Supplemental Material to:

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Effect of salt stress on genes encoding translation-associated proteins in Arabidopsis thaliana

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Supplementary file 1 – Effect of salt stress on genes encoding translation-associated proteins in *Arabidopsis thaliana*

This file includes all tables from the inferential and descriptive analysis of the data set.

i. Differential expression based on linear models

Table S1.Status of all genes differentially expressed in salt-treated versus non-treated samples at the time points given.´0´ indicates no regulation,´1´ indicates up-regulation, and ´-1´, down-regulation. The columns (left to right) indicate the AGI code of the gene and the time points.

AGI	2 h	4 h	6 h	8 h	24 h
AT1G22110	-1	-1	0	-1	0
AT3G08010	1	1	1	0	0
AT1G32990	0	1	0	0	0
AT1G33140	0	1	1	0	0
AT1G48830	0	1	0	0	0
AT1G74970	0	1	0	0	0
AT1G75350	0	1	0	0	0
AT2G24090	0	1	0	0	0
AT3G02660	0	1	1	0	0
AT3G08740	0	1	0	0	0
AT3G13120	0	1	0	0	0
AT3G13580	0	1	1	0	0
AT3G20230	0	1	1	0	0
AT3G25660	0	1	0	0	0
AT3G25920	0	1	0	0	0
AT3G44890	0	1	0	0	0
AT4G11175	0	1	1	1	0
AT4G17560	0	1	0	0	0
AT4G20360	0	1	0	0	0
AT4G34620	0	1	0	0	0
AT5G08650	0	1	0	0	0
AT5G14320	0	1	0	0	0
AT5G14660	0	1	1	0	0
AT5G16710	0	1	1	0	0
AT5G36170	0	1	0	0	0
AT5G40950	0	1	0	0	0
AT1G80620	0	0	1	0	0
AT3G01170	0	0	1	0	0
AT3G09200	0	0	1	0	0

AGI	2 h	4 h	6 h	8 h	24 h
AT4G36420	0	0	1	0	0

ii. Differentially expressed genes over all time points (global regulators)

Table S2.Expression level and the relative significance levels of the four global regulators. The columns (left to right) include the AGI code of the gene and for each time point the relative log-fold changes (lfc) with the *p*-value.

Time points	**2 h**		**4 h**		**6 h**		**8 h**		**24 h**	
AGI code	**lfc**	***p*-value**	**lfc**	***p*-value**	**lfc**	***p*-value**	**lfc**	***p*-value**	**lfc**	**p-value**
AT1G22110	-4.27	3.952E-08	-2.43	1.13E-04	-0.92	0.0883	-1.79	0.0023	-0.69	0.195
AT4G11175	0.32	1.42E-01	1.20	1.20E-05	0.77	0.0015	0.73	0.0025	0.013	0.950
AT3G08010	0.90	6.42E-03	1.72	8.44E-06	0.92	0.0055	0.71	0.0265	0.045	0.880
AT3G20230	0.54	4.26E-02	1.11	2.13E-04	0.81	0.0037	0.65	0.0163	0.53	0.0484

Table S3.Gene names and the relative expression patterns over all time points.´0´ indicates no regulation, ´1´indicates up-regulation, and ´-1´ indicates down-regulation. The columns (left to right) include the AGI code of the gene and the time points.

AGI code	**Gene name**	**2 h**	**4 h**	**6 h**	**8 h**	**24 h**
AT1G22110	structural constituent of ribosome	-1	-1	0	-1	0
AT4G11175	translation initiation factor IF-1, chloroplast, putative	0	1	1	1	0
AT3G08010	ATAB2; RNA binding	1	1	1	1	0
AT3G20230	50S ribosomal protein L18 family	1	1	1	1	1

iii. Differentially expressed genes between consecutive time points across conditions

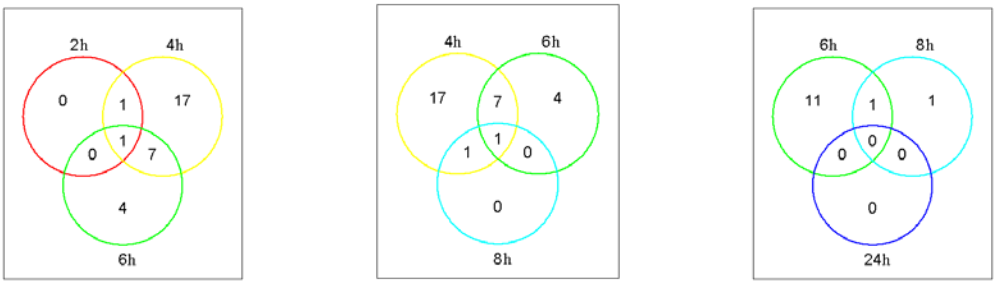

Figure S1.Venn diagrams of the listed differentially expressed genes. Shown are the numbers of genes in the intersection of each three consecutive time points. Each time point is specified by a circle given in a particular color.

Cluster-based approach to identify global effectors

Table S4.Global effectors. Global effectors are the genes which contribute to the difference between control and treatment clusterings, as calculated by Eq. (9) in the main text.

AGI code	**Gene name**
AT3G01170	structural constituent of ribosome
AT5G15260	structural constituent of ribosome
AT1G16720	HCF173 (high chlorophyll fluorescence phenotype 173); binding / catalytic/ transcription repressor
AT1G15390	PDF1A (PEPTIDE DEFORMYLASE 1A); peptide deformylase
AT4G11175	translation initiation factor IF-1, chloroplast, putative
AT1G32990	PRPL11 (PLASTID RIBOSOMAL PROTEIN L11); structural constituent of ribosome
AT1G17220	FUG1 (fu-gaeri1); translation initiation factor
AT5G26830	threonyl-tRNAsynthetase / threonine--tRNA ligase (THRRS)
AT1G26910	60S ribosomal protein L10 (RPL10B)
AT3G58140	phenylalanyl-tRNAsynthetase class IIc family protein
AT4G37660	ribosomal protein L12 family protein
AT3G25660	glutamyl-tRNA(Gln) amidotransferase, putative
AT4G27130	eukaryotic translation initiation factor SUI1, putative
AT2G20060	ribosomal protein L4 family protein
AT3G63490	ribosomal protein L1 family protein
AT3G04230	40S ribosomal protein S16 (RPS16B)
AT5G40950	RPL27 (RIBOSOMAL PROTEIN LARGE SUBUNIT 27); structural constituent of ribosome
AT3G13120	30S ribosomal protein S10, chloroplast, putative
AT3G08010	ATAB2; RNA binding
AT3G04770	RPSAb (40S ribosomal protein SA B); structural constituent of ribosome
AT5G16710	DHAR3 (dehydroascorbatereductase 1); glutathione dehydrogenase (ascorbate)
AT3G15190	chloroplast 30S ribosomal protein S20, putative
AT4G30690	translation initiation factor 3 (IF-3) family protein
AT2G09990	40S ribosomal protein S16 (RPS16A)
AT3G01800	ribosome recycling factor family protein / ribosome releasing factor family protein
AT5G14320	30S ribosomal protein S13, chloroplast (CS13)
AT2G47610	60S ribosomal protein L7A (RPL7aA)
AT4G17560	ribosomal protein L19 family protein
AT2G27710	60S acidic ribosomal protein P2 (RPP2B)
AT3G62910	APG3 (ALBINO AND PALE GREEN); translation release factor/ translation release factor, codon specific
AT5G52520	OVA6 (OVULE ABORTION 6); ATP binding / aminoacyl-tRNA ligase/ nucleotide binding / proline-tRNA ligase
AT2G19740	60S ribosomal protein L31 (RPL31A)

AGI code	**Gene name**
AT1G33120	60S ribosomal protein L9 (RPL90B)
AT5G08650	GTP-binding protein LepA, putative
AT3G11250	60S acidic ribosomal protein P0 (RPP0C)
AT1G29070	ribosomal protein L34 family protein
AT4G36420	ribosomal protein L12 family protein
AT5G14660	PDF1B (PEPTIDE DEFORMYLASE 1B); iron ion binding / peptide deformylase
AT3G02660	emb2768 (EMBRYO DEFECTIVE 2768); ATP binding / RNA binding / aminoacyl-tRNA ligase/ nucleotide binding / tyrosine-tRNA ligase
AT4G29060	emb2726 (embryo defective 2726); RNA binding / translation elongation factor
AT3G13490	OVA5 (OVULE ABORTION 5); ATP binding / aminoacyl-tRNA ligase/ lysine-tRNA ligase/ nucleic acid binding / nucleotide binding
AT1G48520	GATB (GLU-ADT SUBUNIT B); carbon-nitrogen ligase, with glutamine as amido-N-donor / glutaminyl-tRNA synthase (glutamine-hydrolyzing)/ ligase
AT1G07320	RPL4; poly(U) binding / structural constituent of ribosome
AT5G47190	ribosomal protein L19 family protein
AT1G62750	SCO1 (SNOWY COTYLEDON 1); ATP binding / translation elongation factor/ translation factor, nucleic acid binding
AT1G09620	ATP binding / aminoacyl-tRNA ligase/ leucine-tRNA ligase/ nucleotide binding
AT1G74970	RPS9 (RIBOSOMAL PROTEIN S9); structural constituent of ribosome
AT5G13510	ribosomal protein L10 family protein
AT1G14320	SAC52 (SUPPRESSOR OF ACAULIS 52); structural constituent of ribosome
AT4G31700	RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome
AT5G20290	40S ribosomal protein S8 (RPS8A)
AT3G20230	50S ribosomal protein L18 family
AT1G33330	peptide chain release factor, putative
AT1G80620	ribosomal protein S15 family protein
AT2G39140	SVR1 (SUPPRESSOR OF VARIEGATION 1); RNA binding / pseudouridine synthase
AT3G02760	ATP binding / aminoacyl-tRNA ligase/ histidine-tRNA ligase/ nucleotide binding
AT1G05190	emb2394 (embryo defective 2394); structural constituent of ribosome
AT5G24490	30S ribosomal protein, putative
AT5G15200	40S ribosomal protein S9 (RPS9B)
AT5G30510	RPS1 (RIBOSOMAL PROTEIN S1); RNA binding / structural constituent of ribosome
AT1G68590	plastid-specific 30S ribosomal protein 3, putative / PSRP-3, putative

Supplementary file 2 – Effect of salt stress on genes encoding translation-associated proteins in *Arabidopsis thaliana.*

Gene names, annotation and qRT-PCR primer pairs used in this study

Transcript_identifier	Annotation - for multiple identifier mappings only the ann	primer_fw_sequence	primer_fw_start	primer_fw_length
AT1G05190	emb2394__Ribosomal protein L6 family	ACCCACGCGAAGTTGAGCTTAC	327	22
AT1G07070	Ribosomal protein L35Ae family protein	GAACGTGTCAGACTCTATGTCAGG	109	24
AT1G07320	RPL4__ribosomal protein L4	AATGCGAGGTACGGTGTTGATG	828	22
AT1G07920	GTP binding Elongation factor Tu family protein	TCTGCCGCAGGTGAATCAAAGG	1481	22
AT1G09590	Translation protein SH3-like family protein	ACATTTCGCAACCACCAAAGCG	17	22
AT1G09620	ATP binding;leucine-tRNA ligases;aminoacyl-tRNA ligases;nucleotide bin	TGACGCAGAATCCTCCATCTCCAG	3344	24
AT1G13950	ATELF5A-1_EIF-5A_EIF5A_ELF5A-1__eukaryotic elongation factor 5A-1	CTCAACAAGCTGGAACCATCCG	113	22
AT1G14320	RPL10_RPL10A_SAC52__Ribosomal protein L16p/L10e family protein	CCAAGTTGAGGCAAGAGAAGCG	600	22
AT1G14610	TWN2_VALRS__valyl-tRNA synthetase / valine--tRNA ligase (VALRS)	GCTGGTATAGCTACACAGGTGGTG	695	24
AT1G15250	Zinc-binding ribosomal protein family protein	TTCTCGGAGCCGCAAAGATTTC	33	22
AT1G15390	ATDEF1_PDF1A__peptide deformylase 1A	CGCTGCTCCTCAAATTGGTGTTC	404	23
AT1G16720	HCF173__high chlorophyll fluorescence phenotype 173	TTTCGACCGGTCAACCCAGAAG	1294	22
AT1G17220	FUG1__Translation initiation factor 2, small GTP-binding protein	GTGCGAAACGCAATGGAAGGAC	2997	22
AT1G18440	Peptidyl-tRNA hydrolase family protein	AAGGCCTTGTTTGGGAAAGGC	425	21
AT1G18540	Ribosomal protein L6 family protein	TTTCCCTCGTCACGATGCTCAG	163	22
AT1G22110	structural constituent of ribosome	TCCGATACCGTTGCTTGCTCAG	400	22
AT1G23410	Ribosomal protein S27a / Ubiquitin family protein	CGCACAAGAAAGTGAAGCTAGCAG	296	24
AT1G26880	Ribosomal protein L34e superfamily protein	ACTGGCAAGCGTATTCAAGGAATC	186	24
AT1G26910	RPL10B__Ribosomal protein L16p/L10e family protein	AATCAACGCGATGGGACGAAGACC	49	24
AT1G27400	Ribosomal protein L22p/L17e family protein	TGCTGAGAGCAATGCTGAGGTC	388	22
AT1G29070	Ribosomal protein L34	TTTCTCTCGTCGCCTGTTTCCC	267	22
AT1G32990	PRPL11__plastid ribosomal protein l11	CTACGCACAATTGCAGCAGAGAAG	561	24
AT1G33120	Ribosomal protein L6 family	TTCCTTGGCGAGAAGAAGGTGAGG	442	24
AT1G33140	PGY2__Ribosomal protein L6 family	CTTCCTTGGCGAGAAGAAGGTG	441	22
AT1G33330	Class I peptide chain release factor	ATAGCATGAGAGCAGCCAAGGG	750	22
AT1G35680	Ribosomal protein L21	TGCCACTGTACATGCTGTTGTG	508	22

AT1G48350	Ribosomal L18p/L5e family protein	ACACCTCTGGACCAACCATTGAG	408	23
AT1G48520	GATB__GLU-ADT subunit B	GCGAATGACGTCAGTGTTGCAG	1258	22
AT1G48830	Ribosomal protein S7e family protein	TTGGCGGATTAGCCTCAGAGTG	42	22
AT1G56070	LOS1__Ribosomal protein S5/Elongation factor G/III/V family protein	CGACCACGGGAAATCCACTCTTAC	194	24
AT1G58380	XW6__Ribosomal protein S5 family protein	CTCCGAGAGGTTCTGGTATTGTTG	654	24
AT1G61580	ARP2_RPL3B__R-protein L3 B	AGCCATGACCGAGTATGACAGAAC	930	24
AT1G62750	ATSCO1_ATSCO1/CPEF-G_SCO1__Translation elongation factor EFG/EF2	AAGGTGGAGGCTAACGTTGGTG	1794	22
AT1G64510	Translation elongation factor EF1B/ribosomal protein S6 family protein	CATGTCTGAAGATGAACGGCTTGG	385	24
AT1G64600	methyltransferases;copper ion binding	TCGTCTCAGCGTTCCTACAAGC	997	22
AT1G64880	Ribosomal protein S5 family protein	AGAGCTGGCTGAAGACAGAAATGC	1078	24
AT1G68590	Ribosomal protein PSRP-3/Ycf65	CAGAGACACTCACCGCTGAAAC	217	22
AT1G69410	ATELF5A-3_ELF5A-3__eukaryotic elongation factor 5A-3	ACGACGAGCATCACTTCGAATCC	106	23
AT1G70190	Ribosomal protein L7/L12, oligomerisation;Ribosomal protein L7/L12, C-	AGCTCCCAACAGATTACGATCCAG	215	24
AT1G72370	AP40_P40_RP40_RPSAA__40s ribosomal protein SA	GACAGAAGTGGGATGTCATGGTTG	675	24
AT1G74970	RPS9_TWN3__ribosomal protein S9	ATCAACTATCGTGATGCCAAGGAG	418	24
AT1G75350	emb2184__Ribosomal protein L31	CGGTTTCTCTCCCGAACTCGTTTC	96	24
AT1G77750	Ribosomal protein S13/S18 family	TGCGACGACCTTGTTCGACATC	54	22
AT1G78630	emb1473__Ribosomal protein L13 family protein	ATCGTTGAGCATGCTGTTCGTG	608	22
AT1G79850	CS17_PRPS17_RPS17__ribosomal protein S17	TCAAGCTTTCGTCTCCGTTCGC	67	22
AT1G80620	S15/NS1, RNA-binding protein	TCGAGCTTGCAAAGGTCAGAGAAG	1021	24
AT2G01250	Ribosomal protein L30/L7 family protein	TCCAAGGAATATGCCGAGAAGGAG	259	24
AT2G09990	Ribosomal protein S5 domain 2-like superfamily protein	TCCGACTCTCTGCGTTAGGTTTC	45	23
AT2G16360	Ribosomal protein S25 family protein	AGGTGAACAACATGGTTCTGTTCG	154	24
AT2G17360	Ribosomal protein S4 (RPS4A) family protein	ACTCATTCGCTGCAAACATGGC	101	22
AT2G18020	EMB2296__Ribosomal protein L2 family	TCCTGAAGGAGCTGTTGTCTGC	369	22
AT2G19730	Ribosomal L28e protein family	TCAAAGGCTGTTGCTAACCAGGTG	355	24
AT2G19740	Ribosomal protein L31e family protein	TCGAAGACCAGGGAGATCGAAG	38	22
AT2G20060	Ribosomal protein L4/L1 family	TACACTACGTGGTCCGCAGTTC	605	22
AT2G24060	Translation initiation factor 3 protein	GGAGCTTGCAACTGAAGAGAGC	754	22
AT2G24090	Ribosomal protein L35	ACAAGATGAAGACCCACAAGGC	297	22
AT2G25840	OVA4__Nucleotidylyl transferase superfamily protein	AGCCTCTCCTTGCAGATGCTTTG	1112	23
AT2G27710	60S acidic ribosomal protein family	ACTTCTTCATCGCCGTCTGCAC	1	22
AT2G31060	elongation factor family protein	ATTCGCTCTGCTGGGAAAGACG	1836	22

AT2G31170	SYCO ARATH__Cysteinyl-tRNA synthetase, class Ia family protein	GATCTCATTCACACCCGAAAGGG	1361	23
AT2G31610	Ribosomal protein S3 family protein	TGTTCGCAGGGCCTGTTATG	423	20
AT2G32220	Ribosomal L27e protein family	AGAAATCGCGCGTGAAATGCTTC	216	23
AT2G33450	Ribosomal L28 family	TTCAGCCAATCGTCGCACGTAG	222	22
AT2G33800	Ribosomal protein S5 family protein	GGGAATGTTGGTGTTGGTTGTGC	615	23
AT2G36160	Ribosomal protein S11 family protein	TTGCTCAGCGATGCAAGGAAC	345	21
AT2G36620	RPL24A__ribosomal protein L24	TACCGAAAGCAGCACAAGAAGGAC	249	24
AT2G37270	ATRPS5B_RPS5B__ribosomal protein 5B	GAGCTTTGATGACGTTTCGGTTAC	174	24
AT2G38140	PSRP4__plastid-specific ribosomal protein 4	TGCGAGGCCAAGAAACAAGAGC	286	22
AT2G39140	SVR1__pseudouridine synthase family protein	GCTGGAGTGGCATCAAGAAGAACC	559	24
AT2G40510	Ribosomal protein S26e family protein	TCGGCAACAAGAGCGTAAACCC	14	22
AT2G42710	Ribosomal protein L1p/L10e family	TTGAGGCGCATGTGAGATTGGG	669	22
AT2G42740	RPL16A__ribosomal protein large subunit 16A	TTCGCAACCCAAATTCCAAATGGC	46	24
AT2G43030	Ribosomal protein L3 family protein	GCTTTGGGTTCGATTGGTGCTG	650	22
AT2G44120	Ribosomal protein L30/L7 family protein	CAGTAAACATGCTGCGCCGAGTTG	772	24
AT2G47610	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	CAAATCTCGTCTTGGAGCGGTTG	640	23
AT3G01170	Ribosomal protein L34e superfamily protein	AGGCCTCTCTGTGTTTGTGAGTG	377	23
AT3G01800	Ribosome recycling factor	AGAGATTCTCGTCGAGGCTTTGC	320	23
AT3G02560	Ribosomal protein S7e family protein	TCCACAAGGATAAGGGTGTTGCAC	139	24
AT3G02660	emb2768__Tyrosyl-tRNA synthetase, class Ib, bacterial/mitochondrial	AACCCGGCTATGTTCCCAACAC	1238	22
AT3G02760	Class II aaRS and biotin synthetases superfamily protein	CTTGATTACTACACCGGCGTCATC	2151	24
AT3G04230	Ribosomal protein S5 domain 2-like superfamily protein	AGAAGACGGCAACAGCAGTCAC	96	22
AT3G04770	RPSAb__40s ribosomal protein SA B	GAGCCTAGGTTGTTGATTCTCACC	407	24
AT3G04840	Ribosomal protein S3Ae	ACCTTGGCAAGCTCATGGATGTTC	756	24
AT3G04920	Ribosomal protein S24e family protein	GGAAGAGCCAATGTTTCAAAGGC	200	23
AT3G05590	RPL18__ribosomal protein L18	TGGAGTTCATGACTGGCAAGGAAG	256	24
AT3G06040	Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein Cl	TGGTCCTGCACTCAATGAACACC	396	23
AT3G06180	Ribosomal protein L34e superfamily protein	TCTAGATGTGGTTGCCCTGTTGC	629	23
AT3G07110	Ribosomal protein L13 family protein	TCGTTCCTGATGCTCTCAAGGTC	443	23
AT3G08010	ATAB2__RNA binding	TGGTCTCTCTGTTGCTACTTCACG	899	24
AT3G08720	ATPK19_ATPK2_ATS6K2_S6K2__serine/threonine protein kinase 2	AAGGACAAGATCAAGCTTCCACAG	1329	24
AT3G08740	elongation factor P (EF-P) family protein	TTCGCGGTGATACTGTGCAAGGTG	656	24
AT3G09200	Ribosomal protein L10 family protein	TCCCAAACATCTTTCTTCCAGGTG	496	24

AT3G09630	Ribosomal protein L4/L1 family	TTGAAGCTTGCTCCTGGTGGTC	799	22
AT3G11250	Ribosomal protein L10 family protein	CCACTCCGAGAACTCTGGAAACAC	296	24
AT3G11940	AML1_ATRPS5A_RPS5A__ribosomal protein 5A	TGACGACGTTACGGTCACAGAC	193	22
AT3G12370	Ribosomal protein L10 family protein	AGCAGGGAAGACGAAGATCAACC	144	23
AT3G13120	Ribosomal protein S10p/S20e family protein	TCCCGATACCCTAGATCCAACTCC	277	24
AT3G13490	ATKRS-2_OVA5__Lysyl-tRNA synthetase, class II	ATCTCCTTTGGCCAAGCCACATC	1444	23
AT3G13580	Ribosomal protein L30/L7 family protein	TCCGTGATCGCCGAAATGACTG	116	22
AT3G15190	chloroplast 30S ribosomal protein S20, putative	TCGCCTTCTCAACCGGGAATTTG	250	23
AT3G17040	HCF107__high chlorophyll fluorescent 107	AAAGCTGGCCGGTATGAACAGG	1020	22
AT3G17170	RFC3__Translation elongation factor EF1B/ribosomal protein S6 family	TCCCGAGTTTGCTGATGCTGAAG	328	23
AT3G18780	ACT2_DER1_ENL2_LSR2__actin 2	TCTTCCGCTCTTTCTTTCCAAGC	189	23
AT3G20230	Ribosomal L18p/L5e family protein	CTGGGTTCTGCAGTTTCATGGC	157	22
AT3G25520	ATL5_OLI5_PGY3_RPL5A__ribosomal protein L5	TGCAGCTTACTGTACTGGCCTTC	350	23
AT3G25660	Amidase family protein	ACTACAAGCGAGCTCAACAGGTG	1409	23
AT3G25920	RPL15__ribosomal protein L15	TAGAGGAATCGCTGGAGGTATGC	508	23
AT3G27160	GHS1__Ribosomal protein S21 family protein	AAGGCGTCCTCAAGCAAGGTTTAC	483	24
AT3G27830	RPL12_RPL12-A__ribosomal protein L12-A	ATCACTTCCCTTCCCGAACCAC	141	22
AT3G27850	RPL12-C__ribosomal protein L12-C	CTTTCCAAACCCACCGCAATCG	144	22
AT3G44890	RPL9__ribosomal protein L9	ACTCCTACTGCATCCCAAGGAAC	682	23
AT3G49910	Translation protein SH3-like family protein	TCGAGAGAATCACGAGGGAGAAGG	296	24
AT3G54210	Ribosomal protein L17 family protein	TCGGACTTCCAGATTGGCAAAG	264	22
AT3G55400	OVA1__methionyl-tRNA synthetase / methionine--tRNA ligase / MetRS (	AGACACAGTGGAGAAGCTGGTTG	1432	23
AT3G57490	Ribosomal protein S5 family protein	TCTTGGAAACTTCGTCAAGGCAAC	711	24
AT3G58140	phenylalanyl-tRNA synthetase class IIc family protein	ATAATGTTGCTTGGGCCTTCGG	1048	22
AT3G58660	Ribosomal protein L1p/L10e family	AGCTGCCAAAGGGAAGTCGAAAC	1185	23
AT3G60770	Ribosomal protein S13/S15	AGTGAGAGGACGATCACTTCGC	91	22
AT3G62910	APG3__Peptide chain release factor 1	TCCTTCCGATCCTCTTGATGCC	511	22
AT3G63190	AtcpRRF_cpRRF_HFP108_RRF__ribosome recycling factor, chloroplast p	GCGATGCTTGACAAGATTGAGGTG	505	24
AT3G63490	Ribosomal protein L1p/L10e family	CCCGGATATGATGGTCAAGGTTGC	740	24
AT4G01310	Ribosomal L5P family protein	AAAGTCTCGGCGTCTGGAACTG	181	22
AT4G04350	EMB2369__tRNA synthetase class I (I, L, M and V) family protein	TGGCCACCCGGTTATAAGAAAGC	824	23
AT4G11175	Nucleic acid-binding, OB-fold-like protein	ATCCGGCCAATGATACGATGCC	192	22
AT4G17560	Ribosomal protein L19 family protein	TGAGAGTTTGCTGCAGCTATGG	46	22

AT4G20360	ATRAB8D_ATRABE1B_RABE1b__RAB GTPase homolog E1B	ATGGTTATGCCCGGTGATCGAG	1377	22
AT4G20980	Eukaryotic translation initiation factor 3 subunit 7 (eIF-3)	TGAGGAACCGTTGCCTGAAGATG	1718	23
AT4G27090	Ribosomal protein L14	GACGTTGTTGACCAGAACAGAGC	149	23
AT4G27130	Translation initiation factor SUI1 family protein	TGCAACGGAACTGTGGTTCAAG	454	22
AT4G29060	emb2726__elongation factor Ts family protein	AAGCCAGGACTTTGCTGCTGAG	2387	22
AT4G30690	Translation initiation factor 3 protein	GGTCAGCCACTGTTAGGCTTATTG	330	24
AT4G30800	Nucleic acid-binding, OB-fold-like protein	TTCAACCATGGCAGAGCAGACG	75	22
AT4G31700	RPS6_RPS6A__ribosomal protein S6	GATCGACGATGACCAGAAACTACG	63	24
AT4G32915	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: regulation	TCGTCGAGTCATCGACTGGTTTG	295	23
AT4G33760	tRNA synthetase class II (D, K and N) family protein	TTCACAGCTCCTAAGCCGGAAG	1611	22
AT4G34620	SSR16__small subunit ribosomal protein 16	GCGCAGGGACGGTAAACAAATC	159	22
AT4G36420	Ribosomal protein L12 family protein	AAGCGTACGATGCAGTGTCGAAG	404	23
AT4G37660	Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein Cl	ATCCTCCGCTACTCGTCACCTATG	112	24
AT5G02870	Ribosomal protein L4/L1 family	AGGAAAGTCGTCACTAAGGAGGAG	1136	24
AT5G05410	DREB2_DREB2A__DRE-binding protein 2A	TGTCTGGAGAATGGTGCGGAAG	734	22
AT5G08650	Small GTP-binding protein	ACCATCGTACACAGGGATAAGGC	1778	23
AT5G13510	Ribosomal protein L10 family protein	GCCATTGAAGGCACCAAATGGG	335	22
AT5G13650	elongation factor family protein	TCGCGGGACAGCTATCCTTAAC	1685	22
AT5G14320	Ribosomal protein S13/S18 family	TCGAACTAGGGCTCGTCAGATTC	355	23
AT5G14660	ATDEF2_DEF2_PDF1B__peptide deformylase 1B	TACGACCATCTGGAGGGAGTTC	717	22
AT5G15200	Ribosomal protein S4	ACGTTTGCTACTACCGCAACTATG	81	24
AT5G15260		TCCAATCAGGGCTACTTCGATTTG	412	24
AT5G15760	Ribosomal protein PSRP-3/Ycf65	AATCTCCGCCACTTGGAAAGAAG	294	23
AT5G16140	Peptidyl-tRNA hydrolase family protein	AGGAGGTCAAGGCTATCACAACG	536	23
AT5G16710	DHAR3__dehydroascorbate reductase 1	AGTATCCTGAGCCTCCTCTTGC	409	22
AT5G16715	EMB2247__ATP binding;valine-tRNA ligases;aminoacyl-tRNA ligases;nuc	TGGCGGAACCATCACAAATCAG	560	22
AT5G18380	Ribosomal protein S5 domain 2-like superfamily protein	AGAGAGCTAAAGCAAGGAGCAAC	35	23
AT5G20290	Ribosomal protein S8e family protein	ATGCTGCTCCGTTCAAGCAGTG	370	22
AT5G23535		GCTCCTCTTCACGCCTCAAATG	385	22
AT5G24490	30S ribosomal protein, putative	ACTGACTCGAGCGTAGGAGAAG	725	22
AT5G26830	Threonyl-tRNA synthetase	AGAAGCTGCTACAGGACAGGTG	2069	22
AT5G30510	ARRPS1_RPS1__ribosomal protein S1	GAGAATTGCGCAAGCAGAAGCC	1157	22
AT5G36170	ATPRFB_HCF109__high chlorophyll fluorescent 109	GTGTTGCTGTTCGTTGCACAGAG	1097	23

AT5G38290	Peptidyl-tRNA hydrolase family protein	AAATGGTTGTCGCGGCTATCCC	617	22
AT5G39850	Ribosomal protein S4	CGACAAAGGCATATCAGGGTTGGG	424	24
AT5G40950	RPL27__ribosomal protein large subunit 27	ATCGGCCCATAAGAAAGGAGCTG	254	23
AT5G41520	RNA binding Plectin/S10 domain-containing protein	ACAGAGATGGATACCGTGGAGGTC	479	24
AT5G47190	Ribosomal protein L19 family protein	TGGTTTCGAGTTTGGGTTGTGC	17	22
AT5G47880	ERF1-1__eukaryotic release factor 1-1	ACAGTGACTTGGCTTTGGACGTG	1162	23
AT5G49030	OVA2__tRNA synthetase class I (I, L, M and V) family protein	CAGCCAAGAAAGCATCTGAAGGG	430	23
AT5G51610	Ribosomal protein L11 family protein	TTGTTGCTTAAGGCTGCAGGTG	318	22
AT5G52520	OVA6_PRORS1__Class II aaRS and biotin synthetases superfamily protei	ACTTGAGGAGAAACTTGTGGTTCG	528	24
AT5G53070	Ribosomal protein L9/RNase H1	TCATCCGAGAGCAACGCAAGATG	406	23
AT5G54600	Translation protein SH3-like family protein	CCATGTCTTGTTCTTGCAAAGCTC	200	24
AT5G59240	Ribosomal protein S8e family protein	TGTGGAGGAAGAAGCGAAAGTATG	121	24
AT5G63300		TGGTGCCTAAAGACGGCGAATC	264	22
AT5G65220	Ribosomal L29 family protein	CTTCGTCTCCAGAAATCGGCAAG	345	23

primer_fw_Tm	primer_fw_GC	primer_rev_sequence	primer_rev_start	primer_rev_length	primer_rev_Tm	primer_rev_GC
63.704	54.545	ACCATGTTATCGGTAAGCGTCCTG	447	24	63.118	50
61.027	50	ACCATGACACTTCCTCAGTGGTG	232	23	62.748	52.174
61.602	50	TCTTAAGCTTCCTCTGACCCTTCC	907	24	61.973	50
63.758	54.545	ACACAGACACGCGACCAAATACC	1552	23	63.84	52.174
63.371	50	TTCTCGCTCGAACTCCATGTCC	77	22	62.699	54.545
64.411	54.167	CACTTGTGCTGGTCACAAAGATGG	3403	24	62.922	50
62.117	54.545	AGGTTGAAACCTCAACAACCTTGC	193	24	62.545	45.833
62.361	54.545	GTCCATGGCATGAGAGGAACTTAG	668	24	61.342	50
63.125	54.167	TGTACCGCCGTACTGGTTCTTC	823	22	62.637	54.545
61.858	50	TCCCTGTTCCTTTACCCATTGCC	111	23	63.099	52.174
63.095	52.174	ACCGGATTCACCATCACCATGAG	541	23	62.934	52.174
63.105	54.545	AGTCCATCAACAGGCCTCTGTC	1394	22	62.364	54.545
63.458	54.545	TGAGCCAATTGGGATTTGTTCCTC	3056	24	61.961	45.833
62.015	52.381	TTGTGGTTTAGCCAGCATAATCGG	484	24	62.056	45.833
62.953	54.545	AAACTTGGCAGGCTTCTCAACCG	223	23	64.324	52.174
63.267	54.545	TGGTCACCACACGCTTGAGAAC	473	22	63.599	54.545
62.993	50	CAACCTCTGAACTTTCCCACTTCC	366	24	61.883	50
62.051	45.833	TGCTCGGTTTACAGTCCTCCTG	278	22	62.341	54.545
65.842	54.167	TCTTAGGATCGGGAACACCACGAC	149	24	64.326	54.167
63.239	54.545	TGCTGCTTGGTTCACTTGGATG	466	22	62.011	50
63.155	54.545	GATCAAACGCAATGGACAAACCAG	327	24	61.727	45.833
63.052	50	AGCGGATTCAATGGTCGTGCAG	620	22	64.095	54.545
64.78	54.167	TTCTGGTTGATCAGAGCGCACGAC	584	24	65.762	54.167
61.544	54.545	CTGGTTGATCAAAGCGCATGAC	582	22	61.078	50
62.826	54.545	GCCCGAACGTCATCTTTCAAATGC	827	24	63.802	50
61.997	50	TCCTAATCCTCGTATTCGGCTGTC	632	24	62.175	50

62.762	52.174	ACGTCCATGGTAAGGGTAACCAC	529	23	62.56	52.174
63.181	54.545	CAACTTCACTTCAGCACCCTTACC	1323	24	62.168	50
62.733	54.545	TCAGAAAGTTCCACACCCTTCTCC	155	24	62.634	50
63.567	54.167	ACCAGCAACCTCTTGGGCAATG	266	22	64.001	54.545
61.273	50	GTAAGCAGTCAAACGTCGCCTTG	794	23	63.053	52.174
62.832	50	AGTCACCACACGTTTCTTAGGC	1062	22	61.16	50
63.129	54.545	CCTGCTTCCAATGGCTCAAACC	1942	22	62.657	54.545
62.56	50	TCCTGCCACAAGCAACTCTTCG	445	22	63.672	54.545
62.933	54.545	TACCGTCAAGAGGCCACAACTC	1120	22	62.596	54.545
63.788	50	CTTTCAACCCTGCCACCCTTTG	1206	22	62.538	54.545
61.779	54.545	TGTTGTGGAGTGTTGTCGGAAG	277	22	61.352	50
63.451	52.174	AAGTCGATACCTCAACCACCTTGC	237	24	63.256	50
62.612	50	ATCCGTTGGTGGACTTCGATGC	279	22	63.542	54.545
61.994	50	TGAGGGCCAGCTTCATCTTCATC	762	23	62.94	52.174
61.102	45.833	TGCTTGAGCTTGACCTGAGAGAC	567	23	62.783	52.174
63.988	54.167	GCCATCACCGGCTTTCTTAATTGC	171	24	63.614	50
63.72	54.545	CTTGGACTCGTAACCCATGAAACG	124	24	62.257	50
62.407	50	TTGAACAGAGCTCTCCCAAGCC	669	22	62.882	54.545
63.971	54.545	TGTGGTTCGGGAAGGAATTGGG	144	22	63.162	54.545
63.465	50	AGTTGCGCCACTTGAACACG	1099	20	62.392	55
62.384	50	CAAGAGCTTAGCTTCAGGGTCAAC	357	24	61.985	50
62.571	52.174	TGTGTCGCCATGGTTAGGGTTTC	124	23	63.596	52.174
62.107	45.833	TAGCAAGCGACCCATTGATCCG	279	22	63.35	54.545
62.942	50	AGGAGCATTGAGCCTCTTCAAATG	162	24	61.771	45.833
62.866	54.545	TCCTAGTAGTGTCGCTGTCAGG	490	22	61.297	54.545
63.925	50	GCAAGTGCAGCTTTCTTCAAGTCC	422	24	63.43	50
61.623	54.545	TTCTTCTTGAAGGTGCAGCTATGG	158	24	61.466	45.833
62.623	54.545	TGGCATGGCTTCTTGGTTTGGG	672	22	64.275	54.545
62.112	54.545	TGTGGGTGGTTCTTGTGGTTTCC	856	23	63.699	52.174
61.176	50	CACAATCTTCCCTCTACCCGTCAC	361	24	63.064	54.167
63.671	52.174	TCCTGATAACGGGCCTGGATTG	1172	22	62.5	54.545
63.757	54.545	GCGGCAACAACCTTCATCTTCG	88	22	63.215	54.545
63.53	54.545	CCGAATCGTCTTTGGTGTCACCTC	1958	24	64.014	54.167

61.595	52.174	GCTCGAGAACCTCTGAGTAACTTG	1493	24	61.262	50
61.029	55	GAGCTTTCCACTCACGATGACC	507	22	61.598	54.545
63.414	47.826	AAGAGTGTAGCGCGTAGGCATC	286	22	63.063	54.545
63.784	54.545	CCAGCTTCCCACCAAACTCTCTTG	363	24	63.975	54.167
63.502	52.174	CACCCTCTGATCTGTGAGGGAAAG	750	24	62.796	54.167
62.158	52.381	ACCAGGTGTCTTGGTCTTGTTTCC	430	24	63.351	50
63.705	50	CCTCCAAAGTAGCACCGACAATCG	354	24	64.073	54.167
61.014	45.833	AAAGTTGCGTGCTTCGATGGC	251	21	62.996	52.381
64.24	54.545	TATCTTTCCTCGGTGGTGCTGGAG	362	24	64.364	54.167
64.306	54.167	TGATGGATCAACTCGAGTCTGTGG	663	24	62.538	50
63.969	54.545	TCCTTCGCTTGAAAGTCATCTTGC	91	24	62.217	45.833
63.823	54.545	GCCAAAGTACCACGAACTATCAGC	735	24	62.318	50
63.72	45.833	TCACCAACGGAGATGTTGAGAACC	144	24	63.194	50
63.19	54.545	CCTCCCATTCTTCCAGGCATCTTC	726	24	63.409	54.167
65.505	54.167	ACGCTCTTCAAGTTTGGGTATCCG	835	24	63.53	50
62.597	52.174	AGTGGTCAAACACAAGCAAGAAGC	700	24	62.817	45.833
62.983	52.174	TTGGGTCGACGGAATTGCAGAC	450	22	63.723	54.545
63.177	52.174	TCCCTGTTCCTGAATCGTCCTTTG	380	24	62.977	50
63.466	50	TCTCCAAGTCAAACAAAGCCTGAG	210	24	61.585	45.833
63.467	54.545	CAAACCCTCTTCGCCATGTACG	1317	22	62.163	54.545
61.899	50	AGCACCAATTGATCCCACCTCTG	2219	23	63.143	52.174
63.654	54.545	ATAAAGCTCGATCGGCGAACCG	175	22	63.664	54.545
61.518	50	GCACCTTCCTTGATTGGCTGATG	468	23	62.647	52.174
64.057	50	ATCAGCCGGCCTGTCTACCTTAAC	832	24	64.658	54.167
61.218	47.826	TCCTTGACCTCGTACATCCTTGC	264	23	62.602	52.174
63.222	50	GCTTTCTCAATGCGAGCCCTTG	397	22	62.992	54.545
63.547	52.174	TTTGCTCCAATGCCGTCCGATG	467	22	64.361	54.545
63.362	52.174	TTATGACGCCGGCCTCGTTTAG	693	22	63.319	54.545
62.593	52.174	AGAAAGGCGACCCAACAGACAG	513	22	63.119	54.545
62.697	50	TCAAGCCCATTCATCCAAGCTG	958	22	61.57	50
61.409	45.833	TTTGCAGCAGCCCTTTCAGC	1398	20	62.444	55
66.009	54.167	ACAGCAACTATTGCACCCGTTTCC	722	24	64.484	50
61.358	45.833	CGACGGTACCCTTGTTAATCTTGG	556	24	61.798	50

63.395	54.545	TCTCAAAGGCAGACTTGGTCCAG	862	23	62.748	52.174
63.46	54.167	CAAACCAACGTTTCCCTGAAGGAG	365	24	62.636	50
62.841	54.545	AGCATGTTTAGCTGCCTGAACTCC	259	24	63.8	50
62.857	52.174	TTGCTTCACGCTGAGACCGTTG	222	22	64.185	54.545
62.963	54.167	TGGATGAAGAGCTCGGAACCTC	347	22	62.153	54.545
63.703	52.174	TTGCTCTTCCAACCGTGTCCTCTG	1582	24	65.217	54.167
63.56	54.545	TGGCAAGTGCCCATTCTTCCTC	212	22	63.48	54.545
63.887	52.174	AGCAGCAGCCTCACACACAATC	320	22	64.002	54.545
63.521	54.545	TTCCAACTGTGCCCATGCCAAC	1118	22	64.501	54.545
63.636	52.174	ACCACCTCATAGTGCCTCATCC	429	22	61.916	54.545
61.718	47.826	ACCATTGTCACACACGATTGGTTG	265	24	62.635	45.833
62.642	54.545	ACAGAGCCGATTTCGATGGAGAG	218	23	62.706	52.174
63.098	52.174	AGTCTTCTCCAGTGGCCTCAAC	450	22	62.298	54.545
63.311	52.174	TCGTTCTGTTCTAACGCTGCTTTG	1478	24	62.42	45.833
61.986	52.174	CACTTCATCTCCCTCTTGAAACCC	607	24	61.467	50
63.961	50	AGGTACATCTCCACCAGGCATCTC	600	24	63.923	54.167
62.63	54.545	ATGATGAACCACCACCGAAGCG	203	22	63.796	54.545
63.183	54.545	TGCACGGTGGCTAGAAGAAGAG	206	22	62.652	54.545
62.323	52.174	ATCCTCACCACAAGAGGCTACTC	745	23	61.812	52.174
63.618	54.167	TTTCGACGGCTGAATCCCAACG	360	22	64.012	54.545
61.233	50	AGATACGACCACCACCGTCAAC	329	22	62.642	54.545
62.983	52.174	TGGTGCTCGTTGATCCATGTAGG	1558	23	62.912	52.174
62.339	45.833	TGACGCCAGGAGGTATAAGCAAG	853	23	62.665	52.174
61.891	50	TTCCAAACTGGGACGTGAATCG	1164	22	61.48	50
64.079	52.174	TTGACCGCAGCTTTCTGCATAGG	1244	23	63.937	52.174
62.436	54.545	AGCAGATGCCGAGATACCCTTACC	167	24	64.251	54.167
62.231	54.545	GCCACCAGTTCCTGCTCTAACTTC	571	24	63.774	54.167
63.067	50	CCGGAGTACTGATTTGGGCTATGC	583	24	63.712	54.167
63.967	54.167	AGCCTTGGGATTTGGCATGAGC	815	22	64.137	54.545
63.145	54.545	CTTCTGTACCTTTGGAACCTGGTG	330	24	61.643	50
63.431	52.174	TCAGCGTACGCAGTAATCTTCAGC	886	24	63.59	50
63.502	54.545	TGCGGCTTAGCAGGTTTGCTTC	268	22	64.551	54.545
61.295	50	TGGGTATCATATGCAATGCCTGAG	112	24	61.172	45.833

62.859	54.545	ACAAGCCACCGGCACAATAAGC	1436	22	64.576	54.545
63.344	52.174	ACTTGCTTCTGCTCCCTCTGTG	1787	22	62.872	54.545
62.474	52.174	TGGCACACGGTTGATGTCAATG	262	22	62.314	50
62.184	50	ATCGCCTTGAAGCTGAATAACCTG	513	24	61.816	45.833
63.709	54.545	ACCACTGTAGTTGGTGGGCTTG	2503	22	63.085	54.545
62.051	50	CATCCGGCGAAAGAATCACCAG	449	22	62.231	54.545
63.737	54.545	TTACCAGGCCTCTTTCCCTTACC	170	23	62.023	52.174
61.651	50	GGGAAACCTTGCTTATCGCAACC	197	23	62.877	52.174
63.084	52.174	TGCTCTAATAGCTGGCTCCACAC	367	23	62.67	52.174
62.667	54.545	CTCAAACTTCCTCCACCAATCTCG	1714	24	61.748	50
62.975	54.545	ATCCGCATCTTCTTTGCCTTGG	228	22	61.885	50
63.904	52.174	CCCAATGCCGTAATCGTTCTCAC	467	23	62.424	52.174
63.733	54.167	TCGCTCGAGTTTCTTCGTTCGAG	178	23	63.348	52.174
61.713	50	TGATACCAAGCCTTGCCTGCTG	1197	22	63.527	54.545
62.925	54.545	TCGCTCAGCCAATGCTTATCCG	798	22	63.652	54.545
62.429	52.174	GTGCTTCACTAGCAATCACCTTGG	1913	24	62.513	50
63.248	54.545	AAGCCAAGCGTTCATGCCTTTC	397	22	62.893	50
62.517	54.545	TGTTCCATCTTCAAAGGCAACCAG	1790	24	62.131	45.833
62.146	52.174	TGCAAGAGCATTGAACCTCCTCAG	502	24	63.506	50
61.31	54.545	CTTTCAGGGCTTGGCAATCCAG	844	22	62.403	54.545
61.789	45.833	TCCAGAGCTCACGCTTGTTACG	209	22	63.185	54.545
61.284	45.833	TGGTCTACGAGGGAGATTGAGTTC	510	24	61.771	50
61.48	47.826	TTTGGTTTCTCTAGCGGCTTCAC	354	23	61.714	47.826
62.607	52.174	CCAGGTGGTTTACCAATGCCTATG	637	24	62.07	50
61.647	54.545	AAGATCTTCGATCCAACTGAAGCC	469	24	61.282	45.833
61.814	50	AAAGCTTCGACCACAGCTCGAC	667	22	63.692	54.545
61.227	47.826	GCACAGATTCAGTAGCTGGTTGAG	95	24	62.035	50
64.291	54.545	AACAGCTGCCTCTTCACCTTCCTC	485	24	65.029	54.167
62.172	54.545	AACCTTACAAGGCCTCCCAGTG	447	22	62.582	54.545
61.607	54.545	GTCTTGGTACGGACAATCTCCTTG	792	24	61.508	50
62.352	54.545	TCCTCAATGCTCTTCACGGAGTG	2140	23	62.84	52.174
63.537	54.545	AACTCAGCGTCAGTCCACTCTC	1233	22	62.323	54.545
63.474	52.174	TCAGAGCTCTCGTCTTGTTCGC	1156	22	62.923	54.545

63.876	54.545	TGTTCCAGTCCCTCATCCATCTG	748	23	62.073	52.174
64.142	54.167	ACGTGCTTCTGTGACTCTACTCTC	503	24	62.219	50
62.999	52.174	AGATCTTGACGCCGAGTCGTTG	330	22	63.234	54.545
63.655	54.167	TGCTCCAGCCTTGTCACCATAC	540	22	62.941	54.545
62.449	50	TCGGTATCATATGCAATGCCTGAG	91	24	61.22	45.833
63.993	52.174	ACGCCTGTACTCATTGGCAAGC	1232	22	64.052	54.545
62.342	52.174	ACCAGTCTTTGGCAAATCAACCG	506	23	62.466	47.826
62.266	50	TCAGCTCAGGCAGCTTTACTTCTG	435	24	63.252	50
61.575	45.833	GGTTTCGTCCGCATTTCCCATC	671	22	62.743	54.545
63.716	52.174	TAGCATTCGCCAGACGCTTTGC	531	22	64.622	54.545
61.439	45.833	ACCCTTGTCGCGTCCAGATATTAC	331	24	62.883	50
61.219	45.833	TTTACATTCCCACCACGCACAC	226	22	62	50
63.534	54.545	AACACACCCGCTCTGAAACACG	339	22	64.143	54.545
62.117	52.174	CCGAGCAACTTGTTTCTTCATACG	419	24	61.016	45.833

amplicon_length	either_primer_spans_exon	amplicon_3prime_distance	primer_pair_optimal_Ta
121	Yes	608	62.1258
124	Yes	466	62.1868
80	Yes	418	60.9593
72	No	302	58.6311
61	No	691	60.3589
60	Yes	376	61.0404
81	Yes	618	59.5844
69	Yes	372	60.6682
129	Yes	2937	62.9302
79	Yes	509	60.7881
138	Yes	602	60.6538
101	Yes	806	61.2851
60	Yes	689	58.3605
60	Yes	686	56.9415
61	No	698	61.3763
74	No	1656	63.3602
71	No	312	58.9633
93	Yes	482	61.0563
101	Yes	828	61.8735
79	Yes	453	60.1075
61	Yes	505	58.6559
60	No	295	60.6011
143	Yes	529	63.1217
142	Yes	510	62.0837
78	Yes	331	60.0882
125	Yes	368	60.7865

122	Yes	297	62.3484
66	Yes	762	58.7108
114	Yes	849	61.5759
73	Yes	2764	61.2419
141	Yes	455	61.4019
133	Yes	424	62.1637
149	Yes	872	62.8402
61	Yes	479	58.9056
124	Yes	737	64.2776
129	Yes	907	60.0085
61	No	536	59.014
132	Yes	662	63.9587
65	No	821	59.3886
88	Yes	516	61.5541
150	Yes	540	61.5374
76	Yes	576	60.9089
71	Yes	637	60.2884
62	Yes	411	60.1397
78	No	643	62.3967
79	Yes	501	60.5849
99	Yes	822	61.647
80	No	677	61.25
126	Yes	224	61.433
62	Yes	978	58.097
122	Yes	601	63.6163
68	Yes	367	61.0034
121	Yes	559	62.579
68	Yes	677	61.1832
103	Yes	426	59.9162
65	Yes	413	60.7238
61	Yes	403	59.8287
88	Yes	616	61.2681
123	Yes	510	62.3231

133	Yes	564	61.1153
85	Yes	666	60.5898
71	No	389	60.1258
142	Yes	404	61.885
136	Yes	528	61.158
86	Yes	409	62.16
106	Yes	528	63.1487
78	Yes	756	59.1767
77	Yes	289	62.8509
105	Yes	936	60.4401
78	Yes	726	60.6412
67	Yes	856	59.0845
99	Yes	704	61.7199
77	No	381	61.0449
64	Yes	547	59.7769
61	Yes	502	58.9168
74	No	892	60.1723
61	Yes	1040	58.0899
72	Yes	771	58.7765
80	No	500	60.7688
69	Yes	730	59.1718
80	No	574	62.6511
62	Yes	804	60.3358
77	Yes	318	61.3049
65	Yes	539	59.4118
142	Yes	601	62.8602
72	No	468	60.1622
65	No	331	60.9253
71	Yes	447	61.1976
60	Yes	380	59.1996
70	Yes	485	58.9213
67	Yes	302	61.0196
61	Yes	835	58.0746

64	No	761	60.439
70	Yes	947	60.1095
67	Yes	824	59.2415
79	No	761	60.3611
71	Yes	750	61.0654
139	Yes	647	63.9213
97	Yes	946	62.295
71	Yes	637	61.1814
99	Yes	1123	62.6876
102	Yes	797	60.4977
77	Yes	1624	58.3668
62	No	772	58.8215
101	Yes	905	61.5494
70	Yes	582	58.8146
100	Yes	616	59.6729
118	Yes	360	61.8869
63	No	787	60.99
63	No	731	60.0856
64	Yes	238	59.2614
65	No	416	60.5733
66	Yes	554	57.9957
127	Yes	665	61.6004
143	Yes	339	61.5869
117	Yes	685	60.4979
60	No	396	59.9098
77	Yes	824	61.9367
61	Yes	906	58.807
79	Yes	735	59.6977
76	Yes	702	63.2807
150	Yes	871	62.465
63	Yes	2257	60.3192
77	No	545	62.2565
67	Yes	1127	59.1693

60	No	381	59.1082
70	No	408	60.5904
114	Yes	520	61.9835
60	Yes	394	58.7953
117	Yes	961	63.4326
120	Yes	710	61.409
96	Yes	766	60.4659
135	Yes	937	62.1563
73	Yes	450	60.1867
104	Yes	534	61.6627
70	Yes	491	59.8841
64	No	470	58.0997
67	No	663	62.8204
62	Yes	339	60.3944
65	No	716	59.924
136	Yes	522	61.8921
63	No	499	59.7023
106	Yes	746	62.4057
148	Yes	484	61.5956
128	Yes	571	61.2711
129	Yes	831	62.8985
99	Yes	972	59.4075
61	Yes	453	58.1112
102	Yes	415	61.6694
61	Yes	547	58.9927
108	Yes	2644	61.3212
61	No	675	59.4468
116	Yes	596	64.3851
63	Yes	512	59.9414
68	Yes	573	58.7386
72	Yes	326	61.3981
77	Yes	405	62.2755
60	Yes	533	60.0841

132	Yes	394	62.7341
80	Yes	455	60.4269
77	No	645	62.4784
62	No	397	60.2998
75	Yes	902	59.9208
71	No	605	62.0218
77	Yes	3170	59.2994
118	Yes	231	60.1738
144	Yes	1458	61.6902
126	Yes	655	61.2325
132	Yes	629	61.0219
106	Yes	736	61.5905
76	No	566	62.0179
75	Yes	425	59.0941