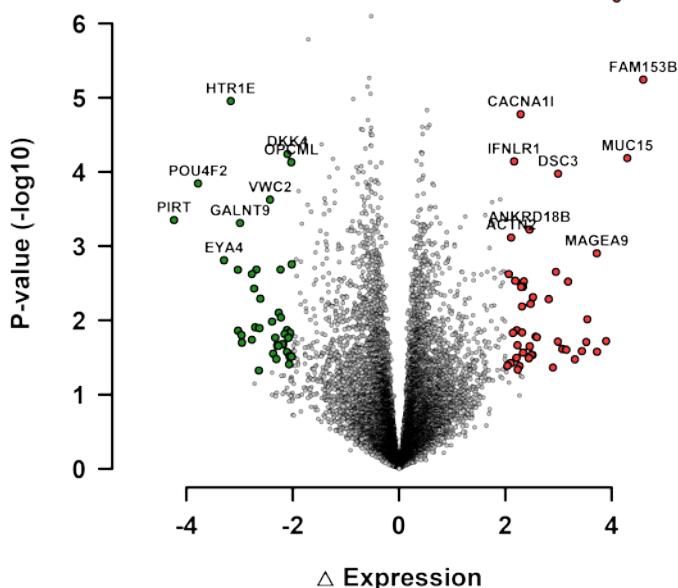


(A)



(B)

A total of 86 genes were significant. (red/green dot)

* Threshold for significance: $|\Delta \text{Expression}| > 2$ & $\text{P-value} < 0.05$

Class	Gene	High risk (avg expr.)	Non-high risk (avg expr.)	diff.expr	T-stat.	P-value	P-value (FDR)	Class	Gene	High risk (avg expr.)	Non-high risk (avg expr.)	diff.expr	T-stat.	P-value	P-value (FDR)
Overexpressed in High risk	FAM153A	1.780	-2.318	4.098	6.413	0.000	0.006	Underexpressed in High risk	HTR1E	-3.903	-0.737	-3.166	-5.212	0.000	0.020
	FAM153B	1.677	-2.924	4.601	5.681	0.000	0.018		DKK4	-4.904	-2.803	-2.101	-4.434	0.000	0.030
	CACNA1I	1.577	-0.715	2.292	4.889	0.000	0.023		OPCML	-0.608	1.417	-2.025	-4.670	0.000	0.032
	MUC15	0.632	-3.666	4.298	4.778	0.000	0.032		POU4F2	-3.866	-0.083	-3.783	-4.271	0.000	0.040
	IFNLR1	1.613	-0.554	2.167	4.743	0.000	0.032		VWC2	-4.768	-2.343	-2.425	-3.988	0.000	0.050
	DSC3	0.446	-2.548	2.994	4.276	0.000	0.037		PIRT	1.015	5.246	-4.231	-4.063	0.000	0.068
	ANKRD18B	-1.714	-4.172	2.459	3.998	0.001	0.070		GALNT9	-2.191	0.799	-2.989	-3.988	0.000	0.068
	ACTN2	4.811	2.699	2.113	3.637	0.001	0.077		EYA4	-1.373	1.918	-3.292	-3.454	0.002	0.100
	MAGEA9	0.847	-2.876	3.723	3.693	0.001	0.093		ERBB4	-2.470	-0.452	-2.018	-3.418	0.002	0.104
	MAGEC1	-1.120	-4.075	2.954	3.413	0.002	0.115		SLC17A6	-4.305	-2.075	-2.229	-3.265	0.002	0.113
	PPP4R4	1.226	-0.842	2.068	3.221	0.002	0.117		GALR1	-3.692	-1.009	-2.683	-3.411	0.002	0.113
	SLC5A12	0.328	-1.861	2.189	3.332	0.003	0.129		SPHKAP	-2.521	0.512	-3.033	-3.418	0.002	0.113
	CRB2	-0.162	-2.513	2.352	3.357	0.003	0.129		SLITRK3	-3.480	-0.714	-2.766	-3.306	0.002	0.117
	POTEM	-0.202	-5.204	3.184	3.484	0.003	0.129		CRABP1	-1.797	0.929	-2.726	-3.071	0.004	0.141
	TRPC5	-0.531	-2.867	2.336	3.146	0.004	0.138		EYA1	0.429	3.036	-2.607	-3.042	0.005	0.165
	LGSN	-0.421	-2.720	2.299	3.210	0.004	0.138		NLGN1	0.082	2.344	-2.262	-2.960	0.008	0.200
	ALX3	-1.354	-3.878	2.524	3.090	0.005	0.161		DIO3	-1.368	0.854	-2.222	-2.778	0.009	0.212
	SLCO1A2	0.773	-2.048	2.821	3.077	0.005	0.166		CSAG1	-3.097	-0.710	-2.387	-2.784	0.010	0.222
	OR4N4	-2.959	-5.437	2.478	3.154	0.006	0.176		FABP7	-1.346	1.360	-2.705	-2.726	0.012	0.242
	SAA1	-0.878	-3.193	2.316	2.922	0.007	0.181		NELL1	-2.484	0.142	-2.626	-2.715	0.013	0.245
	MAGEA4	-0.256	-3.801	3.545	2.858	0.010	0.216		DGKB	1.760	3.869	-2.109	-2.719	0.014	0.249
	NXF2B	0.226	-1.991	2.217	2.588	0.014	0.249		ADCYAP1	2.578	5.604	-3.026	-2.614	0.014	0.251
	CXCR5	1.524	-0.795	2.320	2.565	0.015	0.255		PRND	-0.032	2.017	-2.049	-2.628	0.015	0.255
	CCDC144NL	1.252	-0.891	2.143	2.617	0.015	0.255		INSM1	-0.058	2.094	-2.152	-2.530	0.015	0.259
	TUBA3C	-2.624	-5.197	2.573	2.670	0.017	0.266		CACNG7	-1.230	1.732	-2.962	-2.592	0.016	0.261
	WDR72	-1.554	-4.152	2.598	2.633	0.017	0.266		HOXC10	-1.062	1.265	-2.326	-2.562	0.017	0.267
	DDX3Y	3.472	-0.426	3.898	2.466	0.019	0.281		TMEFF2	1.963	4.041	-2.078	-2.551	0.017	0.268
	MAGEA11	-0.376	-3.367	2.991	2.536	0.019	0.281		SLC5A7	-2.869	-0.101	-2.768	-2.483	0.018	0.276
	KDM5D	2.707	-0.816	3.523	2.459	0.020	0.283		DLK1	1.573	4.527	-2.954	-2.505	0.020	0.286
	FGF10	1.859	-0.371	2.229	2.406	0.022	0.293		ARHGDIG	2.421	4.598	-2.177	-2.515	0.021	0.289
	NAA11	-3.193	-5.655	2.461	2.538	0.023	0.298		MAGEA2B	-4.671	-2.477	-2.194	-2.424	0.021	0.289
	MAGEA10	1.807	-1.270	3.077	2.371	0.025	0.306		SPOCK3	1.061	3.353	-2.292	-2.461	0.022	0.294
	UTY	1.430	-1.718	3.148	2.350	0.025	0.308		MIA	1.669	3.938	-2.269	-2.409	0.022	0.295
	USP9Y	2.468	-0.977	3.445	2.331	0.026	0.315		CLDN19	-3.622	-1.514	-2.108	-2.302	0.027	0.318
	RPS4Y1	4.865	1.135	3.730	2.318	0.027	0.316		CGA	-3.052	-0.683	-2.369	-2.285	0.028	0.323
	XAGE1A	-2.755	-5.090	2.335	2.428	0.027	0.320		SV2C	1.154	3.213	-2.058	-2.303	0.031	0.331
	XAGE1D	-2.199	-4.714	2.515	2.389	0.029	0.327		GABRG1	-1.989	0.035	-2.024	-2.273	0.031	0.331
	XAGE1E	-2.597	-5.090	2.493	2.390	0.030	0.328		NKAIN4	-1.127	1.179	-2.306	-2.265	0.033	0.341
	CA1	-0.849	-3.064	2.215	2.280	0.032	0.335		CDH10	-0.579	1.488	-2.067	-2.177	0.039	0.360
	XAGE1C	-2.595	-5.040	2.446	2.343	0.032	0.337		FOXD3	0.190	2.827	-2.637	-2.089	0.048	0.386

Figure S4. (A) Volcano plot representing the result of DEG (n = 86). Red and green dots indicate significantly over or under expressed genes, respectively, in high risk group. (B) List of DEGs (n = 86). While 46 genes were overexpressed, 40 genes were under-expressed, in high risk group. The significance was determined by two-group T-test (P-value < 0.05) and difference of average expression between risk-groups > 2.

(C)

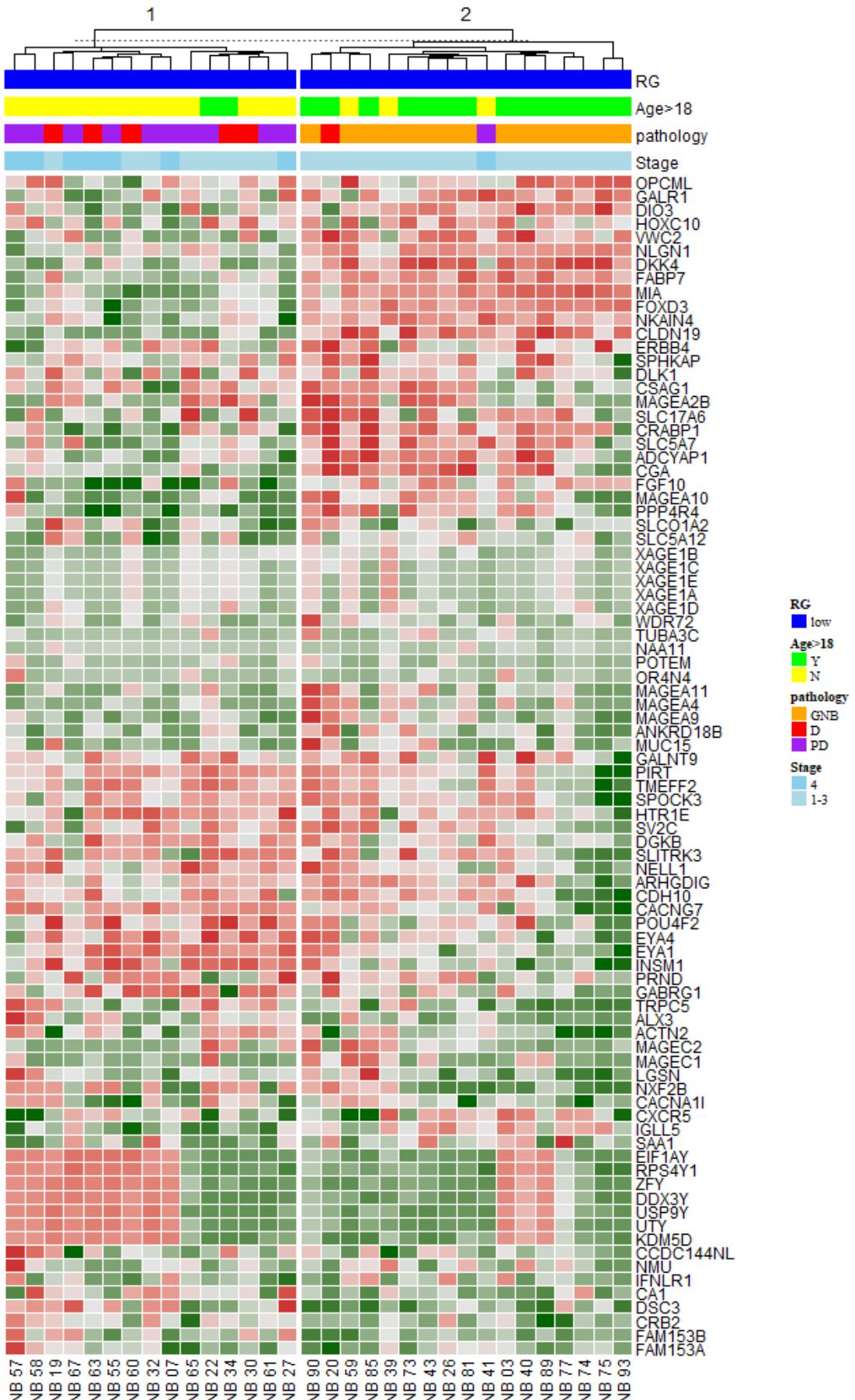


Figure S4. (C) Unsupervised clustering of non-high-risk group. Unsupervised clustering of non-high-risk group revealed two distinct subgroups showing clear differences in age, pathologic differentiation and stage.