

**Supplementary Table s6. Annotations produced by DAVID for the observed CGS between the Apc1 mutant and wild type.**

Annotation Cluster 1 Category	Enrichment Score: 5.261167414991856 Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
INTERPRO	IPR002334:Dol/Ves 1 allergen	6	2.53164557	4.84E-08	CG17191, CG6271, CG6283, CG6295, CG6296, CG17192	210	7	10984	44.83265306	1.84E-05	1.84E-05	6.71E-05	N
GOTERM_MF_DIRECT	GO:0052740-1-acyl-2-lysophosphatidylserine acylhydrolase activity	6	2.53164557	1.87E-07	CG17191, CG6271, CG6283, CG6295, CG6296, CG17192	164	9	9284	37.7398374	3.89E-05	3.89E-05	2.36E-04	Y
GOTERM_MF_DIRECT	GO:0052739-phosphatidylserine 1-acylhydrolase activity	6	2.53164557	1.87E-07	CG17191, CG6271, CG6283, CG6295, CG6296, CG17192	164	9	9284	37.7398374	3.89E-05	3.89E-05	2.36E-04	Y
GOTERM_MF_DIRECT	GO:0008970-phosphatidylcholine 1-acylhydrolase activity	6	2.53164557	1.87E-07	CG17191, CG6271, CG6283, CG6295, CG6296, CG17192	164	9	9284	37.7398374	3.89E-05	3.89E-05	2.36E-04	Y
GOTERM_BP_DIRECT	GO:0016042-lipid catabolic process	8	3.37552743	2.37E-05	CG2772, CG17191, CG6271, CG31091, CG6283, CG6295, CG6296, CG17192	182	53	10996	9.119635082	0.01066386	0.00534622	0.03366616	Y
UP_KEYWORDS	Secreted	17	7.17299578	2.84E-05	HH, CECC, DEF, EPSILONTRY, THETATRY, CG6283, ATTA, CG6295, CG6296, CG17192, IM3, BETATRY, CG6271, CG17191, CCHA1, MTK, TOTC	235	287	13921	3.508888724	0.0037765	0.00126042	0.03325868	N
GOTERM_MF_DIRECT	GO:0016298-lipase activity	6	2.53164557	1.57E-04	CG17191, CG6271, CG6283, CG6295, CG6296, CG17192	164	30	9284	11.32195122	0.03207452	0.01616796	0.1975127	Y
INTERPRO	IPR000734:Lipase	6	2.53164557	3.66E-04	CG17191, CG6271, CG6283, CG6295, CG6296, CG17192	210	33	10984	9.50995671	0.13004485	0.03422888	0.50512127	N
INTERPRO	IPR013818:Lipase, N-terminal	6	2.53164557	3.66E-04	CG17191, CG6271, CG6283, CG6295, CG6296, CG17192	210	33	10984	9.50995671	0.13004485	0.03422888	0.50512127	N
Annotation Cluster 2 Category	Enrichment Score: 4.375939730686171 Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
SMART	SM00587:CHK	9	3.79746835	1.28E-06	CG13658, CG9259, CG13360, CG10514, CG11892, CG33510, CG11893, CG6908, CHKOV1	86	51	5218	10.70725034	9.34E-05	9.34E-05	0.00133604	N
INTERPRO	IPR015897:CHK kinase-like	9	3.79746835	4.74E-06	CG13658, CG9259, CG13360, CG10514, CG11892, CG33510, CG11893, CG6908, CHKOV1	210	51	10984	9.230252101	0.00180383	6.02E-04	0.00656258	N
INTERPRO	IPR004119:Protein of unknown function DUF227	9	3.79746835	4.74E-06	CG13658, CG9259, CG13360, CG10514, CG11892, CG33510, CG11893, CG6908, CHKOV1	210	51	10984	9.230252101	0.00180383	6.02E-04	0.00656258	N
INTERPRO	IPR011009:Protein kinase-like domain	10	4.21940928	0.109071	CG13658, CG9259, CG13360, CG10514, TAKL2, CG11892, CG33510, CG11893, CG6908, CHKOV1	210	294	10984	1.779073534	1	0.86467682	79.7994397	N
Annotation Cluster 3 Category	Enrichment Score: 2.7029011380582055 Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
SMART	SM00631:Zn_pept	5	2.10970464	3.84E-04	CG8560, CG8562, CG8539, CG12374, CG18417	86	22	5218	13.78964059	0.02761704	0.0139052	0.39963795	N
UP_KEYWORDS	Carboxypeptidase	6	2.53164557	4.10E-04	CG8560, CG8562, CG32483, CG8539, CG12374, CG18417	235	38	13921	9.353415454	0.05313364	0.00905828	0.47884572	N
GOTERM_MF_DIRECT	GO:0004181-metalloproteinase activity	5	2.10970464	6.25E-04	CG8560, CG8562, CG8539, CG12374, CG18417	164	23	9284	12.30646872	0.12192132	0.04241395	0.78541692	Y
INTERPRO	IPR000834:Peptidase M14, carboxypeptidase A	5	2.10970464	8.49E-04	CG8560, CG8562, CG8539, CG12374, CG18417	210	23	10984	11.37060041	0.27645777	0.06266944	1.16937329	N
INTERPRO	IPR003146:Proteinase inhibitor, carboxypeptidase propeptide	4	1.68776371	0.003792	CG8560, CG8562, CG12374, CG18417	210	17	10984	12.3070028	0.76484794	0.18680877	5.12567587	N
INTERPRO	IPR009020:Proteinase inhibitor, propeptide	4	1.68776371	0.006096	CG8560, CG8562, CG12374, CG18417	210	20	10984	10.46095238	0.90268236	0.22807192	8.11999054	N
UP_KEYWORDS	Metalloprotease	4	1.68776371	0.062228	CG8560, CG8562, CG12374, CG18417	235	54	13921	4.388022065	0.99980548	0.33429224	52.8218268	N
Annotation Cluster 4 Category	Enrichment Score: 2.5149381300535785 Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
KEGG_PATHWAY	dme00983:Drug metabolism - other enzymes	7	2.9535865	4.57E-05	UGT86DI, UGT37B1, UGT86DG, UGT35B, RY, CG8353, CG5999	41	47	2737	9.942397509	0.00209926	0.00209926	0.04317034	N
KEGG_PATHWAY	dme00830:Retinol metabolism	6	2.53164557	6.63E-05	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG10672, CG5999	41	31	2737	12.92053501	0.00304625	0.00152429	0.06266836	N
KEGG_PATHWAY	dme00982:Drug metabolism - cytochrome P450	7	2.9535865	2.03E-04	UGT86DI, UGT37B1, UGT86DG, UGT35B, GSTD5, GSTE9, CG5999	41	61	2737	7.660535786	0.00930326	0.00311075	0.19186844	N
KEGG_PATHWAY	dme00980:Metabolism of xenobiotics by cytochrome P450	7	2.9535865	2.03E-04	UGT86DI, UGT37B1, UGT86DG, UGT35B, GSTD5, GSTE9, CG5999	41	61	2737	7.660535786	0.00930326	0.00311075	0.19186844	N

KEGG_PATHWAY	dme00040:Uridine and glucuronate interconversions	6	2.53164557	3.30E-04	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG5999, CG10863	41	43	2737	9.314804311	0.01508322	0.00379232	0.31179511	N
KEGG_PATHWAY	dme00053:Ascorbate and aldarate metabolism	5	2.10970464	8.15E-04	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG5999	41	30	2737	11.12601626	0.03683085	0.00747715	0.76810172	N
GOTERM_BP_DIRECT	GO:0052696--flavonoid glucuronidation	5	2.10970464	0.002239	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG5999	182	34	10996	8.884938591	0.63695354	0.18343184	3.13213241	Y
GOTERM_BP_DIRECT	GO:0009813--flavonoid biosynthetic process	5	2.10970464	0.002239	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG5999	182	34	10996	8.884938591	0.63695354	0.18343184	3.13213241	Y
KEGG_PATHWAY	dme00860:Porphyrin and chlorophyll metabolism	5	2.10970464	0.002935	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG5999	41	42	2737	7.947154472	0.12646216	0.02228198	2.73985462	N
GOTERM_MF_DIRECT	GO:0008194--UDP-glycosyltransferase activity	5	2.10970464	0.003482	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG5999	164	36	9284	7.862466125	0.51595086	0.13507611	4.30489748	Y
INTERPRO	IPR002213:UDP-glucuronosyl/UDP-glycosyltransferase	5	2.10970464	0.004202	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG5999	210	35	10984	7.472108844	0.79894095	0.18169453	5.66431691	N
GOTERM_MF_DIRECT	GO:0016758--transferase activity, transferring hexosyl groups	5	2.10970464	0.0061	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG5999	164	42	9284	6.739256678	0.71993176	0.19113264	7.42822325	Y
GOTERM_MF_DIRECT	GO:0015020--glucuronosyltransferase activity	4	1.68776371	0.013893	UGT86DI, UGT86DG, UGT35B, CG5999	164	29	9284	7.80824222	0.94551921	0.34012246	16.1780342	Y
GOTERM_CC_DIRECT	GO:0043231--intracellular membrane-bounded organelle	5	2.10970464	0.024069	UGT86DI, UGT37B1, UGT86DG, UGT35B, CG5999	168	66	10026	4.521103896	0.88838899	0.35502719	23.282994	N
GOTERM_BP_DIRECT	GO:0008152--metabolic process	6	2.53164557	0.093254	UGT86DI, UGT86DG, CG5361, CG4594, CG4830, CG5999	182	146	10996	2.482914346	1	0.92593349	75.0844809	N
UP_KEYWORDS	Glycosyltransferase	6	2.53164557	0.145482	UGT86DI, UGT37B1, UGT86DG, UGT35B, L(2)K12914, CG5999	235	165	13921	2.154119923	1	0.49059543	84.09135	N
UP_KEYWORDS	Transferase	15	6.32911392	0.877964	UGT37B1, AKAP200, UGT86DI, UGT86DG, UGT35B, CG31522, CG1946, CG5999, CG10344, CG1894, GSTD5, TAKL2, GFAT1, L(2)K12914, GSTE9	235	1081	13921	0.821993032	1	0.99323284	100	N
Annotation Cluster 5	Enrichment Score: 2.3004014201024727												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
GOTERM_BP_DIRECT	GO:0006508--proteolysis	24	10.1265823	3.21E-06	SDA, JON99CI, SWIM, BACE, CG32483, EPSILONTRY, THETATRY, CG8539, CG1304, PCL, JON25BII, CG30090, CG3734, CG8560, ADAMTS-A, BETATRY, JON25BI, CG8562, CG6337, JON65AII, CG14528, CG11912, CG12374, CG18417	182	475	10996	3.052677848	0.00145103	0.00145103	0.00456044	Y
UP_KEYWORDS	Protease	19	8.01687764	4.13E-05	HH, SDA, JON99CI, BACE, CG32483, EPSILONTRY, THETATRY, CG8539, PCL, JON25BII, CG30090, CG8560, BETATRY, JON25BI, CG8562, JON65AII, CG11912, CG12374, CG18417	235	362	13921	3.10919243	0.00548416	0.00137387	0.04833538	N
UP_KEYWORDS	Disulfide bond	26	10.9704641	1.59E-04	DEF, EPSILONTRY, FZ, THETATRY, IM3, CG8560, JON25BI, LPR1, CG8562, MEW, JON99CI, CG1304, JON25BII, CG12950, LYSX, CG30090, CG5731, ADAMTS-A, BETATRY, FZ3, CCHA1, MTHL8, JON65AII, CG11912, CG12374, CG18417	235	670	13921	2.298799619	0.02089667	0.00421471	0.18548889	N
UP_SEQ_FEATURE	domain:Peptidase S1	4	1.68776371	0.001854	BETATRY, JON99CI, EPSILONTRY, THETATRY	45	18	3113	15.37283951	0.2678916	0.14436666	2.23455539	N
UP_KEYWORDS	Serine protease	9	3.79746835	0.003406	BETATRY, JON25BI, JON99CI, EPSILONTRY, THETATRY, JON65AII, JON25BII, CG30090, CG11912	235	147	13921	3.626834564	0.36480232	0.04917413	3.9112361	N
UP_SEQ_FEATURE	site:Required for specificity	3	1.26582278	0.008177	BETATRY, EPSILONTRY, THETATRY	45	10	3113	20.75333333	0.74827318	0.36859237	9.51354071	N
INTERPRO	IPR018114:Peptidase S1, trypsin family, active site	10	4.21940928	0.009175	BETATRY, JON25BI, JON99CI, EPSILONTRY, THETATRY, CG1304, JON65AII, JON25BII, CG30090, CG11912	210	186	10984	2.812083973	0.97015471	0.29613791	11.9838965	N
UP_SEQ_FEATURE	disulfide bond	10	4.21940928	0.01018	IM3, FZ3, BETATRY, JON99CI, DEF, EPSILONTRY, FZ, THETATRY, MTHL8, LYSX	45	265	3113	2.61048218	0.82076732	0.34933971	11.7137756	N
UP_SEQ_FEATURE	active site:Charge relay system	4	1.68776371	0.011618	BETATRY, JON99CI, EPSILONTRY, THETATRY	45	34	3113	8.138562092	0.85959999	0.32473626	13.2624433	N
KEGG_PATHWAY	dme04080:Neuroactive ligand-receptor interaction	4	1.68776371	0.013696	BETATRY, EPSILONTRY, THETATRY, DH31-R	41	35	2737	7.629268293	0.46974284	0.0680612	12.2213051	N
UP_SEQ_FEATURE	propeptide:Activation peptide	3	1.26582278	0.013798	BETATRY, EPSILONTRY, THETATRY	45	13	3113	15.96410256	0.90310509	0.32228022	15.5627182	N
SMART	SM00020:Tryp_SpC	10	4.21940928	0.0206	BETATRY, JON25BI, JON99CI, EPSILONTRY, THETATRY, CG1304, JON65AII, JON25BII, CG30090, CG11912	86	252	5218	2.407715024	0.78117263	0.3973934	19.5281146	N
UP_KEYWORDS	Zymogen	4	1.68776371	0.025676	BETATRY, JON99CI, EPSILONTRY, THETATRY	235	38	13921	6.235610302	0.96855356	0.18412833	26.2243563	N

INTERPRO	IPR001314:Peptidase S1A, chymotrypsin-type	10	4.21940928	0.031053	BETATRY, JON25BI, JON99CI, EPSILONTRY, THETATRY, CG1304, JON65AII, JON25BII, CG30090, CG11912	210	229	10984	2.284050738	0.99999397	0.66466149	35.3950296	N
INTERPRO	IPR001254:Peptidase S1	10	4.21940928	0.05698	BETATRY, JON25BI, JON99CI, EPSILONTRY, THETATRY, CG1304, JON65AII, JON25BII, CG30090, CG11912	210	257	10984	2.035204743	1	0.77466349	55.6254482	N
GOTERM_MF_DIRECT	GO:004252--serine-type endopeptidase activity	10	4.21940928	0.058164	BETATRY, JON25BI, JON99CI, EPSILONTRY, THETATRY, CG1304, JON65AII, JON25BII, CG30090, CG11912	164	280	9284	2.021777003	0.99999614	0.58947065	53.04189	N
INTERPRO	IPR009003:Trypsin-like cysteine/serine peptidase domain	10	4.21940928	0.064306	BETATRY, JON25BI, JON99CI, EPSILONTRY, THETATRY, CG1304, JON65AII, JON25BII, CG30090, CG11912	210	263	10984	1.988774217	1	0.77454587	60.1686319	N
Annotation Cluster 6	Enrichment Score: 2.06538775108392												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
GOTERM_BP_DIRECT	GO:0019731--antibacterial humoral response	5	2.10970464	4.92E-04	IM3, CECC, DEF, MTK, ATTA	182	23	10996	13.13425705	0.19952636	0.07149907	0.69653064	Y
UP_KEYWORDS	Antimicrobial	5	2.10970464	6.35E-04	CECC, DEF, MTK, LYSX, ATTA	235	24	13921	12.34131206	0.08096375	0.01198894	0.7395214	N
UP_KEYWORDS	Antibiotic	4	1.68776371	0.001488	CECC, DEF, MTK, ATTA	235	14	13921	16.92522796	0.17968681	0.02445465	1.7262636	N
GOTERM_BP_DIRECT	GO:0050830--defense response to Gram-positive bacterium	6	2.53164557	0.002215	CECC, DEF, MTK, LYSX, ATTA, DPTB	182	56	10996	6.473312402	0.63295951	0.22164361	3.0988395	Y
UP_KEYWORDS	Innate immunity	6	2.53164557	0.004681	IM3, CECC, DEF, MTK, TOTC, ATTA	235	65	13921	5.468150573	0.46425111	0.05515599	5.33892062	N
UP_KEYWORDS	Immunity	6	2.53164557	0.006412	IM3, CECC, DEF, MTK, TOTC, ATTA	235	70	13921	5.077568389	0.57496457	0.06881617	7.24597797	N
GOTERM_BP_DIRECT	GO:0009617--response to bacterium	5	2.10970464	0.006762	IM3, DEF, MTK, PHK-3, TOTC	182	46	10996	6.567128524	0.95343843	0.40020257	9.18308139	Y
GOTERM_BP_DIRECT	GO:0006959--humoral immune response	4	1.68776371	0.006884	CECC, DEF, ATTA, DPTB	182	24	10996	10.06959707	0.95594839	0.3598522	9.34099915	Y
GOTERM_BP_DIRECT	GO:0045087--innate immune response	7	2.9535865	0.007343	IM3, CECC, DEF, MTK, RALA, TOTC, ATTA	182	104	10996	4.066568047	0.96425389	0.34059293	9.93391667	Y
GOTERM_BP_DIRECT	GO:0050829--defense response to Gram-negative bacterium	6	2.53164557	0.03277	CECC, MTK, TEP2, RALA, LYSX, ATTA	182	108	10996	3.356532357	0.99999971	0.71492452	37.6863505	N
UP_SEQ_FEATURE	sequence variant	7	2.9535865	0.093892	CECC, CYP4D1, DEF, MTK, MLE, CLC-A, LYSX	45	225	3113	2.152197531	0.99999994	0.84125735	69.8944054	N
UP_KEYWORDS	Polymorphism	5	2.10970464	0.143657	CECC, CYP4D1, DEF, E(SPL)M3-HLH, MTK	235	120	13921	2.468262411	1	0.50897023	83.6896722	N
GOTERM_BP_DIRECT	GO:0042742--defense response to bacterium	3	1.26582278	0.302419	CECC, DEF, ATTA	182	67	10996	2.705264884	1	0.99382304	99.3978886	N
Annotation Cluster 7	Enrichment Score: 2.0516651961259957												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
UP_KEYWORDS	Membrane	74	31.2236287	0.003852	HH, SDA, CG10344, CG30495, CG33080, LPR1, RALA, CG4991, CG12824, TSP42EI, CG10444, CYP4D1, UGT35B, CG33474, CLC-A, CG31522, WLS, CYP4P1, CYP28A5, CYP6A2, GAL, CYP4P2, DTG, ASTA-R2, CG5999, ADAMTS-A, CG43187, ORK1, CG31259, CG5361, IRK1, CG8195, L(2)K12914, CG16700, PPK12, CG5697, CG31475, SUGB, UGT37B1, UGT86DI, CG10936, CG10073, UGT86DG, MFS9, CG4607, CG17928, FZ, VHA100-4, MFS1, CG1698, IR76A, CG17752, CG6901, BMCP, CG43394, DH31-R, LRCH, MEW, P24-1, CG10062, MIPP1, OUT, CG8925, CG12950, CG1946, CG17664, FZ3, CG1139, SESN, MES2, CG3961, MTHL8, CG5070, CG31446	235	3266	13921	1.342202707	0.40149582	0.05003694	4.41258549	N
GOTERM_CC_DIRECT	GO:0016021--integral component of membrane	62	26.1603376	0.010197	SDA, CG10344, CG30495, CG33080, LPR1, CG4991, CG12824, TSP42EI, UGT35B, CLC-A, CG31522, GAL, DTG, ASTA-R2, CG5999, ADAMTS-A, CG43187, ORK1, CG31259, CG5361, IRK1, CG8195, L(2)K12914, CG16700, PPK12, CG5697, CG31475, SUGB, UGT37B1, UGT86DI, CG10936, UGT86DG, CG10073, MFS9, CG4607, CG17928, FZ, VHA100-4, MFS1, CG1698, IR76A, CG17752, CG6901, BMCP, DH31-R, CG43394, LRCH, P24-1, CG10062, OUT, CG8925, CG12950, CG1946, CG17664, CG1139, FZ3, SESN, MES2, CG3961, MTHL8, CG5070, CG31446	168	2814	10026	1.314879683	0.60243928	0.20594448	10.5504996	Y



Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
UP_KEYWORDS	Iron	9	3.79746835	0.01466	RFESP, CYP4D1, RY, RNRS, AOX3, CYP6A2, CYP28A5, CYP4P1, CYP4P2	235	189	13921	2.820871327	0.85972524	0.11552366	15.8592957	N
GOTERM_MF_DIRECT	GO:0016491-oxidoreductase activity	9	3.79746835	0.02034	CG30495, CG9509, CG17928, RNRS, CYP6A2, CYP28A5, CG10672, CG3270, CG10863	164	193	9284	2.639833186	0.98607822	0.41391331	22.8347146	Y
UP_SEQ_FEATURE	binding site:Heme (covalent; via 1 link)	3	1.26582278	0.020665	CYP4D1, CYP4P1, CYP4P2	45	16	3113	12.97083333	0.97004686	0.39417261	22.4497347	N
GOTERM_CC_DIRECT	GO:0031090-organelle membrane	5	2.10970464	0.042584	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	168	79	10026	3.777124774	0.98008994	0.38710782	37.712556	N
UP_KEYWORDS	Microsome	5	2.10970464	0.043979	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	235	79	13921	3.749259359	0.99747538	0.27008305	40.8966217	N
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	5	2.10970464	0.044987	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	45	96	3113	3.603009259	0.9995619	0.61963843	42.9041027	N
GOTERM_MF_DIRECT	GO:0005506-iron ion binding	7	2.9535865	0.045967	CYP4D1, RY, AOX3, CYP6A2, CYP28A5, CYP4P1, CYP4P2	164	148	9284	2.677488464	0.99994387	0.589264	44.7662993	N
UP_KEYWORDS	Oxidoreductase	17	7.17299578	0.046974	CYP4D1, CG17544, CG9509, RNRS, CG17928, CYP28A5, CYP4P1, CYP6A2, CYP4P2, CG10672, CG14688, RFESP, CG30495, RY, AOX3, CG3270, CG10863	235	601	13921	1.67562573	0.99833681	0.27381536	43.0259345	N
INTERPRO	IPR017972:Cytochrome P450, conserved site	5	2.10970464	0.065941	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	210	80	10984	3.269047619	1	0.76399294	61.1216507	N
GOTERM_MF_DIRECT	GO:0004497-monoxygenase activity	5	2.10970464	0.068814	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	164	88	9284	3.216463415	0.99999964	0.56126977	59.3171917	N
GOTERM_MF_DIRECT	GO:0016705-oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	5	2.10970464	0.075827	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	164	91	9284	3.110426159	0.99999992	0.57821514	63.0171841	N
COG_ONTOLOGY	Secondary metabolites biosynthesis, transport, and catabolism	5	2.10970464	0.082152	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	24	91	1239	2.836538462	0.61052802	0.3759231	41.3753614	N
INTERPRO	IPR001128:Cytochrome P450	5	2.10970464	0.086738	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	210	88	10984	2.971861472	1	0.83788045	71.5372547	N
UP_KEYWORDS	Endoplasmic reticulum	7	2.9535865	0.090816	CYP4D1, CYP6A2, CYP28A5, WLS, CYP4P1, CYP4P2, L(2)K12914	235	184	13921	2.253630897	0.99999683	0.4099849	67.1506532	N
UP_KEYWORDS	Monoxygenase	5	2.10970464	0.09555	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	235	103	13921	2.875645528	0.99999842	0.41390801	69.0960509	N
UP_KEYWORDS	Heme	5	2.10970464	0.131582	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	235	116	13921	2.553374908	0.99999999	0.48836392	80.7882202	N
GOTERM_BP_DIRECT	GO:0055114-oxidation-reduction process	11	4.64135021	0.142254	CYP4D1, CG9509, RY, RNRS, AOX3, CYP6A2, CYP28A5, CYP4P1, CYP4P2, CG3270, CG10863	182	412	10996	1.613090793	1	0.96321859	88.6769114	N
INTERPRO	IPR002401:Cytochrome P450, E-class, group I	4	1.68776371	0.180675	CYP4D1, CYP6A2, CYP4P1, CYP4P2	210	77	10984	2.717130489	1	0.95772184	93.6695816	N
GOTERM_MF_DIRECT	GO:0020037-heme binding	5	2.10970464	0.201944	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	164	132	9284	2.144308943	1	0.8128247	94.1895748	N
GOTERM_CC_DIRECT	GO:0005789-endoplasmic reticulum membrane	5	2.10970464	0.504664	CYP4D1, CYP6A2, CYP28A5, CYP4P1, CYP4P2	168	221	10026	1.350193924	1	0.99227736	99.9520389	N
Annotation Cluster 12	Enrichment Score: 1.1207098573368486												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
GOTERM_MF_DIRECT	GO:0016614-oxidoreductase activity, acting on CH-OH group of donors	3	1.26582278	0.056263	CG9509, RY, AOX3	164	22	9284	7.719512195	0.99999412	0.63349111	51.831838	N
GOTERM_MF_DIRECT	GO:0009055-electron carrier activity	4	1.68776371	0.057173	CG17544, RY, AOX3, CYP28A5	164	50	9284	4.528780488	0.99999519	0.61013616	52.4144593	N
UP_KEYWORDS	FAD	4	1.68776371	0.079909	CG17544, CG9509, RY, AOX3	235	60	13921	3.949219858	0.99998453	0.3822013	62.2358219	N
GOTERM_MF_DIRECT	GO:0050660-flavin adenine dinucleotide binding	4	1.68776371	0.088149	CG17544, CG9509, RY, AOX3	164	60	9284	3.77398374	1	0.59908188	68.777855	N
UP_KEYWORDS	Flavoprotein	4	1.68776371	0.109957	CG17544, CG9509, RY, AOX3	235	69	13921	3.434104224	0.99999981	0.44891723	74.3863425	N
Annotation Cluster 13	Enrichment Score: 1.1200972165701493												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
INTERPRO	IPR020846:Major facilitator superfamily domain	8	3.37552743	0.049797	SUGB, MFS9, CG4607, OUT, CG8925, CG17752, CG6901, MFS1	210	175	10984	2.39107483	1	0.77620715	50.7084961	N
GOTERM_BP_DIRECT	GO:0055085-transmembrane transport	10	4.21940928	0.050401	CG10444, MFS9, CG4607, OUT, CG8925, CG17752, CG6901, BMCP, MFS1, CG17664	182	290	10996	2.083364911	1	0.83438865	52.0087935	N
GOTERM_MF_DIRECT	GO:0022857-transmembrane transporter activity	5	2.10970464	0.064335	MFS9, CG17752, CG6901, BMCP, MFS1	164	86	9284	3.291264889	0.99999902	0.57872815	56.7787194	N
INTERPRO	IPR011701:Major facilitator superfamily	4	1.68776371	0.204887	MFS9, OUT, CG8925, MFS1	210	82	10984	2.5514518	1	0.96962392	95.8215929	N
Annotation Cluster 14	Enrichment Score: 1.1179470584136082												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
INTERPRO	IPR013057:Amino acid transporter, transmembrane	3	1.26582278	0.036291	CG1139, CG4991, CG16700	210	16	10984	9.807142857	0.99999924	0.69076762	40.067289	N
GOTERM_BP_DIRECT	GO:0003333-amino acid transmembrane transport	3	1.26582278	0.102137	CG1139, CG4991, CG16700	182	33	10996	5.492507493	1	0.92292824	78.3342372	N

GOTERM_MF_DIRECT	GO:0015171--amino acid transmembrane transporter activity	3	1.26582278	0.119448	CG1139, CG4991, CG16700	164	34	9284	4.994978479	1	0.68348659	79.903773	N
Annotation Cluster 15	Enrichment Score: 0.9737234206526821												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
SMART	SM00516:SEC14	3	1.26582278	0.080214	CG32407, CG3091, CG5973	86	29	5218	6.276663994	0.99776565	0.78258591	58.220111	N
INTERPRO	IPR011074:CRAL/TRIO, N-terminal domain	3	1.26582278	0.104712	CG32407, CG3091, CG5973	210	29	10984	5.410837438	1	0.86557898	78.3867405	N
INTERPRO	IPR001251:CRAL-TRIO domain	3	1.26582278	0.142753	CG32407, CG3091, CG5973	210	35	10984	4.483265306	1	0.92203753	88.1541102	N
Annotation Cluster 16	Enrichment Score: 0.591296993313303												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
GOTERM_MF_DIRECT	GO:0017147--Wnt-protein binding	4	1.68776371	0.002515	FZ3, SWIM, FZ, WLS	164	16	9284	14.15243902	0.40771687	0.12273189	3.12655417	Y
UP_KEYWORDS	G-protein coupled receptor	5	2.10970464	0.071557	FZ3, FZ, MTHL8, ASTA-R2, DH31-R	235	93	13921	3.184854724	0.99994854	0.36163842	58.0269133	N
INTERPRO	IPR017981:GPCR, family 2-like	3	1.26582278	0.09868	FZ3, FZ, DH31-R	210	28	10984	5.604081633	1	0.86181903	76.280233	N
GOTERM_BP_DIRECT	GO:0016055--Wnt signaling pathway	4	1.68776371	0.118823	FZ3, FZ, PCL, WLS	182	73	10996	3.310552461	1	0.94266449	83.3996741	N
UP_KEYWORDS	Wnt signaling pathway	3	1.26582278	0.156839	FZ3, FZ, WLS	235	42	13921	4.231306991	1	0.50788573	86.3953047	N
GOTERM_MF_DIRECT	GO:0004930--G-protein coupled receptor activity	4	1.68776371	0.16997	FZ3, FZ, MTHL8, ASTA-R2	164	81	9284	2.795543511	1	0.78774373	90.4629385	N
GOTERM_BP_DIRECT	GO:0007186--G-protein coupled receptor signaling pathway	5	2.10970464	0.209666	FZ3, FZ, MTHL8, ASTA-R2, DH31-R	182	143	10996	2.112502882	1	0.98053413	96.4573873	N
GOTERM_CC_DIRECT	GO:0005886--plasma membrane	15	6.32911392	0.437459	MOD(MDG4), HH, AKAP200, SDA, MFS9, FZ, MIPP1, WLS, MFS1, CG1139, ORK1, MTHL8, RALA, PROS, HEXO2	168	786	10026	1.138904035	1	0.9909675	99.8085778	N
UP_KEYWORDS	Cell membrane	8	3.37552743	0.476645	CG1139, HH, MEW, FZ, MIPP1, MTHL8, RALA, WLS	235	391	13921	1.212036785	1	0.85246784	99.9484836	N
UP_SEQ_FEATURE	topological domain:Cytoplasmic	7	2.9535865	0.497739	FZ3, ORK1, MEW, FZ, CLC-A, MTHL8, WLS	45	397	3113	1.219759306	1	0.9995529	99.9771611	N
UP_KEYWORDS	Transducer	5	2.10970464	0.529094	FZ3, FZ, MTHL8, ASTA-R2, DH31-R	235	226	13921	1.310581811	1	0.88129348	99.9850137	N
UP_KEYWORDS	Receptor	8	3.37552743	0.609859	FZ3, MEW, LPR1, IR76A, FZ, MTHL8, ASTA-R2, DH31-R	235	439	13921	1.079513401	1	0.92229323	99.9983395	N
UP_SEQ_FEATURE	topological domain:Extracellular	5	2.10970464	0.656947	FZ3, MEW, FZ, MTHL8, WLS	45	312	3113	1.108618234	1	0.99998678	99.9997798	N
UP_SEQ_FEATURE	transmembrane region	8	3.37552743	0.713023	FZ3, ORK1, MEW, FZ, CLC-A, MTHL8, WLS, L(2)K12914	45	566	3113	0.977777778	1	0.99999129	99.9999749	N
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	6	2.53164557	0.733423	FZ3, ORK1, MEW, FZ, MTHL8, WLS	45	423	3113	0.981245075	1	0.99999162	99.9999898	N
UP_KEYWORDS	Glycoprotein	8	3.37552743	0.746109	CG1139, FZ3, ORK1, MEW, FZ, MIPP1, MTHL8, WLS	235	503	13921	0.942159807	1	0.96998974	99.9999891	N
GOTERM_BP_DIRECT	GO:0007476--imaginal disc-derived wing morphogenesis	3	1.26582278	0.876193	MEW, FZ, WLS	182	217	10996	0.835266116	1	1	100	N
Annotation Cluster 17	Enrichment Score: 0.39890087452955725												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
GOTERM_MF_DIRECT	GO:0003700--transcription factor activity, sequence-specific DNA binding	9	3.79746835	0.110985	LAB, XBP1, FOXK, E(SPL)M3-HLH, PDM2, PCL, REPTOR-BP, PROS, PTX1	164	275	9284	1.852682927	1	0.6711809	77.3266801	N
UP_SEQ_FEATURE	mutagenesis site	6	2.53164557	0.157916	MOD(MDG4), HH, ESG, PCL, DRM, WLS	45	204	3113	2.034640523	1	0.94428505	87.6641581	N
UP_SEQ_FEATURE	DNA-binding region:Homeobox	3	1.26582278	0.16151	LAB, PDM2, PTX1	45	51	3113	4.069281046	1	0.932141	88.2900604	N
GOTERM_BP_DIRECT	GO:0006351--transcription, DNA-templated	10	4.21940928	0.167726	MOD(MDG4), LAB, ESG, E(SPL)M3-HLH, PDM2, PCL, MEF2, DRM, PROS, PTX1	182	376	10996	1.606850596	1	0.97289439	92.619197	N
GOTERM_MF_DIRECT	GO:0043565--sequence-specific DNA binding	8	3.37552743	0.17995	LAB, FOXK, TRAX, E(SPL)M3-HLH, PDM2, CTCF, REPTOR-BP, PTX1	164	263	9284	1.721969767	1	0.79548696	91.8126696	N
UP_KEYWORDS	Developmental protein	14	5.907173	0.199676	LAB, HH, PDM2, E(SPL)M3-HLH, ESG, FZ, MIPP1, PCL, WLS, DRM, FZ3, MEF2, PROS, PTX1	235	593	13921	1.398543289	1	0.58159296	92.6054923	N
UP_KEYWORDS	Homeobox	4	1.68776371	0.254689	LAB, PDM2, PROS, PTX1	235	104	13921	2.278396072	1	0.67274752	96.7843297	N
UP_KEYWORDS	Transcription regulation	10	4.21940928	0.266878	MOD(MDG4), LAB, ESG, E(SPL)M3-HLH, PDM2, PCL, MEF2, DRM, PROS, PTX1	235	416	13921	1.423997545	1	0.68238414	97.348214	N
GOTERM_BP_DIRECT	GO:0045892--negative regulation of transcription, DNA-templated	4	1.68776371	0.316502	ESG, PCL, CTCF, DRM	182	120	10996	2.013919414	1	0.99364701	99.5492482	N
GOTERM_BP_DIRECT	GO:0045944--positive regulation of transcription from RNA polymerase II promoter	6	2.53164557	0.321769	LAB, ESG, MLE, MEF2, DRM, PROS	182	228	10996	1.589936379	1	0.99335706	99.5961297	N
UP_KEYWORDS	Activator	4	1.68776371	0.323375	ESG, PDM2, MEF2, PTX1	235	119	13921	1.99120329	1	0.72715986	98.9617543	N

UP_KEYWORDS	Transcription	10	4.21940928	0.325396	MOD(MDG4), LAB, ESG, E(SPL)M3-HLH, PDM2, PCL, MEF2, DRM, PROS, PTX1	235	442	13921	1.340232984	1	0.7210978	98.9974449	N
SMART	SM00389:HOX	3	1.26582278	0.498463	LAB, PDM2, PTX1	86	102	5218	1.784541724	1	0.99977422	99.9255639	N
INTERPRO	IPR017970:Homeobox, conserved site	3	1.26582278	0.525425	LAB, PDM2, PTX1	210	92	10984	1.705590062	1	0.99997294	99.996711	N
INTERPRO	IPR009057:Homeodomain-like	4	1.68776371	0.542099	LAB, PDM2, PROS, PTX1	210	149	10984	1.404154682	1	0.99997579	99.9979958	N
INTERPRO	IPR001356:Homeodomain	3	1.26582278	0.581469	LAB, PDM2, PTX1	210	102	10984	1.53837535	1	0.99998928	99.9994229	N
GOTERM_BP_DIRECT	GO:0006355--regulation of transcription, DNA-templated	7	2.9535865	0.651525	LAB, CG1894, FOXK, E(SPL)M3-HLH, PDM2, PROS, PTX1	182	401	10996	1.054671015	1	0.99999329	99.9999683	N
UP_KEYWORDS	DNA-binding	9	3.79746835	0.681835	LAB, FOXK, ESG, E(SPL)M3-HLH, PDM2, MEF2, DRM, PROS, PTX1	235	535	13921	0.996532114	1	0.94953439	99.999847	N
GOTERM_BP_DIRECT	GO:0001122--negative regulation of transcription from RNA polymerase II promoter	3	1.26582278	0.707461	ESG, DRM, PROS	182	149	10996	1.216461391	1	0.9999982	99.9999974	N
GOTERM_MF_DIRECT	GO:0003677--DNA binding	7	2.9535865	0.930443	MOD(MDG4), ESG, PDM2, PCL, MEF2, DRM, PROS	164	555	9284	0.713996924	1	0.99999954	100	N
UP_KEYWORDS	Nucleus	14	5.907173	0.949719	MOD(MDG4), HH, LAB, SESN, CG1894, ESG, E(SPL)M3-HLH, PDM2, MLE, PCL, MEF2, DRM, PROS, PTX1	235	1134	13921	0.731337011	1	0.99906686	100	N
UP_KEYWORDS	Zinc-finger	4	1.68776371	0.958705	MOD(MDG4), ESG, PCL, DRM	235	384	13921	0.617065603	1	0.99932993	100	N
GOTERM_CC_DIRECT	GO:0005634--nucleus	22	9.28270042	0.982125	MOD(MDG4), HH, LAB, PDM2, CG12493, E(SPL)M3-HLH, ESG, MLE, PCL, CTCF, DRM, MES2, SESN, CG1894, XBP1, FUSS, MEF2, CG32104, REPTOR-BP, PROS, PTX1, CG12119	168	1832	10026	0.716664067	1	1	100	N
UP_KEYWORDS	Phosphoprotein	8	3.37552743	0.995064	MOD(MDG4), ORK1, SESN, PDM2, RNRS, PCL, MEF2, PROS	235	909	13921	0.521349156	1	0.99999065	100	N
Annotation Cluster 18	Enrichment Score: 0.39229739210790504												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
GOTERM_BP_DIRECT	GO:0007264--small GTPase mediated signal transduction	4	1.68776371	0.101429	DND, CG5160, RALA, CG7787	182	68	10996	3.553975436	1	0.9318215	78.0905794	N
UP_KEYWORDS	GTP-binding	4	1.68776371	0.291165	DND, CG5160, RALA, BETATUB60D	235	112	13921	2.115653495	1	0.70975158	98.211639	N
GOTERM_MF_DIRECT	GO:0005525--GTP binding	5	2.10970464	0.373764	DND, CG10924, CG5160, RALA, BETATUB60D	164	176	9284	1.608231707	1	0.95673093	99.7271237	N
UP_KEYWORDS	Nucleotide-binding	6	2.53164557	0.992686	DND, TAKL2, MLE, CG5160, RALA, BETATUB60D	235	701	13921	0.507032507	1	0.99998157	100	N
INTERPRO	IPR027417:P-loop containing nucleoside triphosphate hydrolase	4	1.68776371	0.997244	DND, MLE, CG5160, RALA	210	512	10984	0.408630952	1	1	100	N
Annotation Cluster 19	Enrichment Score: 0.3211910835193623												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
UP_SEQ_FEATURE	splice variant	12	5.06329114	0.230659	MOD(MDG4), HH, LAB, SESN, MEW, CYP4D1, FZ, MLE, CLC-A, MEF2, WLS, PROS	45	610	3113	1.360874317	1	0.97455148	95.8937629	N
UP_KEYWORDS	Alternative splicing	12	5.06329114	0.496433	MOD(MDG4), HH, LAB, SESN, MEW, CYP4D1, PDM2, MLE, CLC-A, MEF2, WLS, PROS	235	631	13921	1.12656034	1	0.86241973	99.967174	N
UP_KEYWORDS	Nucleus	14	5.907173	0.949719	MOD(MDG4), HH, LAB, SESN, CG1894, ESG, E(SPL)M3-HLH, PDM2, MLE, PCL, MEF2, DRM, PROS, PTX1	235	1134	13921	0.731337011	1	0.99906686	100	N
Annotation Cluster 20	Enrichment Score: 0.1008313109778247												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	Included for comparison (Top 20 significance)
GOTERM_BP_DIRECT	GO:0045892--negative regulation of transcription, DNA-templated	4	1.68776371	0.316502	ESG, PCL, CTCF, DRM	182	120	10996	2.013919414	1	0.99364701	99.5492482	N
INTERPRO	IPR013087:Zinc finger C2H2-type/integrase DNA-binding domain	3	1.26582278	0.930798	ESG, CTCF, DRM	210	225	10984	0.697396825	1	1	100	N
SMART	SM00355:ZnF_C2H2	3	1.26582278	0.940649	ESG, CTCF, DRM	86	271	5218	0.671672531	1	1	100	N
GOTERM_MF_DIRECT	GO:0046872--metal ion binding	8	3.37552743	0.948073	MOD(MDG4), RFESP, CG6839, HH, ESG, RNRS, CTCF, DRM	164	656	9284	0.690362879	1	0.99999986	100	N
INTERPRO	IPR015880:Zinc finger, C2H2-like	3	1.26582278	0.967186	ESG, CTCF, DRM	210	271	10984	0.579019504	1	1	100	N
INTERPRO	IPR007087:Zinc finger, C2H2	3	1.26582278	0.97724	ESG, CTCF, DRM	210	293	10984	0.535543637	1	1	100	N