Supplementary table 1. A complete list of all the RP and EIF genes used in the analysis. The numbers of REs detected by p53famtag tool (Sbisà 2007 [18]) in the promoter or intron region of query genes are listed. p53 ChIP-seq data of corresponding genes was obtained from another study by Nikulenkov 2015 [22], where the enrichment of p53 on the chromatin was calculated by comparing it with control IgG binding. Here the p-value <0.05 is indicated by a “*”, <0.01 is indicated by a “**”, <0.001 is indicated by a “***” and a very high significance p-value is indicated by p-value written next to “****”, while the p-value > 0.05 is indicated by a “X” (Nikulenkov 2015 [22]). Microarray data was obtained from Sbisà 2007 [18] and it is listed in the table, where “+” indicates upregulation and “−” indicates downregulation. For convenience while identifying the pattern, all the genes with microarray data in the table are highlighted by colors (blue indicates downregulation, orange indicates upregulation and yellow indicates the few outliers, which have a mix of up and downregulation). All the genes were screened for REs using another tool, known as p53 retriever (Tebaldi 2015 [21]), where it was found that most of the genes, both RP and EIF, had REs of grade 2 or higher. Grade 2 indicates poor p53 binding, grade 3 indicates low p53 binding and grade 4 indicates moderate p53 binding. The grade 1 REs, which are considered as highly unlikely p53 binding targets were not considered for listing in the table, except in case of genes that have a valid p53 ChIP-seq data but do not have a grade 2 or higher REs. The RPS17 and RPS17L in red are likely to be the same gene according to the gene listing in NCBI, because of which their data have been considered in sync as belonging to RPS17 for analysis.
### Supplementary table 1

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