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Supplementary Information for

Species Groups Distributed Across Elevational Gradients Reveal Convergent and Continuous Genetic Adaptation to High Elevations

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This PDF file includes:

Figure S1 to S2
Tables S1 to S36

Other supplementary materials for this manuscript include the following:

Dataset S1

Figure S1. Species phylogenies and distributions of the two studied groups.

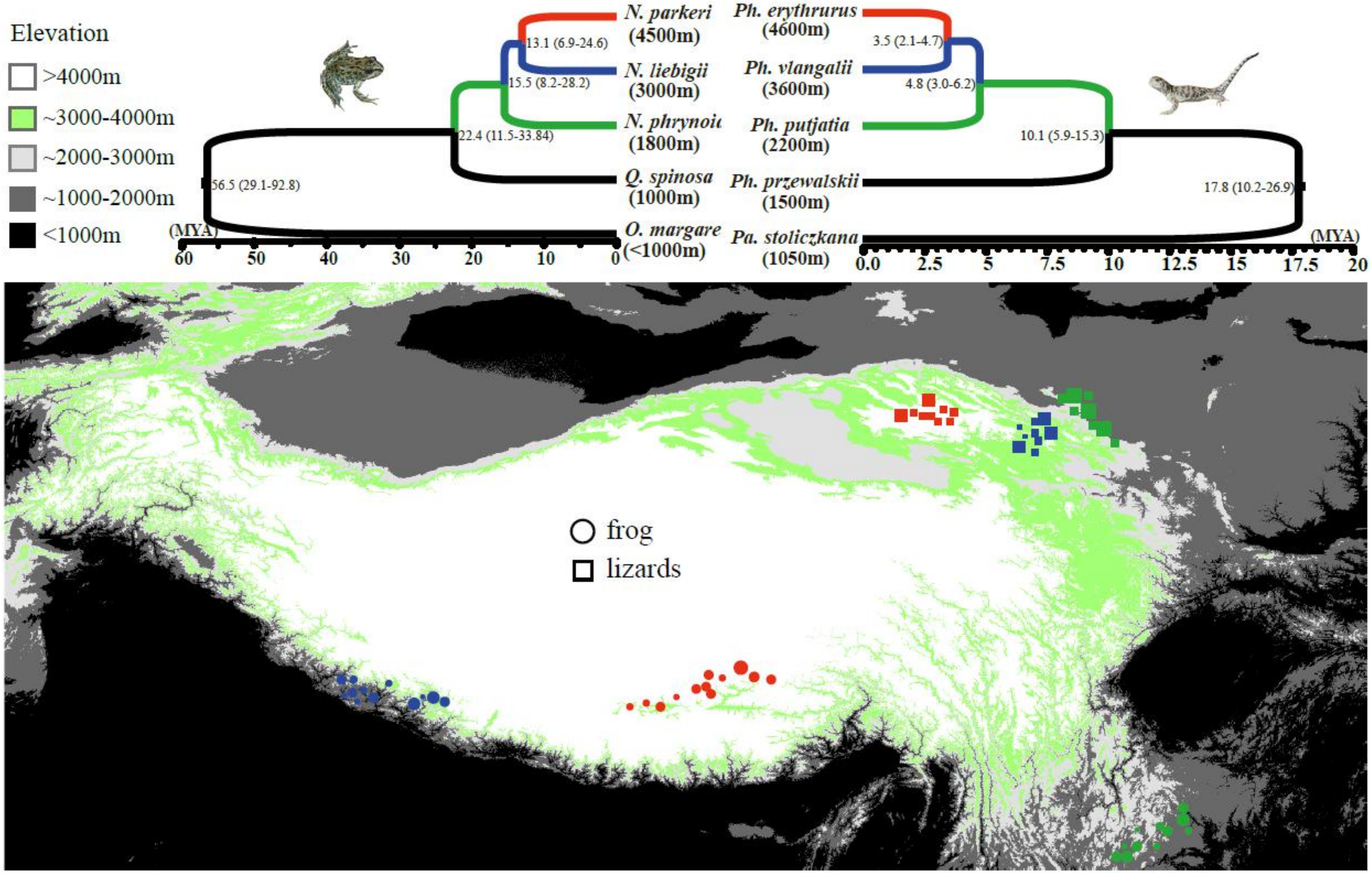

Figure S2. Comparison of the proportion of PSGs among different functions.

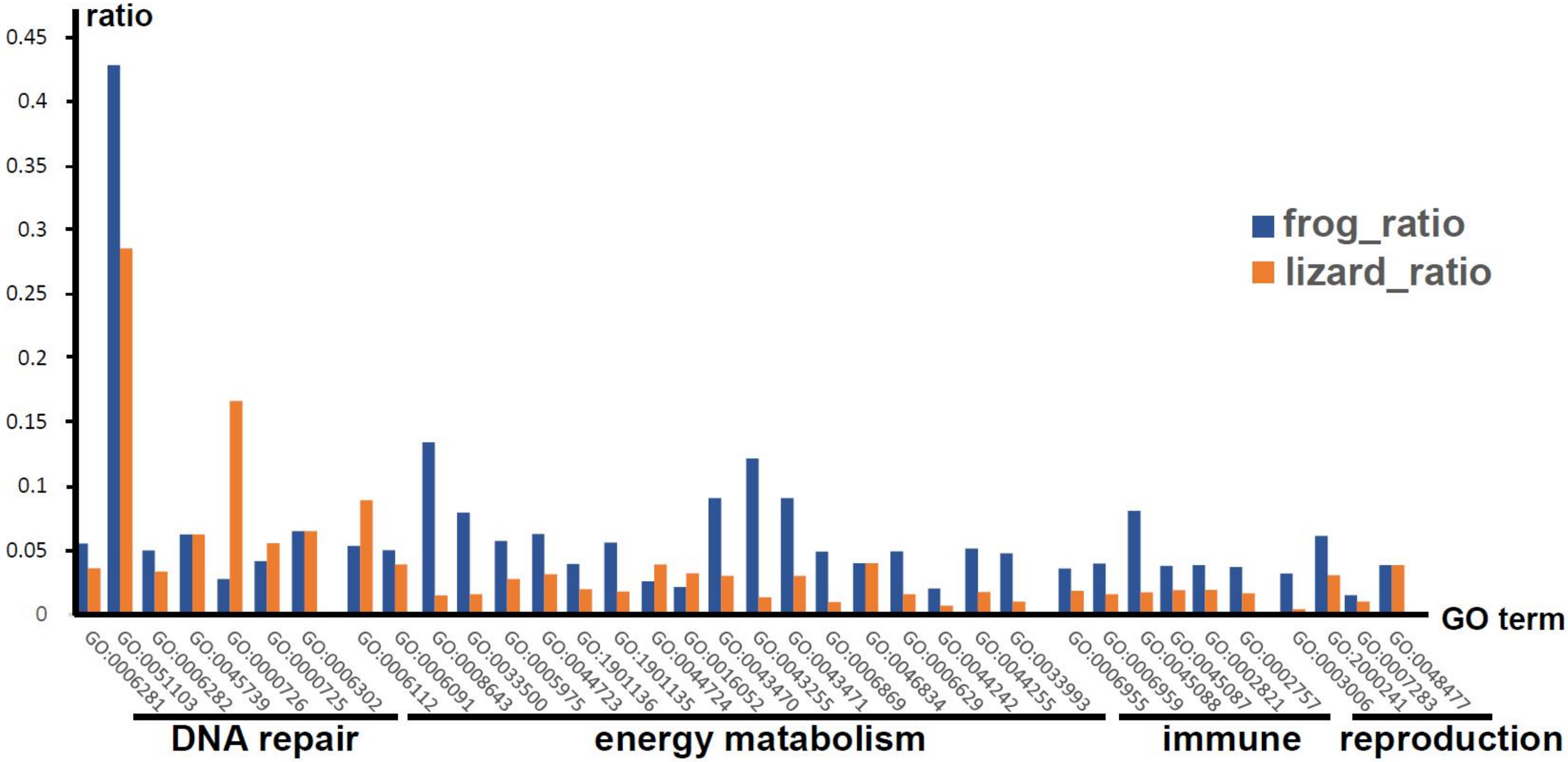

Table S1. Statistics of the sequencing, assembly, and mapping of the transcriptomes of the five studied frog species.

	N. parkeri	*N. pleskei*	*N. liebigii*	*N. phrynoides*	*Q. spinosa*
Statistics for cleaned reads					
Brain	31747793	28372324	30089889	36982011	44806278

Heart	68919061	NA	39001346	37108402	42516294
Liver	37751646	29983581	27273475	21938277	31297635
Ovary	40151610	38496558	24922554	NA	61407966
Skin	41843091	38825058	23503252	NA	43138626
Testis	62470978	59282415	52438831	NA	64628702
Total	282884179	194959936	197229347	96028690	287795501
Statistics for assemblies					
n_seqs	162309	123903	109250	145507	174007
n_bases	185021286	142948117	121932574	149433562	168143443
mean_len	1139.93	1153.71	1116.09	1026.99	966.3
N90	429	436	419	389	393
N50	1984	1968	1914	1788	1483
Statistics for mapping rates					
Brain	0.87	0.89	0.66	0.85	0.9
Heart	0.9	NA	0.92	0.91	0.9
Liver	0.94	0.95	0.97	0.96	0.93
Ovary	0.87	0.91	0.88	NA	0.85
Skin	0.9	0.92	0.92	NA	0.92
Testis	0.84	0.8	0.71	NA	0.84

(n seqs: number of seqs; n bases: number of bases; mean len: mean length; N90: the length of the smallest contig in the set that contains the fewest (largest) contigs whose combined length represents at least 90% of the assembly; N50: the length of the smallest contig in the set that contains the fewest (largest) contigs whose combined length represents at least 50% of the assembly)

Table S2. PSGs identified on branch 7 of frog.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000017607	ENSACAG00000017862	ENSACAT00000017953	NID2
ENSACAP00000001510	ENSACAG00000001589	ENSACAT00000001546	CCDC6

ENSACAP00000011157	ENSACAG00000010939	ENSACAT00000011389	TLN1
ENSACAP00000000577	ENSACAG00000000375	ENSACAT00000000596	SUPT5H
ENSACAP00000006240	ENSACAG00000006382	ENSACAT00000006379	MRPL48
ENSACAP00000013530	ENSACAG00000013806	ENSACAT00000013808	C15orf40
ENSACAP00000010281	ENSACAG00000010443	ENSACAT00000010493	MYPN
ENSACAP00000013942	ENSACAG00000014212	ENSACAT00000014228	
ENSACAP00000004204	ENSACAG00000004343	ENSACAT00000004303	
ENSACAP00000016408	ENSACAG00000016668	ENSACAT00000016733	HTATIP2
ENSACAP00000017016	ENSACAG00000017279	ENSACAT00000017351	RPL13A
ENSACAP00000009390	ENSACAG00000009594	ENSACAT00000009585	
ENSACAP00000006024	ENSACAG00000006175	ENSACAT00000006158	ZNF518A
ENSACAP00000020409	ENSACAG00000025807	ENSACAT00000024910	
ENSACAP00000014496	ENSACAG00000014522	ENSACAT00000014791	KIAA0319L
ENSACAP00000012225	ENSACAG00000012412	ENSACAT00000012475	TINAGL1
ENSACAP00000012152	ENSACAG00000012399	ENSACAT00000012398	PEF1
ENSACAP00000015045	ENSACAG00000015301	ENSACAT00000015349	MRPL28
ENSACAP00000009086	ENSACAG00000009224	ENSACAT00000009279	XPNPEP2
ENSACAP00000001230	ENSACAG00000001340	ENSACAT00000001263	MUL1
ENSACAP00000019661	ENSACAG00000028065	ENSACAT00000026241	IFNGR1
ENSACAP00000001568	ENSACAG00000001189	ENSACAT00000001605	GRIN1
ENSACAP00000007253	ENSACAG00000007287	ENSACAT00000007408	STX4
ENSACAP00000000726	ENSACAG00000000734	ENSACAT00000000750	CEP95
ENSACAP00000004828	ENSACAG00000004882	ENSACAT00000004936	PDIA3
ENSACAP00000007602	ENSACAG00000007494	ENSACAT00000007763	SPTBN2
ENSACAP00000015368	ENSACAG00000015612	ENSACAT00000015681	DPAGT1
ENSACAP00000017456	ENSACAG00000017715	ENSACAT00000017798	EXOC2
ENSACAP00000000221	ENSACAG00000000233	ENSACAT00000000226	RAB11FIP1
ENSACAP00000007082	ENSACAG00000007230	ENSACAT00000007235	
ENSACAP00000007739	ENSACAG00000007802	ENSACAT00000007905	AP1G1
ENSACAP00000007392	ENSACAG00000007495	ENSACAT00000007549	PCIF1

ENSACAP00000001605	ENSACAG00000001652	ENSACAT00000001644	RSRC2
ENSACAP00000009907	ENSACAG00000010107	ENSACAT00000010110	BBS10
ENSACAP00000009618	ENSACAG00000009734	ENSACAT00000009815	AFAP1L2
ENSACAP00000006379	ENSACAG00000006527	ENSACAT00000006522	PTGFR
ENSACAP00000008308	ENSACAG00000008449	ENSACAT00000008487	PLA2G6
ENSACAP00000017541	ENSACAG00000017813	ENSACAT00000017887	STMN1
ENSACAP00000009217	ENSACAG00000009420	ENSACAT00000009410	CTHRC1
ENSACAP00000011007	ENSACAG00000011206	ENSACAT00000011235	STARD5
ENSACAP00000000190	ENSACAG00000000197	ENSACAT00000000193	RPLP1
ENSACAP00000012760	ENSACAG00000012995	ENSACAT00000013016	PTGR1
ENSACAP00000008480	ENSACAG00000008679	ENSACAT00000008662	RERE
ENSACAP00000008439	ENSACAG00000008492	ENSACAT00000008621	NOC2L
ENSACAP00000015231	ENSACAG00000015062	ENSACAT00000015539	COL3A1
ENSACAP00000002246	ENSACAG00000002283	ENSACAT00000002306	MTX1
ENSACAP00000000009	ENSACAG00000000010	ENSACAT00000000010	C9orf114
ENSACAP00000008955	ENSACAG00000009158	ENSACAT00000009147	H6PD
ENSACAP00000003816	ENSACAG00000003931	ENSACAT00000003908	MOCS3
ENSACAP00000006332	ENSACAG00000006410	ENSACAT00000006474	PPL
ENSACAP00000013508	ENSACAG00000013732	ENSACAT00000013786	IMPA1
ENSACAP00000005323	ENSACAG00000005405	ENSACAT00000005440	SDCBP
ENSACAP00000001612	ENSACAG00000001561	ENSACAT00000001651	EDC4
ENSACAP00000016387	ENSACAG00000016630	ENSACAT00000016711	ADHFE1
ENSACAP00000022567	ENSACAG00000029031	ENSACAT00000029984	THY1
ENSACAP00000000097	ENSACAG00000000097	ENSACAT00000000099	ST3GAL4
ENSACAP00000017417	ENSACAG00000017674	ENSACAT00000017759	STX12
ENSACAP00000015283	ENSACAG00000015561	ENSACAT00000015593	C12orf65
ENSACAP00000005642	ENSACAG00000005783	ENSACAT00000005765	NOP56
ENSACAP00000005757	ENSACAG00000005785	ENSACAT00000005884	IDH3B
ENSACAP00000001710	ENSACAG00000001452	ENSACAT00000001750	TPR
ENSACAP00000018531	ENSACAG00000000642	ENSACAT00000026269	MRPS18A

ENSACAP00000013104	ENSACAG00000013226	ENSACAT00000013364	
ENSACAP00000003323	ENSACAG00000003408	ENSACAT00000003406	SPINT1
ENSACAP00000008645	ENSACAG00000008766	ENSACAT00000008829	NDC80
ENSACAP00000004975	ENSACAG00000005023	ENSACAT00000005088	DHX9
ENSACAP00000021856	ENSACAG00000009246	ENSACAT00000029274	MYOM1
ENSACAP00000006621	ENSACAG00000006760	ENSACAT00000006767	HHATL
ENSACAP00000003089	ENSACAG00000003151	ENSACAT00000003168	CIRH1A
ENSACAP00000003435	ENSACAG00000003527	ENSACAT00000003520	
ENSACAP00000014368	ENSACAG00000014635	ENSACAT00000014661	CCKAR
ENSACAP00000003280	ENSACAG00000003259	ENSACAT00000003363	CEP120
ENSACAP00000007588	ENSACAG00000007655	ENSACAT00000007749	CHFR
ENSACAP00000004177	ENSACAG00000004251	ENSACAT00000004276	PAK1IP1
ENSACAP00000017711	ENSACAG00000017988	ENSACAT00000018059	TGS1
ENSACAP00000016402	ENSACAG00000016680	ENSACAT00000016727	C1QL3
ENSACAP00000016956	ENSACAG00000017208	ENSACAT00000017291	FLOT1
ENSACAP00000002766	ENSACAG00000002701	ENSACAT00000002836	ATL3
ENSACAP00000019744	ENSACAG00000026199	ENSACAT00000025542	TMEM158
ENSACAP00000016067	ENSACAG00000016360	ENSACAT00000016387	MYADM
ENSACAP00000015077	ENSACAG00000015336	ENSACAT00000015381	MMP19
ENSACAP00000013343	ENSACAG00000013301	ENSACAT00000013614	COL1A2
ENSACAP00000015291	ENSACAG00000015534	ENSACAT00000015602	EPN1
ENSACAP00000014423	ENSACAG00000014705	ENSACAT00000014718	DLX6
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ENSACAP00000001278	ENSACAG00000001224	ENSACAT00000001311	PPIL2
ENSACAP00000000925	ENSACAG00000000892	ENSACAT00000000953	UFD1L
ENSACAP00000002021	ENSACAG00000002090	ENSACAT00000002069	KIAA0232
ENSACAP00000004779	ENSACAG00000004791	ENSACAT00000004887	PLS1
ENSACAP00000004674	ENSACAG00000004789	ENSACAT00000004780	RWDD3
ENSACAP00000013905	ENSACAG00000014123	ENSACAT00000014191	PDIA4
ENSACAP00000022783	ENSACAG00000029652	ENSACAT00000030201	PIGX

ENSACAP00000001757	ENSACAG00000001800	ENSACAT00000001798	
ENSACAP00000007400	ENSACAG00000007571	ENSACAT00000007557	RPS19BP1
ENSACAP00000009566	ENSACAG00000009697	ENSACAT00000009763	YTHDC1
ENSACAP00000005180	ENSACAG00000005227	ENSACAT00000005297	
ENSACAP00000005095	ENSACAG00000005215	ENSACAT00000005210	XPNPEP3
ENSACAP00000005033	ENSACAG00000005163	ENSACAT00000005146	SFR1
ENSACAP00000011995	ENSACAG00000012203	ENSACAT00000012240	FAM171A2
ENSACAP00000006283	ENSACAG00000006287	ENSACAT00000006423	XPNPEP1
ENSACAP00000014854	ENSACAG00000015138	ENSACAT00000015155	SEPP1
ENSACAP00000013720	ENSACAG00000013826	ENSACAT00000014001	SYT1
ENSACAP00000017010	ENSACAG00000017228	ENSACAT00000017345	SLC4A1
ENSACAP00000000791	ENSACAG00000000862	ENSACAT00000000816	MCU
ENSACAP00000007175	ENSACAG00000007344	ENSACAT00000007330	LRRN2
ENSACAP00000007428	ENSACAG00000007599	ENSACAT00000007585	PPP1R15B
ENSACAP00000003054	ENSACAG00000003149	ENSACAT00000003132	PPHLN1
ENSACAP00000002294	ENSACAG00000002156	ENSACAT00000002354	LMO7
ENSACAP00000002037	ENSACAG00000002035	ENSACAT00000002086	UCHL3
ENSACAP00000000748	ENSACAG00000000689	ENSACAT00000000772	GAS6
ENSACAP00000005130	ENSACAG00000005207	ENSACAT00000005246	ADD1
ENSACAP00000006927	ENSACAG00000007007	ENSACAT00000007078	SAMHD1
ENSACAP00000000344	ENSACAG00000000390	ENSACAT00000000358	STS
ENSACAP00000007342	ENSACAG00000007489	ENSACAT00000007498	PRDX4
ENSACAP00000017656	ENSACAG00000017928	ENSACAT00000018002	
ENSACAP00000014951	ENSACAG00000015209	ENSACAT00000015254	
ENSACAP00000002450	ENSACAG00000002543	ENSACAT00000002513	SOD1
ENSACAP00000002268	ENSACAG00000002352	ENSACAT00000002328	SLC25A4
ENSACAP00000010317	ENSACAG00000010312	ENSACAT00000010529	F5
ENSACAP00000016547	ENSACAG00000016786	ENSACAT00000016873	GLRB
ENSACAP00000015388	ENSACAG00000015617	ENSACAT00000015701	FGG
ENSACAP00000012614	ENSACAG00000012831	ENSACAT00000012870	CCDC109B

ENSACAP00000012376	ENSACAG00000012569	ENSACAT00000012629	ETNPPL
ENSACAP00000011045	ENSACAG00000011296	ENSACAT00000011273	EMB
ENSACAP00000010244	ENSACAG00000010314	ENSACAT00000010455	
ENSACAP00000010102	ENSACAG00000010303	ENSACAT00000010309	C7
ENSACAP00000016155	ENSACAG00000016440	ENSACAT00000016476	CENPH
ENSACAP00000008740	ENSACAG00000008942	ENSACAT00000008928	GCNT4
ENSACAP00000008820	ENSACAG00000008991	ENSACAT00000009010	KEAP1
ENSACAP00000016373	ENSACAG00000016619	ENSACAT00000016697	SEMA4D
ENSACAP00000000355	ENSACAG00000000371	ENSACAT00000000369	GOLM1
ENSACAP00000008420	ENSACAG00000008545	ENSACAT00000008602	DDX24
ENSACAP00000008929	ENSACAG00000008987	ENSACAT00000009120	LGMN
ENSACAP00000009030	ENSACAG00000009184	ENSACAT00000009223	SLC24A4
ENSACAP00000013202	ENSACAG00000013365	ENSACAT00000013466	GALC
ENSACAP00000016429	ENSACAG00000016685	ENSACAT00000016754	YLPM1
ENSACAP00000015870	ENSACAG00000016157	ENSACAT00000016188	FAM161B
ENSACAP00000017274	ENSACAG00000017477	ENSACAT00000017614	
ENSACAP00000012138	ENSACAG00000012275	ENSACAT00000012383	EEF2
ENSACAP00000007715	ENSACAG00000007871	ENSACAT00000007880	GATA1
ENSACAP00000020710	ENSACAG00000016156	ENSACAT00000022687	PAPLN
ENSACAP00000005007	ENSACAG00000005108	ENSACAT00000005120	TRAF6
ENSACAP00000001943	ENSACAG00000002019	ENSACAT00000001989	ARL14EP
ENSACAP00000022624	ENSACAG00000028784	ENSACAT00000030041	
ENSACAP00000012439	ENSACAG00000012658	ENSACAT00000012693	PDE3B
ENSACAP00000000060	ENSACAG00000000061	ENSACAT00000000061	
ENSACAP00000015232	ENSACAG00000015422	ENSACAT00000015540	BAIAP2
ENSACAP00000016462	ENSACAG00000016730	ENSACAT00000016788	TK1
ENSACAP00000016553	ENSACAG00000016808	ENSACAT00000016879	HGS
ENSACAP00000013241	ENSACAG00000013428	ENSACAT00000013507	PKP3
ENSACAP00000009525	ENSACAG00000009732	ENSACAT00000009722	DTX3L
ENSACAP00000015851	ENSACAG00000016117	ENSACAT00000016168	

ENSACAP00000009739	ENSACAG00000009876	ENSACAT00000009938	STX3
ENSACAP00000006856	ENSACAG00000006926	ENSACAT00000007006	CTNND1
ENSACAP00000022448	ENSACAG00000008728	ENSACAT00000029865	
ENSACAP00000005899	ENSACAG00000006044	ENSACAT00000006028	ICT1
ENSACAP00000002161	ENSACAG00000002188	ENSACAT00000002220	
ENSACAP00000015946	ENSACAG00000016212	ENSACAT00000016264	SPDL1
ENSACAP00000004891	ENSACAG00000004938	ENSACAT00000005003	RARS
ENSACAP00000010520	ENSACAG00000010677	ENSACAT00000010737	ACADL
ENSACAP00000005561	ENSACAG00000005569	ENSACAT00000005683	CCT4
ENSACAP00000014514	ENSACAG00000014770	ENSACAT00000014809	ITM2B
ENSACAP00000013145	ENSACAG00000013326	ENSACAT00000013405	ADGRF5
ENSACAP00000011424	ENSACAG00000011554	ENSACAT00000011663	PARP3
ENSACAP00000006881	ENSACAG00000007045	ENSACAT00000007031	
ENSACAP00000014132	ENSACAG00000014404	ENSACAT00000014422	MDN1
ENSACAP00000013835	ENSACAG00000014005	ENSACAT00000014118	TXNRD3
ENSACAP00000010811	ENSACAG00000010996	ENSACAT00000011035	RPS5
ENSACAP00000004644	ENSACAG00000004653	ENSACAT00000004750	EZR
ENSACAP00000004996	ENSACAG00000005018	ENSACAT00000005109	SNX9
ENSACAP00000020699	ENSACAG00000017760	ENSACAT00000026892	
ENSACAP00000022351	ENSACAG00000001489	ENSACAT00000029768	TBCE
ENSACAP00000001610	ENSACAG00000001612	ENSACAT00000001649	VEGFA
ENSACAP00000001283	ENSACAG00000001292	ENSACAT00000001316	DIEXF
ENSACAP00000001907	ENSACAG00000001946	ENSACAT00000001953	
ENSACAP00000003297	ENSACAG00000003328	ENSACAT00000003380	MTIF2
ENSACAP00000001611	ENSACAG00000001550	ENSACAT00000001650	NRXN1

Table S3. GO terms associated with PSGs identified on frog branch 7.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames

GO:0030198	1.37E-05	11	210	extracellular matrix organization	MMP19,COL1A2,GAS6,PRDX4,FGG,ENSACAG00000017760,NRXN1,NID2,COL3A1,SPINT1,FLOT1
GO:0043062	1.47E-05	11	212	extracellular structure organization	MMP19,COL1A2,GAS6,PRDX4,FGG,ENSACAG00000017760,NRXN1,NID2,COL3A1,SPINT1,FLOT1
GO:0045921	1.80E-05	6	59	positive regulation of exocytosis	FGG,HGS,STX4,AP1G1,PLA2G6,SDCBP
GO:0022411	5.11E-05	9	175	cellular component disassembly	MMP19,ICT1,ENSACAG00000017760,MTIF2,STMN1,C12orf65,TPR,MRPL48,FLOT1
GO:1902896	0.000123526	2	2	terminal web assembly	PLS1,EZR
GO:0070126	0.000135325	3	16	mitochondrial translational termination	ICT1,C12orf65,MRPL48
GO:0022406	0.000245636	5	65	membrane docking	STX3,EZR,NRXN1,STX4,STX12
GO:0001951	0.000338055	2	3	intestinal D-glucose absorption	PLS1,EZR
GO:0072657	0.000363474	9	233	protein localization to membrane	PPIL2,GAS6,GLRB,HGS,RPS5,NRXN1,RPL13A,SDCBP,FLOT1
GO:0032984	0.000498456	5	69	macromolecular complex disassembly	ICT1,MTIF2,STMN1,C12orf65,MRPL48
GO:1903078	0.000560531	4	41	positive regulation of protein localization to plasma membrane	PLS1,STX3,EZR,STX4
GO:0034116	0.000574935	2	4	positive regulation of heterotypic cell-cell adhesion	FGG,FLOT1
GO:0006414	0.000724099	4	58	translational elongation	RPLP1,C12orf65,MRPS18A,MRPL48
GO:0051017	0.000734502	4	40	actin filament bundle assembly	PLS1,ADD1,BAIAP2,EZR
GO:1903608	0.000746964	2	4	protein localization to cytoplasmic stress granule	ENSACAG00000017928,DHX9
GO:0050731	0.000846055	5	76	positive regulation of peptidyl-tyrosine phosphorylation	GAS6,SEMA4D,GATA1,CTNND1,VEGFA
GO:0097028	0.000954023	3	21	dendritic cell differentiation	GAS6,GATA1,TRAF6
GO:0036444	0.000986709	2	6	calcium ion transmembrane import into mitochondrion	MCU,CCDC109B
GO:0048278	0.001188464	4	54	vesicle docking	STX3,NRXN1,STX4,STX12
GO:0035457	0.001264808	2	5	cellular response to interferon-alpha	GAS6,TPR
GO:0032532	0.001352776	2	5	regulation of microvillus length	PLS1,EZR
GO:0060627	0.001414933	10	335	regulation of vesicle-mediated transport	GAS6,ENSACAG00000015209,FGG,HGS,EZR,STX4,AP1G1,PLA2G6,SDCBP,FLOT1
GO:0001894	0.00214517	5	95	tissue homeostasis	ADD1,GATA1,TRAF6,ADGRF5,BBS10

GO:0090267	0.00224599	2	7	positive regulation of mitotic cell cycle spindle assembly checkpoint	TPR,NDC80
GO:0019083	0.002465858	3	29	viral transcription	RPS5,RPL13A,TPR
GO:0033690	0.002508122	2	8	positive regulation of osteoblast proliferation	GATA1,CTHRC1
GO:0032536	0.002716264	2	7	regulation of cell projection size	PLS1,EZR
GO:0051023	0.002785628	2	10	regulation of immunoglobulin secretion	TRAF6,STX4
GO:0030953	0.002896043	2	8	astral microtubule organization	EZR,CEP120
GO:0045454	0.002944918	4	70	cell redox homeostasis	PDIA4,PRDX4,TXNRD3,PDIA3
GO:0006364	0.003306535	6	165	rRNA processing	MDN1,RPS5,DIEXF,RPL13A,NOP56,CIRH1A
GO:0006457	0.003632197	6	168	protein folding	PPIL2,PDIA4,PRDX4,CCT4,TBCE,PDIA3
GO:0097067	0.003971133	2	10	cellular response to thyroid hormone stimulus	COL1A2,GATA1
GO:0030534	0.004090956	5	105	adult behavior	UCHL3,GLRB,TBCE,NRXN1,SPTBN2
GO:0034976	0.004370411	5	112	response to endoplasmic reticulum stress	PDIA4,PPP1R15B,PDIA3,PLA2G6,FLOT1
GO:0031629	0.004422914	2	14	synaptic vesicle fusion to presynaptic active zone membrane	STX3,STX4
GO:0030155	0.004663163	11	449	regulation of cell adhesion	LMO7,ENSACAG00000015209,FGG,SEMA4D,TRAF6,PDE3B,STX3,VEGFA,STX4,THY1,FLOT1
GO:0050806	0.005147679	4	71	positive regulation of synaptic transmission	STX3,NRXN1,STX4,FLOT1
GO:0006413	0.005180226	4	86	translational initiation	RPS5,MTIF2,RPL13A,MRPS18A
GO:2000106	0.005245271	3	38	regulation of leukocyte apoptotic process	GAS6,ENSACAG00000007230,NOC2L
GO:0072376	0.005333605	4	94	protein activation cascade	FGG,ENSACAG00000010314,C7,ENSACAG00000017760
GO:0032816	0.005417496	2	11	positive regulation of natural killer cell activation	GAS6,AP1G1
GO:0006851	0.005520766	2	13	mitochondrial calcium ion transport	MCU,CCDC109B
GO:0070168	0.006118731	2	14	negative regulation of biomineral tissue development	GAS6,GATA1
GO:0072344	0.006255895	1	1	rescue of stalled ribosome	C12orf65
GO:0090177	0.006310985	1	1	establishment of planar polarity involved in neural tube closure	CTHRC1
GO:1901193	0.006365886	1	1	regulation of formation of translation preinitiation complex	RPL13A
GO:1901194	0.006365886	1	1	negative regulation of formation of translation	RPL13A

				preinitiation complex	
GO:0051560	0.006392653	2	13	mitochondrial calcium ion homeostasis	MCU,CCDC109B
GO:0002504	0.006636416	3	38	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	TRAF6,SPTBN2,AP1G1
GO:0007016	0.006889169	2	10	cytoskeletal anchoring at plasma membrane	EZR,TLN1
GO:0051764	0.006899841	2	11	actin crosslink formation	PLS1,BAIAP2
GO:1902073	0.007487102	1	1	positive regulation of hypoxia-inducible factor-1alpha signaling pathway	RWDD3
GO:2000255	0.007586801	1	1	negative regulation of male germ cell proliferation	PRDX4
GO:0070613	0.007664738	6	185	regulation of protein processing	GAS6,ENSACAG00000017928,CTNND1,ENSACAG00000017760,SDCBP,TPR
GO:0031424	0.007695752	2	14	keratinization	PPHLN1,PPL
GO:0050860	0.007745056	2	15	negative regulation of T cell receptor signaling pathway	EZR,THY1
GO:0035455	0.007916165	2	13	response to interferon-alpha	GAS6,TPR
GO:0030221	0.008208988	1	1	basophil differentiation	GATA1
GO:0045947	0.008336478	2	15	negative regulation of translational initiation	RPL13A,TPR
GO:0032481	0.008364486	3	39	positive regulation of type I interferon production	ENSACAG00000017928,DHX9,FLOT1
GO:0035786	0.008782063	1	1	protein complex oligomerization	MCU
GO:0032846	0.009120721	5	130	positive regulation of homeostatic process	GATA1,CCT4,STX4,PLA2G6,THY1
GO:0018192	0.009483328	1	1	enzyme active site formation via cysteine modification tc L-cysteine persulfide	MOCS3
GO:0018307	0.009483328	1	1	enzyme active site formation	MOCS3
GO:0043254	0.00955193	8	304	regulation of protein complex assembly	ADD1,ENSACAG00000017928,SNX9,VEGFA,SPTBN2,BBS10,STMN1,TPR
GO:0090274	0.009746136	1	1	positive regulation of somatostatin secretion	CCKAR
GO:0072378	0.009832393	1	1	blood coagulation, fibrin clot formation	FGG
GO:0051262	0.009867759	4	87	protein tetramerization	SAMHD1,TK1,ACADL,NRXN1
GO:0097066	0.010039924	2	16	response to thyroid hormone	COL1A2,GATA1
GO:0040014	0.01009789	3	46	regulation of multicellular organism growth	PLS1,LGMN,EZR
GO:0015993	0.010123852	1	1	molecular hydrogen transport	ADHFE1
GO:0060262	0.010123852	1	1	negative regulation of N-terminal protein palmitoylation	HHATL

GO:0001554	0.010216958	1	1	luteolysis	MMP19
GO:0060353	0.01025318	1	1	regulation of cell adhesion molecule production	FLOT1
GO:0006664	0.01082641	4	96	glycolipid metabolic process	PIGX,STS,GALC,ST3GAL4
GO:1900142	0.011053231	1	1	negative regulation of oligodendrocyte apoptotic process	GAS6
GO:2000533	0.011053231	1	1	negative regulation of renal albumin absorption	GAS6
GO:0009607	0.011346781	10	483	response to biotic stimulus	PPP1R15B,SAMHD1,ENSACAG00000017928,TRAF6,BAIAP2,IFNGR1,PTGFR,PLA2G6,STMN1,CCKAR
GO:0071826	0.011403875	6	206	ribonucleoprotein complex subunit organization	YTHDC1,ENSACAG00000017928,MDN1,RPS5,MTIF2,TGS1
GO:0006683	0.011427452	1	1	galactosylceramide catabolic process	GALC
GO:1903509	0.012155142	4	99	liposaccharide metabolic process	PIGX,STS,GALC,ST3GAL4
GO:0060690	0.012194482	1	1	epithelial cell differentiation involved in salivary gland development	CTNND1
GO:0036261	0.012243751	1	1	7-methylguanosine cap hypermethylation	TGS1
GO:0070124	0.012428638	2	25	mitochondrial translational initiation	MTIF2,MRPS18A
GO:0007596	0.013014058	4	91	blood coagulation	GAS6,F5,FGG,GATA1
GO:0050817	0.013014058	4	91	coagulation	GAS6,F5,FGG,GATA1
GO:0021692	0.014198163	1	1	cerebellar Purkinje cell layer morphogenesis	SPTBN2
GO:0000189	0.014297621	1	1	MAPK import into nucleus	TPR
GO:0045799	0.014297621	1	1	positive regulation of chromatin assembly or disassembl	TPR
GO:0097327	0.01442961	1	2	response to antineoplastic agent	PTGR1
GO:2000352	0.015031572	2	18	negative regulation of endothelial cell apoptotic process	GAS6,FGG
GO:0036260	0.015561444	2	21	RNA capping	SUPT5H,TGS1
GO:0006487	0.015596589	3	56	protein N-linked glycosylation	ENSACAG00000016117,DPAGT1,ST3GAL4
GO:2000677	0.015697179	2	23	regulation of transcription regulatory region DNA bindin	GATA1,TRAF6
GO:0090202	0.016546139	1	2	gene looping	GATA1
GO:0090579	0.016546139	1	2	dsDNA loop formation	GATA1
GO:1903898	0.016900956	1	2	negative regulation of PERK-mediated unfolded protein response	PPP1R15B
GO:0019408	0.017316345	1	2	dolichol biosynthetic process	DPAGT1

GO:0046061	0.017575851	1	2	dATP catabolic process	SAMHD1
GO:1901890	0.01843122	2	20	positive regulation of cell junction assembly	VEGFA,FLOT1
GO:0042758	0.018870728	1	2	long-chain fatty acid catabolic process	ACADL
GO:0071649	0.018888724	1	2	regulation of chemokine (C-C motif) ligand 5 production	ENSACAG00000017928
GO:0000132	0.019354169	2	22	establishment of mitotic spindle orientation	SPDL1,NDC80
GO:0031990	0.019439249	1	2	mRNA export from nucleus in response to heat stress	TPR
GO:0006446	0.019832095	3	59	regulation of translational initiation	ENSACAG00000017928,RPL13A,TPR
GO:0090666	0.019866267	1	2	scaRNA localization to Cajal body	CCT4
GO:0006404	0.020042338	1	2	RNA import into nucleus	TPR
GO:0070164	0.020368657	1	2	negative regulation of adiponectin secretion	RAB11FIP1
GO:0033240	0.020778374	5	162	positive regulation of cellular amine metabolic process	GAS6,SEMA4D,GATA1,CTNND1,VEGFA
GO:0006624	0.021416549	1	3	vacuolar protein processing	LGMN
GO:0060988	0.021641074	1	2	lipid tube assembly	SNX9
GO:0071167	0.021827653	1	2	ribonucleoprotein complex import into nucleus	TGS1
GO:1902966	0.021893707	1	2	positive regulation of protein localization to early endosome	EZR
GO:0007610	0.021909634	9	417	behavior	ENSACAG00000004557,UCHL3,GLRB,GCNT4,TBCE,NRXN1,SPTBN2,PLA2G6,CCKAR
GO:0006412	0.021973342	5	228	translation	EEF2,RPS5,RPL13A,RPLP1,MRPS18A
GO:0032103	0.022339517	5	173	positive regulation of response to external stimulus	GAS6,TRAF6,STX3,STX4,SUPT5H
GO:0032870	0.022402134	6	235	cellular response to hormone stimulus	COL1A2,UCHL3,GATA1,PDE3B,PTGFR,CCKAR
GO:0043207	0.02269421	9	460	response to external biotic stimulus	SAMHD1,ENSACAG00000017928,TRAF6,BAIAP2,IFNGR1,PTGFR,PLA2G6,STMN1,CCKAR
GO:0046813	0.022821055	1	2	receptor-mediated virion attachment to host cell	GAS6
GO:0035701	0.022880872	1	2	hematopoietic stem cell migration	GAS6
GO:0097241	0.022880872	1	2	hematopoietic stem cell migration to bone marrow	GAS6
GO:0030219	0.023003649	1	3	megakaryocyte differentiation	GATA1
GO:0071307	0.023046065	1	2	cellular response to vitamin K	GAS6
GO:0006643	0.023417661	5	181	membrane lipid metabolic process	PIGX,STS,GALC,ENSACAG00000008728,ST3GAL4

GO:0032066	0.024079222	1	2	nucleolus to nucleoplasm transport	NOC2L
GO:0010559	0.02408727	2	28	regulation of glycoprotein biosynthetic process	GATA1,ITM2B
GO:0032447	0.024186519	1	3	protein urmylation	MOCS3
GO:0032226	0.024509395	1	3	positive regulation of synaptic transmission, dopaminergi	FLOT1
GO:0071873	0.024787551	1	2	response to norepinephrine	COL1A2
GO:0060414	0.024793881	1	2	aorta smooth muscle tissue morphogenesis	COL3A1
GO:0071799	0.0255018	1	3	cellular response to prostaglandin D stimulus	PTGFR
GO:0043932	0.025551741	1	3	ossification involved in bone remodeling	CTHRC1
GO:0051105	0.025675921	1	3	regulation of DNA ligation	PARP3
GO:0051106	0.025675921	1	3	positive regulation of DNA ligation	PARP3
GO:1903553	0.026042161	1	3	positive regulation of extracellular exosome assembly	SDCBP
GO:0010693	0.026338126	1	3	negative regulation of alkaline phosphatase activity	SEMA4D
GO:0046832	0.027332994	1	2	negative regulation of RNA export from nucleus	TPR
GO:0044706	0.028064917	3	72	multi-multicellular organism process	EPN1,STS,PTGFR
GO:0019254	0.028292273	1	3	carnitine metabolic process, CoA-linked	ACADL
GO:0006068	0.028397781	1	3	ethanol catabolic process	ENSACAG00000008728
GO:1901976	0.028465277	2	25	regulation of cell cycle checkpoint	TPR,NDC80
GO:1903018	0.028680912	2	31	regulation of glycoprotein metabolic process	GATA1,ITM2B
GO:0018149	0.028949196	2	26	peptide cross-linking	COL3A1,ENSACAG00000013226
GO:0060670	0.028966471	1	4	branching involved in labyrinthine layer morphogenesis	SPINT1
GO:0006213	0.028997134	2	36	pyrimidine nucleoside metabolic process	TK1,ENSACAG00000002188
GO:0002143	0.029316336	1	3	tRNA wobble position uridine thiolation	MOCS3
GO:0046434	0.029741547	4	124	organophosphate catabolic process	SAMHD1,PDE3B,H6PD,IMPA1
GO:0034660	0.03020518	8	391	ncRNA metabolic process	RARS,MDN1,RPS5,DIEXF,RPL13A,MOCS3,NOP56,CIRH1A
GO:0019835	0.030228888	2	33	cytolysis	ENSACAG00000010314,C7
GO:0010725	0.030268974	1	3	regulation of primitive erythrocyte differentiation	GATA1
GO:0034502	0.030419879	2	27	protein localization to chromosome	SPDL1,PARP3
GO:0035754	0.030605732	1	3	B cell chemotaxis	GAS6
GO:1900220	0.030749112	1	3	semaphorin-plexin signaling pathway involved in bone	SEMA4D

				trabecula morphogenesis	
GO:0046104	0.031181637	1	4	thymidine metabolic process	TK1
GO:1902476	0.031610307	2	26	chloride transmembrane transport	SLC4A1,GLRB
GO:0097112	0.032237825	1	3	gamma-aminobutyric acid receptor clustering	GLRB
GO:0070972	0.032508198	2	35	protein localization to endoplasmic reticulum	RPS5,RPL13A
GO:0006420	0.032869537	1	3	arginyl-tRNA aminoacylation	RARS
GO:2000535	0.033238063	1	3	regulation of entry of bacterium into host cell	EXOC2
GO:0070508	0.033435797	1	4	cholesterol import	STARD5
GO:0034227	0.033578292	1	4	tRNA thio-modification	MOCS3
GO:0060689	0.033952584	1	3	cell differentiation involved in salivary gland development	CTNND1
GO:0030865	0.034034553	2	29	cortical cytoskeleton organization	PLS1,EZR
GO:0042773	0.034158812	1	7	ATP synthesis coupled electron transport	ENSACAG00000007045
GO:1903650	0.034514631	3	78	negative regulation of cytoplasmic transport	GAS6,KEAP1,TPR
GO:0090037	0.034740194	1	4	positive regulation of protein kinase C signaling	PLA2G6
GO:0003014	0.034874362	3	75	renal system process	XPNPEP3,GAS6,LGMN
GO:0045838	0.035450545	2	28	positive regulation of membrane potential	NRXN1,ENSACAG00000025807
GO:0043951	0.03554311	1	4	negative regulation of cAMP-mediated signaling	PDE3B
GO:0006839	0.036368332	3	88	mitochondrial transport	MCU,CCDC109B,MTX1
GO:0050878	0.036371799	5	184	regulation of body fluid levels	GAS6,F5,FGG,GATA1,CCKAR
GO:0010815	0.037425996	1	4	bradykinin catabolic process	XPNPEP1
GO:0010737	0.037471364	1	4	protein kinase A signaling	EZR
GO:0070262	0.038386062	1	4	peptidyl-serine dephosphorylation	PPP1R15B
GO:0006700	0.042218761	1	5	C21-steroid hormone biosynthetic process	STARD5
GO:0051098	0.042249583	5	207	regulation of binding	ADD1,GATA1,TRAF6,CTHRC1,FLOT1
GO:1903753	0.042644473	1	4	negative regulation of p38MAPK cascade	EZR
GO:0090154	0.043335707	1	4	positive regulation of sphingolipid biosynthetic process	PLA2G6
GO:0044406	0.043348959	1	4	adhesion of symbiont to host	GAS6
GO:0033227	0.043770372	1	4	dsRNA transport	FLOT1
GO:0030574	0.044604237	2	32	collagen catabolic process	MMP19,COL3A1

GO:0033238	0.04471057	6	269	regulation of cellular amine metabolic process	GAS6,SEMA4D,GATA1,CTNND1,VEGFA,NOC2L
GO:0009120	0.045226967	1	6	deoxyribonucleoside metabolic process	TK1
GO:0006228	0.045273109	1	7	UTP biosynthetic process	ENSACAG00000002188
GO:0070934	0.046025855	1	4	CRD-mediated mRNA stabilization	DHX9
GO:0006273	0.046341283	1	4	lagging strand elongation	PARP3
GO:0034141	0.046805253	1	5	positive regulation of toll-like receptor 3 signaling pathway	FLOT1
GO:0010825	0.046890003	1	4	positive regulation of centrosome duplication	CEP120
GO:2000270	0.047316335	1	5	negative regulation of fibroblast apoptotic process	GAS6
GO:0006102	0.048876096	1	5	isocitrate metabolic process	IDH3B
GO:0015749	0.049079512	2	35	monosaccharide transport	PLS1,EZR
GO:0090237	0.049404779	1	5	regulation of arachidonic acid secretion	PLA2G6

Table S4. PSGs identified on branch 3 of frog.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000003956	ENSACAG00000004065	ENSACAT00000004048	RPL35
ENSACAP00000012390	ENSACAG00000012619	ENSACAT00000012643	HSPG2
ENSACAP00000013434	ENSACAG00000013691	ENSACAT00000013708	
ENSACAP00000013792	ENSACAG00000014064	ENSACAT00000014074	NEURL2
ENSACAP00000013812	ENSACAG00000014065	ENSACAT00000014094	TMCC1
ENSACAP00000005559	ENSACAG00000005630	ENSACAT00000005681	CHRNB3
ENSACAP00000014692	ENSACAG00000014974	ENSACAT00000014992	THUMPD3
ENSACAP00000004154	ENSACAG00000004291	ENSACAT00000004253	
ENSACAP00000011545	ENSACAG00000011710	ENSACAT00000011785	POLD2
ENSACAP00000008525	ENSACAG00000008687	ENSACAT00000008708	BRAT1
ENSACAP00000004794	ENSACAG00000004894	ENSACAT00000004902	MFSD2A
ENSACAP00000002842	ENSACAG00000002932	ENSACAT00000002912	TPRG1
ENSACAP00000013942	ENSACAG00000014212	ENSACAT00000014228	

ENSACAP00000000982	ENSACAG00000000996	ENSACAT00000001010	DTX2
ENSACAP00000016819	ENSACAG00000017064	ENSACAT00000017151	
ENSACAP00000008893	ENSACAG00000009051	ENSACAT00000009084	LMBRD2
ENSACAP00000002580	ENSACAG00000002517	ENSACAT00000002646	CLK2
ENSACAP00000012114	ENSACAG00000012194	ENSACAT00000012359	MTTP
ENSACAP00000010546	ENSACAG00000010745	ENSACAT00000010764	DCTPP1
ENSACAP00000009363	ENSACAG00000009471	ENSACAT00000009558	TBC1D31
ENSACAP00000007441	ENSACAG00000007546	ENSACAT00000007598	CLSTN3
ENSACAP00000007914	ENSACAG00000007857	ENSACAT00000008080	
ENSACAP00000008105	ENSACAG00000008210	ENSACAT00000008277	WDR3
ENSACAP00000000869	ENSACAG00000000837	ENSACAT00000000896	KATNB1
ENSACAP00000019188	ENSACAG00000005871	ENSACAT00000026240	SIN3A
ENSACAP00000006456	ENSACAG00000006462	ENSACAT00000006601	
ENSACAP00000007546	ENSACAG00000007711	ENSACAT00000007707	RNF149
ENSACAP00000011651	ENSACAG00000011733	ENSACAT00000011891	VCP
ENSACAP00000008583	ENSACAG00000008720	ENSACAT00000008766	LPCAT4
ENSACAP00000021749	ENSACAG00000028691	ENSACAT00000029169	
ENSACAP00000008647	ENSACAG00000008819	ENSACAT00000008831	RBMX2
ENSACAP00000016617	ENSACAG00000016855	ENSACAT00000016944	TNFAIP3
ENSACAP00000008691	ENSACAG00000008854	ENSACAT00000008877	ALG3
ENSACAP00000019661	ENSACAG00000028065	ENSACAT00000026241	IFNGR1
ENSACAP00000006555	ENSACAG00000006702	ENSACAT00000006700	IYD
ENSACAP00000023167	ENSACAG00000028678	ENSACAT00000030587	EGFL7
ENSACAP00000007253	ENSACAG00000007287	ENSACAT00000007408	STX4
ENSACAP00000000220	ENSACAG00000000210	ENSACAT00000000225	PSMD12
ENSACAP00000006502	ENSACAG00000006445	ENSACAT00000006647	
ENSACAP00000000442	ENSACAG00000000515	ENSACAT00000000459	POLRMT
ENSACAP00000017567	ENSACAG00000017843	ENSACAT00000017913	
ENSACAP00000009180	ENSACAG00000009367	ENSACAT00000009373	
ENSACAP00000004108	ENSACAG00000004206	ENSACAT00000004205	

ENSACAP00000004168	ENSACAG00000004303	ENSACAT00000004267	ANKRD53
ENSACAP00000015218	ENSACAG00000015364	ENSACAT00000015526	
ENSACAP00000015407	ENSACAG00000015669	ENSACAT00000015720	TMLHE
ENSACAP00000006828	ENSACAG00000006962	ENSACAT00000006978	PCYT1A
ENSACAP00000000221	ENSACAG00000000233	ENSACAT00000000226	RAB11FIP1
ENSACAP00000022899	ENSACAG00000011799	ENSACAT00000030317	
ENSACAP00000017999	ENSACAG00000027397	ENSACAT00000022186	SART1
ENSACAP00000008010	ENSACAG00000007949	ENSACAT00000008181	EPHB3
ENSACAP00000002433	ENSACAG00000002419	ENSACAT00000002496	ATXN2
ENSACAP00000005827	ENSACAG00000005943	ENSACAT00000005956	STIL
ENSACAP00000010827	ENSACAG00000010909	ENSACAT00000011051	RAD21
ENSACAP00000011005	ENSACAG00000011204	ENSACAT00000011233	PECAM1
ENSACAP00000004033	ENSACAG00000003913	ENSACAT00000004125	
ENSACAP00000008903	ENSACAG00000009009	ENSACAT00000009094	THOC5
ENSACAP00000006543	ENSACAG00000006538	ENSACAT00000006688	CLUH
ENSACAP00000008137	ENSACAG00000008305	ENSACAT00000008309	EIF5B
ENSACAP00000001566	ENSACAG00000001034	ENSACAT00000001603	
ENSACAP00000017866	ENSACAG00000020943	ENSACAT00000021176	
ENSACAP00000008163	ENSACAG00000008273	ENSACAT00000008338	RHCG
ENSACAP00000015047	ENSACAG00000015242	ENSACAT00000015351	MYO1E
ENSACAP00000012786	ENSACAG00000013018	ENSACAT00000013042	
ENSACAP00000014702	ENSACAG00000014883	ENSACAT00000015003	LIPC
ENSACAP00000015231	ENSACAG00000015062	ENSACAT00000015539	COL3A1
ENSACAP00000001369	ENSACAG00000001473	ENSACAT00000001402	LYSMD2
ENSACAP00000014072	ENSACAG00000014329	ENSACAT00000014360	SAV1
ENSACAP00000015858	ENSACAG00000016142	ENSACAT00000016175	NIPAL2
ENSACAP00000007239	ENSACAG00000007354	ENSACAT00000007394	FAM114A1
ENSACAP00000011352	ENSACAG00000011361	ENSACAT00000011591	MAPK8
ENSACAP00000002210	ENSACAG00000002308	ENSACAT00000002270	TMEM208
ENSACAP00000003768	ENSACAG00000003791	ENSACAT00000003860	PGM2L1

ENSACAP00000015715	ENSACAG00000015982	ENSACAT00000016030	GLOD4
ENSACAP00000013502	ENSACAG00000013773	ENSACAT00000013780	MEGF9
ENSACAP00000001641	ENSACAG00000001557	ENSACAT00000001680	
ENSACAP00000014578	ENSACAG00000014729	ENSACAT00000014873	SCARB1
ENSACAP00000010109	ENSACAG00000010260	ENSACAT00000010316	
ENSACAP00000021570	ENSACAG00000026480	ENSACAT00000025303	MEN1
ENSACAP00000008354	ENSACAG00000008521	ENSACAT00000008535	COMTD1
ENSACAP00000017732	ENSACAG00000018003	ENSACAT00000018080	FGFR1
ENSACAP00000003539	ENSACAG00000003568	ENSACAT00000003627	YARS
ENSACAP00000014871	ENSACAG00000015065	ENSACAT00000015172	
ENSACAP00000011812	ENSACAG00000012065	ENSACAT00000012056	ZNF598
ENSACAP00000007387	ENSACAG00000007529	ENSACAT00000007543	UPP2
ENSACAP00000004064	ENSACAG00000003987	ENSACAT00000004158	NUP107
ENSACAP00000007135	ENSACAG00000007220	ENSACAT00000007290	SFSWAP
ENSACAP00000013183	ENSACAG00000013293	ENSACAT00000013446	VPS35
ENSACAP00000001626	ENSACAG00000001638	ENSACAT00000001665	ZC3HC1
ENSACAP00000014368	ENSACAG00000014635	ENSACAT00000014661	CCKAR
ENSACAP00000003183	ENSACAG00000003205	ENSACAT00000003264	CLINT1
ENSACAP00000003035	ENSACAG00000003142	ENSACAT00000003113	
ENSACAP00000006720	ENSACAG00000006862	ENSACAT00000006866	KREMEN2
ENSACAP00000003383	ENSACAG00000003402	ENSACAT00000003466	ATP1A1
ENSACAP00000019138	ENSACAG00000022604	ENSACAT00000026439	C19orf44
ENSACAP00000000934	ENSACAG00000000955	ENSACAT00000000962	QSOX1
ENSACAP00000006842	ENSACAG00000006941	ENSACAT00000006992	MYOF
ENSACAP00000006605	ENSACAG00000006744	ENSACAT00000006751	TRIM69
ENSACAP00000002372	ENSACAG00000002358	ENSACAT00000002433	UFL1
ENSACAP00000005274	ENSACAG00000005411	ENSACAT00000005391	
ENSACAP00000003827	ENSACAG00000003867	ENSACAT00000003919	
ENSACAP00000015125	ENSACAG00000015348	ENSACAT00000015431	SERPINC1
ENSACAP00000016661	ENSACAG00000016931	ENSACAT00000016990	ECHDC3

ENSACAP00000008624	ENSACAG00000008771	ENSACAT00000008807	CTSK
ENSACAP00000005035	ENSACAG00000005162	ENSACAT00000005148	SLC39A9
ENSACAP00000003528	ENSACAG00000003614	ENSACAT00000003616	KDM8
ENSACAP00000003497	ENSACAG00000003591	ENSACAT00000003584	NSMCE1
ENSACAP00000009331	ENSACAG00000009549	ENSACAT00000009526	TRAFD1
ENSACAP00000011360	ENSACAG00000011582	ENSACAT00000011599	NSRP1
ENSACAP00000002479	ENSACAG00000002556	ENSACAT00000002543	SLC25A1
ENSACAP00000002155	ENSACAG00000002257	ENSACAT00000002214	SERPIND1
ENSACAP00000012440	ENSACAG00000012624	ENSACAT00000012694	FGD4
ENSACAP00000013049	ENSACAG00000013246	ENSACAT00000013308	DFNA5
ENSACAP00000020564	ENSACAG00000012196	ENSACAT00000022834	IL17RA
ENSACAP00000012275	ENSACAG00000012534	ENSACAT00000012527	BID
ENSACAP00000010278	ENSACAG00000010474	ENSACAT00000010490	FAM173B
ENSACAP00000016170	ENSACAG00000016374	ENSACAT00000016491	PAH
ENSACAP00000016035	ENSACAG00000016283	ENSACAT00000016355	NT5DC3
ENSACAP00000005316	ENSACAG00000005406	ENSACAT00000005433	BCAR3
ENSACAP00000023463	ENSACAG00000028687	ENSACAT00000030883	COA1
ENSACAP00000016238	ENSACAG00000016387	ENSACAT00000016561	MYH9
ENSACAP00000009495	ENSACAG00000009576	ENSACAT00000009692	SDHA
ENSACAP00000022842	ENSACAG00000029076	ENSACAT00000030260	UBE2U
ENSACAP00000002239	ENSACAG00000002353	ENSACAT00000002299	
ENSACAP00000004463	ENSACAG00000004508	ENSACAT00000004564	XRCC6
ENSACAP00000011537	ENSACAG00000011671	ENSACAT00000011777	UTP20
ENSACAP00000003683	ENSACAG00000003767	ENSACAT00000003773	COX15
ENSACAP00000013158	ENSACAG00000013337	ENSACAT00000013420	NEDD1
ENSACAP00000013146	ENSACAG00000013339	ENSACAT00000013406	CDC20
ENSACAP00000003866	ENSACAG00000003954	ENSACAT00000003958	SLF2
ENSACAP00000004166	ENSACAG00000004270	ENSACAT00000004265	SFXN2
ENSACAP00000012479	ENSACAG00000012654	ENSACAT00000012735	CEP83
ENSACAP00000022859	ENSACAG00000028815	ENSACAT00000030277	

ENSACAP00000001925	ENSACAG00000001984	ENSACAT00000001971	
ENSACAP00000001433	ENSACAG00000001470	ENSACAT00000001468	SAR1A
ENSACAP00000021784	ENSACAG00000029340	ENSACAT00000029204	
ENSACAP00000010524	ENSACAG00000010708	ENSACAT00000010741	COQ2
ENSACAP00000007398	ENSACAG00000007567	ENSACAT00000007555	PWWP2B
ENSACAP00000013947	ENSACAG00000013863	ENSACAT00000014233	CNTN2
ENSACAP00000017296	ENSACAG00000017564	ENSACAT00000017636	LHPP
ENSACAP00000017591	ENSACAG00000017868	ENSACAT00000017937	KRT19
ENSACAP00000017690	ENSACAG00000017967	ENSACAT00000018038	COASY
ENSACAP00000007406	ENSACAG00000007498	ENSACAT00000007563	SRCIN1
ENSACAP00000007271	ENSACAG00000007418	ENSACAT00000007427	SOCS7
ENSACAP00000006596	ENSACAG00000006686	ENSACAT00000006742	CDK5RAP3
ENSACAP00000002933	ENSACAG00000002988	ENSACAT00000003009	IRAK4
ENSACAP00000000530	ENSACAG00000000608	ENSACAT00000000548	FBXL3
ENSACAP00000023290	ENSACAG00000000535	ENSACAT00000030710	CLN5
ENSACAP00000007005	ENSACAG00000007124	ENSACAT00000007156	TSPAN12
ENSACAP00000013144	ENSACAG00000013334	ENSACAT00000013404	
ENSACAP00000002048	ENSACAG00000002091	ENSACAT00000002100	
ENSACAP00000014988	ENSACAG00000015240	ENSACAT00000015291	FKBP4
ENSACAP00000011603	ENSACAG00000011834	ENSACAT00000011843	GTPBP6
ENSACAP00000010489	ENSACAG00000010668	ENSACAT00000010705	
ENSACAP00000020940	ENSACAG00000026925	ENSACAT00000027411	PRR5
ENSACAP00000015617	ENSACAG00000015897	ENSACAT00000015931	MCAT
ENSACAP00000001089	ENSACAG00000001195	ENSACAT00000001118	UCMA
ENSACAP00000006202	ENSACAG00000006348	ENSACAT00000006339	FGL2
ENSACAP00000006508	ENSACAG00000006548	ENSACAT00000006653	DNAJC2
ENSACAP00000005078	ENSACAG00000005168	ENSACAT00000005193	OGFR
ENSACAP00000002892	ENSACAG00000002948	ENSACAT00000002963	RSPH1
ENSACAP00000005315	ENSACAG00000005453	ENSACAT00000005432	HMGN1
ENSACAP00000009134	ENSACAG00000009269	ENSACAT00000009327	

ENSACAP00000002583	ENSACAG00000002694	ENSACAT00000002649	CENPU
ENSACAP00000006815	ENSACAG00000006976	ENSACAT00000006965	CDKN2AIP
ENSACAP00000010317	ENSACAG00000010312	ENSACAT00000010529	F5
ENSACAP00000016585	ENSACAG00000016828	ENSACAT00000016911	PDGFC
ENSACAP00000015388	ENSACAG00000015617	ENSACAT00000015701	FGG
ENSACAP00000004913	ENSACAG00000004925	ENSACAT00000005026	HSPH1
ENSACAP00000010079	ENSACAG00000010236	ENSACAT00000010286	PRKAA1
ENSACAP00000010113	ENSACAG00000010254	ENSACAT00000010321	RAD17
ENSACAP00000000778	ENSACAG00000000768	ENSACAT00000000802	SYK
ENSACAP00000001366	ENSACAG00000001474	ENSACAT00000001399	RMI1
ENSACAP00000011838	ENSACAG00000011929	ENSACAT00000012082	ANXA1
ENSACAP00000018554	ENSACAG00000027513	ENSACAT00000026625	PTAR1
ENSACAP00000002264	ENSACAG00000002328	ENSACAT00000002324	BAZ1A
ENSACAP00000017072	ENSACAG00000017316	ENSACAT00000017407	PTBP3
ENSACAP00000005965	ENSACAG00000006091	ENSACAT00000006099	MBD1
ENSACAP00000013028	ENSACAG00000013258	ENSACAT00000013287	SYNE3
ENSACAP00000006487	ENSACAG00000006636	ENSACAT00000006632	ABT1
ENSACAP00000007334	ENSACAG00000007259	ENSACAT00000007490	MYO1A
ENSACAP00000015102	ENSACAG00000015347	ENSACAT00000015406	CARM1
ENSACAP00000008096	ENSACAG00000008220	ENSACAT00000008268	IDH3G
ENSACAP00000004222	ENSACAG00000004323	ENSACAT00000004321	CD44
ENSACAP00000009049	ENSACAG00000009213	ENSACAT00000009242	SWAP70
ENSACAP00000014302	ENSACAG00000014575	ENSACAT00000014595	COG1
ENSACAP00000015327	ENSACAG00000015535	ENSACAT00000015640	
ENSACAP00000015926	ENSACAG00000016215	ENSACAT00000016244	CANT1
ENSACAP00000017147	ENSACAG00000017398	ENSACAT00000017484	ELAC2
ENSACAP00000010337	ENSACAG00000010381	ENSACAT00000010550	KALRN
ENSACAP00000002909	ENSACAG00000002906	ENSACAT00000002983	STK36
ENSACAP00000001599	ENSACAG00000001693	ENSACAT00000001638	CATIP
ENSACAP00000008204	ENSACAG00000008383	ENSACAT00000008380	RHBDF2

ENSACAP00000006565	ENSACAG00000006658	ENSACAT00000006710	OSBP
ENSACAP00000006131	ENSACAG00000006230	ENSACAT00000006268	NUP85
ENSACAP00000001558	ENSACAG00000001586	ENSACAT00000001595	LUC7L3
ENSACAP00000012577	ENSACAG00000012718	ENSACAT00000012833	CYP27A1
ENSACAP00000021704	ENSACAG00000028511	ENSACAT00000029124	MAT2B
ENSACAP00000010845	ENSACAG00000010914	ENSACAT00000011070	MAP2
ENSACAP00000015745	ENSACAG00000016013	ENSACAT00000016061	TYW5
ENSACAP00000018355	ENSACAG00000022605	ENSACAT00000024982	AFF4
ENSACAP00000018017	ENSACAG00000022125	ENSACAT00000025587	
ENSACAP00000000516	ENSACAG00000000582	ENSACAT00000000534	SNRPB2
ENSACAP00000004973	ENSACAG00000005105	ENSACAT00000005086	KBTBD11
ENSACAP00000002004	ENSACAG00000002121	ENSACAT00000002052	NDUFAF4
ENSACAP00000014132	ENSACAG00000014404	ENSACAT00000014422	MDN1
ENSACAP00000006046	ENSACAG00000006164	ENSACAT00000006180	CEP57L1
ENSACAP00000002361	ENSACAG00000002472	ENSACAT00000002421	SLC25A26
ENSACAP00000020059	ENSACAG00000024948	ENSACAT00000028463	
ENSACAP00000000649	ENSACAG00000000731	ENSACAT00000000669	NTPCR
ENSACAP00000002778	ENSACAG00000002876	ENSACAT00000002848	RHOU
ENSACAP00000009136	ENSACAG00000009345	ENSACAT00000009329	TRMT61B
ENSACAP00000006218	ENSACAG00000006189	ENSACAT00000006356	PARP1

Table S5. GO terms associated with PSGs identified on frog branch 3.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames
GO:0050900	0.000156213	8	130	leukocyte migration	IL17RA,MYH9,IRAK4,SYK,ANXA1,NUP85,ENSACAG00000006445,PECAM1
GO:0045056	0.000224823	3	11	transcytosis	MFSD2A,MYO1A,VPS35
GO:0000967	0.000515004	2	3	rRNA 5'-end processing	UTP20,ABT1

GO:0071539	0.001205419	3	16	protein localization to centrosome	NEDD1,CEP83,STIL
GO:0000480	0.001392886	2	5	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	UTP20,ABT1
GO:0090502	0.002111447	3	22	RNA phosphodiester bond hydrolysis, endonucleolytic	UTP20,ABT1,ELAC2
GO:0002888	0.002434923	2	7	positive regulation of myeloid leukocyte mediated immunity	SYK,STX4
GO:0000966	0.002659431	2	6	RNA 5'-end processing	UTP20,ABT1
GO:0009314	0.00307453	10	315	response to radiation	XRCC6,FBXL3,PRKAA1,CLK2,ENSACAG00000013018,COL3A1,MAPK8,MEN1,CCKAR,BRAT1
GO:0061041	0.003305387	5	84	regulation of wound healing	SERPINC1,FGG,SYK,ANXA1,TNFAIP3
GO:0008535	0.004100155	2	15	respiratory chain complex IV assembly	COA1,COX15
GO:0010677	0.00418769	3	29	negative regulation of cellular carbohydrate metabolic process	ENSACAG00000002091,ENSACAG00000022125,CLK2
GO:0030224	0.004302506	2	9	monocyte differentiation	MYH9,THOC5
GO:0000959	0.004366188	3	27	mitochondrial RNA metabolic process	ELAC2,TRMT61B,POLRMT
GO:1901264	0.005226316	3	31	carbohydrate derivative transport	MFSD2A,SLC25A26,SCARB1
GO:0022618	0.005965142	7	199	ribonucleoprotein complex assembly	ABT1,LUC7L3,MDN1,SART1,ATXN2,ENSACAG00000010260,SFSWAP
GO:1902041	0.006169899	3	34	regulation of extrinsic apoptotic signaling pathway via death domain receptors	FGG,TNFAIP3,STX4
GO:1903039	0.00625169	5	110	positive regulation of leukocyte cell-cell adhesion	HSPH1,SYK,ANXA1,ENSACAG00000009367,SART1
GO:0015931	0.006275891	6	141	nucleobase-containing compound transport	ENSACAG00000002091,NUP85,SLC25A26,RBMX2,THOC5,NUP107
GO:0048261	0.006318216	2	10	negative regulation of receptor-mediated endocytosis	ENSACAG00000011799,ATXN2
GO:0051028	0.00696084	5	102	mRNA transport	ENSACAG00000002091,NUP85,RBMX2,THOC5,NUP107
GO:0071826	0.007528466	7	206	ribonucleoprotein complex subunit organization	ABT1,LUC7L3,MDN1,SART1,ATXN2,ENSACAG00000010260,SFSWAP
GO:0006694	0.00759435	5	108	steroid biosynthetic process	PRKAA1,CYP27A1,MAT2B,SCARB1,ENSACAG00000003142

GO:0044380	0.007702217	3	31	protein localization to cytoskeleton	NEDD1,CEP83,STIL
GO:0042752	0.007851063	4	64	regulation of circadian rhythm	FBXL3,PRKAA1,SIN3A,MAPK8
GO:0050992	0.007946335	1	1	dimethylallyl diphosphate biosynthetic process	ENSACAG00000003142
GO:0050993	0.007946335	1	1	dimethylallyl diphosphate metabolic process	ENSACAG00000003142
GO:0034470	0.008248377	9	312	ncRNA processing	UTP20,ABT1,ELAC2,TYW5,MDN1,TRMT61B,WDR3,THUMPD3,SART1
GO:0015805	0.009077769	1	1	S-adenosyl-L-methionine transport	SLC25A26
GO:0034462	0.009347284	1	1	small-subunit processome assembly	ABT1
GO:0000963	0.009503202	2	11	mitochondrial RNA processing	ELAC2,TRMT61B
GO:0071361	0.009707782	2	12	cellular response to ethanol	PRKAA1,ENSACAG00000022125
GO:0006396	0.011096461	12	474	RNA processing	NSRP1,UTP20,PTBP3,ABT1,ELAC2,LUC7L3,SNRPB2,TRMT61B,RBMX2,SART1,THOC5,SFSWAP
GO:0010257	0.011122383	2	17	NADH dehydrogenase complex assembly	COA1,NDUFAF4
GO:0032981	0.011122383	2	17	mitochondrial respiratory chain complex I assembly	COA1,NDUFAF4
GO:0097031	0.011122383	2	17	mitochondrial respiratory chain complex I biogenesis	COA1,NDUFAF4
GO:0090673	0.011428505	1	1	endothelial cell-matrix adhesion	PECAM1
GO:0006657	0.011490944	1	1	CDP-choline pathway	PCYT1A
GO:0070507	0.011696409	5	119	regulation of microtubule cytoskeleton organization	FKBP4,HSPH1,KATNB1,ANKRD53,STIL
GO:0051186	0.011930253	7	226	cofactor metabolic process	PAH,COX15,COQ2,COASY,IDH3G,MAT2B,ENSACAG00000022125
GO:0090274	0.012606337	1	1	positive regulation of somatostatin secretion	CCKAR
GO:0009073	0.012877382	1	1	aromatic amino acid family biosynthetic process	PAH
GO:1904146	0.013595778	1	1	positive regulation of meiotic cell cycle process involved in oocyte maturation	CDC20
GO:0000481	0.013731283	1	1	maturation of 5S rRNA	SART1
GO:0007229	0.013800909	4	71	integrin-mediated signaling pathway	MYH9,SYK,ENSACAG00000006445,COL3A1
GO:0006789	0.013820565	1	1	bilirubin conjugation	ENSACAG00000022125
GO:0070980	0.013820565	1	1	biphenyl catabolic process	ENSACAG00000022125

GO:0034970	0.013846167	1	1	histone H3-R2 methylation	CARM1
GO:0015920	0.01390383	1	1	lipopolysaccharide transport	SCARB1
GO:0060696	0.01390383	1	1	regulation of phospholipid catabolic process	SCARB1
GO:0009631	0.013988724	1	1	cold acclimation	PRKAA1
GO:0046318	0.013988724	1	1	negative regulation of glucosylceramide biosynthetic process	PRKAA1
GO:0061762	0.013988724	1	1	CAMKK-AMPK signaling cascade	PRKAA1
GO:0034660	0.014396715	10	391	ncRNA metabolic process	UTP20,ABT1,ELAC2,TYW5,MDN1,TRMT61B,WDR3,THUMPD3,SART1,YARS
GO:0001820	0.014434996	1	1	serotonin secretion	SYK
GO:0071226	0.014434996	1	1	cellular response to molecule of fungal origin	SYK
GO:0046883	0.014580772	6	179	regulation of hormone secretion	FGG,ANXA1,ENSACAG00000015535,STX4,RAB11FIP1,CCKAR
GO:0044128	0.014641615	1	1	positive regulation of growth of symbiont in host	OSBP
GO:0034148	0.014645235	1	1	negative regulation of toll-like receptor 5 signaling pathway	TNFAIP3
GO:0070429	0.014645235	1	1	negative regulation of nucleotide-binding oligomerization domain containing 1 signaling pathway	TNFAIP3
GO:2000349	0.014645235	1	1	negative regulation of CD40 signaling pathway	TNFAIP3
GO:0034414	0.014645235	1	1	tRNA 3'-trailer cleavage, endonucleolytic	ELAC2
GO:0051595	0.014645303	1	1	response to methylglyoxal	SIN3A
GO:1901675	0.014645303	1	1	negative regulation of histone H3-K27 acetylation	SIN3A
GO:1903923	0.014771808	1	1	positive regulation of protein processing in phagocytic vesicle	MYH9
GO:0045736	0.015567547	2	17	negative regulation of cyclin-dependent protein serine/threonine kinase activity	TNFAIP3,MEN1
GO:1901617	0.015774183	5	121	organic hydroxy compound biosynthetic process	PRKAA1,CYP27A1,TMLHE,PCYT1A,ENSACAG00000003142
GO:0070301	0.016693463	3	47	cellular response to hydrogen peroxide	PRKAA1,SYK,TNFAIP3
GO:0042168	0.016783326	2	20	heme metabolic process	COX15,ENSACAG00000022125
GO:0033119	0.016794658	2	19	negative regulation of RNA splicing	PTBP3,SFSWAP
GO:0001570	0.017320435	3	45	vasculogenesis	EGFL7,ENSACAG00000009367,MYO1E

GO:0051977	0.018480184	1	2	lysophospholipid transport	MFSD2A
GO:0008360	0.018975759	5	130	regulation of cell shape	FGD4,MYH9,ANXA1,SYNE3,RHOU
GO:0031590	0.019217836	1	2	wybutosine metabolic process	TYW5
GO:0031591	0.019217836	1	2	wybutosine biosynthetic process	TYW5
GO:0006109	0.019304091	5	137	regulation of carbohydrate metabolic process	ENSACAG00000002091,PRKAA1,ENSACAG00000022125,CLK2,ENSACAG00000009367
GO:0003347	0.020289082	1	2	epicardial cell to mesenchymal cell transition	FGFR1
GO:0034384	0.020426983	1	2	high-density lipoprotein particle clearance	SCARB1
GO:0051090	0.0205726	8	303	regulation of sequence-specific DNA binding transcription factor activity	CDK5RAP3,STK36,TNFAIP3,SAV1,MAPK8,MEN1,UFL1,ENSACAG00000003867
GO:0005996	0.020614289	5	131	monosaccharide metabolic process	PRKAA1,ENSACAG00000022125,ENSACAG00000003913,PGM2L1,BRAT1
GO:2001274	0.02111832	1	2	negative regulation of glucose import in response to insulin stimulus	PRKAA1
GO:1904426	0.021325811	1	2	positive regulation of GTP binding	CLN5
GO:1903919	0.021594506	1	2	negative regulation of actin filament severing	MYH9
GO:0023035	0.021650079	1	2	CD40 signaling pathway	ENSACAG00000003867
GO:1901659	0.021714149	4	112	glycosyl compound biosynthetic process	COASY,MAT2B,TYW5,UPP2
GO:2000352	0.021968276	2	18	negative regulation of endothelial cell apoptotic process	FGG,TNFAIP3
GO:0061098	0.022668765	2	20	positive regulation of protein tyrosine kinase activity	SRCIN1,HSPH1
GO:0061614	0.022741902	1	2	pri-miRNA transcription from RNA polymerase II promoter	ENSACAG00000009269
GO:0010992	0.022790278	1	2	ubiquitin homeostasis	ENSACAG00000006462
GO:1901143	0.022790278	1	2	insulin catabolic process	ENSACAG00000006462
GO:0030048	0.023053277	3	44	actin filament-based movement	MYH9,MYO1A,MYO1E
GO:0072537	0.023231153	1	3	fibroblast activation	IL17RA
GO:0051182	0.023247194	1	2	coenzyme transport	SLC25A26
GO:1904224	0.023247848	1	2	negative regulation of glucuronosyltransferase activity	ENSACAG00000022125
GO:0044283	0.023252909	8	301	small molecule biosynthetic process	PAH,COQ2,MCAT,PRKAA1,CYP27A1,TMLHE,PCYT1A,ENSACAG000000

					03142
GO:1903747	0.023297454	2	23	regulation of establishment of protein localization to mitochondrion	HSPH1,MAPK8
GO:0006913	0.0234963	6	185	nucleocytoplasmic transport	NSRP1,ENSACAG00000002091,NUP85,RBMX2,THOC5,NUP107
GO:0070271	0.024314193	2	31	protein complex biogenesis	COA1,NDUFAF4
GO:1903047	0.02446241	11	458	mitotic cell cycle process	KDM8,NEDD1,CDK5RAP3,CARM1,ENSACAG00000013691,RHOU,ENSACAG00000004206,ANKRD53,STIL,RAD21,NUP107
GO:0031532	0.024767458	3	53	actin cytoskeleton reorganization	MYH9,ANXA1,CCKAR
GO:0050878	0.024780128	6	184	regulation of body fluid levels	SERPINC1,SERPIND1,F5,FGG,ENSACAG00000009367,CCKAR
GO:0051169	0.025065614	6	188	nuclear transport	NSRP1,ENSACAG00000002091,NUP85,RBMX2,THOC5,NUP107
GO:0050817	0.025161819	4	91	coagulation	SERPINC1,SERPIND1,F5,FGG
GO:0006624	0.025317409	1	3	vacuolar protein processing	TMEM208
GO:0043433	0.025898153	4	102	negative regulation of sequence-specific DNA binding transcription factor activity	CDK5RAP3,TNFAIP3,MEN1,UFL1
GO:0050904	0.025907141	1	2	diapedesis	PECAM1
GO:0006261	0.02667879	2	21	DNA-dependent DNA replication	BAZ1A,POLD2
GO:0007258	0.026998463	1	2	JUN phosphorylation	MAPK8
GO:0006437	0.027041484	1	2	tyrosyl-tRNA aminoacylation	YARS
GO:0031667	0.02719755	7	254	response to nutrient levels	SERPINC1,PRKAA1,MBD1,ENSACAG00000015535,ENSACAG00000022125,ENSACAG00000015364,CCKAR
GO:1990379	0.027413822	1	2	lipid transport across blood brain barrier	MFSD2A
GO:0032886	0.027733503	5	144	regulation of microtubule-based process	FKBP4,HSPH1,KATNB1,ANKRD53,STIL
GO:0060982	0.02776097	1	2	coronary artery morphogenesis	ENSACAG00000009269
GO:0030578	0.02776097	1	2	PML body organization	ENSACAG00000009269
GO:0032796	0.027826382	1	2	uropod organization	MYH9
GO:0035461	0.028004565	1	2	vitamin transmembrane transport	SCARB1

GO:1902415	0.028022577	1	2	regulation of mRNA binding	CARM1
GO:0051552	0.028264094	1	2	flavone metabolic process	ENSACAG00000022125
GO:0006720	0.028490109	4	103	isoprenoid metabolic process	HSPG2,COQ2,ENSACAG00000022125,ENSACAG00000003142
GO:0030262	0.028806097	1	3	apoptotic nuclear changes	CDK5RAP3
GO:0001922	0.029076977	1	2	B-1 B cell homeostasis	TNFAIP3
GO:0070212	0.029077034	1	2	protein poly-ADP-ribosylation	PARP1
GO:0045124	0.029452854	2	26	regulation of bone resorption	SYK,TNFAIP3
GO:1902823	0.029673252	1	2	negative regulation of late endosome to lysosome transport	VPS35
GO:0002023	0.030030206	1	4	reduction of food intake in response to dietary excess	CCKAR
GO:0060349	0.030060928	2	24	bone morphogenesis	CARM1,ENSACAG00000009367
GO:0043484	0.030112525	4	100	regulation of RNA splicing	NSRP1,PTBP3,CLK2,SFSWAP
GO:1900127	0.030154565	1	3	positive regulation of hyaluronan biosynthetic process	ENSACAG00000009367
GO:0045668	0.032476438	2	30	negative regulation of osteoblast differentiation	UCMA,MEN1
GO:0010803	0.032720108	2	24	regulation of tumor necrosis factor-mediated signaling pathway	TNFAIP3,ENSACAG00000003867
GO:0033108	0.032975462	2	36	mitochondrial respiratory chain complex assembly	COA1,NDUFAF4
GO:0071705	0.032976355	9	366	nitrogen compound transport	ENSACAG00000002091,SYK,NUP85,SLC25A26,RBMX2,THOC5,RHCG,NUP107,CCKAR
GO:0051646	0.033676392	2	22	mitochondrion localization	CLUH,BRAT1
GO:0006457	0.03440204	5	168	protein folding	ENSACAG00000002091,FKBP4,HSPH1,ENSACAG00000017064,QSOX1
GO:0032747	0.034417676	1	3	positive regulation of interleukin-23 production	IL17RA
GO:0000973	0.035348384	1	3	posttranscriptional tethering of RNA polymerase II gene DNA at nuclear periphery	NUP107
GO:0090291	0.035813588	1	4	negative regulation of osteoclast proliferation	TNFAIP3
GO:0002676	0.035970778	1	4	regulation of chronic inflammatory response	TNFAIP3
GO:0015748	0.036321305	3	64	organophosphate ester transport	MFSD2A,MTTP,SCARB1
GO:1990966	0.036593133	1	3	ATP generation from poly-ADP-D-ribose	PARP1
GO:0008202	0.036692159	6	208	steroid metabolic process	PRKAA1,CYP27A1,MAT2B,ENSACAG00000022125,SCARB1,ENSACAG00

					000003142
GO:0045329	0.037122081	1	3	carnitine biosynthetic process	TMLHE
GO:0006412	0.037649301	5	228	translation	SLC25A1,COA1,SLC25A26,RPL35,ENSACAG00000004291
GO:0050807	0.037793226	4	100	regulation of synapse organization	CDC20,CLSTN3,ENSACAG00000017843,EPHB3
GO:0051188	0.038116464	4	120	cofactor biosynthetic process	COX15,COQ2,COASY,MAT2B
GO:0030488	0.038283369	2	27	tRNA methylation	TRMT61B,THUMPD3
GO:0000022	0.038327088	1	3	mitotic spindle elongation	ENSACAG00000004206
GO:0032497	0.038455091	1	4	detection of lipopolysaccharide	SCARB1
GO:0019740	0.038481458	1	3	nitrogen utilization	RHCG
GO:2000664	0.038995517	1	3	positive regulation of interleukin-5 secretion	IL17RA
GO:1901563	0.039004629	1	3	response to camptothecin	PRKAA1
GO:0042167	0.039048728	1	4	heme catabolic process	ENSACAG00000022125
GO:0097034	0.039625032	1	9	mitochondrial respiratory chain complex IV biogenesis	COA1
GO:1901137	0.04002151	8	354	carbohydrate derivative biosynthetic process	HSPG2,COASY,CANT1,MAT2B,TYW5,ALG3,ENSACAG00000009367,UPP2
GO:0072573	0.04046207	1	3	tolerance induction to lipopolysaccharide	TNFAIP3
GO:0001767	0.04066379	1	3	establishment of lymphocyte polarity	MYH9
GO:0008299	0.041036543	2	28	isoprenoid biosynthetic process	COQ2,ENSACAG00000003142
GO:2000002	0.041158521	1	3	negative regulation of DNA damage checkpoint	THOC5
GO:0060856	0.041202042	1	3	establishment of blood-brain barrier	MFSD2A
GO:0061077	0.04128796	2	33	chaperone-mediated protein folding	FKBP4,HSPH1
GO:0070508	0.041288947	1	4	cholesterol import	SCARB1
GO:0071396	0.041973069	6	220	cellular response to lipid	PRKAA1,ANXA1,ENSACAG00000022125,TNFAIP3,ENSACAG00000015364,MAPK8
GO:0051932	0.042059963	1	4	synaptic transmission, GABAergic	CLSTN3
GO:0051295	0.042207296	1	3	establishment of meiotic spindle localization	MYH9
GO:0034502	0.042249406	2	27	protein localization to chromosome	SLF2,RAD21
GO:0044206	0.0422531	1	7	UMP salvage	UPP2

GO:0006105	0.042290465	1	3	succinate metabolic process	SDHA
GO:1990166	0.042601527	1	3	protein localization to site of double-strand break	SLF2
GO:0050994	0.042792508	2	27	regulation of lipid catabolic process	PRKAA1,SCARB1
GO:0060215	0.042826095	1	4	primitive hemopoiesis	THOC5
GO:1902963	0.043058822	1	3	negative regulation of metalloendopeptidase activity involved in amyloid precursor protein catabolic process	ENSACAG00000011799
GO:0000462	0.04328212	2	30	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	UTP20,WDR3
GO:0071205	0.043298324	1	3	protein localization to juxtaparanode region of axon	CNTN2
GO:0046146	0.044190331	1	7	tetrahydrobiopterin metabolic process	PAH
GO:0033504	0.044314849	1	4	floor plate development	STIL
GO:0071569	0.044869331	1	5	protein ufmylation	UFL1
GO:1990592	0.044869331	1	5	protein K69-linked ufmylation	UFL1
GO:0032652	0.045099988	2	29	regulation of interleukin-1 production	ANXA1,TNFAIP3
GO:0090500	0.045311583	1	4	endocardial cushion to mesenchymal transition	ENSACAG00000009367
GO:0030157	0.045658452	1	5	pancreatic juice secretion	CCKAR
GO:0010815	0.046121825	1	4	bradykinin catabolic process	ENSACAG00000006462
GO:0071495	0.046613392	10	471	cellular response to endogenous stimulus	PRKAA1,ANXA1,ENSACAG00000015535,ENSACAG00000022125,SIN3A,ENSACAG00000009367,ENSACAG00000015364,COL3A1,MEN1,CCKAR
GO:0071391	0.046755987	2	30	cellular response to estrogen stimulus	ENSACAG00000022125,ENSACAG00000015364
GO:0018212	0.047274805	3	61	peptidyl-tyrosine modification	SYK,CLK2,FGFR1
GO:0006556	0.047354467	1	4	S-adenosylmethionine biosynthetic process	MAT2B
GO:0035493	0.047495302	1	7	SNARE complex assembly	STX4
GO:1903335	0.047499124	1	5	regulation of vacuolar transport	VPS35
GO:0006301	0.047786063	2	31	postreplication repair	NSMCE1,VCP
GO:0002526	0.04793323	2	31	acute inflammatory response	SERPINC1,ENSACAG00000022125
GO:0045786	0.048207617	8	386	negative regulation of cell cycle	CDK5RAP3,PRKAA1,CARM1,ENSACAG00000013691,TNFAIP3,SART1,T

					HOC5,MEN1
GO:0045824	0.048747732	2	29	negative regulation of innate immune response	TRAFD1,TNFAIP3
GO:0043654	0.048793005	1	4	recognition of apoptotic cell	SCARB1
GO:0030198	0.049342607	6	210	extracellular matrix organization	HSPG2,FGG,ENSACAG00000006445,ENSACAG00000009367,MYO1E,COL3A1
GO:0006346	0.049431954	1	4	methylation-dependent chromatin silencing	MBD1
GO:0048008	0.049589015	2	29	platelet-derived growth factor receptor signaling pathway	PDGFC,MYO1E
GO:0061469	0.049655856	1	5	regulation of type B pancreatic cell proliferation	MEN1

Table S6. PSGs identified on branch 7 of lizard.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000008616	ENSACAG00000008793	ENSACAT00000008799	
ENSACAP00000001892	ENSACAG00000001928	ENSACAT00000001938	PPIA
ENSACAP00000009102	ENSACAG00000009174	ENSACAT00000009295	TOP3A
ENSACAP00000011752	ENSACAG00000011849	ENSACAT00000011995	
ENSACAP00000008334	ENSACAG00000008479	ENSACAT00000008515	EPN2
ENSACAP00000009466	ENSACAG00000009326	ENSACAT00000009663	HKDC1
ENSACAP00000016791	ENSACAG00000017044	ENSACAT00000017122	SPG7
ENSACAP00000000589	ENSACAG00000000612	ENSACAT00000000608	EIF4H
ENSACAP00000003351	ENSACAG00000003450	ENSACAT00000003434	FDPS
ENSACAP00000016287	ENSACAG00000016561	ENSACAT00000016611	CCDC120
ENSACAP00000017141	ENSACAG00000017411	ENSACAT00000017478	CCDC155
ENSACAP00000004380	ENSACAG00000004514	ENSACAT00000004480	MTFMT
ENSACAP00000007881	ENSACAG00000008005	ENSACAT00000008047	PHACTR2
ENSACAP00000019723	ENSACAG00000026198	ENSACAT00000027755	
ENSACAP00000019544	ENSACAG00000025211	ENSACAT00000023876	PSMB7
ENSACAP00000012215	ENSACAG00000012469	ENSACAT00000012465	ALG8
ENSACAP00000003421	ENSACAG00000003518	ENSACAT00000003505	SNX15

ENSACAP00000002218	ENSACAG00000002161	ENSACAT00000002278	GGCX
ENSACAP00000012225	ENSACAG00000012412	ENSACAT00000012475	TINAGL1
ENSACAP00000013010	ENSACAG00000013244	ENSACAT00000013269	AIMP2
ENSACAP00000021150	ENSACAG00000025684	ENSACAT00000023023	CDK5R1
ENSACAP00000009014	ENSACAG00000009215	ENSACAT00000009207	MAP7D3
ENSACAP00000014902	ENSACAG00000015167	ENSACAT00000015205	CA4
ENSACAP00000007360	ENSACAG00000007471	ENSACAT00000007516	TMPRSS13
ENSACAP00000021911	ENSACAG00000028360	ENSACAT00000029329	LRRIQ3
ENSACAP00000005537	ENSACAG00000005675	ENSACAT00000005658	SPATA6
ENSACAP00000005172	ENSACAG00000005300	ENSACAT00000005289	PENK
ENSACAP00000009494	ENSACAG00000009686	ENSACAT00000009691	WDYHV1
ENSACAP00000004033	ENSACAG00000003913	ENSACAT00000004125	
ENSACAP00000006642	ENSACAG00000006706	ENSACAT00000006788	PAFAH1B1
ENSACAP00000015047	ENSACAG00000015242	ENSACAT00000015351	MYO1E
ENSACAP00000009822	ENSACAG00000009903	ENSACAT00000010022	
ENSACAP00000010243	ENSACAG00000010426	ENSACAT00000010453	WDR18
ENSACAP00000003556	ENSACAG00000003644	ENSACAT00000003644	NMI
ENSACAP00000006831	ENSACAG00000006971	ENSACAT00000006981	CASP2
ENSACAP00000012450	ENSACAG00000012696	ENSACAT00000012706	
ENSACAP00000016586	ENSACAG00000016861	ENSACAT00000016912	RNF4
ENSACAP00000014398	ENSACAG00000014647	ENSACAT00000014692	HDAC8
ENSACAP00000006372	ENSACAG00000006516	ENSACAT00000006515	SLC38A6
ENSACAP00000000186	ENSACAG00000000189	ENSACAT00000000189	RPUSD4
ENSACAP00000001731	ENSACAG00000001829	ENSACAT00000001771	CPLX1
ENSACAP00000009857	ENSACAG00000010053	ENSACAT00000010060	DCLRE1A
ENSACAP00000013467	ENSACAG00000013657	ENSACAT00000013745	RMDN3
ENSACAP00000007911	ENSACAG00000007985	ENSACAT00000008077	POLR3A
ENSACAP00000008939	ENSACAG00000009078	ENSACAT00000009130	
ENSACAP00000014119	ENSACAG00000014302	ENSACAT00000014409	LONP2
ENSACAP00000009111	ENSACAG00000009325	ENSACAT00000009304	PSMD5

ENSACAP00000003529	ENSACAG00000003604	ENSACAT00000003617	RANBP9
ENSACAP00000003912	ENSACAG00000003975	ENSACAT00000004004	FAM179B
ENSACAP00000006807	ENSACAG00000006885	ENSACAT00000006957	
ENSACAP00000007188	ENSACAG00000007331	ENSACAT00000007343	TRUB2
ENSACAP00000005006	ENSACAG00000005072	ENSACAT00000005119	TRDMT1
ENSACAP00000005435	ENSACAG00000005541	ENSACAT00000005553	DCP1B
ENSACAP00000008622	ENSACAG00000008770	ENSACAT00000008805	UQCRC2
ENSACAP00000014797	ENSACAG00000015073	ENSACAT00000015098	CD79A
ENSACAP00000016065	ENSACAG00000016357	ENSACAT00000016385	CCDC114
ENSACAP00000012512	ENSACAG00000011927	ENSACAT00000012768	
ENSACAP00000016197	ENSACAG00000016429	ENSACAT00000016520	ECT2
ENSACAP00000012123	ENSACAG00000012336	ENSACAT00000012368	NPHS2
ENSACAP00000016631	ENSACAG00000016906	ENSACAT00000016958	LENG9
ENSACAP00000001278	ENSACAG00000001224	ENSACAT00000001311	PPIL2
ENSACAP00000020077	ENSACAG00000017616	ENSACAT00000023898	ZBBX
ENSACAP00000012505	ENSACAG00000012646	ENSACAT00000012761	BZW2
ENSACAP00000006658	ENSACAG00000006806	ENSACAT00000006804	RSRC1
ENSACAP00000011017	ENSACAG00000011260	ENSACAT00000011245	RAP2B
ENSACAP00000007488	ENSACAG00000007569	ENSACAT00000007645	RNF13
ENSACAP00000002874	ENSACAG00000002984	ENSACAT00000002945	
ENSACAP00000009037	ENSACAG00000009195	ENSACAT00000009230	TGFBR1
ENSACAP00000012778	ENSACAG00000013023	ENSACAT00000013034	CENPC
ENSACAP00000006276	ENSACAG00000006300	ENSACAT00000006416	GIGYF2
ENSACAP00000013601	ENSACAG00000013672	ENSACAT00000013881	LTA4H
ENSACAP00000017175	ENSACAG00000017448	ENSACAT00000017512	C10orf88
ENSACAP00000000334	ENSACAG00000000380	ENSACAT00000000348	OLFM4
ENSACAP00000016295	ENSACAG00000016570	ENSACAT00000016619	ETV7
ENSACAP00000000533	ENSACAG00000000625	ENSACAT00000000552	BORA
ENSACAP00000007022	ENSACAG00000007100	ENSACAT00000007173	ZNF277
ENSACAP00000012075	ENSACAG00000012308	ENSACAT00000012320	EMC10

ENSACAP00000012243	ENSACAG00000012446	ENSACAT00000012494	ARNTL2
ENSACAP00000015866	ENSACAG00000016035	ENSACAT00000016184	GNAI1
ENSACAP00000006098	ENSACAG00000006177	ENSACAT00000006235	PHTF2
ENSACAP00000000756	ENSACAG00000000644	ENSACAT00000000780	PROS1
ENSACAP00000010876	ENSACAG00000011065	ENSACAT00000011102	CMSS1
ENSACAP00000014735	ENSACAG00000014951	ENSACAT00000015036	DDX4
ENSACAP00000002495	ENSACAG00000002612	ENSACAT00000002560	CTXN3
ENSACAP00000004504	ENSACAG00000004592	ENSACAT00000004607	
ENSACAP00000010618	ENSACAG00000010781	ENSACAT00000010837	HAUS6
ENSACAP00000014848	ENSACAG00000015126	ENSACAT00000015149	
ENSACAP00000017384	ENSACAG00000017648	ENSACAT00000017725	EXOSC8
ENSACAP00000016946	ENSACAG00000017202	ENSACAT00000017281	ATF1
ENSACAP00000000600	ENSACAG00000000510	ENSACAT00000000620	
ENSACAP00000007748	ENSACAG00000007876	ENSACAT00000007914	MYL6
ENSACAP00000016415	ENSACAG00000016662	ENSACAT00000016740	PGS1
ENSACAP00000010337	ENSACAG00000010381	ENSACAT00000010550	KALRN
ENSACAP00000003778	ENSACAG00000003893	ENSACAT00000003870	TMEM177
ENSACAP00000000432	ENSACAG00000000451	ENSACAT00000000449	HNMT
ENSACAP00000015661	ENSACAG00000015930	ENSACAT00000015976	LCP2
ENSACAP00000016181	ENSACAG00000016379	ENSACAT00000016502	RUFY1
ENSACAP00000016478	ENSACAG00000016751	ENSACAT00000016804	THSD1
ENSACAP00000014275	ENSACAG00000014566	ENSACAT00000014568	LIG4
ENSACAP00000001570	ENSACAG00000001672	ENSACAT00000001607	TRDN
ENSACAP00000012699	ENSACAG00000012645	ENSACAT00000012955	QARS
ENSACAP00000000946	ENSACAG00000000985	ENSACAT00000000974	CTGF
ENSACAP00000007136	ENSACAG00000007254	ENSACAT00000007291	
ENSACAP00000004112	ENSACAG00000004244	ENSACAT00000004209	MRPL18
ENSACAP00000008317	ENSACAG00000008467	ENSACAT00000008497	FRMD1

Table S7. GO terms associated with PSGs identified on lizard branch 7.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames
GO:0070507	4.61E-06	7	119	regulation of microtubule cytoskeleton organization	ECT2,BORA,CDK5R1,PAFAH1B1,ENSACAG00000012696,RNF4,FAM179B
GO:0032886	1.86E-05	7	144	regulation of microtubule-based process	ECT2,BORA,CDK5R1,PAFAH1B1,ENSACAG00000012696,RNF4,FAM179B
GO:0061001	0.000728444	3	27	regulation of dendritic spine morphogenesis	KALRN,CDK5R1,PAFAH1B1
GO:0006625	0.001270913	2	10	protein targeting to peroxisome	ENSACAG00000011849,LONP2
GO:0043574	0.001270913	2	10	peroxisomal transport	ENSACAG00000011849,LONP2
GO:0021819	0.001333661	2	10	layer formation in cerebral cortex	CDK5R1,PAFAH1B1
GO:0000413	0.002762017	2	16	protein peptidyl-prolyl isomerization	PPIL2,PPIA
GO:0070925	0.003044368	6	246	organelle assembly	CENPC,HAUS6,CCDC155,SPATA6,PAFAH1B1,ENSACAG00000012696
GO:0006399	0.003280201	5	176	tRNA metabolic process	EXOSC8,QARS,RPUSD4,TRUB2,TRDMT1
GO:0072015	0.003555081	2	14	glomerular visceral epithelial cell development	NPHS2,MYO1E
GO:0000291	0.003849114	2	18	nuclear-transcribed mRNA catabolic process, exonucleolytic	EXOSC8,DCP1B
GO:0001522	0.004026245	2	18	pseudouridine synthesis	RPUSD4,TRUB2
GO:0071897	0.00451704	3	56	DNA biosynthetic process	TOP3A,LIG4,CTGF
GO:0051867	0.004696361	1	1	general adaptation syndrome, behavioral process	PENK
GO:0032687	0.004873366	1	1	negative regulation of interferon-alpha production	NMI
GO:0009306	0.005107436	4	120	protein secretion	ENSACAG00000011849,LCP2,PAFAH1B1,CPLX1
GO:0090220	0.005309215	1	1	chromosome localization to nuclear envelope involved in homologous chromosome segregation	CCDC155
GO:0051276	0.005372572	6	271	chromosome organization	CENPC,TOP3A,CCDC155,PAFAH1B1,HDAC8,DCLRE1A
GO:0001695	0.005416762	1	1	histamine catabolic process	HNMT
GO:0090176	0.005948274	1	1	microtubule cytoskeleton organization involved in establishment of planar polarity	PAFAH1B1
GO:0002209	0.006236284	2	23	behavioral defense response	KALRN,PENK

GO:0034660	0.006342	7	391	ncRNA metabolic process	DDX4,EXOSC8,QARS,WDR18,RPUSD4,TRUB2,TRDMT1
GO:0051461	0.006645157	1	2	positive regulation of corticotropin secretion	ENSACAG00000011849
GO:0007031	0.006812234	2	22	peroxisome organization	ENSACAG00000011849,LONP2
GO:0006425	0.006866147	1	1	glutaminyl-tRNA aminoacylation	QARS
GO:0090158	0.007606271	1	2	endoplasmic reticulum membrane organization	TRDN
GO:0021722	0.007701049	1	2	superior olivary nucleus maturation	CDK5R1
GO:0050905	0.008899274	3	72	neuromuscular process	GIGYF2,PENK,PAFAH1B1
GO:0014075	0.009175654	2	24	response to amine	HNMT,TRDMT1
GO:0007062	0.010457074	3	76	sister chromatid cohesion	CENPC,PAFAH1B1,HDAC8
GO:1903321	0.010459358	3	83	negative regulation of protein modification by small protein conjugation or removal	RNF4,HDAC8,PSMD5
GO:0008088	0.010855916	2	31	axo-dendritic transport	SPG7,PAFAH1B1
GO:1902524	0.011003462	1	2	positive regulation of protein K48-linked ubiquitination	NMI
GO:0065002	0.011276057	2	34	intracellular protein transmembrane transport	ENSACAG00000011849,LONP2
GO:0000086	0.011580468	3	77	G2/M transition of mitotic cell cycle	BORA,HAUS6,PAFAH1B1
GO:0033383	0.011866226	1	2	geranyl diphosphate metabolic process	FDPS
GO:0033384	0.011866226	1	2	geranyl diphosphate biosynthetic process	FDPS
GO:0045337	0.011866226	1	2	farnesyl diphosphate biosynthetic process	FDPS
GO:0045338	0.011866226	1	2	farnesyl diphosphate metabolic process	FDPS
GO:0046469	0.012513946	1	2	platelet activating factor metabolic process	PAFAH1B1
GO:0006490	0.012987417	1	2	oligosaccharide-lipid intermediate biosynthetic process	ALG8
GO:0051691	0.012987417	1	2	cellular oligosaccharide metabolic process	ALG8
GO:1903697	0.013082687	1	2	negative regulation of microvillus assembly	ENSACAG00000006885
GO:0070682	0.014372943	1	3	proteasome regulatory particle assembly	PSMD5
GO:0051301	0.01529286	6	351	cell division	CENPC,BORA,GNAI1,HAUS6,LIG4,PAFAH1B1
GO:0097010	0.015380222	1	3	eukaryotic translation initiation factor 4F complex assembly	EIF4H
GO:0035928	0.015603117	1	3	rRNA import into mitochondrion	MRPL18
GO:0001692	0.016587775	1	3	histamine metabolic process	HNMT

GO:0050851	0.016857331	3	102	antigen receptor-mediated signaling pathway	CD79A,LCP2,PSMD5
GO:0010927	0.016877385	3	89	cellular component assembly involved in morphogenesis	SPATA6,PAFAH1B1,FAM179B
GO:0017187	0.017049735	1	3	peptidyl-glutamic acid carboxylation	GGCX
GO:0090234	0.017528696	1	3	regulation of kinetochore assembly	RNF4
GO:0034473	0.01770932	1	4	U1 snRNA 3'-end processing	EXOSC8
GO:0043622	0.017733468	1	3	cortical microtubule organization	PAFAH1B1
GO:0051653	0.018075475	1	3	spindle localization	CCDC155
GO:0035927	0.018858089	1	4	RNA import into mitochondrion	MRPL18
GO:0051280	0.019270705	1	5	negative regulation of release of sequestered calcium ion into cytosol	TRDN
GO:0006303	0.019963512	2	35	double-strand break repair via nonhomologous end joining	LIG4,DCLRE1A
GO:0003383	0.020227679	1	3	apical constriction	FRMD1
GO:0000726	0.020662114	2	36	non-recombinational repair	LIG4,DCLRE1A
GO:0071922	0.021026313	1	4	regulation of cohesin loading	HDAC8
GO:0033555	0.021445255	2	43	multicellular organismal response to stress	KALRN,PENK
GO:1903320	0.02177588	4	192	regulation of protein modification by small protein conjugation or removal	NMI,RNF4,HDAC8,PSMD5
GO:0034599	0.022024418	3	109	cellular response to oxidative stress	ECT2,ZNF277,PENK
GO:0072089	0.022793251	2	40	stem cell proliferation	ETV7,PAFAH1B1
GO:0006333	0.022959474	2	42	chromatin assembly or disassembly	CENPC,HDAC8
GO:0018214	0.023800491	1	4	protein carboxylation	GGCX
GO:0071042	0.024455405	1	5	nuclear polyadenylation-dependent mRNA catabolic process	EXOSC8
GO:0036035	0.025061168	1	4	osteoclast development	PAFAH1B1
GO:0071305	0.025741852	1	5	cellular response to vitamin D	PENK
GO:0031087	0.025944624	1	5	deadenylation-independent decapping of nuclear-transcribed mRNA	DCP1B
GO:0051029	0.026657968	1	5	rRNA transport	MRPL18
GO:0006970	0.027105015	2	45	response to osmotic stress	HNMT,MAP7D3
GO:0060359	0.027107214	2	45	response to ammonium ion	HNMT,PENK
GO:0002347	0.027455927	1	5	response to tumor cell	HNMT

GO:0006013	0.027877274	1	5	mannose metabolic process	ENSACAG00000003913
GO:0051865	0.028274314	2	47	protein autoubiquitination	RNF13,RNF4
GO:0033152	0.02848869	1	5	immunoglobulin V(D)J recombination	LIG4
GO:0050885	0.029023695	2	45	neuromuscular process controlling balance	GIGYF2,PAFAH1B1
GO:0035166	0.030274801	1	6	post-embryonic hemopoiesis	MYO1E
GO:0051660	0.031152567	1	5	establishment of centrosome localization	PAFAH1B1
GO:0085020	0.031170211	1	6	protein K6-linked ubiquitination	RNF4
GO:0009451	0.031440402	3	122	RNA modification	RPUSD4,TRUB2,TRDMT1
GO:0030048	0.031622752	2	44	actin filament-based movement	FRMD1,MYO1E
GO:0048013	0.032274808	2	47	ephrin receptor signaling pathway	KALRN,CDK5R1
GO:0016078	0.033818488	1	7	tRNA catabolic process	EXOSC8
GO:0006122	0.033967584	1	8	mitochondrial electron transport, ubiquinol to cytochrome c	UQCRC2
GO:0051383	0.034194114	1	8	kinetochore organization	CENPC
GO:0030029	0.034331166	5	301	actin filament-based process	NPHS2,MYL6,FRMD1,PAFAH1B1,MYO1E
GO:0031848	0.034796002	1	6	protection from non-homologous end joining at telomere	DCLRE1A
GO:0043247	0.034796002	1	6	telomere maintenance in response to DNA damage	DCLRE1A
GO:0006691	0.036331756	1	7	leukotriene metabolic process	LTA4H
GO:0032049	0.038326495	1	7	cardiolipin biosynthetic process	PGS1
GO:0048569	0.039530939	1	8	post-embryonic animal organ development	MYO1E
GO:2000574	0.040112201	1	7	regulation of microtubule motor activity	PAFAH1B1
GO:0034427	0.041431739	1	9	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	EXOSC8
GO:0045576	0.042120474	1	8	mast cell activation	LCP2
GO:0051103	0.042264304	1	7	DNA ligation involved in DNA repair	LIG4
GO:0032486	0.042776035	1	9	Rap protein signal transduction	RAP2B
GO:0043633	0.043141913	1	9	polyadenylation-dependent RNA catabolic process	EXOSC8
GO:0000467	0.04317038	1	9	exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	EXOSC8
GO:0002118	0.043192629	1	8	aggressive behavior	PENK

GO:0052805	0.044501213	1	7	imidazole-containing compound catabolic process	HNMT
GO:0006302	0.045499126	3	138	double-strand break repair	LIG4,CCDC155,DCLRE1A
GO:0014902	0.045553042	1	8	myotube differentiation	TRDN
GO:0001836	0.046381646	1	11	release of cytochrome c from mitochondria	ENSACAG00000002984
GO:0031119	0.046559321	1	8	tRNA pseudouridine synthesis	RPUSD4
GO:0033169	0.04709722	1	7	histone H3-K9 demethylation	ENSACAG00000004592
GO:0035235	0.047916031	1	8	ionotropic glutamate receptor signaling pathway	CDK5R1
GO:0006703	0.049427184	1	10	estrogen biosynthetic process	ENSACAG00000000510

Table S8. PSGs identified on branch 3 of lizard.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000017617	ENSACAG00000017890	ENSACAT00000017963	FRMD6
ENSACAP00000021464	ENSACAG00000022350	ENSACAT00000028958	GCNT2
ENSACAP00000013774	ENSACAG00000014000	ENSACAT00000014055	CCDC150
ENSACAP00000004262	ENSACAG00000004398	ENSACAT00000004361	CCK
ENSACAP00000008877	ENSACAG00000009089	ENSACAT00000009068	FTSJ2
ENSACAP00000008525	ENSACAG00000008687	ENSACAT00000008708	BRAT1
ENSACAP00000007909	ENSACAG00000008064	ENSACAT00000008075	PGPEP1L
ENSACAP00000006257	ENSACAG00000006391	ENSACAT00000006396	
ENSACAP00000001831	ENSACAG00000001902	ENSACAT00000001875	BAIAP2L1
ENSACAP00000016271	ENSACAG00000016477	ENSACAT00000016595	GRIPAP1
ENSACAP00000020903	ENSACAG00000027313	ENSACAT00000027467	APOA1BP
ENSACAP00000012897	ENSACAG00000013107	ENSACAT00000013155	BUB1
ENSACAP00000016378	ENSACAG00000016634	ENSACAT00000016702	CHMP7
ENSACAP00000004552	ENSACAG00000004469	ENSACAT00000004657	
ENSACAP00000004695	ENSACAG00000004715	ENSACAT00000004802	PER1
ENSACAP00000003181	ENSACAG00000003268	ENSACAT00000003262	WRAP53
ENSACAP00000000726	ENSACAG00000000734	ENSACAT00000000750	CEP95
ENSACAP00000019130	ENSACAG00000022469	ENSACAT00000023799	INHBE

ENSACAP00000003224	ENSACAG00000002862	ENSACAT00000003307	KIF5C
ENSACAP00000006395	ENSACAG00000006551	ENSACAT00000006538	
ENSACAP00000004419	ENSACAG00000004481	ENSACAT00000004519	MTO1
ENSACAP00000006195	ENSACAG00000006333	ENSACAT00000006332	NOP16
ENSACAP00000015761	ENSACAG00000016002	ENSACAT00000016077	MATN2
ENSACAP00000003548	ENSACAG00000003615	ENSACAT00000003636	RNF126
ENSACAP00000007021	ENSACAG00000007102	ENSACAT00000007172	PGM2
ENSACAP00000013508	ENSACAG00000013732	ENSACAT00000013786	IMPA1
ENSACAP00000001731	ENSACAG00000001829	ENSACAT00000001771	CPLX1
ENSACAP00000017375	ENSACAG00000017604	ENSACAT00000017716	COPG2
ENSACAP00000012836	ENSACAG00000013059	ENSACAT00000013093	JPH1
ENSACAP00000015309	ENSACAG00000015563	ENSACAT00000015621	MPHOSPH9
ENSACAP00000004170	ENSACAG00000004294	ENSACAT00000004269	PPP1R2
ENSACAP00000000325	ENSACAG00000000339	ENSACAT00000000339	NPDC1
ENSACAP00000003120	ENSACAG00000003220	ENSACAT00000003199	VIMP
ENSACAP00000015856	ENSACAG00000016141	ENSACAT00000016173	STEAP3
ENSACAP00000006742	ENSACAG00000006893	ENSACAT00000006888	PKMYT1
ENSACAP00000023079	ENSACAG00000029390	ENSACAT00000030500	
ENSACAP00000001571	ENSACAG00000001644	ENSACAT00000001608	CCP110
ENSACAP00000004163	ENSACAG00000004288	ENSACAT00000004262	OVCH2
ENSACAP00000023121	ENSACAG00000028892	ENSACAT00000030541	TOR1AIP1
ENSACAP00000005208	ENSACAG00000005306	ENSACAT00000005325	EXD2
ENSACAP00000012123	ENSACAG00000012336	ENSACAT00000012368	NPHS2
ENSACAP00000017589	ENSACAG00000017863	ENSACAT00000017935	RNF125
ENSACAP00000012930	ENSACAG00000013117	ENSACAT00000013188	
ENSACAP00000011701	ENSACAG00000011812	ENSACAT00000011942	HDAC3
ENSACAP00000001278	ENSACAG00000001224	ENSACAT00000001311	PPIL2
ENSACAP00000011214	ENSACAG00000011373	ENSACAT00000011450	AGK
ENSACAP00000008587	ENSACAG00000008478	ENSACAT00000008770	JAK1
ENSACAP00000002239	ENSACAG00000002353	ENSACAT00000002299	

ENSACAP00000002228	ENSACAG00000002322	ENSACAT00000002288	
ENSACAP00000005613	ENSACAG00000005654	ENSACAT00000005735	CAMK1G
ENSACAP00000001539	ENSACAG00000001584	ENSACAT00000001575	PRPS2
ENSACAP00000008363	ENSACAG00000008475	ENSACAT00000008544	SNTA1
ENSACAP00000007611	ENSACAG00000007720	ENSACAT00000007772	TRMU
ENSACAP00000016261	ENSACAG00000016502	ENSACAT00000016585	ETFDH
ENSACAP00000003266	ENSACAG00000003023	ENSACAT00000003349	LRBA
ENSACAP00000003492	ENSACAG00000003495	ENSACAT00000003578	DCLK2
ENSACAP00000002092	ENSACAG00000002189	ENSACAT00000002147	ZMYM2
ENSACAP00000012424	ENSACAG00000012630	ENSACAT00000012677	CCNA2
ENSACAP00000012475	ENSACAG00000012650	ENSACAT00000012731	
ENSACAP00000008867	ENSACAG00000009000	ENSACAT00000009058	DEPDC1B
ENSACAP00000009215	ENSACAG00000009351	ENSACAT00000009408	UTP15
ENSACAP00000001136	ENSACAG00000001252	ENSACAT00000001168	TJP2
ENSACAP00000005113	ENSACAG00000005220	ENSACAT00000005229	
ENSACAP00000022884	ENSACAG00000028675	ENSACAT00000030302	TRIM44
ENSACAP00000008585	ENSACAG00000008760	ENSACAT00000008768	MRVI1
ENSACAP00000000070	ENSACAG00000000071	ENSACAT00000000071	PSMG1
ENSACAP00000021985	ENSACAG00000029328	ENSACAT00000029403	HMMR
ENSACAP00000004933	ENSACAG00000004980	ENSACAT00000005046	MCM3AP
ENSACAP00000015318	ENSACAG00000015374	ENSACAT00000015630	RANBP17
ENSACAP00000016106	ENSACAG00000016325	ENSACAT00000016427	SLC23A1
ENSACAP00000001448	ENSACAG00000001543	ENSACAT00000001483	THAP5
ENSACAP00000005778	ENSACAG00000005778	ENSACAT00000005905	DDX41
ENSACAP00000013318	ENSACAG00000013515	ENSACAT00000013588	XPC
ENSACAP00000011025	ENSACAG00000011199	ENSACAT00000011253	
ENSACAP00000021883	ENSACAG00000028683	ENSACAT00000029301	
ENSACAP00000001283	ENSACAG00000001292	ENSACAT00000001316	DIEXF

Table S9. GO terms associated with PSGs identified on lizard branch 3.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames
GO:0009820	0.00022084	2	6	alkaloid metabolic process	ENSACAG00000011199,APOA1BP
GO:1900864	0.000508584	2	8	mitochondrial RNA modification	TRMU,MTO1
GO:0070525	0.000598271	2	9	tRNA threonylcarbamoyladenosine metabolic process	TRMU,MTO1
GO:0002098	0.000807311	2	10	tRNA wobble uridine modification	TRMU,MTO1
GO:0002097	0.001181535	2	13	tRNA wobble base modification	TRMU,MTO1
GO:0046085	0.001719259	2	16	adenosine metabolic process	TRMU,MTO1
GO:0071629	0.002797871	1	1	cytoplasm-associated proteasomal ubiquitin-dependent protein catabolic process	RNF126
GO:0080129	0.002915312	1	1	proteasome core complex assembly	PSMG1
GO:0032203	0.003517897	1	1	telomere formation via telomerase	WRAP53
GO:0090671	0.003517897	1	1	telomerase RNA localization to Cajal body	WRAP53
GO:0015882	0.00497018	1	1	L-ascorbic acid transport	SLC23A1
GO:0070837	0.00497018	1	1	dehydroascorbic acid transport	SLC23A1
GO:0070904	0.00497018	1	1	transepithelial L-ascorbic acid transport	SLC23A1
GO:0006769	0.005257033	1	2	nicotinamide metabolic process	APOA1BP
GO:0000959	0.00582725	2	27	mitochondrial RNA metabolic process	TRMU,MTO1
GO:0032202	0.006026214	1	2	telomere assembly	WRAP53
GO:0031104	0.00643294	1	1	dendrite regeneration	MATN2
GO:0017144	0.006990731	2	31	drug metabolic process	ENSACAG00000013117,ENSACAG00000011199
GO:0034470	0.007075211	5	312	ncRNA processing	TRMU,UTP15,DIEXF,MTO1,FTSJ2
GO:1904851	0.008100695	1	2	positive regulation of establishment of protein localization to telomere	WRAP53
GO:0038110	0.009521418	1	2	interleukin-2-mediated signaling pathway	JAK1
GO:0006021	0.009654662	1	3	inositol biosynthetic process	IMPA1
GO:0072249	0.010123345	1	2	metanephric glomerular visceral epithelial cell development	NPHS2
GO:0046882	0.01053161	1	3	negative regulation of follicle-stimulating hormone secretion	INHBE

GO:0048178	0.01053161	1	3	negative regulation of hepatocyte growth factor biosynthetic process	INHBE
GO:0006015	0.010763553	1	3	5-phosphoribose 1-diphosphate biosynthetic process	PRPS2
GO:0046391	0.010763553	1	3	5-phosphoribose 1-diphosphate metabolic process	PRPS2
GO:0071763	0.011441129	1	3	nuclear membrane organization	TOR1AIP1
GO:0000453	0.011476722	1	3	enzyme-directed rRNA 2'-O-methylation	FTSJ2
GO:0009451	0.011491803	3	122	RNA modification	TRMU,MTO1,FTSJ2
GO:0034637	0.011881345	2	42	cellular carbohydrate biosynthetic process	PGM2,IMPA1
GO:2000323	0.012233757	1	3	negative regulation of glucocorticoid receptor signaling pathway	PER1
GO:0034504	0.012541147	3	106	protein localization to nucleus	MCM3AP,RANBP17,TOR1AIP1
GO:0060546	0.013064698	1	4	negative regulation of necroptotic process	ENSACAG00000012650
GO:0044262	0.013237757	3	120	cellular carbohydrate metabolic process	PGM2,IMPA1,PPP1R2
GO:0097167	0.013318414	1	3	circadian regulation of translation	PER1
GO:0034227	0.013498027	1	4	tRNA thio-modification	TRMU
GO:0046448	0.013792929	1	3	tropane alkaloid metabolic process	ENSACAG00000011199
GO:0050783	0.013792929	1	3	cocaine metabolic process	ENSACAG00000011199
GO:0019388	0.014523449	1	4	galactose catabolic process	PGM2
GO:0034116	0.015561132	1	4	positive regulation of heterotypic cell-cell adhesion	GCNT2
GO:0003383	0.015762842	1	3	apical constriction	FRMD6
GO:0060278	0.016160052	1	4	regulation of ovulation	INHBE
GO:0036438	0.016322279	1	4	maintenance of lens transparency	GCNT2
GO:0072524	0.016352706	2	54	pyridine-containing compound metabolic process	APOA1BP,PGM2
GO:1900094	0.016797406	1	5	regulation of transcription from RNA polymerase II promoter involved in determination of left/right symmetry	INHBE
GO:0001510	0.018148483	2	51	RNA methylation	MTO1,FTSJ2
GO:0014016	0.019139512	1	5	neuroblast differentiation	ENSACAG00000011199
GO:0046128	0.019360801	3	157	purine ribonucleoside metabolic process	PRPS2,TRMU,MTO1
GO:0034660	0.020190001	5	391	ncRNA metabolic process	TRMU,UTP15,DIEXF,MTO1,FTSJ2
GO:0015931	0.021653218	3	141	nucleobase-containing compound transport	MCM3AP,RANBP17,KIF5C
GO:0051593	0.023441205	1	7	response to folic acid	ENSACAG00000011199
GO:0006112	0.023545918	2	56	energy reserve metabolic process	PGM2,PPP1R2

GO:1901990	0.024769075	3	151	regulation of mitotic cell cycle phase transition	CCNA2,XPC,BUB1
GO:0021930	0.025598581	1	6	cerebellar granule cell precursor proliferation	PSMG1
GO:2000241	0.025615592	2	65	regulation of reproductive process	ENSACAG00000005220,INHBE
GO:1990001	0.027631413	1	7	inhibition of cysteine-type endopeptidase activity involved in apoptotic process	ENSACAG00000012650
GO:0015677	0.028171814	1	6	copper ion import	STEAP3
GO:0060467	0.030402548	1	8	negative regulation of fertilization	ENSACAG00000005220
GO:0006091	0.031217663	3	179	generation of precursor metabolites and energy	ETFDH,PGM2,PPP1R2
GO:0006098	0.031597729	1	9	pentose-phosphate shunt	PGM2
GO:0010996	0.032293919	1	7	response to auditory stimulus	XPC
GO:0046838	0.033703708	1	9	phosphorylated carbohydrate dephosphorylation	IMPA1
GO:0008347	0.034222369	1	8	glial cell migration	MATN2
GO:0006012	0.034686005	1	9	galactose metabolic process	PGM2
GO:0010224	0.035094327	1	9	response to UV-B	XPC
GO:0070633	0.035132567	1	8	transepithelial transport	SLC23A1
GO:0045324	0.038573137	1	10	late endosome to vacuole transport	CHMP7
GO:1903672	0.038626116	1	9	positive regulation of sprouting angiogenesis	JAK1
GO:0035458	0.039174291	1	10	cellular response to interferon-beta	DDX41
GO:0042634	0.039541826	1	9	regulation of hair cycle	PER1
GO:0090557	0.040400773	1	8	establishment of endothelial intestinal barrier	TJP2
GO:0070932	0.040481975	1	9	histone H3 deacetylation	PER1
GO:2000251	0.041177491	1	11	positive regulation of actin cytoskeleton reorganization	BAIAP2L1
GO:1901657	0.041244906	3	218	glycosyl compound metabolic process	PRPS2,TRMU,MTO1
GO:0000717	0.041616079	1	8	nucleotide-excision repair, DNA duplex unwinding	XPC
GO:0000715	0.041700756	1	8	nucleotide-excision repair, DNA damage recognition	XPC
GO:0032053	0.042594554	1	8	ciliary basal body organization	CCP110
GO:0021860	0.042704037	1	8	pyramidal neuron development	DCLK2
GO:0000920	0.04370835	1	12	cell separation after cytokinesis	CHMP7
GO:0030214	0.044161931	1	9	hyaluronan catabolic process	HMMR
GO:0005976	0.045021827	2	81	polysaccharide metabolic process	PGM2,PPP1R2

GO:0043153	0.046552698	1	12	entrainment of circadian clock by photoperiod	PER1
GO:0046386	0.047433296	1	15	deoxyribose phosphate catabolic process	PGM2
GO:0019695	0.047719006	1	10	choline metabolic process	ENSACAG00000011199
GO:0043162	0.047757903	1	15	ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	RNF126
GO:0043248	0.047850153	1	16	proteasome assembly	PSMG1
GO:0042273	0.048493215	1	15	ribosomal large subunit biogenesis	NOP16
GO:0031099	0.048761255	2	95	regeneration	PRPS2,MATN2
GO:0016079	0.048922482	1	12	synaptic vesicle exocytosis	CPLX1
GO:0060334	0.049314998	1	12	regulation of interferon-gamma-mediated signaling pathway	JAK1
GO:0051156	0.049641284	1	14	glucose 6-phosphate metabolic process	PGM2

Table S10. PSGs identified on branch 6 of frog.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000009832	ENSACAG00000009950	ENSACAT00000010033	LGALS4
ENSACAP00000012790	ENSACAG00000012967	ENSACAT00000013046	UBE4B
ENSACAP00000011157	ENSACAG00000010939	ENSACAT00000011389	TLN1
ENSACAP00000007335	ENSACAG00000007457	ENSACAT00000007491	TDRKH
ENSACAP00000011041	ENSACAG00000011220	ENSACAT00000011269	SLC35F6
ENSACAP00000020529	ENSACAG00000022067	ENSACAT00000026115	AEBP1
ENSACAP00000005716	ENSACAG00000005606	ENSACAT00000005841	HK2
ENSACAP00000000381	ENSACAG00000000472	ENSACAT00000000396	FAS
ENSACAP00000009299	ENSACAG00000009333	ENSACAT00000009493	FLII
ENSACAP00000008336	ENSACAG00000008508	ENSACAT00000008517	GSTCD
ENSACAP00000009283	ENSACAG00000009414	ENSACAT00000009476	KMO
ENSACAP00000010744	ENSACAG00000010772	ENSACAT00000010966	
ENSACAP00000007089	ENSACAG00000007224	ENSACAT00000007242	LPCAT3
ENSACAP00000016788	ENSACAG00000017030	ENSACAT00000017119	
ENSACAP00000006254	ENSACAG00000006400	ENSACAT00000006393	RAB28

ENSACAP00000007849	ENSACAG00000007907	ENSACAT00000008015	FLOT2
ENSACAP00000003664	ENSACAG00000003722	ENSACAT00000003754	
ENSACAP00000017289	ENSACAG00000017545	ENSACAT00000017629	
ENSACAP00000011692	ENSACAG00000011940	ENSACAT00000011933	TFB2M
ENSACAP00000000518	ENSACAG00000000548	ENSACAT00000000536	SLC37A2
ENSACAP00000009821	ENSACAG00000010023	ENSACAT00000010021	CFAP53
ENSACAP00000003057	ENSACAG00000003131	ENSACAT00000003135	RPRD2
ENSACAP00000005278	ENSACAG00000005344	ENSACAT00000005395	HM13
ENSACAP00000002920	ENSACAG00000002994	ENSACAT00000002994	VPS52
ENSACAP00000004168	ENSACAG00000004303	ENSACAT00000004267	ANKRD53
ENSACAP00000013931	ENSACAG00000014164	ENSACAT00000014217	LZTFL1
ENSACAP00000013484	ENSACAG00000013728	ENSACAT00000013762	CRTAP
ENSACAP00000020455	ENSACAG00000024096	ENSACAT00000026031	MAPK15
ENSACAP00000019308	ENSACAG00000009983	ENSACAT00000023910	ABRA
ENSACAP00000010018	ENSACAG00000010181	ENSACAT00000010225	INTS9
ENSACAP00000008156	ENSACAG00000008317	ENSACAT00000008331	TXNDC9
ENSACAP00000003556	ENSACAG00000003644	ENSACAT00000003644	NMI
ENSACAP00000005858	ENSACAG00000005760	ENSACAT00000005987	CHD7
ENSACAP00000013614	ENSACAG00000013758	ENSACAT00000013894	RAPGEF1
ENSACAP00000006716	ENSACAG00000006626	ENSACAT00000006862	
ENSACAP00000001737	ENSACAG00000001799	ENSACAT00000001777	ZNF521
ENSACAP00000023204	ENSACAG00000029360	ENSACAT00000030624	
ENSACAP00000008354	ENSACAG00000008521	ENSACAT00000008535	COMTD1
ENSACAP00000005395	ENSACAG00000005301	ENSACAT00000005512	VILL
ENSACAP00000014119	ENSACAG00000014302	ENSACAT00000014409	LONP2
ENSACAP00000003647	ENSACAG00000003431	ENSACAT00000003736	TNC
ENSACAP00000001626	ENSACAG00000001638	ENSACAT00000001665	ZC3HC1
ENSACAP00000020092	ENSACAG00000024726	ENSACAT00000027932	
ENSACAP00000001640	ENSACAG00000001752	ENSACAT00000001679	CCDC78
ENSACAP00000002201	ENSACAG00000002300	ENSACAT00000002261	NLRX1

ENSACAP00000014251	ENSACAG00000014410	ENSACAT00000014544	CRISPLD2
ENSACAP00000021556	ENSACAG00000025660	ENSACAT00000026730	
ENSACAP00000012316	ENSACAG00000012414	ENSACAT00000012569	COPB1
ENSACAP00000008624	ENSACAG00000008771	ENSACAT00000008807	CTSK
ENSACAP00000016107	ENSACAG00000016384	ENSACAT00000016428	SPAG1
ENSACAP00000009331	ENSACAG00000009549	ENSACAT00000009526	TRAFD1
ENSACAP00000013933	ENSACAG00000014198	ENSACAT00000014219	MGME1
ENSACAP00000003369	ENSACAG00000003465	ENSACAT00000003452	ZNF574
ENSACAP00000012268	ENSACAG00000012487	ENSACAT00000012519	BCL2L13
ENSACAP00000012559	ENSACAG00000012773	ENSACAT00000012815	SLC37A3
ENSACAP00000003454	ENSACAG00000003528	ENSACAT00000003540	SASS6
ENSACAP00000015408	ENSACAG00000015569	ENSACAT00000015721	APPL2
ENSACAP00000016382	ENSACAG00000016659	ENSACAT00000016706	HMOX1
ENSACAP00000007993	ENSACAG00000008160	ENSACAT00000008164	C7orf57
ENSACAP00000001168	ENSACAG00000001238	ENSACAT00000001201	LRRC8C
ENSACAP00000009495	ENSACAG00000009576	ENSACAT00000009692	SDHA
ENSACAP00000020588	ENSACAG00000008144	ENSACAT00000026899	EFCAB7
ENSACAP00000008386	ENSACAG00000008484	ENSACAT00000008567	SMYD1
ENSACAP00000012479	ENSACAG00000012654	ENSACAT00000012735	CEP83
ENSACAP00000015527	ENSACAG00000015761	ENSACAT00000015841	PDCD4
ENSACAP00000017077	ENSACAG00000017346	ENSACAT00000017412	KANSL1
ENSACAP00000016873	ENSACAG00000017131	ENSACAT00000017208	SEC23IP
ENSACAP00000005181	ENSACAG00000005084	ENSACAT00000005298	COL1A1
ENSACAP00000005187	ENSACAG00000005261	ENSACAT00000005304	IPO9
ENSACAP00000006657	ENSACAG00000006739	ENSACAT00000006803	RALGAPB
ENSACAP00000022907	ENSACAG00000029016	ENSACAT00000030325	CD99
ENSACAP00000004056	ENSACAG00000004191	ENSACAT00000004150	MAB21L1
ENSACAP00000002517	ENSACAG00000002561	ENSACAT00000002582	CCDC81
ENSACAP00000017420	ENSACAG00000017672	ENSACAT00000017762	PLIN2
ENSACAP00000010758	ENSACAG00000010932	ENSACAT00000010981	CFP

ENSACAP00000018492	ENSACAG00000023141	ENSACAT00000022514	RD3L
ENSACAP00000008929	ENSACAG00000008987	ENSACAT00000009120	LGMN
ENSACAP00000016946	ENSACAG00000017202	ENSACAT00000017281	ATF1
ENSACAP00000014168	ENSACAG00000014373	ENSACAT00000014458	
ENSACAP00000004222	ENSACAG00000004323	ENSACAT00000004321	CD44
ENSACAP00000016889	ENSACAG00000017105	ENSACAT00000017224	STXBP2
ENSACAP00000010518	ENSACAG00000010640	ENSACAT00000010735	MYLK
ENSACAP00000017256	ENSACAG00000017496	ENSACAT00000017595	TBCD
ENSACAP00000006856	ENSACAG00000006926	ENSACAT00000007006	CTNND1
ENSACAP00000007659	ENSACAG00000007694	ENSACAT00000007823	ACOX1
ENSACAP00000022448	ENSACAG00000008728	ENSACAT00000029865	
ENSACAP00000018579	ENSACAG00000009366	ENSACAT00000026649	PLEKHG3
ENSACAP00000010282	ENSACAG00000010434	ENSACAT00000010494	SIRT7
ENSACAP00000008500	ENSACAG00000008693	ENSACAT00000008682	TUSC2
ENSACAP00000006476	ENSACAG00000006619	ENSACAT00000006621	GLYCTK
ENSACAP00000013318	ENSACAG00000013515	ENSACAT00000013588	XPC
ENSACAP00000011671	ENSACAG00000011855	ENSACAT00000011912	CCDC174
ENSACAP00000008228	ENSACAG00000008206	ENSACAT00000008405	ADGRG6
ENSACAP00000011882	ENSACAG00000012116	ENSACAT00000012126	STK19
ENSACAP00000011394	ENSACAG00000011208	ENSACAT00000011633	
ENSACAP00000010371	ENSACAG00000010535	ENSACAT00000010585	ATF6B
ENSACAP00000001116	ENSACAG00000001130	ENSACAT00000001148	ABCB10
ENSACAP00000002674	ENSACAG00000002782	ENSACAT00000002741	ERMARD

Table S11. GO terms associated with PSGs identified on frog branch 6.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames
GO:0032688	0.000402452	2	6	negative regulation of interferon-beta production	NMI,NLRX1
GO:0008643	0.000472479	4	67	carbohydrate transport	SLC37A3,SLC37A2,SLC35F6,HK2

GO:0045824	0.000562715	3	29	negative regulation of innate immune response	TRAFD1,NMI,NLRX1
GO:0001909	0.001090705	2	11	leukocyte mediated cytotoxicity	STXBP2,TUSC2
GO:0051014	0.001254138	2	9	actin filament severing	FLII,VILL
GO:0032618	0.002089888	1	1	interleukin-15 production	TUSC2
GO:0052567	0.002089888	1	1	response to defense-related host reactive oxygen species production	TUSC2
GO:0071609	0.002089888	1	1	chemokine (C-C motif) ligand 5 production	TUSC2
GO:0016485	0.002297722	5	182	protein processing	BCL2L13,LGMN,HM13,AEBP1,LONP2
GO:0006957	0.00275908	2	14	complement activation, alternative pathway	CFP,ENSACAG00000011208
GO:0031113	0.004064604	2	18	regulation of microtubule polymerization	TBCD,ANKRD53
GO:1903564	0.004271243	1	1	regulation of protein localization to cilium	LZTFL1
GO:0006788	0.00455411	1	1	heme oxidation	HMOX1
GO:0007072	0.004641887	1	1	positive regulation of transcription involved in exit from mitosis	SIRT7
GO:0043504	0.004651542	1	1	mitochondrial DNA repair	MGME1
GO:0001906	0.005116983	2	22	cell killing	STXBP2,TUSC2
GO:0018400	0.005225641	1	1	peptidyl-proline hydroxylation to 3-hydroxy-L-proline	CRTAP
GO:0098534	0.005246116	2	17	centriole assembly	SASS6,CCDC78
GO:1903905	0.005447399	1	1	positive regulation of establishment of T cell polarity	FLOT2
GO:0015794	0.005928903	1	1	glycerol-3-phosphate transport	SLC37A2
GO:0048611	0.006195778	1	1	embryonic ectodermal digestive tract development	VPS52
GO:1904925	0.007299423	1	1	positive regulation of mitophagy in response to mitochondrial depolarization	HK2
GO:0060690	0.007311921	1	1	epithelial cell differentiation involved in salivary gland development	CTNND1
GO:0042795	0.007759932	2	27	snRNA transcription from RNA polymerase II promoter	RPRD2,INTS9
GO:0006391	0.008540247	1	2	transcription initiation from mitochondrial promoter	TFB2M
GO:0032602	0.008879293	1	3	chemokine production	TUSC2
GO:1902524	0.009678068	1	2	positive regulation of protein K48-linked ubiquitination	NMI
GO:0008626	0.010321828	1	2	granzyme-mediated apoptotic signaling pathway	UBE4B
GO:0006127	0.010327515	1	2	glycerophosphate shuttle	SLC37A2

GO:0052646	0.010594766	2	29	alditol phosphate metabolic process	LPCAT3,SLC37A2
GO:1904211	0.011015362	1	3	membrane protein proteolysis involved in retrograde protein transport, ER to cytosol	HM13
GO:1901873	0.011482944	1	2	regulation of post-translational protein modification	CRTAP
GO:1901874	0.011482944	1	2	negative regulation of post-translational protein modification	CRTAP
GO:0006091	0.011779115	4	179	generation of precursor metabolites and energy	SDHA,ACOX1,HK2,ENSACAG00000024726
GO:0036494	0.01182251	1	2	positive regulation of translation initiation in response to endoplasmic reticulum stress	ENSACAG00000017545
GO:0035795	0.012956846	1	2	negative regulation of mitochondrial membrane permeability	HK2
GO:0050821	0.013042458	3	96	protein stabilization	IPO9,FLOT2,CRTAP
GO:1902412	0.013121126	1	2	regulation of mitotic cytokinesis	ANKRD53
GO:0044860	0.013218964	1	2	protein localization to plasma membrane raft	FLOT2
GO:0045661	0.01391857	2	37	regulation of myoblast differentiation	SMYD1,FLOT2
GO:0042991	0.014766006	1	2	transcription factor import into nucleus	IPO9
GO:0097006	0.015174572	1	3	regulation of plasma lipoprotein particle levels	LPCAT3
GO:0043420	0.015584362	1	3	anthranilate metabolic process	KMO
GO:0006068	0.015943122	1	3	ethanol catabolic process	ENSACAG00000008728
GO:0072656	0.019165467	1	4	maintenance of protein location in mitochondrion	HK2
GO:0019418	0.019229227	1	4	sulfide oxidation	ENSACAG00000003722
GO:0070221	0.019229227	1	4	sulfide oxidation, using sulfide:quinone oxidoreductase	ENSACAG00000003722
GO:0006105	0.019634254	1	3	succinate metabolic process	SDHA
GO:0034354	0.019830362	1	4	'de novo' NAD biosynthetic process from tryptophan	KMO
GO:0060689	0.020021925	1	3	cell differentiation involved in salivary gland development	CTNND1
GO:0002252	0.020846947	5	322	immune effector process	CFP,STXBP2,TUSC2,ENSACAG00000011208,ENSACAG00000006626
GO:0005981	0.020850007	1	5	regulation of glycogen catabolic process	ENSACAG00000024726
GO:0019805	0.023318553	1	4	quinolinate biosynthetic process	KMO
GO:0060327	0.025015595	1	4	cytoplasmic actin-based contraction involved in cell motility	VILL
GO:1902992	0.025494198	1	4	negative regulation of amyloid precursor protein catabolic process	FLOT2
GO:0036500	0.025713156	1	4	ATF6-mediated unfolded protein response	ATF6B

GO:0001779	0.025945401	1	5	natural killer cell differentiation	TUSC2
GO:0007021	0.026938925	1	8	tubulin complex assembly	TBCD
GO:0048278	0.027099102	2	54	vesicle docking	CEP83,STXBP2
GO:0015712	0.027792024	1	5	hexose phosphate transport	SLC37A2
GO:0015760	0.027792024	1	5	glucose-6-phosphate transport	SLC37A2
GO:0010668	0.027828091	1	5	ectodermal cell differentiation	VPS52
GO:0007023	0.028512214	1	6	post-chaperonin tubulin folding pathway	TBCD
GO:0009617	0.029231918	3	146	response to bacterium	TUSC2,ENSACAG00000006626,VILL
GO:0008616	0.029611281	1	7	queuosine biosynthetic process	TXNDC9
GO:0046116	0.029611281	1	7	queuosine metabolic process	TXNDC9
GO:0035435	0.029691078	1	5	phosphate ion transmembrane transport	SLC37A2
GO:0051660	0.0302713	1	5	establishment of centrosome localization	CEP83
GO:0043124	0.030639563	2	47	negative regulation of I-kappaB kinase/NF-kappaB signaling	NLRX1,ENSACAG00000025660
GO:0070813	0.030736899	1	6	hydrogen sulfide metabolic process	ENSACAG00000003722
GO:0033540	0.031318546	1	5	fatty acid beta-oxidation using acyl-CoA oxidase	ACOX1
GO:0072102	0.031577265	1	6	glomerulus morphogenesis	CTNND1
GO:1900086	0.032262373	1	6	positive regulation of peptidyl-tyrosine autophosphorylation	CTNND1
GO:0006575	0.033112859	3	143	cellular modified amino acid metabolic process	KMO,LPCAT3,CRTAP
GO:0098535	0.033344676	1	5	de novo centriole assembly	CCDC78
GO:0040015	0.033959717	1	7	negative regulation of multicellular organism growth	LGMN
GO:1903044	0.03484943	1	6	protein localization to membrane raft	FLOT2
GO:0046874	0.03613453	1	7	quinolinate metabolic process	KMO
GO:0038180	0.036564244	1	7	nerve growth factor signaling pathway	RAPGEF1
GO:0001765	0.03753899	1	10	membrane raft assembly	FLOT2
GO:0022406	0.038472967	2	65	membrane docking	CEP83,STXBP2
GO:0000002	0.038794642	1	8	mitochondrial genome maintenance	MGME1
GO:0032486	0.03977477	1	9	Rap protein signal transduction	RAPGEF1
GO:0070417	0.039831493	1	7	cellular response to cold	ENSACAG00000017545
GO:0010996	0.041841853	1	7	response to auditory stimulus	XPC

GO:0044550	0.042017856	1	8	secondary metabolite biosynthetic process	KMO
GO:1990440	0.042075718	1	9	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	ATF6B
GO:0001738	0.042495455	1	6	morphogenesis of a polarized epithelium	CTNND1
GO:0010224	0.043569017	1	9	response to UV-B	XPC
GO:0009566	0.047506821	2	61	fertilization	SPAG1,TDRKH
GO:0036230	0.047925562	1	8	granulocyte activation	STXBP2
GO:0043574	0.049703483	1	10	peroxisomal transport	LONP2

Table S12. PSGs on identified branch 2 of frog.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000001895	ENSACAG00000001926	ENSACAT00000001941	TAGLN
ENSACAP00000006222	ENSACAG00000006266	ENSACAT00000006360	EPHA2
ENSACAP00000019091	ENSACAG00000022477	ENSACAT00000023955	MYPOP
ENSACAP00000009478	ENSACAG00000009584	ENSACAT00000009675	AFG3L2
ENSACAP00000009546	ENSACAG00000009706	ENSACAT00000009743	GAS8
ENSACAP00000002283	ENSACAG00000002280	ENSACAT00000002343	TRIT1
ENSACAP00000016408	ENSACAG00000016668	ENSACAT00000016733	HTATIP2
ENSACAP00000011621	ENSACAG00000011877	ENSACAT00000011861	ZFAND6
ENSACAP00000023366	ENSACAG00000028384	ENSACAT00000030786	CAPSL
ENSACAP00000011080	ENSACAG00000011294	ENSACAT00000011309	STRBP
ENSACAP00000010531	ENSACAG00000010711	ENSACAT00000010748	CHMP2A
ENSACAP00000009390	ENSACAG00000009594	ENSACAT00000009585	
ENSACAP00000008105	ENSACAG00000008210	ENSACAT00000008277	WDR3
ENSACAP00000001055	ENSACAG00000000623	ENSACAT00000001084	CPT1B
ENSACAP00000010465	ENSACAG00000010661	ENSACAT00000010681	SIRT6
ENSACAP00000017554	ENSACAG00000017828	ENSACAT00000017900	HPN
ENSACAP00000017624	ENSACAG00000017900	ENSACAT00000017970	BMP4
ENSACAP00000007838	ENSACAG00000007923	ENSACAT00000008004	RXRA

ENSACAP00000003421	ENSACAG00000003518	ENSACAT00000003505	SNX15
ENSACAP00000001781	ENSACAG00000001869	ENSACAT00000001825	
ENSACAP00000012408	ENSACAG00000012591	ENSACAT00000012661	NFYC
ENSACAP00000008175	ENSACAG00000008301	ENSACAT00000008350	PARP2
ENSACAP00000001874	ENSACAG00000001886	ENSACAT00000001920	KANSL3
ENSACAP00000012140	ENSACAG00000012220	ENSACAT00000012385	COL16A1
ENSACAP00000001322	ENSACAG00000001073	ENSACAT00000001355	HYDIN
ENSACAP00000013010	ENSACAG00000013244	ENSACAT00000013269	AIMP2
ENSACAP00000016793	ENSACAG00000017061	ENSACAT00000017124	SP3
ENSACAP00000003596	ENSACAG00000003599	ENSACAT00000003684	PPP4R1
ENSACAP00000006502	ENSACAG00000006445	ENSACAT00000006647	
ENSACAP00000008790	ENSACAG00000008878	ENSACAT00000008978	TAF2
ENSACAP00000000442	ENSACAG00000000515	ENSACAT00000000459	POLRMT
ENSACAP00000015218	ENSACAG00000015364	ENSACAT00000015526	
ENSACAP00000003146	ENSACAG00000003229	ENSACAT00000003227	CFAP45
ENSACAP00000017421	ENSACAG00000017693	ENSACAT00000017763	RIPK1
ENSACAP00000011853	ENSACAG00000012105	ENSACAT00000012097	FAM180A
ENSACAP00000012057	ENSACAG00000012181	ENSACAT00000012302	COL4A6
ENSACAP00000007762	ENSACAG00000007908	ENSACAT00000007928	SENP5
ENSACAP00000005764	ENSACAG00000005840	ENSACAT00000005891	PBX1
ENSACAP00000010921	ENSACAG00000011074	ENSACAT00000011149	EIF3H
ENSACAP00000006379	ENSACAG00000006527	ENSACAT00000006522	PTGFR
ENSACAP00000004258	ENSACAG00000004362	ENSACAT00000004357	PPIF
ENSACAP00000005635	ENSACAG00000005745	ENSACAT00000005758	SCN1B
ENSACAP00000019308	ENSACAG00000009983	ENSACAT00000023910	ABRA
ENSACAP00000015939	ENSACAG00000015936	ENSACAT00000016257	VPS13C
ENSACAP00000022522	ENSACAG00000028662	ENSACAT00000029939	COX19
ENSACAP00000011871	ENSACAG00000012018	ENSACAT00000012115	CA12
ENSACAP00000012414	ENSACAG00000012657	ENSACAT00000012667	
ENSACAP00000007369	ENSACAG00000007538	ENSACAT00000007525	CYHR1

ENSACAP00000004467	ENSACAG00000004556	ENSACAT00000004568	EEF1A1
ENSACAP00000012511	ENSACAG00000012620	ENSACAT00000012767	PLAT
ENSACAP00000012725	ENSACAG00000012939	ENSACAT00000012981	VDAC3
ENSACAP00000014487	ENSACAG00000014561	ENSACAT00000014782	
ENSACAP00000006923	ENSACAG00000006920	ENSACAT00000007074	NEO1
ENSACAP00000015231	ENSACAG00000015062	ENSACAT00000015539	COL3A1
ENSACAP00000000009	ENSACAG00000000010	ENSACAT00000000010	C9orf114
ENSACAP00000012411	ENSACAG00000012671	ENSACAT00000012664	BCAS1
ENSACAP00000008943	ENSACAG00000009143	ENSACAT00000009134	MRPL20
ENSACAP00000019740	ENSACAG00000004115	ENSACAT00000023628	C8orf37
ENSACAP00000011731	ENSACAG00000011986	ENSACAT00000011974	
ENSACAP00000010338	ENSACAG00000010516	ENSACAT00000010551	CALB1
ENSACAP00000014660	ENSACAG00000014939	ENSACAT00000014957	C1QA
ENSACAP00000003548	ENSACAG00000003615	ENSACAT00000003636	RNF126
ENSACAP00000008887	ENSACAG00000008884	ENSACAT00000009078	LIPA
ENSACAP00000004656	ENSACAG00000004703	ENSACAT00000004762	
ENSACAP00000004437	ENSACAG00000004560	ENSACAT00000004537	IQCD
ENSACAP00000004932	ENSACAG00000005037	ENSACAT00000005045	LHX5
ENSACAP00000013115	ENSACAG00000013361	ENSACAT00000013375	PKIA
ENSACAP00000006179	ENSACAG00000006290	ENSACAT00000006316	SCLT1
ENSACAP00000013319	ENSACAG00000013470	ENSACAT00000013589	TNPO3
ENSACAP00000001047	ENSACAG00000001050	ENSACAT00000001075	CTCF
ENSACAP00000016123	ENSACAG00000016403	ENSACAT00000016444	CSPP1
ENSACAP00000009938	ENSACAG00000010008	ENSACAT00000010142	PPP3CB
ENSACAP00000007427	ENSACAG00000007566	ENSACAT00000007584	NUP93
ENSACAP00000008830	ENSACAG00000008935	ENSACAT00000009020	VCL
ENSACAP00000017354	ENSACAG00000017628	ENSACAT00000017695	DNAJC8
ENSACAP00000006308	ENSACAG00000006461	ENSACAT00000006448	NUFIP1
ENSACAP00000006334	ENSACAG00000006468	ENSACAT00000006476	GPALPP1
ENSACAP00000015300	ENSACAG00000015568	ENSACAT00000015612	C7orf26

ENSACAP00000019515	ENSACAG00000024776	ENSACAT00000026278	PSMB9
ENSACAP00000003286	ENSACAG00000003355	ENSACAT00000003369	ZFYVE19
ENSACAP00000016437	ENSACAG00000016709	ENSACAT00000016762	GPATCH3
ENSACAP00000007083	ENSACAG00000007141	ENSACAT00000007236	WDR36
ENSACAP00000006621	ENSACAG00000006760	ENSACAT00000006767	HHATL
ENSACAP00000006629	ENSACAG00000006787	ENSACAT00000006775	CCDC13
ENSACAP00000004628	ENSACAG00000004762	ENSACAT00000004734	SSUH2
ENSACAP00000003647	ENSACAG00000003431	ENSACAT00000003736	TNC
ENSACAP00000002954	ENSACAG00000002779	ENSACAT00000003031	CDH1
ENSACAP00000013656	ENSACAG00000013912	ENSACAT00000013937	CCDC84
ENSACAP00000013311	ENSACAG00000013530	ENSACAT00000013580	
ENSACAP00000003727	ENSACAG00000003828	ENSACAT00000003818	CBLN2
ENSACAP00000001457	ENSACAG00000001432	ENSACAT00000001493	SCGN
ENSACAP00000006083	ENSACAG00000006142	ENSACAT00000006219	PITPNB
ENSACAP00000006513	ENSACAG00000006580	ENSACAT00000006658	NCAPD2
ENSACAP00000011565	ENSACAG00000011593	ENSACAT00000011805	RPN2
ENSACAP00000003909	ENSACAG00000004037	ENSACAT00000004001	LRFN3
ENSACAP00000004136	ENSACAG00000004137	ENSACAT00000004235	STARD13
ENSACAP00000007591	ENSACAG00000007760	ENSACAT00000007752	FGFBP3
ENSACAP00000004162	ENSACAG00000004280	ENSACAT00000004261	KIN
ENSACAP00000007502	ENSACAG00000007562	ENSACAT00000007662	ACVR1
ENSACAP00000002413	ENSACAG00000002495	ENSACAT00000002475	HINFP
ENSACAP00000005274	ENSACAG00000005411	ENSACAT00000005391	
ENSACAP00000014977	ENSACAG00000015222	ENSACAT00000015280	FKBP15
ENSACAP00000022968	ENSACAG00000029620	ENSACAT00000030387	PTN
ENSACAP00000014797	ENSACAG00000015073	ENSACAT00000015098	CD79A
ENSACAP00000005022	ENSACAG00000005154	ENSACAT00000005135	CCDC177
ENSACAP00000005833	ENSACAG00000005770	ENSACAT00000005962	STXBP3
ENSACAP00000000378	ENSACAG00000000366	ENSACAT00000000393	TNFAIP2
ENSACAP00000005552	ENSACAG00000005665	ENSACAT00000005674	FAM102B

ENSACAP00000017480	ENSACAG00000017750	ENSACAT00000017825	TKFC
ENSACAP00000017040	ENSACAG00000017304	ENSACAT00000017375	ETNK1
ENSACAP00000016496	ENSACAG00000016777	ENSACAT00000016822	
ENSACAP00000011794	ENSACAG00000012043	ENSACAT00000012038	EFCAB5
ENSACAP00000012746	ENSACAG00000012993	ENSACAT00000013002	METTL11B
ENSACAP00000004582	ENSACAG00000004623	ENSACAT00000004688	ATP13A1
ENSACAP00000000034	ENSACAG00000000035	ENSACAT00000000035	SLC6A13
ENSACAP00000012912	ENSACAG00000013148	ENSACAT00000013170	SRA1
ENSACAP00000009392	ENSACAG00000009603	ENSACAT00000009587	CHST2
ENSACAP00000011214	ENSACAG00000011373	ENSACAT00000011450	AGK
ENSACAP00000009221	ENSACAG00000009397	ENSACAT00000009414	FKBP9
ENSACAP00000019934	ENSACAG00000025074	ENSACAT00000025296	TMEM263
ENSACAP00000017267	ENSACAG00000017546	ENSACAT00000017607	C7orf25
ENSACAP00000022783	ENSACAG00000029652	ENSACAT00000030201	PIGX
ENSACAP00000017850	ENSACAG00000021120	ENSACAT00000021222	LRRC8D
ENSACAP00000015971	ENSACAG00000016250	ENSACAT00000016290	PVALB
ENSACAP00000001757	ENSACAG00000001800	ENSACAT00000001798	
ENSACAP00000020588	ENSACAG00000008144	ENSACAT00000026899	EFCAB7
ENSACAP00000007417	ENSACAG00000007573	ENSACAT00000007574	ATF4
ENSACAP00000008386	ENSACAG00000008484	ENSACAT00000008567	SMYD1
ENSACAP00000002239	ENSACAG00000002353	ENSACAT00000002299	
ENSACAP00000003808	ENSACAG00000003916	ENSACAT00000003900	NDUFA6
ENSACAP00000012975	ENSACAG00000013225	ENSACAT00000013234	IKBIP
ENSACAP00000005058	ENSACAG00000005165	ENSACAT00000005171	CFAP43
ENSACAP00000014179	ENSACAG00000014452	ENSACAT00000014470	LIN7A
ENSACAP00000016356	ENSACAG00000016584	ENSACAT00000016680	NSF
ENSACAP00000003040	ENSACAG00000003026	ENSACAT00000003118	MED24
ENSACAP00000001315	ENSACAG00000000802	ENSACAT00000001348	USP15
ENSACAP00000001618	ENSACAG00000001636	ENSACAT00000001657	RPAP3
ENSACAP00000016350	ENSACAG00000016606	ENSACAT00000016674	STK38

ENSACAP00000005181	ENSACAG00000005084	ENSACAT00000005298	COL1A1
ENSACAP00000011662	ENSACAG00000011895	ENSACAT00000011902	THAP7
ENSACAP00000000349	ENSACAG00000000410	ENSACAT00000000363	SOD3
ENSACAP00000001158	ENSACAG00000001047	ENSACAT00000001191	ADGRA3
ENSACAP00000005126	ENSACAG00000005107	ENSACAT00000005242	KDM5B
ENSACAP00000010489	ENSACAG00000010668	ENSACAT00000010705	
ENSACAP00000015442	ENSACAG00000015718	ENSACAT00000015756	PHF21B
ENSACAP00000016767	ENSACAG00000017034	ENSACAT00000017098	
ENSACAP00000016151	ENSACAG00000016342	ENSACAT00000016472	SEMA3D
ENSACAP00000014191	ENSACAG00000014415	ENSACAT00000014482	ATP6AP2
ENSACAP00000006211	ENSACAG00000006358	ENSACAT00000006349	FAM185A
ENSACAP00000005291	ENSACAG00000005213	ENSACAT00000005408	COL9A3
ENSACAP00000014901	ENSACAG00000015121	ENSACAT00000015204	SLC26A4
ENSACAP00000013595	ENSACAG00000013842	ENSACAT00000013875	BCL9
ENSACAP00000005737	ENSACAG00000005859	ENSACAT00000005862	SPATA4
ENSACAP00000011523	ENSACAG00000011687	ENSACAT00000011763	ABI3BP
ENSACAP00000014676	ENSACAG00000014952	ENSACAT00000014973	GAP43
ENSACAP00000010797	ENSACAG00000010946	ENSACAT00000011020	CWF19L2
ENSACAP00000011904	ENSACAG00000012117	ENSACAT00000012148	NDST4
ENSACAP00000001885	ENSACAG00000001917	ENSACAT00000001931	SYTL2
ENSACAP00000021261	ENSACAG00000027099	ENSACAT00000022125	CCDC89
ENSACAP00000013273	ENSACAG00000013389	ENSACAT00000013540	ADAMTS3
ENSACAP00000010681	ENSACAG00000010867	ENSACAT00000010902	PAIP1
ENSACAP00000008759	ENSACAG00000008952	ENSACAT00000008947	FAM169A
ENSACAP00000009090	ENSACAG00000009297	ENSACAT00000009283	ENC1
ENSACAP00000017518	ENSACAG00000017794	ENSACAT00000017863	ZDHHC21
ENSACAP00000004589	ENSACAG00000004710	ENSACAT00000004695	
ENSACAP00000005729	ENSACAG00000005869	ENSACAT00000005854	CCDC115
ENSACAP00000006472	ENSACAG00000006406	ENSACAT00000006617	GRM6
ENSACAP00000017196	ENSACAG00000017454	ENSACAT00000017533	SEL1L

ENSACAP00000015658	ENSACAG00000015894	ENSACAT00000015973	PNN
ENSACAP00000017274	ENSACAG00000017477	ENSACAT00000017614	
ENSACAP00000015816	ENSACAG00000016077	ENSACAT00000016133	
ENSACAP00000008189	ENSACAG00000008280	ENSACAT00000008365	SRPK3
ENSACAP00000015556	ENSACAG00000015816	ENSACAT00000015870	TTBK2
ENSACAP00000011215	ENSACAG00000011417	ENSACAT00000011451	PDZD4
ENSACAP00000009344	ENSACAG00000009404	ENSACAT00000009539	SMC1A
ENSACAP00000012329	ENSACAG00000012437	ENSACAT00000012582	G6PD
ENSACAP00000021152	ENSACAG00000027094	ENSACAT00000025138	APOF
ENSACAP00000000050	ENSACAG00000000051	ENSACAT00000000051	USH1C
ENSACAP00000014885	ENSACAG00000015119	ENSACAT00000015187	NPLOC4
ENSACAP00000002650	ENSACAG00000002763	ENSACAT00000002717	TSSC4
ENSACAP00000016789	ENSACAG00000017062	ENSACAT00000017120	
ENSACAP00000014718	ENSACAG00000014995	ENSACAT00000015019	RASSF7
ENSACAP00000014526	ENSACAG00000014764	ENSACAT00000014821	CHKA
ENSACAP00000017197	ENSACAG00000017472	ENSACAT00000017534	IFITM5
ENSACAP00000001930	ENSACAG00000001798	ENSACAT00000001976	CCDC93
ENSACAP00000001501	ENSACAG00000001486	ENSACAT00000001537	TMBIM1
ENSACAP00000008138	ENSACAG00000008270	ENSACAT00000008310	SPHK1
ENSACAP00000003843	ENSACAG00000003940	ENSACAT00000003935	GSTP1
ENSACAP00000009803	ENSACAG00000009982	ENSACAT00000010003	
ENSACAP00000008060	ENSACAG00000008231	ENSACAT00000008232	CARNS1
ENSACAP00000020914	ENSACAG00000013938	ENSACAT00000023342	SPEG
ENSACAP00000001445	ENSACAG00000001396	ENSACAT00000001480	ABCC3
ENSACAP00000012758	ENSACAG00000012986	ENSACAT00000013014	ZFAND2B
ENSACAP00000012577	ENSACAG00000012718	ENSACAT00000012833	CYP27A1
ENSACAP00000016779	ENSACAG00000017036	ENSACAT00000017110	NIF3L1
ENSACAP00000010279	ENSACAG00000010432	ENSACAT00000010491	
ENSACAP00000009915	ENSACAG00000010121	ENSACAT00000010118	CCDC69
ENSACAP00000004825	ENSACAG00000004851	ENSACAT00000004933	PTK7

ENSACAP00000013732	ENSACAG00000013981	ENSACAT00000014013	RCBTB1
ENSACAP00000008288	ENSACAG00000008460	ENSACAT00000008467	MON1A
ENSACAP00000022226	ENSACAG00000028931	ENSACAT00000029643	HEMK1
ENSACAP00000006616	ENSACAG00000006743	ENSACAT00000006762	ALAS1
ENSACAP00000005783	ENSACAG00000005867	ENSACAT00000005911	TRAPPC12
ENSACAP00000013711	ENSACAG00000013979	ENSACAT00000013992	
ENSACAP00000011325	ENSACAG00000011571	ENSACAT00000011563	MGAT1
ENSACAP00000004644	ENSACAG00000004653	ENSACAT00000004750	EZR
ENSACAP00000011800	ENSACAG00000011746	ENSACAT00000012044	SKIV2L
ENSACAP00000001376	ENSACAG00000001463	ENSACAT00000001409	GGPS1
ENSACAP00000001426	ENSACAG00000001523	ENSACAT00000001461	PGBD5
ENSACAP00000008168	ENSACAG00000008250	ENSACAT00000008343	HEATR5B
ENSACAP00000002125	ENSACAG00000002181	ENSACAT00000002184	TAF1A
ENSACAP00000011533	ENSACAG00000011654	ENSACAT00000011773	RTN4

Table S13. GO terms associated with PSGs identified on frog branch 2.

category	pvalue	numDE InCat	Num InCat	term	GeneNames
GO:2000347	0.001288613	2	5	positive regulation of hepatocyte proliferation	PTN,HPN
GO:0032532	0.001910418	2	5	regulation of microvillus length	USH1C,EZR
GO:0032536	0.003802747	2	7	regulation of cell projection size	USH1C,EZR
GO:0001655	0.004739833	2	10	urogenital system development	PBX1,ACVR1
GO:0022406	0.004744015	4	65	membrane docking	STXBP3,NSF,SYTL2,EZR
GO:0051292	0.006462651	2	9	nuclear pore complex assembly	RTN4,NUP93
GO:0035025	0.00701328	2	10	positive regulation of Rho protein signal transduction	ABRA,COL3A1
GO:0030970	0.007135389	2	12	retrograde protein transport, ER to cytosol	SEL1L,NPLOC4
GO:0019682	0.007141923	2	12	glyceraldehyde-3-phosphate metabolic process	TKFC,G6PD
GO:0003247	0.007457984	1	1	post-embryonic cardiac muscle cell growth involved in heart morphogenesis	SIRT6

GO:0030574	0.007613466	3	32	collagen catabolic process	ADAMTS3,COL4A6,COL3A1
GO:1904389	0.007672887	1	1	rod bipolar cell differentiation	PTN
GO:1904391	0.007672887	1	1	response to ciliary neurotrophic factor	PTN
GO:1904397	0.007672887	1	1	negative regulation of neuromuscular junction development	PTN
GO:0010849	0.008076412	1	1	regulation of proton-transporting ATPase activity, rotational mechanism	PPIF
GO:0021966	0.008321442	1	1	corticospinal neuron axon guidance	SCN1B
GO:0006646	0.008335098	2	13	phosphatidylethanolamine biosynthetic process	ETNK1,CHKA
GO:0010939	0.009050737	2	15	regulation of necrotic cell death	RIPK1,PPIF
GO:0072027	0.009067509	1	1	connecting tubule development	CALB1
GO:0072286	0.009067509	1	1	metanephric connecting tubule development	CALB1
GO:0071629	0.009173001	1	1	cytoplasm-associated proteasomal ubiquitin-dependent protein catabolic process	RNF126
GO:0006480	0.009584684	1	1	N-terminal protein amino acid methylation	METTL11B
GO:0033385	0.009718092	1	1	geranylgeranyl diphosphate metabolic process	GGPS1
GO:0033386	0.009718092	1	1	geranylgeranyl diphosphate biosynthetic process	GGPS1
GO:1902044	0.010026839	1	1	regulation of Fas signaling pathway	TMBIM1
GO:0031344	0.010985794	12	461	regulation of cell projection organization	PTN,EPHA2,SEMA3D,ENC1,USH1C,EZR,RTN4,ENSACAG00000015364,SCN1B,EEF1A1,VDAC3,WDR36
GO:0046931	0.011323945	2	12	pore complex assembly	RTN4,NUP93
GO:0046337	0.011579444	2	15	phosphatidylethanolamine metabolic process	ETNK1,CHKA
GO:0006049	0.011794823	1	1	UDP-N-acetylglucosamine catabolic process	MGAT1
GO:0009227	0.011794823	1	1	nucleotide-sugar catabolic process	MGAT1
GO:0006580	0.01180568	1	1	ethanolamine metabolic process	CHKA
GO:1904681	0.01180568	1	1	response to 3-methylcholanthrene	CHKA
GO:1904526	0.012133391	1	1	regulation of microtubule binding	GAS8
GO:0072697	0.01296464	1	1	protein localization to cell cortex	EZR
GO:0061624	0.01324911	1	1	fructose catabolic process to hydroxyacetone phosphate and glyceraldehyde-3-phosphate	TKFC

GO:0070926	0.01359841	1	1	regulation of ATP:ADP antiporter activity	RIPK1
GO:1905206	0.01359841	1	1	positive regulation of hydrogen peroxide-induced cell death	RIPK1
GO:0035048	0.014051739	1	1	splicing factor protein import into nucleus	TNPO3
GO:1902426	0.014060349	1	1	negative regulation of mitotic spindle assembly checkpoint	TRAPPC12
GO:0030046	0.014353655	1	1	parallel actin filament bundle assembly	USH1C
GO:0007507	0.014595575	6	162	heart development	PTN,SMYD1,RXRA,COL3A1,PPP3CB,ACVR1
GO:0035499	0.014674145	1	1	carnosine biosynthetic process	CARNS1
GO:0006616	0.014783691	1	2	SRP-dependent cotranslational protein targeting to membrane, translocation	ZFAND2B
GO:0044236	0.015008189	3	41	multicellular organism metabolic process	ADAMTS3,COL4A6,COL3A1
GO:0000245	0.01520417	2	17	spliceosomal complex assembly	ENSACAG00000017034,SRPK3
GO:0014908	0.016179183	1	1	myotube differentiation involved in skeletal muscle regeneration	BCL9
GO:1905090	0.016357209	1	1	negative regulation of parkin-mediated mitophagy in response to mitochondrial depolarization	VPS13C
GO:0042692	0.016585591	4	84	muscle cell differentiation	BCL9,SPEG,RXRA,HINFP
GO:0006471	0.018398717	2	19	protein ADP-ribosylation	SIRT6,PARP2
GO:0048278	0.018622884	3	54	vesicle docking	STXBP3,NSF,SYTL2
GO:0035338	0.018936417	2	19	long-chain fatty-acyl-CoA biosynthetic process	AGK,ENSACAG00000016077
GO:0034769	0.019947235	1	2	basement membrane disassembly	HPN
GO:0003241	0.020041691	1	2	growth involved in heart morphogenesis	SIRT6
GO:0045041	0.020313563	1	2	protein import into mitochondrial intermembrane space	AFG3L2
GO:0021937	0.020497908	1	2	cerebellar Purkinje cell-granule cell precursor cell signaling involved in regulation of granule cell precursor cell proliferation	LHX5
GO:0061245	0.021493638	2	22	establishment or maintenance of bipolar cell polarity	LIN7A,EZR
GO:0048729	0.021593983	8	292	tissue morphogenesis	EPHA2,PTK7,BMP4,RXRA,PBX1,COL3A1,VCL,STARD13
GO:0034629	0.022654156	2	22	cellular protein complex localization	TNFAIP2,EZR
GO:1905342	0.022772293	1	2	positive regulation of protein localization to kinetochore	TRAPPC12

GO:0071729	0.023071259	1	2	beak morphogenesis	BMP4
GO:2000870	0.023071259	1	2	regulation of progesterone secretion	BMP4
GO:0097195	0.023088262	1	2	pilomotor reflex	HPN
GO:0006447	0.023567798	1	2	regulation of translational initiation by iron	RXRA
GO:0045994	0.023567798	1	2	positive regulation of translational initiation by iron	RXRA
GO:0060978	0.023567798	1	2	angiogenesis involved in coronary vascular morphogenesis	RXRA
GO:0033383	0.023587067	1	2	geranyl diphosphate metabolic process	GGPS1
GO:0033384	0.023587067	1	2	geranyl diphosphate biosynthetic process	GGPS1
GO:0045337	0.023587067	1	2	farnesyl diphosphate biosynthetic process	GGPS1
GO:0045338	0.023587067	1	2	farnesyl diphosphate metabolic process	GGPS1
GO:1901522	0.023757371	2	19	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	ATF4,RXRA
GO:0006001	0.024132656	1	2	fructose catabolic process	TKFC
GO:0006997	0.024496454	3	49	nucleus organization	SRPK3,RTN4,NUP93
GO:1902966	0.02570851	1	2	positive regulation of protein localization to early endosome	EZR
GO:1902896	0.026031429	1	2	terminal web assembly	EZR
GO:0070265	0.026431056	2	22	necrotic cell death	RIPK1,PPIF
GO:0035063	0.027040159	1	2	nuclear speck organization	SRPK3
GO:0035616	0.028483367	1	2	histone H2B conserved C-terminal lysine deubiquitination	USP15
GO:0001915	0.028510054	1	2	negative regulation of T cell mediated cytotoxicity	PPP3CB
GO:0010573	0.028976926	1	2	vascular endothelial growth factor production	ADAMTS3
GO:2000609	0.029525213	1	3	regulation of thyroid hormone generation	HPN
GO:0031503	0.029556648	2	25	protein complex localization	TNFAIP2,EZR
GO:1904158	0.029677019	1	2	axonemal central apparatus assembly	HYDIN
GO:0060414	0.029781475	1	2	aorta smooth muscle tissue morphogenesis	COL3A1
GO:0097498	0.029903877	1	2	endothelial tube lumen extension	STARD13
GO:0048733	0.030355236	1	3	sebaceous gland development	ZDHHC21
GO:0071799	0.030584077	1	3	cellular response to prostaglandin D stimulus	PTGFR
GO:1903361	0.030597537	1	4	protein localization to basolateral plasma membrane	LIN7A
GO:0021553	0.030644599	1	2	olfactory nerve development	RTN4

GO:0097343	0.032556731	1	3	ripoptosome assembly	RIPK1
GO:0048392	0.033334635	1	3	intermediate mesodermal cell differentiation	BMP4
GO:0072198	0.033334635	1	3	mesenchymal cell proliferation involved in ureter development	BMP4
GO:1900748	0.033992064	1	3	positive regulation of vascular endothelial growth factor signaling pathway	ADAMTS3
GO:0009951	0.03434062	1	3	polarity specification of dorsal/ventral axis	BMP4
GO:2000504	0.03444433	1	3	positive regulation of blood vessel remodeling	TMBIM1
GO:1990737	0.035227766	1	3	response to manganese-induced endoplasmic reticulum stress	ATF4
GO:2000290	0.035427647	1	3	regulation of myotome development	BMP4
GO:0060528	0.035454034	1	3	secretory columnal luminar epithelial cell differentiation involved in prostate glandular acinus development	RXRA
GO:1904373	0.035490895	1	3	response to kainic acid	PTN
GO:0035498	0.036476279	1	3	carnosine metabolic process	CARNS1
GO:0034334	0.03664346	1	3	adherens junction maintenance	RASSF7
GO:0060221	0.036954273	1	4	retinal rod cell differentiation	PTN
GO:0090234	0.036965269	1	3	regulation of kinetochore assembly	TRAPPC12
GO:0001951	0.037289698	1	3	intestinal D-glucose absorption	EZR
GO:0006887	0.038172269	5	159	exocytosis	STXBP3,TNFAIP2,LIN7A,SYTL2,PPP3CB
GO:0000959	0.039754206	2	27	mitochondrial RNA metabolic process	POLRMT,TRIT1
GO:0006284	0.039875692	2	28	base-excision repair	SIRT6,PARP2
GO:0043009	0.039971864	5	154	chordate embryonic development	IFITM5,MGAT1,RXRA,ACVR1,HINFP
GO:0097435	0.04094732	1	4	fibril organization	RIPK1
GO:1990000	0.04094732	1	4	amyloid fibril formation	RIPK1
GO:0031987	0.040957699	1	4	locomotion involved in locomotory behavior	PPP3CB
GO:0015722	0.041099232	1	3	canalicular bile acid transport	ABCC3
GO:0090324	0.042076181	1	5	negative regulation of oxidative phosphorylation	PPIF
GO:0010032	0.042282515	1	3	meiotic chromosome condensation	NCAPD2
GO:0065002	0.042653104	2	34	intracellular protein transmembrane transport	ZFAND2B,AFG3L2
GO:0071806	0.042653104	2	34	protein transmembrane transport	ZFAND2B,AFG3L2

GO:0060438	0.042693533	1	4	trachea development	HYDIN
GO:0018231	0.042994475	1	5	peptidyl-S-diacylglycerol-L-cysteine biosynthetic process from peptidyl-cysteine	ZDHHC21
GO:0043312	0.043750265	1	4	neutrophil degranulation	STXBP3
GO:0010737	0.044532504	1	4	protein kinase A signaling	EZR
GO:0070257	0.046599177	1	4	positive regulation of mucus secretion	SYTL2
GO:1904106	0.047377358	1	4	protein localization to microvillus	USH1C
GO:0061032	0.047450959	1	4	visceral serous pericardium development	RXRA
GO:0015701	0.047494055	2	28	bicarbonate transport	SLC26A4,CA12
GO:0050957	0.047559414	1	4	equilibrioception	USH1C
GO:0019722	0.047859286	3	68	calcium-mediated signaling	SPHK1,PTGFR,PPP3CB
GO:0071787	0.048380319	1	4	endoplasmic reticulum tubular network assembly	RTN4
GO:0007179	0.048802168	3	67	transforming growth factor beta receptor signaling pathway	USP15,COL3A1,ACVR1
GO:0045651	0.049207144	1	5	positive regulation of macrophage differentiation	RIPK1
GO:0035337	0.049327441	2	32	fatty-acyl-CoA metabolic process	AGK,ENSACAG00000016077
GO:0010756	0.049530895	1	5	positive regulation of plasminogen activation	HPN
GO:0048146	0.049798573	2	33	positive regulation of fibroblast proliferation	SPHK1,SIRT6

Table S14. PSGs identified on branch 6 of lizard.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000004915	ENSACAG00000004759	ENSACAT00000005028	
ENSACAP00000015677	ENSACAG00000015962	ENSACAT00000015992	WDR73
ENSACAP00000011004	ENSACAG00000011239	ENSACAT00000011232	PRSS16
ENSACAP00000006471	ENSACAG00000006602	ENSACAT00000006616	ZNF282
ENSACAP00000012717	ENSACAG00000012949	ENSACAT00000012973	RAC1
ENSACAP00000022809	ENSACAG00000029432	ENSACAT00000030227	
ENSACAP00000003146	ENSACAG00000003229	ENSACAT00000003227	CFAP45
ENSACAP00000007762	ENSACAG00000007908	ENSACAT00000007928	SENP5
ENSACAP00000003356	ENSACAG00000003438	ENSACAT00000003439	

ENSACAP00000013712	ENSACAG00000013937	ENSACAT00000013993	
ENSACAP00000013105	ENSACAG00000013315	ENSACAT00000013365	
ENSACAP00000002838	ENSACAG00000002945	ENSACAT00000002908	
ENSACAP00000017711	ENSACAG00000017988	ENSACAT00000018059	TGS1
ENSACAP00000005090	ENSACAG00000005142	ENSACAT00000005205	VIM
ENSACAP00000019497	ENSACAG00000026822	ENSACAT00000025669	
ENSACAP00000003491	ENSACAG00000003566	ENSACAT00000003577	ANLN
ENSACAP00000016018	ENSACAG00000016306	ENSACAT00000016338	RNF168
ENSACAP00000005556	ENSACAG00000005666	ENSACAT00000005678	IWS1
ENSACAP00000014032	ENSACAG00000014232	ENSACAT00000014319	RBBP5
ENSACAP00000007200	ENSACAG00000007343	ENSACAT00000007355	MRPL45
ENSACAP00000016693	ENSACAG00000016929	ENSACAT00000017023	GUCY1B3
ENSACAP00000003266	ENSACAG00000003023	ENSACAT00000003349	LRBA
ENSACAP00000014655	ENSACAG00000014864	ENSACAT00000014952	EHD4
ENSACAP00000021933	ENSACAG00000029485	ENSACAT00000029351	
ENSACAP00000010337	ENSACAG00000010381	ENSACAT00000010550	KALRN
ENSACAP00000005266	ENSACAG00000005394	ENSACAT00000005383	ZNF346
ENSACAP00000007182	ENSACAG00000007132	ENSACAT00000007337	PBRM1
ENSACAP00000007261	ENSACAG00000007421	ENSACAT00000007416	LCLAT1

Table S15. GO terms associated with PSGs identified on lizard branch 6.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames
GO:0032707	0.001059493	1	1	negative regulation of interleukin-23 production	RAC1
GO:0036352	0.001657074	1	1	histone H2A-K15 ubiquitination	RNF168
GO:2001253	0.001709599	1	1	regulation of histone H3-K36 trimethylation	IWS1
GO:0036261	0.001720373	1	1	7-methylguanosine cap hypermethylation	TGS1
GO:0031106	0.001749031	1	1	septin ring organization	ANLN
GO:0032784	0.001788216	2	41	regulation of DNA-templated transcription, elongation	RNF168,IWS1

GO:0021894	0.002088467	1	2	cerebral cortex GABAergic interneuron development	RAC1
GO:0036462	0.002227209	1	2	TRAIL-activated apoptotic signaling pathway	ENSACAG00000029485
GO:0002551	0.002614602	1	2	mast cell chemotaxis	RAC1
GO:0071167	0.003232198	1	2	ribonucleoprotein complex import into nucleus	TGS1
GO:0032185	0.003454107	1	2	septin cytoskeleton organization	ANLN
GO:0002093	0.004477182	1	3	auditory receptor cell morphogenesis	RAC1
GO:0038060	0.004663477	1	3	nitric oxide-cGMP-mediated signaling pathway	GUCY1B3
GO:0043652	0.00484099	1	4	engulfment of apoptotic cell	RAC1
GO:0051932	0.005518069	1	4	synaptic transmission, GABAergic	RAC1
GO:0016925	0.005934227	2	68	protein sumoylation	RNF168,SENP5
GO:0021826	0.006030077	1	5	substrate-independent telencephalic tangential migration	RAC1
GO:0090521	0.006764349	1	4	glomerular visceral epithelial cell migration	ANLN
GO:0060263	0.010352434	1	8	regulation of respiratory burst	RAC1
GO:0090239	0.011231878	1	7	regulation of histone H4 acetylation	IWS1
GO:0010793	0.013041759	1	7	regulation of mRNA export from nucleus	IWS1
GO:0006907	0.013154576	1	8	pinocytosis	EHD4
GO:0016926	0.013212904	1	8	protein desumoylation	SENP5
GO:0000103	0.014098885	1	11	sulfate assimilation	ENSACAG00000013937
GO:0097178	0.014291854	1	11	ruffle assembly	RAC1
GO:0032785	0.014324632	1	9	negative regulation of DNA-templated transcription, elongation	RNF168
GO:0007263	0.014433395	1	9	nitric oxide mediated signal transduction	GUCY1B3
GO:0048148	0.015370369	1	9	behavioral response to cocaine	KALRN
GO:0007096	0.015783321	1	11	regulation of exit from mitosis	ANLN
GO:0021517	0.015818125	1	8	ventral spinal cord development	ENSACAG00000002945
GO:0014041	0.015893225	1	9	regulation of neuron maturation	RAC1
GO:0071732	0.016445347	1	11	cellular response to nitric oxide	GUCY1B3
GO:0006972	0.018673388	1	14	hyperosmotic response	RAC1
GO:0010592	0.018911639	1	13	positive regulation of lamellipodium assembly	RAC1

GO:0071731	0.019341701	1	13	response to nitric oxide	GUCY1B3
GO:0045190	0.020218081	1	14	isotype switching	RNF168
GO:0051054	0.020986533	2	150	positive regulation of DNA metabolic process	RNF168,RAC1
GO:0032239	0.021265177	1	11	regulation of nucleobase-containing compound transport	IWS1
GO:1902170	0.021542019	1	14	cellular response to reactive nitrogen species	GUCY1B3
GO:0045453	0.021864454	1	15	bone resorption	RAC1
GO:0006182	0.024411224	1	16	cGMP biosynthetic process	GUCY1B3
GO:0016569	0.024794729	3	371	chromatin modification	RNF168,RBBP5,PBRM1
GO:0016024	0.025158729	1	19	CDP-diacylglycerol biosynthetic process	LCLAT1
GO:0046341	0.026241809	1	20	CDP-diacylglycerol metabolic process	LCLAT1
GO:0048532	0.027087816	1	17	anatomical structure arrangement	RAC1
GO:0051668	0.027569319	1	18	localization within membrane	RAC1
GO:0043414	0.028862832	2	164	macromolecule methylation	RBBP5,TGS1
GO:0036260	0.029042574	1	21	RNA capping	TGS1
GO:0006911	0.031160509	1	23	phagocytosis, engulfment	RAC1
GO:1901890	0.032214177	1	20	positive regulation of cell junction assembly	RAC1
GO:0043552	0.032800576	1	21	positive regulation of phosphatidylinositol 3-kinase activity	RAC1
GO:0001662	0.033641862	1	23	behavioral fear response	KALRN
GO:0002209	0.033641862	1	23	behavioral defense response	KALRN
GO:0032259	0.034280504	2	186	methylation	RBBP5,TGS1
GO:0016601	0.034777051	1	23	Rac protein signal transduction	RAC1
GO:0010762	0.035302563	1	25	regulation of fibroblast migration	RAC1
GO:0031529	0.036901993	1	26	ruffle organization	RAC1
GO:0032456	0.037763918	1	25	endocytic recycling	EHD4
GO:0036297	0.03961406	1	26	interstrand cross-link repair	RNF168
GO:0008202	0.039868585	2	208	steroid metabolic process	ENSACAG00000013937,ENSACAG00000002945
GO:0030041	0.040203781	1	29	actin filament polymerization	RAC1

GO:1904837	0.041439198	1	19	beta-catenin-TCF complex assembly	RBBP5
GO:0006325	0.042379144	3	476	chromatin organization	RNF168,RBBP5,PBRM1
GO:0010324	0.043382808	1	31	membrane invagination	RAC1
GO:0016444	0.044137047	1	29	somatic cell DNA recombination	RNF168

Table S16. PSGs identified on branch 2 of lizard.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000002982	ENSACAG00000003085	ENSACAT00000003059	BLOC1S5
ENSACAP00000001637	ENSACAG00000001708	ENSACAT00000001676	
ENSACAP00000006114	ENSACAG00000006219	ENSACAT00000006251	SLC22A17
ENSACAP00000003601	ENSACAG00000003709	ENSACAT00000003689	FADD
ENSACAP00000009466	ENSACAG00000009326	ENSACAT00000009663	HKDC1
ENSACAP00000016378	ENSACAG00000016634	ENSACAT00000016702	CHMP7
ENSACAP00000009853	ENSACAG00000010057	ENSACAT00000010055	SKA1
ENSACAP00000012480	ENSACAG00000012728	ENSACAT00000012736	C16orf13
ENSACAP00000014425	ENSACAG00000014718	ENSACAT00000014720	KLHL25
ENSACAP00000009907	ENSACAG00000010107	ENSACAT00000010110	BBS10
ENSACAP00000002439	ENSACAG00000002527	ENSACAT00000002502	SYBU
ENSACAP00000002575	ENSACAG00000002642	ENSACAT00000002641	MPHOSPH10
ENSACAP00000012354	ENSACAG00000012565	ENSACAT00000012607	AP3M2
ENSACAP00000023124	ENSACAG00000028274	ENSACAT00000030544	PPP1R1A
ENSACAP00000002938	ENSACAG00000002808	ENSACAT00000003014	AARS
ENSACAP00000008717	ENSACAG00000008837	ENSACAT00000008904	ADK
ENSACAP00000000325	ENSACAG00000000339	ENSACAT00000000339	NPDC1
ENSACAP00000002813	ENSACAG00000002925	ENSACAT00000002883	PPP1R3B
ENSACAP00000000283	ENSACAG00000000306	ENSACAT00000000291	ZNF622
ENSACAP00000004433	ENSACAG00000004543	ENSACAT00000004533	TSTD2
ENSACAP00000005953	ENSACAG00000005972	ENSACAT00000006087	PPP2R2A
ENSACAP00000009165	ENSACAG00000009328	ENSACAT00000009358	PLXDC2

ENSACAP00000001286	ENSACAG00000001336	ENSACAT00000001319	ATF6
ENSACAP00000008748	ENSACAG00000008908	ENSACAT00000008936	
ENSACAP00000019497	ENSACAG00000026822	ENSACAT00000025669	
ENSACAP00000010575	ENSACAG00000010758	ENSACAT00000010793	SLC39A14
ENSACAP00000012089	ENSACAG00000012271	ENSACAT00000012334	
ENSACAP00000000834	ENSACAG00000000877	ENSACAT00000000860	SCRN1
ENSACAP00000004063	ENSACAG00000004173	ENSACAT00000004157	MRPL44
ENSACAP00000023445	ENSACAG00000029320	ENSACAT00000030864	
ENSACAP00000023038	ENSACAG00000028642	ENSACAT00000030458	CCDC24
ENSACAP00000000882	ENSACAG00000000907	ENSACAT00000000909	MICU1
ENSACAP00000022057	ENSACAG00000029108	ENSACAT00000029475	ZYG11A
ENSACAP00000001539	ENSACAG00000001584	ENSACAT00000001575	PRPS2
ENSACAP00000011362	ENSACAG00000011590	ENSACAT00000011601	REPS2
ENSACAP00000011458	ENSACAG00000011708	ENSACAT00000011697	CDKL5
ENSACAP00000015734	ENSACAG00000015951	ENSACAT00000016050	CSE1L
ENSACAP00000014277	ENSACAG00000014447	ENSACAT00000014570	PUS7
ENSACAP00000009396	ENSACAG00000009601	ENSACAT00000009591	SRD5A3
ENSACAP00000014749	ENSACAG00000014964	ENSACAT00000015050	LSAMP
ENSACAP00000003266	ENSACAG00000003023	ENSACAT00000003349	LRBA
ENSACAP00000009875	ENSACAG00000010017	ENSACAT00000010078	
ENSACAP00000008230	ENSACAG00000008386	ENSACAT00000008407	
ENSACAP00000003850	ENSACAG00000003673	ENSACAT00000003942	JAK2
ENSACAP00000015315	ENSACAG00000015401	ENSACAT00000015626	RYR3
ENSACAP00000015303	ENSACAG00000015436	ENSACAT00000015615	DNM2
ENSACAP00000015401	ENSACAG00000015649	ENSACAT00000015714	ZNF106
ENSACAP00000006901	ENSACAG00000007054	ENSACAT00000007052	MED19
ENSACAP00000000953	ENSACAG00000000804	ENSACAT00000000981	DARS
ENSACAP00000015661	ENSACAG00000015930	ENSACAT00000015976	LCP2
ENSACAP00000004986	ENSACAG00000005027	ENSACAT00000005099	
ENSACAP00000013619	ENSACAG00000013868	ENSACAT00000013899	RWDD1

ENSACAP00000011520	ENSACAG00000011707	ENSACAT00000011760	FYN
ENSACAP00000023211	ENSACAG00000029208	ENSACAT00000030630	
ENSACAP00000007136	ENSACAG00000007254	ENSACAT00000007291	
ENSACAP00000015333	ENSACAG00000015618	ENSACAT00000015646	RGS7BP
ENSACAP00000002216	ENSACAG00000002254	ENSACAT00000002276	MIA3

Table S17. GO terms associated with PSGs identified on lizard branch 2.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames
GO:0006167	0.000106847	2	6	AMP biosynthetic process	PRPS2,ADK
GO:0043624	0.000428142	3	49	cellular protein complex disassembly	MRPL44,ENSACAG00000010017,ENSACAG00000008908
GO:0070126	0.000676067	2	16	mitochondrial translational termination	MRPL44,ENSACAG00000008908
GO:0048490	0.000704032	2	15	anterograde synaptic vesicle transport	BLOC1S5,AP3M2
GO:0046033	0.000730478	2	14	AMP metabolic process	PRPS2,ADK
GO:0097049	0.002190912	1	1	motor neuron apoptotic process	FADD
GO:2000454	0.002190912	1	1	positive regulation of CD8-positive, alpha-beta cytotoxic T cell extravasation	FADD
GO:1901253	0.002592272	1	1	negative regulation of intracellular transport of viral material	ENSACAG00000029208
GO:0016095	0.002607642	1	1	polyprenol catabolic process	SRD5A3
GO:0006175	0.002676538	1	1	dATP biosynthetic process	ADK
GO:0015891	0.003038912	1	1	siderophore transport	SLC22A17
GO:0035406	0.004023665	1	1	histone-tyrosine phosphorylation	JAK2
GO:0035409	0.004023665	1	1	histone H3-Y41 phosphorylation	JAK2
GO:0030968	0.004197636	2	32	endoplasmic reticulum unfolded protein response	AARS,ATF6
GO:0036462	0.00482546	1	2	TRAIL-activated apoptotic signaling pathway	FADD
GO:2000452	0.004836915	1	2	regulation of CD8-positive, alpha-beta cytotoxic T cell extravasation	FADD
GO:2000451	0.004854072	1	2	positive regulation of CD8-positive, alpha-beta T cell extravasation	FADD

GO:0038083	0.005393954	2	33	peptidyl-tyrosine autophosphorylation	JAK2,FYN
GO:0007169	0.005656095	5	351	transmembrane receptor protein tyrosine kinase signaling pathway	REPS2,JAK2,ZNF106,LCP2,FYN
GO:0034660	0.005876161	5	391	ncRNA metabolic process	MRPL44,PUS7,DARS,MPHOSPH10,AARS
GO:0006422	0.005938821	1	2	aspartyl-tRNA aminoacylation	DARS
GO:0007260	0.006740784	1	2	tyrosine phosphorylation of STAT protein	JAK2
GO:0006984	0.006760038	2	41	ER-nucleus signaling pathway	AARS,ATF6
GO:0043588	0.006877616	2	33	skin development	RYR3,AARS
GO:2000449	0.007493136	1	3	regulation of CD8-positive, alpha-beta T cell extravasation	FADD
GO:0006046	0.007759731	1	3	N-acetylglucosamine catabolic process	ENSACAG00000001708
GO:0006015	0.008175337	1	3	5-phosphoribose 1-diphosphate biosynthetic process	PRPS2
GO:0046391	0.008175337	1	3	5-phosphoribose 1-diphosphate metabolic process	PRPS2
GO:0070235	0.008345923	1	3	regulation of activation-induced cell death of T cells	FADD
GO:0006414	0.009318349	2	58	translational elongation	MRPL44,ENSACAG00000008908
GO:0060546	0.01048289	1	4	negative regulation of necroptotic process	FADD
GO:0030900	0.010482965	2	44	forebrain development	ENSACAG00000005027,FYN
GO:1901678	0.010671965	1	4	iron coordination entity transport	SLC22A17
GO:0090110	0.010841449	1	3	cargo loading into COPII-coated vesicle	MIA3
GO:0006073	0.0110035	2	52	cellular glucan metabolic process	PPP1R1A,PPP1R3B
GO:0043038	0.011709496	2	52	amino acid activation	DARS,AARS
GO:0006166	0.012413498	1	5	purine ribonucleoside salvage	ADK
GO:0006112	0.012597149	2	56	energy reserve metabolic process	PPP1R1A,PPP1R3B
GO:0060340	0.013231552	1	5	positive regulation of type I interferon-mediated signaling pathway	FADD
GO:0045651	0.013505881	1	5	positive regulation of macrophage differentiation	FADD
GO:0050798	0.013623588	1	4	activated T cell proliferation	FYN
GO:0045087	0.014153873	4	316	innate immune response	FADD,JAK2,FYN,ENSACAG00000029208
GO:0006091	0.014350153	3	179	generation of precursor metabolites and energy	HKDC1,PPP1R1A,PPP1R3B
GO:0097202	0.014614789	2	64	activation of cysteine-type endopeptidase activity	FADD,ENSACAG00000005027

GO:0009202	0.015420649	1	5	deoxyribonucleoside triphosphate biosynthetic process	ADK
GO:0019262	0.015511817	1	6	N-acetylneuraminate catabolic process	ENSACAG00000001708
GO:0051561	0.016308511	1	6	positive regulation of mitochondrial calcium ion concentration	MICU1
GO:0003374	0.017212162	1	5	dynamin family protein polymerization involved in mitochondrial fission	DNM2
GO:0016093	0.017346659	1	7	polyprenol metabolic process	SRD5A3
GO:0071578	0.017566153	1	6	zinc II ion transmembrane import	SLC39A14
GO:0009265	0.017769974	1	7	2'-deoxyribonucleotide biosynthetic process	ADK
GO:0018212	0.017804366	2	61	peptidyl-tyrosine modification	JAK2,FYN
GO:0022411	0.018266385	3	175	cellular component disassembly	MRPL44,ENSACAG00000010017,ENSACAG00000008908
GO:0008300	0.019226425	1	7	isoprenoid catabolic process	SRD5A3
GO:0009124	0.019538532	2	79	nucleoside monophosphate biosynthetic process	PRPS2,ADK
GO:0031638	0.019981529	2	75	zymogen activation	FADD,ENSACAG00000005027
GO:0051131	0.020800729	1	7	chaperone-mediated protein complex assembly	BBS10
GO:0050932	0.021250597	1	6	regulation of pigment cell differentiation	BLOC1S5
GO:0045576	0.021845788	1	8	mast cell activation	LCP2
GO:0030422	0.021957184	1	6	production of siRNA involved in RNA interference	MRPL44
GO:0046777	0.022186481	3	174	protein autophosphorylation	CDKL5,JAK2,FYN
GO:0050966	0.023139806	1	7	detection of mechanical stimulus involved in sensory perception of pain	FYN
GO:0005976	0.024145008	2	81	polysaccharide metabolic process	PPP1R1A,PPP1R3B
GO:1900246	0.025137034	1	6	positive regulation of RIG-I signaling pathway	ENSACAG00000029208
GO:0055065	0.027869372	4	372	metal ion homeostasis	SLC39A14,MICU1,RYR3,SLC22A17
GO:0045324	0.028661983	1	10	late endosome to vacuole transport	CHMP7
GO:0043065	0.028886192	4	387	positive regulation of apoptotic process	FADD,ENSACAG00000005027,ZNF622,ATF6
GO:0031468	0.029275461	1	11	nuclear envelope reassembly	CHMP7
GO:0043279	0.029438798	2	88	response to alkaloid	RYR3,PPP2R2A
GO:0035459	0.02969924	1	8	cargo loading into vesicle	MIA3
GO:0048535	0.029900649	1	11	lymph node development	FADD

GO:0010458	0.03103426	1	10	exit from mitosis	CHMP7
GO:0008631	0.032176207	1	12	intrinsic apoptotic signaling pathway in response to oxidative stress	ZNF622
GO:0006054	0.032278939	1	12	N-acetylneuraminate metabolic process	ENSACAG00000001708
GO:0000920	0.03289032	1	12	cell separation after cytokinesis	CHMP7
GO:0006851	0.034868344	1	13	mitochondrial calcium ion transport	MICU1
GO:1903513	0.035591085	1	9	endoplasmic reticulum to cytosol transport	RYR3
GO:1901659	0.035921325	2	112	glycosyl compound biosynthetic process	PRPS2,ADK
GO:0009200	0.037459376	1	14	deoxyribonucleoside triphosphate metabolic process	ADK
GO:0006488	0.037506251	1	14	dolichol-linked oligosaccharide biosynthetic process	SRD5A3
GO:0035024	0.038692193	1	11	negative regulation of Rho protein signal transduction	ENSACAG00000005027
GO:0042273	0.038883384	1	15	ribosomal large subunit biogenesis	ZNF622
GO:0042953	0.043753589	1	9	lipoprotein transport	MIA3
GO:0044872	0.043753589	1	9	lipoprotein localization	MIA3
GO:0035307	0.043958378	1	14	positive regulation of protein dephosphorylation	ENSACAG00000005027
GO:0051895	0.044059735	1	15	negative regulation of focal adhesion assembly	ENSACAG00000005027
GO:0034976	0.044119841	2	112	response to endoplasmic reticulum stress	AARS,ATF6
GO:0001895	0.044280591	1	16	retina homeostasis	BBS10
GO:0071313	0.0463952	1	12	cellular response to caffeine	RYR3
GO:0009451	0.046998562	2	122	RNA modification	PUS7,AARS
GO:0001522	0.047530739	1	18	pseudouridine synthesis	PUS7
GO:0044262	0.048978373	2	120	cellular carbohydrate metabolic process	PPP1R1A,PPP1R3B
GO:0070296	0.049715744	1	12	sarcoplasmic reticulum calcium ion transport	RYR3
GO:0036120	0.049950111	1	16	cellular response to platelet-derived growth factor stimulus	FYN

Table S18. PSGs identified on branch 1 of frog.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000002963	ENSACAG00000003016	ENSACAT00000003040	
ENSACAP00000020775	ENSACAG00000026588	ENSACAT00000022129	

ENSACAP00000008201	ENSACAG00000008368	ENSACAT00000008377	TAF10
ENSACAP00000001268	ENSACAG00000001379	ENSACAT00000001301	FICD
ENSACAP00000003231	ENSACAG00000003255	ENSACAT00000003314	
ENSACAP00000012691	ENSACAG00000012889	ENSACAT00000012947	
ENSACAP00000004101	ENSACAG00000004183	ENSACAT00000004198	
ENSACAP00000017277	ENSACAG00000017542	ENSACAT00000017617	FOXK1
ENSACAP00000006715	ENSACAG00000006792	ENSACAT00000006861	PIEZO1
ENSACAP00000002886	ENSACAG00000002886	ENSACAT00000002957	
ENSACAP00000004963	ENSACAG00000005058	ENSACAT00000005076	RPL11
ENSACAP00000004923	ENSACAG00000005000	ENSACAT00000005036	PPT1
ENSACAP00000023346	ENSACAG00000004885	ENSACAT00000030766	BMPR2
ENSACAP00000008316	ENSACAG00000008437	ENSACAT00000008496	NPNT
ENSACAP00000005070	ENSACAG00000005194	ENSACAT00000005185	NOP58
ENSACAP00000004794	ENSACAG00000004894	ENSACAT00000004902	MFSD2A
ENSACAP00000001312	ENSACAG00000001400	ENSACAT00000001345	PCBD2
ENSACAP00000012337	ENSACAG00000012598	ENSACAT00000012590	MAN2C1
ENSACAP00000016408	ENSACAG00000016668	ENSACAT00000016733	HTATIP2
ENSACAP00000004015	ENSACAG00000004079	ENSACAT00000004107	RELB
ENSACAP00000009019	ENSACAG00000009164	ENSACAT00000009211	NADK2
ENSACAP00000005351	ENSACAG00000005479	ENSACAT00000005468	COX4I1
ENSACAP00000016271	ENSACAG00000016477	ENSACAT00000016595	GRIPAP1
ENSACAP00000011892	ENSACAG00000011740	ENSACAT00000012136	
ENSACAP00000008948	ENSACAG00000009150	ENSACAT00000009139	MED29
ENSACAP00000013586	ENSACAG00000013788	ENSACAT00000013866	
ENSACAP00000022553	ENSACAG00000028479	ENSACAT00000029970	IFNAR2
ENSACAP00000000414	ENSACAG00000000363	ENSACAT00000000431	IMPDH1
ENSACAP00000000500	ENSACAG00000000594	ENSACAT00000000518	THEM5
ENSACAP00000000793	ENSACAG00000000902	ENSACAT00000000818	LPAR4
ENSACAP00000016905	ENSACAG00000017180	ENSACAT00000017240	LOXL1
ENSACAP00000019544	ENSACAG00000025211	ENSACAT00000023876	PSMB7

ENSACAP00000000405	ENSACAG00000000447	ENSACAT00000000422	BRCC3
ENSACAP00000016795	ENSACAG00000017007	ENSACAT00000017126	SCAMP2
ENSACAP00000016725	ENSACAG00000016980	ENSACAT00000017055	
ENSACAP00000016867	ENSACAG00000017134	ENSACAT00000017202	DDX6
ENSACAP00000006180	ENSACAG00000006198	ENSACAT00000006317	BTAF1
ENSACAP00000006928	ENSACAG00000006934	ENSACAT00000007079	
ENSACAP00000002807	ENSACAG00000002851	ENSACAT00000002877	METTL3
ENSACAP00000011104	ENSACAG00000011339	ENSACAT00000011334	RPL15
ENSACAP00000013361	ENSACAG00000013588	ENSACAT00000013632	
ENSACAP00000007585	ENSACAG00000007221	ENSACAT00000007746	COL5A1
ENSACAP00000009399	ENSACAG00000009349	ENSACAT00000009594	ADCY4
ENSACAP00000016430	ENSACAG00000016688	ENSACAT00000016755	
ENSACAP00000002142	ENSACAG00000001978	ENSACAT00000002201	COG4
ENSACAP00000016626	ENSACAG00000016896	ENSACAT00000016953	FIBCD1
ENSACAP00000012225	ENSACAG00000012412	ENSACAT00000012475	TINAGL1
ENSACAP00000010445	ENSACAG00000010646	ENSACAT00000010659	USE1
ENSACAP00000001330	ENSACAG00000000936	ENSACAT00000001363	OCRL
ENSACAP00000001568	ENSACAG00000001189	ENSACAT00000001605	GRIN1
ENSACAP00000015226	ENSACAG00000015481	ENSACAT00000015534	USB1
ENSACAP00000013201	ENSACAG00000013450	ENSACAT00000013465	SMIM12
ENSACAP00000017268	ENSACAG00000017538	ENSACAT00000017608	
ENSACAP00000006749	ENSACAG00000006776	ENSACAT00000006895	FUS
ENSACAP00000013733	ENSACAG00000013982	ENSACAT00000014014	GCA
ENSACAP00000017486	ENSACAG00000017755	ENSACAT00000017831	EIF4G3
ENSACAP00000013440	ENSACAG00000013675	ENSACAT00000013715	
ENSACAP00000012483	ENSACAG00000012625	ENSACAT00000012739	AQP3
ENSACAP00000008343	ENSACAG00000008519	ENSACAT00000008524	FAM131C
ENSACAP00000014346	ENSACAG00000014490	ENSACAT00000014639	RPA1
ENSACAP00000007281	ENSACAG00000007456	ENSACAT00000007437	RGS9BP
ENSACAP00000011611	ENSACAG00000011700	ENSACAT00000011851	NDRG1

ENSACAP00000017999	ENSACAG00000027397	ENSACAT00000022186	SART1
ENSACAP00000008073	ENSACAG00000008238	ENSACAT00000008245	ZFHX3
ENSACAP00000010118	ENSACAG00000010210	ENSACAT00000010326	KIAA0196
ENSACAP00000001537	ENSACAG00000001545	ENSACAT00000001573	ZCCHC8
ENSACAP00000009815	ENSACAG00000010022	ENSACAT00000010015	NDUFB9
ENSACAP00000011505	ENSACAG00000011615	ENSACAT00000011745	KIAA1468
ENSACAP00000002400	ENSACAG00000002429	ENSACAT00000002461	ADIPOR1
ENSACAP00000008584	ENSACAG00000008659	ENSACAT00000008767	CABIN1
ENSACAP00000016608	ENSACAG00000016791	ENSACAT00000016935	TBC1D22B
ENSACAP00000009201	ENSACAG00000009364	ENSACAT00000009394	FZD6
ENSACAP00000005862	ENSACAG00000005969	ENSACAT00000005991	MLF2
ENSACAP00000001566	ENSACAG00000001034	ENSACAT00000001603	
ENSACAP00000008780	ENSACAG00000008913	ENSACAT00000008968	RRM2B
ENSACAP00000005325	ENSACAG00000005445	ENSACAT00000005442	GMDS
ENSACAP00000011281	ENSACAG00000011533	ENSACAT00000011517	PSMG3
ENSACAP00000011162	ENSACAG00000011399	ENSACAT00000011395	C15orf26
ENSACAP00000005539	ENSACAG00000005680	ENSACAT00000005660	GPER1
ENSACAP00000008480	ENSACAG00000008679	ENSACAT00000008662	RERE
ENSACAP00000004182	ENSACAG00000004222	ENSACAT00000004281	LSG1
ENSACAP00000013023	ENSACAG00000013171	ENSACAT00000013282	CCT3
ENSACAP00000008788	ENSACAG00000008928	ENSACAT00000008976	CALU
ENSACAP00000000009	ENSACAG00000000010	ENSACAT00000000010	C9orf114
ENSACAP00000012411	ENSACAG00000012671	ENSACAT00000012664	BCAS1
ENSACAP00000000890	ENSACAG00000000794	ENSACAT00000000917	DMTN
ENSACAP00000003197	ENSACAG00000003297	ENSACAT00000003280	GUCD1
ENSACAP00000009005	ENSACAG00000009136	ENSACAT00000009198	BRD1
ENSACAP00000005969	ENSACAG00000006111	ENSACAT00000006103	SOX8
ENSACAP00000010338	ENSACAG00000010516	ENSACAT00000010551	CALB1
ENSACAP00000003704	ENSACAG00000003756	ENSACAT00000003794	RPLP0
ENSACAP00000005884	ENSACAG00000006013	ENSACAT00000006013	CLVS1

ENSACAP00000000788	ENSACAG00000000773	ENSACAT00000000813	IL1RAP
ENSACAP00000014578	ENSACAG00000014729	ENSACAT00000014873	SCARB1
ENSACAP00000014383	ENSACAG00000014658	ENSACAT00000014676	EMP2
ENSACAP00000015098	ENSACAG00000015296	ENSACAT00000015402	DDX55
ENSACAP00000009342	ENSACAG00000009522	ENSACAT00000009537	ZSWIM8
ENSACAP00000015272	ENSACAG00000015441	ENSACAT00000015581	SBNO1
ENSACAP00000008830	ENSACAG00000008935	ENSACAT00000009020	VCL
ENSACAP00000007394	ENSACAG00000007463	ENSACAT00000007551	SND1
ENSACAP00000006308	ENSACAG00000006461	ENSACAT00000006448	NUFIP1
ENSACAP00000005642	ENSACAG00000005783	ENSACAT00000005765	NOP56
ENSACAP00000003381	ENSACAG00000003487	ENSACAT00000003464	PVRL1
ENSACAP00000007730	ENSACAG00000007887	ENSACAT00000007896	ABHD3
ENSACAP00000009563	ENSACAG00000009771	ENSACAT00000009760	XIRP1
ENSACAP00000007053	ENSACAG00000007195	ENSACAT00000007205	GPAA1
ENSACAP00000005163	ENSACAG00000005221	ENSACAT00000005280	PLCD1
ENSACAP00000008027	ENSACAG00000008092	ENSACAT00000008198	DLG5
ENSACAP00000004798	ENSACAG00000004884	ENSACAT00000004906	HSPA8
ENSACAP00000014695	ENSACAG00000014958	ENSACAT00000014995	ZMYND19
ENSACAP00000000393	ENSACAG00000000404	ENSACAT00000000410	
ENSACAP00000012178	ENSACAG00000012396	ENSACAT00000012426	NUCKS1
ENSACAP00000006654	ENSACAG00000006809	ENSACAT00000006800	CYP8B1
ENSACAP00000003628	ENSACAG00000003695	ENSACAT00000003716	
ENSACAP00000013808	ENSACAG00000014010	ENSACAT00000014090	SLC37A4
ENSACAP00000013183	ENSACAG00000013293	ENSACAT00000013446	VPS35
ENSACAP00000000846	ENSACAG00000000923	ENSACAT00000000872	
ENSACAP00000004578	ENSACAG00000004685	ENSACAT00000004683	
ENSACAP00000009688	ENSACAG00000009839	ENSACAT00000009885	NFATC3
ENSACAP00000005385	ENSACAG00000005425	ENSACAT00000005502	ATXN2L
ENSACAP00000015970	ENSACAG00000016254	ENSACAT00000016289	FBXO34
ENSACAP00000006839	ENSACAG00000006788	ENSACAT00000006989	ITGB1

ENSACAP00000003860	ENSACAG00000003962	ENSACAT00000003952	RBM24
ENSACAP00000009562	ENSACAG00000009597	ENSACAT00000009759	XRCC5
ENSACAP00000007336	ENSACAG00000007423	ENSACAT00000007492	SVIL
ENSACAP00000017100	ENSACAG00000017294	ENSACAT00000017437	GRIK3
ENSACAP00000007069	ENSACAG00000007003	ENSACAT00000007221	DNM1
ENSACAP00000006603	ENSACAG00000006763	ENSACAT00000006749	COMMD8
ENSACAP00000022713	ENSACAG00000028448	ENSACAT00000030131	OTUD1
ENSACAP00000017694	ENSACAG00000017971	ENSACAT00000018042	RGS20
ENSACAP00000017693	ENSACAG00000017969	ENSACAT00000018041	ATP6V1H
ENSACAP00000000854	ENSACAG00000000821	ENSACAT00000000880	LPCAT1
ENSACAP00000007033	ENSACAG00000007160	ENSACAT00000007185	RGS5
ENSACAP00000003827	ENSACAG00000003867	ENSACAT00000003919	
ENSACAP00000007237	ENSACAG00000007250	ENSACAT00000007392	ATP11B
ENSACAP00000015568	ENSACAG00000015849	ENSACAT00000015882	CLDN12
ENSACAP00000015558	ENSACAG00000015785	ENSACAT00000015872	CDK14
ENSACAP00000009285	ENSACAG00000009472	ENSACAT00000009478	UTP6
ENSACAP00000003937	ENSACAG00000004062	ENSACAT00000004029	CLEC3B
ENSACAP00000002866	ENSACAG00000002729	ENSACAT00000002937	FBXO18
ENSACAP00000014494	ENSACAG00000014695	ENSACAT00000014789	RFWD2
ENSACAP00000004411	ENSACAG00000004517	ENSACAT00000004511	MRPL47
ENSACAP00000008624	ENSACAG00000008771	ENSACAT00000008807	CTSK
ENSACAP00000000477	ENSACAG00000000441	ENSACAT00000000495	CIRBP
ENSACAP00000016051	ENSACAG00000016332	ENSACAT00000016371	TMEM143
ENSACAP00000015517	ENSACAG00000015798	ENSACAT00000015831	DNAJC22
ENSACAP00000014686	ENSACAG00000014919	ENSACAT00000014984	ALDOA
ENSACAP00000017455	ENSACAG00000017727	ENSACAT00000017797	PPP1R32
ENSACAP00000016487	ENSACAG00000016682	ENSACAT00000016813	CYTH2
ENSACAP00000016567	ENSACAG00000016780	ENSACAT00000016893	TNNT1
ENSACAP00000013343	ENSACAG00000013301	ENSACAT00000013614	COL1A2
ENSACAP00000012761	ENSACAG00000013005	ENSACAT00000013017	GORAB

ENSACAP00000014423	ENSACAG00000014705	ENSACAT00000014718	DLX6
ENSACAP00000002155	ENSACAG00000002257	ENSACAT00000002214	SERPIND1
ENSACAP00000006658	ENSACAG00000006806	ENSACAT00000006804	RSRC1
ENSACAP00000006622	ENSACAG00000006780	ENSACAT00000006768	PTX3
ENSACAP00000000029	ENSACAG00000000028	ENSACAT00000000030	WNK1
ENSACAP00000013049	ENSACAG00000013246	ENSACAT00000013308	DFNA5
ENSACAP00000007049	ENSACAG00000007116	ENSACAT00000007201	HLTF
ENSACAP00000002209	ENSACAG00000001756	ENSACAT00000002269	ATP2C1
ENSACAP00000016703	ENSACAG00000016940	ENSACAT00000017033	HIPK2
ENSACAP00000005541	ENSACAG00000005571	ENSACAT00000005662	CCDC18
ENSACAP00000005184	ENSACAG00000005061	ENSACAT00000005301	EPHA4
ENSACAP00000007260	ENSACAG00000007341	ENSACAT00000007415	SEPT7
ENSACAP00000015007	ENSACAG00000015290	ENSACAT00000015311	MTERF2
ENSACAP00000016036	ENSACAG00000016312	ENSACAT00000016356	UBXN7
ENSACAP00000016238	ENSACAG00000016387	ENSACAT00000016561	MYH9
ENSACAP00000009531	ENSACAG00000009662	ENSACAT00000009728	RYK
ENSACAP00000015992	ENSACAG00000016262	ENSACAT00000016312	IFT27
ENSACAP00000015428	ENSACAG00000015666	ENSACAT00000015741	SH3BP1
ENSACAP00000007420	ENSACAG00000007355	ENSACAT00000007577	STAG1
ENSACAP00000004157	ENSACAG00000004193	ENSACAT00000004256	CPN1
ENSACAP00000012985	ENSACAG00000013236	ENSACAT00000013244	CFAP57
ENSACAP00000013843	ENSACAG00000014080	ENSACAT00000014127	NTN4
ENSACAP00000012479	ENSACAG00000012654	ENSACAT00000012735	CEP83
ENSACAP00000011995	ENSACAG00000012203	ENSACAT00000012240	FAM171A2
ENSACAP00000014854	ENSACAG00000015138	ENSACAT00000015155	SEPP1
ENSACAP00000014890	ENSACAG00000015161	ENSACAT00000015192	TOE1
ENSACAP00000011061	ENSACAG00000011252	ENSACAT00000011290	C12orf29
ENSACAP00000015276	ENSACAG00000015495	ENSACAT00000015585	EIF2B3
ENSACAP00000017515	ENSACAG00000017786	ENSACAT00000017860	AIFM2
ENSACAP00000016880	ENSACAG00000017140	ENSACAT00000017215	FKBP10

ENSACAP00000008015	ENSACAG00000008185	ENSACAT00000008186	CC2D1B
ENSACAP00000007491	ENSACAG00000007467	ENSACAT00000007648	
ENSACAP00000007428	ENSACAG00000007599	ENSACAT00000007585	PPP1R15B
ENSACAP00000017662	ENSACAG00000017936	ENSACAT00000018008	ATP6V0A1
ENSACAP00000000334	ENSACAG00000000380	ENSACAT00000000348	OLFM4
ENSACAP00000007271	ENSACAG00000007418	ENSACAT00000007427	SOCS7
ENSACAP00000000706	ENSACAG00000000649	ENSACAT00000000730	DIS3
ENSACAP00000004505	ENSACAG00000004618	ENSACAT00000004608	LSM12
ENSACAP00000002485	ENSACAG00000002592	ENSACAT00000002549	ARGLU1
ENSACAP00000001690	ENSACAG00000001572	ENSACAT00000001730	PLXNB2
ENSACAP00000001397	ENSACAG00000001494	ENSACAT00000001430	ZNF800
ENSACAP00000020514	ENSACAG00000024935	ENSACAT00000027223	F7
ENSACAP00000013323	ENSACAG00000013405	ENSACAT00000013593	AP2A1
ENSACAP00000001974	ENSACAG00000002034	ENSACAT00000002022	CCDC138
ENSACAP00000000629	ENSACAG00000000412	ENSACAT00000000649	DHX15
ENSACAP00000011725	ENSACAG00000011909	ENSACAT00000011967	RGN
ENSACAP00000006202	ENSACAG00000006348	ENSACAT00000006339	FGL2
ENSACAP00000015991	ENSACAG00000016236	ENSACAT00000016311	CDH4
ENSACAP00000002797	ENSACAG00000002817	ENSACAT00000002867	URB1
ENSACAP00000009262	ENSACAG00000009451	ENSACAT00000009455	MPZL1
ENSACAP00000009198	ENSACAG00000009329	ENSACAT00000009391	DCAF6
ENSACAP00000002067	ENSACAG00000002110	ENSACAT00000002121	UFSP2
ENSACAP00000011610	ENSACAG00000011843	ENSACAT00000011850	SENP7
ENSACAP00000010908	ENSACAG00000011125	ENSACAT00000011135	FILIP1L
ENSACAP00000003608	ENSACAG00000003612	ENSACAT00000003696	NR3C2
ENSACAP00000012569	ENSACAG00000012684	ENSACAT00000012825	SEC24B
ENSACAP00000016161	ENSACAG00000016447	ENSACAT00000016482	
ENSACAP00000008722	ENSACAG00000008698	ENSACAT00000008909	HMGCR
ENSACAP00000009807	ENSACAG00000010001	ENSACAT00000010007	BDP1
ENSACAP00000011156	ENSACAG00000011195	ENSACAT00000011388	VCAN

ENSACAP00000012915	ENSACAG00000013091	ENSACAT00000013173	TTC37
ENSACAP00000017487	ENSACAG00000017757	ENSACAT00000017832	PSIP1
ENSACAP00000005301	ENSACAG00000005379	ENSACAT00000005418	OSTF1
ENSACAP00000002825	ENSACAG00000002423	ENSACAT00000002895	SMARCA2
ENSACAP00000001812	ENSACAG00000001896	ENSACAT00000001856	PSMA6
ENSACAP00000018251	ENSACAG00000024248	ENSACAT00000028273	LETMD1
ENSACAP00000009450	ENSACAG00000009586	ENSACAT00000009647	PPP4R3A
ENSACAP00000015113	ENSACAG00000015342	ENSACAT00000015419	
ENSACAP00000017164	ENSACAG00000017431	ENSACAT00000017501	GTF2A1
ENSACAP00000016915	ENSACAG00000017170	ENSACAT00000017250	POMT2
ENSACAP00000016842	ENSACAG00000017113	ENSACAT00000017177	ANGEL1
ENSACAP00000016904	ENSACAG00000017166	ENSACAT00000017239	FARSA
ENSACAP00000016804	ENSACAG00000017054	ENSACAT00000017136	NFIX
ENSACAP00000015583	ENSACAG00000015726	ENSACAT00000015897	SLC44A2
ENSACAP00000012138	ENSACAG00000012275	ENSACAT00000012383	EEF2
ENSACAP00000012387	ENSACAG00000012627	ENSACAT00000012640	C18orf25
ENSACAP00000017361	ENSACAG00000017600	ENSACAT00000017702	POSTN
ENSACAP00000009994	ENSACAG00000009800	ENSACAT00000010200	FLNA
ENSACAP00000022376	ENSACAG00000029651	ENSACAT00000029793	CKAP5
ENSACAP00000009344	ENSACAG00000009404	ENSACAT00000009539	SMC1A
ENSACAP00000012413	ENSACAG00000012614	ENSACAT00000012666	SEPHS2
ENSACAP00000012565	ENSACAG00000012772	ENSACAT00000012821	ATP6AP1
ENSACAP00000021105	ENSACAG00000025589	ENSACAT00000022389	DDX23
ENSACAP00000008971	ENSACAG00000009130	ENSACAT00000009163	PTGES3
ENSACAP00000000046	ENSACAG00000000047	ENSACAT00000000047	KCNJ11
ENSACAP00000015422	ENSACAG00000015684	ENSACAT00000015735	SLC26A11
ENSACAP00000009489	ENSACAG00000009700	ENSACAT00000009686	
ENSACAP00000016415	ENSACAG00000016662	ENSACAT00000016740	PGS1
ENSACAP00000017329	ENSACAG00000017595	ENSACAT00000017669	TEKT3
ENSACAP00000006856	ENSACAG00000006926	ENSACAT00000007006	CTNND1

ENSACAP00000007102	ENSACAG00000007213	ENSACAT00000007255	SLC43A1
ENSACAP00000005039	ENSACAG00000005166	ENSACAT00000005152	MYCBPAP
ENSACAP00000010845	ENSACAG00000010914	ENSACAT00000011070	MAP2
ENSACAP00000015631	ENSACAG00000015637	ENSACAT00000015946	FN1
ENSACAP00000013512	ENSACAG00000013668	ENSACAT00000013790	NR3C1
ENSACAP00000015745	ENSACAG00000016013	ENSACAT00000016061	TYW5
ENSACAP00000005755	ENSACAG00000005717	ENSACAT00000005882	GLS
ENSACAP00000005673	ENSACAG00000005744	ENSACAT00000005797	EHBP1
ENSACAP00000014506	ENSACAG00000014556	ENSACAT00000014801	DPYSL3
ENSACAP00000004705	ENSACAG00000004735	ENSACAT00000004812	COL6A1
ENSACAP00000004412	ENSACAG00000004231	ENSACAT00000004512	COL6A3
ENSACAP00000016181	ENSACAG00000016379	ENSACAT00000016502	RUFY1
ENSACAP00000004544	ENSACAG00000004636	ENSACAT00000004649	TTBK1
ENSACAP00000005421	ENSACAG00000005410	ENSACAT00000005539	FGFR4
ENSACAP00000006467	ENSACAG00000006599	ENSACAT00000006612	B4GALT7
ENSACAP00000000239	ENSACAG00000000198	ENSACAT00000000245	ROCK2
ENSACAP00000001499	ENSACAG00000001356	ENSACAT00000001535	ADAM17
ENSACAP00000006912	ENSACAG00000006988	ENSACAT00000007063	STAB1
ENSACAP00000008355	ENSACAG00000008501	ENSACAT00000008536	ELOVL5
ENSACAP00000007242	ENSACAG00000007357	ENSACAT00000007397	GNL3
ENSACAP00000008014	ENSACAG00000007955	ENSACAT00000008185	ITIH4
ENSACAP00000012886	ENSACAG00000013126	ENSACAT00000013144	RAB43
ENSACAP00000010793	ENSACAG00000010885	ENSACAT00000011016	TKT
ENSACAP00000008329	ENSACAG00000008491	ENSACAT00000008510	B3GAT2
ENSACAP00000013979	ENSACAG00000014247	ENSACAT00000014265	AZI2
ENSACAP00000015105	ENSACAG00000015388	ENSACAT00000015409	LMOD3
ENSACAP00000009930	ENSACAG00000010035	ENSACAT00000010134	BRPF1
ENSACAP00000010433	ENSACAG00000010517	ENSACAT00000010647	ABCF1
ENSACAP00000004516	ENSACAG00000004605	ENSACAT00000004620	
ENSACAP00000011394	ENSACAG00000011208	ENSACAT00000011633	

ENSACAP00000003593	ENSACAG00000003646	ENSACAT00000003681	FMN2
ENSACAP00000002410	ENSACAG00000002405	ENSACAT00000002472	GNPAT
ENSACAP00000002456	ENSACAG00000002531	ENSACAT00000002519	PDCD2
ENSACAP00000002674	ENSACAG00000002782	ENSACAT00000002741	ERMARD
ENSACAP00000002993	ENSACAG00000002861	ENSACAT00000003070	THBS2
ENSACAP00000009442	ENSACAG00000009630	ENSACAT00000009639	TJAP1

Table S19. GO terms associated with PSGs identified on frog branch 1.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames
GO:2001046	3.76E-05	3	5	positive regulation of integrin-mediated signaling pathway	FLNA,DMTN,EMP2
GO:2001044	0.000469871	3	11	regulation of integrin-mediated signaling pathway	FLNA,DMTN,EMP2
GO:0032962	0.000606203	2	3	positive regulation of inositol trisphosphate biosynthetic process	GPER1,PLCD1
GO:0032571	0.000816288	2	3	response to vitamin K	F7,POSTN
GO:0006412	0.000859054	9	228	translation	MRPL47,RPL11,EIF2B3,ENSACAG00000015342,EEF2,ENSACAG00000009700,ABCF1,RPL15,ENSACAG00000004183
GO:0040038	0.001459864	2	3	polar body extrusion after meiotic divisions	FMN2,KIAA0196
GO:1900078	0.001712704	3	15	positive regulation of cellular response to insulin stimulus	ENSACAG00000002886,ADIPOR1,NUCKS1
GO:0051295	0.001731436	2	3	establishment of meiotic spindle localization	MYH9,FMN2
GO:0043534	0.001985744	3	16	blood vessel endothelial cell migration	MYH9,SCARB1,EMP2
GO:0030511	0.002140851	3	18	positive regulation of transforming growth factor beta receptor signaling pathway	HIPK2,NPNT,ADAM17
GO:0033206	0.002348464	2	4	meiotic cytokinesis	FMN2,KIAA0196
GO:0022618	0.00247669	9	199	ribonucleoprotein complex assembly	CIRBP,RPL11,PSIP1,DDX23,DDX6,SART1,ENSACAG00000004183,NUFIP1,ATXN2L
GO:0090407	0.002551013	13	377	organophosphate biosynthetic process	ATP6V0A1,PGS1,NADK2,TKT,GNPAT,IMPDH1,ADCY4,OCRL,RRM2B,GMDS,ABHD3,GP

					AA1,LPCAT1
GO:0071826	0.003247275	9	206	ribonucleoprotein complex subunit organization	CIRBP,RPL11,PSIP1,DDX23,DDX6,SART1,ENSACAG00000004183,NUFIP1,ATXN2L
GO:0015748	0.003387821	5	64	organophosphate ester transport	ATP11B,MFSD2A,ENSACAG00000015342,SCARB1,SLC37A4
GO:0044319	0.003395663	3	18	wound healing, spreading of cells	FLNA,ADAM17,COL5A1
GO:0033627	0.003998623	3	18	cell adhesion mediated by integrin	NPNT,ADAM17,ITGB1
GO:0045851	0.004463254	3	28	pH reduction	PPT1,ATP6V0A1,ATP6AP1
GO:1900024	0.004547265	4	41	regulation of substrate adhesion-dependent cell spreading	OLFM4,POSTN,FLNA,DMTN
GO:0032287	0.004559302	2	6	peripheral nervous system myelin maintenance	ENSACAG00000002886,NDRG1
GO:0035313	0.004572216	2	6	wound healing, spreading of epidermal cells	ADAM17,COL5A1
GO:0021942	0.004744206	2	7	radial glia guided migration of Purkinje cell	SOCS7,RERE
GO:1901998	0.006669428	3	26	toxin transport	RAB43,CCT3,DNM1
GO:1901264	0.007788427	3	31	carbohydrate derivative transport	MFSD2A,SCARB1,SLC37A4
GO:1901137	0.009585572	11	354	carbohydrate derivative biosynthetic process	BMPR2,ATP6V0A1,TYW5,B4GALT7,TKT,B3GAT2,IMPDH1,ADCY4,RRM2B,GMDS,GPAA1
GO:0034477	0.010289475	1	1	U6 snRNA 3'-end processing	USB1
GO:0031444	0.010641053	1	1	slow-twitch skeletal muscle fiber contraction	TNNT1
GO:0072027	0.010896985	1	1	connecting tubule development	CALB1
GO:0072286	0.010896985	1	1	metanephric connecting tubule development	CALB1
GO:0045056	0.011243956	2	11	transcytosis	MFSD2A,VPS35
GO:0035562	0.011756416	2	9	negative regulation of chromatin binding	FBXO18,BTAF1
GO:0030264	0.012385249	1	1	nuclear fragmentation involved in apoptotic nuclear change	GPER1
GO:2000724	0.012385249	1	1	positive regulation of cardiac vascular smooth muscle cell differentiation	GPER1
GO:0035585	0.013072474	1	1	calcium-mediated signaling using extracellular calcium source	DMTN
GO:1901731	0.013072474	1	1	positive regulation of platelet aggregation	DMTN
GO:0032640	0.0130884	1	1	tumor necrosis factor production	AZI2

GO:0015988	0.013160262	3	37	energy coupled proton transmembrane transport, against electrochemical gradient	ATP6V0A1,ATP6AP1,ATP6V1H
GO:0015991	0.013160262	3	37	ATP hydrolysis coupled proton transport	ATP6V0A1,ATP6AP1,ATP6V1H
GO:0006608	0.013617055	1	1	snRNP protein import into nucleus	NOP58
GO:0033595	0.013647369	1	1	response to genistein	F7
GO:0061476	0.013647369	1	1	response to anticoagulant	F7
GO:1904400	0.013647369	1	1	response to Thyroid stimulating hormone	F7
GO:1904612	0.013647369	1	1	response to 2,3,7,8-tetrachlorodibenzodioxine	F7
GO:0031270	0.013812611	1	1	pseudopodium retraction	SEPT7
GO:0018117	0.01415051	1	1	protein adenylylation	FICD
GO:0018175	0.01415051	1	1	protein nucleotidylation	FICD
GO:0007249	0.014272567	3	36	I-kappaB kinase/NF-kappaB signaling	RELB,AZI2,ENSACAG00000003867
GO:0031579	0.014796318	2	14	membrane raft organization	PPT1,EMP2
GO:0000212	0.014865765	2	9	meiotic spindle organization	MYH9,KIAA0196
GO:0006109	0.014867589	6	137	regulation of carbohydrate metabolic process	ENSACAG00000002886,AP2A1,PPP4R3A,ADIPOR1,GPER1,PLCD1
GO:0000481	0.014978143	1	1	maturation of 5S rRNA	SART1
GO:0045585	0.014978143	1	1	positive regulation of cytotoxic T cell differentiation	SART1
GO:0015920	0.015248734	1	1	lipopolysaccharide transport	SCARB1
GO:0060696	0.015248734	1	1	regulation of phospholipid catabolic process	SCARB1
GO:1902930	0.015298759	3	34	regulation of alcohol biosynthetic process	GPER1,PLCD1,LPCAT1
GO:0010954	0.01539396	2	15	positive regulation of protein processing	CLEC3B,CTNND1
GO:1990744	0.015648023	1	1	primary miRNA methylation	METTL3
GO:0036518	0.016028837	1	1	chemorepulsion of dopaminergic neuron axon	RYK
GO:0030308	0.016906835	6	137	negative regulation of cell growth	RYK,PPT1,BMPR2,SMARCA2,ADIPOR1,FOXK1
GO:0051764	0.01770704	2	11	actin crosslink formation	FLNA,DPYSL3
GO:0072044	0.017930786	2	13	collecting duct development	CALB1,DLG5
GO:0043402	0.018364415	1	1	glucocorticoid mediated signaling pathway	NR3C1
GO:0033025	0.019274816	1	1	regulation of mast cell apoptotic process	ADAM17

GO:0045987	0.020012869	2	16	positive regulation of smooth muscle contraction	NPNT,GPER1
GO:1904209	0.020265491	1	1	positive regulation of chemokine (C-C motif) ligand 2 secretion	POSTN
GO:1990523	0.020265491	1	1	bone regeneration	POSTN
GO:0030026	0.020622357	1	1	cellular manganese ion homeostasis	ATP2C1
GO:0032468	0.020622357	1	1	Golgi calcium ion homeostasis	ATP2C1
GO:0055071	0.020622357	1	1	manganese ion homeostasis	ATP2C1
GO:0060690	0.020687669	1	1	epithelial cell differentiation involved in salivary gland development	CTNND1
GO:0008360	0.020883865	6	130	regulation of cell shape	SEPT7,MYH9,PLXNB2,FN1,TTBK1,DMTN
GO:0006954	0.021233505	9	279	inflammatory response	PTX3,FN1,RELB,STAB1,ITIH4,ABCF1,GPER1,IL1RAP,NFATC3
GO:0070482	0.021706357	7	190	response to oxygen levels	ALDOA,HIPK2,F7,POSTN,ADAM17,FMN2,PLCD1
GO:0010501	0.021757271	3	36	RNA secondary structure unwinding	DDX23,DDX6,DDX55
GO:0071277	0.021768614	3	39	cellular response to calcium ion	ENSACAG00000015342,FUS,DMTN
GO:2001108	0.02184223	1	1	positive regulation of Rho guanyl-nucleotide exchange factor activity	EPHA4
GO:0031590	0.022642723	1	2	wybutosine metabolic process	TYW5
GO:0031591	0.022642723	1	2	wybutosine biosynthetic process	TYW5
GO:0043966	0.02299676	3	35	histone H3 acetylation	BRPF1,TAF10,BRD1
GO:0051977	0.023311183	1	2	lysophospholipid transport	MFSD2A
GO:0048254	0.023341121	1	2	snoRNA localization	NOP58
GO:0010748	0.02364092	1	2	negative regulation of plasma membrane long-chain fatty acid transport	ENSACAG00000002886
GO:0006741	0.023819554	1	2	NADP biosynthetic process	NADK2
GO:0042351	0.024097332	1	2	'de novo' GDP-L-fucose biosynthetic process	GMDS
GO:1903898	0.024111357	1	2	negative regulation of PERK-mediated unfolded protein response	PPP1R15B
GO:0034384	0.024525735	1	2	high-density lipoprotein particle clearance	SCARB1
GO:0010641	0.024751965	1	2	positive regulation of platelet-derived growth factor receptor signaling pathway	F7

GO:1901301	0.025031914	1	1	regulation of cargo loading into COPII-coated vesicle	SEC24B
GO:0070560	0.025477356	1	2	protein secretion by platelet	DMTN
GO:0097066	0.025524225	2	16	response to thyroid hormone	COL1A2,F7
GO:0035561	0.025599428	2	15	regulation of chromatin binding	FBXO18,BTAF1
GO:0046166	0.026874237	1	2	glyceraldehyde-3-phosphate biosynthetic process	TKT
GO:0097274	0.026931219	1	2	urea homeostasis	ENSACAG00000015342
GO:0045742	0.027028995	2	18	positive regulation of epidermal growth factor receptor signaling pathway	ADAM17,GPER1
GO:0015917	0.027262047	1	1	aminophospholipid transport	ATP11B
GO:0051758	0.027761935	1	1	homologous chromosome movement towards spindle pole involved in homologous chromosome segregation	FMN2
GO:0097195	0.028345821	1	2	pilomotor reflex	NPNT
GO:0035234	0.028394703	1	3	ectopic germ cell programmed cell death	ENSACAG00000013588
GO:0035338	0.028518466	2	19	long-chain fatty-acyl-CoA biosynthetic process	ELOVL5,THEM5
GO:0023035	0.029057064	1	2	CD40 signaling pathway	ENSACAG00000003867
GO:0072602	0.029843103	1	2	interleukin-4 secretion	IL1RAP
GO:0045112	0.029897774	1	1	integrin biosynthetic process	COL5A1
GO:1990379	0.029946443	1	2	lipid transport across blood brain barrier	MFSD2A
GO:0097068	0.029959964	1	2	response to thyroxine	F7
GO:1904871	0.03041099	1	2	positive regulation of protein localization to Cajal body	CCT3
GO:0045186	0.030414158	1	1	zonula adherens assembly	DLG5
GO:0044565	0.03061195	1	2	dendritic cell proliferation	AZI2
GO:0071470	0.030627759	2	20	cellular response to osmotic stress	RELB,XRCC5
GO:0070269	0.030967899	1	2	pyroptosis	ENSACAG00000013588
GO:0035461	0.031072629	1	2	vitamin transmembrane transport	SCARB1
GO:0001935	0.031123148	2	17	endothelial cell proliferation	BMPR2,SCARB1
GO:2000767	0.031207632	1	2	positive regulation of cytoplasmic translation	METTL3
GO:0016476	0.031377003	1	2	regulation of embryonic cell shape	7-Sep
GO:0010044	0.032014542	1	2	response to aluminum ion	PLCD1
GO:0006543	0.032077718	1	2	glutamine catabolic process	GLS

GO:0048213	0.032107282	1	2	Golgi vesicle prefusion complex stabilization	COG4
GO:1902893	0.032194582	2	18	regulation of pri-miRNA transcription from RNA polymerase II promoter	GNL3,NFATC3
GO:0061640	0.032305756	3	38	cytoskeleton-dependent cytokinesis	SEPT7,FMN2,KIAA0196
GO:0060668	0.032315277	1	2	regulation of branching involved in salivary gland morphogenesis by extracellular matrix-epithelial cell signaling	NTN4
GO:0055094	0.032345716	2	17	response to lipoprotein particle	ADAM17,ITGB1
GO:1903525	0.033108967	1	2	regulation of membrane tubulation	ENSACAG00000013675
GO:2000104	0.033280918	2	15	negative regulation of DNA-dependent DNA replication	FBXO18,SMC1A
GO:0032472	0.033347895	1	2	Golgi calcium ion transport	ATP2C1
GO:0097028	0.033653771	2	21	dendritic cell differentiation	RELB,AZI2
GO:0021747	0.033954692	1	2	cochlear nucleus development	SEC24B
GO:1903015	0.034025263	1	3	regulation of exo-alpha-sialidase activity	PTX3
GO:0001913	0.034283887	1	3	T cell mediated cytotoxicity	EMP2
GO:0071167	0.034331427	1	2	ribonucleoprotein complex import into nucleus	NOP58
GO:0098602	0.034513415	10	319	single organism cell adhesion	MYH9,NPNT,FLNA,CTNND1,RELB,ADAM17,AZI2,VCL,PVRL1,DLG5
GO:0010701	0.035263999	1	3	positive regulation of norepinephrine secretion	PLCD1
GO:0055099	0.035866364	1	2	response to high density lipoprotein particle	ADAM17
GO:0007015	0.035962945	7	200	actin filament organization	FLNA,DPYSL3,LMOD3,FMN2,DMTN,EMP2,ENSACAG00000000923
GO:1904706	0.036361608	1	4	negative regulation of vascular smooth muscle cell proliferation	GPER1
GO:0010710	0.036649815	1	2	regulation of collagen catabolic process	ITGB1
GO:0034696	0.037277611	1	3	response to prostaglandin F	PLCD1
GO:0008610	0.037695969	11	435	lipid biosynthetic process	HMGCR,PTGES3,PGS1,ELOVL5,TKT,GNPAT,OCRL,SCARB1,ABHD3,GPAA1,LPCAT1
GO:0009108	0.038115226	4	98	coenzyme biosynthetic process	PCBD2,NADK2,ELOVL5,THEM5
GO:0010037	0.038200347	1	2	response to carbon dioxide	F7
GO:0030578	0.039176671	1	2	PML body organization	HIPK2

GO:0090382	0.039435404	1	4	phagosome maturation	RAB43
GO:0046368	0.039459681	1	3	GDP-L-fucose metabolic process	GMDS
GO:1903919	0.039746457	1	2	negative regulation of actin filament severing	MYH9
GO:0070542	0.039827825	3	49	response to fatty acid	GNPAT,PLCD1,XRCC5
GO:0022613	0.040070022	3	54	ribonucleoprotein complex biogenesis	GNL3,LSG1,RPLP0
GO:0006953	0.040655034	2	22	acute-phase response	FN1,ITIH4
GO:0023016	0.041018197	1	2	signal transduction by trans-phosphorylation	WNK1
GO:0001974	0.041549998	2	19	blood vessel remodeling	BMPR2,FLNA
GO:0044359	0.043457407	1	4	modulation of molecular function in other organism	PTX3
GO:0006029	0.044318875	3	51	proteoglycan metabolic process	BMPR2,B4GALT7,B3GAT2
GO:0032796	0.044343174	1	2	uropod organization	MYH9
GO:1904953	0.044402634	1	2	Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation	RYK
GO:0051262	0.044472896	4	87	protein tetramerization	ALDOA,FARSA,GLS,DNM1
GO:0001666	0.044693209	6	177	response to hypoxia	ALDOA,HIPK2,F7,POSTN,ADAM17,FMN2
GO:0003252	0.044771946	1	2	negative regulation of cell proliferation involved in heart valve morphogenesis	BMPR2
GO:0045906	0.044771946	1	2	negative regulation of vasoconstriction	BMPR2
GO:0071873	0.044951615	1	2	response to norepinephrine	COL1A2
GO:0060856	0.045242575	1	3	establishment of blood-brain barrier	MFSD2A
GO:0072429	0.045335506	1	3	response to intra-S DNA damage checkpoint signaling	FBXO18
GO:0006432	0.045365613	1	3	phenylalanyl-tRNA aminoacylation	FARSA
GO:1904816	0.045624719	1	3	positive regulation of protein localization to chromosome, telomeric region	GNL3
GO:0016578	0.045897499	2	19	histone deubiquitination	BRCC3,TAF10
GO:0019853	0.046439574	1	4	L-ascorbic acid biosynthetic process	RGN
GO:0006123	0.046787883	1	6	mitochondrial electron transport, cytochrome c to oxygen	COX4I1
GO:2001206	0.046900259	1	4	positive regulation of osteoclast development	ATP6AP1
GO:0070537	0.047032898	1	3	histone H2A K63-linked deubiquitination	BRCC3
GO:0071918	0.047061102	1	4	urea transmembrane transport	AQP3

GO:0021691	0.047143182	1	2	cerebellar Purkinje cell layer maturation	RERE
GO:0005996	0.047193646	5	131	monosaccharide metabolic process	ENSACAG00000002886,RGN,MAN2C1,ENSACAG00000003255,SLC37A4
GO:1904059	0.048146074	1	2	regulation of locomotor rhythm	ZFHX3
GO:0000354	0.04831298	1	2	cis assembly of pre-catalytic spliceosome	DDX23
GO:0070508	0.048489864	1	4	cholesterol import	SCARB1
GO:0061357	0.048612238	1	3	positive regulation of Wnt protein secretion	VPS35
GO:0032543	0.048946128	2	32	mitochondrial translation	MRPL47,ENSACAG00000009700

Table S20. PSGs identified on branch 1 of lizard.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000002137	ENSACAG00000002143	ENSACAT00000002196	L3MBTL1
ENSACAP00000015439	ENSACAG00000015714	ENSACAT00000015753	MFI2
ENSACAP00000016336	ENSACAG00000016618	ENSACAT00000016660	PROSER3
ENSACAP00000012717	ENSACAG00000012949	ENSACAT00000012973	RAC1
ENSACAP00000007383	ENSACAG00000007428	ENSACAT00000007539	STX1B
ENSACAP00000015377	ENSACAG00000015642	ENSACAT00000015690	C4orf27
ENSACAP00000008811	ENSACAG00000009002	ENSACAT00000009000	DSCC1
ENSACAP00000017566	ENSACAG00000017840	ENSACAT00000017912	SYTL1
ENSACAP00000007133	ENSACAG00000007296	ENSACAT00000007288	MPZL2
ENSACAP00000005828	ENSACAG00000005562	ENSACAT00000005957	PFKM
ENSACAP00000003300	ENSACAG00000003345	ENSACAT00000003383	EPC2
ENSACAP00000017808	ENSACAG00000014871	ENSACAT00000021009	
ENSACAP00000014476	ENSACAG00000014759	ENSACAT00000014771	SNCG
ENSACAP00000004419	ENSACAG00000004481	ENSACAT00000004519	MTO1
ENSACAP00000011033	ENSACAG00000011006	ENSACAT00000011261	
ENSACAP00000003616	ENSACAG00000003671	ENSACAT00000003704	RAD54B
ENSACAP00000012671	ENSACAG00000012853	ENSACAT00000012927	TUBD1
ENSACAP00000010262	ENSACAG00000010440	ENSACAT00000010474	NBN

ENSACAP00000006530	ENSACAG00000006669	ENSACAT00000006675	CEP164
ENSACAP00000011352	ENSACAG00000011361	ENSACAT00000011591	MAPK8
ENSACAP00000001731	ENSACAG00000001829	ENSACAT00000001771	CPLX1
ENSACAP00000014202	ENSACAG00000014417	ENSACAT00000014493	SLC40A1
ENSACAP00000007473	ENSACAG00000007570	ENSACAT00000007630	KIFC3
ENSACAP00000007083	ENSACAG00000007141	ENSACAT00000007236	WDR36
ENSACAP00000013980	ENSACAG00000014244	ENSACAT00000014266	ELK4
ENSACAP00000011565	ENSACAG00000011593	ENSACAT00000011805	RPN2
ENSACAP00000020020	ENSACAG00000023926	ENSACAT00000025106	
ENSACAP00000002341	ENSACAG00000002418	ENSACAT00000002401	FAM98C
ENSACAP00000004433	ENSACAG00000004543	ENSACAT00000004533	TSTD2
ENSACAP00000016972	ENSACAG00000017247	ENSACAT00000017307	CCHCR1
ENSACAP00000015181	ENSACAG00000015394	ENSACAT00000015488	PEX1
ENSACAP00000006087	ENSACAG00000006163	ENSACAT00000006224	
ENSACAP00000017400	ENSACAG00000017657	ENSACAT00000017741	
ENSACAP00000020398	ENSACAG00000024242	ENSACAT00000024602	
ENSACAP00000000025	ENSACAG00000000026	ENSACAT00000000026	RAD52
ENSACAP00000002621	ENSACAG00000002580	ENSACAT00000002687	CAPN7
ENSACAP00000002239	ENSACAG00000002353	ENSACAT00000002299	
ENSACAP00000022859	ENSACAG00000028815	ENSACAT00000030277	
ENSACAP00000016459	ENSACAG00000016741	ENSACAT00000016784	RPRML
ENSACAP00000002072	ENSACAG00000002150	ENSACAT00000002126	NSUN4
ENSACAP00000018329	ENSACAG00000023921	ENSACAT00000023397	
ENSACAP00000017296	ENSACAG00000017564	ENSACAT00000017636	LHPP
ENSACAP00000022870	ENSACAG00000017206	ENSACAT00000030288	FGFR2
ENSACAP00000016763	ENSACAG00000017032	ENSACAT00000017093	BAG3
ENSACAP00000001618	ENSACAG00000001636	ENSACAT00000001657	RPAP3
ENSACAP00000005847	ENSACAG00000005931	ENSACAT00000005976	IRF6
ENSACAP00000011603	ENSACAG00000011834	ENSACAT00000011843	GTPBP6
ENSACAP00000001539	ENSACAG00000001584	ENSACAT00000001575	PRPS2

ENSACAP00000007616	ENSACAG00000007783	ENSACAT00000007777	GTSE1
ENSACAP00000009396	ENSACAG00000009601	ENSACAT00000009591	SRD5A3
ENSACAP00000009059	ENSACAG00000009242	ENSACAT00000009252	
ENSACAP00000008781	ENSACAG00000008899	ENSACAT00000008969	
ENSACAP00000010959	ENSACAG00000011160	ENSACAT00000011187	XRCC4
ENSACAP00000008989	ENSACAG00000008993	ENSACAT00000009182	TRPM3
ENSACAP00000000826	ENSACAG00000000931	ENSACAT00000000852	SMC5
ENSACAP00000003853	ENSACAG00000003966	ENSACAT00000003945	PLGRKT
ENSACAP00000013191	ENSACAG00000013313	ENSACAT00000013455	AGAP2
ENSACAP00000003931	ENSACAG00000004053	ENSACAT00000004023	PPP4R4
ENSACAP00000003757	ENSACAG00000003860	ENSACAT00000003849	ZNF408
ENSACAP00000022884	ENSACAG00000028675	ENSACAT00000030302	TRIM44
ENSACAP00000015058	ENSACAG00000015300	ENSACAT00000015362	SLC38A10
ENSACAP00000016415	ENSACAG00000016662	ENSACAT00000016740	PGS1
ENSACAP00000019694	ENSACAG00000017681	ENSACAT00000025897	MFSD6L
ENSACAP00000001956	ENSACAG00000001934	ENSACAT00000002002	ZRANB3
ENSACAP00000021468	ENSACAG00000022559	ENSACAT00000024525	
ENSACAP00000012005	ENSACAG00000012175	ENSACAT00000012250	FNIP1
ENSACAP00000018017	ENSACAG00000022125	ENSACAT00000025587	
ENSACAP00000005109	ENSACAG00000005146	ENSACAT00000005225	MCM3
ENSACAP00000011380	ENSACAG00000011645	ENSACAT00000011619	C2orf44
ENSACAP00000010301	ENSACAG00000010498	ENSACAT00000010513	COQ3
ENSACAP00000013721	ENSACAG00000013992	ENSACAT00000014002	CHST13
ENSACAP00000010691	ENSACAG00000010800	ENSACAT00000010912	ATAT1

Table S21. GO terms associated with PSGs identified on lizard branch 1.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames
GO:0006281	4.33E-05	9	416	DNA repair	RAD52,ENSACAG00000008899,XRCC4,SMC

					5,ZRANB3,EPC2,RAD54B,NBN,CEP164
GO:0010756	0.000117492	2	5	positive regulation of plasminogen activation	PLGRKT,MFI2
GO:0060249	0.000362269	5	154	anatomical structure homeostasis	SMC5,RAC1,PFKM,NBN,WDR36
GO:0000726	0.000504308	3	36	non-recombinational repair	RAD52,XRCC4,NBN
GO:0071260	0.000701814	3	46	cellular response to mechanical stimulus	BAG3,RAC1,MAPK8
GO:0090329	0.000715345	3	41	regulation of DNA-dependent DNA replication	ZRANB3,DSCC1,NBN
GO:0032707	0.002512592	1	1	negative regulation of interleukin-23 production	RAC1
GO:0045002	0.002601058	1	1	double-strand break repair via single-strand annealing	RAD52
GO:0009877	0.003142512	1	1	nodulation	COQ3
GO:0010795	0.003142512	1	1	regulation of ubiquinone biosynthetic process	COQ3
GO:1905302	0.003242383	1	1	negative regulation of macropinocytosis	STX1B
GO:0010165	0.003392055	2	23	response to X-ray	ENSACAG00000008899,XRCC4
GO:0036031	0.003434285	1	2	recruitment of mRNA capping enzyme to RNA polymerase II holoenzyme complex	ENSACAG00000023921
GO:0016095	0.003480589	1	1	polyprenol catabolic process	SRD5A3
GO:0006789	0.004477313	1	1	bilirubin conjugation	ENSACAG00000022125
GO:0070980	0.004477313	1	1	biphenyl catabolic process	ENSACAG00000022125
GO:0034395	0.004620218	1	1	regulation of transcription from RNA polymerase II promoter in response to iron	SLC40A1
GO:0060345	0.004620218	1	1	spleen trabecula formation	SLC40A1
GO:1903988	0.004620218	1	1	ferrous iron export	SLC40A1
GO:0070899	0.004800792	1	1	mitochondrial tRNA wobble uridine modification	MTO1
GO:1904527	0.00486269	1	1	negative regulation of microtubule binding	GTSE1
GO:0021894	0.004921485	1	2	cerebral cortex GABAergic interneuron development	RAC1
GO:0093001	0.004922472	1	1	glycolysis from storage polysaccharide through glucose-1-phosphate	PFKM
GO:0036292	0.005033754	1	1	DNA rewinding	ZRANB3
GO:0032259	0.006264961	4	186	methylation	NSUN4,ENSACAG00000023921,COQ3,MTO1
GO:0006826	0.006440195	2	33	iron ion transport	MFI2,SLC40A1
GO:0002551	0.006717719	1	2	mast cell chemotaxis	RAC1

GO:0043687	0.006782741	2	31	post-translational protein modification	ENSACAG00000009242,DSCC1
GO:0033037	0.007241434	1	2	polysaccharide localization	CHST13
GO:0060025	0.007498225	1	2	regulation of synaptic activity	STX1B
GO:1904224	0.007684283	1	2	negative regulation of glucuronosyltransferase activity	ENSACAG00000022125
GO:2001030	0.007684283	1	2	negative regulation of cellular glucuronidation	ENSACAG00000022125
GO:0080163	0.007731222	1	2	regulation of protein serine/threonine phosphatase activity	PPP4R4
GO:0003158	0.008328068	1	2	endothelium development	SLC40A1
GO:0006473	0.008696978	3	102	protein acetylation	ATAT1,DSCC1,EPC2
GO:0023061	0.008883536	3	112	signal release	STX1B,SYTL1,CPLX1
GO:0007258	0.008895522	1	2	JUN phosphorylation	MAPK8
GO:0060151	0.008934931	1	2	peroxisome localization	PEX1
GO:0060152	0.008934931	1	2	microtubule-based peroxisome localization	PEX1
GO:0051552	0.00938926	1	2	flavone metabolic process	ENSACAG00000022125
GO:0032392	0.009401059	2	34	DNA geometric change	ZRANB3,NBN
GO:0006015	0.00993461	1	3	5-phosphoribose 1-diphosphate biosynthetic process	PRPS2
GO:0046391	0.00993461	1	3	5-phosphoribose 1-diphosphate metabolic process	PRPS2
GO:0033601	0.010048738	1	2	positive regulation of mammary gland epithelial cell proliferation	AGAP2
GO:0006836	0.010401326	3	110	neurotransmitter transport	STX1B,SYTL1,CPLX1
GO:0051052	0.010984957	5	326	regulation of DNA metabolic process	ENSACAG00000008899,ZRANB3,RAC1,DSCC1,NBN
GO:0075713	0.011352097	1	3	establishment of integrated proviral latency	XRCC4
GO:1900024	0.011514351	2	41	regulation of substrate adhesion-dependent cell spreading	MFI2,RAC1
GO:0043652	0.012077454	1	4	engulfment of apoptotic cell	RAC1
GO:0002093	0.012305086	1	3	auditory receptor cell morphogenesis	RAC1
GO:0034086	0.012393217	1	3	maintenance of sister chromatid cohesion	DSCC1
GO:0034088	0.012393217	1	3	maintenance of mitotic sister chromatid cohesion	DSCC1
GO:0061669	0.013258988	1	3	spontaneous neurotransmitter secretion	STX1B
GO:0010822	0.013303175	2	53	positive regulation of mitochondrion organization	NSUN4,MAPK8
GO:0042167	0.013308553	1	4	heme catabolic process	ENSACAG00000022125

GO:0097286	0.013768681	1	3	iron ion import	MFI2
GO:0051932	0.014837425	1	4	synaptic transmission, GABAergic	RAC1
GO:0021826	0.01506116	1	5	substrate-independent telencephalic tangential migration	RAC1
GO:0030330	0.01567673	2	50	DNA damage response, signal transduction by p53 class mediator	GTSE1,NBN
GO:0043543	0.016402067	3	132	protein acylation	ATAT1,DSCC1,EPC2
GO:0042178	0.0173593	1	5	xenobiotic catabolic process	ENSACAG00000022125
GO:0001510	0.017546879	2	51	RNA methylation	NSUN4,MTO1
GO:0031100	0.01771596	2	59	animal organ regeneration	PRPS2,ENSACAG00000022125
GO:0010835	0.018317028	1	5	regulation of protein ADP-ribosylation	C4orf27
GO:0071139	0.018741224	1	4	resolution of recombination intermediates	SMC5
GO:0042256	0.019734795	1	5	mature ribosome assembly	NSUN4
GO:0016093	0.02090815	1	7	polyprenol metabolic process	SRD5A3
GO:0006167	0.022041989	1	6	AMP biosynthetic process	PRPS2
GO:0042770	0.022810584	2	60	signal transduction in response to DNA damage	GTSE1,NBN
GO:0009612	0.023537369	3	154	response to mechanical stimulus	BAG3,RAC1,MAPK8
GO:0016558	0.023758909	1	6	protein import into peroxisome matrix	PEX1
GO:0055072	0.023899385	2	62	iron ion homeostasis	MFI2,SLC40A1
GO:0090045	0.023945129	1	6	positive regulation of deacetylase activity	MAPK8
GO:0033015	0.02403488	1	7	tetrapyrrole catabolic process	ENSACAG00000022125
GO:0046149	0.02403488	1	7	pigment catabolic process	ENSACAG00000022125
GO:0038095	0.025002251	2	82	Fc-epsilon receptor signaling pathway	ENSACAG00000024242,MAPK8
GO:0051276	0.025479054	4	271	chromosome organization	SMC5,ZRANB3,DSCC1,NBN
GO:0045217	0.025987468	1	6	cell-cell junction maintenance	KIFC3
GO:0032049	0.026152347	1	7	cardiolipin biosynthetic process	PGS1
GO:0060263	0.026331094	1	8	regulation of respiratory burst	RAC1
GO:0006002	0.026755447	1	6	fructose 6-phosphate metabolic process	PFKM
GO:0008300	0.026783044	1	7	isoprenoid catabolic process	SRD5A3
GO:0001832	0.027297657	1	6	blastocyst growth	NBN
GO:0051103	0.029795898	1	7	DNA ligation involved in DNA repair	XRCC4

GO:0050951	0.029862947	1	7	sensory perception of temperature stimulus	TRPM3
GO:0009812	0.030953321	1	8	flavonoid metabolic process	ENSACAG00000022125
GO:0045876	0.031084725	1	7	positive regulation of sister chromatid cohesion	SMC5
GO:0006063	0.032734971	1	8	uronic acid metabolic process	ENSACAG00000022125
GO:0018879	0.03345997	1	8	biphenyl metabolic process	ENSACAG00000022125
GO:0006906	0.033796206	2	84	vesicle fusion	STX1B,SYTL1
GO:0014041	0.033813888	1	9	regulation of neuron maturation	RAC1
GO:0000041	0.034366301	2	77	transition metal ion transport	MFI2,SLC40A1
GO:0016925	0.034988255	2	68	protein sumoylation	XRCC4,SMC5
GO:0009312	0.035323968	1	11	oligosaccharide biosynthetic process	COQ3
GO:0090091	0.035763585	1	8	positive regulation of extracellular matrix disassembly	MFI2
GO:0097264	0.036289876	1	9	self proteolysis	CAPN7
GO:0006266	0.036504524	1	9	DNA ligation	XRCC4
GO:0043574	0.036595463	1	10	peroxisomal transport	PEX1
GO:0097178	0.036782668	1	11	ruffle assembly	RAC1
GO:0070525	0.03709151	1	9	tRNA threonylcarbamoyladenosine metabolic process	MTO1
GO:1903749	0.037218686	1	11	positive regulation of establishment of protein localization to mitochondrion	MAPK8
GO:0010664	0.037284084	1	9	negative regulation of striated muscle cell apoptotic process	BAG3
GO:0070932	0.037835751	1	9	histone H3 deacetylation	ELK4
GO:0071496	0.038289316	3	194	cellular response to external stimulus	BAG3,RAC1,MAPK8
GO:0051187	0.040477435	1	12	cofactor catabolic process	ENSACAG00000022125
GO:0072331	0.041977356	2	87	signal transduction by p53 class mediator	GTSE1,NBN
GO:0046339	0.04325344	1	11	diacylglycerol metabolic process	PGS1
GO:0042573	0.043420339	1	11	retinoic acid metabolic process	ENSACAG00000022125
GO:0031099	0.044196754	2	95	regeneration	PRPS2,ENSACAG00000022125
GO:0010592	0.04557161	1	13	positive regulation of lamellipodium assembly	RAC1
GO:0006972	0.048259431	1	14	hyperosmotic response	RAC1
GO:0006007	0.048545852	1	11	glucose catabolic process	PFKM

GO:0016048	0.048782934	1	12	detection of temperature stimulus	TRPM3
GO:0046033	0.048795883	1	14	AMP metabolic process	PRPS2
GO:0071361	0.049161505	1	12	cellular response to ethanol	ENSACAG00000022125
GO:0002097	0.049515438	1	13	tRNA wobble base modification	MTO1

Table S22. Categories showed continuous evolution with the elevation increasing in frogs.

category	**pvalue**	**numDEInCat**	**numInCat**	**term**	***N. phrynoides***	***N. liebigii***	***N. parkeri***
GO:0022618	4.40E-05	22	199	ribonucleoprotein complex assembly	CIRBP,RPL11,PSIP1,DDX23,DDX6,SART1,ENSACAG00000004183,NUFIP1,ATXN2L	ENSACAG00000017034,SRPK3,EIF3H,MRPL20,NUFIP1	YTHDC1,ABT1,LUC7L3,MDN1,RPS5,SART1,ATXN2,ENSACAG00000010260,SFSWAP,TGS1
GO:0043122	0.0450509	14	190	regulation of I-kappaB kinase/NF-kappaB signaling	ATP2C1,OLFM4,FLNA,ENSACAG00000003867	SPHK1,ZFAND6,RIPK1,NLRX1,ENSACAG00000025660	IRAK4,TRAF6,CANT1,MUL1,TNFAIP3,ENSACAG00000003867
GO:0051169	0.0033935	18	188	nuclear transport	RSRC1,NOP58,HTATIP2,ENSACAG00000013788,ENSACAG00000026588,LSG1	IPO9,HTATIP2,TNPO3,NUP93	NSRP1,ENSACAG00000002091,NUP85,HTATIP2,RBMX2,THOC5,NOC2L,TPR,NUP107,TGS1
GO:0006366	0.0054727	17	185	transcription from RNA polymerase II promoter	BMPR2,GTF2A1,NFIX,NR3C1,ZFHX3,NFATC3	ATF4,RPRD2,INTS9,ENSACAG00000014561,NMI	ENSACAG00000009269,MBD1,ABT1,GATA1,AFF4,SUPT5H
GO:0006913	0.0065337	17	185	nucleocytoplasmic transport	RSRC1,NOP58,HTATIP2,ENSACAG00000013788,ENSACAG00000026588,LSG1	IPO9,HTATIP2,TNPO3,NUP93	NSRP1,ENSACAG00000002091,NUP85,HTATIP2,RBMX2,THOC5,TPR,NUP107,TGS1
GO:0045926	0.016445	15	183	negative regulation of growth	RYK,PPT1,BMPR2,SMARCA2,ADIPOR1,FOXK1	SEMA3D,LGMN,RTN4	DNAJC2,SEMA4D,LGMN,IDH3G,MUL1,ATXN2,SAV1
GO:0016485	0.002285	17	182	protein processing	CPN1,F7,PDCD2	BCL2L13,ATP6AP2,ADAMTS3,LGMN,HM13,A	XPNPEP3,CLN5,FGG,LGMN,ENSACAG000000

						FG3L2,AEBP1,LONP2	06462,MUL1,TMEM208
GO:0022411	0.0152713	15	175	cellular component disassembly	ENSACAG00000009700	HPN,NUP93,VILL	MMP19,HSPG2,CDK5RAP3,ENSACAG00000017760,MTIF2,STMN1,C12orf65,TPR,NUP107,MRPL48,FLOT1
GO:0006457	0.0005765	17	168	protein folding	FKBP10,ENSACAG00000003016	FKBP9,TBCD,CRTAP,PPIF,FKBP15	PPIL2,PDIA4,ENSACAG00000002091,FKBP4,PRDX4,HSPH1,CCT4,ENSACAG00000017064,TBCE,PDIA3
GO:0016072	0.0105773	14	168	rRNA metabolic process	UTP6,NOP58,DIS3,SART1,NOP56	WDR3,CHD7,WDR36	UTP20,MDN1,RPS5,DIEXF,RPL13A,WDR3,SART1,NOP56,CIRH1A
GO:0008654	0.0020123	16	162	phospholipid biosynthetic process	PGS1,GNPAT,OCRL,ABHD3,GPAA1,LPCAT1	ETNK1,PIGX,CHKA,GGPS1,LPCAT3	PIGX,LPCAT4,PCYT1A,PLA2G6,IMPA1,ENSACAG00000003142
GO:0043009	0.0372336	13	154	chordate embryonic development	MYH9,OCRL	IFITM5,MGAT1,RXRA,ACVR1,HINFP	EPN1,MYH9,ADD1,GATA1,SIN3A,STIL,MYO1E
GO:0010810	0.008138	14	143	regulation of cell-substrate adhesion	NPNT,OLFM4,POSTN,FLNA,DMTN,EMP2	PTN,TBCD,COL16A1,ENSACAG00000015364	FGG,VEGFA,ENSACAG00000009367,ENSACAG00000015364,MEN1
GO:0006109	0.007111	13	137	regulation of carbohydrate metabolic process	ENSACAG00000002886,AP2A1,PPP4R3A,ADIPOR1,GPER1,PLCD1	SIRT6,ENSACAG00000024726	ENSACAG00000002091,PRKAA1,ENSACAG00000022125,CLK2,ENSACAG00000009367
GO:0000377	0.0456563	11	135	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RSRC1,DHX15,DDX23,METTL3,SART1	ENSACAG00000017034,PNN	SNRPB2,RBMX2,SART1,DHX9,SFSWAP
GO:0000398	0.0456563	11	135	mRNA splicing, via spliceosome	RSRC1,DHX15,DDX23,METTL3,SART1	ENSACAG00000017034,PNN	SNRPB2,RBMX2,SART1,DHX9,SFSWAP

GO:0005996	0.0382534	11	131	monosaccharide metabolic process	ENSACAG00000002886,RGN,MAN2C1,SLC37A4	TKFC,ATF4	PRKAA1,ENSACAG00000022125,ENSACAG00000003913,H6PD,PGM2L1
GO:0008360	0.0001382	17	130	regulation of cell shape	SEPT7,MYH9,PLXNB2,FN1,TTBK1,DMTN	PTN,TTBK2,EZR,HPN,VILL	FGD4,MYH9,SEMA4D,ANXA1,SYNE3,BAIAP2,EZR,RHOU
GO:0032846	0.0407951	11	130	positive regulation of homeostatic process	ATP6AP1,GNL3,GPER1,CCT3	PPP3CB	ENSACAG00000009269,GATA1,CCT4,STX4,PLA2G6,THY1
GO:0009451	0.0171136	11	122	RNA modification	NOP58,TYW5,METTL3,NOP56	HEMK1,TXNDC9,TRIT1	TYW5,TRMT61B,THUMPD3,MOCS3,NOP56,TGS1
GO:0051188	0.0011589	13	120	cofactor biosynthetic process	PCBD2,NADK2,ELOVL5,THEM5	AGK,KMO,ENSACAG00000016077,ALAS1	COX15,COQ2,COASY,MAT2B,MOCS3
GO:0043627	0.034995	10	115	response to estrogen	ALDOA,F7,POSTN,GPER1	PTN,ENSACAG00000015364,MAPK15,PTGFR	MBD1,ENSACAG00000022125,ENSACAG00000015364,PTGFR
GO:0034976	0.0125641	11	112	response to endoplasmic reticulum stress	PPP1R15B,ENSACAG00000003016	ATF4,SEL1L,ATF6B,UBE4B	PDIA4,PPP1R15B,CDK5RAP3,PDIA3,PLA2G6,FLOT1
GO:0017038	0.0261176	10	108	protein import	NOP58	IPO9,AFG3L2,TNPO3,NUP93,LONP2	ENSACAG00000002091,NUP85,TPR,NUP107
GO:0009411	0.0389707	9	102	response to UV	CIRBP	PTN,ATF4,XPC,UBE4B	PRKAA1,NOC2L,MAPK8,MEN1
GO:1903708	0.0314611	9	98	positive regulation of hemopoiesis	ATP6AP1,PDCD2,SART1	RIPK1	GAS6,ENSACAG00000009269,ANXA1,GATA1,TRAF6,SART1
GO:0007051	0.0280914	10	96	spindle organization	MYH9,FLNA,CKAP5,KIAA0196	EZR,ENSACAG00000001869	MYH9,EZR,STIL,STMN1,NDC80,CEP120
GO:0044085	0.0079662	9	89	cellular component biogenesis	GNL3,LSG1,RPLP0	IPO9,COX19	COA1,NDUFAF4,NOC2L,TGS1
GO:0051262	0.0062233	10	87	protein tetramerization	ALDOA,FARSA,GLS,DNM1	RXRA,HM13	SAMHD1,TK1,ACADL,NRXN1

GO:0006413	0.005323	9	86	translational initiation	ABCF1	PAIP1,EIF3H	RPS5,MTIF2,RPL13A,ENSACAG00000004291,ENSACAG00000010260,MRPS18A
GO:0046165	0.0031463	10	80	alcohol biosynthetic process	HMGCR,ABHD3	CHKA,SPHK1,GGPS1	PRKAA1,DPAGT1,PCYT1A,IMPA1,ENSACAG00000003142
GO:0032355	0.0200504	8	77	response to estradiol	F7,POSTN,GPER1	PTN,MAPK15,PTGFR	MBD1,ENSACAG00000022125,PTGFR
GO:0050731	0.0235817	8	76	positive regulation of peptidyl-tyrosine phosphorylation	CTNND1,ADAM17	CTNND1	SRCIN1,GAS6,HSPH1,SEMA4D,GATA1,CTNND1,VEGFA
GO:0090100	0.0056596	9	74	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	HIPK2,BMPR2,NPNT,ADAM17	BMP4,NEO1,NUP93	SDCBP,MEN1
GO:0043255	0.0060655	9	74	regulation of carbohydrate biosynthetic process	ENSACAG00000002886,AP2A1,PPP4R3A,GPER1,PLCD1	ENSACAG00000024726	ENSACAG00000002091,CLK2,ENSACAG00000009367
GO:0050806	0.047133	7	71	positive regulation of synaptic transmission	GPER1	PTN	STX3,NRXN1,CLSTN3,STX4,FLOT1
GO:0045454	0.0214802	7	70	cell redox homeostasis	ENSACAG00000003016	TXNDC9	PDIA4,PRDX4,TXNRD3,PDIA3,ENSACAG00000013018
GO:1903729	0.00018	11	68	regulation of plasma membrane organization	ENSACAG00000013675,GPER1,ITGB1	EPHA2,TMBIM1,EZR,LZTFL1	PLS1,KALRN,STX3,EZR,STX4
GO:0016925	0.0077647	9	68	protein sumoylation	STAG1,NOP58	XPC,SENP5,NUP93	ENSACAG00000002091,RAD21,TPR,NUP107
GO:0008643	0.0031103	9	67	carbohydrate transport	ENSACAG00000002886,AQP3,SLC37A4	STXBP3,SLC37A3,EZR,SLC37A2,SLC35F6	PLS1,EZR
GO:0022406	0.0002783	10	65	membrane docking	CEP83	STXBP3,CEP83,NSF,SYTL2,STXBP2,EZR	CEP83,STX3,EZR,NRXN1,STX4,STX12
GO:0015748	0.0257048	7	64	organophosphate ester transport	ATP11B,MFSD2A,ENSACAG00000015342,SCAR	SLC37A2	MFSD2A,MTTP,SCARB1

					B1,SLC37A4		
GO:0006446	0.005677	8	59	regulation of translational initiation	METTL3,EIF4G3	ATF4,RXRA	RPL13A,EIF5B,ENSACAG00000010260,TPR
GO:0032272	0.0176301	7	57	negative regulation of protein polymerization	LMOD3,DMTN	TBCD,VILL	ADD1,SPTBN2,STMN1
GO:0006487	0.036651	6	56	protein N-linked glycosylation	B4GALT7	RPN2	ENSACAG00000016117,VCP,DPAGT1,ST3GAL4
GO:1901184	0.0331375	6	55	regulation of ERBB signaling pathway	ADAM17,GPER1	LGMN,RNF126	LGMN,RHBDF2,AFAP1L2
GO:0048278	0.0002925	9	54	vesicle docking	CEP83	STXBP3,CEP83,NSF,SYTL2,STXBP2	CEP83,STX3,NRXN1,STX4,STX12
GO:0022613	0.0270442	6	54	ribonucleoprotein complex biogenesis	GNL3,LSG1,RPLP0	IPO9	NOC2L,TGS1
GO:0090277	0.0236804	6	53	positive regulation of peptide hormone secretion	GPER1	PPP3CB	FGG,STX4,PLA2G6,CCKAR
GO:0031532	0.0397664	6	53	actin cytoskeleton reorganization	ATP2C1,MYH9,FLNA	EZR	MYH9,ANXA1,EZR,CCKAR
GO:0006997	0.0032167	8	49	nucleus organization	HIPK2	SRPK3,RTN4,NUP93	ENSACAG00000009269,GOLM1,TPR,NUP107
GO:0098661	0.0041594	7	41	inorganic anion transmembrane transport	SLC26A11,SLC37A4	CPT1B,SLC37A2	SLC4A1,GLRB,RHCG
GO:0022904	0.0365691	4	41	respiratory electron transport chain	COX4I1,NDUFB9	SDHA	SDHA,ENSACAG00000007045
GO:0051017	0.0006147	8	40	actin filament bundle assembly	DPYSL3,FMN2,DMTN	USH1C,EZR	PLS1,ADD1,BAIAP2,EZR
GO:0006909	0.0340946	5	40	phagocytosis	ENSACAG00000003016	TUSC2	GAS6,ANXA1,PECAM1
GO:0043542	0.037613	5	39	endothelial cell migration	MYH9,SCARB1,EMP2	STARD13	MYH9,PECAM1,SCARB1
GO:0002504	0.0351977	5	38	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	SEC24B	ENSACAG00000011986	TRAF6,SPTBN2,AP1G1
GO:0046470	0.0059889	6	36	phosphatidylcholine metabolic	ABHD3,LPCAT1	CHKA,LPCAT3	LPCAT4,PCYT1A

				process			
GO:0010501	0.0372238	5	36	RNA secondary structure unwinding	DDX23,DDX6,DDX55	ENSACAG00000004703	DDX24
GO:0061077	0.0013776	6	33	chaperone-mediated protein folding	FKBP10	FKBP9,CRTAP	PDIA4,FKBP4,HSPH1
GO:0030574	0.0215224	5	32	collagen catabolic process	COL5A1	ADAMTS3,COL4A6,COL3A1	MMP19,COL3A1
GO:1901264	0.0094633	5	31	carbohydrate derivative transport	MFSD2A,SCARB1,SLC37A4	SLC37A2	MFSD2A,SLC25A26,SCARB1
GO:0019674	0.031326	4	30	NAD metabolic process	NADK2	KMO	IDH3G,IDH3B
GO:0000462	0.0393944	4	30	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	UTP6	WDR3	UTP20,DIEXF,WDR3
GO:0070527	0.0067134	5	29	platelet aggregation	MYH9,FLNA	STXBP3	MYH9,FGG,GATA1
GO:0032652	0.0083954	5	29	regulation of interleukin-1 production	ENSACAG00000013588	SPHK1	GAS6,ANXA1,TNFAIP3
GO:0006695	0.0369478	4	28	cholesterol biosynthetic process	HMGCR	GGPS1	PRKAA1,ENSACAG00000003142
GO:0015701	0.0489908	4	28	bicarbonate transport	SLC26A11	SLC26A4,CA12	SLC4A1
GO:0050994	0.0080256	5	27	regulation of lipid catabolic process	ENSACAG00000002886,SCARB1	LONP2	PRKAA1,PDE3B,SCARB1
GO:1901998	0.0059761	5	26	toxin transport	RAB43,CCT3,DNM1	RAB28	CCT4
GO:0060349	0.0207314	4	24	bone morphogenesis	BMPR2	IFITM5	CARM1,ENSACAG00000009367
GO:0010803	0.0222199	4	24	regulation of tumor necrosis factor-mediated signaling pathway	ENSACAG00000003867	SPHK1	GAS6,TNFAIP3,ENSACAG00000003867
GO:0001906	0.0122734	4	22	cell killing	EMP2	STXBP2,TUSC2	ENSACAG00000028691
GO:0060122	0.0228864	4	22	inner ear receptor stereocilium organization	IFT27,SEC24B	USH1C	CTHRC1
GO:0006261	0.0169774	4	21	DNA-dependent DNA replication	RRM2B	MGME1	BAZ1A,POLD2

GO:0090200	0.0223388	3	19	positive regulation of release of cytochrome c from mitochondria	GPER1	PPIF	PLA2G6
GO:0006515	0.0074906	4	18	misfolded or incompletely synthesized protein catabolic process	POMT2	RNF126,LONP2	UFD1L
GO:0097066	0.0344866	3	16	response to thyroid hormone	F7	HPN	GATA1
GO:0031579	0.0016951	4	14	membrane raft organization	PPT1,EMP2	FLOT2	FLOT1
GO:0046931	0.0032926	4	12	pore complex assembly	CCT3	RTN4,NUP93	NUP107
GO:0001765	0.0038785	3	10	membrane raft assembly	EMP2	FLOT2	FLOT1
GO:0071295	0.004781	3	9	cellular response to vitamin	POSTN	PTN	GAS6
GO:0002446	0.0020329	3	7	neutrophil mediated immunity	ADAM17	TUSC2	IRAK4
GO:0030575	0.004434	3	7	nuclear body organization	HIPK2	SRPK3	ENSACAG00000009269
GO:0051660	0.0233717	2	5	establishment of centrosome localization	CEP83	CEP83,EZR	CEP83,EZR
GO:1903912	0.0110545	2	4	negative regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation	PPP1R15B	ENSACAG00000017545	PPP1R15B

Table S23. Categories showed continuous evolution with the elevation increasing in lizards.

category	**pvalue**	**numDE InCat**	**numIn Cat**	**term**	***Ph. putjatia***	***Ph. vlangalii***	***Ph. erythrurus***
GO:0032259	0.001128425	10	186	methylation	NSUN4,ENSACAG00000023921,COQ3,MTO1	RBBP5,TGS1	DDX4,HNMT,MTO1,FTSJ2,TRDMT1
GO:0006091	0.019736421	7	179	generation of precursor metabolites and energy	PFKM	HKDC1,PPP1R1A,PPP1R3B	UQCRC2,HKDC1,PGM2,PPP1R2
GO:0006399	0.000647395	10	176	tRNA metabolic process	MTO1	PUS7,DARS,AARS	TRMU,EXOSC8,QARS,MTO1,RPUSD4,TRUB2,TRDMT1
GO:0060249	0.001115317	9	154	anatomical structure	SMC5,RAC1,PFKM,N	RAC1,BBS10	GIGYF2,GCNT2,DC

				homeostasis	BN,WDR36		LRE1A
GO:0009612	0.044973927	6	154	response to mechanical stimulus	BAG3,RAC1	FADD,FYN,RAC1	XPC,INHBE
GO:0051054	0.03405449	6	150	positive regulation of DNA metabolic process	ENSACAG00000008899,RAC1,DSCC1,NBN	RNF168,RAC1	WRAP53
GO:0006302	0.000548123	9	138	double-strand break repair	RAD52,XRCC4,SMC5,NBN	RNF168	EXD2,LIG4,CCDC155,DCLRE1A
GO:0005996	0.023565571	6	131	monosaccharide metabolic process	ENSACAG00000022125,PFKM	HKDC1	HKDC1,ENSACAG00000003913,PGM2,BRAT1
GO:0009451	2.87E-05	10	122	RNA modification	NSUN4,MTO1	PUS7,AARS,TGS1	TRMU,MTO1,RPUSD4,FTSJ2,TRUB2,TRDMT1
GO:0044262	0.000975316	8	120	cellular carbohydrate metabolic process	COQ3,PFKM	PPP1R1A,PPP1R3B	ALG8,PGM2,IMPA1,PPP1R2
GO:0009306	0.015418936	6	120	protein secretion	SNCG,CPLX1	LCP2	ENSACAG00000011849,LCP2,PAFAH1B1,CPLX1,STEAP3
GO:0017038	0.008216473	6	108	protein import	PEX1	CSE1L	ENSACAG00000011849,MCM3AP,RANBP17,LONP2
GO:0010212	0.021140086	5	101	response to ionizing radiation	ENSACAG00000008899,XRCC4	RNF168	ECT2,BRAT1
GO:0015980	0.003891926	6	96	energy derivation by oxidation of organic compounds	PFKM	PPP1R1A,PPP1R3B	UQCRC2,PGM2,PPP1R2
GO:0001894	0.019069575	5	95	tissue homeostasis	RAC1,WDR36	RAC1,BBS10	GIGYF2,GCNT2
GO:0044085	0.03631386	4	89	cellular component biogenesis	ENSACAG00000009242	ZNF622,TGS1	NOP16
GO:0055076	0.01138443	5	85	transition metal ion homeostasis	MFI2,SLC40A1	SLC39A14,SLC22A17	STEAP3
GO:0005976	0.012567898	5	81	polysaccharide metabolic process	PFKM	PPP1R1A,PPP1R3B	PGM2,PPP1R2
GO:0030516	0.015747927	5	80	regulation of axon extension	WDR36	CDKL5,DNM2	CDK5R1,PAFAH1B1

GO:0000041	0.033538076	4	77	transition metal ion transport	MFI2,SLC40A1	SLC39A14	STEAP3
GO:0050905	0.00828918	5	72	neuromuscular process	NBN	AARS	GIGYF2,PENK,PAFAH1B1
GO:0016925	0.008034912	5	68	protein sumoylation	XRCC4,SMC5	RNF168,SENP5	XPC
GO:0022613	0.009599317	4	54	ribonucleoprotein complex biogenesis	ENSACAG00000009242	ZNF622,TGS1	NOP16
GO:0006073	0.001925423	5	52	cellular glucan metabolic process	PFKM	PPP1R1A,PPP1R3B	PGM2,PPP1R2
GO:0001510	0.001659181	5	51	RNA methylation	NSUN4,MTO1	TGS1	MTO1,FTSJ2,TRDMT1
GO:0050885	0.007655503	4	45	neuromuscular process controlling balance	NBN	AARS	GIGYF2,PAFAH1B1
GO:0048489	0.033420882	3	45	synaptic vesicle transport	CPLX1	BLOC1S5,AP3M2	CPLX1
GO:0006970	0.038017454	3	45	response to osmotic stress	RAC1	RAC1	HNMT,MAP7D3
GO:0002200	0.023242819	3	37	somatic diversification of immune receptors	NBN	RNF168	LIG4
GO:0000726	4.39E-05	6	36	non-recombinational repair	RAD52,XRCC4,NBN	RNF168	LIG4,DCLRE1A
GO:0006303	0.0004354	5	35	double-strand break repair via nonhomologous end joining	XRCC4,NBN	RNF168	LIG4,DCLRE1A
GO:0006826	0.001501831	4	33	iron ion transport	MFI2,SLC40A1	SLC39A14	STEAP3
GO:0016444	0.012669132	3	29	somatic cell DNA recombination	NBN	RNF168	LIG4
GO:0021884	0.043436728	2	20	forebrain neuron development	RAC1	RAC1	DCLK2
GO:0016447	0.003548175	3	19	somatic recombination of immunoglobulin gene segments	NBN	RNF168	LIG4
GO:0006972	0.017237487	2	14	hyperosmotic response	RAC1	RAC1	HNMT
GO:0006488	0.019078854	2	14	dolichol-linked oligosaccharide biosynthetic process	SRD5A3	SRD5A3	ALG8

Table S24. Expression profile across different tissues for frogs (value showed with TPM).

Lineage	PSGs	brain	heart	liver	ovary	skin	testis
N. parkeri	ENSACAP00000001268	1.66942	0	0	0.54158	0	0

ENSACAP00000004182	5.13715	0	0	0.083873	0.064615	0
ENSACAP00000012691	0.883662	4.7322	0.854152	1.39852	14.2309	0.395573
ENSACAP00000000393	1.17447	0.278061	0.023366	0.09667	0.13509	0.010775
ENSACAP00000021105	1.44922	0.617614	0.230895	1.40177	0.884922	0
ENSACAP00000019544	2.47595	0.107731	0.341818	0	0.15758	0
ENSACAP00000005325	3.17391	0.682129	0.374374	0.361927	0.413667	0.18447
ENSACAP00000013343	0.047416	0.016707	0.066948	0.036537	83.0341	0
ENSACAP00000004963	0.305515	1.17723	1.20636	0.24683	0.373459	0
ENSACAP00000014854	1.86186	0.432994	0.24441	1.0035	0	0.985896
ENSACAP00000003231	1.50713	0.277078	0.204506	0	0.459033	0.101471
ENSACAP00000007242	1.74389	0.89156	0.13626	0	0.768176	0.065787
ENSACAP00000013979	0.783252	0.441311	0.539173	0	0.09487	0
ENSACAP00000013586	7.51213	27.2975	19.1852	3.69759	17.6897	4.16386
ENSACAP00000011725	516.143	1.79631	0.406369	1.19498	0.87307	11.2642
ENSACAP00000016051	1.76494	0.520353	0.701302	6.40595	0.718653	0.117363
ENSACAP00000007394	2.26087	1.78311	1.26312	0.261584	1.38326	0.255604
ENSACAP00000017662	0	0.030319	0	0.107039	2.85496	0
ENSACAP00000005070	0.516406	1.32392	0.332108	0.401234	0.217485	0.044196
ENSACAP00000016161	2.74964	0.107021	0.723817	0	0.373459	0.243001
ENSACAP00000002067	0.31038	0.100539	0.204736	0.619422	3.01315	1.40706
ENSACAP00000006467	0.277487	0.636511	0.165589	0.072325	0.223171	0
ENSACAP00000000009	8.81785	4.00504	0.845297	0.279378	2.20248	0.274522
ENSACAP00000016725	0.816875	2.03724	0.068896	0.028784	0.066959	0.047866
ENSACAP00000009344	7.21238	6.63265	4.31523	17.9074	5.51444	0.983719
ENSACAP00000013023	6.01736	2.96299	0.238213	11.4169	0.367675	2.75565
ENSACAP00000012178	0.779566	0.254431	0.294112	0	0	4.23323
ENSACAP00000004705	0.554974	0.358037	0.165589	0.144651	0.167378	0
ENSACAP00000007336	0	0	0.270821	0.285735	1.50881	0
ENSACAP00000010433	35.7092	51.6677	20.4315	84.4721	21.7779	26.4856
ENSACAP00000008788	9.2377	5.2875	3.14106	1.65271	1.74173	0.280013
ENSACAP00000006622	13.0979	5.10435	2.70693	0.431949	4.34102	0.442593

ENSACAP00000016880	5.47588	2.66308	2.86097	15.4103	3.50735	0.879063
ENSACAP00000003197	5.71194	1.73098	2.00104	12.4919	3.68892	0.791226
ENSACAP00000003628	20.2662	12.8954	5.52298	39.9398	16.238	1.92313
ENSACAP00000016904	0.567044	0.765848	0	0	0.279781	0
ENSACAP00000017487	0	18.2489	0.128345	0	0	0
ENSACAP00000000793	6.19645	6.52409	0	0.382167	0.663962	0
ENSACAP00000002963	0	0	0.02682	0	6.47821	0
ENSACAP00000015276	6.94465	4.9163	3.33989	14.2183	5.1689	2.01E-05
ENSACAP00000016415	1.10222	0.356035	1.05274	0.25591	1.65657	1.86721
ENSACAP00000015745	32.6422	31.049	19.4354	60.0552	35.5918	3.44223
ENSACAP00000007730	10.5757	2.1792	3.67992	3.70624	2.85389	3.50107
ENSACAP00000015007	9.68587	0.048718	0.032623	0	0.072952	0.082512
ENSACAP00000008624	1.12004	0.401106	1.82539	0	0	0
ENSACAP00000005301	2.76918	0.062662	0.298004	27.5745	7.6058	1.12755
ENSACAP00000006308	1.74617	0.88231	0.371433	0.366568	0.284266	0.132411
ENSACAP00000011162	2.16701	0.703883	0.105908	1.13451	1.81865	0.101024
ENSACAP00000003937	0.114534	0.106108	0.268466	0.092103	0.045911	0
ENSACAP00000022713	1.84943	6.98685	0.336132	0	0	0
ENSACAP00000005539	14.2074	1.78274	0.110032	2.12456	0.638193	0.254121
ENSACAP00000002825	1.08314	0.424116	0.174252	0.099195	0.345262	0.027171
ENSACAP00000015105	10.413	0	0	0.368963	0	0
ENSACAP00000009198	8.39421	13.92	2.8	9.04662	2.51547	0.49055
ENSACAP00000000046	1.36897	0.394531	0	0	0.50105	0.109883
ENSACAP00000007271	17.6837	4.32029	3.0307	2.4408	4.4562	2.58459
ENSACAP00000001312	19.397	0.489868	0.354338	8.62214	0.957595	0.79428
ENSACAP00000012483	1.32621	1.4718	7.32812	0.676133	243.407	1.4106
ENSACAP00000014578	0.220547	0.130361	1.50558	0.244411	0.993845	0.042126
ENSACAP00000005642	1.65202	0.512067	5.22111	0.219895	1.93054	0.060674
ENSACAP00000005884	12.193	2.84026	6.09655	107.432	14.7043	10.455
ENSACAP00000007428	2.65508	0.631503	0.70796	1.66381	1.05283	0.193254
ENSACAP00000000854	1.98398	0.570762	0.429126	2.31505	0.967413	0.02477

ENSACAP00000017164	3.63169	0.442748	0.045185	0.15247	1.03328	0.231191
ENSACAP00000012761	1.9266	0.575508	0.133694	0.232939	0.996563	0
ENSACAP00000016181	1.57687	0.445389	0.275802	0.330669	0.41003	0.03657
ENSACAP00000009285	0.116659	0	0.337744	0	0	0.294573
ENSACAP00000004516	19.1077	0.156166	0.105671	10.5532	0.045672	0.228474
ENSACAP00000004794	0.146299	0.064253	0	0	0.969528	0
ENSACAP00000012225	1.08336	0	0	0	0.312791	0
ENSACAP00000013843	0.244949	0	7.65481	0	0.163594	0.242691
ENSACAP00000004798	170.223	163.917	42.1363	183.883	25.9092	25.4061
ENSACAP00000009019	8.34406	11.229	7.27089	32.3411	6.38086	34.1099
ENSACAP00000011061	0.49922	0.249985	0.063388	0.058417	0.142146	0
ENSACAP00000017694	3.04968	1.08082	0.757238	135.317	2.5795	1.04336
ENSACAP00000003860	0.1282	0	2.35697	0	0	0.053669
ENSACAP00000010908	0.607234	2.43688	4.60496	0.107532	6.91495	0.139711
ENSACAP00000014494	0	1.11642	0.130235	0.152234	0	0
ENSACAP00000012985	0.174733	0.255143	0.000841	3.1825	4.7283	160.246
ENSACAP00000003608	1.65932	0.53217	0.573272	1.17911	1.11393	1.16225
ENSACAP00000012337	0.149468	0.059485	0.138049	0	0.034801	0
ENSACAP00000015226	1.32797	1.16574	0	0.147384	0.316828	0.178207
ENSACAP00000014890	3.21689	0.964052	1.52274	5.37753	0.646676	0.151311
ENSACAP00000011156	1.49864	0.119681	1.27979	1.21965	0.713977	0.155943
ENSACAP00000013808	7.3827	3.62964	2.64412	0.047145	0	3.43953
ENSACAP00000004015	0	0.229598	0.930233	0.163728	0.685839	0.127395
ENSACAP00000017100	55.7501	19.5831	13.3192	24.2466	12.5126	2.63052
ENSACAP00000015631	9.40E-09	8.88E-06	3.27E-07	0	0	0
ENSACAP00000005421	0	0	5.42053	0.502907	0	0
ENSACAP00000007049	6.24091	1.89612	2.35352	5.05463	3.66604	0.067083
ENSACAP00000015272	13.9726	1.06178	0.488294	1.81388	3.40125	0.233253
ENSACAP00000007102	0.020182	0.214514	1.90866	0	1.08941	0
ENSACAP00000009201	0.039097	4.50572	1.11894	0	0.082168	0.016885
ENSACAP00000002142	14.7502	5.31017	0.904376	0.549051	2.88469	0.525338

ENSACAP00000006180	1.4823	0.554486	0	0.74243	0.407495	0
ENSACAP00000016842	1.41477	0.232207	0.470624	0.560404	0.922353	0.311553
ENSACAP00000008722	2.95572	0.643321	0.416583	0.092815	0.857168	0.049636
ENSACAP00000001499	3.64517	23.9905	0	18.0917	0	0.234759
ENSACAP00000023346	8.93245	16.9729	2.29615	0.939221	13.0426	0.17333
ENSACAP00000000890	1.02528	0.214921	0.495916	0.234616	0.181527	0
ENSACAP00000008201	192.075	129.565	49.6952	92.285	55.0889	91.8792
ENSACAP00000017329	0.716397	0.637891	0.711072	0.048877	1.18942	0.100052
ENSACAP00000004544	0.511542	0.215309	0.13106	0	0.051561	10.7736
ENSACAP00000006856	0.101072	17.5081	1.27045	10.1121	7.12105	0.217168
ENSACAP00000007237	0.212149	0.065852	1.55403	0.073862	0.86918	0
ENSACAP00000022376	0.003353	0	0	0	0	0
ENSACAP00000007053	261.465	36.5447	15.0765	73.4213	15.77	3.23552
ENSACAP00000015992	1.90336	0.489776	0.170089	0.148891	0.287073	0.281544
ENSACAP00000009563	0.235145	2.46658	0	0.348381	0.119494	0.114555
ENSACAP00000007585	0.11496	0	0.010404	0.030867	7.46901	0.047735
ENSACAP00000001537	0	0.01391	0.028126	0.177834	7.1186	0.025989
ENSACAP00000008316	0.278611	0.192494	0.35135	0	0.399779	0
ENSACAP00000008329	17.4216	4.73822	7.70227	50.1293	13.7315	0.997585
ENSACAP00000009005	1.32832	0.518482	0.509949	2.69E-08	0.731309	0
ENSACAP00000007281	4.2878	2.60195	0.442048	0	0.097557	0.041068
ENSACAP00000013361	5.01778	3.84245	1.98091	27.6236	1.79389	15.7587
ENSACAP00000006603	3.48984	0	0	0.053239	0.104108	0
ENSACAP00000012565	2.03486	0.280467	0.035591	0.178614	0.646259	0.032984
ENSACAP00000009562	0.676676	0.180423	0.116734	0.061838	0.302388	0
ENSACAP00000001330	18.1719	8.74336	3.28708	6.9481	3.94074	0.391432
ENSACAP00000006839	7.58873	9.06447	3.89833	1.63459	5.05239	0.5388
ENSACAP00000001974	0.020126	1.75649	0.090565	1.27116	0.314749	0.201079
ENSACAP00000011505	0.157732	0	0.012218	0.004461	0	0
ENSACAP00000009442	6.10223	0.040902	1.46484	0.118436	0.012006	0
ENSACAP00000000846	0.48627	0.085849	3.30829	7.19455	7.42466	0.111841

ENSACAP00000016430	2.18788	0.459982	0.444072	0.141862	0.804883	0.59659
ENSACAP00000015583	0.144867	0	0.029505	0	0.213232	0
ENSACAP00000018251	0.551075	0.896368	0.007232	0	0	0
ENSACAP00000013512	0	0.525428	1.63033	1.97961	0.1698	0
ENSACAP00000002485	8.5208	5.33781	2.57254	14.3908	2.79478	0.559395
ENSACAP00000014506	24.9994	1.56587	0.243947	0.106288	0.500555	0.006815
ENSACAP00000016238	46.7859	54.7062	21.8036	19.3799	8.47648	11.3832
ENSACAP00000012387	1.72747	1.37266	0.099552	10.0714	0.223554	0.387105
ENSACAP00000010845	0.377049	0	0	0	0	0
ENSACAP00000016703	1.40746	0	0	0	0	0
ENSACAP00000015098	0.513579	0.237164	9.74E-05	0.077737	0.175871	0.006067
ENSACAP00000012411	4.75472	1.36408	0	0	0	0.164794
ENSACAP00000001397	0.358894	0.000189	0.1419	2.38272	0.149175	0.208689
ENSACAP00000009399	0.044132	0.003526	1.36483	0	0.025346	0
ENSACAP00000008027	3.42624	0	0	0.063059	0	0
ENSACAP00000015970	8.68882	9.67187	2.43269	71.4532	7.41616	0.762016
ENSACAP00000003593	3.75902	0	0	0	0	0.09447
ENSACAP00000005755	0.071308	0.033679	0.169205	0	0.141875	0.071312
ENSACAP00000008480	2.77854	0.814642	0.294214	0.46103	0.398431	0.532682
ENSACAP00000000029	0.085071	0.039938	0	2.24E-10	0	7.35E-05
ENSACAP00000006928	4.60227	0.259519	0.123609	3.36918	0.137556	0.037
ENSACAP00000014383	0.47547	1.50895	0.911373	0.451241	0.428312	0.055969
ENSACAP00000007491	1.95551	1.56666	1.38646	0.120405	0.676525	0.016759
ENSACAP00000013049	1.22532	0.895067	0.118617	0	0.247046	0.056867
ENSACAP00000010338	0	0	0.056441	0.365118	0.177651	0.22893
ENSACAP00000005673	1.94514	0	0	0	0.197527	0.027925
ENSACAP00000017486	1.86236	1.41651	0.987732	0.361943	1.49718	0.095318
ENSACAP00000017515	0	0.11206	0.73573	0	0	0.167148
ENSACAP00000006654	0.000266	0.305633	0.075803	0	0	0.075819
ENSACAP00000002993	4.12357	1.81784	1.31539	0.294598	2.56793	0
ENSACAP00000009450	1.09656	1.15377	0.645992	5.05928	1.64442	1.73413

ENSACAP00000006715	4.52669	2.09811	1.93615	10.3184	1.88092	0.203462
ENSACAP00000005862	17.1196	9.6989	3206.43	12.5415	9.47798	11.1874
ENSACAP00000007069	49.3781	0.76221	0.364487	0.167628	0.509868	0.110909
ENSACAP00000013440	0	1.33735	0	0.000245	0	0
ENSACAP00000016487	4.76603	0.334133	6.91749	0.623123	0.891011	4.29353
ENSACAP00000006202	3.68469	1.20167	0.920731	11.067	1.57867	0.201623
ENSACAP00000005163	0.290782	4.33685	0.046488	6.24966	5.28112	0.032265
ENSACAP00000000629	4.26544	2.20495	2.40062	0.943973	3.31964	0.039362
ENSACAP00000015558	0.143683	0.111743	0	3.45637	0.163196	0.312603
ENSACAP00000015568	8.60326	4.49984	3.77935	2.31108	4.94489	0.145905
ENSACAP00000001568	0.13563	0	0	0	2.01009	0
ENSACAP00000010445	1.21058	0.179382	0.234453	1.61904	1.21151	0.033197
ENSACAP00000003381	13.9756	0	0	0.038358	0.059415	0
ENSACAP00000009807	13.3297	0.068541	0	0.137056	0.314834	0.357667
ENSACAP00000013183	1.54865	0.513377	0.489512	0.260211	0.267203	0
ENSACAP00000008073	0.418081	0	0.233841	0	0.375064	7.14736
ENSACAP00000007033	10.3199	1.47178	1.23044	0.347373	24.8587	1.99164
ENSACAP00000009489	1.08608	0	0	0.386388	15.312	0.166742
ENSACAP00000002674	0.365829	0.326133	0	0.410862	0.18672	0.176205
ENSACAP00000005541	0.218027	0.017903	0	1.68E-10	0	0.113255
ENSACAP00000011995	0.296571	0.951746	0	0	0.067476	0
ENSACAP00000006658	2.83841	1.27582	0.513216	0.109863	1.23319	0
ENSACAP00000007420	4.29783	1.5232	78.156	0.993773	1.01875	0.780413
ENSACAP00000002456	0.432598	0.693513	0.308927	0.088977	0.611888	0
ENSACAP00000017277	0	0.220498	1.28451	0.631969	0.647539	0
ENSACAP00000008014	0.208758	0.079853	7.40703	0.166175	0	0
ENSACAP00000002400	2.27237	1.17817	0.562765	3.1394	3.04817	0.095745
ENSACAP00000004412	0.149346	0.771751	0.270026	0.091784	8.30735	0.189449
ENSACAP00000011892	1.19632	0.363686	1.42151	0	1.44838	0
ENSACAP00000017999	0.039135	0.01714	0	0	0.00023	0
ENSACAP00000015422	0.799238	0.175923	0.168222	0.813519	0.456484	0.390823

ENSACAP00000005385	0.371905	0.448707	9.56E-09	0.010949	0.053716	0
ENSACAP00000000788	0.824095	0.926787	0.094649	0.040018	0.340869	0
ENSACAP00000002209	12.3185	3.45293	1.29366	0.03386	3.03289	0.040219
ENSACAP00000016915	0.652609	1.66741	0.185736	0.027125	0.152102	0.092617
ENSACAP00000016271	0.046593	0.056995	0.831374	0.134078	0.362583	0.016989
ENSACAP00000003704	11.0294	0.595163	0.260435	0.276927	0.195615	0.161974
ENSACAP00000011394	1.60481	1.19299	0.319894	0	1.23665	0.037745
ENSACAP00000017361	0.307894	0.430525	0	0	0.18821	0
ENSACAP00000002866	0.728177	0.353143	0	0.028512	0.831583	0.163109
ENSACAP00000000239	0.752391	2.62632	0.328705	0.033369	0.721165	0.024411
ENSACAP00000012915	8.35055	2.3209	1.50343	0.391227	2.51708	0.247863
ENSACAP00000015517	6.61682	4.08947	2.04448	4.10559	1.95394	0.148369
ENSACAP00000004157	0.145618	0.012696	0.08585	0.00392	0.126648	0.037658
ENSACAP00000002797	0	4.33166	0.208658	0.105235	0	0.06067
ENSACAP00000022553	2.02087	1.29785	1.64506	0.409706	1.41792	0.046836
ENSACAP00000005969	0	0	0	0	0	0
ENSACAP00000008015	3.90326	0.953472	0	0	0.435032	0.139124
ENSACAP00000002410	2.16456	1.47425	1.33584	5.60613	1.10581	1.11699
ENSACAP00000005184	1.78176	1.99434	2.6605	17.2016	2.52872	0.159433
ENSACAP00000013323	11.8355	1.18657	0.349277	4.39654	0.087648	8.40589
ENSACAP00000002807	0	0.481755	1.1314	0.859136	0.313515	0
ENSACAP00000012886	6.69327	6.71344	30.7381	29.0254	16.1891	3.2124
ENSACAP00000014423	1.71278	1.97622	0	0	0.629506	0
ENSACAP00000011611	15.9482	14.0076	2.88221	15.8057	14.5527	0.776986
ENSACAP00000012569	0.637677	0.199886	0.353109	0	0.530451	0
ENSACAP00000010118	19.7382	8.4545	8.51264	0.613575	8.56468	0
ENSACAP00000000500	0	0.975036	0	0.527124	0	0
ENSACAP00000000706	4.30473	0.497352	1.49563	2.42912	2.45983	2.82654
ENSACAP00000009342	7.68283	4.56453	2.5343	5.77276	3.35767	0.347503
ENSACAP00000007260	27.7007	7.96761	6.83088	50.4782	23.2254	0.478427
ENSACAP00000020775	0.449396	0.901306	0.205576	1.04236	0.168364	0.045676

ENSACAP00000001690	12.1884	13.0505	24.5334	0.678544	11.9357	1.21979
ENSACAP00000016626	0.431373	0.161645	0.061022	1.74502	1.74E-10	9.96E-11
ENSACAP00000009930	5.26691	3.46419	4.21331	0.685732	2.27293	0.268343
ENSACAP00000016567	0.22796	0.241037	0.077889	0.030715	0	0
ENSACAP00000012479	1.47493	0.114557	0.275873	7.20108	0.811249	2.06117
ENSACAP00000009994	198.396	0.148974	0	0.284509	0.789206	0.739157
ENSACAP00000008780	1.4613	0.718679	0	0	0	0
ENSACAP00000016408	7.50626	0.024582	0.017679	0.013566	0.010344	0.008083
ENSACAP00000017268	1.03736	0.217934	0	0	0.092638	1.65E-09
ENSACAP00000014686	9.35618	2.56789	3.32527	1.18396	6.91097	1.3252
ENSACAP00000009688	0.436427	0.722924	0.116094	0.170955	0.085451	0.636182
ENSACAP00000008584	0.468792	0	0	0	0.037142	0
ENSACAP00000006912	0	0.138013	0.085309	0.309729	0	0
ENSACAP00000003827	0.353765	0.489374	0.654805	0.308565	0.459626	0.056409
ENSACAP00000016036	0.533875	0.555835	0.531611	0.320492	3.06856	0.129455
ENSACAP00000000414	0.328858	0	0	0	0	0.038868
ENSACAP00000009531	0.935357	1.40874	1.37912	0	0.304804	0.217536
ENSACAP00000008343	1.67346	2.74156	0.128785	0.078811	0.299101	0.23189
ENSACAP00000004578	2000.68	1119.72	11647.5	688.544	6514.8	550.187
ENSACAP00000016804	6.70211	0.250336	1.77743	0	13.8678	0.044388
ENSACAP00000009262	10.1102	7.04539	4.74557	0	6.47772	72.1353
ENSACAP00000015113	1.31437	6.98134	0.212604	0	1.12173	0.423336
ENSACAP00000002886	0.542978	0	0	0.162678	0.209443	0
ENSACAP00000004101	0	0	0	0	0	0
ENSACAP00000000477	144.697	70.0479	81.8811	2.92159	47.4656	1.10098
ENSACAP00000015428	0.694046	0.092394	0.197601	0	1.49214	0.029049
ENSACAP00000016608	22.0743	26.1483	0.000996	0.001972	0	0
ENSACAP00000004923	0.192404	1.3446	5.70321	0.607304	1.58097	0.796044
ENSACAP00000008971	12.5158	8.75003	26.2686	9.03685	23.1237	1.17719
ENSACAP00000001566	3.58382	5.80327	2.35342	21.6192	1.48779	0.496515
ENSACAP00000011610	10.2448	1.52935	0	10.4988	2.45094	0

	ENSACAP00000006749	0	1.21057	0.579422	0.850638	0	1.02895
	ENSACAP00000008830	0.718456	0.54676	0	0.506822	0	0.053077
	ENSACAP00000002155	3.10382	0.494829	0	0.384788	4.79934	7.46E-06
	ENSACAP00000011104	1543.83	1548.11	2453.48	304.078	2627.63	502.296
	ENSACAP00000012138	3.24544	1.65783	8063.88	5.31195	3.91195	18.3158
	ENSACAP00000005351	156.682	568.847	102.329	88.5355	76.4261	164.227
	ENSACAP00000009815	117.054	779.23	160.308	4.84771	32.7312	15.1656
	ENSACAP00000013733	251.895	259.335	222.694	151.032	171.751	17.7698
	ENSACAP00000020514	70.3664	11.9585	282.195	192.37	14.4516	67.6062
	ENSACAP00000001812	220.254	41.1605	31.8313	164.616	40.9809	23.8003
	ENSACAP00000016905	10.7223	27.1383	39.9283	1.09994	11.1827	5.22945
	ENSACAP00000016867	59.6287	74.803	55.91	128.456	49.1186	13.8621
	ENSACAP00000010793	13.2595	39.8955	164.771	2.38864	21.0927	236.58
	ENSACAP00000012413	353.57	0.572318	1.39805	6.91032	5.16183	2.43066
	ENSACAP00000004411	0.218271	0.059437	248.724	0.813031	0.210012	0.69278
	ENSACAP00000017693	57.8141	25.5225	17.4719	140.797	17.3018	44.6697
	ENSACAP00000013201	2.48248	6.49492	10.2652	0.250875	2.27658	1.10913
	ENSACAP00000004505	25.3356	85.9242	0.034864	0.058284	0.045193	0.080753
	ENSACAP00000000405	24.1265	40.5663	14.6623	10.4226	12.6958	14.694
	ENSACAP00000016795	27.917	15.3637	17.2256	34.8111	22.2396	4.17924
	ENSACAP00000008355	61.4127	7.90423	19.0515	13.9905	1.09042	0.171779
	ENSACAP00000008948	6.79869	9.39945	22.0572	7.30162	74.705	0.820424
	ENSACAP00000014346	0.873208	63.5887	0.297328	0.138297	0.317645	0.072133
	ENSACAP00000011281	2.14008	41.7082	4.34069	0	0.410859	0.493043
	ENSACAP00000000334	31.5842	29.3463	7.1074	54.0222	16.0159	9.36212
	ENSACAP00000014695	24.6374	0.121134	0.084092	0	0	0.039755
	ENSACAP00000015991	0.676248	2.54647	0.745035	3.59794	1.91929	0
	ENSACAP00000005039	0.551889	0.481769	0	0	0.047515	0.033476
	ENSACAP00000017455	1.96165	0.330607	0	0	0.264995	0.177803
N. liebigii	PSGs	brain	heart	liver	ovary	skin	testis
	ENSACAP00000003454	0.266183	0.685454	0.828295	3.73869	1.95209	1.32725

ENSACAP00000006211	1.32933	0.966089	0.263072	0.0947	0.616052	0.041628
ENSACAP00000001640	2.33889	1.48507	3.06346	0.079166	1.53379	4.9713
ENSACAP00000021152	0	0	0	0	1.04336	0.246602
ENSACAP00000012316	0	14.6191	0.074472	0.313691	0.298832	0.103792
ENSACAP00000017289	0.12164	15.2366	0	0.597922	0	5.66767
ENSACAP00000003556	8.35489	9.38121	5.74669	1.68118	8.5574	28.4791
ENSACAP00000017197	12.1652	0.05067	0	0	0.214977	0.033027
ENSACAP00000011692	4.06054	8.48616	2.24533	0	15.594	4.09017
ENSACAP00000008759	4.49081	0	0	1.34674	0	1.36451
ENSACAP00000004168	2.57202	0.021218	0.032384	0.189579	0.064881	46.8124
ENSACAP00000012758	1.56684	0.250761	0.4662	0.699555	11.2846	0.581654
ENSACAP00000015527	2.83408	0.446913	0	0	1.23825	0.159888
ENSACAP00000019308	4.15761	0	0.718295	0	0	0.283045
ENSACAP00000005737	0	0	0	0	8.95742	0
ENSACAP00000013484	5.9664	0	0	0	0	0.027587
ENSACAP00000010921	0.532367	2.39909	0	0.467336	0.557739	1.89608
ENSACAP00000003808	1.36901	1.80536	0.567594	0	0.860163	1.19012
ENSACAP00000014660	1.18859	1.13745	0.355471	0.232322	0.894635	0.396302
ENSACAP00000023366	0	2.06803	0.555689	0	0.139667	0.072037
ENSACAP00000007427	1.88439	1.33131	0	0	0.680276	45.4007
ENSACAP00000012912	0.876594	1.21238	0.302342	1.66084	1.83391	0.438723
ENSACAP00000004437	16.1931	13.0443	13.5672	37.5409	113.57	11.1587
ENSACAP00000003421	0.981879	0.148913	0.310045	0.16732	0	0
ENSACAP00000014191	147.853	33.8432	13.4588	31.0318	29.502	13.7453
ENSACAP00000001426	5.01577	9.1591	1.78994	78.2655	3.44162	8.5046
ENSACAP00000016437	4.35289	1.63657	0.576587	11.4032	0.800071	4.28327
ENSACAP00000008175	1.2338	0	8.04236	0	0.260739	0
ENSACAP00000012975	1.16449	1.11619	0	1.13331	0.136668	0.140246
ENSACAP00000007762	14.4037	0.091575	0.065382	0	0.196709	0.179614
ENSACAP00000001322	1.08462	0.712807	0.162419	0	0	0
ENSACAP00000017267	0	1.16692	0	0	0	0

ENSACAP00000011214	8.19183	7.8181	0.918891	6.59455	1.97472	9.53017
ENSACAP00000010531	0	0	0	0	1.70056	0
ENSACAP00000006716	0.258688	1.14425	0.363933	0.889955	0.365288	0.477697
ENSACAP00000001376	0.231415	1.8591	0.963289	0	1.94357	1.06936
ENSACAP00000002517	1.42639	0.144983	0.47987	0	1.1001	0.031546
ENSACAP00000007089	27.572	0.311217	0.254356	0	0.050992	0.182122
ENSACAP00000006179	0.80252	0.898645	0.044625	4.55089	0.983877	4.56578
ENSACAP00000001781	1.35076	0.681828	0.31479	82.4915	1.10838	11.2285
ENSACAP00000015442	0.896502	0.374938	0.233079	3.51317	0.116846	5.00988
ENSACAP00000004656	0.770194	2.02172	0.851005	4.39372	0	10.7339
ENSACAP00000014487	2.26112	5.52174	0.276558	3.78229	1.61493	0.746824
ENSACAP00000011904	5.24044	0.356357	0.188956	2.02902	0	0.322968
ENSACAP00000013319	3.26861	2.12499	1.65777	1.71993	5.10099	60.051
ENSACAP00000010282	1.01047	0.726071	0.096872	0	0.194505	0.046695
ENSACAP00000004589	0.311781	0.033336	0.034908	0.863034	0.087379	1.17285
ENSACAP00000000349	0.825333	0.593671	0.248049	0	0.623132	0.125267
ENSACAP00000002674	0	0	0	0.157034	5.87156	0.476611
ENSACAP00000012408	0.653807	5.89288	0.64805	0.187885	0.408649	0.180112
ENSACAP00000000518	1.20614	0.254402	0.106424	17.0794	1.28023	8.74749
ENSACAP00000007369	0.663283	1.11606	0	0	0.382301	0.567228
ENSACAP00000009283	0.235212	0.067594	5.82954	0.050141	0.049942	0.044591
ENSACAP00000013273	0.754632	0.873249	0	0.05394	0.42719	0.693893
ENSACAP00000004258	42.0706	21.3797	1.13968	19.4101	3.89462	1.62514
ENSACAP00000002920	4.23399	3.20966	1.96391	19.8896	3.13314	34.2646
ENSACAP00000010338	1.49398	1.60648	0.248649	0.160395	0.240981	2.39406
ENSACAP00000013115	8.31588	12.3781	1.32572	68.9719	3.91913	46.8089
ENSACAP00000017196	13.4616	14.4552	1.23598	1.1147	50.5557	4.56289
ENSACAP00000006254	20.1543	2.89957	0.913997	8.80339	2.13525	9.33246
ENSACAP00000005552	1.98128	0.385357	0	2.913	0	0.222714
ENSACAP00000017624	0.061406	0.021348	0.032571	0.063578	39.2838	0.637661
ENSACAP00000022968	0.132547	0.148647	0.070063	0.146344	114.336	0.614058

ENSACAP00000009090	39.8214	0	0	0.754531	0.100178	0.066994
ENSACAP00000014676	96.5556	2.77333	3.13224	0.302149	6.44141	15.145
ENSACAP00000007659	25.0874	0.337319	0	1.06676	0.018896	0.064344
ENSACAP00000006856	0	6.62515	0.495297	0	0	0.01332
ENSACAP00000008138	1.88801	0.917134	0.233803	1.33791	0.469762	12.4778
ENSACAP00000020455	0.447334	0.339649	0	3.77521	0.209255	0.254291
ENSACAP00000010279	1.83227	2.47876	0.602501	13.4765	1.2107	2.72158
ENSACAP00000012746	2.47237	1.5233	0.093148	0.101665	1.77654	0.223104
ENSACAP00000007591	3.18224	0	0	0	0.177715	155.237
ENSACAP00000008790	0.249331	0.983094	0	0	1.32499	0
ENSACAP00000009390	8.01916	0	0	0	0.611537	0.381872
ENSACAP00000017850	6.79103	1.13267	0.548469	0.705779	0.549307	0.157533
ENSACAP00000019934	13.3692	25.3582	0.406854	15.0057	3.98833	0.713385
ENSACAP00000006621	4.68859	2.32619	0.225587	5.22654	0.339249	262.369
ENSACAP00000017518	8.0436	0.940963	0.600384	27.8692	3.18471	4.22103
ENSACAP00000003909	0.643692	0.900777	0.035929	0.740733	0.179977	0.062845
ENSACAP00000008105	11.8366	0.151014	0	0	0	1.27034
ENSACAP00000002413	1.15949	0	0	3.24197	0	0.110205
ENSACAP00000016946	0.187066	1.87771	0.195489	0.266568	0.196916	1.80525
ENSACAP00000005858	2.47378	1.72308	0	0.245675	2.04733	0.208924
ENSACAP00000016873	4.34186	0.7548	0	0	0.109369	0.10714
ENSACAP00000001874	1.14002	1.5534	0.176395	0.466937	1.10072	0.451445
ENSACAP00000013732	0.926673	0.851501	0.161902	0	1.46609	1.13848
ENSACAP00000011794	0	1.17272	0	0	0.792623	0
ENSACAP00000021556	15.167	1.96028	2.76674	0	6.40424	8.1599
ENSACAP00000009821	0.498977	0	0	0	0.085352	104.439
ENSACAP00000011325	0.518194	0.707865	0.208263	0	1.33935	0.157411
ENSACAP00000008624	8.87893	6.92444	0.300126	16.6678	1.70471	7.42189
ENSACAP00000023204	0	0.536233	0	0	0.547498	28.9969
ENSACAP00000011882	0.503522	1.72627	0.345666	0.244868	1.00729	0.436725
ENSACAP00000014718	3.76819	5.37726	1.34562	7.03879	3.26243	10.6949

ENSACAP00000007993	72.3424	13.0164	0	0	0	80.9335
ENSACAP00000014901	0.49301	2.44425	2.89039	21.9015	1.40534	4.74138
ENSACAP00000022522	3.47348	0.896001	0.281397	4.46952	0.873724	2.35915
ENSACAP00000013933	28.0465	34.9114	4.47756	21.6241	12.9686	63.9758
ENSACAP00000001930	30.1116	37.9904	5.75202	9.14935	9.36182	130.606
ENSACAP00000019740	13.6171	1.31045	0	0.228724	1.9729	6.88899
ENSACAP00000004162	2.85052	0	0.729408	0.561462	1.33227	9.16213
ENSACAP00000005395	0.811147	0.00892	0	0	0.114522	0
ENSACAP00000008336	1.13343	1.69264	0	0	0	3.9625
ENSACAP00000001501	1.04461	1.55451	0	0	2.53752	0.342813
ENSACAP00000003727	2.72084	0.554594	0.675899	1.08815	1.44132	1.63574
ENSACAP00000009938	1.66965	20.1282	1.88068	14.3356	5.84649	9.2685
ENSACAP00000005181	2.83089	22.2892	0.421561	15.6599	72.6909	27.8752
ENSACAP00000015231	1.14164	14.7352	0.056342	6.34803	21.4168	8.67999
ENSACAP00000007502	53.2306	4.57071	0.488714	17.393	9.54044	18.6195
ENSACAP00000006629	2.61377	4.41173	2.44418	1.57091	0	0.464372
ENSACAP00000007083	0.842464	1.49058	0.150636	0.374798	1.23866	6.7609
ENSACAP00000005635	2.48506	0	0	0	0	0
ENSACAP00000011533	45.1539	44.4983	2.65229	15.1378	26.9485	50.4645
ENSACAP00000004222	3.11933	16.7518	1.28179	11.6942	2.00481	7.65491
ENSACAP00000001618	1.13156	0.55349	0.120937	0.375004	0.169127	0.448026
ENSACAP00000008500	0.23914	1.40788	1.40401	0.151323	1.34341	1.1374
ENSACAP00000001626	5.95445	11.855	1.55601	0.988661	8.22966	2.42746
ENSACAP00000003146	0	0.230323	0	0	0.004281	726.855
ENSACAP00000017421	0.827091	1.14894	0.922435	4.84119	2.03385	2.08975
ENSACAP00000020588	18.2177	2.22827	0.132137	0.659059	1.44071	1.13163
ENSACAP00000015300	0	1.25234	0.396014	1.13916	0.249013	0.390554
ENSACAP00000001315	0.553394	1.99276	0.154074	0	0.221772	0.527526
ENSACAP00000006476	1.00009	1.55841	2.60265	0.431297	0	1.25856
ENSACAP00000016107	0.359059	1.33376	0	0	1.59569	14.8542
ENSACAP00000006923	0.224309	0.271751	1.30E-09	0.698504	0.041889	1.28E-10

ENSACAP00000011215	1.89431	8.33863	1.6751	7.83639	1.30037	9.41408
ENSACAP00000016350	1.42865	1.10044	0.432593	0.516295	0.563561	2.98447
ENSACAP00000015816	8.40187	2.00197	0.354919	0	4.29819	5.34192
ENSACAP00000009331	1.84668	5.02908	0.973197	27.1141	13.8375	8.3768
ENSACAP00000010371	0.44544	0	0	0.11501	0	0
ENSACAP00000002201	0.209895	2.27793	0.527094	0.751583	1.17655	2.98747
ENSACAP00000020914	0.001636	0.071342	0	0	0	0.011376
ENSACAP00000015408	47.6232	138.387	12.8434	7.86327	22.2878	10.1269
ENSACAP00000013711	0.275285	0.201968	2.36952	0	0	0
ENSACAP00000016151	2.40468	2.24493	1.36521	5.80511	6.20941	2.49447
ENSACAP00000012725	5.2431	0.48189	0.020445	3.6663	0.877043	0
ENSACAP00000000034	4.16095	0.033544	0	0.248846	0	0
ENSACAP00000008386	0	51.3864	0	0	0	0.800515
ENSACAP00000009392	2.08782	6.93995	0.443473	6.48936	11.7676	2.8663
ENSACAP00000010681	19.6024	13.8624	2.16012	7.9502	7.52763	2.07973
ENSACAP00000006513	13.9838	4.82147	0	3.59771	0.666072	0.115854
ENSACAP00000010797	0	0.327511	0	1.15964	1.03095	0.790484
ENSACAP00000015971	0.418821	1.19239	0.171088	0.389113	0.393413	0.068593
ENSACAP00000016767	0	0.979887	0	0.555163	1.61915	0.117206
ENSACAP00000001116	1.32365	2.5387	1.22992	0.170832	0.259788	5.8258
ENSACAP00000017256	17.1447	9.73716	1.35514	5.98499	5.92116	73.5414
ENSACAP00000005783	0.050145	0.667203	0.529229	1.13098	0	4.33375
ENSACAP00000016382	25.1128	55.5498	5.4524	21.9472	14.3925	58.3356
ENSACAP00000013656	0.024788	0.084206	0.184124	0.319261	0	0
ENSACAP00000014179	2.69843	0	0	0	0	0.045021
ENSACAP00000003596	1.31063	2.8874	0.77356	5.67037	1.71567	0.512756
ENSACAP00000002125	0.935329	3.19211	0.390978	1.59941	0.590749	0.225656
ENSACAP00000003548	8.84893	5.28322	1.45297	20.1786	2.6991	41.2479
ENSACAP00000000381	0.129967	0.212782	0.357488	0	1.03677	0.034877
ENSACAP00000016789	0.613099	0	16.6179	0.560514	0.211505	2.80681
ENSACAP00000005833	1.64882	0.329944	0	0	0.374513	0.022089

ENSACAP00000010744	0.551446	0.376444	0.870816	0	0.879981	0
ENSACAP00000022448	2.90188	0	0	0	0.478706	0
ENSACAP00000014119	2.26007	5.55008	0.758714	0.473781	2.04062	3.44363
ENSACAP00000011394	0.567972	2.4629	0.786923	0.833188	1.11342	3.90785
ENSACAP00000015556	4.5685	0	0.11541	1.92413	0.103425	0.705227
ENSACAP00000008887	0.529507	0.214234	0.556008	0	0.297337	0
ENSACAP00000004628	0.099343	0.677797	0.765977	0.094966	0	0.413803
ENSACAP00000009915	1.26647	145.865	7.98651	3.30877	2.00693	3.75692
ENSACAP00000013931	14.3083	9.85741	0.562828	5.51367	1.0585	166.821
ENSACAP00000001168	2.54217	0.341677	0	1.00157	0.356597	0.085523
ENSACAP00000005291	0	0	0	0.143601	0.497288	2.41104
ENSACAP00000018579	0	0	0	0.335121	0.001927	0.000211
ENSACAP00000005187	1.48264	0	5.54E-10	0.069779	0.164286	1.45238
ENSACAP00000011800	0.370531	2.76627	0.451371	0	0.415916	17.1874
ENSACAP00000012790	0	0.648328	0	0	0	0
ENSACAP00000001055	0	1.87485	0	0	0	0
ENSACAP00000005729	3.30676	2.99955	0.238371	31.1226	2.1492	6.51852
ENSACAP00000011523	0	0	0	0	0	0
ENSACAP00000003040	0.507871	0	0	0	0	0
ENSACAP00000011731	3.79771	1.44131	0.043597	8.35291	0.392917	0.821124
ENSACAP00000007417	0	1.20372	0.090893	0	0.619447	0
ENSACAP00000012511	4.75547	1.92722	0	0	0	0.753326
ENSACAP00000003369	12.9471	3.98945	0.822968	5.75742	7.00862	1.13126
ENSACAP00000002283	1.13853	1.46044	0.389957	0.255344	0	0.096592
ENSACAP00000004136	0	0.231613	0	0	0.313793	0
ENSACAP00000010518	0	2.14329	0.43998	0	0	4.37642
ENSACAP00000003286	7.10E-05	0.381428	0	0.194494	0.262774	0.091975
ENSACAP00000005716	0.611773	0.572151	0	0	0	0
ENSACAP00000017354	5.78033	2.74417	0.792558	3.69764	4.94176	9.21183
ENSACAP00000006083	5.39889	6.98139	0.630887	1.0304	6.59354	3.58188
ENSACAP00000016123	0.979245	1.44139	0.975958	0.39869	1.32453	0.136742

ENSACAP00000010465	1.53302	0	0	0	0.210778	0
ENSACAP00000012411	0.14231	0.824662	0.079454	0.273382	0	1.78725
ENSACAP00000016793	5.28016	3.6569	55.5922	5.46309	1.46942	6.28663
ENSACAP00000004825	0.522424	0	0.078673	0.02112	0.144524	7.98E-06
ENSACAP00000000050	0.52559	1.32716	0.39246	0	1.30741	5.07438
ENSACAP00000003057	0.277977	0.03242	0	0.051292	0	0
ENSACAP00000008168	0.018553	6.33726	0.03941	0.018809	0.118385	0.100902
ENSACAP00000001158	2.07765	1.73731	0.408567	0.392047	0.113649	24.0595
ENSACAP00000005278	16.0177	10.1018	4.70483	20.315	11.1804	32.864
ENSACAP00000007849	1.41294	1.1301	0	0	0	4.5566
ENSACAP00000010018	5.08199	2.71158	0	0.415157	0.415544	11.3322
ENSACAP00000015658	2.25101	73.5154	70.7652	89.7598	6.08076	7.60695
ENSACAP00000017480	7.81629	5.73074	9.0784	2.56647	4.28171	2.71079
ENSACAP00000012559	7.07897	8.33631	0.352225	6.9941	2.77401	13.8364
ENSACAP00000011080	2.04986	7.94324	1.14126	0.444383	3.31327	4.89073
ENSACAP00000020529	131.958	82.8701	59.6026	31.0688	82.6547	47.2933
ENSACAP00000017077	1.47675	2.50925	0	0	0.520146	0.263839
ENSACAP00000008228	0.423443	0.399017	0.770598	0	1.68178	0
ENSACAP00000009344	3.96136	18.2874	7.51881	5.46428	30.7775	3.88035
ENSACAP00000004582	0.209896	0	0	0	0	0
ENSACAP00000007335	0	0	0.025517	0	0.130998	0.021972
ENSACAP00000022907	4.53692	0.049322	0	0	0.34242	0.37789
ENSACAP00000017554	0	0.109053	0.263017	0	0.229811	0
ENSACAP00000004644	3.07656	1.54831	4.52927	6.5923	25.6479	6.4782
ENSACAP00000016408	33.6859	28.2422	6.69787	15.0017	21.3416	40.198
ENSACAP00000001445	1.24353	2.37899	1.1199	0.475968	2.65323	7.24376
ENSACAP00000005126	0	0	0	0.160568	0.677084	0.086562
ENSACAP00000014168	6.90809	2.11096	1.31426	4.33571	4.03697	2.42718
ENSACAP00000016779	2.26456	5.09071	1.10904	4.53967	0.666232	0.326344
ENSACAP00000009546	6.10165	4.51159	1.43156	4.79819	1.23972	12.1944
ENSACAP00000011041	8.66468	1.68325	0.052025	0.122743	0.390606	0.769309

ENSACAP00000013311	0.581787	0.507003	0.05631	0.138234	0.448594	0.094874
ENSACAP00000014251	0	2.91367	0	0.599163	0.752444	0.383923
ENSACAP00000005764	1.96652	0.554304	0.06589	0	0	0
ENSACAP00000008060	0	0.40544	0.000234	0.000171	1.39436	0.23488
ENSACAP00000001885	0.00761	2.89E-07	6.79E-08	8.18E-07	1.65189	0.1073
ENSACAP00000009299	16.3564	54.7343	2.45018	2.77417	12.2657	52.2824
ENSACAP00000012577	3.1799	3.99629	0.295515	0	1.11658	0.476356
ENSACAP00000012479	21.1347	13.2958	4.69455	5.27844	16.005	16.7149
ENSACAP00000002239	0.355237	8.8044	2.70382	10.1785	23.5026	6.86397
ENSACAP00000000442	0.239004	0.887198	0	0	0.710483	0
ENSACAP00000006222	1.0604	1.7125	0.617101	0	0.539153	0.406012
ENSACAP00000002650	18.1303	0.084092	0	0	0	0.859301
ENSACAP00000008354	0.187241	0	0	0	0	0.018998
ENSACAP00000008189	0.008571	0.348789	0	0	0.030125	0.010253
ENSACAP00000009478	0	0	0.042702	0	0	0
ENSACAP00000012057	0.033848	1.2646	0.661897	0.21944	0.594766	5.94E-06
ENSACAP00000012140	0.693727	1.57734	0	1.91526	0.759613	3.61906
ENSACAP00000006657	0.606541	1.92691	0.147584	0.338826	0.37731	0.041949
ENSACAP00000013595	0.440723	3.62887	0	0	0	2.11454
ENSACAP00000014885	0.543718	0	0.702946	0.263922	1135.32	0.846513
ENSACAP00000001047	2.13802	1.64265	0.003149	0.79591	0.306151	4.29601
ENSACAP00000006472	5.18323	7.5614	0.485881	29.8579	5.74657	9.57647
ENSACAP00000001737	1.95142	2.45821	2.33E-08	1.10E-08	0.196246	0
ENSACAP00000009495	63.3984	1.57156	9.42914	2.09215	10.7693	11.4163
ENSACAP00000010489	22.5099	27.3631	2.78499	10.076	4.39993	14.1941
ENSACAP00000006502	0	0	0	0	0	0
ENSACAP00000014526	29.1627	17.4793	4.15606	1.98017	7.86064	66.6454
ENSACAP00000017040	21.4229	31.246	3.10582	2.94648	9.73461	29.437
ENSACAP00000002954	0	0.021462	0.274914	0.518235	4.24633	10.1076
ENSACAP00000011565	0	1.08498	0.123723	0.143601	0.62161	0.062448
ENSACAP00000008830	4.17376	32.9086	0.538839	2.00858	8.4844	16.8039

ENSACAP00000013318	32.2161	20.9545	5.78782	2.92172	4.56347	78.7293
ENSACAP00000009221	16.4102	13.8221	5.31263	2.41263	3.96006	0.573768
ENSACAP00000000009	11.0607	20.0192	2.54276	15.7734	4.89428	2.95594
ENSACAP00000007838	10.3269	13.8896	2.5696	8.33971	2.93468	6.40325
ENSACAP00000014977	0.038951	0	0.238244	0	0	1.038
ENSACAP00000008288	0.59126	1.22163	0	0.287773	1.03669	0
ENSACAP00000017420	0.815697	5.62156	0.058518	0	0.164865	0.045385
ENSACAP00000006334	1.55432	1.27929	0	0	0	16.4456
ENSACAP00000016788	1.12787	2.51438	0.720005	40.196	3.52244	2.48773
ENSACAP00000015939	0.223201	0.022807	0.165061	0	0	0
ENSACAP00000000378	0	7.81413	0	0.090709	0	0.000242
ENSACAP00000011621	0.002506	0.040176	0.004845	0	0.007995	0
ENSACAP00000011871	3.61508	2.2838	0.15178	0.059852	0.398515	0.10202
ENSACAP00000011671	28.5646	0.160435	0	9.77408	0.116579	0.026964
ENSACAP00000003647	1.17094	0	0	0	7.60898	0.923104
ENSACAP00000008929	0.32762	18.5255	0.26038	0.16019	0.5746	0.31182
ENSACAP00000022226	0.149615	2.30819	0	0	0	0.25803
ENSACAP00000019515	0	11.4557	0	0.24914	0.110796	0.05464
ENSACAP00000005274	2.77158	0.736284	0.209649	0.239713	1.43523	1.04772
ENSACAP00000013614	1.77549	0.012778	0	0	0.007957	0
ENSACAP00000012329	83.8397	164.006	32.4238	66.6096	35.2681	224.202
ENSACAP00000016496	3.38227	2.15831	0	0.49654	12.4841	0.872877
ENSACAP00000011662	0.922241	2.33488	0	3.82699	0.764611	1.69394
ENSACAP00000011157	1.05632	134.163	0	0.366902	1.52788	1.35657
ENSACAP00000015218	24.6629	8.03238	0.747037	27.6211	4.97219	12.9152
ENSACAP00000004467	930.036	1053.07	851.98	357.18	1075.3	1168.91
ENSACAP00000009803	425.203	9.64136	3996.98	22.0618	6.57345	72.9969
ENSACAP00000003843	23.1034	242.675	6.40238	22.2437	3.98828	151.385
ENSACAP00000013010	222.747	124	17.0137	84.1111	42.8344	92.1874
ENSACAP00000009832	26.582	8.00811	562.296	2.74288	0.954115	2.79564
ENSACAP00000017274	0.130092	0	0	0.489076	661.882	0

	ENSACAP00000016356	314.876	0.554498	0.254866	0.565429	0.562039	2.05331
	ENSACAP00000001457	42.4337	1.44903	59.2559	7.11569	45.1389	312.384
	ENSACAP00000006616	94.2281	57.978	12.3679	68.8764	33.223	46.2403
	ENSACAP00000008156	0.71902	0.307503	0.253042	0.452523	210.421	0.199105
	ENSACAP00000012414	32.7448	70.0169	9.55894	20.7619	11.7767	178.915
	ENSACAP00000008943	20.8192	75.4446	10.0576	76.6192	11.8327	76.1043
	ENSACAP00000012268	56.7433	52.5249	6.54923	94.2844	11.6687	115.189
	ENSACAP00000003664	6.06873	3.41914	91.045	61.7463	5.5864	3.15372
	ENSACAP00000001895	51.2686	6.70714	0.921844	0.659825	3.02789	1.62014
	ENSACAP00000010758	11.6401	59.3362	2.86333	12.1318	7.47839	67.0762
	ENSACAP00000016889	3.15882	5.87642	23.4102	0.782768	5.77503	6.36612
	ENSACAP00000021261	3.95308	22.0078	0.153595	8.74252	0.46349	1.96337
	ENSACAP00000006308	7.88347	0	0	0	0	0
	ENSACAP00000019091	7.08736	0.291752	0	0.20954	0	0.808289
	ENSACAP00000001757	4.44634	0.90526	0.074581	8.16959	1.04745	2.46045
	ENSACAP00000014797	3.11661	0.052932	0	0	0.199434	0.192623
	ENSACAP00000005022	1.47905	6.18229	0.917932	1.13312	0.928093	0.446324
	ENSACAP00000022783	6.17385	0.408141	0.608298	7.28023	0	5.08931
	ENSACAP00000020092	0.107396	0.273758	0.170513	0	2.33637	0.179724
	ENSACAP00000006379	0	0	4.80292	0.400213	0	0
	ENSACAP00000005058	0	0.070644	0	0.207366	4.2783	0.181947
	ENSACAP00000004056	2.5726	0.0969	0	0.047941	0.095841	0
	ENSACAP00000011853	0.63041	0.421313	0	0.691861	1.27036	0.030586
	ENSACAP00000018492	1.961	0.153738	0	0.440688	0	2.54383
	ENSACAP00000004932	0.48636	1.16017	0	0	0.765353	0
N. phrynoides	PSGs	brain	heart	liver			
	ENSACAP00000004108	1.92951	0.02714	0			
	ENSACAP00000009739	2.66803	0.053922	0			
	ENSACAP00000023290	7.297	0.024739	0			
	ENSACAP00000010546	7.53433	3.76094	0			
	ENSACAP00000003528	4.93488	5.7034	1.19618			

ENSACAP00000004644	10.6941	36.4969	1.90299
ENSACAP00000001089	10.1273	38.1406	4.57709
ENSACAP00000001626	5.82998	5.6912	1.51968
ENSACAP00000014702	37.6553	308.826	14.8
ENSACAP00000012786	76.8458	14.8507	4.86266
ENSACAP00000000060	336.506	1973.14	179.52
ENSACAP00000017016	0.439077	234.053	457.647
ENSACAP00000010811	449.457	1677.3	389.411
ENSACAP00000010281	2.59567	23.6529	4.23222
ENSACAP00000008583	147.219	0.119203	0.245468
ENSACAP00000005899	47.7693	2.0613	0.42675
ENSACAP00000015045	35.1961	28.2431	19.6837
ENSACAP00000004154	3.9437	8.3856	5.60567
ENSACAP00000010244	1.01213	63.4687	0.072337
ENSACAP00000017999	6.82347	10.7306	9.72927
ENSACAP00000002155	0.179261	22.23	98.2864
ENSACAP00000014692	3.56613	20.065	2.42555
ENSACAP00000006379	8.28911	0.375249	0.292961
ENSACAP00000016462	6.3435	1.88635	0.242336
ENSACAP00000009907	2.2854	0	0
ENSACAP00000016661	6.93854	0.312322	0.256172
ENSACAP00000007387	0.217112	1.25233	0
ENSACAP00000002450	0.54735	0.482362	0
ENSACAP00000008096	14.4758	16.9448	0.877635
ENSACAP00000011007	3.61991	2.19824	0.792604
ENSACAP00000005559	5.88607	3.81185	0.600964
ENSACAP00000010278	2.37456	3.3895	0
ENSACAP00000000748	0	2.47279	0
ENSACAP00000016585	0.744605	3.34114	0
ENSACAP00000013502	2.60359	0	0
ENSACAP00000002004	3.7549	6.34282	0.535776

ENSACAP00000008893	0.483065	0	6.10299
ENSACAP00000004484	2.44091	0.42827	0.145252
ENSACAP00000022448	1.49986	0.837607	0.331129
ENSACAP00000008820	4.05881	2.21004	0
ENSACAP00000003323	3.71521	0.188777	0
ENSACAP00000008624	0.158505	1.63848	0.393181
ENSACAP00000002778	1.69501	0.649326	0.041195
ENSACAP00000015858	1.02713	0.498256	2.74132
ENSACAP00000008740	1.80991	0	0
ENSACAP00000015283	2.01188	0	0
ENSACAP00000005035	4.38349	1.02222	1.37541
ENSACAP00000002479	2.10056	0.246251	0
ENSACAP00000004168	0.120647	0	0.159786
ENSACAP00000015870	0.684353	0.24168	0
ENSACAP00000006881	3.45968	3.01867	0
ENSACAP00000016956	0.552901	0.087855	0.473578
ENSACAP00000001366	2.50349	0.730627	0.637766
ENSACAP00000016170	0	0.408908	212.972
ENSACAP00000002246	0.03506	5.44187	0.142788
ENSACAP00000003956	2395.04	3655.25	2134.77
ENSACAP00000006283	1.50791	0	0.332892
ENSACAP00000015368	8.32366	4.52615	3.00251
ENSACAP00000017541	1.05281	0.57696	0.596302
ENSACAP00000009180	4.92216	14.3224	4.00677
ENSACAP00000001369	0.12423	1.06214	0
ENSACAP00000012275	19.5536	27.918	17.038
ENSACAP00000013942	8.015	4.71024	0.822037
ENSACAP00000007398	1.16404	4.63919	0
ENSACAP00000006927	2.74012	0.170831	0.104227
ENSACAP00000017456	1.83605	0.213314	0
ENSACAP00000013792	87.3764	174.52	38.4617

ENSACAP00000001605	1.87823	1.17189	0
ENSACAP00000016547	1.85731	3.42747	4.25378
ENSACAP00000009331	1.27854	0.460749	0.126342
ENSACAP00000014514	3.8599	7.61462	6.53609
ENSACAP00000001757	10.903	2.38371	0.998818
ENSACAP00000007005	4.67917	2.49045	0
ENSACAP00000006720	2.65461	1.76703	0.976056
ENSACAP00000004177	0.972855	0.433469	0
ENSACAP00000000220	2.99722	0.298001	0
ENSACAP00000002909	1.29303	0	0
ENSACAP00000004975	1.74719	0.295988	0.396493
ENSACAP00000022859	5.89822	2.68263	2.06019
ENSACAP00000007715	0.303132	0.62296	0
ENSACAP00000016617	18.7922	0.17093	0.273892
ENSACAP00000008647	0	0.41634	4.49819
ENSACAP00000008204	3.71198	7.78533	0.890272
ENSACAP00000012138	1.40732	2.43907	2.39929
ENSACAP00000008420	4.7436	0.782105	0.366921
ENSACAP00000010102	11.8585	2.64023	0.450601
ENSACAP00000007342	9.257	0.794411	1.88589
ENSACAP00000002583	0.893782	0.982248	0
ENSACAP00000013530	2.34594	0.653974	0.57751
ENSACAP00000002892	1.99498	0.304328	0
ENSACAP00000000869	4.46872	0	0
ENSACAP00000015851	5.49659	0.738581	0.112139
ENSACAP00000006332	1.84045	0	0
ENSACAP00000000778	0	0.803016	0.959395
ENSACAP00000005827	1.15963	1.16745	1.02257
ENSACAP00000015926	6.65251	2.3453	1.79324
ENSACAP00000005033	0.474913	0.273414	0.523493
ENSACAP00000006828	0.548974	0.211659	3.13445

ENSACAP00000005315	162.232	118.225	32.1369
ENSACAP00000020564	0.366315	2.9417	8.26195
ENSACAP00000002210	1.1122	1.38635	0
ENSACAP00000002372	0	1.62489	6.49504
ENSACAP00000009217	2.19581	1.42213	0
ENSACAP00000000577	2.78388	0	0
ENSACAP00000017591	2.00332	0.462474	0.608661
ENSACAP00000012225	9.12122	6.00554	1.49598
ENSACAP00000006596	2.99764	7.0199	0
ENSACAP00000001925	0.523183	0.388874	3.84E-06
ENSACAP00000011157	0.733829	4.86915	0
ENSACAP00000010520	0.515328	0	0
ENSACAP00000008645	0	0	0.096566
ENSACAP00000022842	0.419283	2.47695	0
ENSACAP00000005078	0	3.05141	0.954639
ENSACAP00000021570	0.261497	0.42842	0.220105
ENSACAP00000016155	4.10634	0.126753	0
ENSACAP00000014368	9.48515	5.13369	0
ENSACAP00000004064	1.17084	0.461754	0
ENSACAP00000007082	0.054859	0.129334	0.436233
ENSACAP00000003280	0.869911	2.01057	0.855904
ENSACAP00000000516	0	15.214	11.1565
ENSACAP00000003816	4.38848	8.29132	6.65127
ENSACAP00000002264	0	11.7003	0.96566
ENSACAP00000020940	0.488928	0.990349	0
ENSACAP00000015617	4.14067	7.53481	0.852435
ENSACAP00000007271	0.114675	0.230794	0.331677
ENSACAP00000007546	1.83926	0.470876	0
ENSACAP00000014496	2.97756	12.1236	0.352769
ENSACAP00000006856	2.4145	4.40674	0.177241
ENSACAP00000007588	1.25497	0	0.403529

ENSACAP00000008903	0.88557	0.46789	0
ENSACAP00000012760	0.071714	13.1729	17.2924
ENSACAP00000000442	2.24578	1.73491	0.521739
ENSACAP00000003539	0.124878	2.53182	0.262525
ENSACAP00000002580	30.617	23.9978	3.63028
ENSACAP00000015047	0	2.68237	0.461768
ENSACAP00000013241	1.79391	0.453727	0.581123
ENSACAP00000008163	19.632	0	0
ENSACAP00000013146	0.45681	0.743574	6.33E-08
ENSACAP00000002766	26.9082	16.7505	6.53657
ENSACAP00000004996	1.91314	0.575288	0.41472
ENSACAP00000017656	1.29205	11.2043	0.566146
ENSACAP00000016238	8.84483	16.2699	12.1477
ENSACAP00000011995	70.0106	1.97257	0
ENSACAP00000006621	1.61859	0.180055	0
ENSACAP00000012376	9.82752	4.23906	2.19974
ENSACAP00000000791	11.8562	0.238606	0.345601
ENSACAP00000004222	8.06724	0.346501	0.372376
ENSACAP00000006131	0.310585	0.038896	0
ENSACAP00000005095	0	0.514935	0
ENSACAP00000001510	1.10053	9.77115	0
ENSACAP00000000344	12.4532	1.43034	0.57616
ENSACAP00000023463	9.67143	46.8211	0.823045
ENSACAP00000010113	0.74472	0.49999	0
ENSACAP00000019661	1.51983	0	0
ENSACAP00000000009	1.61417	0.654313	0
ENSACAP00000008308	0.114609	1.30E-07	0
ENSACAP00000022783	1.722	0.457391	0
ENSACAP00000011360	2.71398	0.33601	0
ENSACAP00000000097	0	0	0
ENSACAP00000011537	0	0.803396	0

ENSACAP00000008354	4.06626	1.42196	0.168961
ENSACAP00000013343	3.95549	9.95695	2.01425
ENSACAP00000021784	5.4513	0.821973	0.879325
ENSACAP00000001230	0.673304	1.22167	5.96E-07
ENSACAP00000001558	59.741	25.0209	3.5419
ENSACAP00000005642	2.54229	5.26121	0.106308
ENSACAP00000013183	4.40447	0.870398	0.9604
ENSACAP00000001599	14.5686	16.0709	6.54795
ENSACAP00000017690	3.00338	1.66422	0.382856
ENSACAP00000003089	2.75889	2.51134	1.5429
ENSACAP00000006024	0.778626	0	0
ENSACAP00000013812	13.8946	8.82518	0.889295
ENSACAP00000018355	5.37553	1.85724	1.82081
ENSACAP00000014988	7.26647	3.33978	0.641782
ENSACAP00000010827	5.10009	3.58341	2.54288
ENSACAP00000011651	552.875	163.98	59.0032
ENSACAP00000012440	9.76125	14.0871	2.16543
ENSACAP00000018554	1.63447	0.726121	0.864555
ENSACAP00000000726	19.7924	21.3992	3.87425
ENSACAP00000002433	0.198365	0	0.125283
ENSACAP00000015077	5.6788	10.0505	19.4667
ENSACAP00000003827	6.18297	0.768018	0.136244
ENSACAP00000014423	2.70357	0	0
ENSACAP00000014302	26.0788	0.054447	0.07541
ENSACAP00000012479	5.93826	11.9042	0.754407
ENSACAP00000014578	0.966667	4.08056	19.3917
ENSACAP00000017147	3.039	1.71358	1.13984
ENSACAP00000016402	5.31777	2.43159	0
ENSACAP00000008480	1.20003	0.831629	0.867373
ENSACAP00000001611	0.014903	0.000174	0
ENSACAP00000013158	2.52372	0.591976	0

ENSACAP00000007739	0.465732	0	0
ENSACAP00000017417	1.87324	1.38669	0.761584
ENSACAP00000008105	2.00445	4.23376	2.50345
ENSACAP00000014951	0.598864	0.707457	2.49E-09
ENSACAP00000001283	7.40819	9.98637	1.35737
ENSACAP00000002021	6.6984	2.64948	2.25879
ENSACAP00000023167	0.512729	2.22851	0
ENSACAP00000010524	3.72393	8.50619	1.58044
ENSACAP00000017711	0.130367	0.064658	0.150879
ENSACAP00000017072	0.355613	0.490119	0.161487
ENSACAP00000015946	1.68031	0	0
ENSACAP00000006456	1.9223	1.34124	0.506977
ENSACAP00000016387	2.35653	0.968545	0
ENSACAP00000013434	0.833982	2.49E-06	0
ENSACAP00000015102	0.560224	0.331867	0.539301
ENSACAP00000005965	0	0	0
ENSACAP00000004794	6.23631	4.56035	1.76832
ENSACAP00000013104	45.4536	16.3416	9.54066
ENSACAP00000013145	1.27079	3.78368	0.862611
ENSACAP00000019188	0.804956	1.45858	1.66611
ENSACAP00000004204	6.27321	9.55863	2.34505
ENSACAP00000007602	3.73226	2.98426	3.95726
ENSACAP00000005007	0	0.460466	0
ENSACAP00000004166	0.736164	0.554467	0
ENSACAP00000001278	9.8056	3.79305	0
ENSACAP00000007253	3.49363	9.14279	1.76499
ENSACAP00000011005	0.159655	0.070637	0.127534
ENSACAP00000005757	49.8236	10.6401	1.28395
ENSACAP00000013947	23.1118	0.194744	0
ENSACAP00000022624	1.92422	0.35166	0.303794
ENSACAP00000009030	0	0.873862	0.473381

ENSACAP00000009618	0.697115	5.10923	0
ENSACAP00000000649	1.89208	0.455035	0
ENSACAP00000001612	0.30354	0.071905	0
ENSACAP00000015388	7.24327	1.35434	0.470292
ENSACAP00000006543	2.57717	2927.22	6208.06
ENSACAP00000011812	8.18835	8.27909	1.61806
ENSACAP00000009049	0.056584	0.054716	0.067791
ENSACAP00000003054	0.948986	0.20829	0
ENSACAP00000015745	5.97758	16.74	4.10533
ENSACAP00000006842	0.772869	2.0573	0
ENSACAP00000001710	1.9416	0.567701	0
ENSACAP00000001566	1.07896	1.19845	0.394539
ENSACAP00000000982	0.046018	0	0
ENSACAP00000002294	0.506594	3.16329	0.136318
ENSACAP00000008439	0.860423	0.098958	0.223283
ENSACAP00000003383	4.02812	1.62601	0.819079
ENSACAP00000008137	1.84877	3.0193	0.380864
ENSACAP00000003297	3.01031	1.40768	0
ENSACAP00000003866	0.039548	0.016995	0
ENSACAP00000003768	13.4014	0.062859	0.019306
ENSACAP00000022899	0.509635	9.12E-06	0
ENSACAP00000010317	0	4.8447	28.7411
ENSACAP00000020699	15.5216	121.181	523.536
ENSACAP00000012439	1.46806	3.36201	1.77546
ENSACAP00000020710	3.01923	6.75984	1.60557
ENSACAP00000022567	2.21429	0.564482	0.075139
ENSACAP00000004779	1.04644	0	0.428815
ENSACAP00000021704	0.751166	0	0
ENSACAP00000011424	0	0	0
ENSACAP00000010845	2.65913	0.524254	0
ENSACAP00000007239	1.30313	0.134394	0

ENSACAP00000011603	2.54404	2.80107	1.65755
ENSACAP00000015407	0.953423	0.729608	0.746592
ENSACAP00000007334	4.5163	3.99732	1.8088
ENSACAP00000007175	2.94368	1.0187	0.116929
ENSACAP00000003183	0	0.006294	0
ENSACAP00000017607	1.35468	5.34853	1.65041
ENSACAP00000013720	21.7504	25.0091	5.90553
ENSACAP00000005180	2.29385	1.43851	2.33765
ENSACAP00000022351	1.81416	1.83936	0.205385
ENSACAP00000009136	0.059798	0.304515	0
ENSACAP00000001610	0.967475	5.05906	0.884373
ENSACAP00000008929	0.921976	0.38957	0.147135
ENSACAP00000002048	3.46165	1.50037	0.480253
ENSACAP00000005316	7.59175	3.75359	4.66925
ENSACAP00000003497	0.204777	6.31E-10	0
ENSACAP00000009390	3.31167	0.554834	0.358486
ENSACAP00000006815	0	0	0
ENSACAP00000007914	0	0.200595	0.18548
ENSACAP00000013835	0.654264	0.618352	0
ENSACAP00000013028	0.5237	0.07525	0.102208
ENSACAP00000021856	1.17675	1.52033	2.70296
ENSACAP00000004973	0	0	0.120817
ENSACAP00000009086	0	0.550294	0.69096
ENSACAP00000009363	0.426793	0.278813	0.138555
ENSACAP00000010079	0.773469	0.039825	6.67E-09
ENSACAP00000015125	0.000857	36.2554	122.464
ENSACAP00000010489	0	0	0
ENSACAP00000011352	4.90717	4.77705	3.47577
ENSACAP00000011045	0.258734	0	0.035841
ENSACAP00000002842	45.3954	23.4749	9.70221
ENSACAP00000019138	2.80998	0.757942	0

ENSACAP00000011545	0	0	0
ENSACAP00000005130	0.114728	0	0
ENSACAP00000020409	4.07102	7.07143	1.84005
ENSACAP00000007392	1.3018	1.52579	0
ENSACAP00000015291	0.248859	2.65129	1.20974
ENSACAP00000009566	2.35362	0.6277	0.433199
ENSACAP00000007135	4.94287	0.528928	0
ENSACAP00000005323	0.081177	6.86243	26.1253
ENSACAP00000001907	128.926	4.2925	0.363307
ENSACAP00000013905	0	1.70728	1.60304
ENSACAP00000013049	0.883526	2.55755	0.249701
ENSACAP00000011838	19.7293	3.31787	0.490756
ENSACAP00000013508	62.8143	0.489159	0.00232
ENSACAP00000012114	2.86504	15.0282	2.51594
ENSACAP00000004033	0.196773	0.0298	0
ENSACAP00000021749	3.39844	0.994672	0.91552
ENSACAP00000013144	134.459	71.0199	69.511
ENSACAP00000016373	3.95119	2.19684	1.9486
ENSACAP00000009134	11.1344	10.5837	1.83437
ENSACAP00000020059	1.61234	3.92033	1.62683
ENSACAP00000000934	3.34366	0.982068	3.72027
ENSACAP00000005274	1.90865	2.18412	0.915523
ENSACAP00000015231	20.9588	34.1593	69.838
ENSACAP00000015232	2.03918	0	0
ENSACAP00000004913	3.08366	0.766368	0.267205
ENSACAP00000012614	0	0.953318	5.48938
ENSACAP00000004463	1.33433	3.53916	0
ENSACAP00000001568	0	0.941594	0.624117
ENSACAP00000001641	0.128435	0	0
ENSACAP00000006565	4.42509	3.79742	1.02878
ENSACAP00000007441	1.07749	0.046319	0.504102

ENSACAP00000006202	1.33628	2.13744	2.13899
ENSACAP00000017732	0.533161	1.89098	0
ENSACAP00000001943	12.8843	7.98602	1.18333
ENSACAP00000016429	1.6413	1.18134	0.130892
ENSACAP00000006487	16.2647	6.88629	6.16883
ENSACAP00000015218	4.78976	0.710778	1.07186
ENSACAP00000007400	21.4334	13.7727	20.5211
ENSACAP00000002933	0.040264	0.626729	0
ENSACAP00000012152	14.7385	8.57175	3.87936
ENSACAP00000002239	1.77291	66.1975	353.381
ENSACAP00000016035	2.75414	3.95991	3.17876
ENSACAP00000007406	0.588832	1.27E-06	3.54E-05
ENSACAP00000006605	3.52459	0.867705	0.549843
ENSACAP00000015327	0.458303	0.32494	0.276025
ENSACAP00000018017	6.75804	2.67832	1.84068
ENSACAP00000008010	1.128	1.55996	0
ENSACAP00000008691	0	0	0
ENSACAP00000014854	3.10712	6.08058	1.28514
ENSACAP00000013202	0.052669	0	0.002338
ENSACAP00000015715	2.68985	14.9393	10.3968
ENSACAP00000012577	0.319767	0.619699	0.479282
ENSACAP00000006218	1.42188	0.074296	0.125234
ENSACAP00000008525	0.677403	0	0
ENSACAP00000009525	0.116602	1.81238	0.16454
ENSACAP00000016067	0	0	0
ENSACAP00000016408	8.35753	3.54426	1.88271
ENSACAP00000003683	4.12584	0.526568	0.188141
ENSACAP00000014072	28.3263	0.627486	0.164666
ENSACAP00000010337	0.847309	0	0.047949
ENSACAP00000000221	0.705668	0.043468	0
ENSACAP00000006046	2.07235	0.720252	0.574054

ENSACAP00000017010	3.04018	8.18963	9.1979
ENSACAP00000002361	0	2.53274	0
ENSACAP00000000355	11.3543	0.690189	1.98209
ENSACAP00000017296	3.60593	4.46405	0.092999
ENSACAP00000017567	78.5364	133.944	104.623
ENSACAP00000007428	4.25005	2.39066	2.31596
ENSACAP00000008955	3.20096	0	0
ENSACAP00000012390	0.09838	0.091693	0
ENSACAP00000014132	53.0362	0	0
ENSACAP00000016553	4.24219	2.21102	1.15674
ENSACAP00000016819	20.4093	15.1421	4.62014
ENSACAP00000006502	11.276	81.515	7.86571
ENSACAP00000000190	1.28126	1264.44	4055.95
ENSACAP00000002268	23.2209	13.8907	5.05606
ENSACAP00000002161	593.21	3254.67	959.838
ENSACAP00000004828	795.912	7.21444	2.65449
ENSACAP00000010109	178.814	310.26	246.253
ENSACAP00000017866	66.9977	216.803	28.7273
ENSACAP00000005561	0.265347	116.352	288.28
ENSACAP00000009495	40.8161	47.2902	14.0712
ENSACAP00000001433	101.295	51.7779	43.6446
ENSACAP00000003435	75.9677	80.5918	33.217
ENSACAP00000017274	78.6641	80.1739	17.7361
ENSACAP00000006508	1.19256	79.7944	0
ENSACAP00000018531	56.1486	18.1134	10.1358
ENSACAP00000006555	37.6474	36.6474	13.2159
ENSACAP00000000530	29.183	0.031498	0.033939
ENSACAP00000006240	29.7966	58.1103	9.64772
ENSACAP00000003035	37.8978	31.7497	6.03504
ENSACAP00000004891	9.25568	58.3229	4.95456
ENSACAP00000002037	59.4863	0	0.215128

	ENSACAP00000000925	9.21254	17.9237	3.7244			
	ENSACAP00000004674	2.34221	0.196313	0.280238			
	ENSACAP00000019744	0.703184	1.64845	4.34313			
	ENSACAP00000014871	2.30947	0.842763	0			
Q. spinosa	PSGs	brain	heart	liver	ovary	skin	testis
	ENSACAP00000023038	0.440349	1.21022	0.168382	0	0.318539	0.255496
	ENSACAP00000011007	7.79031	0.827077	0	1.78306	0.081191	37.838
	ENSACAP00000016677	1.28353	0	0	0	0	0
	ENSACAP00000004467	0.092172	1.46938	0.249346	0.074482	1.04235	1.29377
	ENSACAP00000017751	0.312409	0	0.213475	0	0.948952	0
	ENSACAP00000015070	91.5279	74.4423	10.496	4.03419	125.612	195.646
	ENSACAP00000007659	1.55679	8.85625	33.6726	0.564433	3.69219	3.1271
	ENSACAP00000017283	1.00716	0	0	0.023234	0	0.019367
	ENSACAP00000015849	1.99676	0	0	0	0	0
	ENSACAP00000005899	0	0.910017	0	0	0.594949	0.071835
	ENSACAP00000000391	0.133039	0	0	0	0	0.081848
	ENSACAP00000015147	0.060833	0.643698	28.97	1.3438	0.030302	1.7032
	ENSACAP00000022313	0.886834	0	0	0	0	0
	ENSACAP00000002155	3.61065	1.63793	331.49	1.80806	1.0346	0.771401
	ENSACAP00000010053	38.1052	205.283	52.7317	15.8153	65.9849	57.6875
	ENSACAP00000010147	0.596672	0	2.26629	85.7319	339.08	0.338051
	ENSACAP00000006604	27.5526	15.4298	4.75796	55.9505	21.0746	30.8713
	ENSACAP00000012470	41.613	35.6952	8.77621	16.5329	29.7574	61.9815
	ENSACAP00000016067	5.11805	1.23392	0.185032	0.2242	3.25615	1.49719
	ENSACAP00000005089	6.39343	2.42441	0.989231	7.15795	2.89487	1.05333
	ENSACAP00000007005	1.72369	0	0	0	0	0.056886
	ENSACAP00000001580	1.84955	0	0.11338	0.067559	0	0.05841
	ENSACAP00000000932	1.90163	0	0.039926	0.023392	0.150336	0.039297
	ENSACAP00000004466	0.431525	0.85273	0.078306	1.32422	0.926685	7.76382
	ENSACAP00000017496	4.17059	0.061706	0.084697	0.248254	1.4674	0.062615
	ENSACAP00000010758	2.63792	1.54362	0	2.79087	1.12149	3.95209

ENSACAP00000004078	2.39202	0	0	0	0	0
ENSACAP00000004798	0.500513	0.954429	0.287972	0.113937	0.145461	0.489118
ENSACAP00000022284	0	1.5083	0	0	0	0.409259
ENSACAP00000001589	0.443187	1.77921	0.239476	0	0.090959	0.867072
ENSACAP00000023366	4.80972	0	0	0	0	0
ENSACAP00000009761	1.67932	0.890335	0.720305	15.1548	1.22716	15.3119
ENSACAP00000021933	0.194486	0.405652	0	0	0.323003	1.12887
ENSACAP00000001760	0.326379	0.066348	0.522492	0.051789	0.595677	0.792284
ENSACAP00000005047	9.71634	7.72551	9.06E-06	44.0784	8.06356	7.19743
ENSACAP00000015416	9.51647	30.8159	11.4138	7.47099	11.6897	32.3541
ENSACAP00000011696	103.783	0	0.049309	0	0.408878	0
ENSACAP00000006319	0.274655	0.688728	0.156203	0.03059	0.117786	0.619554
ENSACAP00000013296	0.376631	0.565651	0.859477	0.103821	0.393986	0.45968
ENSACAP00000022652	1.85923	2.16199	0.197082	0.83818	1.35895	7.17962
ENSACAP00000013672	10.9959	11.2892	3.39213	10.1721	11.6823	36.3003
ENSACAP00000011083	15.4296	4.40306	16.6597	63.4174	20.613	6.16951
ENSACAP00000008841	3.03592	1.73725	0.182033	0.041718	0.738878	2.12141
ENSACAP00000010618	0.184547	0.993569	0.097239	30.5396	0.877212	8.02182
ENSACAP00000002276	3.59117	0	0.010666	0	0.032025	0.477644
ENSACAP00000023397	1.44034	1.90479	0.153724	1.60462	0.902087	2.14422
ENSACAP00000015246	1.60052	0.883215	0.268119	0.317759	0.135335	1.31517
ENSACAP00000012369	1.40906	0.105855	0	0.021375	0.164915	0.035861
ENSACAP00000001643	2.33517	0.314603	0	1.88466	0	0.928254
ENSACAP00000011628	0	0	0	0.027761	0.05722	0
ENSACAP00000008070	3.00855	10.5791	2.55639	0.711902	3.9326	5.43313
ENSACAP00000009687	1.88911	0	0	0	0	0
ENSACAP00000003229	2.2307	1.32654	0	1.03565	0.790757	18.6525
ENSACAP00000001268	1.83971	0	0.593199	0.058714	0.224799	1.16077
ENSACAP00000012746	0.8623	0.217274	0.248542	0	0.299297	0.147957
ENSACAP00000021909	0.087234	2.61247	0	0.068211	0.787363	0.461553
ENSACAP00000002257	2.38872	1.61748	1.28541	16.0007	1.18971	2.90973

ENSACAP00000002101	3.85813	0.061841	0	23.1133	0.123934	4.13708
ENSACAP00000000934	1.18041	0.633115	0.274736	0.702261	0.800251	0.981576
ENSACAP00000001347	4.51584	0	0	0	0	0
ENSACAP00000009624	3.88916	30.7192	11.6964	3.40598	41.7843	17.1673
ENSACAP00000014830	9.82899	0	0	0.102808	0	0
ENSACAP00000004589	7.43838	30.5904	17.6586	26.0517	9.00527	208.7
ENSACAP00000003355	9.32087	0	0	0.191508	0	0.178242
ENSACAP00000012754	1.09624	0.265336	0.227471	13.4874	4.31711	18.2264
ENSACAP00000008681	2.93025	0	0	0	0	0
ENSACAP00000007066	0	4.14648	0	0	0	0
ENSACAP00000000778	0	0	0.048222	0	0.049446	0.047612
ENSACAP00000000378	0.258478	0.45323	0	131.393	1.85436	8.10228
ENSACAP00000009821	11.1448	0	0	0	0	0
ENSACAP00000014417	1.39401	0.687459	0.989164	0.21842	0.186669	0.030837
ENSACAP00000003664	0.072625	10.1604	0	0.636981	0.147831	343.616
ENSACAP00000003069	6.03207	2.2818	0.490838	3.44625	5.8241	17.0637
ENSACAP00000010744	12.3882	0	0.027496	0	0.041355	0
ENSACAP00000002650	0.161434	1.55173	0	0.210152	0.021013	1.05096
ENSACAP00000023237	0.966179	0	0.016141	0.000151	3.51E-06	0.016966
ENSACAP00000013343	0.425277	2.69861	0.492028	1.3826	2.34279	4.8417
ENSACAP00000009073	0.373993	3.52526	1.09567	68.3207	6.70496	2.87261
ENSACAP00000009092	0.796123	0.43289	0.245734	14.779	1.67311	5.46094
ENSACAP00000003231	0.070953	8.80747	0	0	0	0.38803
ENSACAP00000002914	5.09408	3.66834	2.5552	6.75195	6.06216	9.42969
ENSACAP00000000160	2.03251	0.686544	0	30.65	0.484383	0.334804
ENSACAP00000023204	20.3599	33.9749	1.7155	0.27222	8.421	17.1576
ENSACAP00000004762	3.874	9.35287	7.20275	14.1789	16.7298	8.5573
ENSACAP00000005916	0	2.91951	0	0	0	1.4395
ENSACAP00000000034	2.36469	0	0.11435	0.031791	0	0.16145
ENSACAP00000016681	15.2133	35.2116	5.87213	257.047	88.6657	15.6169
ENSACAP00000006046	8.6472	0.866351	0.014613	12.9828	0.272038	8.62491

ENSACAP00000012342	0.523161	0.563413	0.107837	0.332379	0.410774	1.40327
ENSACAP00000001893	3.92994	0.501431	2.58335	0.108647	0.046428	0.276066
ENSACAP00000012879	1.97824	1.12994	0.504864	7.98081	1.41332	4.13815
ENSACAP00000003660	0.15586	3.6554	0.161009	0.91426	0.063343	0.077678
ENSACAP00000002102	13.4831	19.2021	5.96273	2.15153	7.44738	13.291
ENSACAP00000002921	0	1.28916	1.29922	14.6297	1.71019	5.50916
ENSACAP00000007627	5.92382	0	0	0	0	0
ENSACAP00000002708	2.71426	0	0	1.27604	1.70477	1.66911
ENSACAP00000002763	0.783116	0	0	0.18328	0	0.402483
ENSACAP00000005027	4.79071	6.9157	3.62064	44.6395	8.53143	10.8816
ENSACAP00000001856	0.365067	1.90579	0	0	0.127039	1.77337
ENSACAP00000015880	0.356218	0.782121	0.826479	0.151094	0	0
ENSACAP00000000416	2.65129	0.101064	0	0.076648	0.097473	1.73328
ENSACAP00000004787	0.964013	0	0	0.077158	0.056565	0.076658
ENSACAP00000018247	0.616622	6.01E-08	0.124082	9.29411	2.48159	5.77E-06
ENSACAP00000008669	0.355878	0.36603	0.274984	0.112543	16.5119	0
ENSACAP00000010793	2.30352	0	0.011117	0	0.008345	0
ENSACAP00000003323	3.99237	1.98876	3.16782	9.59885	4.09341	5.21308
ENSACAP00000005436	35.2007	22.2951	9.04921	68.4057	35.2578	29.6118
ENSACAP00000006257	0.383066	14.4769	2.43678	0.164926	4.75492	14.4277
ENSACAP00000017656	28.8265	8.99484	9.90018	26.142	23.8436	17.0346
ENSACAP00000017054	7.13111	2.68048	1.54418	0.680892	1.64091	1.68799
ENSACAP00000016757	17.3509	0.110036	0	0.053535	0.045927	2.13572
ENSACAP00000003601	0	0	0	0.103488	0	0
ENSACAP00000010527	0.031942	0	0	0	0	0
ENSACAP00000012329	3.8463	2.97304	0.477791	11.1629	2.81629	4.06005
ENSACAP00000017703	1.41281	0.178898	0.448184	3.52147	0.192449	0
ENSACAP00000012425	2.52114	2.8517	0.366878	2.71856	1.41321	2.39419
ENSACAP00000009827	0.380333	0.905855	0.170068	1.69447	0.162571	0.378423
ENSACAP00000017274	3.87821	0	0	0	0	0
ENSACAP00000003019	0.401822	0.848773	0.108623	0	0.081238	0.173513

ENSACAP00000009165	0.178457	0	0	0.973775	0.13386	0.255156
ENSACAP00000009562	1.15345	1.40259	0.493394	0.1072	0.583526	0.397227
ENSACAP00000003757	1.59483	0.828687	0.804387	0.050941	0.607499	0.849438
ENSACAP00000012760	0	0	0	0	0	0
ENSACAP00000012693	0.23662	0.111057	0	0	0.053468	0.257517
ENSACAP00000005126	0.439353	0.953055	0	0.198851	0.063559	7.81614
ENSACAP00000010265	13.0495	36.9899	17.942	4.85084	31.7864	9.35351
ENSACAP00000001609	3.58771	1.20201	0	0.05502	0.388706	3.05081
ENSACAP00000002037	0.64033	1.1707	0.535705	1.7495	0.951999	10.1331
ENSACAP00000003389	8.24566	9.5825	4.75653	15.1024	4.12357	3.5215
ENSACAP00000022629	0.284631	0.761323	0	0.000671	0.246512	6.89062
ENSACAP00000000054	4.88552	4.64897	6.56691	85.0674	9.17962	10.457
ENSACAP00000005208	0.076494	0.082197	0	0.014424	0.008367	0.000391
ENSACAP00000017438	0.038427	0.123237	0	2.56E-08	0	8.02126
ENSACAP00000002866	1.65281	2.89751	0.537452	1.38652	0.880087	2.50757
ENSACAP00000007935	0.080245	0.058923	0	0	0	0.053313
ENSACAP00000004015	0	0.542509	0.141905	0	0.092937	6.03E-07
ENSACAP00000012644	4.78085	0.561116	0.217113	0.265075	0.666856	1.4355
ENSACAP00000005716	1.604	0	0	0	0	0
ENSACAP00000011364	3.68509	10.5322	16.2303	14.4947	1.9783	2.60965
ENSACAP00000017584	2.95557	0.519955	1.08799	0.685595	1.3321	0.745756
ENSACAP00000003403	5.69658	5.48441	1.39273	1.3923	236.443	1.8961
ENSACAP00000005206	1.85119	0.577923	0.466108	0.193708	0.34263	1.12908
ENSACAP00000008692	0.334255	0.175068	0	0.134257	0	0.464169
ENSACAP00000010338	6.91937	1.39367	2.06861	0.275555	1.55938	0.433415
ENSACAP00000023146	10.5171	5.15008	5.67275	16.3898	8.55197	5.90349
ENSACAP00000012150	0.1332	1.30616	0.640857	0.271166	1.69078	0.708337
ENSACAP00000011712	0.354837	0	0	0	0	0
ENSACAP00000011394	2.40289	0.241302	154.111	0.721974	0.627643	0.941314
ENSACAP00000013738	1.62147	1.76461	0.627235	9.89592	3.70969	9.94777
ENSACAP00000011987	5.03596	0	0	0	0	0

ENSACAP00000002985	3.4073	2.85869	0	9.73511	2.41373	2.12805
ENSACAP00000002567	5.78031	0	0	0	0	0
ENSACAP00000011523	0	0	0	0	0	0
ENSACAP00000004222	1.08375	1.67596	0.340785	0.139573	19.5622	1.32011
ENSACAP00000016592	1.33391	1.21918	0.549495	9.87196	5.32436	7.10532
ENSACAP00000011153	0.400393	375.247	0.381975	3.74621	1.90604	16.0727
ENSACAP00000000791	1.46219	3.50662	0.291039	21.4067	2.28364	2.27164
ENSACAP00000009973	11.4201	11.2381	4.81155	4.81066	7.84898	9.76519
ENSACAP00000015188	17.9531	24.1314	15.5415	194.93	45.5103	20.902
ENSACAP00000004636	2.97294	4.25525	1.81048	12.2619	3.2607	16.097
ENSACAP00000013915	0	2.89415	0.105514	0	0	0.053563
ENSACAP00000022437	1.47855	0.23821	0.222717	1.48069	0.65856	0.481304
ENSACAP00000015705	6.26825	5.99261	3.66458	11.626	9.64675	5.55506
ENSACAP00000002190	0.949668	9.2248	5.50074	13.5534	14.2201	13.5605
ENSACAP00000001155	6.35044	7.28769	4.76113	67.343	5.50468	8.69783
ENSACAP00000004955	2.90153	3.63143	0	15.7639	0.781752	1.71731
ENSACAP00000019214	4.26022	1.17255	1.31477	2.56202	2.50831	1.75335
ENSACAP00000000684	0	0	0.113027	0.714688	0	0
ENSACAP00000012511	0.133914	0.321512	0.008323	0.291931	0.27595	4.16448
ENSACAP00000011059	1.66618	3.25311	0.387227	0	0.419875	0.64487
ENSACAP00000012209	1.45859	0.427891	0	1.56778	0	0.118317
ENSACAP00000014754	1.74866	4.21728	0.747545	7.39727	6.75346	4.8955
ENSACAP00000015123	9.75622	38.4133	35.3835	14.639	24.9233	51.2612
ENSACAP00000001943	10.7426	2.10787	2.00133	12.3184	6.54734	10.7633
ENSACAP00000002239	0	28.3689	1.10525	0	0.545497	0.12917
ENSACAP00000014952	5.2351	0.937466	0.342499	0.429929	0.466739	0.700752
ENSACAP00000015149	7.52416	0.270668	0	0.861736	0.060782	0.151728
ENSACAP00000004160	37.6426	53.4685	10.8831	27.1449	24.8021	38.8334
ENSACAP00000007082	0	0.006096	0	0	0	0.007443
ENSACAP00000007057	0	0.810694	0.253082	0.40601	0.223983	0
ENSACAP00000000221	0.728497	0	0	0	0	0

ENSACAP00000015527	0.207457	10.2841	0	1.39151	0	0.600147
ENSACAP00000000379	8.65545	3.79751	0.00713	20.5495	6.10213	9.23281
ENSACAP00000015734	7.03373	4.36356	1.96953	1.60691	3.15322	1.39667
ENSACAP00000000255	0.148708	1.77602	0.388464	0	0.951314	0.062439
ENSACAP00000015446	0.214936	0	0.782197	1.59E-09	1.93731	0.043903
ENSACAP00000009585	6.06773	1.33568	0.940671	15.8127	1.90125	2.7967
ENSACAP00000016228	8.7877	0.054399	0.152311	0.11131	0.175712	2.42624
ENSACAP00000010279	1.95471	0.497603	0	0	0.072233	72.1966
ENSACAP00000011446	3.48866	3.91217	1.7917	6.00331	5.60961	19.885
ENSACAP00000021641	0.109423	0.080882	0	0	0.001448	0
ENSACAP00000000796	0.409902	0.178413	2.74165	0	1.04443	0.532123
ENSACAP00000001682	1.19572	2.27391	2.31012	0.589255	0.978474	0.767976
ENSACAP00000005515	0.66398	1.18528	0.196257	0.230967	1.05639	0.337417
ENSACAP00000003806	0.639494	0	0	0	0.16774	0.378318
ENSACAP00000005087	101.674	40.6464	19.6881	29.0051	27.1258	162.935
ENSACAP00000014677	8.65949	3.79341	3.36301	1.7574	3.9098	4.02386
ENSACAP00000009232	0	0.315749	0	0	0	0.196809
ENSACAP00000015109	3.82836	0.793209	1.27575	1.00375	1.38375	1.65167
ENSACAP00000020710	1.22834	4.05651	0.361851	0.130397	3.93959	0.680353
ENSACAP00000007131	0.160081	0.31917	0.288015	1.22586	0.15154	0.883307
ENSACAP00000013736	0.098313	0.832698	3.87316	0.039808	1.17212	0.921427
ENSACAP00000017662	2.18776	8.74243	0.126186	19.1148	3.049	118.346
ENSACAP00000003905	0.893687	0	1.49867	0.208697	0.088591	0.060224
ENSACAP00000021261	11.6768	2.77866	0.474259	0.848791	0.450281	3.24791
ENSACAP00000014073	0	1.35647	0.075281	0	0	0.023888
ENSACAP00000011883	2.35336	0.720004	0.434707	0.892205	1.48529	1.02757
ENSACAP00000001594	0.335525	0.530336	0.135013	0	0.104324	0.241722
ENSACAP00000009969	4.7861	2.99249	1.92123	117.266	8.18141	37.3207
ENSACAP00000001092	7.26602	0.069437	0	0	0.893865	0.11727
ENSACAP00000013095	0.706345	1.64117	249.354	4.31002	0.416162	0.502726
ENSACAP00000008525	0.671866	0.833546	0.219888	0.096731	0.304973	0.7088

ENSACAP00000016346	0.773063	0.891358	0.374868	0.076768	4.49248	0.701084
ENSACAP00000001332	1.64157	0	0.158595	0.049599	0.574361	1.94304
ENSACAP00000015430	4.18201	2.24139	0.991944	24.787	4.05041	14.9145
ENSACAP00000008830	2.1614	29.2913	0.0551	0.008333	0.444405	1.08332
ENSACAP00000006716	0.127148	0.194607	0.111778	0.227218	0.177239	0
ENSACAP00000016369	26.4447	90.5094	14.4671	18.7384	90.5018	57.5612
ENSACAP00000017354	2.8725	1.42018	1.3604	5.13245	1.74497	1.45748
ENSACAP00000017382	0.153389	0.016497	0.087822	2.62552	0.360155	0
ENSACAP00000008985	0.21792	0.291099	0	0.092314	0	0.170603
ENSACAP00000001757	2.65094	10.5381	3.46715	8.48646	19.4333	10.6226
ENSACAP00000015316	22.1778	52.6312	28.5886	50.4968	53.0547	85.8383
ENSACAP00000000241	1.08547	0.411796	0.087159	0.470218	0.240068	0.420361
ENSACAP00000004226	4.72657	3.44879	2.3174	13.4888	5.70245	5.2786
ENSACAP00000000825	0	3.77293	2.03469	0	0.026657	1.02718
ENSACAP00000002742	0.675298	2.10916	0.257886	47.2287	3.4296	4.1763
ENSACAP00000004168	2.57628	0.239646	0.084683	0	0.076511	0
ENSACAP00000002332	0.297081	0.713543	0.633409	2.60627	1.18998	0
ENSACAP00000017058	0.339814	0.10744	0	0.052805	0.257621	0.155545
ENSACAP00000006621	0.728625	2.96734	0.769154	0.145157	0.873806	1.90893
ENSACAP00000001253	6.24554	5.13452	3.32742	38.8433	5.22277	3.29265
ENSACAP00000004238	0.202692	0	5.75E-10	0	0.001956	0
ENSACAP00000004705	1.30867	25.2145	16.0663	67.8015	4.92812	0.165752
ENSACAP00000006425	3.93E-05	0.063801	0	0.031025	1.7808	3.82792
ENSACAP00000009892	0.804388	1.15539	0.089401	2.52384	7.32329	11.9202
ENSACAP00000016988	0	4.14635	0	0	0	0.040226
ENSACAP00000001231	23.9225	46.1347	40.2894	25.0773	30.3028	24.2329
ENSACAP00000016669	1.30844	21.2309	12.1604	8.19852	5.03	6.95501
ENSACAP00000009086	0.143775	7.74061	0.144602	0.362102	4.09579	1.60236
ENSACAP00000014848	9.45735	2.70325	1948.35	5.29214	3.82019	0.231218
ENSACAP00000010464	0	99.6445	4.74673	0	0	2.46402
ENSACAP00000011045	1.52709	0	0.026708	0.122655	0.360049	0.503374

ENSACAP00000015757	12.2973	8.60239	9.64578	16.9381	12.9911	24.2956
ENSACAP00000006746	110.649	18.9849	12.3918	47.1224	22.2986	29.4596
ENSACAP00000021793	23.9503	0.087911	0.125337	0.008273	0	5.23322
ENSACAP00000012089	21.837	0.166852	0	0	0.283702	0
ENSACAP00000000360	5.52625	11.0115	0.928454	9.04136	7.04624	10.378
ENSACAP00000003974	0.980897	0.968367	0	0	0.147718	3.22355
ENSACAP00000000583	9.9588	1.73521	0.960615	2.12086	0.396938	1.65231
ENSACAP00000007352	0.19446	0.702171	50.702	0.019587	0.701065	1.98734
ENSACAP00000017391	37.4824	34.5341	25.8388	25.6889	47.7998	23.9828
ENSACAP00000001606	1.1424	0.324032	0.185862	0.275376	0.368644	1.09624
ENSACAP00000006180	6.75733	2.04512	1.87909	2.91327	2.0009	1.74646
ENSACAP00000010615	0.403341	1.95331	1.6043	0.158551	3.78787	1.04229
ENSACAP00000017757	7.14152	0.517792	0.249757	0.091234	0.28174	1.2373
ENSACAP00000016251	4.43062	1.29516	3.21248	5.05163	3.0352	6.51467
ENSACAP00000010343	0.281753	2.30094	0.381465	4.13236	0.053987	3.72344
ENSACAP00000013128	0	0.360803	0	0.131849	0	0
ENSACAP00000016340	7.87096	11.31	0.31978	0.080758	0.507043	0.693097
ENSACAP00000007747	0.333087	0.245565	0	0	0	0.322403
ENSACAP00000005936	9.19E-11	0	1.47E-07	0	0	0
ENSACAP00000018161	4.49501	1.87553	0.61708	16.3888	1.8197	4.53164
ENSACAP00000009556	0.300749	0	0.233131	0.095775	0	0.269314
ENSACAP00000001664	3.42274	9.03337	1.79606	4.44086	4.82025	5.61613
ENSACAP00000001455	700.57	0	0.786485	0	1.73758	0
ENSACAP00000006737	48.9328	48.131	11.1434	72.9873	28.117	118.324
ENSACAP00000017717	17.3628	18.1014	2.00433	171.25	13.4549	292.792
ENSACAP00000015276	12.6093	15.0261	16.3029	128.268	17.3104	12.6796
ENSACAP00000015381	8.61714	22.484	1.71642	5.81073	18.7858	7.97784

Table S25. Continuous evolved KEGG pathways in frogs.

KEGG pathway	From low to ~2000m	From ~2000m to ~3000m	From ~3000m to ~4500m

ko00030:Pentose phosphate pathway	H6PD	G6PD	ALDOA, TKT
ko00120:Primary bile acid biosynthesis	CYP27A1	CYP27A1	CYP8B1
ko00190:Oxidative phosphorylation	SDHA, LHPP	SDHA, NDUFA6	NDUFB9, ATP6AP1, COX4I1, ATP6V0A1, ATP6V1H
ko00563:Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	PIGX	PIGX	GPAA1
ko00564:Glycerophospholipid metabolism	ETNPPL, PLA2G6, PCYT1A, LPCAT4	CHKA, ETNK1, LPCAT3	PGS1, LPCAT1, GNPAT
ko01130:Biosynthesis of antibiotics	SDHA, IDH3G, IDH3B	SDHA, G6PD, GGPS1, HK2	ALDOA, HMGCR, TKT
ko01200:Carbon metabolism	SDHA, IDH3G, H6PD, IDH3B	SDHA, G6PD, TKFC, HK2	ALDOA, TKT
ko01212:Fatty acid metabolism	MCAT, ACADL	ACOX1, CPT1B	ELOVL5, PPT1
ko03008:Ribosome biogenesis in eukaryotes	WDR3, NOP56, MDN1	WDR36, WDR3	UTP6, LSG1, NOP58, NOP56, GNL3
ko03010:Ribosome	MRPL28, MRPS18A, RPL13A, RPLP1, RPL35, RPS5	MRPL20	RPLP0, RPL15, RPL11
ko03013:RNA transport	ELAC2, EIF5B, NUP85, THOC5, NUP107, TPR, TGS1	EEF1A1, EIF3H, PAIP1, NUP93, PNN	EIF4G3, EIF2B3
ko03018:RNA degradation	EDC4	SKIV2L	DIS3, TTC37, DDX6
ko03050:Proteasome	PSMD12	PSMB9	PSMB7, PSMA6
ko03320:PPAR signaling pathway	CYP27A1, ACADL	ACOX1, CPT1B, CYP27A1, RXRA	CYP8B1
ko03420:Nucleotide excision repair	POLD2	XPC	RPA1
ko04010:MAPK signaling pathway	FGFR1, MAPK8, STMN1, TRAF6	ATF4, PPP3CB, FAS	FGFR4, RELB, NFATC3, HSPA8
ko04014:Ras signaling pathway	FGFR1, VEGFA, GRIN1, PLA2G6, MAPK8, PDGFC, EXOC2	EPHA2	FGFR4
ko04015:Rap1 signaling pathway	FGFR1, TLN1, VEGFA, GRIN1,	TLN1, CTNND1, CDH1, RAPGEF1, EPHA2	ADCY4, FGFR4, LPAR4, CTNND1, ITGB1

	CTNND1, PDGFC		
ko04020:Calcium signaling pathway	CCKAR, SLC25A4, GRIN1, PTGFR	PPIF, SPHK1, PPP3CB, PTGFR, VDAC3, MYLK	ADCY4, PLCD1
ko04022:cGMP-PKG signaling pathway	SLC25A4, PDE3B, ATP1A1	PPIF, ATF4, ATF6B, PPP3CB, VDAC3, MYLK	ADCY4, ROCK2, NFATC3
ko04024:cAMP signaling pathway	GRIN1, PDE3B, ATP1A1, MAPK8	ACOX1	ADCY4, ROCK2
ko04060:Cytokine-cytokine receptor interaction	VEGFA, IL17RA, IFNGR1	FAS, ACVR1	IFNAR2, IL1RAP, BMPR2
ko04064:NF-kappa B signaling pathway	IRAK4, TNFAIP3, TRAF6, SYK	RIPK1	RELB
ko04071:Sphingolipid signaling pathway	BID, MAPK8	SPHK1	ROCK2
ko04080:Neuroactive ligand-receptor interaction	CCKAR, GLRB, GRIN1, CHRNB3, PTGFR	GRM6, PTGFR	GRIK3, LPAR4, NR3C1
ko04110:Cell cycle	RAD21, CDC20	SMC1A	SMC1A, STAG1
ko04114:Oocyte meiosis	CDC20	PPP3CB, SMC1A	ADCY4, SMC1A
ko04115:p53 signaling pathway	BID	FAS	RFWD2, RRM2B
ko04120:Ubiquitin mediated proteolysis	PPIL2, CDC20, KEAP1, TRAF6, UBE2U	UBE4B	RFWD2
ko04141:Protein processing in endoplasmic reticulum	HSPH1, PDIA3, VCP, UFD1L, MAPK8, PDIA4, SAR1A	NPLOC4, ATF4, UBE4B, ATF6B, RPN2, SEL1L	SEC24B, HSPA8
ko04142:Lysosome	CTSK, AP1G1, LGMN, GALC, CLN5	CTSK, LIPA, LGMN	CTSK, ATP6AP1, ATP6V0A1, ATP6V1H, PPT1
ko04144:Endocytosis	HGS, VPS35, TRAF6, RAB11FIP1, EPN1	CHMP2A	FGFR4, AP2A1, KIAA0196, RUFY1, VPS35, CYTH2, HSPA8, DNM1
ko04146:Peroxisome	SOD1	ACOX1	GNPAT
ko04151:PI3K-Akt signaling pathway	FGFR1, COL3A1, VEGFA, COL1A2, PDGFC, PRKAA1,	ATF4, TNC, RXRA, COL3A1, ATF6B, COL1A1, COL4A6,	IFNAR2, FGFR4, COL6A3, COL1A2, LPAR4, COL6A1, ITGB1,

	SYK	EPHA2	THBS2, COL5A1, FN1
ko04152:AMPK signaling pathway	EEF2, PRKAA1	CPT1B	HMGCR, ADIPOR1, EEF2
ko04261:Adrenergic signaling in cardiomyocytes	ATP1A1	ATF4, SCN1B, ATF6B	ADCY4
ko04270:Vascular smooth muscle contraction	PLA2G6	MYLK	ADCY4, ROCK2
ko04310:Wnt signaling pathway	MAPK8	PPP3CB	ROCK2, NFATC3, FZD6
ko04360:Axon guidance	SEMA4D, EPHB3	SEMA3D, PPP3CB, EPHA2	EPHA4, ROCK2, PLXNB2, NTN4, NFATC3, ITGB1
ko04380:Osteoclast differentiation	CTSK, MAPK8, TRAF6, IFNGR1, SYK	CTSK, PPP3CB	IFNAR2, CTSK, RELB
ko04390:Hippo signaling pathway	SAV1	BMP4, CDH1	BMPR2, FZD6
ko04510:Focal adhesion	TLN1, COL3A1, VEGFA, COL1A2, MAPK8, PDGFC	TLN1, TNC, COL3A1, COL1A1, RAPGEF1, COL4A6, MYLK, VCL	ROCK2, COL6A3, COL1A2, COL6A1, ITGB1, THBS2, COL5A1, VCL, FN1
ko04512:ECM-receptor interaction	CD44, COL3A1, HSPG2, COL1A2	CD44, TNC, COL3A1, COL1A1, COL4A6	COL6A3, COL1A2, COL6A1, ITGB1, THBS2, COL5A1, FN1
ko04514:Cell adhesion molecules (CAMs)	PECAM1, CNTN2, NRXN1	CD99, CDH1, NEO1	MPZL1, VCAN, ITGB1, CDH4
ko04520:Adherens junction	FGFR1, BAIAP2, CTNND1, LMO7	CTNND1, CDH1, VCL	CTNND1, VCL
ko04550:Signaling pathways regulating pluripotency of stem cells	FGFR1	BMP4, LHX5, ACVR1	FGFR4, BMPR2, ZFHX3, FZD6
ko04610:Complement and coagulation cascades	C7, FGG, F5, SERPINC1, SERPIND1	C1QA, PLAT	SERPIND1, F7
ko04611:Platelet activation	FGG, TLN1, COL3A1, COL1A2, SYK	TLN1, COL3A1, COL1A1, MYLK	ADCY4, ROCK2, COL1A2, ITGB1, COL5A1
ko04612:Antigen processing and presentation	PDIA3, LGMN	LGMN, NFYC	HSPA8
ko04620:Toll-like receptor signaling pathway	IRAK4, CTSK, MAPK8, TRAF6	CTSK, RIPK1	IFNAR2, CTSK
ko04622:RIG-I-like receptor signaling pathway	MAPK8, TRAF6	TKFC, RIPK1, NLRX1	AZI2

ko04650:Natural killer cell mediated cytotoxicity	BID, IFNGR1, SYK	PPP3CB, FAS	IFNAR2
ko04662:B cell receptor signaling pathway	SYK	PPP3CB, CD79A	NFATC3
ko04670:Leukocyte transendothelial migration	EZR, PECAM1, CTNND1, THY1	EZR, CTNND1, CD99, VCL	ROCK2, CTNND1, ITGB1, VCL
ko04721:Synaptic vesicle cycle	SYT1, STX3	NSF	AP2A1, ATP6V0A1, ATP6V1H, DNM1
ko04724:Glutamatergic synapse	GRIN1	GRM6, PPP3CB	ADCY4, GRIK3, GLS
ko04810:Regulation of actin cytoskeleton	FGFR1, EZR, BAIAP2, PDGFC	EZR, MYLK, VCL	FGFR4, ROCK2, ITGB1, VCL, FN1
ko04911:Insulin secretion	CCKAR, ATP1A1	ATF4, ATF6B	ADCY4, KCNJ11
ko04912:GnRH signaling pathway	MAPK8	ATF4	ADCY4
ko04915:Estrogen signaling pathway	FKBP4	ATF4, ATF6B	ADCY4, HSPA8
ko04918:Thyroid hormone synthesis	ATP1A1, PDIA4, IYD	SLC26A4, ATF4, ATF6B	ADCY4
ko04919:Thyroid hormone signaling pathway	SIN3A, ATP1A1	RXRA, MED24	PLCD1
ko04920:Adipocytokine signaling pathway	MAPK8, PRKAA1	CPT1B, RXRA	ADIPOR1
ko04921:Oxytocin signaling pathway	EEF2, PRKAA1	PPP3CB, MYLK	ADCY4, ROCK2, EEF2, NFATC3
ko04925:Aldosterone synthesis and secretion	SCARB1	ATF4, ATF6B, ATF1	ADCY4, SCARB1
ko04930:Type II diabetes mellitus	MAPK8	HK2	KCNJ11
ko04932:Non-alcoholic fatty liver disease (NAFLD)	BID, SDHA, MAPK8, PRKAA1	SDHA, ATF4, NDUFA6, RXRA, FAS	NDUFB9, COX4I1, ADIPOR1
ko04961:Endocrine and other factor-regulated calcium reabsorption	ATP1A1	CALB1	AP2A1, CALB1, DNM1
ko04962:Vasopressin-regulated water reabsorption	STX4	NSF	AQP3
ko04971:Gastric acid secretion	EZR, ATP1A1	EZR, MYLK	ADCY4
ko04973:Carbohydrate digestion and absorption	ATP1A1	HK2	SLC37A4
ko04974:Protein digestion and absorption	COL3A1, COL1A2, ATP1A1, XPNPEP2	COL9A3, COL3A1, COL1A1, COL4A6	COL6A3, COL1A2, COL6A1, COL5A1
ko04976:Bile secretion	ATP1A1, SCARB1	RXRA, ABCC3	ADCY4, HMGCR, SCARB1
ko05010:Alzheimer's disease	BID, SDHA, GRIN1	SDHA, NDUFA6, PPP3CB, FAS	NDUFB9, ADAM17, COX4I1
ko05012:Parkinson's disease	SDHA, SLC25A4	SDHA, PPIF, NDUFA6, VDAC3	NDUFB9, COX4I1

ko05016:Huntington's disease	SDHA, SIN3A, SLC25A4, GRIN1, SOD1	SDHA, PPIF, NDUFA6, VDAC3	AP2A1, NDUFB9, COX4I1
ko05133:Pertussis	IRAK4, MAPK8, TRAF6	C1QA	ITGB1
ko05134:Legionellosis	VCP, SAR1A	EEF1A1, BCL2L13	HSPA8
ko05145:Toxoplasmosis	IRAK4, MAPK8, TRAF6, IFNGR1	PPIF	ITGB1, HSPA8
ko05146:Amoebiasis	COL3A1, COL1A2	COL3A1, COL1A1, COL4A6, VCL	COL1A2, COL5A1, VCL, FN1
ko05152:Tuberculosis	BID, IRAK4, MAPK8, TRAF6, IFNGR1, SYK	SPHK1, PPP3CB, NFYC	ATP6AP1, ATP6V0A1, ATP6V1H
ko05160:Hepatitis C	MAPK8, SCARB1, TRAF6	RIPK1, RXRA	IFNAR2, SCARB1
ko05161:Hepatitis B	HSPG2, MAPK8	ATF4, ATF6B, FAS, VDAC3	ATP6AP1, NFATC3
ko05162:Measles	IRAK4, TNFAIP3, TRAF6, IFNGR1	EIF3H, FAS	IFNAR2, HSPA8
ko05164:Influenza A	IRAK4, MAPK8, IFNGR1	NLRX1, FAS	IFNAR2, HSPA8
ko05166:HTLV-I infection	TLN1, SLC25A4, POLD2, CDC20	TLN1, ATF4, PPP3CB, VDAC3, ATF1	ADCY4, RELB, NFATC3, FZD6
ko05168:Herpes simplex infection	HMGN1, MAPK8, TRAF6, IFNGR1	CFP, FAS	IFNAR2, TAF10
ko05169:Epstein-Barr virus infection	CD44, PSMD12, MAPK8, TNFAIP3, TRAF6, SYK	CD44, RIPK1	SND1, RELB, HSPA8
ko05200:Pathways in cancer	BID, CCDC6, FGFR1, STK36, VEGFA, MAPK8, TPR, TRAF6	BMP4, RXRA, CDH1, FAS, COL4A6	ADCY4, ROCK2, LPAR4, ITGB1, FZD6, FN1
ko05202:Transcriptional misregulation in cancer	MEN1, SIN3A, SPINT1	PLAT, RXRA, PBX1, ATF1	FUS, CDK14
ko05203:Viral carcinogenesis	CDC20, SYK	HPN, ATF4, ATF6B, VDAC3	GTF2A1, SND1
ko05205:Proteoglycans in cancer	FGFR1, EZR, CD44,	EZR, CD44, FAS, PDCD4	ROCK2, ITGB1, FZD6,

	VEGFA, HSPG2		FN1
ko05206:MicroRNAs in cancer	EZR, CD44, VEGFA, STMN1	EZR, CD44, TNC, PDCD4	GLS, BMPR2
ko05217:Basal cell carcinoma	STK36	BMP4	FZD6
ko05222:Small cell lung cancer	TRAF6	RXRA, COL4A6	ITGB1, FN1
ko05230:Central carbon metabolism in cancer	FGFR1	G6PD, HK2, SIRT6	GLS
ko05231:Choline metabolism in cancer	PCYT1A, MAPK8, PDGFC	CHKA	SLC44A2
ko05323:Rheumatoid arthritis	CTSK, VEGFA	CTSK	CTSK, ATP6AP1, ATP6V0A1, ATP6V1H

Table S26. Continuous evolved KEGG pathways in lizards.

KEGG pathway	From low to ~2000m	From ~2000m to ~3000m	From ~3000m to ~4500m
ko00010:Glycolysis / Gluconeogenesis	PGM2, HKDC1	HKDC1	PFKM
ko00030:Pentose phosphate pathway	PGM2, PRPS2	PRPS2	PFKM, PRPS2
ko00051:Fructose and mannose metabolism	HKDC1	HKDC1	PFKM
ko00052:Galactose metabolism	PGM2, HKDC1	HKDC1	PFKM
ko00230:Purine metabolism	PGM2, POLR3A, PRPS2	ADK, GUCY1B3, PRPS2	PRPS2
ko00564:Glycerophospholipid metabolism	PGS1	LCLAT1	PGS1
ko01130:Biosynthesis of antibiotics	PGM2, HKDC1, FDPS, PRPS2	HKDC1, PRPS2	PFKM, PRPS2
ko01200:Carbon metabolism	HKDC1, PRPS2	HKDC1, PRPS2	PFKM, PRPS2
ko01230:Biosynthesis of amino acids	PRPS2	PRPS2	PFKM, PRPS2
ko03008:Ribosome biogenesis in eukaryotes	UTP15	MPHOSPH10	WDR36
ko04010:MAPK signaling pathway	TGFBR1	RAC1	FGFR2, ELK4, RAC1, MAPK8
ko04015:Rap1 signaling pathway	GNAI1, LCP2	RAC1, LCP2	FGFR2, RAC1
ko04024:cAMP signaling pathway	GNAI1	RAC1	RAC1, MAPK8
ko04062:Chemokine signaling pathway	GNAI1	RAC1, JAK2	RAC1
ko04071:Sphingolipid signaling pathway	GNAI1	FYN, RAC1, PPP2R2A	RAC1, MAPK8

ko04144:Endocytosis	TGFBR1, CHMP7, KIF5C, RUFY1, EPN2	CHMP7, DNM2, EHD4	FGFR2, AGAP2
ko04151:PI3K-Akt signaling pathway	JAK1	RAC1, JAK2, PPP2R2A	FGFR2, RAC1
ko04152:AMPK signaling pathway	CCNA2	PPP2R2A	PFKM
ko04360:Axon guidance	GNAI1	FYN, RAC1	RAC1
ko04380:Osteoclast differentiation	TGFBR1, JAK1, LCP2	FYN, RAC1, LCP2	RAC1, MAPK8
ko04520:Adherens junction	TGFBR1	FYN, RAC1	RAC1
ko04550:Signaling pathways regulating pluripotency of stem cells	INHBE, JAK1	JAK2	FGFR2
ko04622:RIG-I-like receptor signaling pathway	RNF125	FADD	MAPK8
ko04650:Natural killer cell mediated cytotoxicity	LCP2	FYN, RAC1, LCP2	RAC1
ko04662:B cell receptor signaling pathway	CD79A	RAC1	RAC1
ko04664:Fc epsilon RI signaling pathway	LCP2	FYN, RAC1, LCP2	RAC1, MAPK8
ko04670:Leukocyte transendothelial migration	GNAI1	RAC1	RAC1
ko04721:Synaptic vesicle cycle	CPLX1	DNM2	STX1B
ko04728:Dopaminergic synapse	GNAI1, KIF5C	PPP2R2A	MAPK8
ko04910:Insulin signaling pathway	HKDC1	PPP1R3B, HKDC1	MAPK8
ko04930:Type II diabetes mellitus	HKDC1	HKDC1	MAPK8
ko05142:Chagas disease (American trypanosomiasis)	GNAI1, TGFBR1	FADD, PPP2R2A	MAPK8
ko05145:Toxoplasmosis	GNAI1, JAK1	JAK2	MAPK8
ko05152:Tuberculosis	JAK1	FADD, JAK2	MAPK8
ko05160:Hepatitis C	JAK1	PPP2R2A	MAPK8
ko05161:Hepatitis B	TGFBR1, JAK1, CCNA2	FADD	MAPK8
ko05164:Influenza A	FDPS, JAK1, TMPRSS13	JAK2	MAPK8
ko05168:Herpes simplex infection	JAK1, PER1	FADD, JAK2	MAPK8
ko05169:Epstein-Barr virus infection	JAK1, POLR3A, CCNA2	VIM	MAPK8
ko05200:Pathways in cancer	GNAI1, TGFBR1, JAK1	RAC1, FADD	FGFR2, RAC1, MAPK8

ko05203:Viral carcinogenesis	HDAC3, JAK1, HDAC8, CCNA2	RAC1	RAC1
ko05210:Colorectal cancer	TGFBR1	RAC1	RAC1, MAPK8
ko05212:Pancreatic cancer	TGFBR1, JAK1	RAC1	RAC1, MAPK8
ko05230:Central carbon metabolism in cancer	HKDC1	HKDC1	FGFR2, PFKM

Table S27. Categories showed evolutionary convergence between the frogs and lizards at elevation around 2000 m.

category	pvalue	numDE InCat	numIn Cat	term	Frog PSGs	Lizard PSGs
GO:0070507	9.81E-07	15	119	regulation of microtubule cytoskeleton organization	ECT2,BORA,CDK5R1,PAFAH1B1,ENSACAG00000012696,RNF4,FAM179B	FKBP4,HSPH1,PARP3,KATNB1,STIL,STMN1,TPR,CEP120
GO:0032886	1.48E-05	15	144	regulation of microtubule-based process	ECT2,BORA,CDK5R1,PAFAH1B1,ENSACAG00000012696,RNF4,FAM179B	FKBP4,HSPH1,PARP3,KATNB1,STIL,STMN1,TPR,CEP120
GO:0034116	0.000115086	3	4	positive regulation of heterotypic cell-cell adhesion	GCNT2	FGG,FLOT1
GO:0009451	0.000152631	12	122	RNA modification	TRMU,MTO1,RPUSD4,FTSJ2,TRUB2,TRDMT1	TYW5,TRMT61B,THUMPD3,MOCS3,NOP56,TGS1
GO:0051660	0.000308287	3	5	establishment of centrosome localization	PAFAH1B1	CEP83,EZR
GO:0000963	0.000325271	4	11	mitochondrial RNA processing	TRMU,MTO1	ELAC2,TRMT61B
GO:0006364	0.000333132	13	165	rRNA processing	UTP15,EXOSC8,DIEXF,WDR18,FTSJ2	UTP20,MDN1,RPS5,DIEXF,RPL13A,WDR3,SART1,NOP56,CIRH1A
GO:0015931	0.000671108	12	141	nucleobase-containing compound transport	MCM3AP,RANBP17,MRPL18,KIF5C	ENSACAG00000002091,NUP85,SLC25A26,RBMX2,THOC5,TPR,NUP107,FLOT1
GO:0050658	0.000831435	11	124	RNA transport	MCM3AP,RANBP17,MRPL18,KIF5C	ENSACAG00000002091,NUP85,RBMX2,THOC5,TPR,NUP107,FLOT1
GO:0051103	0.000941995	3	7	DNA ligation involved in DNA	LIG4	PARP3,PARP1

				repair		
GO:1904851	0.00096647	2	2	positive regulation of establishment of protein localization to telomere	WRAP53	CCT4
GO:0000959	0.001099414	5	27	mitochondrial RNA metabolic process	TRMU,MTO1	ELAC2,TRMT61B,POLRMT
GO:0022406	0.001366209	7	65	membrane docking	ENSACAG00000011849	CEP83,STX3,EZR,NRXN1,STX4,STX12
GO:0006266	0.001842718	3	9	DNA ligation	LIG4	PARP3,PARP1
GO:0006302	0.002091915	11	138	double-strand break repair	EXD2,LIG4,CCDC155,DCLRE1A	NSMCE1,XRCC6,SFR1,DTX3L,PARP3,VCP,RAD21
GO:0021819	0.002126566	3	10	layer formation in cerebral cortex	CDK5R1,PAFAH1B1	SOCS7
GO:0070525	0.002173845	3	9	tRNA threonylcarbamoyladenosine metabolic process	TRMU,MTO1	TRMT61B
GO:0048278	0.002435528	6	54	vesicle docking	ENSACAG00000011849	CEP83,STX3,NRXN1,STX4,STX12
GO:0043622	0.002600473	2	3	cortical microtubule organization	PAFAH1B1	EZR
GO:0002098	0.002780466	3	10	tRNA wobble uridine modification	TRMU,MTO1	MOCS3
GO:0051169	0.003141844	13	188	nuclear transport	RSRC1,MCM3AP,RANBP17	NSRP1,ENSACAG00000002091,NUP85,HTATIP2,RBMX2,THOC5,NOC2L,TPR,NUP107,TGS1
GO:0050892	0.003329579	4	20	intestinal absorption	TJP2	PLS1,EZR,SCARB1
GO:0022411	0.00370738	12	175	cellular component disassembly	PAFAH1B1	MMP19,HSPG2,CDK5RAP3,ENSACAG00000017760,MTIF2,STMN1,C12orf65,TPR,NUP107,MRPL48,FLOT1
GO:0034227	0.0038338	2	4	tRNA thio-modification	TRMU	MOCS3
GO:0051170	0.004049954	8	87	nuclear import	MCM3AP,RANBP17	ENSACAG00000002091,NUP85,HTATIP2,TPR,NUP107,TGS1
GO:0006413	0.004247735	7	86	translational initiation	EIF4H	RPS5,MTIF2,RPL13A,ENSACAG00000004291,ENSACAG00000010260,MRPS18A

GO:0042249	0.004399966	2	4	establishment of planar polarity of embryonic epithelium	PAFAH1B1	CTHRC1
GO:0032873	0.004432051	5	38	negative regulation of stress-activated MAPK cascade	PER1,PAFAH1B1	HSPH1,EZR,MEN1
GO:0006457	0.004496455	11	168	protein folding	PPIL2,PPIA	PPIL2,PDIA4,ENSACAG00000002091,FKBP4,PRDX4,HSPH1,CCT4,ENSACAG00000017064,TBCE,PDIA3
GO:0043928	0.005148158	3	14	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	EXOSC8,DCP1B	EDC4
GO:0002097	0.005261194	3	13	tRNA wobble base modification	TRMU,MTO1	MOCS3
GO:0051764	0.005373639	3	11	actin crosslink formation	BAIAP2L1	PLS1,BAIAP2
GO:0006488	0.005527815	3	14	dolichol-linked oligosaccharide biosynthetic process	ALG8	ALG3,DPAGT1
GO:0000413	0.00589066	3	16	protein peptidyl-prolyl isomerization	PPIL2,PPIA	PPIL2,ENSACAG00000017064
GO:0071897	0.006255193	6	56	DNA biosynthetic process	TOP3A,LIG4,CTGF	UFD1L,TK1,VCP
GO:0070527	0.006408357	4	29	platelet aggregation	RAP2B	MYH9,FGG,GATA1
GO:0051017	0.007095854	5	40	actin filament bundle assembly	BAIAP2L1	PLS1,ADD1,BAIAP2,EZR
GO:0008299	0.007285847	4	28	isoprenoid biosynthetic process	FDPS	COQ2,DPAGT1,ENSACAG00000003142
GO:0007062	0.007347437	7	76	sister chromatid cohesion	CENPC,BUB1,PAFAH1B1,HDAC8	CENPH,RAD21,NUP107
GO:0046471	0.00748545	3	16	phosphatidylglycerol metabolic process	PGS1	LPCAT4,PLA2G6
GO:0050994	0.007743878	4	27	regulation of lipid catabolic process	LONP2	PRKAA1,PDE3B,SCARB1
GO:0032530	0.008884901	3	14	regulation of microvillus organization	ENSACAG00000006885	PLS1,EZR
GO:0000086	0.009182437	7	77	G2/M transition of mitotic cell cycle	BORA,HAUS6,HMMR,PAFAH1B1,CCP110	KDM8,NEDD1
GO:0000075	0.009630994	9	123	cell cycle checkpoint	GIGYF2,XPC,BUB1	CDK5RAP3,RAD17,SPDL1,ENSACAG00000013691,TPR,CHFR

GO:0000291	0.009775576	3	18	nuclear-transcribed mRNA catabolic process, exonucleolytic	EXOSC8,DCP1B	EDC4
GO:0017038	0.010124882	8	108	protein import	ENSACAG00000011849,MCM3AP,RANBP17,LONP2	ENSACAG00000002091,NUP85,TPR,NUP107
GO:0051382	0.010477716	2	8	kinetochore assembly	CENPC	CENPH
GO:0051383	0.010477716	2	8	kinetochore organization	CENPC	CENPH
GO:0046085	0.01069666	3	16	adenosine metabolic process	TRMU,MTO1	TRMT61B
GO:0050730	0.011320676	8	108	regulation of peptidyl-tyrosine phosphorylation	RAP2B	SRCIN1,GAS6,HSPH1,SEMA4D,GATA1,CTNND1,VEGFA
GO:0021930	0.011542396	2	6	cerebellar granule cell precursor proliferation	PSMG1	RERE
GO:0042752	0.011656016	6	64	regulation of circadian rhythm	ARNTL2,PER1	FBXL3,PRKAA1,SIN3A,MAPK8
GO:0050900	0.011960947	9	130	leukocyte migration	PPIL2	PPIL2,IL17RA,MYH9,IRAK4,GAS6,ANXA1,NUP85,ENSACAG00000006445,PECAM1
GO:0061001	0.012037255	4	27	regulation of dendritic spine morphogenesis	CDK5R1,PAFAH1B1	SRCIN1,KALRN
GO:0090277	0.01223131	5	53	positive regulation of peptide hormone secretion	ENSACAG00000011849	FGG,STX4,PLA2G6,CCKAR
GO:0006515	0.012291356	3	18	misfolded or incompletely synthesized protein catabolic process	RNF126,LONP2	UFD1L
GO:0060249	0.012745447	10	154	anatomical structure homeostasis	GIGYF2,GCNT2,DCLRE1A	XRCC6,ADD1,GATA1,TRAF6,ADGRF5,PARP3,BBS10
GO:0043547	0.012808641	7	91	positive regulation of GTPase activity	ECT2,ENSACAG00000006885	SEMA4D,SNX9,ENSACAG00000015364,THY1,ENSACAG00000001557
GO:0030048	0.012891355	5	44	actin filament-based movement	FRMD6,FRMD1	MYH9,MYO1A,MYO1E
GO:0072376	0.013415824	6	94	protein activation cascade	ENSACAG00000026198	FGG,ENSACAG00000010314,C7,ENSACAG00000017760,ENSACAG00000007857
GO:0045088	0.013538657	11	173	regulation of innate immune	JAK1,NMI	TRAFD1,IRAK4,SAMHD1,EN

				response		SACAG00000017760,SIN3A,TNFAIP3,IFNGR1,ENSACAG00000006445,AP1G1
GO:0072524	0.013543229	5	54	pyridine-containing compound metabolic process	APOA1BP,PGM2	IDH3G,H6PD,IDH3B
GO:0032049	0.014464779	2	7	cardiolipin biosynthetic process	PGS1	PLA2G6
GO:0001894	0.016528339	7	95	tissue homeostasis	GIGYF2,GCNT2	ADD1,GATA1,TRAF6,ADGRF5,BBS10
GO:0031532	0.01755094	5	53	actin cytoskeleton reorganization	NPHS2	MYH9,ANXA1,EZR,CCKAR
GO:0002118	0.018447881	2	8	aggressive behavior	PENK	GCNT4
GO:0071295	0.018632268	2	9	cellular response to vitamin	PENK	GAS6
GO:0050905	0.019518264	6	72	neuromuscular process	GIGYF2,PENK,PAFAH1B1	GLRB,NRXN1,ATXN2
GO:0030100	0.02016771	9	140	regulation of endocytosis	RUFY1,ENSACAG00000006885	GAS6,ENSACAG00000015209,ENSACAG00000011799,ATXN2,SDCBP,SCARB1,FLOT1
GO:0006098	0.020828916	2	9	pentose-phosphate shunt	PGM2	H6PD
GO:0006487	0.020843264	5	56	protein N-linked glycosylation	ALG8	ENSACAG00000016117,VCP,DPAGT1,ST3GAL4
GO:0006732	0.021849627	10	181	coenzyme metabolic process	AGK,PGM2	PAH,COQ2,COASY,IDH3G,MAT2B,H6PD,MOCS3,IDH3B
GO:0090501	0.022028298	4	39	RNA phosphodiester bond hydrolysis	EXOSC8	UTP20,ABT1,ELAC2
GO:0009306	0.022086372	8	120	protein secretion	ENSACAG00000011849,LCP2,PAFAH1B1,CPLX1,STEAP3	PDIA4,FGG,CCKAR
GO:0002504	0.023609965	4	38	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	ENSACAG00000006391	TRAF6,SPTBN2,AP1G1
GO:0030397	0.024392786	3	20	membrane disassembly	PAFAH1B1	TPR,NUP107
GO:0051081	0.024392786	3	20	nuclear envelope disassembly	PAFAH1B1	TPR,NUP107
GO:1901617	0.025883019	8	121	organic hydroxy compound biosynthetic process	FDPS,IMPA1	PRKAA1,CYP27A1,DPAGT1,TMLHE,PCYT1A,IMPA1,ENSACAG00000003142
GO:0006446	0.026865062	5	59	regulation of translational initiation	EIF4H	RPL13A,EIF5B,ENSACAG000

						00010260,TPR
GO:0006333	0.028007139	4	42	chromatin assembly or disassembly	CENPC,HDAC8	CENPH,NOC2L
GO:0006694	0.02917831	7	108	steroid biosynthetic process	ENSACAG00000000510,FDPS	PRKAA1,CYP27A1,MAT2B,SCARB1,ENSACAG00000003142
GO:0070613	0.030824194	10	185	regulation of protein processing	ENSACAG00000012650,BUB1,ENSACAG00000026198	GAS6,CTNND1,ENSACAG00000013691,ENSACAG00000017760,ENSACAG00000011799,SDCBP,TPR
GO:0090150	0.031925254	9	167	establishment of protein localization to membrane	ENSACAG00000011849	GAS6,SYNE3,PKP3,RPS5,EZR,RPL13A,SDCBP,FLOT1
GO:0032846	0.034964282	8	130	positive regulation of homeostatic process	TRDN,WRAP53	ENSACAG00000009269,GATA1,CCT4,STX4,PLA2G6,THY1
GO:0051591	0.034999104	5	68	response to cAMP	PER1,PENK	MMP19,CARM1,EZR
GO:0014075	0.035155648	3	24	response to amine	HNMT,TRDMT1	ENSACAG00000002091
GO:2000251	0.035824764	2	11	positive regulation of actin cytoskeleton reorganization	BAIAP2L1	ENSACAG00000015364
GO:0034504	0.03667234	7	106	protein localization to nucleus	MCM3AP,RANBP17,TOR1AIP1	ENSACAG00000002091,NUP85,TPR,NUP107
GO:0019318	0.03834842	7	108	hexose metabolic process	HKDC1,ENSACAG00000003913,PGM2,BRAT1	PRKAA1,ENSACAG00000003913,H6PD,PGM2L1
GO:0022904	0.0388685	3	41	respiratory electron transport chain	UQCRC2	SDHA,ENSACAG00000007045
GO:0000380	0.039354611	2	11	alternative mRNA splicing, via spliceosome	RSRC1	SFSWAP
GO:0001678	0.039407858	4	46	cellular glucose homeostasis	HKDC1	GAS6,SIN3A,MEN1
GO:0032259	0.040573296	10	186	methylation	DDX4,HNMT,MTO1,FTSJ2,TRDMT1	CARM1,TRMT61B,THUMPD3,MEN1,TGS1
GO:0032479	0.040631594	5	62	regulation of type I interferon production	DDX41,NMI	TNFAIP3,DHX9,FLOT1
GO:0070301	0.041529497	4	47	cellular response to hydrogen peroxide	ECT2,ZNF277	PRKAA1,TNFAIP3
GO:0031055	0.043518123	2	13	chromatin remodeling at	CENPC	CENPH

				centromere		
GO:0051289	0.043584284	4	50	protein homotetramerization	APOA1BP	SAMHD1,TK1,ACADL
GO:0009790	0.044090824	10	185	embryo development	EPN2,CDK5R1	EPN1,MYH9,ADD1,PDGFC,GATA1,SIN3A,STIL,MYO1E
GO:0048872	0.044892596	6	96	homeostasis of number of cells	GIGYF2	ADD1,GCNT4,GATA1,TNFAIP3,ATXN2
GO:0000462	0.045744754	3	30	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	DIEXF	UTP20,DIEXF,WDR3
GO:0009648	0.047631675	2	13	photoperiodism	PER1	FBXL3
GO:2000257	0.048914315	3	28	regulation of protein activation cascade	ENSACAG00000026198	SERPINC1,ENSACAG00000017760
GO:0006265	0.049369877	2	12	DNA topological change	TOP3A	MTX1

Table S28. Categories showed evolutionary convergence between the frogs and lizards at elevation around 3500 m.

category	pvalue	numDEInCat	numInCat	term	Frog PSGs	Lizard PSGs
GO:1990440	0.000384738	3	9	positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress	ATF6	ATF4,ATF6B
GO:0010939	0.001485361	3	15	regulation of necrotic cell death	FADD	RIPK1,PPIF
GO:0016485	0.001657693	10	182	protein processing	FADD,ENSACAG00000005027	BCL2L13,ATP6AP2,ADAMTS3,LGMN,HM13,AFG3L2,AEBP1,LONP2
GO:0005981	0.002249768	2	5	regulation of glycogen catabolic process	PPP1R3B	ENSACAG00000024726
GO:0039531	0.002341062	3	13	regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	ENSACAG00000029208	TKFC,NLRX1
GO:0045651	0.002572418	2	5	positive regulation of macrophage differentiation	FADD	RIPK1
GO:0036500	0.002974759	2	4	ATF6-mediated unfolded protein response	ATF6	ATF6B

GO:0090521	0.003281777	2	4	glomerular visceral epithelial cell migration	ANLN	NUP93
GO:1901888	0.006540381	5	61	regulation of cell junction assembly	ENSACAG00000005027,RAC1	COL16A1,ENSACAG00000015364,RAPGEF1
GO:1901522	0.007189188	3	19	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	ATF6	ATF4,RXRA
GO:0051170	0.008349257	6	87	nuclear import	CSE1L,TGS1	IPO9,HTATIP2,TNPO3,NUP93
GO:0021799	0.008614656	2	9	cerebral cortex radially oriented cell migration	RAC1	RTN4
GO:2001240	0.010663203	3	24	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	FYN	RIPK1,ZC3HC1
GO:0043624	0.010869853	4	49	cellular protein complex disassembly	MRPL44,ENSACAG00000010017,ENSACAG00000008908	VILL
GO:0031468	0.013939645	2	11	nuclear envelope reassembly	CHMP7	CHMP2A
GO:0008360	0.013974349	7	130	regulation of cell shape	ENSACAG00000005027,FYN	PTN,TTBK2,EZR,HPN,VILL
GO:0010458	0.015971503	2	10	exit from mitosis	CHMP7	CHMP2A
GO:0017038	0.016640492	6	108	protein import	CSE1L	IPO9,AFG3L2,TNPO3,NUP93,LONP2
GO:0034976	0.019758571	6	112	response to endoplasmic reticulum stress	AARS,ATF6	ATF4,SEL1L,ATF6B,UBE4B
GO:0090103	0.020127148	2	13	cochlea morphogenesis	RAC1	HPN
GO:0097190	0.0214731	8	190	apoptotic signaling pathway	FADD,ZNF346,ZNF622	FAS,ATF4,PARP2,UBE4B,RIPK1
GO:0032239	0.022664747	2	11	regulation of nucleobase-containing compound transport	IWS1	RIPK1
GO:0009451	0.02457272	6	122	RNA modification	PUS7,AARS,TGS1	HEMK1,TXNDC9,TRIT1
GO:0006044	0.024673619	2	14	N-acetylglucosamine metabolic process	ENSACAG00000001708	CHST2
GO:0006457	0.026225839	7	168	protein folding	AARS,ATF6	FKBP9,TBCD,CRTAP,PPIF,FKBP15
GO:0043467	0.029021199	4	65	regulation of generation of precursor metabolites and energy	PPP1R3B	SIRT6,PPIF,ENSACAG00000024726
GO:0043547	0.029612275	5	91	positive regulation of GTPase activity	CDKL5,RAC1	TBCD,ENSACAG00000015364,RAPGEF1

GO:0006887	0.03291211	7	159	exocytosis	SCRN1,MIA3	STXBP3,LIN7A,SYTL2,STXBP2,PPP3CB
GO:0001895	0.033774468	2	16	retina homeostasis	BBS10	WDR36
GO:0043588	0.036278776	3	33	skin development	RYR3,AARS	COL3A1
GO:0036120	0.040566244	2	16	cellular response to platelet-derived growth factor stimulus	FYN	PTN
GO:0006040	0.044014955	3	44	amino sugar metabolic process	ENSACAG00000001708	CHST2,MGAT1
GO:0043029	0.04433137	2	20	T cell homeostasis	FADD	PPP3CB
GO:0006400	0.044821016	4	74	tRNA modification	AARS	HEMK1,TXNDC9,TRIT1
GO:0036119	0.046455853	2	17	response to platelet-derived growth factor	FYN	PTN

Table S29. Categories showed evolutionary convergence between the frogs and lizards at elevation around 4500 m

category	pvalue	numDE InCat	numIn Cat	term	Frog PSGs	Lizard PSGs
GO:0010954	6.88E-05	4	15	positive regulation of protein processing	PLGRKT,MFI2	CLEC3B,CTNND1
GO:1900024	0.000117483	6	41	regulation of substrate adhesion-dependent cell spreading	MFI2,RAC1	OLFM4,POSTN,FLNA,DMTN
GO:0022618	0.000649805	11	199	ribonucleoprotein complex assembly	NSUN4,ENSACAG00000023921	CIRBP,RPL11,PSIP1,DDX23,DDX6,SART1,ENSACAG00000004183,NUFIP1,ATXN2L
GO:0051932	0.0019179	2	4	synaptic transmission, GABAergic	RAC1	DNM1
GO:0006826	0.002232932	4	33	iron ion transport	MFI2,SLC40A1	PVRL1,ENSACAG00000004685
GO:0006109	0.002529437	8	137	regulation of carbohydrate metabolic process	ENSACAG00000022125,C4orf27	ENSACAG00000002886,AP2A1,PPP4R3A,ADIPOR1,GPER1,PLCD1
GO:1904948	0.005086229	2	6	midbrain dopaminergic neuron differentiation	RAC1	RYK
GO:0060644	0.005695273	2	8	mammary gland epithelial cell differentiation	IRF6	ENSACAG0000002886

GO:0010675	0.006029237	7	128	regulation of cellular carbohydrate metabolic process	ENSACAG00000022125,C4orf27	ENSACAG00000002886,PPP4R3A,ADIPOR1,GPER1,PLCD1
GO:0006953	0.006084761	3	22	acute-phase response	ENSACAG00000022125	FN1,ITIH4
GO:0090329	0.009921794	4	41	regulation of DNA-dependent DNA replication	ZRANB3,DSCC1,NBN	SMC1A
GO:0000041	0.011086842	5	77	transition metal ion transport	MFI2,SLC40A1	ATP2C1,PVRL1,ENSACAG00000004685
GO:0022613	0.012969547	4	54	ribonucleoprotein complex biogenesis	ENSACAG00000009242	GNL3,LSG1,RPLP0
GO:0009451	0.01588654	6	122	RNA modification	NSUN4,MTO1	NOP58,TYW5,METTL3,NOP56
GO:0006473	0.016478222	6	102	protein acetylation	ATAT1,DSCC1,EPC2	BRPF1,TAF10,BRD1
GO:0045727	0.017256202	4	58	positive regulation of translation	NSUN4	CIRBP,ABCF1,METTL3
GO:0009108	0.018600805	5	98	coenzyme biosynthetic process	COQ3	PCBD2,NADK2,ELOVL5,THEM5
GO:0001956	0.018716143	2	12	positive regulation of neurotransmitter secretion	STX1B	GPER1
GO:0007062	0.019688526	5	76	sister chromatid cohesion	SMC5,DSCC1	STAG1,CKAP5,SMC1A
GO:0051262	0.020216924	5	87	protein tetramerization	TRPM3	ALDOA,FARSA,GLS,DNM1
GO:0016072	0.021575442	7	168	rRNA metabolic process	NSUN4,WDR36	UTP6,NOP58,DIS3,SART1,NOP56
GO:0006636	0.022019106	3	37	unsaturated fatty acid biosynthetic process	ENSACAG00000017657	PTGES3,ELOVL5
GO:0002690	0.023738402	3	41	positive regulation of leukocyte chemotaxis	RAC1	F7,ADAM17
GO:0042770	0.025243823	4	60	signal transduction in response to DNA damage	GTSE1,NBN	HIPK2,SMC1A
GO:0060249	0.026047808	7	154	anatomical structure homeostasis	SMC5,RAC1,PFKM,NBN,WDR36	RPA1,LPCAT1
GO:0005996	0.029535623	6	131	monosaccharide metabolic process	ENSACAG00000022125,PFKM	ENSACAG00000002886,RGN,MAN2C1,SLC37A4
GO:0045833	0.033235711	3	39	negative regulation of lipid metabolic process	ENSACAG00000022125	GPER1,LPCAT1
GO:0046427	0.034274719	2	17	positive regulation of JAK-STAT cascade	AGAP2	ADIPOR1

GO:0008344	0.038697933	4	67	adult locomotory behavior	SNCG	HIPK2,EPHA4,DNM1
GO:0031954	0.038958704	2	18	positive regulation of protein autophosphorylation	NBN	CTNND1
GO:0043543	0.04034647	6	132	protein acylation	ATAT1,DSCC1,EPC2	BRPF1,TAF10,BRD1
GO:0007030	0.042136667	5	96	Golgi organization	KIFC3	RAB43,TJAP1,COG4,ENSACAG00000013675
GO:0032355	0.043205949	4	77	response to estradiol	ENSACAG00000022125	F7,POSTN,GPER1
GO:0045216	0.044599456	6	128	cell-cell junction organization	RAC1,KIFC3	FLNA,GNPAT,PVRL1,DLG5
GO:0002063	0.04937034	2	18	chondrocyte development	CHST13	BMPR2

Table S30. Categories showed evolutionary convergence between the frogs and lizards along branches 7, 6, and 1.

category	pvalue	numDE InCat	numIn Cat	term	Frog PSGs	Lizard PSGs
GO:0006412	1.91E-05	20	228	translation	RRBP1,MRPL35,MRPS30,ENSACAG00000008192,RPLP2,MRPL18,SLC25A35	MRPL47,SLC25A3,RPS8,EIF4H,EEF2,ENSACAG00000009700,ENSACAG00000010703,SLC25A26,RPS5,RPL15,RPLP1,ENSACAG00000004183,ENSACAG00000007152
GO:0001938	0.0001616	8	44	positive regulation of endothelial cell proliferation	NRP2,SEMA5A,PDCD6,TGFBR1	F3,FIGF,VEGFC,VEGFA
GO:0007062	0.000267449	11	76	sister chromatid cohesion	DSN1,CENPC,ENSACAG00000011405,PAFAH1B1,HDAC8,NUP107	STAG2,STAG1,PDS5B,CLIP1,PLK1
GO:0032355	0.000587452	10	77	response to estradiol	ENSACAG00000022125,PENK,ENSACAG00000017475,TXNIP	F7,SLC6A1,MAPK15,PTGFR,GPER1,ENSACAG00000028324
GO:0070507	0.000631703	13	119	regulation of microtubule cytoskeleton organization	FBXW5,CENPJ,CDK5R1,PAFAH1B1,ENSACAG00000012696,RNF4,RANBP1	ROCK2,CDK5R1,XPO1,PDCD6IP,VPS4B,CLIP1,PLK1
GO:0051660	0.000692194	3	5	establishment of centrosome localization	PAFAH1B1	CEP83,EZR
GO:0007596	0.000965588	11	91	blood coagulation	PROCR,PROS1	F3,F7,VWF,F5,FGG,WAS,ENSACAG00000003225,ADORA2A,LMAN1

GO:0050817	0.000965588	11	91	coagulation	PROCR,PROS1	F3,F7,VWF,F5,FGG,WAS,ENSACAG00000003225,ADORA2A,LMAN1
GO:1900024	0.001003693	7	41	regulation of substrate adhesion-dependent cell spreading	OLFM4,MFI2,RAC1	OLFM4,FGG,DMTN,NET1,SDC3
GO:0030100	0.001034105	14	140	regulation of endocytosis	ENSACAG00000013638,RUFY1,ANKFY1,ENSACAG00000006885	PPT1,ARFGAP1,ENSACAG00000015209,EHD4,RUFY1,ENSACAG00000012647,ENSACAG00000006690,OPHN1,SDCBP,ENSACAG00000028324,FLOT1
GO:0051186	0.00140481	18	226	cofactor metabolic process	ENSACAG00000022125,GNMT,COQ3,COQ5,ALAD,GPHN,ENSACAG00000008138,ENSACAG00000004307	PPT1,ACOT8,ASPDH,PCBD2,ALDOB,ELOVL5,THEM5,ELOVL2,ENSACAG00000007025,IDH3B,ENSACAG00000004307
GO:0010954	0.00150727	4	15	positive regulation of protein processing	PLGRKT,MFI2	CLEC3B,CTNND1
GO:0044743	0.001540808	5	27	intracellular protein transmembrane import	PEX26,ENSACAG00000011849,HSPA4,LONP2	ENSACAG00000028324
GO:0070925	0.001774729	20	246	organelle assembly	CENPC,CENPJ,HAUS7,ARHGEF10,SPATA6,TSR1,PAFAH1B1,ENSACAG00000012696,ENSACAG00000013026	CIRBP,PLS1,ATG13,ZMYND10,EZR,DDX6,ENSACAG00000004832,PDCD6IP,VPS4B,KIAA0196,ENSACAG00000013026,CHD4
GO:0072313	0.002121981	2	2	metanephric glomerular epithelial cell development	NPHS2	LAMB2
GO:0035336	0.002456979	5	26	long-chain fatty-acyl-CoA metabolic process	ENSACAG00000004307	ACOT8,ELOVL5,THEM5,ELOVL2,ENSACAG00000004307
GO:0002181	0.002523838	4	21	cytoplasmic translation	RPLP2	EIF4H,RPL15,RPLP1
GO:0006096	0.002883309	6	37	glycolytic process	HKDC1,ENSACAG00000002126	ALDOA,ALDOB,PKM,PFKFB3
GO:0043627	0.004525206	11	115	response to estrogen	ENSACAG00000022125,PENK,ENSACAG00000017475,TXNIP	ALDOA,F7,SLC6A1,MAPK15,PTGFR,GPER1,ENSACAG00000028324
GO:0071806	0.004628732	5	34	protein transmembrane transport	PEX26,ENSACAG00000011849,HSPA4,LONP2	ENSACAG00000028324
GO:0006091	0.005097942	14	179	generation of precursor	ENSACAG00000005218,HKDC1,G	ALDOA,NDUFS4,ALDOB,ADGRF5,

				metabolites and energy	AA,OXA1L,ENSACAG00000002126	ENSACAG00000007045,COX19,MTFR1,PKM,PFKFB3
GO:0021819	0.00518773	3	10	layer formation in cerebral cortex	CDK5R1,PAFAH1B1	SOCS7,CDK5R1
GO:0045765	0.005674056	14	172	regulation of angiogenesis	SEMA5A,PDCD6,TERT	HIPK2,F3,FIGF,VEGFC,ANXA3,ITGB2,HTATIP2,COL4A2,STAB1,THBS2,EMP2
GO:0044772	0.005834022	13	148	mitotic cell cycle phase transition	OFD1,CAMK2D,HAUS7,ORC2,PAFAH1B1,ENSACAG00000013026,RANBP1	CDK14,ENSACAG00000025027,CAMK2D,TAF10,ENSACAG00000013026,EIF4E,ENSACAG00000028324,PLK1
GO:0035337	0.00630288	5	32	fatty-acyl-CoA metabolic process	ENSACAG00000004307	ACOT8,ELOVL5,THEM5,ELOVL2,ENSACAG00000004307
GO:0045056	0.006944866	3	11	transcytosis	MYO1A	MFSD2A,VPS35
GO:0051932	0.007409718	2	4	synaptic transmission, GABAergic	RAC1	DNM1
GO:0006414	0.007522494	6	58	translational elongation	MRPS30,RPLP2,MRPS31	ENSACAG00000009700,RPLP1,ENSACAG00000007152
GO:0090003	0.008215618	6	48	regulation of establishment of protein localization to plasma membrane	PPP2R5A	PLS1,EZR,ARF6,GPER1,ITGB1
GO:0017038	0.008249771	10	108	protein import	PEX26,ENSACAG00000011849,HSPA4,KPNA5,TXNIP,LONP2,NUP107,RANBP1	NOP58,ENSACAG00000028324
GO:0016052	0.00992898	9	93	carbohydrate catabolic process	GK5,HKDC1,GAA,ENSACAG00000002126	ALDOA,ENSACAG00000001468,ALDOB,PKM,PFKFB3
GO:0021549	0.010184445	5	35	cerebellum development	CDK5R1,SEMA4C	CNTN1,CDK5R1,RPGRIP1L,ENSACAG00000028324
GO:0043161	1.02E-02	16	223	proteasome-mediated ubiquitin-dependent protein catabolic process	FBXW5,GTSE1,ENSACAG00000008899,KEAP1,RNF4	HSP90B1,CDC20,FBXO4,C18orf25,SPOPL,UBE2J1,EDEM1,PSMD12,UBE4B,NSFL1C,PLK1
GO:0034605	0.010822911	5	37	cellular response to heat	PDCD6,ENSACAG00000011939	ENSACAG00000015832,ENSACAG00000028324,MYOF

GO:0061635	0.011179153	2	5	regulation of protein complex stability	SQSTM1	ENSACAG00000028324
GO:0051560	0.011254107	3	13	mitochondrial calcium ion homeostasis	MICU1	IMMT,CCDC109B
GO:1903532	0.01255461	17	251	positive regulation of secretion by cell	ENSACAG00000011849,PPIA,ENSACAG00000029563	VEGFC,FGG,LPL,ATP6AP1,EZR,ENSACAG00000006690,PDCD6IP,VPS4B,PLA2G6,GPER1,SDCBP,IL1RAP,PLCD1,VPS35
GO:0010762	0.012585045	4	25	regulation of fibroblast migration	CYGB,WDPCP,RAC1	DMTN
GO:0043928	0.012603396	3	14	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	EXOSC8	EXOSC2,CNOT8
GO:0030866	0.013377646	4	24	cortical actin cytoskeleton organization	EPB41L1	PLS1,EZR,ARF6
GO:0048520	0.013978057	8	88	positive regulation of behavior	SEMA5A,RAC1,PENK	F7,FIGF,VEGFC,STX3,ADAM17
GO:0006913	0.014240764	14	185	nucleocytoplasmic transport	RSRC1,KPNA5,TXNIP,NUP107,RANBP1	NOP58,HTATIP2,ENSACAG00000013788,ENSACAG00000026588,XPO1,ENSACAG00000015804,THOC1,ENSACAG00000028324,TGS1
GO:0051651	0.014638942	10	112	maintenance of location in cell	DSN1,TBCCD1,DZIP1,ARL2BP,KEAP1,GAA	SUPT7L,EZR,VPS13C,CEP350
GO:0051169	0.016167646	14	188	nuclear transport	RSRC1,KPNA5,TXNIP,NUP107,RANBP1	NOP58,HTATIP2,ENSACAG00000013788,ENSACAG00000026588,XPO1,ENSACAG00000015804,THOC1,ENSACAG00000028324,TGS1
GO:0032530	0.018682016	3	14	regulation of microvillus organization	ENSACAG00000006885	PLS1,EZR
GO:1902285	0.019974542	3	12	semaphorin-plexin signaling pathway involved in neuron projection guidance	NRP2,PLXNA1	PLXNB2

GO:0000291	0.023745737	3	18	nuclear-transcribed mRNA catabolic process, exonucleolytic	EXOSC8	EXOSC2,CNOT8
GO:0043547	0.024198176	8	91	positive regulation of GTPase activity	ARHGAP27,RAC1,ENSACAG00000006885	SEMA4D,SNX9,TNFRSF14,RAPGEF1,NET1
GO:0070482	0.024360832	13	190	response to oxygen levels	CAMK2D,CYGB,PENK,NARFL,TERT	ALDOA,HIPK2,HSP90B1,F7,FIGF,VEGFC,CAMK2D,ADAM17,PLCD1
GO:0006413	0.02576018	7	86	translational initiation	MRPS30,MRPS31	EIF4H,RPS5,EIF4E2,EIF4E,EIF3G
GO:1903010	0.0259739	3	19	regulation of bone development	TMEM119	ATP6AP1,FAM101B,TMEM119
GO:0051276	0.027180126	18	271	chromosome organization	DSN1,CENPC,TOP3A,DCLRE1B,ENSACAG00000011405,ENSACAG00000012053,PAFAH1B1,HDAC8,NUP107,TERT	STAG2,STAG1,HMGB2,PDS5B,FBXO4,CLIP1,GPER1,PLK1
GO:0072594	0.029213859	15	235	establishment of protein localization to organelle	PEX26,ENSACAG00000011849,NABP2,HSPA4,KPNA5,TXNIP,LONP2,NUP107,RANBP1,TERT	NOP58,RPS5,VPS13C,ENSACAG00000028324,SPCS2
GO:0001666	0.030533707	12	177	response to hypoxia	CAMK2D,CYGB,PENK,NARFL,TERT	ALDOA,HIPK2,HSP90B1,F7,FIGF,VEGFC,CAMK2D,ADAM17
GO:0034427	0.031752012	2	9	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	EXOSC8	EXOSC2
GO:0045358	0.033217193	1	1	negative regulation of interferon-beta biosynthetic process	NMI	NMI
GO:0030947	0.033285875	3	19	regulation of vascular endothelial growth factor receptor signaling pathway	PDCD6	VEGFC,MYOF
GO:0043633	0.033807095	2	9	polyadenylation-dependent RNA catabolic process	EXOSC8	EXOSC2
GO:0010566	0.033963987	2	8	regulation of ketone biosynthetic process	COQ3	SIRT5
GO:1901888	0.034360891	6	61	regulation of cell junction assembly	WDPCP,RAC1	VEGFA,DMTN,RAPGEF1,FLOT1

GO:2000352	0.035373391	3	18	negative regulation of endothelial cell apoptotic process	SEMA5A,TERT	FGG
GO:0050795	0.0375796	12	174	regulation of behavior	SEMA5A,PLXNA1,RAC1,PENK,SEMA4C	F7,FIGF,VEGFC,SEMA4D,STX3,ADAM17,PADI2
GO:0046364	0.040185896	4	35	monosaccharide biosynthetic process	ENSACAG00000002126	RGN,ALDOB,ENSACAG00000010703
GO:0030048	0.041704426	5	44	actin filament-based movement	CAMK2D,MYO1A	MYH9,CAMK2D,WAS,EMP2
GO:0045926	0.043132454	12	183	negative regulation of growth	SEMA5A,SQSTM1,CDK5R1,SEMA4C	PPT1,IFRD1,SEMA4D,SMARCA2,LGMN,CDK5R1,MUL1,ADIPOR1,FOXK1
GO:0045787	0.044578274	15	242	positive regulation of cell cycle	ENSACAG00000014321,GTSE1,CDK5R1,PAFAH1B1,RANBP1,KIF20B,TERT	RAB11FIP4,ROCK2,ADAM17,UBE2E2,CDK5R1,ENSACAG00000004832,VPS4B,EIF4E,CNOT8
GO:0045022	0.045732361	3	20	early endosome to late endosome transport	ENSACAG00000012345	VPS4B,EMP2
GO:0010664	0.046824507	2	9	negative regulation of striated muscle cell apoptotic process	BAG3	ENSACAG00000028324
GO:0015931	0.047860364	10	141	nucleobase-containing compound transport	MRPL18,NUP107,RANBP1,THOC2	SLC35A1,SLC25A26,XPO1,ENSACAG00000015804,THOC1,FLOT1

Table S31. Convergent evolved KEGG pathways between frogs and lizards.

KEGG pathway	Frog	Lizard
ko00010:Glycolysis / Gluconeogenesis	ALDOA, HK2	PGM2, HKDC1, PFKM
ko00030:Pentose phosphate pathway	ALDOA, G6PD, H6PD, TKT	PGM2, PFKM, PRPS2
ko00051:Fructose and mannose metabolism	ALDOA, GMDS, HK2	HKDC1, PFKM
ko00052:Galactose metabolism	HK2	PGM2, HKDC1, PFKM
ko00130:Ubiquinone and other terpenoid-quinone biosynthesis	COQ2	GGCX, COQ3
ko00140:Steroid hormone biosynthesis	STS	SRD5A3
ko00190:Oxidative phosphorylation	SDHA, NDUFA6, ATP6AP1, NDUFB9, COX4I1, ATP6V1H, ATP6V0A1, LHPP	LHPP

ko00230:Purine metabolism	ADCY4, POLD2, NTPCR, PDE3B, RRM2B, IMPDH1	PGM2, ADK, POLR3A, GUCY1B3, PRPS2
ko00240:Pyrimidine metabolism	POLD2, TXNRD3, RRM2B, DCTPP1, TK1	POLR3A
ko00340:Histidine metabolism	CARNS1	HNMT
ko00500:Starch and sucrose metabolism	HK2, PGM2L1	PGM2, HKDC1
ko00510:N-Glycan biosynthesis	MGAT1, ALG3, DPAGT1, RPN2	RPN2, ALG8
ko00520:Amino sugar and nucleotide sugar metabolism	GMDS, HK2	PGM2, HKDC1
ko00524:Butirosin and neomycin biosynthesis	HK2	HKDC1
ko00532:Glycosaminoglycan biosynthesis	B4GALT7	CHST13
ko00561:Glycerolipid metabolism	TKFC, LIPC, AGK	LCLAT1, AGK
ko00562:Inositol phosphate metabolism	IMPA1, PLCD1, OCRL	IMPA1
ko00564:Glycerophospholipid metabolism	ETNPPL, CHKA, PGS1, LPCAT1, ETNK1, PLA2G6, GNPAT, PCYT1A, LPCAT3, LPCAT4	PGS1, LCLAT1
ko00565:Ether lipid metabolism	LPCAT1, PLA2G6, LPCAT4	PAFAH1B1
ko00590:Arachidonic acid metabolism	PTGES3, PLA2G6	LTA4H
ko00900:Terpenoid backbone biosynthesis	HMGCR, GGPS1	FDPS
ko00910:Nitrogen metabolism	CA12	CA4
ko00970:Aminoacyl-tRNA biosynthesis	YARS, RARS, FARSA	DARS, AARS, QARS, MTFMT
ko01130:Biosynthesis of antibiotics	ALDOA, SDHA, G6PD, IDH3G, HMGCR, GGPS1, HK2, IDH3B, TKT	PGM2, HKDC1, FDPS, PFKM, PRPS2
ko01200:Carbon metabolism	ALDOA, SDHA, G6PD, IDH3G, TKFC, H6PD, HK2, IDH3B, TKT	HKDC1, PFKM, PRPS2
ko01230:Biosynthesis of amino acids	ALDOA, IDH3G, IDH3B, TKT, PAH, MAT2B	PFKM, PRPS2
ko03008:Ribosome biogenesis in eukaryotes	WDR36, UTP6, LSG1, WDR3, NOP58, NOP56, MDN1, GNL3	WDR36, UTP15, MPHOSPH10
ko03010:Ribosome	MRPL28, MRPS18A, RPL13A, RPLP0, RPL15, RPLP1, RPL35, RPL11, RPS5, MRPL20	MRPL18

ko03013:RNA transport	EEF1A1, EIF4G3, ELAC2, EIF3H, PAIP1, EIF5B, NUP93, NUP85, NUP107, THOC5, TGS1, TPR, EIF2B3, PNN	TGS1
ko03015:mRNA surveillance pathway	PNN	PPP2R2A
ko03018:RNA degradation	DIS3, SKIV2L, TTC37, EDC4, DDX6	EXOSC8, DCP1B, PFKM
ko03030:DNA replication	RPA1, POLD2	MCM3
ko03050:Proteasome	PSMB7, PSMA6, PSMD12, PSMB9	PSMB7
ko03420:Nucleotide excision repair	RPA1, XPC, POLD2	XPC
ko03440:Homologous recombination	RPA1, POLD2	NBN, TOP3A, RAD54B, RAD52
ko03450:Non-homologous end-joining	XRCC5, XRCC6	XRCC4, LIG4
ko03460:Fanconi anemia pathway	RPA1, RMI1	TOP3A
ko04010:MAPK signaling pathway	FGFR1, FGFR4, ATF4, RELB, PPP3CB, MAPK8, FAS, STMN1, TRAF6, NFATC3, HSPA8	FGFR2, ELK4, TGFBR1, RAC1, MAPK8
ko04012:ErbB signaling pathway	MAPK8	MAPK8
ko04014:Ras signaling pathway	FGFR1, FGFR4, VEGFA, GRIN1, PLA2G6, MAPK8, PDGFC, EXOC2, EPHA2	FGFR2, RAC1, MAPK8
ko04015:Rap1 signaling pathway	ADCY4, FGFR1, FGFR4, TLN1, GRIN1, LPAR4, CTNND1, CDH1, ITGB1, EPHA2, VEGFA, PDGFC, RAPGEF1	FGFR2, GNAI1, RAC1, LCP2
ko04020:Calcium signaling pathway	PPIF, CCKAR, ADCY4, SLC25A4, SPHK1, GRIN1, PPP3CB, PLCD1, PTGFR, VDAC3, MYLK	RYR3
ko04022:cGMP-PKG signaling pathway	PPIF, ADCY4, ATF4, SLC25A4, ROCK2, ATF6B, PPP3CB, PDE3B, ATP1A1, VDAC3, NFATC3, MYLK	GNAI1, MRVI1, GUCY1B3
ko04024:cAMP signaling pathway	ACOX1, ADCY4, ROCK2, GRIN1, PDE3B, ATP1A1, MAPK8	GNAI1, RAC1, MAPK8
ko04060:Cytokine-cytokine receptor interaction	IFNAR2, VEGFA, IL1RAP, BMPR2, FAS, IL17RA, IFNGR1, ACVR1	TGFBR1

ko04062:Chemokine signaling pathway	ADCY4, ROCK2	GNAI1, RAC1, JAK2
ko04066:HIF-1 signaling pathway	VEGFA, HK2, IFNGR1	HKDC1
ko04068:FoxO signaling pathway	MAPK8, PRKAA1	TGFBR1, MAPK8, AGAP2
ko04070:Phosphatidylinositol signaling system	IMPA1, PLCD1, OCRL	IMPA1
ko04071:Sphingolipid signaling pathway	BID, ROCK2, SPHK1, MAPK8	FYN, GNAI1, RAC1, MAPK8, PPP2R2A
ko04110:Cell cycle	RAD21, CDC20, SMC1A, STAG1	BUB1, PKMYT1, MCM3, CCNA2
ko04114:Oocyte meiosis	ADCY4, PPP3CB, CDC20, SMC1A	BUB1, PKMYT1
ko04115:p53 signaling pathway	BID, RFWD2, RRM2B, FAS	STEAP3, GTSE1
ko04120:Ubiquitin mediated proteolysis	RFWD2, PPIL2, UBE4B, CDC20, KEAP1, TRAF6, UBE2U	PPIL2
ko04122:Sulfur relay system	MOCS3	TRMU
ko04130:SNARE interactions in vesicular transport	STX4, STX3, USE1	STX1B
ko04141:Protein processing in endoplasmic reticulum	HSPH1, SEC24B, NPLOC4, ATF4, PDIA3, VCP, UFD1L, UBE4B, ATF6B, MAPK8, PDIA4, RPN2, SAR1A, HSPA8, SEL1L	ATF6, MAPK8, RPN2
ko04142:Lysosome	CTSK, LIPA, AP1G1, ATP6AP1, LGMN, GALC, ATP6V1H, ATP6V0A1, PPT1, CLN5	AP3M2
ko04144:Endocytosis	CHMP2A, FGFR4, AP2A1, KIAA0196, RUFY1, HGS, CYTH2, VPS35, TRAF6, RAB11FIP1, HSPA8, DNM1, EPN1	FGFR2, TGFBR1, CHMP7, KIF5C, RUFY1, AGAP2, EPN2, DNM2, EHD4
ko04145:Phagosome	STX12, ATP6AP1, ATP6V1H, HGS, ATP6V0A1, SCARB1, THBS2, ITGB1	RAC1
ko04146:Peroxisome	ACOX1, GNPAT, SOD1	PEX1
ko04151:PI3K-Akt signaling pathway	FGFR1, FGFR4, RXRA, TNC, COL3A1, LPAR4, ITGB1, EPHA2, COL5A1, COL4A6, IFNAR2, ATF4, VEGFA, ATF6B, COL6A3, COL1A2, COL6A1, PDGFC, PRKAA1, COL1A1, THBS2, SYK, FN1	FGFR2, RAC1, JAK1, JAK2, PPP2R2A

ko04152:AMPK signaling pathway	CPT1B, HMGCR, ADIPOR1, EEF2, PRKAA1	PFKM, CCNA2, PPP2R2A
ko04210:Apoptosis	BID, RIPK1, FAS	FADD
ko04261:Adrenergic signaling in cardiomyocytes	ADCY4, ATF4, SCN1B, ATF6B, ATP1A1	GNAI1, PPP1R1A, PPP2R2A
ko04270:Vascular smooth muscle contraction	ADCY4, ROCK2, PLA2G6, MYLK	MYL6, MRVI1, GUCY1B3
ko04310:Wnt signaling pathway	ROCK2, PPP3CB, MAPK8, NFATC3, FZD6	RAC1, MAPK8
ko04320:Dorso-ventral axis formation	FMN2	ETV7
ko04350:TGF-beta signaling pathway	BMP4, BMPR2, ACVR1	INHBE, TGFBR1
ko04360:Axon guidance	EPHA4, ROCK2, PLXNB2, SEMA3D, NTN4, PPP3CB, SEMA4D, EPHB3, NFATC3, ITGB1, EPHA2	FYN, GNAI1, RAC1
ko04370:VEGF signaling pathway	VEGFA, SPHK1, PPP3CB	RAC1
ko04380:Osteoclast differentiation	IFNAR2, CTSK, RELB, PPP3CB, MAPK8, TRAF6, IFNGR1, SYK	FYN, TGFBR1, RAC1, JAK1, MAPK8, LCP2
ko04390:Hippo signaling pathway	BMP4, SAV1, BMPR2, CDH1, FZD6	FRMD6, CTGF, TGFBR1, FRMD1, PPP2R2A
ko04510:Focal adhesion	TLN1, ROCK2, TNC, COL3A1, ITGB1, COL5A1, COL4A6, VCL, VEGFA, COL6A3, COL1A2, COL6A1, MAPK8, PDGFC, COL1A1, RAPGEF1, THBS2, MYLK, FN1	FYN, RAC1, MAPK8
ko04512:ECM-receptor interaction	TNC, COL3A1, HSPG2, ITGB1, COL4A6, COL5A1, CD44, COL6A3, COL1A2, COL6A1, COL1A1, THBS2, FN1	HMMR
ko04520:Adherens junction	FGFR1, BAIAP2, CTNND1, LMO7, CDH1, VCL	FYN, TGFBR1, RAC1
ko04530:Tight junction	MYH9, TJAP1	GNAI1, TJP2, PPP2R2A
ko04540:Gap junction	ADCY4, PDGFC	GNAI1, GUCY1B3
ko04550:Signaling pathways regulating pluripotency of stem cells	BMP4, FGFR1, FGFR4, BMPR2, LHX5, ZFHX3, ACVR1, FZD6	FGFR2, INHBE, JAK1, JAK2

ko04610:Complement and coagulation cascades	C1QA, PLAT, C7, FGG, F5, SERPINC1, SERPIND1, F7	PROS1
ko04611:Platelet activation	ADCY4, FGG, TLN1, ROCK2, COL3A1, COL1A2, COL1A1, ITGB1, COL5A1, MYLK, SYK	FYN, GNAI1, GUCY1B3, LCP2
ko04620:Toll-like receptor signaling pathway	IRAK4, IFNAR2, CTSK, RIPK1, MAPK8, TRAF6	RAC1, FADD, MAPK8
ko04621:NOD-like receptor signaling pathway	MAPK8, TNFAIP3, TRAF6	MAPK8
ko04622:RIG-I-like receptor signaling pathway	TKFC, RIPK1, NLRX1, MAPK8, TRAF6, AZI2	RNF125, FADD, MAPK8
ko04623:Cytosolic DNA-sensing pathway	RIPK1	POLR3A
ko04630:Jak-STAT signaling pathway	IFNAR2, SOCS7, IFNGR1	JAK1, JAK2
ko04650:Natural killer cell mediated cytotoxicity	BID, IFNAR2, PPP3CB, FAS, IFNGR1, SYK	FYN, RAC1, LCP2
ko04660:T cell receptor signaling pathway	PPP3CB, NFATC3	FYN, LCP2
ko04662:B cell receptor signaling pathway	PPP3CB, CD79A, NFATC3, SYK	RAC1, CD79A
ko04664:Fc epsilon RI signaling pathway	MAPK8, SYK	FYN, RAC1, MAPK8, LCP2
ko04666:Fc gamma R-mediated phagocytosis	SPHK1, SYK	RAC1
ko04668:TNF signaling pathway	ATF4, RIPK1, ATF6B, MAPK8, FAS, TNFAIP3	FADD, MAPK8
ko04670:Leukocyte transendothelial migration	EZR, ROCK2, PECAM1, CTNND1, CD99, ITGB1, VCL, THY1	GNAI1, RAC1
ko04710:Circadian rhythm	PRKAA1, FBXL3	PER1
ko04713:Circadian entrainment	ADCY4, GRIN1	GNAI1, RYR3, PER1, GUCY1B3
ko04720:Long-term potentiation	ATF4, GRIN1, PPP3CB	PPP1R1A
ko04721:Synaptic vesicle cycle	SYT1, STX3, AP2A1, ATP6V1H, ATP6V0A1, DNM1, NSF	CPLX1, STX1B, DNM2
ko04722:Neurotrophin signaling pathway	IRAK4, ATF4, MAPK8, TRAF6, RAPGEF1	RAC1, MAPK8
ko04723:Retrograde endocannabinoid signaling	ADCY4, MAPK8	GNAI1, MAPK8
ko04724:Glutamatergic synapse	ADCY4, GLS, GRIK3, GRM6, GRIN1, PPP3CB	GNAI1

ko04725:Cholinergic synapse	ADCY4, ATF4	FYN, GNAI1, JAK2
ko04727:GABAergic synapse	ADCY4, GLS, NSF	GNAI1
ko04728:Dopaminergic synapse	ATF4, ATF6B, PPP3CB, MAPK8	GNAI1, KIF5C, MAPK8, PPP2R2A
ko04750:Inflammatory mediator regulation of TRP channels	ADCY4, IL1RAP, PLA2G6, MAPK8	MAPK8
ko04810:Regulation of actin cytoskeleton	FGFR1, FGFR4, EZR, ROCK2, BAIAP2, PDGFC, ITGB1, MYLK, FN1, VCL	FGFR2, RAC1
ko04910:Insulin signaling pathway	FLOT2, FLOT1, HK2, PDE3B, MAPK8, PRKAA1, RAPGEF1	PPP1R3B, HKDC1, MAPK8
ko04912:GnRH signaling pathway	ADCY4, ATF4, MAPK8	MAPK8
ko04914:Progesterone-mediated oocyte maturation	ADCY4, PDE3B, MAPK8	GNAI1, BUB1, PKMYT1, MAPK8, CCNA2
ko04915:Estrogen signaling pathway	ADCY4, ATF4, FKBP4, ATF6B, HSPA8	GNAI1
ko04916:Melanogenesis	ADCY4, FZD6	GNAI1
ko04917:Prolactin signaling pathway	SOCS7, MAPK8	JAK2, MAPK8
ko04919:Thyroid hormone signaling pathway	SIN3A, RXRA, MED24, PLCD1, ATP1A1	HDAC3
ko04920:Adipocytokine signaling pathway	CPT1B, RXRA, ADIPOR1, MAPK8, PRKAA1	JAK2, MAPK8
ko04921:Oxytocin signaling pathway	ADCY4, ROCK2, PPP3CB, EEF2, PRKAA1, NFATC3, MYLK	MYL6, CAMK1G, GNAI1, RYR3, GUCY1B3
ko04923:Regulation of lipolysis in adipocytes	ADCY4, PDE3B	GNAI1
ko04924:Renin secretion	PPP3CB, PDE3B	GNAI1, GUCY1B3
ko04925:Aldosterone synthesis and secretion	ADCY4, ATF4, ATF6B, SCARB1, ATF1	CAMK1G, ATF1
ko04930:Type II diabetes mellitus	HK2, MAPK8, KCNJ11	HKDC1, MAPK8
ko04931:Insulin resistance	CPT1B, MAPK8, PRKAA1	PPP1R3B, MAPK8
ko04932:Non-alcoholic fatty liver disease (NAFLD)	BID, SDHA, ATF4, NDUFA6, RXRA, NDUFB9, COX4I1, ADIPOR1, MAPK8, PRKAA1, FAS	RAC1, MAPK8
ko04961:Endocrine and other factor-regulated calcium reabsorption	AP2A1, ATP1A1, CALB1, DNM1	DNM2
ko04964:Proximal tubule bicarbonate reclamation	GLS, ATP1A1	CA4
ko04970:Salivary secretion	ADCY4, ATP1A1	RYR3, GUCY1B3

ko04971:Gastric acid secretion	ADCY4, EZR, ATP1A1, MYLK	GNAI1
ko04972:Pancreatic secretion	CCKAR, ADCY4, ATP1A1	RAC1
ko04973:Carbohydrate digestion and absorption	SLC37A4, HK2, ATP1A1	HKDC1
ko04978:Mineral absorption	HMOX1, ATP1A1	SLC40A1
ko05010:Alzheimer's disease	BID, SDHA, NDUFA6, NDUFB9, GRIN1, PPP3CB, COX4I1, ADAM17, FAS	ATF6, CDK5R1, RYR3, FADD
ko05012:Parkinson's disease	SDHA, PPIF, SLC25A4, NDUFA6, NDUFB9, COX4I1, VDAC3	GNAI1
ko05014:Amyotrophic lateral sclerosis (ALS)	BID, GRIN1, PPP3CB, SOD1	RAC1
ko05020:Prion diseases	C1QA, C7, SOD1	FYN
ko05030:Cocaine addiction	ATF4, ATF6B, GRIN1	CDK5R1, GNAI1
ko05032:Morphine addiction	ADCY4, PDE3B	GNAI1
ko05034:Alcoholism	ATF4, ATF6B, GRIN1, PKIA	HDAC3, GNAI1, HDAC8
ko05100:Bacterial invasion of epithelial cells	CDH1, ITGB1, DNM1, FN1, VCL	RAC1, DNM2
ko05132:Salmonella infection	ROCK2, MAPK8, IFNGR1	RAC1, MAPK8
ko05133:Pertussis	IRAK4, C1QA, MAPK8, TRAF6, ITGB1	GNAI1, MAPK8
ko05140:Leishmaniasis	IRAK4, TRAF6, ITGB1, IFNGR1	JAK1, JAK2
ko05142:Chagas disease (American trypanosomiasis)	IRAK4, C1QA, MAPK8, FAS, TRAF6, IFNGR1	GNAI1, TGFBR1, FADD, MAPK8, PPP2R2A
ko05145:Toxoplasmosis	IRAK4, PPIF, MAPK8, TRAF6, ITGB1, HSPA8, IFNGR1	GNAI1, JAK1, JAK2, MAPK8
ko05152:Tuberculosis	BID, IRAK4, ATP6AP1, SPHK1, PPP3CB, NFYC, ATP6V1H, ATP6V0A1, MAPK8, TRAF6, IFNGR1, SYK	JAK1, FADD, JAK2, MAPK8
ko05160:Hepatitis C	IFNAR2, RIPK1, RXRA, MAPK8, SCARB1, TRAF6	JAK1, MAPK8, PPP2R2A
ko05161:Hepatitis B	ATF4, ATP6AP1, ATF6B, HSPG2, MAPK8, FAS, VDAC3, NFATC3	TGFBR1, JAK1, FADD, MAPK8, CCNA2
ko05162:Measles	IRAK4, IFNAR2, EIF3H, FAS, TNFAIP3, TRAF6, HSPA8, IFNGR1	FYN, JAK1, JAK2

ko05164:Influenza A	IRAK4, IFNAR2, NLRX1, MAPK8, FAS, HSPA8, IFNGR1	FDPS, JAK1, JAK2, MAPK8, TMPRSS13
ko05166:HTLV-I infection	ADCY4, TLN1, ATF4, SLC25A4, RELB, POLD2, PPP3CB, CDC20, VDAC3, NFATC3, ATF1, FZD6	ELK4, TGFBR1, FDPS, JAK1, ATF1
ko05168:Herpes simplex infection	CFP, HMGN1, TAF10, IFNAR2, MAPK8, FAS, TRAF6, IFNGR1	JAK1, PER1, FADD, JAK2, MAPK8
ko05169:Epstein-Barr virus infection	CD44, PSMD12, RIPK1, SND1, RELB, MAPK8, TNFAIP3, TRAF6, HSPA8, SYK	VIM, JAK1, POLR3A, MAPK8, CCNA2
ko05200:Pathways in cancer	BID, BMP4, FGFR1, ADCY4, ROCK2, STK36, RXRA, LPAR4, CDH1, ITGB1, COL4A6, FZD6, CCDC6, VEGFA, MAPK8, FAS, TRAF6, TPR, FN1	FGFR2, GNAI1, TGFBR1, RAC1, JAK1, FADD, MAPK8
ko05202:Transcriptional misregulation in cancer	PLAT, MEN1, FUS, SIN3A, RXRA, SPINT1, PBX1, CDK14, ATF1	ETV7, ELK4, ATF1
ko05203:Viral carcinogenesis	HPN, ATF4, GTF2A1, SND1, ATF6B, CDC20, VDAC3, SYK	HDAC3, RAC1, JAK1, HDAC8, CCNA2
ko05205:Proteoglycans in cancer	FGFR1, EZR, CD44, ROCK2, VEGFA, HSPG2, FAS, PDCD4, ITGB1, FN1, FZD6	RAC1
ko05206:MicroRNAs in cancer	EZR, CD44, GLS, TNC, VEGFA, BMPR2, STMN1, PDCD4	VIM
ko05210:Colorectal cancer	MAPK8	TGFBR1, RAC1, MAPK8
ko05211:Renal cell carcinoma	VEGFA, RAPGEF1	RAC1
ko05212:Pancreatic cancer	VEGFA, MAPK8	TGFBR1, RAC1, JAK1, MAPK8
ko05215:Prostate cancer	FGFR1, ATF4, PDGFC	FGFR2
ko05230:Central carbon metabolism in cancer	FGFR1, G6PD, GLS, HK2, SIRT6	FGFR2, HKDC1, PFKM
ko05231:Choline metabolism in cancer	CHKA, SLC44A2, PCYT1A, MAPK8, PDGFC	RAC1, MAPK8
ko05340:Primary immunodeficiency	CD79A	CD79A
ko05416:Viral myocarditis	BID, EIF4G3	FYN, RAC1

Table S32. The reference list of hypoxia-responsive categories constructed in this study.

category	pvalue	numDEInCat	numInCat	term
GO:0001666	4.79E-28	69	276	response to hypoxia
GO:0070482	3.78E-27	71	301	response to oxygen levels
GO:0044057	7.43E-15	67	441	regulation of system process
GO:1901342	1.86E-13	45	240	regulation of vasculature development
GO:1903522	3.76E-13	43	226	regulation of blood circulation
GO:0042493	1.51E-12	56	372	response to drug
GO:0010038	1.70E-11	46	288	response to metal ion
GO:0048511	3.31E-11	47	294	rhythmic process
GO:1903649	4.97E-11	53	368	regulation of cytoplasmic transport
GO:0006979	5.57E-11	49	341	response to oxidative stress
GO:0007568	2.81E-10	39	243	aging
GO:0009612	2.97E-10	34	177	response to mechanical stimulus
GO:0050795	3.28E-10	40	264	regulation of behavior
GO:0048520	4.65E-10	29	164	positive regulation of behavior
GO:0032970	1.28E-09	46	309	regulation of actin filament-based process
GO:0006096	1.51E-09	15	41	glycolytic process
GO:0043620	7.20E-09	18	64	regulation of DNA-templated transcription in response to stress
GO:2000377	4.03E-08	28	173	regulation of reactive oxygen species metabolic process
GO:0098900	4.24E-08	13	35	regulation of action potential
GO:0048771	4.91E-08	17	65	tissue remodeling
GO:0043618	6.61E-08	16	58	regulation of transcription from RNA polymerase II promoter in response to stress
GO:0090559	8.43E-08	11	30	regulation of membrane permeability
GO:0031667	9.58E-08	47	394	response to nutrient levels
GO:0033238	1.57E-07	49	429	regulation of cellular amine metabolic process
GO:0010950	1.73E-07	25	146	positive regulation of endopeptidase activity
GO:0048193	1.83E-07	42	309	Golgi vesicle transport
GO:0046902	1.90E-07	10	27	regulation of mitochondrial membrane permeability
GO:0006521	2.42E-07	47	405	regulation of cellular amino acid metabolic process

GO:0006874	2.62E-07	41	326	cellular calcium ion homeostasis
GO:0034405	2.70E-07	12	35	response to fluid shear stress
GO:0070849	2.73E-07	12	34	response to epidermal growth factor
GO:0051924	2.84E-07	32	224	regulation of calcium ion transport
GO:0009611	5.20E-07	28	184	response to wounding
GO:0007623	5.46E-07	24	139	circadian rhythm
GO:0043627	5.78E-07	27	176	response to estrogen
GO:0044264	6.42E-07	16	67	cellular polysaccharide metabolic process
GO:0048729	7.68E-07	46	372	tissue morphogenesis
GO:1903426	8.04E-07	17	85	regulation of reactive oxygen species biosynthetic process
GO:0034330	8.15E-07	31	197	cell junction organization
GO:0032844	9.50E-07	48	425	regulation of homeostatic process
GO:1901654	1.06E-06	23	140	response to ketone
GO:0045216	1.13E-06	28	173	cell-cell junction organization
GO:0072593	1.26E-06	20	111	reactive oxygen species metabolic process
GO:0007005	1.52E-06	34	281	mitochondrion organization
GO:0030029	1.71E-06	44	342	actin filament-based process
GO:0006112	1.75E-06	15	64	energy reserve metabolic process
GO:0051384	1.79E-06	22	144	response to glucocorticoid
GO:0035924	2.14E-06	9	22	cellular response to vascular endothelial growth factor stimulus
GO:0005976	2.49E-06	16	74	polysaccharide metabolic process
GO:0006892	2.56E-06	18	88	post-Golgi vesicle-mediated transport
GO:0034112	4.09E-06	34	296	positive regulation of homotypic cell-cell adhesion
GO:0023014	4.81E-06	38	319	signal transduction by protein phosphorylation
GO:0071364	5.22E-06	10	30	cellular response to epidermal growth factor stimulus
GO:0044262	7.03E-06	21	130	cellular carbohydrate metabolic process
GO:0046677	7.06E-06	11	42	response to antibiotic
GO:0001974	9.13E-06	10	33	blood vessel remodeling
GO:0001763	9.24E-06	25	167	morphogenesis of a branching structure
GO:0051146	9.56E-06	12	47	striated muscle cell differentiation

GO:0048017	9.70E-06	21	124	inositol lipid-mediated signaling
GO:0046683	1.11E-05	21	131	response to organophosphorus
GO:0090066	1.17E-05	33	266	regulation of anatomical structure size
GO:0010906	1.18E-05	18	107	regulation of glucose metabolic process
GO:0071260	1.25E-05	14	68	cellular response to mechanical stimulus
GO:0015749	1.46E-05	12	52	monosaccharide transport
GO:0007265	1.54E-05	23	157	Ras protein signal transduction
GO:0000165	1.74E-05	36	313	MAPK cascade
GO:0032409	1.77E-05	27	205	regulation of transporter activity
GO:2000736	1.94E-05	20	127	regulation of stem cell differentiation
GO:0033483	1.99E-05	5	8	gas homeostasis
GO:1990267	2.02E-05	18	114	response to transition metal nanoparticle
GO:0001101	2.04E-05	36	317	response to acid chemical
GO:0048015	2.24E-05	20	121	phosphatidylinositol-mediated signaling
GO:0060306	2.30E-05	9	30	regulation of membrane repolarization
GO:0006109	2.36E-05	24	176	regulation of carbohydrate metabolic process
GO:0040007	2.62E-05	41	360	growth
GO:0048872	2.91E-05	18	111	homeostasis of number of cells
GO:0002931	2.98E-05	9	32	response to ischemia
GO:0031647	3.42E-05	29	238	regulation of protein stability
GO:0007264	3.88E-05	39	382	small GTPase mediated signal transduction
GO:0042391	4.53E-05	36	311	regulation of membrane potential
GO:0021700	4.83E-05	22	159	developmental maturation
GO:0032570	5.09E-05	10	42	response to progesterone
GO:0002634	5.27E-05	5	9	regulation of germinal center formation
GO:0044252	5.67E-05	5	10	negative regulation of multicellular organismal metabolic process
GO:0031958	6.19E-05	5	8	corticosteroid receptor signaling pathway
GO:0051133	7.93E-05	4	6	regulation of NK T cell activation
GO:0010575	8.51E-05	8	26	positive regulation of vascular endothelial growth factor production
GO:1900182	8.73E-05	19	131	positive regulation of protein localization to nucleus

GO:0010506	8.85E-05	30	259	regulation of autophagy
GO:0032507	0.000101979	19	123	maintenance of protein location in cell
GO:0032364	0.000102479	4	6	oxygen homeostasis
GO:0035239	0.000103261	31	263	tube morphogenesis
GO:0031657	0.000107467	5	10	regulation of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle
GO:0090087	0.000111546	29	263	regulation of peptide transport
GO:0048732	0.000115664	27	225	gland development
GO:0035637	0.000118919	14	77	multicellular organismal signaling
GO:0034109	0.000125768	31	286	homotypic cell-cell adhesion
GO:0007589	0.00013653	13	75	body fluid secretion
GO:0042770	0.00014291	16	100	signal transduction in response to DNA damage
GO:0045599	0.000155875	10	49	negative regulation of fat cell differentiation
GO:0000904	0.00015603	22	160	cell morphogenesis involved in differentiation
GO:0019932	0.000157378	22	166	second-messenger-mediated signaling
GO:0006022	0.000158975	22	168	aminoglycan metabolic process
GO:0002260	0.000161037	10	47	lymphocyte homeostasis
GO:0008643	0.000172484	14	88	carbohydrate transport
GO:0046685	0.000182755	7	25	response to arsenic-containing substance
GO:0045778	0.000182823	14	88	positive regulation of ossification
GO:0051235	0.000184324	24	191	maintenance of location
GO:0051660	0.000192424	3	3	establishment of centrosome localization
GO:0016197	0.000192965	28	241	endosomal transport
GO:0033280	0.000195067	7	26	response to vitamin D
GO:0030953	0.000205937	4	6	astral microtubule organization
GO:0032941	0.000206722	12	67	secretion by tissue
GO:0030203	0.000241609	21	161	glycosaminoglycan metabolic process
GO:0051591	0.000263254	15	95	response to cAMP
GO:0034976	0.000264779	20	155	response to endoplasmic reticulum stress
GO:0061077	0.000297262	9	45	chaperone-mediated protein folding

GO:0007034	0.000334571	16	106	vacuolar transport
GO:0035020	0.000335614	5	11	regulation of Rac protein signal transduction
GO:0030330	0.000341439	14	87	DNA damage response, signal transduction by p53 class mediator
GO:0030212	0.000348302	8	31	hyaluronan metabolic process
GO:0031102	0.000352476	7	26	neuron projection regeneration
GO:1902083	0.000398481	3	3	negative regulation of peptidyl-cysteine S-nitrosylation
GO:1903510	0.000473703	16	110	mucopolysaccharide metabolic process
GO:0008626	0.000530247	3	4	granzyme-mediated apoptotic signaling pathway
GO:0043467	0.000556347	13	85	regulation of generation of precursor metabolites and energy
GO:0032909	0.000559071	4	8	regulation of transforming growth factor beta2 production
GO:0001889	0.000566654	14	95	liver development
GO:1903650	0.000597917	14	98	negative regulation of cytoplasmic transport
GO:0050878	0.000662273	32	322	regulation of body fluid levels
GO:0048598	0.000677811	40	418	embryonic morphogenesis
GO:2001057	0.000694294	7	30	reactive nitrogen species metabolic process
GO:0060396	0.00069785	4	8	growth hormone receptor signaling pathway
GO:1901605	0.000714736	26	253	alpha-amino acid metabolic process
GO:0097094	0.000745913	5	14	craniofacial suture morphogenesis
GO:0006820	0.000767576	44	479	anion transport
GO:0018108	0.000782326	13	76	peptidyl-tyrosine phosphorylation
GO:0045444	0.000784843	15	112	fat cell differentiation
GO:0018401	0.000870764	3	5	peptidyl-proline hydroxylation to 4-hydroxy-L-proline
GO:0060191	0.000895013	12	79	regulation of lipase activity
GO:0030522	0.00090879	18	137	intracellular receptor signaling pathway
GO:0002576	0.000914039	14	95	platelet degranulation
GO:0051781	0.000929464	16	128	positive regulation of cell division
GO:0018212	0.000957974	13	78	peptidyl-tyrosine modification
GO:0051100	0.000980188	16	123	negative regulation of binding
GO:0006953	0.000980932	8	43	acute-phase response
GO:0060395	0.000993347	10	59	SMAD protein signal transduction

GO:0072584	0.0010055	3	5	caveolin-mediated endocytosis
GO:0045740	0.001025674	13	91	positive regulation of DNA replication
GO:0007528	0.001078176	8	32	neuromuscular junction development
GO:0032228	0.0010933	7	30	regulation of synaptic transmission, GABAergic
GO:0051302	0.001166085	27	263	regulation of cell division
GO:0036120	0.001178252	5	16	cellular response to platelet-derived growth factor stimulus
GO:0006693	0.001183199	6	27	prostaglandin metabolic process
GO:0060263	0.001249393	4	11	regulation of respiratory burst
GO:0042541	0.001279716	3	5	hemoglobin biosynthetic process
GO:0007041	0.001283824	12	74	lysosomal transport
GO:0015711	0.001480493	34	353	organic anion transport
GO:0010518	0.00148745	9	51	positive regulation of phospholipase activity
GO:0072331	0.001566527	17	138	signal transduction by p53 class mediator
GO:0071236	0.001613253	4	11	cellular response to antibiotic
GO:0090265	0.001614822	2	2	positive regulation of immune complex clearance by monocytes and macrophages
GO:0051769	0.00162532	5	17	regulation of nitric-oxide synthase biosynthetic process
GO:0032846	0.001632284	21	195	positive regulation of homeostatic process
GO:1901184	0.00163285	12	81	regulation of ERBB signaling pathway
GO:0036119	0.001665758	5	17	response to platelet-derived growth factor
GO:0038093	0.001682085	19	171	Fc receptor signaling pathway
GO:0006366	0.001754785	32	332	transcription from RNA polymerase II promoter
GO:0045649	0.001809847	5	19	regulation of macrophage differentiation
GO:0010877	0.001813345	2	2	lipid transport involved in lipid storage
GO:0050821	0.001821354	17	143	protein stabilization
GO:0019722	0.001843729	13	94	calcium-mediated signaling
GO:0010649	0.00186482	4	10	regulation of cell communication by electrical coupling
GO:1901300	0.001949257	3	5	positive regulation of hydrogen peroxide-mediated programmed cell death
GO:1902041	0.001982834	9	53	regulation of extrinsic apoptotic signaling pathway via death domain receptors
GO:0002366	0.001990342	16	137	leukocyte activation involved in immune response
GO:2000191	0.00202748	6	26	regulation of fatty acid transport

GO:0034696	0.002050077	2	2	response to prostaglandin F
GO:1901387	0.002066332	3	6	positive regulation of voltage-gated calcium channel activity
GO:1902966	0.00210754	3	5	positive regulation of protein localization to early endosome
GO:0010455	0.002110521	4	12	positive regulation of cell fate commitment
GO:0043547	0.002131253	16	144	positive regulation of GTPase activity
GO:2000378	0.002139585	8	46	negative regulation of reactive oxygen species metabolic process
GO:0032355	0.002192781	14	113	response to estradiol
GO:0035902	0.002205505	5	19	response to immobilization stress
GO:0000910	0.002222394	12	78	cytokinesis
GO:1902567	0.002225685	2	2	negative regulation of eosinophil activation
GO:0070256	0.002273928	2	2	negative regulation of mucus secretion
GO:0032070	0.002309916	3	6	regulation of deoxyribonuclease activity
GO:0002880	0.002346388	2	2	regulation of chronic inflammatory response to non-antigenic stimulus
GO:0009314	0.002351914	38	427	response to radiation
GO:0071505	0.002357164	2	2	response to mycophenolic acid
GO:0071506	0.002357164	2	2	cellular response to mycophenolic acid
GO:0031589	0.002363065	20	159	cell-substrate adhesion
GO:1900744	0.002375571	6	24	regulation of p38MAPK cascade
GO:0032890	0.00238423	8	47	regulation of organic acid transport
GO:0098903	0.002445018	3	6	regulation of membrane repolarization during action potential
GO:0071498	0.002462121	5	18	cellular response to fluid shear stress
GO:2000352	0.002469463	6	25	negative regulation of endothelial cell apoptotic process
GO:1902745	0.002504551	6	25	positive regulation of lamellipodium organization
GO:0097306	0.002540025	13	98	cellular response to alcohol
GO:0006457	0.002589113	22	228	protein folding
GO:0043124	0.002612888	9	54	negative regulation of I-kappaB kinase/NF-kappaB signaling
GO:0018209	0.002734088	18	149	peptidyl-serine modification
GO:0035873	0.002815105	4	12	lactate transmembrane transport
GO:0009743	0.002816933	17	153	response to carbohydrate
GO:1900542	0.002949754	19	177	regulation of purine nucleotide metabolic process

GO:0048661	0.00297601	10	72	positive regulation of smooth muscle cell proliferation
GO:0001300	0.002976164	2	2	chronological cell aging
GO:0032069	0.002996437	5	20	regulation of nuclease activity
GO:0015920	0.00299805	2	2	lipopolysaccharide transport
GO:0070483	0.003000079	2	2	detection of hypoxia
GO:0019471	0.00302249	4	13	4-hydroxyproline metabolic process
GO:1901655	0.003036835	9	57	cellular response to ketone
GO:0098801	0.00303882	6	31	regulation of renal system process
GO:0002523	0.003039638	4	14	leukocyte migration involved in inflammatory response
GO:1901216	0.003071248	10	67	positive regulation of neuron death
GO:0045188	0.003120654	3	7	regulation of circadian sleep/wake cycle, non-REM sleep
GO:0006986	0.003127168	8	49	response to unfolded protein
GO:0006816	0.003141704	20	177	calcium ion transport
GO:0035428	0.003172074	2	2	hexose transmembrane transport
GO:0019318	0.003186344	18	168	hexose metabolic process
GO:0048286	0.003201022	7	35	lung alveolus development
GO:0009746	0.003238548	15	130	response to hexose
GO:0097296	0.003241624	4	13	activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway
GO:0014706	0.003435535	11	79	striated muscle tissue development
GO:0018277	0.003466472	2	2	protein deamination
GO:0014910	0.003491604	8	48	regulation of smooth muscle cell migration
GO:1903242	0.003493275	3	6	regulation of cardiac muscle hypertrophy in response to stress
GO:0001649	0.003584421	13	102	osteoblast differentiation
GO:0006417	0.00362638	28	306	regulation of translation
GO:1902950	0.003703255	2	2	regulation of dendritic spine maintenance
GO:0006206	0.003733381	5	19	pyrimidine nucleobase metabolic process
GO:0050818	0.003799541	12	92	regulation of coagulation
GO:0051147	0.003830753	18	171	regulation of muscle cell differentiation
GO:1901137	0.003872233	35	420	carbohydrate derivative biosynthetic process

GO:0044557	0.003887294	3	7	relaxation of smooth muscle
GO:0072524	0.003919731	9	62	pyridine-containing compound metabolic process
GO:1903689	0.003951948	3	5	regulation of wound healing, spreading of epidermal cells
GO:0005980	0.003984229	5	18	glycogen catabolic process
GO:0050872	0.004107168	4	13	white fat cell differentiation
GO:0015850	0.004135327	16	138	organic hydroxy compound transport
GO:0035335	0.004155244	5	20	peptidyl-tyrosine dephosphorylation
GO:0006509	0.004257909	5	20	membrane protein ectodomain proteolysis
GO:0003013	0.004263692	16	142	circulatory system process
GO:0007259	0.00427564	7	39	JAK-STAT cascade
GO:0016264	0.004282079	3	7	gap junction assembly
GO:0048873	0.004303269	6	30	homeostasis of number of cells within a tissue
GO:0033206	0.004335883	3	6	meiotic cytokinesis
GO:0043173	0.004442999	4	14	nucleotide salvage
GO:1902728	0.004443661	2	2	positive regulation of growth factor dependent skeletal muscle satellite cell proliferation
GO:0006769	0.004615986	3	7	nicotinamide metabolic process
GO:0044708	0.004624063	35	386	single-organism behavior
GO:0071354	0.004714373	4	14	cellular response to interleukin-6
GO:0046164	0.004715213	9	60	alcohol catabolic process
GO:0010469	0.004896424	11	78	regulation of receptor activity
GO:0042476	0.004978672	12	92	odontogenesis
GO:0046777	0.005046902	23	209	protein autophosphorylation
GO:0071877	0.005049247	3	7	regulation of adrenergic receptor signaling pathway
GO:0051220	0.005104273	6	30	cytoplasmic sequestering of protein
GO:0010621	0.005145439	2	3	negative regulation of transcription by transcription factor localization
GO:0006901	0.005288621	10	70	vesicle coating
GO:0046394	0.005331606	25	276	carboxylic acid biosynthetic process
GO:0009112	0.005446022	7	40	nucleobase metabolic process
GO:0002636	0.005508484	2	3	positive regulation of germinal center formation

GO:0060021	0.005600648	11	77	palate development
GO:0086073	0.005610127	3	6	bundle of His cell-Purkinje myocyte adhesion involved in cell communication
GO:0046033	0.005610641	4	15	AMP metabolic process
GO:1901630	0.005651733	2	3	negative regulation of presynaptic membrane organization
GO:0035655	0.005742708	2	3	interleukin-18-mediated signaling pathway
GO:0030185	0.005915195	2	3	nitric oxide transport
GO:0010226	0.005997206	5	23	response to lithium ion
GO:0035694	0.006163029	2	3	mitochondrial protein catabolic process
GO:0045837	0.006179917	4	16	negative regulation of membrane potential
GO:0030397	0.006278785	8	46	membrane disassembly
GO:0015669	0.006538972	3	9	gas transport
GO:2000286	0.006574971	2	3	receptor internalization involved in canonical Wnt signaling pathway
GO:0007163	0.006578631	16	138	establishment or maintenance of cell polarity
GO:0036302	0.006586321	3	7	atrioventricular canal development
GO:0048844	0.006719602	8	48	artery morphogenesis
GO:2000648	0.006786575	9	59	positive regulation of stem cell proliferation
GO:0000186	0.006839995	7	38	activation of MAPKK activity
GO:0043255	0.006971248	11	86	regulation of carbohydrate biosynthetic process
GO:0042045	0.007074114	3	8	epithelial fluid transport
GO:0015701	0.007148941	7	41	bicarbonate transport
GO:1902992	0.007190118	3	7	negative regulation of amyloid precursor protein catabolic process
GO:0071222	0.007285971	14	128	cellular response to lipopolysaccharide
GO:0006024	0.00746955	13	109	glycosaminoglycan biosynthetic process
GO:0003382	0.007506834	8	50	epithelial cell morphogenesis
GO:2000169	0.007554472	3	7	regulation of peptidyl-cysteine S-nitrosylation
GO:1902110	0.007569453	3	9	positive regulation of mitochondrial membrane permeability involved in apoptotic process
GO:0035434	0.007587222	2	3	copper ion transmembrane transport
GO:0031098	0.007640421	10	76	stress-activated protein kinase signaling cascade
GO:0002638	0.007716163	3	8	negative regulation of immunoglobulin production

GO:0044321	0.007747651	4	16	response to leptin
GO:0038179	0.007771699	5	22	neurotrophin signaling pathway
GO:0048858	0.007857641	26	260	cell projection morphogenesis
GO:0097012	0.00801599	3	8	response to granulocyte macrophage colony-stimulating factor
GO:0002828	0.008264835	5	26	regulation of type 2 immune response
GO:0051052	0.00827441	31	351	regulation of DNA metabolic process
GO:0002467	0.008330621	3	8	germinal center formation
GO:0001508	0.008379269	10	68	action potential
GO:0019827	0.008388996	15	132	stem cell population maintenance
GO:0031343	0.00842011	7	50	positive regulation of cell killing
GO:0009791	0.008430219	10	70	post-embryonic development
GO:0097021	0.008474385	2	3	lymphocyte migration into lymphoid organs
GO:0070208	0.008540098	4	15	protein heterotrimerization
GO:0090135	0.008726563	2	3	actin filament branching
GO:0043094	0.008744126	6	39	cellular metabolic compound salvage
GO:1990785	0.009009295	2	3	response to water-immersion restraint stress
GO:0019858	0.009076148	2	3	cytosine metabolic process
GO:0048839	0.009202015	7	45	inner ear development
GO:1900153	0.009246956	4	16	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
GO:0009267	0.009292778	17	165	cellular response to starvation
GO:0022405	0.009681696	9	64	hair cycle process
GO:0048011	0.009788155	4	16	neurotrophin TRK receptor signaling pathway
GO:0097581	0.009890422	7	41	lamellipodium organization

Table S33. PSGs identified on branch 4 of frog.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000011153	ENSACAG00000011291	ENSACAT00000011385	TPX2
ENSACAP00000010147	ENSACAG00000010046	ENSACAT00000010357	ACTN4

ENSACAP00000008070	ENSACAG00000008152	ENSACAT00000008242	CDH6
ENSACAP00000001268	ENSACAG00000001379	ENSACAT00000001301	FICD
ENSACAP00000015880	ENSACAG00000016135	ENSACAT00000016198	ENTPD2
ENSACAP00000004466	ENSACAG00000004565	ENSACAT00000004567	
ENSACAP00000003231	ENSACAG00000003255	ENSACAT00000003314	
ENSACAP00000009624	ENSACAG00000009754	ENSACAT00000009821	ANXA4
ENSACAP00000009687	ENSACAG00000009844	ENSACAT00000009884	ZWILCH
ENSACAP00000005716	ENSACAG00000005606	ENSACAT00000005841	HK2
ENSACAP00000008525	ENSACAG00000008687	ENSACAT00000008708	BRAT1
ENSACAP00000005206	ENSACAG00000005327	ENSACAT00000005323	SRSF10
ENSACAP00000005936	ENSACAG00000006034	ENSACAT00000006069	N4BP1
ENSACAP00000000379	ENSACAG00000000471	ENSACAT00000000394	CH25H
ENSACAP00000022629	ENSACAG00000029096	ENSACAT00000030046	FTCDNL1
ENSACAP00000010343	ENSACAG00000010493	ENSACAT00000010557	HERC4
ENSACAP00000003601	ENSACAG00000003709	ENSACAT00000003689	FADD
ENSACAP00000006257	ENSACAG00000006391	ENSACAT00000006396	
ENSACAP00000003660	ENSACAG00000003679	ENSACAT00000003750	PACS1
ENSACAP00000001664	ENSACAG00000001777	ENSACAT00000001703	NDUFB3
ENSACAP00000000825	ENSACAG00000000812	ENSACAT00000000851	IGHM
ENSACAP00000018161	ENSACAG00000024548	ENSACAT00000022331	
ENSACAP00000009092	ENSACAG00000009253	ENSACAT00000009285	SLC1A3
ENSACAP00000004015	ENSACAG00000004079	ENSACAT00000004107	RELB
ENSACAP00000004078	ENSACAG00000004072	ENSACAT00000004172	HSPA5
ENSACAP00000023366	ENSACAG00000028384	ENSACAT00000030786	CAPSL
ENSACAP00000017054	ENSACAG00000017314	ENSACAT00000017389	SLC17A7
ENSACAP00000010744	ENSACAG00000010772	ENSACAT00000010966	
ENSACAP00000007747	ENSACAG00000007863	ENSACAT00000007913	
ENSACAP00000007352	ENSACAG00000007262	ENSACAT00000007508	
ENSACAP00000011083	ENSACAG00000011313	ENSACAT00000011312	
ENSACAP00000001332	ENSACAG00000001111	ENSACAT00000001365	GPI

ENSACAP00000001155	ENSACAG00000001070	ENSACAT00000001188	CADM1
ENSACAP00000016988	ENSACAG00000017266	ENSACAT00000017323	
ENSACAP00000011446	ENSACAG00000011631	ENSACAT00000011685	REXO2
ENSACAP00000006180	ENSACAG00000006198	ENSACAT00000006317	BTAF1
ENSACAP00000003664	ENSACAG00000003722	ENSACAT00000003754	
ENSACAP00000002914	ENSACAG00000002921	ENSACAT00000002988	TOX4
ENSACAP00000016346	ENSACAG00000016627	ENSACAT00000016670	R3HCC1
ENSACAP00000001760	ENSACAG00000001775	ENSACAT00000001801	
ENSACAP00000017058	ENSACAG00000017331	ENSACAT00000017393	DDAH2
ENSACAP00000002190	ENSACAG00000002120	ENSACAT00000002250	EIF4G1
ENSACAP00000004787	ENSACAG00000004921	ENSACAT00000004895	ABRACL
ENSACAP00000001609	ENSACAG00000001350	ENSACAT00000001648	ECE2
ENSACAP00000009086	ENSACAG00000009224	ENSACAT00000009279	XPNPEP2
ENSACAP00000009821	ENSACAG00000010023	ENSACAT00000010021	CFAP53
ENSACAP00000008669	ENSACAG00000008711	ENSACAT00000008854	LOXL3
ENSACAP00000012879	ENSACAG00000013111	ENSACAT00000013136	YJEFN3
ENSACAP00000004168	ENSACAG00000004303	ENSACAT00000004267	ANKRD53
ENSACAP00000012425	ENSACAG00000012604	ENSACAT00000012678	HSF1
ENSACAP00000002276	ENSACAG00000002387	ENSACAT00000002336	NUDT7
ENSACAP00000005916	ENSACAG00000005991	ENSACAT00000006048	DNAI1
ENSACAP00000005436	ENSACAG00000005574	ENSACAT00000005554	HS3ST1
ENSACAP00000004636	ENSACAG00000004724	ENSACAT00000004742	DNAJA3
ENSACAP00000000221	ENSACAG00000000233	ENSACAT00000000226	RAB11FIP1
ENSACAP00000017382	ENSACAG00000017650	ENSACAT00000017723	PRPF4B
ENSACAP00000007082	ENSACAG00000007230	ENSACAT00000007235	
ENSACAP00000010464	ENSACAG00000010658	ENSACAT00000010680	HBM
ENSACAP00000010527	ENSACAG00000010719	ENSACAT00000010744	MPG
ENSACAP00000003403	ENSACAG00000003497	ENSACAT00000003486	TERF2
ENSACAP00000021909	ENSACAG00000028799	ENSACAT00000029327	C1orf52
ENSACAP00000015147	ENSACAG00000015409	ENSACAT00000015453	

ENSACAP00000018247	ENSACAG00000022510	ENSACAT00000022382	DLAT
ENSACAP00000003069	ENSACAG00000003166	ENSACAT00000003147	BNIP2
ENSACAP00000017496	ENSACAG00000017773	ENSACAT00000017841	SH3BGRL3
ENSACAP00000015109	ENSACAG00000015385	ENSACAT00000015414	HERC1
ENSACAP00000011007	ENSACAG00000011206	ENSACAT00000011235	STARD5
ENSACAP00000009892	ENSACAG00000010041	ENSACAT00000010095	SMTN
ENSACAP00000009973	ENSACAG00000010115	ENSACAT00000010178	INPP5J
ENSACAP00000012760	ENSACAG00000012995	ENSACAT00000013016	PTGR1
ENSACAP00000004467	ENSACAG00000004556	ENSACAT00000004568	EEF1A1
ENSACAP00000012511	ENSACAG00000012620	ENSACAT00000012767	PLAT
ENSACAP00000007066	ENSACAG00000007212	ENSACAT00000007218	CD276
ENSACAP00000014677	ENSACAG00000014806	ENSACAT00000014975	
ENSACAP00000004160	ENSACAG00000004179	ENSACAT00000004259	PTDSS1
ENSACAP00000010338	ENSACAG00000010516	ENSACAT00000010551	CALB1
ENSACAP00000021793	ENSACAG00000028464	ENSACAT00000029213	RALYL
ENSACAP00000016677	ENSACAG00000016952	ENSACAT00000017007	HSD11B1L
ENSACAP00000014073	ENSACAG00000014323	ENSACAT00000014361	PLP1
ENSACAP00000000416	ENSACAG00000000308	ENSACAT00000000433	IDUA
ENSACAP00000004226	ENSACAG00000004364	ENSACAT00000004325	TFAM
ENSACAP00000011628	ENSACAG00000011894	ENSACAT00000011868	ZCCHC7
ENSACAP00000006716	ENSACAG00000006626	ENSACAT00000006862	
ENSACAP00000011696	ENSACAG00000011898	ENSACAT00000011937	GRHPR
ENSACAP00000003905	ENSACAG00000003984	ENSACAT00000003997	B4GALT3
ENSACAP00000002101	ENSACAG00000002223	ENSACAT00000002158	CHST9
ENSACAP00000015123	ENSACAG00000015382	ENSACAT00000015429	TMED2
ENSACAP00000015149	ENSACAG00000015423	ENSACAT00000015455	RILPL2
ENSACAP00000001682	ENSACAG00000001663	ENSACAT00000001722	IMPACT
ENSACAP00000008830	ENSACAG00000008935	ENSACAT00000009020	VCL
ENSACAP00000001092	ENSACAG00000000304	ENSACAT00000001122	LAMA3
ENSACAP00000017354	ENSACAG00000017628	ENSACAT00000017695	DNAJC8

ENSACAP00000023204	ENSACAG00000029360	ENSACAT00000030624	
ENSACAP00000000255	ENSACAG00000000201	ENSACAT00000000261	NPC1
ENSACAP00000003389	ENSACAG00000003453	ENSACAT00000003472	AK2
ENSACAP00000017751	ENSACAG00000021101	ENSACAT00000021162	
ENSACAP00000015757	ENSACAG00000016016	ENSACAT00000016073	GPN3
ENSACAP00000007131	ENSACAG00000007245	ENSACAT00000007286	SHARPIN
ENSACAP00000009761	ENSACAG00000009859	ENSACAT00000009960	OXSR1
ENSACAP00000003323	ENSACAG00000003408	ENSACAT00000003406	SPINT1
ENSACAP00000004798	ENSACAG00000004884	ENSACAT00000004906	HSPA8
ENSACAP00000000360	ENSACAG00000000388	ENSACAT00000000374	RASSF8
ENSACAP00000002102	ENSACAG00000002133	ENSACAT00000002159	POLA2
ENSACAP00000000796	ENSACAG00000000861	ENSACAT00000000822	ACAD8
ENSACAP00000006621	ENSACAG00000006760	ENSACAT00000006767	HHATL
ENSACAP00000012150	ENSACAG00000012394	ENSACAT00000012396	MAP6
ENSACAP00000007627	ENSACAG00000007724	ENSACAT00000007789	EIF2D
ENSACAP00000009969	ENSACAG00000010176	ENSACAT00000010174	HIRIP3
ENSACAP00000016369	ENSACAG00000016579	ENSACAT00000016693	CAPN1
ENSACAP00000008681	ENSACAG00000008859	ENSACAT00000008867	CENPN
ENSACAP00000002742	ENSACAG00000002493	ENSACAT00000002811	DIP2C
ENSACAP00000000391	ENSACAG00000000286	ENSACAT00000000408	MAP2K2
ENSACAP00000021641	ENSACAG00000004214	ENSACAT00000022236	MIS18BP1
ENSACAP00000009827	ENSACAG00000009919	ENSACAT00000010027	ERCC3
ENSACAP00000009562	ENSACAG00000009597	ENSACAT00000009759	XRCC5
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ENSACAP00000004238	ENSACAG00000004336	ENSACAT00000004337	ANP32B
ENSACAP00000017703	ENSACAG00000017980	ENSACAT00000018051	
ENSACAP00000009165	ENSACAG00000009328	ENSACAT00000009358	PLXDC2
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ENSACAP00000001455	ENSACAG00000001457	ENSACAT00000001490	MDH2
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ENSACAP00000005208	ENSACAG00000005306	ENSACAT00000005325	EXD2
ENSACAP00000016067	ENSACAG00000016360	ENSACAT00000016387	MYADM
ENSACAP00000016228	ENSACAG00000016368	ENSACAT00000016551	PRKCG
ENSACAP00000000378	ENSACAG00000000366	ENSACAT00000000393	TNFAIP2
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ENSACAP00000012746	ENSACAG00000012993	ENSACAT00000013002	METTL11B
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ENSACAP00000002155	ENSACAG00000002257	ENSACAT00000002214	SERPIND1
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ENSACAP00000000034	ENSACAG00000000035	ENSACAT00000000035	SLC6A13
ENSACAP00000003355	ENSACAG00000003341	ENSACAT00000003438	COPB2
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ENSACAP00000007935	ENSACAG00000008070	ENSACAT00000008103	GTPBP1
ENSACAP00000022437	ENSACAG00000029148	ENSACAT00000029854	CHMP5
ENSACAP00000006319	ENSACAG00000006450	ENSACAT00000006460	EFHD1
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ENSACAP00000000160	ENSACAG00000000146	ENSACAT00000000163	PCSK9
ENSACAP00000002239	ENSACAG00000002353	ENSACAT00000002299	
ENSACAP00000022313	ENSACAG00000029391	ENSACAT00000029730	AREG
ENSACAP00000011712	ENSACAG00000011773	ENSACAT00000011954	

ENSACAP00000011987	ENSACAG00000012027	ENSACAT00000012231	AHCYL1
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ENSACAP00000023038	ENSACAG00000028642	ENSACAT00000030458	CCDC24
ENSACAP00000014417	ENSACAG00000014707	ENSACAT00000014712	CCDC59
ENSACAP00000015276	ENSACAG00000015495	ENSACAT00000015585	EIF2B3
ENSACAP00000015527	ENSACAG00000015761	ENSACAT00000015841	PDCD4
ENSACAP00000015446	ENSACAG00000015732	ENSACAT00000015760	TMEM69
ENSACAP00000013736	ENSACAG00000014001	ENSACAT00000014017	PAWR
ENSACAP00000001347	ENSACAG00000001348	ENSACAT00000001380	SPOCK2
ENSACAP00000000791	ENSACAG00000000862	ENSACAT00000000816	MCU
ENSACAP00000017283	ENSACAG00000017561	ENSACAT00000017623	NEUROD2
ENSACAP00000022284	ENSACAG00000028720	ENSACAT00000029701	
ENSACAP00000002985	ENSACAG00000003079	ENSACAT00000003062	BYSL
ENSACAP00000017662	ENSACAG00000017936	ENSACAT00000018008	ATP6V0A1
ENSACAP00000000684	ENSACAG00000000574	ENSACAT00000000706	MON2
ENSACAP00000002037	ENSACAG00000002035	ENSACAT00000002086	UCHL3
ENSACAP00000005089	ENSACAG00000005218	ENSACAT00000005204	
ENSACAP00000007005	ENSACAG00000007124	ENSACAT00000007156	TSPAN12
ENSACAP00000002567	ENSACAG00000002604	ENSACAT00000002632	EFNB2
ENSACAP00000000241	ENSACAG00000000264	ENSACAT00000000247	LAMP1
ENSACAP00000003806	ENSACAG00000003847	ENSACAT00000003898	SYT2
ENSACAP00000013672	ENSACAG00000013921	ENSACAT00000013953	NOSIP
ENSACAP00000005126	ENSACAG00000005107	ENSACAT00000005242	KDM5B
ENSACAP00000011883	ENSACAG00000012036	ENSACAT00000012127	UBE3A
ENSACAP00000015430	ENSACAG00000015683	ENSACAT00000015743	NUP50
ENSACAP00000012342	ENSACAG00000012584	ENSACAT00000012595	CXorf23
ENSACAP00000016592	ENSACAG00000016869	ENSACAT00000016918	SERINC3
ENSACAP00000007057	ENSACAG00000007218	ENSACAT00000007209	NR0B1
ENSACAP00000019214	ENSACAG00000014537	ENSACAT00000014541	MID1IP1

ENSACAP00000015734	ENSACAG00000015951	ENSACAT00000016050	CSE1L
ENSACAP00000017656	ENSACAG00000017928	ENSACAT00000018002	
ENSACAP00000017584	ENSACAG00000017858	ENSACAT00000017930	
ENSACAP00000006746	ENSACAG00000006896	ENSACAT00000006892	RELN
ENSACAP00000014830	ENSACAG00000015115	ENSACAT00000015131	GPR22
ENSACAP00000001856	ENSACAG00000001784	ENSACAT00000001901	CCT8
ENSACAP00000008692	ENSACAG00000008845	ENSACAT00000008878	LONRF1
ENSACAP00000013738	ENSACAG00000013950	ENSACAT00000014019	
ENSACAP00000011523	ENSACAG00000011687	ENSACAT00000011763	ABI3BP
ENSACAP00000011059	ENSACAG00000011149	ENSACAT00000011288	TBC1D23
ENSACAP00000005027	ENSACAG00000005144	ENSACAT00000005140	MARCH1
ENSACAP00000015416	ENSACAG00000015674	ENSACAT00000015729	FGB
ENSACAP00000017757	ENSACAG00000021135	ENSACAT00000021129	
ENSACAP00000002763	ENSACAG00000002772	ENSACAT00000002832	GATB
ENSACAP00000001606	ENSACAG00000001683	ENSACAT00000001645	CENPJ
ENSACAP00000012693	ENSACAG00000012765	ENSACAT00000012949	ANXA5
ENSACAP00000012369	ENSACAG00000012632	ENSACAT00000012622	
ENSACAP00000012644	ENSACAG00000012875	ENSACAT00000012900	CASP6
ENSACAP00000012209	ENSACAG00000012255	ENSACAT00000012459	SEPT11
ENSACAP00000021261	ENSACAG00000027099	ENSACAT00000022125	CCDC89
ENSACAP00000013095	ENSACAG00000013283	ENSACAT00000013355	GC
ENSACAP00000017717	ENSACAG00000017990	ENSACAT00000018065	ACAA2
ENSACAP00000011045	ENSACAG00000011296	ENSACAT00000011273	EMB
ENSACAP00000001594	ENSACAG00000001614	ENSACAT00000001633	SLC27A6
ENSACAP00000000932	ENSACAG00000000922	ENSACAT00000000960	ROR2
ENSACAP00000000778	ENSACAG00000000768	ENSACAT00000000802	SYK
ENSACAP00000013128	ENSACAG00000013328	ENSACAT00000013388	
ENSACAP00000003019	ENSACAG00000003015	ENSACAT00000003096	VLDLR
ENSACAP00000001893	ENSACAG00000001929	ENSACAT00000001939	
ENSACAP00000010618	ENSACAG00000010781	ENSACAT00000010837	HAUS6

ENSACAP00000010758	ENSACAG00000010932	ENSACAT00000010981	CFP
ENSACAP00000004589	ENSACAG00000004710	ENSACAT00000004695	
ENSACAP00000005087	ENSACAG00000005069	ENSACAT00000005202	CDK16
ENSACAP00000015316	ENSACAG00000015591	ENSACAT00000015628	CLPP
ENSACAP00000022652	ENSACAG00000015935	ENSACAT00000030069	SPRED1
ENSACAP00000015705	ENSACAG00000015966	ENSACAT00000016020	KRI1
ENSACAP00000014848	ENSACAG00000015126	ENSACAT00000015149	
ENSACAP00000017274	ENSACAG00000017477	ENSACAT00000017614	
ENSACAP00000020710	ENSACAG00000016156	ENSACAT00000022687	PAPLN
ENSACAP00000003757	ENSACAG00000003860	ENSACAT00000003849	ZNF408
ENSACAP00000012329	ENSACAG00000012437	ENSACAT00000012582	G6PD
ENSACAP00000016757	ENSACAG00000016987	ENSACAT00000017087	
ENSACAP00000005047	ENSACAG00000005179	ENSACAT00000005160	COMMD9
ENSACAP00000004222	ENSACAG00000004323	ENSACAT00000004321	CD44
ENSACAP00000001943	ENSACAG00000002019	ENSACAT00000001989	ARL14EP
ENSACAP00000002708	ENSACAG00000002746	ENSACAT00000002776	TCP11L1
ENSACAP00000002921	ENSACAG00000002823	ENSACAT00000002995	CSTF3
ENSACAP00000009232	ENSACAG00000009338	ENSACAT00000009425	ZNF143
ENSACAP00000000054	ENSACAG00000000055	ENSACAT00000000055	KCNC1
ENSACAP00000021933	ENSACAG00000029485	ENSACAT00000029351	
ENSACAP00000002650	ENSACAG00000002763	ENSACAT00000002717	TSSC4
ENSACAP00000009585	ENSACAG00000009745	ENSACAT00000009782	TOLLIP
ENSACAP00000015070	ENSACAG00000015332	ENSACAT00000015374	RPLP2
ENSACAP00000016669	ENSACAG00000016849	ENSACAT00000016998	PKN1
ENSACAP00000014952	ENSACAG00000015157	ENSACAT00000015255	EPS8L2
ENSACAP00000009556	ENSACAG00000009769	ENSACAT00000009753	
ENSACAP00000017391	ENSACAG00000017579	ENSACAT00000017732	MYH10
ENSACAP00000010265	ENSACAG00000010273	ENSACAT00000010477	COL18A1
ENSACAP00000010053	ENSACAG00000010217	ENSACAT00000010260	NDUFV1
ENSACAP00000007659	ENSACAG00000007694	ENSACAT00000007823	ACOX1

ENSACAP00000005899	ENSACAG00000006044	ENSACAT00000006028	ICT1
ENSACAP00000001589	ENSACAG00000001698	ENSACAT00000001627	TOB1
ENSACAP00000010615	ENSACAG00000010832	ENSACAT00000010834	ADGRE5
ENSACAP00000016681	ENSACAG00000016934	ENSACAT00000017011	BZW1
ENSACAP00000006604	ENSACAG00000006747	ENSACAT00000006750	TMEFF2
ENSACAP00000010279	ENSACAG00000010432	ENSACAT00000010491	
ENSACAP00000004762	ENSACAG00000004847	ENSACAT00000004870	
ENSACAP00000004705	ENSACAG00000004735	ENSACAT00000004812	COL6A1
ENSACAP00000016251	ENSACAG00000016533	ENSACAT00000016574	NHLRC3
ENSACAP00000013296	ENSACAG00000013523	ENSACAT00000013565	MRPL19
ENSACAP00000011364	ENSACAG00000011587	ENSACAT00000011603	UBXN2A
ENSACAP00000012470	ENSACAG00000012600	ENSACAT00000012726	ODC1
ENSACAP00000008985	ENSACAG00000009170	ENSACAT00000009178	OGN
ENSACAP00000023237	ENSACAG00000005667	ENSACAT00000030656	MYT1L
ENSACAP00000006425	ENSACAG00000005967	ENSACAT00000006570	
ENSACAP00000010793	ENSACAG00000010885	ENSACAT00000011016	TKT
ENSACAP00000017438	ENSACAG00000017700	ENSACAT00000017780	FAM184A
ENSACAP00000006046	ENSACAG00000006164	ENSACAT00000006180	CEP57L1
ENSACAP00000005515	ENSACAG00000005657	ENSACAT00000005636	TRNT1
ENSACAP00000014754	ENSACAG00000015012	ENSACAT00000015055	ANO10
ENSACAP00000003229	ENSACAG00000003319	ENSACAT00000003312	PACRG
ENSACAP00000011394	ENSACAG00000011208	ENSACAT00000011633	
ENSACAP00000002257	ENSACAG00000002344	ENSACAT00000002317	GPR137B
ENSACAP00000001580	ENSACAG00000001633	ENSACAT00000001618	B3GALNT2
ENSACAP00000009073	ENSACAG00000009007	ENSACAT00000009266	LTBP1
ENSACAP00000001253	ENSACAG00000001139	ENSACAT00000001286	PRKD3
ENSACAP00000023397	ENSACAG00000029073	ENSACAT00000030817	LYPLAL1
ENSACAP00000002332	ENSACAG00000002384	ENSACAT00000002392	BROX

Table S34. GO terms associated with PSGs identified on frog branch 4.

category	pvalue	numDE InCat	numIn Cat	term	GeneName
GO:0036462	0.000111602	2	2	TRAIL-activated apoptotic signaling pathway	FADD,ENSACAG00000029485,
GO:0071470	0.000147044	4	20	cellular response to osmotic stress	ENSACAG00000017928,RELB,OXSR1,XRCC5,
GO:0035795	0.000274784	2	2	negative regulation of mitochondrial membrane permeability	ACAA2,HK2,
GO:1904430	0.00029842	2	2	negative regulation of t-circle formation	TERF2,XRCC5,
GO:0006081	0.001064851	5	55	cellular aldehyde metabolic process	G6PD,TKT,GPI,DLAT,GRHPR,
GO:0006957	0.001105394	3	14	complement activation, alternative pathway	C8A,CFP,ENSACAG00000011208,
GO:0038026	0.001209879	2	3	reelin-mediated signaling pathway	RELN,VLDLR,
GO:0046184	0.001257641	2	4	aldehyde biosynthetic process	TKT,GPI,
GO:0001945	0.001288649	2	4	lymph vessel development	EFNB2,SYK,
GO:0006006	0.001696709	6	84	glucose metabolic process	G6PD,GPI,DLAT,ENSACAG00000003255,HK2,BRAT1,
GO:0060236	0.001864445	3	16	regulation of mitotic spindle organization	TPX2,CHMP5,ANKRD53,
GO:0033555	0.002850564	4	43	multicellular organismal response to stress	PRKCG,NEUROD2,RELN,EIF4G1,
GO:0050999	0.003771516	3	22	regulation of nitric-oxide synthase activity	NOSIP,DDAH2,TERF2,
GO:0006970	0.004009937	4	45	response to osmotic stress	ENSACAG00000017928,RELB,OXSR1,XRCC5,
GO:0031175	0.0043879	7	137	neuron projection development	EFHD1,AREG,PTPRF,RELN,CDK16,HERC1,PLP1,
GO:1902857	0.004948652	2	7	positive regulation of nonmotile primary cilium assembly	SEPT12,CENPJ,
GO:0042129	0.006033309	5	85	regulation of T cell proliferation	FADD,PAWR,SYK,DNAJA3,CD276,
GO:0045087	0.00606838	11	316	innate immune response	FADD,C8A,SERINC3,ENSACAG00000017928,ENSACAG00000021135,SYK,CFP,TOLLIP,RELB,ENSACAG00000011208,ENSACAG00000007262,
GO:0006090	0.007123617	4	50	pyruvate metabolic process	GPI,DLAT,ENSACAG00000003255,HK2,
GO:0097049	0.007383836	1	1	motor neuron apoptotic process	FADD,
GO:2000454	0.007383836	1	1	positive regulation of CD8-positive, alpha-beta cytotoxic T cell	FADD,

				extravasation	
GO:0021517	0.008225599	2	8	ventral spinal cord development	RELN,VLDLR,
GO:0046034	0.008958334	4	63	ATP metabolic process	ATP6V0A1,HSPA5,AK2,ENSACAG00000021101,
GO:0035562	0.00921317	2	9	negative regulation of chromatin binding	FBXO18,BTAF1,
GO:0060598	0.009435699	1	1	dichotomous subdivision of terminal units involved in mammary gland duct morphogenesis	AREG,
GO:0032787	0.009538867	13	417	monocarboxylic acid metabolic process	ACAA2,SLC27A6,ACOX1,ENSACAG00000004847,GPI,DLAT,ENSACAG00000003255,PLP1,IDUA,GRHPR,NPC1,ACAD8,HK2,
GO:0048265	0.010396075	2	11	response to pain	PRKCG,RELN,
GO:0046487	0.010592178	2	11	glyoxylate metabolic process	DLAT,GRHPR,
GO:0033869	0.011169222	1	1	nucleoside bisphosphate catabolic process	NUDT7,
GO:0034034	0.011169222	1	1	purine nucleoside bisphosphate catabolic process	NUDT7,
GO:0046356	0.011169222	1	1	acetyl-CoA catabolic process	NUDT7,
GO:0021680	0.011623862	2	11	cerebellar Purkinje cell layer development	MYH10,HSPA5,
GO:0072027	0.011896872	1	1	connecting tubule development	CALB1,
GO:0072286	0.011896872	1	1	metanephric connecting tubule development	CALB1,
GO:0006480	0.012660835	1	1	N-terminal protein amino acid methylation	METTL11B,
GO:0006924	0.013094653	1	1	activation-induced cell death of T cells	DNAJA3,
GO:0072755	0.013281179	1	1	cellular response to benomyl	IMPACT,
GO:1901561	0.013281179	1	1	response to benomyl	IMPACT,
GO:1903849	0.013859234	1	1	positive regulation of aorta morphogenesis	EFNB2,
GO:0035786	0.014007207	1	1	protein complex oligomerization	MCU,
GO:0010035	0.014271971	10	299	response to inorganic substance	AREG,AHCYL1,NEUROD2,SYK,KCNC1,COL18A1,GPI,ENSACAG00000017266,IMPACT,NPC1,
GO:0048857	0.014548543	3	37	neural nucleus development	KCNC1,HSPA5,PLP1,
GO:0061620	0.014932553	2	12	glycolytic process through glucose-6-phosphate	GPI,HK2,
GO:0051346	0.015290738	7	179	negative regulation of hydrolase activity	SPOCK2,ENSACAG00000017928,SPRED

					1,GPI,TERF2,FICD,TMED2,
GO:0061300	0.015404067	1	2	cerebellum vasculature development	ENSACAG00000005218,
GO:0001680	0.015516298	1	1	tRNA 3'-terminal CCA addition	TRNT1,
GO:0051156	0.015814385	2	14	glucose 6-phosphate metabolic process	G6PD,GPI,
GO:0018117	0.015841793	1	1	protein adenylylation	FICD,
GO:0018175	0.015841793	1	1	protein nucleotidylation	FICD,
GO:0070613	0.016499143	7	185	regulation of protein processing	N4BP1,PRKCG,C8A,SPOCK2,ENSACAG00000017928,ENSACAG00000011208,GPI,
GO:0019242	0.01673979	1	1	methylglyoxal biosynthetic process	GPI,
GO:0006099	0.016983803	3	36	tricarboxylic acid cycle	MDH2,ENSACAG00000015409,DLAT,
GO:0001820	0.017145152	1	1	serotonin secretion	SYK,
GO:0071226	0.017145152	1	1	cellular response to molecule of fungal origin	SYK,
GO:0030209	0.017226685	1	1	dermatan sulfate catabolic process	IDUA,
GO:0032799	0.017277767	1	1	low-density lipoprotein receptor particle metabolic process	PCSK9,
GO:2000646	0.017277767	1	1	positive regulation of receptor catabolic process	PCSK9,
GO:1903770	0.017288441	1	1	negative regulation of beta-galactosidase activity	TERF2,
GO:0034447	0.017346009	1	1	very-low-density lipoprotein particle clearance	VLDLR,
GO:0035037	0.017346009	1	1	sperm entry	UBE3A,
GO:1902396	0.017346009	1	1	protein localization to bicellular tight junction	ACTN4,
GO:1904925	0.017346009	1	1	positive regulation of mitophagy in response to mitochondrial depolarization	HK2,
GO:0030954	0.017347767	1	1	astral microtubule nucleation	CENPJ,
GO:0051300	0.017347767	1	1	spindle pole body organization	CENPJ,
GO:1903320	0.019252433	7	192	regulation of protein modification by small protein conjugation or removal	N4BP1,PRKCG,UBE2L3,UBE3A,TOLLIP,UBXN2A,HSPA5,
GO:0043278	0.019642871	2	16	response to morphine	PRKCG,GPI,
GO:0045948	0.020702823	2	15	positive regulation of translational initiation	ENSACAG00000017928,IMPACT,
GO:0032886	0.021115779	6	144	regulation of microtubule-based process	TPX2,CHMP5,MID1IP1,CENPJ,ANKRD53,INPP5J,
GO:2000452	0.021183419	1	2	regulation of CD8-positive, alpha-beta cytotoxic T cell	FADD,

				extravasation	
GO:0018107	0.021340109	3	38	peptidyl-threonine phosphorylation	PKN1,ENSACAG00000014806,OXSR1,
GO:0090129	0.021361991	2	14	positive regulation of synapse maturation	NEUROD2,RELN,
GO:2000451	0.021370434	1	2	positive regulation of CD8-positive, alpha-beta T cell extravasation	FADD,
GO:0051341	0.021526069	3	42	regulation of oxidoreductase activity	NOSIP,DDAH2,TERF2,
GO:0006891	0.021756999	3	42	intra-Golgi vesicle-mediated transport	COPB2,ENSACAG00000017858,PACS1,
GO:0007613	0.021814209	4	70	memory	RELN,VLDLR,ENSACAG00000016987,CALB1,
GO:0042986	0.022103676	1	2	positive regulation of amyloid precursor protein biosynthetic process	PAWR,
GO:0072376	0.022507535	4	94	protein activation cascade	C8A,CFP,ENSACAG00000011208,ENSACAG00000007262,
GO:0035561	0.022567455	2	15	regulation of chromatin binding	FBXO18,BTAF1,
GO:0042094	0.022698409	1	2	interleukin-2 biosynthetic process	PAWR,
GO:0072350	0.022884787	3	40	tricarboxylic acid metabolic process	MDH2,ENSACAG00000015409,DLAT,
GO:0001912	0.023026387	2	17	positive regulation of leukocyte mediated cytotoxicity	FADD,CADM1,
GO:0097327	0.023105093	1	2	response to antineoplastic agent	PTGR1,
GO:0010447	0.023203718	2	16	response to acidic pH	ENSACAG00000016987,IMPACT,
GO:0006413	0.023229974	4	86	translational initiation	EIF2B3,MRPL19,EIF4G1,EIF2D,
GO:0031330	0.024274741	5	110	negative regulation of cellular catabolic process	N4BP1,PRKCG,TOB1,HERC1,NPC1,
GO:0033539	0.024678395	2	16	fatty acid beta-oxidation using acyl-CoA dehydrogenase	ACOX1,ACAD8,
GO:0006391	0.025416402	1	2	transcription initiation from mitochondrial promoter	TFAM,
GO:1902078	0.026050719	1	1	positive regulation of lateral motor column neuron migration	RELN,
GO:0006414	0.026210392	3	58	translational elongation	GTPBP1,RPLP2,MRPL19,
GO:2000483	0.026399167	1	2	negative regulation of interleukin-8 secretion	ANXA4,
GO:0015672	0.02708898	9	293	monovalent inorganic cation transport	ATP6V0A1,ENSACAG00000017858,SYK,ENSACAG00000016987,COMMD9,KCNC1,SLC17A7,ENSACAG00000021101,COMMD3,
GO:0006814	0.027147063	5	108	sodium ion transport	ENSACAG00000017858,ENSACAG00000

					016987,COMMD9,SLC17A7,COMMD3,
GO:0007512	0.027964815	2	11	adult heart development	MYH10,ENSACAG00000017266,
GO:0046166	0.028448545	1	2	glyceraldehyde-3-phosphate biosynthetic process	TKT,
GO:0021762	0.028619536	2	20	substantia nigra development	HSPA5,PLP1,
GO:0071649	0.028887326	1	2	regulation of chemokine (C-C motif) ligand 5 production	ENSACAG00000017928,
GO:0031581	0.030174085	2	11	hemidesmosome assembly	ENSACAG00000005967,LAMA3,
GO:0018210	0.030232141	3	43	peptidyl-threonine modification	PKN1,ENSACAG00000014806,OXSR1,
GO:0071494	0.030330313	1	2	cellular response to UV-C	IMPACT,
GO:0006084	0.030457606	2	18	acetyl-CoA metabolic process	NUDT7,DLAT,
GO:1900152	0.030514019	1	2	negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	TOB1,
GO:0031123	0.031572269	4	81	RNA 3'-end processing	AHCYL1,CSTF3,TRNT1,EIF4G1,
GO:0045113	0.032044776	1	3	regulation of integrin biosynthetic process	TMEFF2,
GO:0046686	0.032379888	2	19	response to cadmium ion	GPI,NPC1,
GO:1902412	0.03258221	1	2	regulation of mitotic cytokinesis	ANKRD53,
GO:0001682	0.033462908	1	2	tRNA 5'-leader removal	ENSACAG00000001929,
GO:0071600	0.033857467	1	2	otic vesicle morphogenesis	SHARPIN,
GO:1902903	0.034061414	1	2	regulation of fibril organization	HSPA5,
GO:0070207	0.034157869	2	20	protein homotrimerization	ENSACAG00000016987,HSF1,
GO:0071873	0.034394106	1	2	response to norepinephrine	COL1A2,
GO:2000449	0.034976281	1	3	regulation of CD8-positive, alpha-beta T cell extravasation	FADD,
GO:0003351	0.035499433	2	18	epithelial cilium movement	CCDC39,DNAI1,
GO:0006658	0.035829569	2	20	phosphatidylserine metabolic process	SERINC3,PTDSS1,
GO:0006091	0.035992015	6	179	generation of precursor metabolites and energy	ENSACAG00000005218,NDUFB3,ACOX1,GPI,ENSACAG00000003255,HK2,
GO:0015985	0.036334539	2	26	energy coupled proton transport, down electrochemical gradient	ATP6V0A1,ENSACAG00000021101,
GO:0055003	0.037311755	2	14	cardiac myofibril assembly	MYH10,ENSACAG00000017266,
GO:1903445	0.038832855	1	3	protein transport from ciliary membrane to plasma membrane	RILPL2,
GO:0051452	0.038881033	2	25	intracellular pH reduction	ATP6V0A1,ENSACAG00000013950,

GO:0051258	0.039002358	3	56	protein polymerization	MID1IP1,FGB,CENPJ,
GO:0080135	0.039499082	12	463	regulation of cellular response to stress	FBXO18,PTPRF,PDCD4,PAWR,NUP50,SERINC3,SPRED1,TERF2,ENSACAG00000004565,IMPACT,NPC1,CAPN1,
GO:0042149	0.039651164	2	21	cellular response to glucose starvation	HSPA5,IMPACT,
GO:1901033	0.039701641	1	3	positive regulation of response to reactive oxygen species	PAWR,
GO:0009132	0.039723333	2	24	nucleoside diphosphate metabolic process	NUDT7,AK2,
GO:0072429	0.040243661	1	3	response to intra-S DNA damage checkpoint signaling	FBXO18,
GO:0070681	0.040883428	1	3	glutaminyl-tRNAGln biosynthesis via transamidation	GATB,
GO:0022411	0.042246886	6	175	cellular component disassembly	NUP50,CASP6,ICT1,LAMA3,EIF2D,CAPN1,
GO:0006574	0.042399324	1	3	valine catabolic process	ACAD8,
GO:0007080	0.042727231	2	23	mitotic metaphase plate congression	CHMP5,ANKRD53,
GO:0009826	0.043786731	1	3	unidimensional cell growth	CADM1,
GO:0034436	0.044025394	1	3	glycoprotein transport	VLDLR,
GO:0034508	0.044420402	1	3	centromere complex assembly	CENPN,
GO:0030538	0.044739211	1	4	embryonic genitalia morphogenesis	ROR2,
GO:0090342	0.045077091	2	26	regulation of cell aging	PAWR,TERF2,
GO:0030198	0.045772926	7	210	extracellular matrix organization	COL1A2,SPOCK2,ABI3BP,COL18A1,LAMA3,SPINT1,CAPN1,
GO:0060670	0.045838069	1	4	branching involved in labyrinthine layer morphogenesis	SPINT1,
GO:0046395	0.045874003	6	172	carboxylic acid catabolic process	ACAA2,ACOX1,ENSACAG00000004847,DDAH2,IDUA,ACAD8,
GO:0030162	0.04646724	10	384	regulation of proteolysis	N4BP1,PRKCG,FADD,SPOCK2,UBE3A,ENSACAG00000017928,ENSACAG00000015126,ENSACAG00000029485,GPI,ENSACAG00000014806,
GO:0032200	0.046917447	3	52	telomere organization	TERF2,POLA2,XRCC5,
GO:0033387	0.047045378	1	3	putrescine biosynthetic process from ornithine	ODC1,
GO:0034334	0.047327023	1	3	adherens junction maintenance	RASSF8,
GO:0043062	0.047338548	7	212	extracellular structure organization	COL1A2,SPOCK2,ABI3BP,COL18A1,LAMA3,SPINT1,CAPN1,

GO:0034620	0.048675433	1	4	cellular response to unfolded protein	PACRG,
GO:2000189	0.048956469	1	3	positive regulation of cholesterol homeostasis	NPC1,
GO:0097475	0.048990869	1	3	motor neuron migration	RELN,
GO:0060546	0.049267568	1	4	negative regulation of necroptotic process	FADD,

Table S35. PSGs identified on branch 4 of lizard.

Ensembl Prot ID	Ensembl Gene ID	Ensembl Trans ID	HNGC Name
ENSACAP00000011291	ENSACAG00000011517	ENSACAT00000011528	FHAD1
ENSACAP00000012390	ENSACAG00000012619	ENSACAT00000012643	HSPG2
ENSACAP00000000682	ENSACAG00000000750	ENSACAT00000000704	ARSA
ENSACAP00000002992	ENSACAG00000003104	ENSACAT00000003069	
ENSACAP00000012484	ENSACAG00000012665	ENSACAT00000012740	STK17B
ENSACAP00000015433	ENSACAG00000015663	ENSACAT00000015746	CTSH
ENSACAP00000000960	ENSACAG00000000835	ENSACAT00000000988	
ENSACAP00000014306	ENSACAG00000014599	ENSACAT00000014599	SOCS1
ENSACAP00000005501	ENSACAG00000005357	ENSACAT00000005621	MYOM3
ENSACAP00000022471	ENSACAG00000028660	ENSACAT00000029888	
ENSACAP00000023045	ENSACAG00000013110	ENSACAT00000030466	ACSF3
ENSACAP00000003934	ENSACAG00000004012	ENSACAT00000004026	RABEPK
ENSACAP00000008291	ENSACAG00000008337	ENSACAT00000008470	KDM4B
ENSACAP00000006471	ENSACAG00000006602	ENSACAT00000006616	ZNF282
ENSACAP00000010379	ENSACAG00000010571	ENSACAT00000010593	C1orf43
ENSACAP00000007881	ENSACAG00000008005	ENSACAT00000008047	PHACTR2
ENSACAP00000009591	ENSACAG00000009744	ENSACAT00000009788	
ENSACAP00000016986	ENSACAG00000017256	ENSACAT00000017321	PLEKHA3
ENSACAP00000015845	ENSACAG00000016110	ENSACAT00000016162	IGSF8
ENSACAP00000018353	ENSACAG00000008223	ENSACAT00000027398	CD34

ENSACAP00000021652	ENSACAG00000017540	ENSACAT00000017605	ADAT3
ENSACAP00000010555	ENSACAG00000010722	ENSACAT00000010773	ISYNA1
ENSACAP00000003401	ENSACAG00000003460	ENSACAT00000003484	ANKRD12
ENSACAP00000009853	ENSACAG00000010057	ENSACAT00000010055	SKA1
ENSACAP00000013205	ENSACAG00000013451	ENSACAT00000013471	GJA4
ENSACAP00000000998	ENSACAG00000001095	ENSACAT00000001026	KIAA0895L
ENSACAP00000000281	ENSACAG00000000317	ENSACAT00000000288	C17orf58
ENSACAP00000001060	ENSACAG00000001118	ENSACAT00000001089	POLG2
ENSACAP00000010499	ENSACAG00000010552	ENSACAT00000010716	DVL3
ENSACAP00000012483	ENSACAG00000012625	ENSACAT00000012739	AQP3
ENSACAP00000014597	ENSACAG00000014876	ENSACAT00000014892	SPATA22
ENSACAP00000000214	ENSACAG00000000225	ENSACAT00000000218	BRF2
ENSACAP00000015062	ENSACAG00000015305	ENSACAT00000015366	
ENSACAP00000021940	ENSACAG00000028558	ENSACAT00000029358	EIF4EBP1
ENSACAP00000011037	ENSACAG00000011272	ENSACAT00000011265	C3AR1
ENSACAP00000005668	ENSACAG00000005806	ENSACAT00000005792	HGFAC
ENSACAP00000007661	ENSACAG00000007830	ENSACAT00000007825	FETUB
ENSACAP00000008430	ENSACAG00000008564	ENSACAT00000008612	GLE1
ENSACAP00000017509	ENSACAG00000017781	ENSACAT00000017854	CNKSR1
ENSACAP00000015047	ENSACAG00000015242	ENSACAT00000015351	MYO1E
ENSACAP00000019631	ENSACAG00000000549	ENSACAT00000028168	DENND3
ENSACAP00000010841	ENSACAG00000010764	ENSACAT00000011065	P2RX6
ENSACAP00000019300	ENSACAG00000024425	ENSACAT00000022888	EMC1
ENSACAP00000006188	ENSACAG00000006279	ENSACAT00000006325	GLYR1
ENSACAP00000007179	ENSACAG00000007342	ENSACAT00000007334	
ENSACAP00000013818	ENSACAG00000013984	ENSACAT00000014100	LRRCC1
ENSACAP00000004437	ENSACAG00000004560	ENSACAT00000004537	IQCD
ENSACAP00000011352	ENSACAG00000011361	ENSACAT00000011591	MAPK8
ENSACAP00000007549	ENSACAG00000007617	ENSACAT00000007710	LMAN1
ENSACAP00000004704	ENSACAG00000004785	ENSACAT00000004811	RASGEF1A

ENSACAP00000008436	ENSACAG00000008572	ENSACAT00000008618	MAGT1
ENSACAP00000017488	ENSACAG00000017762	ENSACAT00000017833	ARHGEF16
ENSACAP00000017417	ENSACAG00000017674	ENSACAT00000017759	STX12
ENSACAP00000017385	ENSACAG00000017653	ENSACAT00000017726	
ENSACAP00000008212	ENSACAG00000008373	ENSACAT00000008389	CRK
ENSACAP00000006308	ENSACAG00000006461	ENSACAT00000006448	NUFIP1
ENSACAP00000015300	ENSACAG00000015568	ENSACAT00000015612	C7orf26
ENSACAP00000007053	ENSACAG00000007195	ENSACAT00000007205	GPAA1
ENSACAP00000016401	ENSACAG00000016644	ENSACAT00000016726	ZDHHC18
ENSACAP00000020153	ENSACAG00000014990	ENSACAT00000022361	LRSAM1
ENSACAP00000002176	ENSACAG00000002229	ENSACAT00000002235	SERPINH1
ENSACAP00000007984	ENSACAG00000008166	ENSACAT00000008155	COMMD10
ENSACAP00000003831	ENSACAG00000003908	ENSACAT00000003923	MDM1
ENSACAP00000004473	ENSACAG00000004492	ENSACAT00000004576	CCT2
ENSACAP00000018624	ENSACAG00000001148	ENSACAT00000022260	CTDP1
ENSACAP00000022810	ENSACAG00000028873	ENSACAT00000030228	NME4
ENSACAP00000009111	ENSACAG00000009325	ENSACAT00000009304	PSMD5
ENSACAP00000003383	ENSACAG00000003402	ENSACAT00000003466	ATP1A1
ENSACAP00000002430	ENSACAG00000002451	ENSACAT00000002493	TBL3
ENSACAP00000007154	ENSACAG00000007239	ENSACAT00000007309	
ENSACAP00000020020	ENSACAG00000023926	ENSACAT00000025106	
ENSACAP00000006499	ENSACAG00000006640	ENSACAT00000006644	NFXL1
ENSACAP00000016709	ENSACAG00000016978	ENSACAT00000017039	RHBDL2
ENSACAP00000019497	ENSACAG00000026822	ENSACAT00000025669	
ENSACAP00000004411	ENSACAG00000004517	ENSACAT00000004511	MRPL47
ENSACAP00000013551	ENSACAG00000013799	ENSACAT00000013829	YIPF5
ENSACAP00000005833	ENSACAG00000005770	ENSACAT00000005962	STXBP3
ENSACAP00000021056	ENSACAG00000016378	ENSACAT00000022547	FBXO43
ENSACAP00000011360	ENSACAG00000011582	ENSACAT00000011599	NSRP1
ENSACAP00000000775	ENSACAG00000000756	ENSACAT00000000799	CDC45

ENSACAP00000012662	ENSACAG00000012768	ENSACAT00000012918	
ENSACAP00000002209	ENSACAG00000001756	ENSACAT00000002269	ATP2C1
ENSACAP00000002352	ENSACAG00000002469	ENSACAT00000002412	ADIPOQ
ENSACAP00000022445	ENSACAG00000029434	ENSACAT00000029862	
ENSACAP00000009871	ENSACAG00000009938	ENSACAT00000010074	
ENSACAP00000008472	ENSACAG00000008565	ENSACAT00000008654	EXOC3
ENSACAP00000023118	ENSACAG00000029342	ENSACAT00000030538	ITGB3BP
ENSACAP00000008789	ENSACAG00000008914	ENSACAT00000008977	USO1
ENSACAP00000010441	ENSACAG00000010644	ENSACAT00000010655	
ENSACAP00000012885	ENSACAG00000013098	ENSACAT00000013143	
ENSACAP00000012965	ENSACAG00000013012	ENSACAT00000013224	APAF1
ENSACAP00000013079	ENSACAG00000013303	ENSACAT00000013339	TMEM106A
ENSACAP00000022598	ENSACAG00000016414	ENSACAT00000030015	
ENSACAP00000001815	ENSACAG00000001870	ENSACAT00000001859	MKNK1
ENSACAP00000014276	ENSACAG00000014491	ENSACAT00000014569	NUAK2
ENSACAP00000019602	ENSACAG00000022624	ENSACAT00000027362	GSDMA
ENSACAP00000000780	ENSACAG00000000798	ENSACAT00000000804	WBP4
ENSACAP00000001520	ENSACAG00000001618	ENSACAT00000001556	XRCC6BP1
ENSACAP00000002162	ENSACAG00000002060	ENSACAT00000002221	SLC38A2
ENSACAP00000016104	ENSACAG00000016245	ENSACAT00000016424	
ENSACAP00000022931	ENSACAG00000002987	ENSACAT00000030350	TPP2
ENSACAP00000000748	ENSACAG00000000689	ENSACAT00000000772	GAS6
ENSACAP00000001185	ENSACAG00000001294	ENSACAT00000001218	PACRGL
ENSACAP00000001539	ENSACAG00000001584	ENSACAT00000001575	PRPS2
ENSACAP00000008255	ENSACAG00000008338	ENSACAT00000008432	EDEM2
ENSACAP00000014380	ENSACAG00000014456	ENSACAT00000014673	FBLN1
ENSACAP00000015430	ENSACAG00000015683	ENSACAT00000015743	NUP50
ENSACAP00000015610	ENSACAG00000015880	ENSACAT00000015924	TSPO
ENSACAP00000016592	ENSACAG00000016869	ENSACAT00000016918	SERINC3
ENSACAP00000015866	ENSACAG00000016035	ENSACAT00000016184	GNAI1

ENSACAP00000017579	ENSACAG00000017853	ENSACAT00000017925	PDXK
ENSACAP00000004938	ENSACAG00000005042	ENSACAT00000005051	
ENSACAP00000014949	ENSACAG00000015225	ENSACAT00000015252	C3orf38
ENSACAP00000022414	ENSACAG00000029246	ENSACAT00000029831	CD47
ENSACAP00000011059	ENSACAG00000011149	ENSACAT00000011288	TBC1D23
ENSACAP00000016261	ENSACAG00000016502	ENSACAT00000016585	ETFDH
ENSACAP00000004459	ENSACAG00000004541	ENSACAT00000004560	BRCA2
ENSACAP00000004913	ENSACAG00000004925	ENSACAT00000005026	HSPH1
ENSACAP00000004935	ENSACAG00000005067	ENSACAT00000005048	TEX26
ENSACAP00000003266	ENSACAG00000003023	ENSACAT00000003349	LRBA
ENSACAP00000016452	ENSACAG00000016683	ENSACAT00000016777	PAPD4
ENSACAP00000005994	ENSACAG00000006074	ENSACAT00000006128	PSAT1
ENSACAP00000002234	ENSACAG00000002270	ENSACAT00000002294	KANK1
ENSACAP00000022348	ENSACAG00000029075	ENSACAT00000029765	CD274
ENSACAP00000006487	ENSACAG00000006636	ENSACAT00000006632	ABT1
ENSACAP00000006592	ENSACAG00000006650	ENSACAT00000006739	ESPL1
ENSACAP00000008633	ENSACAG00000008781	ENSACAT00000008816	
ENSACAP00000009667	ENSACAG00000009814	ENSACAT00000009864	C14orf159
ENSACAP00000014905	ENSACAG00000014786	ENSACAT00000015208	
ENSACAP00000014848	ENSACAG00000015126	ENSACAT00000015149	
ENSACAP00000016045	ENSACAG00000016309	ENSACAT00000016365	ZFYVE1
ENSACAP00000014599	ENSACAG00000014815	ENSACAT00000014894	PEX16
ENSACAP00000004222	ENSACAG00000004323	ENSACAT00000004321	CD44
ENSACAP00000008602	ENSACAG00000008776	ENSACAT00000008785	KANSL2
ENSACAP00000008205	ENSACAG00000007961	ENSACAT00000008381	KRT7
ENSACAP00000021933	ENSACAG00000029485	ENSACAT00000029351	
ENSACAP00000009525	ENSACAG00000009732	ENSACAT00000009722	DTX3L
ENSACAP00000010337	ENSACAG00000010381	ENSACAT00000010550	KALRN
ENSACAP00000004880	ENSACAG00000004997	ENSACAT00000004992	HSPBAP1
ENSACAP00000008191	ENSACAG00000008318	ENSACAT00000008367	UBE2O

ENSACAP00000007651	ENSACAG00000007663	ENSACAT00000007814	ADRBK1
ENSACAP00000008347	ENSACAG00000008489	ENSACAT00000008528	ACY3
ENSACAP00000008796	ENSACAG00000008948	ENSACAT00000008984	
ENSACAP00000002970	ENSACAG00000003082	ENSACAT00000003047	GTDC1
ENSACAP00000021654	ENSACAG00000023811	ENSACAT00000026478	ZEB2
ENSACAP00000015946	ENSACAG00000016212	ENSACAT00000016264	SPDL1
ENSACAP00000012528	ENSACAG00000012723	ENSACAT00000012784	RAD50
ENSACAP00000001750	ENSACAG00000001863	ENSACAT00000001790	CEP68
ENSACAP00000001097	ENSACAG00000001044	ENSACAT00000001129	
ENSACAP00000005633	ENSACAG00000005737	ENSACAT00000005756	FAM193B
ENSACAP00000003415	ENSACAG00000003413	ENSACAT00000003499	RB1
ENSACAP00000006790	ENSACAG00000006937	ENSACAT00000006938	GFRA3
ENSACAP00000011479	ENSACAG00000011679	ENSACAT00000011719	RNASEH2B
ENSACAP00000009033	ENSACAG00000009153	ENSACAT00000009226	OASL
ENSACAP00000007772	ENSACAG00000007499	ENSACAT00000007938	
ENSACAP00000020536	ENSACAG00000005884	ENSACAT00000025744	CCDC66
ENSACAP00000010137	ENSACAG00000010294	ENSACAT00000010345	SUMF1
ENSACAP00000014659	ENSACAG00000014913	ENSACAT00000014956	TCAIM
ENSACAP00000008284	ENSACAG00000008420	ENSACAT00000008463	VTA1
ENSACAP00000019777	ENSACAG00000026326	ENSACAT00000022565	
ENSACAP00000010774	ENSACAG00000011003	ENSACAT00000010997	
ENSACAP00000001376	ENSACAG00000001463	ENSACAT00000001409	GGPS1
ENSACAP00000001348	ENSACAG00000001289	ENSACAT00000001381	ARID4B
ENSACAP00000002671	ENSACAG00000002728	ENSACAT00000002738	DISC1
ENSACAP00000012781	ENSACAG00000012647	ENSACAT00000013037	
ENSACAP00000008325	ENSACAG00000008473	ENSACAT00000008506	RMDN2
ENSACAP00000016112	ENSACAG00000016371	ENSACAT00000016433	TRAF5
ENSACAP00000013794	ENSACAG00000013917	ENSACAT00000014076	MSH2

Table S36. GO terms associated with PSGs identified on lizard branch 4.

category	pvalue	numDE InCat	numIn Cat	term	GeneNames
GO:0036462	0.000111602	2	2	TRAIL-activated apoptotic signaling pathway	FADD,ENSACAG00000029485
GO:0071470	0.000147044	4	20	cellular response to osmotic stress	ENSACAG00000017928,RELB,OXSR1,XRCC5
GO:0035795	0.000274784	2	2	negative regulation of mitochondrial membrane permeability	ACAA2,HK2
GO:1904430	0.00029842	2	2	negative regulation of t-circle formation	TERF2,XRCC5
GO:0006081	0.001064851	5	55	cellular aldehyde metabolic process	G6PD,TKT,GPI,DLAT,GRHPR
GO:0006957	0.001105394	3	14	complement activation, alternative pathway	C8A,CFP,ENSACAG00000011208
GO:0038026	0.001209879	2	3	reelin-mediated signaling pathway	RELN,VLDLR
GO:0046184	0.001257641	2	4	aldehyde biosynthetic process	TKT,GPI
GO:0001945	0.001288649	2	4	lymph vessel development	EFNB2,SYK
GO:0006006	0.001696709	6	84	glucose metabolic process	G6PD,GPI,DLAT,ENSACAG00000003255,HK2, BRAT1
GO:0060236	0.001864445	3	16	regulation of mitotic spindle organization	TPX2,CHMP5,ANKRD53
GO:0033555	0.002850564	4	43	multicellular organismal response to stress	PRKCG,NEUROD2,RELN,EIF4G1
GO:0050999	0.003771516	3	22	regulation of nitric-oxide synthase activity	NOSIP,DDAH2,TERF2
GO:0006970	0.004009937	4	45	response to osmotic stress	ENSACAG00000017928,RELB,OXSR1,XRCC5
GO:0031175	0.0043879	7	137	neuron projection development	EFHD1,AREG,PTPRF,RELN,CDK16,HERC1,PLP1
GO:1902857	0.004948652	2	7	positive regulation of nonmotile primary cilium assembly	SEPT12,CENPJ
GO:0042129	0.006033309	5	85	regulation of T cell proliferation	FADD,PAWR,SYK,DNAJA3,CD276
GO:0045087	0.00606838	11	316	innate immune response	FADD,C8A,SERINC3,ENSACAG00000017928, ENSACAG00000021135,SYK,CFP,TOLLIP,RELB,ENSACAG00000011208,ENSACAG00000007262
GO:0006090	0.007123617	4	50	pyruvate metabolic process	GPI,DLAT,ENSACAG00000003255,HK2
GO:0097049	0.007383836	1	1	motor neuron apoptotic process	FADD
GO:2000454	0.007383836	1	1	positive regulation of CD8-positive, alpha-beta	FADD

				cytotoxic T cell extravasation	
GO:0021517	0.008225599	2	8	ventral spinal cord development	RELN,VLDLR
GO:0046034	0.008958334	4	63	ATP metabolic process	ATP6V0A1,HSPA5,AK2,ENSACAG00000021101
GO:0035562	0.00921317	2	9	negative regulation of chromatin binding	FBXO18,BTAF1
GO:0060598	0.009435699	1	1	dichotomous subdivision of terminal units involved in mammary gland duct morphogenesis	AREG
GO:0032787	0.009538867	13	417	monocarboxylic acid metabolic process	ACAA2,SLC27A6,ACOX1,ENSACAG00000004847,GPI,DLAT,ENSACAG00000003255,PLP1,IDUA,GRHPR,NPC1,ACAD8,HK2
GO:0048265	0.010396075	2	11	response to pain	PRKCG,RELN
GO:0046487	0.010592178	2	11	glyoxylate metabolic process	DLAT,GRHPR
GO:0033869	0.011169222	1	1	nucleoside bisphosphate catabolic process	NUDT7
GO:0034034	0.011169222	1	1	purine nucleoside bisphosphate catabolic process	NUDT7
GO:0046356	0.011169222	1	1	acetyl-CoA catabolic process	NUDT7
GO:0021680	0.011623862	2	11	cerebellar Purkinje cell layer development	MYH10,HSPA5
GO:0072027	0.011896872	1	1	connecting tubule development	CALB1
GO:0072286	0.011896872	1	1	metanephric connecting tubule development	CALB1
GO:0006480	0.012660835	1	1	N-terminal protein amino acid methylation	METTL11B
GO:0006924	0.013094653	1	1	activation-induced cell death of T cells	DNAJA3
GO:0072755	0.013281179	1	1	cellular response to benomyl	IMPACT
GO:1901561	0.013281179	1	1	response to benomyl	IMPACT
GO:1903849	0.013859234	1	1	positive regulation of aorta morphogenesis	EFNB2
GO:0035786	0.014007207	1	1	protein complex oligomerization	MCU
GO:0010035	0.014271971	10	299	response to inorganic substance	AREG,AHCYL1,NEUROD2,SYK,KCNC1,COL18A1,GPI,ENSACAG00000017266,IMPACT,NPC1
GO:0048857	0.014548543	3	37	neural nucleus development	KCNC1,HSPA5,PLP1
GO:0061620	0.014932553	2	12	glycolytic process through glucose-6-phosphate	GPI,HK2
GO:0051346	0.015290738	7	179	negative regulation of hydrolase activity	SPOCK2,ENSACAG00000017928,SPRED1,GPI,

					TERF2,FICD,TMED2
GO:0061300	0.015404067	1	2	cerebellum vasculature development	ENSACAG00000005218
GO:0001680	0.015516298	1	1	tRNA 3'-terminal CCA addition	TRNT1
GO:0051156	0.015814385	2	14	glucose 6-phosphate metabolic process	G6PD,GPI
GO:0018117	0.015841793	1	1	protein adenylylation	FICD
GO:0018175	0.015841793	1	1	protein nucleotidylation	FICD
GO:0070613	0.016499143	7	185	regulation of protein processing	N4BP1,PRKCG,C8A,SPOCK2,ENSACAG00000017928,ENSACAG00000011208,GPI
GO:0019242	0.01673979	1	1	methylglyoxal biosynthetic process	GPI
GO:0006099	0.016983803	3	36	tricarboxylic acid cycle	MDH2,ENSACAG00000015409,DLAT
GO:0001820	0.017145152	1	1	serotonin secretion	SYK
GO:0071226	0.017145152	1	1	cellular response to molecule of fungal origin	SYK
GO:0030209	0.017226685	1	1	dermatan sulfate catabolic process	IDUA
GO:0032799	0.017277767	1	1	low-density lipoprotein receptor particle metabolic process	PCSK9
GO:2000646	0.017277767	1	1	positive regulation of receptor catabolic process	PCSK9
GO:1903770	0.017288441	1	1	negative regulation of beta-galactosidase activity	TERF2
GO:0034447	0.017346009	1	1	very-low-density lipoprotein particle clearance	VLDLR
GO:0035037	0.017346009	1	1	sperm entry	UBE3A
GO:1902396	0.017346009	1	1	protein localization to bicellular tight junction	ACTN4
GO:1904925	0.017346009	1	1	positive regulation of mitophagy in response to mitochondrial depolarization	HK2
GO:0030954	0.017347767	1	1	astral microtubule nucleation	CENPJ
GO:0051300	0.017347767	1	1	spindle pole body organization	CENPJ
GO:1903320	0.019252433	7	192	regulation of protein modification by small protein conjugation or removal	N4BP1,PRKCG,UBE2L3,UBE3A,TOLLIP,UBXN2A,HSPA5
GO:0043278	0.019642871	2	16	response to morphine	PRKCG,GPI
GO:0045948	0.020702823	2	15	positive regulation of translational initiation	ENSACAG00000017928,IMPACT
GO:0032886	0.021115779	6	144	regulation of microtubule-based process	TPX2,CHMP5,MID1IP1,CENPJ,ANKRD53,INPP5J
GO:2000452	0.021183419	1	2	regulation of CD8-positive, alpha-beta cytotoxic	FADD

				T cell extravasation	
GO:0018107	0.021340109	3	38	peptidyl-threonine phosphorylation	PKN1,ENSACAG00000014806,OXSR1
GO:0090129	0.021361991	2	14	positive regulation of synapse maturation	NEUROD2,RELN
GO:2000451	0.021370434	1	2	positive regulation of CD8-positive, alpha-beta T cell extravasation	FADD
GO:0051341	0.021526069	3	42	regulation of oxidoreductase activity	NOSIP,DDAH2,TERF2
GO:0006891	0.021756999	3	42	intra-Golgi vesicle-mediated transport	COPB2,ENSACAG00000017858,PACS1
GO:0007613	0.021814209	4	70	memory	RELN,VLDLR,ENSACAG00000016987,CALB1
GO:0042986	0.022103676	1	2	positive regulation of amyloid precursor protein biosynthetic process	PAWR
GO:0072376	0.022507535	4	94	protein activation cascade	C8A,CFP,ENSACAG00000011208,ENSACAG00000007262
GO:0035561	0.022567455	2	15	regulation of chromatin binding	FBXO18,BTAF1
GO:0042094	0.022698409	1	2	interleukin-2 biosynthetic process	PAWR
GO:0072350	0.022884787	3	40	tricarboxylic acid metabolic process	MDH2,ENSACAG00000015409,DLAT
GO:0001912	0.023026387	2	17	positive regulation of leukocyte mediated cytotoxicity	FADD,CADM1
GO:0097327	0.023105093	1	2	response to antineoplastic agent	PTGR1
GO:0010447	0.023203718	2	16	response to acidic pH	ENSACAG00000016987,IMPACT
GO:0006413	0.023229974	4	86	translational initiation	EIF2B3,MRPL19,EIF4G1,EIF2D
GO:0031330	0.024274741	5	110	negative regulation of cellular catabolic process	N4BP1,PRKCG,TOB1,HERC1,NPC1
GO:0033539	0.024678395	2	16	fatty acid beta-oxidation using acyl-CoA dehydrogenase	ACOX1,ACAD8
GO:0006391	0.025416402	1	2	transcription initiation from mitochondrial promoter	TFAM
GO:1902078	0.026050719	1	1	positive regulation of lateral motor column neuron migration	RELN
GO:0006414	0.026210392	3	58	translational elongation	GTPBP1,RPLP2,MRPL19
GO:2000483	0.026399167	1	2	negative regulation of interleukin-8 secretion	ANXA4
GO:0015672	0.02708898	9	293	monovalent inorganic cation transport	ATP6V0A1,ENSACAG00000017858,SYK,ENSACAG00000016987,COMMD9,KCNC1,SLC17A7,ENSACAG00000021101,COMMD3

GO:0006814	0.027147063	5	108	sodium ion transport	ENSACAG00000017858,ENSACAG00000016987,COMMD9,SLC17A7,COMMD3
GO:0007512	0.027964815	2	11	adult heart development	MYH10,ENSACAG00000017266
GO:0046166	0.028448545	1	2	glyceraldehyde-3-phosphate biosynthetic process	TKT
GO:0021762	0.028619536	2	20	substantia nigra development	HSPA5,PLP1
GO:0071649	0.028887326	1	2	regulation of chemokine (C-C motif) ligand 5 production	ENSACAG00000017928
GO:0031581	0.030174085	2	11	hemidesmosome assembly	ENSACAG00000005967,LAMA3
GO:0018210	0.030232141	3	43	peptidyl-threonine modification	PKN1,ENSACAG00000014806,OXSR1
GO:0071494	0.030330313	1	2	cellular response to UV-C	IMPACT
GO:0006084	0.030457606	2	18	acetyl-CoA metabolic process	NUDT7,DLAT
GO:1900152	0.030514019	1	2	negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	TOB1
GO:0031123	0.031572269	4	81	RNA 3'-end processing	AHCYL1,CSTF3,TRNT1,EIF4G1
GO:0045113	0.032044776	1	3	regulation of integrin biosynthetic process	TMEFF2
GO:0046686	0.032379888	2	19	response to cadmium ion	GPI,NPC1
GO:1902412	0.03258221	1	2	regulation of mitotic cytokinesis	ANKRD53
GO:0001682	0.033462908	1	2	tRNA 5'-leader removal	ENSACAG00000001929
GO:0071600	0.033857467	1	2	otic vesicle morphogenesis	SHARPIN
GO:1902903	0.034061414	1	2	regulation of fibril organization	HSPA5
GO:0070207	0.034157869	2	20	protein homotrimerization	ENSACAG00000016987,HSF1
GO:0071873	0.034394106	1	2	response to norepinephrine	COL1A2
GO:2000449	0.034976281	1	3	regulation of CD8-positive, alpha-beta T cell extravasation	FADD
GO:0003351	0.035499433	2	18	epithelial cilium movement	CCDC39,DNAI1
GO:0006658	0.035829569	2	20	phosphatidylserine metabolic process	SERINC3,PTDSS1
GO:0006091	0.035992015	6	179	generation of precursor metabolites and energy	ENSACAG00000005218,NDUFB3,ACOX1,GPI,ENSACAG00000003255,HK2
GO:0015985	0.036334539	2	26	energy coupled proton transport, down electrochemical gradient	ATP6V0A1,ENSACAG00000021101

GO:0055003	0.037311755	2	14	cardiac myofibril assembly	MYH10,ENSACAG00000017266
GO:1903445	0.038832855	1	3	protein transport from ciliary membrane to plasma membrane	RILPL2
GO:0051452	0.038881033	2	25	intracellular pH reduction	ATP6V0A1,ENSACAG00000013950
GO:0051258	0.039002358	3	56	protein polymerization	MID1IP1,FGB,CENPJ
GO:0080135	0.039499082	12	463	regulation of cellular response to stress	FBXO18,PTPRF,PDCD4,PAWR,NUP50,SERINC3,SPRED1,TERF2,ENSACAG00000004565,IMPACT,NPC1,CAPN1
GO:0042149	0.039651164	2	21	cellular response to glucose starvation	HSPA5,IMPACT
GO:1901033	0.039701641	1	3	positive regulation of response to reactive oxygen species	PAWR
GO:0009132	0.039723333	2	24	nucleoside diphosphate metabolic process	NUDT7,AK2
GO:0072429	0.040243661	1	3	response to intra-S DNA damage checkpoint signaling	FBXO18
GO:0070681	0.040883428	1	3	glutaminyl-tRNAGln biosynthesis via transamidation	GATB
GO:0022411	0.042246886	6	175	cellular component disassembly	NUP50,CASP6,ICT1,LAMA3,EIF2D,CAPN1
GO:0006574	0.042399324	1	3	valine catabolic process	ACAD8
GO:0007080	0.042727231	2	23	mitotic metaphase plate congression	CHMP5,ANKRD53
GO:0009826	0.043786731	1	3	unidimensional cell growth	CADM1
GO:0034436	0.044025394	1	3	glycoprotein transport	VLDLR
GO:0034508	0.044420402	1	3	centromere complex assembly	CENPN
GO:0030538	0.044739211	1	4	embryonic genitalia morphogenesis	ROR2
GO:0090342	0.045077091	2	26	regulation of cell aging	PAWR,TERF2
GO:0030198	0.045772926	7	210	extracellular matrix organization	COL1A2,SPOCK2,ABI3BP,COL18A1,LAMA3,SPINT1,CAPN1
GO:0060670	0.045838069	1	4	branching involved in labyrinthine layer morphogenesis	SPINT1
GO:0046395	0.045874003	6	172	carboxylic acid catabolic process	ACAA2,ACOX1,ENSACAG00000004847,DDAH2,IDUA,ACAD8
GO:0030162	0.04646724	10	384	regulation of proteolysis	N4BP1,PRKCG,FADD,SPOCK2,UBE3A,ENSACAG00000017928,ENSACAG00000015126,ENS

					ACAG00000029485,GPI,ENSACAG00000014806
GO:0032200	0.046917447	3	52	telomere organization	TERF2,POLA2,XRCC5
GO:0033387	0.047045378	1	3	putrescine biosynthetic process from ornithine	ODC1
GO:0034334	0.047327023	1	3	adherens junction maintenance	RASSF8
GO:0043062	0.047338548	7	212	extracellular structure organization	COL1A2,SPOCK2,ABI3BP,COL18A1,LAMA3,SPINT1,CAPN1
GO:0034620	0.048675433	1	4	cellular response to unfolded protein	PACRG
GO:2000189	0.048956469	1	3	positive regulation of cholesterol homeostasis	NPC1
GO:0097475	0.048990869	1	3	motor neuron migration	RELN
GO:0060546	0.049267568	1	4	negative regulation of necroptotic process	FADD

Additional data table S1 (separate file)

Dataset S1