Supplementary Table S-2. Up- and down-regulated proteins in space strains when compared to Af293 and CEA10.

Gene	Protein names	Relative protein abundance*			P-value
		CEA10	ISSFT-021	IF1SW-F4	
AFUA_3G00280	Metallo-beta-lactamase domain protein, putative	2.26	3.78	3.75	5.18E-04
AFUA_3G11070	Pyruvate decarboxylase (EC 4.1.1.1)	1.95	3.42	3.43	9.50E-08
AFUA_1G13500	Transketolase (EC 2.2.1.1)	2.21	3.24	3.23	5.10E-09
AFUA_4G11540	Glycerol kinase, putative (EC 2.7.1.30)	1.52	3.18	2.94	5.99E-05
AFUA_3G08470	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	1.41	3.06	3.33	8.66E-07
AFUA_1G09750	Aldehyde reductase (AKR1), putative (EC 1.1.1.2)	1.78	3.04	3.54	1.03E-08
AFUA_4G14530	Glutathione S-transferase-like protein tpcF (EC 2.5.1.-) (Trypacidin synthesis protein E)	0.83	3.02	2.46	2.76E-06
AFUA_3G00590	Asp-hemolysin (Asp-HS)	0.00	3.01	3.24	7.48E-09
AFUA_4G14580	O-methyltransferase tpcA (EC 2.1.1.-) (Trypacidin synthesis protein A)	-0.14	2.95	3.06	6.77E-07
AFUA_4G04300	Alanine racemase family protein, putative	0.78	2.85	3.24	3.63E-04
AFUA_4G11730	Glycerol dehydrogenase (GldB), putative (EC 1.1.1.72)	1.29	2.83	3.70	5.34E-07
AFUA_1G14710	Beta-glucosidase, putative	1.63	2.70	3.52	4.34E-05
AFUA_3G05360	Histone H2A	1.50	2.69	3.49	3.10E-05
AFUA_3G10310	Acetolactate synthase (EC 2.2.1.6)	1.11	2.68	2.31	4.10E-07
AFUA_4G14470	Probable decarboxylase tpcK (EC 1.-.-.-) (Trypacidin synthesis protein K)	0.27	2.58	2.17	3.04E-03
AFUA_5G11430	Quinone oxidoreductase, putative (EC 1.6.5.5)	0.95	2.55	2.51	1.45E-09
AFUA_7G04540	Short chain dehydrogenase/reductase family (EC 1.1.1.69)	0.87	2.53	2.98	2.26E-07
AFUA_2G17580	Scytalone dehydratase arp1 (EC 4.2.1.94) (Conidial pigment biosynthesis oxidase arp1)	0.58	2.49	2.69	2.24E-07
AFUA_7G02070	AIF-like mitochondrial oxidoreductase (Nfrl), putative	0.65	2.37	2.52	2.26E-08
AFUA_8G01210	Enoyl-CoA hydratase/isomerase family protein (EC 4.2.1.17)	-0.38	2.33	2.05	5.72E-03
AFUA_6G06750	14-3-3 family protein	0.77	2.32	2.84	2.93E-06
AFUA_6G04560	37S ribosomal protein S9	0.95	2.24	3.28	4.88E-04
AFUA_5G10540	Glycogen branching enzyme GbeA, putative	0.91	2.23	3.06	1.39E-07
AFUA_2G03290	14-3-3 family protein ArtA, putative	0.67	2.21	2.82	1.90E-07
AFUA_3G10090	Dihydroneopterin aldolase domain protein (EC 4.1.2.25)	0.71	2.20	2.58	2.09E-05
AFUA_2G01220	GTP cyclohydrolase II, putative (EC 3.5.4.25)	1.06	2.20	3.30	5.88E-03
AFUA_3G13620	Cupin domain protein	-0.46	2.20	1.33	1.15E-03
AFUA_4G06380	Sterol carrier protein, putative	0.71	2.15	2.45	7.99E-07
AFUA_2G07720	Cytochrome b5, putative	0.33	2.14	2.11	2.06E-02
AFUA_1G02820	NADH-quinone oxidoreductase Pst2, putative	-0.37	2.10	2.55	9.33E-06
AFUA_6G03540	Malate synthase (EC 2.3.3.9)	0.38	2.10	2.16	1.22E-07
AFUA_1G09480	Vacuolar protein sorting-associated protein 29	0.98	2.02	2.31	3.96E-02
AFUA_1G02140	Glycogen debranching enzyme Gdb1, putative	0.87	1.98	3.18	1.08E-03
AFUA_3G12560	Allantoicase Alc, putative (EC 3.5.3.4)	-0.32	1.93	2.50	3.74E-05
AFUA_6G05090	RNA polymerase II Elongator subunit, putative	-0.19	1.92	2.79	3.47E-03
AFUA_6G10660	ATP citrate lyase subunit (Acl), putatibe (EC 6.2.1.5)	0.19	1.91	2.65	1.23E-04
AFUA_2G14030	Arginyl-tRNA synthetase (EC 6.1.1.19)	0.35	1.91	2.08	2.78E-07
AFUA_3G00370	Phosphoketolase, putative (EC 4.1.2.-)	0.51	1.88	2.84	3.50E-05
AFUA_4G04680	FGGY-family carbohydrate kinase, putative	0.81	1.82	2.61	1.73E-05
AFUA_7G01880	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	-0.48	1.81	1.87	8.56E-04
AFUA_3G11640	Homoserine dehydrogenase (HDH) (EC 1.1.1.3)	-0.21	1.76	2.09	2.66E-06
AFUA_3G11430	Arginase (EC 3.5.3.1)	0.44	1.75	2.07	7.83E-03
AFUA_2G01100	Pirin domain protein, putative	0.33	1.73	2.73	9.67E-04
AFUA_4G07690	Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	0.20	1.65	2.06	7.82E-08
AFUA_1G01750	Peptidyl-prolyl cis-trans isomerase, putative (EC 5.2.1.8)	0.38	1.61	1.81	1.91E-02
AFUA_3G06210	Phosphoribosyl-aminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	-0.11	1.53	2.33	2.96E-06
AFUA_5G03350	Glutamine-dependent NAD(+) synthetase (EC 6.3.5.1) (NAD(+) synthase [glutamine-hydrolyzing])	0.47	1.51	1.84	5.06E-03

AFUA_4G08880	Glucose-6-phosphate 1-epimerase (EC 5.1.3.15)	-0.32	1.46	2.61	7.00E-05
AFUA_5G06130	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial (EC 6.2.1.5) (Succinyl-CoA synthetase subunit alpha) (SCS-alpha)	-0.10	1.42	2.15	4.63E-07
AFUA_7G01830	UTP-glucose-1-phosphate uridylyltransferase Ugp1, putative	0.00	1.35	2.11	4.43E-05
AFUA_2G15980	3' exoribonuclease family protein	0.02	1.24	2.20	4.73E-03
AFUA_4G14070	Glycosyl transferase, putative (EC 2.-.-.-)	-0.24	1.23	1.60	4.77E-04
AFUA_1G05850	Erythromycin esterase, putative	-0.16	1.22	2.48	6.61E-03
AFUA_2G05910	Phosphotransferase (EC 2.7.1.-)	-0.01	1.20	2.12	8.68E-07
AFUA_2G11290	Orotate phosphoribosyltransferase (EC 2.4.2.10)	-0.51	1.15	2.21	5.62E-08
AFUA_5G06710	DUF89 domain protein	-0.36	1.07	1.81	1.10E-04
AFUA_4G13120	Glutamine synthetase (EC 6.3.1.2)	-0.37	1.01	2.23	6.13E-05
AFUA_2G01330	Exosome complex subunit Rrp46, putative (EC 3.1.13.-)	-0.13	1.01	2.12	2.83E-02
AFUA_2G00680	Glycosyl hydrolase, putative	-0.14	1.01	1.63	1.32E-02
AFUA_5G05500	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	-0.44	0.99	1.51	1.70E-04
AFUA_4G06960	UBX domain protein, putative	0.16	-0.99	-2.03	8.96E-03
AFUA_1G06580	High expression lethality protein Hel10, putative	1.24	-1.04	-1.37	4.99E-06
AFUA_6G05030	Polysaccharide deacetylase family protein	-0.09	-1.21	-1.23	1.53E-03
AFUA_1G03140	Glycosyl hydrolase, putative (EC 3.2.1.-)	-0.31	-1.31	-1.44	1.39E-06
AFUA_7G05650	Glutamine-serine rich protein MS8, putative	-0.10	-1.39	-1.40	2.22E-02
AFUA_6G14490	Probable beta-glucosidase H (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase H) (Cellobiase H) (Gentiobiase H)	-0.21	-1.41	-1.33	4.68E-05
AFUA_2G15510	DUF866 domain protein	0.98	-1.44	-1.51	7.12E-07
AFUA_1G06910	Probable arabinogalactan endo-beta-1,4-galactanase A (EC 3.2.1.89) (Endo-1,4-beta-galactanase A) (Galactanase A)	-0.43	-1.53	-2.04	9.05E-06
AFUA_5G09600	2-nitropropane dioxygenase family oxidoreductase, putative (EC 1.3.1.9)	0.41	-1.54	-1.66	1.28E-03
AFUA_2G00820	Extracellular GDSL-like lipase/acylhydrolase, putative	-0.17	-1.68	-1.43	4.80E-05
AFUA_7G05450	Secreted beta-glucosidase sun1 (EC 3.2.1.-)	-0.61	-1.87	-2.15	4.13E-02
AFUA_2G17470	L-PSP endoribonuclease family protein, putative	0.01	-2.24	-2.03	2.01E-03
AFUA_4G03322	WW domain protein	-0.34	-2.27	-2.52	5.11E-03
AFUA_2G13310	RING finger domain protein, putative	0.82	-2.49	-1.61	4.25E-03
AFUA_3G10340	Rho GTPase Rho 2, putative	-0.96	-2.51	-2.14	2.12E-03
AFUA_3G07870	Extracellular serine-rich protein, putative	-1.73	-2.89	-3.23	1.27E-06
AFUA_2G05540	Pre-mRNA-splicing factor cef1	-2.16	-3.57	-3.66	5.22E-03
AFUA_2G14490	Endoglucanase, putative (EC 3.2.1.-)	-2.17	-3.83	-3.33	1.17E-04
AFUA_2G03010	Cytochrome c subunit Vb, putative	-2.09	-3.83	-3.13	8.44E-07
AFUA_3G13850	LRP16 family protein	-2.27	-4.37	-4.88	1.16E-03
AFUA_6G03210	Conidiation-specific protein (Con-10), putative	-2.13	-4.73	-3.82	3.46E-04
AFUA_3G10410	Conserved serine-rich protein	-2.82	-4.81	-3.94	3.68E-05
AFUA_7G01340	RPEL repeat protein	-3.36	-5.15	-5.55	4.07E-10
AFUA_4G08960	GPI anchored cell wall protein, putative	-3.69	-5.18	-5.37	8.40E-05
AFUA_1G17370	Heat shock protein Awh11, putative	-2.95	-5.23	-4.26	4.25E-07
AFUA_3G05570	Spindle poison sensitivity protein Scp3, putative	-2.94	-5.28	-4.83	4.20E-04
AFUA_7G04930	Alkaline serine protease (PR1)/allergen F18-like (EC 3.4.21.-)	-3.63	-5.32	-5.53	1.14E-06
AFUA_4G00860	Cell surface protein, putative	-3.54	-5.64	-4.62	1.37E-07
AFUA_3G05430	ATP-dependent RNA helicase dhh1 (EC 3.6.4.13)	-2.86	-5.81	-4.16	7.98E-04
AFUA_6G12450	Chaperone/heat shock protein Hsp12, putative	-4.05	-5.81	-5.12	5.46E-05
AFUA_4G09600	GPI anchored protein, putative	-3.43	-6.26	-5.82	1.33E-07
AFUA_5G14210	Glucose repressible protein Grg1, putative	-3.21	-7.14	-4.80	1.87E-07

* Log2 fold change of CEA10, ISSFT-021, and IF1SW-F4 compared to Af293 ($P < 0.05$)