Supplemental Methods

1.0 Generation of an ERV1/ChemR23 mutant allele by CRISPR/Cas9-mediated genome editing. Benchling software was used to identify Cas9 guide RNAs flanking the coding sequences of the *Cmklr1 (ERV1/ChemR23)* gene. Three guide RNAs at each end of the target sequence were selected for activity testing. The 5′ and the 3′ guide RNAs were designed to target near the 3′ end of ERV1/ChemR23 intron 2 and the 3′ UTR region after the stop codon in ERV1/ChemR23 exon 3 respectively (Suppl. Fig. 2B, 2C). Guide RNAs were cloned into a T7 promoter vector followed by in vitro transcription and spin column purification. A mouse embryonic fibroblast cell line was transfected with guide RNA and Cas9 protein to perform functional testing. The guide RNA target site was amplified from transfected cells and analyzed by T7 Endonuclease 1 assay. Guide RNAs selected for genome editing in embryos were 5sg81T (protospacer sequence 5′-GAGATCGTTCACAACCC-3′) and 3sg81T (protospacer sequence 5′-gCGGCCCAGGGACGCCTA-3′). A donor oligonucleotide of sequence 5′-CATACGAATGCAAAATAAAGACAAGAAATGGCAAAAGGGGAGATCGTTCACAATAA TGGGAGACATGCCGGGAGCCTTTGGGAATGCTCCAATGCCCACTGAATTTTG-3′.
was included to facilitate homologous recombination to produce a deletion event. However, the founder animal did not have the same deletion junction as the donor oligonucleotide, suggesting the oligonucleotide did not participate in the deletion allele resolution in that founder.

C57BL/6J zygotes were electroporated with 1.2 μM Cas9 protein, 94.5 ng/μl each guide RNA and 400 ng/μl donor oligonucleotide and implanted in recipient pseudopregnant females. Resulting pups were screened by PCR for the presence of a

deletion allele. One male founder was identified with a precise deletion between the cut sites of the electroporated guide RNAs. The founder was mated to wild-type C57BL/6J females to establish a colony with the deletion allele. ERV1/ChemR23 animals were detected by PCR with primers Cmklr1-5ScF1 (5′-GGAGCAGGAAACAGAATAGGAC-3′), Cmklr1-3ScF1 (5′-ATCACCTTCTTCCTCTGCTGG-3′) and Cmklr1-3ScR1 (5′-GGTTTGACTGTCATGTTGCCATA-3′). We observe a 580 bp band for the ERV1/ChemR23 deletion allele and a 725 bp band for the ERV1/ChemR23 wild-type allele in this assay.

1.1 Genes mined for SNP analyses. SNPs were mined in the following genes: PTGS2/COX2 (ENSG00000073756), CYP1A1 (ENSG00000140465), CYP1A2 (ENSG00000140505), CYP2E1 (ENSG00000130649), CYP2C8 (ENSG00000138115), CYP2C9 (ENSG00000138109), CYP2C18 (ENSG00000108242), CYP2C19 (ENSG00000165841), CYP2J2 (ENSG00000134716), CYP4F2 (ENSG00000186115), CYP4F3 (ENSG00000186529), CYP4F8 (ENSG00000186526), CYP4F12 (ENSG00000186204), CYP2S1 (ENSG00000167600), CMKLR1/ChemR23 (ENSG00000174600), LTB4R/BLT1 (ENSG00000213903), ALOX12/15 (ENSG00000108839 & ENSG00000161905), ALOX5 (ENSG00000012779), ALOX5AP/FLAP (ENSG00000132965), LTA4H (ENSG00000111144).