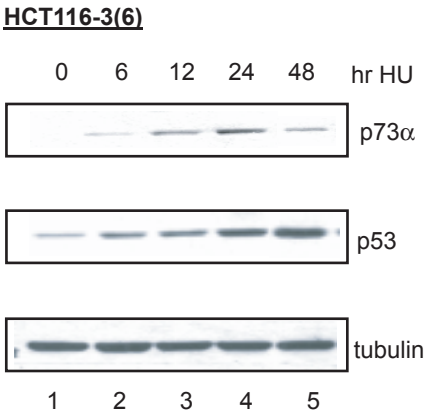
**Figure S1**

**A**

| HCT116-3(6) | p53 | p63 | p73 |
|---|---|---|---|
| β-actin normalized CT value | 20.23 ±0.005 | 30.33 ±0.66 | 28.18 ±0.11 |

**B**




**C**

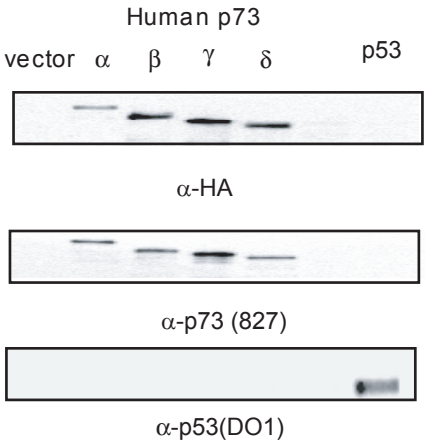
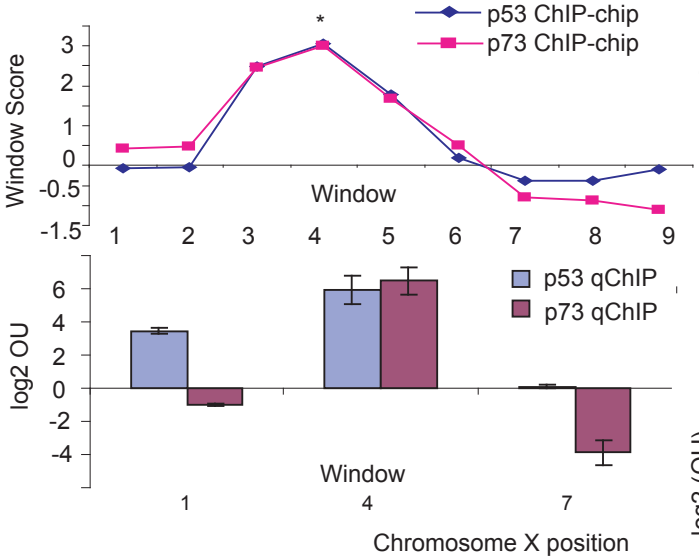



**Figure S1 - Confirmation of antibody specificity used in this study.**
**(a)** Relative expression of p53, p63, and p73 in HCT-116(3) cells. mRNA level was determined by real-time polymerase chain reaction shown as β-actin normalized Ct values. Error represents standard deviation from three biological samples. **(b)** Time-course of p53 and p73 induction by hydroxyurea. HCT116-3(6) cells were treated with 1 mM hydroxyurea at the indicated times. Endogenous levels of p53 and p73 were detected by immunoblotting as described in Figure 1(a). **(c)** Validation of p53 and p73 antibodies used in this study. Extracts of 293T cells transfected with empty vector, HA-tagged p53, or HA-tagged p73 α/β/χ/δ were subjected to SDS-PAGE followed by immunoblotting with the indicated antibodies.

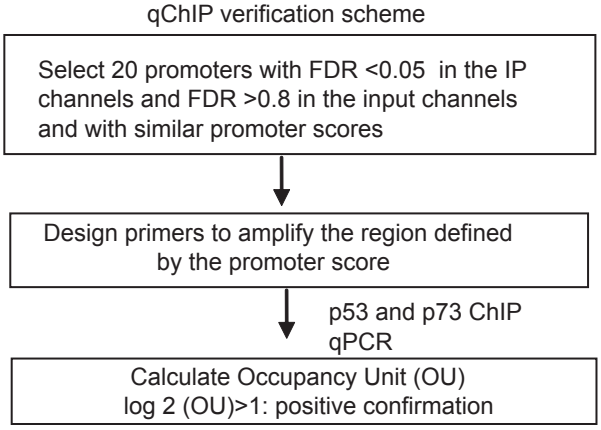
**Figure S2**

**A**

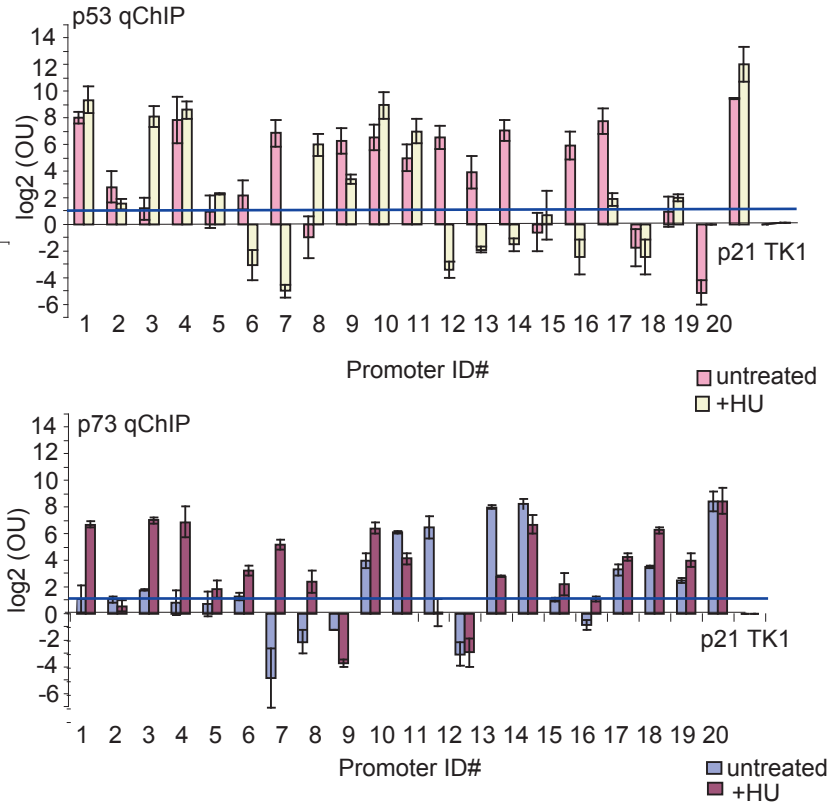



1: 77389053-77389233 (180 nt, p=3)
2: 77389403-77389603 (200 nt, p=3)
3: 77389603-77389823 (220 nt, p=3)
4: 77389753-77389883 (130 nt, p=3)
5: 77389823-77390053 (230 nt, p=3)
6: 77389883-77390103 (220 nt, p=3)
7: 77390053-77390273 (220 nt, p=4)
8: 77390103-77390333 (230 nt, p=4)
9: 77390273-77390483 (210 nt, p=3)

**B**




**C**




**D**

p53 -HU

| MAP Computed FDR | Promoter Score Range | # false/# assayed | qChIP FDR | # promoters in bin |
|---|---|---|---|---|
| 0-0.005 | 1.22-2.15 | 2/12 | 0.17 | **201** |
| 0.005-0.01 | 1.11-1.14 | 1/3 | 0.33 | 65 |
| 0.01-0.05 | 0.96-0.99 | 3/5 | 0.60 | 183 |

p53 +HU

| MAP Computed FDR | Promoter Score Range | # false/# assayed | qChIP FDR | # promoters in bin |
|---|---|---|---|---|
| 0-0.005 | 1.14-2.03 | 6/16 | 0.37 | **216** |
| 0.01-0.05 | 0.98-1.01 | 2/4 | 0.50 | 173 |

p73 -HU

| MAP Computed FDR | Promoter Score Range | # false/# assayed | qChIP FDR | # promoters in bin |
|---|---|---|---|---|
| 0-0.005 | 1.08-2.41 | 7/19 | 0.37 | **360** |

p73 +HU

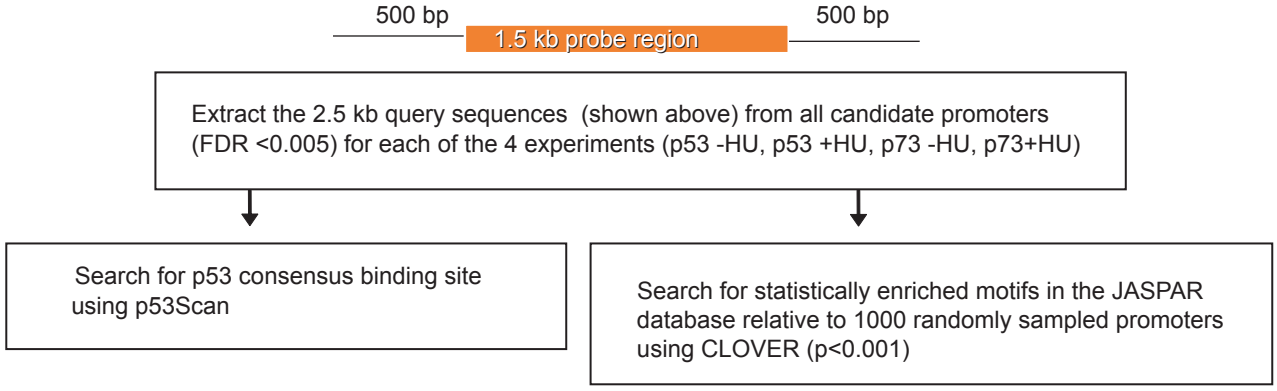
| MAP Computed FDR | Promoter Score Range | # false/# assayed | qChIP FDR | # promoters in bin |
|---|---|---|---|---|
| 0-0.005 | 0.89-2.13 | 4/19 | 0.21 | **526** |

**Figure S2. Verification of model-based algorithm for promoter array window and promoter-scores.**

**(a)** Window score verification. Quantitative chromatin immunoprecipitation (qChIP) scanning of p53 and p73 across a representative promoter region. Window scores across the indicated chromosome regions (top) and the enrichment of selected chromosome regions determined by qChIP (bottom) in a logarithmic-scale (log2) are shown. *denotes genomic region that contains a non-canonical p53 consensus sequence: GGGCTTGCTg (spacer = 32)AGGCAAGTgT (capital letters represent perfect match to the consensus sequence), p = number of probes. **(b)** Verification strategy. **(c)** Promoter-score verification. Summary of p53 and p73 qChIP verification of the 20 selected promoters in the untreated hydroxyurea (-HU) or hydroxyurea-treated (+HU) experiments. Two independent ChIPs were performed for the –HU or +HU condition using the indicated antibodies. Input and ChIP DNA were amplified by ligation-mediated polymerase chain reaction. Enrichment was expressed in terms of log2 occupancy unit (OU). p21cip1 and TK1 were used as controls for the calculation. Data are represented as mean of the log2 OU from two independent ChIPs +/- standard error of the mean. Log2 (OU) > 1 is considered as a positive confirmation (indicated by the blue line). **(d)** Summary table of model-based algorithm for promoter array analysis, qChIP verification, and false discovery rate determination.

**Figure S3**

**A.**




**B.**

| p<0.001 | | | Experiment | | | | |
|---|---|---|---|---|---|---|---|
| JASPAR Motif ID | Motif name | Motif type | Motif Logo | p53 -HU | p53+HU | p73 -HU | p73 +HU |
| MA0010 | Broad-complex_1 | C2H2 ZN-FINGER | | | | | X |
| MA0013 | Broad-complex_4 | C2H2 ZN-FINGER | | X | X | X | X |
| MA0039 | Gklf | C2H2 ZN-FINGER | | | | X | |
| MA0041 | HFH-2 | FORKHEAD | | | | X | X |
| MA0045 | HMG-IY | HMG | | | | X | X |
| MA0049 | Hunchback | C2H2 ZN-FINGER | | X | X | X | X |
| MA0055 | Myf | bHLH | | | X | X | X |
| MA0056 | MZF_1-4 | C2H2 ZN-FINGER | | X | X | X | X |
| MA0068 | Pax-4 | PAIRED-HOMEO | | | | X | X |
| MA0073 | RREB-1 | C2H2 ZN-FINGER | | X | X | X | |
| MA0079 | SP1 | C2H2 ZN-FINGER | | X | X | X | X |
| MA0082 | SQUA | MADS | | X | | X | X |
| MA0086 | Snail | C2H2 ZN-FINGER | | X | X | X | X |

**Figure S3. Motif analysis.**

**(a)** Outline of motif search for the p53- and p73-bound promoters. **(b)** Over-represented JASPAR motifs in p53 and p73-bound promoters. The sequence logo of the JASPAR motif represents the frequency of occurrence in the binding-site matrix. A motif that is over-represented with $P < 0.001$ in the experimental set is marked by X. *P* values are calculated to indicate the degree of over-representation of each PSSM in target versus background sequences randomly selected from 1000 human promoters. Motifs found in all four experiments are highlighted in yellow.