GO ID	Function Name	Genes	Count	Ref	*p-val*
GO: 0008150	**biological process**				
GO:0008152	metabolism	*PGRP-SD; Cyp12a4*; CG3011; CG6687; *wal; PHGPx; ade2; Cyp12d1-p; Tal; CG6214; NA; Nmdmc; CG10444;* CG3036; tok; ade3; *CRMP;* CG10960; *eas;* CG11796; *Gyk; Ance-4;Cyp6d5;* CG8132; *pug; Got1; Hn;* CG12428; *fbp;* CG9009; *ade5;* CG5493; CG2789; CG5567; *Pcaf;* CG11963; *ref(2)P;* CG6045; *PGRP-LB;* CG10638; CG32549; *GstE7;* CG17836; CG11899*; GstE1*	45	3157	0.005
GO:0006807	nitrogen compound metabolism	*Got1;* CG3011; CG12428; *eas;* CG11796; Hn; CG8132; *pug; Nmdmc; CG5493; CG11899;*	11	260	0.002
GO:0044271	nitrogen compound biosynthesis	*Got1*; CG11899; CG3011; *eas; Nmdmc; pug*	6	55	0.001
GO:0009308	amine metabolism	Got1; CG3011; CG12428; eas; CG11796; *Nmdmc; pug; CG5493; Hn; CG11899;*	10	247	0.004
GO:0009309	amine biosynthesis	*Got1;* CG11899; CG3011; *eas;* CG11796; CG5493; *Hn;* CG11899;	6	55	0.001
GO:0006519	amino acid and derivative metabolism	*Got1;* CG3011; CG12428; *eas;* CG11796; *pug; CG5493;CG11899; Nmdmc;*	10	191	0.001
GO:0006520	amino acid metabolism	*Got1;* CG3011; CG12428; CG11796; CG5493; Hn; CG11899; Nmdmc; pug	9	173	0.002
GO:0008652	amino acid biosynthesis	*Got1;* CG11899; CG3011; *Nmdmc; pug*	5	47	0.003
GO:0019752	carboxylic acid metabolism	*Got1;* CG3011; CG12428; CG9009; CG11796; *Nmdmc; pug; CG5493; Hn; CG11899;*	10	252	0.004
GO:0006725	aromatic compound metabolism	CG6045; CG32549; CG11796; *ade5; Hn; Nmdmc; pug*	9	92	1.5×10^{-4}
GO:0046483	heterocycle metabolism	*ade5;* CG6045; *ade2; ade3;* CG32549; Nmdmc; pug	7	91	0.001
GO:0006144	purine base metabolism	*ade5;* CG6045; *ade2; ade3;* CG32549	5	36	0.001
GO:0009127	purine nucleoside monophosphate biosynthesis	*ade5; ade2; ade3*	3	11	0.004
GO:0009168	purine ribonucleoside monophosphate biosynthesis	*ade5; ade2; ade3*	3	11	0.004
GO:0006188	IMP biosynthesis	*ade5; ade2; ade3*	3	7	0.001
GO:0006732	coenzyme metabolism	CG10444; CG2789; *Tal;* CG6687; *Nmdmc;* CG11963; *pug*	7	145	0.008
GO:0009396	folic acid and derivative biosynthesis	*Nmdmc; pug*	2	2	0.003
GO: 0003674	**molecular function**				
GO:0003824	catalytic activity	*PGRP-SD; Cyp12a4;* CG3011; CG4716; *PHGPx; Cyp12d1-p;* CG6687;	40	2375	0.001
GO:0016491	oxidoreductase activity;	*Nmdmc; ade2; CRMP; eas*; CG11796; *Gyk; Tal;* CG8132; *Cyp6d5; wal; CG11899; GstE1 pug; Got1; tok;* CG1681; *ade3;* CG12428; *fbp;* CG9009; ade5; CG6045; PGRP-LB; Pcaf; CG5493; CG5567; *ref(2)P;* CG11963; CG10638; CG32549; CG6214; *GstE7; Hn;*	14	401	0.001
GO:0016645	oxidoreductase activity, acting on the CH-NH group of donors	CG4716; *Nmdmc; pug*	3	12	0.004
GO:0051213	dioxygenase activity	CG11796; CG5493	2	4	0.008
GO:0004486	methylenetetrahydrofolate dehydrogenase activity	CG4716; *Nmdmc; pug*	3	3	2.8×10^{-4}
GO:0016810	hydrolase activity	*PGRP-SD; PGRP-LB; CRMP;* CG8132; Nmdmc; pug	6	53	0.001
GO:0019238	cyclohydrolase activity	*Nmdmc; pug*	2	3	0.005
GO:0004372	transferase activity	*ade3;* CG3011	2	3	0.005

Additional data file 8: MnSOD-regulated xenobiotic detoxification genes. Gene Ontology classifications and functional overrepresentation of MnSOD up-regulated genes that are also up-regulated due to the xenobiotic response to phenobarbital.