Supplementary Tables

Supplementary Table S1. Percentage of *M. m. domesticus* alleles per individual. The percentage of *M. m. domesticus* alleles (PercDom) based on the average of parental genotypes for 37 diagnostic SNPs is shown for all individuals used in this study. ID, identification number of the respective mouse (corresponds to MID in SNP genotype data (dryad cite). A, mouse was previously used in Pallares *et al.* (2014) and Turner and Harr (2014). These mice were genotyped with the panel of 270 SNPs. B, mouse used only in the current study.

ID	Family ID	PercDom	Age (days)	Sex	OtherStudies
1	TUP9	21.7	73	M	A
2	FSP14	59.2	80	M	A
3	GLP6	14.6	64	M	B
4	FSP14	59.2	80	M	A
5	RFP2	15.0	81	M	A
6	HAP9	25.0	84	M	A
7	HAP8	24.2	83	M	A
8	KHP1	22.9	84	M	A
9	REP1	14.2	83	M	A
10	GRP1	8.3	79	M	B
11	GLP4	14.3	83	M	A
12	HHP1	44.2	86	M	A
13	KTP3	24.6	79	M	A
14	STP1	93.3	83	M	A
15	HAP7	27.5	81	M	A
16	TUP5	20.8	81	M	A
17	FSP10	60.8	72	M	A
18	KTP1	27.2	79	M	A
19	FSP10	60.8	75	M	A
20	GRP1	8.3	69	M	B
21	FHP2	37.5	76	M	A
22	FTP1	42.5	84	M	A
24	TUP9	21.7	73	M	A
25	KTP1	27.2	82	M	A
26	HHP1	44.2	86	M	A
27	SOP7	88.8	84	M	B
28	FSP7	61.0	81	M	A
30	HAP4	23.3	76	M	A
31	REP1	14.2	81	M	B
32	KMP4	26.7	82	M	A
33	FHP2	37.5	81	M	A
34	SOP4	99.3	81	M	B
35	REP1	14.2	83	M	B
36	TSP1	60.0	84	M	A
37	KTP3	24.6	79	M	A
38	FSP12	56.8	71	M	A
39	FSP12	56.8	68	M	A
40	STP2	90.8	83	M	A
41	KFP1	43.9	69	M	A
42	HAP6	23.3	64	M	A
43	KHP1	22.9	84	M	A
44	HAP6	23.3	62	M	A

45	HAP5	30.8	84	M	A
46	RTP1	16.7	79	M	A
48	HAP4	23.3	84	M	A
49	FHP1	40.0	82	M	A
50	FHP2	37.5	79	M	A
51	KTP3	24.6	80	M	A
52	SOP6	91.4	81	M	A
53	KMP4	26.7	82	M	A
54	KMP4	26.7	82	M	A
55	TUP6	32.3	69	M	A
56	STP6	88.3	64	M	B
57	STP1	93.3	84	M	B
58	HAP5	30.8	84	M	A
59	HAP1	25.0	84	M	A
60	KFP1	43.9	69	M	A
61	FHP1	40.0	82	M	A
64	FHP1	40.0	82	M	A
65	KTP3	24.6	79	M	A
66	KMP2	32.0	81	M	A
67	FSP11	61.7	68	M	A
68	KHP1	22.9	84	M	A
69	HAP4	23.3	77	M	A
70	KHP2	30.5	82	M	A
71	HAP9	25.0	84	M	A
72	KHP3	25.8	72	M	A
73	REP1	14.2	82	M	B
74	RTP1	16.7	81	M	A
75	KTP3	24.6	79	M	A
76	TUP5	20.8	76	M	A
77	TUP2	29.7	84	M	A
78	SOP5	91.1	76	M	A
80	FSP8	60.0	81	M	A
81	TUP5	20.8	81	M	A
82	TSP2	61.4	84	M	A
84	FHP2	37.5	80	M	A
85	HOP5	69.4	67	M	A
86	FTP1	42.5	84	M	A
87	TSP2	61.4	84	M	A
88	TUP3	18.3	77	M	A
89	FSP4	56.7	84	M	A
90	FTP2	34.2	75	M	A
91	HAP1	25.0	83	M	A
92	HAP3	17.5	83	M	A
93	KTP1	27.2	82	M	A
94	HAP9	25.0	84	M	A
95	HHP1	44.2	86	M	A
96	FSP11	61.7	71	M	A
97	GLP2	15.8	83	M	B
98	FTP2	34.2	75	M	A
99	HAP1	25.0	82	M	A
100	FSP12	56.8	68	M	A
101	KMP1	22.4	81	M	A
102	HHP1	44.2	86	M	A
103	FHP1	40.0	81	M	A
104	SGP1	50.3	80	M	A
106	HAP4	23.3	77	M	A
107	HOP4	69.4	84	M	A
108	KTP1	27.2	82	M	A
109	HOP4	69.4	84	M	A
110	KMP1	22.4	82	M	A
111	GLP6	14.6	62	M	A
112	FSP6	55.8	82	M	A
113	FSP8	60.0	78	M	A
114	FSP3	55.0	84	M	A

115	HAP6	23.3	69	M	A
116	HAP3	17.5	83	M	A
117	KHP1	22.9	83	M	A
118	REP1	14.2	83	M	B
119	KFP1	43.9	79	M	A
120	KTP1	27.2	81	M	A
121	FSP12	56.8	69	M	A
123	TUP3	18.3	77	M	A
124	FHP2	37.5	79	M	A
125	TUP5	20.8	76	M	A
126	HAP6	23.3	69	M	A
127	RTP1	16.7	83	M	A
128	KMP2	32.0	80	M	A
129	HOP5	69.4	67	M	A
130	TSP2	61.4	84	M	A
131	HAP4	23.3	84	M	A
132	FHP1	40.0	80	M	A
133	HAP3	17.5	84	M	A
134	SOP6	91.4	81	M	B
135	TUP4	24.7	84	M	A
136	HAP3	17.5	84	M	A
137	FHP2	37.5	79	M	A
138	TUP5	20.8	77	M	A
140	HAP9	25.0	83	M	A
141	KHP3	25.8	71	M	A
142	TUP5	20.8	81	M	A
143	SOP1	90.5	84	M	B
144	TSP2	61.4	84	M	A
145	TUP1	39.7	84	M	A
146	HAP3	17.5	84	M	A
147	TUP3	18.3	83	M	A
148	SOP1	90.5	84	M	B
149	KFP1	43.9	80	M	A
150	TUP3	18.3	82	M	A
151	KTP1	27.2	82	M	A
152	FSP5	58.5	83	M	A
153	KTP1	27.2	82	M	A
154	TSP1	60.0	84	M	A
156	HAP4	23.3	84	M	A
158	HTP2	49.2	83	M	A
159	GLP4	14.3	83	M	B
160	HAP4	23.3	83	M	A
161	TUP5	20.8	76	M	A
162	TUP3	18.3	83	M	A
163	TUP5	20.8	76	M	A
164	RTP1	16.7	83	M	A
165	RGP1	11.7	69	M	B
166	KHP1	22.9	83	M	A
167	FHP2	37.5	79	M	A
168	RGP1	11.7	69	M	B
169	KHP2	30.5	82	M	A
170	RTP1	16.7	84	M	A
171	FSP6	55.8	82	M	A
172	HAP5	30.8	84	M	A
173	HOP4	69.4	84	M	A
174	FTP2	34.2	75	M	A
175	GSP1	57.0	80	M	A
176	KTP1	27.2	82	M	A
177	KHP2	30.5	82	M	A
178	STP4	90.0	81	M	B
180	SOP7	88.8	84	M	A
181	RTP1	16.7	84	M	A
182	KTP3	24.6	80	M	A
184	FTP1	42.5	84	M	A

185	GLP2	15.8	83	M	A
186	HAP6	23.3	64	M	A
187	SOP1	90.5	84	M	B
188	KHP3	25.8	71	M	A
190	FHP2	37.5	83	M	A
191	KHP2	30.5	83	M	A
192	FSP8	60.0	82	M	A
193	FSP13	57.5	83	M	A
194	KHP3	25.8	71	M	A
195	KHP3	25.8	72	M	A
196	FSP10	60.8	72	M	A
197	FSP5	58.5	83	M	A
198	TUP5	20.8	82	M	A
199	KTP1	27.2	82	M	A
200	KHP2	30.5	83	M	A
211	FSP7	61.0	71	M	A
214	FSP7	61.0	71	M	A
215	FSP17	59.2	73	M	A
222	FSP14	59.2	71	M	A
225	FSP16	51.7	71	M	A
230	KMP3	24.0	74	M	A
233	FSP7	61.0	71	M	A
236	HFP3	60.8	84	M	A
240	FSP16	51.7	72	M	A
244	HOP11	66.1	74	M	A
245	FSP16	51.7	72	M	A
249	KMP4	26.7	83	M	A
250	KMP3	24.0	74	M	A
500	GRP1	8.3	87	F	B
501	GRP1	8.3	87	F	B
502	GRP1	8.3	90	F	B
503	GRP1	8.3	90	F	B
504	RGP1	11.7	64	F	B
505	RGP1	11.7	64	F	B
506	RGP1	11.7	64	F	B
508	GLP4	14.3	85	F	B
509	GLP6	14.6	63	F	B
510	GLP6	14.6	92	F	B
511	GLP2	15.8	72	F	B
512	GLP2	15.8	72	F	B
513	GLP2	15.8	72	F	B
516	FHP1	40.0	75	F	B
517	FHP1	40.0	75	F	B
518	FHP1	40.0	84	F	B
519	FHP1	40.0	84	F	B
520	FHP1	40.0	84	F	B
521	FHP1	40.0	84	F	B
522	KFP1	43.9	92	F	B
523	KFP1	43.9	92	F	B
524	KFP1	43.9	92	F	B
525	KFP1	43.9	92	F	B
526	KFP1	43.9	92	F	B
527	HTP2	49.2	63	F	B
528	HTP2	49.2	63	F	B
529	HTP2	49.2	63	F	B
530	HHP3	50.5	80	F	B
531	HHP3	50.5	80	F	B
532	HHP3	50.5	80	F	B
533	HHP3	50.5	80	F	B
534	HHP3	50.5	80	F	B
535	FSP14	59.2	66	F	B
537	TSP1	60.0	71	F	B
538	TSP1	60.0	71	F	B
539	FSP8	60.0	76	F	B

540	FSP8	60.0	76	F	B
541	FSP10	60.8	91	F	B
548	FSP11	61.7	85	F	B
549	STP5	89.8	93	F	B
550	STP5	89.8	93	F	B
551	STP5	89.8	93	F	B
552	STP5	89.8	93	F	B
553	STP5	89.8	93	F	B
554	STP5	89.8	93	F	B
556	SOP6	91.4	88	F	B
557	SOP6	91.4	88	F	B
558	SOP6	91.4	88	F	B
559	SOP6	91.4	88	F	B
560	SOP6	91.4	88	F	B
561	SOP6	91.4	88	F	B

Supplementary Table S2. Description of the landmarks used for geometric morphometrics analyses.

Landmark	Description
Skull	
1	Nasal bones most anterior suture
2	Nasal bones most posterior suture
3	Frontal bones most posterior suture
4	Parietal bones most posterior suture
5	Interparietal bone most posterior point on the median line
6	Right side, most anterior point of the suture between frontal and parietal bones
7	Left side, most anterior point of the suture between frontal and parietal bones
8	Right side, intersection between parietal, occipital and squamosal bones
9	Left side, intersection between parietal, occipital and squamosal bones
10	Right, most posterior junction of squamosal bone and the zygomatic process of the squamosal bone
11	Left, most posterior junction of squamosal bone and the zygomatic process of the squamosal bone
12	Right side, most anterior suture of the zygomatic process of the squamosal bone and jugal bone
13	Left side, most anterior suture of the zygomatic process of the squamosal bone and jugal bone
14	Right side, most anterior suture of jugal bone and the zygomatic process of the maxillary bone
15	Left side, most anterior suture of jugal bone and the zygomatic process of the maxillary bone
16	Right side, intersection of the frontal, lacrimal and the zygomatic process of the maxillary bone
17	Left side, intersection of the frontal, lacrimal and the zygomatic process of the maxillary bone
18	Right infraorbital foramen most superior point
19	Left infraorbital foramen most superior point
20	Right infraorbital foramen most inferior point
21	Left infraorbital foramen most inferior point
22	Right premaxilla-right nasal bone most anterior point of suture
23	Left premaxilla-left nasal bone most anterior point of suture
24	Most superior point of the right incisor alveolus
25	Most superior edge of the left incisor alveolus
26	Most inferior point of the right incisor alveolus
27	Most inferior point of the left incisor alveolus
28	Right premaxilla-maxilla most ventral juntion
29	Left premaxilla-maxilla most ventral juntion
30	Most anterior point of the right first molar alveolus
31	Most anterior point of the left first molar alveolus
32	Most posterior point of the right third molar alveolus
33	Most posterior point of the left third molar alveolus
34	Most anterior point of the right anterior palatine foramen
35	Most anterior point of the left anterior palatine foramen
36	Most posterior point of the right anterior palatine foramen

37	Most posterior point of the left anterior palatine foramen
38	Right pterygoid process, most posterior point
39	Left pterygoid process, most posterior point
40	Median-line point of the suture between occipital and basisphenoid bones
41	Median-line point of the suture between basisphenoid and presphenoid bones
42	Most posterior point of the suture between palatine bones
43	Foramen magnum most anterior point, Basion
44	Foramen magnum most posterior point, Bregma

Mandible

1	Most superior point of the incisor alveolus
2	Most inferior point of the incisor alveolus
3	Most anterior point of the first molar alveolus
4	Most posterior point of the third molar alveolus
5	Most posterior tip of the coronoid process
6	Most anterior concave point of coronoid process
7	Most anterior point of the articular surface of the condyle
8	Most posterior tip of the condyle
9	Most anterior concave point between condyle and angular process
10	Most posterior tip of angular process
11	Most inferior point of angular process
12	Ascending ramus dorsal-most ventral point
13	Alveolar region most inferior point

Supplementary Table S3. Results of comparisons between the skull shapes of hybrid groups. VarPCs, amount of skull variation represented by the first 10 PCs from a PCA using individuals from both groups. DiffMean, p-value after multiple testing correction from a MANOVA using the first 10 PCs. MisClass, percentage of mice classified to the wrong group in a leave-one-out validation of the discriminant analysis. Procrustes, Procrustes distance between mean skull shapes. Genomic, difference between the mean percentage of *M. m. domesticus* alleles. Angle, angle between *mus*-to-*dom* vector and the vector formed by the mean shape of the groups. SignAngle, p-value after multiple testing correction of the angle between vectors.

GroupPair	VarPCs	DiffMean	Misclass	Procrustes	Genomic	Angle	SignAngle
0-1	0.81162	4.00E-05	8.9	0.0266	7.2	90.3	0.88068
0-2	0.76457	3.37E-09	1.4	0.0254	15.9	87.2	0.88068
0-3	0.89436	2.25E-06	0	0.0298	25.9	78.8	0.282
0-4	0.84081	2.94E-09	0	0.0295	34.8	65.9	0.00351
0-5	0.85707	5.31E-06	6.2	0.0319	46.9	61.8	0.00036
0-6	0.83864	6.46E-10	0	0.0320	54.0	60.3	0.00036
0-8	0.9653	6.94E-08	6.7	0.0326	81.1	44.4	0.00036
0-9	0.90405	2.94E-08	4.3	0.0378	83.5	43.3	0.00036

1-2	0.73235	1.50E-11	15	0.0140	8.7	84.2	0.82564
1-3	0.7898	3.27E-09	9.8	0.0182	18.7	71.0	0.04056
1-4	0.77688	5.03E-14	8.6	0.0231	27.6	58.1	0.00036
1-5	0.78354	4.45E-17	4.6	0.0264	39.7	54.8	0.00036
1-6	0.77005	3.86E-20	0	0.0240	46.8	48.2	0.00036
1-8	0.80186	2.97E-13	0	0.0275	73.9	31.5	0.00036
1-9	0.79815	9.17E-20	0	0.0284	76.3	13.6	0.00036
2-3	0.76008	5.01E-09	11	0.0149	9.9	72.3	0.05283
2-4	0.73954	5.07E-24	2.1	0.0171	18.9	50.9	0.00036
2-5	0.75632	3.78E-26	1.1	0.0249	31.0	56.3	0.00036
2-6	0.74595	8.86E-32	2.1	0.0231	38.1	50.8	0.00036
2-8	0.76545	9.17E-20	0	0.0287	65.2	39.9	0.00036
2-9	0.7726	5.76E-29	0	0.0301	67.6	29.3	0.00036
3-4	0.79658	2.40E-09	5.7	0.0140	8.9	63.3	9.00E-04
3-5	0.81162	2.79E-07	8.3	0.0167	21.1	56.1	0.00036
3-6	0.79394	3.19E-13	3.8	0.0185	28.2	57.0	0.00036
3-8	0.86897	2.29E-09	0	0.0281	55.3	51.4	0.00036
3-9	0.84593	1.25E-12	0	0.0281	57.6	39.6	0.00036
4-5	0.77301	2.25E-06	14	0.0129	12.1	76.4	0.18879
4-6	0.76598	4.93E-08	18	0.0140	19.2	74.2	0.10008
4-8	0.82494	5.79E-08	2.5	0.0253	46.3	63.6	0.00098
4-9	0.81042	4.98E-12	2.1	0.0252	48.7	52.2	0.00036
5-6	0.77073	1.20E-04	19	0.0116	7.1	86.2	0.88068
5-8	0.84327	5.90E-09	0	0.0257	34.2	71.4	0.04367
5-9	0.81915	1.06E-14	0	0.0251	36.6	60.4	0.00036
6-8	0.82006	1.03E-06	5	0.0232	27.1	71.4	0.04367
6-9	0.80188	2.79E-09	4.2	0.0217	29.5	57.6	0.00036
8-9	0.87154	0.2126444	27	0.0202	2.4	78.0	0.26676
mus-dom	0.79065	2.37E-28	0	0.0261	78.7	-	-

Supplementary Table S4. Results of comparisons between the mandible shape of hybrid groups. VarPCs, amount of skull variation represented by the first 10 PCs from a PCA using individuals from both groups. DiffMean, p-value after multiple testing correction from a MANOVA using the first 10 PCs. MisClass, percentage of mice classified to the wrong group in a leave-one-out validation of the discriminant analysis. Procrustes, Procrustes distance between mean skull shapes. Genomic, difference between the mean percentage of *M. m. domesticus* alleles. Angle, angle between *mus*-to-*dom* vector and the vector formed by the mean shape of the groups. SignAngle, p-value after multiple testing correction of the angle between vectors.

GroupPair	VarPCs	DiffMean	Misclass	Procrustes	Genomic	Angle	SignAngle
0-1	0.87664	0.0065	6.7	0.02618	7.2	89.1	1
0-2	0.85102	1.1E-06	1.4	0.02840	16.0	86.1	1
0-3	0.88724	9.4E-05	3.4	0.02702	25.7	74.8	0.4180
0-4	0.86911	1.8E-09	0	0.02642	34.7	58.5	1.3E-02
0-5	0.89918	8.9E-06	6.2	0.03228	46.9	63.0	4.7E-02
0-6	0.8741	4.3E-07	2.7	0.03662	54.0	54.5	3.4E-03
0-8	0.9737	5.3E-05	6.7	0.04751	81.1	33.4	3.6E-04
0-9	0.94324	2.1E-05	0	0.05052	83.5	28.2	3.6E-04
1-2	0.83109	4.5E-08	21	0.01217	8.8	82.9	0.9850
1-3	0.85401	4.0E-08	13	0.01716	18.6	67.0	0.1241
1-4	0.84424	9.8E-12	10	0.02191	27.6	52.3	1.6E-03
1-5	0.86367	8.5E-13	4.6	0.02552	39.7	56.0	6.1E-03
1-6	0.852	1.6E-14	2.9	0.02797	46.8	41.7	3.6E-04
1-8	0.88303	5.8E-15	2.1	0.04162	73.9	19.5	3.6E-04
1-9	0.8867	6.0E-16	0	0.04481	76.3	10.2	3.6E-04
2-3	0.83272	0.0002	23	0.01504	9.8	69.8	0.1728
2-4	0.83292	2.2E-14	11	0.02241	18.8	58.0	0.0120
2-5	0.84601	7.4E-14	13	0.02445	30.9	58.6	0.0127
2-6	0.83645	1.8E-20	4.1	0.02865	38.0	47.5	3.6E-04
2-8	0.85933	1.1E-16	1.3	0.04139	65.1	24.2	3.6E-04
2-9	0.86719	2.5E-23	0	0.04522	67.5	19.6	3.6E-04
3-4	0.84507	0.0002	19	0.01782	9.0	67.9	0.1337
3-5	0.86057	0.0001	16	0.01998	21.2	67.7	0.1337
3-6	0.84548	1.4E-07	11	0.02331	28.3	52.5	1.7E-03
3-8	0.89106	4.0E-08	0	0.03824	55.3	31.7	3.6E-04
3-9	0.88634	3.7E-11	0	0.04100	57.8	24.1	3.6E-04
4-5	0.85158	0.03778	33	0.01332	12.1	86.2	1
4-6	0.83065	6.3E-06	13	0.01722	19.2	64.2	0.0631
4-8	0.8826	1.8E-09	0	0.03425	46.3	41.0	3.6E-04
4-9	0.87883	1.7E-14	0	0.03468	48.7	27.6	3.6E-04
5-6	0.8325	0.0248	28	0.01256	7.1	58.2	0.0125
5-8	0.89743	1.2E-07	0	0.03429	34.2	43.2	3.6E-04
5-9	0.89319	5.3E-11	0	0.03723	36.6	36.7	3.6E-04
6-8	0.87383	1.2E-07	2.5	0.02852	27.1	49.9	6.3E-04
6-9	0.86648	2.6E-08	6.2	0.03086	29.5	41.2	3.6E-04
8-9	0.92581	0.0690	35	0.02107	2.4	76.7	0.4904
mus-dom	0.87326	2.0E-26	0	0.04239	78.7	-	-