Supplementary Table 1

Primers and probes for real-time RT-PCR

Gene target (Accession number)	Forward primer '5 → 3'	Reverse primer '5 → 3'	Probe '5 → 3'
FMO1 (NM010231)	ACATTACCACCGCCAAGTGT	TGCAGTAGCACAAGCCAAAC	TGAACGGAAGAAAAACAAGCATAGCGG
FMO2 (NM018881)	ACTCAGAGCAACGGAAAGGA	CCTGGGAATGACTTGAGTGG	ATGGTTTGCAGCGGCCATCA
FMO3 (NM008030)	AAGACTCCTTTCCAGGACTGAACC	TTCCCTTCCATATTCCTGGTTCCT	AAAGGCAAATGCTTCCACAGCAGGGACT
FMO4 (NM144878)	CCAGTGGGATGTTGTCACAG	AAATGTGGGCTCAGGAATTG	AAGGCAAACGGGACAGGGCA
FMO5 (NM010232)	ATGACCTGCCCAATCGTATC	CCTGGAGCCATCCTCAAATA	AATTCACAGAGACAGCCGCCG
CYP1A1 (NM012540)	GAATGCCAATGTCCAGCTCTCA	TACCAGGTACATGAGGCTCCAA	AGCAGTTGTGATTGTGTCAAACCCAGCTCC

Supplementary Table 2

microRNAs that are predicted to target mouse FMO2 or FMO3 mRNAs

Data are from: http://microrna.sanger.ac.uk. Bold blue font indicates microRNA species or their close structural relatives that are significantly upregulated by TCDD in liver of C57BL/6J mice (Moffat et al. *Toxicol Sci* 99:470-487, 2007).

Mouse FMO3	*Mouse FMO2*
mmu-miR-15b*	mmu-miR-22*
hsa-miR-518d-5p	hsa-miR-548a-3p
hsa-miR-548c-3p	**mmu-miR-203**
mmu-miR-382	hsa-miR-589
mmu-miR-470	mmu-miR-466d-3p
mmu-miR-677	mmu-miR-466b-3-3p
mmu-miR-27a*	mmu-miR-684
mmu-miR-143	hsa-miR-651
mmu-miR-24-1*	mmu-miR-153
mml-miR-189	mmu-miR-590-5p
mmu-miR-203*	
mmu-miR-382	
mmu-miR-488	
hsa-miR-626	
hsa-miR-601	
mmu-miR-509-3p	
hsa-miR-583	
mmu-miR-148a*	
mmu-miR-590-3p	
hsa-miR-581	
mmu-miR-340-5p	
mmu-miR-24-2*	
mmu-miR-431	
mmu-miR-145	
mmu-miR-218-1*	
hsa-miR-583	
mmu-miR-503*	
mmu-miR-370	
mmu-miR-361	
mmu-miR-218-2*	
mmu-miR-27a*	
mmu-miR-654-3p	
mmu-miR-369-5p	
mmu-miR-590-5p	
mmu-miR-137	
hsa-miR-519d	

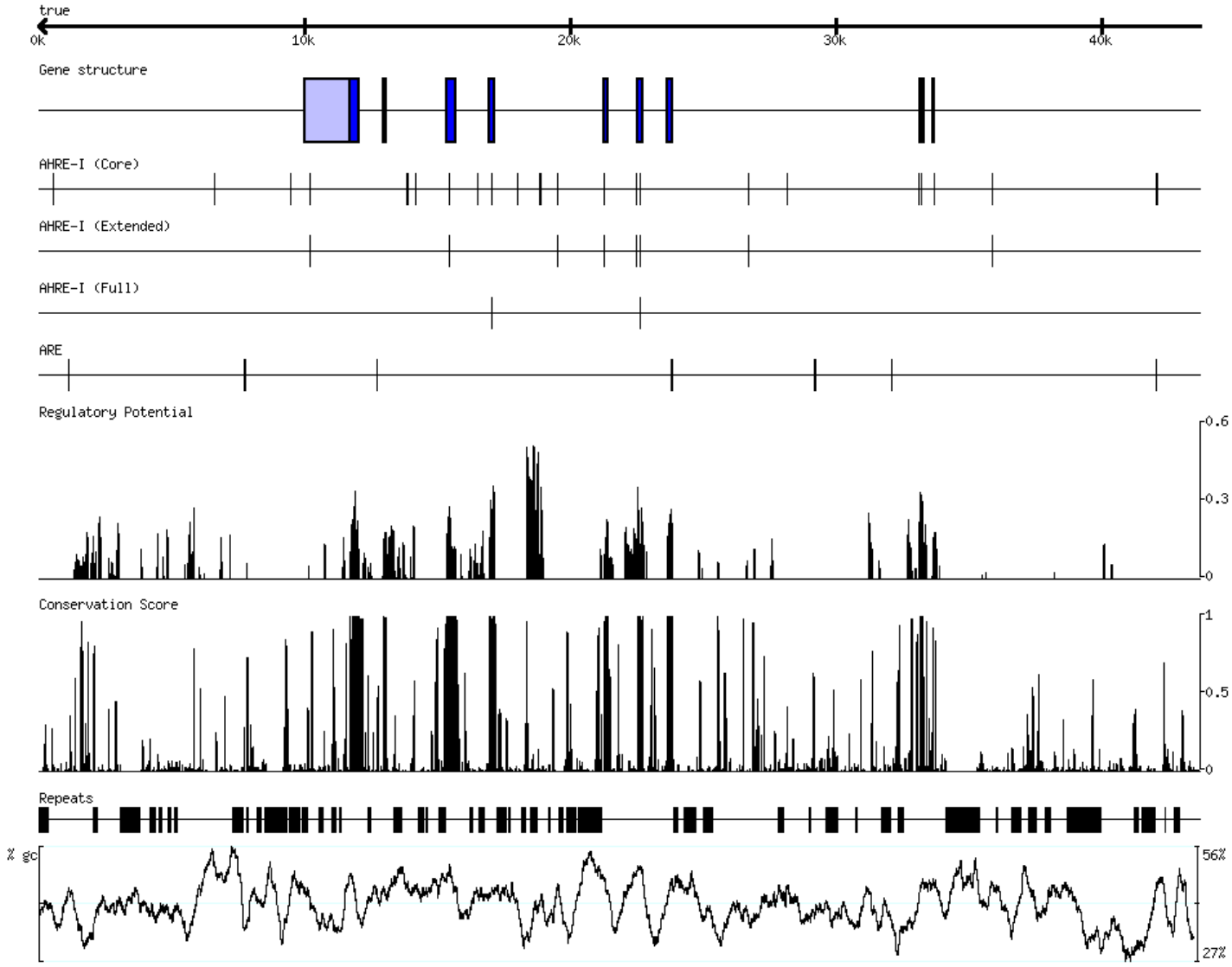
Legend for Supplementary Figures 1 to 4

Sequences for rat and mouse FMO2 and FMO3 genes were downloaded from the UCSC Genome Browser Database (builds rn4 and mm8, respectively). Sequence 10 kbp 3' and 5' to the gene was included for each gene. Also extracted from the same resource were the Regulatory Potential (mouse only) and phyloHMM Conservation scores. The Regulatory Potential indicates the likelihood that any given base plays a regulatory role, while the phyloHMM score gives the posterior probability that a particular base is evolutionarily conserved. In both cases, higher scores indicate higher probabilities. On top of these structures, we also mapped the location of five distinct transcription factor binding motifs: the core, extended, and full AHRE-I motifs; the AHRE-II motif; and the ARE motif. All these motifs and their mappings have been described in detail previously (Boutros et al. *Biochem Biophys Res Comm* 321:707-715, 2004).

Legend for Supplementary Figure 5

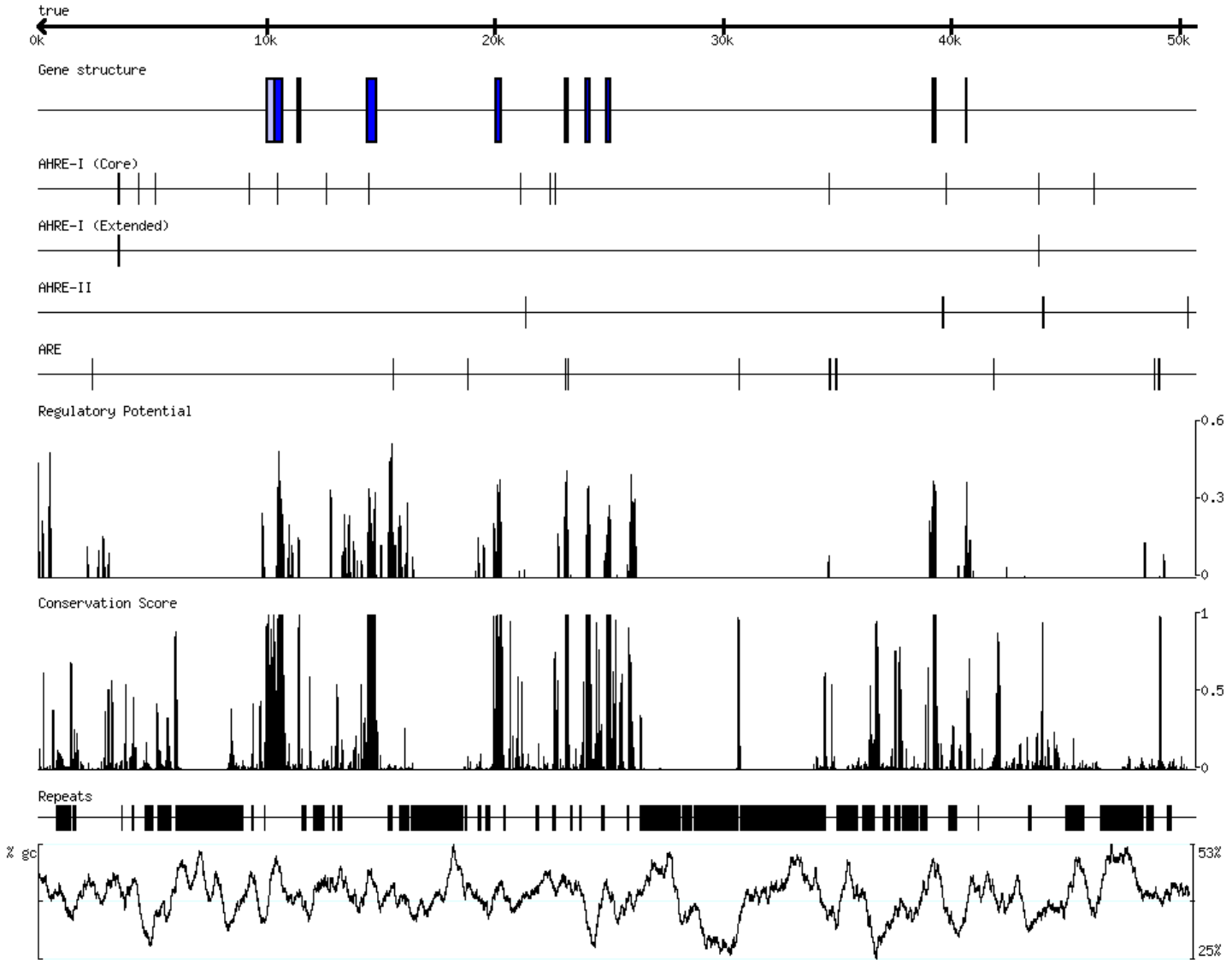
To assess if the region of the FMO3 promoter that bound the AHR in mouse represents a conserved regulatory module we employed a sequence alignment approach. This fragment of the mouse *Fmo3* promoter was extracted from the mouse genome (build mm9). It was then aligned to the rat genome (build rn4) and human genome (build hg18) using the BLAST-Like Alignment Tool (BLAT; Kent, WJ *Genome Research* 12:656-664, 2002), which is specialized for aligning small fragments to genomes. The best-matching alignment for each species was selected. For the human genome this best alignment involved 26 of 78 base-pairs in the mouse region assessed, while for the rat genome it involved 10 of 78 base-pairs. In the human genome the aligned region represents an intron of the OAZ2 gene and in the rat genome it represents a gene-desert.

Mouse – FMO2



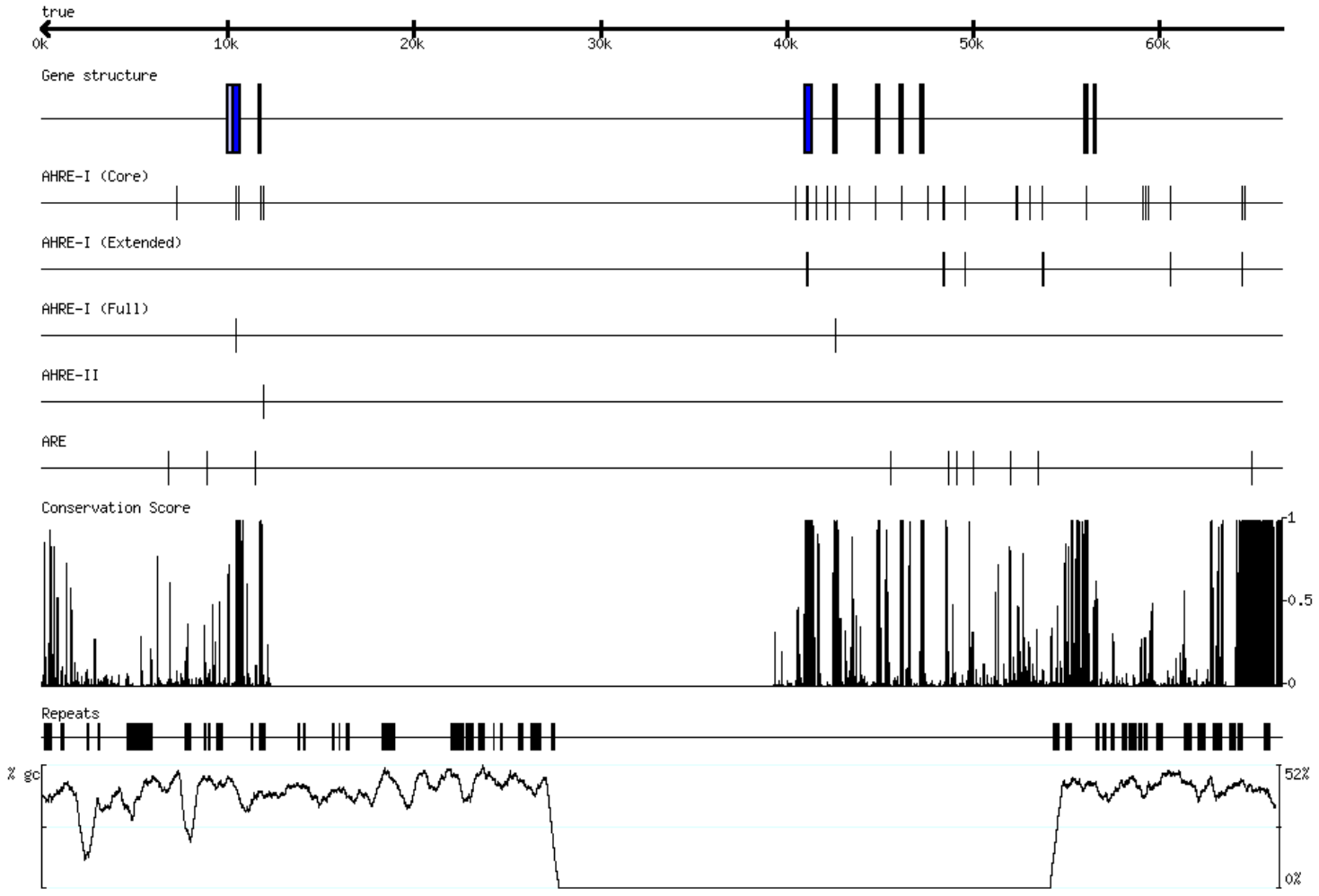
Supp Fig 1

Mouse – FMO3



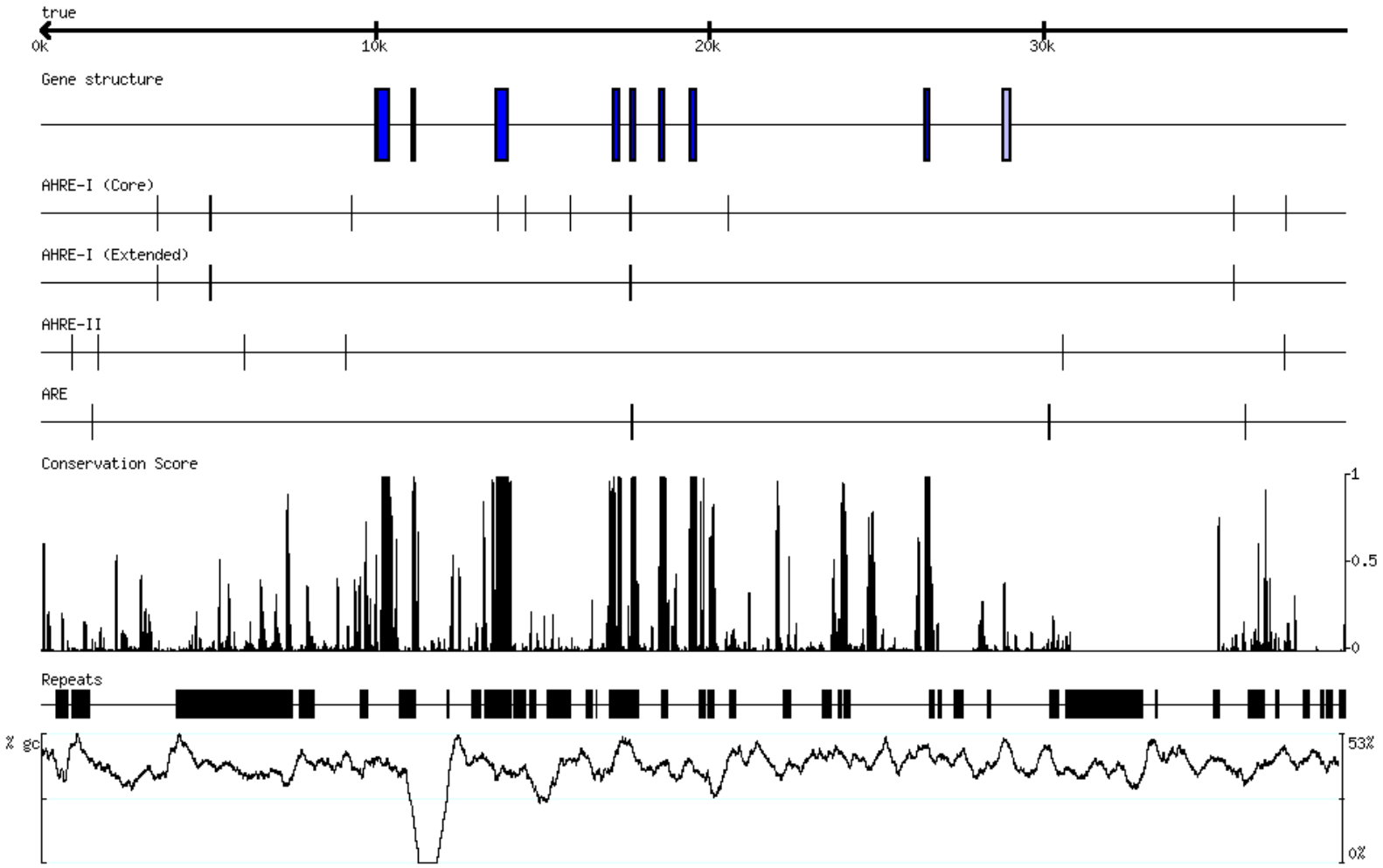
Supp Fig 2

Rat – FMO2



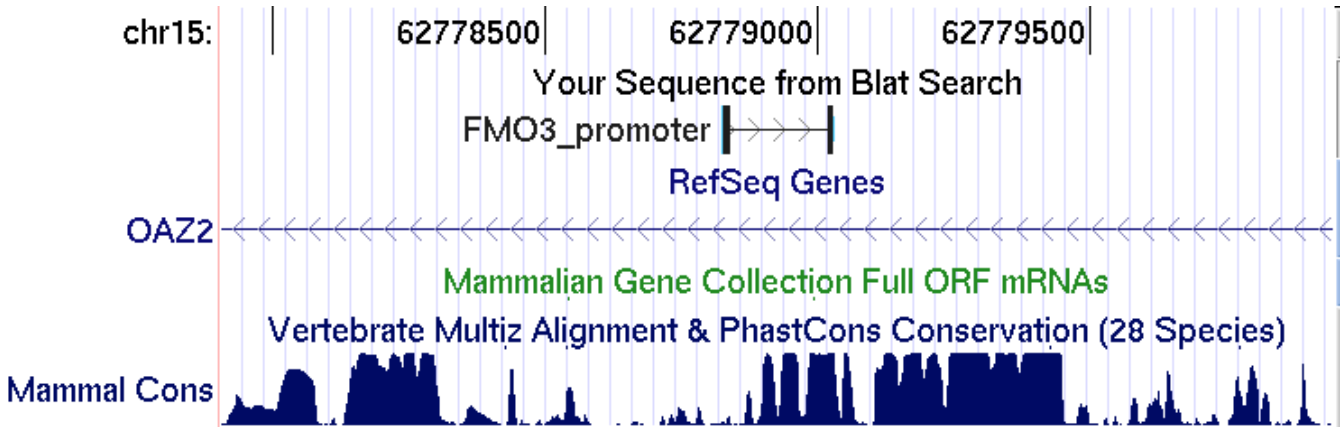
Supp Fig 3

Rat – FMO3

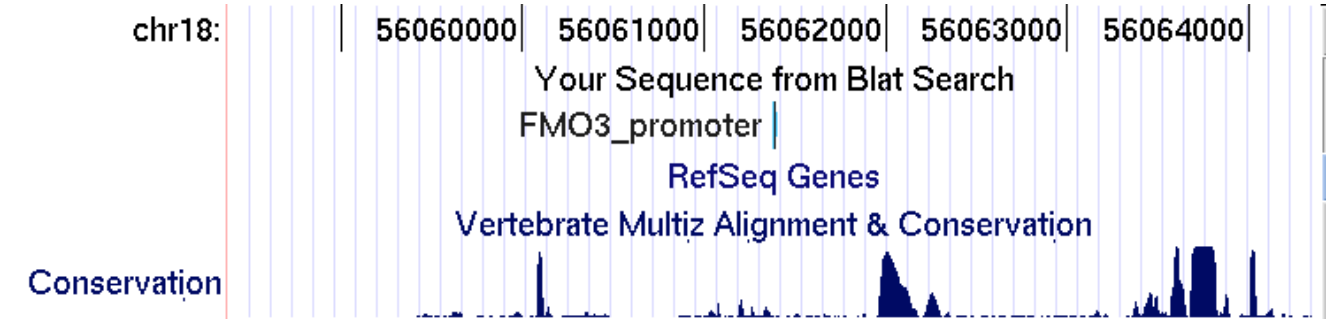


Supp Fig 4

Human
26/78



Rat
20/78



Supp Fig 5