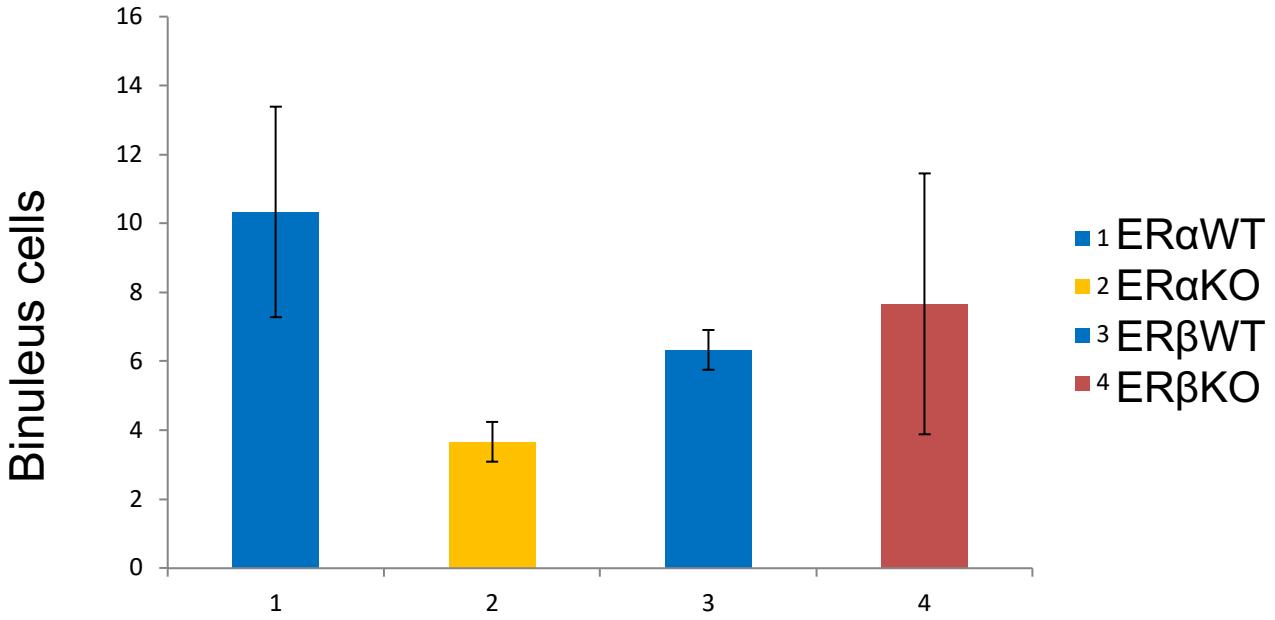
Suppl. Fig. 1, Kao *et al*



Supplemental Figure 1. The binucleated cell number count in regenerating livers (Post 2/3PHx surgery day 4) from WT vs. ERα-KO vs. ERβ-KO.

Supplemental Table 1. Genes and pathway enrichment analysis of ERa with KEGG platform

ERαKO vs Wildtype

KEGG pathway of PHx mice microarray

Term	Link	Count	%	*P* Value	Genes
mmu01040:Biosynthesis of unsaturated fatty acids	Biosynthesis of unsaturated fatty acids	5	0.75	0.003	SCD1, 1600014K23RIK, SCD3, SCD2, ACOT3
mmu04114:Oocyte meiosis	Oocyte meiosis	8	1.20	0.016	CCNB1, ADCY3, CDK1, PLK1, RPS6KA2, BUB1, CDC20, AURKA
mmu04914:Progesterone-mediated oocyte maturation	Progesterone-mediated oocyte maturation	6	0.90	0.045	CCNB1, ADCY3, CDK1, PLK1, RPS6KA2, BUB1
mmu04540:Gap junction	Gap junction	6	0.90	0.047	ADCY3, CDK1, TUBB2A-PS2, TUBB2A, TUBB6, TUBB3
mmu00830:Retinol metabolism	Retinol metabolism	5	0.75	0.071	CYP2C37, CYP26B1, CYP26A1, CYP2B10, CYP2A4
mmu04115:p53 signaling pathway	p53 signaling pathway	5	0.75	0.074	CCNB1, CDK1, CDKN1A, BAI1, GADD45A
mmu04110:Cell cycle	Cell cycle	7	1.05	0.074	CCNB1, CDK1, CDKN1A, PLK1, BUB1, CDC20, GADD45A

Supplemental Table 2. Genes and pathway enrichment analysis of ERbeta with KEGG platform

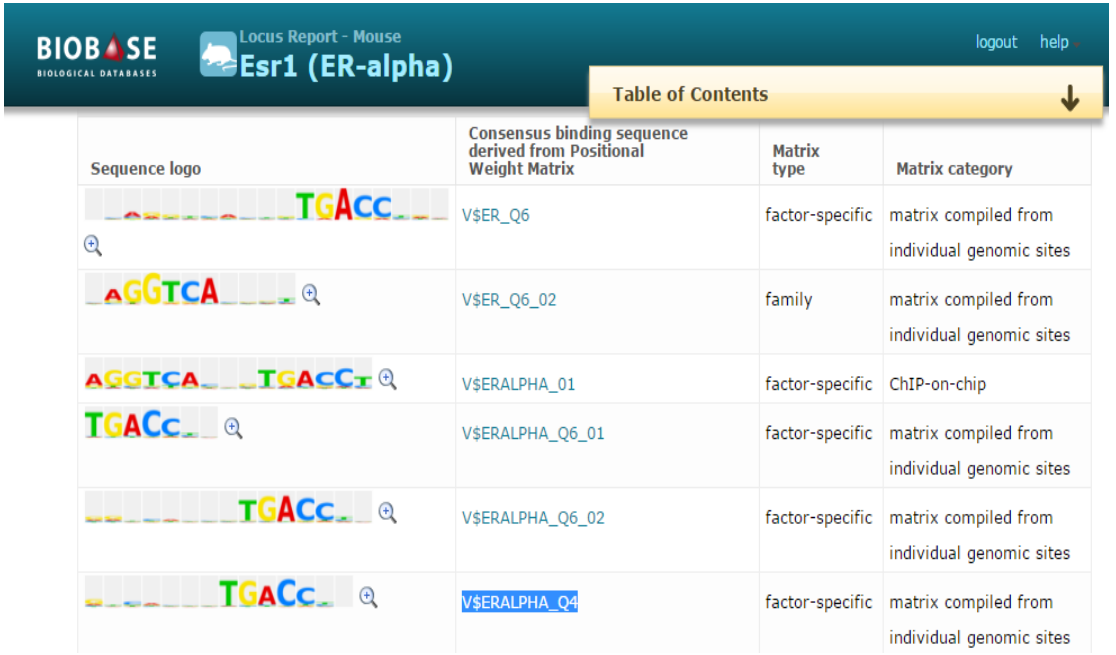
ERβKO vs Wildtype

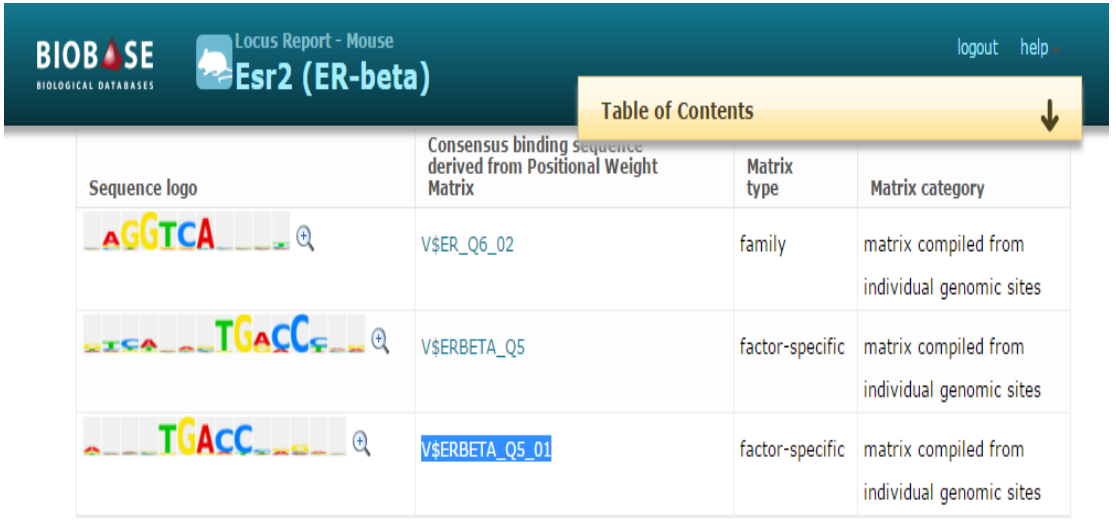
KEGG pathway of PHx mice microarray

Term	Link	Count	%	*P* Value	Genes
mmu00590:Arachidonic acid metabolism	Arachidonic acid metabolism	11	1.95	1.61E-05	CYP2C37, CYP2C54, CYP2B13, GGT1, CYP2C50, CYP4A10, ALOX15, CYP4A32, CYP4A31, CYP2C38, CYP4A14, PLA2G2E, CYP2C39
mmu03320:PPAR signaling pathway	PPAR signaling pathway	9	1.59	3.98E-04	CYP4A10, SCD3, SCD2, CYP4A32, CYP4A31, FABP3, UCP1, CYP4A14, CYP8B1, ADIPOQ, ACSL6
mmu00830:Retinol metabolism	Retinol metabolism	8	1.42	8.38E-04	CYP4A10, CYP2C37, CYP2C54, CYP4A32, CYP4A31, CYP2B13, CYP4A14, CYP2C38, CYP2C39, CYP2C50
mmu00591:Linoleic acid metabolism	Linoleic acid metabolism	6	1.06	3.72E-03	CYP2C37, CYP2C54, PLA2G2E, CYP2C38, CYP2C39, CYP
mmu00980:Metabolism of xenobiotics by cytochrome P450	Metabolism of xenobiotics by cytochrome P450	7	1.24	3.74E-03	CYP2C37, CYP2C54, ALDH1A3, CYP2B13, CYP2C38, CYP2C39, CYP2C50
mmu00982:Drug metabolism	Drug metabolism	7	1.24	7.01E-03	CYP2C37, CYP2C54, ALDH1A3, CYP2B13, CYP2C38, CYP2C39, CYP2C50
mmu04740:Olfactory transduction	Olfactory transduction	34	6.02	8.22E-03	OLFR1370, OLFR315, OLFR611, OLFR805, OLFR823, OLFR690, OLFR1157, OLFR362, OLFR1506, OLFR945, OLFR1032, OLFR575, OLFR384, OLFR533, OLFR676, OLFR843, CAMK2A, OLFR899, OLFR874, OLFR282, OLFR954, OLFR441, OLFR716, GUCY2D, OLFR620, OLFR1145, OLFR665, OLFR608, OLFR584, OLFR644, OLFR1101, OLFR12, OLFR978, OLFR830
mmu05320:Autoimmune thyroid disease	Autoimmune thyroid disease	5	0.88	8.15E-02	IFNAB, CGA, IFNA5, H2-M1, H2-DMB2

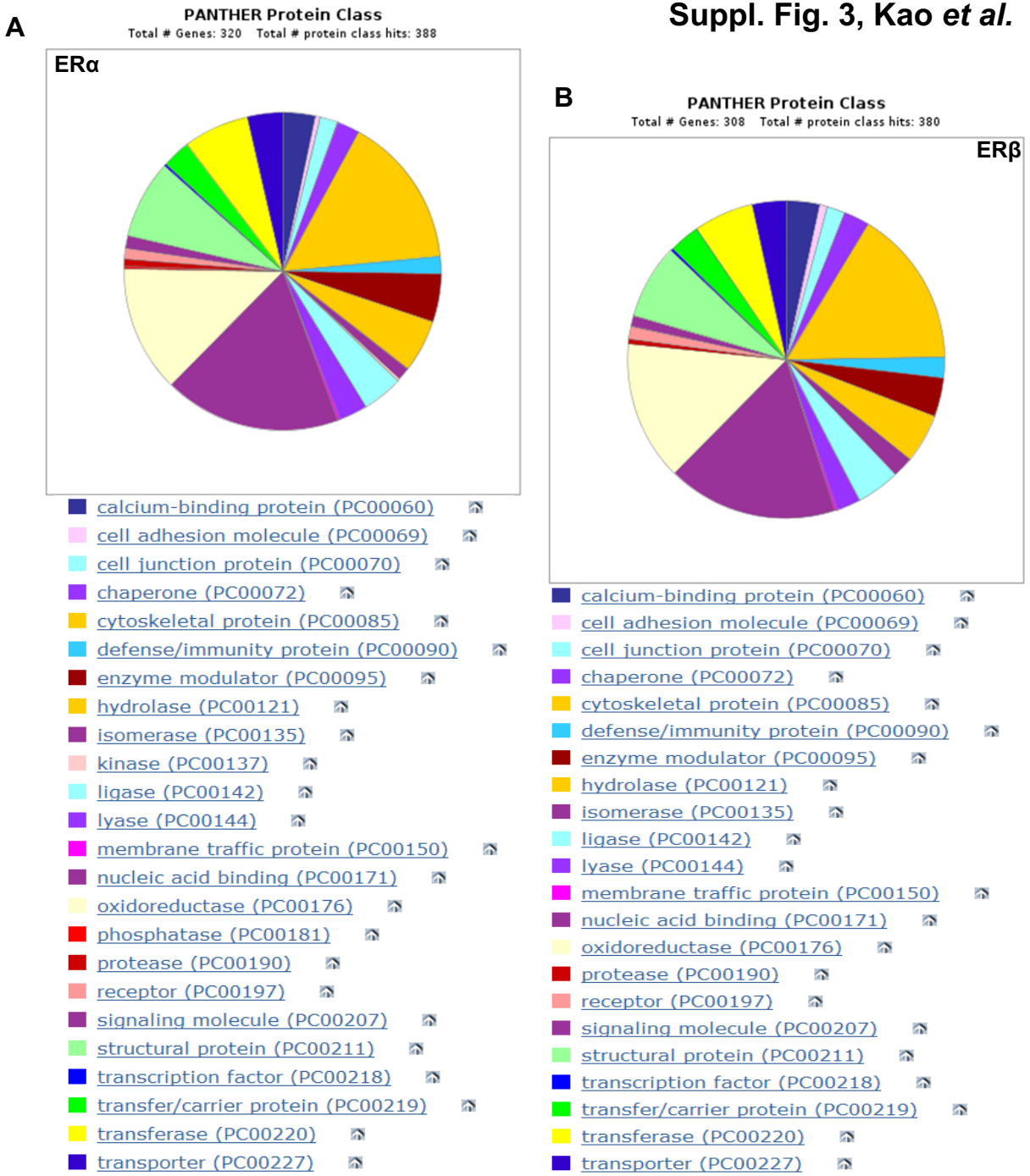
ERα (6 mouse)	
V$ER_Q6	CAGGTCACTGTGACCTGA
V$ER_Q6_02	CAGGTCACGGT
V$ERALPHA_01	AGGTCACAGTGACCT
V$ERALPHA_Q6_01	TGACCTG
V$ERALPHA_Q6_02	GGTCACGTGACCTG
V$ERALPHA_Q4	GTCACCGTGACCT

ERβ (3 mouse)	
V$ER_Q6_02	CAGGTCACGGT
V$ERBETA_Q5	GTCAGAGTGACCCAG
V$ERBETA_Q5_01	ACAGTGACCCGGAA





Supplemental Figure 2. The sequences and scores of ERα-EREs and ERβ-EREs.



Supplemental Figure 3. The ERα- and ERβ-interactome enrichment analysis with the GSEA platform.