

S1 Table. **The genes that have been reported in the works of literature.** The 51 genes have been confirmed in the works of literature to be indeed related to the occurrence and prognosis of breast cancer.

Biomarker	Description	Reported literatures	KEGG pathway	GWAS Catalog	Gene ORGA-Nizer
ADRB1	ADRB1 is identified as a potential biomarker for breast cancer by the co-analysis of tumor mutational burden and immune infiltration.	[1]			
ALDH3A1	Cellular levels of ALDH3A1 as predictors of therapeutic responses to cyclophosphamide-based chemotherapy of breast cancer.	[2]	✓		
APOBEC3D	APOBEC3D is differentially expressed in the lymph nodes of patients with metastatic breast cancer.	[3]			
ARID1B	ARID1B is lost in breast cancer.	[4]			✓
BCL2A1	KCNN4 induces multiple chemoresistance in breast cancer by regulating BCL2A1.	[5, 6, 7]			
BMPR1A	Knockdown of BMPR1A of breast cancer cells suppresses their production of RANKL via p38 pathway and inhibits cancer-induced osteoclastogenesis.	[8, 9, 10]		✓	
C1orf226	C1orf226 is a downregulated gene in the Triple-Negative Breast Cancer (TNBC) tissues compared to normal breast tissues.	[11, 12]			
CGA	The CGA gene as new predictor of the response to endocrine therapy in ER α -positive postmenopausal breast cancer patients.	[13]	✓		
CHGA	Diseases associated with CHGA include acinar cell carcinoma and tubular adenocarcinoma. Among its related pathways are defensins and innate immune system.	[14, 15]			
DCUN1D4	An important paralog of DCUN1D4 is DCUN1D5, DCUN1D5 is significantly hypermethylated in the parous breast.	[16]			
DERL1	DERL1 mRNA overexpression correlates with positive lymph node metastasis in breast cancer.	[17]			
ESRRG	miR-378 targets endogenous ESRRG and GABPA and reduces their expression in human breast cancer cells.	[18]	✓		
FGF6	FGF6 amplifies in human breast-tumors and increases cell death in breast cancer cell lines.	[19]	✓	✓	✓
FGF7	The fibroblast growth factor binding protein is a novel interaction partner of FGF7 and regulates FGF activity: implications for epithelial repair.	[20, 21, 22]	✓		
FOXQ1	FOXQ1 is differentially expressed across breast cancer subtypes with low expression associated with poor overall survival.	[23, 24, 25, 26]			
GAL3ST2	GAL3ST2 is present in NMMuMG and two human breast cancer cell lines, and it is more strongly expressed in more metastatic tumors.	[27]			
GP1BA	the gene expression of GP1BA is shared by all transcriptomic subgroups of breast cancer, suggesting that there is a gene expression program that is common to all breast metastases.	[28]			

Biomarker	Description	Reported literatures	KEGG pathway	GWAS Catalog	Gene ORGA-Nizer
HES3	The anti-tumor efficacy of an enzyme involved in Notch receptor activation can be predicted by the level of expression of HES3 in breast cancer xenograft models.	[29, 30]			
HES5	HES5 is a disease-specific gene in breast cancer.	[31]	✓		
HLA-G	HLA-G expression in classical HLA class I-negative tumors is of prognostic value for clinical outcome of early breast cancer patients.	[32, 33, 34, 35]			
IGFBPL1	Insulin-like growth factor binding protein (IGFBP)-related IGFBPL1 has an independent function in suppressing breast cancer phenotype.	[36, 37, 38]			
KDM6A	Chemotherapy-induced S100A10 recruits KDM6A to facilitate OCT4-mediated breast cancer stemness.	[39, 40]			✓
KLHDC7B	A Kelch domain-containing KLHDC7B acts oppositely on breast cancer cell proliferation via the interferon signaling pathway.	[41]			
KRT15	Low KRT15 expression is associated with poor prognosis in patients with breast invasive carcinoma	[42]			
MAL2	MAL2 drives immune evasion in breast cancer by suppressing tumor antigen presentation.	[43, 44]			
MID2	MORC4 promotes chemoresistance of luminal A/B breast cancer via STAT3-mediated MID2 upregulation.	[45]			
MT3	Increase in fluidity in the membrane of MT3 breast cancer cells correlates with enhanced cell adhesion in vitro.	[46]			
NFKB2	Diseases associated with NFKB2 include immunodeficiency, common variable, 10 and common variable immunodeficiency.	[47, 48]	✓		
NR1H4	NR1H4 is a member of the nuclear receptor superfamily of ligand-dependent transcription factors, it has been recently detected in breast cancer cell lines and tissue specimens.	[49, 50, 51, 52]			
NRAS	MicroRNA-22 suppresses breast cancer cell growth and increases paclitaxel sensitivity by targeting N-RAS.	[53, 54]			✓
PARP3	PARP3 inhibitors ME0328 and olaparib potentiate vinorelbine sensitization in breast cancer cell lines.	[55]	✓		
PCMT1	Breast cancer patients with higher PCMT1 expression have significantly lower survival rates than those with lower PCMT1 expression.	[56]			
PGK1	PGK1 is a potential survival biomarker and invasion promoter by regulating the HIF-1 α -Mediated epithelial-mesenchymal transition process in breast cancer.	[57, 58, 59]			
PIGR	The immune function-related gene PIGR is detected as downregulated in breast cancer.	[60]	✓		
PLXND1	PLXND1 is ubiquitously expressed on tumor vessels and tumor cells in solid malignancies.	[61, 62]			✓
PTGES3	Genes such as JAK2, TBP, PTGES3, and RYBP may be promising prognostic biomarkers for breast cancer patients.	[63]			

Biomarker	Description	Reported literatures	KEGG pathway	GWAS Catalog	Gene ORGA-Nizer
RAB18	Several microarray studies have shown dysregulation of RAB18 in breast cancer.	[64, 65]			
RAPGEFL1	The ERGs RAPGEFL1 is identified ceRNAs of NEAT1, the role of NEAT1 in breast cancer has been widely investigated.	[66]			
SAV1	SAV1 expression is found to be downregulated in a variety of cancers, including breast cancer.	[67]			
SERPINA1	SERPINA1 is a direct estrogen receptor target gene and a predictor of survival in breast cancer patients.	[68]			
SFRP4	Inhibition of breast cancer stem-like cells by a triterpenoid, ursolic acid, via activation of Wnt antagonist and SFRP4.	[69]	✓	✓	✓
SHBG	Decrease of circulating level of SHBG in post-menopausal obese women as a risk factor in breast cancer.	[70]			
SIX2	Homeoprotein SIX2 promotes breast cancer metastasis via transcriptional and epigenetic control of E-cadherin expression.	[71, 72]			
STAG3	Investigating STAG3 expression as a novel human breast cancer Biomarker.	[73, 74]			
TAPBPL	TAPBPL protein was detected in normal breast tissue at low levels, as compared to isotype antibody staining .	[75]	✓		
TSPAN14	The average methylation difference 10% between breast cancer patients and controls mapped to gene TSPAN14, which is previously described as cancer genes.	[76]			
TWIST1	TWIST1-mediated adriamycin-induced epithelial-mesenchymal transition relates to multidrug resistance and invasive potential in breast cancer cells.	[77, 78, 79, 80]	✓		✓
TYRP1	Expression of tyrosinase-related protein 1 (TYRP1) correlates with the absence of metastasis in an isogenic human breast cancer model.	[81]	✓		
WNT11	WNT11 is a novel ligand for ROR2 in human breast cancer.	[82, 83]	✓		
WNT3A	MiR-6838-5p suppresses cell metastasis and the EMT process in triple-negative breast cancer by targeting WNT3A to inhibit the Wnt pathway.	[84, 85]	✓		
WWOX	WWOX is a novel WW domain-containing protein mapping to human chromosome 16q23.3-24.1, a region frequently affected in breast cancer.	[86, 87, 88]		✓	✓

S1 Table Continued. **The genes that haven't been reported in the works of literature.** The 21 genes haven't been confirmed in the works of literature to be indeed related to the occurrence and prognosis of breast cancer.

Biomarker	Description	Reported literatures	KEGG pathway	Gene ORGA-Nizer
AAK1 ADH7 APC2 C20orf85 CEL CLCNKB CR1L EIF4E1B GABRA1 LRRC14B MAFA PSME1 PSME2 SEL1L2 SFTPB SLC20A2 TBX4 TNNI3 TRDN TRMT2B UPK1B	Diseases associated with PSME1 include Immunodeficiency 12. Diseases associated with PSME2 include Immunodeficiency 12.			

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