Table S1. Gonad samples of cats used in this study.

| No | Strains | Tissues |
|----|---------|---------|
| 1  | Mongrel | Testes  |
| 2  | Mongrel | Testes  |
| 3  | Mongrel | Testes  |
| 4  | Mongrel | Testes  |
| 5  | Mongrel | Testes  |
| 6  | Mongrel | Testes  |
| 7  | Mongrel | Testes  |
| 8  | Mongrel | Testes  |
| 9  | Mongrel | Testes  |
| 10 | Mongrel | Testes  |
| 11 | Mongrel | Testes  |
| 12 | Mongrel | Ovary   |
| 13 | Mongrel | Testes  |
| 14 | Mongrel | Testes  |
| 15 | Mongrel | Testes  |
| 16 | Mongrel | Testes  |
| 17 | Mongrel | Testes  |
| 18 | Mongrel | Ovary   |
| 19 | Mongrel | Ovary   |
| 20 | Mongrel | Ovary   |
| 21 | Mongrel | Ovary   |
| 22 | Mongrel | Ovary   |
| 23 | Mongrel | Testes  |
| 24 | Mongrel | Ovary   |
| 25 | Mongrel | Ovary   |
| 26 | Mongrel | Ovary   |
| 27 | Mongrel | Ovary   |
| 28 | Mongrel | Testes  |
| 29 | Mongrel | Testes  |

Testes and ovaries of mongrel cats were obtained from local animal hospitals with permissions from the animal owners. Twenty five samples of 29 were used to determine each SNP.
Table S2. Primers used for PCR, sequencing and mutagenesis of CYP1A2 in this study

| No | Primers | Sequences (5' to 3') | Purpose |
|----|----------|-----------------------|---------|
| 1  | CYP1A2 F | CCAGACTCCATAACCCTGCTGATC | Protein expression |
| 2  | CYP1A2 R | GCAATGCTGCTGTCTCTTCACTTGATGG | Protein expression |
| 3  | ompA F   | GGAATTTCCATATGAAAAGACAGATCAGCG | Protein expression |
| 4  | CYP1A2 ompA+2 linker | GGCGGTGGGGGATTATTGGCCTCCGGGCCTGCTACGTAGCGAA | Protein expression |
| 5  | CYP1A2 Express R | TCTAGATCACTTGATGGAGAACCTGGGC | Protein expression |
| 6  | CYP1A2 Seq3 | GATGGGGGAAGAGGACCTCACAG | Sequence |
| 7  | CYP1A2 Seq4 | GAAGAGGAGTCTGGAAGATC | Sequence |
| 8  | CYP1A2 Seq5 | TGTCACAAGCAGGTCATCTCTG | Sequence |
| 9  | CYP1A2 Exon1 F | GACTGAGTGTGAGTGAAGCTTGAAG | PCR, sequence |
| 10 | CYP1A2 Exon1 R | ATCAGCTGCGTGCTACCTTG | PCR, sequence |
| 11 | CYP1A2 Exon2 F | CCCAGCTTACTGCTAGAGG | PCR, sequence |
| 12 | CYP1A2 Exon2 R | GTGGTGGCAAGTTATCTGATGGAC | PCR |
| 13 | CYP1A2 Exon3/4 F | ATGCTGTGTACATGTTGCTTGGTG | PCR, sequence |
| 14 | CYP1A2 Exon3/4 R | CTGTGAGGAAATTTTCGCTGACATGG | PCR, sequence |
| 15 | CYP1A2 Exon5 F | GAGACTATGGAAGCTGCAACAGTATTG | PCR, sequence |
| 16 | CYP1A2 Exon5 R | GACAGAGACCTTCTGAC | PCR |
| 17 | CYP1A2 Exon6 F | ACAGAAGTCTCCCAGCTGTC | PCR, sequence |
| 18 | CYP1A2 Exon6 R | CTTGCGATCTGCTGTTCCTTCAC | PCR |
| 19 | CYP1A2 680 A>C F | TCCTCGGGGAACCCCTGGAC | Mutagenesis |
| 20 | CYP1A2 680 A>C R | CGCATTCCACGAAATATTGCTGCTGTATG | Mutagenesis |
| 21 | CYP1A2 799 C>A F | GAGAATACAGGACTTGGACG | Mutagenesis |
| 22 | CYP1A2 799 C>A R | CTGGAATTTTCTGAGAAGACCTGAC | Mutagenesis |
| 23 | CYP1A2 1229 T>C F | CCAATCGTAGACAAAGGAGTGG | Mutagenesis |
| 24 | CYP1A2 1229 T>C R | CCTGCCACTGTTATGGAAC | Mutagenesis |
| 25 | CYP1A2 1381 A>G F | CGAGTGGGGAGTCTTCTCTCTC | Mutagenesis |
| 26 | CYP1A2 1381 A>G R | GCCAGAACCTCCCCCTATACAC | Mutagenesis |
Supplemental Fig. S1. Genomic structure of feline CYP1A2 and polymorphic variants identified.

Exons and lines are indicated by white boxes and lines, respectively. Blue columns show putative substrate-recognition sites (SRS1-6). Red columns indicate heme-binding region. The scheme is drawn with reference to Ensembl genome browser (Ensembl genome browser (ENSFCAG00000000344, Chromosome B3: 33,511,989 - 33,516,370 reverse strand).
Supplemental Fig. S2. Saturation curve of coumarin hydroxylation activity by feline CYP1A2 variants.

Heterologously-coexpressed feline CYP1A2 variants in bactosomes of *E. coli* were incubated with 7-ethoxyresorufin (8 graded concentrations in 0.078 μM - 5 μM) for 10 min. Enzymatic activity was indicated in pmol/min/pmol P450. N=4. Vertical bars for each point indicate sem.