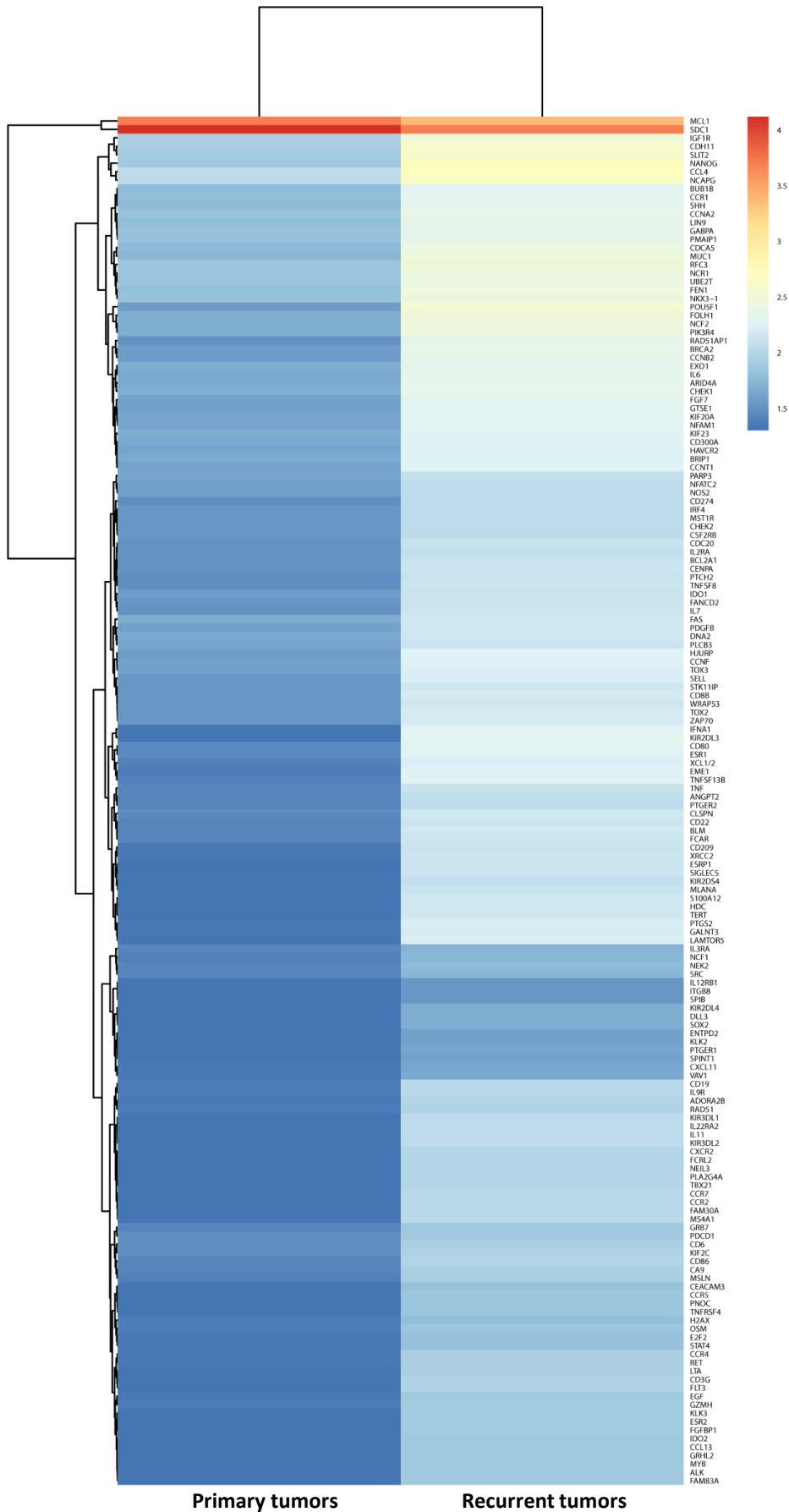
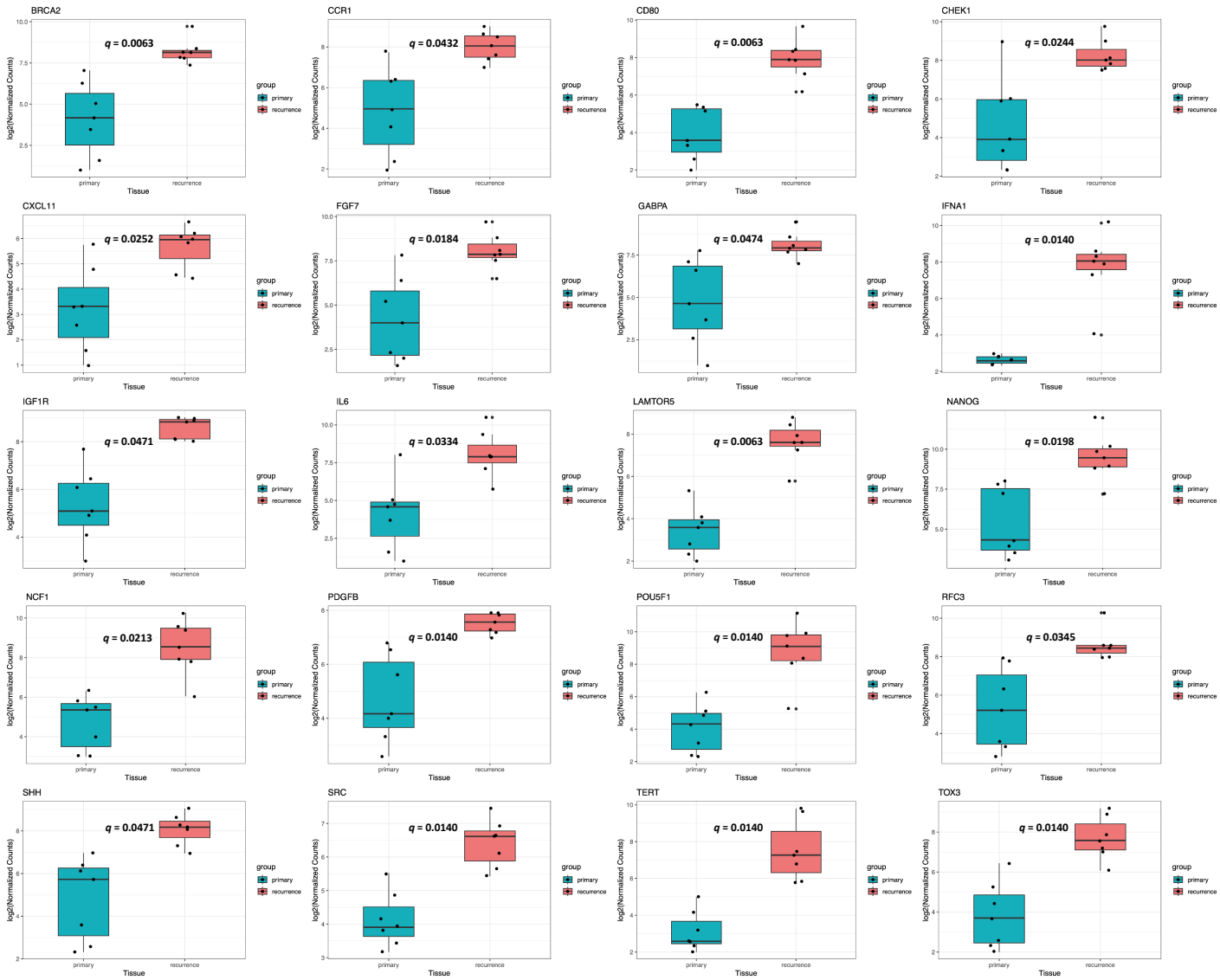


# Supplementary Fig. 1



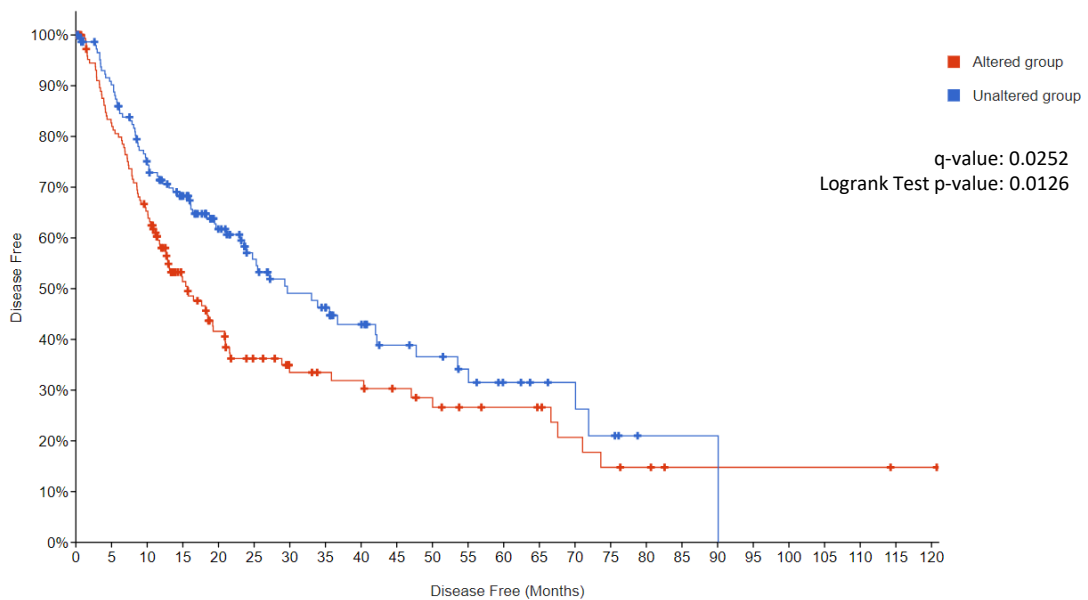
**Supplementary Figure 1. Differentially expressed genes (DEGs).** The heatmap shows the 162 DEGs of HCC recurrent post-transplant tumors compared with the paired primary tumors ( $q$ -value  $\leq 0.05$  and  $|\text{Fold change}| \geq 1.5$ ).

## Supplementary Fig. 2



**Supplementary Figure 2. Identification of 20 genes for recurrent HCC post-transplant in a pathway-centric modeling machine learning-based analysis.**

### Supplementary Fig. 3



**Number at risk (n)**

Altered group	157	119	93	55	40	30	23	21	20	17	15	12	11	10	7	5	4	2	2	2	2	2	1	1
Unaltered group	151	128	101	83	59	44	35	32	24	18	16	13	9	7	6	4	1	1	1	0	0	0	0	0

Survival plot summary	Number of cases, Total	Number of events	Median months disease free (95% CI)
Altered group	157	93	15.70 (12.61 - 20.93)
Unaltered group	151	73	29.66 (23.95 - 47.73)

**Supplementary Figure 3. Association between upregulation of 20-gene signatures and reduced disease-free survival in HCC patients.**