

Table 1. Functional and pathway enrichment analysis of the overlap DEGs.

Category	Term	Count	pValue
GOTERM_BP	GO:0019373~epoxygenase P450 pathway	5	2.13E-06
GOTERM_BP	GO:0055114~oxidation-reduction process	15	2.62E-06
GOTERM_BP	GO:0042738~exogenous drug catabolic process	4	3.06E-05
GOTERM_BP	GO:0006805~xenobiotic metabolic process	6	5.81E-05
GOTERM_BP	GO:0032787~monocarboxylic acid metabolic process	3	8.30E-05
GOTERM_BP	GO:0017144~drug metabolic process	4	3.84E-04
GOTERM_BP	GO:0051988~regulation of attachment of spindle microtubules to kinetochore	3	5.73E-04
GOTERM_BP	GO:0007067~mitotic nuclear division	7	0.002043
GOTERM_BP	GO:0048146~positive regulation of fibroblast proliferation	4	0.002937
GOTERM_BP	GO:0008209~androgen metabolic process	3	0.003176
GOTERM_CC	GO:0031090~organelle membrane	8	2.40E-07
GOTERM_CC	GO:0005576~extracellular region	21	9.18E-05
GOTERM_CC	GO:0030496~midbody	6	4.47E-04
GOTERM_CC	GO:0072562~blood microparticle	5	0.006825
GOTERM_CC	GO:0097149~centralspindlin complex	2	0.014743
GOTERM_CC	GO:0005615~extracellular space	14	0.014768
GOTERM_CC	GO:0072686~mitotic spindle	3	0.017456
GOTERM_CC	GO:0005789~endoplasmic reticulum membran	10	0.026348
GOTERM_CC	GO:0070062~extracellular exosome	22	0.03125
GOTERM_CC	GO:0005579~membrane attack complex	2	0.034067
GOTERM_MF	GO:0020037~heme binding	8	6.26E-06
GOTERM_MF	GO:0016705~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	6	1.04E-05
GOTERM_MF	GO:0005506~iron ion binding	8	1.29E-05
GOTERM_MF	GO:0008392~arachidonic acid epoxygenase activity	4	5.56E-05

GOTERM_MF	GO:0016712~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	4	5.56E-05
GOTERM_MF	GO:0019825~oxygen binding	47	9.48E-05
GOTERM_MF	GO:0004497~monooxygenase activity	58	2.16E-04
GOTERM_MF	GO:0008395~steroid hydroxylase activity	26	3.05E-04
GOTERM_MF	GO:0070330~aromatase activity	27	0.00829
GOTERM_MF	GO:0034875~caffeine oxidase activity	4	0.00829
KEGG_PATHWAY	hsa00830:Retinol metabolism	6	8.28E-05
KEGG_PATHWAY	hsa00232:Caffeine metabolism	3	4.90E-04
KEGG_PATHWAY	hsa01100:Metabolic pathways	19	0.001176
KEGG_PATHWAY	hsa00982:Drug metabolism - cytochrome P450	5	0.001324
KEGG_PATHWAY	hsa00980:Metabolism of xenobiotics by cytochrome P450	5	0.001813
KEGG_PATHWAY	hsa05204:Chemical carcinogenesis	5	0.002416
KEGG_PATHWAY	hsa04115:p53 signaling pathway	4	0.011823
KEGG_PATHWAY	hsa00380:Tryptophan metabolism	3	0.032647

Table 2 The full name and functional roles of hub genes.

Gene Symbol	Full name	Function
ANLN	anillin actin binding protein	This gene encodes an actin-binding protein that plays a role in cell growth and migration, and in cytokinesis. The encoded protein is thought to regulate actin cytoskeletal dynamics in podocytes, components of the glomerulus. Mutations in this gene are associated with focal segmental glomerulosclerosis 8. Alternative splicing results in multiple transcript variants encoding different isoforms.
CCNB1	cyclin B1	The protein encoded by this gene is a regulatory protein involved in mitosis. The gene product complexes with p34(cdc2) to form the

		maturation-promoting factor (MPF). The encoded protein is necessary for proper control of the G2/M transition phase of the cell cycle.
		The DTL gene, which is also known as the <i>CDT2/RAMP/DCAF2/L2DTL</i> gene, is located on chromosome 1q32; this area is frequently amplified in human solid cancers.
DTL	Denticleless E3 ubiquitin protein ligase homolog	DTL encodes a putative 730 amino acid protein that contains six highly conserved five WD40-repeat domains and physically interacts with the DDB1/CULLIN4 complex (CRL4). Cullin-RING ubiquitin ligases (CRLs) are the largest family of E3 ligase.
		This gene encodes a GTPase-activating protein (GAP) that is a component of the centralspindlin complex. This protein binds
RACGAP1	Rac GTPase activating protein 1	activated forms of Rho GTPases and stimulates GTP hydrolysis, which results in negative regulation of Rho-mediated signals. This protein plays a regulatory role in cytokinesis, cell growth, and differentiation. Alternatively spliced transcript variants have been found for this gene. There is a pseudogene for this gene on chromosome 12.
		This gene encodes one of two non-identical subunits for ribonucleotide reductase. This reductase catalyzes the formation of
RRM2	Ribonucleotide reductase regulatory subunit M2	deoxyribonucleotides from ribonucleotides. Synthesis of the encoded protein (M2) is regulated in a cell-cycle dependent fashion. Transcription from this gene can initiate from alternative promoters, which results in two isoforms that differ in the lengths of their N-termini. Related pseudogenes have been identified on chromosomes 1 and X.
		This gene encodes a DNA topoisomerase, an enzyme that controls and alters the topologic states of DNA during transcription. This nuclear enzyme is involved in processes such as chromosome condensation, chromatid separation, and the relief of torsional stress that occurs during DNA transcription and replication. It catalyzes the transient

DNA breaking and rejoining of two strands of duplex DNA which allows the strands to pass through one another, thus altering the topology of DNA. Two forms of this enzyme exist as likely products of a gene duplication event. The gene encoding this form, alpha, is localized to chromosome 17 and the beta gene is localized to chromosome 3. The gene encoding this enzyme functions as the target for several anticancer agents and a variety of mutations in this gene have been associated with the development of drug resistance. Reduced activity of this enzyme may also play a role in ataxia-telangiectasia.

Table 3 List of the 10 most significant small molecule drugs.

Cmap name	Enrichment	<i>p</i>
thioguanosine	-0.964	0
apigenin	-0.94	0
trichostatin A	-0.21	0
resveratrol	-0.71	0.00002
meticrane	-0.845	0.00026
felbinac	0.879	0.0003
medrysone	-0.755	0.00044
phenoxybenzamine	-0.881	0.00048
daunorubicin	-0.875	0.00052
trifluridine	-0.864	0.00062