

Table 1

Correlation expression of KIAA1456 in ovarian tissues, benign and malignant

human epithelial ovarian cancer

Variable	n	KIAA1456 expression					P
		< 10%	10-20%	20-30%	> 30%	Median positive (%)	
Tissue							0.000
Normal ovarian tissue	15	0	0	5	10	29.48	
Benign EOC	15	0	6	9	0	18.72	
Malignant EOC	45	23	21	1	0	8.91	
Histologic grade							0.000
Low-grade	15	3	11	1	0	12.09	
High-grade	30	20	10	0	0	6.04	
Age (years)							0.9414
≤50	37	9	14	10	4		
> 50	38	14	13	8	3		

Table 2 Microarray analysis identified a list of genes significantly differentially expressed after KIAA1456 overexpression.

Gene Symbol	Accession Number	Gene Description	Fold Change	p-value	Gene Feature
IQGAP1	NM_003870	"Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA."	1.702313	0.000584	up
UBE4A	NM_001204077	"Homo sapiens ubiquitination factor E4A (UBE4A), transcript variant 2, mRNA."	1.419223	0.00054	up
PSMD1	NM_001191037	"Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (PSMD1), transcript variant 2, mRNA."	1.365103	0.000545	up
KIAA1456	NM_001099677	"Homo sapiens KIAA1456 (KIAA1456), transcript variant 2, mRNA."	1.314254	0.000115	up
SMARCA1	NM_003069	"Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMARCA1), transcript variant 1, mRNA."	1.286039	0.000653	up
TRIM29	NM_012101	"Homo sapiens tripartite motif containing 29 (TRIM29), mRNA."	1.222872	0.000775	up
SSX1	NM_005635	"Homo sapiens synovial sarcoma, X breakpoint 1 (SSX1), mRNA."	5.73389	5.10E-05	down
CYP1A1	NM_000499	"Homo sapiens cytochrome P450, family 1, subfamily A, polypeptide 1 (CYP1A1), mRNA."	-2.26197	0.013938	down
IGHD2-21	ENST00000390572	cdna:known chromosome:GRCh37:14:106354409:106354436:-1 gene:ENSG00000211912 gene_biotype:IG_D_gene transcript_biotype:IG_D_gene	-1.5694	0.026841	down
IER3	NM_003897	"Homo sapiens immediate early response 3 (IER3), mRNA."	-1.50082	0.020279	down
HMOX1	NM_002133	"Homo sapiens heme oxygenase (decycling) 1 (HMOX1), mRNA."	-1.47563	0.003978	down

Table 3 KEGG pathway analysis of differentially expressed genes in KIAA1456-overexpressing and control cells.

Pathway	Diff Gene Counts in Pathway	Enrichment Score	P-value	FDR	Gene Symbols
RNA transport	16	13.41944	1.95E-13	3.23E-11	EIF2B2 EIF3A GEMIN5 ...
Protein processing in endoplasmic reticulum	12	9.944049	7.95E-09	6.56E-07	SEC24A CANX UBE2G1 ...
Lysosome	9	10.20895	5.72E-07	3.15E-05	CTSL1 AP3M1 DNASE2 ...
Proteoglycans in cancer	11	6.706027	1.91E-06	7.89E-05	ITGAV FN1 IQGAP1 ...
Pathways in cancer	12	5.078459	1.11E-05	0.000366	MET HSP90AA1 ITGAV ...
Proteasome	5	15.72591	3.29E-05	0.000905	PSMB7 PSME2 PSMD1 ...
Antigen processing and presentation	6	10.12595	6.00E-05	0.001413	HSPA4 CTSB HSP90AA1 ...
Purine metabolism	7	5.599515	0.000564	0.011625	PRPS2 POLR2B PNP ...
Ubiquitin mediated proteolysis	6	6.01687	0.00105	0.01575	UBE4A HERC3 UBE3A ...
Metabolic pathways	20	2.327805	0.001258	0.0173	AMD1 PNP EPRS ...
PI3K-Akt signaling pathway	8	3.190502	0.007973	0.058966	ITGB1 MET ITGAV ...