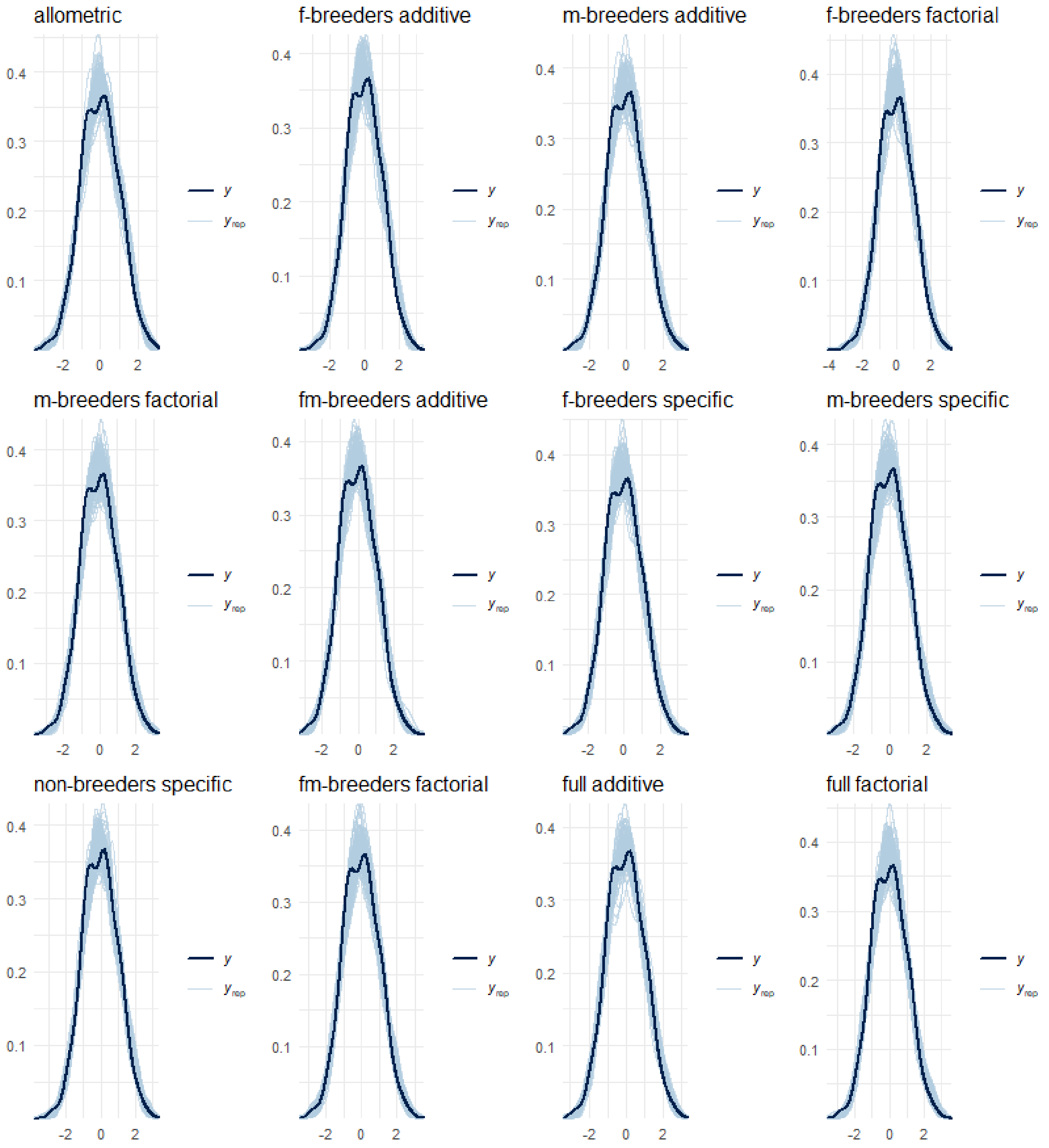
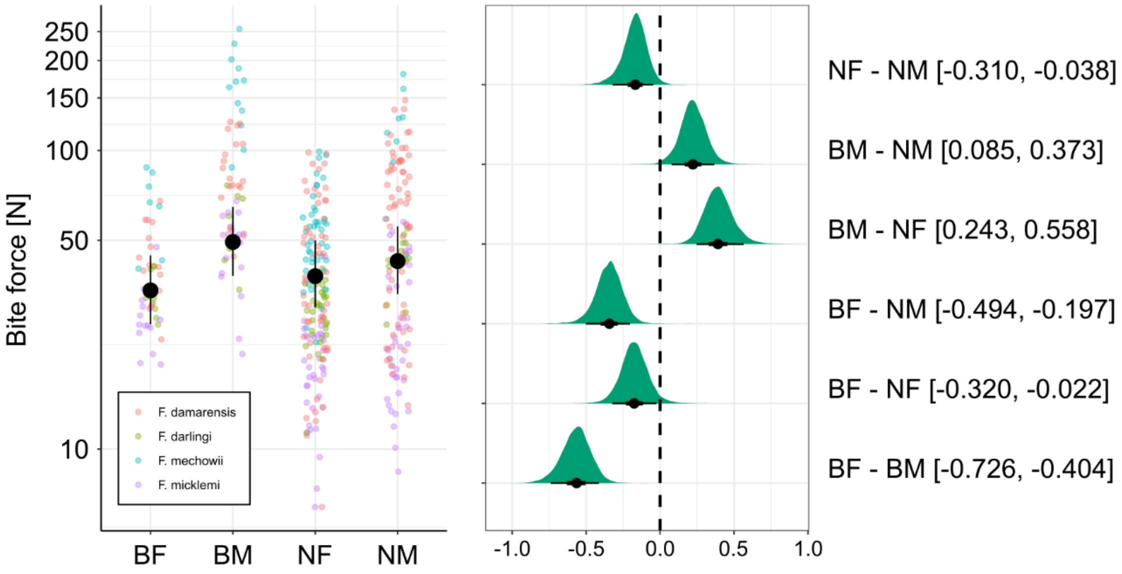
Breeding male mole-rats (*Fukomys)* use stronger bites to defend reproductive monopoly.

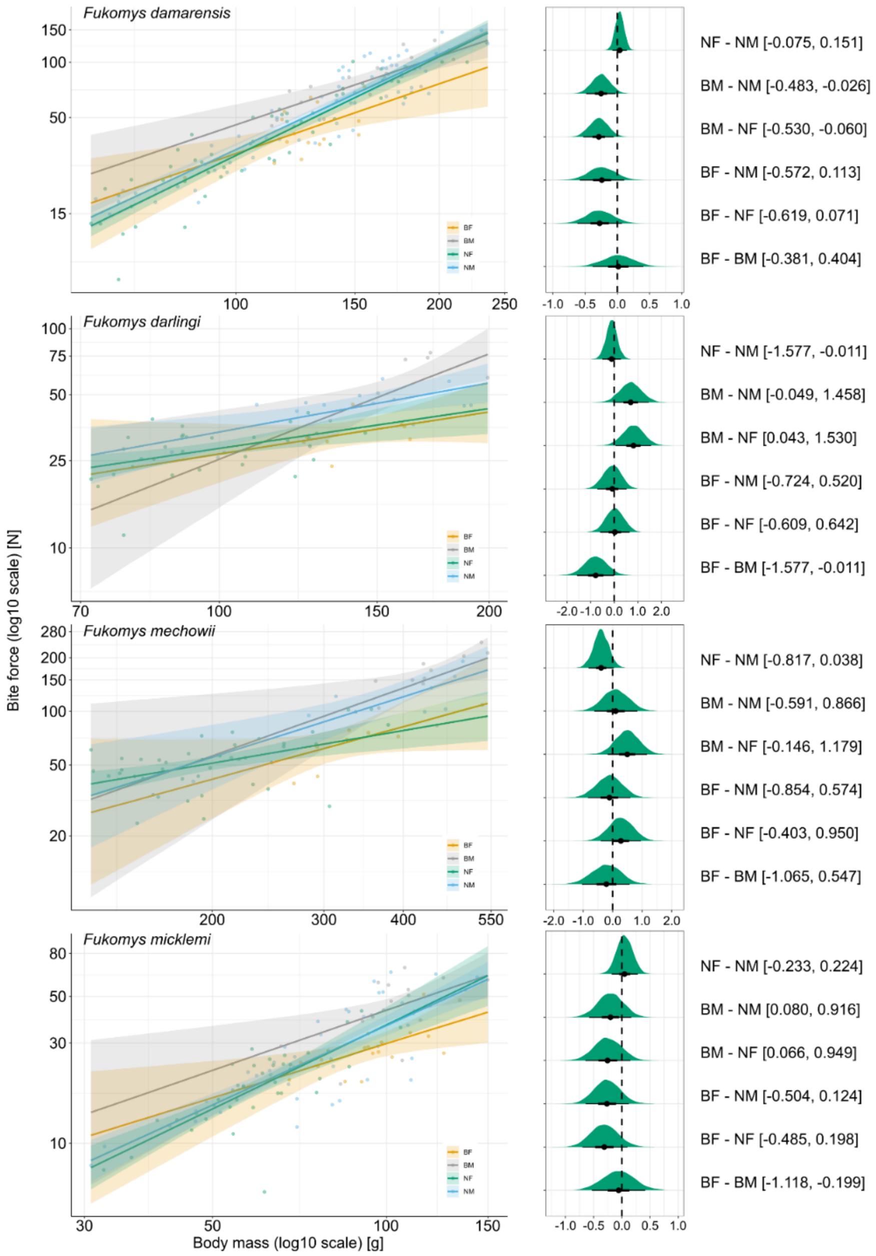
Supplementary figures and tables



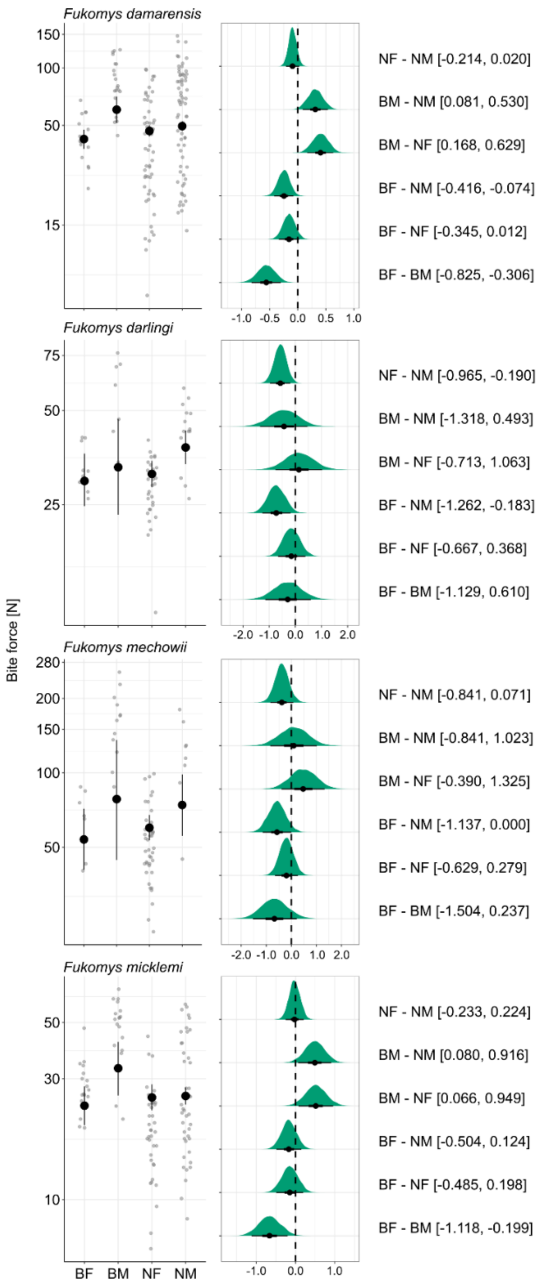
Supplementary Figure 1. Posterior predictive checks for the 12 Bayesian regression models assessing bite force in relation to body mass and all combinations of sex and reproductive status across four *Fukomys* mole-rat species. Each panel shows the posterior predictive distribution (y_{rep}, blue lines; 100 draws) in the background of the observed data (y, black line), generated using the “pp_check” function from the brms package.



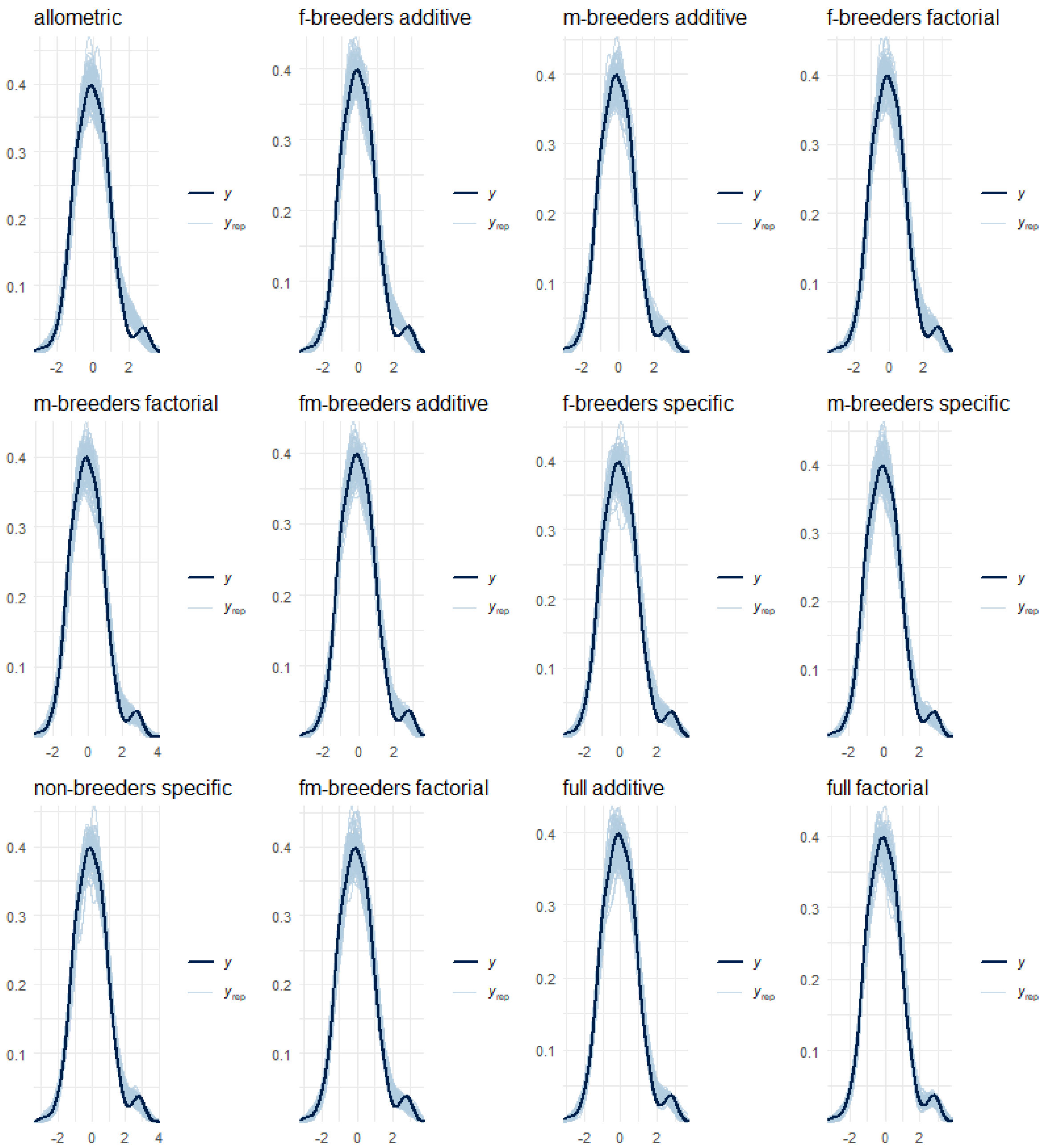
Supplementary Figure 2. Predicted bite force from the second-best performing "full additive" model in *Fukomys* mole-rats (BF – breeding females, BM – breeding males, NF – non-breeding females, and NM – non-breeding males). Bite force was back-transformed from standardised values and is displayed on a log scale. In the left panel, black dots and error bars represent posterior mean estimates and 90% credible intervals, respectively, from a Bayesian mixed-effects model. In the right panel, posterior distributions of pairwise differences are depicted and black points indicate posterior means of each pairwise difference; horizontal lines represent 50% and 90% credible intervals.



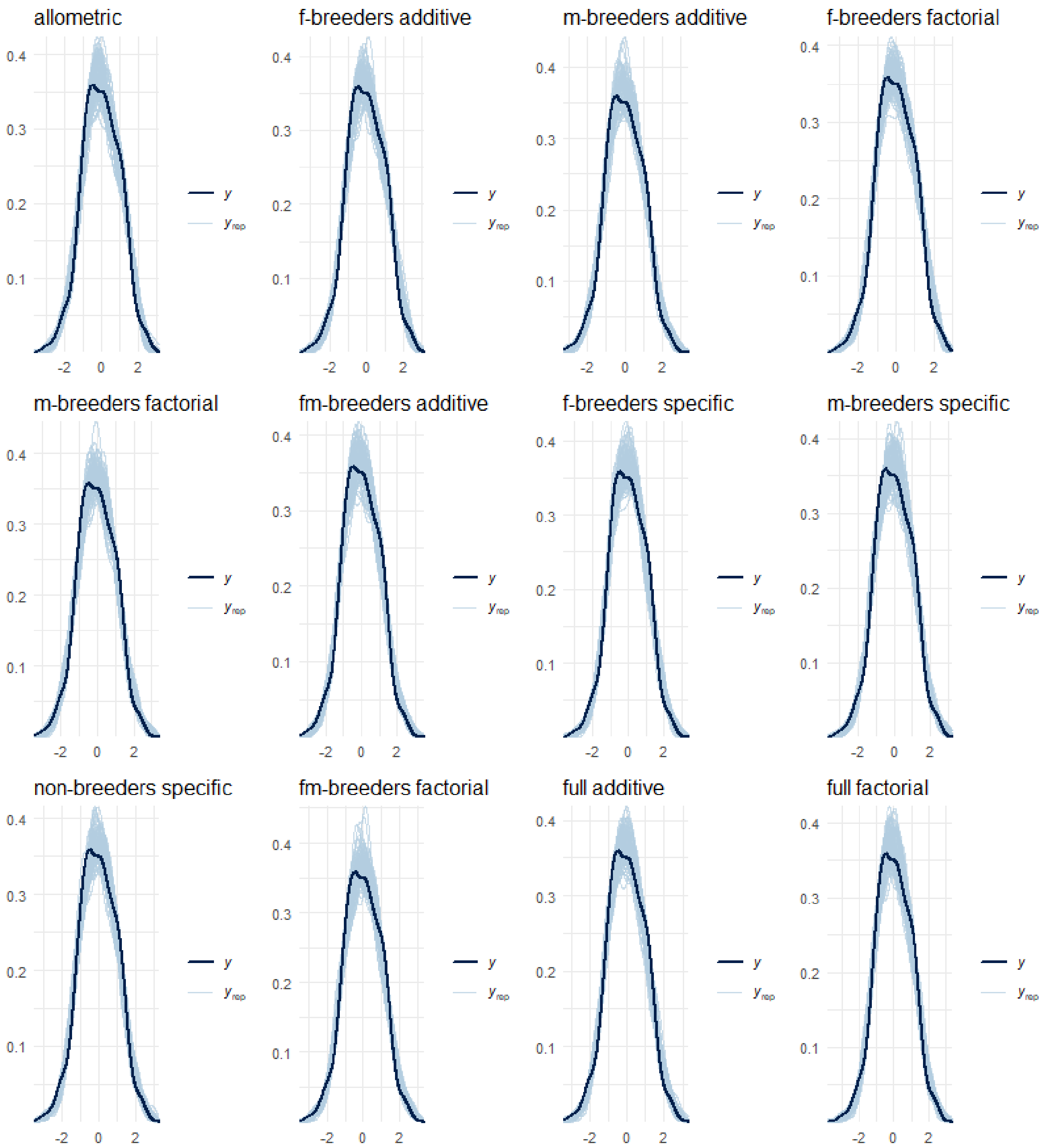
Supplementary Figure 3. Interspecific comparison of the change in predicted bite force with increasing body mass from the "full factorial" models fitted independently for each *Fukomys* mole-rat species, shown in relation to body mass (BF – breeding females, BM – breeding males, NF – non-breeding females and NM – non-breeding males). Pairwise contrasts of the allometric slopes are provided for each comparison, with 90% credible intervals shown in parentheses. Bite force was back-transformed from standardised values and is plotted on a log-log scale. In the left panels, lines represent posterior mean estimates from a Bayesian mixed-effects model and shaded ribbons indicate 90% credible intervals (CIs) around the posterior mean. In the right panels, posterior distributions of pairwise differences are depicted and black points indicate posterior means of each pairwise difference; horizontal lines represent 50% and 90% credible intervals.



Supplementary Figure 4. Intraspecific comparison of the predicted bite force shown in relation to the combination of sex and breeding status, based on the full factorial models fitted independently for each *Fukomys* mole-rat species (BF – breeding females, BM – breeding males, NF – non-breeding females, and NM – non-breeding males). Bite force was back-transformed from standardised values and is displayed on a log scale. In the left panels, black dots and error bars represent posterior mean estimates and 90% credible intervals, respectively, from a Bayesian mixed-effects model. In the right panels, posterior distributions of pairwise differences are depicted and black points indicate posterior means of each pairwise difference; horizontal lines represent 50% and 90% credible intervals.



Supplementary Figure 5. Posterior predictive checks for the 12 Bayesian regression models assessing head width in relation to body mass and all combinations of sex and reproductive status across four *Fukomys* mole-rat species. Each panel shows the posterior predictive distribution (y_{rep}, blue lines; 100 draws) in the background of the observed data (y, black line), generated using the "pp_check" function from the brms package.



Supplementary Figure 6. Posterior predictive checks for the 12 Bayesian regression models assessing upper incisor width in relation to body mass and all combinations of sex and reproductive status across four *Fukomys* mole-rat species. Each panel shows the posterior predictive distribution (y_{rep}, blue lines; 100 draws) in the background of the observed data (y, black line), generated using the "pp_check" function from the brms package.

Supplementary Table 1. Summary of measured bite force, head width, and upper incisor width in four *Fukomys* mole-rat species. Abbreviations: BF – breeding females, BM – breeding males, NF – non-breeding females, NM – non-breeding males. Values are presented as means ± standard deviation (SD), with range in parentheses.

Species	Status and sex	Bite force [N]	Head width [mm]	Upper incisor width [mm]
F. damarensis	BF	44.1 ± 12.6 (23.3–67.7)	29.1 ± 2.3 (24.0–33.3)	5.7 ± 0.5 (4.8–6.7)
	BM	85.5 ± 24.9 (44.2–124.6)	33.5 ± 3.6 (28.4–40.3)	6.9 ± 0.7 (5.7–8.6)
	NF	43.2 ± 24.9 (6.4–98.4)	27.9 ± 3.5 (20.6–33.6)	5.5 ± 1.1 (3.0–7.2)
	NM	63.4 ± 34.2 (14.0–147.3)	30.8 ± 4.4 (21.1–39.1)	6.0 ± 1.2 (3.2–8.0)
F. darlingi	BF	33.3 ± 5.8 (26.1–41.0)	26.8 ± 2.1 (24.6–31.1)	4.8 ± 0.2 (4.5–5.2)
	BM	57.1 ± 16 (34.2–76.4)	31.9 ± 1.1 (30.8–34.1)	5.8 ± 0.2 (5.6–6.1)
	NF	28.6 ± 6 (11.3–40.2)	25.9 ± 1.9 (22.9–30.5)	4.7 ± 0.4 (3.9–5.5)
	NM	43.5 ± 9.7 (26.1–59.0)	28.6 ± 2.9 (24.2–33.5)	5.3 ± 0.7 (3.9–6.3)
F. mechowii	BF	66.2 ± 18.7 (40.2–87.8)	38.4 ± 3 (33.9–43.4)	6.0 ± 0.6 (5.3–6.9)
	BM	163.9 ± 49.9 (87.8–255.3)	50.4 ± 3.1 (45.2–55.1)	8.8 ± 0.5 (7.9–9.4)
	NF	54.2 ± 18.3 (22.8–99.2)	34.2 ± 3.6 (28.2–41.0)	5.5 ± 0.6 (4.4–6.8)
	NM	119.5 ± 41.6 (44.8–180.2)	45.4 ± 8.6 (30.7–54.6)	6.6 ± 1.1 (4.6–7.8)
F. micklemi	BF	28.5 ± 6.9 (19.2–47.5)	23.9 ± 1 (22.2–26.3)	4.3 ± 0.2 (3.8–4.6)
	BM	47.6 ± 12.8 (20.8–67.7)	28.3 ± 1.5 (25.7–31.3)	5.3 ± 0.4 (4.6–6.3)
	NF	20 ± 8 (6.4–44.1)	22.2 ± 2.2 (17.7–27.5)	3.9 ± 0.5 (2.9–5.0)
	NM	28.3 ± 14.6 (8.4–59.0)	23.8 ± 3.4 (15.2–30.5)	4.2 ± 0.7 (2.5–5.5)

Supplementary Table 2. A series of twelve multilevel Bayesian regression models considered to assess the effects of selected predictors on bite force in *Fukomys* mole-rats. The models are listed in order of increasing complexity. sBF denotes standardised log bite force, and sBMass denotes standardised log body mass. For definitions and coding of categorical predictors used in the models, see Table S9.

<table>
<tr><th rowspan="2">Model</th><th rowspan="2">Formula in R notation</th><th colspan="2">No. of fixed terms</th></tr>
<tr><th>intercepts</th><th>slopes</th></tr>
<tr><td>Allometric</td><td>sBF ~ sBMass + (1 | Species) + (0 + sBMass | Species)</td><td>1</td><td>1</td></tr>
<tr><td>f-breeders additive</td><td>sBF ~ sBMass + FBreeders + (1 | Species / FBreeders) + (0 + sBMass | Species)</td><td>2</td><td>1</td></tr>
<tr><td>m-breeders additive</td><td>sBF ~ sBMass + MBreeders + (1 | Species / MBreeders) + (0 + sBMass | Species)</td><td>2</td><td>1</td></tr>
<tr><td>f-breeders factorial</td><td>sBF ~ sBMass * FBreeders + (1 | Species / FBreeders) + (0 + sBMass | Species / FBreeders)</td><td>2</td><td>2</td></tr>
<tr><td>m-breeders factorial</td><td>sBF ~ sBMass * MBreeders + (1 | Species / MBreeders) + (0 + sBMass | Species / MBreeders)</td><td>2</td><td>2</td></tr>
<tr><td>fm-breeders additive</td><td>sBF ~ sBMass + FMBreeders + (1 | Species / FMBreeders) + (0 + sBMass | Species)</td><td>3</td><td>1</td></tr>
<tr><td>f-breeders specific</td><td>sBF ~ sBMass + FMBreeders + sBMass:Fbreeders + (1 | Species / FMBreeders) + (0 + sBMass | Species / FBreeders)</td><td>3</td><td>2</td></tr>
</table>

<table>
<tr><td>m-breeders specific</td><td>sBF ~ sBMass + FMBreeders + sBMass:Mbreeders + (1 | Species / FMBreeders) + (0 + sBMass | Species / MBreeders)</td><td>3</td><td>2</td></tr>
<tr><td>non-breeders specific</td><td>sBF ~ sBMass + FMBreeders + sBMass:Status + (1 | Species / FMBreeders) + (0 + sBMass | Species / Status)</td><td>3</td><td>2</td></tr>
<tr><td>fm-breeders factorial</td><td>sBF ~ sBMass * FMBreeders + (1 | Species / FMBreeders) + (0 + sBMass | Species / FMBreeders)</td><td>3</td><td>3</td></tr>
<tr><td>full additive</td><td>sBF ~ sBMass + Statussex + (1 | Species / statussex) + (0 + sBMass | Species)</td><td>4</td><td>1</td></tr>
<tr><td>full factorial</td><td>sBF ~ sBMass * Statussex + (1 | Species / statussex) + (0 + sBMass | Species / statussex)</td><td>4</td><td>4</td></tr>
</table>

Supplementary Table 3. Comparison of the 12 models describing head width in *Fukomys* mole-rats. The models are listed in order of decreasing performance, based on differences in expected log predictive density (ΔELPD) and Watanabe–Akaike information criterion (ΔWAIC). Both statistics are expressed relative to the best-performing model ("full factorial"), and ΔELPD is also shown scaled by its standard error (ΔELPD/SE).

Rank	Model	ΔELPD	SE	ΔELPD/SE	ΔWAIC
1	full factorial	0.0			0.0
2	non-breeders specific	-13.2	7.0	-1.89	26.3
3	fm-breeders factorial	-13.9	7.0	-1.99	27.9
4	f-breeders specific	-14.5	6.8	-2.13	29.0
5	full additive	-14.5	5.3	-2.74	29.0
6	fm-breeders additive	-18.8	6.8	-2.76	37.6
7	m-breeders specific	-18.9	6.9	-2.74	37.9
8	f-breeders factorial	-25.8	8.2	-3.15	51.6
9	f-breeders additive	-31.3	7.9	-3.96	62.7
10	m-breeders additive	-32.7	9.8	-3.34	65.4
11	m-breeders factorial	-32.9	10.0	-3.29	65.9
12	Allometric	-55.1	11.6	-4.75	110.3

Supplementary Table 4. Summary of pairwise contrasts from the full factorial model comparing estimated head width (Intercept) and its change with increasing body mass (allometric slope) among breeding females (BF), breeding males (BM), and non-breeding females (NF), non-breeding males (NM) in *Fukomys* mole-rats.

Contrast	Estimate	Lower CI (90%)	Upper CI (90%)
Allometric slope			
NF × NM	-0.219	-0.462	0.020
BM × NM	-0.142	-0.432	0.102
BM × NF	0.076	-0.200	0.326
BF × NM	-0.369	-0.666	-0.073
BF × NF	-0.150	-0.455	0.117
BF × BM	-0.224	-0.529	0.060
Intercept			
NF × NM	-0.007	-0.237	0.267
BM × NM	0.200	-0.060	0.473
BM × NF	0.207	-0.068	0.473
BF × NM	-0.246	-0.476	0.036
BF × NF	-0.236	-0.490	0.020
BF × BM	-0.443	-0.712	-0.178

Supplementary Table 5. Comparison of the 12 models describing upper incisor width in *Fukomys* mole-rats. The models are listed in order of decreasing model performance, based on differences in expected log predictive density (ΔELPD) and Watanabe–Akaike information criterion (ΔWAIC). Both statistics are expressed relative to the best-performing model ("full factorial"), and ΔELPD is also shown scaled by its standard error (ΔELPD/SE).

Rank	**Model**	**ΔELPD**	**ΔSE**	**ΔELPD/SE**	**ΔWAIC**
1	fm-breeders factorial	0.0	0.0		0.0
2	non-breeders specific	-0.1	1.6	-0.06	0.3
3	f-breeders specific	-3.5	2.5	-1.40	7.1
4	full factorial	-4.3	2.4	-1.79	8.7
5	m-breeders specific	-10.8	4.9	-2.20	21.6
6	fm-breeders additive	-13.0	5.1	-2.55	26.0
7	full additive	-17.2	5.3	-3.25	34.4
8	m-breeders factorial	-23.7	7.2	-3.29	47.5
9	m-breeders additive	-25.2	7.3	-3.45	50.5
10	f-breeders factorial	-32.9	8.3	-3.96	65.9
11	f-breeders additive	-42.6	9.0	-4.73	85.2
12	Allometric	-64.2	11.3	-5.68	128.4

Supplementary Table 6. Summary of pairwise contrasts from the full factorial model comparing estimated upper incisors width (Intercept) and its change with increasing body mass (allometric slope) among breeding females (BF), breeding males (BM), and pooled non-breeders (N) in *Fukomys* mole-rats.

Contrast	**Estimate**	**Lower CI (90%)**	**Upper CI (90%)**
Allometric slope			
BF × BM	-0.285	-0.670	0.083
BF × N	-0.562	-0.935	-0.215
BM × N	-0.273	-0.602	0.068
Intercept			
BF × BM	-0.581	-1.004	-0.185
BF × N	-0.168	-0.539	0.257
BM × N	0.412	0.038	0.866

Supplementary Table 7. Overview of the willingness of reproductively active (breeding) females of each *Fukomys* species to bite. Females categorised as "reluctant to bite" either bit only once or required extra motivation (i.e., blowing in the face). Reluctant females that were clearly underperforming compared to similar-sized females were consequently removed from the analysis. Females categorised as "refusing to bite" did not bite at all, even after further encouragement.

Species	**Breeding females (n)**	**Breeding females refusing to bite (n)**	**Breeding females reluctant to bite (n)**
Fukomys damarensis	26	6	5
Fukomys darlingi	9	0	0
Fukomys mechowii	13	5	1
Fukomys micklemi	21	2	2

Supplementary Table 8. Locality of origin, numbers of breeders and non-breeders, and minimum body mass of tested specimens for each species (Mass cut off was defined by approximate body mass when reaching adulthood).

Species	**Locality of origin**	**Families (n)**	**Non-breeders ♂ / ♀ (n)**	**Breeders ♂ / ♀ (n)**	**Mass cut off [g]**	**Average family size**	**Average body mass (g)**
Fukomys damarensis	South Africa: Kuruman River Reserve (26.99°S, 21.81°E)	29	67/54	20/15	60[1,2]	8.9±5.7 (n=51)[3] 8.7±5.3 (n=210)[4]	Wild: ♂ subordinate 96±29, ♀ subordinate 91±27[3], ♂ reproductive 155±21, ♀ reproductive 125±17[3]
Fukomys darlingi	Malawi: Nsanje (16°55′S, 35°16′E)	9	14/31	7/9	60[5]	Not known in this population, 5 to 9 in populations from Zimbabwe[6]	Wild: ♂ 138±32, ♀ 101±25[7] Captive: ♂ 154±23, ♀ 114±15[7]
Fukomys mechowii	Zambia: Ndola, Kapiri Mposhi (exact GPS not known)	13	8/43	12/7	120[8]	9±2[9] 9-13[10]	Wild: ♂ 345±95, ♀ 252±34[8] Wild: ♂ 571±21, ♀ 392±12[11]
Fukomys micklemi	Zambia: Sekute area (17°39'S, 25°37'E)	7	15/9	7/5	50[12]	NA	Captive: ♂ 123±25, ♀ 94±16[13]
	Zambia: Lusaka East Forest Reserve (15°28'S, 28°25'E)	17	28/29	12/12	30[14, 15]	9.7 ± 2.5[16]	Wild: ♂72±14, ♀ 62±8[16] Wild: ♂96±13 (n=20), ♀ 76±12 (n=66)[17]

Supplementary Table 9. Sex and reproductive status predictors used in multilevel Bayesian regression models to assess their effect on bite force in *Fukomys* mole-rats.

Predictor	**No. of categories**	**Description**
Bmass	continuous	body mass
Status	2	breeders vs. non-breeders
FBreeders	2	female breeders vs. the rest
MBreeders	2	male breeders vs. the rest
FMBreeders	3	female breeders vs. male breeders vs. non-breeders
Statussex	4	all four combinations of sex and reproductive status

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