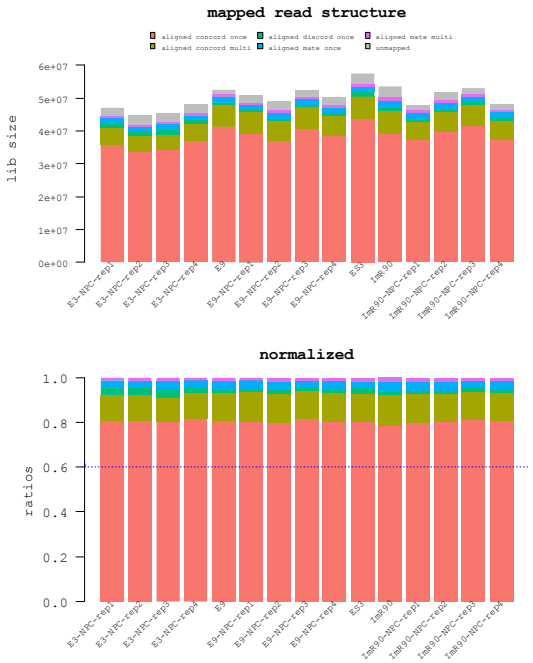
Supplementary figures

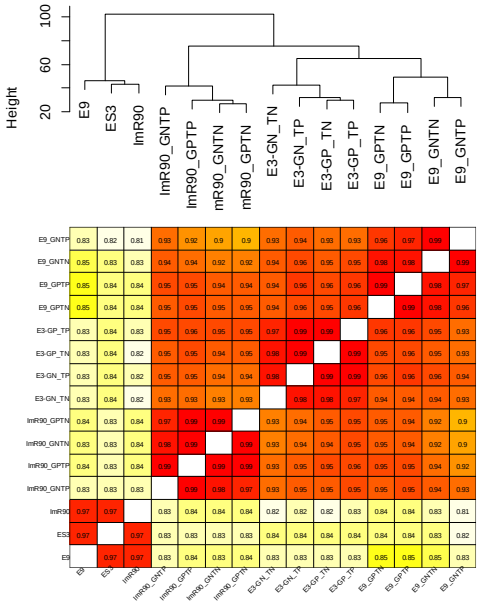
Contents

Figure S1 Superb data quality was observed for the 15 RNA-seq profiles. **A**, the 15 profiles have on average a mapping rate of over 95%, over 80% of which uniquely map to the human genome. **B**, the 15 samples cluster into two distinctive clusters, characterized by pre- and post-differentiation, respectively. The clustering was based on genome-wide Euclidean distances. In the lower panel, pairwise Spearman correlation coefficients were also indicated and visualized. **C**, the 15 profiles have highly comparable expression levels, as shown in this genome-wide box-and-whisker plot.

A



B



C

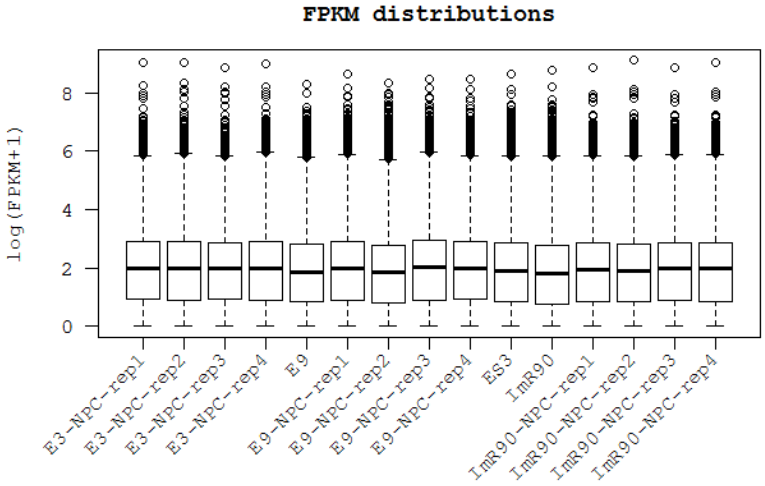


Figure S2 About three thousand differentially expressed genes (DEGs) were detected between the before and after differentiated samples, as shown in this volcano plot. Log2(FC)=log2(after-differentiation/before-differentiation). NPC: our NPC differentiations; hESCs: the three stem cell lines.

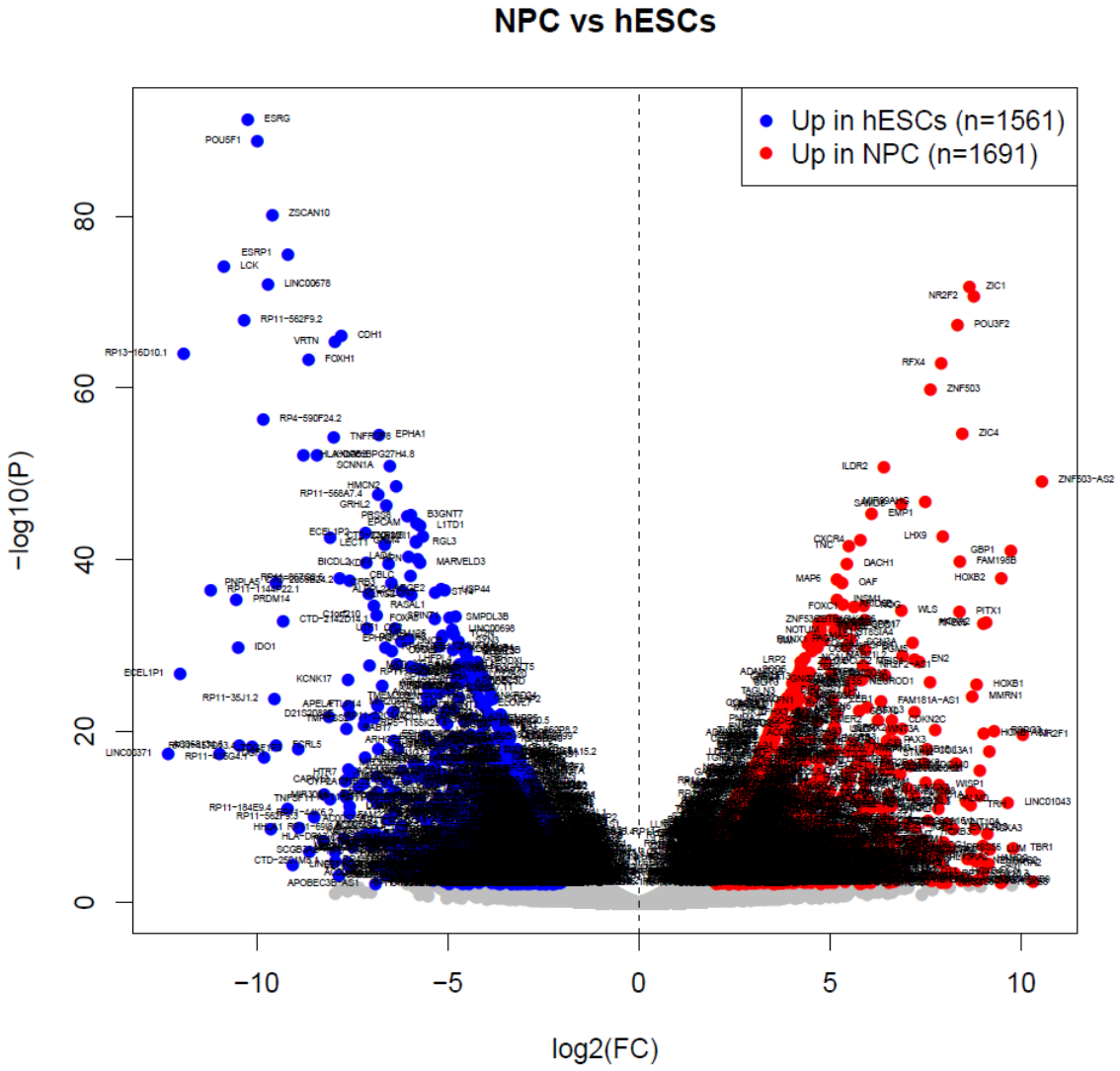


Figure S3 Go term and pathway enrichment analyses show matrisome (the genes of ECMs), and its regulators among the top most significant terms, for the 1691 genes up-regulated in our NPC differentiation.

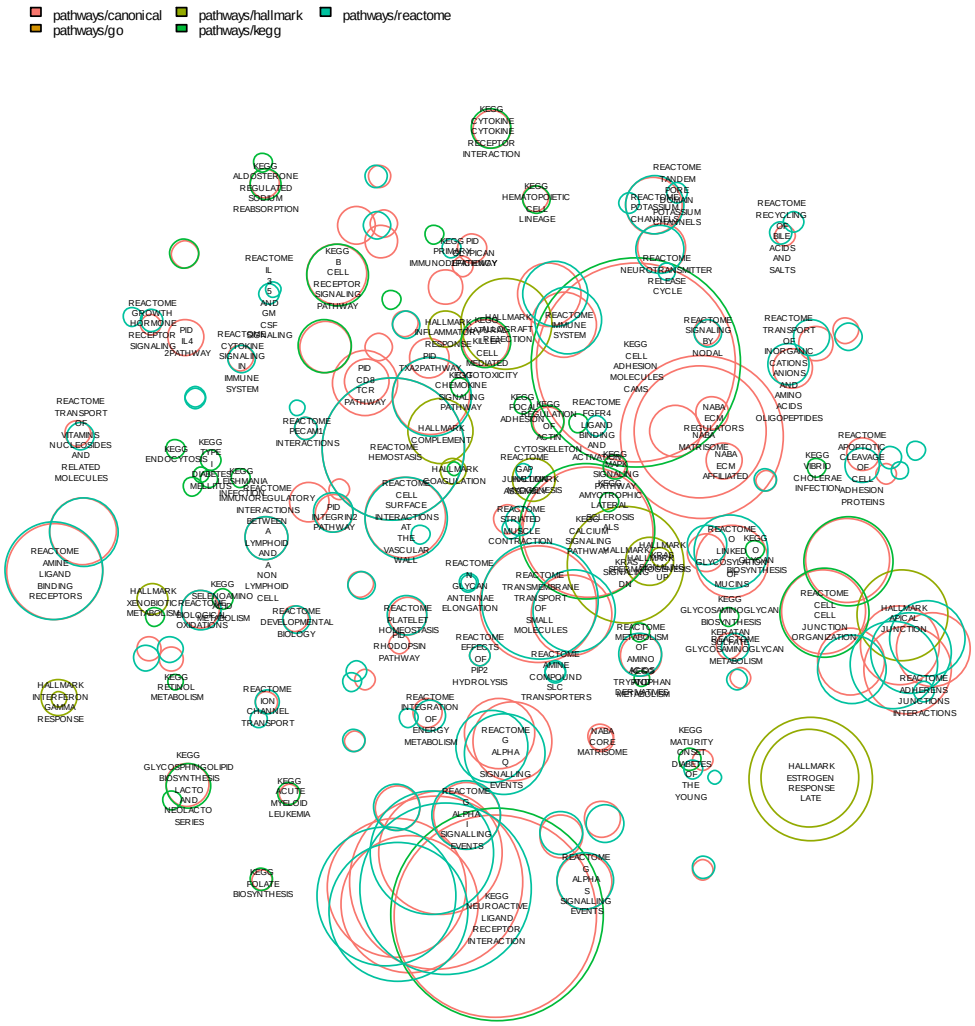


Figure S4, differentiated products of the three stem cell lines have similar responses and up-regulated genes. A, this Venn-diagram shows that 87.8% (1486 out of 1691) of the DEGs up in the NPC differentiations are not varying among the different lines. The lines do have a few hundred DEGs, but B-D show that these genes are only differences in the before differentiation lines.

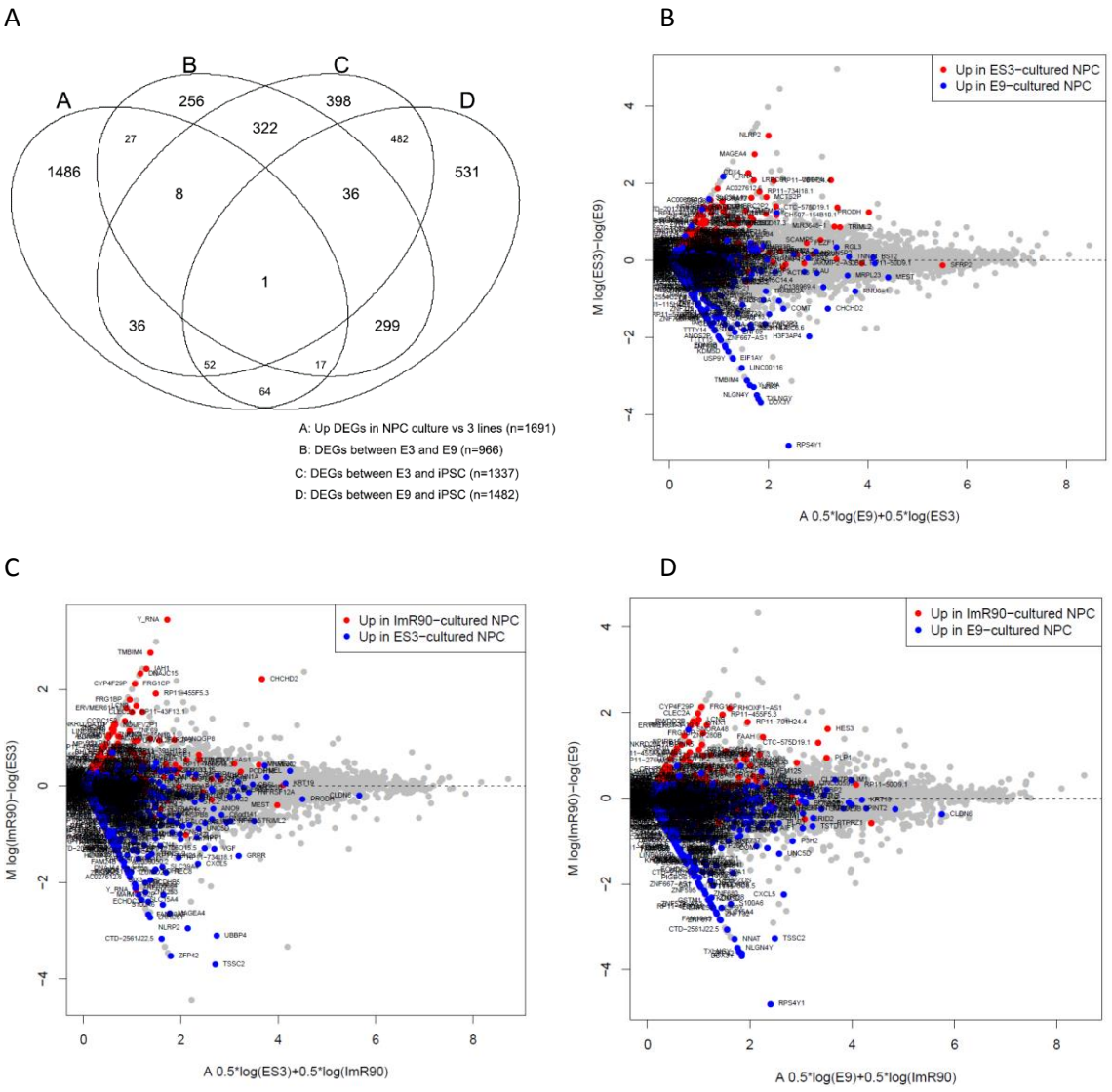


Figure S5, cross-comparisons of our NPC culture against Hoyland lab's normal NP data (microarray, three replicates). Common genes (excluding those below 1FPKM in our data, because these lowly expressed genes could not be captured by the microarray data) between the two datasets were used, and Spearman correlation coefficients were calculated.

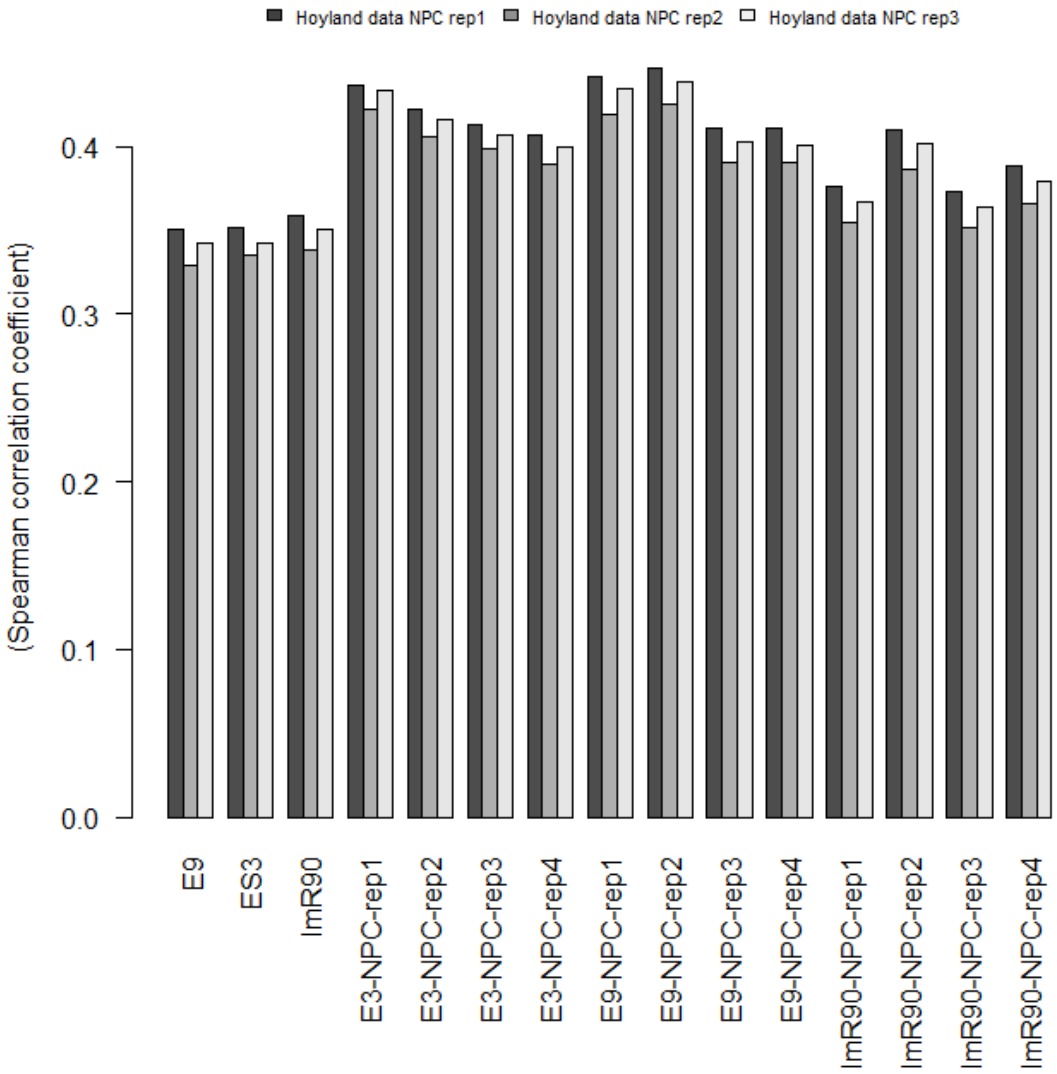


Figure S6, cross-comparisons of our NPC culture against Chan lab's normal NP data (microarray, two replicates). Common genes (excluding those below 1FPKM in our data, because these lowly expressed genes could not be captured by the microarray data) between the two datasets were used, and Spearman correlation coefficients were calculated.