

Supplementary

Table S1 Primer sequences for RT-qPCR

Primer	Sequences (5'-3')
<i>IGF</i>	F: CAACATCTCCCATCTCTCTGGA R: TTGGGTTGGAAGACTGCTGA
<i>INS</i>	F: CAGAAGAGGCCATCAAGCAGA R: TTCACAAAGGCTGCGGCT
<i>GAPDH</i>	F: ATGGTTTACATGTTCCAATATGA R: TTACTIONCTGGAGGCCATGTGG
<i>WNT6</i>	F: AACAGGACATTCGGGAGACG R: CAGCTCGCCCATAGAACAGG
<i>WNT11</i>	F: CCGACATGCGCTGGA R: GGTCCCTCTCTCCAGGTCAA
<i>WNT2B</i>	F: TGGAGTGGTAGCCATAAGCA R: CGCTGACTGTGTAGGTATGC
<i>SESN</i>	F: ACAACCTCTCTGGAGGCACT R: CATGTAGCGGGTGTGGCAC
<i>NCRNA00173</i>	F: GCATCCAGCTACCCAGACTC R: CCTGCAGCACGCAATTAGAC

Table S2 KEGG enrichment of DEGs

ONTOLOGY	ID	Description	Gene Ratio	Background ratio	P value	p. adjust	q value	Count
KEGG	hsa05217	Basal cell carcinoma	8/220	63/8076	0.000284565	0.000284565	0.047869655	8
KEGG	hsa04060	Cytokine-cytokine receptor interaction	19/220	295/8076	0.000421076	0.000421076	0.047869655	19
KEGG	hsa04115	p53 signaling pathway	8/220	73/8076	0.000782327	0.000782327	0.048931026	8
KEGG	hsa04068	FoxO signaling pathway	11/220	131/8076	0.000860824	0.000860824	0.048931026	11
KEGG	hsa04935	Growth hormone synthesis, secretion and action	10/220	119/8076	0.001462265	0.001462265	0.066494562	10
KEGG	hsa05224	Breast cancer	11/220	147/8076	0.002195372	0.002195372	0.06960978	11
KEGG	hsa04010	MAPK signaling pathway	17/220	294/8076	0.002710854	0.002710854	0.06960978	17
KEGG	hsa04917	Prolactin signaling pathway	7/220	70/8076	0.002826702	0.002826702	0.06960978	7
KEGG	hsa04150	mTOR signaling pathway	11/220	155/8076	0.003320642	0.003320642	0.06960978	11
KEGG	hsa04151	PI3K-Akt signaling pathway	19/220	354/8076	0.003575144	0.003575144	0.06960978	19
KEGG	hsa04390	Hippo signaling pathway	11/220	157/8076	0.003664239	0.003664239	0.06960978	11
KEGG	hsa05205	Proteoglycans in cancer	13/220	205/8076	0.003901214	0.003901214	0.06960978	13
KEGG	hsa04657	IL-17 signaling pathway	8/220	94/8076	0.003980004	0.003980004	0.06960978	8
KEGG	hsa04630	JAK-STAT signaling pathway	11/220	162/8076	0.004648847	0.004648847	0.075500066	11
KEGG	hsa04620	Toll-like receptor signaling pathway	8/220	104/8076	0.007311119	0.007311119	0.110821174	8
KEGG	hsa04380	Osteoclast differentiation	9/220	128/8076	0.0081084	0.0081084	0.115224638	9
KEGG	hsa04512	ECM-receptor interaction	7/220	88/8076	0.009929541	0.009929541	0.132803773	7
KEGG	hsa04080	Neuroactive ligand-receptor interaction	17/220	341/8076	0.011635834	0.011635834	0.146978959	17
KEGG	hsa04658	Th1 and Th2 cell differentiation	7/220	92/8076	0.01251336	0.01251336	0.149744358	7
KEGG	hsa05162	Measles	9/220	139/8076	0.013502328	0.013502328	0.15350015	9
KEGG	hsa05202	Transcriptional misregulation in cancer	11/220	192/8076	0.015709759	0.015709759	0.15926526	11
KEGG	hsa04550	Signaling pathways regulating pluripotency of stem cells	9/220	143/8076	0.016008749	0.016008749	0.15926526	9
KEGG	hsa05225	Hepatocellular carcinoma	10/220	168/8076	0.016353571	0.016353571	0.15926526	10
KEGG	hsa04960	Aldosterone-regulated sodium reabsorption	4/220	37/8076	0.017511805	0.017511805	0.15926526	4
KEGG	hsa05216	Thyroid cancer	4/220	37/8076	0.017511805	0.017511805	0.15926526	4
KEGG	hsa05169	Epstein-Barr virus infection	11/220	202/8076	0.022044079	0.022044079	0.192774133	11

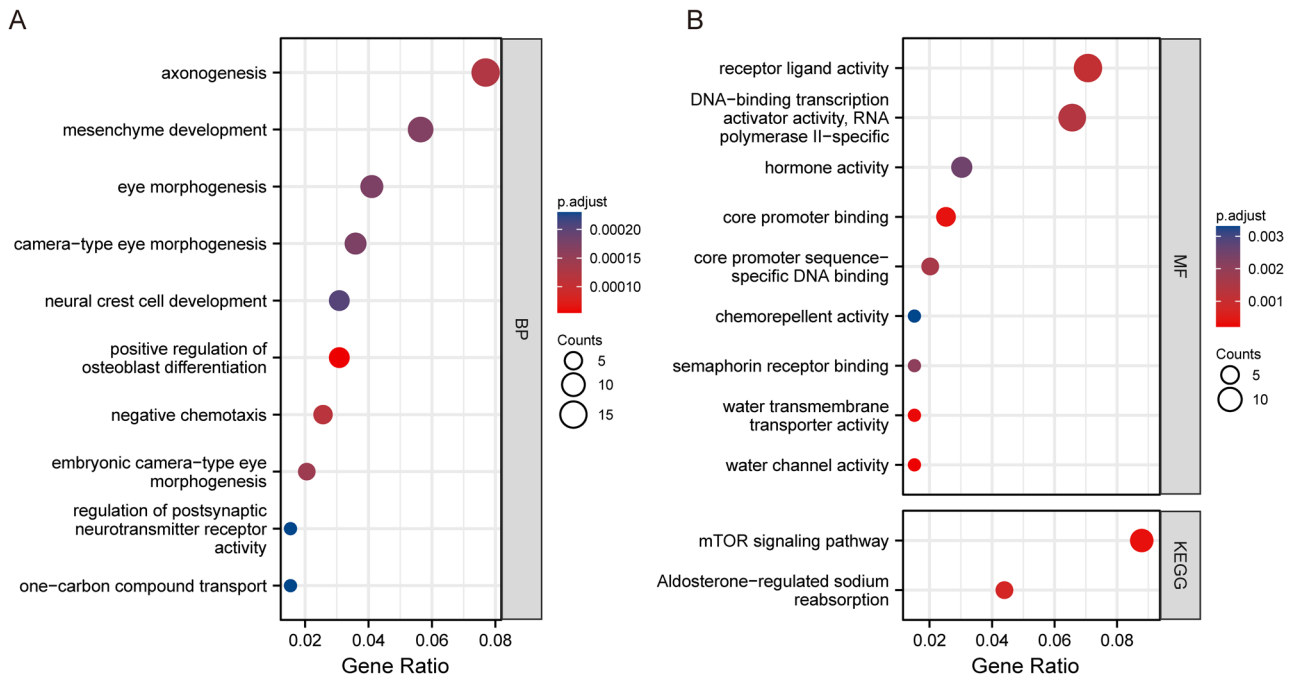


Figure S1 Enrichment of the co-expressed DEGs of the top 10 upregulated DELs. (A) GO-BP enrichment of the co-expressed DEGs of the top 10 upregulated DELs. (B) GO-MF and KEGG enrichment of the co-expressed DEGs of the top 10 upregulated DELs. BP, biological process. MF, molecular function.

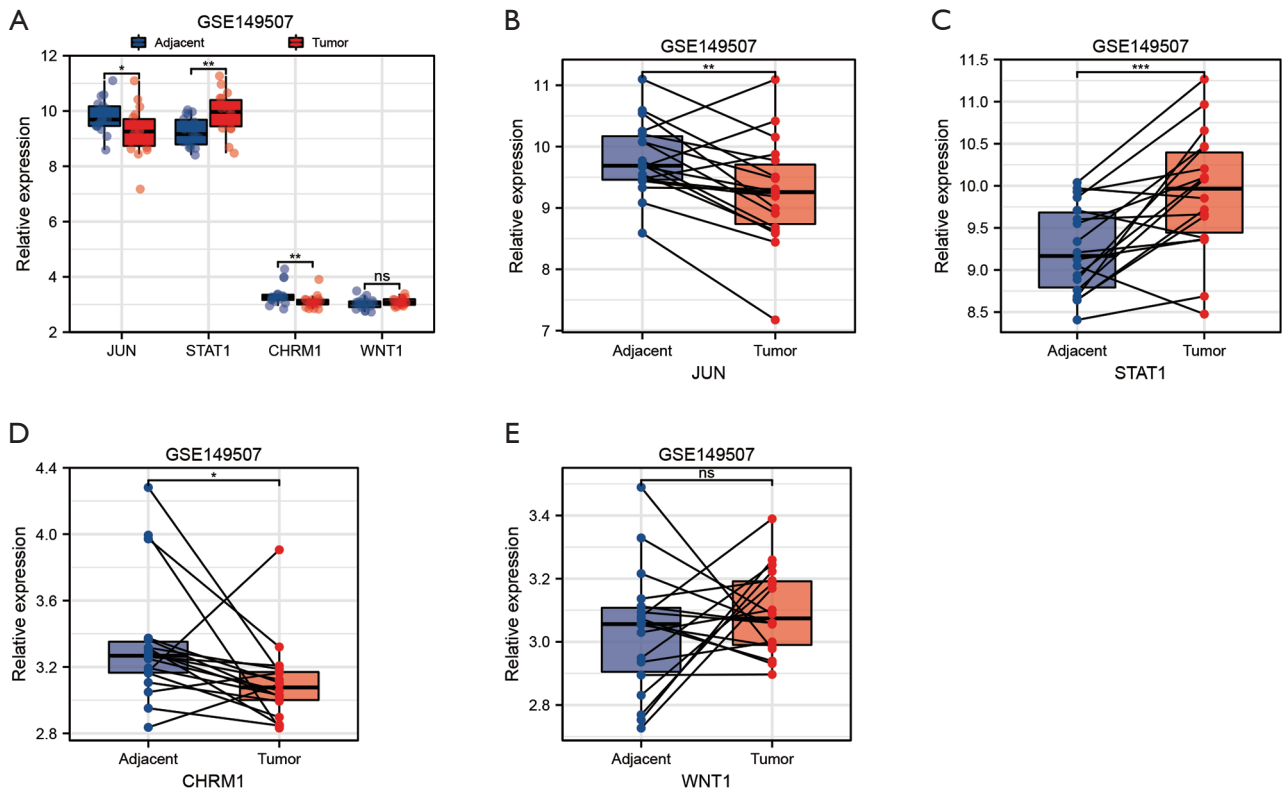


Figure S2 The expression of the hub genes from the DEGs of our microarray data was analyzed in the GSE149507 data set. (A) JUN, STAT1, CHR1, and WNT1 expression in the adjacent tissues and tumor tissues in GSE149507. (B-E) The expression of JUN (B), STAT1 (C), CHR1 (D), and WNT1 (E) in the matched adjacent tissues and tumor tissues in GSE149507. ns, $P > 0.05$; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

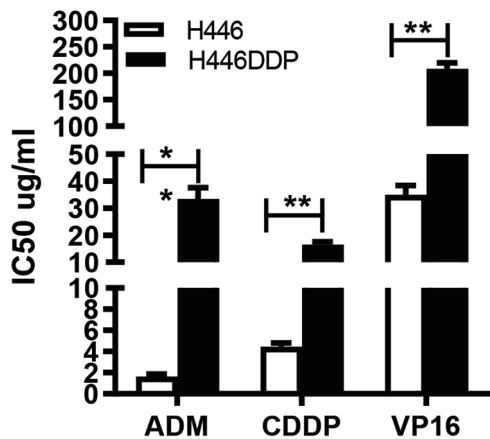


Figure S3 Chemoresistance of H446 cells and H446DDP cells to cisplatin (CDDP), etoposide (VP-16), and Adriamycin (ADM). The data are shown as the mean \pm standard deviation from 3 independent experiments. *, $P < 0.01$.