

Supporting Online Material for

Genetic Restoration of the Florida Panther

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Supplemental Materials and Methods

Field data and analyses

Field-research methodology, which has been ongoing starting in 1981, is described in numerous publications (S1-4). Briefly, adult and juvenile Florida panthers were captured using trained hounds and houndsmen (supplied by Livestock Protection Company, Alpine, Texas), chemically immobilized, and fitted with radio-collars. Vital signs (temperature, heart rate, respiration rate, and capillary refill time) and depth of anesthesia were monitored and recorded and all animals were given a physical examination to assess general health and physical condition. Pumas >4 months old were vaccinated subcutaneously against feline viral rhinotracheitis, feline calicivirus, feline panleukopenia virus (Fel-O-Vax PCT [FDAH]), and rabies (RabvacTM 3 [FDAH])(initiated in 1985). Beginning June 2003, captive and free-ranging pumas also were vaccinated against FeLV (Fel-O-Vax Lv-K [FDAH] or Fevaxyn FeLV, Schering-Plough Animal Health Corporation, Omaha, Nebraska, USA, and rabies (RabvacTM 3 [FDAH]). Captured panthers were dewormed with ivermectin (0.1 mg/kg, Ivomec®, Merial Limited, Iselin, New Jersey) and praziquantel (3.75 mg/kg, CestaJectTM, Phoenix Pharmaceutical, Inc., St. Joseph, Missouri) and treated with Penicillin G procaine/benzathine (USVet®, Hanford Pharmaceuticals, Syracuse, New York). Panthers were implanted with a subcutaneous transponder identification chip (Trovan®, Douglas, United Kingdom), ear-tattooed, measured, and weighed. Neonatal kittens <6 weeks-of age were handled according to (S1) and marked with a subcutaneous (SQ) transponder identification chip.

All recovered Florida panther carcasses were necropsied by board-certified pathologists at the University of Florida Veterinary Medical Teaching Hospital (VMTH, Gainesville, Florida), Disney's Animal Kingdom (Celebration, Florida) or by the FWC Panther Section veterinarian at the Wildlife Research Laboratory (WRL; Gainesville, Florida).

Instrumented animals were monitored approximately every other day (Monday, Wednesday, Friday) from fixed-wing aircraft. Locations were plotted on 7.5-minute USGS topographic maps and recorded as Universal Transverse Mercator coordinates. Mating and denning behavior, aggressive

encounters among panthers, movements and home range shifts, dispersal, survival, recruitment, displacements and replacements of individuals, and other social and ecological interactions were interpreted from radiotelemetry data and field investigations. The study included field observations, radio-telemetry monitoring (>86,000 relocations from 164 individuals representing >3,000 panther-years collected by National Park Service and FWC personnel), and biomedical assessments (404 physical and blood chemistry exams of 173 individuals and >200 necropsies).

Yearly population size estimates are from estimated ages at capture or recovery of carcasses, capture and marking of kittens of known age, and monitoring of radio-collared panthers. Estimated ages of adult panthers were backdated and added to population estimates for previous years.

Genetic data and analyses

Blood and tissue samples were collected from wild-caught and captive panthers from southern Florida since 1978, including pumas from captive populations in Florida and representative pumas from the western United States, including the released Texas females. Total genomic DNA was extracted from blood or tissue samples using one of three standard extraction techniques: phenol-chloroform (S5), salt precipitation (S6), or commercial extraction kits (Qiagen, Valencia, CA).

Twenty-three short-tandem-repeat (STR) loci (F37, F42, FCA43, FCA57, FCA75, FCA90, FCA91, FCA94, FCA95, FCA98, FCA124, FCA133, FCA161, FCA193, FCA 243, FCA249, FCA293, FCA310, FCA369, FCA441, F559, FCA566, FCA668) were selected based on their information content [number of alleles, heterozygosity, and their consistency to amplify in canonical Florida panthers (CFP)] and ease and consistency of scoring from over 250 STRs developed in the domestic cat (*Felis catus*) genome mapping project. STRs were amplified and scored following previously described PCR amplification conditions (S7-8) and were generally repeated 2-5 times for each animal to ensure accuracy and repeatability.

Common measures of STR genetic variation, average observed heterozygosity (Ho), average number of alleles per locus, average allele size range per locus, number of unique alleles, and average

variance were estimated with MICROSAT (S9). Heterozygosity values are relative and highly inflated overall since the 23 STR loci were selected from a larger group of 280 loci based on minimum allele frequency of >0.1. Pairwise genetic distances among individual were estimated based on the proportion of shared alleles (Dps) with [1-ps/kf] option in MICROSAT (S9) and were used to construct neighbor-joining phylogenetic trees with the program NEIGHBOR in the PHYLIP 3.5 package (S10).

A Bayesian procedure, implemented in the program STRUCTURE (S11), was used to identify populations or genetic clusters and to estimate the genetic heritage of individuals (fig. S1, table S2). The Bayesian STRUCTURE approach evaluates conformance of STR loci to Hardy Weinberg and linkage equilibrium in homogenous populations and uses departure as an indication of population substructure. In addition to assigning individuals to various lineages based upon composite STR genotypes, the analysis also estimates the proportion of genetic contribution from each group for individuals of mixed origin.

Animals were assigned to groups of different genetic heritage based on the assignment results from STRUCTURE and from the results of the pedigree analyses that were made using the program CERVUS (version 3.0) (S12). CFP had no direct non-CFP relatives or <5% non-CFP genetic contribution from the STRUCTURE analyses.

Animals were assigned to different chronological groups based on the year they were born, using the midpoint of estimated birth dates when exact birth dates were not known, and in some analyses based on if they were alive during a certain time period.

Probable parents were determined using the program CERVUS (version 3.0) (S12) by first testing all individuals as possible parents using the “neither-parent known” option, followed by the “one-parent known” option, and then using field data (known birth and death dates, sex, geographic location, behavioral observations, i.e. denning behavior, etc.) to eliminate individuals. Only parents exhibiting zero “mismatches” with offspring were considered.

An individual exclusion probability, or the average probability of excluding a single unrelated candidate parent from parentage of a given offspring at one or more loci, assuming no typing errors occur was calculated for each offspring in CERVUS (S12). If one parent was known, or hypothesized, the exclusion probability was calculated taking into account alleles that were unambiguously descended from the known parent. Using a likelihood approach, a LOD (log-likelihood) score was calculated for every assigned parent or pair of parents in CERVUS based on the genotypes of the candidate parent, offspring and other parent (if known).

Relying primarily on our genetic inferences of parents, but also assisted with information from field observations, an interconnected pedigree was constructed (fig. S3-S4). In a few cases when there was no genetic data available, we included suppositions based on field observations. For example, kittens (< 6-months-old) of the same litter based on field observations (and which were not sampled or genotyped) were assumed to have the same parents as their littermates. Individuals that could not be linked in pedigree either did not have a matching candidate parent or offspring in the data set or had multiple options, among which we could not confidently establish paternity or maternity.

Unless otherwise specified, individuals were grouped into age-classes by calendar years (e.g. in survival estimates). Therefore, for most summaries, each animal has a "kitten year", a "juvenile yr", and "adult years", regardless of when they were born or when they died during that year.

The Seminole Indians maintained a group of western North American pumas in an enclosure on their Reservation (SEM on Fig. 1a) adjacent to the northern boundary of the Big Cypress National Preserve (BCNP, Fig. 1a). From 1997-1999 up to eight individuals periodically escaped and although they were subsequently recaptured, our genetic analyses comparing free-ranging panthers and captive SEM showed that the escaped SEM produced several free-living descendants (Fig. 1A-B, Fig. 2, tables S1-S2 (S13).

An abridged pedigree of the population highlighting CFP lineages is displayed in fig. S3 and TX lineages in fig. S4a-d. Excluding founders, 97 of 108 CFP were assigned at least one parent. At least 14 CFP contributed to the AdmFP population with representation from two of the original

matrilines (FP03 and UCFP15) and one patriline (FP04) (fig. S3, table S2). Many first-order inbreeding loops were observed (red-lines in fig. S3), perpetuated primarily by sires breeding daughters (n=17) or mating between siblings (n=6). Among CFP there was one mother-son and 25 aunt-nephew/ uncle-niece/or first- and second-cousin matings. This inbreeding pattern has continued among the TX offspring, as exemplified by FP79 (fig. S3, S4).

Physiological Correlates

Male testicular development, the presence of cowlicks in the hair pattern on the mid-dorsal thoracic line, and the presence of a kinked tail consisting of an abnormal bend caused by a deformity in one or more terminal tail vertebrae were evaluated during field capture, autopsies, and biomedical physical examinations in captivity. CFP had significantly higher incidence of cowlicks (81% vs 6-38%; p<0.05), tail kinks (90% vs 0- 40%; p<0.05), and cryptorchidism (66% vs 6-17%; p<0.05) compared with other panther groups (Table 1).

Prior to 1995, heart murmurs were commonly detected in CFP and eight CFP with congenital atrial septal defects (ASD) (resulting in holes between cardiac atria) were documented at necropsy from 1991-1995 (born 1981-91). Since 1995, nine additional ASD cases have been documented, three in CFP and six in AdmFP (all born since 2001) (table S2-3). Nine of the eleven CFP with an ASD have known sires, and all of these descend from 3 males in FP07's patriline (FP07, FP12 and FP45 in fig. S3). The one AdmFP (FP129) of known parents that exhibited an ASD was the offspring of a father/daughter mating (table S2, fig. S4d). The prevalence of atrial septal defects between CFP and other heritage groups was not significantly different (17% vs 7-14%), but has declined in the population from 21% (in panthers born prior to 1995) to 7.5% (for panthers born 1995-2007) (table S3a-d).

On average, over 70% of CFP had one or more of these four aberrant characters, while 80% of AdmFP exhibited none of these characteristics (table S3b,d). The 1995 TX introduction clearly reduced the incidence of these characters (Table 1, table S3a). For example, 63% of all males (76% of

CFP males) born from 1990-1995 were cryptorchid, including three completely sterile males with no descended testicles (table S2), while 88% of males born 2005-2007, largely AdmFP, had two descended testicles (table S3a).

Sperm was collected from adult males when possible during physical exams, either in the field or in captivity. For sperm collection, each male was induced into a surgical plane of anesthesia following standard protocols (S2, S4). Semen was collected by an electro-ejaculation technique (S14) that relied on a 2.6 cm diameter rectal probe with three longitudinal, stainless-steel electrodes (12.0 x 0.5 cm) and a 60 Hz, sine wave stimulator (P. T. Electronics, Boring, Oregon) which was used to elicit ejaculation following a standardized set of low voltage stimulations (2 to 6 V) over three series of 30 stimuli each. Freshly obtained semen was evaluated for ejaculate volume and sperm concentration via a standard haemocytometer method (S14-S15). Where possible, subjective estimates of sperm motility and forward progression (i.e., the type of forward movement of sperm from rapid, straight direction to quivering, no progression on a scale of 0 to 5; 5 being best) were determined at 400X using a microscope (S14-15). For post-mortem gamete rescue, sperm from minced epididymal tissue collected at necropsy was washed in Ham's F10 medium and similarly analyzed.

An estimate of the frequency of abnormal sperm morphology was determined from fixed aliquots of raw semen as previously described (S15). A 10 ul aliquot of the fresh electroejaculate was added to 100 ul of fixative (0.3% glutaraldehyde in saline) for morphologic examination of spermatozoa by phase-contrast microscopy (1,000X power) (S14-15). Sperm were categorized as normal or as abnormal, with anomalies including macrocephaly, microcephaly, bicephaly, abnormal head shape, abnormal acrosome, coiled flagellum, bent midpiece with cytoplasmic droplet, bent midpiece without cytoplasmic droplet, bent flagellum with cytoplasmic droplet, bent flagellum without cytoplasmic droplet, proximal cytoplasmic droplet, and distal cytoplasmic droplet (S14-15). We are reporting only the most-serious abnormalities (% normal and % head abnormalities).

The CFP testicular volume was significantly smaller than any of the other groups ($p<0.05$ for both living and dead males). The inter-mating between a CFP male and a TX female resulted in F1

males (n=2) with testicular volumes significantly larger than the other groups of males ($p=0.001$, table S5). In other admixed matings (either TX-BC, CFP-BC, or EVG-BC) testicular volume and percent normal sperm declined to values similar to TX males while the percentage of acrosomal defects reverted to former CFP and EVG levels (Table S5-S6).

Florida panthers, both CFP and EVG, produced an extraordinarily low proportion of structurally normal spermatozoa (~5-10%) and a high percentage (>35%) of sperm with a serious deformity in the acrosomal membrane, a structure critical to fertilization. It is noteworthy that wild TX pumas also ejaculate a comparatively high proportion of pleiomorphic spermatozoa (Table 1). However, TX pumas produce considerably fewer sperm with the unusual and serious acrosomal defect than the Florida panther males (13.8% vs 38.9%, table S5-6). CFPxTX-F1 males had fewer acrosomal defects than the TX males and significantly less than all of the other Admixed males (31% vs. 52%, $p<0.002$, table S5-6). Also, percent normal sperm and testicular volume were significantly higher ($p=0.07$ and $p<0.001$ respectively) in the F1s than in all other admixed males (table S5). On balance, despite the high percentage of acrosomal defects and other defective sperm seen in all but the F1 males, there has been a net improvement in male reproductive traits over the CFP and EVG; there are now fewer cryptorchid males with more functional (and larger) testicles per male, all of which should result in better sperm production and improved fertility.

Modeling Panther Jumps between Texas Descendants and Canonical Panthers

We modeled the effect of ancestry (admixed or canonical Florida panthers [AdmFP and CFP, respectively]), sex, and age (as well as their interactions) on the number of times panthers jumped when treed using the SAS GLIMMIX procedure (v9.2) and a Generalized Linear Mixed Model, incorporating the potential explanatory variables and the random variable for each individual panther, and assuming a Poisson distribution for the number of times jumped. The best fit model based on Akaike's information corrected criterion (AICC), as well as the fixed effects, were used to select the best-fitting model based on the potential explanatory variables.

We chose the model that incorporated only ancestry. This models had a lower AICC score and did not have significant effects of either sex or age, or their respective interaction (AICC for Ancestry = 365.88; Ancestry, Sex, Ancestry*Sex = 366.62; Ancestry, Age, Ancestry*Age = 369.12). There was a significant effect of ancestry ($F_{1,81} = 4.33$, $P = 0.041$), with AFP jumping an average of 0.60 ± 0.10 ($N = 115$ captures of 64 different panthers) times while CFP jumped 0.34 ± 0.09 ($N = 61$ captures of 31 different panthers) times. There were also significant panther-specific or individual effects, as seen in the significant random effect (Chi square = 8.31, $p < 0.002$). We note that there has been a non-significant trend towards less jumping in AdmFP panthers born between 2001-2008 in comparison to the cohort of AdmFP born between 1995-2000 (0.45 ± 0.11 vs 0.77 ± 0.15 ; $F_{1,51} = 3.51$, $P = 0.067$), perhaps as more back-cross panthers with CFP heritage were chased.

Kitten Survival

We estimated kitten survival using the live capture, dead recovery, den failure, and radio-tracking data collected during June 1995 to May 2008 and Burnham's live-recapture dead-recovery modeling framework (*S16, S17*). Burnham's model has four parameters: survival probability (S), recapture probability (p), recovery probability (r), and fidelity (F). We fixed F to 1 for all panthers, because the recapture and recovery areas were the same and encompass the entire range of the Florida panther; we also fixed p and r to 1 for radio-collared panthers because we accurately knew fates of radio-collared panthers. Sub-adult and adult panthers were also included in these analyses to more effectively estimate parameters relevant to kitten survival (*S18*).

We present results from a model with additive effects of ancestry (with two ancestry categories: 1) CFP and CFP-BC and 2) EVG-BC, TX-BC, and F1) on kitten survival and an additive effect of ancestry (with two ancestry categories: F1 and all other panthers) on sub-adult and adult survival. Based on Akaike's information criterion adjusted for quasi-likelihood and small sample size (QAICc) ranking, this model was best supported by data (*S18*). We compared this model to one without the effect of ancestry on kitten survival using a likelihood ratio test (*S17*).

Sub-Adult and Adult Survival

We estimated annual survival and examined the effects of covariates using a Cox proportional hazard regression (*S19-S20*) analysis of radio-tracking data. Florida panthers that lost their collars or experienced collar failure were right-censored. We investigated potential effects of genetic ancestry and genetic diversity on survival rates. Given that the first offspring produced by a Texas female were born in 1995 and were not adults until 1997, these analyses were based on a subset of data collected from 1997 until December 31, 2006. Only 2 admixed panthers (born during 1995 and 1996) reached 10 years of age by the end of 2006, and both for periods of <1 year; thus, we excluded older-adult panthers from these analyses. We present results from a model that included interactive effects of sex and age class (sub-adult through adult), and an additive effect of ancestry (2 ancestry categories; F1 and all other panthers). Based on Akaike's information criterion (AIC) ranking, this model was best supported by data (*S21*). We compared this model to an equivalent model without ancestry using a likelihood ratio test.

Sub-Adult and Adult Cause-Specific Mortality Analysis

We attributed mortality of radio-collared panthers to 1 of 4 causes: 1) hit by vehicle, 2) intraspecific aggression, 3) other (included known causes of death such as disease, heart failure, and infections unrelated to intraspecific aggression), and 4) unknown (mortalities for which evidence from field and necropsy examinations was insufficient to assign cause of death). We tested for effects of ancestry and average heterozygosity on cause-specific mortality rates, using the radio-tracking and necropsy data of all sub-adult and adult panthers that could be assigned an ancestry category from 1997-2006. We ran a Cox proportional-hazard regression for each covariate, stratified by the cause of death (*S22*). Risk ratios are presented for covariates that significantly affected cause-specific mortality. For ancestry, we compared cause-specific mortality of all admixed panthers to that of CFP. Risk ratios

for heterozygosity were scaled as the proportional increases in instantaneous hazard from a cause with an increase of 0.1 in the heterozygosity (e.g., 0.2 to 0.3).

We projected female panther survivorship (probability of survival) by ancestry category using estimated survival rates for kittens, sub-adult and adult females by ancestry categories. Survivorship was estimated as the product of annual survival rates. Since we assumed that female panthers become adults at age 2.5, the geometric mean of sub-adult and adult survival was used as the survival rate for ages 2-3. Standard errors were estimated using the delta method with the simplifying assumption that kitten, sub-adult, and adult survivals were independent (S17).

Effective Population Size

The effective population size (N_e) was estimated from demographic data as $N_e=4N_{ef}N_{em}/(N_{ef}+N_{em})$ based on the number of female (N_{ef}) and male (N_{em}) breeders (had bred during or prior to that year) during 1995, 1998, 2001, 2004, and 2007 (S23) (roughly 4 generations).

Supplemental Figures

Figure S1. Genetic heritage of Florida panthers (> 1.5 yr-old) alive in 1995, 1998, 2001, 2004 and 2007 using STR-based Bayesian STRUCTURE analyses (see table S2). The number of genotyped panthers relative to the known number alive is noted at the left for each year. For each year, vertical bars represent unique individuals; Florida panthers to the left of the solid black line are canonical Florida panthers (CFP) or Everglades Florida panthers (EVG) born prior to 1995 and those to the right are genetically admixed Florida panthers (AdmFP). Each bar is colored/shaded in up to nine categories identified by Bayesian STRUCTURE analysis (*S11*). These include groups consisting predominantly of CFP (groups 1-3 in colored boxes), EVG and their descendants (group 4), and five groups of admixed origin, including 2 groups (groups 5-6) with a genetic signal representing predominantly back-crossed CFP (CFP-BC) heritage, one admixed category of approximately 50% TX ancestry (group 7), one reflecting the genetic heritage from the Seminole (SEM) Florida panthers (group 8) (*S13*), and a predominately TX-BC group (group 9). The mean genetic heritage across individuals for each year is depicted in the pie charts, highlighting the numerical percentage representing predominantly CFP genetic heritage. The black diamonds (2007 row) mark the two CFPs (FP113 and FP160) monitored in 2007. FP113 was still being monitored and was breeding in 2010.

Canonical & Everglades Florida panthers

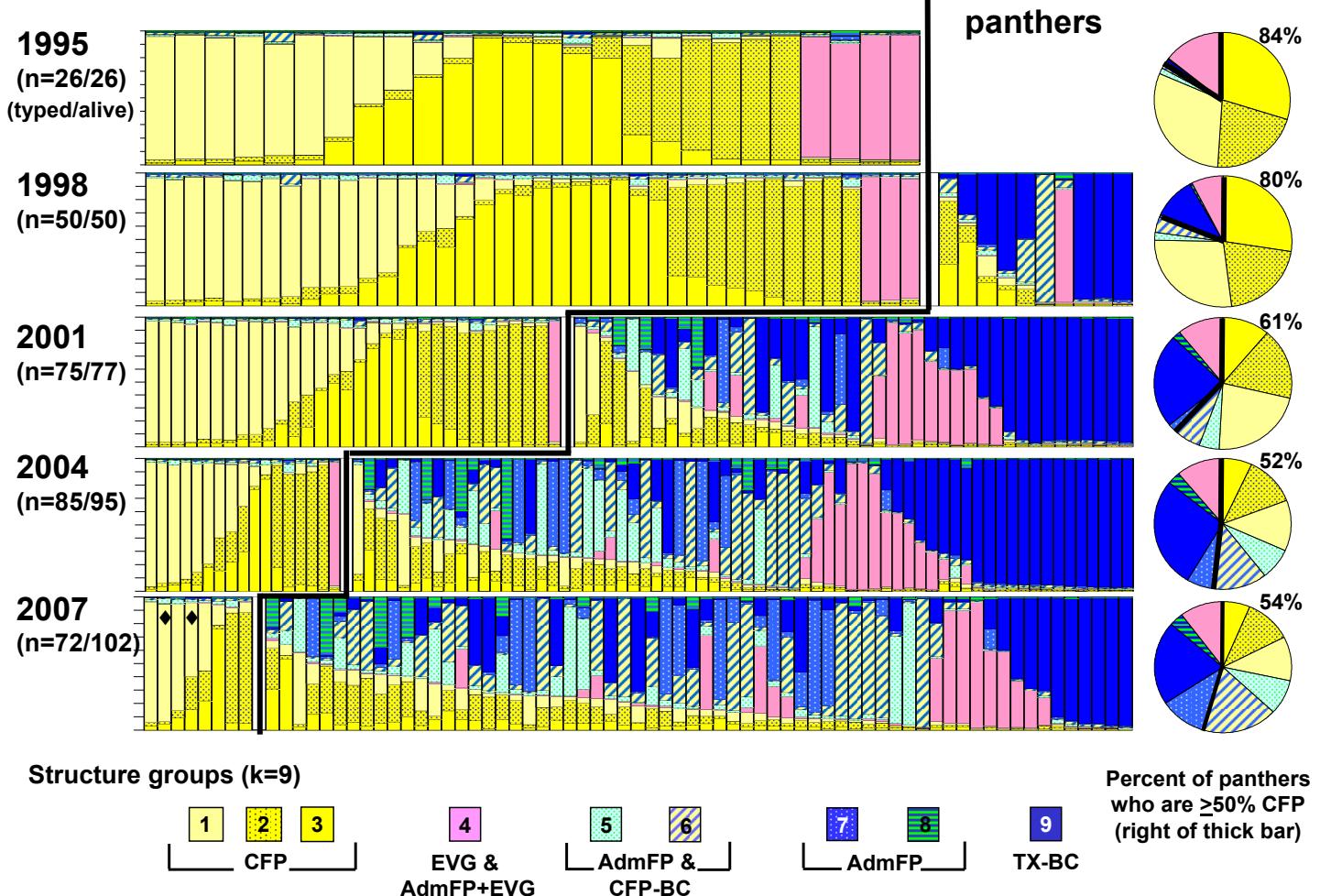


Figure S2. Minimum annual panther population size based on inferred genetic heritage from 1986-2007 of both adults (as in Fig. 3a) and kittens. Genetic heritage of post-dispersal (1- 1.5-year-old) and adult (>1.5-year-old) CFP in yellow, EVG in pink, TX in red, CFPxTX-F1 and EVGxTX-F1 in dark orange, and TX-BC in blue and other admixed panthers (AdmFP) in light orange as determined by pedigree data and Bayesian genetic analyses (fig. S1) of STR allele distributions. Individuals that were not genetically characterized are UNK (in green). Kittens (with striated colors) are split into CFP (yellow), EVG (pink), and admixed (in blue), with undetermined shown in green. Yearly numbers are based on estimated ages at capture or recovery of carcasses (e.g., roadway mortality) and on the capture and marking of kittens of known age, and the monitoring of radio-collared panthers. The estimated ages of panthers examined as adults were backdated and were added to population estimates for previous years.

Adult and kitten Florida Panthers of varying heritage: 1986 - 2007

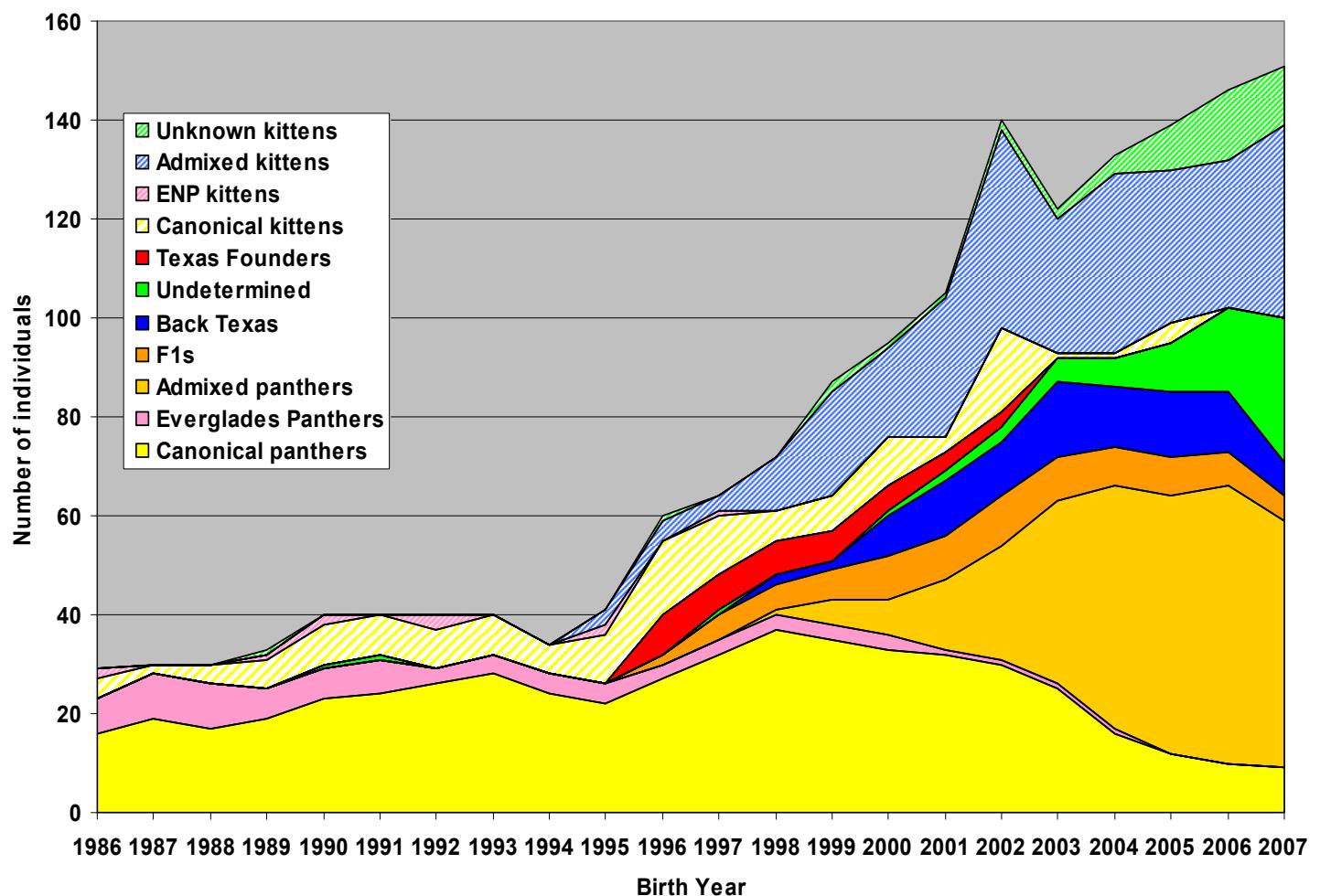


Figure S3. Pedigree of Florida panther population spanning eight generations (>30 years) including principal canonical Florida panthers (CFP; in yellow), introduced Texas (TX) female that successfully bred (in blue), and Everglades panthers (EVG; in pink) that contributed first-generation (F1) admixed offspring. CFP non-breeding females (n=12), neonatal kittens (n=49), and individuals unlinked to this pedigree are excluded (2 parent/offspring pairs). CFP founders (in generations 1-2) are identified by number or as unknown male (Unk CM) or female (Unk CF). The 14 CFP that mated with TX females or their adult descendants (see text) are marked with a “T” and their surviving offspring (n=80) are depicted in Fig. S4a-d. Inbred offspring (first order) are connected with their parents by red lines. One of the two CFP (FP113) that was still being monitored in 2007 is marked by a black diamond (the other is unlinked to this pedigree).

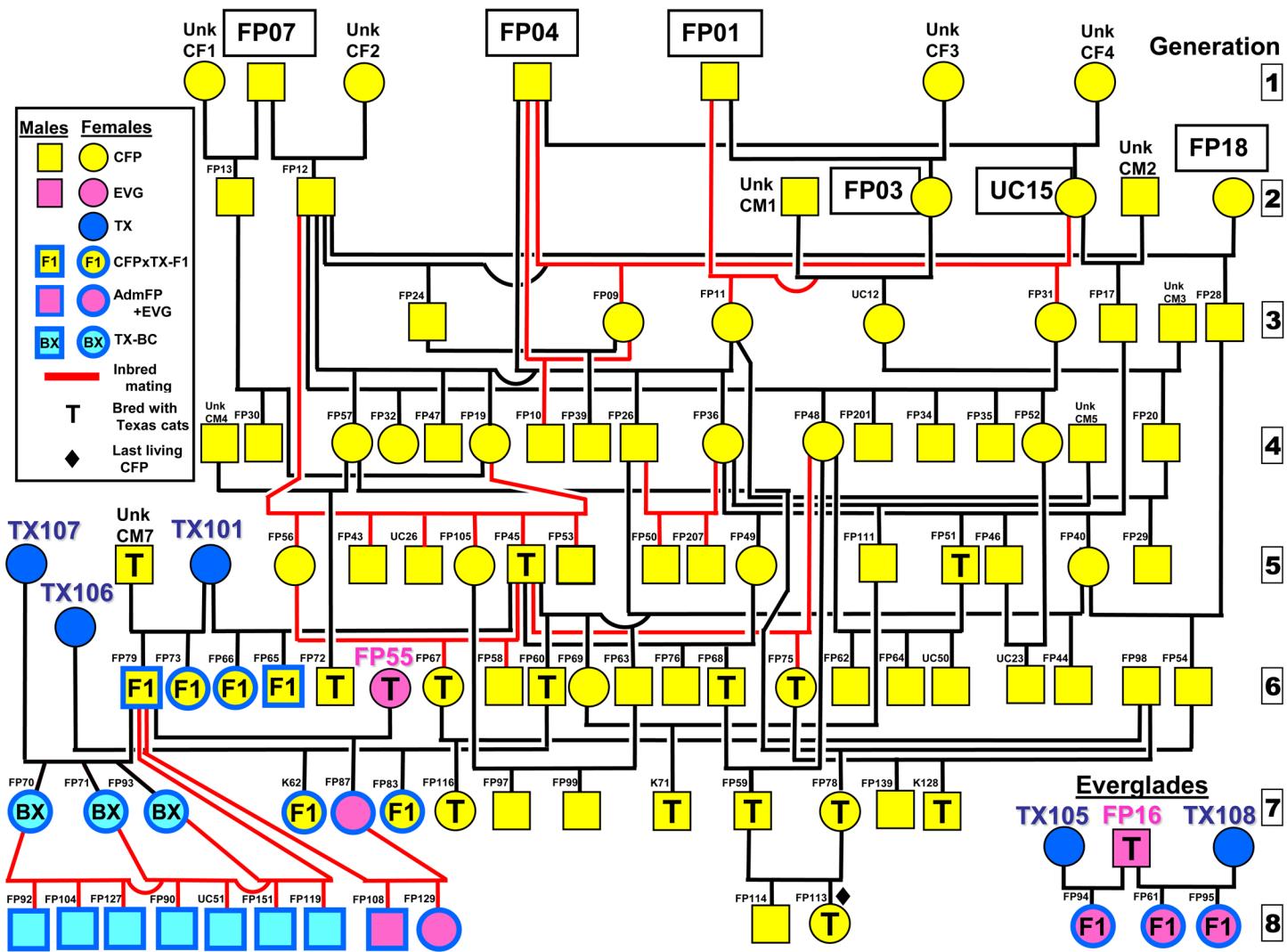
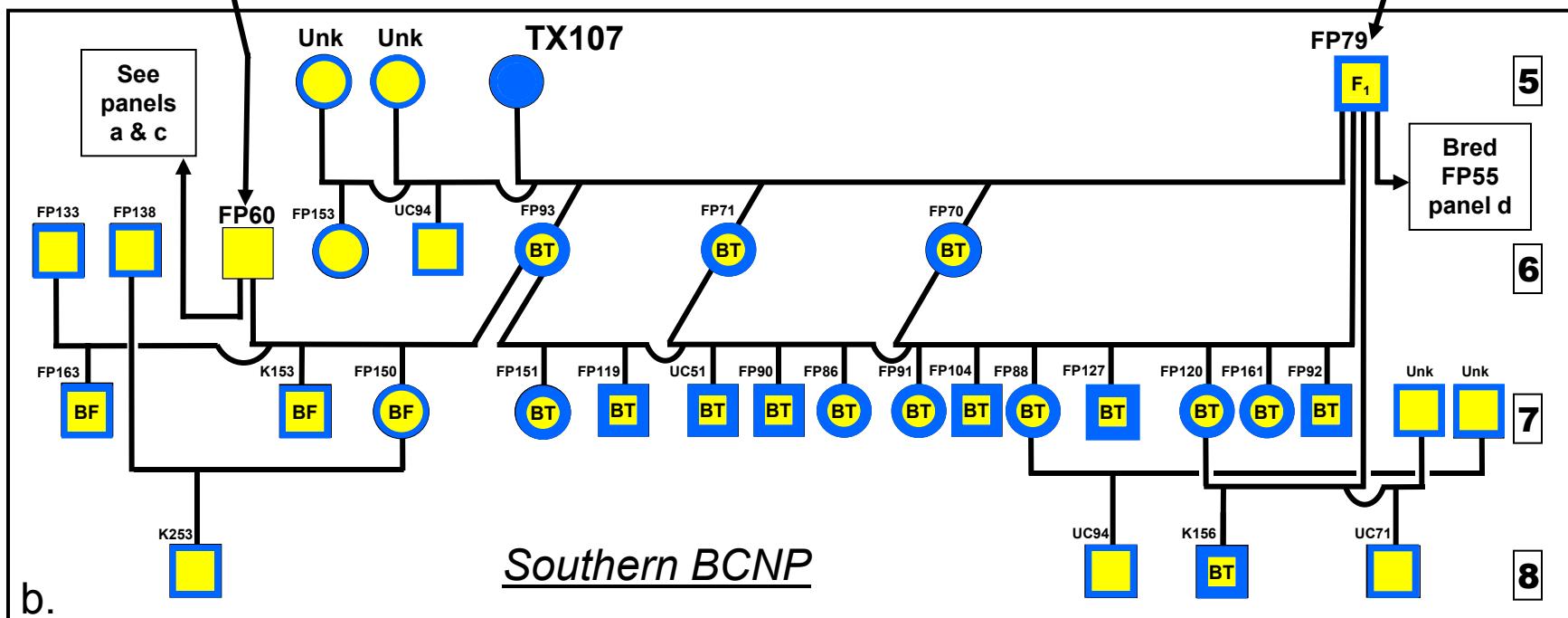
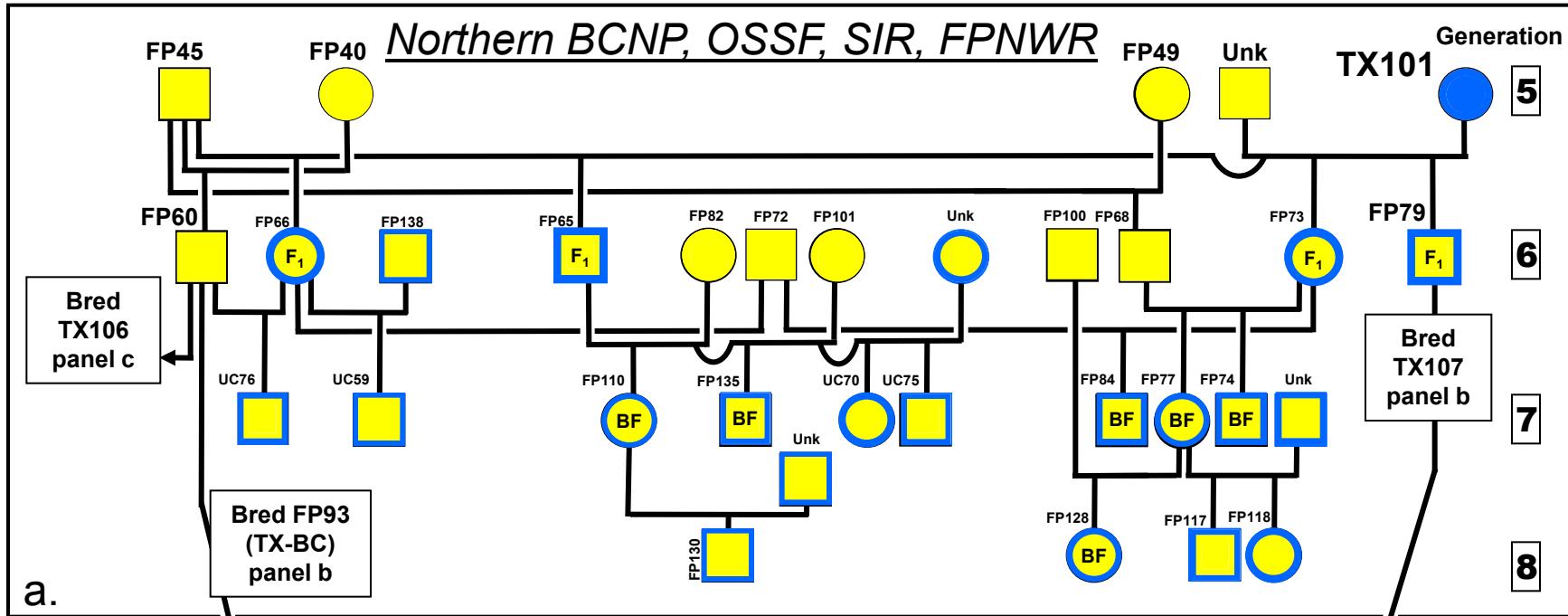


Figure S4. Detailed pedigree of the adult descendants and CFP breeding partners of the five successful TX females introduced into southern Florida in 1995 showing only offspring known to have survived.

a) TX101 produced 4 F1s and bred with two CFPs, b) TX107 bred only with an F1 (FP79) to produce 3 TX-BC offspring, c) TX106 bred with one CFP to produce two F1s and she bred with an unknown Admixed male, d) TX105 and TX-108 both bred FP16 (EVG) to produce 3 F1s.



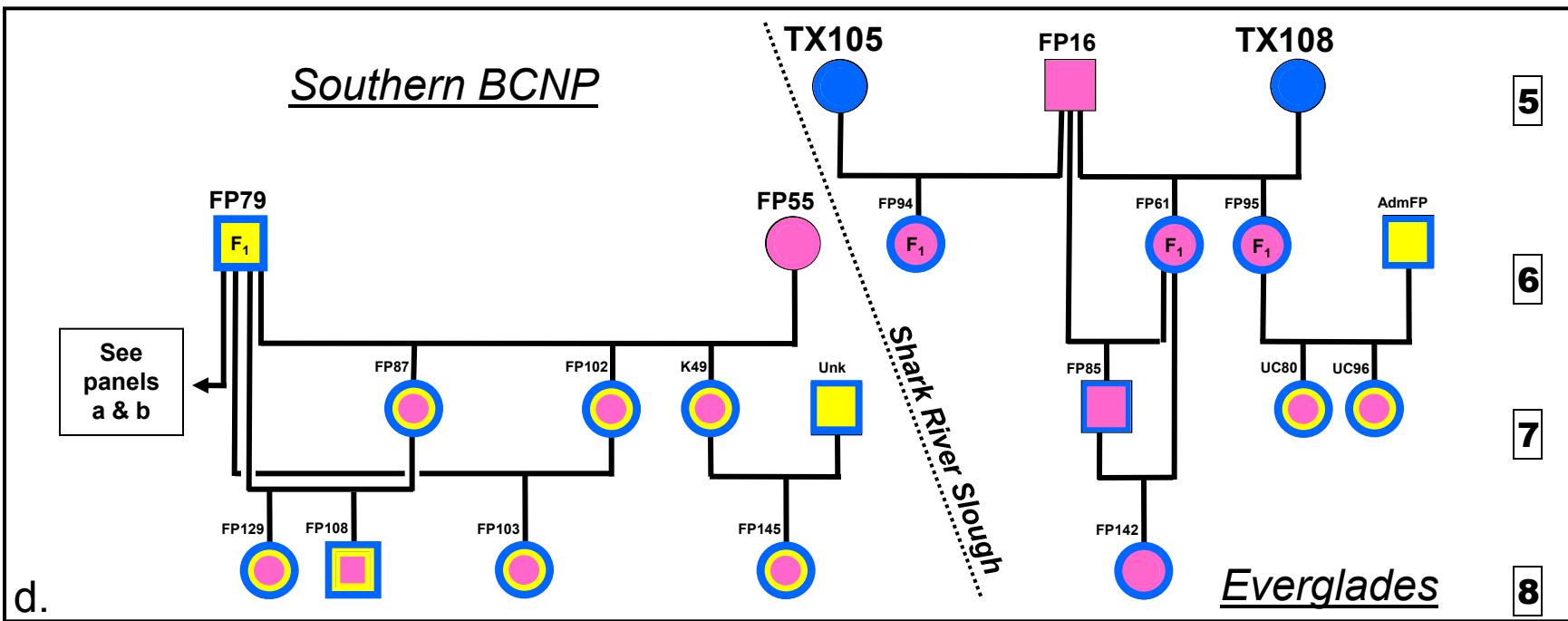
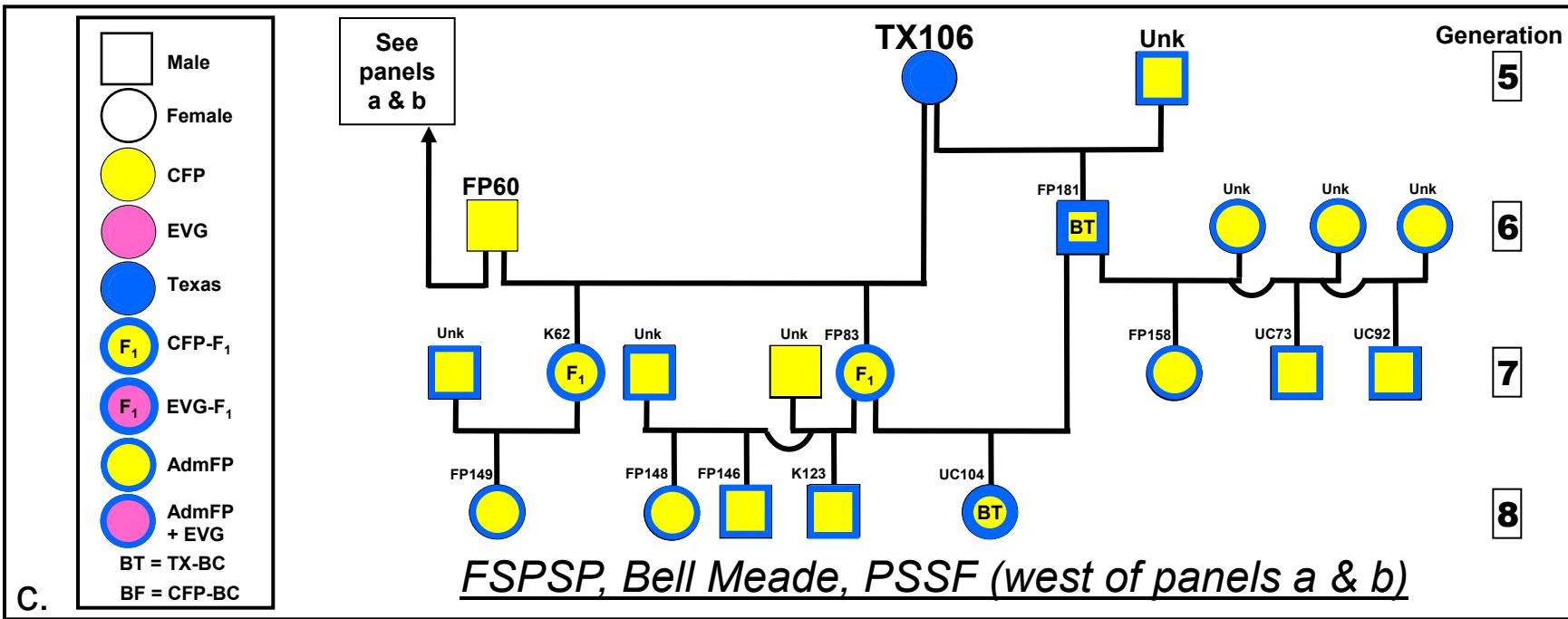
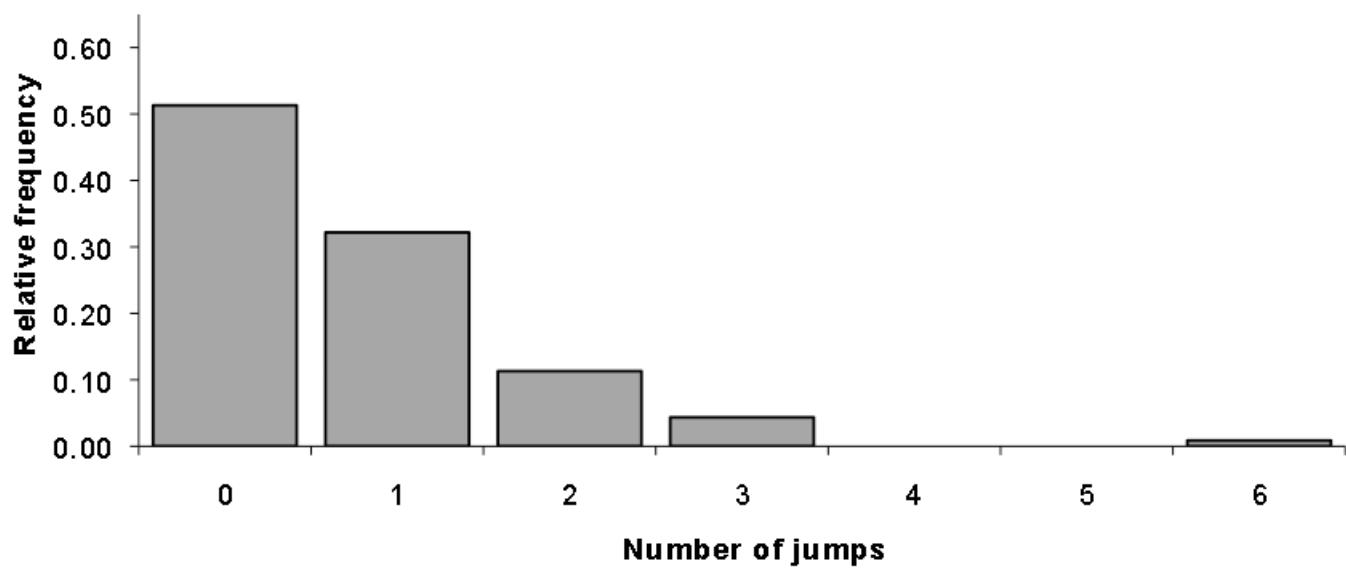


Figure S5. Frequency that the panthers of different genetic heritage jumped from trees after being chased by dogs during capture. a) Admixed panthers, b) CFPs. Per capture event, admixed panthers jumped significantly more often ($p=0.041$) than did the CFPs.

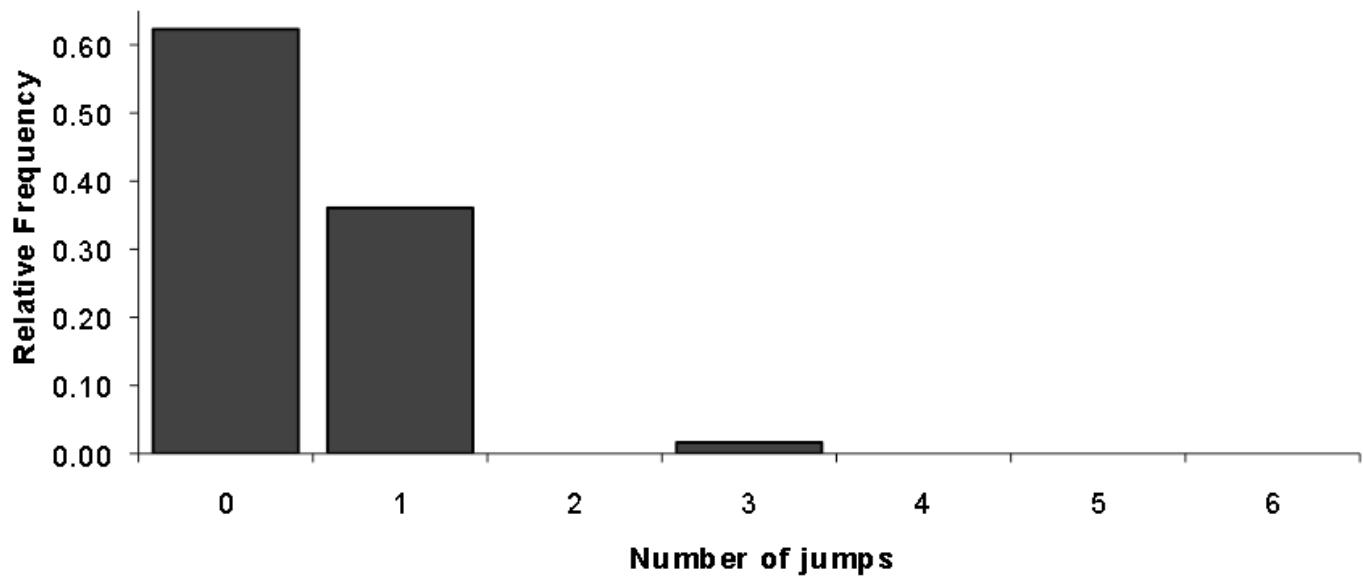
A.

Admixed pumas



B.

Canonical panthers



Supplemental table 1. Chronology of significant events in Florida panther research and management.

1850 - 1900	Florida panther range contracts from much of southeastern United States to peninsular Florida as hunting, bounties, depredation, and habitat loss extirpate panthers from >95% of original 19th century range
1950 - 1972	Florida panther widely considered to be extirpated based on lack of field evidence
1957 - 1967	Seven pumas from Les Piper's private collection (Everglades Wonder Garden, Bonita Springs, FL) released into Everglades National Park
1958	Florida panther provided legal protection in Florida
1967	Florida panther listed as Federal Endangered Species
1972	Presence of Florida panthers confirmed in southern Florida by the capture of aged female at Fish Eating Creek (field survey by World Wildlife Fund(2))
1972	First Florida panther road-kill documented in Moorehaven, FL.
1973	United States Congress passes the Endangered Species Act and gives Florida panther legal protection
1976	Florida Fish and Wildlife Conservation Commission (FWC) begins collection of field observations (>5000 reports processed) and identifies a focal area of panther activity in southwestern Florida (FSSP)
1981	FWC commences capture and radio telemetry of panthers
1982	Florida panther named Florida state animal
1983	Florida panther biomedical studies and specimen collection initiated
1989	Florida Panther National Wildlife Refuge and Corkscrew Regional Ecosystem Watershed established, protecting 80,000 acres of habitat
1992	IUCN Captive Breeding Specialist Group Workshop, Yulee, FL, recommends restoration plan to introduce females of Texas puma subspecies into Florida
1995	Eight female pumas from Texas captured and translocated to Florida
1997 - 1999	Periodic escapes of captive western pumas from the Seminole Indian Reservation
1998	First documented dispersal of a collared panther to the north of the Caloosahatchee River
2002 - 2004	Feline Leukemia Virus outbreak implicated in the death of 5 panthers
2003	Last Texas female puma removed from Florida
2007	The 100 th panther mortality by vehicle collision documented
2008	Male panther from southern Florida shot near Georgia/Alabama state line, approximately 100km southwest of Atlanta, Georgia

Supplemental table 2. List of 591 pumas used in analyses with demographic information, occurrence of traits, diversity estimates, dam and sire identification, pedigree information, and structure results. Symbols and abbreviations are defined in the first panel.

Description of Table Columns	
Color Codes	
Yellow	Canonical Florida panther (CFP)
Pink	Everglades Florida panther (EVG) or part of pedigree can be traced to an EVG founder (pink)
Magenta	AdmFP that is derived from TX, but specific the founders are unknown (magenta)
Orange	AdmFP that is derived from TX, but specific founders are unknown
Red	Texas ancestry can be traced through each generation to a specific Texas female ancestor
Light Green	AdmFP that shares some Seminole heritage in addition to the Texas ancestry (has one unique Seminole allele, or parent or littermate has this)
Green	AdmFP that has a lot of Seminole heritage (either shown by structure or by 2 or more unique Seminole alleles in self, parent or littermate)
Dark Blue	AdmFP is a descendant of FP79, either known from the pedigree or inferred by presence of his unique allele (348 at F42)
Grey	Unknown genetic heritage - either tissue is not available, is of poor quality, or has not been analyzed yet
Purple	Abnormal value or outlier (i.e. released cats)
Field ID	
K #	Kittens handled in the den are given a sequential "K#", if found dead they usually continue to be identified by their K#
FP#	Live captured panthers are assigned a sequential "Florida panther (FP)" number, including those previously marked as kittens (note that FP200-FP210 were captured and brought into captivity in the early 1990s)
UCFP#	Dead panthers not previously handled are given a sequential "Un-collared Florida Panther" #
WC#	Seminole Indian Reservation pumas identified as "WC" for Weed Cat (pumas originated from Frank Weed)
Piper	These animals are descendants of the panthers bred by Lester Piper (PIP) of Everglades Wonder Gardens (EWG), Bonita Springs. They were sampled in the 1980s and resided at multiple zoos and private facilities in Florida, including several still living at EWG. The oldest animal sampled was born in the early 1960s (Pco-11, "Camp Kalaqua") thus is representative of the animals released into Everglades National Park at that time (see Fig 2 for similarity to present day EVGs)
Genetic Group - primary designation: C - Canonical FP, E - Everglades FP, H - admixed (non-Florida), T - Texas founders, U - unknown	
PCO#: Laboratory of Genomic diversity (NCI) database ID for Puma concolor (Pco)	
FLMNH (UF#): Mammal collection ID numbers from the University of Florida Museum of Natural History, Gainesville, FL	
Necropsy ID:	
G# - Early necropsies in the 1980s conducted by Dr. Don Forrester, Dept. of Parasitology, U of F, Gainesville, FL; N# - Veterinary Teaching Hospital, University of Florida Veterinary School; CC# - Southeastern Cooperative Wildlife Disease Study (SCWDS) College of Veterinary Medicine, Athens, Georgia.	
County of residence	
Florida County(ies) where the panther lived (or dispersed to) while radio-collared or where the carcass of an UCFP was found. Abbreviations: Br - Broward, Co - Collier, Da - Dade, Gl - Glades, He - Hendry, Hi - Highlands, Hil - Hillsborough, Le - Lee, Mo - Monroe, PB - Palm Beach, P Beach - Palm Beach	
Status on 4/1/2010	
Alive: radio collared and still monitored; Captivity: removed from the wild (illness, injury, orphaned, or for captive breeding) and is permanently residing in captivity; Radio-failure (RF): either radio-collar has malfunctioned or has dropped off, so animal cannot be followed nor can it be determined if they are still alive or not; Dead: body or remains collected; Kitten unk: handled and marked as a kitten, but it has not been handled since, therefore do not know if they are alive or not (majority or dead)	
Description of Table Columns	
Morphological traits; Atrial Septal defects, Number of descended testicles, presence of thoracic cowlick or kinked tail	
No: body examined and trait not present; Yes: body examined and trait present; Unk: unknown (or unknowable - carcass scavenged); Lost-RF: animal has been lost to carcass retrieval as its radio-collar failed; 1 or 2: number of intra-scrotal testicles found; na: not applicable (female); TBD - to be determined, necropsy pending	
Pedigree	
Colored squares representing ancestry - up to 4 sets of grandparents can be shown. Dams' heritage is always on the left, sire on the right, i.e. if only the parents are known, then the 4 left hand squares represent the dam and the 4 on the right represent the sire. If both sets of grandparents are known - then the first 2 squares are the dams mother and the next are her sires etc.	
Field Dam	
Identified as the dam by field observations and is based on the proximity of the adult female when the juvenile/sub-adult was captured OR the was the adult female attending the den (with kittens). Unknown (Unk) means no field dam was suspected.	
Genetic Dam	
Genotype data was analyzed by CERVUS and it was determined that this female was a good match (with input from field information about which females were alive and conceivably in the area). If parent was unknown (unk) it was because either PNI (parent not identified), MMI (multiple matches were identified but there was no field data to support the selection of any particular female over another), pqd (poor quality DNA), sna (the sample was not available), or ND (not determined yet)	
Dam Consensus - Assignment of parent was inferred based on a combination of Field Dam and Genetic dam evidence (see above), with weight given to genetic data.	
LOD score for support of the Dam - offspring pair	
Dam Support codes:	
Summary of evidence that final decision was based upon. F - field observation, G - genetic, LMG - littermate genetics (if self is lacking), T - telemetric data (i.e. overlapping use area with offspring & mate), or TC - telemetry data at conception date showed evidence of a male overlapping her location on one to several days.	
Field SIRE: is based on the radio-collared males' movements and home range as he associated with the putative dam.	
Genetic Sire, Sire consensus, Sire -offspring LOD score, and sire support: same as for female	
Dam-Sire-Offspring Trio LOD score: LOD score for all three individuals taken together	
Ave Het: Average heterozygosity; Ave # Alleles: average number of alleles for all the STRs analyzed for that individual	
Heritage call	
This is based on a combination of information: the individuals' pedigree (if known), STRUCTURE results (>5% non-Florida = admixed), and an inspection of microsatellite data looking for non-Florida alleles. In all cases, if one sibling shows evidence of admixture, this same status is assigned to all littermates. If panthers are obviously admixed, but lack the pedigree information to determine whether they are back-crossed to CFP, EVG, or TX, they are called "Admixed" or AdmFP. +SEM = Seminole heritage	
Structure results -	
STRUCTURE analysis defined 9 groups (K9): K1, K2, and K3 - 3 family groups of CFP, K4 - EVG and Admixed+EVG (including the EVGxTX-F1s), K5 - mostly CFP-BCs and FP107s family members, K6 - mostly CFP-BC with some AdmFPs and a few CFPxTX-F1s, K7 - AdmFPs and some F1s, K8 - AdmFP and Seminole heritage, K9 - mostly TX-BC and FP79's family (colors/patterns at top of column match the corresponding bar segments in Fig 3.)	

DEMOGRAPHIC INFORMATION

TRAITS

PEDIGREE

Field ID & Genetic group	SEX	PCO#	FLMNH & Necropsy IDs	County	Birth Year	Loss Year	Status on 4/1/2010	Atrial Septal Defect	Number of Descended Testicles	Thoracic Cowlick	Tail tip Kink	Pedigree	
												Dam	Sire
K108	H	M	Pco-1018		2001		Kitten Unk	Unk	Unk	Unk	Unk		
K109	H	M	Pco-1025		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K110	H	M	Pco-1026		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K111	H	F	Pco-1027		2002		Kitten Unk	Unk	na	Unk	Unk		
K112	H	F	Pco-1030		2002		Kitten Unk	Unk	na	Unk	Unk		
K114	H	F	Pco-1032		2002		Kitten Unk	Unk	na	Unk	Unk		
K116	H	F	Pco-1034		2002		Kitten Unk	Unk	na	Unk	Unk		
K117	C	F	Pco-1035		2002		Kitten Unk	Unk	na	Unk	Unk		
K118	C	F	Pco-1036		2002		Kitten Unk	Unk	na	Unk	Unk		
K121	.H	M	Pco-1039		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K122	.H	F	Pco-1040		2002		Kitten Unk	Unk	na	Unk	Unk		
K123	H	M	Pco-1041		2002	2004	Parent in '04	Unk	Unk	Unk	Unk		
K124	C	F	Pco-1042		2002		Kitten Unk	Unk	na	Unk	Unk		
K125	C	M	Pco-1043		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K126	C	M	Pco-1044		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K127	H	F	Pco-1046		2002		Kitten Unk	Unk	na	Unk	Unk		
K128	C	M	Pco-1047		2002	2004	Dead	No	2	Yes	Yes		
K130	C	M	Pco-1049		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K131	C	M	Pco-1050		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K133	C	M	Pco-1052		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K134	C	M	Pco-1053		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K135	.H	M	Pco-1054		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K136	.H	F	Pco-1055		2002		Kitten Unk	Unk	na	Unk	Unk		
K137	H	F	Pco-1056		2002		Kitten Unk	Unk	na	Unk	Unk		
K138	H	M	Pco-1057		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K139	H	F	Pco-1221		2002		Kitten Unk	Unk	na	Unk	Unk		
K140	H	M	Pco-1222		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K141	H	M	No DNA		2002		Kitten Unk	Unk	Unk	Unk	Unk		
K142	H	F	Pco-1223		2002		Kitten Unk	Unk	na	Unk	Unk		
K143	H	F	Pco-1062		2003		Kitten Unk	Unk	na	Unk	Unk		
K144	H	M	Pco-1063		2003		Kitten Unk	Unk	Unk	Unk	Unk		
K145	H	F	No DNA		2003		Kitten Unk	Unk	na	Unk	Unk		
K146	H	F	Pco-1066		2003		Kitten Unk	Unk	na	Unk	Unk		
K148	H	F	Pco-1068		2003		Kitten Unk	Unk	na	Unk	Unk		
K149	H	F	Pco-1072		2003	2004	Kitten Unk	Unk	na	Unk	Unk		
K151	H	F	Pco-1073		2003		Kitten Unk	Unk	na	Unk	Unk		
K153	H	M	Pco-1080		2003	2005	Dead	No	2	No	Yes		
K154	H	M	Pco-1081		2003		Kitten Unk	Unk	Unk	Unk	Unk		
K155	H	F	Pco-1089		2004		Kitten Unk	Unk	na	Unk	Unk		
K156	H	M	Pco-1090		2004	2004	Dead	No	2	No	No		
K157	.H	M	Pco-1099		2004		Kitten Unk	Unk	Unk	Unk	Unk		
K158	.H	M	Pco-1100		2004		Kitten Unk	Unk	Unk	Unk	Unk		
K159	.H	F	Pco-1101		2004		Kitten Unk	Unk	na	Unk	Unk		
K160	H	F	Pco-1104		2004		Kitten Unk	Unk	na	Unk	Unk		
K161	H	F	Pco-1105		2004		Kitten Unk	Unk	na	Unk	Unk		
K162	H	M	Pco-1106		2004		Kitten Unk	Unk	Unk	Unk	Unk		
K163	.H	M	Pco-1109		2004		Kitten Unk	Unk	Unk	Unk	Unk		
K164	.H	M	Pco-1110		2004		Kitten Unk	Unk	Unk	Unk	Unk		
K165	.H	F	Pco-1111		2004		Kitten Unk	Unk	na	Unk	Unk		
K166	.H	F	Pco-1112		2004		Kitten Unk	Unk	na	Unk	Unk		
K167	H	F	Pco-1113		2004		Kitten Unk	Unk	na	Unk	Unk		
K168	H	M	Pco-1114		2004		Kitten Unk	Unk	Unk	Unk	Unk		
K170	H	F	Pco-1117		2004		Kitten Unk	Unk	na	Unk	Unk		
K171	H	M	Pco-1118		2004		Kitten Unk	Unk	Unk	Unk	Unk		
K172	H	F	Pco-1119		2004		Kitten Unk	Unk	na	Unk	Unk		
K173	.H	F	Pco-1120		2004		Kitten Unk	Unk	na	Unk	Unk		
K174	H	M	Pco-1121		2004		Kitten Unk	Unk	Unk	Unk	Unk		
K175	.H	M	Pco-1141		2005		Kitten Unk	Unk	Unk	Unk	Unk		

DEMOGRAPHIC INFORMATION

TRAITS

PEDIGREE

Field ID & Genetic group	SEX	PCO#	FLMNH & Necropsy IDs	County	Birth Year	Loss Year	Status on 4/1/2010	Atrial Septal Defect	Number of Descended Testicles	Thoracic Cowlick	Tail tip Kink	Pedigree	
												Dam	Sire
K176	.H	M	Pco-1142		2005		Kitten Unk	Unk	Unk	Unk	Unk		
K177	.H	F	Pco-1143		2005		Kitten Unk	Unk	na	Unk	Unk		
K178	H	M	Pco-1191	Hendry	2005		Kitten Unk	Unk	Unk	Unk	Unk		
K179	H	F	Pco-1192	Hendry	2005		Kitten Unk	Unk	na	Unk	Unk		
K180	.H	F	Pco-1145		2005		Kitten Unk	Unk	na	Unk	Unk		
K181	H	F	Pco-1146		2005		Kitten Unk	Unk	na	Unk	Unk		
K182	H	F	Pco-1148		2005		Kitten Unk	Unk	na	Unk	Unk		
K183	H	M	Pco-1149		2005		Kitten Unk	Unk	Unk	Unk	Unk		
K185	.U	M	No DNA		2005		Kitten Unk	Unk	Unk	Unk	Unk		
K186	U	F	No DNA		2005		Kitten Unk	Unk	na	Unk	Unk		
K187	C	M	Pco-1153	Hendry	2005		Kitten Unk	Unk	Unk	Unk	Unk		
K188	C	F	Pco-1154	Hendry	2005		Kitten Unk	Unk	na	Unk	Unk		
K189	C	M	Pco-1155	Hendry	2005		Kitten Unk	Unk	Unk	Unk	Unk		
K190	H	M	Pco-1156		2005		Kitten Unk	Unk	Unk	Unk	Unk		
K191	H	M	Pco-1157		2005		Kitten Unk	Unk	na	Unk	Unk		
K192	H	M	Pco-1158		2005		Kitten Unk	Unk	Unk	Unk	Unk		
K193	H	F	No DNA		2005		Kitten Unk	Unk	na	Unk	Unk		
K194	H	F	Pco-1160		2005		Kitten Unk	Unk	na	Unk	Unk		
K195	H	M	No DNA		2005		Kitten Unk	Unk	Unk	Unk	Unk		
K196	H	M	Pco-1162	Hendry	2005		Kitten Unk	Unk	Unk	Unk	Unk		
K197	H	M	Pco-1163	Hendry	2005		Kitten Unk	Unk	Unk	Unk	Unk		
K198	H	M	Pco-1164	Hendry	2005		Kitten Unk	Unk	Unk	Unk	Unk		
K199	H	F	Pco-1165	Hendry	2005	2007	Dead	Unk	na	Yes	Unk		
K200	.H	F	Pco-1172		2006		Kitten Unk	Unk	na	Unk	Unk		
K201	.H	M	Pco-1173		2006		Kitten Unk	Unk	Unk	Unk	Unk		
K202	.H	F	Pco-1176		2006		Kitten Unk	Unk	na	Unk	Unk		
K203	.H	M	No DNA	Hendry	2006	2006	Dead	Unk	Unk	Unk	Unk		
K204	.H	M	Pco-1178		2006		Kitten Unk	Unk	Unk	Unk	Unk		
K205	H	F	Pco-1179		2006		Kitten Unk	Unk	na	Unk	Unk		
K206	H	M	Pco-1180		2006		Kitten Unk	Unk	Unk	Unk	Unk		
K207	H	F	Pco-1181		2006		Kitten Unk	Unk	na	Unk	Unk		
K208	H	F	Pco-1182		2006		Kitten Unk	Unk	Unk	Unk	Unk		
K209	H	F	Pco-1183		2006		Kitten Unk	Unk	na	Unk	Unk		
K210	H	F	Pco-1184		2006		Kitten Unk	Unk	Unk	Unk	Unk		
K211	H	F	No DNA	Collier	2006		Kitten Unk	Unk	na	Unk	Unk		
K212	H	F	Pco-1186	Collier	2006		Kitten Unk	Unk	na	Unk	Unk		
K213	H	F	Pco-1187	Collier	2006		Kitten Unk	Unk	na	Unk	Unk		
K214	H	F	Pco-1188		2006		Kitten Unk	Unk	na	Unk	Unk		
K215	H	F	No DNA		2006		Kitten Unk	Unk	na	Unk	Unk		
K216	H	M	Pco-1190		2006		Kitten Unk	Unk	na	Unk	Unk		
K217	H	M	Pco-1211		2006		Kitten Unk	Unk	na	Unk	Unk		
K218	H	M	Pco-1212		2006		Kitten Unk	Unk	na	Unk	Unk		
K219	.H	F	Pco-1229		2006		Kitten Unk	Unk	na	Unk	Unk		
K220	.H	M	Pco-1230		2006		Kitten Unk	Unk	na	Unk	Unk		
K221	H	F	Pco-1234		2006		Kitten Unk	Unk	na	Unk	Unk		
K222	H	M	Pco-1235		2006		Kitten Unk	Unk	na	Unk	Unk		
K223	H	F	Pco-1236		2006		Kitten Unk	Unk	na	Unk	Unk		
K224	.H	M	No DNA		2007		Kitten Unk	Unk	na	Unk	Unk		
K225	.H	M	No DNA		2007		Kitten Unk	Unk	na	Unk	Unk		
K226	H	M	Pco-1241	Collier	2007		Kitten Unk	Unk	na	Unk	Unk		
K228	H	F	Pco-1243	Collier	2007		Kitten Unk	Unk	na	Unk	Unk		
K229	H	F	Pco-1244	Hendry	2007		Kitten Unk	Unk	na	Unk	Unk		
K230	H	M	Pco-1245	Hendry	2007		Kitten Unk	Unk	na	Unk	Unk		
K231	H	F	No DNA	Hendry	2007		Kitten Unk	Unk	na	Unk	Unk		
K232	H	M	No DNA	Hendry	2007		Kitten Unk	Unk	na	Unk	Unk		
K233	.H	F	Pco-1246		2007		Kitten Unk	Unk	na	Unk	Unk		
K234	.H	M	Pco-1247		2007		Kitten Unk	Unk	na	Unk	Unk		
K236	H	F	Pco-1252		2007		Kitten Unk	Unk	na	Unk	Unk		

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TRAITS

PEDIGREE

Field ID & Genetic group	SEX	PCO#	FLMNH & Necropsy IDs	County	Birth Year	Loss Year	Status on 4/1/2010	Atrial Septal Defect	Number of Descended Testicles	Thoracic Cowlick	Tail tip Kink	Pedigree	
												Dam	Sire
K237	H	F	Pco-1253		2007		Kitten Unk	Unk	na	Unk	Unk		
K238	H	M	Pco-1254		2007		Kitten Unk	Unk	Unk	Unk	Unk		
K239	H	F	Pco-1258		2007		Kitten Unk	Unk	na	Unk	Unk		
K240	H	F	Pco-1259	Collier	2007		Kitten Unk	Unk	na	Unk	Unk		
K241	H	M	Pco-1255		2007		Kitten Unk	Unk	Unk	Unk	Unk		
K242	H	F	Pco-1256		2007		Kitten Unk	Unk	na	Unk	Unk		
K243	H	F	Pco-1257		2007		Kitten Unk	Unk	na	Unk	Unk		
K244	H	M	Pco-1260		2007		Kitten Unk	Unk	Unk	Unk	Unk		
K245	H	M	Pco-1261		2007		Kitten Unk	Unk	Unk	Unk	Unk		
K246	H	F	Pco-1262		2007		Kitten Unk	Unk	na	Unk	Unk		
K247	.H	F	Pco-1263	Collier	2007	2007	Dead	No	na	Unk	Yes		
K248	.H	M	Pco-1264	Collier	2007	2007	Dead	Unk	Unk	Unk	Unk		
K249	.H	F	Pco-1265	Collier	2007	2007	Dead	Unk	na	Unk	Unk		
K250	H	M	Pco-1266		2007		Kitten Unk	Unk	Unk	Unk	Unk		
K251	H	M	Pco-1267		2007		Kitten Unk	Unk	na	Unk	Unk		
K252	H	F	Pco-1268		2007		Kitten Unk	Unk	na	Unk	Unk		
K253	H	M	Pco-1280	Collier	2007	2009	Dead	No	2	No	Yes		
K255	H	F	Pco-1283		2007		Kitten Unk	Unk	na	Unk	Unk		
K256	H	F	Pco-1282		2007		Kitten Unk	Unk	na	Unk	Unk		
K257	H	M	Pco-1284	Hendry	2007		Kitten Unk	Unk	Unk	Unk	Unk		
K258	H	M	Pco-1285	Hendry	2007		Kitten Unk	Unk	Unk	Unk	Unk		
K259	H	M	Pco-1286	Collier	2007	2007	Dead	Unk	Unk	Unk	Unk		
K260	H	U	Pco-1287	Collier	2007	2007	Dead	Unk	na	Unk	Unk		
K261	.H	M	Pco-1289		2007		Kitten Unk	Unk	Unk	Unk	Unk		
K262	H	M	Pco-1290		2007		Alive	Unk	Unk	Unk	Unk		
K263	H	M	Pco-1291		2007		Kitten Unk	Unk	Unk	Unk	Unk		
K265	H	M	Pco-1301		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K266	.H	M	Pco-1304		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K267	.H	M	Pco-1305		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K268	.H	F	Pco-1316	Collier	2008	2008	Dead	No	na	Unk	Unk		
K269	.H	M	Pco-1315	Collier	2008	2008	Dead	Unk	Unk	Unk	Unk		
K270	H	F	Pco-1317		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K271	H	M	Pco-1318		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K272	H	M	Pco-1319		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K273	H	M	Pco-1320		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K274	H	F	Pco-1321		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K275	H	M	Pco-1322		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K276	H	M	Pco-1323		2008		Kitten Unk	Unk	Unk	Unk	Unk		
K277	H	M	Pco-1338		2009		Kitten Unk	Unk	Unk	Unk	Unk		
K278	H	M	Pco-1339		2009		Kitten Unk	Unk	Unk	Unk	Unk		
K280	U	F	Pco-1345		2009		Kitten Unk	Unk	Unk	Unk	Unk		
K281	H	M	Pco-1354		2009		Kitten Unk	Unk	Unk	Unk	Unk		
K282	H	M	Pco-1355		2009		Kitten Unk	Unk	Unk	Unk	Unk		
K283	.U	M	Pco-1356		2009		Kitten Unk	Unk	Unk	Unk	Unk		
K284	.U	M	Pco-1357		2009		Kitten Unk	Unk	Unk	Unk	Unk		
K285	.U	M	Pco-1358	Collier	2009		Kitten Unk	Unk	Unk	Unk	Unk		
K286	.U	M	Pco-1359	Collier	2009		Kitten Unk	Unk	Unk	Unk	Unk		
K287	.U	F	Pco-1360	Collier	2009		Kitten Unk	Unk	na	Unk	Unk		
K288	.U	M	Pco-1376		2010		Kitten Unk	Unk	Unk	Unk	Unk		
K289	.U	M	Pco-1377		2010		Kitten Unk	Unk	Unk	Unk	Unk		
K290	.U	M	Pco-1378		2010		Kitten Unk	Unk	Unk	Unk	Unk		
K291	H	F	Pco-1379	Collier	2010		Kitten Unk	Unk	na	Unk	Unk		
K292	H	M	Pco-1380	Collier	2010		Kitten Unk	Unk	Unk	Unk	Unk		
K293	H	F	Pco-1381	Collier	2010		Kitten Unk	Unk	na	Unk	Unk		
K294	H	U	Pco-1383		2010		Kitten Unk	Unk	Unk	Unk	Unk		
K295	H	U	Pco-1384		2010		Kitten Unk	Unk	Unk	Unk	Unk		
K296	H	U	Pco-1385		2010		Kitten Unk	Unk	Unk	Unk	Unk		
K297	H	F	Pco-1386	Collier	2010		Kitten Unk	Unk	na	Unk	Unk		

DEMOGRAPHIC INFORMATION

TRAITS

PEDIGREE

Field ID & Genetic group		SEX	PCO#	FLMNH & Necropsy IDs	County	Birth Year	Loss Year	Status on 4/1/2010	Atrial Septal Defect	Number of Descended Testicles	Thoracic Cowlick	Tail tip Kink	Pedigree						
													Dam	Sire					
K298	H	F	Pco-1387			2010		Kitten Unk	Unk	na	Unk	Unk	Red	Yellow	Grey	Grey	Grey	Grey	Grey
K299	H	M	Pco-1388		Hendry	2010		Kitten Unk	Unk	Unk			Red	Yellow	Grey	Grey	Grey	Grey	Grey
unmar Ked2	H	U	No DNA			2002		Kitten Unk	Unk	Unk	Unk	Unk	Red	Pink	Red	Grey	Grey	Grey	Grey
FP080 fetus #1	C	U	Pco-0964		Hendry	2000	2000	Dead	Unk	Unk	Unk	Unk	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
FP080 fetus #2	C	U	Pco-0965		Hendry	2000	2000	Dead	Unk	Unk	Unk	Unk	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
FP080 fetus #3	C	U	Pco-0966		Hendry	2000	2000	Dead	Unk	Unk	Unk	Unk	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
FP116 fetus #1	.U	U	Pco-1308		Hendry	2007	2007	Dead	Unk	Unk	Unk	Unk	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
FP116 fetus #2	.U	U	Pco-1309		Hendry	2007	2007	Dead	Unk	Unk	Unk	Unk	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
TEXAS FEMALE PUMAS																			
TX101-BCNP BI	T	F	Pco-0730		Hendry	1991	2000	Dead	No	na	No	No	Red	Red	Red	Red	Red	Red	Red
Tx103 fetus #1	H	U	Pco-0954			1999	1999	Dead	Unk	Unk	Unk	Unk	Red	Red	Red	Grey	Grey	Grey	Grey
TX102-BCNP BI	T	F	Pco-0731		Hendry	1991	1995	Dead	No	na	No	No	Red	Red	Red	Red	Red	Red	Red
TX103-LP	T	F	Pco-0737		Monroe	1991	1999	Dead	Unk	na	No	No	Red	Red	Red	Red	Red	Red	Red
TX104-FSSP	T	F	Pco-0732		Collier	1991	1998	Dead	No	na	No	No	Red	Red	Red	Red	Red	Red	Red
TX105-ENP	T	F	Pco-0739		Dade	1991	2003	Captivity	Unk	na	No	No	Red	Red	Red	Red	Red	Red	Red
TX106-FSSP	T	F	Pco-0733		Collier	1991	2003	Captivity	Unk	na	No	No	Red	Red	Red	Red	Red	Red	Red
TX107-RP	T	F	Pco-0736		Collier	1991	2001	Dead	No	na	No	No	Red	Red	Red	Red	Red	Red	Red
TX108-ENP	T	F	Pco-0740		Dade	1991	2002	Captivity	Unk	na	No	No	Red	Red	Red	Red	Red	Red	Red

DEMOGRAPHIC INFORMATION
TRAITS
PEDIGREE

Field ID & Genetic group	SEX	PCO#	FLMNH & Necropsy IDs	County	Birth Year	Loss Year	Status on 4/1/2010	Atrial Septal Defect	Number of Descended Testicles	Thoracic Cowlick	Tail tip Kink	Pedigree	
												Dam	Sire
SEMINOLE INDIAN RESERVATION PUMAS													
WC00 "Little Boy"	W	M	Pco-0742										
WC01 "castrated 10m"	W	M	Pco-0922										
WC02 "Opal daughter"	W	F	Pco-0959										
WC03	W	F	Pco-0923										
WC04 "neutered"	W	F	Pco-0924										
WC05 "Taz"	W	M	Pco-0925										
WC06 "castrated 10"	W	M	Pco-0926										
WC07 "Opal"	W	F	Pco-0927										
WC08 "Bubba"	W	M	Pco-0928										
PIPER - EVERGLADES WONDER GARDENS PANTHERS													
Piper "Cmp Kalaqua"		M	Pco-0011										
Piper "Offspring"		F	Pco-0034										
Piper "Ocho"		M	Pco-0039										
Piper "Bert Wahl"		M	Pco-0040										
Piper "Dies Dose"		F	Pco-0053										
Piper " Kima"		M	Pco-0054										
Piper "Survivor"		U	Pco-0055										
Piper "Florida"		F	Pco-0078										
Piper "Osceola"		M	Pco-0084										
Piper "Hayeta"		F	Pco-0085										
Piper "Synda"		F	Pco-0169										
Piper "Dellilah / Fatima"		F	Pco-0178										
Piper "Baca"		M	Pco-0179										
Piper "Numa"		M	Pco-0443										

DAM IDENTIFICATION

SIRE IDENTIFICATION

Field ID & Genetic group	Field Dam	Genetic Dam	Dam Consensus	Dam-offspring LOD score	Dam support	Field Sire	Genetic Sire	Sire Consensus	Sire Offspring LOD score	Sire support	Dame Sire and offspring LOD score
FLORIDA											
FP001	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP002	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
FP003	Unk	Unk-PNI	Unk-PNI		G	Unk	FP001	FP001	6.97E+00	G	
FP004	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP005	Unk	Unk-sna	Unk-sna			Unk	Unk-sna	Unk-sna			
FP006	Unk	Unk-sna	Unk-sna			Unk	Unk-sna	Unk-sna			
FP007	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP008	Unk	UCFC12	UCFP12	6.49E+00	G	Unk	FP001	FP001	5.96E+00	G	7.14E+00
FP009	Unk	UCFC15	UCFP15	9.40E+00	G	Unk	FP004	FP004	5.42E+00	G	4.79E+00
FP010	FP009	FP009	FP009	8.85E+00	F G	Unk	FP004	FP004	6.33E+00	G	3.49E+00
FP011	FP003	FP003	FP003	6.37E+00	G	Unk	FP001	FP001	6.58E+00	G	4.74E+00
FP012	Unk	Unk-PNI	UnK-PNI		G	Unk	FP007	FP007	4.56E+00	G	
FP013	Unk	Unk-PNI	UnK-PNI		G	Unk	FP007	FP007	4.92E+00	G	
FP014	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP015	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP016	FP014	FP014	FP014	1.36E+01	F G	Unk	FP025	FP025	1.86E+01	G	2.01E+01
FP017	Unk	UCFC15	UCFP15	7.22E+00	G	Unk	Unk-PNI	Unk-PNI		G	
FP018	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP019	FP011	FP011	FP011	3.80E+00	F G TC	FP012	FP012	FP012	3.15E+00	F G TC	5.47E+00
FP020	Unk	UCFC12	UCFP12	2.63E+00	G	Unk	Unk-PNI	Unk-PNI		G	
FP021	FP014	FP014	FP014	1.10E+01	F G	Unk	FP025	FP025	1.90E+01	G	1.56E+01
FP022	FP015	FP015	FP015	1.97E+01	F G	Unk	Unk-PNI	Unk-PNI		G	
FP023	FP015	FP015	FP015	1.74E+01	F G	Unk	FP012	FP012	8.57E+00	G	1.23E+01
FP024	Unk	UCFC15	UCFP15	3.09E+00	G	Unk	Unk-PNI	Unk-PNI		G	
FP025	Unk	FP014	FP014	7.57E+00	G	Unk	FP004	FP004	6.32E+00	G T	7.27E+00
FP026	Unk	FP011	FP011	3.41E+00	G T	Unk	Unk-PNI	Unk-PNI		G	
FP027	Unk	FP015	FP015	2.06E+01	G	Unk	FP012	FP012	5.65E+00	G T	7.77E+00
FP028	Unk	FP018	FP018	1.31E+01	G T	FP020	FP020	FP020	5.26E+00	F G TC	8.41E+00
FP029	FP011	FP011	FP011	4.55E+00	F G TC	FP013	FP013	FP013	6.16E+00	F G TC	7.34E+00
FP030	FP019	FP019	FP019	3.56E+00	F G TC	Unk	FP004	FP004	5.67E+00	G	4.14E+00
FP031	Unk	UCFC15	UCFP15	6.29E+00	G	Unk	FP012	FP012	2.15E+00	G T	4.77E+00
FP032	Unk	FP031	FP031	4.44E+00	G T	Unk	Unk-MMI	Unk-MMI		G	
FP033	Unk	Unk-MMI	Unk-MMI		G	FP012	FP012	FP012	3.67E-01	F G T	3.08E+00
FP034	FP031	FP031	FP031	6.06E+00	F G T	FP012	FP012	FP012	2.42E+00	F G T	4.31E+00
FP035	FP031	FP031	FP031	4.99E+00	F G T	Unk	FP004	FP004	5.21E+00	G T	6.31E+00
FP036	Unk	FP011	FP011	3.93E+00	G T	Unk	Unk-PNI	Unk-PNI		G	
FP037	Unk	FP015	FP015	1.45E+01	G	Unk	FP007	FP007	7.38E+00	G	
FP038	Unk	Unk-PNI	UnK-PNI		G	Unk	FP024	FP024	1.71E+00	G	5.71E+00
FP039	Unk	FP009	FP009	2.14E+00	G	Unk	FP017	FP017	2.04E+00	G T	3.19E+00
FP040	Unk	FP036	FP036	3.26E+00	G T	Unk	FP017	FP017	6.28E+00	G T	8.25E+00
FP041	Unk	FP036	FP036	3.68E+00	G T	FP016	FP016	FP016	1.10E+01	F G TC	1.16E+01
FP042	FP014	FP014	FP014	4.41E+00	F G TC	FP012	FP012	FP012	8.08E+00	F G TC	7.90E+00
FP043	FP019	FP019	FP019	5.02E+00	F G TC	FP026	FP026	FP026	5.69E+00	F G TC	7.95E+00
FP044	FP040	FP040	FP040	3.99E+00	F G TC	FP012	FP012	FP012	5.25E+00	F G TC	7.19E+00
FP045	FP019	FP019	FP019	5.57E+00	F G TC	Unk	FP017	FP017	6.60E+00	G T	8.67E+00
FP046	Unk	FP036	FP036	3.82E+00	G T	FP012	FP012	FP012	4.89E+00	F G TC	6.68E+00
FP047	FP011	FP011	FP011	4.19E+00	F G TC	FP012	FP012	FP012	3.84E+00	F G TC	6.89E+00
FP048	FP031	FP031	FP031	2.23E+00	F G TC	Unk	FP017	FP017	9.26E+00	G T	1.03E+01
FP049	Unk	FP036	FP036	4.91E+00	G T	FP026	FP026	FP026	5.38E+00	F G TC	4.85E+00
FP050	FP036	FP036	FP036	6.86E+00	F G TC	Unk	FP017	FP017	8.21E+00	G T	9.10E+00
FP051	Unk	FP036	FP036	4.71E+00	G T	FP012	FP012	FP012	3.32E+00	F G TC	5.76E+00
FP052	FP031	FP031	FP031	1.99E+00	F G TC	FP012	FP012	FP012	5.36E+00	F G T	6.68E+00
FP053	FP019	FP019	FP019	7.80E+00	F G T	FP028	FP028	FP028	7.94E+00	F G	1.22E+01
FP054	FP040	FP040	FP040	2.06E+00	F G	FP042	FP042	FP042	1.43E+01	F G TC	2.20E+01
FP055	FP023	FP023	FP023	1.22E+01	F G TC	Unk	FP012	FP012	6.56E+00	G T	8.93E+00
FP056	Unk	FP019	FP019	6.31E+00	GT	Unk	FP012	FP012	3.39E+00	G T	4.23E+00
FP057	Unk	FP011	FP011	3.88E+00	G T						

DAM IDENTIFICATION

SIRE IDENTIFICATION

Field ID & Genetic group	Field Dam	Genetic Dam	Dam Consensus	Dam-offspring LOD score	Dam support	Field Sire	Genetic Sire	Sire Consensus	Sire Offspring LOD score	Sire support	Dame Sire and offspring LOD score
FP116	FP067	FP067	FP067	7.26E+00	F G TC	Unk	FP098	FP098	5.57E+00	G TC	7.35E+00
FP117	Unk	FP077	FP077	8.70E-01	G T	Unk	Unk-PNI	Unk-PNI		G	
FP118	Unk	FP077	FP077	-2.02E+00	G T	Unk	Unk-PNI	Unk-PNI		G	
FP119 / K115	FP093	FP093	FP093	8.98E+00	F G TC	FP079	FP079	FP079 _{F1}	6.46E+00	F G TC	5.72E+00
FP120	Unk	FP070	FP070	1.08E+01	G T	Unk	FP079	FP079 _{F1}	7.74E+00	G T	4.54E+00
FP121	Unk	UCFP57	UCFP57	0.00E+00	G	Unk	Unk-PNI	Unk-PNI		G	
FP122	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP123	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP124	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP125	FP124	FP124	FP124	2.76E+00	F G	Unk	Unk-PNI	Unk-PNI		G	
FP126	FP124	FP124	FP124	9.95E+00	F G	Unk	Unk-PNI	Unk-PNI		G	
FP127	Unk	FP070	FP070	1.30E+01	G T	Unk	FP079	FP079 _{F1}	5.32E+00	G T	3.65E+00
FP128 / K082	FP077	FP077	FP077	4.08E+00	F G T	Unk	FP100	FP100	4.58E+00	G T	7.70E+00
FP129 / K089	FP087	FP087	FP087	9.75E+00	F G	FP079	FP079	FP079 _{F1}	4.72E+00	F G TC	3.18E+00
FP130 / K150	FP110	FP110	FP110	4.47E+00	F G	Unk	Unk-PNI	Unk-PNI		G	
FP131	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP132	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP133	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP134	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP135 / K147	FP101	FP101	FP101	3.34E+00	F G TC	FP065/100	FP065	FP065 _{F1}	5.47E+00	F G TC	1.23E+01
FP136	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP137	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP138	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP139	FP075	FP075	FP075	4.20E+00	F G TC	FP098/100	FP098	FP098	5.28E+00	F G TC	6.45E+00
FP140	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP141	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP142	Unk	FP061	FP061 _{F1}	2.83E+01	G	Unk	FP085	FP085	3.22E+01	G	2.89E+01
FP143	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP144	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP145	Unk	K049	K049	9.77E+00	G	Unk	Unk-PNI	Unk-PNI		G	
FP146	Unk	FP083	FP083 _{F1}	9.08E+00	G	Unk	Unk-MMI	Unk-MMI		G	
FP147 / K184	FP129	FP129	FP129	2.61E+00	F G	Unk	Unk-PNI	Unk-PNI		G	
FP148	Unk	FP083	FP083 _{F1}	1.19E+01	G T	Unk	Unk-PNI	Unk-PNI		G	
FP149	Unk	K062	K062 _{F1}	7.07E+00	G	Unk	Unk-MMI	Unk-MMI		G	
FP150 / K152	FP093	FP093	FP093	8.94E+00	F G TC	FP060	FP060	FP060	2.80E+00	F G TC	8.58E+00
FP151 / K113	FP093	FP093	FP093	1.37E+01	F G TC	FP079	FP079	FP079 _{F1}	8.64E+00	F G TC	9.74E+00
FP152	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP153	Unk	Unk-MMI	Unk-MMI		G	Unk	FP079	FP079 _{F1}	9.51E+00	G	
FP154	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP155	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	UnK-PNI		G	
FP156	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP157	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP158	Unk	Unk-PNI	UnK-PNI		G	Unk	K093	FP181 / K093	7.55E+00	G	
FP159	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP160	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
FP161 / K169	FP070	FP070	FP070	8.06E+00	F G	Unk	FP079	FP079 _{F1}	1.55E+00	G T	3.48E+00
FP162	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
FP163 / K227	FP093	FP093	FP093	1.27E+01	F G T	Unk	FP133	FP133	7.33E+00	G T	1.00E+01
FP164	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
FP165	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP166	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP167	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP168	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP169	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP170	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP171	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP172	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP173	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			

DAM IDENTIFICATION

SIRE IDENTIFICATION

Field ID & Genetic group	Field Dam	Genetic Dam	Dam Consensus	Dam-offspring LOD score	Dam support	Field Sire	Genetic Sire	Sire Consensus	Sire Offspring LOD score	Sire support	Dame Sire and offspring LOD score
FP174	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP175 / K254	FP150	FP150	FP150	5.17E+00	F G	TBD	FP138	FP138	2.15E+00	G	5.23E+00
FP176	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP177 / K235	FP113	FP113	FP113	9.70E-01	F G	FP119	FP154	FP154	9.14E+00	G	1.32E+01
FP178	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP179	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
FP180 / K264	FP151	FP151	FP151	5.94E+00	F G	Unk	FP138	FP138	-1.25E+00	G	2.52E+00
FP181 / K093	TX106	TX106	TX106	1.71E+01	F G	FP060	Unk-PNI	Unk-PNI		G	
FP182 / K279	FP161	Unk-ND	FP161		F	Unk	Unk-ND	Unk-ND			
FP200 "Big Guy"	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
FP201	FP031	FP031	FP031	4.57E+00	F G TC	FP012	FP012	FP012	2.76E+00	F G TC	5.72E+00
FP202	FP009	FP009	FP009	9.77E+00	F G TC	FP037	FP037	FP037	1.78E+01	F G TC	1.95E+01
FP203	FP009	FP009	FP009	9.73E+00	F G TC	FP037	FP037	FP037	1.73E+01	F G TC	1.91E+01
FP204	FP031	FP031	FP031	3.92E+00	F G TC	FP012	FP012	FP012	4.44E+00	F G TC	8.65E+00
FP205	FP019	FP019	FP019	7.20E+00	F G TC	FP012	FP012	FP012	6.10E+00	F G TC	5.92E+00
FP206	FP040	FP040	FP040	5.00E+00	F G TC	FP026	FP026	FP026	5.51E+00	F G TC	7.18E+00
FP207	FP036	FP036	FP036	5.15E+00	F G TC	FP026	FP026	FP026	9.37E+00	F G TC	9.19E+00
FP208	FP032	FP032	FP032	7.47E+00	F G TC	FP012	FP012	FP012	4.26E+00	F G TC	4.59E+00
FP209	FP023	FP023	FP023	2.18E+01	F G TC	FP042	FP042	FP042	3.02E+00	F G TC	6.53E+00
FP210	FP023	FP023	FP023	1.18E+01	F G TC	FP042	FP042	FP042	7.18E+00	F G TC	9.76E+00
UCFP002	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP003	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP004	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP005	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP006	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP007	UCFP06	Unk-pqd	UCFP06		F	Unk	Unk-pqd	Unk-pqd			
UCFP008	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP009	Unk	FP003	Unk-PNI		G	Unk	FP001	FP001	6.28E+00	G	
UCFP010	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP011	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP012	Unk	FP003	FP003	3.22E+00	G	Unk	Unk-PNI	Unk-PNI		G	
UCFP013	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP014	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP015	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP017	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP018	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP019	Unk	Unk-PNI	Unk-PNI		G	Unk	FP033	FP033	7.85E+00	G	
UCFP020	FP011	FP011	FP011	4.50E+00	F G TC	FP012	FP012	FP012	2.24E+00	F G TC	3.26E+00
UCFP021	FP019	FP019	FP019	5.72E+00	F G T	FP012	FP012	FP012	4.99E+00	F G T	4.21E+00
UCFP022	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP023	FP052	FP052	FP052	3.27E+00	F G TC	FP046	FP046	FP046	6.49E+00	F G TC	6.79E+00
UCFP024	FP032	Unk-sna	FP032		F	Unk	Unk-sna	Unk-sna			
UCFP025	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP026	Unk	FP019	FP019	5.81E+00	G T	Unk	FP012	FP012	7.00E+00	G TC	9.36E+00
UCFP027	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP028	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP029	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP030	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP031	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP032	Unk	Unk-sna	Unk-sna			Unk	Unk-sna	Unk-sna			
UCFP033	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP034	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP035	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP036	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP037	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP038	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP039	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP040	Unk	Unk-PNI	Unk-PNI		G	Unk	FP060	FP060	1.64E+00	G	

DAM IDENTIFICATION

SIRE IDENTIFICATION

Field ID & Genetic group	Field Dam	Genetic Dam	Dam Consensus	Dam-offspring LOD score	Dam support	Field Sire	Genetic Sire	Sire Consensus	Sire Offspring LOD score	Sire support	Dame Sire and offspring LOD score
UCFP041	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP042	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP043	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP044	FP036	Unk-pqd	FP036		F	FP045	Unk-pqd	FP045		F T(C?)	
UCFP045	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP046	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP047	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP048	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP049 /K98	FP067	FP067	FP067	4.91E+00	F G	Unk	Unk-PNI	Unk-PNI		G	
UCFP050	FP048	FP048	FP048	7.89E+00	F G T	Unk	FP051	FP051	5.02E+00	G T	5.58E+00
UCFP051	Unk	FP071	FP071	9.72E+00	G T	Unk	FP079	FP079 _{F1}	5.83E+00	G T	7.99E+00
UCFP052	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP053	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP054	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP055	Unk	Unk-PNI	Unk-PNI		G	Unk	UCFP056	Unk-PNI		G	
UCFP056	Unk	Unk-PNI	Unk-PNI		G	Unk	UCFP055	Unk-PNI		G	
UCFP057	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP058	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP059	Unk	FP066 _{F1}	FP066 _{F1}	5.25E+00	G	Unk	FP138	FP138	1.55E+00	G	4.89E+00
UCFP060	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP061	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP062	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP063	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-pqd	Unk-pqd			
UCFP064	Unk	Unk-pqd	Unk-pqd			Unk	Unk-MMI	Unk-MMI			
UCFP065	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI			
UCFP066	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI			
UCFP067	FP113	FP113	FP113	5.43E+00	F G	Unk	Unk-PNI	Unk-PNI		G	
UCFP068	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP069	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP070	Unk	Unk-MMI	Unk-MMI		G	Unk	FP065	FP065 _{F1}	1.11E+01	G	
UCFP071	Unk	FP120	FP120	9.37E+00	G	Unk	Unk-PNI	Unk-PNI		G	
UCFP072	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP073	Unk	Unk-MMI	Unk-MMI		G	Unk	K093	FP181 / K093	9.77E+00	G	
UCFP074	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP075	Unk	Unk-MMI	Unk-MMI		G	Unk	FP065	FP065 _{F1}	1.05E+01	G	
UCFP076	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP077	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP078	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP079	Unk	Unk-PNI	UnK-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP080	Unk	FP095	FP095 _{F1}	1.04E+01	G	Unk	Unk-PNI	Unk-PNI		G	
UCFP081	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP082	Unk	Unk-sna	Unk-sna			Unk	Unk-sna	Unk-sna			
UCFP083	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP084	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP085	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP086	Unk	Unk-pqd	Unk-pqd			Unk	Unk-pqd	Unk-pqd			
UCFP087	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP088	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP089	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP090	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP091	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP092	Unk	Unk-MMI	Unk-MMI		G	Unk	K093	FP181 / K093	1.04E+01	G	
UCFP093	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP094	Unk	Unk-MMI	Unk-MMI		G	Unk	FP079	FP079 _{F1}	4.89E+00	G	
UCFP095	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP096	Unk	FP095	FP095 _{F1}	7.85E+00	G	Unk	Unk-MMI	Unk-MMI		G	
UCFP097	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP098	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	

DAM IDENTIFICATION

SIRE IDENTIFICATION

Field ID & Genetic group	Field Dam	Genetic Dam	Dam Consensus	Dam-offspring LOD score	Dam support	Field Sire	Genetic Sire	Sire Consensus	Sire Offspring LOD score	Sire support	Dame Sire and offspring LOD score
UCFP099	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP100	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP101	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP102	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP103	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
UCFP104	Unk	FP083	FP083 _{F1}	8.13E+00	G	Unk	K093	FP181 / K093	1.13E+01	G	9.98E+00
UCFP105	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP106	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP107	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP108	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP109	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP110	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP111	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP112	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP113	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP114	Unk	Unk-MMI	Unk-MMI		G	Unk	Unk-MMI	Unk-MMI		G	
UCFP115	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP116	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP117	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP118	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP119	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP120	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP121	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP122	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP123	Unk	Unk-MMI	Unk-MMI		G	Unk	FP137	FP137	5.15E+00	G	
UCFP124	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP125	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP126	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP127	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP128	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP129	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP130	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP131	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP132	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP133	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP134	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP135	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP136	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP137	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP138	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP139	Unk	Unk-ND	Unk-ND			Unk	Unk-ND	Unk-ND			
UCFP-LawEnfor	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
K002	FP040	FP040	FP040	2.61E+00	F G	FP028	FP028	FP028	7.44E+00	F G	1.12E+01
K003	FP040	Unk-sna	FP040		F LMG TC	FP026	Unk-sna	FP026		F TC	
K004	FP040	Unk-sna	FP040		F LMG TC	FP026	Unk-sna	FP026		F TC	
K005	FP040	Unk-sna	FP040		F LMG TC	FP026	Unk-sna	FP026		F TC	
K006	FP048	FP048	FP048	6.69E+00	F G TC	FP012	FP012	FP012	2.40E+00	F G TC	2.57E+00
K007	FP048	Unk-sna	FP048		F LMG TC	FP012	Unk-sna	FP12		F LMG TC	
K008	FP048	Unk-sna	FP048		F LMG TC	FP012	Unk-sna	FP12		F LMG TC	
K010	FP056	Unk-sna	FP056		F T	Unk	Unk-sna	FP045		LMG T	
K011 or K009	FP056	Unk-sna	FP056		F T	Unk	Unk-sna	FP045		LMG T	
K013	FP019	FP019	FP019	5.32E+00	F G TC	Unk	FP012	FP012	7.19E+00	G TC	7.50E+00
K014	FP055	Unk-sna	FP055		F TC	FP042	Unk-sna	FP042		F TC	
K015	FP055	Unk-sna	FP055		F TC	FP042	Unk-sna	FP042		F TC	
K017	FP048	FP048	FP048	5.49E+00	F G	Unk	FP68/K002	FP068	1.30E+00	G T	3.44E+00
K020	FP056	Unk-sna	FP056		F TC	FP045	Unk-sna	FP045		F TC	
K021	FP056	Unk-sna	FP056		F TC	FP045	Unk-sna	FP045		F TC	
K022	FP056	Unk-sna	FP056		F TC	FP045	Unk-sna	FP045		F TC	

DAM IDENTIFICATION						SIRE IDENTIFICATION					
Field ID & Genetic group	Field Dam	Genetic Dam	Dam Consensus	Dam-offspring LOD score	Dam support	Field Sire	Genetic Sire	Sire Consensus	Sire Offspring LOD score	Sire support	Dame Sire and offspring LOD score
K298	FP148	Unk-ND	FP148		F	Unk	Unk-ND	Unk-ND			
K299	FP148	Unk-ND	FP148		F	Unk	Unk-ND	Unk-ND			
unmar Ked2	FP095	Unk-sna	FP095 _{F1}		F T	Unk	Unk-sna	FP085		LMG T	
FP080 fetus #1	FP080	FP080	FP080	8.71E+00	F G T	FP081	FP081	FP081	6.19E+00	F G T	4.10E+00
FP080 fetus #2	FP080	FP080	FP080	7.60E+00	F G T	FP081	FP081	FP081	6.46E+00	F G T	4.48E+00
FP080 fetus #3	FP080	FP080	FP080	7.94E+00	F G T	FP081	FP081	FP081	7.14E+00	F G T	4.41E+00
FP116 fetus #1	FP116	FP116	FP116		F G	TBD	Unk-MMI	Unk-MMI		G	
FP116 fetus #2	FP116	FP116	FP116		F G	TBD	Unk-MMI	Unk-MMI		G	
TEXAS FETUS											
TX101-BCNP BI	Unk	Unk-PNI	UnK-Texas		G	Unk	Unk	UnK-Texas		G	
Tx103 fetus #1	TX103	TX103	TX103		F G	Unk	Unk-pqd	Unk-pqd			
TX102-BCNP BI	Unk	Unk-PNI	UnK-Texas		G	Unk	Unk	UnK-Texas		G	
TX103-LP	Unk	Unk-PNI	UnK-Texas		G	Unk	Unk	UnK-Texas		G	
TX104-FSSP	Unk	Unk-PNI	UnK-Texas		G	Unk	Unk	UnK-Texas		G	
TX105-ENP	Unk	Unk-PNI	UnK-Texas		G	Unk	Unk	UnK-Texas		G	
TX106-FSSP	Unk	Unk-PNI	UnK-Texas		G	Unk	Unk	UnK-Texas		G	
TX107-RP	Unk	Unk-PNI	UnK-Texas		G	Unk	Unk	UnK-Texas		G	
TX108-ENP	Unk	Unk-PNI	UnK-Texas		G	Unk	Unk	UnK-Texas		G	

DAM IDENTIFICATION

SIRE IDENTIFICATION

Field ID & Genetic group	Field Dam	Genetic Dam	Dam Consensus	Dam-offspring LOD score	Dam support	Field Sire	Genetic Sire	Sire Consensus	Sire Offspring LOD score	Sire support	Dame Sire and offspring LOD score
SEMINOL											
WC00 "Little Boy"	WC-07	WC-07	WC-07	2.58E+01	G	WC-08	WC-08	WC-08	1.79E+01	F G	1.74E+01
WC01 "castrated 10m"	WC-07	Unk-PNI	Unk-PNI		G	WC-08	WC-08	WC-08	2.27E+01	F G	
WC02 "Opal daughter"	WC-07	WC-07	WC-07	2.20E+01	F G	Unk	NA	WC-08	2.13E+01	F G	2.10E+01
WC03	WC-07	WC-07	WC-07	1.24E+01	F G	WC-08	WC-08	WC-08	2.30E+01	F G	2.42E+01
WC04 "neutered"	WC-07	WC-07	WC-07	1.77E+01	F G	WC-08	WC-08	WC-08	2.09E+01	F G	1.82E+01
WC05 "Taz"	WC-07	WC-07	WC-07	1.64E+01	F G	WC-08	WC-08	WC-08	2.16E+01	F G	1.84E+01
WC06 "castrated 10m"	WC-07	Unk-PNI	Unk-PNI		G	WC-08	WC-08	WC-08	2.87E+01	G	
WC07 "Opal"	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
WC08 "Bubba"	Unk	Unk-PNI	Unk-PNI		G	Unk	Unk-PNI	Unk-PNI		G	
PIPER - E											
Piper "Cmp Kala"											
Piper "Offspring"											
Piper "Ocho"											
Piper "Bert Wah"											
Piper "Dies Dos"											
Piper "Kima"											
Piper "Survivor"											
Piper "Florida"											
Piper "Osceola"											
Piper "Hayeta"											
Piper "Synda"											
Piper "Dellilah / F"											
Piper "Baca"											
Piper "Numa"											

GENETIC DIVERSITY
STRUCTURE ANALYSIS (K=9)

Field ID & Genetic group	Avg Het	Avg # Alleles	Heritage Calls	CFP	CFP	CFP	EVG +AdmFP	CFP-BC +AdmFP	CFP-BC +AdmFP	AdmFP	AdmFP +SEM	TX-BC
				1	2	3	4	5	6	7	8	9
UCFP099	0.196	1.39	AdmFP	0.124	0.009	0.049	0.02	0.008	0.072	0.009	0.005	0.706
UCFP100	0.139	1.28	CFP-BC+SEM	0.01	0.009	0.016	0.01	0.916	0.012	0.01	0.01	0.012
UCFP101	0.190	1.38	AdmFP	0.011	0.009	0.018	0.01	0.655	0.021	0.018	0.008	0.247
UCFP102	0.176	1.35	AdmFP	0.036	0.197	0.07	0.00	0.027	0.149	0.01	0.01	0.496
UCFP103	0.269	1.54	AdmFP	0.048	0.072	0.037	0.01	0.016	0.28	0.014	0.09	0.438
UCFP104	0.167	1.33	TX-BC	0.027	0.034	0.023	0.01	0.02	0.024	0.839	0.005	0.02
UCFP105			Unknown									
UCFP106	0.095	1.19	CFP-BC	0.079	0.03	0.532	0.01	0.102	0.217	0.003	0.006	0.026
UCFP107	0.158	1.32	CFP-BC	0.156	0.228	0.118	0.01	0.034	0.01	0.437	0.005	0.006
UCFP108			Unknown									
UCFP109			Unknown									
UCFP110			Unknown									
UCFP111	0.176	1.35	CFP-BC+SEM	0.017	0.025	0.078	0.01	0.592	0.047	0.007	0.027	0.2
UCFP112	0.147	1.29	CFP-BC	0.095	0.318	0.04	0.01	0.234	0.123	0.039	0.115	0.029
UCFP113			Unknown									
UCFP114	0.067	1.13	CFP	0.037	0.828	0.054	0.00	0.051	0.013	0.005	0.003	0.005
UCFP115			Unknown									
UCFP116			Unknown									
UCFP117			Unknown									
UCFP118			Unknown									
UCFP119			Unknown									
UCFP120			Unknown									
UCFP121			Unknown									
UCFP122			Unknown									
UCFP123	0.100	1.20	AdmFP	0.067	0.021	0.045	0.00	0.012	0.66	0.18	0.004	0.008
UCFP124			Unknown									
UCFP125			Unknown									
UCFP126			Unknown									
UCFP127			Unknown									
UCFP128			Unknown									
UCFP129			Unknown									
UCFP130			Unknown									
UCFP131			Unknown									
UCFP132			Unknown									
UCFP133			Unknown									
UCFP134			Unknown									
UCFP135			Unknown									
UCFP136			Unknown									
UCFP137			Unknown									
UCFP138			Unknown									
UCFP139			Unknown									
UCFP-LawEnfor	0.174	1.35	TX-BC	0.782	0.025	0.163	0.00	0.009	0.008	0.003	0.002	0.004
K002	0.200	1.40	CFP									
K003			CFP									
K004			CFP									
K005			CFP									
K006	0.100	1.20	CFP	0.561	0.067	0.307	0.00	0.039	0.014	0.004	0.002	0.004
K007			CFP									
K008			CFP									
K010			CFP									
K011 or K009			CFP									
K013	0.143	1.29	CFP	0.933	0.015	0.027	0.00	0.008	0.006	0.003	0.002	0.003
K014			EVG									
K015			EVG									
K017	0.143	1.29	CFP	0.592	0.026	0.119	0.00	0.24	0.009	0.004	0.004	0.004
K020			CFP									
K021			CFP									
K022			CFP									

GENETIC DIVERSITY

STRUCTURE ANALYSIS (K=9)

Field ID & Genetic group	Avg Het	Avg # Alleles	Heritage Calls	CFP	CFP	CFP	EVG +AdmFP	CFP-BC +AdmFP	CFP-BC +AdmFP	AdmFP	AdmFP +SEM	TX-BC
				1	2	3	4	5	6	7	8	9
K023F1			CFP-F1									
K024			CFP									
K025			CFP									
K026			CFP									
K027			CFP									
K028			CFP									
K029			CFP									
K030			CFP									
K034F1			EVG-F1									
K037	0.147	1.29	CFP									
K040			CFP									
K041			CFP									
K043			CFP									
K044			EVG x Unk									
K046F1			EVG-F1									
K047F1			CFP-F1									
K049	0.341	1.68	EVG-BC									
K050			EVG-BC									
K051			CFP									
K052			CFP-BC									
K053			CFP-BC									
K054			CFP-BC									
K055			CFPxUnk									
K056			TX-BC									
K057			TX-BC									
K061			EVG-BC									
K062F1	0.318	1.64	CFP-F1									
K069	0.289	1.58	TX-BC									
K070	0.250	1.50	TX-BC									
K071	0.238	1.48	CFP									
K072	0.200	1.40	CFP									
K073	0.114	1.23	CFP									
K074	0.262	1.52	CFP									
K075	0.250	1.50	CFP									
K076	0.190	1.38	CFP-BC									
K077	0.159	1.32	CFP-BC									
K078	0.167	1.33	CFP-BC									
K081	0.175	1.35	CFP-BC									
K083	0.200	1.40	CFP-BC									
K084	0.167	1.33	CFP									
K085	0.182	1.36	CFP									
K087	0.341	1.68	CFP-BC									
K088	0.295	1.59	CFP-BC									
K091	0.273	1.55	TX-BC+EVG									
K092	0.211	1.42	TX-BC									
K094	0.261	1.52	TX-BC									
K095			AdmFP									
K096			AdmFP									
K097			AdmFP									
K099	0.235	1.47	CFP-BC+EVG									
K100	0.273	1.55	CFP-BC+EVG									
K101	0.239	1.48	CFP-BC+EVG									
K102	0.152	1.30	CFP									
K103	0.053	1.11	CFP									
K104	0.344	1.69	EVG-BC									
K105	0.147	1.29	TX-BC+EVG									
K106	0.227	1.46	TX-BC+EVG									
K107	0.227	1.46	CFP-BC+EVG									

GENETIC DIVERSITY

STRUCTURE ANALYSIS (K=9)

Field ID & Genetic group	Avg Het	Avg # Alleles	Heritage Calls	CFP	CFP	CFP	EVG +AdmFP	CFP-BC +AdmFP	CFP-BC +AdmFP	AdmFP	AdmFP +SEM	TX-BC
				1	2	3	4	5	6	7	8	9
K298			AdmFP									
K299			AdmFP									
unmar Ked2			EVG-BC									
FP080 fetus #1	0.088	1.18	CFP									
FP080 fetus #2	0.105	1.21	CFP									
FP080 fetus #3	0.105	1.21	CFP									
FP116 fetus #1	0.100	1.20	Unknown									
FP116 fetus #2	0.184	1.37	Unknown									
TEXAS FETUS												
TX101-BCNP BI	0.348	1.70	TX									
Tx103 fetus #1	0.375	1.75	CFP-F1									
TX102-BCNP BI	0.391	1.78	TX									
TX103-LP	0.381	1.76	TX									
TX104-FSSP	0.342	1.68	TX									
TX105-ENP	0.283	1.57	TX									
TX106-FSSP	0.262	1.52	TX									
TX107-RP	0.326	1.65	TX									
TX108-ENP	0.370	1.74	TX									

GENETIC DIVERSITY

STRUCTURE ANALYSIS (K=9)

Field ID & Genetic group	Avg Het	Avg # Alleles	Heritage Calls	CFP	CFP	CFP	EVG +AdmFP	CFP-BC +AdmFP	CFP-BC +AdmFP	AdmFP	AdmFP +SEM	TX-BC
				1	2	3	4	5	6	7	8	9
SEMINOL												
WC00 "Little Boy"	0.283	1.57	Seminole	0.004	0.004	0.005	0.00	0.008	0.003	0.008	0.961	0.004
WC01 "castrated 10m"	0.310	1.62	Seminole	0.016	0.008	0.013	0.00	0.006	0.017	0.028	0.890	0.018
WC02 "Opal daughter"	0.250	1.50	Seminole	0.009	0.011	0.008	0.00	0.017	0.01	0.016	0.916	0.009
WC03	0.211	1.42	Seminole	0.008	0.008	0.007	0.00	0.012	0.008	0.005	0.946	0.005
WC04 "neutered"	0.325	1.65	Seminole	0.03	0.022	0.013	0.00	0.042	0.015	0.01	0.784	0.08
WC05 "Taz"	0.333	1.67	Seminole	0.03	0.013	0.012	0.01	0.022	0.011	0.007	0.891	0.01
WC06 "castrated 10m"	0.326	1.65	Seminole	0.009	0.014	0.007	0.00	0.006	0.032	0.005	0.910	0.014
WC07 "Opal"	0.341	1.68	Seminole	0.012	0.009	0.008	0.01	0.012	0.015	0.067	0.855	0.016
WC08 "Bubba"	0.381	1.76	Seminole	0.009	0.006	0.006	0.00	0.015	0.009	0.006	0.939	0.007
PIPER - E												
Piper "Cmp Kala"	0.214	1.43	Piper									
Piper "Offspring"	0.250	1.50	Piper									
Piper "Ocho"	0.283	1.57	Piper									
Piper "Bert Wah"	0.194	1.39	Piper									
Piper "Dies Dos"	0.316	1.63	Piper									
Piper "Kima"	0.261	1.52	Piper									
Piper "Survivor"	0.312	1.63	Piper									
Piper "Florida"	0.250	1.50	Piper									
Piper "Osceola"	0.413	1.83	Piper									
Piper "Hayeta"	0.273	1.55	Piper									
Piper "Synda"	0.386	1.77	Piper									
Piper "Dellilah / F"	0.238	1.48	Piper									
Piper "Baca"	0.286	1.57	Piper									
Piper "Numa"	0.357	1.71	Piper									

Supplemental table 3. A) All free-ranging Florida panthers (> 1.5 years-old) of all genetic heritages B) Canonical Florida panthers (CFP), C) Everglades Florida panthers (EVG) and D) Texas (TX) combined with Seminole (SEM) panthers, estimates of molecular genetic variation (mean individual percent observed heterozygosity \pm standard error (SE) and average number of alleles per locus \pm SE estimated from 23 STR loci) and occurrence of physiological traits in Florida panthers alive during three time periods prior to the release of Texas females and two time periods post-release. Sample sizes for each estimate is in parentheses. Percentage of panthers with cowlicks, kinked tails, average number of testicles for males, and percentage of panthers with atrial septal defects were collected during handling of animals in the field or during necropsy.

A.

Heritage Group	No. per group	Average Heterozygosity	Average No. Alleles per locus	^A No. of descended testicles	Proportion of males cryptorchid	Proportion with atrial septal defects	Proportion with Kinked tails	Proportion with cowlick on thorax	Proportion with at least 1 trait
ALL Florida Panthers									
Pre-Introgression									
1970-1984	33	0.231 ± 0.017 (27)	1.46 ± 0.03 (27)	1.67 ± 0.14 (12)	0.33 ± 0.14 (12)	0.33 ± 0.21 (6)	0.86 ± 0.07 (29)	0.79 ± 0.08 (28)	0.71 ± 0.06 (31)
1985-1989	37	0.208 ± 0.014 (36)	1.42 ± 0.03 (36)	1.53 ± 0.12 (18)	0.5 ± 0.12 (18)	0.16 ± 0.09 (18)	0.68 ± 0.08 (37)	0.75 ± 0.07 (36)	0.58 ± 0.06 (37)
1990-1995	62	0.190 ± 0.009 (62)	1.38 ± 0.02 (62)	1.33 ± 0.10 (35)	0.63 ± 0.08 (35)	0.21 ± 0.07 (34)	0.77 ± 0.05 (61)	0.74 ± 0.06 (62)	0.64 ± 0.04 (62)
Post-Introgression									
1996-1998	67	0.220 ± 0.011 (64)	1.44 ± 0.02 (64)	1.38 ± 0.12 (26)	0.54 ± 0.10 (26)	0.06 ± 0.04 (31)	0.59 ± 0.06 (61)	0.63 ± 0.06 (62)	0.48 ± 0.04 (64)
1999-2001	102	0.224 ± 0.009 (101)	1.45 ± 0.02 (101)	1.56 ± 0.09 (41)	0.42 ± 0.08 (41)	0.07 ± 0.04 (46)	0.51 ± 0.05 (95)	0.49 ± 0.05 (93)	0.41 ± 0.03 (96)
2002-2004	139	0.226 ± 0.007 (137)	1.45 ± 0.01 (137)	1.77 ± 0.05 (65)	0.23 ± 0.05 (65)	0.06 ± 0.03 (72)	0.43 ± 0.04 (133)	0.42 ± 0.04 (126)	0.34 ± 0.04 (134)
2005-2007	116	0.240 ± 0.007 (105)	1.48 ± 0.01 (105)	1.88 ± 0.04 (59)	0.12 ± 0.04 (59)	0.09 ± 0.04 (53)	0.31 ± 0.04 (110)	0.26 ± 0.04 (107)	0.23 ± 0.03 (111)

B.

Heritage Group	No. per group	Average Heterozygosity	Average No. Alleles per locus	^A No. of descended testicles	Proportion of males cryptorchid	Proportion with Atrial Septal defects	Proportion with Kinked tails	Proportion with cowlick on thorax	Proportion with at least 1 trait
All Canonical Florida Panthers									
Pre-Introgression									
1970-1984	26	0.188 ± 0.010 (20)	1.38 ± 0.02 (20)	1.6 ± 0.14 (10)	0.40 ± 0.16 (10)	0.40 ± 0.24 (10)	1.00 ± 0 (24)	0.86 ± 0.07 (22)	0.81 ± 0.05 (25)
1985-1989	28	0.182 ± 0.010 (27)	1.36 ± 0.02 (27)	1.4 ± 0.13 (15)	0.60 ± 0.13 (15)	0.20 ± 0.11 (15)	0.89 ± 0.06 (28)	0.93 ± 0.05 (27)	0.74 ± 0.04 (28)
1990-1995	51	0.175 ± 0.007 (51)	1.35 ± 0.01 (51)	1.2 ± 0.10 (29)	0.76 ± 0.08 (29)	0.24 ± 0.08 (29)	0.86 ± 0.05 (50)	0.86 ± 0.05 (51)	0.74 ± 0.03 (51)
Post-Introgression									
1996-1998	41	0.164 ± 0.008 (40)	1.33 ± 0.02 (40)	1.2 ± 0.14 (21)	0.67 ± 0.11 (21)	0.08 ± 0.05 (26)	0.87 ± 0.06 (38)	0.79 ± 0.07 (69)	0.64 ± 0.04 (41)
1999-2001	42	0.161 ± 0.008 (42)	1.32 ± 0.02 (42)	1.2 ± 0.12 (21)	0.71 ± 0.10 (21)	0.08 ± 0.06 (24)	0.93 ± 0.04 (40)	0.73 ± 0.07 (41)	0.69 ± 0.04 (41)
2002-2004	40	0.158 ± 0.007 (40)	1.32 ± 0.01 (40)	1.3 ± 0.11 (18)	0.67 ± 0.11 (18)	0.09 ± 0.06 (22)	0.89 ± 0.05 (38)	0.74 ± 0.07 (38)	0.69 ± 0.04 (39)
2005-2007	11	0.144 ± 0.015 (11)	1.29 ± 0.03 (11)	1.0 ± 0 (2)	1.0 ± 0 (2)	0 ± 0 (3)	0.90 ± 0.10 (10)	0.80 ± 0.13 (10)	0.80 ± 0.10 (10)

C.

Heritage Group	No. per group	Average Heterozygosity	Average No. Alleles per locus	^A No. of descended testicles	Proportion of males cryptorchid	Proportion with Atrial Septal defects	Proportion with Kinked tails	Proportion with cowlick on thorax	Proportion with at least 1 trait
All Everglades Florida Panthers									
Pre-Introgression									
1970-1984	7	0.355 ± 0.022 (7)	1.71 ± 0.04 (7)	2.0 ± 0 (2)	0 (2)	0 (1)	0.20 ± 0.20 (6)	0.50 ± 0.22 (6)	0.31 ± 16.3 (6)
1985-1989	9	0.286 ± 0.035 (9)	1.57 ± 0.07 (9)	2.0 ± 0 (3)	0 (3)	0 (4)	0 (2)	0.22 ± 0.15 (9)	0.06 ± 0.04 (9)
1990-1995	11	0.260 ± 0.030 (11)	1.52 ± 0.06 (11)	2.0 ± 0 (6)	0 (6)	0 (5)	0.36 ± 0.15 (11)	0.18 ± 0.12 (11)	0.18 ± 0.07 (11)
Post-Introgression									
1996-1998	3	0.273 ± 0.059 (3)	1.55 ± 0.12 (3)	2.0 (1)	0 (1)	0 (1)	0.33 ± 0.33 (3)	0.33 ± 0.33 (3)	0.33 ± 0.33 (3)
1999-2001	3	0.273 ± 0.059 (3)	1.55 ± 0.12 (3)	2.0 (1)	0 (1)	0 (1)	0.33 ± 0.33 (3)	0.33 ± 0.33 (3)	0.33 ± 0.33 (3)

D.

Heritage Group	No. per group	Average Heterozygosity	Average No. Alleles per locus	^A No. of descended testicles	Proportion of males cryptorchid	Proportion with Atrial Septal defects	Proportion with Kinked tails	Proportion with cowlick on thorax	Proportion with at least 1 trait
Texas Founders									
Pre-Introgression									
1996-2001	8	0.324 ± 0.015 (8)	1.65 ± 0.03 (8)	NR	NR	NR	0 (5)	0 (5)	0 (5)
All AdmFP Post-Introgression									
1996-1998	10	0.320 ± 0.011 (9)	1.64 ± 0.02 (9)	2.0 ± 0 (3)	0 (3)	0 (2)	0.10 ± 0.10 (10)	0.50 ± 0.17 (10)	0.23 ± 0.08 (10)
1999-2001	49	0.260 ± 0.011 (48)	1.52 ± 0.02 (48)	1.9 ± 0.07 (19)	0.11 ± 0.07 (19)	0.05 ± 0.05 (21)	0.21 ± 0.06 (47)	0.34 ± 0.07 (44)	0.22 ± 0.04 (47)
2002-2004	96	0.253 ± 0.007 (96)	1.51 ± 0.01 (96)	1.9 ± 0.04 (46)	0.07 ± 0.04 (46)	0.04 ± 0.03 (49)	0.23 ± 0.04 (92)	0.29 ± 0.05 (86)	0.18 ± 0.02 (92)
2005-2007	94	0.251 ± 0.007 (94)	1.50 ± 0.01 (94)	1.9 ± 0.04 (51)	0.10 ± 0.04 (51)	0.11 ± 0.05 (45)	0.22 ± 0.04 (89)	0.21 ± 0.04 (86)	0.17 ± 0.02 (90)

Supplemental table 4. Estimated annual survival rates \pm SE by sex and age class. For this analysis, kittens are defined as age 0-1 year for both sexes, sub-adults as age 1-2.5 years for females and 1-3.5 years for males, and prime-adults as age 2.5-10 years for females and 3.5-10 years for males. Panthers that could not be classified as CFP, CFPxTX-F1, EVGxTX-F1, TX-BC or EVG-BC and adults > 10 yrs old were excluded. One single-remaining pre-restoration EVG female was included with the CFP in the sub-adult and prime-adult analysis. Results from a model with two ancestry categories (1: CFP and CFP-BC and 2: EVG-BC, TX-BC, CFPxTX-F1 and EVGxTX-F1) are presented for kitten survival and results from a model with two different ancestry categories (1: CFP, CFP-BC, EVG-BC, and TX-BC and 2: CFPxTX-F1 and EVGxTX-F1) are presented for sub-adults and prime-adults. Both models were significantly ($p<0.05$) better supported by the data than the equivalent models without ancestry effects.

Age Class	Sex	CFP and	TX-BC and	CFPxTX-F1 and
		CFP-BC	EVG-BC	EVGxTX-F1
Kitten	All	0.243 ± 0.061	0.518 ± 0.107	0.518 ± 0.107
Sub-Adult	Female		0.958 ± 0.041	0.995 ± 0.007
Sub-Adult	Male		0.681 ± 0.073	0.957 ± 0.044
Prime-Adult	Female		0.825 ± 0.039	0.978 ± 0.022
Prime-Adult	Male		0.787 ± 0.057	0.973 ± 0.028

Supplemental Table 5. Comparison of testicular volume and two measures of sperm morphology (percentage normal sperm and percentage abnormal acrosomes) among ejaculates from live canonical Florida panthers (CFP), Everglades Florida panthers (EVG), admixed Florida panthers (AdmFP) and Texas pumas, as well as from CFP and AdmFP testes rescued post mortem. Number of individuals examined listed in parentheses. Expanded data in table S6.

¹Testicular volume in each male included only descended testicles. Within columns, similar letters indicate that no differences were observed ($p<0.05$).

²Electro-ejaculation was performed under anesthesia.

³Percentage cryptorchid: CFP = 43.8%; AdmFP = 25%, EVG, CFP-TX-F1, and TX = 0%.

⁴Data from 11 CFP males, 5 EVG males, 9 TX males, and 7 Colorado males are from (S24); an additional 5 CFP males were included for a total of 16 CFP males.

⁵Aspermia: 1 ejaculated and 1 gamete rescue CFP was aspermic and oligospermic, respectively, and 4 of the AdmFP were aspermic (2 ejaculates and 2 gamete rescues).

⁶Testes were collected post-mortem, thus testicular volume does not include the scrotum.

⁷Percentage of these males cryptorchid: CFP = 50% AdmFP = 0%.

⁸Western males were not included in statistical evaluation [raw data from (S24) was not available] and ejaculated and gamete rescued male data were analyzed separately. For ejaculated males, testicular volume CFP<AdmFP ($p=0.05$), CFP<F1s ($p=0.001$), EVG<F1s ($p=0.01$), and AdmFP<F1s ($p=0.07$). For percent normal sperm CFP<EVG ($p=0.03$), F1s>all others ($p<0.001$). For abnormal acrosomes F1s< all others ($p<0.002$). For the gamete rescue males, testicular volume CFP<AdmFP ($p=0.005$), normal sperm CFP<AdmFP ($p=0.08$)(Fishers exact test in each comparison).

Panther population and sampling method	Testicular volume (cm³) ± SE	Spermatozoa morphology percent ± SE	
		Normal	Abnormal acrosomes
Ejaculates from live Florida males²			
Canonical Florida panthers (16) ^{3,4,5}	11.3 ± 1.6 ^A (15)	5.4 ± 0.7 ^C (15)	38.9 ± 3.2 ^{A,C} (15)
Everglades Florida panthers (5) ^{3,4}	14.0 ± 1.9 ^B (4)	9.5 ± 0.6 ^B (5)	38.8 ± 2.8 ^{A,C} (5)
Admixed Florida panthers			
All AdmFP except F1s (4) ^{3,5}	18.2 ± 3.1 ^{B,C} (4)	7.0 ± 6.0 ^{B,C} (2)	51.5 ± 7.5 ^{A,C} (2)
CFPxTX-F1 C (2) ³	27.7 ± 1.8 ^D (2)	20.5 ± 4.5 ^A (2)	7.0 ± 3.0 ^B (2)
Gametes rescued from testes at post-mortem⁶			
Canonical Florida panthers (14) ^{5,7}	8.8 ± 1.0 ^N (10)	10.1 ± 1.9 ^N (13)	35.3 ± 2.8 ^{N,C} (13)
Admixed Florida panthers (14) ^{5,7}	15.1 ± 1.7 ^P (9)	16.9 ± 3.6 ^P (10)	31.0 ± 5.3 ^{N,C} (10)
Ejaculates from live Western U.S. male pumas⁸			
Texas males (9) ^{3,4}	17.8 ± 1.7 (9)	14.0 ± 3.5 (9)	13.8 ± 1.2 (9)
Colorado males (7) ⁴	10.8 ± 0.7 (7)	16.3 ± 2.1 (7)	19.5 ± 0.8 (7)

Supplemental Table 6. Detail of data used to calculate values in Table S5. Codes in column 2 refer to panther heritage categories (C=CFP, E=EVG, BE=EVG-BC, BF=CFP-BC, BxT=TX-BC, AD=AdmFP, % Texas Unknown, * = inbred; †= related to FP79; S = sire; L+ = grand sire). **This animal had high % microcephalic and spermatids - ~18% of each

Collection method	Codes ^A	Panther ID	No. of Testes	Testes vol. per male	Vol / testis	% normal	%Acro+ Head	Date
CANONICAL								
Ejaculation	C	FP07	2	ND	ND	8.3	44.0	26-Jan-85
Ejaculation	C	FP12	1	8.81	8.8	5.7	39.7	28-Jan-86
Ejaculation	C	FP13	2	14.91	7.5	10.3	46.0	27-Feb-86
Ejaculation	C	FP17	2	13.77	6.9	10.0	29.0	26-Jan-89
Ejaculation	C	FP20	1	6.85	6.9	4.5	41.5	10-Jul-87
Ejaculation	C	FP24	2	21.22	10.6	4.0	52.5	30-Jan-88
Ejaculation	C	FP26	1	5.45	5.5	2.0	49.3	1-Mar-88
Ejaculation	C	FP28	1	7.39	7.4	4.5	3.6**	24-Jan-92
Ejaculation	C	FP29	1	5.67	5.7	3.0	31.5	12-Feb-90
Ejaculation	C	FP33	2	12.74	6.4	2.5	51.2	5-Mar-89
Ejaculation	C	FP34	1	5.29	5.3	5.5	35.5	11-Jan-91
Ejaculation	C	FP39	2	7.25	3.6	7.5	30.0	19-Feb-90
Ejaculation	C	FP43	1	3.09	3.09	aspermic		8-Jan-91
Ejaculation	C	FP51	2	20.6	10.3	5	46	28-Jan-98
Ejaculation	C	FP54	2	17.0	8.5	2	37	1-Jan-04
Ejaculation	C	FP60	2	19.0	9.5	6	46	1-Jan-04
		N=	16	15	15	15	14	
		Ave canonici	1.56	11.27	7.05	5.39	38.85	
		S.E.	0.13	1.58	0.58	0.69	3.18	
 GamResc								
GamResc	C	FP4	1	6.85	6.9	6.0	48.0	19-Apr-85
GamResc	C	FP13	2	ND	ND	18.0	35.0	15-Feb-87
GamResc	C	FP20	1	6.01	6.0	6.5	47.5	24-Aug-88
GamResc	C	FP30	1	ND	ND	12.0	22.0	30-Jan-90
GamResc	C	FP33	2	15.09	7.5	25.5	26.0	23-Nov-89
GamResc	C	FP39	2	5.25	2.6	19.5	24.0	18-May-90
GamResc	C	UCFP018	1	8.32	8.3	9.0	52.5	26-Jan-89
GamResc	C	FP59	2	12.4	6.2	3	32	26-Nov-04
GamResc	C	UCFP035	1	ND	ND	6	40	23-Jun-00
GamResc	C	FP98	1	8.0	8.0	7	28	1-Jul-02
GamResc	C	FP99	2	11.9	6.0	oligospermic		28-Nov-02
GamResc	C	K128	2	8.3	4.2	5	42	8-Dec-04
GamResc	C	UCFP050	1	ND	ND	10	28	29-Jan-03
GamResc	C	UCFP063	1	6.3	6.3	4	34	27-Feb-04
		N=	14	10	10	13	13	
		Ave canonici	1.43	8.84	6.19	10.12	35.31	
		S.E.	0.14	1.02	0.55	1.90	2.75	

Collection method	Codes ^A	Panther ID	No. of Testes	Testes vol. per male	Vol / testis	% normal	%Acro+ Head	Date
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Admixed Florida panthers

EVERGLADES

Ejaculation	E	FP16	2	14.47	7.2	9.5	48.5	2-Feb-88
Ejaculation	E	FP25	2	17.75	8.9	11.5	31.0	16-Feb-88
Ejaculation	E	FP37	2	ND	ND	7.5	38.0	30-Jan-90
Ejaculation	E	FP42	2	8.71	4.4	9.5	38.5	5-Feb-91
Ejaculation	E	FP200	2	14.91	7.5	9.5	38.0	17-Jan-90
		N=	5	4	4	5	5	
		Ave canon	2.00	13.96	6.98	9.50	38.80	
		S.E.	0.00	1.89	0.95	0.63	2.80	

CFPxTX-F1

Ejaculation	F1	FP065 _{F1-CT}	2	25.9	13.0	16	4	14-Feb-01
Ejaculation	F1	FP079 _{F1}	2	29.5	14.7	25	10	15-Nov-00
		Ave F1	2.00	27.68	13.84	20.50	7.00	
		S.E.	0.00	1.78	0.89	4.50	3.00	

Other AdmFP

Ejaculation	AD	FP154	1	9.5	9.5	13	44	21-Feb-07
Ejaculation	BE*	FP085 _{B-Enp}	2	24.0	12.0	1	59	18-Feb-03
Ejaculation	AD L	FP131	2	18.0	9.0	aspermic		22-Feb-07
Ejaculation	BT* S	FP104 _{Bx(BxT)}	2	21.1	10.6	aspermic		28-Feb-05
		N=	4	4	4	2	2	
		Ave Admixe	1.75	18.15	10.26	7.00	51.50	
		S.E.	0.25	3.13	0.66	6.00	7.50	

GamResc	AD	UCFP60	2	ND	ND	18	34	13-Dec-03
GamResc	BE	FP084 _{B-FI}	2	ND	ND	9	53	20-Apr-00
GamResc	BF	FP074	2	12.72	6.36	12	17	8-Sep-99
GamResc	BF	UCFP089	2	13.1	6.6	18	19	13-Dec-06
GamResc	BF	FP108 _{TXF1x(B)}	2	10.5	5.3	42	33	20-Nov-02
GamResc	BF	UCFP085	2	ND	ND	22	33	6-Jun-06
GamResc	BF	FP152	2	25.9	13.0	14	20	22/Oct/08
GamResc	BF	UCFP095	2	16.1	8.0	ND	ND	19-Apr-07
GamResc	BE*	FP085 _{B-Enp}	2	13.4	6.7	ND	ND	4-Mar-04
GamResc	BT L	K094 _{Bx(BxTX)}	2	9.7	4.9	6	49	18-Aug-04
GamResc	BT* S	FP090 _{Bx(BxT)}	2	ND	ND	15	3	26-Apr-01
GamResc	BT* S	UCFP051	2	14.5	7.3	10	40	11-Mar-03
GamResc	BT* S	FP104 _{Bx(BxT)}	2	ND	ND	aspermic		10-Mar-06
GamResc	SM	FP132+SEM	2	20.3	10.2	aspermic		23-Jul-04
		N=	14	9	9	10	10	
		Ave admixe	2.00	15.14	7.57	16.60	30.10	
		S.E.	0.00	1.70	0.85	3.20	4.88	

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