SUPPLEMENTARY MATERIAL

Table S1. Sampled sequences

A. thaliana sequences included in the analysis.

GenBank acc. no.	Description	GenBank acc. no.	description
AF154272	Pinehead	AF069468	Sterol-C5-desaturase
AF133708	Protein Phosphatase 2A regulatory subunit	AB027151	Threonine synthase
AF057024	Ran-binding protein	AF085354	Shrunken seed protein
D10910	Serine/threonine protein kinase	AF132606	Transcription factor CRC
AF136152	PUR alpha like protein	U88061	SNF5 homolog BSH
AF080676	Cytidine deaminase 8	AF047834	4-hydroxyphenylpyruvate dioxygenase
AF020433	Cyclophilin	AF019927	GSK3/shaggy-like protein kinase
AF154574	Trans-Golgi localized tSNARE	AF082176	Auxin response factor 9
AF132477	Heme oxygenase 2	AF033587	Serine/arginine-rich protein SRZ-21
AF132212	OPDA-reductase homolog	AF135455	Phytochrome A supressor
AF060874	Glycosylphosphatidylinositol-anchored protein	AF117296	ER type calcium-transporting ATPase 3
AF153677	Vacuolar H+-ATPase subunit c isoform 4	AB026987	Dynamin-like protein
AF138281	Phospholipase D-gamma-2	U92460	12-oxophytodienoate reductase
AF126057	Microtubule-associated protein	AF140219	Nuclear cap-binding protein
AF130878	Phosphoribosylanthranilate isomerase	AF091112	ATP dependent Cu transporter
AB020975	Lipoyltransferase	AB022891	Glucose-1-phosphate adenylyltransferase
AF144382	Glutathione S-transferase	AF134133	Chromosome IV Lil3 protein
AB021120	RNA polymerase sigma subunit	AF134132	Chromosome IV early light-inducable protein
AF085231	Phytochelatin synthase 1	AF134131	PsbS protein
AF051326	Dimethyladenosine transferase	AF134120	PS I antenna protein LHCI-680
AF153284	Progesterone-binding protein homolog	AF081067	IAA-Ala hydrolase
AF109721	RNA-binding protein	AF124524	Gamma-adaptin 1
AF083913	Annexin	AF121355	Peroxiredoxin TPx1
AF149816	IAA28	AF128407	EDS1 lipase homolog
AF145045	Homolog of TatC/YCF43	AF134155	Ring finger protein
AF141375	Protodermal factor 1	AF126009	Clavata3
AF076251	Calcineurin B-like protein 1	D89055	Germin-like protein precursor
AF082525	Homoserine kinase	AF110407	ATP sulphurylase precursor
AB027507	ACE (Adhesion of Calyx Edges)	AB018408	3-phosphoserine phosphatase
AB027506	TSF (Twin Sister of FT)	AF073361	Nitrate transporter NTL1
AB027504	FT (Flowering locus T)	AF126374	At14a protein
AF139188	Thylakoid membrane component protein	AF080249	Kinesin-like heavy chain
AF130973	Peroxisomal targeting signal type 2 receptor	AF076253	Calcineurin B-like protein 3
AF088917	Cellulose synthase catalytic subunit	AF136538	YABBY1
AF141977	AtHVA22a	AF120335	Putative transposase
AF141853	Mevalonate kinase		

Table S1. *Continued*

B. napus sequences included in the analysis

GenBank acc. no.	description	GenBank acc. no.	description
AF155224	Putative diacylglycerol acyltransferase	D63166	Phosphocholine cytidylyltransferase
AF118383	Plasma membrane intrinsic protein 2	D63151	Calcium-binding protein
J04468	Malate synthase	D38220	Nitrate reductase
AF139818	Oxygen evolving protein of photosystem II	D13987	Phosphoenolpyruvate carboxylase
AB014076	Histidine decarboxylase	U59379	Thioredoxin-h-like-1
AF069772	Calcium-binding protein	U68218	ATP sulphurylase
AF108123	Phosphoinositide-specific phospholipase C	U68217	Ferritin
AF136223	Putative cell-wall protein	U66193	S locus-linked 2
S47089	ATPase subunit 6	U86642	Pollen-specific protein Bnm1
AF081796	Fructose-1,6-bisphosphatase precursor	U22105	Germination-specific lipid transfer protein 1
AF101038	Nonspecific lipid-transfer protein precursor	U70666	Pathogenesis-related protein
AF111812	Actin	U65890	10 kDa chaperonin
F105140	Disease resistance homolog	U27107	Transcription factor
AF097522	Laminin receptor-like protein	U59459	Antifungal protein
AF060884	Desiccation protein	U55032	Aspartic protease
AF000307	Steroid sulfotransferase 3	U21849	PR-1a
AF057027	Response regulator protein	U50771	Fatty acid elongase
3650422	BNTFL1-3	U18365	Cyclin dependent protein kinase
U39289	Myrosinase-associated protein	J02798	Napin seed storage protein
U33884	CCAAT-binding factor B subunit homolog	U21743	Germin-like protein
L47352	Arabinogalactan protein	U15604	Tonoplast ATPase 70 kDa
AF076335	Chalcone synthase B1	U20179	Fructose 1,6-bisphosphatase
AF015310	BTH1	U17987	Putative nitrate transporter
AF016011	Constans homolog	L19879	Polygalacturonase
AF055707	Ribosomal protein S4	L33283	STA 41-9
AB013447	Aluminum-induced protein	L10736	S-locus related glycoprotein
AF049028	BURP domain containing protein	L34287	Stigma protein
U59443	Myrosinase-binding protein	U14665	Low-temperature regulated protein
AF052241	Unknown	U22665	AGL15 type 1
AF018174	Thioredoxin-f	U22175	Germination-specific lipid transfer protein 3
AF024625	Arm repeat containing protein	M60068	Acetolactate synthase
AF035414	Heat shock cognate protein	L22962	Omega-3 fatty acid desaturase
AF009563	3-ketoacyl-CoA synthase	L25406	Cyclin
AF019376	Calreticulin	M97667	Serine/threonine kinase receptor
U54827	Histone H3 homolog	L08482	Isocitrate lyase
L08607	S-receptor kinase	AF118381	Tonoplast intrinsic protein
L01418	Linoleate desaturase	M81224	Kin1 protein
M16860	Cruciferin	M83334	ATPase subunit 6
M95835	Endochitinase	U12133	RNA polymerase II subunit RPB10 homolog
M99415	BAG1	U10150	Calmodulin

Table S1. *Continued*

L. esculentum sequences included in the analysis.

GenBank acc. no.	description	GenBank acc. no.	description
AF150096	Small zinc finger-like protein	AF093141	Fruit-ripening protein
AB013346	1-aminocyclopropane-1-carboxylate synthase	U67131	Heat shock induced transcript 2
AF143812	1-D-deoxyxylulose 5-phosphate synthase	U88089	ADP-glucose pyrophosphorylase large subunit 1
AF050496	Ca^{2+}-ATPase mRNA	U83708	Farnesyl protein transferase subunit B
AJ005173	Serine protease	U26423	Dehydrin
AF123266	Remorin 2	U65391	Pseudomonas resistance and fenthion sensitivity protein
AF118844	Ethylene receptor homolog	U55278	DCL
AF136580	Iron-regulated transporter 2	U28403	RNA polymerase II subunit 2
AF123257	17.6 kDa class I small heat shock protein	AF035631	Germacrene C synthase
AF118127	Disease resistance protein	L25128	Auxin-induced proteinase inhibitor
AB022687	LeArcA2 protein	AF090115	Cytosolic class II small heat shock protein
AF088276	NADPH oxidase	AB004558	Acid invertase
AF014810	Proline transporter 3	AF043122	ACC synthase
AB013101	1-aminocyclopropane-1-carboxylate oxidase	U84140	Self-pruning protein
AB010992	3b-hydroxylase	AF020390	Beta-galactosidase
Y17277	Subtilisin-like protease	AF017252	Importin alpha
AJ002281	Phytochrome B1	AF033194	Dehydroquinate dehydratase/shikimate:NADP oxidoreductase
AF118567	Polygalacturonase	AJ003137	Cysteine protease
AF049900	Gibberellin 20-oxidase-3	U58474	Receptor-like protein kinase
AF059489	Expansin precursor	AB012138	Germin-like protein
AF117707	Copper/zinc superoxide dismutase copper chaperone precursor	AF043085	Ethylene receptor homolog
AF110519	Ethylene-inducible CTR1-like protein kinase	AB001389	Ca^{2+}-dependent lipid-binding domain protein
AF098292	Endo-beta-1,4-D-glucanase	U77719	Ethylene-responsive late embryogenesis-like protein
AF098674	Lateral suppressor protein	AF017144	(1-4)-beta-mannan endohydrolase
AF016713	Oligopeptide transporter	AF053993	Disease resistance protein
U76410	Homeobox 2 protein	AF048747	Farnesyl pyrophosphate synthase
U76408	Knotted 3 protein	AF093743	Pathogenesis-related protein osmotin precursor
AF029984	COP1 homolog	U70076	LeMir
AF091048	Disease resistance protein	AF030292	Ornithine decarboxylase
AF079232	Annexin p34	U28007	Pto kinase interactor 1
AF053998	Hcr2-5D		

Table S1. *Continued*

N. tabacum sequences included in the analysis

GenBank acc. no.	description	GenBank acc. no.	description
AB018441	Phi-1	AF009127	NAP1-2
AF068724	MADS-box protein	U73939	Protein kinase
D90196	Pathogenesis-related protein precursor	U64926	Geranylgeranylated protein
AB021178	NAC-domain protein	AF049350	Alpha-expansin precursor
AF153278	DNA-directed RNA polymerase IIb	AF083343	Heat shock protein 101 kDa
AF149981	Sucrose transporter-like protein	D10524	Glutathione S-transferase
AF141654	Beta-1,3-glucanase	AF032465	Putative serine/threonine protein kinase
AF149251	Secretory peroxidase	AF053104	Peroxisomal targeting signal 1 receptor
AF098636	Chaperone GrpE type 2	AB008892	Chitinase 134
AF124371	NT4	AB008200	Phenylalanine ammonia-lyase
AF099969	Sterol-C5(6)-desaturase homolog	AB010717	Sulfite reductase
AF133209	Putative chloride channel protein	U91723	14-3-3 protein isoform b
AB020590	Transcription factor	AF021220	Cation-chloride co-transporter
AB020023	DNA-binding protein NtWRKY3	U90212	DNA binding protein ACBF
AH007670	Calcium/calmodulin-dependent protein kinase	U66264	Ubiquitin
F120093	Elongation factor 1-alpha	U66263	Tumor-related protein
AF120092	CCAAT-binding transcription factor subunit B	U62735	Caffeoyl-CoA O-methyltransferase 3
AB025715	Homeobox 22	U34817	Violaxanthin de-epoxidase precursor
D89984	Ornithine decarboxylase	U69154	Prohibitin
AB024575	Ethylene responsive element binding factor	U35620	Rubisco large subunit N-methyltransfrase
AB015222	NtcycD3-1	U43542	Diphenol oxidase
AB015221	NtRb1	U52078	Kinesin-like protein
AB000834	Thaumatin-like protein	L38260	Acetyl-CoA carboxylase (biotin carboxylase subunit)
AF113545	Vacuole-associated annexin	AF020424	Glutamate decarboxylase isozyme 2
AB025573	KN1-type homeobox protein	AB004797	NTH23
AF117339	FtsH-like protein Pftf precursor	AB017502	Beta-D-glucan exohydrolase
AB017694	WREBP-2	D38123	Ethylene-responsive transcription factor
AB017533	Phosphoprotein EPc	U81312	S-adenosyl-methionine-sterol-C-methyltransferase
AB015855	Ethylene-insensitive transcription factor	U57350	Epoxide hydrolase
AF118129	Tsi1-interacting protein TSIP1	AF112863	Syntaxin-related protein
AF097180	Cystathionine gamma-synthase precursor	AF115482	Topoisomerase I
AF096299	DNA-binding protein WRKY2	AF044129	Protoporphyrinogen oxidase

Table S1. *Continued*

P. sativum sequences included in the analysis.

GenBank acc. no.	description	GenBank acc. no.	description
AF109922	Sucrose transport protein	AF079850	Nodule-enhanced malate dehydrogenase
AF043108	Spermidine synthase 1	AF065444	Root iron transporter protein
AB021873	Ribosome-sedimenting protein	AF063246	Cell wall invertase
AF145976	G protein beta subunit	AF061962	SAR DNA-binding protein
AF144708	Thylakoid membrane protein	AF056493	Pectin methylesterase
AF115574	Pathogenesis-related protein	U24398	Cold-induced peaci11.8
AB026253	Copper amine oxidase	AF034743	UDP-glucuronosyltransferase
D13296	Precursor for 23-kDa protein of photosystem II	AF039746	ERS-like ethylene receptor
D10661	Chalcone synthase	U31565	Reversibly glycosylatable polypeptide
AF014821	Developmentally regulated GTP binding protein	D89619	Cycloartenol synthase
AJ132614	LegA class precursor	AF029242	Dormancy-associated protein
AF107404	Sophorol reductase	AF014399	Mg-chelatase subunit D
AF016458	1-aminocyclopropane-1-carboxylate synthase	U79958	BP-80 vacuolar sorting receptor
L81139	Ubiquitin (PUB1)	U84198	Lipoxygenase
AF043905	Plastoglobule associated protein PG1 precursor	U81287	Glycine-rich RNA-binding protein
AF030516	Leaf cytosolic bifunctional enzyme	AF016460	1-aminocyclopropane-1-carboxylate synthase
AF004843	Stamina pistilloidia	D88262	Chalcone synthase
AF004730	Gibberellin 3B-hydroxylase le-3 allele	U05293	Aspartate carbamoyltransferase
U79562	Defender against death homolog Peadad	U49978	Imidazoleglycerol-phosphate dehydratase
AF095285	Chloroplast inner envelope membrane protein	U85045	2-oxoglutarate-dependent dioxygenase
M81864	Albumin 1	U63298	Farnesyltransferase alpha subunit
AF034419	Cytosine-5 DNA methyltransferase	U63652	Ent-kaurene synthase A
AF030709	Poly(A) polymerase	D86052	Nucleoside diphosphate kinase
AF010578	Polynucleotide phosphorylase	D10003	Phenylalanine ammonia-lyase
U43401	Putative transmembrane protein	D86494	Diminuto
U69554	6a-hydroxymaackiain methyltransferase	U44947	Putative cysteine protease
AF010190	Unifoliata protein	U81049	Actin
U56419	Import intermediate associated protein	U60592	S-adenosylmethionine decarboxylase
U35831	Thioredoxin m	U28925	Cytosolic glutamine synthetase
U31981	Root nodule lectin	X07014	Minor legumin
3608178	Cyclin D	Z25471	Blue copper protein
AB008186	Proliferating cell nuclear antigen	U56697	Pyruvate dehydrogenase E1beta subunit
AF080104	Knotted I class homeodomain protein	L41046	Endo-1,4-beta-glucanase
AF081457	Pectin methylesterase	U13882	Calmodulin
AF063307	Knox class 1 protein	U21105	Chloroplast chaperonin precursor
AF079851	Nodule-enhanced sucrose synthase	AB015428	Endoxyloglucan transferase

Table S1. *Continued*

G. max sequences included in the analysis

GenBank acc. no.	description	GenBank acc. no.	description
AF135862	Precursor monofunctional aspartokinase	AF091304	Aminoacyl peptidase
AF089851	Peroxisomal copper-containing amine oxidase	AF030231	Sucrose synthase
AF089850	Urate-degrading peroxidase	AF069738	Symbiotic ammonium transporter
AB029159	GmMYB291	D50866	Beta-amylase
AB008679	Beta subunit of beta conglycinin	AF034572	Proteasome IOTA subunit
AB008678	Alpha subunit of beta conglycinin	AF074940	Ferric leghemoglobin reductase-2 precursor
U44850	G beta-like protein	AF068249	Biotin carboxylase precursor
D86929	Uricase	AF048978	2,4-D inducible glutathione S-transferase
AF135485	Cytochrome P450 monooxygenase	AF020193	DNA polymerase delta
AF100159	Hydrophobic seed protein precursor	U82810	Early light-induced protein
AF145348	Peroxidase	AB013289	Allergenic protein
AF141602	Cystathionine-gamma-synthase precursor	L28831	Ribosomal protein S11
AF136636	PR1a precursor	U55874	Asparagine synthetase
F051159	Ribonucleotide reductase small subunit	L28003	TGACG-motif binding protein
AF117885	Seed maturation protein	AF035671	Arginase
AB007127	Acidic chitinase	AF007100	Biotin carboxylase precursor
AF068686	Geranylgeranyl hydrogenase	AF014502	Seed coat peroxidase precursor
AF068686	Nodule-enhanced malate dehydrogenase	D00216	Glycinin A2B1a subunit
AF128443	SNF-1-like serine/threonine protein kinase	AF024652	Polyphosphoinositide binding protein
U25027	Phosphatidylinositol-specific phospholipase C	AF035252	Catalase
AB025102	Protoporphyrinogen IX oxidase	AF031241	ER HSC70-cognate binding protein precursor
AF124148	Trehalase 1	AB008540	Phosphoenolpyruvate carboxylase
AB004062	Glycinin	AF019115	Putative cadmium-transporting ATPase
AF127804	Ascorbate peroxidase	AB007907	6-phosphogluconate dehydrogenase
AF105221	Glutamyl-tRNA reductase precursor	AB007503	Squalene synthase
L07647	Chalcone synthase	AF004809	Ca^{2+}-binding EF hand protein
U71195	Napin-type 2S albumin 3	AF004808	Metallothionein-II protein
AF007211	Peroxidase precursor	AF004805	Em protein
U12150	Protease inhibitor	AF019910	GRR1 homolog
AF039027	Cationic peroxidase 2	U40666	Biotin carboxyl carrier protein precursor
AF065435	Nodulin	U64866	Aluminum induced
AF095445	NADP-dependent isocitrate dehydrogenase	D45857	Mg chelatase subunit (46 kDa)
U59626	68 kDa LEA protein	D50868	Mitotic cyclin a1-type
AF034210	Aspartate aminotransferase glyoxysomal isozyme AAT1 precursor	U36430	Dynamin-like protein
U77679	Asparagine synthetase 1	U36191	Lipoxygenase
U43838	Choline kinase	U20260	Glutamate 1-semialdehyde aminotransferase
U42608	Clathrin heavy chain		

Table S1. *Continued*

O. sativa sequences included in the analysis.

GenBank acc. no.	description	GenBank acc. no.	description
AF155333	NADP-specific isocitrate dehydrogenase	AB020502	Catalase
AB018377	Early nodulin	AF067194	S-adenosylmethionine decarboxylase
AF150113	Small zinc finger-like protein	D83727	Elongation factor 1 beta 2
AB029060	F1F0-ATPase inhibitor	D11385	Prolamin
AB028885	Knotted1-type homeobox protein	AF093636	Plastocyanin precursor
AB003495	4-reductase dihydroflavonol	AF093633	Histone H3
AB008845	NADH dependent glutamate synthase	AF093632	High mobility group protein
D67043	Aspartate aminotransferase	AF093631	Rieske Fe-S precursor protein
D50317	ADP glucose pyrophosphorylase large subunit	AF093629	Inorganic pyrophosphatase
D01000	Copper/zinc-superoxide dismutase	D89802	Elongation factor 1B gamma
AF066050	Thymidine kinase	U25970	Early embryogenesis
AF110382	3-hydroxy-3-methylglutaryl-coenzyme A reductase	AF047444	Ribulose-5-phosphate-3-epimerase
AF141965	MADS-box protein	AF069773	Putative type 1a plasma membrane receptor
AF155334	NADP-specific isocitrate dehydrogenase	AF049356	Phytoene desaturase precursor
AF145727	Homeodomain leucine zipper protein	AF046884	Late embryogenesis abundant group 3 protein
AB020973	Heat shock protein 26	AF040700	Methionyl-tRNA synthetase
D38445	Ferredoxin-NADP+ reductase	AF062479	Protein kinase
AF017358	Lipid transfer protein	AF052503	S-phase-specific ribosomal protein
AF133118	Nucleic acid binding protein	AF052203	23 kDa polypeptide of photosystem II
AB027429	beta-1,3-glucanase	AF065992	Floral meristem identity protein
AB027425	Class III chitinase homologue	AB010876	Germin-like protein 1
U46159	Type 1 metallothionein-like	AB003496	Dihydroflavonol 4-reductase
AB027123	Cytochrome c oxidase subunit 5c	AF001396	Metallothionein-like protein
AB027054	Nitrilase-like protein	AF044059	Proteinase inhibitor
AF143746	CER1 homolog	AF097724	33-kDa secretory protein
AB019533	NAD-dependent formate dehydrogenase	U72251	Beta-1,3-glucanase precursor
AB007405	Alanine aminotransferase	U57640	Bowman-Birk type trypsin inhibitor
AB013449	Pi-b	U57639	Hydrophobic LEA-like protein
D85764	Cytosolic monodehydroascorbate reductase	U31773	Protein phosphatase 1
D85763	Glyoxysomal malate dehydrogenase	D13512	Cytoplasmic aldolase
D78136	Cytosolic glutathione reductase	AB023402	Thymidylate synthase
AB021746	Nicotianamine synthase 1	AB022674	Chloroplast ribosomal protein L12
AF134807	Putative dihydroflavonol reductase	AB021736	Seed bZIP protein
D82039	Serine/threonine protein kinase	AB021747	Farnesyl diphosphate synthase
AF073695	Cysteine synthase	AB018442	Phytochrome C
AF121139	RIM2 protein	AB018376	OsENOD93a early nodulin
AB019240	RPR1 homologue	AB017042	Glyoxalase I
AB017914	Nucleotide binding, leucine-rich protein	AB015204	Plastidic ATP sulfurylase
AB024054	OsENOD40	AF042275	Anther-specific protein
AB012765	Vacuolar H^+-translocating inorganic pyrophosphatase		

Table S1. *Continued*

T. aestivum sequences included in the analysis

GenBank acc. no.	description	GenBank acc. no.	description
AF156977	(1,4)-beta-xylan endohydrolase	U81318	Poly(A)-binding protein (wheatpab)
AF107027	Histone H1	U80037	ABA induced plasma membrane protein
AH005224	Serine-threonine protein kinase	U60754	Delta-24-sterol methyltransferase
AF139915	ABA-inducible protein	U42336	ACC synthase
AF145590	Putative hmw glutenin precursor	U73218	Chlorophyll a/b-binding protein WCAB precursor
AF144104	Gamma-gliadin GAG56D-FO allele	AF112966	Chitinase IV precursor
AF076679	Endosperm starch branching enzyme-I	U66376	1,4-alpha-D-glucan6-alpha-D-(1,4-alpha-D-glucanotransf.)
AB019624	Starch synthase	U51304	Alpha-gliadin storage protein
AF112967	Beta-1,3-glucanase precursor	L28009	Wali6
U73217	Cold acclimation protein	AF002820	Starch branching enzyme I
AF112964	Small GTP-binding protein	U22442	Adenine phosphoribosyltransferase form 1
AF112963	Chitinase II precursor	U32310	Single-stranded nucleic acid binding protein
F120148	Myo-inositol 1-phosphate synthase	M62893	DNA binding protein
AF113844	Granule-bound starch synthase precursor	L11882	Unknown
AB019617	Early light-inducible protein	M94959	Protein associated with pathogen defense
AF097363	Heat shock protein 101	M55604	Ubiquitin activating enzyme E1
U91983	Phosphatidylserine synthase	L11872	S-adenosyl-L-homocysteine hydrolase
AF117660	S-adenosylmethionine decarboxylase precursor	M37477	Rubisco
AF031231	S222	J02817	Gibberellin responsive protein
AF031195	Blue copper-binding protein homolog	M63224	Germin
AF004816	Unknown	M60599	Dihydrodipicolinate synthase
U91981	Pollen allergen homolog	F002211	Glutathione-S-transferase
U86762	Gamma-type tonoplast intrinsic protein	D38111	Transcription factor
U76744	Beta-tubulin 1	D16416	Putative zinc-finger protein
U76558	Alpha-tubulin	D13795	Tritin
U76384	o-methyltransferase	D38090	Histone H2A
U23409	p34cdc2	D16457	Endo-xyloglucan transferase
AF109714	Glutathione S-transferase	D86327	Catalase
F030420	Cell wall invertase	D64051	bZIP-type protein HALF-1
D12920	Transcription factor HBP-1a	D84390	Alpha-1 purothionin
AB011670	Protein kinase	U91834	Root abundant protein
AB008497	LMW glutenin	F027193	Receptor-like kinase
AB007506	MADS box transcription factor	AF079318	MAP kinase homolog
AF092524	Manganese superoxide dismutase	D84678	Omega-3 fatty acid desaturase
U51330	Leaf rust resistance kinase	AF058794	COR39
U58278	Actin-binding protein	AF004018	Beta purothionin precursor
U32430	Thiol protease	U87163	Germ initiation factor 2 beta subunit
U32429	Sulfur-rich/thionin-like protein	AB005555	Gibberellin 20-oxidase

Table S1. *Continued*

H. vulgare sequences included in the analysis.

GenBank acc. no.	description	GenBank acc. no.	description
AF102868	Beta-D-glucan exohydrolase isoenzyme ExoI	M96939	Glucan endo-1,3-beta-glucosidase (isoenzyme V)
AB024058	Iron-deficiency specific protein	U01228	Harrington haemoglobin apoprotein
D88272	Formate dehydrogenase	M98254	PSI-D subunit of photosystem I
AB019525	Nicotianamine synthase 7	AF022390	Knotted class 1 homeodomain protein
S72926	Ribitol dehydrogenase homolog	S69616	Dihydroflavonol-4-reductase
L36959	Carbonic anhydrase	X95277	Serpin
D83178	Endonuclease	U01963	Germin subunit
D88383	Glutamyl-tRNA reductase	M29280	Root-specific lectin
AB009309	Plasma-membrane type water channel	M21400	Chymotrypsin inhibitor
L37358	Lipoxygenase 2	M27303	Calmodulin
M31545	Glutamate 1-semialdehyde aminotransferase	J01236	Alpha-amylase type A isozyme
D82941	D hordein	M60175	Ubiquitin (mub1)
D63835	S-adenosylmethionine synthetase	M55685	L-lactate dehydrogenase
D26448	Betaine aldehyde dehydrogenase	U20777	Catalase
D21349	Beta-amylase	U49505	Profilin
U57845	Pollen allergen precursor	U19359	Cysteine proteinase
U43497	Putative 32.7 kDa jasmonate-induced protein	D26448	Betaine aldehyde dehydrogenase
U43493	Ribulose-1,5-bisphosphate carboxylase small subunit	AF136942	Nicotianamine synthase 2
L11873	Vacuolar ATPase B subunit	AF000940	Ribonuclease
L48286	Signal recognition particle 54 kDa subunit	U73749	Xylan endohydrolase isoenzyme X-I
L33251	Disulfide isomerase	U88090	Nonspecific lipid transfer protein
M55449	Rubisco activase	U83414	Cytosolic triosephosphate isomerase
M61146	Photosystem I hydrophobic protein	U49482	Low temperature-responsive RNA-binding protein
L32165	Heat-shock protein HSP70	U22450	Alpha-glucosidase
M19048	Leaf specific thionin	Z23130	Protein synthesis elongation factor-1 alpha
L36093	Peroxidase	X07774	Alcohol dehydrogenase 1
M15207	Probable amylase/protease inhibitor	U26916	Protoporphyrin IX Mg-chelatase subunit precursor
M60410	Beta-ketoacyl-ACP synthase I	U52867	High affinity sulfate transporter
M62905	Ribosome-inactivating protein	AF056325	Myo-inositol 1-phosphate synthase
M62904	26kDa chitinase	AF017430	Early embryogenesis associated protein
M62907	(1-3)-beta-glucanase	U87148	Nucellin
M64372	Embryo globulin	AB009307	Bpw1
M36000	Abscisic acid (ABA) induced protein	D50641	Plant metallothionein-like protein
M24425	Acyl carrier protein I	U89510	Beta-ketoacyl reductase
AF021256	32 kDa protein from a family of jasmonate-regulated genes	AF020791	Ferrochelatase
AF025292	Putative high-affinity potassium transporter	AF035820	Gibberellin action negative regulator SPY
D10057	Dioxygenase gene expressed under iron deficiency conditions	AF023472	Peptide transporter
U54767	Caffeic acid o-methyltransferase		

Table S1. *Continued*

Z. mays sequences included in the analysis

GenBank acc. no.	description	GenBank acc. no.	description
AF073329	Translation initiation factor 3 large subunit	U39958	NADP-malic enzyme root isoform
AF153448	Nitrate reductase	U33816	Beta-D-glucosidase
AF003551	Lysine-ketoglutarate reductase/saccharopine	AF045473	Histone deacetylase
AF126054	Small GTP binding protein	AF082347	C13 endopeptidase NP1 precursor
AF143447	Rough sheath 2	U90944	PDI-like protein
AF133840	Heat shock protein HSP101	AF050129	Cell wall invertase
AF142322	Putative transcription repressor protein	AF047490	Zeta-carotene desaturase precursor
AF079429	RAD51 homolog RAD51B	AF084478	Rubisco activase precursor
AF145756	THA9	U83625	Protein kinase
AF143681	Cell cycle checkpoint protein MAD2 homolog	AF093627	Poly(ADP)-ribose polymerase
AF131201	Plasma membrane MIP protein	AF063865	Tapetum specific protein
AF073522	Chloroplast protein crp1	AF072326	Endo-1,3-1,4-beta-D-glucanase
AF031083	Aluminum-induced protein	AF038585	Pyruvate dehydrogenase kinase isoform 1
AF104924	Unconventional myosin heavy chain	AF055898	Aminotransferase
AF126742	Bundle sheath defective protein 2	U89341	Phosphoglucomutase 1
AF064707	Exohydrolase II	U85494	LON1 protease
AF127021	T7-like RNA polymerase	U58209	Lumenal binding protein
AF016305	ATP sulfurylase	U50064	Type A-like cyclin
AB016810	Ferredoxin	U35063	Opaque-2 heterodimerizing protein
AB021175	Root cap protein 1	U57002	P protein
AB004882	Response regulator homolog	U33318	Sulfur starvation induced isoflavone reductase-like enzyme
AB018589	Seedling Leaf sheath protein	U32579	Protein involved in an early step in gibberellin biosynthesis
AB016802	Kinase	U31541	High-methionine zein
AB014475	Root cap-specific glycine-rich protein	U29159	Ubiquitin
AF100455	Knotted class 1 homeodomain protein liguleless3	AF047852	Terminal ear1
AF069911	Pyruvate dehydrogenase E1 alpha subunit	L05934	Catalase
AF069908	Pyruvate dehydrogenase E1 beta subunit isoform 1	AF037061	Tonoplast intrinsic protein
AF111029	40S ribosomal protein S27 homolog	AF019297	Starch synthase isoform
AF044603	Cytokinin oxidase	AF080567	Pullulanase-type starch debranching enzyme
AF077372	Cytochrome b5 reductase	U62748	Acidic ribosomal protein
AF068119	Beta-amylase	U87949	Proliferating cell nuclear antigen

Table S2. Codon usage in sampled sequences

A. thaliana (28,951 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	21.9	UCU	23.5	UAU	13.5	UGU	8.5
UUC	21.7	UCC	10.7	UAC	13.1	UGC	5.9
UUA	12.8	UCA	18.2	UAA	-	UGA	-
UUG	19.7	UCG	8.5	UAG	-	UGG	11.7
CUU	24.9	CCU	20.9	CAU	13.0	CGU	8.9
CUC	15.5	CCC	5.7	CAC	9.1	CGC	3.5
CUA	9.6	CCA	18.4	CAA	18.4	CGA	5.6
CUG	9.6	CCG	7.6	CAG	15.1	CGG	4.9
AUU	21.3	ACU	19.2	AAU	21.8	AGU	12.5
AUC	18.7	ACC	9.2	AAC	19.2	AGC	11.2
AUA	13.2	ACA	16.3	AAA	28.9	AGA	19.9
AUG	25.0	ACG	6.7	AAG	30.9	AGG	11.3
GUU	30.2	GCU	33.0	GAU	36.4	GGU	22.3
GUC	13.4	GCC	11.4	GAC	15.3	GGC	9.7
GUA	10.3	GCA	19.8	GAA	34.0	GGA	25.6
GUG	18.9	GCG	8.3	GAG	32.3	GGG	10.9

B. napus (28,232 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	16.2	UCU	17.6	UAU	12.6	UGU	8.1
UUC	26.3	UCC	12.7	UAC	20.5	UGC	8.9
UUA	8.7	UCA	14.6	UAA	-	UGA	-
UUG	17.9	UCG	7.7	UAG	-	UGG	12.1
CUU	22.2	CCU	18.9	CAU	11.7	CGU	9.8
CUC	19.9	CCC	7.5	CAC	11.5	CGC	4.2
CUA	10.2	CCA	14.6	CAA	16.8	CGA	4.1
CUG	10.6	CCG	8.3	CAG	17.1	CGG	4.1
AUU	18.1	ACU	16.9	AAU	15.5	AGU	11.5
AUC	22.1	ACC	15.8	AAC	30.2	AGC	12.2
AUA	11.1	ACA	13.9	AAA	25.4	AGA	16.2
AUG	24.7	ACG	10.0	AAG	35.2	AGG	11.1
GUU	22.9	GCU	30.1	GAU	30.1	GGU	24.5
GUC	18.0	GCC	17.0	GAC	25.4	GGC	12.5
GUA	7.1	GCA	15.8	GAA	25.1	GGA	27.7
GUG	19.2	GCG	9.8	GAG	35.9	GGG	10.6

L. esculentum (31,872 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	27.0	UCU	21.5	UAU	19.3	UGU	11.2
UUC	15.8	UCC	9.4	UAC	12.4	UGC	7.3
UUA	15.5	UCA	20.6	UAA	-	UGA	-
UUG	27.3	UCG	5.3	UAG	-	UGG	13.1
							0.0
CUU	27.4	CCU	18.2	CAU	15.8	CGU	6.8
CUC	12.4	CCC	4.7	CAC	7.4	CGC	3.3
CUA	12.0	CCA	15.8	CAA	21.3	CGA	5.0
CUG	11.3	CCG	3.9	CAG	13.7	CGG	3.0
AUU	30.5	ACU	20.6	AAU	31.8	AGU	15.4
AUC	14.5	ACC	7.2	AAC	18.1	AGC	9.6
AUA	15.3	ACA	18.5	AAA	30.5	AGA	16.0
AUG	25.1	ACG	5.0	AAG	29.0	AGG	11.5
GUU	28.6	GCU	30.2	GAU	40.3	GGU	23.4
GUC	10.1	GCC	9.1	GAC	14.5	GGC	10.9
GUA	11.2	GCA	20.6	GAA	34.5	GGA	23.8
GUG	15.0	GCG	4.8	GAG	24.6	GGG	10.3

N. tabacum (26,805 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	23.1	UCU	20.9	UAU	18.6	UGU	9.6
UUC	17.3	UCC	9.9	UAC	12.6	UGC	7.1
UUA	13.2	UCA	18.0	UAA	-	UGA	-
UUG	21.5	UCG	5.3	UAG	-	UGG	11.7
CUU	23.4	CCU	19.2	CAU	13.6	CGU	7.9
CUC	13.1	CCC	6.1	CAC	8.1	CGC	3.6
CUA	9.3	CCA	18.8	CAA	23.3	CGA	5.7
CUG	10.8	CCG	6.0	CAG	16.8	CGG	4.3
AUU	26.0	ACU	18.8	AAU	29.7	AGU	13.5
AUC	13.4	ACC	8.0	AAC	18.8	AGC	9.6
AUA	13.1	ACA	17.9	AAA	30.7	AGA	16.3
AUG	24.8	ACG	4.4	AAG	32.9	AGG	13.1
GUU	27.8	GCU	31.2	GAU	36.6	GGU	22.3
GUC	10.4	GCC	11.7	GAC	16.1	GGC	11.2
GUA	12.3	GCA	25.3	GAA	36.7	GGA	23.7
GUG	15.5	GCG	6.5	GAG	29.2	GGG	11.3

P. sativum (30,728 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	23.1	UCU	23.2	UAU	17.8	UGU	9.7
UUC	18.0	UCC	10.4	UAC	11.7	UGC	5.7
UUA	13.6	UCA	18.0	UAA	-	UGA	-
UUG	22.2	UCG	3.7	UAG	-	UGG	13.4
CUU	26.6	CCU	18.9	CAU	14.4	CGU	8.6
CUC	13.7	CCC	6.5	CAC	9.3	CGC	3.7
CUA	8.3	CCA	17.3	CAA	21.8	CGA	4.3
CUG	8.0	CCG	4.5	CAG	12.5	CGG	2.2
AUU	29.3	ACU	21.0	AAU	26.0	AGU	14.2
AUC	15.5	ACC	11.3	AAC	20.1	AGC	8.7
AUA	13.9	ACA	18.1	AAA	33.0	AGA	16.0
AUG	21.6	ACG	3.8	AAG	34.0	AGG	10.6
GUU	30.3	GCU	34.0	GAU	37.8	GGU	26.4
GUC	11.0	GCC	11.9	GAC	15.9	GGC	9.4
GUA	9.3	GCA	23.2	GAA	37.7	GGA	25.0
GUG	16.2	GCG	5.6	GAG	27.3	GGG	8.8

G. max (32,312 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	21.4	UCU	17.9	UAU	15.4	UGU	7.8
UUC	19.1	UCC	9.3	UAC	14.3	UGC	8.0
UUA	13.0	UCA	14.4	UAA	-	UGA	-
UUG	23.5	UCG	3.9	UAG	-	UGG	11.0
CUU	24.7	CCU	18.8	CAU	13.4	CGU	8.7
CUC	15.0	CCC	8.5	CAC	10.4	CGC	6.6
CUA	8.7	CCA	17.5	CAA	20.2	CGA	4.4
CUG	13.6	CCG	3.3	CAG	18.0	CGG	2.8
AUU	28.6	ACU	17.8	AAU	21.5	AGU	12.4
AUC	15.5	ACC	12.9	AAC	21.7	AGC	10.6
AUA	12.1	ACA	15.0	AAA	25.4	AGA	16.4
AUG	22.0	ACG	3.3	AAG	37.6	AGG	14.3
GUU	29.8	GCU	31.0	GAU	34.8	GGU	22.2
GUC	11.5	GCC	16.8	GAC	19.3	GGC	12.2
GUA	8.0	GCA	22.9	GAA	36.4	GGA	23.5
GUG	20.7	GCG	5.9	GAG	35.3	GGG	11.9

Table S2. *Continued*

O.sativa (29,531 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	13.7	UCU	11.0	UAU	11.3	UGU	5.6
UUC	23.8	UCC	14.2	UAC	17.7	UGC	13.1
UUA	5.6	UCA	10.9	UAA	-	UGA	-
UUG	14.6	UCG	7.8	UAG	-	UGG	11.3
CUU	19.5	CCU	12.9	CAU	10.8	CGU	6.9
CUC	23.8	CCC	11.2	CAC	12.0	CGC	12.8
CUA	7.6	CCA	13.4	CAA	11.3	CGA	4.1
CUG	20.6	CCG	12.7	CAG	19.6	CGG	7.6
AUU	17.8	ACU	12.5	AAU	14.0	AGU	7.9
AUC	22.8	ACC	15.6	AAC	24.1	AGC	15.5
AUA	8.8	ACA	12.0	AAA	17.9	AGA	7.4
AUG	25.9	ACG	8.9	AAG	42.2	AGG	14.5
GUU	19.6	GCU	25.3	GAU	25.5	GGU	17.9
GUC	21.0	GCC	29.9	GAC	27.4	GGC	26.7
GUA	6.8	GCA	19.6	GAA	23.1	GGA	17.1
GUG	24.2	GCG	19.9	GAG	41.9	GGG	16.4

T. aestivum (26,670 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	12.0	UCU	10.8	UAU	9.7	UGU	4.9
UUC	28.8	UCC	18.6	UAC	23.4	UGC	12.7
UUA	2.9	UCA	10.0	UAA	-	UGA	-
UUG	9.4	UCG	8.7	UAG	-	UGG	12.3
CUU	12.1	CCU	11.7	CAU	8.2	CGU	4.6
CUC	27.7	CCC	15.0	CAC	16.3	CGC	14.6
CUA	4.4	CCA	15.6	CAA	18.6	CGA	2.8
CUG	21.7	CCG	16.2	CAG	31.0	CGG	8.5
AUU	9.8	ACU	8.6	AAU	10.7	AGU	5.5
AUC	27.4	ACC	20.8	AAC	26.1	AGC	15.9
AUA	5.1	ACA	7.9	AAA	11.1	AGA	5.5
AUG	27.3	ACG	11.3	AAG	42.4	AGG	12.9
GUU	13.2	GCU	16.2	GAU	17.8	GGU	13.8
GUC	24.3	GCC	38.0	GAC	35.8	GGC	39.4
GUA	5.1	GCA	13.2	GAA	14.5	GGA	13.5
GUG	26.8	GCG	23.3	GAG	41.4	GGG	18.9

H. vulgare (26,561 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	8.1	UCU	6.7	UAU	6.4	UGU	3.6
UUC	33.0	UCC	18.7	UAC	25.9	UGC	13.0
UUA	1.5	UCA	6.4	UAA	-	UGA	-
UUG	8.5	UCG	10.8	UAG	-	UGG	11.7
CUU	10.6	CCU	9.9	CAU	6.2	CGU	5.5
CUC	33.8	CCC	15.0	CAC	15.8	CGC	14.9
CUA	3.8	CCA	11.0	CAA	10.4	CGA	2.3
CUG	24.5	CCG	16.9	CAG	28.8	CGG	9.8
AUU	10.7	ACU	8.4	AAU	8.6	AGU	4.1
AUC	32.6	ACC	26.3	AAC	29.6	AGC	17.4
AUA	5.6	ACA	7.0	AAA	9.1	AGA	4.1
AUG	24.5	ACG	12.2	AAG	43.8	AGG	11.8
GUU	12.5	GCU	15.7	GAU	13.8	GGU	13.9
GUC	28.8	GCC	42.0	GAC	37.8	GGC	42.0
GUA	3.7	GCA	14.3	GAA	11.5	GGA	13.4
GUG	31.5	GCG	23.6	GAG	43.6	GGG	19.6

Z. mays (29,807 codons)

Codon	‰	Codon	‰	Codon	‰	Codon	‰
UUU	11.8	UCU	11.8	UAU	10.2	UGU	4.6
UUC	24.4	UCC	14.5	UAC	20.8	UGC	9.3
UUA	5.2	UCA	10.6	UAA	-	UGA	-
UUG	12.5	UCG	10.5	UAG	-	UGG	11.8
CUU	16.5	CCU	13.2	CAU	9.1	CGU	6.2
CUC	23.9	CCC	12.9	CAC	13.7	CGC	15.2
CUA	5.4	CCA	13.0	CAA	10.7	CGA	3.6
CUG	26.7	CCG	15.6	CAG	25.1	CGG	10.0
AUU	13.5	ACU	10.4	AAU	13.1	AGU	7.5
AUC	26.5	ACC	15.9	AAC	21.7	AGC	16.0
AUA	7.4	ACA	10.4	AAA	14.3	AGA	8.9
AUG	25.5	ACG	10.4	AAG	41.4	AGG	15.5
GUU	15.7	GCU	24.4	GAU	23.1	GGU	16.2
GUC	20.2	GCC	28.6	GAC	34.2	GGC	28.3
GUA	6.2	GCA	16.9	GAA	21.6	GGA	15.2
GUG	26.7	GCG	24.4	GAG	42.8	GGG	16.4

‰: frequency of occurrence (per thousand) for each codon in the sample.

-: not determined (STOP codons).

Table S3. Relative frequency (%) of each codon when the subsequent triplet was headed by A, G, C or T

Aminoacid	Codon position 1,2,3	4	A. thaliana	B. napus	L. esculentum	N. tabacum	P. sativum	G. max	O. sativa	T. aestivum	H. vulgare	Z. mays
Lys	AAA	A	25.7 ⇓	21.3 ⇓	26.5	26.9	29.1	26.1	25.0	22.0	23.0	29.4
		G	39.1 ⇑	41.8 ⇑	38.1 ⇑	37.9	37.8	37.6	36.1	33.6	42.0	40.5
		C	18.5	22.6	15.2	15.8 ⇓	17.8	17.9	15.1	21.0	14.4 ⇓	15.5 ⇓
		T	16.7	14.3	20.1	19.4	15.4	18.4	23.8 ⇑	23.4 ⇑	20.6 ⇑	14.6
	AAG	A	37.0 ⇑	37.2 ⇑	34.1 ⇑	34.3	34.6	31.3	32.2	29.3	28.5	29.5
		G	26.8 ⇓	26.5 ⇓	29.1 ⇓	28.5 ⇓	33.0	33.4	34.9	35.4	35.7	34.6
		C	21.0	20.6	20.1	22.5	17.6	21.3	20.4	19.7	23.6	21.8
		T	15.1	15.7	16.7	14.6	14.6	14.0	12.5 ⇓	15.6	12.3	14.1
Asn	AAC	A	38.6 ⇑	35.6 ⇑	42.3 ⇑	37.6 ⇑	43.8 ⇑	42.2 ⇑	37.1 ⇑	28.3	28.8 ⇑	32.0 ⇑
		G	21.5 ⇓	25.2 ⇓	13.2 ⇓	15.6 ⇓	14.9 ⇓	11.5 ⇓	20.5 ⇓	27.7 ⇓	29.3 ⇓	23.5 ⇓
		C	18.5	21.4	15.9	21.4	20.1	25.4	23.9	24.1	22.6	23.5
		T	21.4	17.8	28.6 ⇑	25.3	21.2	20.9	18.4	19.9	19.3	21.0
	AAT	A	17.2 ⇓	21.0 ⇓	22.4 ⇓	17.2 ⇓	20.4 ⇓	16.3 ⇓	18.7 ⇓	17.2 ⇓	14.0 ⇓	17.2 ⇓
		G	43.5 ⇑	43.3 ⇑	38.1 ⇑	42.9 ⇑	43.7 ⇑	46.1 ⇑	50.2 ⇑	49.8 ⇑	53.3 ⇑	50.8 ⇑
		C	24.2	22.6	20.2	21.3	17.5	18.2	18.0	17.9	21.4	17.4
		T	15.0	13.2	19.2	18.6	18.3	19.5	13.1	15.1	11.4 ⇓	14.6
Glu	GAA	A	23.6 ⇓	22.2 ⇓	29.9	30.8	30.0	27.2 ⇓	25.7	22.7	15.4 ⇓	26.7
		G	48.4 ⇑	49.0 ⇑	35.8	38.5 ⇑	41.4 ⇑	42.2 ⇑	43.3	38.8	50.8 ⇑	43.2
		C	15.3	15.4	16.3	16.5	14.4	16.1	15.3	18.9	17.7	18.2
		T	12.7	13.4	18.0	14.2	14.2	14.4	15.7	19.6	16.1	11.8
	GAG	A	39.1 ⇑	38.6 ⇑	37.1	37.0	34.4	35.5 ⇑	29.1	29.5	27.0	29.4
		G	25.6 ⇓	25.0 ⇓	30.2	25.2 ⇓	30.5 ⇓	31.1 ⇓	37.9	34.3	37.8	35.8
		C	17.8	18.7	15.9	21.8	14.9	16.0	18.7	21.7	21.8	22.2
		T	17.4	17.8	16.8	16.0	20.2 ⇑	17.4	14.2	14.6	13.4	12.6
Asp	GAC	A	33.3 ⇑	30.1 ⇑	42.0 ⇑	34.6 ⇑	43.2 ⇑	43.8 ⇑	34.2 ⇑	27.1 ⇑	29.6 ⇑	30.8 ⇑
		G	25.0 ⇓	30.3 ⇓	15.4 ⇓	23.2 ⇓	16.2 ⇓	16.2 ⇓	29.5 ⇓	32.7 ⇓	32.8 ⇓	31.9 ⇓
		C	20.7	18.3	16.7	18.1	20.5	20.8	20.5	22.4	22.1	22.2
		T	20.9	21.3	26.0	24.1	20.1	19.2	15.8	17.8	15.5	15.1
	GAT	A	20.3 ⇓	18.1 ⇓	20.8 ⇓	20.4 ⇓	22.5 ⇓	18.9 ⇓	15.4 ⇓	15.6 ⇓	16.9 ⇓	19.8 ⇓
		G	41.8 ⇑	46.0 ⇑	40.6 ⇑	43.2 ⇑	42.4 ⇑	45.3 ⇑	48.8 ⇑	50.0 ⇑	52.3 ⇑	46.7 ⇑
		C	19.5	20.7	18.7	18.8	18.1	18.8	21.1	18.8	18.5	18.6
		T	18.4	15.2	19.9	17.7	17.0	16.9	14.6	15.6	12.3	15.0
Gln	CAA	A	26.1	24.9	27.7	27.5	27.3	26.5	23.1	13.9 ⇓	23.6	29.6
		G	40.0 ⇑	46.2 ⇑	34.5	32.0	39.3	37.9 ⇑	39.5	22.6	44.0 ⇑	33.3
		C	19.5	19.4	18.3	23.2	17.9	21.9	22.2	52.8 ⇑	22.2	23.0
		T	14.4	9.5 ⇓	19.5	17.3	15.5	13.7	15.3	10.7	10.2	14.2
	CAG	A	32.5	34.6	34.6	34.2	35.0	35.1 ⇑	27.9	21.7	23.9	23.7
		G	21.1 ⇓	20.1 ⇓	24.5 ⇓	23.8	26.9	25.1 ⇓	29.0	27.5	31.7	34.4
		C	27.9	24.1	20.6	24.4	21.4	24.7	25.7	37.7 ⇓	28.5	27.8
		T	18.5	21.2 ⇑	20.2	17.6	16.7	15.1	17.4	13.0	15.9	14.1
His	CAC	A	36.0 ⇑	29.9 ⇑	42.4 ⇑	44.9 ⇑	38.8 ⇑	33.4 ⇑	28.6	23.6	23.6	23.2
		G	22.0 ⇓	31.2	10.2 ⇓	17.1 ⇓	14.7 ⇓	16.7 ⇓	22.7 ⇓	30.0 ⇓	28.3 ⇓	24.9 ⇓
		C	20.1	19.1	25.0	20.4	24.8	26.0	29.2	28.4	29.8	32.0 ⇑
		T	22.0	19.8	22.5	17.6	21.7	23.9	19.5	17.9	18.3	19.8
	CAT	A	18.0 ⇓	15.1 ⇓	19.3 ⇓	15.9 ⇓	20.0 ⇓	15.0 ⇓	18.2	14.1	12.7	16.6
		G	40.1 ⇑	36.3	40.4 ⇑	38.2 ⇑	39.5 ⇑	43.3 ⇑	48.3 ⇑	48.6 ⇑	55.8 ⇑	46.9 ⇑
		C	24.1	24.2	22.5	23.1	21.1	21.8	22.6	18.6	20.0	18.8 ⇓
		T	17.8	24.5	17.9	22.8	19.5	19.9	11.0	18.6	11.5	17.7
Tyr	TAC	A	39.2 ⇑	36.5 ⇑	43.9 ⇑	38.3 ⇑	40.6 ⇑	42.1 ⇑	36.8 ⇑	26.3 ⇑	28.1	38.4 ⇑
		G	21.3 ⇓	26.5 ⇓	14.0 ⇓	16.2 ⇓	16.4 ⇓	12.4 ⇓	23.0 ⇓	28.8 ⇓	28.8 ⇓	22.8 ⇓
		C	18.2	14.4	20.1	20.6	20.8	19.5	21.1	24.0	23.4	22.8
		T	21.3	22.7	22.1	24.8	22.2	26.0 ⇑	19.2	20.8	19.8	16.0
	TAT	A	18.5 ⇓	16.6 ⇓	23.9 ⇓	19.4 ⇓	18.8 ⇓	14.9 ⇓	10.2 ⇓	11.9 ⇓	14.2 ⇓	18.5 ⇓
		G	44.6 ⇑	41.3 ⇑	35.1 ⇑	44.3 ⇑	43.6 ⇑	50.5 ⇑	56.0 ⇑	49.2 ⇑	60.4 ⇑	52.8 ⇑
		C	20.0	23.6 ⇑	19.5	16.0	19.3	18.5	19.8	21.5	16.0	16.8
		T	16.9	18.5	21.6	20.2	18.2	16.1 ⇓	14.1	17.3	9.5	11.9

Table S3. *Continued*

AA	Codon	Base	1	2	3	4	5	6	7	8	9	10
Cys	TGC	A	43.0 ⇑	38.4	39.7 ⇑	47.1 ⇑	41.1 ⇑	44.0 ⇑	32.4	31.6	27.9	29.3
		G	17.4 ⇩	22.0 ⇩	11.2 ⇩	10.1 ⇩	14.3 ⇩	9.3 ⇩	21.5 ⇩	24.8 ⇩	27.9 ⇩	19.6 ⇩
		C	9.3 ⇩	18.4	22.4	22.2	16.6	26.5	23.6	23.0	25.0	30.4 ⇑
		T	30.2	21.2	26.7	20.6	28.0	20.2	22.5	20.6	19.2	20.7
	TGT	A	20.4 ⇩	30.0	20.7 ⇩	20.9 ⇩	17.8 ⇩	9.5 ⇩	12.1 ⇩	13.6 ⇩	14.7	19.1
		G	39.6 ⇑	38.3 ⇑	41.5 ⇑	42.6 ⇑	38.4 ⇑	59.1 ⇑	60.0 ⇑	56.8 ⇑	65.3 ⇑	53.7 ⇑
		C	22.4	14.3	15.4	20.9	19.2	17.9	13.3	15.9	9.5 ⇩	11.8 ⇩
		T	17.6	17.4	22.4	15.5	24.6	13.5	14.5	13.6	10.5	15.4
Phe	TTC	A	35.1 ⇑	30.4	39.4 ⇑	39.9 ⇑	39.2 ⇑	37.7 ⇑	29.5 ⇑	28.1 ⇑	29.9	28.0 ⇑
		G	19.2 ⇩	22.7 ⇩	12.3 ⇩	11.4 ⇩	11.2 ⇩	13.4 ⇩	24.1 ⇩	25.5 ⇩	30.2 ⇩	28.6 ⇩
		C	18.1	20.5	21.2	22.6	23.3	24.6	25.1	23.3	22.9	22.3
		T	27.5 ⇑	26.4	27.1 ⇑	26.1 ⇑	26.4 ⇑	24.3 ⇑	21.2	23.1	17.0	21.2
	TTT	A	19.0 ⇩	20.4 ⇩	21.5 ⇩	16.8 ⇩	17.6 ⇩	13.6 ⇩	14.8 ⇩	12.5 ⇩	15.8 ⇩	15.4 ⇩
		G	46.9 ⇑	44.6 ⇑	39.4 ⇑	48.1 ⇑	46.4 ⇑	52.8 ⇑	54.6 ⇑	54.7 ⇑	60.9 ⇑	52.4 ⇑
		C	16.4	18.8	19.8	17.9	18.3	17.4	18.3	15.0 ⇩	8.8 ⇩	18.5
		T	17.7 ⇩	16.2 ⇩	19.3	17.3	17.7 ⇩	16.2	12.3 ⇩	17.8	14.4	13.7
Ile	ATA	A	25.5	26.8	25.8	28.3	29.2	27.7	32.0	22.8	23.5	27.5
		G	32.3	34.4	35.8	28.6	31.5	31.3	23.6 ⇩	27.9	27.5	33.3
		C	17.8	17.2	14.5 ⇩	16.3	11.9 ⇩	12.6 ⇩	15.1	25.0	14.8	21.6
		T	24.4	21.7	23.9	26.9 ⇑	27.3 ⇑	28.5 ⇑	29.3 ⇑	24.3	34.2 ⇑	17.6
	ATC	A	36.3 ⇑	33.0 ⇑	40.8 ⇑	42.2 ⇑	45.5 ⇑	42.2 ⇑	36.3 ⇑	32.8 ⇑	33.3 ⇑	30.3 ⇑
		G	21.4 ⇩	25.6 ⇩	19.9 ⇩	15.4 ⇩	16.2 ⇩	17.5 ⇩	26.0 ⇩	28.9 ⇩	29.6 ⇩	27.0 ⇩
		C	16.8	20.5	20.3	20.7	17.5	22.3	22.3	23.8	21.6	26.0
		T	25.5 ⇑	21.0	20.9	21.8	20.8	17.9	15.3	14.5	15.6	16.7
	ATT	A	18.3 ⇩	18.8 ⇩	18.4 ⇩	21.9 ⇩	20.0 ⇩	18.1 ⇩	15.4 ⇩	13.0 ⇩	12.6 ⇩	18.4 ⇩
		G	41.5 ⇑	44.6 ⇑	40.0 ⇑	42.3 ⇑	43.6 ⇑	46.9 ⇑	53.9 ⇑	51.9 ⇑	57.9 ⇑	48.4 ⇑
		C	26.1 ⇑	22.1	22.9	18.9	18.6	19.2	16.5	18.3	16.1	21.1
		T	14.1 ⇩	14.5 ⇩	18.6	16.9 ⇩	17.8	15.8 ⇩	14.2	16.8	13.3	12.2
Thr	ACA	A	32.7	38.5 ⇑	35.5	30.8	36.8	33.5	36.0 ⇑	26.2	33.5	28.2
		G	32.9	29.3	28.0	33.5	25.4 ⇩	30.6	28.9 ⇩	35.7	28.6	29.8
		C	15.7	17.9	18.0	16.5	17.8	20.0	17.3	17.1	18.9	15.2
		T	18.7	14.3	18.5	19.2	20.0	15.9	17.8	21.0	18.9	26.9 ⇑
	ACG	A	32.3	25.4	31.9	33.1	19.7	25.5	22.7	16.6 ⇩	16.4 ⇩	19.9
		G	33.8	30.0	27.5	36.4	41.9	38.7	39.8	36.8	42.1	36.7
		C	17.4	19.8	16.3	8.5	16.2	22.6	23.5	31.1 ⇑	23.8 ⇑	25.7 ⇑
		T	16.4	24.7	24.4	22.0	22.2	13.2	14.0	15.6	17.6	17.7
	ACC	A	37.5 ⇑	34.6	45.9 ⇑	39.7 ⇑	48.8 ⇑	43.5 ⇑	36.2 ⇑	32.6 ⇑	32.6 ⇑	31.5 ⇑
		G	27.3	36.9	16.6 ⇩	16.4 ⇩	22.5 ⇩	15.9 ⇩	30.8 ⇩	35.8	33.8	30.4 ⇩
		C	15.4	11.9 ⇩	18.3	20.1	15.0	22.6	19.1	16.0	15.6	19.2
		T	19.9	16.6	19.2	23.8	13.6	18.0	13.9	15.6	18.0	18.8
	ACT	A	17.4 ⇩	20.5 ⇩	24.6 ⇩	20.9 ⇩	21.0 ⇩	15.5 ⇩	13.0 ⇩	18.7	15.2 ⇩	15.2 ⇩
		G	38.6	32.1	37.8 ⇑	39.4 ⇑	37.7 ⇑	45.5 ⇑	51.8 ⇑	43.9	46.4 ⇑	53.2 ⇑
		C	25.0 ⇑	24.7 ⇑	17.9	16.9	21.4	20.5	22.5	17.8	18.8	17.7
		T	19.0	22.6	19.6	22.9	19.9	18.6	12.7	19.6	19.6	13.9
Gly	GGA	A	33.6	35.8 ⇑	31.1	35.7 ⇑	37.5 ⇑	37.7 ⇑	32.3	28.6	25.1	24.9
		G	38.0 ⇑	38.1	31.8	33.3	32.2	36.8	36.8	33.1	35.2	38.5
		C	11.6 ⇩	14.7	15.0	12.3 ⇩	14.8	12.9 ⇩	12.3 ⇩	20.0	23.9	14.5 ⇩
		T	16.8 ⇩	11.5 ⇩	22.1	18.7	15.5 ⇩	12.6 ⇩	18.6	18.3	15.8	22.0
	GGG	A	44.8 ⇑	44.0 ⇑	38.2 ⇑	34.0	39.6 ⇑	34.2	36.2 ⇑	30.0	27.3	29.3
		G	15.9 ⇩	15.7 ⇩	26.0	27.7	26.7	26.9 ⇩	20.3 ⇩	23.3 ⇩	22.1 ⇩	24.0 ⇩
		C	16.5	18.7	17.1	23.8 ⇑	13.3	18.5	25.1 ⇑	31.2 ⇑	28.8 ⇑	26.8 ⇑
		T	22.9	21.7	18.7	14.5	20.4	20.4	18.4	15.5	21.9 ⇑	19.9
	GGC	A	33.0	34.3	39.9 ⇑	42.1 ⇑	31.8	38.7 ⇑	29.0	29.5	31.3 ⇑	32.1 ⇑
		G	27.3	25.5 ⇩	15.3 ⇩	20.7 ⇩	20.1 ⇩	17.7 ⇩	38.1	39.2	34.6	33.9
		C	17.7	17.8	17.6	18.7	26.3 ⇑	20.5	18.1	18.9	20.4	20.6
		T	22.0	22.4	27.2	18.4	21.8	23.0 ⇑	14.7	12.5	13.6 ⇩	13.3 ⇩
	GGT	A	18.4 ⇩	19.1 ⇩	23.1 ⇩	16.0 ⇩	18.4 ⇩	15.5 ⇩	15.5 ⇩	13.6 ⇩	10.6 ⇩	12.6 ⇩
		G	37.4	40.5 ⇑	37.0 ⇑	44.7 ⇑	40.6 ⇑	48.0 ⇑	49.3 ⇑	54.5 ⇑	55.4 ⇑	53.6 ⇑
		C	19.2	21.1	16.5	18.0	16.2	18.2	14.7	17.3	17.9	16.4
		T	25.0	19.2	23.5	21.2	24.8 ⇑	18.3	20.4	14.6	16.0	17.4

Table S3. *Continued*

Ala	GCA	A	32.9 ⇑	30.8	34.2 ⇑	31.1	35.2 ⇑	33.8	28.0	27.8	28.1	30.3 ⇑
		G	36.0	35.3	29.2	33.4	27.6 ⇓	31.4	35.9	31.5 ⇓	32.5	33.9 ⇓
		C	14.7	19.1	17.0	15.8	18.5	17.7	19.5	21.9	22.3	20.2
		T	16.4 ⇓	14.8	19.5	19.7	18.7	17.1	16.6	18.8	17.1	15.6
	GCG	A	33.2	29.9	31.2	29.5	32.0	22.5	22.7	19.3 ⇓	15.6 ⇓	13.8 ⇓
		G	32.4	37.4	35.7	38.2	39.5	42.9	35.4	34.5 ⇓	33.9	38.4
		C	15.8	12.9	14.9	15.6	12.8	15.2	27.4 ⇑	31.2 ⇑	37.2 ⇑	31.8 ⇑
		T	18.7	19.8	18.2	16.8	15.7	19.4	14.5	15.0	13.4	16.1
	GCC	A	38.0 ⇑	34.6	44.5 ⇑	39.8 ⇑	43.9 ⇑	50.9 ⇑	30.2 ⇑	31.9 ⇑	34.1 ⇑	33.9 ⇑
		G	32.8	39.4	21.0 ⇓	22.6 ⇓	26.2 ⇓	16.4 ⇓	41.2	42.5	39.2	40.2
		C	11.2 ⇓	10.0 ⇓	15.2	17.5	15.3	17.5	13.4 ⇓	13.8 ⇓	12.8 ⇓	11.0 ⇓
		T	17.9	16.0	19.3	20.1	14.7	15.3	15.3	11.8	13.9	14.9
	GCT	A	19.3 ⇓	22.7 ⇓	21.3 ⇓	22.1 ⇓	22.5 ⇓	17.5 ⇓	16.5 ⇓	13.6 ⇓	13.2 ⇓	15.1 ⇓
		G	33.6	34.9	38.9 ⇑	43.3 ⇑	43.4 ⇑	46.7 ⇑	50.1 ⇑	49.9 ⇑	50.1 ⇑	50.1 ⇑
		C	23.1 ⇑	22.8 ⇑	17.7	18.2	15.8	18.0	19.4	21.7	20.9	20.1
		T	24.0 ⇑	19.5	22.1	16.4	18.3	17.9	13.9	14.8	15.8	14.7
Val	GTA	A	24.4	29.0	29.8	30.2	27.5	31.0	26.5	20.7	25.3	30.3
		G	41.1	29.0	29.8	32.0	32.8	32.2	32.0	37.0	39.4	29.7
		C	19.1	21.0	19.4	18.7	16.0	16.7	19.5	21.5	16.2	21.1
		T	15.4	21.0	21.1	19.0	23.7	20.2	22.0 ⇑	20.7	19.2	18.9
	GTG	A	34.9 ⇑	35.1 ⇑	35.9 ⇑	31.7	34.2 ⇑	34.9 ⇑	25.1	24.6	22.9	22.6
		G	35.3	36.8	31.9	36.8	31.6	34.9	35.7	36.1	35.7	36.3
		C	14.1 ⇓	12.0 ⇓	14.2	15.4	15.1	15.1 ⇓	25.2	24.9	28.0 ⇑	25.6
		T	15.7	16.1	18.0	16.1	19.1	15.1	14.0	14.4	13.4	15.6
	GTC	A	32.5	31.2	42.9 ⇑	39.3 ⇑	41.5 ⇑	44.6 ⇑	34.8 ⇑	29.4 ⇑	31.9 ⇑	33.1 ⇑
		G	26.8 ⇓	22.0 ⇓	16.5 ⇓	21.4 ⇓	20.8 ⇓	15.3 ⇓	29.8 ⇓	34.9	33.8	34.2
		C	14.2	20.2	18.6	21.1	15.7	20.7	21.1	18.7 ⇓	16.4 ⇓	18.8
		T	26.5 ⇑	26.5 ⇑	22.0	18.2	22.0	19.4	14.3	17.0	17.9	14.0
	GTT	A	19.8 ⇓	20.7 ⇓	19.8 ⇓	19.4 ⇓	18.3 ⇓	17.3 ⇓	16.2 ⇓	14.8 ⇓	15.9 ⇓	16.2 ⇓
		G	38.6	37.7 ⇑	41.6 ⇑	43.5 ⇑	44.5 ⇑	45.4 ⇑	49.9 ⇑	44.3	54.7 ⇑	51.1 ⇑
		C	23.7 ⇑	23.2	18.3	20.3	18.3	21.7	19.9	25.9	17.7	22.9
		T	17.9	18.4	20.3	16.8	18.9	15.6	14.0	15.1	11.7	9.8 ⇓
Pro	CCA	A	31.1 ⇑	33.9	34.4 ⇑	35.0	31.4	28.8	28.1	19.7	23.3	25.8
		G	31.1	28.3	29.4	27.8	26.9	30.7	34.9	31.3	33.6	29.9
		C	17.1 ⇓	18.4	17.5	17.1	20.1	20.0	19.5	28.4	19.9	23.2
		T	20.6	19.4	18.7	20.1	21.6	20.5	17.5	20.7	23.3 ⇑	21.1
	CCG	A	30.0	27.7	28.8	19.3 ⇓	24.8	22.2	18.4 ⇓	16.7 ⇓	15.8 ⇓	18.7 ⇓
		G	34.1	35.3	41.6	42.9	34.3	35.2	32.4	39.6	38.3	33.3
		C	17.7	14.0	12.8	20.5	21.9	29.6	33.5 ⇑	28.5	30.7 ⇑	29.5 ⇑
		T	18.2	23.0	16.8	17.4	19.0	13.0	15.7	15.3	15.1	18.5
	CCC	A	40.9 ⇑	41.2 ⇑	44.3 ⇑	50.6 ⇑	43.2 ⇑	39.1 ⇑	39.5 ⇑	32.8 ⇑	38.1 ⇑	35.1 ⇑
		G	29.9	27.5	16.1 ⇓	21.3 ⇓	27.1	18.8 ⇓	26.2 ⇓	31.8	32.8	33.5
		C	13.4 ⇓	13.3	16.1	12.8	12.1 ⇓	18.8	13.3 ⇓	17.5 ⇓	11.5 ⇓	14.8 ⇓
		T	15.9	18.0	23.5	15.2	17.6	23.2	21.1	18.0	17.5	16.6
	CCT	A	14.7 ⇓	20.6 ⇓	19.4 ⇓	21.2 ⇓	24.1 ⇓	19.6 ⇓	12.1 ⇓	18.6	17.1 ⇓	16.0 ⇓
		G	31.1	34.7	40.1 ⇑	37.7	33.4	40.7 ⇑	46.7 ⇑	40.4	46.8 ⇑	45.5 ⇑
		C	30.1 ⇑	23.6 ⇑	20.7	19.4	21.9	22.2	23.4	26.9	22.8	21.9
		T	24.1	21.0	19.8	21.7	20.5	17.5	17.8	14.1	13.3	16.5

Table S3. *Continued*

AA	Codon	Base										
Arg	AGA	A	32.1	27.9	34.6	33.4	32.9	29.9	28.3	24.3	22.0	29.9
		G	35.2	39.7 ⇧	32.5	35.7	31.4	41.8 ⇧	34.2	31.1	47.7	33.7
		C	14.0 ⇩	15.1	14.3 ⇩	11.9 ⇩	15.0	13.0 ⇩	16.9 ⇩	12.8	14.7	14.4 ⇩
		T	18.7	17.3	18.6	19.0	20.7	15.3	20.5	31.8 ⇧	15.6	22.0
	AGG	A	37.6 ⇧	43.6 ⇧	32.9	34.5	41.3 ⇧	34.7	36.1 ⇧	34.5 ⇧	28.0 ⇧	30.4
		G	22.0 ⇩	18.2 ⇩	26.6	26.5	24.5	29.1 ⇩	26.3 ⇩	25.2 ⇩	30.9	34.1
		C	25.4	17.2	19.2	23.4	19.6	20.0	23.8	19.1	26.4	21.7
		T	15.0	21.0	21.4	15.7	14.7	16.3	13.8	21.2	14.6	13.9
	CGA	A	28.8	34.2	22.5	29.9	24.4	38.0	23.0	12.0	15.0	25.2
		G	33.1	31.6	31.9	29.9	30.5	35.2	43.4	38.7	38.3	29.9
		C	17.2	21.4	18.8	18.2	20.6	16.2	15.6	20.0	23.3	21.5
		T	20.9	12.8	26.9	22.1	24.4	10.6	18.0	29.3	23.3	23.4
	CGG	A	31.2	38.8	35.1	29.6	35.8	35.2	29.0	22.4	20.7	20.8
		G	22.7	12.9	25.8	24.3	20.9	29.7	25.4 ⇩	30.7	29.9	28.2
		C	19.1	18.1	19.6	27.8	20.9	22.0	26.8	27.6	29.1	34.9 ⇧
		T	27.0	30.2 ⇧	19.6	18.3	22.4	13.2	18.8	19.3	20.3	16.1
	CGC	A	23.8	36.4	35.6	32.3	30.1	31.8	19.0 ⇩	21.0	24.2	23.8
		G	20.8	24.6 ⇩	16.3 ⇩	25.0	19.5 ⇩	22.4 ⇩	32.7	35.9	35.0	31.9
		C	27.7	26.3	26.9	25.0	37.2 ⇧	27.6 ⇧	31.1 ⇧	24.4	28.0	28.0
		T	27.7	12.7	21.2	17.7	13.3	18.2	17.2	18.7	12.8	16.3
	CGT	A	19.0 ⇩	17.7 ⇩	25.3	17.8 ⇩	16.0 ⇩	16.4 ⇩	17.6 ⇩	10.7 ⇩	11.0 ⇩	14.1 ⇩
		G	40.7 ⇧	40.1 ⇧	30.4	42.3 ⇧	47.9 ⇧	46.6 ⇧	53.7 ⇧	58.2 ⇧	62.8 ⇧	45.4 ⇧
		C	19.8	22.7	24.0	19.2	20.2	22.4	17.6	18.0	16.6	25.9
		T	20.5	19.5	20.3	20.7	16.0	14.6	11.2	13.1	9.7	14.6
Ser	AGC	A	38.1 ⇧	27.5	43.6 ⇧	36.8	44.7 ⇧	37.2 ⇧	33.8 ⇧	32.4 ⇧	31.7 ⇧	33.6 ⇧
		G	23.2	26.4	12.5 ⇩	13.2 ⇩	11.7 ⇩	18.0 ⇩	23.6 ⇩	24.1 ⇩	26.6 ⇩	21.4 ⇩
		C	16.1	16.8	19.7	16.3	18.8	22.7	22.5	24.6	26.1	23.5
		T	22.6	29.3	24.3	33.7 ⇧	24.8	22.1	20.1	18.9	15.6	21.4
	AGT	A	25.1	20.2 ⇩	20.6 ⇩	29.2	21.5 ⇩	14.4 ⇩	19.4 ⇩	20.5	20.0	16.5 ⇩
		G	34.3	42.6 ⇧	41.3 ⇧	39.1 ⇧	42.8 ⇧	54.7 ⇧	46.6 ⇧	48.6 ⇧	51.8 ⇧	51.8 ⇧
		C	21.8	15.3	12.6 ⇩	14.3	12.8	12.9 ⇩	12.5 ⇩	15.8	10.9 ⇩	19.2
		T	18.8	21.8	25.5	17.4	22.9	17.9	21.6	15.1	17.3	12.5 ⇩
	TCA	A	34.2	29.9	32.3	35.3	32.4	31.6	30.7	23.2	29.2	25.9
		G	30.4	32.8	22.7 ⇩	29.3	24.8 ⇩	32.0	30.4	31.8	29.2	31.5
		C	16.1	16.5	20.0	17.4	17.5	16.1	16.8	23.2	21.1	21.8
		T	19.4	20.7	25.0	18.0	25.3	20.2	22.0	21.7	20.5	20.8
	TCG	A	30.6	27.8	43.5 ⇧	29.1	26.1	21.6	17.8 ⇩	16.8 ⇩	13.3 ⇩	16.0 ⇩
		G	29.0	32.9	20.2	28.4	33.9	23.2	33.5	28.4	38.8	30.8
		C	17.6	15.3 ⇧	13.1	16.3	17.4	30.4 ⇧	29.6	30.2 ⇧	30.1 ⇧	32.4 ⇧
		T	22.9	24.1	23.2	26.2	22.6	24.8	19.1	24.6	17.8	20.8
	TCC	A	37.9 ⇧	41.5 ⇧	35.3	37.7	45.8 ⇧	37.7 ⇧	39.0 ⇧	32.7 ⇧	32.9 ⇧	28.9
		G	25.4	23.4 ⇩	20.3 ⇩	14.3 ⇩	23.7 ⇩	18.0 ⇩	24.9 ⇩	28.9	29.7	30.1
		C	15.1	13.1	15.7	23.8	10.6 ⇩	17.3	15.8	17.6	18.3	19.2
		T	21.5	22.0	28.7	24.2	19.9	27.0	20.3	20.8	19.1	21.8
	TCT	A	19.7 ⇩	20.8 ⇩	21.2 ⇩	19.1 ⇩	17.7 ⇩	17.8 ⇩	18.1 ⇩	12.5 ⇩	12.9 ⇩	15.6 ⇩
		G	31.7	31.9	35.2 ⇧	37.4 ⇧	37.6 ⇧	41.3 ⇧	48.8 ⇧	44.4 ⇧	46.1 ⇧	47.9 ⇧
		C	25.0 ⇧	24.4 ⇧	21.8	20.9	19.8 ⇧	22.1	17.8	22.2	20.8	17.6
		T	23.6	23.0	21.8	22.5	25.0	18.8	15.3	20.8	20.2	19.0

Table S3. *Continued*

Leu	CTA	A	33.8	31.7	35.5	30.6	28.0	30.9	28.1	27.1	22.0	25.5
		G	29.5	37.6	30.5	32.3	28.3	30.9	26.3 ⇓	33.9	46.0	35.4
		C	15.8	13.6 ⇓	13.6 ⇓	18.5	19.7	17.4	25.4	17.8	16.0	21.7
		T	20.9	17.1	20.4	18.5	24.0	20.9	20.1	21.2	16.0	17.4
	CTG	A	38.8 ⇑	38.3 ⇑	36.1	27.3	28.0	33.5	25.0	21.6	21.8	21.1 ⇓
		G	28.8	27.2	26.1	30.4	24.8	32.6	33.6	36.2	38.1	35.6
		C	14.0	19.8	20.6	22.5	19.9	21.2	27.0	29.8 ⇑	28.3 ⇑	31.3 ⇑
		T	18.3	14.8	17.2	19.7	27.2 ⇑	12.8 ⇓	14.3	12.4	11.8	11.9
	CTC	A	31.6	28.4	41.7 ⇑	38.5 ⇑	37.5 ⇑	37.6 ⇑	28.3	32.1 ⇑	31.3 ⇑	33.1 ⇑
		G	22.9 ⇓	25.8 ⇓	11.6 ⇓	14.8 ⇓	20.4 ⇓	13.0 ⇓	28.7 ⇓	29.6 ⇓	30.5 ⇓	28.4 ⇓
		C	16.7	21.3	20.7	19.9	18.1	24.4	24.1	21.0	22.1	23.1
		T	28.9 ⇑	24.5 ⇑	26.0 ⇑	26.8 ⇑	24.0	25.0 ⇑	18.9	17.3	16.1	15.5
	CTT	A	17.1 ⇓	17.0 ⇓	21.3 ⇓	14.7 ⇓	16.8 ⇓	15.8 ⇓	17.4 ⇓	12.4 ⇓	13.1 ⇓	14.4 ⇓
		G	38.0 ⇑	40.6 ⇑	34.8 ⇑	37.5 ⇑	37.4 ⇑	43.9 ⇑	46.5 ⇑	52.2 ⇑	51.1 ⇑	49.8 ⇑
		C	26.5 ⇑	27.4 ⇑	22.7 ⇑	26.0 ⇑	27.3 ⇑	26.3 ⇑	22.0	21.7	27.3	23.2
		T	18.4	15.0	21.2	21.7	18.5	13.9	14.1	13.7	8.5 ⇓	12.6
	TTA	A	24.6	23.9	31.4	34.6 ⇑	30.5	31.0	22.3	19.2	25.0	30.3
		G	37.3	35.2	28.7	28.5	33.9	31.4	34.9	35.9	42.5	34.8
		C	18.1	19.0	18.2	18.9	14.8 ⇓	16.5	22.3	30.8	15.0	20.6
		T	20.0	21.9	21.7	18.0	20.8	21.2	20.5	14.1	17.5	14.2
	TTG	A	33.5 ⇑	30.1	32.0	32.3	36.0 ⇑	29.9	26.0	27.5	30.0	29.4
		G	35.2	30.9	30.6	34.2	31.4	37.0	39.7	41.4	41.9	36.1
		C	16.1	19.8	17.8	19.8	17.6	17.5 ⇓	18.8 ⇓	21.1	12.3 ⇓	21.1
		T	15.2 ⇓	19.2	19.6	13.7 ⇓	15.0 ⇓	15.7	15.5	10.0	15.9	13.4

Significantly large and small values (P = 0.01) are indicated with an upward or downward arrow, respectively.

Table S4. Optimum codons and certainty factors calculated as indicated in Materials and Methods

A. thaliana

Aminoacid	Optimum codon and certainty factor when subsequent codon is headed by:			
	A	G	C	T
Lys	AAG 87%	AAA 86%	AAG 85%	AAA 83%
Asn	AAC 89%	AAT 90%	AAT 86%	AAC 85%
Glu	GAG 87%	GAA 89%	GAG 84%	GAG 85%
Asp	GAT 86%	nc 93%	nc 89%	nc 89%
Gln	CAG 83%	CAA 90%	CAG 84%	CAG 83%
His	CAC 86%	CAT 91%	CAT 87%	CAT 84%
Tyr	TAC 89%	TAT 89%	TAT 84%	TAC 85%
Cys	TGC 86%	TGT 92%	TGT 92%	TGC 85%
Phe	TTC 88%	TTT 90%	TTC 84%	TTC 87%
Ile	ATC 82%	ATT 84%	ATT 83%	ATC 81%
Thr	ACA 79%	ACT 80%	ACT 82%	ACT 79%
Gly	GGA 80%	GGA 81%	GGT 80%	GGT 79%
Ala	GCA 77%	GCT 81%	GCT 86%	GCT 84%
Val	GTG 78%	GTT 81%	GTT 84%	GTT 80%
Pro	CCA 81%	CCT 79%	CCT 85%	CCT 81%
Arg	AGA 71%	AGA 69%	AGG 64%	AGA 65%
Ser	TCC 58%	TCT 64%	TCT 65%	TCT 63%
Leu	CTG 67%	CTG/CTT 64%	CTT 68%	CTG 65%

B. napus

Aminoacid	Optimum codon and certainty factor when subsequent codon is headed by:			
	A	G	C	T
Lys	AAG 90%	AAA 84%	AAG 85%	AAG 86%
Asn	AAC 92%	nc 84%	nc 88%	nc 91%
Glu	GAG 90%	GAA 86%	GAG 88%	GAG 88%
Asp	GAC 86%	GAT 88%	GAT 85%	GAC 84%
Gln	CAG 86%	CAA 90%	CAG 85%	CAG 90%
His	CAC 88%	CAT 84%	CAT 85%	CAT 85%
Tyr	TAC 93%	TAC 83%	TAT 83%	TAC 89%
Cys	TGC 86%	TGT 87%	TGC 86%	TGC 85%
Phe	TTC 90%	TTT 85%	TTC 88%	TTC 91%
Ile	ATC 84%	ATT 82%	ATC 81%	ATC 82%
Thr	ACC 77%	ACC 77%	ACT 80%	ACT 78%
Gly	GGA 80%	GGA 80%	GGT 79%	GGT 78%
Ala	GCT 77%	nc 80%	nc 84%	nc 82%
Val	GTG 78%	GTT 80%	GTT 80%	GTC 78%
Pro	CCA 78%	CCT 80%	CCT 82%	CCT 79%
Arg	AGG 67%	AGA 68%	CGA 62%	AGG 64%
Ser	TCC 62%	TCT 58%	TCT 62%	TCT 56%
Leu	CTG 69%	CTT 67%	CTT 68%	CTG/CTC 65%

Table S4. *Continued*

L. esculentum	Optimum codon and certainty factor when subsequent codon is headed by:			
Aminoacid	A	G	C	T
Lys	AAG 85%	**AAA** 86%	AAG 85%	**AAA** 85%
Asn	AAC 84%	**AAT** 94%	**AAT** 89%	**AAT** 84%
Glu	**GAA** 84%	nc 87%	nc 86%	nc 86%
Asp	**GAT** 86%	nc 96%	nc 92%	nc 89%
Gln	**CAA** 85%	nc 89%	nc 86%	nc 86%
His	CAC 83%	**CAT** 96%	**CAT** 88%	**CAT** 87%
Tyr	TAC 84%	**TAT** 93%	**TAT** 87%	**TAT** 87%
Cys	TGC 85%	**TGT** 95%	**TGT** 83%	**TGT** 85%
Phe	TTC 84%	**TTT** 95%	**TTT** 87%	**TTT** 85%
Ile	ATC 79%	**ATT** 86%	**ATT** 86%	**ATT** 82%
Thr	ACA 79%	**ACT** 83%	**ACT** 80%	**ACT** 80%
Gly	**GGA** 78%	GGT 80%	GGT 78%	GGT 78%
Ala	GCA 79%	**GCT** 85%	**GCT** 83%	**GCT** 83%
Val	**GTT** 76%	nc 85%	nc 82%	nc 81%
Pro	CCA 81%	**CCT** 83%	**CCT** 82%	**CCT** 81%
Arg	**AGA** 70%	nc 71%	nc 63%	nc 67%
Ser	**TCT** 57%	nc 65%	nc 64%	nc 60%
Leu	CTG 65%	CTG 64%	CTG 65%	CTG 64%

N. tabacum	Optimum codon and certainty factor when subsequent codon is headed by:			
Aminoacid	A	G	C	T
Lys	**AAG** 86%	AAA 85%	**AAG** 87%	AAA 85%
Asn	AAC 86%	**AAT** 94%	**AAT** 87%	**AAT** 84%
Glu	**GAA** 83%	**GAA** 88%	GAG 83%	**GAA** 84%
Asp	**GAT** 85%	nc 93%	nc 90%	nc 87%
Gln	**CAA** 84%	nc 88%	nc 85%	nc 86%
His	CAC 87%	**CAT** 93%	**CAT** 88%	**CAT** 89%
Tyr	TAC 85%	**TAT** 93%	**TAT** 84%	**TAT** 85%
Cys	TGC 87%	**TGT** 95%	**TGT** 85%	**TGT** 83%
Phe	TTC 88%	**TTT** 95%	**TTT** 83%	TTC 84%
Ile	**ATT** 79%	nc 88%	nc 83%	nc 80%
Thr	ACA 79%	**ACT** 81%	**ACT** 79%	**ACT** 80%
Gly	**GGA** 80%	GGT 81%	GGT 78%	GGT 79%
Ala	GCA 79%	**GCT** 83%	**GCT** 81%	**GCT** 79%
Val	**GTT** 76%	nc 83%	nc 81%	nc 80%
Pro	CCA 81%	**CCT** 81%	**CCT** 80%	**CCT** 80%
Arg	**AGA** 70%	**AGA** 67%	AGG 65%	**AGA** 66%
Ser	**TCT** 56%	nc 66%	nc 65%	nc 58%
Leu	CTG 64%	CTG 66%	CTG 66%	**CTT** 66%

Table S4. *Continued*

P. sativum Aminoacid	Optimum codon and certainty factor when subsequent codon is headed by:				G. max Aminoacid	Optimum codon and certainty factor when subsequent codon is headed by:			
	A	G	C	T		A	G	C	T
Lys	**AAG** 85%	AAA 84%	**AAG** 83%	AAA 83%	Lys	**AAG** 88%	nc 85%	nc 88%	nc 84%
Asn	AAC 87%	**AAT** 93%	**AAT** 84%	**AAT** 84%	Asn	**AAC** 91%	AAT 93%	**AAC** 86%	**AAC** 84%
Glu	**GAA** 85%	**GAA** 88%	**GAA** 85%	GAG 83%	Glu	GAG 85%	**GAA** 86%	**GAA** 83%	GAG 84%
Asp	**GAT** 85%	nc 95%	nc 89%	nc 89%	Asp	GAC 85%	**GAT** 94%	**GAT** 87%	**GAT** 87%
Gln	**CAA** 86%	nc 90%	nc 86%	nc 87%	Gln	CAG 84%	**CAA** 87%	CAG 83%	**CAA** 83%
His	CAC 85%	**CAT** 93%	**CAT** 85%	**CAT** 86%	His	CAC 88%	**CAT** 92%	**CAT** 84%	**CAT** 84%
Tyr	TAC 86%	**TAT** 93%	**TAT** 86%	**TAT** 85%	Tyr	TAC 91%	**TAT** 94%	**TAT** 83%	TAC 86%
Cys	TGC 86%	**TGT** 94%	**TGT** 89%	**TGT** 86%	Cys	**TGC** 94%	TGT 95%	**TGC** 86%	**TGC** 87%
Phe	TTC 88%	**TTT** 95%	**TTT** 83%	TTC 84%	Phe	TTC 90%	**TTT** 94%	TTC 85%	TTC 85%
Ile	ATC 80%	**ATT** 88%	**ATT** 85%	**ATT** 80%	Ile	ATC 81%	**ATT** 89%	**ATT** 84%	**ATT** 80%
Thr	ACA 79%	**ACT** 82%	**ACT** 81%	**ACT** 80%	Thr	ACC 79%	**ACT** 83%	**ACT** 78%	**ACT** 79%
Gly	GGA 81%	**GGT** 82%	**GGT** 78%	**GGT** 82%	Gly	**GGA** 80%	GGT 81%	GGT 78%	GGT 77%
Ala	GCA 78%	**GCT** 85%	**GCT** 81%	**GCT** 82%	Ala	GCC 79%	**GCT** 84%	**GCT** 80%	**GCT** 80%
Val	**GTG/GTT** 76%	**GTT** 85%	**GTT** 83%	**GTT** 80%	Val	GTG 78%	**GTT** 84%	**GTT** 83%	**GTT** 80%
Pro	CCA 79%	**CCT** 81%	**CCT** 81%	**CCT** 80%	Pro	CCA 79%	**CCT** 82%	**CCT** 80%	CCA 79%
Arg	**AGA** 71%	nc 66%	nc 62%	nc 70%	Arg	**AGA** 67%	**AGA** 67%	CGG 61%	**AGA** 65%
Ser	TCC 59%	**TCT** 67%	**TCT** 65%	**TCT** 63%	Ser	TCC 59%	**TCT** 62%	**TCT** 60%	**TCT** 58%
Leu	CTG 64%	**CTT** 64%	**CTT** 69%	CTG 65%	Leu	CTG 69%	CTG 68%	CTG 69%	CTG 66%

Table S4. *Continued*

O. sativa Aminoacid	Optimum codon and certainty factor when subsequent codon is headed by: A	G	C	T
Lys	**AAG** 92%	nc 90%	nc 92%	nc 85%
Asn	**AAC** 92%	AAT 86%	**AAC** 90%	**AAC** 90%
Glu	**GAG** 89%	nc 87%	nc 89%	nc 87%
Asp	**GAC** 90%	GAT 87%	**GAC** 83%	**GAC** 84%
Gln	**CAG** 89%	nc 85%	nc 89%	nc 89%
His	**CAC** 88%	CAT 88%	**CAC** 86%	**CAC** 89%
Tyr	**TAC** 95%	TAT 87%	**TAC** 87%	**TAC** 89%
Cys	**TGC** 95%	TGT 84%	**TGC** 93%	**TGC** 93%
Phe	**TTC** 92%	TTT 85%	**TTC** 90%	**TTC** 91%
Ile	**ATC** 86%	ATT 85%	**ATC** 84%	**ATC** 80%
Thr	**ACC** 80%	ACT 78%	**ACC** 76%	**ACC** 76%
Gly	**GGC** 78%	nc 78%	nc 78%	nc 76%
Ala	**GCC** 79%	GCT 77%	GCG 76%	**GCC** 77%
Val	GTC 80%	GTT 78%	**GTG** 79%	**GTG** 77%
Pro	CCC 78%	CCT 78%	CCG 79%	CCC 75%
Arg	**AGG** 68%	CGG 65%	CGG 68%	CGG 66%
Ser	TCC 61%	TCT 58%	TCC 58%	TCC 57%
Leu	CTG 72%	CTG 71%	CTG 73%	CTG 70%

T. aestivum Aminoacid	Optimum codon and certainty factor when subsequent codon is headed by: A	G	C	T
Lys	**AAG** 94%	nc 93%	nc 93%	nc 90%
Asn	**AAC** 93%	nc 86%	nc 92%	nc 92%
Glu	**GAG** 93%	nc 90%	nc 92%	nc 89%
Asp	**GAC** 92%	nc 85%	nn 90%	nc 90%
Gln	**CAG** 91%	nc 89%	nc 84%	nc 89%
His	**CAC** 92%	nc 85%	nc 92%	nc 88%
Tyr	**TAC** 95%	nc 86%	nc 91%	nc 91%
Cys	**TGC** 95%	nc 84%	nc 93%	nc 93%
Phe	**TTC** 95%	nc 84%	nc 93%	nc 92%
Ile	**ATC** 93%	nc 85%	nc 89%	nc 86%
Thr	**ACC** 85%	**ACC** 80%	ACG 78%	**ACC** 79%
Gly	**GGC** 83%	nc 82%	nc 80%	nc 80%
Ala	**GCC** 84%	**GCC** 81%	GCG 79%	**GCC** 78%
Val	GTC 80%	**GTG** 79%	**GTG** 80%	GTC 79%
Pro	CCC 79%	**CCG** 76%	**CCG** 77%	CCA 77%
Arg	AGG 68%	CGG 68%	CGG 71%	CGG 66%
Ser	**TCC** 64%	nc 61%	nc 61%	nc 64%
Leu	**CTC** 76%	CTG 74%	CTG 76%	**CTC** 76%

Table S4. *Continued*

H. vulgare Aminoacid	Optimum codon and certainty factor when subsequent codon is headed by:			
	A	G	C	T
Lys	**AAG** 95%	nc 93%	nc 96%	nc 91%
Asn	**AAC** 96%	nc 88%	nc 93%	nc 95%
Glu	**GAG** 96%	nc 91%	nc 94%	nc 92%
Asp	**GAC** 94%	nc 87%	nc 92%	nc 92%
Gln	**CAG** 91%	nc 89%	nc 93%	nc 94%
His	**CAC** 94%	nc 85%	nc 93%	nc 93%
Tyr	**TAC** 96%	nc 88%	nc 95%	nc 96%
Cys	**TGC** 96%	nc 87%	nc 97%	nc 96%
Phe	**TTC** 96%	nc 89%	nc 97%	nc 94%
Ile	**ATC** 93%	nc 85%	nc 91%	nc 86%
Thr	**ACC** 87%	nc 81%	nc 80%	nc 82%
Gly	**GGC** 85%	nc 82%	nc 81%	nc 80%
Ala	**GCC** 86%	**GCC** 81%	GCG 80%	**GCC** 80%
Val	GTC 82%	**GTG** 79%	**GTG** 84%	GTC 81%
Pro	CCC 81%	**CCG** 77%	**CCG** 82%	CCC 76%
Arg	CGG 70%	CGG 68%	CGG 72%	CGG 72%
Ser	**TCC** 64%	nc 61%	nc 62%	nc 65%
Leu	**CTC** 78%	CTG 76%	CTG 78%	**CTC** 77%

Z. mays Aminoacid	Optimum codon and certainty factor when subsequent codon is headed by:			
	A	G	C	T
Lys	**AAG** 91%	nc 90%	nc 93%	nc 91%
Asn	**AAC** 92%	AAT 85%	**AAC** 89%	**AAC** 90%
Glu	**GAG** 89%	nc 87%	nc 90%	nc 89%
Asp	**GAC** 90%	nc 83%	nc 88%	nc 86%
Gln	**CAG** 88%	nc 90%	nc 91%	nc 90%
His	**CAC** 89%	CAT 85%	**CAC** 90%	**CAC** 87%
Tyr	**TAC** 94%	TAT 84%	**TAC** 91%	**TAC** 91%
Cys	**TGC** 92%	TGT 86%	**TGC** 95%	**TGC** 91%
Phe	**TTC** 93%	nc 84%	nc 90%	nc 92%
Ile	**ATC** 88%	nc 81%	nc 87%	nc 86%
Thr	**ACC** 81%	ACT 77%	**ACC** 77%	**ACC** 77%
Gly	**GGC** 82%	nc 78%	nc 79%	nc 76%
Ala	**GCC** 81%	GCT 77%	GCG 80%	**GCC** 76%
Val	GTC 79%	**GTG** 78%	**GTG** 81%	**GTG** 81%
Pro	CCC 78%	CCT 77%	**CCG** 79%	**CCG** 76%
Arg	CGG 65%	nc 66%	nc 71%	nc 65%
Ser	TCC 59%	TCT 59%	TCC 58%	TCC 61%
Leu	**CTG** 72%	nc 74%	nc 77%	nc 73%