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The effect of transcriptomic annotations in breast cancer differential gene expression study

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Material & Methods

- RNA-seq of MCF7 breast cancer (Cancer reads ERR358487-88) and normal tissues (Normal reads ERR358485-86)
- Illumina HiSeq 2000, 2 x 150 bp
- The library size: 73,974,766 - 97,983,949 reads
- One differential gene expression (DGE) pipeline (FastQC, Trimmomatic, Kallisto, DESeq2) → **four approaches**
- Gene Set Enrichment Analysis (GSEA) of DEGs
- PCA based on expression of all genes
- T-test based on expression of Naderi breast cancer prognosis down- and upregulated genes (doi.org/10.1038/sj.onc.1209920)

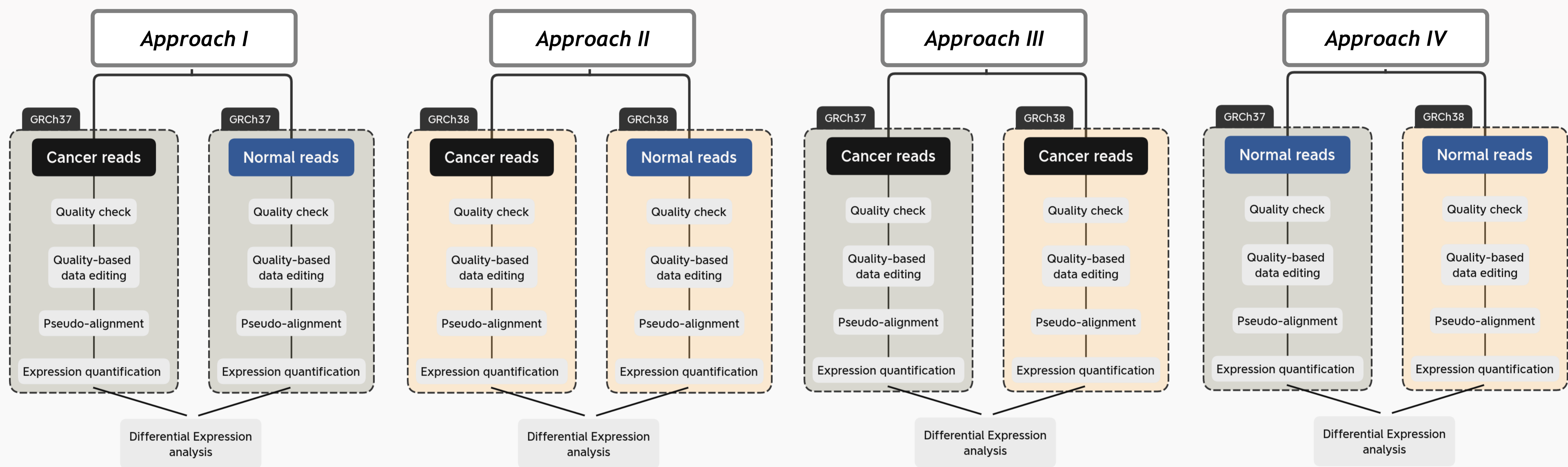
Objectives

Investigation of the transcriptome annotation effect on:

- DGE of all genes
- genes related to survival prognosis in breast cancer

Conclusions

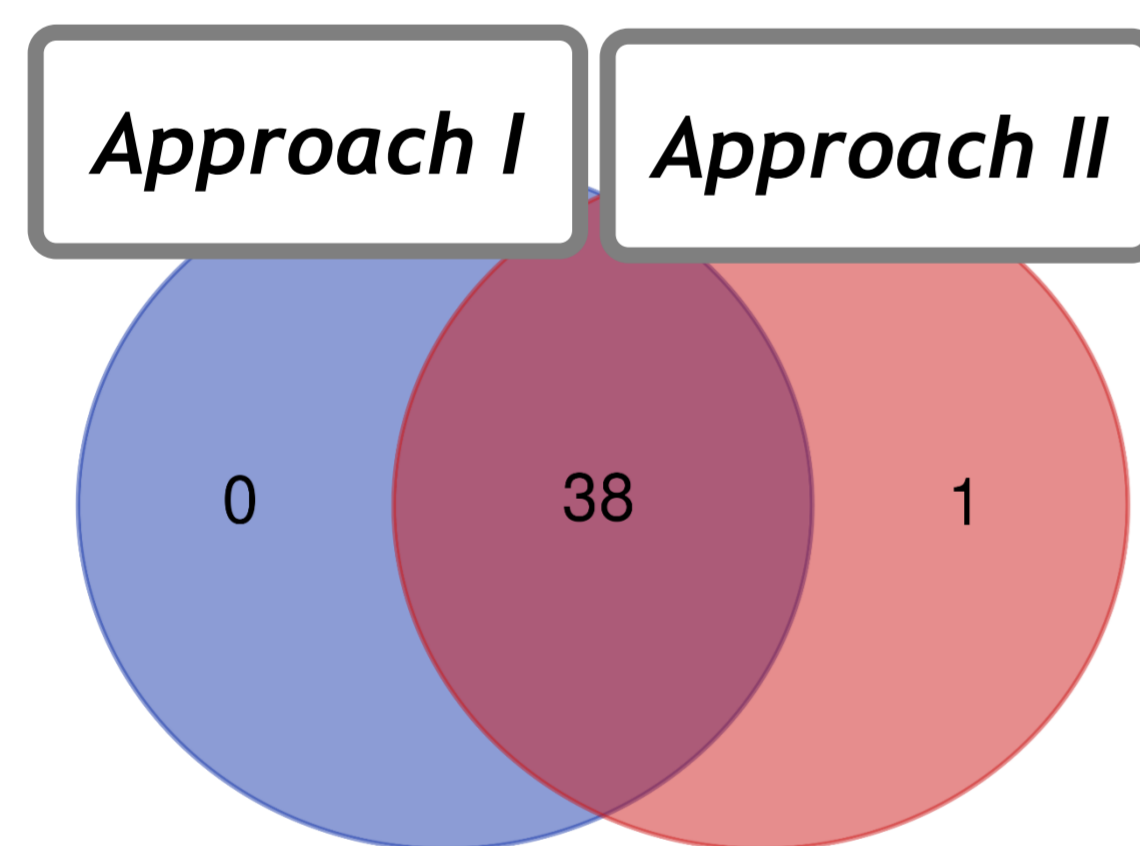
- The overall DGE outcomes were not identical between GRCh37 and GRCh38 annotations
- ...however, the transcriptome annotation had no effect on genes related to survival prognosis in breast cancer



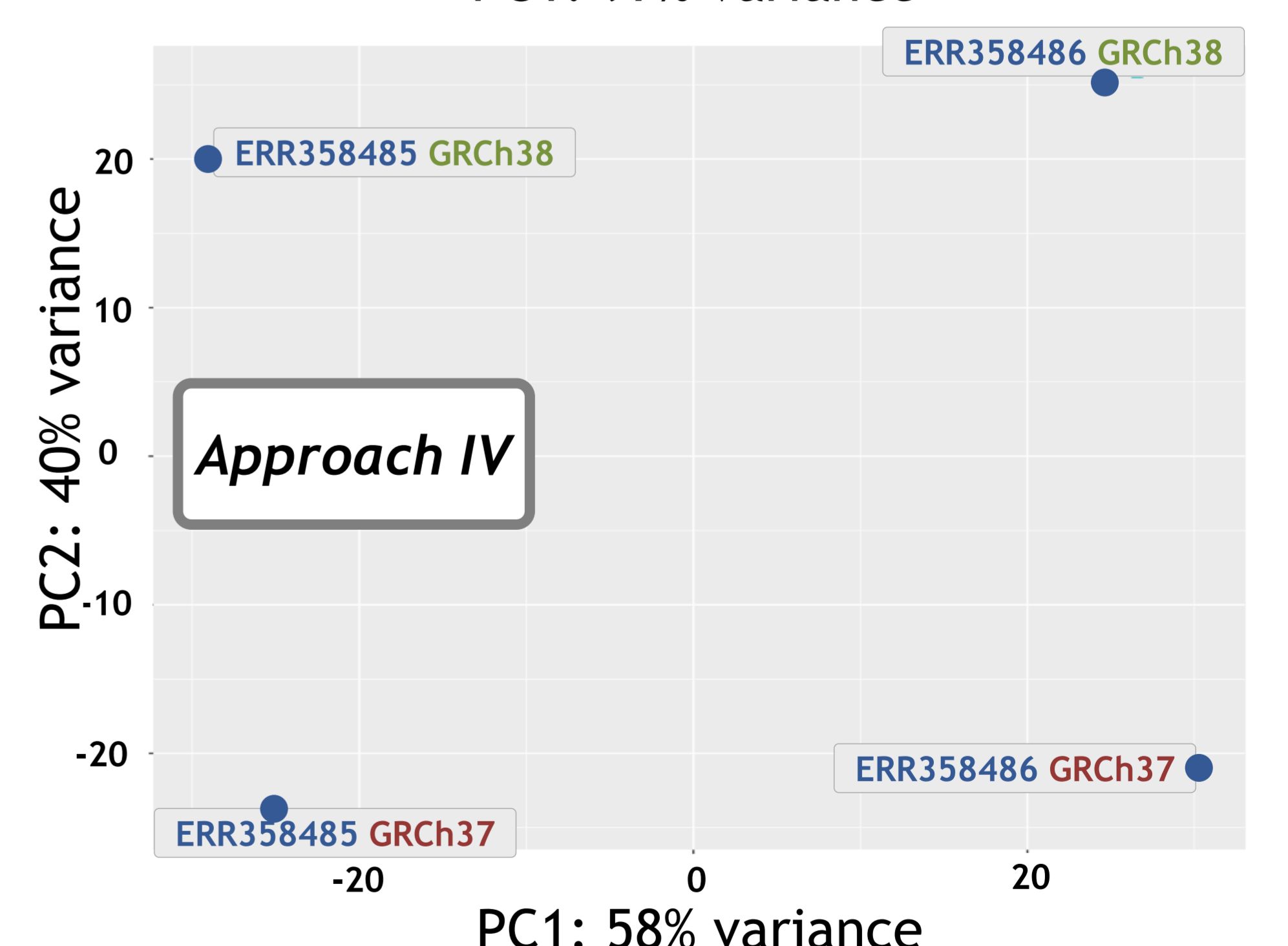
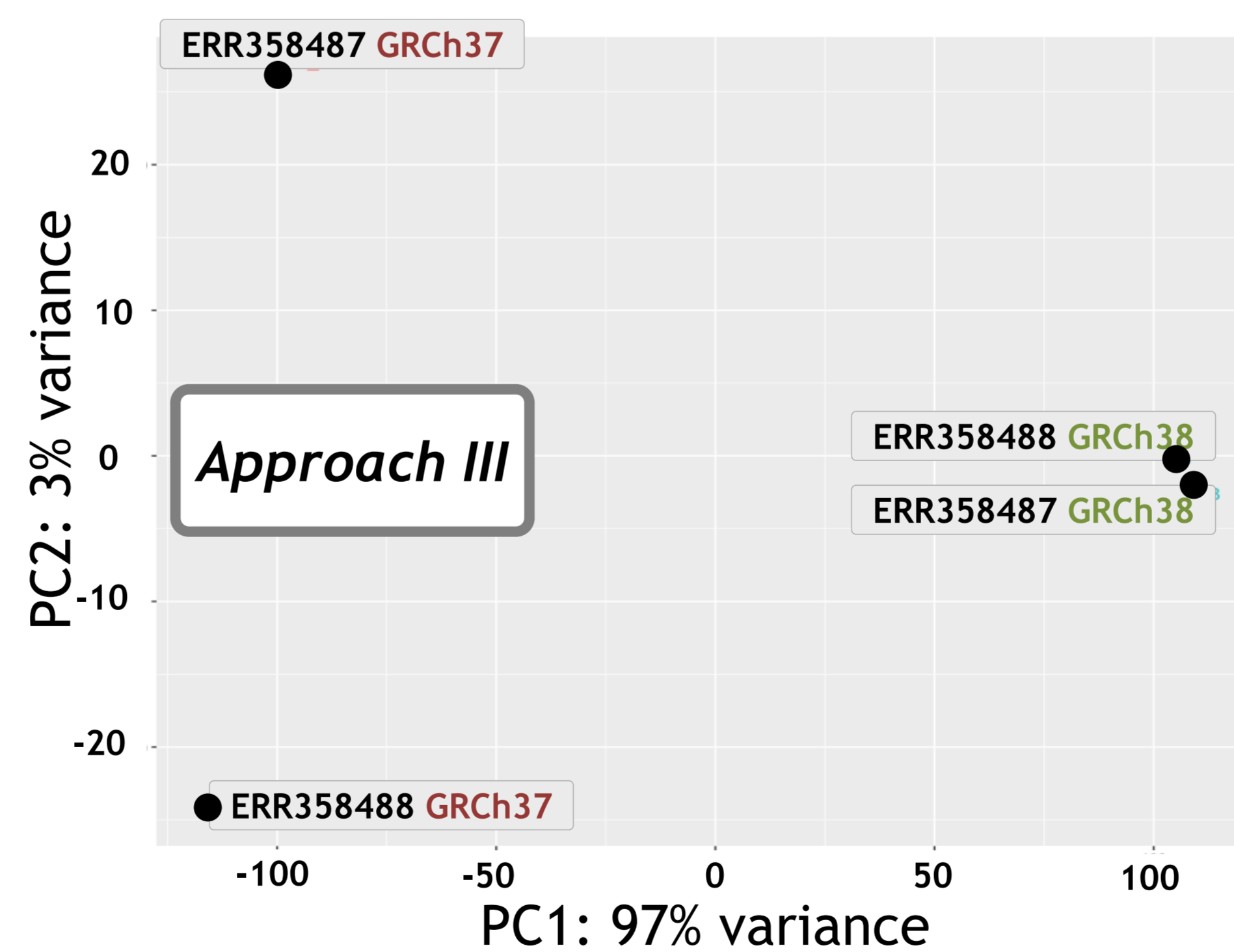
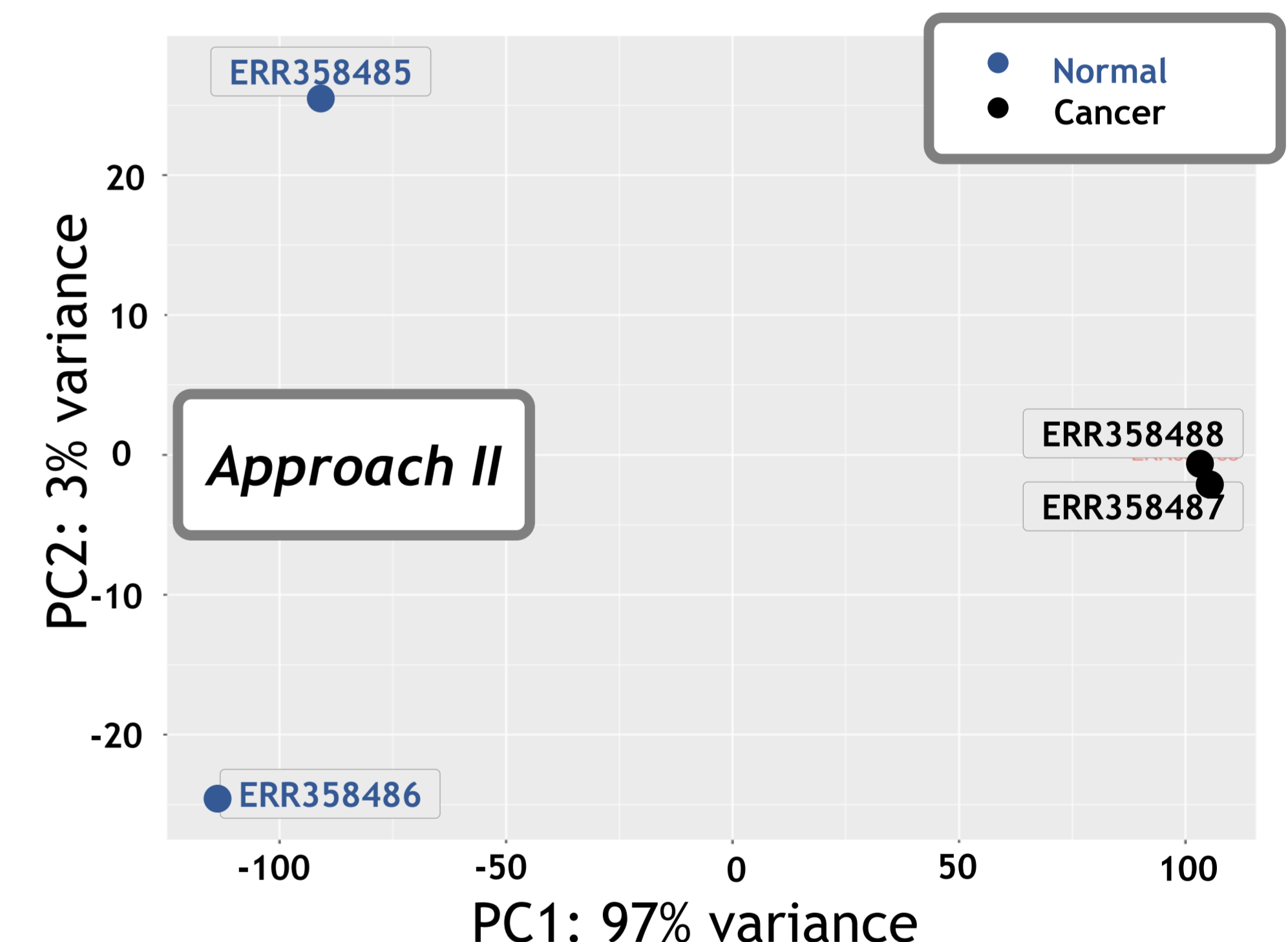
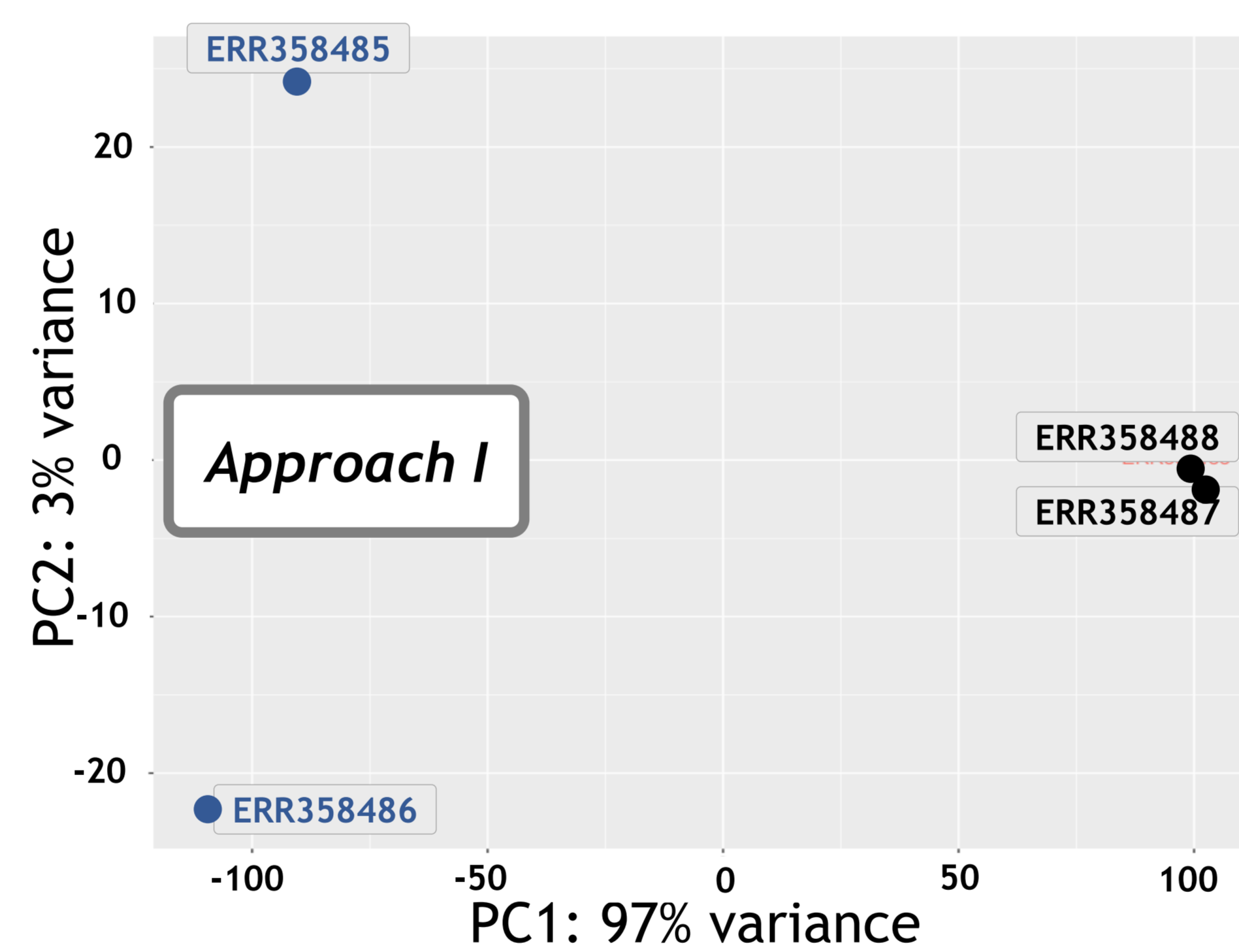
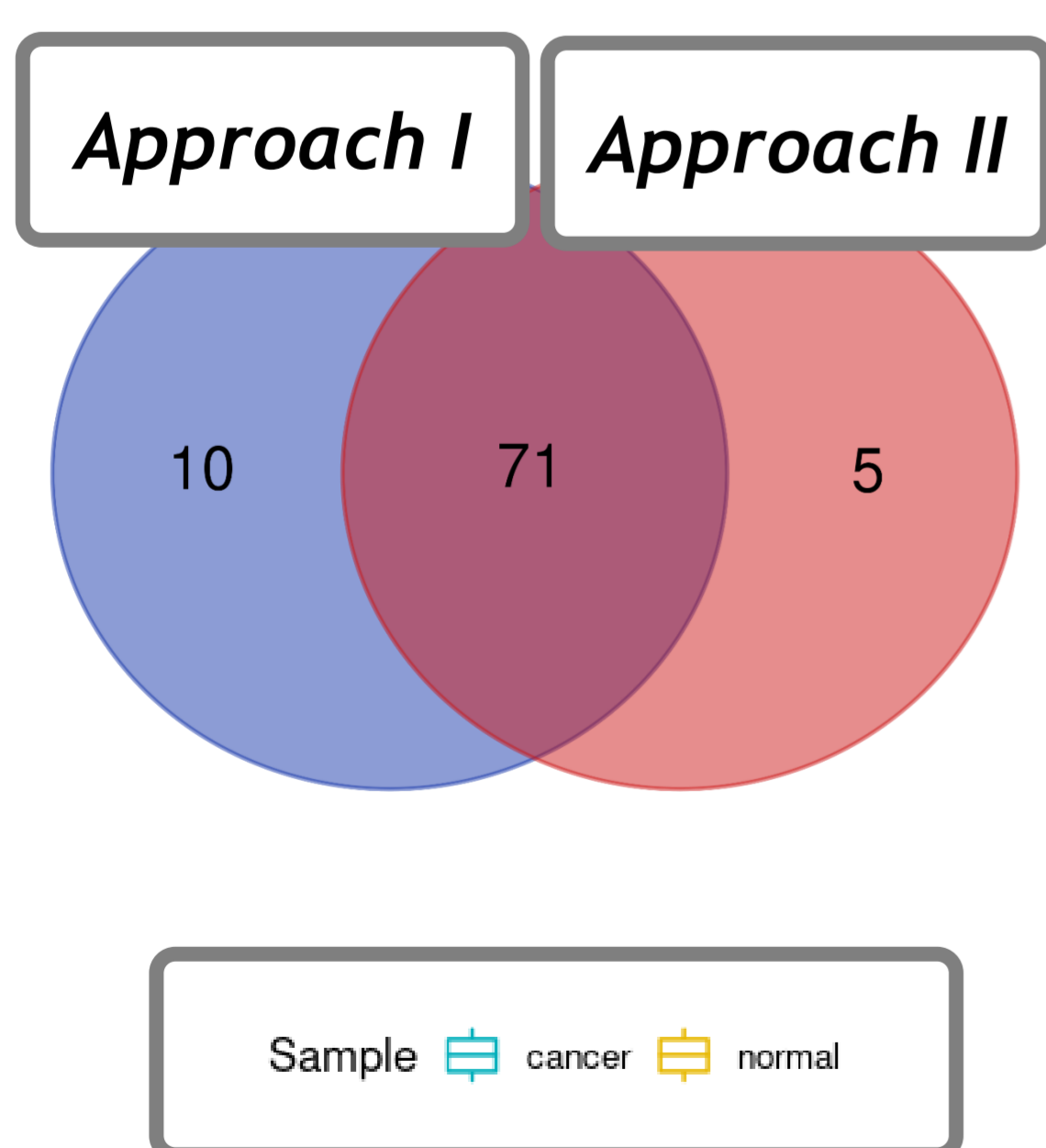
Results

GSEA:

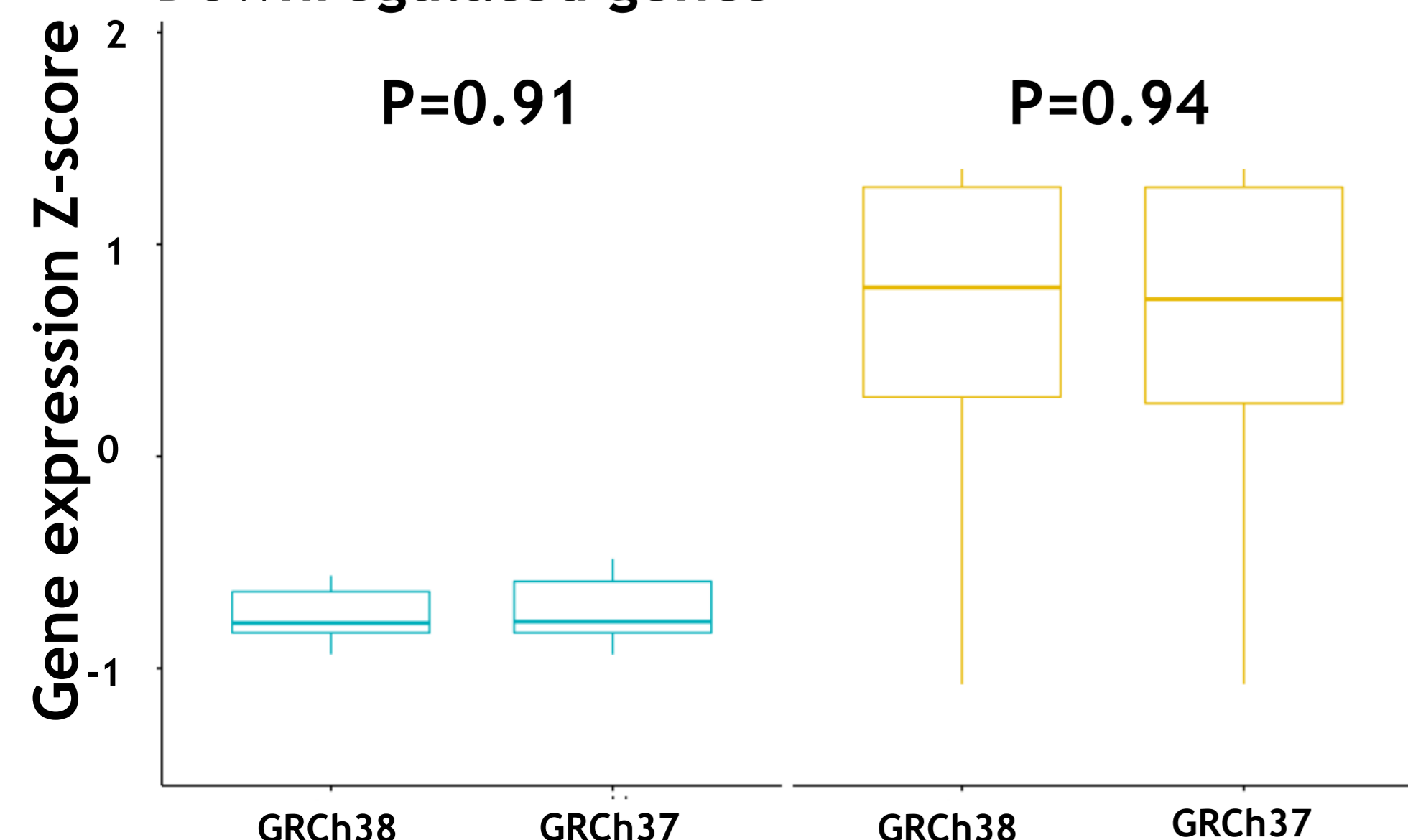
- Hallmark pathways



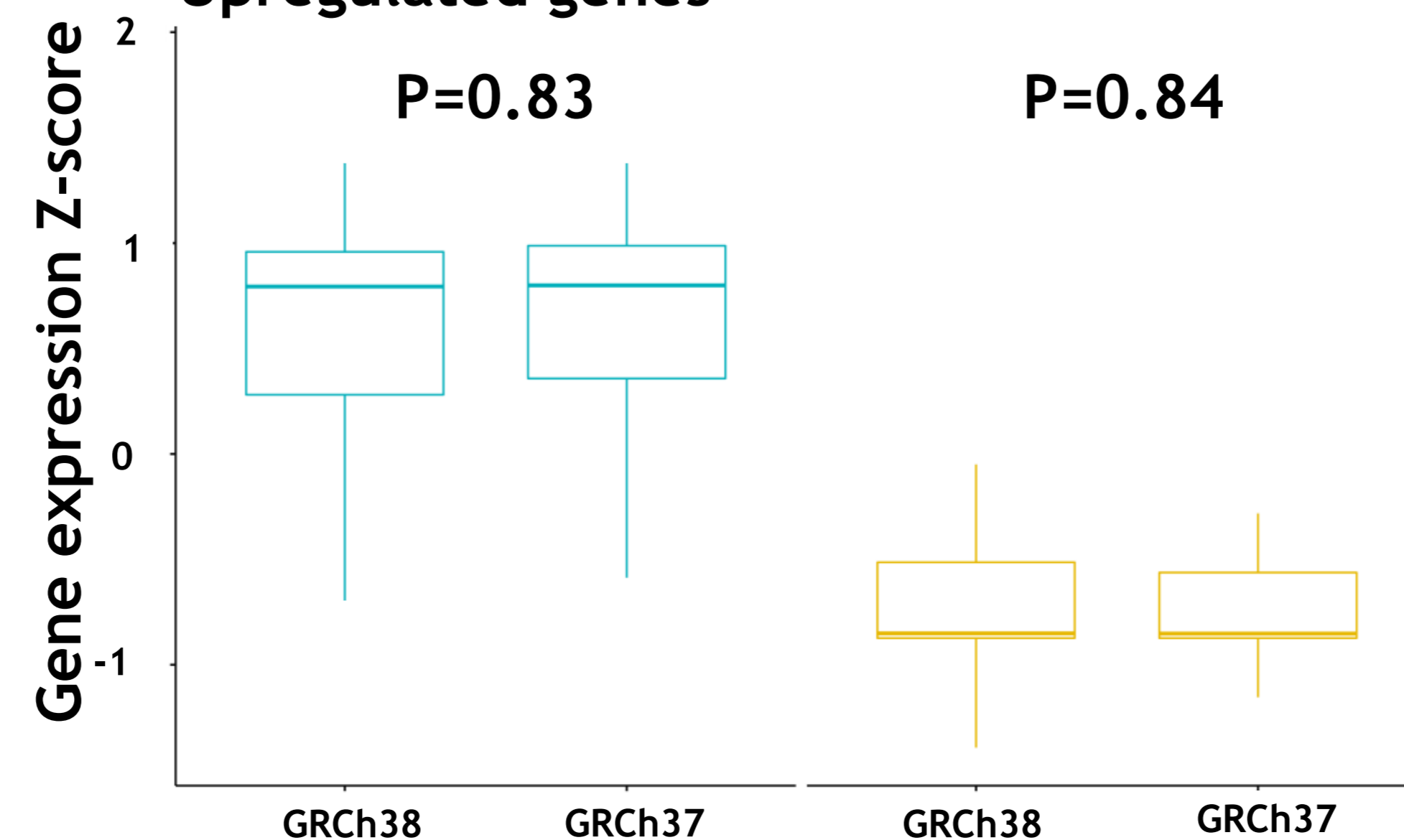
- KEGG pathways



Downregulated genes



Upregulated genes



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