Appendix S1. Parameters used for parentage analysis.

Colony (v. 2.0.6.1):

Error Rates: calculated by Gimlet on the replicates (multitube protocol)

Known population allele frequency: Yes

Allele frequency: calculated by GenAlEx and updating by Colony by accounting for the inferred relationship

Number of loci: 15

N. of offspring in the sample: 2 (the killed cubs)

N. of male candidates: 12 (the adult males considered present in the population in 2015, see the main text for details)

Prob. a dad is included in the male candidates: 1

N. of female candidates: 14 (the adult females considered present in the population in 2015, see the main text for details)

Prob. a mum is included in the female candidates: 1

Male and Female mating system: Polygamy

Outbreeding (0) or inbreeding (1) model: 1

Dioecious (2) or monoecious (1): 2

Species: Diploid

Length of Run, Analysis Method and Likelihood Precision: default values.

Sibship scaling: Yes

Number of run: 2

Seed for random number generator: 1234

Sibship size prior: Yes

Paternal & maternal sibship sizes : 1 1

N. of known paternal sibships: 0

N. of known maternal sibships: 0

N. of offspring with excluded fathers: 0

N. of offspring with excluded mothers: 0

N. of Excluded Paternal Sibships: 0

N. of Excluded Maternal Sibships: 0

N. of threads: 1

Monitor intermediate results by: Every 1 second

FRANz (v. 2.0.0):

N. of individual in the sample: 28 bears (14 candidate mother, 12 candidate father and 2 killed cubs)

--freqin Allele frequency calculated by GenAlEx

--femrepro 3:30 --malerepro 5:30 --Nfmax 14 --Nmmax 12 --maxmismatching 1,1 --typingerror 0.01 --fullsibtest --fullsibparental --fullsibpvmethod 1 --fullsibpvth 0.001,0.001,0.05 --fullsibH0 1,2,1 --simiter 50000 --hwesteps 2000 --hwechunks 200 --hwechunksize 1000 --sachains 2 --samaxiter 100000000 --sachi 0.95 --sabeta 3.000 --sadelta 0.100 --saepsilon 0.001000 --sanepsilon 3 --mhchains 2 --mhburniniter 500000 --mhiter 3000000 --mhsamplefreq 10 --mhswapfreq 25 --mhtemp 0.500 --out summary.txt --lociout locisummary.txt --mismatchout mismatches.txt --freqout freqout.txt --pout parentage --poutformat 1,2 --simulationout simulation.txt --siblingsout siblings --siblingsoutformat 2,3 --pedigreeout pedigree --pedigreeoutformat 1,2 --mcmclog mcmc.log --hwetestout hwetestout.txt --cervusgenotypeout --cervusoffspringout --parenteout --genepopout --seed 1976