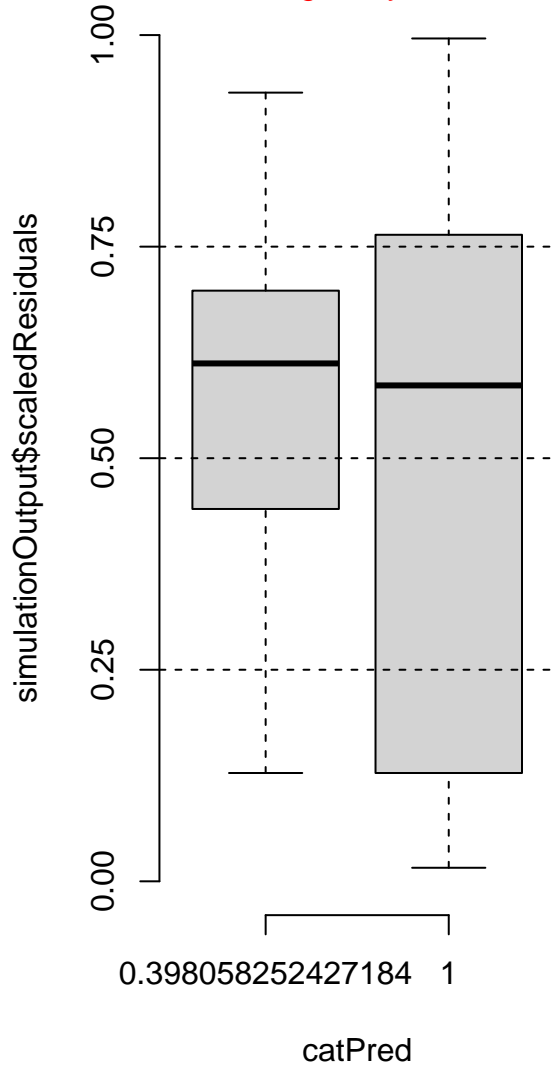
Nb obs control: 22

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
-60.6	-50.0	35.3	-70.6	57

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.392e-02	1.180e-01
day	(Intercept)	9.677e-12	3.111e-06
Residual		1.328e-02	1.152e-01

Number of obs: 62, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0133

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.69770	0.04537	37.42	<2e-16 ***
inf_statusControl	0.12620	0.08040	1.57	0.116

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

Infection in DENV-squirrel

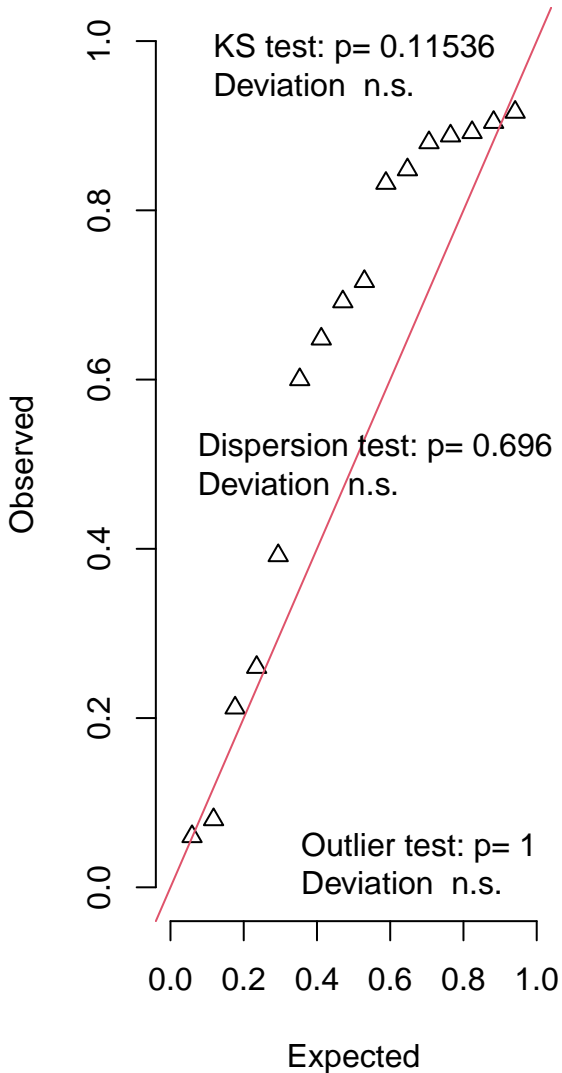
Nb excluded (LOD): 33

Nb obs infection: 15

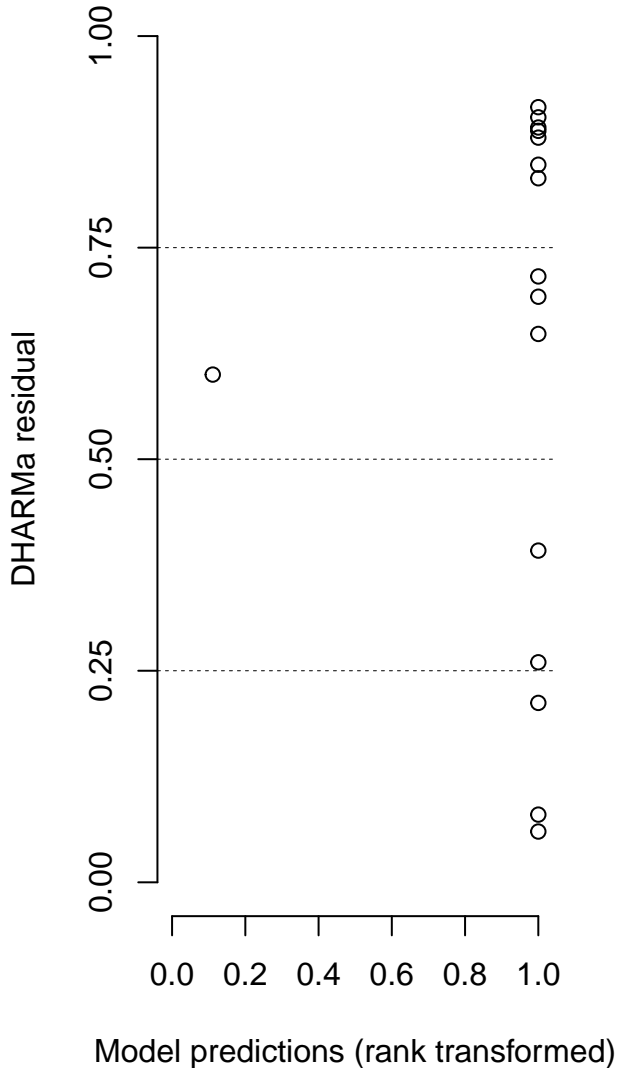
Nb obs control: 1

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
1.4	5.3	4.3	-8.6	11

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.122330	0.34976
day	(Intercept)	0.004869	0.06978
Residual		0.005965	0.07724

Number of obs: 16, groups: ID, 6; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.00597

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.0542	0.1615	12.720	<2e-16 ***
inf_statusControl	-0.6172	0.3962	-1.558	0.119

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

Infection in ZIKV-squirrel

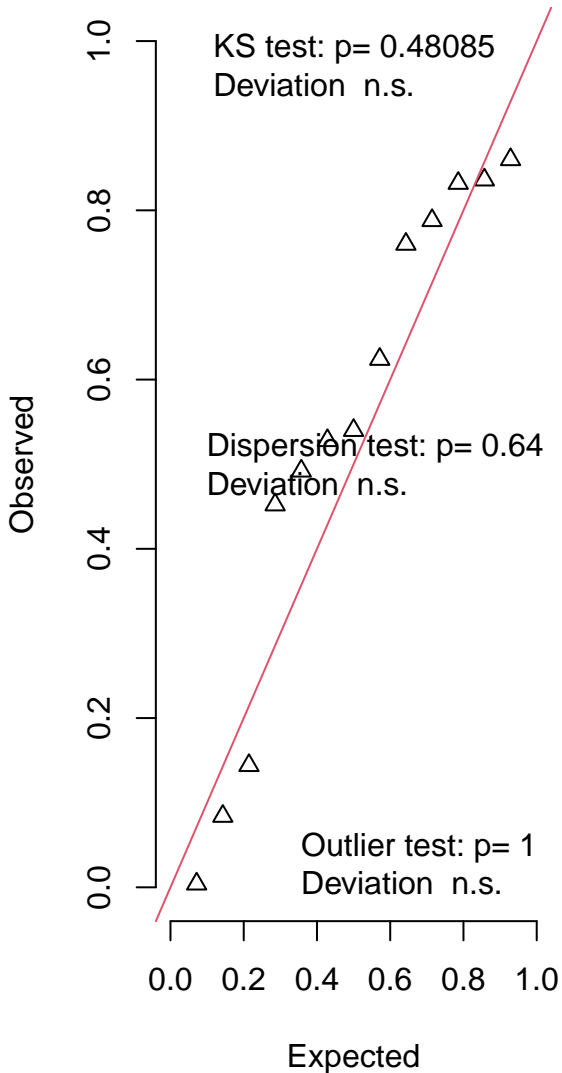
Nb excluded (LOD): 36

Nb obs infection: 12

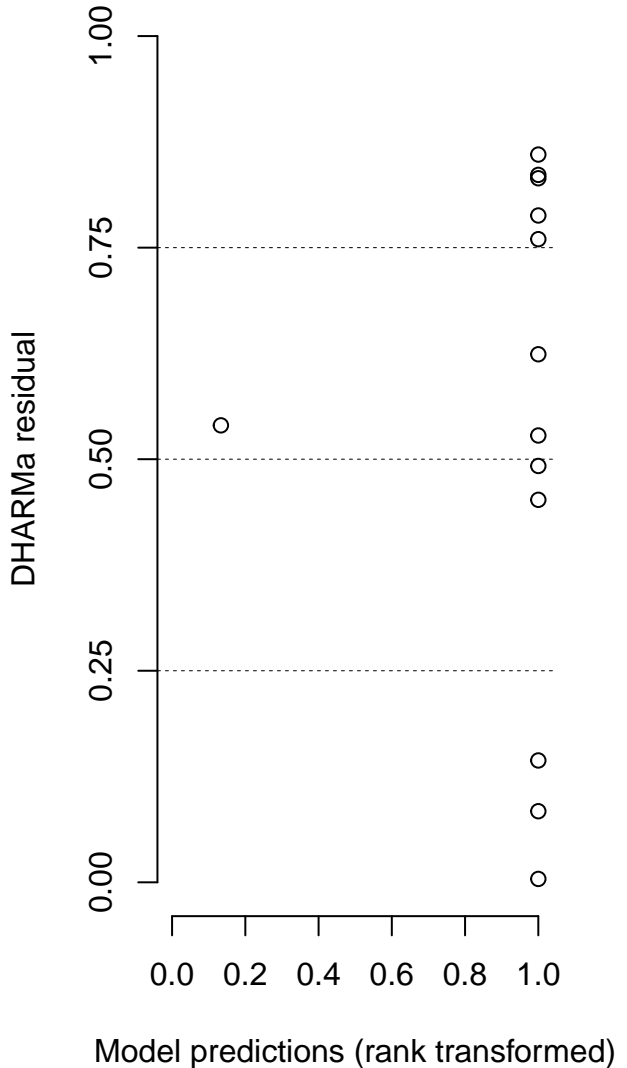
Nb obs control: 1

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected



```

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

```

AIC	BIC	logLik	deviance	df.resid
-1.4	1.4	5.7	-11.4	8

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.900e-13	5.385e-07
day	(Intercept)	8.676e-12	2.945e-06
Residual		2.428e-02	1.558e-01

Number of obs: 13, groups: ID, 5; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0243

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.07208	0.04498	46.06	< 2e-16 ***
inf_statusControl	-0.61481	0.16219	-3.79	0.00015 ***

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

Effect of experiment

Nb excluded (LOD): 66

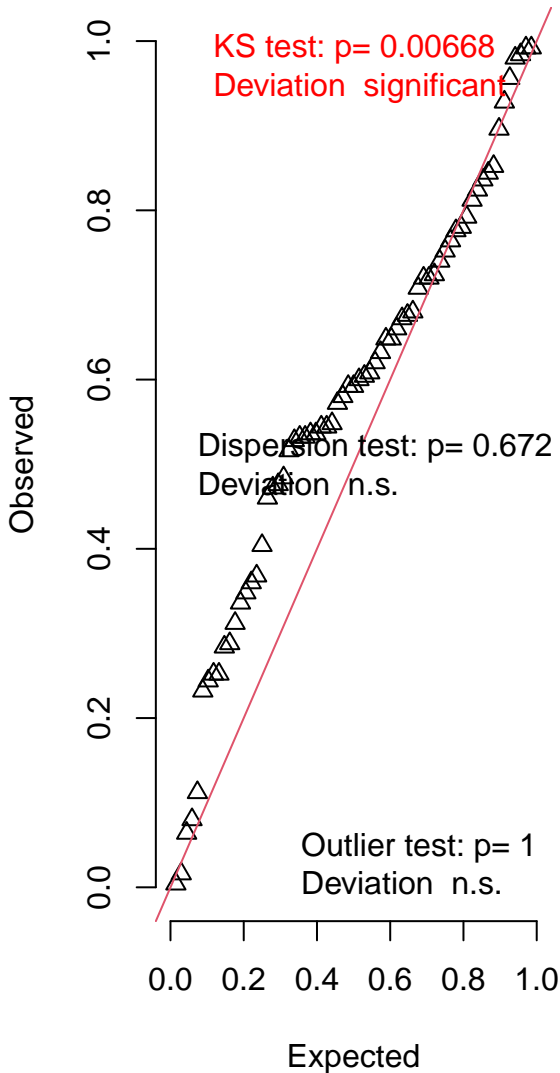
Nb obs DENV-squirrel (infected only): 15

Nb obs DENV-cyno (infected only): 40

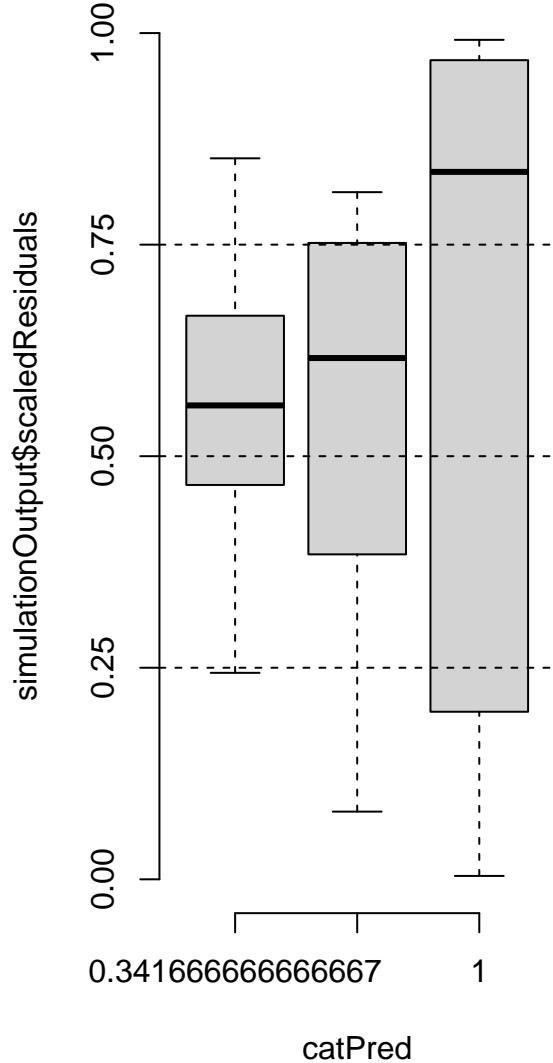
Nb obs ZIKV-squirrel (infected only): 12

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) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-55.9	-42.7	34.0	-67.9	61

Random effects:

```

Conditional model:
Groups   Name          Variance Std.Dev.
ID       (Intercept) 3.998e-02 1.999e-01
day      (Intercept) 2.634e-12 1.623e-06
Residual                1.077e-02 1.038e-01
Number of obs: 67, groups: ID, 18; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.0108

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)      2.08183    0.09449   22.033 < 2e-16 ***
groupCyno.Dengue virus -0.39141    0.11747   -3.332 0.000863 ***
groupSquirrel.Zika virus -0.03852    0.14168   -0.272 0.785718
---

```

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

MIP.1B

Infection in DENV-cyno

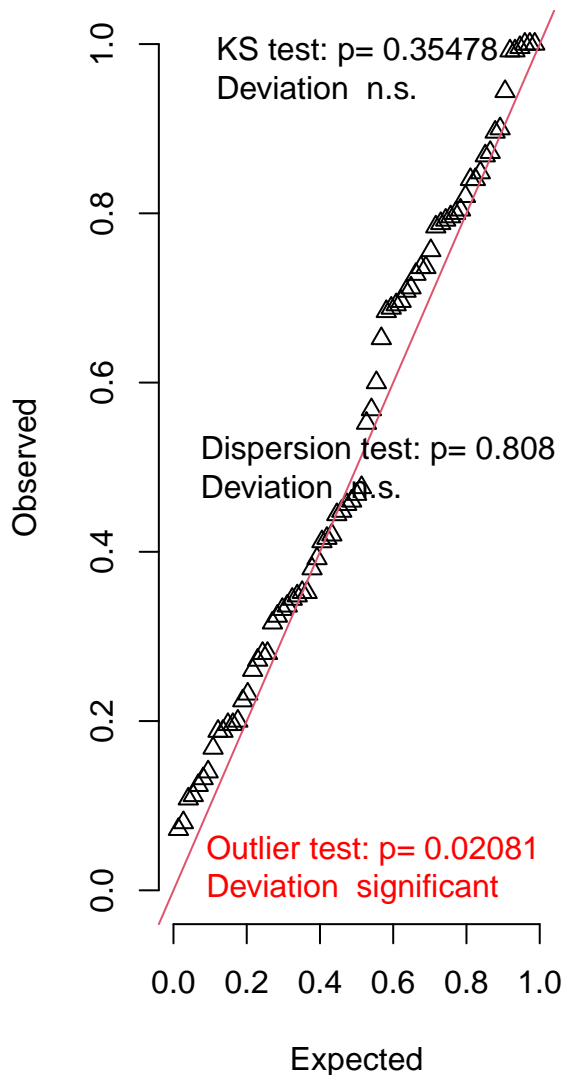
Nb excluded (LOD): 18

Nb obs infection: 49

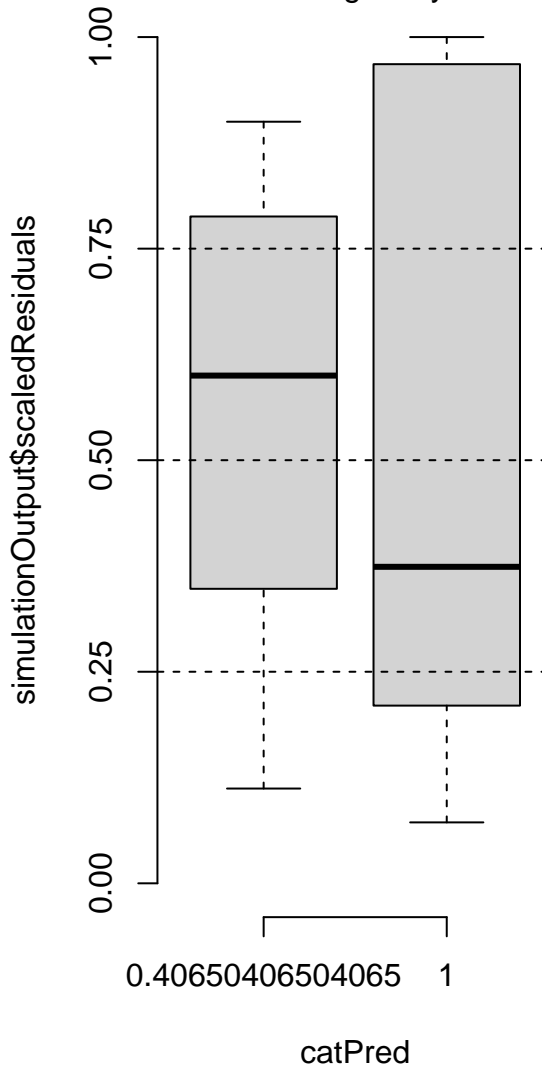
Nb obs control: 24

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
-62.7	-51.2	36.3	-72.7	68

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0584237	0.2417
day	(Intercept)	0.0002044	0.0143
Residual		0.0121085	0.1100

Number of obs: 73, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0121

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.85033	0.08354	22.148	<2e-16 ***
inf_statusControl	0.10770	0.14874	0.724	0.469

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

Infection in DENV-squirrel

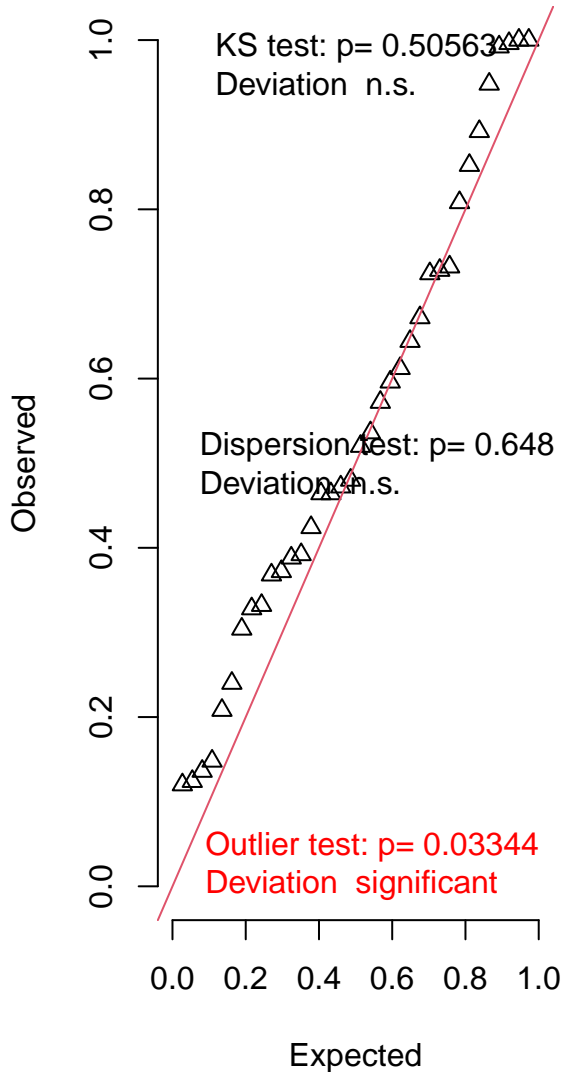
Nb excluded (LOD): 13

Nb obs infection: 27

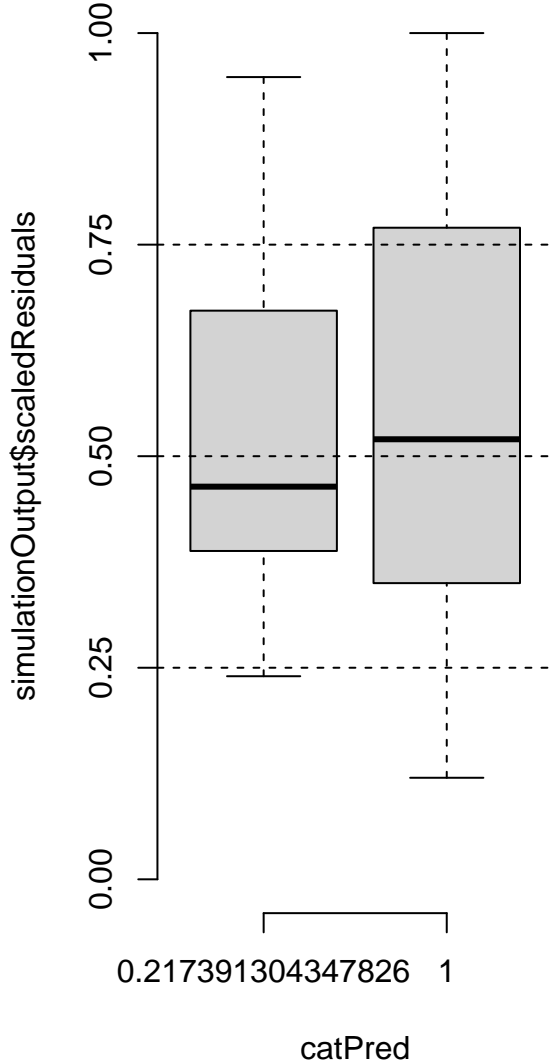
Nb obs control: 9

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
42.4	50.3	-16.2	32.4	31

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.25285	0.5028
day	(Intercept)	0.02639	0.1625
Residual		0.04093	0.2023

Number of obs: 36, groups: ID, 14; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0409

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.2027	0.1783	12.35	<2e-16 ***
inf_statusControl	-0.2538	0.3093	-0.82	0.412

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

Infection in ZIKV-squirrel

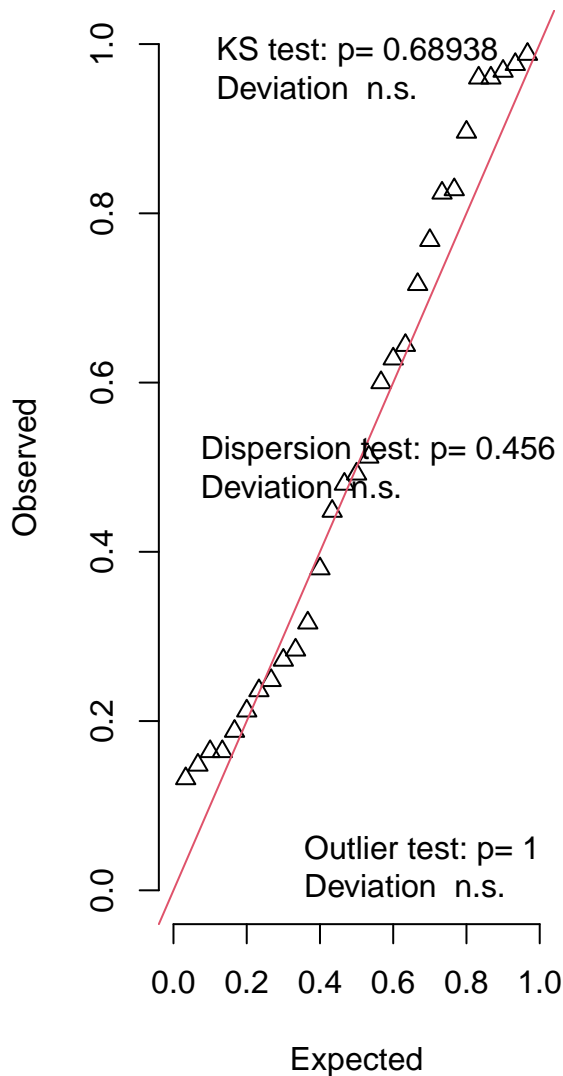
Nb excluded (LOD): 20

Nb obs infection: 20

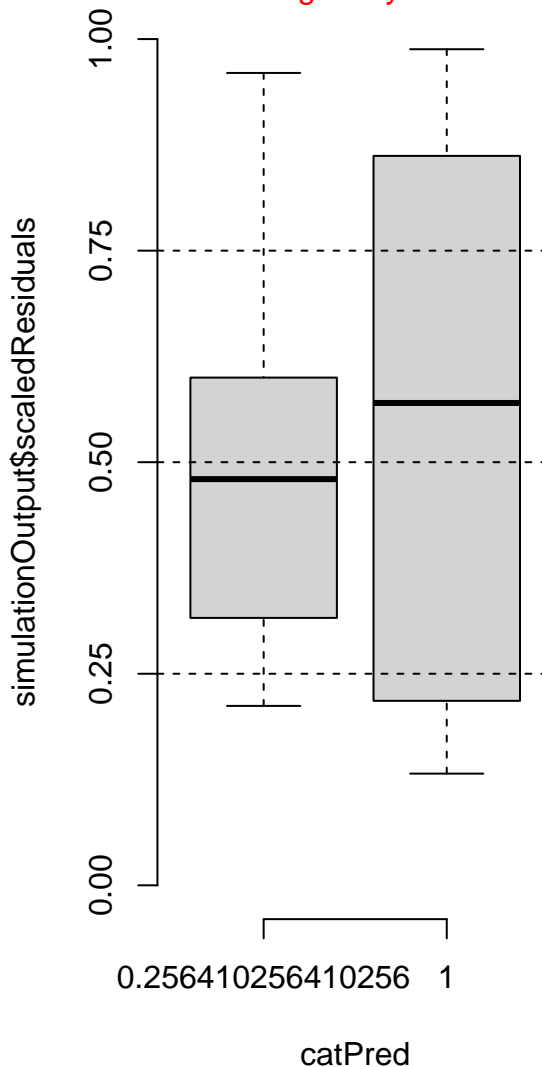
Nb obs control: 9

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: z_sq

```

AIC	BIC	logLik	deviance	df.resid
36.8	43.7	-13.4	26.8	24

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.20967	0.4579
day	(Intercept)	0.01188	0.1090
Residual		0.05449	0.2334

Number of obs: 29, groups: ID, 11; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0545

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.1285	0.1876	11.348	<2e-16 ***
inf_statusControl	-0.1244	0.3042	-0.409	0.683

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

Effect of experiment

Nb excluded (LOD): 37

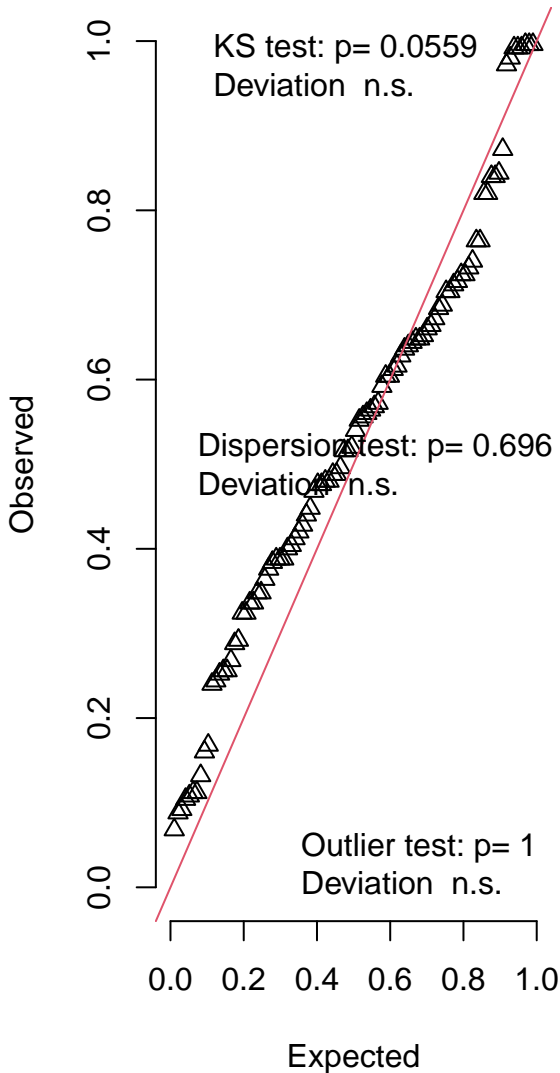
Nb obs DENV-squirrel (infected only): 27

Nb obs DENV-cyno (infected only): 49

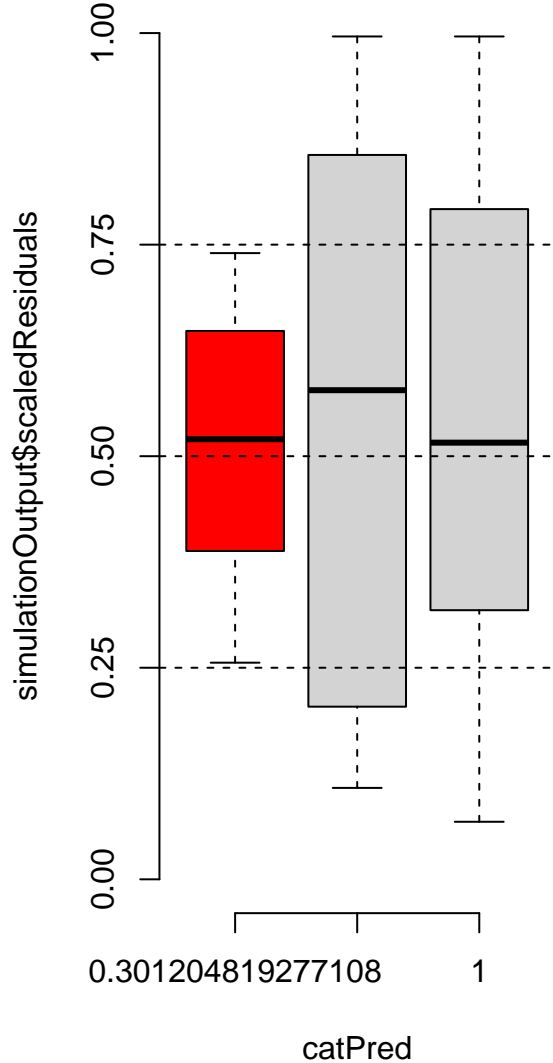
Nb obs ZIKV-squirrel (infected only): 20

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
-7.4	8.0	9.7	-19.4	90

Random effects:

```

Conditional model:
Groups   Name          Variance Std.Dev.
ID       (Intercept) 0.228878 0.47841
day      (Intercept) 0.003964 0.06296
Residual                0.015605 0.12492
Number of obs: 96, groups: ID, 26; day, 8

```

Dispersion estimate for gaussian family (sigma^2): 0.0156

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)      2.2274      0.1565  14.236  <2e-16 ***
groupCyno.Dengue virus -0.3668      0.2247  -1.632   0.103
groupSquirrel.Zika virus -0.1166      0.2401  -0.486   0.627
---

```

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

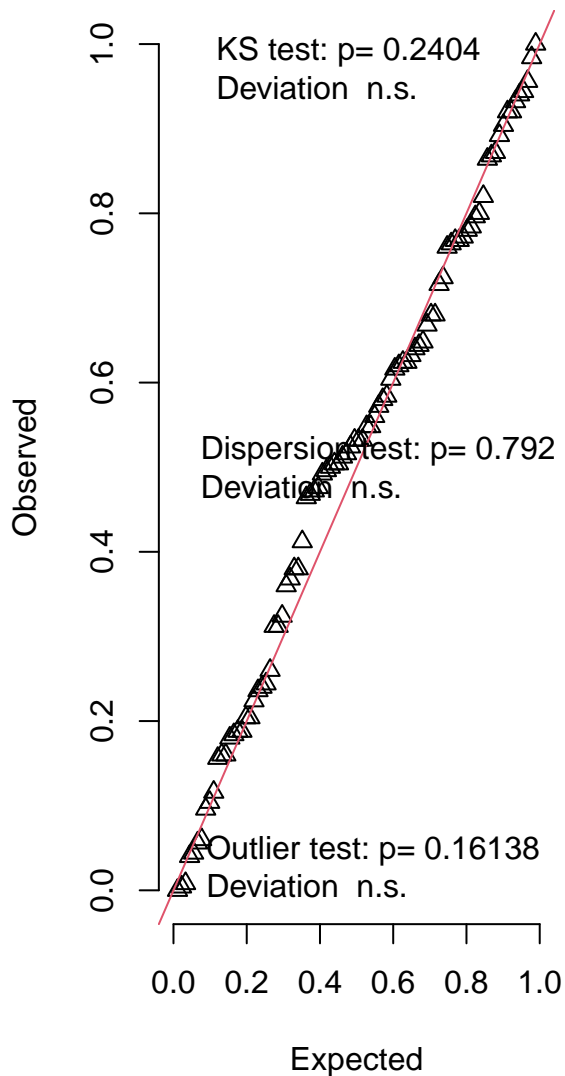
RANTES

Infection in DENV-cyno

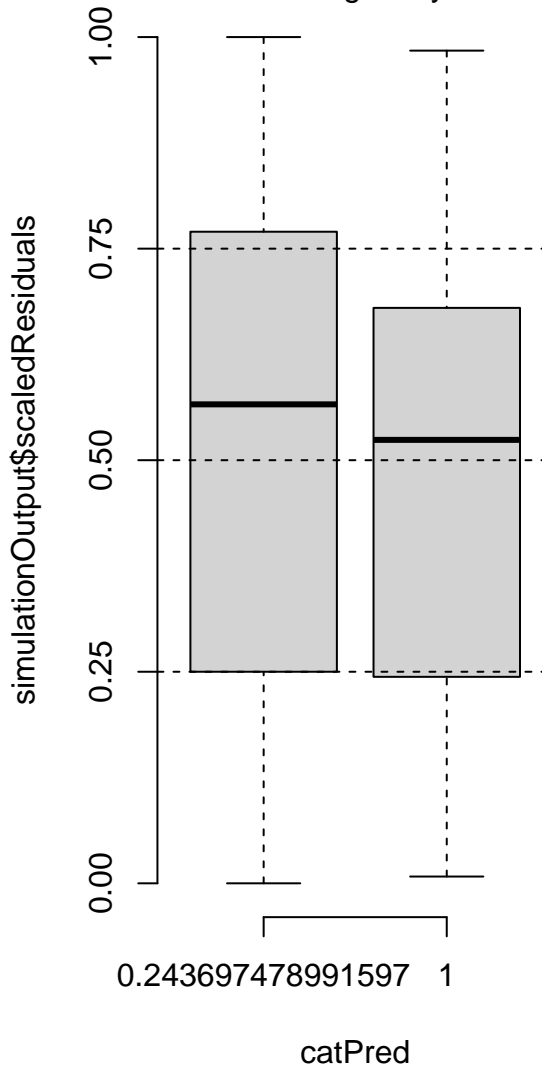
Nb excluded (LOD): 1
Nb obs infection: 62
Nb obs control: 28

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
-53.7	-41.2	31.8	-63.7	85

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.0085609	0.09253
day	(Intercept)	0.0004121	0.02030
Residual		0.0237558	0.15413

Number of obs: 90, groups: ID, 13; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0238

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.55685	0.03734	95.27	<2e-16 ***
inf_statusControl	-0.05973	0.06576	-0.91	0.364

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

Infection in DENV-squirrel

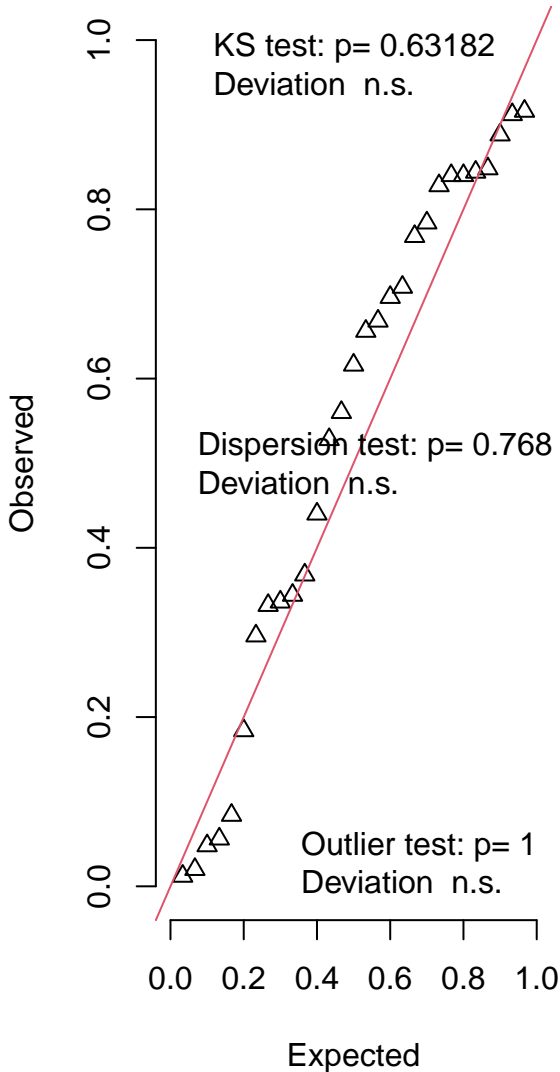
Nb excluded (LOD): 20

Nb obs infection: 18

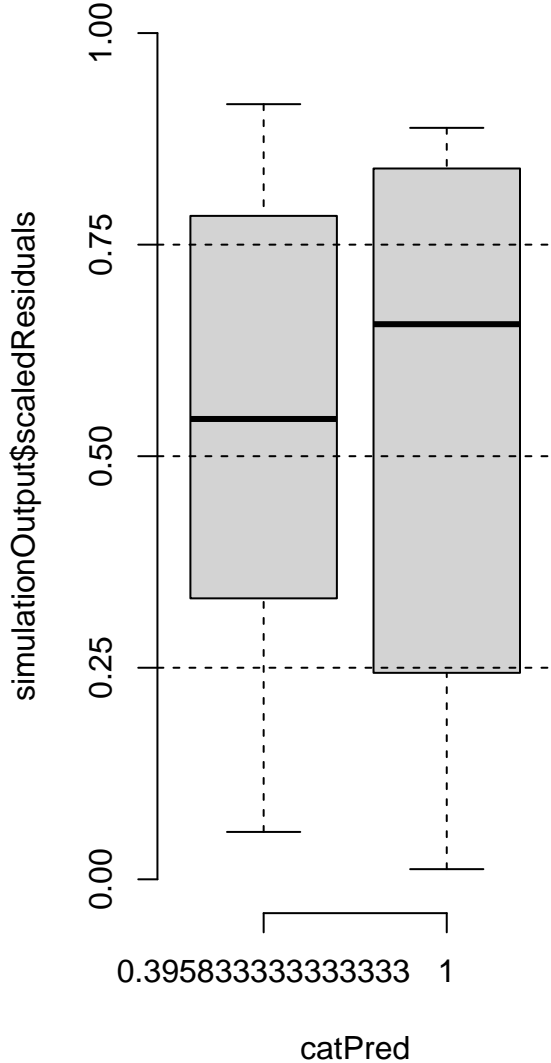
Nb obs control: 11

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
-30.4	-23.5	20.2	-40.4	24

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	4.466e-03	6.683e-02
day	(Intercept)	3.398e-12	1.843e-06
Residual		1.127e-02	1.062e-01

Number of obs: 29, groups: ID, 10; day, 7

Dispersion estimate for gaussian family (sigma^2): 0.0113

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.35050	0.03849	35.09	<2e-16 ***
inf_statusControl	0.05381	0.06074	0.89	0.376

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

Infection in ZIKV-squirrel

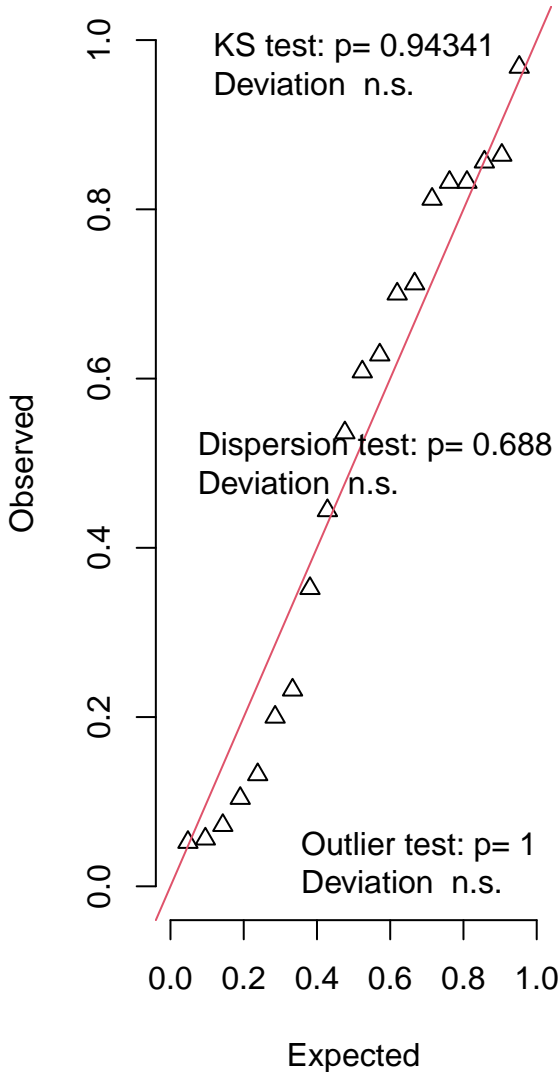
Nb excluded (LOD): 29

Nb obs infection: 9

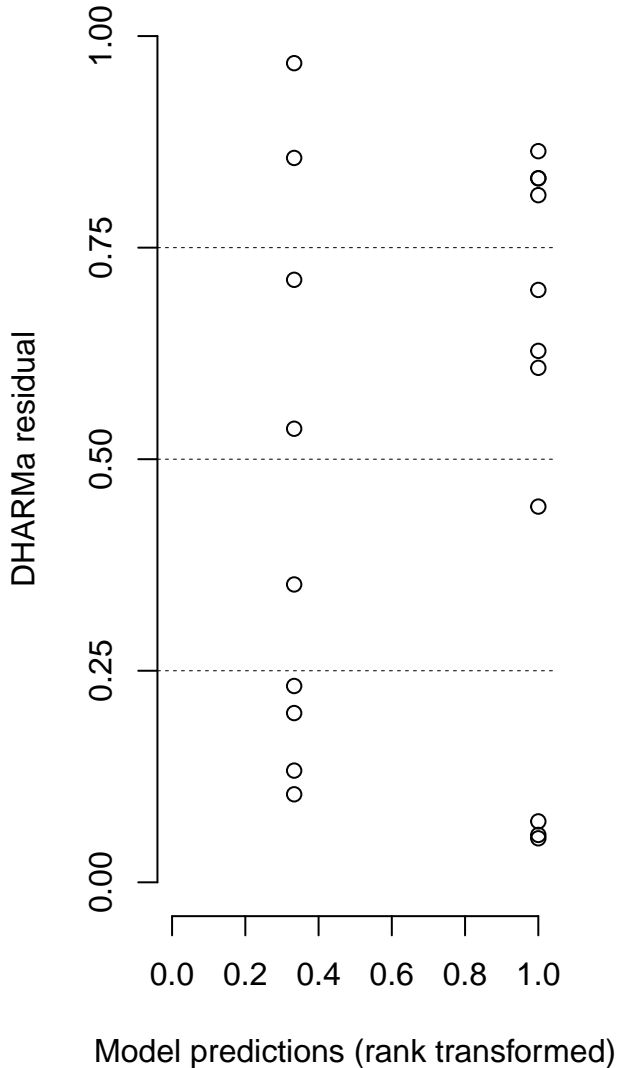
Nb obs control: 11

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected




```

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

```

AIC	BIC	logLik	deviance	df.resid
-11.7	-6.8	10.9	-21.7	15

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	0.002350	0.04847
day	(Intercept)	0.004808	0.06934
Residual		0.014015	0.11838

Number of obs: 20, groups: ID, 7; day, 7

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

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.13966	0.05954	19.140	< 2e-16 ***
inf_statusControl	0.27104	0.06912	3.921	8.82e-05 ***

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

Effect of experiment

Nb excluded (LOD): 44

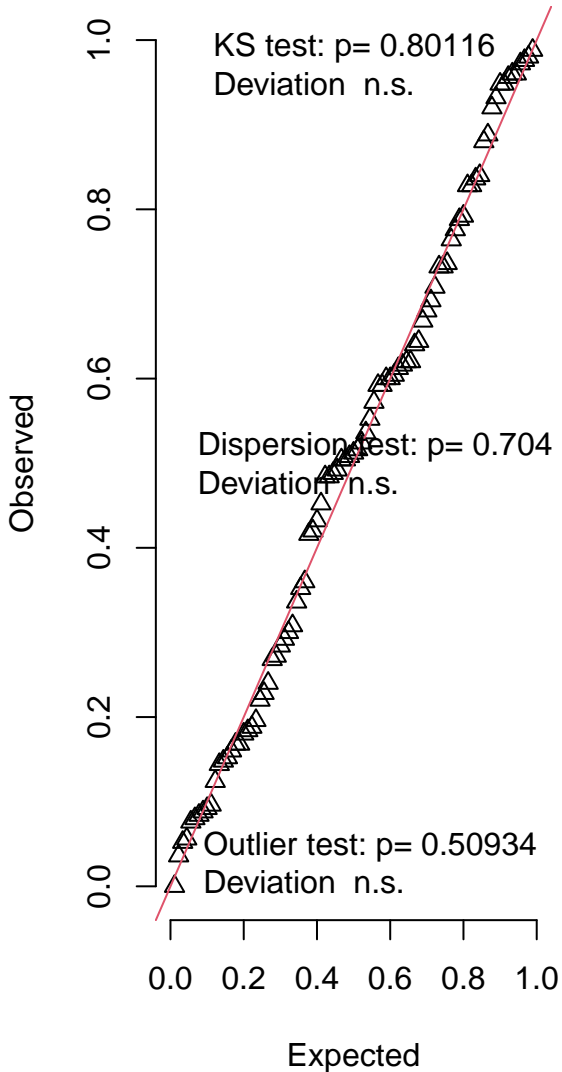
Nb obs DENV-squirrel (infected only): 18

Nb obs DENV-cyno (infected only): 62

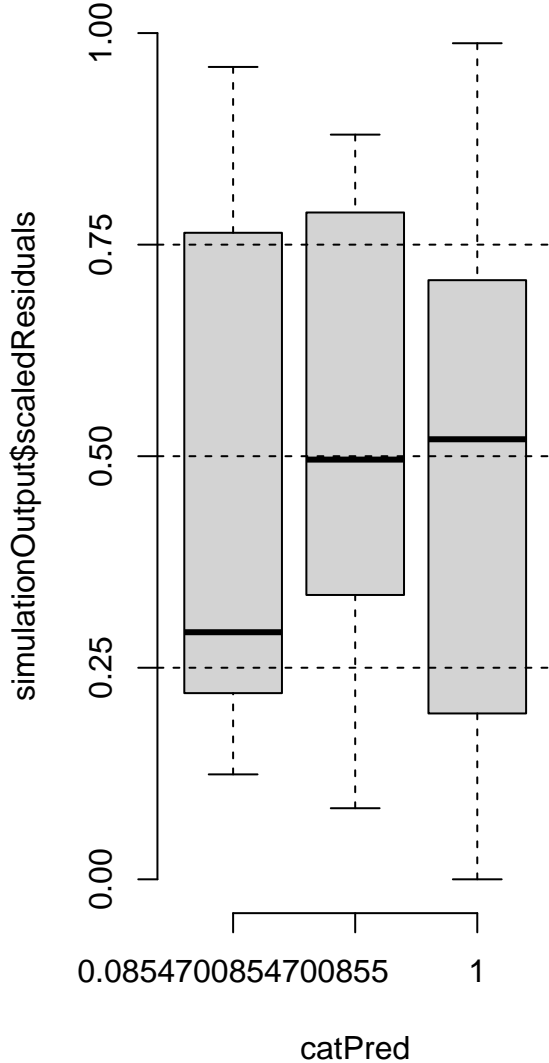
Nb obs ZIKV-squirrel (infected only): 9

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
-79.7	-64.8	45.9	-91.7	83

Random effects:

```

Conditional model:
Groups   Name             Variance Std.Dev.
ID       (Intercept) 0.004532 0.06732
day      (Intercept) 0.000104 0.01020
Residual                   0.017729 0.13315
Number of obs: 89, groups: ID, 18; day, 7

```

Dispersion estimate for gaussian family (sigma^2): 0.0177

```

Conditional model:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.35240    0.04300   31.45 < 2e-16 ***
groupCyno.Dengue virus  2.20438    0.05122   43.03 < 2e-16 ***
groupSquirrel.Zika virus -0.22283    0.07343   -3.03 0.00241 **
---

```

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

TGFbeta

Infection in DENV-cyno

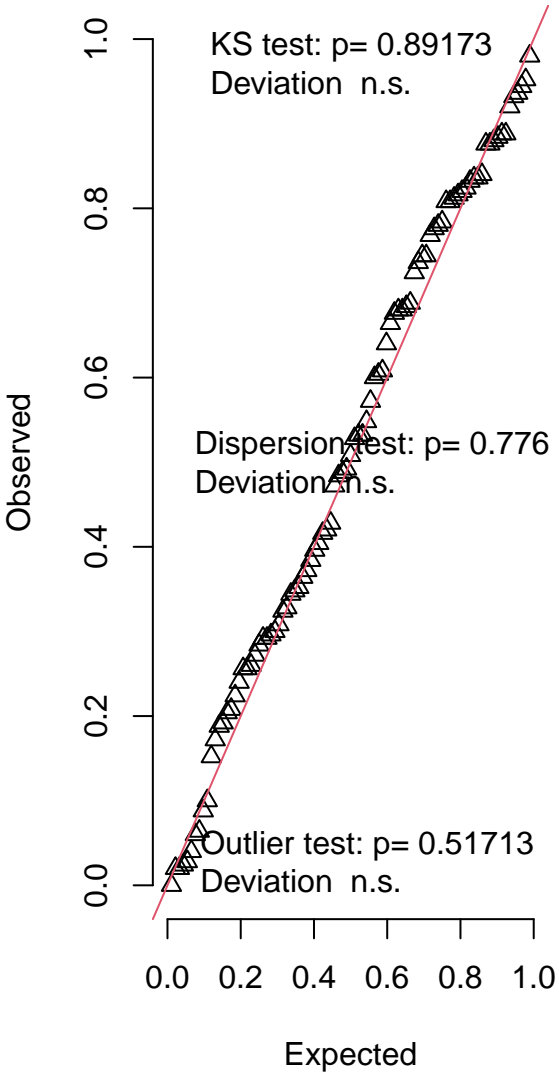
Nb excluded (LOD): 0

Nb obs infection: 63

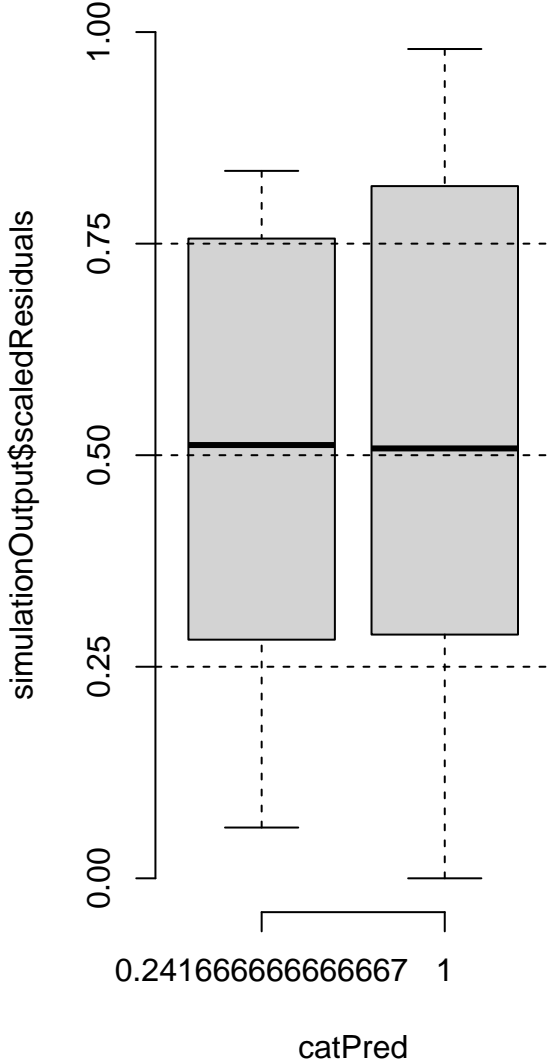
Nb obs control: 28

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 excluded (LOD): 29

Nb obs infection: 20

Nb obs control: 0

TGPbeta ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 31

Nb obs infection: 18

Nb obs control: 0

TGPbeta ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 32

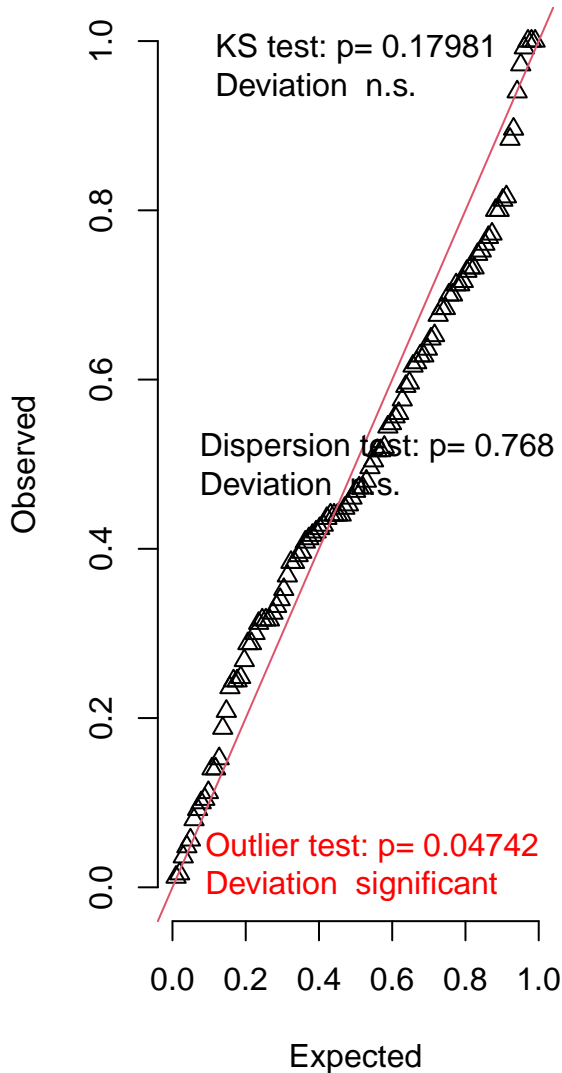
Nb obs DENV-squirrel (infected only): 20

Nb obs DENV-cyno (infected only): 63

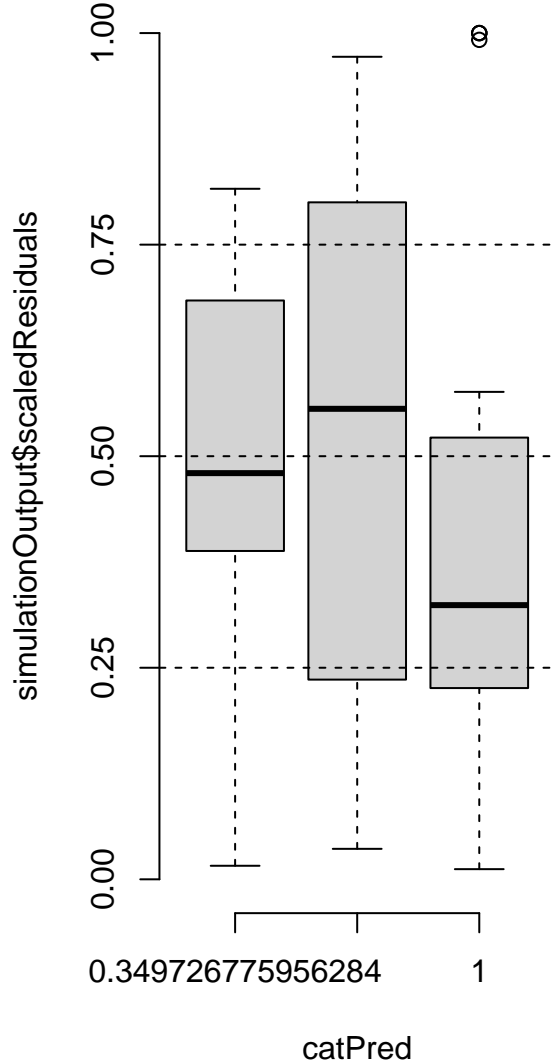
Nb obs ZIKV-squirrel (infected only): 18

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) ~ group + (1 | ID) + (1 | day)
Data: my_df

```

AIC	BIC	logLik	deviance	df.resid
-76.4	-60.7	44.2	-88.4	95

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.066e-01	3.264e-01
day	(Intercept)	2.460e-12	1.568e-06
Residual		1.184e-02	1.088e-01

Number of obs: 101, groups: ID, 19; day, 8

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

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.2233	0.1480	15.022	<2e-16 ***
groupCyno.Dengue virus	-0.2943	0.1842	-1.598	0.11
groupSquirrel.Zika virus	-0.1837	0.2095	-0.877	0.38

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

TNF.alpha

Infection in DENV-cyno

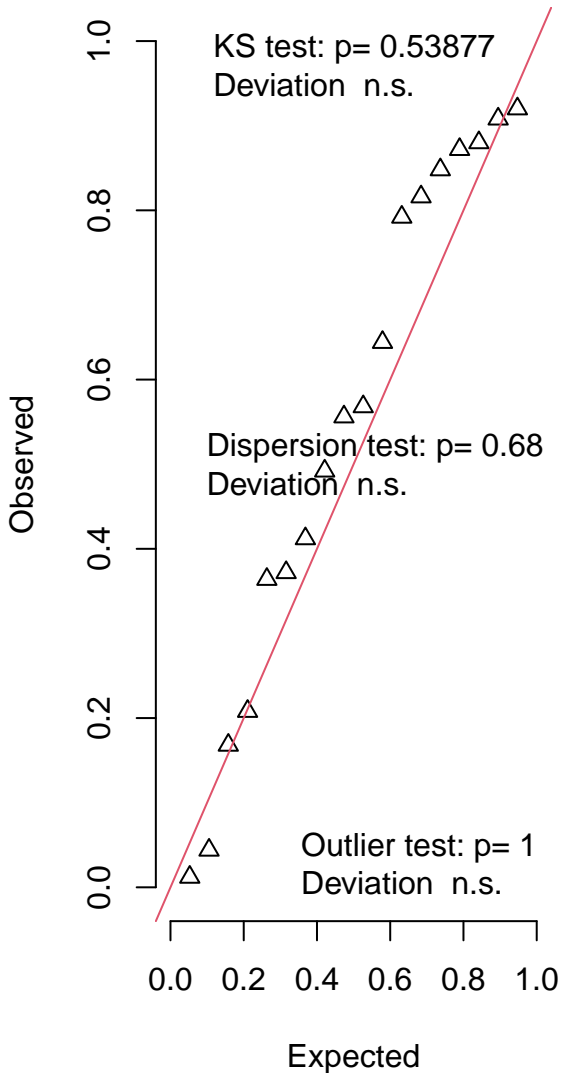
Nb excluded (LOD): 73

Nb obs infection: 13

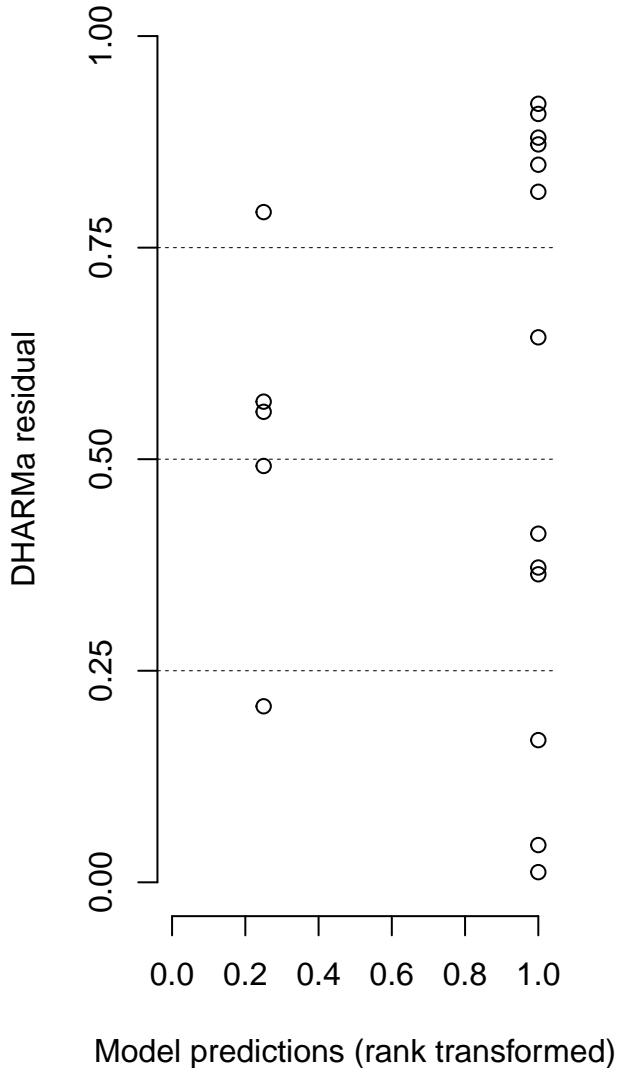
Nb obs control: 5

DHARMA residual

QQ plot residuals



Residual vs. predicted No significant problems detected




```

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

```

AIC	BIC	logLik	deviance	df.resid
-68.4	-63.9	39.2	-78.4	13

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	1.295e-04	1.138e-02
day	(Intercept)	3.293e-13	5.738e-07
Residual		6.521e-04	2.554e-02

Number of obs: 18, groups: ID, 5; day, 6

Dispersion estimate for gaussian family (sigma^2): 0.000652

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.24910	0.01042	119.86	<2e-16 ***
inf_statusControl	-0.03925	0.01763	-2.23	0.0259 *

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

Infection in DENV-squirrel

Nb excluded (LOD): 47

Nb obs infection: 2

Nb obs control: 0

TNF.alpha ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 45

Nb obs infection: 4

Nb obs control: 0

TNF.alpha ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 114

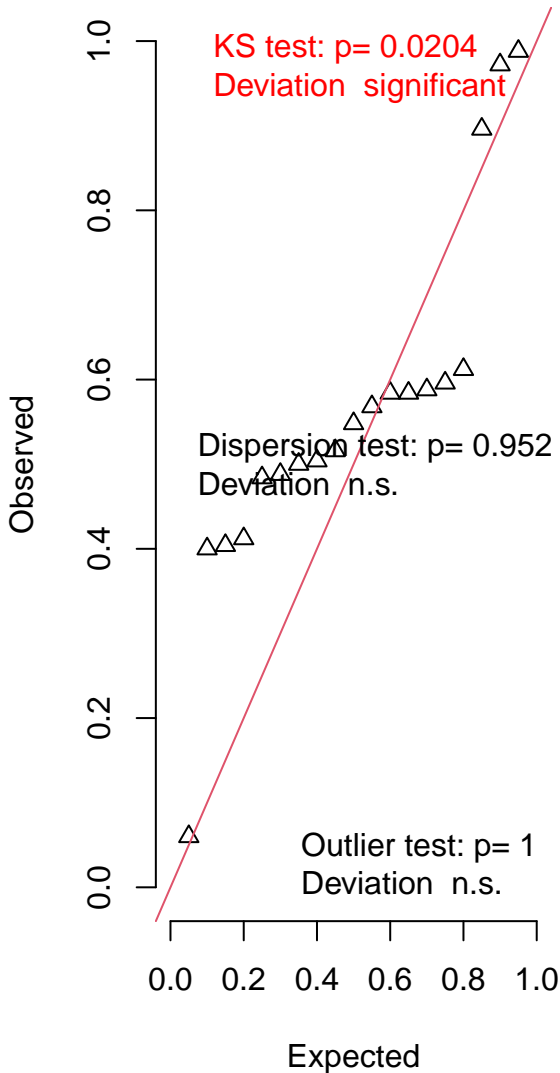
Nb obs DENV-squirrel (infected only): 2

Nb obs DENV-cyno (infected only): 13

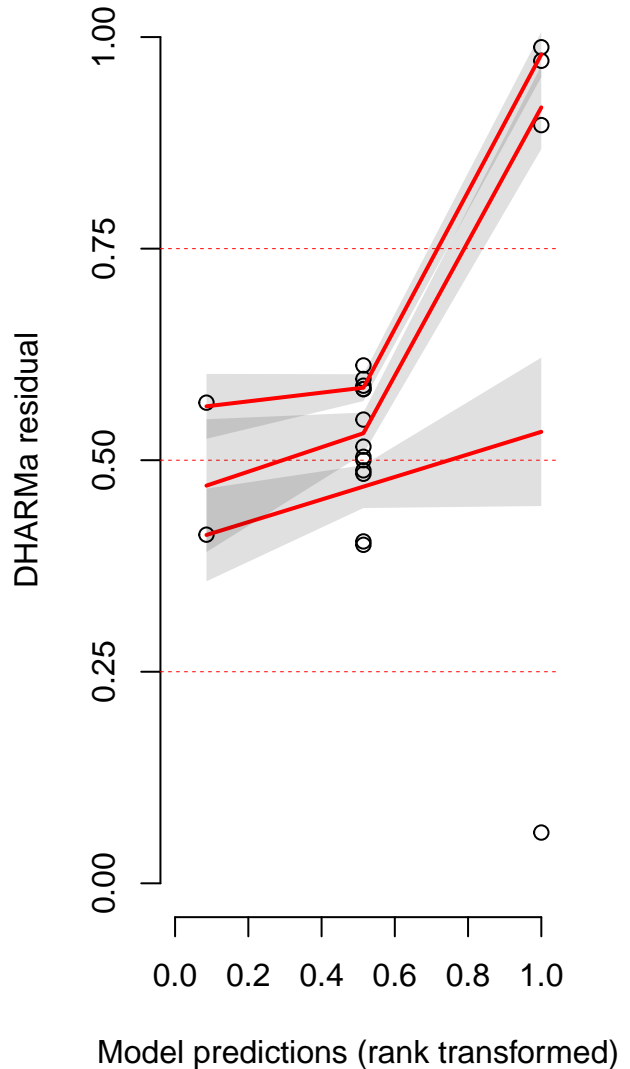
Nb obs ZIKV-squirrel (infected only): 4

DHARMA residual

QQ plot residuals



Residual vs. predicted Quantile deviations detected (red curves) Combined adjusted quantile test significant



```

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

```

AIC	BIC	logLik	deviance	df.resid
-31.8	-26.1	21.9	-43.8	13

Random effects:

Conditional model:

Groups	Name	Variance	Std.Dev.
ID	(Intercept)	2.518e-02	1.587e-01
day	(Intercept)	5.941e-12	2.437e-06
Residual		1.863e-03	4.317e-02

Number of obs: 19, groups: ID, 6; day, 8

Dispersion estimate for gaussian family (sigma^2): 0.00186

Conditional model:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.19844	0.16159	7.417	1.2e-13 ***
groupCyno.Dengue virus	0.04593	0.18623	0.247	0.805
groupSquirrel.Zika virus	0.30477	0.19833	1.537	0.124

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

VEGF

Infection in DENV-cyno

Nb excluded (LOD): 90

Nb obs infection: 1

Nb obs control: 0

VEGF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in DENV-squirrel

Nb excluded (LOD): 49

Nb obs infection: 0

Nb obs control: 0

VEGF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Infection in ZIKV-squirrel

Nb excluded (LOD): 49

Nb obs infection: 0

Nb obs control: 0

VEGF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux

Effect of experiment

Nb excluded (LOD): 132

Nb obs DENV-squirrel (infected only): 0

Nb obs DENV-cyno (infected only): 1

Nb obs ZIKV-squirrel (infected only): 0

VEGF ERROR : les contrastes ne peuvent être appliqués qu'aux facteurs ayant au moins deux niveaux