Integrative Genomic Analysis Reveals Widespread Enhancer Regulation by p53 in Response to DNA Damage

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Supplementary Information

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Supplementary Table 1. Summary of differential gene expression in human and mouse primary fibroblasts in response to doxorubicin treatment.

Supplementary Table 2. PCR Primers and PCR conditions.

Supplementary File 1. Summary of the p53-regulated transcriptome: gene names, genomic coordinates, expression values, fold changes, and corresponding p53 binding sites for p53-regulated transcripts (mRNAs and lincRNAs) in human and mouse primary fibroblasts in response to doxorubicin treatment.

Supplementary File 2. Summary of guilt-by-association predictions for p53-regulated lincRNA functions: gene set enrichment analysis (GSEA) output.

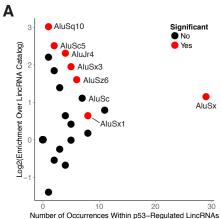
Supplementary File 3. Summary of p53 binding sites within annotated chromatin states: coordinates of p53 binding sites and corresponding chromatin state annotations.

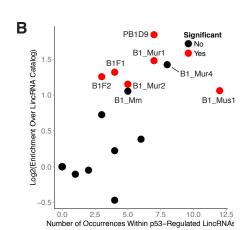
Supplementary Figure 1. Comparison of p53 binding sites across multiple cell types and treatments. (A-C) Comparison of p53 binding sites characterized in this study with sites identified in previous studies using various forms of p53 activation in (A) MCF7, (B) lymphoblastoid, and (C) U2OS cells. (D) Comparison of p53 binding sites in doxorubicin treated human fetal fibroblasts (this study), lymphoblastoid cells, and U2OS cells.

Supplementary Figure 2. Enrichment analysis of Alu/B1 family elements within lincRNAs regulated by p53 relative to reference lincRNA catalogs in (**A**) primary human fibroblasts (Alu) and (**B**) primary mouse embryonic fibroblasts (B1).

Supplementary Figure 1 A Younger et al. Nikulenkov et al. Cell Death Differ. 2012 Dec;19(12):1992-2002. Doxorubicin (hFetal Fibro.): 2,638 Doxorubicin (hFetal Fibro.): 2,638 Doxorubicin (hFetal Fibro.): 2,638 Nutlin (MCF7) : 17,958 5FU (MCF7) : 11,320 RITA (MCF7) : 11,477 Overlap : 1.652 Overlap : 1.366 Overlap: 1,707 **B** • Younger et al. Zeron-Medina et al. Cell. 2013 Oct 10;155(2):410-22. Doxorubicin (hFetal Fibro.): 2,638 Doxorubicin (hFetal Fibro.): 2,638 Doxorubicin (hFetal Fibro.): 2,638 Nutlin (Lymphoblastoid): 1,183 Doxorubicin (Lymphoblastoid): 13,055 IR (Lymphoblastoid): 237 Overlap: 351 Overlap : 1,668 Overlap : 161 Younger et al. Menendez et al. Nucleic Acids Res. 2013 Aug;41(15):7286-301. Doxorubicin (hFetal Fibro.): 2,638 Doxorubicin (hFetal Fibro.): 2,638 Nutlin (U2OS) : 18,156 Doxorubicin (U2OS): 3,087 Overlap : 2,226 Overlap: 1,555 All Doxorubicin Samples (Diagram Not Scaled) D - 660 423 Doxorubicin (hFetal Fibro.): 2,638 - 1.245 Doxorubicin (Lymphoblastoid): 13,055 Doxorubicin (U2OS): 3,087 310 454

Supplementary Figure 2





Supplementary Table 1. Summary of differential gene expression in response to doxorubicin treatment.

| | | Human | | Mouse | |
|----------------|-------------|------------|----------|------------|----------|
| | | mRNA | lincRNA | mRNA | lincRNA |
| Up-regulated | Total | 1365 | 101 | 3124 | 94 |
| | p53 Targets | 262 (19%) | 22 (22%) | 585 (19%) | 21 (22%) |
| Down-regulated | Total | 1598 | 32 | 3334 | 99 |
| | p53 Targets | 106 (6.6%) | 1 (3.1%) | 175 (5.2%) | 4 (4%) |

Supplementary Table 2. PCR Primers and PCR conditions.

| Target | Direction | Use | Sequence |
|----------------------|-----------|-----------|------------------------|
| LincRNA-7 | Forward | RT-qPCR | TGCTGCATTTACAGGTGAGG |
| LincRNA-7 | Reverse | RT-qPCR | AGGATGGCAGGTACATGAGG |
| LincRNA-4 | Forward | RT-qPCR | GGAGCCTAGCATCACTCGTC |
| LincRNA-4 | Reverse | RT-qPCR | CTCCTCTCCAGCAGTTTGG |
| LincRNA-1 | Forward | RT-qPCR | AAGCCAAGCTTCCTGTTTCA |
| LincRNA-1 | Reverse | RT-qPCR | GGGTCTAGGGGATGGGAATA |
| LincRNA-7 Promoter | Forward | ChIP-qPCR | GCACGGACTGAGAAACACAA |
| LincRNA-7 Promoter | Reverse | ChIP-qPCR | GGGGCATTTGGAGATTTTG |
| LincRNA-4 Promoter | Forward | ChIP-qPCR | ACTTACCATGGGCAGTCAGC |
| LincRNA-4 Promoter | Reverse | ChIP-qPCR | GGGTGGTGGTCACTAAA |
| LincRNA-1 Promoter | Forward | ChIP-qPCR | AGTGGACTGGAGCCTGACAT |
| LincRNA-1 Promoter | Reverse | ChIP-qPCR | AGCACCACCTCACACATTGA |
| Enhancer Region-1 | Forward | ChIP-qPCR | CCACAGGCTGCACAAGATAA |
| Enhancer Region-1 | Reverse | ChIP-qPCR | TCTGAAAGTGATGCTGTGGAA |
| Enhancer Region-2 | Forward | ChIP-qPCR | GCCAGGCAATTTTGTTGATT |
| Enhancer Region-2 | Reverse | ChIP-qPCR | TAGCCTGCTGGATGATGAAA |
| Unannotated Region-1 | Forward | ChIP-qPCR | AGGCAGTGGAGAGAA |
| Unannotated Region-1 | Reverse | ChIP-qPCR | GACCCTTGCAACCTGCTTAG |
| GAPDH Promoter | Forward | ChIP-qPCR | TACTAGCGGTTTTACGGGCG |
| GAPDH Promoter | Reverse | ChIP-qPCR | TCGAACAGGAGGAGCAGAGCGA |

| PCR Conditions | Denature | Annealing | Extension | Cycles |
|----------------|------------|------------|------------|--------|
| RT-qPCR | 95°C, 20 s | 57°C, 30 s | 72°C, 45 s | x40 |
| ChIP-qPCR | 95°C, 20 s | 57°C, 30 s | 72°C, 45 s | x40 |