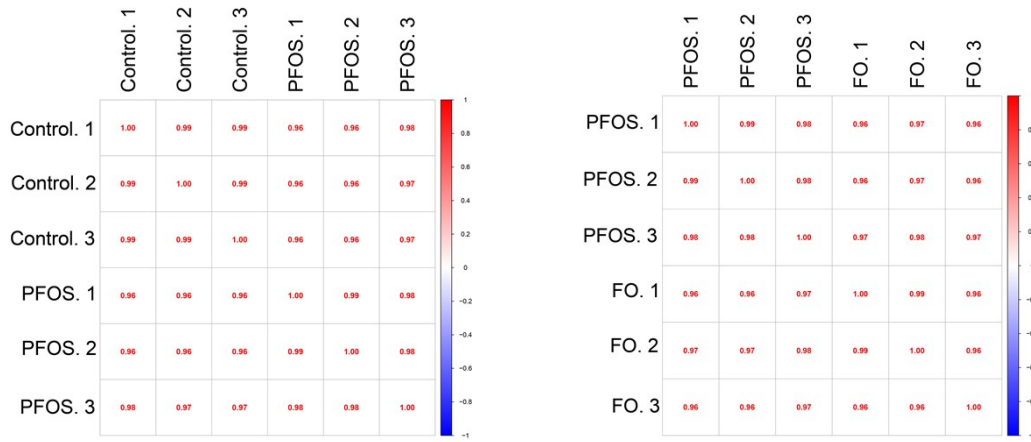
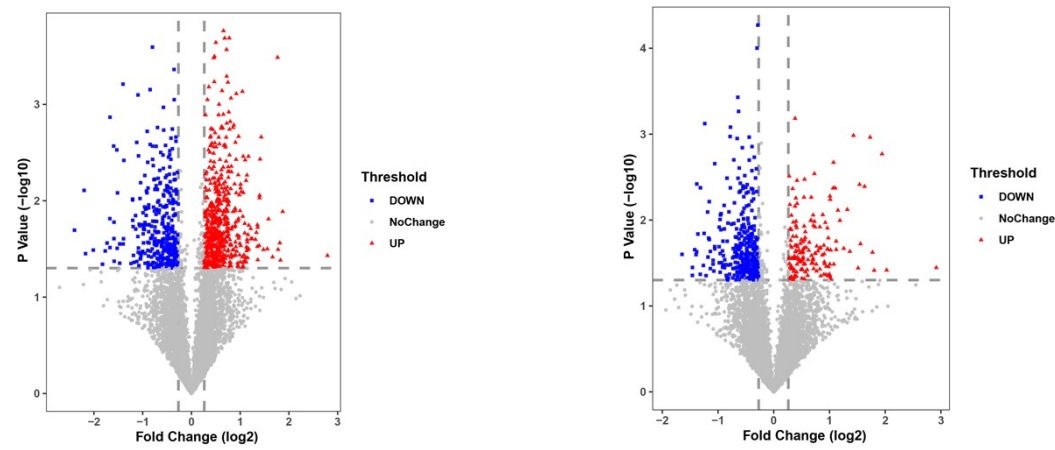


FigureS1

A



B



C

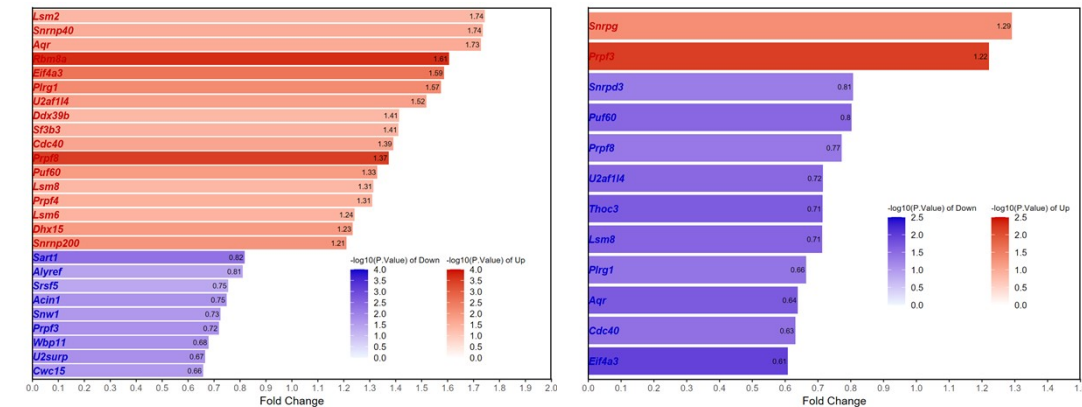


Figure.S1 Distribution of dep. A Pearson's correlation plots between control group and PFOS group, and between PFOS group and FO group. B Volcano plot of differential proteins between control group and PFOS group, PFOS group and FO group. C Changed spliceosome related proteins in PFOS group compared with Control group displayed in heatmap assayed by proteomics. Changed spliceosome related proteins in FO group compared with PFOS group displayed in heatmap assayed by proteomics.

FigureS2

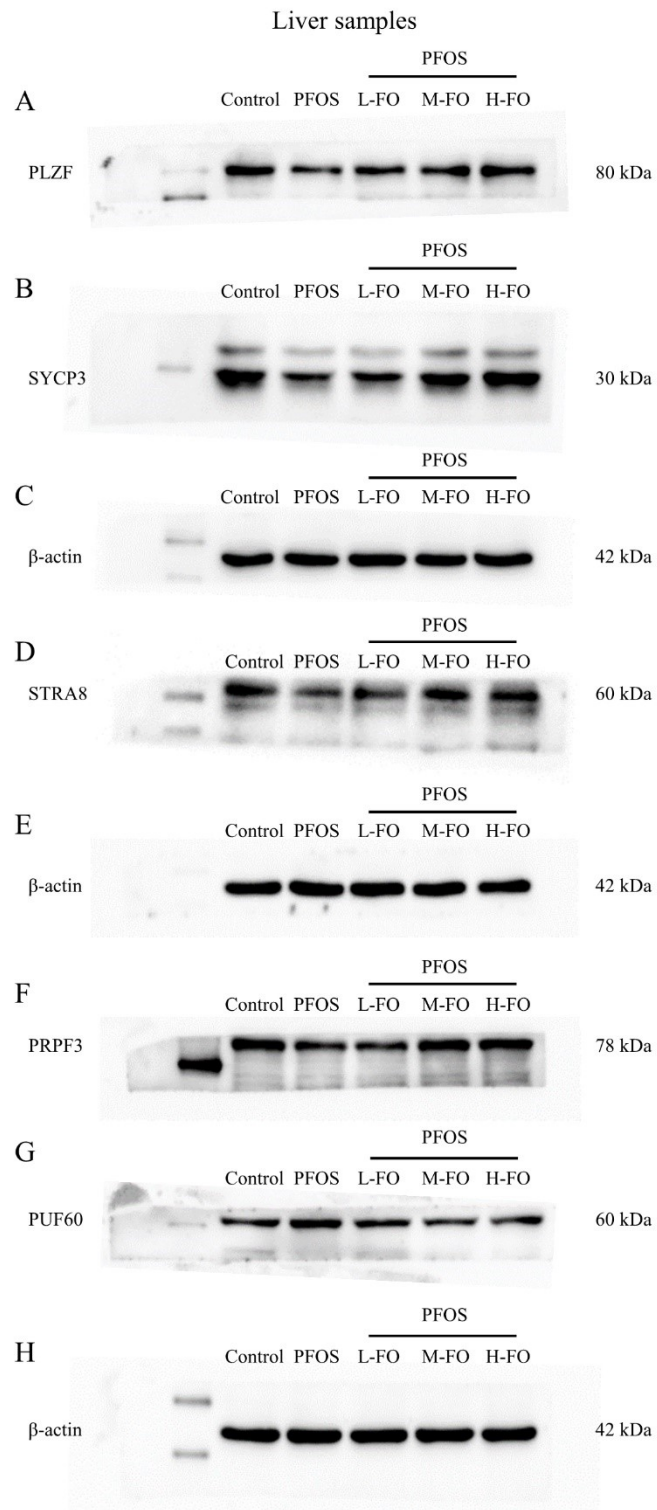


Figure. S2 Original western blot results of PLZF (A), SYCP3(B), β -actin (C), STRA8 (D), β -actin (E), PRPF3 (F), PUF60 (G), and β -actin (H)in Liver for Figure 5C and 8B, respectively.

Table S1

Primary antibodies used in western blot

Antibody	Supplier	Dilution	Calculated
PLZF	ABclonal Technology (Wuhan ,China)	1:2000	80
SYCP3	Proteintech (Wuhan ,China)	1:1000	30
STRA8	Proteintech (Wuhan ,China)	1:1000	60
PRPF3	Proteintech (Wuhan ,China)	1:500	78
PUF60	Proteintech (Wuhan ,China)	1:5000	60
β -actin	ABclonal Technology (Wuhan, China)	1:40000	42

Table S2

Pathways enriched in KEGG analysis for DEPs between control and PFOS groups.

Description	<i>p</i> -value	<i>q</i> -value	Gene ID
Amyotrophic lateral sclerosis	0.000162	1.15E-06	O08583/O55234/P12787/P46412/P47811/P54775/P59235/P62821/P63260/P70195/Q3TXS7/Q3UIU2/Q61337/Q80ZN9/Q8BG32/Q8CBY8/Q8K310/Q8R111/Q8R2U0/Q8R3E3/Q8R480/Q8VDM4/Q99KJ8/Q99LC3/Q99NB8/Q99P88/Q9CQJ8/Q9CQZ5/Q9CR61/Q9CWU9/Q9D1M0/Q9DCJ5/Q9DCS9/Q9QZB7/Q9R1P0/Q9Z1P6/Q9Z2V5
Spliceosome	8.38E-09	1.90E-05	O08583/O35286/O35326/O35900/P62313/Q3UEB3/Q6NV83/Q6P4T2/Q6PE01/Q6ZWM4/Q8BGJ9/Q8CFQ3/Q91VC3/Q921M3/Q922U1/Q922V4/Q923D5/Q99PV0/Q9CSN1/Q9CWZ3/Q9DAW6/Q9DC48/Q9JHS9/Q9JIX8/Q9Z1N5/Q9Z315
Carbon metabolism	2.48E-07	1.90E-05	O08528/P05202/P12382/P16858/P21550/P28474/P35486/P47857/Q00612/Q60597/Q64374/Q8CFX1/Q8QZR5/Q8QZS1/Q8VDL4/Q99KE1/Q99MX0/Q99NB1/Q9D7G0/Q9DCD0/Q9QXG4/Q9R0P3
Ribosome	5.06E-06	0.000277	O09167/P25444/P47962/P47964/P62270/P62702/P62754/P62858/P62908/P63276/P99027/Q3TBW2/Q6ZVW3/Q8BP67/Q99N95/Q99N96/Q9CPR4/Q9CQR2/Q9CR57/Q9D338/Q9D823/Q9DC71
Purine metabolism	1.12E-05	0.000433	O08739/P00493/P03958/P08030/P24547/P46664/P55264/P55772/P56380/Q01768/Q3V1L4/Q5SSUR0/Q61409/Q64737/Q8CIH9/Q91WF3/Q99L27/Q9CWJ9/Q9D0F9/Q9D7G0/Q9WUZ9
Biosynthesis of cofactors	0.000223	0.000438	O35855/P00375/P12265/P36552/P46664/P47738/P60487/P70698/P97494/Q01768/Q5RKZ7/Q64374/Q6ZQM8/Q78JT3/Q7M753/Q8BTZ7/Q91ZJ5/Q9D404/Q9D9M5/Q9DBL7
Nucleocytoplasmic transport	3.27E-05	0.00112	O08583/O35343/O35691/P59235/P63166/Q8CIC2/Q8R2U0/Q8R480/Q91VC3/Q99M28/Q99P88/Q9CR67/Q9CWU9/Q9CWZ3/Q9D1M0/Q9EPU0/Q9JIX8/Q9Z1N5
mRNA surveillance pathway	9.49E-06	0.001627	O08583/O35691/P63087/P63330/Q60996/Q6P1F6/Q76MZ3/Q91VC3/Q925E7/Q99LC2/Q99M28/Q9CWZ3/Q9EPU0/Q9EPU4/Q9JIX8/Q9QXK7/Q9Z1N5
Nucleotide metabolism	0.000132	0.001627	O08739/P00493/P03958/P08030/P24547/P46664/P55264/P55772/P70698/Q01768/Q3V1L4/Q99L27/Q9D020/Q9WUZ9
Aminoacyl-tRNA biosynthesis	2.78E-07	0.002704	Q3U186/Q3U2A8/Q8BIJ6/Q8BIP0/Q8BU30/Q8BYM8/Q8CFI5/Q8VDC0/Q91WQ3/Q9CZD3/Q9D0R2/Q9JL8/Q9WUA2
Glycolysis / Gluconeogenesis	0.000152	0.003022	O08528/P12382/P16125/P16858/P21550/P28474/P35486/P47738/P47857/Q8VDL4/Q99NB1/Q9D0F9/Q9QXG4
Amino sugar and nucleotide sugar metabolism	0.000109	0.003169	O08528/O88958/P47856/Q7TMC8/Q8BTZ7/Q91ZJ5/Q9CYR6/Q9D0F9/Q9DB73/Q9DCJ9/Q9QZ08
Fatty acid metabolism	0.000203	0.003169	O35448/P32020/P41216/P50544/P52825/P97742/Q8K2C9/Q8VCH0/Q920L1/Q9D404/Q9Z0R9
Pentose phosphate pathway	5.94E-05	0.003705	P12382/P47857/Q00612/Q64374/Q8CFX1/Q99MX0/Q9D0F9/Q9D7G0/Q9DCD0

Table S3

Pathways enriched in KEGG analysis for DEPs between PFOS and FO+PFOS groups.

Description	<i>p</i> -value	<i>q</i> -value	Gene ID
Salmonella infection	0.001004	0.027792	O35343/P07901/P16858/P47811/P61161/P62908/P63321/Q02248/Q60823/Q64331/Q78JE5/Q99KJ8/Q9CVB6/Q9D0M5/Q9D4H1/Q9D898/Q9QZB7/Q9QZB9/Q9R0M6/Q9WTX5
Carbon metabolism	9.92E-09	1.37E-06	P05202/P12382/P16332/P16858/P26443/P28474/Q60597/Q64374/Q8BPC6/Q8CFX1/Q8K2B3/Q91Y97/Q99KE1/Q99MX0/Q99NB1/Q9D2G2/Q9D7G0/Q9EPL9/Q9R0P3
Spliceosome	0.001519	0.037007	P62309/P62320/Q3UEB3/Q6ZWM4/Q8BGJ9/Q8CFQ3/Q8VE80/Q91VC3/Q922U1/Q922V4/Q99PV0/Q9DC48
Ribosome	0.002307	0.042759	O55142/P14131/P47955/P62702/P62908/Q8BU88/Q99N96/Q9CR57/Q9D116/Q9D1P0/Q9D338/Q9D823
Biosynthesis of amino acids	0.000316	0.01092	A6H5Y3/O35855/P05202/P12382/P16858/Q61176/Q8BPC6/Q91Y97/Q99MX0/Q9D7G0
Peroxisome	0.00049	0.015058	O35386/O35488/P11930/P41216/P51660/P58137/Q99LB2/Q9DC50/Q9EPL9/Q9WV68
Cysteine and methionine metabolism	7.52E-05	0.005208	A6H5Y3/O35855/P05202/P16125/P50247/P97355/Q71R19/Q9CQ65/Q9QXF8
Glutathione metabolism	0.001604	0.037007	O09131/P24472/P46412/P47791/P97355/Q64471/Q91VS7/Q99L20
2-Oxocarboxylic acid metabolism	6.84E-05	0.005208	A2ATU0/O35855/P05202/Q60597/Q6P3A8/Q8BPC6/Q9D2G2
Pentose phosphate pathway	0.000108	0.005978	P12382/Q64374/Q8CFX1/Q91Y97/Q99MX0/Q9D0F9/Q9D7G0
Fatty acid metabolism	0.002708	0.044958	O35448/P41216/P50544/P51660/P97742/Q9D404/Q9EPL9
Starch and sucrose metabolism	0.000195	0.008983	P70699/Q8C194/Q9D0F9/Q9D6Y9/Q9ET01/Q9WUB3
Propanoate metabolism	0.000311	0.01092	P16125/P16332/P61922/Q6P3A8/Q99NB1/Q9EPL9
Citrate cycle (TCA cycle)	0.002317	0.042759	Q60597/Q8BPC6/Q8K2B3/Q91V92/Q9D2G2

Table S4

KEGG enrichment analysis was used to analyze the pathways of intersection DEPs

Description	<i>p</i> -value	<i>q</i> -value	Gene ID
Salmonella infection	0.001272	0.03681	O35343/P07901/P16858/P47811/P61161/P62908/Q02248/Q64331/Q78JE5/Q99KJ8/Q9CVB6/Q9D898/Q9QZB7
Carbon metabolism	9.57E-07	0.000111	P05202/P12382/P16858/P28474/Q60597/Q64374/Q8CFX1/Q99KE1/Q99MX0/Q99NB1/Q9D7G0/Q9R0P3
Spliceosome	0.000542	0.017915	Q3UEB3/Q6ZWM4/Q8BGJ9/Q8CFQ3/Q91VC3/Q922U1/Q922V4/Q99PV0/Q9DC48
Purine metabolism	0.002667	0.056156	P00493/P08030/P55264/Q5SUR0/Q8CIH9/Q9CWJ9/Q9D0F9/Q9D7G0
Cysteine and methionine metabolism	4.65E-05	0.002693	A6H5Y3/O35855/P05202/P16125/P50247/P97355/Q71R19
Biosynthesis of amino acids	0.000513	0.017915	A6H5Y3/O35855/P05202/P12382/P16858/Q99MX0/Q9D7G0
Pentose phosphate pathway	2.49E-05	0.001923	P12382/Q64374/Q8CFX1/Q99MX0/Q9D0F9/Q9D7G0
Glycolysis / Gluconeogenesis	0.001915	0.049286	P12382/P16125/P16858/P28474/Q99NB1/Q9D0F9
Starch and sucrose metabolism	8.66E-05	0.004013	Q8CI94/Q9D0F9/Q9D6Y9/Q9ET01/Q9WUB3
Fatty acid metabolism	0.003203	0.06181	O35448/P41216/P50544/P97742/Q9D404
2-Oxocarboxylic acid metabolism	0.002175	0.050372	A2ATU0/O35855/P05202/Q60597
Alanine, aspartate and glutamate metabolism	0.004433	0.078972	P05202/P47856/P61922/Q8CIH9
Aminoacyl-tRNA biosynthesis	0.006595	0.109097	Q8CFI5/Q8VDC0/Q9CZD3/Q9JL8
Fatty acid degradation	0.012173	0.172399	P28474/P41216/P50544/P97742

Table S5

Major terms enriched in GO analysis of DEPS in the control and PFOS groups

Description	Ontology	GO IDs	<i>p</i> -value	<i>p</i> -adjust
transcription, DNA-templated	BP	GO:0006351	0.000485	0.007942
positive regulation of transcription by RNA polymerase II	BP	GO:0045944	6.55E-05	0.002084
protein transport	BP	GO:0015031	2.09E-11	3.74E-09
translation	BP	GO:0006412	2.56E-09	3.33E-07
negative regulation of transcription by RNA polymerase II	BP	GO:0000122	0.004399	0.034345
negative regulation of apoptotic process	BP	GO:0043066	0.000416	0.006935
mRNA processing	BP	GO:0006397	2.19E-09	2.93E-07
proteolysis	BP	GO:0006508	9.00E-12	1.68E-09
intracellular protein transport	BP	GO:0006886	0.000194	0.00454
apoptotic process	BP	GO:0006915	0.001844	0.019117
spermatogenesis	BP	GO:0007283	6.52E-05	0.002084
mRNA splicing, via spliceosome	BP	GO:0000398	1.60E-10	2.65E-08
multicellular organism development	BP	GO:0007275	0.001236	0.014823
RNA splicing	BP	GO:0008380	5.35E-10	7.92E-08
cell migration	BP	GO:0016477	4.20E-07	3.40E-05
cytoplasm	CC	GO:0005737	1.32E-98	2.84E-95
nucleus	CC	GO:0005634	2.65E-37	1.63E-34
extracellular exosome	CC	GO:0070062	5.23E-109	2.24E-105
cytosol	CC	GO:0005829	2.66E-71	2.85E-68
membrane	CC	GO:0016020	7.47E-47	5.34E-44
mitochondrion	CC	GO:0005739	4.50E-62	3.87E-59
nucleoplasm	CC	GO:0005654	2.48E-33	1.33E-30
plasma membrane	CC	GO:0005886	0.000884	0.011429
extracellular space	CC	GO:0005615	3.27E-05	0.001298
nucleolus	CC	GO:0005730	2.28E-14	7.01E-12
Golgi apparatus	CC	GO:0005794	1.13E-12	2.71E-10
endoplasmic reticulum	CC	GO:0005783	8.39E-12	1.64E-09
endoplasmic reticulum membrane	CC	GO:0005789	3.95E-13	9.97E-11
perinuclear region of cytoplasm	CC	GO:0048471	5.78E-12	1.18E-09
intracellular membrane-bounded organelle	CC	GO:0043231	1.38E-15	4.94E-13
ATP binding	MF	GO:0005524	0.000152061	0.003933443
metal ion binding	MF	GO:0046872	0.000129704	0.003525002
protein homodimerization activity	MF	GO:0042803	3.77E-12	8.10E-10
cadherin binding involved in cell-cell adhesion	MF	GO:0098641	5.10E-21	2.43E-18
identical protein binding	MF	GO:0042802	1.60E-10	2.65E-08
structural constituent of ribosome	MF	GO:0003735	1.20E-09	1.72E-07

RNA binding	MF	GO:0003723	0.00032339	0.005884055
chromatin binding	MF	GO:0003682	3.62E-05	0.001339888
protein kinase binding	MF	GO:0019901	4.81E-05	0.001678154
protein heterodimerization activity	MF	GO:0046982	5.32E-05	0.001812969
mRNA binding	MF	GO:0003729	6.32E-08	6.31E-06
magnesium ion binding	MF	GO:0000287	0.003463469	0.027955146
signaling receptor binding	MF	GO:0005102	0.000138951	0.003660459
transcription factor binding	MF	GO:0008134	0.000175444	0.004422787
enzyme binding	MF	GO:0019899	8.83E-05	0.002634403

Table S6

Major terms enriched in GO analysis of DEPS in the PFOS and FO groups.

Description	Ontology	GO IDs	<i>p</i> -value	<i>p</i> -adjust
transcription, DNA-templated	BP	GO:0006351	0.008742386	0.046270563
positive regulation of transcription by RNA polymerase II	BP	GO:0045944	0.000611185	0.011182554
proteolysis	BP	GO:0006508	3.53E-11	7.93E-09
translation	BP	GO:0006412	4.54E-05	0.002306786
multicellular organism development	BP	GO:0007275	0.000185962	0.005565815
protein transport	BP	GO:0015031	3.77E-05	0.002043437
response to drug	BP	GO:0042493	1.00E-05	0.000753019
cell division	BP	GO:0051301	2.10E-05	0.001310331
intracellular protein transport	BP	GO:0006886	0.002038954	0.024753005
regulation of cell proliferation	BP	GO:0042127	1.75E-05	0.00122095
spermatogenesis	BP	GO:0007283	0.005267031	0.043619335
mRNA splicing, via spliceosome	BP	GO:0000398	0.000115791	0.004140857
mRNA processing	BP	GO:0006397	0.002702461	0.028467975
cell cycle	BP	GO:0007049	0.003493135	0.033668252
aging	BP	GO:0007568	0.000688679	0.012107387
cytoplasm	CC	GO:0005737	1.34E-44	1.41E-41
extracellular exosome	CC	GO:0070062	3.60E-67	1.13E-63
nucleus	CC	GO:0005634	2.74E-16	1.08E-13
mitochondrion	CC	GO:0005739	7.90E-55	1.24E-51
membrane	CC	GO:0016020	6.17E-24	3.24E-21
cytosol	CC	GO:0005829	1.99E-33	1.57E-30
nucleoplasm	CC	GO:0005654	1.08E-18	4.87E-16
plasma membrane	CC	GO:0005886	0.002002	0.024521
perinuclear region of cytoplasm	CC	GO:0048471	9.72E-11	2.04E-08
nucleolus	CC	GO:0005730	1.22E-06	0.000133
endoplasmic reticulum	CC	GO:0005783	3.27E-06	0.000327
Golgi apparatus	CC	GO:0005794	2.03E-05	0.00131
endoplasmic reticulum membrane	CC	GO:0005789	2.98E-07	4.26E-05
focal adhesion	CC	GO:0005925	2.87E-10	5.64E-08
intracellular membrane-bounded organelle	CC	GO:0043231	6.00E-09	1.11E-06
metal ion binding	MF	GO:0046872	0.001036	0.016215
identical protein binding	MF	GO:0042802	6.18E-12	1.50E-09
protein homodimerization activity	MF	GO:0042803	1.20E-08	2.09E-06
cadherin binding involved in cell-cell adhesion	MF	GO:0098641	1.21E-12	3.45E-10
chromatin binding	MF	GO:0003682	0.00053	0.009866
structural constituent of ribosome	MF	GO:0003735	0.000221	0.005566
enzyme binding	MF	GO:0019899	5.22E-07	6.57E-05

GTPase activity	MF	GO:0003924	0.001457	0.020022
signaling receptor binding	MF	GO:0005102	0.000112	0.004102
transcription factor binding	MF	GO:0008134	0.000135	0.004603
protein kinase binding	MF	GO:0019901	0.004137	0.037843
microtubule binding	MF	GO:0008017	2.42E-05	0.001464
protein C-terminus binding	MF	GO:0008022	5.57E-05	0.002697
actin filament binding	MF	GO:0051015	2.75E-06	0.000288
mRNA binding	MF	GO:0003729	0.001509	0.020542

Table S7
Major terms enriched in GO analysis of intersection DEPs

Description	Ontology	GO IDs	<i>p</i> -value	<i>p</i> -adjust
transcription, DNA-templated	BP	GO:0006351	0.009988	0.0444
positive regulation of transcription by RNA polymerase II	BP	GO:0045944	0.000566	0.012217
proteolysis	BP	GO:0006508	3.32E-08	4.68E-06
regulation of cell proliferation	BP	GO:0042127	3.11E-07	3.65E-05
spermatogenesis	BP	GO:0007283	0.000186	0.005544
intracellular protein transport	BP	GO:0006886	0.002532	0.029433
multicellular organism development	BP	GO:0007275	0.002445	0.029229
cell differentiation	BP	GO:0030154	0.001925	0.025328
translation	BP	GO:0006412	0.008536	0.039616
protein transport	BP	GO:0015031	0.004063	0.029517
response to drug	BP	GO:0042493	0.002098	0.026588
mRNA splicing, via spliceosome	BP	GO:0000398	0.00012	0.003929
mRNA processing	BP	GO:0006397	0.001523	0.023192
positive regulation of gene expression	BP	GO:0010628	0.012266	0.046049
cell division	BP	GO:0051301	0.00635	0.039058
cytoplasm	CC	GO:0005737	8.51E-37	9.00E-34
extracellular exosome	CC	GO:0070062	2.65E-52	5.61E-49
nucleus	CC	GO:0005634	1.02E-13	3.09E-11
cytosol	CC	GO:0005829	7.89E-28	5.56E-25
mitochondrion	CC	GO:0005739	3.98E-27	2.11E-24
membrane	CC	GO:0016020	4.03E-16	1.42E-13
plasma membrane	CC	GO:0005886	0.002047	0.026098
nucleoplasm	CC	GO:0005654	1.89E-10	4.78E-08
perinuclear region of cytoplasm	CC	GO:0048471	2.42E-08	3.65E-06
extracellular space	CC	GO:0005615	0.014534	0.049844
nucleolus	CC	GO:0005730	0.000133	0.004141
Golgi apparatus	CC	GO:0005794	0.000195	0.005577
focal adhesion	CC	GO:0005925	5.93E-08	7.39E-06
mitochondrial matrix	CC	GO:0005759	2.03E-10	4.78E-08
cell-cell adherens junction	CC	GO:0005913	5.76E-08	7.39E-06
metal ion binding	MF	GO:0046872	0.004867	0.031984
identical protein binding	MF	GO:0042802	4.16E-10	8.80E-08
protein homodimerization activity	MF	GO:0042803	1.03E-08	1.81E-06
cadherin binding involved in cell-cell adhesion	MF	GO:0098641	8.60E-09	1.66E-06
chromatin binding	MF	GO:0003682	0.004589	0.030462
transcription factor binding	MF	GO:0008134	0.000119	0.003929
enzyme binding	MF	GO:0019899	7.70E-05	0.003013

pyridoxal phosphate binding	MF	GO:0030170	4.91E-06	0.000452
magnesium ion binding	MF	GO:0000287	0.014311	0.049159
metalloendopeptidase activity	MF	GO:0004222	0.007018	0.039616
microtubule binding	MF	GO:0008017	3.51E-05	0.001866
mRNA binding	MF	GO:0003729	0.001851	0.024951
actin filament binding	MF	GO:0051015	9.41E-05	0.003433
actin binding	MF	GO:0003779	0.007586	0.039616
aminopeptidase activity	MF	GO:0004177	7.83E-05	0.003013
