

Table S8. Performance of the three-marker combination (*GALR1*, *TLX1*, and *ZNF154*) in classifying TCGA tumors using cross validation (validation cohorts)

Type ^a	Tumor samples	Normal samples	Sensitivity		Specificity	
			<i>Mean^b</i>	<i>SD</i>	<i>Mean^b</i>	<i>SD</i>
BLCA	100	10	92.4%	2.1	80.0%	12.2
BRCA	338	48	92.7%	2.3	89.2%	6.0
COAD	137	19	95.6%	1.3	98.9%	2.4
HNSC	213	25	99.0%	0.6	94.4%	2.2
KIRC	148	80	84.9%	2.7	91.3%	3.2
KIRP	78	22	72.3%	14.7	71.8%	23.7
LIHC	75	25	92.3%	2.6	95.2%	5.2
LUAD	218	16	98.5%	1.5	88.8%	10.3
LUSC	179	21	98.9%	0.9	94.3%	2.1
PAAD*	32	4	95.6%	5.2	90.0%	13.7
PRAD	124	24	90.9%	1.7	83.3%	5.1
READ*	48	3	97.5%	2.3	100.0%	0.0
STAD*	130	1	98.6%	1.0	20.0%	44.7
UCEC	202	23	98.6%	0.5	94.8%	7.1

^a Tumor types are abbreviated as in Figure 1

^b TCGA datasets were randomly split in two five times and used as training/validation cohorts. The mean and SD report the average performance across the five iterations.

* Due to <10 samples in either the tumor or normal cohort, the performance results should be interpreted with caution

Abbreviations: SD = Standard Deviation