

Differential effects of metal ions on TCDD-induced cytotoxicity and cytochrome P4501A1 gene expression in a zebrafish liver (ZFL) cell-line

Electronic Supplementary Information

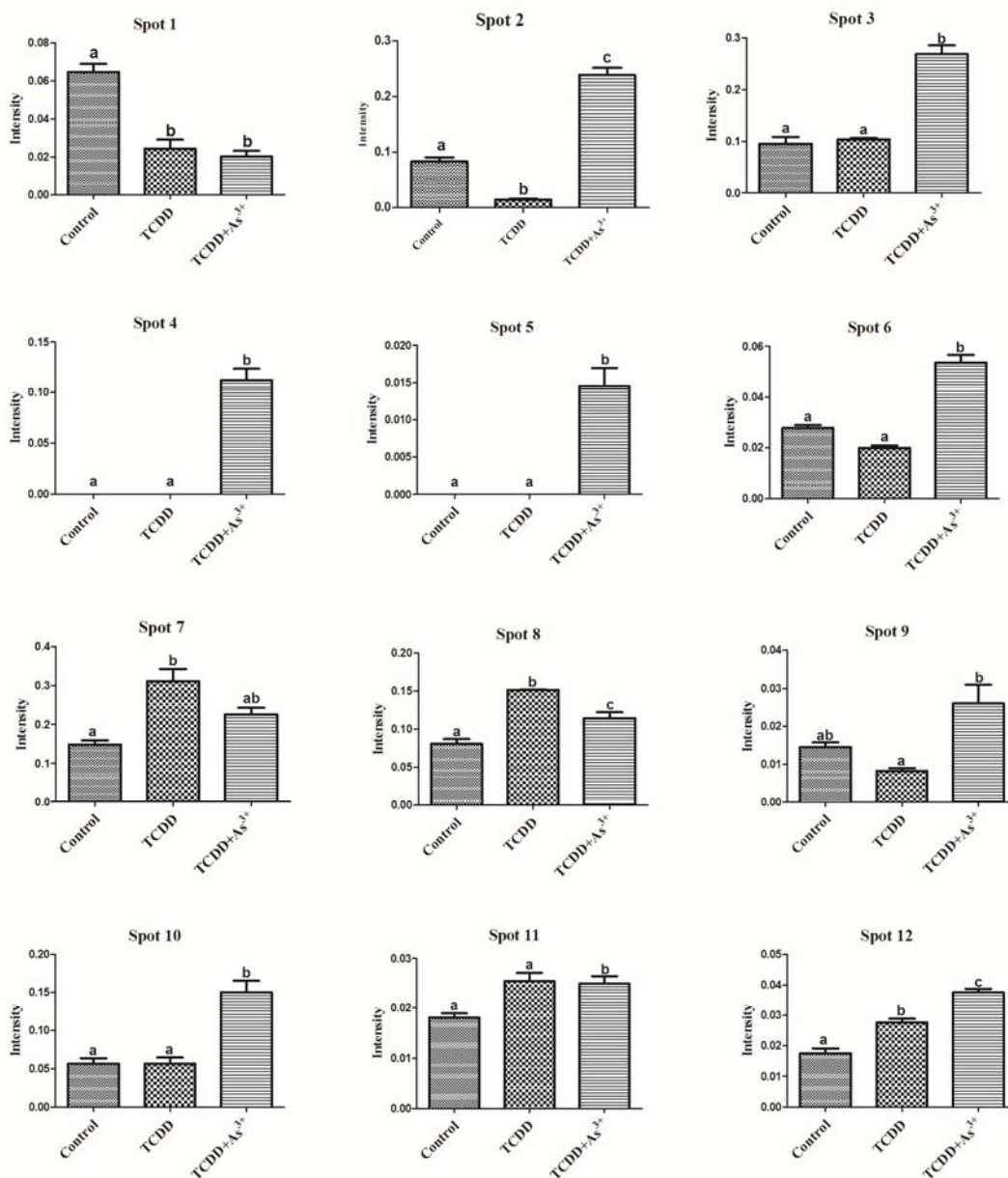


Figure S1-1

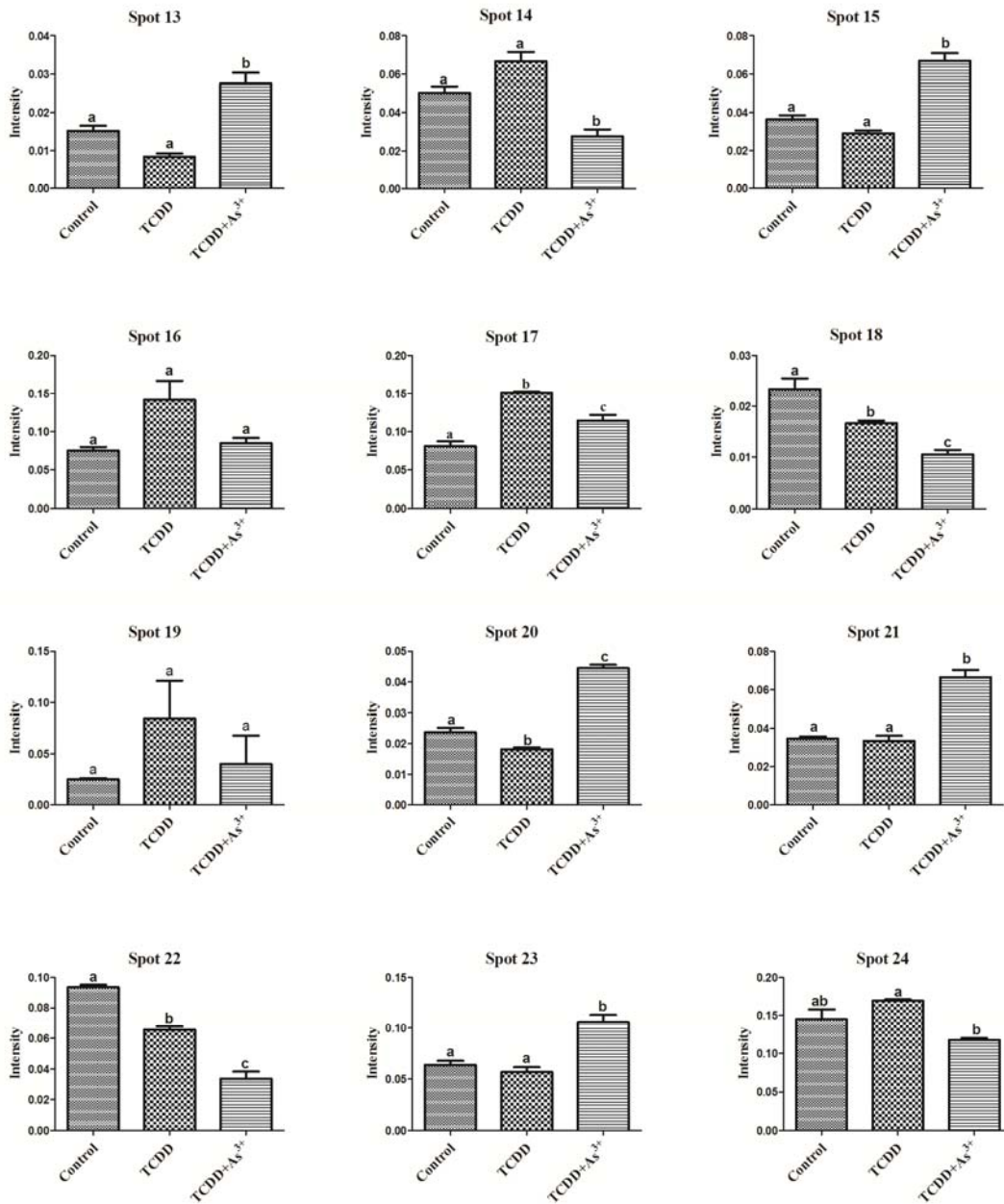


Figure S1-2

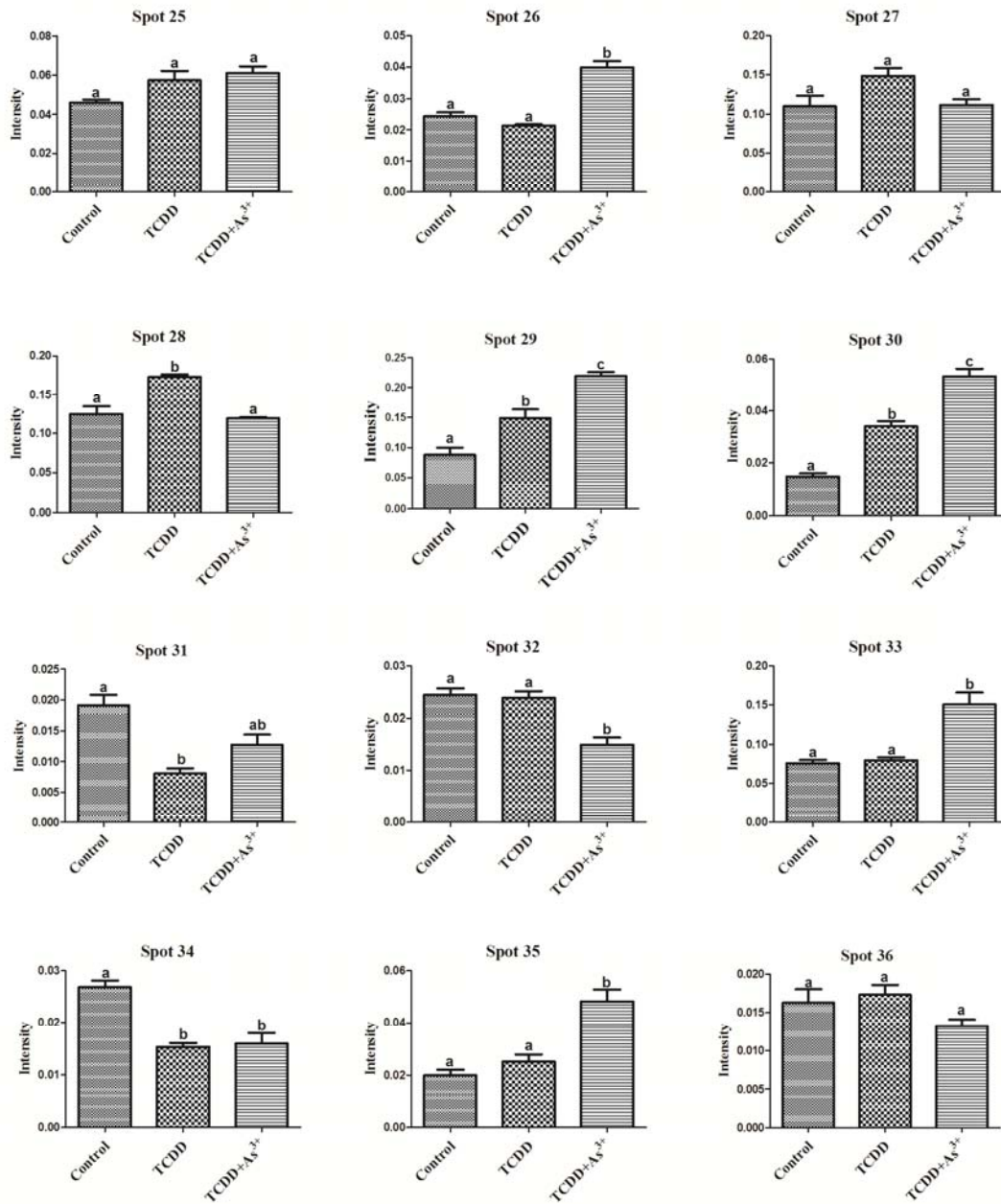


Figure S1-3

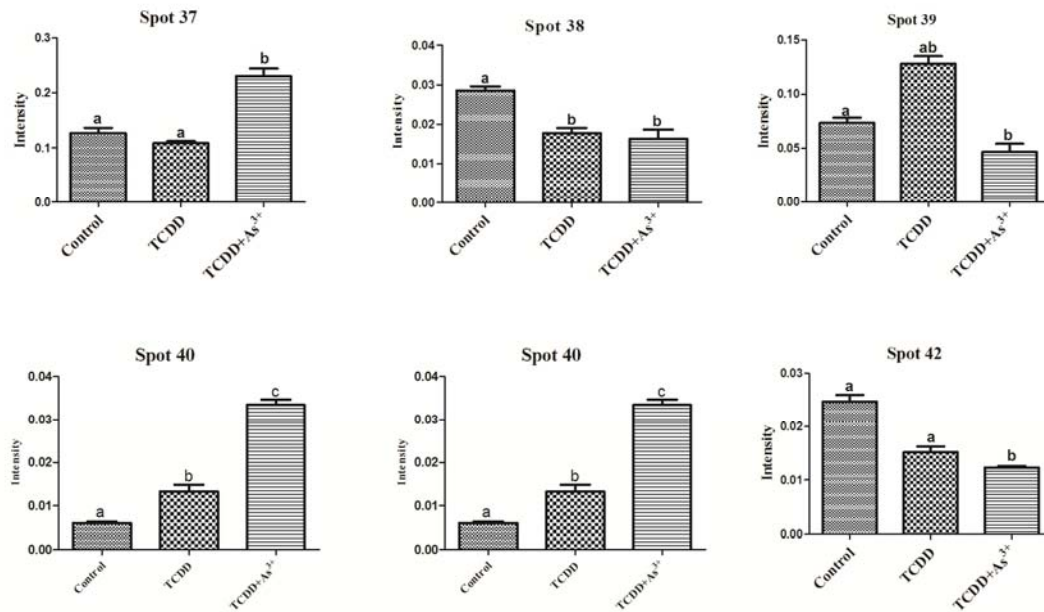


Figure S1-4

Table S1 GO Terms Enrichment Analysis of Gene Clusters of differentially expressed genes

P-value < 0.1 correspond to enrichment scores larger than 1 (red in table).

3 clusters	GO Term	Count	P_Value
	glycolysis	6	9.4E-9
	glucose catabolic process	6	2.3E-8
	hexose catabolic process	6	2.3E-8
	monosaccharide catabolic process	6	2.3E-8
	cellular carbohydrate catabolic process	6	3.7E-8
	alcohol catabolic process	6	3.7E-8
	glucose metabolic process	6	7.3E-8
	carbohydrate catabolic process	6	1.1E-7
	hexose metabolic process	6	2.4E-7
	monosaccharide metabolic process	6	3.1E-7
	generation of precursor metabolites and energy	6	4.2E-6

Cluster 2			
	nucleotide binding	4	4.5E-1
	adenyl nucleotide binding	4	4.5E-1
	nucleoside binding		4.5E-1
	purine nucleotide binding	4	6.4E-1
	ATP binding	3	6.9E-1
	adenyl ribonucleotide binding	3	8.4E-1
	purine ribonucleotide binding	3	8.4E-1
	ribonucleotide binding	3	8.4E-1
Cluster 3			
	metal ion binding	4	9.4E-1
	cation binding	4	9.5E-1
	ion binding	4	9.5E-1

Table S2 Summary of up/down regulated spots number (No)

TCDD	TCCD+ AS ³⁺	Spots no
up	-----	20
up	up	7
up	down	12
up	No effects	1
down	-----	16
down	up	12
down	up	3
down	No-effects	1
No-effects	up	5
No-effects	down	1

Up / down in TCDD treatment alone group represents up-regulation / down –regulation compare with control group.

Up and down in TCCD+ AS³⁺ treatment group represents up-regulation/down –regulation compare with TCDD treatment alone group.