Supplemental Materials: High Expression of NRF2 Is Associated with Increased Tumor-Infiltrating Lymphocytes and Cancer Immunity in ER-Positive/HER2-Negative Breast Cancer

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Table S1. Correlation of the NRF2 expression with gene expressions of Hallmark_apoptosis gene set in ER-positive/HER2-negative breast cancer in the METABRIC and GSE96058 cohorts. Spearman's rank correlation coefficient was used to the analysis.

	METABRIC		GSE96058			METABRIC		GSE96058	
Genes	***r***	***p***	***r***	***p***	**Genes**	***r***	***p***	***r***	***p***
ADD1	-0.401	<0.01	0.24	<0.01	GPX1	0.254	<0.01	-0.025	0.22
AIFM3	0.143	<0.01	-0.113	<0.01	GPX3	0.068	0.01	0.293	<0.01
ANKH	0.184	<0.01	0.116	<0.01	GPX4	-0.13	<0.01	-0.102	<0.01
ANXA1	0.556	<0.01	0.329	<0.01	GSN	0.297	<0.01	0.373	<0.01
APP	0.268	<0.01	0.087	<0.01	GSR	-0.034	0.21	0.061	<0.01
ATF3	0.311	<0.01	0.265	<0.01	GSTM1	0.01	0.72	0.034	0.1
AVPR1A	0.044	0.1	0.227	<0.01	GUCY2D	-0.043	0.12	0.013	0.51
BAX	-0.076	<0.01	-0.188	<0.01	H1F0	-0.134	<0.01	-0.056	<0.01
BCAP31	-0.288	<0.01	-0.225	<0.01	HGF	0.114	<0.01	0.286	<0.01
BCL10	0.508	<0.01	0.282	<0.01	HMGB2	0.212	<0.01	-0.034	0.1
BCL2L1	-0.113	<0.01	-0.134	<0.01	HMOX1	-0.016	0.57	0.004	0.83
BCL2L10	0.041	0.13	0.138	<0.01	HSPB1	-0.174	<0.01	-0.151	<0.01
BCL2L11	0.145	<0.01	0.278	<0.01	IER3	0.009	0.74	0.043	0.04
BCL2L2	0.181	<0.01	0.268	<0.01	IFITM3	0.174	<0.01	0.109	<0.01
BGN	-0.104	<0.01	0	0.98	IFNB1	0.042	0.12	-0.044	0.03
BID	0.1	<0.01	0.057	<0.01	IFNGR1	-	-	0.408	<0.01
BIK	-0.124	<0.01	-0.091	<0.01	IGF2R	-0.177	<0.01	0.129	<0.01
BIRC3	0.126	<0.01	0.246	<0.01	IGFBP6	0.242	<0.01	0.257	<0.01
BMF	-0.184	<0.01	0.155	<0.01	IL18	-	-	0.11	<0.01
BMP2	0.005	0.85	0.263	<0.01	IL1A	0.135	<0.01	0.072	<0.01
BNIP3L	0.296	<0.01	0.186	<0.01	IL1B	0.319	<0.01	0.173	<0.01
BRCA1	-0.219	<0.01	-0.088	<0.01	IL6	0.3	<0.01	0.309	<0.01
BTG2	0.2	<0.01	0.246	<0.01	IRF1	-0.005	0.87	0.125	<0.01
BTG3	0.36	<0.01	0.18	<0.01	ISG20	0.019	0.48	0.003	0.89
CASP1	0.319	<0.01	0.265	<0.01	JUN	0.209	<0.01	0.26	<0.01
CASP2	0.194	<0.01	0.115	<0.01	KRT18	-0.117	<0.01	-0.149	<0.01
CASP3	0.039	0.15	0.088	<0.01	LEF1	0.149	<0.01	0.17	<0.01
CASP4	0.425	<0.01	0.32	<0.01	LGALS3	0.37	<0.01	0.21	<0.01
CASP6	0.396	<0.01	0.103	<0.01	LMNA	-0.306	<0.01	0.152	<0.01
CASP7	0.345	<0.01	0.174	<0.01	LUM	0.472	<0.01	0.078	<0.01
CASP8	0.416	<0.01	0.284	<0.01	MADD	-0.545	<0.01	0.085	<0.01
CASP9	0.115	<0.01	0.139	<0.01	MCL1	0.471	<0.01	0.273	<0.01
CAV1	0.449	<0.01	0.329	<0.01	MGMT	-0.018	0.51	-0.034	0.09
CCNA1	0.07	<0.01	0.208	<0.01	MMP2	0.13	<0.01	0.095	<0.01
CCND1	-0.301	<0.01	-0.045	0.03	NEDD9	0.314	<0.01	0.226	<0.01
CCND2	0.323	<0.01	0.231	<0.01	NEFH	0.05	0.07	0.107	<0.01
CD14	0.278	<0.01	0.147	<0.01	PAK1	-0.092	<0.01	0.02	0.32
CD2	-	-	0.15	<0.01	PDCD4	0.153	<0.01	0.209	<0.01
CD2	0.198	<0.01	.	.	PDGFRB	0.104	<0.01	0.139	<0.01
CD38	0.241	<0.01	0.158	<0.01	PEA15	-0.022	0.42	0.077	<0.01
CD44	-	-	0.095	<0.01	PLAT	0.026	0.33	0.038	0.06
CD44	0.033	0.22	.	.	PLCB2	-0.137	<0.01	0.121	<0.01
CD69	0.364	<0.01	0.244	<0.01	PMAIP1	0.115	<0.01	0.019	0.35
CDC25B	-0.241	<0.01	-0.028	0.16	PPP2R5B	-0.278	<0.01	0.026	0.19
CDK2	-0.03	0.27	0.016	0.42	PPP3R1	0.08	<0.01	0.24	<0.01
CDKN1A	0.161	<0.01	0.079	<0.01	PPT1	0.267	<0.01	0.129	<0.01

CDKN1B	0.416	<0.01	0.104	<0.01	PRF1	0.17	<0.01	0.185	<0.01
CFLAR	-	-	0.384	<0.01	PSEN1	0.37	<0.01	0.056	<0.01
CLU	0.164	<0.01	0.054	<0.01	PSEN2	-0.296	<0.01	-0.113	<0.01
CREBBP	0.153	<0.01	0.212	<0.01	PTK2	-0.316	<0.01	0.01	0.63
CTH	0.306	<0.01	0.119	<0.01	RARA	-0.338	<0.01	-0.081	<0.01
CTNNB1	0.388	<0.01	0.198	<0.01	RELA	0.132	<0.01	0.095	<0.01
CYLD	0.012	0.65	0.131	<0.01	RETSAT	-0.03	0.27	0.065	<0.01
DAP	-0.048	0.08	-0.039	0.05	RHOB	0.321	<0.01	0.092	<0.01
DAP3	0.04	0.15	-0.083	<0.01	RHOT2	-0.326	<0.01	-0.142	<0.01
DCN	0.471	<0.01	0.229	<0.01	RNASEL	-	-	0.165	<0.01
DDIT3	0.029	0.28	0.071	<0.01	ROCK1	0.536	<0.01	0.313	<0.01
DFFA	-0.038	0.17	0.223	<0.01	SAT1	0.285	<0.01	0.154	<0.01
DIABLO	0.056	0.04	-0.059	<0.01	SATB1	0.082	<0.01	0.262	<0.01
DNAJA1	0.27	<0.01	0.04	0.05	SC5D	-	-	0.133	<0.01
DNAJC3	-0.023	0.39	0.129	<0.01	SC5DL	0.121	<0.01	.	.
DNM1L	0.346	<0.01	0.056	<0.01	SLC20A1	-0.039	0.15	0.169	<0.01
DPYD	0.635	<0.01	0.393	<0.01	SMAD7	0.255	<0.01	0.084	<0.01
EBP	-0.112	<0.01	-0.254	<0.01	SOD1	0.136	<0.01	-0.119	<0.01
EGR3	0.265	<0.01	0.25	<0.01	SOD2	0.265	<0.01	0.257	<0.01
EMP1	0.365	<0.01	0.269	<0.01	SPTAN1	-0.165	<0.01	0.114	<0.01
ENO2	-0.247	<0.01	-0.131	<0.01	SQSTM1	-0.244	<0.01	-0.038	0.06
ERBB2	-0.296	<0.01	0.041	0.04	TAP1	-0.064	0.02	-0.002	0.94
ERBB3	-0.258	<0.01	-0.041	0.05	TGFB2	0.305	<0.01	0.164	<0.01
EREG	-	-	0.156	<0.01	TGFBR3	0.139	<0.01	0.322	<0.01
ETF1	0.427	<0.01	0.112	<0.01	TIMP1	-0.107	<0.01	0.113	<0.01
F2	-	-	-0.04	0.05	TIMP2	0.231	<0.01	0.105	<0.01
F2R	-	-	0.293	<0.01	TIMP3	0.195	<0.01	0.064	<0.01
FAS	0.477	<0.01	0.28	<0.01	TNF	-0.079	<0.01	0.119	<0.01
FASLG	0.087	<0.01	0.142	<0.01	TNFRSF12A	0.244	<0.01	0.059	<0.01
FDXR	0.095	<0.01	-0.175	<0.01	TNFSF10	0.165	<0.01	0.22	<0.01
FEZ1	0.209	<0.01	0.194	<0.01	TOP2A	-0.135	<0.01	-0.162	<0.01
GADD45A	0.321	<0.01	0.24	<0.01	TSPO	0.304	<0.01	-0.109	<0.01
GADD45B	0.149	<0.01	0.092	<0.01	TXNIP	0.295	<0.01	0.292	<0.01
GCH1	0.105	<0.01	-0.092	<0.01	VDAC2	0.252	<0.01	-0.055	<0.01
GNA15	-0.093	<0.01	0.074	<0.01	WEE1	0.327	<0.01	0.176	<0.01
					XIAP	-	-	0.091	<0.01

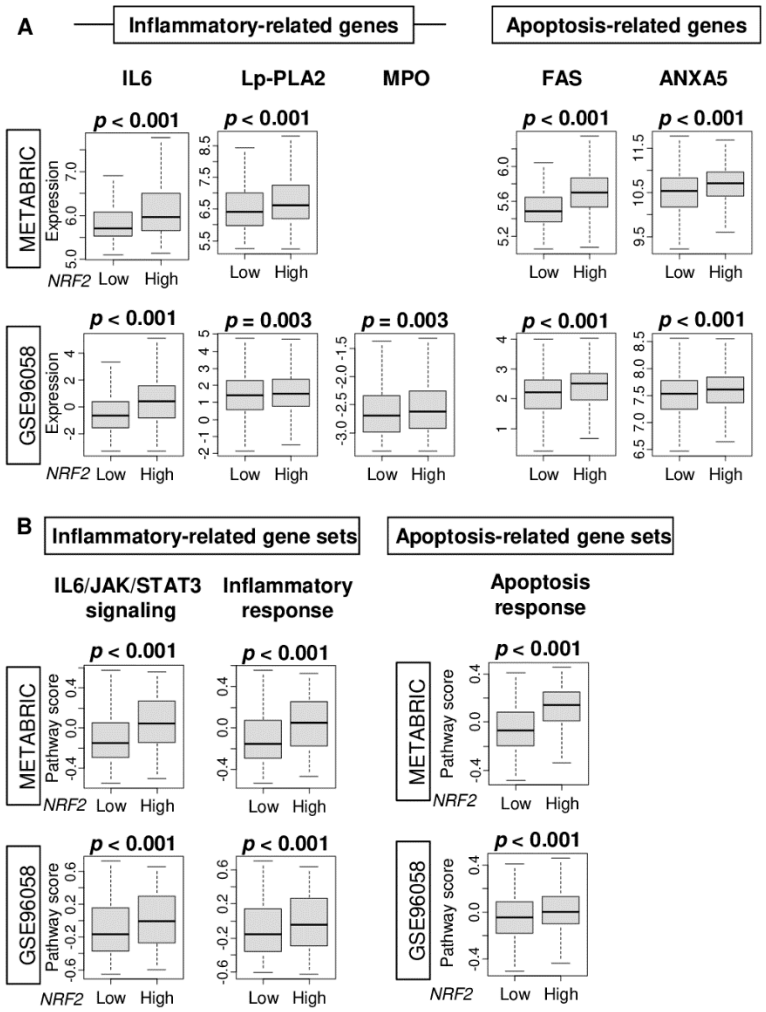

Figure S1. Association of the NRF2 with gene expression and pathway score of inflammatory- and apoptosis-related markers in ER+/HER2- breast cancer in the METABRIC and GSE96058 cohorts. Boxplots comparing (A) inflammatory-related genes (IL6, PLA2G7, and MPO) and apoptosis-related genes (FAS and ANXA5), and (B) inflammatory-related gene sets (IL6/JAK/STAT3 signaling), and inflammatory response pathways, and apoptosis pathway gene setas calculated by the GSVA algorithm, by low and high NRF2 groups. The cut-off of top tertile of NRF2 expression was considered as NRF2 high and low within each cohort. One-way ANOVA test was used for comparison. METABRIC cohort do not have MPO expression data.