Gene_id	readcount_DeltaTgPiT	readcount_Parental	logFC	pval	padj	Annotation Blast swiss prot
TGGT1_216290A-t26_1	336.3203738	0.972197767	8.4344	3.76E-56	5.27E-53	-//-
TGGT1_216290B-t26_1	616.7199557	6.840451961	6.4944	1.14E-80	4.78E-77	-//-
TGGT1_216335-t26_1	3376.925715	49.15317091	6.1023	6.36E-96	5.34E-92	-//-
TGGT1_221840-t26_1	45.13253831	1.046650121	5.4303	0.0004472	0.018602	-//-
TGGT1_221310-t26_1	852.0608753	27.13845078	4.9725	4.01E-80	1.12E-76	sp|Q8H059|PSA_ARATH Puromycin-sensitive aminopeptidase OS=Arabidopsis thaliana GN=MPA1 PE=2 SV=1//0
TGGT1_243720-t26_1	43.08944634	1.45829665	4.885	3.10E-07	3.35E-05	sp|Q54H86|PEX11_DICDI Peroxisomal membrane protein 11 homolog OS=Dictyostelium discoideum GN=pex11 PE=3 SV=1//4.36269e-26
TGGT1_237585-t26_1	19.18173244	1.046650121	4.1959	0.0013243	0.031256	-//-
TGGT1_233153-t26_1	68.03330962	3.774953953	4.1717	0.0006212	0.018314	-//-
TGGT1_245530-t26_1	759.2211462	47.36199725	4.0027	2.69E-51	2.83E-48	-//-
TGGT1_257720-t26_1	66.99716024	4.186600483	4.0002	5.44E-09	9.32E-07	sp|Q9XIE6|ALA3_ARATH Phospholipid-transporting ATPase 3 OS=Arabidopsis thaliana GN=ALA3 PE=1 SV=2//4.2699e-16
TGGT1_305100-t26_1	22.55596087	1.45829665	3.9512	0.0011512	0.028616	-//-
TGGT1_304920-t26_1	40.07720883	2.728303832	3.8767	0.000438	0.013835	-//-
TGGT1_215900-t26_1	35.68572953	2.504946771	3.8325	3.94E-05	0.0020678	-//-
TGGT1_220560-t26_1	37.38401105	2.728303832	3.7763	0.0012584	0.030295	-//-
TGGT1_280570-t26_1	440.518231	34.75849388	3.6638	0.0003487	0.011444	-//-
TGGT1_204300-t26_1	25.92331711	2.093300241	3.6304	0.0006852	0.019783	-//-
TGGT1_223258-t26_1	51.52759448	4.186600483	3.6215	0.0004962	0.01527	-//-
TGGT1_239365-t26_1	32.9976859	2.728303832	3.5963	0.0001277	0.0052355	-//-
TGGT1_203135-t26_1	36.36332409	3.065498008	3.5683	7.53E-05	0.0034879	sp|Q39565|DYHB_CHLRE Dynein beta chain, flagellar outer arm OS=Chlamydomonas reinhardtii GN=ODA4 PE=3 SV=1//0
TGGT1_295995-t26_1	46.45164844	4.037695775	3.5241	5.17E-06	0.000402	-//-
TGGT1_293790-t26_1	186.5374478	16.3347554	3.5134	1.62E-14	5.93E-12	-//-
TGGT1_280500-t26_1	36.7029804	3.214402716	3.5133	7.49E-05	0.0034879	sp|P55189|YBAR_BACSU Putative sulfate transporter YbaR OS=Bacillus subtilis (strain 168) GN=ybaR PE=3 SV=2//1.36417e-25
TGGT1_268800-t26_1	94.915464	8.561490433	3.4707	1.10E-10	2.58E-08	-//-
TGGT1_248430-t26_1	54.19845765	5.307702957	3.3521	1.51E-06	0.0001361	-//-
TGGT1_210478-t26_1	56.88478323	5.644897133	3.333	8.78E-07	8.38E-05	-//-
TGGT1_219610-t26_1	34.67363281	3.477144538	3.3179	0.0001903	0.0070125	-//-
TGGT1_284615-t26_1	24.57328213	2.653851479	3.2109	0.0017551	0.038806	-//-
TGGT1_256700-t26_1	28.62338707	3.139950362	3.1884	0.0012446	0.030112	-//-
TGGT1_252640-t26_1	328.515151	37.1539207	3.1444	4.09E-16	2.02E-13	sp|Q58623|Y1226_METJA Putative cation-transporting ATPase MJ1226 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) GN=MJ1226 PE=3 SV=1//6.9619e-126
TGGT1_225290-t26_1	229.587379	26.57358238	3.111	2.03E-19	1.22E-16	sp|Q27893|NTP1_TOXGO Nucleoside-triphosphatase 1 OS=Toxoplasma gondii GN=NTP3 PE=1 SV=1//1.08395e-142
TGGT1_268970-t26_1	70.03516846	8.522105673	3.0388	4.96E-07	5.03E-05	-//-
TGGT1_233610-t26_1	48.1585202	5.868254194	3.0368	0.0008225	0.022221	-//-
TGGT1_207210-t26_1	104.0294887	12.78315851	3.0247	8.28E-10	1.58E-07	-//-
TGGT1_208020-t26_1	175.4267184	22.01903729	2.994	2.35E-11	6.32E-09	-//-
TGGT1_295945-t26_1	69.02822588	8.859299848	2.9619	1.28E-06	0.0001185	-//-
TGGT1_216140-t26_1	1482.689559	192.3036117	2.9468	1.16E-51	1.39E-48	sp|Q01484|ANK2_HUMAN Ankyrin-2 OS=Homo sapiens GN=ANK2 PE=1 SV=4//1.72523e-07
TGGT1_207130-t26_1	105.0518937	13.79474104	2.9289	4.53E-09	7.94E-07	-//-
TGGT1_235950-t26_1	36.35129776	4.821604074	2.9144	0.0002369	0.008491	sp|Q45670|THES_BACSJ Thermophilic serine proteinase OS=Bacillus sp. (strain AK1) PE=1 SV=1//5.91753e-30
TGGT1_202020-t26_1	484.5922853	64.66031609	2.9058	8.43E-05	0.0037676	sp|Q9TRY0|FKBP4_BOVIN Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Bos taurus GN=FKBP4 PE=1 SV=4//1.36915e-06
TGGT1_274170-t26_1	42.76525246	5.719349487	2.9025	0.0001812	0.0067355	-//-
TGGT1_280580-t26_1	367.4347461	49.1882385	2.9011	0.0022883	0.045303	-//-
TGGT1_219218-t26_1	120.5214594	16.63256482	2.8572	1.83E-10	3.88E-08	-//-
TGGT1_220025-t26_1	58.92272106	8.224296257	2.8409	1.27E-05	0.0008321	-//-
TGGT1_223262-t26_1	123.9077142	17.49524264	2.8242	6.30E-10	1.23E-07	sp|Q8IWG1|WDR63_HUMAN WD repeat-containing protein 63 OS=Homo sapiens GN=WDR63 PE=2 SV=1//1.81223e-47
TGGT1_207160-t26_1	186.1273516	26.57358238	2.8082	2.71E-08	3.92E-06	-//-
TGGT1_248425-t26_1	66.31956568	9.608140554	2.7871	3.76E-06	0.0003101	-//-
TGGT1_240200-t26_1	77.11640943	11.54821892	2.7394	0.0003527	0.011529	-//-
TGGT1_268860-t26_1	106.3967745	16.03694599	2.73	1.56E-08	2.47E-06	sp|Q9UAE6|ENO1_TOXGO Enolase 1 OS=Toxoplasma gondii GN=ENO1 PE=1 SV=1//0
TGGT1_262970-t26_1	2103.927612	317.3410749	2.729	2.43E-56	4.08E-53	-//-
TGGT1_305280-t26_1	48.48958626	7.326550844	2.7265	0.0001275	0.0052355	-//-
TGGT1_253760-t26_1	89.89105937	13.79474104	2.7041	1.82E-07	2.18E-05	-//-
TGGT1_222340-t26_1	30.98036464	4.896056428	2.6617	0.0024226	0.0469	sp|Q0V8R7|NSUN4_BOVIN 5-methylcytosine rRNA methyltransferase NSUN4 OS=Bos taurus GN=NSUN4 PE=2 SV=2//3.23866e-19
TGGT1_313050-t26_1	59.60718781	9.419851086	2.6617	0.0007467	0.020865	sp|Q9Y14D|DHRS7_DROME Dehydrogenase/reductase SDR family protein 7-like OS=Drosophila melanogaster GN=CG7601 PE=2 SV=1//2.64291e-15
TGGT1_312435-t26_1	41.07040703	6.542642546	2.6502	0.0004367	0.013835	-//-
TGGT1_243470-t26_1	50.50690753	8.224296257	2.6185	0.0001444	0.0056681	-//-
TGGT1_232420-t26_1	53.19323311	8.710395141	2.6104	7.53E-05	0.0034879	-//-
TGGT1_245770B-t26_1	48.82924257	8.224296257	2.5698	0.0003992	0.012851	-//-
TGGT1_204290-t26_1	33.66669023	5.719349487	2.5574	0.0018417	0.039787	-//-
TGGT1_224170-t26_1	92.24975498	15.7348194	2.5516	2.05E-07	2.33E-05	-//-
TGGT1_291040-t26_1	47.13611519	8.149843903	2.532	0.0003102	0.010384	sp|Q27797|LDH_TOXGO L-lactate dehydrogenase OS=Toxoplasma gondii PE=1 SV=1//0
TGGT1_238915-t26_1	28.2699864	4.896056428	2.5296	0.0026106	0.049514	-//-
TGGT1_207150-t26_1	217.1180245	38.45899548	2.4971	2.02E-14	7.06E-12	-//-
TGGT1_316635-t26_1	125.9301896	22.76356083	2.4678	1.13E-08	1.83E-06	-//-
TGGT1_203800-t26_1	33.99260215	6.20544837	2.4536	0.0015731	0.035339	-//-
TGGT1_290970-t26_1	2576.477666	477.1197634	2.433	8.00E-38	6.72E-35	sp|B0K590|BIOF_THEPX 8-amino-7-oxononanoate synthase OS=Thermoanaerobacter sp. (strain X514) GN=Teth514_0779 PE=3 SV=1//2.62341e-60
TGGT1_245980-t26_1	391.7245504	72.78372673	2.4282	0.0004915	0.015239	-//-
TGGT1_365480-t26_1	171.9683057	32.40676898	2.4078	0.0005834	0.017444	-//-
TGGT1_293780-t26_1	1252.091801	238.5666226	2.3919	1.80E-15	7.97E-13	-//-
TGGT1_290645-t26_1	39.05823991	7.475455552	2.3854	0.0014494	0.033734	-//-
TGGT1_245770A-t26_1	258.9192855	50.64653515	2.354	3.34E-12	9.68E-10	-//-
TGGT1_250000-t26_1	75.40266549	14.84139116	2.345	9.65E-06	0.0006759	-//-
TGGT1_232170-t26_1	37.36511254	7.401003198	2.3359	0.0015425	0.035027	sp|O28078|Y2205_ARCFU Uncharacterized protein AF_2205 OS=Archaeoglobus fulgidus (strain ATCC 49558 / VC-16 / DSM 4304 / JCM 9628 / NBRC 100126) GN=AF_2205 PE=4 SV=1//1.3111e-56
TGGT1_227630-t26_1	871.105164	173.0430984	2.3317	2.94E-12	8.81E-10	-//-
TGGT1_238440-t26_1	79.11826827	15.73913657	2.3297	1.16E-05	0.0007742	-//-
TGGT1_286460-t26_1	161.9143423	32.37601855	2.3222	6.10E-10	1.22E-07	-//-
TGGT1_285445-t26_1	60.92286185	12.18753968	2.3216	6.53E-05	0.0030991	-//-
TGGT1_236880-t26_1	58.555576	11.77589315	2.314	0.002026	0.042134	-//-
TGGT1_462970-t26_1	36.35301581	7.326550844	2.3109	0.0018762	0.039909	-//-
TGGT1_304930-t26_1	202.7086608	41.00764417	2.3054	1.64E-06	0.0001453	-//-
TGGT1_265320-t26_1	114.1229671	23.5517863	2.2767	2.03E-07	2.33E-05	sp|Q54PH5|CWC2_DICDI Pre-mRNA-splicing factor cwc2 OS=Dictyostelium discoideum GN=cwc2 PE=3 SV=1//2.29242e-47
TGGT1_202430-t26_1	329.5976876	68.1067102	2.2748	4.50E-16	2.10E-13	-//-
TGGT1_265255-t26_1	58.24856259	12.22260727	2.2527	0.0001825	0.006756	-//-
TGGT1_295720-t26_1	95.63257364	20.37245118	2.2309	3.66E-05	0.0019574	sp|Q9VWP4|SUOX_DROME Probable sulfite oxidase, mitochondrial OS=Drosophila melanogaster GN=CG7280 PE=2 SV=1//1.15456e-98
TGGT1_316560-t26_1	93.25669756	20.07464176	2.2158	4.01E-06	0.0003239	-//-
TGGT1_215955-t26_1	45.78264412	9.905949969	2.2084	0.0008773	0.023436	-//-
TGGT1_219450-t26_1	106.3658497	23.02630265	2.2077	3.88E-07	4.12E-05	sp|Q00664|LIS1_EMENI Nuclear distribution protein nudF OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) GN=nudF PE=1 SV=1//8.45696e-14
TGGT1_212275-t26_1	147.4259484	32.03882438	2.2021	5.85E-08	7.80E-06	-//-
TGGT1_411080-t26_1	317.7200253	69.22781267	2.1983	3.09E-06	0.00026	-//-
TGGT1_213700-t26_1	89.89449546	19.62361047	2.1956	5.51E-06	0.0004206	-//-
TGGT1_295960-t26_1	1315.41631	289.532553	2.1837	1.13E-19	7.27E-17	-//-
TGGT1_259020-t26_1	113.790183	25.1196029	2.1795	4.18E-07	4.39E-05	sp|Q84Q77|HS17A_ORYSJ 17.9 kDa class I heat shock protein OS=Oryza sativa subsp. japonica GN=HSP17.9A PE=2 SV=1//8.60982e-17
TGGT1_264150-t26_1	106.0347836	24.03788518	2.1412	1.21E-06	0.0001129	-//-
TGGT1_268985-t26_1	74.39056877	16.96975899	2.1322	2.62E-05	0.0014928	-//-
TGGT1_256800-t26_1	43.09975462	9.905949969	2.1213	0.0025705	0.048973	-//-
TGGT1_305610-t26_1	244.1066978	56.18622951	2.1192	2.41E-11	6.32E-09	-//-
TGGT1_209755A-t26_1	93.58776363	21.63814119	2.1127	1.93E-05	0.0011912	-//-
TGGT1_209755B-t26_1	156.5434092	37.937829	2.0449	1.68E-08	2.60E-06	sp|Q27409|FP1_MYTGA Adhesive plaque matrix protein OS=Mytilus galloprovincialis GN=FP1 PE=2 SV=1//2.72008e-06
TGGT1_295020-t26_1	120.8679879	29.41572333	2.0388	7.07E-07	6.91E-05	sp|Q0EEE2|PTHD3_MOUSE Patched domain-containing protein 3 OS=Mus musculus GN=Ptchd3 PE=1 SV=1//1.12177e-08
TGGT1_207470-t26_1	111.779734	27.28303832	2.0346	5.24E-06	0.0004039	-//-
TGGT1_293560-t26_1	68.33688694	16.70701717	2.0322	9.93E-05	0.0043017	-//-
TGGT1_269680-t26_1	53.18464288	13.01083274	2.0313	0.0008866	0.023575	sp|Q9V9A7|MCCB_DROME Probable methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Drosophila melanogaster GN=l(2)04524 PE=2 SV=1//0
TGGT1_208380-t26_1	160.2349593	39.36537522	2.0252	2.62E-08	3.87E-06	-//-
TGGT1_270670-t26_1	324.5698469	80.10596041	2.0185	3.62E-13	1.17E-10	-//-
TGGT1_295950-t26_1	2018.726973	500.1369015	2.0131	9.98E-25	6.99E-22	-//-
TGGT1_207350-t26_1	49.47934838	12.44596433	1.9911	0.0008185	0.022184	-//-
TGGT1_293480-t26_1	2781.526278	701.3300332	1.9877	7.79E-35	5.95E-32	sp|Q39054|CNX1_ARATH Molybdopterin biosynthesis protein CNX1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=2//3.64665e-10
TGGT1_364790-t26_1	43.0842922	10.87814774	1.9857	0.0024344	0.04702	-//-
TGGT1_268190-t26_1	48.47927798	12.26199203	1.9832	0.0020538	0.042502	-//-
TGGT1_269075-t26_1	104.7191095	26.91077655	1.9603	8.33E-05	0.0037434	-//-
TGGT1_301000-t26_1	75.76981055	19.47470576	1.96	0.0026463	0.049964	sp|Q9Y7J3|CARME_SCHPO Carnosine N-methyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC1778.07 PE=3 SV=1//1.29354e-43
TGGT1_267130-t26_1	158.5521402	41.15654888	1.9458	5.44E-08	7.50E-06	sp|P13664|P30_TOXGO Major surface antigen p30 OS=Toxoplasma gondii PE=1 SV=1//1.83234e-14
TGGT1_225105-t26_1	354.4212876	92.43808763	1.9389	4.97E-07	5.03E-05	-//-
TGGT1_270260-t26_1	253.4847847	66.20601659	1.9369	8.40E-11	2.14E-08	-//-
TGGT1_219110-t26_1	98.94151629	25.8684436	1.9354	0.0020457	0.042439	-//-
TGGT1_258910-t26_1	53.5139909	14.20638757	1.9134	0.0010147	0.02613	-//-
TGGT1_321490-t26_1	215.7353466	57.6051414	1.905	8.77E-05	0.0038697	sp|P13664|P30_TOXGO Major surface antigen p30 OS=Toxoplasma gondii PE=1 SV=1//4.85945e-17
TGGT1_252395-t26_1	81.13215344	21.7169107	1.9015	7.75E-05	0.0035385	-//-
TGGT1_205050-t26_1	91.88432797	25.1196029	1.871	2.05E-05	0.0012319	-//-
TGGT1_267875-t26_1	77.76823329	21.37971654	1.8629	0.0001356	0.0054356	sp|P0DL09|DRC1_CHLRE Dynein regulatory complex protein 1 OS=Chlamydomonas reinhardtii GN=DRC1 PE=1 SV=1//4.93913e-44
TGGT1_321480-t26_1	164.6607995	45.26869701	1.8629	8.78E-05	0.0038697	sp|P13664|P30_TOXGO Major surface antigen p30 OS=Toxoplasma gondii PE=1 SV=1//1.90152e-19
TGGT1_266035-t26_1	76.41476222	21.08622429	1.8576	0.0002431	0.008547	-//-
TGGT1_309030-t26_1	76.74926438	21.19574423	1.8564	0.0001623	0.0062279	-//-
TGGT1_208730-t26_1	6062.769763	1683.378082	1.8486	1.62E-14	5.93E-12	sp|O00834|MIC1_TOXGO Micronemal protein 1 OS=Toxoplasma gondii GN=MIC1 PE=1 SV=1//2.00961e-13
TGGT1_268220-t26_1	175.4146921	48.96919861	1.8408	1.39E-07	1.74E-05	-//-
TGGT1_288520-t26_1	104.3760172	29.30620338	1.8325	3.07E-05	0.0016629	sp|E1C6Q1|PCH2_CHICK Pachytene checkpoint protein 2 homolog OS=Gallus gallus GN=TRIP13 PE=3 SV=1//1.09615e-105
TGGT1_244590-t26_1	54.54498614	15.47639475	1.8174	0.0026235	0.049646	sp|Q9SEX2|KTNA1_ARATH Katanin p60 ATPase-containing subunit A1 OS=Arabidopsis thaliana GN=AAA1 PE=1 SV=1//1.99647e-105
TGGT1_200340-t26_1	114.8039978	32.7045784	1.8116	8.19E-06	0.0005935	-//-
TGGT1_233210-t26_1	74.72850702	21.34464894	1.8078	0.0002365	0.008491	-//-
TGGT1_409260-t26_1	366.0159892	105.1861785	1.799	2.15E-05	0.0012831	-//-
TGGT1_292935-t26_1	160.5986682	47.58967148	1.7547	1.44E-06	0.0001317	sp|Q8BI79|CCD40_MOUSE Coiled-coil domain-containing protein 40 OS=Mus musculus GN=Ccdc40 PE=1 SV=1//2.17375e-41
TGGT1_225070-t26_1	51.16044943	15.21365293	1.7497	0.0022481	0.045146	-//-
TGGT1_220420-t26_1	91.24109435	27.13845078	1.7493	0.0001468	0.0057379	sp|O60658|PDE8A_HUMAN High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A OS=Homo sapiens GN=PDE8A PE=1 SV=2//9.41128e-35
TGGT1_203720-t26_1	456.5107671	137.8600065	1.7274	2.73E-13	9.18E-11	-//-
TGGT1_297350-t26_1	103.6829602	31.51334073	1.7181	5.07E-05	0.00255	-//-
TGGT1_220460-t26_1	73.70610202	22.57958853	1.7068	0.0008176	0.022184	sp|Q54DB1|CM2A2_DICDI Charged multivesicular body protein 2a homolog 2 OS=Dictyostelium discoideum GN=chmp2a2 PE=3 SV=1//3.253e-15
TGGT1_228175-t26_1	114.1384296	35.10000522	1.7012	4.08E-05	0.0021144	-//-
TGGT1_201840-t26_1	1276.135241	393.8652183	1.696	0.0005179	0.015708	sp|Q9DEX3|CATD_CLUHA Cathepsin D OS=Clupea harengus GN=ctsd PE=1 SV=1//1.84555e-65
TGGT1_235650-t26_1	56.89165542	17.8675044	1.6709	0.0025279	0.048492	sp|Q75A82|ANT1_ASHGO Peroxisomal adenine nucleotide transporter 1 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) GN=ANT1 PE=3 SV=1//1.37012e-20
TGGT1_259270-t26_1	102.3535417	32.18772908	1.669	0.0001637	0.0062509	-//-
TGGT1_310160-t26_1	122.8715648	38.80050682	1.663	1.63E-05	0.00103	sp|Q8CJG1|AGO1_MOUSE Protein argonaute-1 OS=Mus musculus GN=Ago1 PE=1 SV=2//1.24542e-52

TGGT1_221220-t26_1	104.0346428	32.85780027	1.6628	0.0001086	0.004585	-//-	sp|Q3V0B4|CC108_MOUSE Coiled-coil domain-containing protein 108 OS=Mus musculus GN=Ccdc108 PE=1 SV=1//1.48037e-22
TGGT1_216710-t26_1	93.59119973	29.75723467	1.6531	0.000242	0.0085419	-//-	
TGGT1_285940-t26_1	68.32142452	22.09348965	1.6287	0.0009669	0.025152	-//-	sp|Q5W6B9|HAP2A_ORYSJ Protein HAPLESS 2-A OS=Oryza sativa subsp. japonica GN=HAP2A PE=2 SV=1//1.81477e-11
TGGT1_266670-t26_1	61.59358422	20.00018941	1.6228	0.0018489	0.039787	-//-	
TGGT1_281400-t26_1	766.2577179	248.9759401	1.6218	5.93E-13	1.85E-10	-//-	sp|Q8W4M5|PFPB1_ARATH Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 1 OS=Arabidopsis thaliana GN=PFP-BETA1 PE=1 SV=1//7.93018e-48
TGGT1_293258-t26_1	112.7901126	36.82104369	1.615	0.0001013	0.0043637	-//-	
TGGT1_293290-t26_1	202.6141682	66.28046894	1.6121	0.0002629	0.0091669	-//-	
TGGT1_218500-t26_1	105.0055064	34.35116451	1.612	0.0011238	0.028019	-//-	
TGGT1_257670-t26_1	106.7312767	35.69562405	1.5802	0.0001443	0.0056681	-//-	
TGGT1_264485-t26_1	384.7618547	130.9715355	1.5547	3.55E-09	6.48E-07	-//-	
TGGT1_213020-t26_1	734.8414864	250.2281484	1.5542	3.84E-15	1.61E-12	-//-	
TGGT1_312930-t26_1	170.0334507	58.05617268	1.5503	1.02E-05	0.0006898	-//-	sp|Q83A83|METC_COXBU Cystathionine beta-lyase OS=Coxiella burnetii (strain RSA 493 / Nine Mile phase I) GN=metC PE=1 SV=1//1.7987e-100
TGGT1_233920-t26_1	421.1354871	144.0740892	1.5475	9.27E-11	2.23E-08	-//-	sp|Q5NCP0|RNF43_MOUSE E3 ubiquitin-protein ligase RNF43 OS=Mus musculus GN=Rnf43 PE=2 SV=1//5.77659e-08
TGGT1_223480-t26_1	223.197477	76.55868068	1.5437	3.05E-07	3.35E-05	-//-	sp|Q9UPZ6|THS7A_HUMAN Thrombospondin type-1 domain-containing protein 7A OS=Homo sapiens GN=THSD7A PE=1 SV=4//1.60688e-14
TGGT1_227370-t26_1	115.8143765	39.73763699	1.5432	0.0001372	0.0054361	-//-	sp|P0A5F6|Y1866_MYCBO Putative serine esterase Mb1866c OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) GN=Mb1866c PE=3 SV=1//9.50486e-08
TGGT1_210400-t26_1	236.3135013	81.27076481	1.5399	1.43E-07	1.77E-05	-//-	
TGGT1_288640-t26_1	2346.647679	812.0467415	1.531	9.22E-06	0.0006597	-//-	sp|P73245|Y1917_SYNY3 Oxygen-independent coproporphyrinogen-III oxidase-like protein sll1917 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) GN=sll1917 PE=2 SV=1//4.43595e-19
TGGT1_269050-t26_1	471.7145526	163.7548834	1.5264	3.01E-06	0.0002551	-//-	sp|Q0ANS1|KAD_MARMM Adenylate kinase OS=Maricaulis maris (strain MCS10) GN=adk PE=3 SV=1//4.42818e-07
TGGT1_208740-t26_1	6201.903431	2153.627173	1.5259	4.43E-08	6.20E-06	-//-	sp|O00834|MIC1_TOXGO Micronemal protein 1 OS=Toxoplasma gondii GN=MIC1 PE=1 SV=1//8.77474e-09
TGGT1_253460-t26_1	154.529524	53.8695722	1.5203	2.04E-05	0.0012319	-//-	
TGGT1_215180-t26_1	60.91598966	21.27019659	1.518	0.0025813	0.049067	-//-	
TGGT1_228160-t26_1	145.0620987	51.06681602	1.5062	0.0008923	0.023651	-//-	sp|P29288|PPA5_RAT Tartrate-resistant acid phosphatase type 5 OS=Rattus norvegicus GN=Acp5 PE=1 SV=1//1.89029e-16
TGGT1_254430-t26_1	89.23236332	32.14834432	1.4728	0.0016962	0.037903	-//-	sp|P03951|FA11_HUMAN Coagulation factor XI OS=Homo sapiens GN=F11 PE=1 SV=1//7.80133e-09
TGGT1_293280-t26_1	2513.65343	908.2905335	1.4686	6.99E-07	6.91E-05	-//-	sp|O80513|CCU41_ARATH Cyclin-U4-1 OS=Arabidopsis thaliana GN=CYCU4-1 PE=1 SV=1//3.50618e-12
TGGT1_223725-t26_1	323.5800848	117.1066592	1.4663	0.0001665	0.0063019	-//-	
TGGT1_213255-t26_1	467.9422543	172.0579491	1.4434	1.45E-10	3.29E-08	-//-	
TGGT1_307590-t26_1	99.6465996	36.71152374	1.4406	0.0007179	0.020477	-//-	
TGGT1_281460-t26_1	124.887168	46.23657761	1.4335	8.33E-05	0.0037434	-//-	
TGGT1_310480-t26_1	228.3026298	84.55098554	1.4331	0.0021311	0.043274	-//-	sp|Q9DAK2|PACRG_MOUSE Parkin coregulated gene protein homolog OS=Mus musculus GN=Pacrg PE=1 SV=1//2.76461e-78
TGGT1_215970-t26_1	798.4317753	298.6454301	1.4187	1.69E-10	3.73E-08	-//-	
TGGT1_220585-t26_1	88.52556197	33.19499444	1.4151	0.0009357	0.024492	-//-	
TGGT1_287960-t26_1	221.2110806	83.43420024	1.4067	4.55E-06	0.0003603	-//-	
TGGT1_203290-t26_1	2497.79662	952.9555076	1.3902	2.31E-19	1.29E-16	-//-	
TGGT1_249840-t26_1	340.6998267	131.3259983	1.3753	7.96E-08	1.03E-05	-//-	sp|Q9P2D7|DYH1_HUMAN Dynein heavy chain 1, axonemal OS=Homo sapiens GN=DNAH1 PE=2 SV=4//0
TGGT1_294400-t26_1	392.4330699	154.2648971	1.347	0.0014892	0.03428	-//-	sp|B6KV60|RON2_TOXGO Rhoptry neck protein 2 OS=Toxoplasma gondii GN=TGME49_100100 PE=1 SV=2//5.00644e-32
TGGT1_253330-t26_1	697.3870354	275.628292	1.3392	0.0007119	0.020415	-//-	
TGGT1_205658-t26_1	82.12878774	32.78334792	1.3249	0.0022528	0.045146	-//-	sp|Q8CGD2|CRLD1_MOUSE Cysteine-rich secretory protein LCCL domain-containing 1 OS=Mus musculus GN=Crisperld1 PE=2 SV=1//3.46047e-07
TGGT1_294805-t26_1	87.85483959	35.21384233	1.319	0.0019923	0.041537	-//-	
TGGT1_206550-t26_1	391.1792455	156.8529306	1.3184	3.00E-08	4.27E-06	-//-	sp|Q4G0P3|HYDIN_HUMAN Hydrocephalus-inducing protein homolog OS=Homo sapiens GN=HYDIN PE=1 SV=3//7.6059e-34
TGGT1_319520-t26_1	310.0934793	125.3352727	1.3069	7.88E-07	7.61E-05	-//-	
TGGT1_248240-t26_1	169.6697417	68.70664619	1.3042	6.26E-05	0.0030247	-//-	
TGGT1_281930-t26_1	205.9987049	84.29256089	1.2892	7.90E-06	0.0005769	-//-	
TGGT1_312330-t26_1	2124.730831	874.7809912	1.2803	1.85E-10	3.88E-08	-//-	
TGGT1_272730-t26_1	183.4685147	77.30752139	1.2469	7.66E-05	0.0035152	-//-	
TGGT1_203890-t26_1	92.56192253	39.17708575	1.2404	0.002359	0.046093	-//-	
TGGT1_308965-t26_1	166.2869231	70.72981125	1.2333	0.000136	0.0054356	-//-	
TGGT1_272370-t26_1	6010.120117	2569.366916	1.226	3.94E-09	7.04E-07	-//-	
TGGT1_275870-t26_1	102.3380793	43.81040036	1.224	0.0021323	0.043274	-//-	sp|Q9D6T1|TBE_MOUSE Tubulin epsilon chain OS=Mus musculus GN=Tube1 PE=2 SV=1//4.57952e-35
TGGT1_220720-t26_1	269.6731781	116.213231	1.2144	7.16E-06	0.0005324	-//-	
TGGT1_300130-t26_1	282.1322244	121.9805996	1.2097	9.81E-06	0.0006811	-//-	sp|B6KAM0|AMA1_TOXGO Apical membrane antigen 1 OS=Toxoplasma gondii GN=AMA1 PE=1 SV=1//1.61724e-53
TGGT1_209040-t26_1	549.9524968	245.5640833	1.1632	0.0023659	0.046122	-//-	sp|Q9CR92|CCD96_MOUSE Coiled-coil domain-containing protein 96 OS=Mus musculus GN=Ccdc96 PE=2 SV=1//1.01051e-10
TGGT1_215340-t26_1	112.7609058	50.69023708	1.1535	0.0018192	0.039599	-//-	
TGGT1_236670A-t26_1	281.4666562	126.7585017	1.1509	2.04E-05	0.0012319	-//-	
TGGT1_205265-t26_1	532.5343316	242.3847482	1.1356	5.58E-08	7.56E-06	-//-	sp|Q00975|CAC1B_HUMAN Voltage-dependent N-type calcium channel subunit alpha-1B OS=Homo sapiens GN=CACNA1B PE=1 SV=1//1.20848e-12
TGGT1_293500-t26_1	249.774336	114.1943831	1.1291	2.00E-05	0.0012264	-//-	
TGGT1_219650-t26_1	498.6654288	230.8235778	1.1113	0.0002821	0.009635	-//-	sp|Q9LYG9|MSL10_ARATH Mechanosensitive ion channel protein 10 OS=Arabidopsis thaliana GN=MSL10 PE=1 SV=1//3.57272e-17
TGGT1_294785-t26_1	151.5104143	70.1298725	1.1113	0.0015984	0.035813	-//-	
TGGT1_306620-t26_1	1229.966036	569.7321285	1.1103	8.38E-09	1.38E-06	-//-	
TGGT1_291170-t26_1	175.4026658	82.6896767	1.0849	0.00075	0.020865	sp|Q54I39|IST1L_DICDI IST1-like protein OS=Dictyostelium discoideum GN=DDB_G0289029 PE=3 SV=1//1.23829e-17	
TGGT1_212160-t26_1	205.0037886	98.35004375	1.0597	0.0002258	0.0082129	-//-	
TGGT1_286740-t26_1	183.4960035	88.48347854	1.0523	0.0010964	0.027746	sp|P07207|NOTCH_DROME Neurogenic locus Notch protein OS=Drosophila melanogaster GN=N PE=1 SV=3//2.39046e-06	
TGGT1_255290-t26_1	221.8388518	106.9859865	1.0521	0.0001764	0.006587	-//-	
TGGT1_245440-t26_1	277.7647978	134.1244373	1.0503	0.0001074	0.0045565	-//-	
TGGT1_267460-t26_1	142.7205835	69.15336032	1.0453	0.0012697	0.030479	-//-	
TGGT1_297910-t26_1	127.2321192	62.27352359	1.0308	0.0019679	0.041335	-//-	
TGGT1_315123-t26_1	247.4396931	121.6083378	1.0248	0.0002392	0.0085165	-//-	
TGGT1_254640-t26_1	183.1305765	90.05129513	1.0241	0.000719	0.020477	sp|Q3T0X9|DPOD4_BOVIN DNA polymerase delta subunit 4 OS=Bos taurus GN=POLD4 PE=1 SV=1//1.19527e-10	
TGGT1_233490-t26_1	3188.210651	1589.295074	1.0044	2.62E-08	3.87E-06	-//-	
TGGT1_250100-t26_1	2119.712782	1058.373147	1.002	8.93E-11	2.21E-08	-//-	
TGGT1_363340-t26_1	306.0141676	153.108727	0.99904	5.82E-05	0.0028611	-//-	
TGGT1_250220-t26_1	3793.505992	1903.646694	0.99477	6.93E-12	1.94E-09	-//-	
TGGT1_215500-t26_1	258.5263698	130.6866775	0.9842	0.0001655	0.0062922	-//-	
TGGT1_222160-t26_1	845.7929546	430.0113434	0.97593	0.0012827	0.030704	sp|O62148|AL1A2_MOUSE Retinal dehydrogenase 2 OS=Mus musculus GN=Aldh1a2 PE=1 SV=2//1.70784e-150	
TGGT1_200350-t26_1	1347.962666	685.731167	0.97507	5.98E-09	1.00E-06	sp|P42779|BPRV_DICNO Extracellular basic protease OS=Dichelobacter nodosus GN=bprV PE=1 SV=1//1.2144e-28	
TGGT1_272440-t26_1	200.3207583	102.5673947	0.96574	0.001017	0.02613	sp|Q1PDV2|SRC28_ARATH Serine/arginine-rich SC35-like splicing factor SCL28 OS=Arabidopsis thaliana GN=SCL28 PE=1 SV=1//6.82459e-22	
TGGT1_223750-t26_1	460.231524	235.8728561	0.96435	1.56E-05	0.0010004	-//-	
TGGT1_212810-t26_1	181.0995108	94.16344326	0.94354	0.0013799	0.032386	-//-	
TGGT1_245428-t26_1	942.253794	492.0172777	0.93741	1.94E-07	2.26E-05	-//-	
TGGT1_232590-t26_1	1107.302355	583.846795	0.92339	1.92E-07	2.26E-05	-//-	sp|Q09768|GSH1_SCHPO Glutamate--cysteine ligase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=gcs1 PE=3 SV=1//1.94145e-85
TGGT1_304730-t26_1	402.9194641	214.9177376	0.90671	0.0014689	0.034002	sp|Q8GYX0|MOB1B_ARATH MOB kinase activator-like 1B OS=Arabidopsis thaliana GN=MOB1B PE=2 SV=1//1.07775e-25	
TGGT1_200320-t26_1	500.27609	267.2416093	0.90458	2.75E-05	0.0015282	sp|O26997|HGXR_TOXGO Hypoxanthine-guanine-xanthine phosphoribosyltransferase OS=Toxoplasma gondii GN=HPRT PE=1 SV=1//5.93678e-164	
TGGT1_239810-t26_1	723.7805804	388.201992	0.89874	2.27E-06	0.0001948	-//-	
TGGT1_218740-t26_1	488.8291404	263.2303468	0.893	2.78E-05	0.0015391	-//-	
TGGT1_235460-t26_1	200.963992	108.5581203	0.88847	0.0018674	0.039854	-//-	
TGGT1_266870-t26_1	630.5479355	341.1815061	0.88607	9.26E-06	0.0006597	-//-	
TGGT1_224710-t26_1	210.7057878	114.5402116	0.87938	0.001903	0.040173	sp|P93484|VSR1_PEA Vacuolar-sorting receptor 1 OS=Pisum sativum GN=BP80 PE=1 SV=1//1.39162e-20	
TGGT1_215910-t26_1	7953.027456	4337.198355	0.87474	2.71E-10	5.55E-08	-//-	
TGGT1_257360-t26_1	369.9372406	202.2354647	0.87124	0.0001057	0.0045317	-//-	
TGGT1_273350-t26_1	398.6585564	218.3031611	0.86882	0.0012953	0.03083	sp|B4NJW0|MOC2B_DROWI Molybdopterin synthase catalytic subunit OS=Drosophila willistoni GN=Mocs2 PE=3 SV=1//1.773e-14	
TGGT1_239090-t26_1	597.527915	330.3427431	0.85504	1.76E-05	0.0011025	-//-	
TGGT1_254960-t26_1	290.8378709	160.8248083	0.85473	0.0025592	0.04887	-//-	
TGGT1_214220-t26_1	14512.67401	8060.70308	0.84834	1.64E-07	2.00E-05	-//-	
TGGT1_269417-t26_1	813.2443631	453.6505335	0.84211	4.25E-06	0.0003401	-//-	
TGGT1_248140-t26_1	240.3687604	136.0645157	0.82096	0.002114	0.043217	-//-	
TGGT1_244710-t26_1	671.2202726	382.9115577	0.80978	5.21E-05	0.0026042	-//-	
TGGT1_214575-t26_1	541.9862945	309.81707	0.80684	7.17E-05	0.0033829	-//-	
TGGT1_266910-t26_1	740.5812826	424.274195	0.80366	1.29E-05	0.0008398	sp|P51137|MSK1_MEDSA Glycogen synthase kinase-3 homolog MsK-1 OS=Medicago sativa GN=MSK-1 PE=2 SV=1//5.81887e-34	
TGGT1_289050-t26_1	5560.864114	3191.086253	0.80126	7.64E-08	1.00E-05	-//-	
TGGT1_233925-t26_1	403.9934105	234.8040899	0.78287	0.000795	0.0219	-//-	
TGGT1_234180-t26_1	732.8310373	427.8694938	0.77631	2.63E-05	0.0014928	-//-	
TGGT1_225790-t26_1	669.5958671	395.06456	0.7612	5.96E-05	0.002912	sp|Q7Y0F2|NRX12_ORYSJ Probable nucleoredoxin 1-2 OS=Oryza sativa subsp. japonica GN=Os03g0405900 PE=2 SV=1//2.42864e-09	
TGGT1_225540-t26_1	2505.026814	1486.776759	0.75264	3.18E-05	0.0017117	-//-	
TGGT1_237510-t26_1	756.6631571	449.2055084	0.75228	0.0008763	0.023436	-//-	
TGGT1_236620-t26_1	820.6704145	505.2557847	0.69979	8.17E-05	0.0037126	-//-	
TGGT1_239020-t26_1	1638.979214	1020.811897	0.68308	6.32E-05	0.0030335	sp|P08183|MDR1_HUMAN Multidrug resistance protein 1 OS=Homo sapiens GN=ABCB1 PE=1 SV=3//1.28154e-88	
TGGT1_220230A-t26_1	853.4246547	536.0947371	0.67078	0.0003044	0.010229	-//-	
TGGT1_236890-t26_1	2101.693817	1321.533359	0.66934	0.0020815	0.042938	-//-	
TGGT1_266880-t26_1	1139.956949	718.9126797	0.66509	0.0001539	0.005959	sp|Q8ZKH4|DUSA_SALTY tRNA-dihydrouridine(20/20a) synthase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=dusA PE=3 SV=1//3.86666e-78	
TGGT1_208450-t26_1	4005.96624	2535.22237	0.66004	7.56E-05	0.0034879	sp|O96790|DPGN_DIPMA Serine protease inhibitor dipetalogastin (Fragment) OS=Dipetalogaster maximus PE=1 SV=2//6.92367e-06	
TGGT1_236010-t26_1	2955.645395	1884.530238	0.64927	1.02E-05	0.0006898	-//-	
TGGT1_283810-t26_1	1166.101377	749.9005368	0.63692	0.0001254	0.0051914	sp|Q93XK2|STSYN_PEA Stachyose synthase OS=Pisum sativum GN=STS1 PE=1 SV=1//1.19629e-09	
TGGT1_293810-t26_1	636.9464278	413.1419397	0.62453	0.001469	0.034002	sp|Q8NSH8|PRPB1_CORGL Probable 2-methylisocitrate lyase 1 OS=Corynebacterium glutamicum (strain ATCC 13032 / DSM 20300 / JCM 1318 / LMG 3730 / NCIMB 10025) GN=prpB1 PE=3 SV=1//2.19565e-70	
TGGT1_230170-t26_1	4119.849197	2693.786645	0.61296	0.0001297	0.0052909	-//-	
TGGT1_273320-t26_1	2009.605559	1316.685321	0.61	4.65E-05	0.0023918	-//-	
TGGT1_213445-t26_1	3766.730356	2478.891553	0.60362	3.81E-05	0.0020115	-//-	
TGGT1_278940-t26_1	1446.650429	952.7925909	0.60248	0.000416	0.013241	sp|O14326|PUB3_SCHPO E3 ubiquitin-protein ligase pub3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pub3 PE=2 SV=1//5.15235e-82	
TGGT1_263220-t26_1	614.359542	404.996413	0.60117	0.0018956	0.040117	sp|Q9NQU5|PAK6_HUMAN Serine/threonine-protein kinase PAK 6 OS=Homo sapiens GN=PAK6 PE=1 SV=1//5.19295e-11	
TGGT1_263270-t26_1	1324.888372	873.4138853	0.60113	0.0002231	0.0081496	sp|Q9ESM6|GDPD2_MOUSE Glycerophosphoinositol inositolphosphodiesterase GDPD2 OS=Mus musculus GN=Gdpd2 PE=1 SV=1//4.53144e-50	
TGGT1_219230-t26_1	1144.926376	761.1158787	0.58907	0.0004749	0.014833	sp|Q9Z3R3|AAC5_RHIME Acetoacetyl-coenzyme A synthetase OS=Rhizobium meliloti (strain 1021) GN=acsA2 PE=3 SV=2//2.03058e-131	
TGGT1_203060-t26_1	3012.364045	2006.83455	0.58597	0.0001168	0.004884	-//-	
TGGT1_262630-t26_1	604.2385748	402.8944784	0.58472	0.0018496	0.039787	-//-	
TGGT1_311100-t26_1	5409.314184	3610.907318	0.58308	0.0002375	0.008491	-//-	
TGGT1_269425-t26_1	1103.732269	738.9436195	0.57885	0.00059	0.017579	-//-	
TGGT1_203870-t26_1	797.2020036	534.5619881	0.57659	0.0021504	0.043537	sp|Q9ULR0|ISY1_HUMAN Pre-mRNA-splicing factor ISY1 homolog OS=Homo sapiens GN=ISY1 PE=1 SV=3//2.06471e-54	
TGGT1_269430-t26_1	1115.635702	751.2315145	0.57054	0.000916	0.024052	sp|Q6S3T6|SPS1_ORYSJ Solanesyl-diphosphate synthase 1, mitochondrial OS=Oryza sativa subsp. japonica GN=SPS1 PE=1 SV=1//1.91225e-40	
TGGT1_316430-t26_1	1144.015644	772.8308012	0.56588	0.0011196	0.027997	sp|O14356|TOR1_SCHPO Phosphatidylinositol 3-kinase tor1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=tor1 PE=1 SV=1//2.17642e-06	
TGGT1_213280-t26_1	3688.333151	2507.024318	0.55699	0.0003321	0.01103	-//-	
TGGT1_204540-t26_1	1423.399693	968.5101416	0.5555	0.000901	0.023785	sp|Q9UJK0|TSR3_HUMAN Ribosome biogenesis protein TSR3 homolog OS=Homo sapiens GN=TSR3 PE=1 SV=1//2.0456e-25	
TGGT1_263740-t26_1	1367.380972	943.7978681	0.53487	0.0007302	0.020588	sp|Q9JI39|ABCBA_MOUSE ATP-binding cassette sub-family B member 10, mitochondrial OS=Mus musculus GN=Abcb10 PE=1 SV=1//2.70364e-51	
TGGT1_208570-t26_1	3363.038805	2328.664352	0.53026	0.0002902	0.0098701	sp|Q8N2K1|UB2J2_HUMAN Ubiquitin-conjugating enzyme E2 J2 OS=Homo sapiens GN=UBE2J2 PE=1 SV=3//3.25291e-48	
TGGT1_203790-t26_1	3172.121904	2199.050758	0.52857	0.0002739	0.0094303	-//-	
TGGT1_237550-t26_1	1539.153938	1068.256981	0.52688	0.0012287	0.030098	-//-	
TGGT1_205680-t26_1	993.6662793	690.2107295	0.52572	0.0012342	0.030112	-//-	
TGGT1_304670-t26_1	1343.411409	933.9836391	0.52443	0.0013393	0.03152	sp|Q4R747|LRC46_MACFA Leucine-rich repeat-containing protein 46 OS=Macaca fascicularis GN=LRRC46 PE=2 SV=1//6.71104e-07	
TGGT1_216770-t26_1	2549.801314	1803.014	0.49997	0.0011083	0.027964	-//-	
TGGT1_300055-t26_1	1707.763477	1222.964275	0.48173	0.0019761	0.041404	-//-	
TGGT1_204050-t26_1	12721.38737	9124.079152	0.47951	0.0004133	0.013204	sp|I3R794|HLY_HALMT Halolysin OS=Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) GN=hly PE=1 SV=1//5.72593e-29	
TGGT1_208370-t26_1	5762.545732	4169.813635	0.46672	0.0007981	0.021914	-//-	
TGGT1_286090-t26_1	9065.382738	6574.291614	0.46353	0.0011186	0.027997	sp|P42678|SUI1_ANOGA Protein translation factor SUI1 homolog OS=Anopheles gambiae GN=AGAP006459 PE=3 SV=1//6.64889e-33	
TGGT1_268980-t26_1	2197.846442	1606.169325	0.45247	0.0023082	0.045418	-//-	
TGGT1_239420-t26_1	11916.54748	8847.030888	0.4297	0.0022805	0.045297	sp|P53683|CDPK2_ORYSJ Calcium-dependent protein kinase isoform 2 OS=Oryza sativa subsp. japonica GN=CPK2 PE=2 SV=2//3.80474e-07	

S2_Table. SwissProt
KOPITvsPar.DEG_up sort