

Figure S1. Volcano plots of three Gene Expression Omnibus datasets and Venn diagrams of the DEG screening. Volcano plot of the (A) GSE41657 and (B) GSE41258 datasets. (C) Overlapping upregulated DEGs in the two datasets. (D) Overlapping downregulated DEGs in the two datasets. DEG, differentially expressed gene.

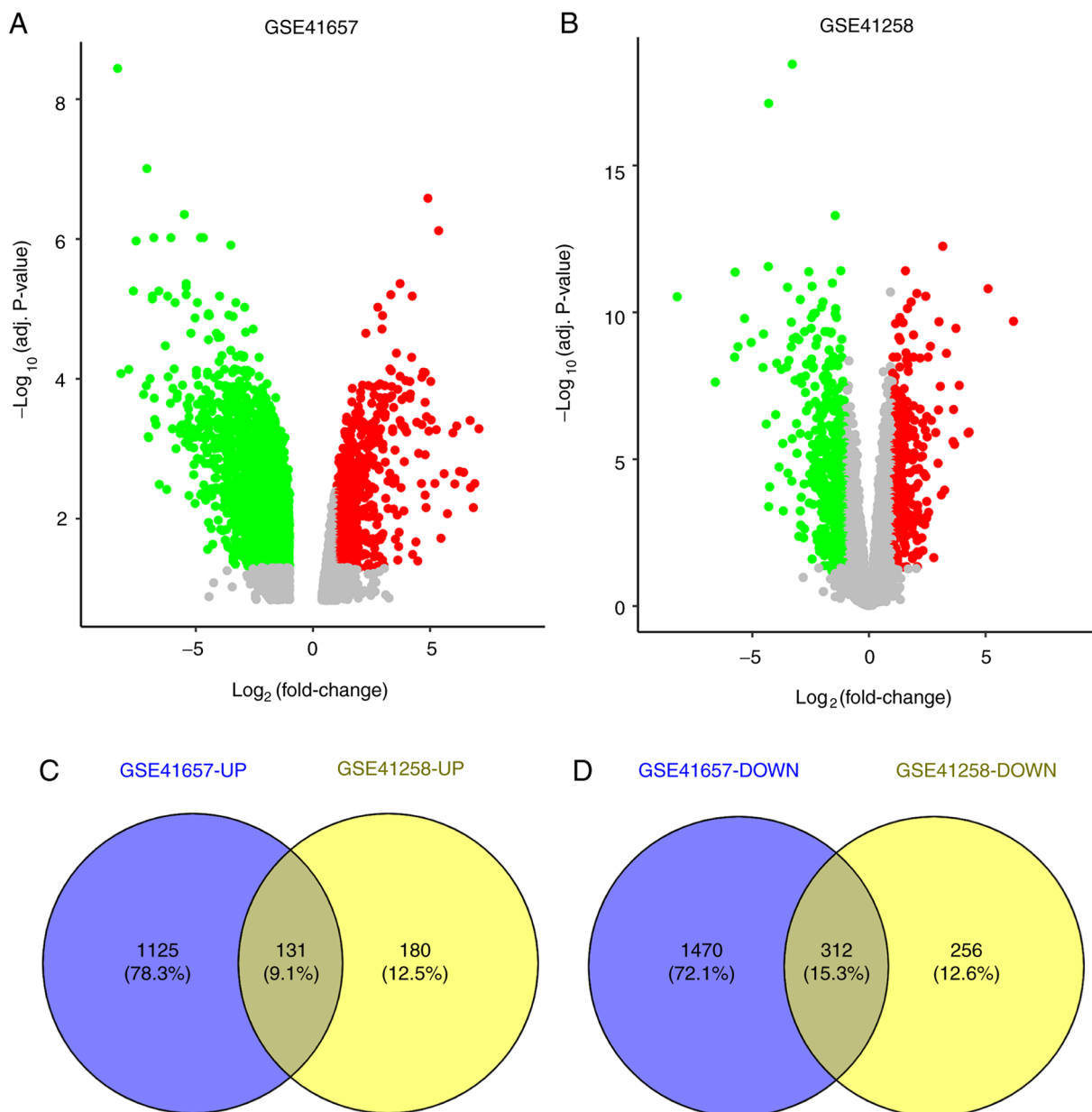


Figure S2. Protein-protein interaction network. Red nodes represent upregulated DEGs, and green nodes downregulated DEGs. DEG, differentially expressed gene.

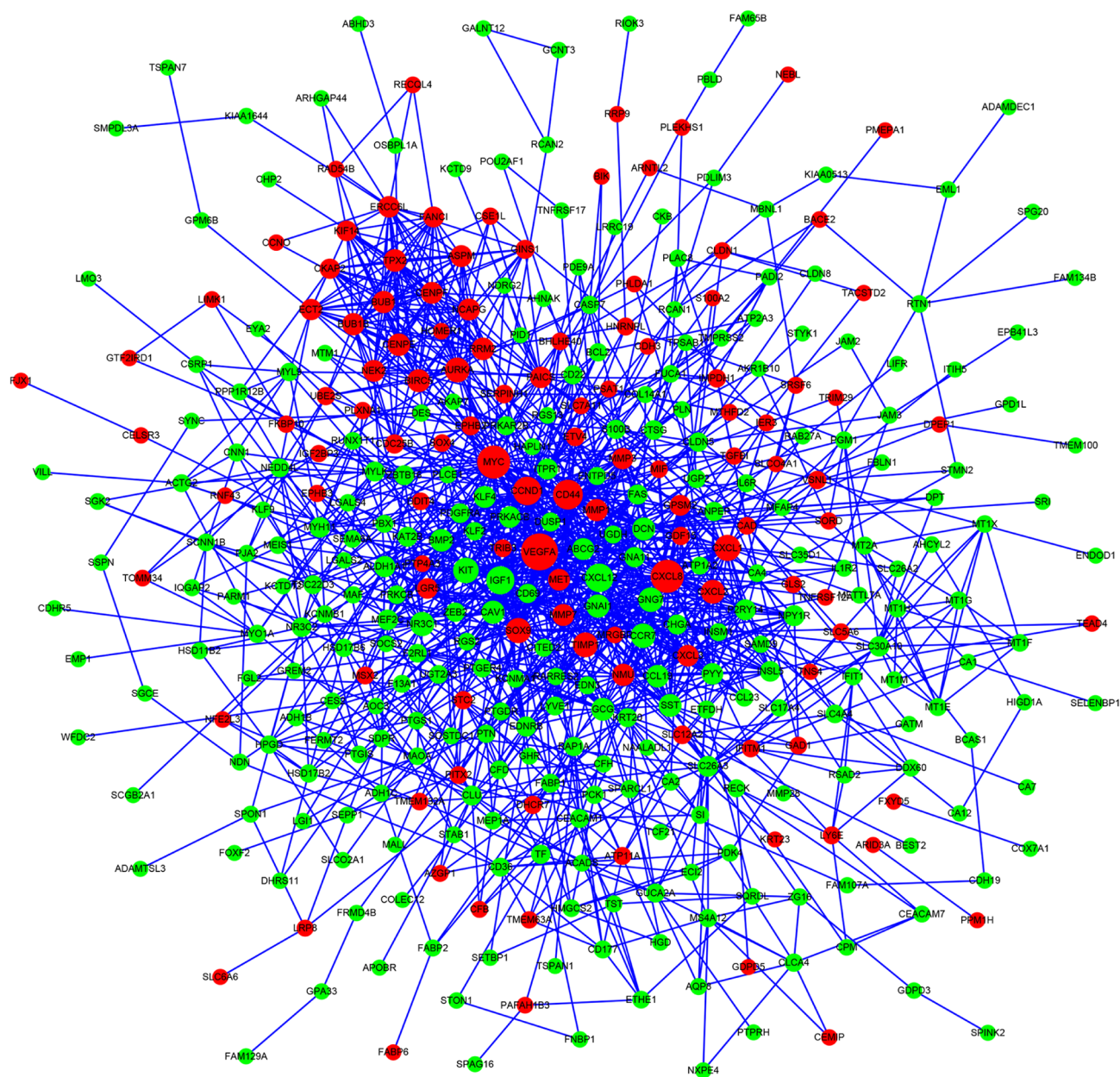


Figure S3. Candidate genes in 'pathways in cancer'. Red regions represent the candidate genes.

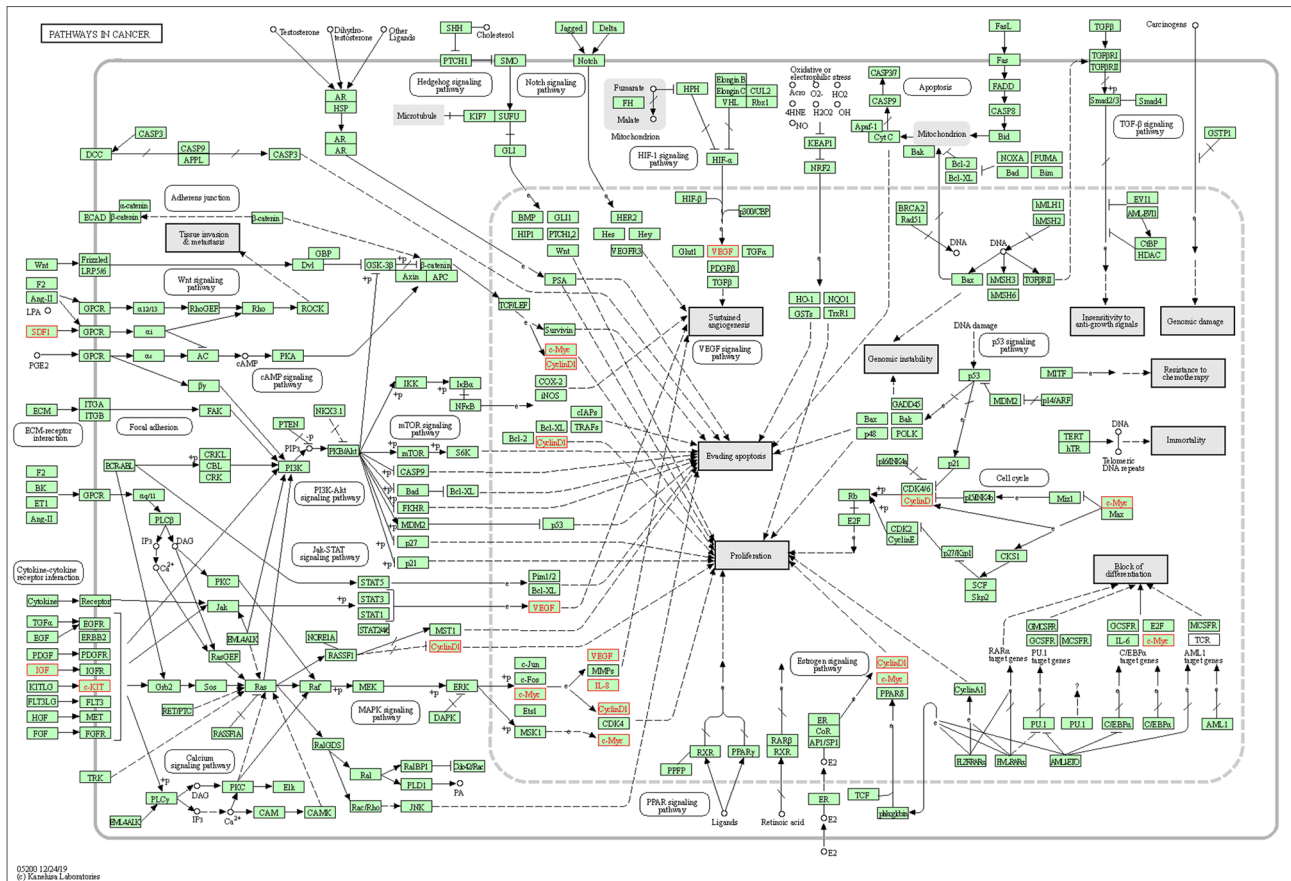


Table SI. Primer sequences for quantitative PCR.

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
CXCL8	AGTTTTTGAAGAGGGCTGAGA	ACCAAGGCACAGTGAACAA
VEGFA	GTCTGGAGCGTGTACGTTG	CTTCCGGGCTCGGTGATTTA
GAPDH	GAAAGCCTGCCGGTGACTAA	TTCCCGTTCTCAGCCTTGAC

Table SII. Significantly enriched GO terms of DEGs.

Category	Term	Count	P-value
BP-GO:0071294	cellular response to zinc ion	7	4.48x10 ⁻⁰⁶
BP-GO:0045926	negative regulation of growth	7	4.48x10 ⁻⁰⁶
BP-GO:0008283~	cell proliferation	25	1.42x10 ⁻⁰⁵
BP-GO:0006730	one-carbon metabolic process	7	7.78x10 ⁻⁰⁵
BP-GO:0015701	bicarbonate transport	8	9.17x10 ⁻⁰⁵
CC-GO:0070062	extracellular exosome	123	6.81x10 ⁻¹²
CC-GO:0005615	extracellular space	73	6.41x10 ⁻¹¹
CC-GO:0016324	apical plasma membrane	20	7.58x10 ⁻⁰⁵
CC-GO:0005737	cytoplasm	159	2.43x10 ⁻⁰⁴
CC-GO:0005887	integral component of plasma membrane	55	3.87x10 ⁻⁰⁴
MF-GO:0005515	protein binding	249	2.44x10 ⁻⁰⁴
MF-GO:0004089	carbonate dehydratase activity	5	2.80x10 ⁻⁰⁴
MF-GO:0045236	CXCR chemokine receptor binding	4	0.001
MF-GO:0008009	chemokine activity	7	0.001
MF-GO:0005540	hyaluronic acid binding	5	0.002

BP, biological process; CC, cellular component; MF, molecular function; GO, gene ontology; DEGs, differentially expressed genes.

Table SIII. Top 10 enriched pathways of the differentially expressed genes.

Pathway	Terms	Count	P-value
KEGG-hsa04978	Mineral absorption	10	5.23×10^{-06}
KEGG-hsa05202	Transcriptional misregulation in cancer	16	1.55×10^{-06}
KEGG-hsa04972	Pancreatic secretion	11	4.83×10^{-04}
KEGG-hsa04964	Proximal tubule bicarbonate reclamation	6	5.31×10^{-04}
KEGG-hsa04022	cGMP-PKG signaling pathway	14	9.86×10^{-04}
KEGG-hsa04960	Aldosterone-regulated sodium reabsorption	7	0.00103264
KEGG-hsa00910	Nitrogen metabolism	5	0.00144328
KEGG-hsa00350	Tyrosine metabolism	6	0.00381063
KEGG-hsa05200	Pathways in cancer	23	0.00386651
KEGG-hsa04971	Gastric acid secretion	8	0.00644278

KEGG, Kyoto Encyclopedia of Genes and Genomes.