Table 2a. Increased genes in the transfectant mRNA analysis

Probe Name	log2(FC)	Gene annotation	GeneID TSK#
CTG_2462	2.962	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative	Tc00.1047053510645.30
IB_MT_02_F08	1.719	40S ribosomal protein S11, putative	Tc00.1047053508405.40
MG_ST_15_C06	1.911	60S ribosomal protein L10a, putative	Tc00.1047053511277.160
MG_24H_15_D04	1.907	60S ribosomal protein L10a, putative	Tc00.1047053511277.160
CTG_1494	2.465	60S ribosomal protein L4, putative	Tc00.1047053504121.30
CTG_1223	1.649	AAA ATPase, putative	Tc00.1047053509437.50
MG_24H_07_B07	1.622	ABC transporter, putative	Tc00.1047053506579.10
CTG_2431	2.262	actin, putative	Tc00.1047053510127.79
CTG_307	1.679	acyl carrier protein, mitochondrial precursor, putative	Tc00.1047053511867.140
CTG_4081	3.083	alcohol dehydrogenase, putative	Tc00.1047053506357.50
CTG_882	3.133	alpha tubulin, putative	Tc00.1047053411235.9
MG_ST_08_B01	3.308	amino acid permease, putative	Tc00.1047053511325.40
IB_ST_02_H05	3.412	amino acid transporter, putative	Tc00.1047053506053.10
MG_ST_08_H12	3.769	amino acid transporter, putative	Tc00.1047053506053.10
CTG_3460	2.712	amino acid transporter, putative	Tc00.1047053507659.20
IB_MT_01_F06	2.151	amino acid transporter, putative	Tc00.1047053507659.20
MG_EP_02_D10	1.911	amino acid transporter, putative	Tc00.1047053507659.20
CTG_1747	1.833	amino acid transporter, putative	Tc00.1047053508017.30
IB_ST_01_H05	3.347	arginine kinase|ATP-guanidine phosphotransferase	Tc00.1047053507241.30
CTG_1307	2.207	arginine kinase|ATP-guanidine phosphotransferase	Tc00.1047053507241.30
MG_ST_10_H03	2.055	arginine kinase|ATP-guanidine phosphotransferase	Tc00.1047053507241.30
CTG_1860	1.693	aspartate carbamoyltransferase, putative	Tc00.1047053511643.30
CTG_1856	1.898	ATP synthase, alpha chain, mitochondrial precursor, putative	Tc00.1047053510395.10
IB_EP_16_E06	2.258	ATPase beta subunit, putative	Tc00.1047053509233.180
MG_ST_05_D07	1.650	ATPase beta subunit, putative	Tc00.1047053509233.180
CTG_3358	2.189	axoneme central apparatus protein, putative	Tc00.1047053510955.40
MG_ST_08_G04	3.814	AY526247 | Trypanosoma cruzi putative amino acid transporter PAT6 gene	AY526247
CTG_586	2.036	beta tubulin, putative	Tc00.1047053506563.40
CTG_1464	2.357	calpain-like cysteine peptidase (pseudogene), putative|calpain-like cysteine peptidase, clan CA, family C2, putative (pseudogene)	Tc00.1047053508999.250
IB_ST_20_G08	2.459	calpain-like cysteine peptidase, putative|calpain-like cysteine peptidase, clan CA, family C2, putative	Tc00.1047053509003.40
CTG_3451	1.758	calpain-like cysteine peptidase, putative|cysteine peptidase, Clan CA, family C2, putative	Tc00.1047053508999.200
IB_MT_02_B11	1.843	casein kinase, putative	Tc00.1047053508541.240
CTG_2698	1.667	centrin, putative	Tc00.1047053506559.380
MG_EP_08_D11	1.898	chaperone DnaJ protein, putative	Tc00.1047053510575.200
CTG_3832	2.191	chaperonin containing T-complex protein, putative	Tc00.1047053511725.250
MG_24H_11_G01	2.035	chaperonin containing T-complex protein, putative	Tc00.1047053511725.250
CTG_1559	1.629	choline dehydrogenase, putative	Tc00.1047053511141.20
CTG_3050	1.596	clathrin heavy chain, putative	Tc00.1047053506167.50
CTG_1907	2.184	cyclosome subunit, putative	Tc00.1047053511507.30

MG_EP_06_G01	1.848	cystathionine beta-synthase|cysteine synthase|serine sulfhydrylase	Tc00.1047053511691.20
CTG_1937	1.924	cysteine proteinase, putative	Tc00.1047053507849.50
MG_EP_08_C09	2.774	cytochrome C oxidase subunit IV, putative	Tc00.1047053506529.360
CTG_1074	1.621	cytochrome c oxidase VIII (COX VIII), putative	Tc00.1047053407477.50
MG_24H_11_A10	1.791	cytoskeleton-associated protein CAP5.5, putative|cysteine peptidase, Clan CA, family C2, putative	Tc00.1047053508555.60
CTG_2371	1.746	delta-6 fatty acid desaturase, putative	Tc00.1047053507609.40
MG_ST_11_D04	2.008	delta-6 fatty acid desaturase, putative	Tc00.1047053507609.40
CTG_281	1.687	dihydrofolate reductase-thymidylate synthase, putative	Tc00.1047053509153.90
MG_EP_08_E07	3.152	dipeptidyl-peptidase, putative	Tc00.1047053508699.120
MG_ST_06_H09	2.613	D-isomer specific 2-hydroxyacid dehydrogenase-protein, putative	Tc00.1047053510099.120
IB_EP_11_B08	1.733	D-isomer specific 2-hydroxyacid dehydrogenase-protein, putative	Tc00.1047053510099.120
CTG_1150	2.922	dispersed gene family protein 1 (DGF-1), putative	Tc00.1047053507035.30
IB_ST_02_B11	1.709	DNA repair protein RAD51, putative	Tc00.1047053503801.30
IB_MT_07_E07	2.004	DnaJ chaperone protein, putative	Tc00.1047053509629.20
CTG_3315	2.364	DREV methyltransferase, putative	Tc00.1047053509965.190
CTG_1422	1.869	elongation factor 1-gamma (EF-1-gamma), putative	Tc00.1047053510463.160
CTG_673	2.492	elongation factor 2, putative	Tc00.1047053508169.20
CTG_2383	2.378	enolase, putative	Tc00.1047053504105.140
IB_MT_19_E01	1.668	enolase, putative	Tc00.1047053504105.140
CTG_3581	1.622	expression site-associated gene (ESAG-like) protein, putative|expression site-associated gene 5 (ESAG5-like) protein, putative	Tc00.1047053508257.220
MG_24H_18_F02	1.778	flagellar radial spoke protein-like, putative	Tc00.1047053510149.120
CTG_140	1.864	folate/pteridine transporter, putative	Tc00.1047053508027.40
MG_R_Y_#20	2.599	glucose-regulated protein 78, putative	Tc00.1047053506585.40
CTG_1650	2.683	glutamamyl carboxypeptidase, putative|metallo-peptidase, clan MH, family M18, putative	Tc00.1047053511391.120
MG_EP_02_D05	2.127	glutamamyl carboxypeptidase, putative|metallo-peptidase, clan MH, family M18, putative	Tc00.1047053511391.120
IB_EP_11_H06	1.691	glutamate dehydrogenase, putative	Tc00.1047053508111.30
CTG_1213	2.379	glyceraldehyde 3-phosphate dehydrogenase, putative	Tc00.1047053509065.70
MG_ST_05_F11	2.070	glycosomal malate dehydrogenase, putative	Tc00.1047053506503.69
CTG_1653	1.866	glycosomal membrane protein, putative	Tc00.1047053509203.40
CTG_650	1.612	Golgi/lysosome glycoprotein, putative	Tc00.1047053511391.180
CTG_274	2.717	heat shock protein 70 (HSP70), putative	Tc00.1047053511211.170
IB_EP_12_D11	2.374	hexokinase, putative	Tc00.1047053508951.20
CTG_1787	2.118	hexokinase, putative	Tc00.1047053508951.20
IB_EP_16_C04	3.652	hexose transporter, putative	Tc00.1047053506355.10
IB_EP_14_D04	2.960	hexose transporter, putative	Tc00.1047053506355.10
CTG_663	1.711	hexose transporter, putative	Tc00.1047053506355.10
CTG_97	3.413	histone H3, putative	Tc00.1047053509471.86
CTG_410	2.583	hypothetical protein	Tc00.1047053504985.10
MG_ST_14_D07	2.028	hypothetical protein	Tc00.1047053506295.150
IB_MT_02_F11	1.850	hypothetical protein	Tc00.1047053506835.50
MG_24H_11_B12	2.344	hypothetical protein	Tc00.1047053508177.70
MG_EP_09_A05	1.683	hypothetical protein	Tc00.1047053509429.280

MG_EP_03_E01	1.747	hypothetical protein	Tc00.1047053511001.40
MG_24H_09_A03	1.813	hypothetical protein	Tc00.1047053511439.40
CTG_2713	1.889	hypothetical protein	Tc00.1047053511439.40
MG_ST_05_C08	2.096	hypothetical protein	Tc00.1047053511807.220
CTG_3256	3.975	hypothetical protein, conserved	Tc00.1047053503565.29
IB_MT_04_D02	2.107	hypothetical protein, conserved	Tc00.1047053504137.90
CTG_175	3.608	hypothetical protein, conserved	Tc00.1047053504153.70
IB_ST_01_A04	1.956	hypothetical protein, conserved	Tc00.1047053504153.70
IB_EP_16_F07	2.477	hypothetical protein, conserved	Tc00.1047053505789.20
IB_MT_04_A01	2.118	hypothetical protein, conserved	Tc00.1047053506147.110
CTG_1667	3.859	hypothetical protein, conserved	Tc00.1047053506147.190
CTG_4002	2.677	hypothetical protein, conserved	Tc00.1047053506175.110
IB_EP_16_C05	1.812	hypothetical protein, conserved	Tc00.1047053506175.110
CTG_292	2.409	hypothetical protein, conserved	Tc00.1047053506195.290
MG_ST_16_G12	1.699	hypothetical protein, conserved	Tc00.1047053506195.290
CTG_3175	1.670	hypothetical protein, conserved	Tc00.1047053506235.20
CTG_3328	2.067	hypothetical protein, conserved	Tc00.1047053506321.280
CTG_2266	2.107	hypothetical protein, conserved	Tc00.1047053506351.20
CTG_2277	2.086	hypothetical protein, conserved	Tc00.1047053506355.130
CTG_793	2.000	hypothetical protein, conserved	Tc00.1047053506399.60
CTG_4463	1.697	hypothetical protein, conserved	Tc00.1047053506407.50
CTG_4382	3.882	hypothetical protein, conserved	Tc00.1047053506469.100
CTG_4324	1.746	hypothetical protein, conserved	Tc00.1047053506513.120
MG_ST_16_H04	1.814	hypothetical protein, conserved	Tc00.1047053506529.330
MG_24H_11_G07	1.844	hypothetical protein, conserved	Tc00.1047053506629.200
CTG_4527	3.615	hypothetical protein, conserved	Tc00.1047053506681.50
CTG_3580	1.792	hypothetical protein, conserved	Tc00.1047053506725.20
MG_ST_11_C01	2.146	hypothetical protein, conserved	Tc00.1047053506789.340
MG_24H_03_D04	1.619	hypothetical protein, conserved	Tc00.1047053506789.340
CTG_404	1.937	hypothetical protein, conserved	Tc00.1047053506853.10
MG_24H_10_D11	1.528	hypothetical protein, conserved	Tc00.1047053506945.50
MG_24H_16_F08	2.303	hypothetical protein, conserved	Tc00.1047053507807.10
CTG_3897	1.587	hypothetical protein, conserved	Tc00.1047053507907.50
CTG_2229	3.245	hypothetical protein, conserved	Tc00.1047053507951.15
CTG_4177	1.678	hypothetical protein, conserved	Tc00.1047053508173.129
CTG_4383	2.038	hypothetical protein, conserved	Tc00.1047053508177.40
MG_24H_09_C08	1.746	hypothetical protein, conserved	Tc00.1047053508177.40
CTG_1889	2.926	hypothetical protein, conserved	Tc00.1047053508177.90
CTG_2413	2.863	hypothetical protein, conserved	Tc00.1047053508177.90
MG_24H_02_F02	1.937	hypothetical protein, conserved	Tc00.1047053508177.90
CTG_1889	1.956	hypothetical protein, conserved	Tc00.1047053508177.90
MG_24H_07_H05	1.960	hypothetical protein, conserved	Tc00.1047053508177.90

IB_EP_15_F06	1.634	hypothetical protein, conserved	Tc00.1047053508277.40
CTG_1825	2.248	hypothetical protein, conserved	Tc00.1047053508355.330
CTG_3880	1.714	hypothetical protein, conserved	Tc00.1047053508569.90
MG_EP_06_E05	2.278	hypothetical protein, conserved	Tc00.1047053508693.50
CTG_1252	2.101	hypothetical protein, conserved	Tc00.1047053508693.50
MG_EP_03_B03	1.652	hypothetical protein, conserved	Tc00.1047053508799.10
MG_ST_14_E05	2.445	hypothetical protein, conserved	Tc00.1047053508799.270
CTG_2394	2.891	hypothetical protein, conserved	Tc00.1047053509033.50
CTG_3340	1.914	hypothetical protein, conserved	Tc00.1047053509207.40
MG_EP_08_B02	1.622	hypothetical protein, conserved	Tc00.1047053509669.70
MG_ST_14_H05	1.927	hypothetical protein, conserved	Tc00.1047053509713.20
MG_ST_08_B06	2.957	hypothetical protein, conserved	Tc00.1047053509713.30
IB_ST_17_B07	2.902	hypothetical protein, conserved	Tc00.1047053509713.30
CTG_3073	1.905	hypothetical protein, conserved	Tc00.1047053509713.30
MG_ST_14_C06	1.698	hypothetical protein, conserved	Tc00.1047053509713.30
MG_24H_15_C12	1.795	hypothetical protein, conserved	Tc00.1047053509761.10
CTG_4323	2.193	hypothetical protein, conserved	Tc00.1047053509837.10
IB_MT_19_C09	2.581	hypothetical protein, conserved	Tc00.1047053509859.30
CTG_1527	2.083	hypothetical protein, conserved	Tc00.1047053509935.20
IB_EP_16_A07	2.132	hypothetical protein, conserved	Tc00.1047053509939.19
MG_EP_09_H05	1.647	hypothetical protein, conserved	Tc00.1047053510087.80
MG_24H_08_A03	1.734	hypothetical protein, conserved	Tc00.1047053510101.470
CTG_2738	1.676	hypothetical protein, conserved	Tc00.1047053510307.200
IB_MT_08_G04	1.779	hypothetical protein, conserved	Tc00.1047053510349.64
CTG_3310	2.285	hypothetical protein, conserved	Tc00.1047053510407.30
CTG_1542	1.662	hypothetical protein, conserved	Tc00.1047053510535.64
IB_MT_08_E06	1.710	hypothetical protein, conserved	Tc00.1047053510595.40
MG_24H_09_B03	1.675	hypothetical protein, conserved	Tc00.1047053510797.30
MG_EP_10_B11	1.972	hypothetical protein, conserved	Tc00.1047053510947.30
CTG_2748	2.028	hypothetical protein, conserved	Tc00.1047053511003.90
MG_ST_08_F06	3.023	hypothetical protein, conserved	Tc00.1047053511053.10
MG_24H_09_F03	1.626	hypothetical protein, conserved	Tc00.1047053511245.230
IB_ST_20_A03	1.906	hypothetical protein, conserved	Tc00.1047053511421.24
CTG_1644	1.636	hypothetical protein, conserved	Tc00.1047053511523.14
IB_ST_02_H07	1.682	hypothetical protein, conserved	Tc00.1047053511559.20
MG_ST_06_E06	2.275	hypothetical protein, conserved	Tc00.1047053511621.244
IB_EP_16_F04	1.998	hypothetical protein, conserved	Tc00.1047053511903.40
MG_EP_06_D11	2.655	inosine-5'-monophosphate dehydrogenase, putative	Tc00.1047053507211.40
MG_24H_08_E12	1.849	kinesin, putative	Tc00.1047053509023.180
CTG_2507	2.654	LA RNA binding protein, putative	Tc00.1047053511367.60
MG_EP_03_C10	2.125	lanosterol 14-alpha-demethylase, putative	Tc00.1047053510101.50
CTG_4180	2.420	methionine aminopeptidase, putative|metallo-peptidase, clan MG, family M24, putative	Tc00.1047053507031.120

CTG_2427	2.841	mevalonate kinase, putative	Tc00.1047053436521.9
MG_EP_09_B06	1.747	mitochondrial ATP-dependent zinc metallopeptidase, putative|metallo-peptidase, clan MA(E), family M41, putative	Tc00.1047053507739.20
CTG_2768	1.692	mitochondrial carrier protein, putative	Tc00.1047053504033.90
MG_EP_05_H03	1.650	mitochondrial processing peptidase alpha subunit, putative|metallo-peptidase, Clan ME, Family M16, putative	Tc00.1047053506735.10
CTG_2473	1.771	mucin TcMUCII, putative	Tc00.1047053508295.30
CTG_2039	2.790	mucin TcMUCII, putative	Tc00.1047053511099.70
CTG_4576	2.521	mucin-associated surface protein (MASP, pseudogene), putative	Tc00.1047053508521.70
IB_MT_06_B12	1.770	N-acetylglucosamine-6-phosphate deacetylase-like protein, putative	Tc00.1047053506507.10
CTG_665	2.768	NAD(P)-dependent steroid dehydrogenase protein, putative	Tc00.1047053510873.10
MG_24H_10_G09	2.394	NAD(P)-dependent steroid dehydrogenase protein, putative	Tc00.1047053510873.10
CTG_2950	2.310	nitrilase, putative	Tc00.1047053509979.150
CTG_851	1.799	nucleobase transporter, putative	Tc00.1047053506445.110
Nop58	1.782	nucleolar RNA binding protein, putative	Tc00.1047053508277.230
CTG_4492	2.325	nucleoside transporter 1, putative	Tc00.1047053508645.40
CTG_148	3.558	orotidine-5-phosphate decarboxylase/orotate phosphoribosyltransferase, putative|OMPDCase-OPRTase, putative	Tc00.1047053507059.60
CTG_1779	1.829	orotidine-5-phosphate decarboxylase/orotate phosphoribosyltransferase, putative|OMPDCase-OPRTase, putative	Tc00.1047053507059.60
CTG_1110	2.328	pantothenate kinase subunit, putative	Tc00.1047053511153.120
MG_EP_05_B06	3.017	peptidase M20/M25/M40, putative	Tc00.1047053509213.120
MG_EP_10_B06	2.083	peptidase T, putative|aminotripeptidase, putative	Tc00.1047053506513.110
IB_ST_17_B09	2.725	phosphoglycerate kinase, putative	Tc00.1047053505999.90
IB_EP_16_H11	1.586	poly(A)-binding protein, putative|polyadenylate-binding protein, putative	Tc00.1047053508461.140
MG_24H_16_B04	1.540	pretranslocation protein, alpha subunit, putative|SEC61-like (pretranslocation process) protein, putative	Tc00.1047053506297.240
IB_MT_07_H07	2.187	prostaglandin F synthase, putative|aldo/keto reductase, putative	Tc00.1047053511287.49
CTG_3494	2.332	prostaglandin F2alpha synthase	Tc00.1047053508461.80
CTG_557	3.059	protein kinase, putative	Tc00.1047053506743.160
IB_EP_16_A09	2.958	protein kinase, putative	Tc00.1047053508405.70
MG_ST_09_C06	1.753	protein kinase, putative	Tc00.1047053508405.70
MG_ST_09_F08	2.009	protein kinase, putative	Tc00.1047053508405.70
MG_ST_08_A04	2.151	protein kinase, putative	Tc00.1047053508405.70
MG_24H_07_G04	2.116	protein kinase, putative	Tc00.1047053510943.40
CTG_150	2.468	protein kinase, putative	Tc00.1047053511351.30
CTG_3546	2.248	PUF1, putative	Tc00.1047053508625.160
CTG_3624	1.755	ribonucleoside-diphosphate reductase small chain, putative	Tc00.1047053511555.80
MG_24H_03_E06	1.586	ribonucleoside-diphosphate reductase small chain, putative	Tc00.1047053511555.80
CTG_4212	3.732	RNA-binding protein, putative	Tc00.1047053509317.60
CTG_1441	1.589	S-adenosylmethionine synthetase, putative	Tc00.1047053506945.160
MG_24H_20_E05	2.022	serine hydroxymethyltransferase, putative	Tc00.1047053510407.90
CTG_3665	1.988	serine/threonine protein kinase, putative	Tc00.1047053511277.140
CTG_1728	2.599	succinyl-CoA ligase [GDP-forming] beta-chain, putative	Tc00.1047053507681.20

CTG_240	2.286	succinyl-CoA synthetase alpha subunit, putative	Tc00.1047053508479.340
CTG_4424	2.263	succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor, putative	Tc00.1047053504153.360
MG_ST_05_H07	1.644	syntaxin, putative	Tc00.1047053508955.10
IB_MT_08_D07	1.586	t-complex protein 1, delta subunit, putative	Tc00.1047053509695.200
CTG_4504	1.728	transketolase, putative	Tc00.1047053511903.120
IB_MT_11_A02	1.666	transketolase, putative	Tc00.1047053511903.120
CTG_1577	1.765	trans-sialidase (pseudogene), putative	Tc00.1047053410923.40
CTG_120	3.142	trans-sialidase (pseudogene), putative	Tc00.1047053422843.10
CTG_2897	2.487	trans-sialidase, putative	Tc00.1047053508045.120
CTG_1217	2.714	triosephosphate isomerase, putative	Tc00.1047053508647.200
IB_MT_07_E04	1.646	triosephosphate isomerase, putative	Tc00.1047053508647.200
CTG_2486	1.710	tRNA (guanine-N(7)-)-methyltransferase, putative|methyltransferase, putative	Tc00.1047053510429.20
CTG_4105	2.265	trypanothione reductase, putative	Tc00.1047053503555.30
CTG_1857	2.208	tryparedoxin peroxidase, putative	Tc00.1047053509499.14
CTG_3669	1.755	tryparedoxin, putative	Tc00.1047053509997.30
MG_EP_06_D07	1.880	tyrosine aminotransferase, putative	Tc00.1047053510187.20
MG_EP_10_A08	1.638	vesicular-fusion ATPase-like protein, putative	Tc00.1047053509831.20
CTG_1590	3.764	zinc carboxypeptidase, putative	Tc00.1047053509979.51

Probe Name: Internal code for T. cruzi microarray probe
Log2(FC): fold change (base 2 logarithm)
Gene annotation: Putative gene function description
GeneID TSK: Gene code from Trypanosoma cruzi Sequencing Consortium
#: When not available, GenBank sequence ID