

Figure S1. Protein-protein interaction network of the differentially expressed genes was constructed using the Search Tool for the Retrieval of Interacting Genes/Proteins database. The network contained 335 nodes and 6,026 edges, and a combined score >0.4 was set as the cut-off value.

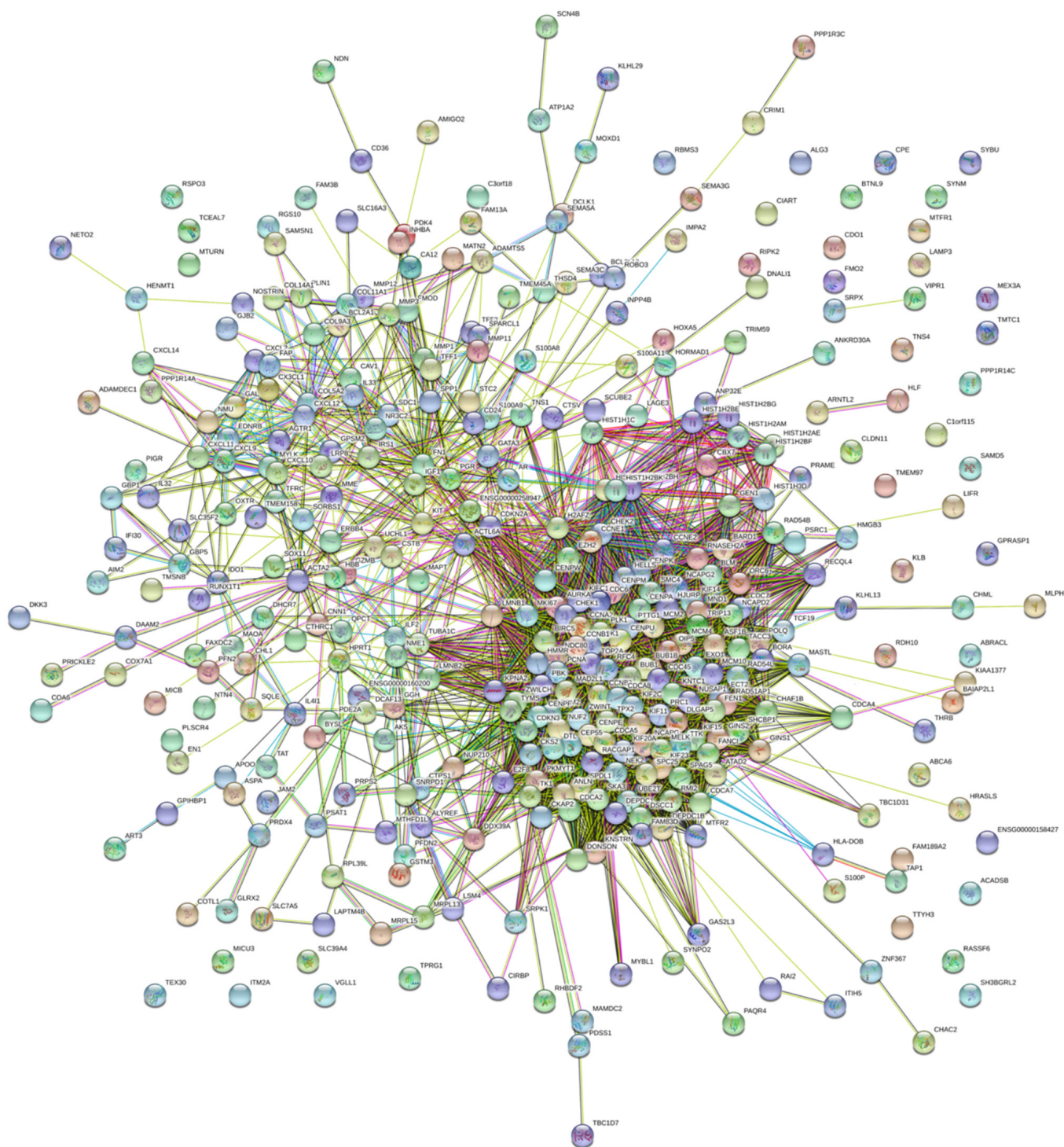


Table SI. Significantly enriched GO terms and KEGG pathways of differentially expressed genes in triple-negative breast cancer.

Category	Pathway ID	Description	Count	P-value
CC	GO:0005694	Chromosome	80	3.49×10^{-25}
CC	GO:0044427	Chromosomal part	72	1.15×10^{-23}
CC	GO:0043232	Intracellular non-membrane-bounded organelle	165	1.11×10^{-21}
CC	GO:0000775	Chromosome, centromeric region	35	4.78×10^{-20}
CC	GO:0000779	Condensed chromosome, centromeric region	29	1.52×10^{-19}
CC	GO:0000793	Condensed chromosome	36	1.68×10^{-19}
CC	GO:0000777	Condensed chromosome kinetochore	26	1.21×10^{-17}
CC	GO:0000776	Kinetochore	27	1.30×10^{-16}
CC	GO:0098687	Chromosomal region	36	1.30×10^{-16}
CC	GO:0005819	Spindle	37	2.36×10^{-15}
MF	GO:0005515	Protein binding	203	1.58×10^{-12}
MF	GO:0005488	Binding	288	4.84×10^{-8}
MF	GO:0046983	Protein dimerization activity	56	7.43×10^{-6}
MF	GO:0008017	Microtubule binding	21	1.35×10^{-5}
MF	GO:0005524	ATP binding	58	3.60×10^{-5}
MF	GO:0032559	Adenyl ribonucleotide binding	59	4.14×10^{-5}
MF	GO:0015631	Tubulin binding	23	6.01×10^{-5}
MF	GO:0008144	Drug binding	63	6.77×10^{-5}
MF	GO:0008092	Cytoskeletal protein binding	40	7.66×10^{-5}
MF	GO:0000166	Nucleotide binding	70	3.80×10^{-4}
BP	GO:0000278	Mitotic cell cycle	83	2.14×10^{-38}
BP	GO:1903047	Mitotic cell cycle process	77	1.92×10^{-36}
BP	GO:0007049	Cell cycle	105	1.34×10^{-33}
BP	GO:0022402	Cell cycle process	88	1.27×10^{-32}
BP	GO:0051301	Cell division	66	4.61×10^{-31}
BP	GO:0051276	Chromosome organization	82	4.70×10^{-25}
BP	GO:0007059	Chromosome segregation	45	1.09×10^{-24}
BP	GO:0048285	Organelle fission	46	3.09×10^{-23}
BP	GO:0000280	Nuclear division	44	6.09×10^{-23}
BP	GO:0071103	DNA conformation change	40	5.79×10^{-20}
Upregulated DEGs				
KEGG pathway	hsa04110	Cell cycle	23	8.09×10^{-18}
KEGG pathway	hsa05322	Systemic lupus erythematosus	12	7.01×10^{-6}
KEGG pathway	hsa04114	Oocyte meiosis	11	8.21×10^{-6}
KEGG pathway	hsa04115	p53 signaling pathway	9	8.61×10^{-6}
KEGG pathway	hsa03030	DNA replication	6	2.22×10^{-4}
KEGG pathway	hsa05203	Viral carcinogenesis	12	3.45×10^{-4}
KEGG pathway	hsa04914	Progesterone-mediated oocyte maturation	8	4.03×10^{-4}
KEGG pathway	hsa05034	Alcoholism	10	1.77×10^{-3}
KEGG pathway	hsa04512	ECM-receptor interaction	6	1.16×10^{-2}
Downregulated DEGs				
KEGG pathway	hsa04960	Aldosterone-regulated sodium reabsorption	4	4.61×10^{-3}
KEGG pathway	hsa04360	Axon guidance	6	4.81×10^{-3}
KEGG pathway	hsa04022	cGMP-PKG signaling pathway	6	1.19×10^{-2}

GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; BP, biological process; CC, cellular component; MF, molecular function; ECM, extracellular matrix.