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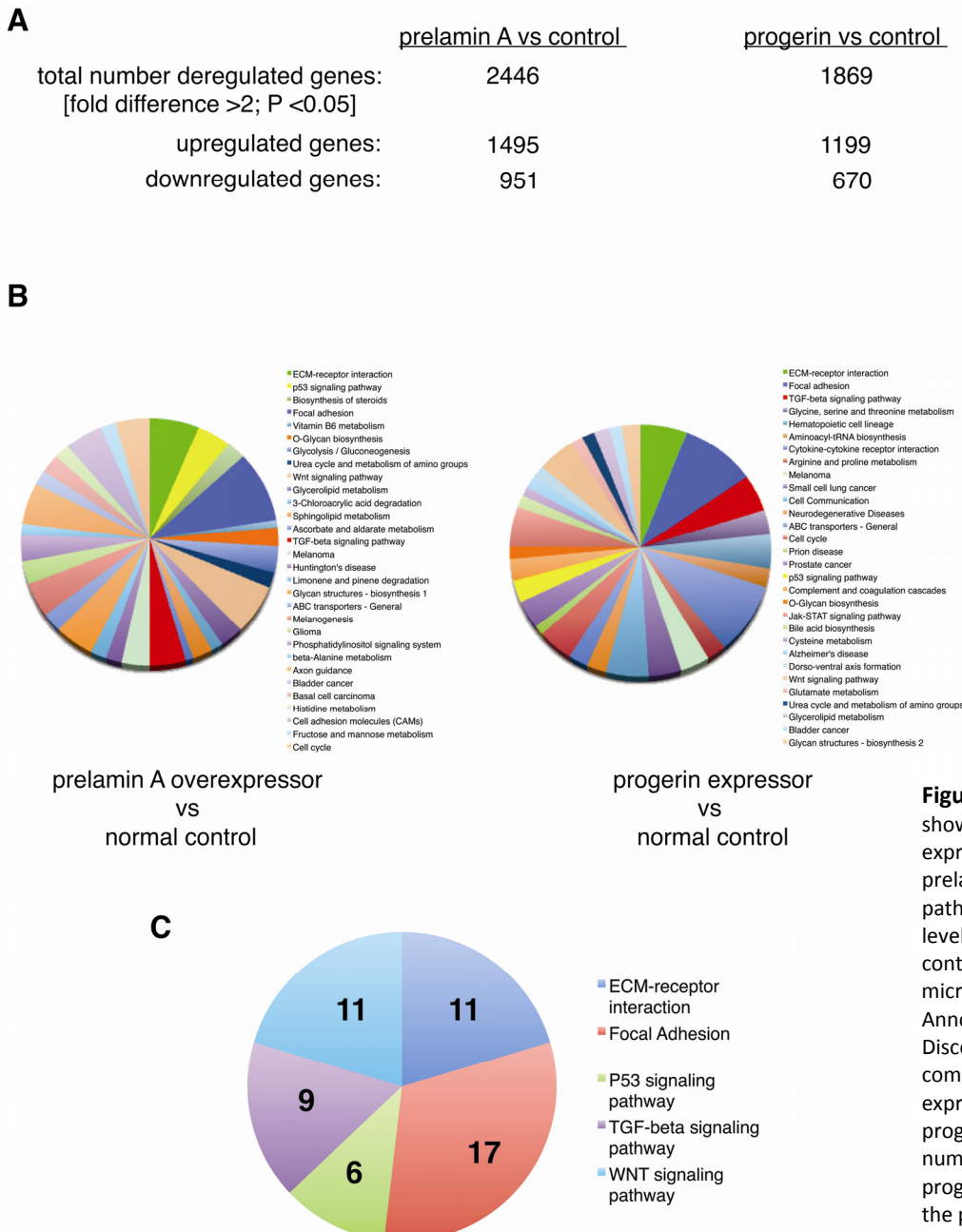
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## SUPPLEMENTARY FIGURES



**A**

| | prelamin A vs control | progerin vs control |
| --- | --- | --- |
| total number deregulated genes: [fold difference >2; P <0.05] | 2446 | 1869 |
| upregulated genes: | 1495 | 1199 |
| downregulated genes: | 951 | 670 |

**B**

prelamin A overexpressor vs normal control

progerin expressor vs normal control

**C**

**Figure S1.** (**A**) Summary of microarray data showing number of genes with altered expression in cells expressing elevated levels of prelamin A or progerin. (**B**) Pie charts showing pathways altered in cells expressing elevated levels of prelamin A or progerin, as compared to control cells. Chart was generated from the DNA microarray data analysis by Database for Annotation, Visualization, and Integrated Discovery (DAVID). (**C**) Pie chart showing common pathways affected in both cells expressing elevated levels of prelamin A or progerin. Numbers in each sector represent number of deregulated genes shared between progerin and elevated levels of prelamin A within the pathway.
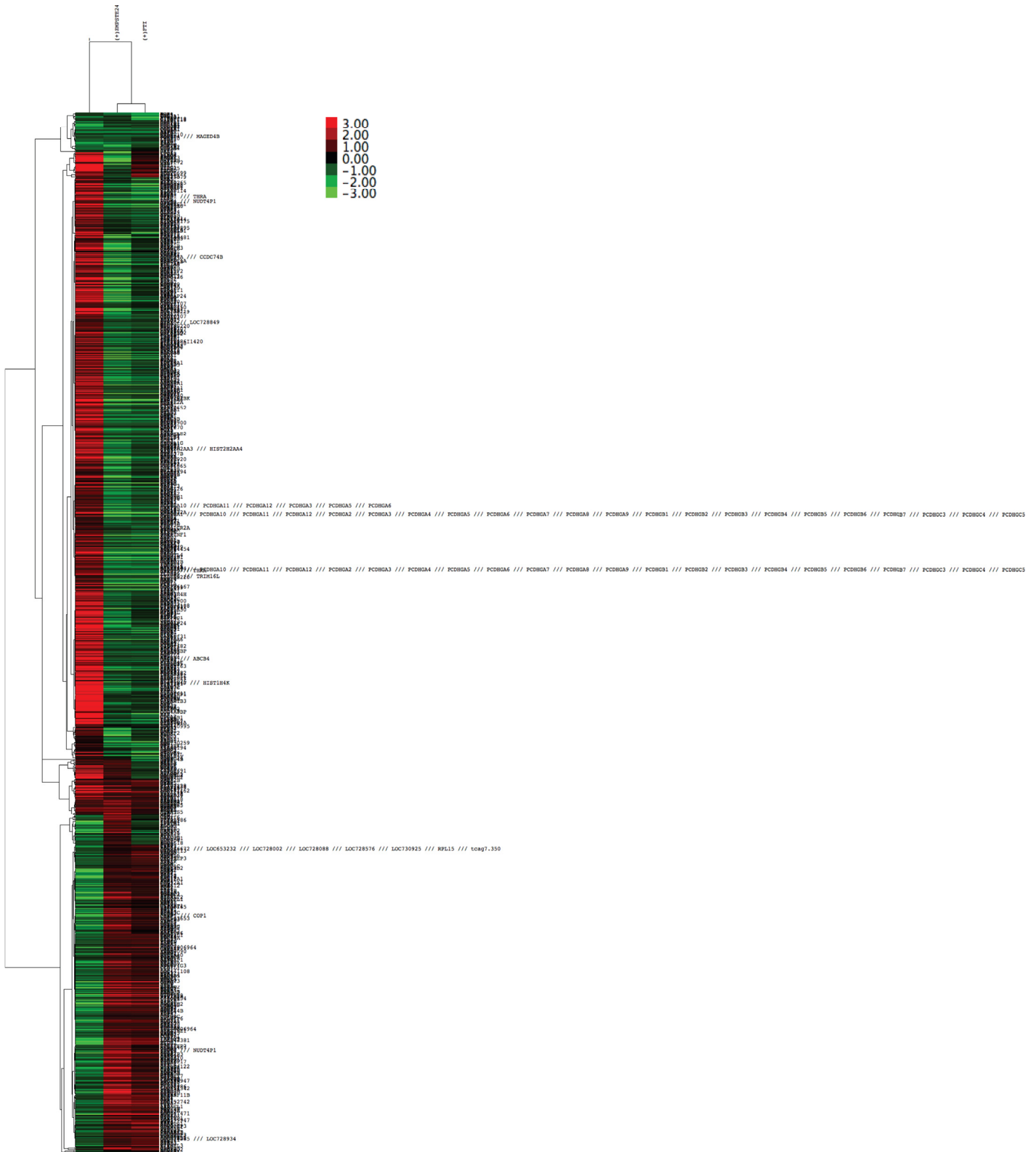
**Figure S2.** Unsupervised hierarchical clustering of differentially expressed genes from DNA microarray data analysis showing gene expression changes in cells expressing elevated levels of prelamin A prior to and after FTI treatment for 48 hours or ZMPSTE24 overexpression compared to control cells. Genes that are up- or down-regulated by ≥2-fold with p<0.05 were subjected to centered Pearson's correlation matrix. Each heat map represents intensity values relative to the median intensity across all samples per probe after background subtraction and normalization.
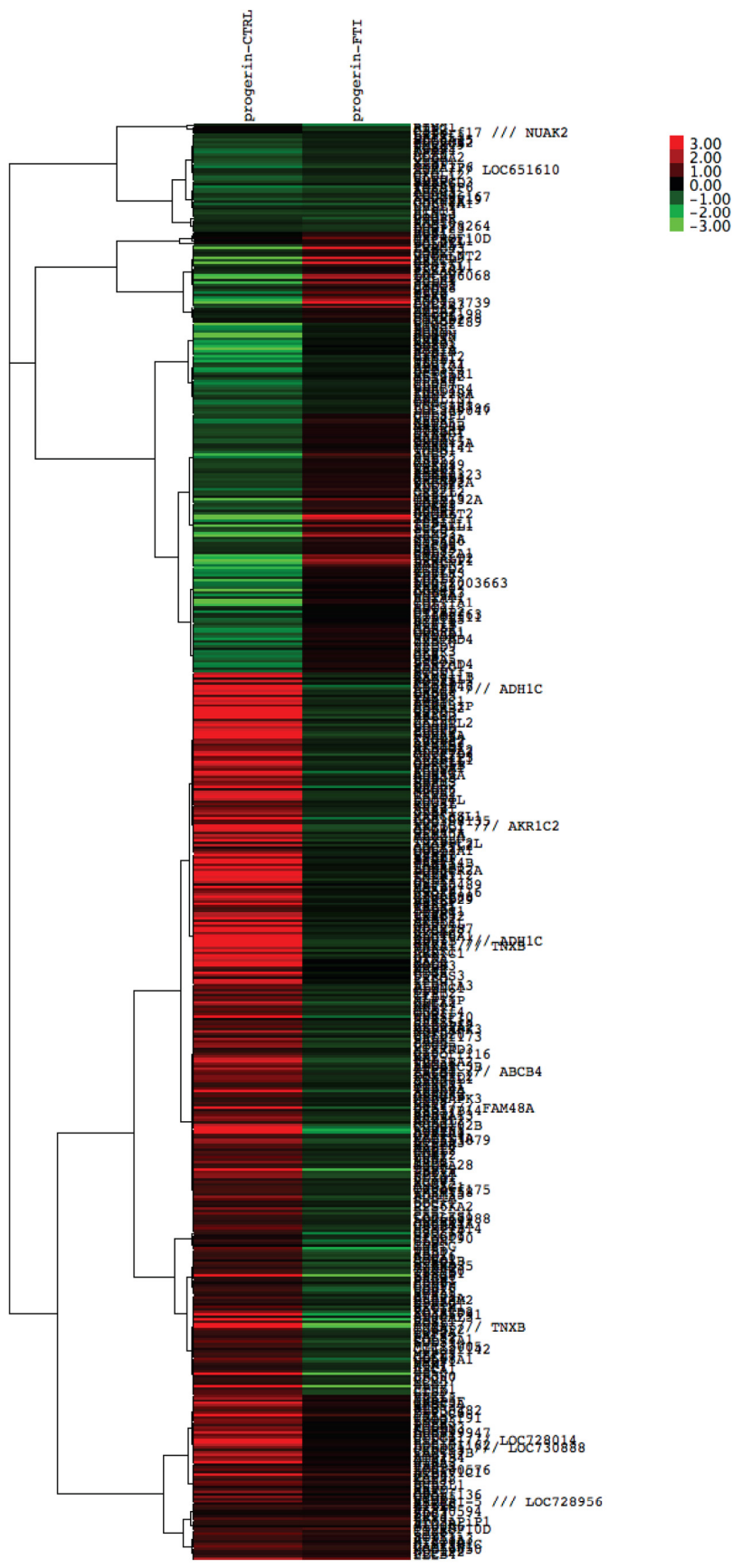
**Figure S3.** Unsupervised hierarchical clustering of differentially expressed genes from DNA microarray data analysis showing gene expression changes in cells expressing progerin prior to and after FTI treatment compared to control cells. Genes that are up- or down-regulated by ≥2-fold with $p < 0.05$ were subjected to centered Pearson's correlation matrix. Each heat map represents intensity values relative to the median intensity across all samples per probe after background subtraction and normalization.