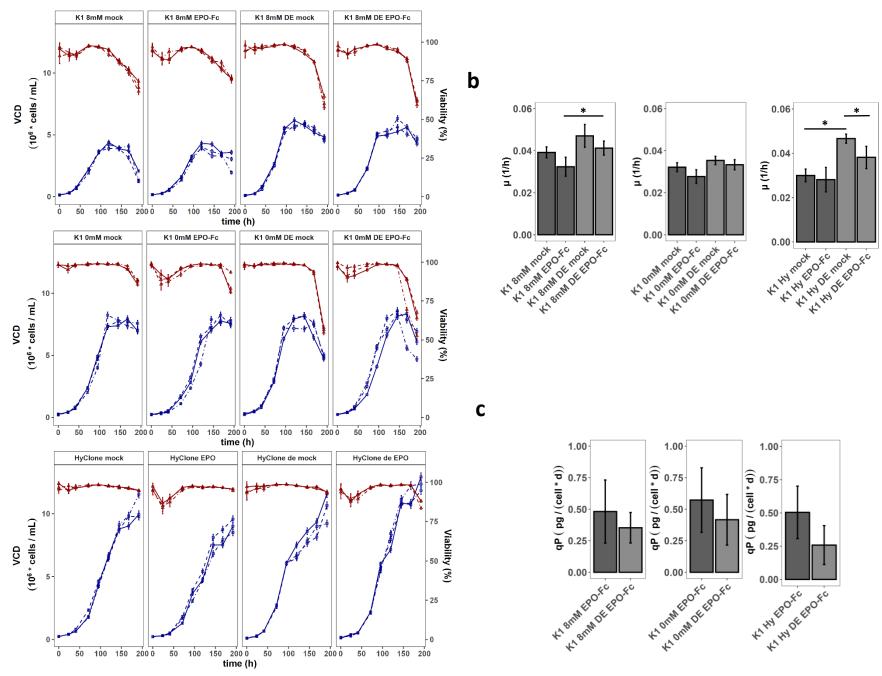


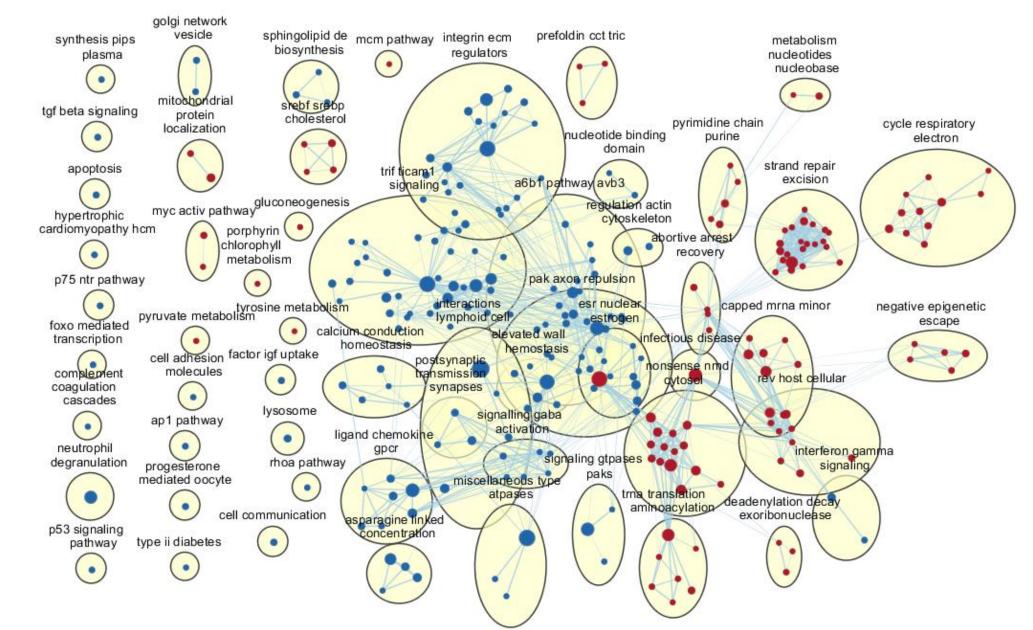
Supplementary Figure 1: Map of the EPO-Fc Plasmid used for transient transfection of the used cell lines



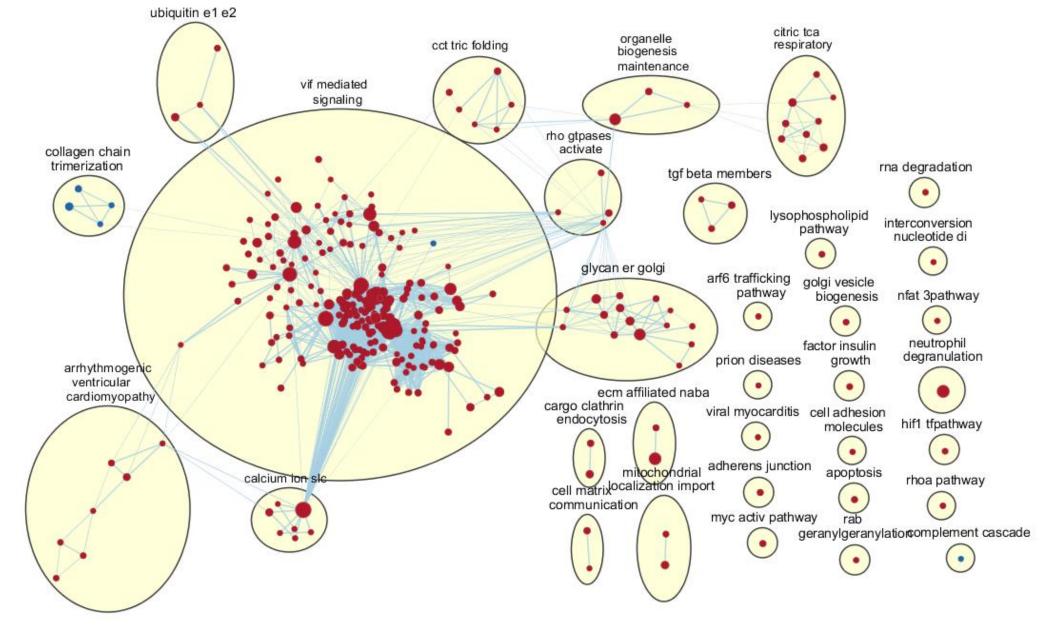


Supplementary Figure 2: (a) VCD (blue) and viability (red) of transient transfection with EPO-Fc . Corresponding growth rates (μ) (b) and specific productivities (qP) (c). Mock indicates mock transfection, EPO-Fc – indicates cells transfected with EPO-Fc

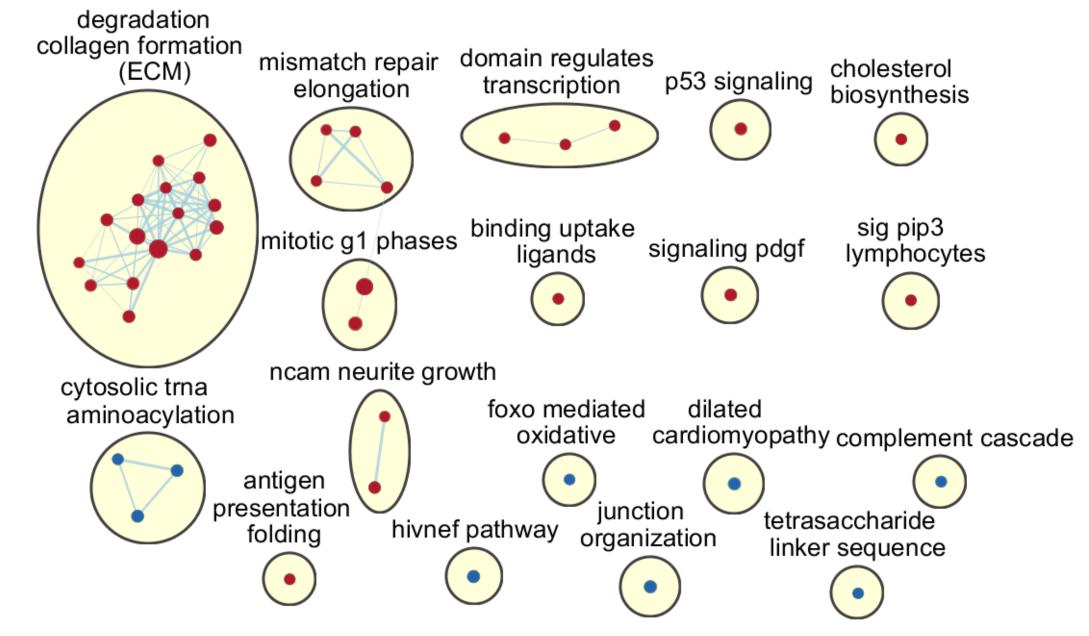
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Supplementary Figure 3: K1 8mM GSEA enriched pathways network produced by Cytoscape 3.7.2. Nodes represent gene sets, Node size indicates the number of genes found in the gene sets, edges show the overlap in between gene sets, edge width represent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

SIZE • 100 • 200 • 300 • 400	Supplementary Figure 6: Complete list of overlapping
NES	GSEA enriched pathways of K1 0mM and K1 8mM.

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REACTOME_TOLL_LIKE_RECEPTOR_CASCADES	A
REACTOME_SIGNALING_BY_VEGF	^
REACTOME_SIGNALING BY RHO_GTPASES REACTOME_SIGNALING BY RECEPTOR TYROSINE_KINASES REACTOME_SIGNALING_BY_RAS_MUTANTS	
REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES	
REACTOME_SIGNALING_BY_RAS_MUTANTS	A
REACTOME SIGNALING BY INTERLEUKINS	
REACTOME_SIGNALING_BY_BRAF_AND_RAF_FUSIONS REACTOME_SIGNAL_TRANSDUCTION_BY_L1	▲
REACTOME SIGNAL TRANSDUCTION BY L1	
REACTOME SEMAPHORIN INTERACTIONS	▲
REACTOME_SEMA33_PAK_DEPENDENT_AXON_REPULSION REACTOME_RESONSE_TO_LEVATED_PLATELET_CYTOSOLIC_CA2PLUS REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_TRANSPORT_AND_UPTAKE_BY_INSULIN_LIKE_GROWTH_FACTOR_BIOTEINS_IGFBPS- REACTOME_PLATELET_CALCIUM_HOMEOSTASIS- DELOTANCE_DILATED_ISTANTION DOWN TO A DECOMPTON LIVENING NUM-HOMEOSTASIS-	
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PID_FAK_PATHWAY PID_EPHB_FWD_PATHWAY	A
PID_EPHB_FWD_PATHWAY	A
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KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	^
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KEGG_APOPTOSIS-	▲
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REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM REACTOME_TRANSLATION	▲
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REACTOME_RRNA_PROCESSING_IN_THE_NUCLEUS_AND_CYTOSOL	A
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REACTOME_RRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	A
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REACTOME HIV LIFE CYCLE-	
REACTOME HIV INFECTION	
REACTOME_GENE_SILENCING_BY_RNA1	<u> </u>
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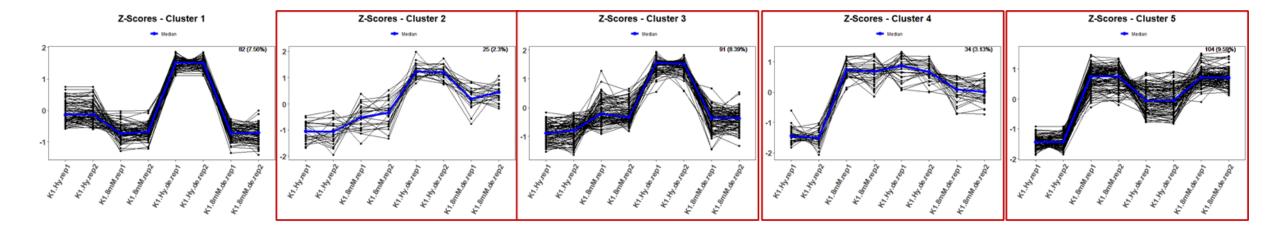
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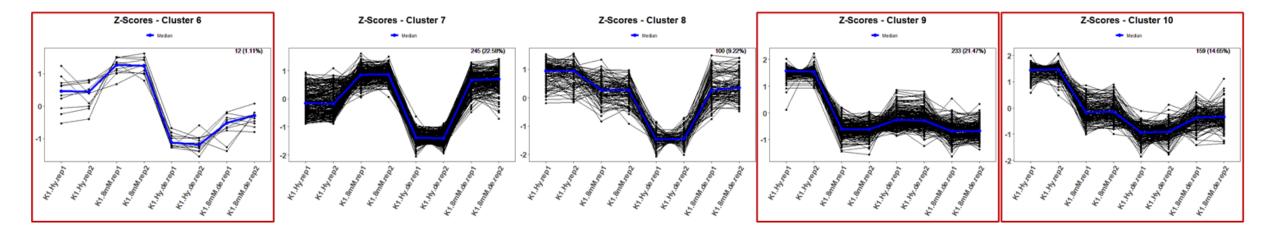
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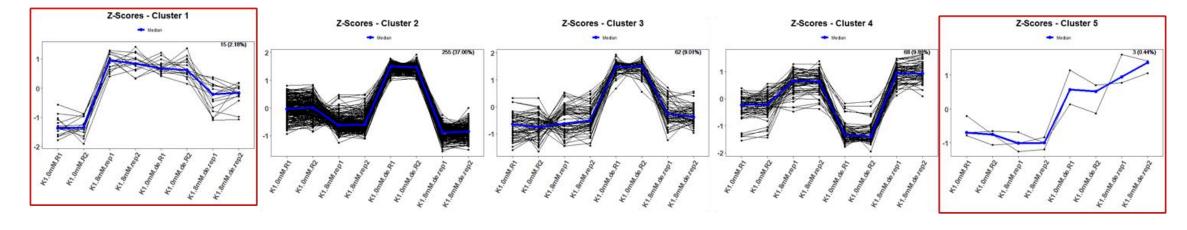
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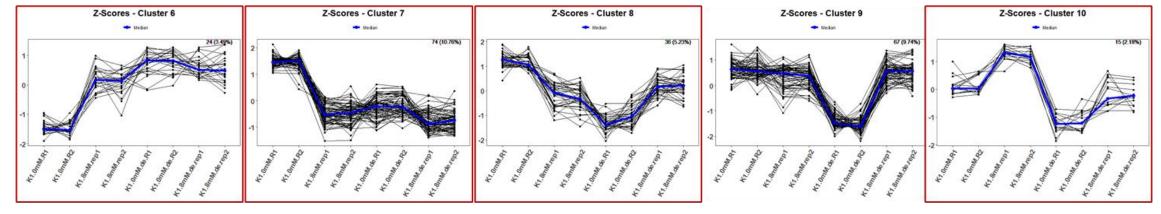
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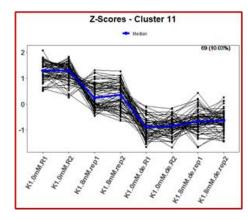




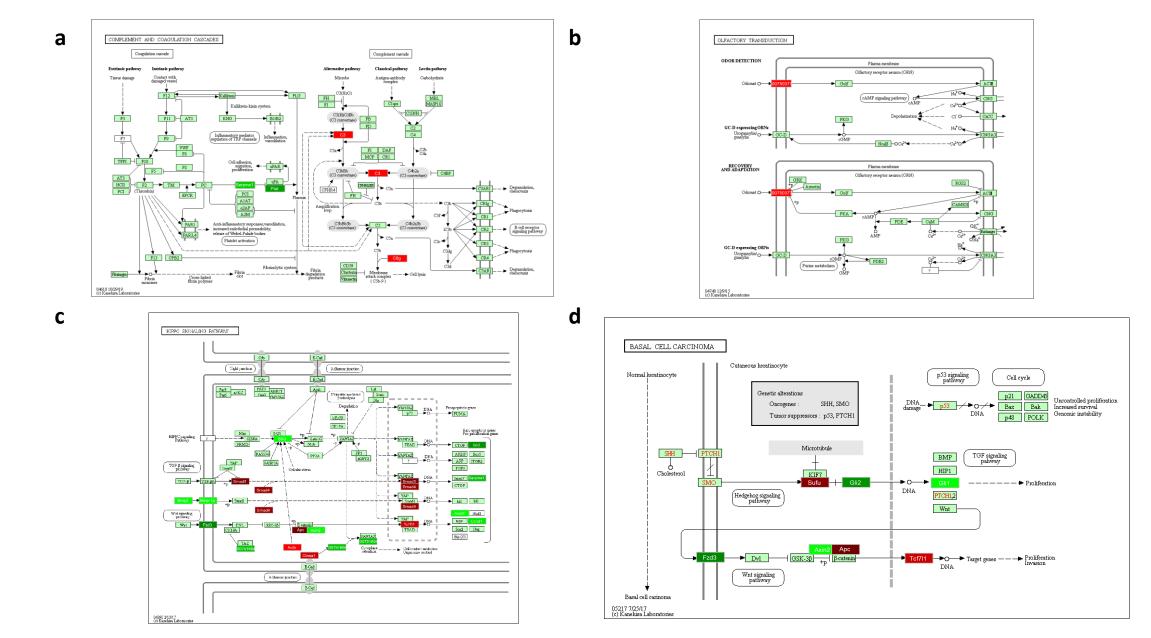
Supplementary Figure 7: Identified clusters of K1 Hy of hard clustered vst - normalised RNA-Seq counts. Clusters of interest are framed in red.







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



Supplementary Figure 9: Identified KEGG Pathways using the hard clustered RNA-Seq counts of K1 0mM.DE (a,b) and K1 Hy.DE (c,d). (a) Compliment and coagulation cascades (b) Olfactory transduction (c) Hippo signalling pathway and (d) Basal Cell Carcinoma. Upregulated genes are shown in strong/bright green, downregulated genes in dark/bright red.