

Electronic supplementary material (ESM) for:

## **Convergent evolution of an extreme dietary specialisation, the olfactory system of worm-eating rodents**

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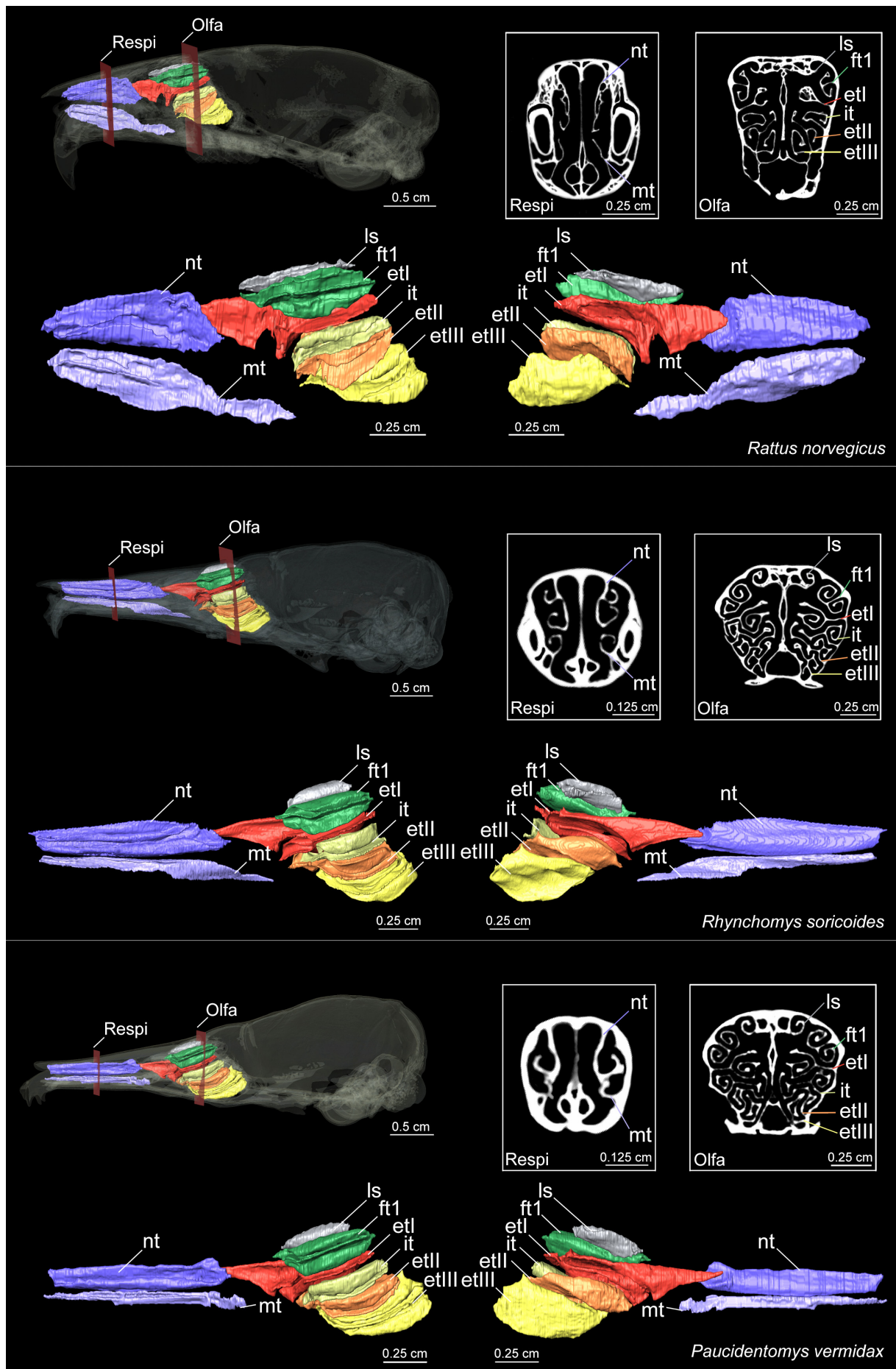
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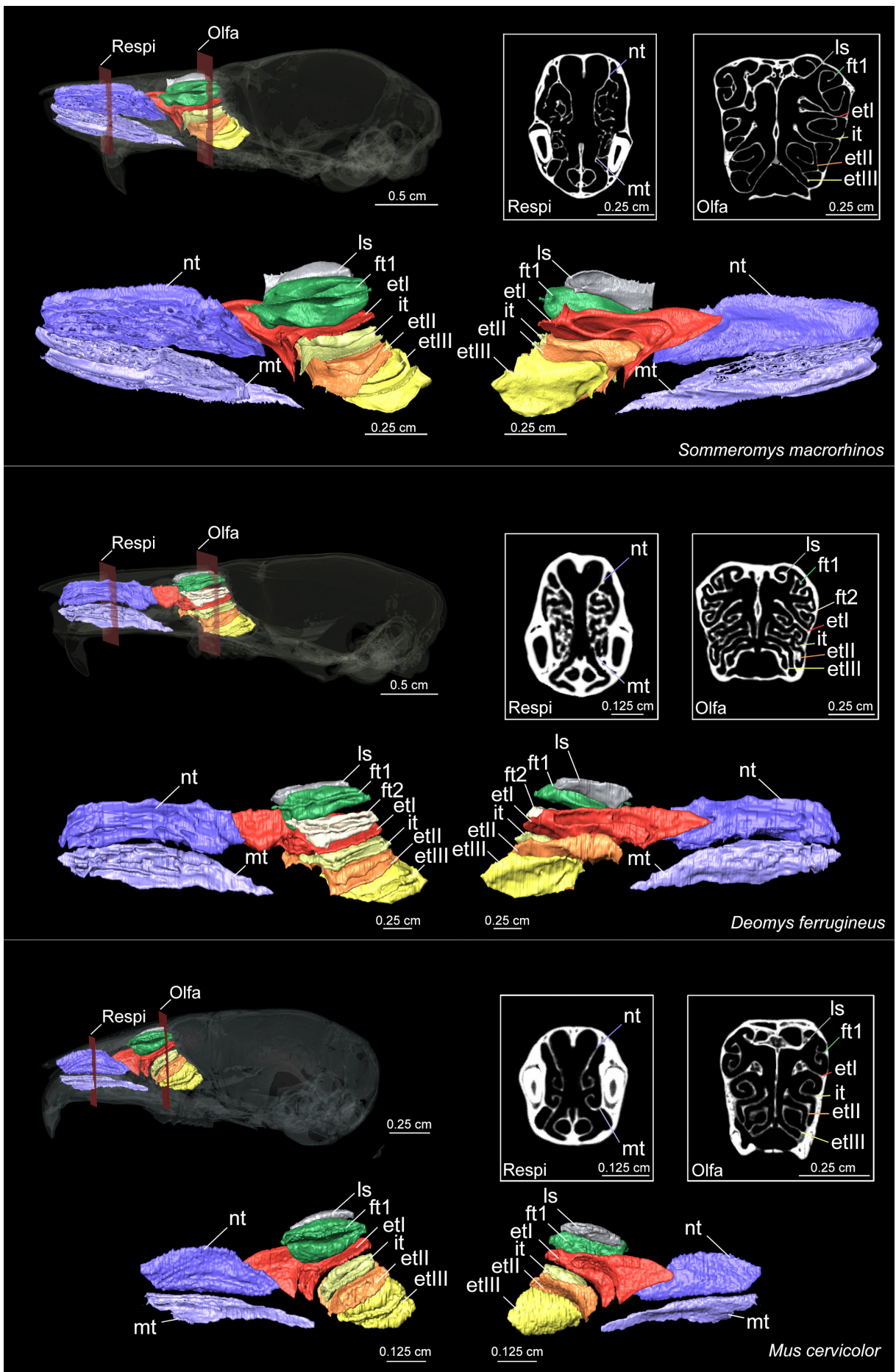
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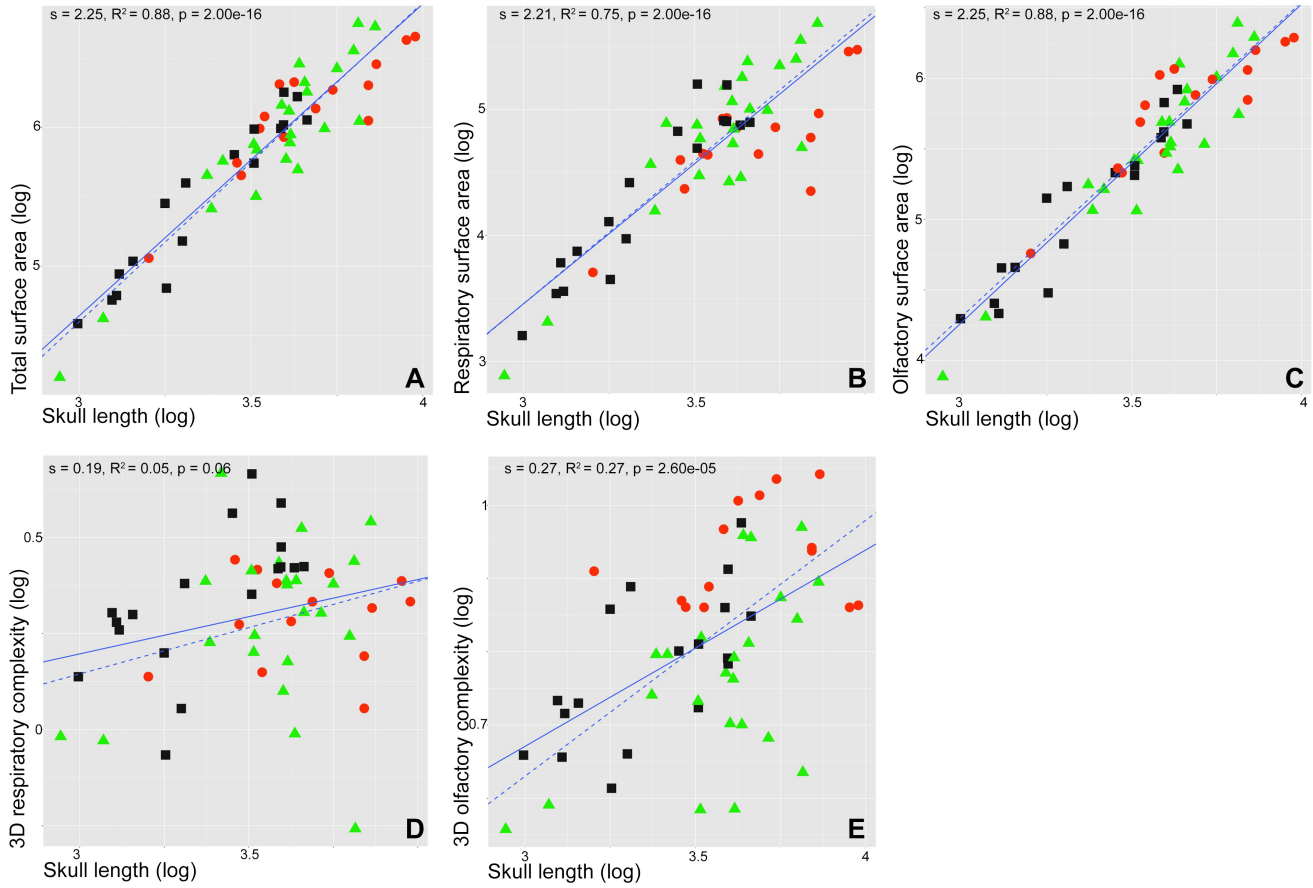
**Figure S1.** Coronal cross section and sagittal plane of skull and 3D representations of turbinal bones in *Rattus norvegicus*, *Rhynchomys soricoides*, and *Paucidentomys vermidax*. Abbreviations: see Table S1.



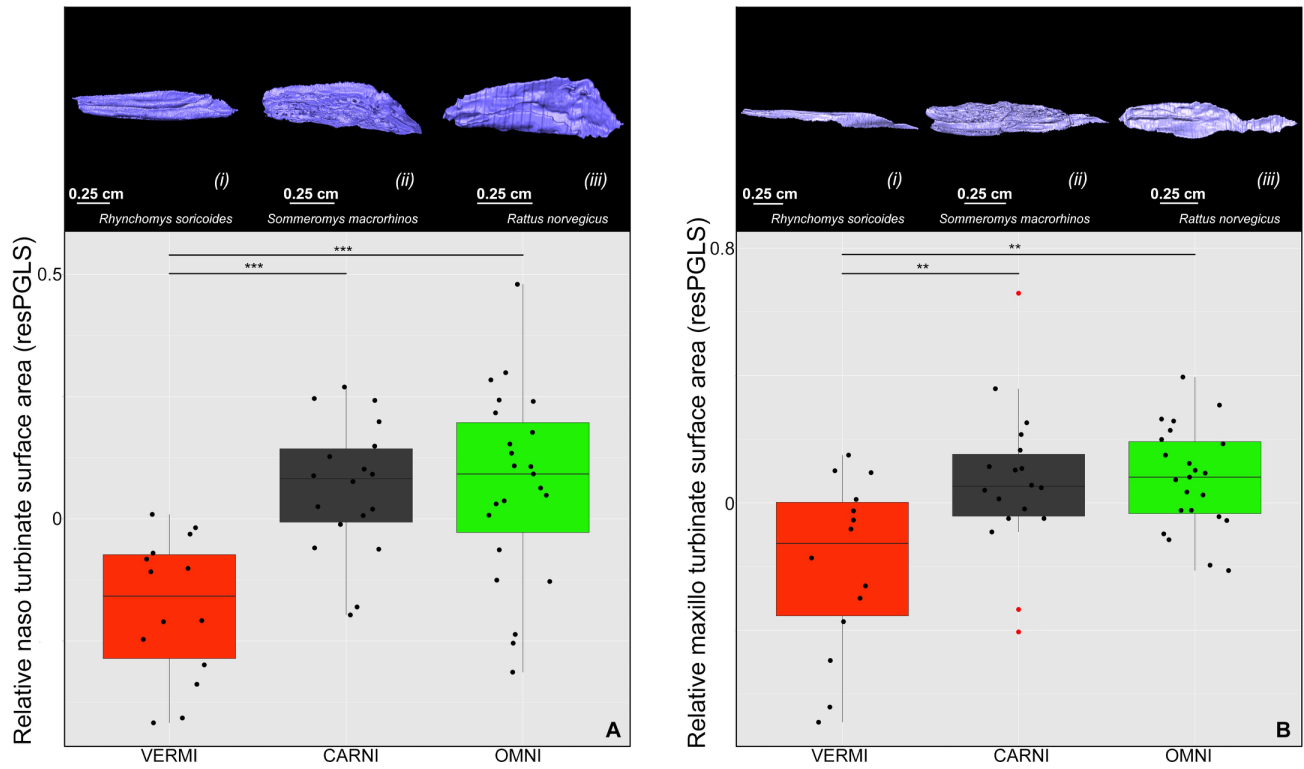
**Figure S2.** Coronal cross section and sagittal plane of skull and 3D representations of turbinal bones in *Sommeromys macrorhinos*, *Deomys ferrugineus*, and *Mus cervicolor*. Abbreviations: see Table S1.



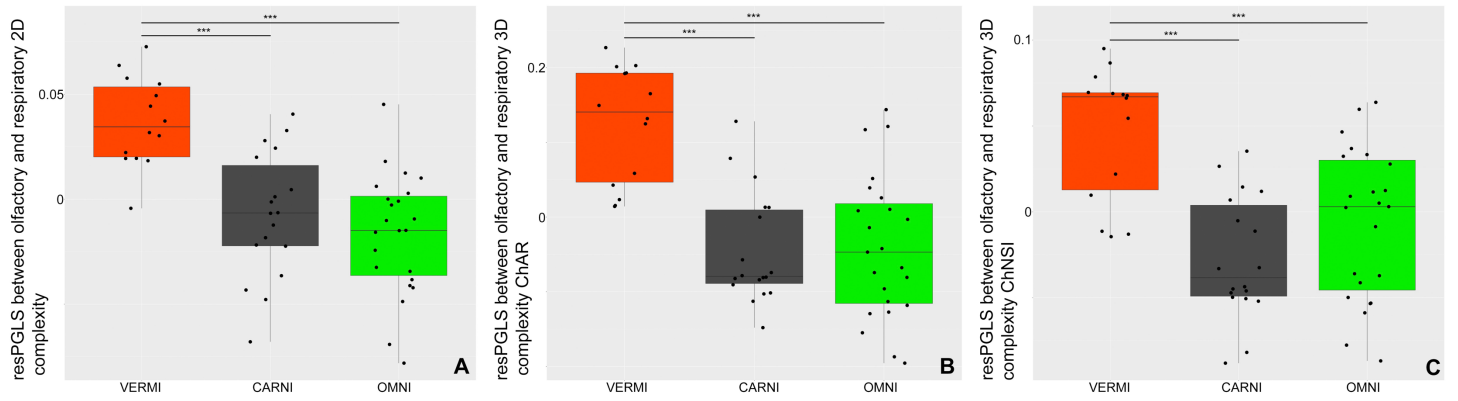
**Figure S3.** Linear regressions (continuous line) and PGLS (dashed line) of (A) total surface area of turbinals against skull length, (B) respiratory turbinals surface area against skull length, (C) olfactory turbinals surface area against skull length, (D) 3D respiratory complexity (CHAR) against skull length, and (E) 3D olfactory complexity (CHAR) against skull.



**Figure S4.** Boxplot with dietary categories: (A) relative nasoturbinale surface area and (B) relative maxilloturbinale surface area. Boxplots are based on PGLS residuals. Significance codes are based on phylogenetic Tukey's HSD test. (i) *Rhynchomys soricoides*, (ii) *Sommeromys macrorhinos*, and (iii) *Rattus norvegicus*. Red points are outliers.

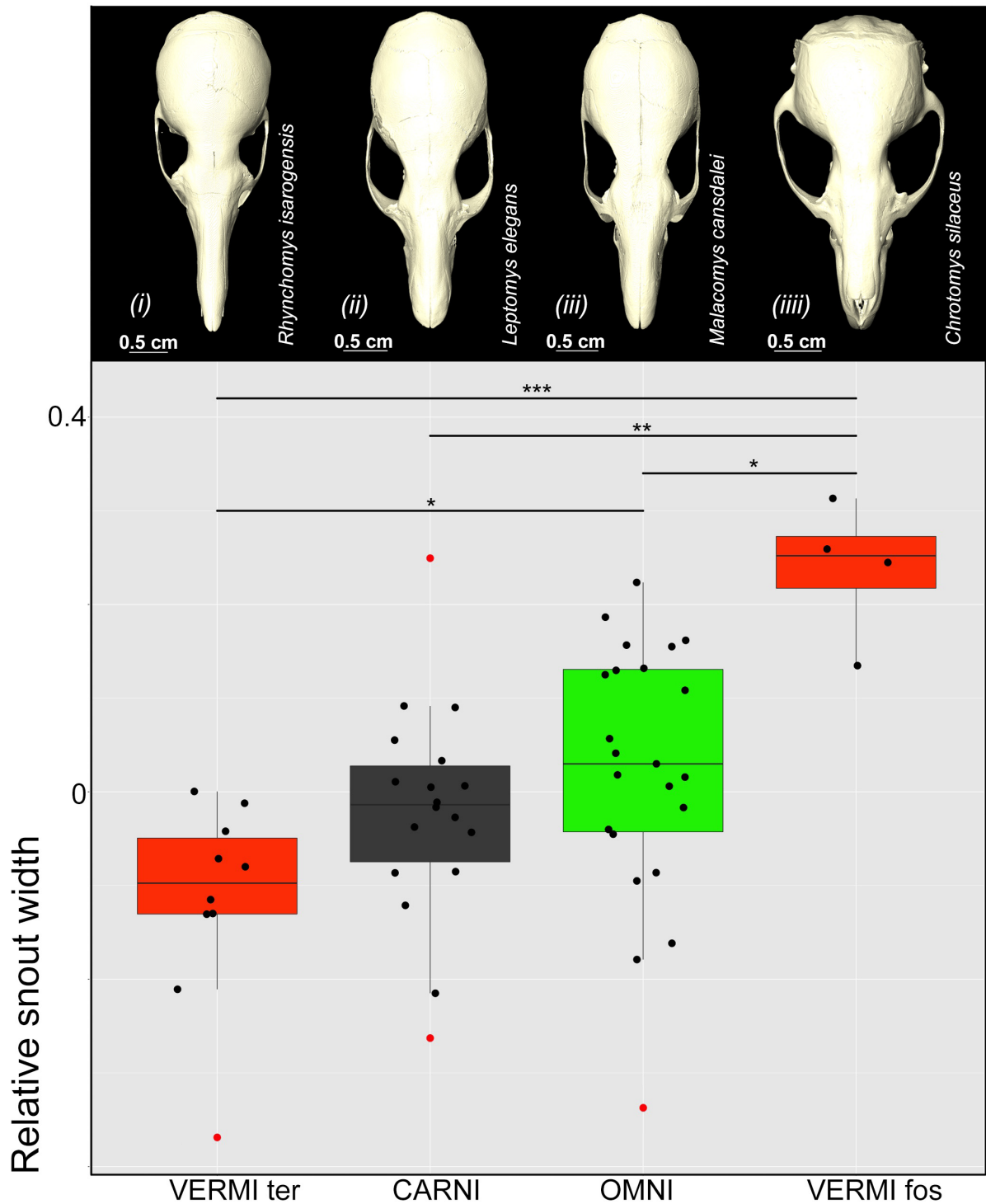


**Figure S5.** Boxplot of the residuals of PGLS (resPGLS) between olfactory and respiratory complexity with dietary categories: (A) 2D complexity method, (B) 3D complexity method (CHAR), and 3D complexity method (CHNSI).





**Figure S6.** Boxplot of snout width (SNW) with dietary categories. Boxplot are based on PGLS residuals. Significance code are based on phylogenetic Tukey's HSD test. (i) *Rhynchomys isarogenesis*, (ii) *Leptomys elegans*, (iii) *Malacomys cansdalei*, and (iiii) *Chrotomys silaceus*.



**Legend S1.** In order to implement phylogenetic comparative analyses to our turbinal dataset, we build a composite phylogenetic tree. Concerning the murinae we used the phylogenetic tree from Rowe et al. (2016). We subsequently used the dated tree from Steppan & Schenk (2017) for the divergence among Cricetidae and the basal split between Muridae and Cricetidae. A species of *Crunomys*, a *Malacomys*, 2 species of *Pseudohydromys*, 3 species of *Leptomys* were missing from these phylogenies. We constrained missing species to their assigned genus, thereby assuming monophyly at the genus level, respectively. We subsequently used the PASTIS R package (Thomas *et al.* 2013) to randomly incorporate them in our composite tree following Maestri *et al.* (2016) protocol.



**Table S1.** PGLS and linear regression results. Abbreviations: SA = surface area, TotSA = total surface area of turbinals, Relat = relative, Cor = corrected, NoCor = non-corrected, CHAR = convex hull area ratio, CHNSI = convex hull normalized shape index, Respi = respiratory, Olfa = olfactory, NT = nasoturbinal, MT = maxilloturbinal, LS = lamina semicircularis, FT1 = frontoturbinal 1, FT1 bis = frontoturbinal 1 bis, FT2 = frontoturbinal 2, ET1 = ethmoturbinal 1, ET2 = ethmoturbinal 2, and ET3 = ethmoturbinal 3, SKL = skull length, SNW = snout width, SNL = snout length, NaRe = nasoturbinal considered as respiratory turbinal, and NaOl = nasoturbinal considered as olfactory turbinal.

Variables	Slope	P-value	Signif-code	R-squared	PGLS slope	PGLS p-value
TotSA/SKL	2.25	2.00e-16	***	0.88	2.30	<0.01
RespiSA/SKL	2.21	2.00e-16	***	0.75	2.26	<0.01
OlfaSA/SKL	2.25	2.00e-16	***	0.88	2.33	<0.01
OlfaSA/RespiSA	0.86	2.00e-16	***	0.83	0.74	<0.01
OlfaSA/TotSA	0.99	2.00e-16	***	0.98	1.00	<0.01
RespiSA/TotSA	1.02	2.00e-16	***	0.92	0.99	<0.01
2DNoCorOlfa/2DNoCorRespi	0.37	2.00e-16	***	0.19	0.33	2.00E-04
2DCorOlfa/SKL	0.34	1.52e-03	**	0.16	0.25	0.08
2DCorRespi/SKL	0.28	0.03	*	0.07	0.21	0.38
2DCorOlfa/RelatOlfaSA	0.41	0.22	-	0.01	0.34	0.16
2DCorRespi/RelatRespiSA	0.48	0.01	**	0.12	0.55	4.00e-03
OlfaCHAR/RespiCHAR	0.29	7.33e-04	***	0.18	0.19	2.80e-03
OlfaCHAR/SKL	0.27	2.60e-05	***	0.27	0.35	1.00e-04
RespiCHAR/SKL	0.19	0.06	-	0.05	0.24	0.18
OlfaCHAR/OlfaSA	0.15	8.21e-10	***	0.50	0.18	<0.01
OlfaCHAR/RelatOlfaSA	0.47	0.02	*	0.08	0.14	0.36
RespiCHAR/RespiSA	0.18	5.33e-07	***	0.36	0.31	<0.01
RespiCHAR/RelatRespiSA	0.55	4.81e-06	***	0.31	0.81	<0.01
OlfaCHNSI/RespiCHNSI	0.40	6.99e-06	***	0.30	0.19	0.01
OlfaCHNSI/SKL	0.17	3.13e-09	***	0.47	0.19	<0.01
RespiCHNSI/SKL	0.15	7.42e-04	***	0.18	0.16	0.06
OlfaCHNSI/OlfaSA	0.08	5.91e-16	***	5.90e-16	0.10	<0.01
OlfaCHNSI/RelatOlfaSA	0.18	0.06	-	0.05	0.10	0.15
RespiCHNSI/RespiSA	0.09	2.55e-09	***	0.48	0.14	<0.01
RespiCHNSI/RelatRespiSA	0.19	4.78e-04	***	0.19	0.35	<0.01

**Table S2.** Analysis of variance (ANOVA) results for dietary variables. Abbreviations: see Table S1.

<b>Variable</b>	<b>Sum Sq</b>	<b>Mean Sq</b>	<b>F value</b>	<b>Pr(&gt;F)</b>	<b>Signif-code</b>
OlfSA/TotSA	0.11	0.06	13.04	2.57e-05	***
RespiSA/TotSA	0.67	0.34	15.90	4.11e-06	***
OlfSA/RespiSA	1.42	0.71	20.57	2.62e-07	***
MT/TotSA	0.73	0.37	7.61	1.25e-03	**
NT/TotSA	0.63	0.31	11.66	6.57e-05	***
2DCorOlfSA/SKL	0.66	0.33	15.54	5.11e-06	***
2DCorRespi/SKL	0.18	0.09	1.86	0.17	-
2DNoCorOlfSA/2DNoDCorRespi	0.03	0.01	17.50	1.54e-06	***
SNL/SKL	0.01	0.01	1.31	0.28	-
SNL/SKL_VERMI_fos_ter	0.04	0.01	3.83	0.01	*
SNW/SNL	0.02	0.01	0.57	0.57	-
SNW/SNL_VERMI_fos_ter	0.38	0.13	8.52	1.09e-04	***
OlfCHAR/RespiCHAR	0.29	0.15	20.01	3.59e-07	***
OlfCHAR/SKL	0.18	0.09	11.28	8.54e-05	***
RespiCHAR/SKL	0.12	0.06	2.04	0.14	-
OlfCHNSI/RespiCHNSI	0.04	0.02	13.66	1.71e-05	***
OlfCHNSI/SKL	0.02	0.01	6.13	4.08e-03	**
RespiCHNSI/SKL	0.01	0.01	1.32	0.27	-

**Table S3.** Phylogenetic Tukey's HSD results. Abbreviations: see Table S1.

Variables	Comparison	p-value	Signif-code
RespiSA/TotSA	OMNI/CARNI	0.99	-
RespiSA/TotSA	VERMI/CARNI	1.18e-05	***
RespiSA/TotSA	VERMI/OMNI	1.00e-05	***
OlfaSA/TotSA	OMNI/CARNI	0.97	-
OlfaSA/TotSA	VERMI/CARNI	9.17e-05	***
OlfaSA/TotSA	VERMI/OMNI	8.40e-05	***
OlfaSA/RespiSA	OMNI/CARNI	0.64	-
OlfaSA/RespiSA	VERMI/CARNI	1.00e-04	***
OlfaSA/RespiSA	VERMI/OMNI	1.00e-04	***
MTSA/TotSA	OMNI/CARNI	0.98	-
MTSA/TotSA	VERMI/CARNI	4.47e-03	**
MTSA/TotSA	VERMI/OMNI	1.34e-03	**
NTSA/TotSA	OMNI/CARNI	0.98	-
NTSA/TotSA	VERMI/CARNI	2.67e-04	***
NTSA/TotSA	VERMI/OMNI	2.19e-04	***
SNL/SKL	OMNI/CARNI	0.32	-
SNL/SKL	VERMIter/CARNI	0.94	-
SNL/SKL	VERMIfos/CARNI	0.04	*
SNL/SKL	VERMIter/OMNI	0.19	-
SNL/SKL	VERMIfos/OMNI	0.30	-
SNL/SKL	VERMIter/VERMIfos	0.03	*
SNW/SNL	OMNI/CARNI	0.65	-
SNW/SNL	VERMIter/CARNI	0.21	-
SNW/SNL	VERMIfos/CARNI	2.00e-03	**

Variables	Comparison	p-value	Signif-code
SNW/SNL	VERMIter/OMNI	0.02	*
SNW/SNL	VERMIfos/OMNI	0.01	*
SNW/SNL	VERMIter/VERMIfos	6.03e-05	***
2DCorOlfa/SKL	OMNI/CARNI	2.67e-04	***
2DCorOlfa/SKL	VERMI/CARNI	0.31	-
2DCorOlfa/SKL	VERMI/OMNI	1.00e-04	***
2DCorRespi/SKL	OMNI/CARNI	0.07	-
2DCorRespi/SKL	VERMI/CARNI	0.29	-
2DCorRespi/SKL	VERMI/OMNI	0.88	-
2DNoCorOlfa/2NoDCorRespi	OMNI/CARNI	0.52	-
2DNoCorOlfa/2NoDCorRespi	VERMI/CARNI	1.00e-04	***
2DNoCorOlfa/2NoDCorRespi	VERMI/OMNI	1.00e-04	***
OlfaCHAR/RespiCHAR	OMNI/CARNI	0.99	-
OlfaCHAR/RespiCHAR	VERMI/CARNI	2.70e-06	***
OlfaCHAR/RespiCHAR	VERMI/OMNI	1.60e-06	***
OlfaCHAR/SKL	OMNI/CARNI	0.05	*
OlfaCHAR/SKL	VERMI/CARNI	0.06	-
OlfaCHAR/SKL	VERMI/OMNI	5.42e-05	***
OlfaCHNSI/RespiCHNSI	OMNI/CARNI	0.25	-
OlfaCHNSI/RespiCHNSI	VERMI/CARNI	1.36e-05	***
OlfaCHNSI/RespiCHNSI	VERMI/OMNI	8.26e-04	***
OlfaCHNSI/SKL	OMNI/CARNI	0.39	-
OlfaCHNSI/SKL	VERMI/CARNI	0.09	-
OlfaCHNSI/SKL	VERMI/OMNI	2.73e-03	**

**Table S4.** Phylogenetic Tukey's HSD differences between considering the nasoturbinal whether as olfactory whether as respiratory turbinals. Abbreviations: see Table S1.

<b>Variables</b>	<b>Comparison</b>	<b>NaRe p-value</b>	<b>NaOI p-value</b>
RespiSA/TotSA	OMNI/CARNI	0.76	0.83
RespiSA/TotSA	VERMI/CARNI	0.01	0.03
RespiSA/TotSA	VERMI/OMNI	0.00	0.00
OlfSA/TotSA	OMNI/CARNI	0.90	1.00
OlfSA/TotSA	VERMI/CARNI	0.01	0.03
OlfSA/TotSA	VERMI/OMNI	0.00	0.04
OlfSA/RespiSA	OMNI/CARNI	0.86	0.75
OlfSA/RespiSA	VERMI/CARNI	0.00	0.00
OlfSA/RespiSA	VERMI/OMNI	0.00	0.00

**Table S5.** Comparison between the results of phylogenetic Tukey's HSD and non-phylogenetic Tukey's HSD. Abbreviations: see Table S1.

<b>Variables</b>	<b>Comparison</b>	<b>PhyloTukey p-value</b>	<b>Tukey p-value</b>
RespiSA/TotSA	OMNI/CARNI	0.76	0.94
RespiSA/TotSA	VERMI/CARNI	0.01	0.00
RespiSA/TotSA	VERMI/OMNI	0.00	0.00
OlfSA/TotSA	OMNI/CARNI	0.90	0.98
OlfSA/TotSA	VERMI/CARNI	0.01	0.00
OlfSA/TotSA	VERMI/OMNI	0.00	0.00
OlfSA/RespiSA	OMNI/CARNI	0.86	0.44
OlfSA/RespiSA	VERMI/CARNI	0.00	0.00
OlfSA/RespiSA	VERMI/OMNI	0.00	0.00

**Table S6.** Results of phylogenetic ANCOVA. Three models were contrasted: a model without dietary categories (H0), a model with omnivorous and carnivorous dietary categories (Carni), and a model with omnivorous, carnivorous, and vermivorous dietary categories (Vermi). Model were compared using the Akaike information criterion (AIC) and the Likelihood-ratio test.

	<b>AIC</b>	<b>Lr test likelihood</b>	<b>Lr test p-value</b>		
			H0	Carni	Vermi
	RespiSA/TotSA				
H0	512.34	-253.17	-	2.12e-04	6.02e-09
Carni	499.42	-244.71	-	-	8.46e-07
Vermi	477.17	-232.58	-	-	-

	<b>AIC</b>	<b>Lr test likelihood</b>	<b>Lr test p-value</b>		
			H0	Carni	Vermi
	OlfaSA/TotSA				
H0	512.34	-253.17	-	2.12e-04	6.02e-09
Carni	499.42	-244.71	-	-	8.46e-07
Vermi	477.17	-232.58	-	-	-

	<b>AIC</b>	<b>Lr test likelihood</b>	<b>Lr test p-value</b>		
			H0	Carni	Vermi
	OlfaSA/RespiSA				
H0	636.07	-315.03	-	3.20e-06	2.06e-12
Carni	614.76	-302.38	-	-	1.43e-08
Vermi	584.62	-286.31	-	-	-

	<b>AIC</b>	<b>Lr test likelihood</b>	<b>Lr test p-value</b>		
			H0	Carni	Vermi
	RespiSKL				
H0	565.52	-279.76	-	1.55e-05	5.06e-09
Carni	591.67	-290.84	-	-	1.47e-15
Vermi	530.00	-259.00	-	-	-

	<b>AIC</b>	<b>Lr test likelihood</b>	<b>Lr test p-value</b>		
			H0	Carni	Vermi
	OlfaSKL				
H0	636.07	-315.03	-	3.10e-11	2.48e-12
Carni	591.67	-290.84	-	-	3.22e-03
Vermi	585.00	-286.50	-	-	-

	<b>AIC</b>	<b>Lr test likelihood</b>	<b>Lr test p-value</b>		
			H0	Carni	Vermi
	OlfaCHAR/RespiCHAR				
H0	59.32	-26.66	-	9.84e-13	4.98e-14
Carni	8.03	0.99	-	-	1.82e-03
Vermi	0.31	5.85	-	-	-

**Table S7.** Results of 1.000 simulations of single-rate BM and three alternative OU models with the ratio between snout width (SNW) and snout length (SNL). BM and OU1 with omnivorous and all carnivorous dietary categories (carnivorous + vermivorous); OU2 with omnivorous, carnivorous, and vermivorous dietary categories; and OU3 with omnivorous, carnivorous, terrestrial vermivorous, and semi-fossorial vermivorous dietary categories. AICc = Akaike's information criterion corrected.  $\Delta$ AICc = difference between AICc compared to minimum AICc.

Model	SNW/SNL	
	AICc	$\Delta$ AICc
<b>BM</b>	-90.22	27.60
<b>OU1</b>	-104.65	13.17
<b>OU2</b>	-104.60	13.21
<b>OU3</b>	-117.82	00.00

**Table S8.** Dataset used for quantitative analyses. Abbreviations: see Table S1. American Museum of Natural History (AMNH), Centre de Biologie et de Gestion des Populations (CBGP), Field Museum of Natural History (FMNH), Museums Victoria (NMV), Museum Zoologicum Bogoriense (MZB), Natural History Museum London (NHMUK previously BMNH), Natural History Museum of Paris (MNHN), Smithsonian Institution National Museum of Natural History (NMNH), and University of Montpellier (UM).

Taxa	MUSEUM	VOUCHER	Time	DIET	Sex	mISA	iISA	sISA	rISA	eISA	fISA	eISA	hISA	totISA	SNL	SNL	SNW	2DRepl	2DOils	2DCarRepl	2DCarOils	ChkRepl	ChkOils	ChkSRepl	ChkSOils
Apomys_jabrae	AMNH	D4099.00	AP0bra	OMNI	-	45.86	112.45	25.73	54.49	73.22	36.87	50.99	54.84	454.45	37.00	6.09	1.47	1.52	2498.64	3681.00	147.20	2.14	1.54	1.72	
Apomys_banahao	CBGP	P0045	AP0bna	OMNI	-	71.18	93.17	22.40	55.86	84.52	40.42	50.63	62.37	480.56	36.51	13.08	6.50	1.53	2768.21	4242.00	1.48	2.09	1.59	1.76	
Apomys_banahao	CBGP	P0067	AP0bna	OMNI	-	51.74	82.52	21.15	41.47	66.34	32.26	35.17	43.19	373.83	33.74	12.16	5.65	-	-	-	1.48	2.03	1.55	1.63	
Apomys_banahao	CBGP	P0066	AP0bna	OMNI	-	95.83	141.24	27.78	60.51	89.26	39.57	43.07	71.20	568.47	38.38	13.30	6.81	-	-	-	1.67	2.17	1.66	1.70	
Apomys_date	FMNH	232475.00	AP0dta	OMNI	F	57.64	143.09	42.91	80.95	126.60	60.02	69.49	88.23	669.03	38.48	14.26	7.62	1.56	3277.09	5127.00	1.62	2.74	1.65	1.89	
Apomys_date	FMNH	130256.00	AP0dta	OMNI	M	73.04	110.79	31.89	82.47	117.05	55.07	59.41	80.02	608.73	31.73	13.65	6.54	-	-	-	1.32	2.48	1.49	1.83	
Apomys_hylocoetes	USNM	102544.00	AP0hly	OMNI	F	39.44	93.68	13.59	32.53	54.47	18.86	28.01	36.11	316.78	30.51	11.02	5.40	1.48	1.46	2300.00	3709.00	1.95	2.22	1.84	1.71
Apomys_lyllozalis	USNM	487855.00	AP0lly	OMNI	M	35.44	60.65	13.42	32.47	58.77	20.12	29.07	35.99	285.94	29.14	9.34	5.21	1.46	1.42	2393.68	3197.00	1.47	2.10	1.58	1.69
Archibdomys_lucenensis	USNM	578840.00	AR0luc	INSEC	F	33.27	48.03	15.44	38.81	52.07	19.01	26.29	33.29	266.21	26.67	9.10	5.13	1.46	1.53	2695.39	3935.00	1.51	2.45	1.58	1.79
Archibdomys_lucenensis	USNM	578837.00	AR0luc	INSEC	M	32.78	52.09	12.07	38.71	54.39	19.37	27.30	37.88	274.58	28.10	9.30	4.93	-	-	-	1.42	2.42	1.56	1.79	
Buromys_andrewsi	NMNH	31692.00	BU0andr	OMNI	-	62.54	132.80	21.63	59.70	80.96	45.31	50.49	66.65	520.08	36.08	15.05	6.63	1.43	1.46	2083.80	2979.00	1.68	2.32	1.72	1.77
Buromys_andrewsi	NMNH	31692.00	BU0andr	OMNI	-	88.70	150.71	34.02	64.89	100.92	43.97	53.23	61.35	597.48	40.75	16.13	7.94	-	-	-	1.70	2.18	1.74	1.72	
Buromys_perotus	NMNH	36868.00	BU0peri	OMNI	-	77.80	179.94	42.15	137.21	86.21	51.81	109.92	85.00	45.23	18.67	8.31	5.53	1.58	1.58	2296.93	3512.00	1.55	2.64	1.67	1.86
Chromomys_gonzalesi	USNM	488955.00	CHR0gz	WORM	F	50.11	53.48	24.36	80.38	78.84	37.79	51.63	60.37	436.95	34.45	12.00	7.49	1.36	1.52	2238.40	3044.00	1.16	2.43	1.43	1.80
Chromomys_mindorensis	FMNH	22107.00	CHR0md	WORM	F	43.34	85.29	38.74	94.64	91.61	49.60	70.22	86.33	559.77	37.54	12.52	8.19	1.36	1.55	2010.33	2725.00	1.32	2.74	1.50	1.88
Chromomys_silvaceus	NMNHUK	97.5.2.16	CHR0sl	WORM	M	47.19	61.08	24.81	68.76	75.80	38.55	51.14	49.98	417.10	34.62	11.06	6.91	1.48	1.53	2644.03	3954.00	1.50	2.33	1.58	1.77
Chromomys_silvaceus	NMNHUK	97.5.2.39	CHR0sl	WORM	F	41.72	59.29	18.89	56.20	61.89	37.46	51.64	56.79	385.87	33.31	11.21	6.02	-	-	-	1.53	2.40	1.63	1.71	
Chromomys_whitladi	NMNHUK	95.8.2.29	CHR0wh	WORM	F	49.03	70.45	28.03	82.65	105.97	51.56	62.95	90.61	547.26	35.29	12.30	7.88	1.42	1.60	2483.92	3825.00	1.57	2.88	1.62	1.95
Chromomys_whitladi	NMNHUK	95.8.2.19	CHR0wh	WORM	M	64.47	85.89	38.71	94.25	92.76	56.15	67.34	91.50	500.87	36.84	12.12	7.59	-	-	-	1.44	2.53	1.55	1.85	
Chromomys_whitladi	NMNHUK	97.5.2.17	CHR0wh	WORM	F	57.88	80.57	33.00	80.92	83.35	47.17	53.42	79.17	516.08	35.78	12.24	7.73	-	-	-	1.38	2.48	1.56	1.82	
Crunomys_falax	NMNHUK	97.4.8.1	CR0fal	INSEC	-	15.78	22.72	9.17	16.24	24.17	9.69	12.78	16.09	126.63	25.89	8.82	4.06	1.28	1.43	1256.45	1606.00	0.94	1.85	1.35	1.56
Crunomys_melanus	NMNHUK	7.2.2.14	CR0mel	INSEC	M	23.39	29.81	8.99	23.20	35.78	13.63	19.34	24.01	177.89	27.12	9.24	6.61	1.37	1.39	1841.28	2515.00	1.06	1.94	1.38	1.57
Deomys_ferrugineus	NMNHUK	1400.00	DE0ferr	INSEC	-	46.38	100.29	13.92	24.11	79.92	39.04	41.62	376.38	37.55	16.04	5.22	1.45	1.56	2271.12	3282.00	1.62	2.23	1.62	1.79	
Deomys_ferrugineus	NMNHUK	1402.00	DE0ferr	INSEC	-	49.53	81.63	14.42	23.50	63.38	23.92	36.12	34.94	326.49	35.94	15.29	5.07	-	-	-	1.60	2.15	1.60	1.83	
Echthoxy_centosa	NMNHUK	40.385	ECH0ce	WORM	F	95.13	152.01	39.44	106.40	142.58	62.49	81.37	112.51	719.92	51.82	21.44	7.39	1.45	1.55	2250.53	3651.00	1.54	2.32	1.71	1.83
Echthoxy_centosa	NMNHUK	153013.00	ECH0ce	WORM	M	91.34	132.22	42.59	93.33	143.38	56.80	70.30	94.85	734.82	52.29	22.83	6.75	-	-	-	1.40	2.41	1.63	1.83	
Echthoxy_lucura	NMNHUK	97.1.2.46	ECH0luc	WORM	M	96.81	159.22	46.65	101.20	152.26	55.06	82.46	90.03	783.89	53.68	22.50	6.95	1.43	1.56	2420.25	3452.00	1.39	2.36	1.68	1.82
Echthoxy_lucura	NMNHUK	97.1.2.45	ECH0luc	WORM	M	93.01	128.75	41.30	107.86	126.19	68.36	86.23	119.37	770.86	53.13	22.54	7.12	-	-	-	1.40	2.38	1.66	1.80	
Gracilomys_nalis	NMNHUK	31695.00	GR0nal	OMNI	-	24.73	41.97	12.26	29.49	54.12	17.95	24.24	20.26	226.69	29.51	10.00	5.32	1.38	1.47	1070.77	2581.00	1.25	2.22	1.45	1.68
Halmaheromys_bakimkot	MZB	82366.00	HAL0bak	OMNI	-	116.12	178.68	50.38	103.91	149.48	68.25	85.72	82.26	834.99	51.12	19.26	8.43	1.49	1.53	2475.95	3681.00	1.72	2.45	1.71	1.83
Hyrrhomyomys_stampelae	NMNHUK	237.58	HYR0st	WORM	-	45.62	73.22	24.02	82.33	98.39	58.87	73.39	91.13	546.94	46.99	18.35	7.35	1.29	1.49	1891.19	2450.00	1.21	2.57	1.45	1.80
Leptomys_falensis	NMNHUK	295.27.22	LEP0fal	INSEC	F	47.48	86.64	21.57	53.28	81.39	38.61	46.87	50.30	426.14	38.58	14.31	6.43	1.44	1.56	2234.15	3225.00	1.33	2.47	1.53	1.75
Leptomys_falensis	NMNHUK	5.11.28.22	LEP0fal	INSEC	M	51.69	91.06	26.38	49.84	71.44	35.71	41.03	54.68	421.91	36.79	13.93	6.32	1.50	1.52	2480.17	3221.00	1.55	2.19	1.62	1.74
Leptomys_elegans	NMNHUK	50.1254	LEP0leg	INSEC	M	51.95	75.32	27.63	47.17	66.37	34.88	41.22	55.87	400.20	36.01	12.74	6.17	-	-	-	1.50	2.22	1.56	1.74	
Leptomys_eudimorphi	NMNHUK	50.1252	LEP0leg	INSEC	M	60.87	93.98	26.98	56.28	76.80	42.07	44.16	49.29	448.22	36.67	13.70	6.80	1.48	1.54	2848.95	4728.00	1.64	2.46	1.60	1.79
Leptomys_eudimorphi	AMNH	194936.00	LEP0leg	INSEC	F	46.79	71.26	24.83	41.69	59.80	29.08	35.74	44.07	353.33	35.55	11.91	6.22	-	-	-	1.40	2.26	1.53	1.73	
Leptomys_signatus	AMNH	105370.00	LEP0sig	INSEC	F	44.43	64.80	17.93	32.67	56.63	26.42	30.50	38.62	312.00	33.40	12.02	5.62	1.46	1.47	2384.04	3490.00	1.42	2.06	1.54	1.66
Malcomys_candollei	USNM	486151.00	MAL0can	OMNI	M	57.40	91.74	29.17	78.86	84.95	42.11	61.43	74.79	521.46	38.98	15.14	6.70	1.41	1.58	2271.92	3210.00	1.36	2.60	1.62	1.88
Malcomys_edwardsi	AMNH	46726.00	MAL0eda	OMNI	F	37.05	80.22	15.26	50.81	61.99	21.35	31.80	44.34	343.43	33.69	13.41	5.18	1.45	1.54	2206.53	3205.00	1.28	2.27	1.53	1.78
Maomys_muscibroekii	CBGP	37009.00	MA0mus	OMNI	-	89.41	121.07	26.45	77.42	102.55	41.92	62.22	96.41	617.44	42.53	16.11	6.17	1.48	1.55	2262.00	3355.00	1.46	2.40	1.56	1.82
Maomys_sulzeri	CBGP	6399.00	MA0sul	OMNI	F	17.11	91.74	35.17	87.11	108.53	52.94	67.63	90.47	651.60	44.98	15.99	7.30	1.46	1.49	2481.32	3641.00	1.39	2.14	1.61	1.73
Maomys_sulzeri	CBGP	03135	MA0sul	OMNI	F	115.27	139.17	39.25	108.19	137.39	53.23	51.92	96.44	757.47	44.29	17.64	7.30	1.33	1.47	1886.63	2646.00	1.17	2.52	1.50	1.86
Mayeromys_ellermani	AMNH	53278.00	MA0yell	INSEC	M	11.77	18.40	6.14	14.23	19.11	8.45	11.68	10.37	100.15	21.40	6.84	4.54	1.33	1.47	1986.61	2400.00	1.39	2.20	1.48	1.59
Mayeromys_ellermani	NMNHUK	53280.00	MA0yell	INSEC	M	16.30	22.38	6.82	19.28	25.57	13.02	14.													



**Table S9.** List of references for dietary categorizations.

Species	DIET	Region	Reference
APOabra	OMNI	PHIL	Heaney et. al. 2016
APObana	OMNI	PHIL	Heaney et. al. 2016
APOdata	OMNI	PHIL	Heaney et. al. 2016
APOhylo	OMNI	PHIL	L. Heaney pers. comm.; IUCN red list
APOlitt	OMNI	PHIL	Based on other Apomys
ARCluzo	CARNI	PHIL	Rickart et. al. 1991; Heaney et. al. 1999; Balete et. al. 2012
BUNandr	OMNI	SULAW	Musser 2014
BUNpeni	OMNI	SULAW	Musser 2014
CHRgonz	VERMI	PHIL	Rickart et. al. 1991; Heaney et. al. 1999
CHRmind	VERMI	PHIL	Rickart et. al. 1991; Heaney et. al. 1999; Heaney et. al. 2016
CHRsila	VERMI	PHIL	Heaney et. al. 2010; Rickart et. al. 2011
CHRwhit	VERMI	PHIL	Heaney et. al. 2010; Rickart et. al. 2011
CRUfall	CARNI	PHIL	-
DEOferr	CARNI	AFRIC	Happold 2013
CRUmela	CARNI	PHIL	Musser & Durden 2002
ECHcent	VERMI	SULAW	Musser & Durden 2014
ECHleuc	VERMI	SULAW	Musser 1990
GRAradi	OMNI	SULAW	Rowe et. al. 2016
HALboki	OMNI	MOLUC	Fabre et. al. 2013
HYOstue	VERMI	SULAW	Esselstyn et. al. 2015
LEParf	CARNI	PAPUA	Musser et. al. 2008
LEPeleg	CARNI	PAPUA	Musser et. al. 2008
LEPerns	CARNI	PAPUA	Musser et. al. 2008
LEPsign	CARNI	PAPUA	Musser et. al. 2008
MALedwa	OMNI	AFRIC	Happold 1987; Cole 1975
MAXmuss	OMNI	SULAW	Musser 1982
MAXsuri	OMNI	ORIEN	Pimsai et. al. 2014
MELburt	OMNI	MOLUC	Kerle 2008
MELobie	OMNI	MOLUC	Pers. Data.
MELnaso	VERMI	SULAW	Musser 1982
MICrich	CARNI	PAPUA	Helgen et. al. 2010
MUScerv	OMNI	ORIEN	Francis 2008; Lekagul & McNeely 1988
MUSpaha	CARNI	ORIEN	Smith & Xie 2008
NANminu	OMNI	AFRIC	Happold 2013
OXYdasy	CARNI	AMERI	Based on other Oxymycterus species; Wilson et. al. 2017
OXYquae	CARNI	AMERI	Based on other Oxymycterus species; Wilson et. al. 2017
PARwilh	CARNI	PAPUA	Musser et. al. 2008
PAUverm	VERMI	SULAW	Esselstyn et. al. 2012
PSEelea	CARNI	PAPUA	Based on other Pseudohydromys
PSEelle	CARNI	PAPUA	Based on other Pseudohydromys
PSEfusc	CARNI	PAPUA	Wilson et. al. 2017
PSEmuri	CARNI	PAPUA	Wilson et. al. 2017
RATmarm	OMNI	SULAW	Musser 1982
RATmoro	OMNI	MOLUC	Pers. Comm.
RATnorv	OMNI	ORIEN	Francis 2008; Zhang et. al. 2005
RATprae	OMNI	PAPUA	Taylor et. al. 1982; Flannery 1995
RATtane	OMNI	ORIEN	Pimsai et. al. 2014
RHYisar	VERMI	PHIL	Rickart et. Al. 1991; Heaney et. al. 1999; Rickart et. al. 2011; Balete et. al. 2009
RHYsori	VERMI	PHIL	Rickart et. Al. 1991; Heaney et. al. 1999; Rickart et. al. 2011; Balete et. al. 2009
SIGhisp	OMNI	AMERI	Cameron & Spencer 1981
SOMmacr	CARNI	SULAW	Musser & Durden 2002; Achmadi et. al. 2014
SORleon	VERMI	PHIL	Balete et. al. 2012
TATmacr	VERMI	SULAW	Musser 1982
TATrhin	VERMI	SULAW	Musser 1982