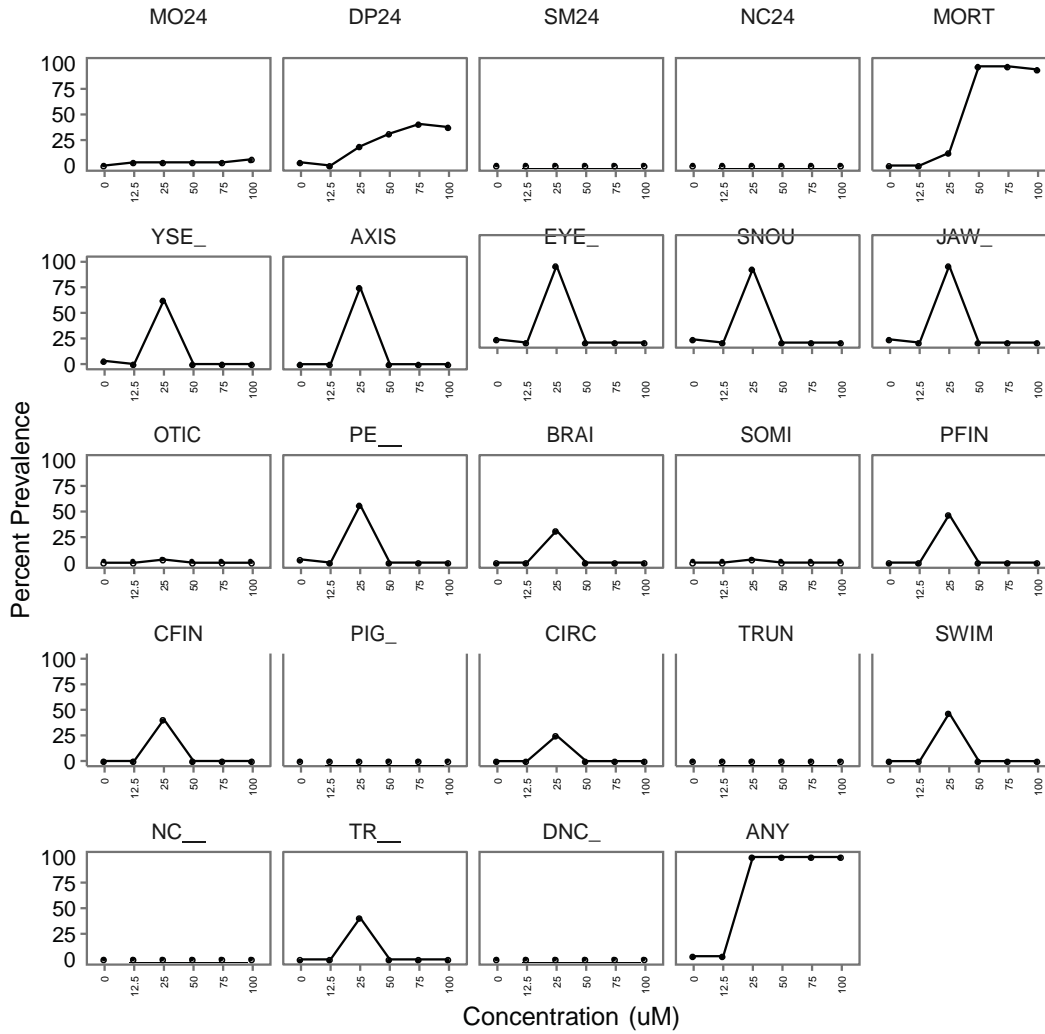


Supplemental Data 2.

Developmental toxicity profiles, logistic model output, calculated EC values, and logistic regression curves for the 25 test chemicals. Each page represents an individual test chemical. Developmental toxicity for the 24 uniquely measured endpoints at 24 or 120 hpf are shown in the top panel. The Left-bottom panel indicates the model output from logistic regression of the binarized data for any observed morbidity or mortality by 120 hpf. Right bottom panel indicates the calculated EC values and the logistic regression curves of the fitted data.

Abbreviations: MO24, 24 hpf mortality; DP24, 24 hpf developmental delay; SM24; 24 hpf somites; NC24, 24 hpf notochord; MORT, 120 hpf mortality; YSE_, 120 hpf yolk sac edema; AXIS, 120 hpf axis; EYE_; 120 hpf eye; SNOU, 120 hpf snout; JAW_, 120 hpf jaw; OTIC, 120 hpf otic vesicle; PE_, 120 hpf pericardial edema; BRAI, 120 hpf brain; PFIC, 120 hpf pectoral fin; CFIN, 120 hpf caudal fin; PIG_, 120 hpf pigmentation; CIRC, 120 hpf circulation; TRUN, 120 hpf truncation; SWIM, 120 hpf swim bladder; NC_, 120 hpf notochord; TR_, 120 hpf touch response; DNC_, not counted due to technical or other error during sampling; ANY, summation of any morbidity or mortality effect

5a_dihydrotestosterone



Model Output:

Call:
`glm(formula = ANY ~ CONC, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -0.4420 -0.0259 0.0000 0.0008 3.9997

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -7.99842 1.56751 -5.103 3.35e-07 ***
 CONC 0.45774 0.09398 4.871 1.11e-06 ***

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

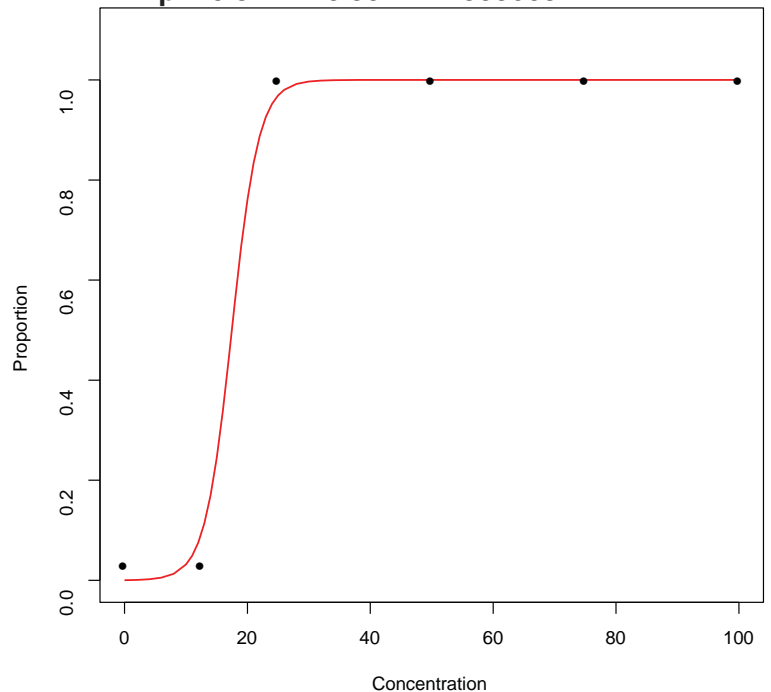
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 241.555 on 191 degrees of freedom
 Residual deviance: 28.834 on 190 degrees of freedom
 AIC: 32.834

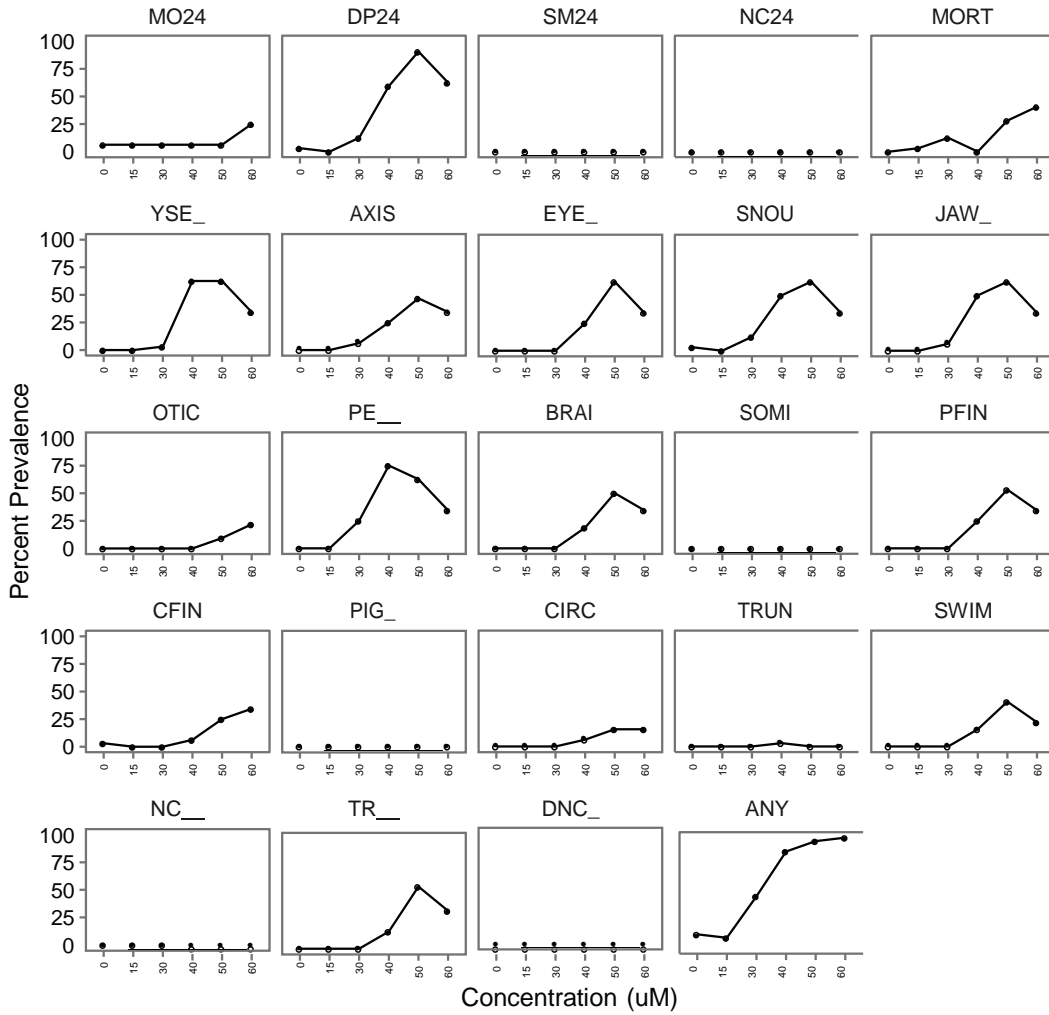
Number of Fisher Scoring iterations: 10

EC Values:

	Concentration	SE
p = 0.5:	17.47358	1.195250
p = 0.6:	18.35937	1.261757
p = 0.7:	19.32461	1.358456
p = 0.8:	20.50211	1.503608



17_methyltestosterone



Model Output:

Call:
`glm(formula = ANY ~ CONC, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -2.3849 -0.6199 0.1884 0.6218 2.6239

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -3.41001 0.54660 -6.239 4.42e-10 ***
 CONC 0.12388 0.01668 7.426 1.12e-13 ***

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

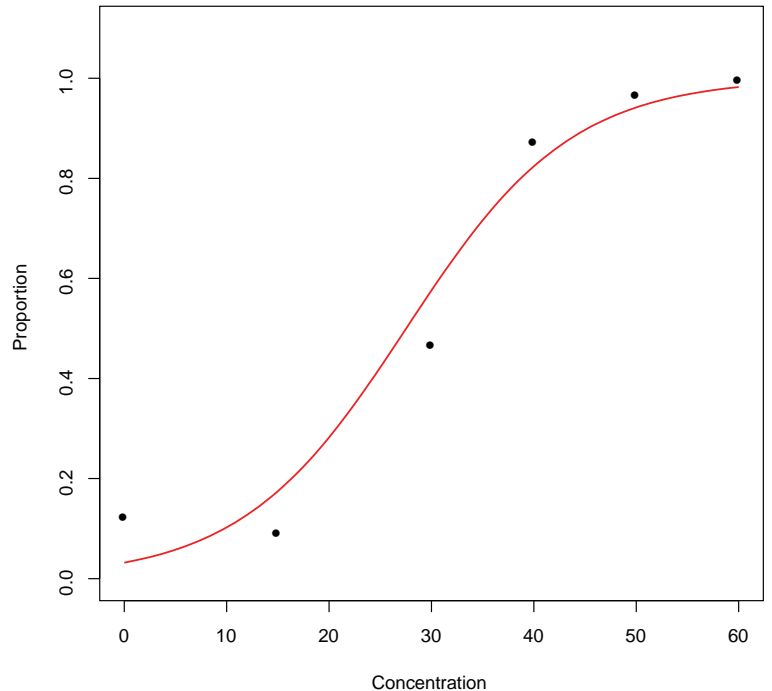
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 260.12 on 191 degrees of freedom
 Residual deviance: 131.97 on 190 degrees of freedom
 AIC: 135.97

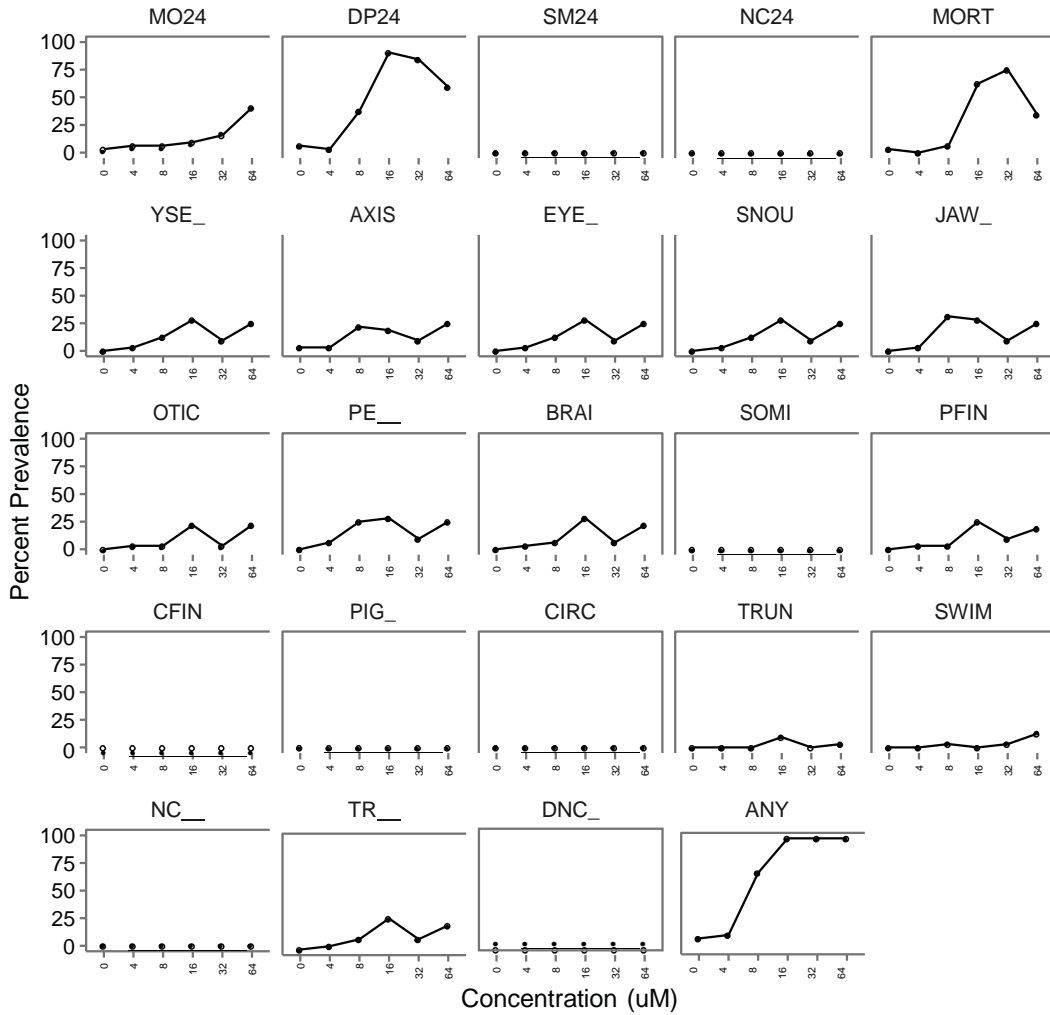
Number of Fisher Scoring iterations: 5

EC Values:

	Concentration	SE
p = 0.5:	27.52669	1.818322
p = 0.6:	30.79973	1.792332
p = 0.7:	34.36635	1.884816
p = 0.8:	38.71730	2.142905



17a_ethinylestradiol



Model Output:

Call:
`glm(formula = ANY ~ CONC, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.4726 -0.2772 0.0000 0.1426 2.5606

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -3.23983 0.59880 -5.411 6.28e-08 ***
 CONC 0.48892 0.08969 5.451 5.00e-08 ***

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

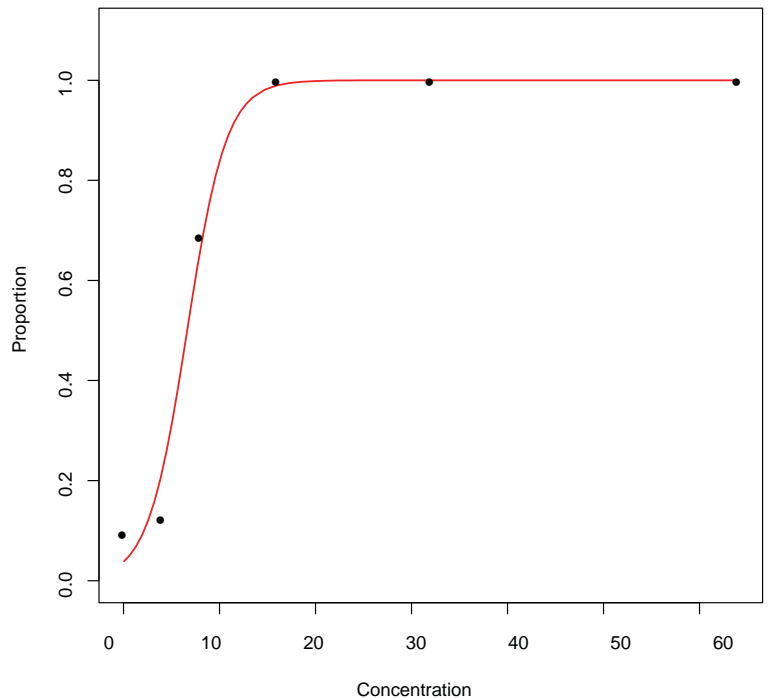
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 248.371 on 191 degrees of freedom
 Residual deviance: 88.311 on 190 degrees of freedom
 AIC: 92.311

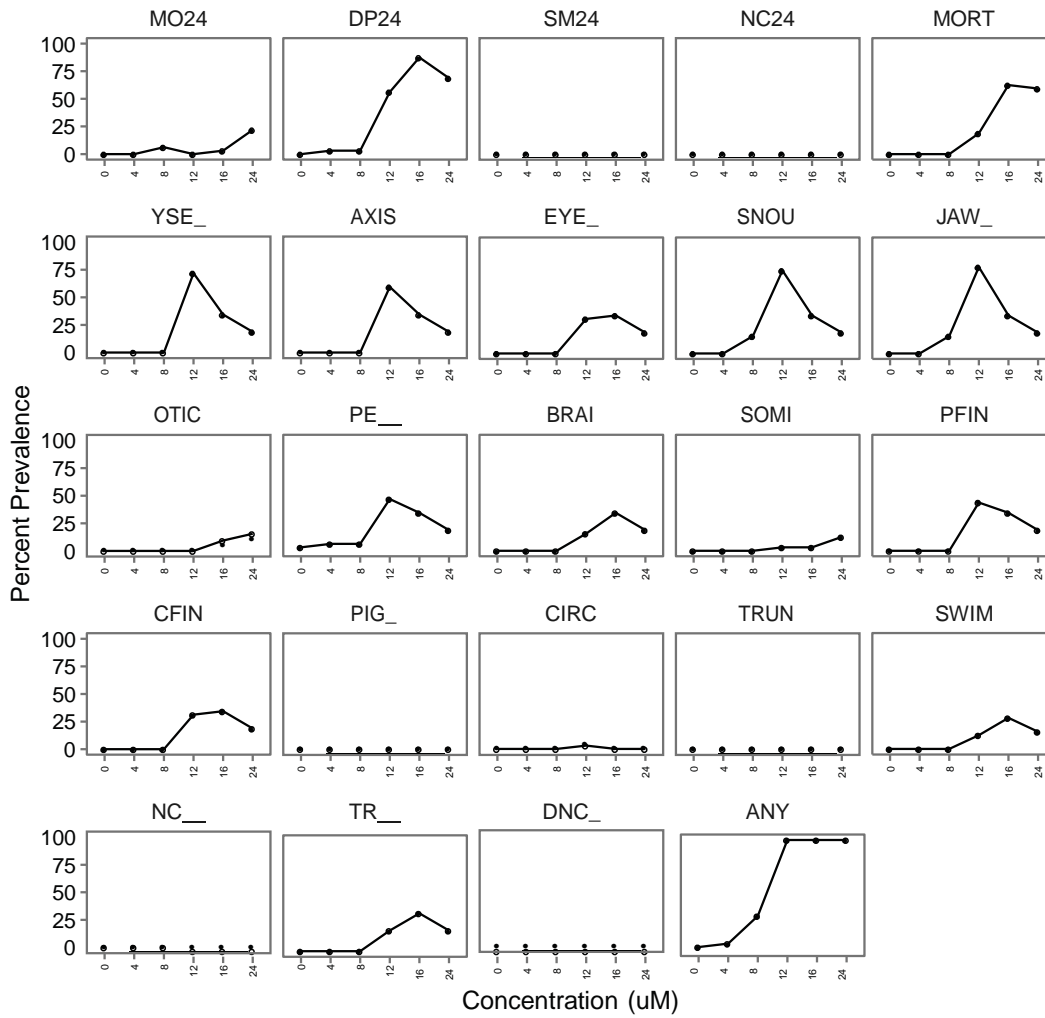
Number of Fisher Scoring iterations: 9

EC Values:

	Concentration	SE
p = 0.5:	6.626547	0.5579331
p = 0.6:	7.455861	0.6087623
p = 0.7:	8.359558	0.6985086
p = 0.8:	9.461989	0.8399172



17b_estradiol



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.51390 -0.11850 0.07363 0.41304 3.15034

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -4.9553 0.9283 -5.338 9.40e-08 ***
 CONC_log 5.9929 0.9984 6.002 1.94e-09 ***

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

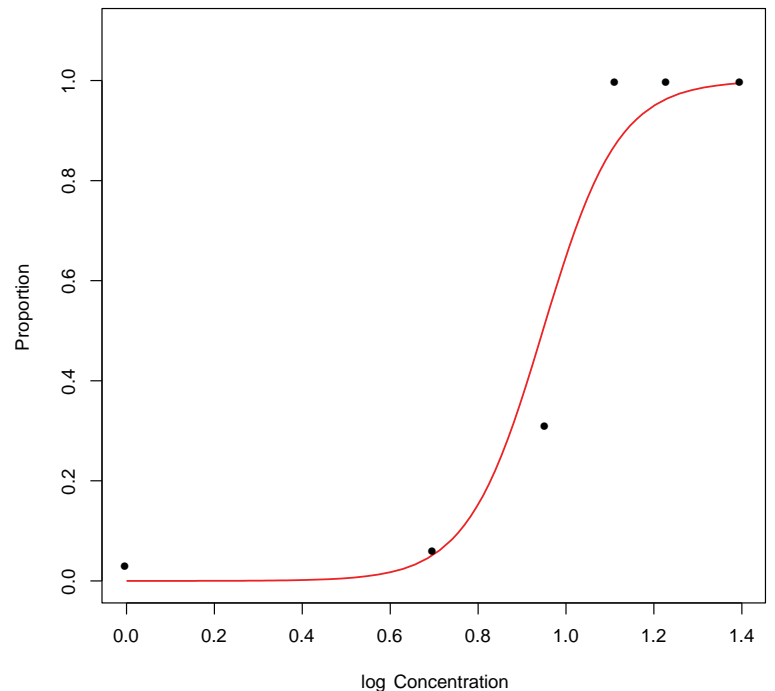
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 248.37 on 191 degrees of freedom
 Residual deviance: 107.13 on 190 degrees of freedom
 AIC: 111.13

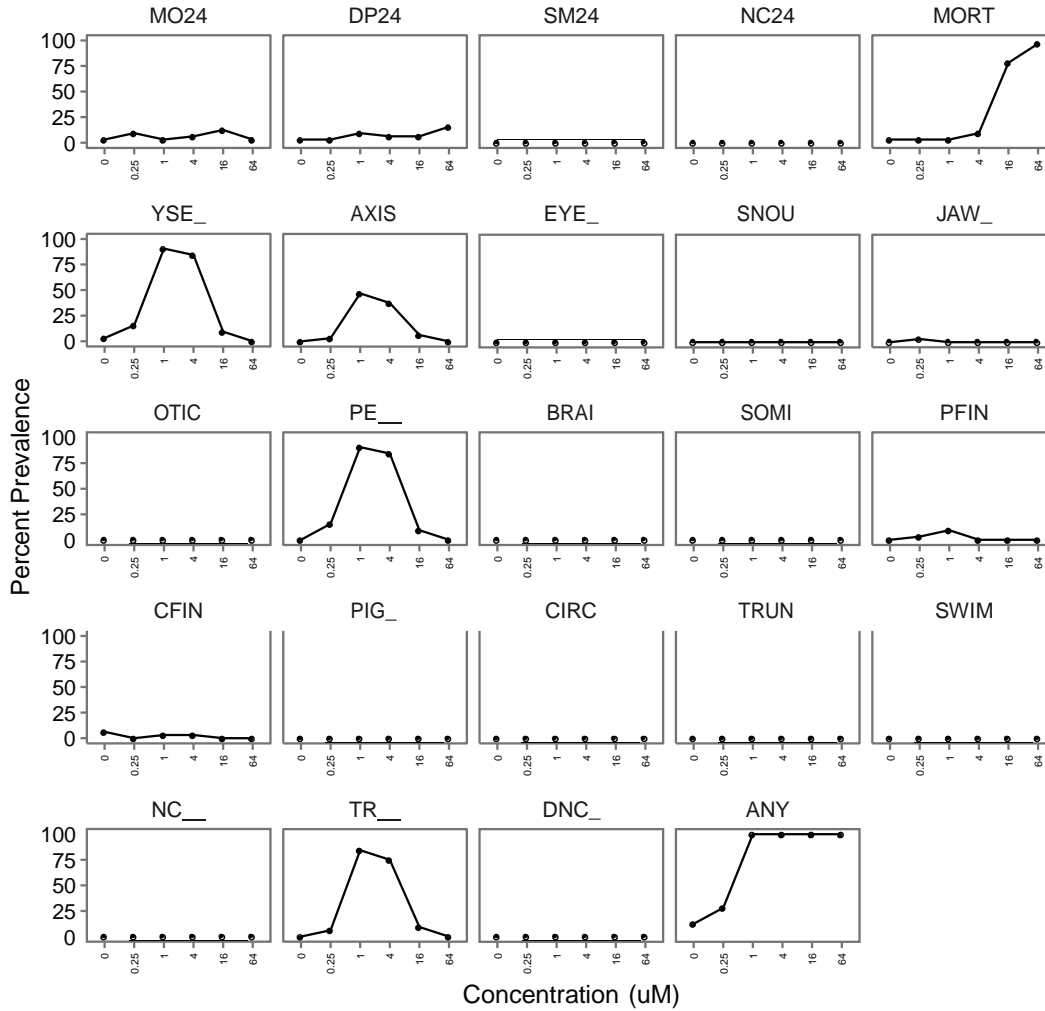
Number of Fisher Scoring iterations: 6

EC Values:

	Concentration	SE.log
p = 0.5:	7.856496	0.05616197
p = 0.6:	8.596602	0.05370714
p = 0.7:	9.473682	0.05470802
p = 0.8:	10.652897	0.06080110



abamectin



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -0.94613 -0.38387 0.00002 0.00378 2.29985

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -2.5710 0.5097 -5.044 4.57e-07 ***
 CONC_log 20.6295 4.3423 4.751 2.03e-06 ***

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

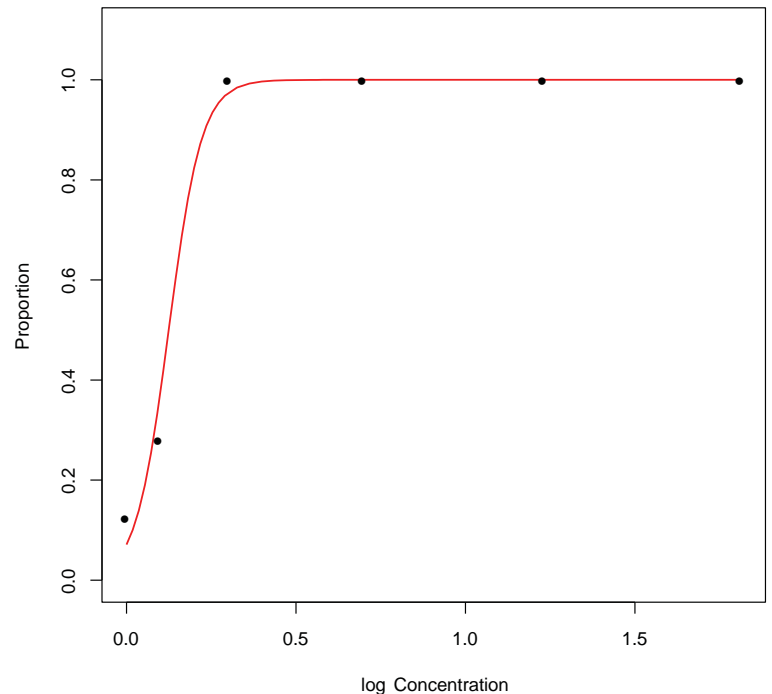
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 222.282 on 191 degrees of freedom
 Residual deviance: 65.881 on 190 degrees of freedom
 AIC: 69.881

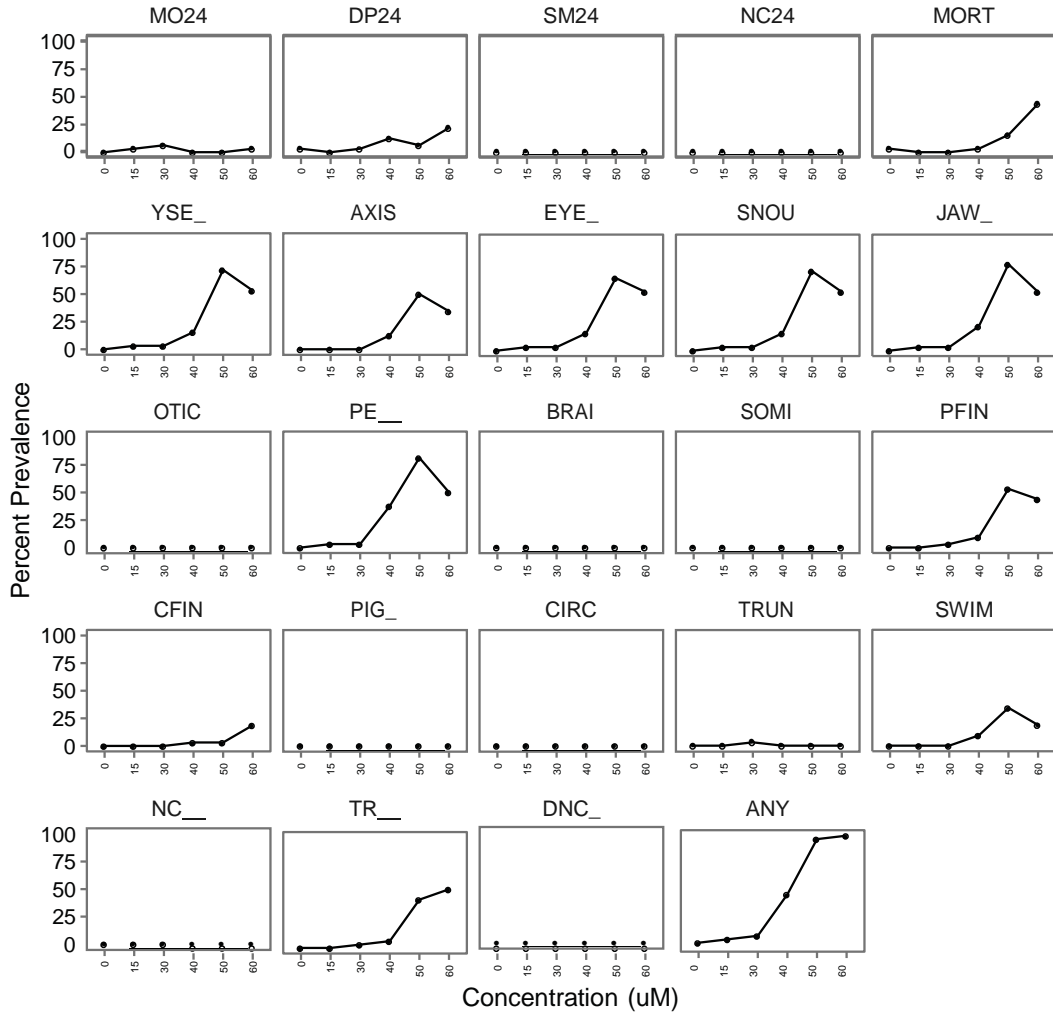
Number of Fisher Scoring iterations: 9

EC Values:

	Concentration	SE.log
p = 0.5:	0.3323731	0.03877618
p = 0.6:	0.3940567	0.04372087
p = 0.7:	0.4645288	0.05080763
p = 0.8:	0.5553399	0.06103778



Bisphenol_A



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.7626 -0.2432 -0.0008 0.6894 5.4841

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-15.038	2.560	-5.875	4.23e-09 ***
CONC_log	9.577	1.588	6.029	1.65e-09 ***

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

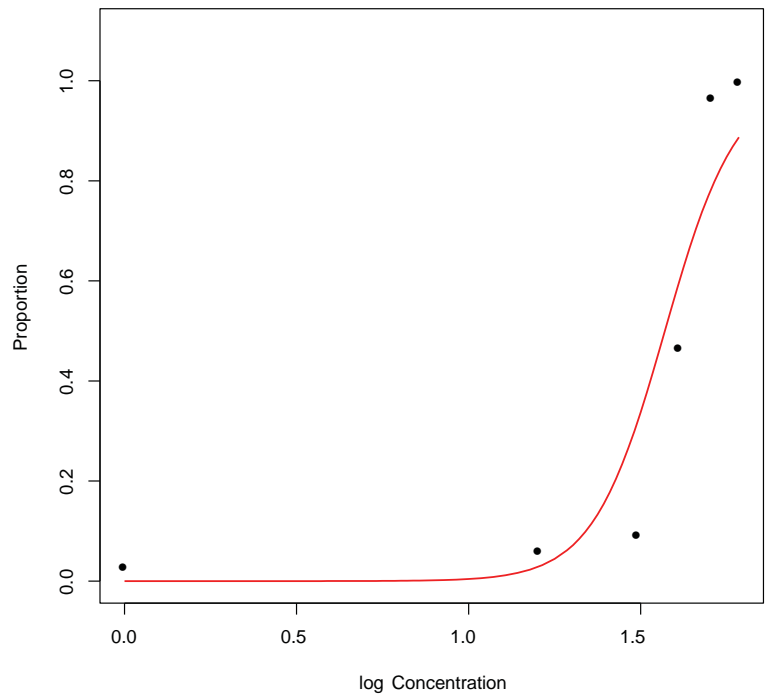
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 263.16 on 191 degrees of freedom
 Residual deviance: 147.20 on 190 degrees of freedom
 AIC: 151.2

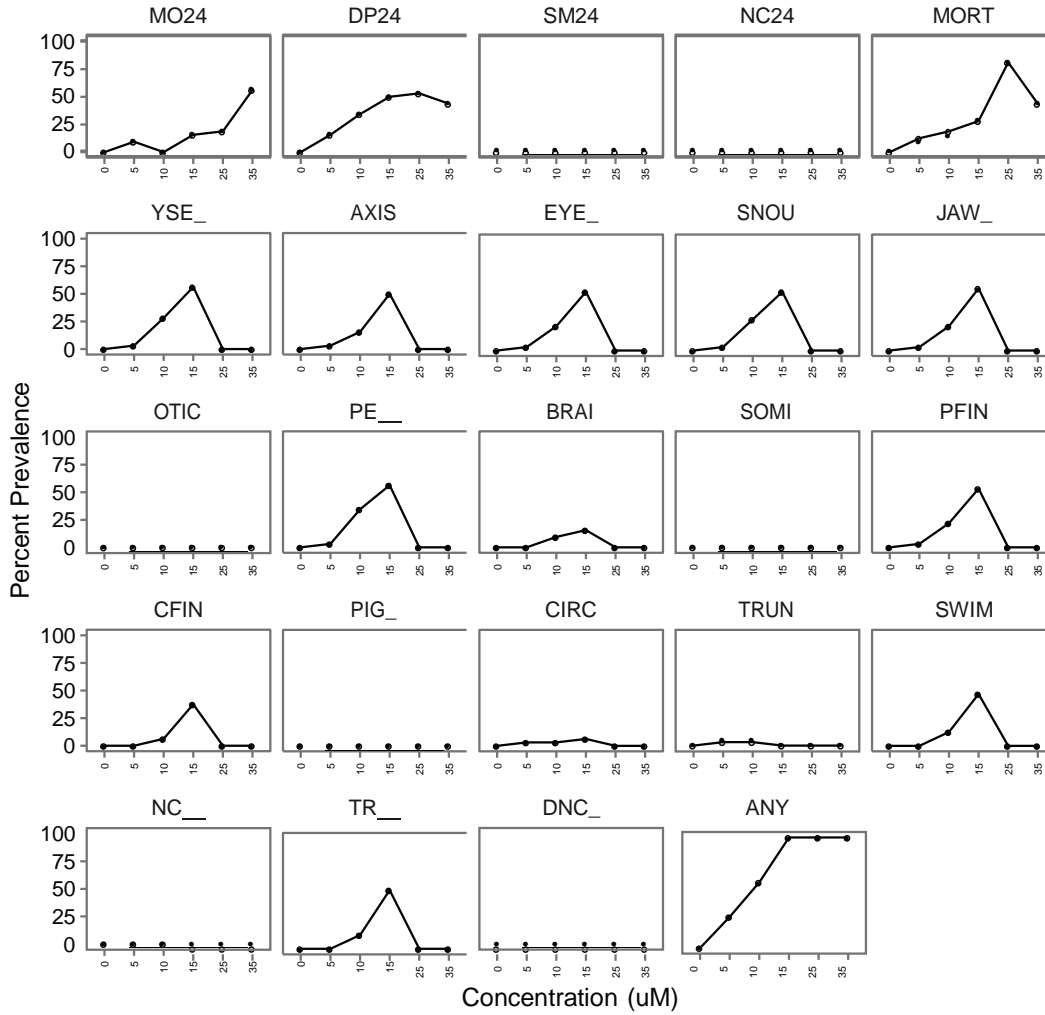
Number of Fisher Scoring iterations: 7

EC Values:

	Concentration	SE.log
p = 0.5:	36.16904	0.05221240
p = 0.6:	39.97500	0.05026920
p = 0.7:	44.56738	0.05433598
p = 0.8:	50.87221	0.06630027



Bisphenol_AF



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.65862 -0.02165 0.07961 0.38597 1.75674

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -8.358 1.471 -5.684 1.32e-08 ***
 CONC_log 9.067 1.479 6.131 8.72e-10 ***

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

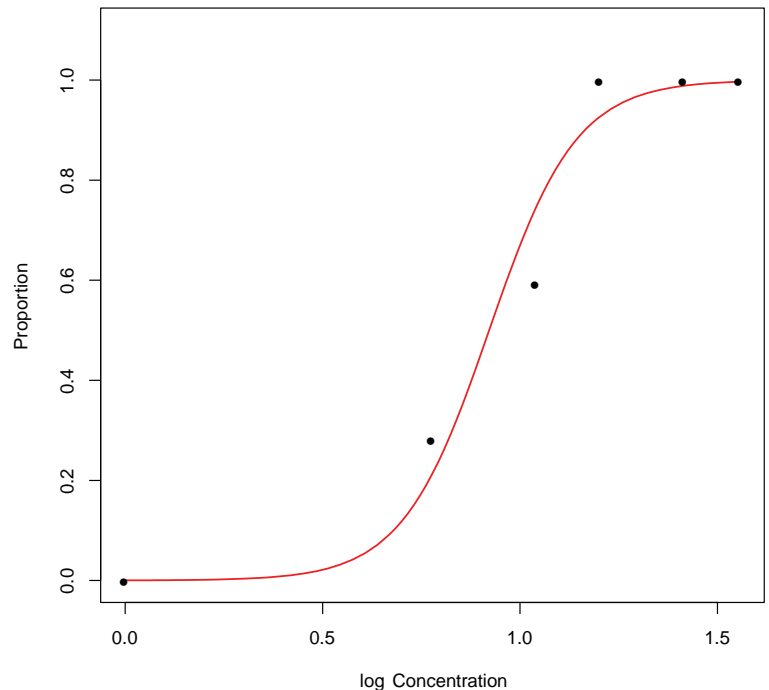
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 249.595 on 191 degrees of freedom
 Residual deviance: 91.381 on 190 degrees of freedom
 AIC: 95.381

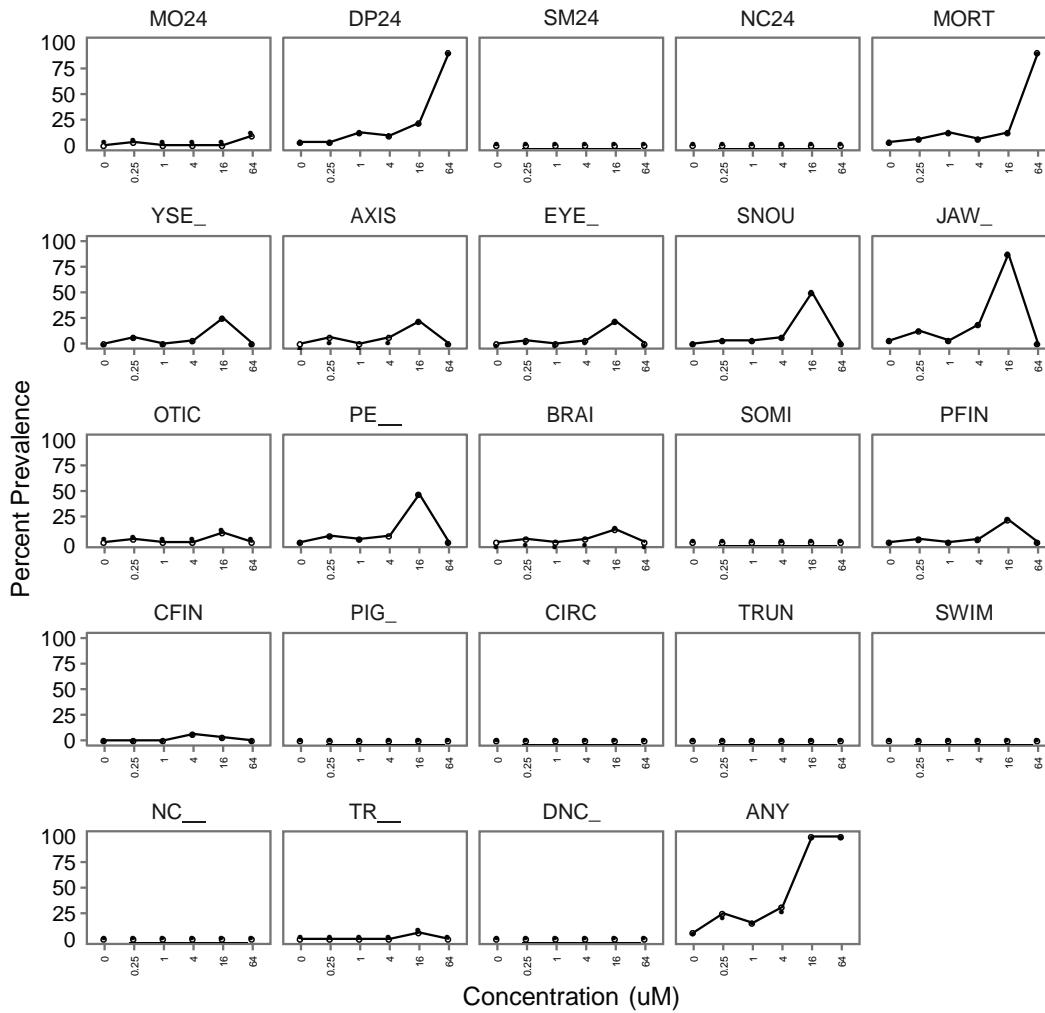
Number of Fisher Scoring iterations: 7

EC Values:

	Concentration	SE.log
p = 0.5:	7.352511	0.07359671
p = 0.6:	8.258394	0.07032117
p = 0.7:	9.357744	0.07172202
p = 0.8:	10.877113	0.08000540



butylparaben



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.2279 -0.6605 -0.3842 0.4670 2.2990

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.5689	0.3577	-7.181	6.90e-13 ***
CONC_log	3.8442	0.5195	7.400	1.37e-13 ***

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

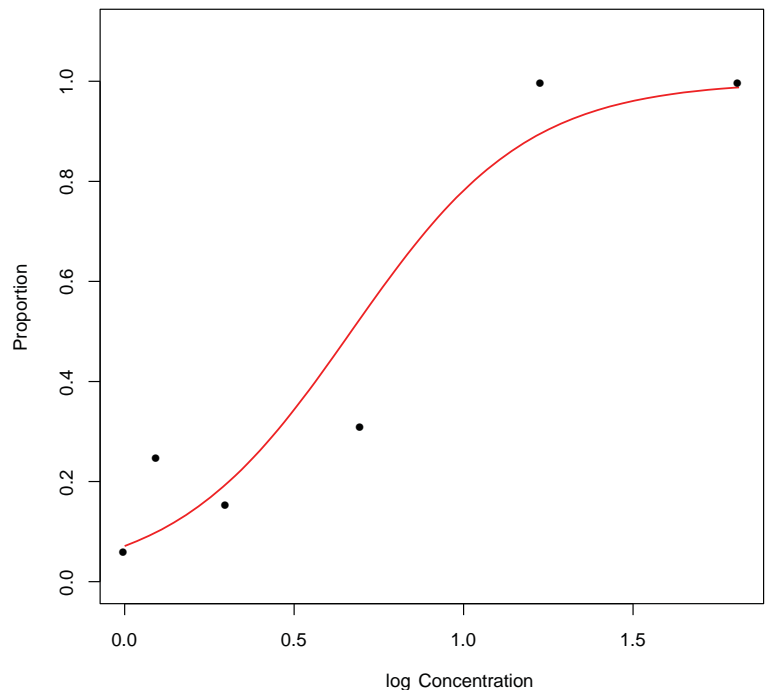
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 265.15 on 191 degrees of freedom
 Residual deviance: 138.62 on 190 degrees of freedom
 AIC: 142.62

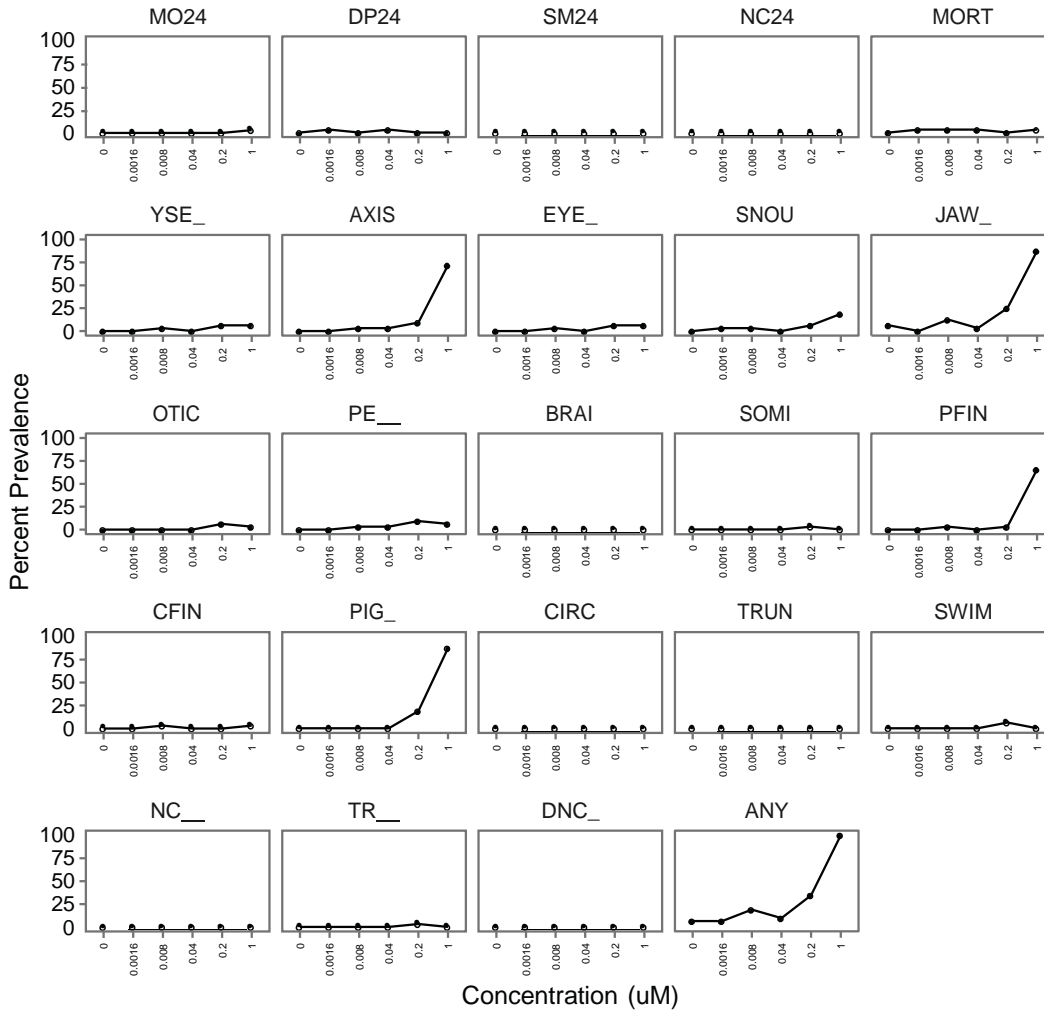
Number of Fisher Scoring iterations: 5

EC Values:

	Concentration	SE.log
p = 0.5:	3.658728	0.1443856
p = 0.6:	4.939393	0.1587761
p = 0.7:	6.738862	0.1821907
p = 0.8:	9.687784	0.2188184



CP-634384



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -0.9697 -0.5092 -0.4242 0.1328 2.2218

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -2.3796 0.2983 -7.977 1.50e-15 ***
 CONC_log 23.6075 4.7844 4.934 8.04e-07 ***

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

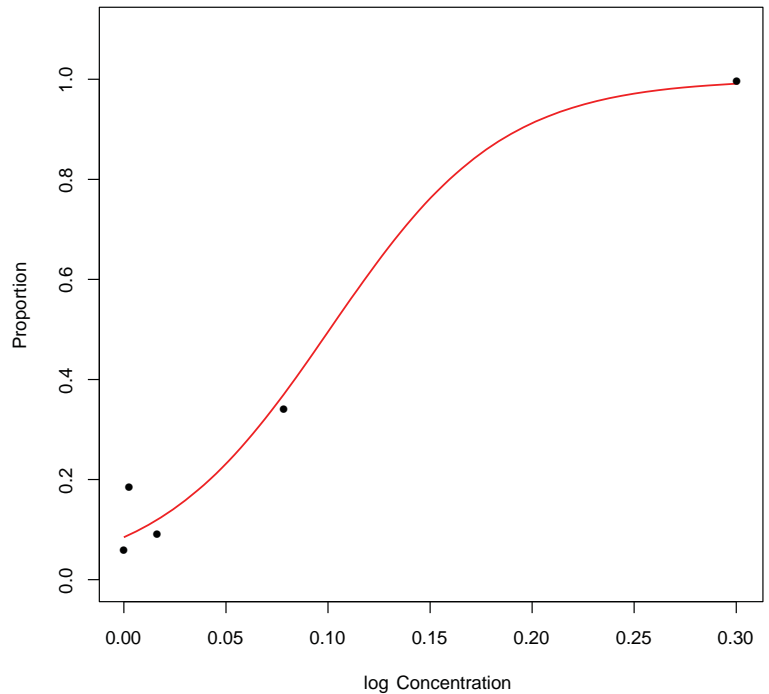
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 231.80 on 191 degrees of freedom
 Residual deviance: 126.14 on 190 degrees of freedom
 AIC: 130.14

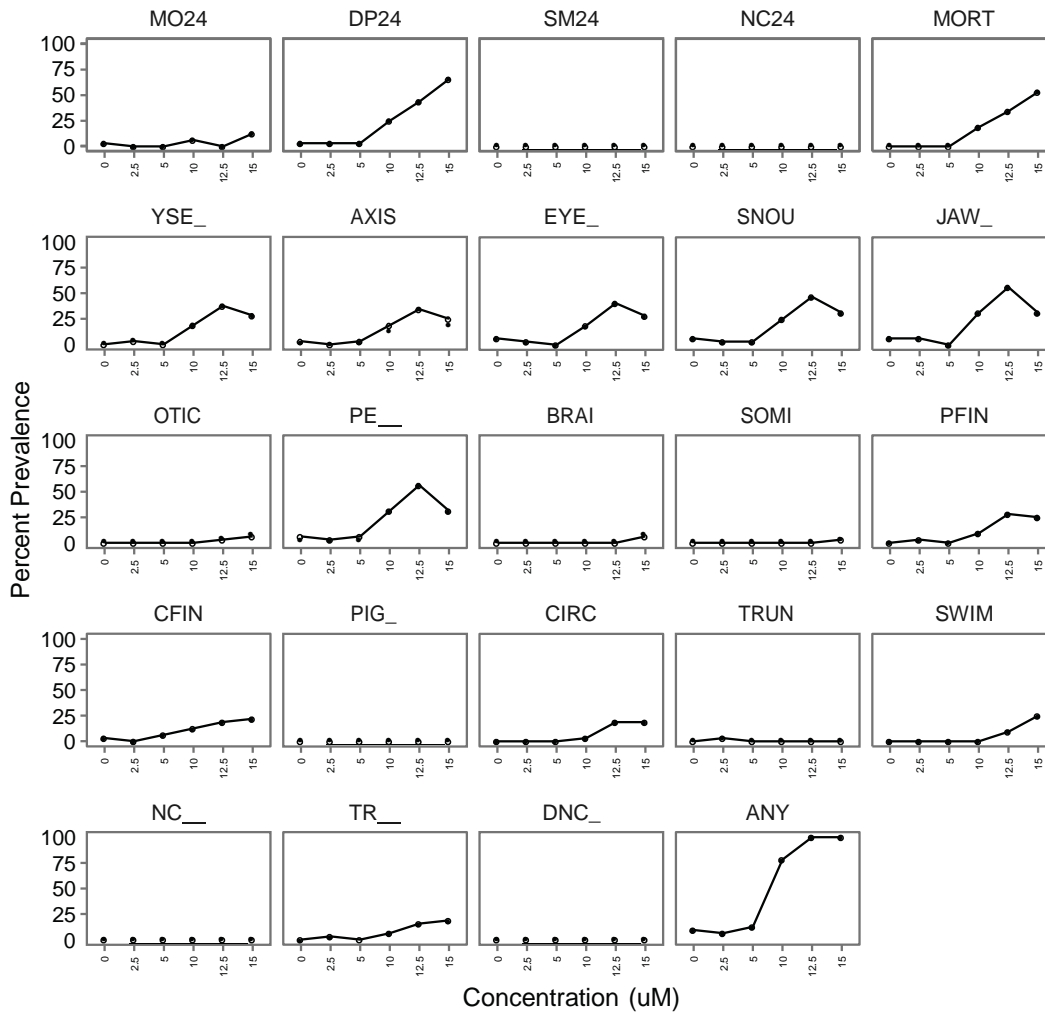
Number of Fisher Scoring iterations: 6

EC Values:

	Concentration	SE.log
p = 0.5:	0.2612395	0.03699463
p = 0.6:	0.3121177	0.04384646
p = 0.7:	0.3698991	0.05186088
p = 0.8:	0.4438436	0.06214655



Diisobutyl_phtalate



Model Output:

Call:
`glm(formula = ANY ~ CONC, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.8456 -0.3776 0.1691 0.3319 2.8259

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.97413	0.55447	-7.167	7.65e-13 ***
CONC	0.54763	0.06859	7.984	1.42e-15 ***

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

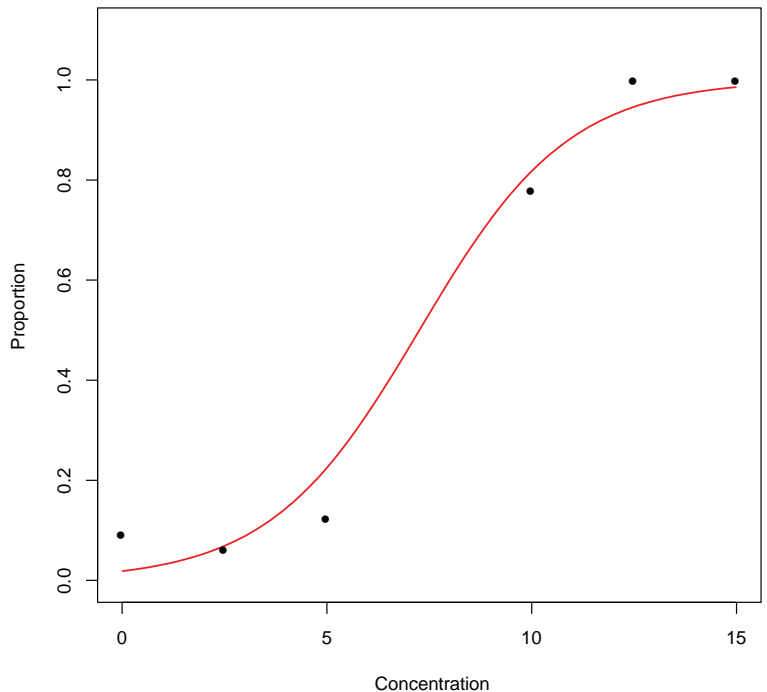
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 266.09 on 191 degrees of freedom
 Residual deviance: 104.57 on 190 degrees of freedom
 AIC: 108.57

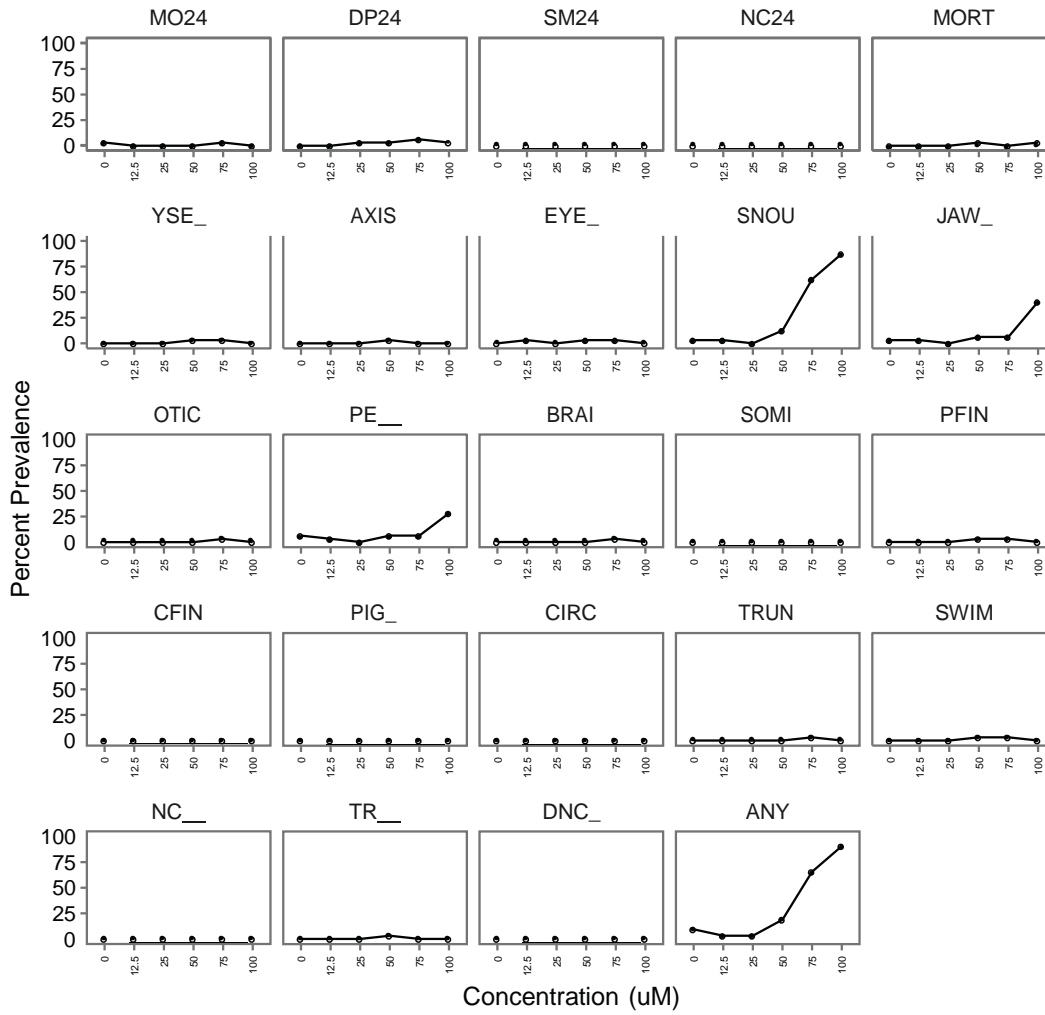
Number of Fisher Scoring iterations: 6

EC Values:

	Concentration	SE
p = 0.5:	7.256982	0.4708762
p = 0.6:	7.997385	0.4823395
p = 0.7:	8.804197	0.5139485
p = 0.8:	9.788435	0.5746450



Dimethipin



Model Output:

Call:
`glm(formula = ANY ~ CONC, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -2.0517 -0.4032 -0.2814 0.5098 2.8175

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.949975	0.533689	-7.401	1.35e-13 ***
CONC	0.059248	0.008045	7.364	1.78e-13 ***

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

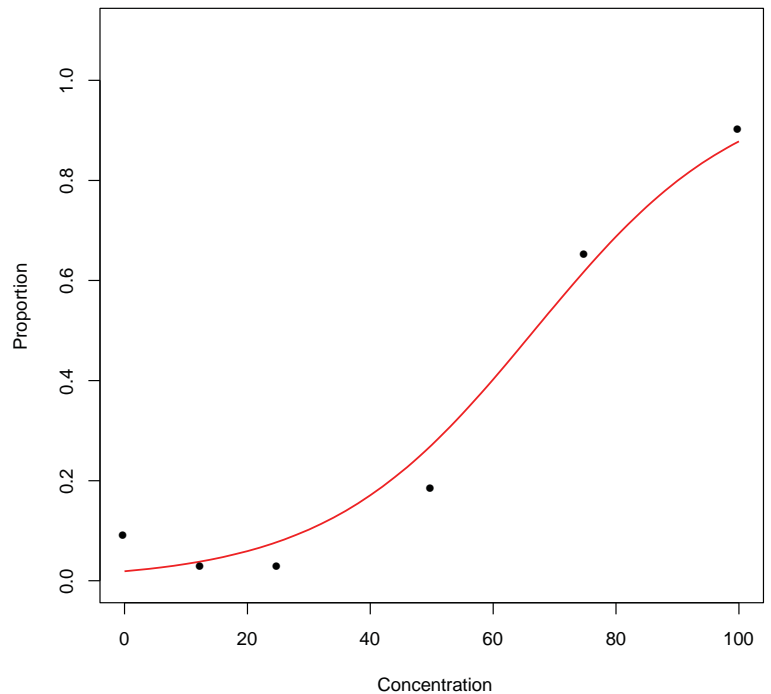
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 240.05 on 191 degrees of freedom
 Residual deviance: 137.65 on 190 degrees of freedom
 AIC: 141.65

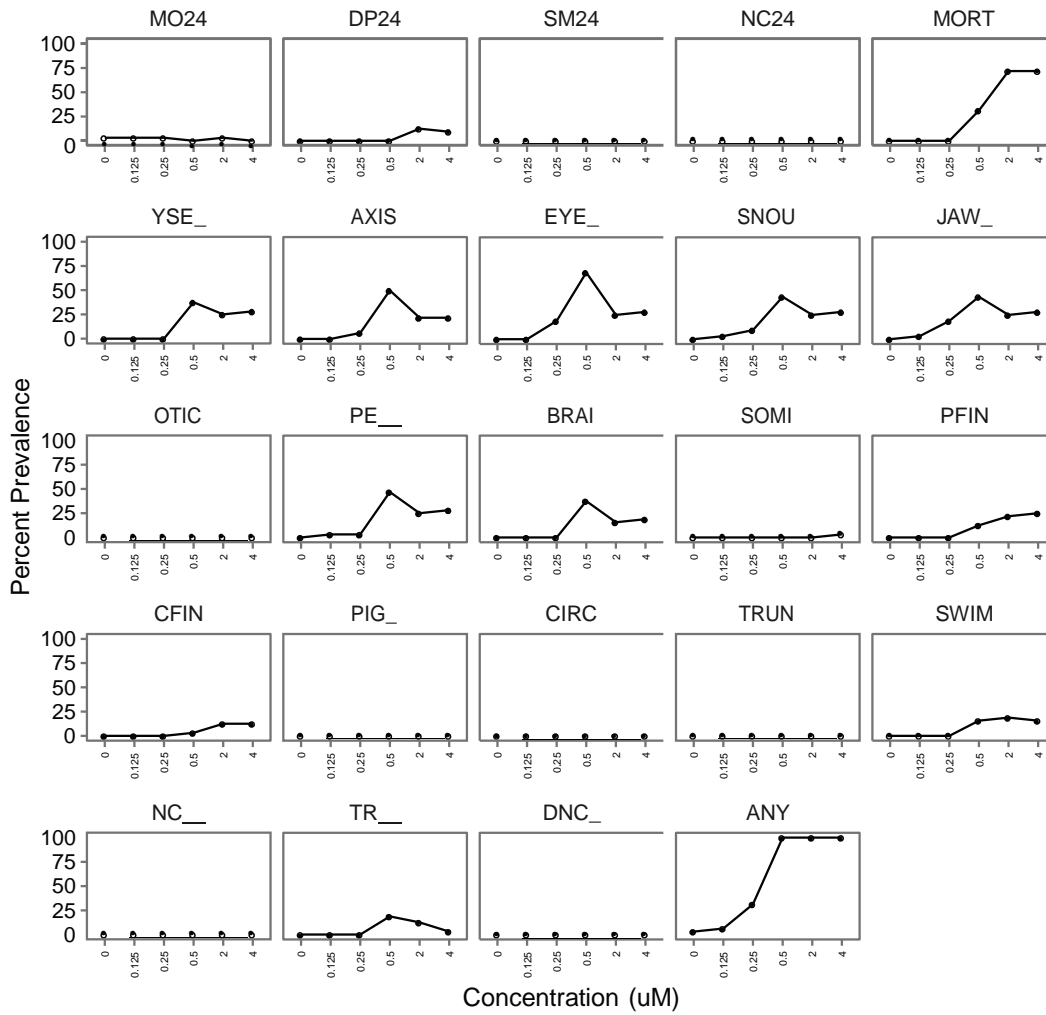
Number of Fisher Scoring iterations: 5

EC Values:

	Concentration	SE
p = 0.5:	66.66883	3.741229
p = 0.6:	73.51239	4.047338
p = 0.7:	80.96977	4.576616
p = 0.8:	90.06711	5.412083



Endrin



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -0.9689 -0.3515 0.0000 0.0002 3.2445

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -5.2582 0.9312 -5.647 1.63e-08 ***
 CONC_log 48.9692 9.2158 5.314 1.07e-07 ***

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

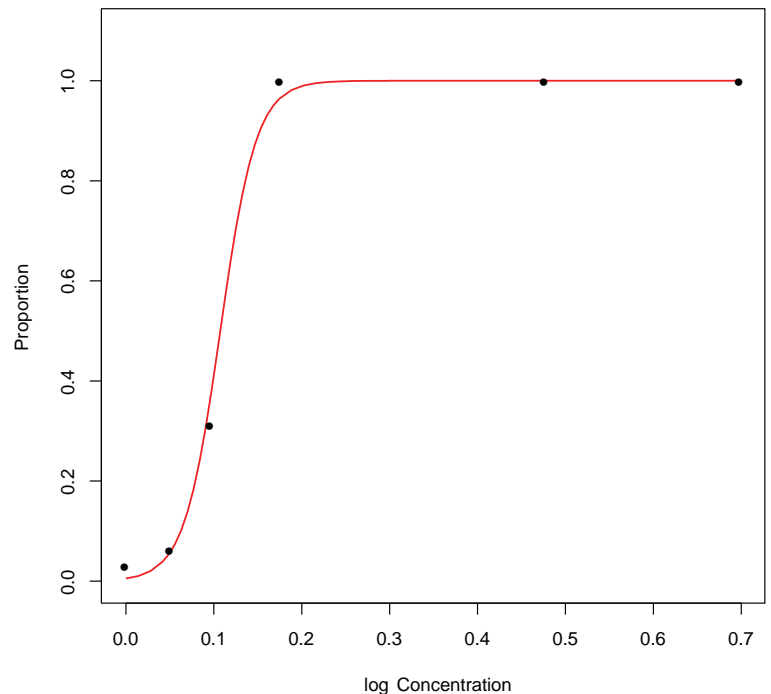
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 262.64 on 191 degrees of freedom
 Residual deviance: 68.28 on 190 degrees of freedom
 AIC: 72.28

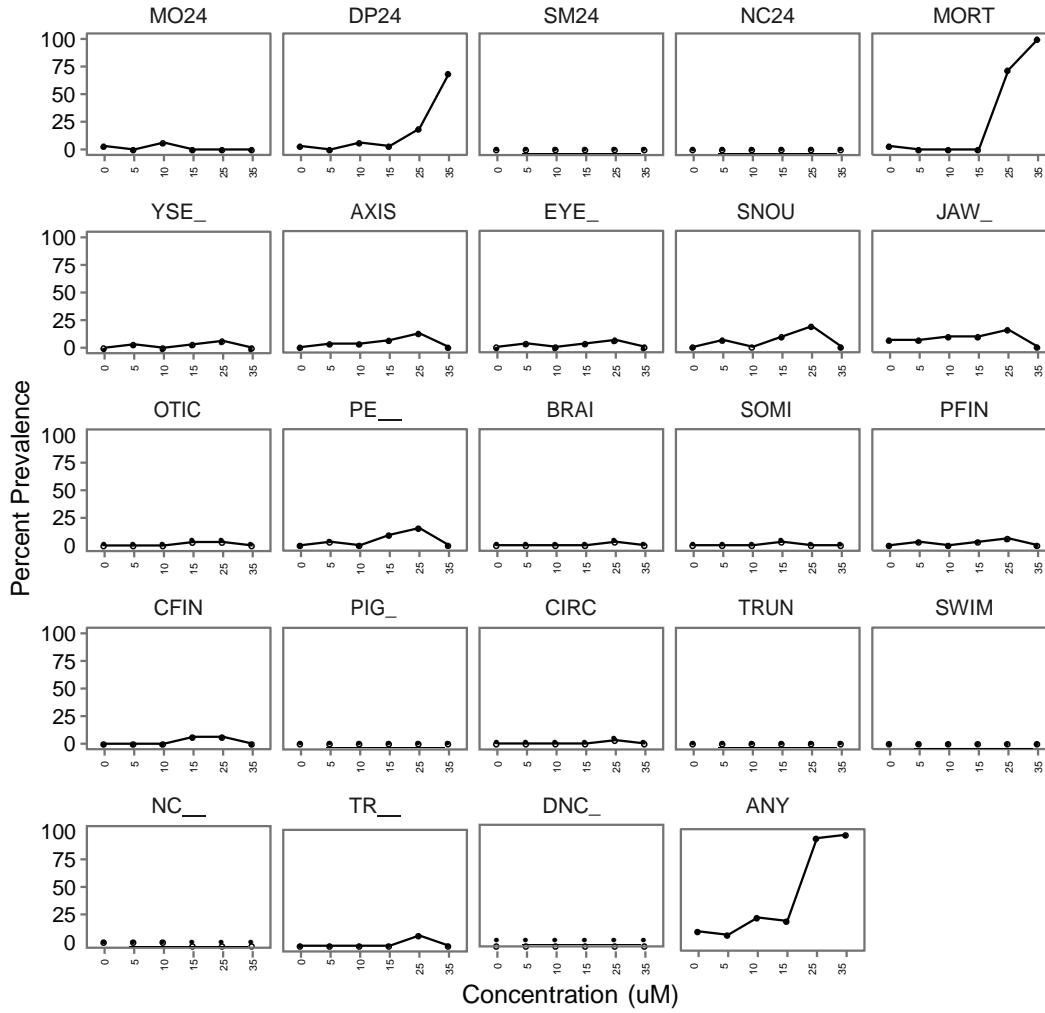
Number of Fisher Scoring iterations: 9

EC Values:

	Concentration	SE.log
p = 0.5:	0.2804947	0.01554328
p = 0.6:	0.3051420	0.01712235
p = 0.7:	0.3325405	0.01948519
p = 0.8:	0.3667443	0.02298653



Genistein



Model Output:

Call:
`glm(formula = ANY ~ CONC, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -2.0022 -0.7185 -0.2722 0.5380 2.5746

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -3.27736 0.44706 -7.331 2.29e-13 ***
 CONC 0.20548 0.02813 7.304 2.80e-13 ***

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

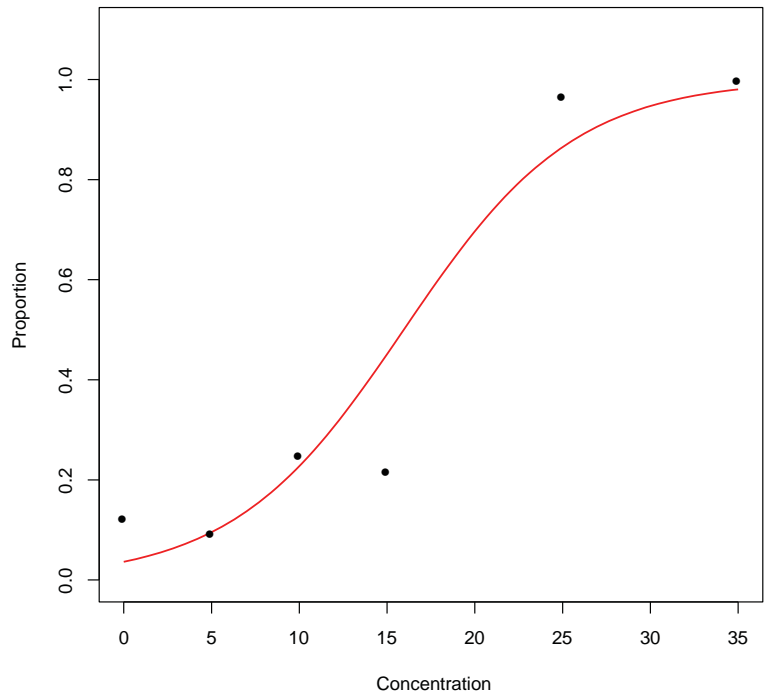
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 263.64 on 191 degrees of freedom
 Residual deviance: 139.98 on 190 degrees of freedom
 AIC: 143.98

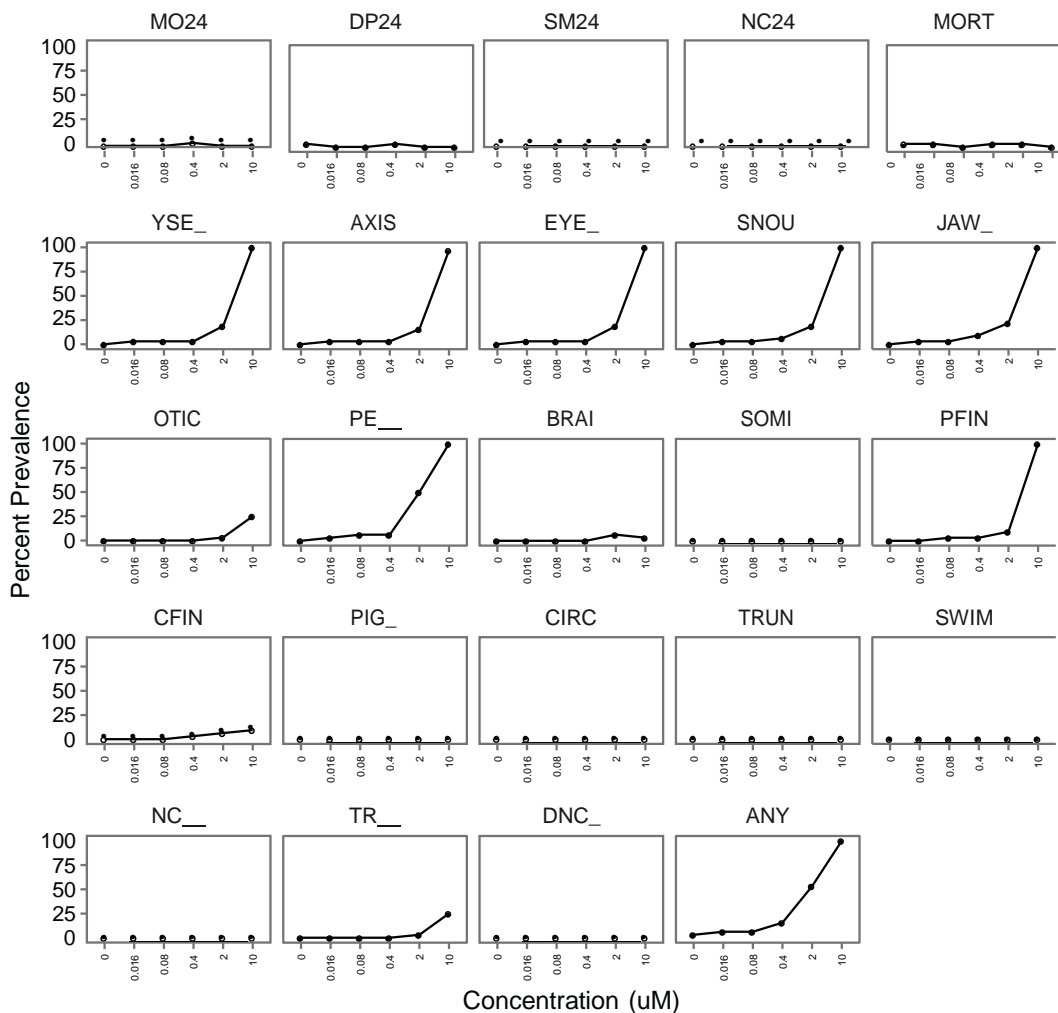
Number of Fisher Scoring iterations: 5

EC Values:

	Concentration	SE
p = 0.5:	15.94980	1.078416
p = 0.6:	17.92307	1.176533
p = 0.7:	20.07332	1.338486
p = 0.8:	22.69644	1.588446



haloperidol



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.3082 -0.3543 -0.3243 0.1753 2.4561

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.9660	0.3806	-7.792	6.58e-15 ***
CONC_log	6.8501	1.0066	6.805	1.01e-11 ***

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

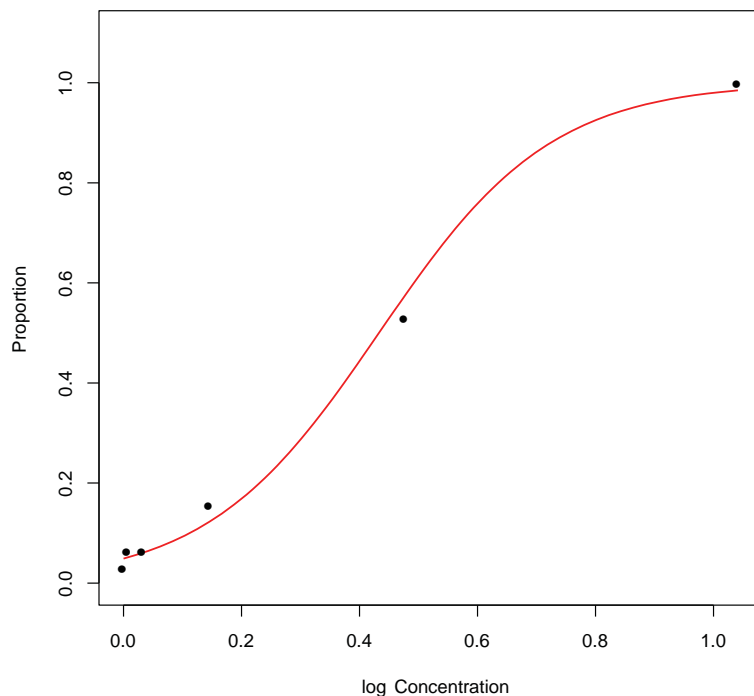
(Dispersion parameter for binomial family taken to be 1)

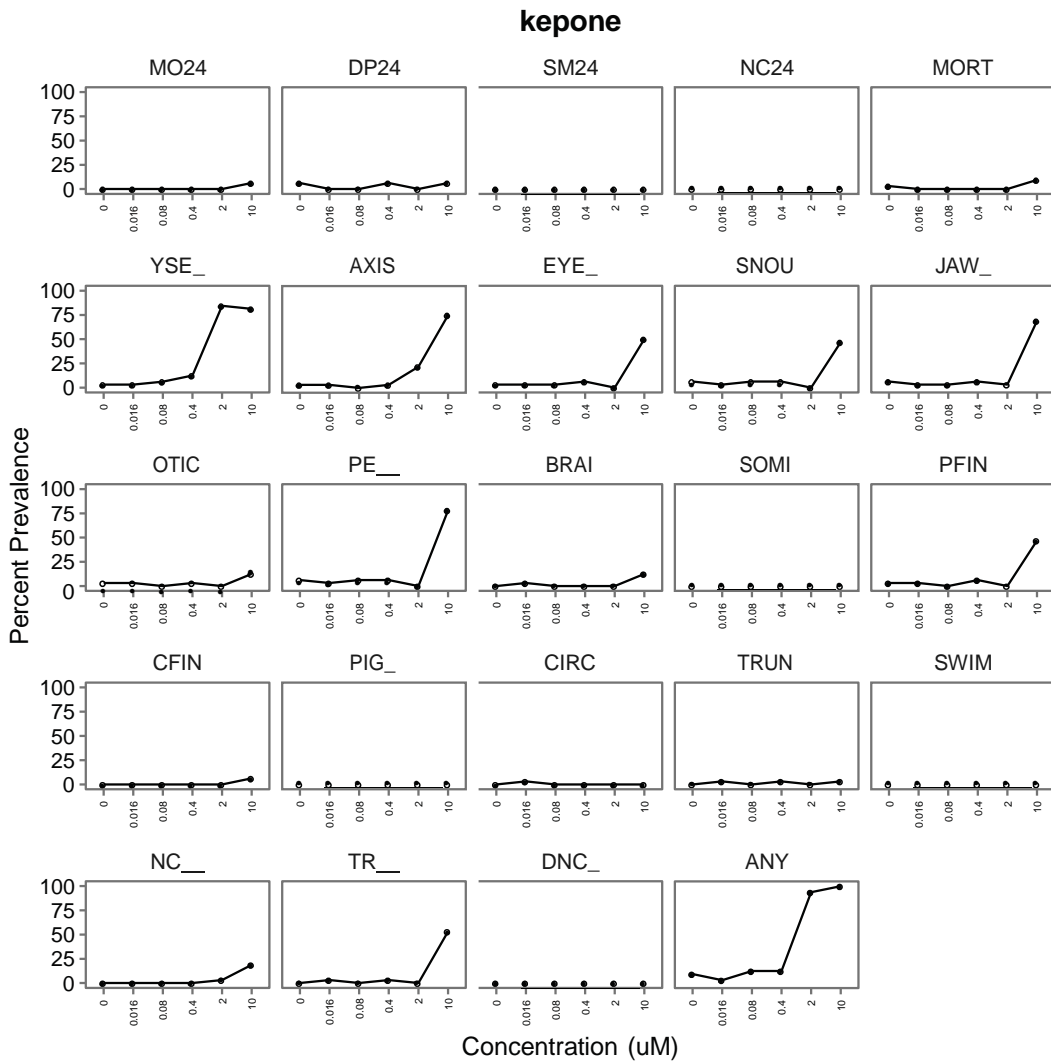
Null deviance: 236.90 on 191 degrees of freedom
 Residual deviance: 112.67 on 190 degrees of freedom
 AIC: 116.67

Number of Fisher Scoring iterations: 6

EC Values:

	Concentration	SE.log
p = 0.5:	1.710062	0.1004594
p = 0.6:	2.105777	0.1132710
p = 0.7:	2.603049	0.1302349
p = 0.8:	3.318713	0.1539999





Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -2.21041 -0.39247 -0.32852 0.01963 2.42748

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.8924	0.3722	-7.770	7.84e-15 ***
CONC_log	10.9917	1.6290	6.748	1.50e-11 ***

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

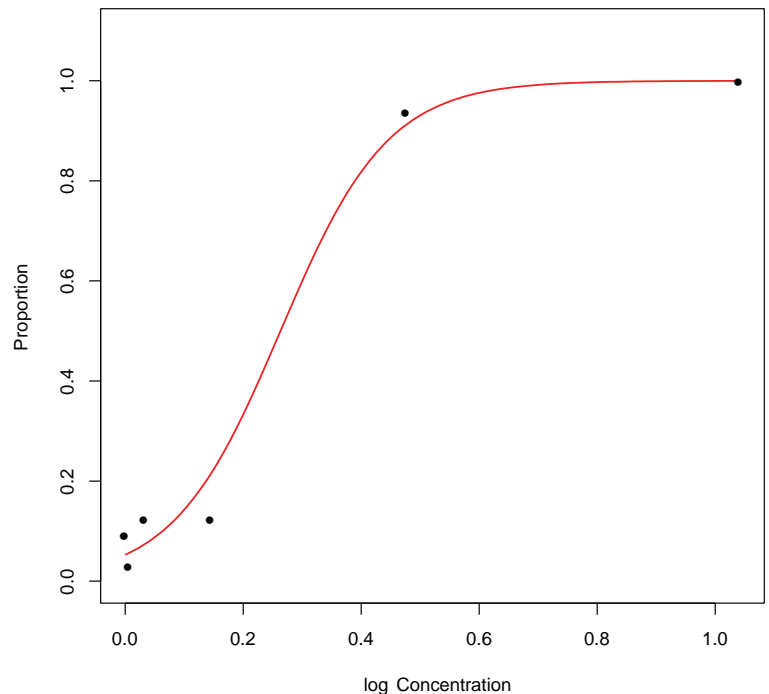
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 255.995 on 191 degrees of freedom
 Residual deviance: 96.431 on 190 degrees of freedom
 AIC: 100.43

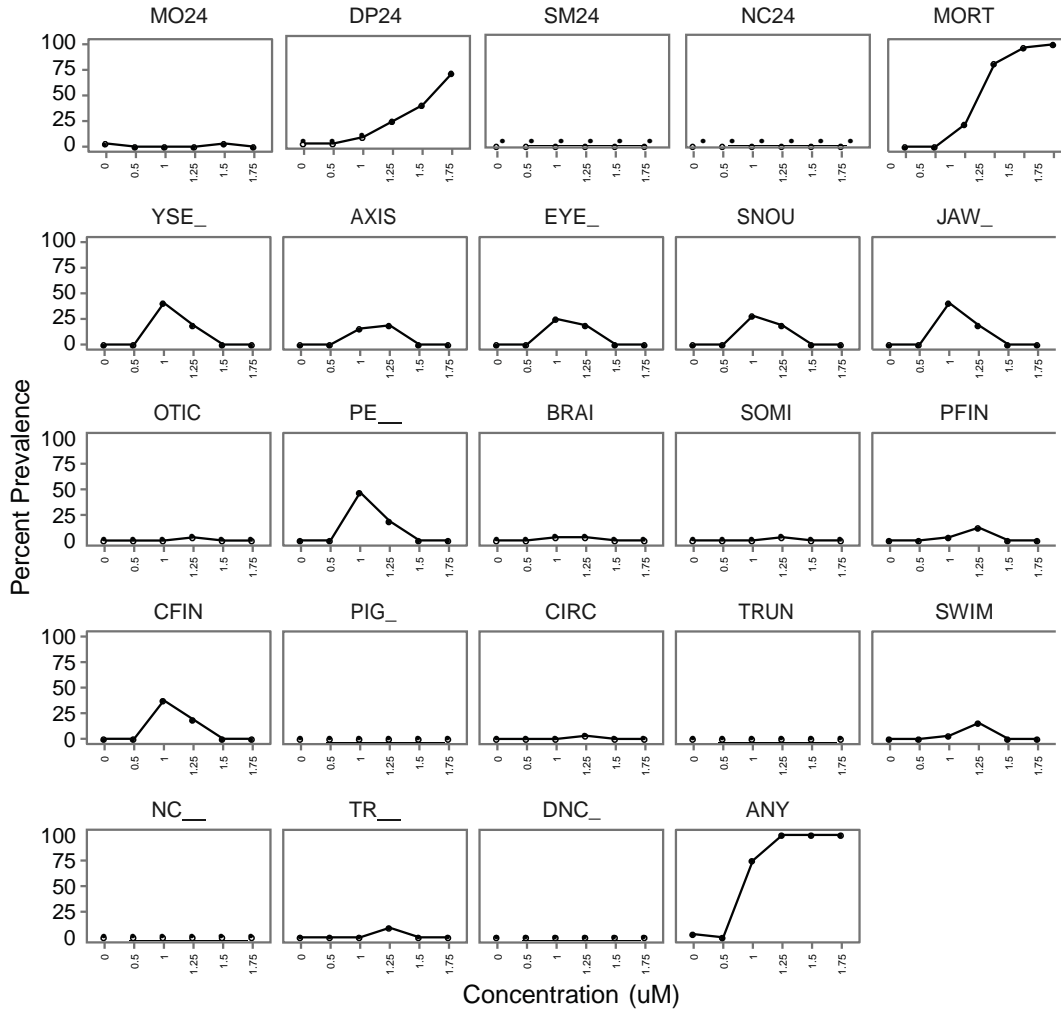
Number of Fisher Scoring iterations: 7

EC Values:

	Concentration	SE.log
p = 0.5:	0.8329025	0.07020508
p = 0.6:	0.9953889	0.07831717
p = 0.7:	1.1888922	0.08871710
p = 0.8:	1.4505350	0.10301181



Pentachlorophenol



Model Output:

Call:
`glm(formula = ANY ~ CONC, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.7269 -0.0329 0.0286 0.2531 3.8783

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-7.520	1.523	-4.938	7.87e-07 ***
CONC	8.756	1.547	5.660	1.52e-08 ***

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

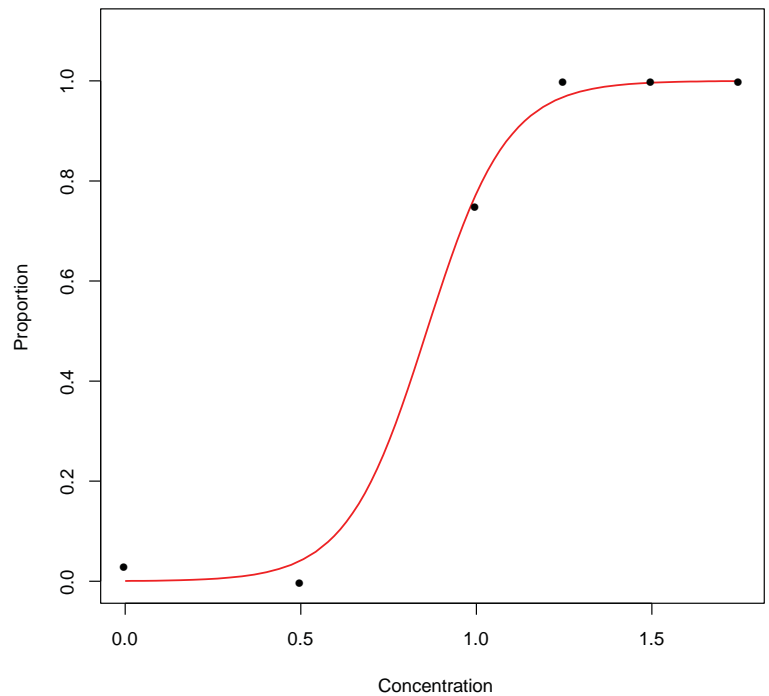
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 253.00 on 191 degrees of freedom
 Residual deviance: 56.19 on 190 degrees of freedom
 AIC: 60.19

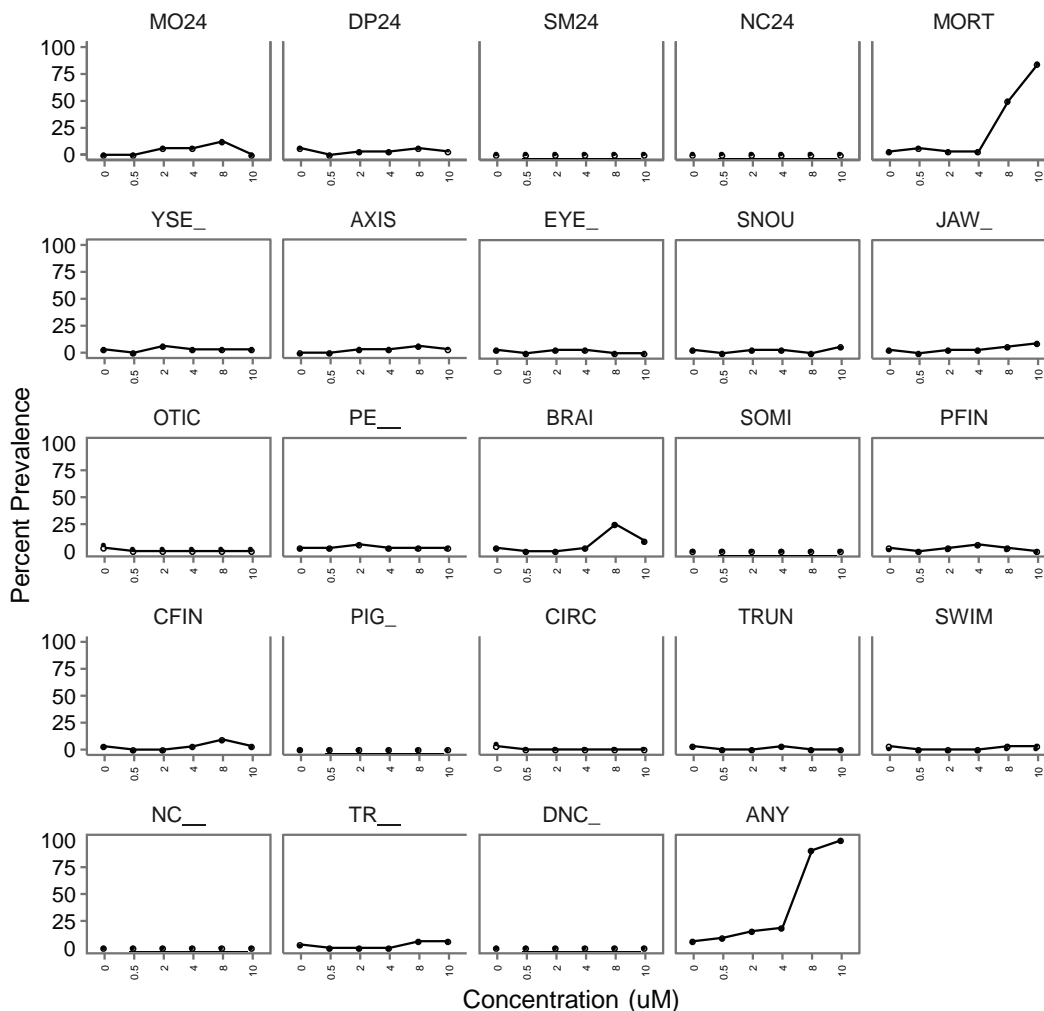
Number of Fisher Scoring iterations: 7

EC Values:

	Concentration	SE
p = 0.5:	0.8588398	0.04402178
p = 0.6:	0.9051472	0.04147522
p = 0.7:	0.9556081	0.04043983
p = 0.8:	1.0171659	0.04179931



Perfluorooctanesulfonic_acid



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.8455 -0.6369 -0.1497 0.4924 2.9992

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.4864	0.6522	-6.879	6.01e-12 ***
CONC_log	6.2754	0.8555	7.336	2.21e-13 ***

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

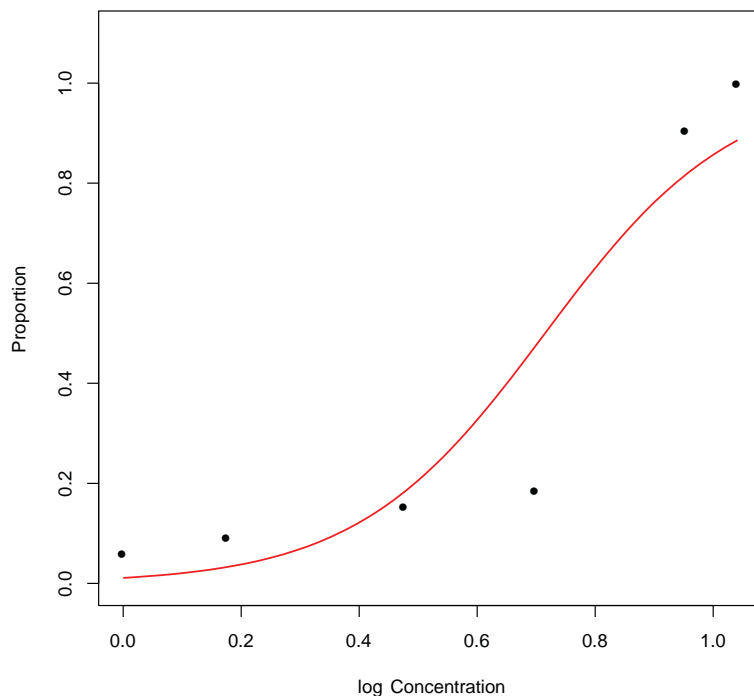
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 258.60 on 191 degrees of freedom
 Residual deviance: 141.07 on 190 degrees of freedom
 AIC: 145.07

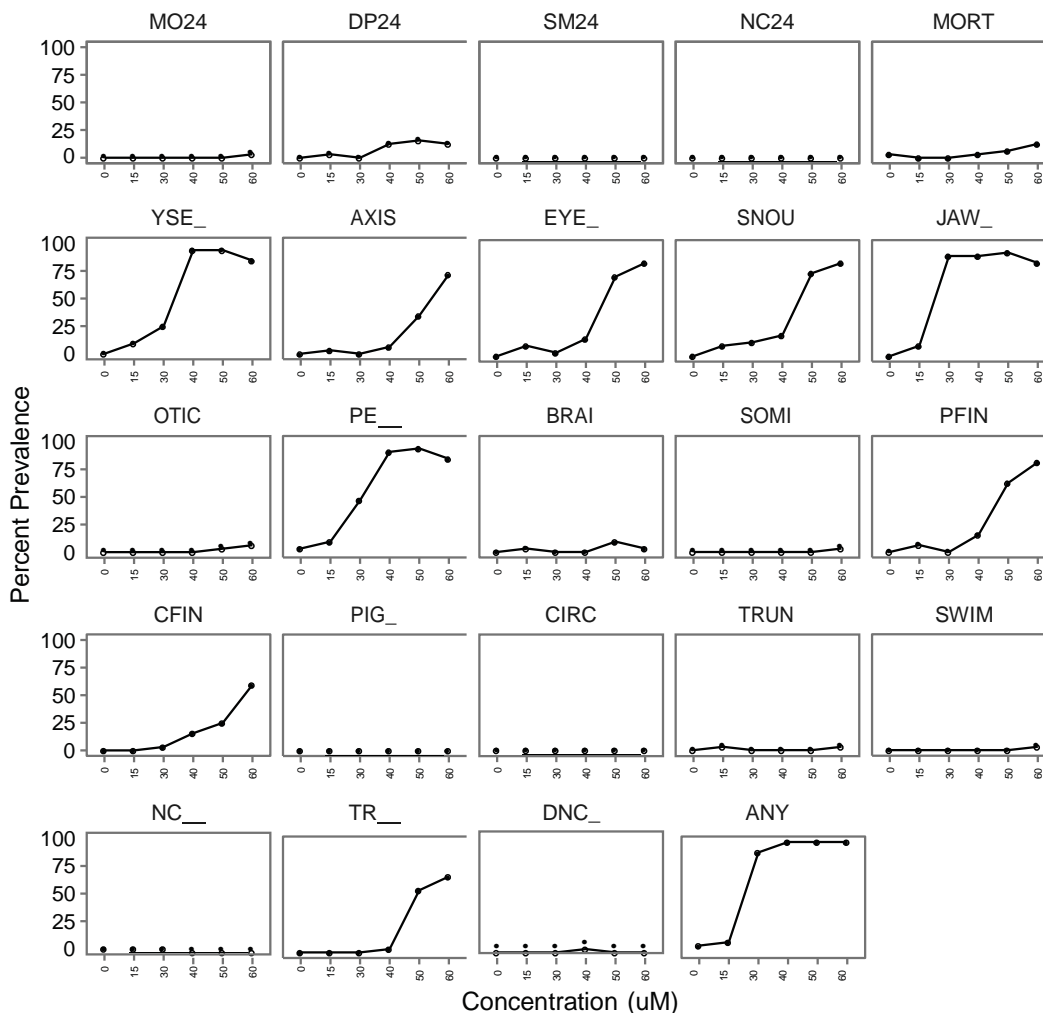
Number of Fisher Scoring iterations: 5

EC Values:

	Concentration	SE.log
p = 0.5:	4.187089	0.08110138
p = 0.6:	5.019158	0.08340946
p = 0.7:	6.078532	0.09185229
p = 0.8:	7.626487	0.10863450



Propiconazole



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.9077 -0.0086 0.2611 0.3771 4.5197

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-10.214	1.833	-5.571	2.54e-08 ***
CONC_log	7.950	1.300	6.118	9.49e-10 ***

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

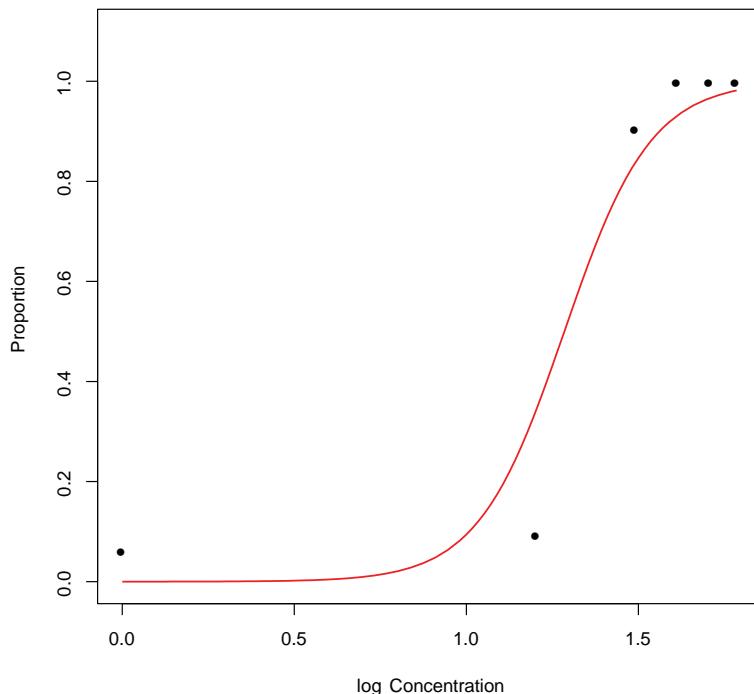
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 241.55 on 191 degrees of freedom
 Residual deviance: 100.88 on 190 degrees of freedom
 AIC: 104.88

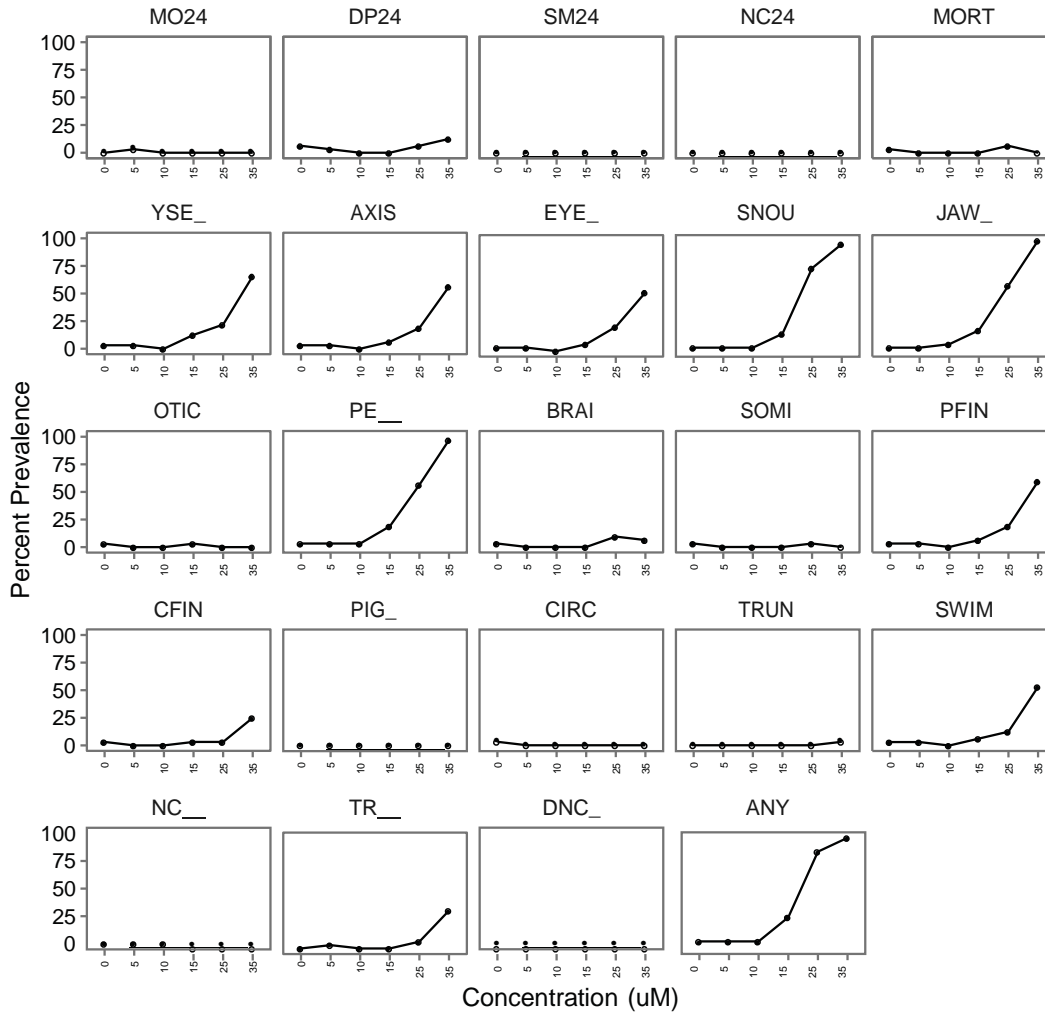
Number of Fisher Scoring iterations: 7

EC Values:

	Concentration	SE.log
p = 0.5:	18.26342	0.08914680
p = 0.6:	20.66380	0.08080198
p = 0.7:	23.62127	0.07705336
p = 0.8:	27.78113	0.08089292



Propylparaben



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.7005 -0.6783 -0.0212 0.4730 4.0997

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -8.404 1.272 -6.606 3.95e-11 ***
 CONC_log 6.771 1.011 6.701 2.08e-11 ***

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

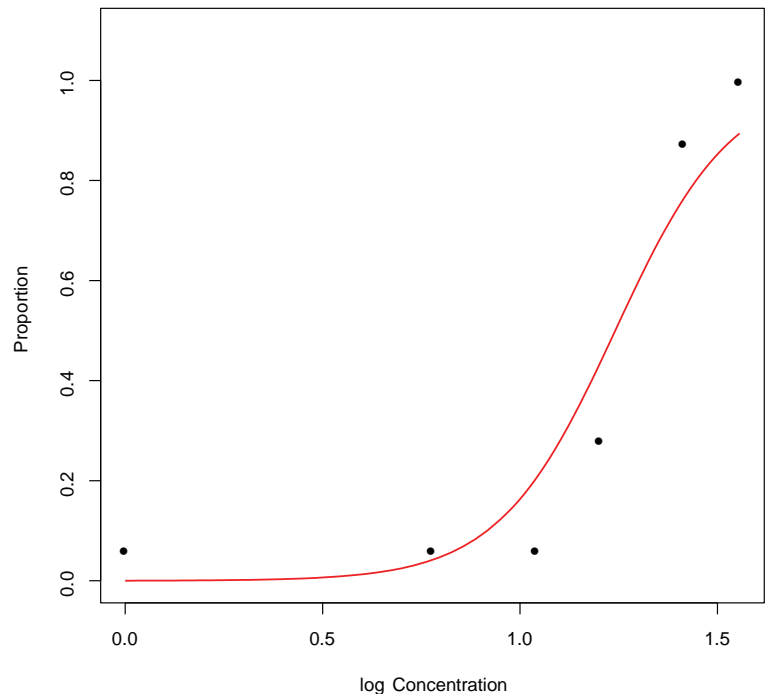
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 256.91 on 191 degrees of freedom
 Residual deviance: 144.15 on 190 degrees of freedom
 AIC: 148.15

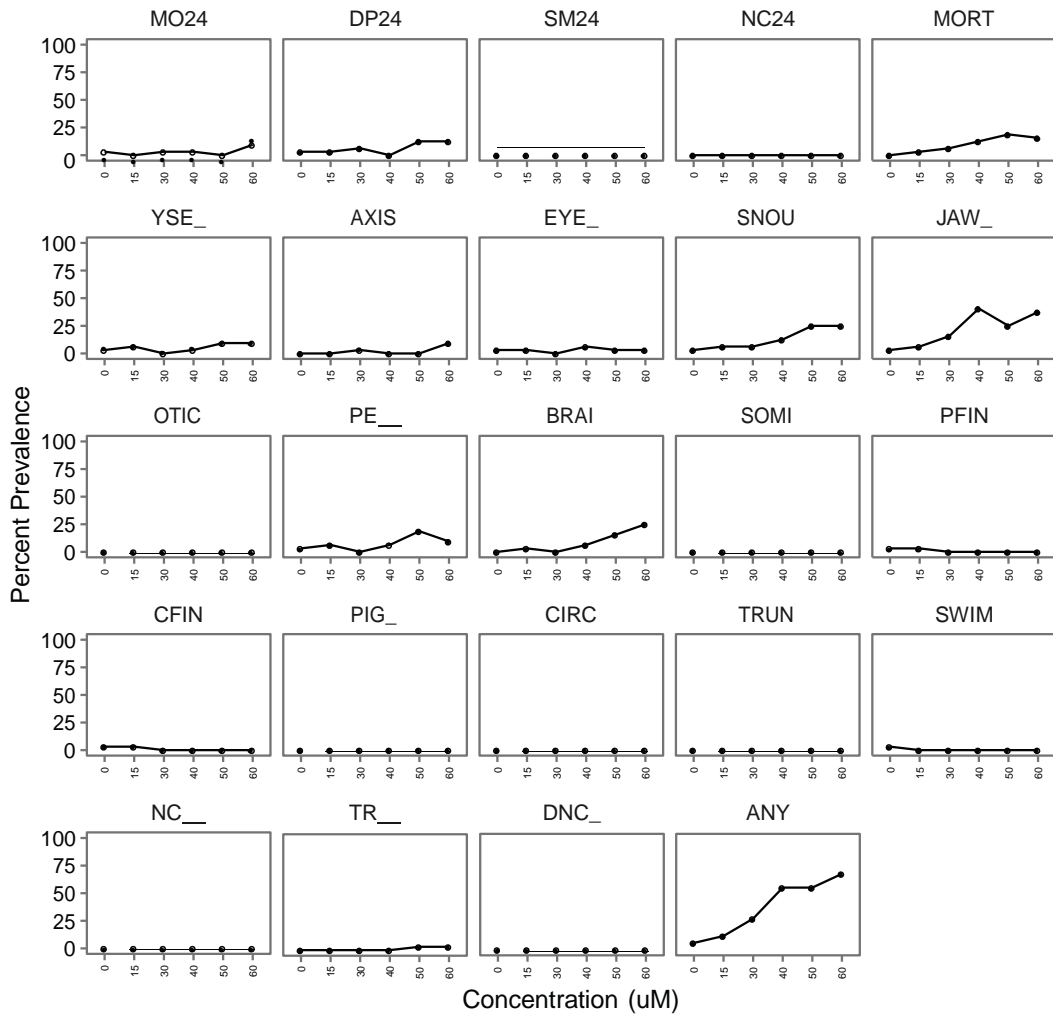
Number of Fisher Scoring iterations: 6

EC Values:

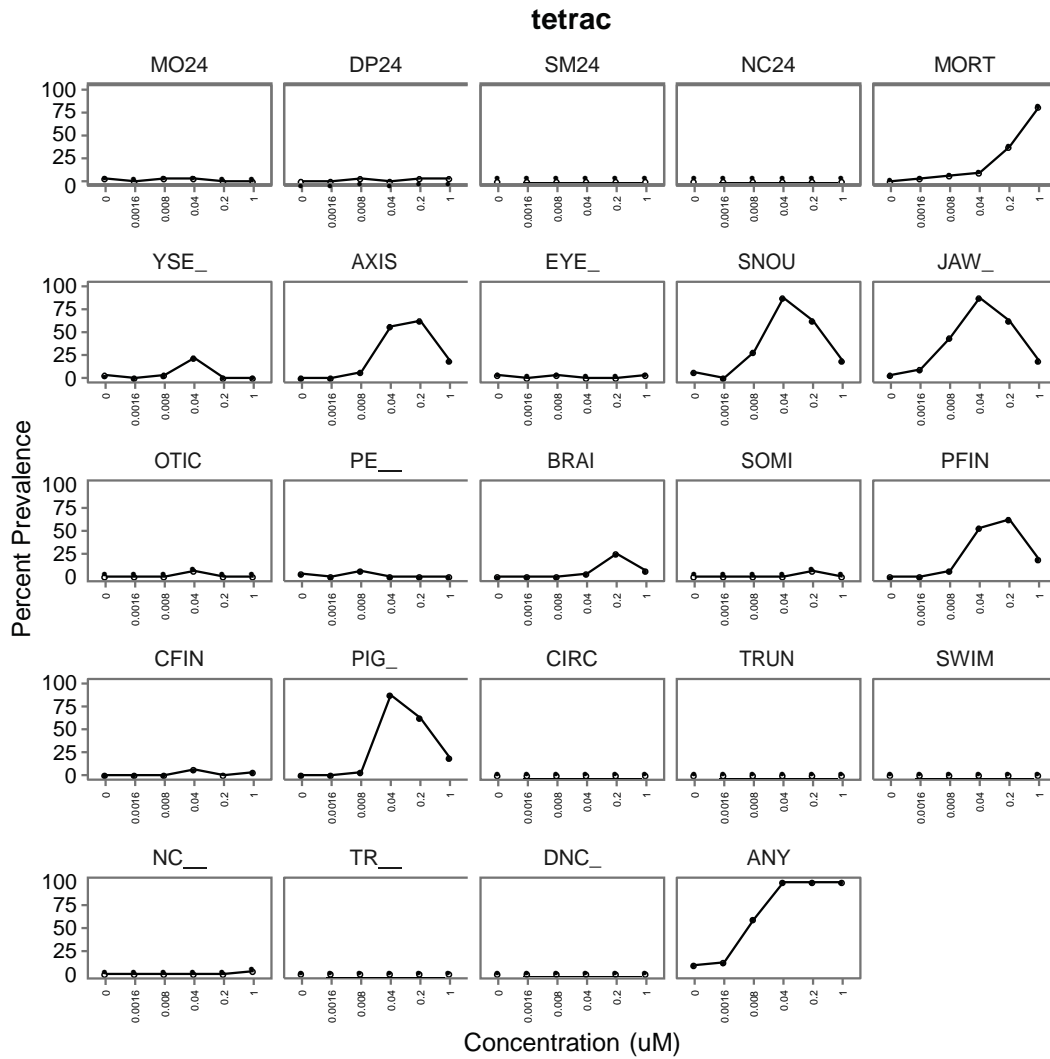
	Concentration	SE.log
p = 0.5:	16.42256	0.07319316
p = 0.6:	18.99837	0.07625754
p = 0.7:	22.24067	0.08604209
p = 0.8:	26.91596	0.10460158



Raloxifene_hydrochloride



**Precipitation at 60 uM
EC set to 50 uM**



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.33781 -0.41845 0.00000 0.00523 2.22666

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -2.3915 0.4545 -5.262 1.43e-07 ***
 CONC_log 797.8440 174.7635 4.565 4.99e-06 ***

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

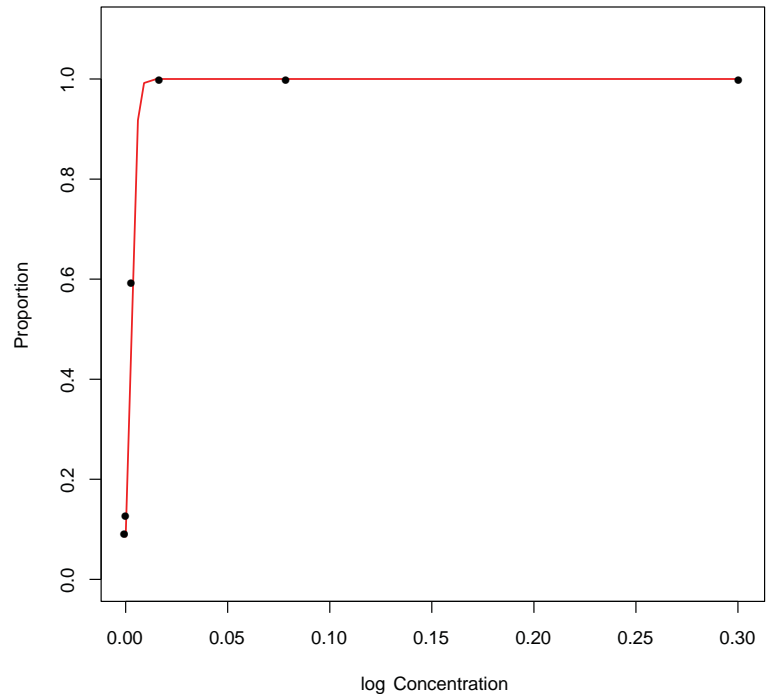
(Dispersion parameter for binomial family taken to be 1)

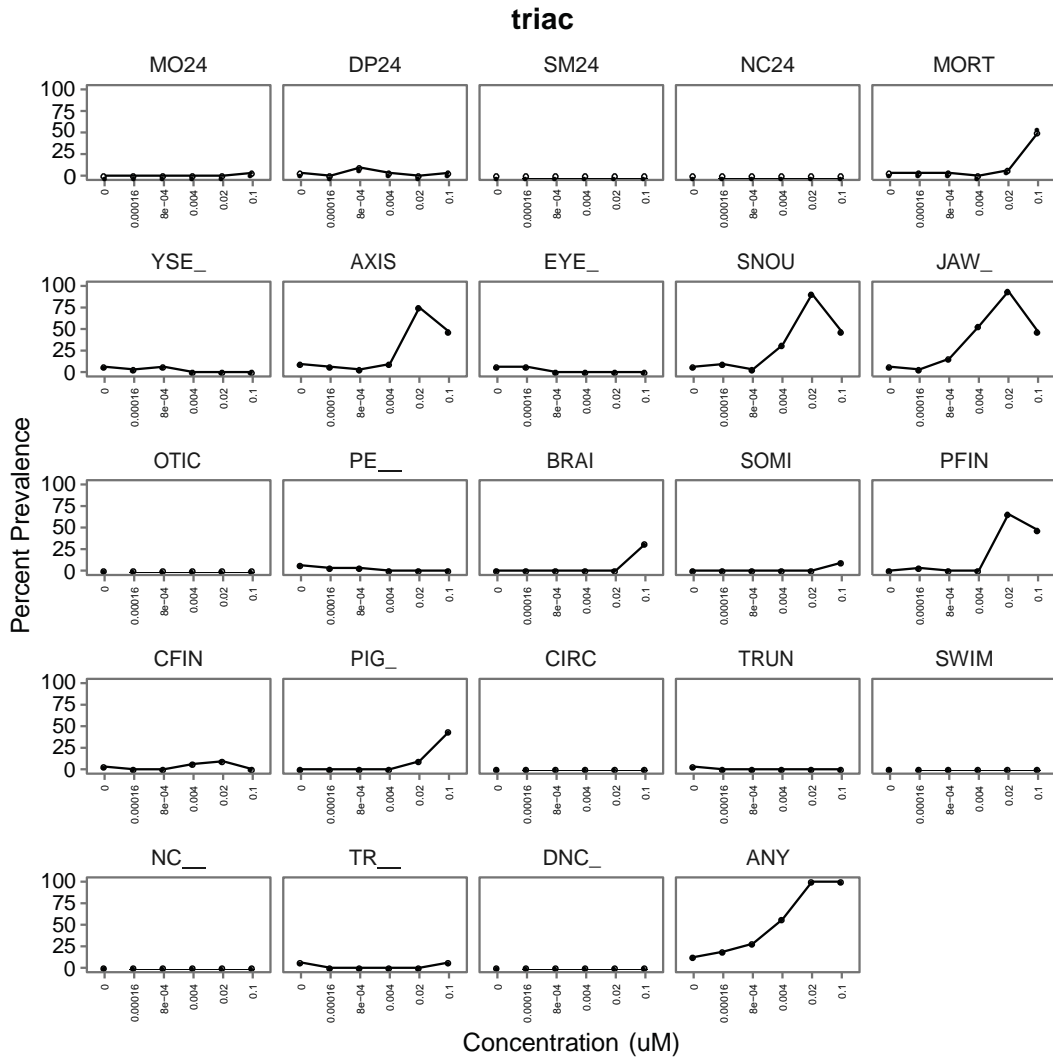
Null deviance: 251.908 on 191 degrees of freedom
 Residual deviance: 87.339 on 190 degrees of freedom
 AIC: 91.339

Number of Fisher Scoring iterations: 12

EC Values:

	Concentration	SE.log
p = 0.5:	0.006925638	0.0008944543
p = 0.6:	0.008104608	0.0010476304
p = 0.7:	0.009390896	0.0012536536
p = 0.8:	0.010962274	0.0015368660





Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.30825 -0.63217 0.00000 0.02898 1.88198

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.5844	0.2812	-5.635	1.75e-08 ***
CONC_log	1088.3107	267.2499	4.072	4.66e-05 ***

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

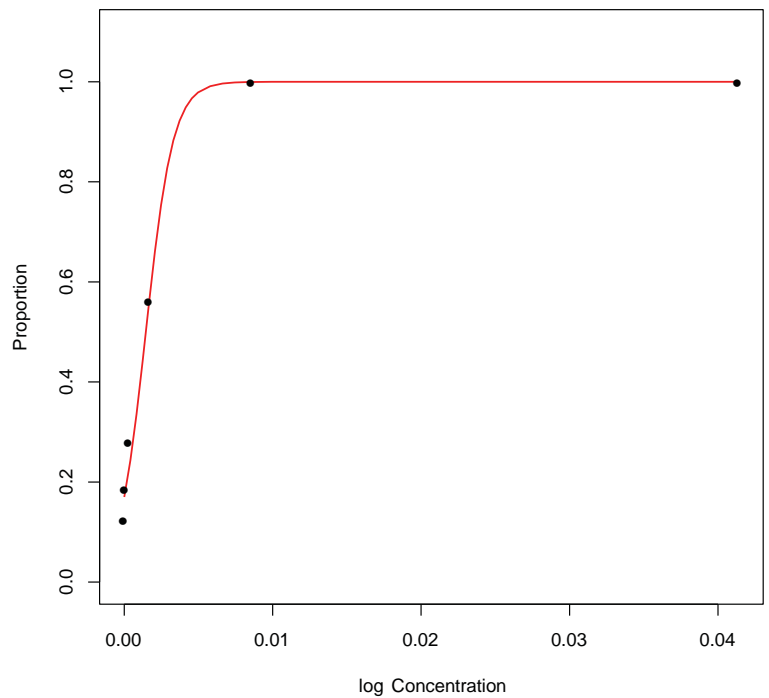
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 265.65 on 191 degrees of freedom
 Residual deviance: 137.89 on 190 degrees of freedom
 AIC: 141.89

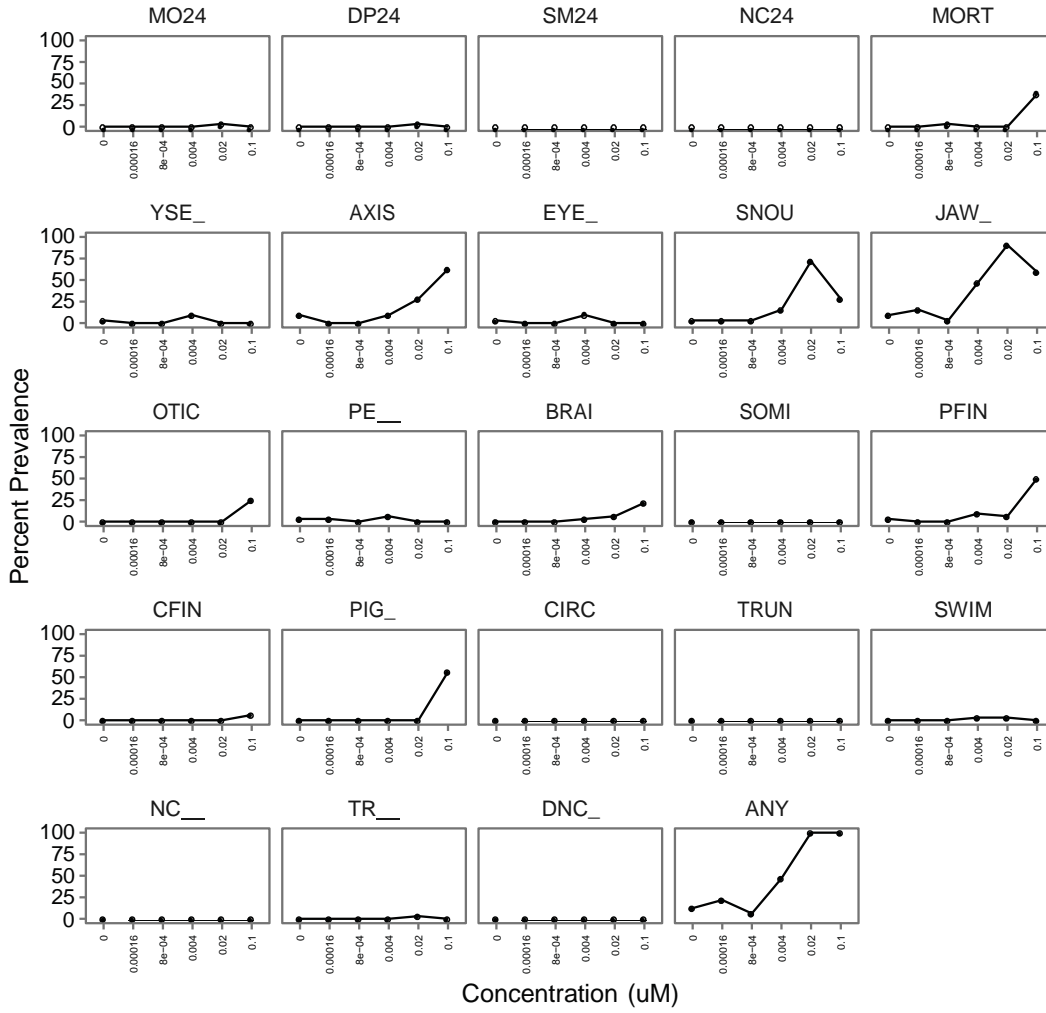
Number of Fisher Scoring iterations: 9

EC Values:

	Concentration	SE.log
p = 0.5:	0.003357774	0.0006154304
p = 0.6:	0.004218884	0.0007765824
p = 0.7:	0.005158071	0.0009740526
p = 0.8:	0.006304985	0.0012302781



335_triiodothyronine



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -1.10392 -0.52880 -0.51132 0.04428 2.04905

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -1.9686 0.3144 -6.261 3.83e-10 ***
 CONC_log 1034.3437 268.4446 3.853 0.000117 ***

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

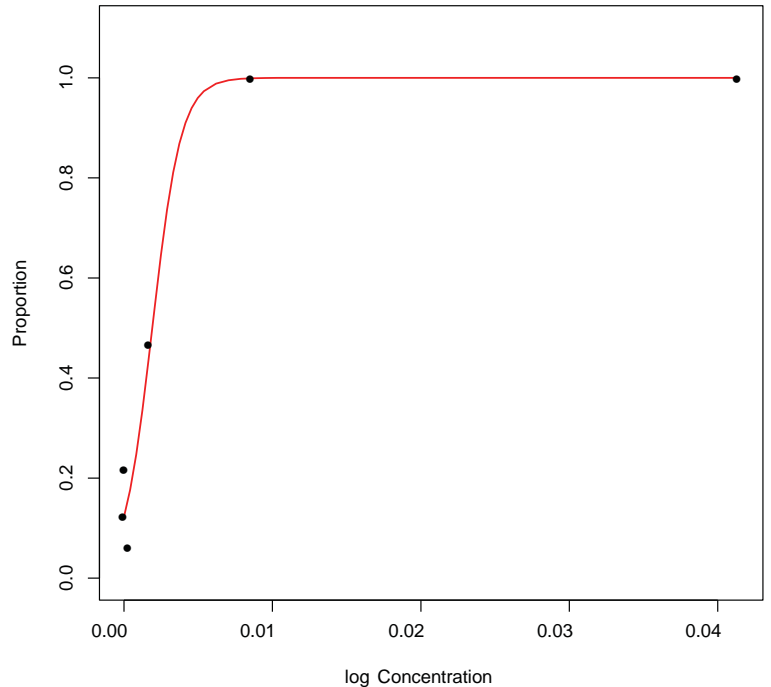
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 265.84 on 191 degrees of freedom
 Residual deviance: 122.04 on 190 degrees of freedom
 AIC: 126.04

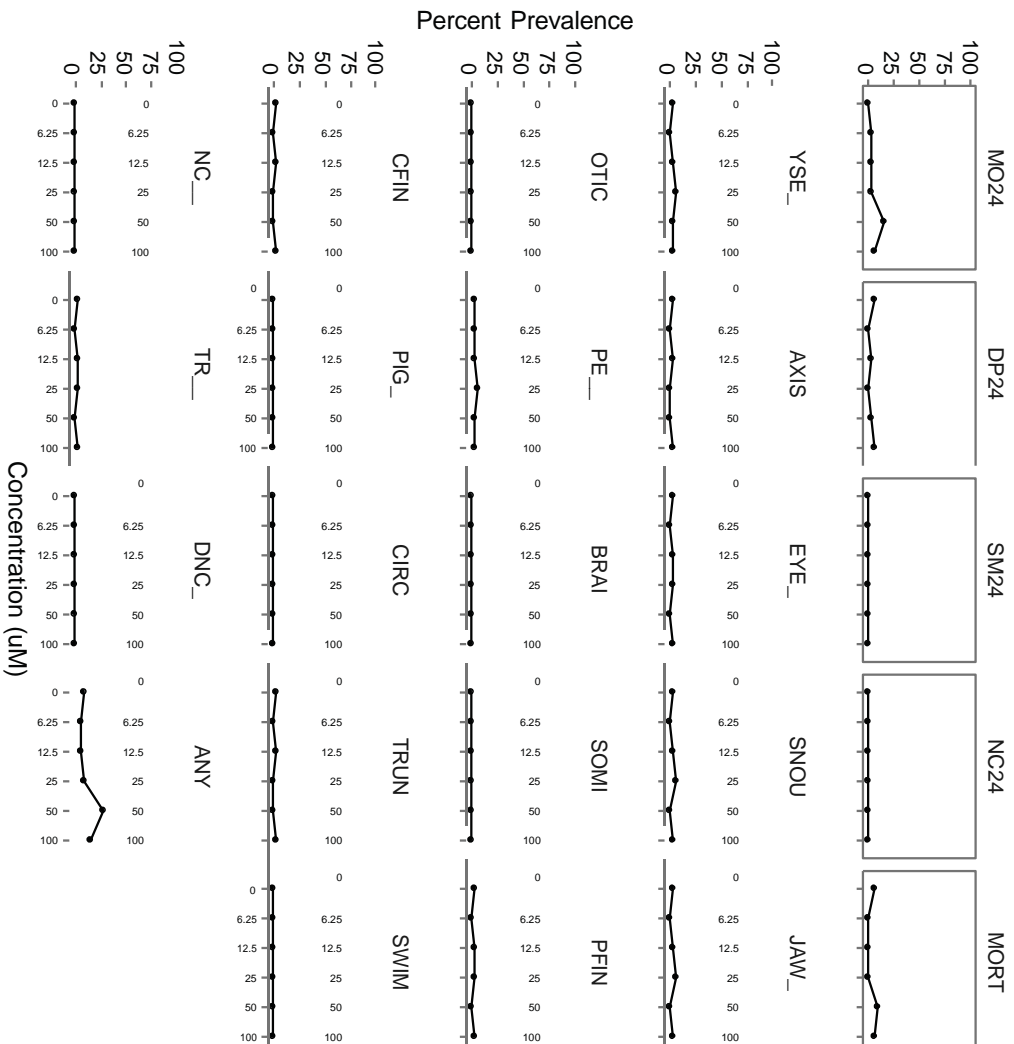
Number of Fisher Scoring iterations: 9

EC Values:

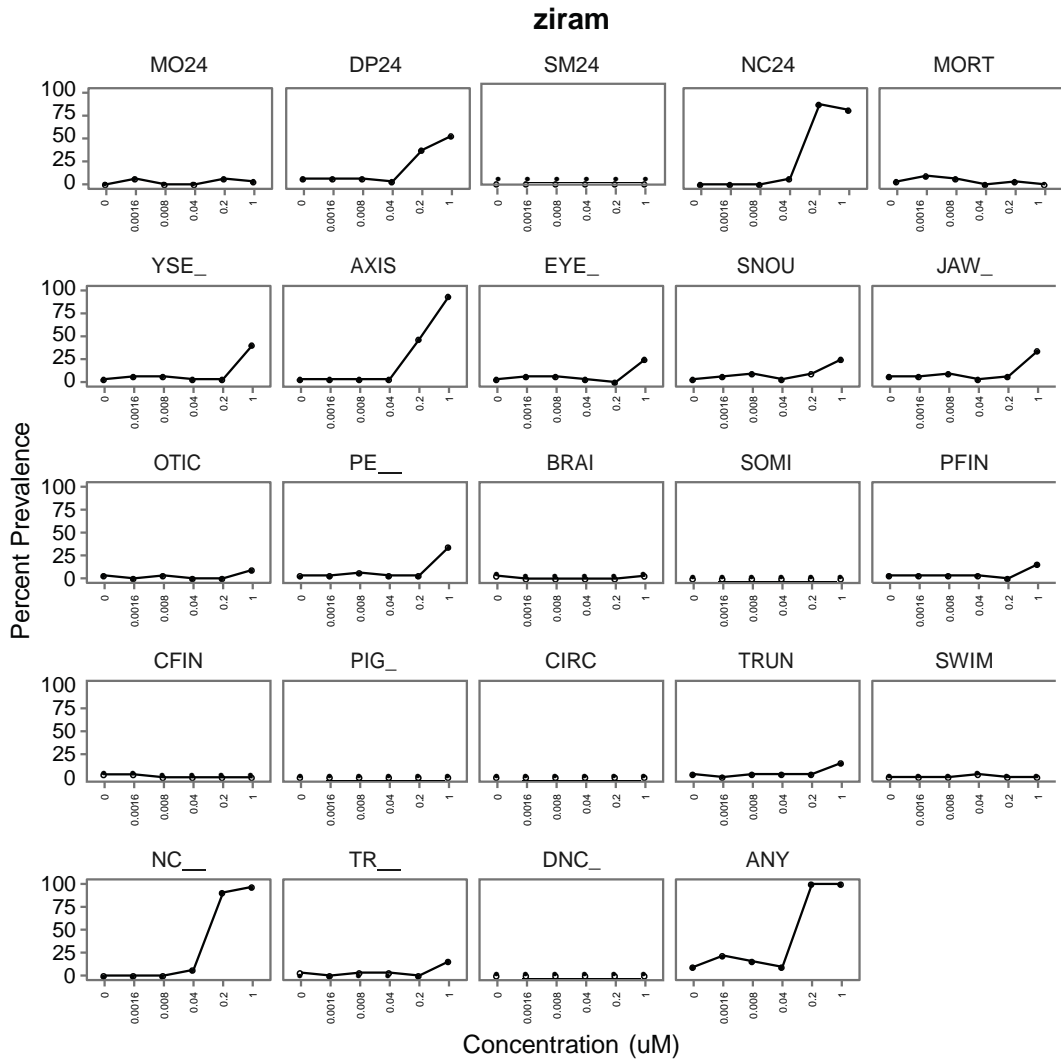
	Concentration	SE.log
p = 0.5:	0.004391939	0.000824545
p = 0.6:	0.005298931	0.001020142
p = 0.7:	0.006288207	0.001248666
p = 0.8:	0.007496354	0.001539073



Vinclozolin



**No significant mortality or malformations at 100 uM
EC set to 50 uM**



Model Output:

Call:
`glm(formula = ANY ~ CONC_log, family = binomial("logit"), data = logit_df)`

Deviance Residuals:
 Min 1Q Median 3Q Max
 -0.7892 -0.5156 -0.4602 0.2670 2.1436

Coefficients:
 Estimate Std. Error z value Pr(>|z|)
 (Intercept) -2.1917 0.2911 -7.529 5.13e-14 ***
 CONC_log 69.5629 12.8123 5.429 5.66e-08 ***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 262.07 on 191 degrees of freedom
 Residual deviance: 113.30 on 190 degrees of freedom
 AIC: 117.3

Number of Fisher Scoring iterations: 8

EC Values:

	Concentration	SE.log
p = 0.5:	0.07524232	0.01153387
p = 0.6:	0.08977064	0.01342361
p = 0.7:	0.10582567	0.01568328
p = 0.8:	0.12573198	0.01861909

