Table S1. A list of all the genes analyzed in the microarray analysis and whose signal ratios (-N/+N) are shown

Gene number[a]	Gene product[a]	Ratio (-N/+N)[b]		
CMG018C	Nitrate transporter	7.64	±	1.17
CMK117C	Similar to Protein phosphatase 2C	6.41	±	0.69
CMT527C	Hypothetical protein	4.97	±	0.49
CMT526C	High affinity ammonium transporter	4.92	±	1.59
CMS301C	Hypothetical protein	4.51	±	0.96
CME096C	Similar to RNA binding protein HUA1	4.34	±	0.44
CMN035C	Hypothetical protein	4.21	±	0.66
CMS095C	Hypothetical protein	3.92	±	0.17
CMJ282C	MYB-related protein	3.87	±	0.23
CML236C	Hypothetical protein	3.32	±	0.08
CMC183C	Hypothetical protein	3.29	±	0.12
CMJ222C	Hypothetical protein	3.19	±	0.34
CMQ313C	Hypothetical protein	3.04	±	0.20
CMM277C	Hypothetical protein	3.02	±	0.83
CMQ066C	Hypothetical protein	2.95	±	0.19
CMD108C	Probable lactoylglutathione lyase	2.83	±	0.09
CMS246C	Hypothetical protein	2.79	±	0.21
CMS149C	Hypothetical protein	2.78	±	1.85
CME036C	Hypothetical protein	2.77	±	0.50
CMQ191C	Citrate synthase, mitochondrial precursor	2.74	±	0.46
CMI233C	Glutamine synthetase	2.74	±	0.35
CMI268C	Hypothetical protein	2.67	±	0.22
CMF144C	Hypothetical protein	2.67	±	0.07
CMC149C	Phosphoglycerate dehydrogenase	2.64	±	0.45
CMI140C	60S acidic ribosomal protein P1	2.59	±	0.59
CMI066C	Hypothetical protein	2.55	±	0.41
CMK296C	Ubiquitin with short C-terminal extension	2.52	±	0.29
CMQ064C	Acetylornithine transaminase	2.51	±	0.60
CMI118C	Similar to cell death-regulatory protein GRIM19	2.51	±	0.24
CME180C	Hypothetical protein	2.42	±	0.24
CMR492C	Similar to MAP kinase phosphatase	2.35	±	0.69
CML209C	Glycerol-3-phosphate dehydrogenase	2.31	±	0.55
CMH176C	Similar to synaptobrevin-type protein transport protein	2.30	±	0.54
CMN082C	Similar to GTP pyrophosphokinase	2.30	±	0.67
CMI072C	Mitochondrial alternative oxidase	2.28	±	0.47
CMG021C	Nitrite reductase (ferredoxin)	2.28	±	0.98
CMO028C	Hypothetical protein	2.27	±	0.59
CMM034C	NADH dehydrogenase I Fe-S protein, 75kDa subunit	2.27	±	0.32
CMP037C	Hypothetical protein	2.26	±	0.05
CMQ079C	Similar to subunit of cleavage and polyadenylation factor Mpe1p	2.25	±	0.34
CML066C	Similar to phosphate starvation-inducible ATPase PhoH	2.24	±	0.15

CMS432C	Hypothetical protein	2.22	±	0.33
CMR143C	Ribonuclease P subunit POP1	2.13	±	0.56
CML201C	Hypothetical protein	2.10	±	0.21
CML203C	Hypothetical protein	2.08	±	0.15
CMI163C	Similar to TBP-associated factor TAF9	2.08	±	0.32
CMK303C	Similar to ADP ribosylation factor 1 GTPase activating protein	2.07	±	0.23
CMP179C	60S ribosomal protein L10A	2.07	±	0.20
CMJ068C	Hypothetical protein	2.06	±	0.27
CMO230C	Hypothetical protein	2.06	±	0.23
CMT454C	Similar to chondroitin 4-sulfotransferase	2.05	±	0.20
CMQ189C	Small GTP-binding protein of Rab family	2.04	±	0.33
CMF092C	Hypothetical protein	2.04	±	0.74
CMM003C	Eukaryotic translation elongation factor 1 gamma (eEF-1g)	2.04	±	0.20
CMH234C	Hypothetical protein	2.03	±	0.16
CMT361C	Mitochondrial phosphate carrier protein	2.01	±	0.55
CMI266C	Hypothetical protein	1.98	±	0.06
CMH032C	Similar to protein phosphatase 2C (PP2C)	1.98	±	0.72
CMQ413C	Hypothetical protein	1.96	±	0.48
CMC021C	Pyruvate kinase	1.95	±	0.46
CMN011C	Similar to ubiquinone/menaquinone biosynthesis methlytransferase family protein	1.94	±	0.23
CMA004C	Hypothetical protein	1.93	±	0.07
CMR500C	Membrane-associated calcium-independent phospholipase A2	1.93	±	0.11
CMN222C	Similar to regulator of chloroplast RNA processing, CRP1 (Zea mays)	1.91	±	0.47
CMN228C	Anthranilate synthase component I	1.91	±	0.27
CMN330C	Hypothetical protein	1.91	±	0.19
CMD139C	Similar to endonuclease III	1.91	±	0.27
CMH044C	Hypothetical protein	1.90	±	0.14
CMO302C	60S ribosomal protein l18a	1.90	±	0.38
CML246C	MYB-related protein	1.89	±	0.48
CMM061C	Hypothetical protein	1.89	±	0.18
CMM332C	Hypothetical protein	1.89	±	0.23
CMT397C	Hypothetical protein	1.89	±	0.16
CMH080C	Hypothetical protein	1.87	±	0.09
CMH199C	Hypothetical protein	1.85	±	0.22
CMB077C	Similar to mitochondrial inner membrane protease IMP1	1.85	±	0.25
CMC096C	Cytoplasmic aminopeptidase P	1.85	±	0.20
CMS125C	Alcohol dehydrogenase class III	1.84	±	0.22
CMS131C	Unknown protein for iron-sulfur cluster formation sufe	1.84	±	0.23
CMB099C	Similar to brain protein	1.84	±	0.09
CMK012C	Hypothetical protein	1.83	±	0.04
CMP084C	Mitochondrial phosphate translocator MIR1	1.83	±	0.15
CMP181C	Similar to ubiquitin conjugating enzyme E2	1.81	±	0.04
CMR122C	60S ribosomal protein L13A	1.81	±	0.20

CMI170C	Hypothetical protein	1.80	±	0.38
CMM316C	Homeotic gene regulator (BRAHMA protein)	1.80	±	0.29
CMN188C	Similar to steroid binding protein	1.80	±	0.24
CML242C	Hypothetical protein	1.80	±	0.31
CML049C	Glutamate dehydrogenase ($NADP^+$) 1	1.80	±	0.02
CMR129C	Probable rRNA (adenosine-N6,N6)-dimethyltransferase	1.79	±	0.21
CMF080C	Hypothetical protein	1.79	±	0.03
CML244C	Hypothetical protein	1.79	±	0.39
CMR158C	Mitochondrial Mn superoxide dismutase	1.77	±	0.31
CMB107C	Hypothetical protein	1.76	±	0.35
CMG016C	Hypothetical protein	1.75	±	0.12
CMM060C	Hypothetical protein	1.75	±	0.30
CML016C	Probable DNA-(apurinic or apyrimidinic site) lyase (ARP)	1.75	±	0.28
CMI134C	Hypothetical protein	1.74	±	0.17
CMH265C	Hypothetical protein	1.74	±	0.20
CMQ353C	Similar to ring-box protein 1	1.73	±	0.25
CMT312C	Membrane-associated calcium-independent phospholipase A2	1.73	±	0.52
CMT623C	DnaJ (Hsp40) homolog, subfamily B	1.73	±	0.24
CMK059C	RNA polymerase I, III common subunit	1.73	±	0.27
CMN079C	Hypothetical protein	1.73	±	0.10
CMN126C	40S ribosomal protein S26	1.73	±	0.31
CMN084C	ADP/ATP translocase	1.73	±	0.39
CMH065C	60S ribosomal protein L14	1.73	±	0.31
CMS025C	Hypothetical protein	1.72	±	0.33
CMH135C	Unknown transcriptional coactivator, ALY homolog	1.72	±	0.17
CMT631C	Sphingosine-1-phosphate lyase	1.72	±	0.52
CMD127C	Hypothetical protein	1.72	±	0.34
CMP287C	Hypothetical protein	1.72	±	0.37
CMG075C	Unknown kinase with aarF domain	1.71	±	0.20
CMR309C	Similar to mitochondrial carrier protein (Mrs1p)	1.71	±	0.20
CMN056C	Hypothetical protein	1.71	±	0.08
CMO338C	Hypothetical protein	1.71	±	0.07
CMM079C	Unknown transcriptional regulator	1.71	±	0.18
CMD063C	Hypothetical protein	1.71	±	0.04
CMS197C	Isoamylase	1.70	±	0.12
CMM217C	Similar to single-stranded telomeric DNA-binding protein Gbp1 (hnRNP M)	1.70	±	0.25
CMH226C	Eukaryotic translation elongation factor 1 alpha (eEF-1a)	1.70	±	0.31
CML170C	Similar to phosphoribosylanthranilate transferase	1.70	±	0.10
CMT430C	Zinc finger protein	1.70	±	0.09
CMN176C	Histone H3	1.70	±	0.16
CMP207C	Hypothetical protein	1.69	±	0.19
CMN173C	Histone H2B	1.69	±	0.02
CMN332C	Serine hydroxymethyltransferase, cytosolic (glycine hydroxymethyltransferase)	1.69	±	0.22

CML325C	Hypothetical protein	1.69	±	0.12
CMM087C	Hypothetical protein	1.69	±	0.08
CMT298C	Large fused protein of putative glutamine amidotransferase and glutamate carboxypeptidase	1.69	±	0.25
CMQ461C	Chloroplast ribosome releasing factor RRF	1.68	±	0.51
CMS163C	Zinc-finger protein	1.68	±	0.39
CMI113C	Similar to peroxiredoxin Q	1.68	±	0.16
CMH275C	Hypothetical protein	1.67	±	0.19
CMR319C	Unknown globin-like protein	1.67	±	0.23
CMR229C	Hypothetical protein	1.67	±	0.04
CMT163C	Hypothetical protein	1.67	±	0.01
CMM253C	60S ribosomal protein L3	1.67	±	0.10
CMQ134C	Similar to ubiquinone/menaquinone biosynthesis methyltransferase	1.66	±	0.06
CMT032C	Hypothetical protein	1.66	±	0.14
CML191C	Hypothetical protein	1.66	±	0.24
CMN197C	Hypothetical protein	1.65	±	0.05
CML172C	Hypothetical protein	1.65	±	0.24
CMG157C	60S ribosomal protein L26	1.65	±	0.30
CMM296C	Alcohol dehydrogenase [NADP$^+$] (aldehyde reductase)	1.65	±	0.18
CMD112C	Unknown hydrolase	1.65	±	0.27
CML322C	dTMP kinase	1.64	±	0.06
CMS272C	Isocitrate dehydrogenase (NAD$^+$) subunit 2, mitochondrial precursor	1.64	±	0.14
CMT188C	Similar to KRR1-interacting protein	1.64	±	0.31
CMJ056C	Similar to vesicle transport v-SNARE protein	1.63	±	0.20
CMQ463C	60S ribosomal protein L17	1.63	±	0.36
CMT048C	Probable de-N-glycosylation enzyme Png1p	1.63	±	0.36
CMQ293C	60S ribosomal protein L4	1.63	±	0.21
CML239C	Hypothetical protein	1.63	±	0.27
CMS462C	Fusion protein of dihydrofolate reductase and thymidylate synthase	1.63	±	0.13
CMS441C	Hypothetical protein	1.63	±	0.08
CMJ171C	Hypothetical protein	1.62	±	0.25
CMT378C	Mitochondrial ribosomal protein L11 precursor	1.62	±	0.16
CMO167C	Hypothetical protein	1.62	±	0.05
CMJ070C	Hypothetical protein	1.62	±	0.29
CMS100C	Hypothetical protein	1.62	±	0.03
CMM002C	Hypothetical protein	1.62	±	0.06
CMN169C	Histone H4	1.61	±	0.06
CMS193C	Hypothetical protein	1.61	±	0.10
CMT366C	Hypothetical protein	1.61	±	0.17
CMD175C	Hypothetical protein	1.61	±	0.21
CMJ008C	Similar to retinoblastoma-binding protein 5	1.61	±	0.14
CMC022C	Probable endoplasmic reticulum oxidoreductin 1-Lbeta (ERO1-L)	1.61	±	0.29
CMM088C	Probable purine phosphoribosyltransferase	1.61	±	0.26
CMC136C	Probable nucleotide binding protein	1.60	±	0.20

CMH122C	Similar to DNA invertase	1.60	±	0.21
CMD102C	Adaptor-related protein complex 3, sigma subunit	1.60	±	0.20
CML334C	Hypothetical protein	1.60	±	0.25
CML189C	Hypothetical protein	1.59	±	0.06
CMQ468C	Hypothetical protein	1.59	±	0.29
CMS321C	Probable non-canonical ubiquitin conjugating enzyme	1.59	±	0.23
CMQ024C	Glutamate-5-semialdehyde dehydrogenase	1.59	±	0.27
CMD005C	Similar to Trithorax protein	1.59	±	0.20
CMJ033C	Hypothetical protein	1.58	±	0.06
CMT042C	Hypothetical protein	1.58	±	0.21
CMT322C	Chaperonin containing TCP1, subunit 2 (beta)	1.58	±	0.09
CMK118C	40S ribosomal protein S12	1.58	±	0.07
CMG064C	Cytochrome c oxidase (Complex IV) assembly protein	1.58	±	0.04
CMF161C	Similar to cleavage and polyadenylation specific factor 4, 30kDa subunit	1.57	±	0.07
CMP126C	Similar to 3-oxoacyl-(acyl-carrier-protein) reductase	1.57	±	0.21
CMP293C	Hypothetical protein	1.57	±	0.07
CMN240C	Hypothetical protein	1.56	±	0.26
CMQ349C	Hypothetical protein	1.56	±	0.19
CMI107C	Similar to 3'-5' exoribonuclease subunit Dis3	1.56	±	0.18
CMG022C	Hypothetical protein	1.56	±	0.21
CMN267C	Hypothetical protein	1.56	±	0.25
CMF107C	Hypothetical protein	1.56	±	0.07
CMT447C	Hypothetical protein	1.56	±	0.13
CMN018C	Hypothetical protein	1.56	±	0.07
CMM298C	Hypothetical protein	1.56	±	0.26
CMT260C	Hypothetical protein	1.56	±	0.15
CME167C	Hypothetical protein	1.56	±	0.17
CML176C	Hypothetical protein	1.55	±	0.04
CMI030C	Hypothetical protein	1.55	±	0.30
CMS109C	Similar to geranylgeranyl hydrogenase	1.55	±	0.36
CMB076C	Similar to histidyl-tRNA synthetase	1.55	±	0.09
CMK253C	Probable ubiquitin conjugating enzyme E2	1.55	±	0.13
CML161C	Hypothetical protein	1.55	±	0.03
CMI204C	Similar to UMP-CMP kinase	1.55	±	0.15
CMI054C	Similar to guanine nucleotide exchanging fractor	1.55	±	0.15
CMN175C	Similar to cyclin C	1.55	±	0.25
CMM265C	Gamma-glutamyltransferase	1.55	±	0.15
CMS503C	Probable ubiquitin-conjugating enzyme E2	1.54	±	0.05
CMT380C	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	1.54	±	0.11
CML219C	Similar to cyclin E2	1.54	±	0.24
CMH197C	Mitochondrial F-type ATPase F1 subunit beta, precursor	1.54	±	0.34
CMJ023C	Hypothetical protein	1.54	±	0.24
CML162C	Hypothetical protein	1.54	±	0.23

CMI299C	Serine O-acetyltransferase	1.53	±	0.12
CMS101C	Probable proliferating cell nuclear antigen	1.53	±	0.39
CMQ159C	Hypothetical protein	1.53	±	0.20
CMB059C	Aluminum resistance protein	1.53	±	0.06
CMM100C	Similar to nuclear receptor binding factor 1	1.53	±	0.28
CMO287C	40S ribosomal protein S11	1.53	±	0.27
CMH165C	Hypothetical protein	1.53	±	0.01
CMT402C	40S ribosomal protein S17	1.52	±	0.22
CMK013C	Hypothetical protein	1.52	±	0.31
CML175C	Hypothetical protein	1.52	±	0.26
CMB018C	60S ribosomal protein L18	1.52	±	0.24
CMS040C	Hypothetical protein	1.52	±	0.26
CMR182C	Hypothetical protein	1.52	±	0.25
CMJ159C	Hypothetical protein	1.52	±	0.04
CMD174C	Hypothetical protein	1.52	±	0.22
CMR377C	Hypothetical protein	1.52	±	0.03
CMO149C	20S core proteasome subunit beta 5	1.52	±	0.08
CMJ054C	Glutamyl-tRNA reductase	1.51	±	0.38
CMS284C	60S ribosomal protein L12	1.51	±	0.09
CMN156C	Hypothetical protein	1.51	±	0.33
CMM280C	Hypothetical protein	1.51	±	0.10
CMT450C	Similar to nuclear transport factor 2	1.50	±	0.13
CMJ087C	Probable beta-amylase	1.50	±	0.21
CMP300C	Probable pullulanase	1.50	±	0.31
CMH021C	Hypothetical protein	1.50	±	0.06
CMM139C	Probable arginine deiminase	1.50	±	0.13
CML075C	Hypothetical protein	1.50	±	0.14
CMH237C	Zinc finger protein	1.49	±	0.23
CMP308C	Mitochondrial ribosomal protein L27 precursor	1.49	±	0.20
CMG125C	Similar to 22 kDa peroxisomal membrane protein PMP22	1.49	±	0.13
CMH240C	Hypothetical protein	1.49	±	0.30
CMJ065C	Hypothetical protein	1.49	±	0.06
CMT293C	Hypothetical protein	1.49	±	0.10
CMC044C	60S ribosomal protein L44	1.49	±	0.18
CMN024C	Hypothetical protein	1.49	±	0.31
CMK095C	Hypothetical protein	1.48	±	0.35
CME072C	Hypothetical protein	1.48	±	0.09
CMS130C	Probable signal peptidase I	1.48	±	0.11
CMD098C	Hypothetical protein	1.48	±	0.01
CMA082C	40S ribosomal protein S2	1.48	±	0.21
CMK061C	DNA repair and recombination protein reca, chloroplast precursor	1.48	±	0.29
CMI047C	Hypothetical protein	1.48	±	0.07
CMM252C	Hypothetical protein	1.48	±	0.10

CMK008C	Similar to ubiquitin fusion-degradation protein 1	1.48	±	0.22
CMS045C	Proteasome regulatory particle subunit	1.48	±	0.12
CMS429C	Serine-glyoxylate aminotransferase	1.48	±	0.12
CMO178C	Similar to bacterial putative methyl transferase	1.48	±	0.29
CMA125C	Similar to Rab11-binding protein	1.48	±	0.24
CME166C	Probable pre-mRNA splicing factor ATP-dependent RNA helicase PRP43	1.47	±	0.23
CMQ247C	Plasma membrane H^+-ATPase	1.47	±	0.14
CMJ110C	60S ribosomal protein L15	1.47	±	0.23
CMH218C	40S ribosomal protein S4	1.47	±	0.17
CMT234C	Cysteine desulfurase IscS, mitochondrial precursor	1.47	±	0.14
CMR096C	Hypothetical protein	1.47	±	0.08
CMG078C	Hypothetical protein	1.47	±	0.09
CMT553C	Hypothetical protein	1.47	±	0.16
CMR145C	Hypothetical protein	1.47	±	0.24
CMJ170C	60S ribosomal protein L38	1.47	±	0.02
CMM104C	Mitochondrial processing peptidase beta subunit (Complex III core subunit 1), precursor	1.47	±	0.15
CMO111C	Outer mitochondrial membrane protein porin	1.47	±	0.09
CMJ219C	Similar to component of oligomeric golgi complex 4	1.47	±	0.16
CMK219C	Calmodulin	1.47	±	0.26
CME126C	Similar to epidermal growth factor receptor substrate 15	1.46	±	0.06
CMN127C	Mitochondrial F-type ATPase F1 subunit delta, precursor	1.46	±	0.20
CMT504C	Alpha-tubulin	1.46	±	0.08
CMQ251C	Hypothetical protein	1.46	±	0.22
CMD061C	Hypothetical protein	1.46	±	0.20
CMM275C	Hypothetical protein	1.46	±	0.22
CMH036C	O-acetylserine (thiol) lyase 2 (cysteine synthase)	1.46	±	0.13
CMR442C	Hypothetical protein	1.45	±	0.07
CMI128C	Hypothetical protein	1.45	±	0.24
CMO062C	60S ribosomal protein L41	1.45	±	0.12
CMP159C	U6 snRNA-associated Sm-like protein LSm5	1.45	±	0.20
CMN263C	Beta-tubulin	1.45	±	0.16
CMR296C	Hypothetical protein	1.45	±	0.11
CMO304C	Hypothetical protein	1.45	±	0.21
CMH256C	Squalene monooxygenase	1.45	±	0.20
CMC176C	Similar to HERC2	1.45	±	0.08
CMT119C	Inorganic pyrophosphatase fused with fructose-1,6-bisphosphatase	1.45	±	0.08
CMJ125C	40S ribosomal protein S9	1.44	±	0.16
CMT124C	Hypothetical protein	1.44	±	0.12
CML157C	Chloroplast pre-mRNA splicing protein Mbb1	1.44	±	0.18
CMC088C	Hypothetical protein	1.44	±	0.17
CMQ211C	Adenylosuccinate lyase	1.44	±	0.07
CMK291C	Delta12 fatty acid desaturase, chloroplast or ER	1.44	±	0.25
CMB015C	Probable ubiquitin-conjugating enzyme E2	1.44	±	0.03

CMS144C	TATA-box binding protein-associated factor 12	1.44	±	0.05
CMM257C	Hypothetical protein	1.44	±	0.10
CMM039C	Hypothetical protein	1.44	±	0.29
CMI154C	Hypothetical protein	1.44	±	0.17
CMI195C	Hypothetical protein	1.43	±	0.13
CMJ279C	Hypothetical protein	1.43	±	0.07
CMO305C	Similar to adipocyte-specific protein 4	1.43	±	0.17
CMM140C	Similar to alpha-hemolysin	1.43	±	0.17
CMT131C	Probable RNA helicase with DEAD box	1.43	±	0.32
CML264C	Hypothetical protein	1.43	±	0.03
CMT197C	40S ribosomal protein S27	1.43	±	0.07
CMP012C	60S ribosomal protein L34	1.43	±	0.19
CMQ380C	Similar to COPII coated vesicle component Sec24	1.43	±	0.23
CMC076C	Similar to Na$^+$-translocating NADH:quinone oxidoreductase, subunit Nqr6	1.43	±	0.04
CMP138C	U6 snRNA-associated Sm-like protein LSm6	1.43	±	0.13
CMQ148C	Trehalose-phosphatase	1.42	±	0.21
CMR399C	Similar to pyrazinamidase/nicotinamidase	1.42	±	0.11
CMP031C	Hypothetical protein	1.42	±	0.15
CMS304C	Probable ubiquitin conjugating enzyme E2	1.42	±	0.12
CMQ152C	Hypothetical protein	1.42	±	0.31
CMR340C	Similar to procollagen (type III) N-endopeptidase	1.42	±	0.07
CMQ111C	Meiotic DNA topoisomerase VI subunit A	1.42	±	0.12
CMO238C	Hypothetical protein	1.42	±	0.07
CMS015C	Hypothetical protein	1.42	±	0.05
CMQ138C	Hypothetical protein	1.42	±	0.06
CMQ074C	Small GTP-binding protein Arf1	1.42	±	0.27
CMG215C	Cytochrome c reductase (Complex III) hinge protein	1.42	±	0.13
CMN208C	20S core proteasome subunit alpha 1	1.42	±	0.17
CMQ106C	Hypothetical protein	1.42	±	0.16
CMF021C	Hypothetical protein	1.42	±	0.02
CMJ078C	Probable prohibitin	1.41	±	0.22
CMF076C	Similar to DnaJ protein	1.41	±	0.31
CMN315C	60S ribosomal protein L37A	1.41	±	0.18
CMP311C	TBP-1 interacting protein	1.41	±	0.15
CMT227C	Carboxyl-terminal processing protease	1.41	±	0.13
CMT636C	Similar to membrane-bound alpha-1,6-mannosyltransferase	1.41	±	0.23
CMK045C	Pseudouridine synthase 3	1.41	±	0.12
CML299C	Hypothetical protein	1.41	±	0.11
CMK136C	Hypothetical protein	1.41	±	0.19
CML020C	Hypothetical protein	1.41	±	0.07
CMM176C	Hypothetical protein	1.41	±	0.30
CMS157C	Hypothetical protein	1.41	±	0.40
CMA060C	Hypothetical protein	1.41	±	0.26

CMD031C	Probable arginine methyltransferase (pam1)	1.41	±	0.23
CMB060C	Hypothetical protein	1.40	±	0.19
CMM152C	Similar to ribonuclease P subunit RPP1	1.40	±	0.03
CMI232C	Hypothetical protein	1.40	±	0.30
CMT209C	Succinate--CoA ligase (ADP- or GDP-forming), mitochondrial precursor	1.40	±	0.13
CMT492C	Similar to 3-methyladenine DNA glycosylase alka	1.40	±	0.05
CMQ056C	RNA polymerase I, II, III common subunit	1.40	±	0.13
CMO290C	ssra RNA (tmRNA)-binding protein, small protein B	1.40	±	0.15
CME055C	ATP-dependent Zn protease FtsH2	1.40	±	0.14
CME114C	Hypothetical protein	1.40	±	0.05
CMR210C	Hypothetical protein	1.40	±	0.24
CMH024C	Chloroplast peptide chain release factor RF-1	1.40	±	0.16
CMT034C	Glyceraldehyde-3-phosphate dehydrogenase (GAPN)	1.40	±	0.25
CMO357C	Similar to ER membrane protein; Hsd1p	1.40	±	0.05
CMG051C	Similar to sucrose-phosphate synthase	1.40	±	0.15
CMM196C	Pyrophosphate--fructose-6-phosphate 1-phosphotransferase	1.39	±	0.09
CMG094C	Hypothetical protein	1.39	±	0.09
CMQ014C	Hypothetical protein	1.39	±	0.22
CMN213C	Similar to molybdenum cofactor biosynthesis protein C (moac)	1.39	±	0.04
CMC140C	Hypothetical protein	1.39	±	0.22
CML153C	Hypothetical protein	1.39	±	0.07
CMN048C	N-acetyl-gamma-glutamyl-phosphate reductase	1.39	±	0.31
CML171C	Hypothetical protein	1.39	±	0.23
CMH138C	Pantoate--beta-alanine ligase	1.39	±	0.08
CMA098C	Deoxyhypusine synthase	1.39	±	0.13
CMH261C	Similar to ribose methyltransferase	1.38	±	0.10
CMR502C	Hypothetical protein	1.38	±	0.12
CMJ108C	Hypothetical protein	1.38	±	0.26
CMK137C	Hypothetical protein	1.38	±	0.13
CMM216C	Hypothetical protein	1.38	±	0.16
CMR323C	Hypothetical protein	1.38	±	0.14
CMQ181C	Hypothetical protein	1.38	±	0.05
CMF152C	3-hydroxyanthranilate 3,4-dioxygenase	1.38	±	0.09
CML284C	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1.38	±	0.14
CML052C	Hypothetical protein	1.38	±	0.24
CML211C	Hypothetical protein	1.37	±	0.19
CMQ388C	Similar to DNA/RNA-binding protein translin/TB-RBP	1.37	±	0.12
CMQ234C	Dihydrolipoamide dehydrogenase	1.37	±	0.21
CMF016C	Hypothetical protein	1.37	±	0.07
CML221C	Hypothetical protein	1.37	±	0.19
CMS241C	Hypothetical protein	1.37	±	0.05
CMR232C	RNA polymerase I, II, III common subunit	1.37	±	0.22
CMF032C	Hypothetical protein	1.37	±	0.15

CMR175C	Hypothetical protein	1.37	±	0.08
CME177C	Hypothetical protein	1.37	±	0.04
CMI149C	Hypothetical protein	1.37	±	0.04
CMC053C	60S ribosomal protein L35	1.37	±	0.24
CME051C	Hypothetical protein	1.37	±	0.25
CMT410C	40S ribosomal protein SA (P40)	1.37	±	0.12
CMT264C	Probable iron-sulfur cluster assembly protein IscA	1.37	±	0.11
CMN198C	Galactokinase	1.37	±	0.17
CMI152C	Hypothetical protein	1.37	±	0.03
CMO032C	Hypothetical protein	1.37	±	0.18
CME185C	Hypothetical protein	1.36	±	0.16
CMO191C	Hypothetical protein	1.36	±	0.10
CMP314C	Similar to tyrosine phosphatase Oca1p	1.36	±	0.11
CMQ323C	V-type ATPase V0 subunit c	1.36	±	0.26
CMQ091C	Hypothetical protein	1.36	±	0.20
CMS435C	Hypothetical protein	1.36	±	0.02
CMS178C	Trehalose-phosphatase	1.36	±	0.21
CME091C	Hypothetical protein	1.36	±	0.10
CMS329C	Similar to 3-beta hydroxysterioid dehydrogenase/isomerase family	1.36	±	0.07
CMQ253C	MYB-related protein	1.36	±	0.40
CMH128C	Cyclin dependent kinase, B-type	1.36	±	0.05
CMR383C	Hypothetical protein	1.36	±	0.20
CMS283C	Hypothetical protein	1.36	±	0.04
CMS296C	Probable C-4 sterol methyl oxidase	1.36	±	0.15
CMC145C	60S ribosomal protein L9	1.36	±	0.20
CMK193C	Smt3-conjugating enzyme E2	1.36	±	0.17
CMN264C	Phosphoribosylformylglycinamidine cyclo-ligase (phosphoribosyl-aminoimidazole synthetase) (AIR synthase)	1.36	±	0.09
CMD080C	Phosphatidylinositol polyphosphate 5-phosphatase	1.36	±	0.06
CMK204C	Similar to iron-sulfur cluster scaffold protein	1.35	±	0.07
CMS211C	Similar to D-aminoacid oxidoreductase, DadA	1.35	±	0.15
CMT407C	Hypothetical protein	1.35	±	0.06
CMO131C	Hypothetical protein	1.35	±	0.16
CML118C	Hypothetical protein	1.35	±	0.09
CMO027C	Hypothetical protein	1.35	±	0.20
CMC028C	Similar to F-box only protein 9	1.35	±	0.02
CMF155C	Hypothetical protein	1.35	±	0.20
CMO101C	DnaJ (Hsp40) homolog, subfamily B	1.35	±	0.21
CMG012C	Hypothetical protein	1.35	±	0.08
CMT199C	Hypothetical protein	1.35	±	0.11
CMT282C	Hypothetical protein	1.34	±	0.15
CMM305C	Hypothetical protein	1.34	±	0.31
CMN059C	Similar to COP9 signalosome subunit Csn5	1.34	±	0.18
CME179C	Dihydrodipicolinate synthase	1.34	±	0.12

CMH235C	ATP-binding cassette, sub-family A	1.34	±	0.27
CMC146C	Phospholipase A2-activating protein	1.34	±	0.04
CME145C	Fructose-1,6-biphosphate aldolase	1.34	±	0.20
CMI156C	26S proteasome ATP-dependent regulatory subunit	1.34	±	0.02
CML124C	Similar to dual-specificity protein phosphatase	1.34	±	0.16
CMQ414C	Hypothetical protein	1.34	±	0.12
CMG067C	Similar to mitochondrial carrier Yel006N	1.33	±	0.09
CMS174C	Hypothetical protein	1.33	±	0.21
CMJ260C	Similar to prenylated rab acceptor PRA1	1.33	±	0.19
CMM111C	Eukaryotic petide chain release factor erf subunit 1	1.33	±	0.32
CMH210C	Similar to peptidyl-prolyl cis-trans isomerase Ess1p	1.33	±	0.22
CMF025C	Hypothetical protein	1.33	±	0.01
CME019C	Dynamin-related protein involved in mitochondrial division CmDnm1/DRP3	1.33	±	0.07
CMH266C	Hypothetical protein	1.33	±	0.03
CMT426C	Similar to Bax inhibitor-1 (suppressor of BAX induced cell death)	1.33	±	0.10
CMO261C	Hypothetical protein	1.33	±	0.18
CMF078C	26S proteasome ATP-dependent regulatory subunit	1.33	±	0.22
CMT156C	Hypothetical protein	1.33	±	0.09
CMC043C	Glutathione reductase	1.33	±	0.29
CMD024C	Ribosomal large subunit pseudouridine synthase A	1.33	±	0.06
CMJ188C	Similar to probable RUBISCO expression protein cbby	1.33	±	0.06
CMS457C	Hypothetical protein	1.32	±	0.06
CMR095C	Similar to proline transport helper PTH1	1.32	±	0.20
CMT630C	Hypothetical protein	1.32	±	0.05
CMJ178C	Similar to ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase	1.32	±	0.17
CMC137C	3-hydroxybutyryl-CoA dehydrogenase	1.32	±	0.16
CMT198C	NADH dehydrogenase I (Complex I) alpha subcomplex 5 (B13)	1.32	±	0.05
CMC099C	NADH dehydrogenase I (Complex I) beta subcomplex 7 (B18)	1.32	±	0.07
CMS425C	NADH-dependent hydroxypyruvate reductase	1.32	±	0.14
CML310C	BTF3-like transcription factor	1.32	±	0.24
CML067C	Hypothetical protein	1.32	±	0.15
CME015C	Methionine--tRNA ligase, chloroplast or mitochondrial	1.31	±	0.16
CML300C	Hypothetical protein	1.31	±	0.10
CMP165C	Hypothetical protein	1.31	±	0.02
CMS368C	DNA repair protein RAD52	1.31	±	0.06
CMT539C	Hypothetical protein	1.31	±	0.25
CML055C	Carbamoyl-phosphate synthase, pyrimidine-specific, large chain	1.31	±	0.36
CME065C	Hypothetical protein	1.31	±	0.04
CMP227C	Probable ferritin, chloroplast precursor	1.31	±	0.12
CMJ167C	Hypothetical protein	1.31	±	0.09
CMS389C	Hypothetical protein	1.31	±	0.12
CMF127C	Similar to DNA polymerase alpha subunit	1.31	±	0.13
CMN164C	Hypothetical protein	1.31	±	0.04

CMH239C	Hypothetical protein	1.31	±	0.08
CMD155C	Hypothetical protein	1.31	±	0.09
CMN293C	Hypothetical protein	1.31	±	0.29
CMQ063C	Hypothetical protein	1.31	±	0.09
CMP307C	Similar to Reg receptor	1.31	±	0.10
CMI076C	Hypothetical protein	1.30	±	0.03
CMT340C	Hypothetical protein	1.30	±	0.05
CMC108C	Hypothetical protein	1.30	±	0.19
CMT529C	Similar to DNA repair protein Rad17-like protein	1.30	±	0.11
CMR433C	Probable DEAD/DEAH box RNA helicase	1.30	±	0.10
CMT086C	Probable isopentenyl diphosphate isomerase	1.30	±	0.17
CMS424C	Glutamate N-acetyltransferase/amino-acid N-acetyltransferase	1.30	±	0.19
CML308C	Hypothetical protein	1.30	±	0.17
CMD113C	Glycerol-3-phosphate dehydrogenase	1.30	±	0.13
CMG076C	Hypothetical protein	1.30	±	0.16
CMG071C	Hypothetical protein	1.30	±	0.04
CME029C	Chromosome condensation protein SMC4	1.30	±	0.13
CMF053C	Similar to hormone-sensitive lipase	1.30	±	0.13
CMS362C	9-cis-epoxycarotenoid dioxygenase, neoxanthin cleavage enzyme-like protein	1.29	±	0.09
CMA005C	Calcium-binding mitochondrial carrier Aralar	1.29	±	0.03
CMQ371C	Hypothetical protein	1.29	±	0.13
CMQ453C	Probable blue light photoreceptor cryptochrome	1.29	±	0.19
CML297C	Hypothetical protein	1.29	±	0.15
CMS139C	Hypothetical protein	1.29	±	0.10
CMT021C	Similar to AKIN beta2 (protein kinase)	1.29	±	0.14
CMO346C	Similar to fatty acid hydroxylase (FAH1)	1.29	±	0.15
CMF007C	Hypothetical protein	1.29	±	0.07
CMK224C	Hypothetical protein	1.29	±	0.14
CMA136C	Hypothetical protein	1.29	±	0.07
CMT030C	40S ribosomal protein S30	1.29	±	0.07
CMH172C	Hypothetical protein	1.29	±	0.08
CMJ085C	Hypothetical protein	1.29	±	0.02
CMF030C	Hypothetical protein	1.29	±	0.17
CMK196C	Hypothetical protein	1.29	±	0.03
CMJ020C	Hypothetical protein	1.29	±	0.12
CMB098C	Hypothetical protein	1.29	±	0.19
CMP175C	60S ribosomal protein L31	1.28	±	0.14
CMJ185C	NADH dehydrogenase I (Complex I) flavoprotein 51kDa subunit	1.28	±	0.03
CMP133C	Hypothetical protein	1.28	±	0.13
CMI112C	Similar to peroxiredoxin Q	1.28	±	0.06
CML140C	RNA helicase	1.28	±	0.18
CMJ265C	Hypothetical protein	1.28	±	0.15
CME020C	Hypothetical protein	1.28	±	0.19

CMN009C	Hypothetical protein	1.28	±	0.31
CME082C	Similar to cell division cycle protein CDC6	1.28	±	0.09
CMP080C	Hypothetical protein	1.28	±	0.29
CMO116C	Hypothetical protein	1.28	±	0.06
CMT383C	Hypothetical protein	1.28	±	0.04
CMT384C	Adenylate kinase	1.28	±	0.19
CMT434C	Mitochondrial F-type ATPase F1 subunit alpha, precursor	1.27	±	0.03
CMF122C	Similar to nitrogen fixation associated protein HesB	1.27	±	0.07
CMF079C	Hypothetical protein	1.27	±	0.04
CMR024C	Transcription antiterminator protein, probably for organellar transcription	1.27	±	0.04
CMR188C	NADH dehydrogenase I (Complex I) flavoprotein 24kDa subunit	1.27	±	0.15
CMQ170C	Hypothetical protein	1.27	±	0.03
CMR285C	Mitochondrial ribosomal protein L18	1.27	±	0.09
CMT582C	Succinate dehydrogenase (Complex II) flavoprotein subunit precursor	1.27	±	0.05
CMT031C	Hypothetical protein	1.27	±	0.01
CMP286C	Hypothetical protein	1.27	±	0.07
CMS380C	Hypothetical protein	1.27	±	0.03
CMH022C	Ruvb-like DNA/RNA helicase pontin	1.27	±	0.01
CMT392C	Hypothetical protein	1.27	±	0.18
CMS228C	Similar to monoglyceride lipase	1.27	±	0.17
CMT468C	Hypothetical protein	1.27	±	0.24
CMK251C	Probable DNA repair protein rada	1.27	±	0.23
CMB042C	Hypothetical protein	1.27	±	0.05
CMD157C	Hypothetical protein	1.26	±	0.18
CMQ221C	Probable polyadenylation factor I subunit 2 Pfs2p	1.26	±	0.03
CMJ057C	60S ribosomal protein L19	1.26	±	0.01
CMH254C	Hypothetical protein	1.26	±	0.05
CME095C	Phosphoenolpyruvate carboxylase	1.26	±	0.11
CMN262C	Dynamin-related protein involved in chloroplast division CmDnm2/DRP5	1.26	±	0.16
CMK220C	Hypothetical protein	1.26	±	0.11
CMJ013C	Similar to CCR4-NOT transcription complex, subunit 2; NOT2	1.26	±	0.10
CMC106C	Hypothetical protein	1.26	±	0.17
CMT195C	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d	1.26	±	0.24
CMJ211C	NADH dehydrogenase I (Complex I) iron-sulfur protein 49kDa subunit	1.26	±	0.06
CMQ308C	Hypothetical protein	1.26	±	0.09
CML173C	Hypothetical protein	1.26	±	0.11
CMH025C	Hypothetical protein	1.26	±	0.05
CMR165C	Sigma subunit for chloroplast RNA polymerase	1.26	±	0.10
CMJ207C	Similar to calcium-binding protein MO25	1.26	±	0.03
CME186C	Long chain acyl-CoA synthetase	1.26	±	0.04
CMN202C	Hypothetical protein	1.26	±	0.15
CMI121C	Similar to leucine-rich repeats containing F-box protein	1.26	±	0.23
CMS191C	Similar to methyltransferase	1.25	±	0.23

CMP171C	Hypothetical protein	1.25	±	0.04
CMH017C	RNA polymerase I, II, III common subunit	1.25	±	0.25
CMN268C	Probable carotenoid cis-trans isomerase, CrtH	1.25	±	0.11
CMG009C	Similar to glucose inhibited division protein B (gidB)	1.25	±	0.08
CMR439C	Hypothetical protein	1.25	±	0.16
CMR153C	Similar to BEL1-related homeotic protein	1.25	±	0.16
CME034C	Similar to calmodulin	1.25	±	0.02
CMR036C	Myo-inositol 1-phosphate synthase	1.25	±	0.25
CMO159C	Unknown WD repeat protein	1.25	±	0.11
CME038C	Hypothetical protein	1.25	±	0.26
CMT391C	Hypothetical protein	1.25	±	0.08
CML177C	Hypothetical protein	1.25	±	0.19
CMI192C	14S cohesin SMC1 subunit; SMC protein	1.25	±	0.12
CMC015C	Similar to biotin carboxyl carrier protein of acetyl-CoA carboxylase	1.25	±	0.23
CMC046C	Hypothetical protein	1.25	±	0.04
CMM258C	Similar to longevity assurance protein LAG1	1.24	±	0.07
CMB073C	Similar to ribosome assembly protein RRB1	1.24	±	0.05
CMT023C	Similar to nucleolar-matrix protein with nucleic-acid binding properties, subunit 6	1.24	±	0.05
CMH045C	Hypothetical protein	1.24	±	0.13
CMO125C	Phosphomethylpyrimidine kinase (hmp-phosphate kinase) (hmp-P kinase)	1.24	±	0.13
CMT113C	Probable phosphoribosyl diphosphate synthetase; ribose-phosphate pyrophosphokinase	1.24	±	0.32
CMT103C	Probable glutathione-S-transferase	1.24	±	0.21
CMI067C	40S ribosomal protein S29	1.24	±	0.06
CMO160C	Similar to archease	1.24	±	0.19
CML040C	Uroporphyrinogen III synthase	1.24	±	0.08
CMS501C	Similar to mitochondrial carrier precursor	1.24	±	0.13
CMO321C	Hypothetical protein	1.24	±	0.04
CMR324C	Hypothetical protein	1.24	±	0.18
CMK105C	Hypothetical protein	1.24	±	0.11
CMT551C	Hypothetical protein	1.24	±	0.05
CMT588C	4-hydroxybenzoate octaprenyltransferase	1.24	±	0.06
CML222C	Hypothetical protein	1.24	±	0.16
CML129C	Similar to v-SNARE protein of ER-Golgi docking complex	1.24	±	0.13
CMM146C	Probable inosine triphosphatase	1.24	±	0.09
CMN203C	Cytochrome c reductase (Complex III) Rieske iron-sulfur subunit	1.24	±	0.15
CMM113C	Similar to inorganic phosphate transporter	1.24	±	0.11
CME171C	Similar to ring finger protein	1.24	±	0.21
CMI059C	40S ribosomal protein S23	1.24	±	0.16
CMS112C	Similar to origin recognition complex subunit 1	1.24	±	0.13
CMI032C	Hypothetical protein	1.24	±	0.17
CMO171C	Hypothetical protein	1.24	±	0.22
CMM208C	Hypothetical protein	1.24	±	0.18
CMQ118C	60S ribosomal protein L39	1.24	±	0.02

CME071C	Hypothetical protein	1.24	±	0.09
CMO250C	Phycocyanin-associated rod linker protein, fragment	1.24	±	0.07
CMR014C	Glucose-6-phosphate 1-dehydrogenase	1.24	±	0.12
CMI102C	Hypothetical protein	1.24	±	0.08
CMN218C	Similar to maf protein	1.24	±	0.09
CMQ199C	Diacyl-glycerol acyltransferase	1.24	±	0.03
CMM005C	Probable protein kinase CK2 regulatory subunit CK2B1	1.23	±	0.06
CMT270C	Hypothetical protein	1.23	±	0.16
CMJ014C	Mercuric reductase	1.23	±	0.11
CMN183C	Similar to histone H1	1.23	±	0.04
CMQ447C	Hypothetical protein	1.23	±	0.11
CMG080C	Hypothetical protein	1.23	±	0.26
CMM288C	Similar to magnesium transporter Mrs2p	1.23	±	0.03
CMQ009C	Hypothetical protein	1.23	±	0.07
CMG195C	Hypothetical protein	1.23	±	0.05
CMI111C	Probable phytochelatin synthase	1.23	±	0.16
CMM121C	Hypothetical protein	1.23	±	0.04
CMQ032C	Hypothetical protein	1.23	±	0.06
CMJ152C	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	1.23	±	0.17
CMS303C	Hypothetical protein	1.23	±	0.06
CMQ432C	NADH dehydrogenase type II	1.23	±	0.15
CMP183C	Probable 2-epi-valiolone synthase	1.23	±	0.07
CMT613C	DnaJ (Hsp40) homolog, subfamily A	1.23	±	0.18
CMB139C	Similar to signal peptidase	1.23	±	0.03
CMT252C	Phosphoserine aminotransferase	1.23	±	0.22
CME187C	Hypothetical protein	1.23	±	0.05
CMP052C	DNA mismatch repair (recognition) protein	1.23	±	0.20
CMG171C	Thiamin biosynthesis protein	1.23	±	0.09
CMQ412C	Similar to O-linked glcnac transferase, Mbb1 protein	1.23	±	0.11
CMK032C	Hypothetical protein	1.23	±	0.08
CMH156C	Hypothetical protein	1.23	±	0.15
CMB040C	Small GTP-binding protein of Sar1/Arf family	1.23	±	0.05
CMR011C	Probable choline kinase	1.23	±	0.06
CML313C	Similar to ATP-dependent RNA helicase	1.22	±	0.14
CMP328C	Poly-A RNA export protein DBP5	1.22	±	0.12
CMQ215C	Chromodomain helicase DNA binding protein CHD	1.22	±	0.31
CME163C	Hypothetical protein	1.22	±	0.20
CMP318C	Sphingolipid delta 4 desaturase protein DES-1	1.22	±	0.25
CMM082C	Alpha glucosidase 2, alpha neutral subunit	1.22	±	0.25
CML046C	Hypothetical protein	1.22	±	0.14
CMR287C	60S ribosomal protein L8	1.22	±	0.04
CMO303C	Similar to mitochondrial carrier protein	1.22	±	0.08
CMJ232C	Hypothetical protein	1.22	±	0.08

CML237C	Similar to ABI3-interacting protein 3	1.22	±	0.03
CMM269C	Farnesyl-diphosphate synthetase	1.22	±	0.16
CMT584C	Dihydroorotase	1.22	±	0.18
CMO289C	Hypothetical protein	1.22	±	0.06
CMJ077C	Hypothetical protein	1.22	±	0.08
CMG089C	Similar to respiratory burst oxidase protein	1.22	±	0.08
CMT598C	Similar to heterogeneous nuclear ribonucleoprotein	1.22	±	0.20
CMN012C	Mitochondrial ribosomal protein L35 precursor	1.22	±	0.14
CMQ260C	Unknown kinase with aarf domain	1.22	±	0.13
CMS013C	Hypothetical protein	1.22	±	0.17
CMQ117C	Eukaryotic translation initiation factor eIF-1A	1.22	±	0.24
CMT393C	Hypothetical protein	1.22	±	0.14
CMD067C	Probable prohibitin protein	1.22	±	0.23
CMM286C	3-oxoacyl-[acyl-carrier-protein] synthase I, precursor	1.22	±	0.19
CMM223C	Hypothetical protein	1.22	±	0.09
CMD187C	Hypothetical protein	1.22	±	0.07
CME068C	Hypothetical protein	1.22	±	0.04
CMO272C	Phosphoacetylglucosamine mutase	1.22	±	0.12
CMQ450C	Hypothetical protein	1.22	±	0.10
CMQ442C	Similar to glycosyl transferase	1.22	±	0.06
CMQ003C	Hypothetical protein	1.21	±	0.03
CMJ184C	Hypothetical protein	1.21	±	0.08
CMC130C	Hypothetical protein	1.21	±	0.16
CMP168C	Hypothetical protein	1.21	±	0.17
CMM271C	Ubiquitin-protein isopeptide ligase E3	1.21	±	0.06
CMI095C	NADH dehydrogenase I (Complex I) iron-sulfur protein 20kDa subunit (PSST)	1.21	±	0.15
CMQ258C	Similar to mitochondrial carrier protein	1.21	±	0.15
CMP128C	Casein kinase II, alpha subunit	1.21	±	0.15
CMJ153C	Hypothetical protein	1.21	±	0.16
CMT055C	Hypothetical protein	1.21	±	0.11
CMR047C	Hypothetical protein	1.21	±	0.05
CMD023C	Similar to ferripyochelin binding protein	1.21	±	0.13
CMC147C	Polypeptide chain releasing factor eRF3	1.21	±	0.07
CMS270C	Chaperonin containing TCP1, subunit 4 (delta)	1.21	±	0.29
CMJ061C	Hypothetical protein	1.21	±	0.04
CMS306C	Hypothetical protein	1.21	±	0.03
CMB003C	Similar to GTP-binding protein	1.21	±	0.03
CMD125C	Similar to heat shock protein DnaJ	1.21	±	0.10
CME148C	Chloroplast peptide chain release factor RF-2	1.21	±	0.46
CMS262C	60S ribosomal protein L23	1.21	±	0.02
CMG106C	Probable flap structure-specific endonuclease 1	1.21	±	0.03
CMO080C	NADH dehydrogenase I (Complex I) iron-sulfur protein 18kDa subunit	1.21	±	0.14
CMN265C	Hypothetical protein	1.21	±	0.10

CMP288C	Hypothetical protein	1.21	±	0.13
CMI166C	Hypothetical protein	1.21	±	0.11
CMT172C	Rubisco expression protein cfxQ (cbbX)	1.20	±	0.03
CMR495C	Hypothetical protein	1.20	±	0.06
CMT524C	Hypothetical protein	1.20	±	0.06
CMN247C	Coatomer protein complex, subunit zeta	1.20	±	0.07
CMS132C	Mitochondrial intermediate peptidase	1.20	±	0.01
CMJ169C	Probable heat shock protein hsIV, proteasome-related peptidase subunit	1.20	±	0.14
CMK172C	Probable steroid dehydrogenase SPM2	1.20	±	0.09
CMO318C	Similar to glutathione S-transferase family protein	1.20	±	0.02
CMC045C	60S ribosomal protein L40, ubiquitin fusion protein	1.20	±	0.04
CMI187C	Hypothetical protein	1.20	±	0.03
CMS273C	Hypothetical protein	1.20	±	0.04
CMT369C	Similar to O-demethylpuromycin-O-methyltransferase	1.20	±	0.17
CMQ201C	Similar to myo-inositol monophosphatase	1.20	±	0.07
CME056C	Hypothetical protein	1.20	±	0.18
CMN196C	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	1.20	±	0.19
CMS080C	60S ribosomal protein L22	1.20	±	0.26
CMP098C	Similar to A/G-specific adenine glycosylase	1.20	±	0.06
CMK053C	Hypothetical protein	1.20	±	0.07
CMQ334C	Hypothetical protein	1.20	±	0.09
CMQ048C	Hypothetical protein	1.20	±	0.02
CMR268C	Similar to heat shock protein Hsp33	1.20	±	0.07
CML230C	Hypothetical protein	1.20	±	0.21
CMQ360C	Hypothetical protein	1.20	±	0.06
CMT533C	Probable tyrosine aminotransferase	1.20	±	0.15
CMI160C	Hypothetical protein	1.20	±	0.06
CMB153C	Hypothetical protein	1.20	±	0.19
CMN287C	Hypothetical protein	1.20	±	0.14
CMB023C	Hypothetical protein	1.20	±	0.19
CMS353C	Hypothetical protein	1.20	±	0.06
CMI138C	Hypothetical protein	1.20	±	0.09
CMM285C	Hypothetical protein	1.20	±	0.09
CMK063C	Hypothetical protein, putative membrane transporter	1.19	±	0.18
CMR484C	Similar to 13S condensin XCAP-D2 subunit	1.19	±	0.12
CMT049C	Hypothetical protein	1.19	±	0.13
CMD103C	Hypothetical protein	1.19	±	0.06
CMR114C	Hypothetical protein	1.19	±	0.23
CML198C	Ribosomal large subunit pseudouridine synthase C	1.19	±	0.11
CML135C	Probable CCR4-NOT transcription complex, subunit 3	1.19	±	0.11
CMT271C	Similar to nascent-polypeptide-associated complex alpha polypeptide	1.19	±	0.18
CMS257C	Hypothetical protein	1.19	±	0.13
CMQ292C	Chloroplast ribosomal protein L15 precursor	1.19	±	0.16

CMO255C	Similar to nuclear polyadenylated RNA-binding protein NAB3	1.19	±	0.14
CMI283C	Receptor for activated protein kinase C	1.19	±	0.10
CMS067C	Hypothetical protein	1.19	±	0.11
CMK039C	Photoregulatory zinc-finger protein COP1	1.19	±	0.10
CMS406C	Probable proline synthetase associated protein	1.19	±	0.16
CMK176C	Photosystem II protein Psb27	1.19	±	0.20
CMC055C	Probable lathosterol oxidase	1.19	±	0.16
CMO240C	Hypothetical protein	1.19	±	0.06
CMS332C	V-type ATPase V0 subunit c	1.19	±	0.07
CMX002C	Hypothetical protein	1.19	±	0.08
CMJ174C	Hypothetical protein	1.19	±	0.10
CMN064C	Hypothetical protein	1.19	±	0.13
CMK056C	Hypothetical protein	1.19	±	0.04
CMT038C	Similar to retinoblastoma-family protein	1.19	±	0.13
CMJ180C	Hypothetical protein	1.19	±	0.11
CMI106C	Homogentisate 1,2-dioxygenase	1.19	±	0.17
CMJ066C	Phenylalanine hydroxylase	1.18	±	0.07
CMP005C	Hypothetical protein	1.18	±	0.05
CMS181C	Rubredoxin	1.18	±	0.04
CMR130C	Similar to 1-acylglycerol-3-phosphate O-acyltransferase	1.18	±	0.09
CMI244C	Plastid terminal oxidase	1.18	±	0.15
CMR371C	Similar to rRNA processing protein 7	1.18	±	0.05
CMG147C	Probable long-chain acyl-CoA synthetase	1.18	±	0.19
CMN087C	Hypothetical protein	1.18	±	0.04
CMP154C	Similar to cytochrome B5	1.18	±	0.13
CMH264C	DNA replication licensing factor MCM3	1.18	±	0.19
CMI125C	Phosphatidylinositol 4-kinase	1.18	±	0.12
CMK049C	Similar to biotin synthase	1.18	±	0.13
CMB012C	Similar to coiled-coil protein; putative spindle pole body associated protein	1.18	±	0.03
CMP329C	Putrescine aminopropyltransferase (spermidine synthase)	1.18	±	0.08
CMD116C	Hypothetical protein	1.18	±	0.07
CMJ289C	60S ribosomal protein L32	1.18	±	0.13
CMH260C	WD-repeat protein	1.18	±	0.03
CMG143C	Similar to anti-silencing factor	1.18	±	0.09
CMG097C	Hypothetical protein	1.18	±	0.24
CMK055C	Hypothetical protein	1.18	±	0.09
CMQ409C	Hypothetical protein	1.18	±	0.11
CMS143C	Hypothetical protein	1.18	±	0.07
CMJ235C	Mitochondrial ribosomal protein L1 precursor	1.18	±	0.04
CMN294C	Hypothetical protein	1.18	±	0.07
CMJ250C	Glyceraldehyde 3-phosphate dehydrogenase	1.18	±	0.10
CMS229C	Similar to quinone oxidoreductase	1.18	±	0.11
CMO117C	Hypothetical protein	1.18	±	0.05

CMP350C	Hypothetical protein	1.18	±	0.07
CMR201C	Probable mitochondrial ribosomal protein S21	1.18	±	0.12
CMR457C	Histone H2A.Z variant	1.18	±	0.13
CMK062C	Hypothetical protein	1.18	±	0.03
CMO207C	GIN4-like protein kinase	1.18	±	0.03
CMS356C	Hypothetical protein	1.18	±	0.10
CMT313C	Cysteine synthase A (O-acetylserine sulfhydrylase A) (O-acetylserine (thiol)-lyase A) (csase A) (sulfate starvation-induced protein 5) (SSI5)	1.17	±	0.11
CMN159C	Unknown kinase with aarf domain	1.17	±	0.05
CMR131C	Hypothetical protein	1.17	±	0.07
CMJ186C	26S proteasome ATP-dependent regulatory subunit	1.17	±	0.04
CMD152C	Probable ubiquitin-conjugating enzyme E2	1.17	±	0.14
CMO177C	Hypothetical protein	1.17	±	0.09
CMN290C	Oxygen-evolving complex 23K protein	1.17	±	0.19
CMT606C	Hypothetical protein	1.17	±	0.07
CMT305C	Argininosuccinate synthase	1.17	±	0.03
CMT616C	Hypothetical protein	1.17	±	0.16
CMS357C	Hypothetical protein	1.17	±	0.09
CMR028C	Probable replication factor C large subunit	1.17	±	0.02
CMT085C	UDP-N-acetylglucosamine pyrophosphorylase (N-acetylglucosamine-1-phosphate uridyltransferase)	1.17	±	0.10
CMC083C	Glutamate--tRNA ligase, cytoplasmic	1.17	±	0.19
CMQ424C	Nuclear poly(A) polymerase	1.17	±	0.12
CMR424C	Hypothetical protein	1.17	±	0.04
CMM052C	Transcription factor APFI	1.17	±	0.05
CMF018C	Probable nicotinamide mononucleotide adenylyl transferase	1.17	±	0.08
CMS269C	Hypothetical protein	1.17	±	0.07
CMM324C	Hypothetical protein	1.17	±	0.04
CMA017C	Similar to 1-acyl-sn-glycerol-3-phosphate acyltransferase	1.17	±	0.10
CMO025C	Hypothetical protein	1.17	±	0.20
CME175C	60S ribosomal protein L37	1.17	±	0.02
CMQ434C	Hypothetical protein	1.17	±	0.13
CMK175C	Hypothetical protein	1.17	±	0.04
CMP214C	Thiamine-phosphate pyrophosphorylase	1.17	±	0.08
CMG015C	Hypothetical protein	1.17	±	0.04
CMQ363C	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a	1.17	±	0.10
CMS061C	Probable peptide methionine sulfoxide reductase	1.17	±	0.12
CML250C	Hypothetical protein	1.17	±	0.10
CMH038C	Hypothetical protein	1.17	±	0.11
CMH263C	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	1.17	±	0.07
CMT540C	Hypothetical protein	1.17	±	0.09
CMT515C	Chromatin assembly factor 1 55 kDa subunit	1.17	±	0.22
CMG070C	Hypothetical protein	1.17	±	0.08
CMN062C	Hypothetical protein	1.17	±	0.06
CMH246C	Probable DNA repair protein SPR18	1.17	±	0.23

CME150C	Hypothetical protein	1.16	±	0.17
CMM175C	Similar to divalent cation tolerance protein	1.16	±	0.13
CMT045C	Probable ATP-dependent Clp protease regulatory subunit CLPX	1.16	±	0.18
CMH150C	Hypothetical protein	1.16	±	0.06
CMS483C	Similar to DNA mismatch repair protein	1.16	±	0.16
CMP256C	Hypothetical protein	1.16	±	0.06
CMH023C	Hypothetical protein	1.16	±	0.04
CMQ373C	Hypothetical protein	1.16	±	0.05
CMN269C	Hypothetical protein	1.16	±	0.04
CMM292C	DegP protease	1.16	±	0.34
CMI209C	TATA-box binding protein-associated factor 5	1.16	±	0.05
CMS115C	Hypothetical protein	1.16	±	0.11
CMJ245C	Hypothetical protein	1.16	±	0.03
CMS113C	Unknown cyanobacterial protein	1.16	±	0.07
CMB050C	Hypothetical protein	1.16	±	0.09
CMS231C	Similar to carotenoid biosynthesis protein, crtk gene product	1.16	±	0.08
CME044C	Unknown WD repeat protein	1.16	±	0.13
CMP006C	60S ribosomal protein L13	1.16	±	0.16
CMF086C	Probable myo-inositol dehydrogenase	1.16	±	0.07
CMS251C	Hypothetical protein	1.16	±	0.08
CMO063C	Similar to yeast chromosome segregation protein MLO2	1.16	±	0.06
CMQ192C	Hypothetical protein	1.16	±	0.04
CMT135C	Hypothetical protein	1.16	±	0.08
CMS133C	Hypothetical protein	1.16	±	0.12
CMK306C	Hypothetical protein	1.16	±	0.12
CMI293C	Alpha,alpha-trehalose-phosphate synthase (UDP-forming)	1.16	±	0.08
CMG065C	Hypothetical protein	1.16	±	0.07
CMN066C	Hypothetical protein	1.15	±	0.06
CMH198C	Box H/ACA snoRNP component Nop10p	1.15	±	0.10
CMS455C	Hypothetical protein	1.15	±	0.11
CMT196C	Small GTP-binding protein Sar1	1.15	±	0.14
CMM156C	Hypothetical protein	1.15	±	0.16
CMN185C	Hypothetical protein	1.15	±	0.10
CMO126C	Dutp pyrophosphatase	1.15	±	0.17
CMR054C	Similar to phosphatidic acid phosphatase type 2B	1.15	±	0.02
CMI094C	Methionine--tRNA ligase, cytoplasmic	1.15	±	0.12
CMB088C	Probable nucleotide binding protein Maf	1.15	±	0.04
CMF058C	Probable zinc transporter	1.15	±	0.10
CMT010C	Retroelement, alive	1.15	±	0.13
CMI181C	Similar to magnesium transporter Mrs2p	1.15	±	0.08
CMK248C	Similar to phosphate/phosphoenolpyruvate translocator protein	1.15	±	0.07
CMQ246C	Hypothetical protein	1.15	±	0.08
CMR162C	Similar to mitochondrial carrier protein	1.15	±	0.07

CMG028C	Hypothetical protein	1.15	±	0.24
CML307C	Probable replication factor C protein	1.15	±	0.08
CMJ109C	60S ribosomal protein L10	1.15	±	0.03
CMS278C	Hypothetical protein	1.15	±	0.16
CMJ160C	Hypothetical protein	1.15	±	0.08
CMK247C	Similar to 11-beta-hydroxysteroid dehydrogenase	1.15	±	0.09
CMP152C	Cytochrome c reductase (Complex III) cytochrome c1 subunit	1.15	±	0.11
CMC104C	Hypothetical protein	1.15	±	0.06
CMH227C	Probable ubiquitin conjugating enzyme E2	1.15	±	0.17
CMI194C	Similar to rubredoxin	1.15	±	0.31
CMS058C	Similar to origin recognition complex subunit 2	1.15	±	0.10
CMT330C	Mitochondrial ribosomal protein S2, mitochondrial precursor	1.15	±	0.11
CMT511C	Hypothetical protein	1.15	±	0.04
CMO211C	Hypothetical protein	1.15	±	0.07
CMQ470C	Similar to thioredoxin peroxidase Dot5p	1.15	±	0.23
CMK155C	Hypothetical protein	1.15	±	0.06
CMJ157C	Hypothetical protein	1.15	±	0.03
CMT043C	GTP-binding protein of Nug1 family	1.15	±	0.10
CMA069C	SOUL family heme-binding protein	1.15	±	0.11
CMR010C	Probable ubiquitin conjugating enzyme E2	1.14	±	0.06
CMS428C	Eukaryotic translation elongation factor 2 (eEF-2)	1.14	±	0.22
CMQ144C	Hypothetical protein	1.14	±	0.16
CML196C	60S ribosomal protein L11	1.14	±	0.06
CME057C	Hypothetical protein	1.14	±	0.11
CMQ329C	Hypothetical protein	1.14	±	0.10
CMS145C	Similar to shuttle craft like transcriptional regulator NFX1	1.14	±	0.11
CMJ151C	Similar to thylakoid lumenal 17.4 kDa protein, chloroplast precursor	1.14	±	0.12
CMO196C	Probable microtubule organization 1 protein	1.14	±	0.12
CMD007C	V-type ATPase V1 subunit D	1.14	±	0.06
CMM126C	Similar to elongation of very long chain fatty acids Elo3p (Sur4p)	1.14	±	0.18
CMJ229C	Riboflavin kinase	1.14	±	0.08
CMN224C	Hypothetical protein	1.14	±	0.03
CMQ382C	Similar to U3 snoRNP component Utp15p	1.14	±	0.19
CMJ060C	Hypothetical protein	1.14	±	0.05
CME079C	Serine/threonine protein phosphatase PP1 catalytic subunit	1.14	±	0.14
CMT358C	Similar to N-terminal acetyltransferase complex ARD1 subunit	1.14	±	0.20
CMS223C	NADH dehydrogenase I (Complex I) iron-sulfur protein 23kDa subunit (TYKY)	1.14	±	0.02
CMJ197C	Similar to smooth muscle caldesmon	1.14	±	0.05
CMR413C	Hypothetical protein	1.14	±	0.15
CMJ096C	Similar to thioredoxin h	1.14	±	0.05
CMC127C	Probable tRNA methyltransferase Trm7	1.14	±	0.03
CMH069C	Conserved GTP binding protein of unknown function	1.14	±	0.16
CMK047C	Hypothetical protein	1.14	±	0.11

CML260C	Similar to ATPase with chaperone activity	1.14	±	0.11
CML138C	Similar to farnesyltransferase alpha subunit	1.14	±	0.11
CMS204C	Hypothetical protein	1.14	±	0.06
CMQ427C	Carnitine carrier; Crc1p	1.14	±	0.21
CME052C	Hypothetical protein	1.14	±	0.07
CMR161C	WD-repeat protein	1.14	±	0.06
CMT574C	Hypothetical protein	1.14	±	0.02
CMD094C	Hypothetical protein	1.14	±	0.03
CMJ228C	Similar to mitochondrial carrier protein	1.14	±	0.05
CMR050C	Similar to chitobiosyldiphosphodolichol beta-mannosyltransferase	1.14	±	0.07
CMS190C	Similar to sugar fermentation stimulation protein, Sfs1	1.14	±	0.03
CMN138C	Probable AAA protein spastin	1.14	±	0.12
CMO124C	Glucose-6-phosphate isomerase	1.14	±	0.11
CMH006C	Unknown protein involving with Iron-Sulfur proteins SufD	1.14	±	0.27
CMQ149C	RNA helicase	1.14	±	0.09
CMT262C	U6 snRNA-associated Sm-like protein LSm3	1.14	±	0.08
CMJ195C	Similar to outward rectifying potassium channel KCO	1.13	±	0.10
CMJ062C	Similar to acetyltransferase, GNAT family	1.13	±	0.13
CMS328C	Unknown protein of cyanobacteria	1.13	±	0.04
CMM142C	Hypothetical protein	1.13	±	0.13
CMT565C	DNA recombination protein DMC1	1.13	±	0.06
CMO077C	Hypothetical protein	1.13	±	0.15
CMK076C	Hypothetical protein	1.13	±	0.08
CMS165C	Hypothetical protein	1.13	±	0.06
CMM300C	Hypothetical protein	1.13	±	0.08
CMT046C	Similar to a negative regulator of cell cycle, cullin 1	1.13	±	0.08
CMC039C	Probable 1-cys peroxiredoxin	1.13	±	0.06
CMR421C	Probable 4-nitrophenyl phosphatase	1.13	±	0.10
CMB114C	Hypothetical protein	1.13	±	0.17
CMG203C	Similar to protein phosphatase 2C	1.13	±	0.21
CMG162C	Similar to ferredoxin component (biphenyl dioxygenase, Rieske iron-sulfur component related protein)	1.13	±	0.09
CMP244C	Hypothetical protein	1.13	±	0.03
CMI245C	Hypothetical protein	1.13	±	0.10
CMQ445C	60S acidic ribosomal protein P0	1.13	±	0.10
CMK089C	Hypothetical protein	1.13	±	0.12
CML184C	Hypothetical protein	1.13	±	0.04
CMH173C	Similar to mitochondrial uncoupling protein	1.13	±	0.03
CMR055C	Similar to cationic amino acid transporter	1.13	±	0.04
CMT014C	Hypothetical protein	1.13	±	0.06
CMJ221C	Hypothetical protein	1.13	±	0.06
CMP201C	Similar to transcriptional regulator	1.13	±	0.02
CMM211C	Hypothetical protein	1.13	±	0.07
CMS446C	Thimet oligopeptidase	1.13	±	0.07

CMK292C	Hypothetical protein	1.13	±	0.09
CMP303C	Similar to cell division control protein cdc45	1.13	±	0.08
CML042C	Ubiquitin-like protein Rub1	1.13	±	0.06
CMS407C	Hypothetical protein	1.13	±	0.09
CMR193C	Similar to ribosomal protein S6 kinase	1.13	±	0.03
CMQ010C	Probable V-type ATPase V1 subunit E	1.13	±	0.11
CMQ240C	Similar to DnaJ (Hsp40) homolog	1.13	±	0.13
CMN160C	Hypothetical protein	1.13	±	0.13
CMS411C	Hypothetical protein	1.13	±	0.05
CMT388C	Unknown phosphatase CbbY	1.13	±	0.06
CMO098C	Threonine--tRNA ligase, chloroplast or mitochondrial	1.13	±	0.15
CMM240C	40S ribosomal protein S25	1.13	±	0.15
CML193C	Hypothetical protein	1.13	±	0.17
CMM259C	Hypothetical protein	1.13	±	0.05
CME094C	Hypothetical protein	1.13	±	0.03
CMS022C	Hypothetical protein	1.13	±	0.12
CMH008C	Branched-chain alpha-keto acid dehydrogenase E1-alpha subunit	1.13	±	0.07
CMQ197C	Similar to mitochondrial division protein Fis1p	1.12	±	0.02
CMD100C	Similar to ATP-dependent proteinase BsgA	1.12	±	0.09
CMP229C	Probable alpha-soluble NSF attachment protein	1.12	±	0.03
CMR339C	Threonine synthase	1.12	±	0.26
CMG184C	Similar to U3 snoRNP component Utp6p	1.12	±	0.11
CMH209C	Heme oxygenase	1.12	±	0.05
CMC057C	Hypothetical protein	1.12	±	0.14
CMC078C	Hypothetical protein	1.12	±	0.07
CMM281C	Hypothetical protein	1.12	±	0.06
CMT109C	Similar to cyclin M2	1.12	±	0.08
CMI042C	Tyrosine--tRNA ligase	1.12	±	0.11
CMS502C	Mitochondrial translation elongation factor Tu (EF-Tu)	1.12	±	0.16
CMB122C	Hypothetical protein	1.12	±	0.10
CMB105C	Hypothetical protein	1.12	±	0.01
CML285C	Hypothetical protein	1.12	±	0.04
CMI145C	Hypothetical protein	1.12	±	0.04
CMJ205C	Probable iron-sulfur cluster scaffold protein	1.12	±	0.07
CML186C	Hypothetical protein	1.12	±	0.10
CMT268C	Hypothetical protein	1.12	±	0.13
CMR150C	60S ribosomal protein L21	1.12	±	0.12
CMO201C	Hypothetical protein	1.12	±	0.03
CMT272C	Eukaryotic translation initiation factor eIF-2B beta subunit	1.12	±	0.05
CMB052C	DNA polymerase delta small subunit	1.12	±	0.09
CMN226C	Similar to N6-adenine-specific methylase	1.12	±	0.04
CMR269C	Eukaryotic translation initiation factor eIF-2B alpha subunit	1.12	±	0.10
CMG114C	Hypothetical protein	1.12	±	0.05

CMO099C	Similar to apoptosis-inducing factor AIF	1.12	±	0.08
CMT084C	Hypothetical protein	1.12	±	0.13
CMC027C	Dihydroorotate oxidase	1.12	±	0.17
CMN054C	Similar to cell cycle checkpoint and DNA repair exonuclease RAD1	1.12	±	0.06
CMR478C	Similar to transcription factor IIA small subunit	1.12	±	0.08
CMH220C	Retromer component VPS35	1.12	±	0.06
CMT466C	Similar to transmembrane calcium/manganese transporter Ccc1p	1.12	±	0.01
CMF168C	Similar to autoantigen	1.12	±	0.06
CMH273C	Similar to nuclear import protein NPL4	1.12	±	0.03
CMR270C	Similar to actin-related protein Arp4	1.12	±	0.04
CMS135C	Hypothetical protein	1.12	±	0.02
CMO096C	Hypothetical protein	1.12	±	0.25
CMP355C	Similar to J-type co-chaperone HSC20	1.11	±	0.12
CMR112C	Hypothetical protein	1.11	±	0.05
CMQ358C	Similar to candidate tumor suppressor	1.11	±	0.02
CMT118C	Similar to bacterial peptide chain release factor	1.11	±	0.03
CMQ318C	Hypothetical protein	1.11	±	0.05
CMC085C	Hypothetical protein	1.11	±	0.02
CMI202C	40S ribosomal protein S15A	1.11	±	0.05
CMJ281C	Hypothetical protein	1.11	±	0.07
CMK128C	Hypothetical protein	1.11	±	0.12
CMT634C	Similar to rRNA methylase SpoU	1.11	±	0.03
CMI108C	Hypothetical protein	1.11	±	0.01
CME074C	Hypothetical protein	1.11	±	0.05
CMR452C	Hypothetical protein	1.11	±	0.02
CMH231C	Hypothetical protein	1.11	±	0.09
CMP004C	Hypothetical protein	1.11	±	0.07
CMC151C	Probable V-type ATPase V1 subunit C	1.11	±	0.06
CMG007C	Phosphatidylinositol transfer protein	1.11	±	0.10
CMN201C	GTP-binding protein of Era family	1.11	±	0.06
CMP180C	Hypothetical protein	1.11	±	0.14
CMS008C	Similar to 1-acyl-sn-glycerol-3-phosphate acyltransferase	1.11	±	0.03
CMC013C	Probable 26S proteasome, non-ATPase regulatory subunit	1.11	±	0.07
CMR136C	Hypothetical protein	1.11	±	0.03
CMK232C	Argininosuccinate lyase	1.11	±	0.10
CMI215C	Probable GDP dissociation inhibitor	1.11	±	0.09
CMO288C	Hypothetical protein	1.11	±	0.10
CMK072C	Hypothetical protein	1.11	±	0.22
CMP209C	Hypothetical protein	1.11	±	0.03
CMR375C	Hypothetical protein	1.11	±	0.04
CMG030C	Similar to beta-tubulin folding cofactor E	1.11	±	0.07
CMO308C	Probable homocysteine S-methyltransferase	1.11	±	0.05
CMT121C	Similar to sphingosine kinase	1.11	±	0.08

CMS364C	Hypothetical protein	1.11	±	0.02
CMK273C	60S ribosomal protein L23A	1.11	±	0.18
CMM192C	Hypothetical protein	1.11	±	0.17
CMP041C	Hypothetical protein	1.11	±	0.06
CMC162C	Hypothetical protein	1.11	±	0.17
CMQ320C	Hypothetical protein	1.11	±	0.13
CMO344C	Similar to acetohydroxy acid synthase, large subunit	1.11	±	0.18
CMF043C	Probable glutathione synthetase	1.11	±	0.03
CMG093C	Proteasome regulatory particle subunit	1.10	±	0.12
CML320C	Similar to stromal cell derived factor 2 SDF2	1.10	±	0.14
CMS444C	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	1.10	±	0.02
CMO309C	Hypothetical protein	1.10	±	0.18
CMH071C	60S ribosomal protein L5	1.10	±	0.17
CMT453C	Similar to nucleolar RNA-associated protein NRAP	1.10	±	0.06
CMA035C	Probable mRNA guanylyltransferase	1.10	±	0.10
CMM114C	Calcium-transporting ATPase	1.10	±	0.13
CMR231C	Hypothetical protein	1.10	±	0.05
CMS253C	Similar to cytidine/deoxycytidylate deaminase family protein	1.10	±	0.14
CMK305C	Similar to DnaJ (Hsp40) homolog, subfamily B	1.10	±	0.09
CML289C	Hypothetical protein	1.10	±	0.11
CML148C	Hypothetical protein	1.10	±	0.08
CMH027C	Similar to transcriptional activator FHA1	1.10	±	0.12
CMS122C	Probable farnesyl-protein transferase beta-subunit	1.10	±	0.08
CMT059C	Hypothetical protein	1.10	±	0.04
CMT092C	Hypothetical protein	1.10	±	0.06
CMP018C	Probable coclaurine N-methyltransferase	1.10	±	0.04
CMK207C	Hypothetical protein	1.10	±	0.09
CMH202C	Probable isoprenylcysteine methyltransferase	1.10	±	0.24
CMS319C	Cytochrome P450 involved in sterol biosynthesis	1.10	±	0.08
CMT537C	Hypothetical protein	1.10	±	0.20
CMT611C	Malate dehydrogenase, cytoplasmic	1.10	±	0.05
CMO296C	Hypothetical protein	1.10	±	0.04
CMR280C	Hypothetical protein	1.10	±	0.07
CMT356C	Dynein light chain	1.10	±	0.04
CMD141C	Hypothetical protein	1.10	±	0.05
CML029C	Mitochondrial F-type ATPase F1 subunit gamma, precursor	1.10	±	0.14
CMK067C	Aquaporin 5	1.10	±	0.04
CML160C	Hypothetical protein	1.10	±	0.02
CMA138C	Cell cycle switch protein	1.10	±	0.04
CMP157C	Similar to triacylglycerol lipase	1.10	±	0.06
CMM023C	Hypothetical protein	1.10	±	0.09
CMT477C	20S core proteasome subunit beta 6	1.10	±	0.03
CMM016C	Hypothetical protein	1.10	±	0.05

CMA122C	40S ribosomal protein S7	1.10	±	0.02
CMF103C	Clathrin heavy chain	1.10	±	0.19
CMM236C	Hypothetical protein	1.10	±	0.08
CMO110C	Hypothetical protein	1.10	±	0.05
CMN078C	Hypothetical protein	1.10	±	0.06
CMR349C	Actin interacting protein	1.10	±	0.14
CMN245C	Similar to mutator MutT protein	1.10	±	0.05
CMR178C	Cytochrome c reductase (Complex III) ubiquinone-binding protein	1.10	±	0.09
CMG178C	Squalene synthase	1.10	±	0.06
CMO311C	Similar to mitochondrial presequence translocase subunit Tim23	1.10	±	0.08
CMO020C	Hypothetical protein	1.09	±	0.08
CMR335C	Hypothetical protein	1.09	±	0.14
CMR291C	ATP-binding cassette, sub-family G (WBC), member 2	1.09	±	0.02
CMR405C	Similar to retromer component VPS29	1.09	±	0.02
CMI159C	Hypothetical protein	1.09	±	0.05
CMX010C	Hypothetical protein	1.09	±	0.08
CMN248C	Hypothetical protein	1.09	±	0.03
CMF136C	Similar to UDP-N-acetylglucosamine pyrophosphorylase	1.09	±	0.06
CMJ086C	Probable gamma hydroxybutyrate dehydrogenase	1.09	±	0.07
CMM169C	Hypothetical protein	1.09	±	0.04
CMD161C	Hypothetical protein	1.09	±	0.05
CMN284C	Probable cinnamyl-alcohol dehydrogenase	1.09	±	0.10
CME060C	Similar to ER-derived vesicles protein Erv14	1.09	±	0.06
CMR039C	Similar to cell surface protein that may regulate cell wall beta-glucan synthesis and bud site selection; Hanenula mrakii killer toxin-resistance protein; Hkr1p	1.09	±	0.07
CMN134C	Hypothetical protein	1.09	±	0.03
CMP069C	MYB-related protein	1.09	±	0.08
CMB143C	Probable molybdenum cofactor biosynthesis protein Cnx1	1.09	±	0.15
CMM328C	Similar to acid phosphatase 2, lysosomal	1.09	±	0.08
CMM090C	Hypothetical protein	1.09	±	0.06
CMH183C	Small GTP-binding protein of Rho family	1.09	±	0.10
CMO242C	Translational inhibitor protein p14.5	1.09	±	0.08
CMD028C	Hypothetical protein	1.09	±	0.13
CMT550C	Unknown homeobox protein	1.09	±	0.03
CMH189C	Hypothetical protein	1.09	±	0.14
CMQ204C	Ste20/SPS1-like serine/threonine kinase	1.09	±	0.08
CMB016C	Hypothetical protein	1.09	±	0.04
CMP191C	Similar to high light inducible protein	1.09	±	0.04
CMA087C	Hypothetical protein	1.09	±	0.02
CMS047C	Mitochondrial ribosomal protein L21 precursor	1.09	±	0.07
CMK038C	Hypothetical protein	1.09	±	0.06
CMR366C	Hypothetical protein	1.09	±	0.05
CMN192C	MutS family DNA mismatch repair protein MSH5	1.09	±	0.03
CME076C	Hypothetical protein	1.09	±	0.01

CML188C	Hypothetical protein	1.09	±	0.09
CMD131C	Hypothetical protein	1.09	±	0.07
CMM228C	Unknown hydrolase	1.09	±	0.02
CMP115C	Similar to Ap-4-A phosphorylase II	1.09	±	0.02
CMN324C	Conserved GTP-binding protein of unknown function (Developmentally regulated GTP-binding protein 1)	1.09	±	0.05
CMB069C	Hypothetical protein	1.09	±	0.04
CMP167C	Hypothetical protein	1.09	±	0.18
CMP074C	Hypothetical protein	1.09	±	0.05
CML336C	Similar to RNA helicase (RH16)	1.09	±	0.05
CMJ019C	Hypothetical protein	1.09	±	0.15
CMT275C	Valine--tRNA ligase	1.09	±	0.12
CMT317C	Hypothetical protein	1.08	±	0.23
CMR053C	DNA repair protein RAD51	1.08	±	0.04
CMD090C	Hypothetical protein	1.08	±	0.07
CMT476C	Probable phosphate transporter Pht2	1.08	±	0.09
CMQ101C	Gamma-glutamyltransferase	1.08	±	0.07
CMI199C	Similar to ribosomal protein S1	1.08	±	0.11
CMJ165C	Hypothetical protein	1.08	±	0.01
CMJ168C	Hypothetical protein	1.08	±	0.05
CMG095C	Similar to 6-pyruvoyl tetrahydrobiopterin synthase	1.08	±	0.09
CMF063C	Hypothetical protein	1.08	±	0.06
CMK240C	Hypothetical protein	1.08	±	0.07
CMN171C	Hypothetical protein	1.08	±	0.03
CMQ438C	Hypothetical protein	1.08	±	0.06
CMQ058C	Hypothetical protein	1.08	±	0.04
CMK054C	Nucleotide excision repair protein yeast rad23/human HHR23A homolog	1.08	±	0.09
CMN057C	Hypothetical protein	1.08	±	0.03
CMR491C	Hypothetical protein	1.08	±	0.03
CMF125C	Probable RNA helicase RH2	1.08	±	0.06
CMT174C	Similar to kynurenine 3-hydroxylase	1.08	±	0.05
CMQ174C	Hypothetical protein	1.08	±	0.22
CMN043C	Hypothetical protein	1.08	±	0.09
CMH119C	20S core proteasome subunit beta 4	1.08	±	0.13
CMP239C	14-3-3 protein	1.08	±	0.10
CMA133C	Similar to syntaxin 6	1.08	±	0.07
CMR176C	Unknown homeobox protein	1.08	±	0.05
CMD137C	Hypothetical protein	1.08	±	0.03
CMS370C	Similar to rRNA methylase	1.08	±	0.07
CMR468C	Hypothetical protein	1.08	±	0.05
CMR190C	Probable ER lumen protein retaining receptor	1.08	±	0.06
CMP352C	4-alpha-glucanotransferase	1.08	±	0.10
CML226C	Hypothetical protein	1.08	±	0.11
CMX011C	Chloroplast ribosomal protein L10	1.08	±	0.07

CMK178C	Mitochondrial F-type ATPase F0 subunit d	1.08	±	0.02
CMO007C	Hypothetical protein	1.08	±	0.08
CMH187C	Similar to shaggy-related protein kinase	1.08	±	0.14
CML294C	Hypothetical protein	1.08	±	0.02
CMQ167C	Sulfate binding protein of chloroplast sulfate ABC transporter (SbpA)	1.08	±	0.21
CMN211C	Hypothetical protein	1.08	±	0.02
CMI022C	Hypothetical protein	1.08	±	0.06
CMP251C	Similar to Ras-related GTP-binding protein ragA	1.08	±	0.03
CMO001C	Hypothetical protein	1.08	±	0.08
CMP234C	Imidazoleglycerol-phosphate dehydratase (IGPD)	1.08	±	0.02
CMM294C	Probable ferredoxin--NADP reductase	1.08	±	0.04
CMD036C	Similar to Membrane transporters of cations and cationic drugs	1.08	±	0.07
CMR251C	Hypothetical protein	1.08	±	0.16
CMR282C	Glycine dehydrogenase (decarboxylating), mitochondrial precursor	1.08	±	0.07
CMK101C	Hypothetical protein	1.08	±	0.14
CMT367C	Ankyrin-repeat protein	1.08	±	0.08
CMQ151C	Hypothetical protein	1.08	±	0.05
CML131C	ATPases of the AAA+ class	1.08	±	0.05
CMI114C	AMP deaminase	1.08	±	0.16
CMD071C	Unknown ribonuclease	1.08	±	0.12
CMS005C	Similar to human p47 protein	1.08	±	0.08
CMF121C	Alpha-xylosidase	1.08	±	0.12
CMI119C	Similar to DNA repair protein rad16	1.08	±	0.03
CMH042C	Hypothetical protein	1.08	±	0.04
CMO013C	Probable nicotinate-nucleotide pyrophosphorylase (carboxylating)	1.08	±	0.05
CMP247C	Methionyl aminopeptidase	1.08	±	0.04
CML050C	Ribonucleoside-diphosphate reductase beta chain	1.07	±	0.03
CMR065C	Hypothetical protein	1.07	±	0.05
CMG088C	Hypothetical protein	1.07	±	0.04
CMS123C	Hypothetical protein	1.07	±	0.11
CMN162C	Similar to oxidoreductase	1.07	±	0.16
CMT134C	MYB-related protein	1.07	±	0.07
CMS213C	Hypothetical protein	1.07	±	0.07
CMO145C	Probable replication factor C subunit 3	1.07	±	0.03
CMO085C	Hypothetical protein	1.07	±	0.09
CMM321C	RNA polymerase III subunit	1.07	±	0.10
CML069C	Hypothetical protein	1.07	±	0.09
CMO087C	Hypothetical protein	1.07	±	0.09
CMQ394C	Probable platelet activating factor acetylhydrolase	1.07	±	0.10
CMH258C	Hypothetical protein	1.07	±	0.14
CMT076C	Hypothetical protein	1.07	±	0.12
CML245C	Hypothetical protein	1.07	±	0.17
CMM249C	Phosphoribosylpyrophosphate synthetase or ribose-phosphate pyrophosphokinase	1.07	±	0.09

CMQ156C	Similar to Polycomb-group developmental gene, enhancer of zeste	1.07	±	0.03
CMG033C	Mitochondrial intermembrane space complex subunit Tim10	1.07	±	0.05
CMH001C	Similar to hedgehog protein	1.07	±	0.04
CMT546C	Hypothetical protein	1.07	±	0.15
CMT126C	Hypothetical protein	1.07	±	0.01
CMP170C	Similar to formamidopyrimidine-DNA glycosylase	1.07	±	0.04
CML146C	Branched-chain alpha-keto acid dihydrolipoyl acyltransferase, E2 subunit	1.07	±	0.07
CMT239C	Similar to palmitoyl-protein thioesterase precursor	1.07	±	0.06
CMN178C	Serine--tRNA ligase, cytoplasmic	1.07	±	0.12
CML167C	GMP synthase (glutamine-hydrolysing)	1.07	±	0.06
CML317C	60S ribosomal protein L7A	1.07	±	0.09
CMH251C	Similar to tRNA-pseudouridine synthase I	1.07	±	0.07
CMI027C	Probable AAA ATPase associated with peroxisome biosynthesis PEX1	1.07	±	0.03
CMN258C	Dihydrodipicolinate reductase	1.07	±	0.03
CMH208C	Hypothetical protein	1.07	±	0.21
CMC005C	Similar to trefoil factor	1.07	±	0.04
CMS052C	Ethanolamine-phosphate cytidylyltransferase (CTP:phosphoethanolamine cytidylyltransferase)	1.07	±	0.17
CMT627C	40S ribosomal protein S5	1.07	±	0.10
CMH245C	Similar to DNA excision repair protein HAYWIRE (ERCC-3 homolog protein)	1.07	±	0.05
CMR217C	Hypothetical protein	1.07	±	0.07
CMQ172C	Triose-phosphate isomerase	1.07	±	0.09
CMP190C	Myo-inositol 1-phosphate synthase	1.07	±	0.02
CMP204C	Similar to bestrophin	1.07	±	0.09
CMS346C	Small GTP-binding protein of Rab family	1.07	±	0.06
CMC123C	Probable replication protein A (RPA)	1.07	±	0.22
CMH090C	Cysteine--tRNA ligase, cytoplasmic	1.07	±	0.14
CMR196C	Hypothetical protein	1.07	±	0.20
CMI043C	Hypothetical protein	1.06	±	0.05
CMK229C	Hypothetical protein	1.06	±	0.02
CMO170C	Hypothetical protein	1.06	±	0.14
CMQ309C	Similar to glucosyltransferase	1.06	±	0.05
CMT473C	Hypothetical protein	1.06	±	0.09
CMS263C	Similar to ketohexokinase (fructokinase)	1.06	±	0.11
CMH012C	Hypothetical protein	1.06	±	0.04
CMS309C	Similar to microsomal glutathione S-transferase	1.06	±	0.08
CMN246C	Hypothetical protein	1.06	±	0.02
CMJ309C	Hypothetical protein	1.06	±	0.15
CMM007C	Hypothetical protein	1.06	±	0.12
CMH232C	Probable adenylate kinase	1.06	±	0.13
CMI031C	Similar to VAMP-associated protein	1.06	±	0.09
CMG118C	60S acidic ribosomal protein P2	1.06	±	0.12
CMA127C	Cyclin-dependent kinase regulatory subunit	1.06	±	0.09
CMT182C	Hypothetical protein	1.06	±	0.09

CMK112C	Hypothetical protein	1.06	±	0.09
CMQ100C	Similar to DNA repair and recombination protein (Rad51-like) Trad	1.06	±	0.10
CMM026C	Polyphosphate kinase	1.06	±	0.04
CMG025C	Unknown RNA binding protein	1.06	±	0.08
CMS136C	Probable N2,N2-dimethylguanosine tRNA methyltransferase	1.06	±	0.14
CMM335C	Similar to CCR4-NOT transcription complex, subunit 4	1.06	±	0.02
CMK016C	Probable adenosine kinase	1.06	±	0.11
CME017C	Unknown dehydrogenase	1.06	±	0.12
CMQ062C	Hypothetical protein	1.06	±	0.09
CMN069C	Hypothetical protein	1.06	±	0.11
CMF065C	Mitochondrial ribosomal protein L3 precursor	1.06	±	0.05
CMA065C	Hypothetical protein	1.06	±	0.06
CME075C	Hypothetical protein	1.06	±	0.08
CMF101C	Similar to Muconate cycloisomerase related protein	1.06	±	0.01
CML106C	60S ribosomal protein L36	1.06	±	0.13
CMJ285C	40S ribosomal protein S10	1.06	±	0.07
CMF131C	Hypothetical protein	1.06	±	0.14
CMA025C	Hypothetical protein	1.06	±	0.06
CMS331C	Similar to inner centromere protein	1.06	±	0.05
CME008C	Hypoxanthine phosphoribosyltransferase (HPRT)	1.06	±	0.10
CMF173C	DNA replication licensing factor MCM5	1.06	±	0.14
CMM309C	Similar to WD-repeat protein aladin	1.06	±	0.04
CMA114C	40S ribosomal protein S24	1.06	±	0.09
CMH121C	Cystathionine beta-lyase	1.06	±	0.13
CMD037C	Similar to prefoldin 2	1.06	±	0.04
CMM227C	Hypothetical protein	1.06	±	0.17
CML164C	DNA mismatch repair protein MutS, chloroplast precursor	1.06	±	0.06
CMF128C	Probable kynureninase	1.06	±	0.06
CMT217C	Rab geranylgeranyltransferase, beta subunit	1.06	±	0.07
CMC092C	Hypothetical protein	1.06	±	0.08
CME025C	Hypothetical protein	1.06	±	0.05
CMJ156C	Similar to microtubule-associated protein, RP/EB family	1.06	±	0.12
CME009C	Hypothetical protein	1.06	±	0.15
CMA086C	Hypothetical protein	1.06	±	0.10
CMM250C	Hypothetical protein	1.06	±	0.02
CMC098C	Anthranilate phosphoribosyltransferase	1.06	±	0.15
CMF180C	Hypothetical protein	1.06	±	0.04
CMO322C	Similar to S-adenosylmethionine tRNA ribosyltransferase	1.06	±	0.12
CMJ175C	Hypothetical protein	1.06	±	0.06
CMS090C	Hypothetical protein	1.06	±	0.13
CMS170C	Hypothetical protein	1.06	±	0.06
CMN271C	Hypothetical protein	1.05	±	0.02
CMT597C	Heat shock transcription factor	1.05	±	0.08

CMP045C	Probable replication factor C	1.05	±	0.13
CME104C	Similar to protein phosphatase 2A regulatory subunit B'	1.05	±	0.03
CMF099C	Casein kinase-related protein	1.05	±	0.04
CMI137C	Hypothetical protein	1.05	±	0.04
CMH233C	Similar to tRNA intron endonuclease	1.05	±	0.07
CMR289C	NADH dehydrogenase I (Complex I) iron-sulfur protein 75kDa subunit	1.05	±	0.08
CMP326C	Hypothetical protein	1.05	±	0.06
CMN212C	Similar to diaphanous-related formin	1.05	±	0.08
CMD123C	Probable ATP-dependent DNA helicase RecQ	1.05	±	0.04
CMO291C	Ribose 5-phosphate isomerase	1.05	±	0.03
CMQ378C	Hypothetical protein	1.05	±	0.03
CMB026C	Hypothetical protein	1.05	±	0.06
CMH221C	Similar to PUA domain containing RNA binding protein MCT-1	1.05	±	0.12
CMI240C	(3R)-hydroxymyristoyl-ACP dehydratase, precursor	1.05	±	0.22
CMR238C	Hypothetical protein	1.05	±	0.05
CMT452C	Twinkle (putative T7 phage-type DNA helicase for mitochondrial DNA)	1.05	±	0.06
CML082C	Hypothetical protein	1.05	±	0.05
CMI061C	X-prolyl aminopeptidase, cytosolic aminopeptidase P	1.05	±	0.14
CMO278C	Similar to nuclear receptor binding factor-like protein	1.05	±	0.04
CMT510C	Similar to O-linked glcnac transferase, Mbb1 protein	1.05	±	0.23
CMI158C	Probable pyrroline-5-carboxylate reductase	1.05	±	0.14
CMK066C	L-arabinose permease	1.05	±	0.05
CMM105C	Similar to mutT (8-oxo-dGTPase)	1.05	±	0.08
CMO175C	Cell division protein pelota	1.05	±	0.09
CMF111C	Similar to putative vesicle transport protein	1.05	±	0.02
CMR041C	Hypothetical protein	1.05	±	0.06
CMB141C	Similar to peroxisomal biogenesis factor 3	1.05	±	0.06
CMK096C	Hypothetical protein	1.05	±	0.06
CMI063C	4-hydroxyphenylpyruvate dioxygenase, 4HPPD	1.05	±	0.04
CMI200C	NADH dehydrogenase I (Complex I) alpha subcomplex 2 (B8)	1.05	±	0.07
CMT494C	Similar to pheromone shutdown protein TraB	1.05	±	0.12
CMO079C	Hypothetical protein	1.05	±	0.08
CML125C	Hypothetical protein	1.05	±	0.07
CMM329C	Similar to ATP-dependent RNA helicase	1.05	±	0.01
CML027C	Structural maintenance of chromosome 3 (SMC3)	1.05	±	0.15
CMQ239C	Hypothetical protein	1.05	±	0.02
CMR488C	Similar to phosphatidic acid phosphatase	1.05	±	0.10
CMP254C	Similar to telomeric repeat binding factor 1 (TRF1)	1.05	±	0.04
CMC117C	Similar to peptidylprolyl isomerase	1.05	±	0.04
CMR124C	MYB-related protein	1.05	±	0.07
CMK307C	Probable thylakoid lumen rotamase	1.05	±	0.07
CMP249C	Probable endothelin converting enzyme-1	1.05	±	0.17
CML115C	Similar to diphosphoinositol polyphosphate phosphohydrolase	1.05	±	0.08

CML258C	Hypothetical protein	1.05	±	0.08
CMK197C	Probable dolichyl phosphate glucosyltransferase	1.05	±	0.05
CMP054C	Probable tRNA splicing endonuclease positive effector Sen1p	1.05	±	0.05
CMF017C	Similar to glutaredoxin	1.05	±	0.10
CMT499C	Hypothetical protein	1.05	±	0.04
CMM199C	Hypothetical protein	1.05	±	0.06
CMF118C	Similar to serine/threonine protein kinase AKT	1.05	±	0.06
CMT448C	Hypothetical protein	1.04	±	0.01
CML265C	Uracil phosphoribosyltransferase	1.04	±	0.03
CME013C	Hypothetical protein	1.04	±	0.04
CMG153C	Small GTP-binding protein of Rab family	1.04	±	0.05
CMJ072C	Similar to ubiquinone/menaquinone biosynthesis methyl transferase	1.04	±	0.05
CME101C	RNA polymerase III second largest subunit	1.04	±	0.18
CMD135C	ATP-binding cassette, sub-family G	1.04	±	0.32
CML077C	TFIIB	1.04	±	0.08
CMO218C	Shaggy protein kinase	1.04	±	0.06
CMN125C	40S ribosomal protein S27A, ubiquitin fusion protein	1.04	±	0.06
CMH190C	Similar to histidine triad (HIT) protein	1.04	±	0.15
CMI109C	Similar to glutenin low molecular weight chain precursor	1.04	±	0.20
CMS068C	Histone deacetylase	1.04	±	0.05
CMS081C	Hypothetical protein	1.04	±	0.08
CMR147C	Hypothetical protein	1.04	±	0.06
CMS162C	Hypothetical protein	1.04	±	0.08
CMD110C	Probable telomerase reverse transcriptase	1.04	±	0.09
CMR290C	Hypothetical protein	1.04	±	0.09
CMK174C	Hypothetical protein	1.04	±	0.11
CMA093C	ATP-dependent DNA helicase	1.04	±	0.03
CML267C	Hypothetical protein	1.04	±	0.08
CMO084C	Similar to C3HC4 zinc-binding integral peroxisomal membrane protein PEX12	1.04	±	0.05
CMO104C	Flavin-containing amine oxidase	1.04	±	0.10
CMS453C	Similar to mitochondrial carrier protein	1.04	±	0.11
CMT357C	Similar to splicing factor 3b subunit 2, 145kDa	1.04	±	0.02
CMF071C	Hypothetical protein	1.04	±	0.04
CMB127C	Amino-acid N-acetyltransferase	1.04	±	0.08
CMM129C	Hypothetical protein	1.04	±	0.06
CML195C	Hypothetical protein	1.04	±	0.02
CML272C	Hypothetical protein	1.04	±	0.14
CMT486C	Similar to ribosome binding factor A	1.04	±	0.04
CMJ011C	Similar to 26S proteasome regulatory subunit RPN12	1.04	±	0.06
CMT240C	Indole-3-glycerol phosphate synthase	1.04	±	0.13
CME111C	Polypeptide deformylase (formylmethionine deformylase)	1.04	±	0.08
CMI146C	Similar to folate transporter/carrier	1.04	±	0.08
CMO135C	Probable catabolite repressor protein (CCR4)-associative factor 1	1.04	±	0.06

CMI016C	Similar to 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase, mitochondrial	1.04	±	0.08
CMI127C	Hypothetical protein	1.04	±	0.03
CMM331C	Hypothetical protein	1.04	±	0.10
CML163C	Hypothetical protein	1.04	±	0.03
CMI164C	Hypothetical protein	1.04	±	0.02
CMN121C	Hypothetical protein	1.04	±	0.02
CMS485C	Unknown nucleolar protein	1.04	±	0.08
CMI068C	Hypothetical protein	1.04	±	0.03
CMI300C	Uracil-DNA-glycosylase	1.04	±	0.15
CMN296C	Hypothetical protein	1.04	±	0.10
CMT292C	Ribose-phosphate pyrophosphokinase	1.04	±	0.11
CMP263C	Hypothetical protein	1.04	±	0.08
CMH250C	Cytochrome-b5 reductase	1.04	±	0.07
CMA067C	Mitochondrial ribosomal protein L32 precursor	1.04	±	0.08
CMJ039C	ATP-binding cassette, sub-family A	1.04	±	0.08
CMM256C	Similar to RNA polymerase I specific transcription initiation factor RRN3	1.04	±	0.18
CMO269C	Probable glucose 6 phosphate/phosphate translocator	1.04	±	0.17
CMG146C	GTP-binding protein of Obg family	1.04	±	0.09
CME134C	Hypothetical protein	1.04	±	0.04
CMM289C	Molybdopterin synthase sulphurylase MoeB	1.04	±	0.04
CMQ331C	Similar to DEAH-box RNA helicase Dhr1	1.04	±	0.22
CMJ261C	DNA replication licensing factor MCM6	1.04	±	0.06
CMJ215C	Unknown homeobox protein	1.04	±	0.09
CMP345C	Valine--tRNA ligase, cytoplasmic	1.04	±	0.15
CMR389C	Hypothetical protein	1.04	±	0.02
CMR012C	Sulfolipid biosynthesis protein SQD1 (UDP-sulfoquinovose synthesis), chloroplast	1.04	±	0.05
CME004C	Ubiquitin-like protein Smt3	1.04	±	0.01
CMM197C	Hypothetical protein	1.04	±	0.09
CMS172C	Similar to ankyrin 1	1.04	±	0.17
CMT585C	Hypothetical protein	1.04	±	0.04
CMK284C	Similar to DNA primase large subunit	1.04	±	0.04
CMM014C	Eukaryotic translation initiation factor eIF-2B gamma subunit	1.04	±	0.16
CMQ232C	Similar to GTP-binding protein	1.04	±	0.13
CMN285C	Phosphoenolpyruvate carboxykinase (ATP)	1.04	±	0.10
CMP192C	Hypothetical protein	1.04	±	0.09
CMD085C	Hypothetical protein	1.04	±	0.07
CMA044C	Probable deoxyribodipyrimidine photolyase	1.03	±	0.05
CMS486C	Hypothetical protein	1.03	±	0.08
CMC059C	GTP-binding protein of engA family	1.03	±	0.02
CMO265C	Hypothetical protein	1.03	±	0.04
CMQ122C	Small GTP-binding protein of Rab family	1.03	±	0.12
CML252C	Probable peroxisomal biogenesis factor 6	1.03	±	0.15
CMO034C	Similar to postmeiotic segregation increased 2	1.03	±	0.06

CMS011C	Hypothetical protein	1.03	±	0.10
CMR015C	Sulfoquinovosyldiacylglycerol biosynthesis protein	1.03	±	0.04
CME124C	Hypothetical protein	1.03	±	0.05
CMM072C	Sigma subunit for chloroplast RNA polymerase	1.03	±	0.02
CMD053C	Hypothetical protein	1.03	±	0.02
CMH157C	Hypothetical protein	1.03	±	0.16
CMT541C	Similar to mitochondrial carrier protein precursor	1.03	±	0.16
CMC131C	Hypothetical protein	1.03	±	0.04
CMA135C	Similar to androgen-regulated short-chain dehydrogenase/reductase 1	1.03	±	0.04
CMQ128C	Conserved unknown protein	1.03	±	0.01
CMJ091C	Small GTP-binding protein of Rho family	1.03	±	0.13
CMC048C	Hypothetical protein	1.03	±	0.06
CMO164C	Similar to acylphosphatase	1.03	±	0.04
CMQ248C	Hypothetical protein	1.03	±	0.04
CML101C	MYB-related protein	1.03	±	0.02
CMT379C	20S core proteasome subunit alpha 4	1.03	±	0.12
CML210C	Biotin synthetase	1.03	±	0.11
CMM116C	Hypothetical protein	1.03	±	0.07
CME063C	Similar to splicing factor 3b subunit 4 (U2 snRNP)	1.03	±	0.10
CMK041C	Pyruvate kinase	1.03	±	0.14
CMT451C	RNA polymerase I, II, III common subunit	1.03	±	0.05
CMQ160C	Cytochrome c reductase (Complex III) subunit 10(XI)	1.03	±	0.05
CMR497C	Kinesin-related protein	1.03	±	0.10
CMR127C	Similar to putative v-snare binding protein	1.03	±	0.02
CMN085C	Fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase	1.03	±	0.03
CME046C	60S ribosomal protein L29	1.03	±	0.03
CMG197C	Hypothetical protein	1.03	±	0.11
CMM325C	Similar to RNA polymerase III transcription factor TFIIIC	1.03	±	0.02
CMQ243C	Vesicular-fusion protein NSF (N-ethylmaleimide sensitive fusion protein)	1.03	±	0.08
CMC148C	Aspartate aminotransferase	1.03	±	0.03
CMS311C	Similar to bacterioferritin comigratory protein	1.03	±	0.08
CML263C	Hypothetical protein	1.03	±	0.05
CMT294C	Similar to apoptotic cell death regulator DAD1	1.03	±	0.08
CMN300C	Similar to hedgehog protein	1.03	±	0.08
CMI087C	Hypothetical protein	1.03	±	0.00
CMT186C	Hypothetical protein	1.03	±	0.06
CMS326C	Chorismate mutase (CM)/prephenate dehydrogenase (PDH) (T-protein)	1.03	±	0.07
CMP188C	Hypothetical protein	1.03	±	0.21
CMS236C	Probable excision repair protein (ERCC5)	1.03	±	0.10
CMG079C	Similar to DNA excision repair protein ERCC-1	1.03	±	0.07
CMT233C	Hypothetical protein	1.03	±	0.11
CMS339C	Probable pyridoxal kinase	1.03	±	0.03
CMB135C	Hypothetical protein	1.03	±	0.06

CMQ301C	Probable alcohol dehydrogenase	1.03	±	0.32
CMB156C	Probable phosphoinositide phosphatase SAC1	1.03	±	0.06
CMQ102C	Hypothetical protein	1.03	±	0.05
CMN194C	Cathepsin D precursor	1.03	±	0.05
CMG189C	Chromosome assembly protein SMC2	1.03	±	0.06
CMS007C	Similar to 4-methyl-5(beta-hydroxyethyl)-thiazol monophosphate biosynthesis protein	1.03	±	0.02
CMG019C	Nitrate reductase	1.03	±	0.05
CMK085C	Hypothetical protein	1.03	±	0.03
CMN181C	Branched-chain-amino-acid transaminase, mitochondrial precursor	1.03	±	0.08
CMO333C	Hypothetical protein	1.03	±	0.07
CMG008C	Unknown Zinc finger protein	1.03	±	0.02
CMC079C	Hypothetical protein	1.03	±	0.04
CMS327C	Pyruvate dehydrogenase E1 beta subunit, mitochondrial precursor	1.02	±	0.15
CMR037C	Probable serine rich pumilio family rna binding domain pr otein	1.02	±	0.18
CME061C	Similar to protein-tyrosine-phosphatase-like protein	1.02	±	0.18
CMP014C	Hypothetical protein	1.02	±	0.10
CMP351C	Hypothetical protein	1.02	±	0.06
CMM045C	Stearoyl-CoA desaturase	1.02	±	0.09
CMM151C	Probable histone acetyltransferase GCN5	1.02	±	0.06
CMH087C	Hypothetical protein	1.02	±	0.09
CMR476C	Similar to glycerol-3-phosphate dehydrogenase	1.02	±	0.04
CMP290C	Hypothetical protein	1.02	±	0.05
CMT485C	Mitochondrial ribosomal protein S7, precursor	1.02	±	0.13
CMP162C	Hypothetical protein	1.02	±	0.06
CMR489C	Hypothetical protein	1.02	±	0.04
CMS417C	Mitochondrial ribosomal protein L22 precursor	1.02	±	0.02
CMS279C	Transmembrane protein FT27/PFT27-like	1.02	±	0.05
CMG084C	Hypothetical protein	1.02	±	0.11
CMI207C	Hypothetical protein	1.02	±	0.11
CMB043C	Activity of bc1 complex ABC1	1.02	±	0.07
CMR183C	WNK-like protein kinase	1.02	±	0.07
CMN311C	Similar to phosphoglycerate mutase	1.02	±	0.25
CMP270C	Hypothetical protein	1.02	±	0.07
CMI278C	Hypothetical protein	1.02	±	0.03
CMH223C	Hypothetical protein	1.02	±	0.08
CMD011C	Probable MPBQ/MSBQ methyltransferase	1.02	±	0.24
CMF178C	Glutamyl-tRNA amidotransferase subunit B	1.02	±	0.08
CMN199C	DNA polymerase delta catalytic chain	1.02	±	0.06
CMI291C	Similar to replication protein A 30kDa	1.02	±	0.08
CMR313C	Probabale oligoendopeptidase F	1.02	±	0.08
CMS493C	Hypothetical protein, conserved in bacteria	1.02	±	0.03
CMO215C	Similar to RNA methyltransferase	1.02	±	0.04
CMH277C	Hypothetical protein	1.02	±	0.02

CMP161C	Similar to dual specificity protein phosphatase	1.02	±	0.07
CMQ153C	Hypothetical protein	1.02	±	0.06
CMD026C	RNA polymerase II subunit G	1.02	±	0.03
CMK227C	Hypothetical protein	1.02	±	0.07
CMG027C	Hypothetical protein	1.02	±	0.11
CMT278C	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	1.02	±	0.02
CMR222C	Hypothetical protein	1.02	±	0.03
CMR180C	ATP-binding subunit of unknown ABC transporter	1.02	±	0.10
CMI023C	Hypothetical protein	1.02	±	0.06
CMP309C	Hypothetical protein	1.02	±	0.06
CMT321C	Protein translation factor Sui1 homolog	1.02	±	0.27
CMJ103C	Hypothetical protein	1.02	±	0.19
CMN273C	Hypothetical protein	1.02	±	0.14
CMM241C	Hypothetical protein	1.02	±	0.09
CMT029C	N-formylglutamate deformylase	1.02	±	0.18
CMQ105C	Hypothetical protein	1.02	±	0.06
CMG085C	Similar to BET3 involved in targeting and fusion of ER to Golgi transport vesicles	1.02	±	0.02
CMF181C	Small GTP-binding protein of Rab family	1.02	±	0.05
CMP160C	Protease IV	1.02	±	0.08
CMJ233C	Hypothetical protein	1.02	±	0.07
CMR440C	Sulfite reductase (NADPH) flavoprotein alpha-component	1.02	±	0.18
CMR305C	Similar to pleiotropic regulator 1 (PRL1)	1.02	±	0.04
CMF129C	Mitochondrial chaperonin hsp10, precursor	1.02	±	0.04
CMP105C	Hypothetical protein	1.02	±	0.01
CMS023C	Similar to ARE1-like protein	1.02	±	0.05
CME050C	Similar to nuclear LIM interactor-interacting factor	1.02	±	0.23
CMF022C	tRNA pseudouridine 55 synthase	1.02	±	0.04
CMS315C	Similar to electron-transfer-flavoprotein, beta polypeptide, mitochondrial precursor	1.02	±	0.07
CMD048C	Cytochrome c reductase (Complex III) subunit 9(X)	1.02	±	0.07
CMR425C	Probable rRNA methyltransferase	1.02	±	0.14
CMC168C	Hypothetical protein	1.02	±	0.11
CMD058C	Fumarate hydratase precursor	1.01	±	0.06
CMR406C	Hypothetical protein	1.01	±	0.02
CMH028C	Probable alpha-1,3-glucosyltransferase ALG6	1.01	±	0.04
CMG050C	Alpha-galactosidase	1.01	±	0.19
CMR200C	Hypothetical protein	1.01	±	0.09
CMS299C	Biotin carboxylase, chloroplast precursor	1.01	±	0.12
CMR308C	Hypothetical protein	1.01	±	0.04
CML182C	Hypothetical protein	1.01	±	0.02
CMM164C	Hypothetical protein	1.01	±	0.03
CMT482C	Hypothetical protein	1.01	±	0.02
CMR218C	Hypothetical protein	1.01	±	0.03
CMT220C	Chlorophyll a synthase	1.01	±	0.03

CML035C	Hypothetical protein	1.01	±	0.12
CMP086C	Hypothetical protein	1.01	±	0.08
CMO204C	Similar to retinoblastoma binding protein 2	1.01	±	0.09
CMI060C	Hypothetical protein	1.01	±	0.09
CMO130C	ATP-binding cassette, sub-family G	1.01	±	0.09
CMD118C	Beta-ketoacyl-CoA synthase	1.01	±	0.07
CMM295C	Hypothetical protein	1.01	±	0.12
CMS049C	Hypothetical protein	1.01	±	0.04
CMT130C	GTP-binding protein of Nug1 family	1.01	±	0.06
CMP081C	Hypothetical protein	1.01	±	0.10
CMG090C	Hypothetical protein	1.01	±	0.13
CMR044C	Hypothetical protein	1.01	±	0.19
CMN291C	Hypothetical protein	1.01	±	0.17
CMS102C	Eukaryotic translation initiatiobn factor eIF-3 subunit 6	1.01	±	0.14
CMN275C	Hypothetical protein	1.01	±	0.09
CMQ103C	Probable pantothenate kinase	1.01	±	0.09
CME086C	Hypothetical protein	1.01	±	0.05
CMS335C	Hypothetical protein	1.01	±	0.01
CML085C	Similar to UDP-galactose transporter	1.01	±	0.09
CMT228C	Similar to acylaminoacyl-peptidase	1.01	±	0.16
CMR148C	40S ribosomal protein S19	1.01	±	0.08
CMT602C	Similar to lanthionine synthetase	1.01	±	0.07
CMQ195C	Cyclin dependent kinase, C-type	1.01	±	0.03
CMR288C	Probable molybdopterin synthase Cnx2	1.01	±	0.07
CMN136C	Hypothetical protein	1.01	±	0.05
CMO190C	Hypothetical protein	1.01	±	0.09
CMD021C	GTP-binding protein of LepA family	1.01	±	0.04
CMK139C	Enoyl-CoA hydratase, mitochondrial precursor	1.01	±	0.11
CMN051C	Similar to 6-pyruvoyltetrahydropterin synthase	1.01	±	0.06
CMQ078C	60S ribosomal protein L6	1.01	±	0.06
CMM010C	Hypothetical protein	1.01	±	0.06
CMS344C	Probable O-sialoglycoprotein endopeptidase	1.01	±	0.04
CMQ044C	Aurora kinase	1.01	±	0.06
CMJ298C	Hypothetical protein	1.01	±	0.07
CMO089C	Plastid division protein FtsZ	1.01	±	0.11
CMG156C	Probable nicotinate phosphoribosyltransferase	1.01	±	0.05
CMO315C	Similar to magnesium transporter Mrs2p	1.01	±	0.10
CMS385C	Proline iminopeptidase	1.01	±	0.03
CMB005C	RNA polymerase III subunit C34	1.01	±	0.02
CML165C	Hypothetical protein	1.01	±	0.06
CMS408C	Hypothetical protein	1.01	±	0.07
CMT308C	Hypothetical protein	1.01	±	0.13
CMC034C	Probable tyrosine aminotransferase	1.01	±	0.06

CML200C	Hypothetical protein	1.01	±	0.09
CMQ359C	Mannose-6-phosphate isomerase	1.01	±	0.07
CMH018C	Hypothetical protein	1.01	±	0.03
CMR401C	Transposon	1.01	±	0.11
CMS281C	Hypothetical protein	1.01	±	0.06
CMM042C	Hypothetical protein	1.00	±	0.06
CML073C	Similar to actin-related protein	1.00	±	0.02
CMB123C	Similar to tRNA (1-methyladenosine) methyltransferase subunit GCD14	1.00	±	0.04
CMT350C	DNA polymerase delta, subunit D	1.00	±	0.03
CMP346C	Hypothetical protein	1.00	±	0.01
CMQ162C	Hypothetical protein	1.00	±	0.04
CMI265C	Hypothetical protein	1.00	±	0.09
CMM173C	Hypothetical protein	1.00	±	0.05
CMT419C	Mitochondrial ribosome releasing factor RRF	1.00	±	0.07
CMO342C	Similar to Sm protein G	1.00	±	0.04
CME118C	Hypothetical protein	1.00	±	0.03
CMD183C	Small GTP-binding protein of Rab family	1.00	±	0.05
CMB112C	Similar to nucleoporin	1.00	±	0.06
CMP061C	Hypothetical protein	1.00	±	0.10
CMS249C	Unknown protein (similar to predicted phosphoesterase)	1.00	±	0.06
CMM136C	Hypothetical protein	1.00	±	0.04
CMB074C	Hypothetical protein	1.00	±	0.05
CMO314C	Photosystem II stability/assembly factor HCF136	1.00	±	0.20
CMG057C	40S ribosomal protein S20	1.00	±	0.08
CML065C	Probable arginine-tRNA-protein transferase	1.00	±	0.11
CMC036C	Similar to ATP-dependent RNA helicase	1.00	±	0.12
CMP315C	Hypothetical protein	1.00	±	0.06
CME168C	Hypothetical protein	1.00	±	0.00
CMC072C	Similar to Transmembrane protein Tmp21 precursor	1.00	±	0.13
CMT373C	GTP binding protein HflX	1.00	±	0.07
CMK217C	Similar to 1-acyl-sn-glycerol-3-phosphate acyltransferase	1.00	±	0.11
CMO009C	Similar to splicing factor RSp31	1.00	±	0.06
CMK173C	Hypothetical protein	1.00	±	0.05
CMI271C	MGDG synthase	1.00	±	0.08
CMT443C	RING zinc finger protein	1.00	±	0.13
CMM041C	Hypothetical protein	1.00	±	0.08
CMF061C	Hypothetical protein	1.00	±	0.06
CML034C	Similar to vesicle docking protein SEC34	1.00	±	0.07
CMM203C	Hypothetical protein	1.00	±	0.05
CMO310C	60S ribosomal protein L7	1.00	±	0.05
CMT562C	Probable telomerase regulation-associated protein	1.00	±	0.09
CMI099C	Hypothetical protein	1.00	±	0.03
CMK124C	Similar to peroxisomal targeting signal type 1 (PTS1) receptor PEX5	1.00	±	0.09

CML338C	Unknown rhomboid family protein	1.00	±	0.09
CMG201C	Hypothetical protein	1.00	±	0.24
CMQ444C	Hypothetical protein	1.00	±	0.05
CMS152C	Probable sodium/hydrogen antiporter	1.00	±	0.06
CMK299C	Hypothetical protein	1.00	±	0.08
CMC041C	Hypothetical protein	1.00	±	0.08
CMJ073C	Hypothetical protein	1.00	±	0.04
CMA099C	Hypothetical protein	1.00	±	0.12
CMF185C	1-acylglycerol-3-phosphate O-acyltransferase	1.00	±	0.07
CMT165C	2-dehydro-3-deoxyphosphoheptonate aldolase	1.00	±	0.09
CMT493C	Organelle division protein FtsZ	1.00	±	0.05
CMK116C	Hypothetical protein	1.00	±	0.06
CML149C	Mitochondrial ribosomal protein L30 precursor	1.00	±	0.05
CMM147C	Similar to signal recognition particle (SRP) receptor beta subunit	1.00	±	0.02
CMT396C	Similar to class 2 transcription repressor NC2 alpha subunit	1.00	±	0.07
CMS182C	Hypothetical protein	1.00	±	0.04
CMN232C	Hypothetical protein	1.00	±	0.04
CMP026C	Probable low-affinity phosphate transporter Pho91p	1.00	±	0.03
CMT184C	GTP-binding protein	1.00	±	0.09
CMT019C	Hypothetical protein	1.00	±	0.08
CMN200C	Hypothetical protein	1.00	±	0.07
CMQ250C	Probable phosphoserine phosphatase	1.00	±	0.03
CMJ201C	Delta 9 acyl-lipid fatty acid desaturase	1.00	±	0.08
CMK009C	Hypothetical protein	1.00	±	0.08
CMQ266C	Hypothetical protein	1.00	±	0.07
CMI254C	Hypothetical protein	1.00	±	0.03
CMQ154C	Fumarylacetoacetase	1.00	±	0.04
CMI262C	NADH dehydrogenase I (Complex I) alpha subcomplex 6 (B14)	1.00	±	0.03
CMH274C	Similar to deoxyribodipyrimidine photolyase	1.00	±	0.06
CMK163C	Hypothetical protein	1.00	±	0.05
CMK036C	Hypothetical protein	1.00	±	0.04
CML122C	Similar to oxysterol binding protein	0.99	±	0.03
CMO312C	Similar to pre-mRNA cleavage complex II protein Clp1	0.99	±	0.12
CMP253C	Similar to ion transporter	0.99	±	0.07
CMK060C	Nucleoside-diphosphate kinase	0.99	±	0.01
CMI051C	Similar to thiamine triphosphatase	0.99	±	0.11
CMG072C	Hypothetical protein	0.99	±	0.09
CMS499C	Hypothetical protein	0.99	±	0.05
CMT626C	Probable ribonuclease H	0.99	±	0.05
CMT412C	Isocitrate dehydrogenase (NAD^+) subunit 1, mitochondrial	0.99	±	0.02
CME191C	Hypothetical protein	0.99	±	0.07
CME069C	Hypothetical protein	0.99	±	0.12
CMQ291C	dCMP deaminase	0.99	±	0.02

CMH030C	Hypothetical protein	0.99	±	0.10
CMC080C	Similar to biotin holocarboxylase synthetase	0.99	±	0.08
CMS295C	MAP kinase	0.99	±	0.02
CMD073C	Hypothetical protein	0.99	±	0.02
CMT522C	Hypothetical protein	0.99	±	0.05
CMR284C	Similar to arsenical pump-driving ATPase	0.99	±	0.11
CML326C	Hypothetical protein	0.99	±	0.06
CMQ082C	Histidinol dehydrogenase	0.99	±	0.03
CMD121C	Probable photolyase/blue-light receptor (PHR2)	0.99	±	0.05
CMQ147C	Hypothetical protein	0.99	±	0.07
CMP119C	GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase (dhbp synthase)	0.99	±	0.03
CMT508C	Mitochondrial ribosomal protein L17 precursor	0.99	±	0.06
CMR226C	Hypothetical protein	0.99	±	0.02
CMH011C	Hypothetical protein	0.99	±	0.08
CMK050C	Lycopene beta cyclase, chloroplast precursor	0.99	±	0.10
CMB025C	Protoporphyrinogen IX oxidase (PPO)	0.99	±	0.04
CMS337C	Hypothetical protein	0.99	±	0.03
CML081C	Hypothetical protein	0.99	±	0.04
CMD122C	Hypothetical protein	0.99	±	0.04
CMS347C	Probable mitotic spindle assembly checkpoint protein MAD2	0.99	±	0.05
CMS361C	Organelle division protein FtsZ (AB032071)	0.99	±	0.10
CMO256C	Hypothetical protein	0.99	±	0.14
CMI162C	Pyrophosphate-fructose-6-phosphate 1-phosphotransferase	0.99	±	0.07
CMC138C	Similar to FUSCA protein FUS6	0.99	±	0.06
CML227C	Hypothetical protein	0.99	±	0.08
CME117C	ATP-binding cassette, sub-family D (PMP)	0.99	±	0.07
CME040C	Hypothetical protein	0.99	±	0.04
CMR350C	Similar to CCAAT-binding transcription factor subunit A(CBF-A)	0.99	±	0.09
CMC008C	NADH dehydrogenase I (Complex I) alpha subcomplex 7 (B14.5a)	0.99	±	0.04
CMA036C	Similar to tubulin folding cofactor B	0.99	±	0.03
CMA039C	Hypothetical protein	0.99	±	0.01
CMO326C	Hypothetical protein	0.99	±	0.07
CMF102C	Similar to cell division cycle protein (CDC 16), TPR protein, APC6	0.99	±	0.06
CMS217C	Hypothetical protein	0.99	±	0.05
CMQ350C	Probable 1,4-benzoquinone reductase	0.99	±	0.15
CMT573C	Hypothetical protein	0.99	±	0.02
CMH241C	Hypothetical protein	0.99	±	0.06
CMH078C	Hypothetical protein	0.99	±	0.02
CMG198C	Methionyl-tRNA formyltransferase	0.99	±	0.03
CMG124C	GTP-binding protein of Obg-family	0.99	±	0.15
CMC068C	Hypothetical protein	0.99	±	0.03
CMP260C	Pyruvate kinase I	0.99	±	0.04
CMG056C	DNA topoisomerase III alpha	0.99	±	0.02

CML329C	3-oxoacyl-[acyl-carrier-protein] synthase II	0.99	±	0.07
CMQ242C	WD-repeat cell cycle regulatory protein	0.99	±	0.09
CMR260C	Similar to enhancer of rudimentaryp1 homolog	0.99	±	0.05
CMI230C	Similar to endonuclease III	0.99	±	0.06
CML323C	Ornithine aminotransferase	0.99	±	0.04
CMR093C	Hypothetical protein	0.99	±	0.02
CMH126C	Probable eukaryotic translation initiation factor 3, subunit 8	0.99	±	0.08
CMS409C	Similar to survival protein SurE	0.99	±	0.07
CML224C	Similar to flightless-I protein	0.99	±	0.04
CMD097C	Similar to Traf and Tnf receptor associated protein	0.99	±	0.03
CMQ137C	Similar to chloroplast outer envelope protein Toc34	0.99	±	0.07
CMK265C	Hypothetical protein	0.99	±	0.07
CMP282C	Similar to ZIP Zinc transporter	0.99	±	0.05
CMR070C	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like	0.99	±	0.07
CMI101C	Hypothetical protein	0.99	±	0.05
CMP040C	Hypothetical protein	0.99	±	0.10
CMI176C	DNA polymerase alpha, subunit A	0.98	±	0.04
CMT283C	Hypothetical protein	0.98	±	0.06
CMS484C	Similar to guanylate kinase (GMP kinase)	0.98	±	0.06
CMR042C	Similar to carbonyl reductase	0.98	±	0.05
CMS082C	Hypothetical protein	0.98	±	0.03
CMQ255C	CAD complex (carbamoyl-phosphate synthase II/aspartate carbamoyltransferase catalytic chain/dihydroorotase)	0.98	±	0.05
CMH148C	Hypothetical protein	0.98	±	0.07
CMS128C	ATP-dependent Clp protease, ATP-binding subunit ClpB	0.98	±	0.04
CMM069C	Hypothetical protein	0.98	±	0.06
CMP347C	Similar to lipoic acid synthase	0.98	±	0.10
CMS075C	Hypothetical protein	0.98	±	0.05
CMQ068C	Probable ubiquinone biosynthesis monooxgenase COQ6	0.98	±	0.04
CMS393C	Chloroplast 3-oxoacyl-[acyl-carrier protein] reductase orecursor	0.98	±	0.10
CMG130C	Hypothetical protein	0.98	±	0.06
CMA056C	Unknown kinase with aarF domain, fused with possible beta-lactamase	0.98	±	0.13
CMB051C	Mitochondrial translation elongation factor Ts (EF-Ts)	0.98	±	0.01
CMD025C	DNA replication licensing factor MCM2	0.98	±	0.14
CMO284C	Probable 3-oxo-5-alpha-steroid 4-dehydrogenase	0.98	±	0.06
CMO030C	Hypothetical protein	0.98	±	0.09
CMS192C	Glutamate--tRNA ligase, chloroplast or mitochondrial	0.98	±	0.14
CMO092C	DNA repair and recombination protein RAD26	0.98	±	0.02
CMM029C	Notchless	0.98	±	0.10
CMO141C	Probable adrenodoxin	0.98	±	0.07
CMG145C	Hypothetical protein	0.98	±	0.10
CMD140C	60S ribosomal protein L27A	0.98	±	0.08
CMK082C	Hypothetical protein	0.98	±	0.20
CMB101C	Hypothetical protein	0.98	±	0.08

CMQ107C	Hypothetical protein	0.98	±	0.30
CMQ124C	Hypothetical protein	0.98	±	0.05
CMD012C	Hypothetical protein	0.98	±	0.04
CMT399C	Hypothetical protein	0.98	±	0.07
CMP295C	Similar to iron-sulfur cluster scaffold protein	0.98	±	0.05
CMO005C	Hypothetical protein	0.98	±	0.01
CML072C	Hypothetical protein	0.98	±	0.07
CMN061C	Hypothetical protein	0.98	±	0.04
CMK051C	Similar to frataxin	0.98	±	0.08
CMF176C	Similar to lysophospholipase II	0.98	±	0.05
CMR126C	Probable sulfite oxidase	0.98	±	0.08
CMP110C	Similar to retinol dehydrogenase 8 (all-trans)	0.98	±	0.16
CME176C	Hypothetical protein	0.98	±	0.05
CMO105C	Unknown ABC transporter	0.98	±	0.04
CMS141C	Hypothetical protein	0.98	±	0.05
CMO266C	Hypothetical protein	0.98	±	0.01
CMD041C	Fructose-1,6-bisphosphatase	0.98	±	0.10
CME192C	Uridine kinase	0.98	±	0.04
CMO316C	Hypothetical protein	0.98	±	0.08
CML023C	Transitional endoplasmic reticulum ATPase (valosin-containing protein)	0.98	±	0.07
CMP070C	Stress-inducible pyridoxine biosynthesis protein SOR	0.98	±	0.15
CMJ183C	Mitochondrial ribosomal protein L33, precursor	0.98	±	0.13
CMK309C	Unknown zinc-finger protein	0.98	±	0.12
CMB055C	Similar to uroporphyrin-III C-methyltransferase	0.98	±	0.04
CMN143C	Similar to t-SNARE SED5	0.98	±	0.11
CMQ316C	Exonuclease	0.98	±	0.14
CMT548C	Hypothetical protein	0.98	±	0.06
CMP016C	Hypothetical protein	0.98	±	0.12
CMK073C	Probable transcription factor Hap5a	0.98	±	0.09
CMS206C	Hypothetical protein	0.98	±	0.12
CMP173C	Similar to protein-S-isoprenylcysteine O-methyltransferase	0.98	±	0.11
CMB106C	Hypothetical protein	0.98	±	0.04
CMH201C	Hypothetical protein	0.98	±	0.08
CML147C	Hypothetical protein	0.98	±	0.06
CMH252C	Hypothetical protein	0.98	±	0.09
CMM051C	Hypothetical protein	0.98	±	0.20
CMO285C	Hypothetical protein	0.98	±	0.09
CML280C	Hypothetical protein	0.98	±	0.07
CMR382C	Similar to sodium/hydrogen antiporter	0.98	±	0.04
CMT080C	Hypothetical protein	0.98	±	0.11
CME012C	Na^+/glucose co-transporter	0.98	±	0.02
CMP246C	Hypothetical protein	0.98	±	0.06
CMH048C	Hypothetical protein	0.98	±	0.04

CMI015C	L-asparaginase	0.97	±	0.11
CMM318C	Glutamyl-tRNA amidotransferase subunit A	0.97	±	0.15
CMS053C	Hypothetical protein	0.97	±	0.04
CMD091C	Hypothetical protein	0.97	±	0.10
CMI197C	Hypothetical protein	0.97	±	0.15
CMC134C	Probable constituent of 66S pre-ribosomal particles Nsa2p	0.97	±	0.14
CMG154C	Hypothetical protein	0.97	±	0.05
CMT481C	Similar to p53-related protein kinase	0.97	±	0.07
CMD014C	Coatomer protein complex, subunit epsilon	0.97	±	0.07
CMK020C	Similar to glycogenin	0.97	±	0.09
CMT338C	Hypothetical protein	0.97	±	0.06
CMQ337C	2-isopropylmalate synthase	0.97	±	0.04
CMJ210C	Similar to tRNA dihydrouridine synthase Dus1p	0.97	±	0.05
CME047C	Isoleucine--tRNA ligase	0.97	±	0.07
CML214C	Ornithine carbamoyltransferase	0.97	±	0.06
CMA077C	Aspartate transaminase	0.97	±	0.09
CMS138C	Hypothetical protein	0.97	±	0.07
CMQ325C	Hypothetical protein	0.97	±	0.07
CMF038C	Similar to sedlin	0.97	±	0.02
CMK294C	26S proteasome ATP-dependent regulatory subunit	0.97	±	0.04
CMT528C	Hypothetical protein	0.97	±	0.05
CMK029C	Similar to GTPase activating protein	0.97	±	0.04
CMT610C	Methylenetetrahydrofolate reductase	0.97	±	0.05
CMB095C	Similar to alpha-glucosidase	0.97	±	0.08
CMS097C	Hypothetical protein	0.97	±	0.08
CMS297C	Similar to cleavage and polyadenylation specificity factor subunit	0.97	±	0.07
CMT232C	Protoheme IX farnesyltransferase (Complex IV)	0.97	±	0.05
CMQ042C	UDP-glcnac:dolichol phosphate N-acetylglucosamine-1-phosphate transferase	0.97	±	0.09
CMO313C	DNA primase small subunit	0.97	±	0.03
CMT491C	Similar to thylakoidal sec-independent protein transporter Tha4	0.97	±	0.08
CMT570C	Hypothetical protein	0.97	±	0.07
CMJ284C	Cytochrome p450	0.97	±	0.03
CMR216C	Hypothetical protein	0.97	±	0.06
CMP225C	Probable ATPase	0.97	±	0.02
CMS169C	Probable dolichyl-phosphate mannosyltransferase	0.97	±	0.03
CMS286C	Cytochrome-b5 reductase	0.97	±	0.13
CMH137C	Similar to pyrroline-5-carboxylate reductase	0.97	±	0.04
CMP008C	RNA polymerase II subunit	0.97	±	0.02
CMS108C	Immunophilin	0.97	±	0.03
CMT536C	Similar to cation transport protein	0.97	±	0.06
CMI260C	Hypothetical protein	0.97	±	0.05
CMK102C	Hypothetical protein	0.97	±	0.05
CMA090C	NADH dehydrogenase I (Complex I) alpha subcomplex 8 (PGIV)	0.97	±	0.01

CMC160C	Mitochondrial peptide chain release factor RF-2	0.97	±	0.02
CMG109C	40S ribosomal protein S15	0.97	±	0.02
CMM297C	Hypothetical protein	0.97	±	0.04
CMT469C	Probable tyrosyl-DNA phosphodiesterase	0.97	±	0.06
CMR018C	Phosphatidylinositol 3-kinase	0.97	±	0.05
CML305C	60S ribosomal protein L27	0.97	±	0.18
CMK069C	Diacylglycerol kinase	0.97	±	0.01
CMQ381C	Hypothetical protein	0.97	±	0.09
CMB007C	Hypothetical protein	0.97	±	0.02
CME067C	Exonuclease I	0.97	±	0.18
CMN206C	Hypothetical protein	0.97	±	0.08
CMS048C	Hypothetical protein	0.97	±	0.08
CMS334C	Similar to regulator of nonsense transcripts	0.97	±	0.06
CML339C	Steroid monooxygenase	0.97	±	0.08
CMK122C	Hypothetical protein	0.97	±	0.03
CMR404C	Cytochrome c oxidase (Complex IV) subunit VIb	0.97	±	0.12
CMI034C	Ubiquitin-activating enzyme E1	0.97	±	0.05
CMR354C	Hypothetical protein	0.97	±	0.09
CMR139C	Hypothetical protein	0.97	±	0.11
CMJ182C	Hypothetical protein	0.97	±	0.05
CMS271C	Similar to thioredoxin	0.97	±	0.12
CMI264C	ATP-binding cassette, sub-family F (GCN), member 2	0.97	±	0.07
CMT489C	Hypothetical protein	0.97	±	0.02
CMR445C	Oxygen independent coprophorphyrinogen III oxidase	0.97	±	0.08
CMN320C	NADH dehydrogenase I (Complex I) iron-sulfur protein 13kDa subunit	0.97	±	0.04
CMO093C	Hypothetical protein	0.97	±	0.05
CMI196C	Sedoheptulose-1,7-bisphosphatase	0.97	±	0.10
CMC030C	Hypothetical protein	0.97	±	0.08
CMD162C	Similar to DnaJ protein	0.97	±	0.05
CMR262C	Similar to conserved oligomeric Golgi complex component COG2	0.97	±	0.12
CMJ262C	Hypothetical protein	0.97	±	0.08
CMT254C	Hypothetical protein	0.97	±	0.04
CMJ269C	Similar to calcineurin B subunit	0.97	±	0.08
CMR155C	Similar to TATA element modulatory factor	0.97	±	0.03
CMT223C	Similar to translation initiation factor IF-3	0.97	±	0.12
CMC105C	Similar to angio-associated migratory cell protein	0.97	±	0.09
CMQ465C	Similar to senescence-associated protein Din1	0.97	±	0.18
CMT628C	Hypothetical protein	0.96	±	0.12
CMO258C	Hypothetical protein	0.96	±	0.07
CMS035C	Ferrochelatase	0.96	±	0.07
CMG052C	MYB-related protein	0.96	±	0.13
CMK040C	Unknown TatD related DNase	0.96	±	0.12
CMN295C	ATP-binding cassette, sub-family G (WBC)	0.96	±	0.13

CMQ208C	Similar to endoplasmic reticulum translocon component SEC63	0.96	±	0.10
CMC182C	Hypothetical protein	0.96	±	0.05
CMS255C	Similar to proteasome 26S subunit, non-ATPase, 10	0.96	±	0.07
CMM185C	Similar to protein phosphatase 1, regulatory subunit	0.96	±	0.03
CMT523C	Hypothetical protein	0.96	±	0.08
CMB038C	Hypothetical protein	0.96	±	0.11
CMO298C	Hypothetical protein	0.96	±	0.05
CMO221C	Hypothetical protein	0.96	±	0.03
CMT078C	Probable glutamate carboxypeptidase II	0.96	±	0.04
CMQ226C	Similar to sodium-dependent transporter	0.96	±	0.15
CMQ420C	Hypothetical protein	0.96	±	0.09
CMS449C	Similar to molybdopterin biosynthesis CNX1 protein	0.96	±	0.09
CMB061C	Hypothetical protein	0.96	±	0.06
CMC018C	Similar to vesicle-associated membrane protein 7	0.96	±	0.06
CMR098C	Cell division control protein 5 (Cdc5)	0.96	±	0.05
CMI276C	Probable SAC1 (supressor of actin mutations 1) protein	0.96	±	0.07
CMH120C	Hypothetical protein	0.96	±	0.04
CMT247C	Hypothetical protein	0.96	±	0.03
CMR475C	Probable inositol 2-dehydrogenase	0.96	±	0.09
CMS167C	Similar to N2,N2-dimethylguanosine tRNA methyltransferase	0.96	±	0.03
CMT106C	Hypothetical protein	0.96	±	0.05
CMS391C	Similar to leucine-rich repeat-containing G protein-coupled receptor	0.96	±	0.03
CMH110C	Hypothetical protein	0.96	±	0.10
CMA109C	Hypothetical protein	0.96	±	0.08
CMM119C	Glutamate dehydrogenase ($NADP^+$) 2	0.96	±	0.05
CMN128C	Hypothetical protein	0.96	±	0.10
CMM155C	Probable pyridoxine 5'-phosphate oxidase	0.96	±	0.03
CMO069C	Hypothetical protein	0.96	±	0.02
CMO048C	Hypothetical protein	0.96	±	0.06
CMB119C	Similar to cell division control protein 48, AAA family (cdc48-1)	0.96	±	0.05
CMT037C	Similar to thioredoxin-like protein	0.96	±	0.04
CMS388C	Hypothetical protein	0.96	±	0.04
CMN158C	Chloroplast ribosomal protein S15 precursor	0.96	±	0.15
CMJ225C	Probable dipeptidyl aminopeptidase	0.96	±	0.06
CMO355C	Guanine nucleotide exchange factor	0.96	±	0.04
CMR470C	Similar to adaptor-related protein complex 3, beta subunit	0.96	±	0.03
CMJ055C	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)	0.96	±	0.04
CMJ121C	Hypothetical protein	0.96	±	0.06
CMG116C	Hypothetical protein	0.96	±	0.05
CMT207C	Chaperonin containing TCP1, subunit 1 (alpha)	0.96	±	0.12
CMR471C	Hypothetical protein	0.96	±	0.06
CMS448C	Hypothetical protein	0.96	±	0.06
CMS195C	6-phosphogluconate dehydrogenase, decarboxylating	0.96	±	0.18

CMF081C	Hypothetical protein	0.96	±	0.04
CMQ200C	NADH dehydrogenase I (Complex I) iron-sulfur protein 30kDa subunit (NADH-coenzyme Q reductase)	0.96	±	0.05
CME088C	Hypothetical protein	0.96	±	0.09
CMA008C	ORF1050	0.96	±	0.02
CMJ154C	Geranylgeranyl hydrogenase	0.96	±	0.03
CMS261C	Hypothetical protein	0.96	±	0.09
CML249C	Probable 8-oxoguanine-DNA-glycosylase	0.96	±	0.04
CMQ345C	GTP-binding protein of Nug1 family	0.96	±	0.06
CMT251C	Similar to light-inducible protein ATLS1-like	0.96	±	0.15
CML218C	Similar to N-terminal acetyltransferase complex ARD1 subunit	0.96	±	0.03
CML332C	Protein phosphatase 2a	0.96	±	0.05
CMO233C	Hypothetical protein	0.96	±	0.18
CMP228C	Hypothetical protein	0.96	±	0.06
CML130C	Similar to transcription initiation factor TFIIE beta subunit	0.96	±	0.06
CMC082C	CCAAT-box-binding transcription factor	0.96	±	0.03
CMR075C	Probable nucleotide sugar epimerase	0.96	±	0.02
CMM226C	Hypothetical protein	0.96	±	0.09
CMO263C	Hypothetical protein	0.96	±	0.15
CMT518C	Similar to tetrapyrrole methylase	0.96	±	0.07
CME083C	Similar to retromer component VPS5	0.96	±	0.05
CMR314C	Hypothetical protein	0.96	±	0.05
CMK278C	Probable protein disulfide isomerase	0.96	±	0.07
CMM067C	Hypothetical protein	0.96	±	0.08
CMN276C	Hypothetical protein	0.96	±	0.15
CMN029C	Hypothetical protein	0.96	±	0.01
CMM153C	Similar to mitochondrial RNA splicing protein Mrs2p	0.96	±	0.02
CMO139C	2-amino-3-ketobutyrate CoA ligase (akb ligase) (glycine acetyltransferase)	0.96	±	0.03
CMF120C	Hypothetical protein	0.96	±	0.09
CMG035C	Probable Ran GTPase activating protein	0.96	±	0.05
CMO068C	Similar to glycolipid transfer protein	0.95	±	0.07
CMA050C	Hypothetical protein	0.95	±	0.01
CMF072C	Glutamate decarboxylase	0.95	±	0.11
CMG054C	Hypothetical protein	0.95	±	0.04
CMN302C	Similar to Sm protein D2	0.95	±	0.13
CMQ030C	Galactose-1-phosphate uridylyltransferase	0.95	±	0.11
CMN041C	Hypothetical protein	0.95	±	0.04
CMB070C	Ubiquitin protein ligase E3A	0.95	±	0.07
CMT543C	Similar to rRNA methylase	0.95	±	0.04
CMT460C	Similar to RAB geranylgeranyl transferase alpha subunit	0.95	±	0.01
CMT090C	Probable vacuolar protein-sorting protein VPS45	0.95	±	0.05
CMT157C	Small GTP-binding protein of Sar1/Arf family	0.95	±	0.10
CMR392C	Probable heterogeneous nuclear RNP protein A	0.95	±	0.05
CMI284C	Hypothetical protein	0.95	±	0.10

CMH010C	Similar to syntaxin protein	0.95	±	0.04
CMF015C	Small GTP-binding protein of Sar1/Arf family	0.95	±	0.08
CMO276C	Glucokinase	0.95	±	0.06
CMM261C	Cation-transporting ATPase	0.95	±	0.05
CMD185C	TATA-box binding protein-associated factor 13	0.95	±	0.13
CML314C	Similar to RING zinc finger protein	0.95	±	0.06
CMR315C	CP12 protein, chloroplast precursor	0.95	±	0.09
CML282C	Hypothetical protein	0.95	±	0.05
CML304C	60S ribosomal protein L35A	0.95	±	0.05
CMN148C	40S ribosomal protein S3	0.95	±	0.05
CMJ242C	Hypothetical protein	0.95	±	0.01
CMM273C	Similar to alkane hydroxylase	0.95	±	0.23
CMT514C	Hypothetical protein	0.95	±	0.07
CME141C	Similar to GTP-binding protein	0.95	±	0.03
CMR064C	Hypothetical protein	0.95	±	0.08
CMQ261C	Hypothetical protein	0.95	±	0.07
CMO334C	Similar to nucleolar RNA-binding protein	0.95	±	0.23
CMI301C	Similar to glycosyl transferase	0.95	±	0.07
CMD049C	Hypothetical protein	0.95	±	0.09
CML277C	Similar to heat shock transcription factor	0.95	±	0.01
CMO097C	Imidazole glycerol phosphate synthase subunit (IGP synthase cyclase subunit)	0.95	±	0.08
CMJ146C	Hypothetical protein	0.95	±	0.06
CML259C	Eukaryotic polypeptide chain release factor 3	0.95	±	0.05
CMH105C	Hypothetical protein	0.95	±	0.03
CMD095C	V-type ATPase V0 subunit a	0.95	±	0.08
CMB079C	MYB-related protein	0.95	±	0.08
CMM024C	Similar to nuclear protein UKp68	0.95	±	0.11
CMA105C	Hypothetical protein	0.95	±	0.07
CMA075C	Similar to quaking protein	0.95	±	0.05
CML054C	Hypothetical protein	0.95	±	0.06
CMT560C	Probable delta(24)-sterol C-methyltransferase	0.95	±	0.04
CMQ254C	Hypothetical protein	0.95	±	0.07
CMM038C	Hypothetical protein	0.95	±	0.05
CMT620C	Hypothetical protein	0.95	±	0.04
CMH276C	Hypothetical protein	0.95	±	0.02
CMS330C	Probable metal-transporting ATPase	0.95	±	0.05
CMJ226C	Probable mRNA-decapping enzyme DCP2	0.95	±	0.10
CMN266C	Hypothetical protein	0.95	±	0.04
CME073C	ATP-dependent RNA helicase p47	0.95	±	0.03
CMS245C	Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	0.95	±	0.03
CMM299C	Dihydrolipoamide dehydrogenase	0.95	±	0.06
CML076C	3-methyl-2-oxobutanoate hydroxymethyltransferase	0.95	±	0.09
CMK132C	Probable transcription initiation factor TFIID, subunit TAF10	0.95	±	0.07

CMA053C	Hypothetical protein	0.95	±	0.01
CML261C	Hypothetical protein	0.95	±	0.03
CMS395C	Probable electron transport flavoprotein	0.95	±	0.06
CMJ049C	Hypothetical protein	0.95	±	0.05
CMN146C	Hypothetical protein	0.95	±	0.02
CMG165C	Probable NOL1/NOP2/sun family protein (proliferating-cell nucleolar protein)	0.95	±	0.07
CMR254C	Cytidine deaminase	0.95	±	0.03
CMF089C	1-deoxyxylulose-5-phosphate synthase	0.95	±	0.05
CMJ144C	Hypothetical protein	0.95	±	0.06
CMQ071C	Probable U3 snoRNP component Imp4p	0.95	±	0.11
CMI302C	Hypothetical protein	0.95	±	0.06
CMI273C	Dihydrolipoamide S-acetyltransferase, precursor	0.95	±	0.08
CMT191C	Hypothetical protein	0.95	±	0.07
CMK079C	Unknown zinc-finger protein	0.95	±	0.09
CMA033C	Hypothetical protein	0.95	±	0.03
CMD151C	Similar to transcription initiation protein SPT5	0.95	±	0.11
CMC135C	Hypothetical protein	0.95	±	0.03
CMP047C	Hypothetical protein	0.95	±	0.15
CMM086C	Hypothetical protein	0.95	±	0.04
CMS099C	Hypothetical protein	0.95	±	0.12
CMG137C	Hypothetical protein	0.95	±	0.05
CMR257C	Hypothetical protein	0.95	±	0.03
CMM224C	Hypothetical protein	0.95	±	0.09
CMI169C	Probable DNA mismatch repair protein	0.95	±	0.12
CMC103C	Hypothetical protein	0.95	±	0.05
CMO094C	3-isopropylmalate dehydratase small subunit	0.95	±	0.10
CMA030C	Pyruvate kinase, chloroplast precursor	0.95	±	0.25
CMQ131C	Hypothetical protein	0.95	±	0.05
CMQ051C	40S ribosomal protein S21	0.95	±	0.05
CMN144C	Similar to lysyl oxidase	0.95	±	0.07
CMK109C	Hypothetical protein	0.95	±	0.03
CML255C	Similar to inositolphosphorylceramide synthase	0.95	±	0.13
CMO086C	Similar to microsomal signal peptidase	0.95	±	0.02
CMJ173C	Glycerol kinase	0.95	±	0.08
CMH255C	Similar to inositol-1(or 4)-monophosphatase	0.95	±	0.03
CMM157C	Similar to pterin-4-alpha-carbinolamine dehydratase	0.95	±	0.07
CMA081C	Similar to protein kinase (AKINbetagamma-2 of maize)	0.95	±	0.07
CMB086C	Hypothetical protein	0.95	±	0.02
CMF069C	Condensin complex subunit 2	0.95	±	0.02
CMS093C	Hypothetical protein	0.94	±	0.03
CMT315C	Probable oligoribonuclease, mitochondrial precursor	0.94	±	0.10
CMM267C	NADH dehydrogenase I (Complex I) alpha subcomplex 9, mitochondrial precursor	0.94	±	0.05
CMH046C	40S ribosomal protein S14	0.94	±	0.09

CMK301C	Hypothetical protein	0.94	±	0.05
CMT104C	Probable tryptophan 2,3-dioxygenase	0.94	±	0.12
CMT414C	Monodehydroascorbate reductase	0.94	±	0.05
CMH039C	Similar to PREG1-like negative regulator	0.94	±	0.18
CMB035C	Probable Double-strand break repair protein MRE11	0.94	±	0.04
CMK119C	Hypothetical protein	0.94	±	0.05
CMG212C	Similar to iron transporter ferroportin 1	0.94	±	0.08
CMO317C	Similar to carboxyphosphonoenolpyruvate mutase	0.94	±	0.06
CMO108C	Hypothetical protein	0.94	±	0.08
CMK235C	DNA ligase I	0.94	±	0.05
CMQ023C	Similar to lipoate-protein ligase A	0.94	±	0.15
CMA078C	Hypothetical protein	0.94	±	0.04
CMD181C	Similar to RNA polymerase III transcription factor IIIB chain B"	0.94	±	0.08
CML293C	Probable chaperone protein DnaJ	0.94	±	0.06
CMK071C	Hypothetical protein	0.94	±	0.09
CMS445C	Hypothetical protein	0.94	±	0.02
CMB054C	Hypothetical protein	0.94	±	0.05
CML223C	GDP dissociation inhibitor	0.94	±	0.05
CMH013C	Hypothetical protein	0.94	±	0.04
CMJ129C	Histone deacetylase	0.94	±	0.05
CMK182C	Serine/arginine-rich protein specific kinase	0.94	±	0.08
CMF088C	Hypothetical protein	0.94	±	0.07
CMO300C	Cyclophilin	0.94	±	0.02
CME110C	Hypothetical protein	0.94	±	0.02
CME127C	Similar to fructose 1,6-bisphosphatase	0.94	±	0.05
CME113C	Probable dolichol-phosphate mannosyltransferase	0.94	±	0.09
CMT096C	Nuclear transport factor importin alpha	0.94	±	0.04
CMG206C	Hypothetical protein	0.94	±	0.16
CMH016C	Similar to thiamin pyrophosphokinase	0.94	±	0.10
CMO331C	Probable cohesin subunit SA	0.94	±	0.04
CMM308C	Hypothetical protein	0.94	±	0.12
CMQ354C	Phenylalanine--tRNA ligase, mt?	0.94	±	0.19
CMK022C	Similar to Sm protein B	0.94	±	0.02
CMG014C	Similar to G10 protein	0.94	±	0.06
CMT050C	Unknown transporter	0.94	±	0.04
CMR408C	Hypothetical protein	0.94	±	0.06
CMQ219C	Probable tRNA/rRNA cytosine-C5-methylase	0.94	±	0.05
CMT297C	Ribosomal protein S6 kinase RSK-1	0.94	±	0.10
CMK279C	Hypothetical protein	0.94	±	0.19
CMM132C	Mitochondrial propionyl-CoA carboxylase, beta subunit, precursor	0.94	±	0.01
CMR449C	Hypothetical protein	0.94	±	0.04
CME064C	Chorismate synthase	0.94	±	0.11
CMO037C	Hypothetical protein	0.94	±	0.02

CMM099C	Hypothetical protein	0.94	±	0.08
CMR006C	Hypothetical protein	0.94	±	0.05
CMJ164C	Cell differentiation protein rcd1	0.94	±	0.11
CMN106C	Similar to regulator of nonsense transcript stability	0.94	±	0.14
CMC089C	Unknown DUF21 containing protein	0.94	±	0.02
CMO162C	Similar to ring zinc finger protein	0.94	±	0.04
CMS375C	Phospholipid-transporting ATPase IIA, E1-E2 ATPase	0.94	±	0.10
CMR327C	Hypothetical protein	0.94	±	0.17
CMH076C	Similar to FKBP-type peptidyl-prolyl cis-trans isomerase	0.94	±	0.08
CMT362C	Sedoheptulose-1,7-bisphosphatase	0.94	±	0.07
CMP129C	Fructose-1,6-bisphosphatase	0.94	±	0.08
CMS442C	Hypothetical protein	0.94	±	0.10
CMO082C	Similar to nuclear LIM interactor-interacting factor	0.94	±	0.12
CMT155C	Hypothetical protein	0.94	±	0.04
CMJ101C	Similar to heat shock protein	0.94	±	0.08
CMR215C	Hypothetical protein	0.94	±	0.08
CMT566C	TATA-box binding protein-associated factor 2	0.94	±	0.02
CMK185C	Hypothetical protein	0.94	±	0.18
CMK183C	23S RNA pseudouridine 2633 synthase	0.94	±	0.04
CMQ198C	Similar to prenylated Rab receptor 2	0.94	±	0.07
CMF039C	Similar to hypothetical protein, conserved in cyanobacteria	0.94	±	0.05
CMN260C	Hypothetical protein	0.94	±	0.05
CMG117C	Hypothetical protein	0.94	±	0.06
CMP149C	Probabale $Mg2^+$ transporter MgtE	0.94	±	0.02
CMC186C	Similar to trefoil factor	0.94	±	0.05
CML090C	Probable degp protease precursor	0.94	±	0.10
CMM212C	Hypothetical protein	0.94	±	0.09
CMT279C	Similar to prostatic acid phosphatase precursor	0.94	±	0.02
CMR454C	Hypothetical protein	0.94	±	0.04
CMF052C	Hypothetical protein	0.94	±	0.08
CMM334C	Similar to mitochondrial carrier protein	0.94	±	0.16
CMP072C	Hypothetical protein	0.94	±	0.14
CMT415C	Similar to psbb mRNA maturation factor Mbb1, chloroplast precursor	0.94	±	0.10
CMJ102C	Adaptor-related protein complex 1, mu subunit	0.94	±	0.06
CMC114C	26S proteasome ATP-dependent regulatory subunit	0.94	±	0.04
CMS420C	Hypothetical protein	0.94	±	0.06
CMQ178C	Hypothetical protein	0.94	±	0.09
CMP334C	DnaJ (Hsp40) homolog, subfamily D	0.94	±	0.05
CMP284C	Similar to chloroplast outer membrane protein Toc34	0.94	±	0.06
CMX012C	6-phosphogluconate dehydrogenase	0.94	±	0.08
CMI082C	Hypothetical protein	0.94	±	0.08
CMI186C	Cytochrome c-type biogenesis protein ccmE	0.94	±	0.03
CMM049C	Hypothetical protein	0.94	±	0.13

CMO206C	Similar to ribosomal RNA processing exonuclease RRP41	0.94	±	0.03
CMP066C	Hypothetical protein	0.94	±	0.05
CMK140C	Hypothetical protein	0.94	±	0.07
CMT074C	AU-specific RNA-binding enoyl-CoA hydratase	0.94	±	0.04
CMM074C	Hypothetical protein	0.94	±	0.05
CMG202C	Hypothetical protein	0.94	±	0.11
CMP233C	Hypothetical protein	0.94	±	0.08
CMN157C	Hypothetical protein	0.94	±	0.03
CMT222C	Unknown ring-finger protein	0.93	±	0.01
CMQ070C	Hypothetical protein	0.93	±	0.04
CME070C	Unknown [2Fe-2S] ferredoxin	0.93	±	0.15
CMG121C	Hypothetical protein	0.93	±	0.08
CMN151C	Probable ribonuclease R	0.93	±	0.20
CMR318C	Similar to nifu-like iron-sulfur cluster protein Isu1	0.93	±	0.02
CMB115C	Hypothetical protein	0.93	±	0.06
CML155C	ATP-dependent Clp protease proteolytic subunit	0.93	±	0.12
CMJ114C	Hypothetical protein	0.93	±	0.11
CMQ209C	MAP kinase	0.93	±	0.05
CMP096C	Similar to C-methyltransferase	0.93	±	0.17
CMI038C	Mg-protoporphyrin O-methyltransferase	0.93	±	0.11
CMS438C	Similar to pre-mRNA splicing factor U2AF large chain	0.93	±	0.08
CMP032C	Hypothetical protein	0.93	±	0.05
CMR069C	Hypothetical protein	0.93	±	0.04
CMM174C	Hypothetical protein	0.93	±	0.01
CMB008C	Hypothetical protein	0.93	±	0.13
CMR330C	Hypothetical protein	0.93	±	0.05
CMN286C	Sodium/hydrogen antiporter NHE8	0.93	±	0.04
CMQ125C	Probable transcriptional regulator, SIN3	0.93	±	0.09
CMJ112C	Vesicle coat complex COPII, subunit Sec13	0.93	±	0.06
CMO036C	Probable ATP dependent RNA helicase	0.93	±	0.05
CMF059C	Hypothetical protein	0.93	±	0.09
CMD096C	Similar to cytochrome P450 monooxygenase	0.93	±	0.10
CMS014C	Hypothetical protein	0.93	±	0.09
CMH177C	Similar to fructose-2,6-bisphosphatase	0.93	±	0.06
CMI212C	Similar to polyribonucleotide nucleotidyltransferase	0.93	±	0.10
CMQ283C	26S proteasome regulatory subunit	0.93	±	0.06
CMR140C	Similar to selenocysteine-specific elongation factor	0.93	±	0.08
CMH052C	Pyrophosphate--fructose-6-phosphate 1-phosphotransferase, beta subunit	0.93	±	0.19
CMQ410C	Hypothetical protein	0.93	±	0.04
CMT147C	Similar to protein N-methyltransferase	0.93	±	0.08
CMA101C	Probable maintenance of ploidy protein MOB1	0.93	±	0.06
CML058C	Excinuclease ABC subunit C	0.93	±	0.11
CMT530C	Similar to phenylamine binding protein, sterol isomerase	0.93	±	0.11

CMD106C	Hypothetical protein	0.93	±	0.10
CMQ252C	Nitrilase	0.93	±	0.04
CMS290C	Hypothetical protein	0.93	±	0.04
CMN205C	Hypothetical protein	0.93	±	0.14
CMT311C	Hypothetical protein	0.93	±	0.04
CMQ473C	Transmembrane 9 superfamily protein	0.93	±	0.03
CMK065C	Hypothetical protein	0.93	±	0.03
CMA068C	Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor	0.93	±	0.03
CML102C	Histone acetyltransferase HAC108/MYST	0.93	±	0.05
CME106C	Hypothetical protein	0.93	±	0.06
CMB126C	Dehydrodolichyl diphosphate synthase	0.93	±	0.08
CMH139C	Hypothetical protein	0.93	±	0.03
CMO024C	40S ribosomal protein S28	0.93	±	0.02
CMI172C	Unknown cyanobacterial protein	0.93	±	0.02
CMF159C	AAA-metalloprotease ftsh, mitochondrial precursor	0.93	±	0.08
CMT168C	Probable alpha-1,3-mannosyltransferase ALG2	0.93	±	0.04
CMS275C	Hypothetical protein	0.93	±	0.04
CMT012C	Similar to C3HC4 zinc-binding integral peroxisomal membrane protein PEX10	0.93	±	0.06
CMF024C	Hypothetical protein	0.93	±	0.07
CMN321C	Hypothetical protein	0.93	±	0.05
CMR135C	Hypothetical protein	0.93	±	0.09
CMT193C	Hypothetical protein	0.93	±	0.11
CMS079C	Hypothetical protein	0.93	±	0.03
CMQ129C	Unknown metyltransferase	0.93	±	0.02
CMN118C	Hypothetical protein	0.93	±	0.05
CMO088C	Hypothetical protein	0.93	±	0.02
CMM028C	Hypothetical protein	0.93	±	0.10
CMP310C	Probable WD repeat domain protein	0.93	±	0.06
CMT204C	4-alpha-glucanotransferase	0.93	±	0.08
CMM103C	Hypothetical protein	0.93	±	0.03
CMI088C	ATP-binding cassette, sub-family G	0.93	±	0.04
CMM150C	Similar to I kappa B kinase complex-associated protein	0.93	±	0.08
CMC155C	Hypothetical protein	0.93	±	0.08
CMT463C	Hypothetical protein	0.93	±	0.10
CMR271C	Hypothetical protein	0.93	±	0.08
CMI227C	Probable G2/mitotic-specific cyclin 1	0.93	±	0.04
CMB158C	Similar to trehalose synthase	0.93	±	0.04
CMJ044C	Phycocyanobilin lyase beta subuni	0.93	±	0.03
CMK210C	Cysteine--tRNA ligase, mitochondrial or chloroplast	0.93	±	0.05
CMO142C	Serine hydroxymethyltransferase, cytosolic (glycine hydroxymethyltransferase)	0.93	±	0.04
CMI049C	Fructose-1,6-biphosphate aldolase, chloroplast precursor	0.93	±	0.16
CMH179C	Similar to nucleoporin 155kDa	0.93	±	0.01
CMQ397C	Probable S-formylglutathione hydrolase	0.93	±	0.08

CMT381C	Enoyl-[acyl-carrier-protein] reductase [NADH]	0.92	±	0.09
CMS471C	Mitochondrial presequence translocase subunit Tim17	0.92	±	0.04
CMT269C	Probable MAP kinase kinase (MAP2K)	0.92	±	0.15
CME080C	Hypothetical protein	0.92	±	0.14
CME109C	Probable 1-acylglycerol-3-phosphate O-acyltransferase	0.92	±	0.07
CMO340C	Hypothetical protein	0.92	±	0.01
CMN325C	ATP-binding cassette, sub-family B (TAP), member 10, mitochondrial precursor	0.92	±	0.08
CMQ177C	Similar to ribosome biogenesis protein SSF1	0.92	±	0.06
CMS164C	Unknown kinase with aarF domain	0.92	±	0.02
CMR234C	DNA replication licensing factor MCM7	0.92	±	0.07
CMQ405C	Unknown protease	0.92	±	0.05
CMD165C	Hypothetical protein	0.92	±	0.09
CMI258C	Hypothetical protein	0.92	±	0.09
CMT171C	Hypothetical protein	0.92	±	0.06
CMF166C	Hypothetical protein	0.92	±	0.07
CMC049C	Similar to dtdp-4-dehydrorhamnose reductase	0.92	±	0.15
CMD015C	Raf-related MAP kinase kinase kinase (MAP3K), theta-type	0.92	±	0.04
CMR089C	Similar to Raf/ATN-like protein kinase	0.92	±	0.13
CMI219C	Hypothetical protein	0.92	±	0.16
CMR455C	Similar to serine dehydratase	0.92	±	0.07
CMB009C	Asparagine synthase	0.92	±	0.04
CMQ257C	Hypothetical protein	0.92	±	0.08
CMD068C	Hypothetical protein	0.92	±	0.05
CMM284C	Similar to DNA-damage-inducible protein P	0.92	±	0.05
CMQ355C	Hypothetical protein	0.92	±	0.05
CMQ016C	Hypothetical protein	0.92	±	0.11
CML098C	Cytochrome c oxidase (Complex IV) subunit Vb	0.92	±	0.08
CMT159C	40S ribosomal protein S8	0.92	±	0.01
CMS092C	Hypothetical protein	0.92	±	0.11
CMM163C	Hypothetical protein	0.92	±	0.04
CMT411C	Hypothetical protein	0.92	±	0.05
CMR474C	Undecaprenyl pyrophophate synthetase	0.92	±	0.02
CMJ163C	Hypothetical protein	0.92	±	0.01
CMT287C	Unknown zinc-finger protein	0.92	±	0.04
CMC133C	Similar to oxygen-evolving complex component psbQ	0.92	±	0.06
CMN326C	Similar to MAP kinase phosphatase-1	0.92	±	0.05
CML180C	Similar to 3'-5' exoribonuclease CSL4	0.92	±	0.07
CMN120C	Similar to Vacuolar protein sorting-associated protein VPS28	0.92	±	0.09
CMS254C	Similar to triacylglycerol lipase	0.92	±	0.13
CML104C	Similar to nuclear prelamin A recognition factor	0.92	±	0.06
CMH007C	Hypothetical protein	0.92	±	0.07
CMI165C	Similar to endoplasmic reticulum resident protein	0.92	±	0.05
CML056C	Hypothetical protein	0.92	±	0.06

CMS308C	Unknown suger epimerase	0.92	±	0.07
CMS436C	Hypothetical protein	0.92	±	0.07
CMN251C	ATP-binding cassette, sub-family C (MRP), member 1	0.92	±	0.05
CMF174C	Similar to tight junction plaque protein Symplekin	0.92	±	0.05
CMS323C	Hypothetical protein	0.92	±	0.02
CMI292C	Branchpoint bridging protein Msl5p	0.92	±	0.04
CMP017C	Probable CGI-27 protein	0.92	±	0.14
CMS320C	Similar to inositol 1,3,4-trisphosphate 5/6-kinase	0.92	±	0.06
CML150C	Prokaryote-type translation initiation factor IF-2	0.92	±	0.05
CMO297C	Hypothetical protein	0.92	±	0.07
CMC132C	Mitochondrial ribosomal protein L15 precursor	0.92	±	0.04
CMJ097C	Hypothetical protein	0.92	±	0.07
CMM015C	Hypothetical protein	0.92	±	0.05
CMN068C	Similar to U3 snoRNP protein Utp20p	0.92	±	0.10
CMB124C	Hypothetical protein	0.92	±	0.08
CMR316C	Hypothetical protein	0.92	±	0.06
CMM048C	Pre-mRNA splicing factor ATP-dependent RNA helicase PRP43	0.92	±	0.04
CMT255C	Hypothetical protein	0.92	±	0.08
CMT549C	Hypothetical protein	0.92	±	0.08
CML133C	26S proteasome regulatory module subunit	0.92	±	0.04
CMR244C	Probable dehydrogenase	0.92	±	0.19
CMT088C	Hypothetical protein	0.92	±	0.05
CMN283C	Hypothetical protein	0.92	±	0.08
CMI157C	ATP-dependent zinc protease	0.92	±	0.04
CMI177C	Hypothetical protein	0.92	±	0.04
CMO186C	Hypothetical protein	0.92	±	0.10
CMP237C	Similar to UDP N-acetylclucosamine transporter	0.92	±	0.02
CMI290C	Manganese-stabilzing protein precursor	0.92	±	0.03
CMT257C	Small GTP-binding protein of Ran family	0.92	±	0.07
CMM290C	Hypothetical protein	0.92	±	0.02
CMO184C	Similar to hedgehog protein	0.92	±	0.02
CMN297C	Hypothetical protein	0.92	±	0.06
CMB028C	Unknown bromodomain-containing protein	0.91	±	0.10
CMP019C	Hypothetical protein	0.91	±	0.07
CMQ072C	Hypothetical protein	0.91	±	0.07
CMT035C	Hypothetical protein	0.91	±	0.02
CMN086C	Hypothetical protein	0.91	±	0.01
CMQ365C	Phosphoribosylformylglycinamidine synthase	0.91	±	0.04
CMQ268C	Hypothetical protein	0.91	±	0.05
CMJ067C	Hypothetical protein	0.91	±	0.17
CMQ421C	Mitochondrial ribosomal protein L4 precursor	0.91	±	0.03
CMT376C	Exosome complex exonuclease Rrp4	0.91	±	0.06
CMJ115C	Hypothetical protein	0.91	±	0.02

CMN072C	Similar to mitochondrial distribution and morphology mutant Mdm38	0.91	±	0.12
CMQ290C	Probable DNA mismatch repair protein MLH1	0.91	±	0.06
CMA085C	Hypothetical protein	0.91	±	0.02
CMH146C	Polyribonucleotide nucleotidyltransferase	0.91	±	0.15
CMN150C	Probable adenylate kinase	0.91	±	0.04
CMP320C	Hypothetical protein	0.91	±	0.04
CMD017C	Hypothetical protein	0.91	±	0.03
CMS076C	Hypothetical protein	0.91	±	0.04
CMR479C	P68 RNA helicase	0.91	±	0.13
CMM058C	Hypothetical protein	0.91	±	0.03
CMS208C	Threonine--tRNA ligase, cytoplasmic	0.91	±	0.01
CMD117C	Similar to enhancer of polycomb	0.91	±	0.08
CMR358C	Hypothetical protein	0.91	±	0.08
CME190C	Mitochondrial ribosomal protein L19 precursor	0.91	±	0.08
CMN334C	Hypothetical protein	0.91	±	0.02
CMS348C	Hypothetical protein	0.91	±	0.06
CMM040C	60S ribosomal protein L30	0.91	±	0.10
CMR378C	Hypothetical protein	0.91	±	0.07
CMT405C	Unknown hydrolase	0.91	±	0.03
CMB032C	Chloroplast ribosomal protein S21 precursor	0.91	±	0.02
CMC010C	Similar to U3 snoRNP component Imp3p	0.91	±	0.14
CMT110C	Sulfate adenylyltransferase	0.91	±	0.16
CMC020C	Probable cytosolic IMP-GMP specific 5'-nucleotidase	0.91	±	0.04
CMF147C	Hypothetical protein	0.91	±	0.11
CMS386C	Anaphase promoting complex subunit 11	0.91	±	0.01
CMC102C	Similar to anaphase-promoting complex subunit 2	0.91	±	0.04
CMI218C	Hypothetical protein	0.91	±	0.04
CMD146C	Similar to 3-oxo-5-alpha-steroid 4-dehydrogenase	0.91	±	0.02
CMP118C	E3 ubiquitin ligase SCF complex SKP1 subunit	0.91	±	0.05
CMB094C	Similar to membrane protein	0.91	±	0.09
CMF105C	Similar to mtn3-like protein	0.91	±	0.02
CMK263C	Plastid envelope protein CRUMPLED LEAF	0.91	±	0.08
CMG063C	Similar to RNA helicase II binding protein	0.91	±	0.04
CMA107C	Probable proline aminopeptidase P	0.91	±	0.07
CMS034C	Probable structure specific recognition protein, recombination signal sequence recognition protein, chromatin-specific transcription elongation factor	0.91	±	0.09
CMT578C	Similar to methylated-DNA--protein-cysteine methyltransferase	0.91	±	0.03
CMO029C	Hypothetical protein	0.91	±	0.09
CMS194C	Similar to cell polarity protein alp13	0.91	±	0.07
CMR088C	Hypothetical protein	0.91	±	0.07
CMN112C	Mitochondrial ribosomal protein L23 precursor	0.91	±	0.03
CMK070C	Hypothetical protein	0.91	±	0.07
CMS029C	Similar to RNA guanylyltransferase and 5'-phosphatase	0.91	±	0.06
CMO152C	Signal recognition particle recognition component SRP54	0.91	±	0.10

CMT339C	Hypothetical protein	0.91	±	0.04
CMO325C	Hypothetical protein	0.91	±	0.09
CMA116C	Hypothetical protein	0.91	±	0.12
CMQ286C	DNA primase, bacterial-type	0.91	±	0.03
CMS360C	Hypothetical protein	0.91	±	0.04
CMG194C	Similar to phosphoribosylanthranilate isomerase	0.91	±	0.04
CMA028C	Hypothetical protein	0.91	±	0.08
CME147C	Hypothetical protein	0.91	±	0.09
CME031C	Hypothetical protein	0.91	±	0.03
CMT117C	Probable hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase II) (GLX II)	0.91	±	0.06
CMM134C	Hypothetical protein	0.91	±	0.18
CMR295C	Hypothetical protein	0.91	±	0.05
CMQ230C	Diaminopimelate epimerase	0.91	±	0.02
CMO210C	Hypothetical protein	0.91	±	0.09
CMR412C	Hypothetical protein	0.91	±	0.02
CMD163C	Probable molybdopterin converting factor small subunit MoaD	0.91	±	0.01
CMS377C	Casein kinase I	0.91	±	0.02
CMN031C	Similar to glucosamine-phosphate N-acetyltransferase	0.91	±	0.04
CMS116C	Similar to protein transport protein SEC61 gamma subunit	0.91	±	0.04
CMP178C	Similar to ubiquitin conjugating enzyme E2	0.91	±	0.07
CMT154C	40S ribosomal protein S6	0.91	±	0.01
CMN039C	Probable endopeptidase IV, signal peptide peptidase, SppA	0.91	±	0.03
CMH075C	Similar to mitochondrial carrier protein	0.91	±	0.08
CMM070C	Similar to decapping enzyme complex component DCP1	0.91	±	0.06
CMH050C	Hypothetical protein	0.91	±	0.05
CMI007C	Hypothetical protein	0.91	±	0.07
CMT041C	Hypothetical protein	0.91	±	0.04
CMK058C	Geranylgeranyl diphosphate synthase, chloroplast precursor	0.91	±	0.02
CMR211C	Similar to DnaJ-like protein Jem1p	0.91	±	0.03
CMM206C	Similar to trefoil factor	0.91	±	0.03
CMK282C	Hypothetical protein	0.91	±	0.02
CMH115C	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	0.91	±	0.02
CMH026C	Similar to (N6-adenosine)-methyltransferase	0.91	±	0.02
CMD062C	Small GTP-binding protein of Rab family	0.91	±	0.09
CMD104C	Delta-aminolevulinic acid dehydratase (porphobilinogen synthase)	0.91	±	0.09
CMP164C	Similar to ribonuclease III (rnc)	0.91	±	0.16
CMN014C	Probable serine palmitoyltransferase	0.91	±	0.05
CML137C	ATP-dependent RNA helicase	0.91	±	0.09
CMD143C	Hypothetical protein	0.91	±	0.04
CMK205C	RNA lariat debranching enzyme	0.91	±	0.05
CMR021C	Adaptor-related protein complex 2, beta subunit	0.91	±	0.02
CMT286C	Hypothetical protein	0.91	±	0.03
CMJ100C	Similar to heat shock protein, low molwcular weight	0.91	±	0.03

CMO040C	Hypothetical protein	0.91	±	0.15
CMS146C	Similar to receptor lectin kinase 3	0.91	±	0.07
CMC077C	Probable 1-aminocyclopropane-1-carboxylate deaminase	0.91	±	0.08
CMH107C	Ubiquinone biosynthesis protein COQ7	0.91	±	0.04
CMR117C	4-aminobutyrate aminotransferase	0.91	±	0.09
CMD081C	Probable O-sialoglycoprotein endopeptidase	0.91	±	0.04
CMK154C	Hypothetical protein	0.91	±	0.07
CMP321C	Similar to anaphase-promoting complex subunit 10	0.91	±	0.02
CMP022C	Hypothetical protein	0.91	±	0.02
CMB092C	Flavin-dependent tRNA:m5U methyltransferase trmFO	0.91	±	0.05
CMJ244C	Hypothetical protein	0.91	±	0.09
CMG214C	Hypothetical protein	0.91	±	0.03
CMT503C	Hypothetical protein	0.91	±	0.05
CME142C	Similar to retinoblastoma binding protein 2	0.90	±	0.04
CMQ245C	Hypothetical protein	0.90	±	0.09
CMC091C	NADH dehydrogenase I (Complex I) alpha subcomplex 9	0.90	±	0.05
CMT564C	Hypothetical protein	0.90	±	0.06
CMJ177C	Hypothetical protein	0.90	±	0.03
CMS118C	Hypothetical protein	0.90	±	0.07
CMJ247C	Hypothetical protein	0.90	±	0.08
CMT568C	Hypothetical protein	0.90	±	0.06
CMT343C	Unknown methyl transferase	0.90	±	0.07
CMI217C	Hypothetical protein	0.90	±	0.13
CMS234C	Hypothetical protein	0.90	±	0.00
CMI248C	Photosystem II 12 kDa extrinsic protein	0.90	±	0.06
CMI257C	Hypothetical protein	0.90	±	0.06
CMQ249C	Hypothetical protein	0.90	±	0.07
CMQ472C	Similar to chromatin accessibility complex 1	0.90	±	0.03
CMK269C	Fusion protein of 3-dehydroquinate dehydratase and shikimate 5-dehydrogenase	0.90	±	0.04
CMF090C	Probable phosphatidylethanolamine methyltransferase	0.90	±	0.09
CMP044C	Hypothetical protein	0.90	±	0.02
CMH074C	Ubiquitin-specific protease UBP15	0.90	±	0.05
CMK237C	Hypothetical protein	0.90	±	0.08
CMH083C	Similar to mutator MutT protein	0.90	±	0.09
CMJ272C	Phosphoglucomutase	0.90	±	0.10
CME048C	Hypothetical protein	0.90	±	0.02
CMQ306C	Similar to ribosomal protein L11 methyltransferase	0.90	±	0.05
CMF060C	Similar to dishevelled associated activator of morphogenesis	0.90	±	0.06
CMR255C	Probable inorganic pyrophosphatase precursor	0.90	±	0.07
CMT224C	Probable ubiquitin-specific protease	0.90	±	0.05
CMA009C	NAD-dependent sorbitol dehydrogenase	0.90	±	0.01
CME005C	Hypothetical protein	0.90	±	0.04
CMR113C	Hypothetical protein	0.90	±	0.09

CMN016C	Hypothetical protein	0.90	±	0.02
CMJ095C	Hypothetical protein	0.90	±	0.07
CMK255C	Hypothetical protein	0.90	±	0.03
CMJ199C	Similar to UMP/CMP kinase	0.90	±	0.04
CMR062C	Hypothetical protein	0.90	±	0.04
CMR391C	Hypothetical protein	0.90	±	0.06
CMN081C	Hypothetical protein	0.90	±	0.05
CMM201C	Hypothetical protein	0.90	±	0.01
CMF042C	Similar to programed cell death protein 5 (TFAR19)	0.90	±	0.07
CMS366C	Hypothetical protein	0.90	±	0.08
CMK120C	Hypothetical protein	0.90	±	0.01
CMJ141C	ATP-dependent Clp protease proteolytic subunit	0.90	±	0.06
CMH142C	Hypothetical protein	0.90	±	0.03
CMD171C	Probable N-ethylammeline chlorohydrolase	0.90	±	0.03
CMR105C	Hypothetical protein	0.90	±	0.09
CMQ053C	5-amino-6-(5-phosphoribosylamino)uracil reductase	0.90	±	0.05
CML318C	Hypothetical protein	0.90	±	0.08
CMK272C	Hypothetical protein	0.90	±	0.02
CMA083C	Hypothetical protein	0.90	±	0.06
CMQ362C	Hypothetical protein	0.90	±	0.04
CMH166C	DNA gyrase subunit B	0.90	±	0.10
CMN309C	Hypothetical protein	0.90	±	0.07
CMT087C	Similar to DNA replication licensing factor MCM8	0.90	±	0.08
CMN231C	Similar to tRNA intron endonuclease	0.90	±	0.08
CMD057C	Hypothetical protein	0.90	±	0.12
CML232C	RIM15-like serine/threonine kinase	0.90	±	0.11
CMH064C	Similar to guanine nucleotide exchange factor	0.90	±	0.15
CMP002C	Similar to hedgehog protein	0.90	±	0.11
CMM205C	Hypothetical protein	0.90	±	0.05
CMI223C	Retroelement	0.90	±	0.03
CMP339C	Similar to Golgi vesicular membrane trafficking protein Bet1p	0.90	±	0.05
CMS226C	Hypothetical protein	0.90	±	0.06
CMS077C	Hypothetical protein	0.90	±	0.05
CMQ001C	Similar to dolichyl-phosphate-mannose:protein mannosyltransferase	0.90	±	0.06
CMT201C	Hypothetical protein	0.90	±	0.14
CMS267C	Phosphatidylinositol 4-kinase	0.90	±	0.05
CMM274C	Lysine--tRNA ligase, cytoplasmic	0.90	±	0.07
CMT115C	Similar to transcriptional coactivator p100	0.90	±	0.07
CMD142C	Hypothetical protein	0.90	±	0.05
CMK283C	Hypothetical protein	0.90	±	0.05
CMG087C	Similar to lysosomal sphingomyelin phosphodiesterase	0.90	±	0.03
CMS394C	Hypothetical protein	0.90	±	0.09
CMT382C	Hypothetical protein	0.90	±	0.08

CMT285C	Phosphoglucomutase	0.90	±	0.18
CMN046C	Sporulation-induced transcript 4-associated protein SAPLb	0.90	±	0.05
CMP274C	Hypothetical protein	0.90	±	0.13
CMQ017C	Hypothetical protein	0.90	±	0.03
CMM012C	Ring finger protein	0.90	±	0.06
CMT583C	RNA polymerase II subunit	0.90	±	0.07
CMG129C	MYB-related protein	0.90	±	0.07
CMP186C	Hypothetical protein	0.90	±	0.04
CMC069C	Hypothetical protein	0.90	±	0.02
CMR100C	Similar to mannose-P-dolichol utilization defect 1 protein	0.90	±	0.07
CML117C	Hypothetical protein	0.90	±	0.04
CMH072C	Hypothetical protein	0.90	±	0.04
CMD008C	Hypothetical protein	0.90	±	0.04
CML126C	Similar to indoleglycerol phosphate synthase	0.90	±	0.03
CMT331C	Hypothetical protein	0.90	±	0.07
CMN030C	Hypothetical protein	0.90	±	0.04
CMD167C	Hypothetical protein	0.90	±	0.05
CMJ036C	Cytochrome c oxidase (Complex IV) subunit VIa	0.90	±	0.06
CMG188C	20S core proteasome subunit beta 3	0.90	±	0.11
CMI013C	Hypothetical protein	0.90	±	0.02
CMO202C	Coatomer protein complex, subunit delta	0.90	±	0.02
CMR141C	Hypothetical protein	0.90	±	0.09
CMJ076C	Similar to coenzyme F420-reducing hydrogenase, beta subunit	0.90	±	0.06
CMA007C	Serine acetyltransferase (SAT)	0.90	±	0.12
CMG066C	Aspartate aminotransferase, HisC in bacteria	0.89	±	0.03
CMR030C	Probable membrane-associated zinc metalloprotease	0.89	±	0.04
CMF050C	Similar to ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase	0.89	±	0.07
CMO281C	Vacuolar protein sorting-associated protein Vps4p	0.89	±	0.07
CMR213C	Mitochondrial intermembrane space complex subunit Tim9	0.89	±	0.13
CMN049C	Similar to formin	0.89	±	0.02
CMR038C	Hypothetical protein	0.89	±	0.07
CML144C	Hypothetical protein	0.89	±	0.04
CMQ175C	Mitochondrial ribosomal protein S9 precursor	0.89	±	0.02
CMR033C	Hypothetical protein	0.89	±	0.03
CMQ225C	20S core proteasome subunit alpha 5	0.89	±	0.06
CMT166C	Hypothetical protein	0.89	±	0.03
CMO137C	Probable DNA replication licensing factor MCM2	0.89	±	0.03
CMR351C	Hypothetical protein	0.89	±	0.05
CML064C	Hypothetical protein	0.89	±	0.03
CMB004C	40S ribosomal protein S18	0.89	±	0.06
CMA091C	Hypothetical protein	0.89	±	0.05
CMR204C	Hypothetical protein	0.89	±	0.10
CMD044C	Hypothetical protein	0.89	±	0.06

CMA011C	Probable aminoacylase I	0.89	±	0.06
CMB085C	Hypothetical protein	0.89	±	0.13
CME058C	Hypothetical protein	0.89	±	0.03
CMJ241C	Hypothetical protein	0.89	±	0.06
CMM209C	Hypothetical protein	0.89	±	0.08
CMJ256C	Hypothetical protein	0.89	±	0.05
CMG169C	Probable RNA polymerase II subunit I	0.89	±	0.08
CMQ018C	Hypothetical protein	0.89	±	0.07
CMH106C	Hypothetical protein	0.89	±	0.09
CMR077C	Ubiquitin-protein ligase E3	0.89	±	0.02
CMA103C	Raf-related MAP kinase kinase kinase (MAP3K), theta-type	0.89	±	0.11
CMA046C	Hypothetical protein	0.89	±	0.04
CMF108C	Similar to cleavage stimulation factor subunit 2	0.89	±	0.05
CMT180C	Manganese transport protein	0.89	±	0.09
CML093C	Similar to TPR (tetratricopeptide repeat) protein	0.89	±	0.03
CMM097C	Hypothetical protein	0.89	±	0.03
CMO189C	Similar to ubiquinone biosynthesis protein COQ4	0.89	±	0.02
CMR462C	Hypothetical protein	0.89	±	0.04
CMG187C	Hypothetical protein	0.89	±	0.06
CMB154C	Unknown alpha/beta hydrolase	0.89	±	0.04
CMM222C	Similar to mitochondrial carrier protein	0.89	±	0.05
CMJ276C	Hypothetical protein	0.89	±	0.08
CMQ457C	Raf-related MAP kinase kinase kinase (MAP3K), delta-type	0.89	±	0.02
CMT437C	Hypothetical protein	0.89	±	0.04
CMS387C	Similar to PRIP-interacting protein with methyltransferase domain	0.89	±	0.05
CMI288C	Hypothetical protein	0.89	±	0.02
CMO351C	Hypothetical protein	0.89	±	0.05
CMK256C	Hypothetical protein	0.89	±	0.10
CMQ332C	Unknown heme-binding protein	0.89	±	0.09
CMJ149C	Hypothetical protein	0.89	±	0.14
CMT218C	Temperature sensitive supressor Bem46	0.89	±	0.09
CMQ182C	Hypothetical protein	0.89	±	0.04
CMK134C	Hypothetical protein	0.89	±	0.03
CMQ287C	Hypothetical protein	0.89	±	0.03
CMS383C	Similar to methyl transferase	0.89	±	0.05
CMO055C	Unknown nucleotide sugar transporter	0.89	±	0.04
CMK156C	Similar to rRNA methylase SpoU	0.89	±	0.12
CMP122C	Unknown kinase with aarF domain	0.89	±	0.04
CMP280C	Hypothetical protein	0.89	±	0.02
CMS046C	Hypothetical protein	0.89	±	0.07
CMC052C	Hypothetical protein	0.89	±	0.09
CMM263C	DNA topoisomerase	0.89	±	0.04
CMR191C	Hypothetical protein	0.89	±	0.08

CMR072C	Hypothetical protein	0.89	±	0.07
CMQ237C	V-type ATPase V1 subunit F	0.89	±	0.04
CMQ452C	Hypothetical protein	0.89	±	0.07
CMQ168C	Similar to glutathione-S-transferase	0.89	±	0.08
CML080C	Acyl-CoA dehydrogenase, mitochondrial precursor	0.89	±	0.02
CMR087C	Hypothetical protein	0.89	±	0.06
CMC150C	Cytosolic ascorbate hydrogen peroxidase	0.89	±	0.08
CMF169C	Hypothetical protein	0.89	±	0.03
CMP007C	40S ribosomal protein S16	0.89	±	0.03
CMF114C	Probable calcium/calmodulin-dependent protein kinase kinase	0.89	±	0.04
CMA070C	Hypothetical protein	0.89	±	0.12
CMM229C	3-isopropylmalate dehydrogenase	0.89	±	0.15
CMP057C	Hypothetical protein	0.89	±	0.07
CMH092C	Hypothetical protein	0.89	±	0.08
CMQ038C	Similar to ubiquitin conjugating enzyme E2	0.89	±	0.03
CMS124C	Valosin-containing protein	0.89	±	0.02
CMM078C	Similar to Gbp1p protein	0.89	±	0.09
CMP235C	Probable arsenite translocating ATPase	0.89	±	0.08
CML128C	tRNA nucleotidyltransferase	0.89	±	0.12
CMS189C	40S ribosomal protein S3A	0.89	±	0.03
CMM036C	Hypothetical protein	0.89	±	0.03
CMG180C	Similar to key negative regulator of the Notch pathway SEL1L	0.89	±	0.07
CMJ080C	Similar to tRNA modification enzyme Trm5	0.89	±	0.10
CMC125C	Heat shock protein 101	0.89	±	0.12
CMQ210C	Chorismate mutase	0.89	±	0.08
CMA132C	Unknown metallopeptidase	0.89	±	0.06
CMC067C	Hypothetical protein	0.89	±	0.09
CMK144C	Hypothetical protein	0.89	±	0.06
CMS248C	DEAD/H box protein	0.89	±	0.17
CMM080C	Similar to trefoil factor	0.89	±	0.07
CMR487C	Hypothetical protein	0.89	±	0.03
CMO341C	Similar to protease	0.89	±	0.09
CMT284C	Similar to permease involved in the uptake of glycerophosphoinositol Git1p	0.89	±	0.06
CMH073C	Hypothetical protein	0.89	±	0.03
CMF057C	Hypothetical protein	0.89	±	0.09
CMP102C	Hypothetical protein	0.89	±	0.03
CMI205C	60S ribosomal protein L24	0.89	±	0.05
CMK181C	Hypothetical protein	0.89	±	0.04
CMA079C	Similar to actin-binding protein frabin	0.89	±	0.04
CMP155C	Hypothetical protein	0.88	±	0.03
CMJ139C	Tyrosine--tRNA ligase	0.88	±	0.12
CMJ050C	Hypothetical protein	0.88	±	0.06
CMP291C	Hypothetical protein	0.88	±	0.09

CMT498C	Hypothetical protein	0.88	±	0.07
CMB071C	Bromodomain protein 103	0.88	±	0.04
CMO163C	Similar to initiator tRNA phosphoribosyl-transferase	0.88	±	0.14
CMI261C	Hypothetical protein	0.88	±	0.12
CMP236C	Hypothetical protein	0.88	±	0.07
CMS488C	Similar to glucose-6-phosphate/phosphate translocator	0.88	±	0.04
CMT328C	Serine/threonine kinase KIN82	0.88	±	0.03
CMQ059C	Hypothetical protein	0.88	±	0.02
CMQ183C	Hypothetical protein	0.88	±	0.06
CMS324C	Hypothetical protein	0.88	±	0.03
CMK288C	Probable potassium transporter	0.88	±	0.09
CML087C	Hypothetical protein	0.88	±	0.05
CME193C	Hypothetical protein	0.88	±	0.08
CMK233C	Hypothetical protein	0.88	±	0.05
CMP046C	Probable mycolic acid methyl transferase	0.88	±	0.09
CMF115C	Hypothetical protein	0.88	±	0.03
CMG179C	RNA polymerase III largest subunit	0.88	±	0.08
CMR083C	Similar to NADH:ubiquinone oxidoreductase b17.2 subunit	0.88	±	0.08
CMR374C	Similar to RNA helicase with DEAD motif	0.88	±	0.03
CMM154C	Unknown metalloprotease	0.88	±	0.05
CMM031C	Hypothetical protein	0.88	±	0.03
CMT467C	Probable GDP-fucose transporter	0.88	±	0.12
CMC032C	Hypothetical protein	0.88	±	0.02
CMH248C	Hypothetical protein	0.88	±	0.06
CMH019C	Similar to UVB-resistance protein UVR8	0.88	±	0.08
CMM221C	Hypothetical protein	0.88	±	0.02
CMP335C	Box C/D snoRNP and U4 snRNP component Snu13p	0.88	±	0.13
CMP275C	Probable 24-sterol C-methyltransferase	0.88	±	0.01
CMK151C	Phytoene desaturase	0.88	±	0.06
CMF170C	Vesicle coat complex COPII, subunit Sec23	0.88	±	0.05
CMM245C	Similar to RING finger-like protein	0.88	±	0.02
CMR400C	Unknown kinase with aarF domain	0.88	±	0.02
CMM138C	Similar to cyclin dependent kinase	0.88	±	0.07
CMA124C	Probable cell division protein glsA	0.88	±	0.08
CMS026C	Hypothetical protein	0.88	±	0.04
CMQ185C	Box C/D snoRNP component Nop56	0.88	±	0.15
CMT608C	SEC14 protein (PI/PC transfer protein)	0.88	±	0.08
CMI139C	Hypothetical protein	0.88	±	0.06
CMT368C	Similar to oxygen-evolving complex component psbP	0.88	±	0.08
CMG043C	Tryptophane--tRNA ligase, cytoplasmic	0.88	±	0.02
CMG152C	Hypothetical protein	0.88	±	0.03
CMH063C	Similar to Surfeit 1, a protein involved in cytochrome c oxidase assembly	0.88	±	0.05
CME030C	Unknown RING finger protein	0.88	±	0.15

CMQ264C	Glycerol-3-phosphate transporter	0.88	±	0.14
CMS117C	Similar to alpha-1,2 glucosyltransferase	0.88	±	0.02
CMD084C	Chloroplast translation initiation factor IF-1	0.88	±	0.04
CMK033C	Hypothetical protein	0.88	±	0.08
CMP050C	Hypothetical protein	0.88	±	0.10
CMQ035C	Similar to exosome complex exonuclease RRP45	0.88	±	0.10
CML139C	Hypothetical protein	0.88	±	0.03
CMM237C	Actin	0.88	±	0.03
CMC025C	Succinyl-diaminopimelate desuccinylase	0.88	±	0.06
CMJ230C	Similar to GTPase activating protein	0.88	±	0.03
CMG213C	Probable proline dehydrogenase	0.88	±	0.06
CMT470C	Hypothetical protein	0.88	±	0.11
CMQ026C	Ubiquitin carboxy-terminal hydrolase (UCH) L3	0.88	±	0.04
CMT273C	Type II DNA topoisomerase VI subunit B	0.88	±	0.04
CMO248C	Hypothetical protein	0.88	±	0.03
CMI173C	Hypothetical protein	0.88	±	0.05
CMI295C	Phenylalanine--tRNA ligase alpha subunit	0.88	±	0.07
CMR329C	Similar to 67 kDa integral membrane protein; Rft1p	0.88	±	0.09
CMQ236C	Hypothetical protein	0.88	±	0.08
CMH164C	Hypothetical protein	0.88	±	0.03
CMQ395C	Proteasome regulatory particle subunit	0.88	±	0.06
CMS416C	ATP-dependent RNA helicase	0.88	±	0.03
CMH238C	Similar to glucose-6-phosphate/phosphate translocator	0.88	±	0.17
CMI062C	Hypothetical protein	0.88	±	0.01
CMT561C	Aconitate hydratase	0.88	±	0.02
CMM143C	Hypothetical protein	0.88	±	0.03
CMR159C	Similar to COP9 signalosome subunit Csn2	0.88	±	0.06
CMA001C	Similar to trefoil factor	0.88	±	0.07
CMS221C	Similar to nuclear receptor binding factor 1	0.88	±	0.05
CML302C	Hypothetical protein	0.88	±	0.06
CMO070C	Kinesin-related protein	0.88	±	0.05
CMJ029C	Hypothetical protein	0.88	±	0.07
CMT169C	Methionyl aminopeptidase	0.88	±	0.09
CMR490C	Hypothetical protein	0.88	±	0.01
CMR380C	Fusion protein of glyoxysomal fatty acid oxidation tetrafunctional protein, and acetyl-CoA acyltransferase	0.88	±	0.03
CMO018C	Ubiquitin carboxy-terminal hydrolase (UCH) L5	0.88	±	0.06
CMR359C	Hypothetical protein	0.88	±	0.07
CMF104C	Similar to Tsi1-interacting protein TSIP1	0.88	±	0.05
CMP099C	Hypothetical protein	0.88	±	0.04
CML079C	Valine-pyruvate transaminase	0.88	±	0.05
CMB039C	Hypothetical protein	0.88	±	0.04
CMT093C	Shikimate kinase	0.88	±	0.05
CMQ312C	Hypothetical protein	0.88	±	0.05

CMG131C	Hypothetical protein	0.88	±	0.05
CMK166C	Glucosamine--fructose-6-phosphate aminotransferase	0.88	±	0.03
CMM214C	Hypothetical protein	0.88	±	0.08
CME024C	DNA-directed RNA polymerase I subunit	0.88	±	0.02
CMM282C	Rub1-activating enzyme E1 C subunit	0.88	±	0.10
CMQ098C	DNA polymerase epsilon homolog	0.88	±	0.08
CMB102C	Hypothetical protein	0.87	±	0.08
CMH131C	Similar to basal transcription factor ABT1	0.87	±	0.01
CMS119C	Similar to Stat3-interacting protein	0.87	±	0.08
CMM093C	Hypothetical protein	0.87	±	0.04
CMR027C	Hypothetical protein	0.87	±	0.04
CMT054C	Hypothetical protein	0.87	±	0.03
CMT151C	Similar to triacylglycerol lipase	0.87	±	0.05
CMO173C	Similar to Raf-related MAP kinase kinase kinase (MAP3K)	0.87	±	0.04
CMF073C	Probable high-affinity potassium transporter	0.87	±	0.03
CMQ176C	ATP-binding cassette, sub-family B, member 7, mitochondrial precursor	0.87	±	0.03
CMJ037C	Probable GTP-binding protein	0.87	±	0.10
CMF142C	Hypothetical protein	0.87	±	0.07
CMT068C	Hypothetical protein	0.87	±	0.02
CMK081C	TATA-box binding protein-associated factor 6	0.87	±	0.11
CMH153C	Probable leucine aminopeptidase	0.87	±	0.03
CMS472C	Hypothetical protein	0.87	±	0.04
CMB113C	Hypothetical protein	0.87	±	0.10
CMT083C	Similar to uridine-monophosphate kinase (uridylate kinase); Ura6p	0.87	±	0.03
CMK090C	Hypothetical protein	0.87	±	0.08
CMQ133C	Probable CLC-type chloride channel	0.87	±	0.05
CMJ237C	Hypothetical protein	0.87	±	0.21
CMR312C	Hypothetical protein	0.87	±	0.06
CMS492C	Hypothetical protein	0.87	±	0.01
CMF083C	Adaptor-related protein complex 1, gamma subunit	0.87	±	0.10
CMG155C	Hypothetical protein	0.87	±	0.09
CMM307C	Similar to DNA binding protein, dead ringer	0.87	±	0.03
CML185C	Serine protease	0.87	±	0.05
CMG166C	Fructokinase	0.87	±	0.06
CMD133C	ATP-binding cassette, sub-family C (MRP), member 2	0.87	±	0.05
CMQ222C	Zn-dependent peptidase	0.87	±	0.08
CMB093C	Magnesium chelatase subunit H	0.87	±	0.04
CMO106C	Hypothetical protein	0.87	±	0.03
CMG167C	Cell cycle controlling protein kinase RIO	0.87	±	0.04
CMA037C	Hypothetical protein	0.87	±	0.08
CMP151C	Unknown DNA-binding protein	0.87	±	0.02
CMB072C	Similar to cell polarity protein tea1p	0.87	±	0.05
CMO075C	RNA polymerase III subunit	0.87	±	0.04

CMI044C	Similar to vacuolar sorting protein SNF7	0.87	±	0.04
CMO128C	Transketolase	0.87	±	0.11
CMO227C	Hypothetical protein	0.87	±	0.07
CMM037C	Hypothetical protein	0.87	±	0.08
CMN108C	Similar to 60S ribosomal subunit biogenesis protein Nip7p	0.87	±	0.11
CMO187C	Heat shock transcription factor	0.87	±	0.08
CMH005C	Hypothetical protein	0.87	±	0.04
CMK149C	Hypothetical protein	0.87	±	0.03
CMT249C	Similar to S-M checkpoint control protein Rad4p	0.87	±	0.06
CMK092C	Hypothetical protein	0.87	±	0.03
CMG133C	Excinuclease ABC subunit B	0.87	±	0.07
CMS176C	Hypothetical protein	0.87	±	0.13
CMP136C	Hypothetical protein	0.87	±	0.10
CMK212C	Similar to bromodomain containing transcription factor	0.87	±	0.03
CMA080C	Hypothetical protein	0.87	±	0.06
CMD016C	Hypothetical protein	0.87	±	0.03
CMM009C	Hypothetical protein	0.87	±	0.03
CMR118C	Similar to polynucleotide phosphorylase	0.87	±	0.15
CMT395C	Methionyl aminopeptidase	0.87	±	0.06
CMP187C	Hypothetical protein	0.87	±	0.05
CMI198C	Probable ubiquitin fusion degradation protein Ufd4p	0.87	±	0.09
CMO115C	Hypothetical protein	0.87	±	0.06
CMB014C	Similar to ubiquitin-conjugating enzyme E2	0.87	±	0.06
CMD033C	Similar to periplasmic alpha-amylase precursor	0.87	±	0.05
CMR059C	Hypothetical protein	0.87	±	0.06
CMN256C	Reverse transcriptase	0.87	±	0.08
CMT265C	Hypothetical protein	0.87	±	0.03
CMP034C	Hypothetical protein	0.87	±	0.08
CMF040C	Hypothetical protein	0.87	±	0.02
CMO274C	V-type ATPase V0 subunit d	0.87	±	0.07
CMQ228C	Similar to intermediate filament binding protein, plectin (human), trichohyalin (sheep)	0.87	±	0.03
CMG039C	Aspartyl aminopeptidase	0.87	±	0.08
CMR361C	Hypothetical protein	0.87	±	0.11
CMD034C	Hypothetical protein	0.87	±	0.05
CMI130C	Probable zinc protease	0.87	±	0.06
CMT441C	Hypothetical protein	0.87	±	0.04
CMQ462C	Hypothetical protein	0.87	±	0.05
CMS497C	Hypothetical protein	0.87	±	0.04
CMP135C	Hypothetical protein	0.87	±	0.05
CMI018C	Similar to U3 snoRNP component Utp14p	0.87	±	0.08
CMF148C	Hypothetical protein	0.87	±	0.05
CMN130C	Similar to chaperone protein DnaK	0.87	±	0.05
CMN233C	Dihydrolipoamide S-acetyltransferase, chloroplast precursor	0.87	±	0.15

CMQ020C	Hypothetical protein	0.87	±	0.10
CMC174C	Hypothetical protein	0.87	±	0.05
CMG036C	Similar to WD-repeat protein	0.87	±	0.06
CMK260C	Probable mitochondrial processing peptidase alpha subunit	0.87	±	0.05
CMQ295C	Cell division protein FtsH	0.87	±	0.07
CMQ415C	Hypothetical protein	0.87	±	0.03
CMC075C	Similar to cation efflux system protein (zinc/cadmium); Cef	0.87	±	0.09
CMH154C	20S core proteasome subunit beta 1	0.87	±	0.08
CMF048C	Similar to E3 ubiquitin protein ligase Itch	0.87	±	0.04
CMK245C	ATP phosphoribosyl transferase	0.87	±	0.11
CMJ046C	Similar to kinetoplast-associated protein	0.87	±	0.07
CMO026C	Hypothetical protein	0.87	±	0.03
CMT309C	Zinc finger protein	0.87	±	0.03
CMS050C	Hypothetical protein	0.87	±	0.10
CMS352C	Diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase	0.87	±	0.09
CME132C	Porphobilinogen deaminase	0.87	±	0.09
CMI079C	ATP-binding cassette, sub-family G	0.87	±	0.03
CMG042C	Ubiquitin-specific protease	0.87	±	0.06
CMR396C	Hypothetical protein	0.87	±	0.09
CMD119C	Hypothetical protein	0.87	±	0.06
CMQ011C	Hypothetical protein	0.87	±	0.08
CMT471C	UDP-glucose dehydrogenase	0.87	±	0.05
CMH170C	Probable class II DNA photolyase	0.87	±	0.03
CMM160C	Similar to TFIIH subunit TFB2	0.87	±	0.07
CMB030C	Unknown WD repeat protein	0.86	±	0.08
CMC095C	Hypothetical protein	0.86	±	0.06
CMH062C	Hypothetical protein	0.86	±	0.05
CML240C	Hypothetical protein	0.86	±	0.06
CMA045C	Hypothetical protein	0.86	±	0.11
CMH055C	Hypothetical protein	0.86	±	0.04
CMM145C	Asparagine synthase (glutamine-hydrolysing)	0.86	±	0.14
CMJ238C	Mitochondrial ribosomal protein L28 precursor	0.86	±	0.12
CMA129C	Hypothetical protein	0.86	±	0.07
CMJ259C	Hypothetical protein	0.86	±	0.08
CMS083C	Similar to histone acetyltransferase; Hat1p	0.86	±	0.12
CMP349C	Similar to RNA methyltransferase	0.86	±	0.02
CMJ203C	Similar to transposase	0.86	±	0.04
CMD018C	Probable ubiquitin	0.86	±	0.03
CMG172C	Similar to Glu-tRNAgln amidotransferase subunit A	0.86	±	0.02
CML213C	Hypothetical protein	0.86	±	0.05
CMQ121C	Hypothetical protein	0.86	±	0.08
CML168C	Branched-chain alpha-keto acid decarboxylase E1 beta subunit	0.86	±	0.04
CMH111C	Similar to 4-hydroxybenzoyl-CoA thioesterase	0.86	±	0.05

CMK097C	Serine--tRNA ligase, chloroplast or mitochondrial	0.86	±	0.10
CMA089C	Hypothetical protein	0.86	±	0.08
CMD182C	Hypothetical protein	0.86	±	0.12
CMS065C	Hypothetical protein	0.86	±	0.09
CMH127C	Hypothetical protein	0.86	±	0.30
CMJ089C	Similar to DNA Helicase	0.86	±	0.06
CMI167C	Hypothetical protein	0.86	±	0.03
CMO083C	Similar to processing protease	0.86	±	0.08
CMO150C	Hypothetical protein	0.86	±	0.04
CMO205C	Hypothetical protein	0.86	±	0.04
CMJ136C	Similar to poly(A)-binding protein dependent poly(A)-ribonuclease subunit	0.86	±	0.03
CMS372C	Mitochondrial acyl carrier protein precursor, NADH-ubiquinone oxidoreductase (Complex I) 9.6 kDa subunit	0.86	±	0.05
CMT173C	ATP-dependent RNA helicase	0.86	±	0.09
CMD156C	Coatomer protein complex, subunit alpha	0.86	±	0.03
CMG210C	Unknown zinc finger protein	0.86	±	0.02
CMO328C	Similar to sucrose transporter	0.86	±	0.05
CMN155C	Probable beta-alanine synthase, closer	0.86	±	0.03
CMM254C	Hypothetical protein	0.86	±	0.06
CMI298C	Thioredoxin reductase (NADPH)	0.86	±	0.05
CMG046C	Hypothetical protein	0.86	±	0.09
CMB062C	Isopentenyl-diphosphate delta isomerase	0.86	±	0.03
CMR472C	Hypothetical protein	0.86	±	0.09
CMP062C	Similar to TGF beta receptor associated protein-1	0.86	±	0.07
CMR198C	Similar to 3(2),5-bisphosphate nucleotidase	0.86	±	0.12
CML145C	Mannose-1-phosphate guanylyltransferase	0.86	±	0.05
CMG191C	Hypothetical protein	0.86	±	0.09
CMS358C	Chromatin-specific transcription elongation factor	0.86	±	0.04
CMO121C	Transketolase	0.86	±	0.10
CMH109C	Raptor	0.86	±	0.07
CMS456C	Hypothetical protein	0.86	±	0.08
CME116C	Similar to (N6-adenosine)-methyltransferase	0.86	±	0.02
CMS091C	Probable mitochondrial carrier protein	0.86	±	0.08
CMT208C	Hypothetical protein	0.86	±	0.04
CMH058C	Eukaryotic translation initiation factor eIF-5	0.86	±	0.20
CMF084C	Sm protein D1	0.86	±	0.04
CMT478C	Hypothetical protein	0.86	±	0.01
CMB091C	Similar to eukaryotic translation elongation factor 1 alpha (eEF-1a)	0.86	±	0.07
CMT592C	Similar to mitochondrial calcium-dependent solute carrier	0.86	±	0.08
CMG053C	Hypothetical protein	0.86	±	0.05
CMM233C	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c	0.86	±	0.02
CMG193C	Hypothetical protein	0.86	±	0.07
CMO140C	Mitochondrial translation elongation factor G2 (EF-G2)	0.86	±	0.03
CMM098C	Asparagine--tRNA ligase, cytoplasmic	0.86	±	0.06

CMK259C	Hypothetical protein	0.86	±	0.08
CMS500C	Similar to cyclin H	0.86	±	0.07
CMJ051C	NADP-dependent malic enzyme	0.86	±	0.06
CMR267C	Similar to U3 snoRNP-associated 55-kDa protein RRP9	0.86	±	0.13
CMS307C	Hypothetical protein	0.86	±	0.06
CMO109C	Pre-rRNA processing protein bystin	0.86	±	0.09
CMT594C	Hypothetical protein	0.86	±	0.03
CMS316C	Similar to rotamase/parvulin-type peptidyl-prolyl cis-trans isomerase	0.86	±	0.06
CMO253C	Similar to 22 kDa peroxisomal membrane protein	0.86	±	0.02
CMN180C	Similar to methyl transferase	0.86	±	0.05
CMK147C	Similar to GTP pyrophosphokinase	0.86	±	0.12
CME136C	Dtdp-glucose 4,6-dehydratase	0.86	±	0.08
CMA095C	Similar to MADS box transcription enhancer factor	0.86	±	0.05
CMO229C	Ribulose-5-phosphate 3-epimerase	0.86	±	0.07
CMT075C	Degp protease precursor	0.86	±	0.05
CMI203C	Probable mitotic cyclin a2-type	0.86	±	0.07
CML324C	Similar to SUMO-1-specific protease	0.86	±	0.07
CMR032C	Hypothetical protein	0.86	±	0.02
CMM171C	Hypothetical protein	0.86	±	0.02
CMR026C	Probable DNA (cytosine-5)-methyltransferase 3	0.86	±	0.04
CMS187C	Similar to TIA1 cytotoxic granule-associated RNA-binding protein	0.86	±	0.03
CMR356C	Hypothetical protein	0.86	±	0.11
CMK138C	Hypothetical protein	0.86	±	0.10
CMC158C	Unknown WD-repeat protein WDS	0.86	±	0.08
CMJ090C	Hypothetical protein	0.86	±	0.01
CMP139C	Hypothetical protein	0.86	±	0.04
CMQ361C	Hypothetical protein	0.86	±	0.01
CMC090C	Hypothetical protein	0.86	±	0.08
CMP219C	Alpha,alpha-Trehalose-phosphate synthase (UDP-forming)	0.86	±	0.06
CMT586C	Probable eukaryotic translation initiation factor eIF-2A	0.86	±	0.03
CMG059C	Hypothetical protein	0.86	±	0.06
CMI253C	Hypothetical protein	0.86	±	0.07
CMS247C	Hypothetical protein	0.86	±	0.13
CMM127C	Hypothetical protein	0.86	±	0.11
CMJ214C	Hypothetical protein	0.85	±	0.04
CMH043C	Unknown RNA-binding protein	0.85	±	0.04
CMS064C	Hypothetical protein	0.85	±	0.03
CMG136C	Probable ubiquitin-conjugating enzyme E2	0.85	±	0.02
CMN100C	Unknown hydrolase	0.85	±	0.02
CML111C	Hypothetical protein	0.85	±	0.04
CMO090C	Probable 3-phosphoinositide-dependent protein kinase	0.85	±	0.05
CMA074C	Hypothetical protein	0.85	±	0.04
CMO197C	20S core proteasome subunit alpha 7	0.85	±	0.01

CMI035C	Hypothetical protein	0.85	±	0.03
CMO232C	Hypothetical protein	0.85	±	0.02
CMD170C	Similar to methylthioadenosine phosphorylase mtaP	0.85	±	0.01
CMD006C	Probable serine protease	0.85	±	0.09
CMQ285C	Hypothetical protein	0.85	±	0.02
CMS434C	Hypothetical protein	0.85	±	0.09
CMH095C	Similar to inositol monophosphatase	0.85	±	0.05
CMQ319C	Hypothetical protein	0.85	±	0.03
CMT177C	Unknown kinase with aarF domain	0.85	±	0.14
CMI110C	Hypothetical protein	0.85	±	0.12
CMP053C	Coatomer protein complex, subunit gamma	0.85	±	0.11
CMX007C	Similar to dolichyl-phosphate-mannose:protein mannosyltransferase	0.85	±	0.11
CMF094C	Hypothetical protein	0.85	±	0.06
CMQ392C	Hypothetical protein	0.85	±	0.08
CMM017C	Dtdp-glucose 4,6-dehydratase	0.85	±	0.03
CMP111C	Similar to second and third steps of methylation pathway for phosphatidylcholine biosynthesis; Opi3p	0.85	±	0.09
CMN021C	Similar to UDP-sugar transporter	0.85	±	0.04
CMI126C	Hypothetical protein	0.85	±	0.06
CMC159C	Probable mitochrondrial 2-oxoglutarate/malate carrier protein	0.85	±	0.05
CMR322C	Hypothetical protein	0.85	±	0.07
CMN195C	Probable glycosylasparaginase precursor	0.85	±	0.10
CME001C	Similar to trefoil factor	0.85	±	0.04
CMS426C	Hypothetical protein	0.85	±	0.00
CMM220C	Hypothetical protein	0.85	±	0.09
CMT143C	Similar to inorganic polyposphate/ATP-NAD kinase	0.85	±	0.04
CMC180C	Probable protein disulfide-isomerase	0.85	±	0.07
CMR302C	20S core proteasome subunit alpha 3	0.85	±	0.05
CMJ181C	Probable diphthine synthase	0.85	±	0.03
CMI267C	Similar to L-isoaspartate (D-aspartate) O-methyltransferase	0.85	±	0.08
CMN313C	Similar to histone methyltransferase Set2p	0.85	±	0.07
CMD134C	ATP-binding cassette, sub-family G	0.85	±	0.09
CMT359C	Hypothetical protein	0.85	±	0.04
CMO332C	Similar to micrococcal nuclease, mitochondrial precursor	0.85	±	0.05
CMI117C	ATP-binding protein of ABC transporter	0.85	±	0.12
CMR465C	Sulfate ABC transporter ATP-binding subunit cysA	0.85	±	0.07
CMK042C	Hypothetical protein	0.85	±	0.13
CMQ238C	Hypothetical protein	0.85	±	0.05
CMR220C	DNA-directed RNA polymerase II largest subunit	0.85	±	0.05
CME159C	Hypothetical protein	0.85	±	0.04
CMC054C	Glycine--tRNA ligase	0.85	±	0.04
CMJ179C	Similar to Nedd4 binding protein 1	0.85	±	0.03
CMI294C	Isoamylase	0.85	±	0.04
CMD148C	ATP-binding cassette, sub-family B (MDR/TAP), member 1	0.85	±	0.04

CMS369C	Similar to translin-associated factor X	0.85	±	0.06
CMS036C	Similar to syntaxin-binding protein, UNC-18 homolog	0.85	±	0.03
CMM270C	Magnesium chelatase subunits I and D	0.85	±	0.07
CMJ012C	Hypothetical protein	0.85	±	0.06
CMJ030C	Hypothetical protein	0.85	±	0.05
CMC120C	6-Phospho-gluconolactonase	0.85	±	0.02
CMM172C	Hypothetical protein	0.85	±	0.02
CMR046C	Similar to COP9 signalosome subunit Csn12	0.85	±	0.02
CMP113C	Hypothetical protein	0.85	±	0.01
CMF051C	Probable calcium/calmodulin-dependent protein kinase	0.85	±	0.04
CMD186C	Similar to small multidrug export protein qacE	0.85	±	0.04
CMI136C	Similar to protein with DnaJ domain	0.85	±	0.04
CMI103C	Hypothetical protein	0.85	±	0.06
CMR160C	Similar to polyadenylation factor I complex subunit FIP1	0.85	±	0.02
CMD055C	Similar to mitotic check point protein BUB2	0.85	±	0.09
CMT060C	Hypothetical protein	0.85	±	0.09
CMI096C	Hypothetical protein	0.85	±	0.08
CMF012C	Phosphoenolpyruvate synthase	0.85	±	0.05
CMP231C	Similar to tetracycline resistance protein	0.85	±	0.05
CMM165C	Similar to adenylyl cyclase-associated protein CAP2	0.85	±	0.06
CME128C	20S core proteasome subunit alpha 6	0.85	±	0.05
CMJ083C	Similar to midasin Mdn1p	0.85	±	0.06
CMK274C	Mitochondrial ribosomal protein S5 precursor	0.85	±	0.04
CML181C	Hypothetical protein	0.85	±	0.13
CMK228C	Mitochondrial translation initiation factor IF-2	0.85	±	0.03
CMP208C	Hypothetical protein	0.85	±	0.04
CMP117C	Block of proliferation 1	0.85	±	0.04
CMB029C	Similar to GATA transcription factor areB gamma	0.85	±	0.09
CMM202C	Probable glycosyl hydrolase, family 31	0.85	±	0.03
CMQ132C	Hypothetical protein	0.85	±	0.02
CMT280C	Isoleucine--tRNA ligase, cytoplasmic	0.85	±	0.03
CMS298C	Hypothetical protein	0.85	±	0.10
CMG126C	Similar to zinc finger protein	0.85	±	0.08
CMQ123C	Hypothetical protein	0.85	±	0.02
CMN131C	Similar to monooxygenase	0.85	±	0.09
CMP142C	Similar to acyltransferase Tafazzin	0.85	±	0.12
CMB120C	Similar to rotamase/parvulin-type peptidyl-prolyl cis-trans isomerase	0.85	±	0.06
CMQ019C	Hypothetical protein	0.85	±	0.06
CMD129C	Similar to BRCA1-binding helicase-like protein BACH1	0.85	±	0.06
CMT461C	Probable retinoblastoma-binding protein 2	0.85	±	0.05
CMR372C	Hypothetical protein	0.85	±	0.06
CMN167C	RIO-like serine/threonine protein kinase	0.85	±	0.06
CMB118C	ATP citrate lyase	0.85	±	0.09

CMM122C	Similar to 3-oxoacyl-(acyl carrier protein) reductase	0.85	±	0.02
CML225C	Probable 8-amino-7-oxononanoate synthase	0.85	±	0.05
CMM055C	Hypothetical protein	0.85	±	0.03
CMA016C	Similar to transcription factor IIA large subunit	0.85	±	0.09
CMP301C	Mitochondrial ribosomal protein L36 precursor	0.85	±	0.08
CMK088C	Hypothetical protein	0.85	±	0.08
CMN075C	Similar to DNA damage checkpoint kinase RAD3	0.84	±	0.05
CMP123C	V-type ATPase V1 subunit B	0.84	±	0.06
CMK031C	Cytochrome c reductase (Complex III) subunit 7(VI)	0.84	±	0.07
CMK108C	Probable dolichyl-diphosphooligosaccharide--protein glycosyltransferase	0.84	±	0.09
CMS293C	Hypothetical protein	0.84	±	0.04
CMT025C	Probable exodeoxyribonuclease V, alpha subunit	0.84	±	0.02
CMR067C	Similar to vegetatible incompatibility protein HET-E-1	0.84	±	0.06
CMS004C	Plastid division protein FtsZ (AB032072)	0.84	±	0.10
CMB116C	Probable nuclear movement protein NudC	0.84	±	0.06
CME143C	Smt3-activating enzyme E1 C subunit	0.84	±	0.05
CMD115C	Hypothetical protein	0.84	±	0.01
CMT394C	Similar to Sm-like protein LSm1	0.84	±	0.03
CMQ300C	Mitochondrial peptide chain release factor RF-1	0.84	±	0.05
CMB146C	Conserved GTP-binding protein of unknown function (Nucleolar GTP-binding protein)	0.84	±	0.13
CMT479C	Similar to transcription initiation factor TFIID, subunit TAF7	0.84	±	0.10
CMA027C	Hypothetical protein	0.84	±	0.12
CMO283C	Unknown ABC anion transporter	0.84	±	0.08
CML100C	Nuclear receptor co-repressor/HDAC3 complex subunit	0.84	±	0.05
CMM102C	Probable ATP-dependent DNA helicase	0.84	±	0.02
CMP222C	Probable ATP-dependent RNA helicase ROK1	0.84	±	0.08
CMS480C	Hypothetical protein	0.84	±	0.05
CMA062C	Similar to DNA polymerase iota, RAD30	0.84	±	0.06
CMJ088C	Hypothetical protein	0.84	±	0.03
CMT102C	Unknown aldo/keto reductase	0.84	±	0.05
CMO161C	Hypothetical protein	0.84	±	0.07
CMP078C	Probable beta-galactosidase	0.84	±	0.07
CMP112C	5-oxo-L-prolinase	0.84	±	0.06
CMG161C	Unknown kinase with aarF domain	0.84	±	0.04
CMP265C	Eukaryotic translation initiation factor eIF-3 subunit 5	0.84	±	0.04
CMS154C	Probable sodium/hydrogen antiporter	0.84	±	0.09
CMR411C	Hypothetical protein	0.84	±	0.06
CMN124C	Hypothetical protein	0.84	±	0.05
CMT502C	Hypothetical protein	0.84	±	0.04
CMT371C	Small GTP-binding protein of Ras family	0.84	±	0.06
CMO114C	Hypothetical protein	0.84	±	0.04
CMB002C	Probable splicing factor 3b subunit 1	0.84	±	0.08
CMA041C	UDP-glucose 4-epimerase	0.84	±	0.12

CMH116C	Similar to indigoidine systhesis protein IdgA	0.84	±	0.05
CMH020C	Cleavage and polyadenylation specifity factor protein	0.84	±	0.06
CML092C	Hypothetical protein	0.84	±	0.01
CMT484C	Probable flavin-linked sulfhydryl oxidase ERV1	0.84	±	0.02
CMS041C	Probable ubiquitin-fusion degradation protein (ubiquitination factor E4B)	0.84	±	0.05
CMJ111C	Similar to ethylene-responsive transcription coactivator	0.84	±	0.01
CMN088C	Hypothetical protein	0.84	±	0.06
CMR435C	Hypothetical protein	0.84	±	0.04
CMO012C	S-adenosylmethionine decarboxylase	0.84	±	0.13
CMA115C	Hypothetical protein	0.84	±	0.01
CMN182C	Queuine tRNA-ribosyltransferase	0.84	±	0.03
CMA072C	RNA helicase	0.84	±	0.06
CMT629C	Glutaredoxin type 1	0.84	±	0.05
CMK243C	Phosphatidylserine decarboxylase	0.84	±	0.03
CMP217C	Probable NAD(P) dependent 3-beta-hydroxysteroid dehydrogenase	0.84	±	0.05
CMH278C	Hypothetical protein	0.84	±	0.06
CMS054C	Hypothetical protein	0.84	±	0.12
CMS463C	Similar to serine/threonine protein kinase	0.84	±	0.03
CMT472C	Similar to FKBP-type peptidyl-prolyl cis-trans isomerase	0.84	±	0.03
CMS199C	U3 snoRNP component PWP2	0.84	±	0.06
CMS057C	Hypothetical protein	0.84	±	0.06
CMJ074C	Probable carbon catabolite repressor Ccr4p	0.84	±	0.08
CMH014C	Cysteine desulfurase for iron-sulfur cluster formation sufS	0.84	±	0.05
CMR049C	Similar to nucleolar complex Nop3	0.84	±	0.04
CMK068C	Hypothetical protein	0.84	±	0.11
CMT590C	CDK tyrosine kinase WEE1	0.84	±	0.05
CMD083C	Probable serine/threonine protein phosphatase	0.84	±	0.03
CMS062C	Similar to chromosome segregation protein SepB	0.84	±	0.05
CML231C	Similar to multidrug resistance protein	0.84	±	0.12
CMJ200C	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a	0.84	±	0.18
CME121C	Probable kynurenine aminotransferase	0.84	±	0.09
CMS418C	Hypothetical protein	0.84	±	0.12
CMS224C	Hypothetical protein	0.84	±	0.05
CMG211C	Lipid-A-disaccharide synthase	0.84	±	0.05
CMT635C	Hypothetical protein	0.84	±	0.03
CMQ206C	Hypothetical protein	0.84	±	0.08
CMQ379C	Probable Ca2^{+}-transporting ATPase	0.84	±	0.03
CMG142C	Similar to DNA-(apurinic or apyrimidinic site) lyase ARP	0.84	±	0.03
CMQ013C	Hypothetical protein	0.84	±	0.09
CMO337C	Similar to J-domain protein D3	0.84	±	0.05
CMR091C	Probable signal recognition particle targeting component SRP19	0.84	±	0.11
CMT341C	Similar to RNA binding protein	0.84	±	0.09
CMP325C	Hypothetical protein	0.84	±	0.05

CMI236C	Unknown WD-repeat protein	0.84	±	0.13
CMX009C	Hypothetical protein	0.84	±	0.04
CMS185C	Probable actin-related protein Arp6	0.84	±	0.01
CMQ433C	Hypothetical protein	0.84	±	0.02
CMT387C	Hypothetical protein	0.84	±	0.06
CMT098C	Probable ubiquitin isopeptidase T	0.84	±	0.07
CMP065C	DNA excision repair protein ERCC2/XPD	0.84	±	0.06
CMF163C	Similar to heterogeneous nuclear ribonucleoprotein H3, isoform a	0.84	±	0.03
CMF123C	Similar to maleylacetoacetate isomerase	0.84	±	0.04
CMT261C	Similar to Pfam GTP-CDC domain protein	0.84	±	0.03
CML311C	Hypothetical protein	0.84	±	0.08
CMN210C	Eukaryotic translation initiation factor eIF-2 alpha subunit	0.84	±	0.02
CMI014C	Hypothetical protein	0.84	±	0.03
CMH163C	Hypothetical protein	0.84	±	0.14
CMS460C	Similar to endo-beta-N-acetylglucosaminidase	0.84	±	0.05
CMI263C	Similar to atrer1a (Arabidopsis)	0.84	±	0.05
CMS009C	Hypothetical protein	0.84	±	0.07
CMK127C	Hypothetical protein	0.84	±	0.05
CMD077C	Similar to methionine--tRNA ligase, partial	0.84	±	0.03
CMI234C	Similar to PABP1-dependent poly A-specific ribonuclease subunit PAN3	0.84	±	0.07
CMT206C	Hypothetical protein	0.83	±	0.08
CMT456C	Hypothetical protein	0.83	±	0.02
CMT256C	Pyruvate dehydrogenase E1 alpha subunit, mitochondrial precursor	0.83	±	0.08
CMO144C	Branched-chain-amino-acid transaminase	0.83	±	0.07
CMM125C	CDP-diacylglycerol--Inositol 3-phosphatidyltransferase	0.83	±	0.07
CMJ027C	Glycerol-3-phosphate O-acyltransferase	0.83	±	0.03
CMA029C	Hypothetical protein	0.83	±	0.03
CMR362C	Hypothetical protein	0.83	±	0.05
CMR428C	Similar to telomere-binding protein alpha subunit (TEBP alpha)	0.83	±	0.08
CMT363C	Similar to glycogenin-interacting protein	0.83	±	0.04
CMM276C	Hypothetical protein	0.83	±	0.01
CMJ126C	Hypothetical protein	0.83	±	0.09
CMK297C	Probable ribonuclease HI large subunit	0.83	±	0.11
CMF035C	Hypothetical protein	0.83	±	0.08
CMG164C	Hypothetical protein	0.83	±	0.05
CMQ356C	Hypothetical protein	0.83	±	0.06
CMN141C	Hypothetical protein	0.83	±	0.06
CML197C	Probable long-chain fatty acid coenzyme A ligase	0.83	±	0.04
CMO200C	Similar to nucleolar ribosome transport complex component Noc2p	0.83	±	0.09
CMO324C	4-amino-4-deoxychorismate (ADC) synthase	0.83	±	0.04
CMR410C	Similar to translational repressor pumilio	0.83	±	0.06
CMK199C	MutS family DNA mismatch repair protein MSH4	0.83	±	0.03
CMC126C	Similar to PRLI-interacting factor N	0.83	±	0.15

CMM320C	Hypothetical protein	0.83	±	0.12
CMT300C	Similar to origin recognition complex subunit 4	0.83	±	0.07
CMH049C	Unknown homeobox protein	0.83	±	0.03
CMM317C	Similar to glycogen synthase	0.83	±	0.10
CMM242C	Hypothetical protein	0.83	±	0.08
CMQ161C	Hypothetical protein	0.83	±	0.05
CMT316C	Apospory-associated protein C	0.83	±	0.07
CMI286C	Hypothetical protein	0.83	±	0.04
CMN091C	Similar to iron-sulfur cluster-binding protein	0.83	±	0.08
CMO348C	Cryptochrome	0.83	±	0.07
CMK015C	Similar to protein disulfide isomerase	0.83	±	0.04
CMT375C	Hypothetical protein	0.83	±	0.07
CMJ301C	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	0.83	±	0.10
CMD088C	Hypothetical protein	0.83	±	0.07
CMJ064C	Hypothetical protein	0.83	±	0.07
CMS012C	Hypothetical protein	0.83	±	0.01
CMM235C	Hypothetical protein	0.83	±	0.06
CMT576C	Hypothetical protein	0.83	±	0.04
CMQ267C	Hypothetical protein	0.83	±	0.08
CMP332C	Similar to fibrillin	0.83	±	0.04
CMI281C	Cytochrome b6/f complex iron-sulfur subunit, precursor	0.83	±	0.05
CMI270C	Similar to carbonic anhydrase precursor	0.83	±	0.02
CMS452C	Similar to TFIIH subunit TFB4	0.83	±	0.01
CMD168C	Similar to elongin C	0.83	±	0.03
CMN333C	Phosphatidylinositol-4-phosphate 5-kinase	0.83	±	0.02
CMQ256C	Unknown cyanobacterial protein	0.83	±	0.08
CMI064C	Hypothetical protein	0.83	±	0.07
CMI242C	Hypothetical protein	0.83	±	0.08
CMH059C	Similar to RNA polymerase I-associated factor PAF67	0.83	±	0.05
CMQ275C	Tyrosine--tRNA ligase, mitochondrial or chloroplast	0.83	±	0.03
CMP087C	Probable dehydrogenase	0.83	±	0.05
CMH114C	Similar to FKBP-type peptidyl-prolyl cis-trans isomerase	0.83	±	0.07
CMH182C	Similar to ubiquitin specific protease	0.83	±	0.02
CMK087C	Aspartate--tRNA ligase, mitochondrial and chloroplast?	0.83	±	0.09
CMO155C	Probable protein phosphatase 2A regulatory subunit	0.83	±	0.03
CMF157C	Probable U3 snoRNP component Utp7p	0.83	±	0.02
CMR460C	Similar to transparent testa glabra 1	0.83	±	0.06
CMK179C	Hypothetical protein	0.83	±	0.06
CMJ248C	Similar to cytochrome c-type biogenesis protein	0.83	±	0.04
CMS412C	Actin-like protein	0.83	±	0.04
CML276C	Chaperonin containing TCP1, subunit 5 (epsilon)	0.83	±	0.16
CMQ008C	Hypothetical protein	0.83	±	0.01
CMH222C	TATA-box binding protein-associated factor 11	0.83	±	0.01

CMR031C	Hypothetical protein	0.83	±	0.05
CMR108C	Hypothetical protein	0.83	±	0.04
CMK280C	MYB-related protein	0.83	±	0.05
CMT440C	Hypothetical protein	0.83	±	0.04
CMJ239C	Glucose-1-phosphate adenylyltransferase	0.83	±	0.05
CMQ443C	Similar to alkane 1-monooxygenase	0.83	±	0.02
CMG115C	Hypothetical protein	0.83	±	0.03
CMQ057C	Hypothetical protein	0.83	±	0.08
CMK203C	Hypothetical protein	0.83	±	0.04
CML279C	Hypothetical protein	0.83	±	0.06
CME092C	Similar to ankirin	0.83	±	0.01
CMF066C	Glucose inhibited division protein A	0.83	±	0.06
CME059C	Conserved unknown protein RtcB	0.83	±	0.04
CMP089C	Hypothetical protein	0.83	±	0.04
CMC157C	Kinesin-related protein, BimC subfamily	0.83	±	0.03
CMT389C	Cystathionine gamma-lyase	0.83	±	0.02
CMQ028C	Adaptor-related protein complex 3, delta subunit	0.83	±	0.04
CMT406C	Hypothetical protein	0.83	±	0.03
CMQ227C	Hypothetical protein	0.83	±	0.05
CMN147C	Actin depolymerizing factor	0.83	±	0.09
CMC178C	Hypothetical protein	0.83	±	0.11
CMT421C	Hypothetical protein	0.83	±	0.04
CMP042C	Similar to U3 snoRNP component Utp13p	0.83	±	0.04
CML086C	Probable signal recognition particle targeting component SRP68	0.83	±	0.04
CMM287C	Similar to magnesium transporter Mrs2p	0.83	±	0.14
CMP067C	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	0.83	±	0.03
CMA059C	Probable viral mRNA translation inhibitor SKI2	0.83	±	0.11
CMJ302C	Hypothetical protein	0.83	±	0.06
CMP075C	Protein phosphatase 5	0.83	±	0.08
CMP030C	Probable chromatin assembly factor 1 subunit B	0.83	±	0.02
CME018C	Hypothetical protein	0.83	±	0.07
CMT600C	Probable NAD-dependent histone deacetylase SIR2	0.83	±	0.05
CMS342C	V-type ATPase V1 subunit A	0.83	±	0.03
CMI048C	Hypothetical protein	0.83	±	0.04
CMG170C	Proteasome regulatory particle subunit	0.83	±	0.07
CMD010C	Hypothetical protein	0.83	±	0.05
CMS037C	Cystathionine beta-synthase	0.83	±	0.05
CMN322C	Hypothetical protein	0.83	±	0.03
CMB057C	Hypothetical protein	0.83	±	0.01
CMM071C	Hypothetical protein	0.83	±	0.02
CMS256C	Similar to transcriptional activator GCN5, a bromodomain protein	0.83	±	0.05
CMO072C	Unknown WD-40 protein	0.83	±	0.12
CMA111C	Probable transitional endoplasmic reticulum ATPase	0.83	±	0.04

CMT097C	Kinesin-related protein, C-terminal motor subfamily	0.83	±	0.05
CMO225C	Hypothetical protein	0.83	±	0.05
CMN234C	Similar to chlorophyll a/b-binding protein, CP24	0.83	±	0.09
CMP220C	Similar to actin-binding protein, profilin	0.82	±	0.04
CMO147C	Unknown permease	0.82	±	0.06
CMQ187C	Rad50	0.82	±	0.05
CMF146C	Similar to phosphate/phosphoenolpyruvate translocator precursor	0.82	±	0.10
CMR456C	Ribosomal RNA assembly protein mis3/dribble/Krr1p	0.82	±	0.07
CMN163C	Similar to variable flagellar number protein	0.82	±	0.06
CMR144C	Adaptor-related protein complex 1, sigma subunit	0.82	±	0.06
CMQ045C	ATP-dependent Clp protease proteolytic subunit	0.82	±	0.04
CMD060C	20S core proteasome subunit beta 7	0.82	±	0.02
CMM115C	Similar to glycosyltransferase	0.82	±	0.10
CMA134C	Similar to phosphatidyl-N-methylethanolamine N-methyltransferase	0.82	±	0.05
CMO102C	Vacuolar-type H^+-translocating inorganic pyrophosphatase	0.82	±	0.04
CMJ277C	Hypothetical protein	0.82	±	0.05
CMF110C	Probable replication factor C/activator 1 subunit	0.82	±	0.04
CMI073C	Hypothetical protein	0.82	±	0.05
CMX001C	Hypothetical protein	0.82	±	0.21
CMR317C	Hypothetical protein	0.82	±	0.04
CMH132C	Succinyl-CoA synthetase alpha chain	0.82	±	0.04
CMQ077C	Cleavage and polyadenylation specific factor 2, 100kDa subunit	0.82	±	0.04
CMB075C	Unknown transporter	0.82	±	0.09
CMP169C	Similar to expression regulator of ATP synthase Nca2p	0.82	±	0.05
CMB010C	Tryptophane--tRNA ligase, chloroplast or mitochondrial	0.82	±	0.07
CMM190C	Chloroplast ribosomal protein L17 precursor	0.82	±	0.02
CMN027C	Probable chromosome segregation protein CSE1	0.82	±	0.07
CMC172C	Hypothetical protein	0.82	±	0.05
CMQ375C	Hypothetical protein	0.82	±	0.05
CMH057C	Hypothetical protein	0.82	±	0.06
CMO003C	Mannose-1-phosphate guanylyltransferase	0.82	±	0.04
CMP261C	Similar to small conductance mechanosensitive ion channel	0.82	±	0.03
CMT120C	ABC transporter, LktB-related	0.82	±	0.07
CMJ162C	Similar to diacylglycerol acyltransferase type 2B	0.82	±	0.09
CMK164C	Similar to mitochondrial carrier protein	0.82	±	0.04
CMT386C	Hypothetical protein	0.82	±	0.06
CMT140C	Hypothetical protein	0.82	±	0.03
CMO239C	Hypothetical protein	0.82	±	0.09
CME119C	Cyclin dependent kinase, A-type	0.82	±	0.02
CMT462C	DNA polymerase I (POL I)	0.82	±	0.03
CMD042C	Hypothetical protein	0.82	±	0.08
CME022C	Hypothetical protein	0.82	±	0.05
CML290C	Hypothetical protein	0.82	±	0.07

CMB157C	S-adenosyl-L-homocysteine hydrolase	0.82	±	0.12
CMQ110C	Similar to nuclear LIM interactor-interacting factor	0.82	±	0.08
CMJ009C	Cycloartenol synthase	0.82	±	0.14
CMC122C	Hypothetical protein	0.82	±	0.04
CMI179C	Probable fibronectin-binding protein	0.82	±	0.06
CMT513C	Hypothetical protein	0.82	±	0.05
CMF177C	Similar to polymyositis-scleroderma overlap syndrome associated autoantigen	0.82	±	0.03
CMR090C	Hypothetical protein	0.82	±	0.05
CMH009C	Probable adenosine deaminase	0.82	±	0.09
CMC121C	Phosphoglucomutase	0.82	±	0.08
CMT094C	Similar to 2-dehydropantoate 2-reductase	0.82	±	0.05
CMA034C	Hypothetical protein	0.82	±	0.08
CMP257C	Hypothetical protein	0.82	±	0.07
CMN288C	Hypothetical protein	0.82	±	0.14
CMF020C	Probable NADPH-dependent FMN and FAD containing oxidoreductase, NADPH-cytochrome P450 reductase	0.82	±	0.03
CME016C	Signal recognition particle (SRP) receptor alpha subunit	0.82	±	0.01
CMS496C	Hypothetical protein	0.82	±	0.08
CMQ338C	Similar to ATP-dependent RNA helicase deaD	0.82	±	0.04
CMO078C	Hypothetical protein	0.82	±	0.10
CMK044C	Sigma subunit for chloroplast RNA polymerase, precursor	0.82	±	0.15
CMK086C	Hypothetical protein	0.82	±	0.03
CMS359C	Similar to putative mitochondrial carrier protein	0.82	±	0.08
CMH097C	Hypothetical protein	0.82	±	0.05
CMS384C	MAP kinase kinase kinase (MAP3K), cdc15-like epsilon-type	0.82	±	0.04
CMQ393C	Chloroplast preprotein translocase SecA subunit	0.82	±	0.09
CMO045C	Hypothetical protein	0.82	±	0.09
CMC019C	Vesicle transport protein Rop	0.82	±	0.06
CMR370C	Probable bile acid sodium symporter	0.82	±	0.12
CME156C	Similar to mitochondrial ribosome small subunit component Rsm22	0.82	±	0.04
CMM326C	Serine/threonine-protein kinase IRE1	0.82	±	0.08
CMN304C	Gamma-tubulin	0.82	±	0.05
CMJ257C	Single subunit mitochondrial RNA polymerase	0.82	±	0.01
CMS134C	Hypothetical protein	0.82	±	0.04
CMR061C	Hypothetical protein	0.82	±	0.13
CME085C	Probable XPA-binding protein 1	0.82	±	0.08
CMS032C	Similar to nuclear mitotic apparatus protein	0.82	±	0.12
CMP182C	Hypothetical protein	0.82	±	0.05
CMP077C	Hypothetical protein	0.82	±	0.05
CMA066C	DNA repair protein SMC6	0.82	±	0.07
CMR009C	Probable Na^+ driven anion exchanger NDAE1	0.82	±	0.11
CMJ015C	Hypothetical protein	0.82	±	0.03
CML319C	Hypothetical protein	0.82	±	0.01
CMT497C	Glucose-6-phosphate isomerase	0.82	±	0.03

CMP116C	Similar to transposase	0.82	±	0.03
CMC071C	N-myristoyltransferase	0.82	±	0.04
CMR443C	Hypothetical protein	0.82	±	0.04
CMR286C	Hypothetical protein	0.82	±	0.04
CMA019C	RNA polymerase III transcription factor IIIB	0.82	±	0.03
CMT122C	ATP-dependent Hsl protease ATP-binding subunit HslU, heat shock protein HslU	0.82	±	0.02
CMT071C	Methylcrotonyl-CoA carboxylase	0.82	±	0.06
CMO350C	Hypothetical protein	0.81	±	0.04
CMM260C	Hypothetical protein	0.81	±	0.03
CMT563C	Hypothetical protein	0.81	±	0.03
CML274C	Betaine aldehyde dehydrogenase	0.81	±	0.06
CMI091C	Serine hydroxymethyltransferase, cytosolic (glycine hydroxymethyltransferase)	0.81	±	0.12
CMT185C	Probable MAP kinase kinase kinase (MAP3K)	0.81	±	0.09
CMI020C	Hypothetical protein	0.81	±	0.06
CMH242C	Oxysterol binding protein	0.81	±	0.06
CMF068C	2-oxoglutarate dehydrogenase, E1 component	0.81	±	0.02
CMP193C	Malate dehydrogenase, mitochondrial precursor	0.81	±	0.13
CML166C	Hypothetical protein	0.81	±	0.06
CMM065C	Sm protein D3	0.81	±	0.03
CML112C	Hypothetical protein	0.81	±	0.05
CMH143C	Hypothetical protein	0.81	±	0.04
CMO073C	Hypothetical protein	0.81	±	0.03
CMJ296C	Hypothetical protein	0.81	±	0.12
CMM166C	Phytoene synthase	0.81	±	0.09
CMO059C	Unknown heatshock protein	0.81	±	0.05
CMT325C	Serine/threonine kinase 11	0.81	±	0.03
CMR398C	Similar to dehydrogenase	0.81	±	0.04
CMR194C	Hypothetical protein	0.81	±	0.06
CMP281C	Similar to guanine nucleotide exchange factor	0.81	±	0.08
CMG205C	Hypothetical protein	0.81	±	0.03
CMI077C	Probable mRNA-associated protein MRNP 41, RAE1 homolog	0.81	±	0.08
CMP216C	CTP synthase	0.81	±	0.08
CMR438C	Hypothetical protein	0.81	±	0.02
CMN092C	Similar to calcium-activated potassium channel	0.81	±	0.07
CMP297C	Probable carboxyl-terminal protease	0.81	±	0.06
CMS341C	Puromycin-sensitive aminopeptidase	0.81	±	0.06
CMG032C	Hypothetical protein	0.81	±	0.07
CMT203C	Similar to aspartyl protease	0.81	±	0.06
CMM182C	Hypothetical protein	0.81	±	0.07
CMF055C	GTP cyclohydrolase I	0.81	±	0.04
CMS030C	Hypothetical protein	0.81	±	0.06
CMP356C	DNA replication licensing factor MCM4	0.81	±	0.11
CMD052C	Hypothetical protein	0.81	±	0.02

CMC060C	Hypothetical protein	0.81	±	0.07
CMT495C	Similar to 5'-AMP-activated protein kinase, gamma-1 subunit	0.81	±	0.06
CMK159C	Hypothetical protein	0.81	±	0.10
CMN223C	Mitochondrial F-type ATPase F1 subunit epsilon, precursor	0.81	±	0.07
CMH047C	Similar to mRNA binding protein CSP41 precursor	0.81	±	0.02
CMN219C	Hypothetical protein	0.81	±	0.19
CMK230C	Hypothetical protein	0.81	±	0.03
CMG110C	Probable phycocyanobilin:ferredoxin oxidoreductase	0.81	±	0.03
CMS400C	Unknown ABC transporter permease subunit	0.81	±	0.02
CMQ374C	Similar to chaperone DnaJ	0.81	±	0.12
CMG073C	Probable clathrin coat assembly protein AP180	0.81	±	0.02
CMO120C	Hypothetical protein	0.81	±	0.03
CMT267C	Similar to glycosyl transferase	0.81	±	0.06
CMT487C	Similar to DNA cross-link repair protein SNM1	0.81	±	0.05
CMQ104C	Hypothetical protein	0.81	±	0.11
CME099C	Histone H3 variant	0.81	±	0.02
CML103C	Similar to splicing factor 3b subunit 3	0.81	±	0.08
CMR264C	UV-damaged DNA binding protein	0.81	±	0.15
CMO222C	Hypothetical protein	0.81	±	0.10
CMS292C	Hypothetical protein	0.81	±	0.04
CME102C	Similar to GATA transcription factor	0.81	±	0.07
CMR045C	Similar to protein phosphatase 1, regulatory (inhibitor) subunit 11	0.81	±	0.08
CME014C	Hypothetical protein	0.81	±	0.04
CMS421C	Hypothetical protein	0.81	±	0.01
CMO181C	Hypothetical protein	0.81	±	0.01
CMB149C	Hypothetical protein	0.81	±	0.12
CMK236C	Hypothetical protein	0.81	±	0.04
CMJ079C	Hypothetical protein	0.81	±	0.04
CMJ018C	Hypothetical protein	0.81	±	0.09
CMK254C	Similar to tRNA-splicing endonuclease subunit	0.81	±	0.01
CMR469C	Hypothetical protein	0.81	±	0.03
CMP343C	Hypothetical protein	0.81	±	0.04
CMP043C	RNA polymerase II third large subunit	0.81	±	0.03
CMO053C	Alpha,alpha-trehalose-phosphate synthase (UDP-forming)	0.81	±	0.07
CMR390C	Hypothetical protein	0.81	±	0.02
CMR407C	Cell division cycle protein cdc27, TPR protein, APC3	0.81	±	0.05
CMS160C	Hypothetical protein	0.81	±	0.09
CMJ069C	Small GTP-binding protein (Rho+Ras, tandemly repeated)	0.81	±	0.01
CMN252C	Similar to cpce-related prtein	0.81	±	0.03
CMJ208C	Hypothetical protein	0.81	±	0.04
CMT024C	Arsenic methyltransferase Cyt19	0.81	±	0.07
CMB109C	Similar to polyphosphoinositide binding protein Ssh2	0.81	±	0.05
CMI184C	Box H/ACA snoRNP component GAR1	0.81	±	0.04

CMS498C	Similar to thiamine phosphate pyrophosphorylase	0.81	±	0.06
CMJ052C	Hypothetical protein	0.81	±	0.07
CMJ217C	Hypothetical protein	0.81	±	0.04
CMG037C	Hypothetical protein	0.81	±	0.09
CMM247C	Hypothetical protein	0.81	±	0.08
CMS371C	MYB-related protein	0.81	±	0.06
CMP212C	Hypothetical protein	0.81	±	0.03
CMB083C	Chaperonin containing TCP1, subunit 3 (gamma)	0.81	±	0.03
CMM194C	Hypothetical protein	0.81	±	0.06
CMR236C	Similar to tRNA-specific adenosine-34 deaminase subunit Tad3p	0.81	±	0.07
CMF130C	Hypothetical protein	0.81	±	0.01
CMB081C	Hypothetical protein	0.81	±	0.02
CMI213C	Calnexin	0.81	±	0.15
CMF139C	Serine/threonine protein kinase SNF1	0.81	±	0.07
CMR259C	Probable DNA repair protein RAD5	0.81	±	0.03
CMO132C	Probable DNA mismatch repair protein MutS	0.81	±	0.03
CMR344C	Hypothetical protein	0.81	±	0.15
CMI151C	Nucleotide excision repair protein XP-D	0.81	±	0.07
CMQ441C	Probable lipoic acid synthase, mitochondrial precursor	0.81	±	0.11
CMT047C	Eukaryotic translation initiation factor eIF-2B delta subunit	0.81	±	0.10
CMB037C	Hypothetical protein	0.81	±	0.02
CMR473C	Hypothetical protein	0.81	±	0.09
CMO015C	Hypothetical protein	0.81	±	0.04
CMM062C	Probable aminobutyraldehyde dehydrogenase	0.81	±	0.07
CMP015C	Similar to Raf/ATN-like protein kinase, with ankyrin repeats	0.81	±	0.06
CMH262C	TATA-box binding protein-associated factor 1	0.81	±	0.04
CMI221C	Diaminopimelate decarboxylase	0.81	±	0.12
CMI135C	Single strand binding protein, SSB	0.81	±	0.03
CMT245C	Retroelement	0.80	±	0.08
CMS351C	Eukaryotic translation initiation factor eIF-5A	0.80	±	0.09
CMI017C	Similar to exosome complex exonuclease RRP40	0.80	±	0.04
CMF031C	Hypothetical protein	0.80	±	0.01
CMG151C	Hypothetical protein	0.80	±	0.03
CMO061C	Hypothetical protein	0.80	±	0.06
CMN184C	Hypothetical protein	0.80	±	0.04
CMB013C	Topoisomerase II	0.80	±	0.06
CMH091C	Hypothetical protein	0.80	±	0.02
CMO246C	Probable RNA binding protein Mrd1p	0.80	±	0.08
CMG096C	Similar to ribonuclease P subunit POP4	0.80	±	0.10
CMQ194C	Similar to signal recognition particle targeting component SRP72	0.80	±	0.06
CMP177C	Transposon	0.80	±	0.06
CMD047C	Hypothetical protein	0.80	±	0.08
CML330C	DNA topoisomerase II	0.80	±	0.08

CMB078C	Similar to suppressor of lin12 SEL1	0.80	±	0.05
CMF046C	Similar to beta-tubulin folding cofactor D	0.80	±	0.05
CML074C	Similar to trithorax protein ash2	0.80	±	0.05
CMN074C	Box C/D snoRNP rRNA methylase component fibrillarin	0.80	±	0.14
CMM291C	E3 ubiquitin ligase SCF complex Cullin subunit	0.80	±	0.02
CMC129C	Similar to nuclear pore complex protein NUP107	0.80	±	0.12
CMK113C	Alpha-1,3-mannosyltransferase	0.80	±	0.06
CMA015C	Hypothetical protein	0.80	±	0.03
CMN329C	Hypothetical protein	0.80	±	0.13
CMN090C	Similar to syntaxin binding protein	0.80	±	0.02
CML028C	Hypothetical protein	0.80	±	0.08
CMQ297C	Hypothetical protein	0.80	±	0.02
CML143C	Hypothetical protein	0.80	±	0.08
CML247C	Riboflavin synthase alpha chain	0.80	±	0.04
CMQ041C	Pseudouridylate synthase I	0.80	±	0.09
CMT459C	Long-chain-fatty-acid CoA ligase	0.80	±	0.04
CMK180C	Probable transcription regulator exsB	0.80	±	0.05
CMG141C	Gamma-glutamylcysteine synthetase	0.80	±	0.02
CMN305C	Hypothetical protein	0.80	±	0.06
CMM243C	Hypothetical protein	0.80	±	0.05
CMJ231C	Similar to 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase	0.80	±	0.02
CMP145C	Probable 70kDa heat shock cognate protein	0.80	±	0.14
CMR266C	Hypothetical protein	0.80	±	0.00
CMS276C	Exportin 1 (Xpo1)	0.80	±	0.07
CME062C	Probable cationic amino acid transporter ctra	0.80	±	0.04
CMO268C	Hypothetical protein	0.80	±	0.05
CMG086C	Aminomethyltransferase	0.80	±	0.13
CMP232C	Hypothetical protein	0.80	±	0.06
CMP277C	Mitochondrial ribosomal protein L2 precursor	0.80	±	0.09
CMB155C	Similar to uncharacterized hematopoietic stem/progenitor cell protein	0.80	±	0.13
CMK106C	Hypothetical protein	0.80	±	0.10
CME135C	Probable purple acid phosphatase	0.80	±	0.02
CMI238C	6,7-dimethyl-8-ribityllumazine (DMRL/Lumazine/Riboflavin) synthase	0.80	±	0.04
CMQ075C	Hypothetical protein	0.80	±	0.08
CMT444C	Hypothetical protein	0.80	±	0.05
CMR432C	Similar to cation transporting ATPase	0.80	±	0.02
CMS031C	Similar to peroxisoaml membrane protein PMP22	0.80	±	0.07
CMT409C	Hypothetical protein	0.80	±	0.05
CMP223C	Mitochondrial ribosomal protein S18 precursor	0.80	±	0.03
CMI056C	Hypothetical protein	0.80	±	0.04
CMP114C	Mismatch repair protein Msh2	0.80	±	0.08
CMS239C	Hypothetical protein	0.80	±	0.03
CMJ305C	Phosphoglycerate kinase	0.80	±	0.05

CMC115C	Hypothetical protein	0.80	±	0.03
CMJ246C	Trans-prenyltransferase	0.80	±	0.02
CMN038C	Hypothetical protein	0.80	±	0.01
CML025C	Similar to CBL-interacting protein kinase	0.80	±	0.11
CMT061C	Zeta-carotene desaturase	0.80	±	0.08
CMM141C	Similar to zinc finger protein	0.80	±	0.03
CMT066C	ATP-binding cassette, sub-family B (MDR/TAP), member 6	0.80	±	0.05
CMQ095C	Hypothetical protein	0.80	±	0.05
CMT067C	Transcription factor E2F	0.80	±	0.09
CME108C	Similar to protein phosphatase 2A regulatory subunit B	0.80	±	0.05
CMO247C	Hypothetical protein	0.80	±	0.04
CMQ022C	Probable peptidyl-tRNA hydrolase	0.80	±	0.03
CMT202C	Hypothetical protein	0.80	±	0.05
CMS422C	Probable chromosome condensation protein G	0.80	±	0.05
CMJ082C	Hypothetical protein	0.80	±	0.03
CMN053C	Similar to DNA repair and recombination protein Rad57p/XRCC2	0.80	±	0.04
CMM195C	Hypothetical protein	0.80	±	0.07
CMA021C	Similar to DnaJ (Hsp40) homolog	0.80	±	0.13
CMR227C	Hypothetical protein	0.80	±	0.08
CMS345C	Sps1-like serine/threonine kinase	0.80	±	0.04
CMG045C	Hypothetical protein	0.80	±	0.07
CMT534C	Hypothetical protein	0.80	±	0.13
CMR017C	Hypothetical protein	0.80	±	0.03
CMH096C	Hypothetical protein	0.80	±	0.09
CMJ145C	Hypothetical protein	0.80	±	0.02
CMG127C	Hypothetical protein	0.80	±	0.04
CMS285C	Hypothetical protein	0.80	±	0.03
CMR363C	Hypothetical protein	0.80	±	0.08
CMJ120C	Similar to 26S proteasome associated protein	0.80	±	0.06
CMR057C	Ubiquitin-specific protease	0.80	±	0.05
CMJ128C	Phenylalanine--tRNA ligase beta-subunit	0.80	±	0.02
CMD184C	Glycogen phosphorylase	0.80	±	0.05
CMI105C	Hypothetical protein	0.80	±	0.04
CMI241C	Similar to carboxy-terminal proteinase	0.80	±	0.06
CMA052C	Probable ornithine decarboxylase	0.80	±	0.10
CME081C	Hypothetical protein	0.80	±	0.04
CMO260C	Eukaryotic translation initiation factor eIF-3 subunit 7	0.80	±	0.12
CMK135C	Similar to NADH dehydrogenase I (Complex I) alpha subcomplex 1 (MWFE)	0.80	±	0.05
CMI250C	Similar to Golgi SNARE protein	0.80	±	0.05
CMK275C	Hypothetical protein	0.80	±	0.06
CMG168C	Probable purple acid phosphatase protein	0.79	±	0.08
CMH133C	Hypothetical protein	0.79	±	0.13
CMT072C	Isovaleryl-CoA dehydrogenase	0.79	±	0.03

CMM314C	Alanine--tRNA ligase cytoplasmic (plus mito?)	0.79	±	0.02
CME154C	Hypothetical protein	0.79	±	0.04
CMG177C	Hypothetical protein	0.79	±	0.05
CMJ306C	Similar to ribonuclease PH	0.79	±	0.02
CMA023C	MYB-related protein	0.79	±	0.05
CMG119C	Similar to histidine triad protein (HIT)	0.79	±	0.02
CMJ005C	Similar to cell surface glycoprotein	0.79	±	0.05
CMR306C	Similar to calcium-transporting P-type ATPase	0.79	±	0.02
CML068C	Hypothetical protein	0.79	±	0.04
CMA128C	Hypothetical protein	0.79	±	0.02
CMM094C	Elongator protein Elp3p	0.79	±	0.06
CMG185C	Hypothetical protein	0.79	±	0.15
CMQ328C	Hypothetical protein	0.79	±	0.02
CMH192C	Unknown zinc finger protein	0.79	±	0.14
CMP285C	Glutamate-1-semialdehyde 2,1-aminomutase	0.79	±	0.10
CME139C	Similar to spindle checkpoint protein Xmad1	0.79	±	0.05
CMR360C	Hypothetical protein	0.79	±	0.05
CMQ364C	Hypothetical protein	0.79	±	0.09
CMG148C	1-deoxy-D-xylulose 5-phosphate reductoisomerase	0.79	±	0.10
CME194C	Uroporphyrinogen decarboxylase	0.79	±	0.05
CMM193C	Hypothetical protein	0.79	±	0.03
CMP085C	Similar to phosphoserine phosphatase	0.79	±	0.12
CMT231C	Hypothetical protein	0.79	±	0.15
CMC163C	Hypothetical protein	0.79	±	0.11
CMA022C	Hypothetical protein	0.79	±	0.05
CMR320C	Hypothetical protein	0.79	±	0.05
CMQ367C	Similar to nucleosome/chromatin assembly factor C	0.79	±	0.03
CMP028C	ATP-binding cassette, sub-family D (PMP)	0.79	±	0.09
CMP337C	Similar to desmoplakin	0.79	±	0.03
CMS495C	Probable transcriptional adaptor ADA2	0.79	±	0.05
CMD105C	Similar to peroxisomal membrane protein PEX2	0.79	±	0.05
CMT579C	Heat shock protein 70	0.79	±	0.09
CME130C	Hypothetical protein	0.79	±	0.04
CMF095C	TATA-box binding protein	0.79	±	0.05
CMQ376C	Hypothetical protein	0.79	±	0.10
CMC141C	Bis(5'-adenosyl)-triphosphatase	0.79	±	0.02
CMQ039C	MAP kinase	0.79	±	0.09
CMS401C	Unknown ABC transporter ATP-binding subunit	0.79	±	0.04
CMT289C	PGR5	0.79	±	0.09
CMC051C	Similar to programmed cell death 6 interacting protein	0.79	±	0.06
CMQ065C	Hypothetical protein	0.79	±	0.07
CMO168C	Hypothetical protein	0.79	±	0.02
CMB136C	Hypothetical protein	0.79	±	0.03

CMK186C	Hypothetical protein	0.79	±	0.01
CMK064C	Eukaryotic translation initiation factor eIF-2B alpha subunit	0.79	±	0.08
CMQ351C	Hypothetical protein	0.79	±	0.02
CMK046C	Uridine 5'-monophosphate synthase (UMP synthase)	0.79	±	0.02
CMR415C	Similar to BTB domain and Ankaryin repeat containing protein	0.79	±	0.02
CMG092C	Similar to periplasmic protein p19	0.79	±	0.06
CMJ116C	Hypothetical protein	0.79	±	0.04
CMO236C	Hypothetical protein	0.79	±	0.01
CMG083C	Hypothetical protein	0.79	±	0.04
CMO241C	Hypothetical protein	0.79	±	0.01
CMR205C	Asparagine--tRNA ligase, chloroplast precursor	0.79	±	0.04
CMI224C	Glucose-6-phosphate 1-dehydrogenase	0.79	±	0.06
CMT501C	Probable transcription elongation factor S-II (TFIIS)	0.79	±	0.04
CMT420C	Malonyl-CoA:Acyl carrier protein transacylase (MCT)	0.79	±	0.02
CMT465C	Similar to dual-specificity phosphatase laforin	0.79	±	0.05
CMO235C	26S proteasome component	0.79	±	0.03
CMS060C	Hypothetical protein	0.79	±	0.07
CMF167C	Hypothetical protein	0.79	±	0.02
CMS059C	Hypothetical protein	0.79	±	0.07
CMI040C	Chloroplast ADP,ATP carrier protein	0.79	±	0.06
CMS287C	Hypothetical protein	0.79	±	0.01
CMD029C	Hypothetical protein	0.79	±	0.08
CMQ139C	Hypothetical protein	0.79	±	0.06
CMG040C	Hypothetical protein	0.79	±	0.06
CML097C	Similar to nucleotide excision repair complex subunit XPC	0.79	±	0.03
CMK271C	Hypothetical protein	0.79	±	0.05
CMM091C	Hypothetical protein	0.79	±	0.04
CMI065C	Similar to mitochondrial RNA splicing protein Mrs2p	0.79	±	0.01
CMT500C	Hypothetical protein	0.79	±	0.05
CMK200C	Hypothetical protein	0.79	±	0.06
CMR076C	Probable phosphotyrosyl phosphatase activator protein	0.79	±	0.02
CMP003C	Hypothetical protein	0.79	±	0.12
CMM004C	Hypothetical protein	0.79	±	0.02
CMK131C	Enolase	0.79	±	0.06
CMS390C	Probable essential nucleolar protein required for biogenesis of the 60S ribosomal subunit; Brx1p	0.79	±	0.06
CMI211C	Hypothetical protein	0.79	±	0.00
CML110C	Nucleoside-diphosphate kinase	0.79	±	0.03
CMH249C	Hypothetical protein	0.79	±	0.07
CMT416C	Similar to carbonic anhydrase precursor	0.79	±	0.07
CMS464C	TBP-associated factor 172, similar to SWI2/SNF2 family	0.79	±	0.07
CMB087C	Hypothetical protein	0.79	±	0.05
CMR168C	Hypothetical protein	0.78	±	0.11
CMQ127C	Hypothetical protein	0.78	±	0.05

CMN123C	eIF-2alpha kinase GCN2	0.78	±	0.04
CMG182C	Hypothetical protein	0.78	±	0.03
CMT137C	Hypothetical protein	0.78	±	0.06
CMQ464C	Hypothetical protein	0.78	±	0.07
CML107C	Hypothetical protein	0.78	±	0.06
CML257C	Hypothetical protein	0.78	±	0.05
CMR225C	Probable pyruvate dehydrogenase kinase	0.78	±	0.03
CMS159C	UTP--glucose-1-phosphate uridylyltransferase	0.78	±	0.06
CMK037C	RNA polymerase I largest subunit	0.78	±	0.01
CMP230C	Probable protein phosphatase methylesterase-1	0.78	±	0.03
CMT063C	Chloroplast membrane protein ALBINO3 or ARTEMIS	0.78	±	0.06
CMJ300C	Hypothetical protein	0.78	±	0.01
CMR388C	ATP-binding subunit of unknown ABC transporter	0.78	±	0.11
CMP166C	Phycocyanin-associated rod linker protein	0.78	±	0.10
CME037C	Cysteine--tRNA ligase, chloroplast or mitochondrial	0.78	±	0.05
CMN116C	Hypothetical protein	0.78	±	0.02
CMB108C	Spindle checkpoint protein kinase MPS1	0.78	±	0.04
CMJ123C	Hypothetical protein	0.78	±	0.08
CMC016C	Similar to programmed cell death 2	0.78	±	0.04
CMT353C	Unknown snf2 family helicase	0.78	±	0.04
CMO193C	Hypothetical protein	0.78	±	0.04
CMM215C	Hypothetical protein	0.78	±	0.06
CMR099C	Probable pirin	0.78	±	0.11
CMG100C	Hypothetical protein	0.78	±	0.07
CMO319C	Hypothetical protein	0.78	±	0.06
CMR172C	Similar to 26S proteasome subunit 4	0.78	±	0.06
CMB006C	Hypothetical protein	0.78	±	0.07
CMS403C	Hypothetical protein	0.78	±	0.02
CMQ180C	Hypothetical protein	0.78	±	0.07
CMO203C	Hypothetical protein	0.78	±	0.05
CMR459C	Similar to fructosamine 3 kinase	0.78	±	0.05
CMT442C	Hypothetical protein	0.78	±	0.05
CMT291C	Hypothetical protein	0.78	±	0.05
CMA119C	Similar to oxidant-induced cell-cycle arrest Oca1p	0.78	±	0.03
CMQ116C	Similar to phytoene synthase	0.78	±	0.04
CMQ012C	Hypothetical protein	0.78	±	0.06
CME157C	Hypothetical protein	0.78	±	0.05
CMQ169C	Hypothetical protein	0.78	±	0.06
CMR331C	Similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	0.78	±	0.11
CME131C	Hypothetical protein	0.78	±	0.03
CMT190C	Riboflavin kinase/FMN adenylyltransferase	0.78	±	0.02
CMJ216C	ATP-binding protein of ABC transporter	0.78	±	0.06
CMP176C	Similar to TFIIF interacting component of CTD phosphatase Fcp1p	0.78	±	0.06

CMM013C	Queuine tRNA ribosyltransferase	0.78	±	0.06
CML057C	Unknown kinase with aarF domain	0.78	±	0.01
CMI255C	Importin beta-3 subunit (Karyopherin beta-3 subunit) (Ran-binding protein 5)	0.78	±	0.07
CMR203C	Vesicle coat complex COPII, subunit Sec31	0.78	±	0.03
CMI124C	Hypothetical protein	0.78	±	0.05
CMQ096C	Hypothetical protein	0.78	±	0.07
CMP198C	Hypothetical protein	0.78	±	0.03
CML142C	Similar to vacuolar protein sorting 13	0.78	±	0.09
CMS179C	Similar to protein phosphatase 2C	0.78	±	0.05
CMT336C	Hypothetical protein	0.78	±	0.06
CMR151C	Similar to cytochrome b5	0.78	±	0.09
CMQ233C	Hypothetical protein	0.78	±	0.16
CMJ198C	Similar to protoporphyrinogen oxidase HemK	0.78	±	0.08
CMT079C	Hypothetical protein	0.78	±	0.05
CMF047C	Probable mercaptopyruvate sulfurtransferase	0.78	±	0.05
CMN306C	Hypothetical protein	0.78	±	0.08
CMR402C	Similar to rotamase/parvulin-type peptidyl-prolyl cis-trans isomerase	0.78	±	0.02
CMI142C	Dihydroxy-acid dehydratase	0.78	±	0.06
CME138C	Hypothetical protein	0.78	±	0.12
CMS232C	K efflux antiporter KEA1	0.78	±	0.16
CMM030C	NADH dehydrogenase I (Complex I) beta subcomplex 9 (B22)	0.78	±	0.08
CMI086C	Phosphoserine phosphatase (PSP) (O-phosphoserine phosphohydrolase)	0.78	±	0.07
CMQ274C	Similar to oxidoreductase	0.78	±	0.04
CMN132C	Box H/ACA snoRNP component NHP2	0.78	±	0.04
CMF141C	Similar to prefoldin subunit3	0.78	±	0.13
CMH066C	Mitochondrial ribosomal protein S15 precursor	0.78	±	0.07
CMA106C	Similar to alpha-glucosidase	0.78	±	0.04
CMR298C	Heat shock protein DnaJ	0.78	±	0.06
CMT266C	MYB-related protein	0.78	±	0.08
CMA118C	Hypothetical protein	0.78	±	0.08
CMF026C	Hypothetical protein	0.78	±	0.05
CMQ050C	Hypothetical protein	0.78	±	0.10
CMS402C	Hypothetical protein	0.78	±	0.05
CMQ142C	Similar to light harvesting protein	0.78	±	0.02
CMR197C	RNA polymerase I, III common subunit	0.78	±	0.08
CMT591C	Hypothetical protein	0.78	±	0.06
CMT323C	Hypothetical protein	0.78	±	0.07
CMR224C	RNA polymerase II largest subunit	0.78	±	0.05
CMT100C	Hypothetical protein	0.78	±	0.07
CMR181C	Unknown transporter	0.77	±	0.08
CMB089C	Hypothetical protein	0.77	±	0.08
CMS086C	Hypothetical protein	0.77	±	0.05
CMO058C	Rub1-activating enzyme E1 N subunit	0.77	±	0.05

CMQ386C	Similar to V-type ATPase V1 subunit H	0.77	±	0.09
CME087C	Probable acetyl-CoA C-acetyltransferase	0.77	±	0.08
CML179C	Lipoic acid synthetase	0.77	±	0.03
CMS437C	Hypothetical protein	0.77	±	0.07
CMT445C	Acetoacetyl-CoA synthetase	0.77	±	0.08
CMP210C	Hypothetical protein	0.77	±	0.11
CMB140C	Hypothetical protein	0.77	±	0.05
CMP158C	Similar to dehydrogenase	0.77	±	0.06
CMJ253C	Similar to mitochondrial presequence translocase subunit Tim44	0.77	±	0.05
CMS227C	Ubiquinone/menaquinone biosynthesis methyltransferase	0.77	±	0.06
CMS459C	Similar to RNA export mediator	0.77	±	0.09
CMJ148C	Hypothetical protein	0.77	±	0.09
CMO226C	Oligosaccharyl transferase STT3	0.77	±	0.05
CMK115C	Acyl-CoA oxidase ACX3	0.77	±	0.05
CMM081C	Hypothetical protein	0.77	±	0.11
CMP273C	Hypothetical protein	0.77	±	0.10
CMT302C	Hypothetical protein	0.77	±	0.06
CMT617C	Coatomer protein complex, subunit beta 2	0.77	±	0.05
CMC177C	Similar to calcium binding mitochondrial carrier ARALAR1	0.77	±	0.10
CMF075C	Hypothetical protein	0.77	±	0.05
CMT314C	Phosphomannomutase	0.77	±	0.08
CMG113C	Protein phosphatase 2C, with protein kinase domain	0.77	±	0.06
CMC156C	Similar to trefoil factor	0.77	±	0.08
CMK242C	Unknown RNA-binding protein	0.77	±	0.04
CMC063C	Probable ribosome biogenesis protein NEP1	0.77	±	0.17
CMA121C	Unknown zinc finger protein	0.77	±	0.08
CML287C	Helicase-like protein	0.77	±	0.06
CMP205C	Leucine--tRNA ligase	0.77	±	0.09
CMS469C	Similar to Raf/ATN-like protein kinase, with ACT domain	0.77	±	0.03
CMS468C	Similar to DRAP deaminase involved in riboflavin biosynthesis	0.77	±	0.05
CMK188C	Phosphoglycerate mutase	0.77	±	0.05
CMH034C	Probable DNA repair endonuclease XPF	0.77	±	0.05
CMN235C	Similar to chlorophyll a/b-binding protein, CP24	0.77	±	0.07
CMF156C	Cystathionine gamma-synthase	0.77	±	0.06
CMO214C	Hypothetical protein	0.77	±	0.04
CMK206C	Hypothetical protein	0.77	±	0.02
CMQ184C	Hypothetical protein	0.77	±	0.05
CMQ141C	Hypothetical protein	0.77	±	0.06
CMN243C	Propionyl-Coenzyme A carboxylase, alpha subunit, mitochondrial precursor	0.77	±	0.05
CMK221C	Hypothetical protein	0.77	±	0.03
CMB036C	Similar to DnaJ family molecular chaperone	0.77	±	0.05
CMQ158C	Unknown deacetylase	0.77	±	0.11
CMH185C	Hypothetical protein	0.77	±	0.13

CMT349C	Hypothetical protein	0.77	±	0.03
CME181C	Similar to serine/threonine protein phosphatase	0.77	±	0.09
CMP292C	2-dehydro-3-deoxyphosphogluconate aldolase, 4-hydroxy-2-oxoglutarate aldolase	0.77	±	0.09
CMN280C	Hypothetical protein	0.77	±	0.02
CMI275C	Hypothetical protein	0.77	±	0.04
CMK083C	DEAD box protein	0.77	±	0.23
CMR328C	Hypothetical protein	0.77	±	0.04
CMN215C	Phosphatidate cytidylyltransferase	0.77	±	0.02
CMC031C	Hypothetical protein	0.77	±	0.02
CMO271C	Cell cycle protein kinase CDC7	0.77	±	0.04
CMG186C	Hypothetical protein	0.77	±	0.04
CMK211C	Hypothetical protein	0.77	±	0.10
CML032C	Sodium-dependent transporter	0.77	±	0.04
CMS476C	Similar to regulator for ribosome biogenesis regulatory protein RRS1 of yeast	0.77	±	0.06
CMJ172C	Hypothetical protein	0.77	±	0.13
CMK184C	Hypothetical protein	0.77	±	0.03
CMS155C	Similar to Low-affinity zinc transport protein; Zrt2p	0.77	±	0.07
CMK078C	Hypothetical protein	0.77	±	0.10
CML309C	Hypothetical protein	0.77	±	0.03
CMS494C	Hypothetical protein	0.77	±	0.09
CML243C	IMP dehydrogenase	0.77	±	0.03
CMJ191C	Tryptophan synthase beta chain	0.77	±	0.04
CMT161C	Chloroplast signal recognition particle component SRP43	0.77	±	0.09
CMG174C	Similar to glycogenin glucosyltransferase	0.77	±	0.03
CMC062C	Similar to Tat-interacting protein TIP30	0.77	±	0.04
CMB027C	Similar to oxidation resistance protein Oxr1	0.77	±	0.08
CMD072C	Hypothetical protein	0.77	±	0.04
CML119C	Probable transcription regulator SIR2	0.77	±	0.07
CMI058C	ATP-binding cassette, sub-family E (RLI), member 1	0.77	±	0.02
CMS349C	Hypothetical protein	0.77	±	0.05
CMI243C	Plastid terminal oxidase	0.77	±	0.06
CMT277C	Hypothetical protein	0.77	±	0.06
CMN259C	Similar to phospholpid scramblase	0.77	±	0.03
CME112C	Hypothetical protein	0.77	±	0.12
CMC119C	Hypothetical protein	0.77	±	0.08
CML156C	Similar to ATP-dependent RNA helicase	0.77	±	0.06
CMD144C	Hypothetical protein	0.77	±	0.07
CMN137C	Hypothetical protein	0.77	±	0.03
CMJ189C	Probable mRNA cap binding protein 80	0.77	±	0.04
CMF087C	Hypothetical protein	0.77	±	0.05
CMJ117C	Sulfite reductase (ferredoxin)	0.77	±	0.08
CMQ278C	7,8-dihydropteroate synthase/2-amino-4-hydroxy-6-hydroxymethyldihydropteridine (fusion)	0.77	±	0.03
CMS219C	Similar to dsRNA-specific ribonuclease	0.77	±	0.02

CMT354C	Probable GTPase activating protein	0.76	±	0.03
CMD074C	Hypothetical protein	0.76	±	0.06
CMN042C	Hypothetical protein	0.76	±	0.03
CMR447C	Deoxyribonuclease	0.76	±	0.06
CMJ240C	Serine palmitoyltransferase	0.76	±	0.12
CMP184C	Hypothetical protein, Lactoylglutathione lyase	0.76	±	0.09
CMN111C	Similar to protein disulfide isomerase-related protein P5 precursor	0.76	±	0.03
CMM177C	Similar to D-amino acid oxidase	0.76	±	0.04
CMJ143C	Hypothetical protein	0.76	±	0.02
CMR177C	Similar to ferredoxin	0.76	±	0.07
CMQ385C	Probable pre-mRNA splicing factor ATP-dependent RNA helicase PRP16	0.76	±	0.01
CMO275C	Similar to cytidine deaminase	0.76	±	0.06
CMG098C	Similar to COP-coated vesicle membrane protein p24	0.76	±	0.02
CMR125C	Similar to nucleoporin complex subunit	0.76	±	0.05
CMR079C	Similar to thylakoid lumen rotamase	0.76	±	0.03
CMN279C	Similar to thioredoxin f	0.76	±	0.10
CMQ330C	Hypothetical protein	0.76	±	0.08
CMC070C	Similar to ubiquitin-specific processing protease Ubp2p	0.76	±	0.06
CMK129C	Nitrate ABC transporter ATP-binding protein	0.76	±	0.04
CMT069C	Hypothetical protein	0.76	±	0.07
CME090C	Hypothetical protein	0.76	±	0.06
CMR179C	Mitochondrial ribosomal protein L12 precursor	0.76	±	0.12
CME115C	Hypothetical protein	0.76	±	0.03
CMR199C	Similar to transitional endoplasmic reticulum ATPase	0.76	±	0.04
CMQ086C	Retromer component VPS26	0.76	±	0.03
CMF162C	Similar to general negative regulator of transcription cdc39	0.76	±	0.04
CMF067C	Hypothetical protein	0.76	±	0.07
CMT127C	Hypothetical protein	0.76	±	0.06
CMJ303C	Hypothetical protein	0.76	±	0.05
CMI252C	DNA topoisomerase I	0.76	±	0.05
CMS215C	Similar to CDK7/cyclin H assembly factor MAT1/TFIIH subunit	0.76	±	0.05
CML217C	Hypothetical protein	0.76	±	0.05
CMS183C	Hypothetical protein	0.76	±	0.04
CMT558C	Chaperonin containing TCP1, subunit 7 (eta)	0.76	±	0.13
CMJ047C	Histidine--tRNA ligase	0.76	±	0.00
CMM188C	Acetyl-CoA carboxylase, multifunctional enzyme, cytoplasmic	0.76	±	0.04
CMR174C	Hypothetical protein	0.76	±	0.07
CMP206C	Similar to U6 snRNA-associated Sm-like protein lsm7	0.76	±	0.05
CMM178C	NADH dehydrogenase type II, chloroplast precursor	0.76	±	0.05
CMI231C	Ubiquinone/menaquinone biosynthesis methlytransferase	0.76	±	0.08
CMI092C	Similar to protein-tyrosine phosphatase, CDC14 homolog	0.76	±	0.05
CMS088C	Hypothetical protein	0.76	±	0.06
CMC029C	Hypothetical protein	0.76	±	0.02

CMN017C	Dihydrolipoamide S-acetyltransferase	0.76	±	0.07
CMS225C	Similar to glycosyl transferase	0.76	±	0.09
CMR094C	Hypothetical protein	0.76	±	0.15
CML108C	Hypothetical protein	0.76	±	0.04
CMT398C	Hypothetical protein	0.76	±	0.09
CMT170C	Hypothetical protein	0.76	±	0.10
CMG139C	Similar to flavin-containing monooxygenase FMO-1	0.76	±	0.08
CMF070C	Probable mannosyl-oligosaccharide glucosidase	0.76	±	0.04
CMK304C	Similar to syntaxin	0.76	±	0.02
CMQ150C	Hypothetical protein	0.76	±	0.04
CMT418C	Similar to bifunctional aspartokinase/homoserine dehydrogenase	0.76	±	0.04
CMO091C	Similar to myosin heavy chain	0.76	±	0.05
CMG006C	Hypothetical protein	0.76	±	0.03
CML253C	Hypothetical protein	0.76	±	0.05
CMS475C	Similar to tRNA isopentenyltransferase	0.76	±	0.08
CMG103C	Similar to amino acid transporter protein	0.76	±	0.07
CMN316C	Hypothetical protein	0.76	±	0.03
CMK208C	Similar to U5 snRNP-specific protein	0.76	±	0.03
CMT138C	Hypothetical protein	0.76	±	0.07
CMI122C	Similar to RNA-binding protein with RRM	0.76	±	0.06
CMN323C	Unknown transaminase	0.76	±	0.10
CMQ317C	Hypothetical protein	0.76	±	0.02
CMK252C	Hypothetical protein	0.76	±	0.07
CMP068C	Hypothetical protein	0.76	±	0.06
CMM315C	Hypothetical protein	0.76	±	0.09
CMA063C	Hypothetical protein	0.76	±	0.10
CMK110C	Hypothetical protein	0.76	±	0.03
CMR169C	Hypothetical protein	0.76	±	0.07
CMO323C	Hypothetical protein	0.75	±	0.05
CMC171C	Similar to ATP-dependent RNA helicase A	0.75	±	0.07
CMR461C	Hypothetical protein	0.75	±	0.03
CMD046C	Hypothetical protein	0.75	±	0.06
CMO228C	Hypothetical protein	0.75	±	0.05
CMO122C	Hypothetical protein	0.75	±	0.07
CMS120C	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	0.75	±	0.05
CML270C	Hypothetical protein	0.75	±	0.05
CMG011C	Hypothetical protein	0.75	±	0.06
CMB034C	Hypothetical protein	0.75	±	0.03
CMQ390C	Hypothetical protein	0.75	±	0.05
CMC124C	Smt3-activating enzyme E1 N subunit	0.75	±	0.01
CMN105C	ATP-binding cassette, sub-family B (ATM)	0.75	±	0.08
CMA031C	Hypothetical protein	0.75	±	0.04
CMQ294C	Similar to ankyrin	0.75	±	0.04

CMJ010C	Hypothetical protein	0.75	±	0.05
CMJ263C	Acyl-Coenzyme A thioesterase, mitochondrial precursor	0.75	±	0.06
CMF082C	Similar to oxygen regulated protein precursor	0.75	±	0.08
CMF098C	Similar to glycine cleavage system H protein	0.75	±	0.08
CMJ098C	Proline--tRNA ligase	0.75	±	0.02
CMO270C	Probable DNA polymerase (POL I)	0.75	±	0.03
CMN115C	Similar to Na^+-driven multidrug efflux pump	0.75	±	0.03
CMD159C	Similar to separin (cut1)	0.75	±	0.06
CMT236C	Hypothetical protein	0.75	±	0.08
CMR311C	Probable Multidrug Resistance Associated Protein (MRP protein) (ATP/GTP-binding protein)	0.75	±	0.07
CMO257C	Similar to zinc finger protein myoneurin	0.75	±	0.07
CMP036C	Hypothetical protein	0.75	±	0.07
CMM323C	Ribonucleoside-diphosphate reductase alpha chain	0.75	±	0.04
CMB031C	UDP-glucose 6-dehydrogenase	0.75	±	0.02
CMI029C	Probable C-14 sterol reductase	0.75	±	0.03
CMN104C	Hypothetical protein	0.75	±	0.03
CME041C	Hypothetical protein	0.75	±	0.05
CMQ471C	Vesicle coat complex COPII, subunit Sec24	0.75	±	0.04
CMG102C	Similar to ZIP Zinc transporter	0.75	±	0.02
CMN319C	Hypothetical protein	0.75	±	0.07
CMN113C	Cullin 4	0.75	±	0.12
CMG108C	Similar to Raf/ATN-like protein kinase	0.75	±	0.04
CMS447C	Hypothetical protein	0.75	±	0.07
CMQ093C	Thioredoxin	0.75	±	0.00
CMS220C	Probable phosphate transporter	0.75	±	0.02
CMH061C	Eukaryotic translation initiation factor eIF-2 beta subunit	0.75	±	0.03
CMQ214C	Similar to aspartyl beta-hydroxylase	0.75	±	0.12
CMF158C	Dihydroneopterin aldolase	0.75	±	0.06
CMH188C	Hypothetical protein	0.75	±	0.08
CMN050C	Eukaryotic translation initiation factor eIF-4E	0.75	±	0.04
CMN023C	Manganese superoxide dismutase	0.75	±	0.04
CMH082C	Similar to DNA polymerase epsilon small subunit	0.75	±	0.06
CMP107C	Probable glutamate decarboxylase	0.75	±	0.02
CMS343C	Heat-shock protein (HSP110 family)	0.75	±	0.05
CME149C	Hypothetical protein	0.75	±	0.03
CMO219C	Insulin degrading enzyme	0.75	±	0.05
CMT377C	Hypothetical protein	0.75	±	0.05
CMP140C	Probable mitochondrial ATP-dependent RNA helicase Suv3	0.75	±	0.02
CMQ282C	Similar to nuclear cap-binding protein; CBP20	0.75	±	0.05
CMB019C	Similar to U3 snoRNP component Mpp10	0.75	±	0.03
CMF138C	Hypothetical protein	0.75	±	0.07
CMT320C	Hypothetical protein	0.75	±	0.08
CMR304C	Hypothetical protein	0.75	±	0.02

CMQ213C	Sigma subunit for chloroplast RNA polymerase	0.75	±	0.07
CMC024C	Ribosomal large subunit pseudouridine synthase D	0.75	±	0.00
CMT370C	Hypothetical protein	0.75	±	0.08
CMK285C	Eukaryotic translation initiation factor eIF-3 subunit 9	0.75	±	0.05
CME172C	P21-activated protein kinase	0.75	±	0.06
CMO209C	Hypothetical protein	0.75	±	0.08
CMM006C	Hypothetical protein	0.75	±	0.02
CMJ024C	Similar to plant adhesion molecule 1 (PAM1)	0.75	±	0.04
CMN207C	Similar to ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplast precursor	0.75	±	0.06
CMT274C	Similar to alpha/beta hydrolase	0.75	±	0.06
CMP189C	Similar to selenophosphate synthetase	0.75	±	0.05
CMP090C	Cyclin G associated kinase	0.75	±	0.08
CMD101C	Unknown GTP-binding protein	0.74	±	0.04
CMO220C	Similar to UDP-galactose transporter	0.74	±	0.05
CMR086C	Hypothetical protein	0.74	±	0.08
CME165C	Probable dimethyladenosine transferase	0.74	±	0.05
CMI089C	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)	0.74	±	0.10
CMG200C	1-pyrroline-5-carboxylate dehydrogenase	0.74	±	0.03
CMP124C	Probable lactoylglutathione lyase	0.74	±	0.04
CMI098C	Similar to eukaryotic translation elongation factor 2 (eEF-2)	0.74	±	0.03
CMS027C	Hypothetical protein	0.74	±	0.05
CMR132C	Hypothetical protein	0.74	±	0.12
CMR463C	Hypothetical protein	0.74	±	0.08
CMC152C	Hypothetical protein	0.74	±	0.11
CMS317C	Hypothetical protein	0.74	±	0.08
CMM293C	Hypothetical protein	0.74	±	0.09
CMI070C	Similar to syntaxin binding protein	0.74	±	0.05
CMT347C	Hypothetical protein	0.74	±	0.01
CMO100C	Hypothetical protein	0.74	±	0.03
CMQ321C	Hypothetical protein	0.74	±	0.06
CMR106C	Hypothetical protein	0.74	±	0.02
CMT374C	Zinc-finger protein	0.74	±	0.02
CMO169C	Similar to proliferation related acidic leucine rich protein PAL31	0.74	±	0.02
CMP130C	Similar to microtubule-associated protein	0.74	±	0.06
CMF097C	D-ribulokinase, ribitol kinase	0.74	±	0.04
CMJ223C	Similar to actin-related protein	0.74	±	0.10
CMH040C	Similar to glutamine amidotransferase class I	0.74	±	0.06
CMQ451C	Hypothetical protein	0.74	±	0.02
CMO249C	Similar to short-chain dehydrogenase	0.74	±	0.05
CMP312C	DBF2-related serine/threonine kinase Orb6	0.74	±	0.03
CMR152C	Homeobox protein	0.74	±	0.05
CMR397C	Eukaryotic translation initiation factor eIF-2B epsilon subunit	0.74	±	0.03
CMN254C	Hypothetical protein	0.74	±	0.04

CMJ132C	Hypothetical protein	0.74	±	0.02
CME158C	Similar to UGA suppressor tRNA-associated antigenic protein	0.74	±	0.05
CMF056C	NADH dehydrogenase type II	0.74	±	0.09
CMO146C	Similar to glutamine cyclotransferase	0.74	±	0.11
CMF014C	Hypothetical protein	0.74	±	0.05
CMT390C	Hypothetical protein	0.74	±	0.06
CMT571C	Probable adenylate kinase, chloroplast precursor	0.74	±	0.12
CMI229C	MutS family DNA mismatch repair protein MSH6	0.74	±	0.09
CMQ436C	Glycolate oxidase, peroxysomal	0.74	±	0.03
CMQ081C	Hypothetical protein	0.74	±	0.02
CMT633C	Ribulose-5-phosphate 3-epimerase	0.74	±	0.03
CMS354C	Eukaryotic translation initiation factor eIF-3 subunit 3	0.74	±	0.02
CMS467C	ATP-binding cassette, sub-family G (WBC), member 2	0.74	±	0.03
CMR253C	Hypothetical protein	0.74	±	0.02
CMT244C	Vesicle-inducing protein in plastids 1VIPP1	0.74	±	0.03
CML268C	Hypothetical protein	0.74	±	0.04
CMK277C	Hypothetical protein	0.74	±	0.13
CMK215C	Hypothetical protein	0.74	±	0.06
CMT077C	Similar to auxin-regulated protein	0.74	±	0.03
CMP289C	Similar to phytoene desaturase precursor	0.74	±	0.02
CMI220C	Hypothetical protein	0.74	±	0.07
CMT318C	Chaperonin containing TCP1, subunit 8 (theta)	0.74	±	0.04
CMT116C	Hypothetical protein	0.74	±	0.02
CMP137C	Similar to RAN binding protein	0.74	±	0.07
CMN109C	Similar to ahpc/TSA family protein	0.74	±	0.04
CML292C	Hypothetical protein	0.74	±	0.02
CMH282C	Similar to trefoil factor	0.74	±	0.09
CML194C	Phosphoribosylaminoimidazolecarboxamide formyltransferase (AICAR transformylase) / IMP cyclohydrolase (inosinicase) (IMP synthetase) (ATIC)	0.74	±	0.07
CME053C	Unknown M20/M25/M40 family peptidase	0.74	±	0.08
CMH056C	Protein kinase YAK1	0.74	±	0.02
CMT351C	Eukaryotic translation initiation factor eIF-6	0.74	±	0.02
CMQ459C	UDP-glucose:glycoprotein glucosyltransferase, precursor	0.74	±	0.08
CMB128C	ATP citrate lyase	0.74	±	0.09
CMJ196C	Hypothetical protein	0.74	±	0.05
CMK194C	Hypothetical protein	0.74	±	0.07
CMR384C	Ubiquitin-specific protease	0.73	±	0.09
CMS212C	Mitochondrial ribosomal protein S17 precursor	0.73	±	0.08
CMK268C	Hypothetical protein	0.73	±	0.07
CMO056C	Probable importin beta gene	0.73	±	0.05
CMS024C	Prolyl-tRNA synthetase	0.73	±	0.04
CMQ391C	Hypothetical protein	0.73	±	0.04
CMT512C	Hypothetical protein	0.73	±	0.09
CMS168C	Hypothetical protein	0.73	±	0.07

CMI050C	Catalase	0.73	±	0.04
CMT205C	Hypothetical protein	0.73	±	0.11
CMQ406C	Similar to splicing factor 3a, subunit 3	0.73	±	0.08
CMQ389C	Hypothetical protein	0.73	±	0.15
CMK267C	Hypothetical protein	0.73	±	0.01
CMO192C	Hypothetical protein	0.73	±	0.07
CMP092C	Hypothetical protein	0.73	±	0.08
CME123C	Hypothetical protein	0.73	±	0.04
CMA010C	Hypothetical protein	0.73	±	0.06
CMD079C	Hypothetical protein	0.73	±	0.01
CMR092C	Hypothetical protein	0.73	±	0.04
CMP354C	Probable Na^+-dependent inorganic phosphate cotransporter	0.73	±	0.08
CMI021C	Hypothetical protein	0.73	±	0.06
CMC017C	Similar to avirulence induced gene (AIG) 2	0.73	±	0.03
CMS207C	Similar to plant adhesion molecule 1, PAM1	0.73	±	0.07
CMS114C	RNA polymerase I second largest subunit	0.73	±	0.05
CMI132C	U3 snoRNP component Sof1p	0.73	±	0.06
CMN063C	Hypothetical protein	0.73	±	0.13
CMK019C	Similar to low affinity potassium transport; Trk2p	0.73	±	0.03
CMN301C	Similar to oxysterol-binding protein	0.73	±	0.01
CMT625C	Ppgpp synthetase/hydrolase Rel	0.73	±	0.03
CMM076C	Probable cryptochrome 1	0.73	±	0.11
CMO185C	Similar to hedgehog protein	0.73	±	0.01
CMK133C	Hypothetical protein	0.73	±	0.03
CMC040C	Hypothetical protein	0.73	±	0.02
CMS264C	Unknown dehydrogenase	0.73	±	0.13
CMQ171C	Sm protein F	0.73	±	0.08
CMJ133C	Similar to epsin	0.73	±	0.08
CMP013C	Probable suppressor protein of mitochondrial histone mutant	0.73	±	0.05
CMQ343C	Hypothetical protein	0.73	±	0.09
CMQ155C	Hypothetical protein	0.73	±	0.05
CMS166C	Similar to tetracycline resistance protein TetA	0.73	±	0.06
CMQ396C	Hypothetical protein	0.73	±	0.08
CMT213C	Hypothetical protein	0.73	±	0.07
CMT435C	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	0.73	±	0.07
CMS312C	Hypothetical protein	0.73	±	0.09
CMR103C	DNA polymerase zeta catalytic subunit	0.73	±	0.08
CMR355C	Hypothetical protein	0.73	±	0.04
CMT128C	Hypothetical protein	0.73	±	0.06
CMI080C	Hypothetical protein	0.73	±	0.08
CMS010C	Hypothetical protein	0.72	±	0.03
CMC111C	Transcription-repair coupling factor	0.72	±	0.03
CMQ324C	Polyribonucleotide nucleotidyltransferase	0.72	±	0.03

CMO347C	MYB-related protein	0.72	±	0.10
CMB130C	SnRNP core Sm-like protein SmX5	0.72	±	0.06
CMS202C	FAD synthetase (FMN adenyleltransferase) FAD1	0.72	±	0.03
CMF124C	Hypothetical protein	0.72	±	0.06
CMO208C	2-isopropylmalate synthase	0.72	±	0.11
CMC033C	Hypothetical protein	0.72	±	0.08
CMI026C	Similar to cyclin M2	0.72	±	0.05
CMK010C	Hypothetical protein	0.72	±	0.01
CMT581C	Hypothetical protein	0.72	±	0.03
CMC144C	Hypothetical protein	0.72	±	0.07
CMT210C	Hypothetical protein	0.72	±	0.07
CMH060C	Eukaryotic translation initiation factor eIF-3 subunit 10	0.72	±	0.04
CMN336C	Acetyl-CoA synthetase (ADP-forming)	0.72	±	0.03
CMQ456C	Probable apyrase	0.72	±	0.03
CMM130C	Hypothetical protein	0.72	±	0.06
CMB097C	Hypothetical protein	0.72	±	0.05
CMS180C	Hypothetical protein	0.72	±	0.05
CMB080C	Hypothetical protein	0.72	±	0.05
CMI304C	Mitochondrial ribosomal protein S1 precursor	0.72	±	0.06
CMI225C	Similar to RNA polymerase II transcriptional coactivator	0.72	±	0.08
CMQ369C	Similar to submergence induced, nickel-binding protein	0.72	±	0.10
CMR123C	Similar to histidinol-phosphate aminotransferase	0.72	±	0.13
CMI216C	Probable mitochondrial intermembrane space complex subunit Tim8	0.72	±	0.08
CMP083C	Uroporphyrinogen decarboxylase	0.72	±	0.04
CMT605C	Box C/D snoRNP component Nop58	0.72	±	0.06
CML327C	Hypothetical protein	0.72	±	0.08
CMS084C	Hypothetical protein	0.72	±	0.07
CMH168C	Pre-mRNA splicing factor PRP8	0.72	±	0.00
CMQ173C	Tousled-like kinase	0.72	±	0.05
CMR245C	LAMMER-like dual specificity kinase	0.72	±	0.05
CMH140C	Hypothetical protein	0.72	±	0.05
CMR066C	Succinate-semialdehyde dehydrogenase ($NADP^+$) (SSDH)	0.72	±	0.08
CMT547C	Probable starch associated protein R1	0.72	±	0.05
CMA130C	Hypothetical protein	0.72	±	0.02
CMI201C	Hypothetical protein	0.72	±	0.07
CMS028C	Hypothetical protein	0.72	±	0.05
CMC110C	Similar to transcription elongation factor TFIIS.h	0.72	±	0.03
CMR185C	E3 ubiquitin ligase SCF complex F-box protein subunit	0.72	±	0.06
CMJ053C	Hypothetical protein	0.71	±	0.10
CMB144C	Similar to suppressor of Ty 6 Spt6	0.71	±	0.04
CMQ073C	Hypothetical protein	0.71	±	0.07
CML296C	Hypothetical protein	0.71	±	0.01
CMO223C	Hypothetical protein	0.71	±	0.07

CMS440C	ATP-dependent Clp protease proteolytic subunit	0.71	±	0.08
CMS078C	3-isopropylmalate dehydratase	0.71	±	0.03
CMS489C	Hypothetical protein	0.71	±	0.04
CMR019C	Similar to ribosomal processing, RNA binding, nucleolar protein Nop77	0.71	±	0.05
CMC181C	Similar to translocon at the inner envelope membrane Tic22	0.71	±	0.06
CML083C	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	0.71	±	0.03
CMK189C	Hypothetical protein	0.71	±	0.05
CMP267C	Similar to phosphatidic acid-preferring phospholipase A1	0.71	±	0.01
CMJ255C	Similar to gamma-tubulin complex protein 2	0.71	±	0.02
CMS333C	Hypothetical protein	0.71	±	0.03
CMQ429C	Centromere protein E, CENP-E protein	0.71	±	0.04
CMI249C	Similar to syntaxin	0.71	±	0.04
CMS089C	Hypothetical protein	0.71	±	0.06
CMR272C	Probable cyclophilin B; CYPB	0.71	±	0.06
CMR423C	Probable DNA helicase required for mitotic chromosome segregation CHL1	0.71	±	0.01
CMD050C	Protein phosphatase 2 regulatory subunit A	0.71	±	0.07
CMK170C	Hypothetical protein	0.71	±	0.06
CMG196C	Mitochondrial translation elongation factor G1 (EF-G1)	0.71	±	0.05
CMQ029C	Arginine decarboxylase	0.71	±	0.08
CMK017C	Similar to tuberin	0.71	±	0.08
CMN307C	Hypothetical protein	0.71	±	0.07
CMT194C	Nonsense-mediated mRNA decay protein 3	0.71	±	0.05
CMM306C	Hypothetical protein	0.71	±	0.10
CMD030C	Hypothetical protein	0.71	±	0.09
CML190C	Cell division cycle protein cdc23, TPR protein, APC8	0.71	±	0.04
CMK223C	Similar to mitochondrial GTP binding protein trmE	0.71	±	0.03
CMO019C	Unknown conserved AAA protein	0.71	±	0.05
CMR233C	Hypothetical protein	0.71	±	0.03
CMN250C	Chloroplast signal recognition particle (SRP) receptor FtsY	0.71	±	0.01
CME133C	Hypothetical protein	0.71	±	0.05
CMJ286C	Polyadenylate-binding protein	0.71	±	0.09
CMB053C	Probable xylulose kinase	0.71	±	0.04
CMK141C	Glycerate kinase, phosphoribulokinase/uridine kinase-like	0.71	±	0.03
CMT333C	Similar to inorganic phosphate transporter	0.71	±	0.05
CMF150C	B regulatory subunit of protein phosphatase 2A	0.71	±	0.06
CMT427C	Ruvb-like DNA/RNA helicase reptin	0.71	±	0.04
CMO148C	Transposon	0.71	±	0.12
CMB047C	Hypothetical protein	0.71	±	0.04
CMP127C	Hypothetical protein	0.71	±	0.06
CMP215C	Copper-transporting P-type ATPase	0.71	±	0.06
CMF117C	Phosphoribulokinase	0.71	±	0.01
CMH129C	Hypothetical protein	0.71	±	0.05
CMR221C	Similar to dolichyl-phosphate-mannose--protein mannosyltransferase	0.71	±	0.03

CMB151C	Adenylylsulfate kinase	0.71	±	0.03
CMJ202C	Similar to chloroplast import-associated channel Toc75	0.71	±	0.04
CMS043C	Probable transporter, Pfam sugar transporter	0.71	±	0.04
CMP094C	Hypothetical protein	0.71	±	0.06
CMC113C	Hypothetical protein	0.71	±	0.09
CMP021C	Probable two-component sensor histidine kinase	0.71	±	0.03
CMB145C	Hypothetical protein	0.71	±	0.06
CMR052C	Ferredoxin-NADP$^+$ reductase	0.71	±	0.02
CMG044C	Pre-mRNA splicing factor ATP-dependent RNA helicase PRP22	0.71	±	0.08
CMC065C	Hypothetical protein	0.71	±	0.05
CME195C	Hypothetical protein	0.71	±	0.06
CMM179C	Probable sulfur deprivation response regulator sac1	0.70	±	0.05
CMH195C	SWI/SNF complex compenent Snf2	0.70	±	0.09
CMT099C	Hypothetical protein	0.70	±	0.13
CMC037C	Glycine--tRNA ligase, class II	0.70	±	0.06
CMF133C	Ethanolaminephosphotransferase	0.70	±	0.04
CMQ146C	Hypothetical protein	0.70	±	0.09
CMT241C	Calcium-transporting ATPase, endoplasimc reticulum type	0.70	±	0.02
CMM239C	Hypothetical protein	0.70	±	0.03
CMD173C	Hypothetical protein	0.70	±	0.05
CMJ161C	Hypothetical protein	0.70	±	0.06
CMT431C	Proteasome regulatory particle subunit	0.70	±	0.02
CMT480C	Hypothetical protein	0.70	±	0.09
CMS282C	Probable DNA repair protein REV1, deoxycytidyl transferase	0.70	±	0.05
CMI147C	Secreted protein (mpt70)	0.70	±	0.06
CME033C	Hypothetical protein	0.70	±	0.03
CMI052C	Probable sulfate permease	0.70	±	0.04
CMO046C	Similar to PCAF histone acetylase complex subunit	0.70	±	0.07
CMP106C	Hypothetical protein	0.70	±	0.04
CMC035C	Hypothetical protein	0.70	±	0.07
CMO023C	Similar to rRNA biogenesis protein; rrp5 homolog; multiple S1 rna binding domain protein	0.70	±	0.05
CMH155C	Similar to ATP-dependent DNA helicase RecQ	0.70	±	0.05
CMK225C	Hypothetical protein	0.70	±	0.06
CMN139C	CDK-activating kinase	0.70	±	0.02
CMA054C	Hypothetical protein	0.70	±	0.10
CMR137C	Similar to developmental gene, multi-sex-combs	0.70	±	0.09
CMI144C	Similar to ring finger protein	0.70	±	0.08
CMM068C	Citrate synthase	0.70	±	0.02
CMR004C	Hypothetical protein	0.70	±	0.07
CMD164C	Similar to syntaxin binding protein Unc-18	0.70	±	0.05
CMT107C	Hypothetical protein	0.70	±	0.09
CMC011C	ATP-binding cassette, sub-family D (ALD), member 3	0.70	±	0.11
CMT372C	Hypothetical protein	0.70	±	0.08

CMP323C	Hypothetical protein	0.70	±	0.07
CML116C	Hypothetical protein	0.70	±	0.05
CMJ107C	Hypothetical protein	0.70	±	0.02
CME045C	Hypothetical protein	0.70	±	0.02
CMS218C	Similar to mitochondrial distribution and morphology; Mdm38p	0.70	±	0.03
CMB121C	Hypothetical protein	0.70	±	0.08
CMD070C	Probable FKBP-type peptidyl-prolyl cis-trans isomerase	0.70	±	0.04
CMO136C	Coproporphyrinogen III oxidase	0.70	±	0.17
CMN161C	Similar to vegetatible incompatibility protein HET-E-1	0.70	±	0.03
CMH174C	Hypothetical protein	0.70	±	0.03
CMP283C	Unknown zinc finger protein	0.70	±	0.09
CMK258C	Hypothetical protein	0.69	±	0.07
CMR246C	Hypothetical protein	0.69	±	0.06
CMR078C	Hypothetical protein	0.69	±	0.03
CMQ289C	Glyoxylate reductase/hydroxypyruvate reductase	0.69	±	0.02
CML192C	U5 small nuclear ribonucleoprotein 200 kDa helicase	0.69	±	0.01
CMN299C	Similar to hedgehog protein	0.69	±	0.07
CMK074C	Similar to glutathione S-transferase	0.69	±	0.07
CMT488C	Glutamine-dependent NAD synthetase	0.69	±	0.07
CMP088C	Hypothetical protein	0.69	±	0.05
CMM019C	Chloroplast ribosomal protein S1 precursor	0.69	±	0.19
CMT344C	Hypothetical protein	0.69	±	0.07
CMR248C	Probable PET127 (probable mitochondrial translation system component)	0.69	±	0.03
CMK293C	AAA-type ATPase family protein	0.69	±	0.05
CMK192C	Sec61 alpha subunit	0.69	±	0.07
CMH236C	Hypothetical protein	0.69	±	0.04
CMS184C	Hypothetical protein	0.69	±	0.08
CMQ347C	Probable D-lactate dehydrogenase (cytochrome)	0.69	±	0.03
CMM191C	Hypothetical protein	0.69	±	0.04
CMR110C	Similar to glutathione S-transferase	0.69	±	0.07
CMS073C	Eukaryotic translation initiation factor eIF-4G	0.69	±	0.10
CMO352C	ATP-dependent RNA helicase	0.69	±	0.06
CMS482C	Probable N-acetyltransferase MAK3	0.69	±	0.04
CMR212C	Similar to vacuolar assembly protein Vps41	0.69	±	0.07
CMT167C	Hypothetical protein	0.69	±	0.07
CMR219C	Hypothetical protein	0.69	±	0.03
CMN193C	Pepsin A precursor	0.69	±	0.05
CMK146C	Hypothetical protein	0.69	±	0.01
CMT439C	Probable histidinol-phosphate aminotransferase	0.69	±	0.04
CMS051C	Hypothetical protein	0.69	±	0.06
CMD032C	Hypothetical protein	0.69	±	0.06
CMT329C	Unknown hydrolase	0.69	±	0.02
CMA024C	Hypothetical protein	0.69	±	0.07

CMG159C	Hypothetical protein	0.69	±	0.05
CMR441C	Hypothetical protein	0.69	±	0.04
CMJ045C	Hypothetical protein	0.69	±	0.07
CMH123C	Hypothetical protein	0.68	±	0.08
CMB142C	Similar to S2P metalloprotease	0.68	±	0.06
CMD066C	Hypothetical protein	0.68	±	0.04
CMD040C	Similar to apospory-associated protein C	0.68	±	0.03
CMQ272C	Hypothetical protein	0.68	±	0.05
CMF033C	Nucleolar RNA helicase II/Gu	0.68	±	0.10
CML121C	Hypothetical protein	0.68	±	0.08
CMN308C	Hypothetical protein	0.68	±	0.02
CMR173C	Hypothetical protein	0.68	±	0.05
CMM162C	Adenylosuccinate synthetase	0.68	±	0.05
CMQ407C	Hypothetical protein	0.68	±	0.05
CMQ352C	Hypothetical protein	0.68	±	0.02
CMK030C	Hypothetical protein	0.68	±	0.07
CMR337C	Hypothetical protein	0.68	±	0.07
CMR409C	Hypothetical protein	0.68	±	0.05
CMR167C	Methylenetetrahydrofolate dehydrogenase (NADP$^+$)/methenyltetrahydrofolate cyclohydrolase	0.68	±	0.11
CMK238C	Hypothetical protein	0.68	±	0.04
CMT158C	Hypothetical protein	0.68	±	0.03
CMQ067C	Phosphomannomutase	0.68	±	0.05
CMS413C	Hypothetical protein	0.68	±	0.08
CMQ054C	Hypothetical protein	0.68	±	0.07
CMO043C	Hypothetical protein	0.68	±	0.05
CMJ093C	Similar to Na$^+$/H$^+$ antiporter	0.68	±	0.03
CMI226C	Similar to ankyrin	0.68	±	0.03
CML205C	Heat shock protein DnaK (HSP70)	0.68	±	0.00
CMN153C	Hypothetical protein	0.68	±	0.09
CMN129C	Fusion protein of aspartate kinase and homoserine dehydrogenase	0.68	±	0.11
CMR084C	Hypothetical protein	0.68	±	0.04
CML228C	Similar to serine/threonine kinase KIN82	0.68	±	0.04
CMS398C	1-aminocyclopropane-1-carboxylate synthase	0.68	±	0.06
CMT622C	Hypothetical protein	0.68	±	0.00
CMH186C	Hypothetical protein	0.68	±	0.06
CMT577C	Hypothetical protein	0.68	±	0.03
CMJ134C	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	0.68	±	0.06
CMA064C	Unknown cyanobacterial protein	0.68	±	0.10
CMM186C	Hypothetical protein	0.68	±	0.06
CMT215C	Hypothetical protein	0.68	±	0.05
CMI055C	Mitochondrial ribosomal protein L24 precursor	0.68	±	0.10
CMB066C	Hypothetical protein	0.68	±	0.06
CMG105C	Probable WD-repeat membrane protein	0.68	±	0.04

CMO008C	Similar to ribonuclease P	0.68	±	0.02
CMC009C	Similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase	0.68	±	0.05
CMF182C	Aminopeptidase N	0.68	±	0.06
CMJ034C	bZIP transcription factor	0.68	±	0.06
CMK075C	Hypothetical protein	0.68	±	0.03
CMG048C	Coatomer protein complex, subunit beta	0.68	±	0.08
CMH194C	Similar to translational activator GCN1	0.67	±	0.02
CMH117C	RNA polymerase II second largest subunit	0.67	±	0.06
CMN255C	Hypothetical protein	0.67	±	0.05
CMS338C	Hypothetical protein	0.67	±	0.06
CMR299C	Stress-induced phosphoprotein STI1	0.67	±	0.10
CMP278C	Similar to acyl-coenzyme A-binding protein	0.67	±	0.04
CMR240C	Amidophoribosyltransferase	0.67	±	0.02
CMP064C	Similar to solute carrier protein	0.67	±	0.04
CMM189C	3-hydroxy-3-methylglutaryl-Coenzyme A synthase, cytoplasmic or mitochondrial	0.67	±	0.04
CMS177C	Hypothetical protein	0.67	±	0.02
CMA013C	Hypothetical protein	0.67	±	0.07
CMN318C	Hypothetical protein	0.67	±	0.09
CMO107C	ATP-dependent RNA helicase	0.67	±	0.07
CMT342C	Hypothetical protein	0.67	±	0.09
CMR085C	Similar to nuclear RNA binding protein	0.67	±	0.06
CMR121C	Ketol-acid reductoisomerase	0.67	±	0.08
CMT288C	Hypothetical protein	0.67	±	0.03
CMQ426C	Similar to DNA polymerase lambda	0.67	±	0.04
CMT290C	Similar to TFIIH subunit SSL1	0.67	±	0.06
CMR119C	Hypothetical protein	0.67	±	0.03
CMN110C	Hypothetical protein	0.67	±	0.11
CMT281C	Hypothetical protein	0.67	±	0.01
CMJ038C	Similar to hydrolase	0.67	±	0.08
CMH161C	Hypothetical protein	0.67	±	0.11
CMJ294C	Hypothetical protein	0.67	±	0.04
CMI161C	Hypothetical protein	0.67	±	0.10
CMI123C	Probable ribokinase	0.67	±	0.08
CMT178C	Hypothetical protein	0.67	±	0.05
CMI180C	Similar to magnesium transporter Mrs2p	0.67	±	0.07
CMF045C	Probable alpha-1,2-mannosidase, endoplasmic reticulum	0.67	±	0.08
CMM310C	Hypothetical protein	0.67	±	0.02
CMT114C	Similar to ribonuclease PH	0.67	±	0.04
CMN227C	S-adenosylmethionine synthetase	0.67	±	0.11
CMT538C	Hypothetical protein	0.67	±	0.08
CMT432C	Similar to charged amino acid rich leucine zipper factor-1	0.67	±	0.16
CMD180C	GATA transcription factor	0.67	±	0.05
CMN058C	Hypothetical protein	0.67	±	0.09

CMN257C	Similar to DNMT1 associated protein 1	0.66	±	0.05
CMK289C	20S core proteasome subunit beta 2	0.66	±	0.09
CME144C	Hypothetical protein	0.66	±	0.01
CMQ120C	3-deoxy-7-phosphoheptulonate synthase	0.66	±	0.05
CMS243C	DNA gyrase subunit A precursor	0.66	±	0.04
CMQ136C	Unknown PPR repeat protein	0.66	±	0.04
CMM180C	Hypothetical protein	0.66	±	0.07
CMP341C	Similar to phytoene dehydrogenase	0.66	±	0.11
CMI251C	Heat shock protein ClpB	0.66	±	0.05
CML183C	Hypothetical protein	0.66	±	0.07
CMQ423C	Hypothetical protein	0.66	±	0.02
CMP200C	Similar to bestrophin	0.66	±	0.02
CMJ043C	Phycocyanobilin lyase alpha subunit	0.66	±	0.05
CMQ259C	Hypothetical protein	0.66	±	0.09
CML262C	Integral membrane protein	0.66	±	0.09
CMQ399C	Hypothetical protein	0.66	±	0.02
CME162C	Rub1-conjugating enzyme E2	0.66	±	0.07
CML088C	Similar to chaperone grpE	0.66	±	0.06
CMD092C	Hypothetical protein	0.66	±	0.04
CMQ087C	Chloroplast F-type ATPase CF1 subunit gamma, precursor	0.66	±	0.01
CMK011C	3-dehydroquinate synthase	0.66	±	0.02
CME153C	Phosphatidylinositol-4-phosphate 5-kinase	0.66	±	0.04
CMO244C	Inner mitochondrial membrane protein Sco1p	0.66	±	0.10
CMR427C	Hypothetical protein	0.66	±	0.12
CMP143C	Hypothetical protein	0.66	±	0.03
CMJ016C	Aspartate kinase	0.66	±	0.05
CMP331C	Hypothetical protein	0.66	±	0.06
CML120C	Hypothetical protein	0.66	±	0.07
CMR493C	GATA transcription factor	0.66	±	0.04
CML204C	Prephenate dehydratase PDT	0.66	±	0.13
CMT028C	Mn superoxide dismutase	0.66	±	0.03
CMJ042C	Glyceraldehyde-3-phosphate dehydrogenase	0.65	±	0.06
CMS127C	Similar to nucleolar phosphoprotein	0.65	±	0.17
CMK191C	Hypothetical protein	0.65	±	0.02
CMP100C	Hypothetical protein	0.65	±	0.02
CMK308C	Short chain dehydrogenase	0.65	±	0.02
CMS074C	Hypothetical protein	0.65	±	0.06
CMM044C	Box H/ACA snoRNP rRNA pseudouridine syntase component dyskerin	0.65	±	0.13
CMP058C	Similar to ferredoxin-thioredoxin reductase, variable chain	0.65	±	0.14
CMG199C	Hypothetical protein	0.65	±	0.05
CMP294C	26S proteasome ATP-dependent regulatory subunit	0.65	±	0.03
CMM158C	Chloroplast ascorbate hydrogen peroxidase, precursor	0.65	±	0.06
CMO306C	Probable myo-inositol dehydrogenase	0.65	±	0.06

CMT211C	Similar to U3 snoRNP component Utp11p	0.65	±	0.11
CMA040C	Citrate synthase	0.65	±	0.12
CMP134C	Similar to transcriptional adaptor like protein	0.65	±	0.06
CMT615C	Hypothetical protein	0.65	±	0.07
CMS209C	Mitochondrial inner membrane insertion complex subunit Tim22	0.65	±	0.01
CMJ099C	Formate--tetrahydrofolate ligase	0.65	±	0.03
CMK034C	Hypothetical protein	0.65	±	0.05
CMT018C	Probable N-terminal acetyltransferase	0.65	±	0.02
CMQ284C	Similar to cation/proton antiporter	0.65	±	0.06
CMO042C	Hypothetical protein	0.65	±	0.05
CMO151C	Hypothetical protein	0.65	±	0.05
CML256C	Hypothetical protein	0.64	±	0.09
CMG041C	Unknown permease	0.64	±	0.03
CMT089C	Electron transfer flavoprotein-ubiquinone oxidoreductase	0.64	±	0.06
CML254C	Hypothetical protein	0.64	±	0.06
CMC047C	Hypothetical protein	0.64	±	0.02
CMT175C	Similar to long chain fatty acid elongation enzyme Elo1p	0.64	±	0.11
CMR293C	Hypothetical protein	0.64	±	0.09
CMO006C	Hypothetical protein	0.64	±	0.02
CMO183C	Hypothetical protein	0.64	±	0.09
CML273C	20S core proteasome subunit alpha 2	0.64	±	0.04
CMQ383C	Histidine biosynthesis bifunctional protein HisiE	0.64	±	0.06
CMG132C	Similar to acetylpolyamine aminohydolase	0.64	±	0.06
CME103C	Hypothetical protein	0.64	±	0.14
CMQ089C	Probable protease	0.64	±	0.07
CMM279C	Similar to tellurium resistance protein TerC	0.64	±	0.10
CMQ097C	Probable ATP-dependent protease Lon	0.64	±	0.09
CMT073C	Methylcrotonoyl-Coenzyme A carboxylase 1 (alpha or biotin-containing subunit)	0.64	±	0.03
CMS430C	Protein phosphatase 2A B55 regulatory subunit	0.64	±	0.04
CMJ138C	Similar to putative metal ion transporter	0.64	±	0.06
CMK098C	Acetyl-CoA synthetase	0.64	±	0.05
CMT214C	Proliferating cell nuclear protein P120	0.64	±	0.06
CMS147C	Similar to SANT domain protein SMRTER	0.64	±	0.11
CMT595C	Hypothetical protein	0.64	±	0.07
CMT105C	Nucleolar protein pescadillo	0.64	±	0.06
CME100C	Acyl-coenzyme A:cholesterol acyltransferase; ACAT	0.63	±	0.03
CMB021C	Chroloplast chaperonin CPN60, precursor	0.63	±	0.02
CMN022C	Hypothetical protein	0.63	±	0.11
CMQ203C	Hypothetical protein	0.63	±	0.06
CMQ179C	Hypothetical protein	0.63	±	0.10
CMM020C	Hypothetical protein	0.63	±	0.05
CMO273C	Hypothetical protein	0.63	±	0.01
CMG010C	Similar to TFIIE large subunit	0.63	±	0.09

CML113C	Hypothetical protein	0.63	±	0.10
CMO267C	Similar to ATP-dependent RNA helicase	0.63	±	0.07
CMS096C	Sulfate adenylyltransferase	0.63	±	0.09
CML266C	Hypothetical protein	0.63	±	0.04
CMR008C	Hypothetical protein	0.63	±	0.04
CME151C	GTP-binding protein of Nug1 family	0.63	±	0.03
CMQ114C	Hypothetical protein	0.63	±	0.09
CMQ021C	Glutamate 5-kinase	0.63	±	0.03
CME089C	Similar to TBP-binding phosphoprotein DR1	0.63	±	0.05
CMT604C	Hypothetical protein	0.63	±	0.04
CMT436C	Hypothetical protein	0.63	±	0.05
CMR073C	Probable mitochondrial carrier proteins; Pet8p	0.63	±	0.08
CMO044C	Lysine--tRNA ligase class II, chloroplast or mitochondrial	0.63	±	0.04
CMT058C	Phosphoribosylglycinamide formyltransferase (GAR transformylase, GART) (5'-phosphoribosylglycinamide transformylase)	0.63	±	0.05
CMD154C	Hypothetical protein	0.63	±	0.06
CMJ081C	Indole-3-glycerol phosphate synthase	0.63	±	0.10
CMT433C	Transcription factor E2F	0.63	±	0.04
CMS289C	Glutamine--tRNA ligase, chloroplast or mitochondrial?	0.63	±	0.10
CMS431C	Cytochrome c oxidase (Complex IV) assembly protein	0.63	±	0.06
CMN230C	Hypothetical protein	0.62	±	0.05
CMQ244C	Hypothetical protein	0.62	±	0.05
CMT057C	Hypothetical protein	0.62	±	0.04
CML043C	Hypothetical protein	0.62	±	0.06
CMH144C	1,4-alpha-Glucan branching enzyme	0.62	±	0.11
CMF179C	Hypothetical protein	0.62	±	0.01
CMM184C	Hypothetical protein	0.62	±	0.03
CMO165C	TATA-box binding protein-associated factor 9	0.62	±	0.07
CMQ342C	Similar to chloroplast inner membrane protein Tic110	0.62	±	0.17
CMP304C	Eukaryotic translation initiation factor eIF-2 gamma subunit	0.62	±	0.09
CMO212C	Magnesium chelatase subunit H	0.62	±	0.04
CML127C	Hypothetical protein	0.62	±	0.07
CMJ142C	Hypothetical protein	0.62	±	0.04
CMQ270C	Mitochondrial chaperonin Hsp60, precursor	0.62	±	0.04
CMA061C	Heat shock protein of Hsp90 family	0.62	±	0.09
CMP049C	Hypothetical protein	0.62	±	0.04
CMT183C	Hypothetical protein	0.62	±	0.06
CMA042C	Acetyl-CoA acetyltransferase	0.62	±	0.10
CMQ031C	Hypothetical protein	0.62	±	0.02
CMF062C	Mitochondrial general import pore subunit Tom40	0.62	±	0.05
CMJ017C	Hypothetical protein	0.62	±	0.04
CMC066C	Signal recognition particle SRP54 homolog ffh	0.61	±	0.05
CMH162C	Hypothetical protein	0.61	±	0.03
CMR301C	Hypothetical protein	0.61	±	0.01

CMT081C	Plastid-lipid-associated protein PAP	0.61	±	0.10
CMP091C	Similar to mRNA cap methyltransferase	0.61	±	0.05
CMT176C	Hypothetical protein	0.61	±	0.01
CMB048C	60S acidic ribosomal protein PO	0.61	±	0.02
CMP174C	Hypothetical protein	0.61	±	0.03
CML178C	Probable long chain fatty acid elongation enzyme Elo1p	0.61	±	0.07
CMK157C	Hypothetical protein	0.61	±	0.04
CML202C	Similar to SR family splicing factor SC35	0.61	±	0.04
CMN317C	Hypothetical protein	0.61	±	0.05
CMT246C	Hypothetical protein	0.61	±	0.07
CME146C	Polo-like protein kinase	0.61	±	0.01
CMQ336C	Leucyl--tRNA ligase	0.60	±	0.04
CMO259C	Hypothetical protein	0.60	±	0.01
CMK262C	Hypothetical protein	0.60	±	0.15
CMI185C	Probable leucine aminopeptidase	0.60	±	0.01
CMK028C	Eukaryotic translation initiation factor eIF-4A	0.60	±	0.11
CMT056C	Probable sodium-dependent transporter	0.60	±	0.05
CMN237C	ATP-dependent Clp protease proteolytic subunit	0.60	±	0.01
CMQ281C	Hypothetical protein	0.60	±	0.01
CMS490C	Probable malic acid transport protein, malate permease	0.60	±	0.16
CMR368C	Unknown amidotransferase	0.60	±	0.05
CMH200C	Similar to V-type ATPase V1 subunit G	0.60	±	0.01
CMQ040C	Hypothetical protein	0.60	±	0.10
CMT160C	60S ribosomal protein L24 homolog	0.60	±	0.03
CMO349C	Similar to Machado-Joseph disease protein ataxin-3	0.60	±	0.05
CMS105C	Hypothetical protein	0.60	±	0.08
CML030C	DnaJ (Hsp40) homolog, subfamily A	0.60	±	0.09
CML234C	Hypothetical protein	0.60	±	0.02
CMP269C	Hypothetical protein	0.60	±	0.00
CMJ252C	Probable rRNA methyltransferase pmt2	0.60	±	0.08
CMQ348C	Eukaryotic translation initiation factor eIF-4F	0.60	±	0.10
CMT559C	Similar to integrase interactor	0.59	±	0.03
CMS203C	Hypothetical protein	0.59	±	0.07
CMJ135C	Hypothetical protein	0.59	±	0.00
CME023C	Fusion protein of phosphoribosylaminoimidazole carboxylase and phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplast or mitochondrial precursor	0.59	±	0.11
CME188C	GTP-binding protein of Obg family	0.59	±	0.04
CMD093C	L-Galactono-1,4-lactone dehydrogenase	0.59	±	0.07
CMT181C	Similar to ADP-ribosylation factor	0.59	±	0.01
CMH159C	Eukaryotic translation initiation factor eIF-3 subunit 4	0.59	±	0.06
CMT552C	Hypothetical protein	0.59	±	0.07
CMJ084C	Phosphoribosylamine--glycine ligase (GARS) (glycinamide ribonucleotide synthetase) (phosphoribosylglycinamide synthetase)	0.59	±	0.07
CMM200C	Probable DNA binding protein	0.59	±	0.07

CMC142C	Hypothetical protein	0.59	±	0.05
CMG031C	Hypothetical protein	0.59	±	0.03
CMT216C	Isocitrate dehydrogenase, cytosolic	0.59	±	0.02
CMK168C	Hypothetical protein	0.59	±	0.05
CMH178C	Similar to GTPase-activating protein	0.59	±	0.05
CMM011C	Hypothetical protein	0.59	±	0.06
CMT304C	Hypothetical protein	0.58	±	0.06
CMR081C	Similar to meiotic check point regulator	0.58	±	0.05
CMG058C	Unknown transmembrane protein	0.58	±	0.02
CMR109C	GTP-binding protein of typa (tyrosine phosphorylated protein A) family	0.58	±	0.04
CMK114C	Similar to glucose-6-phosphate/phosphate-translocator precursor	0.58	±	0.09
CMS291C	Similar to FKBP-type peptidyl-prolyl cis-trans isomerase Mip	0.58	±	0.08
CMN179C	Mitochondrial presequence translocase subunit Tim50	0.58	±	0.03
CMQ277C	Hypothetical protein	0.58	±	0.07
CME043C	Hypothetical protein	0.57	±	0.02
CMK161C	Hypothetical protein	0.57	±	0.01
CMQ033C	Folylpolyglutamate synthase/dihydrofolate synthase	0.57	±	0.03
CMR373C	Short-chain dehydrogenases/reductases family (SDR),	0.57	±	0.03
CML047C	Similar to mRNA-binding protein	0.57	±	0.08
CMH207C	Probable peptidylprolyl isomerase	0.57	±	0.11
CMJ105C	Similar to chloroplast inner membrane protein Tic22 (Guillardia theta)	0.57	±	0.02
CMP203C	Hypothetical protein	0.57	±	0.07
CMF187C	Similar to ubiquitin-conjugating enzyme E2 variant	0.57	±	0.03
CMH230C	Hypothetical protein	0.57	±	0.05
CMM066C	Alanine aminotransferase	0.57	±	0.12
CMJ295C	Hypothetical protein	0.57	±	0.01
CMG190C	Unknown zinc finger protein	0.57	±	0.08
CMC064C	Eukaryotic translation initiation factor eIF-3 subunit 2	0.57	±	0.03
CMG099C	Hypothetical protein	0.57	±	0.03
CMS294C	Hypothetical protein	0.57	±	0.11
CMN019C	Probable inorganic phosphate transporter protein	0.57	±	0.06
CMH145C	Hypothetical protein	0.57	±	0.08
CMG123C	Aspartate-semialdehyde dehydrogenase (AsA dehydrogenase)	0.57	±	0.09
CMT532C	Hypothetical protein	0.56	±	0.06
CMB148C	Probable mitochondrial intermembrane space complex subunit Tim13	0.56	±	0.02
CMJ137C	Hypothetical protein	0.56	±	0.02
CME183C	Hypothetical protein	0.56	±	0.04
CMN204C	Hypothetical protein	0.56	±	0.05
CMC118C	Similar to oxidase (cytochrome c) assembly OXA1, mitochondrial precursor	0.56	±	0.06
CMR341C	Similar to surfeit locus protein 4	0.56	±	0.04
CMQ368C	Unknown periplasmic-binding protein of ABC transporter	0.56	±	0.07
CMG023C	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	0.56	±	0.02
CMK187C	Chloroplast translation elongation factor P (EF-P)	0.55	±	0.10

CMK024C	Hypothetical protein	0.55	±	0.09
CML063C	Hypothetical protein	0.55	±	0.00
CMQ113C	Similar to translationally controlled tumor protein (TCTP) (p23)	0.55	±	0.05
CMT520C	Hypothetical protein	0.55	±	0.10
CME006C	Hypothetical protein	0.55	±	0.02
CMJ218C	Aspartate--tRNA ligase, cytoplasmic	0.55	±	0.06
CMQ271C	Similar to endonuclease	0.54	±	0.03
CMP010C	Hypothetical protein	0.54	±	0.03
CMK043C	MYB-related protein	0.54	±	0.05
CMF116C	Unknown iron-sulfur protein	0.54	±	0.03
CMC169C	Hypothetical protein	0.54	±	0.06
CMR256C	Spermine synthase	0.54	±	0.15
CMK035C	Ribonucleoside-diphosphate reductase beta chain	0.54	±	0.00
CMK302C	Hypothetical protein	0.54	±	0.01
CMI129C	Hypothetical protein	0.54	±	0.09
CMS150C	Hypothetical protein	0.53	±	0.06
CMQ279C	Probable cytosolic purine 5' nucleotidase	0.53	±	0.02
CMO345C	Probable aldehyde dehydrogenase	0.53	±	0.04
CMQ241C	Probable plastid-specific ribosomal protein PSRP-1 precursor, chloroplast	0.53	±	0.01
CMH158C	Hypothetical protein	0.53	±	0.03
CMJ234C	Vitamine B12-independent methionine synthase	0.52	±	0.07
CMT192C	Unknown mitchondrial carrier protein	0.52	±	0.01
CMN310C	Hypothetical protein	0.52	±	0.03
CMH224C	Mitochondrial ribosomal protein L13 precursor	0.52	±	0.04
CMP340C	26S proteasome regulatory subunit	0.52	±	0.02
CMI148C	Probable trigger factor (proryl isomerase)	0.52	±	0.10
CMR237C	Threonine 3-dehydrogenas	0.51	±	0.03
CMR353C	Similar to respiratory burst oxidase protein	0.51	±	0.02
CMA048C	3-phosphoshikimate 1-carboxyvinyltransferase, chloroplast precursor	0.51	±	0.03
CMC093C	Hypothetical protein	0.51	±	0.06
CMG111C	Alanine--tRNA ligase (chloroplast)	0.51	±	0.07
CMJ288C	Similar to DNA photolyase	0.50	±	0.03
CMS188C	Probable chloroplast chaperonin CPN21, precursor	0.50	±	0.03
CMJ293C	Citrate synthase	0.50	±	0.07
CMO071C	Probable halotolerance protein HAL3	0.49	±	0.01
CMT026C	Hypothetical protein	0.49	±	0.01
CMS487C	Hypothetical protein	0.49	±	0.12
CMA140C	Mitotic control protein dis3	0.49	±	0.04
CMP271C	Similar to cyclophilin B	0.49	±	0.07
CMQ196C	Hypothetical protein	0.48	±	0.01
CMJ130C	Probable DNA photolyase (deoxyribodipyrimidine photolyase)	0.48	±	0.07
CMK023C	Hypothetical protein	0.48	±	0.08
CMI084C	Ribulose-5-phosphate-3-epimerase precursor	0.48	±	0.01

CMP333C	Similar to ubiquitin carboxyl-terminal hydrolase 10 (ubiquitin thioesterase 10)	0.48	±	0.04
CME120C	Eukaryotic translation elongation factor 1 beta (eEF-1b)	0.48	±	0.09
CMB159C	MYB-related protein	0.47	±	0.04
CMT424C	Hypothetical protein	0.47	±	0.12
CMN177C	Arginine--tRNA ligase	0.46	±	0.05
CMQ190C	Hsp90 co-chaperone p23	0.46	±	0.01
CMR252C	Hypothetical protein	0.46	±	0.03
CMQ088C	Hypothetical protein	0.45	±	0.12
CMK150C	Chloroplast translation elongation factor G (EF-G)	0.44	±	0.15
CMD051C	Hypothetical protein	0.43	±	0.11
CMP252C	Hypothetical protein	0.43	±	0.10
CMO245C	Fructose-1,6-bisphosphatase precursor	0.42	±	0.04
CMQ224C	Heat shock protein of Hsp90 family	0.41	±	0.03
CMR346C	Probabale LPS (Lipopolysaccharide) glycosyltransferase	0.41	±	0.08
CMJ206C	Hypothetical protein	0.37	±	0.03
CMT423C	Chloroplast molecular chaperone grpE	0.37	±	0.01
CMT162C	APS reductase	0.36	±	0.02
CMN328C	Probable phosphate/phosphoenolpyruvate translocator precursor	0.36	±	0.06

[a] Gene number and gene product in http://merolae.biol.s.u-tokyo.ac.jp/

[b] Values shown are means ± S.E. (*n*=4)