



Figure S2: Heritabilities and associated intervals for mandibular traits, obtained from three different G -matrix estimation algorithms. For both Wombat and the REML algorithm written in R, intervals refer to a normal approximation of the likelihood function; for BFGS, intervals are obtained from the posterior distribution of G -matrices.

Table S1: Descriptive statistics, repeatabilities, and effective sample size for cranial traits.

	Mean	Variance	CV	Repeatability	N_{eff}
ISPM	4.7831	0.4169	0.1350	0.9813	20.7315
PMZS	6.7766	0.8043	0.1323	0.9900	18.9310
PMZI	8.8525	1.1411	0.1207	0.9931	14.0073
PMMT	7.0880	0.3556	0.0841	0.9823	21.0701
MTPNS	1.6680	0.0223	0.0894	0.6538	29.7420
ISPNS	11.7723	1.5909	0.1071	0.9937	31.2796
NSLZI	14.7935	3.2506	0.1219	0.9978	17.8501
ISNSL	3.0014	0.2001	0.1490	0.9722	7.6078
NSLNA	9.3617	1.6327	0.1365	0.9942	23.6907
NSLZS	12.1392	2.3570	0.1265	0.9971	21.0287
NAPNS	8.0508	0.4377	0.0822	0.9920	17.4201
PTZYGO	6.8091	0.6421	0.1177	0.9890	14.7499
ZSZI	3.0291	0.3211	0.1871	0.9704	2.4434
ZIMT	4.4680	0.4140	0.1440	0.9825	17.0637
ZIZYGO	3.1533	0.2004	0.1420	0.9383	23.5841
ZITSP	3.4402	0.3975	0.1833	0.9849	13.9055
EAMZYGO	3.8778	0.1540	0.1012	0.9509	36.1888
ZYGOTSP	3.8296	0.2861	0.1397	0.9662	6.0911
PTTSP	4.1248	0.1232	0.0851	0.9578	23.1891
NABR	7.7062	0.5475	0.0960	0.9749	16.2234
BRPT	4.0049	0.0623	0.0623	0.8683	36.3455
BRAPET	7.8848	0.2468	0.0630	0.9677	36.1158
PTAPET	8.4384	0.5422	0.0873	0.9891	26.8944
PTBA	11.2926	1.1548	0.0952	0.9947	23.4941
PTEAM	8.6082	0.7725	0.1021	0.9911	19.4437
LDAS	5.3572	0.0767	0.0517	0.8968	62.7865
BRLD	7.1663	0.2042	0.0631	0.9572	47.7202
OPILD	3.6473	0.3391	0.1597	0.9697	15.7402
PTAS	7.8272	0.3809	0.0789	0.9743	31.2381
JPAS	4.6982	0.3511	0.1261	0.9744	10.8988
PNSAPET	5.3178	0.5627	0.1411	0.9807	20.6741
APETBA	3.6937	0.3099	0.1507	0.9691	16.4576
APETTS	3.4693	0.0381	0.0563	0.7866	30.1533
BAEAM	5.7093	0.1689	0.0720	0.9557	17.6073
BAOPI	4.2967	0.0706	0.0618	0.9046	57.2964

Table S2: Descriptive statistics, repeatabilities, and effective sample sizes for mandibular traits. Basic statistics here refer only to the subset of 30 individuals used to estimate repeatability, except for the effective sample sizes; see 'Materials and Methods' for details

	Mean	Variance	CV	Repeatability	N_{eff}
DAMA	3.1582	0.1396	0.1183	0.9425	46.0166
DAMP	4.7575	0.2095	0.0962	0.9643	77.3228
MAMP	1.6089	0.0207	0.0894	0.8788	111.2591
DAVC	3.9638	0.2076	0.1150	0.9502	31.1409
MAVC	3.1968	0.1695	0.1288	0.9739	31.4147
MPVC	3.9326	0.2178	0.1187	0.9702	43.4467
DAVA	2.2533	0.1142	0.1500	0.9396	28.7245
MAVA	2.9556	0.1584	0.1347	0.9760	26.2380
MPVA	4.2982	0.2168	0.1083	0.9845	44.1206
VCVA	1.8208	0.0490	0.1215	0.9010	8.6261
CORMCA	1.4322	0.1103	0.2319	0.9635	137.3761
CORMCP	2.8385	0.2231	0.1664	0.9678	98.4473
MCAMCP	1.4438	0.0479	0.1516	0.9276	4.7604
CORANG	5.5261	0.9524	0.1766	0.9895	50.7683
MCAANG	4.3748	0.5434	0.1685	0.9902	16.9527
MCPANG	3.7203	0.3883	0.1675	0.9837	17.1653
CORIDM	6.1405	0.7929	0.1450	0.9921	18.1222
MCAIDM	6.0728	0.9212	0.1580	0.9921	30.2408
MCPIDM	6.6343	1.0551	0.1548	0.9911	29.3048
ANGIDM	4.9149	1.1668	0.2198	0.9916	17.4681

Table S3: Heritabilities estimated for latent traits under the BSFG model, along with 95% posterior intervals derived from the posterior distribution of h^2 . Bold values indicate those h^2 values whose posterior intervals do not contain the null value.

λ	Skull			Mandible		
	Mean	PI-	PI+	Mean	PI-	PI+
1	0.30	0.11	0.51	0.65	0.38	0.94
2	0.44	0.18	0.72	0.83	0.61	0.99
3	0.51	0.22	0.84	0.50	0.20	0.82
4	0.79	0.53	0.99	0.83	0.59	0.99
5	0.63	0.00	0.97	0.10	0.00	0.41
6	0.11	0.00	0.36	0.27	0.00	0.77
7	0.08	0.00	0.37	0.14	0.00	0.49
8	0.15	0.00	0.45	0.41	0.00	0.86
9	0.28	0.00	0.67	0.05	0.00	0.29
10	0.08	0.00	0.38	0.49	0.00	0.90
11	0.24	0.00	0.54	0.45	0.00	0.89
12	0.38	0.00	0.71	0.43	0.00	0.95
13	0.32	0.00	0.88	0.17	0.00	0.86
14	0.34	0.00	0.62	0.31	0.00	0.90
15	0.47	0.00	0.86	0.21	0.00	0.86
16	0.10	0.00	0.67	0.13	0.00	0.77
17	0.01	0.00	0.00	0.05	0.00	0.45