	Supplementary	table 6:	GO results of o	overlapping gen	es		
	Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	URL	Genes
r - genes shared by at least two species within each dataset (n = 93)	1.5E-32	27	178	38.56	GO:0002181 cytoplasmic translation	http://amigo.gen	RPL31,RPL6,RI
	9.8E-18	29	784	9.40	GO:0006412 translation	http://amigo.gen	RPL31,RPL6,EI
	1.8E-17	29	814	9.06	GO:0043043 peptide biosynthetic proc.	http://amigo.gen	RPL31,RPL6,EI
	3.1E-16	30	999	7.63	GO:0006518 peptide metabolic proc.	http://amigo.gen	RPL31,RPL6,EI
	9.3E-16	29	959	7.69	GO:0043604 amide biosynthetic proc.	http://amigo.gen	RPL31,RPL6,EI
	1.2E-13	30	1259	6.06	GO:0034645 cellular macromolecule biosynthetic proc.	http://amigo.gen	RPL31,RPL6,EI
	2.4E-13	30	1301	5.86	GO:0043603 cellular amide metabolic proc.	http://amigo.gen	RPL31,RPL6,E
	2.2E-12	34	1888	4.58	GO:1901566 organonitrogen compound biosynthetic proc.	http://amigo.gen	RPL31,RPL6,EI
	1.6E-04	12	509	5.99	GO:0022613 ribonucleoprotein complex biogenesis	http://amigo.gen	CELF2,RPL6,R
	7.2E-04	5	63	20.18	GO:0042255 ribosome assembly	http://amigo.gen	RPL6,RPS19,R
	7.2E-04	8	240	8.47	GO:0022618 ribonucleoprotein complex assembly	http://amigo.gen	CELF2,RPL6,R
	7.8E-04	9	327	7.00	GO:0042254 ribosome biogenesis	http://amigo.gen	RPL6,RPS19,R
	7.9E-04	8	248	8.20	GO:0071826 ribonucleoprotein complex subunit organization	http://amigo.gen	CELF2,RPL6,R
BP:G0	9.6E-04	5	70	18.16	GO:0030865 cortical cytoskeleton organization	http://amigo.gen	RAC2,FHOD1,I
ВР	1.7E-03	5	79	16.09	GO:0042273 ribosomal large subunit biogenesis	http://amigo.gen	RPL6,RPL5,RP
- human-specific genes discovered in at least two, datasets (n = 198)	4.0E-08	39	1757	3.34	GO:0022008 neurogenesis	http://amigo.gen	ACTB,MET,UNG
	1.1E-07	35	1522	3.46	GO:0048699 generation of neurons	http://amigo.gen	ACTB,MET,UN
	2.8E-07	33	1449	3.43	GO:0030182 neuron differentiation	http://amigo.gen	ACTB,MET,UN
	2.8E-07	46	2618	2.64	GO:0007399 nervous system development	http://amigo.gen	ACTB,CALM3,A
	1.2E-05	34	1806	2.83	GO:0048870 cell motility	http://amigo.gen	CD99,ACTB,MI
	1.2E-05	34	1806	2.83	GO:0051674 localization of cell	http://amigo.gen	CD99,ACTB,ME
	1.9E-05	45	2945	2.30	GO:0032879 reg. of localization	http://amigo.gen	CD99,SYT17,R
	2.1E-05	27	1271	3.20	GO:0060429 epithelium development	http://amigo.gen	DLX3,MYO6,V0
	2.1E-05	31	1602	2.91	GO:0016477 cell migration	http://amigo.gen	CD99,MET,SEN
	2.1E-05	35	1992	2.64	GO:0040011 locomotion	http://amigo.gen	CD99,ACTB,ME
	2.1E-05	38	2254	2.54	GO:0006928 movement of cell or subcellular component	http://amigo.gen	CD99,ACTB,DY
	2.1E-05	52	3774	2.07	GO:0048513 animal organ development	http://amigo.gen	ACTB,CALM3,
	2.3E-05	59	4617	1.92	GO:0048731 system development	http://amigo.gen	ACTB,CALM3,A
E II	3.6E-05	43	2867	2.26	GO:0009653 anatomical structure morphogenesis	http://amigo.gen	ACTB,CAPZB,L
BP:GO - h	7.8E-05	57	4552	1.88	GO:0030154 cell differentiation	http://amigo.gen	RRAS2,DLX3,A
	8.7E-05	57	4576	1.88	GO:0048869 cellular developmental proc.	http://amigo.gen	RRAS2,DLX3,A
	9.5E-05	19	745	3.84	GO:0051129 negative reg. of cellular component organization	http://amigo.gen	ZNF207,CAPZE
	9.5E-05	22	977	3.39	GO:0030334 reg. of cell migration	http://amigo.gen	CD99,SEMA3E