	Domestic cat (F.catus_Fca126_mat1.0)	Asian leopard cat (Fcat_Pben_1.1_paternal_pri)	Fishing cat (UM_Priviv_1.0)
Complete	8,616	8,610	8,623
Percent Complete	93.39%	93.32%	93.50%
Single-copy	8,589	8,589	8,599
Duplicated	27	21	24
Fragmented	156	153	167
Missing	454	463	436
Percent Present (Comp + Frag)	95.08%	94.98%	95.30%

Supplementary Table 1: BUSCO scores. Here are the BUSCO scores for the selected feline assemblies. Using the same BUSCO mammalia_odb10 dataset, the final scores for completeness, duplication, fragmented, and missing are all consistent with each other.

RefSeq Annotation Report					
Feature	Count	Mean length (bp)	Median length (bp)	Min length (bp)	Max length (bp)
Genes	26,992	44,238	13,021	49	2,066,153
All transcripts	68,764	3,182	2,579	49	103,095
mRNA	56,277	3,505	2,861	147	103,095
misc_RNA	3,687	3,283	2,801	117	15,837
tRNA	751	76	73	59	91
lncRNA	6,003	1,493	896	97	20,187
snoRNA	589	111	105	49	329
snRNA	1,113	114	107	60	199
rRNA	311	905	119	119	4,645
Single-exon transcripts	1,927	1,188	948	147	14,422
coding transcripts (NM_/XM_)	1,927	1,188	948	147	14,422
CDSs	56,290	2,049	1,509	96	103,095
Exons	264,672	306	137	1	22,878
in coding transcripts (NM_/XM_)	242,283	296	136	1	22,878
in non-coding transcripts (NR_/XR_)	44,225	305	135	2	18,596
Introns	236,897	6,513	1,562	30	937,235
in coding transcripts (NM_/XM_)	220,721	6,370	1,528	30	937,235
in non-coding transcripts (NR_/XR_)	37,542	6,607	1,761	30	861,863
	Mean	Median	Min	Max	
Number of transcripts per gene	2.59	1	1	50	
Number of exons per transcript	11.87	9	1	312	

Supplementary Table 2: NCBI RefSeq annotation summary.
Detailed in this table are the statistics for the NCBI RefSeq output for NCBI Prionailurus
viverrinus Annotation Release 100. This table also shows the number of transcripts per gene and exons
per transcript in the fishing cat gene annotation.

Species	Total Protein Coding
Fishing cat (UM_Priviv_1.0)	20,055
Asian leopard cat (Fcat_Pben_1.1_paternal_pri)	20,003
Domestic cat (F.catus_Fca126_mat1.0)	20,453

Supplementary Table 3: Total Protein Coding Genes Across Feline Species. Compared to the Asian leopard cat and Domestic cat phased genome assemblies the number of protein coding genes remains consistent across all 3 species.

Structural Variant Type		Fishing Cat vs Asian Leopard Cat	
Insertion	Size	Count	Total bp
	50-500 bp:	37142	8204841
	500-10,000 bp:	2216	6140544
	Total:	39358	14345385
Deletion	Size	Count	Total bp
	50-500 bp:	26655	5580183
	500-10,000 bp:	1624	4851702
	Total:	28279	10431885
Tandem Expansion	Size	Count	Total bp
	50-500 bp:	1991	470792
	500-10,000 bp:	541	822596
	Total:	2532	1293388
Tandem Contraction	Size	Count	Total bp
	50-500 bp:	1151	263668
	500-10,000 bp:	242	398212
	Total:	1393	661880
Repeat Expansion	Size	Count	Total bp
	50-500 bp:	5081	1321120
	500-10,000 bp:	3287	10569301
	Total:	8368	11890421
Repeat Contraction	Size	Count	Total bp
	50-500 bp:	9636	3031296
	500-10,000 bp:	5990	13116375
	Total:	15626	16147671

Supplementary Table 4: Genome structural comparisons. This table summarizes the AssembyTics output comparing the fishing cat reference genome to Asian leopard cat reference. Overall, least differences are detected in tandem expansions (2,532 identified) and tandem contractions (1,393 identified).

Studbook ID	Name	Sex	DOB	Age (years)	Sequencing	TCC status
687	Pavarti	F	5/2/05	13	WGS	Affected
722	Maliha	F	2/23/06	13	WGS	Affected
693	Sushi	M	7/15/05	11	WGS	Affected
688	Padma	F	5/2/05	12	WGS	Affected
721	Gorton	M	2/23/06	11	WGS	Affected
1196	Juniper	F	3/10/16	6	WGS	Normal
356	Fritz	M	8/15/94	10	WGS	Normal
5	Splash	F	1/14/96	11	WGS	Normal
1095	Wasabi	M	5/17/13	9	WGS	Normal
1195	SB #1195	M	3/10/16	6	WGS	Normal
1059	Jonas	F	7/31/12	10	WGS	Normal
780	Kiet	M	6/29/09	12	RNAseq	Affected
950	Anna	F	9/14/10	11	RNAseq	Normal

Supplementary Table 5: Fishing cat sequencing cohort. Listed in this table are the WGS cats and RNAseq cats, along with their studbook ID, name, sex, date of birth (DOB), current age, and TCC status. It is important to note that samples from normal presenting cats (except for studbook #356 and studbook #5 - both confirmed as non-TCC cats) were collected prior to 10 years old, when clinical signs of transitional cell carcinoma tend to occur. Studbook #950 is also the cat selected as the reference individual.

Consequence type	Count
transcript_ablation	2
splice_donor_variant	554
splice_acceptor_variant	555
stop_gained	547
frameshift_variant	2,587
stop_lost	101
start_lost	146
inframe_insertion	1,555
inframe_deletion	1,969
missense_variant	67,664
protein_altering_variant	54
splice_region_variant	30,675
start_retained_variant	9
synonymous_variant	101,309
stop_retained_variant	59
coding_sequence_variant	171
5_prime_UTR_variant	61,396
3_prime_UTR_variant	228,124
non_coding_transcript_exon_variant	69,156
intron_variant	18,048,749
non_coding_transcript_variant	1,695,493
upstream_gene_variant	1,517,673
downstream_gene_variant	1,508,744
intergenic_variant	5,224,881

Supplementary Table 6: Fishing cat VEP output. Detailed here are all the consequence types identified in the fishing cat cohort from Ensembl's VEP program. Most consequence types are found to be intron variants (63.2%) followed by intergenic variants (18.3%). In addition, a total of 67,664 missense variants were identified (0.2%).