Supplementary Tables (1-7)

Table S1: Primer details for microsatellite loci used to genotype black-backed jackals (*Canis Mesomelas*)

Microsatellite marker	Primer sequence	Size range (bp)	Repeat unit	Fluorescent label	T_a (°C)	Reference
PEZ1	F: 5'- ggc tgt cac ttt tcc ctt tc -3'	95 - 136	Tetra	NED	55	Halverson and Basten, 2005
PEZ1	R: 5'- cac caca at ctc tct cat aaa tac -3'					
PEZ6	F: 5'- atg agc act ggg tgt tat ac -3'	166 - 215	Tetra	NED	50	Halverson and Basten, 2005
PEZ6	R: 5'- aca caa ttg cat tgt caa ac -3'					
FHC2054	F: 5'- gcc tta ttc att gca gtt agg g -3'	140 - 184	Tetra	VIC	50	Francisco et al., 1996
FHC2054	R: 5'- atg ctg agt ttt gaa ctt tcc c -3'					
VGL0760	F: 5'- gca gat tca gga caa aga cca -3'	276 - 340	Tetra	FAM	58	Wictum et al., 2012
VGL0760	R: 5'- ggc cca gaa aag gat agg ag -3'					
VGL1063	F: 5'- agc cac aga gcc tga gag tg -3'	86 - 138	Tetra	PET	50	Wictum et al., 2012
VGL1063	R: 5'- caa tca cc acct tcc ctc ct -3'					
VGL1165	F: 5'- atc ttc ctc tgg cac cac ct -3'	191 - 271	Di	VIC	55	Wictum et al., 2012
VGL1165	R: 5'- ggc cct aaa tcc cat gac tg -3'					
VGL1828	F: 5'- aga ttg cgc ctt tgg aag t -3'	220 - 284	Tetra	NED	50	Wictum et al., 2012
VGL1828	R: 5'- ctt ttg gct tcc tgc tct gt -3'					
VGL2009	F: 5'- cca ttt acc aga att tga agc tg -3'	144–184	Tetra	PET	45	Wictum et al., 2012
VGL2009	R: 5'- ccc ggg aaa ctt ttc tga at -3'					
VGL2409	F: 5'- aag cag gtg ctt caa cct ctg -3'	108–156	Tetra	NED	45	Wictum et al., 2012
VGL2409	R: 5'- agg ata gac ctc cat aac tga cca -3'					
VGL2918	F: 5'- gat tct tcc tgg ata tgc tgc ttt -3'	188–260	Di	PET	50	Wictum et al., 2012
VGL2918	R: 5'- gga aas atg tgt ttt ccc ttc a -3'					
VGL3008	F: 5'- aga aca cgg tta ttt gct agg c -3'	110–178	Tetra	FAM	45	Wictum et al., 2012
VGL3008	R: 5'- aag agc caa cag cag cag a -3'					
VGL3112	F: 5'- agc caa tag agc att aag tag agc tg -3'	185–217	Tetra	NED	48	Wictum et al., 2012
VGL3112	R: 5'- ttg tgt aat gtg tga att taa ggg aat -3'					
VGL3235	F: 5'- ggc gac tct tct ccc ttt ctt -3'	267–327	Tetra	VIC	58	Wictum et al., 2012
VGL3235	R: 5'- tct gga ctg aga cag tct gaa aat -3'					
VGL3438	F: 5'- acg ctt gtg ggt gct aca ct -3'	136–188	Tetra	VIC	50	Wictum et al., 2012
VGL3438	R: 5'- agc agt gat gag cag aga tgg -3'					

Table S2: Per-locus summary statistics as calculated in Cervus v3.0.7. The non-exclusion probabilities and combined non-exclusion probabilities (final row, italics) are relevant indicators of the power of the loci for parentage and sibship analyses.

Locus	N_A	N	H_O	H_E	PIC	NE-1P	NE-2P	NE-PP	NE-I	NE-SI
PEZ1	9	177	0.791	0.801	0.769	0.572	0.395	0.213	0.07	0.368
PEZ6	15	178	0.747	0.761	0.727	0.622	0.443	0.25	0.09	0.393
FHC2054	7	174	0.782	0.788	0.755	0.595	0.416	0.232	0.077	0.376
VGL0760	9	178	0.612	0.673	0.616	0.75	0.585	0.41	0.163	0.455
VGL1063	6	178	0.36	0.382	0.365	0.921	0.777	0.621	0.399	0.659
VGL1828	14	178	0.775	0.848	0.83	0.462	0.298	0.126	0.04	0.337
VGL2009	5	176	0.756	0.751	0.708	0.657	0.478	0.295	0.103	0.402
VGL2409	8	177	0.701	0.76	0.725	0.629	0.448	0.257	0.091	0.394
VGL2918	10	178	0.77	0.812	0.783	0.551	0.375	0.196	0.063	0.361
VGL3008	5	178	0.551	0.634	0.58	0.782	0.617	0.442	0.187	0.481
VGL3112	7	177	0.746	0.785	0.75	0.603	0.423	0.239	0.08	0.379
VGL3235	9	178	0.792	0.808	0.782	0.548	0.371	0.185	0.061	0.363
VGL3438	6	178	0.747	0.722	0.682	0.682	0.502	0.31	0.116	0.419
Mean/*combined*	**8.46**	**177.3**	**0.702**	**0.733**	**0.698**	*0.00270*	*3.86E-05*	*4E-08*	*7.91E-14*	*8.68E-06*

N_A: Number of alleles; N: Number of individuals typed (sample size); H_O/H_E: Observed/expected heterozygosity, PIC: Polymorphic information content, NE-1P: Non-exclusion probability (first parent), NE-2P: Non-exclusion probability (second parent), given the genotype of a known parent of the opposite sex, NE-PP: Non-exclusion probability (parent pair), NE-I: Non-exclusion probability (identity), NE-SI: Non-exclusion probability (sib identity).

Table S3: Summary statistics for 20 sampling localities (farms) with >1 sample and for all farms pooled. Produced using the basicStats command of the diveRsity package v1.9.90 in R v3.6.2 and RStudio v1.2.5033. Standard deviation was calculated across loci in Microsoft Excel (stdev.s). Sampling localities with only one sample are not shown.

Farm	N	H_O	H_O SD	H_E	H_E SD	F_{IS}	F_{IS} 95% CI low	F_{IS} 95% CI high	A_R*	A_R 95% CI low	A_R 95% CI low
All	178	0.702	0.126	0.731	0.120	0.041	0.014	0.063	NA	NA	NA
GV	26	0.76	0.200	0.676	0.129	-0.103	-0.196	-0.056	2.649	1.846	3.079
BB	19	0.761	0.157	0.731	0.079	-0.038	-0.137	0.008	2.773	1.769	3.308
BR	5	0.754	0.145	0.603	0.125	-0.26	-0.562	-0.26	2.425	1.538	3.154
BD	2	0.615	0.363	0.558	0.208	-0.089	-1	-0.089	2.231	1.385	2.846
DS	12	0.596	0.155	0.565	0.141	-0.061	-0.267	-0.004	2.277	1.462	3.231
GG	3	0.769	0.316	0.556	0.214	-0.399	-1	-0.399	2.332	1.692	2.846
HK	8	0.702	0.120	0.689	0.099	-0.021	-0.28	0.029	2.579	1.615	3.077
KW	4	0.731	0.279	0.519	0.163	-0.386	-0.771	-0.386	2.174	1.692	2.462
NG	18	0.638	0.240	0.641	0.154	0.026	-0.068	0.064	2.43	1.615	2.923
ND	6	0.718	0.172	0.647	0.115	-0.103	-0.403	-0.02	2.531	1.385	3.077
OG	18	0.692	0.148	0.673	0.130	-0.033	-0.129	0	2.541	1.692	3.077
RV	17	0.67	0.167	0.636	0.153	-0.066	-0.148	-0.035	2.436	1.615	2.846
RE	3	0.846	0.220	0.637	0.139	-0.33	-1	-0.33	2.575	1.692	3.308
SG	3	0.718	0.185	0.658	0.154	-0.102	-1	-0.102	2.517	1.615	3.154
SK	3	0.769	0.250	0.641	0.063	-0.195	-1	-0.063	2.441	1.615	3.154
VR	5	0.754	0.203	0.605	0.125	-0.248	-0.644	-0.187	2.396	1.692	3.077
WK	4	0.686	0.272	0.63	0.109	-0.071	-0.628	-0.032	2.33	1.538	2.923
CL	8	0.61	0.294	0.623	0.200	0.03	-0.172	0.044	2.349	1.538	3
KR	2	0.731	0.259	0.587	0.156	-0.251	-1	-0.251	2.369	1.615	3
WB	6	0.705	0.361	0.532	0.209	-0.297	-0.545	-0.253	2.216	1.615	2.615

N: Sample size, H_O: Observed heterozygosity, SD: Standard deviation, H_E: Expected heterozygosity, F_{IS}: Inbreeding coefficient, CI: Confidence interval, A_R: Allelic richness. *NA: Not applicable. No data is available for all samples pooled ("All"), since allelic richness is a measure of relative genetic diversity between groups and thus cannot be calculated when there is only one group.

Table S4: Summary statistics per year and for all years pooled. Produced using the basicStats command of the diveRsity package v1.9.90 in R v3.6.2 and RStudio v1.2.5033. Standard deviation was calculated across loci in Microsoft Excel (STDEV.S).

Year	N	H_O	H_O SD	H_E	H_E SD	F_{IS}	F_{IS} 95% CI low	F_{IS} 95% CI high	A_R*	A_R 95% CI low	A_R 95% CI low
All	**178**	**0.702**	**0.126**	**0.731**	**0.120**	**0.041**	**0.014**	**0.063**	**NA**	**NA**	**NA**
Year 1	4	0.705	0.247	0.587	0.130	-0.194	-0.799	-0.14	2.88	2.154	3.385
Year 2	93	0.705	0.126	0.732	0.119	0.037	-0.001	0.064	3.892	3.231	4.538
Year 3	52	0.705	0.185	0.715	0.144	0.023	-0.025	0.053	3.854	3.154	4.387
Year 4	29	0.687	0.110	0.71	0.091	0.033	-0.037	0.072	3.739	2.921	4.615

N: Sample size, H_O: Observed heterozygosity, SD: Standard deviation, H_E: Expected heterozygosity, F_{IS}: Inbreeding coefficient, CI: Confidence interval, A_R: Allelic richness. * NA: Not applicable. No data is available for all samples pooled ("All"), since allelic richness is a measure of relative genetic diversity between groups and thus cannot be calculated when there is only one group.

Table S5. Pairwise F_{ST} values between farms with the full data set (below diagonal) and associated significance at a level of 0.05 (above diagonal), where significant values are indicated by a "+" and non-significant values by a "-". Calculated in Arlequin 3.5.2.2.

	GV	BB	BR	BD	DS	GG	HK	KD	KW	KK	KT	NG	ND	OG	RV	RE	RT	RD	SG	SK	VR	WK	CL	KR	WB	TD
GV	0	+	+	-	+	+	+	-	+	-	-	+	+	+	+	-	-	-	-	+	+	+	+	+	+	-
BB	0.06914	0	+	-	+	-	-	-	+	-	-	+	+	+	+	-	-	-	-	-	-	-	+	-	+	-
BR	0.11527	0.03027	0	-	+	+	-	-	+	-	-	+	+	+	+	-	-	-	-	-	-	-	+	+	+	-
BD	0.05021	0.01687	0.07625	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
DS	0.16415	0.12198	0.13401	0.18622	0	+	+	-	+	-	-	+	+	+	+	+	-	-	-	+	+	+	-	+	+	-
GG	0.0439	0.03715	0.08033	0.04877	0.1301	0	-	-	+	-	-	-	+	-	+	-	-	-	-	-	-	-	-	-	+	-
HK	0.07223	0.02209	0.03448	0.03842	0.11182	0.0181	0	-	+	-	-	+	-	-	+	-	-	-	-	-	-	-	-	-	+	-
KD	0.16587	0.11808	0.1592	0.15408	-0.07428	0.13026	0.11179	0	-	-	-	+	-	+	+	-	-	-	-	-	-	-	-	-	-	-
KW	0.18656	0.13417	0.23106	0.20431	0.24805	0.18926	0.12818	0.31232	0	-	-	+	+	+	+	+	-	-	-	+	+	+	+	+	+	-
KK	0.01644	-0.04993	-0.17347	-0.07801	0.0491	-0.02169	-0.03423	0.16667	0.21556	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
KT	-0.00558	0.03036	0.03049	0.03406	0.07587	-0.05843	-0.04657	0.08571	0.18987	-0.15152	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
NG	0.05834	0.07861	0.10616	0.06219	0.13326	0.04687	0.04007	0.16615	0.2076	0.01208	-0.01878	0	-	+	+	-	-	-	-	-	-	+	-	+	+	-
ND	0.04118	0.03288	0.06264	0.03406	0.1441	0.07651	0.0223	0.14257	0.14913	-0.03367	-0.02186	0.01851	0	-	+	-	-	-	-	-	-	+	-	+	+	-
OG	0.05332	0.03706	0.07273	0.00204	0.13929	0.04419	0.02832	0.15568	0.13476	-0.02721	-0.01514	0.03636	0.02622	0	+	-	-	-	-	-	-	+	+	-	+	-
RV	0.07939	0.0554	0.13265	0.05135	0.11193	0.0668	0.06176	0.11428	0.14686	0.06972	0.02829	0.07652	0.07017	0.04036	0	+	-	-	-	-	-	+	+	+	+	-
RE	0.02501	0.02025	0.02882	-0.05593	0.1601	0.00653	0.00789	0.12718	0.15979	-0.06131	-0.13771	0.04981	0.02481	0.01557	0.0705	0	-	-	-	-	-	-	-	-	-	-
RT	0.09829	0.0104	0.06504	-0.06294	0.18674	0.07738	0.04666	0.21053	0.29461	-0.02857	0.09524	0.12529	0.07108	0.03832	0.09442	0.00189	0	-	-	-	-	-	-	-	-	-
RD	-0.03321	-0.01399	0.07494	-0.04828	0.17772	-0.10824	0.00299	0.21053	0.19553	-0.02857	-0.08571	0.00228	-0.01931	-0.06257	0.00934	-0.09091	-0.02857	0	-	-	-	-	-	-	-	-
SG	-0.01249	0.00381	0.0364	-0.06109	0.07847	-0.0454	0.00966	0.02916	0.15995	-0.09586	-0.1007	0.0185	0.00625	-0.00545	-0.00032	-0.05391	-0.03923	-0.14799	0	-	-	-	-	-	+	-
SK	0.09014	-0.00558	0.04912	0.01914	0.14057	0.02041	-0.00813	0.10875	0.13573	-0.03812	0	0.08039	0.05829	0.06006	0.06463	0.025	-0.00283	-0.01143	0.00599	0	-	-	-	-	+	-
VR	0.07991	0.02325	0.0721	0.0628	0.13294	0.03661	0.02829	0.16994	0.17023	-0.01837	0.05965	0.07346	0.04062	0.0551	0.07483	0.04776	0.10172	0.01039	0.01814	0.06563	0	-	-	-	+	-
WK	0.04839	0.02733	0.05936	0.06494	0.0736	-0.00529	0.03726	0.07666	0.1602	-0.07486	-0.06268	0.01577	0.01144	0.01735	0.05234	0.01944	0.06198	-0.04283	-0.03183	0.04362	0.04393	0	-	-	+	-
CL	0.07974	0.06591	0.0901	0.02393	0.14044	0.02119	0.04206	0.18078	0.10585	-0.02778	0.01912	0.06664	0.09134	0.02187	0.07617	0.03832	0.11254	0.03546	0.0175	0.0817	0.08589	0.04089	0	-	+	-
KR	0.06264	0.02627	0.09062	-0.0303	0.11651	0.07395	0.01223	0.1218	0.15947	-0.00158	0.03715	0.02314	0.01282	0.02157	0.05546	0.0085	-0.08405	-0.01445	-0.02212	0.0289	0.00181	0.00374	0.05419	0	+	-
WB	0.105	0.11818	0.13708	0.09434	0.22615	0.07022	0.06008	0.27074	0.24794	0.1168	-0.11544	0.09568	0.11248	0.08147	0.13254	-0.02688	0.20803	0.01252	0.05538	0.11554	0.1518	0.11419	0.09833	0.16004	0	-
TD	0.07131	-0.01746	-0.00821	-0.01629	0.18851	0.02834	-0.00212	0.27273	0.21472	-0.11765	-0.11111	0.07187	-0.00339	0.03316	0.09196	-0.03868	0	-0.05556	-0.01006	-0.06195	0.04956	0.05726	0.06685	0.03715	0.10469	0

Table S6. Pairwise F$_{ST}$ values between farms with relatives removed (below diagonal) and associated significance at a level of 0.05 (above diagonal), where significant values are indicated by a "+" and non-significant values by a "-". Calculated in Arlequin 3.5.2.2.

	GV	BB	BD	DS	GG	HK	KW	KT	NG	ND	OG	RV	RE	RD	SG	SK	VR	WK	CL
GV	0	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
BB	0.02164	0	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
BD	0.02607	-0.01374	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DS	0.00654	0.01103	-0.04567	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
GG	-0.12882	-0.01885	-0.07692	-0.0782	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-
HK	0.01027	0.01072	0.03936	-0.00725	-0.05158	0	-	-	-	-	-	-	-	-	-	-	-	-	-
KW	-0.00479	-0.02953	-0.02439	0.02556	-0.14286	-0.02431	0	-	-	-	-	-	-	-	-	-	-	-	-
KT	-0.08616	0.01191	0.02326	-0.09275	-0.17647	-0.05627	-0.08108	0	-	-	-	-	-	-	-	-	-	-	-
NG	-0.03466	0.01174	0.01785	0.00903	-0.03713	0.01041	0.00302	-0.08827	0	-	-	-	-	-	-	-	-	-	-
ND	-0.03918	0.02847	0.03137	0.01762	-0.032	0.02752	0.02087	-0.06064	-0.02671	0	-	-	-	-	-	-	-	-	-
OG	-0.05227	-0.02121	-0.08387	-0.04459	-0.15088	-0.02073	-0.10438	-0.10438	-0.0378	-0.06636	0	-	-	-	-	-	-	-	-
RV	0.02812	0.03875	0.05937	0.01913	-0.01117	0.04017	0.03301	-0.01117	0.03274	0.01009	0.0198	0	-	-	-	-	-	-	-
RE	-0.04141	-0.02963	-0.04545	-0.0675	-0.12821	-0.01172	-0.02326	-0.1	0.0199	-0.05222	-0.06502	0.01244	0	-	-	-	-	-	-
RD	-0.10153	-0.01695	0.04762	-0.01445	-0.26667	-0.01311	-0.02703	-0.08571	-0.01943	-0.02632	-0.08108	-0.02408	-0.13514	0	-	-	-	-	-
SG	0.04936	0.05433	0.05	0.02067	0.07692	0.05108	0.12195	0	0.05476	0.06567	0.0574	0.01941	0.11111	0.08108	0	-	-	-	-
SK	-0.04943	-0.0681	-0.17073	-0.11717	-0.17949	-0.06755	-0.17949	-0.09524	-0.08377	-0.05745	-0.14286	-0.03755	-0.19048	-0.07317	-0.02439	0	-	-	-
VR	-0.04398	-0.04224	0.02222	-0.04567	-0.13514	-0.07759	-0.13514	-0.13514	-0.02058	-0.03755	-0.0566	0.05937	-0.09524	-0.08108	-0.02703	-0.06667	0	-	-
WK	-0.0188	-0.03349	-0.00358	-0.01632	-0.14286	0.00718	-0.00741	-0.088	-0.01477	0.00349	-0.11111	0.01422	0.04	-0.01149	0	0.01661	-0.04869	0	-
CL	-0.00387	0.0355	-0.05556	-0.00489	-0.16129	-0.04699	0	0	0.01129	0.05771	-0.01629	0.13824	-0.02564	0.05556	0.13514	-0.07692	0.02564	0.07246	0

Table S7 Comparison of mean pairwise relatedness (*r*) between years and mean individual inbreeding coefficients (*F*) between years. *P*-values for the Wilcoxon tests for difference in means are shown on the inside of the table (bordered by grey), with *p*-values for inbreeding comparisons shown below the diagonal (bottom-left) and *p*-values for relatedness comparisons shown above the diagonal (top-right). The mean *F* for each year is shown in the left-most column "outside" the main table, with the mean *r* for each year shown in the top row "outside" the main table. The numbers in parentheses after each year are the number of observations/ data points for that year (number of samples for *F* and number of pairwise relatedness comparisons for *r*).

Mean *F*	Mean *r*	0.259	0.087	0.093	0.100
	Year	Year 1 (6)	Year 2 (4278)	Year 3 (1326)	Year 4 (406)
0.076	Year 1 (4)	-------	0.040	0.048	0.053
0.091	Year 2 (93)	0.935	-------	0.921	0.475
0.076	Year 3 (52)	0.715	0.644	-------	0.510
0.104	Year 4 (29)	0.852	0.801	0.787	-------