Dataset S1.1(a). List of positively selected genes identified by the two-branch and branch-site tests in the Carnivore lineage

- A4GALT
- AASDH
- ABCG2
- ACR
- ADAM28
- ADH4
- ADH4
- AEN
- AGA
- AGFG2
- AHSG
- AKAP1
- AKAP12
- AMPD1
- ANGPT2
- ANGPTL2
- ANK3
- ANKS1A
- ANKS6
- ANPEP
- ANXA1
- ANXA13
- ANXA5
- ANXA7
- APH1B
- APOB
- APOBEC1
- ARHGAP18
- ARHGAP31
- ARMC3
- ARMCX1
- ATF6
- ATP2C2
- AXIN1
- B4GALT4
- BCAS1
- BCL3
- BLZF1
- BPI
- BRCA2
- BRIP1
- BRWD1
- C15orf52
- C18orf32
- C18orf54
- C2orf62
- C4orf47
- C9
- C9orf123
- C9orf89
- CA14
- CABP4
- CACNB2
- CAPZA3
- CARD6
- CATSPER2
- CATSPER4
- CC2D1B
- CC2D2A
- CCBL2
- CCDC108
- CCDC117
- CCDC137
- CCDC15
- CCDC40
- CCDC67
- CCKBR
- CCNF
- CCR6
- CCR8
- CD47
- CD63
- CD84
- CDC26
- CDH16
- CDH17
- CDH24
- CDSN
- CECR1
- CELA1
- CEP152
- CEP250
- CHCHD2
- CHM
- CHRM5
- CKAP2L
- CLCC1
- CLDN8
- CMYA5
- CNGB
- CNGB3
- COG7
- COL15A1
- COL23A1
- COL6A1
- COL9A3
- COX7A1
- CPD
- CPLX4
- CRTAP
- CTSA
- CX3CR1
- CXADR
- CXCR6
- CXorf30
- CYGB
- CYP27A1
- DAG1
- DBNDD2
- DCAF5
- DCDC2B
- DCK
- DCLRE1B
- DDRGK1
- DGCR2
- DHRS9
- DIAPH3
- DIRAS1
- DLEC1
- DNAJC12
- DNHD1
- DOK1
- DPH2
- DPM2
- DQX1
- DSG2
- DYNLRB2
- EDC4
- EDN1
- EIF2B3
- EIF3I
- EMR1
- ENAH
- ENOSF1
- ENPP4
- ENPP7
- ERAL1
- F10
- F5
- FAM101B
- FAM111B
- FAM129B
- FAM149A
- FAM188B
- FAM195B
- FAM83C
- FAN1
- FECH
- FGF23
- FGFBP1
- FMO3
- FN3KRP
- FOXRED1
- FSD1
- FSD2
- FTO
- GALNT14
- GALNT5
- GALT
- GAPDHS
- GCAT
- GGCT
- GGH
- GLB1
- GLB1L
- GOLM1
- GPR111
- GPR179
- GPRC5A
- GTF3A
- GUCA1B
- HAUS8
- HEATR2
- HEPHL1
- HJURP
- HMGCL
- HOOK1
- IGLON5
- IL1R1
- IL4I1
- IL7
- ILF2
- IMPG1
- INPP5A
- INSL6
- IQGAP3
- IRF8
- ITGA8
- ITGAM
- ITGB1BP2
- ITGB2
- ITPR2
- IWS1
- JAK2
- JARID2
- KARS
- KCNJ15
- KCNK7
- KCNN4
- KCTD3
- KIAA1143
- KIAA1984
- KLF4
- KLHL22
- KRTAP11-1
- LAMA3
- LAX1
- LBR
- LCA5
- LCLAT1
- LETM1
- LGR6
- LPXN
- LRP2
- LRRC15
- LRRC32
- LRRC43
- LRRC63
- LRRK2
- LSS
- LTF
- LY6E
- LYVE1
- MANBA
- MANEA
- MAP1B
- MARCH8
- MARCO
- MAT2B
- MBD1
- MDM1
- MED17
- MKKS
- MLH1
- MMP24
- MORN1
- MRPL2
- MRPL28
- MRPL41
- MRPL51

Dataset S1.1(b). List of positively selected genes identified by the two-branch and branch-site tests in the Carnivore lineage

MRPS12
MSMP
MSR1
MUM1L1
MUTYH
MYD88
MYH8
MYO15A
MYO3B
MYO7A
NANOS3
NBEAL1
NDOR1
NDST3
NDUFA6
NDUFAF4
NDUFV2
NFAM1
NGLY1
NGRN
NID1
NIN
NKTR
NLRP14
NMI
NODAL
NOL7
NOV
NSD1
NSUN5
NUP153
OAZ3
OAZ3
OBFC1
OIT3
OLFM1
OR10V1
OR13H1
OSGEP
OSMR
OTOF
OTUB2
OVCA2
OXCT1
PADI2
PCDH12
PCNXL2
PDCL3
PDE4C
PDE6B
PDILT
PEX6
PGLYRP1
PGM2
PHF15
PIBF1
PIGQ
PIK3CB
PITPNA
PITX1
PKHD1
PKMYT1
PLA2G2F
PLBD1
POC1B
PPA2
PPEF1
PPID
PPL
PPM1E
PPM1K
PPP1R2
PPP1R3A
PRC1
PRF1
PRICKLE2
PSD3
PSMD6
PTCD2
PTGR1
PTPRC
PTPRH
PXN
PYCARD
QSER1
RAB11FIP5
RAB18
RAB19
RAD52
RAG1
RANGAP1
RASAL1
RASSF5
RCSD1
RECQL4
REEP1
RELL2
RGS4
RHBDD1
RHCG
RHEBL1
RHOT2
ROS1
RRAGD
RRS1
RSPO4
RTBDN
RTN4
RTP3
SCGB1C1
SCML2
SCN3B
SCNM1
SDR39U1
SEC61A2
SEL1L2
SELP
SEPT12
SERPINB9
SH2D2A
SHARPIN
SHC4
SIGIRR
SKAP2
SLC10A4
SLC12A4
SLC13A2
SLC15A1
SLC16A5
SLC22A23
SLC22A8
SLC25A23
SLC25A42
SLC29A2
SLC2A10
SLC44A4
SLC47A1
SLC4A1
SLC4A5
SLC6A4
SLC7A1
SLC7A4
SLCO1C1
SMPDL3B
SNAPC4
SNAPC5
SNCAIP
SNRNP25
SOAT1
SOCS6
SPATA7
SPTA1
SRGN
SS18L1
ST3GAL1
STK24
SUCLG1
TAL2
TAS2R38
TBC1D21
TBL3
TBXAS1
TCN2
TEP1
TFAM
TFB2M
TG
TGM6
THADA
THBS3
THSD1
TK2
TLR2
TLR4
TLR6
TLR8
TMCO6
TMEM109
TMEM116
TMEM150B
TMEM156
TMEM167B
TMEM176A
TMEM182
TMEM215
TMIGD1
TMOD1
TMX1
TNFRSF13B
TNKS1BP1
TOM1
TOX4
TP53BP1
TPX2
TRA2A
TRAF7
TRDMT1
TREM2
TRIM25
TRIM33
TSEN2
TSHZ2
TSPAN10
TSPYL4
TTC34
TTF2
TUBGCP3
UBA7
UBE2L6
UGT2A3
UMOD
UNC13D
UPRT
UTP11L
VAMP8
VPS13C
VRK2
WFDC11
YIPF3
ZC3HAV1
ZMYM3
ZNF331
ZNF398
ZNF473
ZNF687
ZNF777
ZSWIM5

Dataset S1.2(a). List of positively selected genes identified by the two-branch and branch-site tests in the Felidae lineage

- ABCA5
- ACADL
- ACCS
- ACSF3
- ADAM22
- ADC
- AHSP
- AIM1L
- AKAP9
- AKNA
- AKNAD1
- ALB
- ALDH1A2
- ALG3
- ALPK2
- ANGPT2
- ANKS4B
- ANPEP
- AP3B2
- ARF4
- ARMCX2
- ATE1
- ATP2B3
- AZGP1
- BAK1
- BBS7
- BBS9
- BCAT2
- BCL2L14
- BCL2L15
- BIN1
- BIRC3
- BMF
- BMP15
- BMPR2
- BPI
- BRD7
- BRIP1
- BRWD1
- C10orf137
- C12orf56
- C14orf166B
- C17orf64
- C1orf146
- C1orf194
- C1QB
- C2orf43
- C3orf62
- C5
- CA4
- CALML5
- CAPN13
- CATSPER3
- CCDC107
- CCDC112
- CCDC113
- CCDC150
- CCNE2
- CD200
- CD244
- CD274
- CD48
- CD8B
- CD97
- CDC25B
- CDH1
- CDH17
- CDH5
- CDKN1B
- CEACAM18
- CENPE
- CES2
- CHRD
- CLEC5A
- CLUL1
- CMTM2
- CMYA5
- CNKSR1
- CRTAM
- CST7
- CTSZ
- CTTNBP2NL
- CXorf23
- CXorf57
- CYP17A1
- CYP1A2
- DCST2
- DDO
- DDX49
- DEPDC1
- DEPDC7
- DHRS1
- DHX32
- DLGAP5
- DMP1
- DNAH8
- DNAJB4
- DNHD1
- DUSP2
- DYSF
- E2F7
- ECM2
- EFCAB2
- EHBP1L1
- EHHADH
- EPHX1
- FA2H
- FAIM3
- FAM161B
- FAM181A
- FBN3
- FIGF
- FKBP3
- FKBP4
- FKBP7
- GAP43
- GGA3
- GJA10
- GJA5
- GLIPR1L2
- GMIP
- GPA33
- GPAA1
- GPRIN3
- GRIA2
- GRIA2
- GRIN2C
- GSDMC
- GTPBP8
- GUCA1A
- HAUS5
- HCFC2
- HDGF
- HFM1
- HHIPL2
- HSD17B14
- HSPBP1
- IFNK
- IGF1
- IGFBP5
- IL17RB
- IL22
- INHBB
- INVS
- IPO7
- IQCH
- IRF8
- IRS4
- ISG15
- ITGAE
- ITGB7
- ITIH4
- ITPR3
- KIF1A
- KREMEN2
- L1CAM
- LARS2
- LAT2
- LAX1
- LCNL1
- LGALS2
- LIMS2
- LIN28B
- LMBRD2
- LMF1
- LONRF3
- LPAR5
- LRAT
- LRRC14B
- LRRC6
- LRRTM2
- LTA4H
- LY9
- MAMDC2
- MAP7D3
- MAPK8IP2
- MAPKBP1
- MCM7
- MECR
- MEIS1
- MKNK2
- MORN3
- MRPL50
- MRPL55
- MSGN1
- MTRR
- MUTYH
- MVK
- MYH8
- MYO15A
- MYO1F
- MYO7A
- N4BP2
- NIF3L1
- NOLC1
- NPNT
- NPY
- NPY1R
- NTRK1
- NUBP2
- NUDCD3
- NUDT22
- OAZ3
- OMA1
- OOEP
- PARP2
- PC
- PFN2
- PIK3C2G
- PLAC8L1
- PNLIP
- PPAPDC1A
- PPP1R13L
- PRF1
- PROM1
- PRRG3
- PRX
- PSMB8
- PSME3
- PSMG3
- PTPRC
- PTPRH
- PTPRN
- PTPRQ
- RAB20
- RASGRP1
- RBM28
- RELA
- RIBC1
- RNF141
- RNF217
- RNPEP
- ROS1
- RPUSD4
- RSPH6A
- S100A12
- SACS
- SCAMP2
- SCAP
- SCD5

Dataset S1.2(b). List of positively selected genes identified by the two-branch and branch-site tests in the Felidae lineage

SCG2
SCGB1A1
SDC2
SELL
SERHL2
SF3A2
SFTPB
SH2D2A
SIPA1L2
SIT1
SLC16A5
SLC1A7
SLC27A1
SLC2A4
SLC38A8
SLC43A3
SLC7A11
SLCO2B1
SMOC2
SNAPC3
SNCG
SNRNP70
SPATA7
SPEF2
SPHK1
SPTBN4
SPTBN5
SPTLC3
SRCRB4D
STAM
STARD13
STARD3
STK31
STOX1
SVEP1
SYDE2
SYNM
SYTL3
TAPBPL
TCF3
TDG
TEX11
TFAP2A
TGM7
THTPA
TM6SF2
TMEM140
TMEM150B
TMEM156
TMEM161B
TMEM176A
TMEM19
TMEM190
TMEM211
TMX3
TNFAIP3
TNIP2
TNIP3
TRA2A
TRAF3IP2
TRAT1
TRMU
TRPM4
TRPS1
TSPAN8
TSSK4
TTC34
TTC39C
TTYH1
TUSC5
UBE2S
UCHL1
UMPS
UNC93B1
USHBP1
VTI1A
WDFY4
WFDC8
WHAMM
WIPF2
WRN
XKR7
XRCC5
YIF1B
ZFYVE16
ZNF304
ZNF408
ZNF780B
ZNF804B
ZSCAN29
ZSWIM2

Dataset S1.3(a). List of positively selected genes identified by the two-branch and branch-site tests in the Felinae lineage

ABHD1
ACOT11
ACOT13
ACOT8
ACOX2
ACOX3
ADAMDEC1
ADAMTS13
ADAMTSL3
AK1
ALDH16A1
ALS2CR12
AMACR
ANKRD2
ANKRD49
ANKRD50
APEH
APOBEC4
ARHGAP26
ASB11
ATXN7L1
BARD1
BCAP31
BPI
BRAF
BRCA1
C11orf54
C11orf63
C16orf71
C1orf109
C22orf31
C2orf40
C2orf62
C3orf62
C8B
C9orf96
CAGE1
CASP7
CBX2
CCDC38
CCDC64B
CCDC70
CD27
CD48
CD93
CDH6
CELA1
CENPE
CENPM
CEP68
CEP97
CHMP4B
CIB4
CLDN17
CLEC5A
CNGA2
COL6A3
COL9A3
CROCC
CSPP1
CTTN
CYB5R1
CYP27B1
DACT1
DAPK1
DNAJB9
DNTTIP2
DPEP3
DUSP19
ECHDC1
EDC3
EHBP1L1
ENKUR
ENTPD7
EPHB4
ETV4
FAIM3
FAM131B
FAM179A
FAM69A
FANCB
FAT4
FBN3
FBXL22
FBXO28
FER
FGA
FN3K
FRMD7
GCNT7
GEMIN7
GGT6
GOLGA1
GPATCH8
GPR133
GPR15
GPR174
GPRASP2
GPRC5A
GPRIN2
GRHL3
GRIA2
HADH
HEATR5B
HECA
HEPACAM2
HEPH
HMMR
HPS5
HSD3B7
HSPA13
IFT81
IGHMBP2
INHBC
INPP4B
INPP5J
IPO4
IQCB1
ISG15
ITGA2B
ITGA9
ITGBL1
ITPR3
JMJD1C
KIAA0226
KIF1C
KIF22
KIF27
KIRREL2
KRIT1
KYNU
LAMC2
LAP3
LATS2
LCAT
LIAS
LIMD1
LRRC32
LRRC36
LSM3
MAP7D2
MARVELD3
MERTK
METTL8
MIIP
MORC1
MRPL11
MRPL52
MTIF2
MTRF1
MURC
MVK
MYLK3
MYO15A
MYO9A
NAPRT1
NEK1
NEK4
NFAM1
NFKBIZ
NOLC1
NOSTRIN
NOTCH2
NPFFR2
NRG2
NUDT15
OPTC
OR10K1
OR2B11
OR4D6
OTOF
PAFAH2
PARVG
PCDHB4
PHLDB3
PITRM1
PJA2
PLA2G2E
PLA2G3
PLAC1
PLAC8L1
PLIN3
PML
PPAP2A
PPAPDC1B
PPFIBP1
PPP1R13B
PRICKLE4
PRKAG1
PRKG2
PRR11
PRX
PSPH
PSTK
PTPRR
PTPRS
PUSL1
RABL3
RBM11
RBP5
RCSD1
RELL1
RHBDD1
RIMKLA
RNASE6
RNPC3
RSL1D1
RTP3
S100A12
SCN9A
SCRIB
SDK2
SEC24A
SENP5
SENP7
SEPT10
SERINC3
SH2D5
SHC4
SIAE
SLC22A13
SLC22A18
SLC25A38
SLC35F5
SLC39A7
SLC39A8
SLC46A1
SLCO1A2
SMG1
SMG6
SPATA21
SPATA7
SPERT
SPHKAP
SPINT1
SPTBN5
SREBF1
SRRM2
STARD5
STK11IP

Dataset S1.3(b). List of positively selected genes identified by the two-branch and branch-site tests in the Felinae lineage

STS
SUN3
SURF2
SYNM
SYTL1
TAS2R1
TAS2R3
TEX14
TF
THBS2
THUMPD1
TMEM59L
TMEM71
TOE1
TP53BP1
TRPV6
TSTD2
TXN2
TXNRD2
TYK2
UBXN10
USP45
UVRAG
VEZT
WDR17
WDR62
WDR90
WFDC8
WIPF2
WIPF3
WWC1
XCR1
XPC
ZFAT
ZFYVE19
ZMYND10
ZNF436
ZNF555
ZNF622
ZNF780B
ZZEF1

Dataset S1.4(a). Predicted structural/functional influence of the domestic cat nonsynonymous substitutions for positively selected sensory and lipid metabolism genes

Gene Name	Number of Significant Amino Acid Properties	Identified Categories	Intense Protein Functional Changes	Number of Suggested Deleterious Amino Acid Substitutions
ABHD1	2	9,22	negative	0
ACOT11	3	12,17,26	negative	0
ACOT8	1	9	negative	0
ACOX2	5	7,10,12,15,31	negative	0
ACOX3	**6**	**4,10,12,15,17,21**	**positive**	**2**
AMACR	**5**	**10,17,24,30,31**	**positive**	**4**
BARD1	2	9,12	negative	0
BBS7	0		negative	0
BBS9	2	3,7	negative	0
BRAF	**2**	**9,22**	**positive**	**1**
BRCA1	**28**	**1-9,11-15,17-26,28-31**	**positive**	**11**
CA4	**2**	**13,27**	**positive**	**1**
CABP4	0		negative	0
CDKN1B	0		negative	0
CHM	4	1,4,11,12	negative	0
CNGA2	**2**	**10,15**	**positive**	**1**
CNGB3	**1**	**31**	**positive**	**1**
COL6A3	**31**	**1-31**	**positive**	**1**
COL9A3	**4**	**13,15,17,31**	**positive**	**1**
CPLX4	0		negative	0
CYP27B1	1	17	negative	0
GJA10	0		positive	1
GRIA2	**1**	**2**	**positive**	**2**
GRIN2C	2	9,17	negative	0
GUCA1A	0		negative	0
GUCA1B	0		negative	0
HADH	1	28	negative	0
HMMR	**5**	**1,7,9,15,17**	**positive**	**2**
HSD3B7	2	9,15	negative	0
IMPG1	0		negative	0
INPP5J	4	1,2,4,12	negative	0
IQCB1	2	15,22	negative	0
ITGA2B	14	3,6,7,8,10,12,16,17,19,22,24,28,29,31	negative	0
ITGA9	3	1,3,15	negative	0
LAMC2	**14**	**3,7-10,12,13,15,16,17,19,26,29,31**	**positive**	**1**
LCAT	0		negative	0
LRAT	0		negative	0

Significant genes common to both approaches are highlighted in red.
a- TreeSAAP is used to measure structural and biochemical properties of amino acid replacement using a threshold of P<0.001. 31 categories are tested as follows: 1. Alpha-helical tendencies, 2. Average number of surrounding residues, 3. Beta-structure tendencies, 4. Bulkiness, 5. Buriedness, 6. Chromatographic index, 7. Coil tendencies, 8. Composition, 9. Compressibility, 10. Equilibrium constant, 11. Helical contact area, 12. Hydropathy, 13. Isoelectric point, 14. Long-range non-bonded energy, 15. Mean r.m.s. fluctuation displacement, 16. Molecular volume, 17. Molecular weight, 18. Normalized consensus hydrophobicity, 19. Partial specific volume, 20. Polar requirement, 21. Polarity, 22. Power to be at the C-terminal, 23. Power to be at the middle of alpha-helix, 24. Power to be at the N-terminal, 25. Refractive index, 26. Short and medium range non-bonded energy, 27. Solvent accessible reduction ratio, 28. Surrounding hydrophobicity, 29. Thermodynamic transfer hydrohphobicity, 30. Total non-bonded energy, 31. Turn tendencies
b - Amino acid substitutions labeled as “deleterious” based on Provean.

Dataset S1.4(b). Predicted structural/functional influence of the domestic cat nonsynonymous substitutions for positively selected sensory and lipid metabolism genes

Gene Name	Number of Significant Amino Acid Properties	Identified Categories	Intense Protein Functional Changes	Number of Suggested Deleterious Amino Acid Substitutions
MERTK	2	9,17	negative	0
MKKS	3	3,4,25	negative	0
MVK	27	1-6,8-19,20,21,22,25-30	negative	0
MYLK3	0		negative	0
MYO15A	**17**	**1,4,5,9,12,14-17,19,20-23,26,30,31**	**positive**	**2**
MYO3B	**0**		**positive**	**1**
MYO7A	**5**	**7,9,12,17,26**	**positive**	**2**
MYO9A	**13**	**1,3,10-13,15,16,17,19,20,22,31**	**positive**	**3**
NPFFR2	**4**	**11,16,19,26**	**positive**	**1**
NPY	0		negative	0
NPY1R	0		negative	0
OR10K1	**2**	**3,22**	**positive**	**2**
OR10V1	2	9,17	negative	0
OR13H1	0		negative	0
OR2B11	**1**	**15**	**positive**	**1**
PAFAH2	2	12,15	negative	0
PARVG	1	12	negative	0
PCDH4B	0		negative	0
PDE6B	2	15,26	negative	0
PLA2G2E	4	9,17,26,27	negative	0
PLA2G3	**1**	**17**	**positive**	**2**
PPAP2A	**2**	**5,26**	**positive**	**4**
PPAPDC1B	1	9	negative	0
PPEF1	6	4,11,15,22,23,28	negative	0
PRKAG1	0		negative	0
PRKG2	0		negative	0
PROM1	**16**	**3,4,6,7,8,11,14-17,20,22,23,28,30,31**	**positive**	**6**
PTPRQ	**25**	**2-17,19,21,22,23,27~31**	**positive**	**4**
RTP3	**1**	**1**	**positive**	**1**
SHC4	0		negative	0
SIAE	**2**	**9,24**	**positive**	**1**
SLCO1A2	5	7,10,11,16,23	negative	0
SMG1	12	3,10,11,12,14-17,22,23,24,29	negative	0
STARD5	1	9	negative	0
TAS2R3	**10**	**2,3,5,8,10,12,18,19,25,30**	**positive**	**3**
TAS2R38	**11**	**3,5,6,7,8,10,11,15,26,30,31**	**positive**	**1**
THBS2	12	2,3,7-11,15,17,22,26,31	negative	0

Significant genes common to both approaches are highlighted in red.
a- TreeSAAP is used to measure structural and biochemical properties of amino acid replacement using a threshold of P<0.001. 31 categories are tested as follows: 1. Alpha-helical tendencies, 2. Average number of surrounding residues, 3. Beta-structure tendencies, 4. Bulkiness, 5. Buriedness, 6. Chromatographic index, 7. Coil tendencies, 8. Composition, 9. Compressibility, 10. Equilibrium constant, 11. Helical contact area, 12. Hydropathy, 13. Isoelectric point, 14. Long-range non-bonded energy, 15. Mean r.m.s. fluctuation displacement, 16. Molecular volume, 17. Molecular weight, 18. Normalized consensus hydrophobicity, 19. Partial specific volume, 20. Polar requirement, 21. Polarity, 22. Power to be at the C-terminal, 23. Power to be at the middle of alpha-helix, 24. Power to be at the N-terminal, 25. Refractive index, 26. Short and medium range non-bonded energy, 27. Solvent accessible reduction ratio, 28. Surrounding hydrophobicity, 29. Thermodynamic transfer hydrohphobicity, 30. Total non-bonded energy, 31. Turn tendencies
b - Amino acid substitutions labeled as “deleterious” based on Provean.

Dataset S1.5. Enriched pathways among genes under positive selection in the domestic cat (Felinae) lineage

PATHWAY COMMONS CATEGORY	C	O	E	GENES
BETA-OXIDATION OF PRISTANOYL-COA	8	4	0.11	ACOX2, AMACR, ACOX3, ACOT8
BILE ACID AND BILE SALT METABOLISM	27	5	0.37	SLCO1A2, ACOX2, AMACR, HSD3B7, ACOT8
SYNTHESIS OF BILE ACIDS AND BILE SALTS VIA 7ALPHA-HYDROXYCHOLESTEROL	15	4	0.21	ACOX2, AMACR, HSD3B7, ACOT8
PEROXISOMAL LIPID METABOLISM	20	4	0.28	ACOX2, AMACR, ACOX3, ACOT8
METABOLISM OF LIPIDS AND LIPOPROTEINS	258	12	3.57	LCAT, CYP27B1, PPAP2A, SLCO1A2, MVK, HADH, STARD5, ACOX2, AMACR, ACOX3, HSD3B7, ACOT8
KEGG CATEGORY				
ECM-RECEPTOR INTERACTION	85	6	1.18	HMMR, ITGA9, THBS2, LAMC2, ITGA2B, COL6A3
LONG-TERM DEPRESSION	70	6	0.97	PRKG2, PLA2G2E, BRAF, GRIA2, ITPR3, PLA2G3
PRIMARY BILE ACID BIOSYNTHESIS	16	3	0.22	ACOX2, AMACR, HSD3B7
ETHER LIPID METABOLISM	36	4	0.5	PLA2G2E, PPAP2A, PAFAH2, PLA2G3
FOCAL ADHESION	200	9	2.77	SHC4, BRAF, PARVG, MYLK3, ITGA9, THBS2, LAMC2, ITGA2B, COL6A3
ALPHA-LINOLENIC ACID METABOLISM	20	3	0.28	PLA2G2E, ACOX3, PLA2G3
PEROXISOME	79	5	1.09	ACOX2, MVK, AMACR, ACOX3, ACOT8
GO CATEGORY				
LIPID MODIFICATION	143	11	2.16	LCAT, PPAP2A, HADH, PRKAG1, ACOX2, AMACR, INPP5J, ACOX3, SMG1, PPAPDC1B, ACOT8
FATTY ACID BETA-OXIDATION USING ACYL-COA OXIDASE	11	4	0.17	ACOX2, AMACR, ACOX3, ACOT8
CARBOXYLIC ESTER HYDROLASE ACTIVITY	116	8	1.71	LCAT, PAFAH2, ACOT11, PLA2G2E, SIAE, ABHD1, PLA2G3, ACOT8
PRISTANOYL-COA OXIDASE ACTIVITY	2	2	0.03	ACOX2, ACOX3
BRCA1-BARD1 COMPLEX	2	2	0.03	BRCA1, BARD1

USER DATA & PARAMETERS - N = 281 genes submitted, Genes mapped to unique Entrez Gene IDs: 281, Organism: hsapiens, Id Type: gene_symbol, Ref Set: entrezgene_protein-coding, Significance Level: .05, Statistics Test: Hypergeometric, MTC: BH, Minimum: 2

COLUMN HEADINGS - number of reference genes in the category (C), number of genes in the gene set and also in the category (O), expected number in the category (E).

Dataset S1.6. Enriched gene ontology categories among genes under positive selection in Carnivora

GO CATEGORY	PATHWAY ID	C	O	E	R	rawP	adjP
pattern recognition receptor activity	GO:0008329	15	4	0.39	10.29	0.0005	0.0482
glycosaminoglycan binding	GO:0005539	174	13	4.51	2.88	0.0006	0.0482
diacyl lipopeptide binding	GO:0042498	2	2	0.05	38.60	0.0007	0.0482
secondary active oligopeptide transmembrane transporter activity	GO:0015322	2	2	0.05	38.60	0.0007	0.0482
bacterial cell surface binding	GO:0051635	17	4	0.44	9.08	0.0008	0.0482
proton-dependent oligopeptide secondary active transmembrane transporter activity	GO:0005427	2	2	0.05	38.60	0.0007	0.0482
carbohydrate derivative binding	GO:0097367	189	14	4.90	2.86	0.0004	0.0482
cytoplasmic part	GO:0044444	6728	210	170	1.23	5.38E-05	0.0157
plasma membrane part	GO:0044459	1908	72	48.38	1.49	0.0003	0.0292
intrinsic to plasma membrane	GO:0031226	1255	53	31.82	1.67	0.0002	0.0292
integral to plasma membrane	GO:0005887	1214	49	30.78	1.59	0.0008	0.0389
Toll-like receptor 2-Toll-like receptor 6 protein	GO:0035355	2	2	0.05	2.41	0.0008	0.0389
mitochondrial matrix	GO:0005759	278	17	7.05	2.41	0.0008	0.0389
cytoplasm	GO:0005737	9051	261	229.5	1.14	0.001	0.0417
membrane	GO:0016020	7631	224	193.5	1.16	0.0015	0.0487
cell periphery	GO:0071944	4286	136	108.68	1.25	0.0015	0.0487

USER DATA & PARAMETERS - N = 467 genes submitted, Genes mapped to unique Entrez Gene IDs: 466, Organism: hsapiens, Id Type: gene_symbol, Ref Set: entrezgene_protein-coding, Significance Level: .05, Statistics Test: Hypergeometric, MTC: BH, Minimum: 2

COLUMN HEADINGS - number of reference genes in the category (C), number of genes in the gene set and also in the category (O), expected number in the category (E), Ratio of enrichment (R), p value from hypergeometric test (rawP), and p value adjusted by the multiple test adjustment (adjP).

Dataset S1.7. Enriched gene ontology categories among genes under positive selection in Felidae

PATHWAY COMMONS	Pathway ID	C	O	E	R	rawP	adjP
AlphaE beta7 integrin cell surface interactions	1632	3	3	0.5	61.46	4.27E-06	0.0012
Adaptive Immune System	515	237	14	3	3.63	3.64E-05	0.0049
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	1098	52	6	0.82	7.09	0.0002	0.0180
Immune System	522	522	20	8.49	2.35	0.0004	0.027
Interaction between L1 and Ankyrins	45	12	3	0.2	15.37	0.0008	0.0432
KEGG CATEGORY							
Cell adhesion molecules (CAMs)	4514	133	9	2.16	4.16	0.0003	0.0246
GO CATEGORY							
epoxide hydrolase activity	GO:0004301	5	3	0.09	33.78	5.40E-05	0.0155
ether hydrolase activity	GO:0016803	7	3	0.12	24.13	0.0002	0.0287
external side of plasma membrane	GO:0009897	199	12	3.42	3.51	0.0002	0.0442

USER DATA & PARAMETERS - N = 331 genes submitted, Genes mapped to unique Entrez Gene IDs: 331, Organism: hsapiens, Id Type: gene_symbol, Ref Set: entrezgene_protein-coding, Significance Level: .05, Statistics Test: Hypergeometric, MTC: BH, Minimum: 2

COLUMN HEADINGS - number of reference genes in the category (C), number of genes in the gene set and also in the category (O), expected number in the category (E), Ratio of enrichment (R), p value from hypergeometric test (rawP), and p value adjusted by the multiple test adjustment (adjP).

Dataset S1.8(a). *Felis catus* gene members that underwent rapid gene family expansions along the Felidae lineage.

Ensembl Gene ID	Ensembl Family Description	Ensembl Protein Family ID(s)

CAFE Family ID:48		
ENSFCAG00000025324	IG HEAVY CHAIN V REGION	ENSFM00670001235368
ENSFCAG00000027432	"	ENSFM00670001235368
ENSFCAG00000028301	"	ENSFM00670001235368
ENSFCAG00000028921	"	ENSFM00670001235368
ENSFCAG00000023488	"	ENSFM00670001235368
ENSFCAG00000026432	"	ENSFM00670001235368
ENSFCAG00000029107	"	ENSFM00670001235368
ENSFCAG00000028889	"	ENSFM00670001235368
ENSFCAG00000029901	"	ENSFM00670001235368
ENSFCAG00000028814	"	ENSFM00670001235368
ENSFCAG00000023635	"	ENSFM00670001235368
ENSFCAG00000027142	"	ENSFM00670001235368
ENSFCAG00000028661	"	ENSFM00670001235368
ENSFCAG00000023737	"	ENSFM00670001235368
ENSFCAG00000026570	"	ENSFM00670001235368
ENSFCAG00000025755	"	ENSFM00670001235368
ENSFCAG00000027760	"	ENSFM00670001235368
ENSFCAG00000026585	"	ENSFM00670001235368
ENSFCAG00000031242	"	ENSFM00670001235368
ENSFCAG00000023332	"	ENSFM00670001235368
ENSFCAG00000023265	"	ENSFM00670001235368
ENSFCAG00000023423	"	ENSFM00670001235368
ENSFCAG00000023729	"	ENSFM00670001235368
ENSFCAG00000030410	"	ENSFM00670001235368
ENSFCAG00000029880	"	ENSFM00670001235368
ENSFCAG00000022386	"	ENSFM00670001235368
ENSFCAG00000026880	"	ENSFM00670001235368
ENSFCAG00000022825	HEAVY V	ENSFM00670001235643
ENSFCAG00000024010	IG HEAVY CHAIN V I REGION	ENSFM00670001235685
ENSFCAG00000022778	"	ENSFM00670001235685
ENSFCAG00000023329	"	ENSFM00670001235685
ENSFCAG00000022071	UNKNOWN	ENSFM00700001406400

Dataset S1.8(b). *Felis catus* gene members that underwent rapid gene family expansions along the Felidae lineage.

CAFE Family ID:60		
ENSFCAG00000001090	PEPTIDYL PROLYL CIS TRANS ISOMERASE 1 PPIASE EC_5.2.1.8 ROTAMASE	ENSFM00500000270856
ENSFCAG00000005373	"	ENSFM00500000271254
ENSFCAG00000028008	"	ENSFM00500000272090
ENSFCAG00000004182	"	ENSFM00500000269861
ENSFCAG00000008910	"	ENSFM00500000269861
ENSFCAG00000006027	PEPTIDYL PROLYL CIS TRANS ISOMERASE PPIASE EC_5.2.1.8 CYCLOPHILIN CYCLOSPORIN A BINDING ROTAMASE	ENSFM00600000921134
ENSFCAG00000009159	"	ENSFM00600000921134
ENSFCAG00000023140	"	ENSFM00600000921134
ENSFCAG00000028094	"	ENSFM00600000921134
ENSFCAG00000028260	"	ENSFM00600000921134
ENSFCAG00000030523	"	ENSFM00600000921134
ENSFCAG00000027344	"	ENSFM00600000921134
ENSFCAG00000028314	"	ENSFM00600000921134
ENSFCAG00000029878	"	ENSFM00600000921134
ENSFCAG00000030193	"	ENSFM00600000921134
ENSFCAG00000028578	"	ENSFM00600000921134
ENSFCAG00000012326	"	ENSFM00600000921134
ENSFCAG00000026216	"	ENSFM00600000921134
ENSFCAG00000025543	"	ENSFM00600000921134
ENSFCAG00000022115	"	ENSFM00600000921134
ENSFCAG00000000811	PEPTIDYL PROLYL CIS TRANS ISOMERASE PPIASE EC_5.2.1.8 ROTAMASE	ENSFM00710001441744
ENSFCAG00000022870	"	ENSFM00710001441744
ENSFCAG00000028615	"	ENSFM00710001441744
ENSFCAG00000028926	"	ENSFM00710001441744
ENSFCAG00000028168	"	ENSFM00710001441744
ENSFCAG00000009056	PEPTIDYLPROLYL ISOMERASE DOMAIN AND WD REPEAT CONTAINING 1 EC_5.2.1.8	ENSFM00500000270357
ENSFCAG00000027963	RANBP2 AND GRIP DOMAIN CONTAINING RAN BINDING 2 RANBP2 RANB	ENSFM00500000270422

Dataset S1.8(c). *Felis catus* gene members that underwent rapid gene family expansions along the Felidae lineage.

CAFE Family ID:77		
ENSFCAG00000000768	DYNEIN HEAVY CHAIN AXONEMAL AXONEMAL BETA DYNEIN HEAVY CHAIN CILIARY DYNEIN HEAVY CHAIN	ENSFM00710001441583
ENSFCAG00000002303	"	ENSFM00710001441583
ENSFCAG00000003487	"	ENSFM00710001441583
ENSFCAG00000008938	"	ENSFM00710001441583
ENSFCAG00000009626	"	ENSFM00710001441583
ENSFCAG00000011050	"	ENSFM00710001441583
ENSFCAG00000011062	"	ENSFM00710001441583
ENSFCAG00000011997	"	ENSFM00710001441583
ENSFCAG00000014410	"	ENSFM00710001441583
ENSFCAG00000015163	"	ENSFM00710001441583
ENSFCAG00000015341	"	ENSFM00710001441583
ENSFCAG00000015710	"	ENSFM00710001441583
ENSFCAG00000024375	"	ENSFM00710001441583
ENSFCAG00000031892	"	ENSFM00710001441583
ENSFCAG00000028573	"	ENSFM00710001441583
ENSFCAG00000030613	"	ENSFM00710001441583
ENSFCAG00000022940	"	ENSFM00710001441583
ENSFCAG00000030413	"	ENSFM00710001441583
ENSFCAG00000023988	"	ENSFM00710001441583
ENSFCAG00000027018	"	ENSFM00710001441583
ENSFCAG00000025942	"	ENSFM00710001441583
ENSFCAG00000029696	"	ENSFM00710001441583
ENSFCAG00000025884	"	ENSFM00710001441583
ENSFCAG00000029772	DYNEIN HEAVY CHAIN 14 AXONEMAL AXONEMAL BETA DYNEIN HEAVY CHAIN 14 CILIARY DYNEIN HEAVY CHAIN 14	ENSFM00250000013821
ENSFCAG00000027160	UNKNOWN	ENSFM00700001403725
ENSFCAG00000003480	UNKNOWN	ENSFM00700001395909

CAFE Family ID:96		
ENSFCAG00000024916	T CELL RECEPTOR ALPHA CHAIN V REGION PY14 PRECURSOR	ENSFM00670001239630
ENSFCAG00000025340	UNCHARACTERIZED FRAGMENT	ENSFM00670001238133
ENSFCAG00000028266	"	ENSFM00670001240217
ENSFCAG00000026476	"	ENSFM00670001257046
ENSFCAG00000030178	"	ENSFM00670001244595
ENSFCAG00000030540	UNKNOWN	ENSFM00670001238314
ENSFCAG00000023413	"	ENSFM00700001403106
ENSFCAG00000028123	"	ENSFM00670001238314

Dataset S1.8(d). *Felis catus* gene members that underwent rapid gene family expansions along the Felidae lineage.

CAFE Family ID:107		
ENSFCAG00000007354	VOMERONASAL TYPE 1 RECEPTOR V1R RECEPTOR	ENSFM00420000140525
ENSFCAG00000013746	"	ENSFM00420000140525
ENSFCAG00000026501	"	ENSFM00390000126342
ENSFCAG00000023564	"	ENSFM00420000140525
ENSFCAG00000030794	"	ENSFM00420000140525
ENSFCAG00000030467	"	ENSFM00420000140525
ENSFCAG00000029349	"	ENSFM00420000140525
ENSFCAG00000028999	"	ENSFM00500000270777
ENSFCAG00000025970	"	ENSFM00500000270777
ENSFCAG00000031455	"	ENSFM00420000140525
ENSFCAG00000029994	"	ENSFM00420000140525
ENSFCAG00000028171	"	ENSFM00500000269919
ENSFCAG00000025619	"	ENSFM00420000140525
ENSFCAG00000022751	"	ENSFM00420000140525
ENSFCAG00000030971	"	ENSFM00420000140525
ENSFCAG00000031841	"	ENSFM00570000851064
ENSFCAG00000026750	"	ENSFM00420000140525
ENSFCAG00000022670	"	ENSFM00420000140525
ENSFCAG00000000122	"	ENSFM00420000140525
ENSFCAG00000022668	"	ENSFM00500000270777
ENSFCAG00000029277	"	ENSFM00420000140525
ENSFCAG00000031101	"	ENSFM00500000269919

CAFE Family ID:159		
ENSFCAG00000002807	TRANSCRIPTION FACTOR SOX	ENSFM00500000269754
ENSFCAG00000004219	"	ENSFM00500000269754
ENSFCAG00000015685	"	ENSFM00500000269754
ENSFCAG00000022613	"	ENSFM00670001235710
ENSFCAG00000009619	SOX 15	ENSFM00500000274021

CAFE Family ID:323		
ENSFCAG00000001958	COLLAGEN ALPHA CHAIN PRECURSOR	ENSFM00250000000231
ENSFCAG00000004005	"	ENSFM00250000000231
ENSFCAG00000009383	"	ENSFM00250000000231
ENSFCAG00000026038	"	ENSFM00250000000231
ENSFCAG00000029007	"	ENSFM00250000000231
ENSFCAG00000025042	"	ENSFM00250000000231
ENSFCAG00000031671	UNKNOWN	ENSFM00700001406119
ENSFCAG00000030864	"	ENSFM00700001407229
ENSFCAG00000025023	"	ENSFM00700001406121

Dataset S1.8(e). *Felis catus* gene members that underwent rapid gene family expansions along the Felidae lineage.

CAFE Family ID:415		
ENSFCAG00000003805	HISTONE H1	ENSFM00670001235652
ENSFCAG00000005967	"	ENSFM00670001235652
ENSFCAG00000006079	"	ENSFM00670001235652
ENSFCAG00000006768	"	ENSFM00670001235652
ENSFCAG00000015177	"	ENSFM00670001235652
ENSFCAG00000005970	HISTONE H1T TESTICULAR H1 HISTONE	ENSFM00600000922221
ENSFCAG00000005962	HISTONE H1 1 HISTONE H1A	ENSFM00670001237167
ENSFCAG00000023697	UNKNOWN	ENSFM00700001402417

CAFE Family ID:494		
ENSFCAG00000027832	DIAPHANOUS HOMOLOG DIAPHANOUS RELATED FORMIN	ENSFM00260000050429
ENSFCAG00000031011	"	ENSFM00260000050429
ENSFCAG00000025687	"	ENSFM00260000050429
ENSFCAG00000027130	UNKNOWN	ENSFM00700001407483
ENSFCAG00000031194	"	ENSFM00700001406364
ENSFCAG00000029496	"	ENSFM00700001403036
ENSFCAG00000029591	"	ENSFM00700001406366
ENSFCAG00000027080	"	ENSFM00700001406365

CAFE Family ID:507		
ENSFCAG00000009104	PARTITIONING DEFECTIVE 3 HOMOLOG B AMYOTROPHIC LATERAL SCLEROSIS 2 CHROMOSOMAL REGION CANDIDATE GENE 19 PAR3 BETA PARTITIONING DEFECTIVE 3 PAR3 L	ENSFM00610000952891
ENSFCAG00000026384	"	ENSFM00610000952891
ENSFCAG00000025827	"	ENSFM00610000952891
ENSFCAG00000022493	"	ENSFM00610000952891
ENSFCAG00000026773	"	ENSFM00610000952891
ENSFCAG00000025870	"	ENSFM00610000952891
ENSFCAG00000024471	UNKNOWN	ENSFM00700001403157
ENSFCAG00000027778	"	ENSFM00700001404186

Dataset S1.8(f). *Felis catus* gene members that underwent rapid gene family expansions along the Felidae lineage.

CAFE Family ID:598		
ENSFCAG00000015547	MYOTILIN MYOFIBRILLAR TITIN IG DOMAINS TITIN IMMUNOGLOBULIN DOMAIN	ENSFM00570000851448
ENSFCAG00000026398	"	ENSFM00570000851448
ENSFCAG00000023378	MYOSIN LIGHT CHAIN KINASE SMOOTH MUSCLE FRAGMENT MLCK EC_2.7.11.18	ENSFM00710001444534
ENSFCAG00000023052	MYOSIN LIGHT CHAIN KINASE EC_2.7.11.18	ENSFM00550000743135
ENSFCAG00000031720	PALLADIN	ENSFM00690001356798
ENSFCAG00000027262	"	ENSFM00570000851711
ENSFCAG00000024606	"	ENSFM00570000851711
ENSFCAG00000003424	"	ENSFM00570000851679
ENSFCAG00000031314	UNKNOWN	ENSFM00700001403043

CAFE Family ID:757		
ENSFCAG00000030661	MYOMEGALIN PHOSPHODIESTERASE 4D INTERACTING	ENSFM00250000001701
ENSFCAG00000026455	"	ENSFM00250000001701
ENSFCAG00000028868	"	ENSFM00250000001701
ENSFCAG00000023617	"	ENSFM00250000001701
ENSFCAG00000031847	"	ENSFM00250000001701
ENSFCAG00000027086	"	ENSFM00250000001701
ENSFCAG00000031642	NEUROBLASTOMA BREAKPOINT FAMILY MEMBER 6	ENSFM00500000284802
ENSFCAG00000031382	UNKNOWN	ENSFM00700001403283

CAFE Family ID:764		
ENSFCAG00000005848	SET PHOSPHATASE 2A INHIBITOR I2PP2A I 2PP2A TEMPLATE ACTIVATING FACTOR I TAF I	ENSFM00500000270208
ENSFCAG00000005959	"	ENSFM00500000270208
ENSFCAG00000021897	"	ENSFM00500000270208
ENSFCAG00000024431	"	ENSFM00500000270208
ENSFCAG00000031705	"	ENSFM00500000270208
ENSFCAG00000024762	"	ENSFM00500000270208

Dataset S1.8(g). *Felis catus* gene members that underwent rapid gene family expansions along the Felidae lineage.

CAFE Family ID:950		
ENSFCAG00000006215	PIEZO TYPE MECHANOSENSITIVE ION CHANNEL COMPONENT 1 MEMBRANE INDUCED BY BETA AMYLOID TREATMENT MIB FAM38A	ENSFM00250000000782
ENSFCAG00000031105	"	ENSFM00250000000782
ENSFCAG00000026991	"	ENSFM00250000000782
ENSFCAG00000022624	"	ENSFM00250000000782
ENSFCAG00000027894	UNKNOWN	ENSFM00700001403972
ENSFCAG00000029479	"	ENSFM00700001407161

CAFE Family ID:1069		
ENSFCAG00000009998	NUCLEAR RECEPTOR COREPRESSOR 1 N COR N COR1	ENSFM00250000001120
ENSFCAG00000026816	"	ENSFM00250000001120
ENSFCAG00000030219	"	ENSFM00250000001120
ENSFCAG00000025434	"	ENSFM00250000001120
ENSFCAG00000027575	"	ENSFM00250000001120
ENSFCAG00000029502	"	ENSFM00250000001120
ENSFCAG00000031193	"	ENSFM00250000001120

CAFE Family ID:1264		
ENSFCAG00000000945	E3 UBIQUITIN LIGASE RNF213 EC_6.3.2.-	ENSFM00440000236907
ENSFCAG00000024632	"	ENSFM00440000236907
ENSFCAG00000022783	"	ENSFM00440000236907
ENSFCAG00000026190	"	ENSFM00440000236907
ENSFCAG00000022578	"	ENSFM00440000236907
ENSFCAG00000023279	"	ENSFM00440000236907
ENSFCAG00000022915	"	ENSFM00440000236907
ENSFCAG00000024960	UNKNOWN	ENSFM00700001402418

CAFE Family ID:1785		
ENSFCAG00000027649	HERV R_7Q21 2 PROVIRUS ANCESTRAL ENV POLYPROTEIN PRECURSOR ERV 3 ENVELOPE ERV3 ENVELOPE ERV3 1 ENVELOPE ENVELOPE POLYPROTEIN HERV R ENVELOPE ERV R ENVELOPE [CONTAINS SURFACE SU ; TRANSMEMBRANE TM]	ENSFM00250000016078
ENSFCAG00000025816	"	ENSFM00250000016078
ENSFCAG00000027786	"	ENSFM00250000016078
ENSFCAG00000029632	"	ENSFM00250000016078
ENSFCAG00000026669	"	ENSFM00250000016078
ENSFCAG00000031768	"	ENSFM00250000016078

Dataset S1.8(h). *Felis catus* gene members that underwent rapid gene family expansions along the Felidae lineage.

CAFE Family ID:2247		
ENSFCAG00000018707	EYES SHUT HOMOLOG FRAGMENT EPIDERMAL GROWTH FACTOR 10 EGF 10 EPIDERMAL GROWTH FACTOR 11 EGF 11 SPACEMAKER HOMOLOG	ENSFM00570000852066
ENSFCAG00000024318	"	ENSFM00690001356937
ENSFCAG00000022442	"	ENSFM00690001356937
ENSFCAG00000030693	EYES SHUT	ENSFM00570000851871
ENSFCAG00000024482	"	ENSFM00570000851871
ENSFCAG00000030936	UNKNOWN	ENSFM00700001405307

CAFE Family ID:2388		
ENSFCAG00000013038	GLYCINE CLEAVAGE SYSTEM H PROTEIN MITOCHONDRIAL PRECURSOR	ENSFM00500000271167
ENSFCAG00000025063	"	ENSFM00500000271167
ENSFCAG00000024721	UNKNOWN	ENSFM00700001404018

CAFE Family ID:2487		
ENSFCAG00000014455	10 KDA HEAT SHOCK PROTEIN MITOCHONDRIAL HSP10.10 KDA CHAPERONIN CHAPERONIN 10 CPN10	ENSFM00670001235755
ENSFCAG00000028974	"	ENSFM00670001235755
ENSFCAG00000025005	UNKNOWN	ENSFM00700001401236
ENSFCAG00000024093	"	ENSFM00700001401235
ENSFCAG00000023339	"	ENSFM00700001401234

CAFE Family ID:2491		
ENSFCAG00000001973	LEUCINE RICH REPEAT SERINE/THREONINE KINASE 1 EC_2.7.11.1	ENSFM00250000001794
ENSFCAG00000030173	UNKNOWN	ENSFM00700001403499
ENSFCAG00000027327	"	ENSFM00700001401791

CAFE Family ID:2587		
ENSFCAG00000023000	UBIQUITIN CARBOXYL TERMINAL HYDROLASE 40 EC_3.4.19.12 DEUBIQUITINATING ENZYME 40 UBIQUITIN THIOESTERASE 40 UBIQUITIN SPECIFIC PROCESSING PROTEASE 40	ENSFM00250000005400
ENSFCAG00000025764	"	ENSFM00250000005400
ENSFCAG00000028768	"	ENSFM00250000005400

CAFE Family ID:2614		
ENSFCAG00000005785	NONSENSE 2 UP FRAMESHIFT SUPPRESSOR 2	ENSFM00250000002346
ENSFCAG00000030556	"	ENSFM00250000002346
ENSFCAG00000024774	"	ENSFM00250000002346

Dataset S1.8(i). *Felis catus* gene members that underwent rapid gene family expansions along the Felidae lineage.

CAFE Family ID:2825		
ENSFCAG00000023028	SYNAPTONEMAL COMPLEX 1 SCP 1	ENSFM00250000006405
ENSFCAG00000022262	"	ENSFM00250000006405
ENSFCAG00000029189	"	ENSFM00250000006405

CAFE Family ID:2831		
ENSFCAG00000004711	TRANSCRIPTION ELONGATION FACTOR B POLYPEPTIDE 2 ELONGIN 18 KDA SUBUNIT ELONGIN B ELOB RNA POLYMERASE II TRANSCRIPTION FACTOR SIII SUBUNIT B SIII P18	ENSFM00500000273664
ENSFCAG00000029930	"	ENSFM00500000273664
ENSFCAG00000026327	"	ENSFM00500000273664

CAFE Family ID:3042		
ENSFCAG00000026757	COILED COIL DOMAIN CONTAINING 168	ENSFM00570000852061
ENSFCAG00000022657	"	ENSFM00570000852061
ENSFCAG00000023173	UNKNOWN	ENSFM00700001404181

CAFE Family ID:9827		
ENSFCAG00000001617	STELLA FRAGMENT	ENSFM00680001305395
ENSFCAG00000026706	"	ENSFM00680001305395
ENSFCAG00000026149	UNKNOWN	ENSFM00700001402535

Dataset S1.9. Summary of 1-Kbps windows, copy number distribution in control regions and gain/loss cutoffs for the domestic cat (Abyssinian sample)

Sequencing	
Sequencing technology	Illumina
# Reads	1,485,609,004
Coverage	21.8X
1-Kbps windows	
# Total windows	1,122,501
# Control windows	993,102
# Non control windows	129,399
Gain/loss cutoffs	
Mean copy number in control regions	2
StDev copy number in control regions	0.24
(# windows excluded*)	9,932
Gain cutoff	2.71
Loss cutoff	1.29

*1-Kbps windows exceeding the 1% highest copy number value

Dataset S1.10. Summary of duplications and deletions using sample-specific gain/loss cutoffs based on the copy number distribution from the control regions within the domestic cat genome (Abyssinian sample)

Duplications	
# Duplications	85
# Duplications (gaps removed)	1002
# Bps*	9,065,598
% size of autosomes	0.39
# Bps in shared duplications*	4,377,574
% of duplicated bps	48.29

Deletions	
# Deletions	1
# Deletions (gaps removed)	18
# Bps*	54,896
% size of autosomes	<0.01
# Bps in shared deletions*	0
% of deleted bps	0

*All bps are after excluding the size of the gaps (M1 method)

Dataset S1.11(a). Genes underlying regions of segmental duplications in the domestic cat genome

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description
A2	1999024	2024218	ENSFCAG00000026539	ZNF77	zinc finger protein 77
A2	2178186	2233965	ENSFCAG00000026952		
A2	4837081	4840788	ENSFCAG00000022669		
A2	4850030	4850775	ENSFCAG00000027538		
A2	4879236	4926614	ENSFCAG00000005041		
A2	4940497	4947843	ENSFCAG00000024220		
A2	4951852	4957168	ENSFCAG00000024591		
A2	10342173	10343114	ENSFCAG00000027467		
A2	10403957	10404904	ENSFCAG00000024728		
A2	10424192	10425154	ENSFCAG00000026934		
A2	10444212	10445147	ENSFCAG00000028346		
A2	10454027	10454932	ENSFCAG00000026032		
A2	10465336	10466262	ENSFCAG00000030313		
A2	10484879	10486405	ENSFCAG00000030477		
A2	10503936	10505982	ENSFCAG00000022920		
A2	10557343	10558290	ENSFCAG00000031912		
A2	10561828	10562778	ENSFCAG00000029420		
A2	10571496	10572431	ENSFCAG00000030284		
A2	10588491	10589447	ENSFCAG00000027325		
A2	10608719	10609642	ENSFCAG00000029342		
A2	10637607	10639184	ENSFCAG00000025226		
A2	10666812	10667738	ENSFCAG00000026535		
A2	10677429	10678364	ENSFCAG00000027309	OR7C1	olfactory receptor, family 7, subfamily C, member 1
A2	10691698	10693042	ENSFCAG00000024926		
A2	10735731	10736645	ENSFCAG00000025361		
A2	10749819	10750754	ENSFCAG00000028413		
A2	10774323	10775967	ENSFCAG00000026904		
A2	10802221	10803189	ENSFCAG00000030343		
A2	10811748	10813240	ENSFCAG00000031709		
A2	11305320	11311224	ENSFCAG00000025482		
A2	11312522	11362773	ENSFCAG00000008623	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3
A2	11380632	11382628	ENSFCAG00000031558		
A2	11390153	11391070	ENSFCAG00000024776		
A2	11408178	11409176	ENSFCAG00000029860		
A2	11427607	11428557	ENSFCAG00000029127		
A2	11444217	11445483	ENSFCAG00000026640		
A2	11454602	11455552	ENSFCAG00000023347		
A2	11469229	11470179	ENSFCAG00000028009		
A2	11478143	11479132	ENSFCAG00000030787		
A2	55532891	55578035	ENSFCAG00000013910	IQSEC1	IQ motif and Sec7 domain 1
A2	58451403	58575137	ENSFCAG00000001776	ALDH1L1	aldehyde dehydrogenase 1 family, member L1
A2	58512851	58512965	ENSFCAG00000020614	5S_rRNA	5S ribosomal RNA
A2	156323262	156324206	ENSFCAG00000025442		
A2	156336015	156336959	ENSFCAG00000024190		
A2	157059766	157060707	ENSFCAG00000026036		
A2	157078181	157079122	ENSFCAG00000025223		
A2	162660127	162661174	ENSFCAG00000003990	GIMAP2	GTPase, IMAP family member 2
A2	162671690	162672605	ENSFCAG00000031058		
A2	162686216	162686593	ENSFCAG00000027719		
A2	162720551	162752217	ENSFCAG00000011443		
A3	30261827	30272148	ENSFCAG00000025532		
A3	30278131	30288600	ENSFCAG00000030407		
A3	30353317	30361064	ENSFCAG00000001879		
A3	30372145	30383790	ENSFCAG00000031263		
A3	40441218	40441327	ENSFCAG00000024869	5S_rRNA	5S ribosomal RNA
B1	40121	43236	ENSFCAG00000019039		
B1	47201	48493	ENSFCAG00000007120	ZNF781	zinc finger protein 781
B1	36295742	36296780	ENSFCAG00000023307		
B2	328785	331268	ENSFCAG00000003660	OR12D2	olfactory receptor, family 12, subfamily D, member 2
B2	713302	714237	ENSFCAG00000011606		
B2	749421	750359	ENSFCAG00000005124		
B2	837074	838335	ENSFCAG00000025316		
B2	884452	885396	ENSFCAG00000030837		

Dataset S1.11(b). Genes underlying regions of segmental duplications in the domestic cat genome

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description
B2	906325	906436	ENSFCAG00000027033	5S_rRNA	5S ribosomal RNA
B2	916798	917733	ENSFCAG00000023506		
B2	977120	979761	ENSFCAG00000026047		
B2	1060434	1061724	ENSFCAG00000028748		
B2	1085480	1086424	ENSFCAG00000030186		
B2	1104867	1106243	ENSFCAG00000000501	OR2B3	olfactory receptor, family 2, subfamily B, member 3
B2	1129129	1130064	ENSFCAG00000023353		
B2	1140538	1144027	ENSFCAG00000028271		
B2	1230045	1231165	ENSFCAG00000028202		
B2	1243051	1243163	ENSFCAG00000029309	5S_rRNA	5S ribosomal RNA
B2	1257504	1257616	ENSFCAG00000028666	5S_rRNA	5S ribosomal RNA
B2	1277229	1278164	ENSFCAG00000028799		
B2	1343658	1344622	ENSFCAG00000025334		
B2	1353504	1357463	ENSFCAG00000029693		
B2	1459936	1460865	ENSFCAG00000010634	OR2W1	olfactory receptor, family 2, subfamily W, member 1
B2	2299340	2300272	ENSFCAG00000026697		
B2	2322927	2323862	ENSFCAG00000029062		
B2	2332065	2348095	ENSFCAG00000028781		
B2	2364168	2365106	ENSFCAG00000023042		
B2	2374024	2374136	ENSFCAG00000030916	5S_rRNA	5S ribosomal RNA
B2	2398409	2399350	ENSFCAG00000027883		
B2	2437587	2438525	ENSFCAG00000023744		
B2	2529387	2530319	ENSFCAG00000030548		
B2	2539008	2539946	ENSFCAG00000025071		
B2	32597800	32602576	ENSFCAG00000021900		
B2	32667396	32670292	ENSFCAG00000000629	FLA-Z	MHC class I antigen
B2	32703681	32706770	ENSFCAG00000027223		
B2	32774101	32776385	ENSFCAG00000015379		
B2	32835681	32838540	ENSFCAG00000000877		
B2	32870997	32871109	ENSFCAG00000027024	5S_rRNA	5S ribosomal RNA
B2	32907635	32910483	ENSFCAG00000018113		
B2	32945158	32948534	ENSFCAG00000027242	FLA-I	MHC class I antigen precursor
B2	33007185	33013570	ENSFCAG00000022105		
B3	148227485	148229683	ENSFCAG00000025368		
B3	148232277	148232726	ENSFCAG00000028661		
B3	148259497	148259934	ENSFCAG00000025324		
B3	148322272	148322384	ENSFCAG00000031776	5S_rRNA	5S ribosomal RNA
B4	24696117	24799719	ENSFCAG00000014236	ANKRD26	ankyrin repeat domain 26
B4	24819736	24859130	ENSFCAG00000027161	RAB18	RAB18, member RAS oncogene family
B4	46929808	46931537	ENSFCAG00000013935		
B4	46958758	46960567	ENSFCAG00000030370		
D1	4486594	4486706	ENSFCAG00000022937	5S_rRNA	5S ribosomal RNA
D1	4776114	4776224	ENSFCAG00000030025	5S_rRNA	5S ribosomal RNA
D1	4803021	4803133	ENSFCAG00000025220	5S_rRNA	5S ribosomal RNA
D1	20649778	20650728	ENSFCAG00000029628		
D1	21354029	21355006	ENSFCAG00000002614		
D1	21380576	21381508	ENSFCAG00000008131	OR8B12	olfactory receptor, family 8, subfamily B, member 12
D1	64918054	64918998	ENSFCAG00000025048		
D1	64938061	64939629	ENSFCAG00000028751		
D1	66883484	66884427	ENSFCAG00000024203		
D1	66892866	66893789	ENSFCAG00000000727	OR10A3	olfactory receptor, family 10, subfamily A, member 3
D1	66908368	66909313	ENSFCAG00000028608		
D1	87753796	88005871	ENSFCAG00000030334	ELP4	elongator acetyltransferase complex subunit 4
D1	88012047	88025138	ENSFCAG00000007094	PAX6	paired box 6
D1	102240555	102241478	ENSFCAG00000001814		
D1	102283570	102284514	ENSFCAG00000024648		
D1	102337235	102338164	ENSFCAG00000014680	OR4A47	olfactory receptor, family 4, subfamily A, member 47
D1	103550482	103551426	ENSFCAG00000028369		
D1	103568480	103569423	ENSFCAG00000024411		
D1	113601303	113688582	ENSFCAG00000004765	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
D2	129076	129188	ENSFCAG00000029175	5S_rRNA	5S ribosomal RNA
D2	8749213	9075406	ENSFCAG00000029000		
D2	8960580	8980244	ENSFCAG00000023704		
D2	20153518	20206464	ENSFCAG00000023459	TTC13	tetratricopeptide repeat domain 13

Dataset S1.11(c). Genes underlying regions of segmental duplications in the domestic cat genome

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description
D2	22330902	22331016	ENSFCAG00000027550	5S_rRNA	5S ribosomal RNA
D2	22332106	22332224	ENSFCAG00000029290	5S_rRNA	5S ribosomal RNA
D2	22333313	22333421	ENSFCAG00000017601	5S_rRNA	5S ribosomal RNA
D2	22367720	22368642	ENSFCAG00000028109		
D2	22379806	22380681	ENSFCAG00000011440		
D2	89795938	89805869	ENSFCAG00000013762	CYP2E2	cytochrome P450 2E2
D2	89809103	89814632	ENSFCAG00000031109	ZNF717	zinc finger protein 717
D2	89817222	89822044	ENSFCAG00000013763	SYCE1	synaptonemal complex central element protein 1
D3	80759	80867	ENSFCAG00000021705	5S_rRNA	5S ribosomal RNA
D3	23225438	23225981	ENSFCAG00000025218		
D3	23273316	23273795	ENSFCAG00000026724		
D3	23297965	23298282	ENSFCAG00000025197		
D3	23382135	23382440	ENSFCAG00000029689		
D3	23419057	23419488	ENSFCAG00000023616		
D3	23509526	23510019	ENSFCAG00000031794		
D3	26658713	26658825	ENSFCAG00000027766	5S_rRNA	5S ribosomal RNA
D3	26681356	26709785	ENSFCAG00000006400	PIWIL3	piwi-like RNA-mediated gene silencing 3
D3	28148397	28167337	ENSFCAG00000005999	MED15	mediator complex subunit 15
D3	28167822	28174177	ENSFCAG00000030668		
D3	28235497	28244430	ENSFCAG00000006009	P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6
D3	28280102	28284449	ENSFCAG00000022091	TUBA3E	tubulin, alpha 3e
D4	7198	11817	ENSFCAG00000029042		
D4	88592476	88595451	ENSFCAG00000023879		
D4	88654911	88657790	ENSFCAG00000001496		
D4	88692182	88695035	ENSFCAG00000027840		
D4	88712762	88715537	ENSFCAG00000031788		
D4	95006881	95010017	ENSFCAG00000012216		
D4	95011716	95016678	ENSFCAG00000012219		
E1	2184	3160	ENSFCAG00000008583		
E1	42029674	42032124	ENSFCAG00000030823		
E1	56288309	56290286	ENSFCAG00000023215		
E1	56322164	56324255	ENSFCAG00000030685		
E1	56334152	56334460	ENSFCAG00000001618		
E1	56382117	56385015	ENSFCAG00000029475		
E2	4520136	4522367	ENSFCAG00000023824		
E2	4673182	4688006	ENSFCAG00000028391		
E2	4739276	4739981	ENSFCAG00000016263		
E2	4893549	4895709	ENSFCAG00000025435		
E2	4950706	4951646	ENSFCAG00000030225		
E2	4960706	4962448	ENSFCAG00000024112		
E2	5330162	5331094	ENSFCAG00000025619	FELCATV1R6	vomeronasal 1 receptor felCatV1R6
E2	5360235	5361671	ENSFCAG00000023132		
E2	5412456	5420577	ENSFCAG00000023403		
E2	5480972	5529785	ENSFCAG00000023819		
E2	5486927	5492030	ENSFCAG00000029493		
E2	5537527	5537593	ENSFCAG00000017968		
E2	5564448	5571174	ENSFCAG00000031161		
E2	5604920	5606596	ENSFCAG00000025806		
E2	5641792	5645484	ENSFCAG00000023019		
E2	5712974	5714008	ENSFCAG00000028544		
E2	5880689	5881638	ENSFCAG00000025070		
E2	5887792	5888197	ENSFCAG00000028057		
E2	5918068	5919030	ENSFCAG00000022670	FELCATV1R7	vomeronasal 1 receptor felCatV1R7
E2	8497229	8501013	ENSFCAG00000007363		
E2	8513256	8529986	ENSFCAG00000022344	FUT2	fucosyltransferase 2 (secretor status included)
E2	8515155	8527136	ENSFCAG00000027085		
E2	12316795	12325442	ENSFCAG00000029888	CEACAM21	carcinoembryonic antigen-related cell adhesion molecule 21
E2	13122830	13132919	ENSFCAG00000013094	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1
E3	26876172	26876284	ENSFCAG00000029594	5S_rRNA	5S ribosomal RNA
E3	26994957	27039168	ENSFCAG00000008109	ACSM1	acyl-CoA synthetase medium-chain family member 1
E3	32693517	33115346	ENSFCAG00000010119	SNX29	sorting nexin 29

Dataset S1.12. Pathway enrichment results using all genes underlying regions of segmental duplications in the domestic cat genome (Abyssinian sample)

KEGG Pathway	Pathway ID	C	O	E	R	rawP	adjP	Genes
Olfactory transduction	4740	388	7	0.27	25.94	7.7E-09	1.54E-08	**OR4A47, OR7C1, OR8B12, OR10A3, OR12D2, OR2W1, OR2B3**
Metabolic pathways	1100	1130	3	0.79	3.82	0.0431	0.0431	**FUT2, CYP4F3, ACSM1**
Wikipathways Pathway								
GPCRs, Class A Rhodopsin-like	WP455	259	3	0.18	16.65	0.0008	0.0014	**OR7C1, OR2W1, OR2B3**
cytochrome P450	WP43	65	2	0.05	44.23	0.0009	0.0014	**CYP2S1, CYP4F3**
GO Category (Sub-root)								
olfactory receptor activity (molecular function)	GO:0004984	419	7	0.71	9.82	4.64E-06	0.0003	**OR4A47, OR7C1, OR8B12, OR10A3, OR12D2, OR2W1, OR2B3**
guanyl nucleotide binding (molecular function)	GO:0019001	392	4	0.67	6	0.0041	0.023	**RAB18, TUBA3E, ACSM1, GIMAP2**

USER DATA & PARAMETERS - N = 35 genes submitted, Genes mapped to unique Entrez Gene IDs: 33, Organism: hsapiens, Id Type: gene_symbol, Ref Set: entrezgene, Significance Level: .05, Statistics Test: Hypergeometric, MTC: BH, Minimum: 2

COLUMN HEADINGS - number of reference genes in the category (C), number of genes in the gene set and also in the category (O), expected number in the category (E), Ratio of enrichment (R), p value from hypergeometric test (rawP), and p value adjusted by the multiple test adjustment (adjP).