Supplementary Table 2. The distribution of p 73 binding sites in ME180 cells relative to p63 and well-characterized genes ${ }^{\mathrm{a}, \mathrm{b}}$

| TFBS ${ }^{\text {c }}$ | $\mathrm{P} \leq 10^{-3} \mathrm{~d}$ | $\mathrm{P} \leq 10^{-4}$ d | $\mathrm{P} \leq 10^{-5} \mathrm{~d}$ | $\begin{gathered} \text { Max } \\ \text { (rand) } \end{gathered}$ | $\begin{gathered} \text { Min } \\ (\text { rand })^{\mathrm{f}} \end{gathered}$ |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Total | 2758 | 986 | 488 | N/A | N/A |
| overlap with p63 | $\begin{gathered} 1068 \\ (38.7 \%) \end{gathered}$ | $\begin{gathered} 615 \\ (62.4 \%) \\ \hline \end{gathered}$ | $\begin{gathered} 385 \\ (78.9 \%) \end{gathered}$ | N/A | N/A |
| gene vicinity | $\begin{gathered} 1905 \\ (69.1 \%) \\ \hline \end{gathered}$ | $\begin{gathered} 637 \\ (64.6 \%) \\ \hline \end{gathered}$ | $\begin{gathered} 308 \\ (63.1 \%) \\ \hline \end{gathered}$ | 42.6\% | 38.2\% |
| up5K | $\begin{gathered} 612 \\ (32.1 \%) \end{gathered}$ | $\begin{gathered} 173 \\ (27.2 \%) \end{gathered}$ | $\begin{gathered} 69 \\ (22.4 \%) \end{gathered}$ | 13.7\% | 9.3\% |
| up1K | $\begin{gathered} 406 \\ (21.3 \%) \\ \hline \end{gathered}$ | $\begin{gathered} 88 \\ (13.8 \%) \\ \hline \end{gathered}$ | $\begin{gathered} 26 \\ (8.4 \%) \\ \hline \end{gathered}$ | 3.6\% | 1.7\% |
| all introns | $\begin{gathered} 1091 \\ (57.3 \%) \end{gathered}$ | $\begin{gathered} 426 \\ (66.9 \%) \end{gathered}$ | $\begin{gathered} 230 \\ (74.7 \%) \end{gathered}$ | 90.1\% | 86.3\% |
| intron 1 | $\begin{gathered} 613 \\ (32.2 \%) \end{gathered}$ | $\begin{gathered} 220 \\ (34.5 \%) \end{gathered}$ | $\begin{gathered} 107 \\ (34.7 \%) \end{gathered}$ | 30.1\% | 24.3\% |
| intron 2 | $\begin{gathered} 197 \\ (10.3 \%) \end{gathered}$ | $\begin{gathered} 80 \\ (12.6 \%) \end{gathered}$ | $\begin{gathered} 45 \\ (14.6 \%) \end{gathered}$ | 21.0\% | 15.9\% |
| intron 3 | $\begin{gathered} 129 \\ (6.8 \%) \end{gathered}$ | $\begin{gathered} 57 \\ (8.9 \%) \end{gathered}$ | $\begin{gathered} 33 \\ (10.7 \%) \end{gathered}$ | 15.8\% | 11.3\% |
| all exons | $\begin{gathered} 542 \\ (28.5 \%) \\ \hline \end{gathered}$ | $\begin{gathered} 133 \\ (20.9 \%) \\ \hline \end{gathered}$ | $\begin{gathered} 45 \\ (14.6 \%) \\ \hline \end{gathered}$ | 7.5\% | 4.0\% |
| exon 1 | $\begin{gathered} 365 \\ (19.2 \%) \end{gathered}$ | $\begin{gathered} 72 \\ (11.3 \%) \end{gathered}$ | $\begin{gathered} 15 \\ (4.9 \%) \end{gathered}$ | 2.1\% | 0.7\% |
| exon 2 | $\begin{gathered} 79 \\ (4.1 \%) \end{gathered}$ | $\begin{gathered} 23 \\ (3.6 \%) \end{gathered}$ | $\begin{gathered} 11 \\ (3.6 \%) \end{gathered}$ | 1.4\% | 0.3\% |
| exon 3 | $\begin{gathered} 29 \\ (1.5 \%) \end{gathered}$ | $\begin{gathered} 8 \\ (1.3 \%) \end{gathered}$ | $\begin{gathered} 5 \\ (1.6 \%) \end{gathered}$ | 1.2\% | 0.1\% |
| 5' UTR | $\begin{gathered} 171 \\ (9.0 \%) \\ \hline \end{gathered}$ | $\begin{gathered} 34 \\ (5.3 \%) \\ \hline \end{gathered}$ | $\begin{gathered} 5 \\ (1.6 \%) \end{gathered}$ | 1.4\% | 0.2\% |

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[^0]:    ${ }^{a}$ Gene structure information was taken from UCSC knownGene and RefSea annotations.
    ${ }^{\mathrm{b}}{ }^{\text {a }}$ Gene structure information was taken from UCSC knownGene and RefSeq annotations.
    c b distance calculations and gene associations are relative to the midpoint of p73 binding sites
    d c TFBS = transcription factor binding site
    ${ }^{e} \quad{ }^{d} P$-value threshold used in binding site generation.
    ${ }^{\dagger}{ }^{e}$ maximum percentage from 1000 random runs; data from Yang et al, 2006 (ref 24);N/A = not applicable ${ }^{\dagger}$ minimum percentage from 1000 random runs; data from Yang et al, 2006 (ref 24);N/A = not applicable

