Additional file 3

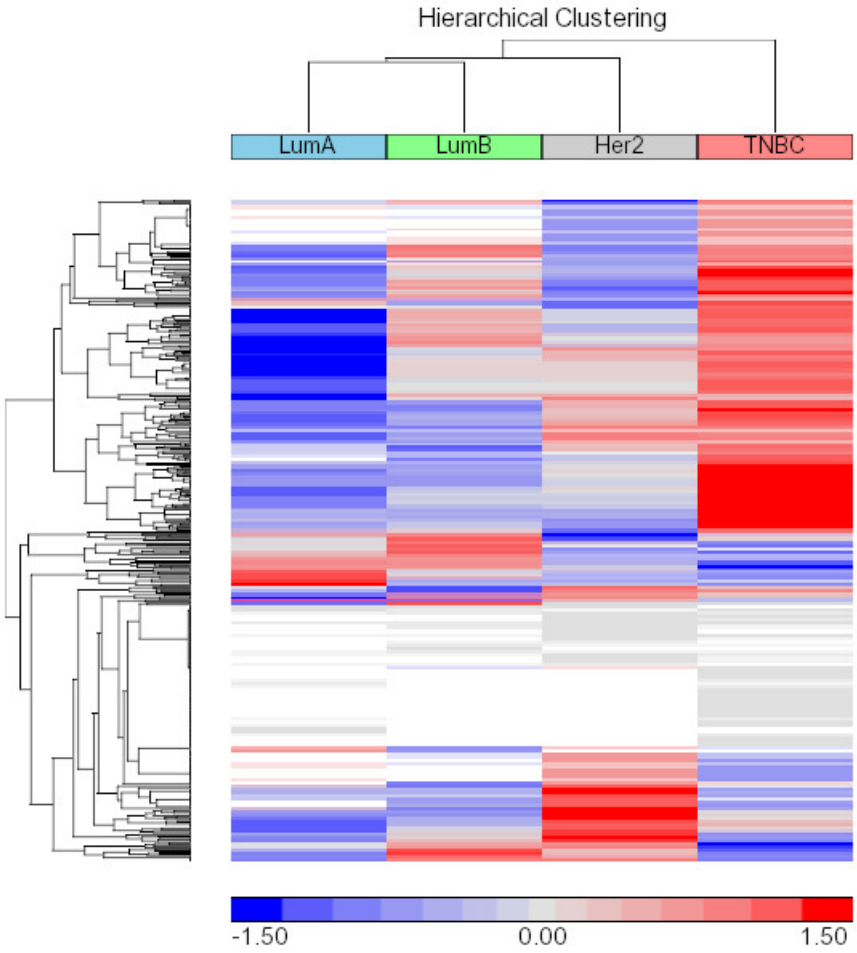


Fig. S1. **Yin pathway significant score profiling among LumA, LumB, Her2, TNBC breast cancer subtype using TCGA data.**

The significant values of Yin (upregulated) pathways (**rows, C2 canonical pathways v5.2**) were transformed into –log10 FDRs and standardized by mean of 0 and standard deviation of 1. The hierarchical Euclidean clustering with complete linkage was performed on breast cancer subtypes (**columns**) using the pathway significant values.

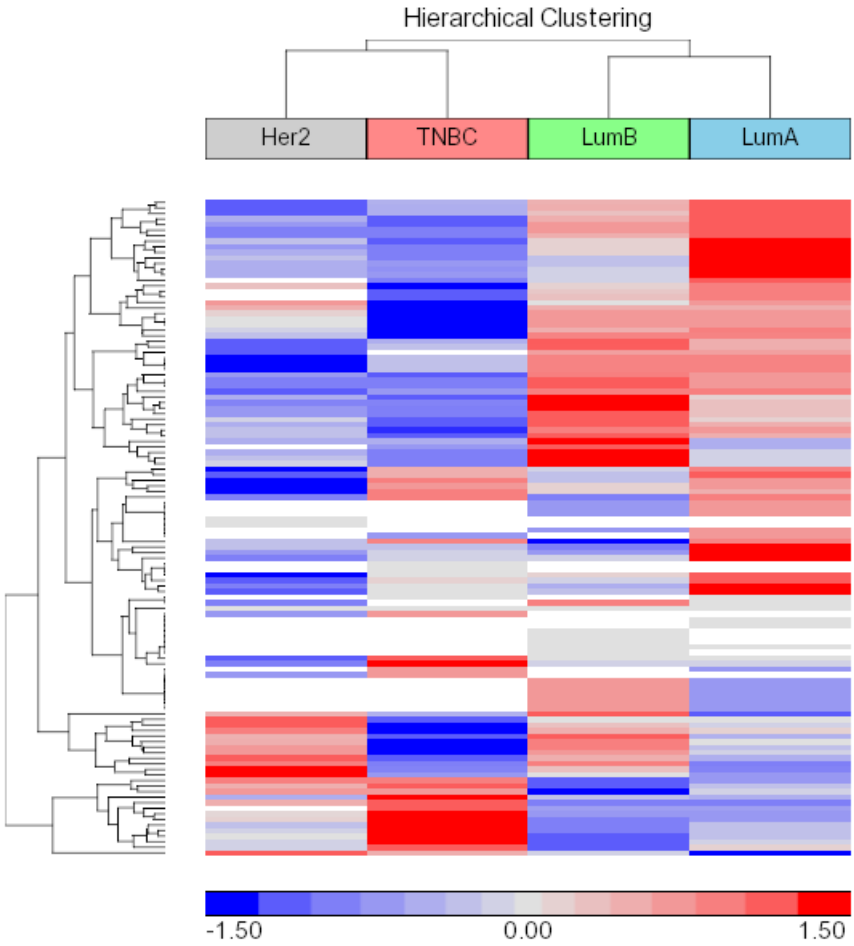


Fig. S2. **Yang pathway significant score profiling among LumA, LumB, Her2, TNBC breast cancer subtype using TCGA data.**

The significant values of Yang (upregulated) pathways (**rows, C2 biocarta pathways v5.2**) were transformed into –log10 FDRs and standardized by mean of 0 and standard deviation of 1. The hierarchical Euclidean clustering with complete linkage was performed on breast cancer subtypes (**columns**) using the pathway significant values.

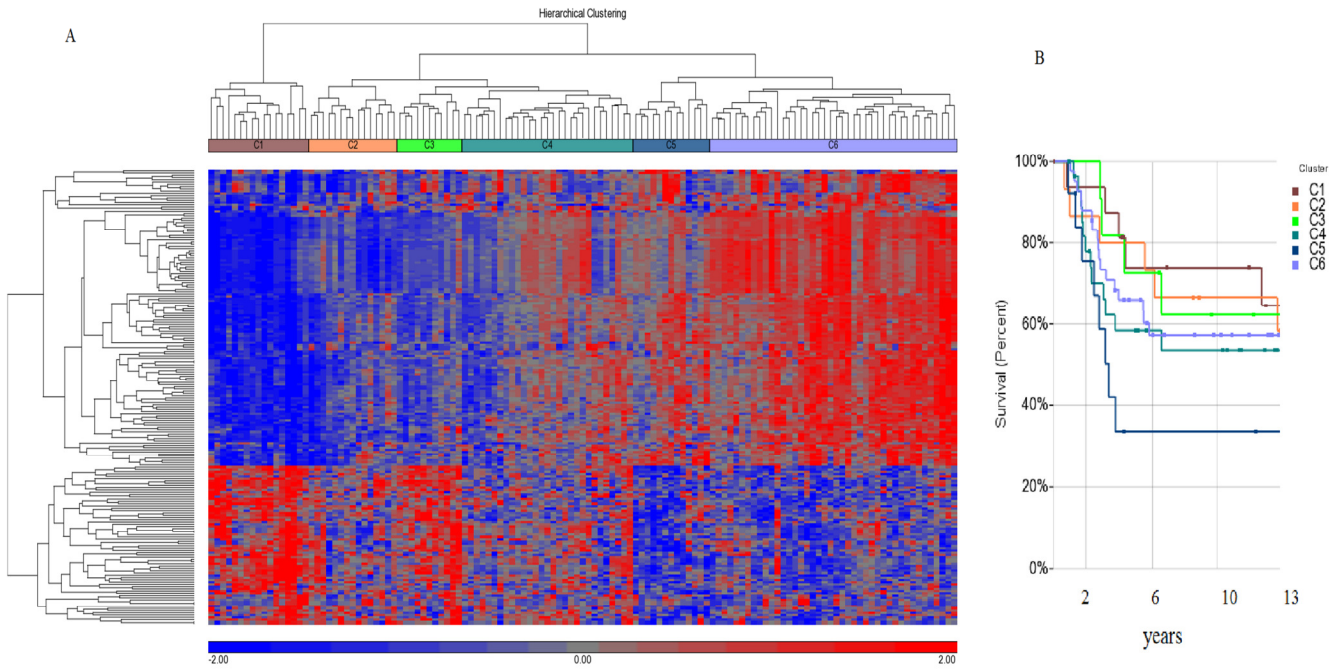


Fig. S3 Yin Yang pathway classifier for TNBCs.

The "core" genes selected from 133 Yin pathways (different cell cycle phage pathways) and 71 top Yang pathways. The weighted sum score was calculated for each of the 204 pathways. The 126 TNBC samples of the METABRIC data set were clustered by the pathways scores using 2D Euclidean complete linkage (A). The clinical outcomes of the 6 clusters were evaluated by the Cox regression model using Partek Genomic Suite.

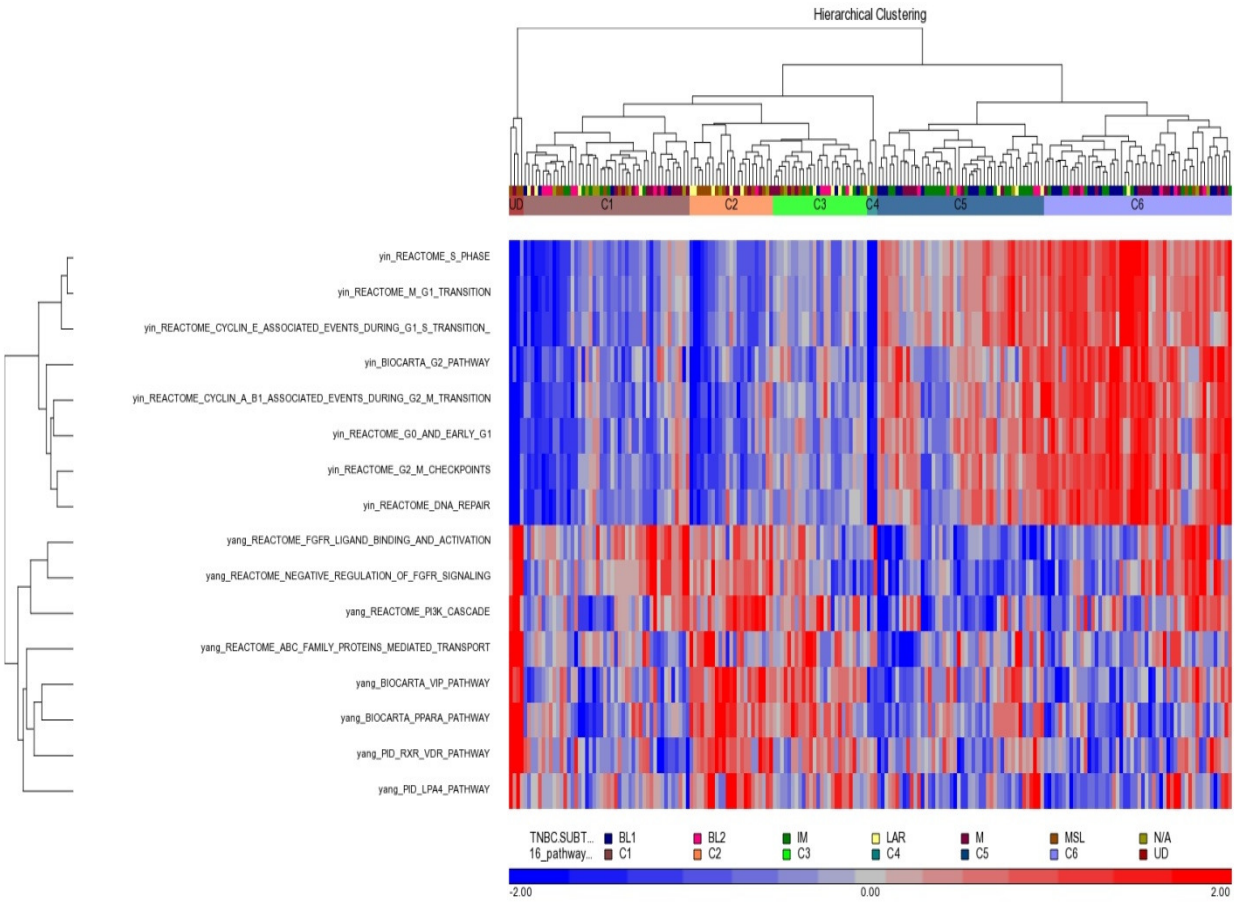
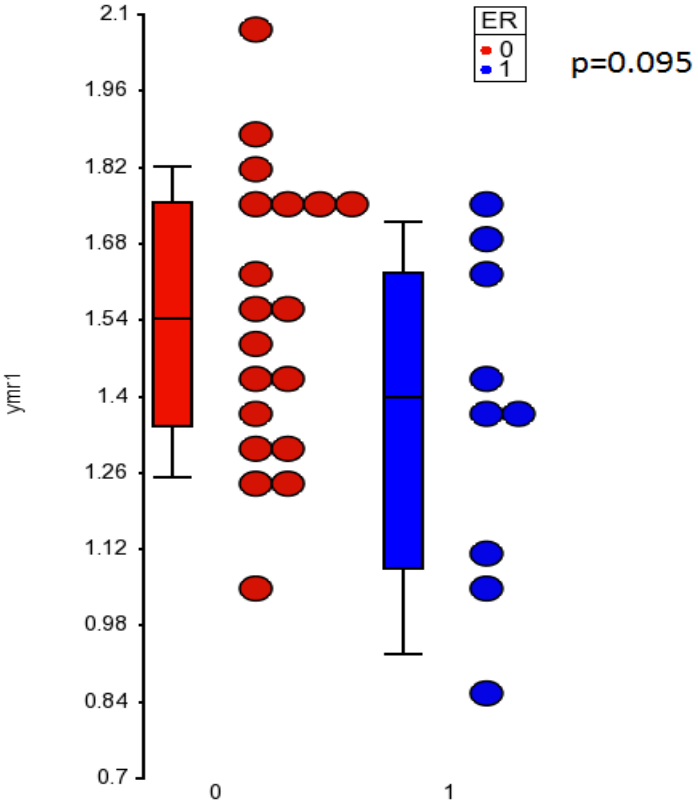


Fig. S4. **Pathway classifier comparison**. 16-pathway classifier was applied to the 201 TNBC samples that were subtyped by previous Lehmann method. Color boxes with C1 to C6 were clusters by 16 pathway scores. The color bars above represented previous 7 subtypes.



Access	breast cancer cell_line	2-pathway ymr	ER(+/1,-/0)
GSM276061	BT474	1.400	1
GSM276035	MDAMB361.1	1.032	1
GSM276025	ZR75	1.085	1
GSM276018	HCC1428	1.679	1
GSM276007	MDAMB415	1.412	1
GSM276000	BT474EI	0.824	1
GSM275992	T47D	1.760	1
GSM275979	BT483	1.374	1
GSM275978	MCF7	1.626	1
GSM276032	UACC812	1.068	0
GSM276028	HCC38	1.446	0
GSM276027	HCC1569	1.748	0
GSM276023	HCC1143	1.792	0
GSM276021	HCC1500	1.247	0
GSM276019	HCC1954	1.763	0

GSM276015	SKBR31	1.282	0
GSM276013	HCC70	1.643	0
GSM276009	MDAMB468	1.779	0
GSM276003	MDAMB453	1.258	0
GSM275998	MDA361	1.398	0
GSM275997	HCC1937	1.738	0
GSM275994	MDA468	1.514	0
GSM275993	MDA231	1.562	0
GSM275989	MDA435	2.105	0
GSM275986	MDA436	1.543	0
GSM275983	SKBR3	1.293	0
GSM275977	HS578T	1.433	0
GSM275974	BT549	1.853	0

Fig. S5 YMR scores of FOXM1 and PPARa pathway among Breast caner cell lines (GSE10890). 28 unique cell lines with known ER marker status were selected. The cell line marker information was from Neve RM, et al (Cancer Cell. 2006, 10(6): 515–527).

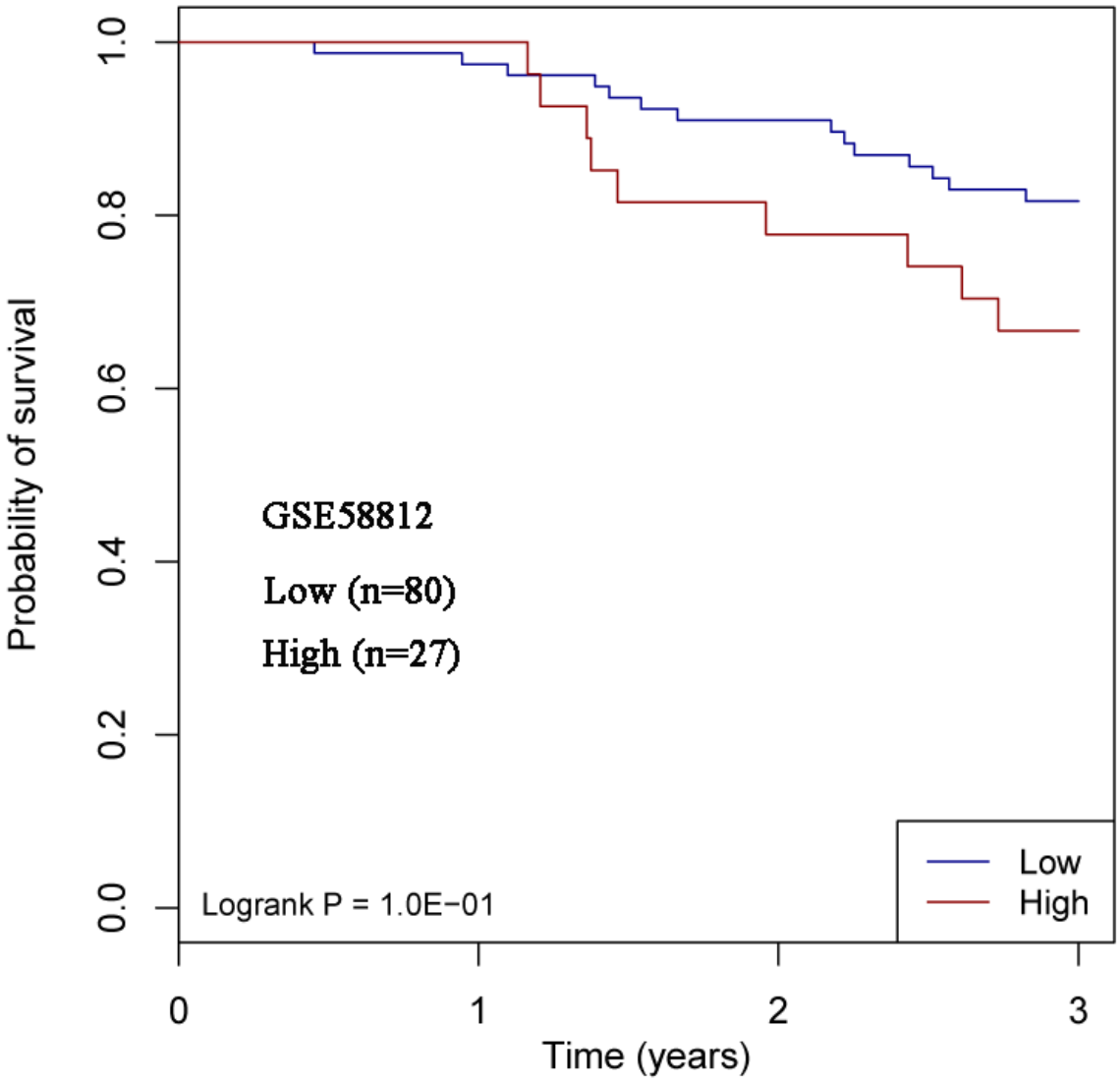


Fig. S6. FOXM1 and PPARa YMR model for GSE58812 data set. The patients were stratified into low and high risk but with no significance.

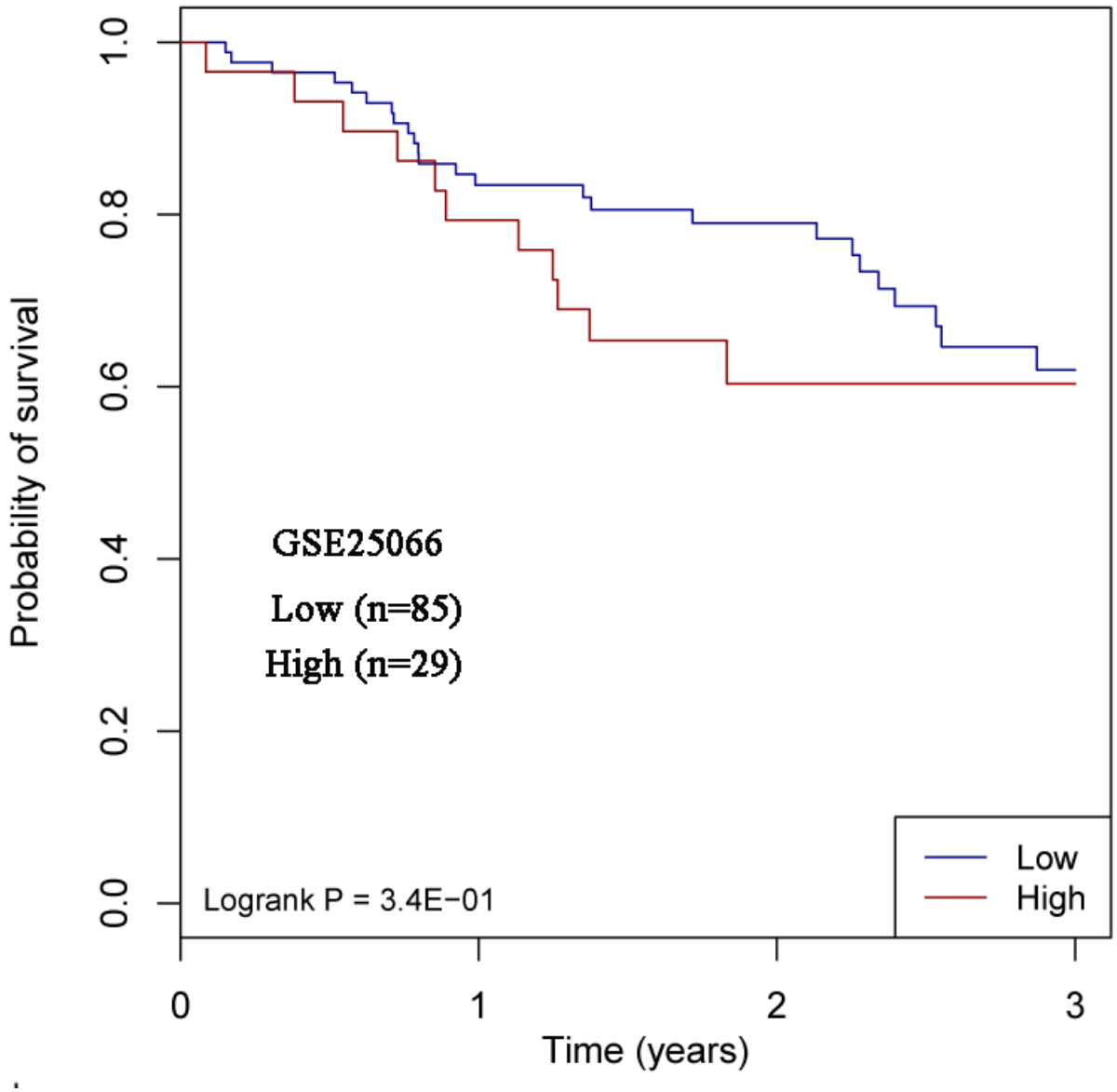


Fig. S7. FOXM1 and PPARa YMR model for GSE25066 data set. The patients were stratified into low and high risk but with no significance. 100% of patients underwent therapy.