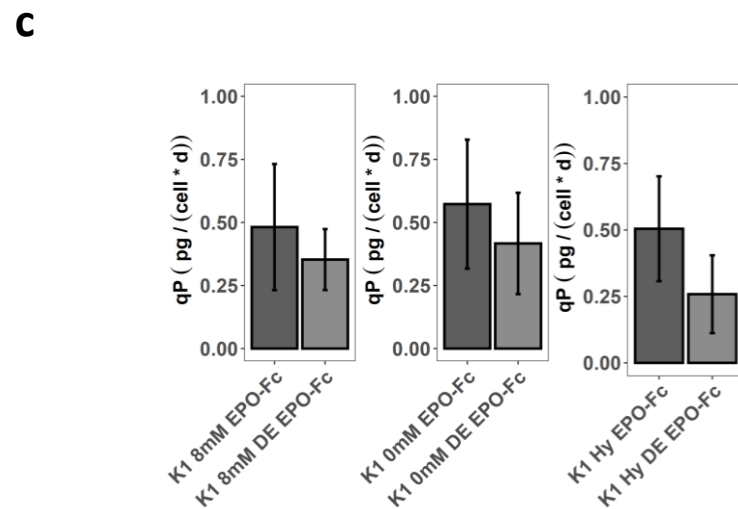
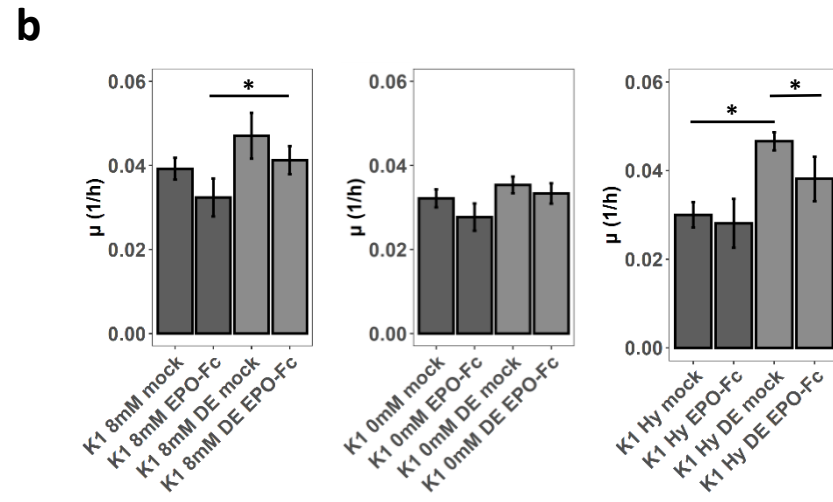
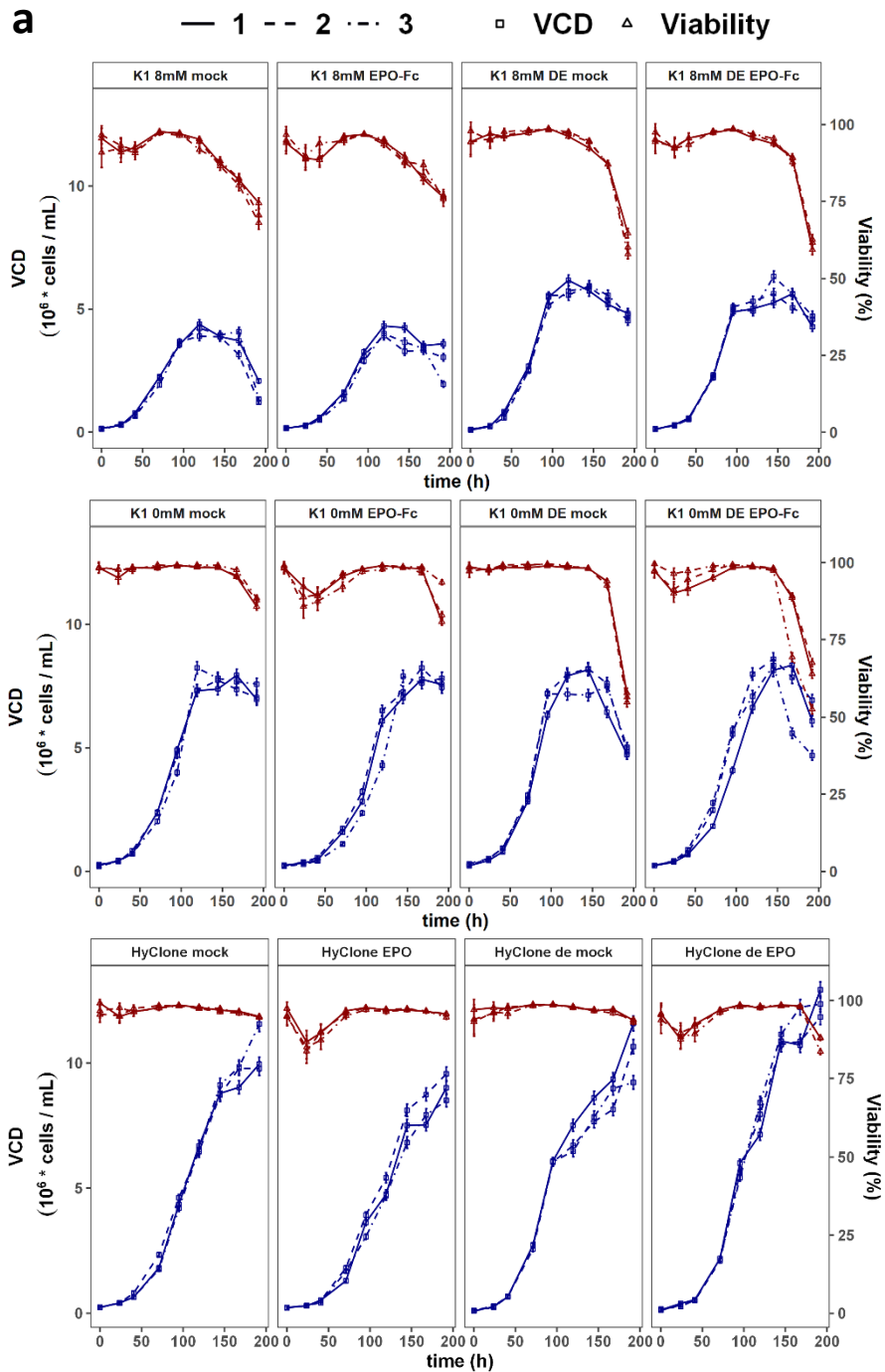
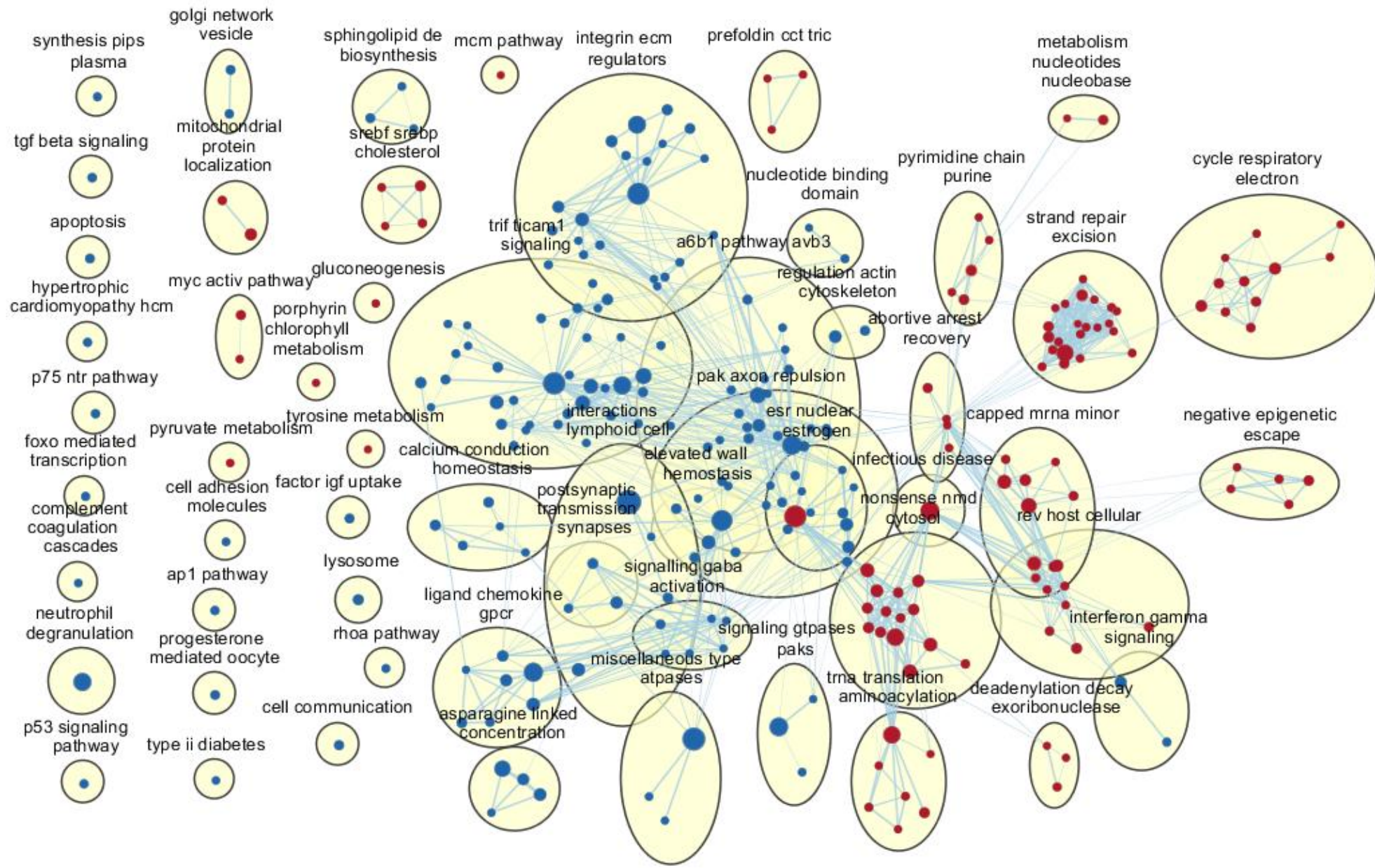


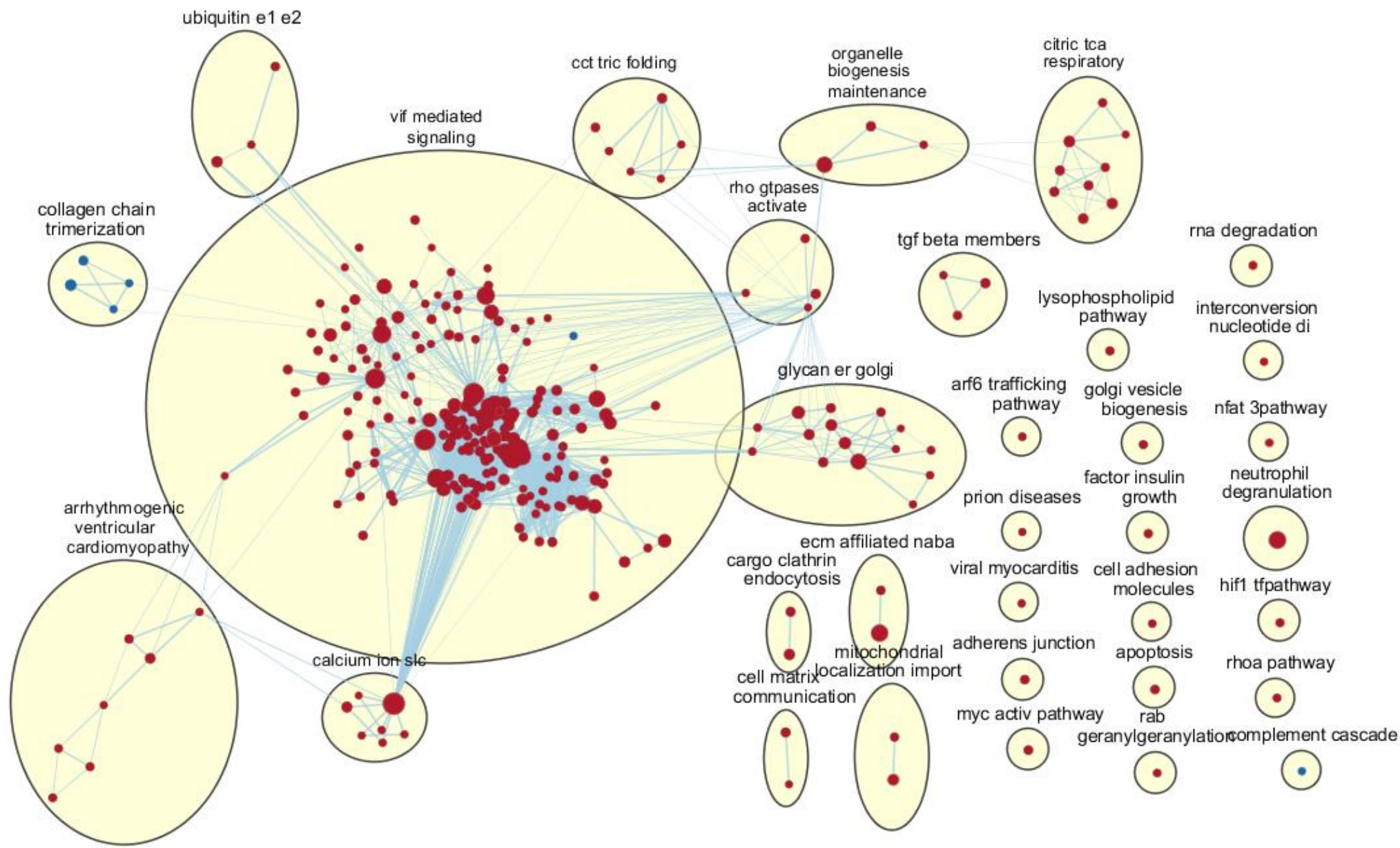
**Supplementary Figure 1:** Map of the EPO-Fc Plasmid used for transient transfection of the used cell lines



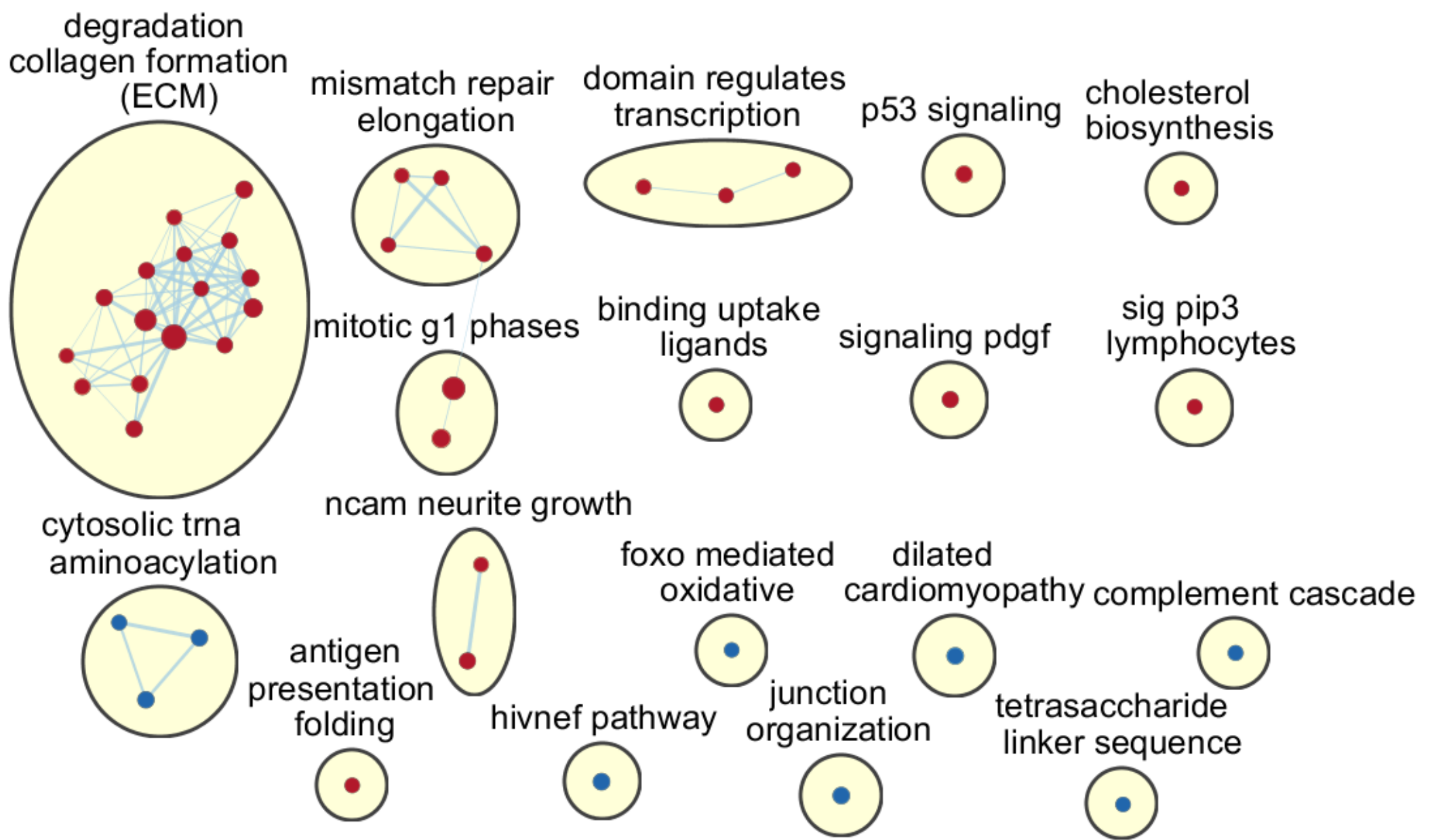
**Supplementary Figure 2: (a)** VCD (blue) and viability (red) of transient transfection with EPO-Fc . Corresponding growth rates ( $\mu$ ) (b) and specific productivities (qP) (c). Mock - indicates mock transfection, EPO-Fc – indicates cells transfected with EPO-Fc



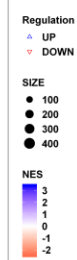
**Supplementary Figure 3:** K1 8mM GSEA enriched pathways network produced by Cytoscape 3.7.2 . Nodes represent gene sets, Node size indicates the number of genes found in the gene sets, edges show the overlap in between gene sets, edge width represent the size of the overlap. Node size indicates positive (red) or negative (blue) enrichment.



**Supplementary Figure 4:** K1 0mM GSEA enriched pathways network produced by Cytoscape 3.7.2 .Nodes represent gene sets, Node size indicates the number of genes found in the gene sets, edges show the overlap in between gene sets, edge width represent the size of the overlap. Node size indicates positive (red) or negative (blue) enrichment.

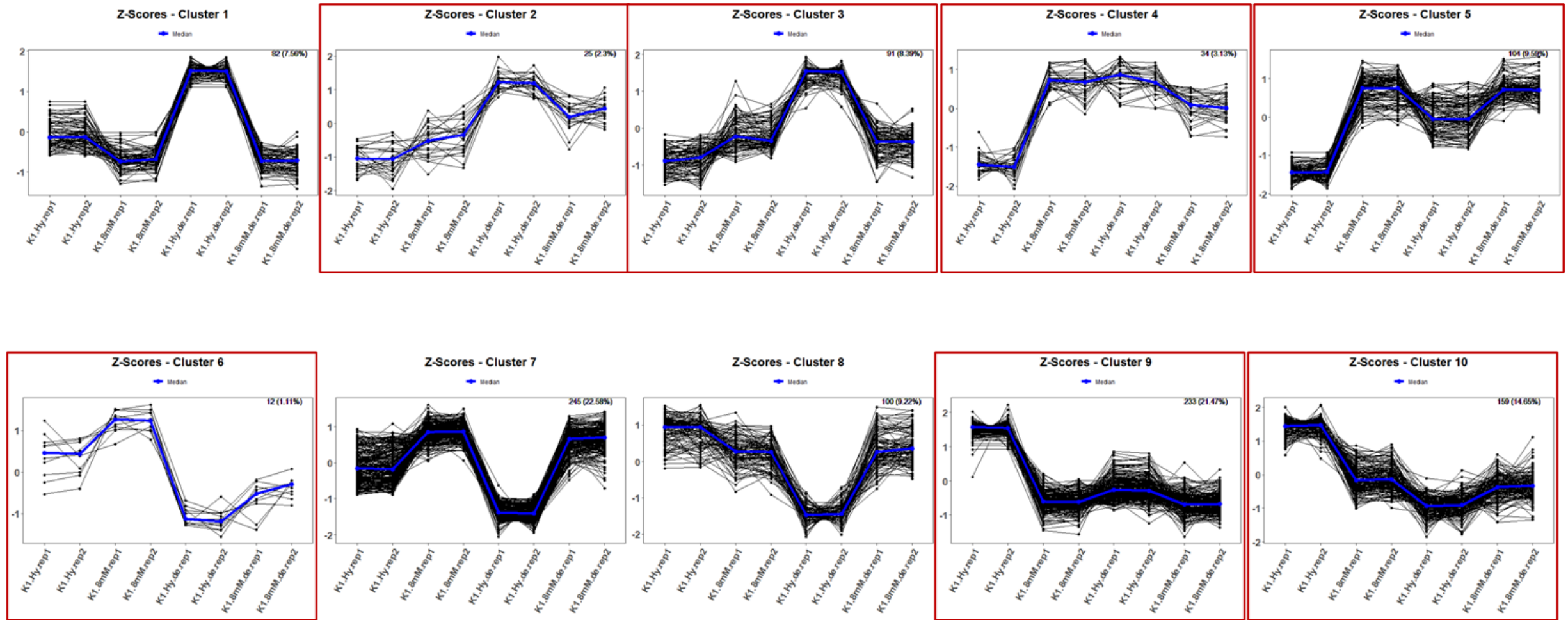


**Supplementary Figure 5:** K1 Hy GSEA enriched pathways network produced by Cytoscape 3.7.2 . Nodes represent gene sets, Node size indicates the number of genes found in the gene sets, edges show the overlap in between gene sets, edge width represent the size of the overlap. Node size indicates positive (red) or negative (blue) enrichment.

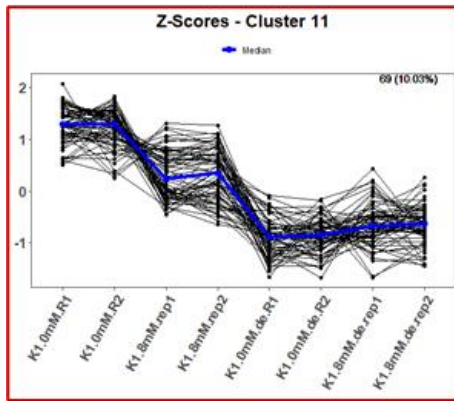
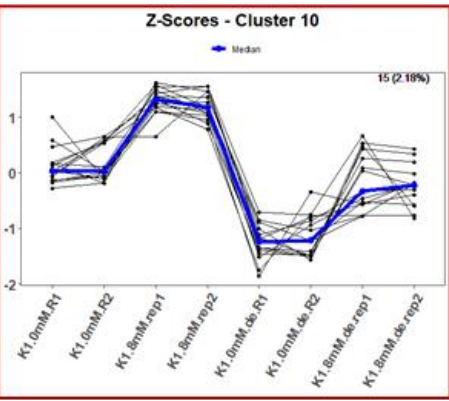
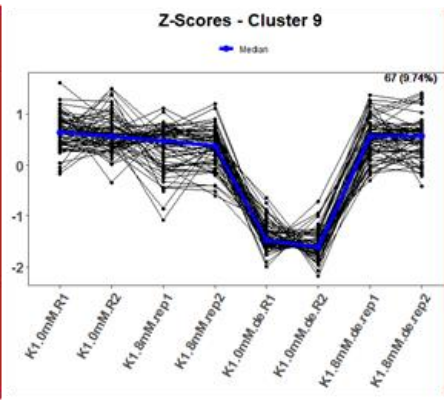
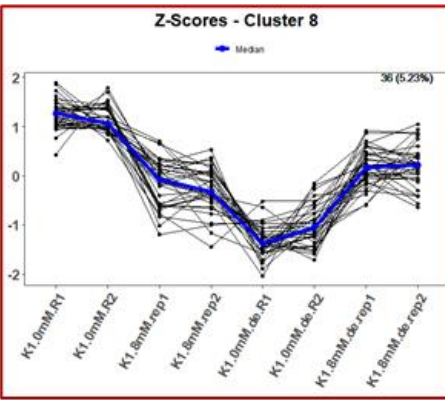
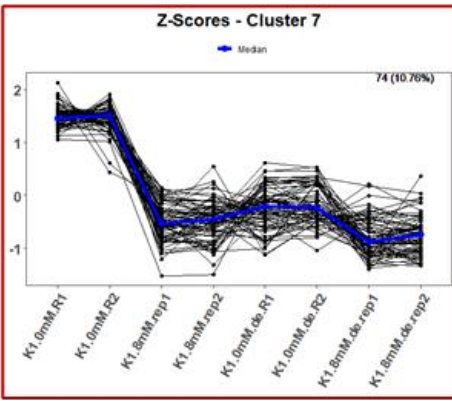
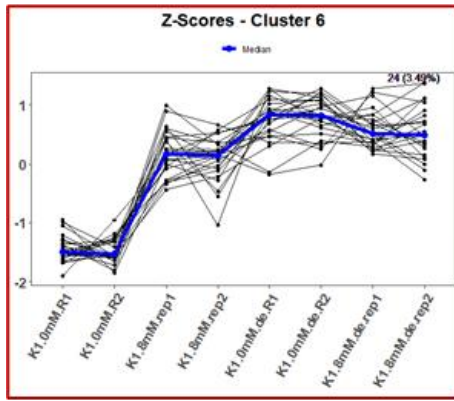
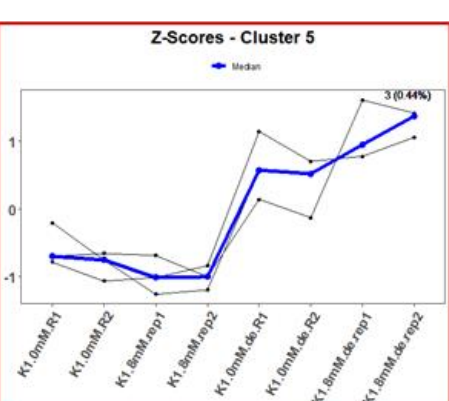
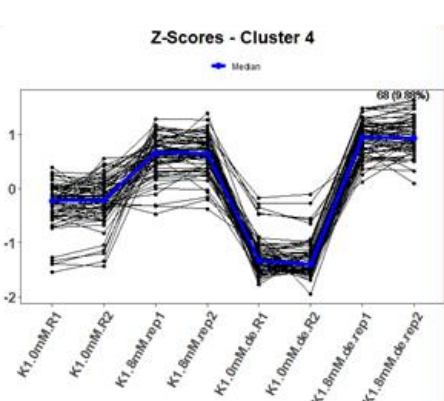
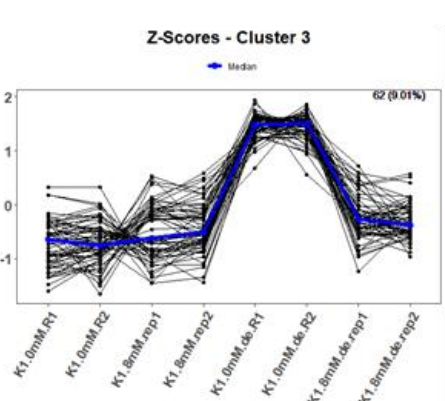
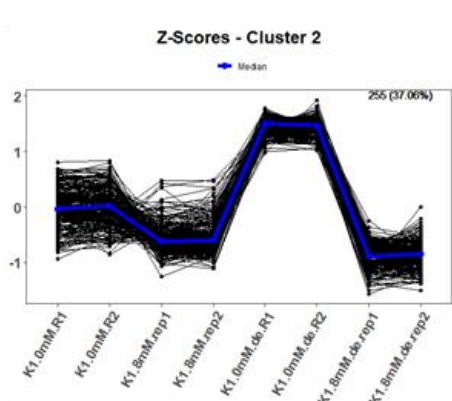
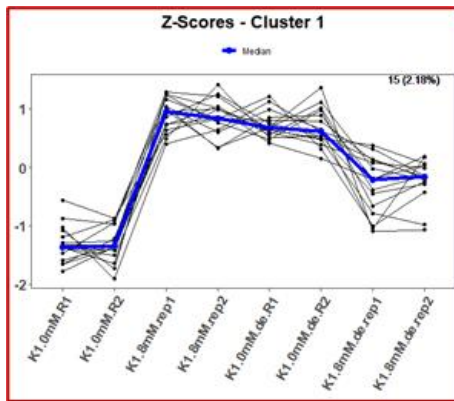


**Supplementary Figure 6: Complete list of overlapping GSEA enriched pathways of K1 0mM and K1 8mM.**

K1 0mM K1 8mM



**Supplementary Figure 7:** Identified clusters of K1 Hy of hard clustered vst - normalised RNA-Seq counts. Clusters of interest are framed in red.



**Supplementary Figure 8:** Identified clusters of K1 0mM of hard clustered vst - normalised RNA-Seq counts. Clusters of interest are framed in red.



