Supporting Information

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DNAS



Fig. S1. Biological process GO terms of the 179 common genes.









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Fig. S3. Motif enrichment for the TRANSFAC p53 binding motifs.

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Scale chr12: p53	I 97570000I 97580000I APAF1	50 kb) 975900001 976000001	976100001 976200001 p53	976300001 9	⊣ 76400001 976500	9766000	
Scale chr6: p53	367450001	10 kbl- 36750000l CDI	36755000l		36760000l		
Scale thr12: p53 MDM2	674900001 674950001	675000001 10 kb}	15000l 67510000l		67520000I	675250001	
scale hr10: p53 FAS	907450001	10 kbl 90750000l	90755000l p53	9076	300001	907650001	
3			A DE AVAL MENTEMONY ALL	870 A. C. M. P. L. SYA	er de etable tolar		
	KEGG Pathway				p-value		
	p53 signaling pathway				1.5E-07		
	Type II diabetes mellitus				0.016		
	Vascular smooth muscle contraction Ribosome			ion	0.026		
					0.058		
	Lysosome	_ysosome Pathways in cancer			0.079		
	Pathways in				0.098		

Fig. S4. (A) Example p53 binding sites near well-known targets. (B) KEGG pathway analysis of genes found near binding sites.



Fig. S5. (A) Biological process GO terms for genes found near the p53 cistrome. (B) Distribution of the p53 cistrome throughout the genome.



Fig. S6. Comparison of genes associated with ER and p53 binding sites. The red and blue circles represent the number of commonly regulated genes that are found within 100 kB of an ER and p53 binding site, respectively. The purple overlap demonstrates the 36 genes that are regulated by both transcription factors.

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Fig. S7. GO term analysis of the 36 overlapping genes.

Table S1. p53 cistrome

Table S1

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Table S2. SeqPos analysis of the p53 cistrome

Table S2