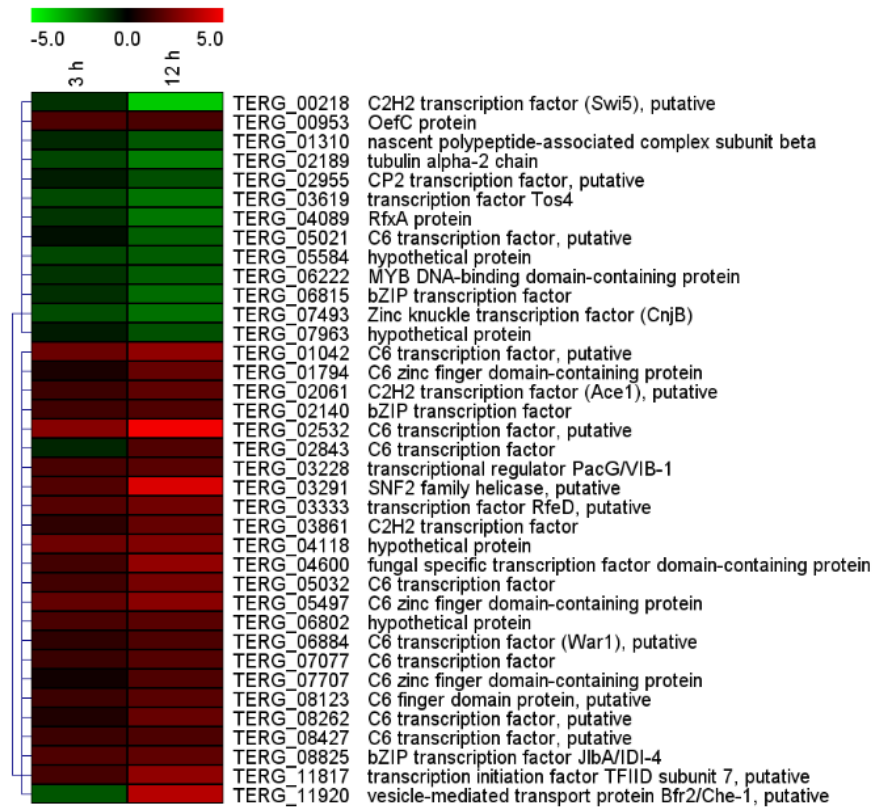
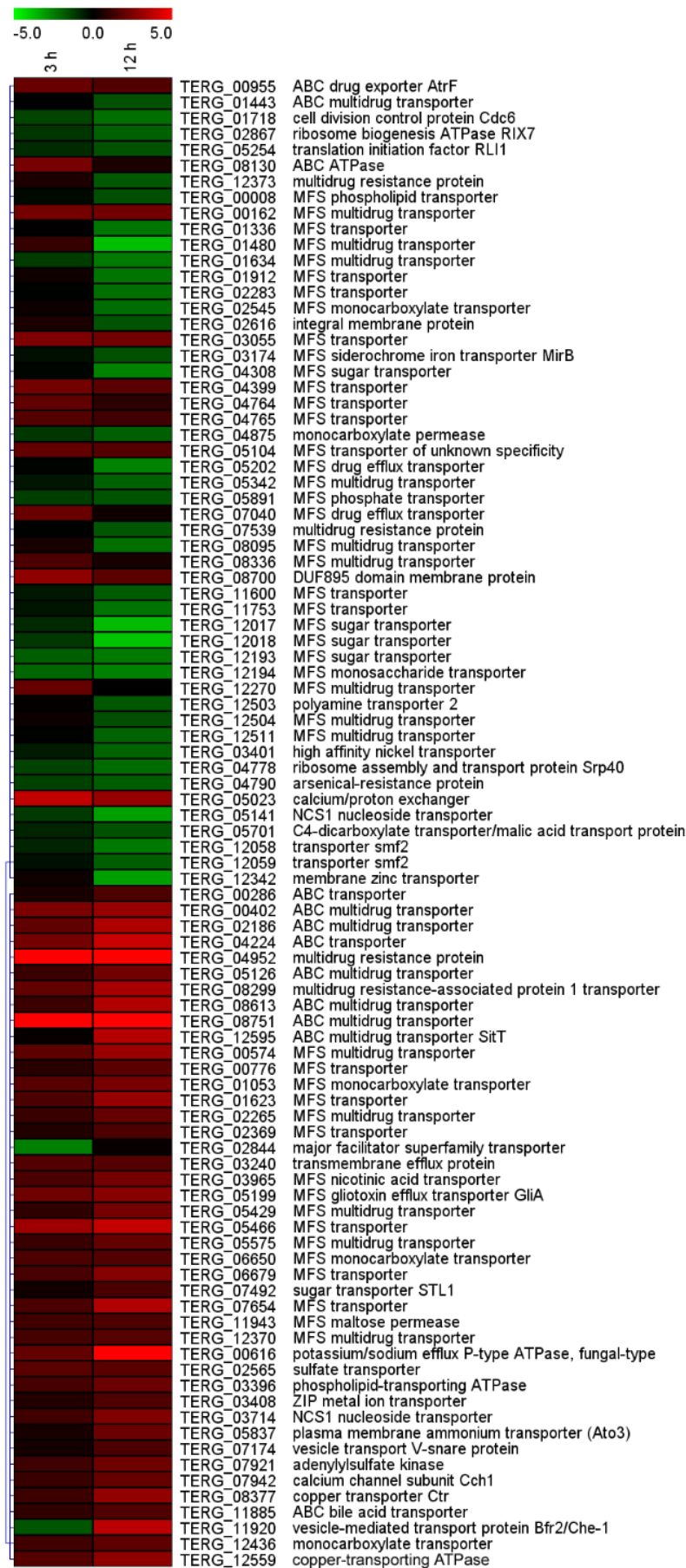


**Figure S1:** Kinase related genes modulated in response to SRT.



**Figure S2:** Transcription factors related genes modulated in response to SRT.



**Figure S3:** *Trichophyton rubrum* membrane transporter genes modulated in response to SRT.

**Table S1:** List of primers used in RT-qPCR assays.

ID	Gene Product Name	Primers (5' - 3')	Efficiency (%)
TERG_05742	DNA-dependent RNA polymerase II RPB140	FW: TGCAGGAGCTGGTGGGAAGA REV: GCTGGGAGGTACTGTTTGATCAA	94.99
TERG_04402	glyceraldehyde 3-phosphate dehydrogenase	FW: GCGTGACCCAGCCAACA REV: CGGTGGACTCGACGATGTAGT	99.90
TERG_11735	microtubule associated protein ( <i>T. tonsurans</i> )	FW: GGGCCAAAGAAACAACAACA REV: CGCTCGGCATATTACCCTAA	98.2
TERG_07544	lipase ( <i>T. tonsurans</i> )	FW: CTTGACGGATGGAAAAAGGA REV: CACCGTTATTTGGATCAGCA	101.6
TERG_06673	pachytene checkpoint component Pch2 ( <i>T. tonsurans</i> )	FW: ATGGGGAGATGCAGTTATGG REV: ACAACGCTCACTTGTGCAAC	102.8
TERG_01762	sulfite reductase (NADPH) hemoprotein. beta-component	FW: ACGTGGATTCTGGGAAACAG REV: AGGCCGAAAACGGAATACTT	95.3
TERG_05522	lysophospholipase ( <i>T. equinum</i> )	FW: CAACGCGGACAATGTCTCTA REV: CTCCATTCATCAAAGCACGA	104.0
TERG_11924	ankyrin repeat protein ( <i>T. tonsurans</i> )	FW: GACCGGAAAGGTGGATGTTA REV: CTCGTGTCGATAGCTTGCAG	100.0
TERG_06548	hypothetical protein	FW: ATCCGGTTCACAGACCAAAC REV: GCTGGATTGAAAGGAGGACA	102.0
TERG_03936	CAMK protein kinase	FW: AGACAGCTGGCTTGCAAAAT REV: TGAAACAGTCGTTTGGGACA	98.9
TERG_06540	glutathione transferase ( <i>T. tonsurans</i> )	FW: AGGGATTGAACAAAGCCAGA REV: AGGACCAATCTCATCCATCG	102.0
TERG_07570	G-protein signaling regulator. putative ( <i>T. verrucosum</i> )	FW: TGGCATCAAGCACAAACTGT REV: CTTTTTGGGCTTTGGACTTG	103.0
TERG_07539	multidrug resistance protein ( <i>T. tonsurans</i> )	FW: CTCCTACCACCCATTGCTA REV: CTCAAGGCCGATAAGGAACA	100.0
TERG_03815	subtilisin-like protease 3	FW: TGGTGTTGACACCGGTATTG REV: GTTGCCATCAGTGTTGTCGT	102.0

**Table S2:** General features of RNA-seq reads mapped to the *Trichophyton rubrum* reference genome.

Sample	Raw reads	High-quality reads	Mapped reads STAR	Total mapped reads (%)
Control 3 hours I	49,001,399	46,661,059	45,099,456	96.65
Control 3 hours II	53,711,149	50,929,711	48,747,310	95.71
Control 3 hours III	54,065,522	51,244,460	48,776,743	95.18
Control 12 hours I	49,723,884	47,231,185	45,011,034	95.30
Control 12 hours II	48,820,202	46,313,505	38,542,411	83.22
Control 12 hours III	49,378,560	46,733,086	38,063,153	81.45
SRT 3 hours I	44,238,209	41,936,258	40,012,345	95.41
SRT 3 hours II	46,989,637	44,653,620	41,137,174	92.13
SRT 3 hours III	46,798,013	44,244,584	42,078,809	95.10
SRT 12 hours I	42,267,590	40,220,692	38,407,036	95.49
SRT 12 hours II	43,358,547	41,011,155	38,955,931	94.99
SRT 12 hours III	36,247,455	34,371,291	32,688,609	95.10

**Table S3:** *Trichophyton rubrum* genes modulated in response to SRT exposure at each time point.

ID	3h	12h	Gene Product Name
TERG_00785	8.60		endoplasmic reticulum vesicle protein 25
TERG_02041	4.28		glutathione S-transferase ( <i>T. equinum</i> )
TERG_12218	4.26		hypothetical protein
TERG_11932	3.77		hypothetical protein
TERG_11576	3.48		hypothetical protein
TERG_11896	3.47		aminotransferase ( <i>T. equinum</i> )
TERG_06701	3.42		gamma-glutamyltransferase
TERG_12400	3.42		hypothetical protein
TERG_07781	3.36		hypothetical protein
TERG_00578	3.10		aspartic endopeptidase (AP1), putative ( <i>T. verrucosum</i> )
TERG_05650	2.97		blasticidin-resistance protein ( <i>T. tonsurans</i> )
TERG_04003	2.92		AMP dependent CoA ligase ( <i>T. tonsurans</i> )
TERG_00911	2.85		hypothetical protein
TERG_02517	2.84		N-acetyltransferase, GNAT family, putative ( <i>A. benhamiae</i> )
TERG_12606	2.78		protease DPPV, putative ( <i>A. benhamiae</i> )
TERG_05943	2.73		aminotransferase, class III ( <i>T. verrucosum</i> )
TERG_11700	2.69		ATP-dependent RNA helicase SUB2 ( <i>T. equinum</i> )
TERG_06116	2.69		indoleamine 2,3-dioxygenase ( <i>T. equinum</i> )
TERG_12661	2.60		hypothetical protein
TERG_00830	2.55		cytochrome P450 monooxygenase, putative ( <i>A. benhamiae</i> )
TERG_04022	2.53		carboxypeptidase S1, putative ( <i>A. benhamiae</i> )
TERG_01896	2.47		hypothetical protein
TERG_03070	2.47		flotillin domain-containing protein ( <i>T. equinum</i> )
TERG_03489	2.46		hypothetical protein
TERG_02990	2.42		subtilisin-like protease 6
TERG_06781	2.40		metallo-beta-lactamase domain protein, putative ( <i>A. benhamiae</i> )
TERG_05445	2.40		DUF323 domain-containing protein ( <i>T. equinum</i> )
TERG_12173	2.36		glycerol-3-phosphate dehydrogenase, mitochondrial
TERG_08130	2.36		ABC ATPase ( <i>T. equinum</i> )
TERG_12556	2.33		hypothetical protein
TERG_12135	2.33		hypothetical protein
TERG_08014	2.28		haloacid dehalogenase, type II
TERG_00227	2.28		glutamine amidotransferase subunit pdxT ( <i>T. equinum</i> )
TERG_07451	2.27		acetoacetate-CoA ligase
TERG_01555	2.26		L-serine dehydratase, putative ( <i>T. verrucosum</i> )
TERG_02615	2.24		oxidoreductase, 2OG-Fe(II) oxygenase family, putative ( <i>A. benhamiae</i> )
TERG_01281	2.23		malate synthase, glyoxysomal
TERG_00579	2.23		glutathione S-transferase ( <i>T. tonsurans</i> )
TERG_03490	2.22		hypothetical protein
TERG_07655	2.20		FAD dependent oxidoreductase, putative ( <i>T. verrucosum</i> )
TERG_02360	2.19		hypothetical protein
TERG_01511	2.19		hypothetical protein
TERG_07782	2.19		GA-binding protein beta chain ( <i>M. gypseum</i> )
TERG_08240	2.18		methyltransferase, putative ( <i>T. verrucosum</i> )
TERG_11757	2.17		hypothetical protein
TERG_02803	2.15		3-oxoacyl-(acyl-carrier-protein) reductase ( <i>T. verrucosum</i> )

TERG_01762	2.14	sulfite reductase (NADPH) hemoprotein, beta-component
TERG_08444	2.09	CipC protein ( <i>M. canis</i> )
TERG_07980	2.09	hypothetical protein
TERG_05121	2.09	cytochrome P450 monooxygenase, putative ( <i>A. benhamiae</i> )
TERG_04324	2.08	extracellular metalloproteinase 4
TERG_07040	2.07	MFS drug efflux transporter ( <i>T. equinum</i> )
TERG_08757	2.06	hypothetical protein
TERG_07673	2.04	hypothetical protein
TERG_05347	2.03	epoxide hydrolase, putative ( <i>T. verrucosum</i> )
TERG_08466	2.03	hypothetical protein
TERG_07001	2.03	hydroxyisocaproate dehydrogenase ( <i>T. tonsurans</i> )
TERG_07544	2.02	lipase ( <i>T. tonsurans</i> )
TERG_06673	2.00	pachytene checkpoint component Pch2 ( <i>T. tonsurans</i> )
TERG_04448	1.97	CMGC/DYRK protein kinase ( <i>M. gypseum</i> )
TERG_01463	1.97	cytochrome c peroxidase ( <i>T. tonsurans</i> )
TERG_08151	1.96	GNAT family acetyltransferase, putative ( <i>T. verrucosum</i> )
TERG_00614	1.96	dihydrodipicolinate synthetase ( <i>T. tonsurans</i> )
TERG_07031	1.95	hypothetical protein
TERG_11539	1.95	3-oxoacyl-(acyl-carrier-protein) reductase ( <i>T. tonsurans</i> )
TERG_00887	1.95	high expression lethality protein Hel10 ( <i>T. tonsurans</i> )
TERG_04164	1.94	hypothetical protein
TERG_04764	1.93	MFS transporter ( <i>T. tonsurans</i> )
TERG_06506	1.91	hypothetical protein
TERG_05677	1.91	phenazine biosynthesis protein ( <i>T. equinum</i> )
TERG_12483	1.90	nonribosomal brevianamide peptide synthase FtmA ( <i>T. verrucosum</i> )
TERG_00563	1.90	GNAT family N-acetyltransferase, putative ( <i>A. benhamiae</i> )
TERG_04098	1.88	Swi5 domain-containing protein ( <i>T. equinum</i> )
TERG_03855	1.88	WW domain-containing protein ( <i>M. canis</i> )
TERG_02196	1.87	l-allo-threonine aldolase ( <i>T. tonsurans</i> )
TERG_04021	1.87	GNAT family acetyltransferase, putative ( <i>A. benhamiae</i> )
TERG_01270	1.87	AMP dependent ligase ( <i>T. tonsurans</i> )
TERG_00413	1.86	DSBA oxidoreductase ( <i>T. equinum</i> )
TERG_03886	1.84	proline permease, putative ( <i>T. verrucosum</i> )
TERG_06806	1.82	hypothetical protein
TERG_12285	1.82	hypothetical protein
TERG_12581	1.82	hypothetical protein
TERG_07911	1.82	hypothetical protein
TERG_05357	1.81	succinate:fumarate antiporter ( <i>T. tonsurans</i> )
TERG_01937	1.80	short chain dehydrogenase ( <i>T. tonsurans</i> )
TERG_07327	1.80	pyridoxamine phosphate oxidase ( <i>T. tonsurans</i> )
TERG_01445	1.79	hypothetical protein
TERG_11776	1.78	hypothetical protein
TERG_01088	1.78	3,4-dihydroxy-2-butanone-4-phosphate synthase
TERG_07734	1.78	O-methyltransferase, putative ( <i>T. verrucosum</i> )
TERG_05641	1.78	amino acid permease (Can1), putative ( <i>T. verrucosum</i> )
TERG_00875	1.76	glutamate-cysteine ligase
TERG_05077	1.76	D-amino-acid oxidase ( <i>T. equinum</i> )
TERG_05528	1.76	hypothetical protein
TERG_07267	1.75	hypothetical protein

TERG_05545	1.75	GNAT family acetyltransferase, putative ( <i>A. benhamiae</i> )
TERG_03791	1.74	NADH-ubiquinone oxidoreductase 20 kDa subunit ( <i>T. equinum</i> )
TERG_11800	1.74	serine/threonine protein kinase ( <i>T. equinum</i> )
TERG_01805	1.73	mucin ( <i>M. canis</i> )
TERG_05484	1.73	acyl-CoA dehydrogenase ( <i>T. tonsurans</i> )
TERG_04124	1.73	hypothetical protein
TERG_12248	1.72	transcription factor fet5 ( <i>M. gypseum</i> )
TERG_00535	1.72	calcium-translocating P-type ATPase, PMCA-type
TERG_02837	1.71	3-beta hydroxysteroid dehydrogenase/isomerase family protein, putative ( <i>T. verrucosum</i> )
TERG_00073	1.71	NADH-dependent flavin oxidoreductase, putative ( <i>T. verrucosum</i> )
TERG_12005	1.71	hypothetical protein
TERG_12647	1.70	hypothetical protein
TERG_04765	1.70	MFS transporter, putative ( <i>A. benhamiae</i> )
TERG_08614	1.69	hypothetical protein
TERG_06206	1.69	peptide-methionine (S)-S-oxide reductase
TERG_01330	1.66	GPI anchored protein, putative ( <i>A. benhamiae</i> )
TERG_11538	1.66	3-oxoacyl-(acyl-carrier-protein) reductase ( <i>T. tonsurans</i> )
TERG_08058	1.66	alpha-1,2-mannosidase family protein ( <i>T. verrucosum</i> )
TERG_12250	1.66	hypothetical protein
TERG_01949	1.65	hypothetical protein
TERG_12295	1.65	hypothetical protein
TERG_01364	1.65	hypothetical protein
TERG_03893	1.64	C6 transcription factor, putative ( <i>A. benhamiae</i> )
TERG_02214	1.64	carboxypeptidase 2
TERG_02249	1.63	phenylacetyl-CoA ligase ( <i>T. tonsurans</i> )
TERG_02746	1.63	hypothetical protein
TERG_08405	1.63	leucine aminopeptidase 2
TERG_01429	1.63	hypothetical protein
TERG_05259	1.62	cytochrome P450, putative ( <i>A. benhamiae</i> )
TERG_01733	1.60	alcohol dehydrogenase, putative ( <i>T. verrucosum</i> )
TERG_08045	1.60	DUF455 domain-containing protein ( <i>T. equinum</i> )
TERG_01436	1.60	oxidoreductase ( <i>T. equinum</i> )
TERG_02798	1.59	DUF895 domain membrane protein ( <i>T. equinum</i> )
TERG_01652	1.59	Atg10p ( <i>M. gypseum</i> )
TERG_00953	1.58	OefC protein ( <i>T. equinum</i> )
TERG_05305	1.58	glutathione-dependent formaldehyde-activating enzyme ( <i>T. tonsurans</i> )
TERG_05714	1.57	hypothetical protein
TERG_05735	1.57	dipeptidyl peptidase 4
TERG_07282	1.56	cytochrome P450 monooxygenase, putative ( <i>T. verrucosum</i> )
TERG_02179	1.56	keylime pathogenicity protein ( <i>M. canis</i> )
TERG_08438	1.56	hypothetical protein
TERG_00070	1.56	maleylacetoacetate isomerase
TERG_08222	1.55	hypothetical protein
TERG_05522	1.55	lysophospholipase ( <i>T. equinum</i> )
TERG_05409	1.55	FAD dependent oxidoreductase ( <i>T. equinum</i> )
TERG_03422	1.54	hypothetical protein
TERG_04447	1.54	protein kinase subdomain-containing protein ( <i>T. equinum</i> )
TERG_04948	1.53	hypothetical protein



TERG_02773	1.53	tartrate dehydrogenase
TERG_02725	1.53	hypothetical protein
TERG_08336	1.53	MFS multidrug transporter, putative ( <i>A. benhamiae</i> )
TERG_06296	1.53	hypothetical protein
TERG_06761	1.53	CAMK protein kinase ( <i>T. tonsurans</i> )
TERG_06047	1.52	hypothetical protein
TERG_08208	1.52	glutathione S-transferase ( <i>T. verrucosum</i> )
TERG_00506	1.52	hypothetical protein
TERG_11639	1.51	isocitrate lyase
TERG_01732	1.51	amidohydrolase ( <i>T. equinum</i> )
TERG_00487	1.50	hypothetical protein
TERG_12454	1.50	cutinase, putative ( <i>A. benhamiae</i> )
TERG_08528	-1.51	fatty acid synthase beta subunit dehydratase ( <i>T. tonsurans</i> )
TERG_00129	-1.56	hypothetical protein
TERG_08633	-1.59	hypothetical protein
TERG_05965	-1.60	hypothetical protein
TERG_08038	-1.83	polysaccharide deacetylase family protein ( <i>T. equinum</i> )
TERG_07598	-1.84	serine carboxypeptidase ( <i>T. equinum</i> )
TERG_02646	-1.96	hypothetical protein
TERG_02952	-2.05	oxidoreductase, short chain dehydrogenase/reductase family ( <i>A. benhamiae</i> )
TERG_12514	-2.40	hypothetical protein
TERG_01347	-2.42	TIGR01456 family HAD hydrolase
TERG_11735	-2.50	microtubule associated protein ( <i>T. tonsurans</i> )
TERG_02650	-3.56	NmrA family protein ( <i>T. equinum</i> )
TERG_04066	-4.67	filamentation protein (Rhfl), putative ( <i>T. verrucosum</i> )
TERG_02652	-4.91	O-methyltransferase, putative ( <i>T. verrucosum</i> )

Gene expression values are expressed in log<sub>2</sub> fold change.

ID	3h	12h	Gene Product Name
TERG_07028		6.08	hypothetical protein
TERG_12356		4.89	hypothetical protein
TERG_04373		4.52	hypothetical protein
TERG_06992		4.36	pyridine nucleotide-disulphide oxidoreductase ( <i>T. tonsurans</i> )
TERG_03254		4.22	hypothetical protein
TERG_01717		4.13	RTA1 domain protein, putative ( <i>A. benhamiae</i> )
TERG_12014		3.99	hypothetical protein
TERG_06772		3.88	hypothetical protein
TERG_03252		3.85	hypothetical protein
TERG_11924		3.85	ankyrin repeat protein ( <i>T. tonsurans</i> )
TERG_03293		3.83	hypothetical protein
TERG_12197		3.72	tyrosyl-DNA phosphodiesterase ( <i>T. tonsurans</i> )
TERG_11920		3.68	vesicle-mediated transport protein Bfr2/Che-1, putative ( <i>T. verrucosum</i> )
TERG_05823		3.67	integral membrane protein ( <i>A. benhamiae</i> )
TERG_06769		3.64	hypothetical protein
TERG_06839		3.60	extracellular proline-rich protein ( <i>T. verrucosum</i> )
TERG_04183		3.59	yqcI protein ( <i>T. equinum</i> )
TERG_08613		3.50	ABC multidrug transporter, putative ( <i>A. benhamiae</i> )

TERG_07654	3.48 MFS transporter, putative ( <i>T. verrucosum</i> )
TERG_01154	3.40 RTA1 domain protein, putative ( <i>T. verrucosum</i> )
TERG_03712	3.39 hydantoinase ( <i>T. equinum</i> )
TERG_08049	3.38 cation diffusion facilitator, putative ( <i>T. verrucosum</i> )
TERG_03552	3.36 serine carboxypeptidase ( <i>T. tonsurans</i> )
TERG_05428	3.34 hypothetical protein
TERG_08508	3.28 hypothetical protein
TERG_01394	3.27 cytochrome P450 alkane hydroxylase, putative ( <i>T. verrucosum</i> )
TERG_03251	3.19 hypothetical protein
TERG_02830	3.19 hypothetical protein
TERG_06167	3.16 hypothetical protein
TERG_07133	3.16 hypothetical protein
TERG_06770	3.16 cytochrome P450, putative ( <i>T. verrucosum</i> )
TERG_00801	3.11 hypothetical protein
TERG_06189	3.04 endo-1,3(4)-beta-glucanase, putative ( <i>T. verrucosum</i> )
TERG_08347	2.99 cytochrome P450 monooxygenase, putative ( <i>A. benhamiae</i> )
TERG_04600	2.96 fungal specific transcription factor domain-containing protein ( <i>T. equinum</i> )
TERG_12118	2.96 hypothetical protein
TERG_08801	2.94 hypothetical protein
TERG_08377	2.92 copper transporter Ctr ( <i>T. tonsurans</i> )
TERG_11817	2.91 transcription initiation factor TFIID subunit 7, putative ( <i>T. verrucosum</i> )
TERG_01678	2.90 histone-lysine N-methyltransferase ( <i>T. tonsurans</i> )
TERG_04714	2.89 mitochondrial phosphate carrier protein ( <i>T. tonsurans</i> )
TERG_00917	2.89 aureobasidin A resistance protein ( <i>T. equinum</i> )
TERG_02306	2.86 integral membrane protein ( <i>T. equinum</i> )
TERG_03491	2.81 hypothetical protein
TERG_11513	2.79 esterase ( <i>T. equinum</i> )
TERG_11774	2.77 hypothetical protein
TERG_12718	2.77 hypothetical protein
TERG_04109	2.74 C3HC4 finger protein ( <i>A. benhamiae</i> )
TERG_00149	2.72 hypothetical protein
TERG_12070	2.72 hypothetical protein
TERG_03183	2.71 hypothetical protein
TERG_01970	2.70 hypothetical protein
TERG_02150	2.67 hypothetical protein
TERG_06679	2.64 MFS transporter, putative ( <i>A. benhamiae</i> )
TERG_12068	2.63 PLC-E ( <i>T. equinum</i> )
TERG_12237	2.63 hypothetical protein
TERG_12679	2.62 JmjC domain-containing protein ( <i>T. tonsurans</i> )
TERG_05618	2.61 Lcc2 ( <i>T. equinum</i> )
TERG_02213	2.60 extracellular metalloproteinase 1
TERG_07919	2.59 thioesterase family protein ( <i>T. verrucosum</i> )
TERG_07982	2.59 hypothetical protein
TERG_08855	2.58 hypothetical protein
TERG_03868	2.56 cupin domain-containing protein ( <i>T. tonsurans</i> )
TERG_00527	2.55 hypothetical protein
TERG_03714	2.53 NCS1 nucleoside transporter ( <i>T. tonsurans</i> )
TERG_12028	2.53 metallothionein family protein ( <i>T. equinum</i> )
TERG_05298	2.53 rhomboid family membrane protein ( <i>T. tonsurans</i> )

TERG_04721	2.52	glutamate carboxypeptidase ( <i>T. equinum</i> )
TERG_01694	2.51	ankyrin repeat-containing protein ( <i>T. equinum</i> )
TERG_01807	2.51	hypothetical protein
TERG_11537	2.49	hypothetical protein
TERG_05988	2.49	solid-state culture expressed protein (Aos23), putative ( <i>T. verrucosum</i> )
TERG_04939	2.47	hypothetical protein
TERG_11514	2.47	lipase/esterase, putative ( <i>T. verrucosum</i> )
TERG_07331	2.45	integral membrane protein ( <i>T. tonsurans</i> )
TERG_12522	2.45	4-hydroxyphenylpyruvate dioxygenase ( <i>T. tonsurans</i> )
TERG_06290	2.44	hypothetical protein
TERG_08230	2.44	hypothetical protein
TERG_03132	2.43	hypothetical protein
TERG_03830	2.43	hypothetical protein
TERG_07479	2.41	hypothetical protein
TERG_01225	2.40	GTPase-activating protein GYP7 ( <i>T. equinum</i> )
TERG_11517	2.40	hypothetical protein
TERG_12639	2.39	choriogenin Hminor ( <i>M. canis</i> )
TERG_06807	2.39	cutinase, putative ( <i>A. benhamiae</i> )
TERG_02562	2.38	chitin synthase C
TERG_07242	2.37	di-trans,poly-cis-decaprenylcistransferase
TERG_03722	2.37	hypothetical protein
TERG_02448	2.36	hypothetical protein
TERG_05032	2.36	C6 transcription factor ( <i>T. equinum</i> )
TERG_01265	2.36	HhH-GPD family base excision DNA repair protein ( <i>T. tonsurans</i> )
TERG_03329	2.36	hypothetical protein
TERG_03218	2.35	extracellular salicylate hydroxylase/monooxygenase, putative ( <i>T. verrucosum</i> )
TERG_03732	2.35	hypothetical protein
TERG_03570	2.34	mitochondria fission 1 protein
TERG_00638	2.34	cellobiose dehydrogenase, putative ( <i>A. benhamiae</i> )
TERG_05429	2.33	MFS multidrug transporter, putative ( <i>T. verrucosum</i> )
TERG_03415	2.33	serine/threonine protein kinase
TERG_12692	2.33	hypothetical protein
TERG_02757	2.33	NADP-dependent alcohol dehydrogenase ( <i>T. equinum</i> )
TERG_08922	2.32	hypothetical protein
TERG_05013	2.32	stress response RCI peptide ( <i>T. equinum</i> )
TERG_03965	2.31	MFS nicotinic acid transporter ( <i>T. tonsurans</i> )
TERG_12337	2.30	hypothetical protein
TERG_03628	2.30	serine/threonine protein kinase ( <i>T. tonsurans</i> )
TERG_07705	2.30	hypothetical protein
TERG_00620	2.30	NAD <sup>+</sup> kinase Utr1 ( <i>T. equinum</i> )
TERG_00847	2.30	SOH1 family protein ( <i>T. equinum</i> )
TERG_00959	2.30	RNA binding protein, putative ( <i>A. benhamiae</i> )
TERG_05135	2.30	glutathione S-transferase GliG ( <i>A. benhamiae</i> )
TERG_08686	2.29	hypothetical protein
TERG_00950	2.29	hypothetical protein
TERG_07273	2.29	glycerol kinase ( <i>T. equinum</i> )
TERG_08622	2.28	transferase ( <i>M. canis</i> )
TERG_06402	2.28	Ser/Thr protein phosphatase family protein ( <i>T. verrucosum</i> )
TERG_05239	2.28	DNA polymerase POL4, putative ( <i>T. verrucosum</i> )

TERG_07311	2.28 fibronectin type III domain-containing protein ( <i>T. equinum</i> )
TERG_05126	2.27 ABC multidrug transporter, putative ( <i>A. benhamiae</i> )
TERG_03511	2.27 calcineurin binding protein ( <i>T. equinum</i> )
TERG_05310	2.27 kynurenine 3-monooxygenase ( <i>T. tonsurans</i> )
TERG_07804	2.26 PBSP domain-containing protein ( <i>T. tonsurans</i> )
TERG_12045	2.26 hypothetical protein
TERG_05244	2.26 hypothetical protein
TERG_05349	2.26 oxidoreductase, 2OG-Fe(II) oxygenase family, putative ( <i>A. benhamiae</i> )
TERG_05680	2.26 IBR domain containing protein ( <i>T. equinum</i> )
TERG_06900	2.25 hypothetical protein
TERG_00471	2.25 hypothetical protein
TERG_12694	2.24 hypothetical protein
TERG_01171	2.24 autophagy regulatory protein Atg2, putative ( <i>T. verrucosum</i> )
TERG_03662	2.23 hypothetical protein
TERG_03620	2.23 glycosyl transferase ( <i>T. tonsurans</i> )
TERG_11831	2.22 hypothetical protein
TERG_11543	2.22 hypothetical protein
TERG_01346	2.22 lipase/serine esterase ( <i>T. tonsurans</i> )
TERG_06994	2.22 hypothetical protein
TERG_00416	2.22 phenylacetaldoxime dehydratase family protein, putative ( <i>A. benhamiae</i> )
TERG_03512	2.21 hypothetical protein
TERG_07987	2.21 GNAT family acetyltransferase ( <i>T. equinum</i> )
TERG_00410	2.21 hypothetical protein
TERG_01822	2.21 serine/threonine protein kinase
TERG_06766	2.20 high affinity methionine permease ( <i>T. tonsurans</i> )
TERG_06995	2.19 metalloredutase, putative ( <i>T. verrucosum</i> )
TERG_08278	2.19 serine/threonine protein kinase ( <i>T. tonsurans</i> )
TERG_07501	2.19 nitrate reductase ( <i>T. tonsurans</i> )
TERG_12243	2.18 hypothetical protein
TERG_02558	2.18 oxysterol binding protein ( <i>T. tonsurans</i> )
TERG_07891	2.18 DUF255 domain-containing protein ( <i>T. equinum</i> )
TERG_07921	2.18 adenylylsulfate kinase
TERG_03064	2.17 MCAK-like kinesin ( <i>T. equinum</i> )
TERG_06969	2.17 CMGC/CDK/CDK5 protein kinase
TERG_12722	2.17 transferase ( <i>M. canis</i> )
TERG_03177	2.17 RING finger domain protein, putative ( <i>A. benhamiae</i> )
TERG_01849	2.17 hypothetical protein
TERG_02469	2.15 hypothetical protein
TERG_11680	2.15 DEAD/DEAH box DNA helicase ( <i>T. tonsurans</i> )
TERG_08065	2.14 auxin Efflux Carrier superfamily protein ( <i>T. equinum</i> )
TERG_03763	2.14 AAA family ATPase ( <i>T. tonsurans</i> )
TERG_05837	2.12 plasma membrane ammonium transporter (Ato3), putative ( <i>A. benhamiae</i> )
TERG_05541	2.12 hypothetical protein
TERG_02340	2.11 polysaccharide deacetylase ( <i>T. equinum</i> )
TERG_06741	2.11 ubiquitin C-terminal hydrolase ( <i>T. tonsurans</i> )
TERG_03790	2.11 DUF1275 domain-containing protein ( <i>T. equinum</i> )
TERG_03396	2.11 phospholipid-transporting ATPase ( <i>T. equinum</i> )
TERG_04473	2.11 hypothetical protein
TERG_03367	2.11 hypothetical protein

TERG_03443	2.10 ankyrin repeat protein ( <i>T. equinum</i> )
TERG_04698	2.10 hypothetical protein
TERG_12711	2.10 hypothetical protein
TERG_01626	2.09 AT hook domain-containing protein family protein ( <i>T. equinum</i> )
TERG_11681	2.09 DEAD/DEAH box DNA helicase ( <i>T. tonsurans</i> )
TERG_02092	2.09 hypothetical protein
TERG_11764	2.09 proline-threonine-rich repeat protein ( <i>T. tonsurans</i> )
TERG_02609	2.08 actin patches distal protein 1 ( <i>T. equinum</i> )
TERG_12721	2.08 transferase ( <i>M. canis</i> )
TERG_05706	2.08 hypothetical protein
TERG_04941	2.08 mitochondrial pyruvate dehydrogenase kinase ( <i>T. tonsurans</i> )
TERG_12455	2.08 hypothetical protein
TERG_04283	2.07 hypothetical protein
TERG_03537	2.07 alpha/beta hydrolase ( <i>T. equinum</i> )
TERG_07252	2.07 hypothetical protein
TERG_05736	2.07 alkaline serine protease ( <i>T. tonsurans</i> )
TERG_08301	2.07 fatty-acid synthase subunit alpha ( <i>M. canis</i> )
TERG_00273	2.07 mucin ( <i>M. canis</i> )
TERG_00188	2.06 hypothetical protein
TERG_08538	2.06 Diacylglycerol kinase domain-containing protein ( <i>T. equinum</i> )
TERG_08262	2.06 C6 transcription factor, putative ( <i>A. benhamiae</i> )
TERG_02651	2.05 NRPS-like enzyme, putative ( <i>A. benhamiae</i> )
TERG_11941	2.05 MCAK-like kinesin ( <i>T. equinum</i> )
TERG_08666	2.05 hypothetical protein
TERG_05111	2.05 hypothetical protein
TERG_03125	2.05 hypothetical protein
TERG_02113	2.04 TIGR01456 family HAD hydrolase
TERG_01794	2.04 C6 zinc finger domain-containing protein ( <i>M. canis</i> )
TERG_03681	2.04 leucine aminopeptidase ( <i>T. equinum</i> )
TERG_07779	2.03 LCCL domain-containing protein ( <i>T. tonsurans</i> )
TERG_05876	2.03 hypothetical protein
TERG_03861	2.03 C2H2 transcription factor ( <i>T. tonsurans</i> )
TERG_02018	2.02 hypothetical protein
TERG_05425	2.02 guanine deaminase
TERG_02315	2.02 extracellular aspartic endopeptidase, putative ( <i>A. benhamiae</i> )
TERG_05441	2.02 cytochrome P450 alkane hydroxylase, putative ( <i>T. verrucosum</i> )
TERG_05157	2.02 hypothetical protein
TERG_02265	2.02 MFS multidrug transporter ( <i>T. equinum</i> )
TERG_08384	2.02 hypothetical protein
TERG_06145	2.02 arrestin ( <i>T. equinum</i> )
TERG_12615	2.01 ankyrin repeat-containing protein ( <i>T. equinum</i> )
TERG_06735	2.01 oxysterol binding protein ( <i>T. tonsurans</i> )
TERG_06778	2.01 PAP2 domain protein ( <i>T. verrucosum</i> )
TERG_00362	2.01 glutaminase ( <i>T. equinum</i> )
TERG_07942	2.01 calcium channel subunit Cch1 ( <i>T. tonsurans</i> )
TERG_07990	2.00 proline-rich protein ( <i>T. tonsurans</i> )
TERG_02974	2.00 hypothetical protein
TERG_06457	2.00 hypothetical protein
TERG_12588	2.00 spindle pole body associated protein SnaD, putative ( <i>T. verrucosum</i> )

TERG_03061	2.00	hypothetical protein
TERG_04268	2.00	cell wall glucanase, putative ( <i>A. benhamiae</i> )
TERG_02483	1.99	hypothetical protein
TERG_08317	1.99	hypothetical protein
TERG_02371	1.99	hypothetical protein
TERG_05422	1.98	hypothetical protein
TERG_02298	1.98	GPI anchored cell wall protein, putative ( <i>T. verrucosum</i> )
TERG_02902	1.98	hypothetical protein
TERG_05575	1.98	MFS multidrug transporter ( <i>T. tonsurans</i> )
TERG_06955	1.97	hypothetical protein
TERG_03854	1.97	laccase ( <i>T. tonsurans</i> )
TERG_07983	1.96	hypothetical protein
TERG_03121	1.96	DNA repair and recombination protein RAD26 ( <i>M. canis</i> )
TERG_05563	1.95	hypothetical protein
TERG_03857	1.95	phosphotransferase enzyme family protein ( <i>T. equinum</i> )
TERG_05079	1.95	extracellular OTU-like cysteine protease, putative ( <i>A. benhamiae</i> )
TERG_03848	1.95	hypothetical protein
TERG_12072	1.93	hypothetical protein
TERG_03969	1.93	hypothetical protein
TERG_04376	1.93	aldehyde reductase I (ARI), putative ( <i>T. verrucosum</i> )
TERG_07871	1.93	hypothetical protein
TERG_12616	1.92	ankyrin repeat-containing protein ( <i>T. equinum</i> )
TERG_00995	1.92	hypothetical protein
TERG_04785	1.92	hypothetical protein
TERG_07870	1.92	glycosyl transferase, putative ( <i>A. benhamiae</i> )
TERG_02183	1.92	C2H2 finger domain-containing protein ( <i>T. equinum</i> )
TERG_02885	1.91	E3 ubiquitin-protein ligase pub1 ( <i>T. tonsurans</i> )
TERG_00828	1.90	hypothetical protein
TERG_00233	1.90	glyoxalase ( <i>T. tonsurans</i> )
TERG_05553	1.90	integral membrane protein ( <i>T. equinum</i> )
TERG_05446	1.90	sarcosine oxidase ( <i>T. equinum</i> )
TERG_08341	1.90	hypothetical protein
TERG_07991	1.89	proline-rich protein ( <i>T. tonsurans</i> )
TERG_01695	1.89	hypothetical protein
TERG_02061	1.89	C2H2 transcription factor (Ace1), putative ( <i>T. verrucosum</i> )
TERG_08328	1.89	basic proline-rich protein ( <i>M. canis</i> )
TERG_00176	1.88	hydroxyisourate hydrolase
TERG_03549	1.88	hypothetical protein
TERG_12436	1.88	monocarboxylate transporter ( <i>M. canis</i> )
TERG_02211	1.88	serine/threonine protein kinase ( <i>T. tonsurans</i> )
TERG_00439	1.87	hypothetical protein
TERG_04417	1.87	DUF455 domain protein ( <i>A. benhamiae</i> )
TERG_06771	1.87	FAD binding domain protein ( <i>A. benhamiae</i> )
TERG_06368	1.87	hypothetical protein
TERG_06552	1.87	aspartic-type endopeptidase (OpsB), putative ( <i>T. verrucosum</i> )
TERG_12139	1.86	hypothetical protein
TERG_02714	1.86	proteinase, putative ( <i>A. benhamiae</i> )
TERG_01173	1.86	hypothetical protein
TERG_03179	1.85	NlpC/P60-like cell-wall peptidase, putative ( <i>A. benhamiae</i> )

TERG_00059	1.84 hypothetical protein
TERG_04429	1.84 MORN repeat-containing protein ( <i>T. equinum</i> )
TERG_05452	1.84 GABA permease ( <i>T. tonsurans</i> )
TERG_05909	1.83 hypothetical protein
TERG_03562	1.83 hypothetical protein
TERG_06978	1.83 SirQ protein ( <i>T. equinum</i> )
TERG_03945	1.83 hypothetical protein
TERG_03789	1.83 glutamine-serine rich protein MS8, putative ( <i>A. benhamiae</i> )
TERG_11762	1.83 lysine-specific permease ( <i>M. gypseum</i> )
TERG_08601	1.83 hypothetical protein
TERG_02453	1.83 hypothetical protein
TERG_00776	1.82 MFS transporter ( <i>T. tonsurans</i> )
TERG_03684	1.82 stress activated MAP kinase interacting protein ( <i>T. equinum</i> )
TERG_00590	1.82 hypothetical protein
TERG_03456	1.82 hypothetical protein
TERG_07265	1.82 sucrase/ferredoxin domain-containing protein ( <i>T. equinum</i> )
TERG_00517	1.81 hypothetical protein
TERG_02561	1.81 ubiquinone biosynthesis protein Coq7 ( <i>T. tonsurans</i> )
TERG_07143	1.81 potassium/sodium efflux P-type ATPase, fungal-type
TERG_04543	1.81 aminotransferase GliI ( <i>T. equinum</i> )
TERG_08069	1.81 glutathione-disulfide reductase
TERG_03486	1.80 Lectin C-type domain protein ( <i>T. verrucosum</i> )
TERG_02412	1.80 HHE domain protein ( <i>T. verrucosum</i> )
TERG_00252	1.80 hypothetical protein
TERG_06044	1.80 hypothetical protein
TERG_03228	1.80 transcriptional regulator PacG/VIB-1 ( <i>T. verrucosum</i> )
TERG_08123	1.80 C6 finger domain protein, putative ( <i>A. benhamiae</i> )
TERG_04774	1.80 isoflavone reductase family protein ( <i>T. verrucosum</i> )
TERG_12349	1.80 hypothetical protein
TERG_12114	1.79 hypothetical protein
TERG_06460	1.79 LEM3/CDC50 family protein ( <i>T. tonsurans</i> )
TERG_05304	1.79 cyanate hydratase
TERG_03653	1.79 hypothetical protein
TERG_12075	1.79 hypothetical protein
TERG_06802	1.79 hypothetical protein
TERG_07188	1.79 xanthine dehydrogenase ( <i>T. tonsurans</i> )
TERG_06594	1.78 DUF1183 domain-containing protein ( <i>T. equinum</i> )
TERG_12176	1.78 hypothetical protein
TERG_11634	1.77 DUF907 domain protein ( <i>T. verrucosum</i> )
TERG_00331	1.77 golgi apparatus membrane protein TVP18 ( <i>T. tonsurans</i> )
TERG_02632	1.77 autophagy cysteine endopeptidase Atg4, putative ( <i>A. benhamiae</i> )
TERG_01049	1.77 hypothetical protein
TERG_06801	1.77 cyclic nucleotide-binding domain-containing protein ( <i>T. tonsurans</i> )
TERG_12055	1.77 vegetative cell wall protein gp1 ( <i>M. canis</i> )
TERG_02063	1.76 hypothetical protein
TERG_04915	1.76 alpha/beta hydrolase ( <i>T. tonsurans</i> )
TERG_08100	1.76 CDP-diacylglycerol-inositol 3-phosphatidyltransferase PIS ( <i>T. equinum</i> )
TERG_12712	1.76 hypothetical protein
TERG_00483	1.76 hypothetical protein

TERG_04338	1.75 subtilisin-like serine protease pepC
TERG_05136	1.75 cytochrome P450 oxidoreductase GliC ( <i>A. benhamiae</i> )
TERG_12265	1.75 glutathione-dependent formaldehyde-activating enzyme ( <i>T. tonsurans</i> )
TERG_01546	1.75 oxidoreductase ( <i>T. tonsurans</i> )
TERG_07489	1.75 hypothetical protein
TERG_06543	1.75 phosphatidate cytidyltransferase ( <i>T. tonsurans</i> )
TERG_12516	1.75 DNA binding protein SART-1 ( <i>T. tonsurans</i> )
TERG_01551	1.75 hypothetical protein
TERG_08255	1.75 carboxypeptidase S1, putative ( <i>A. benhamiae</i> )
TERG_06239	1.75 hypothetical protein
TERG_01328	1.74 metalloredutase transmembrane component, putative ( <i>A. benhamiae</i> )
TERG_04385	1.74 serine/threonine protein kinase ( <i>T. tonsurans</i> )
TERG_08535	1.74 RING finger protein ( <i>A. benhamiae</i> )
TERG_05098	1.74 arginine metabolism regulation protein iii ( <i>T. verrucosum</i> )
TERG_11795	1.74 hypothetical protein
TERG_01889	1.74 RING finger domain-containing protein ( <i>T. tonsurans</i> )
TERG_06089	1.74 PH domain-containing protein ( <i>T. equinum</i> )
TERG_00338	1.74 glutamate carboxypeptidase ( <i>T. tonsurans</i> )
TERG_03705	1.74 cytochrome P450 monooxygenase, putative ( <i>A. benhamiae</i> )
TERG_00148	1.74 hypothetical protein
TERG_02918	1.74 alkaline phytoceramidase ( <i>T. equinum</i> )
TERG_00100	1.73 flavin-containing monooxygenase ( <i>T. equinum</i> )
TERG_02222	1.73 TBC domain-containing protein ( <i>T. equinum</i> )
TERG_05842	1.73 png1 ( <i>T. equinum</i> )
TERG_00836	1.73 QDE-2-interacting protein ( <i>M. gypseum</i> )
TERG_00954	1.72 hypothetical protein
TERG_03283	1.72 diene lactone hydrolase ( <i>M. gypseum</i> )
TERG_07666	1.72 hypothetical protein
TERG_12370	1.72 MFS multidrug transporter, putative ( <i>A. benhamiae</i> )
TERG_06354	1.72 SVP1-like protein ( <i>T. tonsurans</i> )
TERG_07762	1.71 hypothetical protein
TERG_00680	1.71 fimbrin ( <i>T. tonsurans</i> )
TERG_11557	1.71 luciferin 4-monooxygenase ( <i>T. equinum</i> )
TERG_01644	1.71 SNF2 family helicase/ATPase ( <i>T. equinum</i> )
TERG_01357	1.71 hypothetical protein
TERG_05854	1.71 beta-lactamase ( <i>T. tonsurans</i> )
TERG_05118	1.71 actin cytoskeleton organization protein ( <i>T. tonsurans</i> )
TERG_04654	1.71 ubiquitin carboxyl-terminal hydrolase ( <i>T. tonsurans</i> )
TERG_02243	1.70 hypothetical protein
TERG_07077	1.70 C6 transcription factor ( <i>T. equinum</i> )
TERG_00313	1.70 hemolysin-III channel protein Izh2 ( <i>T. tonsurans</i> )
TERG_03141	1.70 hypothetical protein
TERG_05554	1.70 integral membrane protein ( <i>T. equinum</i> )
TERG_05851	1.69 hypothetical protein
TERG_01843	1.69 inositol-3-phosphate synthase ( <i>T. tonsurans</i> )
TERG_05800	1.68 ubiquitin-protein ligase (Hul4), putative ( <i>A. benhamiae</i> )
TERG_03332	1.68 mitochondrial carrier protein ( <i>T. tonsurans</i> )
TERG_02016	1.68 Atg15p ( <i>M. gypseum</i> )
TERG_07332	1.68 hypothetical protein



TERG_12324	1.68 hypothetical protein
TERG_00267	1.68 hypothetical protein
TERG_04703	1.68 DUF1715 domain-containing protein ( <i>T. equinum</i> )
TERG_06247	1.67 DUF821 domain-containing protein ( <i>T. equinum</i> )
TERG_08378	1.67 hypothetical protein
TERG_03709	1.67 hypothetical protein
TERG_00803	1.66 DUF907 domain protein ( <i>A. benhamiae</i> )
TERG_03702	1.66 hypothetical protein
TERG_01153	1.66 hypothetical protein
TERG_04590	1.66 dihydrofolate synthetase Fol3 ( <i>T. equinum</i> )
TERG_01618	1.66 hypothetical protein
TERG_06681	1.66 glycogen debranching enzyme
TERG_07307	1.66 hypothetical protein
TERG_08824	1.65 hypothetical protein
TERG_03182	1.65 serine/threonine protein kinase ( <i>T. equinum</i> )
TERG_08381	1.65 NUDIX domain-containing protein ( <i>T. equinum</i> )
TERG_06111	1.65 DUF1711 domain-containing protein ( <i>M. canis</i> )
TERG_02816	1.64 diene lactone hydrolase ( <i>T. equinum</i> )
TERG_08708	1.64 SesA protein ( <i>T. equinum</i> )
TERG_06209	1.63 UTR2 protein ( <i>M. gypseum</i> )
TERG_07224	1.63 hypothetical protein
TERG_06016	1.63 glycosyl hydrolase ( <i>T. tonsurans</i> )
TERG_06675	1.63 GliK protein ( <i>T. equinum</i> )
TERG_12629	1.63 NAD(P) transhydrogenase ( <i>T. equinum</i> )
TERG_07567	1.63 DUF647 domain-containing protein ( <i>T. equinum</i> )
TERG_04123	1.63 hypothetical protein
TERG_04103	1.63 hypothetical protein
TERG_03533	1.62 DRAP deaminase, putative ( <i>A. benhamiae</i> )
TERG_02511	1.62 salicylate hydroxylase, putative ( <i>A. benhamiae</i> )
TERG_07996	1.62 hypothetical protein
TERG_01292	1.62 glycosyl hydrolase, putative ( <i>A. benhamiae</i> )
TERG_02843	1.62 C6 transcription factor ( <i>T. equinum</i> )
TERG_01856	1.62 CMGC/SRPK protein kinase
TERG_08044	1.61 GPI anchored protein, putative ( <i>A. benhamiae</i> )
TERG_05562	1.61 2-hydroxychromene-2-carboxylate isomerase, putative ( <i>A. benhamiae</i> )
TERG_11885	1.61 ABC bile acid transporter, putative ( <i>T. verrucosum</i> )
TERG_02481	1.61 F-box domain-containing protein ( <i>M. canis</i> )
TERG_01996	1.60 serine/threonine protein kinase
TERG_06899	1.60 alkaline phosphatase ( <i>T. tonsurans</i> )
TERG_00780	1.60 hypothetical protein
TERG_01105	1.60 serine/threonine protein kinase ( <i>T. tonsurans</i> )
TERG_02567	1.60 phytanoyl-CoA dioxygenase ( <i>T. tonsurans</i> )
TERG_02140	1.59 bZIP transcription factor ( <i>T. tonsurans</i> )
TERG_11682	1.59 hypothetical protein
TERG_00860	1.59 LRP16 family protein ( <i>T. tonsurans</i> )
TERG_02410	1.59 cytoskeleton assembly control protein Sla2 ( <i>T. tonsurans</i> )
TERG_12057	1.58 hypothetical protein
TERG_08902	1.58 hypothetical protein
TERG_03408	1.58 ZIP metal ion transporter ( <i>T. equinum</i> )

TERG_08811	1.58 hypothetical protein
TERG_11770	1.58 hypothetical protein
TERG_01841	1.58 hypothetical protein
TERG_07761	1.58 hypothetical protein
TERG_06765	1.58 ULK/ULK protein kinase
TERG_08287	1.58 ATP-citrate synthase ( <i>T. equinum</i> )
TERG_02524	1.58 proline-specific permease ( <i>T. equinum</i> )
TERG_03032	1.58 autophagy protein Atg13, putative ( <i>A. benhamiae</i> )
TERG_02445	1.58 hypothetical protein
TERG_06294	1.57 V-SNARE ( <i>T. equinum</i> )
TERG_04210	1.57 CAMKK/CAMKK-META protein kinase
TERG_07917	1.57 hypothetical protein
TERG_08066	1.57 STE/STE7 protein kinase
TERG_08011	1.57 metallocarboxypeptidase A-like protein
TERG_07707	1.57 C6 zinc finger domain-containing protein ( <i>T. equinum</i> )
TERG_08878	1.57 hypothetical protein
TERG_01914	1.57 trichodiene oxygenase ( <i>T. equinum</i> )
TERG_02550	1.57 ZZ type zinc finger domain protein ( <i>T. verrucosum</i> )
TERG_05963	1.57 WD repeat protein ( <i>T. tonsurans</i> )
TERG_06836	1.56 CAMK/CAMK1/CAMK1-RCK protein kinase
TERG_12636	1.56 hypothetical protein
TERG_04434	1.56 DNA repair protein
TERG_00349	1.55 hypothetical protein
TERG_06472	1.55 ketoreductase ( <i>T. tonsurans</i> )
TERG_05813	1.55 1-phosphatidylinositol-3-phosphate 5-kinase ( <i>T. equinum</i> )
TERG_11943	1.55 MFS maltose permease ( <i>T. tonsurans</i> )
TERG_06533	1.55 glyoxalase family protein ( <i>A. benhamiae</i> )
TERG_07706	1.54 hypothetical protein
TERG_01433	1.54 WD domain, G-beta repeat protein ( <i>A. benhamiae</i> )
TERG_08427	1.54 C6 transcription factor, putative ( <i>A. benhamiae</i> )
TERG_08288	1.54 ATP-citrate synthase subunit 1
TERG_12630	1.54 nicotinamide nucleotide transhydrogenase ( <i>T. tonsurans</i> )
TERG_06884	1.54 C6 transcription factor (War1), putative ( <i>T. verrucosum</i> )
TERG_01603	1.53 UBX domain-containing protein ( <i>T. equinum</i> )
TERG_02087	1.53 hypothetical protein
TERG_05230	1.53 hypothetical protein
TERG_05552	1.53 DNA mismatch repair protein MutL ( <i>T. tonsurans</i> )
TERG_07174	1.53 vesicle transport V-snare protein ( <i>T. equinum</i> )
TERG_02527	1.53 WD40 repeat protein ( <i>A. benhamiae</i> )
TERG_00097	1.53 hypothetical protein
TERG_03835	1.53 hypothetical protein
TERG_07223	1.53 hypothetical protein
TERG_00286	1.53 ABC transporter ( <i>T. tonsurans</i> )
TERG_03200	1.53 DNA repair and recombination protein RAD26 ( <i>T. tonsurans</i> )
TERG_05802	1.53 hypothetical protein
TERG_00580	1.52 7-dehydrocholesterol reductase ( <i>T. equinum</i> )
TERG_00589	1.52 phosphoesterase ( <i>T. tonsurans</i> )
TERG_00570	1.52 autophagy protein ( <i>T. equinum</i> )
TERG_00969	1.52 hypothetical protein

TERG_05144	1.52 hypothetical protein
TERG_07086	1.52 hypothetical protein
TERG_01811	1.51 triacylglycerol lipase, putative ( <i>A. benhamiae</i> )
TERG_00654	1.51 hypothetical protein
TERG_12393	1.51 hypothetical protein
TERG_11582	1.51 hypothetical protein
TERG_05580	1.51 hypothetical protein
TERG_08848	1.51 thioredoxin, putative ( <i>A. benhamiae</i> )
TERG_05405	1.51 methionine permease ( <i>T. equinum</i> )
TERG_02369	1.51 MFS transporter ( <i>T. tonsurans</i> )
TERG_07492	1.50 sugar transporter STL1 ( <i>T. tonsurans</i> )
TERG_06777	1.50 hypothetical protein
TERG_04414	1.50 isoflavone reductase family protein (CipA), putative ( <i>A. benhamiae</i> )
TERG_07337	-1.50 54S ribosomal protein RML2 ( <i>T. equinum</i> )
TERG_02122	-1.50 adenylate-forming enzyme, putative ( <i>A. benhamiae</i> )
TERG_01643	-1.50 hypothetical protein
TERG_04382	-1.50 c-14 sterol reductase ( <i>T. tonsurans</i> )
TERG_12344	-1.51 kinesin family protein ( <i>T. tonsurans</i> )
TERG_07335	-1.51 G2/M-specific cyclin NimE ( <i>T. tonsurans</i> )
TERG_08318	-1.51 HAD superfamily hydrolase ( <i>T. tonsurans</i> )
TERG_05384	-1.51 hypothetical protein
TERG_00211	-1.51 proteasome subunit alpha type 6 ( <i>T. equinum</i> )
TERG_07895	-1.51 prefoldin, alpha subunit
TERG_08991	-1.51 ATPase 2 nuclear control ( <i>M. gypseum</i> )
TERG_02465	-1.51 aminoalcoholphosphotransferase ( <i>T. equinum</i> )
TERG_04192	-1.51 lactonohydrolase, putative ( <i>A. benhamiae</i> )
TERG_06122	-1.52 hypothetical protein
TERG_12392	-1.52 hypothetical protein
TERG_08675	-1.52 hypothetical protein
TERG_12355	-1.52 hypothetical protein
TERG_00524	-1.52 trans-sialidase ( <i>M. canis</i> )
TERG_07157	-1.52 U3 small nucleolar RNA-associated protein 5 ( <i>T. equinum</i> )
TERG_05366	-1.52 hypothetical protein
TERG_06976	-1.52 separin, putative ( <i>T. verrucosum</i> )
TERG_04508	-1.52 AAA ATPase ( <i>T. equinum</i> )
TERG_00170	-1.53 hypothetical protein
TERG_03642	-1.53 hypothetical protein
TERG_00008	-1.53 MFS phospholipid transporter ( <i>T. tonsurans</i> )
TERG_00885	-1.53 60S ribosome biogenesis protein Rrp14 ( <i>T. tonsurans</i> )
TERG_00004	-1.53 alanine aminotransferase ( <i>T. tonsurans</i> )
TERG_02250	-1.53 cyclopropane-fatty-acyl-phospholipid synthase ( <i>T. tonsurans</i> )
TERG_07587	-1.53 hypothetical protein
TERG_06305	-1.53 DNA-directed RNA polymerase I and III ( <i>T. tonsurans</i> )
TERG_04087	-1.53 DnaJ domain-containing protein ( <i>T. tonsurans</i> )
TERG_00192	-1.53 ATP-dependent rRNA helicase spb4 ( <i>T. tonsurans</i> )
TERG_08845	-1.54 pyridoxamine phosphate oxidase ( <i>T. tonsurans</i> )
TERG_03498	-1.54 pre-rRNA processing protein Tsr1 ( <i>T. tonsurans</i> )
TERG_12121	-1.54 DNA replication licensing factor mcm5 ( <i>T. tonsurans</i> )
TERG_12504	-1.54 MFS multidrug transporter ( <i>T. equinum</i> )

TERG_00538	-1.54 oxidoreductase ( <i>T. tonsurans</i> )
TERG_00819	-1.54 PE repeat family protein ( <i>T. verrucosum</i> )
TERG_04586	-1.54 ribonucleoside-diphosphate reductase large chain
TERG_01761	-1.54 hypothetical protein
TERG_06366	-1.54 CAMK protein kinase
TERG_07799	-1.54 fatty acids protein 3 elongation ( <i>T. equinum</i> )
TERG_05809	-1.55 hypothetical protein
TERG_12434	-1.55 hypothetical protein
TERG_12395	-1.55 hypothetical protein
TERG_04636	-1.55 4-hydroxybenzoate polyprenyl transferase
TERG_04378	-1.55 aldehyde reductase I (ARI), putative ( <i>T. verrucosum</i> )
TERG_02037	-1.55 nucleic acid-binding protein ( <i>A. benhamiae</i> )
TERG_06553	-1.55 hypothetical protein
TERG_07120	-1.56 hypothetical protein
TERG_02057	-1.56 hypothetical protein
TERG_06933	-1.56 hypothetical protein
TERG_11862	-1.56 integral membrane protein ( <i>T. tonsurans</i> )
TERG_02176	-1.56 small nuclear ribonucleoprotein LSM2 ( <i>T. equinum</i> )
TERG_05790	-1.56 HMG box protein, putative ( <i>A. benhamiae</i> )
TERG_03174	-1.57 MFS siderochrome iron transporter MirB ( <i>T. verrucosum</i> )
TERG_12340	-1.57 hypothetical protein
TERG_11847	-1.57 hypothetical protein
TERG_03256	-1.57 carbonate dehydratase ( <i>T. equinum</i> )
TERG_01303	-1.57 hypothetical protein
TERG_04060	-1.57 C2H2 type zinc finger domain-containing protein ( <i>T. equinum</i> )
TERG_01771	-1.57 FAD binding monooxygenase, putative ( <i>T. verrucosum</i> )
TERG_04908	-1.57 signal recognition particle, putative ( <i>A. benhamiae</i> )
TERG_03777	-1.57 hypothetical protein
TERG_06918	-1.58 hypothetical protein
TERG_07963	-1.58 hypothetical protein
TERG_00983	-1.58 eukaryotic translation initiation factor 3 subunit K
TERG_12053	-1.58 HEAT repeat protein ( <i>T. verrucosum</i> )
TERG_07341	-1.58 DNA replication helicase Dna2 ( <i>T. tonsurans</i> )
TERG_02076	-1.58 hypothetical protein
TERG_00372	-1.58 hypothetical protein
TERG_01231	-1.58 ribosomal large subunit biogenesis protein MAK16 ( <i>T. tonsurans</i> )
TERG_02538	-1.59 carboxylesterase ( <i>T. equinum</i> )
TERG_00386	-1.59 hypothetical protein
TERG_11809	-1.59 hydroxymethylglutaryl-CoA synthase
TERG_01812	-1.59 nucleolar complex protein 14 ( <i>T. equinum</i> )
TERG_02788	-1.59 DNA-directed RNA polymerase I ( <i>T. tonsurans</i> )
TERG_04349	-1.59 hypothetical protein
TERG_00894	-1.59 translation initiation factor IF-2
TERG_05370	-1.59 hypothetical protein
TERG_05254	-1.60 translation initiation factor RLII
TERG_04684	-1.60 shugoshin family protein ( <i>A. benhamiae</i> )
TERG_12200	-1.60 hypothetical protein
TERG_01697	-1.60 hypothetical protein
TERG_01239	-1.60 Mis6 domain-containing protein ( <i>T. equinum</i> )

TERG_08234	-1.60 TCTP family protein ( <i>T. verrucosum</i> )
TERG_07613	-1.60 nuclear envelope protein ( <i>T. equinum</i> )
TERG_03345	-1.60 hypothetical protein
TERG_01443	-1.61 ABC multidrug transporter ( <i>T. tonsurans</i> )
TERG_07061	-1.61 CMGC/SRPK protein kinase
TERG_02293	-1.61 hypothetical protein
TERG_02393	-1.61 hypothetical protein
TERG_02575	-1.61 hypothetical protein
TERG_02973	-1.61 morphogenesis protein (Msb1), putative ( <i>T. verrucosum</i> )
TERG_02854	-1.61 dynein light chain ( <i>T. tonsurans</i> )
TERG_11721	-1.61 acyl-CoA dehydrogenase ( <i>T. tonsurans</i> )
TERG_06144	-1.61 cell wall serine-threonine-rich galactomannoprotein Mp1 ( <i>A. benhamiae</i> )
TERG_06129	-1.61 60S ribosomal protein
TERG_11758	-1.62 DUF866 domain-containing protein ( <i>T. equinum</i> )
TERG_03084	-1.62 pentatricopeptide repeat protein ( <i>A. benhamiae</i> )
TERG_01507	-1.62 extracellular proline-glycine rich protein ( <i>T. verrucosum</i> )
TERG_05388	-1.62 ribosome biogenesis protein ( <i>T. tonsurans</i> )
TERG_04410	-1.62 hypothetical protein
TERG_06230	-1.62 hypothetical protein
TERG_04819	-1.62 Fe superoxide dismutase ( <i>T. tonsurans</i> )
TERG_05701	-1.62 C4-dicarboxylate transporter/malic acid transport protein, putative ( <i>T. verrucosum</i> )
TERG_00249	-1.62 ATP-dependent rRNA helicase RRP3
TERG_06621	-1.62 60S ribosomal subunit assembly/export protein loc1 ( <i>T. tonsurans</i> )
TERG_05967	-1.63 hypothetical protein
TERG_02590	-1.63 peptidyl-prolyl cis-trans isomerase D
TERG_02251	-1.63 hypothetical protein
TERG_00974	-1.63 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
TERG_04062	-1.63 low-temperature viability protein Itv1 ( <i>T. tonsurans</i> )
TERG_06964	-1.63 NTF2 domain-containing protein ( <i>T. tonsurans</i> )
TERG_02326	-1.63 WD domain-containing protein ( <i>T. tonsurans</i> )
TERG_02616	-1.63 integral membrane protein ( <i>T. equinum</i> )
TERG_05846	-1.63 G1/S-specific cyclin CLN1 ( <i>T. equinum</i> )
TERG_01257	-1.63 nascent polypeptide-associated complex subunit alpha
TERG_08884	-1.63 GPI-anchored cell surface glycoprotein, putative ( <i>T. verrucosum</i> )
TERG_06528	-1.64 Delta(24(24(1)))-sterol reductase ( <i>T. equinum</i> )
TERG_08429	-1.64 eukaryotic translation initiation factor 3 subunit H
TERG_00893	-1.64 mitochondrial carrier protein, putative ( <i>T. verrucosum</i> )
TERG_05434	-1.64 ribosome associated DnaJ chaperone Zuotin ( <i>T. equinum</i> )
TERG_06375	-1.64 hypothetical protein
TERG_01959	-1.64 RNA polymerase Rpb1 C-terminal repeat domain-containing protein ( <i>T. equinum</i> )
TERG_01679	-1.64 Trm112p-like protein ( <i>T. equinum</i> )
TERG_12131	-1.64 alcohol dehydrogenase ( <i>T. tonsurans</i> )
TERG_05891	-1.65 MFS phosphate transporter ( <i>T. equinum</i> )
TERG_12325	-1.65 hypothetical protein
TERG_08623	-1.65 O-methyltransferase GliM2 ( <i>T. equinum</i> )
TERG_08443	-1.66 adenosylhomocysteinase
TERG_04307	-1.66 hypothetical protein
TERG_03339	-1.66 alternative oxidase, mitochondrial

TERG_03587	-1.66 WD repeat protein ( <i>T. verrucosum</i> )
TERG_07444	-1.66 nuclear segregation protein ( <i>T. tonsurans</i> )
TERG_05002	-1.67 UDP-glucose 4-epimerase GalE
TERG_05925	-1.67 EF-hand protein ( <i>T. tonsurans</i> )
TERG_03205	-1.67 DNA polymerase alpha catalytic subunit ( <i>T. equinum</i> )
TERG_12620	-1.67 hypothetical protein
TERG_00757	-1.68 hypothetical protein
TERG_07557	-1.68 hypothetical protein
TERG_04339	-1.68 signal transduction protein Syg1, putative ( <i>A. benhamiae</i> )
TERG_07473	-1.68 DNA-directed RNA polymerase I ( <i>T. tonsurans</i> )
TERG_06744	-1.68 fructose-bisphosphate aldolase 1
TERG_00124	-1.68 peroxisomal matrix protein ( <i>T. equinum</i> )
TERG_07131	-1.68 phosphotransmitter protein Ypd1 ( <i>T. equinum</i> )
TERG_03453	-1.68 eukaryotic translation initiation factor 5 ( <i>T. tonsurans</i> )
TERG_01968	-1.68 RNA binding protein, putative ( <i>T. verrucosum</i> )
TERG_05948	-1.68 protein kinase subdomain-containing protein ( <i>T. equinum</i> )
TERG_06358	-1.68 dicer ( <i>T. tonsurans</i> )
TERG_04131	-1.68 heat shock trehalose synthase, putative ( <i>T. verrucosum</i> )
TERG_03270	-1.68 small nucleolar ribonucleoprotein complex subunit ( <i>T. tonsurans</i> )
TERG_07616	-1.68 diphosphomevalonate decarboxylase
TERG_04995	-1.68 ribosome biogenesis protein Urb1, putative ( <i>A. benhamiae</i> )
TERG_01310	-1.69 nascent polypeptide-associated complex subunit beta
TERG_07024	-1.69 endoribonuclease L-PSP ( <i>T. tonsurans</i> )
TERG_08368	-1.69 TTK protein kinase
TERG_08497	-1.69 mRNA turnover protein 4 ( <i>T. equinum</i> )
TERG_05558	-1.69 ornithine decarboxylase, putative ( <i>T. verrucosum</i> )
TERG_11915	-1.69 nucleolus protein required for cell viability ( <i>T. tonsurans</i> )
TERG_05956	-1.69 rRNA processing protein Ebp2p ( <i>T. equinum</i> )
TERG_06150	-1.69 deoxyuridine 5'-triphosphate nucleotidohydrolase
TERG_01206	-1.69 pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43 ( <i>T. equinum</i> )
TERG_06662	-1.70 eukaryotic translation initiation factor 3 subunit B
TERG_06578	-1.70 glutathione S-transferase, putative ( <i>A. benhamiae</i> )
TERG_02617	-1.70 DNA primase subunit Pri1 ( <i>T. tonsurans</i> )
TERG_04959	-1.70 hypothetical protein
TERG_03124	-1.70 histone
TERG_00977	-1.70 hypothetical protein
TERG_00703	-1.70 nuclear migration protein, putative ( <i>A. benhamiae</i> )
TERG_03172	-1.71 sodium/phosphate symporter ( <i>T. tonsurans</i> )
TERG_03499	-1.71 U3 small nucleolar RNA-associated protein 7 ( <i>T. equinum</i> )
TERG_00834	-1.71 60S ribosomal protein L24b ( <i>T. equinum</i> )
TERG_12503	-1.71 polyamine transporter 2
TERG_01612	-1.71 enolase
TERG_00373	-1.71 hypothetical protein
TERG_08755	-1.71 M-phase inducer phosphatase ( <i>T. tonsurans</i> )
TERG_05261	-1.72 karyopherin alpha subunit ( <i>T. tonsurans</i> )
TERG_04402	-1.72 glyceraldehyde-3-phosphate dehydrogenase
TERG_07361	-1.72 hybrid PKS-NRPS enzyme, putative ( <i>A. benhamiae</i> )
TERG_01957	-1.72 proteinase T ( <i>M. gypseum</i> )
TERG_04746	-1.72 nucleolar GTP-binding protein ( <i>T. tonsurans</i> )

TERG_07539	-1.72 multidrug resistance protein ( <i>T. tonsurans</i> )
TERG_02319	-1.72 metallo-beta-lactamase superfamily protein ( <i>T. equinum</i> )
TERG_05242	-1.73 PUF6 ( <i>M. gypseum</i> )
TERG_02772	-1.73 DNA polymerase V ( <i>T. tonsurans</i> )
TERG_07958	-1.73 myosin class II heavy chain (MHC), putative ( <i>T. verrucosum</i> )
TERG_02023	-1.73 extracellular matrix protein, putative ( <i>T. verrucosum</i> )
TERG_01787	-1.73 integral membrane protein ( <i>T. equinum</i> )
TERG_08918	-1.73 hypothetical protein
TERG_12373	-1.73 multidrug resistance protein ( <i>T. tonsurans</i> )
TERG_07547	-1.73 RGS domain-containing protein ( <i>T. tonsurans</i> )
TERG_03625	-1.74 hypothetical protein
TERG_07736	-1.74 hypothetical protein
TERG_00573	-1.75 hypothetical protein
TERG_03497	-1.75 hemolysin-III family protein ( <i>T. equinum</i> )
TERG_12631	-1.75 conserved lysine-rich protein, putative ( <i>T. verrucosum</i> )
TERG_05865	-1.76 integral membrane protein, Mpv17/PMP22 family, putative ( <i>T. verrucosum</i> )
TERG_08125	-1.76 nucleolar complex protein 2 ( <i>T. equinum</i> )
TERG_02866	-1.76 ribosome biogenesis protein ERB1
TERG_01377	-1.76 hypothetical protein
TERG_07641	-1.76 GPI-anchored cell wall protein Pst1, putative ( <i>A. benhamiae</i> )
TERG_04616	-1.76 hypothetical protein
TERG_06906	-1.76 DNA mismatch repair protein msh6 ( <i>T. equinum</i> )
TERG_01046	-1.76 H/ACA ribonucleoprotein complex subunit 1
TERG_00257	-1.77 conserved predicted protein ( <i>A. benhamiae</i> )
TERG_01010	-1.77 Leucine Rich Repeat domain protein ( <i>A. benhamiae</i> )
TERG_00181	-1.77 nucleolar protein 58
TERG_11525	-1.77 hypothetical protein
TERG_05074	-1.77 NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG ( <i>M. gypseum</i> )
TERG_05941	-1.78 stress responsive A/B barrel domain-containing protein ( <i>T. equinum</i> )
TERG_11600	-1.78 MFS transporter ( <i>T. tonsurans</i> )
TERG_12447	-1.78 F-box domain-containing protein ( <i>M. gypseum</i> )
TERG_08391	-1.78 hypothetical protein
TERG_02399	-1.78 RNA-directed RNA polymerase ( <i>T. tonsurans</i> )
TERG_00456	-1.78 cysteine dioxygenase, putative ( <i>A. benhamiae</i> )
TERG_11907	-1.78 FAD binding domain containing protein ( <i>T. equinum</i> )
TERG_08289	-1.78 Rpp14 family protein ( <i>T. equinum</i> )
TERG_08236	-1.79 hypothetical protein
TERG_04964	-1.79 RNA-binding protein ( <i>A. benhamiae</i> )
TERG_02888	-1.80 PWI domain mRNA processing protein, putative ( <i>T. verrucosum</i> )
TERG_00117	-1.80 SNF2 family helicase, putative ( <i>T. verrucosum</i> )
TERG_03935	-1.80 hypothetical protein
TERG_06810	-1.80 hypothetical protein
TERG_12632	-1.80 conserved lysine-rich protein, putative ( <i>A. benhamiae</i> )
TERG_06158	-1.81 60S ribosomal protein L29
TERG_04790	-1.81 arsenical-resistance protein
TERG_03977	-1.81 hypothetical protein
TERG_01440	-1.81 vegetative cell wall protein gp1 ( <i>M. canis</i> )
TERG_11869	-1.81 cysteine protease atg4 ( <i>T. equinum</i> )
TERG_00063	-1.82 lysine-tRNA ligase

TERG_12119	-1.82 hypothetical protein
TERG_06264	-1.82 steroid monooxygenase, putative ( <i>T. verrucosum</i> )
TERG_06222	-1.82 MYB DNA-binding domain-containing protein ( <i>T. equinum</i> )
TERG_01591	-1.82 small nucleolar ribonucleoprotein complex subunit ( <i>T. equinum</i> )
TERG_06844	-1.82 40S ribosomal protein S21
TERG_02058	-1.82 ribosome biogenesis protein RPF2 ( <i>T. equinum</i> )
TERG_03364	-1.83 hypothetical protein
TERG_03102	-1.83 sterol 24-C-methyltransferase ( <i>T. equinum</i> )
TERG_12633	-1.83 conserved lysine-rich protein, putative ( <i>A. benhamiae</i> )
TERG_12526	-1.83 hypothetical protein
TERG_00605	-1.83 imidazoleglycerol-phosphate dehydratase ( <i>T. equinum</i> )
TERG_12059	-1.83 transporter smf2 ( <i>T. tonsurans</i> )
TERG_00640	-1.83 eukaryotic translation initiation factor 3 subunit L
TERG_01853	-1.84 hypothetical protein
TERG_07047	-1.84 cholesterol delta-isomerase, putative ( <i>T. verrucosum</i> )
TERG_07939	-1.84 ribosomal RNA processing protein ( <i>T. equinum</i> )
TERG_06090	-1.84 C2H2 transcription factor (TFIIIA), putative ( <i>T. verrucosum</i> )
TERG_03734	-1.84 pre-rRNA processing protein Rrp12 ( <i>T. tonsurans</i> )
TERG_01490	-1.84 LysR family regulatory protein ( <i>M. gypseum</i> )
TERG_12252	-1.85 GTP-binding protein ( <i>T. tonsurans</i> )
TERG_02914	-1.85 tRNA (guanine-N(7)-)-methyltransferase
TERG_12390	-1.85 hypothetical protein
TERG_01076	-1.85 aconitate hydratase, mitochondrial
TERG_00922	-1.85 meiotically up-regulated 65 protein ( <i>T. equinum</i> )
TERG_04893	-1.85 polyadenylate-binding protein, cytoplasmic and nuclear
TERG_11948	-1.85 hypothetical protein
TERG_08655	-1.86 ADP,ATP carrier protein
TERG_02139	-1.86 eukaryotic translation initiation factor 3 subunit D
TERG_08961	-1.86 hypothetical protein
TERG_11690	-1.86 protein kinase subdomain-containing protein ( <i>T. tonsurans</i> )
TERG_04002	-1.86 ribosome assembly protein SQT1 ( <i>T. equinum</i> )
TERG_07810	-1.86 phospholipase ( <i>T. tonsurans</i> )
TERG_04437	-1.87 nucleolar protein NOP2 ( <i>T. tonsurans</i> )
TERG_07171	-1.87 hypothetical protein
TERG_07125	-1.87 peptidyl-tRNA hydrolase
TERG_06651	-1.87 cytochrome P450, putative ( <i>T. verrucosum</i> )
TERG_00720	-1.87 60S ribosomal protein L19 ( <i>T. tonsurans</i> )
TERG_07409	-1.87 amino acid permease ( <i>T. equinum</i> )
TERG_00105	-1.87 40S ribosomal protein S30
TERG_04875	-1.88 monocarboxylate permease ( <i>T. equinum</i> )
TERG_06917	-1.88 elongation factor G, mitochondrial
TERG_01372	-1.88 hypothetical protein
TERG_05021	-1.88 C6 transcription factor, putative ( <i>A. benhamiae</i> )
TERG_05146	-1.88 protein methyltransferase ( <i>T. tonsurans</i> )
TERG_04025	-1.88 hypothetical protein
TERG_07882	-1.89 myosin type II heavy chain ( <i>T. tonsurans</i> )
TERG_06522	-1.89 FMN dependent dehydrogenase, putative ( <i>T. verrucosum</i> )
TERG_06893	-1.89 aspartyl-tRNA synthetase ( <i>T. tonsurans</i> )
TERG_02125	-1.89 hypothetical protein



TERG_07947	-1.89 Sas10/Utp3 family protein ( <i>T. tonsurans</i> )
TERG_03225	-1.89 betaine aldehyde dehydrogenase, putative ( <i>A. benhamiae</i> )
TERG_04899	-1.89 ubiquitin-60S ribosomal protein L40
TERG_06539	-1.90 fructosamine-3-kinase ( <i>T. equinum</i> )
TERG_06026	-1.90 ribosomal protein S24 ( <i>T. tonsurans</i> )
TERG_04979	-1.90 RNA exonuclease 4 ( <i>T. tonsurans</i> )
TERG_01494	-1.90 hypothetical protein
TERG_02921	-1.90 hypothetical protein
TERG_07362	-1.90 UV damage endonuclease UvdE
TERG_04676	-1.91 cell division control protein 10 ( <i>T. tonsurans</i> )
TERG_05039	-1.91 ribonucleoprotein-associated protein
TERG_05342	-1.91 MFS multidrug transporter, putative ( <i>A. benhamiae</i> )
TERG_02867	-1.91 ribosome biogenesis ATPase RIX7 ( <i>T. tonsurans</i> )
TERG_07950	-1.91 translation elongation factor 1 subunit Eef1-beta ( <i>T. equinum</i> )
TERG_05799	-1.91 chlorophyll synthesis pathway protein BchC
TERG_06796	-1.91 kinesin family protein ( <i>T. equinum</i> )
TERG_00962	-1.91 protein kinase subdomain-containing protein ( <i>T. tonsurans</i> )
TERG_12199	-1.91 hypothetical protein
TERG_06032	-1.91 ribosomal small subunit assembly protein, putative ( <i>A. benhamiae</i> )
TERG_07922	-1.92 glycine cleavage system T protein
TERG_03400	-1.92 subtilisin-like protease 1
TERG_12501	-1.92 catechol dioxygenase, putative ( <i>T. verrucosum</i> )
TERG_12294	-1.92 histidine acid phosphatase, putative ( <i>T. verrucosum</i> )
TERG_12533	-1.93 hypothetical protein
TERG_06218	-1.93 60S ribosomal protein L34 ( <i>T. equinum</i> )
TERG_05278	-1.93 microtubule associated protein ( <i>T. tonsurans</i> )
TERG_12120	-1.93 DNA replication licensing factor mcm5
TERG_12491	-1.93 carboxylesterase, putative ( <i>A. benhamiae</i> )
TERG_08363	-1.93 tyrosinase ( <i>T. verrucosum</i> )
TERG_04238	-1.93 H/K ATPase alpha subunit ( <i>T. equinum</i> )
TERG_02587	-1.94 hypothetical protein
TERG_07059	-1.94 hypothetical protein
TERG_08794	-1.94 pyruvate dehydrogenase kinase ( <i>T. equinum</i> )
TERG_00708	-1.94 serine hydroxymethyltransferase ( <i>T. tonsurans</i> )
TERG_04548	-1.94 SH3 domain-containing protein cyk3 ( <i>T. equinum</i> )
TERG_06109	-1.94 RNA polymerase I subunit Rpa43, putative ( <i>T. verrucosum</i> )
TERG_12511	-1.95 MFS multidrug transporter ( <i>T. equinum</i> )
TERG_02672	-1.95 ATP-dependent RNA helicase has1
TERG_11979	-1.95 cell division control protein 54 ( <i>T. tonsurans</i> )
TERG_03401	-1.95 high affinity nickel transporter ( <i>T. tonsurans</i> )
TERG_12321	-1.96 hypothetical protein
TERG_06172	-1.96 60S ribosomal protein L12
TERG_00943	-1.96 DNA mismatch repair protein msh-2 ( <i>M. canis</i> )
TERG_08269	-1.97 polysaccharide deacetylase ( <i>T. tonsurans</i> )
TERG_07012	-1.97 rRNA 2'-O-methyltransferase fibrillar
TERG_12602	-1.97 4-coumarate-CoA ligase ( <i>T. equinum</i> )
TERG_08133	-1.97 40S ribosomal protein S25
TERG_08990	-1.97 hypothetical protein
TERG_08375	-1.97 ATP-dependent RNA helicase eIF4A

TERG_01446	-1.97	GMP synthase [glutamine-hydrolyzing]
TERG_12226	-1.97	SNF2 family helicase ( <i>T. equinum</i> )
TERG_05685	-1.97	60S ribosomal protein L13 ( <i>T. tonsurans</i> )
TERG_00679	-1.97	AhpC/TSA family protein ( <i>T. equinum</i> )
TERG_00550	-1.98	hypothetical protein
TERG_00633	-1.98	40S ribosomal protein S16
TERG_07477	-1.98	copper-sulfate regulated protein 1 ( <i>T. equinum</i> )
TERG_04450	-1.98	60S ribosomal protein L23 ( <i>T. tonsurans</i> )
TERG_02640	-1.98	pre-rRNA processing protein Utp22 ( <i>T. verrucosum</i> )
TERG_02759	-1.98	hexokinase XprF ( <i>T. equinum</i> )
TERG_11645	-1.99	Phytanoyl-CoA dioxygenase PhyH ( <i>T. equinum</i> )
TERG_12682	-1.99	hypothetical protein
TERG_11558	-1.99	hypothetical protein
TERG_08334	-2.00	proline oxidase Put1, putative ( <i>A. benhamiae</i> )
TERG_05363	-2.00	hypothetical protein
TERG_11685	-2.00	hypothetical protein
TERG_02397	-2.00	60S ribosomal protein L37
TERG_06365	-2.00	ribosomal protein L15
TERG_05511	-2.00	AT DNA binding protein ( <i>T. equinum</i> )
TERG_00531	-2.00	40S ribosomal protein S7
TERG_12259	-2.00	CMGC/CLK protein kinase ( <i>T. equinum</i> )
TERG_04281	-2.01	woronin body major protein
TERG_04043	-2.01	hypothetical protein
TERG_08924	-2.01	MIZ zinc finger domain protein ( <i>A. benhamiae</i> )
TERG_02322	-2.02	hypothetical protein
TERG_05401	-2.02	rRNA processing protein Bystin ( <i>T. tonsurans</i> )
TERG_04924	-2.02	threonine aldolase, putative ( <i>T. verrucosum</i> )
TERG_03672	-2.02	hypothetical protein
TERG_04647	-2.02	60S ribosomal protein L18 ( <i>T. equinum</i> )
TERG_07626	-2.02	hypothetical protein
TERG_08545	-2.02	C-4 methyl sterol oxidase Erg25 ( <i>T. equinum</i> )
TERG_01125	-2.03	SprT family metallopeptidase, putative ( <i>T. verrucosum</i> )
TERG_05003	-2.03	NmrA family protein ( <i>T. equinum</i> )
TERG_08672	-2.03	HFR-3 ( <i>M. canis</i> )
TERG_08722	-2.04	hypothetical protein
TERG_04411	-2.04	dipeptidase ( <i>T. equinum</i> )
TERG_12263	-2.05	hypothetical protein
TERG_06262	-2.05	mitochondrial carrier protein ( <i>T. tonsurans</i> )
TERG_00881	-2.05	zinc-containing alcohol dehydrogenase, putative ( <i>T. verrucosum</i> )
TERG_11906	-2.06	FAD binding domain containing protein ( <i>T. equinum</i> )
TERG_06760	-2.06	ATP binding L-PSP endoribonuclease family protein, putative ( <i>T. verrucosum</i> )
TERG_07231	-2.06	hemolysin-III family protein ( <i>T. equinum</i> )
TERG_02237	-2.06	40S ribosomal protein S28
TERG_04130	-2.06	plasma membrane ATPase
TERG_00106	-2.07	60S ribosomal protein L24
TERG_07999	-2.07	hypothetical protein
TERG_12334	-2.07	hypothetical protein
TERG_01952	-2.07	40S ribosomal protein S15
TERG_11646	-2.07	hypothetical protein

TERG_07385	-2.07 60S acidic ribosomal protein P1
TERG_05046	-2.07 hypothetical protein
TERG_01149	-2.07 choline dehydrogenase, putative ( <i>T. verrucosum</i> )
TERG_00738	-2.08 60S ribosomal protein L44
TERG_06275	-2.08 40S ribosomal protein
TERG_04478	-2.08 40S ribosomal protein S1
TERG_00088	-2.08 beta-xylosidase, putative ( <i>A. benhamiae</i> )
TERG_03929	-2.08 hypothetical protein
TERG_01415	-2.08 ribosomal protein L24
TERG_06846	-2.08 inosine-5'-monophosphate dehydrogenase
TERG_01779	-2.08 sentrin-specific protease ( <i>T. equinum</i> )
TERG_00880	-2.08 actin filament organization protein App1-like, putative ( <i>T. verrucosum</i> )
TERG_03624	-2.09 SUN domain protein (Uth1), putative ( <i>T. verrucosum</i> )
TERG_06261	-2.09 phosphoesterase ( <i>T. equinum</i> )
TERG_08282	-2.09 hypothetical protein
TERG_07509	-2.09 serine/threonine protein kinase ( <i>M. canis</i> )
TERG_02260	-2.10 hypothetical protein
TERG_06236	-2.10 40S ribosomal protein S19
TERG_02542	-2.10 integral membrane protein Pth11-like, putative ( <i>T. verrucosum</i> )
TERG_02861	-2.10 40S ribosomal protein S23
TERG_11916	-2.11 nucleolus protein required for cell viability ( <i>T. tonsurans</i> )
TERG_01256	-2.11 ribosomal protein L14 ( <i>T. tonsurans</i> )
TERG_12251	-2.11 GTP-binding protein ( <i>T. tonsurans</i> )
TERG_06815	-2.11 bZIP transcription factor ( <i>T. tonsurans</i> )
TERG_04073	-2.11 glutathione synthetase
TERG_02024	-2.12 hypothetical protein
TERG_04778	-2.12 ribosome assembly and transport protein Srp40, putative ( <i>T. verrucosum</i> )
TERG_00491	-2.12 hypothetical protein
TERG_02631	-2.12 histone H2B
TERG_05737	-2.13 hypothetical protein
TERG_02231	-2.13 ribosome biogenesis protein ( <i>T. tonsurans</i> )
TERG_07380	-2.13 40S ribosomal protein S26E
TERG_03116	-2.13 zf-PARP-type zinc finger protein ( <i>T. tonsurans</i> )
TERG_00221	-2.13 hypothetical protein
TERG_06874	-2.14 UTP-glucose-1-phosphate uridylyltransferase ( <i>T. tonsurans</i> )
TERG_07726	-2.14 hypothetical protein
TERG_02545	-2.14 MFS monocarboxylate transporter ( <i>T. equinum</i> )
TERG_08821	-2.14 ribosome biogenesis ( <i>T. equinum</i> )
TERG_02385	-2.14 hypothetical protein
TERG_08047	-2.14 hypothetical protein
TERG_05236	-2.14 60S ribosomal protein L35
TERG_06265	-2.14 LPS glycosyltransferase ( <i>T. equinum</i> )
TERG_02611	-2.14 WD repeat protein ( <i>A. benhamiae</i> )
TERG_04740	-2.15 ergosterol biosynthesis protein Erg28 ( <i>T. tonsurans</i> )
TERG_06512	-2.15 hypothetical protein
TERG_06640	-2.15 phosphoribosylamine-glycine ligase
TERG_03880	-2.15 60S ribosomal protein L5
TERG_02886	-2.15 hypothetical protein
TERG_01018	-2.15 monooxygenase, putative ( <i>A. benhamiae</i> )

TERG_05801	-2.15 60S ribosomal protein L15
TERG_00650	-2.15 40S ribosomal protein S17-A
TERG_07135	-2.15 hypothetical protein
TERG_02263	-2.16 hypothetical protein
TERG_07383	-2.16 aconitate hydratase, mitochondrial
TERG_04506	-2.16 60S ribosomal protein L4-A ( <i>T. tonsurans</i> )
TERG_07066	-2.17 40S ribosomal protein S5
TERG_05424	-2.17 hypothetical protein
TERG_02283	-2.18 MFS transporter, putative ( <i>T. verrucosum</i> )
TERG_05723	-2.18 hypothetical protein
TERG_06221	-2.18 CTP synthase
TERG_07072	-2.18 ATP-dependent RNA helicase DRS1
TERG_08771	-2.18 extracellular serine-threonine rich protein ( <i>T. tonsurans</i> )
TERG_05626	-2.18 chitinase ( <i>T. equinum</i> )
TERG_02534	-2.18 hypothetical protein
TERG_11688	-2.18 nitrilase ( <i>T. tonsurans</i> )
TERG_06421	-2.18 hypothetical protein
TERG_07154	-2.18 iron donor protein CyaY
TERG_01718	-2.19 cell division control protein Cdc6 ( <i>T. tonsurans</i> )
TERG_01604	-2.19 60S ribosomal protein L36
TERG_08095	-2.19 MFS multidrug transporter, putative ( <i>A. benhamiae</i> )
TERG_04040	-2.19 Spo12 family protein ( <i>T. tonsurans</i> )
TERG_11551	-2.19 telomere and ribosome associated protein Stm1 ( <i>T. tonsurans</i> )
TERG_06437	-2.20 ribosomal protein L28e ( <i>T. equinum</i> )
TERG_05345	-2.20 60S ribosomal protein L43
TERG_02404	-2.20 40S ribosomal protein S4
TERG_02496	-2.20 histone H1 ( <i>T. tonsurans</i> )
TERG_05625	-2.20 class V chitinase, putative ( <i>T. verrucosum</i> )
TERG_08533	-2.20 poly(A) polymerase Cid1 ( <i>T. equinum</i> )
TERG_01419	-2.20 protein pyrABCN
TERG_04310	-2.20 alcohol dehydrogenase ( <i>T. tonsurans</i> )
TERG_02895	-2.21 60S ribosomal protein L9-B ( <i>T. equinum</i> )
TERG_05283	-2.21 60S ribosomal protein L32
TERG_07493	-2.21 Zinc knuckle transcription factor (CnjB) ( <i>T. tonsurans</i> )
TERG_02953	-2.21 hypothetical protein
TERG_07235	-2.21 fructose-1,6-bisphosphatase ( <i>T. tonsurans</i> )
TERG_07630	-2.21 FMN dependent dehydrogenase, putative ( <i>T. verrucosum</i> )
TERG_00242	-2.22 60S ribosomal protein L27-A ( <i>T. tonsurans</i> )
TERG_02118	-2.22 GPI anchored protein, putative ( <i>A. benhamiae</i> )
TERG_03747	-2.22 phospholipase A2 ( <i>T. equinum</i> )
TERG_12607	-2.22 ThiF domain-containing protein ( <i>T. tonsurans</i> )
TERG_12500	-2.22 sorbitol dehydrogenase ( <i>T. equinum</i> )
TERG_04576	-2.22 CRAL/TRIO domain protein ( <i>T. verrucosum</i> )
TERG_12619	-2.22 hypothetical protein
TERG_04772	-2.23 40S ribosomal protein S8-B
TERG_01995	-2.23 hypothetical protein
TERG_08428	-2.23 hypothetical protein
TERG_07182	-2.23 40S ribosomal protein S6-B
TERG_00383	-2.24 60S ribosomal protein L16

TERG_03738	-2.24 60S ribosomal protein L3
TERG_07363	-2.24 hypothetical protein
TERG_02376	-2.25 60S ribosomal protein ( <i>T. equinum</i> )
TERG_00103	-2.25 hypothetical protein
TERG_07988	-2.25 60S ribosomal protein L10a
TERG_06626	-2.25 hypothetical protein
TERG_02630	-2.25 histone H2A
TERG_12027	-2.25 hypothetical protein
TERG_05184	-2.25 glycine cleavage system H protein
TERG_06414	-2.26 DUF1338 domain-containing protein ( <i>T. equinum</i> )
TERG_06475	-2.26 zinc knuckle domain-containing protein ( <i>T. tonsurans</i> )
TERG_06755	-2.26 C-8 sterol isomerase (Erg-1), putative ( <i>T. verrucosum</i> )
TERG_01838	-2.26 LIM domain protein ( <i>A. benhamiae</i> )
TERG_07944	-2.26 60S ribosomal protein L6 ( <i>T. equinum</i> )
TERG_12314	-2.26 hypothetical protein
TERG_03619	-2.27 transcription factor Tos4 ( <i>T. equinum</i> )
TERG_05655	-2.27 AN1 zinc finger protein ( <i>T. equinum</i> )
TERG_06952	-2.27 rRNA processing protein Pwp1 ( <i>T. tonsurans</i> )
TERG_04775	-2.27 beta-N-hexosaminidase, putative ( <i>A. benhamiae</i> )
TERG_07127	-2.27 homocitrate synthase, mitochondrial
TERG_11753	-2.28 MFS transporter ( <i>T. tonsurans</i> )
TERG_07957	-2.28 hypothetical protein
TERG_05251	-2.28 phosphoglycerate kinase
TERG_01638	-2.28 hypothetical protein
TERG_05866	-2.28 40S ribosomal protein S2
TERG_02971	-2.28 60S ribosomal protein L35a ( <i>T. equinum</i> )
TERG_01912	-2.29 MFS transporter ( <i>T. equinum</i> )
TERG_01953	-2.29 60S acidic ribosomal protein P2
TERG_06824	-2.30 60S ribosomal protein L23
TERG_01336	-2.30 MFS transporter ( <i>T. equinum</i> )
TERG_02937	-2.30 importin beta-4 subunit ( <i>T. tonsurans</i> )
TERG_07904	-2.31 tubulin beta chain
TERG_07357	-2.31 hypothetical protein
TERG_05825	-2.31 40S ribosomal protein S11
TERG_06101	-2.31 ribosomal protein P0 ( <i>T. equinum</i> )
TERG_04089	-2.32 RfxA protein ( <i>T. equinum</i> )
TERG_03494	-2.32 hypothetical protein
TERG_08667	-2.32 hypothetical protein
TERG_08843	-2.32 hypothetical protein
TERG_04606	-2.32 general amino acid permease AGP2 ( <i>T. equinum</i> )
TERG_04441	-2.33 centromere/microtubule-binding protein CBF5
TERG_08390	-2.33 hypothetical protein
TERG_01102	-2.33 60S ribosomal protein L8-B
TERG_02197	-2.33 nitrilase, putative ( <i>T. verrucosum</i> )
TERG_04036	-2.34 adenosine kinase ( <i>T. tonsurans</i> )
TERG_03340	-2.35 oxidoreductase ( <i>T. equinum</i> )
TERG_07002	-2.35 60S ribosomal protein L17
TERG_04153	-2.35 60S ribosome biogenesis protein Brx1 ( <i>T. tonsurans</i> )
TERG_02878	-2.35 eukaryotic translation initiation factor 3 subunit F

TERG_02377	-2.36 40S ribosomal protein S9
TERG_03204	-2.36 60S ribosomal protein L7
TERG_05544	-2.36 plk/plk-unclassified protein kinase ( <i>T. tonsurans</i> )
TERG_08090	-2.36 plasma membrane iron permease ( <i>T. tonsurans</i> )
TERG_01368	-2.36 Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein ( <i>T. equinum</i> )
TERG_08254	-2.37 40S ribosomal protein S18
TERG_05893	-2.37 CMGC protein kinase ( <i>T. tonsurans</i> )
TERG_07876	-2.37 hypothetical protein
TERG_00635	-2.38 40S ribosomal protein S14
TERG_00956	-2.38 extracellular thaumatin domain-containing protein ( <i>T. equinum</i> )
TERG_12058	-2.38 transporter smf2 ( <i>T. tonsurans</i> )
TERG_12358	-2.38 DNA repair protein Rad5 ( <i>T. tonsurans</i> )
TERG_05756	-2.39 calmodulin-binding protein Sha1, putative ( <i>T. verrucosum</i> )
TERG_07504	-2.39 sialidase ( <i>T. tonsurans</i> )
TERG_06163	-2.39 MYB family conidiophore development protein FlbD ( <i>T. equinum</i> )
TERG_08333	-2.39 1-pyrroline-5-carboxylate dehydrogenase
TERG_06246	-2.39 extracellular serine-threonine rich protein ( <i>A. benhamiae</i> )
TERG_01634	-2.40 MFS multidrug transporter, putative ( <i>T. verrucosum</i> )
TERG_00783	-2.40 guanine nucleotide-binding protein subunit beta-like protein
TERG_00462	-2.41 40S ribosomal protein
TERG_06496	-2.41 coproporphyrinogen III oxidase ( <i>T. tonsurans</i> )
TERG_01066	-2.42 DNA methyltransferase Dim-2 ( <i>T. equinum</i> )
TERG_11751	-2.42 PCI domain-containing protein ( <i>T. tonsurans</i> )
TERG_02604	-2.42 40S ribosomal protein S20
TERG_03343	-2.43 fatty acid desaturase ( <i>T. equinum</i> )
TERG_06266	-2.43 hypothetical protein
TERG_11740	-2.44 hypothetical protein
TERG_06315	-2.44 integral membrane protein ( <i>A. benhamiae</i> )
TERG_12195	-2.44 developmental regulator flbA ( <i>M. gypseum</i> )
TERG_02530	-2.46 hypothetical protein
TERG_11945	-2.46 hypothetical protein
TERG_00217	-2.47 ubiquitin-40S ribosomal protein S27a
TERG_02521	-2.47 60S ribosomal protein L27a
TERG_07029	-2.47 hypothetical protein
TERG_11760	-2.48 HIT finger domain protein, putative ( <i>T. verrucosum</i> )
TERG_01985	-2.48 hypothetical protein
TERG_08108	-2.48 40S ribosomal protein S22
TERG_01550	-2.49 60S ribosomal protein L38 ( <i>T. tonsurans</i> )
TERG_02189	-2.49 tubulin alpha-2 chain
TERG_12231	-2.49 DUF221 domain-containing protein ( <i>T. equinum</i> )
TERG_05998	-2.49 chlorophyll synthesis pathway protein BchC
TERG_12033	-2.49 atypical/RIO/RIO1 protein kinase ( <i>T. tonsurans</i> )
TERG_03780	-2.49 pyruvate dehydrogenase dihydrolipoamide acetyltransferase component ( <i>M. gypseum</i> )
TERG_00504	-2.49 hypothetical protein
TERG_05788	-2.50 60S ribosomal protein L18A ( <i>T. tonsurans</i> )
TERG_12318	-2.50 chitin synthase ( <i>T. tonsurans</i> )
TERG_08273	-2.52 zinc finger protein ZPR1 ( <i>T. tonsurans</i> )
TERG_06585	-2.52 hypothetical protein

TERG_03758	-2.52	hypothetical protein
TERG_07689	-2.53	ribosomal biogenesis protein Gar2 ( <i>T. tonsurans</i> )
TERG_07069	-2.53	carbonic anhydrase ( <i>T. tonsurans</i> )
TERG_00976	-2.54	serine hydroxymethyltransferase, cytosolic
TERG_05627	-2.54	LysM domain-containing protein ( <i>M. canis</i> )
TERG_05615	-2.55	hsp70-like protein ( <i>T. equinum</i> )
TERG_01562	-2.55	60S ribosomal protein L11
TERG_07786	-2.55	NAP family protein ( <i>T. equinum</i> )
TERG_08353	-2.55	cytochrome P450 55A3 ( <i>T. tonsurans</i> )
TERG_01609	-2.56	Na/K ATPase alpha 1 subunit ( <i>T. equinum</i> )
TERG_02053	-2.56	hypothetical protein
TERG_06234	-2.56	2,5-diketo-D-gluconic acid reductase A ( <i>T. equinum</i> )
TERG_04855	-2.56	hypothetical protein
TERG_05523	-2.56	hypothetical protein
TERG_11828	-2.57	hypothetical protein
TERG_06055	-2.57	NmrA-like family protein ( <i>A. benhamiae</i> )
TERG_05202	-2.58	MFS drug efflux transporter ( <i>T. equinum</i> )
TERG_01344	-2.58	60S ribosomal protein L22 ( <i>T. tonsurans</i> )
TERG_03117	-2.58	kinesin family protein ( <i>T. tonsurans</i> )
TERG_04308	-2.59	MFS sugar transporter ( <i>T. tonsurans</i> )
TERG_08179	-2.59	tRNA pseudouridine synthase D ( <i>T. equinum</i> )
TERG_11747	-2.59	hypothetical protein
TERG_07209	-2.60	GTPase binding protein Rid1 ( <i>M. canis</i> )
TERG_11830	-2.61	hypothetical protein
TERG_03380	-2.62	FK506-binding protein 1A ( <i>T. equinum</i> )
TERG_05222	-2.63	S-adenosylmethionine synthase
TERG_02166	-2.63	oxidoreductase ( <i>T. equinum</i> )
TERG_02105	-2.63	hypothetical protein
TERG_06847	-2.63	Ras GTPase activating protein ( <i>T. tonsurans</i> )
TERG_07639	-2.65	atypical/ABC1/ABC1-B protein kinase ( <i>T. tonsurans</i> )
TERG_07099	-2.65	hypothetical protein
TERG_11550	-2.66	telomere and ribosome associated protein Stm1, putative ( <i>T. verrucosum</i> )
TERG_12372	-2.66	multidrug resistance protein ( <i>T. tonsurans</i> )
TERG_05849	-2.67	thioredoxin reductase ( <i>T. equinum</i> )
TERG_07035	-2.67	hypothetical protein
TERG_04187	-2.68	hypothetical protein
TERG_06207	-2.68	proline oxidase PrnD ( <i>T. verrucosum</i> )
TERG_01165	-2.69	40S ribosomal protein S10b ( <i>T. equinum</i> )
TERG_01777	-2.69	GTP-binding protein rhoC
TERG_04531	-2.69	hypothetical protein
TERG_03707	-2.70	geranylgeranyl diphosphate synthase, putative ( <i>A. benhamiae</i> )
TERG_04680	-2.72	hypothetical protein
TERG_07802	-2.73	siderophore biosynthesis acetylase AceI, putative ( <i>T. verrucosum</i> )
TERG_05268	-2.74	hypothetical protein
TERG_08029	-2.74	HMG box protein, putative ( <i>T. verrucosum</i> )
TERG_12357	-2.75	DNA repair protein Rad5 ( <i>T. tonsurans</i> )
TERG_06137	-2.77	RNA binding protein ( <i>A. benhamiae</i> )
TERG_04700	-2.77	hypothetical protein
TERG_06611	-2.77	hypothetical protein

TERG_04320	-2.78	hypothetical protein
TERG_12084	-2.79	hypothetical protein
TERG_01886	-2.80	hypothetical protein
TERG_03921	-2.83	hypothetical protein
TERG_07981	-2.83	hypothetical protein
TERG_04966	-2.85	hypothetical protein
TERG_03004	-2.86	3-methyl-2-oxobutanoate hydroxymethyltransferase
TERG_07588	-2.86	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase
TERG_11710	-2.86	hypothetical protein
TERG_03148	-2.89	molybdenum cofactor sulfurase ( <i>T. equinum</i> )
TERG_01139	-2.90	kinesin family protein ( <i>T. tonsurans</i> )
TERG_07320	-2.91	hypothetical protein
TERG_06784	-2.91	transcriptional activator of ethanol catabolism AlcS ( <i>A. benhamiae</i> )
TERG_08200	-2.94	hypothetical protein
TERG_00566	-2.94	hypothetical protein
TERG_08241	-2.96	cell division control protein 14 ( <i>T. tonsurans</i> )
TERG_04738	-2.96	hypothetical protein
TERG_07045	-2.96	hypothetical protein
TERG_06403	-2.97	HASPIN protein kinase
TERG_07285	-2.97	hypothetical protein
TERG_01322	-2.98	NEK protein kinase ( <i>T. tonsurans</i> )
TERG_06376	-2.99	hypothetical protein
TERG_05094	-2.99	hypothetical protein
TERG_02528	-2.99	ubiE/COQ5 methyltransferase, putative ( <i>T. verrucosum</i> )
TERG_02845	-3.00	cercosporin toxin biosynthesis protein ( <i>T. equinum</i> )
TERG_12159	-3.01	hypothetical protein
TERG_06049	-3.02	dimethylallyl tryptophan synthase, putative ( <i>T. verrucosum</i> )
TERG_02279	-3.03	hypothetical protein
TERG_05419	-3.04	glycine dehydrogenase
TERG_08649	-3.04	cell division control protein (Cdc15), putative ( <i>A. benhamiae</i> )
TERG_04666	-3.05	hypothetical protein
TERG_12566	-3.05	hypothetical protein
TERG_07469	-3.06	SUN domain-containing protein ( <i>T. equinum</i> )
TERG_07905	-3.07	1-pyrroline-5-carboxylate dehydrogenase
TERG_08479	-3.09	kinesin family protein ( <i>T. verrucosum</i> )
TERG_01659	-3.10	heat shock protein Hsp30-like, putative ( <i>A. benhamiae</i> )
TERG_12391	-3.10	hypothetical protein
TERG_03217	-3.11	hypothetical protein
TERG_00429	-3.11	pisatin demethylase ( <i>M. gypseum</i> )
TERG_12342	-3.13	membrane zinc transporter ( <i>T. tonsurans</i> )
TERG_12313	-3.13	hypothetical protein
TERG_05141	-3.13	NCS1 nucleoside transporter ( <i>T. equinum</i> )
TERG_04374	-3.18	STE/STE20/YSK protein kinase
TERG_03671	-3.18	hypothetical protein
TERG_03670	-3.19	hypothetical protein
TERG_03434	-3.25	GTP binding protein ( <i>T. equinum</i> )
TERG_06235	-3.27	hypothetical protein
TERG_11506	-3.27	phosphoenolpyruvate carboxykinase [ATP]
TERG_03660	-3.28	hypothetical protein



TERG_08091	-3.31 conidial pigment biosynthesis oxidase Abr1/brown ( <i>T. verrucosum</i> )
TERG_11621	-3.32 hypothetical protein
TERG_03060	-3.36 hypothetical protein
TERG_04234	-3.41 hydrophobin, putative ( <i>T. verrucosum</i> )
TERG_06646	-3.42 arrestin ( <i>T. equinum</i> )
TERG_07364	-3.42 oxidoreductase, zinc-binding dehydrogenase family superfamily ( <i>T. verrucosum</i> )
TERG_04028	-3.43 cytochrome P450, putative ( <i>T. verrucosum</i> )
TERG_06540	-3.44 glutathione transferase ( <i>T. tonsurans</i> )
TERG_01731	-3.45 hypothetical protein
TERG_07570	-3.47 G-protein signaling regulator, putative ( <i>T. verrucosum</i> )
TERG_07354	-3.48 hypothetical protein
TERG_12618	-3.50 hypothetical protein
TERG_04530	-3.54 hypothetical protein
TERG_03506	-3.54 hypothetical protein
TERG_12043	-3.55 beta-1,6 glucan synthetase ( <i>T. tonsurans</i> )
TERG_08985	-3.56 hypothetical protein
TERG_04956	-3.57 hypothetical protein
TERG_03700	-3.58 hypothetical protein
TERG_00241	-3.59 hypothetical protein
TERG_08004	-3.60 hypothetical protein
TERG_01341	-3.61 protein-tyrosine phosphatase ( <i>T. equinum</i> )
TERG_12017	-3.68 MFS sugar transporter, putative ( <i>A. benhamiae</i> )
TERG_08648	-3.73 cell division control protein (Cdc15), putative ( <i>A. benhamiae</i> )
TERG_01480	-3.74 MFS multidrug transporter, putative ( <i>A. benhamiae</i> )
TERG_08054	-3.75 homoserine acetyltransferase ( <i>T. tonsurans</i> )
TERG_00689	-3.75 AUR protein kinase
TERG_11505	-3.77 phosphoenolpyruvate carboxykinase [ATP]
TERG_08258	-3.79 hypothetical protein
TERG_07083	-3.80 hypothetical protein
TERG_00520	-3.82 hypothetical protein
TERG_12018	-3.85 MFS sugar transporter, putative ( <i>A. benhamiae</i> )
TERG_07665	-3.86 hypothetical protein
TERG_11640	-3.89 hypothetical protein
TERG_03403	-3.92 hypothetical protein
TERG_03493	-3.94 hypothetical protein
TERG_08260	-3.96 subtilisin-like protease 2
TERG_00218	-3.97 C2H2 transcription factor (Swi5), putative ( <i>A. benhamiae</i> )
TERG_04263	-4.01 hypothetical protein
TERG_05350	-4.03 hypothetical protein
TERG_00243	-4.05 pathogenesis associated protein Cap20, putative ( <i>T. verrucosum</i> )
TERG_01406	-4.08 phospholipase D ( <i>T. equinum</i> )
TERG_07108	-4.11 WD-repeat containing protein slp1 ( <i>T. tonsurans</i> )
TERG_00499	-4.17 hypothetical protein
TERG_03936	-4.19 CAMK protein kinase
TERG_03105	-4.39 hypothetical protein
TERG_02671	-4.40 hypothetical protein
TERG_00500	-4.44 hypothetical protein
TERG_02278	-4.60 hypothetical protein
TERG_08806	-4.65 hypothetical protein

TERG_08097	-4.67	hypothetical protein
TERG_12035	-4.87	NB-ARC and TPR domain protein ( <i>A. benhamiae</i> )
TERG_01599	-4.95	hypothetical protein
TERG_01148	-5.26	hypothetical protein
TERG_11771	-5.51	hypothetical protein

Gene expression values are expressed in log<sub>2</sub> fold change.

ID	3h	12h	Gene Product Name
TERG_06548	10.86	11.80	hypothetical protein
TERG_01782	8.34	9.02	hypothetical protein
TERG_04952	6.87	7.69	multidrug resistance protein ( <i>T. equinum</i> )
TERG_08954	6.61	5.90	hypothetical protein
TERG_08751	5.82	6.33	ABC multidrug transporter, putative ( <i>A. benhamiae</i> )
TERG_01543	5.42	7.48	s-adenosylmethionine (SAM)-dependent methyltransferase ( <i>M. gypseum</i> )
TERG_08041	5.42	6.24	aminotransferase, putative ( <i>A. benhamiae</i> )
TERG_04937	5.41	6.40	alpha/beta hydrolase ( <i>T. equinum</i> )
TERG_07830	5.41	8.22	hypothetical protein
TERG_11650	4.97	5.91	hypothetical protein
TERG_03829	4.86	6.92	FAD binding domain-containing protein ( <i>T. equinum</i> )
TERG_00010	4.76	8.72	amidase family protein ( <i>T. verrucosum</i> )
TERG_06347	4.53	5.85	hypothetical protein
TERG_08283	4.46	2.17	acetamidase ( <i>T. tonsurans</i> )
TERG_01783	4.26	4.90	hypothetical protein
TERG_04117	4.12	5.41	tannase, putative ( <i>A. benhamiae</i> )
TERG_07465	3.93	3.62	serine peptidase, family S28, putative ( <i>A. benhamiae</i> )
TERG_05023	3.86	2.95	calcium/proton exchanger
TERG_06779	3.85	4.61	hypothetical protein
TERG_08195	3.74	2.54	peptidase S41 family protein ( <i>M. gypseum</i> )
TERG_05037	3.73	4.31	hypothetical protein
TERG_01280	3.73	4.55	IgE-binding protein ( <i>A. benhamiae</i> )
TERG_02199	3.71	2.04	glutamate carboxypeptidase ( <i>T. equinum</i> )
TERG_04950	3.60	4.48	cytochrome P450 monooxygenase ( <i>T. equinum</i> )
TERG_05137	3.53	4.96	microsomal dipeptidase ( <i>T. tonsurans</i> )
TERG_04951	3.51	3.38	U-box domain-containing protein ( <i>T. equinum</i> )
TERG_01460	3.48	3.04	carboxylesterase ( <i>T. equinum</i> )
TERG_02488	3.43	4.42	hypothetical protein
TERG_04960	3.36	1.75	glutathione S-transferase Ure2-like, putative ( <i>A. benhamiae</i> )
TERG_07408	3.34	4.18	acetyltransferase, GNAT family ( <i>A. benhamiae</i> )
TERG_02814	3.30	4.98	hypothetical protein
TERG_06106	3.27	6.45	sulfate permease 2 ( <i>T. tonsurans</i> )
TERG_12228	3.26	5.00	hypothetical protein
TERG_11667	3.26	3.45	hypothetical protein
TERG_06466	3.26	1.93	hypothetical protein
TERG_07556	3.24	3.97	hypothetical protein
TERG_03970	3.23	5.40	DUF636 domain-containing protein ( <i>T. equinum</i> )
TERG_01405	3.19	2.44	glutathione S-transferase ( <i>T. equinum</i> )
TERG_05063	3.16	4.97	extracellular serine-rich protein ( <i>T. verrucosum</i> )

TERG_04146	3.15	3.93	FAD/FMN-containing isoamyl alcohol oxidase MreA-like, putative ( <i>A. benhamiae</i> )
TERG_03024	3.15	2.52	hypothetical protein
TERG_08235	3.14	3.26	long chain fatty alcohol oxidase ( <i>T. tonsurans</i> )
TERG_05698	3.12	1.50	transesterase (LovD), putative ( <i>T. verrucosum</i> )
TERG_05466	3.12	3.90	MFS transporter, putative ( <i>T. verrucosum</i> )
TERG_12230	3.11	3.51	peptidase S41 family protein ( <i>A. benhamiae</i> )
TERG_02993	3.09	4.40	allergenic cerato-platanin Asp F13 ( <i>T. verrucosum</i> )
TERG_11731	3.05	4.19	zinc/cadmium resistance protein ( <i>T. tonsurans</i> )
TERG_03963	3.05	3.20	mannosyl phosphorylinositol ceramide synthase SUR1 ( <i>T. equinum</i> )
TERG_11633	3.03	4.50	hypothetical protein
TERG_03802	3.03	4.10	hypothetical protein
TERG_00389	3.01	3.41	hypothetical protein
TERG_02384	3.00	2.77	hypothetical protein
TERG_05639	3.00	2.73	hypothetical protein
TERG_12229	2.99	3.56	peptidase S41 family protein ( <i>A. benhamiae</i> )
TERG_00060	2.93	3.54	GPI anchored cell wall protein, putative ( <i>A. benhamiae</i> )
TERG_01572	2.89	4.25	carboxylesterase, putative ( <i>T. verrucosum</i> )
TERG_01113	2.88	3.36	mitochondrial RNA splicing protein ( <i>T. tonsurans</i> )
TERG_02589	2.84	4.78	formamidase ( <i>T. equinum</i> )
TERG_08787	2.84	1.60	aminotransferase ( <i>T. tonsurans</i> )
TERG_08700	2.83	1.79	DUF895 domain membrane protein ( <i>T. equinum</i> )
TERG_04907	2.82	3.06	glyoxalase ( <i>T. tonsurans</i> )
TERG_07094	2.81	3.55	hypothetical protein
TERG_02747	2.80	2.42	cytochrome P450 alkane hydroxylase ( <i>A. benhamiae</i> )
TERG_02332	2.79	3.23	hypothetical protein
TERG_02572	2.78	1.77	hypothetical protein
TERG_12215	2.78	2.87	hypothetical protein
TERG_00254	2.75	1.74	peroxisomal dehydratase ( <i>T. equinum</i> )
TERG_05442	2.74	1.81	hypothetical protein
TERG_11552	2.73	3.23	hypothetical protein
TERG_02532	2.72	4.90	C6 transcription factor, putative ( <i>T. verrucosum</i> )
TERG_12216	2.71	3.06	hypothetical protein
TERG_07487	2.69	2.84	hypothetical protein
TERG_02664	2.68	2.26	hypothetical protein
TERG_00161	2.66	3.23	hypothetical protein
TERG_01943	2.66	2.71	1-aminocyclopropane-1-carboxylate deaminase
TERG_05418	2.64	2.67	hypothetical protein
TERG_04942	2.63	3.29	hypothetical protein
TERG_06208	2.63	3.47	DUF636 domain-containing protein ( <i>M. gypseum</i> )
TERG_04953	2.62	3.54	cyclin, putative ( <i>T. verrucosum</i> )
TERG_12217	2.62	2.86	hypothetical protein
TERG_06005	2.60	4.04	hypothetical protein
TERG_00244	2.59	2.42	stomatin family protein ( <i>T. tonsurans</i> )
TERG_03353	2.58	5.16	endoglucanase ( <i>T. equinum</i> )
TERG_07788	2.58	2.73	lysophospholipase ( <i>T. tonsurans</i> )
TERG_06638	2.57	2.17	endochitinase ( <i>T. equinum</i> )
TERG_03069	2.56	1.92	hypothetical protein
TERG_05450	2.55	1.72	acetyltransferase ( <i>T. tonsurans</i> )

TERG_01876	2.53	4.07	short-chain dehydrogenase/reductase SDR ( <i>T. tonsurans</i> )
TERG_07326	2.53	3.30	glutathione S-transferase PARB ( <i>T. equinum</i> )
TERG_01467	2.53	4.44	cytochrome P450 monooxygenase, putative ( <i>A. benhamiae</i> )
TERG_00013	2.53	2.98	ThiJ/PfpI family protein ( <i>A. benhamiae</i> )
TERG_08539	2.51	4.42	Diacylglycerol kinase domain-containing protein ( <i>T. equinum</i> )
TERG_03055	2.51	2.25	MFS transporter, putative ( <i>T. verrucosum</i> )
TERG_07755	2.50	3.15	ergot alkaloid biosynthetic protein A ( <i>T. verrucosum</i> )
TERG_00402	2.49	3.00	ABC multidrug transporter, putative ( <i>T. verrucosum</i> )
TERG_07796	2.48	1.68	oxidoreductase, short-chain dehydrogenase/reductase family ( <i>A. benhamiae</i> )
TERG_08077	2.47	2.90	hypothetical protein
TERG_12291	2.46	3.27	mitochondrial cytochrome b2 ( <i>T. tonsurans</i> )
TERG_02989	2.45	2.35	cytochrome P450 oxidoreductase, putative ( <i>T. verrucosum</i> )
TERG_03322	2.44	2.79	hypothetical protein
TERG_12290	2.44	3.22	mitochondrial cytochrome b2 ( <i>T. tonsurans</i> )
TERG_02555	2.43	2.55	DUF636 domain containing protein ( <i>T. equinum</i> )
TERG_12600	2.41	3.21	U3 small nucleolar ribonucleoprotein IMP4 ( <i>T. tonsurans</i> )
TERG_03907	2.39	4.54	neutral amino acid permease ( <i>T. tonsurans</i> )
TERG_00583	2.39	1.96	hypothetical protein
TERG_03027	2.35	2.06	hypothetical protein
TERG_12172	2.33	1.53	glycerol-3-phosphate dehydrogenase ( <i>T. equinum</i> )
TERG_01934	2.33	2.69	C2H2 finger domain-containing protein ( <i>T. equinum</i> )
TERG_05518	2.32	2.32	oxidoreductase, short chain dehydrogenase/reductase family ( <i>A. benhamiae</i> )
TERG_00199	2.32	2.61	serine/threonine protein kinase
TERG_04224	2.32	3.96	ABC transporter
TERG_04399	2.31	1.81	MFS transporter, putative ( <i>A. benhamiae</i> )
TERG_00162	2.30	2.26	MFS multidrug transporter, putative ( <i>A. benhamiae</i> )
TERG_04521	2.30	3.15	HypA-like protein, putative ( <i>A. benhamiae</i> )
TERG_08779	2.29	1.84	hypothetical protein
TERG_03390	2.28	2.10	glutathione S-transferase ( <i>T. equinum</i> )
TERG_04936	2.28	2.66	meiotic chromosome segregation protein ( <i>T. equinum</i> )
TERG_03255	2.27	2.72	hypothetical protein
TERG_02838	2.24	2.22	hypothetical protein
TERG_02012	2.23	2.25	adenosine deaminase family protein ( <i>A. benhamiae</i> )
TERG_02210	2.22	2.73	hypothetical protein
TERG_05669	2.22	3.29	homeobox transcription factor, putative ( <i>T. verrucosum</i> )
TERG_03230	2.21	3.14	hypothetical protein
TERG_05199	2.20	2.70	MFS gliotoxin efflux transporter GliA ( <i>T. verrucosum</i> )
TERG_04118	2.20	2.59	hypothetical protein
TERG_08229	2.20	2.82	hypothetical protein
TERG_04837	2.19	2.26	thioesterase ( <i>T. equinum</i> )
TERG_06927	2.19	2.02	hypothetical protein
TERG_12368	2.18	3.73	hypothetical protein
TERG_11577	2.17	1.94	cysteinyl-tRNA synthetase ( <i>M. gypseum</i> )
TERG_06507	2.17	2.24	oxidoreductase, 2OG-Fe(II) oxygenase family ( <i>T. verrucosum</i> )
TERG_02610	2.16	2.12	WD repeat protein ( <i>T. verrucosum</i> )
TERG_12065	2.16	4.89	hypothetical protein
TERG_05091	2.16	2.16	DUF636 domain-containing protein ( <i>T. equinum</i> )
TERG_01042	2.14	2.91	C6 transcription factor, putative ( <i>T. verrucosum</i> )
TERG_02520	2.13	2.17	DNA helicase ( <i>T. equinum</i> )

TERG_11570	2.12	3.31	hypothetical protein
TERG_02212	2.12	2.79	short chain dehydrogenase/reductase family protein ( <i>T. verrucosum</i> )
TERG_08360	2.12	4.15	metallo-beta-lactamase superfamily protein ( <i>T. equinum</i> )
TERG_01956	2.12	3.61	C2H2 finger domain protein, putative ( <i>A. benhamiae</i> )
TERG_06407	2.11	1.95	protein kinase subdomain-containing protein ( <i>M. canis</i> )
TERG_02899	2.11	3.50	hypothetical protein
TERG_02566	2.10	2.93	hypothetical protein
TERG_06547	2.07	2.90	glycerophosphoryl diester phosphodiesterase ( <i>T. tonsurans</i> )
TERG_00955	2.07	1.62	ABC drug exporter AtrF ( <i>T. verrucosum</i> )
TERG_11801	2.06	1.70	serine/threonine protein kinase ( <i>T. equinum</i> )
TERG_07134	2.05	2.67	serine/threonine protein kinase
TERG_03785	2.04	2.77	isochorismatase family hydrolase, putative ( <i>T. verrucosum</i> )
TERG_06690	2.04	3.80	RTA1 domain protein, putative ( <i>A. benhamiae</i> )
TERG_06990	2.04	2.81	hypothetical protein
TERG_08756	2.04	1.94	cercosporin toxin biosynthesis protein ( <i>T. equinum</i> )
TERG_08300	2.03	3.95	branched-chain amino acid aminotransferase
TERG_12158	2.02	2.65	hypothetical protein
TERG_02062	2.02	1.98	hypothetical protein
TERG_05551	2.01	3.61	hypothetical protein
TERG_07428	2.00	1.73	C6 transcription factor (UaY), putative ( <i>T. verrucosum</i> )
TERG_02116	2.00	2.96	PX domain-containing protein ( <i>T. tonsurans</i> )
TERG_04696	2.00	1.72	MHYT domain signaling protein, putative ( <i>T. verrucosum</i> )
TERG_01077	2.00	1.79	metallo-beta-lactamase domain-containing protein ( <i>T. equinum</i> )
TERG_05497	1.99	2.77	C6 zinc finger domain-containing protein ( <i>T. equinum</i> )
TERG_08298	1.99	3.14	RTA1 domain-containing protein ( <i>T. equinum</i> )
TERG_02728	1.99	2.05	3-hydroxyisobutyrate dehydrogenase
TERG_00616	1.98	5.04	potassium/sodium efflux P-type ATPase, fungal-type
TERG_01172	1.98	2.37	hypothetical protein
TERG_04356	1.97	2.20	amino acid permease, putative ( <i>A. benhamiae</i> )
TERG_11861	1.97	2.07	DNA repair helicase (rad3) ( <i>T. tonsurans</i> )
TERG_02661	1.96	1.86	hypothetical protein
TERG_03253	1.96	3.57	hypothetical protein
TERG_12064	1.96	4.56	hypothetical protein
TERG_05104	1.96	1.67	MFS transporter of unknown specificity ( <i>T. verrucosum</i> )
TERG_08299	1.96	3.30	multidrug resistance-associated protein 1 transporter ( <i>M. canis</i> )
TERG_04509	1.94	3.55	hypothetical protein
TERG_05556	1.94	1.73	hypothetical protein
TERG_02635	1.94	3.83	hypothetical protein
TERG_12286	1.94	2.06	hypothetical protein
TERG_07787	1.94	2.28	nitrogen metabolite repression protein nmrA
TERG_04695	1.94	1.75	hypothetical protein
TERG_07198	1.92	1.92	DNA polymerase iota ( <i>T. tonsurans</i> )
TERG_08050	1.92	2.16	acetamidase ( <i>T. equinum</i> )
TERG_01919	1.92	2.96	serine/threonine protein kinase
TERG_02447	1.92	3.39	sulfate adenyltransferase
TERG_04034	1.92	2.86	hypothetical protein
TERG_00914	1.92	2.71	hypothetical protein
TERG_11804	1.92	2.05	hypothetical protein
TERG_03229	1.92	1.65	hexokinase ( <i>T. tonsurans</i> )

TERG_02186	1.91	3.47	ABC multidrug transporter, putative ( <i>A. benhamiae</i> )
TERG_02704	1.91	2.68	short-chain dehydrogenase/reductase, putative ( <i>A. benhamiae</i> )
TERG_06369	1.90	2.40	PQ loop repeat protein ( <i>A. benhamiae</i> )
TERG_02112	1.90	2.69	hypothetical protein
TERG_01594	1.88	2.35	hypothetical protein
TERG_02449	1.88	3.75	phosphoadenosine phosphosulfate reductase
TERG_05492	1.87	2.39	hypothetical protein
TERG_05134	1.87	2.35	O-methyltransferase GliM ( <i>A. benhamiae</i> )
TERG_11782	1.87	3.36	hypothetical protein
TERG_00574	1.86	3.07	MFS multidrug transporter, putative ( <i>T. verrucosum</i> )
TERG_00127	1.86	2.81	secretory phospholipase A2 ( <i>T. tonsurans</i> )
TERG_04763	1.85	2.01	fructosyl amine:oxygen oxidoreductase ( <i>T. tonsurans</i> )
TERG_07847	1.85	3.04	hypothetical protein
TERG_12083	1.85	2.21	hypothetical protein
TERG_01964	1.85	1.60	cystathionine gamma-lyase ( <i>T. equinum</i> )
TERG_11832	1.84	4.18	cytosolic Fe-S cluster assembling factor NBP35 ( <i>T. tonsurans</i> )
TERG_07647	1.83	1.55	hypothetical protein
TERG_12287	1.83	2.27	hypothetical protein
TERG_05456	1.83	2.28	hypothetical protein
TERG_02311	1.83	2.92	hypothetical protein
TERG_04174	1.83	1.81	citrinin biosynthesis oxydoreductase CtnB ( <i>T. equinum</i> )
TERG_12066	1.82	2.01	AMP-binding enzyme, putative ( <i>T. verrucosum</i> )
TERG_06004	1.82	2.61	hypothetical protein
TERG_01986	1.81	3.40	Fe-S protein assembly co-chaperone HscB
TERG_03771	1.80	2.47	ankyrin repeat protein ( <i>T. verrucosum</i> )
TERG_12654	1.79	2.16	hypothetical protein
TERG_08503	1.79	2.51	secalin ( <i>M. canis</i> )
TERG_00523	1.78	3.29	hypothetical protein
TERG_03892	1.78	1.62	CAMK/CAMKL protein kinase ( <i>T. tonsurans</i> )
TERG_03815	1.78	1.75	subtilisin-like protease 3
TERG_01925	1.77	3.53	hypothetical protein
TERG_02565	1.77	1.82	sulfate transporter ( <i>T. equinum</i> )
TERG_12583	1.76	2.34	hypothetical protein
TERG_12044	1.75	2.90	hypothetical protein
TERG_08568	1.75	2.47	CMGC/SRPK protein kinase
TERG_11792	1.75	1.72	hypothetical protein
TERG_06377	1.75	1.63	metalloproteinase, putative ( <i>A. benhamiae</i> )
TERG_02920	1.75	2.98	RTA1 domain-containing protein ( <i>T. equinum</i> )
TERG_05459	1.74	2.89	hypothetical protein
TERG_05824	1.74	2.46	hypothetical protein
TERG_03331	1.72	1.75	F-box protein ( <i>T. equinum</i> )
TERG_03333	1.72	2.26	transcription factor RfeD, putative ( <i>A. benhamiae</i> )
TERG_08181	1.72	2.14	hypothetical protein
TERG_07859	1.72	3.02	ubiquitin C-terminal hydrolase L3 ( <i>T. tonsurans</i> )
TERG_01319	1.71	2.68	hypothetical protein
TERG_12213	1.71	1.59	hypothetical protein
TERG_01468	1.71	1.60	hypothetical protein
TERG_12385	1.71	3.03	hypothetical protein
TERG_03312	1.70	3.03	RTA1 domain protein, putative ( <i>A. benhamiae</i> )

TERG_08286	1.70	1.53	GPI anchored CFEM domain protein ( <i>T. verrucosum</i> )
TERG_02593	1.69	2.21	C2H2 finger domain protein, putative ( <i>T. verrucosum</i> )
TERG_00528	1.69	1.75	hypothetical protein
TERG_04769	1.69	1.85	extracellular serine carboxypeptidase, putative ( <i>T. verrucosum</i> )
TERG_08654	1.69	1.84	hypothetical protein
TERG_04766	1.67	2.07	calcium/proton exchanger
TERG_06792	1.67	1.88	hypothetical protein
TERG_12099	1.66	2.38	hypothetical protein
TERG_08451	1.65	1.51	hypothetical protein
TERG_01459	1.64	2.60	conserved leucine-rich repeat protein ( <i>T. verrucosum</i> )
TERG_05198	1.64	1.67	hypothetical protein
TERG_03240	1.64	1.70	transmembrane efflux protein ( <i>T. tonsurans</i> )
TERG_12067	1.63	1.97	AMP-binding enzyme, putative ( <i>T. verrucosum</i> )
TERG_12327	1.63	3.18	alkaline serine protease (PR1)/allergen F18, putative ( <i>T. verrucosum</i> )
TERG_03291	1.63	4.41	SNF2 family helicase, putative ( <i>T. verrucosum</i> )
TERG_11949	1.63	2.65	hypothetical protein
TERG_06105	1.63	2.66	hypothetical protein
TERG_12320	1.62	1.83	hypothetical protein
TERG_01636	1.62	2.54	ADP-ribosylglycohydrolase ( <i>M. gypseum</i> )
TERG_08178	1.62	2.14	endoglucanase ( <i>T. equinum</i> )
TERG_03078	1.61	1.77	cytochrome P450 oxidoreductase OrdA-like, putative ( <i>T. verrucosum</i> )
TERG_06740	1.61	2.48	hypothetical protein
TERG_04504	1.61	3.97	extracellular protein ( <i>T. equinum</i> )
TERG_05421	1.60	2.11	alpha-galactosidase A ( <i>M. canis</i> )
TERG_08351	1.60	2.50	hypothetical protein
TERG_12591	1.59	2.88	peptidase S8 family protein ( <i>T. equinum</i> )
TERG_01637	1.59	3.74	hypothetical protein
TERG_07964	1.59	2.20	vacuolar endopolyphosphatase, putative ( <i>T. verrucosum</i> )
TERG_03330	1.59	1.84	hypothetical protein
TERG_08781	1.59	1.97	hypothetical protein
TERG_02847	1.59	1.95	Fasciclin domain family protein ( <i>T. verrucosum</i> )
TERG_02995	1.58	2.27	hypothetical protein
TERG_08825	1.58	1.93	bZIP transcription factor JlbA/IDI-4 ( <i>T. verrucosum</i> )
TERG_01082	1.57	1.66	hypothetical protein
TERG_04194	1.57	2.99	acyltransferase ( <i>T. tonsurans</i> )
TERG_01266	1.57	2.26	amidophosphoribosyltransferase
TERG_02794	1.57	2.46	hypothetical protein
TERG_08324	1.56	1.88	hypothetical protein
TERG_02147	1.56	2.36	3-demethylubiquinone-9 3-methyltransferase, putative ( <i>T. verrucosum</i> )
TERG_07443	1.56	2.17	hypothetical protein
TERG_02059	1.55	1.74	AbpA protein ( <i>T. equinum</i> )
TERG_12032	1.55	2.36	hypothetical protein
TERG_02848	1.55	1.54	short chain dehydrogenase/reductase family protein ( <i>A. benhamiae</i> )
TERG_03884	1.55	-2.04	hypothetical protein
TERG_06065	1.55	4.07	conserved glycine-rich protein ( <i>T. verrucosum</i> )
TERG_07095	1.55	1.90	hypothetical protein
TERG_04954	1.55	4.09	hypothetical protein
TERG_00575	1.54	1.61	F-box domain protein ( <i>T. verrucosum</i> )
TERG_01623	1.54	2.98	MFS transporter ( <i>T. equinum</i> )

TERG_02900	1.53	3.12	hypothetical protein
TERG_06650	1.53	1.63	MFS monocarboxylate transporter, putative ( <i>A. benhamiae</i> )
TERG_06147	1.53	1.50	pyridine nucleotide-disulfide oxidoreductase, putative ( <i>A. benhamiae</i> )
TERG_07352	1.53	4.12	aldehyde reductase (AKR1), putative ( <i>T. verrucosum</i> )
TERG_00384	1.52	1.58	Ser/Thr protein phosphatase family protein ( <i>A. benhamiae</i> )
TERG_12640	1.52	2.29	choriogenin Hminor ( <i>M. canis</i> )
TERG_02185	1.52	1.99	hypothetical protein
TERG_04245	1.52	1.73	hypothetical protein
TERG_12002	1.51	1.61	hypothetical protein
TERG_01895	1.51	2.33	pheromone processing carboxypeptidase (Sxa2), putative ( <i>T. verrucosum</i> )
TERG_07197	1.50	3.02	disintegrin and metalloproteinase domain-containing protein B
TERG_05303	1.50	1.88	phospholipase PldA, putative ( <i>T. verrucosum</i> )
TERG_05374	1.50	2.35	hypothetical protein
TERG_02489	1.50	2.02	sister chromatid cohesion acetyltransferase Eco1, putative ( <i>A. benhamiae</i> )
TERG_11724	-1.51	-3.66	polyketide synthase, putative ( <i>A. benhamiae</i> )
TERG_04742	-1.52	-5.29	hypothetical protein
TERG_06187	-1.52	-1.84	nucleolar ATPase Kre33 ( <i>T. tonsurans</i> )
TERG_00507	-1.53	-3.57	hypothetical protein
TERG_12319	-1.53	-2.81	chitin synthase 2
TERG_02327	-1.53	-2.63	rRNA biogenesis protein RRP5 ( <i>T. tonsurans</i> )
TERG_00569	-1.55	-3.66	C2H2 finger domain protein, putative ( <i>A. benhamiae</i> )
TERG_03278	-1.55	-2.57	hypothetical protein
TERG_02425	-1.55	-2.44	RNA binding protein ( <i>A. benhamiae</i> )
TERG_01012	-1.56	-2.03	hypothetical protein
TERG_00342	-1.56	-2.02	phosphoglucomutase
TERG_04791	-1.56	-1.58	hypothetical protein
TERG_04558	-1.57	-2.48	nucleoside diphosphate kinase
TERG_05819	-1.57	-1.99	isocitrate dehydrogenase ( <i>T. tonsurans</i> )
TERG_11986	-1.58	-3.34	GABA permease, putative ( <i>A. benhamiae</i> )
TERG_02623	-1.61	-3.91	hypothetical protein
TERG_11987	-1.61	-3.90	GABA permease, putative ( <i>A. benhamiae</i> )
TERG_01883	-1.61	-3.23	hsp75-like protein
TERG_05717	-1.61	-3.10	squalene epoxidase ( <i>T. equinum</i> )
TERG_04857	-1.61	-2.85	ribose 5-phosphate isomerase
TERG_11689	-1.63	-1.97	U3 small nucleolar RNA-associated protein 10 ( <i>T. equinum</i> )
TERG_01911	-1.64	-3.59	NmrA family protein ( <i>T. equinum</i> )
TERG_07048	-1.65	-2.42	dsDNA-dependent ATPase ( <i>T. equinum</i> )
TERG_00189	-1.65	-2.87	40S ribosomal protein S0
TERG_01202	-1.68	-2.11	histone H3-like centromeric protein cnp1
TERG_04041	-1.69	-2.21	Sad1/UNC domain protein ( <i>T. verrucosum</i> )
TERG_05435	-1.70	-1.62	hypothetical protein
TERG_07351	-1.71	-2.81	hypothetical protein
TERG_00760	-1.71	-3.40	protein arginine methyltransferase ( <i>T. tonsurans</i> )
TERG_08139	-1.71	-2.67	NAD dependent epimerase/dehydratase ( <i>M. gypseum</i> )
TERG_02353	-1.73	-3.00	UbiD family decarboxylase, putative ( <i>T. verrucosum</i> )
TERG_01002	-1.74	-1.89	chaperone dnaK ( <i>T. tonsurans</i> )
TERG_00253	-1.74	-2.77	HNRNP arginine N-methyltransferase ( <i>T. tonsurans</i> )
TERG_12232	-1.75	-2.69	DUF221 domain-containing protein ( <i>T. equinum</i> )
TERG_03175	-1.75	-3.97	DUF833 domain protein ( <i>A. benhamiae</i> )



TERG_00657	-1.77	-2.38	hypothetical protein
TERG_08680	-1.77	-2.05	amino acid permease ( <i>T. tonsurans</i> )
TERG_00694	-1.77	-3.65	glutamate 5-kinase
TERG_05780	-1.78	-2.25	hypothetical protein
TERG_07200	-1.78	-2.48	C2 domain-containing protein ( <i>T. tonsurans</i> )
TERG_11785	-1.78	-1.83	hypothetical protein
TERG_01252	-1.78	-3.32	catalase A
TERG_01062	-1.78	-3.08	hypothetical protein
TERG_11852	-1.80	-2.22	glyoxalase family protein ( <i>T. verrucosum</i> )
TERG_02114	-1.83	-4.27	glycerol dehydrogenase ( <i>T. tonsurans</i> )
TERG_12193	-1.84	-2.38	MFS sugar transporter ( <i>T. equinum</i> )
TERG_12156	-1.87	-3.31	hypothetical protein
TERG_05585	-1.94	-2.99	short-chain dehydrogenase/reductase SDR ( <i>T. equinum</i> )
TERG_01273	-1.97	-3.29	alpha-1,2-mannosidase, putative subfamily ( <i>T. verrucosum</i> )
TERG_00567	-1.98	-2.76	hypothetical protein
TERG_12194	-2.01	-2.53	MFS monosaccharide transporter, putative ( <i>T. verrucosum</i> )
TERG_05808	-2.02	-3.25	hypothetical protein
TERG_02081	-2.03	-3.19	RNA binding protein
TERG_11963	-2.06	-4.79	hypothetical protein
TERG_00855	-2.08	-3.48	aromatic amino acid aminotransferase, putative ( <i>A. benhamiae</i> )
TERG_00852	-2.08	-3.99	Phytanoyl-CoA dioxygenase PhyH ( <i>T. equinum</i> )
TERG_11536	-2.09	-5.69	hypothetical protein
TERG_12038	-2.21	-2.85	protein phosphatase regulatory subunit Gac1, putative ( <i>T. verrucosum</i> )
TERG_07652	-2.22	-2.16	Delta(12) fatty acid desaturase ( <i>T. equinum</i> )
TERG_05139	-2.24	-2.13	non ribosomal peptide synthase ( <i>T. equinum</i> )
TERG_02357	-2.24	-2.32	amino acid permease ( <i>T. equinum</i> )
TERG_06715	-2.27	-2.79	LEA domain protein ( <i>A. benhamiae</i> )
TERG_04282	-2.35	-4.76	GPI ethanolamine phosphate transferase ( <i>T. tonsurans</i> )
TERG_03919	-2.51	-5.20	phytoene dehydrogenase ( <i>T. equinum</i> )
TERG_00856	-2.54	-2.86	phytanoyl-CoA dioxygenase ( <i>T. equinum</i> )
TERG_03677	-2.57	-3.11	protein phosphatase regulatory subunit Gac1, putative ( <i>T. verrucosum</i> )
TERG_01917	-2.60	-2.32	O-methyltransferase, putative ( <i>A. benhamiae</i> )
TERG_04580	-2.64	-3.58	NADP-specific glutamate dehydrogenase
TERG_03826	-2.77	-3.57	hypothetical protein
TERG_00490	-3.13	-5.24	erythromycin esterase ( <i>T. tonsurans</i> )
TERG_01619	-3.20	-2.35	toxin biosynthesis protein (Tri7), putative ( <i>T. verrucosum</i> )
TERG_12339	-3.31	-2.95	hypothetical protein
TERG_05816	-3.74	-1.95	hypothetical protein
TERG_02959	-4.16	-5.90	hypothetical protein
TERG_02653	-6.21	-2.23	hypothetical protein

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Gene expression values are expressed in log<sub>2</sub> fold change.