Table S3. Enriched peaks and their associated genes identified by SPCH ChIP-Seq

1: For peak location, the first and second numbers indicate the chromosome number and the nucleotide position on the chromosome, respectively.

2: Category of gene structure: promoter (< 0.5 kb to TSS), distal promoter (0.5-3kb to TSS), 5'UTR, exon, intron, 3'UTR, downstream (1kb to TSS), or intergenic. TSS, transcription start site.

2: Category	of gene structure: promoter (< 0.5 kb to TSS)			
AGI	Gene symbol	Description Peak location ¹		Gene structure ²
AT1G80070	ABNORMAL SUSPENSOR 2 (SUS2)	a genetic locus 1_30129721	124.01	intergenic
AT1G80080	TOO MANY MOUTHS (TMM)	Encodes a trans 1_30129721	124.01	promoter
AT4G25610	na	C2H2-like zinc f 4_13069981	105.03	intergenic
AT4G25620	na CHLOBODHVII ASE 4 (CLU4)	hydroxyproline-i 4_13069981	105.03 82.46	promoter
AT1G19670 AT1G19680	CHLOROPHYLLASE 1 (CLH1) na	Chlorophyllase i 1_6803197 RING/U-box sui 1_6803197	82.46	intergenic proximal promoter
AT1G19660	na	Wound-respons 1_6803197	82.46	proximal promoter
AT3G26744	INDUCER OF CBF EXPRESSION 1 (ICE		81.19	five_prime_UTR
AT3G26742	na	unknown proteir 3 9835078	81.19	intergenic
AT5G26160	na	unknown proteir 5_9142944	69.37	five_prime_UTR
AT5G23860	TUBULIN BETA 8 (TUB8)	beta-tubulin, pre 5_8042044	60.83	proximal promoter
AT1G20657	na	Pseudogene of 1_7163767	57.72	proximal promoter
AT1G20670	na	DNA-binding bri 1_7163767	57.72	intergenic
AT5G06710	HOMEOBOX FROM ARABIDOPSIS THA		57.06	intergenic
AT1G25550	na	myb-like transcr 1_8975771	53.14	proximal promoter
AT1G25540	PHYTOCHROME AND FLOWERING TIM		53.14	proximal promoter
AT5G53210	SPEECHLESS (SPCH)	Encodes a basi 5_21589130	53.01	promoter
AT3G15790 AT3G15780	METHYL-CPG-BINDING DOMAIN 11 (ME na	unknown proteir 3_5342783	52.72 52.72	promoter downstream
AT2G34510	na	FUNCTIONS IN 2 14545598	51.78	intron
AT4G00480	(ATMYC1)	MYC-related pr. 4_221016	51.76	proximal promoter
AT4G00490	BETA-AMYLASE 2 (BAM2)	Encodes a chlor 4_221016	51.1	proximal promoter
AT1G12840	DE-ETIOLATED 3 (DET3)	Encodes subun 1_4379555	50.7	intergenic
AT1G12845	na	unknown proteir 1_4379555	50.7	promoter
AT1G12850	na	Phosphoglycera 1_4379555	50.7	downstream
AT5G01990	na	Auxin efflux carı 5_379718	49.97	five_prime_UTR
AT5G02000	na	unknown proteir 5_379718	49.97	intergenic
AT1G01040	DICER-LIKE 1 (DCL1)	Encodes a Dice 1_21171	49.8	proximal promoter
AT1G11840	GLYOXALASE I HOMOLOG (GLX1)	Encodes a glyo: 1_3995144	49.79	promoter
AT1G11820	na	O-Glycosyl hydi 1_3995144	49.79	proximal promoter
AT1C22710	na	unknown proteir 2_640895	49.36 48.43	intergenic
AT1G23710 AT1G10652	na na	Protein of unknown 1_8384902 unknown proteir 1_3527672	48.43 48.28	promoter promoter
AT3G57550	GUANYLATE KINASE (AGK2)	guanylate kinas 3_21309941	47.88	intergenic
AT3G57560	N-ACETYL-L-GLUTAMATE KINASE (NAC		47.88	intergenic
AT3G08680	na	Leucine-rich reg 3_2636889	46.79	proximal promoter
AT3G08670	na	unknown proteir 3_2636889	46.79	downstream
AT1G06410	TREHALOSE-PHOSPHATASE/SYNTHAS		45.77	proximal promoter
AT2G23460	EXTRA-LARGE G-PROTEIN 1 (XLG1)	encodes a nove 2_9995300	44.53	promoter
AT1G12855	na	F-box family prc 1_4384491	43.14	intergenic
AT1G12860	SCREAM 2 (SCRM2)	Encodes ICE2 (1_4384491	43.14	five_prime_UTR
AT1G19220	AUXIN RESPONSE FACTOR 19 (ARF19)		42.74	downstream
AT1G19210 AT4G08949	na na	encodes a mem 1_6627905	42.74 42.07	promoter
AT4G08949 AT4G18940	na na	This gene encor 4_5738933 RNA ligase/cycl 4_10374879	42.07	downstream intergenic
AT4G18950	na	Integrin-linked p 4_10374879	42.05	promoter
AT3G22760	(SOL1)	CXC domain co 3_8043179	41.52	proximal promoter
AT4G14770	TESMIN/TSO1-LIKE CXC 2 (TCX2)	TESMIN/TSO1- 4_8486311	41.52	proximal promoter
AT2G04880	ZINC-DEPENDENT ACTIVATOR PROTE	Encodes WRKY 2_1717691	41.29	promoter
AT3G20820	na	Leucine-rich rer 3_7282625	40.84	intergenic
AT1G33930	na	P-loop containir 1_12324210	40.19	intron
AT5G60880	BREAKING OF ASYMMETRY IN THE ST		40.05	promoter
AT1G69010	BES1-INTERACTING MYC-LIKE PROTEI		39.71	promoter
AT1G69000	na CYTOCHROME D450, FAMILY 740, CHR	pre-tRNA; tRNA 1_25941517	39.71	intergenic
AT2G34500 AT2G34490	CYTOCHROME P450, FAMILY 710, SUB CYTOCHROME P450, FAMILY 710, SUB		39.69 39.69	intergenic proximal promoter
AT1G34245	EPIDERMAL PATTERNING FACTOR 2 (I		39.59	proximal promoter
AT1G54100	ALDEHYDE DEHYDROGENASE 7B4 (AL		39.34	promoter
AT1G54110	na	Membrane fusic 1 20199174	39.34	promoter
AT3G20015	na	Eukaryotic aspa 3_6977786	38.54	intergenic
AT2G46360	na	unknown proteir 2_19027906	38.13	proximal promoter
AT2G46340	SUPPRESSOR OF PHYA-105 1 (SPA1)	Encodes a merr 2_19027906	38.13	promoter
AT1G66160	CYS, MET, PRO, AND GLY PROTEIN 1 (37.94	promoter
AT1G66170		encodes a PHD 1_24637048	37.94	intergenic
AT1C72450	GIBBERELLIN 20-OXIDASE 3 (GA20OX3		37.51	intergenic
AT1G72450 AT1G80630	JASMONATE-ZIM-DOMAIN PROTEIN 6 (na	NAZ6 transcript 1_2/2/6/6/ RNI-like superfa 1_30310990	37.17 37	promoter promoter
AT1G80630 AT1G80640	na na	Protein kinase s 1_30310990	37	promoter proximal promoter
AT4G28250	EXPANSIN B3 (EXPB3)	putative beta-ex 4_14004403	36.97	proximal promoter
AT4G28260	na	unknown proteir 4_14004403	36.97	promoter
AT2G42770	na	Peroxisomal me 2_17800346	36.57	promoter
AT2G42780	na	FUNCTIONS IN 2_17800346	36.57	promoter
AT5G53150	na	DNAJ heat shor 5_21558048	36.55	intergenic
AT5G53160	REGULATORY COMPONENTS OF ABA		36.55	proximal promoter
AT3G14750	na	unknown proteir 3_4955876	36.2	promoter
AT3G14760	na	unknown proteir 3_4955876	36.2	promoter
AT2G20560	na	DNAJ heat shot 2_8852149	36.13	proximal promoter
AT2G20562 AT1G13350	na na	unknown proteir 2_8852149 Protein kinase s 1_4577996	36.13 36.01	proximal promoter proximal promoter
AT1G13350 AT1G13360	na na	unknown proteir 1_4577996	36.01	promoter
AT5G07280	EXCESS MICROSPOROCYTES1 (EMS1		35.84	promoter
AT5G07270	XB3 ORTHOLOG 3 IN ARABIDOPSIS TH		35.84	intergenic
AT2G46710	na	Rho GTPase ac 2_19190703	35.49	proximal promoter
AT5G01090	na	Concanavalin A 5_34473	35.48	downstream
AT5G01100	na	O-fucosyltransfe 5_34473	35.48	downstream
AT3G06070	na	unknown proteir 3_1833908	35.34	proximal promoter
AT3G06080	na	Encodes a merr 3_1833908	35.34	intergenic
AT5G47500	PECTIN METHYLESTERASE 5 (PME5)	predicted to enc 5_19273702 Protein of unkny 5_4564817	35.32 35.26	proximal promoter
AT5G14150 AT2G40660	na na	Protein of unknc 5_4564817 Nucleic acid-bin 2_16969979	35.26 35.21	intergenic intergenic
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AT2G40670	RESPONSE REGULATOR 16 (RR16)	response regula 2_16969979	35.21	promoter
AT1G78070	na	Transducin/WD 1_29359345	34.82	intergenic
AT1G68550	CYTOKININ RESPONSE FACTOR 10 (CF			intergenic
AT1G76600 AT5G53880	na na	unknown proteir 1_28745920 unknown proteir 5_21875540		proximal promoter proximal promoter
AT2G45590	na	Protein kinase s 2_18786455		promoter
AT1G03600	(PSB27)	PSB27; FUNCT 1_898361	32.86	proximal promoter
AT1G03590	na	Protein phospha 1_898361		proximal promoter
AT1G03610 AT1G03620	na na	Protein of unknc 1_898361 ELMO/CED-12 1_898361		proximal promoter intergenic
AT5G54145	na	unknown proteir 5_21969857		proximal promoter
AT4G29020	na	glycine-rich prot 4_14304181	32.69	proximal promoter
AT5G54530	na	Protein of unknc 5_22151104		proximal promoter
AT1G17420 AT5G60840	LIPOXYGENASE 3 (LOX3) na	LOX3 encode a 1_5979424 unknown proteir 5_24476916		intron proximal promoter
AT5G23280	na	TCP family tran: 5_7842204		proximal promoter
AT5G23270	SUGAR TRANSPORTER 11 (STP11)	sugar transporte 5_7842204		intergenic
AT3G09720 AT3G09730	na na	P-loop containir 3_2983831 unknown proteir 3_2983831		promoter promoter
AT2G24790	CONSTANS-LIKE 3 (COL3)	Positive regular 2_10566726		promoter
AT2G24791	na	Pseudogene of 2_10566726		intergenic
AT3G06850	(BCE2)	dihydrolipoamid 3_2157780		downstream
AT3G06830 AT3G06840	na na	Plant invertase/ 3_2157780 unknown proteir 3_2157780		intergenic three_prime_UTR
AT2G45880	BETA-AMYLASE 7 (BAM7)	Encodes a beta 2_18882711		promoter
AT5G07180	ERECTA-LIKE 2 (ERL2)	Encodes a rece 5_2227599		three_prime_UTR
AT1C60160	na	Cell cycle regul: 5_2227599		intergenic
AT1G69160 AT1G58270	na (ZW9)	unknown proteir 1_25999877 ZW9 mRNA, co 1_21614228		promoter promoter
AT1G58265	na	Cytochrome P4: 1_21614228		intergenic
AT1G18740	na	FUNCTIONS IN 1_6463675		promoter
AT1G18745 AT3G20390	na na	na 1_6463675 endoribonuclea: 3_7111843		intergenic
AT3G20390 AT3G20395	na	RING/U-box su ₁ 3_7111843		promoter downstream
AT5G57630	CBL-INTERACTING PROTEIN KINASE 21			promoter
AT5G57650	na	eukaryotic trans 5_23343384		intergenic
AT5G57655 AT5G10890	na na	xylose isomeras 5_23343384 myosin heavy cl 5_3435312		intergenic promoter
AT5G10890	na	Calcineurin-like 5 3435312		intergenic
AT1G78690	(At1g78690p)	Encodes a lyso(1_29599053	30.14	intergenic
AT1G78700	BES1/BZR1 HOMOLOG 4 (BEH4)	BES1/BZR1 hor 1_29599053		promoter
AT1G79630 AT1G79640	na na	Protein phospha 1_29966371 Protein kinase s 1_29966371		proximal promoter intergenic
AT4G25260	na	Plant invertase/ 4_12936967		promoter
AT4G25270	ORGANELLE TRANSCRIPT PROCESSIN			intergenic
AT3G14070	CATION EXCHANGER 9 (CAX9)	Involved in catic 3_4660914		downstream
AT3G14060 AT3G14067	na	unknown proteir 3_4660914 Subtilase family 3_4660914		intergenic promoter
AT1G69890	na	CONTAINS Inte 1_26325083		promoter
AT1G69900	na	Actin cross-linki 1_26325083		intergenic
AT3G12920 AT3G12930	BOI-RELATED GENE 3 (BRG3)	Encodes one of 3_4119586 Lojap-related pr 3_4119586		intergenic intergenic
AT2G21340	na	MATE efflux fan 2_9132537		promoter
AT5G46750	ARF-GAP DOMAIN 9 (AGD9)	A member of AF 5_18972545	29.46	proximal promoter
AT1G64670	BODYGUARD1 (BDG1)	Encodes a epid 1_24033544		five_prime_UTR
AT1G64680 AT1G21010	na na	unknown proteir 1_24033544 unknown proteir 1_7348694		proximal promoter intergenic
AT1G12420	ACT DOMAIN REPEAT 8 (ACR8)	ACT domain rer 1_4230143		proximal promoter
AT1G12423	na	unknown proteir 1_4230143		intergenic
AT3G49220 AT3G49670	na BARELY ANY MERISTEM 2 (BAM2)	Plant invertase/ 3_18252453 Encodes a CLA 3_18421572		intron
AT3G49670	BRANCHED-CHAIN AMINOTRANSFERA			
AT4G26700		Encodes a chlor3 18421572		intergenic proximal promoter
	FIMBRIN 1 (FIM1)	fimbrin-like prot 4_13463191	28.88	proximal promoter intron
AT5G42030	ABL INTERACTOR-LIKE PROTEIN 4 (ABI	fimbrin-like prot 4_13463191 ABL interactor-li 5_16813659	28.88 28.84 28.82	proximal promoter intron promoter
AT5G42050	ABL INTERACTOR-LIKE PROTEIN 4 (ABI	fimbrin-like prote 4_13463191 ABL interactor-li 5_16813659 DCD (Developn 5_16813659	28.88 28.84 28.82 28.82	proximal promoter intron promoter proximal promoter
	ABL INTERACTOR-LIKE PROTEIN 4 (ABI	fimbrin-like prot 4_13463191 ABL interactor-li 5_16813659	28.88 28.84 28.82 28.82 28.82	proximal promoter intron promoter
AT5G42050 AT5G42053 AT5G42060 AT5G42040	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE	fimbrin-like prott 4_13463191 ABL interactor-l 5_16813659 DCD (Developn 5_16813659 This gene encot 5_16813659 DEK, chromatin 5_16813659 regulatory partic 5_16813659	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.82	proximal promoter intron promoter proximal promoter intergenic intergenic downstream
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610	ABL INTERÁCTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na	fimbrin-like prott 4_13463191 ABL interactor-l 5_16813659 DCD (Developo 5_16813659 This gene encor 5_16813659 DEK, chromatin 5_16813659 Protein kinase s 3_16187049	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.82 28.76	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400	ABL INTERÁCTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR	fimbrin-like prot 4_13463191 ABL interactor-l 5_16813659 DCD (Developn 5_16813659 This gene encoi 5_16813659 DEK, chromatin 5_16813659 regulatory partic 5_16813659 Protein kinase s 3_16187049 Encodes a plasi 4_18328810	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.82 28.76 28.59	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39404 AT4G39403	ABL INTERÁCTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na	fimbrin-like prot 4_13463191 ABL interactor-l 5_16813659 DCD (Developn 5_16813659 This gene encor 5_16813659 DEK, chromatin 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Encodes a 36 a 4_18328810 Encodes a 36 a 4_18328810	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.76 28.59 28.59	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39404 AT4G39403 AT5G62370	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene encoi 5_16813659 DEK, chromatin 5_16813659 regulatory partic 5_16813659 Protein kinase s 3_16187049 Encodes a plasi 4_18328810 other RNA 4_18328810 Tetratricopeptid 5_25046469	28.88 28.84 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic intergenic proximal promoter
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39404 AT4G39404 AT4G39403 AT5G62370 AT5G53220	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na	fimbrin-like prot 4, 13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene enco: 5_16813659 DEK, chromatin 5_16813659 Protein kinase s 3, 16187049 Encodes a plasi 4_18328810 other RNA 4_18328810 Encodes a 36 a 4_18328810 Encodes a 36 a 4_18328810 Encodes a 56	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59 28.59 28.59	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic intergenic intergenic proximal promoter proximal promoter proximal promoter
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39404 AT4G39403 AT5G62370	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene enco 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Encodes a 36 a 4_18328810 Encodes a 36 a 4_18328810 Tetratricopeptid 5_25046469 unknown proteir 5_21593782 Encodes one of 1_29756891	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.57 28.37 28.37	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic intergenic proximal promoter
AT5G42050 AT5G42063 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39403 AT5G62370 AT5G53220 AT1G79110 AT3G15210 AT3G15210	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na	fimbrin-like prot 4, 13463191 ABL interactor-1 5_16813659 DCD (Developn 5_16813659 DEN, chromatin 5_16813659 DEN, chromatin 5_16813659 Protein kinase s 3, 16187049 Encodes a plasi 4_18328810 other RNA 4_18328810 Encodes a 36 a 4_18328810 Encodes a 36 a 4_18328810 Encodes a 64 18328810 Encodes a 65 18328810 Encodes a 65 18328810 Encodes a 66 18328810 Encodes a 75 18328810 Encodes 3 1	28.88 28.84 28.82 28.82 28.82 28.82 28.79 28.59 28.59 28.59 28.59 28.59 28.7 28.37 28.37	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic intergenic proximal promoter proximal promoter proximal promoter intergenic intergenic intergenic intergenic
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39403 AT5G62370 AT5G52220 AT1G79110 AT3G15210 AT3G15210 AT3G58850	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2)	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene enco 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Encodes a 36 a 4_18328810 Encodes a mer 3_5125515 Encodes PHYTI 3_21761400	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59 28.77 28.34 27.91 27.75	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic intergenic proximal promoter proximal promoter proximal promoter intergenic intergenic intergenic proximal promoter proximal promoter proximal promoter intergenic intergenic proximal promoter
AT5G42050 AT5G42063 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39403 AT5G62370 AT5G53220 AT1G79110 AT3G15210 AT3G15210	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene encoi 5_16813659 DEK, chromatin 5_16813659 DEK, chromatin 5_16813659 Protein kinase s 3_16187049 Encodes a plasi 4_18328810 other RNA 4_18328810 Tetratricopeptid 5_25046469 unknown proteir 5_21593782 Encodes one of 1_29756891 Encodes a merr 3_5125515 Tetratricopeptid 3_5125515	28.88 28.84 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59 28.59 27.91 27.91 27.91 27.91 27.91	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter intergenic intergenic intergenic intergenic proximal promoter exon
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39403 AT5G62370 AT5G5220 AT1G79110 AT3G15210 AT3G15210 AT3G58850 AT5G59732 AT5G59732 AT5G59732 AT5G474930	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene enco 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Encodes a 36 a 4_18328810 Encodes a mer 3_5125515 Encodes PHYTI 3_21761400	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59 27.91 27.75 27.61 27.61 27.61	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic intergenic proximal promoter proximal promoter proximal promoter intergenic intergenic intergenic proximal promoter proximal promoter proximal promoter intergenic intergenic proximal promoter
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39403 AT5G52370 AT5G53220 AT1G79110 AT3G15200 AT3G58850 AT5G59732 AT5G59732 AT5G59733 AT5G59733 AT2G41930 AT2G41945	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene encoi 5_16813659 DEK, chromatin 5_16813659 DEK, chromatin 5_16813659 Protein kinase s 3_16187049 Encodes a plasi 4_18328810 other RNA 4_18328810 Tetratricopeptid 5_25046469 unknown proteir 5_21593782 Encodes one of 1_29756891 Encodes a merr 3_5125515 Tetratricopeptid 3_5125515 Tetratricopeptid 3_5125515 Tetratricopeptid 3_6125515 Tetratricopeptid 3_6125515 Tetratricopeptid 3_6125515 Tetratricopeptid 3_6125616 A member of EV 5_24064167 Potential natura 5_24064167 Protein kinase s 2_17510289 unknown proteir 2_17510289	28.88 28.84 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59 28.5 27.75 27.91 27.91 27.91 27.91 27.61 27.61	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter intergenic intergenic intergenic proximal promoter exon promoter intergenic intron
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39403 AT5G53220 AT5G53220 AT5G53220 AT3G15210 AT3G15210 AT3G58850 AT5G59730 AT5G59732 AT5G41930 AT5G41934	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na ZINC FINGER PROTEIN 8 (ZFP8)	fimbrin-like prot 4, 13463191 ABL interactor-1 5_16813659 DCD (Developn 5_16813659 DEN, Chromatin 5_16813659 DEN, chromatin 5_16813659 Protein kinase s 3, 16187049 Encodes a plasi 4_18328810 other RNA 4_18328810 Encodes a 36 a 4_18328810 Tetratricopeptid 5_25046469 unknown proteir 5_21593782 Encodes one of 1_29756891 Encodes a men 3_5125515 Tetratricopeptid 3_5125515 Tetratricopeptid 3_5125515 Tencodes PHYT1 3_21761400 A member of E) 5_24064167 Protein kinase s 2_17510289 unknown proteir 2_17510289 Encodes a zinc 2_17510289	28.88 28.82 28.82 28.82 28.82 28.82 28.82 28.7 28.59 28.59 28.59 28.59 28.79 27.91 27.91 27.91 27.61 27.61 27.61 27.61 27.61	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter proximal promoter intergenic intergenic proximal promoter exon promoter intergenic intergenic intron intergenic intron intergenic intron intergenic
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39403 AT5G62370 AT5G5220 AT1G79110 AT3G15210 AT3G15210 AT3G558730 AT5G59730 AT5G59732 AT2G41945 AT2G41944 AT3G22886	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene enco 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Encodes a plasi 4_18328810 Encodes a 36 a 4_18328810 Encodes a 36 a 4_18328810 Encodes of 1_287646469 unknown proteir 5_21593782 Encodes one of 1_29756891 Encodes a mer 3_5125515 Encodes PHYTI 3_21761400 A member of Ey 5_24064167 Protein kinase s_2_17510289 unknown proteir 2_17510289 Encodes a micr 2_17510289 Encodes a micr 2_17510289 Encodes a micr 2_18107804	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59 28.77 28.34 27.91 27.75 27.61 27.61 27.61 27.61 27.61 27.61 27.61	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter proximal promoter intergenic intergenic proximal promoter exon promoter intergenic intron intergenic intron intergenic intron intergenic promoter
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39400 AT4G39403 AT5G53220 AT5G53220 AT3G15210 AT3G15210 AT3G58850 AT5G59730 AT5G59732 AT2G41930 AT2G41930 AT2G41940 AT3G22886 AT2G41940 AT3G22886 AT2G41940 AT3G22886	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na na ZINC FINGER PROTEIN 8 (ZFP8) MICRORNA167A (MIR167A)	fimbrin-like prot 4_13463191 ABL interactor-1 5_16813659 DCD (Developn 5_16813659 DEN, Chromatin 5_16813659 DEN, chromatin 5_16813659 Protein kinase s 3_16187049 Encodes a plasi 4_18328810 other RNA 4_18328810 Encodes a 36 a 4_18328810 Encodes a 36 a 4_18328810 Encodes a 6 36 a 4_18328810 Encodes a 7 = 1593782 Encodes one of 1_29756891 Encodes a men 3_5125515 Tetratricopeptid 3_5125515 Tetratricopeptid 3_5125515 Encodes PHYT1 3_21761400 A member of E) 5_24064167 Protein kinase s 2_17510289 Encodes a zinc 3_8107804 FUNCTIONS IN 4_526517 unknown proteir 1_7375328	28.88 28.82 28.82 28.82 28.82 28.82 28.82 28.70 28.59 28.59 28.59 28.59 28.70 27.91 27.91 27.91 27.761 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.54 27.54 27.52	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter proximal promoter intergenic intergenic proximal promoter intergenic intergenic intergenic intergenic intergenic intron intergenic promoter proximal promoter proximal promoter proximal promoter proximal promoter exon
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39403 AT5G62370 AT5G5220 AT1G79110 AT3G15210 AT3G15210 AT3G559730 AT5G59730 AT5G59732 AT2G41940 AT3G241945 AT3G1241940 AT3G22886 AT4G01245 AT1G21070	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na na INC. ZINC FINGER PROTEIN 8 (ZFP8) MICRORNA167A (MIR167A) na na na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene enco 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Encodes a plasi 4_18328810 Encodes a 36 a 4_18328810 Encodes a 36 a 4_18328810 Encodes of 1_2876891 Encodes of 1_29756891 Encodes of 1_29756891 Encodes a mer 3_5125515 Encodes PHYTI 3_21761400 A member of Ey 5_24064167 Protein kinase s_2_17510289 unknown proteir 2_17510289 Encodes a micr 3_8107804 FUNCTIONS IN 4_526517 unknown proteir 1_7375328 Nucleotide-sugt 1_7375328	28.88 28.84 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59 28.77 27.91 27.91 27.91 27.91 27.91 27.61 27.61 27.61 27.61 27.61 27.61 27.54 27.54 27.54	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter proximal promoter intergenic intergenic proximal promoter exon promoter intergenic intron intergenic promoter proximal promoter proximal promoter exon promoter proximal promoter intergenic intron intergenic promoter proximal promoter exon intergenic
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39400 AT4G39403 AT5G52370 AT5G53220 AT1G79110 AT3G15200 AT3G58850 AT5G59730 AT5G59732 AT2G41940 AT2G41945 AT2G41940 AT3G22886 AT4G01245 AT4G21060	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na na na ZINC FINGER PROTEIN 8 (ZFP8) MICRORNA167A (MIR167A) na na na na na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene encor 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Tetratricopeptid 5_25046469 unknown proteir 5_21593782 Encodes one of 1_29756891 Encodes a merr 3_5125515 Encodes PHYTT 3_21761400 A member of E) 5_24064167 Potential natura 5_34064167	28.88 28.82 28.82 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59 27.75 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.52 27.52 27.52	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter intergenic intergenic intergenic intergenic intergenic intergenic intergenic proximal promoter intergenic intergenic proximal promoter exon promoter intergenic
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39403 AT5G62370 AT5G5220 AT1G79110 AT3G15210 AT3G15210 AT3G559730 AT5G59730 AT5G59730 AT2G41945 AT5G1941940 AT3G22886 AT4G01245 AT1G21070 AT1G21060 AT1G21060 AT1G21060 AT1G21070 AT1G21060 AT1G21060 AT1G21070 AT1G21060 AT1G21070 AT1G21060 AT1G74960 AT1G74960 AT1G74960	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na na INC. ZINC FINGER PROTEIN 8 (ZFP8) MICRORNA167A (MIR167A) na na na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene enco 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Encodes a plasi 4_18328810 Encodes a 36 a 4_18328810 Encodes a 36 a 4_18328810 Encodes of 1_2876891 Encodes of 1_29756891 Encodes of 1_29756891 Encodes a mer 3_5125515 Encodes PHYTI 3_21761400 A member of Ey 5_24064167 Protein kinase s_2_17510289 unknown proteir 2_17510289 Encodes a micr 3_8107804 FUNCTIONS IN 4_526517 unknown proteir 1_7375328 Nucleotide-sugt 1_7375328	28.88 28.82 28.82 28.82 28.82 28.82 28.82 28.70 28.59 28.59 28.59 28.59 28.70 27.91 27.91 27.91 27.91 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.54 27.52 27.52 27.52 27.52	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter proximal promoter intergenic intergenic proximal promoter exon promoter intergenic intron intergenic promoter proximal promoter proximal promoter exon promoter proximal promoter intergenic intron intergenic promoter proximal promoter exon intergenic
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39400 AT4G39403 AT5G52370 AT5G53220 AT1G79110 AT3G15200 AT3G15200 AT3G58850 AT5G59730 AT5G59732 AT2G41940 AT2G41940 AT3G22886 AT4G01245 AT1G21060 AT1G21070 AT1G21060 AT1G74960	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na na ZINC FINGER PROTEIN 8 (ZFP8) MICRORNA167A (MIR167A) na na na na FATTY ACID BIOSYNTHESIS 1 (FAB1) na na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene encor 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Tetratricopeptid 5_25046469 unknown proteir 5_21593782 Encodes one of 1_29756891 Encodes a merr 3_5125515 Encodes PHYTT 3_21761400 A member of EP 5_24064167 Potential natura 5_24064167 Protein kinase s_2_17510289 Encodes a micr 3_8107804 FUNCTIONS IN 4_526517 unknown proteir 1_7375328 Protein of unknr 1_7375328 Protein of unknr 1_7375328 Encodes a plasi 1_28156977 Involved in resp 1_4760436 Plant protein of 1_4760436	28.88 28.82 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.59 28.59 27.75 28.37 27.91 27.91 27.91 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.52 27.52 27.52 27.51 27.49	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter intergenic proximal promoter proximal promoter exon intergenic intergenic proximal promoter proximal promoter intergenic proximal promoter intergenic
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39400 AT4G39403 AT5G53220 AT5G53220 AT5G53220 AT3G15210 AT3G15210 AT3G58850 AT5G59730 AT5G59730 AT5G59732 AT2G41930 AT2G41930 AT2G41940 AT3G22886 AT4G01245 AT1G21070 AT1G21070 AT1G21070 AT1G21070 AT1G21070 AT1G21070 AT1G13930 AT1G13930 AT1G13940 AT1G13940 AT1G13940 AT1G30240	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na 2INC FINGER PROTEIN 8 (ZFP8) MICRORNA167A (MIR167A) na na na FATTY ACID BIOSYNTHESIS 1 (FAB1) na na na na	fimbrin-like prot 4_13463191 ABL interactor-1 5_16813659 DCD (Developn 5_16813659 DCD (Developn 5_16813659 This gene enco: 5_16813659 DEK, chromatin 5_16813659 Protein kinase s 3_16187049 Encodes a plasi 4_18328810 Encodes a plasi 4_18328810 Encodes a 36 a 4_18328810 Encodes a 36 a 4_18328810 Encodes a 6 a 4_18328810 Encodes a 6 a 4_18328810 Encodes a mar 3_5125515 Encodes a mer 3_5125515 Encodes a mer 3_5125515 Encodes PHYTI 3_21761400 A member of E) 5_24064167 Protein kinase s 2_17510289 Encodes a micr 3_8107804 Encodes a micr 3_8107804 Encodes a micr 3_8107804 FUNCTIONS IN 4_526517 unknown proteir 1_7375328 Rucleotide-suga 1_7375328 Encodes a plasi 1_28156977 Involved in resp 1_4760436 Syntaxint-SNAI 4_14807480	28.88 28.82 28.82 28.82 28.82 28.82 28.82 28.7 28.59 28.59 28.59 28.59 28.7 28.37 28.34 27.91 27.91 27.761 27.61 27.61 27.61 27.61 27.61 27.61 27.54 27.52 27.52 27.52 27.51 27.49 27.49	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter intergenic intergenic proximal promoter exon promoter intergenic proximal promoter proximal promoter exon intergenic proximal promoter proximal promoter proximal promoter proximal promoter intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic
AT5G42050 AT5G42053 AT5G42060 AT5G42040 AT3G44610 AT4G39400 AT4G39400 AT4G39403 AT5G52370 AT5G53220 AT1G79110 AT3G15200 AT3G15200 AT3G58850 AT5G59730 AT5G59732 AT2G41940 AT2G41940 AT3G22886 AT4G01245 AT1G21060 AT1G21070 AT1G21060 AT1G74960	ABL INTERACTOR-LIKE PROTEIN 4 (ABI na na na REGULATORY PARTICLE NON-ATPASE na BRASSINOSTEROID INSENSITIVE 1 (BR na POLARIS (PLS) na na BOI-RELATED GENE 2 (BRG2) ETHYLENE RESPONSIVE ELEMENT BIN na PHY RAPIDLY REGULATED 2 (PAR2) EXOCYST SUBUNIT EXO70 FAMILY PRO na na na ZINC FINGER PROTEIN 8 (ZFP8) MICRORNA167A (MIR167A) na na na na FATTY ACID BIOSYNTHESIS 1 (FAB1) na na	fimbrin-like prot 4_13463191 ABL interactor-I 5_16813659 DCD (Developn 5_16813659 This gene encor 5_16813659 DEK, chromatin 5_16813659 Protein kinase s_3_16187049 Encodes a plasi 4_18328810 Tetratricopeptid 5_25046469 unknown proteir 5_21593782 Encodes one of 1_29756891 Encodes a merr 3_5125515 Encodes PHYTT 3_21761400 A member of EP 5_24064167 Potential natura 5_24064167 Protein kinase s_2_17510289 Encodes a micr 3_8107804 FUNCTIONS IN 4_526517 unknown proteir 1_7375328 Protein of unknr 1_7375328 Protein of unknr 1_7375328 Encodes a plasi 1_28156977 Involved in resp 1_4760436 Plant protein of 1_4760436	28.88 28.84 28.82 28.82 28.82 28.82 28.82 28.76 28.59 28.59 28.57 28.37 27.91 27.91 27.91 27.91 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.61 27.54 27.54 27.52 27.52 27.52 27.52 27.49 27.49 27.44	proximal promoter intron promoter proximal promoter proximal promoter intergenic intergenic downstream intergenic three_prime_UTR intergenic proximal promoter proximal promoter proximal promoter intergenic proximal promoter proximal promoter exon intergenic intergenic proximal promoter proximal promoter intergenic proximal promoter intergenic

AT1G12110				
	NITRATE TRANSPORTER 1.1 (NRT1.1)	Encodes NRT1. 1 4107982	27.09	intron
AT1G26600	CLAVATA3/ESR-RELATED 9 (CLE9)	Member of a lar 1_9191493	26.95	promoter
AT3G57530	CALCIUM-DEPENDENT PROTEIN KINAS	Calcium-depend 3_21295466	26.7	intergenic
AT2G22330	CYTOCHROME P450, FAMILY 79, SUBF		26.7	proximal promoter
AT3G53390	na	Transducin/WD 3_19791471	26.69	proximal promoter
AT3G53380	na	Concanavalin A 3_19791471	26.69	promoter
AT5G67180	TARGET OF EARLY ACTIVATION TAGG		26.66	proximal promoter
AT1G09470	na	unknown proteir 1_3057087	26.58	intron
AT5G11550	na	ARM repeat sur 5_3708156	26.58	three_prime_UTR
AT5G11560	na	catalytics; FUN(5_3708156	26.58	intergenic
AT5G62230	ERECTA-LIKE 1 (ERL1)	Encodes a rece 5_24995786	26.57	promoter
AT1G75080	BRASSINAZOLE-RESISTANT 1 (BZR1)	Encodes a posil 1_28183994	26.54	proximal promoter
AT1G75060	na	unknown proteir 1_28183994	26.54	promoter
AT1G75070	na	pre-tRNA; tRNA 1_28183994	26.54	proximal promoter
AT1G24405 AT3G17120	na	unknown proteir 1_8654674	26.51 26.4	proximal promoter
AT3G17120	na B-S GLUCOSIDASE 44 (BGLU44)	unknown proteir 3_5843850 B-S glucosidase 3 6190670		intergenic proximal promoter
AT1G66400	CALMODULIN LIKE 23 (CML23)	Encodes a calm 1_24770551	26.21 26.11	downstream
AT1G00400	na	Protein of unknr 1 8598686	26.02	proximal promoter
AT3G16860	COBRA-LIKE PROTEIN 8 PRECURSOR		25.87	proximal promoter
AT3G16870	GATA TRANSCRIPTION FACTOR 17 (GA		25.87	downstream
AT5G65280	GCR2-LIKE 1 (GCL1)	Encodes a prote 5 26088953	25.74	proximal promoter
AT5G60680	na	Protein of unknc 5_24384407	25.72	proximal promoter
AT1G64390	GLYCOSYL HYDROLASE 9C2 (GH9C2)	glycosyl hydrola 1_23912783	25.71	intron
AT4G28770	na	Tetraspanin farr 4_14213922	25.66	intron
AT3G47295	na	unknown proteir 3_17427907	25.65	promoter
AT3G29105	na	pseudogene, nc 3_11081140	25.65	intron
AT3G47300	SELT-LIKE PROTEIN PRECURSOR (SEL		25.65	intergenic
AT3G12965	na	Unknown gene 3_4138372	25.59	proximal promoter
AT3G28070	na	nodulin MtN21-l 3_10449152	25.58	intron
AT1G32690	na	unknown proteir 1_11821872	25.28	promoter
AT1G70090	GLUCOSYL TRANSFERASE FAMILY 8 (L	Encodes a prote 1_26400580	25.24	promoter
AT1G70100	na	unknown proteir 1_26400580	25.24	proximal promoter
AT5G07300	BONZAI 2 (BON2)	Encodes a copii 5_2299751	25.23	promoter
AT5G07290	MEI2-LIKE 4 (ML4)	AML4 A membi 5_2299751	25.23	intergenic
AT1G05240	na	Peroxidase sup 1_1520063	25.05	proximal promoter
AT3G21700	(SGP2)	Monomeric G pi 3_7642912	25.02	proximal promoter
AT3G21690	na	MATE efflux fan 3_7642912	25.02	intergenic
AT1G68560	ALPHA-XYLOSIDASE 1 (XYL1)	Encodes a bifur 1_25741117	24.93	intergenic
AT4G03010	na	RNI-like superfa 4_1329430	24.91	proximal promoter
AT4G03020	na	transducin famil 4_1329430	24.91	intergenic
AT1G73750	na	Uncharacterise: 1_27739100	24.87	downstream
AT1G73760	na	RING/U-box su ₁ 1_27739100	24.87	downstream
AT2G01850	ENDOXYLOGLUCAN TRANSFERASE A3	pre-tRNA; tRNA 1_29443582	24.7 24.67	proximal promoter
AT1G78250 AT4G23750	na CYTOKININ RESPONSE FACTOR 2 (CRI		24.62	intergenic
AT4G23760	na	Cox19-like CHC 4 12379801	24.62	intergenic proximal promoter
AT2G18876	na	Afadin/alpha-ac 2_8169433	24.61	promoter
AT5G16350	na	O-acyltransfera: 5_5352399	24.57	promoter
AT2G02450	LONG VEGETATIVE PHASE 1 (LOV1)	NAC domain co 2_649194	24.55	intron
AT5G03040	IQ-DOMAIN 2 (iqd2)	IQ-domain 2 (iq: 5_712802	24.49	intron
AT1G73150	GLOBAL TRANSCRIPTION FACTOR GR		24.09	promoter
AT3G47620	TEOSINTE BRANCHED, CYCLOIDEA AN		24.06	proximal promoter
	(APRR2)			
AT4G18020		Encodes pseud 4 10003514	23.98	three prime UTR
AT4G18020 AT3G10720	na	Plant invertase/ 3_3356218	23.98 23.85	three_prime_UTR intron
	,	Plant invertase/ 3_3356218		
AT3G10720	na	Plant invertase/ 3_3356218 Encodes a merr 1_6774597	23.85	intron
AT3G10720 AT1G19570	na DEHYDROASCORBATE REDUCTASE (D	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804	23.85 23.84	intron promoter
AT3G10720 AT1G19570 AT1G19580	na DEHYDROASCORBATE REDUCTASE (D GAMMA CARBONIC ANHYDRASE 1 (GA na na	Plant invertase/ 3_3356218 Encodes a merr 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804	23.85 23.84 23.84	intron promoter promoter
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT4G38850	na DEHYDROASCORBATE REDUCTASE (D GAMMA CARBONIC ANHYDRASE 1 (GA na	Plant invertase/ 3_3356218 Encodes a merr 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804	23.85 23.84 23.84 23.8	intron promoter promoter intergenic
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT4G38850 AT3G22104	na DEHYDROASCORBATE REDUCTASE (D GAMMA CARBONIC ANHYDRASE 1 (GA na na	Plant invertase/ 3_3356218 Encodes a men 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 MRNA is rapidly 4_18125804 Phototropic-resj 3_7790107	23.85 23.84 23.84 23.8 23.8 23.8 23.71	intron promoter promoter intergenic promoter promoter promoter intron
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT4G38850 AT3G22104 AT5G10960	na DEHYDROASCORBATE REDUCTASE (D GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 mRNA is rapidly 4_18125804 Phototropic-resj 3_7790107 Polynucleotidyl 5_3464049	23.85 23.84 23.84 23.8 23.8 23.8 23.71 23.64	intron promoter promoter intergenic promoter promoter intron promoter
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT4G38850 AT3G22104 AT5G10960 AT1G18710	na DEHYDROASCORBATE REDUCTASE (D GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUR na na MYB DOMAIN PROTEIN 47 (MYB47)	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 mRNA is rapidly 4_18125804 Phototropic-resj 3_7790107 Polynucleotidy! 5_3464049 Member of the F1_6446303	23.85 23.84 23.8 23.8 23.8 23.8 23.71 23.64 23.61	intron promoter promoter intergenic promoter intron promoter intron promoter intergenic
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT4G38850 AT3G22104 AT5G10960 AT1G18710 AT3G55290	na DEHYDROASCORBATE REDUCTASE (D GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na MYB DOMAIN PROTEIN 47 (MYB47) na	Plant invertase/ 3_3356218 Encodes a men 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-resi 3_7790107 Polynucleotidyl 5_3464049 Member of the f 1_6446303 NAD(P)-binding 3_20501880	23.85 23.84 23.8 23.8 23.8 23.7 23.6 23.64 23.61 23.6	intron promoter promoter intergenic promoter intron promoter intergenic promoter intergenic proximal promoter
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT4G38850 AT3G22104 AT5G10960 AT1G18710 AT3G55290 AT3G55280	na DEHYDROASCORBATE REDUCTASE (D GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AB	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 MRNA is rapidly 4_18125804 Phototropic-res; 3_7790107 Polynucleotidyl 5_3464049 Member of the f 1_6446303 NAD(P)-binding 3_20501880 60S ribosomal r_3_20501880	23.85 23.84 23.8 23.8 23.8 23.71 23.64 23.61 23.6 23.6	intron promoter promoter intergenic promoter promoter intron promoter intergenic promoter intergenic proximal promoter downstream
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38850 AT3G22104 AT5G10960 AT1G18710 AT3G55290 AT3G55290 AT4G12270	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUR na na MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AE na	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 MRNA is rapidly 4_18125804 Phototropic-res; 3_7790107 Polynucleotidyl 5_3464049 Member of the f 1_6446303 NAD(P)-binding 3_20501880 GOS ribosomal; 3_20501880 Copper amine c 4_7288840	23.85 23.84 23.84 23.8 23.8 23.71 23.64 23.61 23.6 23.6 23.6 23.6	intron promoter promoter promoter intergenic promoter promoter intron promoter intergenic proximal promoter downstream exon
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT4G38850 AT3G22104 AT5G10960 AT1G18710 AT3G55280 AT3G55280 AT4G12270 AT5G65130	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AE na na	Plant invertase/ 3_3356218 Encodes a men 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-resi 3_7790107 Polynucleotidyl: 5_3464049 Member of the I 1_6446303 NAD(P)-binding 3_20501880 60S ribosomal g 3_20501880 copper amine c 4_7298840 encodes a mem 5_26018834	23.85 23.84 23.84 23.8 23.8 23.71 23.64 23.61 23.6 23.6 23.57 23.57	intron promoter promoter promoter intergenic promoter intron promoter intron promoter intergenic proximal promoter downstream exom intergenic
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38860 AT4G38850 AT3G22104 AT5G10960 AT1G18710 AT3G55290 AT3G55290 AT3G55280 AT4G12270 AT5G65130 AT2G42880	na DEHYDROASCORBATE REDUCTASE (D GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AE na MAP KINASE 20 (MPK20)	Plant invertase/ 3_3356218 Encodes a men 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 MRNA is rapidly 4_18125804 Phototropic-res; 3_7790107 Polynucleotidy! 5_3464049 Member of the f 1_6446303 NAD(P)-binding 3_20501880 60S ribosomal r, 3_20501880 Copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466	23.85 23.84 23.8 23.8 23.8 23.71 23.64 23.61 23.6 23.6 23.6 23.6 23.5 23.6 23.5 23.6	intron promoter promoter promoter intergenic promoter promoter intron promoter intergenic proximal promoter downstream exon intergenic intergenic intergenic intergenic
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38860 AT4G38850 AT3G22104 AT5G10960 AT1G18710 AT3G55290 AT3G55280 AT4G12270 AT5G65130 AT2G42880 AT5G21940	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUR na na NYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AB na na MAP KINASE 20 (MPK20) na	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-res; 3_7790107 Polynucleotidyl 5_3464049 Member of the f1_6446303 NAD(P)-binding 3_20501880 GOS ribosomal r_3_20501880 Copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466 unknown proteir 5_7252106	23.85 23.84 23.84 23.8 23.8 23.71 23.64 23.61 23.6 23.6 23.57 23.57 23.48	intron promoter promoter promoter intergenic promoter intron promoter intergenic proximal promoter downstream exon intergenic proximal promoter downstream exon intergenic proximal promoter
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT3G38520 AT3G22104 AT5G10960 AT1G18710 AT3G55290 AT3G55280 AT4G12270 AT5G65130 AT2G42880 AT5G21940 AT5G21930	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AE na na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (PA	Plant invertase/ 3_3356218 Encodes a men 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-res; 3_7790107 Polynucleotidyi 5_3464049 Member of the 1_6446303 NAD(P)-binding 3_20501880 60S ribosomal g 3_20501880 60S ribosomal g 3_20501880 copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466 unknown proteir 5_7252106 P-Type ATPase 5_7252106	23.85 23.84 23.84 23.8 23.8 23.71 23.64 23.6 23.6 23.6 23.6 23.5 23.57 23.57 23.48 23.48	intron promoter promoter promoter intergenic promoter intron promoter intron promoter intergenic proximal promoter downstream exon intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38860 AT3G22104 AT5G10960 AT1G18710 AT3G55290 AT3G55290 AT3G55290 AT4G12270 AT5G65130 AT2G42880 AT5G21940 AT5G21940 AT5G21940 AT5G21930 AT2G42870	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AE na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (P. PHY RAPIDLY REGULATED 1 (PAR1)	Plant invertase/ 3_3356218 Encodes a men 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 MRNA is rapidly 4_18125804 Phototropic-resj 3_7790107 Polynucleotidyl 5_3464049 Member of the I 1_6446303 NAD(P)-binding 3_20501880 60S ribosomal r_3_20501880 Copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466 unknown proteit 5_7252106 P-Type ATPass 5_7252106 Encodes PHYTi 2_17836466	23.85 23.84 23.8 23.8 23.8 23.71 23.64 23.61 23.6 23.6 23.6 23.7 23.48 23.48 23.48 23.48	intron promoter promoter promoter intergenic promoter intron promoter intron promoter intergenic proximal promoter downstream exon intergenic proximal promoter intergenic proximal promoter intergenic three_prime_UTR
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38860 AT4G38850 AT3G22104 AT5G10960 AT1G18710 AT3G55280 AT3G55280 AT4G12270 AT5G65130 AT2G42880 AT5G21940 AT5G21940 AT3G621930 AT2G42870 AT3G65500	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUR na na MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AE na na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (P, PHY RAPIDLY REGULATED 1 (PAR1) ALKALINE/NEUTRAL INVERTASE C (A/N	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-res; 3_7790107 Polynucleotidyl 5_3464049 Member of the f1_6446303 NAD(P)-binding 3_20501880 GOS ribosomal r_3_20501880 Copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466 unknown proteir 5_7252106 P-Type ATPase 5_7252106 Encodes PHYTI 2_17836466 Plant neutral inv 3_2011631	23.85 23.84 23.84 23.8 23.8 23.71 23.64 23.6 23.6 23.6 23.57 23.57 23.48 23.48 23.48 23.48	intron promoter promoter promoter intergenic promoter intron promoter intergenic proximal promoter downstream exon intergenic proximal promoter intergenic
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT3G38520 AT3G22104 AT5G10960 AT3G55280 AT3G55280 AT3G55280 AT3G65280 AT4G12270 AT5G65130 AT2G42880 AT5G21940 AT5G21930 AT3G428790 AT3G6500 AT3G48790	na DEHYDROASCORBATE REDUCTASE (D GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AE na na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (P, PHY RAPIDLY REGULATED 1 (PAR1) ALKALINE/NEUTRAL INVERTASE C (A/N na	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-resi 3_7790107 Polynucleotidyl 5_3464049 Member of the 1_646303 NAD(P)-binding 3_20501880 60S ribosomal r 3_20501880 60S ribosomal r 3_20501880 encodes a mem 5_26018834 member of MAF 2_17836466 unknown proteir 5_7252106 P-Type ATPase 5_7252106 Encodes PHYTi 2_17836466 Plant neutral in 3_2011631 Pyridoxal phosp 3_18092380	23.85 23.84 23.84 23.8 23.8 23.71 23.64 23.6 23.6 23.6 23.57 23.57 23.48 23.48 23.48 23.48 23.48 23.48	intron promoter promoter promoter intergenic promoter intron promoter intron promoter intergenic proximal promoter downstream exon intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic proximal promoter intergenic proximal promoter proximal promoter
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38860 AT4G38850 AT3G22104 AT5G10960 AT1G18710 AT3G55290 AT3G55280 AT4G12270 AT5G65130 AT2G42880 AT5G21940 AT5G21940 AT5G21940 AT3G48790 AT3G48790	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na RIBOSOMAL PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AB na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (P. PHY RAPIDLY REGULATED 1 (PAR1) ALKALINE/NEUTRAL INVERTASE C (A/N na SERINE PALMITOYLTRANSFERASE 1 (S	Plant invertase/ 3_3356218 Encodes a men 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-res; 3_7790107 Polynucleotidy! 5_3464049 Member of the I 1_6446303 NAD(P)-binding 3_20501880 60S ribosomal r_3_20501880 Copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466 unknown proteir 5_7252106 P-Type ATPase 5_7252106 Encodes PHYTI 2_17836466 Plant neutral inv 3_2011631 Pyridoxal phos; 3_18092380 Encodes one of 3_18092380	23.85 23.84 23.84 23.8 23.8 23.71 23.64 23.61 23.6 23.6 23.57 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.38	intron promoter promoter promoter intergenic promoter intron promoter intergenic proximal promoter downstream exon intergenic intergenic intergenic intergenic intergenic thergenic three_prime_UTR promoter proximal promoter three_prime_UTR
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38860 AT4G38850 AT3G22104 AT5G10960 AT1G18710 AT3G55280 AT3G55280 AT4G12270 AT5G65130 AT2G42880 AT5G21940 AT5G21940 AT3G6500 AT3G48780 AT3G48780 AT3G48780 AT4G3270	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUR na na MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AE na na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (P. PHY RAPIDLY REGULATED 1 (PAR1) ALKALINE/NEUTRAL INVERTASE C (A/N na SERINE PALMITOYLTRANSFERASE 1 (S CYCLIN D6;1 (CYCD6;1)	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-res; 3_7790107 Polynucleotidyl 5_3464049 Member of the f1_6446303 NAD(P)-binding 3_20501880 GOS ribosomal r_3_20501880 Copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466 unknown proteir 5_7252106 P-Type ATPase 5_7252106 P-Type ATPase 5_7252106 Plant neutral inv 3_2011631 Pyridoxal phosp 3_18092380 Cyclin D6;1 (CY 4_1431871	23.85 23.84 23.8 23.8 23.71 23.64 23.6 23.6 23.57 23.57 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.38	intron promoter promoter promoter intergenic promoter intron promoter intergenic proximal promoter downstream exon intergenic proximal promoter intergenic proximal promoter intergenic proximal promoter intergenic promoter proximal promoter proximal promoter three_prime_UTR intergenic
AT3G10720 AT1G19570 AT1G19580 AT4G38840 AT4G38840 AT4G38840 AT3G22104 AT5G10960 AT3G55280 AT3G55280 AT3G55280 AT4G12270 AT5G65130 AT2G42880 AT5G21940 AT5G21940 AT3G6500 AT3G48790 AT3G48780 AT3G48780 AT3G48780 AT4G03270 AT5G08139	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na RIBOSOMAL PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AB na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (P. PHY RAPIDLY REGULATED 1 (PAR1) ALKALINE/NEUTRAL INVERTASE C (A/N na SERINE PALMITOYLTRANSFERASE 1 (S	Plant invertase/ 3_3356218 Encodes a men 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-res; 3_7790107 Polynucleotidy! 5_3464049 Member of the 1_646303 NAD(P)-binding 3_20501880 60S ribosomal ; 3_20501880 60S ribosomal ; 3_20501880 encodes a mem 5_26018834 member of MAF 2_17836466 P-Type ATPase 5_7252106 P-Type ATPase 5_7252106 Encodes PHYT1 2_17836466 Plant neutral inv 3_2011631 Pyridoxal phosp 3_18092380 Encodes one of 3_18092380 Cyclin D6;1 (CY 4_1431871 RING/U-box suj 5_2614836	23.85 23.84 23.84 23.8 23.8 23.71 23.64 23.6 23.6 23.6 23.57 23.57 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.38 23.38	intron promoter promoter promoter intergenic promoter intron promoter intergenic proximal promoter downstream exon intergenic intergenic intergenic intergenic intergenic thergenic three_prime_UTR promoter proximal promoter three_prime_UTR
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AT3G10720 AT1G19570 AT1G19580 AT4G38840 AT4G38840 AT4G38850 AT3G22104 AT5G10960 AT3G55280 AT3G55280 AT3G55280 AT4G12270 AT5G65130 AT2G42880 AT5G21940 AT5G21940 AT5G21940 AT5G21940 AT3G6550 AT3G48780 AT3G48780 AT3G48780 AT3G48780 AT3G48780 AT3G48780 AT3G48780 AT3G61540 AT3G28910 AT3G28910 AT3G361540 AT3G61550 AT3G61550	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUR na na MAP KINASE 20 (MPK20) na ALKALINE/NEUTRAL INVERTASE C (ANN na SERINE PALMITOYLTRANSFERASE 1 (SCYCLIN D6;1 (CYCD6;1) na na MAP KINASE CYCLIN D6;1 (CYCD6;1) na na MAP KINASE CYCLIN D6;1 (CYCD6;1) na na na (PDF1.4) CAX INTERACTING PROTEIN 4 (CXIP4) na	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 Encodes mitoch 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-res; 3_7790107 Polynucleotidyl 5_3464049 Member of the f1_6446303 NAD(P)-binding 3_20501880 GOS ribosomal r_3_20501880 GOS ribosomal r_3_20501880 Copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466 unknown proteir 5_7252106 P-Type ATPase 5_7252106 Cyclin D6;1 (CY 4_1431871 R)ING/U-box suj 5_2614836 Outer arm dyne 4_1431871 encodes allene 3_9403681 Encodes a mer 2_17646264 Protein kinase s 1_19776858 Predicted to ent 1_6782771 Encodes a CAX 2_12418352 alpha/beta-Hydr 3_22776282 pre-tRNA; tRNA 3_22776282 Reticulon family 3_22776282 Reticulon family 3_22776282	23.85 23.84 23.8 23.84 23.8 23.8 23.71 23.64 23.6 23.6 23.57 23.57 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.18 23.35 23.25 23.25 23.18 23.11 23.1 23.1 23.1 22.99 22.99 22.99	intron promoter promoter promoter intergenic promoter intergenic promoter intergenic promoter intergenic proximal promoter intergenic intergenic intergenic proximal promoter intergenic proximal promoter intergenic promoter proximal promoter three_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter intergenic promoter intergenic promoter intergenic proximal promoter
AT3G10720 AT1G19570 AT1G19580 AT4G38840 AT4G38840 AT4G38840 AT3G22104 AT5G10960 AT3G55280 AT3G55280 AT3G55280 AT3G55280 AT3G65130 AT2G42880 AT5G21940 AT5G21930 AT3G48780 AT3G53650 AT1G53060 AT1G53060 AT3G61560 AT3G61550 AT3G61550 AT3G61550	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (PAPHY RAPIDLY REGULATED 1 (PAR1) ALKALINE/NEUTRAL INVERTASE C (A/N na SERINE PALMITOYLTRANSFERASE 1 (SCYCLIN D6;1 (CYCD6;1) na na na (PDF1.4) CAX INTERACTING PROTEIN 4 (CXIP4) na n	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-res; 3_7790107 Polynucleotidy! 5_3464049 Member of the !1_6446303 NAD(P)-binding 3_20501880 60S ribosomal ; 3_20501880 60S ribosomal ; 3_20501880 copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466 P-Type ATPase 5_7252106 P-Type ATPase 5_7252106 P-Type ATPase 5_7252106 P-Type ATPase 5_7252106 Plant neutral in 3_2011631 Pyridoxal phosp 3_18092380 Encodes one of 3_18092380 Encodes one of 3_18092380 Encodes anem 5_2614836 Outer arm dyne 4_1431871 RING/U-box su; 5_2614836 Outer arm dyne 4_1431871 RING/U-box su; 5_2614836 Uter arm dyne 4_1431871 RING/U-box su; 5_2614836 Uter arm dyne 4_1431871 RING/U-box su; 5_2614836 Uter arm dyne 4_1431871 RING/U-box su; 5_21766264 Protein kinase s 1_19776858 Legume lectin fr 1_2776262 zipha/beta-Hyd; 3_22776282 RING/U-box su; 3_22776282 Protein kinase r 1_7570992	23.85 23.84 23.8 23.84 23.8 23.71 23.64 23.6 23.6 23.6 23.57 23.57 23.57 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.38 23.35 23.35 23.35 23.35 23.35 23.35 23.25	intron promoter promoter promoter intergenic promoter intergenic promoter intron promoter intergenic proximal promoter intergenic promoter proximal promoter proximal promoter intergenic proximal promoter intergenic promoter intergenic proximal promoter exon intergenic promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT3G10720 AT1G19570 AT1G19580 AT4G38860 AT4G38840 AT4G38840 AT3G52900 AT3G55280 AT3G55280 AT3G55280 AT3G21940 AT5G21930 AT2G42870 AT3G65130 AT3G48790 AT3G48790 AT3G48780 AT4G3270 AT3G68130 AT3G48790 AT3G48780 AT4G3270 AT3G68139 AT4G325760 AT3G42380 AT3G453060 AT1G53050 AT3G5861550 AT3G61550 AT3G61560 AT1G21590 AT1G21590 AT1G21600	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na na SMALL AUXIN UPREGULATED 15 (SAUF na na ma MYB DOMAIN PROTEIN 47 (MYB47) na RIBOSOMAL PROTEIN L23AB (RPL23AE na na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (P. PHY RAPIDLY REGULATED 1 (PAR1) ALKALINE/NEUTRAL INVERTASE C (A/N na SERINE PALMITOYLTRANSFERASE 1 (SCYCLIN D6;1 (CYCD6;1) na na ALLENE OXIDE CYCLASE 1 (AOC1) (BZIP34) na na na (PDF1.4) CAX INTERACTING PROTEIN 4 (CXIP4) na	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 MRNA is rapidly 4_18125804 Phototropic-res; 3_7790107 Polynucleotidyl 5_3464049 Member of the f1_6446303 NAD(P)-binding 3_20501880 GOS ribosomal; 3_20501880 Copper amine c 4_7298840 encodes a mem 5_26018834 encodes a mem 5_26018834 encodes a mem 5_26018834 member of MAF 2_17836466 unknown proteir 5_7252106 P-Type ATPase 5_7252106 P	23.85 23.84 23.8 23.84 23.8 23.81 23.61 23.66 23.66 23.67 23.57 23.57 23.57 23.48 23.38 23.35 23.25 23.35 23.25 23	intron promoter promoter promoter promoter promoter intergenic promoter intergenic promoter intergenic proximal promoter downstream exon intergenic proximal promoter intergenic proximal promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter intergenic proximal promoter intergenic proximal promoter intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic proximal promoter exon intergenic promoter proximal promoter intergenic intergenic
AT3G10720 AT1G19570 AT1G19580 AT4G38840 AT4G38840 AT4G38840 AT3G22104 AT5G10960 AT3G55280 AT3G55280 AT3G55280 AT3G55280 AT3G65130 AT2G42880 AT5G21940 AT5G21930 AT3G48780 AT3G53650 AT1G53060 AT1G53060 AT3G61560 AT3G61550 AT3G61550 AT3G61550	na DEHYDROASCORBATE REDUCTASE (IC GAMMA CARBONIC ANHYDRASE 1 (GA na na SMALL AUXIN UPREGULATED 15 (SAUF na na MAP KINASE 20 (MPK20) na P-TYPE ATPASE OF ARABIDOPSIS 2 (PAPHY RAPIDLY REGULATED 1 (PAR1) ALKALINE/NEUTRAL INVERTASE C (A/N na SERINE PALMITOYLTRANSFERASE 1 (SCYCLIN D6;1 (CYCD6;1) na na na (PDF1.4) CAX INTERACTING PROTEIN 4 (CXIP4) na n	Plant invertase/ 3_3356218 Encodes a mer 1_6774597 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 SAUR-like auxir 4_18125804 Phototropic-res; 3_7790107 Polynucleotidy! 5_3464049 Member of the !1_6446303 NAD(P)-binding 3_20501880 60S ribosomal ; 3_20501880 60S ribosomal ; 3_20501880 copper amine c 4_7298840 encodes a mem 5_26018834 member of MAF 2_17836466 P-Type ATPase 5_7252106 P-Type ATPase 5_7252106 P-Type ATPase 5_7252106 P-Type ATPase 5_7252106 Plant neutral in 3_2011631 Pyridoxal phosp 3_18092380 Encodes one of 3_18092380 Encodes one of 3_18092380 Encodes anem 5_2614836 Outer arm dyne 4_1431871 RING/U-box su; 5_2614836 Outer arm dyne 4_1431871 RING/U-box su; 5_2614836 Uter arm dyne 4_1431871 RING/U-box su; 5_2614836 Uter arm dyne 4_1431871 RING/U-box su; 5_2614836 Uter arm dyne 4_1431871 RING/U-box su; 5_21766264 Protein kinase s 1_19776858 Legume lectin fr 1_2776262 zipha/beta-Hyd; 3_22776282 RING/U-box su; 3_22776282 Protein kinase r 1_7570992	23.85 23.84 23.8 23.84 23.8 23.71 23.64 23.6 23.6 23.6 23.57 23.57 23.57 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.48 23.38 23.35 23.35 23.35 23.35 23.35 23.35 23.25	intron promoter promoter promoter intergenic promoter intergenic promoter intron promoter intergenic proximal promoter intergenic promoter proximal promoter proximal promoter intergenic proximal promoter intergenic promoter intergenic proximal promoter exon intergenic promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter

ATEC 11520	EMPRYONIC ELOWER 1 (EME1)	Involved in some 5 2605210	22.70	provimal promotor
AT5G11530 AT3G47800	EMBRYONIC FLOWER 1 (EMF1) na	Involved in regu 5_3695219 Galactose muta 3_17634472	22.78 22.78	proximal promoter promoter
AT1G02180	na	ferredoxin-relate 1_414826	22.75	promoter
AT1G02100	na	Fatty acid hydro 1_414826	22.75	promoter
AT5G40340	na	Tudor/PWWP/N 5_16135294	22.72	promoter
AT1G70530	CYSTEINE-RICH RLK (RECEPTOR-LIKE		22.66	proximal promoter
AT1G70540	EMBRYO SAC DEVELOPMENT ARREST		22.66	proximal promoter
AT1G27300	na	unknown proteir 1_9481305	22.56	proximal promoter
AT1G27285	na	transposable el 1_9481305	22.56	intergenic
AT1G27290	na	unknown proteir 1 9481305	22.56	promoter
AT3G14050	RELA/SPOT HOMOLOG 2 (RSH2)	RELA/SPOT ho 3_4655852	22.52	proximal promoter
AT5G45480	na	Protein of unknc 5_18429840	22.5	proximal promoter
AT5G45490	na	P-loop containir 5_18429840	22.5	intron
AT2G34160	na	Alba DNA/RNA- 2 14427646	22.48	intergenic
AT5G47370	(HAT2)	homeobox-leuci 5_19218876	22.44	proximal promoter
AT2G36040	na	transposable el 2_15132084	22.4	proximal promoter
AT1G35610	na	Cysteine/Histidii 1_13140441	22.38	intergenic
AT5G62000	AUXIN RESPONSE FACTOR 2 (ARF2)	Encodes an aux 5_24906273	22.35	intergenic
AT5G61997	na	This gene encor 5_24906273	22.35	intergenic
AT1G56220	na	Dormancy/auxir 1_21043145	22.28	promoter
AT4G03400	DWARF IN LIGHT 2 (DFL2)	Encodes a GH3 4_1500047	22.27	promoter
AT5G41810	na	unknown proteir 5_16739911	22.27	intergenic
AT5G41820	RAB GERANYLGERANYL TRANSFERAS		22.27	proximal promoter
AT2G36480	na	ENTH/VHS fam 2_15302469	22.21	downstream
AT2G36470	na	Plant protein of 2_15302469	22.21	proximal promoter
AT3G52450	PLANT U-BOX 22 (PUB22)	Encodes a cyto _l 3_19440701	22.21	downstream
AT3G05320	na	O-fucosyltransft 3_1516562	21.94	proximal promoter
AT3G05327	na	Cyclin family prc 3_1516562	21.94	intergenic
AT2G25460	na	CONTAINS Inte 2_10836245	21.91	proximal promoter
AT1G75820	CLAVATA 1 (CLV1)	Putative recept 1_28467556	21.88	proximal promoter
AT1G74930	(ORA47)	encodes a mem 1_28143985	21.84	promoter
AT3G24050	GATA TRANSCRIPTION FACTOR 1 (GAT		21.84	intron
AT1G74929	na	unknown proteir 1_28143985	21.84	downstream
AT1G74940 AT5G52120	na PHI OEM PROTEIN 2 A44 (PR2 A44)	Protein of unknr 1_28143985	21.84	proximal promoter
AT5G52120	PHLOEM PROTEIN 2-A14 (PP2-A14)	phloem protein: 5_21181724	21.84 21.83	proximal promoter
AT1G29630	na	P-loop nucleosi 5_16524524 5'-3' exonucleas 1_10353971	21.03	proximal promoter intergenic
AT1G29640	na	Protein of unknr 1_10353971	21.73	intergenic
AT1G29040 AT5G13730	SIGMA FACTOR 4 (SIG4)	Encodes sigma 5 4431199	21.66	promoter
AT5G13730	ZINC INDUCED FACILITATOR 1 (ZIF1)	Encodes ZIF1 (: 5_4431199	21.66	proximal promoter
AT4G23870	na	unknown proteir 4_12412268	21.5	proximal promoter
AT2G46520	na	cellular apoptos 2 19095855	21.47	proximal promoter
AT1G64405	na	unknown proteir 1_23923232	21.43	promoter
AT1G64710	na	GroES-like zinc: 1_24043554	21.42	proximal promoter
AT4G30180	na	sequence-speci 4_14768433	21.42	proximal promoter
AT1G68500	na	unknown proteir 1_25703222	21.4	intergenic
AT5G13240	na	transcription rec 5_4227823	21.39	promoter
AT3G20320	ATP-BINDING CASSETTE I15 (ABCI15)	Encodes a pern 3_7087431	21.38	downstream
AT3G20310	ETHYLENE RESPONSE FACTOR 7 (ERF	Encodes a merr 3_7087431	21.38	proximal promoter
AT2G39865	na	unknown proteir 2_16642545	21.36	proximal promoter
AT2G39870	na	unknown proteir 2_16642545	21.36	proximal promoter
AT5G04770	CATIONIC AMINO ACID TRANSPORTER	Encodes a merr 5_1380833	21.35	intron
AT5G04780	na	Pentatricopeptic 5_1380833	21.35	intergenic
AT3G15350	na	Core-2/I-branch 3_5165439	21.31	proximal promoter
AT1G08210	na	Eukaryotic aspa 1_2576798	21.26	downstream
AT1G08200	UDP-D-APIOSE/UDP-D-XYLOSE SYNTH		21.26	promoter
AT5G59730	EXOCYST SUBUNIT EXO70 FAMILY PRO		21.25	proximal promoter
AT4G17250	na	unknown proteir 4_9669192	21.23	proximal promoter
AT4G17240	na	unknown proteir 4_9669192	21.23	proximal promoter
AT4G17245	na	RING/U-box sui 4_9669192	21.23	promoter
AT5G03370	na	acylphosphatas 5_828817	21.19	proximal promoter
AT3G06740	GATA TRANSCRIPTION FACTOR 15 (GA		21.17	intergenic
AT5G45800	MATERNAL EFFECT EMBRYO ARREST		21.17	intron
AT3G06750	na	hydroxyproline-i 3_2127785	21.17 21.17	intergenic
AT3G06760 AT3G44610	na na	Drought-respon 3_2127785 Protein kinase s 3_16190467	21.17	intergenic intron
AT1G52855	na	unknown proteir 1_19684013	21.13	proximal promoter
AT1G52860	na	pre-tRNA; tRNA 1_19684013	21.08	intergenic
AT1G52870	na	Peroxisomal me 1_19684013	21.08	proximal promoter
AT3G50620	na	P-loop containir 3 18784581	21.05	downstream
AT1G12430	ARMADILLO REPEAT KINESIN 3 (ARK3)		21.04	promoter
AT4G35930	F-BOX STRESS INDUCED 4 (FBS4)	F-box family prc 4_17018281	21.02	proximal promoter
AT4G00810	na	60S acidic ribos 4_347448	21	promoter
AT4G38900	na	Basic-leucine zi 4_18142087	20.99	promoter
AT4G03205	(hemf2)	hemf2; FUNCTI 4_1415642	20.96	intergenic
AT4G03210	XYLOGLUCAN ENDOTRANSGLUCOSYL		20.96	promoter
AT3G46100	HISTIDYL-TRNA SYNTHETASE 1 (HRS1)		20.93	proximal promoter
AT3G46110	na	LOCATED IN: p 3_16933212	20.93	exon
AT1G32920	na	unknown proteir 1_11927935	20.9	proximal promoter
AT1G68670	na	myb-like transcr 1_25781274	20.73	proximal promoter
AT1G20490	na	AMP-dependen 1_7099928	20.71	promoter
AT5G57660	CONSTANS-LIKE 5 (COL5)	CONSTANS-lik(5_23359534	20.68	intergenic
AT5G25210	na	unknown proteir 5_8725017	20.67	intron
AT2G45685	na	Potential natura 2_18820553	20.61	promoter
AT5G47640	NUCLEAR FACTOR Y, SUBUNIT B2 (NF-		20.61	promoter
AT2G45690	SHRUNKEN SEED 1 (SSE1)	Encodes a prote 2_18820553	20.61	intergenic
AT2G45680	TCP DOMAIN PROTEIN 9 (TCP9)	TCP family tran: 2_18820553	20.61	three_prime_UTR
AT3G06120	MUTE (MUTE)	Encodes a basi 3_1846311	20.6	promoter
AT4G35837	na	This gene encor 4_16983241	20.6	proximal promoter
AT4G35840	na	RING/U-box sui 4_16983241	20.6	intergenic
AT4G35850	na	Pentatricopeptic 4_16983241	20.6	promoter
AT3G17998	CONSERVED PEPTIDE UPSTREAM OPE		20.59	intergenic
AT3G18000	XIPOTL 1 (XPL1)	Arabidopsis thal 3_6158600	20.59	intergenic
AT2G43330	INOSITOL TRANSPORTER 1 (INT1)	Encodes a tono 2_18005027	20.58	intergenic

AT2G43340 AT3G54400	20	Drotoin of unkny 2 19005027	20.58	provimal promotor
	na na	Protein of unknc 2_18005027 Eukaryotic aspa 3_20143201	20.56	proximal promoter proximal promoter
AT3G52190	PHOSPHATE TRANSPORTER TRAFFIC		20.54	intergenic
AT3G52180	STARCH-EXCESS 4 (SEX4)	Encodes a plant 3_19353669	20.54	promoter
AT2G45400	(BEN1)	involved in the r 2 18706339	20.51	promoter
AT3G14205	na	Phosphoinositid 3_4723879	20.5	proximal promoter
AT1G62430	CDP-DIACYLGLYCEROL SYNTHASE 1 (0		20.48	intergenic
AT3G17860	JASMONATE-ZIM-DOMAIN PROTEIN 3 (20.48	promoter
AT1G62420	na	Protein of unknc 1_23105385	20.48	proximal promoter
AT3G19590	BUB (BUDDING UNINHIBITED BY BENZY		20.41	proximal promoter
AT3G19580	ZINC-FINGER PROTEIN 2 (ZF2)	Encodes zinc fir 3_6804799	20.41	proximal promoter
AT1G29395	COLD REGULATED 314 INNER MEMBRA		20.31	promoter
AT1G29400	MEI2-LIKE PROTEIN 5 (ML5)	A member of mt 1_10289670	20.31	intergenic
AT5G39860	PACLOBUTRAZOL RESISTANCE1 (PRE na	unknown proteir 5_9208290	20.3 20.2	promoter
AT5G26270 AT5G26280	na	TRAF-like family 5_9208290	20.2	downstream promoter
AT3G20280	na	Phototropic-resi 3_18502818	20.2	promoter
AT5G04830	na	Nuclear transpc 5 1401433	20.2	intergenic
AT5G04820	OVATE FAMILY PROTEIN 13 (OFP13)	ovate family pro 5_1401433	20.15	intergenic
AT5G19690	STAUROSPORIN AND TEMPERATURE S		20.15	promoter
AT5G51560	na	Leucine-rich reg 5_20943443	20.12	proximal promoter
AT5G07580	na	encodes a mem 5_2399460	20.09	promoter
AT1G13950	EUKARYOTIC ELONGATION FACTOR 5 A	Encodes eukary 1_4772861	20.08	proximal promoter
AT5G11740	ARABINOGALACTAN PROTEIN 15 (AGP		20.05	promoter
AT1G15570	CYCLIN A2;3 (CYCA2;3)	A2-type cyclin. I 1_5360627	20.05	proximal promoter
AT2G46420	na	Plant protein 15 2_19052291	20.04	proximal promoter
AT1G33590	na	Leucine-rich rer 1_12177655	19.96	promoter
AT1G33600	na	Leucine-rich rer 1_12177655	19.96	intergenic
AT1G55330 AT1G55325	ARABINOGALACTAN PROTEIN 21 (AGP:		19.88	intergenic
AT1G55325 AT5G53510	GRAND CENTRAL (GCT) OLIGOPEPTIDE TRANSPORTER 9 (OPT	Encodes the Ari 1_20648208	19.88 19.86	intron proximal promoter
AT1G76380	na	DNA-binding bri 1 28654702	19.81	promoter
AT5G16567	na	This gene encor 5_5420057	19.78	intergenic
AT4G27450	na	Aluminium induc 4 13729297	19.74	promoter
AT5G05410	DRE-BINDING PROTEIN 2A (DREB2A)	Encodes a trans 5_1601439	19.73	proximal promoter
AT5G05420	na	FKBP-like peptir 5_1601439	19.73	intergenic
AT2G23760	BEL1-LIKE HOMEODOMAIN 4 (BLH4)	Encodes a merr 2_10115649	19.72	proximal promoter
AT1G05630	INOSITOL-POLYPHOSPHATE 5-PHOSPH	Encodes an ino: 1_1681776	19.69	proximal promoter
AT5G61970	na	signal recognitic 5_24887160	19.69	proximal promoter
AT1G05620	URIDINE-RIBOHYDROLASE 2 (URH2)	Encodes a cyto: 1_1681776	19.69	downstream
AT2G36026	na	Ovate family prc 2_15128095	19.66	intergenic
AT2G36030	na	unknown proteir 2_15128095	19.66	promoter
AT1G63850	na	BTB/POZ doma 1_23696775	19.64	promoter
AT4G01060	CAPRICE-LIKE MYB3 (CPL3) CYTOKININ OXIDASE/DEHYDROGENAS	Encodes a Myb 4_460274	19.52 19.44	promoter
AT3G63440 AT3G63445	na	Potential natura 3 23426945	19.44	intergenic proximal promoter
AT3G63445	na	RNA-binding (R 3_23426945	19.44	three_prime_UTR
AT3G12200	NIMA-RELATED KINASE 7 (Nek7)	Encodes AtNek 3_3888544	19.42	exon
AT4G19170	NINE-CIS-EPOXYCAROTENOID DIOXYG		19.41	intergenic
AT1G20823	na	RING/U-box suj 1_7239307	19.33	exon
AT3G46450	na	SEC14 cytosolic 3_17095708	19.33	promoter
AT3G46460	UBIQUITIN-CONJUGATING ENZYME 13		19.33	downstream
AT1G16370	ORGANIC CATION/CARNITINE TRANSP	organic cation/c 1_5596553	19.3	promoter
AT3G13450	DARK INDUCIBLE 4 (DIN4)	branched chain 3_4384489	19.29	promoter
AT3G13460	EVOLUTIONARILY CONSERVED C-TERI	Physically intera 3_4384489	19.29	
				downstream
AT1G16500	na	unknown proteir 1_5638356	19.25	proximal promoter
AT2G26100	na	Galactosyltrans 2_11118357	19.25 19.2	proximal promoter promoter
AT2G26100 AT1G07890	na ASCORBATE PEROXIDASE 1 (APX1)	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107	19.25 19.2 19.19	proximal promoter promoter promoter
AT2G26100 AT1G07890 AT1G07885	na ASCORBATE PEROXIDASE 1 (APX1) na	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107	19.25 19.2 19.19 19.19	proximal promoter promoter promoter promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580	na ASCORBATE PEROXIDASE 1 (APX1) na na	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107 Plant protein 15 5_579254	19.25 19.2 19.19 19.19 19.18	proximal promoter promoter promoter promoter proximal promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1)	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402	19.25 19.2 19.19 19.19 19.18 19.17	proximal promoter promoter promoter promoter proximal promoter proximal promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750 AT1G70210	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1)	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410	19.25 19.2 19.19 19.19 19.18 19.17 19.17	proximal promoter promoter promoter proximal promoter proximal promoter three_prime_UTR
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750 AT1G70210 AT1G18670	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1)	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 unknown proteii 1_2437107 Plant protein 15 5_579254 beta-galactosici 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532	19.25 19.2 19.19 19.19 19.18 19.17 19.17	proximal promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750 AT1G70210	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410	19.25 19.2 19.19 19.19 19.18 19.17 19.17	proximal promoter promoter promoter proximal promoter proximal promoter three_prime_UTR
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750 AT1G70210 AT1G18670 AT1G18680	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.13	proximal promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic
AT2G26100 AT1G07880 AT1G07885 AT5G02580 AT3G13750 AT1G70210 AT1G18670 AT1G18680 AT4G00730 AT2G31080 AT5G60850	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4)	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteii 1_2437107 Plant proteiin 15_579254 beta-galactosick: 3_4510402 Encodes a 0-tyl 1_26442410 Encodes a cytil 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable elk 2_13231325 Encodes a zinc 5_24482527	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.13 19.09 19.09	proximal promoter promoter promoter promoter promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic intergenic intergenic
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750 AT1G70210 AT1G18670 AT1G18680 AT4G00730 AT2G31080 AT5G60850 AT5G60860	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f)	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable elt 2_13231325 Encodes a zinc 5_24482527 RAB GTPase ht 5_24482527	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09	proximal promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic intergenic proximal promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750 AT1G70210 AT1G18670 AT4G00730 AT2G31080 AT5G60850 AT5G60860 AT4G00720	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 unknown proteii 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc: 5_24482527 RAB GTPase h: 5_24482527 Encodes ASKth 4_299268	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.09	proximal promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic intergenic proximal promoter proximal promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750 AT1G70210 AT1G18680 AT4G00730 AT2G31080 AT5G60860 AT4G00720 AT1G12451	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK) na	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 Plant protein 1_2437107 Plant protein 15 5_579254 beta-galactosici 3_4510402 Encodes a 0-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc 5_24482527 RAB GTPase hr 5_24482527 Encodes ASKth 4_299268 unknown protein 1_4247123	19.25 19.2 19.19 19.19 19.18 19.17 19.13 19.13 19.09 19.09 19.09 19.09 19.09 19.09	proximal promoter promoter promoter promoter promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter
ATZG26100 AT1G07890 AT1G07885 AT5G02580 AT3G013750 AT1G70210 AT1G18680 AT3G00730 ATZG31080 ATZG31080 AT5G60850 AT4G00720 AT1G12451 AT1G12451	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK) na na	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a dycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable elt 2_13231325 Encodes a zinc 5_24482527 RAB GTPase ht 5_24482527 Encodes ASKth 4_299268 unknown proteir 1_4247123 Leucine-rich reg 1_4247123	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.09 19.09 19.08	proximal promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic intergenic proximal promoter proximal promoter proximal promoter promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G70210 AT1G70210 AT1G18680 AT4G00730 AT2G31080 AT5G60850 AT4G00720 AT1G12451 AT1G12450 AT1G12450 AT1G07630	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK: na POL-LIKE 5 (PLL5)	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Unknown proteii 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc: 5_24482527 Encodes a Zinc: 5_24482527 Encodes a SKKth 4_299268 unknown proteii 1_4247123 Encodes a proti 1_2351723	19.25 19.2 19.19 19.19 19.18 19.17 19.13 19.03 19.09 19.09 19.09 19.09 19.09 19.08 19.08 19.08	proximal promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic intergenic proximal promoter proximal promoter proximal promoter promoter downstream
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750 AT1G70210 AT1G18680 AT4G00730 AT2G31080 AT5G60860 AT5G60860 AT4G00720 AT1G12451 AT1G12460 AT1G7630 AT1G77630 AT1G77120	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK. na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338)	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Unknown proteii 1_2437107 Plant protein 15 5_579254 beta-galactosici 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc 5_24482527 RAB GTPase hi 5_24482527 RAB GTPase hi 5_24482527 Encodes ASKIh 4_299268 unknown proteii 1_4247123 Leucine-rich ret 1_4247123 Rucleic acid-bin 1_26983526	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.09 19.08 19.08 19.08	proximal promoter promoter promoter promoter promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream promoter
ATZGZ6100 AT1G07890 AT1G07885 AT5G02580 AT3G013750 AT1G70210 AT1G18680 AT3G00730 ATZG31080 ATZG31080 AT5G60850 AT4G00720 AT1G12451 AT1G12451 AT1G17240 AT1G07630 AT1G76140	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK) na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a d-vyl 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable elt 2_13231325 Encodes a zinc 5_24482527 RAB GTPase hr 5_24482527 Encodes ASKth 4_299268 unknown proteir 1_4247123 Leucine-rich reg 1_4247123 Encodes a prott 1_2351723 Nucleic acid-bin 1_26983526 Leucine-rich reg 1_21007982	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.09 19.08 19.08 19.01 19	proximal promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter downstream promoter promoter promoter promoter promoter promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G70210 AT1G70210 AT1G18680 AT4G00730 AT2G31080 AT5G60850 AT4G00720 AT1G12451 AT1G12451 AT1G12460 AT1G07630 AT1G56140 AT1G561440 AT1G56145	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK. na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Unknown proteii 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D+ly 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc: 5_24482527 Encodes a Zinc: 5_24482527 Encodes a SKth 4_299268 unknown proteii 1_4247123 Encodes a Grant 1_2427123 Encodes a protei 1_2351723 Nucleic acid-bin 1_26983526 Leucine-rich rer; 1_241007982 Leucine-rich rer; 1_21007982	19.25 19.2 19.19 19.19 19.18 19.17 19.13 19.09 19.09 19.09 19.09 19.09 19.09 19.08 19.08 19.01 19.08 19.01	proximal promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic intergenic proximal promoter proximal promoter proximal promoter downstream promoter downstream promoter promoter downstream downstream
ATZGZ6100 AT1G07890 AT1G07885 AT5G02580 AT3G013750 AT1G70210 AT1G18680 AT3G00730 ATZG31080 ATZG31080 AT5G60850 AT4G00720 AT1G12451 AT1G12451 AT1G17240 AT1G07630 AT1G76140	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK. na na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na na	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Unknown proteii 1_2437107 Plant protein 15 5_579254 beta-galactosici 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc 5_24482527 RAB GTPase hi 5_24482527 Encodes ASKth 4_299268 unknown proteii 1_4247123 Leucine-rich ret 1_4247123 Nucleic acid-bin 1_26983526 Leucine-rich ret 1_21007982 Leucine-rich ret 1_21007982 Kinesin motor fe 2_9140823	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.09 19.08 19.08 19.01 19	proximal promoter promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter downstream promoter downstream promoter downstream promoter downstream proximal promoter promoter downstream proximal promoter downstream proximal promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G13750 AT1G70210 AT1G18680 AT4G00730 AT4G00730 AT5G60860 AT5G60860 AT5G60860 AT4G00720 AT1G12461 AT1G12460 AT1G7630 AT1G7630 AT1G56146 AT1G56145 AT1G56145 AT1G261380	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK. na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Unknown proteii 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D+ly 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc: 5_24482527 Encodes a Zinc: 5_24482527 Encodes a SKth 4_299268 unknown proteii 1_4247123 Encodes a Grant 1_2427123 Encodes a protei 1_2351723 Nucleic acid-bin 1_26983526 Leucine-rich rer; 1_241007982 Leucine-rich rer; 1_21007982	19.25 19.2 19.19 19.19 19.18 19.17 19.13 19.09 19.09 19.09 19.09 19.08 19.08 19.08 19.01 19 19 18.98 18.98 18.98	proximal promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic intergenic proximal promoter proximal promoter proximal promoter downstream promoter downstream promoter promoter downstream downstream
ATZG26100 AT1G07890 AT1G07885 AT5G02580 AT3G03750 AT1G70210 AT1G18680 AT3G00730 ATZG31080 ATZG31080 ATZG60850 AT4G00720 AT1G12451 AT1G12460 AT1G07630 AT1G7630 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56148 ATZG21380	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK) na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na na XYLULOSE KINASE-1 (XK-1)	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 unknown proteir 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a 0-tyl 1_26442410 Encodes a 0-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable elt 2_13231325 Encodes a zinc 5_24482527 RAB GTPase hr 5_24482527 Encodes ASKth 4_299268 unknown proteir 1_4247123 Leucine-rich ret 1_24247123 Encodes a prott 1_2351723 Nucleic acid-bin 1_26983526 Leucine-rich ret 1_21007982 Leucine-rich ret 1_21007982 Leucine-rich ret 1_21007982 Kinesin motor fi 2_9140823 Although this ge 2_9140823	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.09 19.08 19.08 19.01 19 19 19.08 19.01 19 19 19 19 19 19 19 19 19 19 19 19 19	proximal promoter promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream promoter downstream promoter downstream proximal promoter promoter downstream proximal promoter proximal promoter proximal promoter proximal promoter
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ATZG26100 AT1G07890 AT1G07885 AT5G02580 AT3G013750 AT1G70210 AT1G18680 AT3G00730 ATZG31080 ATZG31080 ATZG31080 ATG60850 ATG60860 AT4G00720 AT1G12451 AT1G12461 AT1G12460 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56140 AT1G56145 AT2G21370 AT3G12300 AT1G180700 AT1G27370 AT3G14950 AT1G1580	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK: na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na na xYLULOSE KINASE-1 (XK-1) (BUG22) na SQUAMOSA PROMOTER BINDING PRO GOLGI ALPHA-MANNOSIDASE II (GMII) FERRIC REDUCTION OXIDASE 2 (FRO2	Galactosyltrans 2_11118357 Encodes a cytic 1_2437107 Unknown proteii 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a 0-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable elt 2_13231325 Encodes a zinc 5_24482527 RAB GTPase hr 5_24482527 Encodes ASKth 4_299268 unknown proteii 1_4247123 Leucine-rich ret 1_4247123 Rucelic acid-bin 1_26983526 Leucine-rich ret 1_21007982 Leucine-rich ret 1_21007982 Leucine-rich ret 1_21007982 Leucine-rich ret 1_21007982 Leucine-rich ret 1_33923475 unknown proteii 3_3923475 unknown proteii 1_30331759 In conjunction w 1_9507671 Encodes a golg 5_4841169 Encodes the lov 1_206958	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.08 19.08 19.01 19 18.98 18.98 18.96 18.93 18.93 18.87 18.84 18.84 18.81 18.78	proximal promoter promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream promoter promoter downstream promoter five_prime_UTR intron proximal promoter
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AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G70210 AT1G70210 AT1G18680 AT2G31080 AT2G31080 AT2G31080 AT2G31080 AT3G60850 AT4G00720 AT1G12451 AT1G12451 AT1G12460 AT1G07630 AT1G56140 AT1G56145 AT2G21380 AT3G21370 AT3G12300 AT3G12320 AT3G514950 AT1G27370 AT3G14950 AT1G27370 AT3G14950 AT1G3614950 AT4G36220 AT3G3614950 AT4G36220 AT3G04290 AT3G1580 AT4G36220 AT3G04290 AT3G161570 AT5G57700	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK. na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na na XYLULOSE KINASE-1 (XK-1) (BUG22) na SQUAMOSA PROMOTER BINDING PRO GOLGI ALPHA-MANNOSIDASE II (GMII) FERRIC REDUCTION OXIDASE 2 (FRO2 FERULIC ACID 5-HYDROXYLASE 1 (FAH LI-TOLERANT LIPASE 1 (LTL1) na	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Incodes a cyte: 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc: 5_24482527 Encodes a Zinc: 5_2482527 Encodes a Zinc: 5_24482527 Encodes zinc: 5_24482527 Encodes zinc: 5_24482527 Encodes zinc: 5_24482527 Encodes zinc: 5_244824169 Encodes zinc: 5_24824169 Encodes zinc: 5_244824169 Encodes zinc: 5_244824169 Encode	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.08 19.08 19.01 19 19.08 19.08 19.01 19.8 18.98 18.96 18.93 18.93 18.83 18.87 18.84 18.78 18.78 18.78 18.78	proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream promoter promoter downstream promoter pr
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G70210 AT1G18680 AT3G0730 AT2G31080 AT3G60850 AT5G60850 AT4G00720 AT1G12451 AT1G12460 AT1G07630 AT1G56145 AT2G21370 AT1G56145 AT2G21370 AT3G12300 AT3G12320	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK. na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na XYLULOSE KINASE-1 (XK-1) (BUG22) na na SQUAMOSA PROMOTER BINDING PRO GOLGI ALPHA-MANNOSIDASE II (GMII) FERRIC REDUCTION OXIDASE 2 (FRO2 FERULIC ACID 5-HYDROXYLASE 1 (FAPL LI-TOLERANT LIPASE 1 (LTL1) na na na	Galactosyltrans 2_11118357 Encodes a cyto: 1_2437107 Unknown proteii 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a 0-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable elt 2_13231325 Encodes a inc 5_24482527 RAB GTPase hi 5_24482527 Encodes ASKIth 4_299268 transposable elt 2_13231325 Encodes a protein 1_4247123 Leucine-rich ref 1_4247123 Leucine-rich ref 1_24247123 Leucine-rich ref 1_21007982 Leucine-rich ref 1_21007982 Leucine-rich ref 1_21007982 Leucine-rich ref 1_300313759 Leucine-rich ref 1_30331759 In conjunction w 1_9507671 Encodes a golg 5_4841169 Encodes the low 1_206958 encodes ferulat 4_17137647 Li-tolerant lipasi 3_1135649 FUNCTIONS IN 1_206958 BNR/Asp-box rs 5_23379053 Protein of unknt 1_4192387	19.25 19.2 19.19 19.19 19.18 19.17 19.13 19.09 19.09 19.09 19.08 19.08 19.08 19.01 19 18.98 18.98 18.96 18.93 18.87 18.87 18.87 18.78 18.78 18.78 18.78 18.78	proximal promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream proximal promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter promoter promoter promoter promoter five_prime_UTR intron proximal promoter exon intergenic intergenic
ATZG26100 AT1G07890 AT1G07885 AT5G02580 AT3G013750 AT1G18680 AT3G07070 AT1G18680 AT3G07030 ATZG31080 AT3G60850 AT3G00720 AT1G12451 AT1G12451 AT1G12460 AT1G07630 AT1G12451 AT1G12451 AT1G12461 AT1G56145 AT2G21380 AT3G12320 AT3G12320 AT3G12320 AT3G12300 AT3G12320 AT3G12300 AT3G12320 AT1G27370 AT3G12300 AT3G12300 AT3G12300 AT3G12300 AT1G1570 AT5G14950 AT1G1580 AT4G36220 AT1G01570 AT5G57700 AT5G57700 AT1G12320 AT1G12330	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK: na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na na xYLULOSE KINASE-1 (XK-1) (BUG22) na SQUAMOSA PROMOTER BINDING PRO GOLGI ALPHA-MANNOSIDASE II (GMII) FERRIC REDUCTION OXIDASE 2 (FRO2 FERULIC ACID 5-HYDROXYLASE 1 (FAH- LI-TOLERANT LIPASE 1 (LTL1) na na na na	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Incodes a cyte: 1_2437107 Plant protein 12 437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable elt 2_13231325 Encodes a sinc 5_24482527 RAB GTPase hr 5_24482527 Encodes ASKth 4_299268 unknown proteir 1_4247123 Leucine-rich ret 1_4247123 Leucine-rich ret 1_4247123 Rucleic acid-bin 1_26983526 Leucine-rich ret 1_21007982 Leucine-rich	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.08 19.08 19.01 19 18.98 18.98 18.96 18.96 18.93 18.87 18.84 18.87 18.78 18.78 18.78 18.78 18.78 18.78 18.78 18.72 18.71	proximal promoter promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream promoter promoter downstream promoter promoter downstream proximal promoter five_prime_UTR intron proximal promoter exon intergenic intergenic proximal promoter exon intergenic proximal promoter promote
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G70210 AT1G18680 AT3G0730 AT2G31080 AT3G60850 AT5G60850 AT4G00720 AT1G12451 AT1G12460 AT1G07630 AT1G56145 AT2G21370 AT1G56145 AT2G21370 AT3G12300 AT3G12320	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDINIG PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK. na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na na XYLULOSE KINASE-1 (XK-1) (BUG22) na SQUAMOSA PROMOTER BINDING PRO GOLGI ALPHA-MANNOSIDASE II (GMII) FERRIC REDUCTION OXIDASE 2 (FRO2 FERULIC ACID 5-HYDROXYLASE 1 (FAH LI-TOLERANT LIPASE 1 (LTL1) na na na na na na na na na	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Incodes a cyte: 1_2437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc: 5_24482527 Encodes a Zinc: 5_2482527 Encodes a Zinc: 5_24482527 Encodes a protein 1_2037822 Eucline-rich ret: 1_21007982 Leucine-rich ret: 1_21007982 Kinesin motor fr: 2_9140823 unknown proteir 3_3923475 unknown proteir 3_3923475 unknown proteir 3_3923475 unknown proteir 3_3923475 In conjunction w 1_9507671 Encodes a golg: 5_4841169 Encodes the low 1_206958 Encodes ferulat 4_17137647 Li-tolerant lipast: 3_1135649 Encodes ferulat 4_17137647 Li-tolerant lipast: 3_1135649 Encodes ferulat 4_17137647 Li-tolerant lipast: 3_1135649 ENCOMENTE SEAS379053 Protein of unkn: 1_4192387 unknown proteir 1_4192387 unknown proteir 1_4192387 Encodes a puta 3_22257260	19.25 19.2 19.19 19.19 19.18 19.17 19.13 19.09 19.09 19.09 19.08 19.08 19.08 19.01 19 18.98 18.98 18.96 18.93 18.87 18.87 18.87 18.78 18.78 18.78 18.78 18.78	proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream promoter prom
AT2G26100 AT1G07895 AT1G07885 AT3G02580 AT3G013750 AT1G18680 AT3G07070 AT1G18680 AT3G07030 AT2G31080 AT3G60850 AT3G60850 AT3G0720 AT1G12451 AT1G12461 AT1G26140 AT1G56140 AT1G13200 AT1G1580 AT3G12320 AT3G1250 AT1G1580 AT1G12320 AT1G12320 AT1G12320 AT1G12320	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK: na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na na xYLULOSE KINASE-1 (XK-1) (BUG22) na SQUAMOSA PROMOTER BINDING PRO GOLGI ALPHA-MANNOSIDASE II (GMII) FERRIC REDUCTION OXIDASE 2 (FRO2 FERULIC ACID 5-HYDROXYLASE 1 (FAH- LI-TOLERANT LIPASE 1 (LTL1) na na na na	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Incodes a cyte: 1_2437107 Plant protein 12 437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable elt 2_13231325 Encodes a sinc 5_24482527 RAB GTPase hr 5_24482527 Encodes ASKth 4_299268 unknown proteir 1_4247123 Leucine-rich ret 1_4247123 Leucine-rich ret 1_4247123 Rucleic acid-bin 1_26983526 Leucine-rich ret 1_21007982 Leucine-rich	19.25 19.25 19.19 19.19 19.18 19.17 19.13 19.13 19.09 19.09 19.09 19.08 18.98 18.98 18.98 18.98 18.98 18.98 18.98 18.98 18.98 18.93 18.87 18.87 18.78 18.77 18.71 18.71	proximal promoter promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream promoter promoter downstream promoter promoter downstream proximal promoter five_prime_UTR intron proximal promoter exon intergenic intergenic proximal promoter exon intergenic proximal promoter promote
AT2626100 AT1607890 AT1607885 AT5602580 AT3G13750 AT1G18670 AT1G18670 AT1G18680 AT3G60850 AT5G60850 AT5G60850 AT5G60860 AT4G00720 AT1G12451 AT1G12451 AT1G12460 AT1G67630 AT1G56140 AT1G56145 AT2G21380 AT2G21370 AT3G12300 AT1G27370 AT3G12300 AT1G27370 AT3G12300 AT1G27370 AT3G12300 AT1G157700 AT1G1580 AT1G13320 AT1G12320 AT1G12320 AT1G12330 AT1G63530	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDINIG PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK. na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na na XYLULOSE KINASE-1 (XK-1) (BUG22) na SQUAMOSA PROMOTER BINDING PRO GOLGI ALPHA-MANNOSIDASE II (GMII) FERRIC REDUCTION OXIDASE 2 (FRO2 FERULIC ACID 5-HYDROXYLASE 1 (FAHLI-TOLERANT LIPASE 1 (LTL1) na na na TOXICOS EN LEVADURA 4 (ATL4) FARNESYLATED PROTEIN 3 (FP3) PHOSPHOLIPASE A 24 (PLA2A) DSRNA-BINDING PROTEIN 5 (DRB5)	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Incodes a cyte: 1_2437107 Plant protein 12 437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc: 5_24482527 Encodes a Zinc: 5_24482527 Encodes a SKth 4_299268 unknown protein 1_4247123 Encodes a SKth 4_299268 unknown protein 1_26983526 Leucine-rich ret: 1_2427123 Encodes a protein 1_26983526 Leucine-rich ret: 1_21007982 Leucine-rich ret: 1_21007982 Kinesin motor f: 2_9140823 unknown protein 3_3923475 unknown protein 1_30331759 In conjunction w 1_9507671 Encodes a golg 5_4841169 Encodes ferulat 4_17137647 Li-tolerant lipast 3_1135649 Encodes ferulat 4_17137647 Li-tolerant lipast 3_1135649 Encodes a lipat 3_21257260 Farnesylated pr 5_25437058 Encodes a dout 5_16440205	19.25 19.2 19.19 19.19 19.18 19.17 19.13 19.09 19.09 19.09 19.09 19.08 19.08 19.01 19 18.98 18.98 18.96 18.93 18.87 18.87 18.87 18.78 18.78 18.78 18.78 18.78 18.78 18.71 18.71	proximal promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream promoter five_prime_UTR intron proximal promoter exon intergenic intergenic proximal promoter
AT2G26100 AT1G07890 AT1G07885 AT5G02580 AT3G013750 AT1G18680 AT3G07070 AT1G18680 AT3G60850 AT3G60850 AT3G60860 AT3G612461 AT1G56145 AT1G21380 AT3G12320 AT3G12320 AT3G12320 AT3G12300 AT3G12320 AT3G12300 AT3G12320 AT1G27370 AT5G14950 AT3G14950 AT3G15700 AT5G57700	na ASCORBATE PEROXIDASE 1 (APX1) na na BETA GALACTOSIDASE 1 (BGAL1) CYCLIN D1;1 (CYCD1;1) IMPAIRED IN BABA-INDUCED STERILITY na ANTHOCYANINLESS 2 (ANL2) na OBF BINDING PROTEIN 4 (OBP4) RAB GTPASE HOMOLOG A1F (RABA1f) SHAGGY-LIKE PROTEIN KINASE 32 (SK: na na POL-LIKE 5 (PLL5) PIGMENT DEFECTIVE 338 (PDE338) na na na CXYLULOSE KINASE-1 (XK-1) (BUG22) na na SQUAMOSA PROMOTER BINDING PRO GOLGI ALPHA-MANNOSIDASE II (GMII) FERRIC REDUCTION OXIDASE 2 (FRO2 FERULIC ACID 5-HYDROXYLASE 1 (FAHLI-TOLERANT LIPASE 1 (LTL1) na na na na 10XICOS EN LEVADURA 4 (ATL4) FARNESYLATED PROTEIN 3 (FP3) PHOSPHOLIPASE A 2A (PLA2A)	Galactosyltrans 2_11118357 Encodes a cyte: 1_2437107 Incodes a cyte: 1_2437107 Plant protein 12 437107 Plant protein 15 5_579254 beta-galactosid: 3_4510402 Encodes a D-tyl 1_26442410 Encodes a cycli 1_6431532 HNH endonucle 1_6431532 HNH endonucle 1_6431532 Encodes a hom 4_299268 transposable eli 2_13231325 Encodes a zinc: 5_24482527 Encodes a Zinc: 5_24482527 Encodes a SKth 4_299268 unknown protein 1_4247123 Encodes a SKth 4_299268 unknown protein 1_26983526 Leucine-rich ret: 1_2427123 Encodes a protein 1_26983526 Leucine-rich ret: 1_21007982 Leucine-rich ret: 1_21007982 Kinesin motor f: 2_9140823 unknown protein 3_3923475 unknown protein 1_30331759 In conjunction w 1_9507671 Encodes a golg 5_4841169 Encodes ferulat 4_17137647 Li-tolerant lipast 3_1135649 Encodes ferulat 4_17137647 Li-tolerant lipast 3_1135649 Encodes a lipat 3_21257260 Farnesylated pr 5_25437058 Encodes a dout 5_16440205	19.25 19.2 19.19 19.19 19.18 19.17 19.17 19.13 19.09 19.09 19.09 19.09 19.08 19.08 19.01 19 18.98 18.98 18.96 18.93 18.87 18.84 18.81 18.78 18.78 18.78 18.78 18.78 18.71 18.71 18.71 18.71 18.71 18.71	proximal promoter promoter promoter promoter promoter proximal promoter proximal promoter three_prime_UTR proximal promoter intergenic downstream intergenic proximal promoter proximal promoter proximal promoter promoter downstream promoter downstream promoter promoter downstream promoter five_prime_UTR intron proximal promoter exon intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic promoter

AT3G51140	na	Protein of unknc 3_18999651	18.64	three_prime_UTR
AT3G51150	na	ATP binding mic 3 18999651	18.64	proximal promoter
AT5G41071	na	This gene encor 5_16440205	18.64	exon
AT2G35930	PLANT U-BOX 23 (PUB23)	Encodes a cyto _l 2_15084762	18.64	promoter
AT1G30350	na	Pectin lyase-like 1_10713642	18.63	proximal promoter
AT5G54630 AT5G54640	na RESISTANT TO AGROBACTERIUM TRA	zinc finger prote 5_22195726	18.58 18.58	proximal promoter proximal promoter
AT4G00400	GLYCEROL-3-PHOSPHATE ACYLTRAN		18.57	intron
AT4G00413	na	pseudogene, sii 4_175763	18.57	intergenic
AT1G68400	na	leucine-rich rep 1_25649859	18.55	proximal promoter
AT1G68410	na	Protein phospha 1_25649859	18.55	downstream
AT5G47050	na	SBP (S-ribonuc 5_19106330	18.51	promoter
AT1G71040	LOW PHOSPHATE ROOT2 (LPR2)	Encodes LPR2. 1_26796482	18.5	intergenic
AT1G71030 AT5G01712	MYB-LIKE 2 (MYBL2) CONSERVED PEPTIDE UPSTREAM OPI	Encodes a puta 1_26796482	18.5 18.47	promoter
AT3G26530	na	transposable eli 3_9737590	18.47	proximal promoter proximal promoter
AT5G01720	na	RNI-like superfa 5_266777	18.47	three_prime_UTR
AT5G01710	na	methyltransfera: 5_266777	18.47	proximal promoter
AT5G01715	na	pseudogene, ar 5_266777	18.47	promoter
AT1G22640	MYB DOMAIN PROTEIN 3 (MYB3)	MYB-type trans 1_8010800	18.46	intergenic
AT4G15236	ATP-BINDING CASSETTE G43 (ABCG43	VQ motif-contail 1_29501814	18.45 18.45	proximal promoter
AT1G78410 AT1G20650	na ALTERED SEED GERMINATION 5 (ASG		18.43	proximal promoter promoter
AT3G14000	(ATBRXL2)	Belongs to five- 3_4634766	18.42	proximal promoter
AT1G61740	na	Sulfite exporter 1_22799452	18.35	intron
AT5G66310	na	ATP binding mic 5_26492411	18.35	proximal promoter
AT1G79370	CYTOCHROME P450, FAMILY 79, SUBF		18.33	proximal promoter
AT3G07370	CARBOXYL TERMINUS OF HSC70-INTE PLANT U-BOX 9 (PUB9)		18.29	intergenic
AT3G07360 AT5G02021	na	Encodes a prote 3_2357314 This gene encor 5_388960	18.29 18.26	intergenic promoter
AT5G02021	na	pre-tRNA; tRNA 5_388960	18.26	intergenic
AT5G02010	RHO GUANYL-NUCLEOTIDE EXCHANG		18.26	intergenic
AT5G02020	SALT INDUCED SERINE RICH (SIS)	Encodes a prote 5_388960	18.26	proximal promoter
AT3G60130	BETA GLUCOSIDASE 16 (BGLU16)	beta glucosidas 3_22209297	18.25	proximal promoter
AT3G48980	na	CONTAINS Inte 3_18155830	18.23	intron
AT2G43910 AT2G43920	HARMLESS TO OZONE LAYER 1 (HOL1 HARMLESS TO OZONE LAYER 2 (HOL2		18.22 18.22	proximal promoter intergenic
AT4G28290	na	unknown proteir 4_14013051	18.22	promoter
AT4G28300	na	Encodes a prote 4 14013051	18.22	proximal promoter
AT1G61910	na	pre-tRNA; tRNA 1_22885862	18.2	proximal promoter
AT1G61900	na	unknown proteir 1_22885862	18.2	proximal promoter
AT4G34170	na	Galactose oxida 4_16364642	18.2	intergenic
AT4G25630	FIBRILLARIN 2 (FIB2)	encodes a fibrill 4_13073216	18.19	proximal promoter
AT4G30340 AT2G18260	DIACYLGLYCEROL KINASE 7 (DGK7) SYNTAXIN OF PLANTS 112 (SYP112)	encodes a diac ₁ 4_14841500 member of SYP 2_7943894	18.18 18.17	promoter intergenic
AT4G16144	ASSOCIATED MOLECULE WITH THE SH		18.13	proximal promoter
AT4G16146	na	cAMP-regulatec 4_9142585	18.13	three_prime_UTR
AT2G48030	na	DNAse I-like su 2_19649083	18.13	intron
AT1G68020	(ATTPS6)	Encodes an enz 1_25496759	18.11	proximal promoter
AT2G03660	na	pre-tRNA; tRNA 2_1112428	18.11	intergenic
AT5G50090 AT2G28160	na FER-LIKE REGULATOR OF IRON UPTAI	unknown proteir 5_20369814	18.1 18.09	promoter proximal promoter
AT2G28150	na	FUNCTIONS IN 2_12002529	18.09	downstream
AT5G65660	na	hydroxyproline-i 5_26248106	18.07	proximal promoter
AT1G20010	TUBULIN BETA-5 CHAIN (TUB5)	beta tubulin 1_6939525	18.06	intron
AT3G53550	na	FBD-like domair 3_19855650	18.05	proximal promoter
AT1G66760	na	MATE efflux fan 1_24898774	18.01	intergenic
AT4G00370 AT4G18710	(ANTR2) BRASSINOSTEROID-INSENSITIVE 2 (BII	Encodes an ino 4_163602	18 18	intron promoter
AT4G18710 AT4G00360	CYTOCHROME P450, FAMILY 86, SUBF		18	intergenic
AT4G37740	GROWTH-REGULATING FACTOR 2 (GR		18	proximal promoter
AT1G12020	na	unknown proteir 1_4062482	18	three_prime_UTR
AT2G28070	ATP-BINDING CASSETTE G3 (ABCG3)	ABC-2 type tran 2_11955030	17.97	proximal promoter
AT1G35510	na	O-fucosyltransfe 1_13071197	17.93	five_prime_UTR
AT4G14050	na	Pentatricopeptic 4_8103467	17.89	downstream
AT4G14040 AT5G47380	SELENIUM-BINDING PROTEIN 2 (SBP2) na	Protein of unknc 5 19224871	17.89 17.83	proximal promoter promoter
AT2G46225	ABI-1-LIKE 1 (ABIL1)	Encodes a subl 2_18981492	17.82	promoter
AT2G46220	na	Uncharacterizec 2_18981492	17.82	intergenic
AT2G46210	SPHINGOID LCB DESATURASE 2 (SLD2		17.82	intergenic
AT1G75800	na	Pathogenesis-rc 1_28461421	17.81	intergenic
AT1G75810 AT1G75790	na SKLIE SIMILAD 19 (aka19)	unknown proteir 1_28461421 SKU5_similar 1; 1_28461421	17.81 17.81	promoter
AT3G16690	SKU5 SIMILAR 18 (sks18) (SWEET16)	Nodulin MtN3 fa 3 5686630	17.74	intergenic promoter
AT3G16700	na	Fumarylacetoac 3_5686630	17.74	proximal promoter
AT3G02570	MATERNAL EFFECT EMBRYO ARREST		17.72	promoter
AT3G02580	STEROL 1 (STE1)	Brassinosteroid 3_545745	17.72	proximal promoter
AT1G54390	INHIBITOR OF GROWTH 2 (ING2)	ING2 encodes a 1_20304128	17.69	intergenic
AT5G14430	na	S-adenosyl-L-m 5_4652145	17.69	proximal promoter
AT1G54385 AT5G14420	na RING DOMAIN LIGASE2 (RGLG2)	ARM repeat sur 1_20304128 Encodes RGLG 5_4652145	17.69 17.69	promoter proximal promoter
AT1G73470	na	unknown proteir 1 27627911	17.65	downstream
AT1G73480	na	alpha/beta-Hydr 1_27627911	17.65	proximal promoter
AT1G31650	RHO GUANYL-NUCLEOTIDE EXCHANG	l Encodes a merr 1_11329454	17.65	intron
AT1G66350	RGA-LIKE 1 (RGL1)	Negative regula 1_24743969	17.64	intergenic
AT5G05430	na	RNA-binding pri 5_1608507	17.58	proximal promoter
AT5G05435 AT5G05450	na na	Potential natura 5_1608507 P-loop containir 5_1608507	17.58 17.58	intergenic intergenic
AT5G05450 AT5G05440	PYRABACTIN RESISTANCE 1-LIKE 5 (P)		17.58	proximal promoter
AT1G16500	na	unknown proteir 1_5636564	17.55	proximal promoter
AT3G58080	na	unknown proteir 3_21510431	17.48	intron
AT2G32940	ARGONAUTE 6 (AGO6)	Encodes a nucl 2_13971782	17.47	downstream
AT2G32930	ZINC FINGER NUCLEASE 2 (ZFN2)	Encodes a zinc 2_13971782 A member of mc 5_24884752	17.47 17.45	proximal promoter
AT5G61960	MEI2-LIKE PROTEIN 1 (ML1)	/ member of fix 3_24004/32	17.40	promoter

AT1G58210	EMBRYO DEFECTIVE 1674 (EMB1674)	Encodes a merr 1_21553277	17.41	promoter
AT4G24150	GROWTH-REGULATING FACTOR 8 (GR	Growth regulatir 4_12536906	17.41	intron
AT5G65310	HOMEOBOX PROTEIN 5 (HB5)	Encodes a clast 5_26100618	17.41	intergenic
AT1G58200	MSCS-LIKE 3 (MSL3)	A member of M: 1_21553277	17.41	promoter
AT2G45980	ATG8-INTERACTING PROTEIN 1 (ATI1)		17.37	intergenic
AT2G45970	CYTOCHROME P450, FAMILY 86, SUBF		17.37	five_prime_UTR
AT2G45960	PLASMA MEMBRANE INTRINSIC PROTE		17.37	intergenic
AT2G45950	SKP1-LIKE 20 (SK20)	SKP1-like 20 (S 2_18914684	17.37	intergenic
AT3G23040 AT2G33180	na na	unknown proteir 3_8186832 unknown proteir 2_14065843	17.35 17.35	exon proximal promoter
AT5G43700	AUXIN INDUCIBLE 2-11 (ATAUX2-11)	Auxin inducible 5_17550077	17.33	promoter
AT5G43695	na	unknown proteir 5_17550077	17.33	intergenic
AT3G62980	TRANSPORT INHIBITOR RESPONSE 1 (17.33	promoter
AT3G05640	na	Protein phospha 3_1644438	17.32	proximal promoter
AT4G26400	na	RING/U-box su ₁ 4_13344694	17.31	downstream
AT2G41990	na	CONTAINS Inte 2_17527078	17.27	promoter
AT4G22010	SKU5 SIMILAR 4 (sks4)	SKU5 similar 4 4_11662556	17.26	proximal promoter
AT3G60400	na	Mitochondrial tra 3_22328139	17.25	proximal promoter
AT1G67410	na	Exostosin family 1_25256137	17.23	proximal promoter
AT1G67420	na	Zn-dependent e 1_25256137	17.23	intron
AT4G34710	ARGININE DECARBOXYLASE 2 (ADC2)	encodes a argin 4_16566053	17.19	intergenic
AT5G53400	BOBBER1 (BOB1)	Encodes BOBB 5_21663766	17.17 17.16	downstream
AT2G41820 AT2G31570	na GLUTATHIONE PEROXIDASE 2 (GPX2)	Leucine-rich reg 2_17446655 glutathione perc 2_13437953	17.16	promoter downstream
AT2G31570 AT2G31560	na	Protein of unknc 2_13437953	17.14	three_prime_UTR
AT4G39390	NUCLEOTIDE SUGAR TRANSPORTER-		17.12	downstream
AT1G10060	BRANCHED-CHAIN AMINO ACID TRANS		17.11	promoter
AT5G05370	na	Cytochrome b-c 5_1592113	17.1	promoter
AT5G05380	PRENYLATED RAB ACCEPTOR 1.B3 (PF		17.1	promoter
AT5G05200	na	Protein kinase s 5_1547283	17.09	promoter
AT5G05210	na	Surfeit locus prc 5_1547283	17.09	promoter
AT5G21090	na	Leucine-rich rer 5_7164144	17.08	promoter
AT5G22740	CELLULOSE SYNTHASE-LIKE A02 (CSL		17.06	intron
AT2G44660	na	ALG6, ALG8 gl ₃ 2_18423371	17.04	proximal promoter
AT5G61600	ETHYLENE RESPONSE FACTOR 104 (E		17.02	intergenic
AT5G61590	na	encodes a mem 5_24764159	17.02	intergenic
AT5G61580	PHOSPHOFRUCTOKINASE 4 (PFK4)	phosphofructoki 5_24764159	17.02	downstream
AT3G07350 AT1G80290	na	Protein of unkno 3_2348978	17.01	downstream
AT1G80290 AT1G01260	na na	a member of the 1_30188280 basic helix-loop 1_108239	17.01 17	promoter proximal promoter
AT1G01260 AT1G28440	HAESA-LIKE 1 (HSL1)	HAESA-like 1 (F1 10001675	16.99	intergenic
AT1G28447	na	Pseudogene of 1_10001675	16.99	proximal promoter
AT5G45100	BOI-RELATED GENE 1 (BRG1)	Encodes one of 5_18215847	16.92	proximal promoter
AT3G19540	na	Protein of unknc 3_6783542	16.92	intergenic
AT1G60190	PLANT U-BOX 19 (PUB19)	Encodes PUB1! 1_22200334	16.91	exon
AT1G22330	na	RNA-binding (R 1_7888922	16.9	intron
AT5G19380	CRT (CHLOROQUINE-RESISTANCE TRA	Encodes one of 5_6531542	16.89	proximal promoter
AT5G19390	na	Encodes a prote 5_6531542	16.89	five_prime_UTR
AT1G21060	na	Protein of unknc 1_7370620	16.88	proximal promoter
AT4G05320	POLYUBIQUITIN 10 (UBQ10)	One of five poly 4_2718056	16.85	promoter
AT5G22940	FRA8 HOMOLOG (F8H)	Homolog of FR/ 5_7678938	16.84	three_prime_UTR
AT4G37330	CYTOCHROME P450, FAMILY 81, SUBFA FASCICLIN-LIKE ARABINOGALACTAN P		16.81 16.8	intron
AT3G11700 AT5G40470	na	RNI-like superfa 5 16207152	16.78	proximal promoter intergenic
AT2G47060	PTO-INTERACTING 1-4 (PTI1-4)	Encodes Pto-int 2_19336371	16.76	proximal promoter
AT2G47000	SQUAMOSA PROMOTER BINDING PRO		16.7	promoter
AT2G35920	na	RNA helicase fa 2_15081204	16.69	intergenic
AT2G35930	PLANT U-BOX 23 (PUB23)	Encodes a cyto _l 2_15081204	16.69	intergenic
AT3G59900	AUXIN-REGULATED GENE INVOLVED IN		16.67	proximal promoter
AT4G18205	na	Nucleotide-suga 4_10078435	16.67	intergenic
AT4G18220	na	Drug/metabolite 4_10078435	16.67	promoter
AT4G18210	PURINE PERMEASE 10 (PUP10)	Member of a far 4_10078435	16.67	intergenic
AT5G66580	na	unknown proteir 5_26572366	16.65	promoter
AT5G66590	na	CAP (Cysteine- 5_26572366	16.65	proximal promoter
AT5G66600 AT3G60520	na na	Protein of unkno 5_26572366	16.65	intergenic proximal promoter
AT5G67250	na SKP1/ASK1-INTERACTING PROTEIN 2 (unknown proteir 3_22363532	16.64 16.62	proximal promoter promoter
AT1G67890	na	PAS domain-co 1_25464402	16.61	intergenic
AT1G67900	na	Phototropic-resi 1_25464402	16.61	promoter
AT3G24670	na	Pectin lyase-like 3_9007802	16.59	intron
AT1G19330	na	unknown proteir 1_6683678	16.54	promoter
AT1G19340	na	Methyltransfera: 1_6683678	16.54	proximal promoter
AT3G02120	na	hydroxyproline-ı 3_375803	16.54	proximal promoter
AT3G02110	SERINE CARBOXYPEPTIDASE-LIKE 25 (16.54	proximal promoter
AT3G54820	PLASMA MEMBRANE INTRINSIC PROTE		16.48	intron
AT3G18490	ASPARTIC PROTEASE IN GUARD CELL		16.47	five_prime_UTR
AT3G30775	EARLY RESPONSIVE TO DEHYDRATION		16.47	proximal promoter
AT4G27520 AT4G27510	EARLY NODULIN-LIKE PROTEIN 2 (ENO na	unknown proteir 4_13749433	16.46 16.46	intergenic promoter
AT4G27510 AT5G55120	VITAMIN C DEFECTIVE 5 (VTC5)	Encodes a GDF 5_22369071	16.45	promoter
AT4G16490	na	ARM repeat sur 4_9295851	16.43	promoter
AT1G22400	(UGT85A1)	UGT85A1; FUN 1_7904996	16.42	intron
AT3G16240	DELTA TONOPLAST INTEGRAL PROTEI		16.42	proximal promoter
AT4G01950	GLYCEROL-3-PHOSPHATE ACYLTRANS		16.42	intron
AT4G01940	NFU DOMAIN PROTEIN 1 (NFU1)	Encodes a prote 4_845627	16.42	proximal promoter
AT3G16250	PHOTOSYNTHETIC NDH SUBCOMPLEX		16.42	intergenic
AT1G22380	UDP-GLUCOSYL TRANSFERASE 85A3 (16.42	proximal promoter
AT1G20340	DNA-DAMAGE-REPAIR/TOLERATION PR		16.41	intergenic
AT1G20330			16.41	intergenic
AT4000040	STEROL METHYLTRANSFERASE 2 (SM			promotor
AT1G32640	STEROL METHYLTRANSFERASE 2 (SM (MYC2)	Encodes a MYC 1_11801052	16.39	promoter
AT1G32630	STEROL METHYLTRANSFERASE 2 (SM (MYC2) na	Encodes a MYC 1_11801052 unknown proteir 1_11801052	16.39 16.39	intergenic
AT1G32630 AT2G45600	STEROL METHYLTRANSFERASE 2 (SM (MYC2) na na	Encodes a MYC 1_11801052 unknown proteir 1_11801052 alpha/beta-Hydr 2_18790584	16.39 16.39 16.35	intergenic exon
AT1G32630	STEROL METHYLTRANSFERASE 2 (SM (MYC2) na	Encodes a MYC 1_11801052 unknown proteir 1_11801052	16.39 16.39	intergenic

AT2G44200	na	CBF1-interactin 2_18278511	16.35	three_prime_UTR
AT1G72180	na	Leucine-rich rec 1_27160200	16.34	proximal promoter
AT5G05140	na	Transcription el 5_1523018	16.33	intergenic
AT1G01115	na	unknown proteir 1_55538	16.33	proximal promoter
AT3G51010	na	unknown proteir 3_18948299	16.3	promoter
AT4G25490	C-REPEAT/DRE BINDING FACTOR 1 (CE		16.29	proximal promoter
AT1G30370	DAD1-LIKE ACYLHYDROLASE (DLAH)	Encodes a mito 1_10715617	16.28	intergenic
AT1G30360	EARLY-RESPONSIVE TO DEHYDRATION		16.28	promoter
AT1G22570	na	Major facilitator 1_7975302	16.27	intergenic
AT3G62070	na	unknown proteir 3_22985465	16.24	proximal promoter
AT3G62080	na	SNF7 family prc 3_22985465	16.24	proximal promoter
AT5G67310	CYTOCHROME P450, FAMILY 81, SUBFA		16.23	intergenic
AT5G67300	MYB DOMAIN PROTEIN R1 (MYBR1)	Member of the F 5_26853797	16.23	promoter
AT4G27740	na	Yippee family pt 4_13838808	16.22	promoter
AT2G01670	NUDIX HYDROLASE HOMOLOG 17 (NUI OLIGOPEPTIDE TRANSPORTER 1 (OPT		16.22 16.22	proximal promoter
AT4G27730 AT2G23170	(GH3.3)		16.22	proximal promoter
AT2G23170 AT2G23171	na	encodes an IAA 2_9866788 unknown proteir 2_9866788	16.21	promoter exon
AT3G57400	na na	unknown proteir 3_21237026	16.17	proximal promoter
AT3G19540	na	Protein of unknc 3_6780464	16.17	promoter
AT2G35880	na	TPX2 (targeting 2_15066338	16.15	promoter
AT2G21660	GLYCINE-RICH RNA-BINDING PROTEIN		16.14	promoter
AT2G21670	na	pre-tRNA; tRNA 2_9266542	16.14	intergenic
AT4G34250	3-KETOACYL-COA SYNTHASE 16 (KCS1		16.13	promoter
AT4G34240	ALDEHYDE DEHYDROGENASE 3I1 (ALD		16.13	intergenic
AT3G01830	na	Calcium-binding 3_295660	16.12	promoter
AT3G01820	na	P-loop containir 3_295660	16.12	promoter
AT4G36250	ALDEHYDE DEHYDROGENASE 3F1 (ALI		16.09	promoter
AT4G36240	GATA TRANSCRIPTION FACTOR 7 (GAT	Encodes a merr 4_17150706	16.09	proximal promoter
AT4G36245	na	pre-tRNA; tRNA 4_17150706	16.09	intergenic
AT5G24530	DOWNY MILDEW RESISTANT 6 (DMR6)	Encodes a puta 5_8376521	16.08	proximal promoter
AT4G39400	BRASSINOSTEROID INSENSITIVE 1 (BR	Encodes a plasi 4_18322715	16.04	proximal promoter
AT3G57450	na	unknown proteir 3_21261339	16.04	proximal promoter
AT3G57460	na	catalytics;metal 3_21261339	16.04	intergenic
AT5G59540	na	2-oxoglutarate (5_23999864	16.03	proximal promoter
AT2G42840	PROTODERMAL FACTOR 1 (PDF1)	Encodes a puta 2_17825836	16.03	intergenic
AT5G59550	RING AND DOMAIN OF UNKNOWN FUN		16.03	promoter
AT5G59560	SENSITIVITY TO RED LIGHT REDUCED		16.03	intergenic
AT3G26932	DSRNA-BINDING PROTEIN 3 (DRB3)	dsRNA-binding 3_9930200	16.02	downstream
AT2G27385	na	Pollen Ole e 1 a 2_11717439	16.02	promoter
AT2G41550	na	Rho termination 2_17331371	16.02	promoter
AT3G07450	na	Bifunctional inhi 3_2388687	16.02	intergenic
AT3G07460	na	Protein of unknc 3_2388687	16.02	proximal promoter
AT3G07470	na	Protein of unknr 3_2388687 2Fe-2S ferredo 3_2388687	16.02	promoter
AT3G07480 AT3G26934	na na	unknown proteir 3_9930200	16.02 16.02	promoter
AT1G21390	EMBRYO DEFECTIVE 2170 (emb2170)	embryo defectiv 1 7488922	16.02	proximal promoter downstream
AT1G21380	na	Target of Myb p 1_7488922	16.01	promoter
AT2G22800	(HAT9)	Encodes homec 2_9702847	15.97	intergenic
AT3G15850	FATTY ACID DESATURASE 5 (FAD5)	Chloroplastic er 3_5358834	15.96	promoter
AT3G15840	POST-ILLUMINATION CHLOROPHYLL FI		15.96	promoter
AT1G05010	ETHYLENE-FORMING ENZYME (EFE)	Encodes 1-amir 1_1434694	15.95	proximal promoter
AT1G05020	na	ENTH/ANTH/VI 1_1434694	15.95	intergenic
AT2G01570	REPRESSOR OF GA1-3 1 (RGA1)	Member of the \ 2 259132	15.93	proximal promoter
AT5G44030	CELLULOSE SYNTHASE A4 (CEŚA4)	Encodes a cellu 5_17711801	15.91	proximal promoter
AT5G44020	na	HAD superfamil 5_17711801	15.91	proximal promoter
AT4G29190	OXIDATION-RELATED ZINC FINGER 2 (0	Zinc finger C-x8 4_14396889	15.91	intergenic
AT1G53830	PECTIN METHYLESTERASE 2 (PME2)	encodes a pecti 1_20097025	15.9	proximal promoter
AT5G49760	na	Leucine-rich rer 5_20216325	15.89	promoter
AT1G53170	ETHYLENE RESPONSE FACTOR 8 (ERF		15.87	intergenic
AT1G15750	TOPLESS (TPL)	Encodes a prote 1_5421457	15.86	promoter
AT4G05060	na	PapD-like super 4_2589394	15.82	intergenic
AT4G05049	na	unknown pseud 4_2589394	15.82	intergenic
AT4G05053	na	pseudogene of 4_2589394	15.82	promoter
AT5G52250	REPRESSOR OF UV-B PHOTOMORPHO	Encodes a trant 5_21216059	15.82	proximal promoter
AT4G05050	UBIQUITIN 11 (UBQ11)	not unbiquitie 4 0500004		
		polyubiquitin gel 4_2589394	15.82	promoter
AT5G11050	MYB DOMAIN PROTEIN 64 (MYB64)	Member of R2R 5_3505416	15.82 15.79	promoter intergenic
AT4G18975	MYB DOMAIN PROTEIN 64 (MYB64) na	Member of R2R 5_3505416 Pentatricopeptic 4_10390937	15.82 15.79 15.76	promoter intergenic intergenic
AT4G18975 AT4G18970	MYB DOMAIN PROTEIN 64 (MYB64) na na	Member of R2R 5_3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937	15.82 15.79 15.76 15.76	promoter intergenic intergenic intron
AT4G18975 AT4G18970 AT3G24630	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34)	Member of R2R 5_3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229	15.82 15.79 15.76 15.76 15.76	promoter intergenic intergenic intron proximal promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na	Member of R2R 5_3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257	15.82 15.79 15.76 15.76 15.76 15.75	promoter intergenic intergenic intron proximal promoter proximal promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na	Member of R2R 5_3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362	15.82 15.79 15.76 15.76 15.76 15.75 15.74	promoter intergenic intergenic intron proximal promoter proximal promoter proximal promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109	15.82 15.79 15.76 15.76 15.76 15.75 15.74 15.7	promoter intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na	Member of R2R 5_3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like cha 5_19302109 RING/U-box su 5_19302109	15.82 15.79 15.76 15.76 15.76 15.75 15.74 15.7	promoter intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610 AT5G47620	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipax 4_10390937 unknown proteir 3, 8886229 Zinc finger (C31 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RNA-binding (R 5_19302109	15.82 15.79 15.76 15.76 15.76 15.75 15.74 15.7 15.7	promoter intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610 AT5G47610 AT1G76110	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like cha 5_19302109 RING/U-box su 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035	15.82 15.79 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.7	promoter intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter downstream intergenic
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610 AT5G47620	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na	Member of R2R 5_3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035	15.82 15.79 15.76 15.76 15.76 15.75 15.74 15.7 15.7	promoter intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47610 AT5G47610 AT5G47620 AT1G76110 AT1G76100	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na na PLASTOCYANIN 1 (PETE1)	Member of R2R 5_3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035	15.82 15.79 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.7 15.69	promoter intergenic intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream intergenic intergenic
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610 AT5G47621 AT1G76110 AT1G76100 AT3G02550	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na na pa PLASTOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipax 4_10390937 unknown proteir 3, 8886229 Zinc finger (C31 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 LOB domain-co 3_538416	15.82 15.79 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.7 15.69 15.69	promoter intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intergenic intergenic promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610 AT1G76110 AT1G76110 AT1G76100 AT3G02550 AT3G48450	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na na na pLASTOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like cha 5_19302109 RING/U-box su 5_19302109 RING/U-box su 5_19302109 HMG (high mob 1_28553035) One of two Arat 1_28553035 One of two Arat 1_28553036 LOB domain-co 3_538416 RPM1-interactir 3_17947112	15.82 15.76 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.69 15.69 15.68	promoter intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intergenic intergenic promoter proximal promoter proximal promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47620 AT1G76110 AT1G76100 AT3G022550 AT3G48450 AT1G01840	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na PLASTOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na na	Member of R2R 5_3505416 Pentatricopeptic 4.10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 LOB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737	15.82 15.79 15.76 15.76 15.76 15.75 15.7 15.7 15.7 15.7 15.69 15.69 15.68 15.68	promoter intergenic intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter promoter downstream intergenic intergenic promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610 AT5G47610 AT1G76110 AT1G76100 AT3G02550 AT3G48450 AT1G01840 AT1G01830	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na PLASTOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na na na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035) One of two Arat 1_28553035 One of two Arat 1_28553035 One of two Arat 1_302737 ARM repeat su; 1_302737 Encodes a mem 3_538416	15.82 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.69 15.68 15.68 15.68 15.68	promoter intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream intergenic intergenic promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47600 AT1G76110 AT1G76110 AT1G76110 AT1G76100 AT3G02550 AT3G48450 AT1G01840 AT1G01840 AT3G02540	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na na na na na nb PLASTOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipax 4_10390937 unknown proteir 3, 8986229 Zinc finger (C31 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RNA-binding (R 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 LOB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737 ARM repeat sup 1_302737 Encodes a merr 3_538416 In conjunction w 1_9501581 This gene encoi 3_18860690	15.82 15.76 15.76 15.76 15.76 15.75 15.75 15.7 15.7 15.7 15.69 15.69 15.68 15.68 15.68 15.68	promoter intergenic intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter downstream intergenic intergenic promoter proximal promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47600 AT1G76110 AT1G76110 AT1G76100 AT3G02550 AT3G48450 AT1G01840 AT1G01830 AT3G02540 AT1G27360 AT1G27360 AT1G14910	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na RADIATION SENSITIVE23C (RAD23C) SQUAMOSA PROMOTER-LIKE 11 (SPL1 na na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 One of two Arat 1_28553035 CDB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737 Encodes a merr 3_538416 In conjunction w 1_9501581 This qene encoi 3_18960690 ENTH/ANTH/V+ 1_5147996	15.82 15.76 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.69 15.68 15.68 15.68 15.68 15.68 15.68 15.68	promoter intergenic intergenic intergenic interopenic intron proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream intergenic intergenic promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intron intergenic intergenic intergenic intergenic
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610 AT1G76110 AT1G76100 AT3G48450 AT1G01840 AT1G01840 AT1G01830 AT3G02540 AT1G27360 AT3G51057 AT1G14910 AT2G46535	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na RADIATION SENSITIVE23C (RAD23C) SQUAMOSA PROMOTER-LIKE 11 (SPL1 na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 One of two Arat 1_28553035 CDB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737 ARM repeat suj 1_302737 ARM repeat suj 1_302737 ARM gene encor 3_18960690 ENTH/ANTH/V1 1_5147996 unknown proteir 1_219109229	15.82 15.76 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.69 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.68	promoter intergenic intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream intergenic intergenic promoter proximal promoter proximal promoter proximal promoter proximal promoter intron intergenic intergenic intergenic intergenic promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47610 AT5G47610 AT5G47610 AT3G02550 AT3G48450 AT1G01840 AT1G01840 AT1G01840 AT1G01840 AT1G01840 AT1G1840 AT1G1840 AT1G1840 AT1G1840 AT3G02540 AT3G51057 AT1G14910 AT2G46535 AT5G45950	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na PLASTOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na na RADIATION SENSITIVE23C (RAD23C) SQUAMOSA PROMOTER-LIKE 11 (SPL1 na na na na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipax 4_10390937 unknown proteir 3, 8986229 Zinc finger (C31 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RNA-binding (R 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 LOB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737 ARM repeat sup 1_302737 Encodes a merr 3_538416 In conjunction w 1_9501581 This gene encor 3_18860690 ENTH/ANTH/VF 1_5147996 unknown proteir 2_19109229 GDSL-like Lipas 5_18853521	15.82 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.69 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.65 15.65 15.65 15.65 15.55 15.68	promoter intergenic intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intergenic intergenic promoter proximal promoter proximal promoter proximal promoter intron intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic intron
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT5G47600 AT5G47600 AT5G47600 AT3G476110 AT1G76110 AT1G76110 AT1G76100 AT3G02550 AT1G01840 AT1G01840 AT1G01830 AT3G02540 AT1G27360 AT3G51057 AT1G14910 AT2G46535 AT3G45950 AT3G452380	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na RADIATION SENSITIVE23C (RAD23C) SQUAMOSA PROMOTER-LIKE 11 (SPL1 na na na na TIME FOR COFFEE (TIC)	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chal 5_19302109 RING/U-box suj 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 One of two Arat 1_28553035 CDB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737 Encodes a merr 3_538416 In conjunction w 1_9501581 This gene enco: 3_18960690 ENTH/ANTH/V+ 1_5147996 unknown proteir 2_19109229 GDSL-like Lipas 5_18635321 Encodes a nucl 3_7911306	15.82 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.7 15.69 15.68 15.68 15.68 15.68 15.68 15.68 15.55 15.55 15.55	promoter intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream intergenic intergenic promoter proximal promoter proximal promoter proximal promoter proximal promoter intron intergenic intergenic intergenic intergenic promoter intron proximal promoter
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610 AT1G76110 AT1G76110 AT3G92550 AT3G48450 AT1G01840 AT1G01840 AT1G27360 AT3G51057 AT1G14910 AT2G46535 AT5G45950 AT3G22380 AT3G22380 AT3G22380 AT3G2380	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na na PLASTOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na na na na na na na TOMAIN SENSITIVE23C (RAD23C) SQUAMOSA PROMOTER-LIKE 11 (SPL1 na na na TIME FOR COFFEE (TIC) CYCLIN D3;1 (CYCD3;1)	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RING/U-box suj 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 One of two Arat 1_28553035 CDB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737 ARM repeat suj 1_302737 ARM repeat suj 1_302737 Encodes a mem 3_538416 In conjunction w 1_9501581 This gene encoi 3_18860690 ENTH/ANTH/W 1_5147996 unknown proteir 2_19109229 GDSL-like Lipas 5_18635321 Encodes a nucl 3_7911306 encodes a cyclii 4_16361687	15.82 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.69 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.55 15.51 15.55 15.51	promoter intergenic intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intergenic intergenic intergenic promoter proximal promoter proximal promoter proximal promoter intron intergenic intergenic intergenic intergenic intron proximal promoter intron proximal promoter intron proximal promoter intron proximal promoter intergenic intergenic
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47610 AT5G47610 AT3G47610 AT3G02550 AT3G48450 AT1G01840 AT1G01840 AT1G01840 AT1G27360 AT3G51057 AT1G14910 AT2G46535 AT5G45950 AT3G22380 AT3G22380 AT3G22380 AT3G22380	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na PLASTOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na na RADIATION SENSITIVE23C (RAD23C) SQUAMOSA PROMOTER-LIKE 11 (SPL1 na na na TIME FOR COFFEE (TIC) CYCLIN D3:1 (CYCD3:1) ASYMMETRIC LEAVES 2-LIKE 15 (ASL15	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipax 4_10390937 unknown proteir 3, 8986229 Zinc finger (C31 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RNA-binding (R 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 LOB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737 ARM repeat sup 1_302737 Encodes a merr 3_538416 In conjunction w 1_9501581 This gene encoi 3_18860690 ENTH/ANTH/VF 1_5147996 Unknown proteir 2_19109229 GDSL-like Lipax 5_18635321 Encodes a nucli 3_7911306 encodes a nucli 3_7911306 encodes a nucli 3_7911306	15.82 15.79 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.69 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.65 15.65 15.65 15.65 15.51 15.51 15.51 15.51 15.51 15.51	promoter intergenic intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intergenic intergenic promoter proximal promoter proximal promoter proximal promoter intron intergenic intergenic intergenic promoter intron intergenic intergenic promoter intron proximal promoter intron intergenic intergenic intergenic intergenic intergenic intergenic
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT5G47600 AT5G47600 AT5G47610 AT1G76110 AT1G76110 AT1G76100 AT3G02550 AT1G01840 AT1G01840 AT1G01830 AT3G02540 AT1G27360 AT3G51057 AT1G14910 AT2G46535 AT5G45950 AT3G22380 AT3G22380 AT3G22380 AT3G242440 AT5G60210	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na RADIATIOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na na RADIATION SENSITIVE23C (RAD23C) SQUAMOSA PROMOTER-LIKE 11 (SPL1 na na na TIME FOR COFFEE (TIC) CYCLIN D3;1 (CYCD3;1) ASYMMETRIC LEAVES 2-LIKE 15 (ASL18 ROP INTERACTIVE PARTNER 5 (RIP5)	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipax 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chal 5_19302109 RING/U-box sul 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 One of two Arat 1_28553035 CDB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737 Encodes a merr 3_538416 In conjunction w 1_9501581 This gene encol 3_18960690 ENTH/ANTH/V+ 1_5147996 unknown proteir 2_19109229 GDSL-like Lipax 5_18635321 Encodes a nucl 3_7911306 encodes a cyclir 4_16361687 Lateral organ bx 2_17667909 ROP interactive 5_24245984	15.82 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.69 15.68 15.62 15.65 15.	promoter intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter intron intergenic intergenic intergenic intergenic intergenic promoter intron proximal promoter intergenic intron proximal promoter intergenic
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT1G02060 AT5G47600 AT5G47610 AT1G76110 AT1G76110 AT3G92550 AT3G48450 AT1G01840 AT1G01840 AT1G27360 AT3G51057 AT1G14910 AT2G46535 AT5G45950 AT3G22380 AT3G22380 AT3G22380 AT3G22380 AT3G24040 AT1G3660210 AT1G76580	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na na na na na na na PLASTOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na na na na na TOMAIN TOMAIN TOMAIN TOMAIN TOMAIN TOMAIN NA NA TOMAIN TOMAIN TOMAIN TOMAIN TOMAIN NA NA TIME FOR COFFEE (TIC) CYCLIN D3;1 (CYCD3;1) ASYMMETRIC LEAVES 2-LIKE 15 (ASL15 ROP INTERACTIVE PARTNER 5 (RIP5) na	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipas 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chaj 5_19302109 RING/U-box suj 5_19302109 RING/U-box suj 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 One of two Arat 1_28553035 One of two Arat 1_302737 ARM repeat suj 1_302737 ARM repeat suj 1_302737 Encodes a mem 3_538416 In conjunction w 1_9501581 This gene encol 3_18960690 ENTH/ANTH/W 1_5147996 unknown proteir 2_19109229 GDSL-like Lipas 5_18635321 Encodes a nucl 3_7911306 encodes a cyclii 4_16361687 Lateral organ bx 2_17667990 ROP interactive 5_24245984 Squamosa pron 1_28738993	15.82 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.69 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.68 15.65 15.55 15.51 15.55 15.51 15.55 15.51 15.55 15.51 15.55 15.54 15.55 15.55 15.55 15.55 15.55 15.55 15.55 15.55 15.55 15.55 15.55 15.56 15.56 15.55 15.	promoter intergenic intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter downstream intergenic intergenic promoter proximal promoter proximal promoter proximal promoter intron intergenic intergenic intergenic intergenic intergenic intron proximal promoter intron proximal promoter intron proximal promoter intergenic promoter intergenic promoter downstream
AT4G18975 AT4G18970 AT3G24630 AT5G60710 AT5G47600 AT5G47600 AT5G47600 AT3G476110 AT1G76110 AT1G76110 AT3G02550 AT3G984850 AT1G01830 AT3G02540 AT1G27360 AT3G51057 AT1G14910 AT2G46535 AT5G45950 AT3G22380 AT3G22380 AT3G22380 AT3G22380 AT3G242440 AT5G60210	MYB DOMAIN PROTEIN 64 (MYB64) na na TON1 RECRUITING MOTIF 34 (TRM34) na RADIATIOCYANIN 1 (PETE1) LOB DOMAIN-CONTAINING PROTEIN 41 na na RADIATION SENSITIVE23C (RAD23C) SQUAMOSA PROMOTER-LIKE 11 (SPL1 na na na TIME FOR COFFEE (TIC) CYCLIN D3;1 (CYCD3;1) ASYMMETRIC LEAVES 2-LIKE 15 (ASL18 ROP INTERACTIVE PARTNER 5 (RIP5)	Member of R2R 5, 3505416 Pentatricopeptic 4_10390937 GDSL-like Lipax 4_10390937 unknown proteir 3_8986229 Zinc finger (C3+ 5_24417257 Tetratricopeptid 1_364362 HSP20-like chal 5_19302109 RING/U-box sul 5_19302109 RNA-binding (R 5_19302109 HMG (high mob 1_28553035 One of two Arat 1_28553035 One of two Arat 1_28553035 CDB domain-co 3_538416 RPM1-interactir 3_17947112 unknown proteir 1_302737 Encodes a merr 3_538416 In conjunction w 1_9501581 This gene encol 3_18960690 ENTH/ANTH/V+ 1_5147996 unknown proteir 2_19109229 GDSL-like Lipax 5_18635321 Encodes a nucl 3_7911306 encodes a cyclir 4_16361687 Lateral organ bx 2_17667909 ROP interactive 5_24245984	15.82 15.76 15.76 15.76 15.75 15.74 15.7 15.7 15.7 15.69 15.68 15.62 15.65 15.	promoter intergenic intergenic intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter intron intergenic intergenic intergenic intergenic intergenic promoter intron proximal promoter intergenic intron proximal promoter intergenic

AT40	G29700	na	Alkaline-phosph 4_14545927	15.42	proximal promoter
AT10	G31930	EXTRA-LARGE GTP-BINDING PROTEIN		15.41	downstream
	G31805	na	WRKY family tra 4_15385295	15.41	five_prime_UTR
	G11270	na	F-box and asso 1_3776150	15.41	intergenic
	G31935	na	other RNA 1_11469371	15.41	promoter
	G19806	na	transposable eli 2_8544726	15.41	proximal promoter
	G31940	na	unknown proteir 1_11469371	15.41	intergenic
	G11260	SUGAR TRANSPORTER 1 (STP1)	Encodes a H+/r 1_3776150	15.41	proximal promoter
	G31800 G01430	WRKY DNA-BINDING PROTEIN 18 (WRK TRICHOME BIREFRINGENCE-LIKE 25 (T		15.41 15.4	intergenic downstream
	G01430	UDP-GLUCOSYL TRANSFERASE 72B3 (15.4	proximal promoter
	G18690	na	unknown proteir 2_8097204	15.39	promoter
	G59940	na	Galactose oxida 3 22141792	15.37	proximal promoter
	G59930	na	Encodes a defe 3 22141792	15.37	proximal promoter
	G59950	na	Peptidase family 3 22141792	15.37	intergenic
	G75640	na	Leucine-rich rec 1_28406088	15.36	exon
AT30	G29320	ALPHA-GLUCAN PHOSPHORYLASE 1 (F	Encodes a plast 3_11252683	15.35	promoter
AT40	G24660	HOMEOBOX PROTEIN 22 (HB22)	homeobox prote 4_12727198	15.35	proximal promoter
AT20	G32150	na	Haloacid dehalc 2_13658293	15.35	proximal promoter
	G24670	TRYPTOPHAN AMINOTRANSFERASE R		15.35	intergenic
	G69270	RECEPTOR-LIKE PROTEIN KINASE 1 (R		15.34	promoter
	G19530	na	Encodes a TIR- 4_10649584	15.32	proximal promoter
	G66300	na	F-box/RNI-like/F 1_24720820	15.31	proximal promoter
	G14310	na	Transducin/WD 4_8240613	15.3	promoter
	G54740	na	Protein of unknr 3_20261949	15.28	promoter
	G42950	na	GYF domain-co 5_17224051	15.28	promoter
	G47610 G12120	na (SEC1B)	transcription rec 3_17551357 member of KEU 4 7256183	15.27 15.25	three_prime_UTR intergenic
	G21320	na	BEST Arabidop: 3_7502053	15.25	promoter
	G12115	na	pre-tRNA; tRNA 4_7256183	15.25	promoter
	G12110	STEROL-4ALPHA-METHYL OXIDASE 1-1		15.25	three_prime_UTR
	G23740	na	unknown proteir 3_8551408	15.22	intergenic
	G62988	na	This gene encor 3_23281755	15.22	downstream
	G23730	XYLOGLUCAN ENDOTRANSGLUCOSYL		15.22	downstream
	G12290	na	Amino acid deh 3_3919326	15.21	promoter
AT30	G12280	RETINOBLASTOMA-RELATED 1 (RBR1)	Encodes a retin 3_3919326	15.21	promoter
AT40	G21570	na	Protein of unknc 4_11472935	15.19	five_prime_UTR
AT40	G21560	VACUOLAR PROTEIN SORTING-ASSOC	vacuolar proteir 4_11472935	15.19	proximal promoter
AT40	G03113	na	unknown proteir 4_1382629	15.17	three_prime_UTR
AT40	G03115	na	Mitochondrial st 4_1382629	15.17	three_prime_UTR
AT40	G27270	na	Quinone reduct: 4_13658749	15.16	intergenic
	G38370	na	Plant protein of 2_16074282	15.16	promoter
	G51940	na	unknown proteir 3_19276602	15.16	proximal promoter
	G51950	na	Zinc finger (CC(3_19276602	15.16	intergenic
	G22886	MICRORNA167A (MIR167A)	Encodes a micr 3_8104535	15.15	intergenic
	G18370	DEGP PROTEASE 5 (DEG5)	Encodes DEG5 4_10148862	15.09	promoter
	G18360 G01500	na CARBONIC ANHYDRASE 1 (CA1)	Aldolase-type T 4_10148862 Encodes a puta 3_193593	15.09 15.08	promoter intergenic
	G01490	na	Protein kinase s 3_193593	15.08	promoter
	G54040	EPITHIOSPECIFIER PROTEIN (ESP)	Epithiospecifier 1_20177102	15.06	intergenic
	G49500	na	unknown proteir 1_18323497	15.06	proximal promoter
	G11060	KNOTTED1-LIKE HOMEOBOX GENE 4 (F		15.05	proximal promoter
	G54280	MYOSIN 2 (ATM2)	Type VII myosin 5_22046983	15.05	proximal promoter
AT10	G78040	na	Pollen Ole e 1 a 1 29345709	15.04	promoter
AT10	G78050	PHOSPHOGLYCERATE/BISPHOSPHOG	phosphoglycera 1_29345709	15.04	proximal promoter
AT30	G18490	ASPARTIC PROTEASE IN GUARD CELL	Encodes ASPG 3_6346325	15.03	intergenic
AT40	G14440	3-HYDROXYACYL-COA DEHYDRATASE		15.01	promoter
AT20	G46660	CYTOCHROME P450, FAMILY 78, SUBFA		15.01	exon
	G17890	DA1-RELATED PROTEIN 4 (DAR4)	Encodes a prote 5_5915055	15.01	proximal promoter
	G50060	MYB DOMAIN PROTEIN 77 (MYB77)	Encodes a merr 3_18559324	15.01	promoter
	G65305	na	pre-tRNA; tRNA 5_26096647	15	intergenic
	G43680	IQ-DOMAIN 14 (IQD14)	IQ-domain 14 (I 2_18107242	14.99	proximal promoter
	G23755	na	unknown proteir 2_10105268	14.99	proximal promoter
	G59052	CONSERVED PEPTIDE UPSTREAM OPE		14.98	intergenic
	G17380 G59068	JASMONATE-ZIM-DOMAIN PROTEIN 5 (na	Potential natura 3_21830520	14.98 14.98	proximal promoter proximal promoter
	G59070	na	Cytochrome b5(3_21830520	14.98	intergenic
	G59060	PHYTOCHROME INTERACTING FACTOR		14.98	promoter
	G59050	POLYAMINE OXIDASE 3 (PAO3)	Encodes a poly; 3_21830520	14.98	intergenic
	G32010	HSI2-LIKE 1 (HSL1)	HSI2-like 1 (HSI 4_15485990	14.95	intergenic
	G32020	na	unknown proteir 4_15485990	14.95	proximal promoter
	G01290	COFACTOR OF NITRATE REDUCTASE /	COFACTOR OF 1_118660	14.94	intergenic
	G01300	na	Eukaryotic aspa 1_118660	14.94	three_prime_UTR
	G28056	MICRORNA172A (MIR172A)	Encodes a micr 2_11947551	14.93	intergenic
	G34760	na	SAUR-like auxir 4_16583049	14.92	promoter
	G63150	MIRO-RELATED GTP-ASE 2 (MIRO2)	Encodes a calci 3_23332837	14.91	five_prime_UTR
	G22760	na	basic helix-loop 2_9677081	14.91	proximal promoter
	G61910	NAC DOMAIN PROTEIN 66 (NAC066)	NAC transcriptic 3_22929421	14.9	exon
	G27960	EVOLUTIONARILY CONSERVED C-TERI GLYCOSYLPHOSPHATIDYLINOSITOL-AI		14.89 14.89	intergenic proximal promoter
	G27950 G78170	na	unknown proteir 1 29413435	14.89	proximal promoter
	G78170	na	unknown proteir 1_29413435	14.88	proximal promoter
	G16830	TOPLESS-RELATED 2 (TPR2)	TOPLESS-relati 3_5731143	14.88	promoter
	G10572	ABERRANT PEROXISOME MORPHOLOG		14.85	promoter
	G10572	CYTOCHROME P450, FAMILY 77, SUBF		14.85	downstream
	G20830	na	transferases;foli 2_8971456	14.84	proximal promoter
	G20835	na	unknown proteir 2_8971456	14.84	promoter
	G64380	na	encodes a mem 1_23893680	14.83	proximal promoter
	G51805	na	Leucine-rich rer 1_19225888	14.78	promoter
	G37250	na	Leucine-rich rer 4_17530374	14.77	five_prime_UTR
	G30330	AUXIN RESPONSE FACTOR 6 (ARF6)	Encodes a merr 1_10693199	14.76	proximal promoter
	G28340	GATA TRANSCRIPTION FACTOR 13 (GA		14.75	intergenic
	G67420	LOB DOMAIN-CONTAINING PROTEIN 37		14.73	intergenic
ATT	G04150	na	C2 calcium/lipid 1_1084701	14.72	promoter

AT3G57800	na	basic helix-loop 3_21408549	14.72	intron
AT3G57810	na	Cysteine proteir 3_21408549	14.72	intergenic
AT1G25450	3-KETOACYL-COA SYNTHASE 5 (KCS5)		14.71	downstream
AT3G22104	na	Phototropic-resi 3_7788106	14.71 14.71	proximal promoter
AT5G58620 AT5G19090	na na	zinc finger (CCC 5_23691946 Heavy metal tra 5_6393378	14.71	proximal promoter intergenic
AT1G79060	na	unknown proteir 1_29741417	14.66	promoter
AT1G79070	na	SNARE-associa 1_29741417	14.66	intergenic
AT1G24170	(LGT9)	Encodes a prote 1_8559044	14.65	promoter
AT3G60164	na	Pseudogene of 3_22231830	14.65	downstream
AT3G60170	na	transposable el 3_22231830	14.65	proximal promoter
AT5G62100	BCL-2-ASSOCIATED ATHANOGENE 2 (E		14.63	proximal promoter
AT5G62090 AT2G02540	SEUSS-LIKE 2 (SLK2) HOMEOBOX PROTEIN 21 (HB21)	SEUSS-like 2 (\$ 5_24939425 Zinc finger hom 2_686050	14.63 14.62	promoter intergenic
AT2G02540	na	PIN domain-like 2 686050	14.62	proximal promoter
AT5G51790	na	basic helix-loop 5 21038189	14.61	proximal promoter
AT5G49170	na	unknown proteir 5_19938811	14.6	three_prime_UTR
AT5G55920	OLIGOCELLULA 2 (OLI2)	Encodes a hom 5_22651216	14.58	proximal promoter
AT2G14080	na	Disease resista 2_5925127	14.57	promoter
AT3G58620	TETRATRICOPETIDE-REPEAT THIORED		14.57	proximal promoter
AT3G05210	(ERCC1)	encodes a hom 3_1479254	14.56	promoter
AT3G05200 AT1G25425	ARABIDOPSIS TOXICOS EN LEVADURA CLAVATA3/ESR-RELATED 43 (CLE43)	CLAVATA3/ESF 1_8924294	14.56 14.54	intergenic intergenic
AT4G18830	OVATE FAMILY PROTEIN 5 (OFP5)	Member of the (4_10337186	14.52	promoter
AT5G65700	BARELY ANY MERISTEM 1 (BAM1)	Encodes a CLA 5_26285617	14.51	downstream
AT2G41870	na	Remorin family 2_17473205	14.51	promoter
AT1G76180	EARLY RESPONSE TO DEHYDRATION		14.5	downstream
AT1G11330	na	S-locus lectin pr 1_3810165	14.5	intron
AT1G76170	na	2-thiocytidine tR 1_28586550	14.5	promoter
AT2G46270	G-BOX BINDING FACTOR 3 (GBF3)	encodes a bZIP 2_18998832	14.49	proximal promoter
AT2G46260	LIGHT-RESPONSE BTB 1 (LRB1)	Involvement in r 2_18998832	14.49 14.48	downstream
AT5G64780 AT5G64770	ROOT MERISTEM GROWTH FACTOR 9	Uncharacterise 5_25898291	14.48	intergenic promoter
AT1G06200	na	Peptidase S24/: 1_1897000	14.46	promoter
AT1G05136	na	unknown proteir 1_1479033	14.46	exon
AT1G05135	na	pseudogene of 1_1479033	14.46	promoter
AT1G79150	na	binding; FUNCT 1_29778309	14.45	promoter
AT1G79160	na	unknown proteir 1_29778309	14.45	intergenic
AT5G59790	na	CONTAINS Inte 5_24089417	14.44	proximal promoter
AT5G66730	INDETERMINATE DOMAIN 1 (IDD1)	C2H2-like zinc f 5_26646187	14.43	proximal promoter
AT5G66740	na	Protein of unknc 5_26646187	14.43	proximal promoter
AT4G17680 AT1G46264	na	SBP (S-ribonucl 4_9839987	14.42 14.41	intergenic
AT1G46264 AT1G75570	HEAT SHOCK TRANSCRIPTION FACTOR	pre-tRNA; tRNA 1_28374904	14.41	intergenic proximal promoter
AT5G14640	SHAGGY-LIKE KINASE 13 (SK13)	shaggy-like kina 5_4722415	14.4	promoter
AT5G25220	KNOTTED1-LIKE HOMEOBOX GENE 3 (F		14.39	intergenic
AT3G28910	MYB DOMAIN PROTEIN 30 (MYB30)	transcription fac 3_10908827	14.39	proximal promoter
AT5G02960	na	Ribosomal prote 5_694809	14.39	promoter
AT5G02970	na	alpha/beta-Hydr 5_694809	14.39	promoter
AT2G32010	CVP2 LIKE 1 (CVL1)	Encodes an ino: 2_13628302	14.38	intron
AT5G67270	END BINDING PROTEIN 1C (EB1C)	encodes a hom 5_26846322	14.38	intergenic
AT5G62670 AT5G13760	H(+)-ATPASE 11 (HA11) na	H(+)-ATPase 115_25158765 Plasma-membra 5_4441771	14.38 14.38	promoter promoter
AT1G06000	na	encodes a flavo 1 1820250	14.38	downstream
AT1G06002	na	Potential natura 1_1820250	14.38	proximal promoter
AT1G06010	na	unknown proteir 1_1820250	14.38	proximal promoter
AT5G67290	na	FAD-dependent 5_26846322	14.38	intergenic
AT5G67280	RECEPTOR-LIKE KINASE (RLK)	receptor-like kin 5_26846322	14.38	proximal promoter
AT5G13750	ZINC INDUCED FACILITATOR-LIKE 1 (ZI		14.38	downstream
AT3G52870 AT4G37640	na	IQ calmodulin-b 3_19598734 Encodes a calm 4 17687756	14.37 14.36	proximal promoter
AT5G06390	CALCIUM ATPASE 2 (ACA2) FASCICLIN-LIKE ARABINOGALACTAN P		14.36	proximal promoter promoter
AT1G78600	LIGHT-REGULATED ZINC FINGER PROT		14.35	promoter
AT1G78590	NAD(H) KINASE 3 (NADK3)	Encodes a NAD 1_29566883	14.35	intergenic
AT4G16970	na	Protein kinase s 4_9556685	14.33	proximal promoter
AT4G16980	na	arabinogalactar 4_9556685	14.33	promoter
AT4G36710	(HAM4)	GRAS family tra 4_17304751	14.32	proximal promoter
AT2G26250	3-KETOACYL-COA SYNTHASE 10 (KCS1		14.32	promoter
AT5G11700 AT1G15800	na na	BEST Arabidop: 5_3771629 unknown proteir 1_5442307	14.32	promoter
AT1G15800 AT1G15810	na	S15/NS1, RNA- 1_5442307	14.32 14.32	intron proximal promoter
AT1G01490	na	Heavy metal tra 1 182401	14.3	promoter
AT1G72680	CINNAMYL-ALCOHOL DEHYDROGENAS		14.29	downstream
AT1G72670	IQ-DOMAIN 8 (iqd8)	IQ-domain 8 (iq: 1_27359021	14.29	promoter
AT1G18075	MICRORNA159B (MIR159B)	Encodes a micr 1_6219522	14.29	proximal promoter
AT3G03210	na	unknown proteir 3_740590	14.28	promoter
AT3G60220	TOXICOS EN LEVADURA 4 (ATL4)	Encodes a puta 3_22255983	14.28	five_prime_UTR
AT2G33509 AT2G33510	na na	unknown proteir 2_14193948 unknown proteir 2_14193948	14.27 14.27	exon promoter
AT4G20930	na	6-phosphoglucc 4_11201327	14.27	promoter
AT2G41540	(GPDHC1)	Encodes a prote 2_17325939	14.26	promoter
AT5G19095	na	pre-tRNA; tRNA 5_6395226	14.26	intergenic
AT2G41530	S-FORMYLGLUTATHIONE HYDROLASE		14.26	promoter
AT5G25280	na	serine-rich prot∈ 5_8773613	14.22	promoter
AT5G25290	na (TIE)(T)	CONTAINS Inte 5_8773613	14.22	intergenic
AT1G70700	(TIFY7)	JAZ9 is a protei 1_26657725	14.21	intergenic
AT1G70710 AT5G15310	GLYCOSYL HYDROLASE 9B1 (GH9B1) MYB DOMAIN PROTEIN 16 (MYB16)	endo-1,4-beta-g 1_26657725 Member of the F 5_4973055	14.21 14.2	intergenic proximal promoter
AT1G16515	na	unknown proteir 1_5648174	14.2	proximal promoter promoter
AT1G16520	na	unknown proteir 1_5648174	14.19	proximal promoter
AT1G30020	na	Protein of unknc 1_10517713	14.18	proximal promoter
AT4G16500	na	Cystatin/monelli 4_9302113	14.16	promoter
AT4G16510 AT3G05230	na	YbaK/aminoacy 4_9302113	14.16	proximal promoter
	na	Signal peptidas: 3_1490556	14.16	proximal promoter

ATACOFAAO	20	Hanny motel tro 2, 1400EE6	14.16	oven
AT3G05220 AT5G67260	na CVCLIN D3:3 (CVCD3:3)	Heavy metal tra 3_1490556 Encode CYCD3 5_26835706	14.16 14.13	exon
AT1G18710	CYCLIN D3;2 (CYCD3;2) MYB DOMAIN PROTEIN 47 (MYB47)	Member of the F 1_6453618	14.13	promoter intergenic
AT1G10710 AT1G10410	na	Protein of unknr 1_3421346	14.13	proximal promoter
AT3G06160	na	AP2/B3-like trar 3_1864375	14.12	intron
AT3G07390	AUXIN-INDUCED IN ROOT CULTURES 1		14.1	five_prime_UTR
AT3G07400	na	lipase class 3 fa 3 2365387	14.1	proximal promoter
AT3G50750	BES1/BZR1 HOMOLOG 1 (BEH1)	BES1/BZR1 hor 3_18863746	14.07	proximal promoter
AT3G50751	na	This gene encor 3_18863746	14.07	exon
AT5G45100	BOI-RELATED GENE 1 (BRG1)	Encodes one of 5_18213962	14.06	intergenic
AT3G46560	(TIM9)	Encodes a smal 3_17138011	14.05	proximal promoter
AT5G20190	na	Tetratricopeptid 5_6813567	14.05	proximal promoter
AT5G49525	na	unknown proteir 5_20098792	14.05	proximal promoter
AT3G46540	na	ENTH/VHS fam 3_17138011	14.05	proximal promoter
AT1G75180	na	Erythronate-4-p 1_28216969	14.05	intron
AT1G75190	na	unknown proteir 1_28216969	14.05	proximal promoter
AT1G75200	na	flavodoxin famil 1_28216969	14.05	intergenic
AT5G67070 AT3G46550	RALF-LIKE 34 (RALFL34)	Member of a div 5_26767936 Isolated in a scr 3_17138011	14.05 14.05	promoter
AT5G46550 AT5G19730	SALT OVERLY SENSITIVE 5 (SOS5) na	Pectin lyase-like 5_6669254	14.03	promoter proximal promoter
AT5G19730	na	This gene encor 5_6669254	14.03	intergenic
AT1G01550	BYPASS 1 (BPS1)	Encodes a prote 1_199595	14.02	promoter
AT2G45830	DOWNSTREAM TARGET OF AGL15 2 (D		14.02	exon
AT1G01560	MAP KINASE 11 (MPK11)	member of MAF 1_199595	14.02	proximal promoter
AT1G01540	na	Protein kinase s 1_199595	14.02	intergenic
AT2G33040	GAMMA SUBUNIT OF MT ATP SYNTHAS	gamma subunit 2_14021687	14.01	proximal promoter
AT2G33050	RECEPTOR LIKE PROTEIN 26 (RLP26)	receptor like prc 2_14021687	14.01	promoter
AT3G48360	BTB AND TAZ DOMAIN PROTEIN 2 (bt2)	encodes a prot∈ 3_17911785	14	proximal promoter
AT3G48350	CYSTEINE ENDOPEPTIDASE 3 (CEP3)	Cysteine proteir 3_17911785	14	intergenic
AT3G23085	na	transposable eli 3_8213567	13.99	proximal promoter
AT3G24490	na	Alcohol dehydrc 3_8908670	13.99	proximal promoter
AT2G44920	na (a) (Ta)	Tetratricopeptid 2_18523541	13.98	proximal promoter
AT5G04220	(SYTC)	SYTC; FUNCTI 5_1159523	13.97	proximal promoter
AT5G46720	na (ATTODA)	AIG2-like (avirul 5_18958099	13.97	proximal promoter
AT5G51460	(ATTPPA)	homologous to 15_20900531	13.95	promoter
AT3G08130	(BIM1) APR-LIKE 5 (APRL5)	Arabidopsis thal 5_2609196 Encodes a prote 3 995114	13.95 13.94	intron
AT3G03860 AT3G03870	na	unknown proteir 3 995114	13.94	intergenic promoter
AT3G03870	MYB DOMAIN PROTEIN 106 (MYB106)	Encodes a MIX 3 49819	13.94	proximal promoter
AT3G52060	na	Core-2/I-branch 3_19312503	13.93	promoter
AT3G52070	na	unknown proteir 3_19312503	13.93	promoter
AT3G52072	na	Potential natura 3_19312503	13.93	downstream
AT5G27345	na	transposable eli 5_9645281	13.93	proximal promoter
AT1G14280	PHYTOCHROME KINASE SUBSTRATE 2		13.93	intergenic
AT3G01150	POLYPYRIMIDINE TRACT-BINDING PRO		13.93	proximal promoter
AT3G23727	SCR-LIKE 12 (SCRL12)	Encodes a merr 3_8546934	13.93	intergenic
AT1G14290	SPHINGOID BASE HYDROXYLASE 2 (SE	Encodes one of 1_4879554	13.93	intergenic
AT5G63810	BETA-GALACTOSIDASE 10 (BGAL10)	member of Glyc 5_25536127	13.92	proximal promoter
AT5G63800	MUCILAGE-MODIFIED 2 (MUM2)	Involved in muc 5_25536127	13.92	intergenic
AT2G46970	PHYTOCHROME INTERACTING FACTOR		13.92	proximal promoter
AT5G23260	TRANSPARENT TESTA16 (TT16)	Encodes a MAE 5_7833431	13.89	proximal promoter
AT4G24240	WRKY DNA-BINDING PROTEIN 7 (WRK)		13.88	three_prime_UTR
AT1G25570	na	Di-glucose bind 1_8996335	13.87	proximal promoter
AT5G12040	na	Nitrilase/cyanide 5_3888629	13.86	intergenic
AT5G12043 AT5G12050	na na	This gene encor 5_3888629 unknown proteir 5_3888629	13.86 13.86	downstream proximal promoter
AT4G23190	CYSTEINE-RICH RLK (RECEPTOR-LIKE		13.85	promoter
AT4G23190	na	Unknown gene 4_12143941	13.85	intergenic
AT1G28281	na	unknown proteir 1_9887651	13.84	exon
AT1G28280	na	VQ motif-contail 1 9887651	13.84	promoter
AT4G28230	na	unknown proteir 4_13998495	13.84	proximal promoter
AT4G28240	na	Wound-respons 4_13998495	13.84	promoter
AT2G18780	na	F-box and asso 2_8139645	13.83	proximal promoter
AT3G27210	na	unknown proteir 3_10047464	13.83	promoter
AT2G18790	PHYTOCHROME B (PHYB)	Red/far-red pho 2_8139645	13.83	promoter
AT3G02468	CONSERVED PEPTIDE UPSTREAM OPE		13.82	promoter
AT3G02460	na	Ypt/Rab-GAP d 3_508613	13.82	downstream
AT3G03702	na S-ADENOSYLMETHIONINE DECARBOX	Potential natura 3_915608	13.82 13.82	intergenic
AT3G02470	UNFERTILIZED EMBRYO SAC 7 (UNE7)			promoter
AT3G03690 AT5G07180	ERECTA-LIKE 2 (ERL2)	Encodes a rece 5 2233879	13.82 13.81	proximal promoter promoter
AT4G38470	SERINE/THREONINE/TYROSINE KINASE		13.81	proximal promoter
AT1G18890	CALCIUM-DEPENDENT PROTEIN KINAS		13.79	proximal promoter
AT1G18900	na	Pentatricopeptic 1_6528507	13.79	promoter
AT1G77410	BETA-GALACTOSIDASE 16 (BGAL16)	beta-galactosida 1 29093541	13.78	promoter
AT1G66200	GLUTAMINE SYNTHASE CLONE F11 (G		13.78	intergenic
AT1G77420	na	alpha/beta-Hydr 1_29093541	13.78	five_prime_UTR
AT1G66190	na	unknown proteir 1_24654082	13.78	promoter
AT1G75700	HVA22-LIKE PROTEIN G (HVA22G)	HVA22-like prot 1_28425785	13.77	intergenic
AT4G35100	PLASMA MEMBRANE INTRINSIC PROTE		13.77	intergenic
AT4G03965	na	RING/U-box suj 4_1890262	13.76	three_prime_UTR
AT4G03960	PLANT AND FUNGI ATYPICAL DUAL-SP		13.76	intergenic
AT1G74448	na	unknown proteir 1_27982242	13.75	exon
AT1G74450	na na	FUNCTIONS IN 1_27982242	13.75 13.75	promoter
AT1G74453 AT1G74456	na na	snoRNA; snoRN 1_27982242 snoRNA; snoRN 1_27982242	13.75	intergenic intergenic
AT1G74436 AT5G54930	na	AT hook motif-c 5 22309630	13.75	proximal promoter
AT5G54940	na	Translation initia 5_22309630	13.75	promoter
AT5G54950	na	Aconitase family 5_22309630	13.75	downstream
AT4G25650	ACD1-LIKE (ACD1-LIKE)	Similar to ACD1 4_13080518	13.73	intergenic
AT4G25640		Encodes a multi 4_13080518	13.73	proximal promoter
	DETOXII TINO ELLEGA OMINICIEN OU (DI			
AT3G13790	(ATBFRUCT1)	Encodes a prote 3_4532432	13.71	intergenic
AT4G37790	(ATBFRUCT1) (HAT22)	Encodes a prote 3_4532432 Encodes homec 4_17770783	13.71	intergenic
	(ATBFRUCT1)	Encodes a prote 3_4532432		

AT1G21000	na	PLATZ transcrit 1_7340716	13.68	intergenic
AT5G03350	na	Legume lectin f: 5_816925	13.67	promoter
AT5G03360	na GLUTATHIONE S-TRANSFERASE F3 (G	DC1 domain-co 5_816925	13.67	proximal promoter
AT2G02930 AT2G02950	PHYTOCHROME KINASE SUBSTRATE 1		13.66 13.66	proximal promoter intergenic
AT3G55560	AT-HOOK PROTEIN OF GA FEEDBACK		13.62	promoter
AT1G19110	na	inter-alpha-tryps 1_6601874	13.62	promoter
AT1G12440	na	A20/AN1-like zir 1_4243264	13.62	promoter
AT1G12450	na	SNARE associa 1_4243264	13.62	proximal promoter
AT4G30650	na	Low temperatur 4_14955253	13.61	intergenic
AT4G30660	na	Low temperatur 4_14955253	13.61	promoter
AT2G30600 AT5G04820	na OVATE FAMILY PROTEIN 13 (OFB13)	BTB/POZ doma 2_13036943	13.6 13.6	intron
AT4G26690	OVATE FAMILY PROTEIN 13 (OFP13) SHAVEN 3 (SHV3)	ovate family pro 5_1397816 Glycerophosph(4_13461049	13.6	proximal promoter proximal promoter
AT5G19110	na	Eukaryotic aspa 5_6414366	13.59	proximal promoter
AT5G19120	na	Eukaryotic aspa 5_6414366	13.59	promoter
AT5G19130	na	GPI transamida 5_6414366	13.59	intergenic
AT2G02070	INDETERMINATE(ID)-DOMAIN 5 (IDD5)	indeterminate(IE 2_509851	13.58	intergenic
AT5G47060	na	Protein of unknc 5_19115671	13.56	proximal promoter
AT5G11230	na na	Nucleotide-suge 5_3579913	13.55 13.54	proximal promoter
AT1G18310 AT1G18300	NUDIX HYDROLASE HOMOLOG 4 (NUD	glycosyl hydrola 1_6299115	13.54	intergenic proximal promoter
AT3G49260	IQ-DOMAIN 21 (iqd21)	IQ-domain 21 (ii 3_18262385	13.53	promoter
AT5G67020	na	unknown proteir 5_26752854	13.53	intergenic
AT4G36170	na	unknown proteir 4_17119662	13.52	exon
AT4G36180	na	Leucine-rich rec 4_17119662	13.52	intergenic
AT2G33860	ETTIN (ETT)	ettin (ett) mutati 2_14331435	13.51	proximal promoter
AT3G16050	PYRIDOXINE BIOSYNTHESIS 1.2 (PDX1.		13.51	promoter
AT1G14720	XYLOGLUCAN ENDOTRANSGLUCOSYL		13.51	proximal promoter
AT1G08920 AT1G49560	ERD (EARLY RESPONSE TO DEHYDRA'	Homeodomain-l 1_18342339	13.5 13.5	intergenic promoter
AT1G08910	na	FUNCTIONS IN 1 2862726	13.5	intergenic
AT2G26530	(AR781)	unknown functic 2 11284844	13.48	proximal promoter
AT1G80420	(ATXRCC1)	ATXRCC1; FUN 1_30239120	13.48	proximal promoter
AT1G80430	na	pre-tRNA; tRNA 1_30239120	13.48	intergenic
AT1G80440	na	Galactose oxida 1_30239120	13.48	proximal promoter
AT1G80450	na	VQ motif-contail 1_30239120	13.48	intergenic
AT1G80370	CYCLIN A2;4 (CYCA2;4)	Encodes a A2-tr 1_30217121	13.47 13.47	intergenic
AT1G80380 AT5G15948	na CONSERVED PEPTIDE UPSTREAM OPE	encodes a glyce 1_30217121	13.46	intron proximal promoter
AT5G15950	na	Adenosylmethic 5_5205321	13.46	proximal promoter
AT1G59910	na	Actin-binding Ft 1_22057340	13.45	promoter
AT5G39070	na	transposable ele 5_15641163	13.42	promoter
AT5G39080	na	HXXXD-type ac 5_15641163	13.42	promoter
AT5G39090	na	HXXXD-type ac 5_15641163	13.42	proximal promoter
AT2G47370	na	Calcium-depend 2_19440504	13.42	promoter
AT3G47080 AT4G22350	na na	Tetratricopeptid 3_17340681 Ubiquitin C-term 4_11807465	13.38 13.38	promoter promoter
AT4G22360	na	SWIB complex I 4_11807465	13.38	promoter
AT2G26730	na	Leucine-rich reg 2_11388427	13.38	five_prime_UTR
AT2G39770	CYTOKINESIS DEFECTIVE 1 (CYT1)	Encodes a GDF 2_16587086	13.37	proximal promoter
AT5G48790	na	FUNCTIONS IN 5_19782634	13.37	proximal promoter
AT1G10030	HOMOLOG OF YEAST ERGOSTEROL28		13.33	proximal promoter
AT1G10020	na	Protein of unkno 1_3272626	13.33	proximal promoter
AT1G18670 AT1G76490	IMPAIRED IN BABA-INDUCED STERILITY HYDROXY METHYLGLUTARYL COA REI		13.32 13.29	downstream exon
AT5G46880	HOMEOBOX-7 (HB-7)	homeobox-7 (H 5_19030689	13.25	proximal promoter
AT4G38620	MYB DOMAIN PROTEIN 4 (MYB4)	Encodes a R2R 4_18055572	13.26	intergenic
AT4G38630	REGULATORY PARTICLE NON-ATPASE		13.26	intergenic
AT2G45310	UDP-D-GLUCURONATE 4-EPIMERASE 4	UDP-D-glucuroi 2_18681686	13.26	promoter
AT4G14490	na	SMAD/FHA don 4_8333740	13.25	promoter
AT4G14500	na	Polyketide cycla 4_8333740	13.25	promoter
AT5G09620 AT2G23770	na	Octicosapeptide 5_2985574	13.25	promoter
AT1G72680	LYSM-CONTAINING RECEPTOR-LIKE KI CINNAMYL-ALCOHOL DEHYDROGENAS		13.24 13.23	intergenic proximal promoter
AT1G23080	PIN-FORMED 7 (PIN7)	Encodes a nove 1_8181446	13.22	intron
AT1G75490	na	encodes a mem 1_28335225	13.21	promoter
AT1G75500	WALLS ARE THIN 1 (WAT1)	An Arabidopsis 1_28335225	13.21	intergenic
AT1G78790	na	unknown proteir 1_29625401	13.2	promoter
AT1G78800	na	UDP-Glycosyltr: 1_29625401	13.2	intergenic
AT3G13320	CATION EXCHANGER 2 (CAX2)	low affinity calci 3_4312394 Chaperone Dna 3_4312394	13.19	proximal promoter
AT3G13310 AT1G09070	na SOYBEAN GENE REGULATED BY COLD		13.19 13.19	proximal promoter proximal promoter
AT3G13300	VARICOSE (VCS)	Encodes VCS (' 3_4312394	13.19	intergenic
AT4G37690	na	Galactosyl trans 4 17709293	13.17	exon
AT5G63790	NAC DOMAIN CONTAINING PROTEIN 10		13.17	promoter
AT5G63780	SHOOT APICAL MERISTEM ARREST 1 (13.17	intergenic
AT1G71960	ATP-BINDING CASETTE G25 (ABCG25)		13.16	five_prime_UTR
AT1G72970	HOTHEAD (HTH)	Originally identif 1_27451206	13.16	proximal promoter
AT1G20515	na OPC-8:0 COA LIGASE1 (OPCL1)	Potential natura 1_7106026 OPC-8:0 CoA li ₁ 1_7106026	13.16	promoter
AT1G20510 AT1G17200	OPC-8:0 COA LIGASE1 (OPCL1) na	Uncharacterise(1_5877375	13.16 13.15	promoter proximal promoter
AT1G17200 AT1G69320	CLAVATA3/ESR-RELATED 10 (CLE10)	Member of a lar 1 26062629	13.13	downstream
AT1G20100	na	unknown proteir 1_6971145	13.13	promoter
AT1G20110	na	RING/FYVE/PH 1_6971145	13.13	promoter
AT2G34710	PHABULOSA (PHB)	Dominant PHB 2_14645210	13.13	proximal promoter
AT4G35470	PLANT INTRACELLULAR RAS GROUP-R		13.13	promoter
AT1G20090	RHO-RELATED PROTEIN FROM PLANTS		13.13	intergenic
AT3G50450 AT3G53420	HOMOLOG OF RPW8 1 (HR1) PLASMA MEMBRANE INTRINSIC PROTE	Homolog of RP\ 3_18721686 a member of the 3_19807224	13.12 13.12	proximal promoter proximal promoter
AT4G38760	na	Protein of unknr 4_18083173	13.12	intergenic
AT4G38730	na	Protein of unknc 4_18083173	13.11	proximal promoter
AT1G69870	NITRATE TRANSPORTER 1.7 (NRT1.7)	Encodes a low a 1_26313328	13.11	proximal promoter
AT4G38740	ROTAMASE CYP 1 (ROC1)	Encodes cytoso 4_18083173	13.11	downstream

AT5G08335	(ATSTE14B)	Encodes an isc 5_2680661	13.1	provimal promotor
AT1G10370	EARLY-RESPONSIVE TO DEHYDRATION		13.1	proximal promoter downstream
AT1G10360	GLUTATHIONE S-TRANSFERASE TAU 1		13.1	promoter
AT5G08330	TCP DOMAIN PROTEIN 11 (TCP11)	TCP family tran: 5_2680661	13.1	promoter
AT2G34630	GERANYL DIPHOSPHATE SYNTHASE 1		13.09	promoter
AT1G55450	na	S-adenosyl-L-m 1_20707005	13.09	promoter
AT1G55460	na	DNA/RNA-bindi 1_20707005	13.09	promoter
AT2G34620	na	Mitochondrial tra 2_14578262	13.09	three_prime_UTR
AT5G66650	na	Protein of unknr 5_26604968	13.08	proximal promoter
AT5G57510 AT2G01420	na BIN EORMED 4 (DINA)	unknown proteir 5_23288656	13.07 13.07	intergenic
AT4G22592	PIN-FORMED 4 (PIN4) CONSERVED PEPTIDE UPSTREAM OPE	Encodes a puta 2_181165	13.07	intron proximal promoter
AT4G22850	na	SNARE associa 4_11996406	13.05	downstream
AT4G22860	na	Cell cycle regula 4_11996406	13.05	proximal promoter
AT4G22590	TREHALOSE-6-PHOSPHATE PHOSPHAT		13.05	proximal promoter
AT2G22790	na	unknown proteir 2_9696737	13.04	exon
AT2G22795	na	unknown proteir 2_9696737	13.04	intergenic
AT5G06980	na	unknown proteir 5_2167250	13.04	promoter
AT5G07590	na	Transducin/WD 5_2404074	13.04	promoter
AT4G38430 AT4G15630	RHO GUANYL-NUCLEOTIDE EXCHANGI na	Uncharacterise(4_8918902	13.04 13.02	promoter
AT4G15630	na	unknown proteir 4_8918902	13.02	downstream downstream
AT5G01750	na	Protein of unkno 5 291498	13	downstream
AT5G01760	na	ENTH/VHS/GA ⁻ 5_291498	13	promoter
AT1G17840	ATP-BINDING CASSETTE G11 (ABCG11)		12.98	promoter
AT4G27765	MICRORNA828A (MIR828A)	Encodes a micr 4_13847222	12.98	downstream
AT3G45780	PHOTOTROPIN 1 (PHOT1)	Blue-light photo 3_16817634	12.95	intron
AT5G54960	PYRUVATE DECARBOXYLASE-2 (PDC2)		12.94	promoter
AT5G13110	GLUCOSE-6-PHOSPHATE DEHYDROGE		12.93	proximal promoter
AT5G13090 AT5G13100	na	unknown proteir 5_4156483	12.93 12.93	proximal promoter
AT4G37270	na HEAVY METAL ATPASE 1 (HMA1)	unknown proteir 5_4156483 Encodes a P1B 4 17539917	12.93	promoter intergenic
AT4G37270	MYB DOMAIN PROTEIN 73 (MYB73)	Member of the F 4_17539917	12.92	proximal promoter
AT1G05710	na	basic helix-loop 1_1713579	12.92	proximal promoter
AT3G17820	GLUTAMINE SYNTHETASE 1.3 (GLN1.3)		12.91	intergenic
AT3G17830	na	Molecular chape 3_6099885	12.91	proximal promoter
AT2G32090	na	Lactoylglutathio 2_13645825	12.91	intron
AT2G32100	OVATE FAMILY PROTEIN 16 (OFP16)	ovate family pro 2_13645825	12.91	proximal promoter
AT5G62470	MYB DOMAIN PROTEIN 96 (MYB96)	Encodes a R2R 5_25078229	12.9	intergenic
AT5G62460 AT4G37070	na (DLD4)	RING/FYVE/PH 5_25078229	12.9 12.89	intergenic
AT3G19820	(PLP1) DWARF 1 (DWF1)	Patatin-related ; 4_17469258 Involved in the c3_6884410	12.89	proximal promoter proximal promoter
AT1G10090	na	Early-responsiv 1_3296435	12.89	promoter
AT5G19180	E1 C-TERMINAL RELATED 1 (ECR1)	Encodes a subt 5_6457141	12.88	intergenic
AT3G27050	na	unknown proteir 3_9981436	12.88	proximal promoter
AT3G45050	na	unknown proteir 3_16475821	12.88	promoter
AT3G45040	na	Encodes a puta 3_16475821	12.88	promoter
AT5G19190 AT5G19200	na TSC10B (TSC10B)	unknown proteir 5_6457141 Encodes one of 5_6457141	12.88 12.88	promoter proximal promoter
AT3G27060	TSO MEANING 'UGLY' IN CHINESE 2 (TS		12.88	promoter
AT1G28010	ATP-BINDING CASSETTE B14 (ABCB14)		12.87	proximal promoter
AT1G28007	na	unknown proteir 1_9762341	12.87	downstream
AT2G45430	AT-HOOK MOTIF NUCLEAR-LOCALIZED		12.86	proximal promoter
AT2G35950	EMBRYO SAC DEVELOPMENT ARREST		12.85	intergenic
AT5G01950	na	Leucine-rich reg 5_370154	12.85	five_prime_UTR
AT1C60030	na	RING/U-box suj 5_370154	12.85	promoter
AT1G69930 AT1G32230	GLUTATHIONE S-TRANSFERASE TAU 1 RADICAL-INDUCED CELL DEATH1 (RCD		12.84 12.84	downstream intergenic
AT3G52850	VACUOLAR SORTING RECEPTOR HOM		12.83	promoter
AT4G19020	CHROMOMETHYLASE 2 (CMT2)	chromomethylas 4_10414422	12.82	promoter
AT4G19010	na	AMP-dependen 4 10414422	12.82	promoter
AT4G37250	na	Leucine-rich rer 4_17535110	12.82	intergenic
AT5G05140	na	Transcription el 5_1518165	12.82	proximal promoter
AT1G67350	na	unknown proteir 1_25234863	12.81	promoter
AT3G17185	TRANS-ACTING SIRNA3 (TAS3)	Encodes a trans 3_5862606	12.81	downstream
AT1G49200	na	RING/U-box su _l 1_18198019 CONTAINS Inte 5_25430699	12.79 12.79	promoter proximal promoter
AT5G63520 AT4G12420	na (SKU5)	Encodes a prot 4_7355324	12.79	proximal promoter
AT4G12420 AT4G32160	na	Phox (PX) dom: 4_15528664	12.78	promoter
AT2G02700	na	Cysteine/Histidii 2_758017	12.78	downstream
AT2G02710	PAS/LOV PROTEIN B (PLPB)	Encodes a puta 2_758017	12.78	intergenic
AT4G32150	VESICLE-ASSOCIATED MEMBRANE PRO	AtVAMP711 is a 4_15528664	12.78	proximal promoter
AT1G22767	na	unknown proteir 1_8060883	12.76	downstream
AT2G44120	na	Ribosomal prote 2_18252677	12.75	proximal promoter
AT2G44130	na	Galactose oxida 2_18252677 Peptidase family 2_18252677	12.75	proximal promoter
AT2G44140 AT5G65470	na na	O-fucosyltransf(5_26172047	12.75 12.75	intergenic promoter
AT1G76620	na	Protein of unkno 1_28755050	12.73	proximal promoter
AT5G14710	na	CONTAINS Inte 5_4746051	12.74	promoter
AT3G48690	(CXE12)	Encodes a prote 3_18038273	12.73	promoter
AT1G25220	ANTHRANILATE SYNTHASE BETA SUBL	Catalyzes the fii 1_8839661	12.73	promoter
AT3G23160	na	Protein of unknc 3_8259623	12.73	downstream
AT5G66080	na	Protein phosphs 5_26425472	12.72	promoter
AT5G66090	na	unknown proteir 5_26425472	12.72	promoter
AT5G11090 AT2G17470	na ALUMINIUM ACTIVATED MALATE TRAN:	serine-rich prote 5_3529607 Encodess ALM 2_7588262	12.72 12.71	intergenic promoter
AT2G17470	AUXIN RESPONSE FACTOR 11 (ARF11)		12.71	intergenic
AT2G46520	na	cellular apoptos 2_19101070	12.71	intergenic
AT2G33400	na	unknown proteir 2_14154592	12.7	promoter
AT1G75220	ERD6-LIKE 6 (ERDL6)	Encodes a vacu 1_28233750	12.67	proximal promoter
AT1G75230	na	DNA glycosylas 1_28233750	12.67	proximal promoter
AT1G77200				
AT2C 42620	na MODE AVII I ADV DDANICHES 2 (MAY2)	encodes a mem 1_29005249	12.67	promoter
AT2G42620 AT5G02260	na MORE AXILLARY BRANCHES 2 (MAX2) EXPANSIN A9 (EXPA9)		12.67 12.62 12.61	promoter intergenic proximal promoter

AT4G15233	ATP-BINDING CASSETTE G42 (ABCG42)	ABC-2 and Plar 4_8687760	12.59	proximal promoter
AT1G02210	na	NAC (No Apical 1_426662	12.58	intergenic
AT4G11230	na	Riboflavin synth 4_6839856	12.55	intergenic
AT4G11220	VIRB2-INTERACTING PROTEIN 2 (BTI2)	VIRB2-interactir 4_6839856	12.55	promoter
AT5G20110	na	Dynein light cha 5_6791960	12.54	intron
AT3G02130	RECEPTOR-LIKE PROTEIN KINASE 2 (R		12.54	intergenic
AT3G02140	TWO OR MORE ABRES-CONTAINING G		12.54	proximal promoter
AT1G70610	ATP-BINDING CASSETTE B26 (ABCB26)		12.53	promoter
AT1G70600	na	Ribosomal prote 1_26621868	12.53	promoter
AT5G40900	na	Nucleotide-diph 5_16388721	12.52	intergenic
AT5G08530	51 KDA SUBUNIT OF COMPLEX I (CI51)		12.5	intergenic
AT5G09810	ACTIN 7 (ACT7)	Member of Actir 5_3051924	12.5	promoter
AT1G14440 AT5G13220	HOMEOBOX PROTEIN 31 (HB31) JASMONATE-ZIM-DOMAIN PROTEIN 10	homeobox prote 1_4941390	12.5 12.5	promoter proximal promoter
AT5G13220 AT5G08520	na	Duplicated hom 5 2758971	12.5	proximal promoter
AT4G16430	na	basic helix-loop 4_9267446	12.49	five_prime_UTR
AT5G07030	na	Eukaryotic aspa 5_2184727	12.48	intron
AT1G75710	na	C2H2-like zinc f 1_28430315	12.48	intron
AT5G36250	PP2C74, PROTEIN PHOSPHATASE 2C 7		12.48	proximal promoter
AT5G59820	RESPONSIVE TO HIGH LIGHT 41 (RHL4		12.45	promoter
AT2G16280	3-KETOACYL-COA SYNTHASE 9 (KCS9)	Encodes KCS9, 2_7050710	12.44	promoter
AT3G29575	ABI FIVE BINDING PROTEIN 3 (AFP3)	ABI five binding 3_11384223	12.43	promoter
AT3G50790	na	esterase/lipase/ 3_18882183	12.43	promoter
AT3G50800	na	unknown proteir 3_18882183	12.43	downstream
AT5G15440	EID1-LIKE 1 (EDL1)	EID1-like 1 (EDI 5_5011937	12.42	promoter
AT5G15430	na	Plant calmodulir 5_5011937	12.42	downstream
AT4G21850	METHIONINE SULFOXIDE REDUCTASE		12.41	proximal promoter
AT2G46150	na	Late embryoger 2_18965133	12.4	intergenic
AT2G46160	na	RING/U-box su ₁ 2_18965133	12.4	intergenic
AT2G46170	na	Reticulon family 2_18965133	12.4	promoter
AT4G32800 AT1G64380	na na	encodes a mem 4_15817641	12.4 12.4	proximal promoter
AT1G04380 AT1G21130	INDOLE GLUCOSINOLATE O-METHYLTE	encodes a mem 1_23895854	12.4	intergenic proximal promoter
AT1G21130 AT1G06360	na	Fatty acid desat 1_1938757	12.39	downstream
AT4G30400	na	RING/U-box su; 4 14869239	12.39	intergenic
AT4G30410	na	sequence-speci 4_14869239	12.39	intergenic
AT4G36648	na	Unknown gene 4_17282972	12.39	promoter
AT2G30500	NETWORKED 4B (NET4B)	Kinase interactii 2 13000652	12.39	promoter
AT4G36650	PLANT-SPECIFIC TFIIB-RELATED PROT		12.39	downstream
AT1G68530	3-KETOACYL-COA SYNTHASE 6 (KCS6)		12.38	promoter
AT5G45428	CONSERVED PEPTIDE UPSTREAM OPE		12.38	promoter
AT5G65430	GENERAL REGULATORY FACTOR 8 (GI		12.38	promoter
AT2G47730	GLUTATHIONE S-TRANSFERASE PHI 8		12.38	five_prime_UTR
AT5G65440	na	unknown proteir 5_26150535	12.38	proximal promoter
AT5G45430	na	Protein kinase s 5_18407348	12.38	intron
AT1G68520	na	B-box type zinc 1_25714988	12.38	intergenic
AT1G68526	na	unknown proteir 1_25714988	12.38	proximal promoter
AT2G47740	na	pre-tRNA; tRNA 2_19558135	12.38	intergenic
AT5G51330	SWITCH1 (SWI1)	Encodes novel 5_20862064	12.38	promoter
AT1G56590	ZIG SUPPRESSOR 4 (ZIP4)	Involved in vesi 1_21205420	12.38	proximal promoter
AT1G15340	METHYL-CPG-BINDING DOMAIN 10 (MB		12.37	promoter
AT3G11760	na	unknown proteir 3_3717958	12.37	promoter
AT4G02100	na	Heat shock prot 4_930012	12.34	promoter
AT3G61460 AT3G25870	BRASSINOSTEROID-RESPONSIVE RING	unknown proteir 3_9464284	12.33 12.33	promoter
AT3G23870 AT3G61470	PHOTOSYSTEM I LIGHT HARVESTING (12.33	promoter intergenic
AT3G14560	na	unknown proteir 3 4889134	12.32	five_prime_UTR
AT5G01810	CBL-INTERACTING PROTEIN KINASE 15		12.3	promoter
AT2G28405	LOW-MOLECULAR-WEIGHT CYSTEINE-		12.3	intergenic
AT5G01800	na	saposin B doma 5_308967	12.3	downstream
AT2G22900	na	Galactosyl trans 2_9746494	12.3	promoter
AT3G62700	ATP-BINDING CASSETTE C14 (ABCC14)		12.27	promoter
AT1G44760	na	Adenine nucleol 1_16900935	12.27	proximal promoter
AT3G26740	CCR-LIKE (CCL)	transcripts are 3_9827547	12.26	promoter
AT3G26730	na	RING/U-box sui 3_9827547	12.26	downstream
AT4G26080	ABA INSENSITIVE 1 (ABI1)	Involved in absc 4_13222036	12.25	five_prime_UTR
AT2G01560	na	Plant protein 15 2_252971	12.25	proximal promoter
AT3G60520	na	unknown proteir 3_22367504	12.25	intergenic
AT4G26095	na PVP1-LIKE 4 (PVL4)	Potential natura 4_13222036 Encodes a merr 2_16051882	12.25	intergenic
AT2G38310 AT4G26090	PYR1-LIKE 4 (PYL4) RESISTANT TO P. SYRINGAE 2 (RPS2)	Encodes a merr 2_16051882 Encodes a plasi 4_13222036	12.25 12.25	intergenic proximal promoter
AT4G26090 AT3G05937	na	unknown proteir 3_1776681	12.25	five_prime_UTR
AT4G35060	HEAVY METAL ASSOCIATED ISOPRENY		12.24	proximal promoter
AT5G26660	MYB DOMAIN PROTEIN 86 (MYB86)	myb domain prc 5 9327689	12.22	intergenic
AT4G30610	BRI1 SUPPRESSOR 1 (BRS1)	Encodes a secr 4_14943939	12.21	promoter
AT2G20580	26S PROTEASOME REGULATORY SUBI		12.2	proximal promoter
AT2G20570	GBF'S PRO-RICH REGION-INTERACTING		12.2	intergenic
AT1G04130	TETRATRICOPEPTIDE REPEAT 2 (TPR2		12.2	promoter
AT4G39800	D-MYO-INOSITOL 3-PHOSPHATE SYNTH		12.19	promoter
AT3G50780			12.19	promoter
AT3G18930	na	BEST Arabidop: 3_18877759		
	na na	RING/U-box suj 3_6526533	12.18	proximal promoter
AT3G18940	na na	RING/U-box su ₁ 3_6526533 clast3-related; (3_6526533	12.18 12.18	intergenic
AT3G18940 AT4G18670	na	RING/U-box su _I 3_6526533 clast3-related; C 3_6526533 Leucine-rich rer. 4_10275339	12.18 12.18 12.17	intergenic downstream
AT3G18940 AT4G18670 AT4G18660	na na na na	RING/U-box sul 3_6526533 clast3-related; C 3_6526533 Leucine-rich rer 4_10275339 unknown proteir 4_10275339	12.18 12.18 12.17 12.17	intergenic downstream intergenic
AT3G18940 AT4G18670 AT4G18660 AT3G23230	na na na na TRANSCRIPTIONAL REGULATOR OF DE	RING/U-box su ₁ 3_6526533 clast3-related; (3_6526533 Leucine-rich rer 4_10275339 unknown proteir 4_10275339 encodes a mem 3_8290210	12.18 12.18 12.17 12.17 12.17	intergenic downstream intergenic promoter
AT3G18940 AT4G18670 AT4G18660 AT3G23230 AT2G38000	na na na na TRANSCRIPTIONAL REGULATOR OF DE na	RING/U-box su; 3_6526533 clast3-related; C 3_6526533 Leucine-rich rer 4_10275339 unknown proteir 4_10275339 encodes a mem 3_8290210 chaperone prote 2_15905553	12.18 12.18 12.17 12.17 12.17 12.16	intergenic downstream intergenic promoter promoter
AT3G18940 AT4G18670 AT4G18660 AT3G23230 AT2G38000 AT1G79120	na na na na TRANSCRIPTIONAL REGULATOR OF DI na na	RING/U-box suj 3, 6526533 clast3-related; C 3, 6526533 Leucine-rich ret 4, 10275339 unknown proteir 4, 10275339 encodes a mem 3, 8290210 chaperone prote 2, 15905553 Ubiquitin carbox 1, 29766788	12.18 12.18 12.17 12.17 12.17 12.16 12.16	intergenic downstream intergenic promoter promoter three_prime_UTR
AT3G18940 AT4G18670 AT4G18660 AT3G23230 AT2G38000 AT1G79120 AT1G28280	na na na na TRANSCRIPTIONAL REGULATOR OF DE na na na	RING/U-box suj 3_6526533 clast3-related; C 3_6526533 Leucine-rich rer 4_10275339 unknown proteir 4_10275339 encodes a mem 3_8290210 chaperone prote 2_15905553 Ubiquitin carbox 1_29766788 VQ motif-contair 1_9884921	12.18 12.18 12.17 12.17 12.17 12.16 12.16 12.16	intergenic downstream intergenic promoter promoter three_prime_UTR intergenic
AT3G18940 AT4G18670 AT4G18660 AT3G23230 AT2G38000 AT1G79120 AT1G28280 AT2G28550	na na na na TRANSCRIPTIONAL REGULATOR OF DE na na na RELATED TO AP2.7 (RAP2.7)	RING/U-box suj 3, 6526533 Leucine-rich rer 4, 10275339 unknown proteir 4, 10275339 unknown proteir 4, 10275339 encodes a mem 3, 8290210 chaperone prote 2, 15905553 Ubiquitin carbos 1, 29766788 VQ motif-contair 1, 9884921 related to AP2.7 2, 12230378	12.18 12.18 12.17 12.17 12.17 12.16 12.16 12.16 12.16	intergenic downstream intergenic promoter promoter three_prime_UTR intergenic proximal promoter
AT3G18940 AT4G18670 AT4G18660 AT3G23230 AT2G38000 AT1G79120 AT1G28280 AT2G28550 AT1G25560	na na na na na TRANSCRIPTIONAL REGULATOR OF Di na na na RELATED TO AP2.7 (RAP2.7) TEMPRANILLO 1 (TEM1)	RING/U-box suj 3, 6526533 clast3-related; (3, 6526533 Leucine-rich ret 4, 10275339 unknown proteir 4, 10275339 encodes a mem 3, 8290210 chaperone prot 2, 15905553 Ubiquitin carbox 1, 29766788 VQ motif-contail 1, 9884921 related to AP2.7 2, 12230378 Encodes a mem 1, 8983771	12.18 12.18 12.17 12.17 12.17 12.16 12.16 12.16 12.16 12.16	intergenic downstream intergenic promoter promoter three_prime_UTR intergenic proximal promoter proximal promoter
AT3G18940 AT4G18670 AT4G18660 AT3G23230 AT2G38000 AT1G79120 AT1G28280 AT2G28550 AT1G25560 AT4G13840	na na na na TRANSCRIPTIONAL REGULATOR OF DE na na na RELATED TO AP2.7 (RAP2.7) TEMPRANILLO 1 (TEM1) na	RING/U-box suj 3_6526533 clast3-related; C 3_6526533 Leucine-rich rer, 4_10275339 unknown proteir 4_10275339 encodes a mem 3_8290210 chaperone prote 2_15905553 Ubiquitin carbox 1_29766788 VQ motif-contair 1_9884921 related to AP2.7 2_12230378 Encodes a mem 1_8983771 HXXXD-type ac 4_8015407	12.18 12.18 12.17 12.17 12.17 12.16 12.16 12.16 12.16 12.16 12.16 12.15	intergenic downstream intergenic promoter promoter three_prime_UTR intergenic proximal promoter proximal promoter intron
AT3G18940 AT4G18670 AT4G18660 AT3G23230 AT2G38000 AT1G79120 AT1G28280 AT2G28550 AT1G25560 AT1G13840 AT3G55980	na na na na TRANSCRIPTIONAL REGULATOR OF DE na na na RELATED TO AP2.7 (RAP2.7) TEMPRANILLO 1 (TEM1) na SALT-INDUCIBLE ZINC FINGER 1 (SZF1)	RING/U-box suj 3, 6526533 Leucine-rich ref 4, 10275339 unknown proteir 4, 10275339 unknown proteir 4, 10275339 encodes a mem 3, 8290210 chaperone prote 2, 15905553 Ubiquitin carbox 1, 29766788 Voi untif-contail 1, 9884921 related to AP2.7 2, 12230378 Encodes a mem 1, 8983771 HXXXD-type ac 4, 8015407 salt-inducible zii 3, 20775804	12.18 12.18 12.17 12.17 12.17 12.16 12.16 12.16 12.16 12.16 12.15 12.15	intergenic downstream intergenic promoter promoter three_prime_UTR intergenic proximal promoter proximal promoter intron promoter
AT3G18940 AT4G18670 AT4G18660 AT3G23230 AT2G38000 AT1G79120 AT1G28280 AT2G28550 AT1G25560 AT4G13840	na na na na TRANSCRIPTIONAL REGULATOR OF DE na na na RELATED TO AP2.7 (RAP2.7) TEMPRANILLO 1 (TEM1) na	RING/U-box suj 3_6526533 clast3-related; C 3_6526533 Leucine-rich rer, 4_10275339 unknown proteir 4_10275339 encodes a mem 3_8290210 chaperone prote 2_15905553 Ubiquitin carbox 1_29766788 VQ motif-contair 1_9884921 related to AP2.7 2_12230378 Encodes a mem 1_8983771 HXXXD-type ac 4_8015407	12.18 12.18 12.17 12.17 12.17 12.16 12.16 12.16 12.16 12.16 12.16 12.15	intergenic downstream intergenic promoter promoter three_prime_UTR intergenic proximal promoter proximal promoter intron

AT1G50450	na	Saccharopine d 1_18690853	12.13	promoter
AT5G28040	na	DNA-binding stc 5_10039158	12.12	promoter
AT1G66173	na	other RNA 1_24644808	12.11	intergenic
AT3G51890	na	Clathrin light ch: 3_19251065	12.1	promoter
AT3G51895	SULFATE TRANSPORTER 3;1 (SULTR3;	Encodes a sulfa 3_19251065	12.1	downstream
AT1G17140	INTERACTOR OF CONSTITUTIVE ACTIV		12.09	proximal promoter
AT3G50665	na	pre-tRNA; tRNA 3_18822067	12.09	intergenic
AT1G17145	na	RING/U-box su ₁ 1_5859863	12.09	intergenic
AT3G46630	na	Protein of unknc 3_17182718	12.09	promoter
AT3G46640	PHYTOCLOCK 1 (PCL1)	Encodes a myb 3_17182718	12.09	promoter
AT5G13220	JASMONATE-ZIM-DOMAIN PROTEIN 10		12.08	three_prime_UTR
AT1G78020	na	Protein of unknc 1_29336682	12.08	proximal promoter
AT1G78010	na	tRNA modificatii 1_29336682	12.08	downstream
AT5G13225	na	snoRNA; snoRN 5_4220715	12.08	intergenic
AT5G13230	na	Tetratricopeptid 5_4220715	12.08 12.07	proximal promoter
AT4G30950	FATTY ACID DESATURASE 6 (FAD6)	Chloroplastic er 4_15061714		proximal promoter
AT4G40030 AT4G40040	na	Histone superfa 4_18558976	12.07 12.07	proximal promoter
AT4G40040	na na	Histone superfa 4_18558976 Microsomal sigr 4_18558976	12.07	promoter promoter
AT4G36220	FERULIC ACID 5-HYDROXYLASE 1 (FAF		12.06	intergenic
AT5G28840	GDP-D-MANNOSE 3',5'-EPIMERASE (GN		12.06	three_prime_UTR
AT1G69690	TEOSINTE BRANCHED1/CYCLOIDEA/PC		12.06	proximal promoter
AT2G30580	DREB2A-INTERACTING PROTEIN 2 (DRI		12.05	three_prime_UTR
AT5G52520	OVULE ABORTION 6 (OVA6)	OVULE ABORT 5_21310356	12.05	proximal promoter
AT2G30590	WRKY DNA-BINDING PROTEIN 21 (WRK		12.05	proximal promoter
AT3G13810	INDETERMINATE(ID)-DOMAIN 11 (IDD11		12.04	proximal promoter
AT3G26450	na	Polyketide cycla 3_9681760	12.04	exon
AT3G26460	na	Polyketide cycla 3 9681760	12.04	intergenic
AT3G13800	na	Metallo-hydrola: 3 4541652	12.04	downstream
AT4G27870	na	Vacuolar iron tra 4_13878143	12.04	proximal promoter
AT3G61880	CYTOCHROME P450 78A9 (CYP78A9)	Encodes a cyto 3_22910817	12.02	proximal promoter
AT4G30350	na	Double Clp-N m 4_14846146	12.02	proximal promoter
AT2G46500	PHOSPHOINOSITIDE 4-KINASE GAMMA		12.02	promoter
AT2G44480	BETA GLUCOSIDASE 17 (BGLU17)	beta glucosidas 2_18363781	12.02	intergenic
AT1G79910	na	Regulator of Vp 1_30054546	12.01	promoter
AT2G44490	PENETRATION 2 (PEN2)	Encodes a glyc 2_18363781	12.01	proximal promoter
AT5G62130	na	Per1-like family 5_24953167	12	five_prime_UTR
AT5G62140	na	unknown proteir 5_24953167	12	intergenic
AT1G57680	CANDIDATE G-PROTEIN COUPLED REC		11.99	promoter
AT3G60530	GATA TRANSCRIPTION FACTOR 4 (GAT		11.98	three_prime_UTR
AT3G46630	na	Protein of unknc 3_17180189	11.98	intergenic
AT3G60540	na	Preprotein trans 3_22374349	11.98	intergenic
AT3G46620	RING AND DOMAIN OF UNKNOWN FUN		11.98	promoter
AT1G72150	PATELLIN 1 (PATL1)	novel cell-plate- 1_27152645	11.97	intergenic
AT1G01480	1-AMINO-CYCLOPROPANE-1-CARBOXY		11.96	proximal promoter
AT4G36870	BEL1-LIKE HOMEODOMAIN 2 (BLH2)	Encodes a merr 4_17367046	11.96	proximal promoter
AT2G01905	CYCLIN J18 (CYCJ18)	cyclin J18 (cycJ 2 412371	11.96	intron
AT3G53720	CATION/H+ EXCHANGER 20 (CHX20)	member of Puta 3_19910560	11.95	promoter
AT3G59884	MICRORNA827A (MIR827A)	Encodes a micr 3_22122183	11.95	intergenic
AT3G59880	na	unknown proteir 3_22122183	11.95	intergenic
AT1G76560	CP12 DOMAIN-CONTAINING PROTEIN 3		11.94	promoter
AT1G76550	na	Phosphofructok 1_28728160	11.94	proximal promoter
AT1G76570	na	Chlorophyll A-B 1_28728160	11.94	proximal promoter
AT3G62630	na	Protein of unknc 3 23166189	11.91	proximal promoter
AT3G62640	na	Protein of unknc 3_23166189	11.91	downstream
AT2G35950	EMBRYO SAC DEVELOPMENT ARREST		11.9	promoter
AT2G26650	K+ TRANSPORTER 1 (KT1)	Encodes AKT1, 2_11336699	11.9	promoter
AT1G01471	na	unknown proteir 1_173476	11.9	downstream
AT1G03457	na	RNA-binding (R 1_865309	11.89	proximal promoter
AT3G45775	na	transposable eli 3_16815246	11.89	proximal promoter
AT1G03470	NETWORKED 3A (NET3A)	Encodes a men 1_865309	11.89	intergenic
AT1G04240	SHORT HYPOCOTYL 2 (SHY2)	SHY2/IAA3 regt 1_1129603	11.89	promoter
AT5G20250	DARK INDUCIBLE 10 (DIN10)	encodes a mem 5_6832522	11.88	proximal promoter
AT4G22820	na	A20/AN1-like zir 4_11986618	11.88	intergenic
AT2G05518	na	Unknown gene 2_2024145	11.88	downstream
AT1G76954	na	Encodes a defe 1_28917042	11.88	intergenic
AT5G20260	na	Exostosin family 5_6832522	11.88	intergenic
AT4G33220	PECTIN METHYLESTERASE 44 (PME44)		11.88	intron
AT3G28910	MYB DOMAIN PROTEIN 30 (MYB30)	transcription fac 3_10910978	11.87	promoter
AT4G27652	na	unknown proteir 4_13812957	11.87	intergenic
AT4G27654	na	unknown proteir 4_13812957	11.87	intergenic
AT4G27657	na	unknown proteir 4_13812957	11.87	promoter
AT1G27213	na	unknown proteir 1_9459288	11.85	intergenic
AT5G16370	ACYL ACTIVATING ENZYME 5 (AAE5)	acyl activating € 5_5359091	11.84	proximal promoter
AT1G11000	MILDEW RESISTANCE LOCUS O 4 (MLC		11.84	promoter
AT5G16380	na	Protein of unknc 5_5359091	11.84	intergenic
AT5G16375	na	pre-tRNA; tRNA 5_5359091	11.84	downstream
AT2G32970	na	unknown proteir 2_13996460	11.84	proximal promoter
AT1G11010	na	pre-tRNA; tRNA 1_3676163	11.84	promoter
AT1G11020	na	RING/FYVE/PH 1_3676163	11.84	proximal promoter
AT1G49730	na	Protein kinase s 1_18406362	11.84	proximal promoter
AT1G49740	na	PLC-like phospl 1_18406362	11.84	proximal promoter
AT4G29140	ACTIVATED DISEASE SUSCEPTIBILITY		11.83	intergenic
AT4G22570	ADENINE PHOSPHORIBOSYL TRANSFE		11.83	intron
AT4G22560	na	unknown proteir 4_11882459	11.83	intergenic
AT5G28300	na	Duplicated hom 5_10297187	11.82	proximal promoter
AT4G19390	na	Uncharacteriser 4_10574996	11.82	exon
AT3G61630	CYTOKININ RESPONSE FACTOR 6 (CRI		11.81	proximal promoter
AT3G50480	HOMOLOG OF RPW8 4 (HR4)	Homolog of RP\ 3_18731401	11.81	proximal promoter
AT2G38040	ACETYL CO-ENZYME A CARBOXYLASE		11.79	promoter
AT2G38025	na	Cysteine proteir 2_15917034	11.79	promoter
AT2G38030	na na	pre-tRNA; tRNA 2_15917034	11.79	downstream
AT5G49090 AT5G52900	na MEMBRANE-ASSOCIATED KINASE REG	transposable eli 5_19895683 Encodes a merr 5_21454509	11.79 11.78	proximal promoter proximal promoter
		253d65 d mon 5_21454309	11.70	proximal promoter

AT5G52901	na	This gene enco 5_21454509	11.78	exon
AT5G24300	STARCH SYNTHASE 1 (SS1)	SSI is a plastidi: 5_8266403	11.78	promoter
AT1G22380	UDP-GLUCOSYL TRANSFERASE 85A3 (11.78	intergenic
AT1G22370	UDP-GLUCOSYL TRANSFERASE 85A5 (11.78	promoter
AT1G44760	na (TUI4)	Adenine nucleol 1_16897055	11.77	intron
AT5G54770 AT1G17620	(THI1)	Encodes a thiar 5_22245972 Late embryoger 1_6062083	11.76 11.76	proximal promoter promoter
AT5G54760	na na	Translation initia 5 22245972	11.76	downstream
AT3G22380	TIME FOR COFFEE (TIC)	Encodes a nucli 3 7910149	11.76	proximal promoter
AT5G04530	3-KETOACYL-COA SYNTHASE 19 (KCS1		11.75	three_prime_UTR
AT3G23440	EMBRYO SAC DEVELOPMENT ARREST		11.75	exon
AT4G05010	F-BOX STRESS INDUCED 3 (FBS3)	F-box family prc 4_2567109	11.75	promoter
AT5G04520	na	Protein of unknc 5 1291829	11.75	proximal promoter
AT4G17453	na	This gene enco 4_9738140	11.73	exon
AT4G39900	na	unknown proteir 4_18511229	11.73	proximal promoter
AT1G76940	na	RNA-binding (R 1_28904459	11.72	promoter
AT2G14210	AGAMOUS-LIKE 44 (AGL44)	MADS box gene 2_6018287	11.71	promoter
AT1G71710	na	DNAse I-like su 1_26980938	11.7	intron
AT4G38660	na	Pathogenesis-re 4_18066046	11.7	downstream
AT4G38650	na	Glycosyl hydrol: 4_18066046	11.7	downstream
AT1G53840	PECTIN METHYLESTERASE 1 (PME1)	encodes a pecti 1_20101156	11.7	promoter
AT1G53830	PECTIN METHYLESTERASE 2 (PME2)	encodes a pecti 1_20101156	11.7	intergenic
AT3G47600	MYB DOMAIN PROTEIN 94 (MYB94)	Encodes a puta 3_17541503	11.69	promoter
AT5G37980	na	Zinc-binding del 5_15129092	11.69 11.69	proximal promoter
AT4G27270 AT4G27280	na na	Quinone reduct: 4_13664359 Calcium-binding 4_13664359	11.69	proximal promoter promoter
AT5G43760	3-KETOACYL-COA SYNTHASE 20 (KCS2		11.68	intron
AT3G26200	CYTOCHROME P450, FAMILY 71, SUBF.		11.68	intergenic
AT3G26210	CYTOCHROME P450, FAMILY 71, SUBF		11.68	intergenic
AT2G45820	na	Remorin family 2_18864742	11.68	promoter
AT2G45810	na	DEA(D/H)-box F 2_18864742	11.68	intergenic
AT5G43770	na	proline-rich fami 5_17587121	11.68	proximal promoter
AT1G26945	KIDARI (KDR)	Encodes a basic 1_9351989	11.67	intron
AT4G22550	LIPID PHOSPHATE PHOSPHATASE BET	Phosphatidic ac 4_11879644	11.67	proximal promoter
AT3G06670	na	binding; FUNCT 3_2113663	11.67	intron
AT2G18969	na	Encodes a atypi 2_8230406	11.67	proximal promoter
AT4G22560	na	unknown proteir 4_11879644	11.67	promoter
AT5G52280	na	Myosin heavy c 5_21226218	11.66	proximal promoter
AT1G48330	na	unknown proteir 1_17863601	11.65	promoter
AT2G22990	SINAPOYLGLUCOSE 1 (SNG1)	sinapoylglucose 2_9784649	11.65	proximal promoter
AT1G22640	MYB DOMAIN PROTEIN 3 (MYB3)	MYB-type trans: 1_8006009	11.63	promoter
AT1G61890	na	MATE efflux fan 1_22877575	11.62	intergenic
AT3G61260	na	Remorin family 3_22677125	11.62	promoter
AT2G14890	ARABINOGALACTAN PROTEIN 9 (AGP9		11.61	intron
AT4G23060	IQ-DOMAIN 22 (IQD22)	IQ-domain 22 (I 4_12086816	11.61	promoter
AT3G52105	na	unknown proteir 3_19323104	11.61	promoter
AT3G52100 AT3G52110	na na	RING/FYVE/PH 3_19323104 unknown proteir 3_19323104	11.61 11.61	intergenic
AT1G77800	na	PHD finger fami 1_29253226	11.6	intergenic promoter
AT1G72610	GERMIN-LIKE PROTEIN 1 (GER1)	germin-like proti 1_27340540	11.58	promoter
AT2G43540	na	unknown proteir 2_18073062	11.58	downstream
AT2G43550	na	Encodes a defe 2_18073062	11.58	promoter
AT1G72600	na	hydroxyproline-i 1_27340540	11.58	downstream
AT3G12600	NUDIX HYDROLASE HOMOLOG 16 (NUI		11.58	promoter
AT3G23030	INDOLE-3-ACETIC ACID INDUCIBLE 2 (I	auxin inducible 3_8181920	11.57	promoter
AT3G55734	MICRORNA393B (MIR393B)	Encodes a micr 3_20685363	11.57	intergenic
AT3G55730	MYB DOMAIN PROTEIN 109 (MYB109)	putative transcri 3_20685363	11.57	proximal promoter
AT3G10015	na	pre-tRNA; tRNA 3_3090080	11.57	promoter
AT3G10020	na	unknown proteir 3_3090080	11.57	intergenic
AT3G10030	na	aspartate/glutar 3_3090080	11.57	intergenic
AT4G37290	na	unknown proteir 4_17550421	11.57	promoter
AT2G26710	PHYB ACTIVATION TAGGED SUPPRES		11.56	intergenic
AT1G51690	PROTEIN PHOSPHATASE 2A 55 KDA RE		11.56	proximal promoter
AT5G01810	CBL-INTERACTING PROTEIN KINASE 1		11.54	intergenic
AT5G01820 AT5G41760	SERINE/THREONINE PROTEIN KINASE	Nucleotide-suga 5_16710547	11.54 11.53	intergenic
AT5G41760 AT5G41761	na na	unknown proteir 5 16710547	11.53	intergenic proximal promoter
AT1G02880	THIAMIN PYROPHOSPHOKINASE1 (TPK		11.53	intron
AT1G02880 AT1G70520	CYSTEINE-RICH RLK (RECEPTOR-LIKE		11.53	promoter
AT1G70530	CYSTEINE-RICH RLK (RECEPTOR-LIKE		11.51	intergenic
AT5G63340	na	unknown proteir 5 25379592	11.51	intron
AT5G63350	na	unknown proteir 5_25379592	11.51	intergenic
AT5G63320	NUCLEAR PROTEIN X1 (NPX1)	Encodes NPX1 5_25379592	11.51	promoter
AT4G21750	MERISTEM LAYER 1 (ATML1)	Encodes a hom 4_11555160	11.5	promoter
AT2G23290	MYB DOMAIN PROTEIN 70 (MYB70)	Member of the F 2_9908492	11.5	proximal promoter
AT2G22180	na	hydroxyproline-ı 2_9428129	11.5	proximal promoter
AT2G22760	na	basic helix-loop 2_9680404	11.5	intergenic
AT4G25030	na	unknown proteir 4_12864495	11.5	promoter
AT5G47190	na	Ribosomal prote 5_19163888	11.5	intergenic
AT5G47180	na DLAT DOMAIN PROTEIN 2 (DLAT2)	Plant VAMP (ve 5_19163888	11.5 11.5	promoter
AT2G22170 AT4G00740	PLAT DOMAIN PROTEIN 2 (PLAT2) QUASIMODO 3 (QUA3)	Lipase/lipooxyg 2_9428129 Encodes a Golg 4_311799	11.5 11.5	promoter
AT4G00740 AT5G04530	3-KETOACYL-COA SYNTHASE 19 (KCS		11.5	proximal promoter
AT3G52910	GROWTH-REGULATING FACTOR 4 (GR		11.49	proximal promoter proximal promoter
AT5G52910 AT5G04540	MYOTUBULARIN 2 (MTM2)	Myotubularin-lik 5_1296269	11.49	downstream
AT4G21510	F-BOX STRESS INDUCED 2 (FBS2)	F-box family prc 4_11447252	11.48	promoter
AT5G44060	na	unknown proteir 5_17731596	11.48	exon
AT5G44065	na	This gene enco 5_17731596	11.48	proximal promoter
AT4G21520	na	Transducin/WD 4_11447252	11.48	downstream
AT1G80290	na	a member of th€ 1_30190331	11.47	intergenic
AT1G80300	NUCLEOTIDE TRANSPORTER 1 (NTT1)	Encodes an ATI 1_30190331	11.47	proximal promoter
AT1G70940	PIN-FORMED 3 (PIN3)	A regulator of at 1_26745163	11.47	intron
AT1G23490	ADP-RIBOSYLATION FACTOR 1 (ARF1)		11.45	promoter
AT1G23480	CELLULOSE SYNTHASE-LIKE A3 (CSLA	encodes a gene 1_8336570	11.45	downstream

AT1G32230	RADICAL-INDUCED CELL DEATH1 (RCD	Encodes a prote 1_11612000	11.45	promoter
AT4G23630	VIRB2-INTERACTING PROTEIN 1 (BTI1)		11.45	five_prime_UTR
AT2G46250	na	myosin heavy c 2_18990331	11.42	proximal promoter
AT2G41110	CALMODULIN 2 (CAM2)	Encodes a touc 2_17140125	11.41	promoter
AT2G41090	na	Calcium-binding 2_17140125	11.41	intergenic
AT1G62030	na	Cysteine/Histidii 1_22926788	11.41	promoter
AT2G41100	TOUCH 3 (TCH3)	encodes a calm 2_17140125	11.41	intergenic
AT5G07440	GLUTAMATE DEHYDROGENASE 2 (GDI		11.4	proximal promoter
AT2G20930	na	SNARE-like sur 2_9002968	11.4	proximal promoter
AT2G20940	na	Protein of unknc 2_9002968	11.4	promoter
AT2G20950	na	Arabidopsis phc 2_9002968	11.4	promoter
AT5G57565	na	Protein kinase s 5_23308263	11.4	proximal promoter
AT5G57560	TOUCH 4 (TCH4)	Encodes a cell \ 5_23308263	11.4	five_prime_UTR
AT5G57550	XYLOGLUCAN ENDOTRANSGLUCOSYL		11.4	proximal promoter
AT2G30990 AT5G52930	na	Protein of unknc 2_13191714 Protein of unknc 5_21470126	11.39 11.39	proximal promoter
	na PINOID3 (PID3)	_	11.39	promoter
AT2G26700	PINOID2 (PID2)	Encodes PID2, 2_11368395		promoter
AT3G48050 AT1G13250	'SHUTTLE' IN CHINESE (SUO)	Encodes a large 3_17739865	11.38	promoter
AT1G13250 AT4G32020	GALACTURONOSYLTRANSFERASE-LIK		11.38 11.38	intergenic
AT4G32020	na na	unknown proteir 4_15492009 unknown proteir 4_15492009	11.38	intergenic intron
AT2G20670	na	Protein of unknc 2 8913638	11.38	promoter
AT1G13240	na	pre-tRNA; tRNA 1_4526183	11.38	•
AT1G13240 AT1G13230	na	Encodes a leuci 1 4526183	11.38	intergenic intergenic
AT1G13230 AT1G13245	ROTUNDIFOLIA LIKE 17 (RTFL17)	ROTUNDIFOLI/ 1_4526183	11.38	promoter
AT4G24790	na	AAA-type ATPa 4_12775630	11.37	
AT2G20080	na	unknown proteir 2_8668371	11.35	proximal promoter intergenic
AT2G20080 AT2G29550			11.35	promoter
AT4G23670	TUBULIN BETA-7 CHAIN (TUB7) na	Encodes a beta 2_12646303 Polyketide cycla 4 12334902	11.33	proximal promoter
AT5G16830	SYNTAXIN OF PLANTS 21 (SYP21)	member of SYP 5_5535382	11.34	promoter
AT4G21860	METHIONINE SULFOXIDE REDUCTASE		11.33	promoter
AT1G69570	na	Dof-type zinc fir 1 26164539	11.33	proximal promoter
AT1G28680	na	HXXXD-type ac 1_10078166	11.33	promoter
AT1G28685	na	Potential natura 1_10078166	11.33	exon
AT1G28883	na	Pyridoxal-5'-phc 1_27402328	11.33	proximal promoter
AT1G72810 AT1G72820	na	Mitochondrial st 1_27402328	11.33	proximal promoter
AT4G21865	na	unknown proteir 4_11601748	11.33	promoter
AT5G04550	na	Protein of unknc 5 1306087	11.33	five prime UTR
AT1G29450	na	SAUR-like auxir 1_10305510	11.33	
AT1G29430 AT1G29440	SMALL AUXIN UP RNA 63 (SAUR63)	SAUR-like auxir 1 10305510	11.32	intergenic promoter
AT5G63160	BTB AND TAZ DOMAIN PROTEIN 1 (bt1)		11.32	proximal promoter
AT1G54050	na		11.31	
AT1G54050 AT5G63168	na	HSP20-like cha 1_20178016	11.31	intergenic
AT3G05108	RAPID ALKALINIZATION FACTOR 23 (RA	unknown proteir 5_25336960	11.31	intergenic
AT1G01950	ARMADILLO REPEAT KINESIN 2 (ARK2)		11.31	intergenic promoter
AT1G01930 AT2G24580	na	FAD-dependent 2_10446279	11.3	•
AT2G24380 AT2G38304	na	unknown proteir 2 16047128	11.3	promoter intergenic
AT2G36304 AT2G21300	na	ATP binding mic 2_9119981	11.3	promoter
AT5G08075	na	pre-tRNA; tRNA 5_2588093	11.29	promoter
AT5G08075	SYNTAXIN OF PLANTS 132 (SYP132)	member of SYP 5_2588093	11.29	promoter
AT2G37678	FAR-RED ELONGATED HYPOCOTYL 1 (11.28	proximal promoter
AT2G37676	na	CONTAINS Inte 2_15803455	11.28	three_prime_UTR
AT3G19860	BASIC HELIX-LOOP-HELIX 121 (bHLH12)		11.27	proximal promoter
AT3G19850	na	Phototropic-resi 3 6902339	11.27	proximal promoter
AT3G19850	MYB DOMAIN PROTEIN 17 (MYB17)	LATE MERISTE 3_22670457	11.26	proximal promoter
AT3G08610	na	unknown proteir 3_2615206	11.26	downstream
AT4G24570	DICARBOXYLATE CARRIER 2 (DIC2)	Encodes one of 4_12686366	11.25	promoter
AT3G18220	LIPID PHOSPHATE PHOSPHATASE 4 (LI		11.25	proximal promoter
AT4G24565	na	pre-tRNA; tRNA 4_12686366	11.25	downstream
AT4G24580	ROP1 ENHANCER 1 (REN1)	Encodes a Rho 4_12686366	11.25	intergenic
AT3G04110	GLUTAMATE RECEPTOR 1.1 (GLR1.1)	putative glutama 3_1080769	11.24	intergenic
AT3G04120	GLYCERALDEHYDE-3-PHOSPHATE DEF		11.24	promoter
AT2G45720	na	ARM repeat sur 2_18833130	11.24	promoter
AT5G44255	na	transposable el 5_17828964	11.24	intergenic
AT5G44260	na	Zinc finger C-x8 5_17828964	11.24	intergenic
AT3G49530	NAC DOMAIN CONTAINING PROTEIN 62	Transcription fa 3_18365035	11.24	promoter
AT4G35760	LUMEN THIOL OXIDOREDUCTASE 1 (LT		11.23	intergenic
AT4G35750	na	SEC14 cytosolic 4_16942006	11.23	promoter
AT3G50070	CYCLIN D3;3 (CYCD3;3)	Encode CYCD3 3_18563332	11.22	intergenic
AT1G01310	na	CAP (Cysteine- 1_120659	11.22	exon
AT1G01320	na	Tetratricopeptid 1_120659	11.22	intergenic
AT5G37540	na	Eukaryotic aspa 5_14915084	11.22	intergenic
AT2G35860	FASCICLIN-LIKE ARABINOGALACTAN P		11.21	intergenic
AT3G09560		The PAH1 gene 3_2940224	11.21	proximal promoter
	na			
AT3G09570	na	Lung seven trar 3_2940224	11.21	promoter
AT2G35859	na na	Lung seven trar 3_2940224 Potential natura 2_15062609	11.21 11.21	proximal promoter
AT2G35859 AT2G35880	na na na	Lung seven trar 3_2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609	11.21 11.21 11.21	proximal promoter intergenic
AT2G35859 AT2G35880 AT4G12970	na na na STOMAGEN (STOMAGEN)	Lung seven trar 3_2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879	11.21 11.21 11.21 11.21	proximal promoter intergenic intergenic
AT2G35859 AT2G35880 AT4G12970 AT5G58070	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (1	Lung seven trar 3_2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cysti 4_7585879 Encodes a tem; 5_23501407	11.21 11.21 11.21 11.21 11.21	proximal promoter intergenic intergenic promoter
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840	na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (T GLYOXALASE I HOMOLOG (GLX1)	Lung seven trar 3_2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cystr 4_7585879 Encodes a tem; 5_23501407 Encodes a glyo: 1_3998172	11.21 11.21 11.21 11.21 11.21 11.19	proximal promoter intergenic intergenic promoter intergenic
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850	na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (1 GLYOXALASE I HOMOLOG (GLX1) na	Lung seven trar 3 _2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a temt 5_23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172	11.21 11.21 11.21 11.21 11.21 11.19 11.19	proximal promoter intergenic intergenic promoter intergenic promoter intergenic proximal promoter
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT5G17300	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (T GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1)	Lung seven trar 3_2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a tem; 5_23501407 Encodes a glyo: _13998172 Myb-like transcr 5_5696252	11.21 11.21 11.21 11.21 11.21 11.19 11.19	proximal promoter intergenic intergenic promoter intergenic proximal promoter intergenic
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT5G17300 AT3G52340	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (T GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHOF	Lung seven trar 3 2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a tem; 5_23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 unknown proteir 1_3998172 sucrose-phospf 3_19406944	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.18	proximal promoter intergenic intergenic promoter intergenic proximal promoter intergenic proximal promoter intergenic promoter
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT5G17300 AT3G52340 AT1G19310	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (1 GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHOTE	Lung seven trar 3 _2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a tem; 5_23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 Myb-like transcr 5_5696252 sucrose-phospt 3_19406944 RING/U-box suj 1_6677837	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.18 11.17	proximal promoter intergenic intergenic promoter intergenic proximal promoter intergenic promoter promoter
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT5G17300 AT3G52340 AT1G19310 AT5G13710	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (1 GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHATE PHOSPHOH na STEROL METHYLTRANSFERASE 1 (SM	Lung seven trar 3 _2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cysti 4_7585879 Encodes a tem; 5_23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 Myb-like transcr 5_5696252 sucrose-phosph 3_19406944 RING/U-box sul 1_6677837 SMT1 controls t 5_4426470	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.18 11.17	proximal promoter intergenic intergenic promoter intergenic proximal promoter intergenic promoter promoter intron
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT5G17300 AT3G52340 AT1G19310 AT5G13710 AT4G27320	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (1 GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHATE PHOSPHOH na STEROL METHYLTRANSFERASE 1 (SM' (PHOS34)	Lung seven trar 3 _2940224 Potential natura 2_15062609 PTX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a tem; 5_23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 unknown proteir 1_3998172 unknown proteir 1_3998172 unknown proteir 1_3998172 unknown proteir 1_3998172 unknown proteir 1_3998172 Sucrose-phosph 3_19406944 RING/U-box sur 1_6677837 SMT1 controls t 5_4426470 Contains a univ 4_13677171	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.18 11.17 11.17	proximal promoter intergenic promoter intergenic proximal promoter intergenic promoter promoter promoter intron intergenic
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT5G17300 AT3G52340 AT1G19310 AT5G13710 AT5G23710 AT4G27320 AT4G27310	na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (T GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHATE PHOSPHORA STEROL METHYLTRANSFERASE 1 (SMT (PHOS34) na	Lung seven trar 3 _2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cysti 4_7585879 Encodes a tem; 5_23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 unknown proteir 1_3998172 Myb-like transcr 5_5696252 sucrose-phospt 3_19406944 RING/U-box suj 1_6677837 SMT1 controls t 5_4426470 Contains a univ 4_13677171 B-box type zinc 4_13677171	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.18 11.17 11.17 11.16	proximal promoter intergenic promoter intergenic proximal promoter intergenic promoter promoter intron intergenic intergenic
AT2G35859 AT2G35880 AT4G12970 AT3G58070 AT1G11840 AT1G11850 AT3G17300 AT3G52340 AT1G19310 AT5G13710 AT4G27320 AT4G27320 AT4G27310 AT2G18090	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (T GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHATE PHOSPHOH na STEROL METHYLTRANSFERASE 1 (SM* (PHOS34) na na	Lung seven trar 3_2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a temt 5_23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 Myb-like transcr 5_5696252 sucrose-phosph 3_19406944 RING/U-box suj 1_6677837 SMT1 controls t 5_4426470 Contains a univ 4_13677171 PHD finger fami 2_7864211	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.17 11.17 11.16 11.16 11.15	proximal promoter intergenic promoter intergenic promoter intergenic promoter promoter promoter intron intergenic intergenic promoter
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT5G17300 AT3G52340 AT1G19310 AT4G27310 AT4G27310 AT2G18090 AT3G16620	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (T GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHATE PHOSPHOI- na STEROL METHYLTRANSFERASE 1 (SM* (PHOS34) na na TRANSLOCON OUTER COMPLEX PROT	Lung seven trar 3 _2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a cyst 4_7585879 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 wyb-like transcr 5_5696252 sucrose-phosph 3_19406944 RING/U-box sut 1_6677837 SMT1 controls t 5_4426470 Contains a univ 4_13677171 B-box type zinc 4_13677171 B-box type zinc 4_13677171 DHD finger fami 2_7864211 component of T 3_5662152	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.18 11.17 11.16 11.16 11.16 11.15	proximal promoter intergenic promoter intergenic proximal promoter intergenic promoter intergenic promoter promoter intron intergenic intergenic promoter promoter promoter promoter promoter promoter promoter
AT2G35859 AT2G35880 AT4G12970 AT3G568070 AT1G11840 AT1G11850 AT3G57300 AT3G52340 AT1G19310 AT3G13710 AT4G27320 AT4G27310 AT4G27310 AT3G16620 AT3G16620 AT2G44930	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (T GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHATE PHOSPHOHA STEROL METHYLTRANSFERASE 1 (SMT (PHOS34) na na TRANSLOCON OUTER COMPLEX PROT na	Lung seven trar 3 _2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cysti 4_7585879 Encodes a tems 5_23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 unknown proteir 1_3998172 Myb-like transcr 5_5696252 sucrose-phosph 3_19406944 RING/U-box sur 1_6677837 SMT1 controls t 5_4426470 Contains a univ 4_13677171 B-box type zinc 4_13677171 PHD finger fami 2_7864211 component of T 3_5662152 Plant protein of 2_18534144	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.17 11.17 11.16 11.16 11.15 11.15	proximal promoter intergenic promoter intergenic promoter intergenic proximal promoter intergenic promoter promoter intergenic intergenic intergenic intergenic promoter promoter promoter promoter promoter promoter promoter
ATZG35859 ATZG35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT5G17300 AT3G52340 AT1G19310 AT4G27320 AT4G27310 AT2G18090 AT3G16620 ATZG44930 AT5G24470	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (1 GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHATE PHOSPHOH na STEROL METHYLTRANSFERASE 1 (SM' (PHOS34) na na TRANSLOCON OUTER COMPLEX PROT na PSEUDO-RESPONSE REGULATOR 5 (P	Lung seven trar 3 _2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a temt 5 _23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 Myb-like transor 5_5696252 sucrose-phosph 3_19406944 RING/U-box suj 1_6677837 SMT1 controls t 5_4426470 Contains a univ 4_13677171 PHD finger fami 2_7864211 component of T 3_5662152 Plant protein of 2_18534144 Encodes a pset 5_8359931	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.17 11.17 11.17 11.16 11.16 11.15 11.15	proximal promoter intergenic promoter intergenic promoter intergenic promoter intergenic promoter promoter intron intergenic intron intergenic promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter
AT2G35859 AT2G35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT3G17300 AT3G52340 AT1G19310 AT4G27310 AT4G27310 AT2G18090 AT3G16620 AT2G44930 AT5G24470 AT1G67265	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (1 GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHATE PHOSPHOR NA STEROL METHYLTRANSFERASE 1 (SM (PHOS34) na na TRANSLOCON OUTER COMPLEX PROT na PSEUDO-RESPONSE REGULATOR 5 (P ROTUNDIFOLIA LIKE 21 (RTFL21)	Lung seven trar 3 _2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a cyst 4_7585879 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 wyb-like transcr 5_5696252 sucrose-phosph 3_19406944 RING/U-box sut 1_6677837 SMT1 controls t 5_4426470 Contains a univ 4_13677171 B-box type zinc 4_13677171 B-box type zinc 4_13677171 Component of T_3_5662152 Plant protein of 2_18534144 Encodes a pset 5_8359931 ROTUNDIFOLI 1_25174909	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.18 11.17 11.16 11.16 11.15 11.15 11.14 11.14	proximal promoter intergenic promoter intergenic proximal promoter intergenic promoter intergenic promoter intergenic promoter intron intergenic intergenic promoter promoter promoter promoter promoter promoter proximal promoter intergenic intergenic intergenic
ATZG35859 ATZG35880 AT4G12970 AT5G58070 AT1G11840 AT1G11850 AT5G17300 AT3G52340 AT1G19310 AT4G27320 AT4G27310 AT2G18090 AT3G16620 ATZG44930 AT5G24470	na na na STOMAGEN (STOMAGEN) TEMPERATURE-INDUCED LIPOCALIN (1 GLYOXALASE I HOMOLOG (GLX1) na REVEILLE 1 (RVE1) SUCROSE-6F-PHOSPHATE PHOSPHOH na STEROL METHYLTRANSFERASE 1 (SM' (PHOS34) na na TRANSLOCON OUTER COMPLEX PROT na PSEUDO-RESPONSE REGULATOR 5 (P	Lung seven trar 3 _2940224 Potential natura 2_15062609 TPX2 (targeting 2_15062609 Encodes a cyst 4_7585879 Encodes a temt 5 _23501407 Encodes a glyo: 1_3998172 unknown proteir 1_3998172 Myb-like transor 5_5696252 sucrose-phosph 3_19406944 RING/U-box suj 1_6677837 SMT1 controls t 5_4426470 Contains a univ 4_13677171 PHD finger fami 2_7864211 component of T 3_5662152 Plant protein of 2_18534144 Encodes a pset 5_8359931	11.21 11.21 11.21 11.21 11.21 11.19 11.19 11.19 11.17 11.17 11.17 11.16 11.16 11.15 11.15	proximal promoter intergenic promoter intergenic promoter intergenic promoter intergenic promoter promoter intron intergenic intron intergenic promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter

AT1G70310	SPERMIDINE SYNTHASE 2 (SPDS2)	Spermidine synt 1_26484966	11.12	intergenic
AT1G04110	STOMATAL DENSITY AND DISTRIBUTIO		11.12	proximal promoter
AT1G73670	MAP KINASE 15 (MPK15)	member of MAF 1_27699171	11.11	proximal promoter
AT2G16630	na	Pollen Ole e 1 a 2_7208905	11.11	promoter
AT5G06865	na	Potential natura 5_2132354	11.11	five_prime_UTR
AT5G06860	POLYGALACTURONASE INHIBITING PR		11.11	five_prime_UTR
AT5G06870	POLYGALACTURONASE INHIBITING PR		11.11	proximal promoter
AT3G21320	na	BEST Arabidop: 3_7503470	11.1	proximal promoter
AT1G66940 AT2G01580	na na	protein kinase-r 1_24974806 unknown proteir 2_263351	11.1 11.1	promoter intergenic
AT2G15668	na	unknown proteir 2_7223821	11.1	downstream
AT1G62035	MICRORNA171C (MIR171C)	Encodes a micr 1_22928873	11.09	intergenic
AT2G45440	DIHYDRODIPICOLINATE SYNTHASE (DI		11.08	downstream
AT2G32690	GLYCINE-RICH PROTEIN 23 (GRP23)	Glycine-rich pro 2_13865441	11.08	proximal promoter
AT2G45450	LITTLE ZIPPER 1 (ZPR1)	ZPR1, a small k 2_18733141	11.08	downstream
AT1G33240	GT-2-LIKE 1 (GTL1)	Encodes a plan 1_12056993	11.07	proximal promoter
AT1G33250	na	Protein of unknc 1_12056993	11.07	intergenic
AT2G43010	PHYTOCHROME INTERACTING FACTOR	Isolated as a se 2_17886330	11.06	promoter
AT1G15700	(ATPC2)	One of two gent 1_5398851	11.05	intergenic
AT1G15690	(AVP1)	Encodes a H(+) 1_5398851	11.05	promoter
AT1G74950	(TIFY10B)	TIFY10B; CON1 1_28151154	11.05	proximal promoter
AT1G74960	FATTY ACID BIOSYNTHESIS 1 (FAB1)	Encodes a plast 1_28151154	11.05	intergenic
AT1G15710 AT5G23480	na	prephenate deh 1_5398851	11.05 11.05	intergenic
AT4G36030	na ARMADILLO REPEAT ONLY 3 (ARO3)	SWIB/MDM2 dc 5_7915899 Armadillo repea 4_17048931	11.05	promoter proximal promoter
AT4G36040	DNAJ11 (J11)	Chaperone Dna 4_17048931	11.04	intergenic
AT4G36032	na	Potential natura 4_17048931	11.04	intergenic
AT4G36050	na	endonuclease/e 4_17048931	11.04	intergenic
AT4G36052	na	Potential natura 4_17048931	11.04	intergenic
AT1G22810	na	encodes a mem 1_8075840	11.04	proximal promoter
AT1G22830	na	Tetratricopeptid 1_8075840	11.04	proximal promoter
AT2G23430	(ICK1)	Encodes a cycli 2_9978106	11.03	promoter
AT4G16780	HOMEOBOX PROTEIN 2 (HB-2)	Encodes a hom 4_9447431	11.03	proximal promoter
AT1G59880	na	pre-tRNA; tRNA 1_22034356	11.03	intergenic
AT1G59870	PENETRATION 3 (PEN3)	ATP binding cas 1_22034356	11.03	promoter
AT4G19120	EARLY-RESPONSIVE TO DEHYDRATION		11.02	intron
AT1G10850	na	Leucine-rich rer 1_3611133	11.02	proximal promoter
AT3G60030	SQUAMOSA PROMOTER-BINDING PRO		11.02	proximal promoter
AT1G10840	TRANSLATION INITIATION FACTOR 3 SU		11.02	proximal promoter
AT4G13340 AT4G33030	LEUCINE-RICH REPEAT/EXTENSIN 3 (LI SULFOQUINOVOSYLDIACYLGLYCEROL		11.01 11.01	intergenic proximal promoter
AT2G46830	CIRCADIAN CLOCK ASSOCIATED 1 (CC		11.01	promoter
AT5G04310	na	Pectin lyase-like 5_1205559	11	intron
AT2G46820	PHOTOSYSTEM I P SUBUNIT (PSI-P)	Encodes the P : 2_19245396	11	intergenic
AT3G07360	PLANT U-BOX 9 (PUB9)	Encodes a prot 3_2353811	11	proximal promoter
AT1G28290	ARABINOGALACTAN PROTEIN 31 (AGP		10.99	proximal promoter
AT4G37310	CYTOCHROME P450, FAMILY 81, SUBFA		10.99	three_prime_UTR
AT4G37300	MATERNAL EFFECT EMBRYO ARREST	maternal effect 4_17555972	10.99	downstream
AT4G36370	na	unknown proteir 4_17189526	10.99	intergenic
AT1G32360	na	Zinc finger (CC(1_11672770	10.99	promoter
AT3G62000	na	S-adenosyl-L-m 3_22961329	10.99	promoter
AT4G36380	ROTUNDIFOLIA 3 (ROT3)	Encodes a cyto 4_17189526	10.99	intron
AT4G16140	na	proline-rich fami 4_9128411	10.98	proximal promoter
AT5G13400 AT3G14090	na EXOCYST SUBUNIT EXO70 FAMILY PRO	Major facilitator 5_4299344	10.98 10.97	promoter
AT5G02200	FAR-RED-ELONGATED HYPOCOTYL1-L		10.97	proximal promoter promoter
AT3G14100	na	RNA-binding (R 3_4672675	10.97	promoter
AT3G12910	na	NAC (No Apical 3_4109108	10.97	promoter
AT5G02190	PROMOTION OF CELL SURVIVAL 1 (PC		10.97	intergenic
AT1G79650	RADIATION SENSITIVE23B (RAD23B)	Encodes a men 1_29975515	10.97	promoter
AT2G05520	GLYCINE-RICH PROTEIN 3 (GRP-3)	Encodes a glyci 2_2025992	10.96	promoter
AT4G37470	KARRIKIN INSENSITIVE 2 (KAI2)	HTL belonging t 4_17616841	10.96	three_prime_UTR
AT4G37460	SUPPRESSOR OF RPS4-RLD 1 (SRFR1)		10.96	proximal promoter
AT1G75580	na	SAUR-like auxir 1_28377173	10.95	promoter
AT2G36410	na	Family of unkno 2_15278487	10.95	promoter
AT3G55430 AT3G55440	na TRIOSEPHOSPHATE ISOMERASE (TPI)	O-Glycosyl hydi 3_20552086 Encodes trioser 3_20552086	10.95 10.95	five_prime_UTR proximal promoter
AT3G55440 AT3G57880	na	Calcium-depent 3 21430493	10.95	intergenic
AT1G70944	na	unknown proteir 1_26749405	10.94	promoter
AT3G57870	SUMO CONJUGATION ENZYME 1 (SCE1		10.94	promoter
AT5G10550	GLOBAL TRANSCRIPTION FACTOR GRO		10.93	proximal promoter
AT2G40100	LIGHT HARVESTING COMPLEX PHOTO:		10.93	proximal promoter
AT5G10540	na	Zincin-like meta 5_3336129	10.93	intergenic
AT5G10560	na	Glycosyl hydrol: 5_3336129	10.93	downstream
AT2G40095	na	Alpha/beta hydr 2_16743967	10.93	intron
AT5G56260	na	Ribonuclease E 5_22777592	10.93	promoter
AT4G27950	CYTOKININ RESPONSE FACTOR 4 (CRE		10.92	proximal promoter
AT1G72280	ENDOPLASMIC RETICULUM OXIDORED		10.92	promoter
AT1G30690 AT5G57710	na na	Sec14p-like phc 1_10887512 Double Clp-N m 5_23389100	10.92 10.92	promoter intergenic
AT3G57710	na na	binding; FUNCT 3_21123286	10.92	proximal promoter
AT3G57060 AT3G57062	na	unknown proteir 3_21123286	10.91	intergenic
AT3G57002	na	Glutaredoxin far 3_21123286	10.91	proximal promoter
AT1G62301	na	unknown proteir 1_23020402	10.9	downstream
AT4G35760	LUMEN THIOL OXIDOREDUCTASE 1 (LT		10.89	promoter
AT3G61962	na	This gene enco 3_22946077	10.89	intergenic
AT4G35770	SENESCENCE 1 (SEN1)	Senescence-as 4_16944861	10.89	promoter
AT4G35780	SERINE/THREONINE/TYROSINE KINASE		10.89	intergenic
AT2G26190	na	calmodulin-bind 2_11150580	10.88	promoter
AT2G40475				proximal promoter
	ALTERED SEED GERMINATION 8 (ASG		10.87	
AT1G12520	ALTERED SEED GERMINATION 8 (ASG8 COPPER CHAPERONE FOR SOD1 (CCS	Copper-zinc sur 1_4266867	10.87	intergenic
AT2G23321	ALTERED SEED GERMINATION 8 (ASGE COPPER CHAPERONE FOR SOD1 (CCS na	Copper-zinc sur 1_4266867 unknown proteir 2_9924789	10.87 10.87	intergenic proximal promoter
	ALTERED SEED GERMINATION 8 (ASG8 COPPER CHAPERONE FOR SOD1 (CCS	Copper-zinc sur 1_4266867	10.87	intergenic

AT3G17640	na	Leucine-rich reg 3_6032202	10.87	promoter
AT4G35470	PLANT INTRACELLULAR RAS GROUP-R		10.87	three_prime_UTR
AT3G20070	TITAN9 (TTN9)	Encodes a plan 3_7007078	10.87	promoter
AT2G23320	WRKY DNA-BINDING PROTEIN 15 (WRK		10.87	promoter
AT2G28470	BETA-GALACTOSIDASE 8 (BGAL8)	putative beta-gs 2_12173679	10.86	promoter
AT5G03730	CONSTITUTIVE TRIPLE RESPONSE 1 (C		10.86	intergenic
AT5G03720	HEAT SHOCK TRANSCRIPTION FACTOR		10.86	promoter
AT1G18720	na	Protein of unkno 1_6457170	10.86	intergenic
AT1G68840	RELATED TO ABI3/VP1 2 (RAV2)	Rav2 is part of a 1_25877727	10.86	proximal promoter
AT1G68830	STT7 HOMOLOG STN7 (STN7)	STN7 protein kii 1_25877727	10.86	proximal promoter
AT2G27660	na	Cysteine/Histidii 2_11799446	10.85	exon
AT2G18890	na	Protein kinase s 2_8183743	10.85	promoter
AT3G47750	ATP-BINDING CASSETTE A4 (ABCA4)	member of ATH 3_17606317	10.84	promoter
AT2G46020	BRAHMA (BRM)	Encodes a SWI 2_18922712	10.84	proximal promoter
AT5G66640	DA1-RELATED PROTEIN 3 (DAR3)	DA1-related pro 5_26598328	10.84 10.84	proximal promoter proximal promoter
AT2G46000 AT5G66631	na na	FUNCTIONS IN 2_18922712	10.84	
AT3G12020	na	Tetratricopeptid 5_26598328 P-loop containir 3_3826059	10.84	downstream
AT2G27770	na	Plant protein of 2 11829819	10.84	promoter intergenic
AT1G04690		potassium chan 1_1313025	10.84	proximal promoter
AT3G51960	BASIC LEUCINE ZIPPER 24 (BZIP24)	bZIP transcriptic 3_19281475	10.83	intergenic
AT2G23290	MYB DOMAIN PROTEIN 70 (MYB70)	Member of the F2 9906639	10.83	proximal promoter
AT3G51950	na	Zinc finger (CC(3_19281475	10.83	promoter
AT2G22780	PEROXISOMAL NAD-MALATE DEHYDRO		10.83	intergenic
AT1G71695	na	Peroxidase sup 1_26963425	10.82	proximal promoter
AT3G12190	na	BEST Arabidop: 3_3885210	10.82	proximal promoter
AT4G38690	na	PLC-like phospl 4_18076136	10.82	promoter
AT5G51740	na	Peptidase family 5_21020088	10.82	intergenic
AT4G38700	na	Disease resista 4_18076136	10.82	intergenic
AT4G38710	na	glycine-rich prot 4_18076136	10.82	intergenic
AT5G51750	SUBTILASE 1.3 (SBT1.3)	subtilase 1.3 (S 5_21020088	10.82	promoter
AT1G71696	SUPPRESSOR OF LLP1 1 (SOL1)	Encodes a Puta 1_26963425	10.82	intergenic
AT1G78260	na	RNA-binding (R 1 29448349	10.81	intron
AT3G61310	na	AT hook motif D 3 22693112	10.81	promoter
AT5G16720	na	Protein of unknr 5_5497539	10.81	intergenic
AT5G16720	na	LOCATED IN: c 5_5497539	10.81	promoter
AT5G62230	ERECTA-LIKE 1 (ERL1)	Encodes a rece 5 25002354	10.8	downstream
AT3G51550	` ,	_	10.8	
AT5G62240	FERONIA (FER)	Encodes a syne 3_19121154	10.8	promoter
	na	Cell cycle regul: 5_25002354 Calcium-bindinc 2 17135586		downstream promoter
AT2G41090	na		10.8	
AT3G14310	PECTIN METHYLESTERASE 3 (PME3)	encodes a pecti 3_4773384	10.8	intron
AT1G25390	na	Protein kinase s 1_8911469	10.79	proximal promoter
AT1G25400	na	unknown proteir 1_8911469	10.79	exon
AT3G15470	na	Transducin/WD 3_5221156	10.79	proximal promoter
AT1G11250	SYNTAXIN OF PLANTS 125 (SYP125)	member of SYP 1_3770420	10.79	intergenic
AT1G79840	GLABRA 2 (GL2)	Glabra 2, a horr 1_30035812	10.78	proximal promoter
AT1G61260	na	Protein of unkno 1_22598476	10.78	intergenic
AT5G61270	PHYTOCHROME-INTERACTING FACTOR		10.77	promoter
AT5G40260	(SWEET8)	Nodulin MtN3 fa 5_16088624	10.76	proximal promoter
AT3G16470	JASMONATE RESPONSIVE 1 (JR1)	JA-responsive c 3_5598752	10.76	intron
AT2G40004	na	unknown proteir 2_16706071	10.76	intergenic
AT3G62860	na	alpha/beta-Hydr 3_23240851	10.76	intron
AT1G22570	na	Major facilitator 1_7979475	10.76	proximal promoter
AT4G39330	CINNAMYL ALCOHOL DEHYDROGENAS		10.74	proximal promoter
AT2G41430	EARLY RESPONSIVE TO DEHYDRATION		10.74	promoter
AT2G27050	ETHYLENE-INSENSITIVE3-LIKE 1 (EIL1)		10.74	five_prime_UTR
AT1G02360	na	Chitinase family 1_471595	10.74	intergenic
AT1G02350	na	protoporphyrino 1_471595	10.74	intergenic
AT1G80490	TOPLESS-RELATED 1 (TPR1)	TOPLESS-relat 1_30267454	10.74	promoter
AT5G28646	WAVE-DAMPENED 2 (WVD2)	Encodes a nove 5_10674336	10.74	promoter
AT2G41420	WINDHOSE 2 (WIH2)	proline-rich fami 2_17269221	10.74	proximal promoter
AT1G29330	ENDOPLASMIC RETICULUM RETENTIO		10.73	promoter
AT4G01720	(WRKY47)	member of WRI 4_744137	10.72	proximal promoter
AT2G24540	ATTENUATED FAR-RED RESPONSE (AF		10.72	intergenic
AT5G53560	CYTOCHROME B5 ISOFORM E (CB5-E)		10.72	intergenic
AT5G53570 AT2G24545	na	Ypt/Rab-GAP d 5_21763577 Potential natura 2 10429377	10.72 10.72	promoter
	na na		10.72	proximal promoter promoter
AT2G24550 AT5G45860	na PYR1-LIKE 11 (PYL11)	unknown proteir 2_10429377 Encodes a merr 5_18603621		
AT3G45860 AT3G12560	TRF-LIKE 9 (TRFL9)	Encodes a mer 5_18603621 Encodes a telor 3_3985908	10.72 10.72	intergenic promoter
	BOTRYTIS-INDUCED KINASE1 (BIK1)	Encodes a telor 3_3985908 Encodes a plasi 2_16529400	10.72	promoter proximal promoter
AT2G39660 AT2G39650		Protein of unknr 2 16529400	10.71 10.71	five prime UTR
	na na	unknown proteir 3_5297806	10.71	
AT3G15630	na na	Rubredoxin-like 3 5297806		promoter
AT3G15640 AT3G15620	na	Rubredoxin-like 3_5297806 Required for ph 3 5297806	10.71 10.71	proximal promoter
AT4G33960	UV REPAIR DEFECTIVE 3 (UVR3)	unknown proteir 4_16278918	10.71 10.7	proximal promoter intergenic
AT4G33960 AT5G65920	na na	ARM repeat sur 5_26368366	10.7	proximal promoter
AT5G65920 AT5G65925	na na	unknown proteir 5_26368366	10.7	proximal promoter
AT5G65925 AT5G65930	na ZWICHEL (ZWI)	encodes a nove 5 26368366	10.7	intergenic
AT4G02890	(UBQ14)	Polyubiquitin ge 4_1280157	10.7	promoter
AT5G66055	ANKYRIN REPEAT PROTEIN (AKRP)	A locus involve: 5_26416966	10.69	downstream
AT4G04330	HOMOLOGUE OF CYANOBACTERIAL RI		10.69	proximal promoter
AT1G78610	MECHANOSENSITIVE CHANNEL OF SM		10.69	proximal promoter
AT1G78610 AT1G22060	na	LOCATED IN: v 1_7782522	10.69	proximal promoter
	na na			
AT1G78620	na na	Protein of unknc 1_29573157 unknown proteir 4_1280157	10.69	three_prime_UTR intergenic
AT4G02880 AT2G29510	na	Protein of unknown 2_12634185	10.69 10.69	promoter
AT2G29510 AT5G66052	na na	unknown proteir 5_26416966	10.69	downstream
AT5G66052	na na	unknown proteir 5_26416966	10.69	promoter
AT3G57420		Protein of unknown 3_21252076	10.69	intergenic
		Stone of within 0 Z1Z0ZU/0	10.00	
	na PHE AMMONIA I YASE 1 (pal1)		10 68	provimal promotor
AT2G37040	PHE AMMONIA LYASE 1 (pal1)	Encodes PAL1, 2_15562923	10.68	proximal promoter
AT2G37040 AT3G57410	PHE AMMONIA LYASE 1 (pal1) VILLIN 3 (VLN3)	Encodes PAL1, 2_15562923 Encodes a prote 3_21252076	10.68	proximal promoter
AT2G37040	PHE AMMONIA LYASE 1 (pal1)	Encodes PAL1, 2_15562923 Encodes a prot 3_21252076 translation initia 2_16700877		

AT5G22630	AROGENATE DEHYDRATASE 5 (ADT5)	Encodes a placi 5, 7524802	10.66	exon
AT4G27340	na	Met-10+ like fan 4 13685960	10.66	intergenic
AT4G27330	SPOROCYTELESS (SPL)	Encodes a puta 4_13685960	10.66	proximal promoter
AT5G62370	na	Tetratricopeptid 5_25038922	10.65	intergenic
AT5G62350	na	Plant invertase/ 5_25038922	10.65	intergenic
AT5G62360 AT4G33625	na na	Plant invertase/ 5_25038922 FUNCTIONS IN 4 16154947	10.65 10.65	proximal promoter
AT5G43450	na	encodes a prote 5_17458932	10.65	promoter promoter
AT5G43455	na	pre-tRNA; tRNA 5 17458932	10.65	intergenic
AT5G27030	TOPLESS-RELATED 3 (TPR3)	TOPLESS-relat 5_9515667	10.65	promoter
AT5G24590	TCV-INTERACTING PROTEIN (TIP)	Member of NAc 5_8419061	10.64	promoter
AT1G75750	GAST1 PROTEIN HOMOLOG 1 (GASA1)		10.63	proximal promoter
AT3G44705	na	transposable el 3_16250222	10.63	downstream
AT3G44710 AT1G77480	na na	Plant protein of 3_16250222 Eukaryotic aspa 1_29117512	10.63 10.62	intergenic promoter
AT1G77480	na	unknown proteir 1_29781867	10.62	promoter
AT3G16940	na	calmodulin bind 3_5781191	10.62	proximal promoter
AT4G30790	na	INVOLVED IN: ; 4_14999347	10.62	proximal promoter
AT1G77490	THYLAKOIDAL ASCORBATE PEROXIDA		10.62	promoter
AT5G48250	na	B-box type zinc 5_19563930	10.61	promoter
AT5G02760 AT5G16230	na na	Protein phospha 5_624681 Plant stearoyl-a 5_5306741	10.61 10.61	proximal promoter intergenic
AT5G16235	na	Potential natura 5 5306741	10.61	proximal promoter
AT5G16240	na	Plant stearoyl-a 5_5306741	10.61	promoter
AT2G41170	na	F-box family prc 2_17161272	10.6	promoter
AT2G41178	na	Potential natura 2_17161272	10.6	intergenic
AT4G32300	S-DOMAIN-2 5 (SD2-5)	S-domain-2 5 (\$ 4_15599458	10.6	promoter
AT2G41180 AT2G44080	SIGMA FACTOR BINDING PROTEIN 2 (S ARGOS-LIKE (ARL)		10.6 10.59	intergenic
AT5G02610	na	Encodes ARL, ¿ 2_18236933 Ribosomal L29 : 5 589076	10.59	promoter intergenic
AT5G41140	na	Myosin heavy c 5_16466540	10.59	proximal promoter
AT5G02615	na	pre-tRNA; tRNA 5_589076	10.59	promoter
AT5G20180	na	Ribosomal prote 5_6812432	10.59	intergenic
AT5G20181	na	This gene encor 5_6812432	10.59	exon
AT4G16780	HOMEOBOX PROTEIN 2 (HB-2)	Encodes a hom 4_9443449	10.58	intergenic
AT3G15540 AT3G03626	INDOLE-3-ACETIC ACID INDUCIBLE 19	unknown proteir 3 877578	10.58 10.58	promoter exon
AT3G03020	XYLOGLUCAN ENDOTRANSGLUCOSYL		10.58	proximal promoter
AT1G70300	K+ UPTAKE PERMEASE 6 (KUP6)	potassium trans 1 26477633	10.57	intergenic
AT1G70290	TREHALOSE-6-PHOSPHATASE SYNTHA		10.57	proximal promoter
AT1G74670	GA-STIMULATED ARABIDOPSIS 6 (GAS	Gibberellin-regu 1_28052430	10.56	proximal promoter
AT3G16370	na	GDSL-like Lipas 3_5556650	10.56	promoter
AT4G37580	HOOKLESS 1 (HLS1)	involved in apic: 4_17657863	10.54	proximal promoter
AT1G75530 AT5G20950	na na	Forkhead-assoc 1_28358539 Glycosyl hydrol: 5_7109480	10.54 10.54	proximal promoter intron
AT5G23930	na	Mitochondrial tra 5 8077731	10.54	proximal promoter
AT5G23940	PERMEABLE LEAVES3 (PEL3)	Encodes PERM 5_8077731	10.54	intron
AT5G07290	MEI2-LIKE 4 (ML4)	AML4 A membi 5_2290831	10.53	proximal promoter
AT1G33607	na	Encodes a defe 1_12184290	10.53	intergenic
AT3G56710	SIGMA FACTOR BINDING PROTEIN 1 (S		10.53	promoter
AT2G40970 AT3G13720	(MYBC1) (PRA8)	MYBC1; CONT, 2_17099371 PRA8; CONTAI 3_4496207	10.52 10.52	proximal promoter promoter
AT2G26330	ERECTA (ER)	Homologous to 2_11214393	10.52	promoter
AT1G68872	na	Unknown gene 1_25890565	10.52	exon
AT2G26340	na	unknown proteir 2_11214393	10.52	proximal promoter
AT1G51510	(Y14)	This gene is pre 1_19105622	10.51	proximal promoter
AT5G11260	ELONGATED HYPOCOTYL 5 (HY5)	Basic leucine zi ₁ 5_3595179	10.51	promoter
AT3G56360 AT1G75891	na na	unknown proteir 3_20896205	10.51 10.51	promoter
AT5G11270	OVEREXPRESSOR OF CATIONIC PERC	Potential natura 1_28496267	10.51	proximal promoter downstream
AT2G28830	PLANT U-BOX 12 (PUB12)	Encodes a U-bc 2_12370747	10.51	promoter
AT5G04560	DEMETER (DME)	Encodes a DNA 5_1308427	10.5	proximal promoter
AT2G46780	na	RNA-binding (R 2_19227539	10.5	proximal promoter
AT2G05786	na	unknown proteir 2_2198349	10.49	exon
AT1G70590	na	F-box family prc 1_26617637	10.48	proximal promoter
AT3G23820 AT5G58140	UDP-D-GLUCURONATE 4-EPIMERASE (PHOTOTROPIN 2 (PHOT2)	Membrane-bour 5_23524287	10.48 10.47	three_prime_UTR promoter
AT5G58130	REPRESSOR OF SILENCING 3 (ROS3)	Encodes ROS3 5_23524287	10.47	promoter
AT1G55740	SEED IMBIBITION 1 (SIP1)	seed imbibition 1_20838774	10.46	five_prime_UTR
AT2G28950	EXPANSIN A6 (EXPA6)	Encodes an exr 2_12433901	10.45	promoter
AT1G69760	na	unknown proteir 1_26243616	10.45	proximal promoter
AT2G16660 AT2G16650	na PROTEINACEOUS RNASE P 2 (PRORP2	Major facilitator 2_7219708	10.45 10.45	intron proximal promoter
AT5G28640	ANGUSTIFOLIA 3 (AN3)	Encodes a prote 5 10648802	10.43	intron
AT3G47250	na	Plant protein of 3 17401854	10.44	promoter
AT3G54320	WRINKLED 1 (WRI1)	WRINKLED1 er 3_20117046	10.44	intron
AT5G01260	na	Carbohydrate-b 5_105157	10.43	promoter
AT1G78230	na	Outer arm dyne 1_29429411	10.43	proximal promoter
AT3G07010	na BES1/BZR1 HOMOLOG 3 (BEH3)	Pectin lyase-like 3_2215617 BES1/BZR1 hor 4 10352060	10.43	intron proximal promoter
AT4G18890 AT4G39120	MYO-INOSITOL MONOPHOSPHATASE I		10.42 10.4	intergenic
AT1G55340	na	Protein of unknr 1_20651534	10.4	promoter
AT4G39100	SHORT LIFE (SHL1)	Putative transcr 4_18220353	10.4	promoter
AT5G05190	na	Protein of unknc 5_1540805	10.39	proximal promoter
AT5G62340	na	Plant invertase/ 5_25035850	10.39	intergenic
AT1G01720	(ATAF1)	Belongs to a lar 1_268244	10.38	promoter
AT1G13740 AT1G01725	ABI FIVE BINDING PROTEIN 2 (AFP2) na	Encodes a merr 1_4713189 unknown proteir 1_268244	10.38 10.38	promoter intergenic
AT1G01725 AT1G01710	na na	Acyl-CoA thioes 1_268244	10.38	intergenic
AT3G60760	na	unknown proteir 3_22457965	10.38	intergenic
AT3G60750	na	Transketolase; 3_22457965	10.38	intergenic
AT4G11280	1-AMINOCYCLOPROPANE-1-CARBOXY		10.36	promoter
AT2G36880	METHIONINE ADENOSYLTRANSFERAS	methionine adei 2_15481521 unknown proteir 2_15481521	10.36	promoter
AT2G36881	na	unkilown protell 2_15461521	10.36	downstream

AT2G40120	na	Protein kinase s 2_16759127	10.36	proximal promoter
AT2G30530	na	unknown proteir 2_13006690	10.36	proximal promoter
AT5G44680	na	DNA glycosylas 5_18028283	10.36	proximal promoter
AT3G43720	na	Bifunctional inhi 3_15618207	10.36	proximal promoter
AT5G19160	TRICHOME BIREFRINGENCE-LIKE 11 (T	Encodes a merr 5_6430459	10.36	promoter
AT1G19180	JASMONATE-ZIM-DOMAIN PROTEIN 1 (JAZ1 is a nucle; 1_6621020	10.35	proximal promoter
AT1G03440	na	Leucine-rich rer 1_851775	10.35	proximal promoter
AT4G22190	na	unknown proteir 4_11745518	10.35	proximal promoter
AT4G22200	POTASSIUM TRANSPORT 2/3 (KT2/3)	Encodes AKT2, 4_11745518	10.35	intergenic
AT3G26810	AUXIN SIGNALING F-BOX 2 (AFB2)	auxin signaling 3_9867643	10.34	promoter
AT4G25470	C-REPEAT/DRE BINDING FACTOR 2 (CE		10.34	promoter
AT1G73600	na	S-adenosyl-L-m 1_27667759	10.34	proximal promoter
AT5G50860	na	Protein kinase s 5_20698625	10.34	proximal promoter
AT3G23030	INDOLE-3-ACETIC ACID INDUCIBLE 2 (I/		10.33	proximal promoter
AT2G27700	na	eukaryotic trans 2_11813279	10.33	intergenic
AT1G08920	ERD (EARLY RESPONSE TO DEHYDRA		10.32	five_prime_UTR
AT1G73530	na	RNA-binding (R 1_27647129	10.32	proximal promoter
AT1G73540 AT5G13300	NUDIX HYDROLASE HOMOLOG 21 (NUI		10.32	promoter
AT1G70920	SCARFACE (SFC) HOMEOBOX-LEUCINE ZIPPER PROTEIN	Belongs to 15-rr 5_4262572	10.32 10.31	promoter intron
AT5G01240	LIKE AUXIN RESISTANT 1 (LAX1)	Encodes LAX1 5_97260	10.31	proximal promoter
AT1G68490	na	unknown proteir 1 25691374	10.31	proximal promoter
AT1G08490 AT1G78080	RELATED TO AP2 4 (RAP2.4)	Encodes a merr 1_29367282	10.31	intergenic
AT1G21100	INDOLE GLUCOSINOLATE O-METHYLTE		10.31	downstream
AT1G21100	na	Cupredoxin sup 1_7386711	10.3	downstream
AT2G27770	na	Plant protein of 2_11838725	10.3	intergenic
AT1G48490	na	Protein kinase s 1_17921647	10.3	intergenic
AT1G48480	RECEPTOR-LIKE KINASE 1 (RKL1)	Arabidopsis thal 1 17921647	10.29	intergenic
AT1G03730	na	unknown proteir 1_931767	10.28	five_prime_UTR
AT1G03730	na	Protein kinase s 1_931767	10.28	proximal promoter
AT3G17510	CBL-INTERACTING PROTEIN KINASE 1		10.27	proximal promoter
AT4G25480	DEHYDRATION RESPONSE ELEMENT E		10.27	intergenic
AT2G28355	LOW-MOLECULAR-WEIGHT CYSTEINE-		10.27	intergenic
AT4G19395	MICRORNA168A (MIR168A)	Encodes a micr 4 10578364	10.27	
AT5G04720			10.27	promoter
AT4G36780	ADR1-LIKE 2 (ADR1-L2) BES1/BZR1 HOMOLOG 2 (BEH2)	Encodes a merr 5_1360489 BES1/BZR1 hor 4_17332280	10.25	promoter
AT4G36760 AT4G18540	na	unknown proteir 4 10223729	10.25	intergenic
	• • • • • • • • • • • • • • • • • • • •	RING/U-box su; 5 16085541		proximal promoter promoter
AT5G40250	na		10.25	
AT4G36770	na	UDP-Glycosyltr: 4_17332280	10.25	proximal promoter
AT5G41450	na	RING/U-box suj 5_16590732	10.24 10.24	proximal promoter
AT5G41460	na	Protein of unknr 5_16590732		intron
AT3G62620	na	sucrose-phosph 3_23159085	10.24	proximal promoter
AT3G15770	na	unknown proteir 3_5339972	10.24	promoter
AT3G15780	na	unknown proteir 3_5339972	10.24	proximal promoter
AT4G34240	ALDEHYDE DEHYDROGENASE 3I1 (ALD		10.23	promoter
AT2G39810	HIGH EXPRESSION OF OSMOTICALLY I		10.23	promoter
AT2G39805	na	Integral membra 2_16612610	10.23	promoter
AT2G45730	na	eukaryotic initial 2_18839380	10.22	promoter
AT1G55546	na	unknown proteir 1_20745297	10.22	downstream
AT3G06450	na	HCO3- transpor 3_1980072	10.22	promoter
AT3G06455	na	ubiquitin family 3_1980072	10.22	promoter
AT2G45740	PEROXIN 11D (PEX11D)	member of the r 2_18839380	10.22	promoter
AT3G15095	HIGH CHLOROPHYLL FLUORESCENCE		10.21	promoter
AT3G15110	na	unknown proteir 3_5081697	10.21	intergenic
AT3G63190	RIBOSOME RECYCLING FACTOR, CHLC		10.21	promoter
AT2G39450	(MTP11)	Encodes a Golg 2_16473950	10.2	promoter
AT4G26000	PEPPER (PEP)	Encodes a nove 4_13196316	10.2	proximal promoter
AT2G39460	RIBOSOMAL PROTEIN L23AA (RPL23AA		10.2	promoter
AT1G30825	DISTORTED TRICHOMES 2 (DIS2)	Involved in trich 1_10959866	10.19	proximal promoter
AT4G37980	ELICITOR-ACTIVATED GENE 3-1 (ELI3-1		10.19 10.19	five_prime_UTR
AT2G17780	MID1-COMPLEMENTING ACTIVITY 2 (MC			promoter
AT4G16520	AUTOPHAGY 8F (ATG8F)	autophagy 8f (A 4_9308694	10.18	promoter
AT5G64570	BETA-D-XYLOSIDASE 4 (XYL4)	Encodes a beta 5_25814479	10.18	proximal promoter
AT4G36780	na RES1/RZP1 HOMOLOG 2 (REH2)	Cysteine/Histidii 2_1640222	10.18	exon
AT4G36780 AT3G57990	BES1/BZR1 HOMOLOG 2 (BEH2)	BES1/BZR1 hor 4_17334473 unknown proteir 3_21473021	10.17 10.17	promoter proximal promoter
AT4G36790	na na	Major facilitator 4 17334473	10.17	proximal promoter proximal promoter
AT1G30630	na	Coatomer epsik 1_10860493	10.17	promoter
AT1G30630	na	Protein kinase f: 1_10860493	10.17	promoter
AT5G05965	na	unknown proteir 5_1792703	10.17	promoter
AT5G15410	DEFENSE NO DEATH 1 (DND1)	'defense, no de: 5_5006992	10.16	promoter
AT5G15410	na	Plant calmodulir 5_5006992	10.16	proximal promoter
AT5G15420	na	unknown proteir 5_5006992	10.16	intergenic
AT4G34050	CAFFEOYL COENZYME A O-METHYLTR		10.15	promoter
AT1G73360	HOMEODOMAIN GLABROUS 11 (HDG11		10.15	three prime UTR
AT1G73350	na	unknown proteir 1_27578830	10.15	proximal promoter
AT1G69850	NITRATE TRANSPORTER 1:2 (NRT1:2)	Encodes an ind 1_26299199	10.15	intron
AT3G13520				proximal promoter
AT5G64260	ARABINOGALACTAN PROTEIN 12 (AGP	Encodes a GPI- 3 4406486	10.14	
	ARABINOGALACTAN PROTEIN 12 (AGP EXORDIUM LIKE 2 (EXL2)	Encodes a GPI- 3_4406486 EXORDIUM like 5_25702707	10.14	proximal promoter
AT3G46700				
	EXORDIUM LIKE 2 (EXL2)	EXORDIUM like 5_25702707	10.14	proximal promoter
AT3G46700	EXORDIUM LIKE 2 (EXL2) na	EXORDIUM like 5_25702707 UDP-Glycosyltri 3_17204724	10.14 10.14	proximal promoter proximal promoter
AT3G46700 AT1G07570	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12)	EXORDIUM like 5_25702707 UDP-Glycosyltri 3_17204724 Protein kinase c 1_2333728	10.14 10.14 10.13	proximal promoter proximal promoter intron
AT3G46700 AT1G07570 AT5G67360 AT1G09560	EXORDIUM LIKE 2 (EXL2) na (APK1A)	EXORDIUM like 5_25702707 UDP-Glycosyltr: 3_17204724 Protein kinase c 1_2333728 Encodes a subt 5_26872278 germin-like prot: 1_3093785	10.14 10.14 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT5G50900	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5)	EXORDIUM like 5_25702707 UDP-Glycosyltr: 3_17204724 Protein kinase c 1_2333728 Encodes a subt 5_26872278 germin-like prot 1_3093785 ARM repeat sur 5_20706804	10.14 10.14 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT5G50900 AT1G15250	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5) na	EXORDIUM like 5_25702707 UDP-Glycosyltr 3_17204724 Protein kinase c 1_2333728 Encodes a subt 5_26872278 germin-like prot 1_3093785 ARM repeat sur 5_20706804 Zinc-binding rib 1_5249665	10.14 10.14 10.13 10.13 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter promoter
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT5G50900 AT1G15250 AT1G15260	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5) na na	EXORDIUM like 5_25702707 UDP-Glycosyltr 3_17204724 Protein kinase c 1_2333728 Encodes a subt 5_26872278 germin-like prot 1_3093785 ARM repeat su; 5_20706804 Zinc-binding rib 1_5249665 unknown proteir 1_5249665	10.14 10.14 10.13 10.13 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter promoter promoter promoter
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT5G50900 AT1G15250 AT1G15260 AT1G65830	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5) na na na	EXORDIUM like 5 _25702707 UDP-Glycosyltra _17204724 Protein kinase c 1 _2333728 Encodes a subt 5 _26872278 germin-like prot 1 _3093785 ARM repeat sur 5 _20706804 Zinc-binding rib 1 _5249665 unknown proteir 1 _524965 pre-tRNA; tRNA 1 _24487858	10.14 10.14 10.13 10.13 10.13 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter promoter promoter proximal promoter
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT5G50900 AT1G15250 AT1G15260 AT1G65830 AT1G07580	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5) na na na na	EXORDIUM like 5_25702707 UDP-Glycosyltr 3_17204724 Protein kinase c 1_2333728 Encodes a subt 5_26872278 germin-like prot 1_3093785 ARM repeat sur, 5_20706804 Zinc-binding rib 1_5249665 unknown proteit 1_5249665 pre-tRNA; tRNA 1_24487858 pre-tRNA; tRNA 1_2333728	10.14 10.14 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT5G50900 AT1G15250 AT1G15260 AT1G65830 AT1G07580 AT1G15270	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5) na na na	EXORDIUM like 5_25702707 UDP-Glycosyltr 3_17204724 Protein kinase c 1_2333728 Encodes a subt 5_26872278 germin-like prot 1_3093785 ARM repeat sur 5_20706804 Zinc-binding ribt 1_5249665 unknown proteir 1_5249665 pre-tRNA; tRNA 1_24487858 Pre-tRNA; tRNA 1_233728 Translation mac 1_5249665	10.14 10.14 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter promoter promoter proximal promoter proximal promoter intergenic
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT5G50900 AT1G15250 AT1G15260 AT1G65830 AT1G07580 AT1G15270 AT5G10946	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5) na na na na na	EXORDIUM like 5 _25702707 UDP-Glycosyltra _17204724 Protein kinase c 1 _2333728 Encodes a subt 5 _26872278 germin-like prot 1 _3093785 ARM repeat sur 5 _20706804 Zinc-binding rib 1 _5249665 unknown proteir 1 _524965 pre-tRNA; tRNA 1 _24487858 pre-tRNA; tRNA 1 _2333728 Translation mac 1 _524965 unknown proteir 5 _3459240	10.14 10.14 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter promoter proximal promoter proximal promoter intergenic proximal promoter proximal promoter proximal promoter intergenic proximal promoter
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT5G50900 AT1G15250 AT1G15260 AT1G65830 AT1G07580 AT1G15270 AT5G10946 AT5G10950	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5) na na na na na na na na	EXORDIUM like 5_25702707 UDP-Glycosyltr 3_17204724 Protein kinase 1_2333728 Encodes a subt 5_26872278 germin-like prot 1_3093785 ARM repeat sur 5_20706804 Zinc-binding rib 1_5249665 unknown proteit 1_5249665 unknown proteit 1_5249685 pre-IRNA; tRNA 1_24487858 pre-IRNA; tRNA 1_24487858 translation mac 1_5249665 unknown proteit 5_3459240 Tudor/PWWP/N 5_3459240	10.14 10.14 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter promoter promoter proximal promoter proximal promoter intergenic proximal promoter downstream
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT1G09560 AT1G15250 AT1G15260 AT1G07580 AT1G07580 AT1G15270 AT5G10946 AT5G10950 AT1G09570	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5) na	EXORDIUM like 5_25702707 UDP-Glycosyltr 3_17204724 Protein kinase c 1_2333728 Encodes a subt 5_26872278 germin-like prot 1_3093785 ARM repeat sur 5_20706804 Zinc-binding rib 1_5249665 unknown proteir 1_5249665 pre-tRNA; tRNA 1_2343728 Translation mac 1_5249665 unknown proteir 5_3459240 Tudor/PWWP/N 5_3459240 Light-labile cyto 1_3093785	10.14 10.14 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter promoter promoter proximal promoter proximal promoter intergenic proximal promoter downstream intergenic
AT3G46700 AT1G07570 AT5G67360 AT1G09560 AT5G50900 AT1G15250 AT1G15260 AT1G65830 AT1G07580 AT1G15270 AT5G10946 AT5G10950	EXORDIUM LIKE 2 (EXL2) na (APK1A) (ARA12) GERMIN-LIKE PROTEIN 5 (GLP5) na na na na na na na na	EXORDIUM like 5_25702707 UDP-Glycosyltr 3_17204724 Protein kinase c 1_2333728 Encodes a subt 5_26872278 germin-like prot 1_3093785 ARM repeat sur 5_20706804 Zinc-binding rib 1_5249665 unknown proteir 1_5249665 pre-tRNA; tRNA 1_2343728 Translation mac 1_5249665 unknown proteir 5_3459240 Tudor/PWWP/N 5_3459240 Light-labile cyto 1_3093785	10.14 10.14 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13 10.13	proximal promoter proximal promoter intron exon promoter promoter promoter promoter proximal promoter proximal promoter intergenic proximal promoter downstream

AT5G16210	na	HEAT repeat-cc 5 5290470	10.12	intergenic
AT5G16200	na	50S ribosomal r 5_5290470	10.12	promoter
AT3G46600	na	GRAS family tra 3_17157862	10.12	promoter
AT5G62865 AT4G31890	na na	unknown proteir 5_25235343 ARM repeat sur 4 15427044	10.11 10.11	intergenic intron
AT4G31830	MAP KINASE 5 (MPK5)	MAP kinase 4_6891878	10.11	promoter
AT5G49280	na	hydroxyproline-ı 5_19977998	10.1	proximal promoter
AT4G23910	na	unknown proteir 4_12430702	10.1	intergenic
AT4G23915	na	Encodes an ala 4_12430702	10.1	intergenic
AT4G23920 AT1G65590	UDP-D-GLUCOSE/UDP-D-GALACTOSE BETA-HEXOSAMINIDASE 3 (HEXO3)	Encodes a prot 4_12430702 Encodes a prot 1_24387536	10.1 10.09	proximal promoter intron
AT3G47340	GLUTAMINE-DEPENDENT ASPARAGINE		10.09	promoter
AT3G47341	na	unknown proteir 3_17441423	10.09	exon
AT5G03110	na	FUNCTIONS IN 5_731832	10.09	intergenic
AT5G03120 AT4G03390	na STRUBBELIG-RECEPTOR FAMILY 3 (SR	unknown proteir 5_731832	10.09 10.09	proximal promoter promoter
AT3G59340	na	Eukaryotic prote 3_21931683	10.09	promoter
AT3G59350	na	Protein kinase s 3_21931683	10.08	proximal promoter
AT1G71691	na	GDSL-like Lipas 1_26952234	10.08	proximal promoter
AT5G50740	na	Heavy metal tra 5_20638402	10.07	promoter
AT2G36400 AT1G62370	GROWTH-REGULATING FACTOR 3 (GR	RING/U-box su ₁ 1_23072985	10.06 10.06	intron exon
AT2G36390	STARCH BRANCHING ENZYME 2.1 (SBI		10.06	intergenic
AT2G28840	XB3 ORTHOLOG 1 IN ARABIDOPSIS TH		10.06	proximal promoter
AT4G36920	APETALA 2 (AP2)	Encodes a flora 4_17398905	10.05	proximal promoter
AT2G22850	BASIC LEUCINE-ZIPPER 6 (bZIP6)	basic leucine-zij 2_9731789	10.05	intron
AT5G65630 AT2G22840	GLOBAL TRANSCRIPTION FACTOR GR GROWTH-REGULATING FACTOR 1 (GR		10.05 10.05	proximal promoter intergenic
AT3G05220	na	Heavy metal tra 3_1488551	10.05	promoter
AT5G19240	na	Glycoprotein m∈ 5_6470069	10.05	promoter
AT5G19250	na	Glycoprotein m€ 5_6470069	10.05	proximal promoter
AT5G55040	na NAD KINA CE 4 (NADK4)	DNA-binding br 5_22331925	10.05	promoter
AT3G21070 AT1G69130	NAD KINASE 1 (NADK1)	Encodes a prot 3_7385189 pre-tRNA; tRNA 1_25988923	10.05 10.04	proximal promoter proximal promoter
AT1G69130 AT1G63860	na	Disease resista: 1 23706229	10.04	promoter
AT1G77210	SUGAR TRANSPORT PROTEIN 14 (STP		10.04	intergenic
AT3G61150	HOMEODOMAIN GLABROUS 1 (HDG1)	Encodes a hom 3_22635384	10.03	intergenic
AT3G61160	na	Protein kinase s 3_22635384	10.03	promoter
AT5G05250	na	unknown proteir 5_1558407	10.01	promoter
AT1G27100 AT3G54200	na na	Actin cross-linki 1_9408783 Late embryoger 3_20065044	10.01 10	intron proximal promoter
AT3G54210	na	Ribosomal prote 3_20065044	10	intergenic
AT1G02390	GLYCEROL-3-PHOSPHATE ACYLTRANS		9.99	promoter
AT1G80400	na	RING/U-box su _l 1_30224121	9.99	proximal promoter
AT3G10960	AZA-GUANINE RESISTANT1 (AZG1)	Encodes a hom 3_3429034	9.98	proximal promoter
AT1G49450	na	Transducin/WD 1_18307179	9.98	three_prime_UTR
AT1G19490 AT3G08590	na 2,3-BIPHOSPHOGLYCERATE-INDEPENI	Basic-leucine zi 1_6754311	9.97 9.96	promoter proximal promoter
AT5G47990	CYTOCHROME P450, FAMILY 705, SUBI		9.96	intergenic
AT3G08600	na	Protein of unknc 3_2612157	9.96	promoter
AT5G42090	na	Lung seven trar 5_16828579	9.96	downstream
AT5G42092	na	Potential natura 5_16828579	9.96	proximal promoter
AT1G29395 AT1G29390	COLD REGULATED 314 INNER MEMBRA COLD REGULATED 314 THYLAKOID ME		9.95 9.95	downstream
AT1G29390 AT1G66500	na	Pre-mRNA clea 1_24812718	9.95	intron promoter
AT1G66510	na	AAR2 protein fa 1_24812718	9.95	promoter
AT5G15220	na	Ribosomal prote 5_4942964	9.95	promoter
AT3G18710	PLANT U-BOX 29 (PUB29)	Encodes a prote 3_6438017	9.95	proximal promoter
AT2G23450	na	Protein kinase s 2_9991351	9.94	intron
AT3G06130 AT1G15520	na ATP-BINDING CASSETTE G40 (ABCG40	Heavy metal tra 3_1855051	9.94 9.93	five_prime_UTR proximal promoter
AT3G27170	CHLORIDE CHANNEL B (CLC-B)	member of Anio 3_10022674	9.93	proximal promoter
AT1G42540	GLUTAMATE RECEPTOR 3.3 (GLR3.3)	member of Puta 1_15976966	9.93	intergenic
AT5G01880	na	RING/U-box su _I 5_339400	9.93	exon
AT5G01881	na	unknown proteir 5_339400	9.93	promoter
AT1G15530 AT5G39050	na PHENOLIC GLUCOSIDE MALONYLTRAN	Concanavalin A 1_5339612 Encodes a malc 5_15630834	9.93 9.93	intergenic intergenic
AT1G42550	PLASTID MOVEMENT IMPAIRED1 (PMI1		9.93	promoter
AT1G12610	DWARF AND DELAYED FLOWERING 1	Encodes a merr 1_4289479	9.91	intergenic
AT2G35470	na	unknown proteir 2_14908762	9.91	downstream
AT2G35480	na	unknown proteir 2_14908762	9.91	proximal promoter
AT2G29660 AT3G49870	na ADP-RIBOSYLATION FACTOR-LIKE A10	zinc finger (C2H 2_12680350	9.91 9.9	exon promoter
AT3G49870	SPHINGOID LCB DESATURASE 1 (SLD1		9.9	promoter
AT3G24503	ALDEHYDE DEHYDROGENASE 2C4 (AL		9.88	promoter
AT3G62630	na	Protein of unknc 3_23162932	9.88	intergenic
AT2G22080	na	unknown proteir 2_9386480	9.88	promoter
AT2G33570	na	Domain of unkn 2_14216682	9.88	proximal promoter
AT2G22430 AT2G47440	HOMEOBOX PROTEIN 6 (HB6) na	Encodes a hom 2_9527842 Tetratricopeptid 2_19469711	9.87 9.87	promoter promoter
AT4G39838	na	Potential natura 4_18487053	9.87	proximal promoter
AT4G39840	na	unknown proteir 4_18487053	9.87	intergenic
AT1G52890	NAC DOMAIN CONTAINING PROTEIN 19	encodes a NAC 1_19699380	9.87	proximal promoter
AT4G26610	D6 PROTEIN KINASE LIKE 1 (D6PKL1)	D6 protein kinas 4_13423935	9.85	proximal promoter
AT4G26600	na PETICI II AN I IKE PROTEIN R2 (RTNI R2	S-adenosyl-L-m 4_13423935	9.85	downstream
AT1G64090 AT3G16720	RETICULAN LIKE PROTEIN B3 (RTNLB3 TOXICOS EN LEVADURA 2 (ATL2)	Reticulan like pr 1_23789186 RING-H2 proteil 3 5693834	9.85 9.85	intron three_prime_UTR
AT4G21437	na	unknown pseud 4_11417356	9.84	intron
AT2G47480	na	Protein of unknc 2_19485602	9.84	proximal promoter
AT2G47485	na	unknown proteir 2_19485602	9.84	promoter
AT2G47490	NAD+ TRANSPORTER 1 (NDT1)	Encodes a chlor 2_19485602	9.84	proximal promoter
AT2G47470 AT5G65670	UNFERTILIZED EMBRYO SAC 5 (UNE5) INDOLE-3-ACETIC ACID INDUCIBLE 9 (I.		9.84 9.83	intergenic promoter
AT1G62660	na	Glycosyl hydrol: 1_23200993	9.83	intron
		, ,		

AT5G05480	na	Peptide-N4-(N-: 5_1624353	9.83	promoter
AT1G44760	na	Adenine nucleo 1_16898610	9.83	five_prime_UTR
AT4G08910	na	unknown proteir 4_5717878	9.83	intergenic
AT5G25615	na	transposable el 5_8923455	9.83	intergenic
AT4G29190	OXIDATION-RELATED ZINC FINGER 2 (C		9.83	promoter
AT5G05490 AT1G71697	SYNAPTIC 1 (SYN1) CHOLINE KINASE 1 (CK1)	Encodes a RAD 5_1624353 Encodes choline 1 26971194	9.83 9.82	exon promoter
AT2G30040	MITOGEN-ACTIVATED PROTEIN KINASE		9.82	intergenic
AT2G30020	na	Encodes AP2C 2_12813677	9.82	proximal promoter
AT2G30032	na	unknown proteir 2_12813677	9.82	intergenic
AT5G44680	na	DNA glycosylas 5_18026132	9.82	promoter
AT5G45660	na	unknown proteir 5_18527619	9.82	intergenic
AT5G45670 AT5G19780	na Tubulun Al DHA E (TUAE)	GDSL-like Lipas 5_18527619	9.82 9.82	proximal promoter promoter
AT2G45660	TUBULIN ALPHA-5 (TUA5) AGAMOUS-LIKE 20 (AGL20)	Encodes an isol 5_6686956 Controls flowerii 2_18806888	9.81	intergenic
AT2G45650	AGAMOUS-LIKE 6 (AGL6)	Sequence sugg 2_18806888	9.81	intergenic
AT2G27050	ETHYLENE-INSENSITIVE3-LIKE 1 (EIL1)		9.81	intergenic
AT2G27060	na	Leucine-rich rer 2_11548788	9.81	proximal promoter
AT5G60760	na (OALA)	P-loop containir 5_24436881	9.81	proximal promoter
AT5G63980 AT4G19112	(SAL1) CONSERVED PEPTIDE UPSTREAM OPE	Encodes a bifur 5_25609481	9.8 9.8	promoter promoter
AT5G54510	DWARF IN LIGHT 1 (DFL1)	Encodes an IAA 5_22134790	9.8	proximal promoter
AT5G09590	MITOCHONDRIAL HSO70 2 (MTHSC70-2		9.8	promoter
AT4G19110	na	Protein kinase s 4_10459414	9.8	promoter
AT5G09585	U2 SMALL NUCLEOLAR RNA5 (U2.5)	U2.5; snRNA; g 5_2975183	9.8	exon
AT4G33200	(XI-I)	member of Myo: 4_16002373	9.79	downstream
AT4G30490 AT4G30500	na na	AFG1-like ATPa 4_14902678 Protein of unkno 4_14902678	9.79 9.79	proximal promoter proximal promoter
AT5G54580	na na	RNA-binding (R 5_22173306	9.79	intergenic
AT5G54585	na	unknown proteir 5 22173306	9.79	proximal promoter
AT4G33180	na	alpha/beta-Hydr 4_16002373	9.79	downstream
AT5G60850	OBF BINDING PROTEIN 4 (OBP4)	Encodes a zinc 5_24480344	9.79	promoter
AT1G76185	na	unknown proteir 1_28588669	9.78	proximal promoter
AT5G13080 AT1G67940	WRKY DNA-BINDING PROTEIN 75 (WRK	WRKY/5 is one 5_4151/92 member of NAP 1 25477637	9.78	proximal promoter
AT5G20330	ATP-BINDING CASSETTE 117 (ABCI17) BETA-1,3-GLUCANASE 4 (BETAG4)	beta-1,3-glucan 5_6871022	9.77 9.77	promoter proximal promoter
AT1G67930	na	Golgi transport : 1_25477637	9.77	promoter
AT3G56880	na	VQ motif-contail 3_21059964	9.77	five_prime_UTR
AT4G31800	WRKY DNA-BINDING PROTEIN 18 (WRK		9.77	proximal promoter
AT1G51700	DOF ZINC FINGER PROTEIN 1 (DOF1)	Encodes dof zin 1_19175416	9.75	downstream
AT3G04730 AT1G73060	INDOLEACETIC ACID-INDUCED PROTEI LOW PSII ACCUMULATION 3 (LPA3)	eariy auxin-indu 3_1292091 Low PSII Accur 1_27478826	9.75 9.75	proximal promoter promoter
AT3G04721	na	unknown proteir 3_1292091	9.75	intergenic
AT3G04732	na	unknown proteir 3_1292091	9.75	intergenic
AT5G67630	na	P-loop containir 5_26967185	9.75	downstream
AT5G67620	na	unknown proteir 5_26967185	9.75	proximal promoter
AT1G51710	UBIQUITIN-SPECIFIC PROTEASE 6 (UBF		9.75	downstream
AT3G58750 AT1G29690	CITRATE SYNTHASE 2 (CSY2) CONSTITUTIVELY ACTIVATED CELL DE.	Encodes a pero 3_21727813	9.74 9.74	promoter intergenic
AT4G09965	na	unknown proteir 4_6245698	9.74	promoter
AT4G09970	na	unknown proteir 4_6245698	9.74	promoter
AT1G29670	na	GDSL-like Lipas 1_10374939	9.74	proximal promoter
AT1G29680	na	Protein of unknc 1_10374939	9.74	intergenic
AT5G08150	SUPPRESSOR OF PHYTOCHROME B 5		9.74	proximal promoter
AT1G21470 AT3G16270	na na	BEST Arabidop: 1_7515760 ENTH/VHS fam 3_5513242	9.73 9.73	intergenic promoter
AT3G61840	na	Protein of unknc 3 22893759	9.73	intergenic
AT3G16260	TRNASE Z4 (TRZ4)	Encodes a tRN: 3_5513242	9.73	downstream
AT4G31550	WRKY DNA-BINDING PROTEIN 11 (WRK		9.73	proximal promoter
AT1G19350	BRI1-EMS-SUPPRESSOR 1 (BES1)	Encodes brassii 1_6687260	9.72	proximal promoter
AT1G22651 AT1G22660	na na	unknown proteir 1_8016825	9.72 9.72	intergenic proximal promoter
AT3G57630	na	Polynucleotide (1_8016825 exostosin family 3_21344156	9.72	promoter
AT1G19340	na	Methyltransfera: 1 6687260	9.72	downstream
AT3G14860	na	NHL domain-co 3_5002214	9.72	proximal promoter
AT3G14870	na	Plant protein of 3_5002214	9.72	promoter
AT1G13260 AT3G59970	RELATED TO ABI3/VP1 1 (RAV1) METHYLENETETRAHYDROFOLATE REI	Encodes an AP: 1_4542032	9.72 9.71	promoter
AT1G01490	na	Heavy metal tra 1_183471	9.71	promoter proximal promoter
AT4G29130	HEXOKINASE 1 (HXK1)	Encodes a hexc 4_14359719	9.7	intergenic
AT5G43020	na	Leucine-rich reg 5_17257916	9.7	promoter
AT1G77630	LYSIN-MOTIF (LYSM) DOMAIN PROTEIN		9.69	promoter
AT5G62280	na	Protein of unknc 5_25019236	9.69	intergenic
AT5G62290 AT5G44130	na FASCICLIN-LIKE ARABINOGALACTAN P	nucleotide-sens 5_25019236	9.69	promoter
AT4G30200	VERNALIZATION5/VIN3-LIKE 1 (VEL1)	Encodes a prot 4_14790585	9.68 9.68	proximal promoter promoter
AT1G73965	CLAVATA3/ESR-RELATED 13 (CLE13)	Member of a lar 1_27816669	9.67	downstream
AT2G02080	INDETERMINATE(ID)-DOMAIN 4 (IDD4)	indeterminate(IE 2_519600	9.67	intron
AT1G73970	na	unknown proteir 1_27816669	9.67	promoter
AT4G15545	na	unknown proteir 4_8875607	9.67	promoter
AT4G30430 AT4G30440	TETRASPANIN9 (TET9) UDP-D-GLUCURONATE 4-EPIMERASE 1	Member of TET 4_14884714 UDP-D-glucuroi 4_14884714	9.67 9.67	intergenic proximal promoter
AT3G08970	(ATERDJ3A)	J domain proteil 3_2737195	9.66	promoter
AT5G62530	ALDEHYDE DEHYDROGENASE 12A1 (A		9.66	intergenic
AT4G33430	BRI1-ASSOCIATED RECEPTOR KINASE	Leu-rich recept 4_16090892	9.66	promoter
AT3G50690	na	Leucine-rich rer 3_18837506	9.66	promoter
AT4G33440	na PASTICCINO 1 (PAS1)	Pectin lyase-like 4_16090892	9.66	proximal promoter
AT3G54010 AT5G62520	PASTICCINO 1 (PAS1) SIMILAR TO RCD ONE 5 (SRO5)	Immunophilin-lik 3_19999743 Encodes a prote 5_25097644	9.66 9.66	proximal promoter promoter
AT4G33050	EMBRYO SAC DEVELOPMENT ARREST		9.65	promoter
AT2G01810	na	RING/FYVE/PH 2_347498	9.65	promoter
AT5G02460	na	Dof-type zinc fir 5_537185	9.64	intergenic
AT3G50480	HOMOLOG OF RPW8 4 (HR4)	Homolog of RP\ 3_18733011	9.63	promoter
AT3G51670	na	SEC14 cytosolic 3_19168337	9.63	proximal promoter

AT1G56630	na	alpha/beta-Hydr 1_21228185	9.62	proximal promoter
AT2G32580	na	Protein of unknc 2_13826280	9.62	proximal promoter
AT2G32560	na	F-box family prc 2_13826280	9.62	intron
AT5G23870	na	Pectinacetyleste 5_8048901	9.62	intron
AT5G55400	na	Actin binding C ₆ 5_22459531	9.62	proximal promoter
AT2G46720	3-KETOACYL-COA SYNTHASE 13 (KCS1		9.61	five_prime_UTR
AT3G21100	na	RNA-binding (R 3_7397487	9.61	proximal promoter
AT2G27310	na	F-box family prc 2_11684227	9.6	exon
AT1G55810	URIDINE KINASE-LIKE 3 (UKL3)	One of the hom 1_20860486	9.6	promoter
AT1G05065	CLAVATA3/ESR-RELATED 20 (CLE20)	Member of a lar 1_1455933	9.59	proximal promoter
AT1G02350	na	protoporphyrino 1_468894	9.59	proximal promoter
AT5G47229	na	This gene enco 5_19178239	9.59	intergenic
AT1G05070 AT2G34720	na NUCLEAR FACTOR Y, SUBUNIT A4 (NF-	Protein of unkno 1_1455933	9.59 9.59	intergenic
AT4G01070	(GT72B1)	the glycosyltran 4 465131	9.59	promoter proximal promoter
AT3G56260	na	unknown proteir 3_20869720	9.58	proximal promoter
AT3G56270	na	Plant protein of 3_20869720	9.58	promoter
AT4G14230	na	FUNCTIONS IN 4_8203380	9.58	promoter
AT3G56800	CALMODULIN 3 (CAM3)	encodes a calm 3_21036228	9.57	promoter
AT5G65460	KINESIN LIKE PROTEIN FOR ACTIN BAS		9.57	proximal promoter
AT3G51600	LIPID TRANSFER PROTEIN 5 (LTP5)	Predicted to enc 3_19137435	9.57	intergenic
AT3G26511	na	unknown proteir 3 9714068	9.57	proximal promoter
AT4G22780	ACT DOMAIN REPEAT 7 (ACR7)	Member of a far 4_11971534	9.56	promoter
AT1G08490	CHLOROPLASTIC NIFS-LIKE CYSTEINE		9.56	promoter
AT1G08500	EARLY NODULIN-LIKE PROTEIN 18 (EN		9.56	promoter
AT4G24972	TAPETUM DETERMINANT 1 (TPD1)	Encodes a nov€ 4_12836875	9.56	promoter
AT4G14680	(APS3)	ATP sulfurylase 4_8415936	9.55	proximal promoter
AT5G66320	GATA TRANSCRIPTION FACTOR 5 (GAT		9.55	proximal promoter
AT5G66330	na	Leucine-rich reg 5_26500292	9.55	downstream
AT1G02560	NUCLEAR ENCODED CLP PROTEASE 5		9.55	promoter
AT4G15620	na	Uncharacterise 4 8914867	9.54	intron
AT5G54470	na	B-box type zinc 5 22116002	9.53	proximal promoter
AT1G04990	na	Zinc finger C-x8 1_1422274	9.52	promoter
AT4G27300	na	S-locus lectin pi 4_13672749	9.52	promoter
AT1G35160	GF14 PROTEIN PHI CHAIN (GF14 PHI)	GF14 protein pl 1 12867051	9.51	promoter
AT5G62220	GLYCOSYLTRANSFERASE 18 (GT18)	Encodes a Golg 5_24991190	9.51	proximal promoter
AT2G20635	na	ATP binding;prc 2_8900175	9.51	promoter
AT2G17300	na	unknown proteir 2_7523050	9.51	promoter
AT2G20630	PP2C INDUCED BY AVRRPM1 (PIA1)	PP2C induced t 2_8900175	9.51	promoter
AT1G65590	BETA-HEXOSAMINIDASE 3 (HEXO3)	Encodes a prote 1 24388582	9.5	intron
AT4G39040	na	RNA-binding CF 4_18191123	9.5	proximal promoter
AT3G08730	PROTEIN-SERINE KINASE 1 (PK1)	Encodes a prote 3_2651208	9.5	intergenic
AT3G08730	SERINE/THREONINE PROTEIN KINASE		9.5	promoter
AT4G18700	CBL-INTERACTING PROTEIN KINASE 12		9.49	intergenic
AT3G60190	DYNAMIN-LIKE 1E (DL1E)	At3g60190 encc 3_22248636	9.49	proximal promoter
AT3G52370	FASCICLIN-LIKE ARABINOGALACTAN P		9.49	proximal promoter
AT1G56165	na	Potential natura 1 21024562	9.49	promoter
AT3G60200	na	unknown proteir 3_22248636	9.49	proximal promoter
AT1G30250	na	unknown proteir 1_10649302	9.49	proximal promoter
AT3G62650	na	unknown proteir 3_23167833	9.49	promoter
AT1G56170	NUCLEAR FACTOR Y, SUBUNIT C2 (NF-		9.49	promoter
AT5G67480	BTB AND TAZ DOMAIN PROTEIN 4 (BT4		9.48	proximal promoter
AT5G67488	na	Potential natura 5_26935055	9.48	downstream
AT5G67480	na	unknown proteir 5 26935055	9.48	promoter
AT5G18440	NUCLEAR FMRP-INTERACTING PROTE		9.48	promoter
AT5G18440	VOLTAGE DEPENDENT ANION CHANNE		9.48	promoter
AT1G07720	3-KETOACYL-COA SYNTHASE 3 (KCS3)		9.47	intergenic
AT5G42100	BETA-1,3-GLUCANASE_PUTATIVE (BG_		9.47	promoter
AT3G26230	CYTOCHROME P450, FAMILY 71, SUBF		9.47	downstream
AT3G26220	CYTOCHROME P450, FAMILY 71, SUBFA		9.47	promoter
AT5G28620	na	protein kinase C 5 10613931	9.47	proximal promoter
AT5G42110	na	unknown proteir 5_16831308	9.47	intergenic
AT4G03550	GLUCAN SYNTHASE-LIKE 5 (GSL05)	Encodes a callo 4 1579886	9.46	downstream
AT5G64250	na	Aldolase-type T 5_25701190	9.46	proximal promoter
AT1G67580	na	Protein kinase s 1_25332725	9.46	proximal promoter
AT1G67590	na	Remorin family 1_25332725	9.46	intergenic
AT5G02240	na	Protein is tyrosii 5_451340	9.46	promoter
AT4G03560	TWO-PORE CHANNEL 1 (TPC1)	Encodes a dept 4_1579886	9.46	promoter
AT3G20290	EPS15 HOMOLOGY DOMAIN 1 (EHD1)	Encodes AtEHE 3_7078977	9.45	promoter
AT3G20300	na	Protein of unknc 3_7078977	9.45	intergenic
AT5G57780	P1R1 (P1R1)	Encodes a atypi 5_23406428	9.45	promoter
AT5G24910	CYTOCHROME P450, FAMILY 714, SUBF		9.44	promoter
AT1G23020	FERRIC REDUCTION OXIDASE 3 (FRO3		9.44	promoter
AT5G48460	na	Actin binding Ca 5_19639604	9.44	promoter
AT4G14900	na	FRIGIDA-like pr 4_8523937	9.44	promoter
AT1G69260	ABI FIVE BINDING PROTEIN (AFP1)	ABI five binding 1_26037829	9.43	proximal promoter
AT1G69252	na	other RNA 1_26037829	9.43	downstream
AT1G69270	RECEPTOR-LIKE PROTEIN KINASE 1 (R		9.43	intergenic
AT4G13395	ROTUNDIFOLIA LIKE 12 (RTFL12)	ROTUNDIFOLI/ 4_7787424	9.43	proximal promoter
AT1G28480	(GRX480)	Encodes GRX4 1_10014243	9.42	promoter
AT5G03730	CONSTITUTIVE TRIPLE RESPONSE 1 (C		9.42	proximal promoter
AT5G03740	HISTONE DEACETYLASE 2C (HD2C)	HD2-type histor 5_981725	9.42	promoter
AT1G61350	na	ARM repeat sur 1_22632794	9.41	proximal promoter
AT5G22950	(VPS24.1)	VPS24.1; CON 5_7680405	9.4	proximal promoter
AT1G78280	na	transferases, tra 1_29452662	9.4	five_prime_UTR
AT1G78265	na	Potential natura 1_29452662	9.4	intergenic
AT4G33150	na	Encodes two pr 4_15991938	9.4	promoter
AT3G62260	na	Protein phospha 3_23040879	9.4	promoter
AT4G28910	NOVEL INTERACTOR OF JAZ (NINJA)	novel interactor 4_14266792	9.4	promoter
AT1G09960	SUCROSE TRANSPORTER 4 (SUT4)	low affinity (10rr 1_3242946	9.4	proximal promoter
AT1G78270			0.4	promoter
A110/02/0	UDP-GLUCOSYL TRANSFERASE 85A4 (UDP-glucosyl tr 1_29452662	9.4	promoter
AT4G28730	UDP-GLUCOSYL TRANSFERASE 85A4 (GLUTAREDOXIN C5 (GrxC5)	Encodes a gluta 4_14198571	9.4	proximal promoter
AT4G28730 AT3G12110	GLUTAREDOXIN C5 (GrxC5) ACTIN-11 (ACT11)	Encodes a gluta 4_14198571 Encodes an act 3_3857598	9.39 9.38	proximal promoter promoter
AT4G28730	GLUTAREDOXIN C5 (GrxC5)	Encodes a gluta 4_14198571 Encodes an act 3_3857598	9.39	proximal promoter

AT5G65940	BETA-HYDROXYISOBUTYRYL-COA HYC hydrolyzes beta 5_26	376477 9	.38	downstream
AT1G24400	LYSINE HISTIDINE TRANSPORTER 2 (LI High-affinity trar 1_86		.38	downstream
AT3G09970	na Calcineurin-like 3_30			downstream
AT1G56150	na SAUR-like auxir 1_21			proximal promoter
AT2G36220	na unknown proteir 2_15			three_prime_UTR
AT1G07250	UDP-GLUCOSYL TRANSFERASE 71C4 (UDP-glucosyl tr 1_22			proximal promoter
AT1G07240	UDP-GLUCOSYL TRANSFERASE 71C5 (UDP-glucosyl tr 1_22			exon
AT5G65930	ZWICHEL (ZWI) encodes a nove 5_26			five_prime_UTR
AT4G37540 AT5G58730	LOB DOMAIN-CONTAINING PROTEIN 39 LOB domain-co 4_17			proximal promoter downstream
AT5G58730	MYO-INOSITOL KINASE (MIK) pfkB-like carbor 5_23 smr (Small Mut\$ 5_23			promoter
AT4G37550	na Acetamidase/Fc 4_17			promoter
AT4G18630	na Protein of unknc 4_10			proximal promoter
AT1G28260	na Telomerase acti 1_98			promoter
AT1G08500	EARLY NODULIN-LIKE PROTEIN 18 (EN early nodulin-lik 1 26			intergenic
AT1G08510	FATTY ACYL-ACP THIOESTERASES B (I Encodes an acy 1_26			three_prime_UTR
AT5G15310	MYB DOMAIN PROTEIN 16 (MYB16) Member of the F 5_49			intergenic
AT5G15320	na unknown proteir 5_49		.35	promoter
AT4G36988	CONSERVED PEPTIDE UPSTREAM OPE Upstream open 4_17		.34	three_prime_UTR
AT3G59420	CRINKLY4 (CR4) Encodes a merr 3_21			promoter
AT2G18960	H(+)-ATPASE 1 (HA1) Encodes a plasi 2_82			intergenic
AT4G36990	HEAT SHOCK FACTOR 4 (HSF4) encodes a prote 4_17			three_prime_UTR
AT2G35020	N-ACETYLGLUCOSAMINE-1-PHOSPHA1 Encodes a prote 2_14			intron
AT1G12990	na beta-1,4-N-acet 1_4		'	promoter
AT5G56590	na O-Glycosyl hydi 5_22			promoter
AT4G37590	NAKED PINS IN YUC MUTANTS 5 (NPY5 A member of the 4_17			promoter
AT5G37020 AT4G32480	AUXIN RESPONSE FACTOR 8 (ARF8) Encodes a merr 5_14 na Protein of unknr 4 15			proximal promoter promoter
AT5G11160	ADENINE PHOSPHORIBOSYLTRANSFE adenine phosph 5 35			five_prime_UTR
AT5G15230	GAST1 PROTEIN HOMOLOG 4 (GASA4) Encodes gibber 5_49			intergenic
AT3G61890	HOMEOBOX 12 (HB-12) Encodes a hom 3_22			proximal promoter
AT1G31350	KAR-UP F-BOX 1 (KUF1) KAR-UP F-box 1_11			five_prime_UTR
AT5G15240	na Transmembrane 5 49			proximal promoter
AT3G49790	na Carbohydrate-b 3_18			downstream
AT3G49796	na This gene enco 3_18			intergenic
AT3G49800	na BSD domain-co 3_18		.32	intergenic
AT3G57930	na unknown proteir 3_21	448771 9	.31	promoter
AT3G57940	na CONTAINS Inte 3_21	448771 9	.31	proximal promoter
AT2G31080	na transposable eli 2_13	3230113 9	.31	intergenic
AT1G67090	RIBULOSE BISPHOSPHATE CARBOXYL Encodes a merr 1_25		.31	downstream
AT5G16560	KANADI (KAN) Encodes a KAN 5_54	11565 9	1.3	promoter
AT5G20700	na Protein of unkno 5_70			promoter
AT4G37610	BTB AND TAZ DOMAIN PROTEIN 5 (bt5) BTB and TAZ di 4_17			promoter
AT1G50290	na unknown proteir 1_18			three_prime_UTR
AT5G64430	na Octicosapeptide 5_25			promoter
AT4G37608	na unknown proteir 4_17			intergenic
AT4G37620	na transposable el 4_17			intergenic
AT1G13110	CYTOCHROME P450, FAMILY 71 SUBFA member of CYP 1_44			promoter
AT1G13100	CYTOCHROME P450, FAMILY 71, SUBF, putative cytochr 1_44			intergenic
AT2G15090 AT5G23850	3-KETOACYL-COA SYNTHASE 8 (KCS8) Encodes KCS8, 2_65 na FUNCTIONS IN 5_86			proximal promoter
AT3G23650 AT3G12150	na FUNCTIONS IN 5_80 na unknown proteir 3_38			intron promoter
AT1G68620	na alpha/beta-Hydi 1_25			promoter
AT5G48540	na receptor-like prc 5_19		-	promoter
AT4G30350	na Double Clp-N m 4_14			intergenic
AT3G18710	PLANT U-BOX 29 (PUB29) Encodes a prote 3_64			promoter
AT1G17120	CATIONIC AMINO ACID TRANSPORTER Encodes a merr 1_58			promoter
AT5G15350	EARLY NODULIN-LIKE PROTEIN 17 (EN early nodulin-lik 5_49			downstream
AT1G06590	na unknown proteir 1_20			proximal promoter
AT1G06610	na pre-tRNA; tRNA 1_20	25493 9	.24	downstream
AT1G06620	na encodes a prot∈ 1_20)25493 9		promoter
AT5G40460	na unknown proteir 5_16	3200767 9		proximal promoter
AT5G15340	na Pentatricopeptic 5_49			proximal promoter
AT5G41600	VIRB2-INTERACTING PROTEIN 3 (BTI3) VIRB2-interactir 5_16			promoter
AT1G17370	OLIGOURIDYLATE BINDING PROTEIN 1 oligouridylate bii 1_59			promoter
AT3G60530	GATA TRANSCRIPTION FACTOR 4 (GAT Encodes a merr 3_22			proximal promoter
AT3G19130 AT2G42570	RNA-BINDING PROTEIN 47B (RBP47B) RNA-binding pri 3_66 TRICHOME BIREFRINGENCE-LIKE 39 (T Encodes a meri 2_17			promoter
AT5G65610	na unknown proteir 5_26			proximal promoter intergenic
AT5G65615	na pre-tRNA; tRNA 5_26			downstream
AT5G65620	na Zincin-like meta 5_26			promoter
AT3G03020 AT3G22370	ALTERNATIVE OXIDASE 1A (AOX1A) Encodes AOX1; 3_79			promoter
AT1G10060	BRANCHED-CHAIN AMINO ACID TRANS encodes a mito: 1_32			intergenic
AT1G10070	BRANCHED-CHAIN AMINO ACID TRANS Encodes a chlor 1_32			proximal promoter
AT4G39350	CELLULOSE SYNTHASE A2 (CESA2) Encodes a cellu 4_18			intergenic
AT5G11890	EMBRYO DEFECTIVE 3135 (EMB3135) FUNCTIONS IN 5_38			promoter
AT4G39360	na unknown proteir 4_18	302623 9	1.2	promoter
AT3G47960	na Major facilitator 3_17			intergenic
AT1G76880	na Duplicated hom 1_28			intergenic
AT5G11900	na Translation initis 5_38			proximal promoter
AT3G05840	(ATSK12) encodes a SHA 3_17			proximal promoter
AT3G61640	ARABINOGALACTAN PROTEIN 20 (AGP: arabinogalactan 3_22			downstream
AT3G57330	AUTOINHIBITED CA2+-ATPASE 11 (ACA Lesion mimic pt 3_21			intron
AT4G09153	LOW-MOLECULAR-WEIGHT CYSTEINE- Encodes a merr 4_58			proximal promoter
AT3G05835	na pre-tRNA; tRNA 3_17 na Encodes alpha- 3_17			downstream
AT3G05830 AT4G09150	na Encodes alpha- 3_17 na T-complex prote 4_58			intergenic three_prime_UTR
AT5G13180	NAC DOMAIN CONTAINING PROTEIN 8: Encodes a NAC 5_41			proximal promoter
AT5G13180	BELL 1 (BEL1) Homeodomain r 5_16			intergenic
AT5G56980	na unknown proteir 5_23			promoter
AT3G61420	na BSD domain (B' 3_22			promoter
AT3G61430				
A13001430	PLASMA MEMBRANE INTRINSIC PROTE a member of the 3_22	2732308 9).18	proximal promoter
AT5G46880	HOMEOBOX-7 (HB-7) homeobox-7 (HI 5_19	9035749 9	.17	downstream
		9035749 9	.17	

AT1G02660	na	alpha/beta-Hydr 1_575640	9.17	proximal promoter
AT1G02670	na	P-loop containir 1_575640	9.17	promoter
AT3G03170	na	unknown proteir 3_731677	9.17	promoter
AT3G03180 AT3G45730	na na	Got1/Sft2-like vi 3_731677 unknown proteir 3_16789837	9.17 9.17	proximal promoter promoter
AT3G45740	na	hydrolase family 3_16789837	9.17	proximal promoter
AT4G36970	na	Remorin family 4_17433014	9.17	proximal promoter
AT5G46890	na	Bifunctional inhi 5_19035749	9.17	intergenic
AT2G45660 AT5G01520	AGAMOUS-LIKE 20 (AGL20) ABA INSENSITIVE RING PROTEIN 2 (AIR	Controls flowerii 2_18814456	9.16 9.15	intergenic intergenic
AT2G40810	HOMOLOG OF YEAST AUTOPHAGY 180		9.15	promoter
AT5G01530	LIGHT HARVESTING COMPLEX PHOTO		9.15	downstream
AT2G04675	na	unknown proteir 2_1637783	9.15	exon
AT5G01542 AT5G25810	na TINY (tny)	Potential natura 5_210493 encodes a mem 5_8993218	9.15 9.15	proximal promoter intergenic
AT1G67370	ASYNAPTIC 1 (ASY1)	meiotic asynapt 1_25238248	9.14	intergenic
AT1G10370	EARLY-RESPONSIVE TO DEHYDRATION		9.14	promoter
AT4G02440 AT1G67360	EMPFINDLICHER IM DUNKELROTEN LIC	EID1 is an F-bo 4_1072378 Rubber elongati 1_25238248	9.14 9.14	promoter
AT1G67365	na	Potential natura 1_25238248	9.14	promoter promoter
AT1G20780	SENESCENCE-ASSOCIATED E3 UBIQUI		9.14	promoter
AT4G02430	SERINE/ARGININE-RICH PROTEIN SPLI		9.14	downstream
AT4G36930 AT3G04620	SPATULA (SPT) D NUCLDUO1-ACTIVATEEIC ACID BIND	Encodes a trans 4_17410677	9.14 9.13	intergenic proximal promoter
AT2G02540	HOMEOBOX PROTEIN 21 (HB21)	Zinc finger hom 2_682521	9.13	proximal promoter
AT3G62090	PHYTOCHROME INTERACTING FACTOR		9.13	proximal promoter
AT3G04630	WVD2-LIKE 1 (WDL1)	Member of a srr 3_1258087	9.13	promoter
AT5G57590 AT1G28430	BIOTIN AUXOTROPH 1 (BIO1) CYTOCHROME P450, FAMILY 705, SUBI	Mutant complen 5_23318302 member of CYP 1_9991984	9.12 9.12	downstream intergenic
AT5G03080	LIPID PHOSPHATE PHOSPHATASE GAM		9.12	promoter
AT2G23770	LYSM-CONTAINING RECEPTOR-LIKE KI		9.12	promoter
AT2G19800 AT1G68470	MYO-INOSITOL OXYGENASE 2 (MIOX2) na		9.12 9.12	proximal promoter
AT4G23820	na	Exostosin family 1_25677293 Pectin lyase-like 4_12399201	9.12	intron intron
AT4G30130	na	Protein of unknc 4_14734175	9.12	proximal promoter
AT5G57580	na (ATOTTO II)	Calmodulin-binc 5_23318302	9.12	promoter
AT4G01320 AT4G26210	(ATSTE24) na	CAAX protease 4_550305 Mitochondrial A 4 13279795	9.1 9.1	intergenic proximal promoter
AT3G07580	na	unknown proteir 3 2422888	9.1	promoter
AT4G01330	na	Protein kinase s 4_550305	9.1	promoter
AT4G01328	na	unknown proteir 4_550305	9.1	exon
AT2G26910 AT1G30570	ATP-BINDING CASSETTE G32 (ABCG32 HERCULES RECEPTOR KINASE 2 (HER		9.09 9.09	promoter proximal promoter
AT4G11820	HYDROXYMETHYLGLUTARYL-COA SYN		9.09	proximal promoter
AT5G19040	ISOPENTENYLTRANSFERASE 5 (IPT5)		9.09	three_prime_UTR
AT1G20460	na BELATED TO ADS 4 (BADS 4)	unknown proteir 1_7090053	9.09	proximal promoter
AT1G78080 AT2G16370	RELATED TO AP2 4 (RAP2.4) THYMIDYLATE SYNTHASE 1 (THY-1)	Encodes a merr 1_29363018 Encodes a bifur 2_7084684	9.09 9.09	proximal promoter promoter
AT2G18290	ANAPHASE PROMOTING COMPLEX 10		9.08	proximal promoter
AT1G69150	na	Cysteine/Histidii 1_25997693	9.08	proximal promoter
AT1G51400 AT1G51402	na na	Photosystem II ! 1_19052717 unknown proteir 1_19052717	9.08 9.08	promoter intron
AT1G31402 AT2G36053	na	unknown proteir 2_15140288	9.08	intergenic
AT1G51390	NFU DOMAIN PROTEIN 5 (NFU5)	Encodes a prote 1_19052717	9.08	intergenic
AT5G03690	FRUCTOSE-BISPHOSPHATE ALDOLASE		9.07	proximal promoter
AT1G01610 AT5G44220	GLYCEROL-3-PHOSPHATE ACYLTRANS na	F-box family prc 5_17809127	9.07 9.07	intron proximal promoter
AT4G30780	na	unknown proteir 4_14990190	9.07	promoter
AT1G01630	na	Sec14p-like phc 1_223339	9.07	intergenic
AT5G03700 AT1G01620	na PLASMA MEMBRANE INTRINSIC PROTE	D-mannose bin: 5_966123	9.07 9.07	exon intergenic
AT1G69120	APETALA1 (AP1)	Floral homeotic 1_25986450	9.06	promoter
AT3G49670	BARELY ANY MÉRISTEM 2 (BAM2)	Encodes a CLA 3_18415781	9.06	proximal promoter
AT5G10450	G-BOX REGULATING FACTOR 6 (GRF6)		9.06	promoter
AT3G49660 AT4G05100	HUMAN WDR5 (WD40 REPEAT) HOMOL MYB DOMAIN PROTEIN 74 (MYB74)	Member of the I 4_2620567	9.06 9.06	downstream intergenic
AT4G10940	na	RING/U-box prc 4_6711281	9.05	promoter
AT4G10950	na	SGNH hydrolas 4_6711281	9.05	downstream
AT2G36050	OVATE FAMILY PROTEIN 15 (OFP15) PROTEIN PHOSPHATASE 2CA (PP2CA)	ovate family pro 2_15136880	9.05	promoter
AT3G11410 AT4G39090	RESPONSIVE TO DEHYDRATION 19 (RE		9.05 9.05	promoter promoter
AT4G39100	SHORT LIFE (SHL1)	Putative transcr 4_18217571	9.05	intergenic
AT4G39080	VACUOLAR PROTON ATPASE A3 (VHA-		9.05	intergenic
AT5G64750 AT1G67560	ABA REPRESSOR1 (ABR1) LIPOXYGENASE 6 (LOX6)	Encodes a puta 5_25890755 PLAT/LH2 dom: 1 25319784	9.04 9.04	proximal promoter promoter
AT4G29140	ACTIVATED DISEASE SUSCEPTIBILITY		9.03	intergenic
AT4G01860	na	Transducin fami 4_808381	9.03	promoter
AT4G01865	na	pre-tRNA; tRNA 4_808381	9.03	promoter
AT4G01870 AT4G01880	na na	tolB protein-rela 4_808381 methyltransfera: 4 808381	9.03 9.03	three_prime_UTR intergenic
AT1G76170	na	2-thiocytidine tR 1_28583591	9.03	intergenic
AT1G76160	SKU5 SIMILAR 5 (sks5)	SKU5 similar 5 1_28583591	9.03	proximal promoter
AT5C62280	na	Tubulin binding 3_21438040	9.02	promoter
AT5G62280 AT5G62270	na na	Protein of unknc 5_25015532 FUNCTIONS IN 5_25015532	9.02 9.02	proximal promoter intergenic
AT5G60978	na	Encodes a ECA 5_24540525	9.01	proximal promoter
AT2G44610	(RAB6A)	Encodes a GTP 2_18410625	9	intergenic
AT1G08640 AT1G13380	CHLOROPLAST J-LIKE DOMAIN 1 (CJD1 na	Encodes a choli 1_2747009 Protein of unknr 1 4590515	9 9	intergenic promoter
AT1G13380 AT2G44600	na na	unknown proteir 2_18410625	9	intergenic
AT1G08630	THREONINE ALDOLASE 1 (THA1)	Encodes a threc 1_2747009	9	intron
ATSG06080	na ATP PINIDING CASSETTE G22 (ABCG22	Encodes a men 3_1838457	8.99	promoter
AT5G06530 AT3G51090	ATP-BINDING CASSETTE G22 (ABCG22 na	Protein of unknr 3_18977283	8.97 8.97	proximal promoter intergenic

ATOC 40000	(PZIP24)	Fd 0 47040404	0.00	
AT2G42380 AT1G08570	(BZIP34) ATYPICAL CYS HIS RICH THIOREDOXIN	Encodes a merr 2_17649191	8.96 8.96	promoter promoter
AT1G53520	FATTY-ACID-BINDING PROTEIN 3 (FAP3		8.96	intergenic
AT4G21200	GIBBERELLIN 2-OXIDASE 8 (GA2OX8)		8.96	intron
AT1G53510	MITOGEN-ACTIVATED PROTEIN KINASE		8.96	proximal promoter
AT1G53200	na	unknown proteir 1_19848600	8.96	intergenic
AT1G53210	na	sodium/calcium 1 19848600	8.96	intergenic
AT1G53220	na	pre-tRNA; tRNA 1_19848600	8.96	intergenic
AT1G53230	TEOSINTE BRANCHED 1, CYCLOIDEA A	Encodes a merr 1_19848600	8.96	intergenic
AT2G03340	WRKY DNA-BINDING PROTEIN 3 (WRKY	Encodes WRKY 2_1018489	8.96	proximal promoter
AT1G27130	GLUTATHIONE S-TRANSFERASE TAU 1	Encodes glutath 1_9425382	8.95	promoter
AT2G03070	MEDIATOR SUBUNIT 8 (MED8)	Encodes a subl 2_908996	8.95	three_prime_UTR
AT1G66725	MICRORNA163 (MIR163)	Encodes a micr 1_24883696	8.95	promoter
AT2G03080	na	transposable el 2_908996	8.95	proximal promoter
AT5G57410	na	Afadin/alpha-ac 5_23267961	8.95	promoter
AT1G75640	na	Leucine-rich rec 1_28402567	8.95	intergenic
AT5G62960	na	unknown proteir 5_25267523	8.95	proximal promoter
AT3G17185 AT1G75630	TRANS-ACTING SIRNA3 (TAS3)	Encodes a trans 3_5861330	8.95 8.95	promoter downstream
AT3G05830	VACUOLAR H+-PUMPING ATPASE 16 KI	Encodes alpha- 3_1735964	8.94	proximal promoter
AT3G03630	DNA-DAMAGE REPAIR/TOLERATION 10		8.93	proximal promoter
AT1G21975	na	unknown proteir 1_7732386	8.93	exon
AT2G19650	na	Cysteine/Histidii 2_8495965	8.93	promoter
AT3G12600	NUDIX HYDROLASE HOMOLOG 16 (NUI		8.93	intergenic
AT3G50240	(KICP-02)	Encodes a kine: 3_18629351	8.92	promoter
AT4G23260	CYSTEINE-RICH RLK (RECEPTOR-LIKE	Encodes a cyst 4_12170364	8.92	promoter
AT4G23270	CYSTEINE-RICH RLK (RECEPTOR-LIKE	Encodes a cyst 4_12170364	8.92	proximal promoter
AT5G04560	DEMETER (DME)	Encodes a DNA 5_1319062	8.92	intergenic
AT1G07670	ENDOMEMBRANE-TYPE CA-ATPASE 4 (8.92	promoter
AT2G23000	SERINE CARBOXYPEPTIDASE-LIKE 10 (8.92	promoter
AT2G13790	SOMATIC EMBRYOGENESIS RECEPTOR		8.92	promoter
AT5G04590	SULFITE REDUCTASE (SIR)	A.thaliana gene 5_1319062	8.92	promoter
AT3G58120	(BZIP61)	Encodes a merr 3_21523512	8.91	promoter
AT1G12570	na	Glucose-methar 1_4282396	8.91	proximal promoter
AT1G12580	PHOSPHOENOLPYRUVATE CARBOXYL		8.91	proximal promoter
AT3G54420 AT3G54440	HOMOLOG OF CARROT EP3-3 CHITINA		8.9 8.9	intergenic
AT4G19420	na	glycoside hydro 3_20148125 Pectinacetylest 4_10591186	8.9	downstream
AT3G54430	na SHI-RELATED SEQUENCE 6 (SRS6)	A member of SF 3 20148125	8.9	proximal promoter five_prime_UTR
AT2G24270	ALDEHYDE DEHYDROGENASE 11A3 (A		8.89	five_prime_UTR
AT5G49360	BETA-XYLOSIDASE 1 (BXL1)	Encodes a bifur 5_20016751	8.89	promoter
AT4G34390	EXTRA-LARGE GTP-BINDING PROTEIN		8.89	promoter
AT2G29120	GLUTAMATE RECEPTOR 2.7 (GLR2.7)	member of Puta 2_12518221	8.89	proximal promoter
AT4G34380	na	Transducin/WD 4_16441053	8.89	intergenic
AT5G49350	na	Glycine-rich pro 5_20016751	8.89	intergenic
AT3G22190	IQ-DOMAIN 5 (IQD5)	IQ-domain 5 (IQ 3_7834062	8.88	promoter
AT1G70944	na	unknown proteir 1_26750435	8.88	proximal promoter
AT1G15360	SHINE 1 (SHN1)	Encodes a merr 1_5281970	8.88	proximal promoter
AT5G64310	ARABINOGALACTAN PROTEIN 1 (AGP1)		8.87	promoter
AT1G42990	BASIC REGION/LEUCINE ZIPPER MOTIF		8.87	promoter
AT2G46080	BYPASS 2 (BPS2)	Encodes a prot 2_18950649	8.87	proximal promoter
AT2G46090	LONG-CHAIN BASE (LCB) KINASE 2 (LC		8.87	promoter
AT5G64320	na	Pentatricopeptic 5_25721734	8.87	intergenic
AT2G19460	na	Protein of unkno 2_8429882	8.87	proximal promoter
AT5G26731	na NITDII ASE 4 (NIT4)	unknown proteir 5_9296179	8.87	three_prime_UTR
AT3G44310 AT1G28230	NITRILASE 1 (NIT1) PURINE PERMEASE 1 (PUP1)	Mutants are res 3_15986699 Encodes a trans 1 9868044	8.87 8.87	promoter
AT1G26230 AT2G19450	TRIACYLGLYCEROL BIOSYNTHESIS DE		8.87	intergenic
AT5G41790		encodes a prote 5 16725737	8.86	downstream proximal promoter
AT1G32780	na	GroES-like zinc: 1_11873018	8.86	promoter
AT3G52700	na	unknown proteir 3_19535570	8.86	three_prime_UTR
AT3G52710	na	unknown proteir 3_19535570	8.86	three_prime_UTR
AT4G20250	na	unknown proteir 4_10940446	8.85	exon
AT4G20260	PLASMA-MEMBRANE ASSOCIATED CAT		8.85	promoter
AT2G47240	LONG-CHAIN ACYL-COA SYNTHASE 1 (Encodes an acy 2_19390703	8.84	proximal promoter
AT5G55620	na	unknown proteir 5_22528755	8.84	proximal promoter
AT5G02530	na	RNA-binding (R 5_566045	8.84	promoter
AT5G60966	na	pre-tRNA; tRNA 5_24533169	8.84	intergenic
AT1G25450	3-KETOACYL-COA SYNTHASE 5 (KCS5)		8.83	promoter
AT1G20693	HIGH MOBILITY GROUP B2 (HMGB2)	Encodes a prote 1_7176624	8.83	promoter
AT4G01530	na	transposable eli 4_663218	8.83	promoter
AT1G20691 AT1G72050	na TRANSCRIPTION FACTOR IIIA (TFIIIA)	Potential natura 1_7176624 Encodes a trans 1_27114761	8.83 8.83	promoter promoter
AT1G72030 AT1G55250	HISTONE MONO-UBIQUITINATION 2 (HU		8.82	downstream
AT1G33230	LEAFY COTYLEDON 2 (LEC2)	Transcription fa: 1 9897675	8.82	intron
AT1G20070	na	unknown proteir 1_6959475	8.82	promoter
AT5G46910	na	Transcription fa 5_19045611	8.82	proximal promoter
AT1G55260	na	Bifunctional inhi 1_20612564	8.82	proximal promoter
AT5G65380	na	MATE efflux fan 5_26124562	8.82	intron
AT5G18650	na	CHY-type/CTCl- 5_6217827	8.8	promoter
AT2G24100	ALTERED SEED GERMINATION 1 (ASG1		8.79	promoter
AT1G09350	GALACTINOL SYNTHASE 3 (GolS3)	Predicted to enc 1_3019590	8.79	promoter
AT3G58790	GALACTURONOSYLTRANSFERASE 15		8.79	promoter
AT1G23070	na	Protein of unknc 1_8175938	8.79	promoter
AT2G31981	na	unknown proteir 2_13610027	8.79	exon
AT2G22426	na	unknown proteir 2_9517529	8.79	intergenic
AT1G57980	na	Nucleotide-suga 1_21443580	8.79	proximal promoter
AT3G58795	na PHYTOCYCTATINI 2 (CYC2)	Potential natura 3_21746559	8.79	downstream
AT2G31980	PHYTOCYSTATIN 2 (CYS2)	PHYTOCYSTA 2_13610027	8.79	promoter
AT1G57990	PURINE PERMEASE 18 (PUP18)	Member of a far 1_21443580	8.79 8.79	proximal promoter promoter
AT1G75440				
V 1.2(-14.2.32V)	UBIQUITIN-CONJUGATING ENZYME 16			•
AT2G42350 AT5G53450	na	RING/U-box su; 2_17640165	8.78	downstream
AT2G42350 AT5G53450 AT1G24170				•

AT1G29170	(WAVE2)	Encodes a merr 1_10195418	8.77	proximal promoter
AT1G24160	na	unknown proteir 1_8556654	8.77	promoter
AT3G47610	na	transcription rec 3_17553071		intergenic
AT1G25275	na	unknown proteir 1_8860659	8.76	promoter
AT1G77746 AT1G77750	na na	unknown proteir 1_29229644 Ribosomal prote 1_29229644	8.76 8.76	intergenic intergenic
AT3G06500	ALKALINE/NEUTRAL INVERTASE C (A/N		8.75	downstream
AT3G12120	FATTY ACID DESATURASE 2 (FAD2)	Major enzyme r 3_3863050	8.75	promoter
AT1G27320	HISTIDINE KINASE 3 (HK3)	Encodes a histic 1_9492769	8.75	downstream
AT1G27330	na	Ribosome asso 1_9492769	8.75	promoter
AT3G12130	na	KH domain-cont 3_3863050		intergenic
AT3G06510	SENSITIVE TO FREEZING 2 (SFR2)	Encodes a prote 3_2015850	8.75	promoter
AT2G41290	STRICTOSIDINE SYNTHASE-LIKE 2 (SSI		8.75	exon
AT3G19150 AT1G06370	KIP-RELATED PROTEIN 6 (KRP6) na	Kip-related proti 3_6617867 pseudogene, sii 1_1940582	8.74 8.73	promoter intergenic
AT1G06360	na	Fatty acid desat 1_1940582		promoter
AT3G18050	na	unknown proteir 3_6182965	8.73	downstream
AT4G11300	na	CONTAINS Inte 4_6877760		intergenic
AT4G12230	na	alpha/beta-Hydr 4_7284456	8.73	promoter
AT2G36640	EMBRYONIC CELL PROTEIN 63 (ECP63)		8.72	exon
AT2G36632	na	unknown proteir 2_15357173	8.72	intergenic
AT2G46580	na	Pyridoxamine 5' 2_19131113	8.72	proximal promoter
AT2G39260 AT3G57020	na na	binding;RNA bir 2_16391621 Calcium-depent 3_21100525	8.72 8.72	intergenic promoter
AT1G01030	NGATHA3 (NGA3)	NGATHA3 (NG, 1_13731	8.72	promoter
AT2G39250	SCHNARCHZAPFEN (SNZ)	Encodes a AP2 2_16391621	8.72	proximal promoter
AT4G15550	INDOLE-3-ACETATE BETA-D-GLUCOSY		8.71	promoter
AT3G09975	na	unknown proteir 3_3068854	8.71	intergenic
AT3G09980	na	Family of unkno 3_3068854	8.71	promoter
AT2G39705	ROTUNDIFOLIA LIKE 8 (RTFL8)	ROTUNDIFOLI/ 2_16553611	8.71	intergenic
AT4G39260	COLD, CIRCADIAN RHYTHM, AND RNA		8.7	promoter
AT2G35840 AT2G35850	na na	Sucrose-6F-phc 2_15057192 unknown proteir 2_15057192	8.7 8.7	intron downstream
AT2G33830	na	Potential natura 2 16707354	8.7	proximal promoter
AT3G28193	na	unknown proteir 3_10515273	8.7	proximal promoter
AT1G31930	EXTRA-LARGE GTP-BINDING PROTEIN			promoter
AT5G11790	N-MYC DOWNREGULATED-LIKE 2 (NDL		8.69	proximal promoter
AT1G31920	na	Tetratricopeptid 1_11464974	8.69	proximal promoter
AT3G61380	TON1 RECRUITING MOTIF 14 (TRM14)		8.69	proximal promoter
AT1G78100	AUXIN UP-REGULATED F-BOX PROTEIN		8.68	promoter
AT1G25425	CLAVATA3/ESR-RELATED 43 (CLE43)	CLAVATA3/ESF 1_8922288	8.68	promoter
AT2G38110 AT2G36950	GLYCEROL-3-PHOSPHATE ACYLTRANS	Heavy metal tra 2_15516678	8.68 8.68	intergenic exon
AT5G18550	na	Zinc finger C-x8 5_6157539	8.68	proximal promoter
AT1G10657	na	Plant protein 15 1_3530415	8.68	promoter
AT5G20700	na	Protein of unknr 5 7008440	8.68	proximal promoter
AT2G25490	EIN3-BINDING F BOX PROTEIN 1 (EBF1)		8.67	downstream
AT5G51550	EXORDIUM LIKE 3 (EXL3)	EXORDIUM like 5_20941461	8.67	proximal promoter
AT5G51545	LOW PSII ACCUMULATION2 (LPA2)	Encodes LPA2 5_20941461		intergenic
AT1G25460	na	NAD(P)-binding 1_8941500		proximal promoter
AT2G25482 AT2G45120	na na	Encodes a ECA 2_10847225 C2H2-like zinc f 2_18602444	8.67 8.67	proximal promoter proximal promoter
AT2G43120 AT2G38120	AUXIN RESISTANT 1 (AUX1)	Encodes an aux 2_15977446	8.66	intergenic
AT5G07860	na	HXXXD-type ac 5_2511080	8.66	promoter
AT1G60160	na	Potassium trans 1_22191510	8.66	promoter
AT2G03980	na	GDSL-like Lipas 2_1259616	8.66	intron
AT4G29330	DERLIN-1 (DER1)	DERLIN-1 (DEF 4_14443080	8.65	proximal promoter
AT4G25640	DETOXIFYING EFFLUX CARRIER 35 (DT		8.65	proximal promoter
AT3G03150	na	unknown proteir 3_729685	8.64	promoter
AT3G03160 AT3G03140	na na	FUNCTIONS IN 3_729685	8.64	promoter
AT1G03990			8.64	
	na	Tudor/PWWP/N 3_729685		intergenic
AT1G19840	na na	Long-chain fatty 1_1028474	8.64	intergenic intergenic
AT1G19840 AT1G04000		-	8.64	intergenic
AT1G04000 AT5G50335	na na na	Long-chain fatty 1_1028474 SAUR-like auxir 1_6868137 unknown proteir 1_1028474 unknown proteir 5_20490826	8.64 8.64 8.64 8.64	intergenic intergenic intergenic
AT1G04000 AT5G50335 AT2G30420	na na na ENHANCER OF TRY AND CPC 2 (ETC2)	Long-chain fatty 1_1028474 SAUR-like auxir 1_6868137 unknown proteir 1_1028474 unknown proteir 5_20490826 In a tandem rep 2_12962268	8.64 8.64 8.64 8.64 8.63	intergenic intergenic intergenic exon proximal promoter promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na	Long-chain fatty 1_1028474 SAUR-like auxir 1_6868137 unknown proteir 1_1028474 unknown proteir 5_20490826 In a tandem rep 2_12962268 pre-tRNA; tRNA 3_22859634	8.64 8.64 8.64 8.64 8.63 8.63	intergenic intergenic intergenic exon proximal promoter promoter promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G45745	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na	Long-chain fatty 1_1028474 SAUR-like auxir 1_6868137 unknown proteir 1_1028474 unknown proteir 5_20490826 In a tandem rep 2_12962268 pre-tRNA; tRNA 3_2859634 pre-tRNA; tRNA 5_18558995	8.64 8.64 8.64 8.63 8.63 8.63	intergenic intergenic intergenic exon proximal promoter promoter promoter downstream
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G45745 AT5G65166	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-tRNA; tRNA 3 22859634 pre-tRNA; tRNA 5 18558995 This gene encoi 5 26036284	8.64 8.64 8.64 8.63 8.63 8.63 8.63	intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G45745 AT5G65166 AT5G45750	na na ENHANCER OF TRY AND CPC 2 (ETC2) na na RAB GTPASE HOMOLOG A1C (RABA1c)	Long-chain fatty 1_1028474 SAUR-like auxir 1_6868137 unknown proteir 1_1028474 unknown proteir 5_20490826 In a tandem rep 2_12962268 pre-tRNA; tRNA 3_22859634 pre-tRNA; tRNA 5_18558995 This gene encoi 5_26036284 RAB GTPase hi 5_18558995	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63	intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G45745 AT5G65166	na na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2)	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-tRNA; tRNA 3 22859634 pre-tRNA; tRNA 5 18558995 This gene encoi 5 26036284	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.63	intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G45745 AT5G65166 AT5G45750 AT2G30424	na na ENHANCER OF TRY AND CPC 2 (ETC2) na na RAB GTPASE HOMOLOG A1C (RABA1c)	Long-chain fatty 1 1028474 SAUR-like auxir 16868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-IRNA; IRNA 5 22859634 pre-IRNA; IRNA 5 18558995 This gene encol 5 26036284 RAB GTPase hi 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.63	intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G45745 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32928 AT1G32930	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87)	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-IRNA; IRNA 5 21855634 pre-IRNA; IRNA 5 18558995 This gene encor 5 26036284 RAB GTPase h 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62	intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G45745 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32932 AT1G32930 AT2G03810	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na	Long-chain fatty 1_1028474 SAUR-like auxir 1_6868137 unknown proteir 1_1028474 unknown proteir 5_20490826 In a tandem rep 2_12962268 pre-tRNA; tRNA 3_22859634 pre-tRNA; tRNA 5_18558995 This gene encor 5_26036284 RAB GTPase hr 5_18558995 In a tandem rep 2_12962268 encoded by the 4_17761835 unknown proteir 1_11931086 Galactosyltrans 1_11931086 18S pre-riboson 2_1161454	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62	intergenic intergenic intergenic intergenic exon proximal promoter promoter downstream downstream promoter intergenic proximal promoter promoter intergenic proximal promoter intergenic interpenic intergenic intergenic intergenic intergenic intergenic interpenic interpenic interpenic interpenic interpenic intergenic interpenic in
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G45745 AT5G45750 AT2G30424 AT4G37780 AT1G32930 AT1G32930 AT2G308110 AT3G51660	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-tRNA; tRNA 3 22859634 pre-tRNA; tRNA 5 18558995 This gene enco 5 26036284 Ras GTPase h 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 1161454 Tautomerase/M 3 19166295	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.63 8.63	intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intergenic intron proximal promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G65166 AT2G30424 AT4G37780 AT1G32928 AT1G32930 AT2G03810 AT3G51660 AT1G35460	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na FLOWERING BHLH 1 (FBH1)	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-IRNA; IRNA 5 2859634 pre-IRNA; IRNA 5 18558995 This gene encor 5 26036284 RAB GTPase h 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 18S pre-riboson 2 1161454 Tautomerase/M 3 19166295 basic helik-loop 1 13039843	8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.62	intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter intergenic proximal promoter intergenic intron proximal promoter proximal promoter promoter promoter promoter promoter promoter promoter promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G45745 AT5G65166 AT4G30424 AT1G32930 AT1G32930 AT2G38310 AT3G51660 AT1G35460 AT1G35460 AT1G35460	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6)	Long-chain fatty 1_1028474 SAUR-like auxir 1_6688137 unknown proteir 1_1028474 unknown proteir 5_20490826 In a tandem rep 2_12962268 pre-tRNA; tRNA 3_22859634 pre-tRNA; tRNA 5_18558995 This gene encor 5_26036284 RAB GTPase hr 5_18558995 In a tandem rep 2_12962268 encoded by the 4_17761835 unknown proteir 1_1931086 Galactosyltrans 1_11931086 18S pre-riboson 2_1161454 Tautomerase/M 3_19166295 basic helix-loop 1_13039843 SKU5-similar 6 1_15606681	8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.62 8.62 8.62	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter downstream downstream promoter intergenic proximal promoter promoter intergenic intergenic intergenic intron proximal promoter promoter intron intron
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G65166 AT2G30424 AT4G37780 AT1G32928 AT1G32930 AT2G03810 AT3G51660 AT1G35460	na na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A)	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 1 2028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-tRNA; tRNA 5 22859634 pre-tRNA; tRNA 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Tautomerase/M 3 19166295 basic helix-loop 1 13039843 SKU5-similar 6 1 15606681 AP4.3A; FUNCI 2 13916288	8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.62	intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter intergenic proximal promoter intergenic intron proximal promoter proximal promoter promoter promoter promoter promoter promoter promoter promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32930 AT2G3810 AT3G51660 AT1G35460 AT1G35460 AT1G35480 AT2G32800	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6)	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 1 2028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-tRNA; tRNA 5 22859634 pre-tRNA; tRNA 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Tautomerase/M 3 19166295 basic helix-loop 1 13039843 SKU5-similar 6 1 15606681 AP4.3A; FUNCI 2 13916288	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.62 8.61 8.61 8.61	intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intron proximal promoter promoter intergenic intron proximal promoter promoter promoter promoter interpromoter promoter promoter promoter promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32930 AT2G3810 AT3G51660 AT1G35460 AT1G35460 AT4G32830 AT2G32830 AT2G32830 AT3G5150 AT3G5150 AT3G5150 AT3G5150 AT3G5150 AT3G5150 AT3G5150	na na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43)	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1,1028474 unknown proteir 1,1028474 unknown proteir 5,20490826 In a tandem rep 2 12962268 pre-tRNA; tRNA 5, 28259634 pre-tRNA; tRNA 5, 18558995 In a tandem rep 2, 18558995 In a tandem rep 2, 12962268 encoded by the 4,17761835 unknown proteir 1,11931086 Galactosyltrans 1,11931086 Galactosyltrans 1,11931086 Salactosyltrans 1,11931086 Salactosyltrans 1,11931086 APA:3A; FUNC 1,3039843 SKU5-similar 6 1,15606681 APA:3A; FUNC 1,219316288 AGP17 is a lysir 2,9842001 Encodes a puta 3,197042 CLAVATA3/EST 1,8826691	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.61 8.61 8.61 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter intron promoter intron intergenic
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32928 AT1G32930 AT2G3810 AT3G51660 AT1G35460 AT1G35460 AT1G35460 AT1G35450 AT2G32800 AT2G23130 AT3G01500 AT3G51650 AT3G51650 AT3G51650 AT3G51650	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na ra FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBI	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 11028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-IRNA; IRNA 5 218558935 This gene encor 5 26036284 RAB GTPase h 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Galscheid 11 11931086 Galschei	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.62 8.62 8.63 8.63	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intron proximal promoter intron promoter intergenic intron intron intron intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G45745 AT5G65166 AT4G30424 AT1G32930 AT1G32930 AT2G3810 AT3G51660 AT1G35460 AT1G35460 AT1G253130 AT2G23130 AT3G51500 AT1G251330 AT3G51500 AT1G251330 AT3G51500 AT1G51504	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBF LSD1-LIKE2 (LDL2)	Long-chain fatty 1_1028474 SAUR-like auxir 1_6868137 unknown proteir 1_1028474 unknown proteir 5_20490826 In a tandem rep 2_12962268 pre-tRNA; tRNA 3_22859634 pre-tRNA; tRNA 5_18558995 This gene encor 5_26036284 RAB GTPase hr 5_18558995 In a tandem rep 2_12962268 encoded by the 4_17761835 unknown proteir 1_11931086 Galactosyltrans 1_11931086 18S pre-riboson 2_1161454 Tautomerase/M 3_19166295 basic helix-loop 1_13039843 SKU5-similar 6 1_15606681 AP4_3A; FUNC1 2_13916288 AP4_3A; FUNC1 2_13916288 AP4_3A; FUNC1 2_13916288 AP4_3A; FUNC1 2_13916288 CP17 is a lysir 2_9842001 Encodes a puta 3_197042 CLAVATA3/ES1 1_8926691 Encodes a horn 3_4481999	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.61 8.61 8.61 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter promoter intergenic intron proximal promoter promoter intron promoter intron promoter intron intergenic intron intergenic intron intergenic intron intergenic intergenic intergenic promoter promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32930 AT2G3810 AT3G51660 AT1G35460 AT1G35460 AT1G35460 AT1G253130 AT2G3130 AT2G3130 AT3G31500 AT1G25425 AT5G14400 AT3G13682 AT3G13682 AT3G23118	na na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBILSD1-LIKE2 (LDL2) na	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1,1028474 unknown proteir 1,1028474 unknown proteir 1,2028474 unknown proteir 5,20490826 In a tandem rep 2 12962268 pre-tRNA; tRNA 5, 28259634 pre-tRNA; tRNA 5, 18558995 In a tandem rep 2, 18558995 In a tandem rep 2, 12962268 encoded by the 4,17761835 unknown proteir 1,11931086 Galactosyltrans 1,11931086 Galactosyltrans 1,11931086 Sautomorphism 1,11931086 Galactosyltrans 1,11931086 ABS pre-riboson 2,1161454 Tautomerase/M 3,19166295 basic helix-loop 1,13039843 SKU5-similar 6 1,15606681 AP4.3A; FUNCT 2,13916288 AGP17 is a lysir 2,9842001 Encodes a puta 3,197042 CLAVATA3/EST 1,8826691 Encodes a bras 5,4647552 Encodes a bras 5,4647552 Encodes a bras 5,4847999 unknown proteir 2,9842001	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.61 8.61 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intron proximal promoter promoter intergenic intron promoter promoter intergenic intron promoter intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic promoter exon
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32928 AT1G32928 AT1G32930 AT2G3810 AT3G51660 AT1G35460 AT1G41830 AT2G23130 AT3G51560 AT1G25425 AT5G14400 AT3G13682 AT5G14400 AT3G13682 AT3G23118	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na RABING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBILSD1-LIKE2 (LDL2) na	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-IRNA; IRNA 5 2859634 pre-IRNA; IRNA 5 18558995 This gene encor 5 26036284 RAB GTPase h 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Galscheid 1 11931086 Galscheid 1 1 16506681 APA-3A; FUNC 2 1 3191628 AGP17 is a lysir 2 9842001 Encodes a puta 3 197042 CLAVATA3/EST 1 826691 Encodes a bras 5 4647552 Encodes a bras 5 4481990 unknown proteir 2 9842001 Late embryoger 2 9842001 Late embryoger 2 9842001	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.62 8.61 8.61 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intron proximal promoter intron proximal promoter intron intergenic intron intergenic promoter exon promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G45745 AT5G65166 AT5G30424 AT4G37780 AT1G32930 AT1G32930 AT2G3810 AT3G51660 AT1G35460 AT1G35460 AT1G32330 AT2G23130 AT3G51501 AT3G3582800 AT1G254330 AT3G3582800 AT1G254330 AT3G3582800 AT1G25425 AT3G3582800 AT1G25425 AT3G358240 AT5G01720	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBF LSD1-LIKE2 (LDL2) na na	Long-chain fatty 1 1028474 SAUR-like auxir 1 16868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-tRNA; tRNA 5 2855634 pre-tRNA; tRNA 5 18558995 This gene encor 5 26036284 RAB GTPase hr 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Say 1161454 Tautomerase/M 3 19166295 basic helix-loop 1 13039843 SKU5-similar 6 1 15606681 AP4.3A; FUNCT 2 13916288 AP4.3A; FUNCT 2 13916288 AP4.3A; FUNCT 2 18926691 Encodes a puta 3 197042 CLAVATA3/ESI 1 8926691 Encodes a forma 5 4487552 Encodes a hom 3 4481999 unknown proteir 2 9842001 RNI-like superfe 5 270670	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.61 8.61 8.61 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter downstream downstream promoter intergenic proximal promoter proximal promoter proximal promoter intergenic intron proximal promoter promoter intron promoter intron promoter proximal promoter promoter exon promoter promoter promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32928 AT1G32928 AT1G32930 AT2G3810 AT3G51660 AT1G35460 AT1G41830 AT2G23130 AT3G51560 AT1G25425 AT5G14400 AT3G13682 AT5G14400 AT3G13682 AT3G23118	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na RABING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBILSD1-LIKE2 (LDL2) na	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-IRNA; IRNA 5 2859634 pre-IRNA; IRNA 5 18558995 This gene encor 5 26036284 RAB GTPase h 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Galscheid 1 11931086 Galscheid 1 1 16506681 APA-3A; FUNC 2 1 3191628 AGP17 is a lysir 2 9842001 Encodes a puta 3 197042 CLAVATA3/EST 1 826691 Encodes a bras 5 4647552 Encodes a bras 5 4481990 unknown proteir 2 9842001 Late embryoger 2 9842001 Late embryoger 2 9842001	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.62 8.61 8.61 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intron proximal promoter intron proximal promoter intron intergenic intron intergenic promoter exon promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G645745 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32930 AT3G51660 AT1G35460 AT1G35460 AT1G35460 AT1G25425 AT5G14400 AT3G13682 AT2G23118 AT2G23118 AT2G23120 AT5G14410	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBILSD1-LIKE2 (LDL2) na na na na	Long-chain fatty 1 _ 1028474 SAUR-like auxir _ 16868137 unknown proteir 1 _ 1028474 unknown proteir 5 _ 20490826 In a tandem rep 2 _ 12962268 pre-tRNA; tRNA 5 _ 18558995 This gene encor 5 _ 26036284 RAB GTPase In 5 _ 18558995 In a tandem rep 2 _ 12962268 encoded by the 4 _ 17761835 unknown proteir 1 _ 11931086 Galactosyltrans 1 _ 11931086 Galactosyltrans 1 _ 11931086 SB pre-riboson 2 _ 1161454 Tautomerase/M 3 _ 19166295 basic helik-loop 1 _ 13039843 SKU5-similar 6 1 _ 15606681 AP4-3A; FUNCT 2 _ 13916288 AP6-17 is a lysir 2 _ 9842001 Encodes a puta 3 _ 197042 CLAVATA3/ESI _ 1826691 Encodes a hom 3 _ 4481999 unknown proteir 2 _ 9842001 RNI-like superfa 5 _ 270670 unknown proteir 5 _ 270670 Encodes RGLG 5 _ 4647552 Encodes RGLG 5 _ 4647552 Encodes RGLG 5 _ 4647552 Encodes Inmily 3 _ 3173026	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.61 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intron proximal promoter promoter intergenic intron promoter intergenic intron promoter intergenic intergenic intergenic intergenic promoter proximal promoter proximal promoter proximal promoter intergenic intergenic promoter exon promoter promoter promoter promoter promoter
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G645745 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32930 AT3G51660 AT1G35460 AT1G35460 AT1G35460 AT1G25425 AT5G14400 AT3G13682 AT2G23118 AT2G23120 AT5G14410 AT5G14420 AT5G14450 AT5G14450 AT5G14450 AT5G14450	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBILSD1-LIKE2 (LDL2) na na na RING DOMAIN LIGASE2 (RGLG2) na na	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 1 1028474 unknown proteir 1 2024228 In a tandem rep 2 12962288 pre-tRNA; tRNA 3 22859634 pre-tRNA; tRNA 5 18558995 This gene enco 5 26036284 Ras GTPase h 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Salactosyltrans 1 116454 Tautomerase/M 3 19166295 basic helix-loop 1 15606681 AP4.3A; FUNCT 2 13916288 AGP17 is a lysir 2 9842001 Encodes a puta 3 197042 CLAVATA3/EST 1 8926691 Encodes a bras 5 4647552 Encodes a hom 3 4481999 unknown proteir 2 9842001 Late embryoger 2 9842001 Late embryoger 2 9842001 Unknown proteir 5 2 4647552 Encodes RGLG 5 5 6182710	8.64 8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.61 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6 8.6	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intron proximal promoter intron promoter intergenic intron promoter intergenic intron promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic intergenic intergenic promoter promoter promoter promoter promoter promoter promoter intergenic promoter intergenic promoter five_prime_UTR
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32928 AT1G329380 AT2G3810 AT3G51660 AT1G35460 AT1G35460 AT1G35400 AT2G23130 AT3G01500 AT3G51660 AT1G25425 AT5G14400 AT3G13682 AT5G14410 AT5G14420 AT3G1260 AT5G14410 AT5G14420 AT3G10260 AT5G14410 AT5G14420 AT3G10260	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na na na RABIGHERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBF LSD1-LIKE2 (LDL2) na na na RING DOMAIN LIGASE2 (RGLG2) na na na RING DOMAIN LIGASE2 (RGLG2) na na	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-IRNA; IRNA 5 218558935 This gene enco; 5 26036284 RAB GTPase h 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Jasper-riboson 2 1161454 Tautomerase/M 3 19166295 basic helix-loop 1 13039843 SKU5-similar 6 1 15606681 AP4.3A; FUNC 2 13918288 AGP17 is a lysir 2 9842001 Encodes a puta 3 197042 CLAVATA3/EST 1 826691 Encodes a hom 3 .4481999 unknown proteir 2 9842001 RNI-like superfe 5 270670 unknown proteir 5 4647552 Encodes RGLG 5 4647552 Encodes RGLG 5 4647552 Reticulon family 3 .3173026 Galactose oxids 5 6182710 Encodes e he lar 5 6467497	8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.61 8.61 8.61 8.63 8.62 8.62 8.62 8.61 8.61 8.62 8.63 8.63 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.63 8.63 8.64 8.65 8.65 8.66	intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter promoter intergenic intron proximal promoter promoter intron promoter intron promoter intron promoter intron promoter intron promoter promoter intron promoter promoter promoter intergenic intergenic promoter exon promoter promo
AT1G04000 AT5G50335 AT2G30420 AT3G61755 AT5G645745 AT5G65166 AT5G45750 AT2G30424 AT4G37780 AT1G32930 AT3G51660 AT1G35460 AT1G35460 AT1G35460 AT1G25425 AT5G14400 AT3G13682 AT2G23118 AT2G23120 AT5G14410 AT5G14420 AT5G14450 AT5G14450 AT5G14450 AT5G14450	na na na ENHANCER OF TRY AND CPC 2 (ETC2) na na na na RAB GTPASE HOMOLOG A1C (RABA1c) TRICHOMELESS 2 (TCL2) MYB DOMAIN PROTEIN 87 (MYB87) na na na na FLOWERING BHLH 1 (FBH1) SKU5-SIMILAR 6 (SKS6) (AP4.3A) ARABINOGALACTAN PROTEIN 17 (AGP CARBONIC ANHYDRASE 1 (CA1) CLAVATA3/ESR-RELATED 43 (CLE43) CYTOCHROME P450, FAMILY 724, SUBILSD1-LIKE2 (LDL2) na na na RING DOMAIN LIGASE2 (RGLG2) na na	Long-chain fatty 1 1028474 SAUR-like auxir 1 6868137 unknown proteir 1 1028474 unknown proteir 5 20490826 In a tandem rep 2 12962268 pre-IRNA; IRNA 5 218558935 This gene enco; 5 26036284 RAB GTPase h 5 18558995 In a tandem rep 2 12962268 encoded by the 4 17761835 unknown proteir 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Galactosyltrans 1 11931086 Jasper-riboson 2 1161454 Tautomerase/M 3 19166295 basic helix-loop 1 13039843 SKU5-similar 6 1 15606681 AP4.3A; FUNC 2 13918288 AGP17 is a lysir 2 9842001 Encodes a puta 3 197042 CLAVATA3/EST 1 826691 Encodes a hom 3 .4481999 unknown proteir 2 9842001 RNI-like superfe 5 270670 unknown proteir 5 4647552 Encodes RGLG 5 4647552 Encodes RGLG 5 4647552 Reticulon family 3 .3173026 Galactose oxids 5 6182710 Encodes e he lar 5 6467497	8.64 8.64 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.62 8.62 8.62 8.62 8.61 8.61 8.61 8.63 8.62 8.62 8.62 8.61 8.61 8.62 8.63 8.63 8.63 8.63 8.63 8.63 8.63 8.63 8.62 8.63 8.63 8.64 8.65 8.65 8.66	intergenic intergenic intergenic intergenic intergenic exon proximal promoter promoter promoter downstream downstream promoter intergenic proximal promoter intergenic intron proximal promoter intron promoter intergenic intron promoter intergenic intron promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic intergenic intergenic promoter promoter promoter promoter promoter promoter promoter intergenic promoter intergenic promoter five_prime_UTR

AT2G31005	na	Encodes a Cyst 2_13194184	8.58	intergenic
AT2G31010	na	Protein kinase s 2_13194184	8.58	promoter
AT3G26960	na	Pollen Ole e 1 a 3_9945813	8.58	promoter
AT5G19230	na	Glycoprotein m€ 5_6467497	8.58	promoter
AT3G12480	NUCLEAR FACTOR Y, SUBUNIT C11 (NF	nuclear factor Y 3_3957653	8.58	promoter
AT4G36930	SPATULA (SPT)	Encodes a trans 4_17414019	8.57	promoter
AT4G27260	(WES1)	encodes an IAA 4_13652501	8.56	proximal promoter
AT1G54210	AUTOPHAGY 12 A (ATG12A)	AUTOPHAGY 1 1_20239738	8.56	proximal promoter
AT1G33610	na	Leucine-rich rer 1_12188869	8.56	promoter
AT4G27720	na	Major facilitator 4_13830950	8.56	promoter
AT2G27900	na	CONTAINS Inte 2_11886089	8.55	downstream
AT4G32350	na	Regulator of Vp 4_15617290	8.55	promoter
AT2G27920	SERINE CARBOXYPEPTIDASE-LIKE 51 (8.55	intron
AT1G01060		LHY encodes a 1_38083 Encodes a micr 1 3962287	8.54	promoter
AT1G11735 AT2G04050	MICRORNA171B (MIR171B) na	MATE efflux fan 2_1339789	8.54 8.54	proximal promoter
AT5G03310		SAUR-like auxir 5 801163		proximal promoter
AT5G03310	na na	Protein kinase s 5 801163	8.54 8.54	proximal promoter proximal promoter
AT4G29520	na	LOCATED IN: e 4_14495940	8.54	promoter
AT4G29530	na	Pyridoxal phosp 4_14495940	8.54	promoter
AT4G30390	na	unknown proteir 4_14863194	8.54	promoter
AT1G09390	na	GDSL-like Lipas 1_3031079	8.53	promoter
AT4G36980	na	FUNCTIONS IN 4_17437307	8.53	promoter
AT5G53290	CYTOKININ RESPONSE FACTOR 3 (CRE		8.52	promoter
AT1G36050	na	Endoplasmic rel 1_13453288	8.52	intron
AT1G36060	na	encodes a mem 1_13453288	8.52	intergenic
AT2G28550	RELATED TO AP2.7 (RAP2.7)	related to AP2.7 2_12224346	8.52	intergenic
AT2G24330	na	Protein of unknc 2_10350382	8.51	proximal promoter
AT3G62400	na	unknown proteir 3_23089439	8.51	promoter
AT2G22880	na	VQ motif-contail 2_9741602	8.51	promoter
AT2G22890	na	Kua-ubiquitin cc 2_9741602	8.51	intergenic
AT3G52450	PLANT U-BOX 22 (PUB22)	Encodes a cyto _l 3_19439098	8.51	intergenic
AT3G62390	TRICHOME BIREFRINGENCE-LIKE 6 (TE		8.51	promoter
AT5G65890	ACT DOMAIN REPEAT 1 (ACR1)	Member of ACT 5_26356181	8.5	intron
AT3G04930	na	DNA-binding str 3_1362812	8.5	promoter
AT3G04920	na	Ribosomal prote 3_1362812	8.5	intergenic
AT1G25520	na	Uncharacterized 1_8961977	8.5	promoter
AT1G25510	na	Eukaryotic aspa 1_8961977	8.5	proximal promoter
AT3G19550	na	unknown proteir 3_6785860	8.5	intergenic
AT2G21500 AT2G21510	na	RING/U-box suj 2_9210399	8.49 8.49	promoter
AT1G70370	na POLYCALACTURONASE 2 (BC2)	DNAJ heat shor 2_9210399		intergenic
AT1G70370 AT1G68690	POLYGALACTURONASE 2 (PG2) PROLINE-RICH EXTENSIN-LIKE RECEP	polygalacturona 1_26513158	8.49 8.49	exon proximal promoter
AT2G17550	TON1 RECRUITING MOTIF 26 (TRM26)	unknown proteir 2_7637716	8.49	five_prime_UTR
AT4G37390	(BRU6)	Encodes an IAA 4_17579492	8.48	promoter
AT3G63010	GA INSENSITIVE DWARF1B (GID1B)	Encodes a gibb 3 23287617	8.48	proximal promoter
AT4G16780	HOMEOBOX PROTEIN 2 (HB-2)	Encodes a hom 4_9446082	8.48	intergenic
AT5G55840	na	Pentatricopeptic 5_22597807	8.48	promoter
AT3G63006	na	pre-tRNA; tRNA 3_23287617	8.48	proximal promoter
AT3G51400	na	Arabidopsis pro 3_19079541	8.48	proximal promoter
AT2G18300	na	basic helix-loop 2_7955222	8.48	promoter
AT2G18310	na	pre-tRNA; tRNA 2_7955222	8.48	intergenic
AT2G25470	RECEPTOR LIKE PROTEIN 21 (RLP21)	receptor like prc 2_10838181	8.48	promoter
AT2G47500	na	P-loop nucleosic 2_19491325	8.47	proximal promoter
AT5G58900	na	Homeodomain-I 5_23786687	8.47	proximal promoter
AT4G29240	na	Leucine-rich reg 4_14418165	8.47	promoter
AT5G41060	na	DHHC-type zinc 5_16434438	8.47	proximal promoter
AT5G41050	na	Pollen Ole e 1 a 5_16434438	8.47	promoter
AT5G18240	MYB-RELATED PROTEIN 1 (MYR1)	Encodes MYR1 5_6028153	8.46	
AT3G15578			0.10	downstream
	na	unknown proteir 3_5272991	8.46	proximal promoter
AT1G54730	na	Major facilitator 1_20431679	8.46 8.46	proximal promoter intergenic
AT1G54740	na na	Major facilitator 1_20431679 Protein of unknr 1_20431679	8.46 8.46 8.46	proximal promoter intergenic exon
AT1G54740 AT1G54750	na na na	Major facilitator 1_20431679 Protein of unknc 1_20431679 transposable el 1_20431679	8.46 8.46 8.46 8.46	proximal promoter intergenic exon proximal promoter
AT1G54740 AT1G54750 AT5G18245	na na na na	Major facilitator 1_20431679 Protein of unknc 1_20431679 transposable elc 1_20431679 Potential natura 5_6028153	8.46 8.46 8.46 8.46 8.46	proximal promoter intergenic exon proximal promoter promoter
AT1G54740 AT1G54750 AT5G18245 AT2G42620	na na na na MORE AXILLARY BRANCHES 2 (MAX2)	Major facilitator 1_20431679 Protein of unknc 1_20431679 transposable eli 1_20431679 Potential natura 5_6028153 The mutations a 2_17755119	8.46 8.46 8.46 8.46 8.46 8.45	proximal promoter intergenic exon proximal promoter promoter proximal promoter
AT1G54740 AT1G54750 AT5G18245 AT2G42620 AT1G28580	na na na na MORE AXILLARY BRANCHES 2 (MAX2) na	Major facilitator 1_20431679 Protein of unknx 1_20431679 transposable eli 1_20431679 Potential natura 5_6028153 The mutations a 2_17755119 GDSL-like Lipas 1_10046530	8.46 8.46 8.46 8.46 8.45 8.45	proximal promoter intergenic exon proximal promoter promoter proximal promoter promoter promoter
AT1G54740 AT1G54750 AT5G18245 AT2G42620 AT1G28580 AT5G40890	na na na na MORE AXILLARY BRANCHES 2 (MAX2) na CHLORIDE CHANNEL A (CLC-A)	Major facilitator 1 20431679 Protein of unkm 1 20431679 transposable elt 1 20431679 Potential natura 5 6028153 The mutations a 2 177755119 GDSL-like Lipas 1 10046530 Encodes a mem 5 16386880	8.46 8.46 8.46 8.46 8.46 8.45 8.45 8.45	proximal promoter intergenic exon proximal promoter proximal promoter promoter promoter proximal promoter proximal promoter
AT1G54740 AT1G54750 AT5G18245 AT2G42620 AT1G28580 AT5G40890 AT3G06780	na na na MORE AXILLARY BRANCHES 2 (MAX2) na CHLORIDE CHANNEL A (CLC-A) na	Major facilitator 1_20431679 Protein of unknx 1_20431679 Protein of unknx 1_20431679 Potential natura 5_6028153 The mutations a 2_17755119 GDSL-like Lipas 1_10046530 Encodes a mer 5_16386880 glycine-rich prol 3_2143403	8.46 8.46 8.46 8.46 8.46 8.45 8.45 8.45 8.44	proximal promoter intergenic exon proximal promoter promoter proximal promoter promoter promoter proximal promoter promoter promoter
AT1G54740 AT1G54750 AT5G18245 AT2G42620 AT1G28580 AT5G40890 AT3G06780 AT3G19274	na na na MORE AXILLARY BRANCHES 2 (MAX2) na CHLORIDE CHANNEL A (CLC-A) na na	Major facilitator 1 20431679 Protein of unknr 1 20431679 Protein of unknr 1 20431679 Potential natura 5 6028153 The mutations a 2 17755119 GDSL-like Lipas 1 10046530 Encodes a merr 5 16386880 glycine-rich prot 3 2143403 unknown proteir 3 6678741	8.46 8.46 8.46 8.46 8.46 8.45 8.45 8.45 8.44 8.44	proximal promoter intergenic exon proximal promoter promoter promoter promoter promoter proximal promoter proximal promoter promoter exon
AT1G54740 AT1G54750 AT5G18245 AT2G42620 AT1G28580 AT5G40890 AT3G06780 AT3G19274 AT4G24050	na na na na MORE AXILLARY BRANCHES 2 (MAX2) na CHLORIDE CHANNEL A (CLC-A) na na na	Major facilitator 1 20431679 Protein of unkn 1 20431679 Protein of unkn 1 20431679 Potential natura 5 6028153 The mutations a 2 177755119 GDSL-like Lipas 1 10046530 Encodes a merr 5 16386880 qlycine-rich prot 3 2143403 unknown proteir 3 6678741 NAD(P)-binding 4 12501737	8.46 8.46 8.46 8.46 8.45 8.45 8.45 8.44 8.44	proximal promoter intergenic exon proximal promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter exon intergenic
AT1G54740 AT1G54750 AT5G18245 AT2G42620 AT1G28580 AT5G40890 AT3G06780 AT3G19274 AT4G24050 AT4G24060	na na na na MORE AXILLARY BRANCHES 2 (MAX2) na CHLORIDE CHANNEL A (CLC-A) na na na	Major facilitator 1_20431679 Protein of unkm 1_20431679 Protein of unkm 1_20431679 Potential natura 5_6028153 The mutations a 2_17755119 GDSL-like Lipas 1_10046530 Encodes a mem 5_16386880 glycine-rich prot 3_2143403 unknown protein 3_6678741 NAD(P)-binding 4_12501737 Dof-type zinc fir 4_12501737	8.46 8.46 8.46 8.46 8.45 8.45 8.45 8.44 8.44 8.44	proximal promoter intergenic exon proximal promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter exon intergenic proximal promoter proximal promoter
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AT1G54740 AT1G54750 AT5G18245 AT2G42620 AT1G28580 AT3G06780 AT3G19274 AT4G24050 AT4G24050 AT4G24050 AT4G24050 AT4G32550 AT3G47430 AT1G04530 AT3G0180 AT5G19970 AT5G09975 AT2G39360 AT5G14910 AT4G38770 AT5G54290 AT5G54300 AT3G10415 AT3G10415 AT3G10410 AT1G53300 AT3G10415 AT3G10410 AT1G53300 AT3G10415 AT3G10410 AT1G53300 AT3G10415	na na na na na na na MORE AXILLARY BRANCHES 2 (MAX2) na CHLORIDE CHANNEL A (CLC-A) na na na na na peroxim 11B (PEX11B) na na TETRATRICOPEPTIDE REPEAT 4 (TPR4 YABBY3 (YAB3) na na na na na na na serine CARBOXYPEPTIDASE-LIKE 49 (TETRATRICOPEPTIDE-REPEAT THIORE TRICHOME BIREFRINGENCE-LIKE 41 (TFAR1-RELATED SEQUENCE 11 (FRS11)	Major facilitator 1 20431679 Protein of unknr 2 20431679 Protein of unknr 2 20431679 Potential natura 5 6028153 The mutations a 2 177755119 GOSL-like Lipas 1 10046530 Encodes a mer 5 16386880 glycine-rich prol 3 2143403 unknown proteir 3 6678741 NAD(P)-binding 4 12501737 Portein of unknr 1 12059623 member of the r 3 17478755 unknown proteir 1 25657879 Plant VAMP (ve 4 72298 Encodes one of 1 1236515 YABBY gene fai 4 72298 Protein of unknr 5 3864606 pre-tRNA; tRNA 5 3118259 Protein kinase s 2 16440230 Gibberellin-regu 5 4825469 Heavy metal tra 5 4825469 Encodes one of 4 18100878 Encodes CodA, 5 22054558 Protein of unknr 5 23828 SERINE CARBR 3 3238288 Encodes one of 1 19883806 Encodes a mer 3 4996410 FAR1-related sr 1 3336530	8.46 8.46 8.46 8.46 8.46 8.45 8.45 8.45 8.44 8.44 8.44 8.44 8.44 8.43 8.43 8.43 8.43 8.43 8.42 8.42 8.42 8.42 8.41 8.41 8.41 8.41 8.42	proximal promoter intergenic exon proximal promoter promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter exon intergenic proximal promoter proximal promoter downstream proximal promoter intergenic exon downstream promoter intergenic intron downstream
AT1G54740 AT1G54750 ATG18245 AT2G42620 AT1G28580 AT3G06780 AT3G19274 AT4G24060 AT4G24060 AT4G24060 AT1G33250 AT4G00170 AT1G04530 AT4G0180 AT5G11970 AT5G09975 AT2G39360 AT5G14920 AT5G14920 AT5G14920 AT5G14910 AT4G38770 AT5G54290 AT3G10415 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410	na na na na na na MORE AXILLARY BRANCHES 2 (MAX2) na CHLORIDE CHANNEL A (CLC-A) na na na na na na PEROXIN 11B (PEX11B) na TETRATRICOPEPTIDE REPEAT 4 (TPR4 YABBY3 (YAB3) na na PROLINE-RICH PROTEIN 4 (PRP4) (CcdA) na na SERINE CARBOXYPEPTIDASE-LIKE 49 (TETRATRICOPEPTIDE-REPEAT THIORE TRICHOME BIREFRINGENCE-LIKE 41 (TETRATRICOPEPTIDE-REPEAT THIORE BIREFRINGENCE-LIKE 41 (TETRATRICOPE	Major facilitator 1 _ 20431679 Protein of unkn 1 _ 20431679 Protein of unkn 1 _ 20431679 Potential natura 5 _ 6028153 The mutations a 2 _ 17755119 Potential natura 5 _ 6028153 The mutations a 2 _ 17755119 GDSL-like Lipas 1 _ 10046530 Encodes a mer 5 _ 16386880 glycine-rich prot 3 _ 2143403 unknown protein 3 _ 6678741 NAD(P)-binding 4 _ 12501737 Dof-type zinc fir 4 _ 12501737 Protein of unkn 1 _ 12059623 member of the ; 3 _ 17478755 unknown protein 1 _ 25657879 Plant VAMP (ve 4 _ 72298 Encodes one of 1 _ 1236515 YABBY gene fau 4 _ 72298 Protein inknase s 2 _ 16440230 Gibberellin-regu 5 _ 4825469 Heavy metal tra 5 _ 4825469 Heavy metal tra 5 _ 4825469 Encodes one of 4 _ 18100878 Encodes CodA, 5 _ 22054558 Protein of unkn 5 _ 33238288 ERINE CARBA 3 _ 3238288 ERINE CARBA 3 _ 3338288 Encodes one of 1 _ 18883806 Encodes a mer 3 _ 4996410 FAR1-related s 1 _ 3356530 RING/U-box suj 2 _ 6798351	8.46 8.46 8.46 8.46 8.46 8.45 8.45 8.44 8.44 8.44 8.44 8.44 8.43 8.43 8.43 8.43 8.43 8.43 8.43 8.43 8.43 8.45 8.41 8.41 8.41 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.43 8.44 8.44 8.44 8.44 8.44 8.45 8.45 8.45 8.46 8.47 8.48 8.49 8.40	proximal promoter intergenic exon proximal promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter promoter promoter intergenic proximal promoter promoter promoter intergenic proximal promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic exon downstream promoter intergenic intergenic intron downstream intron
AT1G54740 AT1G54750 AT5G18245 AT2G42620 AT1G28580 AT3G06780 AT3G06780 AT3G19274 AT4G24050 AT4G24050 AT4G24050 AT4G24050 AT4G24050 AT3G47430 AT1G68440 AT4G00170 AT5G09975 AT2G39360 AT5G14920 AT5G14910 AT4G38770 AT5G54290 AT3G14911 AT4G38770 AT5G54290 AT3G14910 AT4G38770 AT5G54290 AT3G14910 AT4G38770 AT5G54290 AT3G14910 AT4G38770 AT5G54290 AT3G14850 AT4G165800	na na na na na MORE AXILLARY BRANCHES 2 (MAX2) na CHLORIDE CHANNEL A (CLC-A) na	Major facilitator 1 20431679 Protein of unknr 1 20431679 Protein of unknr 1 20431679 Potential natura 5 6028153 The mutations a 2 17755119 GDSL-like Lipas 1 10046530 Encodes a merr 5 16386880 glycine-rich prot 3 2143403 unknown proteir 3 6678741 NAD(P)-binding 4 12501737 Protein of unknr 1 12059623 member of the r 3 17478755 unknown proteir 1 25657879 Plant VAMP (ve 4 72298 Encodes one of 1 12365157879 Plant VAMP (ve 4 72298 Protein of unknr 5 3864606 pre-IRNA; IRNA 5 3118259 Protein frams s 2 2 16440230 Gibberellin-regu 5 4825469 Heavy metal tra 5 4825469 Heavy metal tra 5 4825469 Encodes one of 4 18100878 Encodes one of 4 18100878 Encodes one of 5 19883806 Encodes one of 1 19883806 Encodes a merr 3 4996410 FAR1-related st 1 3356530 INING/U-box su 2 6798351 unknown proteir 1 235699757	8.46 8.46 8.46 8.46 8.46 8.45 8.45 8.44 8.44 8.44 8.44 8.44 8.43 8.43 8.43 8.43 8.43 8.43 8.42 8.42 8.42 8.42 8.42 8.41 8.41 8.41 8.42 8.43 8.43 8.43 8.43 8.43 8.43 8.43 8.43 8.43 8.44 8.44 8.44 8.44 8.44 8.44 8.45 8.45 8.45 8.45 8.46 8.47 8.47 8.48 8.49 8.49 8.40	proximal promoter intergenic exon proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter exon intergenic proximal promoter proximal promoter proximal promoter proximal promoter intergenic exon downstream promoter intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic intron downstream intron proximal promoter
AT1G54740 AT1G54750 ATG18245 AT2G42620 AT1G28580 AT3G06780 AT3G19274 AT4G24060 AT4G24060 AT4G24060 AT4G347430 AT4G00170 AT4G00170 AT4G00180 AT3G47430 AT4G0180 AT5G11970 AT5G09975 AT2G39360 AT5G14920 AT5G14920 AT5G14920 AT5G14910 AT4G38770 AT5G54290 AT3G10415 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410 AT3G10410	na na na na na na MORE AXILLARY BRANCHES 2 (MAX2) na CHLORIDE CHANNEL A (CLC-A) na na na na na na PEROXIN 11B (PEX11B) na TETRATRICOPEPTIDE REPEAT 4 (TPR4 YABBY3 (YAB3) na na PROLINE-RICH PROTEIN 4 (PRP4) (CcdA) na na SERINE CARBOXYPEPTIDASE-LIKE 49 (TETRATRICOPEPTIDE-REPEAT THIORE TRICHOME BIREFRINGENCE-LIKE 41 (TETRATRICOPEPTIDE-REPEAT THIORE BIREFRINGENCE-LIKE 41 (TETRATRICOPE	Major facilitator 1 _ 20431679 Protein of unkn 1 _ 20431679 Protein of unkn 1 _ 20431679 Potential natura 5 _ 6028153 The mutations a 2 _ 17755119 Potential natura 5 _ 6028153 The mutations a 2 _ 17755119 GDSL-like Lipas 1 _ 10046530 Encodes a mer 5 _ 16386880 glycine-rich prot 3 _ 2143403 unknown protein 3 _ 6678741 NAD(P)-binding 4 _ 12501737 Dof-type zinc fir 4 _ 12501737 Protein of unkn 1 _ 12059623 member of the ; 3 _ 17478755 unknown protein 1 _ 25657879 Plant VAMP (ve 4 _ 72298 Encodes one of 1 _ 1236515 YABBY gene fau 4 _ 72298 Protein inknase s 2 _ 16440230 Gibberellin-regu 5 _ 4825469 Heavy metal tra 5 _ 4825469 Heavy metal tra 5 _ 4825469 Encodes one of 4 _ 18100878 Encodes CodA, 5 _ 22054558 Protein of unkn 5 _ 33238288 ERINE CARBA 3 _ 3238288 ERINE CARBA 3 _ 3338288 Encodes one of 1 _ 18883806 Encodes a mer 3 _ 4996410 FAR1-related s 1 _ 3356530 RING/U-box suj 2 _ 6798351	8.46 8.46 8.46 8.46 8.46 8.45 8.45 8.44 8.44 8.44 8.44 8.44 8.43 8.43 8.43 8.43 8.43 8.43 8.43 8.43 8.43 8.45 8.41 8.41 8.41 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.42 8.43 8.44 8.44 8.44 8.44 8.44 8.45 8.45 8.45 8.46 8.47 8.48 8.49 8.40	proximal promoter intergenic exon proximal promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter promoter promoter intergenic proximal promoter promoter promoter intergenic proximal promoter intergenic proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter intergenic exon downstream promoter intergenic intergenic intron downstream intron

AT3G12630				
	STRESS ASSOCIATED PROTEIN 5 (SAP	Encodes a prote 3_4012534	8.4	promoter
AT4G25570	(ACYB-2)	Encodes cytoch 4_13055818	8.39	promoter
AT1G19000	na	Homeodomain-I 1_6562908	8.39	promoter
AT1G22470	na	unknown proteir 1_7932490	8.39	intergenic
AT5G15040	na	Paired amphipa 5_4871423	8.39	proximal promoter
AT5G15050	na	Core-2/I-branch 5_4871423	8.39	downstream
AT5G59350	na	unknown proteir 5_23943460	8.38	intergenic
AT2G26710	PHYB ACTIVATION TAGGED SUPPRESS		8.38	promoter
AT3G26400	EUKARYOTIC TRANSLATION INITIATION		8.37	promoter
AT5G58450	na	Tetratricopeptid 5_23626924	8.37	intron
AT5G48200	na	unknown proteir 5_19545132	8.37	promoter
AT1G70280	na	NHL domain-co 1_26471002	8.37	proximal promoter
AT1G79245	na	pseudogene of 1_29809426	8.37	intron
AT2G30000	na	PHF5-like prote 2_12805145	8.37	promoter
AT2G35290	na	unknown proteir 2_14862190	8.37	promoter
AT3G01560 AT5G60850	na Ope pinding drotein 4 (Opp4)	CONTAINS Inte 3_219606 Encodes a zinc 5_24478874	8.37 8.37	five_prime_UTR
AT5G50850	OBF BINDING PROTEIN 4 (OBP4) SORTING NEXIN 2A (SNX2a)	sorting nexin 2A 5_23626924	8.37	proximal promoter
AT1G70290	TREHALOSE-6-PHOSPHATASE SYNTHA		8.37	promoter downstream
AT2G30010	TRICHOME BIREFRINGENCE-LIKE 45 (T		8.37	proximal promoter
AT4G32410	CELLULOSE SYNTHASE 1 (CESA1)	Encodes a cellu 4_15646747	8.36	promoter
AT1G52800	na	2-oxoglutarate (1_19663673	8.36	promoter
AT1G69690	TEOSINTE BRANCHED1/CYCLOIDEA/PO		8.36	proximal promoter
AT1G07000	EXOCYST SUBUNIT EXO70 FAMILY PRO		8.35	promoter
AT5G19020	MITOCHONDRIAL EDITING FACTOR 18		8.35	downstream
AT5G19015	na	transposable eli 5_6352744	8.35	proximal promoter
AT5G47818	na	unknown pseud 5_19365097	8.35	promoter
AT1G07010	SHEWENELLA-LIKE PROTEIN PHOSPHA		8.35	promoter
AT4G37460	SUPPRESSOR OF RPS4-RLD 1 (SRFR1)		8.35	promoter
AT1G28670	(ARAB-1)	Arabidopsis tha 1_10076498	8.34	promoter
AT1G14685	BASIC PENTACYSTEINE 2 (BPC2)	Encodes a men 1 5042496	8.34	five_prime_UTR
AT1G70782	CONSERVED PEPTIDE UPSTREAM OPE		8.34	intergenic
AT1G70780	na	unknown proteir 1_26694861	8.34	intergenic
AT1G71828	na	Potential natura 1_27017946	8.34	exon
AT5G03680	PETAL LOSS (PTL)	Recessive muta 5_957634	8.34	promoter
AT1G71830	SOMATIC EMBRYOGENESIS RECEPTO		8.34	promoter
AT5G57180	CHLOROPLAST IMPORT APPARATUS 2		8.33	intron
AT5G57181	na	This gene encor 5 23169919	8.33	proximal promoter
AT2G47690	na	NADH-ubiquino 2_19551130	8.33	promoter
AT1G79750	NADP-MALIC ENZYME 4 (NADP-ME4)	The malic enzyr 1 30011654	8.33	promoter
AT1G28660	na	GDSL-like Lipas 1_10073521	8.32	promoter
AT2G47630	na	alpha/beta-Hydr 2_19535387	8.32	intron
AT4G34760	na	SAUR-like auxir 4_16587045	8.32	intergenic
AT2G47620	SWITCH/SUCROSE NONFERMENTING :		8.32	intergenic
AT4G19880	na	Glutathione S-tr 4_10786447	8.31	five_prime_UTR
AT5G55530	na	Calcium-depent 5_22493242	8.31	intron
AT5G43190	na	Galactose oxida 5 17342533	8.31	proximal promoter
AT2G27860	UDP-D-APIOSE/UDP-D-XYLOSE SYNTH		8.31	promoter
AT3G10300	na	Calcium-binding 3_3186222	8.3	promoter
AT2G22420	na	Peroxidase sup 2_9511589	8.3	proximal promoter
AT2G39950	na	unknown proteir 2_16680663	8.3	promoter
AT1G01140	CBL-INTERACTING PROTEIN KINASE 9		8.29	proximal promoter
AT2G18650	MATERNAL EFFECT EMBRYO ARREST		8.29	promoter
	na	CONTAINS Inte 1 68497	8.29	intergenic
AT1G01130			8.28	promoter
AT1G01130 AT3G48520	CYTOCHROME P450, FAMILY 94, SUBFA	CYP94B3 IS a [23 1/9/6/91		
	CYTOCHROME P450, FAMILY 94, SUBFAEXORDIUM (EXO)	EXORDIUM (E) 4_5740123	8.28	promoter
AT3G48520		EXORDIUM (E) 4_5740123	8.28 8.28	promoter
AT3G48520 AT4G08950	EXORDIUM (EXO)	EXORDIUM (E) 4_5740123		
AT3G48520 AT4G08950 AT1G03870	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN	EXORDIUM (E) 4_5740123 fasciclin-like ara 1_984219	8.28	promoter proximal promoter
AT3G48520 AT4G08950 AT1G03870 AT3G18040	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9)	EXORDIUM (E) 4_5740123 fasciclin-like ara 1_984219 Encodes a prote 3_6174022	8.28 8.28	promoter proximal promoter proximal promoter
AT3G48520 AT4G08950 AT1G03870 AT3G18040 AT1G05805 AT1G61170 AT3G48515	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na	EXORDIUM (E) 4_5740123 fasciclin-like ara 1_984219 Encodes a prott 3_6174022 basic helix-loop 1_1744722 unknown proteit 1_22549080 pre-tRNA; tRNA 3_17976791	8.28 8.28 8.28 8.28 8.28	promoter proximal promoter proximal promoter promoter proximal promoter proximal promoter
AT3G48520 AT4G08950 AT1G03870 AT3G18040 AT1G05805 AT1G61170 AT3G48515 AT1G03860	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na na PROHIBITIN 2 (PHB2)	EXORDIUM (E) 4_5740123 fasciclin-like ara 1_984219 Encodes a prot 3_6174022 basic helix-loop 1_1744722 unknown proteir 1_22549080 pre-tRNA; tRNA 3_17976791 prohibitin 2 1_984219	8.28 8.28 8.28 8.28 8.28 8.28	promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT3G48520 AT4G08950 AT1G03870 AT3G18040 AT1G05805 AT1G61170 AT3G48515 AT1G03860 AT5G63770	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na na PROHIBITIN 2 (PHB2) DIACYLGLYCEROL KINASE 2 (DGK2)	EXORDIUM (E) 4_5740123 fasciclin-like ara 1_984219 Encodes a prot 3_6174022 basic helix-loop 1_1744722 unknown proteir 1_22549080 pre-tRNA; tRNA 3_17976791 prohibitin 2 1_984219 a member of the 5_25518517	8.28 8.28 8.28 8.28 8.28 8.28 8.27	promoter proximal promoter proximal promoter promoter proximal promoter proximal promoter proximal promoter promoter
AT3G48520 AT4G08950 AT1G03870 AT3G18040 AT1G05805 AT1G61170 AT3G48515 AT1G03860 AT5G63770 AT3G49940	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na na PROHIBITIN 2 (PHB2) DIACYLGLYCEROL KINASE 2 (DGK2) LOB DOMAIN-CONTAINING PROTEIN 38	EXORDIUM (E) 4_5740123 fasciclin-like ara 1_984219 Encodes a prot 3_6174022 basic helix-loop 1_1744722 unknown proteir 1_22549080 pre-tRNA; tRNA 3_17976791 prohibitin 2 1_984219 a member of the 5_25518517 LOB domain-co 3_18516321	8.28 8.28 8.28 8.28 8.28 8.28 8.27 8.27	promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter intergenic
AT3G48520 AT4G08950 AT1G03870 AT3G18040 AT1G05805 AT1G61170 AT3G48515 AT1G03860 AT5G63770 AT3G49940 AT2G34930	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na PROHIBITIN 2 (PHB2) DIACYLGLYCEROL KINASE 2 (DGK2) LOB DOMAIN-CONTAINING PROTEIN 38 na	EXORDIUM (E) 4_5740123 fasciclin-like ara 1_984219 Encodes a prot 3_6174022 basic helix-loop 1_1744722 unknown proteir 1_22549080 pre-IRNA; IRNA 3_17976791 prohibitin 2 1_984219 a member of the 5_25518517 LOB domain-co 3_18516321 disease resistar 2_147440084	8.28 8.28 8.28 8.28 8.28 8.28 8.27 8.27	promoter proximal promoter proximal promoter promoter proximal promoter proximal promoter proximal promoter promoter intergenic promoter
AT3G48520 AT4G08950 AT1G03870 AT3G18040 AT1G05805 AT1G61170 AT3G48515 AT1G03860 AT5G63770 AT3G49940 AT2G34930 AT1G72420	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na na PROHIBITIN 2 (PHB2) DIACYLGLYCEROL KINASE 2 (DGK2) LOB DOMAIN-CONTAINING PROTEIN 38 na na	EXORDIUM (E) 4_5740123 fasciclin-like ara 1_984219 Encodes a protk 3_6174022 basic helix-loop 1_1744722 unknown proteir 1_22549080 pre-tRNA; tRNA 3_17976791 prohibitin 2 1_984219 a member of the 5_25518517 LOB domain-co 3_18516321 disease resistar 2_14740084 NADH:ubiquinoi 1_27265737	8.28 8.28 8.28 8.28 8.28 8.28 8.27 8.27	promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic promoter proximal promoter proximal promoter proximal promoter
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AT3G48520 AT4G08950 AT14G08950 AT14G08950 AT13G18040 AT1G61170 AT3G48515 AT1G03860 AT5G63770 AT3G49940 AT1G72420 AT1G72420 AT1G72430 AT1G72430 AT2G31870 AT3G28770 AT3G66045 AT5G66045 AT5G66040 AT5G24930 AT5G66040 AT5G24930 AT5G24930 AT3G29770 AT1G76160 AT3G29786 AT5G668040 AT3G29786 AT5G668040 AT3G24930 AT3G24970 AT3G24970 AT14G76160 AT3G18850 AT3G18850 AT3G18850 AT3G18860 AT3G18860 AT3G18860 AT3G18860 AT3G18860 AT3G18860 AT3G18860 AT3G18860 AT3G18864470 AT5G484470 AT5G484470	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na na PROHIBITIN 2 (PHB2) DIACYLGLYCEROL KINASE 2 (DGK2) LOB DOMAIN-CONTAINING PROTEIN 38 na na na SANSKRIT FOR 'BRIGHT' (TEJ) na na TRICHOME BIREFRINGENCE-LIKE 25 (T UDP-GLUCOSYL TRANSFERASE 71B8 ((ATGRIP) MICRORNA170 (MIR170) na na na SULFURTRANSFERASE PROTEIN 16 (S CONSTANS-LIKE 4 (COL4) METHYL ESTERASE 11 (MES11) na na SKUJS SIMILAR 5 (sks5) XYLOGLUCAN ENDOTRANSGLUCOSYL LYSOPHOSPHATIDYL ACYLTRANSFER. na OXIDATIVE STRESS 2 (OXS2) DHNA-COA THIOESTERASE 1 (DHNAT1 na na	EXORDIUM (E) 4, 5740123 fasciclin-like ara 1_984219 Encodes a prots 3_6174022 basic helix-loop 1_1744722 unknown proteir 1_22549080 pre-tRNA; tRNA 3_17976791 prohibitin 2 1_984219 a member of the 5_25518517 LOB domain-co 3_18516321 disease resistar 2_14740084 NADH-ubiquino 1_27265737 SAUR-like auxir 1_27265737 The gene encoc 2_13554079 signal recognitic 4_14941485 unknown proteir 5_9410087 Encodes a men 1_159524 UDP-glucosyl tr 3_7681924 Involved in golg 5_26411904 Encodes a mich 5_26411904 Encodes a mich 5_26411904 Encodes a prote 5_26411904 Encodes a prote 5_26411904 Encodes a prote 5_26411904 CONSTANS-like 5_8387146 Encodes a prote 5_2669261 SKU5 similar 5_11650948 unknown proteir 5_26669261 SKU5 similar 5_11650948 unknown proteir 5_26669261 SKU5 similar 5_11650948 unknown proteir 5_26669261 SKU5 similar 5_11650948 unknown proteir 5_1669487 unknown proteir 5_16644637 Lectoylglutarthio 5_19644637 Lectoylglutarthio 5_19644637	8.28 8.28 8.28 8.28 8.28 8.27 8.27 8.27	promoter proximal promoter three_prime_UTR proximal promoter promoter three_prime_utrR promoter proximal promoter downstream proximal promoter proximal promoter intergenic promoter pr
AT3G48520 AT4G08950 AT1G03870 AT3G18040 AT1G05805 AT1G61170 AT3G48515 AT1G03860 AT5G63770 AT3G49940 AT2G34930 AT1G72420 AT1G72420 AT1G72420 AT1G72430 AT2G31870 AT3G26770 AT1G01430 AT5G66045 AT3G18890 AT1G19000 AT5G26790 AT1G19000 AT5G24930 AT3G29770 AT3G29770 AT3G29786 AT5G68045 AT3G18850 AT3G48470 AT5G4847800 AT1G48320 AT5G484780	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na PROHIBITIN 2 (PHB2) DIACYLGLYCEROL KINASE 2 (DGK2) LOB DOMAIN-CONTAINING PROTEIN 38 na na SANSKRIT FOR 'BRIGHT' (TEJ) na na TRICHOME BIREFRINGENCE-LIKE 25 (T UDP-GLUCOSYL TRANSFERASE 71B8 ((ATGRIP) MICRORNA170 (MIR170) na na na SULFURTRANSFERASE PROTEIN 16 (S CONSTANS-LIKE 4 (COL4) METHYL ESTERASE 11 (MES11) na na SKUS SIMILAR 5 (sks5) XYLOGLUCAN ENDOTRANSGLUCOSYL LYSOPHOSPHATIDYL ACYLTRANSFER. na OXIDATIVE STRESS 2 (OXS2) DHNA-COA THIOESTERASE 1 (DHNAT1 na na na	EXORDIUM (E) 4, 5740123 fasciclin-like ara 1_984219 Encodes a prots 3, 6174022 basic helix-loop 1_1744722 unknown proteir 1_22549080 pre-tRNA; tRNA 3_17976791 prohibitin 2 1_984219 a member of the 5_25518517 LOB domain-co 3_18516321 disease resistar 2_14740084 NADH:ubiquinoi 1_27265737 SAUR-like auxir 1_27265737 The gene encoc 2_13554079 signal recognitic 4_14941485 unknown proteir 5_9410087 Encodes a mer 1_159524 UDP-glucosyl tr 3_7681924 Involved in golg 5_26411904 Protein of unkn 1_6560956 Heavy metal tra 5_834714 Encodes a mrot 5_26411904 CONSTANS-like 5_8887405 Encodes a prots 5_26411904 Encodes a prots 5_2669261 SKUS similar 5_1_28881164 vxloglucan endc 4_17776352 lysophosphatidy 3_6501468 transducin famil 3_6501468 transducin famil 3_6501468 CCCH-type zinc 2_17489716 Encodes one of 1_17855726 unknown proteir 5_19644637 Potential natura 1_17855726	8.28 8.28 8.28 8.28 8.28 8.27 8.27 8.27	promoter proximal promoter pro
AT3G48520 AT4G08950 AT14G08950 AT14G08950 AT3G18040 AT1G05805 AT1G61170 AT3G48515 AT1G03860 AT5G63770 AT3G49940 AT1G72420 AT1G72420 AT1G72430 AT1G72430 AT3G28770 AT3G28770 AT3G66030 AT5G66030 AT5G66030 AT5G66040 AT5G1800 AT5G68030 AT5G66040 AT5G24930 AT1G71600 AT3G29780 AT3G48800 AT3G48800 AT3G48800 AT3G48800 AT3G48800 AT3G48800 AT3G48870 AT5G484815 AT5G484815	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na PROHIBITIN 2 (PHB2) DIACYLGLYCEROL KINASE 2 (DGK2) LOB DOMAIN-CONTAINING PROTEIN 38 na na SANSKRIT FOR 'BRIGHT' (TEJ) na na TRICHOME BIREFRINGENCE-LIKE 25 (T UDP-GLUCOSYL TRANSFERASE 71B8 ((ATGRIP) MICRORNA170 (MIR170) na na SULFURTRANSFERASE PROTEIN 16 (S CONSTANS-LIKE 4 (COL4) METHYL ESTERASE 11 (MES11) na SKU5 SIMILAR 5 (sks5) XYLOGLUCAN ENDOTRANSGLUCOSYL LYSOPHOSPHATIDYL ACYLTRANSFERI na OXIDATIVE STRESS 2 (OXS2) DHNA-COA THIOESTERASE 1 (DHNAT1 na na na	EXORDIUM (E) 4, 5740123 fasciclin-like ara 1_984219 Encodes a prott 3, 6174022 basic helix-loop 1_1744722 unknown protein 1_22549080 pre-tRNA; tRNA 3, 17976791 prohibitin 2 1_984219 a member of the 5, 25518517 LOB domain-co 3_18516321 disease resistar 2_14740084 NADH:ubiquinoi 1_27265737 The gene encoc 2_13554079 signal recognitic 4_14941485 unknown protein 5_9410087 Encodes a meri 1_159524 UDP-glucosyl tr 3_7681924 Unvolved in polg 5_26411904 Protein of unkn 1_6560956 Heavy metal tra 5_834714 Encodes a prott 5_26411904 Protein of unkn 1_6560956 Heavy metal tra 5_834714 Encodes a prott 5_26411904 Protein of unkn 1_6560956 Heavy metal tra 5_834714 Encodes a prott 5_26411904 Protein of unkn 1_6560956 Heavy metal tra 5_834714 Encodes a prott 5_2669261 SKU5 similar 5 1_28581164 xyloglucan endc 4_17776352 Uysophosphatids 3_6501468 transducin famil 3_6501468 CCCH-type zinc 2_17489716 Encodes one of 1_17855726 unknown protein 5_19644637 Lactoylqlutathio 5_19644637 Potential natura 1_17855726 Eukaryotic aspa 5_14914178	8.28 8.28 8.28 8.28 8.28 8.27 8.27 8.27	promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter exon exon
AT3G48520 AT4G08950 AT1G03870 AT3G18040 AT1G05805 AT1G61170 AT3G48515 AT1G03860 AT5G63770 AT3G49940 AT2G34930 AT1G72420 AT1G72420 AT1G72420 AT1G72430 AT2G31870 AT3G26770 AT1G01430 AT5G66045 AT3G18890 AT1G19000 AT5G26790 AT1G19000 AT5G24930 AT3G29770 AT3G29770 AT3G29786 AT5G68045 AT3G18850 AT3G48470 AT5G4847800 AT1G48320 AT5G484780	EXORDIUM (EXO) FASCICLIN-LIKE ARABINOOGALACTAN MAP KINASE 9 (MPK9) na na PROHIBITIN 2 (PHB2) DIACYLGLYCEROL KINASE 2 (DGK2) LOB DOMAIN-CONTAINING PROTEIN 38 na na SANSKRIT FOR 'BRIGHT' (TEJ) na na TRICHOME BIREFRINGENCE-LIKE 25 (T UDP-GLUCOSYL TRANSFERASE 71B8 ((ATGRIP) MICRORNA170 (MIR170) na na na SULFURTRANSFERASE PROTEIN 16 (S CONSTANS-LIKE 4 (COL4) METHYL ESTERASE 11 (MES11) na na SKUS SIMILAR 5 (sks5) XYLOGLUCAN ENDOTRANSGLUCOSYL LYSOPHOSPHATIDYL ACYLTRANSFER. na OXIDATIVE STRESS 2 (OXS2) DHNA-COA THIOESTERASE 1 (DHNAT1 na na na	EXORDIUM (E) 4, 5740123 fasciclin-like ara 1_984219 Encodes a prots 3, 6174022 basic helix-loop 1_1744722 unknown proteir 1_22549080 pre-tRNA; tRNA 3_17976791 prohibitin 2 1_984219 a member of the 5_25518517 LOB domain-co 3_18516321 disease resistar 2_14740084 NADH:ubiquinoi 1_27265737 SAUR-like auxir 1_27265737 The gene encoc 2_13554079 signal recognitic 4_14941485 unknown proteir 5_9410087 Encodes a mer 1_159524 UDP-glucosyl tr 3_7681924 Involved in golg 5_26411904 Protein of unkn 1_6560956 Heavy metal tra 5_834714 Encodes a mrot 5_26411904 CONSTANS-like 5_8887405 Encodes a prots 5_26411904 Encodes a prots 5_2669261 SKUS similar 5_1_28881164 vxloglucan endc 4_17776352 lysophosphatidy 3_6501468 transducin famil 3_6501468 transducin famil 3_6501468 CCCH-type zinc 2_17489716 Encodes one of 1_17855726 unknown proteir 5_19644637 Potential natura 1_17855726	8.28 8.28 8.28 8.28 8.28 8.27 8.27 8.27	promoter proximal promoter pro

AT4G36540	BR ENHANCED EXPRESSION 2 (BEE2)	BP enhanced et / 172/3506	8.21	promoter
AT4G25386	na	This gene encor 4_12976984	8.21	downstream
AT2G36690	na	2-oxoglutarate (2_15378697	8.21	proximal promoter
AT1G06070	na	Basic-leucine zi 1_1838229	8.21	proximal promoter
AT1G77280 AT1G77290	na na	Protein kinase r 1_29035738 Glutathione S-tr 1_29035738	8.21 8.21	intron proximal promoter
AT2G18440	GENE WITH UNSTABLE TRANSCRIPT 1		8.2	promoter
AT1G60150	na	transposable ell 1_22185822	8.2	proximal promoter
AT2G18450 AT5G24930	SUCCINATE DEHYDROGENASE 1-2 (SE CONSTANS-LIKE 4 (COL4)		8.2	downstream
AT3G50660	DWARF 4 (DWF4)	CONSTANS-liki 5_8588703 Encodes a 22&# 3_18817830	8.19 8.19	proximal promoter proximal promoter
AT3G17330	EVOLUTIONARILY CONSERVED C-TER		8.19	promoter
AT5G01600	FERRETIN 1 (FER1)	Encodes a ferre 5_230356	8.19	promoter
AT3G07005 AT5G17980	LOW-MOLECULAR-WEIGHT CYSTEINE- na	- Encodes a merr 3_2212637 C2 calcium/lipid 5_5955728	8.19 8.19	downstream exon
AT2G28140	na	Protein of unknr 2_11994223	8.19	proximal promoter
AT5G01595	na	Potential natura 5_230356	8.19	intergenic
AT5G01610	na	Protein of unknc 5_230356	8.19	proximal promoter
AT3G17340 AT3G07010	na	ARM repeat sur 3_5920297	8.19 8.19	downstream
AT5G17990	na TRYPTOPHAN BIOSYNTHESIS 1 (TRP1)	Pectin lyase-like 3_2212637 Encodes the try 5_5955728	8.19	downstream proximal promoter
AT5G47040	LON PROTEASE 2 (LON2)	Encodes a merr 5_19099649	8.18	proximal promoter
AT5G04750	na	F1F0-ATPase ir 5_1378065	8.18	intergenic
AT5G04760 AT5G18620	na CHROMATIN REMODELING FACTOR17	Duplicated hom 5_1378065	8.18 8.17	intergenic promoter
AT3G43720	na	Bifunctional inhi 3_15617145	8.17	five_prime_UTR
AT5G11640	na	Thioredoxin sup 5_3744811	8.17	intergenic
AT5G11650	na	alpha/beta-Hydr 5_3744811	8.17	promoter
AT5G18630 AT5G65683	na WAV3 HOMOLOG 2 (WAVH2)	alpha/beta-Hydr 5_6202401 Zinc finger (C3F 5_26263306	8.17 8.17	promoter exon
AT2G41475	na	Embryo-specific 2_17296409	8.16	five_prime_UTR
AT2G42990	na	GDSL-like Lipas 2_17878363	8.16	proximal promoter
AT5G53510	OLIGOPEPTIDE TRANSPORTER 9 (OPT		8.16	intergenic
AT4G23660 AT5G63120	POLYPRENYLTRANSFERASE 1 (PPT1) na	Encodes para-h 4_12331969 P-loop containir 5_25324103	8.16 8.15	promoter proximal promoter
AT5G63120	na	Octicosapeptide 5 25324103	8.15	three_prime_UTR
AT2G23690	na	unknown proteir 2_10072077	8.15	promoter
AT3G53810	na	Concanavalin A 3_19936428	8.15	proximal promoter
AT5G23730 AT5G58530	REPRESSOR OF UV-B PHOTOMORPHO	Encodes REPR 5_8003654 Glutaredoxin fai 5 23658642	8.15 8.14	proximal promoter proximal promoter
AT2G39390	na	Ribosomal L29 2 16452516	8.14	proximal promoter
AT2G39400	na	alpha/beta-Hydr 2_16452516	8.14	promoter
AT2G47830	na	Cation efflux far 2_19595259	8.14	proximal promoter
AT2G47844 AT2G47840	na TRANSLOCON AT THE INNER ENVELO	unknown proteir 2_19595259	8.14 8.14	promoter promoter
AT2G47010	na	unknown proteir 2 19316390	8.13	proximal promoter
AT4G35090	CATALASE 2 (CAT2)	Encodes a pero 4_16704233	8.12	proximal promoter
AT4G30900	na	DNAse I-like su _I 4_15039392	8.12	promoter
AT4G25830 AT4G27435	na na	Uncharacterise: 4_13132442 Protein of unkn: 4_13725376	8.12 8.12	proximal promoter intergenic
AT5G49690	na	UDP-Glycosyltr: 5_20191832	8.12	promoter
AT5G49700	na	Predicted AT-hc 5_20191832	8.12	proximal promoter
AT4G27440	PROTOCHLOROPHYLLIDE OXIDOREDU		8.12	promoter
AT4G30890 AT4G25820	UBIQUITIN-SPECIFIC PROTEASE 24 (UE XYLOGLUCAN ENDOTRANSGLUCOSYL		8.12 8.12	promoter intergenic
AT5G58430	EXOCYST SUBUNIT EXO70 FAMILY PRO		8.11	promoter
AT3G14270	FORMS APLOID AND BINUCLEATE CEL		8.11	promoter
AT3G25070 AT5G58440	RPM1 INTERACTING PROTEIN 4 (RIN4) SORTING NEXIN 2A (SNX2a)	Encodes a merr 3_9132201 sorting nexin 2/ 5_23623599	8.11 8.11	promoter intergenic
AT1G16150	WALL ASSOCIATED KINASE-LIKE 4 (WA		8.11	promoter
AT2G37640	(EXP3)	member of Alph 2_15789877	8.1	promoter
AT5G20230	BLUE-COPPER-BINDING PROTEIN (BC		8.1	promoter
AT5G20220 AT5G20225	na na	zinc knuckle (Ct 5_6826478 Potential natura 5 6826478	8.1 8.1	intergenic proximal promoter
AT5G20223	SMALL AUXIN UP RNA 21 (SAUR21)	ARM repeat sur 5_318397	8.1	proximal promoter
AT3G51375	MICRORNA171A (MIR171A)	Encodes a micr 3_19072803	8.09	proximal promoter
AT3G56370	na	Leucine-rich rer 3_20903097	8.09	promoter
AT4G27500 AT5G19095	PROTON PUMP INTERACTOR 1 (PPI1) na	interacts with H- 4_13742168 pre-tRNA; tRNA 5_6399609	8.09 8.08	proximal promoter proximal promoter
AT3G52470	na	Late embryoger 3_19453304	8.08	intergenic
AT3G52480	na	unknown proteir 3_19453304	8.08	promoter
AT5G20140	na	SOUL heme-bir 5_6801614	8.08	proximal promoter
AT4G39730 AT5G20150	PLAT DOMAIN PROTEIN 1 (PLAT1) SPX DOMAIN GENE 1 (SPX1)	Lipase/lipooxyg/4_18433830 Expression is u/5_6801614	8.08 8.08	downstream proximal promoter
AT4G34131	UDP-GLUCOSYL TRANSFERASE 73B3		8.08	promoter
AT4G34135	UDP-GLUCOSYLTRANSFERASE 73B2 (8.08	downstream
AT3G50910 AT5G04470	na SIAMESE (SIM)	unknown proteir 3_18919288 Encodes a nove 5_1270839	8.07	promoter
AT1G56580	SIAMESE (SIM) SMALLER WITH VARIABLE BRANCHES		8.07 8.07	intergenic proximal promoter
AT1G05230	HOMEODOMAIN GLABROUS 2 (HDG2)	Encodes a hom 1_1518705	8.06	intron
AT1G64050	na	unknown proteir 1_23762076	8.06	promoter
AT2G28350 AT3G61880	AUXIN RESPONSE FACTOR 10 (ARF10) CYTOCHROME P450 78A9 (CYP78A9)	Involved in root 2_12111449 Encodes a cyto 3_22906537	8.05 8.05	proximal promoter
AT5G66620	DA1-RELATED PROTEIN 6 (DAR6)	DA1-related pro 5 26588343	8.05	exon promoter
AT2G45160	HAIRY MERISTEM 1 (HAM1)	Belongs to one 2_18620428	8.05	promoter
AT3G52290	IQ-DOMAIN 3 (IQD3)	IQ-domain 3 (IQ 3_19392901	8.05	proximal promoter
AT2G45161 AT3G27800	na na	unknown proteir 2_18620428 unknown proteir 3_10304013	8.05 8.05	promoter proximal promoter
AT3G27800 AT3G52285	na na	pre-tRNA; tRNA 3_19392901	8.05	proximal promoter promoter
AT1G11890	SECRETION 22 (SEC22)	member of SEC 1_4010632	8.05	promoter
AT1G11910	ASPARTIC PROTEINASE A1 (APA1)	Encodes an asr 1_4021074	8.04	promoter
AT3G04790 AT1G23900	EMBRYO DEFECTIVE 3119 (EMB3119) GAMMA-ADAPTIN 1 (GAMMA-ADAPTIN	Ribose 5-phosp 3_1315789 Encodes large s 1_8440985	8.04 8.04	intergenic promoter
AT1G23300 AT1G37140	MEI2 C-TERMINAL RRM ONLY LIKE 1 (M		8.04	intergenic

AT2G42910	na	Phosphoribosyll 2_17855388	8.04	proximal promoter
AT2G42900	na	Plant basic secr 2_17855388	8.04	exon
AT1G23890	na	NHL domain-co 1_8440985	8.04	promoter
AT2G24800		Peroxidase sup 2_10572704	8.04	promoter
AT2G28080	na	UDP-Glycosyltr; 2_11961757	8.04	intron
AT5G44290	na	Protein kinase s 5_17843709	8.04	intron
AT3G04800	TRANSLOCASE INNER MEMBRANE SU		8.04	proximal promoter
AT4G39980	3-DEOXY-D-ARABINO-HEPTULOSONAT		8.03	intergenic
AT4G37470	KARRIKIN INSENSITIVE 2 (KAI2)	HTL belonging t 4_17619061	8.03	proximal promoter
AT1G73885	na	unknown proteir 1_27785994	8.03	proximal promoter
AT1G73875	na	DNAse I-like sul 1_27785994	8.03	intergenic
AT4G39985	na	pre-tRNA; tRNA 4_18542450	8.03	downstream
AT4G39986	na	This gene encor 4_18542450	8.03	exon
AT4G37480	na	Chaperone Dna 4_17619061	8.03	promoter
AT2G03550	na	alpha/beta-Hydr 2_1076873 unknown proteir 5 17980217	8.03	promoter
AT5G44578			8.03	intergenic
AT5G44580 AT5G44582		unknown proteir 5_17980217	8.03	three_prime_UTR
	na OVATE FAMILY PROTEIN 6 (OFP6)	unknown proteir 5_17980217	8.03	proximal promoter
AT3G52525 AT4G39990		ovate family pro 3_19475638	8.03 8.03	exon
AT1G73880			8.03	promoter exon
AT1G18150	(ATMPK8)	Encodes mitoge 1_6247926	8.02	promoter
AT1G18130			8.02	•
AT1G18335	na	Acyl-CoA N-acy 1 6308184	8.02	promoter intergenic
AT1G18333		Protein kinase s 1_6247926	8.02	proximal promoter
AT1G78850		curculin-like (ma 1_29644325	8.02	proximal promoter
AT3G50560	na	NAD(P)-binding 3_18766001	8.02	proximal promoter
AT1G10700	PHOSPHORIBOSYL PYROPHOSPHATE		8.02	proximal promoter
AT2G38170	CATION EXCHANGER 1 (CAX1)	Encodes a high 2_15988844	8.01	intergenic
AT3G13405	MICRORNA169A (MIR169A)	Encodes a micr 3_4361408	8.01	proximal promoter
AT2G38160		unknown proteir 2_15988844	8.01	promoter
AT3G13410		unknown proteir 3 4361408	8.01	intergenic
AT2G19810	OXIDATION-RELATED ZINC FINGER 1 (8.01	promoter
AT1G78240	•		8.01	proximal promoter
AT2G20300		Encodes ABNO 2 8760285	7.99	promoter
AT1G30520			7.99	intergenic
AT1G30320	MICRORNA159A (MIR159A)	Encodes a micr 1_27713787	7.99	promoter
AT1G73007		unknown proteir 1_7267547	7.99	promoter
AT1G20090	na	agenet domain- 1_25752583	7.99	promoter
AT2G39020	na	Although this lot 2_16293108	7.99	proximal promoter
AT5G11420	na na	FUNCTIONS IN 5 3645955	7.99	exon
AT2G39010		_	7.99	intron
AT1G30530			7.99	five_prime_UTR
AT1G30330		UGT85A1; FUN 1_7907309	7.98	
AT4G16520	(UGT85A1) AUTOPHAGY 8F (ATG8F)	autophagy 8f (A 4_9306249	7.98	proximal promoter intergenic
AT4G16320		Octicosapeptide 4_2661588	7.98	exon
AT1G12110			7.98	proximal promoter
AT4G16515	ROOT MERISTEM GROWTH FACTOR 6		7.98	promoter
AT2G46510	ABA-INDUCIBLE BHLH-TYPE TRANSCR		7.97	proximal promoter
AT1G51500	ATP-BINDING CASSETTE G12 (ABCG12		7.97	proximal promoter
AT4G02350			7.97	promoter
AT4G02330		alpha/beta-Hydr 4_1037969	7.97	intergenic
AT3G14220		GDSL-like Lipas 3_4732420	7.97	promoter
AT3G14220	na na	unknown proteir 3 5248921	7.97	promoter
AT3G10985	SENESCENCE ASSOCIATED GENE 20 (7.97	intergenic
AT1G01480	1-AMINO-CYCLOPROPANE-1-CARBOX		7.96	exon
AT5G18670	BETA-AMYLASE 3 (BMY3)	putative beta-ar 5_6224079	7.96	proximal promoter
AT4G00150	` ,	Belongs to one 4_56915	7.96	intergenic
AT3G20395		RING/U-box su ₁ 3_7114033	7.96	promoter
AT4G08949		This gene encor 4_5736686	7.96	intergenic
AT5G41401	na	This gene encor 5_16575713	7.96	intergenic
AT5G01849	na	This gene enco 5_332173	7.95	intergenic
AT5G01850	na	Protein kinase s 5 332173	7.95	promoter
AT3G10500	NAC DOMAIN CONTAINING PROTEIN 5		7.95	promoter
AT5G59910	(HTB4)	HTB4; FUNCTI(5_24126934	7.94	promoter
AT1G07210		Ribosomal prote 1_2214268	7.94	proximal promoter
AT2G13363		unknown proteir 2_5543792	7.94	intergenic
AT2G30430		unknown proteir 2_12967453	7.94	proximal promoter
AT3G13740		Ribonuclease III 3_4506904	7.94	intergenic
AT2G30424	TRICHOMELESS 2 (TCL2)	In a tandem rep 2_12967453	7.94	proximal promoter
AT5G59920	UV-B LIGHT INSENSITIVE 3 (ULI3)	Isolated in a scr 5_24126934	7.94	proximal promoter
AT2G01910		Binds microtubl 2_416715	7.93	promoter
AT5G49100		unknown proteir 5_19897014	7.93	intergenic
AT5G22070		Core-2/I-branch 5_7307650	7.93	promoter
AT5G43270			7.93	intron
AT4G37800			7.93	proximal promoter
AT1G20050		C-8 sterol isom 1_6948388	7.92	proximal promoter
AT5G04200	. ,	Encodes a puta 5_1152798	7.92	proximal promoter
AT1G20040		pre-tRNA; tRNA 1_6948388	7.92	intergenic
AT1G11710		Pentatricopeptic 1_3947248	7.92	proximal promoter
AT5G04190			7.92	intergenic
AT2G24765			7.91	proximal promoter
AT4G17500			7.91	promoter
AT3G54804		This gene enco 3_20293272	7.9	promoter
AT5G49435		pre-tRNA; tRNA 5_20046786	7.9	promoter
AT3G14840		Leucine-rich rer 3_4988876	7.9	intron
AT2G03890			7.9	downstream
AT5G66460		Encodes a endc 5_26541320	7.89	promoter
AT1G31420		Encodes a plasi 1_11249481	7.89	promoter
AT1G31410		putrescine-bindi 1_11249481	7.89	promoter
AT2G35900		unknown proteir 2_15073970	7.89	proximal promoter
AT2G35910		RING/U-box sul 2_15073970	7.89	five_prime_UTR
AT3G11690		unknown proteir 3_3696714	7.89	intergenic
AT2G01670	NUDIX HYDROLASE HOMOLOG 17 (NU	i nudix nydrolase z_296498	7.89	downstream

AT3G53620	PYROPHOSPHORYLASE 4 (PPa4)	Encodes a solul 3_19880373	7.89	promoter
AT4G23980	AUXIN RESPONSE FACTOR 9 (ARF9)	Encodes auxin 4_12450377	7.88	proximal promoter
AT5G57015	CASEIN KINASE I-LIKE 12 (ckl12)	casein kinase I- 5_23070635	7.88	promoter
AT5G20630	GERMIN 3 (GER3)	Encodes a gern 5_6977960	7.88	proximal promoter
AT5G57010	na	calmodulin-bind 5_23070635	7.88	downstream
AT1G01540	na	Protein kinase s 1_194974	7.88	proximal promoter
AT1G15840	na	unknown proteir 1_5451209	7.88	promoter
AT3G11670	DIGALACTOSYL DIACYLGLYCEROL DEI	_	7.87	promoter
AT2G05380	GLYCINE-RICH PROTEIN 3 SHORT ISOF		7.87	promoter
AT1G42420	na	transposable eli 1_15880492	7.87	proximal promoter
AT2G20724	na	pseudogene of 2_8933386	7.87	promoter
AT2G20725	na	CAAX amino tei 2_8933386	7.87	downstream
AT5G43000	na	unknown proteir 5_17246200	7.87	downstream
AT4G14350	na	AGC (cAMP-de 4_8261074 INVOLVED IN: 5 8910009	7.87	promoter
AT5G25590	na	S-adenosyl-L-m 1_26134616	7.87 7.87	promoter
AT1G69526 AT4G14743	na		7.87	intergenic
	na	pseudogene, hy 4_8456797		intergenic
AT5G42990 AT1G09750	UBIQUITIN-CONJUGATING ENZYME 18	Eukaryotic aspa 1_3156709	7.87 7.86	promoter proximal promoter
AT1G59730	TUBULIN ALPHA-2 CHAIN (TUA2)	Encodes alpha- 1_18517458	7.86	promoter
AT4G37750	AINTEGUMENTA (ANT)	ANT is required 4_17735347	7.85	intergenic
AT1G70300	K+ UPTAKE PERMEASE 6 (KUP6)	potassium trans 1 26480241	7.85	intron
AT5G62890	na	Xanthine/uracil 5_25241542	7.85	proximal promoter
AT2G42600	PHOSPHOENOLPYRUVATE CARBOXYL		7.85	proximal promoter
AT2G27490	(ATCOAE)	AT2G27490 enc 2_11750915	7.84	proximal promoter
AT2G36270	ABA INSENSITIVE 5 (ABI5)	Encodes a merr 2 15207614	7.84	promoter
AT2G34925	CLAVATA3/ESR-RELATED 42 (CLE42)	Belongs to a lar 2_14735301	7.84	intergenic
AT5G58760	DAMAGED DNA BINDING 2 (DDB2)	Encodes a DDE 5 23733951	7.84	promoter
AT5G01560	LECTIN RECEPTOR KINASE A4.3 (LECR		7.84	proximal promoter
AT5G01570	na	unknown proteir 5_221117	7.84	promoter
AT2G36280	na	pre-tRNA; tRNA 2_15207614	7.84	intergenic
AT1G14270	na	CAAX amino ter 1_4877370	7.84	promoter
AT5G47660	na	Homeodomain-I 5_19312821	7.84	promoter
AT1G14280	PHYTOCHROME KINASE SUBSTRATE 2		7.84	promoter
AT2G44940	na	encodes a mem 2_18535906	7.83	proximal promoter
AT3G16400	NITRILE SPECIFIER PROTEIN 1 (NSP1)		7.83	proximal promoter
AT2G42200	SQUAMOSA PROMOTER BINDING PRO		7.83	promoter
AT5G41905	MICRORNA166E (MIR166E)	Encodes a micr 5_16776353	7.82	proximal promoter
AT1G31710	na	Copper amine c 1_11353972	7.82	intron
AT1G31710	na	Protein of unknc 1 11353972	7.82	proximal promoter
AT2G38820	na	Protein of unknc 2 16221630	7.82	promoter
AT5G02811	na	This gene encor 5 642339	7.82	downstream
AT5G02811	na	pre-tRNA; tRNA 5_642339	7.82	downstream
AT5G02813	na na	Protein of unknr 5_6739577	7.82	
AT5G19930 AT5G19940	na	Plastid-lipid ass 5_6739577	7.82	promoter
AT2G39010	PLASMA MEMBRANE INTRINSIC PROTE		7.82	promoter
AT5G02820	ROOT HAIRLESS 2 (RHL2)	Involved in the r 5 642339	7.82	proximal promoter promoter
AT4G23020	TON1 RECRUITING MOTIF 11 (TRM11)		7.82	intron
AT2G34770	FATTY ACID HYDROXYLASE 1 (FAH1)	unknown proteir 4_12067727	7.82	
		encodes a fatty 2_14665632	7.81	promoter
AT1G07580 AT2G44500	na na	pre-tRNA; tRNA 1_2335806 O-fucosyltransf(2_18372749	7.81	intergenic
AT5G43120	na	ARM-repeat/Tel 5_17315120	7.81	proximal promoter
AT2G34760	na na	pseudogene, tul 2_14665632	7.81	intergenic intron
AT5G43130			7.81	
AT3G06850	TBP-ASSOCIATED FACTOR 4 (TAF4)	TBP-associated 5_17315120 dihydrolipoamid 3_2160704	7.8	intergenic
AT3G13970	(BCE2) AUTOPHAGY 12 B (APG12B)	AUTOPHAGY 13_4616460	7.8	promoter proximal promoter
AT4G39350	CELLULOSE SYNTHASE A2 (CESA2)	Encodes a cellu 4_18296466	7.8	promoter
AT1G15175	na	Potential natura 1 5224262	7.8	•
AT1G15175	na	MATE efflux fan 1_5224262	7.8	promoter
AT4G38950	na na	ATP binding mic 4 18160068	7.8	promoter
AT4G38930	na	unknown proteir 4_12612329	7.8	promoter promoter
AT4G24380	na	INVOLVED IN: 4_12612329	7.8	promoter
AT1G05370	na	Sec14p-like phc 1 1569986	7.8	exon
AT1G03370	na	Pectin lyase-lik€ 1_17768464	7.8	intron
AT3G24542	na	Beta-galactosid 3_8958140	7.8	intergenic
AT3G24550	PROLINE-RICH EXTENSIN-LIKE RECEP		7.8	proximal promoter
AT5G60410	(SIZ1)	Encodes a plar 5_24294752	7.79	promoter
AT2G35690	ACYL-COA OXIDASE 5 (ACX5)	Encodes an acy 2 14999136	7.79	proximal promoter
AT2G35680	na	Phosphotyrosin 2 14999136	7.79	promoter
AT5G15080	na	Protein kinase s 5_4886828	7.79	intron
AT5G66820	na	unknown proteir 5_26688273	7.79	proximal promoter
AT2G28350	AUXIN RESPONSE FACTOR 10 (ARF10)		7.78	promoter
AT1G25250	INDETERMINATE(ID)-DOMAIN 16 (IDD16		7.78	intergenic
AT1G22180	na	Sec14p-like phc 1_7832852	7.78	proximal promoter
AT3G63510	na	FMN-linked oxic 3_23450378	7.78	promoter
AT1G63640	na	P-loop nucleosic 1_23597482	7.78	proximal promoter
AT3G63500	TITANIA 2 (TTA2)	Encodes a PHD 3_23450378	7.78	promoter
AT5G65140	TREHALOSE-6-PHOSPHATE PHOSPHA		7.78	promoter
AT5G46330	FLAGELLIN-SENSITIVE 2 (FLS2)	Encodes a leuci 5_18791581	7.77	promoter
AT5G02490	(Hsp70-2)	Heat shock prot 5_552959	7.76	promoter
AT5G02500	HEAT SHOCK COGNATE PROTEIN 70-1		7.76	intergenic
AT4G13940	HOMOLOGY-DEPENDENT GENE SILEN		7.76	promoter
AT1G33450	na	transposable ele 1_12138646	7.76	proximal promoter
AT2G46787	na	unknown proteir 2_19232454	7.76	exon
AT1G05410	na	Protein of unknc 1_1588025	7.76	promoter
AT1G80610	na	unknown proteir 1_30302938	7.76	intron
AT2G15950	na	pre-tRNA; tRNA 2_6946732	7.76	downstream
AT2G15960		unknown proteir 2 6946732	7.76	proximal promoter
7112010000	na			
AT5G27350	na (SFP1)	Encodes a suga 5_9652917	7.75	intron
	(SFP1) (SFP2)	Encodes a suga 5_9652917 Encodes a suga 5_9652917	7.75	intron intergenic
AT5G27350 AT5G27360 AT5G47230	(SFP1) (SFP2) ETHYLENE RESPONSIVE ELEMENT BIN	Encodes a suga 5_9652917 Encodes a suga 5_9652917 encodes a mem 5_19180901	7.75 7.75	intergenic exon
AT5G27350 AT5G27360 AT5G47230 AT5G20270	(SFP1) (SFP2) ETHYLENE RESPONSIVE ELEMENT BIN HEPTAHELICAL TRANSMEMBRANE PRO	Encodes a suga 5_9652917 Encodes a suga 5_9652917 encodes a mem 5_19180901 heptahelical trar 5_6842924	7.75 7.75 7.75	intergenic exon promoter
AT5G27350 AT5G27360 AT5G47230 AT5G20270 AT4G02425	(SFP1) (SFP2) ETHYLENE RESPONSIVE ELEMENT BIN HEPTAHELICAL TRANSMEMBRANE PRO na	Encodes a suga 5_9652917 Encodes a suga 5_9652917 encodes a mem 5_19180901 heptahelical trar 5_6842924 unknown proteir 4_1067002	7.75 7.75 7.75 7.75	intergenic exon promoter intergenic
AT5G27350 AT5G27360 AT5G47230 AT5G20270	(SFP1) (SFP2) ETHYLENE RESPONSIVE ELEMENT BIN HEPTAHELICAL TRANSMEMBRANE PRO	Encodes a suga 5_9652917 Encodes a suga 5_9652917 encodes a mem 5_19180901 heptahelical trar 5_6842924	7.75 7.75 7.75	intergenic exon promoter

AT5G47229	na	This gene enco 5_19180901	7.75	proximal promoter
AT3G60640	AUTOPHAGY 8G (ATG8G)	AUTOPHAGY 8 3_22417450	7.74	intergenic
AT5G56500	CHAPERONIN-60BETA3 (CPN60BETA3)		7.74	promoter
AT5G56490	L -GULONO-1,4-LACTONE (L -GULL) OX		7.74	downstream
AT3G03456	na	unknown proteir 3_822777	7.74	promoter
AT3G03460 AT4G04560	na	unknown proteir 3_822777	7.74 7.74	downstream
AT3G14230	na RELATED TO AP2 2 (RAP2.2)	transposable ell 4_2289066 encodes a mem 3 4740602	7.74	proximal promoter proximal promoter
AT5G02150	FES1C (Fes1C)	Encodes one of 5_427393	7.73	proximal promoter
AT1G06180	MYB DOMAIN PROTEIN 13 (MYB13)	member of MYE 1_1888771	7.73	proximal promoter
AT3G47940	na	DNAJ heat shot 3_17690953	7.73	proximal promoter
AT4G38930	na	Ubiquitin fusion 4_18151992	7.73	downstream
AT4G38932	na	Potential natura 4_18151992	7.73	exon
AT4G38940 AT3G61962	na na	Galactose oxida 4_18151992 This gene encor 3_22949547	7.73 7.73	proximal promoter proximal promoter
AT5G56220	na	P-loop containir 5 22758207	7.73	intergenic
AT5G56240	na	INVOLVED IN: 15_22758207	7.73	intergenic
AT5G02160	na	unknown proteir 5_427393	7.73	downstream
AT5G02170	na	Transmembran∈ 5_427393	7.73	promoter
AT2G02950	PHYTOCHROME KINASE SUBSTRATE 1		7.73	promoter
AT5G56230	PRENYLATED RAB ACCEPTOR 1.G2 (PI		7.73	intergenic
AT4G36860 AT4G27960	na UBIQUITIN CONJUGATING ENZYME 9 (I	LIM domain-cor 4_17363724	7.72 7.72	proximal promoter promoter
AT3G12380	ACTIN-RELATED PROTEIN 5 (ARP5)	Encodes a gene 3_3942128	7.72	promoter
AT3G62100	INDOLE-3-ACETIC ACID INDUCIBLE 30 (7.71	proximal promoter
AT3G12385	na	pre-tRNA; tRNA 3_3942128	7.71	downstream
AT3G12390	na	Nascent polype 3_3942128	7.71	promoter
AT4G18670	na	Leucine-rich rer 4_10279378	7.71	proximal promoter
AT5G64220	na	Calmodulin-binc 5_25685991	7.71	promoter
AT3G62097 AT4G00180	na YABBY3 (YAB3)	This gene enco 3_22995175 YABBY gene fa 4_76606	7.71 7.71	proximal promoter proximal promoter
AT1G08920	ERD (EARLY RESPONSE TO DEHYDRA)		7.7	intergenic
AT1G66230	MYB DOMAIN PROTEIN 20 (MYB20)	Encodes a puta 1_24677124	7.7	promoter
AT1G12760	na	Zinc finger, C3F 1_4348459	7.7	promoter
AT3G13040	na	myb-like HTH tr. 3_4176407	7.7	proximal promoter
AT3G13050	NICOTINATE TRANSPORTER (NiaP)	Encodes a plan 3_4176407	7.7	promoter
AT1G12750	RHOMBOID-LIKE PROTEIN 6 (RBL6)	RHOMBOID-like 1_4348459	7.7	promoter
AT5G02500 AT5G07290	HEAT SHOCK COGNATE PROTEIN 70-1 MEI2-LIKE 4 (ML4)	AML4 A membi 5 2292417	7.69 7.69	promoter proximal promoter
AT3G07230	na	unknown proteir 3_9718048	7.69	intergenic
AT1G02630	na	Nucleoside tran 1_559881	7.69	intergenic
AT3G60966	na	RING/U-box su ₁ 3_22553383	7.69	three_prime_UTR
AT5G65110	ACYL-COA OXIDASE 2 (ACX2)	Encodes an acy 5_26012721	7.67	promoter
AT5G65670	INDOLE-3-ACETIC ACID INDUCIBLE 9 (I/		7.67	proximal promoter
AT5G65120	na	unknown proteir 5_26012721	7.67	promoter
AT3G11690 AT5G13340	na na	unknown proteir 3_3691917	7.67 7.67	intergenic
AT1G60190	PLANT U-BOX 19 (PUB19)	unknown proteir 5_4277104 Encodes PUB1! 1_22198174	7.67	intergenic promoter
AT5G16190	CELLULOSE SYNTHASE LIKE A11 (CSL		7.66	proximal promoter
AT2G45050	GATA TRANSCRIPTION FACTOR 2 (GAT		7.66	proximal promoter
AT3G57540	na	Remorin family 3_21303165	7.66	promoter
AT5G59700	na	Protein kinase s 5_24055937	7.66	proximal promoter
AT4G36830	(HOS3-1)	HOS3-1; FUNC 4_17350198	7.65	exon
AT1G79110 AT4G36820	BOI-RELATED GENE 2 (BRG2)	Encodes one of 1_29761047 Protein of unkno 4 17350198	7.65 7.65	intergenic intergenic
AT5G18830	SQUAMOSA PROMOTER BINDING PRO		7.65	proximal promoter
AT3G47160	na	RING/U-box su ₁ 3_17362216	7.64	promoter
AT1G16260	na	Wall-associated 1_5562906	7.64	proximal promoter
AT1G16270	na	Protein kinase s 1_5562906	7.64	promoter
AT3G54920	POWDERY MILDEW RESISTANT 6 (PMF		7.64	intron
AT4G34410	REDOX RESPONSIVE TRANSCRIPTION CYSTEINE-RICH RLK (RECEPTOR-LIKE		7.64	proximal promoter
AT5G40380 AT4G02425	na	unknown proteir 4_1068921	7.63 7.63	promoter promoter
AT3G01430	na	BEST Arabidop: 3_165642	7.63	exon
AT1G15757	na	Encodes a defe 1_5423283	7.63	intergenic
AT2G24280	na	alpha/beta-Hydr 2_10331909	7.63	proximal promoter
AT2G31800	na	Integrin-linked p 2_13523988	7.63	promoter
AT2G31810	na	ACT domain-co 2_13523988	7.63	promoter
AT3G01850 AT3G01860	na na	Aldolase-type T 3_303503 unknown proteir 3 303503	7.63 7.63	proximal promoter intron
AT4G18570	na	Tetratricopeptid 4 10231366	7.63	five_prime_UTR
AT5G51910	na	TCP family tran: 5_21095048	7.63	exon
AT4G04890	PROTODERMAL FACTOR 2 (PDF2)	Encodes a hom 4_2482377	7.63	promoter
AT4G02430	SERINE/ARGININE-RICH PROTEIN SPLI		7.63	promoter
AT2G01930	BASIC PENTACYSTEINE1 (BPC1)	BASIC PENTAC 2_428723	7.62	five_prime_UTR
AT2G29420 AT1G08810	GLUTATHIONE S-TRANSFERASE TAU 7 MYB DOMAIN PROTEIN 60 (MYB60)		7.62	promoter
AT1G08810 AT3G50340	na	putative transcri 1_2820433 unknown proteir 3_18664990	7.62 7.62	promoter downstream
AT4G20880	na	ethylene-respor 4 11180787	7.62	five prime UTR
AT1G05860	na	unknown proteir 1_1768871	7.62	promoter
AT1G05850	POM-POM1 (POM1)	Encodes an enc 1_1768871	7.62	promoter
AT2G46860	PYROPHOSPHORYLASE 3 (PPa3)	Encodes a prote 2_19255680	7.62	intergenic
AT3G53350	ROP INTERACTIVE PARTNER 4 (RIP4)	ROP interactive 3_19782933	7.62	promoter
AT1G10960	COLD-REGULATED 413-PLASMA MEMB		7.61 7.61	intergenic
AT1G10960	FERREDOXIN 1 (FD1)	ferredoxin 1 (FE 1_3664222 Legume lectin f: 1_19782864	7.61 7.61	promoter intergenic
AT1G53080	na			
AT1G53080 AT3G50825	na na		7.61	intergenic
		snoRNA; snoRN 3_18892501 basic helix-loop 1_2991476	7.61 7.61	intergenic intergenic
AT3G50825 AT1G09250 AT3G20340	na	snoRNA; snoRl 3_18892501 basic helix-loop 1_2991476 Expression of th 3_7094418	7.61 7.61	intergenic proximal promoter
AT3G50825 AT1G09250 AT3G20340 AT2G43340	na na na na	snoRNA; snoRt 3_18892501 basic helix-loop 1_2991476 Expression of th 3_7094418 Protein of unknc 2_18007553	7.61 7.61 7.61	intergenic proximal promoter promoter
AT3G50825 AT1G09250 AT3G20340 AT2G43340 AT5G47190	na na na na na	snoRNA; snoRt 3_18892501 basic helix-loop 1_2991476 Expression of tt 3_7094418 Protein of unknc 2_18007553 Ribosomal prots 5_19166900	7.61 7.61 7.61 7.61	intergenic proximal promoter promoter proximal promoter
AT3G50825 AT1G09250 AT3G20340 AT2G43340 AT5G47190 AT5G40960	na na na na na na	snoRNA; snoRt 3_18892501 basic helix-loop 1_2991476 Expression of tf 3_7094418 Protein of unknr 2_18007553 Ribosomal prote 5_19166900 Protein of unknr 3_16413480	7.61 7.61 7.61 7.61 7.61	intergenic proximal promoter promoter proximal promoter promoter
AT3G50825 AT1G09250 AT3G20340 AT2G43340 AT5G47190	na na na na na	snoRNA; snoR\ 3_18892501 basic helix-loop 1_2991476 Expression of tf 3_7094418 Protein of unknc 2_18007553 Ribosomal prote 5_19166900 Protein of unknc 5_16413480 Protein of unknc 5_16413480	7.61 7.61 7.61 7.61	intergenic proximal promoter promoter proximal promoter

AT3G20330	PYRIMIDINE B (PYRB)	encodes aspart: 3_	7004418	7.61	proximal promoter
AT5G47200	RAB GTPASE HOMOLOG 1A (RAB1A)	AtRabD2b enco 5_		7.61	promoter
AT1G53090	SPA1-RELATED 4 (SPA4)	Encodes a merr 1_		7.61	promoter
AT1G10950	TRANSMEMBRANE NINE 1 (TMN1)	Encodes an Ara 1_		7.61	intergenic
AT3G53402	CONSERVED PEPTIDE UPSTREAM OPE			7.6	five_prime_UTR
AT4G23220	CYSTEINE-RICH RLK (RECEPTOR-LIKE			7.6	promoter
AT4G29740	CYTOKININ OXIDASE 4 (CKX4)	It encodes a prc 4_		7.6	proximal promoter
AT3G47540	na	Chitinase family 3_	17523323	7.6	intergenic
AT3G47550	na	RING/FYVE/PH 3_	17523323	7.6	promoter
AT3G53400	na	BEST Arabidop: 3_	19798163	7.6	five_prime_UTR
AT4G29735	na	unknown proteir 4_	14564762	7.6	promoter
AT5G59030	COPPER TRANSPORTER 1 (COPT1)	encodes a putal 5_			intergenic
AT3G23050	INDOLE-3-ACETIC ACID 7 (IAA7)	Transcription re 3_		7.59	three_prime_UTR
AT3G27090	na	DCD (Developn 3_		7.59	promoter
AT3G23750	na	Leucine-rich rer 3_		7.59	proximal promoter
AT1G76900	TUBBY LIKE PROTEIN 1 (TLP1)	Member of TLP 1_		7.59	proximal promoter
AT2G07050		Involved in the t 2_		7.58	promoter
AT3G14990	DJ-1 HOMOLOG A (DJ1A)	Encodes a hom 3_			promoter
AT1G51940	LYSM-CONTAINING RECEPTOR-LIKE KI	Pectin lyase-like 2		7.58	proximal promoter proximal promoter
AT2G43880 AT4G39160	na na	Homeodomain-I 4_		7.58 7.58	intron
AT4G39170	na	Sec14p-like phc 4_		7.58	promoter
AT5G24870	na	RING/U-box su ₁ 5_		7.58	proximal promoter
AT3G15000	RNA-EDITING FACTOR INTERACTING P			7.58	intergenic
AT1G71080	na	RNA polymeras 1_		7.57	promoter
AT3G42160	na	Pectin lyase-like 3_			intergenic
AT4G17670	na	Protein of unknc 4_		7.57	proximal promoter
AT5G52430	na	hydroxyproline-ı 5_		7.57	promoter
AT3G26720	na	Glycosyl hydrol: 3_		7.57	intergenic
AT3G26730	na	RING/U-box sur 3_		7.57	promoter
AT3G61070	PEROXIN 11E (PEX11E)	member of the r 3_	22602824	7.57	intergenic
AT3G61060	PHLOEM PROTEIN 2-A13 (PP2-A13)	phloem protein: 3_	22602824	7.57	promoter
AT3G11910	UBIQUITIN-SPECIFIC PROTEASE 13 (UE	ubiquitin-specifi 3_	3770578	7.57	promoter
AT5G08130	(BIM1)	Arabidopsis tha 5_			proximal promoter
AT4G29900	AUTOINHIBITED CA(2+)-ATPASE 10 (AC			7.56	intergenic
AT3G63060	EID1-LIKE 3 (EDL3)	EDL3 is an F-bc 3_		7.56	proximal promoter
AT4G38680	GLYCINE RICH PROTEIN 2 (GRP2)	Encodes a glyci 4_		7.56	downstream
AT2G20980	MINICHROMOSOME MAINTENANCE 10			7.56	promoter
AT5G01734	na	unknown proteir 5_		7.56	proximal promoter
AT5G01740	na	Nuclear transpc 5_			proximal promoter
AT4G38670	na	Pathogenesis-re 4_			promoter
AT4G38690	na	PLC-like phospl 4_		7.56	intergenic
AT2G20990	SYNAPTOTAGMIN A (SYTA)	Encodes a plasi 2_		7.56	promoter
AT5G63420	EMBRYO DEFECTIVE 2746 (emb2746)	embryo defectiv 5_		7.55	proximal promoter
AT5G20900	JASMONATE-ZIM-DOMAIN PROTEIN 12			7.55	promoter
AT2G14050 AT1G53500	MINICHROMOSOME MAINTENANCE 9 (I MUCILAGE-MODIFIED 4 (MUM4)	encodes a putal 1_		7.55 7.55	intergenic five_prime_UTR
AT2G14060	na	encodes a pote 1_			intergenic
AT5G44010	na	unknown proteir 5_		7.55	three_prime_UTR
AT5G63410	na	Leucine-rich reg 5_		7.55	proximal promoter
AT5G20890	na	TCP-1/cpn60 cf 5_		7.55	proximal promoter
AT1G54080	OLIGOURIDYLATE-BINDING PROTEIN 1.			7.55	five_prime_UTR
AT1G08650	PHOSPHOENOLPYRUVATE CARBOXYL			7.55	intergenic
AT5G22770	ALPHA-ADAPTIN (alpha-ADR)	alpha-adaptin (ε 5_		7.54	promoter
AT3G23637	DEVIL 21 (DVL21)	Member of a far 3			proximal promoter
AT5G66120	na	3-dehydroquina 5_	26433880	7.54	promoter
AT2G03240	na	EXS (ERD1/XP 2		7.54	promoter
AT1G21400	na	Thiamin diphost 1_	7494248	7.54	intron
AT1G35140	PHOSPHATE-INDUCED 1 (PHI-1)	EXL1 is involve 1_	12851857	7.54	promoter
AT4G14560	INDOLE-3-ACETIC ACID INDUCIBLE (IAA	auxin (indole-3- 4_	8360932	7.53	promoter
AT3G52800	na	A20/AN1-like zir 3_		7.53	three_prime_UTR
AT3G21560	UDP-GLUCOSYL TRANSFERASE 84A2 (intergenic
AT1G29300	UNFERTILIZED EMBRYO SAC 1 (UNE1)			7.53	three_prime_UTR
AT1G26810	GALACTOSYLTRANSFERASE1 (GALT1)			7.52	intergenic
AT5G27920	na	F-box family prc 5_		7.52	promoter
AT3G19010	na	2-oxoglutarate (3_		7.52	intron
AT1G07870 AT1G26800	na na	Protein kinase s 1_ RING/U-box sui 1		7.52 7.52	promoter promoter
AT1G20000 AT5G47390	na	myb-like transcr 5_		7.52	downstream
AT5G47400	na	unknown proteir 5_		7.52	promoter
AT3G55500	EXPANSIN A16 (EXPA16)	expansin-like pr 3		7.51	proximal promoter
AT5G59480	na	Haloacid dehalc 5		7.51	promoter
AT1G15730	na	Cobalamin bios 1		7.51	proximal promoter
AT1G15740	na	Leucine-rich reg 1		7.51	promoter
AT5G57660	CONSTANS-LIKE 5 (COL5)	CONSTANS-like 5		7.5	intergenic
AT5G41774		· · · · · · · · · · · · · · · · · · ·			
	na	This gene encor 5	16/2220/	7.5	exon
AT5G12040	na na	This gene encor 5_ Nitrilase/cyanide 5_		7.5 7.5	exon five_prime_UTR
AT5G12040 AT5G19770		Nitrilase/cyanide 5_	3885072		
	na	Nitrilase/cyanide 5_ tubulin 3 5_	3885072 6684640	7.5	five_prime_UTR promoter proximal promoter
AT5G19770 AT5G59220 AT4G03420	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (F na	Nitrilase/cyanide 5_ tubulin 3 5_ highly ABA-indu 5_ Protein of unkno 4_	3885072 6684640 23898693 1510241	7.5 7.5 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter
AT5G19770 AT5G59220 AT4G03420 AT3G15450	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (F na na	Nitrilase/cyanide 5_ tubulin 3 5_ highly ABA-indu 5_ Protein of unknc 4_ Aluminium induc 3_	_3885072 _6684640 _23898693 _1510241 _5213023	7.5 7.5 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (F na na na	Nitrilase/cyanide 5_ tubulin 3	_3885072 _6684640 _23898693 _1510241 _5213023 _5213023	7.5 7.5 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G16800	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (F na na na	Nitrilase/cyanidt 5_ tubulin 3	3885072 6684640 23898693 1510241 5213023 5213023 5719057	7.5 7.5 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G16800 AT3G15430	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (F na na na na	Nitrilase/cyanid 5_ tubulin 3 5_ highly ABA-indu 5_ Protein of unku 4_ Aluminium indu 3_ Ribosomal RNA 3_ Protein phosphs 3_ Regulator of chi 3_	.3885072 .6684640 .23898693 .1510241 .5213023 .5213023 .5719057 .5213023	7.5 7.5 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G16800 AT3G15430 AT1G32700	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (F na na na na na	Nitrilase/cyanid 5_ tubulin 3 5_ highly ABA-indu 5_ Protein of unknr 4_ Aluminium indur 3_ Ribosomal RNA 3_ Protein phosphr 3_ Regulator of chr 3_ PLATZ transcrir 1_	3885072 6684640 23898693 1510241 5213023 5213023 5719057 5213023 11827414	7.5 7.5 7.49 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic promoter
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G16800 AT3G15430 AT1G32700 AT2G25200	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (F na na na na na na na	Nitrilase/cyanid 5_tubulin 3 5_tubulin 3 5_Frotein of unkn 4_Aluminium indu 3_Ribosomal RNA 3_Protein phosph 3_Regulator of chi 3_PLATZ transcrip 1_Plant protein of 2_	3885072 6684640 23898693 1510241 5213023 5213023 5719057 5213023 11827414 10737756	7.5 7.5 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic promoter promoter promoter
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G16800 AT3G15430 AT1G32700 AT2G25200 AT3G16785	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (Fna na na na na na na PHOSPHOLIPASE D P1 (PLDP1)	Nitrilase/cyanids 5_ tubulin 3 highly ABA-indu 5_ Protein of unknt 4_ Aluminium indut 3_ Ribosomal RNA 3_ Protein phosphs 3_ Regulator of chr 3_ PLATZ transcrif 1_ Plant protein of 2_ Encodes a merr 3_	3885072 6684640 23898693 1510241 5213023 5213023 5719057 5213023 11827414 10737756 5719057	7.5 7.5 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic proximal promoter promoter promoter downstream
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G16800 AT3G15430 AT1G32700 AT2G25200 AT3G16785 AT3G22380	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (Fina) na	Nitrilase/cyanid 5. highly ABA-indu 5. Protein of unknr 4. Aluminium indu 3. Ribosomal RNA 3. Protein phosph 3. Regulator of chi 3. PLATZ transcrif 1. Plant protein of 2. Encodes a meri 3. Encodes a nucli 3.	3885072 6684640 23898693 1510241 5213023 5213023 5719067 5213023 11827414 10737756 5719057 7919883	7.5 7.5 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic promoter promoter downstream intergenic
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G15460 AT3G15430 AT1G32700 AT2G25200 AT3G16785 AT3G22380 AT3G08980	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (Fina) na na na na na na na na na THOSPHOLIPASE D P1 (PLDP1) TIME FOR COFFEE (TIC) na	Nitrilase/cyanid 5, tubulin 3 5, tubulin 3 5, tubulin 3 5, tubulin 3 5, trotein of unknc 4, Aluminium indu 3, Ribosomal RNA 3, Protein phosph 3, Regulator of ch 3, PLATZ transcrif 1, Plant protein of 2, Encodes a mer 3, Peptidase S24% 3, Peptidase S24% 3,	3885072 6684640 23898693 1510241 5213023 5213023 5719057 5213023 11827414 10737756 5719057 7919883 2742833	7.5 7.5 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic promoter downstream intergenic downstream intergenic
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15450 AT3G15460 AT3G15430 AT1G32700 AT2G25200 AT3G16785 AT3G22380 AT3G089980 AT3G08990	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (Fina) na THOSPHOLIPASE D P1 (PLDP1) TIME FOR COFFEE (TIC) na na	Nitrilase/cyanid 5, tubulin 3 highly ABA-indu 5, Protein of unknd 4, Aluminium indu 3, Ribosomal RNA 3, Protein phosph 3, Regulator of ch 3, PLATZ transcrit 1, Plant protein of 2, Encodes a meri 3, Encodes a nucl 3, Peptidase S24/; 3, Yippee family pi 3	3885072 66884640 23898693 1510241 5213023 5213023 5719057 5213023 11827414 10737756 5719057 7919883 2742833	7.5 7.5 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic promoter promoter promoter downstream intergenic downstream promoter
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G16800 AT3G16800 AT2G25200 AT2G25200 AT3G16785 AT3G08980 AT3G08980 AT3G18990 AT2G18960	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (Fina) na na na na na na PHOSPHOLIPASE D P1 (PLDP1) TIME FOR COFFEE (TIC) na na H(+)-ATPASE 1 (HA1)	Nitrilase/cyanid 5. highly ABA-indu 5. hrotein of unknr 4. Aluminium indu 3. Rrotein phosph 3. Protein phosph 3. Regulator of chi 3. PLATZ transcrif 1. Plant protein of 2. Encodes a meri 3. Encodes a nucli 3. Peptidase \$24/\$ 3. Yippee family pi 3. Encodes a plasi 2.	3885072 6684640 23898693 1510241 5213023 5213023 5719057 5213023 11827414 10737756 5719057 7919883 2742833 2742833 8222940	7.5 7.5 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic promoter downstream intergenic downstream intergenic downstream promoter intron
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G15430 AT1G32700 AT2G25200 AT3G16785 AT3G22380 AT3G08980 AT3G08990 AT2G18960 AT3G63210	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (Final na	Nitrilase/cyanid 5, tubulin 3 highly ABA-indu 5, Protein of unknc 4, Aluminium indu 3, Protein phosph; 3, Regulator of chi 3, PLATZ transcrif; 1, Plant protein of 2, Encodes a meri 3, Peptidase S24/; 3, Yippee family pi 3, Encodes a plasi 2, encodes a noce 3, encodes a posi 2, encodes a posi 2, encodes a noce 3, encodes a posi 3, encodes a posi 3, encodes a posi 3, encodes a noce 3, enco	3885072 6684640 23898693 1510241 5213023 5213023 5719057 5213023 11827414 10737756 5719057 7919883 2742833 8222940 23355263	7.5 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic promoter downstream intergenic downstream promoter downstream promoter intergenic downstream promoter intergenic
AT5G19770 AT5G59220 AT4G03420 AT3G15450 AT3G15460 AT3G16800 AT3G16800 AT2G25200 AT2G25200 AT3G16785 AT3G08980 AT3G08980 AT3G18990 AT2G18960	na TUBULIN ALPHA-3 (TUA3) HIGHLY ABA-INDUCED PP2C GENE 1 (Fina) na na na na na na PHOSPHOLIPASE D P1 (PLDP1) TIME FOR COFFEE (TIC) na na H(+)-ATPASE 1 (HA1)	Nitrilase/cyanid 5. highly ABA-indu 5. hrotein of unknr 4. Aluminium indu 3. Rrotein phosph 3. Protein phosph 3. Regulator of chi 3. PLATZ transcrif 1. Plant protein of 2. Encodes a meri 3. Encodes a nucli 3. Peptidase \$24/\$ 3. Yippee family pi 3. Encodes a plasi 2.	3885072 66884640 23898693 1510241 5213023 5719057 5213023 11827414 10737756 5719057 7719087 7742833 2742833 8222940 23355263 8298393	7.5 7.5 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49 7.49	five_prime_UTR promoter proximal promoter proximal promoter five_prime_UTR intergenic proximal promoter intergenic promoter downstream intergenic downstream intergenic downstream promoter intron

AT1G55110				
	INDETERMINATE(ID)-DOMAIN 7 (IDD7)	indeterminate(IE 1_20561324	7.46	intron
AT1G23380	KNOTTED1-LIKE HOMEOBOX GENE 6 (I		7.46	intron
AT3G19025	na	pseudogene, sir 3_6564616	7.46	intergenic
AT3G19030	na	unknown proteir 3_6564616	7.46	promoter
AT3G19035	na	unknown proteir 3_6564616	7.46	proximal promoter
AT3G01690	na	alpha/beta-Hydr 3_255777	7.46	proximal promoter
AT3G63220	na	Galactose oxida 3_23355263	7.46	intergenic
AT4G13110	na NONHOST RESISTANCE TO P. S. PHAS	BSD domain-co 4_7641376	7.46 7.46	promoter
AT1G80460 AT3G01680	SIEVE-ELEMENT-OCCLUSION-RELATEI		7.46	promoter intergenic
AT5G63050	EMBRYO DEFECTIVE 2759 (EMB2759)	embryo defectiv 5_25291733	7.45	proximal promoter
AT1G26770	EXPANSIN A10 (EXPA10)	Encodes an ext 1_9261440	7.45	downstream
AT2G43330	INOSITOL TRANSPORTER 1 (INT1)	Encodes a tono 2_18000743	7.45	promoter
AT4G27940	MANGANESE TRACKING FACTOR FOR		7.45	promoter
AT2G43320	na	S-adenosyl-L-m 2_18000743	7.45	proximal promoter
AT5G63180	na	Pectin lyase-lik€ 5_25344162	7.45	proximal promoter
AT5G63190	na	MA3 domain-co 5_25344162	7.45	proximal promoter
AT1G15500	(ATNTT2)	ATNTT2; FUNC 1_5325265	7.44	proximal promoter
AT1G79350	EMBRYO DEFECTIVE 1135 (EMB1135)	embryo defectiv 1_29853642	7.44	promoter
AT4G40060	HOMEOBOX PROTEIN 16 (HB16)	Encodes a hom 4_18569726	7.44	intergenic
AT5G65310	HOMEOBOX PROTEIN 5 (HB5)	Encodes a clas: 5_26105348	7.44	proximal promoter
AT2G28056	MICRORNA172A (MIR172A)	Encodes a micr 2_11941304	7.44	intergenic
AT2G28053 AT3G11825	na na	transposable el 2_11941304 Encodes a Prot 3_3731068	7.44 7.44	proximal promoter proximal promoter
AT5G43450	na	encodes a prote 5_17456798	7.44	intergenic
AT5G51770	na	Protein kinase s 5_21029858	7.44	proximal promoter
AT5G43440	na	encodes a prote 5_17456798	7.44	promoter
AT1G79360	ORGANIC CATION/CARNITINE TRANSP		7.44	intergenic
AT1G31340	RELATED TO UBIQUITIN 1 (RUB1)	Encodes a ubiq 1_11220221	7.44	proximal promoter
AT3G11820	SYNTAXIN OF PLANTS 121 (SYP121)	Encodes a synt 3_3731068	7.44	five_prime_UTR
AT2G40140	(CZF1)	CZF1; CONTAII 2_16776499	7.43	intergenic
AT2G40160	(TBL30)	Encodes a merr 2_16776499	7.43	proximal promoter
AT1G48410	ARGONAUTE 1 (AGO1)	Encodes an RN 1_17892644	7.43	promoter
AT1G20620	CATALASE 3 (CAT3)	Catalase, cataly 1_7141532	7.43	proximal promoter
AT5G55670	na	RNA-binding (R 5_22547176	7.43	promoter
AT1G64385	na	unknown proteir 1_23902989	7.43	intergenic
AT5G50840	na	CONTAINS Inte 5_20685607	7.43	promoter
AT1G19400	na	Erythronate-4-p 1_6712698	7.43	intron
AT5G40460	na PROTEIN KINASE 24 (ARK24)	unknown proteir 5_16202019	7.43	promoter
AT1G14370 AT2G40150	PROTEIN KINASE 2A (APK2A) TRICHOME BIREFRINGENCE-LIKE 28 (T	Encodes proteir 1_4915495	7.43 7.43	promoter intron
AT2G46130	ARABINOGALACTAN PROTEIN 16 (AGP		7.43	proximal promoter
AT1G13080	CYTOCHROME P450, FAMILY 71, SUBF		7.42	promoter
AT3G26932	DSRNA-BINDING PROTEIN 3 (DRB3)	dsRNA-binding 3_9932489	7.42	promoter
AT1G14840	MICROTUBULE-ASSOCIATED PROTEIN		7.42	promoter
AT3G54000	na	CONTAINS Inte 3_19996405	7.42	promoter
AT5G38130	na	HXXXD-type ac 5_15217318	7.42	intergenic
AT3G26935	na	DHHC-type zinc 3_9932489	7.42	downstream
AT4G38550	na	Arabidopsis phc 4_18025461	7.42	promoter
AT4G38552	na	Potential natura 4_18025461	7.42	downstream
AT5G60680	na	Protein of unknr 5_24390578	7.42	intergenic
AT4G13395	ROTUNDIFOLIA LIKE 12 (RTFL12)	ROTUNDIFOLI/ 4_7786081	7.42	five_prime_UTR
AT2G26660	SPX DOMAIN GENE 2 (SPX2)	SPX domain gel 2_11338604	7.42	promoter
AT4G31390 AT5G22040	ABC1-LIKE KINASE RELATED TO CHLOI	unknown proteir 5_7299260	7.41 7.41	proximal promoter
AT4G03110	RNA-BINDING PROTEIN-DEFENSE RELA		7.41	promoter promoter
AT5G38740	AGAMOUS-LIKE 77 (AGL77)	AGAMOUS-like 5_15515026	7.4	proximal promoter
7110000110	HOMOLOG OF YEAST AUTOPHAGY 18			
AT4G30510			7.4	promoter
AT4G30510 AT2G36320	na		7.4 7.4	promoter five prime UTR
		A20/AN1-like zir 2_15228805 unknown proteir 4_17524375		promoter five_prime_UTR promoter
AT2G36320	na na URIDINE-RIBOHYDROLASE 1 (URH1)	A20/AN1-like zii 2_15228805 unknown proteir 4_17524375 Encodes a cytol 2_15228805	7.4	five_prime_UTR
AT2G36320 AT4G37240	na na	A20/AN1-like zii 2_15228805 unknown proteir 4_17524375 Encodes a cytol 2_15228805	7.4 7.4	five_prime_UTR promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360	na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE	A20/AN1-like zii 2_15228805 unknown proteir 4_17524375 Encodes a cyto 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044	7.4 7.4 7.4 7.4 7.39	five_prime_UTR promoter proximal promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440	na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4)	A20/AN1-like zii 2_15228805 unknown proteir 4_17524375 Encodes a cyto 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829	7.4 7.4 7.4 7.4 7.39 7.39	five_prime_UTR promoter proximal promoter promoter promoter proximal promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740	na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPH	A20/AN1-like zii 2_15228805 unknown proteii 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831	7.4 7.4 7.4 7.4 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter promoter promoter proximal promoter promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT2G34430	na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF	A20/AN1-like zii 2_15228805 unknown proteir 4_17524375 Encodes a cytol 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter promoter promoter proximal promoter promoter promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT2G34430 AT3G19530	na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPH- LIGHT-HARVESTING CHLOROPHYLL-PI na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter promoter promoter proximal promoter promoter promoter promoter promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT2G34430 AT3G19530 AT1G32190	na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na	A20/AN1-like zii 2_15228805 unknown proteii 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydr 1_11598503	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter promoter promoter proximal promoter promoter proximal promoter proximal promoter
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ATZG36320 AT4G37240 ATZG36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT2G34430 AT3G19530 AT3G58610 AT3G58610 AT3G66670 AT4G34750 AT4G00720 AT5G66880 AT1G20900 AT5G56980 AT1G566980 AT1G566980 AT1G566920 AT1G76420	na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PI na na na na SHAGGY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1(SNF1)-I ESCAROLA (ESC) na na CUP SHAPED COTYLEDON3 (CUC3)	A20/AN1-like zii 2_15228805 unknown proteii 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hyd1 1_11598503 Adaptin ear-binx 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcris 3_22427870 SAUR-like auxir 4_16576831 Encodes ASKth 4_297361 encodes a mm 5_26709997 Encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an t1_28677348	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter promoter promoter promoter promoter intergenic
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AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT3G34430 AT3G358610 AT3G58610 AT3G60670 AT4G34750 AT4G09720 AT5G66880 AT1G20900 AT1G58602 AT1G58602 AT1G76420 AT1G76420 AT1G76420 AT1G76420 AT1G76420	na na na na na na na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na sha SHAGGY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1(SNF1)-F ESCAROLA (ESC) na na na CUP SHAPED COTYLEDON3 (CUC3) IQ-DOMAIN 24 (IQD24) na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2936829 Encodes glutarr 4_16576831 Photosystem II 12_14524539 BEST Arabidop: 3_6777362 alpha/beta-Hydi 1_11598503 Adaptin ear-bin: 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcrir 3_22427870 SAUR-like auxir 4_16576831 encodes ASKIh 4_297361 encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an ∈ 1_28677348 Undnown proteir 2_9454340	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter intergenic intron exon
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AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT3G34430 AT3G19530 AT1G32190 AT3G58600 AT3G58600 AT3G58610 AT3G60670 AT4G34750 AT4G34750 AT4G0900 AT5G56980 AT1G586980 AT1G58692 AT5G7240 AT5G7240 AT5G03690 AT2G03700	na na na na na na na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na na shaGGY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1(SNF1)-F ESCAROLA (ESC) na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydr 1_11598503 Adaptin ear-binr 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcrir 3_22427870 SAUR-like auxir 4_16576831 Encodes ASKth 4_297361 encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an <1_28677348 IQ-domain 24 (15_2272614 unknown proteir 2_9454340 Ubiquinone bios 2_1123212 pre-IRNA_1 tRNA_2 T123212	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter promoter promoter promoter promoter promoter promoter proximal promoter promoter intergenic intron exon promoter downstream
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT2G34430 AT3G19530 AT3G58600 AT3G58610 AT3G60670 AT4G34750 AT4G09720 AT5G66880 AT1G20900 AT1G58602 AT1G76420 AT5G7240 AT5G7240 AT2G03690 AT2G03700 AT2G03700 AT1G07040	na na na na na na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na sha SHAGGY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1(SNF1)-F ESCAROLA (ESC) na na na CUP SHAPED COTYLEDON3 (CUC3) IQ-DOMAIN 24 (IQD24) na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2936829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydi 1_11598503 Adaptin ear-bin: 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcrir 3_22427870 SAUR-like auxir 4_16576831 encodes ASKIh 4_297361 encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an ∈ 1_28677348 Uc-domain 24 (I-5_2272614 unknown proteir 2_9454340 Ubiquinone bios 2_1123212 unknown proteir 1_2164109	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter promoter intergenic intron exon promoter downstream proximal promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT3G34430 AT3G19530 AT1G32190 AT3G58600 AT3G58600 AT3G58610 AT3G60670 AT4G34750 AT4G34750 AT4G0900 AT5G56980 AT1G586980 AT1G58692 AT5G7240 AT5G7240 AT5G03690 AT2G03700	na na na na na na na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na na shaGGY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1(SNF1)-F ESCAROLA (ESC) na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hyd 1_11598503 Adaptin ear-bin: 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcris 3_22427870 SAUR-like auxir 4_16576831 encodes a MSth 4_297361 encodes a mem 5_26709997 Encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an €1_28677348 IQ-domain 24 (I) 5_2272614 unknown proteir 2_9454340 Ubiquinone bios 2_1123212 pre-tRNA; tRNA 2_1123212 unknown proteir 1_2164109 CCT motif famil 1_2164109	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter promoter promoter promoter promoter promoter promoter proximal promoter promoter intergenic intron exon promoter downstream
ATZG36320 AT4G37240 ATZG36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT2G34430 AT3G19530 AT3G58610 AT3G58610 AT3G58610 AT3G66670 AT4G34750 AT4G00720 AT5G658980 AT1G565980 AT1G76420 AT5G65980 AT1G76420 AT5G07240 AT5G07240 AT2G22241 AT2G03700 AT2G22241 AT2G03700 AT1G07040 AT1G07040 AT1G07050	na na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PI na na na na sha shaGGY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1(SNF1)-I ESCAROLA (ESC) na cup SHAPED COTYLEDON3 (CUC3) IQ-DOMAIN 24 (IQD24) na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2936829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydi 1_11598503 Adaptin ear-bin: 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcrir 3_22427870 SAUR-like auxir 4_16576831 encodes ASKIh 4_297361 encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an ∈ 1_28677348 Uc-domain 24 (I-5_2272614 unknown proteir 2_9454340 Ubiquinone bios 2_1123212 unknown proteir 1_2164109	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter promoter intergenic intron exon promoter downstream proximal promoter downstream
ATZG36320 AT4G37240 ATZG36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT2G34430 AT3G19530 AT3G58610 AT3G58610 AT3G58610 AT3G56800 AT4G34750 AT4G00720 AT5G656980 AT1G566980 AT1G76420 AT5G76420 AT5G7240 AT5G7240 AT5G7240 AT5G7240 AT5G7740 AT1G76420 AT5G7740 AT1G76420 AT5G7740 AT1G76420 AT5G7740 AT1G76420 AT5G7740 AT1G765690 AT1G56590 AT1G56590 AT1G56590 AT1G565690 AT1G565690 AT1G565690 AT3G50651	na na na na na na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PI na na na na na na na na companie to the companie	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mitor 5_26510044 EXORDIUM like 5_2935829 Encodes qlutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydr 1_11598503 Adaptin ear-bins 3_21671316 ketol-acid reduc 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcri; 3_22427870 SAUR-like auxir 4_16576831 Encodes A SKth 4_297361 encodes a n AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AT 1_27746190 Identified in an <1_28677348 IQ-domain 24 (I-5_2272614 unknown proteir 5_29454340 Ubiquinone bios 2_1123212 pre-18NA; tRNA 2_1123212 unknown proteir 1_2164109 CCT motif famil 1_2164109 Protein kinase s 1_20448123 unknown proteir 3_18809903 unknown proteir 3_18809903	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter prominal promoter promoter promoter promoter prominal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic intron exon promoter downstream proximal promoter downstream intron proximal promoter downstream intron proximal promoter intergenic
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT3G34430 AT3G19530 AT1G32190 AT3G58600 AT3G58600 AT3G58610 AT3G60670 AT4G34750 AT4G34750 AT4G34750 AT1G20900 AT1G566880 AT1G56980 AT1G76420 AT5G7240 AT5G7240 AT2G03690 AT1G07040 AT1G07040 AT1G07050 AT1G5740 AT1G07040 AT1G5740 AT1G5740 AT1G5740 AT1G5740 AT1G5740 AT1G5740 AT1G5740 AT1G5740 AT1G55690 AT1G55695 AT1G55655 AT1G55655	na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na na shaGQY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1(SNF1)-F ESCAROLA (ESC) na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydr 1_11598503 Adaptin ear-binr 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcrir 3_22427870 SAUR-like auxir 4_16576831 Encodes ASKth 4_297361 encodes a mem 5_26709997 Encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an c1_28677348 IQ-domain 24 (1.5_2272614 unknown proteir 5_2123212 unknown proteir 5_2123212 unknown proteir 5_2123212 unknown proteir 5_20448123 Sec14p-like phc 1_20415239 CCT motif famih 1_2164109 Protein kinase s 1_20448123 Sec14p-like phc 1_20815239 unknown proteir 3_18809903 Encodes a puta 1_5195951	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter downstream proximal promoter downstream proximal promoter intergenic intron proximal promoter intergenic proximal promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT2G34430 AT3G19530 AT1G32190 AT3G58610 AT3G566070 AT4G34750 AT4G34750 AT4G0900 AT5G66880 AT1G20900 AT1G76420 AT5G7240 AT2G03690 AT1G07040 AT1G07050 AT1G07040 AT1G07050 AT1G07040 AT1G56980 AT1G56980 AT1G56980 AT1G56980 AT1G07640 AT1G07640 AT1G07640 AT1G07640 AT1G07650 AT1G56890 AT1G56890 AT1G56890 AT1G56890 AT1G56890 AT1G56890 AT1G56890 AT1G56890 AT3G3700 AT1G56890 AT3G3700 AT1G56890 AT3G3700 AT1G56890 AT3G3700 AT1G56890 AT3G3700 AT1G56890 AT3G3700 AT1G56890 AT3G3700 AT1G56890 AT3G3700 AT1G56890 AT3G3880	na na na na na na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na sha shaGGY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1 (SNF1)-F ESCAROLA (ESC) na na na CUP SHAPED COTYLEDON3 (CUC3) IQ-DOMAIN 24 (IQD24) na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_293829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydi 1_11598503 Adaptin ear-bin: 3_21671316 PLATZ transcrir 3_22427870 SAUR-like auxir 4_16576831 encodes ASKth 4_297361 encodes an AT 1_7270589 Encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an ∈ 1_28677348 IU-domain 24 (1 § 5_2272614 unknown proteir 2_9454340 Ubiquinone bios 2_1123212 unknown proteir 1_2164109 CCT motif famih 1_2164109 PCT motif famih 1_2164109 PCT motif famih 1_2164109 PCT motif famih 1_2164109 PCT motif famih 1_2164109 Protein kinase s 1_20448123 Sec14p-like phc 1_20815239 unknown proteir 3_18809903 Encodes a puta 1_5195951 VPS20.1; CON 5_25563423	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter prominal promoter proximal promoter downstream proximal promoter downstream intron proximal promoter intergenic intergenic proximal promoter intergenic proximal promoter proximal promoter proximal promoter
ATZG36320 AT4G37240 ATG363610 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT3G19530 AT3G58610 AT3G58610 AT3G58610 AT3G58610 AT3G58610 AT3G56880 AT1G20900 AT5G56980 AT1G56980 AT1G76420 AT5G07240 AT5G07240 AT5G07240 AT5G07240 AT5G07240 AT5G07240 AT5G07240 AT5G07240 AT5G07240 AT5G07240 AT5G07240 AT5G07240 AT5G56980 AT1G56980 AT1G56980 AT1G56880 AT1G56880 AT1G56890 AT3G56910	na na na na na na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRYY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na sha shaGGY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1(SNF1)-F ESCAROLA (ESC) na na CUP SHAPED COTYLEDON3 (CUC3) IQ-DOMAIN 24 (IQD24) na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cyto; 2_15228805 Pathogen-induc 1_30383579 Encodes a mito; 5_26510044 EXORDIUM like; 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop; 3_6777362 alpha/beta-Hydr 1_11598503 Adaptin ear-bins 3_21671316 ketol-acid reduc 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcri; 3_22427870 SAUR-like auxir 4_16576831 Encodes A SKth 4_297361 encodes a n AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF1_21746190 Identified in an { 1_28677348 IQ-domain 24 (Ir 5_2272614 unknown proteir 5_9454340 Ubiquinone bios 2_1123212 pre-IRNA; tRNA 2_1123212 pre-IRNA; 18NA 2_1123212	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter intergenic intron promoter downstream proximal promoter intergenic proximal promoter intergenic proximal promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT3G34430 AT3G19530 AT1G32190 AT3G58600 AT3G58600 AT3G58600 AT4G34750 AT4G34750 AT4G34750 AT4G20900 AT5G56980 AT1G56980 AT1G76420 AT5G7240 AT2G22241 AT2G22241 AT2G32690 AT1G07040 AT1G07040 AT1G07050 AT1G565980 AT1G565980 AT1G565910 AT1G565980 AT1G565910 AT1G565980 AT1G556910 AT1G565880 AT1G565880 AT1G565880 AT1G565880 AT1G556910 AT3G50651 AT1G11100 AT5G653880 AT3G565810 AT5G55910	na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na sha na na na cha na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mitor 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydr 1_11598503 Adaptin ear-binr 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcrir 3_22427870 SAUR-like auxir 4_16576831 Encodes ASKth 4_297361 encodes a mem 5_26709997 Encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an c1_28677348 IQ-domain 24 (1: 5_2272614 unknown proteir 5_2123212 unknown proteir 5_25658423 UCT motif famih 1_2164109 Protein kinase s 1_20448123 Sec14p-like phc 1_20815239 unknown proteir 3_18809903 Encodes a puta 1_5195951 VPS20.1; CON1 5_25563423 URSOWN proteir 4_11545852	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter intergenic intron exon promoter downstream proximal promoter downstream proximal promoter intergenic intergenic intron proximal promoter promoter promoter promoter promoter proximal promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT4G34740 AT2G34430 AT3G19530 AT1G32190 AT3G58600 AT3G586010 AT3G60670 AT4G34750 AT4G34750 AT4G34750 AT4G30720 AT5G66880 AT1G20900 AT1G56980 AT1G56980 AT1G76420 AT2G3700 AT1G07040 AT1G07050 AT1G07040 AT1G07050 AT1G56880 AT1G56880 AT1G56880 AT1G57240 AT2G3700 AT1G5764820 AT1G556980 AT3G565810 AT5G63880 AT5G63880 AT5G63880 AT5G655810 AT5G63880 AT5G655910 AT3G63880 AT4G61740 AT3G08020	na na na na na na na na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na sha shaGGY-LIKE PROTEIN KINASE 32 (SK: SUCROSE NONFERMENTING 1(SNF1)-F ESCAROLA (ESC) na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cyto; 2_15228805 Pathogen-induc 1_30383579 Encodes a mito 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydi 1_11598503 Adaptin ear-bin 3_21671316 PLATZ transcrir 3_22427870 SAUR-like auxir 4_16576831 encodes ASKth 4_297361 encodes an AT 1_7270589 Encodes ASKth 4_297361 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an 4_28677348 Ubiquinone bios 2_1123212 unknown proteir 2_9454340 Ubiquinone bios 2_1123212 unknown proteir 1_2164109 CCT motif famih 1_2164109 PCT motif famih 1_2164109 Protein kinase s 1_20448123 Sec14p-like phc 1_20815239 unknown proteir 3_18809903 Encodes a puta 1_519951 VPS20.1; CON¹5_25563423 D6PK is a prote 5_22645041 unknown proteir 4_11454852 PHD finger fami 3_2562919	7.4 7.4 7.4 7.4 7.3 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter prominal promoter proximal promoter promoter intergenic intron exon promoter downstream proximal promoter downstream intron proximal promoter intergenic proximal promoter
AT2G36320 AT4G37240 AT2G36310 AT1G80840 AT5G66360 AT5G09440 AT3G34430 AT3G19530 AT1G32190 AT3G58600 AT3G58600 AT3G58600 AT4G34750 AT4G34750 AT4G34750 AT4G20900 AT5G56980 AT1G56980 AT1G76420 AT5G7240 AT2G22241 AT2G22241 AT2G32690 AT1G07040 AT1G07040 AT1G07050 AT1G565980 AT1G565980 AT1G565910 AT1G565980 AT1G565910 AT1G565980 AT1G556910 AT1G565880 AT1G565880 AT1G565880 AT1G565880 AT1G556910 AT3G50651 AT1G11100 AT5G653880 AT3G565810 AT5G55910	na URIDINE-RIBOHYDROLASE 1 (URH1) WRKY DNA-BINDING PROTEIN 40 (WRK ADENOSINE DIMETHYL TRANSFERASE EXORDIUM LIKE 4 (EXL4) GLN PHOSPHORIBOSYL PYROPHOSPI- LIGHT-HARVESTING CHLOROPHYLL-PF na na na na sha na na na cha na	A20/AN1-like zir 2_15228805 unknown proteir 4_17524375 Encodes a cytoj 2_15228805 Pathogen-induc 1_30383579 Encodes a mitor 5_26510044 EXORDIUM like 5_2935829 Encodes glutarr 4_16576831 Photosystem II 12_14524596 BEST Arabidop: 3_6777362 alpha/beta-Hydr 1_11598503 Adaptin ear-binr 3_21671316 ketol-acid reduc 3_21671316 PLATZ transcrir 3_22427870 SAUR-like auxir 4_16576831 Encodes ASKth 4_297361 encodes a mem 5_26709997 Encodes an AT 1_7270589 unknown proteir 5_23059514 LRR and NB-AF 1_21746190 Identified in an c1_28677348 IQ-domain 24 (1.5_2272614 unknown proteir 5_212212 pre-IRNA; IRNA 2_1123212 pre-IRNA; IRNA 2_1123212 unknown proteir 3_1809903 Encodes a puta 1_5195951 VPS20.1; CONT 5_25563423 URSDOR 15 25863423 URSDOR 1595951 VPS20.1; CONT 5_25563423	7.4 7.4 7.4 7.4 7.39 7.39 7.39 7.39 7.39 7.39 7.39 7.39	five_prime_UTR promoter proximal promoter intergenic intron exon promoter downstream proximal promoter downstream proximal promoter intergenic intergenic intron proximal promoter promoter promoter promoter promoter proximal promoter

AT4040000	10T DOMAIN DEDEATO 44 (10D44)	F I AOT 4 . 5770.405	7.05	
AT1G16880 AT1G15010	ACT DOMAIN REPEATS 11 (ACR11)	Encodes a ACT 1_5773425	7.35	promoter
	na	unknown proteir 1_5171074	7.35 7.35	promoter
AT1G16870 AT1G17830	na na	mitochondrial 28 1_5773425 Protein of unknot 1_6137540	7.35	promoter intron
AT1G17630 AT4G39070	na		7.35	
AT5G63860	UVB-RESISTANCE 8 (UVR8)	B-box zinc finge 4_18208871 UV-B-specific si 5_25558795	7.35	proximal promoter five_prime_UTR
AT4G39080	VACUOLAR PROTON ATPASE A3 (VHA-		7.35	proximal promoter
AT2G03360	na	Glycosyltransfer 2 1025845	7.34	proximal promoter
AT2G03300	na	Glycosyltransfer 2_1025845	7.34	exon
AT5G65740	na	zinc ion binding: 5_26301436	7.34	downstream
AT5G65720	NITROGEN FIXATION S (NIFS)-LIKE 1 (N		7.34	intergenic
AT1G79590	SYNTAXIN OF PLANTS 52 (SYP52)	Encodes one of 1_29949335	7.34	intergenic
AT2G41630	TRANSCRIPTION FACTOR IIB (TFIIB)	Encodes the tra 2_17357789	7.34	promoter
AT5G65730	XYLOGLUCAN ENDOTRANSGLUCOSYL		7.34	intergenic
AT2G41660	MIZU-KUSSEI 1 (MIZ1)	Essential for hy: 2_17369568	7.33	intergenic
AT3G19390	na	Granulin repeat 3_6720056	7.33	proximal promoter
AT1G16750	na	Protein of unknot 1_5731898	7.33	promoter
AT1G10750	na	unknown proteir 2_7641368	7.33	proximal promoter
AT4G19460	na	UDP-Glycosyltr: 4_10612238	7.33	promoter
AT1G72750	TRANSLOCASE INNER MEMBRANE SUI		7.33	promoter
AT3G09260	(PYK10)	Encodes beta-g 3_2844685	7.32	proximal promoter
AT1G02510	(TPK4)	Encodes AtTPK 1_522024	7.32	promoter
AT5G01520	ABA INSENSITIVE RING PROTEIN 2 (AIR		7.32	promoter
AT4G23750	CYTOKININ RESPONSE FACTOR 2 (CRI		7.32	intergenic
AT4G08980	F-BOX WITH WD-40 2 (FBW2)	Encodes an F-b 4_5757896	7.32	promoter
AT5G67200	na	Leucine-rich reg 5_26817182	7.32	proximal promoter
AT1G22320	na	pre-tRNA; tRNA 1_7884334	7.32	downstream
AT2G37030	na	SAUR-like auxir 2_15552671	7.32	proximal promoter
AT1G67340	na	HCP-like superf 1_25230157	7.32	promoter
AT5G67630	na	P-loop containir 5_26969671	7.32	promoter
AT5G67640	na	unknown proteir 5_26969671	7.32	intron
AT2G37025	TRF-LIKE 8 (TRFL8)	TRF-like 8 (TRF 2_15552671	7.32	intergenic
AT5G25460	DUF642 L-GALL RESPONSIVE GENE 2	Protein of unknc 5_8864175	7.31	intron
AT2G29670	na	Tetratricopeptid 2_12682594	7.31	intron
AT2G18860	na	Syntaxin/t-SNAI 2_8164121	7.31	promoter
AT5G54148	na	unknown proteir 5_21975208	7.31	intergenic
AT3G50080	VIER F-BOX PROTEINE 2 (VFB2)	Encodes an F-b 3_18572662	7.31	promoter
AT1G49620	(ICK5)	Kip-related prot 1_18366789	7.3	promoter
AT5G03210	DBP-INTERACTING PROTEIN 2 (DIP2)	Encodes a smal 5_763540	7.3	promoter
AT5G22890	na	C2H2 and C2H(5_7655642	7.3	proximal promoter
AT3G16400	NITRILE SPECIFIER PROTEIN 1 (NSP1)		7.3	downstream
AT1G21100	INDOLE GLUCOSINOLATE O-METHYLTI		7.29	promoter
AT2G29679	na	unknown proteir 2_12688756	7.29	intergenic
AT4G33565	na	RING/U-box su ₁ 4_16136409	7.29	promoter
AT5G01420	na na	Glutaredoxin far 5_176387	7.29	promoter
AT5G01430 AT1G29150	NON-ATPASE SUBUNIT 9 (ATS9)	Got1/Sft2-like v ₁ 5_176387 specifically inter 1_10180403	7.29 7.29	downstream promoter
AT5G47110	(LIL3:2)	Chlorophyll A-B 5_19135912	7.28	proximal promoter
AT5G47110	BAX INHIBITOR 1 (BI1)	Encodes BI-1, a 5_19135912	7.28	promoter
AT5G51990	C-REPEAT-BINDING FACTOR 4 (CBF4)	encodes a mem 5_21118239	7.28	promoter
AT3G60680	na	Plant protein of 3_22432300	7.28	intergenic
AT1G26160	na	Metal-depender 1_9043980	7.28	intergenic
AT1G77200	na	encodes a mem 1_29006374	7.28	proximal promoter
AT4G13530	na	unknown proteir 4_7869491	7.28	intergenic
AT4G13540	na	unknown proteir 4_7869491	7.28	promoter
AT5G67290	na	FAD-dependent 5_26849951	7.28	promoter
AT1G26150	PROLINE-RICH EXTENSIN-LIKE RECEPT	Encodes a merr 1_9043980	7.28	proximal promoter
AT2G40090	ABC2 HOMOLOG 9 (ATH9)	member of ATH 2_16741099	7.27	proximal promoter
AT1G01600	CYTOCHROME P450, FAMILY 86, SUBFA		7.27	promoter
AT1G01610	GLYCEROL-3-PHOSPHATE ACYLTRANS		7.27	intergenic
AT5G44190	GOLDEN2-LIKE 2 (GLK2)	Encodes GLK2, 5_17792821	7.27	intergenic
AT5G03220	na	Mediator comple 5_767094	7.27	intergenic
AT2G44500	na	O-fucosyltransfe 2_18374285	7.27	promoter
AT3G03680	na	C2 calcium/lipid 3_910890	7.27	downstream
AT3G47341	na	unknown proteir 3_17442318	7.27	intergenic
AT5G46250	na	RNA-binding pr. 5_18753977	7.27	proximal promoter
AT4G00570	NAD-DEPENDENT MALIC ENZYME 2 (NA		7.27	promoter
AT3G55000	TONNEAU 1A (TON1A)	Encodes a prote 3_20378990	7.27	proximal promoter
AT3G03690 AT2G02800	UNFERTILIZED EMBRYO SAC 7 (UNE7)	Encodes proteir 2 799575	7.27 7.26	intergenic
	PROTEIN KINASE 2B (APK2B)	Member of the c 2 18067684		promoter
AT2G43510	TRYPSIN INHIBITOR PROTEIN 1 (TI1)		7.26	three_prime_UTR
AT3G16520 AT5G53050	UDP-GLUCOSYL TRANSFERASE 88A1 (7.26 7.25	promoter
AT1G61100	na na	alpha/beta-Hydr 5_21513651 disease resistar 1_22512326	7.25	promoter intron
AT1G71000	na	unknown proteir 1 26731648	7.25	
AT1G70900 AT5G52510	SCARECROW-LIKE 8 (SCL8)	SCARECROW- 5 21306849	7.25 7.25	promoter promoter
AT1G01650	SIGNAL PEPTIDE PEPTIDASE-LIKE 4 (SI		7.25	promoter
AT4G18170	WRKY DNA-BINDING PROTEIN 28 (WRK		7.25	proximal promoter
AT1G07090	LIGHT SENSITIVE HYPOCOTYLS 6 (LSH		7.23	promoter
AT1G12380	na	unknown proteir 1 4217253	7.24	promoter
AT2G34480	na	Ribosomal prote 2 14534747	7.24	proximal promoter
AT2G46380	na	Protein of unknc 2_19038932	7.24	promoter
AT3G57880	na	Calcium-depend 3_21434962	7.24	promoter
AT5G22920	na	CHY-type/CTCl 5_7667533	7.24	intergenic
AT5G24430	na	Calcium-depend 5_8344020	7.24	proximal promoter
AT5G42000	na	ORMDL family r 5_16799217	7.24	promoter
AT3G05740	RECQ HELICASE L1 (RECQI1)	RECQ helicase 3_1697854	7.24	promoter
AT5G64810	WRKY DNA-BINDING PROTEIN 51 (WRK	member of WRI 5_25908050	7.24	promoter
AT5G43890	YUCCA5 (YUC5)	Encodes a YUC 5_17655989	7.24	intergenic
AT1G75660	5'-3' EXORIBONUCLEASE 3 (XRN3)	Encodes a prot 1_28407949	7.23	promoter
AT2G39570	ACT DOMAIN REPEATS 9 (ACR9)	Encodes a ACT 2_16507703	7.23	promoter
AT3G25110	FATA ACYL-ACP THIOESTERASE (FaTA		7.23	promoter
AT3G04210	na	Disease resista: 3_1108278 Esterase/lipase: 5_16464971	7.23 7.23	promoter proximal promoter
AT5G41130	na	L3te183e/iip83e/ 3_1040437 1	7.23	proximal promoter

AT5G51830	na	pfkB-like carbor 5_21071829	7.23	downstream
AT5G51840	na	unknown proteir 5_21071829	7.23	promoter
AT1G75650	na	pre-tRNA; tRNA 1_28407949	7.23	promoter
AT1G75640	na	Leucine-rich rec 1_28407949	7.23	proximal promoter
AT3G17020	na	Adenine nucleol 3_5804344	7.23	promoter
AT3G17030	na	Nucleic acid-bin 3_5804344	7.23	downstream
AT1G72150	PATELLIN 1 (PATL1)	novel cell-plate- 1_27148445	7.23	promoter
AT3G29360	UDP-GLUCOSE DEHYDROGENASE 2 (U		7.23	promoter
AT5G57490	VOLTAGE DEPENDENT ANION CHANNE		7.23	promoter
AT3G52840	BETA-GALACTOSIDASE 2 (BGAL2)	beta-galactosid: 3_19581081	7.22	promoter
AT4G34990	MYB DOMAIN PROTEIN 32 (MYB32)	Member of the F 4_16663613	7.22	proximal promoter
AT3G42570	na	peroxidase fami 3_14690027	7.22	exon
AT3G42580	na	transposable eli 3_14690027	7.22	proximal promoter
AT5G58650	PLANT PEPTIDE CONTAINING SULFATE		7.21	promoter
AT2G47650	UDP-XYLOSE SYNTHASE 4 (UXS4)	encodes a prote 2_19540310	7.21	intron
AT1G63130	na	Transacting siR 1_23412379	7.2	promoter
AT3G62470	na	Pentatricopeptic 3_23108676	7.2	promoter
AT5G49370	na	Pleckstrin home 5_20020667	7.2	proximal promoter
AT4G35780	SERINE/THREONINE/TYROSINE KINASE		7.2	promoter
AT2G25490	EIN3-BINDING F BOX PROTEIN 1 (EBF1)		7.19	promoter
AT1G53170	ETHYLENE RESPONSE FACTOR 8 (ERF		7.19	intergenic
AT1G69530	EXPANSIN A1 (EXPA1)	Member of Alph 1_26140851	7.19	proximal promoter
AT5G13190	GSH-INDUCED LITAF DOMAIN PROTEIN		7.19	intergenic
AT4G29090	na	Ribonuclease H 4_14331487	7.19	proximal promoter
AT1G15370	na	SNARE-like sur 1_5286841	7.19	promoter
AT1G30475	na	BEST Arabidop: 1_10795279	7.19	intergenic
AT3G15520	na	Cyclophilin-like 3_5252843	7.19	promoter
AT3G15530	na	S-adenosyl-L-m 3_5252843	7.19	downstream
AT4G29030	na	Putative membr 4_14308514	7.19	intergenic
AT3G45780	PHOTOTROPIN 1 (PHOT1)	Blue-light photo 3_16819947	7.19	exon
AT2G39480	ATP-BINDING CASSETTE B6 (ABCB6)	P-glycoprotein (2_16485752	7.18	proximal promoter
AT3G26180	CYTOCHROME P450, FAMILY 71, SUBF		7.18	intergenic
AT3G18950	na	Transducin/WD 3_6538399	7.18	three_prime_UTR
AT5G54700	na	Ankyrin repeat f 5_22226556	7.18	proximal promoter
AT3G55110	ATP-BINDING CASSETTE G18 (ABCG18)		7.17	proximal promoter
AT1G73830	BR ENHANCED EXPRESSION 3 (BEE3)		7.17	promoter
AT5G64860	DISPROPORTIONATING ENZYME (DPE1		7.17	promoter
AT5G43750	PHOTOSYNTHETIC NDH SUBCOMPLEX		7.17	proximal promoter
AT5G61810	ATP/PHOSPHATE CARRIER 1 (APC1)	Encodes a mito 5_24834001	7.16	promoter
AT1G12820	AUXIN SIGNALING F-BOX 3 (AFB3)	Auxin receptor i 1_4371445	7.16	promoter
AT2G17840	EARLY-RESPONSIVE TO DEHYDRATION	Identified as drc 2_7757913	7.16	promoter
AT2G18735	na	other RNA 2_8122970	7.16	exon
AT2G18740	na	Small nuclear ril 2_8122970	7.16	promoter
AT2G17830	na	F-box and asso 2_7757913	7.16	intergenic
AT1G25260	na	Ribosomal prote 1_8853826	7.16	downstream
AT4G08910	na	unknown proteir 4_5712228	7.16	promoter
AT5G24570	na	unknown proteir 5_8405209	7.16	intergenic
AT5G61820	na	FUNCTIONS IN 5_24834001	7.16	intergenic
AT5G02940	na	Protein of unknc 5_690071	7.16	promoter
AT5G05180	na	unknown proteir 5_1535995	7.16	promoter
AT1G14740	TITANIA 1 (TTA1)	Encodes a PHD 1_5077859	7.16	promoter
AT2G44910	HOMEOBOX-LEUCINE ZIPPER PROTEIN	Encodes a hom 2_18521608	7.15	proximal promoter
AT5G37490	na	ARM repeat sur 5_14888196	7.15	exon
AT3G58120	(BZIP61)	Encodes a merr 3_21520340	7.14	intergenic
AT1G55360	na	Protein of Unkn 1_20670048	7.14	proximal promoter
AT2G45850	na	AT hook motif D 2_18873964	7.14	five_prime_UTR
AT2G32190	na	unknown proteir 2_13676278	7.14	intergenic
AT2G32200	na	unknown proteir 2_13676278	7.14	promoter
AT5G67190	DREB AND EAR MOTIF PROTEIN 2 (DE/	encodes a mem 5_26808389	7.13	intergenic
AT3G24140	FAMA (FMA)	Encodes a basi 3_8719251	7.13	proximal promoter
AT3G11405	na	unknown proteir 3_3582899	7.13	intergenic
AT1G15970	na	DNA glycosylas 1_5489040	7.13	promoter
AT1G15980	PHOTOSYNTHETIC NDH SUBCOMPLEX	encodes a nove 1_5489040	7.13	promoter
AT3G18485	IAA-LEUCINE RESISTANT 2 (ILR2)	Encodes a nov€ 3_6344437	7.12	proximal promoter
AT2G17120	LYSM DOMAIN GPI-ANCHORED PROTE		7.12	five_prime_UTR
AT3G20360	na	TRAF-like family 3_7102414	7.12	proximal promoter
AT4G29780	na	unknown proteir 4_14579627	7.12	promoter
AT4G29790	na	unknown proteir 4_14579627	7.12	intergenic
AT5G03230	na	Protein of unknc 5_769369	7.12	promoter
AT4G18910	NOD26-LIKE INTRINSIC PROTEIN 1;2 (N		7.12	proximal promoter
AT1G30810	JUMONJI DOMAIN-CONTAINING PROTE		7.11	promoter
AT5G03140	na	Concanavalin A 5_740114	7.11	promoter
AT3G02125	na	unknown proteir 3_380012	7.11	intergenic
AT3G02130	RECEPTOR-LIKE PROTEIN KINASE 2 (R		7.11	proximal promoter
AT5G55910	D6 PROTEIN KINASE (D6PK)	D6PK is a prote 5_22642258	7.1	five_prime_UTR
AT1G17455	ELF4-LIKE 4 (ELF4-L4)	ELF4-like 4 (ELI 1_5997072	7.1	promoter
AT5G57070	na	hydroxyproline-ı 5_23098374	7.1	three_prime_UTR
AT5G57080	na	unknown proteir 5_23098374	7.1	proximal promoter
AT4G37680			_	
AT4G37670	HEPTAHELICAL PROTEIN 4 (HHP4)	heptahelical trar 4_17699259	7.09	proximal promoter
	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2	heptahelical trar 4_17699259 N-acetyl-l-glutar 4_17699259	7.09	promoter
AT3G61670	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na	heptahelical trar 4_17699259 N-acetyl-l-glutar 4_17699259 Protein of unknc 3_22817871	7.09 7.09	promoter proximal promoter
AT1G68490	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na	heptahelical trar 4_17699259 N-acetyl-l-glutar 4_17699259 Protein of unknc 3_22817871 unknown proteir 1_25690158	7.09 7.09 7.09	promoter proximal promoter intergenic
AT1G68490 AT5G40660	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na	heptahelical trar 4_17699259 N-acetyl-l-glutar 4_17699259 Protein of unknc 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770	7.09 7.09 7.09 7.09	promoter proximal promoter intergenic promoter
AT1G68490 AT5G40660 AT5G40670	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na	heptahelical trar 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unknr 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 PQ-loop repeat 5_16285770	7.09 7.09 7.09 7.09 7.09	promoter proximal promoter intergenic promoter five_prime_UTR
AT1G68490 AT5G40660 AT5G40670 AT4G09570	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na CALCIUM-DEPENDENT PROTEIN KINAS	heptahelical trar 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unknr 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 PQ-loop repeat 5_16285770 Encodes a merr 4_6049428	7.09 7.09 7.09 7.09 7.09 7.08	promoter proximal promoter intergenic promoter five_prime_UTR promoter
AT1G68490 AT5G40660 AT5G40670 AT4G09570 AT1G67790	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na na CALCIUM-DEPENDENT PROTEIN KINAS na	heptahelical trar 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unkn 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 PQ-loop repeat 5_16285770 Encodes a mer 4_6049428 unknown proteir 1_25417594	7.09 7.09 7.09 7.09 7.09 7.08 7.08	promoter proximal promoter intergenic promoter five_prime_UTR promoter exon
AT1G68490 AT5G40660 AT5G40670 AT4G09570 AT1G67790 AT1G67792	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na CALCIUM-DEPENDENT PROTEIN KINAS na na	heptahelical trai 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unknc 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 PC-loop repeat 5_16285770 Encodes a merr 4_6049428 unknown proteir 1_25417594 Potential natura 1_25417594	7.09 7.09 7.09 7.09 7.09 7.08 7.08 7.08	promoter proximal promoter intergenic promoter five_prime_UTR promoter exon promoter
AT1G68490 AT5G40660 AT5G40670 AT4G09570 AT1G67790 AT1G67792 AT1G65295	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na CALCIUM-DEPENDENT PROTEIN KINAS na na na	heptahelical trar 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unknr 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 Encodes a mem 4_6049428 unknown proteir 1_25417594 Potential natura 1_25417594 unknown proteir 1_24253036	7.09 7.09 7.09 7.09 7.09 7.08 7.08 7.08 7.08	promoter proximal promoter intergenic promoter five_prime_UTR promoter exon promoter intergenic
AT1G68490 AT5G40660 AT5G40670 AT4G09570 AT1G67790 AT1G67792 AT1G65295 AT1G29340	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na cALCIUM-DEPENDENT PROTEIN KINAS na na na na PLANT U-BOX 17 (PUB17)	heptahelical trar 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unkn 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 PQ-loop repeat 5_16285770 Encodes a merr 4_6049428 unknown proteir 1_25417594 Potential natura 1_25417594 unknown proteir 1_24253036 Encodes a proteir 1_124264026	7.09 7.09 7.09 7.09 7.09 7.08 7.08 7.08 7.08 7.08	promoter proximal promoter intergenic promoter five_prime_UTR promoter exon promoter intergenic promoter
AT1G68490 AT5G40660 AT5G40670 AT4G09570 AT1G67790 AT1G67792 AT1G65295 AT1G29340 AT5G13700	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na CALCIUM-DEPENDENT PROTEIN KINAS na na na PLANT U-BOX 17 (PUB17) POLYAMINE OXIDASE 1 (PAO1)	heptahelical trai 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unknc 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 PC-loop repeat 5_16285770 Encodes a merr 4_6049428 unknown proteir 1_25417594 Potential natura 1_25417594 unknown proteir 1_24253036 Encodes a prote 1_10264026 Encodes a prote 5_4423818	7.09 7.09 7.09 7.09 7.09 7.08 7.08 7.08 7.08 7.08 7.08	promoter proximal promoter intergenic promoter five_prime_UTR promoter exon promoter intergenic promoter proximal promoter proximal promoter
AT1G68490 AT5G40660 AT5G40670 AT4G09570 AT1G67790 AT1G67792 AT1G65295 AT1G29340 AT5G13700 AT5G13710	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na CALCIUM-DEPENDENT PROTEIN KINAS na na na PLANT U-BOX 17 (PUB17) POLYAMINE OXIDASE 1 (PA01) STEROL METHYLTRANSFERASE 1 (SM	heptahelical trar 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unknc 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 Encodes a mem 4_6049428 unknown proteir 1_25417594 vnknown proteir 1_24253036 Encodes a prot 1_10264026 Encodes a prot 5_4423818 SMT1 controls t 5_4423818	7.09 7.09 7.09 7.09 7.09 7.08 7.08 7.08 7.08 7.08 7.08 7.08	promoter proximal promoter intergenic promoter five_prime_UTR promoter exon promoter intergenic promoter proximal promoter three_prime_UTR
AT1G68490 AT5G40660 AT5G40670 AT4G09570 AT1G67790 AT1G67792 AT1G65295 AT1G29340 AT5G137700 AT5G137710 AT4G04955	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na cALCIUM-DEPENDENT PROTEIN KINAS na na pLANT U-BOX 17 (PUB17) POLYAMINE OXIDASE 1 (PAO1) STEROL METHYLTRANSFERASE 1 (SM' ALLANTOINASE (ALN)	heptahelical trar 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unkn 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 PQ-loop repeat 5_16285770 Encodes a merr 4_6049428 unknown proteir 1_25417594 Potential natura 1_25417594 unknown proteir 1_24253036 Encodes a prot 1_10264026 Encodes a prot 5_4423818 SMT1 controls t 5_4423818 Encodes an alla 4_2525460	7.09 7.09 7.09 7.09 7.09 7.08 7.08 7.08 7.08 7.08 7.08 7.08	promoter proximal promoter intergenic promoter five_prime_UTR promoter exon promoter intergenic promoter proximal promoter proximal promoter three_prime_UTR promoter
AT1G68490 AT5G40660 AT5G40670 AT4G09570 AT1G67790 AT1G65295 AT1G65295 AT1G29340 AT5G13700 AT5G13710 AT4G04955 AT3G05800	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na CALCIUM-DEPENDENT PROTEIN KINAS na na na PLANT U-BOX 17 (PUB17) POLYAMINE OXIDASE 1 (PAO1) STEROL METHYLTRANSFERASE 1 (SM' ALLANTOINASE (ALN) ATBS1 (ACTIVATION-TAGGED BRI1 SUP	heptahelical trai 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unknc 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 PC-loop repeat 5_16285770 Encodes a merr 4_6049428 unknown proteir 1_25417594 Potential natura 1_25417594 unknown proteir 1_24253036 Encodes a prote 1_10264026 Encodes a prote 5_4423818 SMT1 controls t 5_4423818 SMT1 controls t 5_4423818 Encodes an alla 4_2525460 AlBS1(activatio 3_1729866	7.09 7.09 7.09 7.09 7.09 7.08 7.08 7.08 7.08 7.08 7.08 7.08 7.07	promoter proximal promoter intergenic promoter five_prime_UTR promoter exon promoter intergenic promoter proximal promoter three_prime_UTR promoter intergenic promoter intergenic
AT1G68490 AT5G40660 AT5G40670 AT4G09570 AT1G67790 AT1G67792 AT1G65295 AT1G29340 AT5G137700 AT5G137710 AT4G04955	HEPTAHELICAL PROTEIN 4 (HHP4) N-ACETYL-L-GLUTAMATE SYNTHASE 2 na na na na cALCIUM-DEPENDENT PROTEIN KINAS na na pLANT U-BOX 17 (PUB17) POLYAMINE OXIDASE 1 (PAO1) STEROL METHYLTRANSFERASE 1 (SM' ALLANTOINASE (ALN)	heptahelical trar 4_17699259 N-acetyl-I-glutar 4_17699259 Protein of unkn 3_22817871 unknown proteir 1_25690158 ATP12 protein-r 5_16285770 PQ-loop repeat 5_16285770 Encodes a merr 4_6049428 unknown proteir 1_25417594 Potential natura 1_25417594 unknown proteir 1_24253036 Encodes a prot 1_10264026 Encodes a prot 5_4423818 SMT1 controls t 5_4423818 Encodes an alla 4_2525460	7.09 7.09 7.09 7.09 7.09 7.08 7.08 7.08 7.08 7.08 7.08 7.08	promoter proximal promoter intergenic promoter five_prime_UTR promoter exon promoter intergenic promoter proximal promoter proximal promoter three_prime_UTR promoter

AT1G62870	na	unknown proteir 1_23286936	7.07	promoter
AT1G15290	na	Tetratricopeptid 1_5265149	7.07	promoter
AT3G12835	na	unknown proteir 3_4084077	7.07	proximal promoter
AT3G05810	na	FUNCTIONS IN 3_1729866	7.07	intergenic
AT3G22840	EARLY LIGHT-INDUCABLE PROTEIN (EL		7.06	proximal promoter
AT2G46662	na	unknown proteir 2_19158245	7.06	promoter
AT3G44380 AT3G24480	na na	Late embryoger 3_16037002 Leucine-rich rer 3 8902722	7.06 7.06	promoter promoter
AT3G57040	RESPONSE REGULATOR 9 (ARR9)	response regula 3_21108849	7.06	proximal promoter
AT1G07140	(SIRANBP)	Encodes a puta 1_2196844	7.05	intergenic
AT1G07150	MITOGEN-ACTIVATED PROTEIN KINASI		7.05	proximal promoter
AT1G78895	na	Reticulon family 1_29660081	7.05	promoter
AT2G32760	na	unknown proteir 2_13891709	7.05	promoter
AT2G18721	na	unknown proteir 2_8117919	7.05	intergenic
AT1G66345	na	Pentatricopeptic 1_24740484	7.05	intergenic
AT2G12462	na	BEST Arabidop: 2_5052961	7.05	proximal promoter
AT3G60318	na	This gene encor 3_22291550	7.05	promoter
AT3G60320	na	Protein of unknc 3_22291550	7.05	intergenic
AT5G24210	na	alpha/beta-Hydr 5_8220631	7.05	intergenic
AT5G20740	na	Plant invertase/ 5_7026655	7.05	promoter
AT5G43310 AT2G23000	na SERINE CARBOXYPEPTIDASE-LIKE 10 (COP1-interactir 5_17385620	7.05 7.05	promoter
AT2G23000 AT2G22990	SINAPOYLGLUCOSE 1 (SNG1)	sinapoylglucose 2_9790498	7.05	proximal promoter intergenic
AT1G76500	SUPPRESSOR OF PHYB-4#3 (SOB3)	Encodes an AT 1_28701717	7.05	intergenic
AT1G78900	VACUOLAR ATP SYNTHASE SUBUNIT A		7.05	promoter
AT1G74950	(TIFY10B)	TIFY10B; CON7 1_28147830	7.04	intergenic
AT4G34610	BEL1-LIKÉ HOMEODOMAIN 6 (BLH6)	BEL1-like home 4_16534192	7.04	proximal promoter
AT1G74940	na	Protein of unknc 1_28147830	7.04	intergenic
AT3G52990	na	Pyruvate kinase 3_19647725	7.04	proximal promoter
AT4G34620	SMALL SUBUNIT RIBOSOMAL PROTEIN		7.04	intergenic
AT1G62380	ACC OXIDASE 2 (ACO2)	Encodes a prot 1_23082135	7.03	promoter
AT1G19870	IQ-DOMAIN 32 (iqd32)	IQ-domain 32 (ii 1_6898761	7.03	promoter
AT4G38620	MYB DOMAIN PROTEIN 4 (MYB4)	Encodes a R2R 4_18053588	7.03	five_prime_UTR
AT1G66880	na	Protein kinase s 1_24952384	7.03	intron
AT1G66890	na (ADA40)	FUNCTIONS IN 1_24952384	7.03	intergenic
AT5G67360	(ARA12) (ATSIK)	Encodes a subt 5_26876665	7.02 7.02	proximal promoter
AT3G08760 AT1G79370	CYTOCHROME P450, FAMILY 79, SUBFA	Encodes an osr 3_2660912	7.02	promoter intergenic
AT4G04850	K+ EFFLUX ANTIPORTER 3 (KEA3)	member of Puta 4 2452642	7.02	promoter
AT1G21835	na	Encodes a Plan 1_7664170	7.02	proximal promoter
AT2G26720	na	Cupredoxin sup 2 11382686	7.02	proximal promoter
AT5G67370	na	Protein of unknc 5_26876665	7.02	intergenic
AT1G77500	na	Protein of unknc 1_29121298	7.02	promoter
AT5G14210	na	Leucine-rich rer 5_4581745	7.02	promoter
AT2G26710	PHYB ACTIVATION TAGGED SUPPRESS	Encodes a merr 2_11382686	7.02	exon
AT1G79380	RING DOMAIN LIGASE 4 (RGLG4)	Encodes a ubiq 1_29860644	7.02	five_prime_UTR
AT1G20850	XYLEM CYSTEINE PEPTIDASE 2 (XCP2)		7.02	proximal promoter
AT3G14010	CTC-INTERACTING DOMAIN 4 (CID4)	hydroxyproline-ı 3_4641864	7.01	intergenic
AT5G02230	na	Haloacid dehalc 5_448794	7.01	intron
AT1G28050	na	B-box type zinc 1_9777983	7.01	promoter
AT1G28060	na	Pre-mRNA-splic 1_9777983	7.01	proximal promoter
AT1G52000 AT2G26975	na na	Mannose-bindin 1_19336085 Ctr copper trans 2_11512889	7.01 7.01	five_prime_UTR five_prime_UTR
AT1G70550	na	Protein of Unkn 1_26596456	7.01	proximal promoter
AT4G14746	na	CONTAINS Inte 4 8465278	7.01	proximal promoter
AT3G14020	NUCLEAR FACTOR Y, SUBUNIT A6 (NF-		7.01	promoter
AT1G31580	(ECS1)	Encodes cell wa 1_11311859	7	three_prime_UTR
AT2G34185	na	unknown proteir 2_14436024	7	intron
AT2G34186	na	unknown proteir 2_14436024	7	promoter
AT3G04470	na	Ankyrin repeat f 3_1192548	7	five_prime_UTR
AT3G13690	na	Protein kinase r 3_4490391	7	downstream
AT3G13700	na	RNA-binding (R 3_4490391	7	intergenic
AT3G13710	PRENYLATED RAB ACCEPTOR 1.F4 (PF		7	intergenic
AT5G19140	(AILP1) ETHYLENE RESPONSE DNA BINDING F	AILP1; FUNCTI 5_6423153	6.99	promoter
AT3G25730 AT3G63170	FATTY-ACID-BINDING PROTEIN 1 (FAP1		6.99 6.99	promoter five_prime_UTR
AT4G20140	GASSHO1 (GSO1)	Encodes GASS 4_10883924	6.99	promoter
AT4G00630	K+ EFFLUX ANTIPORTER 2 (KEA2)	Encodes a K(+), 4_268217	6.99	promoter
AT3G25740	METHIONINE AMINOPEPTIDASE 1C (MA		6.99	proximal promoter
AT1G76878	na	Potential natura 1_28868548	6.99	proximal promoter
AT1G76880	na	Duplicated hom 1_28868548	6.99	intergenic
AT2G45460	na	SMAD/FHA don 2_18741949	6.99	promoter
AT5G19150	na	pfkB-like carbor 5_6423153	6.99	downstream
AT2G28250	(NCRK)	NCRK; CONTA 2_12042367	6.98	proximal promoter
AT3G24840	na	Sec14p-like phc 3_9066395	6.98	promoter
AT4G24200	na	Transcription el 4_12561036	6.98	promoter
AT4G32620	na	Enhancer of pol 4_15731221	6.98	promoter
AT2G05540	na na	Glycine-rich pro 2_2033053 Bifunctional inhi 2_18626057	6.98	promoter
AT2G45180 AT4G32480	na na	Protein of unknr 4_15678023	6.98 6.98	promoter downstream
AT2G20180	PHYTOCHROME INTERACTING FACTOR		6.98	promoter
AT1G27730	SALT TOLERANCE ZINC FINGER (STZ)		6.98	promoter
AT5G52830	WRKY DNA-BINDING PROTEIN 27 (WRK		6.98	proximal promoter
AT1G48280	na	hydroxyproline-ı 1_17834881	6.97	promoter
AT2G46610	ARGININE/SERINE-RICH SPLICING FAC	Barta et al (201/2_19138917	6.96	promoter
AT4G23260	CYSTEINE-RICH RLK (RECEPTOR-LIKE		6.96	downstream
AT4G23250	EMBRYO DEFECTIVE 1290 (emb1290)	EMBRYO DEFE 4_12167132	6.96	promoter
AT1G21670	na	LOCATED IN: c 1_7612790	6.96	downstream
AT1G21680	na	DPP6 N-termina 1_7612790	6.96	promoter
AT2G46620	na ALITODHACY BELATED 12 (ATC12)	P-loop containir 2_19138917	6.96	three_prime_UTR
AT3G49590 AT4G00060	AUTOPHAGY-RELATED 13 (ATG13) MATERNAL EFFECT EMBRYO ARREST	Autophagy-relat 3_18377319	6.95 6.95	promoter promoter
AT4G00060 AT4G30240	na	Syntaxin/t-SNAI 4_14810048	6.95	promoter
AT2G01755	na	unknown proteir 2_332854	6.95	promoter
5050				F

AT5G13950	na	unknown proteir 5_4500762	6.95	promoter
AT2G01760	RESPONSE REGULATOR 14 (RR14)	member of Resi 2_332854	6.95	promoter
AT5G13960	SU(VAR)3-9 HOMOLOG 4 (SUVH4)	Encodes a histc 5_4500762	6.95	proximal promoter
AT1G09960	SUCROSE TRANSPORTER 4 (SUT4)	low affinity (10rr 1_3247960	6.95	intergenic
AT3G50530	CDPK-RELATED KINASE (CRK)	CDPK-related k 3_18752186	6.94	proximal promoter
AT1G19410	na	FBD / Leucine F 1_6714510	6.94	exon
AT1G19400	na	Erythronate-4-p 1_6714510	6.94	promoter
AT4G23740	na	Leucine-rich rer 4_12366344	6.94	promoter
AT5G60270 AT2G33700	na PROTEIN PHOSPHATASE 2C G GROUP	Concanavalin A 5_24257597	6.94 6.94	promoter
AT3G19100	na	Protein kinase s 3_6605518	6.93	promoter five_prime_UTR
AT3G62600	(ATERDJ3B)	J domain proteii 3_23153697	6.92	promoter
AT4G33650	DYNAMIN-RELATED PROTEIN 3A (DRP3		6.92	downstream
AT5G25220	KNOTTED1-LIKE HOMEOBOX GENE 3 (I		6.92	intergenic
AT4G33660	na	unknown proteir 4_16167145	6.92	downstream
AT5G59790	na	CONTAINS Inte 5_24092239	6.92	exon
AT5G59430	TELOMERIC REPEAT BINDING PROTEIN	Encodes a telor 5_23966335	6.92	proximal promoter
AT1G64080	MEMBRANE-ASSOCIATED KINASE REG		6.91	proximal promoter
AT4G19440	na	Tetratricopeptid 4_10604740	6.91	promoter
AT5G23530	CARBOXYESTERASE 18 (CXE18)	carboxyesterasi 5_7933048	6.9	three_prime_UTR
AT2G22668	MICRORNA405A (MIR405A)	Encodes a micr 2_9631665	6.9	intergenic
AT5G23520	na	smr (Small Mut\$ 5_7933048	6.9	proximal promoter
AT1G16920 AT1G58290	RAB GTPASE HOMOLOG A1B (RABA1b) (HEMA1)	Encodes a prote 1_21626347	6.9 6.89	promoter
AT3G10650	(NUP1)	Encodes a profit 1_21020347 Encodes a nucli 3_3331182	6.89	promoter promoter
AT4G24510	ECERIFERUM 2 (CER2)	Involved in C28 4_12660737	6.89	promoter
AT4G11355	na	pre-tRNA; tRNA 4_6905667	6.89	promoter
AT4G24500	na	hydroxyproline-ı 4_12660737	6.89	downstream
AT5G47500	PECTIN METHYLESTERASE 5 (PME5)	predicted to enc 5_19271530	6.89	exon
AT4G11360	RING-H2 FINGER A1B (RHA1B)	Encodes a puta 4_6905667	6.89	promoter
AT1G63670	TON1 RECRUITING MOTIF 12 (TRM12)	CONTAINS Inte 1_23613014	6.89	proximal promoter
AT1G64200	VACUOLAR H+-ATPASE SUBUNIT E ISC	vacuolar H+-AT 1_23830144	6.89	promoter
AT3G63440	CYTOKININ OXIDASE/DEHYDROGENAS		6.88	proximal promoter
AT1G04270	CYTOSOLIC RIBOSOMAL PROTEIN S15		6.88	proximal promoter
AT5G15210	HOMEOBOX PROTEIN 30 (HB30)	Encodes ZFHD: 5_4939123	6.88	promoter
AT1G71040	LOW PHOSPHATE ROOT2 (LPR2)	Encodes LPR2. 1_26801925	6.88	proximal promoter
AT3G63445	na	Potential natura 3_23422858	6.88	exon
AT1G04280	na	P-loop containir 1_1143905	6.88	intron
AT3G17770	na	Dihydroxyaceto 3_6086195	6.88	promoter proximal promoter
AT3G17780 AT2G02710	na PAS/LOV PROTEIN B (PLPB)	FUNCTIONS IN 3_6086195 Encodes a puta 2_761885	6.88 6.88	proximal promoter
AT5G67560	ADP-RIBOSYLATION FACTOR-LIKE A1D		6.87	promoter
AT1G55120	BETA-FRUCTOFURANOSIDASE 5 (FRUC		6.87	intron
AT1G31880	BREVIS RADIX (BRX)	Belongs to five- 1_11445304	6.87	promoter
AT1G70210	CYCLIN D1;1 (CYCD1;1)	Encodes a D-ty ₁ 1_26439586	6.87	promoter
AT3G10050	L-O-METHYLTHREONINE RESISTANT 1		6.87	intergenic
AT1G73630	na	EF hand calciur 1_27685957	6.87	intergenic
AT4G33080	na	AGC (cAMP-de 4_15959685	6.87	promoter
AT1G70209	na	unknown proteir 1_26439586	6.87	downstream
AT1G22885	na	unknown proteir 1_8102648	6.87	intergenic
AT1G22890	na	unknown proteir 1_8102648	6.87	promoter
AT1G22910	na	RNA-binding (R 1_8102648	6.87	proximal promoter
AT1G22882	na	Galactose-bindi 1_8102648	6.87	intergenic
AT3G10040 AT3G29577	na	sequence-speci 3_3098194 transposable eli 3_11386935	6.87 6.87	promoter
AT4G17720	na na	RNA-binding (R 4_9865100	6.87	proximal promoter promoter
AT5G23640	na	unknown proteir 5_7968300	6.87	exon
AT5G23630	PHOSPHATE DEFICIENCY RESPONSE		6.87	promoter
AT4G17730	SYNTAXIN OF PLANTS 23 (SYP23)	member of SYP 4_9865100	6.87	promoter
AT5G03630	(ATMDAR2)	ATMDAR2; FUN 5_925605	6.86	proximal promoter
AT4G23990	CELLULOSE SYNTHASE LIKE G3 (CSLG	encodes a prot∈ 4_12458168	6.86	exon
AT1G65930	CYTOSOLIC NADP+-DEPENDENT ISOC	Encodes a NAD 1_24538297	6.86	proximal promoter
AT2G31570	GLUTATHIONE PEROXIDASE 2 (GPX2)		6.86	promoter
AT1G44350	IAA-LEUCINE RESISTANT (ILR)-LIKE GE		6.86	intron
AT5G66440	na	unknown proteir 5_26531943	6.86	proximal promoter
AT1G29880 AT1G63420	na na	glycyl-tRNA syn 1_10462940 CONTAINS Inte 1_23516881	6.86 6.86	promoter
AT1G63420 AT5G60460	na na	Preprotein trans 5_24316176	6.86	exon intergenic
AT5G60460 AT5G64850	na na	FUNCTIONS IN 5_25922569	6.86	intron
AT4G21960	(PRXR1)	Encodes AT4g2 4_11646062	6.85	downstream
AT4G19020	CHROMOMETHYLASE 2 (CMT2)	chromomethyla: 4_10421469	6.85	intergenic
AT3G11590	na	unknown proteir 3_3658063	6.85	proximal promoter
AT1G31660	na	CONTAINS Inte 1_11333818	6.85	promoter
AT4G21950	na	unknown proteir 4_11646062	6.85	intergenic
AT4G19030	NOD26-LIKE MAJOR INTRINSIC PROTEI		6.85	downstream
AT1G71960	ATP-BINDING CASETTE G25 (ABCG25)		6.84	intron
AT2G27080	na	Late embryoger 2_11566280	6.84	intron
AT2G27090 AT1G77640	na	Protein of unknc 2_11566280 encodes a mem 1 29179724	6.84 6.84	intergenic downstream
AT1G77640 AT4G34800	na	SAUR-like auxir 4_16596493		
AT4G34800 AT3G13320	na CATION EXCHANGER 2 (CAX2)	low affinity calci 3_4319333	6.84 6.83	promoter intergenic
AT1G48000	MYB DOMAIN PROTEIN 112 (MYB112)	Encodes a puta 1_17702707	6.83	intergenic
AT3G50340	na	unknown proteir 3_18669898	6.83	intergenic
AT1G18210	na	Calcium-binding 1_6267797	6.83	intron
AT1G52290	PROLINE-RICH EXTENSIN-LIKE RECEP		6.83	three_prime_UTR
AT3G13330	PROTEASOME ACTIVATING PROTEIN 2		6.83	intergenic
AT1G18220	PURINE PERMEASE 9 (PUP9)	Member of a far 1_6267797	6.83	intergenic
AT1G18200		RAB GTPase h: 1 6267797	6.83	proximal promoter
	RAB GTPASE HOMOLOG A6B (RABA6b)			
AT1G52280	RAB GTPASE HOMOLOG G3D (RABG3d	RAB GTPase h: 1_19470129	6.83	proximal promoter
AT2G36570	RAB GTPASE HOMOLOG G3D (RABG3d na	RAB GTPase h: 1_19470129 Leucine-rich rer 2_15338543	6.82	intergenic
AT2G36570 AT2G36571	RAB GTPASE HOMOLOG G3D (RABG3d na na	RAB GTPase hi 1_19470129 Leucine-rich rer 2_15338543 unknown proteir 2_15338543	6.82 6.82	intergenic promoter
AT2G36570 AT2G36571 AT2G36580	RAB GTPASE HOMOLOG G3D (RABG3d na na na	RAB GTPase h: 1_19470129 Leucine-rich rer 2_15338543 unknown proteir 2_15338543 Pyruvate kinase 2_15338543	6.82 6.82 6.82	intergenic promoter proximal promoter
AT2G36570 AT2G36571	RAB GTPASE HOMOLOG G3D (RABG3d na na	RAB GTPase hi 1_19470129 Leucine-rich rer 2_15338543 unknown proteir 2_15338543	6.82 6.82	intergenic promoter

AT4044750	001.0 DANIOEDO (000)	F	0.00	
AT1G14750 AT5G16910	SOLO DANCERS (SDS) CELLULOSE-SYNTHASE LIKE D2 (CSLD	Encodes a meic 1_5082616	6.82 6.81	promoter proximal promoter
AT1G14440		homeobox prote 1_4938338	6.81	intergenic
AT5G63490		CBS / octicosar 5_25423371	6.81	proximal promoter
AT5G63500		Protein of unkno 5 25423371	6.81	promoter
AT1G01500		Erythronate-4-p 1_184988	6.81	promoter
AT4G18250		receptor serine/ 4_10090781	6.81	intron
AT5G51560		Leucine-rich reg 5_20946534	6.81	intron
AT4G24230	ACYL-COA-BINDING DOMAIN 3 (ACBP3)		6.8	promoter
AT5G40480		embryo defectiv 5_16213089	6.8	promoter
AT3G02050		potassium trans 3_350280	6.8 6.8	promoter
AT5G01240 AT4G04750		Encodes LAX1 5_100271 Major facilitator 4_2417214	6.8	exon proximal promoter
AT4G04730		This gene enco 4_12568937	6.8	exon
AT3G02040	SENESCENCE-RELATED GENE 3 (SRG:		6.8	promoter
AT4G24210		F-box protein th 4_12568937	6.8	intergenic
AT1G22360	UDP-GLUCOSYL TRANSFERASE 85A2 (6.8	promoter
AT1G22370	UDP-GLUCOSYL TRANSFERASE 85A5 (6.8	intergenic
AT4G24220		encodes a prog 4_12568937	6.8	intergenic
AT1G18710		Member of the I 1_6443767	6.79	intergenic
AT3G14360		alpha/beta-Hydr 3_4790551	6.79	proximal promoter
AT1G18700 AT1G56540		DNAJ heat shor 1_6443767 Disease resistar 1_21181538	6.79 6.78	intron
AT3G30778		This gene enco 3_12457264	6.78	promoter intergenic
AT4G04210	PLANT UBX DOMAIN CONTAINING PRO		6.78	promoter
AT5G60200		Encodes a Dof- 5_24240144	6.78	proximal promoter
AT4G30280	XYLOGLUCAN ENDOTRANSGLUCOSYL		6.78	proximal promoter
AT5G08790	(ATAF2)	induced by wou 5_2860407	6.77	promoter
AT4G25692	CONSERVED PEPTIDE UPSTREAM OPE	Upstream open 4_13091964	6.77	promoter
AT3G13510		Protein of Unkn 3_4402847	6.77	proximal promoter
AT5G08780		winged-helix DN 5_2860407	6.77	intergenic
AT4G25690		unknown proteir 4_13091964	6.77	promoter
AT1G09520		LOCATED IN: c 1_3072596	6.77	proximal promoter
AT1G30340 AT3G16850		transposable ell 1_10695765 Pectin lyase-like 3_5747484	6.77 6.77	proximal promoter proximal promoter
AT2G03120		homologous to 12 937318	6.76	promoter
AT3G07650		This gene belon 3 2441393	6.75	promoter
AT5G16050	GENERAL REGULATORY FACTOR 5 (GI		6.75	promoter
AT2G46370		Encodes a jasm 2_19031889	6.75	proximal promoter
AT5G07860		HXXXD-type ac 5_2513511	6.75	intergenic
AT5G07870	na	HXXXD-type ac 5_2513511	6.75	promoter
AT4G15240		Protein of unkno 4_8705554	6.75	promoter
AT5G64343	CONSERVED PEPTIDE UPSTREAM OPE		6.74	three_prime_UTR
AT5G64342 AT5G64341	CONSERVED PEPTIDE UPSTREAM OPE CONSERVED PEPTIDE UPSTREAM OPE		6.74 6.74	three_prime_UTR
AT1G32540		Encodes a prot 1 11767608	6.74	three_prime_UTR five_prime_UTR
AT1G32340 AT1G01100		60S acidic ribos 1_51388	6.74	promoter
AT2G12461		unknown proteir 2_5050797	6.74	proximal promoter
AT2G12462		BEST Arabidop: 2_5050797	6.74	exon
AT5G64330	NON-PHOTOTROPIC HYPOCOTYL 3 (NF		6.74	downstream
AT1G30500	NUCLEAR FACTOR Y, SUBUNIT A7 (NF-	nuclear factor Y 1_10806510	6.74	promoter
AT3G47640		Encodes POPE 3_17567110	6.74	promoter
AT1G01090	PYRUVATE DEHYDROGENASE E1 ALPI		6.74	proximal promoter
AT5G64340	SUPPRESSOR OF ACAULIS 51 (SAC51)		6.74	three_prime_UTR
AT5G55700		In vitro assay in 5_22551028	6.73	proximal promoter
AT5G62500 AT1G21050		encodes a hom 5_25091947 Protein of unkn 1_7366184	6.73 6.73	proximal promoter proximal promoter
AT1G21030 AT5G64735		pre-tRNA; tRNA 5_25876609	6.73	proximal promoter
AT2G38465		unknown proteir 2_16108143	6.73	proximal promoter
AT2G38480		Uncharacterisec 2_16108143	6.73	intergenic
AT1G30320		Remorin family 1_10685007	6.73	intergenic
AT3G52400		syntaxin protein 3_19427437	6.73	promoter
AT2G38470	WRKY DNA-BINDING PROTEIN 33 (WRK		6.73	promoter
AT4G11280	1-AMINOCYCLOPROPANE-1-CARBOXYI		6.72	proximal promoter
AT1G07180 AT2G47760	ALTERNATIVE NAD(P)H DEHYDROGEN ASPARAGINE-LINKED GLYCOSYLATION		6.72 6.72	promoter
AT3G01370		Encodes a prote 3_143615	6.72	promoter three_prime_UTR
AT3G51080	GATA TRANSCRIPTION FACTOR 6 (GAT		6.72	exon
AT1G14520	MYO-INOSITOL OXYGENASE 1 (MIOX1)		6.72	promoter
AT4G17440		Protein of unknc 4_9731671	6.72	intergenic
AT3G56060		Glucose-methar 3_20806523	6.72	proximal promoter
AT4G36925		unknown proteir 4_17405145	6.72	intergenic
AT3G56070		rotamase cyclor 3_20806523	6.72	downstream
AT1G14530	TOM THREE HOMOLOG 1 (THH1) TSPO(OUTER MEMBRANE TRYPTOPHA	TOM THREE H: 1_4970463	6.72	intergenic
AT2G47770 AT1G65620		required for forn 1 24397083	6.72 6.71	promoter proximal promoter
AT3G54810		Encodes a prote 3_20296179	6.71	promoter
AT5G10170	MYO-INOSITOL-1-PHOSPHATE SYNTHA		6.71	proximal promoter
AT3G15820			0.74	intron
AT5G61380	REDUCED OLEATE DESATURATION 1 (6.71	intron
	TIMING OF CAB EXPRESSION 1 (TOC1)	Pseudo respons 5_24674951	6.71	promoter
AT5G66730	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1)	Pseudo respons 5_24674951 C2H2-like zinc f 5_26641593	6.71 6.7	promoter downstream
AT5G66730 AT2G47440	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na	Pseudo respons 5_24674951 C2H2-like zinc f 5_26641593 Tetratricopeptid 2_19468136	6.71 6.7 6.7	promoter downstream proximal promoter
AT5G66730 AT2G47440 AT3G49810	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na	Pseudo respons 5_24674951 C2H2-like zinc f 5_26641593 Tetratricopeptid 2_19468136 ARM repeat sur 3_18478545	6.71 6.7 6.7 6.7	promoter downstream proximal promoter proximal promoter
AT5G66730 AT2G47440 AT3G49810 AT4G30060	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na na	Pseudo respons 5_24674951 C2H2-like zinc f 5_26641593 Tetratricopeptid 2_19468136 ARM repeat sur 3_18478545 Core-2/I-branch 4_14691804	6.71 6.7 6.7 6.7 6.7	promoter downstream proximal promoter proximal promoter intron
AT5G66730 AT2G47440 AT3G49810 AT4G30060 AT5G66720	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na na na	Pseudo respon: 5_24674951 C2H2-like zinc f 5_26641593 Tetratricopeptid 2_19468136 ARM repeat sur 3_18478545 Core-2/I-branch 4_14691804 Protein phosph: 5_26641593	6.71 6.7 6.7 6.7 6.7 6.7	promoter downstream proximal promoter proximal promoter intron proximal promoter
AT5G66730 AT2G47440 AT3G49810 AT4G30060	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na na na NGATHA3 (NGA3)	Pseudo respons 5, 24674951 C2H2-like zinc f 5, 26641593 Tetratricopeptid 2, 19468136 ARM repeat sur 3, 18478545 Core-27l-branch 4, 14691804 Protein phosphs 5, 26641593 NGATHA3 (NG, 1, 16732	6.71 6.7 6.7 6.7 6.7	promoter downstream proximal promoter proximal promoter intron proximal promoter intergenic
AT5G66730 AT2G47440 AT3G49810 AT4G30060 AT5G66720 AT1G01030	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na na na NGATHA3 (NGA3) HVA22-LIKE PROTEIN H (ATHVA22H) (H	Pseudo respons 5, 24674951 C2H2-like zinc f 5, 26641593 Tetratricopeptid 2, 19468136 ARM repeat sur 3, 18478545 Core-27l-branch 4, 14691804 Protein phosphs 5, 26641593 NGATHA3 (NG, 1, 16732	6.71 6.7 6.7 6.7 6.7 6.7 6.7	promoter downstream proximal promoter proximal promoter intron proximal promoter
AT5G66730 AT2G47440 AT3G49810 AT4G30060 AT5G66720 AT1G01030 AT1G19950 AT2G46685 AT1G20030	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na na na NGATHA3 (NGA3) HVA22-LIKE PROTEIN H (ATHVA22H) (H MICRORNA166A (MIR166A) na	Pseudo respons 5, 24674951 C2H2-like zinc f 5, 26641593 Tetratricopeptid 2, 19468136 ARM repeat sur 3, 18478545 Core-2/I-branch 4, 14691804 Protein phosphs 5, 26641593 NGATHA3 (NG, 1, 16732 HVA22-like prot 1, 6923998 Encodes a micr 2, 19175873 Pathogenesis-rt 1, 6946445	6.71 6.7 6.7 6.7 6.7 6.7 6.7 6.7 6.69 6.69 6	promoter downstream proximal promoter proximal promoter intron proximal promoter intergenic promoter
AT5G66730 AT2G47440 AT3G49810 AT4G30060 AT5G66720 AT1G01030 AT1G19950 AT2G46685 AT1G20030 AT1G70740	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na na na NGATHA3 (NGA3) HVA22-LIKE PROTEIN H (ATHVA22H) (H MICRORNA166A (MIR166A) na na	Pseudo respons 5 _24674951 CZH2-like zinc f _26641593 Tetratricopeptid 2 _19468136 ARM repeat sur 3 _18478545 Core-2/l-branch 4 _14691804 Protein phosphs 5 _26641593 NGATHA3 (NG. 1_16732 HVA22-like prot 1_6923998 Encodes a micn 2 _19175873 Pathogenesis-r 1_6946445 Protein kinase s 1_26678618	6.71 6.7 6.7 6.7 6.7 6.7 6.7 6.69 6.69 6.69	promoter downstream proximal promoter proximal promoter intron proximal promoter intergenic promoter promoter exon proximal promoter
AT5G66730 AT2G47440 AT3G49810 AT4G30060 AT5G66720 AT1G01030 AT1G19950 AT2G46685 AT1G20030 AT1G70740 AT3G05470	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na na na NGATHA3 (NGA3) HVA22-LIKE PROTEIN H (ATHVA22H) (H MICRORNA166A (MIR166A) na na na	Pseudo respons 5, 24674951 C2H2-like zinc f 5_26641593 Tetratricopeptid 2_19468136 ARM repeat sur 3, 18478545 Core-2/I-branch 4_14691804 Protein phosphs 5_26641593 NGATHA3 (NG, 1_16732 HVA22-like prot 1_6923998 Encodes a micr 2_19175873 Pathogenesis-rr 1_6946445 Protein kinase s 1_26678618 Actin-binding Ff 3_1583142	6.71 6.7 6.7 6.7 6.7 6.7 6.7 6.69 6.69 6.69	promoter downstream proximal promoter proximal promoter intron proximal promoter intergenic promoter promoter exon proximal promoter proximal promoter
AT5G66730 AT2G47440 AT3G49810 AT4G30060 AT5G66720 AT1G01030 AT1G19950 AT2G46685 AT1G20030 AT1G70740 AT3G05470 AT3G16560	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na na na NGATHA3 (NGA3) HVA22-LIKE PROTEIN H (ATHVA22H) (H MICRORNA166A (MIR166A) na na na na	Pseudo respons 5, 24674951 C2H2-like zinc f 5_26641593 Tetratricopeptid 2, 19468136 ARM repeat sur, 3_18478545 Core-27l-branch 4_14691804 Protein phosphs 5, 26641593 NGATHA3 (NG, 1_16732 HVA22-like prot 1_6923998 Encodes a micr 2_19175873 Pathogenesis-rt 1_6946445 Protein kinase s 1_26678618 Actin-binding Ft 3_1583142 Protein phosphs 3_5637974	6.71 6.7 6.7 6.7 6.7 6.7 6.7 6.69 6.69 6.69	promoter downstream proximal promoter proximal promoter intron proximal promoter intergenic promoter promoter exon proximal promoter proximal promoter intron
AT5G66730 AT2G47440 AT3G49810 AT4G30060 AT5G66720 AT1G01030 AT1G19950 AT2G46685 AT1G20030 AT1G70740 AT3G05470	TIMING OF CAB EXPRESSION 1 (TOC1) INDETERMINATE DOMAIN 1 (IDD1) na na na na NGATHA3 (NGA3) HVA22-LIKE PROTEIN H (ATHVA22H) (H MICRORNA166A (MIR166A) na na na na POLY(A) BINDING PROTEIN 6 (PAB6)	Pseudo respons 5, 24674951 C2H2-like zinc f 5_26641593 Tetratricopeptid 2_19468136 ARM repeat sur 3, 18478545 Core-2/I-branch 4_14691804 Protein phosphs 5_26641593 NGATHA3 (NG, 1_16732 HVA22-like prot 1_6923998 Encodes a micr 2_19175873 Pathogenesis-rr 1_6946445 Protein kinase s 1_26678618 Actin-binding Ff 3_1583142	6.71 6.7 6.7 6.7 6.7 6.7 6.7 6.69 6.69 6.69	promoter downstream proximal promoter proximal promoter intron proximal promoter intergenic promoter promoter exon proximal promoter proximal promoter

AT2C611E0	HOMEODOMAIN GLABROUS 1 (HDG1)	Encodes a ham 2, 22620521	6.68	promotor
AT3G61150 AT5G25240	na	unknown proteir 5_8747337	6.68	promoter promoter
AT4G01330	na	Protein kinase s 4_553212	6.68	downstream
AT4G01335	na	FUNCTIONS IN 4_553212	6.68	promoter
AT1G78140	na	S-adenosyl-L-m 1_29403984	6.68	promoter
AT1G78150	na	unknown proteir 1_29403984	6.68	proximal promoter
AT1G23860	RS-CONTAINING ZINC FINGER PROTEIL		6.68	proximal promoter
AT5G38420	RUBISCO SMALL SUBUNIT 2B (RBCS2B		6.68	promoter
AT1G20980	SQUAMOSA PROMOTER BINDING PRO		6.68	proximal promoter
AT1G23870 AT5G26210	TREHALOSE-PHOSPHATASE/SYNTHAS ALFIN-LIKE 4 (AL4)	Encodes a merr 5_9160339	6.68 6.67	proximal promoter five_prime_UTR
AT5G10240	ASPARAGINE SYNTHETASE 3 (ASN3)	Encodes aspara 5_3216642	6.67	promoter
AT2G41010	CALMODULIN (CAM)-BINDING PROTEIN		6.67	promoter
AT4G18700	CBL-INTERACTING PROTEIN KINASE 12		6.67	proximal promoter
AT3G29030	EXPANSIN A5 (EXPA5)	Encodes an ext 3_11012079	6.67	intron
AT3G18170	na	Glycosyltransfel 3_6228535	6.67	exon
AT1G05870	na	Protein of unknr 1_1773856	6.67	proximal promoter
AT2G41000 AT2G01570	na REPRESSOR OF GA1-3 1 (RGA1)	Chaperone Dna 2_17115235 Member of the \ 2_261952	6.67 6.67	intergenic intergenic
AT4G24740	FUS3-COMPLEMENTING GENE 2 (FC2)		6.66	promoter
AT2G28340	GATA TRANSCRIPTION FACTOR 13 (GA		6.66	intergenic
AT5G06700	na	Encodes a merr 5_2066363	6.66	intergenic
AT5G62710	na	Leucine-rich rer 5_25187028	6.66	promoter
AT1G29465	na	unknown proteir 1_10308382	6.66	promoter
AT3G05500	na	Rubber elongati 3_1590668	6.66	proximal promoter
AT3G05510 AT1G30110	na NUDIX HYDROLASE HOMOLOG 25 (NUI	Phospholipid/gl\ 3_1590668	6.66 6.66	intergenic promoter
AT3G47290	PHOSPHATIDYLINOSITOL-SPECIWC PH		6.66	promoter
AT3G05490	RALF-LIKE 22 (RALFL22)	Member of a div 3_1590668	6.66	proximal promoter
AT5G62700	TUBULIN BETA CHAIN 3 (TUB3)	encodes tubulin 5_25187028	6.66	intergenic
AT5G25460	DUF642 L-GALL RESPONSIVE GENE 2	Protein of unknc 5_8861365	6.65	proximal promoter
AT5G57010	na	calmodulin-bind 5_23067631	6.65	promoter
AT5G65700	BARELY ANY MERISTEM 1 (BAM1)	Encodes a CLA 5_26280319	6.64	proximal promoter
AT1G75750	GAST1 PROTEIN HOMOLOG 1 (GASA1)		6.64	intergenic
AT2G38540 AT2G22805	LIPID TRANSFER PROTEIN 1 (LP1)	Non-specific lipi 2_16130283 Encodes a defe 2_9710595	6.64 6.64	promoter proximal promoter
AT2G30760	na	unknown proteir 2_13106919	6.64	intron
AT2G30766	na	unknown proteir 2_13106919	6.64	proximal promoter
AT3G55140	na	Pectin lyase-like 3_20438656	6.64	promoter
AT5G19970	na	unknown proteir 5_6748733	6.64	downstream
AT1G75730	na	unknown proteir 1_28439833	6.64	promoter
AT1G75740	na	pre-tRNA; tRNA 1_28439833	6.64	proximal promoter
AT4G29905 AT5G45960	na na	unknown proteir 4_14626308 GDSL-like Lipas 5_18638953	6.64 6.64	intergenic exon
AT2G30260	U2 SMALL NUCLEAR RIBONUCLEOPRC		6.64	downstream
AT2G30250	WRKY DNA-BINDING PROTEIN 25 (WRK		6.64	promoter
AT2G35700	ERF FAMILY PROTEIN 38 (ERF38)	encodes a mem 2_15006536	6.63	intergenic
AT3G17390	METHIONINE OVER-ACCUMULATOR 3 (6.63	promoter
AT1G35430	na	unknown proteir 1_13030019	6.63	intergenic
AT3G17410	na	Protein kinase s 3_5954492	6.63	proximal promoter
AT5G54855 AT5G55620	na na	Pollen Ole e 1 a 5_22284490 unknown proteir 5_22529886	6.63 6.63	downstream promoter
AT5G54860	na	Major facilitator 5_22284490	6.63	promoter
AT5G64550	na	loricrin-related; 5_25805120	6.63	promoter
AT1G13260	RELATED TO ABI3/VP1 1 (RAV1)	Encodes an AP: 1_4538785	6.63	intergenic
AT2G30490	CINNAMATE-4-HYDROXYLASE (C4H)	Encodes a cinn; 2_12995843	6.62	promoter
AT3G62610	MYB DOMAIN PROTEIN 11 (MYB11)	Member of the F3_23155533	6.62	intron
AT5G16120	na	alpha/beta-Hydr 5_5265475	6.62	promoter
AT4G18890	BES1/BZR1 HOMOLOG 3 (BEH3)	BES1/BZR1 hor 4_10355774 beta-galactosid: 5 23003362	6.61	downstream
AT5G56870 AT5G22910	BETA-GALACTOSIDASE 4 (BGAL4) CATION/H+ EXCHANGER 9 (CHX9)	member of Puta 5_7664378	6.61 6.61	proximal promoter proximal promoter
AT5G21482	CYTOKININ OXIDASE 7 (CKX7)	This gene used 5_7229142	6.61	intron
AT4G18550	DAD1-LIKE SEEDING ESTABLISHMENT-		6.61	proximal promoter
AT4G09000	GENERAL REGULATORY FACTOR 1 (GI	Encodes a 14-3 4_5775117	6.61	promoter
AT1G17500	na	ATPase E1-E2 1_6017229	6.61	proximal promoter
AT3G63240	na	DNAse I-like su 3_23367541	6.61	five_prime_UTR
AT4G03100 AT4G18900	na na	Rho GTPase at 4_1374054 Transducin/WD 4_10355774	6.61 6.61	promoter proximal promoter
AT5G07780	na	Actin-binding Ft 5_2483048	6.61	downstream
AT5G07790	na	unknown proteir 5_2483048	6.61	promoter
AT2G03440	NODULIN-RELATED PROTEIN 1 (NRP1)	Induced at the ti 2_1040585	6.61	promoter
AT5G39860	PACLOBUTRAZOL RESISTANCE1 (PRE		6.61	proximal promoter
AT4G15800	RALF-LIKE 33 (RALFL33)	Member of a div 4_8986033	6.61	intergenic
AT1G28340	RECEPTOR LIKE PROTEIN 4 (RLP4)	receptor like prc 1_9938922	6.61	proximal promoter
AT3G05870 AT4G16780	ANAPHASE-PROMOTING COMPLEX/CY HOMEOBOX PROTEIN 2 (HB-2)	Encodes a hom 4_9450007	6.6 6.6	intron intron
AT1G29660	na	GDSL-like Lipas 1_10365171	6.6	intergenic
AT1G19373	na	snoRNA; snoRN 1_6697979	6.6	intergenic
AT1G19380	na	Protein of unknot 1_6697979	6.6	promoter
AT3G05880	RARE-COLD-INDUCIBLE 2A (RCI2A)	Induced by low 3_1755496	6.6	intron
AT1G76080	CUI ODODI ACTIC DDOLLOUT INDLICED	Encodes a thior 1 28547791	6.59	three_prime_UTR
AT1G44790	CHLOROPLASTIC DROUGHT-INDUCED			
ATECOCCO15	na	ChaC-like family 1_16913654	6.59	five_prime_UTR
AT1G76070	na na	ChaC-like famil, 1_16913654 pre-tRNA; tRNA 5_25972830	6.59	downstream
AT1G76070	na na na	ChaC-like family 1_16913654 pre-tRNA; tRNA 5_25972830 unknown proteir 1_28547791	6.59 6.59	downstream downstream
	na na	ChaC-like famil, 1_16913654 pre-tRNA; tRNA 5_25972830	6.59	downstream downstream promoter
AT1G76070 AT4G33666	na na na na	ChaC-like family 1_16913654 pre-tRNA; tRNA 5_25972830 unknown proteir 1_28547791 unknown proteir 4_16168912	6.59 6.59 6.59	downstream downstream
AT1G76070 AT4G33666 AT5G35805 AT5G57790 AT5G23460	na na na na na na na	ChaC-like famil) 1_16913654 pre-tRNA; tRNA 5_25972830 unknown proteir 1_28547791 unknown proteir 4_16168912 transposable elt 5_13988709 unknown proteir 5_23411641 unknown proteir 5_7913417	6.59 6.59 6.59 6.59 6.58 6.58	downstream downstream promoter intergenic intergenic three_prime_UTR
AT1G76070 AT4G33666 AT5G35805 AT5G57790 AT5G23460 AT5G23470	na na na na na na na	ChaC-like family 1_16913654 pre-tRNA; tRNA 5_25972830 unknown proteir 1_28547791 unknown proteir 4_16168912 transposable els 5_13988709 unknown proteir 5_23411641 unknown proteir 5_7913417 Haloacid dehalc 5_7913417	6.59 6.59 6.59 6.59 6.58 6.58 6.58	downstream downstream promoter intergenic intergenic three_prime_UTR promoter
AT1G76070 AT4G33666 AT5G35805 AT5G57790 AT5G23460 AT5G23470 AT4G16880	na na na na na na na na	ChaC-like famil) 1_16913654 pre-IRNA; IRNA 5_25972830 unknown proteir 1_28547791 unknown proteir 1_18547791 unknown proteir 4_16168912 transposable els 5_13988709 unknown proteir 5_23411641 unknown proteir 5_7913417 Haloacid dehalc 5_7913417 Leucine-rich reg 4_9496377	6.59 6.59 6.59 6.59 6.58 6.58 6.58 6.58	downstream downstream promoter intergenic intergenic three_prime_UTR promoter three_prime_UTR
AT1G76070 AT4G33666 AT5G35805 AT5G57790 AT5G23460 AT5G23470 AT4G16880 AT5G22390	na n	ChaC-like famil) 1_16913654 pre-tRNA; tRNA 5_25972830 unknown proteir 1_28547791 unknown proteir 4_16168912 transposable elt 5_13988709 unknown proteir 5_23411641 unknown proteir 5_7913417 Haloacid dehalc 5_7913417 Protein of unknc 5_7419083	6.59 6.59 6.59 6.59 6.58 6.58 6.58 6.58 6.58	downstream downstream promoter intergenic intergenic three_prime_UTR promoter three_prime_UTR five_prime_UTR
AT1G76070 AT4G33666 AT5G35805 AT5G57790 AT5G23460 AT5G23470 AT4G16880 AT5G22390 AT1G19835	na na na na na na na na	ChaC-like family 1_16913654 pre-tRNA; tRNA 5_25972830 unknown proteir 1_28547791 unknown proteir 4_16168912 transposable elt 5_13988709 unknown proteir 5_23411641 unknown proteir 5_7913417 Haloacid dehalc 5_7913417 Leucine-rich rer 4_9496377 Protein of unknc 5_7419083 Plant protein of 1_6863115	6.59 6.59 6.59 6.59 6.58 6.58 6.58 6.58 6.58 6.58	downstream downstream promoter intergenic intergenic three_prime_UTR promoter three_prime_UTR five_prime_UTR proximal promoter
AT1G76070 AT4G33666 AT5G35805 AT5G57790 AT5G23460 AT5G23470 AT4G16880 AT5G22390	na n	ChaC-like famil) 1_16913654 pre-tRNA; tRNA 5_25972830 unknown proteir 1_28547791 unknown proteir 4_16168912 transposable elt 5_13988709 unknown proteir 5_23411641 unknown proteir 5_7913417 Haloacid dehalc 5_7913417 Protein of unknc 5_7419083	6.59 6.59 6.59 6.59 6.58 6.58 6.58 6.58 6.58	downstream downstream promoter intergenic intergenic three_prime_UTR promoter three_prime_UTR five_prime_UTR

AT5G57010	na	calmodulin-bind 5_23066893	6.58	proximal promoter
AT5G02480	na	HSP20-like cha 5_547510	6.58	promoter
AT3G14440	NINE-CIS-EPOXYCAROTENOID DIOXYG		6.58	intergenic
AT3G26690	NUDIX HYDROLASE HOMOLOG 13 (NUI		6.58	proximal promoter
AT1G12710	PHLOEM PROTEIN 2-A12 (PP2-A12)	This gene is pre 1_4329441	6.58	proximal promoter
AT4G16860	RECOGNITION OF PERONOSPORA PAR		6.58	proximal promoter
AT3G12690	AGC KINASE 1.5 (AGC1.5)	Encodes a puta 3_4034460	6.57	proximal promoter
AT3G62420	BASIC REGION/LEUCINE ZIPPER MOTIF		6.57	promoter
AT5G62390	BCL-2-ASSOCIATED ATHANOGENE 7 (E		6.57	five_prime_UTR
AT3G62422	CONSERVED PEPTIDE UPSTREAM OPE		6.57	promoter
AT3G62410	CP12 DOMAIN-CONTAINING PROTEIN 2		6.57	intergenic
AT1G76490	HYDROXY METHYLGLUTARYL COA REI		6.57	three_prime_UTR
AT5G62400	na	unknown proteir 5_25054277	6.57	intergenic
AT1G27210	na	ARM repeat sur 1_9455074	6.57	intergenic
AT3G62400	na	unknown proteir 3_23093039	6.57	intergenic
AT4G29310	na	Protein of unknc 4_14440479	6.57	proximal promoter
AT4G38520	na	Protein phosph; 4_18018441	6.57	promoter
AT3G22380	TIME FOR COFFEE (TIC)	Encodes a nucli 3_7912589	6.57	promoter
AT1G75360 AT4G25280	na	unknown proteir 1_28274265 P-loop containir 4_12941084	6.56 6.55	promoter
AT4G25280 AT4G25290	na na	DNA photolyase 4_12941084	6.55	promoter downstream
AT2G44940	• • • • • • • • • • • • • • • • • • • •	encodes a mem 2 18537029	6.55	
AT5G37270	na na	RING/U-box su ₁ 5_14755702	6.55	promoter
AT5G37270	(AKINBETA1)	Encodes AKINb 5 7205565	6.54	intergenic five_prime_UTR
AT1G01120	3-KETOACYL-COA SYNTHASE 1 (KCS1)		6.54	
AT1G01120 AT2G40475			6.54	downstream downstream
AT2G33470	ALTERED SEED GERMINATION 8 (ASGE GLYCOLIPID TRANSFER PROTEIN 1 (GI		6.54	
AT2G33470 AT2G18350	HOMEOBOX PROTEIN 24 (HB24)		6.54	proximal promoter
AT1G02590	na	homeobox prote 2_7972386 Aldehyde oxida: 1 552832	6.54	promoter
		pre-tRNA; tRNA 1 552832	6.54	promoter
AT1G02600 AT2G25250	na	unknown proteir 2 10753853		downstream
	na		6.54	five_prime_UTR
AT2G25255 AT1G01115	na	Encodes a defe 2_10753853	6.54	intergenic
	na	unknown proteir 1_57143	6.54	intergenic
AT1G02610	na	RING/FYVE/PH 1_552832	6.54	downstream
AT4G22730	na	Leucine-rich rer 4_11941026	6.54	promoter
AT5G09760	na	Plant invertase/ 5_3032198	6.54	promoter
AT2G33480	NAC DOMAIN CONTAINING PROTEIN 41		6.54	proximal promoter
AT4G16370	OLIGOPEPTIDE TRANSPORTER (OPT3)		6.54	promoter
AT4G18197	PURINE PERMEASE 7 (PUP7)	Member of a far 4_10071573	6.54	promoter
AT5G08130	(BIM1)	Arabidopsis thal 5_2611653	6.53	proximal promoter
AT5G11950	LONELY GUY 8 (LOG8)	Encodes a prote 5_3857198	6.53	downstream
AT3G17800	na	mRNA level of t 3_6093679	6.53	proximal promoter
AT4G21910	na	MATE efflux fan 4_11633015	6.53	proximal promoter
AT3G17790	PURPLE ACID PHOSPHATASE 17 (PAP1		6.53	intergenic
AT3G17810	PYRIMIDINE 1 (PYD1)	Encodes a prote 3_6093679	6.53	promoter
AT1G05810	RAB GTPASE HOMOLOG A5E (RABA5E)		6.53	exon
AT3G17840	RECEPTOR-LIKE KINASE 902 (RLK902)		6.53	proximal promoter
AT2G01470	SEC12P-LIKE 2 PROTEIN (STL2P)	Sec12p-like pro 2_214631	6.53	promoter
AT5G45340	CYTOCHROME P450, FAMILY 707, SUBF		6.52	promoter
AT4G00310	EMBRYO SAC DEVELOPMENT ARREST		6.52	proximal promoter
AT4G01220	MALE GAMETOPHYTE DEFECTIVE 4 (M		6.52	downstream
AT1G10590	na	Nucleic acid-bin 1_3503517	6.52	promoter
AT5G48385	na	FRIGIDA-like pr 5_19608440	6.52	promoter
AT4G17100	na	EXPRESSED IN 4_9612656	6.52	intron
AT1G22190	na	The gene encor 1_7834272	6.52	proximal promoter
AT4G01210 AT4G18810	na	glycosyl transfe 4_513087 NAD(P)-binding 4_10321691	6.52 6.52	promoter intergenic
	na			•
AT5G64410	OLIGOPEPTIDE TRANSPORTER 4 (OPT		6.52	intron
AT3G16500 AT4G18800	PHYTOCHROME-ASSOCIATED PROTEII RAB GTPASE HOMOLOG A1D (RABA1d)		6.52 6.52	intergenic
AT1G68560	ALPHA-XYLOSIDASE 1 (XYL1)	Encodes RabA 4_10321091 Encodes a bifur 1 25732394	6.51	promoter intergenic
AT1G00300	na	FUNCTIONS IN 1_2219027	6.51	intron
AT4G32272	na	Nucleotide/suga 4_15579922	6.51	promoter
AT5G07360	na	Amidase family 5_2326593	6.51	downstream
AT1G27210	na		6.51	
AT2G03565	na	ARM repeat sur 1_9456661 unknown proteir 2_1083247	6.51	exon intergenic
AT3G14440	NINE-CIS-EPOXYCAROTENOID DIOXYG		6.51	promoter
AT2G01150	RING-H2 FINGER PROTEIN 2B (RHA2B)		6.51	promoter
AT5G07350	TUDOR-SN PROTEIN 1 (TUDOR1)	RNA binding prc 5_2326593	6.51	proximal promoter
AT4G14890	FERREDOXIN C 1 (FdC1)	2Fe-2S ferredo 4_8520446	6.5	promoter
AT5G59220	HIGHLY ABA-INDUCED PP2C GENE 1 (F		6.5	exon
AT3G13000	na	Protein of unknc 3 4161313	6.5	intron
AT4G03292	na	Polynucleotidyl 4 1444537	6.5	downstream
AT5G45350	na	proline-rich fami 5_18378843	6.5	intergenic
AT4G14880	O-ACETYLSERINE (THIOL) LYASE (OAS		6.5	five_prime_UTR
AT3G63130	RAN GTPASE ACTIVATING PROTEIN 1 (6.5	promoter
AT1G18640	3-PHOSPHOSERINE PHOSPHATASE (P		6.49	promoter
AT2G42790	CITRATE SYNTHASE 3 (CSY3)	Encodes a pero 2_17806227	6.49	promoter
AT4G04970	GLUCAN SYNTHASE-LIKE 1 (GSL1)	encodes a gene 4_2536735	6.49	promoter
AT3G17040	HIGH CHLOROPHYLL FLUORESCENT 1		6.49	promoter
AT4G40060	HOMEOBOX PROTEIN 16 (HB16)	Encodes a hom 4_18573088	6.49	promoter
AT3G17050	na	transposable eli 3_5812823	6.49	proximal promoter
AT4G34975	na	pre-tRNA; tRNA 4_16656964	6.49	intergenic
AT1G27500	na	Tetratricopeptid 1_9554281	6.49	promoter
AT3G17580	na	unknown proteir 3_6016804	6.49	intergenic
AT4G40070	na	RING/U-box su ₁ 4_18573088	6.49	intergenic
AT5G57040	na	Lactoylglutathio 5_23086240	6.49	proximal promoter
AT1G12370	PHOTOLYASE 1 (PHR1)	encodes an ami 1_4211903	6.49	proximal promoter
AT1G18650			6.49	exon
	PLASMODESMATA CALLOSE-BINDING I			
AT4G34980	SUBTILISIN-LIKE SERINE PROTEASE 2	Serine protease 4_16656964	6.49	exon
		Serine protease 4_16656964	6.49 6.49	exon intergenic
AT4G34980	SUBTILISIN-LIKE SERINE PROTEASE 2	Serine protease 4_16656964 Sucrose transport 1_27048293 xyloglucan endc 3_16446325		
AT4G34980 AT1G71880 AT3G44990 AT1G07510	SUBTILISIN-LIKE SERINE PROTEASE 2 I SUCROSE-PROTON SYMPORTER 1 (SL XYLOGLUCAN ENDO-TRANSGLYCOSYL FTSH PROTEASE 10 (ftsh10)	Serine protease 4_16656964 Sucrose transpt 1_27048293 xyloglucan endt 3_16446325 encodes an Ftsl 1_2305257	6.49 6.49 6.48	intergenic intergenic promoter
AT4G34980 AT1G71880 AT3G44990	SUBTILISIN-LIKE SERINE PROTEASE 2 (SUCROSE-PROTON SYMPORTER 1 (SU XYLOGLUCAN ENDO-TRANSGLYCOSYL	Serine protease 4_16656964 Sucrose transport 1_27048293 xyloglucan endc 3_16446325	6.49 6.49	intergenic intergenic

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AT5G41120	na	Esterase/lipase/5_16459262	6.48	promoter
AT2G30362	na	Potential natura 2_12937315	6.48	promoter
AT3G52920	na	Family of unkno 3_19623705	6.48	proximal promoter
AT4G02200	na	Drought-respon 4_972488	6.48	promoter
AT5G51190 AT2G30360	na SOS3-INTERACTING PROTEIN 4 (SIP4)	encodes a mem 5_20801625	6.48 6.48	promoter
AT4G02195	SYNTAXIN OF PLANTS 42 (SYP42)	Encodes a SOS 2_12937315 Encodes a merr 4_972488	6.48	exon promoter
AT4G02193	(SGT1A)	Closely related 4_12299323	6.47	promoter
AT1G19780	CYCLIC NUCLEOTIDE GATED CHANNEL		6.47	intergenic
AT5G10440	CYCLIN D4;2 (CYCD4;2)	Encodes a cycli 5_3284057	6.47	proximal promoter
AT3G49250	DEFECTIVE IN MERISTEM SILENCING 3		6.47	proximal promoter
AT5G10450	G-BOX REGULATING FACTOR 6 (GRF6)	Encodes a merr 5_3284057	6.47	three_prime_UTR
AT5G62480	GLUTATHIONE S-TRANSFERASE TAU 9		6.47	intergenic
AT1G74430	MYB DOMAIN PROTEIN 95 (MYB95)	Encodes a puta 1_27974359	6.47	proximal promoter
AT2G41312	na	Unknown gene 2_17225403	6.47	promoter
AT2G34650	PINOID (PID)	Encodes a prot 2_14593775	6.47	proximal promoter
AT1G19770	PURINE PERMEASE 14 (PUP14)	Member of a far 1_6832313	6.47	promoter
AT1G49480 AT2G41310	RELATED TO VERNALIZATION1 1 (RTV1 RESPONSE REGULATOR 3 (RR3)	Encodes an A-+2 17225403	6.47 6.47	five_prime_UTR intergenic
AT3G61690	na	nucleotidyltrans 3_22834973	6.46	intergenic
AT3G61700	na	Plant protein 15 3_22834973	6.46	promoter
AT1G17060	CYTOCHROME P450 72C1 (CYP72C1)	Encodes a prote 1 5835498	6.45	promoter
AT2G46310	CYTOKININ RESPONSE FACTOR 5 (CR	CRF5 encodes 2_19011134	6.45	promoter
AT2G46308	na	unknown proteir 2_19011134	6.45	downstream
AT4G30410	na	sequence-speci 4_14872229	6.45	promoter
AT4G01100	ADENINE NUCLEOTIDE TRANSPORTER		6.44	proximal promoter
AT3G17130	na	Plant invertase/ 3_5845794	6.44	proximal promoter
AT2G22660	na	Protein of unknr 2_9627191	6.44	promoter
AT1G61900	na	unknown proteir 1_22881844	6.44	intergenic
AT2G23755 AT5G67200	na na	unknown proteir 2_10106526 Leucine-rich rer 5_26813731	6.44 6.44	proximal promoter three prime UTR
AT1G72440	EMBRYO SAC DEVELOPMENT ARREST		6.43	promoter
AT1G28360	ERF DOMAIN PROTEIN 12 (ERF12)	encodes a mem 1 9952915	6.43	downstream
AT1G72450	JASMONATE-ZIM-DOMAIN PROTEIN 6 (_	6.43	downstream
AT2G01450	MAP KINASE 17 (MPK17)	member of MAF 2_203139	6.43	promoter
AT2G31945	na	unknown proteir 2_13582673	6.43	intergenic
AT2G24230	na	Leucine-rich rer 2_10304995	6.43	promoter
AT1G08910	na	FUNCTIONS IN 1_2856031	6.43	promoter
AT2G36770	na	UDP-Glycosyltri 2_15416872	6.43	promoter
AT1G62301	na	unknown proteir 1_23022721	6.43	proximal promoter
AT3G06125	na	Unknown gene 3_1852145	6.43	intergenic
AT4G28260	na BINC MEMBRANE ANCHOR 2 (BMA2)	unknown proteir 4_14007183	6.43	downstream
AT4G28270 AT4G13830	RING MEMBRANE-ANCHOR 2 (RMA2) DNAJ-LIKE 20 (J20)	Encodes a RIN(4_14007183 DnaJ-like protei 4_8011136	6.43 6.42	intergenic promoter
AT5G45580	na	Homeodomain-I 5_18484229	6.42	proximal promoter
AT5G56530	na	Protein of Unkn 5_22888586	6.42	proximal promoter
AT1G60000	na	RNA-binding (R 1 22096539	6.42	proximal promoter
AT1G60010	na	unknown proteir 1_22096539	6.42	five_prime_UTR
AT3G05900	na	neurofilament pi 3_1764053	6.42	promoter
AT3G05905	na	Potential natura 3_1764053	6.42	exon
AT3G05910	na	Pectinacetyleste 3_1764053	6.42	intergenic
AT4G30400	na	RING/U-box su ₁ 4_14866928	6.42	promoter
AT5G13920	na	GRF zinc finger 5_4487791	6.42	promoter
AT5G13930 AT5G66700	TRANSPARENT TESTA 4 (TT4)	Encodes chalco 5_4487791 Encodes a hom 5_26635179	6.42 6.41	proximal promoter intron
AT3G00700	HOMEOBOX 53 (HB53) na	beta-1,4-N-acet 3 10205083	6.41	promoter
				promoter
		Protein of unknr 4 10370499	6 41	intergenic
AT4G18920	na na	Protein of unknr 4_10370499 RNA ligase/cvcl 4_10370499	6.41 6.41	intergenic promoter
	na	RNA ligase/cycl 4_10370499	6.41 6.41 6.41	intergenic promoter proximal promoter
AT4G18920 AT4G18930	na na	RNA ligase/cycl 4_10370499 Protein of unknc 5_4555036	6.41	promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7)	RNA ligase/cycl 4_10370499 Protein of unknc 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421	6.41 6.41 6.41 6.4	promoter proximal promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200	na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2)	RNA ligase/cycl 4_10370499 Protein of unknt 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381	6.41 6.41 6.4 6.4	promoter proximal promoter intron exon proximal promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210	na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381	6.41 6.41 6.41 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210 AT5G03190	na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085	6.41 6.41 6.41 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210 AT5G03190 AT4G32290	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na	RNA ligase/cycl 4_10370499 Protein of unknt 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085 Core-2/I-branch 4_15591661	6.41 6.41 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210 AT5G03190 AT4G32290 AT5G61450	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421	6.41 6.41 6.41 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210 AT5G03190 AT4G32290	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na	RNA ligase/cycl 4_10370499 Protein of unknt 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085 Core-2/I-branch 4_15591661	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G63190 AT4G32290 AT5G61450 AT1G78250	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-IRNA; tRNA 1_29440961	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter promoter intergenic
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G661455 AT5G66200 AT5G66210 AT5G03190 AT4G32290 AT5G61450 AT1G78250 AT5G07620	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085 Core-2/I-branch 4_15591661 P-loop containir 5_24713421 pre-tRNA; tRNA 1_29440961 Protein kinase s 5_2409640	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter intergenic proximal promoter proximal promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G66200 AT5G66200 AT5G66210 AT4G32290 AT4G32290 AT5G61450 AT1G78250 AT1G07620 AT5G07620 AT5G07630 AT4G13020	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na na na na (MHK)	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-tRNA; tRNb 1_29440961 Protein kinase s 5_2409640 pre-tRNA; tRNb 5_2409640 lipid transporter 5_2409640 Encodes a mer 4_7602850	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210 AT5G63190 AT4G32290 AT5G61450 AT1G78250 AT5G07620 AT5G07620 AT5G07620 AT5G07620 AT4G13020 AT1G56210	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na na (MHK)	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g_5_24713421 Armadillo repea 5_26456381 conserved pept 5_758085 Core-2/I-branch 4_15591661 P-loop containir 5_24713421 pre-tRNA; tRNA 1_29440961 Protein kinase s_5_2409640 Ipid transporter 5_2409640 Lipid transporter 5_2409640 Encodes a men 4_7602850 Heavy metal tra 1_21038947	6.41 6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter intergenic
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210 AT4G32290 AT4G32290 AT4G32290 AT4G78250 AT5G07620 AT5G07625 AT5G07630 AT4G13020 AT4G13020 AT4G130210 AT4G130110	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na (MHK) na na na	RNA ligase/cycl 4_10370499 Protein of unkn: 5_455036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-IRNA; tRNA 1_29440961 Protein kinase s 5_2409640 Ipid transporter 5_2409640 lipid transporter 5_2409640 Encodes a mer 4_7602850 Heavy metal tra 1_21038947 Oxidoreductase 4_7602850	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter promoter intergenic downstream
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G66200 AT5G66200 AT5G66210 AT4G32290 AT4G32290 AT5G07620 AT5G07620 AT5G07630 AT4G13020 AT4G13010 AT4G13010 AT4G31610	na na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) CALCIUM-DEPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na na na na na na	RNA ligase/cycl 4_10370499 Protein of unkin 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-IRNA; tRNb 1_29440961 Protein kinase s 5_2409640 pre-IRNA; tRNb 5_2409640 pre-IRNA; tRNb 5_2409640 Encodes a men 4_7602850 Heavy metal tra 1_21038947 Oxidoreductase 4_7602850 UDP-N-acetylgl 4_15314589	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic downstream intergenic
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210 AT5G63190 AT4G32290 AT5G61450 AT1G78250 AT5G07620 AT5G07620 AT5G07620 AT5G07620 AT4G13010 AT4G13010 AT4G13010 AT4G13010 AT4G13600 AT1G77450	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na (MHK) na na na na NAC DOMAIN CONTAINING PROTEIN 32	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g_5_24713421 Armadillo repea 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-tRNA; tRNA 1_29440961 Protein kinase s_5_2409640 Protein kinase s_5_2409640 lipid transporter 5_2409640 lipid transporter 5_2409640 Encodes a mer 4_7602850 Heavy metal tra 1_21038947 Oxidoreductase 4_7602850 UDP-N-acetylgl 4_15314589 NAC domain co 1_29100955	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter intergenic downstream intergenic exon
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G66420 AT5G66210 AT5G66210 AT4G32290 AT4G32290 AT4G32290 AT4G3250 AT5G07620 AT5G07620 AT5G07620 AT5G07620 AT5G07630 AT4G13020 AT4G13020 AT4G13020 AT4G13020 AT4G13020 AT4G13020 AT4G13070	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na (MHK) na na na NAC DOMAIN CONTAINING PROTEIN 32 ASYNAPTIC 1 (ASY1)	RNA ligase/cycl 4_10370499 Protein of unknc 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-IRNA; tRNA 1_29440961 Protein kinase s 5_2409640 Protein kinase s 5_2409640 lipid transporter 5_2409640 lipid transporter 5_2409640 Encodes a mer 4_7602850 UDP-N-acetylgl 4_15314589 NAC domain co 1_29100955 meiotic asynapt 1_25244073	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.3 6.39 6.39 6.39 6.39 6.39 6.39	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic downstream intergenic exon promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210 AT5G63190 AT4G32290 AT5G61450 AT1G78250 AT5G07620 AT5G07620 AT5G07620 AT5G07620 AT4G13010 AT4G13010 AT4G13010 AT4G13010 AT4G13600 AT1G77450	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na (MHK) na na na na NAC DOMAIN CONTAINING PROTEIN 32	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g_5_24713421 Armadillo repea 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-tRNA; tRNA 1_29440961 Protein kinase s_5_2409640 Protein kinase s_5_2409640 lipid transporter 5_2409640 lipid transporter 5_2409640 Encodes a mer 4_7602850 Heavy metal tra 1_21038947 Oxidoreductase 4_7602850 UDP-N-acetylgl 4_15314589 NAC domain co 1_29100955	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter intergenic downstream intergenic exon
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AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G61455 AT5G66200 AT5G66210 AT5G66210 AT5G66210 AT5G66210 AT5G66200 AT5G66200 AT5G67620 AT5G07620 AT5G07620 AT5G07620 AT5G07620 AT4G13010 AT4G31800 AT1G77450 AT1G67370 AT1G77450 AT3G50660 AT3G36060 AT3G303900 AT5G63640 AT3G03990 AT3G04000 AT4G23490 AT3G23520	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na na na NAC DOMAIN CONTAINING PROTEIN 32 ASYNAPTIC 1 (ASY1) CYTOKININ OXIDASE 5 (CKX5) DWARF 4 (DWF4) LIGHT-HARVESTING CHLOROPHYLL-PE na	RNA ligase/cycl 4_10370499 Protein of unknr 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-tRNA; tRNA 1_29440961 Protein kinases 5_2409640 Ipid transporter 5_2409640 lipid transporter 5_2409640 Lencodes a mer 4_7602850 UDP-N-acetylgl 4_15314589 NAC domain co 1_29100955 meiotic asynapt 1_25244073 This gene used 1_28319023 Encodes a 22& 3_18814565 Encodes a chiol 3_17495156 P-loop containir 5_25477532 RND(P)-binding 3_1034711 ChlADR is an al 3_1034711 Protein of unknr 4_12252448 Pryridoxal phosp 2_10017265 Encodes pheny 3_19747076	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.3 6.39 6.39 6.39 6.39 6.38 6.38 6.38 6.38 6.38 6.38 6.38 6.38	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter intergenic downstream intergenic exon promoter proximal promoter intron promoter proximal promoter intron promoter intergenic three_prime_UTR proximal promoter intron promoter intron promoter
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AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G67620 AT5G7620 AT5G7620 AT5G7620 AT5G7620 AT5G7630 AT4G13010 AT4G13010 AT4G31600 AT1G77450 AT3G5360600 AT3G47470 AT5G63630 AT3G47470 AT5G63840 AT3G63860	na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na na (MHK) na na na NAC DOMAIN CONTAINING PROTEIN 32 ASYNAPTIC 1 (ASY1) CYTOKININ OXIDASE 5 (CKX5) DWARF 4 (DWF4) LIGHT-HARVESTING CHLOROPHYLL-PF na	RNA ligase/cycl 4_10370499 Protein of unkn: 5_455036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-IRNA; tRNA 1_29440961 Protein kinase s 5_2409640 Ipid transporter 5_2409640 Ipid transporter 5_2409640 Ipid transporter 5_2409640 Ipid transporter 5_2409640 Encodes a mer 4_7602850 UDP-N-acetylgi 4_15314589 NAC domain co 1_29100955 meiotic asynapt 1_25244073 This gene used 1_28319023 Encodes a 228: 3_18814565 Encodes a chio 3_17495156 P-loop containir 5_25477532 ENTH/MFS/GA* 5_25477532 ENTH/MFS/GA* 5_25477532 ENTH/MFS/GA* 5_25477532 ENTH/MFS/GA* 5_25477532 Encodes a chio 3_1034711 Alpha/beta-Hydr 3_1034711 Protein of unkn: 4_12252448 Pyridoxal phose 2_10017265 Encodes pheny 3_19747076 protein kinase 1_212424319 Induced by low 3_1757473 Encodes a mer 5_19173008	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.3 6.39 6.39 6.39 6.39 6.38 6.38 6.38 6.38 6.38 6.38 6.38 6.38	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter intergenic proximal promoter intergenic three_prime_UTR proximal promoter intron promoter intron promoter intron proximal promoter intron proximal promoter intron proximal promoter downstream promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G66200 AT5G66210 AT5G66210 AT5G66210 AT5G66210 AT5G66200 AT5G66200 AT5G66200 AT5G67620 AT5G07620 AT5G07620 AT5G07620 AT4G13010 AT4G31600 AT1G77450 AT1G67370 AT1G77450 AT3G50660 AT3G47470 AT5G63630 AT5G63640 AT3G303980 AT3G03990 AT3G04000 AT1G22820 AT3G28930 AT3G28930 AT3G28930 AT3G65880 AT3G05880 AT3G05880 AT3G05880 AT3G05880 AT3G05880 AT3G05880	na na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na na na na na na NAC DOMAIN CONTAINING PROTEIN 32 ASYNAPTIC 1 (ASY1) CYTOKININ OXIDASE 5 (CKX5) DWARF 4 (DWF4) LIGHT-HARVESTING CHLOROPHYLL-PF na	RNA ligase/cycl 4_10370499 Protein of unkn: 5_4555036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 member of Calc 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-tRNA; tRNA 1_29440961 Protein kinase s 5_2409640 pre-tRNA; tRNA 5_2409640 lipid transporter 5_2409640 lipid transporter 5_2409640 Uph-N-acetylejl 4_15314589 NAC domain co 1_29100955 meiotic asynapt 1_25244073 This gnen used 1_28319023 Encodes a chiol 3_17495156 Encodes a print a chioliprofice in the chioliprofice in t	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.3 6.39 6.39 6.39 6.39 6.38 6.38 6.38 6.38 6.38 6.38 6.38 6.38	promoter proximal promoter intron exon promoter promoter promoter promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter intergenic downstream intergenic exon promoter proximal promoter proximal promoter intron promoter intergenic downstream intergenic exon promoter proximal promoter intron promoter proximal promoter intergenic three_prime_UTR proximal promoter intron promoter intron promoter intron promoter intron proximal promoter intron proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT4G18920 AT4G18930 AT5G14110 AT5G47560 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G66200 AT5G67620 AT5G7620 AT5G7620 AT5G7620 AT5G7620 AT5G7630 AT4G13010 AT4G13010 AT4G31600 AT1G77450 AT3G5360600 AT3G47470 AT5G63630 AT3G47470 AT5G63840 AT3G63860	na na TONOPLAST DICARBOXYLATE TRANSF (U2.7) ARMADILLO REPEAT ONLY 2 (ARO2) CALCIUM-DEPENDENT PROTEIN KINAS CONSERVED PEPTIDE UPSTREAM OPE na na na na na (MHK) na na na NAC DOMAIN CONTAINING PROTEIN 32 ASYNAPTIC 1 (ASY1) CYTOKININ OXIDASE 5 (CKX5) DWARF 4 (DWF4) LIGHT-HARVESTING CHLOROPHYLL-PF na	RNA ligase/cycl 4_10370499 Protein of unkn: 5_455036 Encodes a tono 5_19289691 U2.7; snRNA; g 5_24713421 Armadillo repea 5_26456381 conserved pept 5_758085 Core-2/l-branch 4_15591661 P-loop containir 5_24713421 pre-IRNA; tRNA 1_29440961 Protein kinase s 5_2409640 Ipid transporter 5_2409640 Ipid transporter 5_2409640 Ipid transporter 5_2409640 Ipid transporter 5_2409640 Encodes a mer 4_7602850 UDP-N-acetylgi 4_15314589 NAC domain co 1_29100955 meiotic asynapt 1_25244073 This gene used 1_28319023 Encodes a 228: 3_18814565 Encodes a chio 3_17495156 P-loop containir 5_25477532 ENTH/MFS/GA* 5_25477532 ENTH/MFS/GA* 5_25477532 ENTH/MFS/GA* 5_25477532 ENTH/MFS/GA* 5_25477532 Encodes a chio 3_1034711 Alpha/beta-Hydr 3_1034711 Protein of unkn: 4_12252448 Pyridoxal phose 2_10017265 Encodes pheny 3_19747076 protein kinase 1_212424319 Induced by low 3_1757473 Encodes a mer 5_19173008	6.41 6.41 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.4 6.3 6.39 6.39 6.39 6.39 6.38 6.38 6.38 6.38 6.38 6.38 6.38 6.38	promoter proximal promoter intron exon proximal promoter three_prime_UTR promoter promoter promoter intergenic proximal promoter intergenic three_prime_UTR proximal promoter intron promoter intron promoter intron proximal promoter intron proximal promoter intron proximal promoter downstream promoter

AT5G03760	(ATCSLA09)	encodes a beta 5 987819	6.36	intron
AT5G16590	(LRR1)	Leucine-rich reg 5_5430271	6.36	proximal promoter
AT5G66680	DEFECTIVE GLYCOSYLATION (DGL1)	Encodes a prote 5_26617063	6.36	intergenic
AT2G27500	na	Glycosyl hydrol: 2_11754863	6.36	proximal promoter
AT4G31510	na	unknown proteir 4_15277636	6.36	promoter
AT5G66675 AT4G36670	na POLYOL/MONOSACCHARIDE TRANSPO	Protein of unknr 5_26617063	6.36 6.36	promoter proximal promoter
AT1G74160	TON1 RECRUITING MOTIF 4 (TRM4)	unknown proteir 1 27885548	6.36	proximal promoter
AT2G41225	na	unknown proteir 2 17189286	6.35	intergenic
AT1G21540	na	AMP-dependen 1_7551952	6.35	proximal promoter
AT2G44070	na	NagB/RpiA/CoA 2_18234505	6.34	proximal promoter
AT3G52110	na	unknown proteir 3_19325836	6.34	promoter
AT1G02110	na	Protein of unknr 1_395593	6.34	downstream
AT1G21810 AT1G21830	na	Plant protein of 1_7660017 unknown proteir 1_7660017	6.34 6.34	proximal promoter
AT2G24600	na na	Ankyrin repeat f 2_10454717	6.34	intergenic promoter
AT1G01320	na	Tetratricopeptid 1 130680	6.34	promoter
AT1G19835	na	Plant protein of 1_6864946	6.34	intergenic
AT5G08660	na	Protein of unknc 5_2813954	6.34	promoter
AT5G49410	na	unknown proteir 5_20032509	6.34	five_prime_UTR
AT3G25717	ROTUNDIFOLIA LIKE 16 (RTFL16)	ROTUNDIFOLI/ 3_9375767	6.34	promoter
AT2G18700	TREHALOSE PHOSPHATASE/SYNTHAS		6.34	proximal promoter
AT1G02120	VASCULAR ASSOCIATED DEATH1 (VAD		6.34	promoter
AT1G67230	LITTLE NUCLEI1 (LINC1)	Encodes a nucli 1_25156365	6.33	promoter
AT3G25715 AT3G25716	na	pre-tRNA; tRNA 3_9373307	6.33 6.33	proximal promoter
AT1G18470	na na	unknown proteir 3_9373307 Transmembrane 1_6360272	6.33	exon promoter
AT5G18030	na	SAUR-like auxir 5 5968153	6.33	promoter
AT4G22920	NON-YELLOWING 1 (NYE1)	Similar to the to 4 12018574	6.33	promoter
AT2G40540	POTASSIUM TRANSPORTÉR 2 (KT2)	putative potassi 2_16930837	6.33	promoter
AT2G30980	SHAGGY-RELATED PROTEIN KINASE D	Encodes a GSK 2_13185904	6.33	five_prime_UTR
AT1G18480	SHEWENELLA-LIKE PROTEIN PHOSPHA		6.33	proximal promoter
AT5G18020	SMALL AUXIN UP RNA 20 (SAUR20)	SAUR-like auxir 5_5968153	6.33	proximal promoter
AT2G26260	3BETA-HYDROXYSTEROID-DEHYDROG		6.32	proximal promoter
AT1G69040	ACT DOMAIN REPEAT 4 (ACR4)	ACT-domain co 1_25955174	6.32	proximal promoter
AT3G14180 AT3G26290	ARABIDOPSIS 6B-INTERACTING PROTI CYTOCHROME P450, FAMILY 71, SUBFA		6.32 6.32	promoter
AT4G32890	GATA TRANSCRIPTION FACTOR 9 (GAT		6.32	promoter intergenic
AT1G02400		Encodes a gibb 1_488850	6.32	exon
AT3G07750	na	3'-5'-exoribonuc 3_2475607	6.32	downstream
AT3G07760	na	Sterile alpha mc 3_2475607	6.32	proximal promoter
AT1G07135	na	glycine-rich prot 1_2191087	6.32	promoter
AT1G78830	na	Curculin-like (m 1_29638664	6.32	promoter
AT1G64380	na	encodes a mem 1_23890493	6.32	downstream
AT1G67510	na	Leucine-rich rer 1_25297225	6.32	intergenic
AT1G78840 AT5G59230	na na	F-box/RNI-like/F 1_29638664 transcription fac 5_23901201	6.32 6.32	intergenic promoter
AT2G37710	RECEPTOR LECTIN KINASE (RLK)	Induced in resp. 2_15818132	6.32	proximal promoter
AT1G67500	RECOVERY PROTEIN 3 (REV3)	Encodes the car 1 25297225	6.32	promoter
AT2G37720	TRICHOME BIREFRINGENCE-LIKE 15 (T		6.32	exon
AT3G17203	GIBBERELLIN 2-OXIDASE 5 (GA2OX5)	a pseudogene ii 3_5873075	6.31	downstream
AT2G43060	ILI1 BINDING BHLH 1 (IBH1)	ILI1 binding bHL 2_17906290	6.31	proximal promoter
AT4G36820	na	Protein of unkno 4_17346686	6.31	promoter
AT4G11570	na	Haloacid dehalc 4_7004081	6.31	promoter
AT2G29670 AT1G03220	na na	Tetratricopeptid 2_12685209 Eukaryotic aspa 1_785746	6.31 6.31	promoter proximal promoter
AT2G24240	na	BTB/POZ doma 2_10310494	6.31	promoter
AT4G17810	na	C2H2 and C2H(4 9908728	6.31	intergenic
AT5G62880	RAC-LIKE 10 (RAC10)	A member of R(5_25236956	6.31	promoter
AT3G17205	UBIQUITIN PROTEIN LIGASE 6 (UPL6)	ubiquitin protein 3_5873075	6.31	promoter
AT5G64660	CYS, MET, PRO, AND GLY PROTEIN 2 (0		6.3	proximal promoter
AT1G64470	na	Ubiquitin-like su 1_23947656	6.3	proximal promoter
AT1G67590	na	Remorin family 1_25335129	6.3	promoter
AT4G29950 AT1G69910	na na	Ypt/Rab-GAP di 4_14656252 Protein kinase s 1_26328740	6.3 6.3	proximal promoter proximal promoter
AT1G09910 AT4G29940	PATHOGENESIS RELATED HOMEODON	Protein kinase s 1_26328740 Homeodomain r 4 14656252	6.3	proximal promoter
AT1G67960	POLLEN DEFECTIVE IN GUIDANCE 1 (P		6.3	promoter
AT4G37450	ARABINOGALACTAN PROTEIN 18 (AGF	AGP18 is a lysir 4_17605334	6.29	intergenic
AT1G14620	DECOY (DECOY)	DECOY (DECO 1_5018092	6.29	proximal promoter
AT5G67370	na	Protein of unknc 5 26879717	6.29	promoter
				downstream
AT2G26110	na	Protein of unknc 2_11122247	6.29	
AT4G25870	na na	Protein of unknc 2_11122247 Core-2/l-branch 4_13151961	6.29	intron
AT4G25870 AT1G14430	na na na	Protein of unknc 2_11122247 Core-2/I-branch 4_13151961 glyoxal oxidase- 1_4934582	6.29 6.29	intron exon
AT4G25870 AT1G14430 AT4G37445	na na na na	Protein of unknc 2_11122247 Core-2/I-branch 4_13151961 glyoxal oxidase- 1_4934582 BEST Arabidop: 4_17605334	6.29 6.29 6.29	intron exon promoter
AT4G25870 AT1G14430	na na na na EIN3-BINDING F BOX PROTEIN 2 (EBF2)	Protein of unknc 2_11122247 Core-2/I-branch 4_13151961 glyoxal oxidase- 1_4934582 BEST Arabidop: 4_17605334	6.29 6.29	intron exon promoter promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680	na na na na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG	Protein of unknc 2_11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidop: 4_17605334 Arabidopsis thal 5_8797111 Encodes a plasl 2_14965511 The Arabidopsis 1_29593739	6.29 6.29 6.29 6.28	intron exon promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620	na na na na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2)	Protein of unknc 2_11122247 Core-2/l-branch 4_13151961 qlyoxal oxidase-1_4934582 BEST Arabidop: 4_17605334 Arabidopsis thal 5_8797111 Encodes a plasi 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739	6.29 6.29 6.29 6.28 6.28	intron exon promoter promoter promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510	na na na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na	Protein of unknr 2_11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidop: 4_17605334 Arabidopsis thal 5_8797111 Encodes a plasi 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter intergenic promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT5G01790	na na na e EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na	Protein of unknc 2_11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidop: 4_17605334 Arabidopsis thai 5_8797111 Encodes a plası 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter intergenic promoter promoter promoter promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT5G01790 AT3G21055	na na na na na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na PHOTOSYSTEM II SUBUNIT T (PSBTN)	Protein of unknc 2_11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidop: 4_17605334 Arabidopsis thal 5_8797111 Encodes a plası 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter intergenic promoter proximal promoter promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT5G01790 AT3G21055 AT3G21060	na na na na na na leins-binding f box protein 2 (ebf2) fei 2 (fei2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na PHOTOSYSTEM II SUBUNIT T (PSBTN) RBBP5 LIKE (RBL)	Protein of unkn: 2_11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidop: 4_17605334 Arabidopsis thai 5_8797111 Encodes a plasi 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384 Encodes a brote 3_7377278 Encodes a strux 3_7377278	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter intergenic promoter proximal promoter promoter promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78670 AT3G25510 AT5G01790 AT3G21055 AT3G21060 AT3G25520	na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na PHOTOSYSTEM II SUBUNIT T (PSBTN) RBBP5 LIKE (RBL) RIBOSOMAL PROTEIN L5 (ATL5)	Protein of unknc 2_11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidops 4_17605334 Arabidopsis thai 5_8797111 Encodes a plası 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278 Encodes a struc 3_7377278 Encodes riboso 3_9268999	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter intergenic promoter proximal promoter promoter promoter promoter intergenic
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT5G01790 AT3G21055 AT3G21060	na na na na na na na na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na PHOTOSYSTEM II SUBUNIT T (PSBTN) RBBP5 LIKE (RBL) RIBOSOMAL PROTEIN L5 (ATL5) SUPPRESSORS OF SECRETION-DEFEC	Protein of unknt 2 11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidop: 4_17605334 Arabidopsis thal 5_8797111 Encodes a plası 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown protei 5_306384 Encodes photos 3_7377278 Encodes a strut 3_7377278 Encodes riboso 3_9268999 Sec61 Beta Sut 2_18589591	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter intergenic proximal promoter proximal promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT5G01790 AT3G21060 AT3G25520 AT3G25520 AT2G45070	na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na PHOTOSYSTEM II SUBUNIT T (PSBTN) RBBP5 LIKE (RBL) RIBOSOMAL PROTEIN L5 (ATL5)	Protein of unknt 2 11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidop: 4_17605334 Arabidopsis thal 5_8797111 Encodes a plası 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown protei 5_306384 Encodes photos 3_7377278 Encodes a strut 3_7377278 Encodes riboso 3_9268999 Sec61 Beta Sut 2_18589591	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter intergenic promoter proximal promoter promoter promoter promoter intergenic
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78680 AT3G25510 AT3G21060 AT3G21060 AT3G25520 AT2G45070 AT2G46400 AT4G35600 AT1G16300	na n	Protein of unknt 2_11122247 Core-27l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidops 4_17605334 Arabidopsis thai 5_8797111 Encodes a plasi 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278 Encodes a struc 3_7377278 Encodes a fibros 3_9268999 Sec61 Beta Sut 2_18589591 member of WR1 2_19045469 Encodes a rece 4_16895299 Encodes a nec 4_16895299 Encodes one of 1_5574137	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter intergenic proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT3G21050 AT3G21050 AT3G25520 AT2G45070 AT2G46400 AT4G35600 AT1G53580	na na na na na na na na na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na PHOTOSYSTEM II SUBUNIT T (PSBTN) RBBP5 LIKE (RBL) RIBOSOMAL PROTEIN L5 (ATL5) SUPPRESSORS OF SECRETION-DEFEC WRKY DNA-BINDING PROTEIN 46 (WRK CAST AWAY (CST) GLYCERALDEHYDE-3-PHOSPHATE DEF GLYCERALDEHYDE-3-PHOSPHATE DEF GLYCERALDEHYDE-3-PHOSPHATE DEF	Protein of unknc 2_11122247 Core-2/l-branch 4_13151961 qlyoxal oxidase 1_4934582 BEST Arabidops 4_17605334 Arabidopsis thai 5_8797111 The Arabidopsis 1_29593739 glisease resistar 3_9268999 unknown proteir 5_306384 Encodes a plotos 3_7377278 Encodes photos 3_7377278 Encodes a struc 3_7377278 Encodes iboso 3_9268999 unknown proteir 5_18589591 member of WRP 2_19045469 Encodes a rece 4_16895299 Encodes a rece 4_16895299 Encodes one of 1_5574137 Mononuclear Fe 1_19993408	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter promoter proximal promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT3G21060 AT3G21060 AT3G25520 AT2G45070 AT3G35500 AT1G35500 AT1G353600 AT1G53580 AT1G53380 AT1G53380	na n	Protein of unknt 2_11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidops 4_17605334 Arabidopsis thai 5_8797111 Encodes a plasi 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278 Encodes a strux 3_7377278 Encodes inboso 3_9268999 Sec61 Beta Sut 2_18589591 member of WRI 2_19045469 Encodes a rece 4_16895299 Encodes one of 1_5574137 Mononuclear Fe 1_19993408 P-loop containir 1_701386	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter promoter promoter proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT3G21060 AT3G251060 AT3G25520 AT2G45070 AT2G45070 AT2G45070 AT1G53580 AT1G53580 AT1G53580 AT1G53580 AT1G53580	na n	Protein of unknt 2_11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidops 4_17605334 Arabidopsis thal 5_8797111 Encodes a plass 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278 Encodes iboso 3_9268999 Sec61 Beta Sut 2_18589591 member of WR1 2_19045499 Encodes a rece 4_16895299 Encodes one of 1_5574137 Mononuclear Fe 1_19993408 O-Glycosyl hydi 5_22390165	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter intergenic promoter promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter exon
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT3G21050 AT3G25520 AT2G45070 AT2G46400 AT4G35600 AT1G53580 AT1G03030 AT1G53580 AT1G03030 AT1G53580 AT1G03030	na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na PHOTOSYSTEM II SUBUNIT T (PSBTN) RBBP5 LIKE (RBL) RIBOSOMAL PROTEIN L5 (ATL5) SUPPRESSORS OF SECRETION-DEFEC WRKY DNA-BINDING PROTEIN 46 (WRK CAST AWAY (CST) GLYCERALDEHYDE-3-PHOSPHATE DEH GLYOXALASE II 3 (GLY3) na na na	Protein of unknc 2_11122247 Core-2/I-branch 4_13151961 qlyoxal oxidase 1_4934582 BEST Arabidops 4_17605334 Arabidopsis thai 5_8797111 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278 Encodes photos 3_7377278 Encodes gastus 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278 Encodes a struc 3_7377278 Encodes iboso 3_9268999 unknown proteir 5_18589591 member of WRP 2_19045469 Encodes a rece 4_16895299 Encodes one of 1_5574137 Mononuclear Fe 1_19993408 P-loop containir 1_701386 O-Glycosyl hyds 5_22390165 unknown proteir 1_7032134	6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78680 AT1G78670 AT3G25510 AT3G21060 AT3G21060 AT3G25520 AT2G45070 AT2G46400 AT1G53580 AT1G53580 AT1G53580 AT1G53580 AT1G20310 AT2G41640	na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na PHOTOSYSTEM II SUBUNIT T (PSBTN) RBBP5 LIKE (RBL) RIBOSOMAL PROTEIN L5 (ATL5) SUPPRESSORS OF SECRETION-DEFEC WRKY DNA-BINDING PROTEIN 46 (WRK CAST AWAY (CST) GLYCERALDEHYDE-3-PHOSPHATE DEI GLYOXALASE II 3 (GLY3) na na na na na	Protein of unknt 2_11122247 Core-2/l-branch 4_13151961 glyoxal oxidase 1_4934582 BEST Arabidops 4_17605334 Arabidopsis thai 5_8797111 Encodes a plass 2_14965511 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278 Encodes inboso 3_97377278 Encodes a strux 3_7377278 Encodes riboso 3_9268999 Sec61 Beta Sut 2_18589591 member of WRI 2_19045469 Encodes a rece 4_16895299 Encodes one of 1_5574137 Mononuclear Fe 1_19993408 P-loop containir 1_701386 O-Glycosyl hydi 5_22390165 unknown proteir 1_7032134 Glycosyltransfei 2_17359938	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter
AT4G25870 AT1G14430 AT4G37445 AT5G25350 AT2G35620 AT1G78680 AT1G78670 AT3G25510 AT3G21050 AT3G25520 AT2G45070 AT2G46400 AT4G35600 AT1G53580 AT1G03030 AT1G53580 AT1G03030 AT1G53580 AT1G03030	na EIN3-BINDING F BOX PROTEIN 2 (EBF2) FEI 2 (FEI2) GAMMA-GLUTAMYL HYDROLASE 2 (GG GAMMA-GLUTAMYL HYDROLASE 3 (GG na na PHOTOSYSTEM II SUBUNIT T (PSBTN) RBBP5 LIKE (RBL) RIBOSOMAL PROTEIN L5 (ATL5) SUPPRESSORS OF SECRETION-DEFEC WRKY DNA-BINDING PROTEIN 46 (WRK CAST AWAY (CST) GLYCERALDEHYDE-3-PHOSPHATE DEH GLYOXALASE II 3 (GLY3) na na na	Protein of unknc 2_11122247 Core-2/I-branch 4_13151961 qlyoxal oxidase 1_4934582 BEST Arabidops 4_17605334 Arabidopsis thai 5_8797111 The Arabidopsis 1_29593739 gamma-glutamy 1_29593739 disease resistar 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278 Encodes photos 3_7377278 Encodes gastus 3_9268999 unknown proteir 5_306384 Encodes photos 3_7377278 Encodes a struc 3_7377278 Encodes iboso 3_9268999 unknown proteir 5_18589591 member of WRP 2_19045469 Encodes a rece 4_16895299 Encodes one of 1_5574137 Mononuclear Fe 1_19993408 P-loop containir 1_701386 O-Glycosyl hyds 5_22390165 unknown proteir 1_7032134	6.29 6.29 6.29 6.28 6.28 6.28 6.28 6.28 6.28 6.28 6.28	intron exon promoter proximal promoter proximal promoter proximal promoter proximal promoter

AT4G27430	COP1-INTERACTING PROTEIN 7 (CIP7) Positive regulati 4_13717716	6.26	proximal promoter
AT4G17840	na FUNCTIONS IN 4_9920526	6.26	promoter
AT4G12300	CYTOCHROME P450, FAMILY 706, SUBI member of CYP 4_7309973	6.25	promoter
AT4G34100	ECERIFERUM 9 (CER9) Encodes a prote 4_16330354	6.25	promoter
AT2G39700	EXPANSIN A4 (EXPA4) putative expans 2_16547004	6.25	proximal promoter
AT5G66568	na pre-tRNA; tRNA 5_26568496	6.25	downstream
AT2G22620	na Rhamnogalactu 2_9606901	6.25	intron
AT5G01790	na unknown proteir 5_304291	6.25	intergenic
AT4G34090	na unknown proteir 4_16330354	6.25	promoter
AT5G01780	na 2-oxoglutarate-(5_304291	6.25	promoter
AT5G66570	PS II OXYGEN-EVOLVING COMPLEX 1 (Encodes a prote 5_26568496	6.25	promoter
AT1G23400	(CAF2) Promotes the sr 1_8311841	6.24	intergenic
AT1G76650	CALMODULIN-LIKE 38 (CML38) calmodulin-like : 1_28767757	6.24	intron
AT2G41140	CDPK-RELATED KINASE 1 (CRK1) Encodes CDPK 2_17147873	6.24	proximal promoter
AT1G68552	CONSERVED PEPTIDE UPSTREAM OPE Upstream open 1_25728231	6.24 6.24	proximal promoter
AT1G68550 AT2G39860	CYTOKININ RESPONSE FACTOR 10 (CF encodes a mem 1_25728231 na pre-tRNA; tRNA 2 16640273	6.24	proximal promoter
	· · · · · · · · · · · · · · · · · · ·		promoter
AT1G78310 AT1G23390	na VQ motif-contail 1_29466052 na Kelch repeat-co 1 8311841	6.24 6.24	proximal promoter
AT1G23390 AT2G21120	na Protein of unknc 2_9054655	6.24	proximal promoter
AT2G21120 AT2G21130	na Cyclophilin-like 2_9054655	6.24	promoter intergenic
AT2G21130 AT2G37580	na RING/U-box su ₁ 2_15763768	6.24	proximal promoter
AT2G37585	na Core-2/I-branch 2_15763768	6.24	proximal promoter
AT3G13686	na unknown proteir 3_4484227	6.24	downstream
AT3G15080	na unknown proteir 3_4464227	6.24	intergenic
AT3G06870	na proline-rich fami 3_2169983	6.24	proximal promoter
AT3G06880	na Transducin/WD 3_2169983	6.24	intron
AT4G34500	na Protein kinase s 4_16490083	6.24	intron
AT2G37570	SODIUM- AND LITHIUM-TOLERANT 1 (S encodes a prote 2_15763768	6.24	promoter
AT1G60950	(FED A) encodes a majo 1_22444361	6.23	•
AT1G00930	(MCCA) MCCA is the bit 1 739534	6.23	promoter promoter
AT1G03090 AT2G47940	DEGP PROTEASE 2 (DEGP2) Encodes DegP2 2_19622344	6.23	promoter
AT5G16260	EARLY FLOWERING 9 (ELF9) Encodes DegP2 2_19622344 EARLY FLOWERING 9 (ELF9) Encodes a RNA 5_5311156	6.23	promoter
AT2G01860	` '	6.23	promoter
AT2G01860 AT2G01850	EMBRYO DEFECTIVE 975 (EMB975) EMBRYO DEFE 2_387879 ENDOXYLOGLUCAN TRANSFERASE A3 EXGT-A3 has h 2_387879	6.23	intergenic
AT1G60960	IRON REGULATED TRANSPORTER 3 (IF Encodes a plasi 1_22444361	6.23	
AT1G60960 AT5G43620	na Pre-mRNA clea 5_17522495	6.23	intergenic
			promoter
AT1G03100	na Pentatricopeptic 1_739534 na unknown proteir 3 8269782	6.23	intergenic
AT3G23171 AT3G23310		6.23 6.23	exon
		6.23	proximal promoter
AT5G16250	na unknown proteir 5_5311156		promoter
AT1G62950	na leucine-rich rep 1_23314910	6.22	promoter
AT2G25430	na epsin N-termina 2_10825203	6.22	intergenic
AT1G78230	na Outer arm dyne 1_29430229	6.22	exon
AT3G60318	na This gene encor 3_22293181	6.22	intergenic
AT3G60320	na Protein of unkno 3_22293181	6.22	intron
AT4G36500	na unknown proteir 4_17226743	6.22	promoter
AT5G01070	na RING/FYVE/PH 5_27587	6.22	proximal promoter
AT5G01075	na Glycosyl hydrol: 5_27587	6.22	promoter
AT2G25440	RECEPTOR LIKE PROTEIN 20 (RLP20) receptor like prc 2_10825203	6.22	proximal promoter
AT5G46410	SCP1-LIKE SMALL PHOSPHATASE 4 (St Encodes a SCP 5_18825015	6.22	promoter
AT4G03070	(AOP1) Encodes a poss 4_1358274	6.21	promoter
AT1G76890	(GT2) encodes a plant 1_28876273	6.21	proximal promoter
AT2G42000	ARABIDOPSIS THALIANA METALLOTHIC AtMT4a is a me 2_17530853	6.21	promoter
AT1G05670	na Pentatricopeptic 1_1699459	6.21	exon
AT1G78400	na Pectin lyase-like 1_29497892 na pre-tRNA; tRNA 5_23954122	6.21	intergenic
AT5G59385		6.21	downstream
AT3G61070	PEROXIN 11E (PEX11E) member of the r 3_22606932	6.21	promoter
AT5G25610 AT3G09690	RESPONSIVE TO DESSICATION 22 (RD; responsive to di 5_8918677 na alpha/beta-Hydr 3_2971653	6.21 6.2	proximal promoter
AT1G05350		6.2	promoter
AT3G55420	na NAD(P)-binding 1_1564330 na unknown proteir 3_20548518	6.2	promoter exon
AT5G35420 AT5G48500		6.2	
AT4G01120	na unknown proteir 5_19652420 G-BOX BINDING FACTOR 2 (GBF2) bZIP (basic leuc 4_484969	6.19	proximal promoter promoter
AT3G02885		6.19	
AT1G33240	GAST1 PROTEIN HOMOLOG 5 (GASA5) GASA5, is invol 3_633962 GT-2-LIKE 1 (GTL1) Encodes a plan: 1_12051202	6.19	intergenic intergenic
AT3G02875	IAA-LEUCINE RESISTANT 1 (ILR1) Hydrolyzes amii 3_633962	6.19	three_prime_UTR
AT3G02880	na Leucine-rich rer 3 633962	6.19	proximal promoter
AT4G01130	na GDSL-like Lipas 4_484969	6.19	proximal promoter
AT4G37760	SQUALENE EPOXIDASE 3 (SQE3) squalene epoxic 4_17743339	6.19	proximal promoter
AT2G30590	WRKY DNA-BINDING PROTEIN 21 (WRK Encodes WRKY 2_13033508	6.19	five_prime_UTR
AT5G15970	(KIN2) Encodes a gene 5_5211766	6.18	promoter
AT1G56340	CALRETICULIN 1A (CRT1a) Encodes one of 1_21092787	6.18	promoter
AT1G70895	CLAVATA3/ESR-RELATED 17 (CLE17) Member of a lar 1_26727661	6.18	promoter
AT1G03800	ERF DOMAIN PROTEIN 10 (ERF10) encodes a mem 1_958117	6.18	promoter
AT1G70890	MLP-LIKE PROTEIN 43 (MLP43) MLP-like proteir 1_26727661	6.18	proximal promoter
AT1G56345	na Pseudouridine s 1_21092787	6.18	downstream
AT3G45230	na hydroxyproline-i 3_16568844	6.18	promoter
AT1G32930	na Galactosyltrans 1_11934793	6.18	promoter
AT1G21730	na P-loop containir 1_7629628	6.18	promoter
AT1G70885	na pseudogene, sii 1_26727661	6.18	proximal promoter
AT2G46870	NGATHA1 (NGA1) NGATHA1 (NG, 2_19258004	6.18	proximal promoter
AT1G15110		6.18	five_prime_UTR
	PHOSPHATIDYLSERINE SYNTHASE 1 (F PSS1 encodes 1_5199089	0.10	
AT5G38410	PHOSPHATIDYLSERINE SYNTHASE 1 (F PSS1 encodes : 1_5199089 RUBISCO SMALL SUBUNIT 3B (RBCS3B Encodes a mem 5_15378522	6.18	promoter
AT5G38410	RUBISCO SMALL SUBUNIT 3B (RBCS3B Encodes a merr 5_15378522	6.18	promoter
AT5G38410 AT1G08250	RUBISCO SMALL SUBUNIT 3B (RBCS3B Encodes a men 5_15378522 AROGENATE DEHYDRATASE 6 (ADT6) Encodes a plast 1_2590398 MULTIFUNCTIONAL PROTEIN 2 (MFP2) Encodes a multi 3_2166496 na unknown protein 5_442657	6.18 6.17	promoter promoter
AT5G38410 AT1G08250 AT3G06860	RUBISCO SMALL SUBUNIT 3B (RBCS3B Encodes a merr 5_15378522 AROGENATE DEHYDRATASE 6 (ADT6) Encodes a plast 1_2590398 MULTIFUNCTIONAL PROTEIN 2 (MFP2) Encodes a multi 3_2166496 na unknown proteir 5_442657 na Agenet domain- 5_21161269	6.18 6.17 6.17	promoter promoter downstream
AT5G38410 AT1G08250 AT3G06860 AT5G02220	RUBISCO SMALL SUBUNIT 3B (RBCS3B Encodes a men 5_15378522 AROGENATE DEHYDRATASE 6 (ADT6) Encodes a plast 1_2590398 MULTIFUNCTIONAL PROTEIN 2 (MFP2) Encodes a multi 3_2166496 na unknown protein 5_442657	6.18 6.17 6.17 6.17	promoter promoter downstream proximal promoter
AT5G38410 AT1G08250 AT3G06860 AT5G02220 AT5G52070	RUBISCO SMALL SUBUNIT 3B (RBCS3B Encodes a merr 5_15378522 AROGENATE DEHYDRATASE 6 (ADT6) Encodes a plast 1_2590398 MULTIFUNCTIONAL PROTEIN 2 (MFP2) Encodes a multi 3_2166496 na unknown proteir 5_442657 na Agenet domain- 5_21161269 na unknown proteir 3_2166496 na Putative auxin-7 2_9086108	6.18 6.17 6.17 6.17 6.17	promoter promoter downstream proximal promoter promoter
AT5G38410 AT1G08250 AT3G06860 AT5G02220 AT5G52070 AT3G06868 AT2G21210 AT3G23930	RUBISCO SMALL SUBUNIT 3B (RBCS3B Encodes a merr 5_15378522 AROGENATE DEHYDRATASE 6 (ADT6) Encodes a plast 1_2590398 MULTIFUNCTIONAL PROTEIN 2 (MFP2) Encodes a multi 3_2166496 na unknown proteir 5_442657 na Agenet domain- 5_21161269 na unknown proteir 3_2166496 na Putative auxin-r 2_9086108 na unknown proteir 3_8646607	6.18 6.17 6.17 6.17 6.17 6.17 6.17	promoter promoter downstream proximal promoter promoter proximal promoter promoter promoter
AT5G38410 AT1G08250 AT3G06860 AT5G02220 AT5G52070 AT3G06868 AT2G21210 AT3G23930 AT5G10150	RUBISCO SMALL SUBUNIT 38 (RECS3B Encodes a merr 5, 15378522 AROGENATE DEHYDRATASE 6 (ADT6) Encodes a plast 1_2590398 MULTIFUNCTIONAL PROTEIN 2 (MFP2) Encodes a multi 3,2166496 na Agnet domain- 5_21161269 na unknown proteir 3,2166496 na Putattive auxin-r 2_9086108 na unknown proteir 3,2166496 na FUNCTIONS IN 5_3184090	6.18 6.17 6.17 6.17 6.17 6.17 6.17 6.17	promoter promoter downstream proximal promoter promoter promoter promoter promoter
AT5G38410 AT1G08250 AT3G06860 AT5G02220 AT5G52070 AT3G06868 AT2G21210 AT3G23930 AT5G10150 AT2G27840	RUBISCO SMALL SUBUNIT 3B (RBCS3B Encodes a merr 5_15378522 AROGENATE DEHYDRATASE 6 (ADT6)	6.18 6.17 6.17 6.17 6.17 6.17 6.17 6.17 6.16	promoter promoter downstream proximal promoter promoter proximal promoter promoter promoter promoter proximal promoter
AT5G38410 AT1G08250 AT3G06860 AT5G02220 AT5G52070 AT3G06868 AT2G21210 AT3G23930 AT5G10150	RUBISCO SMALL SUBUNIT 38 (RECS3B Encodes a merr 5, 15378522 AROGENATE DEHYDRATASE 6 (ADT6) Encodes a plast 1_2590398 MULTIFUNCTIONAL PROTEIN 2 (MFP2) Encodes a multi 3,2166496 na Agnet domain- 5_21161269 na unknown proteir 3,2166496 na Putattive auxin-r 2_9086108 na unknown proteir 3,2166496 na FUNCTIONS IN 5_3184090	6.18 6.17 6.17 6.17 6.17 6.17 6.17 6.17	promoter promoter downstream proximal promoter promoter promoter promoter promoter

AT5G45820	CBL-INTERACTING PROTEIN KINASE 2(Encodes a	CBL 5_18589648	6.16	proximal promoter
AT5G45830		OG1 5_18589648	6.16	three_prime_UTR
AT1G03850	GLUTAREDOXIN 13 (GRXS13) Encodes gl	utare 1_979053	6.16	proximal promoter
AT2G45910		ain-c 2_18894006	6.16	promoter
AT5G58090		hydı 5_23507389	6.16	promoter
AT2G05810		t sur 2_2215085	6.16	intron
AT2G05812		tura 2_2215085	6.16	promoter
AT2G27830		oteir 2_11860547	6.16	five_prime_UTR
AT3G61826		nco: 3_22887283	6.16	proximal promoter
AT3G61827		nco 3_22887283	6.16	promoter
AT3G61829		oteir 3_22887283	6.16	exon
AT1G03860	PROHIBITIN 2 (PHB2) prohibitin 2	1_979053	6.16	intergenic
AT2G33050		e prc 2_14025439	6.16	intergenic
AT2G33060		e prc 2_14025439	6.16	promoter
AT2G02180	TOBAMOVIRUS MULTIPLICATION PROT Necessary UDP-D-GLUCOSE/UDP-D-GALACTOSE (Encodes a		6.16	promoter
AT1G63180		_	6.16 6.15	five_prime_UTR proximal promoter
AT1G32200		chloi 1_11605806	6.15	downstream
AT1G32210 AT5G07920	DEFENDER AGAINST APOPTOTIC DEAT Encodes pr DIACYLGLYCEROL KINASE1 (DGK1) diacylglycei	rol ki 5_2529512	6.15	promoter
AT4G13340	LEUCINE-RICH REPEAT/EXTENSIN 3 (LI Leucine-ric		6.15	proximal promoter
AT3G23530		ne-f: 3_8437785	6.15	intron
AT3G47960		ator 3_17700889	6.15	promoter
AT5G11000		n of 5_3478506	6.15	intergenic
AT4G37820		oteir 4_17784984	6.15	promoter
AT5G10990		auxir 5_3478506	6.15	intergenic
AT5G04410	NAC DOMAIN CONTAINING PROTEIN 2 NAC family		6.15	promoter
AT5G03520		se h: 5_882899	6.15	proximal promoter
AT4G00370		n ino 4_166412	6.14	promoter
AT5G62000		aux 5_24916026	6.14	intergenic
AT5G62020	HEAT SHOCK TRANSCRIPTION FACTOI member of	Heat 5_24916026	6.14	promoter
AT3G18250	na Putative me	embr 3_6259175	6.14	proximal promoter
AT4G33040	na Thioredoxir	sup 4_15941492	6.14	promoter
AT1G02620	na Ras-related	l sm: 1_557156	6.14	intron
AT1G02610		E/PH 1_557156	6.14	proximal promoter
AT3G19680	na Protein of u	nknc 3_6842105	6.14	exon
AT3G19690		eine- 3_6842105	6.14	downstream
AT2G47670		ase/ 2_19545633	6.14	proximal promoter
AT5G42650		merr 5_17098358	6.13	exon
AT2G40840	DISPROPORTIONATING ENZYME 2 (DPI Encodes a		6.13	promoter
AT1G07110	FRUCTOSE-2,6-BISPHOSPHATASE (F2I Encodes th		6.13	intergenic
AT2G15890	MATERNAL EFFECT EMBRYO ARREST maternal ef		6.13	promoter
AT5G65300		oteir 5_26095873	6.13	promoter
AT1G07100		RNA 1_2177631	6.13	promoter
AT2G15880		h rer 2_6922176	6.13	proximal promoter
AT2G45040 AT3G09440		nily r 2_18579190 prot 3_2906644	6.13 6.13	intergenic
AT4G34950		ator 4_16643175	6.13	proximal promoter intron
AT2G40830		puta 2_17044943	6.13	downstream
AT4G16890	SUPPRESSOR OF NPR1-1, CONSTITUT Encodes a		6.13	promoter
AT5G59430	TELOMERIC REPEAT BINDING PROTEIN Encodes a		6.13	promoter
AT3G48350		oteir 3_17905259	6.12	promoter
AT2G40610		Alph 2_16952444	6.12	proximal promoter
AT1G76610		nknc 1_28752400	6.12	intergenic
AT5G44050		x fan 5 17723581	6.12	intron
AT1G80530	na Major facilit	ator 1_30281116	6.12	proximal promoter
AT4G38660	na Pathogenes	sis-re 4_18068542	6.12	promoter
AT4G38670	na Pathogenes	sis-re 4_18068542	6.12	intergenic
AT5G54620	na Ankyrin rep	eat f 5_22191319	6.12	proximal promoter
AT1G73080	PEP1 RECEPTOR 1 (PEPR1) Encodes a	leuci 1_27484275	6.12	promoter
AT1G76680	12-OXOPHYTODIENOATE REDUCTASE Encodes a		6.11	promoter
AT2G38400	ALANINE:GLYOXYLATE AMINOTRANSFI alanine:glyo		6.11	proximal promoter
AT2G28350	AUXIN RESPONSE FACTOR 10 (ARF10) Involved in		6.11	intergenic
AT3G23250		the F 3_8309111	6.11	promoter
AT1G35560		tran: 1_13115674	6.11	downstream
AT1G76670		suga 1_28776829	6.11	proximal promoter
AT3G28430		oteir 3_10662769	6.11	promoter
AT3G26530		le eli 3_9739462	6.11	intergenic
AT4G02410	na Concanava RESPONSE TO ABA AND SALT 1 (RAS1 RESPONS	lin A 4_1062285	6.11	promoter
AT1G09950 AT5G40390		prot: 5_16163367	6.11 6.11	intergenic intron
AT4G30960		BL-ir 4_15066919	6.11	
AT5G07990		or flay 5 2562146	6.11	promoter exon
AT3G09390		nein, 3_2890380	6.1	promoter
AT1G77060		olpy 1 28953596	6.1	promoter
AT2G24360		se s 2_10367029	6.1	promoter
AT2G18630		nknc 2 8079905	6.1	proximal promoter
AT2G30880		omc 2_13141346	6.09	intergenic
AT3G23220	ETHYLENE AND SALT INDUCIBLE 1 (ES encodes a		6.09	promoter
AT2G30870	GLUTATHIONE S-TRANSFERASE PHI 1(early dehyd		6.09	promoter
AT2G30860	GLUTATHIONE S-TRANSFERASE PHI 9 Encodes gl		6.09	intergenic
AT3G13810	INDETERMINATE(ID)-DOMAIN 11 (IDD11 indetermina	ite(IE 3_4547893	6.09	intergenic
AT1G51660	MITOGEN-ACTIVATED PROTEIN KINASI Encodes a		6.09	promoter
AT1G47970		oteir 1_17687037	6.09	promoter
AT1G51650		se e 1_19154230	6.09	intergenic
AT4G26480		g KF 4_13376140	6.09	promoter
AT3G13820	na F-box and a	asso 3_4547893	6.09	proximal promoter
AT2G46810		loop 2_19242469	6.09	three_prime_UTR
AT5G17840		0 cy: 5_5897699	6.09	proximal promoter
AT5G54200	na Transducin	WD 5_21999089	6.09	proximal promoter
AT5G61120			6.09	promoter
A TOO 40000		idop: 5_24585807		
AT2G46820	PHOTOSYSTEM I P SUBUNIT (PSI-P) Encodes th	e P : 2_19242469	6.09	proximal promoter
AT3G23810	PHOTOSYSTEM I P SUBUNIT (PSI-P) Encodes th S-ADENOSYL-L-HOMOCYSTEINE (SAH) S-adenosyl	e P : 2_19242469 -l-ho 3_8595488	6.09 6.09	proximal promoter intergenic
AT3G23810 AT2G42580	PHOTOSYSTEM I P SUBUNIT (PSI-P) Encodes th S-ADENOSYL-L-HOMOCYSTEINE (SAH) S-adenosyl TETRATRICOPETIDE-REPEAT THIOREC Encodes a	e P : 2_19242469 -l-ho 3_8595488 merr 2_17726807	6.09 6.09 6.09	proximal promoter intergenic proximal promoter
AT3G23810	PHOTOSYSTEM I P SUBUNIT (PSI-P) Encodes th S-ADENOSYL-L-HOMOCYSTEINE (SAH) S-adenosyl TETRATRICOPETIDE-REPEAT THIOREC Encodes a	e P : 2_19242469 -l-ho 3_8595488	6.09 6.09	proximal promoter intergenic

AT3G54900	CAX INTERACTING PROTEIN 1 (CXIP1)	A.thaliana PICC 3 20341147	6.08	intergenic
AT3G22968	CONSERVED PEPTIDE UPSTREAM OPE		6.08	promoter
AT1G75450	CYTOKININ OXIDASE 5 (CKX5)	This gene used 1_28315868	6.08	intron
AT5G08280	HYDROXYMETHYLBILANE SYNTHASE (Encodes a prote 5_2665858	6.08	promoter
AT3G22970	na	Protein of unknc 3_8151855	6.08	promoter
AT5G10745	na	unknown proteir 5_3400239	6.08	intergenic
AT5G10750	na	Protein of unknc 5_3400239	6.08	downstream
AT5G10760	na	Eukaryotic aspa 5_3400239	6.08	downstream
AT3G54890	PHOTOSYSTEM I LIGHT HARVESTING (6.08	promoter
AT1G59900	PYRUVATE DEHYDROGENASE COMPLI		6.08	promoter
AT1G59890	SIN3-LIKE 5 (SNL5)	SIN3-like 5 (SNI 1_22051266	6.08	downstream
AT1G75440	UBIQUITIN-CONJUGATING ENZYME 16		6.08	intergenic
AT5G08290	YELLOW-LEAF-SPECIFIC GENE 8 (YLS8		6.08	promoter
AT4G23750	CYTOKININ RESPONSE FACTOR 2 (CRI		6.07	proximal promoter
AT2G29450	GLUTATHIONE S-TRANSFERASE TAU (6.07	three_prime_UTR
AT5G56240		INVOLVED IN: 15_22765304	6.07	proximal promoter
AT2G29452 AT2G29390	na STEROL 4-ALPHA-METHYL-OXIDASE 2-:	unknown proteir 2_12624640	6.07	intergenic
AT5G42100	BETA-1,3-GLUCANASE_PUTATIVE (BG_		6.07 6.06	intron intron
AT1G75380	BIFUNCTIONAL NUCLEASE IN BASAL D		6.06	proximal promoter
AT1G75380 AT1G54115	CATION CALCIUM EXCHANGER 4 (CCX-		6.06	downstream
AT5G43060	ESPONSIVE TO DEHYDRATION 21B (RE		6.06	proximal promoter
AT3G43000 AT3G08762	na	unknown proteir 3_2662000	6.06	
AT1G45688	na	unknown proteir 1_17192972	6.06	exon three_prime_UTR
AT1G45088	na	transposable eli 1_17192972	6.06	proximal promoter
AT3G63460	na	transducin famil 3_23437624	6.06	promoter
AT2G29628	na	unknown proteir 2_12666823	6.06	downstream
AT2G29028 AT2G14080	na na	Disease resista 2 5924214	6.06	proximal promoter
AT2G14080 AT2G40460	na na	_	6.06	
		Major facilitator 2_16895758 Protein of unknc 4 1514807	6.06	proximal promoter
AT4G03420	na			intergenic
AT5G59050	na	unknown proteir 5_23840764	6.06	intron
AT5G10310 AT5G10320	na	unknown proteir 5_3242338	6.06	promoter
	na	unknown proteir 5_3242338	6.06	intergenic
AT2G29630	THIAMINC (THIC)	Encodes a prote 2_12666823	6.06	promoter
AT4G11660	(AT-HSFB2B)	member of Heat 4_7042490	6.05	promoter
AT2G38040	ACETYL CO-ENZYME A CARBOXYLASE		6.05 6.05	intergenic
AT3G44720	AROGENATE DEHYDRATASE 4 (ADT4)			exon
AT1G15950	CINNAMOYL COA REDUCTASE 1 (CCR1		6.05	exon
AT2G38050	DE-ETIOLATED 2 (DET2)	Similar to mamn 2_15921464	6.05	exon
AT5G22500	FATTY ACID REDUCTASE 1 (FAR1)	Encodes a merr 5_7466700	6.05	intergenic
AT3G53800	FES1B (Fes1B)	Encodes one of 3_19930790	6.05	promoter
AT4G36730	G-BOX BINDING FACTOR 1 (GBF1)	member of a ge 4_17312537	6.05	promoter
AT5G59840	na	Ras-related sm: 5_24109398	6.05	promoter
AT1G55700	na	Cysteine/Histidii 1_20818173	6.05	intergenic
AT3G22560	na	Acyl-CoA N-acy 3_7997610	6.05	intergenic
AT1G47310	na	unknown proteir 1_17342981	6.05	five_prime_UTR
AT2G38060	PHOSPHATE TRANSPORTER 4;2 (PHT4		6.05	intergenic
AT4G21960	(PRXR1)	Encodes AT4g2 4_11650391	6.04	proximal promoter
AT5G01370	ALC-INTERACTING PROTEIN 1 (ACI1)	Nuclear protein 5_154949	6.04	intergenic
AT1G73830	BR ENHANCED EXPRESSION 3 (BEE3)		6.04	intergenic
AT3G18550	BRANCHED 1 (BRC1)	Encodes a TCP 3_6381248	6.04	proximal promoter
AT2G22125	CELLULOSE SYNTHASE-INTERACTIVE		6.04	promoter
AT3G19980	FLOWER-SPECIFIC, PHYTOCHROME-A		6.04	promoter
AT1G61900	na	unknown proteir 1_22880809	6.04	intergenic
AT2G29670	na	Tetratricopeptid 2_12686591	6.04	proximal promoter
AT3G19970	na	alpha/beta-Hydr 3_6961730	6.04	downstream
AT4G19140	na	unknown proteir 4_10469518	6.04	promoter
AT1G09430	ATP-CITRATE LYASE A-3 (ACLA-3)	Encodes subun 1_3041921	6.03	promoter
AT2G46450	CYCLIC NUCLEOTIDE-GATED CHANNEL		6.03	promoter
AT2G26140	FTSH PROTEASE 4 (ftsh4)	encodes an Ftsl 2_11135376	6.03	promoter
AT1G09420	GLUCOSE-6-PHOSPHATE DEHYDROGE	Encodes a proti 1_3041921		
AT2G26150			6.03	promoter
	HEAT SHOCK TRANSCRIPTION FACTOR		6.03	promoter
AT4G23030	na	MATE efflux fan 4_12074828	6.03 6.03	promoter intergenic
AT2G30060	na na	MATE efflux fan 4_12074828 Pleckstrin homc 2_12829167	6.03 6.03 6.03	promoter intergenic intergenic
AT2G30060 AT2G46810	na na na	MATE efflux fan 4_12074828 Pleckstrin homc 2_12829167 basic helix-loop: 2_19240928	6.03 6.03 6.03	promoter intergenic intergenic intron
AT2G30060 AT2G46810 AT3G11402	na na na na	MATE efflux fan 4_12074828 Pleckstrin homc 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidii 3_3573346	6.03 6.03 6.03 6.03 6.03	promoter intergenic intergenic intron promoter
AT2G30060 AT2G46810 AT3G11402 AT5G03140	na na na na na	MATE efflux fan 4_12074828 Pleckstrin homc 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidii 3_3573346 Concanavalin A 5_742508	6.03 6.03 6.03 6.03 6.03 6.03	promoter intergenic intergenic intron promoter proximal promoter
AT2G30060 AT2G46810 AT3G11402 AT5G03140 AT4G33220	na na na na na PECTIN METHYLESTERASE 44 (PME44)	MATE efflux fan 4_12074828 Pleckstrin homc 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidii 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056	6.03 6.03 6.03 6.03 6.03 6.03 6.03	promoter intergenic intergenic intron promoter proximal promoter promoter
AT2G30060 AT2G46810 AT3G11402 AT5G03140 AT4G33220 AT4G39980	na na na na na PECTIN METHYLESTERASE 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT	MATE efflux fan 4_12074828 Pleckstrin homc 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544	6.03 6.03 6.03 6.03 6.03 6.03 6.03 6.02	promoter intergenic intergenic intron promoter proximal promoter promoter promoter
AT2G30060 AT2G46810 AT3G11402 AT5G03140 AT4G33220 AT4G39980 AT1G14920	na na na na na PECTIN METHYLESTERASE 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT GIBBERELLIC ACID INSENSITIVE (GAI)	MATE efflux fan 4_12074828 Pleckstrin homc 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a puta 1_5151852	6.03 6.03 6.03 6.03 6.03 6.03 6.03 6.03	promoter intergenic intergenic intron promoter proximal promoter promoter intergenic intergenic
AT2G30060 AT2G46810 AT3G11402 AT5G03140 AT4G33220 AT4G39980 AT1G14920 AT1G14930	na na na na na na PECTIN METHYLESTERASE 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT GIBBERELLIC ACID INSENSITIVE (GAI) na	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a puta 1_5151852 Polyketide cycle 1_5151852	6.03 6.03 6.03 6.03 6.03 6.03 6.03 6.03	promoter intergenic intergenic intron promoter proximal promoter promoter promoter intergenic intergenic intergenic
AT2G30060 AT2G46810 AT3G11402 AT5G03140 AT4G33220 AT4G39980 AT1G14920 AT1G14930 AT2G24395	na na na na na na na na na A PECTIN METHYLESTERASE 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT GIBBERELLIC ACID INSENSITIVE (GAI) na na	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a pute 1_5151852 Polyketide cycla 1_5151852 chaperone prott 2_10375353	6.03 6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.02	promoter intergenic intergenic intergenic intron promoter proximal promoter promoter promoter intergenic intergenic promoter
AT2G30060 AT2G46810 AT3G11402 AT5G03140 AT4G33220 AT4G39980 AT1G14920 AT1G14930 AT2G24395 AT4G39970	na na na na na na pectin Methylesterase 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT GIBBERELLIC ACID INSENSITIVE (GAI) na na na	MATE efflux fan 4_12074828 Pleckstrin homc 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidii 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a puta 1_5151852 Polyketide cycla 1_5151852 Polyketide cycla 1_5151853 Haloacid dehalc 4_18539544	6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.02 6.02	promoter intergenic intergenic intron promoter proximal promoter promoter intergenic intergenic proximal promoter promoter promoter
AT2G30060 AT2G46810 AT3G11402 AT5G03140 AT4G33220 AT4G39980 AT1G14920 AT1G14930 AT2G24395 AT4G39970 AT4G28630	na n	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a puta 1_5151852 Polyketide cycle 1_5151852 chaperone prote 2_10375353 Haloacid dehalc 4_18539544 Half-molecule A 4_14141117	6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.02 6.02 6.02 6.02	promoter intergenic intergenic intergenic intergenic intron promoter proximal promoter promoter promoter intergenic intergenic promoter proximal promoter proximal promoter promoter promoter
AT2G30060 AT2G46810 AT3G11402 AT5G03140 AT4G33920 AT4G39980 AT1G14920 AT1G14930 AT2G24395 AT4G39970 AT4G28630 AT4G17490	na ha pECTIN METHYLESTERASE 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT GIBBERELLIC ACID INSENSITIVE (GAI) na na ATP-BINDING CASSETTE B23 (ABCB23) ETHYLENE RESPONSIVE ELEMENT BIN	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a pute 1_5151852 chaperone prote 2_10375353 Haloacid dehalc 4_18539544 Half-molecule A 4_14141117 Encodes a merr 4_9753001	6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.02 6.02 6.01 6.01	promoter intergenic intergenic intergenic intergenic intron promoter proximal promoter promoter promoter intergenic intergenic promoter proximal promoter proximal promoter proximal promoter exon
AT2G30060 AT2G468110 AT3G11402 AT5G03140 AT4G33220 AT4G39980 AT1G14920 AT1G14930 AT2G24395 AT4G28630 AT4G17490 AT1G02400	na na na na na na na na PECTIN METHYLESTERASE 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT GIBBERELLIC ACID INSENSITIVE (GAI) na na ATP-BINDING CASSETTE B23 (ABCB23) ETHYLENE RESPONSIVE ELEMENT BIN GIBBERELLIN 2-OXIDASE 6 (GAZOX6)	MATE efflux fan 4_12074828 Pleckstrin homc 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidii 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a pute 1_5151852 Polyketide cycla 1_5151852 chaperone prote 2_10375353 Haloacid dehalc 4_18539544 Half-molecule A 4_14141117 Encodes a mer 4_9753001 Encodes a gibb 1_485744	6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.02 6.02 6.02 6.01 6.01	promoter intergenic intergenic intergenic intergenic intron promoter proximal promoter promoter intergenic intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter exon proximal promoter
ATZG30060 ATZG46810 AT3G11402 AT5G03140 AT4G33220 AT1G14920 AT1G14920 AT1G24395 AT4G298970 AT4G28630 AT4G17490 AT1G02400 AT4G28640	na n	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a put 1_5151852 Polyketide cycle 1_5151852 chaperone prote 2_10375353 Haloacid dehalc 4_18539544 Half-molecule A 4_14141117 Encodes a mer 4_9753001 Encodes a gibb 1_485744 Auxin induced c_4_14141117	6.03 6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.02 6.02 6.01 6.01 6.01	promoter intergenic intergenic intergenic intergenic intron promoter proximal promoter promoter promoter intergenic intergenic promoter proximal promoter proximal promoter promoter proximal promoter
ATZG30060 ATZG46810 AT3G11402 AT5G03140 AT4G33220 AT1G14920 AT1G14920 AT1G24395 AT4G28630 AT4G17490 AT1G02400 AT1G02400 AT3G228640 AT3G2288640 AT3G22886	na pECTIN METHYLESTERASE 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT GIBBERELLIC ACID INSENSITIVE (GAI) na na na ATP-BINDING CASSETTE B23 (ABCB23) ETHYLENE RESPONSIVE ELEMENT BIN GIBBERELLIN 2-OXIDASE 6 (GA2OX6) INDOLE-3-ACETIC ACID INDUCIBLE 11 (MICRORNA167A (MIR167A)	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a pute 1_5151852 Chaperone prote 2_10375353 Haloacid dehalc 4_18539544 Half-molecule A 4_14141117 Encodes a merr 4_9753001 Encodes a gibb 1_485744 Auxin induced g 4_14141117 Encodes a micr 3_8106289	6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.02 6.01 6.01 6.01 6.01	promoter intergenic intergenic intergenic intergenic intron promoter proximal promoter promoter intergenic intergenic promoter proximal promoter proximal promoter exon proximal promoter proximal proximal promoter proximal proxim
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ATZG30060 ATZG46810 AT3G11402 AT3G11402 AT5G03140 AT4G33220 AT1G14930 AT1G14930 AT2G24395 AT4G28630 AT4G28630 AT4G28640 AT4G28640 AT4G28640 AT4G28640 AT4G28640 AT4G38810 AT4G38810 AT4G38810 AT4G387260 AT3G25250 AT3G61990 AT3G25250 AT3G5250 AT3G5250 AT3G57280 AT4G357280 AT4G357280 AT4G357280 AT4G357280 AT4G357280	na pECTIN METHYLESTERASE 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT GIBBERELLIC ACID INSENSITIVE (GAI) na na na ATP-BINDING CASSETTE B23 (ABCB23) ETHYLENE RESPONSIVE ELEMENT BIN GIBBERELLIN 2-OXIDASE 6 (GA2OX6) INDOLE-3-ACETIC ACID INDUCIBLE 11 (MICRORNA167A (MIR167A) na NITRATE TRANSPORTER 1:2 (NRT1:2) O-MTASE FAMILY 3 PROTEIN (OMTF3) (AGC2-1) MYB DOMAIN PROTEIN 73 (MYB73) na na na na na na	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a pute 1_5151852 chaperone prote 2_10375353 Haloacid dehalc 4_18539544 Half-molecule A 4_141117 Encodes a merr 4_9753001 Encodes a gibb 1_485744 Auxin induced q 4_14141117 Encodes a mich 3_8106289 serine protease 3_22956965 Calcium-binding 4_18119943 Encodes an ind 1_26302892 Encodes a prote 3_22956965 Arabidopsis pro 3_9195200 Member of the f 4_17538046 proline-rich fami 3_2745543 Phosphatidylino 1_9092594 Unknown gene 1_1879487 Transmembrane 3_21193711 unknown protei 4_10597155 RNA-binding (R_181655318	6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.02 6.01 6.01 6.01 6.01 6.01 6.01 6.01 6.01	promoter intergenic intergenic intergenic intergenic intergenic intron promoter promoter promoter promoter intergenic intergenic intergenic promoter proximal promoter promoter promoter promoter promoter promoter promoter intergenic promoter
ATZG30060 ATZG46810 AT3G11402 AT5G03140 AT4G33220 AT1G14920 AT1G14930 AT2G24395 AT4G28630 AT4G17490 AT4G28640 AT3G22886 AT4G38810 AT4G38810 AT4G38810 AT4G37260 AT3G61990 AT3G25250 AT4G37260 AT3G6199000 AT1G06148 AT3G6199000 AT1G06148 AT3G67280 AT4G61943	na n	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidi 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a pute 1_5151852 chaperone prote 2_10375353 Haloacid dehalc 4_18539544 Half-molecule A 4_141117 Encodes a merr 4_9753001 Encodes a gibb 1_485744 Auxin induced q 4_14141117 Encodes a mich 3_8106289 serine protease 3_22956965 Calcium-binding 4_18119943 Encodes an ind 1_26302892 Encodes a prote 3_22956965 Arabidopsis pro 3_9195200 Member of the f 4_17538046 proline-rich fami 3_2745543 Phosphatidylino 1_9092594 Unknown gene 1_1879487 Transmembrane 3_21193711 unknown protei 4_10597155 RNA-binding (R_181655318	6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.02 6.01 6.01 6.01 6.01 6.01 6.01 6.01 6.01	promoter intergenic intergenic intergenic intergenic intergenic promoter promoter promoter promoter promoter promoter proximal promoter promoter promoter promoter promoter promoter promoter promoter intergenic
ATZG30060 ATZG46810 AT3G11402 AT5G03140 AT4G33220 AT1G14930 AT1G14930 AT4G28630 AT4G28630 AT4G28630 AT4G2740 AT4G28640 AT4G28640 AT4G28640 AT4G28640 AT4G28640 AT4G38810 AT4G38810 AT4G38810 AT4G387260 AT3G61990 AT3G25250 AT3G61990 AT3G25250 AT4G37260 AT3G90000 AT1G26270 AT4G37260 AT4G357280 AT4G357280 AT4G35738	na pECTIN METHYLESTERASE 44 (PME44) 3-DEOXY-D-ARABINO-HEPTULOSONAT GIBBERELLIC ACID INSENSITIVE (GAI) na na ATP-BINDING CASSETTE B23 (ABCB23) ETHYLENE RESPONSIVE ELEMENT BIN GIBBERELLIN 2-OXIDASE 6 (GAZOX6) INDOLE-3-ACETIC ACID INDUCIBLE 11 (MICRORNA167A (MIR167A) na	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidii 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a put 1_5151852 Polyketide cycle 1_5151852 chaperone prote 2_10375353 Haloacid dehalc 4_18539544 Half-molecule A 4_14141117 Encodes a mer 4_9753001 Encodes a gibb 1_485744 Auxin induced c 4_14141117 Encodes a micr 3_8106289 serine protease 3_2295695 Calcium-bindinc 4_18119943 Encodes an ind 1_26302892 Encodes an prot 3_2295695 Arabidopsis pro 3_9195200 Member of the f 4_17538046 proline-rich fami 3_2745543 Phosphatidylino 1_9092594 Unknown gene 1_1879487 Transmembrans 3_21193711 unknown proteir 4_16955318 Encodes a prote 4_16955318 Encodes a prote 4_16955318 Encodes a prote 4_16955318 RARE-COLD-IN 3_1759657	6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.01 6.01 6.01 6.01 6.01 6.01 6.01 6.01	promoter intergenic intergenic intergenic intergenic intergenic intron promoter proximal promoter promoter intergenic promoter promoter promoter proximal promoter promoter promoter proximal promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter pr
ATZG30060 ATZG46810 AT3G11402 AT5G03140 AT4G33220 AT1G14920 AT1G14930 AT4G28630 AT4G24395 AT4G28630 AT4G17490 AT3G22886 AT4G38810 AT1G69850 AT3G61980 AT3G61990 AT3G25250 AT4G37260 AT3G05280 AT4G37260 AT3G05280 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G37260 AT4G35785 AT4G35785	na n	MATE efflux fan 4_12074828 Pleckstrin home 2_12829167 basic helix-loop 2_19240928 Cysteine/Histidii 3_3573346 Concanavalin A 5_742508 pectin methyles 4_16022056 Encodes a 2-de 4_18539544 Similar to a put 1_5151852 Polyketide cycle 1_5151852 chaperone prote 2_10375353 Haloacid dehalc 4_18539544 Half-molecule A 4_14141117 Encodes a mer 4_9753001 Encodes a gibb 1_485744 Auxin induced c 4_14141117 Encodes a micr 3_8106289 serine protease 3_2295695 Calcium-bindinc 4_18119943 Encodes an ind 1_26302892 Encodes an prot 3_2295695 Arabidopsis pro 3_9195200 Member of the f 4_17538046 proline-rich fami 3_2745543 Phosphatidylino 1_9092594 Unknown gene 1_1879487 Transmembrans 3_21193711 unknown proteir 4_16955318 Encodes a prote 4_16955318 Encodes a prote 4_16955318 Encodes a prote 4_16955318 RARE-COLD-IN 3_1759657	6.03 6.03 6.03 6.03 6.03 6.03 6.03 6.02 6.02 6.02 6.02 6.01 6.01 6.01 6.01 6.01 6.01 6.01 6.01	promoter intergenic intergenic intergenic intergenic intergenic intron promoter promoter promoter promoter intergenic intergenic intergenic promoter proximal promoter promoter promoter intergenic promoter downstream promoter downstream proximal promoter of promoter intergenic promoter downstream proximal promoter proximal promoter promoter downstream proximal promoter

AT5G65420	CYCLIN D4;1 (CYCD4;1)	Encodes a D-ty _l 5_26141138	5.99	intergenic
AT1G28360	ERF DOMAIN PROTEIN 12 (ERF12)	encodes a mem 1_9950928	5.99	proximal promoter
AT2G38540	LIPID TRANSFER PROTEIN 1 (LP1)	Non-specific lipi 2_16131561	5.99	intergenic
AT3G02170	LONGIFOLIA2 (LNG2)	Encodes LONG 3_401678	5.99	proximal promoter
AT2G38544	na	unknown proteir 2_16131561	5.99	exon
AT5G45410	na	unknown proteir 5_18403858	5.99	promoter
AT5G56160	na	Sec14p-like phc 5_22731845	5.99	promoter
AT2G38290	AMMONIUM TRANSPORTER 2 (AMT2)	encodes a high- 2_16042424	5.98	promoter
AT3G62690	ATL5 (ATL5)	Encodes a RIN(3_23185753	5.98	three_prime_UTR
AT1G55530	na	RING/U-box sui 1_20731340	5.98	promoter
AT4G25980	na	Peroxidase sup 4_13188986	5.98	promoter
AT3G19340	na	LOCATED IN: p 3_6704615	5.98	promoter
AT1G71020	na	ARM repeat sur 1_26793184	5.98	promoter
AT2G17880	na	Chaperone Dna 2_7767903 Mitochondrial st 2 19014860	5.98	five_prime_UTR
AT2G46320	na		5.98	proximal promoter
AT5G11070 AT5G11080	na na	unknown proteir 5_3516908	5.98 5.98	five_prime_UTR
		Ubiquitin-like su 5_3516908		intergenic
AT5G60060 AT4G25970	na PHOSPHATIDYLSERINE DECARBOXYLA	CONTAINS Inte 5_24188280	5.98 5.98	intergenic intron
AT5G21990	TETRATRICOPEPTIDE REPEAT 7 (TPR7		5.98	proximal promoter
AT3G03090	VACUOLAR GLUCOSE TRANSPORTER		5.98	intron
AT1G53700	WAG 1 (WAG1)	The WAG1 and 1 20049948	5.98	exon
AT4G28710	(XIH)	member of Myo: 4_14171034	5.97	proximal promoter
AT1G76730	CLUSTERS OF ORTHOLOGOUS GROUP		5.97	promoter
AT4G11140	CYTOKININ RESPONSE FACTOR 1 (CRI		5.97	exon
AT1G53430	na	Leucine-rich reg 1_19935787	5.97	intron
AT3G22440	na	FRIGIDA-like pr 3_7959613	5.97	promoter
AT4G28706	na	pfkB-like carbor 4_14171034	5.97	intron
AT5G10980	na	Histone superfa 5 3473664	5.97	promoter
AT5G47240	NUDIX HYDROLASE HOMOLOG 8 (NUD	. –	5.97	proximal promoter
AT4G30530	GAMMA-GLUTAMYL PEPTIDASE 1 (GGF		5.96	proximal promoter
AT2G16720	MYB DOMAIN PROTEIN 7 (MYB7)	Encodes a merr 2_7260497	5.96	intergenic
AT4G32870	na	Polyketide cycla 4_15863021	5.96	intergenic
AT1G22490	na	basic helix-loop 1_7938808	5.96	intron
AT2G40800	na	unknown proteir 2_17027077	5.96	promoter
AT4G34412	na	CONTAINS Inte 4 16451891	5.96	intergenic
AT5G03660	na	Family of unkno 5 941562	5.96	intergenic
AT4G32990	na	Transducin/WD 4 15921987	5.96	exon
AT4G32990	REDOX RESPONSIVE TRANSCRIPTION		5.96	five_prime_UTR
AT3G51370	na	Protein phosph: 3 19068939	5.95	promoter
AT5G62730	na	Major facilitator 5 25196407	5.95	proximal promoter
AT1G76970	na	Target of Myb p 1_28925414	5.95	promoter
AT1G70970	na	unknown proteir 1_11974094	5.95	proximal promoter
AT1G76980	na	BEST Arabidop: 1_28925414	5.95	intergenic
AT4G28200	na	FUNCTIONS IN 4_13987453	5.95	downstream
AT5G66910	na	Disease resista 5_26718007	5.95	downstream
AT5G52055	na	transposable el 5 21150752	5.95	intergenic
AT5G66900	na	Disease resista 5_26718007	5.95	promoter
AT3G05630	PHOSPHOLIPASE D P2 (PLDP2)	Encodes a merr 3_1635019	5.95	promoter
AT5G23730	REPRESSOR OF UV-B PHOTOMORPHO		5.95	exon
AT4G28190	ULTRAPETALA1 (ULT1)	Encodes a nove 4_13987453	5.95	downstream
AT3G05480	(RAD9)	Involved in the r 3_1585127	5.94	promoter
AT1G76990	ACT DOMAIN REPEAT 3 (ACR3)	ACT domain reg 1_28931743	5.94	•
AT4G14622	CONSERVED PEPTIDE UPSTREAM OPE		5.94	promoter promoter
AT2G42485	na		5.94	•
AT1G30016	na	Unknown gene 2_17691250 unknown proteir 1_10521172	5.94	downstream exon
AT2G29065	na	GRAS family tra 2_12484763	5.94	promoter
AT4G14620	na	Protein of unkno 4_8391105	5.94	promoter
AT2G44490	PENETRATION 2 (PEN2)	Encodes a glyc(2_18368990	5.94	intergenic
AT2G25900	(ATCTH)	putative Cys3Hi 2_11040274	5.93	
AT2G23900 AT2G30490	CINNAMATE-4-HYDROXYLASE (C4H)	Encodes a cinn; 2_12997458	5.93	proximal promoter proximal promoter
AT3G23830	GLYCINE-RICH RNA-BINDING PROTEIN		5.93	promoter
AT3G23830	na	Mitochondrial tr: 3 22326271	5.93	proximal promoter
AT5G62550	• • • • • • • • • • • • • • • • • • • •		5.93	
AT2G30500	na NETWORKED 4B (NET4B)	unknown proteir 5_25108498 Kinase interactii 2_12997458	5.93	proximal promoter intergenic
AT1G22280	PHYTOCHROME-ASSOCIATED PROTEIL		5.93	proximal promoter
AT1G06570	PHYTOENE DESATURATION 1 (PDS1)	Mutation of the 1 2013707	5.93	promoter
AT2G45470	FASCICLIN-LIKE ARABINOGALACTAN P		5.92	promoter
AT2G33580	LYSM-CONTAINING RECEPTOR-LIKE KI		5.92	promoter
AT2G41250	na	Haloacid dehalc 2_17203394	5.92	proximal promoter
AT3G26890	na	unknown proteir 3_9912083	5.92	promoter
AT5G47380	na	Protein of unknc 5_19220961	5.92	intergenic
AT2G33360	na	Protein of unknc 2_14139748	5.92	promoter
AT3G13800	na	Metallo-hydrola: 3_4538009	5.92	proximal promoter
AT5G20050	na	Protein kinase s 5_6774058	5.92	promoter
AT5G56880	na	unknown proteir 5_23010305	5.92	proximal promoter
AT5G39580	na	Peroxidase sup 5 15849173	5.92	promoter
AT5G39581	na	This gene encor 5_15849173	5.92	exon
AT5G56890		Protein kinase s 5 23010305	5.92	downstream
	na			intron
AT3G26900		Encodes a prote 3 9912083	5.92	
AT3G26900 AT5G13820	SHIKIMATE KINASE-LIKE 1 (SKL1)	Encodes a prot 3_9912083 Encodes a prot 5_4460646	5.92 5.92	
AT5G13820	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (Encodes a prote 5_4460646	5.92	promoter
AT5G13820 AT1G74700	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE Z1 (TRZ1)	Encodes a prote 5_4460646 Encodes a prote 1_28065108	5.92 5.92	promoter promoter
AT5G13820 AT1G74700 AT4G00900	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE Z1 (TRZ1) ER-TYPE CA2+-ATPASE 2 (ECA2)	Encodes a prot 5_4460646 Encodes a prot 1_28065108 Type IIA (SERC 4_386852	5.92 5.92 5.91	promoter promoter promoter
AT5G13820 AT1G74700 AT4G00900 AT2G47015	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE Z1 (TRZ1) ER-TYPE CA2+ATPASE 2 (ECA2) MICRORNA408 (MIR408)	Encodes a prot 5_4460646 Encodes a prot 1_28065108 Type IIA (SERC 4_386852 Encodes a micn 2_19319539	5.92 5.92 5.91 5.91	promoter promoter promoter promoter
AT5G13820 AT1G74700 AT4G00900 AT2G47015 AT2G31130	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE Z1 (TRZ1) ER-TYPE CA2+-ATPASE 2 (ECA2)	Encodes a prott 5_4460646 Encodes a prott 1_28065108 Type IIA (SERC 4_386852 Encodes a micr 2_19319539 unknown proteir 2_13266681	5.92 5.92 5.91 5.91 5.91	promoter promoter promoter promoter promoter
AT5G13820 AT1G74700 AT4G00900 AT2G47015 AT2G31130 AT2G47010	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE 21 (TRZ1) ER-TYPE CA2+-ATPASE 2 (ECA2) MICRORNA408 (MIR408) na na	Encodes a proft 5_4460646 Encodes a proft 1_28065108 Type IIA (SERC 4_386852 Encodes a micn 2_19319539 unknown proteir 2_19366881 unknown proteir 2_19319539	5.92 5.92 5.91 5.91 5.91 5.91	promoter promoter promoter promoter promoter downstream
AT5G13820 AT1G74700 AT4G00900 AT2G47015 AT2G31130 AT2G47010 AT1G11090	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE Z1 (TRZ1) ER-TYPE CA2+ATPASE 2 (ECA2) MICRORNA408 (MIR408) na na na	Encodes a prott 5_4460646 Encodes a prott 1_28065108 Type IIA (SERC 4_386852 Encodes a micn 2_19319539 unknown proteit 2_19319539 alpha/beta-Hydt 1_3702322	5.92 5.92 5.91 5.91 5.91 5.91 5.91	promoter promoter promoter promoter promoter downstream promoter
AT5G13820 AT1G74700 AT4G00900 AT2G47015 AT2G31130 AT2G47010 AT1G11090 AT1G54410	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE Z1 (TRZ1) ER-TYPE CA2+ATPASE 2 (ECA2) MICRORNA408 (MIR408) na na na	Encodes a prott 5_4460646 Encodes a prott 1_28065108 Type IIA (SERC 4_386852 Encodes a micr 2_19319539 unknown proteir 2_13266681 unknown proteir 2_19319530 alpha/beta-Hydr 1_3702322 dehydrin family 1_20309257	5.92 5.92 5.91 5.91 5.91 5.91 5.91 5.91	promoter promoter promoter promoter promoter downstream promoter intergenic
AT5G13820 AT1G74700 AT4G00900 AT2G47015 AT2G31130 AT2G47010 AT1G11090 AT1G54410 AT2G39980	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE Z1 (TRZ1) ER-TYPE CA2+ATPASE 2 (ECA2) MICRORNA408 (MIR408) na na na	Encodes a prott 5_4460646 Encodes a prott 1_28065108 Type IIA (SERC 4_386852 Encodes a micr 2_19319539 unknown proteir 2_13266681 unknown proteir 2_19319539 alpha/beta-Hydt 1_3702322 dehydrin family 1_20309257 HXXXD-bype ac 2_16690077	5.92 5.92 5.91 5.91 5.91 5.91 5.91 5.91 5.91	promoter promoter promoter promoter promoter downstream promoter intergenic promoter
AT5G13820 AT1G74700 AT4G00900 AT2G47015 AT2G31130 AT2G47010 AT1G11090 AT1G54410 AT2G39980 AT4G00300	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE 21 (TRZ1) ER-TYPE CA2+-ATPASE 2 (ECA2) MICRORNA408 (MIR408) na na na na na	Encodes a prott 5_4460646 Encodes a prott 1_28065108 Type IIA (SERC 4_386852 Encodes a micr 2_19319539 unknown proteir 2_19319539 unknown proteir 2_19319539 alpha/beta-Hydr 1_3702322 dehydrin family 1_20309257 HXXXD-type ac 2_16690077 fringe-related pr 4_128561	5.92 5.92 5.91 5.91 5.91 5.91 5.91 5.91 5.91	promoter promoter promoter promoter downstream promoter intergenic promoter intron
AT5G13820 AT1G74700 AT4G00900 AT2G47015 AT2G31130 AT2G47010 AT1G11090 AT1G54410 AT2G39980	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE 21 (TRZ1) ER-TYPE CA2+ATPASE 2 (ECA2) MICRORNA408 (MIR408) na na na na na	Encodes a prott 5_4460646 Encodes a prott 1_28065108 Type IIA (SERC 4_386852 Encodes a micr 2_19319539 unknown proteir 2_13266681 unknown proteir 2_19319539 alpha/beta-Hydt 1_3702322 dehydrin family 1_20309257 HXXXD-bype ac 2_16690077	5.92 5.92 5.91 5.91 5.91 5.91 5.91 5.91 5.91	promoter promoter promoter promoter promoter downstream promoter intergenic promoter
AT5G13820 AT1G74700 AT4G00900 AT2G47015 AT2G31130 AT2G47010 AT1G11090 AT1G54410 AT2G39980 AT4G00300 AT4G00905	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE Z1 (TRZ1) ER-TYPE CA2+ATPASE 2 (ECA2) MICRORNA408 (MIR408) na na na na na	Encodes a prott 5_4460646 Encodes a prott 1_28065108 Type IIA (SERC 4_386852 Encodes a micn 2_19319539 unknown proteir 2_19319539 alpha/beta-Hydt 1_3702322 dehydrin family 1_20309257 HXXXD-type ac 2_16690077 fringe-related pr 4_128561 NC domain-con 4_386852	5.92 5.92 5.91 5.91 5.91 5.91 5.91 5.91 5.91 5.91	promoter promoter promoter promoter downstream promoter intergenic promoter intron proximal promoter
AT5G13820 AT1G74700 AT4G00900 AT2G47015 AT2G31130 AT2G47010 AT1G11090 AT1G54410 AT2G39980 AT4G00300 AT4G00905 AT4G16563	SHIKIMATE KINASE-LIKE 1 (SKL1) TELOMERIC DNA BINDING PROTEIN 1 (TRNASE Z1 (TRZ1) ER-TYPE CA2+-ATPASE 2 (ECA2) MICRORNA408 (MIR408) na na na na na na na na	Encodes a prott 5_4460646 Encodes a prott 1_28065108 Type IIA (SERC 4_386852 Encodes a micr 2_19319539 unknown proteir 2_19319539 alpha/beta-Hydi 1_3702322 dehydrin family 1_20309254 HXXXD-type ac 2_1669077 fringe-related pr 4_128561 NC domain-con 4_386852 Eukaryotic aspa 4_9330117 HSP20-like chal 4_9330117	5.92 5.92 5.91 5.91 5.91 5.91 5.91 5.91 5.91 5.91	promoter promoter promoter promoter downstream promoter intergenic promoter intron proximal promoter exon

AT4G22130	STRUBBELIG-RECEPTOR FAMILY 8 (SR		5.91	intergenic
AT1G18870	, ,	Encodes a prote 1_6512631	5.9	proximal promoter
AT5G08510	na	Pentatricopeptic 5_2753060	5.9	promoter
AT1G51550	na	Kelch repeat-co 1_19119503	5.9	promoter
AT1G51560	na	Pyridoxamine 5' 1_19119503	5.9	downstream
AT2G17295 AT3G50120	na na	snoRNA; snoRN 2_7520044 Plant protein of 3_18585997	5.9 5.9	proximal promoter exon
AT4G03280	PHOTOSYNTHETIC ELECTRON TRANSF		5.9	promoter
AT2G30070	POTASSIUM TRANSPORTER 1 (KT1)	Encodes a high 2_12831157	5.9	intergenic
AT5G52400	CYTOCHROME P450, FAMILY 715, SUBF		5.89	intron
AT1G32240	KANADI 2 (KAN2)	Encodes a merr 1_11628440	5.89	intron
AT3G55850	LONG AFTER FAR-RED 3 (LAF3)	Encodes a prod 3_20725679	5.89	intron
AT3G56050	na	Protein kinase f: 3_20801397	5.89	promoter
AT5G51790	na	basic helix-loop 5_21039524	5.89	promoter
AT5G52410	na	INVOLVED IN: I 5_21274942	5.89	proximal promoter
AT5G67220	na	FMN-linked oxic 5_26822184	5.89	promoter
AT2G41890	na	curculin-like (ma 2_17483507	5.89	intergenic
AT5G48360	na	Actin-binding FI 5_19595612	5.89	promoter
AT5G52882	na NAC DOMAIN CONTAINING PROTEIN 2	P-loop containir 5_21437772	5.89	intron
AT3G15510 AT4G19660	NPR1-LIKE PROTEIN 4 (NPR4)	Encodes a anky 4_10698837	5.89 5.89	intergenic proximal promoter
AT5G54380	THESEUS1 (THE1)	Encodes THESI 5 22080252	5.89	promoter
AT2G22680	WAV3 HOMOLOG 1 (WAVH1)	Zinc finger (C3F 2_9642887	5.89	proximal promoter
AT4G01360	BYPASS 3 (BPS3)	Encodes a prot 4_567052	5.88	intergenic
AT4G31820	ENHANCER OF PINOID (ENP)	A member of the 4_15396163	5.88	proximal promoter
AT2G42590	GENERAL REGULATORY FACTOR 9 (GI	14-3-3 gene. Bii 2_17733954	5.88	five_prime_UTR
AT4G01370	MAP KINASE 4 (MPK4)	Encodes a nucli 4_567052	5.88	promoter
AT1G19710	na	UDP-Glycosyltr; 1_6814453	5.88	promoter
AT2G42600	PHOSPHOENOLPYRUVATE CARBOXYL		5.88	intergenic
AT1G04010	PHOSPHOLIPID STEROL ACYL TRANSF		5.88	exon
AT1G54130	RELA/SPOT HOMOLOG 3 (RSH3)	RELA/SPOT ho 1_20209370	5.88	proximal promoter
AT3G19930	SUGAR TRANSPORTER 4 (STP4)	Encodes a sucr 3_6934004	5.88	proximal promoter
AT5G57050	ABA INSENSITIVE 2 (ABI2)	Encodes a prot 5_23087408	5.87	five_prime_UTR
AT3G48090	ENHANCED DISEASE SUSCEPTIBILITY		5.87	promoter
AT2G17230 AT4G04840	EXORDIUM LIKE 5 (EXL5) METHIONINE SULFOXIDE REDUCTASE	EXORDIUM like 2_7493762	5.87 5.87	intergenic
AT2G25095	MICRORNA156A (MIR156A)	Encodes a micr 2_10676987	5.87	proximal promoter promoter
AT1G74780	na	Nodulin-like / Mi 1 28095685	5.87	promoter
AT3G55573	na	This gene enco 3_20611415	5.87	exon
AT5G16210	na	HEAT repeat-cc 5_5298035	5.87	promoter
AT5G16220	na	Octicosapeptide 5 5298035	5.87	intergenic
AT5G61570	na	Protein kinase s 5_24757679	5.87	proximal promoter
AT3G19553	POLYAMINE UPTAKE TRANSPORTER 5	Encodes POLY, 3_6793057	5.87	promoter
AT3G24550	PROLINE-RICH EXTENSIN-LIKE RECEP	Encodes a merr 3_8960292	5.87	five_prime_UTR
AT3G24560	RASPBERRY 3 (RSY3)	novel gene invo 3_8960292	5.87	intergenic
AT3G48100	RESPONSE REGULATOR 5 (RR5)	Encodes a trans 3_17757950	5.87	intergenic
AT3G21560	UDP-GLUCOSYL TRANSFERASE 84A2 (5.87	promoter
AT2G20960	(pEARLI4)	pEARLI4; CON 2_9006055	5.86	proximal promoter
AT2G46530	AUXIN RESPONSE FACTOR 11 (ARF11)		5.86	promoter
AT1G01380 AT1G29400	ENHANCER OF TRY AND CPC 1 (ETC1) MEI2-LIKE PROTEIN 5 (ML5)	A member of me 1_10294729	5.86 5.86	proximal promoter
AT1G29400 AT1G19980	na	cytomatrix prote 1_6932856	5.86	promoter promoter
AT3G52230	na	unknown proteir 3_19371175	5.86	promoter
AT5G14011	na	This gene encor 5_4523320	5.86	promoter
AT5G17233	na	This gene encor 5_5664277	5.86	downstream
AT1G70990	na	proline-rich fami 1_26768741	5.86	proximal promoter
AT2G20950	na	Arabidopsis phc 2_9006055	5.86	downstream
AT3G24190	na	Protein kinase s 3_8743045	5.86	promoter
AT4G04630	na	Protein of unkno 4_2331936	5.86	three_prime_UTR
AT5G67455	na	pre-tRNA; tRNA 5_26921665	5.86	promoter
AT5G67460	na	O-Glycosyl hydi 5_26921665	5.86	three_prime_UTR
AT5G56550	OXIDATIVE STRESS 3 (OXS3)	Encodes OXID/ 5_22896802	5.86	promoter
AT1G49780	PLANT U-BOX 26 (PUB26)	plant U-box 26 (1_18433009	5.86	proximal promoter
AT3G05750	TON1 RECRUITING MOTIF 6 (TRM6)	unknown proteir 3_1703990	5.86	promoter five prime LITP
AT5G46110 AT5G48380	ACCLIMATION OF PHOTOSYNTHESIS T BAK1-INTERACTING RECEPTOR-LIKE K		5.85 5.85	five_prime_UTR promoter
AT2G43400	ELECTRON-TRANSFER FLAVOPROTEIN		5.85	promoter
AT3G05670	na	RING/U-box prc 3_1653130	5.85	promoter
AT1G18382	na	Potential natura 1_6324782	5.85	intergenic
AT1G18390	na	Protein kinase s 1_6324782	5.85	proximal promoter
AT3G27770	na	unknown proteir 3_10287809	5.85	promoter
AT3G11590	na	unknown proteir 3_3656694	5.85	intergenic
AT4G00500	na	alpha/beta-Hydr 4_227533	5.85	promoter
AT4G00520	na	Acyl-CoA thioes 4_227533	5.85	promoter
AT4G28180	na	unknown proteir 4_13983868	5.85	promoter
AT4G28181	na DHI OEM DDOTEIN 2 B44 (DD2 B44)	This gene encor 4_13983868	5.85	downstream
AT1G80110 AT2G32940	PHLOEM PROTEIN 2-B11 (PP2-B11) ARGONAUTE 6 (AGO6)	phloem protein: 1_30135256 Encodes a nucli 2_13977836	5.85 5.84	promoter promoter
AT2G32940 AT2G32950	CONSTITUTIVE PHOTOMORPHOGENIC		5.84	promoter
AT1G29980	na	INVOLVED IN: I 1_10504237	5.84	exon
AT5G37850	SALT OVERLY SENSITIVE 4 (SOS4)	Encodes a pyric 5_15065264	5.84	promoter
AT5G16370	ACYL ACTIVATING ENZYME 5 (AAE5)	acyl activating e 5_5356529	5.83	downstream
AT2G22670	INDOLEACETIC ACID-INDUCED PROTEI		5.83	proximal promoter
AT1G07520	na	GRAS family tra 1_2312247	5.83	promoter
AT1G32740	na	SBP (S-ribonuc 1_11846032	5.83	exon
AT1G68585	na	unknown proteir 1_25756529	5.83	promoter
AT1G68580	na	agenet domain- 1_25756529	5.83	intergenic
AT3G51980	na	ARM repeat sur 3_19287791	5.83	promoter
AT3G51990	na na	Protein kinase s 3_19287791 ENTHA/HS fam 3_17133487	5.83	promoter
AT3G46540	na na	ENTH/VHS fam 3_17133487 CCT motif family 5_4630143	5.83	intergenic
AT5G14370 AT5G14360	na na	Ubiquitin-like su 5_4630143	5.83 5.83	intergenic proximal promoter
AT5G14360	na	NC domain-con 5_5356529	5.83	promoter
AT1G68590	PLASTID-SPECIfiC RIBOSOMAL		5.83	intergenic
				-

AT3G46530	RECOGNITION OF PERONOSPORA PAI	Confers resistar 3 17133487	5.83	promoter
AT2G30880	(SWAP70)	Pleckstrin home 2_13146052	5.82	promoter
AT1G33980	(UPF3)	Involved in mRN 1_12355743	5.82	intergenic
AT1G59640	BIG PETAL P (BPEP)	A basic helix-lot 1_21911425	5.82	promoter
AT3G11550	CASPARIAN STRIP MEMBRANE DOMAII	Uncharacterise(3_3639371	5.82	downstream
AT3G49620	DARK INDUCIBLE 11 (DIN11)	encodes a prot∈ 3_18393147	5.82	proximal promoter
AT3G52770	LITTLE ZIPPER 3 (ZPR3)	ZPR3 is a small 3_19559217	5.82	promoter
AT1G33990	METHYL ESTERASE 14 (MES14)	Encodes a prote 1_12355743	5.82	five_prime_UTR
AT4G22240	na	Plastid-lipid ass 4_11767474	5.82	promoter
AT4G22250	na	RING/U-box su ₁ 4_11767474	5.82	downstream
AT3G60930	na	transposable eli 3_22513918	5.82	promoter
AT1G29290	na	unknown proteir 1_10243620	5.82	proximal promoter
AT1G04650	na	unknown proteir 1_1299514	5.82	proximal promoter
AT1G62045	na	BEST Arabidop: 1_22936871	5.82	proximal promoter
AT1G62050	na	Ankyrin repeat f 1_22936871	5.82 5.82	intron
AT3G11560 AT4G34360	na na	LETM1-like prot 3_3639371 S-adenosyl-L-m 4 16431469	5.82	promoter promoter
AT1G333060	- 1		5.82	•
	NAC 014 (NAC014)	NAC 014 (NAC(1_11978699		promoter
AT2G33870 AT3G21090	RAB GTPASE HOMOLOG A1H (ArRABA		5.82 5.81	intergenic
AT2G39800	ATP-BINDING CASSETTE G15 (ABCG15 DELTA1-PYRROLINE-5-CARBOXYLATE		5.81	promoter five prime LITP
				five_prime_UTR
AT1G68050	FLAVIN-BINDING, KELCH REPEAT, F BC		5.81	promoter
AT1G69800	na	Cystathionine b 1_26276330 Galactose oxida 1 28005205	5.81	promoter
AT1G74510	na		5.81	promoter
AT4G28703	na	RmIC-like cupin 4_14165752	5.81	proximal promoter
AT1G70250	na	Encodes a Prot 1_26451139	5.81	proximal promoter
AT3G18990	REDUCED VERNALIZATION RESPONSE		5.81	promoter
AT2G30440	THYLAKOID PROCESSING PEPTIDE (TF		5.81	promoter
AT3G46590	TRF-LIKE 1 (TRFL1)	Encodes a prote 3_17152615	5.81	promoter
AT1G70230	TRICHOME BIREFRINGENCE-LIKE 27 (T		5.81	exon
AT1G45249	ABSCISIC ACID RESPONSIVE ELEMENT		5.8	proximal promoter
AT2G44810	DEFECTIVE ANTHER DEHISCENCE 1 (D		5.8	proximal promoter
AT5G06710	HOMEOBOX FROM ARABIDOPSIS THAL		5.8	promoter
AT4G10340	LIGHT HARVESTING COMPLEX OF PHO		5.8	promoter
AT2G45360	na	Protein of unknc 2_18699245	5.8	exon
AT1G45170	na	unknown proteir 1_17098096	5.8	promoter
AT2G44798	na	Potential natura 2_18465103	5.8	intergenic
AT2G44800	na	2-oxoglutarate (2_18465103	5.8	proximal promoter
AT4G10330	na	glycine-rich prot 4_6407934	5.8	downstream
AT4G00430	PLASMA MEMBRANE INTRINSIC PROTE		5.8	proximal promoter
AT1G24400	LYSINE HISTIDINE TRANSPORTER 2 (LI	High-affinity trar 1_8653830	5.79	promoter
AT4G15760	MONOOXYGENASE 1 (MO1)	Encodes a prote 4_8974631	5.79	five_prime_UTR
AT1G22680	na	unknown proteir 1_8026544	5.79	promoter
AT2G33500	na	B-box type zinc 2_14190273	5.79	promoter
AT4G15765	na	FAD/NAD(P)-bii 4_8974631	5.79	intergenic
AT5G10946	na	unknown proteir 5_3457587	5.79	promoter
AT5G60390	na	GTP binding Ek 5_24292214	5.79	intergenic
AT5G60400	na	unknown proteir 5_24292214	5.79	promoter
AT2G41900	OXIDATIVE STRESS 2 (OXS2)	CCCH-type zinc 2_17485471	5.79	intergenic
AT2G38170	CATION EXCHANGER 1 (CAX1)	Encodes a high 2_15991966	5.78	intron
AT2G17570	na	Undecaprenyl p 2_7643903	5.78	promoter
AT5G46295	na	unknown proteir 5_18777590	5.78	intergenic
AT1G72140	na	Major facilitator 1_27140955	5.78	proximal promoter
AT4G24110	na	unknown proteir 4_12523631	5.78	proximal promoter
AT5G03700	na	D-mannose binc 5_968822	5.78	proximal promoter
AT4G32050	na	neurochondrin f 4_15501024	5.78	downstream
AT4G32060	na	calcium-binding 4_15501024	5.78	promoter
AT4G18140	SCP1-LIKE SMALL PHOSPHATASE 4B (\$	Encodes a SCP 4_10049596	5.78	promoter
AT3G61740	SET DOMAIN PROTEIN 14 (SDG14)	SET domain prc 3_22857179	5.78	promoter
AT4G24120	YELLOW STRIPE LIKE 1 (YSL1)	Member of a srr 4_12523631	5.78	proximal promoter
AT1G04610	YUCCA 3 (YUC3)	YUCCA 3 (YUC 1_1274215	5.78	intergenic
AT1G70410	BETA CARBONIC ANHYDRASE 4 (BCA4	Encodes a puta 1_26539066		
AT4G27820	BETA GLUCOSIDASE 9 (BGLU9)		5.77	proximal promoter
AT5G43100		beta glucosidas 4_13860836	5.77 5.77	proximal promoter promoter
	na	beta glucosidas 4_13860836 Eukaryotic aspa 5_17299078		
AT3G28200	na na		5.77	promoter
AT3G28200 AT1G29660		Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809	5.77 5.77	promoter promoter promoter intergenic
	na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040	5.77 5.77 5.77	promoter promoter promoter
AT1G29660 AT4G30350 AT5G09960	na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809	5.77 5.77 5.77 5.77	promoter promoter promoter intergenic
AT1G29660 AT4G30350	na na na na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999	5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter intergenic intergenic
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910	na na na na na RESPIRATORY BURST OXIDASE HOMO	Eukaryotic asps 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 NADPH/respiral 5_1399200	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter intergenic intergenic promoter downstream intron
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128	na na na na na na na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double CIp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 NADPH/respiral 5_19399200 cysteine protein 1_17288453	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430	na na na na na RESPIRATORY BURST OXIDASE HOMO	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter intergenic intergenic promoter downstream intron
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560	na na na na na na na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430	na na na na na na RESPIRATORY BURST OXIDASE HOMC ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H	Eukaryotic asps 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatior 5_21607332	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560	na na na na na na na RESPIRATORY BURST OXIDASE HOMC ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatior 5_21607332 O-fucosyltransft 2_989369	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270	na na na na na na na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_1728453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatior 5_21607332 O-fucosyltransft 2_998369 unknown proteir 2_12196893	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270 AT2G03280	na na na na na na na RESPIRATORY BURST OXIDASE HOMC ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (Fina na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatior 5_21607332 O-fucosyltransft 2_989369	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270 AT2G03280 AT2G28507	na na na na na na na na na RESPIRATORY BURST OXIDASE HOMC ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H na na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_1728453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatior 5_21607332 O-fucosyltransft 2_998369 unknown proteir 2_12196893	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter intergenic promoter intergenic promoter intergenic
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270 AT2G03280 AT2G28507 AT2G38500	na na na na na na na na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H na na na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607333 Seed maturation 5_21607333 C-fucosyltransft 2_998369 unknown protein 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_5833209 unknown protein 3_19472812	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter intergenic promoter
AT1G29660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270 AT2G03280 AT2G28507 AT2G38500 AT3G17100	na RESPIRATORY BURST OXIDASE HOMC ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H na na na na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 INADPH/respirat 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatior 5_21607332 O-fucosyltransfr 2_989369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_5833209	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter
AT1G29660 AT4G30350 AT5G9960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270 AT2G3280 AT2G28507 AT2G38500 AT3G17100 AT3G52520	na na na na na na na na na RESPIRATORY BURST OXIDASE HOMC ESPONSIVE TO DEHYDRATION 21A (RI HIGHLY ABA-INDUCED PP2C GENE 2 (H na na na na na na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607333 Seed maturation 5_21607333 C-fucosyltransft 2_998369 unknown protein 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_5833209 unknown protein 3_19472812	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter intergenic promoter intergenic promoter promoter intergenic proximal promoter proximal promoter promoter intergenic proximal promoter
AT1629660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270 AT2G03280 AT2G28507 AT2G38500 AT3G52520 AT3G52520 AT3G52520	na na na na na na na na na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H na na na na na na na na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607332 C-hucosyltransft 2_998369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_583209 unknown proteir 3_19472812 unknown proteir 3_19472812 unknown proteir 5_4621088 An integral oute 5_21607332	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter
AT1G29660 AT4G30350 AT5G9960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT2G3280 AT2G28507 AT2G38500 AT3G17100 AT3G52520 AT3G17100 AT3G52520 AT4G28085 AT5G14330	na na na na na na na na na RESPIRATORY BURST OXIDASE HOMC ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatio 5_21607332 O-fucosyltransfr 2_998369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_5833209 unknown proteir 4_13959385 unknown proteir 5_4621088	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter
AT1G29660 AT4G30350 AT5G99960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT2G32800 AT2G32800 AT2G32800 AT2G38500 AT3G17100 AT3G52520 AT4G28085 AT5G14330 AT5G53280	na na na na na na na na na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RC HIGHLY ABA-INDUCED PP2C GENE 2 (F) na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607332 C-hucosyltransft 2_998369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_583209 unknown proteir 3_19472812 unknown proteir 3_19472812 unknown proteir 5_4621088 An integral oute 5_21607332	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter
AT1629660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270 AT2G03280 AT2G28507 AT2G38500 AT3G52520 AT3G52520 AT4G28085 AT5G14330 AT1G438600 AT3G53280 AT1G49600	na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (F na	Eukaryotic asps 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatio 5_21607332 O-fucosyltransft 2_998369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_5833209 unknown proteir 3_19472812 unknown proteir 4_13959385 unknown proteir 4_13959385 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-binding pri 1_18357749	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter promoter intron
AT1G29660 AT4G30350 AT5G9960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT2G3280 AT2G28507 AT2G38500 AT3G17100 AT3G52520 AT3G17400 AT3G53280 AT5G53280 AT5G14330 AT5G53280 AT1G49600 AT3G18370	na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607332 O-fucosyltransft 2_983869 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_583209 unknown proteir 3_19472812 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-binding pr 1_18357749 ATSYTF; FUNC 3_6304821 Encodes a nucl 3_18126662	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter promoter intergenic proximal promoter intergenic proximal promoter intron proximal promoter
AT1G29660 AT4G30350 AT5G99960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270 AT2G32800 AT2G28507 AT2G38500 AT3G17100 AT3G52520 AT4G28085 AT5G14330 AT5G53280 AT1G49600 AT3G18370 AT3G48870	na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (F na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607332 O-fucosyltransft 2_983869 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_583209 unknown proteir 3_19472812 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-binding pr 1_18357749 ATSYTF; FUNC 3_6304821 Encodes a nucl 3_18126662	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intron proximal promoter intron
AT1629660 AT4G30350 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT5G53270 AT2G03280 AT2G28507 AT2G38500 AT3G52520 AT3G52520 AT3G52520 AT3G53280 AT5G53280 AT1G49600 AT3G18370 AT3G84870 AT1G689410	na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (F na	Eukaryotic asps 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 nighly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607332 O-fucosyltransf 2_998369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 social sunknown proteir 3_19472812 unknown proteir 3_19472812 unknown proteir 3_19472812 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-binding pn 1_18357749 ATSYTF; FUNC 3_6304821 Encodes a nucl 3_18126662 Encodes elFSA-1_26091065	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter intron proximal promoter intron intergenic
AT1G29660 AT4G30350 AT5G9960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT2G3280 AT2G3280 AT2G28507 AT2G38500 AT3G17100 AT3G52520 AT4G28085 AT5G14330 AT5G53280 AT3G17400 AT3G53280 AT3G48870 AT3G48870 AT3G48870 AT3G48870 AT3G69410 AT1G69410	na na na na na na na na na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (H na RHASTIID DIVISION1 (PDV1) RNA-BINDING PROTEIN 47A (RBP47A) (ATSYTF) (HSP93-III) EUKARYOTIC ELONGATION FACTOR 56 LESION INITIATION 2 (LIN2)	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 INADPH/respirat 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatio 5_21607332 O-fucosyltransft 2_998369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_5833209 unknown proteir 3_19472812 unknown proteir 4_13959385 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-binding pn 1_18357749 ATSYTF; FUNC 3_6304821 Encodes a nucli 3_18126662 Encodes coprof 1_868915	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.75	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter promoter intergenic proximal promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intron proximal promoter intron intron intergenic downstream
AT1G29660 AT4G30350 AT5G99960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT2G32800 AT2G32800 AT2G38500 AT3G17100 AT3G52520 AT4G28085 AT5G14330 AT5G53280 AT1G48600 AT3G18370 AT3G8870 AT3G8870 AT3G8870 AT3G8870 AT3G8870 AT3G68410	na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RC HIGHLY ABA-INDUCED PP2C GENE 2 (F) na na na na na na na na na PLASTID DIVISION1 (PDV1) RNA-BINDING PROTEIN 47A (RBP47A) (ATSYTF) (HSP93-III) EUKARYOTIC ELONGATION FACTOR 56 LESION INITIATION 2 (LIN2) METHIONINE SYNTHESIS 1 (ATMS1)	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607332 O-tucosyltransft 2_988369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_583209 unknown proteir 3_19472812 unknown proteir 3_19472812 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-binding pri 1_18357749 ATSYTF; FUNC 3_6304821 Encodes a nucli 3_18126662 Encodes elF5A-1_26091065 Encodes copro; 1_868915 Encodes copro; 1_868915 Encodes a oyto: 5_55939635	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter proximal promoter proximal promoter intron proximal promoter intron intergenic downstream downstream
AT1629660 AT4G30350 AT5G09960 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT2G03280 AT2G03280 AT2G28507 AT2G38500 AT3G17100 AT3G52520 AT4G28085 AT5G14330 AT5G53280 AT5G4330 AT5G4870 AT3G48870 AT3G48870 AT1G69410 AT1G63475 AT5G17920 AT1G17920 AT1G17702	na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (F na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 nighly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607332 O-fucosyltransf 2_998369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_5833209 unknown proteir 3_19472812 unknown proteir 3_19472812 unknown proteir 4_13959385 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-binding pn 1_18357749 ATSYTF; FUNC 3_6304821 Encodes a nucl 3_18126662 Encodes copro 1_868915 Encodes a cyto: 5_5939635 Protein of unkn 1_33945116	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter intron proximal promoter intron intergenic downstream downstream proximal promoter intron intergenic downstream proximal promoter proximal promoter intron intergenic downstream proximal promoter proximal promoter intron intergenic downstream proximal promoter interg
AT1G29660 AT4G30350 AT5G09960 AT5G99960 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT2G3280 AT2G3280 AT2G28507 AT2G38500 AT3G17100 AT3G52520 AT4G28085 AT5G14330 AT5G53280 AT3G14330 AT3G48870 AT3G48870 AT1G94900 AT3G48870 AT1G9410 AT1G03475 AT5G17920 AT1G1700 AT1G1700 AT5G43870	na na na na na na na na na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (Hona na na na na na na na na PLASTID DIVISION1 (PDV1) RNA-BINDING PROTEIN 47A (RBP47A) (ATSYTF) (HSP93-III) EUKARYOTIC ELONGATION FACTOR 5/ LESION INITIATION 2 (LIN2) METHIONINE SYNTHESIS 1 (ATMS1) na na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 INADPH/respirat 5_19399200 cysteine protein 1_17288453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatio 5_21607332 O-fucosyltransft 2_998369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_5833209 unknown proteir 4_13959385 unknown proteir 4_13959385 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-binding pn 1_18357749 ATSYTF; FUNC 3_6304821 Encodes a nucli 3_18126662 Encodes copror 1_868915 Encodes 155454	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.75	promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter promoter intergenic proximal promoter intergenic proximal promoter proximal promoter proximal promoter intron intron intergenic downstream downstream downstream downstream proximal promoter proximal promoter proximal promoter intron proximal promoter
AT1G29660 AT4G30350 AT5G9960 AT5G99960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT2G3280 AT2G28507 AT2G38500 AT3G17100 AT3G52520 AT4G28085 AT5G14330 AT5G53280 AT1G48600 AT3G18370 AT3G8870 AT3G8870 AT3G8870 AT1G69410 AT1G69410 AT1G11700 AT5G17920 AT1G11700 AT5G17920 AT1G11700 AT1G69420	na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RC HIGHLY ABA-INDUCED PP2C GENE 2 (F) na	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 unknown proteir 5_7371999 NADPH/respiral 5_19399200 cysteine protein 1_1728453 highly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturatior 5_21607332 O-fucosyltransft 2_988369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_583209 unknown proteir 3_19472812 unknown proteir 3_19472812 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-bindring pri 1_18357749 ATSYTF; FUNC 3_6304821 Encodes a nucli 3_18126662 Encodes copro; 1_868915 Encodes a cyto: 5_5939635 Protein of unkn 1_3945116 FUNCTIONS IN 5_17635964 DHHC-type zinc 1_26091065	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.76	promoter promoter promoter promoter intergenic intergenic promoter downstream intron promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter intron intergenic downstream downstream downstream downstream proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT1629660 AT4G30350 AT5G09960 AT5G09960 AT5G22270 AT5G47910 AT1G47128 AT1G07430 AT4G17560 AT3G52270 AT2G03280 AT2G28507 AT2G38500 AT3G17100 AT3G52520 AT3G14330 AT5G53280 AT5G4330 AT5G48600 AT3G48870 AT1G69400 AT3G4870 AT1G69410 AT1G69420 AT1G17700 AT1G69420 AT5G12440	na RESPIRATORY BURST OXIDASE HOMO ESPONSIVE TO DEHYDRATION 21A (RE HIGHLY ABA-INDUCED PP2C GENE 2 (Hona na n	Eukaryotic aspa 5_17299078 Peroxidase sup 3_10518040 GDSL-like Lipas 1_10368809 Double Clp-N m 4_14844524 FUNCTIONS IN 5_3106209 NADPH/respiral 5_19399200 cysteine protein 1_17288453 nighly ABA-indu 1_2283071 Ribosomal prote 4_9780038 Seed maturation 5_21607332 O-fucosyltransft 2_998369 unknown proteir 2_12196893 2-oxoglutarate (2_16119307 sequence-speci 3_5833209 unknown proteir 3_19472812 unknown proteir 5_4621088 An integral oute 5_21607332 RNA-binding pri 1_18357749 ATSYTF; FUNC 3_6304821 Encodes a nucli 3_18126662 Encodes copro; 1_868915 Encodes a cvito: 5_5939635 Protein of unkn t_3945116 FUNCTIONS IN 5_17635964 DHHC-type zint 1_26091065 CCCH-type zint 1_5_403905	5.77 5.77 5.77 5.77 5.77 5.77 5.77 5.76 5.75	promoter promoter promoter promoter promoter intergenic intergenic promoter downstream intron proximal promoter promoter promoter promoter promoter promoter promoter intergenic promoter intergenic proximal promoter proximal promoter proximal promoter intron proximal promoter intron intergenic downstream downstream proximal promoter proximal promoter intron intergenic downstream proximal promoter promoter proximal promoter proximal promoter proximal promoter intron

ATOC 40000		DNI III	F 7F	
AT3G48880 AT1G03470	na NETWORKED 3A (NET3A)	RNI-like superfa 3_18126662 Encodes a merr 1 868915	5.75 5.75	promoter proximal promoter
AT1G03470 AT2G34420	PHOTOSYSTEM II LIGHT HARVESTING			promoter
AT4G00430	PLASMA MEMBRANE INTRINSIC PROTE			intron
AT3G17000	UBIQUITIN-CONJUGATING ENZYME 32			promoter
AT4G34160	CYCLIN D3;1 (CYCD3;1)	encodes a cyclii 4_16355001		proximal promoter
AT3G26210	CYTOCHROME P450, FAMILY 71, SUBFA			proximal promoter
AT3G26220	CYTOCHROME P450, FAMILY 71, SUBFA			downstream
AT4G00820	IQ-DOMAIN 17 (iqd17)	IQ-domain 17 (ii 4_349077		promoter
AT1G73500	MAP KINASE KINASE 9 (MKK9)	member of MAF 1 27641855		proximal promoter
AT5G13760	na	Plasma-membra 5_4445305		intergenic
AT5G13770	na	Pentatricopeptic 5_4445305		promoter
AT4G31000	na	Calmodulin-binc 4_15103030	5.74	promoter
AT1G70200	na	RNA-binding (R 1_26434960	5.74	proximal promoter
AT1G78210	na	alpha/beta-Hydr 1_29424933	5.74	proximal promoter
AT2G21520	na	Sec14p-like phc 2_9215139	5.74	promoter
AT4G34140	na	D111/G-patch d 4_16355001	5.74	intergenic
AT4G20040	na	Pectin lyase-lik € 4_10850185	5.74	proximal promoter
AT4G27560	na	UDP-Glycosyltr; 4_13761885		promoter
AT4G34150	na	Calcium-depend 4_16355001		five_prime_UTR
AT4G30996	NA(+)- AND K(+)-SENSITIVE 1 (NKS1)	NKS1, a plant-s 4_15103030		intergenic
AT2G01180	PHOSPHATIDIC ACID PHOSPHATASE 1			promoter
AT4G20050	QUARTET 3 (QRT3)	Encodes a poly 4_10850185		exon
AT1G53390	ATP-BINDING CASSETTE G24 (ABCG24)			proximal promoter
AT1G14350	FOUR LIPS (FLP)	Encodes a puta 1_4906954		proximal promoter
AT3G28920	HOMEOBOX PROTEIN 34 (HB34)	homeobox prote 3_10941960		promoter
AT1G04810	na	26S proteasom(1_1355758		intergenic
AT3G62000	na	S-adenosyl-L-m 3_22962144		proximal promoter
AT1G53380	na	Plant protein of 1_19916686		promoter
AT2G27830	na	unknown proteir 2_11859541		proximal promoter
AT5G56240	na	INVOLVED IN: 15_22764474 Encodes a plast 2 11859541		five_prime_UTR
AT2G27820 AT1G13260	PREPHENATE DEHYDRATASE 1 (PD1) RELATED TO ABI3/VP1 1 (RAV1)	Encodes a plasi 2_11859541 Encodes an AP: 1_4540813		intergenic
				proximal promoter
AT1G71880 AT1G04820	SUCROSE-PROTON SYMPORTER 1 (SU TUBULIN ALPHA-4 CHAIN (TUA4)	Encodes an alpl 1 1355758		promoter
AT3G21781	na	Potential natura 3_7675860		intergenic
AT2G22530	na	Alkaline-phosph 2_9577670		promoter promoter
AT1G22250	na	unknown proteir 1_7858793		promoter
AT1G22230 AT1G15530	na	Concanavalin A 1 5342112		promoter
AT5G57480	na	P-loop containir 5_23283348		proximal promoter
AT5G06270	na	unknown proteir 5_1914572		intergenic
AT1G50420	SCARECROW-LIKE 3 (SCL3)	Encodes a scar 1_18681048		proximal promoter
AT3G21780	UDP-GLUCOSYL TRANSFERASE 71B6 (exon
AT5G57490	VOLTAGE DEPENDENT ANION CHANNE			intergenic
AT4G24280	CHLOROPLAST HEAT SHOCK PROTEIN			intergenic
AT3G01472	CONSERVED PEPTIDE UPSTREAM OPE			three_prime_UTR
AT3G01070	EARLY NODULIN-LIKE PROTEIN 16 (EN			downstream
AT5G04140	GLUTAMATE SYNTHASE 1 (GLU1)	Encodes a gene 5_1129746		promoter
AT3G01470	HOMEOBOX 1 (HB-1)	Encodes a hom 3_182955	5.71	three_prime_UTR
AT2G20370	MURUS 3 (MUR3)	Encodes a xylo; 2_8791837		promoter
AT1G15405	na	Unknown gene 1_5297848		downstream
AT2G34250	na	SecY protein tra 2_14462050	5.71	promoter
AT3G47830	na	DNA glycosylas 3_17646384	5.71	proximal promoter
AT3G61198	na	Unknown gene 3_22655288	5.71	intergenic
AT4G24290	na	MAC/Perforin d ₁ 4_12594170	5.71	promoter
AT3G63200	PATATIN-LIKE PROTEIN 9 (PLP9)	PATATIN-like pi 3_23347351		exon
AT1G63090	PHLOEM PROTEIN 2-A11 (PP2-A11)	phloem protein: 1_23395453	5.71	proximal promoter
AT3G47820	PLANT U-BOX 39 (PUB39)	PLANT U-BOX 3_17646384		downstream
AT4G17870	PYRABACTIN RESISTANCE 1 (PYR1)	Encodes a merr 4_9930403	5.71	intergenic
AT3G19820	DWARF 1 (DWF1)	Involved in the (3_6882206		intron
AT4G13050	na	Acyl-ACP thioes 4_7617574		five_prime_UTR
AT1G17090	na	unknown proteir 1_5844341		promoter
AT1G17100	na	SOUL heme-bir 1_5844341		promoter
AT1G27350	na	Ribosome asso 1_9499597		promoter
AT2G24165	na	pseudogene, sir 2_10272614		downstream
AT3G04920	na	Ribosomal prote 3_1358594		proximal promoter
AT3G27400 AT1G32060	na PHOSPHORIBULOKINASE (PRK)	Pectin lyase-like 3_10141076 phosphoribuloki 1_11531991		intron proximal promoter
	SECRETORY CARRIER MEMBRANE PR			intergenic
AT1G32050 AT3G04910	WITH NO LYSINE (K) KINASE 1 (WNK1)			intergenic
AT4G34000	= (IN) INITAL (VINIT)			promoter
	ARSCISIC ACID RESPONISIVE ELEMENT	Encodes an AR / 16205276		PIOIIIOIGI
AT5G62040	ABSCISIC ACID RESPONSIVE ELEMENT			proximal promotor
AT1G67900	HIGH CAMBIAL ACTIVITY2 (HCA2)	HCA2 induces t 5_25259322	5.69	proximal promoter
AT1G67900	HIGH CAMBIAL ACTIVITY2 (HCA2) na	HCA2 induces t 5_25259322 Phototropic-resi 1_25466745	5.69 5.69	intron
AT1G67900 AT1G71070	HIGH CAMBIAL ACTIVITY2 (HCA2) na na	HCA2 induces t 5_25259322 Phototropic-res ₁ 1_25466745 Core-2/l-branch 1_26809634	5.69 5.69 5.69	intron promoter
AT1G67900 AT1G71070 AT1G71080	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na	HCA2 induces t 5_25259322 Phototropic-resi 1_25466745 Core-2/l-branch 1_26809634 RNA polymeras 1_26809634	5.69 5.69 5.69 5.69	intron promoter downstream
AT1G67900 AT1G71070 AT1G71080 AT2G30100	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na	HCA2 induces t 5_25259322 Phototropic-resj 1_25466745 Core-2/l-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372	5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na	HCA2 induces t 5_25259322 Phototropic-resp 1_25466745 Core-2/l-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372 pre-tRNA; tRNA 5_3287686	5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na	HCA2 induces t 5_25259322 Phototropic-resi 1_25466745 Core-2/I-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372 pre-tRNA; tRNA 5_3287686 Haloacid dehalc 5_3287686	5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na	HCA2 induces t 5_25259322 Phototropic-resj 1_25466745 Core-2/I-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372 pre-tRNA; tRNA 5_3287686 Haloacid dehalc 5_3287686 receptor like prc 4_10309565	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460 AT4G18760	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51)	HCA2 induces t 5_26259322 Pho2 induces t 5_26269322 Poore-2/I-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372 pre-IRNA; IRNA 5_3287686 Haloacid dehalc 5_3287686 receptor like prc 4_10309565 selenium-bindin 4_810507	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460 AT4G18760 AT4G14030	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1)	HCA2 induces t 5_26259322 Pho2 induces t 5_26269322 Poore-2/l-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372 pre-IRNA; IRNA 5_3287686 Haloacid dehalc 5_3287686 receptor like prc 4_10309565 selenium-bindin 4_810507	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460 AT4G18760 AT4G14030 AT4G14040	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2)	HCA2 induces t 5_25259322 Phototropic-resi 1_25466745 Core-2/I-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372 pre-tRNA; tRNA 5_3287686 Haloacid dehalc 5_3287686 receptor like prc 4_10309565 selenium-bindin 4_8100507 Selenium-bindin 4_8100507 Encodes a merr 5_6937874	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter promoter three_prime_UTR
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460 AT4G18760 AT4G14030 AT4G14040 AT5G20490	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK)	HCA2 induces t 5 _ 26259322 Pho2 induces t 5 _ 26259322 Core-2/l-branch 1 _ 26809634 RNA polymeras 1 _ 26809634 Pho2 induced by 126809634 Pho2 induced by 12680963 Pho2 induced by 126809	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter three_prime_UTR promoter
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460 AT4G18760 AT4G14030 AT4G14040 AT5G20490 AT4G38460	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR	HCA2 induces t 5 _ 26259322 Pho2 induces t 5 _ 26259322 Core-2/l-branch 1 _ 26809634 RNA polymeras 1 _ 26809634 Pho2 induced by 126809634 Pho2 induced by 12680963 Pho2 induced by 126809	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter promoter promoter promoter three_prime_UTR three_prime_UTR
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460 AT4G18760 AT4G14030 AT4G14040 AT5G20490 AT4G38460 AT1G76490	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR HYDROXY METHYLGLUTARYL COA REI	HCA2 induces t 5_25259322 Phototropic-resi 1_25466745 Core-2/I-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372 pre-IRNA; IRNA 5_3287686 Haloacid dehalc 5_3287686 receptor like prc 4_10309565 selenium-bindin 4_8100507 selenium-bindin 4_8100507 Encodes a mer 5_6937874 geranylgeranyl i 4_17996035 Encodes a 3-hy 1_28699598	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR intergenic
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460 AT4G18760 AT4G14030 AT4G14040 AT5G20490 AT4G38460 AT1G76490 AT5G14545	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR HYDROXY METHYLGLUTARYL COA REI MICRORNA398B (MIR398B)	HCA2 induces t 5_25259322 Phototropic-resi 1_25466745 Core-2/I-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372 pre-IRNA; IRNA 5_3287686 Haloacid dehalc 5_3287686 receptor like prc 4_10309565 selenium-bindin 4_8100507 selenium-bindin 4_8100507 Encodes a merr 5_6937874 geranylgeranyl i 4_17996035 Encodes a 3-hy 1_28699598 Encodes a micr 5_4690709 unknown proteir 5_4495792 aminopeptidase 5_4495792	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR promoter promoter three_prime_utre promoter
AT1G67900 AT1G71070 AT1G71080 AT2G30100 AT5G10450 AT4G18760 AT4G14030 AT4G14040 AT1G20490 AT4G38460 AT1G76490 AT5G13950	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR HYDROXY METHYLGLUTARYL COA REI MICRORNA398B (MIR398B) na	HCA2 induces t 5 _ 26259322 Phototropic-res; 1 _ 25466745 Core-2/I-branch 1 _ 26809634 RNA polymeras 1 _ 26809634 pentatricopeptic 2 _ 12847372 pre-IRNA; IRNA 5 _ 3287686 Haloacid dehalc 5 _ 3287686 Haloacid dehalc 5 _ 3287686 selenium-bindin 4 _ 8100507 selenium-bindin 4 _ 8100507 selenium-bindin 4 _ 8100507 seleniem-bindin 4 _ 8100507 seleniem-bindin 4 _ 8100507 seleniem-bindin 4 _ 8100507 seleniem-bindin 5 _ 4810507 geranylgeranyl 1 _ 17996035 Encodes a 3-hy 1 _ 26699598 Encodes a micr 5 _ 4690709 unknown proteir 5 _ 4495792	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR intergenic promoter downstream
AT1667900 AT1G71070 AT1G71070 AT1G71080 AT2G30100 AT5G10450 AT4G18760 AT4G14040 AT4G14040 AT5G20490 AT4G38460 AT1G76490 AT5G13550 AT5G13950 AT5G13940	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR HYDROXY METHYLGLUTARYL COA REI MICRORNA398B (MIR398B) na na	HCA2 induces t 5 _ 26259322 Phototropic-res; 1 _ 25466745 Core-2/I-branch 1 _ 26809634 RNA polymeras 1 _ 26809634 RNA polymeras 1 _ 26809634 pentatricopeptic 2 _ 12847372 pre-IRNA; IRNA 5 _ 3287686 Haloacid dehalc 5 _ 3287686 receptor like prc 4 _ 10309565 selenium-bindin 4 _ 8100507 selenium-bindin 5 _ 48109507 geranylgeranyl 1 _ 17996035 Encodes a 3-by 1 _ 28699598 Encodes a micn 5 _ 4690709 unknown proteir 5 _ 4495792 aminopeptidase 5 _ 4495792 Plant stearoyl-a 3 _ 561850 Plant stearoyl-a 3 _ 561850	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR intergenic promoter downstream promoter
AT1G67900 AT1G71070 AT1G71070 AT1G71080 AT2G30100 AT5G10450 AT5G10460 AT4G14030 AT4G14040 AT5G20490 AT4G38460 AT1G76490 AT5G13545 AT5G13950 AT5G13940 AT3G02620	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR HYDROXY METHYLGLUTARYL COA REI MICRORNA398B (MIR398B) na na na	HCA2 induces t 5 _25259322 Phototropic-resi 1 _25466745 Core-2/I-branch 1 _26809634 RNA polymeras 1 _26809634 pentatricopeptic 2 _12847372 pre-IRNA; IRNA 5 _3287686 Haloacid dehalc 5 _3287686 receptor like prc 4 _10309565 selenium-bindin 4 _8100507 selenium-bindin 4 _8100507 selenium-bindin 4 _8100507 Encodes a mer 5 _6937874 geranylgeranyl 4 _17996035 Encodes a micn 5 _4690709 unknown proteir 5 _4495792 aminopeptidase 5 _4495792 Plant stearoyl-a 3 _561850 Plant stearoyl-a 3 _561850 Sterile alpha mc 3 _2280090	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_utR intergenic promoter downstream promoter three_prime_UTR
AT1G67900 AT1G71070 AT1G71070 AT1G71080 AT2G30100 AT5G10450 AT5G10460 AT4G14030 AT4G14030 AT4G14040 AT5G20490 AT4G38460 AT5G13950 AT5G13950 AT5G13950 AT3G02630 AT3G02630 AT3G02630 AT3G07170 AT5G14550	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR HYDROXY METHYLGLUTARYL COA REI MICRORNA398B (MIR398B) na na na na	HCA2 induces t 5_25259322 Phototropic-resi 1_25466745 Core-2/I-branch 1_26809634 RNA polymeras 1_26809634 pentatricopeptic 2_12847372 pre-tRNA; tRNA 5_3287686 Haloacid dehalc 5_3287686 receptor like prc 4_10309565 selenium-bindin 4_8100507 selenium-bindin 4_8100507 Encodes a merr 5_6937874 geranylgeranyl 1_477996035 Encodes a 3-hy 1_28699598 Encodes a micn 5_4690709 unknown proteir 5_4495792 Plant stearoyl-a 3_561850 Plant stearoyl-a 3_561850 Plant stearoyl-a 3_280090 Core-2/I-branch 5_4690709	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter three_prime_UTR promoter three_prime_UTR intergenic promoter three_prime_UTR promoter promoter three_prime_UTR promoter promoter intergenic
AT1G67900 AT1G71070 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460 AT4G14030 AT4G14040 AT4G20490 AT4G38460 AT1G76490 AT5G13940 AT5G13940 AT3G02620 AT3G02620 AT3G02630 AT3G07170 AT5G14545 AT5G14540	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR HYDROXY METHYLGLUTARYL COA REI MICRORNA398B (MIR398B) na na na na	HCA2 induces t 5 _ 26259322 Pho2 induces t 5 _ 26259322 Pho2 induces t 5 _ 26369634 RNA polymeras 1 _ 26809634 RNA polymeras 1 _ 26809634 pentatricopeptic 2 _ 12847372 pre-IRNA; IRNA 5 _ 3287686 Haloacid dehalc 5 _ 3287686 receptor like prc 4 _ 10309565 selenium-bindin 4 _ 8100507 selenium-bindin 4 _ 8100507 selenium-bindin 4 _ 8100507 selenium-bindin 4 _ 8100507 selenium-bindin 5 _ 48109507 selenium-bindin 5 _ 48109507 selenium-bindin 5 _ 4895794 geranylgeranyl 1 _ 17996035 Encodes a 3-by 1 _ 2699598 Encodes a micn 5 _ 4690709 unknown proteir 5 _ 4495792 aminopeptidase 5 _ 4495792 aminopeptidase 5 _ 4495792 Plant stearoyl-a 3 _ 561850 Plant stearoyl-a 3 _ 561850 Sterile alpha mc 3 _ 2280090 FUNCTIONS IN 5 _ 4690709 FUNCTIONS IN 5 _ 4690709	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR intergenic promoter downstream promoter three_prime_UTR promoter three_prime_UTR promoter
AT1667900 AT1671070 AT1671080 AT2G30100 AT5G10455 AT5G10460 AT4G18760 AT4G14030 AT4G14040 AT5G20490 AT4G38460 AT1G76490 AT5G13950 AT5G13950 AT5G13940 AT3G02620 AT3G02630 AT3G07170 AT5G14540 AT3G04504 AT3G04504 AT3G04504	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR HYDROXY METHYLGLUTARYL COA REI MICRORNA398B (MIR398B) na na na na na na	HCA2 induces t 5 _25259322 Phototropic-resi 1 _25466745 Core-2/I-branch 1 _26809634 RNA polymeras 1 _26809634 pentatricopeptic 2 _12847372 pre-tRNA; fRNA 5 _3287686 Haloacid dehalc 5 _3287686 receptor like prc 4 _10309565 selenium-bindin 4 _8100507 selenium-bindin 4 _8100507 selenium-bindin 4 _8100507 Encodes a mer 5 _6937874 geranylgeranyl 4 _1798035 Encodes a micn 5 _4690709 unknown proteir 5 _4495792 aminopeptidase 5 _4495792 plant stearoyl-a 3 _561850 Sterile alpha mc 3 _2280090 Core-2/I-branch 5 _4690709 GUNCTIONS IN 5 _4690709 GUItaredoxin far 5 _6937874	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter promoter promoter promoter three_prime_UTR intergenic promoter three_prime_UTR promoter three_prime_UTR promoter three_prime_UTR promoter three_prime_UTR promoter intergenic promoter promoter proximal promoter proximal promoter proximal promoter
AT1G67900 AT1G71070 AT1G71070 AT1G71080 AT2G30100 AT5G10455 AT5G10460 AT4G14030 AT4G14040 AT4G20490 AT4G38460 AT1G76490 AT5G13940 AT5G13940 AT3G02620 AT3G02620 AT3G02630 AT3G07170 AT5G14545 AT5G14540	HIGH CAMBIAL ACTIVITY2 (HCA2) na na na na na na RECEPTOR LIKE PROTEIN 51 (RLP51) SELENIUM-BINDING PROTEIN 1 (SBP1) SELENIUM-BINDING PROTEIN 2 (SBP2) (XIK) GERANYLGERANYL REDUCTASE (GGR HYDROXY METHYLGLUTARYL COA REI MICRORNA398B (MIR398B) na na na na na na	HCA2 induces t 5 _ 26259322 Pho2 induces t 5 _ 26259322 Pho2 induces t 5 _ 26369634 RNA polymeras 1 _ 26809634 RNA polymeras 1 _ 26809634 pentatricopeptic 2 _ 12847372 pre-IRNA; IRNA 5 _ 3287686 Haloacid dehalc 5 _ 3287686 receptor like prc 4 _ 10309565 selenium-bindin 4 _ 8100507 selenium-bindin 4 _ 8100507 selenium-bindin 4 _ 8100507 selenium-bindin 4 _ 8100507 selenium-bindin 5 _ 48109507 selenium-bindin 5 _ 48109507 selenium-bindin 5 _ 4895794 geranylgeranyl 1 _ 17996035 Encodes a 3-by 1 _ 2699598 Encodes a micn 5 _ 4690709 unknown proteir 5 _ 4495792 aminopeptidase 5 _ 4495792 aminopeptidase 5 _ 4495792 Plant stearoyl-a 3 _ 561850 Plant stearoyl-a 3 _ 561850 Sterile alpha mc 3 _ 2280090 FUNCTIONS IN 5 _ 4690709 FUNCTIONS IN 5 _ 4690709	5.69 5.69 5.69 5.69 5.69 5.69 5.69 5.69	intron promoter downstream promoter promoter promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR intergenic promoter downstream promoter three_prime_UTR promoter three_prime_UTR promoter

AT4G34410	REDOX RESPONSIVE TRANSCRIPTION	encodes a mem 4_16449844	5.68	proximal promoter
AT1G67400	na	ELMO/CED-12 1_25249933	5.67	intron
AT5G18610	na	Protein kinase s 5_6189628	5.67	proximal promoter
AT5G46170	na	F-box family prc 5_18716981	5.67	promoter
AT3G27845	na	pre-tRNA; tRNA 3_10324713	5.67	downstream
AT5G41401	na	This gene enco 5_16572144	5.67	exon
AT4G36010	na	Pathogenesis-re 4_17039577	5.67	exon
AT4G22200	POTASSIUM TRANSPORT 2/3 (KT2/3)	Encodes AKT2, 4_11750301	5.67	five_prime_UTR
AT3G27850	RIBOSOMAL PROTEIN L12-C (RPL12-C)		5.67	promoter
AT2G26770	STOMATAL CLOSURE-RELATED ACTIN		5.67	promoter
AT3G11415	na	na 3_3589489	5.66	exon
AT3G47610	na	transcription rec 3_17547141	5.66	proximal promoter
AT3G50550 AT3G50560	na	unknown proteir 3_18760876	5.66 5.66	intergenic
AT1G51090	na na	NAD(P)-binding 3_18760876 Heavy metal tra 1_18932694	5.66	downstream promoter
AT3G61820	na	Eukaryotic aspa 3_22881944	5.66	promoter
AT3G61825	na	pre-tRNA; tRNA 3_22881944	5.66	downstream
AT5G59450	na	GRAS family tra 5_23974604	5.66	promoter
AT4G35930	F-BOX STRESS INDUCED 4 (FBS4)	F-box family prc 4 17021303	5.65	intergenic
AT3G24520	HEAT SHOCK TRANSCRIPTION FACTOR		5.65	five prime UTR
AT4G11820	HYDROXYMETHYLGLUTARYL-COA SYN		5.65	promoter
AT1G15580	INDOLE-3-ACETIC ACID INDUCIBLE 5 (IA		5.65	promoter
AT2G43290	MULTICOPY SUPPRESSORS OF SNF4 I		5.65	proximal promoter
AT5G11460	na	Protein of unknc 5_3661984	5.65	intergenic
AT1G27050	na	Encodes a prote 1_9393541	5.65	promoter
AT4G35940	na	unknown proteir 4_17021303	5.65	promoter
AT2G47890	na	B-box type zinc 2_19608051	5.65	five_prime_UTR
AT3G24518	na	Potential natura 3_8941247	5.65	five_prime_UTR
AT3G06770	na	Pectin lyase-lik€ 3_2137524	5.65	promoter
AT4G14743	na	pseudogene, hy 4_8459437	5.65	proximal promoter
AT4G11990	na	Cell cycle regul: 4_7190047	5.65	promoter
AT4G16442	na	Uncharacterise(4_9274296	5.65	proximal promoter
AT4G16444	na	FUNCTIONS IN 4_9274296	5.65	downstream
AT2G38120	AUXIN RESISTANT 1 (AUX1)	Encodes an aux 2_15969738	5.64	intergenic
AT5G54150	na	unknown proteir 5_21979825	5.64	proximal promoter
AT1G25480	na	Aluminium activ 1_8947602	5.64	proximal promoter
AT1G79040	PHOTOSYSTEM II SUBUNIT R (PSBR)	Encodes for the 1_29735811	5.64	promoter
AT1G53230	TEOSINTE BRANCHED 1, CYCLOIDEA A	Encodes a merr 1_19853432	5.64	proximal promoter
AT3G26420	(ATRZ-1A)	Zinc finger-cont 3_9676482	5.63	intergenic
AT3G61050	(NTMC2T4)	Encodes a nov€ 3_22601834	5.63	intergenic
AT5G21920	(YLMG2)	YLMG2; FUNC 5_7242931	5.63	promoter
AT3G51860	CATION EXCHANGER 3 (CAX3)	cation exchange 3_19240113	5.63	intron
AT4G30340	DIACYLGLYCEROL KINASE 7 (DGK7)	encodes a diac _\ 4_14843771	5.63	proximal promoter
AT2G47585	MICRORNA164A (MIR164A)	Encodes a micr 2_19519355	5.63	proximal promoter
AT3G26440	na	Protein of unknc 3_9676482	5.63	promoter
AT3G26430	na	GDSL-like Lipas 3_9676482	5.63	intergenic
AT1G48430	na	Dihydroxyaceto 1_17906973	5.63	promoter
AT1G48440	na	B-cell receptor-; 1_17906973	5.63	promoter
AT1G13880	na	ELM2 domain-c 1_4748809	5.63	promoter
AT3G02832	na	na 3_617527	5.63	downstream
AT3G62240	na	RING/U-box suj 3_23036944	5.63	promoter
AT3G62245	na	pre-tRNA; tRNA 3_23036944	5.63	exon
AT5G38520	na	alpha/beta-Hydr 5_15423594	5.63	downstream
AT5G21930	P-TYPE ATPASE OF ARABIDOPSIS 2 (PA	P-Type ATPase 5_7242931	5.63	promoter
AT3G61060	PHLOEM PROTEIN 2-A13 (PP2-A13)	phloem protein: 3_22601834	5.63	proximal promoter
AT5G38530	TRYPTOPHAN SYNTHASE BETA TYPE 2	TSBtype2 encor 5_15423594	5.63	promoter
AT3G62250	UBIQUITIN 5 (UBQ5)	ubiquitin 5 (UBC 3_23036944	5.63	promoter
AT3G02830	ZINC FINGER PROTEIN 1 (ZFN1)	Encodes a zinc 3_617527	5.63	intergenic
AT3G12740	ALA-INTERACTING SUBUNIT 1 (ALIS1)	Physically intera 3_4049376	5.62	promoter
AT5G46690	BETA HLH PROTEIN 71 (bHLH071)	beta HLH protei 5_18947104	5.62	intron
AT5G27420	CARBON/NITROGEN INSENSITIVE 1 (CN			
AT3G01370			5.62	promoter
	CRM FAMILY MEMBER 2 (CFM2)	Encodes a prote 3_138891	5.62 5.62	promoter promoter
AT5G14570	HIGH AFFINITY NITRATE TRANSPORTE	Encodes a prote 3_138891 Encodes ATNR 5_4695768	5.62 5.62 5.62	promoter promoter exon
AT3G13405	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A)	Encodes a prote 3_138891 Encodes ATNR' 5_4695768 Encodes a micr 3_4360159	5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter
AT3G13405 AT5G14565	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C)	Encodes a prote 3_138891 Encodes ATNR' 5_4695768 Encodes a micn 3_4360159 Encodes a micn 5_4695768	5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon
AT3G13405 AT5G14565 AT3G01360	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prote 3_138891 Encodes ATNR 5_4695768 Encodes a micn 3_4360159 Encodes a micn 5_4695768 Family of unkno 3_138891	5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na	Encodes a prot 3_138891 Encodes ATNR 5_4695768 Encodes a micr 3_4360159 Encodes a micr 5_4695768 Family of unkno 3_138891 beta-1,4-N-acet 1_25455787	5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na	Encodes a prott 3_138891 Encodes ATNR 5_4695768 Encodes a micr 3_4360159 Encodes a micr 5_4695768 Family of unkno 3_138891 beta-1,4-N-acet 1_25455787 Protein of unkno 1_3008495	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter promoter proximal promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57210	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na	Encodes a prot 3_138891 Encodes ATNR 5_4695768 Encodes a micn 3_4360159 Encodes a micr 5_4695768 Family of unkno 3_138891 beta-1,4-N-acet 1_25455787 Protein of unkno 1_3008495 Protein of unkno 3_21174385	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter promoter proximal promoter promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57210 AT3G57220	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfe 3, 21174385	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter promoter promoter proximal promoter promoter promoter promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57210 AT3G57220 AT4G14420	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na na na	Encodes a prot 3, 138891 Encodes ATNR 5,4695768 Encodes a micr 3, 4360159 Encodes a micr 5,4695768 Family of unkno 3,138891 beta-1,4-N-acet 1,25455787 Protein of unknt 1,3008495 Protein of unknt 3,21174385 Glycosyl transfe 3,21174385 HR-like lesion-ir 4,8303929	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57210 AT3G57220 AT4G14420 AT3G18780	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na na na ACTIN 2 (ACT2)	Encodes a prott 3_138891 Encodes ATNR 5_4695768 Encodes a micr 3_4360159 Encodes a micr 5_4695768 Family of unkno 3_138891 beta-1,4-N-acet 1_25455787 Protein of unknc 1_3008495 Protein of unknc 3_21174385 Glycosyl transfe 3_21174385 HR-like lesion-ir 4_8303929 Encodes an act 3_6474724	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter promoter proximal promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57210 AT3G57220 AT4G14420 AT3G18780 AT2G39990	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na na na ACTIN 2 (ACT2) EUKARYOTIC TRANSLATION INITIATION	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter intergenic
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G9310 AT3G57210 AT3G57220 AT4G14420 AT3G18780 AT2G39990 AT1G79840	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na na na na na CTIN 2 (ACT2) EUKARYOTIC TRANSLATION INITIATION GLABRA 2 (GL2)	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta 1, 4.N-acet 1, 25455787 Protein of unknr 1, 3008495 Protein of unknr 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57220 AT4G14420 AT3G18780 AT2G39990 AT1G79840 AT4G37740	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na na na na na na na ACTIN 2 (ACT2) EUKARYOTIC TRANSLATION INITIATION GLABRA 2 (GL2) GROWTH-REGULATING FACTOR 2 (GR	Encodes a prott 3_138891 Encodes ATNR 5_4695768 Encodes a micr 3_4360159 Encodes a micr 5_4695768 Family of unkno 3_138891 beta-1,4-N-acet 1_25455787 Protein of unknt 1_3008495 Protein of unknt 3_21174385 Glycosyl transfe 3_21174385 HR-like lesion-ir 4_8303929 Encodes an act 3_6474724 translation initia 2_16696886 Glabra 2, a horr 1_30036740 Growth regulatir 4_17730917	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57220 AT4G14420 AT3G18780 AT2G39990 AT1G79840 AT4G37740 AT1G06390	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic five_prime_UTR
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57210 AT3G57220 AT4G14420 AT3G18780 AT2G39990 AT1G79840 AT4G37740 AT1G6390 AT1G18570	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta 1,4.N-acet 1, 25455787 Protein of unknc 1, 3008495 Protein of unknc 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 1669886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a mer 1, 6391034	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic prime_UTR
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G69310 AT3G572210 AT3G57220 AT4G14420 AT3G18780 AT2G39990 AT1G79840 AT4G37740 AT1G06390 AT1G7840 AT1G65390 AT5G57610	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micn 3, 4360159 Encodes a micn 5, 4695768 Family of unkno 3, 138891 Deta-1, 4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfs 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horn 1, 30036740 Growth regulatin 4, 17730917 encodes a GSK 1, 1946797 Encodes a men 1, 6391034 Protein kinase s 5, 23324565	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic five_prime_UTR three_prime_UTR promoter_
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57220 AT3G157220 AT3G18780 AT2G39990 AT1G79840 AT1G06390 AT1G18570 AT1G18570 AT3G1857610 AT3G06125	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Enmily of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a merr 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter promoter promoter promoter promoter promoter promoter promoter promoter intergenic promoter intergenic five_prime_UTR three_prime_UTR promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57210 AT3G57220 AT3G18780 AT1G78840 AT4G37740 AT1G08390 AT1G18570 AT1G6390 AT1G18570 AT5G57610 AT3G06125 AT3G18779	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta 1,4.N-acet 1, 25455787 Protein of unknc 1, 3008495 Protein of unknc 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 1669886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 177730917 encodes a merr 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic prime_UTR three_prime_UTR promoter promoter promoter promoter promoter promoter promoter promoter promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G69310 AT3G57220 AT3G57220 AT3G18780 AT2G39990 AT1G79840 AT1G68390 AT1G68390 AT1G18570 AT1G6857610 AT3G08125 AT3G18779 AT3G32389	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micn 3, 4360159 Encodes a micn 5, 4695768 Family of unkno 3, 138891 beta-1, 4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfs 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a mer 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable eli 3, 13330926	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter promoter promoter promoter promoter promoter promoter promoter promoter intergenic promoter intergenic promoter intergenic promoter
AT3G13405 AT5G14565 AT5G01360 AT1G67880 AT1G09310 AT3G57220 AT3G157220 AT3G18780 AT2G39990 AT1G79840 AT1G06390 AT1G08390 AT1G18570 AT3G18779 AT3G18779 AT3G367610 AT3G06125 AT3G18778 AT3G18778	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a merr 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable el 3, 13330926 ARM repeat sur, 1, 301054	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter intergenic promoter intergenic five_prime_UTR three_prime_UTR promoter intron
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G09310 AT3G57220 AT3G18780 AT3G57220 AT3G18780 AT1G79840 AT4G37740 AT1G08390 AT1G18570 AT5G57610 AT3G06125 AT3G18779 AT3G32388 AT1G1830 AT1G1830 AT1G1830 AT2G42300	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na na na consider the second of the s	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 Beta 1,4-N-acet 1, 25455787 Protein of unknc 1, 3008495 Protein of unknc 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16698886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 177730917 encodes a merr 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable els 3, 13330926 ARM repeat sur 1, 301054 basic helix-loop 2, 17624239	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic five prime_UTR three_prime_UTR promoter promoter promoter promoter promoter proximal promoter intron intron
AT3G13405 AT5G14565 AT5G01360 AT1G67880 AT1G67880 AT1G6787210 AT3G57220 AT4G14420 AT3G16780 AT1G79840 AT1G68390 AT1G68390 AT1G18570 AT3G18779 AT3G36725 AT3G18779 AT3G32389 AT1G01830 AT2G42300 AT2G42310	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta-1, 4-N-acet 1, 25455787 Protein of unknr 1, 3008495 Protein of unknr 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a merr 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable eli 3, 13330926 ARM repeat sur 1, 301054 Basic helix-loop 2, 17624239 unknown proteir 2, 17624239	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic promoter intergenic promoter proximal promoter intron intron proximal promoter
AT3G13405 AT5G14565 AT5G01360 AT1G67880 AT1G09310 AT3G57220 AT3G157220 AT3G18780 AT2G39990 AT1G79840 AT1G06390 AT1G08390 AT1G18570 AT3G06125 AT3G18778 AT3G06125 AT3G18778 AT1G01830 AT2G42300 AT2G42301 AT2G42310 AT2G42311	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes aTNR 5, 4695768 Encodes a micn 3, 4360159 Encodes a micn 5, 4695768 Encodes a micn 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horn 1, 30036740 Growth regulatin 4, 17730917 encodes a GSK 1, 1946797 Encodes a mern 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable el 3, 13330926 ARM repeat sur, 1, 301054 basic helix-loop 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter intergenic promoter intergenic five_prime_UTR three_prime_UTR promoter intron proximal promoter intergenic
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G69810 AT3G57210 AT3G57220 AT3G18780 AT2G39990 AT1G78840 AT4G37740 AT1G6390 AT1G18570 AT5G57610 AT3G08125 AT3G18779 AT3G32389 AT1G1830 AT2G42300 AT2G42300 AT2G42310 AT2G42300 AT2G42300	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na na na ACTIN 2 (ACT2) EUKARYOTIC TRANSLATION INITIATION GLABRA 2 (GL2) GROWTH-REGULATING FACTOR 2 (GR GSK3/SHAGGY-LIKE PROTEIN KINASE MYB DOMAIN PROTEIN 51 (MYB51) na na na na na na na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micn 3, 4360159 Encodes a micn 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unknc 1, 3008495 Protein of unknc 1, 3008495 Protein of unknc 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 1669886 Glabra 2, a horn 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a GSK 1, 1946797 Encodes a mern 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable els 3, 13330926 ARM repeat sur, 1, 301054 basic helix-loop 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239 SAUR-like auxir 2, 9090362 CONTAINS Inte 2, 17544284	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic five prime_UTR three_prime_UTR promoter promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter intron intron proximal promoter intergenic intergenic intron
AT3G13405 AT5G14565 AT5G01360 AT1G67880 AT1G09310 AT3G57220 AT3G157220 AT3G18780 AT2G39990 AT1G79840 AT1G06390 AT1G08390 AT1G18570 AT3G06125 AT3G18778 AT3G06125 AT3G18778 AT1G01830 AT2G42300 AT2G42301 AT2G42310 AT2G42311	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta-1, 4-N-acet 1, 25455787 Protein of unknr 1, 3008495 Protein of unknr 3, 21174385 Glycosyl transfs 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a merr 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable els 3, 13330926 ARM repeat sur 1, 301054 Basic helix-loop 2, 17624239 unknown proteir 2, 17624239 SAUR-like auxir 2, 9090362 CONTAINS Inte 2, 17544284 Homeodomain-1 4, 18236271	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic promoter intron intron proximal promoter intergenic intron promoter
AT3G13405 AT5G14565 AT5G01360 AT1G67880 AT1G69810 AT3G572210 AT3G57220 AT4G14420 AT3G18780 AT2G39990 AT1G79840 AT1G68390 AT1G18570 AT3G6125 AT3G18779 AT3G18779 AT3G32389 AT1G01830 AT2G42300 AT2G42310 AT2G42310 AT2G42240 AT4G33160	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micn 3, 4360159 Encodes a micn 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unknc 1, 3008495 Protein of unknc 1, 3008495 Protein of unknc 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 1669886 Glabra 2, a horn 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a GSK 1, 1946797 Encodes a mern 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable els 3, 13330926 ARM repeat sur, 1, 301054 basic helix-loop 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239 SAUR-like auxir 2, 9090362 CONTAINS Inte 2, 17544284	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic five prime_UTR three_prime_UTR promoter promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter intron intron proximal promoter intergenic intergenic intron
AT3G13405 AT5G14565 AT5G01360 AT1G67880 AT1G09310 AT3G57220 AT3G157220 AT3G18780 AT2G39990 AT1G79840 AT1G06390 AT1G678610 AT3G06125 AT3G18779 AT3G18779 AT3G2389 AT1G01830 AT2G42300 AT2G42300 AT2G42301 AT2G42300	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micn 3, 4360159 Encodes a micn 5, 4695768 Encodes a micn 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horn 1, 30036740 Growth regulatin 4, 17730917 encodes a GSK 1, 1946797 Encodes a mern 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable els 3, 13330926 ARM repeat sur 1, 301054 basic helix-loop 2, 17624239 unknown proteir 2, 17624239 SAUR-like auxir 2, 9090362 CONTAINS Inte 2, 17544284 Homeodomain-1 4, 18236271 transposable els 5, 5216061	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter intergenic promoter intergenic five_prime_UTR three_prime_UTR promoter intron intron proximal promoter intergenic intron promoter proximal promoter proximal promoter
AT3G13405 AT5G14565 AT5G01360 AT1G67880 AT1G69810 AT3G572210 AT3G572210 AT3G57220 AT4G14420 AT3G18780 AT2G39990 AT1G79840 AT1G18570 AT3G6125 AT3G18779 AT3G32389 AT1G01830 AT2G42300 AT2G42300 AT2G42300 AT2G42310 AT2G42300 AT2G42310 AT2G51250 AT3G15999 AT1G515990 AT1G63505 AT2G1500	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unknt 1, 3008495 Protein of unknt 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a mer 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable elt 3, 13330926 ARM repeat sur, 1, 301054 basic helix-loop 2, 17624239 unknown proteir 2, 17624239 SAUR-like auxir 2, 9090362 CONTAINS Inte 2, 17544284 Homeodomain-1, 4, 18236271 transposable elt 5, 5216061 pre-tRNA; tRNA; 5, 25784269 PFS2 encodes ; 2, 227204	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic promoter proximal promoter intron intergenic intron proximal promoter proximal promoter proximal promoter proximal promoter downstream proximal promoter
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G67880 AT1G69810 AT3G57210 AT3G57220 AT4G14420 AT2G39990 AT1G78840 AT4G37740 AT1G6890 AT1G18570 AT3G18779 AT3G2389 AT1G1830 AT2G42300 AT2G42310 AT2G42310 AT2G42310 AT2G42310 AT2G42300 AT2G42310 AT2G42300 AT2G42310 AT2G423160 AT5G615990 AT5G64505	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unknt 1, 3008495 Protein of unknt 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a mer 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable elt 3, 13330926 ARM repeat sur, 1, 301054 basic helix-loop 2, 17624239 unknown proteir 2, 17624239 SAUR-like auxir 2, 9090362 CONTAINS Inte 2, 17544284 Homeodomain-1, 4, 18236271 transposable elt 5, 5216061 pre-tRNA; tRNA; 5, 25784269 PFS2 encodes ; 2, 227204	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic promoter promoter promoter promoter promoter intergenic promoter downstream
AT3G13405 AT5G14565 AT5G01360 AT1G67880 AT1G09310 AT3G57220 AT3G157220 AT3G18780 AT2G39990 AT1G79840 AT1G06390 AT1G67870 AT3G6757610 AT3G06125 AT3G18779 AT3G2389 AT1G01830 AT2G42300 AT2G42301 AT2G42301 AT2G42300 AT2G42300 AT3G57610 AT3G57610 AT3G57610 AT3G57610 AT3G64505 AT3G64505 AT2G61500 AT3G64505	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na	Encodes a prot 3, 138891 Encodes a TMR 5, 4695768 Encodes a micr 3, 4360159 Encodes a micr 5, 4695768 Encodes a micr 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 16696886 Glabra 2, a horr 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a merr 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 6474724 transposable els 3, 13330926 ARM repeat sur 1, 301054 basic helix-loop 2, 17624239 unknown proteir 2, 17624239 SAUR-like auxir 2, 9090362 CONTAINS Inte 2, 1754284 Homeodomain-1 4, 18236271 transposable els 5, 52784269 PFS2 encodes : 2, 227204 UDP-D-glucuro 3, 8597282	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic five_prime_UTR three_prime_UTR promoter intron proximal promoter intergenic intron promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream proximal promoter intergenic intergenic
AT3G13405 AT5G14565 AT3G01360 AT1G67880 AT1G67880 AT1G69810 AT3G57220 AT3G18780 AT2G39990 AT1G78840 AT4G37740 AT3G57610 AT3G6870 AT5G57610 AT3G08125 AT3G18779 AT3G2389 AT1G1830 AT2G42300 AT2G42310 AT2G42310 AT2G42310 AT2G42316 AT3G01500 AT5G64505 AT2G01500 AT3G043820 AT3G42820 AT3G42820 AT3G42820	HIGH AFFINITY NITRATE TRANSPORTE MICRORNA169A (MIR169A) MICRORNA398C (MIR398C) na na na na na na ACTIN 2 (ACT2) EUKARYOTIC TRANSLATION INITIATION GLABRA 2 (GL2) GROWTH-REGULATING FACTOR 2 (GR GSK3/SHAGGY-LIKE PROTEIN KINASE MYB DOMAIN PROTEIN 51 (MYB51) na	Encodes a prot 3, 138891 Encodes ATNR 5, 4695768 Encodes a micn 3, 4360159 Encodes a micn 5, 4695768 Family of unkno 3, 138891 beta-1,4-N-acet 1, 25455787 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 1, 3008495 Protein of unkno 3, 21174385 Glycosyl transfe 3, 21174385 HR-like lesion-ir 4, 8303929 Encodes an act 3, 6474724 translation initia 2, 1669886 Glabra 2, a horn 1, 30036740 Growth regulatir 4, 17730917 encodes a GSK 1, 1946797 Encodes a mern 1, 6391034 Protein kinase s 5, 23324565 Unknown gene 3, 1848775 unknown proteir 3, 13330926 ARM repeat sur, 1, 301054 basic helix-loop 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239 unknown proteir 2, 17624239 Unknown gene 3, 1848775 Unknown proteir 2, 17624239 Unknown proteir 3, 18727630	5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.62 5.61	promoter promoter exon proximal promoter exon promoter intergenic promoter intergenic promoter intergenic promoter promo

AT1G17210	IAP-LIKE PROTEIN 1 (ILP1)	IAP-like protein 1_5884907	5.6	promoter
AT1G77690	LIKE AUX1 3 (LAX3)	Encodes an aux 1_29203514	5.6	promoter
AT3G52510	na	F-box associate 3_19469277	5.6	intergenic
AT5G61530	na	small G protein 5_24741977	5.6	promoter
AT1G09440	na	Protein kinase s 1_3047564	5.6	intron
AT3G13440	na	S-adenosyl-L-m 3_4379755	5.6	downstream
AT2G28150	na	FUNCTIONS IN 2_11999782	5.6	promoter
AT3G46610	na	Pentatricopeptic 3_17163371	5.6	proximal promoter
AT4G36550	na	ARM repeat sur 4_17248595	5.6	promoter
AT1G22530	PATELLIN 2 (PATL2)	PATELLIN 2 (P) 1_7958494	5.6	promoter
AT5G08590	SNF1-RELATED PROTEIN KINASE 2.1 (S		5.6	promoter
AT3G13445	TATA BINDING PROTEIN 1 (TBP1)	TBP (TATA binc 3_4379755	5.6	promoter
AT1G45130	BETA-GALACTOSIDASE 5 (BGAL5)	beta-galactosid: 1_17062567	5.59	proximal promoter
AT2G28260	CYCLIC NUCLEOTIDE-GATED CHANNEL		5.59	promoter
AT5G54500	FLAVODOXIN-LIKE QUINONE REDUCTA	PAS domain-co 4 12079847	5.59	promoter
AT4G23050	na		5.59	promoter
AT2G40640	na	RING/U-box su ₁ 2_16963223	5.59	promoter
AT2G40650 AT1G79030	na na	PRP38 family pi 2_16963223 Chaperone Dna 1 29734460	5.59 5.59	downstream proximal promoter
AT3G16180	na	Major facilitator 3_5483815	5.59	intron
AT4G13530	na	unknown proteir 4_7866608	5.59	promoter
AT4G35300	TONOPLAST MONOSACCHARIDE TRAN		5.59	intron
AT2G31230	ETHYLENE-RESPONSIVE ELEMENT BIN		5.58	promoter
AT5G49300	GATA TRANSCRIPTION FACTOR 16 (GA		5.58	promoter
AT1G30135	JASMONATE-ZIM-DOMAIN PROTEIN 8 (5.58	promoter
AT1G62035	MICRORNA171C (MIR171C)	Encodes a micr 1 22931493	5.58	proximal promoter
AT3G48240	na	Octicosapeptide 3_17868260	5.58	three_prime_UTR
AT4G33540	na	metallo-beta-lac 4_16130616	5.58	promoter
AT1G11410	na	S-locus lectin pi 1 3841097	5.58	promoter
AT3G20260	na	FUNCTIONS IN 3_7066783	5.58	promoter
AT3G01310	na	Phosphoglycera 3_102005	5.58	promoter
AT5G46710	na	PLATZ transcrit 5_18954705	5.58	promoter
AT3G46030	(HTB11)	HTB11; FUNCT 3_16914364	5.57	promoter
AT5G01550	LECTIN RECEPTOR KINASE A4.1 (LECR		5.57	proximal promoter
AT5G01560	LECTIN RECEPTOR KINASE A4.3 (LECR		5.57	downstream
AT3G14810	MECHANOSENSITIVE CHANNEL OF SM		5.57	proximal promoter
AT3G09670	na	Tudor/PWWP/N 3_2966350	5.57	promoter
AT2G40980	na	Protein kinase s 2_17101455	5.57	proximal promoter
AT3G46020	na	RNA-binding (R 3_16914364	5.57	proximal promoter
AT4G38480	na	Transducin/WD 4_18003809	5.57	promoter
AT3G46040	RIBOSOMAL PROTEIN S15A D (RPS15A		5.57	promoter
AT1G12950	ROOT HAIR SPECIFIC 2 (RSH2)	root hair specific 1_4419242	5.57	proximal promoter
AT4G38470	SERINE/THREONINE/TYROSINE KINASE		5.57	downstream
AT1G14000	VH1-INTERACTING KINASE (VIK)	Encodes a prot 1_4796805	5.57	proximal promoter
AT5G45010	DSS1 HOMOLOG ON CHROMOSOME V		5.56	promoter
AT3G62660	GALACTURONOSYLTRANSFERASE-LIK		5.56	intergenic
AT1G73390	na	Endosomal targ 1_27596180	5.56	proximal promoter
AT4G02055	na	pre-tRNA; tRNA 4_901240	5.56	exon
AT5G65650	na	Protein of unknc 5_26242199	5.56	intergenic
AT2G01840	na	transposable eli 2_379138	5.56	proximal promoter
AT2G39710	na	Encodes a Cyst 2_16561560	5.56	downstream
AT4G02060	PROLIFERA (PRL)	Member of the r 4_901240	5.56	exon
AT4G02050	SUGAR TRANSPORTER PROTEIN 7 (ST		5.56	promoter
AT2G40610	EXPANSIN A8 (EXPA8)	member of Alph 2 16951092	5.55	proximal promoter
AT1G75680	GLYCOSYL HYDROLASE 9B7 (GH9B7)	glycosyl hydrola 1_28420000	5.55	promoter
AT3G10920	MANGANESE SUPEROXIDE DISMUTASI		5.55	promoter
AT4G26542	na	Potential natura 4_13393575	5.55	proximal promoter
AT1G01800	na	NAD(P)-binding 1_293099	5.55	promoter
AT1G52780	na	Protein of unknc 1_19658092	5.55	proximal promoter
AT3G08030	na	Protein of unknc 3_2564046	5.55	five_prime_UTR
AT3G10915	na	Reticulon family 3_3417889	5.55	promoter
AT5G44290	na	Protein kinase s 5_17839752	5.55	intergenic
AT5G23750	na	Remorin family 5_8009653	5.55	downstream
AT5G44283	na	pre-tRNA; tRNA 5_17839752	5.55	promoter
AT5G44286	na	snoRNA; snoRI 5_17839752	5.55	promoter
AT5G23740	RIBOSOMAL PROTEIN S11-BETA (RPS1		5.55	promoter
AT5G44340	TUBULIN BETA CHAIN 4 (TUB4)	beta tubulin gen 5_17861714	5.55	proximal promoter
AT1G07725	EXOCYST SUBUNIT EXO70 FAMILY PRO		5.54	exon
AT5G13840	FIZZY-RELATED 3 (FZR3)	FIZZY-related 3 5_4471153	5.54	intron
AT5G13845	na	pre-tRNA; tRNA 5_4471153	5.54	downstream
AT1G07728	na	Potential natura 1_2395298	5.54	promoter
AT3G11390	na	Cysteine/Histidii 3_3569423	5.54	promoter
AT3G13594	na	unknown proteir 3_4441358	5.54	downstream
AT5G47700	na	60S acidic ribos 5_19329196	5.54	promoter
AT5G13850	NASCENT POLYPEPTIDE-ASSOCIATED		5.54	promoter
AT1G30120	PYRUVATE DEHYDROGENASE E1 BETA SEPALLATA3 (SEP3)	Encodes a puta 1_10586747 Member of the I 1 8596575	5.54	promoter
AT1G24260 AT3G10280	3-KETOACYL-COA SYNTHASE 14 (KCS1		5.54 5.53	promoter
AT2G45430	AT-HOOK MOTIF NUCLEAR-LOCALIZED		5.53	intergenic intergenic
AT2G45430 AT2G39350	ATP-BINDING CASSETTE G1 (ABCG1)		5.53	proximal promoter
AT2G39350 AT2G37590	DNA BINDING WITH ONE FINGER 2.4 (D		5.53	intergenic
AT3G10282	na	unknown pseud 3_3182470	5.53	intron
AT2G46600	na	Calcium-binding 2 19135829	5.53	promoter
AT4G39140	na	RING/U-box su ₁ 4_18233258	5.53	proximal promoter
AT5G41040	na na	Encodes a ferul 5_16430389	5.53	proximal promoter
AT2G23310	(ATRER1C1)	Encodes AtREF 2_9916658	5.52	proximal promoter
AT5G52570	BETA-CAROTENE HYDROXYLASE 2 (BE		5.52	promoter
			5.52	promoter
AT3G25500				P. JIIIOIOI
AT3G25500 AT5G41905	FORMIN HOMOLOGY 1 (AFH1)	Poly-L-proline-c 3_9255100 Encodes a micr. 5_16772664		intergenic
AT5G41905	FORMIN HOMOLOGY 1 (AFH1) MICRORNA166E (MIR166E)	Encodes a micr 5_16772664	5.52	intergenic promoter
AT5G41905 AT3G18210	FORMIN HOMOLOGY 1 (AFH1) MICRORNA166E (MIR166E) na	Encodes a micr 5_16772664 2-oxoglutarate (3_6240750	5.52 5.52	promoter
AT5G41905 AT3G18210 AT3G18215	FORMIN HOMOLOGY 1 (AFH1) MICRORNA166E (MIR166E) na na	Encodes a micr 5_16772664 2-oxoglutarate (3_6240750 Protein of unknc 3_6240750	5.52 5.52 5.52	promoter promoter
AT5G41905 AT3G18210	FORMIN HOMOLOGY 1 (AFH1) MICRORNA166E (MIR166E) na	Encodes a micr 5_16772664 2-oxoglutarate (3_6240750	5.52 5.52	promoter
AT5G41905 AT3G18210 AT3G18215 AT5G52580	FORMIN HOMOLOGY 1 (AFH1) MICRORNA166E (MIR166E) na na na	Encodes a micr 5_16772664 2-oxoglutarate (3_6240750 Protein of unknc 3_6240750 RabGAP/TBC d 5_21337272	5.52 5.52 5.52 5.52	promoter promoter proximal promoter

AT2G29280	na	pseudogene, trc 2_12585574	5.52	promoter
AT2G29290	na	NAD(P)-binding 2_12585574	5.52	promoter
AT2G38330	na	MATE efflux fan 2_16063787	5.52	proximal promoter
AT4G08871 AT4G28775	na na	transposable el 4_5650106 unknown proteir 4_14215525	5.52 5.52	proximal promoter downstream
AT4G28780	na	GDSL-like Lipas 4_14215525	5.52	promoter
AT5G57100	na	Nucleotide/sugs 5_23109035	5.52	promoter
AT1G58250	SABRE (SAB)	SABRE, putativ 1_21601703	5.52	promoter
AT2G28630 AT4G12730	3-KETOACYL-COA SYNTHASE 12 (KCS1 FASCICLIN-LIKE ARABINOGALACTAN 2		5.51 5.51	intergenic three_prime_UTR
AT2G37090	IRREGULAR XYLEM 9 (IRX9)	The IRX9 gene 2_15587241	5.51	downstream
AT5G58850	MYB DOMAIN PROTEIN 119 (MYB119)	Encodes a puta 5_23762561	5.51	proximal promoter
AT1G75170	na	Sec14p-like phc 1_28213788	5.51	promoter
AT4G33920 AT1G74640	na na	Protein phospha 4_16260597 alpha/beta-Hydr 1 28035645	5.51 5.51	promoter intergenic
AT1G62370	na	RING/U-box suj 1_23077280	5.51	intergenic
AT5G24810	na	ABC1 family prc 5_8522863	5.51	promoter
AT5G54720 AT1G14860	na NUDIX HYDROLASE HOMOLOG 18 (NUI	Ankyrin repeat f 5_22233420	5.51 5.51	promoter
AT4G03510	RING MEMBRANE-ANCHOR 1 (RMA1)	RMA1 encodes 4_1560623	5.51	intergenic proximal promoter
AT2G37080	ROP INTERACTIVE PARTNER 3 (RIP3)	Encodes RIP3 (2_15587241	5.51	proximal promoter
AT4G02380	SENESCENCE-ASSOCIATED GENE 21 (5.51	proximal promoter
AT5G24030 AT4G14960	SLAC1 HOMOLOGUE 3 (SLAH3) TUBULIN ALPHA-6 (TUA6)	Encodes a prote 5_8122887 Encodes an alpl 4_8550550	5.51 5.51	promoter promoter
AT4G11140	CYTOKININ RESPONSE FACTOR 1 (CRI		5.5	intergenic
AT1G11710	na	Pentatricopeptic 1_3951109	5.5	three_prime_UTR
AT1G18940	na	Nodulin-like / M: 1_6543703	5.5	promoter
AT1G02475 AT1G02480	na na	Polyketide cycla 1_515481 pre-tRNA; tRNA 1_515481	5.5 5.5	promoter promoter
AT4G36808	na	Potential natura 4_17342927	5.5	intergenic
AT1G25440	na	B-box type zinc 1_8935586	5.5	promoter
AT3G28040 AT4G36800	na	Leucine-rich rec 3_10434970	5.5	promoter
AT1G11720	RUB1 CONJUGATING ENZYME 1 (RCE1 STARCH SYNTHASE 3 (SS3)	Encodes a starc 1_3951109	5.5 5.5	promoter promoter
AT4G16265	(NRPB9B)	One of two high 4_9204212	5.49	promoter
AT2G25090	CBL-INTERACTING PROTEIN KINASE 16		5.49	proximal promoter
AT3G20770 AT2G29980	ETHYLENE-INSENSITIVE3 (EIN3)	Encodes EIN3 (3_7263230	5.49 5.49	five_prime_UTR
AT5G65710	FATTY ACID DESATURASE 3 (FAD3) HAESA-LIKE 2 (HSL2)	Endoplasmic rel 2_12783723 HAESA-like 2 (F 5 26288297	5.49	intron intergenic
AT5G57030	LUTEIN DEFICIENT 2 (LUT2)	Lutein-deficient 5_23077087	5.49	promoter
AT5G57020	MYRISTOYL-COA:PROTEIN N-MYRISTO		5.49	downstream
AT1G74840 AT2G23808	na na	Homeodomain-I 1_28117456 pseudogene of 12_10137507	5.49 5.49	promoter intergenic
AT2G25000	na	Xanthine/uracil 2_2180650	5.49	promoter
AT4G14746	na	CONTAINS Inte 4_8467123	5.49	proximal promoter
AT4G15420	na	Ubiquitin fusion 4_8826240	5.49	downstream
AT4G15430 AT5G07940	na na	ERD (early-resr 4_8826240 BEST Arabidop: 5_2533540	5.49 5.49	proximal promoter promoter
AT1G71100	RADIAL SWELLING 10 (RSW10)	Encodes a ribos 1_26815671	5.49	intron
AT2G23810	TETRASPANIN8 (TET8)	Member of TET 2_10137507	5.49	five_prime_UTR
AT3G20780	TOPOISOMERASE 6 SUBUNIT B (TOP6		5.49	intergenic
AT5G04490 AT1G30825	VITAMIN E PATHWAY GENE 5 (VTE5) DISTORTED TRICHOMES 2 (DIS2)	Encodes a prote 5_1279695 Involved in trich 1_10956460	5.49 5.48	promoter intergenic
AT2G28110	FRAGILE FIBER 8 (FRA8)	Homolog to AT5 2_11978110	5.48	exon
AT1G70300	K+ UPTAKE PERMEASE 6 (KUP6)	potassium trans 1_26483303	5.48	proximal promoter
AT3G54460 AT2G36080	na na	SNF2 domain-c 3_20167520 Encodes a plant 2_15150376	5.48 5.48	promoter intron
AT4G32920	na	glycine-rich prot 4_15887247	5.48	downstream
AT4G32915	na	FUNCTIONS IN 4_15887247	5.48	intergenic
AT1G54120	na	unknown proteir 1_20206730	5.48	promoter
AT1G70150 AT1G70160	na na	zinc ion binding; 1_26419799 unknown proteir 1_26419799	5.48 5.48	downstream promoter
AT3G04020	na	unknown proteir 3_1040443	5.48	promoter
AT4G36370	na	unknown proteir 4_17184482	5.48	proximal promoter
AT5G44070	CADMIUM SENSITIVE 1 (CAD1) na	Phytochelatin s ₁ 5_17734343	5.47 5.47	promoter
AT2G05790 AT2G05800	na	O-Glycosyl hydı 2_2201092 transposable eli 2_2201092	5.47	intron proximal promoter
AT4G24790	na	AAA-type ATPa 4_12777532	5.47	promoter
AT2G31110	na	Encodes a merr 2_13263532	5.47	proximal promoter
AT1G03457 AT2G31130	na na	RNA-binding (R 1_864287 unknown proteir 2 13263532	5.47 5.47	promoter downstream
AT5G43940	SENSITIVE TO HOT TEMPERATURES 5		5.47	promoter
AT2G30010	TRICHOME BIREFRINGENCE-LIKE 45 (T	Encodes a merr 2_12808738	5.47	intron
AT2G47260	WRKY DNA-BINDING PROTEIN 23 (WRK		5.47	five_prime_UTR
AT1G35670 AT1G11680	CALCIUM-DEPENDENT PROTEIN KINAS CYTOCHROME P450 51G1 (CYP51G1)		5.46 5.46	proximal promoter proximal promoter
AT5G24530	DOWNY MILDEW RESISTANT 6 (DMR6)		5.46	intron
AT4G37890	EMBRYO SAC DEVELOPMENT ARREST		5.46	exon
AT2G47240 AT4G37895	LONG-CHAIN ACYL-COA SYNTHASE 1 (5.46	intron
AT1G08230	na na	Potential natura 4_17813520 Codes for a H+- 1 2586155	5.46 5.46	promoter intron
AT1G18720	na	Protein of unknc 1_6459129	5.46	intron
AT5G17490	RGA-LIKE PROTEIN 3 (RGL3)	DELLA subfami 5_5764211	5.46	three_prime_UTR
AT2G46800 AT1G22880	ZINC TRANSPORTER OF ARABIDOPSIS CELLULASE 5 (CEL5)	Encodes a merr 2_19237407 cellulase 5 (CEI 1_8098145	5.46 5.45	promoter intergenic
AT1G22880 AT3G22820	CHALLAH-LIKE 1 (CLL1)	allergen-related 3_8072671	5.45	intergenic
AT1G03310	DEBRANCHING ENZYME 1 (DBE1)	Encodes a prote 1_813305	5.45	promoter
AT2G35860	FASCICLIN-LIKE ARABINOGALACTAN P		5.45	promoter
AT4G18880 AT2G35859	HEAT SHOCK TRANSCRIPTION FACTOR	member of Heal 4_10349635 Potential natura 2_15059721	5.45 5.45	promoter exon
AT1G02070	na	unknown proteir 1_368349	5.45	intergenic
AT1G14820	na	Sec14p-like phc 1_5106959	5.45	promoter
AT2G39420 AT1G22882	na na	alpha/beta-Hydr 2_16460238 Galactose-bindi 1_8098145	5.45 5.45	promoter proximal promoter
111022002	na .	Galactose-billar 1_0030143	5.75	proximal promoter

AT1G19050	RESPONSE REGULATOR 7 (ARR7)	Encodes a merr 1_6579378	5.45	promoter
AT3G50740	UDP-GLUCOSYL TRANSFERASE 72E1 (5.45	proximal promoter
AT3G04910	WITH NO LYSINE (K) KINASE 1 (WNK1)	Serine/threonine 3_1354724	5.45	five_prime_UTR
AT3G28860	ATP-BINDING CASSETTE B19 (ABCB19)	Belongs to the f 3_10876131	5.44	intron
AT5G51990	C-REPEAT-BINDING FACTOR 4 (CBF4)	encodes a mem 5_21116408		intergenic
AT2G47180	GALACTINOL SYNTHASE 1 (GolS1)	GolS1 is a gala: 2_19371310	5.44	proximal promoter
AT4G02130	GALACTURONOSYLTRANSFERASE 6 (C		5.44	intron
AT4G32690	HEMOGLOBIN 3 (GLB3)	Encodes a hem 4_15765244	5.44	promoter
AT5G45307	MICRORNA168B (MIR168B)	Encodes a micr 5_18359089	5.44	promoter
AT5G45310	na	unknown proteir 5_18359089	5.44	downstream
AT2G45300	na	encodes 3-phos 2_18677233	5.44	promoter
AT5G08240	na	unknown proteir 5_2651109		three_prime_UTR
AT5G42440	na	Protein kinase s 5_16974626	5.44	promoter
AT4G16141	na	GATA type zinc 4_9131363	5.44	intergenic
AT1G17850	na	Rhodanese/Cell 1_6149163	5.44	promoter
AT1G17860	na	Kunitz family try 1_6149163		promoter
AT1G32360 AT3G12835	na	Zinc finger (CC(1_11671589	5.44	proximal promoter
AT4G32680	na na	unknown proteir 3_4082762	5.44 5.44	intergenic promoter
AT5G40150	na	unknown proteir 4_15765244 Peroxidase sup 5_16060849	5.44	five_prime_UTR
AT5G51980	na	Transducin/WD 5_21116408	5.44	promoter
AT5G51980	THESEUS1 (THE1)	Encodes THESI 5 22082658	5.44	•
AT1G24120	ARG1-LIKE 1 (ARL1)	encodes a Dna. 1_8532242		proximal promoter
AT1G24120 AT2G16400	BEL1-LIKE HOMEODOMAIN 7 (BLH7)	BEL1-like home 2_7104426	5.43	promoter
AT1G64142	CONSERVED PEPTIDE UPSTREAM OPE		5.43	proximal promoter proximal promoter
AT2G37380	MEMBRANE-ASSOCIATED KINASE REG			intergenic
AT4G35490	MITOCHONDRIAL RIBOSOMAL PROTEIN		5.43	
AT1G51130	na		5.43	proximal promoter
AT1G31130	na	Nse4, compone 1_18942678	5.43	proximal promoter
AT1G13470 AT1G31540		Protein of unkno 1_4621874		promoter
	na	Disease resista 1_11293885	5.43	promoter
AT1G64140	na	BEST Arabidop: 1_23807790 Leucine-rich reg 1 9446400	5.43	proximal promoter
AT1G27190	na			intergenic
AT1G69570	na	Dof-type zinc fir 1_26163437	5.43	five_prime_UTR
AT5G62560	na	RING/U-box su ₁ 5_25109760	5.43	promoter
AT2G45140	PLANT VAP HOMOLOG 12 (PVA12)	Encodes a Plan 2_18610830	5.43	five_prime_UTR
AT4G00050	UNFERTILIZED EMBRYO SAC 10 (UNE1		5.43	intron
AT2G25900	(ATCTH)	putative Cys3Hi 2_11041762	5.42	five_prime_UTR
AT3G18290	BRUTUS (BTS)	Encodes BRUT 3_6272813		proximal promoter
AT3G61897	MICRORNA166B (MIR166B)	Encodes a micr 3_22921947		promoter
AT2G39200	MILDEW RESISTANCE LOCUS O 12 (ML			promoter
AT4G19420	na	Pectinacetyleste 4_10593223		proximal promoter
AT2G24380	na	pre-tRNA; tRNA 2_10373564	5.42	promoter
AT2G24390	na	AIG2-like (avirul 2_10373564	5.42	promoter
AT5G07760	na	formin homolog 5_2467807	5.42	promoter
AT1G10690	na	unknown proteir 1_3550761	5.42	promoter
AT3G55020	na	Ypt/Rab-GAP d 3_20394906		five_prime_UTR
AT3G61898	na	unknown proteir 3_22921947	5.42	proximal promoter
AT5G06320	NDR1/HIN1-LIKE 3 (NHL3)	encodes a prote 5_1931741		five_prime_UTR
AT5G06310	PROTECTION OF TELOMERES 1B (AtPC			intergenic
AT5G53160	REGULATORY COMPONENTS OF ABA I		5.42	promoter
AT3G53232	ROTUNDIFOLIA LIKE 1 (RTFL1)	ROTUNDIFOLI/ 3_19732233	5.42	proximal promoter
AT2G01830	WOODEN LEG (WOL)	Histidine kinase 2_368971		intron
AT3G54360	na	zinc ion binding: 3_20132174	5.41	promoter
AT3G54363	na	This gene enco 3_20132174	5.41	downstream
AT1G68400	na	leucine-rich rep 1_25647447		intron
AT5G18460	na	Protein of Unkn 5_6124009	5.4	exon
AT1G62480	na	Vacuolar calciur 1_23126627	5.4	proximal promoter
AT3G44100	na	MD-2-related lip 3_15867536	5.4	promoter
AT5G10745	na	unknown proteir 5_3396377	5.4	promoter
AT4G19390	na	Uncharacterised 4_10576519	5.4	promoter
AT3G59765	na	Unknown gene 3_22078335	5.4	exon
AT1G30590	na	RNA polymeras 1_10840897	5.4	
AT1G30600	na	Subtilase family 1_10840897	F 4	proximal promoter
AT5G28770			5.4	intergenic
	(BZO2H3)	bZIP protein BZ 5_10799599	5.39	intergenic proximal promoter
AT5G10860	CBS DOMAIN CONTAINING PROTEIN 3	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601	5.39 5.39	intergenic proximal promoter promoter
AT5G10870	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes choris 5_3430601	5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR
AT5G10870 AT3G05120	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes chorisl 5_3430601 Encodes a gibb 3_1430374	5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter
AT5G10870 AT3G05120 AT2G24240	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes chorisi 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284	5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter
AT5G10870 AT3G05120 AT2G24240 AT1G12080	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes chorisi 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciui 1_4082666	5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter
AT5G10870 AT3G05120 AT2G24240 AT1G12080 AT1G76870	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes chorisi 5_3430601 Encodes chorisi 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciuri 1_4082666 BEST Arabidop: 1_28859503	5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic
AT5G10870 AT3G05120 AT2G24240 AT1G12080 AT1G76870 AT2G19582	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes chorisi 5_343061 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 BTB/POZ doma 2_10308284 BTB/T Arabidop: 1_28859503 Potential natura 2_8475165	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic exon
AT5G10870 AT3G05120 AT2G24240 AT1G12080 AT1G76870 AT2G19582 AT5G64400	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA (INSENSITIVE DWARF1A (GID1A) na na na na	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes chorisi 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciu 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic exon promoter
AT5G10870 AT3G05120 AT2G24240 AT1G12080 AT1G76870 AT2G19582 AT5G64400 AT5G13390	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na NO EXINE FORMATION 1 (NEF1)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes choris: 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciu 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic exon promoter promoter promoter promoter
AT5G10870 AT3G05120 AT2G24240 AT1G12080 AT1G76870 AT2G19582 AT5G64400 AT5G13390 AT2G33150	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na NO EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes chorisi 5_3430601 Encodes chorisi 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciul 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic exon promoter promoter promoter promoter promoter
AT5G10870 AT3G05120 AT2G24240 AT1G12080 AT1G76870 AT2G19582 AT5G64400 AT5G13390 AT2G33150 AT2G19580	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na NO EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO TETRASPANIN2 (TET2)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes chorisi 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciu 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433 Member of TET 2_8475165	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic exon promoter promoter promoter promoter promoter promoter promoter promoter promoter
AT5G10870 AT3G05120 AT2G24240 AT1G12080 AT1G76870 AT2G19582 AT5G64400 AT5G13390 AT2G33150 AT2G19580 AT4G19700	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na NO EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO TETRASPANIN2 (TET2) (RING)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes choris: 5_3430601 Encodes choris: 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciu 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433 Member of TET 2_8475165 Encodes BOI (E 4_10716026	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic exon promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter
AT5G10870 AT3G05120 AT2G24240 AT1G12080 AT1G76870 AT2G19582 AT5G64400 AT5G13390 AT2G33150 AT2G19580 AT4G19700 AT3G07390	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na NO EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO TETRASPANIN2 (TET2) (RING) AUXIN-INDUCED IN ROOT CULTURES 1	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes choris 5_3430601 Encodes choris 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciul 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433 Member of TET 2_8475165 Encodes BOI (E 4_10716026) isolated from dif 3_2364282	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic exon promoter proximal promoter proximal promoter
AT5G10870 AT3G05120 AT2G24240 AT1G12080 AT1G76870 AT2G19582 AT5G64400 AT5G13390 AT2G33150 AT2G19580 AT4G19700 AT3G07390 AT5G59570	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na NO EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO TETRASPANIN2 (TET2) (RING) AUXIN-INDUCED IN ROOT CULTURES 1 BROTHER OF LUX ARRHYTHMO (BOA)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes a dibb 3_1430374 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciu 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433 Member of TET 2_8475165 Encodes BOI (E 4_10716026 isolated from dif 3_2364282 Encodes BOA (5_24003782	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic exon promoter promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter promoter
AT5G10870 AT3G05120 AT3G024240 AT1G12080 AT1G76870 AT2G19582 AT5G64400 AT5G13390 AT2G33150 AT2G19580 AT4G19700 AT3G07390 AT3G07390 AT5G59570 AT1G12840	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na NO EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO TETRASPANIN2 (TET2) (RING) AUXIN-INDUCED IN ROOT CULTURES 1 BROTHER OF LUX ARRHYTHMO (BOA) DE-ETIOLATED 3 (DET3)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes choris: 5_3430601 Encodes choris: 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciui 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433 Member of TET 2_8475165 Encodes BOI (E 4_10716026 isolated from dif 3_2364282 Encodes BOA (5_24003782 Encodes subun 1_4375359	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter intergenic exon promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter
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ATSG10870 AT3G05120 AT3G05120 AT1G2824240 AT1G12080 AT1G16870 AT2G19582 AT5G64400 AT5G13390 AT2G33150 AT2G19580 AT3G07390 AT3G07390 AT5G59570 AT1G12840 AT3G06110 AT3G06120 AT4G33467 AT1G12830 AT3G05120 AT4G33467 AT1G12830 AT3G12170 AT3G0553410 AT3G02550	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na no NO EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO TETRASPANIN2 (TET2) (RING) AUXIN-INDUCED IN ROOT CULTURES 1 BROTHER OF LUX ARRHYTHMO (BOA) DE-ETIOLATED 3 (DET3) FARNESYLATED PROTEIN 3 (FP3) GENOMES UNCOUPLED 5 (GUN5) MAPK PHOSPHATASE 2 (MKP2) MUTE (MUTE) na na na na na na POLY(A) POLYMERASE 2 (PAPS2)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes a dibb 3_1430374 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciu 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433 Member of TET 2_8475165 Encodes BOI (E 4_10716026 isolated from dif 3_2364282 Encodes BOO (5_24003782 Encodes BOD (5_2403782 Encodes an org 3_1845047 Encodes an anucl 3_1845047 Unknown proteir 4_16102323 unknown proteir 4_16102323 unknown proteir 1_122240 unknown proteir 5_21665466 Encodes a polyl 2_11030841	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.38	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter proximal promoter exon promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter promote
ATSG10870 AT3G05120 AT3G05120 AT3G05120 AT1G12080 AT1G176870 AT2G19582 AT5G64400 AT5G13390 AT2G19580 AT2G19580 AT3G07390 AT3G07390 AT3G07390 AT3G055570 AT1G12840 AT5G63530 AT3G061120 AT3G06120 AT3G06120 AT4G33467 AT1G12830 AT2G25870 AT1G12850 AT4G32550 AT5G53410 AT3G05250 AT5G53410 AT3G25850 AT4G34870	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na na na na NO EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO TETRASPANIN2 (TET2) (RING) AUXIN-INDUCED IN ROOT CULTURES 1 BROTHER OF LUX ARRHYTHMO (BOA) DE-ETIOLATED 3 (DET3) FARNESYLATED PROTEIN 3 (FP3) GENOMES UNCOUPLED 5 (GUN5) MAPK PHOSPHATASE 2 (MKP2) MUTE (MUTE) na na na na na na na pOLY(A) POLYMERASE 2 (PAPS2) ROTAMASE CYCLOPHILIN 5 (ROC5)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes chorisi 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciui 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433 Member of TET 1_2 8475165 Encodes BOI (E 4_10716026 isolated from dif 3_2364282 Encodes BOA (5_24003782 Encodes BOA (5_24003782 Encodes BOA (5_2403782 Encodes an org 3_1845047 Encodes a nucl 3_1845047 Encodes a basii 3_1845047 Encodes a basii 3_1845047 Encodes a poil (1_4375359 haloacid dehalo 2_11030841 Chaperone Dna 3_3880759 unknown proteir 4_1122240 unknown proteir 4_11620841	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.38	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter proximal promoter intergenic exon promoter promo
ATSG10870 AT3G05120 AT3G24240 AT1G12080 AT1G76870 AT2G19582 AT5G64400 AT5G13390 AT2G33150 AT2G19580 AT3G07390 AT3G07390 AT3G07390 AT3G05870 AT1G12840 AT3G06110 AT3G06110 AT3G06120 AT4G33467 AT1G12830 AT5G55570 AT5G55410 AT3G05120 AT4G25570 AT3G05120 AT4G33467 AT3G05120 AT4G33467 AT3G58710	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na no EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO TETRASPANIN2 (TET2) (RING) AUXIN-INDUCED IN ROOT CULTURES 1 BROTHER OF LUX ARRHYTHMO (BOA) DE-ETIOLATED 3 (DET3) FARNESYLATED PROTEIN 3 (FP3) GENOMES UNCOUPLED 5 (GUN5) MAPK PHOSPHATASE 2 (MKP2) MUTE (MUTE) na na na na na na na ROTAMASE CYCLOPHILIN 5 (ROC5) WRKY DNA-BINDING PROTEIN 69 (WRK	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes choris: 5_3430601 Encodes choris: 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciu 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433 Member of TET 2_8475165 Encodes BOI (E_4_10716026 isolated from dif 3_2364282 Encodes BOI (E_4_10716026 isolated from dif 3_2364282 Encodes BOI (5_24003782 Encodes BOI (5_24003782 Encodes a ubun 1_4375359 Famesylated or 5_25433136 Encodes a ubun 1_4375359 Famesylated or 5_25433136 Encodes a nucl 3_1845047 Encodes a nucl 3_1845047 Encodes a point 3_1845047	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.38	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter proximal promoter intergenic exon promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter intron
ATSG10870 AT3G05120 AT3G05120 AT3G05120 AT1G12080 AT1G176870 AT2G19582 AT5G64400 AT5G13390 AT2G19580 AT2G19580 AT3G07390 AT3G07390 AT3G07390 AT3G055570 AT1G12840 AT5G63530 AT3G061120 AT3G06120 AT3G06120 AT4G33467 AT1G12830 AT2G25870 AT1G12850 AT4G32550 AT5G53410 AT3G05250 AT5G53410 AT3G25850 AT4G34870	CBS DOMAIN CONTAINING PROTEIN 3 CHORISMATE MUTASE 2 (CM2) GA INSENSITIVE DWARF1A (GID1A) na na na na na na na na NO EXINE FORMATION 1 (NEF1) PEROXISOMAL 3-KETOACYL-COA THIO TETRASPANIN2 (TET2) (RING) AUXIN-INDUCED IN ROOT CULTURES 1 BROTHER OF LUX ARRHYTHMO (BOA) DE-ETIOLATED 3 (DET3) FARNESYLATED PROTEIN 3 (FP3) GENOMES UNCOUPLED 5 (GUN5) MAPK PHOSPHATASE 2 (MKP2) MUTE (MUTE) na na na na na na na pOLY(A) POLYMERASE 2 (PAPS2) ROTAMASE CYCLOPHILIN 5 (ROC5)	bZIP protein BZ 5_10799599 Encodes a singl 5_3430601 Encodes a singl 5_3430601 Encodes a gibb 3_1430374 BTB/POZ doma 2_10308284 Vacuolar calciu 1_4082666 BEST Arabidop: 1_28859503 Potential natura 2_8475165 BEST Arabidop: 5_25748652 Required for no 5_4292697 Encodes an org 2_14051433 Member of TET 2_8475165 Encodes BOI (E 4_10716026 isolated from dif 3_2364282 Encodes BOO (5_24003782 Encodes BOD (5_25433136 Encodes an org 3_1845047 Encodes an org 3_1845047 unknown proteir 4_16102323 unknown proteir 4_16102323 unknown proteir 4_16102323 unknown proteir 4_1122240 unknown proteir 5_21665466 Encodes a polyl 2_11030841 belongs to cyclc 4_16614121 member of WRI 3_21715638 Encodes an aub 2_15972778	5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.39 5.38	intergenic proximal promoter promoter three_prime_UTR promoter proximal promoter proximal promoter proximal promoter intergenic exon promoter promo

AT1G27750	na	nucleic acid bin 1_9662073	5.37	downstream
AT1G27752	na	Ubiquitin systen 1_9662073	5.37	promoter
AT1G38149	na	transposable ell 1_14307625	5.37	intergenic
AT1G61353	na	unknown proteir 1_22636555	5.37	downstream
AT2G31585	na	Unknown gene 2_13447088	5.37	intergenic
AT2G31590	na	unknown proteir 2_13447088	5.37	exon
AT2G31580	na	tRNAHis guanyl 2_13447088	5.37	proximal promoter
AT3G55700	na	UDP-Glycosyltr; 3_20669824	5.37	proximal promoter
AT2G28900	OUTER PLASTID ENVELOPE PROTEIN		5.37	promoter
AT4G30210	P450 REDUCTASE 2 (ATR2)	Encodes NADP 4_14796759	5.37	promoter
AT4G30220	SMALL NUCLEAR RIBONUCLEOPROTE		5.37	intergenic
AT2G02860	SUCROSE TRANSPORTER 2 (SUT2)	encodes a sucr 2_832620	5.37	promoter
AT1G14900	HIGH MOBILITY GROUP A (HMGA)	Encodes a prote 1_5138124	5.36	downstream
AT5G45630	na	CONTAINS Inte 5_18507076	5.36	proximal promoter
AT1G68190	na	B-box zinc finge 1_25559124	5.36	promoter
AT1G72100	na	late embryogen 1_27127837	5.36	exon
AT3G13880	na	Tetratricopeptid 3_4571703	5.36	promoter
AT1G14890	na	Plant invertase/ 1_5138124	5.36	downstream
AT4G02720	na	unknown proteir 4_1204147	5.36	downstream
AT4G02715	na	unknown proteir 4_1204147	5.36	proximal promoter
AT5G66530	na	Galactose muta 5_26555958	5.36	promoter
AT5G66535	na	pre-tRNA; tRNA 5_26555958	5.36	downstream
AT2G42600	PHOSPHOENOLPYRUVATE CARBOXYL		5.36	five_prime_UTR
AT3G44990	XYLOGLUCAN ENDO-TRANSGLYCOSY		5.36	promoter
AT2G28630	3-KETOACYL-COA SYNTHASE 12 (KCS1		5.35	intergenic
AT4G25960	ATP-BINDING CASSETTE B2 (ABCB2)	P-glycoprotein 2 4_13177344	5.35	promoter
AT3G15850	FATTY ACID DESATURASE 5 (FAD5)	Chloroplastic er 3_5360362	5.35	intron
AT2G02100	LOW-MOLECULAR-WEIGHT CYSTEINE-		5.35	promoter
AT3G61678	na	This gene enco 3_22823423	5.35	exon
AT3G61680	na	alpha/beta-Hydr 3_22823423	5.35	promoter
AT5G07770	na	Actin-binding FI 5_2474017	5.35	proximal promoter
AT1G15420	na	CONTAINS Inte 1_5304249	5.35	proximal promoter
AT1G15430	na	Protein of unknc 1_5304249	5.35	promoter
AT1G63820	na	CCT motif family 1_23685219	5.35	proximal promoter
AT1G63830	na	PLAC8 family pi 1_23685219	5.35	five_prime_UTR
AT3G15860	na	FUNCTIONS IN 3_5360362	5.35	intergenic
AT1G05675	na	UDP-Glycosyltr: 1_1702854	5.35	promoter
AT1G34640	na	peptidases; FUI 1_12688596	5.35	promoter
AT2G37020	na	Translin family r 2_15549004	5.35	three_prime_UTR
AT2G42020	na	pre-tRNA; tRNA 2_17538860	5.35	promoter
AT2G42030	na	RING/U-box sui 2_17538860	5.35	downstream
AT2G37025	TRF-LIKE 8 (TRFL8)	TRF-like 8 (TRF 2_15549004	5.35	promoter
AT1G05680	URIDINE DIPHOSPHATE GLYCOSYLTRA		5.35	intergenic
AT1G69740	(HEMB1)	Encodes a puta 1_26235836	5.34	intergenic
AT1G68560	ALPHA-XYLOSIDASE 1 (XYL1)	Encodes a bifur 1_25736456	5.34	intron
AT3G13520	ARABINOGALACTAN PROTEIN 12 (AGP		5.34	proximal promoter
AT4G17615	CALCINEURIN B-LIKE PROTEIN 1 (CBL1		5.34	proximal promoter
AT1G69750	CYTOCHROME C OXIDASE 19-2 (COX1)		5.34	five_prime_UTR
AT3G27785	MYB DOMAIN PROTEIN 118 (MYB118)	putative transcri 3_10291202	5.34	promoter
AT4G23490	na	Protein of unkno 4_12254675	5.34	promoter
AT4G30470	na	NAD(P)-binding 4_14892412	5.34	proximal promoter
AT1G70040	na na	Protein of unknr 1_26382060	5.34	three_prime_UTR
AT1G70050	• • • • • • • • • • • • • • • • • • • •	pre-tRNA; tRNA 1_26382060	5.34	downstream
AT3G01810	na	FUNCTIONS IN 3_288386	5.34 5.34	promoter
AT4G08240 AT4G08250	na na	unknown proteir 4_5196643 GRAS family tra 4_5196643	5.34	intron promoter
AT4G08230	na	pre-tRNA; tRNA 4 9815305	5.34	promoter
AT5G16220	na na	Octicosapeptide 5_5300729	5.34	•
AT4G36640	na	Sec14p-like phc 4_17279311	5.34	promoter promoter
AT3G51260	20S PROTEASOME ALPHA SUBUNIT PA		5.33	promoter
AT1G22600	na	Late embryoger 1_7991159	5.33	proximal promoter
AT4G27840	na	SNARE-like sur 4_13866507	5.33	promoter
AT4G26555	na	FKBP-like pepti 4 13406283	5.33	promoter
AT3G26510	na	Octicosapeptide 3_9710063	5.33	intergenic
AT3G27330	na	zinc finger (C3F 3_10119862	5.33	exon
AT3G27340	na	FUNCTIONS IN 3_10119862	5.33	proximal promoter
AT3G29805	na	transposable ele 3_11725317	5.33	intergenic
AT3G26511	na	unknown proteir 3 9710063	5.33	intergenic
AT4G18205	na	Nucleotide-suge 4_10073604	5.33	promoter
AT5G44572	na	unknown proteir 5_17969694	5.33	downstream
AT5G44574	na	unknown proteir 5_17969694	5.33	proximal promoter
AT3G61970	NGATHA2 (NGA2)	NGATHA2 (NG, 3_22951436	5.33	promoter
AT3G26500	PLANT INTRACELLULAR RAS GROUP-F		5.33	promoter
AT4G18197	PURINE PERMEASE 7 (PUP7)	Member of a far 4_10073604	5.33	intergenic
AT1G66970	SHV3-LIKE 2 (SVL2)	Encodes a merr 1_24996613	5.33	promoter
AT3G22420	WITH NO LYSINE (K) KINASE 2 (WNK2)	Encodes a merr 3_7946072	5.33	promoter
AT3G23920	BETA-AMYLASE 1 (BAM1)	Encodes a chloi 3_8641489	5.32	promoter
AT1G01240	na	unknown proteir 1_99810	5.32	promoter
AT4G38310	na	Galactosyl trans 4_17947270	5.32	proximal promoter
AT1G29600	na	Zinc finger C-x8 1_10343370	5.32	proximal promoter
AT3G54400	na	Eukaryotic aspa 3_20141715	5.32	intron
AT1G13260	RELATED TO ABI3/VP1 1 (RAV1)	Encodes an AP: 1_4535896	5.32	intergenic
AT4G35000	ASCORBATE PEROXIDASE 3 (APX3)	Encodes a micr 4_16667710	5.31	five_prime_UTR
AT3G62150	ATP-BINDING CASSETTE B21 (ABCB21)		5.31	promoter
AT1G04400	CRYPTOCHROME 2 (CRY2)	Blue light recept 1_1188568	5.31	promoter
AT2G47430	CYTOKININ-INDEPENDENT 1 (CKI1)	Encodes a puta 2_19465294	5.31	proximal promoter
AT1G04410	CYTOSOLIC-NAD-DEPENDENT MALATE		5.31	intergenic
AT5G43330	CYTOSOLIC-NAD-DEPENDENT MALATE		5.31	promoter
AT4G30190	H(+)-ATPASE 2 (HA2)	belongs to the F 4_14782282	5.31	intergenic
AT1G79310	METACASPASE 7 (MC7)	Encodes a puta 1_29833863	5.31	promoter
AT1G17940	na	Endosomal targ 1_6174632	5.31	proximal promoter
AT1G79290	na	pre-tRNA; tRNA 1_29833863	5.31	intergenic
AT1G79300	na	pre-tRNA; tRNA 1_29833863	5.31	downstream
AT3G62160	na	HXXXD-type ac 3_23013974	5.31	downstream

AT4G18810	na	NAD(P)-binding 4_10325957	5.31	promoter
AT4G18815	na	pre-tRNA; tRNA 4_10325957	5.31	downstream
AT1G79280	NUCLEAR PORE ANCHOR (NUA)	Encodes a 237- 1_29833863	5.31	proximal promoter
AT3G05800	ATBS1(ACTIVATION-TAGGED BRI1 SUP		5.3	proximal promoter
AT5G41070	DSRNA-BINDING PROTEIN 5 (DRB5)	Encodes a dout 5_16438109	5.3	promoter
AT5G39360 AT1G70140	EID1-LIKE 2 (EDL2)	EID1-like 2 (EDI 5_15754788 Encodes a grou 1_26415371	5.3 5.3	promoter
AT5G59505	FORMIN 8 (FH8) MICRORNA172E (MIR172E)	Encodes a grou 1_20415371 Encodes a micr 5_23989004	5.3	promoter intergenic
AT2G48000	na	Pentatricopeptic 2 19640991	5.3	promoter
AT2G03020	na	Heat shock prot 2_884296	5.3	promoter
AT1G77640	na	encodes a mem 1_29177273	5.3	proximal promoter
AT3G63233	na	This gene enco 3_23363217	5.3	proximal promoter
AT4G14615	na	unknown proteir 4_8386650	5.3	intergenic
AT5G41060 AT4G25672	na CONSERVED PEPTIDE UPSTREAM OPE	DHHC-type zinc 5_16438109	5.3 5.29	intergenic
AT1G63900	DIAP1-LIKE PROTEIN 1 (DAL1)	E3 Ubiquitin liga 1_23716253	5.29	promoter promoter
AT4G24660	HOMEOBOX PROTEIN 22 (HB22)	homeobox prote 4_12723689	5.29	intergenic
AT5G55090	MITOGEN-ACTIVATED PROTEIN KINASI		5.29	proximal promoter
AT4G01680	MYB DOMAIN PROTEIN 55 (MYB55)	Encodes a puta 4_719659	5.29	proximal promoter
AT2G41830	na	Uncharacterizec 2_17457717	5.29	proximal promoter
AT2G41835	na	zinc finger (C2F 2_17457717	5.29	downstream
AT4G25670 AT4G25680	na	unknown proteir 4_13087157	5.29 5.29	promoter
AT1G67720	na na	PPPDE putativ€ 4_13087157 Leucine-rich reg 1_25386396	5.29	proximal promoter five_prime_UTR
AT1G10747	na	Encodes a Mate 1 3575199	5.29	intergenic
AT1G10750	na	Protein of Unkn 1_3575199	5.29	exon
AT1G63880	na	Encodes a TIR- 1_23716253	5.29	promoter
AT1G76230	na	unknown proteir 1_28600690	5.29	promoter
AT2G21780	na	unknown proteir 2_9290747	5.29	promoter
AT1G28260	na na	Telomerase acti 1_9880607 ARM repeat sur 2_2217143	5.29 5.29	proximal promoter five_prime_UTR
AT2G05810 AT2G05812	na	Potential natura 2_2217143	5.29	five_prime_UTR
AT4G24652	na	Pseudogene of 4_12723689	5.29	proximal promoter
AT5G64180	na	unknown proteir 5 25676959	5.29	promoter
AT4G00710	BR-SIGNALING KINASE 3 (BSK3)	Encodes BR-sic 4_289798	5.28	promoter
AT1G28330	DORMANCY-ASSOCIATED PROTEIN-LIF		5.28	proximal promoter
AT3G22990	LEAF AND FLOWER RELATED (LFR)	Armadillo-repea 3_8167420	5.28	intergenic
AT3G01202	na	Potential natura 3_71528	5.28	downstream
AT3G01210 AT1G25422	na na	RNA-binding (R 3_71528	5.28 5.28	promoter promoter
AT1G25422 AT1G35614	na	unknown proteir 1_8918470 unknown proteir 1_13147708	5.28	proximal promoter
AT1G80831	na	unknown proteir 1_30376388	5.28	exon
AT1G25420	na	Regulator of Vp 1_8918470	5.28	intergenic
AT3G23690	na	basic helix-loop 3_8531205	5.28	promoter
AT3G23700	na	Nucleic acid-bin 3_8531205	5.28	downstream
AT3G01200	PPDK REGULATORY PROTEIN 2 (RP2)	Encodes a PPD 3_71528	5.28	promoter
AT3G05020	ACYL CARRIER PROTEIN 1 (ACP1)	encodes an acy 3_1393030	5.27	promoter
AT3G15580 AT1G02800	AUTOPHAGY 8H (APG8H) CELLULASE 2 (CEL2)	Encodes APG8, 3_5275221 Encodes a prote 1_616822	5.27 5.27	promoter proximal promoter
AT1G10690	na	unknown proteir 1_3548067	5.27	intergenic
AT3G15585	na	pre-tRNA; tRNA 3_5275221	5.27	intron
AT2G36854	na	unknown proteir 2_15470090	5.27	downstream
AT2G36860	na	pre-tRNA; tRNA 2_15470090	5.27	downstream
AT5G06700	na	Encodes a merr 5_2063459	5.27	promoter
AT5G63380	na	Encodes a pero 5_25387321	5.27	downstream
AT5G56975 AT5G63370	na na	pre-tRNA; tRNA 5_23054530 Protein kinase s 5_25387321	5.27 5.27	intergenic
AT2G27810	NUCLEOBASE-ASCORBATE TRANSPOR		5.27	promoter intergenic
AT2G27820	PREPHENATE DEHYDRATASE 1 (PD1)		5.27	promoter
AT3G05030	SODIUM HYDROGEN EXCHANGER 2 (N		5.27	intergenic
AT4G15910	DROUGHT-INDUCED 21 (DI21)	encodes a gen∈ 4_9029170	5.26	exon
AT1G02205	ECERIFERUM 1 (CER1)	Expression of th 1_418595	5.26	promoter
AT5G10140	FLOWERING LOCUS C (FLC)	MADS-box prot 5_3173359	5.26	downstream
AT1G17550	HOMOLOGY TO ABI2 (HAB2)	Protein Phosph; 1_6034134	5.26	promoter
AT4G18530 AT4G18520	na na	Protein of unknc 4_10217328 Pentatricopeptic 4_10217328	5.26 5.26	promoter promoter
AT4G18320 AT4G24350	na	Phosphorylase : 4_12609549	5.26	five_prime_UTR
AT1G79620	na	Leucine-rich rer 1_29957390	5.26	downstream
AT2G28625	na	unknown proteir 2_12273769	5.26	intergenic
AT1G02190	na	Fatty acid hydrc 1_418595	5.26	intergenic
AT1G22403	na	other RNA 1_7909844	5.26	promoter
AT4G35025 AT4G35030	na na	This gene enco 4_16675525 Protein kinase s 4_16675525	5.26 5.26	downstream promoter
AT5G64320	na	Pentatricopeptic 5 25725725	5.26	promoter
AT5G10130	na	Pollen Ole e 1 a 5_3173359	5.26	proximal promoter
AT1G79610	NA+/H+ ANTIPORTER 6 (NHX6)	Encodes an enc 1 29957390	5.26	promoter
AT5G64330	NON-PHOTOTROPIC HYPOCOTYL 3 (NI		5.26	proximal promoter
AT4G35020	RAC-LIKE 3 (RAC3)	A member of R(4_16675525	5.26	intergenic
AT2G23320	WRKY DNA-BINDING PROTEIN 15 (WRK		5.26	proximal promoter
AT3G09520	EXOCYST SUBUNIT EXO70 FAMILY PRO		5.25	promoter
AT1G66880 AT1G66890	na na	Protein kinase s 1_24955637 FUNCTIONS IN 1 24955637	5.25 5.25	downstream proximal promoter
AT1G66890 AT2G01220	na na	Nucleotidylyl tra 2 126772	5.25	intergenic
AT2G01220	1100	Reticulon family 2 126772	5.25	intergenic
	na			promoter
AT4G09630	na na	Protein of unkno 4_6083587	5.25	promoter
		Protein of unknc 4_6083587 NOL1/NOP2/su 1_2007373	5.25 5.25	promoter
AT4G09630 AT1G06560 AT1G19230	na na na	Protein of unknc 4_6083587 NOL1/NOP2/su 1_2007373 Riboflavin synth 1_6641145	5.25 5.25	promoter intergenic
AT4G09630 AT1G06560 AT1G19230 AT3G29240	na na na na	Protein of unknc 4_6083587 NOL1/NOP2/su 1_2007373 Riboflavin synth 1_6641145 Protein of unknc 3_11191482	5.25 5.25 5.25	promoter intergenic promoter
AT4G09630 AT1G06560 AT1G19230 AT3G29240 AT5G59960	na na na na na	Protein of unknc 4_6083587 NOL1/NOP2/su 1_2007373 Riboflavin synth 1_6641145 Protein of unknc 3_11191482 unknown proteir 5_24145984	5.25 5.25 5.25 5.25	promoter intergenic promoter proximal promoter
AT4G09630 AT1G06560 AT1G19230 AT3G29240 AT5G59960 AT5G59970	na na na na na na	Protein of unkn: 4_6083587 NOL1/NOP2/su 1_2007373 Riboflavin synth 1_6641145 Protein of unkn: 3_11191482 unknown proteir 5_24145984 Histone superfa 5_24145984	5.25 5.25 5.25 5.25 5.25	promoter intergenic promoter proximal promoter downstream
AT4G09630 AT1G06560 AT1G19230 AT3G29240 AT5G59960 AT5G59970 AT4G13350	na na na na na NSP (NUCLEAR SHUTTLE PROTEIN)-IN	Protein of unknr 4_6083587 NOL1/NOP2/su 1_2007373 Riboflavin synth 1_6641145 Protein of unknr 3_11191482 unknown proteir 5_24145984 Histone superfa 5_24145984 Encodes a GTP 4_7773694	5.25 5.25 5.25 5.25	promoter intergenic promoter proximal promoter downstream intron
AT4G09630 AT1G06560 AT1G19230 AT3G29240 AT5G59960 AT5G59970	na na na na na na	Protein of unknr 4_6083587 NOL1/NOP2/su 1_2007373 Riboflavin synth 1_6641145 Protein of unknr 3_11191482 unknown proteir 5_24145984 Histone superfa 5_24145984 Encodes a GTP 4_7773694 Aldolase superf 2_97887 Auxin biosynthe 4_14195893	5.25 5.25 5.25 5.25 5.25 5.25	promoter intergenic promoter proximal promoter downstream
AT4G09630 AT1G06560 AT1G19230 AT3G29240 AT5G59960 AT5G59970 AT4G13350 AT2G01140	na na na na na na NSP (NUCLEAR SHUTTLE PROTEIN)-IN PIGMENT DEFECTIVE 345 (PDE345)	Protein of unknc 4_6083587 NOL1/NOP2/su 1_2007373 Riboflavin synth 1_6641145 Protein of unknc 3_11191482 unknown proteir 5_24145984 Histone superfa 5_24145984 Encodes a GTP 4_7773694 Aldolase superfi 2_97887	5.25 5.25 5.25 5.25 5.25 5.25 5.25 5.25	promoter intergenic promoter proximal promoter downstream intron proximal promoter

AT1G64660	METHIONINE GAMMA-LYASE (MGL)	Encodes a func 1_24028579	5.24	promoter
AT3G27700	na	zinc finger (CC(3_10255845	5.24	intergenic
AT5G57710	na	Double Clp-N m 5_23383344	5.24	proximal promoter
AT5G10040	na	unknown proteir 5_3140646	5.24	intergenic
AT1G11050	na	Protein kinase s 1_3681725	5.24	promoter
AT1G17147	na	VQ motif-contail 1_5864781	5.24	proximal promoter
AT1G66100	na	Predicted to enc 1_24606654	5.24	promoter
AT2G04080	na	MATE efflux fan 2_1359649	5.24	promoter
AT2G20920	na	Protein of unknc 2_8998491	5.24	promoter
AT3G06770	na	Pectin lyase-like 3_2138290	5.24	proximal promoter
AT4G17765	na	pre-tRNA; tRNA 4_9873644	5.24	promoter
AT4G36550	na	ARM repeat sur 4_17249812	5.24	proximal promoter
AT5G25820	na	Exostosin family 5_9000983	5.24	proximal promoter
AT4G35580	NAC TRANSCRIPTION FACTOR-LIKE 9		5.24	promoter
AT1G12110	NITRATE TRANSPORTER 1.1 (NRT1.1)		5.24	promoter
AT3G27690	PHOTOSYSTEM II LIGHT HARVESTING		5.24	promoter
AT5G10030	TGACG MOTIF-BINDING FACTOR 4 (TG		5.24	intron
AT5G64530	XYLEM NAC DOMAIN 1 (XND1)	xylem NAC dor 5_25792654	5.24	proximal promoter
AT1G48410	ARGONAUTE 1 (AGO1)	Encodes an RN 1_17895038	5.23	proximal promoter
AT1G56030	na	RING/U-box sui 1_20956706	5.23	intergenic
AT1G06980	na	unknown proteir 1_2141985	5.23	intergenic
AT1G16630	na	unknown proteir 1_5685367	5.23	proximal promoter
AT1G16635	na	na 1_5685367	5.23	downstream
AT1G16640	na	AP2/B3-like trar 1_5685367	5.23	proximal promoter
AT1G65010 AT3G49720	na na	Putative role in 1_24149162	5.23 5.23	promoter
AT3G49725	na	unknown proteir 3_18442211 GTP-binding prr 3_18442211	5.23	promoter
AT2G38060	PHOSPHATE TRANSPORTER 4;2 (PHT4		5.23	downstream promoter
AT3G16500	PHYTOCHROME-ASSOCIATED PROTEI		5.23	proximal promoter
AT5G53280	PLASTID DIVISION1 (PDV1)	An integral oute 5_21611332	5.23	intergenic
AT3G53280 AT3G62720	XYLOSYLTRANSFERASE 1 (XT1)	Encodes a prot 3 23200961	5.23	promoter
AT5G02720	(NAK)	Encodes a canc 5_472751	5.22	intron
AT5G64740	CELLULOSE SYNTHASE 6 (CESA6)	Encodes a call 5_472731	5.22	five_prime_UTR
AT3G50830	COLD-REGULATED 413-PLASMA MEMB		5.22	•
AT1G52760	LYSOPHOSPHOLIPASE 2 (LysoPL2)	Encodes a lysor 1_19650532	5.22	promoter proximal promoter
AT4G16150	na	calmodulin bindi 4_9147554	5.22	proximal promoter
AT1G32670	na	unknown proteir 1_11816495	5.22	intergenic
AT1G52610	na	transposable eli 1_19600589	5.22	proximal promoter
AT1G52615	na na	unknown gene 1_19600589	5.22	
AT1G52015 AT5G66770	na na	GRAS family tra 5_26659607	5.22	exon proximal promoter
AT2G23430	(ICK1)	Encodes a cycli 2_9976150	5.22	intergenic
AT2G23430 AT2G37478	CONSERVED PEPTIDE UPSTREAM OPE		5.21	promoter
AT3G07060	EMBRYO DEFECTIVE 1974 (emb1974)	embryo defectiv 3_2232454	5.21	promoter
AT4G31820	ENHANCER OF PINOID (ENP)	A member of the 4_15397306	5.21	proximal promoter
AT1G72020	na	unknown proteir 1_27110579	5.21	promoter
AT2G13660	na	unknown proteir 2_5691992	5.21	downstream
AT2G13665	na	Potential natura 2 5691992	5.21	promoter
AT2G37470	na	Histone superfa 2_15737650	5.21	intergenic
AT2G37480	na	unknown proteir 2_15737650	5.21	promoter
AT3G07055	na	pre-tRNA; tRNA 3_2232454	5.21	downstream
AT2G42040	na	CONTAINS Inte 2_17542259	5.21	proximal promoter
AT4G20880	na	ethylene-respor 4_11179128	5.21	three_prime_UTR
AT5G35370	na	S-locus lectin pi 5_13591406	5.21	promoter
AT5G62200	na	Embryo-specific 5 24985823	5.21	promoter
AT3G07050	NUCLEOSTEMIN-LIKE 1 (NSN1)	Arabidopsis NS 3_2232454	5.21	promoter
AT4G38420	SKU5 SIMILAR 9 (sks9)	SKU5 similar 9 4_17982052	5.21	proximal promoter
AT4G13520	SMALL ACIDIC PROTEIN 1 (SMAP1)	Encodes a smal 4_7862503	5.21	proximal promoter
AT3G59280	THAXTOMIN A RESISTANT 1 (TXR1)	mutant exhibiter 3_21910728	5.21	promoter
AT2G24570	WRKY DNA-BINDING PROTEIN 17 (WRI		5.21	exon
AT1G21410	(SKP2A)	AtSKP2;1 is a h 1 7496996	5.2	promoter
AT5G54800	GLUCOSE 6-PHOSPHATE/PHOSPHATE	Encodes glucos 5_22258601	5.2	proximal promoter
AT4G15250	na	B-box type zinc 4_8711629	5.2	proximal promoter
AT1G23030	na	ARM repeat sur 1_8159233	5.2	downstream
AT1G21400	na	Thiamin diphost 1_7496996	5.2	intergenic
AT3G02270	na	Trimeric LpxA-li 3_451241	5.2	promoter
AT2G27360	na	GDSL-like Lipas 2_11706027	5.2	promoter
AT2G42425	na	Unknown gene 2_17662711	5.2	promoter
AT3G01516	na	unknown proteir 3_208315	5.2	downstream
AT3G17250	na	Protein phospha 3_5894944	5.2	promoter
AT3G01520	na	Adenine nucleol 3_208315	5.2	promoter
AT3G04420	NAC DOMAIN CONTAINING PROTEIN 48		5.2	proximal promoter
AT5G67440	NAKED PINS IN YUC MUTANTS 3 (NPY3		5.2	promoter
AT4G12420	(SKU5)	Encodes a prote 4_7349346	5.19	intron
AT1G35580	CYTOSOLIC INVERTASE 1 (CINV1)	CINV1 / A/N-Inv 1_13126633	5.19	proximal promoter
AT5G16760	INOSITOL (1,3,4) P3 5/6-KINASE 1 (ITPK		5.19	promoter
AT1G75830	LOW-MOLECULAR-WEIGHT CYSTEINE-		5.19	proximal promoter
AT2G42190	na	unknown proteir 2_17582715	5.19	promoter
AT1G18610	na	Galactose oxida 1_6409522	5.19	downstream
AT1G29430	na	SAUR-like auxir 1_10303587	5.19	promoter
AT2G28620 AT4G22190	na na	P-loop containir 2_12270846 unknown proteir 4_11743173	5.19 5.19	proximal promoter exon
AT4G22190 AT5G49510	PREFOLDIN 3 (PFD3)	prefoldin 3 (PFE 5 20084339	5.19	intergenic
AT1G06040	SALT TOLERANCE (STO)	Encodes salt tol 1_1829927	5.19	promoter
AT1G06040 AT1G29440	SMALL AUXIN UP RNA 63 (SAUR63)	SAUR-like auxir 1_10303587	5.19	intergenic
AT1G29440 AT1G18620	TON1 RECRUITING MOTIF 3 (TRM3)	unknown proteir 1_6409522	5.19	promoter
AT1G16620 AT4G14660	(NRPE7)	Non-catalytic su 4_8405965	5.19	intergenic
AT1G04220	3-KETOACYL-COA SYNTHASE 2 (KCS2)		5.18	exon
AT3G55950	CRINKLY4 RELATED 3 (CCR3)	CRINKLY4 relat 3_20757885	5.18	proximal promoter
AT4G11350	na	Protein of unknc 4_6903310	5.18	intron
AT2G44420			5.18	intergenic
	na	protein in-termii z maaaauss		
A12G44430	na na	protein N-termir 2_18335099 DNA-binding bri 2_18335099	5.18	
AT2G44430 AT4G05070		DNA-binding bri 2_18335099 Wound-respons 4_2594259		intron promoter
	na	DNA-binding bri 2_18335099 Wound-respons 4_2594259 This gene encoi 4_2594259	5.18	intron
AT4G05070	na na	DNA-binding bri 2_18335099 Wound-respons 4_2594259	5.18 5.18	intron promoter

AT1G04150	na	C2 calcium/lipid 1_1081030	5.18	downstream
AT1G27930	na	Function unkno 1_9731054	5.18	downstream
AT1G45010	na	TRAM, LAG1 ar 1_17015528	5.18	promoter
AT1G72240 AT2G37430	na na	unknown proteir 1_27191345 C2H2 and C2H(2_15706108	5.18 5.18	intergenic promoter
AT1G26930	na	Galactose oxida 1_9338447	5.18	proximal promoter
AT5G20020	RAS-RELATED GTP-BINDING NUCLEAR	A member of R/ 5_6760213	5.18	proximal promoter
AT5G20010	RAS-RELATED NUCLEAR PROTEIN-1 (F		5.18	promoter
AT1G79590 AT4G37790	SYNTAXIN OF PLANTS 52 (SYP52) (HAT22)	Encodes one of 1_29945309 Encodes homec 4 17764480	5.18 5.17	proximal promoter intergenic
AT1G04250	AUXIN RESISTANT 3 (AXR3)	Transcription re 1_1133876	5.17	proximal promoter
AT1G67730	BETA-KETOACYL REDUCTASE 1 (KCR1		5.17	five_prime_UTR
AT2G19980	na	CAP (Cysteine- 2_8629373	5.17	proximal promoter
AT5G58160 AT3G13370	na na	actin binding; Fl 5_23533525 unknown proteir 3_4344140	5.17 5.17	promoter intergenic
AT1G28140	na	unknown proteir 1_9832600	5.17	downstream
AT1G66090	na	Disease resistal 1_24602085	5.17	promoter
AT3G06435	na DBS1 LIKE 1 (DBI 1)	Expressed prote 3_1970898 PBS1-like 1 (PE 3_20557547	5.17 5.17	promoter
AT3G55450 AT4G29220	PBS1-LIKE 1 (PBL1) PHOSPHOFRUCTOKINASE 1 (PFK1)	phosphofructoki 4_14406534	5.17	promoter five_prime_UTR
AT5G58140	PHOTOTROPIN 2 (PHOT2)	Membrane-bour 5_23533525	5.17	intergenic
AT3G55440	TRIOSEPHOSPHATE ISOMERASE (TPI)		5.17	intergenic
AT2G40140 AT5G67480	(CZF1) BTB AND TAZ DOMAIN PROTEIN 4 (BT4	CZF1; CONTAll 2_16770491 BTB and TAZ di 5_26930704	5.16 5.16	proximal promoter intergenic
AT1G16858	CONSERVED PEPTIDE UPSTREAM OPE		5.16	proximal promoter
AT3G55830	ECTOPICALLY PARTING CELLS (EPC1)		5.16	promoter
AT1G15190	na	Fasciclin-like ar 1_5228111	5.16	three_prime_UTR
AT1G67510 AT3G20830	na na	Leucine-rich rer 1_25300941 AGC (cAMP-de 3_7285125	5.16 5.16	proximal promoter exon
AT3G55820	na	Fasciclin-like ar 3_20714919	5.16	downstream
AT5G04386	na	This gene encor 5_1238149	5.16	exon
AT5G47790 AT5G47800	na na	SMAD/FHA don 5_19353308 Phototropic-resi 5_19353308	5.16 5.16	three_prime_UTR
AT5G47600	REGULATORY PARTICLE NON-ATPASE		5.16	promoter promoter
AT1G44170	ALDEHYDE DEHYDROGENASE 3H1 (AL		5.15	proximal promoter
AT5G59040	COPPER TRANSPORTER 3 (COPT3)	encodes a mem 5_23838777	5.15	intergenic
AT2G45200 AT5G15150	GOLGI SNARE 12 (GOS12) HOMEOBOX 3 (HB-3)	Encodes a merr 2_18637255 homeobox-cont: 5 4918147	5.15 5.15	intergenic proximal promoter
AT1G17230	na	Leucine-rich rec 1 5890841	5.15	promoter
AT5G59050	na	unknown proteir 5_23838777	5.15	intergenic
AT2G05940	RPM1-INDUCED PROTEIN KINASE (RIPI		5.15	promoter
AT4G25360 AT1G04180	TRICHOME BIREFRINGENCE-LIKE 18 (T YUCCA 9 (YUC9)	YUCCA 9 (YUC 1_1103339	5.15 5.15	promoter proximal promoter
AT4G12720	(NUDT7)	Encodes a prot 4_7489946	5.14	three_prime_UTR
AT1G49160	(WNK7)	Encodes a merr 1_18182799	5.14	promoter
AT1G68310	AS1/2 ENHANCER7 (AE7)	Encodes a prote 1_25599399	5.14	promoter
AT3G11700 AT5G66700	FASCICLIN-LIKE ARABINOGALACTAN P HOMEOBOX 53 (HB53)	Encodes a hom 5_26631300	5.14 5.14	downstream intergenic
AT3G11710	LYSYL-TRNA SYNTHETASE 1 (ATKRS-1		5.14	intergenic
AT5G24710	na	Transducin/WD 5_8468421	5.14	promoter
AT5G24735 AT1G68300	na na	Unknown gene 5_8468421 Adenine nucleo 1_25599399	5.14 5.14	exon promoter
AT1G08300 AT1G75090	na	DNA glycosylas 1_28188642	5.14	intron
AT2G36340	na	DNA-binding str 2_15237813	5.14	downstream
AT2G36350	na	Protein kinase s 2_15237813	5.14	promoter
AT1G30350 AT2G46735	na na	Pectin lyase-lik€ 1_10707821 unknown proteir 2_19204860	5.14 5.14	intergenic exon
AT5G13600	na	Phototropic-resi 5_4380005	5.14	promoter
AT5G49555	na	FAD/NAD(P)-bii 5_20110814	5.14	promoter
AT5G49560 AT5G51110	na na	Putative methylt 5_20110814 Transcriptional (5_20779569	5.14 5.14	downstream
AT5G51110	POLYADENYLATE-BINDING PROTEIN 1		5.14	promoter intron
AT3G05650	RECEPTOR LIKE PROTEIN 32 (RLP32)	receptor like prc 3_1649060	5.14	promoter
AT3G05660	RECEPTOR LIKE PROTEIN 33 (RLP33)		5.14	three_prime_UTR
AT1G01650 AT5G43260	SIGNAL PEPTIDE PEPTIDASE-LIKE 4 (SI	chaperone prot 5_17358246	5.14 5.13	proximal promoter promoter
AT5G55520	na	CONTAINS Inte 5_22491392	5.13	promoter
AT1G73760	na	RING/U-box sui 1_27741427	5.13	promoter
AT3G14415 AT5G62950	na	Aldolase-type T 3_4818206 RNA polymeras 5 25266276	5.13 5.13	promoter
AT5G02950 AT5G03705	na na	pre-tRNA: tRNA 5 970890	5.13	proximal promoter promoter
AT5G11670	NADP-MALIC ENZYME 2 (NADP-ME2)	The malic enzyr 5_3754245	5.13	promoter
AT3G48530	SNF1-RELATED PROTEIN KINASE REGI		5.13	promoter
AT4G32400 AT3G02350	SODIUM HYPERSENSITIVE 1 (SHS1) GALACTURONOSYLTRANSFERASE 9 (0	Encodes a plas 4_15638382	5.13 5.12	promoter
AT4G32980	HOMEOBOX GENE 1 (ATH1)	Encodes transc 4_15918238	5.12	promoter promoter
AT3G16360	HPT PHOSPHOTRANSMITTER 4 (AHP4)		5.12	intron
AT1G20830	MULTIPLE CHLOROPLAST DIVISION SIT		5.12	promoter
AT4G35589 AT1G16740	na na	unknown proteir 4_16892868 Ribosomal prote 1_5727556	5.12 5.12	exon promoter
AT5G21105	na	Plant L-ascorba 5_7174826	5.12	intron
AT5G66755	na	pre-tRNA; tRNA 5_26653501	5.12	promoter
AT1G20820	na	pre-tRNA; tRNA 1_7242757	5.12 5.12	downstream
AT1G78460 AT1G78450	na na	SOUL heme-bir 1_29520006 SOUL heme-bir 1_29520006	5.12 5.12	proximal promoter proximal promoter
AT3G52500	na	Eukaryotic aspa 3_19467535	5.12	promoter
AT5G01450	na	RING/U-box su _i 5_186572	5.12	promoter
AT5G01460 AT2G28890	na POLTERGEIST LIKE 4 (PLL4)	LMBR1-like mei 5_186572 Encodes a prote 2_12409499	5.12 5.12	promoter proximal promoter
AT2G28890	POLTERGEIST LIKE 4 (PLL4) POLTERGEIST LIKE 4 (PLL4)	Encodes a prote 2_12408419	5.12	promoter
AT3G02230	REVERSIBLY GLYCOSYLATED POLYPE	RGP1 is a UDP 3_416181	5.12	intron
AT1G68825	ROTUNDIFOLIA LIKE 15 (RTFL15)	ROTUNDIFOLI/ 1_25870384	5.12	intron
AT4G35590 AT5G07120	RWP-RK DOMAIN-CONTAINING 5 (RKD! SORTING NEXIN 2B (SNX2b)	Encodes sorting 5_2209592	5.12 5.12	promoter promoter
	ζ/	*		•

AT3G11900				
	AROMATIC AND NEUTRAL TRANSPORT	encodes an ami 3 3760572	5.11	downstream
AT3G22968	CONSERVED PEPTIDE UPSTREAM OPE		5.11	intergenic
AT1G08930	EARLY RESPONSE TO DEHYDRATION (encodes a putal 1_2872661	5.11	proximal promoter
AT5G24920	GLUTAMINE DUMPER 5 (GDU5)	Encodes a merr 5_8584439	5.11	promoter
AT5G67060	HECATE 1 (HEC1)	HECATE 1 (HE: 5_26765456	5.11	proximal promoter
AT1G74490	na	Protein kinase s 1_27996786	5.11	promoter
AT3G05700	na	Drought-respon 3_1684765	5.11	promoter
AT3G59455	na	Encodes a Proti 3_21977540	5.11	downstream
AT3G59460	na	BEST Arabidop: 3_21977540	5.11	intron
AT4G30940	na	BTB/POZ doma 4_15054838	5.11	promoter
AT2G33830	na	Dormancy/auxir 2_14310871	5.11	proximal promoter
AT3G19500	na	basic helix-loop 3_6761521	5.11	proximal promoter
AT3G60750	na	Transketolase; 3_22453569	5.11	promoter
AT4G21170	na	Tetratricopeptid 4_11288755	5.11	promoter
AT4G27900	na	CCT motif family 4_13889244	5.11	proximal promoter
AT5G06210 AT5G06220	na	RNA binding (R 5_1879791	5.11	downstream
	na	LETM1-like prot 5_1879791	5.11	promoter
AT5G41800	na	Transmembrane 5_16733736	5.11	promoter
AT1G79410 AT1G23820	ORGANIC CATION/CARNITINE TRANSPORT SPERMIDINE SYNTHASE 1 (SPDS1)		5.11	promoter
AT3G05710	SYNTAXIN OF PLANTS 43 (SYP43)	Spermidine synl 1_8420130 Encodes a merr 3_1684765	5.11 5.11	promoter
				promoter
AT3G11910 AT4G30935	UBIQUITIN-SPECIFIC PROTEIN 33 (WEB		5.11	intergenic
	WRKY DNA-BINDING PROTEIN 32 (WRK		5.11	proximal promoter
AT4G30270	XYLOGLUCAN ENDOTRANSGLUCOSYL XYLOGLUCAN ENDOTRANSGLUCOSYL		5.11 5.11	proximal promoter
AT4G37800				intergenic
AT2G06530	(VPS2.1)	VPS2.1; CONT/ 2_2588475	5.1	downstream
AT5G18270	ARABIDOPSIS NAC DOMAIN CONTAININ		5.1 5.1	intergenic
AT3G13970	AUTOPHAGY 12 B (APG12B)	AUTOPHAGY 13_4613418	5.1	downstream
AT3G22840	EARLY LIGHT-INDUCABLE PROTEIN (EL			intergenic
AT1G06780 AT1G26945	GALACTURONOSYLTRANSFERASE 6 (C KIDARI (KDR)		5.1	promoter
AT1G26945 AT2G13460	,	Encodes a basii 1_9350298	5.1	proximal promoter
	na	transposable eli 2_5606522	5.1	proximal promoter
AT3G13965	na	pseudogene, hy 3_4613418	5.1	proximal promoter
AT5G53540	na	P-loop containir 5_21753021	5.1	proximal promoter
AT5G59260	na	Concanavalin A 5_23910701	5.1	proximal promoter
AT3G54140	PEPTIDE TRANSPORTER 1 (PTR1)	Encodes a di- a 3_20048737	5.1	promoter
AT2G06520	PHOTOSYSTEM II SUBUNIT X (PSBX)	Encodes a prote 2_2588475	5.1	promoter
AT2G47470	UNFERTILIZED EMBRYO SAC 5 (UNE5)		5.1	promoter
AT2G26910	ATP-BINDING CASSETTE G32 (ABCG32		5.09	proximal promoter
AT3G18290	BRUTUS (BTS)	Encodes BRUT 3_6273894	5.09	promoter
AT4G16650	na	O-fucosyltransfe 4_9372074	5.09	promoter
AT4G33400	na	Vacuolar import 4_16080698	5.09	promoter
AT1G10560	PLANT U-BOX 18 (PUB18)	Encodes a prote 1_3484441	5.09	promoter
AT1G58180	BETA CARBONIC ANHYDRASE 6 (BCA6		5.08	promoter
AT1G05470	COTYLEDON VASCULAR PATTERN 2 (C		5.08	intron
AT3G24520	HEAT SHOCK TRANSCRIPTION FACTOR		5.08	intergenic
AT3G60390	HOMEOBOX-LEUCINE ZIPPER PROTEIN		5.08	intron
AT3G27820	MONODEHYDROASCORBATE REDUCT		5.08	intergenic
AT3G24518	na	Potential natura 3_8943345	5.08	proximal promoter
AT2G41905	na	BEST Arabidop: 2_17495434	5.08	promoter
AT1G63290	na	Aldolase-type T 1_23473922	5.08	promoter
AT1G63295	na	Remorin family 1_23473922	5.08	downstream
AT1G72130	na	Major facilitator 1_27137145	5.08	promoter
AT2G18240	na	Rer1 family prot 2_7935068	5.08	promoter
AT2G44770	na	ELMO/CED-12 2_18456791	5.08	proximal promoter
AT1G73870	na	B-box type zinc 1_27778336	5.08	proximal promoter
AT3G27825		pre-tRNA; tRNA 3_10318427	5.08	
AT3G60380	na			downstream
A TO CO 7000	na	FUNCTIONS IN 3_22321420	5.08	proximal promoter
AT3G27830	na RIBOSOMAL PROTEIN L12-A (RPL12-A)	50S ribosomal r 3_10318427	5.08 5.08	proximal promoter promoter
AT1G05460	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3)	50S ribosomal r 3_10318427 Encodes a prot 1_1608306	5.08 5.08 5.08	proximal promoter promoter intergenic
AT1G05460 AT5G06290	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys	50S ribosomal r 3_10318427 Encodes a prott 1_1608306 Encodes a 2-Cy 5_1921870	5.08 5.08 5.08 5.07	proximal promoter promoter intergenic intergenic
AT1G05460 AT5G06290 AT5G61440	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXII	50S ribosomal r 3_10318427 Encodes a prot 1_1608306 Encodes a 2-Cy 5_1921870 Encodes a merr 5_24707171	5.08 5.08 5.08 5.07 5.07	proximal promoter promoter intergenic intergenic promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2)	50S ribosomal r 3_10318427 Encodes a prott 1_1608306 Encodes a 2-Cy 5_1921870 Encodes a merr 5_24707171 encodes a prott 1_564648	5.08 5.08 5.08 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT5G22250	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1	50S ribosomal ; 3_10318427 Encodes a prott 1_1608306 Encodes a 2-Cy 5_1921870 Encodes a merr 5_24707171 encodes a prott 1_564648 Encodes one of 5_7366638	5.08 5.08 5.08 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT5G22250 AT3G53280	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXII BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5)	50S ribosomal r 3_10318427 Encodes a prott 1_1608306 Encodes a 2-CV 5_1921870 Encodes a men 5_24707171 encodes a prott 1_564648 Encodes one of 5_7366638 cytochrome P4t 3_19755644	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT5G22250 AT3G53280 AT1G26770	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXII BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10)	50S ribosomal r 3_10318427 Encodes a prot 1_1608306 Encodes a 2-Cy 5_1921870 Encodes a mem 5_24707171 encodes a prot 1_564648 Encodes one of 5_7366638 cytochrome P4\$ 3_19755644 Encodes an ext 1_9258582	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT5G22250 AT3G53280 AT1G26770 AT5G06300	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7)	50S ribosomal r 3_10318427 Encodes a prot	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT5G22250 AT3G53280 AT1G26770 AT5G06300 AT5G26140	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9)	50S ribosomal r 3_10318427 Encodes a prott 1_1608306 Encodes a 2-CV, 5_1921870 Encodes a prott 1_564648 Encodes a prott 1_564648 Encodes one of 5_7366638 cytochrome P4\$ 3_19755644 Encodes an exp 1_9258582 Putative lysine t 5_1921870 LONELY GUY \$ 5_9132546	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT5G22250 AT3G53280 AT1G26770 AT5G06300 AT5G26140 AT3G20640	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXII BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na	50S ribosomal r 3_10318427 Encodes a prott 1_1608306 Encodes a 2-cv 5_1921870 Encodes a men 5_24707171 encodes a prote 1_564648 Encodes one of 5_7366638 cytochrome P4ť 3_19755644 Encodes an exr 1_9258582 Putative lysine c5_1921870 LONELY GUY 5_9132546 basic helix-loop 3_7214071	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter proximal promoter three_prime_UTR intergenic proximal promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT5G22250 AT3G53280 AT1G26770 AT5G06300 AT5G26140 AT3G20640 AT3G20640 AT3G08636	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na	50S ribosomal r 3_10318427 Encodes a prot	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter exon
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT5G22250 AT3G53280 AT1G26770 AT5G06300 AT5G26140 AT3G20640 AT3G08636 AT3G08640	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a 2-CV 5_1921870 Encodes a prott _1564648 Encodes a prott _1564648 Encodes one of 5_7366638 cytochrome P4£ 3_19755644 Encodes an exp 1_9258582 Putative lysine < 5_1921870 LONELY GUY £ 5_9132546 basic helix-loop 3_7214071 unknown proteir 3_2622748 Protein of unknc 3_2622748	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter exon promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT5G22250 AT3G53280 AT1G26770 AT5G06300 AT5G26140 AT3G08636 AT3G08636 AT3G08636 AT3G08636	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIR BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na na	50S ribosomal r 3_10318427 Encodes a prott 1_1608306 Encodes a 2-C\p 5_1921870 Encodes a men 5_24707171 encodes a prote 1_564648 Encodes one of 5_7366638 cytochrome P4ť 3_19755644 Encodes an exr 1_9258582 Putative lysine <_5_1921870 LONELY GUY \$ 5_9132546 basic helix-loop 3_7214071 unknown proteir 3_2622748 Protein of unkn 3_2622748 unknown proteir 1_11423843	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter three_prime_UTR intergenic proximal promoter three_prime_utra proximal promoter exon promoter promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT3G53280 AT1G26770 AT5G06300 AT5G26140 AT3G08640 AT3G08640 AT3G08646 AT3G08648 AT1G31835 AT1G31840	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na na na na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a 2-Cv 5_1921870 Encodes a mer 5_24707171 encodes a mer 5_24707171 encodes a prott _1_564648 Encodes one of 5_7366638 cytochrome P44 3_19755644 Encodes an ex; 1_9258582 Putative lysine c 5_1921870 LONELY GUY c 5_9132546 basic helix-loop 3_7214071 unknown proteir 3_2622748 Protein of unknc 3_2622748 Tetratricopeptid 1_11423843	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter exon promoter promoter promoter promoter promoter
AT1G05460 AT5G61440 AT5G61440 AT1G02640 AT3G632280 AT1G26770 AT5G06300 AT3G026140 AT3G08636 AT3G08636 AT3G08640 AT1G31835 AT1G31835 AT1G31840 AT2G32179	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na na na na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a 2-CV, 5_1921870 Encodes a prott _1564648 Encodes a prott _1564648 Encodes one of 5_7366638 cytochrome P46 3_19755644 Encodes an exr 1_9258582 Putative lysine c 5_1921870 LONELY GUY 6_9132546 basic helix-loop 3_7214071 unknown proteir 3_2622748 Protein of unknc 3_2622748 unknown proteir 1_11423843 Potential natura 2_13673427	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter exon promoter promoter promoter downstream
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT3G53280 AT1G26770 AT5G06300 AT3G26140 AT3G20640 AT3G08636 AT1G31840 AT1G31840 AT2G32179 AT2G41380	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na na na na na na na na	50S ribosomal r 3_10318427 Encodes a prott 1_1608306 Encodes a 2-CV, 5_1921870 Encodes a prott 1_564648 Encodes a prott 1_564648 Encodes one of 5_7366638 cytochrome P4ť 3_19755644 Encodes an exr 1_9258582 Putative lysine c 5_1921870 LONELY GUY '5_9132546 basic helix-loop 3_7214071 unknown proteir 3_2622748 unknown proteir 1_11423843 Tetratricopeptid 1_11423843 Tetratricopeptid 1_11423843 S-adenosyl-L-m 2_17249137	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter three_prime_UTR intergenic proximal promoter proximal promoter exon promoter promoter promoter downstream proximal promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT3G53280 AT3G53280 AT3G526140 AT3G08640 AT3G08640 AT1G31835 AT1G31840 AT2G32179 AT2G41380 AT1G76980	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a 2-Cv 5_1921870 Encodes a prott _1564648 Encodes a prott _1564648 Encodes one of 5_7366638 cytochrome P44 3_19755644 Encodes one sx 1_9258582 Putative lysine t 5_1921870 LONELY GUY \$ 5_9132546 basic helix-loop 3_7214071 unknown proteir 3_2622748 Protein of unknt 3_2622748 Protein of unknt 3_2622748 auknown proteir 1_11423843 Potential natura 2_13673427 S-adenosyl-Lm 2_17249137 BEST Arabidop: 1_28927652	5.08 5.08 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter exon promoter promoter downstream proximal promoter downstream proximal promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT3G52250 AT1G26770 AT5G06300 AT1G268140 AT3G20640 AT3G308636 AT1G31835 AT1G31840 AT2G32179 AT2G41380 AT1G76980 AT1G76980 AT1G76980 AT1G76980	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 7185 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na	50S ribosomal r 3_10318427 Encodes a prott 1_1608306 Encodes a 2-CV 5_1921870 Encodes a prott 1_564648 Encodes a prott 1_564648 Encodes one of 5_7366638 cytochrome P46 3_19755644 Encodes one of 5_7366638 cytochrome P46 3_19755644 Encodes an exp 1_9258582 Putative lysine c 5_1921870 LONELY GUY 6_9132546 basic helix-loop 3_7214071 unknown protei 3_2622748 Protein of unknc 3_2622748 unknown protei 1_11423843 Potential natura 2_13673427 S-adenosyl-L-m 2_17249137 BEST Arabidop: 1_28927652 plastid transcrip 2_13673427	5.08 5.08 5.08 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter exon promoter promoter downstream proximal promoter downstream proximal promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT3G53280 AT1G26770 AT5G06300 AT3G26140 AT3G20640 AT3G08636 AT1G31840 AT1G31840 AT2G32179 AT2G41380 AT1G76980 AT1G76980 AT1G76980 AT3G232180 AT3G232180	na RIBOSOMAL PROTEIN L12-A (RPL12-A) RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na na na na na na na PLASTID TRANSCRIPTIONALLY ACTIVE RALF-LIKE 24 (RALFL24)	50S ribosomal r 3_10318427 Encodes a prott 1_1608306 Encodes a 2-CV, 5_1921870 Encodes a prott 1_564648 Encodes a prott 1_564648 Encodes one of 5_7366638 cytochrome P4\$ 3_19755644 Encodes an exr 1_9258582 Putative lysine c 5_1921870 LONELY GUY \$ 5_9132546 basic helix-loop 3_7214071 unknown proteir 3_2622748 unknown proteir 1_11423843 Tetratricopeptid 1_11423843 Tetratricopeptid 1_11423843 Tetratricopeptid 1_11423843 Set 13	5.08 5.08 5.08 5.07 5.07 5.07 5.07 5.07 5.07 5.07 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter three_prime_UTR intergenic proximal promoter proximal promoter exon promoter promoter downstream proximal promoter proximal promoter proximal promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT3G652250 AT3G53280 AT1G26770 AT5G06300 AT5G26140 AT3G08640 AT3G08640 AT1G31835 AT1G31840 AT2G32179 AT2G41380 AT1G76980 AT1G76980 AT3G232805 AT1G16130	na RIBOSOMAL PROTEIN L12-A (RPL12-A) RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na na na na na na na RA RA RA RA RALFILETID TRANSCRIPTIONALLY ACTIVE RALF-LIKE 24 (RALFL24) WALL ASSOCIATED KINASE-LIKE 2 (WA	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a 2-Cv 5_1921870 Encodes a merr 5_24707171 encodes a merr 5_24707171 encodes a prott _1564648 Encodes one of 5_7366638 cytochrome P44 3_19755644 Encodes an ex; 1_9258582 Putative lysine c 5_1921870 LONELY GUY c 5_9132546 basic helix-loop 3_7214071 unknown proteir 3_2622748 Protein of unknc 3_2622748 Protein of unknc 3_2622748 anknown proteir 1_11423843 Potential natura 2_13673427 S-adenosyl-L-m 2_17249137 BEST Arabidop: 1_28927652 plastid transcrip 2_13673427 Member of a div 3_8585782 wall-associated 1_5525313	5.08 5.08 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter exon promoter promoter promoter downstream proximal promoter proximal promoter proximal promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT3G52250 AT3G53280 AT1G26770 AT5G06300 AT3G26140 AT3G20640 AT3G308636 AT1G31840 AT1G31835 AT1G31840 AT2G32179 AT2G41380 AT2G32179 AT2G41380 AT1G76980 AT1G76980 AT1G525620	na RIBOSOMAL PROTEIN L12-A (RPL12-A) RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na na na na na na na na PLASTID TRANSCRIPTIONALLY ACTIVE RALF-LIKE 24 (RALFL24) WALL ASSOCIATED KINASE-LIKE 2 (WAYUCCA6 (YUC66)	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a 2-Cv 5_1921870 Encodes a prott _1564648 Encodes a prott _1564648 Encodes one of 5_7366638 cytochrome P46 3_19755644 Encodes one of 5_7366638 cytochrome P46 3_19755644 Encodes an exp 1_9258582 Putative lysine c 5_1921870 LONELY GUY \$ 5_9132546 basic helix-loop 3_7214071 unknown protei 3_2622748 Protein of unknc 3_2622748 unknown protei 1_11423843 Potential natura 2_13673427 S-adenosyl-L-m 2_17249137 BEST Arabidop: 1_28927652 plastid transcrip 2_13673427 Member of a dis 3_8585782 wall-associated 1_5525313 YUCCA6 (YUCt 5_8934934	5.08 5.08 5.08 5.07	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter exon promoter promoter downstream proximal promoter downstream promoter promoter promoter promoter promoter promoter promoter promoter downstream proximal promoter promoter downstream downstream downstream
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AT1G05460 AT5G61440 AT5G61440 AT1G02640 AT3G52250 AT3G52280 AT1G26770 AT5G06300 AT3G26410 AT3G20640 AT3G20640 AT3G20840 AT1G31835 AT1G31840 AT1G31835 AT1G31840 AT1G76980 AT1G76980 AT1G6130 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G76980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT3G6980 AT3G6980 AT3G6980 AT3G6980 AT3G6980 AT3G6980 AT3G6980	na RIBOSOMAL PROTEIN L12-A (RPL12-A) RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na na na na na na na na na pLASTID TRANSCRIPTIONALLY ACTIVE RALF-LIKE 24 (RALFL24) WALL ASSOCIATED KINASE-LIKE 2 (WA YUCCA6 (YUC6) BCL-2-ASSOCIATED ATHANOGENE 3 (E COPPER/ZINC SUPEROXIDE DISMUTAS na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a 2-Cv 5_1921870 Encodes a prott _1564648 Encodes a prott _1564648 Encodes on of 5_7366638 cytochrome P44 3_19755644 Encodes on ext _19258582 Putative lysine t 5_1921870 LONELY GUY \$ 5_9132546 basic helix-loop 3_7214071 unknown proteii 3_2622748 Protein of unknt 3_2622748 Protein of unknt 3_2622748 unknown proteii 1_11423843 Potential natura 2_13673427 S-adenosyl-Lm 2_17249137 BEST Arabidop: 1_28927652 plastid transcrip 2_13673427 Member of a div 3_8585782 wall-associated 1_5525313 YUCCA6 (YUCt 5_8934934 A member of Ar 5_2265964 Encodes a cyto: 1_2827059 unknown proteii 3_10132965 FUNCTIONS IN 5_16451150 unknown proteii 5_16451150 unknown proteii 5_16451150 unknown proteii 1_13031098 Zinc finger C-x8_3_1951230 alpha/beta-Hydt 2_17778099	5.08 5.08 5.08 5.07 5.06	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter downstream proximal promoter downstream exon promoter downstream exon promoter downstream exon promoter downstream intergenic promoter five_prime_UTR proximal promoter promoter promoter promoter five_prime_UTR proximal promoter promoter promoter promoter promoter promoter five_prime_UTR proximal promoter
AT1G05460 AT5G61440 AT5G61440 AT1G02250 AT3G53280 AT1G26770 AT5G06300 AT3G526140 AT3G20640 AT3G20640 AT3G20640 AT3G20640 AT3G208640 AT1G31840 AT1G31840 AT1G31840 AT1G31840 AT2G32179 AT2G41380 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G6980 AT1G641110 AT1G435430 AT3G42690 AT2G42690 AT2G42700	na RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 7185 (CYP7185) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a prott _1608306 Encodes a prott _1564648 Encodes a prott _1564648 Encodes one of 5_7366638 cytochrome P4f 3_19755644 Encodes one of 5_7366638 cytochrome P4f 3_19755644 Encodes an exr 1_9258582 Putative lysine c 5_1921870 LONELY GUY f 5_9132546 basic helix-loop 3_7214071 unknown protei 1 3_2622748 Protein of unkm 3_2622748 Protein of unkm 3_2622748 unknown protei 1_11423843 Potential natura 2_13673427 S-adenosyl-L-m 2_17249137 BEST Arabidop 1_28927652 plastid transcrip 2_13673427 Member of a div 3_8585782 wall-associated 1_5525313 YUCCA6 (YUCt 5_8934934 A member of Ar 5_2265964 Encodes a cyto 1_2827059 unknown proteir 3_10132965 FUNCTIONS IN 5_16451150 unknown proteir 1_13031098 Zinc finger C-x8 3_1951230 alpha/beta-Hydt 2_17778099 FUNCTIONS IN 2_17778099	5.08 5.08 5.08 5.07 5.06	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR proximal promoter three_prime_UTR intergenic proximal promoter exon promoter promoter promoter downstream proximal promoter five_prime_UTR proximal promoter five_prime_UTR proximal promoter
AT1G05460 AT5G06290 AT5G61440 AT1G02640 AT3G53280 AT1G26770 AT5G06300 AT3G526140 AT3G20640 AT3G20640 AT3G20640 AT3G208640 AT1G31840 AT1G31840 AT2G32179 AT2G41380 AT1G76980 AT1G6130 AT3G23805 AT1G16130 AT3G23805 AT1G16130 AT5G25620 AT5G07220 AT1G08830 AT3G27390 AT5G41110 AT5G41110 AT3G41110 AT3G41110 AT3G41110 AT3G42690 AT3G42700 AT3G42700 AT5G42700 AT5G42700	na RIBOSOMAL PROTEIN L12-A (RPL12-A) RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 7185 (CYP7185) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a prott _1608306 Encodes a prott _1564648 Encodes a prott _1564648 Encodes one of 5_7366638 cytochrome P44 3_19755644 Encodes an ext _1_9258582 Putative lysine (5_1921870 LONELY GUY * 5_9132546 basic helix-loop _3_7214071 unknown protei _3_2622748 Protein of unkn: 3_2622748 Protein of unkn: 3_2622748 Protein of unkn: 3_2622748 Tratiricopeptid _1_11423843 Tetratricopeptid _1_11423843 Tetratricopeptid _1_11423843 Potential natura _2_13673427 S-adenosyL-L-m _2_17249137 BEST Arabidop: 1_28927652 plastid transcrip _2_13673427 Member of a di \u00e3_8585782 wall-associated _1_5525313 YUCCA6 (YUCI _5_8934934 A member of Ar 5_2265964 Encodes a cyto: 1_2827059 unknown protei _3_10132965 FUNCTIONS IN _5_16451150 unknown protei _1_13031098 Zinc finger C-x8 _3_1951230 alpha/beta-Hyd: 2_17778099 FUNCTIONS IN _2_17778099 FUNCTIONS IN _2_177778099	5.08 5.08 5.08 5.07 5.06	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter three_prime_UTR intergenic proximal promoter proximal promoter promoter promoter promoter downstream proximal promoter downstream exon promoter downstream intergenic promoter five_prime_UTR proximal promoter promo
AT1G05460 AT5G61440 AT5G61440 AT1G02640 AT3G52250 AT3G52280 AT1G26770 AT5G06300 AT3G264140 AT3G20640 AT3G20640 AT3G308640 AT1G31835 AT1G31840 AT1G31840 AT1G32179 AT2G41380 AT1G76980 AT1G41380 AT1G76980 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G61100	na RIBOSOMAL PROTEIN L12-A (RPL12-A) RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a prott _1608306 Encodes a prott _1564648 Encodes a prott _1564648 Encodes on of 5_7366638 cytochrome P44 3_19755644 Encodes on ext _19258582 Putative lysine t 5_1921870 LONELY GUY 5 5_9132546 basic helix-loop 3_7214071 unknown proteir 3_2622748 Protein of unknt 3_2622748 Protein of unknt 3_2622748 unknown proteir 1_11423843 Potential natura 2_13673427 S-adenosyl-Lm 2_17249137 BEST Arabidop: 1_28927652 plastid transcrip 2_13673427 Member of a div 3_8585782 wall-associated 1_5525313 YUCCA6 (YUCt 5_8934934 A member of Ar 5_2265964 Encodes a cyto: 1_2827059 unknown proteir 3_10132965 FUNCTIONS IN 5_16451150 unknown proteir 5_16451150 unknown proteir 1_13031098 Eline finger C-x8 3_1951230 alpha/beta-Hydt 2_17778099 FUNCTIONS IN 2_177778099 FUNCTIONS IN 5_177721719 B-box type zinc 5_22113099	5.08 5.08 5.08 5.07 5.06	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter downstream proximal promoter downstream exon promoter downstream exon promoter five_prime_UTR proximal promoter intergenic
AT1G05460 AT5G61440 AT1G0622950 AT3G632280 AT1G26770 AT5G63000 AT3G52380 AT1G26770 AT5G06300 AT3G226140 AT3G20640 AT3G20640 AT3G20640 AT3G20836 AT1G31840 AT1G31840 AT1G31840 AT2G32179 AT2G41380 AT1G6980 AT1G6130 AT1G6980 AT1G6130 AT1G6980 AT1G6130 AT1G6980 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G41110 AT1G41110 AT1G42690 AT2G42700 AT5G44050 AT5G44040	na RIBOSOMAL PROTEIN L12-A (RPL12-A) RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a prott _1608306 Encodes a prott _1564648 Encodes a prott _1564648 Encodes on ed 5_7366638 cytochrome P4f 3_19755644 Encodes on ex f _19258582 Putative lysine c 5_1921870 LONELY GUY f 5_9132546 basic helix-loop 3_7214071 unknown protei 1 _2622748 Protein of unkm 3_2622748 Protein of unkm 3_2622748 unknown protei 1_11423843 Potential natura 2_13673427 S-adenosyl-L-m 2_17249137 BEST Arabidop 1_28927652 plastid transcrip 2_13673427 Member of a di 3_8585782 wall-associated 1_5525313 YUCCA6 (YUCt 5_8934934 A member of Ar 5_2265964 Encodes a cyto 1_2827059 unknown proteir 3_10132965 FUNCTIONS IN 5_16451150 unknown proteir 1_13031098 Zinc finger C-x8 3_1951230 alpha/beta-Hydt 2_17778099 MATE efflux fan 5_17721719 B-box type zinc 5_22113099 unknown proteir 5_1645179099 MATE efflux fan 5_17721719	5.08 5.08 5.08 5.07 5.06	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR proximal promoter three_prime_UTR intergenic proximal promoter exon promoter promoter promoter downstream proximal promoter downstream exon promoter downstream intergenic promoter five_prime_UTR proximal promoter intergenic promoter intergenic promoter
AT1G05460 AT5G61440 AT5G61440 AT1G02640 AT3G52250 AT3G52280 AT1G26770 AT5G06300 AT3G264140 AT3G20640 AT3G20640 AT3G308640 AT1G31835 AT1G31840 AT1G31840 AT1G32179 AT2G41380 AT1G76980 AT1G41380 AT1G76980 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G6130 AT1G61100	na RIBOSOMAL PROTEIN L12-A (RPL12-A) RIBOSOMAL PROTEIN L12-A (RPL12-A) SILENCING DEFECTIVE (SDE3) 2-CYSTEINE PEROXIREDOXIN B (2-Cys ATYPICAL CYS HIS RICH THIOREDOXIN BETA-XYLOSIDASE 2 (BXL2) CCR4- ASSOCIATED FACTOR 1B (CAF1 CYTOCHROME P450 71B5 (CYP71B5) EXPANSIN A10 (EXPA10) LONELY GUY 7 (LOG7) LONELY GUY 9 (LOG9) na	50S ribosomal r 3_10318427 Encodes a prott _1608306 Encodes a prott _1608306 Encodes a prott _1564648 Encodes a prott _1564648 Encodes on ed 5_7366638 cytochrome P4f 3_19755644 Encodes on ex f _19258582 Putative lysine c 5_1921870 LONELY GUY f 5_9132546 basic helix-loop 3_7214071 unknown protei 1 _2622748 Protein of unkm 3_2622748 Protein of unkm 3_2622748 unknown protei 1_11423843 Potential natura 2_13673427 S-adenosyl-L-m 2_17249137 BEST Arabidop 1_28927652 plastid transcrip 2_13673427 Member of a di 3_8585782 wall-associated 1_5525313 YUCCA6 (YUCt 5_8934934 A member of Ar 5_2265964 Encodes a cyto 1_2827059 unknown proteir 3_10132965 FUNCTIONS IN 5_16451150 unknown proteir 1_13031098 Zinc finger C-x8 3_1951230 alpha/beta-Hydt 2_17778099 MATE efflux fan 5_17721719 B-box type zinc 5_22113099 unknown proteir 5_1645179099 MATE efflux fan 5_17721719	5.08 5.08 5.08 5.07 5.06	proximal promoter promoter intergenic intergenic promoter exon five_prime_UTR promoter proximal promoter three_prime_UTR intergenic proximal promoter downstream proximal promoter downstream exon promoter downstream exon promoter five_prime_UTR proximal promoter intergenic

AT2G15440	na	Protein of unknc 2_6743597	5.05	downstream
AT5G41140	na	Myosin heavy c 5_16467576	5.05	proximal promoter
AT5G45940	NUDIX HYDROLASE HOMOLOG 11 (NUI	Encodes a CoA 5_18632080	5.05	proximal promoter
AT1G02840	SERINE/ARGININE-RICH PROTEIN SPLI	SR34/SR1 is a 1_626736	5.05	promoter
AT1G76890	(GT2)	encodes a plant 1_28878007	5.04	proximal promoter
AT5G66210	CALCIUM-DEPENDENT PROTEIN KINAS		5.04	promoter
AT2G03800	GEKO1 (GEK1)	encodes a D-an 2_1156726	5.04	five_prime_UTR
AT1G77370	na	Glutaredoxin far 1_29073781	5.04	promoter
AT5G03668	na	Potential natura 5_950468	5.04	proximal promoter
AT5G46510	na	Disease resista 5_18860174	5.04	promoter
AT1G65486	na	unknown proteir 1_24349221	5.04	promoter
AT5G60800	na	Heavy metal tra 5_24460445	5.04	intergenic
AT5G66211 AT4G00335	na RING-H2 FINGER B1A (RHB1A)	This gene encor 5_26459798	5.04 5.04	exon
AT5G03670	TON1 RECRUITING MOTIF 28 (TRM28)	RING-H2 finger 4_145764 unknown proteir 5_950468	5.04	promoter intergenic
AT5G03070	TOUCH 2 (TCH2)	Encodes a prote 5_14999589	5.04	five_prime_UTR
AT4G19710	ASPARTATE KINASE-HOMOSERINE DEI		5.03	promoter
AT1G05570	CALLOSE SYNTHASE 1 (CALS1)	Encodes a callo 1_1661109	5.03	proximal promoter
AT1G80560	ISOPROPYLMALATE DEHYDROGENASE		5.03	proximal promoter
AT5G16600	MYB DOMAIN PROTEIN 43 (MYB43)	Encodes a puta 5_5436575	5.03	proximal promoter
AT1G19650	na	Sec14p-like phc 1_6799818	5.03	promoter
AT1G19660	na	Wound-respons 1_6799818	5.03	downstream
AT1G20670	na	DNA-binding br 1_7168106	5.03	promoter
AT1G66890	na	FUNCTIONS IN 1_24957446	5.03	promoter
AT3G61810	na	Glycosyl hydrol: 3_22878655	5.03	downstream
AT1G05575	na	unknown proteir 1_1661109	5.03	intergenic
AT1G05577	na	CONTAINS Inte 1_1661109	5.03	intergenic
AT1G21738	na	unknown proteir 1_7641153	5.03	promoter
AT1G80555	na	Isocitrate/isopro 1_30286894	5.03	promoter
AT1G21740	na	Protein of unknc 1_7641153	5.03	promoter
AT3G52500	na	Eukaryotic aspa 3_19463908	5.03	intergenic
AT4G35720	na	Arabidopsis pro 4_16927798	5.03	promoter
AT5G24610	na	unknown proteir 5_8427943	5.03	promoter
AT1G03080	NETWORKED 1D (NET1D)	kinase interactir 1_738139	5.03	promoter
AT1G48920	NUCLEOLIN LIKE 1 (NUC-L1)	Encodes ATNU 1_18097949	5.03	promoter
AT2G18040	PEPTIDYLPROLYL CIS/TRANS ISOMERA	phosphorylation 2_7842049	5.03	promoter
AT5G04940	SU(VAR)3-9 HOMOLOG 1 (SUVH1)	Encodes a SU(\ 5_1457190	5.03	promoter
AT1G12240	(ATBETAFRUCT4)	Encodes a vacu 1_4151276	5.02	proximal promoter
AT3G47500	CYCLING DOF FACTOR 3 (CDF3)	Dof-type zinc fir 3_17507848	5.02	proximal promoter
AT5G25350	EIN3-BINDING F BOX PROTEIN 2 (EBF2)	Arabidopsis tha 5_8798321	5.02	proximal promoter
AT4G25080	MAGNESIUM-PROTOPORPHYRIN IX ME	Encodes a prote 4_12876892	5.02	intron
AT1G12230	na	Aldolase superf: 1_4151276	5.02	downstream
AT1G67920	na	unknown proteir 1_25472472	5.02	proximal promoter
AT1G15120	na	Ubiquinol-cytocl 1_5202623	5.02	promoter
AT1G67910	na	unknown proteir 1_25472472	5.02	promoter
AT2G23690	na	unknown proteir 2_10074567	5.02	intergenic
AT1G27440	(GUT2)	GUT2; FUNCTI: 1_9531527	5.01	promoter
AT5G12230	(MED19A)	MED19A; BEST 5_3956208	5.01	promoter
AT3G51840	ACYL-COA OXIDASE 4 (ACX4)	Encodes a shor 3_19229181	5.01	promoter
AT1G27450	ADENINE PHOSPHORIBOSYL TRANSFE	Adenosine phos 1_9531527	5.01	promoter
AT3G56660	BASIC REGION/LEUCINE ZIPPER MOTIF	basic region/leu 3_20988402	5.01	promoter
AT1G78670	GAMMA-GLUTAMYL HYDROLASE 3 (GG	gamma-glutamy 1_29590758	5.01	promoter
AT5G33285	na	transposable eli 5_12553582	5.01	intergenic
AT5G48655	na	RING/U-box su _I 5_19733104	5.01	promoter
AT5G15810	na	N2,N2-dimethyl _! 5_5161585	5.01	downstream
AT5G15815	na	pre-tRNA; tRNA 5_5161585	5.01	downstream
AT2G18670	na	RING/U-box su _l 2_8094341	5.01	intron
AT2G18680	na	unknown proteir 2_8094341	5.01	promoter
AT1G66180	na	The gene encor 1_24648543	5.01	three_prime_UTR
AT3G06778	na	Chaperone Dna 3_2142137	5.01	proximal promoter
AT5G60670	na	Ribosomal prote 5_24381788	5.01	promoter
AT3G15730	PHOSPHOLIPASE D ALPHA 1 (PLDALPH		5.01	promoter
AT5G43090	PUMILIO 13 (PUM13)	Encodes a merr 5_17295340	5.01	proximal promoter
AT5G66350	SHORT INTERNODES (SHI)	A member of SI 5_26506584	5.01	promoter
AT5G67180	TARGET OF EARLY ACTIVATION TAGGI		5.01	promoter
AT1G24120	ARG1-LIKE 1 (ARL1) MICRORNA164B (MIR164B)	encodes a Dna. 1_8533377	5	proximal promoter
AT4G09460	- ' '	Encodes a micr 5_285399 Encodes myb6 4 5992911	5 5	proximal promoter
AT4G09460	MYB DOMAIN PROTEIN 6 (MYB6)		5	promoter
AT5G01350 AT5G50450	na na	unknown proteir 5_147279 HCP-like superf 5_20544797	5	promoter promoter
AT1G30050		unknown proteir 1 10542282	5	
AT1G30050 AT1G21010	na na		5	proximal promoter
AT1G21010 AT2G44220	na na	unknown proteir 1_7346214 Protein of Unkn 2_18286377	5	five_prime_UTR intergenic
AT2G44220 AT2G44230	na na	Plant protein of 2 18286377	5	promoter
AT3G06540	RAB ESCORT PROTEIN (REP)	Encodes a cyto _l 3_2034572	5	intergenic
AT1G11350	S-DOMAIN-1 13 (SD1-13)	S-domain-1 13 (1_3820892	5	promoter
AT1G11350 AT5G01360	TRICHOME BIREFRINGENCE-LIKE 3 (TE		5	downstream
AT5G51360	WRKY DNA-BINDING PROTEIN 2 (WRK)		5	promoter
AT2G39770	CYTOKINESIS DEFECTIVE 1 (CYT1)	Encodes a GDF 2 16588489	4.99	promoter
AT4G19040	ENHANCED DISEASE RESISTANCE 2 (E		4.99	promoter
AT4G19040	FARNESYLATED PROTEIN 6 (FP6)	putative farnesy 4_18033859	4.99	proximal promoter
AT4G38380	GLYCINE-RICH RNA-BINDING PROTEIN		4.99	promoter
AT4G13830	LOSS OF THE TIMING OF ET AND JA BI		4.99	proximal promoter
AT5G55230	MICROTUBULE-ASSOCIATED PROTEIN:		4.99	proximal promoter
AT3G60340	na	alpha/beta-Hydr 3_22304017	4.99	promoter
AT3G00340 AT3G03140	na	Tudor/PWWP/N 3_723847	4.99	promoter
AT4G12735	na	unknown proteir 4_7494397	4.99	promoter
AT4G12733	na	HhH-GPD base 4_7494397	4.99	downstream
AT1G54150	na	E3 Ubiquitin liga 1_20215311	4.99	promoter
AT2G36970	na	UDP-Glycosyltri 2_15528219	4.99	proximal promoter
AT5G55220	na	trigger factor tyr 5_22400907	4.99	downstream
AT5G53900	na	Serine/threonin: 5_21884112	4.99	proximal promoter
AT4G14540	NUCLEAR FACTOR Y, SUBUNIT B3 (NF-		4.99	promoter
AT4G38570	PROBABLE CDP-DIACYLGLYCEROLIN		4.99	promoter
		=		-

AT3G15060	RAB GTPASE HOMOLOG A1G (RABA1g	RAB GTPase h: 3_5069107	4.99	promoter
AT5G07000	SULFOTRANSFERASE 2B (ST2B)	Encodes a merr 5_2171659	4.99	exon
AT1G54140	TATA BINDING PROTEIN ASSOCIATED		4.99	promoter
AT3G08710	THIOREDOXIN H-TYPE 9 (TH9)	Associated to pl 3_2647621	4.99	intergenic
AT1G09850	XYLEM BARK CYSTEINE PEPTIDASE 3 (Arabidopsis tha 1_3201716	4.99	promoter
AT4G33300	ADR1-LIKE 1 (ADR1-L1)	Encodes a merr 4_16054103	4.98	five_prime_UTR
AT3G51920	CALMODULIN 9 (CAM9)	encodes a diver 3_19266937	4.98	intergenic
AT3G51910	HEAT SHOCK TRANSCRIPTION FACTOR		4.98	intergenic
AT3G12980	HISTONE ACETYLTRANSFERASE OF TH		4.98	promoter
AT1G03515	na	pre-tRNA; tRNA 1_877763	4.98	downstream
AT1G03520	na	Core-2/I-branch 1_877763	4.98	downstream
AT4G33310	na	unknown proteir 4_16054103	4.98	proximal promoter
AT5G12340	na	unknown proteir 5_3994009	4.98	promoter
AT1G75860 AT1G75870	na	unknown proteir 1_28486094	4.98 4.98	promoter
AT1G75670 AT2G38260	na na	unknown proteir 1_28486094	4.98	promoter promoter
	na na	pseudogene, sir 2_16028841		•
AT3G12977 AT3G12130		NAC (No Apical 3_4146284 KH domain-cont 3_3866699	4.98 4.98	intergenic promoter
AT3G51915	na na	unknown proteir 3_19266937	4.98	•
AT5G49690	na	UDP-Glycosyltr; 5 20189981	4.98	intergenic exon
AT4G39615	na	pre-tRNA; tRNA 4_18395142	4.98	downstream
AT5G61560	na	U-box domain-c 5_24752063	4.98	proximal promoter
AT1G49240	ACTIN 8 (ACT8)	Member of a su 1_18215746	4.97	promoter
AT4G29900	AUTOINHIBITED CA(2+)-ATPASE 10 (AC		4.97	five_prime_UTR
AT5G57180	CHLOROPLAST IMPORT APPARATUS 2		4.97	promoter
AT4G02130	GALACTURONOSYLTRANSFERASE 6 (0		4.97	proximal promoter
AT3G16360	HPT PHOSPHOTRANSMITTER 4 (AHP4)		4.97	intergenic
AT2G19780	na	Leucine-rich reg 2_8524278	4.97	five_prime_UTR
AT2G47660	na	unknown proteir 2_19543620	4.97	intergenic
AT2G31370	na	Basic-leucine zi 2 13381809	4.97	intergenic
AT2G47670	na	Plant invertase/ 2 19543620	4.97	intergenic
AT3G07320	na	O-Glycosyl hydi 3_2332644	4.97	exon
AT5G15870	na	glycosyl hydrola 5_5184890	4.97	promoter
AT5G15880	na	unknown proteir 5_5184890	4.97	proximal promoter
AT5G44320	na na	Eukaryotic trans 5_17856862	4.97	promoter
AT2G02220	PHYTOSULFOKIN RECEPTOR 1 (PSKR1		4.97	promoter
AT3G04280	RESPONSE REGULATOR 22 (RR22)	Encodes an aty 3_1132739	4.97	proximal promoter
AT2G31380	SALT TOLERANCE HOMOLOGUE (STH)		4.97	promoter
AT2G29090	CYTOCHROME P450, FAMILY 707, SUBI		4.96	intergenic
AT2G29080	FTSH PROTEASE 3 (ftsh3)	encodes an Ftsl 2_12494263	4.96	proximal promoter
AT1G28440	HAESA-LIKE 1 (HSL1)	HAESA-like 1 (F 1_9996799	4.96	promoter
AT4G05470	na	RNI-like superfa 4_2765505	4.96	promoter
AT2G46060	na	transmembrane 2_18945269	4.96	promoter
AT3G45260	na	C2H2-like zinc f 3_16599292	4.96	proximal promoter
AT3G48460	na	GDSL-like Lipas 3_17948330	4.96	proximal promoter
AT4G30710	QWRF DOMAIN CONTAINING 8 (QWRF8		4.96	proximal promoter
AT4G25350	SHORT HYPOCOTYL UNDER BLUE1 (SH		4.96	proximal promoter
AT4G37330	CYTOCHROME P450, FAMILY 81, SUBF		4.95	three_prime_UTR
AT4G37320	CYTOCHROME P450, FAMILY 81, SUBFA		4.95	proximal promoter
AT3G08940	LIGHT HARVESTING COMPLEX PHOTO		4.95	promoter
AT5G65070	MADS AFFECTING FLOWERING 4 (MAF		4.95	proximal promoter
AT1G11970	na	Ubiquitin-like su 1_4044387	4.95	exon
AT1G77250	na	RING/FYVE/PH 1_29023626	4.95	promoter
AT2G41710	na	Integrase-type [2_17403179	4.95	promoter
AT3G08630	na	Protein of unknc 3_2620711	4.95	promoter
AT4G37225	na	Potential natura 4_17517052	4.95	promoter
AT4G37230	na	Photosystem II I 4_17517052	4.95	intron
AT1G26916	na	unknown proteir 1_9327227	4.95	exon
AT3G08930	na	LMBR1-like mer 3_2717501	4.95	downstream
AT5G53310	na	myosin heavy cl 5_21634315	4.95	promoter
AT5G62570	na	Calmodulin bind 5_25114070	4.95	promoter
AT5G53300	UBIQUITIN-CONJUGATING ENZYME 10	Encodes a ubiq 5_21634315	4.95	promoter
AT3G14590	(NTMC2T6.2)	NTMC2T6.2; C(3_4908101	4.94	promoter
AT1G68552	CONSERVED PEPTIDE UPSTREAM OPE		4.94	intergenic
AT4G23220	CYSTEINE-RICH RLK (RECEPTOR-LIKE		4.94	intergenic
AT1G68550	CYTOKININ RESPONSE FACTOR 10 (CF		4.94	intergenic
AT3G22100	na	basic helix-loop 3_7784645	4.94	promoter
AT1G04985	na	unknown proteir 1_1418605	4.94	promoter
AT1G04990	na	Zinc finger C-x8 1_1418605	4.94	intergenic
AT1G79700	na	Integrase-type [1_29990817	4.94	exon
AT4G37175	na	pre-tRNA; tRNA 4_17502541	4.94	proximal promoter
AT4G23215	na	pseudogene of 4_12153587	4.94	promoter
AT1G04480	na	Ribosomal prote 1_1215856	4.94	promoter
AT1G05960	na	ARM repeat sur 1_1815540	4.94	promoter
AT1G72500	na	LOCATED IN: p 1_27300170	4.94	proximal promoter
AT5G44570	na	unknown proteir 5_17964240	4.94	promoter
AT5G51795	na na	DNA/RNA-bindi 5_21042239	4.94	intergenic
AT5G56220	na	P-loop containir 5_22754680	4.94	promoter
AT5G53110	na na	na 5_17964240 RING/U-box su; 5_21532346	4.94	intergenic
AT5G53110 AT1G06160	na OCTADECANOID-RESPONSIVE ARABID		4.94 4.94	intron promoter
AT1G06160 AT5G53120	SPERMIDINE SYNTHASE 3 (SPDS3)	encodes a nove 5_21532346	4.94	proximal promoter
AT4G00440	TON1 RECRUITING MOTIF 15 (TRM15)	FUNCTIONS IN 4_193436	4.94	promoter
AT4G00440 AT3G18010	WUSCHEL RELATED HOMEOBOX 1 (W		4.94 4.94	downstream
AT1G30330	AUXIN RESPONSE FACTOR 6 (ARF6)	Encodes a wor 3_6160987 Encodes a merr 1_10685776	4.94	downstream
AT1G30330 AT1G75240	HOMEOBOX PROTEIN 33 (HB33)	Encodes a rinc 1_10685776 Encodes a zinc 1_28239742	4.93	proximal promoter
AT1G75240 AT1G69030		BSD domain-co 1_25952036	4.93	proximal promoter
AT1G69030 AT5G40800	na na	unknown proteir 5_16333514	4.93	intergenic
AT2G41410	na	Calcium-binding 2_17262792	4.93	five_prime_UTR
AT5G62820	na	Uncharacterise: 5_25225140	4.93	promoter
AT5G62620	na	Acyl-CoA N-acy 5_26912614	4.93	intergenic
AT5G67440	NAKED PINS IN YUC MUTANTS 3 (NPY3		4.93	downstream
AT4G37760	SQUALENE EPOXIDASE 3 (SQE3)	squalene epoxic 4_17748713	4.93	intergenic
AT1G75010	ACCUMULATION AND REPLICATION OF		4.92	proximal promoter
		=		

AT5G46690	BETA HLH PROTEIN 71 (bHLH071)	beta HLH protei 5_18944301	4.92	proximal promoter
AT5G03280	ETHYLENE INSENSITIVE 2 (EIN2)	Involved in ethy 5_793635	4.92	intergenic
AT1G75750	GAST1 PROTEIN HOMOLOG 1 (GASA1)	GA-responsive 1_28443530	4.92	proximal promoter
AT1G75700	HVA22-LIKE PROTEIN G (HVA22G)	HVA22-like prot 1_28423408	4.92	promoter
AT5G03290	ISOCITRATE DEHYDROGENASE V (IDH-		4.92	promoter
AT1G75690	LOW QUANTUM YIELD OF PHOTOSYST		4.92	promoter
AT1G75020	LYSOPHOSPHATIDYL ACYLTRANSFER		4.92	promoter
AT1G01980	na	member of Retic 1_342252	4.92	promoter
AT1G23440	na	Peptidase C15, 1_8321580	4.92	promoter
AT2G36600	na	pre-tRNA; tRNA 2_15345753	4.92	promoter
AT4G27595	na	Plant protein of 4_13777541	4.92	promoter
AT5G03285	na	other RNA 5_793635	4.92	exon
AT1G66150	TRANSMEMBRANE KINASE 1 (TMK1)	receptor-like tra 1_24631344	4.92	promoter
AT3G27520 AT3G24490	na	unknown proteir 3_10192207	4.91	promoter
	na PATATIN LIKE PROTEIN 6 (DI D6)	Alcohol dehydrc 3_8910711	4.91	promoter
AT2G39220 AT4G24040	PATATIN-LIKE PROTEIN 6 (PLP6)	PATATIN-like pi 2_16377025	4.91 4.91	promoter
AT1G58520	TREHALASE 1 (TRE1)	Encodes a treha 4_12488025 RXW8; FUNCT 1_21732451	4.91	promoter intron
AT5G35360	(RXW8) ACETYL CO-ENZYME A CARBOXYLASE		4.9	promoter
AT2G34490	CYTOCHROME P450, FAMILY 710, SUBF		4.9	three_prime_UTR
AT1G09810	EVOLUTIONARILY CONSERVED C-TERI		4.9	intergenic
AT2G20750	EXPANSIN B1 (EXPB1)	member of BET 2 8940996	4.9	promoter
AT3G24927	na	pseudogene of 3_9103659	4.9	intron
AT1G09800	na	Pseudouridine s 1_3180559	4.9	promoter
AT1G15670	na	Galactose oxida 1_5387002	4.9	proximal promoter
AT5G41140	na	Myosin heavy c 5_16469533	4.9	intron
AT4G34490	CYCLASE ASSOCIATED PROTEIN 1 (CA		4.89	intergenic
AT4G09180	FLOWERING BHLH 2 (FBH2)	basic helix-loop 4_5847259	4.89	promoter
AT5G66320	GATA TRANSCRIPTION FACTOR 5 (GAT		4.89	downstream
AT4G34480	na	O-Glycosyl hydi 4_16484043	4.89	promoter
AT5G23610	na	INVOLVED IN: 15_7960336	4.89	promoter
AT2G22320	na	unknown proteir 2_9481106	4.89	intergenic
AT1G49010	na	Duplicated hom 1_18132492	4.89	promoter
AT1G71970	na	unknown proteir 1_27092614	4.89	promoter
AT2G26690	na	Major facilitator 2_11350071	4.89	intron
AT2G26692	na	Potential natura 2 11350071	4.89	proximal promoter
AT2G41200	na	unknown proteir 2_17171628	4.89	five_prime_UTR
AT2G01410	na	NHL domain-co 2_176548	4.89	promoter
AT3G59470	na	Far-red impaire(3_21980791	4.89	promoter
AT5G23630	PHOSPHATE DEFICIENCY RESPONSE 2		4.89	downstream
AT1G04010	PHOSPHOLIPID STEROL ACYL TRANSF		4.89	promoter
AT3G02180	SPIRAL1-LIKE3 (SP1L3)	SPIRAL1-LIKE3 3_402683	4.89	proximal promoter
AT4G01100	ADENINE NUCLEOTIDE TRANSPORTER		4.88	intergenic
AT5G60910	AGAMOUS-LIKE 8 (AGL8)	MADS box gene 5_24508609	4.88	proximal promoter
AT3G45970	EXPANSIN-LIKE A1 (EXLA1)	member of EXP 3_16896064	4.88	promoter
AT5G58560	FARNESOL KINASE (FOLK)	FOLK is a farne 5_23670310	4.88	promoter
AT3G59400	GENOMES UNCOUPLED 4 (GUN4)	GUN, genomes 3 21948418	4.88	intergenic
AT1G78380	GLUTATHIONE S-TRANSFERASE TAU 1		4.88	proximal promoter
AT1G05340	na	unknown proteir 1_1559960	4.88	promoter
AT1G05350	na	NAD(P)-binding 1_1559960	4.88	intergenic
AT3G23750	na	Leucine-rich reg 3_8561635	4.88	downstream
AT3G23760	na	FUNCTIONS IN 3_8561635	4.88	intergenic
AT4G23103	na	This gene encor 4_12109276	4.88	proximal promoter
AT1G56350	na	Peptide chain re 1 21094609	4.88	promoter
AT1G75880	na	SGNH hydrolas 1_28489261	4.88	proximal promoter
AT2G01300	na	unknown proteir 2_151833	4.88	promoter
AT1G56345	na	Pseudouridine s 1_21094609	4.88	promoter
AT3G59390	na	unknown proteir 3_21948418	4.88	downstream
AT4G01110	na	unknown proteir 4 480426	4.88	exon
AT4G34220	na	Leucine-rich rer 4 16385110	4.88	proximal promoter
AT4G11010	NUCLEOSIDE DIPHOSPHATE KINASE 3		4.88	promoter
AT5G54290	(CcdA)	Encodes CcdA, 5_22050539	4.87	promoter
AT3G08580	ADP/ATP CARRIER 1 (AAC1)	mitochondrial Al 3 2607888	4.87	promoter
AT5G50920	CLPC HOMOLOGUE 1 (CLPC1)	Encodes a prot 5_20720872	4.87	promoter
AT1G12610	DWARF AND DELAYED FLOWERING 1 (4.87	proximal promoter
AT4G14270	na	Protein containii 4_8218318	4.87	promoter
AT1G16950	na	unknown proteir 1_5794644	4.87	proximal promoter
AT2G38250	na	Homeodomain-I 2_16017071	4.87	proximal promoter
AT4G28330	na	unknown proteir 4_14023173	4.87	promoter
AT5G39530	na	Protein of unknc 5_15828734	4.87	proximal promoter
AT1G49750	na	Leucine-rich rer 1_18411727	4.87	exon
AT1G74330	na	Protein kinase s 1_27947427	4.87	promoter
AT1G26916	na	unknown proteir 1_9326001	4.87	proximal promoter
AT3G26486	na	transposable eli 3_9699575	4.87	intergenic
AT5G04880	na	pseudogene of .5_1422748	4.87	promoter
AT5G04238	na	This gene encor 5_1169059	4.87	downstream
AT5G04885	na	Glycosyl hydrol: 5_1422748	4.87	promoter
AT4G27800	THYLAKOID-ASSOCIATED PHOSPHATA		4.87	promoter
AT3G01700	ARABINOGALACTAN PROTEIN 11 (AGP		4.86	promoter
AT3G25690	CHLOROPLAST UNUSUAL POSITIONING		4.86	intergenic
AT1G04310	ETHYLENE RESPONSE SENSOR 2 (ERS		4.86	promoter
AT1G04050	HOMOLOG OF SU(VAR)3-9 1 (SUVR1)		4.86	proximal promoter
AT5G56490	L -GULONO-1,4-LACTONE (L -GULL) OX		4.86	promoter
AT5G65676	na	transposable eli 5_26257485	4.86	proximal promoter
AT5G11475	na	pre-tRNA; tRNA 5_3668936	4.86	downstream
AT1G12080	na	Vacuolar calciur 1_4086529	4.86	intergenic
AT3G01690	na	alpha/beta-Hydr 3_258567	4.86	downstream
AT3G25700	na	Eukaryotic aspa 3_9359548	4.86	exon
AT3G18830	POLYOL/MONOSACCHARIDE TRANSPO		4.86	proximal promoter
AT4G16990	RESISTANCE TO LEPTOSPHAERIA MAC		4.86	promoter
AT4G36360	BETA-GALACTOSIDASE 3 (BGAL3)	putative beta-ga 4_17182228	4.85	proximal promoter
AT2G40080	EARLY FLOWERING 4 (ELF4)	Encodes a nov€ 2_16735019	4.85	promoter
AT3G30775	EARLY RESPONSIVE TO DEHYDRATION		4.85	proximal promoter
AT3G51880	HIGH MOBILITY GROUP B1 (HMGB1)	Encodes a prote 3_19249154	4.85	promoter

AT2G28355	LOW-MOLECULAR-WEIGHT CYSTEINE-	low-molecular-w 2_12117971	4.85	proximal promoter
AT5G07260	na	START (StAR-r ₁ 5_2280560	4.85	intergenic
AT3G62940	na	Cysteine proteir 3_23265053	4.85	promoter
AT2G40081	na	unknown proteir 2_16735019	4.85	exon
AT1G71150	na	unknown proteir 1_26826852	4.85	promoter
AT3G51890	na	Clathrin light ch: 3_19249154	4.85	intergenic
AT5G18460	na	Protein of Unkn 5_6122694	4.85	promoter
AT5G04020	na	calmodulin bind 5_1087556	4.85	proximal promoter
AT1G34370	SENSITIVE TO PROTON RHIZOTOXICIT		4.85	promoter
AT5G07270	XB3 ORTHOLOG 3 IN ARABIDOPSIS TH.		4.85	promoter
AT2G36870	XYLOGLUCAN ENDOTRANSGLUCOSYL		4.85	promoter
AT1G28130	(GH3.17)	encodes an IAA 1_9828354	4.84	intergenic
AT3G63210	(MARD1)	encodes a nove 3_23352461	4.84	intergenic
AT4G29330	DERLIN-1 (DER1)	DERLIN-1 (DEF 4_14444626	4.84	promoter
AT3G60530	GATA TRANSCRIPTION FACTOR 4 (GAT	Encodes a merr 3_22368832	4.84	intergenic
AT3G50700	INDETERMINATE(ID)-DOMAIN 2 (IDD2)	zinc finger prote 3_18843298	4.84	intergenic
AT4G11985	na	pre-tRNA; tRNA 4_7185600	4.84	promoter
AT2G43795	na	unknown proteir 2_18143532	4.84	proximal promoter
AT1G28135	na	unknown proteir 1_9828354	4.84	proximal promoter
AT1G56210	na	Heavy metal tra 1_21036996	4.84	exon
AT5G50000	na	Protein kinase s 5_20344341	4.84	intron
AT4G11980	NUDIX HYDROLASE HOMOLOG 14 (NUI	nudix hydrolase 4_7185600	4.84	promoter
AT3G29250	SHORT-CHAIN DEHYDROGENASE RED	NAD(P)-binding 3_11195489	4.84	promoter
AT5G52560	UDP-SUGAR PYROPHOSPHORYLASE (Encodes a prot 5_21330425	4.84	promoter
AT1G73602	CONSERVED PEPTIDE UPSTREAM OPE	Upstream open 1_27670440	4.83	promoter
AT3G61610	na	Galactose muta 3_22798336	4.83	proximal promoter
AT4G09190	na	F-box and asso 4_5851840	4.83	intergenic
AT5G44670	na	Domain of unkn 5_18022137	4.83	proximal promoter
AT2G17723	na	Encodes a defe 2_7701264	4.83	intergenic
AT2G19090	na	Protein of unknc 2 8269400	4.83	proximal promoter
AT1G10650	na	SBP (S-ribonuc 1_3526453	4.83	promoter
AT1G73600	na	S-adenosyl-L-m 1_27670440	4.83	intron
AT4G16670	na	CONTAINS Inte 4_9383201	4.83	proximal promoter
AT4G40050	na	FUNCTIONS IN 4_18566679	4.83	proximal promoter
AT5G16550	na	unknown proteir 5_5405330	4.83	promoter
AT3G61600	POZ/BTB CONTAININ G-PROTEIN 1 (PO		4.83	downstream
AT4G30960	SOS3-INTERACTING PROTEIN 3 (SIP3)		4.83	intergenic
AT5G16540	ZINC FINGER NUCLEASE 3 (ZFN3)	Encodes a zinc 5 5405330	4.83	downstream
AT4G29670	ATYPICAL CYS HIS RICH THIOREDOXIN		4.82	promoter
AT4G29660	EMBRYO DEFECTIVE 2752 (EMB2752)	EMBRYO DEFE 4_14537339	4.82	proximal promoter
AT2G39270	na	P-loop containir 2_16399890	4.82	promoter
AT2G39260	na	binding;RNA bir 2_16399890	4.82	promoter
AT2G23790	na	Protein of unknc 2_10127752	4.82	promoter
AT4G21926	na	unknown proteir 4_11638944	4.82	three_prime_UTR
AT4G21930	na	Protein of unknc 4_11638944	4.82	proximal promoter
AT4G24760	na	alpha/beta-Hydr 4_12764246	4.82	promoter
AT5G38520	na	alpha/beta-Hydr 5_15421436	4.82	promoter
AT5G48900	na	Pectin lyase-like 5_19826807	4.82	intron
AT5G38510	na	Rhomboid-relate 5_15421436	4.82	proximal promoter
AT3G57990	na	unknown proteir 3_21471639	4.82	promoter
AT4G14620	na	Protein of unknr 4_8387881	4.82	intergenic
AT5G23100	na	Protein of unknc 5_7753376	4.82	promoter
AT1G73010	PHOSPHATE STARVATION-INDUCED G		4.82	proximal promoter
AT2G23320	WRKY DNA-BINDING PROTEIN 15 (WRK		4.82	proximal promoter
AT5G25460	DUF642 L-GALL RESPONSIVE GENE 2		4.81	promoter
AT1G78630	EMBRYO DEFECTIVE 1473 (emb1473)	embryo defectiv 1 29575905	4.81	promoter
AT1G78630	na	Histone superfa 1_2368590	4.81	promoter
AT1G77000	na na		4.81	
	• • • • • • • • • • • • • • • • • • • •	Protein of unknr 1_29872938	4.81	intron
AT1G80250 AT1G03440	na	pre-tRNA; tRNA 1_30173980	4.81	downstream
AT1G03440 AT1G78620	na na	Leucine-rich reg 1_850763 Protein of unkno 1 29575905	4.81	proximal promoter
AT3G14830	na	unknown proteir 3_4986016	4.81	promoter downstream
AT3G14840	na	Leucine-rich reg 3 4986016	4.81	proximal promoter
AT1G73990	SIGNAL PEPTIDE PEPTIDASE (SPPA)	Encodes a puta 1_27824239	4.81	promoter
AT1G73990	FORMS APLOID AND BINUCLEATE CEL		4.8	
AT3G48070	na	RING/U-box su ₁ 3_17750587	4.8	proximal promoter promoter
AT4G15260	na	UDP-Glycosyltr: 4 8715123	4.8	exon
AT5G22690	na	Disease resista 5_7541116	4.8	promoter
AT1G50020	na	unknown proteir 1_18521886	4.8	promoter
AT1G05070	na	Protein of unknr 1_1458859	4.8	promoter
AT5G11680	na	FUNCTIONS IN 5_3758787	4.8	promoter
AT4G36660	na	Protein of unknc 4 17287980	4.8	proximal promoter
AT5G45360	na	F-box family prc 5_18387862	4.8	proximal promoter
AT5G45370	na	nodulin MtN21-l 5_18387862	4.8	promoter
AT4G36670	POLYOL/MONOSACCHARIDE TRANSPO		4.8	exon
AT1G04240	SHORT HYPOCOTYL 2 (SHY2)	SHY2/IAA3 regt 1 1131853	4.8	proximal promoter
AT5G56210	WPP DOMAIN INTERACTING PROTEIN		4.8	promoter
AT2G28560	(RAD51B)	Encodes a prot 2_12240409	4.79	proximal promoter
AT3G25620	ATP-BINDING CASSETTE G21 (ABCG21		4.79	intergenic
AT1G32900	GRANULE BOUND STARCH SYNTHASE		4.79	promoter
AT1G32300 AT1G75240	HOMEOBOX PROTEIN 33 (HB33)	Encodes a zinc 1 28241336	4.79	five_prime_UTR
AT4G26760	MICROTUBULE-ASSOCIATED PROTEIN		4.79	promoter
AT4G35510	na	unknown proteir 4_16860275	4.79	downstream
AT1G69730	na	Wall-associated 1_26230137	4.79	exon
AT1G09730	na	Domain of unkn 1_7954539	4.79	promoter
AT1G22320 AT1G71980	na	Protease-assoc 1_27096808	4.79	proximal promoter
AT1G71300 AT1G74370	na	RING/U-box su ₁ 1_27959479	4.79	promoter
AT1G74370 AT1G27200	na	CONTAINS Inte 1 9452059	4.79	promoter
AT1G27200 AT3G25610	na	ATPase E1-E2 3_9315797	4.79	proximal promoter
AT3G25610 AT3G49890	na	unknown proteir 3_18499095	4.79	promoter
AT5G49690	na	alpha/beta-Hydr 5_2011174	4.79	promoter
AT5G06570	na na	Encodes a prot 5_2011174	4.79	downstream
AT2G41680	NADPH-DEPENDENT THIOREDOXIN RE		4.79	promoter
AT5G15860	PRENYLCYSTEINE METHYLESTERASE		4.79	promoter
50.5000		p.o o_o101000	0	F. 2

AT1G03060	SPIRRIG (SPI)	Encodes a WD/ 1_727552	4.79	proximal promoter
AT1G74380	XYLOGLÜCAN XYLOSYLTRANSFERASE		4.79	promoter
AT4G25050	ACYL CARRIER PROTEIN 4 (ACP4)	encodes an acy 4_12869991	4.78	promoter
AT2G47000	ATP-BINDING CASSETTE B4 (ABCB4)	Encodes an au 2_19310130		exon
AT5G41410 AT1G48300	BELL 1 (BEL1) DIACYLGLYCEROL ACYLTRANSFERASI	Homeodomain r 5_16579955	4.78 4.78	promoter
AT5G22500	FATTY ACID REDUCTASE 1 (FAR1)	Encodes a merr 5_7470303	4.78	promoter promoter
AT2G28740	HISTONE H4 (HIS4)	histone 4 2_12330159		promoter
AT5G61820	na	FUNCTIONS IN 5_24836787	4.78	promoter
AT5G61830	na	NAD(P)-binding 5_24836787	4.78	promoter
AT5G13970	na	unknown proteir 5_4507996	4.78	promoter
AT4G28030	na	Acyl-CoA N-acy 4_13939812		proximal promoter
AT4G28040	na	nodulin MtN21-l 4_13939812		proximal promoter
AT1G56660 AT2G28720	na na	unknown proteir 1_21237827 Histone superfa 2_12330159	4.78 4.78	promoter intergenic
AT2G28730	na	pre-tRNA; tRNA 2 12330159		intergenic
AT2G46995	na	unknown proteir 2_19310130		proximal promoter
AT4G21620	na	glycine-rich prot 4_11491409	4.78	promoter
AT5G64040	(PSAN)	Encodes the on 5_25629645	4.77	promoter
AT4G29140	ACTIVATED DISEASE SUSCEPTIBILITY		4.77	exon
AT5G15160	BANQUO 2 (BNQ2)	BNQ2 belongs t 5_4922711	4.77	promoter
AT2G47450	CHAOS (CAO)	A component of 2_19471589		proximal promoter
AT5G51430 AT5G64050	EMBRYO YELLOW (EYE) GLUTAMATE TRNA SYNTHETASE (ERS)	Encodes a prot 5_20890993 Glutamate-tRN/ 5_25629645		promoter downstream
AT2G17220	KINASE 3 (KIN3)	Encodes a puta 2_7490156	4.77	five_prime_UTR
AT5G55230	MICROTUBULE-ASSOCIATED PROTEIN		4.77	promoter
AT1G67310	na	Calmodulin-binc 1_25203122	4.77	exon
AT5G07730	na	unknown proteir 5_2458529	4.77	promoter
AT5G07740	na	actin binding; Fl 5_2458529	4.77	downstream
AT5G27889	na	This gene enco 5_9903425	4.77	promoter
AT2G23710 AT2G30270	na	transposable el 2_10083858 Protein of unknc 2_12907815		proximal promoter
AT3G01740	na na	Mitochondrial rit 3 267672	4.77 4.77	downstream promoter
AT3G15356	na	Legume lectin fa 3 5175635	4.77	promoter
AT2G47440	na	Tetratricopeptid 2 19471589		exon
AT4G35240	na	Protein of unknc 4_16767577		promoter
AT5G47330	na	alpha/beta-Hydr 5_19206977	4.77	promoter
AT1G02230	NAC DOMAIN CONTAINING PROTEIN 4		4.77	promoter
AT2G30260	U2 SMALL NUCLEAR RIBONUCLEOPRO			promoter
AT2G15480	UDP-GLUCOSYL TRANSFERASE 73B5 (4.77	promoter
AT1G76890	(GT2)	encodes a plant 1_28872826	4.76	downstream
AT1G77850 AT4G23650	AUXIN RESPONSE FACTOR 17 (ARF17) CALCIUM-DEPENDENT PROTEIN KINAS			proximal promoter promoter
AT5G27320	GA INSENSITIVE DWARF1C (GID1C)	Encodes a gibb 5_9628989	4.76	promoter
AT1G15820	LIGHT HARVESTING COMPLEX PHOTO		4.76	promoter
AT4G34120	LOSS OF THE TIMING OF ET AND JA BI		4.76	promoter
AT1G22180	na	Sec14p-like phc 1_7830402	4.76	promoter
AT5G52980	na	CONTAINS Inte 5_21483795	4.76	promoter
AT5G52990	na	SNARE-like sur 5_21483795		promoter
AT2G42247	na	Potential natura 2_17599735	4.76	exon
AT2G42240	na	RNA-binding (R 2_17599735		downstream
AT1G27890 AT1G27900	na na	Polynucleotidyl 1_9715258 RNA helicase fa 1_9715258	4.76 4.76	promoter downstream
AT1G15825	na	hydroxyproline-i 1_5447888	4.76	intergenic
AT1G70505	na	unknown proteir 1_26570522		promoter
AT1G76892	na	Potential natura 1_28872826		promoter
AT2G17705	na	unknown proteir 2_7692411	4.76	promoter
AT2G17710	na	unknown proteir 2_7692411	4.76	proximal promoter
AT1G15810	na	S15/NS1, RNA- 1_5447888	4.76	intergenic
AT3G45820	na	unknown proteir 3_16840777	4.76	intron
AT4G34110 AT4G23660	POLY(A) BINDING PROTEIN 2 (PAB2) POLYPRENYLTRANSFERASE 1 (PPT1)	Putative poly-A 4_16340989 Encodes para-h 4_12327546	4.76 4.76	intergenic downstream
AT5G62430	CYCLING DOF FACTOR 1 (CDF1)	Dof-type zinc fir 5 25068328		intergenic
AT5G22640	EMBRYO DEFECTIVE 1211 (emb1211)	EMB1211 is a N 5 7529208	4.75	promoter
AT5G38480	GENERAL REGULATORY FACTOR 3 (GI	general regulate 5_15409617	4.75	promoter
AT4G28490	HAESA (HAE)	member of Reci 4_14077449	4.75	promoter
AT3G27350	na	unknown proteir 3_10130039		intergenic
AT3G27360	na	Histone superfa 3_10130039		promoter
AT2G28400	na na	Protein of unknc 2_12149165		promoter
AT3G59580 AT1G63010	na na	Plant regulator I 3_22009016 Major Facilitator 1_23352656		promoter intron
AT2G17960	na	unknown proteir 2 7816606	4.75	intergenic
AT3G28050	na	nodulin MtN21-I 3_10443969		intron
AT4G00200	na	AT hook motif D 4_85047	4.75	promoter
AT4G09160	na	SEC14 cytosolic 4_5839676	4.75	promoter
AT4G16745	na	Exostosin family 4_9415400	4.75	intergenic
AT4G32270	na PHE AMMONIA I VASE 1 (pol1)	Ubiquitin-like su 4_15574827		downstream
AT2G37040 AT4G32260	PHE AMMONIA LYASE 1 (pal1) PIGMENT DEFECTIVE 334 (PDE334)	Encodes PAL1, 2_15561375 ATPase, F0 cor 4 15574827		proximal promoter promoter
AT3G19380	PLANT U-BOX 25 (PUB25)	plant U-box 25 (3 6716821	4.75 4.75	promoter proximal promoter
AT5G67400	ROOT HAIR SPECIFIC 19 (RHS19)	root hair specific 5_26894453		promoter
AT3G27380	SUCCINATE DEHYDROGENASE 2-1 (SD			three_prime_UTR
AT3G11570	TRICHOME BIREFRINGENCE-LIKE 8 (TE		4.75	promoter
AT3G04670	WRKY DNA-BINDING PROTEIN 39 (WRK	member of WRI 3_1269111	4.75	proximal promoter
AT1G28130	(GH3.17)	encodes an IAA 1_9822418	4.74	proximal promoter
AT5G09250	(KIWI)	putative transcri 5_2876638	4.74	promoter
AT2G45190 AT5G45340	ABNORMAL FLORAL ORGANS (AFO) CYTOCHROME P450, FAMILY 707, SUBI	Encodes a prot 5 18373000		intron
AT4G11600	GLUTATHIONE PEROXIDASE 6 (GPX6)		4.74	proximal promoter promoter
AT2G39930	ISOAMYLASE 1 (ISA1)	Encodes an iso: 2_16665629		promoter
AT2G42890	MEI2-LIKE 2 (ML2)	A member of mt 2_17854513		three_prime_UTR
AT2G16720	MYB DOMAIN PROTEIN 7 (MYB7)	Encodes a merr 2_7255949	4.74	exon
AT3G59020	na	ARM repeat sur 3_21817633		promoter
AT1G32650	na	unknown proteir 1_11810002	4.74	intergenic

AT3G15430	na	Regulator of chi 3_5208597	4.74	promoter
AT4G26380	na	Cysteine/Histidii 4_13337931	4.74	promoter
AT1G01880	na	5'-3' exonucleas 1_309758	4.74	proximal promoter
AT1G01890	na	pre-tRNA; tRNA 1_309758	4.74	promoter
AT2G42900	na	Plant basic secr 2_17854513	4.74	promoter
AT4G11610 AT4G34770	na na	C2 calcium/lipid 4_7018487 SAUR-like auxir 4 16587838	4.74 4.74	promoter
AT5G56365	na	pre-tRNA; tRNA 5_22828262	4.74	intergenic downstream
AT5G58640	na	Selenoprotein, F 5 23697745	4.74	promoter
AT3G15500	NAC DOMAIN CONTAINING PROTEIN 3		4.74	intergenic
AT2G43040	NO POLLEN GERMINATION 1 (NPG1)	encodes a calm 2_17899515	4.74	promoter
AT2G34650	PINOID (PID)	Encodes a prot 2_14591922	4.74	promoter
AT5G24520	TRANSPARENT TESTA GLABRA 1 (TTG		4.74	proximal promoter
AT3G23730 AT4G24280	XYLOGLUCAN ENDOTRANSGLUCOSYL CHLOROPLAST HEAT SHOCK PROTEIN		4.74 4.73	proximal promoter promoter
AT1G61340	F-BOX STRESS INDUCED 1 (FBS1)	Encodes a F-bo 1 22627979	4.73	promoter
AT5G10300	METHYL ESTERASE 5 (MES5)	Encodes a prot 5_3239226	4.73	promoter
AT1G55525	na	Unknown gene 1_20728155	4.73	downstream
AT2G20515	na	unknown proteir 2_8839857	4.73	promoter
AT3G29647	na	transposable eli 3_11510280	4.73	intergenic
AT5G10290	na	leucine-rich rep 5_3239226	4.73 4.73	proximal promoter
AT4G31340 AT5G15780	na na	myosin heavy cl 4_15205445 Pollen Ole e 1 a 5_5147419	4.73	promoter proximal promoter
AT1G04430	na	S-adenosyl-L-m 1_1197721	4.73	promoter
AT1G26790	na	Dof-type zinc fir 1_9275370	4.73	promoter
AT1G60010	na	unknown proteir 1_22100041	4.73	intergenic
AT3G24420	na	alpha/beta-Hydr 3_8866883	4.73	proximal promoter
AT4G08850 AT4G18975	na	Leucine-rich rer 4_5640543	4.73	five_prime_UTR
AT4G18975 AT4G24275	na na	Pentatricopeptic 4_10393974 Identified as a s 4_12589876	4.73 4.73	intron intergenic
AT5G23340	na	RNI-like superfa 5 7856009	4.73	promoter
AT5G48412	na	na 5 19624240	4.73	promoter
AT5G52530	na	dentin sialophos 5_21317005	4.73	promoter
AT3G54110	PLANT UNCOUPLING MITOCHONDRIAL		4.73	promoter
AT2G16600	ROTAMASE CYP 3 (ROC3)	Encodes cytosc 2_7200638	4.73	promoter
AT1G55520	TATA BINDING PROTEIN 2 (TBP2)	TATA-box bindii 1_20728155	4.73	promoter
AT2G20510 AT1G73030	TRANSLOCASE INNER MEMBRANE SUB (VPS46.2)	Encodes an ES 1_27473750	4.73 4.72	proximal promoter
AT4G00730	ANTHOCYANINLESS 2 (ANL2)	Encodes a hom 4 304439	4.72	promoter five prime UTR
AT1G21910	DEHYDRATION RESPONSE ELEMENT-E		4.72	proximal promoter
AT5G54510	DWARF IN LIGHT 1 (DFL1)	Encodes an IAA 5_22129588	4.72	intergenic
AT2G28950	EXPANSIN A6 (EXPA6)	Encodes an ext 2_12435673	4.72	proximal promoter
AT1G32550	FERREDOXIN C 2 (FdC2)	Encodes FdC2, 1_11774323	4.72	promoter
AT2G44910	HOMEOBOX-LEUCINE ZIPPER PROTEIN		4.72	intron
AT5G17460 AT1G73020	na na	unknown proteir 5_5759994 unknown proteir 1 27473750	4.72 4.72	promoter
AT1G73020 AT1G64850	na	Calcium-binding 1_24097824	4.72	promoter promoter
AT1G21740	na	Protein of unkno 1_7645474	4.72	intergenic
AT2G45126	na	unknown proteir 2_18605720	4.72	downstream
AT3G60540	na	Preprotein trans 3_22376144	4.72	promoter
AT4G13010	na	Oxidoreductase 4_7600494	4.72	promoter
AT1G31885	NOD26-LIKE INTRINSIC PROTEIN 3;1 (N		4.72	intergenic
AT1G21750 AT3G20250	PDI-LIKE 1-1 (PDIL1-1) PUMILIO 5 (PUM5)	Encodes a prote 1_7645474 Encodes a merr 3_7063504	4.72 4.72	promoter promoter
AT1G64860	SIGMA FACTOR A (SIGA)	Subunit of chlor 1_24097824	4.72	promoter
AT4G22756	STEROL C4-METHYL OXIDASE 1-2 (SMC		4.72	proximal promoter
AT1G56440	TETRATRICOPEPTIDE REPEAT 5 (TPR5		4.72	promoter
AT1G32400	TOBAMOVIRUS MULTIPLICATION 2A (TO		4.72	promoter
AT3G04910	WITH NO LYSINE (K) KINASE 1 (WNK1)		4.72	proximal promoter
AT3G10920	MANGANESE SUPEROXIDE DISMUTASI		4.71	downstream
AT3G29770 AT2G26511	METHYL ESTERASE 11 (MES11) na	Encodes a prote 3_11648338 unknown proteir 2_11277802	4.71 4.71	promoter exon
AT3G63450	na	RNA-binding (R 3_23429965	4.71	proximal promoter
AT3G63460	na	transducin famil 3_23429965	4.71	intergenic
AT3G10930	na	unknown proteir 3_3420059	4.71	downstream
AT3G10030	na	aspartate/glutar 3_3094919	4.71	five_prime_UTR
AT2G26510 AT2G22680	PIGMENT DEFECTIVE EMBRYO 135 (PD WAV3 HOMOLOG 1 (WAVH1)	permease 2_11277802 Zinc finger (C3F 2_9646748	4.71 4.71	downstream exon
AT3G61050	(NTMC2T4)	Encodes a nove 3_22596797	4.71	promoter
AT3G16150	ASPARAGINASE B1 (ASPGB1)	N-terminal nucle 3_5472389	4.7	exon
AT3G01480	CYCLOPHILIN 38 (CYP38)	Encodes a chloi 3_188332	4.7	promoter
AT3G51590	LIPID TRANSFER PROTEIN 12 (LTP12)	Encodes a merr 3_19135784	4.7	three_prime_UTR
AT2G17480	MILDEW RESISTANCE LOCUS O 8 (MLC		4.7	promoter
AT1G02816	na	Protein of unknc 1_621426	4.7	promoter
AT1G74790 AT1G74780	na na	catalytics; FUN(1_28098633 Nodulin-like / M; 1_28098633	4.7 4.7	promoter intergenic
AT2G47100	na	pre-tRNA; tRNA 2_19344511	4.7	downstream
AT3G57770	na	Protein kinase s 3 21397627	4.7	exon
AT3G57760	na	Protein kinase s 3_21397627	4.7	intergenic
AT4G14930	na	Survival protein 4_8538278	4.7	promoter
AT4G31860	na	Protein phospha 4_15409175	4.7	promoter
AT4G32460	na	FUNCTIONS IN 4_15663656	4.7	intron
AT5G40540 AT1G52290	na PROLINE-RICH EXTENSIN-LIKE RECEP	Protein kinase s 5_16236870 Encodes a merr 1_19473487	4.7 4.7	promoter proximal promoter
AT1G52290 AT3G23810	S-ADENOSYL-L-HOMOCYSTEINE (SAH)		4.7	intergenic
AT5G23610	TUBULIN BETA CHAIN 2 (TUB2)	encodes tubulin 5_25181018	4.7	promoter
AT3G57765	U2 SMALL NUCLEOLAR RNA3 (U2.3)	encodes a smal 3_21397627	4.7	exon
AT2G47110	UBIQUITIN 6 (UBQ6)	polyubiquitin ge 2_19344511	4.7	promoter
AT1G17720	(ATB BETA)	type 2A protein 1_6098521	4.69	promoter
AT1G62520	na	unknown proteir 1_23145215	4.69	exon
AT5G03330	no.			
AT4G2Q000	na na	Cysteine proteir 5_805969 Tesmin/TSO1-lil 4_14293332	4.69 4.69	proximal promoter
AT4G29000 AT5G24830	na na na	Tesmin/TSO1-lil 4_14293332	4.69 4.69 4.69	promoter
AT4G29000 AT5G24830 AT1G17730	na	Tesmin/TSO1-lil 4_14293332 Tetratricopeptid 5_8529517	4.69	

AT2G35600				
	BREVIS RADIX-LIKE 1 (BRXL1)	Belongs to five- 2_14945502	4.68	promoter
AT4G00330	CALMODULIN-BINDING RECEPTOR-LIK		4.68	five_prime_UTR
AT3G52370	FASCICLIN-LIKE ARABINOGALACTAN P	FASCICLIN-like 3_19417233	4.68	promoter
AT1G65960	GLUTAMATE DECARBOXYLASE 2 (GAD		4.68	intron
AT2G18840	na	Integral membra 2_8158157	4.68	promoter
AT1G15240	na	Phox-associate 1_5243357	4.68	promoter
AT1G77520	na	O-methyltransfe 1_29130116	4.68	promoter
AT2G43120	na	RmlC-like cupin 2_17927216	4.68	promoter
AT2G17730	NEP-INTERACTING PROTEIN 2 (NIP2)	Intrinsic thylakoi 2_7703954	4.68	five_prime_UTR
AT3G53180	NODULIN/GLUTAMINE SYNTHASE-LIKE		4.68	promoter
AT1G20980 AT1G13210	SQUAMOSA PROMOTER BINDING PRO AUTOINHIBITED CA2+/ATPASE II (ACA.I)		4.68 4.67	intergenic proximal promoter
AT3G23150	ETHYLENE RESPONSE 2 (ETR2)	Involved in ethy 3 8254592	4.67	promoter
AT2G22840	GROWTH-REGULATING FACTOR 1 (GR		4.67	proximal promoter
AT1G07090	LIGHT SENSITIVE HYPOCOTYLS 6 (LSH		4.67	proximal promoter
AT1G13220	LITTLE NUCLEI2 (LINC2)	Encodes a nucli 1_4515265	4.67	promoter
AT1G13360	na	unknown proteir 1_4581071	4.67	intergenic
AT1G54420	na	unknown proteir 1_20311715	4.67	intron
AT1G54410	na	dehydrin family 1_20311715	4.67	proximal promoter
AT4G32570	TIFY DOMAIN PROTEIN 8 (TIFY8)	TIFY domain pr. 4_15717910	4.67	intron
AT2G29740	UDP-GLUCOSYL TRANSFERASE 71C2 (UDP-glucosyl tr 2_12707877	4.67	exon
AT3G19450	(ATCAD4)	Encodes a catal 3_6743596	4.66	proximal promoter
AT3G60120	BETA GLUCOSIDASE 27 (BGLU27)	beta glucosidas 3_22205758	4.66	promoter
AT2G20900	DIACYLGLYCEROL KINASE 5 (DGK5)	diacylglycerol ki 2_8993173	4.66	promoter
AT2G31230	ETHYLENE-RESPONSIVE ELEMENT BIN		4.66	proximal promoter
AT3G12970	na	unknown proteir 3_4142576	4.66	promoter
AT1G49840	na	Protein of unknc 1_18452002	4.66	promoter
AT1G65870	na	Disease resista 1_24503405	4.66	promoter
AT1G73600	na	S-adenosyl-L-m 1_27665771	4.66	intergenic
AT3G23080	na	Polyketide cycla 3_8209319	4.66	intron
AT3G27880	na	Protein of unknc 3_10338356	4.66 4.66	five_prime_UTR
AT4G00085 AT4G00090	na na	pre-tRNA; tRNA 4_33940 Transducin/WD 4_33940	4.66	downstream promoter
AT1G16880		Encodes a ACT 1 5775524	4.65	intron
AT3G03050	ACT DOMAIN REPEATS 11 (ACR11) CELLULOSE SYNTHASE-LIKE D3 (CSLD		4.65	promoter
AT1G12920	EUKARYOTIC RELEASE FACTOR 1-2 (E		4.65	promoter
AT3G56090	FERRITIN 3 (FER3)	Encodes FERR 3_20816025	4.65	five_prime_UTR
AT3G56085	na	pre-tRNA; tRNA 3_20816025	4.65	proximal promoter
AT5G55830	na	Concanavalin A 5_22594454	4.65	promoter
AT1G50659	na	na 1 18771128	4.65	five_prime_UTR
AT1G50660	na	unknown proteir 1_18771128	4.65	five_prime_UTR
AT1G48960	na	Adenine nucleo 1_18112445	4.65	promoter
AT1G26208	na	Potential natura 1_9069403	4.65	promoter
AT3G04920	na	Ribosomal prote 3_1359844	4.65	proximal promoter
AT3G27200	na	Cupredoxin sup 3_10043809	4.65	exon
AT3G62580	na	Late embryoger 3_23146751	4.65	promoter
AT4G30370	na	RING/U-box su _i 4_14859897	4.65	promoter
AT5G13181	na	This gene encor 5_4201833	4.65	proximal promoter
AT5G58575	na	CONTAINS Inte 5_23673533	4.65	promoter
AT2G30520	ROOT PHOTOTROPISM 2 (RPT2)	light inducible rc 2_13005734	4.65	promoter
AT2G22970	SERINE CARBOXYPEPTIDASE-LIKE 11 (4.65	intergenic
AT2G22980	SERINE CARBOXYPEPTIDASE-LIKE 13 (4.65	
				promoter
AT5G56180	ACTIN-RELATED PROTEIN 8 (ARP8)	encodes a prote 5_22741203	4.64	promoter
AT5G56180 AT1G23740	ALKENAL/ONE OXIDOREDUCTASE (AO	AOR is an alker 1_8399917	4.64 4.64	promoter promoter
AT5G56180 AT1G23740 AT5G13010	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011)	AOR is an alker 1_8399917 embryo defectiv 5_4121598	4.64 4.64 4.64	promoter promoter proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12)	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598	4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419	4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156	4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203	4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na na na na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264	4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter intergenic
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unknc 3_18027857	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter intergenic proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na na na na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc: 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn: 3_18027857 Protein kinase s 1_28648202	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter intergenic proximal promoter proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT2G35710	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na na na na na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn 3_18027857 Protein kinase s 1_28648202 Nucleotide-diph 2_15015949	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter intergenic proximal promoter proximal promoter proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na na na na na na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc: 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn: 3_18027857 Protein kinase s 1_28648202	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter intergenic proximal promoter proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT2G21172 AT3G48660 AT2G35710 AT4G17960 AT4G17960 AT4G31075 AT4G31080	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn 3_18027857 Protein kinase s 1_28648202 Nucleotide-diph 2_15015949 unknown proteir 4_9969619 pre-tRNA; tRNA 4_15120745 Protein in of unkn 4_15120745	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter intergenic proximal promoter proximal promoter proximal promoter downstream promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13010 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G31075 AT4G31075 AT4G31080 AT2G35720	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gen 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn 3_18027857 Protein kinase s 1_28648202 Nucleotide-diph 2_15015949 unknown proteir 4_9969619 pre-tRNA; tRNA 4_15120745 Protein of unkn 4_15120745 Encodes OWL1 2_15015949	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G17960 AT4G31080 AT2G35720 AT2G35720 AT2G21770	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1,7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3,18027857 Protein kinase s 1,28648202 Nucleotide-diph 2, 15015949 unknown proteir 4,9969619 pre-tRNA; tRNA 4, 15120745 Protein of unkn 4,15120745 Protein of unkn 4,15120745 Encodes OWL1 2,15015949 Encodes a plasi 2,9073264	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter downstream promoter proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT1G256190 AT2G21172 AT3G48660 AT2G35710 AT4G17960 AT4G31075 AT4G31080 AT2G35720 AT2G35720 AT2G21170 AT1G64780	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn 3_18027857 Protein kinase s 1_28648202 Nucleotide-diph 2_15015949 unknown proteir 4_9969619 pre-tRNA; tRNA 4_15120745 Protein of unkn 4_15120745 Encodes OWL1 2_15015949 encodes a plasi 2_9073264 encodes an ami 1_24061067	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter intergenic proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13010 AT4G37420 AT1G22430 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT1G76360 AT4G31075 AT4G31080 AT2G35710 AT2G21170 AT1G64780 AT4G3170 AT1G64780 AT4G35310	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn 3_18027857 Protein kinase s 1_28648202 Nucleotide-diph 2_15015949 unknown proteir 4_9969619 pre-tRNA; tRNA 4_15120745 Protein of unkn 4_15120745 Encodes OWL1 2_15015949 Encodes an ami 1_24061067 calmodulin-dom 4_16801874	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter proximal promoter intron proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G17960 AT4G31080 AT2G35720 AT2G35720 AT2G35720 AT3G4783510 AT3G17998	ALKENAL/ONE OXIDOREDUCTASE (AO) EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1,7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3,18027857 Protein kinase s 1,28648202 Nucleotide-diph 2, 15015949 unknown proteir 4,9969619 pre-tRNA; tRNA 4, 15120745 Protein of unkn 4,15120745 Protein of unkn 4,1512074	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter promoter exon promoter proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G17960 AT4G31075 AT4G31075 AT4G31075 AT4G35720 AT1G64780 AT1G64780 AT3G17998 AT1G28200	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn 3_18027857 Protein kinase s 1_28648202 Nucleotide-diph 2_15015949 unknown proteir 4_9969619 pre-tRNA; tRNA 4_15120745 Protein of unkn 4_15120745 Protein of unkn 4_15120745 encodes OWL1 2_15015949 encodes an ami 1_24061067 calmodulin-dom 4_16801874 Upstream open 3_6153792 VirF-interacting 1_9852486	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter promoter exon promoter proximal promoter exon promoter proximal promoter proximal promoter proximal promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13010 AT4G37420 AT1G22430 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT1G76360 AT4G31075 AT4G31075 AT4G31080 AT2G35710 AT2G21170 AT3G21170 AT4G4780 AT4G35310 AT4G35310 AT4G35310 AT4G35310 AT4G35310 AT4G35310 AT4G35310 AT4G35310 AT4G35310 AT4G3617998 AT4G28200 AT2G01430	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn 3_18027857 Protein kinase s 1_28648202 Nucleotide-diph 2_15015949 unknown proteir 4_9969619 pre-tRNA; tRNA 4_15120745 Protein of unkn 4_15120745 Encodes OWL1 2_15015949 Encodes a plasi 2_9073264 encodes an am 1_24061067 calmodulin-dom 4_16801874 Upstream open 3_6153792 VirF-interacting 1_9852486 homeobox-leuci 2_193435	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter proximal promoter intron proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G17960 AT4G31080 AT2G35720 AT2G21170 AT1G64780 AT3G17998 AT1G28200 AT3G17998 AT1G28201 AT3G17998 AT1G28200 AT3G01430 AT3G02550	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 Domain of unkn 4, 17594419 GroES-like zinc: 1,7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn: 3,18027857 Protein kinases: 1,28648202 Nucleotide-diph 2, 15015949 unknown proteir 4,9969619 pre-tRNA; tRNA 4,15120745 Protein of unkn:	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter promoter exon promoter promoter promoter promoter intergenic proximal promoter promoter promoter intergenic proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter promoter promoter promoter promoter promoter promoter proximal promoter promote
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT2G35710 AT4G17960 AT4G31075 AT4G31075 AT4G35720 AT2G21170 AT1G64780 AT1G64780 AT1G28200 AT2G01430 AT2G01430 AT2G01430	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1,8399917 embryo defectiv 5,4121598 encodes a gene 5,4121598 encodes a gene 5,4121598 Domain of unkn 4,17594419 GroES-like zinc 1,7920156 Transducin/WD 5,22741203 Pseudogene of 2,9073264 Protein of unkn 3,18027857 Protein kinase s 1,28648202 Nucleotide-diph 2,15015949 unknown proteir 4,9969619 pre-tRNA; tRNA 4,15120745 Protein of unkn 4,15120745 Protein of unkn 4,15120745 Encodes OWL1 2,15015949 encodes a plasi 2,9073264 encodes an ami 1,24061067 calmodulin-dom 4,16801874 Upstream open 3,6153792 VirF-interacting 1,9852486 homeobox-leuci 2,193435 LOB domain-co 3,539488 member of MAF 2,202311	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter proximal promoter proximal promoter intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter exon promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic proximal promoter intron
AT5G56180 AT1G23740 AT5G13010 AT5G13010 AT4G37420 AT1G22430 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT1G76360 AT4G31075 AT4G31075 AT4G31080 AT2G35710 AT1G64780 AT2G35720 AT2G21170 AT1G64780 AT4G35310 AT3G17998 AT1G28200 AT2G01430 AT2G01430 AT2G01450 AT1G07170	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1_8399917 embryo defectiv 5_4121598 encodes a gene 5_4121598 Domain of unkn 4_17594419 GroES-like zinc 1_7920156 Transducin/WD 5_22741203 Pseudogene of 2_9073264 Protein of unkn 3_18027857 Protein kinase s 1_28648202 Nucleotide-diph 2_15015949 unknown proteir 4_9969619 pre-tRNA; tRNA 4_15120745 Protein of unkn 4_15120745 Protein of unkn 4_15120745 Encodes OWL1 2_15015949 Encodes a plasi 2_9073264 encodes an am 1_24061067 calmodulin-dom 4_16801874 Upstream open 3_6153792 VirF-interating 1_9852486 homeobox-leuci 2_193435 LOB domain-co 3_539488 member of MAF 2_202311 Similar to humai 1_2200027	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter promoter proximal promoter intergenic proximal promoter intron promoter
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G17960 AT4G31080 AT2G35720 AT2G21170 AT1G64780 AT3G17998 AT1G28200 AT3G17998 AT1G28200 AT3G17998 AT1G28200 AT3G17998 AT1G28200 AT3G17998 AT1G28200 AT3G17998 AT1G28200 AT3G17998 AT1G28200 AT3G17998 AT1G28200 AT3G1430 AT3G17998 AT1G61480	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 encodes a gene 6, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1,7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3,18027857 Protein kinases s 1,28648202 Nucleotide-diph 2, 15015949 unknown proteir 4,9969619 pre-tRNA; tRNA 4, 15120745 Protein of unkn 4, 15120745 Protein of unkn 4, 15120745 Encodes a plasi 2, 9073264 encodes an am 1, 24061067 calmodulin-dom 4,16801874 Upstream open 3, 6153792 VirF-interacting 1,9852486 homeobox-leuci 2,193435 LOB domain-co 3,539488 member of MAF 2, 202311 Similar to humai 1,2200027 pre-tRNA; tRNA 1,22866716	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter promoter exon promoter promoter promoter intergenic proximal promoter intergenic proximal promoter intergenic proximal promoter intron promoter downstream
AT5G56180 AT1G23740 AT5G13010 AT5G13010 AT4G37420 AT1G22430 AT1G22430 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G17960 AT4G31075 AT4G35100 AT2G21170 AT1G64780 AT4G35310 AT2G21170 AT1G64780 AT2G21170 AT1G64780 AT2G21170 AT1G64780 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1,8399917 embryo defectiv 5,4121598 encodes a gene 5,4121598 encodes a gene 5,4121598 Domain of unkn 4,17594419 GroES-like zinc 1,7920156 Transducin/WD 5,22741203 Pseudogene of 2,9073264 Protein of unkn 3,18027857 Protein kinase s 1,28648202 Nucleotide-diph 2,15015949 unknown proteir 4,9969612 Protein of unkn 4,15120745 Protein of unkn 4,15120745 Protein of unkn 4,15120745 Encodes OWL1 2,15015949 encodes a plasi 2,9073264 encodes an ami 1,24061067 calmodulin-dom 4,16801874 Upstream open 3,6153792 VirF-interacting 1,9852486 homeobox-leuci 2,193435 LOB domain-co 3,539488 member of MAF 2,202311 Similar to humai 1,2200027 pre-tRNA; tRNA 1,22866716 DEAD/DEAH bx 2,193435	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter promoter proximal promoter exon intron proximal promoter promoter exon promoter proximal promoter intergenic proximal promoter intergenic proximal promoter intron promoter downstream intergenic
ATSG56180 AT1G23740 AT5G13010 AT5G13010 AT4G37420 AT1G22430 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT1G76360 AT4G31075 AT4G31075 AT4G31080 AT2G35710 AT1G64780 AT1G64780 AT4G21770 AT1G64780 AT4G31080 AT4G3107998 AT1G28200 AT2G011430 AT3G01790 AT1G61880 AT1G61880	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 encodes a gene 6, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1,7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3,18027857 Protein kinases s 1,28648202 Nucleotide-diph 2, 15015949 unknown proteir 4,9969619 pre-tRNA; tRNA 4, 15120745 Protein of unkn 4, 15120745 Protein of unkn 4, 15120745 Encodes a plasi 2, 9073264 encodes an am 1, 24061067 calmodulin-dom 4,16801874 Upstream open 3, 6153792 VirF-interacting 1,9852486 homeobox-leuci 2,193435 LOB domain-co 3,539488 member of MAF 2, 202311 Similar to humai 1,2200027 pre-tRNA; tRNA 1,22866716	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter intergenic proximal promoter intergenic proximal promoter intron promoter downstream intergenic intergenic intergenic intergenic
AT5G56180 AT1G23740 AT5G13010 AT5G13010 AT4G37420 AT1G22430 AT1G22430 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G17960 AT4G31075 AT4G35100 AT2G21170 AT1G64780 AT4G35310 AT2G21170 AT1G64780 AT2G21170 AT1G64780 AT2G21170 AT1G64780 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1 . 8399917 embryo defectiv 5 _4121598 encodes a gene 5 .4121598 encodes a gene 5 .4121598 Domain of unkn 4_17594419 GroES-like zinc 1 _7920156 Transducin/WD 5 _22741203 Pseudogene of 2_9073264 Protein of unkn 3_18027857 Protein kinase s 1_28648202 Nucleotide-diph 2_15015949 unknown proteir 4_9969619 unknown proteir 4_9969619 unknown proteir 4_9969619 pre-tRNA; tRNA 4_15120745 Protein of unkn 4_15120745 Encodes OWL1 2_15015949 Encodes an ami 1_24061067 calmodulin-dom 4_16801874 Upstream open 3_6153792 VirF-interacting 1_9952486 homeobox-leuci 2_193435 LOB domain-co 3_539488 member of MAF 2_202311 Similar to humai 1_2200027 pre-tRNA; tRNA 1_22866716 EAD/DEAH bc 2_193435 MATE efflux fan 1_22866716	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter promoter proximal promoter exon intron proximal promoter promoter exon promoter proximal promoter intergenic proximal promoter intergenic proximal promoter intron promoter downstream intergenic
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G17960 AT4G31080 AT2G35720 AT2G21170 AT1G64780 AT3G17998 AT1G28200 AT3G17998 AT1G28200 AT2G01450 AT2G01450 AT2G01450 AT2G01450 AT2G01450 AT1G61880 AT2G01440 AT3G02555	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 Domain of unkn 4, 17594419 GroES-like zinc: 1,7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn: 3,18027857 Protein kinases: 1,28648202 Nucleotide-diph 2, 15015949 unknown proteir 4,9969619 pre-tRNA; tRNA 4, 15120745 Protein of unkn: 4,15120745 Protein of unkn:	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter intergenic proximal promoter intergenic intergenic intergenic intergenic intergenic intergenic intergenic downstream intergenic downstream
AT5G56180 AT1G23740 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT2G35710 AT4G17998 AT4G35370 AT2G21170 AT1G64780 AT2G21170 AT1G64780 AT2G21170 AT1G64780 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21430 AT2G21440 AT1G61890 AT2G01440 AT3G12555 AT4G10270	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1 .8399917 embryo defectiv 5 _4121598 encodes a gene 5 _4121598 Domain of unkn 4 _17594419 GroES-like zinc 1 _7920156 Transducinr\(^{1}\)D 5 _22741203 Pseudogene of 2 _9073264 Protein of unkn 3 _18027857 Protein kinase s 1 _28648202 Nucleotide-diph 2 _15015949 unknown proteir 4 _9969619 unknown proteir 4 _9969619 pre-tRNA; tRNA 4 _15120745 Protein of unkn 4 _15120745 Locales OWL1 2 _15015949 Unknown proteir 4 _19861874 Upstream open 3 _6153792 VirF-interacting 1 _9852486 homeobox-leuci 2 _193435 LOB domain-co 3 _539488 member of MAF 2 _202311 Similar to humai 1 _2200027 pre-tRNA; tRNA 1 _22866716 Unknown proteir 3 _539488 Wound-respons 4 _6374600 NGATHA1 (NG, 2 _19260886	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter promoter exon promoter proximal promoter proximal promoter intergenic proximal promoter intron promoter downstream intergenic intergenic intergenic downstream promoter
ATSG56180 AT1G23740 AT5G13010 AT5G13010 AT4G37420 AT1G22430 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT1G76360 AT4G31075 AT4G31080 AT2G21170 AT1G64780 AT3G4780 AT3G17998 AT1G28200 AT2G21170 AT1G64780 AT3G17998 AT1G28200 AT2G1170 AT1G61880 AT3G01440 AT1G61880 AT3G02555 AT4G10270 AT1G246870	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 encodes a gene 5, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1, 7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3, 18027857 Protein kinases s 1, 28648202 Nucleotide-diph 2, 15015949 unknown proteir 4, 9969619 pre-tRNA; tRNA 4, 15120745 Protein of unkn 4, 15120745 Protein of unkn 4, 15120745 Encodes a plasi 2, 9073264 encodes an am 1, 24061067 calmodulin-dom 4,16801874 Upstream open 3, 6153792 VirF-interacting 1, 9852486 homeobox-leuci 2, 193435 LOB domain-co 3, 539488 member of MAF 2, 202311 Similar to humai 1, 22806716 DEAD/DEAH bc 2, 193435 MATE efflux fan 1, 22866716 unknown proteir 3, 539488 Wound-respons 4, 6374600 NGATHA1 (NG, 2, 19260886) pectin methyles 3, 21807013	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter intergenic proximal promoter intron promoter downstream intergenic intergenic intergenic downstream promoter
ATSG56180 AT1G23740 AT5G13010 AT5G13010 AT5G13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT4G31080 AT4G31080 AT2G35710 AT4G31080 AT2G35720 AT2G21170 AT1G64780 AT3G5720 AT3G17998 AT1G28200 AT2G01450 AT2G01450 AT2G01450 AT3G17998 AT1G61880 AT2G01450 AT2G01450 AT3G17970 AT1G61880 AT3G02555 AT4G10270 AT3G2646870 AT3G59010	ALKENAL/ONE OXIDOREDUCTASE (ADI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1, 7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3, 18027857 Protein kinases 1, 28648202 Nucleotide-diph 2, 15015949 unknown proteir 4, 99699619 pre-IRNA; IRNA 4, 15120745 Protein of unkn 4, 15120745 Protein of unk	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter promoter promoter promoter promoter promoter promoter proximal promoter promoter promoter promoter intergenic proximal promoter intergenic intergenic intergenic intergenic downstream intergenic downstream promoter pr
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ATISG56180 ATIG23740 ATISG13010 ATISG13010 ATISG13010 ATISG13000 ATISG56190 ATISG2430 ATISG56190 ATISG5720	ALKENAL/ONE OXIDOREDUCTASE (ADI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1, 7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3, 18027857 Protein kinases 1, 28648202 Nucleotide-diph 2, 15015949 unknown proteir 4, 9969619 pre-IRNA; IRNA 4, 15120745 Protein of unkn 4, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter intergenic proximal promoter intergenic downstream intergenic downstream promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic intergenic proximal promoter proximal promoter proximal promoter intergenic proximal promoter promoter promoter promoter proximal promoter promoter promoter proximal promoter promoter promoter proximal promoter promoter promoter promoter proximal promoter promoter promoter promoter proximal promoter
ATSG56180 ATIG23740 ATSG13010 ATSG13010 ATSG13000 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT4G31075 AT4G31080 AT2G35710 AT1G64780 AT2G35710 AT1G64780 AT3G17998 AT1G28200 AT2G01450 AT2G01450 AT2G01450 AT2G01450 AT3G01850 AT2G01450 AT3G02555 AT4G10270 AT1G61870 AT3G58010 AT3G58010 AT3G58010 AT3G58010 AT3G58010 AT3G58010 AT3G58080 AT3G58080	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 encodes a gene 5, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1, 7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3, 18027857 Protein kinases s 1, 28648202 Nucleotide-diph 2, 15015949 unknown proteir 4, 9969619 pre-tRNA; tRNA 4, 15120745 Protein of unkn 2, 15015949 Encodes a plasi 2, 9073264 encodes an ami 1, 24061067 calmodulin-dom 4, 16801874 Upstream open 3, 6153792 VirF-interacting 1, 9852486 homeobox-leuci 2, 193435 LOB domain-co 3, 539488 member of MAF 2, 202311 Similar to humai 1, 22806716 DEAD/DEAH bc 2, 193435 MATE efflux fan 1, 22866716 unknown proteir 3, 539488 Wound-respons 4, 6374600 NGATHA1 (NG, 2, 19260866 pectin methyles 3, 21807013 pentatricopeptic 1, 22866716 Arabidopsis thai 3, 6153792 Inositol phosph 3, 20008581 Encodes a cyto 5, 19792178 Elixologes a trans 5, 23419192	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic proximal promoter intergenic downstream intergenic intergenic downstream promoter promoter promoter promoter promoter promoter proximal proxim
ATSG56180 AT1G23740 AT5G13010 AT5G13010 AT5G13010 AT5G13010 AT4G37420 AT1G22430 AT5G56190 AT2G21172 AT3G48660 AT1G76360 AT4G35710 AT4G17960 AT4G31075 AT4G31075 AT4G31075 AT4G31080 AT2G35720 AT2G21170 AT1G64780 AT4G35310 AT3G17998 AT3G2555 AT4G10270 AT1G61880 AT3G02555 AT4G10270 AT1G61880 AT3G02555 AT4G10270 AT1G61880 AT3G02555 AT4G10270 AT1G61880 AT3G59010 AT3G59010 AT3G54020 AT3G54020 AT5G548810 AT1G355800 AT5G57800 AT5G55730	ALKENAL/ONE OXIDOREDUCTASE (AOI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 encodes a gene 6, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1, 7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3, 18027857 Protein kinases 1, 28648202 Nucleotide-diph 2, 15015949 unknown proteir 4, 9969619 Pre-tRNA; 1RNA 4, 15120745 Protein of unkn 4, 15120745 Protein of unkn 4, 15120745 Encodes OWL1 2, 15015949 encodes a plasi 2, 9073264 encodes an ami 1, 24061067 calmodulin-dom 4, 1680187, Upstream open 3, 6153792 VirF-interacting 1, 9852486 homeobox-leuci 2, 193435 LOB domain-co 3, 539488 member of MAF 2, 202311 Similar to humai 1, 22006716 DEAD/DEAH bc 2, 193435 MATE efflux fan 1, 22866716 DEAD/DEAH bc 2, 193435 MATE efflux fan 1, 22866716 DRAD/DEAH bc 2, 1936888 Wound-respons 4, 6374600 NGATHA1 (NG. 2, 19260886 Pectin methyles 3, 21807013 pentatricopeptic 1, 22866716 Arabidopsis thai 3, 6153792 Incodes a trans 5, 23419192 Encodes fascid 5, 22560558	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic proximal promoter intergenic downstream intergenic intergenic downstream promoter proximal promoter promoter
ATISG56180 ATIG23740 ATISG13010 ATISG13010 ATISG13010 ATISG13000 ATISG56190 ATISG2430 ATISG56190 ATISG56190 ATISG56190 ATISG56190 ATISG56190 ATISG56190 ATISG56190 ATISG56190 ATISG56190 ATISG5700 ATISG5700 ATISG5700 ATISG5700 ATISG64780 ATISG65730 ATISG65730	ALKENAL/ONE OXIDOREDUCTASE (ADI EMBRYO DEFECTIVE 3011 (EMB3011) GLUCAN SYNTHASE-LIKE 12 (GSL12) na	AOR is an alker 1, 8399917 embryo defectiv 5, 4121598 encodes a gene 5, 4121598 Domain of unkn 4, 17594419 GroES-like zinc 1, 7920156 Transducin/WD 5, 22741203 Pseudogene of 2, 9073264 Protein of unkn 3, 18027857 Protein kinases 1, 28648202 Nucleotide-diph 2, 15015949 unknown proteir 4, 9969619 pre-tRNA; tRNA 4, 15120745 Protein of unkn 4, 12001594 Encodes a plasi 2, 9073264 encodes an am 1, 24061067 calmodulin-dom 4, 16801874 Upstream open 3, 6153792 VirF-interacting 1, 9852486 homeobox-leuci 2, 193435 LOB domain-co 3, 539488 member of MAF 2, 202311 Similar to humal 1, 2200027 pre-tRNA; tRNA 1, 22866716 Unknown proteir 3, 539488 Wound-respons 4, 6374600 NGATHA1 (NG, 2, 19260886 pectin methyles 3, 21807013 pentatricopeptic 1, 22866716 Arabidopsis thal 3, 6153792 Inositol phosph 3, 20008581 Encodes a cvto 5, 19792178 CINV1 / AN-Inv 1, 13125423 encodes a trans 5, 23419192 Encodes fascicl 5, 22560558 Kip-related prot 5, 19792178	4.64 4.64 4.64 4.64 4.64 4.64 4.64 4.64	promoter promoter promoter proximal promoter exon intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic proximal promoter intergenic downstream promoter proximal promoter downstream
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AT1G19160				
	na	F-box family prc 1_6614167	4.62	exon
AT1G55675		unknown proteir 1_20803670	4.62	downstream
AT1G55680		Transducin/WD 1_20803670	4.62	intergenic
AT1G66180		The gene encor 1_24650245	4.62	intergenic
AT1G19150	PHOTOSYSTEM I LIGHT HARVESTING (4.62	downstream
AT1G55670		Encodes subun 1_20803670	4.62	promoter
AT2G33330	PLASMODESMATA-LOCATED PROTEIN		4.62	intergenic
AT5G46790		Encodes a merr 5_18982405	4.62	intergenic
AT2G40330	PYR1-LIKE 6 (PYL6)	Encodes a merr 2_16846073	4.62	promoter
AT1G76030		One of three ge 1_28533799	4.62	five_prime_UTR
AT3G02720	(DJ1D)	Class I glutamin 3_586201	4.61	promoter
AT1G20440	COLD-REGULATED 47 (COR47)	Belongs to the c 1_7086709	4.61	proximal promoter
AT5G09463	CONSERVED PEPTIDE UPSTREAM OPE	Upstream open 5_2943960	4.61	three_prime_UTR
AT5G09462	CONSERVED PEPTIDE UPSTREAM OPE		4.61	three_prime_UTR
AT5G09461	CONSERVED PEPTIDE UPSTREAM OPE		4.61	three_prime_UTR
AT5G15850	CONSTANS-LIKE 1 (COL1)	Homologous to 5_5177696	4.61	five_prime_UTR
AT5G15845	na	Potential natura 5_5177696	4.61	five_prime_UTR
AT5G15853	na	unknown proteir 5_5177696	4.61	promoter
AT2G02370	na	SNARE associa 2_620904	4.61	promoter
AT4G01090	na	Protein of unknc 4_473820	4.61	promoter
AT4G35610	na	zinc finger (C2F 4_16900491	4.61	promoter
AT5G52840	na	NADH-ubiquino 5_21412898	4.61	proximal promoter
AT1G15280	na	CASC3/Barents 1_5252215	4.61	promoter
AT1G48450	na	Protein of unknc 1_17911214	4.61	proximal promoter
AT1G48460	na	unknown proteir 1_17911214	4.61	promoter
AT1G63750	na	Disease resistal 1_23650525	4.61	promoter
AT1G15270	na	Translation mac 1_5252215	4.61	promoter
AT3G02715	na	pre-tRNA; tRNA 3_586201	4.61	downstream
AT2G21300	na	ATP binding mic 2_9121353	4.61	proximal promoter
AT3G08670	na	unknown proteir 3_2633261	4.61	promoter
AT4G33040	na	Thioredoxin sup 4_15939711	4.61	intergenic
AT5G09450	na	Tetratricopeptid 5_2943960	4.61	intergenic
AT5G09460	na	sequence-speci 5_2943960	4.61	three_prime_UTR
AT4G29390		Ribosomal prote 4_14466096	4.61	promoter
AT5G40450		unknown proteir 5_16195735	4.61	promoter
AT5G55896		transposable eli 5_22634136	4.61	proximal promoter
AT5G67411		GRAS family tra 5_26899801	4.61	proximal promoter
AT2G02360		phloem protein : 2_620904	4.61	promoter
AT5G15860	PRENYLCYSTEINE METHYLESTERASE		4.61	intergenic
AT3G62440	SECONDARY WALL THICKENING-ASSO		4.61	promoter
AT2G22300		Encodes a puta 2_9471355	4.61	intron
AT5G52830	WRKY DNA-BINDING PROTEIN 27 (WRK		4.61	intergenic
AT4G37410	CYTOCHROME P450, FAMILY 81, SUBFA		4.6	proximal promoter
AT3G47490		HNH endonucle 3_17501556	4.6	intergenic
AT5G19730		Pectin lyase-lik€ 5_6671581	4.6	intron
AT5G01110		Tetratricopeptid 5 40975	4.6	intergenic
AT3G17070		Peroxidase fam 3_5820429	4.6	proximal promoter
AT4G17890		A member of AF 4_9936410	4.59	proximal promoter
AT3G53460	CHLOROPLAST RNA-BINDING PROTEIN		4.59	downstream
AT5G42900		cold regulated g 5_17199863	4.59	promoter
AT2G40880		Encodes a prot 2_17057326	4.59	promoter
AT1G13090	CYTOCHROME P450, FAMILY 71, SUBFA		4.59	promoter
AT3G04290		Li-tolerant lipase 3_1134211	4.59	intron
AT1G18835		Encodes a smal 1_6497108	4.59	proximal promoter
AT2G40860		protein kinase f: 2_17057326	4.59	promoter
AT3G26910		hydroxyproline-ı 3_9918850	4.59	promoter
AT4G18820		AAA-type ATPa 4 10328375		
			4.59	proximal promoter
AT3G02560			4.59 4.59	proximal promoter
AT3G02560 AT3G04605	na	Ribosomal prote 3_541544	4.59	promoter
AT3G04605	na na	Ribosomal prote 3_541544 transposable ele 3_1246598	4.59 4.59	promoter promoter
AT3G04605 AT3G13670	na na na	Ribosomal prote 3_541544 transposable ele 3_1246598 Protein kinase f. 3_4469124	4.59 4.59 4.59	promoter promoter promoter
AT3G04605 AT3G13670 AT3G02555	na na na na	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544	4.59 4.59 4.59 4.59	promoter promoter promoter promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760	na na na na na	Ribosomal prote 3_541544 transposable ele 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788	4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter proximal promoter
AT3G04605 AT3G13670 AT3G02555	na na na na na na	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zint 3_18074788 Adenine nucleol 3_19989473	4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter proximal promoter three_prime_UTR
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G53990	na na na na na na na	Ribosomal prote 3_541544 transposable ele 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788	4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter proximal promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G53990 AT5G04390	na na na na na na na na	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleol 3_19989473 C2H2-type zinc 5_1238925	4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter proximal promoter three_prime_UTR promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G53990 AT5G04390 AT5G40720	na na na na na na na na	Ribosomal prote 3_541544 transposable elt 3_1246598 Protein kinase f: 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleo: 3_19889473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G53990 AT5G04390 AT5G40720 AT5G39770	na NO VEIN-LIKE (NVL) PHOTOSYSTEM II SUBUNIT P-1 (PSBP-1	Ribosomal prots 3_541544 transposable els 3_1246598 Protein kinase f: 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleo: 3_19899473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE : 1_2614523 Encodes a 23 k 1_2047796	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G53990 AT5G04390 AT5G40720 AT5G39770 AT1G08300	na NO VEIN-LIKE (NVL) PHOTOSYSTEM II SUBUNIT P-1 (PSBP-1	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleol 3_1998473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE 11_2614523	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G53990 AT5G04390 AT5G39770 AT1G08300 AT1G06680	na NO VEIN-LIKE (NVL) PHOTOSYSTEM II SUBUNIT P-1 (PSBP-1	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleoi 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nt 5_15927934 NO VEIN-LIKE 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter promoter promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G53990 AT5G04390 AT5G39770 AT1G08680 AT1G06680 AT1G44750	na PHOTOSYSTEM II SUBUNIT P-1 (PSBP-1 PURINE PERMEASE 11 (PUP11)	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleo 3_1998473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl. 1_7324459	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter promoter promoter promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G53990 AT5G04390 AT5G40720 AT5G39770 AT1G06880 AT1G44750 AT1G20980	na n	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleo 3_1989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE i 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nuclei 1_73244459 sugar-depender 3_21150642	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter promoter promoter promoter promoter promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G53990 AT5G04390 AT5G40720 AT1G08300 AT1G06680 AT1G44750 AT1G20980 AT3G57140	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleo 3_1998473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl. 1_7324459	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter promoter promoter promoter promoter three_prime_UTR
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G03990 AT5G04390 AT5G40720 AT5G39770 AT1G08300 AT1G44750 AT1G20980 AT3G57140 AT3G57140 AT4G28390	na n	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleor 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE 11_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_14043385	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter proximal promoter promoter exon promoter promote
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3GG53990 AT5G04390 AT1G08300 AT1G06880 AT1G44750 AT1G2980 AT3G257140 AT4G28390 AT4G28390 AT3G23760	na n	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleor 3_1998473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a ment 4_14043385 Encodes a ment 2_10108148	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR promoter exon
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G6539970 AT5G040720 AT5G39770 AT1G08680 AT1G44750 AT1G20880 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G57140 AT3G50660	na n	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleor 3_19898473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents na fs_15927934 NO VEIN-LIKE i 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mer 2_10108148 Encodes a 22& 3_18819638 Encodes a 4IFH, 4_1424880	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR promoter exon proximal promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G653990 AT5G04707 AT1G08300 AT1G08300 AT1G08300 AT1G02080 AT1G20980 AT3G57140 AT4G28390 AT2G23760 AT3G50660 AT4G03240	na n	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleor 3_19898473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents na fs_15927934 NO VEIN-LIKE i 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mer 2_10108148 Encodes a 22& 3_18819638 Encodes a 4IFH, 4_1424880	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter proximal promoter promoter exon promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G63990 AT5G40720 AT5G39770 AT1G06880 AT1G44750 AT1G2980 AT3G57140 AT4G28390 AT3G57660 AT3G50660 AT3G50660 AT3G50660 AT3G63240 AT1G68200	na n	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleor 3_1998473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mer 2_10108148 Encodes a z28k 3_18819638 Encodes AtFH, 4_1424880 encodes a cytot 1_24658463	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter proximal promoter three_prime_UTR promoter exon promoter promoter promoter promoter promoter promoter three_prime_UTR promoter exon proximal promoter promoter promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G635990 AT5G04390 AT5G40720 AT1G08800 AT1G06680 AT1G44750 AT1G2980 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT4G03240 AT1G50460 AT1G50460 AT1G50460 AT3G01510 AT3G01510	na n	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleo 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 CONTAINS Inte 5_16299627 Represents an 5_15927934 NO VEIN-LIKE 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_114043385 Encodes a mer 2_10108148 Encodes a 228k 3_18819638 Encodes at Fith 4_1424880 encodes a cytot 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 3_201832	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter promoter proximal promoter three_prime_UTR promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR promoter exon proximal promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G639990 AT5G40720 AT1G08300 AT1G08300 AT1G08680 AT1G44750 AT1G20980 AT3G57140 AT4G283760 AT3G57140 AT4G283760 AT4G03240 AT4G6200 AT1G66200 AT1G66200 AT1G6400 AT3G01510	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleol 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE 1_2614523 Encodes a 23 k l _2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_14043385 Encodes a mer 2_10108148 Encodes a cytox 1_2468463 Involved in gluc 1_18691722 Encodes a quta 1_2468463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 3_201832 unknown proteir 3_201832 unknown proteir 2_10108148	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter promoter promoter promoter promoter exon promoter prominal promoter prominal promoter proximal promoter proximal promoter proximal promoter proximal promoter prominal promoter prominal promoter prominal promoter promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G635990 AT5G04390 AT5G40720 AT1G08800 AT1G06680 AT1G44750 AT1G2980 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT4G03240 AT1G50460 AT1G50460 AT1G50460 AT3G01510 AT3G01510	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleoi 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents an s_15927934 NO VEIN-LIKE i 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucle 1_7324459 sugar-depender 3_21150642 Encodes a merc 2_10108148 Encodes a 22& 3_18819638 Encodes AIFH, 4_1424880 encodes a cytos 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 2_10108148 unknown proteir 2_1108148	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter downstream
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G635990 AT5G40720 AT5G39770 AT1G0680 AT1G44750 AT1G2980 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT3G03240 AT1G50460 AT3G01510 AT3G01511 AT3G01511 AT3G01513 AT3G23755	na n	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleo 3_1998473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Sepresents a nr 5_15927934 NO VEIN-LIKE I _2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_14043385 Encodes a mem 2_10108148 Encodes a relito 4_14043385 Encodes a relito 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 2_10108148 unknown proteir 2_14851896 RNA-binding Kf 1_3131209	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter promoter proximal promoter three_prime_UTR promoter promoter promoter promoter promoter promoter three_prime_UTR promoter three_prime_UTR promoter exon proximal promoter promoter promoter promoter downstream intergenic
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G639990 AT5G049720 AT1G08300 AT1G08300 AT1G08300 AT1G20980 AT3G57140 AT4G28390 AT2G23760 AT4G6200 AT4G65200 AT4G65200 AT3G01510 AT3G01513 AT3G01513 AT3G23755 AT2G332560	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleoi 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents an s_15927934 NO VEIN-LIKE i 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucle 1_7324459 sugar-depender 3_21150642 Encodes a merc 2_10108148 Encodes a 22& 3_18819638 Encodes AIFH, 4_1424880 encodes a cytos 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 2_10108148 unknown proteir 2_1108148	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter downstream intergenic three_prime_UTR
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G035990 AT5G04390 AT5G40720 AT1G08800 AT1G06680 AT1G44750 AT1G2980 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT4G03240 AT1G50460 AT3G01510 AT3G01511 AT3G01513 AT3G01513 AT3G035260 AT1G03660	na n	Ribosomal prots 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleo 3_1998473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Sepresents a nr 5_15927934 NO VEIN-LIKE I _2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_14043385 Encodes a mem 2_10108148 Encodes a relito 4_14043385 Encodes a relito 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 2_10108148 unknown proteir 2_14851896 RNA-binding Kf 1_3131209	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter proximal promoter proximal promoter proximal promoter pro
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G035990 AT5G040720 AT5G39770 AT1G06680 AT1G06680 AT1G44750 AT3G2980 AT3G57140 AT4G28390 AT3G50660 AT3G03240 AT1G50460 AT3G01510 AT3G01510 AT3G01511 AT2G23755 AT2G35260 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560 AT3G0560	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleol 3_1998473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mer 2_10108148 Encodes a mer 2_10108148 Encodes a mer 2_10108148 Encodes a type 1_41424880 encodes a cytic 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 3_201832 unknown proteir 2_10108148 unknown proteir 2_10108148 unknown proteir 2_1131209 AMP-dependen 1_28518862	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter promoter promoter promoter promoter proximal promoter exon promoter proximal promoter proximal promoter proximal promoter promoter downstream intergenic three_prime_UTR promoter exon
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G639990 AT5G40720 AT1G08300 AT1G08300 AT1G08300 AT1G20980 AT3G57140 AT4G28390 AT2G23760 AT4G6200 AT4G6200 AT4G65200 AT3G01513 AT3G5150460 AT3G01513 AT3G23755 AT2G323755 AT2G32560 AT1G08660 AT1G5960 AT1G5960 AT1G5960 AT1G75970	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleoi 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents an s_15927934 NO VEIN-LIKE i 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mer 2_10108148 Encodes a 22& 3_18819638 Encodes a Cytor 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 2_10108148 unknown proteir 2_14851896 RNA-binding Kh 1_3131209 AMP-dependen 1_28518862 pre-IRNA; tRNA 1_28518862	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.58	promoter pro
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G035990 AT5G04390 AT5G40720 AT5G039770 AT1G06880 AT1G44750 AT1G06880 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT4G03240 AT1G50460 AT4G03240 AT1G50460 AT4G03250 AT1G75970 AT1G75970 AT4G03250	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleoi 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents an s_15927934 NO VEIN-LIKE i 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucle 1_7324459 sugar-depender 3_21150642 Encodes a merc 2_10108148 Encodes a 22& 3_18819638 Encodes a 22& 3_18819638 Encodes a vitor 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 2_14081480 encodes a cytor 1_24658463 Unknown proteir 2_14851896 RNA-binding KF 1_3131209 AMP-dependen 1_28518862 Homeodomain-1 4_1424880 Mitochondrial in 5_9674282 Mog1/Psb/VD 5_9674282	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter pro
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G035990 AT5G040720 AT5G03770 AT1G06680 AT1G06680 AT1G04750 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT4G03240 AT1G50460 AT3G01510 AT3G01511 AT2G23755 AT2G35260 AT1G75960 AT1G75960 AT1G75970 AT4G03255 AT5G27395	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleol 3_1998473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_14043385 Encodes a mem 2_10108148 Encodes a 228 s 1_8819638 Encodes a description of a far 1_16892566 Encodes a mem 2_10108148 Encodes a cytos 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 3_201832 unknown proteir 2_10108148 unknown proteir 2_10108148 unknown proteir 2_14851896 RNA-binding kh 1_3131209 AMP-dependen 1_28518862 pre-tRNA; tRNA 1_28518862 Momeodomain-1_41424880 Mitochondrial in 5_9674282	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G635990 AT5G40720 AT5G39770 AT1G06880 AT1G44750 AT1G20980 AT2G23760 AT3G50660 AT4G03240 AT1G66200 AT3G50460 AT3G01513 AT2G23755 AT2G35260 AT1G5960 AT1G5960 AT1G5960 AT1G5960 AT1G75970 AT1G75970 AT3G032390 AT3G27399	na n	Ribosomal prots 3_541544 transposable els 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleor 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE: 1_2614523 Encodes a 28 k 1_2047796 Member of a far 1_16892566 Encodes a nucl: 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_14043385 Encodes a mito 4_14043385 Encodes a 22& 3_18819638 Encodes a 22& 3_18819638 Encodes a Vito: 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 3_2115018148 unknown proteir 2_14851896 RNA-binding KH = 1_3131209 AMP-dependen 1_28518862 pre-tRNA; tRNA 1_28518862	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.58	promoter prominal promoter proximal promoter proximal promoter promoter downstream intergenic three_prime_UTR promoter exon intergenic promoter promoter promoter promoter promoter promoter promoter promoter promoter downstream intergenic promoter promoter downstream downstream intergenic promoter promoter downstream
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G635990 AT5G04390 AT5G40720 AT5G039770 AT1G06880 AT1G44750 AT1G06880 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT4G03240 AT1G50460 AT3G01510 AT3G01511 AT2G23755 AT3G235260 AT1G75970 AT1G75970 AT4G03250 AT5G27399 AT5G273990 AT5G273990	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleoi 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents an s_15927934 NO VEIN-LIKE 11_2614523 Encodes a 28 k 1_2047796 Member of a far 1_16892566 Encodes a nucle 1_7324459 sugar-depender 3_21150642 Encodes a merc 2_10108148 Encodes a 22& 3_18819638 Encodes AIFH, 4_1424880 encodes a ovtor 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 2_14081481 unknown proteir 2_141851896 RNA-binding KF 1_33131209 AMP-dependen 1_28518862 Homeodomain-1 4_1424880 Mitochondrial in 5_9674282 unknown proteir 2_14851896 RNA-binding KF 1_33131209 AMP-dependen 1_28518862 Homeodomain-1 4_1424880 Mitochondrial in 5_9674282 unknown proteir 5_22323484 Encodes an ER 1_7692525 member of SYP 1_2711148	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.58	promoter downstream intergenic
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G035990 AT5G040720 AT5G039770 AT1G08680 AT1G06680 AT1G06680 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT3G50660 AT4G03240 AT1G50460 AT3G01510 AT3G01511 AT2G23755 AT2G35260 AT1G75960 AT1G75960 AT1G75970 AT4G03250 AT5G27395	na n	Ribosomal prots 3_541544 transposable els 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleor 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE: 1_2614523 Encodes a 28 k 1_2047796 Member of a far 1_16892566 Encodes a nucl: 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_14043385 Encodes a mito 4_14043385 Encodes a 22& 3_18819638 Encodes a 22& 3_18819638 Encodes a Vito: 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 3_2115018148 unknown proteir 2_14851896 RNA-binding KH = 1_3131209 AMP-dependen 1_28518862 pre-tRNA; tRNA 1_28518862	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59	promoter proximal promoter proximal promoter promoter downstream intergenic three_prime_UTR promoter exon intergenic promoter downstream intergenic promoter
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G035990 AT5G040720 AT5G03770 AT1G08680 AT1G06680 AT1G06680 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT4G03240 AT1G50460 AT3G01510 AT3G01510 AT3G01513 AT2G23755 AT2G35260 AT1G75960 AT1G75970 AT1G75970 AT4G03250 AT5G27395 AT5G27395 AT5G27395 AT5G27395 AT5G27390 AT1G21900 AT1G08560 AT1G1085601 AT1G108560	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleoi 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE: 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_14043385 Encodes a mito 4_14043385 Encodes a 22&3_18819638 Encodes a 22&3_18819638 Encodes a 24&3_18819638 Encodes a 24&3_18819638 Encodes a 25&3_18819638 Encodes a 25&3_201832 unknown proteir 2_14851896 RNA-binding K1_3131209 AMP-dependen 1_28518862 pre-tRNA; tRNA 1_28518862 pre-tRNA; tRNA 1_28518862 pre-tRNA; tRNA 1_28518862 unknown proteir 5_22323484 Encodes an ER_1_692525 member of SYP 1_2711148 AGAMOUS-like 1_17235423 aldolase like (Al 4_12512243	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.58	promoter pro
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G035990 AT5G04390 AT5G04390 AT1G06880 AT1G44750 AT1G20980 AT3G357140 AT1G20980 AT3G357140 AT1G66200 AT1G50460 AT3G01510 AT3G01511 AT3G01513 AT2G23755 AT5G237390 AT1G29370 AT4G03250 AT1G29370 AT4G03250 AT1G23750 AT5G27395 AT5G27395 AT5G27390 AT5G27390 AT5G257390 AT5G257390 AT1G21900 AT1G21900 AT1G21900 AT1G46408 AT1G46408 AT1G464080 AT1G464080 AT1G464080	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleoi 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents an s_15927934 NO VEIN-LIKE i 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucle 1_7324459 sugar-depender 3_21150642 Encodes a merc 2_10108148 Encodes a 22& 3_18819638 Encodes a 22& 3_18819638 Encodes a 22& 3_18819638 Encodes a vitor 1_24658463 Involved in gluc 1_18691722 Encodes a puta 3_201832 unknown proteir 3_201832 unknown proteir 2_14851896 RNA-binding KF 1_3131209 AMP-dependen 1_28518862 Homeodomain-1 4_1424880 Mitochondrial in 5_9674282 unknown proteir 2_14851896 RNA-binding KF 1_3131209 AMP-dependen 1_28518862 Homeodomain-1 4_1424880 Mitochondrial in 5_9674282 unknown proteir 5_22323484 Encodes an ER 1_7692525 member of SYP 1_2711148 AGAMOUS-like 1_17235423 Encodes a thior 1_28549667	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.58 4.57 4.57 4.57 4.57	promoter pro
AT3G04605 AT3G13670 AT3G02555 AT3G48760 AT3G035990 AT5G040720 AT5G03770 AT1G08680 AT1G06680 AT1G06680 AT3G57140 AT4G28390 AT3G57140 AT4G28390 AT3G50660 AT4G03240 AT1G50460 AT3G01510 AT3G01510 AT3G01513 AT2G23755 AT2G35260 AT1G75960 AT1G75970 AT1G75970 AT4G03250 AT5G27395 AT5G27395 AT5G27395 AT5G27395 AT5G27390 AT1G21900 AT1G08560 AT1G1085601 AT1G108560	na n	Ribosomal prote 3_541544 transposable eli 3_1246598 Protein kinase fi 3_4469124 unknown proteir 3_541544 DHHC-type zinc 3_18074788 Adenine nucleoi 3_19989473 C2H2-type zinc 5_1238925 CONTAINS Inte 5_16299627 Represents a nr 5_15927934 NO VEIN-LIKE: 1_2614523 Encodes a 23 k 1_2047796 Member of a far 1_16892566 Encodes a nucl 1_7324459 sugar-depender 3_21150642 Encodes a mito 4_14043385 Encodes a mito 4_14043385 Encodes a 22&3_18819638 Encodes a 22&3_18819638 Encodes a 24&3_18819638 Encodes a 24&3_18819638 Encodes a 25&3_18819638 Encodes a 25&3_201832 unknown proteir 2_14851896 RNA-binding K1_3131209 AMP-dependen 1_28518862 pre-tRNA; tRNA 1_28518862 pre-tRNA; tRNA 1_28518862 pre-tRNA; tRNA 1_28518862 unknown proteir 5_22323484 Encodes an ER_1_692525 member of SYP 1_2711148 AGAMOUS-like 1_17235423 aldolase like (Al 4_12512243	4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.58	promoter pro

AT5G46417	na	unknown proteir 5_18829795	4.57	exon
AT2G40620	na	Basic-leucine zi 2_16953919	4.57	intergenic
AT4G24090	na	unknown proteir 4_12512243	4.57	promoter
AT5G49334	na	This gene encor 5_20005293	4.57	proximal promoter
AT4G21865	na	unknown proteir 4_11604474	4.57	intergenic
AT4G21870	na	HSP20-like chal 4_11604474	4.57	promoter
AT4G21880	na	Pentatricopeptic 4_11604474	4.57	proximal promoter
AT1G35350	na	EXS (ERD1/XPI 1_12986647	4.57	proximal promoter
AT1G69300	na	pre-tRNA; tRNA 1_26050894	4.57	intergenic
AT3G10470	na	C2H2-type zinc 3_3259729	4.57	proximal promoter
AT2G28920 AT2G36690	na na	RING/U-box su ₁ 2_12419910 2-oxoglutarate (2_15375200	4.57 4.57	intergenic intergenic
AT3G18815	na	pre-tRNA; tRNA 3_6484098	4.57	promoter
AT3G44190	na	FAD/NAD(P)-bii 3 15903601	4.57	five_prime_UTR
AT4G22850	na	SNARE associa 4_11993804	4.57	promoter
AT4G22840	na	Sodium Bile aci 4 11993804	4.57	promoter
AT1G06160	OCTADECANOID-RESPONSIVE ARABID	_	4.57	proximal promoter
AT1G69295	PLASMODESMATA CALLOSE-BINDING I		4.57	intron
AT3G18820	RAB GTPASE HOMOLOG G3F (RAB7B)		4.57	five_prime_UTR
AT1G76090	STEROL METHYLTRANSFERASE 3 (SM	Encodes S-adei 1_28549667	4.57	intergenic
AT5G06600	UBIQUITIN-SPECIFIC PROTEASE 12 (UE	Encodes a ubiq 5_2028070	4.57	promoter
AT5G03630	(ATMDAR2)	ATMDAR2; FUI 5_924815	4.56	promoter
AT2G16280	3-KETOACYL-COA SYNTHASE 9 (KCS9)	Encodes KCS9, 2_7053116	4.56	downstream
AT5G14250	CONSTITUTIVE PHOTOMORPHOGENIC		4.56	downstream
AT3G50700	INDETERMINATE(ID)-DOMAIN 2 (IDD2)	zinc finger prote 3_18839781	4.56	proximal promoter
AT4G01090	na	Protein of unkno 4_470121	4.56	intergenic
AT1G74910	na	ADP-glucose py 1_28138800	4.56	intron
AT3G50695	na	This gene enco 3_18839781	4.56	proximal promoter
AT4G17540 AT5G14260	na	unknown proteir 4_9775644 Rubisco methyll 5 4600892	4.56	promoter
	na BAB CTDASE HOMOLOG 4C (BAB4C)	AtRabD2c enco 4 9775644	4.56	promoter
AT4G17530 AT4G01080	RAB GTPASE HOMOLOG 1C (RAB1C) TRICHOME BIREFRINGENCE-LIKE 26 (T		4.56 4.56	promoter
AT5G38880	AUGMIN SUBUNIT 5 (AUG5)	unknown proteir 5 15569272	4.55	proximal promoter promoter
AT5G05980	DHFS-FPGS HOMOLOG B (DFB)	Encodes one of 5_1804607	4.55	promoter
AT1G47990	GIBBERELLIN 2-OXIDASE 4 (GA2OX4)	Encodes a gibb 1_17700008	4.55	exon
AT4G01575	na	serine protease 4_682860	4.55	promoter
AT1G79700	na	Integrase-type [1_29992909	4.55	intron
AT4G02620	na	vacuolar ATPas 4 1151467	4.55	promoter
AT4G02630	na	Protein kinase s 4 1151467	4.55	promoter
AT4G17250	na	unknown proteir 4_9673307	4.55	exon
AT4G17260	na	Lactate/malate (4_9673307	4.55	proximal promoter
AT5G05985	na	pre-tRNA; tRNA 5_1804607	4.55	promoter
AT5G38890	na	Nucleic acid-bin 5_15569272	4.55	promoter
AT1G60800	NSP-INTERACTING KINASE 3 (NIK3)	NSP-interacting 1_22388294	4.55	proximal promoter
AT1G06530	PEROXISOMAL AND MITOCHONDRIAL I	Encodes PERO 1_2000699	4.55	proximal promoter
AT2G29700	PLECKSTRIN HOMOLOGUE 1 (PH1)	Encodes a prote 2_12697403	4.55	promoter
AT2G22010	RELATED TO KPC1 (RKP)	Encodes a prote 2_9369418	4.55	intron
AT2G35780	SERINE CARBOXYPEPTIDASE-LIKE 26 (4.55	promoter
AT2G42200	SQUAMOSA PROMOTER BINDING PRO	Encodes a puta 2 17585665	4.55	proximal promoter
AT2G34070	TRICHOME BIREFRINGENCE-LIKE 37 (T	Encodes a merr 2_14388739	4.55	intron
AT2G34070 AT2G27040	ARGONAUTE 4 (AGO4)	Encodes a merr 2_14388739 AGO4 is a merr 2_11542464	4.55 4.54	intron promoter
AT2G34070 AT2G27040 AT3G26300	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBFA	Encodes a merr 2_14388739 AGO4 is a merr 2_11542464 putative cytochr 3_9641089	4.55 4.54 4.54	intron promoter promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBFA CYTOCHROME P450, FAMILY 71, SUBFA	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089	4.55 4.54 4.54 4.54	intron promoter promoter intron
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBFA CYTOCHROME P450, FAMILY 71, SUBFA GLUTAMATE RECEPTOR 1.1 (GLR1.1)	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutama 3_1077194	4.55 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN	Encodes a merr 2_14388739 AGO4 is a merr 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of 2_7044737	4.55 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of 1_2_7044737 Encodes heat-s 4_11340271	4.55 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320 AT4G16480	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4)	Encodes a merr 2_14388739 AGO4 is a merr 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutam: 3_1077194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter promoter downstream
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT2G22510	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF/ CYTOCHROME P450, FAMILY 71, SUBF/ GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a mer 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutam: 3_1077194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter downstream intergenic
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF/ CYTOCHROME P450, FAMILY 71, SUBF/ GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_10777194 pseudogene of 1_27044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1_2_9668548 MATE efflux fan 1_24901960	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter promoter downstream intergenic promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G39420	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter downstream intergenic promoter intergenic
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G39420 AT4G39420 AT4G32190	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na na na	Encodes a mer 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutam: 3_1077194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter downstream intergenic promoter intergenic promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G39420 AT4G32190 AT5G63620	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF/ CYTOCHROME P450, FAMILY 71, SUBF/ GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na na na na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of 1_27044737 Encodes heal-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1_2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc 5_25468386	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter promoter downstream intergenic promoter intergenic promoter intergenic promoter five_prime_UTR
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G39420 AT4G39420 AT4G32190	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na na na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc 5_25468386 unknown proteir 1_1974526	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter downstream intergenic promoter intergenic promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT4G32190 AT4G32190 AT5G63620 AT5G63620 AT1G06475	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na na na na na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of 1_27044737 Encodes heal-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1_2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc 5_25468386	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter downstream intergenic promoter intergenic promoter five_prime_UTR promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT3G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G39420 AT4G32190 AT5G63620 AT1G06475 AT1G56670	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na na na na na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-l 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc 5_25468386 unknown proteir 1_1974526 GDSL-like Lipas 1_21242096 F-box/FBD-like 1_23963424 RING/U-box suj 3_9122050	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter promoter downstream intergenic promoter intergenic promoter five_prime_UTR promoter intron
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G263110 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G39420 AT4G32190 AT5G63620 AT1G645676 AT1G645676 AT1G64540 AT1G64540 AT4G216490	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na na na na na na na	Encodes a mer 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutam: 3_1077194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc 5_25468386 unknown proteir 1_1974526 GDSL-like Lipas 1_21242096 F-box/FBD-like 1_23963424 RING/U-box suj 3_9122050 ARM repeat sur 4_9293410	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter promoter promoter downstream intergenic promoter intergenic promoter five_prime_UTR promoter intron intergenic promoter downstream
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G39420 AT5G63620 AT1G06475 AT1G66570 AT1G64540 AT3G25030 AT3G25030 AT4G16490 AT5G41400	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutam: 3_10777194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1_2 9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc 5_25468386 unknown proteir 1_1974526 GDSL-like Lipsa 1_21242096 F-box/FBD-like 1_23963424 RING/U-box suj 3_9122050 ARM repeat suj 4_9293410 RING/U-box suj 5_16569022	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter promoter promoter downstream intergenic promoter five_prime_UTR promoter intron intergenic promoter downstream intergenic
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G64110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G32190 AT5G63620 AT1G666760 AT1G666760 AT1G666760 AT1G666760 AT1G66760 AT1G66760 AT1G66760 AT1G66760 AT1G66760 AT1G66760 AT1G66760 AT1G66760 AT1G66760 AT1G66760 AT1G66760 AT1G66760 AT3G25030 AT4G16490 AT3G29370	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc-5_25468336 unknown proteir 1_1974526 GDSL-like Lipas 1_21242096 F-box/FBD-like 1_23963424 RING/U-box su; 3_9122050 ARM repeat su; 4_9293410 RING/U-box su; 5_16569022 Encodes a atyp 3_1127632	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter promoter downstream intergenic promoter intergenic promoter five_prime_UTR promoter intron intergenic promoter downstream intergenic promoter downstream intergenic promoter downstream intergenic proximal promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G263110 AT3G04110 AT2G16260 AT4G21320 AT4G16480 AT1G66760 AT4G39420 AT1G66760 AT4G39420 AT1G6475 AT1G66476 AT1G66476 AT1G66470 AT1G64540 AT3G25030 AT3G25030 AT3G26307 AT3G29370 AT3G29370 AT1G28340	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a mer 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc-5_25468386 unknown proteir 1_1974526 GDSL-like Lipas 1_21242096 F-box/FBD-like 1_23963424 RING/U-box su; 3_9122050 ARM repeat su; 4_9293410 RING/U-box su; 5_16569022 Encodes a atyp 3_11276832 receptor like pr: 1_9939986	4.55 4.54	intron promoter promoter intron promoter promoter promoter promoter promoter downstream intergenic promoter five_prime_UTR promoter intron intergenic promoter downstream intergenic promoter downstream intergenic promoter downstream intergenic promoter downstream intergenic proximal promoter promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G26310 AT3G6260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G39420 AT5G63620 AT1G64540 AT3G25030 AT4G64540 AT3G25030 AT4G641400 AT3G29370 AT1G28340 AT4G29370 AT4G29370 AT4G28340	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutams 3_10777194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1_29568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc 5_25468386 unknown proteir 1_1974526 GDSL-like Lipsa 1_21242096 F-box/FBD-like 1_23963424 RING/U-box suj 3_9122050 ARM repeat sur 4_9293410 RING/U-box suj 5_16569022 Encodes a atypi 3_11276832 enceptor like prc 1_9939986 Encodes a plasi 4_18355477	4.55 4.54	intron promoter promoter intron promoter promoter promoter promoter promoter promoter downstream intergenic promoter five_prime_UTR promoter intron intergenic promoter downstream intergenic promoter downstream intergenic proximal promoter proximal promoter intergenic
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G64110 AT2G16260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G32190 AT5G63620 AT1G66670 AT1G66670 AT1G66670 AT1G664540 AT3G25030 AT4G16490 AT3G29370 AT1G28340 AT3G29370 AT1G28340 AT3G29370 AT3G39460 AT3G48000	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF- CYTOCHROME P450, FAMILY 71, SUBF- GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutam: 3_1077194 pseudogene of :2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc 5_25468386 unknown proteir 1_1974526 GDSL-like Lipas 1_21242096 F-box/FBD-like 1_23963424 RING/U-box suj 3_9122050 ARM repeat suj 4_9293410 RING/U-box suj 5_1659022 Encodes a atyp 3_11276832 receptor like prc 1_9939986 Encodes a puta 3_17720062	4.55 4.54	intron promoter promoter intron promoter promoter promoter promoter downstream intergenic promoter intergenic promoter intergenic promoter intron intergenic promoter downstream intergenic promoter downstream intergenic proximal promoter promoter intergenic proximal promoter promoter intergenic promoter intergenic
ATZG34070 ATZG27040 AT3G26300 AT3G26310 AT3G263110 AT3G04110 ATZG16260 AT4G21320 AT4G16480 ATG2622510 AT1G66760 AT4G39420 ATG63620 ATIG64540 ATJG25030	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a mer 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1_2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc-5_25468386 unknown proteir 1_1974526 GDSL-like Lipas 1_21242096 F-box/FBD-like 1_23963424 RING/U-box su; 3_9122050 ARM repeat su; 4_9293410 RING/U-box su; 5_16569022 Encodes a atyp 3_11276832 receptor like prc 1_9939986 Encodes a plasi 4_18355477 Encodes a plasi 4_17720062 CBL-interacting 5_23340676	4.55 4.54 4.55 4.56	intron promoter promoter intron promoter promoter promoter promoter promoter promoter downstream intergenic promoter five_prime_UTR promoter intron intergenic promoter downstream intergenic promoter intron intergenic promoter downstream intergenic proximal promoter proximal promoter promoter intergenic promoter downstream intergenic promoter downstream intergenic promoter downstream
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G26310 AT3G6260 AT4G21320 AT4G16480 AT2G22510 AT1G66760 AT4G394290 AT5G63620 AT1G64540 AT3G25030 AT4G16490 AT5G41400 AT5G41400 AT3G29370 AT4G38460 AT4G38460 AT3G3848000 AT3G48000 AT3G48000 AT3G48000 AT3G857630 AT2G32720	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutam: 3_10777194 pseudogene of: 2_7044737 Encodes a high 4_9293410 Encodes a high 4_18355477 Encodes a plasi 1_124901960 Encodes a Encodes a High 4_18355477 Encodes a plasi 4_18355479	4.55 4.54 4.55	intron promoter promoter intron promoter promoter promoter promoter promoter promoter downstream intergenic promoter five_prime_UTR promoter intron intergenic promoter downstream intergenic promoter downstream intergenic proximal promoter promoter intergenic proximal promoter promoter intergenic promoter downstream intergenic promoter downstream promoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G626310 AT3G16260 AT4G21320 AT4G16480 AT4G329420 AT4G32190 AT5G63620 AT1G66670 AT1G66670 AT1G66670 AT1G66670 AT1G64540 AT3G25030 AT4G16490 AT3G29370 AT1G28340 AT3G29370 AT3G24615	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na na na na na na na na na P1R3 (P1R3) RECEPTOR LIKE PROTEIN 4 (RLP4) S-ADENOSYLMETHIONINE CARRIER 1 ALDEHYDE DEHYDROGENASE 2B4 (AL CBL-INTERACTING PROTEIN KINASE 21 CYTOCHROME B5 ISOFORM B (CB5-B) na	Encodes a merr 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutamr 3_1077194 pseudogene of 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like Lipas 1_21242096 F-box/FBD-like 1_23963424 RING/U-box suj 3_9122050 ARM repeat suj 4_9293410 RING/U-box suj 3_9122050 ARM repeat suj 4_9293410 RING/U-box suj 5_1659022 Encodes a atyp 3_11276832 receptor like prc 1_9939986 Encodes a puta 3_17720062 CBL-interacting 5_23340676 member of Cyto 2_13878799 Encodes a 243_3_8979867	4.55 4.54 4.55	intron promoter promoter intron promoter promoter promoter promoter promoter promoter downstream intergenic promoter five_prime_UTR promoter intron intergenic promoter downstream intergenic promoter downstream intergenic proximal promoter promoter intergenic proximal promoter promoter downstream promoter downstream promoter promoter formoter
AT2G34070 AT2G27040 AT3G26300 AT3G26310 AT3G26310 AT3G26310 AT4G1320 AT4G16480 AT4G39420 AT4G39420 AT5G63620 AT1G66567 AT1G66567 AT1G64540 AT3G25030 AT3G25030 AT3G16490 AT3G29370 AT1G28340 AT3G3948000 AT3G39763 AT2G32720 AT3G24615 AT3G324615	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF- CYTOCHROME P450, FAMILY 71, SUBF- GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a mer 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutams 3_1077194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc-5_25468386 unknown proteir 1_1974526 GDSL-like Lipas 1_21242096 F-box/FBD-like 1_23963424 RING/U-box su; 3_9122050 ARM repeat su; 4_9293410 RING/U-box su; 5_16569022 Encodes a atyp 3_11276832 receptor like prc 1_9939986 Encodes a plasi 4_18355477 Encodes a plasi 4_18356476 member of Cyto 2_13878799 Encodes a 243 3_8979867 Ribonuclease III 3_4504165	4.55 4.54 4.53	intron promoter promoter intron promoter promoter promoter promoter promoter promoter promoter downstream intergenic promoter five_prime_UTR promoter intron intergenic promoter downstream intergenic promoter downstream intergenic promoter downstream intergenic proximal promoter promoter intergenic proximal promoter promoter downstream promoter promoter promoter promoter promoter promoter promoter promoter
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ATZG34070 ATZG27040 AT3G26300 AT3G26310 AT3G04110 AT3G16260 AT4G21320 AT4G16480 AT4G39420 AT4G332190 AT5G63620 AT1G66567 AT1G665760 AT4G32190 AT5G63620 AT1G64540 AT3G25303 AT3G16490 AT5G41400 AT3G29370 AT1G28340 AT3G32720 AT3G32720 AT3G32730 ATZG32720 AT3G348100 AT3G348100 AT3G34810 AT3G451210 AT3G34810 AT3G451210 AT3G51210	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF/ CYTOCHROME P450, FAMILY 71, SUBF/ GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a merr 2_14388739 AGO4 is a memr 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutams 3_1077194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-1 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc-5_25468386 unknown proteir 1_1974526 GDSL-like lipas 1_21242096 F-box/FBD-like 1_23963424 RING/U-box su; 5_16569022 Encodes a atps; 3_9122050 ARM repeat su; 4_9293410 RING/U-box su; 5_16569022 Encodes a atps; 3_9122650 ARM repeat su; 4_9293410 RING/U-box su; 5_16569022 Encodes a plasi 4_18355477 Encodes a plasi 4_18356476 member of Cyto 2_13878799 Encodes a 243 3_8979867 Ribonuclease III 3_4504165 P-loop containir 3_19020214 Tyrosyl-IRNA s; 2_14314855 SBP (S-ribonucl 1_3522914 This gene enco: 3_22864392 NAD(P)-binding 4_7658277 Plant protein of 5_6136794 unknown proteir 5_26887416 Encodes a sphil 4_11462852 VP1/ABI3-like 3 4_11462852	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter intron promoter promoter promoter promoter promoter promoter promoter intergenic promoter five_prime_UTR promoter intergenic promoter downstream intergenic promoter downstream intergenic promoter intergenic promoter intergenic promoter intergenic promoter intergenic promoter intergenic promoter intergenic promoter intergenic promoter intergenic promoter
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AT2G34070 AT2G27040 AT3G26310 AT3G26310 AT3G26310 AT3G26310 AT3G21320 AT4G16260 AT4G21320 AT4G68760 AT1G66760 AT1G66760 AT1G66760 AT3G29370 AT1G28340 AT3G29370 AT1G28340 AT3G29370 AT1G28340 AT3G367630 AT2G37270 AT1G66560 AT3G4760 AT3G476	ARGONAUTE 4 (AGO4) CYTOCHROME P450, FAMILY 71, SUBF, CYTOCHROME P450, FAMILY 71, SUBF, GLUTAMATE RECEPTOR 1.1 (GLR1.1) GLYCINE-RICH RNA-BINDING PROTEIN HEAT-STRESS-ASSOCIATED 32 (HSA32 INOSITOL TRANSPORTER 4 (INT4) na	Encodes a mer 2_14388739 AGO4 is a mem 2_11542464 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative cytochr 3_9641089 putative glutam: 3_1077194 pseudogene of: 2_7044737 Encodes heat-s 4_11340271 Encodes a high 4_9293410 hydroxyproline-l 2_9568548 MATE efflux fan 1_24901960 unknown proteir 4_18355477 Myosin heavy c 4_15544653 GroES-like zinc: 5_25468386 unknown proteir 1_974526 GDSL-like tipas: 1_21242096 F-box/FBD-like: 1_23963424 RING/U-box suj 3_9122050 ARM repeat sur 4_9293410 RING/U-box suj 3_9122050 ARM repeat sur 4_9293410 RING/U-box suj 3_9122050 ARM repeat sur 4_9293410 RING/U-box suj 3_9122050 CBL-interacting 5_23340676 member of Cyto 2_13878799 Encodes a palsa 4_178355477 Encodes a puta 3_17720062 CBL-interacting 5_23340676 member of Cyto 2_13878799 Encodes a Z43_3_8979867 Ribonuclease III 3_4504165 P-loop containir 3_19020214 Tyrosyl-tRNA s_2_14314855 SBP (S-ribonucl 1_3522914 Tyrosyl-tRNA s_2_14314855 SBP (S-ribonucl 1_3522914 unknown proteir 5_6136794 unknown proteir 5_6136794 unknown proteir 5_688277 Plant protein of 5_6136794 unknown proteir 5_26887416 Encodes an en 1_10690905 Encodes a men 1_10690905 Encodes a men 1_10690905 Encodes a unce 4_16205149 Aldolase superf 2_15298580	4.55 4.54 4.54 4.54 4.54 4.54 4.54 4.54	intron promoter promoter intron promoter promoter promoter promoter promoter promoter downstream intergenic promoter five_prime_UTR promoter intron intergenic promoter intron intergenic promoter downstream intergenic promoter downstream intergenic promoter downstream intergenic promoter promoter promoter intergenic promoter promoter promoter promoter intergenic
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AT3G62120	na	Class II aaRS a 3_23004411	4.52	promoter
AT4G33780	na	FUNCTIONS IN 4_16205149	4.52	proximal promoter
AT5G13810	na	Glutaredoxin far 5_4457875	4.52	intergenic
AT3G15040	na	Protein of unkno 3_5064898	4.52	three_prime_UTR
AT2G36470	na	Plant protein of 2_15298580	4.52	intergenic
AT2G36950	na	Heavy metal tra 2_15515040	4.52	promoter
AT4G02760	na	RNI-like superfa 4_1230146	4.52	proximal promoter
AT4G06744	na	Leucine-rich rer 4_4070275	4.52	intergenic
AT4G39530	na	Tetratricopeptid 4_18377386	4.52	promoter
AT4G39830	na	Cupredoxin sup 4_18480937	4.52	exon
AT5G07090	na	Ribosomal prote 5_2204149	4.52	downstream
AT4G02770	PHOTOSYSTEM I SUBUNIT D-1 (PSAD-1		4.52	promoter
AT3G15030	TCP FAMILY TRANSCRIPTION FACTOR		4.52	intergenic
AT4G39770	TREHALOSE-6-PHOSPHATE PHOSPHAT		4.52	promoter
AT5G07100	WRKY DNA-BINDING PROTEIN 26 (WRK		4.52	promoter
AT4G28720	YUCCA 8 (YUC8)	Auxin biosynthe 4_14192099	4.52	promoter
AT5G09870	CELLULOSE SYNTHASE 5 (CESA5)	Encodes a cellu 5_3072187	4.51	proximal promoter
AT1G01160	GRF1-INTERACTING FACTOR 2 (GIF2)	Arabidopsis tha 1_75467	4.51	intergenic
AT5G17350	na	unknown proteir 5_5719001	4.51	exon
AT1G34010	na	unknown proteir 1_12359023	4.51	intergenic
AT2G18070	na	unknown proteir 2_7851637	4.51	proximal promoter
AT4G24780	na	Pectin lyase-like 4_12774413	4.51	proximal promoter
AT1G01170	na	Protein of unknc 1_75467	4.51	proximal promoter
AT1G01180	na	S-adenosyl-L-m 1_75467	4.51	promoter
AT1G53233	na	Potential natura 1_19851770	4.51	exon
AT4G01460	na	basic helix-loop 4_619789	4.51	proximal promoter
AT5G15810	na	N2,N2-dimethyle 5_5157730	4.51	promoter
AT5G51770	na	Protein kinase s 5_21030918	4.51	promoter
AT5G15805	na	pre-tRNA; tRNA 5_5157730	4.51	downstream
AT3G24220	NINE-CIS-EPOXYCAROTENOID DIOXYG		4.51	exon
AT1G34000	ONE-HELIX PROTEIN 2 (OHP2)	Encodes a nov€ 1_12359023	4.51	promoter
AT1G53230	TEOSINTE BRANCHED 1, CYCLOIDEA A		4.51	promoter
AT5G12250	BETA-6 TUBULIN (TUB6)	Encodes a beta 5_3963666	4.5	promoter
AT3G07330	CELLULOSE-SYNTHASE-LIKE C6 (CSLC	encodes a gene 3_2334885	4.5	intergenic
AT1G29920	CHLOROPHYLL A/B-BINDING PROTEIN	Encodes Ihcb1. 1_10476110	4.5	promoter
AT2G33800	EMBRYO DEFECTIVE 3113 (EMB3113)	Ribosomal prote 2_14302967	4.5	proximal promoter
AT2G21060	GLYCINE-RICH PROTEIN 2B (GRP2B)	Glycine-rich pro 2_9038361	4.5	proximal promoter
AT2G21050	LIKE AUXIN RESISTANT 2 (LAX2)	Encodes LAX2 2_9038361	4.5	intergenic
AT3G52880	MONODEHYDROASCORBATE REDUCT.	Encodes a pero 3_19604618	4.5	promoter
AT1G07650	na	Leucine-rich reg 1_2365676	4.5	intron
AT3G07320	na	O-Glycosyl hydı 3_2334885	4.5	proximal promoter
AT3G52960	na	Thioredoxin sup 3_19639538	4.5	promoter
AT4G18280	na	glycine-rich cell 4_10103336	4.5	proximal promoter
AT5G06440	na	FUNCTIONS IN 5_1967289	4.5	five_prime_UTR
AT5G51845	na	Encodes a defe 5_21075991	4.5	proximal promoter
AT1G69850	NITRATE TRANSPORTER 1:2 (NRT1:2)	Encodes an ind 1 26300503	4.5	promoter
AT2G33810	SQUAMOSA PROMOTER BINDING PRO		4.5	proximal promoter
AT1G32200	(ATS1)	Encodes a chloi 1_11601408	4.49	intergenic
AT5G06250	DEVELOPMENT-RELATED PCG TARGET		4.49	intergenic
AT1G05190	EMBRYO DEFECTIVE 2394 (emb2394)	embryo defectiv 1_1504790	4.49	proximal promoter
AT1G05200	GLUTAMATE RECEPTOR 3.4 (GLR3.4)	Encodes a puta 1_1504790	4.49	promoter
AT1G68460	ISOPENTENYLTRANSFERASE 1 (IPT1)	Encodes a puta 1_25669025	4.49	exon
AT1G78560	na	Sodium Bile aci 1_29548886	4.49	promoter
AT1G60783	na	unknown proteir 1_22374103	4.49	proximal promoter
AT1G08845	na	Ribosomal L18r 1_2839005	4.49	intron
AT1G56500	na	haloacid dehalo 1_21167514	4.49	downstream
AT1G68780	na	RNI-like superfa 1 25834471	4.49	proximal promoter
AT2G16380	na	Sec14p-like phc 2 7085663	4.49	promoter
AT4G20170	na	Domain of unkn 4_10899278	4.49	downstream
AT4G20180	na	transposable eli 4_10899278	4.49	proximal promoter
AT5G18770	na	F-box/FBD-like 5_6261163	4.49	promoter
AT1G78570	RHAMNOSE BIOSYNTHESIS 1 (RHM1)	Encodes a UDF 1_29548886	4.49	proximal promoter
AT3G23820	UDP-D-GLUCURONATE 4-EPIMERASE 6		4.49	proximal promoter
AT1G56510	WHITE RUST RESISTANCE 4 (WRR4)	TIR-NB-LRR pri 1_21167514	4.49	promoter
AT1G54990	AUXIN RESISTANT 4 (AXR4)	auxin response 1_20511159	4.48	promoter
AT5G66680	DEFECTIVE GLYCOSYLATION (DGL1)	Encodes a prot 5_26620679	4.48	promoter
AT5G02260	EXPANSIN A9 (EXPA9)	member of Alph 5 465565	4.48	intergenic
AT5G25220	KNOTTED1-LIKE HOMEOBOX GENE 3 (F		4.48	proximal promoter
AT5G48945	LOW-MOLECULAR-WEIGHT CYSTEINE-		4.48	proximal promoter
AT3G04765	MICRORNA167C (MIR167C)	Encodes a micr 3_1307608	4.48	proximal promoter
AT5G59780	MYB DOMAIN PROTEIN 59 (MYB59)	Encodes a puta 5 24084882	4.48	proximal promoter
AT5G52815	na	pre-tRNA; tRNA 5_21401212	4.48	exon
AT5G52820	na	WD-40 repeat f: 5_21401212	4.48	promoter
AT4G29270	na	HAD superfamil 4 14424963	4.48	promoter
AT2G33320	na	Calcium-depend 2 14119638	4.48	exon
AT3G44640	na	transposable eli 3 16204255	4.48	intergenic
AT1G08610	na	Pentatricopeptic 1_2735905	4.48	promoter
AT1G54985	na	pseudogene, hy 1_20511159	4.48	intron
AT1G23000	na	Heavy metal tra 1_8141177	4.48	proximal promoter
AT1G23000 AT1G72510	na	Protein of unknr 1_27303326	4.48	promoter
AT3G42170	na na	transposase-like 3_14321657	4.48	intron
AT3G55470	na	Calcium-depend 3_20564144	4.48	promoter
AT4G02880	na	unknown proteir 4_1274387	4.48	promoter
AT4G028570		Long-chain fatty 4_14119465	4.48	five_prime_UTR
			4.48	intergenic
	na na		T.TO	
AT5G20700	na	Protein of unkno 5_7005379 HCP-like superf 5_20547009		nroximal promoter
AT5G20700 AT5G50450	na na	HCP-like superf 5_20547009	4.48	proximal promoter
AT5G20700 AT5G50450 AT5G21950	na na na	HCP-like superf 5_20547009 alpha/beta-Hydr 5_7256745	4.48 4.48	proximal promoter
AT5G20700 AT5G50450 AT5G21950 AT1G77740	na na na PHOSPHATIDYLINOSITOL-4-PHOSPHAT	HCP-like superf 5_20547009 alpha/beta-Hydr 5_7256745 Encodes PIP5K 1_29217927	4.48 4.48 4.48	proximal promoter proximal promoter
AT5G20700 AT5G50450 AT5G21950 AT1G77740 AT5G65270	na na na PHOSPHATIDYLINOSITOL-4-PHOSPHAT RAB GTPASE HOMOLOG A4A (RABA4a)	HCP-like superf 5_20547009 alpha/beta-Hydr 5_7256745 Encodes PIP5K 1_29217927 RAB GTPase hr 5_26083198	4.48 4.48 4.48 4.48	proximal promoter proximal promoter promoter
AT5G20700 AT5G50450 AT5G21950 AT1G77740 AT5G65270 AT1G78000	na na PHOSPHATIDYLINOSITOL-4-PHOSPHAT RAB GTPASE HOMOLOG A4A (RABA4a) SULFATE TRANSPORTER 1;2 (SULTR1;	HCP-like superf 5_20547009 alpha/beta-Hydr 5_7256745 Encodes PIP5K 1_29217927 RAB GTPase hr 5_26083198 Encodes a sulfa 1_29327688	4.48 4.48 4.48 4.48 4.48	proximal promoter proximal promoter proximal promoter proximal promoter
AT5G20700 AT5G50450 AT5G21950 AT1G77740 AT5G65270 AT1G78000 AT5G02260	na na PHOSPHATIDYLINOSITOL-4-PHOSPHAT RAB GTPASE HOMOLOG A4A (RABA4a) SULFATE TRANSPORTER 1;2 (SULTR1; EXPANSIN A9 (EXPA9)	HCP-like superf 5_20547009 alpha/beta-Hydı 5_7256745 Encodes PIP5K 1_29217927 RAB GTPase hı 5_26083198 Encodes a sulfe 1_29327688 member of Alph 5_462591	4.48 4.48 4.48 4.48 4.48 4.47	proximal promoter proximal promoter promoter proximal promoter proximal promoter
AT5G20700 AT5G50450 AT5G21950 AT1G77740 AT5G65270 AT1G78000 AT5G02260 AT1G70790	na na PHOSPHATIDYLINOSITOL-4-PHOSPHAT RAB GTPASE HOMOLOG A4A (RABA4a) SULFATE TRANSPORTER 1;2 (SULTR1; EXPANSIN A9 (EXPA9) na	HCP-like superf 5_20547009 alpha/beta-Hyd 5_7256745 Encodes PIPSK 1_29217927 RAB GTPase hi 5_26083198 Encodes a sulfa 1_29327688 member of Alph 5_462591 Calcium-depent 1_26699438	4.48 4.48 4.48 4.48 4.48 4.47 4.47	proximal promoter proximal promoter promoter proximal promoter proximal promoter proximal promoter
AT5G20700 AT5G50450 AT5G21950 AT1G77740 AT5G65270 AT1G78000 AT5G02260 AT1G70790 AT3G21690	na na na PHOSPHATIDYLINOSITOL-4-PHOSPHAT RAB GTPASE HOMOLOG A4A (RABA4a) SULFATE TRANSPORTER 1;2 (SULTR1; EXPANSIN A9 (EXPA9) na na	HCP-like superf 5_20547009 alpha/beta-Hydt 5_7256745 Encodes PIP5K 1_29217927 RAB GTPase ht 5_26083198 Encodes a sulfa 1_29327688 member of Alph 5_462591 Calcium-depent 1_26699438 MATE efflux fan 3_7637767	4.48 4.48 4.48 4.48 4.48 4.47 4.47	proximal promoter proximal promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT5G20700 AT5G50450 AT5G21950 AT1G77740 AT5G65270 AT1G78000 AT5G02260 AT1G70790	na na PHOSPHATIDYLINOSITOL-4-PHOSPHAT RAB GTPASE HOMOLOG A4A (RABA4a) SULFATE TRANSPORTER 1;2 (SULTR1; EXPANSIN A9 (EXPA9) na	HCP-like superf 5_20547009 alpha/beta-Hyd 5_7256745 Encodes PIPSK 1_29217927 RAB GTPase hi 5_26083198 Encodes a sulfa 1_29327688 member of Alph 5_462591 Calcium-depent 1_26699438	4.48 4.48 4.48 4.48 4.48 4.47 4.47	proximal promoter proximal promoter promoter proximal promoter proximal promoter proximal promoter

AT5G08060				
	na	unknown proteir 5_2580373	4.47	promoter
AT1G72830	NUCLEAR FACTOR Y, SUBUNIT A3 (NF-		4.47	proximal promoter
AT1G80300	NUCLEOTIDE TRANSPORTER 1 (NTT1)	Encodes an ATI 1_30191681	4.47	promoter
AT1G02130	RAS 5 (RA-5)	Belongs to the F1_401218	4.47	exon
AT5G26920	CAM-BINDING PROTEIN 60-LIKE G (CBF		4.46	intron
AT3G14450	CTC-INTERACTING DOMAIN 9 (CID9)	RNA-binding pr 3_4846159	4.46	intergenic
AT4G34200	EMBRYO SAC DEVELOPMENT ARREST		4.46	downstream
AT3G27260	GLOBAL TRANSCRIPTION FACTOR GRO		4.46	intron
AT4G00830	LHP1-INTERACTING FACTOR 2 (LIF2)	RNA-binding (R 4_351922	4.46	promoter
AT1G11310	MILDEW RESISTANCE LOCUS O 2 (MLC		4.46	promoter
AT2G22426	na	unknown proteir 2_9520891	4.46	intergenic
AT3G50625		transposable eli 3_18790412	4.46	proximal promoter
AT1G79720 AT4G39550	na	Eukaryotic aspa 1_29999991	4.46 4.46	proximal promoter
AT4G39550 AT4G11680	na na	Galactose oxida 4_18382063 Zinc finger, C3F 4 7053221	4.46	promoter downstream
AT4G11680		FUNCTIONS IN 4_7053221	4.46	promoter
AT1G04770	na	Tetratricopeptid 1_1338028	4.46	promoter
AT1G29650		transposable ek 1_10363575	4.46	intergenic
AT2G40110	na	Yippee family pt 2_16749857	4.46	intergenic
AT2G40113	na	Pollen Ole e 1 a 2_16749857	4.46	promoter
AT3G13432	na	unknown proteir 3_4372689	4.46	intergenic
AT5G22000	RING-H2 GROUP F2A (RHF2A)	encodes a RIN(5_7277198	4.46	five_prime_UTR
AT4G34190	STRESS ENHANCED PROTEIN 1 (SEP1)		4.46	promoter
AT3G60600	VAMP/SYNAPTOBREVIN-ASSOCIATED I		4.46	promoter
AT3G27020	YELLOW STRIPE LIKE 6 (YSL6)	Arabidopsis tha 3_9964784	4.46	promoter
AT1G66600	ABA OVERLY SENSITIVE MUTANT 3 (AB		4.45	promoter
AT1G17190	GLUTATHIONE S-TRANSFERASE TAU 2		4.45	three_prime_UTR
AT4G38600	KAKTUS (KAK)	encodes a mem 4_18049888	4.45	proximal promoter
AT3G50870	MONOPOLE (MNP)	Encodes a GAT 3_18909953	4.45	proximal promoter
AT3G54500	, ,	FUNCTIONS IN 3 20179110	4.45	promoter
AT3G56275	na	pseudogene of 3_20872515	4.45	promoter
AT2G22280		pre-tRNA; tRNA 2_9466283	4.45	proximal promoter
AT1G17620		Late embryoger 1_6061348	4.45	proximal promoter
AT1G31940		unknown proteir 1 11472655	4.45	proximal promoter
AT5G20950	na	Glycosyl hydrol: 5 7111840	4.45	promoter
AT1G50160		BEST Arabidop: 1_18581887	4.45	intergenic
AT3G07260	na	SMAD/FHA don 3_2309495	4.45	promoter
AT4G34140	na	D111/G-patch d 4_16350216	4.45	proximal promoter
AT2G22290	RAB GTPASE HOMOLOG H1D (RABH1d		4.45	promoter
AT1G50170	SIROHYDROCHLORIN FERROCHELATA		4.45	promoter
AT2G18700	TREHALOSE PHOSPHATASE/SYNTHAS		4.45	promoter
AT4G00730	ANTHOCYANINLESS 2 (ANL2)	Encodes a hom 4 305317	4.44	proximal promoter
AT1G06850	BASIC LEUCINE-ZIPPER 52 (bZIP52)	basic leucine-zi _l 1_2104996	4.44	promoter
AT1G50430	DWARF 5 (DWF5)	Mutants are def 1_18685677	4.44	promoter
AT5G54110	MEMBRANE-ASSOCIATED MANNITOL-II		4.44	•
AT1G50440	na	RING/FYVE/PH 1 18685677	4.44	promoter
AT5G67020		unknown proteir 5_26750983	4.44	promoter exon
AT1G21326	na	VQ motif-contail 1_7470405	4.44	proximal promoter
AT1G21320 AT1G23980		RING/U-box su ₁ 1_8487315	4.44	proximal promoter
AT1G68660	na	Ribosomal prote 1_25779324	4.44	
AT2G16365		F-box family prc 2_7074071	4.44	promoter promoter
AT3G10303	na	Calcium-binding 3_3155284	4.44	promoter
AT3G10190	na	SAUR-like auxir 3_22927985	4.44	intergenic
AT5G47225		transposable el 5_19176775	4.44	-
	RESPONSE REGULATOR 3 (RR3)	Encodes an A-12_17221261	4.44	intergenic proximal promoter
			4.44	
AT2G41310			1 12	
AT2G41310 AT1G32790	CTC-INTERACTING DOMAIN 11 (CID11)		4.43	downstream
AT2G41310 AT1G32790 AT3G01120	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (encodes a cysta 3_42636	4.43	proximal promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na	encodes a cysta 3_42636 unknown proteir 1_27349344	4.43 4.43	proximal promoter downstream
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na	encodes a cysta 3_42636 unknown proteir 1_27349344 Encodes a prote 5_1578802	4.43 4.43 4.43	proximal promoter downstream promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na	encodes a cysta 3_42636 unknown proteir 1_27349344 Encodes a prote 5_1578802 Encodes for a n 1_27991058	4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15300	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na na	encodes a cyste 3_42636 unknown proteir 1_27349344 Encodes a prote 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571	4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15300 AT2G15830	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na na na	encodes a cyst: 3_42636 unknown proteir 1_27349344 Encodes a prot: 5_1578802 Encodes for a n 1_27991058 Leucine-rich ret 2_6651571 unknown proteir 2_6894787	4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15300 AT2G15830 AT1G32780	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na na na na	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688	4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15300 AT2G15830 AT1G32780 AT3G49000	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na na na na na	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543	4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15300 AT2G15300 AT1G32780 AT3G49000 AT4G18740	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na	encodes a cysts 3, 42636 unknown proteir 1_27349344 Encodes a prote 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroE5-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669	4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15300 AT2G15830 AT1G32780 AT3G49000 AT4G18740 AT5G14495	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-IRNA; tRNA 5_4673109	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter proximal promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15300 AT2G15830 AT1G32780 AT3G49000 AT4G18740 AT5G14495 AT5G59500	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_23985808	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter promoter promoter promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15800 AT2G15800 AT3G49000 AT4G18740 AT5G14495 AT5G59500 AT1G18800	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na	encodes a cysts 3,42636 unknown proteir 1_27349344 Encodes a prott 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_23985808 Double npf-1 r 1_6484352	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G49000 AT3G49000 AT5G14495 AT5G59500 AT1G18800 AT1G05340	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na NAP1-RELATED PROTEIN 2 (NRP2) PEROXIDASE 52 (PRX52)	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-IRNA; IRNA 5_4673109 protein C-termir 5_23985808 Double nrp1-1 r 1_6484352 Peroxidase sup 5_1578802	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter promoter promoter promoter downstream
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15800 AT2G15800 AT3G49000 AT4G18740 AT5G14495 AT5G59500 AT1G18800	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na NAP1-RELATED PROTEIN 2 (NRP2) PEROXIDASE 52 (PRX52) SLAC1 HOMOLOGUE 2 (SLAH2)	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-1RNA; tRNA 5_4673109 protein C-termir 5_23985808 Double nrp1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prote 4_13920700	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream proximal promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15300 AT2G15830 AT1G32780 AT3G49000 AT4G18740 AT5G14495 AT5G59500 AT1G18800 AT1G18800 AT1G18800 AT4G27970 AT1G72650	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na na na na na na na na na NAP1-RELATED PROTEIN 2 (NRP2) PEROXIDASE 52 (PRX52) SLAC1 HOMOLOGUE 2 (SLAH2) TRF-LIKE 6 (TRFL6)	encodes a cysts 3,42636 unknown proteir 1_27349344 Encodes a prott 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_23985808 Double nrp1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prott 4_13920700 Arabidopsis thal 1_27349344	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter downstream proximal promoter promoter promoter promoter
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AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G49000 AT3G418740 AT5G14495 AT5G59500 AT1G18800 AT4G27970 AT1G72650 AT5G05340 AT5G0547770 AT5G0477760 AT5G047760 AT5G05160 AT5G05160 AT5G05160 AT3G09510 AT3G095410	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na NAP1-RELATED PROTEIN 2 (NRP2) PEROXIDASE 52 (PRX52) SLAC1 HOMOLOGUE 2 (SLAH2) TRF-LIKE 6 (TRFL6) (THO1) TRF-LIKE 6 (TRFL6) (THO1) SAPPHOSPHOGLYCOLATE PHOSPHATASE FARNESYL DIPHOSPHATE SYNTHASE II (na na na na	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer, 2_6651571 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-IRNA; IRNA 5_4673109 protein C-termir 5_23985808 Double nrp1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prote 4_13920700 Arabidopsis thai 1_27349344 Encodes a com 5_3065845 serine/threonine 5_19345193 Encodes an ino: 4_9994426 CCCH-type zinc 2_1862236 Tetratricopeptid 5_26189905 Pectinacetylests 3_2901172 unknown proteir 3_2901172	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter
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AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G215830 AT3G32780 AT3G49000 AT4G18740 AT5G15490 AT1G18800 AT1G18800 AT1G2650 AT5G05340 AT5G05407760 AT5G47770 AT1G72650 AT5G05160 AT5G65520 AT3G09410 AT3G09410 AT3G09430 AT3G1395 AT3G11395 AT3G11402 AT3G51700 AT4G24780 AT4G24780 AT4G24780 AT4G24780 AT4G24780 AT4G24780	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer_2_6651571 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_23985808 Doublen np1-1r 1_6484352 Peroxidase sup 5_1578802 Encodes a prote 4_13920700 Arabidopsis thal 1_27349344 Encodes a com 5_3065845 serine/threonine 5_19345193 Encodes a note 5_19345193 Encodes an ino 4_9994426 CCCH-type zinc 2_1862236 Tetratricopeptid 5_26189005 Pectinacetylest 3_2901172 unknown proteir 3_2901172 unknown proteir 3_2901172 unknown proteir 3_2901172 unknown proteir 3_2901172 pre-tRNA; tRNA 3_3575936 Cysteine/Histidi 3_3575936 PleT1 helicase; (3_19181819 Pectin lyase-like 4_12769657 Transcription elt 5_3065845	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter exon promoter promoter downstream intron proximal promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G49000 AT3G49000 AT3G1495 AT5G59500 AT1G18800 AT4G27970 AT1G72650 AT5G65400 AT5G47770 AT3G947760 AT5G65520 AT3G09410	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na n	encodes a cysts 3, 42636 unknown proteir 1_27349344 Encodes a prott 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_2388508 Double nrp1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prott 4_13920700 Arabidopsis thal 1_27349344 Encodes a com 5_3065845 serine/threonine 5_19345193 Encodes a prott 4_13920700 Arabidopsis thal 1_27349344 Encodes a rom 5_3065845 serine/threonine 5_19345193 Encodes an ino: 4_9994426 CCCH-type zinc 2_1862236 Tetratricopeptid 5_26189905 Pectinacetylests 2_9901172 pre-tRNA; tRNA 3_3575936 Cysteine/Histidi 3_3575936 PIF1 helicase; (3_19181819 Pectin lyase-like 4_12769657 Transcription el 5_3065845 Encodes PP2C! 2_16782241	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter downstream proximal promoter p
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT2G15830 AT2G15830 AT3G49000 AT4G18740 AT3G49700 AT4G18740 AT5G05340 AT1G32780 AT1G2650 AT5G05340 AT1G2650 AT5G47770 AT4G18010 AT5G47770 AT4G18010 AT5G47770 AT4G18010 AT5G47760 AT5G47770 AT4G18010 AT3G09410 AT3G09410 AT3G11402 AT3G11402 AT3G11402 AT3G11402 AT3G11402 AT3G11402 AT3G11402 AT3G11402 AT3G11402 AT3G11402 AT3G11403 AT3G11403 AT3G11403 AT3G11403	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na NAP1-RELATED PROTEIN 2 (NRP2) PEROXIDASE 52 (PRX52) SLAC1 HOMOLOGUE 2 (SLAH2) TRF-LIKE 6 (TRFL6) (THO1) 2-PHOSPHOGLYCOLATE PHOSPHATAS FARNESYL DIPHOSPHATE SYNTHASE II (na na n	encodes a cyst 3, 42636 unknown proteir 1,27349344 Encodes a prott 5,1578802 Encodes for an 1,27991058 Leucine-rich rer 2,6651571 unknown proteir 2,6681571 unknown proteir 2,6894787 GroES-like zinc 1,11874688 RNA polymeras 3,18162543 Rho termination 4,10304669 pre-tRNA; tRNA 5,4673109 protein C-termir 5,23985808 Double nrp1-1 r 1,6484352 Peroxidase sup 5,1578802 Encodes a prott 4,13920700 Arabidopsis thal 1,27349344 Encodes a com 5,3065845 serine/threonine 5,19345193 Encodes a prott 5,19345193 Encodes a prott 6,19345193 Encodes an ino: 4,9994426 CCCH-type zinc 2,1862236 Tetratricopeptid 5,26189905 Pectinacetylests 3,2901172 unknown proteir 3,2901172 pre-tRNA; tRNA 3,3575936 Cysteine/Histidi 3,3575936 Cysteine/Histidi 3,3575936 Transcription els 5,3065845 Transcription els 5,3065845 Transcription els 5,3065845 Encodes PP2C! 2,16782241 Arabidopsis thal 3,5061913	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter downstream intron proximal promoter intergenic five_prime_UTR promoter intergenic five_prime_UTR promoter intergenic five_prime_UTR promoter intron
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G49000 AT4G187490 AT5G14495 AT5G59500 AT1G18800 AT1G2650 AT5G05340 AT4G27970 AT1G72650 AT5G05860 AT5G477760 AT5G65520 AT3G09410 AT3G05160 AT5G65520 AT3G09410 AT3G09430 AT3G1395 AT3G11395 AT3G11402 AT3G51700 AT4G24780 AT4G24780 AT4G24780 AT4G24780 AT4G24780 AT4G24780 AT3G051503 AT3G655520	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na n	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer_2_6651571 GroES-like zinc: 1_11874688 RNA polymeras 3_18162543 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_23985808 Doublen np1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prote 4_13920700 Arabidopsis thal 1_27349344 Encodes a com 5_3065845 serine/threonine 5_19345193 Encodes a prote 5_19345193 Encodes Brezier 1_878905 Pectin lacetylest 3_2901172 unknown proteir 3_2901172 unknown proteir 3_2901172 pre-tRNA; tRNA 3_3575936 Cysteine/Histidi 3_3575936 Plef1 helicase; (3_19181819 Pectin lyase-like 4_12769657 Transcription ell 5_3065845 Encodes PP2C: 2_16782241 Arabidopsis thal 3_5061913 encodes a pero 1_24361281	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter downstream proximal promoter p
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G49000 AT3G49700 AT5G14495 AT5G59500 AT1G18800 AT3G49770 AT1G72650 AT3G497770 AT3G497770 AT3G497770 AT3G497770 AT3G497770 AT3G497770 AT3G497770 AT3G497770 AT3G497770 AT3G547770 AT3G547770 AT3G547770 AT3G547770 AT3G547770 AT3G547700 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G51700 AT4G4780 AT3G1402 AT3G51700 AT4G4780 AT3G4780 AT3G4780 AT3G4780	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na n	encodes a cysts 3, 42636 unknown proteir 1_27349344 Encodes a prott 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_2388508 Double nrp1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prott 4_13920700 Arabidopsis thal 1_27349344 Encodes a com 5_3065845 serine/threonine 5_19345193 Encodes a prott 4_13920700 Arabidopsis thal 1_27349344 Encodes a prott 4_13920700 Arabidopsis thal 1_27349345193 Encodes a prott 5_19345193 Encodes a prott 5_19345193 Encodes an ino: 4_9994426 CCCH-type zinc 2_1862236 Tetratricopeptid 5_26189905 Pectinacetylests 2_3901172 pre-tRNA; tRNA 3_3575936 Cysteine/Histidi 3_3575936 PIE1 helicase; (3_19181819 Pectin lyase-like 4_12769657 Transcription el 5_3065845 Encodes PP2C! 2_16782241 Arabidopsis thal 3_5061913 encodes lDN2 (3_18030379	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter five_prime_UTR promoter downstream intron proximal promoter intergenic five_prime_UTR promoter intergenic five_prime_UTR promoter intron exon promoter
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G3780 AT3G18830 AT3G18749000 AT4G187490 AT5G14495 AT5G05340 AT4G18740 AT5G14495 AT5G05340 AT4G27970 AT4G27970 AT4G27970 AT4G18010 AT5G05340 AT5G47760 AT5G47760 AT5G47760 AT5G47767 AT4G18010 AT3G05160 AT5G47767 AT4G18010 AT3G051700 AT3G1395 AT3G11395 AT3G11402 AT3G51700 AT4G24780 AT5G08850 AT5G40180 AT5G4780 AT5G49850 AT2G40180 AT3G45520 AT3G48670 AT3G48670 AT4G65520 AT3G48670 AT3G48670 AT4G65520 AT3G48670 AT4G65520 AT3G48670	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na NAP1-RELATED PROTEIN 2 (NRP2) PEROXIDASE 52 (PRX52) SLAC1 HOMOLOGUE 2 (SLAH2) TRF-LIKE 6 (TRFL6) (THO1) 2-PHOSPHOGLYCOLATE PHOSPHATAS FARNESYL DIPHOSPHATE SYNTHASE 1 INOSITOL(1,4,5)P3 5-PHOSPHATASE II (na na n	encodes a cyst 3 ,42636 unknown proteir 1_27349344 Encodes a prott 5_1578802 Encodes for an 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_11874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_23985808 Double nrp1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prott 4_13920700 Arabidopsis thal 1_27349344 Encodes a com 5_3065845 serine/threonine 5_19345193 Encodes a prott 5_19365193 encodes a prott 5_19361913 encodes a prott 1_24361281 Encodes IDN2 (3_18030379 Euklaryotic aspa 4_16110741	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter intergenic five_prime_UTR promoter intergenic five_prime_UTR promoter intergenic five_prime_UTR promoter intron exon promoter three_prime_UTR
ATZG41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 ATZG15830 AT3G49000 AT4G18740 AT5G14495 AT5G59500 AT1G18800 AT1G2780 AT1G2780 AT1G2780 AT1G286160 AT5G6520 AT5G9860 AT5G647770 AT1G72656 AT5G9860 AT5G65520 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G9410 AT3G11395 AT3G11402 AT3G15100 AT4G24780 AT3G15030 AT3G15030 AT3G15030 AT3G15030 AT3G15030 AT3G15030 AT3G15030 AT3G65520 AT3G434040 AT3G43490 AT4G33490 AT2G33175	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na NAP1-RELATED PROTEIN 2 (NRP2) PEROXIDASE 52 (PRX52) SLAC1 HOMOLOGUE 2 (SLAH2) TRF-LIKE 6 (TRFL6) (THO1) 2-PHOSPHOGLYCOLATE PHOSPHATAS FARNESYL DIPHOSPHATE SYNTHASE 1 INOSITOL(1,4,5)P3 5-PHOSPHATASE II (na na n	encodes a cyst 3_42636 unknown proteir 1_27349344 Encodes a prot 5_1578802 Encodes for a n 1_27991058 Leucine-rich reg _6651571 GroES-like zinc: 1_11874688 RNA polymeras 3_18162543 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_23985808 Doublen np1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prote 4_13920700 Arabidopsis thal 1_27349344 Encodes a com 5_3065845 serine/threonine 5_19345193 Encodes a prote 5_19345193 Encodes 10172 unknown proteir 3_2901172 unknown proteir 3_2901172 proteirs-RNA; tRNA 3_3575936 Cysteine/Histidi 3_3575936 PlE1 helicase; (3_19181819 Pectin lyase-like 4_12769657 Transcription ell 5_3065845 Encodes PP2C! 2_16782241 Arabidopsis thal 3_5061913 encodes a pero 1_24361281 Encodes IDNZ (3_18030379 Eukaryotic aspa 4_16110741 unknown proteir 2_14061874	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter p
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G49000 AT3G14950 AT3G49700 AT5G14495 AT5G59500 AT1G18800 AT5G65520 AT3G9860 AT5G47760 AT5G647770 AT4G188101 AT2G05160 AT5G65520 AT3G09410	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na n	encodes a cyst: 3, 42636 unknown proteir 1_27349344 Encodes a prott 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_1874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_23985808 Double nrp1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prott 4_13920700 Arabidopsis thal 1_27349344 Encodes a com 5_3065845 serine/threonine 5_19345193 Encodes a prot 4_13920700 Arabidopsis thal 1_27349344 Encodes a prot 4_13920700 Arabidopsis thal 1_27349345193 Encodes a prot 4_13920700 Arabidopsis thal 1_27349345193 Encodes an ino 4_9994426 CCCH-type zinc 2_1862236 Tetratricopeptid 5_26189905 Pectinacetylests 3_2901172 unknown proteir 3_2901172 pre-tRNA; tRNA 3_3575936 Cysteine/Histidi 3_3575936 Cysteine/Histidi 3_3575936 Tysteine/Histidi 3_3575936 Transcription ell 5_3065845 Encodes PP2C! 2_16782241 Arabidopsis thal 3_5061913 encodes a pero 1_24361281 Encodes IDN2 (3_18030379 Eukaryotic aspa 4_16110741 unknown proteir 3_1567523	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.42 4.41 4.41 4.41 4.41 4.41 4.41 4.41	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter promoter five_prime_UTR promoter downstream intron proximal promoter intergenic five_prime_UTR promoter intergenic promoter three_prime_UTR promoter three_prime_UTR intergenic exon
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G31830 AT3G349000 AT3G187470 AT5G14495 AT5G05340 AT4G18740 AT5G14495 AT5G05340 AT4G18740 AT5G05340 AT4G187770 AT4G18010 AT2G05160 AT5G47760 AT3G05430 AT3G1395 AT3G11402 AT3G51700 AT3G05430 AT3G1395 AT3G11402 AT3G51700 AT4G4780 AT5G08850 AT5G08850 AT5G4780 AT5G08850 AT5G4780 AT5G08850 AT3G11395 AT3G11395 AT3G11395 AT3G11395 AT3G11395 AT3G11395 AT3G139340 AT3G33490 AT3G33490 AT2G33175 AT3G05435	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na n	encodes a cyst 3 _ 42636 unknown proteir 1 _ 27349344 Encodes a prott 5 _ 1578802 Encodes for an 1 _ 27991058 Leucine-rich rer 2 _ 6651571 unknown proteir 2 _ 6894787 GroES-like zinc 1 _ 11874888 RNA polymeras 3 _ 18162543 Rho termination 4 _ 10304669 pre-tRNA; tRNA 5 _ 4673109 protein C-termir 5 _ 23985808 Double nrp1-1 r 1 _ 6484352 Peroxidase sup 5 _ 1578802 Encodes a prott 4 _ 13920700 Arabidopsis thal 1 _ 27349344 Encodes a com 5 _ 3065845 serine/threonine 5 _ 19345193 Encodes a prott 5 _ 19345193 Encodes a prott 5 _ 19345193 Encodes an ino: 4 _ 9994426 CCCH-type zinc 2 _ 1862236 Tetratricopeptid 5 _ 26189905 Pectinacetylest 3 _ 2901172 unknown proteir 3 _ 2901172 pre-tRNA; tRNA 3 _ 3575936 Cysteine/Histidi 3 _ 3575936 Cysteine/Histidi 3 _ 3575936 Cysteine/Histidi 3 _ 3575936 Cysteine/Histidi 3 _ 3675937 Transcription elt 5 _ 3065845 Encodes PP2C! 2 _ 16782241 Arabidopsis thal 3 _ 5061913 encodes a prot 1 _ 24361281 Encodes IDN2 (3 _ 18030379 Eukaryotic aspa 4 _ 16110741 unknown proteir 3 _ 1567523 Tudor/PWWP/N 3 _ 1567523 Tudor/PWWP/N 3 _ 1567523	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter promoter promoter promoter proximal promoter downstream proximal promoter intergenic five_prime_UTR promoter intergenic five_prime_UTR promoter intergenic promoter p
AT2G41310 AT1G32790 AT3G01120 AT1G72645 AT5G05330 AT1G74470 AT2G15830 AT3G49000 AT3G14950 AT3G49700 AT5G14495 AT5G59500 AT1G18800 AT5G65520 AT3G9860 AT5G47760 AT5G647770 AT4G188101 AT2G05160 AT5G65520 AT3G09410	CTC-INTERACTING DOMAIN 11 (CID11) METHIONINE OVERACCUMULATION 1 (na na NAP1-RELATED PROTEIN 2 (NRP2) PEROXIDASE 52 (PRX52) SLAC1 HOMOLOGUE 2 (SLAH2) TRF-LIKE 6 (TRFL6) (THO1) 2-PHOSPHOGLYCOLATE PHOSPHATAS FARNESYL DIPHOSPHATE SYNTHASE 1 (NOSITOL (1,4,5)P3 5-PHOSPHATASE III (na na n	encodes a cyst: 3, 42636 unknown proteir 1_27349344 Encodes a prott 5_1578802 Encodes for a n 1_27991058 Leucine-rich rer 2_6651571 unknown proteir 2_6894787 GroES-like zinc 1_1874688 RNA polymeras 3_18162543 Rho termination 4_10304669 pre-tRNA; tRNA 5_4673109 protein C-termir 5_23985808 Double nrp1-1 r 1_6484352 Peroxidase sup 5_1578802 Encodes a prott 4_13920700 Arabidopsis thal 1_27349344 Encodes a com 5_3065845 serine/threonine 5_19345193 Encodes a prot 4_13920700 Arabidopsis thal 1_27349344 Encodes a prot 4_13920700 Arabidopsis thal 1_27349345193 Encodes a prot 4_13920700 Arabidopsis thal 1_27349345193 Encodes an ino 4_9994426 CCCH-type zinc 2_1862236 Tetratricopeptid 5_26189905 Pectinacetylests 3_2901172 unknown proteir 3_2901172 pre-tRNA; tRNA 3_3575936 Cysteine/Histidi 3_3575936 Cysteine/Histidi 3_3575936 Tysteine/Histidi 3_3575936 Transcription ell 5_3065845 Encodes PP2C! 2_16782241 Arabidopsis thal 3_5061913 encodes a pero 1_24361281 Encodes IDN2 (3_18030379 Eukaryotic aspa 4_16110741 unknown proteir 3_1567523	4.43 4.43 4.43 4.43 4.43 4.43 4.43 4.43	proximal promoter downstream promoter promoter exon intergenic proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter promoter five_prime_UTR promoter downstream intron proximal promoter intergenic five_prime_UTR promoter intergenic promoter three_prime_UTR promoter three_prime_UTR intergenic exon

AT5G14470	na	GHMP kinase fa 5 4664788	4.41	promoter
AT2G32960	PLANT AND FUNGI ATYPICAL DUAL-SP	Encodes an aty 2_13989292	4.41	intron
AT4G33495	ROOT PRIMORDIUM DEFECTIVE 1 (RPI	A member of the 4_16110741	4.41	three_prime_UTR
AT5G61780	TUDOR-SN PROTEIN 2 (TUDOR2)	Involved in the r 5_24820561	4.41	proximal promoter
AT2G34960	CATIONIC AMINO ACID TRANSPORTER		4.4	promoter
AT5G65710	HAESA-LIKE 2 (HSL2)	HAESA-like 2 (F 5_26294344	4.4	exon
AT3G21720	ISOCITRATE LYASE (ICL)	Encodes a glyo: 3_7657866	4.4	proximal promoter
AT1G19530	na	unknown proteir 1_6763215	4.4	proximal promoter
AT1G75210	na	HAD-superfamil 1_28223791	4.4	promoter
AT1G75200	na	flavodoxin famil: 1_28223791	4.4	promoter
AT5G55896	na na	transposable eli 5_22627274	4.4 4.4	intergenic
AT5G55893 AT3G07440	na	unknown proteir 5_22627274 unknown proteir 3_2381186	4.4	proximal promoter promoter
AT4G31136	na	This gene encor 4_15140613	4.4	downstream
AT4G33940	na	RING/U-box suj 4_16265982	4.4	promoter
AT5G25820	na	Exostosin family 5_8994727	4.4	intergenic
AT5G66550	na	Maf-like protein; 5_26561919	4.4	proximal promoter
AT5G65720	NITROGEN FIXATION S (NIFS)-LIKE 1 (N		4.4	proximal promoter
AT5G22370	QUATRE-QUART 1 (QQT1)	Encodes QQT1 5_7405923	4.4	promoter
AT3G27010	TEOSINTE BRANCHED 1, CYCLOIDEA, I	Belongs to a TC 3_9959857	4.4	proximal promoter
AT5G22360	VESICLE-ASSOCIATED MEMBRANE PR	Member of Syna 5_7405923	4.4	promoter
AT5G04340	ZINC FINGER OF ARABIDOPSIS THALIA	putative c2h2 zi 5_1217414	4.4	promoter
AT2G43130	(ARA4)	encodes a prot∈ 2_17933170	4.39	proximal promoter
AT2G02010	GLUTAMATE DECARBOXYLASE 4 (GAD		4.39	proximal promoter
AT3G07770	HEAT SHOCK PROTEIN 89.1 (Hsp89.1)	HEAT SHOCK I 3_2484402	4.39	downstream
AT2G01480	na	O-fucosyltransfe 2_221114	4.39	downstream
AT5G60190	na	Encodes a prote 5_24237156	4.39	intergenic
AT2G29995	na	unknown proteir 2_12798995	4.39	intron
AT2G43140	na	basic helix-loop 2_17933170	4.39	intron
AT1G70550	na	Protein of Unkn 1_26600421	4.39	downstream
AT3G21300 AT5G02680	na na	RNA methyltran 3_7496435 LOCATED IN: e 5_604790	4.39 4.39	promoter promoter
AT5G02540	na na	NAD(P)-binding 5_569357	4.39	intron
AT5G58120	na	Disease resista 5_23517135	4.39	promoter
AT5G65820	na	Pentatricopeptic 5_26341956	4.39	promoter
AT3G07780	OBERON1 (OBE1)	Encodes a nucli 3_2484402	4.39	promoter
AT2G01490	PHYTANOYL-COA 2-HYDROXYLASE (PA		4.39	promoter
AT5G65830	RECEPTOR LIKE PROTEIN 57 (RLP57)	receptor like prc 5 26341956	4.39	downstream
AT1G78770	ANAPHASE PROMOTING COMPLEX 6 (A		4.38	five_prime_UTR
AT3G10912	CONSERVED PEPTIDE UPSTREAM OPE		4.38	five_prime_UTR
AT3G51240	FLAVANONE 3-HYDROXYLASE (F3H)	Encodes flavan 3_19024977	4.38	promoter
AT5G47820	FRAGILE FIBER 1 (FRA1)	encodes a kines 5_19366261	4.38	promoter
AT4G21440	MYB-LIKE 102 (MYB102)	Encodes a MYE 4_11420937	4.38	proximal promoter
AT4G14980	na	Cysteine/Histidii 4_8565433	4.38	proximal promoter
AT4G14990	na	Topoisomerase 4_8565433	4.38	downstream
AT1G26730	na	EXS (ERD1/XPI 1_9241039	4.38	promoter
AT3G51230	na	BEST Arabidop: 3_19024977	4.38	proximal promoter
AT4G17940	na	Tetratricopeptid 4_9965612	4.38	promoter
AT5G49100	na	unknown proteir 5_19899104	4.38	five_prime_UTR
AT1G78420	na	RING/U-box su _i 1_29504489	4.38	promoter
AT3G10910	na	RING/U-box sul 3_3413851	4.38	five_prime_UTR
AT1G52720	na	unknown proteir 1_19640850	4.38	promoter
AT1G29060	na	Target SNARE 1_10143779	4.38	intergenic
AT2G05920	na	Subtilase family 2_2272374	4.38	promoter
AT3G58730	na	vacuolar ATP s) 3_21720054	4.38	promoter
AT4G34040 AT5G14050	na	RING/U-box su _i 4_16309074	4.38 4.38	promoter
	na	Transducin/WD 5_4533149 Protein kinase f: 5_9050892	4.38	promoter
AT5G25930 AT5G48490	na na	Bifunctional inhi 5 19648329	4.38	exon promoter
AT3G44320	NITRILASE 3 (NIT3)	This enzyme ca 3_15991709	4.38	proximal promoter
AT5G14040	PHOSPHATE TRANSPORTER 3;1 (PHT3		4.38	promoter
AT3G58100	PLASMODESMATA CALLOSE-BINDING		4.38	promoter
AT5G02010	RHO GUANYL-NUCLEOTIDE EXCHANG		4.38	proximal promoter
AT5G13170	SENESCENCE-ASSOCIATED GENE 29 (4.38	proximal promoter
AT2G22540	SHORT VEGETATIVE PHASE (SVP)	Encodes a nucli 2_9580185	4.38	five_prime_UTR
AT2G45900	TON1 RECRUITING MOTIF 13 (TRM13)		4.38	proximal promoter
AT1G68720	TRNA ARGININE ADENOSINE DEAMINA		4.38	proximal promoter
AT1G36340	UBIQUITIN-CONJUGATING ENZYME 31		4.38	intergenic
AT2G28840	XB3 ORTHOLOG 1 IN ARABIDOPSIS TH.		4.38	intergenic
AT3G24503	ALDEHYDE DEHYDROGENASE 2C4 (AL		4.37	intergenic
AT1G44110	CYCLIN A1;1 (CYCA1;1)	Cyclin A1;1 (CY 1_16777397	4.37	promoter
AT1G03475	LESION INITIATION 2 (LIN2)	Encodes copror 1_871353	4.37	promoter
AT3G24500	MULTIPROTEIN BRIDGING FACTOR 1C		4.37	promoter
AT1G56310	na	Polynucleotidyl 1_21082427	4.37	promoter
AT2G42760	na	unknown proteir 2_17796161	4.37	three_prime_UTR
AT4G19160	na	unknown proteir 4_10480190	4.37	downstream
AT5G08460	na	GDSL-like Lipas 5_2734250	4.37	intron
AT5G01210	na	HXXXD-type ac 5_82662	4.37	proximal promoter
AT5G12150 AT5G57130	na na	Encodes a prote 5_3930413 Clp amino termi 5_23149796	4.37 4.37	promoter downstream
AT3G37130	NAC DOMAIN CONTAINING PROTEIN 49		4.37	downstream
AT4G19170	NINE-CIS-EPOXYCAROTENOID DIOXYG		4.37	proximal promoter
AT1G08090	NITRATE TRANSPORTER 2:1 (NRT2:1)	High-affinity nitr 1_2522815	4.37	proximal promoter
AT5G57140	PURPLE ACID PHOSPHATASE 28 (PAP2		4.37	promoter
AT1G74100	SULFOTRANSFERASE 16 (SOT16)	encodes a desu 1_27866012	4.37	promoter
AT4G28720	YUCCA 8 (YUC8)	Auxin biosynthe 4_14184520	4.37	intergenic
AT4G37750	AINTEGUMENTA (ANT)	ANT is required 4_17736637	4.36	proximal promoter
AT1G27770	AUTOINHIBITED CA2+-ATPASE 1 (ACA1		4.36	promoter
AT3G50660	DWARF 4 (DWF4)	Encodes a 22& 3_18821123	4.36	intergenic
AT5G19820	EMBRYO DEFECTIVE 2734 (emb2734)	embryo defectiv 5_6695098	4.36	downstream
AT2G31570	GLUTATHIONE PEROXIDASE 2 (GPX2)	glutathione perc 2_13440898	4.36	proximal promoter
AT5G47010	LOW-LEVEL BETA-AMYLASE 1 (LBA1)	Required for no 5_19079650	4.36	intergenic
AT5G51350	MORE LATERAL GROWTH1 (MOL1)	Encodes a rece 5_20870804	4.36	promoter
AT1G72490	na	unknown proteir 1_27292767	4.36	proximal promoter

AT3G14150	na	Aldolase-type T 3 4693172	4.36	promotor
AT4G33905	na	Peroxisomal me 4_16256189	4.36	promoter proximal promoter
AT5G19810	na	Proline-rich exte 5_6695098	4.36	intergenic
AT1G07280	na	Tetratricopeptid 1_2237827	4.36	promoter
AT1G21920	na	Histone H3 K4-: 1_7706253	4.36	promoter
AT1G80850	na	DNA glycosylas 1_30387910	4.36	promoter
AT2G31218	na	unknown proteir 2_13302137	4.36	exon
AT1G55690	na	Sec14p-like phc 1_20813041	4.36	promoter
AT2G22530	na	Alkaline-phosph 2_9578605	4.36	proximal promoter
AT3G15720	na	Pectin lyase-like 3_5328169	4.36 4.36	proximal promoter downstream
AT2G31580 AT3G60210	na na	tRNAHis guanyl 2_13440898 GroES-like fami 3_22251040	4.36	downstream
AT3G60210	na	unknown proteir 3_22251040	4.36	intergenic
AT4G30010	na	unknown proteir 4_14672609	4.36	promoter
AT4G30000	na	Dihydropterin py 4_14672609	4.36	five_prime_UTR
AT5G25210	na	unknown proteir 5_8728466	4.36	intergenic
AT5G47020	na	unknown proteir 5_19079650	4.36	proximal promoter
AT1G80860	PHOSPHOLIPID N-METHYLTRANSFERA	Encodes a singl 1_30387910	4.36	downstream
AT1G75250	RAD-LIKE 6 (RL6)	RAD-like 6 (RLf 1_28243553	4.36	intergenic
AT5G25910	RECEPTOR LIKE PROTEIN 52 (RLP52)	putative disease 5_9038814	4.36	promoter
AT1G27760	SALT-TOLERANCE 32 (SAT32)	Encodes a prote 1_9676208	4.36 4.35	intergenic
AT1G72310 AT5G04660	(ATL3) CYTOCHROME P450, FAMILY 77, SUBF/	Encodes a puta 1_27224402	4.35	proximal promoter exon
AT5G12860	DICARBOXYLATE TRANSPORTER 1 (Di		4.35	promoter
AT3G57290	EUKARYOTIC TRANSLATION INITIATION		4.35	promoter
AT1G20693	HIGH MOBILITY GROUP B2 (HMGB2)	Encodes a prote 1_7179406	4.35	intergenic
AT1G20696	HIGH MOBILITY GROUP B3 (HMGB3)	Encodes a prote 1_7179406	4.35	promoter
AT1G27340	LEAF CURLING RESPONSIVENESS (LC)		4.35	promoter
AT5G10490	MSCS-LIKE 2 (MSL2)	A member of M: 5_3300158	4.35	downstream
AT2G22820	na	unknown proteir 2_9722204	4.35	proximal promoter
AT3G04040	na	unknown proteir 3_1047499	4.35	promoter
AT3G08890 AT4G18530	na na	Protein of unknc 3_2706492 Protein of unknc 4_10220339	4.35 4.35	promoter three_prime_UTR
AT4G18530	na	unknown proteir 4_10220339	4.35	intergenic
AT4G20760	na	NAD(P)-binding 4 11128941	4.35	promoter
AT5G08460	na	GDSL-like Lipas 5_2733021	4.35	promoter
AT5G08450	na	CONTAINS Inte 5_2733021	4.35	promoter
AT5G66950	na	Pyridoxal phosp 5_26732166	4.35	proximal promoter
AT5G10480	PASTICCINO 2 (PAS2)	Protein tyrosine 5_3300158	4.35	promoter
AT4G00760	PSEUDO-RESPONSE REGULATOR 8 (A		4.35	promoter
AT2G28550	RELATED TO AP2.7 (RAP2.7)	related to AP2.7 2_12233054	4.35	intergenic
AT4G00770	TON1 RECRUITING MOTIF 9 (TRM9)	unknown proteir 4_333666	4.35	downstream
AT4G11150	VACUOLAR ATP SYNTHASE SUBUNIT E	Encodes a Vac. 4_6798610 Encodes a ACT 2_16509988	4.35 4.34	proximal promoter
AT2G39570 AT5G63400	ACT DOMAIN REPEATS 9 (ACR9) ADENYLATE KINASE 1 (ADK1)	encodes a prote 5_25394928	4.34	three_prime_UTR promoter
AT1G08920	ERD (EARLY RESPONSE TO DEHYDRA'		4.34	proximal promoter
AT1G47128	ESPONSIVE TO DEHYDRATION 21A (RE		4.34	proximal promoter
AT1G31730	na	Adaptin family p 1_11359603	4.34	promoter
AT5G63410	na	Leucine-rich rer 5_25394928	4.34	downstream
AT1G76920	na	F-box family prc 1_28892188	4.34	five_prime_UTR
AT2G24560	na	GDSL-like Lipas 2_10430851	4.34	proximal promoter
AT2G39580	na	CONTAINS Inte 2_16509988	4.34	promoter
AT5G20050	na	Protein kinase s 5_6776118	4.34	intergenic
AT5G01380 AT5G01390	na na	Homeodomain-I 5_158973 DNAJ heat shor 5_158973	4.34 4.34	proximal promoter intergenic
AT5G20060	na	alpha/beta-Hydr 5_6776118	4.34	promoter
AT1G73590	PIN-FORMED 1 (PIN1)	Encodes an aux 1_27664618	4.34	intergenic
AT4G02460	POSTMEIOTIC SEGREGATION 1 (PMS1)		4.34	promoter
AT1G43890	RAB GTPASE HOMOLOG B18 (RAB18)	ras-related sma 1_16646663	4.34	promoter
AT5G24270	SALT OVERLY SENSITIVE 3 (SOS3)	encodes a calci 5_8241746	4.34	intron
AT2G43130	(ARA4)	encodes a prot€ 2_17929606	4.33	downstream
AT1G60710	(ATB2)	Encodes ATB2. 1_22356756	4.33	five_prime_UTR
AT3G63140	CHLOROPLAST STEM-LOOP BINDING F		4.33	promoter
AT5G48890 AT3G63150	LATE FLOWERING (LATE) MIRO-RELATED GTP-ASE 2 (MIRO2)	Encodes a C(2) 5_19822715 Encodes a calci 3_23328797	4.33 4.33	intergenic downstream
AT3G50340	na	unknown proteir 3_18667733	4.33	proximal promoter
AT1G07830	na	ribosomal protei 1_2422126	4.33	promoter
AT2G47390	na	Prolyl oligopepti 2_19446374	4.33	promoter
AT2G47410	na	WD40/YVTN re 2_19446374	4.33	proximal promoter
AT3G15810	na	Protein of unknc 3_5348147	4.33	exon
AT3G05220	na	Heavy metal tra 3_1487237	4.33	proximal promoter
AT4G27700 AT5G53451	na	Rhodanese/Cell 4_13827980	4.33	promoter
AT3G53451	na SCARECROW (SCR)	This gene enco 5_21693205 Encodes a mer 3_20069264	4.33 4.33	promoter proximal promoter
AT2G45980	ATG8-INTERACTING PROTEIN 1 (ATI1)	Encodes an Atg 2 18919206	4.32	promoter
AT2G42970	na	pre-tRNA; tRNA 2_17873817	4.32	downstream
AT2G42975	na	unknown proteir 2_17873817	4.32	promoter
AT1G29060	na	Target SNARE - 1_10147561	4.32	promoter
AT2G45990	na	unknown proteir 2_18919206	4.32	promoter
AT3G06890	na	unknown proteir 3_2177703	4.32	downstream
AT3G06895	na	unknown proteir 3_2177703	4.32	promoter
AT3G06880 AT3G46020	na	Transducin/WD 3_2177703 RNA-binding (R 3 16912236	4.32 4.32	proximal promoter downstream
AT1G68140	na na	Protein of unknr 1_25541725	4.32	five prime UTR
AT1G00140	na	encodes a mem 1_103837	4.32	intergenic
AT4G22820	na	A20/AN1-like zir 4_11989077	4.32	promoter
AT1G03630	PROTOCHLOROPHYLLIDE OXIDOREDL		4.32	promoter
AT3G06900	U4 SMALL NUCLEOLAR RNA2 (U4.2)	U4.2; snRNA; g 3_2177703	4.32	intergenic
AT1G65630	DEGP PROTEASE 3 (DegP3)	Encodes a puta 1_24404404	4.31	intergenic
AT4G03430	EMBRYO DEFECTIVE 2770 (EMB2770)	Encodes a nucl 4_1520738	4.31	promoter
AT5G26030	EMBRYO DEFECTIVE 2770 (EMB2770) FERROCHELATASE 1 (FC1)	encodes ferroch 5_9096535	4.31	five_prime_UTR
AT5G26030 AT1G02390	EMBRYO DEFECTIVE 2770 (EMB2770) FERROCHELATASE 1 (FC1) GLYCEROL-3-PHOSPHATE ACYLTRANS	encodes ferroch 5_9096535 Encodes a men 1_483080	4.31 4.31	five_prime_UTR exon
AT5G26030	EMBRYO DEFECTIVE 2770 (EMB2770) FERROCHELATASE 1 (FC1)	encodes ferroch 5_9096535	4.31	five_prime_UTR

AT3G09370	MYB DOMAIN PROTEIN 3R-3 (MYB3R-3)	putative c-myb-l 3_2879163	4.31	promoter
AT1G74430	MYB DOMAIN PROTEIN 95 (MYB95)	Encodes a puta 1_27973012	4.31	proximal promoter
AT1G02391	na	unknown proteir 1_483080	4.31	intergenic
AT2G45290	na	Transketolase; 2_18672194	4.31	promoter
AT1G53290	na	Galactosyltrans 1_19871332	4.31	five_prime_UTR
AT4G03435		pre-tRNA; tRNA 4_1520738	4.31	downstream
AT5G43830		Aluminium induc 5_17625135	4.31	proximal promoter
AT2G14910		unknown proteir 2_6409141	4.31	five_prime_UTR
AT1G14590	na	Nucleotide-diph 1_4997619	4.31	intergenic
AT5G14920	na	Gibberellin-regu 5_4828478	4.31	intergenic
AT5G54855	na	Pollen Ole e 1 a 5_22282643	4.31	promoter
AT5G13640	PHOSPHOLIPID:DIACYLGLYCEROL ACY		4.31	five_prime_UTR
AT2G21140	PROLINE-RICH PROTEIN 2 (PRP2)	Proline-rich prot 2_9062962	4.31	proximal promoter
AT2G45280	RAS ASSOCIATED WITH DIABETES PRO		4.31	three_prime_UTR
AT5G14930	SENESCENCE-ASSOCIATED GENE 101		4.31	promoter
AT3G26520	TONOPLAST INTRINSIC PROTEIN 2 (TIP		4.31	intergenic
AT2G18730	DIACYLGLYCEROL KINASE 3 (DGK3)	diacylglycerol ki 2_8118746	4.3	promoter
AT3G60900	FASCICLIN-LIKE ARABINOGALACTAN-P	FASCICLIN-like 3_22499144	4.3	downstream
AT4G25100	FE SUPEROXIDE DISMUTASE 1 (FSD1)		4.3	three_prime_UTR
AT1G12900	GLYCERALDEHYDE 3-PHOSPHATE DEF		4.3	promoter
AT1G71340	GLYCEROPHOSPHODIESTER PHOSPH		4.3	five_prime_UTR
AT5G03040	IQ-DOMAIN 2 (iqd2)	IQ-domain 2 (iq: 5_709868	4.3	downstream
AT2G27680		NAD(P)-linked c 2_11807173	4.3	proximal promoter
AT1G65110		Ubiquitin carbox 1_24188450	4.3	promoter
AT2G38240	na	2-oxoglutarate (2_16013911	4.3	intron
AT3G60897	na	This gene encor 3_22499144	4.3	promoter
AT3G60910	na	S-adenosyl-L-m 3_22499144	4.3	proximal promoter
AT4G33170		Tetratricopeptid 4_15999276	4.3	proximal promoter
AT1G15030	na	Encodes a Cyst 1_5176320	4.3	proximal promoter
AT1G26797	na	Plant self-incom 1_9280290	4.3	proximal promoter
AT1G26860	na	transposable eli 1_9306662	4.3	proximal promoter
AT1G78030	na	unknown proteir 1_29343158	4.3	exon
AT2G45520	na	unknown proteir 2_18756358	4.3	promoter
AT4G11680	na	Zinc finger, C3F 4_7055702	4.3	promoter
AT4G04340	na	ERD (early-resr 4_2122688	4.3	five_prime_UTR
AT4G15590	na	transposable el 4_8907813	4.3	proximal promoter
AT4G25090	na	Riboflavin synth 4_12884398	4.3	proximal promoter
AT5G03030	na	Chaperone Dna 5_709868	4.3	promoter
AT5G24490	na	30S ribosomal r 5_8365602	4.3	five_prime_UTR
AT5G27150	NA+/H+ EXCHANGER 1 (NHX1)	Encodes a vacu 5_9553399	4.3	promoter
AT1G69490	NAC-LIKE, ACTIVATED BY AP3/PI (NAP)	Encodes a merr 1_26120910	4.3	proximal promoter
AT4G05180	PHOTOSYSTEM II SUBUNIT Q-2 (PSBQ-	Encodes the Ps 4_2673298	4.3	promoter
AT5G58600	POWDERY MILDEW RESISTANT 5 (PMR	Belongs to a lar 5_23685841	4.3	promoter
AT1G15020	QUIESCIN-SULFHYDRYL OXIDASE 1 (Q:	Encodes a prote 1_5176320	4.3	promoter
AT3G43210	TETRASPORE (TES)	Encodes a kine: 3_15190713	4.3	promoter
AT2G42570	TRICHOME BIREFRINGENCE-LIKE 39 (T	Encodes a men 2_17719479	4.3	intron
AT1G80840	WRKY DNA-BINDING PROTEIN 40 (WRK	Pathogen-induc 1_30380543	4.3	intergenic
AT4G29010	ABNORMAL INFLORESCENCE MERISTE	Functions in bet 4_14302301	4.29	promoter
AT5G05700	ARGININE-TRNA PROTEIN TRANSFERA	Encodes an arg 5_1712431	4.29	intergenic
AT4G34700	B22 SUBUNIT OF EUKARYOTIC MITOCH	Encodes the B2 4_16556757	4.29	promoter
AT1G21910	DEHYDRATION RESPONSE ELEMENT-E	encodes a mem 1_7699279	4.29	intergenic
AT4G39640	GAMMA-GLUTAMYL TRANSPEPTIDASE		4.29	promoter
AT4G15440		Encodes a hydr 4_8838094	4.29	exon
AT1G49430	LONG-CHAIN ACYL-COA SYNTHETASE		4.29	promoter
AT4G24415	MICRORNA824A (MIR824A)	Encodes a micr 4_12622862	4.29	proximal promoter
AT5G44080		Basic-leucine zi 5_17739986	4.29	promoter
AT2G14878		na 2_6392896	4.29	exon
AT4G02090	na	unknown proteir 4 924795	4.29	intergenic
AT4G15450	na	Senescence/de 4_8838094	4.29	proximal promoter
AT1G26390		FAD-binding Be 1_9132747	4.29	proximal promoter
AT2G38070		Protein of unknc 2_15927073	4.29	proximal promoter
AT1G61460	na	S-locus protein 1_22677645	4.29	five_prime_UTR
AT1G03220	na	Eukaryotic aspa 1_786981	4.29	promoter
AT2G36145	na	unknown proteir 2_15169574	4.29	downstream
AT2G36150	na			
AT1G15840	iia	pre-tRNA; tRNA 2_15169574	4.29	promoter
ATTO 10040		pre-tRNA; tRNA 2_15169574 unknown proteir 1_5452536		
AT1G13640 AT1G78260	na na	unknown proteir 1_5452536 RNA-binding (R 1_29446986	4.29	promoter
	na na	unknown proteir 1_5452536	4.29 4.29	promoter downstream
AT1G78260	na na na	unknown proteir 1_5452536 RNA-binding (R 1_29446986	4.29 4.29 4.29	promoter downstream five_prime_UTR
AT1G78260 AT2G20060	na na na na na	unknown proteir 1_5452536 RNA-binding (R 1_29446986 Ribosomal prote 2_8657360	4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter
AT1G78260 AT2G20060 AT4G34695	na na na na na	unknown proteir 1_5452536 RNA-binding (R 1_29446986 Ribosomal prote 2_8657360 pre-tRNA; tRNA 4_16556757	4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream
AT1G78260 AT2G20060 AT4G34695 AT5G11416	na na na na na	unknown proteir 1_5452536 RNA-binding (R 1_29446986 Ribosomal prote 2_8657360 pre-tRNA; tRNA 4_16556757 This gene enco 5_3642908	4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon
AT1G78260 AT2G20060 AT4G34695 AT5G11416 AT1G23550	na na na na na SIMILAR TO RCD ONE 2 (SRO2)	unknown proteir 1,5452536 RNA-binding (R 1_29446986 Ribosomal prote 2,8657360 pre-tRNA; tRNA 4_16556757 This gene encor 5_3642908 Encodes a prote 1_8350255 encodes a mem 5_3728799	4.29 4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter
AT1G78260 AT2G20060 AT4G34695 AT5G11416 AT1G23550 AT5G11590	na na na na na na SIMILAR TO RCD ONE 2 (SRO2) TINY2 (TINY2)	unknown proteir 1_5452536 RNA-binding (R 1_29446986 Ribosomal prote 2_8657360 pre-IRNA; IRNA 4_16556757 This gene encor 5_3642908 Encodes a prote 1_8350255 encodes a mem 5_3728799 Encodes a prote 4_12729898	4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter promoter
AT1G78260 AT2G20060 AT4G34695 AT5G11416 AT1G23550 AT5G11590 AT4G24670	na na na na na na similar to RCD ONE 2 (SRO2) TINY2 (TINY2) TRYPTOPHAN AMINOTRANSFERASE R CELLULOSE SYNTHASE-LIKE A3 (CSLA) DON-GLUCOSYLTRANSFERASE 1 (DOC	unknown proteir 1,5452536 RNA-binding (R 1_29446986 Ribosomal prote 2,8657360 pre-tRNA; tRNA 4_16556757 This gene encor 5_3642908 Encodes a prote 1,8350255 encodes a mem 5_3728799 Encodes a prote 4_12729898 encodes a gene 1_8333617 Encodes a DON 2_15425271	4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter promoter intron
AT1G78260 AT2G20060 AT4G34695 AT5G11416 AT1G23550 AT5G11590 AT4G24670 AT1G23480	na na na na na na similar to rcd one 2 (sro2) Tiny2 (Tiny2) Tryptophan Aminotransferase r CELLULOSE SYNTHASE-LIKE A3 (CSLA)	unknown proteir 1,5452536 RNA-binding (R 1_29446986 Ribosomal prote 2,8657360 pre-tRNA; tRNA 4_16556757 This gene encor 5_3642908 Encodes a prote 1,8350255 encodes a mem 5_3728799 Encodes a prote 4_12729898 encodes a gene 1_8333617 Encodes a DON 2_15425271	4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter promoter intron
AT1G78260 AT2G20060 AT4G34695 AT5G11416 AT1G23550 AT5G11590 AT4G24670 AT1G23480 AT2G36800	na TIMILAR TO RCD ONE 2 (SRO2) TINY2 (TINY2) TRYPTOPHAN AMINOTRANSFERASE R CELLULOSE SYNTHASE-LIKE A3 (CSLA: DON-GLUCOSYLTRANSFERASE 1 (DOC G PROTEIN ALPHA SUBUNIT 1 (GP ALP na	unknown proteir 1,5452536 RNA-binding (R 1_29446986 Ribosomal prote 2,8657360 pre-tRNA; tRNA 4,16556757 This gene enco; 5_3642908 Encodes a prote 1,8350255 encodes a mem 5,3728799 Encodes a prote 4_12729898 encodes a gene 1,8333617 Encodes a DON 2,15425271 Encodes an DON 2,15425271 Encodes an alpi 2_11197052 ATP binding mic 3,23444110	4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter promoter intron intron promoter five_prime_UTR promoter
AT1G78260 AT2G20060 AT4G34695 AT5G11416 AT1G23550 AT5G11590 AT4G24670 AT1G23480 AT2G36800 AT2G26300	na TIMILAR TO RCD ONE 2 (SRO2) TINY2 (TINY2) TRYPTOPHAN AMINOTRANSFERASE R CELLULOSE SYNTHASE-LIKE A3 (CSLA: DON-GLUCOSYLTRANSFERASE 1 (DOC G PROTEIN ALPHA SUBUNIT 1 (GP ALP na	unknown proteir 1,5452536 RNA-binding (R 1_29446986 Ribosomal prote 2,8657360 pre-tRNA; tRNA 4_16556757 This gene encor 5,3642908 Encodes a prote 1_8350255 encodes a mem 5_3728799 Encodes a prote 4_12729898 encodes a gene 1_8333617 Encodes a DON 2_15425271 Encodes an alp 2_11197052	4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter promoter intron intron promoter five_prime_UTR
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AT1G78260 AT2G20060 AT4G34695 AT5G11416 AT1G23550 AT5G11590 AT4G24670 AT1G23480 AT2G36800 AT2G26300 AT3G63480 AT3G63480 AT4G34320 AT1G18070	na n	unknown proteir 1, 5452536 RNA-binding (R 1_29446986 Ribosomal prote 2, 8657360 pre-tRNA; tRNA 4_16556757 This gene encor 5, 3642908 Encodes a prote 1_8350255 encodes a prote 4_12729898 encodes a prote 4_12729898 encodes a prote 4_12729898 encodes a pore 1_8333617 Encodes a DON 2_15425271 Encodes an alpi 2_11197052 ATP binding mic 3_23444110 Protein of unknc 4_16419895 Translation elon 1_6218416	4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter promoter intron intron promoter five_prime_UTR promoter proximal promoter proximal promoter proximal promoter promoter promoter
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AT1G78260 AT2G20060 AT2G20060 AT4G34695 AT5G11416 AT1G23550 AT3G1590 AT4G24670 AT1G23480 AT2G26800 AT3G63480 AT3G63480 AT4G34320 AT1G64150 AT1G64150 AT3G51290 AT2G47820 AT2G40270	na SIMILAR TO RCD ONE 2 (SRO2) TINY2 (TINY2) TRYPTOPHAN AMINOTRANSFERASE R CELLULOSE SYNTHASE-LIKE A3 (CSLAI DON-GLUCOSYLTRANSFERASE 1 (DOC G PROTEIN ALPHA SUBUNIT 1 (GP ALP na na na na na na na	unknown proteir 1_5452536 RNA-binding (R 1_29446986 Ribosomal prote 2_8657360 pre-tRNA; tRNA 4_16556757 This gene enco; 5_3642908 Encodes a prote 1_8350255 encodes a mem 5_3728799 Encodes a prote 4_12729898 encodes a gene 1_8333617 Encodes a DON 2_15425271 Encodes a DON 2_15425271 Encodes an John 2_15425271 Protein of unkn 3_19041181 unknown proteir 2_19587009 Protein kinase f; 2_15825196	4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter promoter intron intron promoter five_prime_UTR promoter proximal promoter proximal promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
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AT1G78260 AT2G20060 AT2G20060 AT4G34695 AT5G11416 AT1G23550 AT3G11590 AT4G24670 AT2G26300 AT2G26300 AT2G26300 AT3G63480 AT4G34320 AT1G64150 AT2G47820 AT2G40270 AT2G40270 AT2G42800 AT2G428735	na similar TO RCD ONE 2 (SRO2) TINY2 (TINY2) TRYPTOPHAN AMINOTRANSFERASE R CELLULOSE SYNTHASE-LIKE A3 (CSLA: DON-GLUCOSYLTRANSFERASE 1 (DOC G PROTEIN ALPHA SUBUNIT 1 (GP ALP na na na na na na na na na	unknown proteir 1,5452536 RNA-binding (R 1_29446986 Ribosomal prote 2,8657360 pre-tRNA; tRNA 4_16556757 This gene encor 5_3642908 Encodes a prote 1,8350255 encodes a prote 1,8350255 encodes a prote 4,12729898 encodes a prote 4,12729898 encodes a porte 4,12729898 encodes a porte 1,8333617 Encodes a DON 2_15425271 Encodes an alpi 2_11197052 ATP binding mic 3_23444110 Protein of unknc 4_16419895 Translation elon 1_6218416 Uncharacterizec 1_23812807 Protein of unknc 3_19041181 unknown proteir 2_19587009 Protein kinase fi 2_16825196 Peroxisomal me 2_6389762 unknown proteir 2_10975874	4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.29	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter promoter intron intron promoter five_prime_UTR promoter proximal promoter proximal promoter
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AT1G78260 AT2G20060 AT2G20060 AT4G34695 AT5G11416 AT1G23550 AT3G11590 AT4G24670 AT2G26300 AT2G26300 AT2G26300 AT3G51290 AT1G64150 AT2G47820 AT2G40270 AT2G40270 AT2G4860 AT2G25735 AT2G25735 AT2G25735 AT2G25735 AT2G25735 AT2G369160 AT3G51606 AT3G51606 AT5G38990	na na na na na na na na na similar to rcd one 2 (sro2) tiny2 (tiny2) tryptophan aminotransferase r cellulose synthase-like a3 (csla) don-glucosyltransferase 1 (doc G Protein alpha subunit 1 (GP alp na	unknown proteir 1_5452536 RNA-binding (R 1_29446986 Ribosomal prote 2_8657360 pre-tRNA; tRNA 4_16556757 pre-tRNA; tRNA 4_16556757 Bincodes a prote 1_8350255 encodes a prote 1_8350255 encodes a prote 4_12729898 encodes a gene 1_8333617 Encodes a DON 2_15425271 Encodes an alp 2_115425271 Encodes an alp 2_115425271 Encodes an alp 2_115425271 Encodes an alp 2_116425271 Encodes an alp 2_116475271 Encodes an alp 2_11976757 Encodes an alp 2_11976757 Encodes an alp 2_11976757 Encodes an alp 2_11976757 Encodes an alp 2_11976767 Encodes an alp 2_11976767 Protein of unknc 4_16419895 Translation elon 1_6218416 Uncharacterized 1_23812807 Protein of unknc 3_19041181 unknown proteir 2_19587009 Protein kinase f 2_16825196 Peroxisomal me 2_6389762 unknown proteir 2_10975874 ARM repeat sur 2_15425271 NHL domain-co 2_178024 ARM repeat sur 2_15425271 NHL domain-co 2_178024 Potential natura 3_7773078 Major facilitator 3_1453584 Malectin/recepts 5_15608746 unknown proteir 5_23400465 encodes a S-ad 1_518126	4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.29 4.28	promoter downstream five_prime_UTR proximal promoter downstream exon proximal promoter promoter intron intron promoter five_prime_UTR promoter proximal promoter proximal promoter promoter intron promoter promoter promoter promoter promoter proximal promoter exon promoter
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AT3G11730	(ATEDO) Facadas a	0 0744000	4.07	
AT3G61190	(ATFP8) Encodes a BON ASSOCIATION PROTEIN 1 (BAP1) Encodes a	merr 3_3711626		promoter downstream
AT5G47100	CALCINEURIN B-LIKE PROTEIN 9 (CBL9 member o			intron
AT1G12740	CYTOCHROME P450, FAMILY 87, SUBF, encodes a			proximal promoter
AT2G29980		nic rel 2_12781512		downstream
AT3G16360	HPT PHOSPHOTRANSMITTER 4 (AHP4) Encodes A			proximal promoter
AT1G32240		merr 1 11630657		promoter
AT3G24090	L-GLUTAMINE D-FRUCTOSE-6-PHOSPF Encodes a	glute 3_8701119		promoter
AT5G23680	na Sterile alp	ha mc 5_7986601	4.27	five_prime_UTR
AT1G63390	na FAD/NAD	(P)-bii 1_23507142	4.27	promoter
AT1G75510				promoter
AT1G23000		_		downstream
AT3G08910		t shor 3_2712076		promoter
AT3G08920		e/Cell 3_2712076		promoter
AT3G25600		inding 3_9307122		promoter
AT3G08930		_		proximal promoter
AT4G22980 AT4G39270				proximal promoter downstream
AT4G39270 AT4G39280				downstream
AT5G59080				proximal promoter
AT1G16390	ORGANIC CATION/CARNITINE TRANSPi organic ca			promoter
AT5G15600		LIKE4 5_5077367		proximal promoter
AT1G08880				promoter
AT4G34530	CRYPTOCHROME-INTERACTING BASIC Encodes a	trans 4_16498315	4.26	promoter
AT3G54050	HIGH CYCLIC ELECTRON FLOW 1 (HCE Encodes a	a chloi 3_20016732	4.26	promoter
AT4G27230	HISTONE H2A 2 (HTA2) Encodes H	HTA2, 4_13638502	4.26	promoter
AT4G22260				promoter
AT3G09230		f MYE 3_2833245		promoter
AT1G52330		yoger 1_19489288		exon
AT3G11590				promoter
AT5G64120 AT1G08870		tRNA 1 2848234		promoter proximal promoter
AT1G08890	• • • • •	itator 1_2848234		promoter
AT1G69430				promoter
AT1G76940		ng (R 1_28902096		intergenic
AT2G27500		ydrok 2_11753974		five_prime_UTR
AT3G16370		Lipas 3 5559064		intergenic
AT4G34540	na encodes a	prot∈ 4_16498315		promoter
AT5G62770		unknc 5_25211346		exon
AT5G57240	OSBP(OXYSTEROL BINDING PROTEIN): OSBP(oxy	stero 5_23192323	4.26	proximal promoter
AT3G02150	PLASTID TRANSCRIPTION FACTOR 1 (F a chloropla	ast tra 3_390909	4.26	promoter
AT3G16380				intron
AT1G41830				intron
AT5G62170		oroteir 5_24977211		proximal promoter
AT4G38920	VACUOLAR-TYPE H(+)-ATPASE C3 (VH/ vacuolar-t			promoter
AT1G58270 AT5G46290	(ZW9) ZW9 mRN 3-KETOACYL-ACYL CARRIER PROTEIN Encodes b	IA, co 1_21617211		intergenic downstream
AT1G73680	ALPHA DIOXYGENASE (ALPHA DOX2) Encodes a			five_prime_UTR
AT3G28860	ATP-BINDING CASSETTE B19 (ABCB19) Belongs to			intron
AT2G24610	CYCLIC NUCLEOTIDE-GATED CHANNEl member o			intron
AT2G28650	EXOCYST SUBUNIT EXO70 FAMILY PRC A member			exon
AT1G02390	GLYCEROL-3-PHOSPHATE ACYLTRANS Encodes a			proximal promoter
AT1G73687				intergenic
AT5G46280	MINICHROMOSOME MAINTENANCE 3 (I MINICHRO	OMO\$ 5_18773889	4.25	promoter
AT4G20480	na Putative e	ndonı 4_11035318	4.25	exon
AT1G02380				downstream
AT1G15125		/l-L-m 1_5204427		promoter
AT1G18820	na pre-tRNA;			promoter
AT1G18830		n/WD 1_6488217		
	na Transduci			proximal promoter
AT1G73210	na Transduci na Protein of	unknc 1_27533157	4.25	proximal promoter
AT1G73210 AT2G19790	na Transduci na Protein of na SNARE-lik	unkn: 1_27533157 se sur 2_8526925	4.25 4.25	proximal promoter promoter
AT1G73210 AT2G19790 AT1G15120	na Transduci na Protein of na SNARE-lii na Ubiquinol-	unkn: 1_27533157 se sur 2_8526925 cytocl 1_5204427	4.25 4.25 4.25	proximal promoter promoter intergenic
AT1G73210 AT2G19790 AT1G15120 AT4G13263	na Transduci na Protein of na SNARE-lii na Ubiquinol- na Protein of	unkn: 1_27533157 te sur: 2_8526925 cytocl 1_5204427 unkn: 4_7716008	4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA;	unknc 1_27533157 te sur 2_8526925 cytocl 1_5204427 unknc 4_7716008 tRNA 5_6398517	4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-t-RNA; na Enhancer	unkn: 1_27533157 te sur: 2_8526925 cytocl 1_5204427 unkn: 4_7716008	4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G04670	na Transduci na Protein of na SNARE-lik na Ubiquinol- na protein of na protein of na Enhancer na GRAM do na Tautomera	unkn: 1_27533157 te sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G04670 AT5G23350 AT5G57170 AT3G61910	na Transduci na Protein of na SNARE-lik na Ubiquinol- na pro-tRNA; na Enhancer na GRAM do na Tautomers NAC DOMAIN PROTEIN 66 (NAC066) NAC trans	unkn: 1_27533157 ke sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-i 5_7860104 ase/M 5_23163376 cripti: 3_22931244	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter promoter promoter proximal promoter proximal promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G04670 AT5G23350 AT5G57170 AT3G61910 AT5G62170	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) unknown p	unkn: 1_27533157 ke sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 ase/M 5_23163376 criptic 3_22931244 proteir 5_24972804	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter promoter promoter proximal promoter proximal promoter downstream
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G04670 AT5G23350 AT5G57170 AT3G61910 AT5G62170 AT4G23010	na Transduci na Protein of na SNARE-lik na Ubiquinol- na pre-tRNA; na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUTING MOTIF 25 (TRM25) unknown UDP-GALACTOSE TRANSPORTER 2 (U' UDP-galar)	unkn: 1_27533157 te sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 ase/M 5_23163376 cripit: 3_22931244 oroteir 5_24972804 ctose 4_12062827	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter promoter promoter promoter proximal promoter downstream intron
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G04670 AT5G23350 AT5G57170 AT3G61910 AT5G62170 AT4G23010 AT1G76410	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) unknown ju UDP-GALACTOSE TRANSPORTER 2 (U') UDP-gala (ATL8) ATL8; FUI	unknt 1_27533157 xe sur 2_8526925 cytocl 1_5204427 unknt 4_7716008 tRNA 5_6398517 of pol 5_1341671 main- 5_7860104 ase/M 5_23163376 cripiti 3_22931244 vorteir 5_24972804 ctose 4_12062827 vCTIC 1_28669396	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G04670 AT5G23350 AT5G57170 AT3G61910 AT5G62170 AT4G23010 AT1G76410 AT3G12570	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na TON1 RECRUITING MOTIF 25 (TRM25) unknown; UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala (ATL8) (FYD) FYD; LOC	unkn: 1_27533157 ke sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-1 5_7860104 ase/M 5_23163376 cirpiti: 3_22931244 voteir 5_24972804 ctose 4_12062827 NCTIC 1_28669396 ATEE 3_3988678	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G23350 AT5G57170 AT3G61910 AT1G62170 AT4G23010 AT1G76410 AT1G76410 AT1G76410 AT1G76205	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) unknown; UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala (ATL8; FUI (FYD) TRANSPORTER 2 (U' UPP-gala CECERIFERUM 1 (CER1) Expressio	unkn: 1_27533157 te sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671 main- 5_7860104 ase/M 5_23163376 cripit: 3_22931244 orotei: 5_24972804 ctose 4_12062827 NCTIC 1_28669396 ATEL 3_3988678 n of tf 1_420307	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron intron
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G04670 AT5G57170 AT3G61910 AT4G23010 AT1G76410 AT1G76410 AT3G12570 AT1G02205 AT4G17500	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) unknown; UDP-gala (ATL8) (ATL8) ATL8; FUI (FYD) FYD; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes at the codes a	unknc 1_27533157 se sur 2_8526925 cytocl 1_5204427 unknc 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 ase/M 5_23163376 cripiti 3_22931244 vorteir 5_24972804 ctose 4_12062827 vCTIC 1_28669396 ATEE 3_3988678 n of it 1_420307 t men 4_9757305	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron intron proximal promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G23350 AT5G57170 AT3G69110 AT5G62170 AT4G23010 AT1G76410 AT3G12570 AT1G02205 AT4G17500 AT1G54690	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomers NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) unknown i UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala (ATL8) ATL8; FUI (FYD) FYD; LOC ECERIFERUM 1 (CER1) EXpressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GAMMA HISTONE VARIANT H2AX (GAM Encodes I	unkn: 1_27533157 te sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671 main- 5_7860104 ase/M 5_23163376 criptis 3_22931244 oroteir 5_24972804 ctose 4_12062827 NCTIC 1_28669396 ATEL 3_3988678 n of th 1_420307 n menr 4_9757305 tTA3, 1_20415447	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron intron proximal promoter promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G57170 AT3G61910 AT5G57170 AT3G61910 AT1G76410 AT1G76410 AT1G76410 AT1G76450 AT1G75409 AT1G75490 AT1G18970	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na Tautomera NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) unknown; UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala VATL8; FUI (FYD) TYD; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes & GAMMA HISTONE VARIANT H2AX (GAM Encodes & GERMIN-LIKE PROTEIN 4 (GLP4) Encodes &	unkn: 1_27533157 te sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 ase/M 5_23163376 criptis 3_22931244 oroteir 5_24972804 ctose 4_12062827 NCTIC 1_28669396 ATEE 3_398678 n of tr 1_420307 n merr 4_9757305 t TA3, 1_20415447 t gern 1_6555946	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron intron proximal promoter promoter promoter proximal promoter proximal promoter proximal promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G23350 AT5G57170 AT3G69110 AT5G62170 AT4G23010 AT1G76410 AT3G12570 AT1G02205 AT4G17500 AT1G54690	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na Tautomera NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) unknown; UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala VATL8; FUI (FYD) TYD; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes & GAMMA HISTONE VARIANT H2AX (GAM Encodes & GERMIN-LIKE PROTEIN 4 (GLP4) Encodes &	unknc 1_27533157 se sur 2_8526925 cytocl 1_5204427 unknc 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 ase/M 5_23163376 criptit 3_22931244 vorteit 5_24972804 ctose 4_12062827 uCTIC 1_28669396 ATEL 3_3988678 n of it 1_420307 t men 4_9757305 tTA3, 1_20415447 a g gern 1_6555946 to x su 1_26065648	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron intron proximal promoter proximal promoter promote
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G04670 AT5G23350 AT5G657170 AT3G61910 AT1G62010 AT1G76410 AT3G12570 AT1G02205 AT1G54690 AT1G18970 AT1G8970 AT1G89330 AT2G01422	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomers NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) unknown i UDP-GALACTOSE TRANSPORTER 2 (U** UDP-gala (ATL8) ATL8; FUI (FYD) FYD; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes i GAMMA HISTONE VARIANT H2AX (GAM Encodes i GERMIN-LIKE PROTEIN 4 (GLP4) Encodes i na RING/U-b	unkn(1_27533157 te sur 2_8526925 cytocl 1_5204427 unkn(4_7716008 tRNA 5_6398517 of pol 5_1341671 main- 5_7860104 ase/M 5_23163376 criptis 3_22931244 broteir 5_24972804 broteir 5_2497	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron intron intron proximal promoter proximal promoter promoter proximal promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G23350 AT5G23350 AT5G23770 AT3G61910 AT3G61910 AT4G23010 AT1G76410 AT3G12570 AT1G02205 AT1G54690 AT1G18970 AT1G18970 AT1G18970 AT1G189330	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) unknown; UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala VIDP-gala (ATL8) 4TL8; FUI (FYD) FYD; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GAMMA HISTONE VARIANT H2AX (GAM Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na na na protein of	unknc 1_27533157 se sur 2_8526925 cytocl 1_5204427 unknc 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 ase/M 5_23163376 criptit 3_22931244 vorteit 5_24972804 ctose 4_12062827 uCTIC 1_28669396 ATEL 3_3988678 n of it 1_420307 t men 4_9757305 tTA3, 1_20415447 a g gern 1_6555946 to x su 1_26065648	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron intron proximal promoter proximal promoter promote
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G657170 AT3G61910 AT3G657170 AT3G61910 AT1G76410 AT1G76410 AT1G76410 AT1G76410 AT1G76490 AT1G18970 AT1G69330 AT1G69330 AT2G01422 AT5G18460	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomen NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) UUP-GALACTOSE TRANSPORTER 2 (U UP)-gala (ATL8) ATL8; FUI (FYD) FYD; LOS ECERIFERUM 1 (CER1) Expression ECERIFERUM 2 (CER1) Expression ETHYLENE RESPONSIVE ELEMENT BIN Encodes and RING/U-b na RING/U-b na RING/U-b na na na na na na na Curculin-li	unknt 1_27533157 ke sur 2_8526925 cytocl 1_5204427 unknt 4_7716008 tRNA 5_6398517 of pol 5_1341671 main- 5_7860104 ase/M 5_23163376 ccripit 3_22931244 vorteir 5_24972804 ctose 4_12062827 vCTIC 1_28669396 ATEE 3_3988678 n of it 1_420307 u mer 4_9757305 tTA3, 1_20415447 a t gern 1_6555946 box suj 1_26065648 2_183412 Unkni 5_6127115 ke (m 5_6127115	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron intron proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter intergenic
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G23350 AT5G57170 AT3G61910 AT3G61910 AT3G61910 AT4G23010 AT1G76410 AT1G76410 AT1G7500 AT1G54690 AT1G18970 AT1G689330 AT2G01422 AT5G18460 AT5G18460	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRN25) UU UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala (ATL8) ATL8; FUI (FYD) FYD; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GAMMA HISTONE VARIANT H2AX (GAM Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na na na Protein of na RING/U-b na Curculin-li na Curculin-li na Curculin-li na Curculin-li na Unknown p	unkn: 1_27533157 te sut 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671 main- 5_7860104 ase/M 5_23163376 criptic 3_22931244 vroteir 5_24972804 vroteir 5_24972804 vroteir 5_24972804 vroteir 5_3988678 n of it 1_420307 in men' 4_9757305 a gern 1_6555946 ox sut 1_26065648	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron intron proximal promoter intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G04670 AT5G23350 AT5G57170 AT3G61910 AT3G61910 AT3G62170 AT4G23010 AT1G76410 AT1G76410 AT1G54690 AT1G18970 AT1G54690 AT1G18970 AT1G89330 AT2G01422 AT5G18460 AT5G18470 AT1G08180 AT1G281840 AT1G281840 AT1G281840 AT1G281840 AT1G261240	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) UUP-GALACTOSE TRANSPORTER 2 (U UP-gala (ATL8) ATL8; FUI (FYD) FYD; LOC ECERIFERUM 1 (CER1) Expression ECERIFERUM 2 (CER1) Expression ETHYLENE RESPONSIVE ELEMENT BIN Encodes and Encodes and RING/U-b Encodes and na RING/U-b na RING/U-b na Curculin-li na Reticulon na Reticulon na Family of the control of th	unknc 1_27533157 ke sur 2_8526925 cytocl 1_5204427 unknc 4_7716008 tRNA 5_6398517 of pol 5_1341671 main- 5_7860104 ase/M 5_23163376 cripiti 3_22931244 vorteir 5_24972804 ctose 4_12062827 NCTIC 1_28669396 ATEE 3_3988678 n of th 1_420307 u men 4_9757305 tTA3, 1_20415447 at 20415447 at 20415447 box sul 1_26065648 cu sul 1_26065648 cu sul 1_26065648 cu sul 1_26127115 ke (m 5_6127115 ke (m 5_6127115 ramily 2_131220 oroteir 1_2565647 unkno 1_9004670	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter downstream intron intron intron proximal promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G6470 AT5G23350 AT5G57170 AT4G23010 AT1G62170 AT1G62170 AT1G62070 AT1G62170 AT1G6200 AT1G54690 AT1G18970 AT1G68970 AT1G68970 AT1G6930 AT2G01422 AT5G18460 AT5G18470 AT2G01240 AT1G08180	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) Unbp-gala UDP-GALACTOSE TRANSPORTER 2 (U'UDP-gala UDP-gala (ATL8) FYP; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GAMMA HISTONE VARIANT H2AX (GAM GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na RING/U-b na R na Protein of na R <	unkn(1_27533157 te sur 2_8526925 cytocl 1_5204427 unkn(4_7716008 tRNA 5_6398517 of pol 5_1341671 main- 5_7860104 ase/M 5_23163376 cripiti 3_22931244 oroteir 5_24972804 close 4_12062827 NCTIK 1_28669396 ATEL 3_3988678 n of tf 1_420307 n mer 4_9757305 tTA3, 1_20415447 agern 1_6555946 ox sur 1_26065648 2_183412 Unkn 5_6127115 family 2_131220 oroteir 1_2565647 ankno 1_9004670 asso 3_8025961	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron intron proximal promoter promoter promoter promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G557170 AT3G657170 AT3G61910 AT3G62170 AT4G23010 AT1G76410 AT1G76410 AT1G76410 AT1G76490 AT1G18970 AT1G69330 AT2G01422 AT5G18470 AT1G08180 AT5G18470 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G7590 AT4G15790	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) Un UNRown; UPD-GALACTOSE TRANSPORTER 2 (U' U' UP)-gala ATL8; FUI (FYD) FYD; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GAMMA HISTONE VARIANT H2AX (GAM Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na RING/IU-b na Protein of na Curculin-li na Reticulon na unknown; na Family of r na Family of r na Herbert	unkn: 1_27533157 te sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1345171 main-15_7860104 ase;M 5_23163376 circipti: 3_22931244 vortei: 5_24972804 ctose 4_12062827 NCTIC 1_28669396 ATEE 3_3988678 no fit 1_420307 n merr 4_9757305 tTA3, 1_20415447 a gern 1_6555946 ox sur 1_26065648	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.24 4.26	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron exon intron proximal promoter promoter promoter promoter promoter promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G19095 AT5G23350 AT5G57170 AT3G61910 AT3G61910 AT3G62170 AT4G23010 AT1G76410 AT3G12570 AT1G54690 AT1G18970 AT1G54690 AT1G18970 AT1G9330 AT2G01422 AT5G18460 AT5G18470 AT5G18470 AT5G18470 AT5G18470 AT5G18470 AT5G18470 AT5G18470 AT4G17500 AT1G58300 AT1G18970 AT4G17570 AT4G01420 AT5G18470 AT5G18470 AT5G18470 AT5G18470 AT4G195790 AT4G15790 AT4G39670	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRN25) Unknown; UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala UP-gala (ATL8) ATL8; FUI (FYD) FYD; LOS ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na RING/U-b na Reficulon na Reficulon na Family of na Glycolipid	unknt 1_27533157 ke sur 2_8526925 cytocl 1_5204427 unknt 4_7716008 tRNA 5_6398517 of pol 5_1341671 main- 5_7860104 ase/M 5_23163376 cripiti 3_22931244 vorteir 5_24972804 ctose 4_12062827 vCTIC 1_28669396 ATEE 3_3988678 n of it 1_420307 u mer 4_9757305 tTA3, 1_20415447 a t gern 1_6555946 to x suj 1_26065648 2_183412 Unkni 5_6127115 ke (m 5_6127115 ke (m 5_6127115 tamily 2_131220 oroteir 1_2565647 unkno 1_9004670 asso 3_8025961 oroteir 4_8981716 transl 4_188410033	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter downstream intron intron intron proximal promoter promoter promoter promoter promoter promoter promoter promoter promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G6470 AT5G23350 AT5G57170 AT4G23010 AT1G62170 AT1G62170 AT1G62070 AT1G62170 AT1G62070 AT1G6410 AT3G12570 AT1G63930 AT1G18970 AT1G68930 AT2G01422 AT5G18460 AT1G18970 AT2G01240 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G08180 AT1G15790 AT1G635207 AT3G65207	na Transduci na Protein of na SNARE-lik na Ubiquinol na Ubiquinol na Ubiquinol na pre-tRNA; na Enhancer na Enhancer na GRAM do na Tautomera NAC DOMAIN PROTEIN 66 (NACO66) WARD UDP-GALACTOSE TRANSPORTER 2 (U'UDP-gala (ATL8) (TFY) FY; LOC ECERIFERUM 1 (CER1) ETYLENE RESPONSIVE ELEMENT BIL Encodes & GAMMA HISTONE VARIANT H2AX (GAM Encodes I GAMMA HISTONE VARIANT H2AX (GAM Encodes I RING/U-b na na Curculin-lik na Reticulon na HISTONE VARIANT H2AX (GAM Encodes I Family of in RING/U-b na na RING/U-b na na RING/U-b na na Curculin-lik na Reticulon na HISTONE VARIANT H2AX (GAM Encodes RING/U-b na na RING/U-b	unkn(1_27533157	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron intron proximal promoter promoter promoter promoter promoter promoter promoter promoter five_prime_UTR
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G657170 AT3G61910 AT5G62170 AT4G23010 AT1G76410 AT3G12570 AT1G02205 AT4G17500 AT1G69330 AT1G69330 AT1G69330 AT1G6930422 AT5G18470 AT1G08180 AT1G08180 AT1G25682 AT4G15790 AT4G39670 AT4G39670 AT4G39670 AT4G39670 AT5G65207 AT5G65207	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomera NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRN25) Ununknown; UDP-GALACTOSE TRANSPORTER 2 (U' U'DP-gala ATL8; FUI (FYD) FYD; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GAMMA HISTONE VARIANT H2AX (GAM Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na RING/IU-b na Curculin-li na Curculin-li na Reticulon na Honown na Honown na Glycolipid na Glycolipid na Honown na Glycolipid na Honown	unkn: 1_27533157 te sur 2_8526925 cytocl 1_5204427 unkn: 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 asse/M 5_23163376 circiptis 3_22931244 proteir 5_24972804 ctose 4_12062827 NCTIC 1_28669396 ATEL 3_3988678 n of th 1_420307 n merr 4_9757305 tTA3, 1_20415447 a gern 1_6555946 ox sur 1_26065648	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.24 4.26	proximal promoter promoter intergenic intergenic proximal promoter downstream intron intron intron proximal promoter pro
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G19095 AT5G57170 AT3G61910 AT3G61910 AT3G61910 AT3G62170 AT4G23010 AT1G76410 AT3G61910 AT1G76410 AT3G61910 AT1G7500 AT1G54890 AT1G18970 AT1G8970 AT1G9330 AT2G01422 AT5G18460 AT1G918470 AT2G01420 AT1G08180 AT1G25682 AT3G22700 AT4G35670 AT4G36670 AT4G365207 AT5G65207 AT5G65207 AT5G65207 AT5G65207 AT5G65207 AT5G65207 AT5G65207	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRN25) unknown; UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala UP-gala (ATL8) ATL8; FUI (FYD) FYD; LOZ ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na RING/U-b na Reticulon na Reticulon na F-box and na F-box and na F-box and na Glycolipid na Glycolipid na Glycolipid na Glycolipid na Glycolipid n	unknt 1_27533157 ke sur 2_8526925 cytocl 1_5204427 unknt 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-5_7860104 ase/M 5_23163376 cripiti 3_22931244 vorteir 5_24972804 ctose 4_12062827 NCTIC 1_28669396 ATEE 3_3988678 n of th 1_420307 n merr 4_9757305 tTA3, 1_20415447 at 24972804 to xu 1_26065648 c xu 1_26065648 c xu 1_26065648 c xu 1_26065647 unkno 1_9004670 asso 3_8025961 oroteir 1_2565647 unkno 1_9004670 asso 3_8025961 oroteir 4_8981716 transl 4_18410033 oroteir 5_26052628 a para 5_18228862 a puta 2_183412	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter downstream intron intron intron proximal promoter pro
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G64670 AT5G23350 AT5G62170 AT3G61910 AT1G62070 AT1G62070 AT1G62070 AT1G62070 AT1G62070 AT1G6410 AT3G12570 AT1G6200 AT1G54690 AT1G18970 AT1G68970 AT1G68930 AT2G01422 AT5G18460 AT1G18970 AT2G01240 AT1G08180 AT1G25682 AT3G22700 AT4G15790 AT4G15790 AT4G15790 AT4G15790 AT4G15790 AT4G65207 AT5G65207 AT5G65217 AT5G65217 AT5G6545110 AT2G01420 AT4G27410	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na Tautomera NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) Unknown UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala ATL8; FUI (FYD) FYP; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a Bencodes a GAMMA HISTONE VARIANT H2AX (GAM Encodes a Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na Protein of na Reticulon na Reticulon na Fabous na Reticulon na Fabous na GIVcolipid na Unknown I na Inknown I na Inknown I na Inknown I na Inkno	unkn(1_27533157	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron intron proximal promoter p
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G657170 AT3G61910 AT3G61910 AT3G61910 AT3G62170 AT4G23010 AT1G76410 AT3G12570 AT1G6205 AT4G17500 AT1G54690 AT1G18970 AT1G69330 AT1G18970 AT1G69330 AT1G18970 AT1G9870	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRN25) Ununhowan UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala NAC trans (ATL8) ATL8; FUI (FYD) FYD; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na na na RING/IU-b na Reticulon na Reticulon na GRICHINGON na GIycolipid na GIycolipid na GIycolipid na GIycolipid na Encodes a ESPONSIVE TO DESICCATION 26 (RD: Encodes a	unknc 1_27533157 de sur 2_8526925 cytocl 1_5204427 unknc 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 ase/M 5_23163376 criptit 3_22931244 vroteir 5_24972804 ctose 4_12062827 vCTIC 1_28669396 ATEC 3_3988678 n of th 1_420307 n merr 4_9757305 tTA3, 1_20415447 n gern 1_6555946 ox suj 1_26065648 v_183412 Unkn 1_6127115 ke (m 5_6127115 temily 2_131220 vroteir 1_2566647 unkn 0_1_9004670 asso 3_8025961 vroteir 4_8981716 transl 4_18410033 proteir 5_26052628 n para 5_18228862 n para 5_18228862 n para 5_18228862 n para 5_1823412 n NAC 4_13709256 st-tarc 3_19845015	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.24	proximal promoter promoter intergenic intergenic proximal promoter downstream intron intron intron proximal promoter
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G64670 AT5G23350 AT5G62170 AT3G61910 AT1G62070 AT1G62070 AT1G62070 AT1G62070 AT1G62070 AT1G6410 AT3G12570 AT1G6200 AT1G54690 AT1G18970 AT1G68970 AT1G68930 AT2G01422 AT5G18460 AT1G18970 AT2G01240 AT1G08180 AT1G25682 AT3G22700 AT4G15790 AT4G15790 AT4G15790 AT4G15790 AT4G15790 AT4G65207 AT5G65207 AT5G65217 AT5G65217 AT5G6545110 AT2G01420 AT4G27410	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na Enhancer na GRAM do na Tautomer NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) Unknown; UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala (ATL8) (FYD) FYD; LOC ECERIFERUM 1 (CER1) Expression ECTHYLENE RESPONSIVE ELEMENT BIN Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na RING/U-b na Reticulon na Reticulon na Reticulon na F-box and na F-box and na Glycolipid na Glycolipid na F-box and na Glycolipid na Glycolipid na <td>unknc 1_27533157 de sur 2_8526925 cytocl 1_5204427 unknc 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 ase/M 5_23163376 criptit 3_22931244 vroteir 5_24972804 ctose 4_12062827 vCTIC 1_28669396 ATEC 3_3988678 n of th 1_420307 n merr 4_9757305 tTA3, 1_20415447 n gern 1_6555946 ox suj 1_26065648 v_183412 Unkn 1_6127115 ke (m 5_6127115 temily 2_131220 vroteir 1_2566647 unkn 0_1_9004670 asso 3_8025961 vroteir 4_8981716 transl 4_18410033 proteir 5_26052628 n para 5_18228862 n para 5_18228862 n para 5_18228862 n para 5_1823412 n NAC 4_13709256 st-tarc 3_19845015</td> <td>4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25</td> <td>proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron intron proximal promoter p</td>	unknc 1_27533157 de sur 2_8526925 cytocl 1_5204427 unknc 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-15_7860104 ase/M 5_23163376 criptit 3_22931244 vroteir 5_24972804 ctose 4_12062827 vCTIC 1_28669396 ATEC 3_3988678 n of th 1_420307 n merr 4_9757305 tTA3, 1_20415447 n gern 1_6555946 ox suj 1_26065648 v_183412 Unkn 1_6127115 ke (m 5_6127115 temily 2_131220 vroteir 1_2566647 unkn 0_1_9004670 asso 3_8025961 vroteir 4_8981716 transl 4_18410033 proteir 5_26052628 n para 5_18228862 n para 5_18228862 n para 5_18228862 n para 5_1823412 n NAC 4_13709256 st-tarc 3_19845015	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25	proximal promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter downstream intron intron proximal promoter p
AT1G73210 AT2G19790 AT1G15120 AT4G13263 AT5G19095 AT5G19095 AT5G57170 AT3G61910 AT3G61910 AT3G61910 AT3G62170 AT4G23010 AT1G76410 AT3G61910 AT1G76410 AT3G61910 AT1G7500 AT1G18970 AT1G18970 AT1G18970 AT1G91420 AT5G18460 AT1G18970 AT1G91420 AT5G18470 AT2G01420 AT5G18470 AT2G01420 AT4G15790 AT4G365207 AT5G65207	na Transduci na Protein of na SNARE-lik na Ubiquinol- na Protein of na pre-tRNA; na Enhancer na Tautomera NAC DOMAIN PROTEIN 66 (NAC066) NAC trans TON1 RECRUITING MOTIF 25 (TRM25) Unknown UDP-GALACTOSE TRANSPORTER 2 (U' UDP-gala ATL8; FUI (FYD) FYP; LOC ECERIFERUM 1 (CER1) Expressio ETHYLENE RESPONSIVE ELEMENT BIN Encodes a GERMIN-LIKE PROTEIN 4 (GLP4) Encodes a na RING/U-b na RREction na Curculin-li na Reticulon na Reticulon na Reticulon na F-box and na Inknown n na Inknown n na Inknown n na Encodes a SCHILLINE PROTEIN 3 (NPR3) Encodes a FIN-FORMED 4 (PIN4) Encodes a<	unknt 1_27533157 ke sur 2_8526925 cytocl 1_5204427 unknt 4_7716008 tRNA 5_6398517 of pol 5_1341671 main-5_7860104 ase/M 5_23163376 cripiti 3_22931244 vorteir 5_24972804 ctose 4_12062827 NCTIC 1_28669396 ATEE 3_3988678 n of th 1_420307 n men 4_9757305 tTA3, 1_20415447 at 20415447 at 20415447 at 20415447 control 1_6555946 box sul 1_26065648 cox sul 1_26065648 cox sul 1_26065647 unkno 1_9004670 asso 3_8025961 oroteir 1_2565647 unkno 1_9004670 asso 3_8025961 oroteir 4_9881716 transl 4_18410033 oroteir 5_26052628 at para 5_18228862 at puta 2_183412 unka 4_13709256 st-targ 3_19845015 t VAN 4_8981716	4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.25 4.24 4.26 4.27 4.28 4.29	proximal promoter promoter intergenic intergenic proximal promoter downstream intron intron intron proximal promoter five_prime_UTR

474000000	ANIDAGE 4 (ANIA)	F 1	4.00	
AT1G08980	AMIDASE 1 (AMI1)	Encodes an enz 1_2884387	4.23	promoter
AT3G50100	CYCLING DOF FACTOR 1 (CDF1)	Dof-type zinc fir 5_25071472	4.23 4.23	proximal promoter
AT3G59100 AT2G30860	GLUCAN SYNTHASE-LIKE 11 (GSL11) GLUTATHIONE S-TRANSFERASE PHI 9	encodes a prote 3_21853975 Encodes glutath 2_13139031	4.23	downstream
AT2G30800 AT2G18950			4.23	five_prime_UTR
AT1G73500	HOMOGENTISATE PHYTYLTRANSFERA MAP KINASE KINASE 9 (MKK9)	member of MAF 1_27638483	4.23	promoter intergenic
AT4G00870	na	basic helix-loop 4_363793	4.23	promoter
AT1G26950	na	transposable ell 1_9355006	4.23	proximal promoter
AT2G31090	na	unknown proteir 2_13256194	4.23	five_prime_UTR
AT2G35360	na	ubiquitin family 2_14890992	4.23	promoter
AT2G27770	na	Plant protein of 2_11834365	4.23	five_prime_UTR
AT3G59110	na	Protein kinase s 3_21853975	4.23	proximal promoter
AT4G03250	na	Homeodomain-I 4_1428059	4.23	intergenic
AT4G03250	na	Outer arm dyne 4_1428059	4.23	promoter
AT4G03260 AT4G16162	na na	Leucine-rich reg 4 9159011	4.23	•
				downstream
AT5G47060	na	Protein of unknc 5_19116700	4.23	promoter
AT5G62950	na	RNA polymeras 5_25264132	4.23	promoter
AT5G66910	na	Disease resista 5_26721461	4.23	promoter
AT1G08970	NUCLEAR FACTOR Y, SUBUNIT C9 (NF		4.23	downstream
AT4G37870	PHOSPHOENOLPYRUVATE CARBOXYK		4.23	promoter
AT2G20610	SUPERROOT 1 (SUR1)	Confers auxin o 2_8880494	4.23	promoter
AT4G16740	TERPENE SYNTHASE 03 (TPS03)	Encodes an (E,I 4_9407119	4.23	proximal promoter
AT5G53190	(SWEET3)	Nodulin MtN3 fa 5_21576609	4.22	proximal promoter
AT1G23310	GLUTAMATE:GLYOXYLATE AMINOTRAI		4.22	promoter
AT2G05290	na	transposable el 2_1926598	4.22	exon
AT1G08270	na	CONTAINS Inte 1_2607774	4.22	promoter
AT1G71520	na	encodes a mem 1_26938019	4.22	proximal promoter
AT1G72416	na	Chaperone Dna 1_27259584	4.22	intron
AT3G11420	na	Protein of unknc 3_3590606	4.22	proximal promoter
AT3G50350	na	Protein of unknc 3_18673048	4.22	intron
AT5G38200	na	Class I glutamin 5_15258031	4.22	intron
AT5G04440	na	Protein of unknc 5_1254801	4.22	promoter
AT4G25700	BETA-HYDROXYLASE 1 (BETA-OHASE)	*Converts beta-c 4_13095964	4.21	promoter
AT5G64905	ELICITOR PEPTIDE 3 PRECURSOR (PR	elicitor peptide (5_25938213	4.21	proximal promoter
AT4G19960	K+ UPTAKE PERMEASE 9 (KUP9)	Encodes a pota 4_10813138	4.21	promoter
AT2G47610	na	Ribosomal prote 2_19528971	4.21	proximal promoter
AT4G36850	na	PQ-loop repeat 4_17357804	4.21	proximal promoter
AT4G36860	na	LIM domain-cor 4_17357804	4.21	intergenic
AT1G62301	na	unknown proteir 1_23024038	4.21	intergenic
AT1G04280	na	P-loop containir 1_1145863	4.21	intron
AT1G68490	na	unknown proteir 1_25695716	4.21	intergenic
AT3G53430	na	Ribosomal prote 3_19808408	4.21	intergenic
AT3G58610	na	ketol-acid reduc 3_21675361	4.21	intergenic
AT4G11300	na	CONTAINS Inte 4_6875005	4.21	proximal promoter
AT4G27020	na	unknown proteir 4_13571696	4.21	promoter
AT5G24040	na	Protein of unknc 5_8125589	4.21	intergenic
AT5G64900	PRECURSOR OF PEPTIDE 1 (PROPEP1		4.21	downstream
AT3G09880	(ATB' BETA)	Encodes B' regi 3_3028549	4.2	
AT3G09880	(RPA32B)		4.2	proximal promoter
		RPA32B; FUNC 3_654560	4.2	promoter
AT1G53280	DJ-1 HOMOLOG B (DJ1B)	Encodes a hom 1_19867514	4.2	promoter
AT3G52930	FRUCTOSE-BISPHOSPHATE ALDOLASI		4.2	promoter
AT3G63030	METHYL-CPG-BINDING DOMAIN 4 (MBD			promoter
AT1G70420	na	Protein of unknc 1_26541470	4.2	proximal promoter
AT4G38330	na	Integral membra 4_17951230	4.2	promoter
AT3G09870	na	SAUR-like auxir 3_3028549	4.2	proximal promoter
AT1G17360	na	BEST Arabidop: 1_5946303	4.2	promoter
AT1G27470	na	transducin famil 1_9544337	4.2	promoter
AT1G64600	na	methyltransfera: 1_23995805	4.2	promoter
AT2G38646	na	unknown proteir 2_16160150	4.2	promoter
AT3G02315	na	pre-tRNA; tRNA 3_469745	4.2	downstream
AT3G09032	na	unknown proteir 3_2757183	4.2	intergenic
AT3G23480	na	Cyclopropane-f: 3_8418772	4.2	promoter
AT3G63020	na	Protein of unknc 3_23295189	4.2	downstream
AT5G01890	na	Leucine-rich rec 5_344904	4.2	five_prime_UTR
AT3G16640	TRANSLATIONALLY CONTROLLED TUM		4.2	promoter
AT5G05810	(ATL43)	ATL43; FUNCT 5_1747980	4.19	exon
AT3G25860	(LTA2)	Nuclear encode 3_9462879	4.19	downstream
AT1G11650	(RBP45B)	Encodes an RN 1_3914685	4.19	promoter
AT5G54510	DWARF IN LIGHT 1 (DFL1)	Encodes an IAA 5_22136618	4.19	proximal promoter
AT3G56700	FATTY ACID REDUCTASE 6 (FAR6)	Encodes a fatty 3_21002249	4.19	promoter
AT2G44180	METHIONINE AMINOPEPTIDASE 2A (MA		4.19	promoter
AT3G50845	na	Protein of unknc 3_18902158	4.19	proximal promoter
AT3G50860	na	Clathrin adaptor 3_18902158	4.19	five_prime_UTR
AT3G50850	na	Putative methyll 3_18902158	4.19	promoter
AT2G42450	na	alpha/beta-Hydr 2_17676041	4.19	proximal promoter
AT1G11640	na	pre-tRNA; tRNA 1_3914685	4.19	exon
AT1G49210	na	RING/U-box sui 1_18201737	4.19	promoter
AT1G63170	na	Zinc finger, C3F 1_23425353	4.19	five_prime_UTR
AT2G25625	na	unknown proteir 2_10906195	4.19	promoter
AT2G41400	na	Pollen Ole e 1 a 2_17260954	4.19	intergenic
AT3G25870	na	unknown proteir 3_9462879	4.19	intergenic
AT3G53190	na	Pectin lyase-like 3_19716065	4.19	intron
AT4G03405	na	pre-tRNA; tRNA 4_1501657	4.19	five_prime_UTR
AT4G03410	na	Peroxisomal me 4_1501657	4.19	five_prime_UTR
AT4G11970	na	YTH family prot 4_7180292	4.19	promoter
AT4G32760	na	ENTH/VHS/GA 4_15798514	4.19	proximal promoter
AT4G25550	na	Cleavage/polya 4_13048347	4.19	promoter
AT4G32750	na	unknown proteir 4_15798514	4.19	promoter
AT5G05800	na	unknown proteir 5_1747980	4.19	proximal promoter
AT5G20885	na	RING/U-box su ₁ 5_7085232	4.19	promoter
AT4G01250				
		AtWRKY22 is a 4 524123	4.18	exon
	(WRKY22)	AtWRKY22 is a 4_524123 beta-galactosid; 5_23008678	4.18 4.18	exon downstream
AT5G56870	(WRKY22) BETA-GALACTOSIDASE 4 (BGAL4)	beta-galactosid: 5_23008678	4.18	downstream
AT5G56870 AT2G31081	(WRKY22) BETA-GALACTOSIDASE 4 (BGAL4) CLAVATA3/ESR-RELATED 4 (CLE4)	beta-galactosid: 5_23008678 Member of a lar 2_13233762	4.18 4.18	downstream intergenic
AT5G56870	(WRKY22) BETA-GALACTOSIDASE 4 (BGAL4)	beta-galactosid: 5_23008678	4.18	downstream

AT3G09595	na	pre-tRNA; tRNA 3_2946345	4.18	proximal promoter
AT3G58193	na	snoRNA; snoRN 3_21554854	4.18	intergenic
AT5G53590	na	SAUR-like auxir 5_21769908	4.18	proximal promoter
AT3G02500	na	unknown proteir 3_518528	4.18	proximal promoter
AT3G55390	na	Uncharacterise(3_20534707	4.18	five_prime_UTR
AT1G66260	na	RNA-binding (R 1_24698520	4.18	intron
AT3G62050	na	Putative endonu 3_22978107	4.18	promoter
AT5G56880	na	unknown proteir 5_23008678	4.18	intergenic
AT5G58787	na	RING/U-box su ₁ 5_23742349	4.18	promoter
AT5G58784	na	Undecaprenyl p 5_23742349	4.18	proximal promoter
AT5G67050	na	alpha/beta-Hydr 5_26762681	4.18	proximal promoter
AT3G09600	REVEILLE 8 (RVE8)	Encodes a MYE 3_2946345	4.18	promoter
AT1G13280	ALLENE OXIDE CYCLASE 4 (AOC4)	Encodes allene 1 4547447	4.17	promoter
AT3G55360	ECERIFERUM 10 (CER10)	Enoyl-CoA redu 3_20522973	4.17	five_prime_UTR
AT1G79000	HISTONE ACETYLTRANSFERASE OF TI		4.17	promoter
AT3G01100	HYPOTHETICAL PROTEIN 1 (HYP1)	unknown proteir 3_38922	4.17	promoter
AT4G22880	LEUCOANTHOCYANIDIN DIOXYGENAS		4.17	promoter
AT3G01120	METHIONINE OVERACCUMULATION 1 (4.17	three_prime_UTR
AT3G06490	MYB DOMAIN PROTEIN 108 (MYB108)	putative transcri 3 2000504	4.17	proximal promoter
AT1G24600	na	unknown proteir 1 8719494	4.17	proximal promoter
AT4G14135	na	Pseudogene of 4_8140149	4.17	proximal promoter
AT3G02335	na	pre-tRNA; tRNA 3_476792	4.17	promoter
AT1G26090	na	P-loop containir 1_9020356	4.17	promoter
AT1G79010	na	Alpha-helical fei 1_29724887	4.17	three_prime_UTR
AT2G39690	na	Protein of unknc 2_16540783	4.17	promoter
AT1G27190	na	Leucine-rich reg 1_9449332	4.17	proximal promoter
AT1G27200	na	CONTAINS Inte 1_9449332	4.17	downstream
AT3G47630	na	CONTAINS Inte 3_17562856	4.17	downstream
AT3G60957	na	pseudogene of 3_22535658	4.17	downstream
AT3G60960	na	Tetratricopeptid 3_22535658	4.17	promoter
AT4G01590	na	unknown proteir 4_690534	4.17	promoter
AT4G01593	na	Potential natura 4_690534	4.17	promoter
AT4G01595	na	Protein kinase s 4_690534	4.17	downstream
AT5G37540	na	Eukaryotic aspa 5_14916059	4.17	intergenic
AT5G51260	na	HAD superfamil 5 20833862	4.17	promoter
AT3G58840	PEROXISOMAL AND MITOCHONDRIAL		4.17	promoter
AT3G58780	SHATTERPROOF 1 (SHP1)	One of two gene 3_21737402	4.17	proximal promoter
AT3G01680	SIEVE-ELEMENT-OCCLUSION-RELATED		4.17	promoter
AT5G21990	TETRATRICOPEPTIDE REPEAT 7 (TPR7		4.17	intergenic
AT5G62850	VEGETATIVE CELL EXPRESSED1 (AtVE		4.17	promoter
AT2G44610	(RAB6A)	Encodes a GTP 2_18414175	4.16	promoter
AT4G15920	(SWEET17)	Nodulin MtN3 fa 4_9031245	4.16	intron
AT1G31230	ASPARTATÉ KINASE-HOMOSERINE DE		4.16	proximal promoter
AT1G51140	FLOWERING BHLH 3 (FBH3)	Encodes a basi 1_18945830	4.16	promoter
AT4G31877	MICRORNA156C (MIR156C)	Encodes a micr 4_15417646	4.16	proximal promoter
AT2G44620	MITOCHONDRIAL ACYL CARRIER PRO		4.16	promoter
AT5G01340	MITOCHONDRIAL SUCCINATE-FUMARA		4.16	downstream
AT1G60783	na	unknown proteir 1_22377693	4.16	intergenic
AT3G14240	na	Subtilase family 3_4745002	4.16	proximal promoter
AT1G31240	na	Bromodomain tr 1_11163998	4.16	three_prime_UTR
AT1G03370	na	C2 calcium/lipid 1_830525	4.16	promoter
AT1G75400	na	RING/U-box su ₁ 1_28295953	4.16	proximal promoter
AT3G48550	na	BEST Arabidop: 3_17998445	4.16	intergenic
AT3G54880	na	unknown proteir 3 20338676	4.16	promoter
AT3G55646	na	unknown proteir 3_20644014	4.16	proximal promoter
AT3G61950	na	basic helix-loop 3_22941575	4.16	downstream
AT3G61960	na	Protein kinase s 3_22941575	4.16	downstream
AT4G20290	na	unknown proteir 4 10955335	4.16	exon
AT4G20300	na	Protein of unknc 4_10955335	4.16	promoter
AT4G26960	na	unknown proteir 4_13539582	4.16	intron
AT4G26965	na	NADH:ubiquino 4_13539582	4.16	promoter
AT4G35320	na	unknown proteir 4_16806683	4.16	promoter
AT3G54890	PHOTOSYSTEM I LIGHT HARVESTING (4.16	intergenic
AT2G36960	TSL-KINASE INTERACTING PROTEIN 1		4.16	promoter
AT1G07130	(STN1)	Encodes a prote 1_2188437	4.15	three_prime_UTR
AT1G58440	(XF1)	Encodes a puta 1_21717415	4.15	promoter
AT3G48190	ATAXIA-TELANGIECTASIA MUTATED (A		4.15	intron
AT2G37300	ATP-BINDING CASSETTE I16 (ABCI16)	unknown proteir 2_15664530	4.15	intron
AT3G06650	ATP-CITRATE LYASE B-1 (ACLB-1)	One of the two (3_2083296	4.15	promoter
AT4G24510	ECERIFERUM 2 (CER2)	Involved in C28 4_12661824	4.15	exon
AT2G30200	EMBRYO DEFECTIVE 3147 (EMB3147)	catalytics;transf 2_12885746	4.15	intron
AT3G43270	na	Plant invertase/ 3_15226602	4.15	proximal promoter
AT3G66652	na	fip1 motif-contai 3_2083296	4.15	promoter
AT4G23432	na	This gene enco 4_12233369	4.15	exon
AT1G02750	na	Drought-respon 1_602393	4.15	promoter
AT1G06840	na	Leucine-rich rer 1_2103388	4.15	five_prime_UTR
AT1G07128	na	Potential natura 1_2188437	4.15	promoter
AT3G13980	na	unknown proteir 3_4623450	4.15	intergenic
AT3G15220	na	Protein kinase s 3_5132479	4.15	promoter
AT3G61930	na	unknown proteir 3_22934147	4.15	proximal promoter
AT3G63270	na	CONTAINS Inte 3_23377576	4.15	promoter
AT5G03380	na	Heavy metal tra 5_831071	4.15	intergenic
AT5G54064	na	pseudogene, sir 5_21940017	4.15	promoter
AT1G30380	PHOTOSYSTEM I SUBUNIT K (PSAK)	Encodes subun 1_10722067	4.15	promoter
AT2G45640	SIN3 ASSOCIATED POLYPEPTIDE P18 (4.15	promoter
AT1G10760	STARCH EXCESS 1 (SEX1)	Encodes an &#! 1_3590671</td><td>4.15</td><td>intron</td></tr><tr><td>AT1G24460</td><td>TGN-LOCALIZED SYP41 INTERACTING</td><td></td><td>4.15</td><td>promoter</td></tr><tr><td>AT1G25280</td><td>TUBBY LIKE PROTEIN 10 (TLP10)</td><td>Member of TLP 1_8863813</td><td>4.15</td><td>five_prime_UTR</td></tr><tr><td>AT1G75540</td><td>B-BOX DOMAIN PROTEIN 21 (BBX21)</td><td>Encodes a B-bc 1_28363274</td><td>4.14</td><td>proximal promoter</td></tr><tr><td>AT4G19230</td><td>CYTOCHROME P450, FAMILY 707, SUBI</td><td></td><td>4.14</td><td>promoter</td></tr><tr><td>AT2G21330</td><td>FRUCTOSE-BISPHOSPHATE ALDOLASI</td><td></td><td>4.14</td><td>promoter</td></tr><tr><td>AT2G46550</td><td>na</td><td>unknown proteir 2_19114274</td><td>4.14</td><td>promoter</td></tr><tr><td>AT3G10915</td><td>na</td><td>Reticulon family 3_3415798</td><td>4.14</td><td>downstream</td></tr><tr><td>AT5G39570</td><td>na</td><td>FUNCTIONS IN 5_15843893</td><td>4.14</td><td>promoter</td></tr><tr><td></td><td></td><td></td><td></td><td></td></tr></tbody></table>		

AT2G30380	na	CONTAINS Inte 2_12946551	4.14	proximal promoter
AT1G59860	na	HSP20-like cha 1_22031402	4.14	promoter
AT2G03667	na	Asparagine syn 2_1114049	4.14	promoter
AT2G19340	na	Oligosaccharyltı 2_8375992	4.14	promoter
AT3G02250	na	O-fucosyltransfe 3_429771	4.14	proximal promoter
AT2G03660	na	pre-tRNA; tRNA 2_1114049	4.14	exon
AT2G36220	na	unknown proteir 2_15189878	4.14 4.14	proximal promoter proximal promoter
AT3G10910 AT3G50130	na na	RING/U-box su ₁ 3_3414990 Plant protein of 3 18589844	4.14	exon
AT4G08910	na	unknown proteir 4_5710913	4.14	proximal promoter
AT4G09890	na	Protein of unknc 4_6218000	4.14	promoter
AT5G35735	na	Auxin-responsiv 5_13902927	4.14	exon
AT5G61220	na	LYR family of F ₆ 5_24627085	4.14	promoter
AT5G65360	na	Histone superfa 5_26120803	4.14	promoter
AT3G45980	(HTB9)	Encodes a histc 3_16898112 Encodes an am 1 23320408	4.13	promoter
AT1G62960 AT3G50070	ACC SYNTHASE 10 (ACS10) CYCLIN D3;3 (CYCD3;3)	Encode CYCD3 3 18567181	4.13 4.13	promoter promoter
AT3G30070	EXPANSIN-LIKE A1 (EXLA1)	member of EXP 3_16898112	4.13	intergenic
AT5G22830	MAGNESIUM (MG) TRANSPORTER 10 (I		4.13	proximal promoter
AT3G03070	na	NADH-ubiquino 3_696034	4.13	intergenic
AT3G58700	na	Ribosomal L5P 3_21711468	4.13	promoter
AT3G58690	na	Protein kinase s 3_21711468	4.13	downstream
AT4G22980	na	FUNCTIONS IN 4_12047679	4.13	proximal promoter
AT1G33760	na	encodes a mem 1_12239433	4.13	intergenic
AT1G58420 AT2G16290	na na	Uncharacterise: 1_21707297 CONTAINS Inte 2_7056317	4.13 4.13	promoter intergenic
AT3G09180	na	CONTAINS Inte 3_2819155	4.13	five_prime_UTR
AT2G39980	na	HXXXD-type ac 2_16692501	4.13	proximal promoter
AT3G47070	na	LOCATED IN: tl 3_17337814	4.13	promoter
AT3G47080	na	Tetratricopeptid 3_17337814	4.13	intergenic
AT3G54910	na	RNI-like superfa 3_20345027	4.13	promoter
AT3G60110	na	DNA-binding br 3_22197605	4.13	promoter
AT4G00530	na	unknown proteir 4_233877	4.13	promoter
AT4G13710 AT4G39420	na na	Pectin lyase-like 4_7964404	4.13 4.13	intron promoter
AT5G14880	na	unknown proteir 4_18339172 Potassium trans 5_4812859	4.13	proximal promoter
AT5G22820	na	ARM repeat sur 5_7627082	4.13	promoter
AT5G49950	na	alpha/beta-Hydr 5_20323907	4.13	promoter
AT5G49960	na	unknown proteir 5_20323907	4.13	downstream
AT5G56290	PEROXIN 5 (PEX5)	Encodes the pe 5_22792284	4.13	downstream
AT3G54920	POWDERY MILDEW RESISTANT 6 (PMF		4.13	promoter
AT2G40340	(DREB2C)	Encodes a merr 2_16850618	4.12	promoter
AT4G35450 AT3G63310	ANKYRIN REPEAT-CONTAINING PROTE BRZ-INSENSITIVE-LONG HYPOCOTYLS		4.12 4.12	promoter
AT4G35440	CHLORIDE CHANNEL E (CLC-E)	Enclodes a choi 4_16839450	4.12	promoter promoter
AT3G13920	EUKARYOTIC TRANSLATION INITIATION		4.12	proximal promoter
AT1G01580	FERRIC REDUCTION OXIDASE 2 (FRO2		4.12	intron
AT5G48930	HYDROXYCINNAMOYL-COA SHIKIMATE		4.12	promoter
AT4G18230	na	FUNCTIONS IN 4_10081972	4.12	promoter
AT1G35180	na	TRAM, LAG1 ar 1_12878826	4.12	promoter
AT1G30720	na	FAD-binding Be 1_10897769	4.12	promoter
AT3G13930	na	Dihydrolipoamid 3_4595750	4.12	promoter
AT3G19520 AT3G44570	na na	Protein of unknr 3_6772573 Arabidopsis retr 3_16158383	4.12 4.12	promoter promoter
AT3G23840	na	HXXXD-type ac 3_8609658	4.12	proximal promoter
AT4G36925	na	unknown proteir 4_17407947	4.12	intergenic
AT4G28100	na	unknown proteir 4_13965946	4.12	intron
AT5G44570	na	unknown proteir 5_17966779	4.12	intergenic
AT5G44572	na	unknown proteir 5_17966779	4.12	proximal promoter
AT5G58340	na	myb-like HTH tr. 5_23584649	4.12	intron
AT4G18240 AT5G58350	STARCH SYNTHASE 4 (SS4) WITH NO LYSINE (K) KINASE 4 (WNK4)	starch synthase 4_10081972 Encodes a merr 5_23584649	4.12 4.12	promoter promoter
AT3G38330	ZINC FINGER PROTEIN 1 (ZFN1)	Encodes a rineri 3_23364649 Encodes a zinc 3_613638	4.12	promoter
AT5G43630	(TZP)	Encodes a zinc 5_17525007	4.11	proximal promoter
AT1G33980	(UPF3)	Involved in mRN 1_12351438	4.11	promoter
AT3G10740	ALPHA-L-ARABINOFURANOSIDASE 1 (A		4.11	proximal promoter
AT4G25960	ATP-BINDING CASSETTE B2 (ABCB2)	P-glycoprotein 2 4_13179012	4.11	intron
AT1G55350	DEFECTIVE KERNEL 1 (DEK1)	Similar to maize 1_20665137	4.11	promoter
AT4G00850 AT3G20810	GRF1-INTERACTING FACTOR 3 (GIF3) JUMONJI DOMAIN CONTAINING 5 (JMJI		4.11 4.11	promoter intergenic
AT3G20810 AT3G10745	MICRORNA158A (MIR158A)	Encodes a micr 3 3366597	4.11	promoter
AT5G55970	na	RING/U-box suj 5_22665424	4.11	proximal promoter
AT1G70750	na	Protein of unknc 1_26684024	4.11	proximal promoter
AT3G27328	na	unknown proteir 3_10111774	4.11	exon
AT4G00840	na	DHHC-type zinc 4_357393	4.11	promoter
AT4G22290	na	Ubiquitin-specifi 4_11785823	4.11	promoter
AT2G40935	na	PLAC8 family pi 2_17082844	4.11	promoter
AT4G39270 AT1G19480	na na	Leucine-rich rer 4_18276295 DNA glycosylas 1_6744339	4.11 4.11	promoter promoter
AT1G19460 AT1G33970	na	P-loop containir 1 12351438	4.11	promoter
AT1G55370	na	unknown proteir 1_22673046	4.11	promoter
AT2G17240	na	unknown proteir 2_7497600	4.11	proximal promoter
AT1G06640	na	encodes a prot∈ 1_2034132	4.11	downstream
AT1G06645	na	2-oxoglutarate (1_2034132	4.11	promoter
AT2G41820	na	Leucine-rich rer 2_17445216	4.11	proximal promoter
AT3G20820	na	Leucine-rich rer 3_7278665	4.11	proximal promoter
AT4G13100 AT4G14342	na na	RING/U-box su ₁ 4_7638583 Splicing factor 3 4_8255649	4.11 4.11	intron promoter
AT4G14342 AT4G14345	na na	pre-tRNA; tRNA 4 8255649	4.11	promoter
AT4G25170	na	Uncharacterise(4_12909566	4.11	promoter
AT5G20736	na	This gene encor 5_7023368	4.11	intergenic
AT5G60410	(SIZ1)	Encodes a plar 5_24301390	4.1	intergenic
AT4G17640	CASEIN KINASE II BETA CHAIN 2 (CKB2	Encodes casein 4_9825127	4.1	promoter
AT2G20190	CLIP-ASSOCIATED PROTEIN (CLASP)	Encodes a micr 2_8719102	4.1	promoter

AT4G21810	DERLIN-2.1 (DER2.1)	DERLIN-2.1 (DI 4_11577235	4.1	promoter
AT5G62070	IQ-DOMAIN 23 (IQD23)	IQ-domain 23 (I 5_24932705	4.1	promoter
AT1G63720	na	BEST Arabidop: 1_23638038	4.1	proximal promoter
AT1G55265	na	Protein of unknr 1_20617246	4.1	promoter
AT1G67900	na	Phototropic-resi 1_25470109	4.1	downstream
AT1G67910	na	unknown proteir 1_25470109	4.1	intergenic
AT4G17620	na	glycine-rich prot 4_9825127	4.1	downstream
AT1G29950	na	basic helix-loop 1_10489910	4.1	proximal promoter
AT5G59055	na	pre-tRNA; tRNA 5_23845038	4.1	intergenic
AT5G59060 AT5G59070	na na	BEST Arabidop: 5_23845038 UDP-Glycosyltr: 5_23845038	4.1 4.1	promoter promoter
AT1G28760	na na	Uncharacterizer 1_10102918	4.1	promoter
AT1G20700	na	unknown proteir 1_11738140	4.1	five_prime_UTR
AT1G32470	na	Single hybrid m 1 11738140	4.1	intergenic
AT1G78260	na	RNA-binding (R 1_29449780	4.1	intron
AT1G78265	na	Potential natura 1 29449780	4.1	proximal promoter
AT2G28390	na	SAND family prc 2_12145732	4.1	proximal promoter
AT3G28918	na	unknown proteir 3_10934870	4.1	intergenic
AT3G56408	na	Potential natura 3_20921410	4.1	downstream
AT3G56410	na	Protein of unknc 3_20921410	4.1	promoter
AT5G08520	na	Duplicated hom 5_2756860	4.1	intron
AT5G25625	na	pre-tRNA; tRNA 5_8947239	4.1	promoter
AT5G25630	na	Tetratricopeptid 5_8947239	4.1	intron
AT5G60430	na	drug transmemt 5_24301390	4.1	promoter
AT1G56010	NAC DOMAIN CONTAINING PROTEIN 1		4.1	proximal promoter
AT1G78270	UDP-GLUCOSYL TRANSFERASE 85A4 (4.1	intergenic
AT2G33540	C-TERMINAL DOMAIN PHOSPHATASE-L		4.09	promoter
AT3G23000	CBL-INTERACTING PROTEIN KINASE 7		4.09	proximal promoter promoter
AT4G15560 AT3G11040	CLOROPLASTOS ALTERADOS 1 (CLA1) ENDO-BETA-N-ACETYGLUCOSAMINIDA		4.09 4.09	•
AT3G17860	JASMONATE-ZIM-DOMAIN PROTEIN 3 (4.09	promoter proximal promoter
AT3G17860	LYSOPHOSPHATIDYL ACYLTRANSFERA		4.09	intergenic
AT5G10050	na	Tudor/PWWP/N 5 3461808	4.09	promoter
AT2G25690	na	Protein of unknc 2_10942351	4.09	promoter
AT1G03140	na	splicing factor P 1_754321	4.09	downstream
AT1G06480	na	pre-tRNA; tRNA 1_1978184	4.09	downstream
AT2G02910	na	Protein of unknc 2_849806	4.09	promoter
AT2G44670	na	Protein of unknc 2_18424676	4.09	proximal promoter
AT3G17850	na	Protein kinase s 3_6116877	4.09	promoter
AT3G18845	na	Encodes a Prot 3_6499170	4.09	promoter
AT3G27110	na	Peptidase family 3_9997836	4.09	promoter
AT3G51390	na	DHHC-type zinc 3_19075430	4.09	promoter
AT4G21445	na	unknown proteir 4_11425928	4.09	downstream
AT4G21450	na	PapD-like super 4_11425928	4.09	promoter
AT4G26375	na	pre-tRNA; tRNA 4_13336335	4.09	downstream
AT4G32285	na	ENTH/ANTH/VI 4_15585636	4.09	promoter
AT1G03130	PHOTOSYSTEM I SUBUNIT D-2 (PSAD-2		4.09	promoter
AT1G03780	TARGETING PROTEIN FOR XKLP2 (TPX		4.09	promoter
AT4G24040	TREHALASE 1 (TRE1)	Encodes a treh: 4_12489118	4.09	exon
AT4G14622	CONSERVED PEPTIDE UPSTREAM OPE		4.08	three_prime_UTR
AT4G37410	CYTOCHROME P450, FAMILY 81, SUBFA		4.08	proximal promoter
AT3G11400	EUKARYOTIC TRANSLATION INITIATION		4.08	promoter
AT2G37090	IRREGULAR XYLEM 9 (IRX9)	The IRX9 gene 2_15588336	4.08	exon
AT3G01820	na	P-loop containir 3_293218	4.08	intergenic
AT1G14590	na	Nucleotide-diph 1_4996098	4.08	intergenic
AT2G22760	na	basic helix-loop 2_9675958	4.08	proximal promoter
AT3G11402	na	Cysteine/Histidii 3_3578309	4.08	downstream
AT4G14620	na	Protein of unkno 4_8389281	4.08	three_prime_UTR
AT5G41040 AT5G10690	na na	Encodes a ferul 5_16431336 pentatricopeptid 5_3377606	4.08 4.08	promoter
AT5G10695	na	unknown proteir 5 3377606	4.08	promoter promoter
AT5G10093	na	Peptidyl-tRNA h 5_3377606	4.08	intergenic
AT5G32450	na	RNA binding (R 5_12079487	4.08	promoter
AT5G53460	NADH-DEPENDENT GLUTAMATE SYNTI		4.08	proximal promoter
AT3G63180	TIC-LIKE (TKL)	TIC-like (TKL); I 3_23341128	4.08	proximal promoter
AT5G04740	ACT DOMAIN REPEATS 12 (ACR12)	Encodes a ACT 5_1372048	4.07	proximal promoter
AT1G30330	AUXIN RESPONSE FACTOR 6 (ARF6)	Encodes a merr 1_10691857	4.07	proximal promoter
AT5G16260	EARLY FLOWERING 9 (ELF9)	Encodes a RNA 5_5316186	4.07	intergenic
AT1G78300	GENERAL REGULATORY FACTOR 2 (GI	G-box binding fa 1_29461339	4.07	promoter
AT5G27670	HISTONE H2A 7 (HTA7)	Encodes HTA7, 5_9793555	4.07	promoter
AT2G21050	LIKE AUXIN RESISTANT 2 (LAX2)	Encodes LAX2 2_9035571	4.07	exon
AT5G15580	LONGIFOLIA1 (LNG1)	Encodes LONG 5_5072846	4.07	promoter
AT4G37910	MITOCHONDRIAL HEAT SHOCK PROTE		4.07	promoter
AT5G14370	na	CCT motif family 5_4633757	4.07	promoter
AT5G55896	na	transposable el 5_22633422	4.07	promoter
AT5G27660	na	Trypsin family p 5_9793555	4.07	proximal promoter
AT2G40230	na	HXXXD-type ac 2_16803381	4.07	exon
AT2G47870	na	Thioredoxin sup 2_19602526	4.07	proximal promoter
AT4G29780	na	unknown proteir 4_14578516	4.07	proximal promoter
AT4G35110	na na	F1F0-ATPase ir 5_1372048	4.07 4.07	promoter
AT4G35110 AT4G37920	na na	Arabidopsis phc 4_16715132 unknown proteir 4_17828306	4.07 4.07	promoter downstream
AT4G37920 AT5G15581	na na	unknown proteir 4_17828306 unknown proteir 5_5072846	4.07	
AT5G15581 AT5G59020	na na	Protein of unknown 5_23830621	4.07 4.07	intergenic promoter
AT5G59020 AT5G61345	na	pre-tRNA; tRNA 5_24667152	4.07	promoter
AT5G64600	na na	O-fucosyltransfe 5_25824956	4.07	promoter
AT2G22860	PHYTOSULFOKINE 2 PRECURSOR (PSI		4.07	promoter
			4.07	promoter
AT2G02850		Encodes planta 2 827834	4.07	
AT2G02850 AT3G08730	PLANTACYANIN (ARPN) PROTEIN-SERINE KINASE 1 (PK1)	Encodes planta 2_827834 Encodes a prote 3_2654243	4.07	promoter
	PLANTACYANIN (ARPN)			promoter
AT3G08730	PLANTACYANIN (ARPN) PROTEIN-SERINE KINASE 1 (PK1)	Encodes a prote 3_2654243 DNA helicase 5_9793555	4.07	
AT3G08730 AT5G27680	PLANTACYANIN (ARPN) PROTEIN-SERINE KINASE 1 (PK1) RECQ HELICASE SIM (RECQSIM)	Encodes a prote 3_2654243 DNA helicase 5_9793555	4.07 4.07	promoter intergenic
AT3G08730 AT5G27680 AT5G16270 AT2G02860 AT3G26280	PLANTACYANIN (ARPN) PROTEIN-SERINE KINASE 1 (PK1) RECQ HELICASE SIM (RECQSIM) SISTER CHROMATID COHESION 1 PRO SUCROSE TRANSPORTER 2 (SUT2) CYTOCHROME P450, FAMILY 71, SUBF,	Encodes a prott 3_2654243 DNA helicase 5_9793555 Encodes a SCC 5_5316186 encodes a sucri 2_827834 cytochrome P4£ 3_9632075	4.07 4.07 4.07 4.07 4.06	promoter intergenic promoter intergenic promoter
AT3G08730 AT5G27680 AT5G16270 AT2G02860	PLANTACYANIN (ARPN) PROTEIN-SERINE KINASE 1 (PK1) RECQ HELICASE SIM (RECQSIM) SISTER CHROMATID COHESION 1 PRO SUCROSE TRANSPORTER 2 (SUT2)	Encodes a prott 3_2654243 DNA helicase 5_9793555 Encodes a SCC 5_5316186 encodes a sucri 2_827834 cytochrome P4£ 3_9632075	4.07 4.07 4.07 4.07	promoter intergenic promoter intergenic

AT5G15630	IRREGULAR XYLEM 6 (IRX6)	Encodes a merr 5_5086856	4.06	downstream
AT5G12330	LATERAL ROOT PRIMORDIUM 1 (LRP1)		4.06	promoter
AT2G39440	na	CONTAINS Inte 2_16469918	4.06	promoter
AT3G49160	na	Expression of th 3_18224931	4.06	promoter
AT5G15640 AT1G29240	na na	Mitochondrial st 5_5086856 Protein of unknot1_10219844	4.06 4.06	proximal promoter five_prime_UTR
AT1G64610	na	Transducin/WD 1_24003210	4.06	proximal promoter
AT1G04680	na	Pectin lyase-lik€ 1_1307969	4.06	promoter
AT1G06890	na	Nucleotide/suga 1_2114693	4.06	promoter
AT2G17670 AT2G19940	na na	Tetratricopeptid 2_7674183 oxidoreductase: 2_8612815	4.06 4.06	promoter
AT2G30930	na	unknown proteir 2_13162124	4.06	promoter promoter
AT2G42420	na	pre-tRNA; tRNA 2_17660774	4.06	promoter
AT3G27570	na	Sucrase/ferredc 3_10216834	4.06	promoter
AT4G15790	na	unknown proteir 4_8984805	4.06	intergenic
AT4G20830 AT4G35837	na na	FAD-binding Be 4_11154509 This gene encor 4_16979924	4.06 4.06	proximal promoter intergenic
AT5G53490	na	thylakoid lumen: 5 21725853	4.06	proximal promoter
AT5G53500	na	Transducin/WD 5_21725853	4.06	three_prime_UTR
AT1G62720	NOVEL GENE 1 (NG1)	Encodes a PPR 1_23227384	4.06	promoter
AT4G15800	RALF-LIKE 33 (RALFL33)	Member of a div 4_8984805	4.06	promoter
AT1G61380 AT3G61860	S-DOMAIN-1 29 (SD1-29) ARGININE/SERINE-RICH SPLICING FAC	S-domain-1 29 (1_22649809 encodes an ard 3_22902456	4.06 4.05	promoter promoter
AT5G53400	BOBBER1 (BOB1)	Encodes BOBB 5_21661326	4.05	promoter
AT3G27530	GOLGIN CANDIDATE 6 (GC6)	This gene is pre 3_10200089	4.05	promoter
AT5G22880	HISTONE B2 (HTB2)	Encodes a histc 5_7652803	4.05	promoter
AT1G64760 AT2G32210	HYPERSENSITIVE TO EXCESS BORON na	U-Glycosyl hydi 1_24056462 unknown proteir 2_13677976	4.05 4.05	promoter promoter
AT2G32220	na	Ribosomal L27e 2_13677976	4.05	proximal promoter
AT1G52910	na	Protein of unknc 1_19708078	4.05	five_prime_UTR
AT1G52905	na	unknown proteir 1_19708078	4.05	intergenic
AT1G14160	na	Uncharacterise: 1_4842412	4.05	proximal promoter
AT1G22480 AT1G26850	na na	Cupredoxin sup 1_7934093 S-adenosyl-L-m 1_9304638	4.05 4.05	downstream promoter
AT2G15060	na	transposable eli 2 6523786	4.05	intergenic
AT1G22470	na	unknown proteir 1_7934093	4.05	proximal promoter
AT2G41810	na	FUNCTIONS IN 2_17439537	4.05	exon
AT3G26670 AT5G10020	na na	Protein of unknc 3_9801160 Leucine-rich rec 5_3132395	4.05 4.05	intron proximal promoter
AT1G80460	NONHOST RESISTANCE TO P. S. PHAS		4.05	proximal promoter
AT1G48635	PEROXIN 3 (PEX3)	peroxin 3 (PEX: 1_17983592	4.05	promoter
AT3G46780	PLASTID TRANSCRIPTIONALLY ACTIVE		4.05	promoter
AT2G32230	PROTEINACEOUS RNASE P 1 (PRORP1		4.05	intergenic
AT1G48630 AT4G04900	RECEPTOR FOR ACTIVATED C KINASE ROP-INTERACTIVE CRIB MOTIF-CONTA		4.05 4.05	promoter intergenic
AT1G67265	ROTUNDIFOLIA LIKE 21 (RTFL21)	ROTUNDIFOLI/ 1 25176441	4.05	promoter
AT3G26680	SENSITIVE TO NITROGEN MUSTARD 1		4.05	promoter
AT1G68720	TRNA ARGININE ADENOSINE DEAMINA		4.05	proximal promoter
AT1G55190	(PRA7)	PRA7; INVOLVI 1_20588012	4.04	promoter
AT3G16170 AT1G29690	ACYL ACTIVATING ENZYME 13 (AAE13) CONSTITUTIVELY ACTIVATED CELL DE		4.04 4.04	promoter five_prime_UTR
AT5G16820	HEAT SHOCK FACTOR 3 (HSF3)	Encodes a puta 5_5530136	4.04	promoter
AT1G79480	na	Carbohydrate-b 1_29898405	4.04	exon
AT2G04250	na	pseudogene, hy 2_1467491	4.04	intergenic
AT1G05135 AT1G77750	na na	pseudogene of 1_1477690 Ribosomal prote 1_29232133	4.04 4.04	intron proximal promoter
AT3G07790	na	DGCR14-relate 3 2487250	4.04	promoter
AT3G24480	na	Leucine-rich reg 3_8904570	4.04	proximal promoter
AT4G02540	na	Cysteine/Histidii 4_1117091	4.04	promoter
AT5G51795	na	DNA/RNA-bindi 5_21044842	4.04	proximal promoter
AT5G16810 AT5G41890	na na	Protein kinase s 5_5530136 GDSL-like Lipas 5_16767035	4.04 4.04	promoter promoter
AT3G07780	OBERON1 (OBE1)	Encodes a nucl 3_2487250	4.04	downstream
AT3G29370	P1R3 (P1R3)	Encodes a atypi 3_11277871	4.04	proximal promoter
AT5G05590	PHOSPHORIBOSYLANTHRANILATE ISO		4.04	proximal promoter
AT1G52290 AT2G26580	PROLINE-RICH EXTENSIN-LIKE RECEP YABBY5 (YAB5)	YABBY5 (YAB5 2 11309701	4.04 4.04	promoter proximal promoter
AT4G14720	(PPD2)	PPD2 (and its p 4_8435059	4.03	five_prime_UTR
AT5G13790	AGAMOUS-LIKE 15 (AGL15)	AGL15 (AGAM(5_4448736	4.03	intergenic
AT5G52060	BCL-2-ASSOCIATED ATHANOGENE 1 (E		4.03	intergenic
AT3G55610	DELTA 1-PYRROLINE-5-CARBOXYLATE		4.03	proximal promoter five prime UTR
AT4G08500 AT4G36925	MAPK/ERK KINASE KINASE 1 (MEKK1) na	unknown proteir 4_17406279	4.03 4.03	intergenic
AT2G42170	na	Actin family prot 2_17577673	4.03	promoter
AT3G16780	na	Ribosomal prote 3_5708752	4.03	promoter
AT5G13780	na	Acyl-CoA N-acy 5_4448736	4.03	promoter
AT2G27450 AT2G30140	NITRILASE-LIKE PROTEIN 1 (NLP1) UDP-GLUCOSYL TRANSFERASE 87A2 (Encodes N-cart 2_11739685	4.03 4.03	five_prime_UTR promoter
AT2G15090	3-KETOACYL-COA SYNTHASE 8 (KCS8)		4.02	proximal promoter
AT1G54060	6B-INTERACTING PROTEIN 1-LIKE 1 (AS	Member of the t 1_20180751	4.02	five_prime_UTR
AT1G70410	BETA CARBONIC ANHYDRASE 4 (BCA4)		4.02	intron
AT5G63450	CYTOCHROME P450, FAMILY 94, SUBF		4.02	proximal promoter
AT3G02600 AT5G65970	LIPID PHOSPHATE PHOSPHATASE 3 (LI MILDEW RESISTANCE LOCUS O 10 (ML		4.02 4.02	promoter promoter
AT3G03770	na	ankyrin repeat f: 3_961860	4.02	promoter
AT3G24480	na	Leucine-rich reg 3_8900575	4.02	intergenic
AT3G02590	na	Fatty acid hydrc 3_550632	4.02	downstream
AT1G03820	na na	unknown proteir 1_961895	4.02	proximal promoter
AT1G21560 AT2G36980	na na	unknown proteir 1_7554512 Tetratricopeptid 2_15530257	4.02 4.02	promoter proximal promoter
AT2G36360 AT2G46040	na	ARID/BRIGHT [2_18938150	4.02	intron
AT1G54050	na	HSP20-like cha 1_20180751	4.02	promoter
AT2G36970	na	UDP-Glycosyltr: 2_15530257 pre-tRNA; tRNA 2_17659423	4.02	exon
AT2G42420	na	pro-univa, univa 2_17009423	4.02	proximal promoter

AT3G57730	na	Protein kinase s 3_21391619	4.02	promoter
AT4G35250	na	NAD(P)-binding 4_16773364	4.02	promoter
AT5G03970	na	F-box associate 5_1073565	4.02	promoter
AT5G57035	na	U-box domain-c 5_23080658	4.02	promoter
AT5G39860	PACLOBUTRAZOL RESISTANCE1 (PRE	Encodes PRE1 5_15955478	4.02	proximal promoter
AT1G59820	AMINOPHOSPHOLIPID ATPASE 3 (ALA3	Encodes a phos 1_22011159	4.01	promoter
AT4G31590	CELLULOSE-SYNTHASE-LIKE C5 (CSLC	encodes a gen∈ 4_15312862	4.01	promoter
AT3G25690	CHLOROPLAST UNUSUAL POSITIONING		4.01	intron
AT1G56280	DROUGHT-INDUCED 19 (DI19)	Encodes a gene 1_21075057	4.01	promoter
AT1G03970	G-BOX BINDING FACTOR 4 (GBF4)	encodes a basic 1_1018042	4.01	promoter
AT1G15080	LIPID PHOSPHATE PHOSPHATASE 2 (LI		4.01	downstream
AT2G37380	MEMBRANE-ASSOCIATED KINASE REG		4.01	proximal promoter
AT1G02228	na	pseudogene of 1_434282	4.01	promoter
AT1G32410	na	Vacuolar proteir 1_11693711	4.01	promoter
AT3G48380	na	Peptidase C78, 3_17920378	4.01	downstream
AT3G48390	na	MA3 domain-co 3_17920378	4.01	promoter
AT4G17080	na	Histone H3 K4-: 4_9600085	4.01	proximal promoter
AT1G03960	na	Calcium-binding 1_1018042	4.01	downstream
AT1G14330	na	Galactose oxida 1_4894883	4.01	proximal promoter
AT3G06778	na	Chaperone Dna 3_2140770	4.01	intron
AT1G15090	na	pre-tRNA; tRNA 1_5189815	4.01	promoter
AT2G35820	na	ureidoglycolate 2_15051909	4.01	intron
AT2G35830	na	unknown proteir 2_15051909	4.01	promoter
AT3G20650	na	mRNA capping 3_7224155	4.01	promoter
AT3G20655	na	pre-tRNA; tRNA 3_7224155	4.01	downstream
AT3G60510	na	ATP-dependent 3_22360225	4.01	promoter
AT4G05040	na	ankyrin repeat f: 4_2578476	4.01	promoter
AT4G05400	na	copper ion bindi 4_2741054	4.01	promoter
AT5G65990	na	Transmembrane 5_26394523	4.01	promoter
AT5G66480	na	unknown proteir 5_26547126	4.01	promoter
AT5G66490	na	unknown proteir 5_26547126	4.01	downstream
AT5G66500	na	Tetratricopeptid 5_26547126	4.01	intergenic
AT3G23590	REF4-RELATED 1 (RFR1)	Encodes a prote 3_8467507	4.01	five_prime_UTR
AT3G61440	CYSTEINE SYNTHASE C1 (CYSC1)	Encodes a cyst 3_22735661	4	promoter
AT1G27980	DIHYDROSPHINGOSINE PHOSPHATE L		4	proximal promoter
AT1G19180	JASMONATE-ZIM-DOMAIN PROTEIN 1 (JAZ1 is a nucle: 1_6621959	4	promoter
AT2G43240	na	Nucleotide-suga 2_17976064	4	promoter
AT3G17640	na	Leucine-rich reg 3_6033821	4	intergenic
AT3G49810	na	ARM repeat sur 3_18476974	4	promoter
AT4G28430	na	Reticulon family 4_14059930	4	downstream
AT4G28440	na	Nucleic acid-bin 4_14059930	4	promoter
AT3G16840	na	P-loop containir 3_5743265	4	promoter
AT1G19430	na	S-adenosyl-L-m 1_6728032	4	five_prime_UTR
AT1G73740	na	UDP-Glycosyltri 1_27733987	4	promoter
AT3G27250	na	unknown proteir 3_10063068	4	intergenic
AT3G43670	na	Copper amine c 3_15567582	4	intron
AT3G61105	na	pre-tRNA; tRNA 3_22611522	4	downstream
AT4G23870	na	unknown proteir 4_12416516	4	intergenic
AT4G23880	na	unknown proteir 4_12416516	4	promoter
AT4G26675	na	pre-tRNA; tRNA 4_13454530	4	promoter
AT4G27480	na	Core-2/I-branch 4_13739135	4	promoter
AT1G27970	NUCLEAR TRANSPORT FACTOR 2B (NT	Encodes an orth 1_9748151	4	intron
AT3G61430	PLASMA MEMBRANE INTRINSIC PROTE	a member of th€ 3_22735661	4	intergenic
AT3G06300	PROLYL 4-HYDROXYLASE 2 (P4H2)	Encodes a proly 3_1907531	4	promoter
AT1G20090	RHO-RELATED PROTEIN FROM PLANTS	Member of the F 1_6965861	4	proximal promoter
AT3G61110	RIBOSOMAL PROTEIN S27 (RS27A)	Arabidopsis ribc 3_22611522	4	promoter
AT1G47490	RNA-BINDING PROTEIN 47C (RBP47C)	RNA-binding pr 1_17424629	4	promoter
AT1G73805	SAR DEFICIENT 1 (SARD1)	Encodes SAR I 1_27749463	4	promoter
AT1G34210	SOMATIC EMBRYOGENESIS RECEPTO	Plasma membra 1_12458687	4	five_prime_UTR
AT1G08470	STRICTOSIDINE SYNTHASE-LIKE 3 (SSI	Although this er 1_2681090	4	intergenic
AT5G60120	TARGET OF EARLY ACTIVATION TAGGI	target of early a 5_24205547	4	proximal promoter
AT3G06290	YEAST SAC3 HOMOLOG B (SAC3B)	SAC3/GANP/Ni 3_1907531	4	promoter
AT3G17650	YELLOW STRIPE LIKE 5 (YSL5)	Arabidopsis tha 3_6033821	4	promoter
AT2G28560	(RAD51B)	Encodes a prote 2_12234322	3.99	intergenic
AT4G36880	CYSTEINE PROTEINASE1 (CP1)	cysteine protein 4_17378877	3.99	proximal promoter
AT2G32720	CYTOCHROME B5 ISOFORM B (CB5-B)		3.99	intergenic
AT2G23180	CYTOCHROME P450, FAMILY 96, SUBFA		3.99	promoter
AT4G36890	IRREGULAR XYLEM 14 (IRX14)	The IRX14 gene 4_17378877	3.99	intergenic
AT3G06110	MAPK PHOSPHATASE 2 (MKP2)	Encodes a nucli 3_1842071	3.99	proximal promoter
AT3G06490	MYB DOMAIN PROTEIN 108 (MYB108)	putative transcri 3_2007772	3.99	intergenic
AT3G59490	na	unknown proteir 3_21986469	3.99	promoter
AT3G59500	na	Integral membra 3_21986469	3.99	promoter
AT4G29090	na	Ribonuclease H 4_14333301	3.99	promoter
AT5G03660	na	Family of unkno 5_942398	3.99	intergenic
AT5G26960	na	Galactose oxida 5_9484914	3.99	exon
AT3G28040	na	Leucine-rich rec 3_10433980	3.99	proximal promoter
AT5G47550	na	Cystatin/monelli 5_19286340	3.99	downstream
AT1G26580	na	FUNCTIONS IN 1_9184532	3.99	promoter
AT2G32710	na	Kip-related prot 2_13875954	3.99	downstream
AT1G26940	na	Cyclophilin-like 1_9344927	3.99	intron
AT3G06105	na	pre-tRNA; tRNA 3_1842071	3.99	intergenic
AT3G18952	na	pre-tRNA; tRNA 3_6540857	3.99	downstream
AT3G53965	na	pre-tRNA; tRNA 3_19985016	3.99	downstream
AT5G24650	na	Mitochondrial in 5_8437511	3.99	exon
AT3G06100	NOD26-LIKE INTRINSIC PROTEIN 7;1 (N		3.99	exon
AT2G42500	PROTEIN PHOSPHATASE 2A-3 (PP2A-3)		3.99	promoter
AT3G55000	TONNEAU 1A (TON1A)	Encodes a prote 3_20380179	3.99	proximal promoter
AT5G47560	TONOPLAST DICARBOXYLATE TRANSF		3.99	intergenic
AT1G26570	UDP-GLUCOSE DEHYDROGENASE 1 (U		3.99	downstream
AT5G47110	(LIL3:2)	Chlorophyll A-B 5_19133817	3.98	downstream
AT5G27350	(SFP1)	Encodes a suga 5_9646057	3.98	proximal promoter
AT5G40840	(SYN2)	Cohesion family 5_16364654	3.98	proximal promoter
AT4G23810	(WRKY53)	member of WRI 4_12396486	3.98	proximal promoter
AT5G48880	3-KETO-ACYL-COENZYME A THIOLASE	Lilicoues a peio 5_1901/31/	3.98	intron

AT2G41560	AUTOINHIBITED CA(2+)-ATPASE, ISOFO	Encodes a calm 2 17337326	3.98	promoter
AT5G52060	BCL-2-ASSOCIATED ATHANOGENE 1 (E		3.98	proximal promoter
AT1G44446	CHLORINA 1 (CH1)	Encodes chloro 1_16851348	3.98	promoter
AT3G47060	FTSH PROTEASE 7 (ftsh7)	encodes an Ftsl 3_17332787	3.98	promoter
AT2G45050	GATA TRANSCRIPTION FACTOR 2 (GAT		3.98	promoter
AT1G15380	GLYOXYLASE I 4 (GLYI4)	Lactoylglutathio 1_5290177	3.98	proximal promoter
AT5G63715	MICRORNA166G (MIR166G)	Encodes a micr 5_25503457	3.98	proximal promoter
AT1G52347	na	Unknown gene 1_19496385	3.98	promoter
AT4G37880	na	LisH/CRA/RING 4_17809610	3.98	promoter
AT5G66800	na	unknown proteir 5_26672855	3.98	intergenic
AT5G66810	na	CONTAINS Inte 5_26672855	3.98	promoter
AT3G26580	na	Tetratricopeptid 3_9758777	3.98	promoter
AT3G48275	na	pre-tRNA; tRNA 3_17894146	3.98	promoter
AT5G59395	na	pre-tRNA; tRNA 5_23957603	3.98	downstream
AT5G59400	na	FUNCTIONS IN 5_23957603	3.98	promoter
AT1G11390	na	Protein kinase s 1_3837670	3.98	promoter
AT2G43560	na	FKBP-like peptii 2_18075609	3.98	promoter
AT1G12500	na	Nucleotide-suga 1_4265267	3.98	promoter
AT1G45160	na	Protein kinase s 1_17091014	3.98	promoter
AT1G45163	na	unknown proteir 1_17091014	3.98	exon
AT1G45165	na	Expressed prote 1_17091014	3.98	exon
AT1G72570	na	Integrase-type [1_27332856	3.98	intron
AT1G14580	na	C2H2-like zinc f 1_4994611	3.98	intergenic
AT3G02390	na	unknown proteir 3_488895	3.98	exon
AT3G02400	na	SMAD/FHA don 3_488895	3.98	proximal promoter
AT2G31370	na	Basic-leucine zi 2_13378952	3.98	intron
AT4G23820	na	Pectin lyase-like 4_12396486	3.98	intergenic
AT4G40011	na	unknown proteir 4_18552454	3.98	proximal promoter
AT5G01910	na	unknown proteir 5_359073	3.98	promoter
AT4G28080	na	Tetratricopeptid 4_13958135	3.98	promoter
AT4G31650	na	Transcriptional 14_15329947	3.98	proximal promoter
AT5G40348	na	Potential natura 5_16136387	3.98	promoter
AT5G56840	na	myb-like transcr 5_22983943	3.98	intergenic
AT1G11400	PARTNER OF Y14-MAGO (PYM)	The PYM gene 1_3837670	3.98	promoter
AT3G26570	PHOSPHATE TRANSPORTER 2;1 (PHT2		3.98	downstream
AT5G01920	STATE TRANSITION 8 (STN8)	Chloroplast thyl: 5_359073	3.98	promoter
AT1G74020	STRICTOSIDINE SYNTHASE 2 (SS2)	Encodes AtSS-: 1_27838290	3.98	proximal promoter
AT1G53320	TUBBY LIKE PROTEIN 7 (TLP7)	Member of TLP 1_19893551	3.98	promoter
AT1G78100	AUXIN UP-REGULATED F-BOX PROTEI		3.97	proximal promoter
AT1G18400	BR ENHANCED EXPRESSION 1 (BEE1)		3.97	three_prime_UTR
AT5G50380	EXOCYST SUBUNIT EXO70 FAMILY PRO		3.97	promoter
AT1G54030	MODIFIED VACUOLE PHENOTYPE 1 (M		3.97	exon
AT1G63240	na	unknown proteir 1_23458670	3.97	promoter
AT3G60410	na	Protein of unkno 3_22331405	3.97	promoter
AT3G60400	na	Mitochondrial tr. 3_22331405	3.97	intergenic
AT1G51170	na	Protein kinase s 1_18953738	3.97	exon
AT1G55430	na	Cysteine/Histidii 1_20698000	3.97	exon
AT2G01820	na	Leucine-rich rer 2_360903	3.97	promoter
AT3G17450	na	hAT dimerisatio 3_5976125	3.97	promoter
AT4G27585	na	SPFH/Band 7/P 4_13769999	3.97	promoter
AT4G38825	na	SAUR-like auxir 4_18121233	3.97	promoter
AT5G11250	na THOREDOVINI O4 (TO4)	Disease resistal 5_3592077	3.97	promoter
AT2G35010	THIOREDOXIN 01 (TO1)	thioredoxin O1 (2_14754216	3.97	promoter
AT4G00180	YABBY3 (YAB3)	YABBY gene fai 4_75404	3.97	promoter
AT1G19920 AT1G63680	(APS2) (MURE)	encodes a chlor 1_6916854	3.96 3.96	promoter
AT4G09030	ARABINOGALACTAN PROTEIN 10 (AGP	Encodes AtMurl 1_23618183	3.96	intergenic
AT2G46950			3.96	intergenic three_prime_UTR
AT3G21270	CYTOCHROME P450, FAMILY 709, SUB DOF ZINC FINGER PROTEIN 2 (DOF2)	Encodes Dof zir 3_7473165	3.96	proximal promoter
AT2G20000	HOBBIT (HBT)	Required for cel 2_8637072	3.96	five_prime_UTR
AT1G52990	na	thioredoxin fami 1_19740889	3.96	intron
AT2G46940	na	unknown proteir 2_19289337	3.96	proximal promoter
AT1G24530	na	Transducin/WD 1 8694352	3.96	exon
AT1G24330	na	Protein kinase s 1_12064259	3.96	promoter
AT1G55205	na	unknown proteir 1_20593635	3.96	proximal promoter
AT2G37650	na	GRAS family tra 2_15792510	3.96	promoter
AT1G32470	na	Single hybrid m: 1_11740362	3.96	promoter
AT1G80930	na	MIF4G domain- 1_30409864	3.96	promoter
AT3G11780	na	MD-2-related lip 3_3725762	3.96	promoter
AT2G32560	na	F-box family prc 2_13824482	3.96	promoter
AT4G20960	na	encodes diamin 4_11211832	3.96	promoter
AT4G39790	na	Protein of unknc 4_18462091	3.96	downstream
AT5G06260	na	TLD-domain coi 5_1901812	3.96	intergenic
AT2G01290	RIBOSE-5-PHOSPHATE ISOMERASE 2		3.96	promoter
AT1G63690	SIGNAL PEPTIDE PEPTIDASE-LIKE 2 (S		3.96	promoter
AT2G46030	UBIQUITIN-CONJUGATING ENZYME 6 (Ubiquitin conjug 2_18934324	3.96	proximal promoter
AT4G13260	YUCCA2 (YUC2)	Encodes YUC2. 4_7717613	3.96	intergenic
AT1G36160	ACETYL-COA CARBOXYLASE 1 (ACC1)		3.95	promoter
AT5G05690	CONSTITUTIVE PHOTOMORPHOGENIC		3.95	intron
AT1G30610	EMBRYO DEFECTIVE 2279 (emb2279)	Mutations in this 1_10846450	3.95	promoter
AT5G28490	LIGHT-DEPENDENT SHORT HYPOCOTY		3.95	intergenic
AT2G28500	LOB DOMAIN-CONTAINING PROTEIN 1		3.95	intergenic
AT5G57880	MULTIPOLAR SPINDLE 1 (MPS1)	Encodes MULT 5_23446710	3.95	intron
AT1G49610	na	F-box family prc 1_18364735	3.95	proximal promoter
AT1G34630	na	BEST Arabidop: 1_12685148	3.95	promoter
AT5G10070	na	RNase L inhibit 5_3150527	3.95	promoter
AT1G09980	na	Putative serine 1_3261799	3.95	promoter
AT5G57887	na	unknown proteir 5_23446710	3.95	promoter
AT5G57890	na	Glutamine amid 5_23446710	3.95	intergenic
AT1G56240	PHLOEM PROTEIN 2-B13 (PP2-B13)	phloem protein: 1_21058980	3.95	proximal promoter
AT1G67740	PHOTOSYSTEM II BY (PSBY)	PsbY precursor 1_25395149	3.95	five_prime_UTR
AT4G17230	SCARECROW-LIKE 13 (SCL13)	Encodes a scar 4_9663806	3.95	promoter
AT4G24190	SHEPHERD (SHD)	encodes an orth 4_12556115	3.95	promoter
AT5G15330	SPX DOMAIN GENE 4 (SPX4)	SPX domain ge 5_4979406	3.95	proximal promoter

AT5G16620	TRANSLOCON AT THE INNER ENVELOR	chloroplast prot 5 5450586	3.95	promoter
AT3G54826	ZINC RIBBON 3 (ZR3)	Zim17-type zinc 3_20310273	3.95	promoter
AT2G04030	(CR88)	Encodes a chloi 2_1281772	3.94	promoter
AT3G10650	(NUP1)	Encodes a nucl 3_3325191	3.94	three_prime_UTR
AT5G16630	(RAD4)	RAD4; FUNCTI 5_5459831	3.94	downstream
AT3G10640	(VPS60.1)	VPS60.1; CON 3_3325191	3.94	promoter
AT4G34490	CYCLASE ASSOCIATED PROTEIN 1 (CA		3.94	promoter
AT5G01040 AT3G53130	LACCASE 8 (LAC8)	putative laccase 5_15151	3.94	intron
AT5G22830	LUTEIN DEFICIENT 1 (LUT1) MAGNESIUM (MG) TRANSPORTER 10 (I	Lutein-deficient 3_19696647	3.94 3.94	three_prime_UTR three_prime_UTR
AT3G22830	MYB DOMAIN PROTEIN 0 (MYB0)	Encodes a Myb 3_10360943	3.94	intergenic
AT3G53140	na	O-methyltransfe 3_19696647	3.94	three_prime_UTR
AT1G78450	na	SOUL heme-bir 1 29516206	3.94	intergenic
AT4G34500	na	Protein kinase s 4_16487524	3.94	downstream
AT5G59010	na	Protein kinase r 5_23826665	3.94	intergenic
AT5G21020	na	unknown proteir 5_7139468	3.94	intron
AT5G24970	na	Protein kinase s 5_8608920	3.94	promoter
AT5G24980	na	unknown proteir 5_8608920	3.94	promoter
AT1G61260	na	Protein of unknc 1_22597059	3.94	proximal promoter
AT4G20830	na	FAD-binding Be 4_11155444	3.94	promoter
AT4G20840	na	FAD-binding Be 4_11155444	3.94	proximal promoter
AT2G13300	na	transposable eli 2_5522731	3.94	proximal promoter
AT3G10120 AT3G60647	na na	unknown proteir 3_3128718 unknown proteir 3_22419192	3.94 3.94	proximal promoter promoter
AT5G16640	na	Pentatricopeptic 5_5459831	3.94	proximal promoter
AT5G22840	na	Protein kinase s 5_7630799	3.94	three_prime_UTR
AT1G60790	TRICHOME BIREFRINGENCE-LIKE 2 (TE		3.94	promoter
AT2G42260	UV-B-INSENSITIVE 4 (UVI4)	Encodes a nov€ 2_17603806	3.94	promoter
AT1G19730	(ATTRX4)	encodes a cytos 1_6824146	3.93	promoter
AT4G26640	(WRKY20)	member of WRI 4_13442031	3.93	proximal promoter
AT3G47730	ATP-BINDING CASSETTE A2 (ABCA2)	member of ATH 3_17598992	3.93	promoter
AT5G15530	BIOTIN CARBOXYL CARRIER PROTEIN	biotin carboxyl c 5_5047092	3.93	intergenic
AT5G49730	FERRIC REDUCTION OXIDASE 6 (FRO6	Encodes a plasi 5_20204713	3.93	promoter
AT5G61850	LEAFY (LFY)	Encodes transc 5_24845643	3.93	intron
AT2G45450	LITTLE ZIPPER 1 (ZPR1)	ZPR1, a small k 2_18735786	3.93	proximal promoter
AT3G48810	na	Pentatricopeptic 3_18096915	3.93	promoter
AT1G19740	na	ATP-dependent 1_6824146	3.93	promoter
AT1G75590	na	SAUR-like auxir 1_28387214	3.93	intergenic
AT2G01820 AT2G36410	na	Leucine-rich rer 2_362292 Family of unkno 2 15282321	3.93 3.93	proximal promoter
AT4G22580	na na	Exostosin family 4_11890888	3.93	intergenic promoter
AT4G38860	na	SAUR-like auxir 4_18131693	3.93	intergenic
AT1G75040	PATHOGENESIS-RELATED GENE 5 (PR		3.93	proximal promoter
AT5G07250	RHOMBOID-LIKE PROTEIN 3 (RBL3)	RHOMBOID-like 5_2276073	3.93	promoter
AT1G59650	(CW14)	Encodes CW14 1_21915662	3.92	intergenic
AT4G30080	AUXIN RESPONSE FACTOR 16 (ARF16)		3.92	proximal promoter
AT3G58170	BET1P/SFT1P-LIKE PROTEIN 14A (BS14		3.92	promoter
AT2G36830	GAMMA TONOPLAST INTRINSIC PROTE	Encodes a tono 2_15445217	3.92	promoter
AT2G16640	MULTIMERIC TRANSLOCON COMPLEX		3.92	promoter
AT2G19660	na	Cysteine/Histidii 2_8498890	3.92	promoter
AT4G30090	na	FUNCTIONS IN 4_14707885	3.92	intergenic
AT5G64735	na	pre-tRNA; tRNA 5_25875385	3.92	downstream
AT5G66270	na	Zinc finger C-x8 5_26475904	3.92	promoter
AT1G68450 AT2G16650	PIGMENT DEFECTIVE 337 (PDE337) PROTEINACEOUS RNASE P 2 (PRORP2	VQ motif-contail 1_25663978	3.92 3.92	proximal promoter downstream
AT3G62030	ROTAMASE CYP 4 (ROC4)	nuclear-encode 3_22973549	3.92	intron
AT1G64720	(CP5)	membrane relat 1_24048728	3.91	promoter
AT1G31812	ACYL-COA-BINDING PROTEIN 6 (ACBP6		3.91	promoter
AT3G05380	ALWAYS EARLY 2 (ALY2)	ALWAYS EARL 3 1538878	3.91	proximal promoter
AT3G04080	APYRASE 1 (APY1)	Encodes an enz 3_1071879	3.91	proximal promoter
AT5G42380	CALMODULIN LIKE 37 (CML37)	calmodulin like (5_16943630	3.91	promoter
AT1G31814	FRIGIDA LIKE 2 (FRL2)	family member (1_11412241	3.91	intergenic
AT5G62560	na	RING/U-box su ₁ 5_25111661	3.91	exon
AT1G06640	na	encodes a prot∈ 1_2032253	3.91	promoter
AT5G38720	na	unknown proteir 5_15510714		
AT5G38730			3.91	promoter
VI1020100	na	Tetratricopeptid 5_15510714	3.91	promoter
AT1G72190	na	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067	3.91 3.91	promoter promoter
AT1G72200	na na	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box su ₁ 1_27170067	3.91 3.91 3.91	promoter promoter exon
AT1G72200 AT1G09575	na na na	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box su ₁ 1_27170067 Protein of unknc 1_3103259	3.91 3.91 3.91 3.91	promoter promoter exon promoter
AT1G72200 AT1G09575 AT3G53740	na na	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box su ₁ 1_27170067	3.91 3.91 3.91 3.91 3.91	promoter promoter exon
AT1G72200 AT1G09575	na na na na	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box su ₁ 1_27170067 Protein of unknc 1_3103259 Ribosomal prote 3_19915151 Transmembranc 3_20313669	3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron
AT1G72200 AT1G09575 AT3G53740 AT3G54830	na na na na na	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box su ₁ 1_27170067 Protein of unknc 1_3103259 Ribosomal prote 3_19915151	3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G62110	na na na na na na	Tetratricopeptid 5, 15510714 D-isomer specif 1_27170067 RING/U-box suj 1_27170067 Protein of unknx 1_3103259 Ribosomal protx 3_19915151 Transmembranx 3_20313669 Pectin Iyase-likk 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673	3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460	na na na na na na na na	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box suj 1_27170067 Protein of unknc 1_3103259 Ribosomal prote 3_19915151 Transmembran 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460 AT5G14440	na	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box suy 1_27170067 Protein of unknr 1_3103259 Ribosomal prote 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prr 5_4657999	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460 AT5G14440 AT5G12840	na n	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box suj 1_27170067 Protein of unknt 1_3103259 Ribosomal prots 3_19915151 Transmembrant 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteit 5_16205782 Surfeit locus prc 5_4657999 Encodes a subt 5_4053772	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460 AT5G14440 AT5G12840 AT2G39290	na n	Tetratricopeptid 5, 15510714 D-isomer specif 1_27170067 RING/U-box sup 1_27170067 Protein of unknc 1_3103259 Ribosomal prote 3_19915151 Transmembrane 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prc 5_4657992 Encodes a subt. 5_4053772 Encodes a phos 2_16407076	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter promoter promoter promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460 AT5G124440 AT5G12840 AT5G39290 AT5G49510	na n	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box suj 1_27170067 Protein of unknt 1_3103259 Ribosomal prote 3_19915151 Transmembrant 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown protei 5_16205782 Surfeit locus prc 5_4657999 Encodes a subt 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFE 5_20080493	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter promoter promoter promoter promoter promoter
AT1G72200 AT1G09575 AT3G53740 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G14440 AT5G12840 AT5G39290 AT4G39290 AT3G05370	na n	Tetratricopeptid 5, 15510714 D-isomer specif 1_27170067 RING/U-box suj 1_27170067 Protein of unkn 1_3103259 Ribosomal prots 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prc 5_4657999 Encodes a subt 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFL 5_20080493) receptor like prc 3_1538878	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter promoter promoter promoter promoter promoter promoter promoter promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G54830 AT4G12690 AT4G12690 AT5G14440 AT5G14440 AT2G39290 AT5G49510 AT3G05370 AT3G04090	na n	Tetratricopeptid 5, 15510714 D-isomer specif 1_27170067 RING/U-box sup 1_27170067 Protein of unknr 1_3103259 Ribosomal prote 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prr 5_4657999 Encodes a subt 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFL 5_20080493) receptor like prc 3_1538878 Belongs to a far 3_1071879	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter intron five_prime_UTR promoter intergenic intergenic promoter downstream
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G54830 AT4G12690 AT4G36860 AT5G40460 AT5G12840 AT5G12840 AT5G12840 AT5G39290 AT5G49510 AT3G05370 AT3G04090 AT4G15515	na n	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box sup 1_27170067 Protein of unknc 1_3103259 Ribosomal prote 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prc 5_4657999 Encodes a sub. 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFL 5_20080493) receptor like prc 3_1538878 Belongs to a far 3_1071879 B' regulatory su 4_8816911	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G54830 AT4G12690 AT4G12690 AT5G40460 AT5G12840 AT5G12840 AT5G39290 AT3G04090 AT3G04090 AT4G15415 AT1G27840	na n	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box suj 1_27170067 Protein of unkn 1_3103259 Ribosomal prots 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prc 5_4657999 Encodes a subt 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFL 5_20080493) receptor like prc 3_1538878 Belongs to a far 3_1071879 B' regulatory su 4_8816911 Encodes a DDB 1_9696571	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G54830 AT4G12690 AT4G36860 AT5G40460 AT5G12840 AT5G12840 AT5G12840 AT5G39290 AT5G49510 AT3G05370 AT3G04090 AT4G15515	na n	Tetratricopeptid 5, 15510714 D-isomer specif 1_27170067 RING/U-box sup 1_27170067 Protein of unknr 1_3103259 Ribosomal prote 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prr 5_4657999 Encodes a sub 5_4053772 Encodes a sub 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFE 5_20080493) sreceptor like prr 3_1538878 Belongs to a far 3_1071879 B' regulatory su 4_8816911 Encodes a DDE 1_9696571 encodes a prote 2_6454586	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G54830 AT4G12690 AT4G12690 AT5G14440 AT5G12840 AT5G49510 AT3G04950 AT3G04900 AT3G05370 AT3G04090 AT4G15415 AT1G27840 AT2G14960	na n	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box suj 1_27170067 Protein of unknc 1_3103259 Ribosomal prote 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prc 5_4657999 Encodes a sub. 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFL 5_20080493) receptor like prc 3_1538878 Belongs to a far 3_1071879 B' regulatory su 4_8816911 Encodes a DDE 1_9696571 encodes a DDE 1_9696571 encodes a DDE 1_9696571 encodes a DDE 1_9696571 encodes a note 2_6454586 Encodes an adé 1_30111315	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter intron five_prime_UTR promoter intergenic intergenic promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G54830 AT4G12690 AT4G36860 AT5G14440 AT5G12840 AT5G49510 AT3G049510 AT3G05370 AT3G05370 AT3G04990 AT4G15415 AT1G27840 AT2G14960 AT1G80050 AT1G32150 AT1G62540	na n	Tetratricopeptid 5, 15510714 D-isomer specif 1_27170067 RING/U-box sup 1_27170067 Protein of unknx 1_3103259 Ribosomal prots 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prx 5_4657999 Encodes a sub. 5_4053772 Encodes a sub. 5_4053772 Encodes a sub. 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFL 5_20080493 receptor like prx 3_1538878 Belongs to a far 3_1071879 B' regulatory su 4_8816911 Encodes a DDE 1_9696571 encodes a prote 2_6454586 Encodes an ade 1_30111315 Encodes a Gg r1_11568620 belongs to the fil 1_23150310	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter downstream promoter proximal promoter downstream proxiteam
AT1G72200 AT1G09575 AT3G53740 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460 AT5G14440 AT5G12840 AT5G39290 AT3G04990 AT3G49510 AT3G04900 AT4G15415 AT1G27840 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150	na n	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box suj 1_27170067 Protein of unknr 1_3103259 Ribosomal prote 3_19915151 Transmembran 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prr 5_4657999 Encodes a subt 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFL 5_20080493) receptor like prc 3_1538878 Belongs to a far 3_1071879 B' regulatory su 4_8816911 Encodes a DDE 1_9696571 encodes a prote 2_6445866 Encodes an ade 1_30111315 Encodes a G gr 1_11568620 belongs to the fil 1_23150310 LOB domain-co 1_11212861	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter downstream proximal promoter downstream downstream downstream
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460 AT5G12840 AT5G12840 AT5G49510 AT3G05370 AT3G04090 AT4G15415 AT1G27840 AT2G14960 AT1G32150 AT1G62540 AT1G62540 AT1G62540 AT1G631320 AT1G47040	na n	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box suj 1_27170067 Protein of unkn 1_3103259 Ribosomal prots 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prc 5_4657999 Encodes a subt 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFL 5_20080493) receptor like prc 3_1538878 Belongs to a far 3_1071879 B' regulatory su 4_8816911 Encodes a DDB 1_9696571 encodes a prots 2_6454586 Encodes an ads 1_30111315 Encodes a G gr 1_11568620 belongs to the fil 1_23150310 LOB domain-co 1_11212861 Encodes a mer 5_19101033	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter excon promoter promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter promoter promoter promoter promoter promoter promoter promoter downstream promoter downstream downstream downstream downstream promoter promoter proximal promoter promoter promoter proximal promoter promoter promoter proximal promoter promoter promoter promoter promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G54830 AT4G12690 AT4G36860 AT5G14440 AT5G12840 AT5G149510 AT3G05370 AT3G04090 AT4G15415 AT1G27840 AT2G14960 AT1G327840 AT1G327840 AT1G327840 AT1G32150 AT1G32150 AT1G332150 AT1G332150 AT1G332150 AT1G33220 AT5G47040 AT5G52890	na n	Tetratricopeptid 5_15510714 D-isomer specif 1_27170067 RING/U-box sup 1_27170067 Protein of unknx 1_3103259 Ribosomal prots 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prx 5_4657999 Encodes a sub. 5_4053772 Encodes a sub. 5_4053772 Encodes a sub. 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PET 5_20080493) Receptor like prx 3_1538878 Belongs to a far 3_1071879 B' regulatory su 4_8816911 Encodes a DDE 1_9606571 encodes a DDE 1_9606571 encodes an ade 1_30111315 Encodes a Gg r1_11568200 belongs to the fil 1_23150310 LOB domain-co 1_11212861 Encodes a mem 5_19101033 AT hook motif-c 5_21449965	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter intron five_prime_UTR promoter intergenic intergenic promoter downstream promoter proximal promoter downstream proximal promoter
AT1G72200 AT1G09575 AT3G53740 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460 AT5G14440 AT5G12840 AT5G49510 AT3G04990 AT4G15415 AT1G27840 AT1G27840 AT1G32150 AT1G62540 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G4735	na n	Tetratricopeptid 5, 15510714 D-isomer specif 1,27170067 RING/U-box suj 1,27170067 Protein of unknr 1,3103259 Ribosomal prote 3,19915151 Transmembran 3,20313669 Pectin lyase-like 3,22999759 Plant protein of 4,7480516 LIM domain-cor 4,17365673 unknown proteir 5,16205782 Surfeit locus prr 5,4657992 Encodes a subt. 5,4053772 Encodes a phos 2,16407076 prefoldin 3 (PFL 5,20080493 receptor like prc 3,1538878 Belongs to a far 3,1071879 B' regulatory su 4,8816911 Encodes a DBL 9,696571 encodes a DBL 1,15686666 Encodes and 1,30111315 Encodes a G gr 1,11568666 Encodes and 1,30111315 Encodes a G gr 1,11568660 Encodes a mer 5,19101033 AT hook motif-c 5,21449965 BEST Arabidop: 2,14438834	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter downstream proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
AT1G72200 AT1G09575 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460 AT5G12840 AT5G12840 AT5G12840 AT3G03290 AT3G04090 AT4G15415 AT1G27840 AT2G14960 AT1G82540 AT1G62540 AT1G62540 AT5G47040 AT5G47040 AT5G47040 AT5G47040 AT5G47040 AT5G52890 AT1G67340	na n	Tetratricopeptid 5, 15510714 D-isomer specif 1_27170067 RING/U-box sup 1_27170067 Protein of unkn 1_3103259 Ribosomal prots 3_19915151 Transmembrans 3_20313669 Pectin lyase-like 3_22999759 Plant protein of 4_7480516 LIM domain-cor 4_17365673 unknown proteir 5_16205782 Surfeit locus prc 5_4657999 Encodes a subt 5_4053772 Encodes a phos 2_16407076 prefoldin 3 (PFL 5_20080493) receptor like prc 3_1538878 Belongs to a far 3_1071879 B' regulatory su 4_8816911 Encodes a DDB 1_9696571 encodes a prots 2_6454586 Encodes an ada 1_30111315 Encodes a G gr 1_11568620 belongs to the fil 1_23150310 LOB domain-co 1_11212861 Encodes a mem 5_19101033 AT hook motif-c 5_214449863 BEST Arabidops 2_18438834 HCP-like superf 1_25225523	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter excon promoter promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter promoter promoter promoter promoter promoter promoter promoter promoter downstream promoter proximal promoter proximal promoter promoter proximal promoter excon intergenic
AT1G72200 AT1G09575 AT3G53740 AT3G53740 AT3G54830 AT3G62110 AT4G12690 AT4G36860 AT5G40460 AT5G14440 AT5G12840 AT5G49510 AT3G04990 AT4G15415 AT1G27840 AT1G27840 AT1G32150 AT1G62540 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G32150 AT1G4735	na n	Tetratricopeptid 5, 15510714 D-isomer specif 1,27170067 RING/U-box suj 1,27170067 Protein of unknr 1,3103259 Ribosomal prote 3,19915151 Transmembran 3,20313669 Pectin lyase-like 3,22999759 Plant protein of 4,7480516 LIM domain-cor 4,17365673 unknown proteir 5,16205782 Surfeit locus prr 5,4657992 Encodes a subt. 5,4053772 Encodes a phos 2,16407076 prefoldin 3 (PFL 5,20080493 receptor like prc 3,1538878 Belongs to a far 3,1071879 B' regulatory su 4,8816911 Encodes a DBL 9,696571 encodes a DBL 1,15686666 Encodes and 1,30111315 Encodes a G gr 1,11568666 Encodes and 1,30111315 Encodes a G gr 1,11568660 Encodes a mer 5,19101033 AT hook motif-c 5,21449965 BEST Arabidop: 2,14438834	3.91 3.91 3.91 3.91 3.91 3.91 3.91 3.91	promoter promoter exon promoter promoter intron five_prime_UTR promoter intergenic intergenic promoter downstream proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter

AT1G21080	na	DNAJ heat shot 1_7382486	3.9	intron
AT1G80040	na	FUNCTIONS IN 1_30111315	3.9	promoter
AT3G28200	na	Peroxidase sup 3_10516820	3.9	proximal promoter
AT3G11580	na	AP2/B3-like trar 3_3655836	3.9	intergenic
AT4G20430	na	Subtilase family 4_11021448	3.9	promoter
AT1G32160	na	Protein of unknc 1_11568620		promoter
AT1G74570	na	pre-tRNA; tRNA 1_28020290	3.9	downstream
AT3G18773	na	RING/U-box sul 3_6466119	3.9	five_prime_UTR
AT3G53990	na	Adenine nucleol 3_19992894	3.9	proximal promoter
AT4G32470 AT4G32475	na na	Cytochrome bd 4_15671304	3.9 3.9	promoter
AT5G17070	na	pre-tRNA; tRNA 4_15671304 CONTAINS Inte 5_5616212	3.9	promoter promoter
AT4G15410	SERINE/THREONINE PROTEIN PHOSPI		3.9	downstream
AT2G21950	SKP1 INTERACTING PARTNER 6 (SKIP6		3.9	promoter
AT1G30210	TEOSINTE BRANCHED 1, CYCLOIDEA, A		3.9	promoter
AT2G36420		unknown proteir 2_15284242	3.9	proximal promoter
AT3G02870	(VTC4)	Encodes a L-ga 3_630011	3.89	promoter
AT1G60270	BETA GLUCOSIDASE 6 (BGLU6)	beta glucosidas 1_22225683	3.89	proximal promoter
AT4G26100	CASEIN KINASE 1 (CK1)	Encodes a merr 4_13230832	3.89	promoter
AT2G42540	COLD-REGULATED 15A (COR15A)	A cold-regulater 2_17712373	3.89	promoter
AT1G26770	EXPANSIN A10 (EXPA10)	Encodes an ext 1_9259357	3.89	promoter
AT3G14720	MAP KINASE 19 (MPK19)	member of MAF 3_4945476	3.89	promoter
AT5G28145	na	transposable eli 5_10128233	3.89	proximal promoter
AT2G46290 AT5G48610	na	Transducin/WD 2_19008011		promoter
AT5G46610 AT5G36240	na na	unknown proteir 5_19711493 zinc knuckle (Ct 5_14280317	3.89	promoter proximal promoter
AT3G30240	na	Peptidyl-tRNA h 3_680750	3.89	promoter
AT3G03020	na	unknown proteir 3 680750	3.89	promoter
AT3G49200	na	O-acyltransfera: 3_18238469	3.89	proximal promoter
AT3G49210	na	O-acyltransfera: 3 18238469	3.89	exon
AT3G61898	na	unknown proteir 3_22923831	3.89	intergenic
AT4G38640	na	Plasma-membra 4_18062388	3.89	promoter
AT4G39780	na	encodes a mem 4_18460924	3.89	proximal promoter
AT5G38096	na	Pseudogene of 5_15201154	3.89	exon
AT4G37860	na	SPT2 chromatir 4_17802799	3.89	proximal promoter
AT5G38100	na	S-adenosyl-L-m 5_15201154	3.89	exon
AT5G52850	na	Pentatricopeptic 5_21418503	3.89	proximal promoter
AT5G59760	na	Protein of unknc 5_24075746	3.89	exon
AT4G37870	PHOSPHOENOLPYRUVATE CARBOXYK PSEUDO-RESPONSE REGULATOR 5 (P		3.89	three_prime_UTR
AT5G24470 AT3G46590	TRF-LIKE 1 (TRFL1)	Encodes a prote 3_17151363	3.89 3.89	proximal promoter proximal promoter
AT5G42020	(BIP2)	Luminal binding 5_16810687	3.88	promoter
AT2G17520	(IRE1A)	Encodes a endc 2_7617143	3.88	promoter
AT3G14370	(WAG2)	The WAG2 and 3_4800089	3.88	proximal promoter
AT5G42030	ABL INTERACTOR-LIKE PROTEIN 4 (ABI		3.88	intergenic
AT1G73680	ALPHA DIOXYGENASE (ALPHA DOX2)	Encodes an alpl 1_27710117	3.88	proximal promoter
AT3G17700	CYCLIC NUCLEOTIDE-BINDING TRANSF	cyclic nucleotide 3_6048807	3.88	promoter
AT1G13950	EUKARYOTIC ELONGATION FACTOR 5/		3.88	proximal promoter
AT3G13810	INDETERMINATE(ID)-DOMAIN 11 (IDD11		3.88	intron
AT2G15050	LIPID TRANSFER PROTEIN (LTP)	Predicted to enc 2_6518833	3.88	promoter
AT5G65590	na	Dof-type zinc fir 5_26215588		proximal promoter
AT1G17660	na na	pre-tRNA; tRNA 1_6075900	3.88 3.88	downstream
AT1G17670 AT1G78820	na	pre-tRNA; tRNA 1_6075900 D-mannose bin: 1_29635842	3.88	downstream promoter
AT3G50230	na	Leucine-rich reg 3_18620016	3.88	proximal promoter
AT4G18380	na	F-box family prc 4_10161077	3.88	intergenic
AT5G47590	na	Heat shock prot 5 19299264	3.88	promoter
AT5G39020	na	Malectin/recepts 5_15616844	3.88	promoter
AT5G50995	na	pre-tRNA; tRNA 5_20741623	3.88	downstream
AT5G57280		Gene encodes : 5_23204366	3.88	promoter
AT4G19640	(ARA7)	Encodes Ara7. 4_10689634	3.87	promoter
AT3G11020	DRE/CRT-BINDING PROTEIN 2B (DREB2	_	3.87	promoter
AT1G56200	EMBRYO DEFECTIVE 1303 (emb1303)	Encodes a chloi 1_21030725	3.87	promoter
AT4G35920	MID1-COMPLEMENTING ACTIVITY 1 (MC		3.87	promoter
AT1G02030 AT1G61400	na na	C2H2-like zinc f 1_356908 S-locus lectin pi 1_22658435	3.87 3.87	five_prime_UTR proximal promoter
AT1G61400 AT1G61410	na	DNA double-str: 1 22658435	3.87	downstream
AT2G05920	na	Subtilase family 2_2269524	3.87	three prime UTR
AT5G17190	na	FUNCTIONS IN 5_5652191	3.87	promoter
AT4G23895	na	Pleckstrin home 4_12421515	3.87	proximal promoter
AT4G19645	na	TRAM, LAG1 at 4_10689634	3.87	downstream
AT4G36850	na	PQ-loop repeat 4_17355879	3.87	five_prime_UTR
AT4G23890	NADH DEHYDROGENASE-LIKE COMPLI	unknown proteir 4_12421515	3.87	promoter
AT2G20890	PHOTOSYSTEM II REACTION CENTER F	unknown proteir 4_12421515 Chloroplast-loca 2_8987576	3.87	promoter
AT2G20890 AT2G30070	PHOTOSYSTEM II REACTION CENTER F POTASSIUM TRANSPORTER 1 (KT1)	unknown proteir 4_12421515 Chloroplast-loca 2_8987576 Encodes a high 2_12834990	3.87 3.87	promoter promoter
AT2G20890 AT2G30070 AT1G80670	PHOTOSYSTEM II REACTION CENTER F POTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1)	unknown proteir 4_12421515 Chloroplast-loca 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872	3.87 3.87 3.87	promoter promoter promoter
AT2G20890 AT2G30070 AT1G80670 AT2G28630	PHOTOSYSTEM II REACTION CENTER F POTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1	unknown proteir 4_12421515 Chloroplast-loce 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436	3.87 3.87 3.87 3.86	promoter promoter promoter promoter
AT2G20890 AT2G30070 AT1G80670 AT2G28630 AT3G61190	PHOTOSYSTEM II REACTION CENTER F POTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1)	unknown proteir 4_12421515 Chloroplast-loce 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS11 2_12277436 Encodes a prote 3_22652199	3.87 3.87 3.87 3.86 3.86	promoter promoter promoter promoter proximal promoter
AT2G20890 AT2G30070 AT1G80670 AT2G28630 AT3G61190 AT5G20650	PHOTOSYSTEM II REACTION CENTER F POTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5)	unknown proteir 4_12421515 Chloroplast-loce 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436	3.87 3.87 3.87 3.86 3.86 3.86	promoter promoter promoter promoter proximal promoter promoter
AT2G20890 AT2G30070 AT1G80670 AT2G28630 AT3G61190	PHOTOSYSTEM II REACTION CENTER F POTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1)	unknown proteir 4_12421515 Chloroplast-locs 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes a prote 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560	3.87 3.87 3.87 3.86 3.86	promoter promoter promoter promoter proximal promoter
AT2G20890 AT2G30070 AT1G80670 AT2G28630 AT3G61190 AT5G20650 AT5G22640	PHOTOSYSTEM II REACTION CENTER I POTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5) EMBRYO DEFECTIVE 1211 (emb1211)	unknown proteir 4, 12421515 Chloroplast-locs 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes a prote 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily cc 3_4184548	3.87 3.87 3.87 3.86 3.86 3.86 3.86	promoter promoter promoter promoter proximal promoter proximal promoter
AT2G20890 AT2G30070 AT1G80670 AT2G28630 AT3G61190 AT5G20650 AT5G22640 AT3G13060	PHOTOSYSTEM II REACTION CENTER F POTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI	unknown proteir 4_12421515 Chloroplast-locs _8887576 Encodes a high _2 _12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes a protei 3_22652199 Encodes COPT 5_6986071 EMB1211 is a \(\hat{N} \)_5_7528560 evolutionarily ct 3_4184548 glutamate decai 1_24553237	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic
AT2G20890 AT2G30070 AT1G80670 AT2G28630 AT3G61190 AT5G20650 AT5G22640 AT3G13060 AT1G65960 AT4G25840 AT3G57650	PHOTOSYSTEM II REACTION CENTER I POTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (GAD GLYCEROL-3-PHOSPHATASE 1 (GPP1) LYSOPHOSPHATIDYL ACYLTRANSFER/	unknown proteir 4, 12421515 Chloroplast-locs 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes a prot 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily cs 3_4184548 glutamate decai 1_24553237 glycerol-3-phosi 4_13138062 Encodes an enc 3_21349461	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic intron proximal promoter promoter
AT2G20890 AT2G30070 AT1G80670 AT1G28630 AT3G61190 AT5G20650 AT5G22640 AT3G13060 AT1G65960 AT4G25840 AT3G57650 AT5G01340	PHOTOSYSTEM II REACTION CENTER F POTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (GAD GLYCEROL-3-PHOSPHATASE 1 (GPP1) LYSOPHOSPHATIDYL ACYLTRANSFER. MITOCHONDRIAL SUCCINATE-FUMARA	unknown proteir 4_12421515 Chloroplast-loce 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes protei 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily cc 3_4184548 glutamate decai 1_24553237 glycerol-3-phosi 4_13138062 Encodes an enc 3_21349461 Mitochondrial st, 5_141816	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter promoter proximal promoter proximal promoter intergenic intron proximal promoter promoter intergenic
AT2G20890 AT2G30070 AT1G80670 AT1G80670 AT3G26630 AT3G2190 AT5G22640 AT3G13060 AT1G65960 AT4G25840 AT3G57650 AT5G01340 AT1G20370	PHOTOSYSTEM II REACTION CENTER FOTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (GAD GLYCEROL-3-PHOSPHATASE 1 (GPP1) LYSOPHOSPHATIDYL ACYLTRANSFER. MITOCHONDRIAL SUCCINATE-FUMARA na	unknown proteir 4_12421515 Chloroplast-locs 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes CCS1: 2_12277436 Encodes a prots 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily cs 3_4184548 glutamate decai 1_24553237 glycerol-3-phosi 4_13138062 Encodes an ens 3_21349461 Mitochondrial st 5_141816 Pseudouridine s 1_7054356	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic intron proximal promoter promoter intergenic proximal promoter
AT2G20890 AT2G30070 AT1G80670 AT1G80670 AT3G208630 AT3G20650 AT3G22640 AT3G13060 AT1G65960 AT3G57650 AT5G01340 AT1G2370 AT1G55140	PHOTOSYSTEM II REACTION CENTER I POTASSIUM TRANSPORTER 1 (KT1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (ADP1) LYSOPHOSPHATIDYL ACYLTRANSFER/ MITOCHONDRIAL SUCCINATE-FUMARA na	unknown proteir 4, 12421515 Chloroplast-locs 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes a prot 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily co 3_4184548 glutamate decai 1_24553237 glycerol-3-phosi 4_13138062 Encodes an enc 3_21349461 Mitochondrial st 5_141816 Pseudouridine s 1_7054356 Ribonuclease III 1_20574471	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter proximal promoter proximal promoter intergenic intron proximal promoter promoter intergenic proximal promoter promoter
AT2G20890 AT2G30070 AT1G80670 AT3G26830 AT3G61190 AT5G20650 AT5G22640 AT3G13060 AT4G25840 AT3G57650 AT5G01340 AT1G501340 AT1G501340 AT1G55152	PHOTOSYSTEM II REACTION CENTER FOTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (GAD GLYCEROL-3-PHOSPHATASE 1 (GPP1) LYSOPHOSPHATIDYL ACYLTRANSFER/ MITOCHONDRIAL SUCCINATE-FUMARA na na na na	unknown proteir 4_12421515 Chloroplast-loce 2_8887576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes a prote 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily cc 3_4184548 glutamate decai 1_24553237 glycerol-3-phosi 4_13138062 Encodes an enc 3_21349461 Mitochondrial si 5_141816 Pseudouridine s 1_7054356 Ribonuclease III 1_20577596	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic intron proximal promoter promoter intergenic proximal promoter promoter promoter promoter three_prime_UTR
AT2G20890 AT2G30070 AT1G80670 AT1G80670 AT2G28630 AT3G61190 AT5G20650 AT5G22640 AT3G13060 AT4G25840 AT3G57650 AT5G01340 AT1G501340 AT1G55142 AT4G55152 AT4G12980	PHOTOSYSTEM II REACTION CENTER FOTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (GAD GLYCEROL-3-PHOSPHATASE 1 (GPP1) LYSOPHOSPHATIDYL ACYLTRANSFER MITOCHONDRIAL SUCCINATE-FUMARA na na na na	unknown proteir 4_12421515 Chloroplast-locs 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes COS1: 2_12277436 Encodes COPT 5_6886071 EMB1211 is a N 5_7528560 evolutionarily cc 3_4184548 glutamate decai 1_24553237 glycerol-3-phosi 4_13138062 Encodes an enc 3_21349461 Mitochondrial st 5_141816 Pseudouridine s 1_7054356 Ribonuclease Illi 1_20574471 unknown proteir 1_20577596 Auxin-responsiv 4_7589964	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic intron proximal promoter three_prime_UTR intron
AT2G20890 AT2G30070 AT1G80670 AT1G80670 AT2G28630 AT3G61190 AT3G22640 AT3G22640 AT3G57650 AT4G25840 AT3G57650 AT5G01340 AT1G55152 AT1G55140 AT1G55152 AT4G12980 AT1G31300	PHOTOSYSTEM II REACTION CENTER FOTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (GAD GLYCEROL-3-PHOSPHATASE 1 (GPP1) LYSOPHOSPHATIDYL ACYLTRANSFER MITOCHONDRIAL SUCCINATE-FUMARA na na na na na	unknown proteir 4, 12421515 Chloroplast-locs 2_8887576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes RCS1: 2_12277436 Encodes a prot 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily co 3_4184548 glutamate decai 1_24553237 glycerol-3-phosi 4_13138062 Encodes an enc 3_21349461 Mitochondrial st 5_141816 Pseudouridine s 1_7054356 Ribonuclease III 1_20577471 unknown proteir 1_20577596 Auxin-responsiv 4_7589964 TRAM, LAG1 ai 1_11197828	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic innovimal promoter promoter promoter promoter intergenic proximal promoter promoter promoter three_prime_UTR intergenic intergenic intergenic
AT2G20890 AT2G30070 AT1G80670 AT1G80670 AT2G28630 AT3G61190 AT5G20650 AT5G22640 AT3G13060 AT4G25840 AT3G57650 AT5G01340 AT1G501340 AT1G55142 AT4G55152 AT4G12980	PHOTOSYSTEM II REACTION CENTER FOTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (GAD GLYCEROL-3-PHOSPHATASE 1 (GPP1) LYSOPHOSPHATIDYL ACYLTRANSFER MITOCHONDRIAL SUCCINATE-FUMARA na na na na	unknown proteir 4_12421515 Chloroplast-loce 2_8887576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1'. 2_12277436 Encodes a prote 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily cc 3_4184548 glutamate decai 1_24553237 glycerol-3-phosi 4_13138062 Encodes an enc 3_21349461 Mitochondrial st 5_141816 Pseudouridine s 1_7054356 Ribonuclease III 1_2057467 unknown proteir 1_20577596 Auxin-responsiv 4_7589964 TRAM, LAG1 at 1_11197828 hydroxyproline-1 1_11197828	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic intron proximal promoter promoter intergenic proximal promoter promoter promoter three_prime_UTR intron intergenic intergenic intergenic
AT2G20890 AT2G30070 AT1G80670 AT1G80670 AT2G28630 AT3G26190 AT5G20650 AT5G22640 AT3G313060 AT4G25840 AT3G57650 AT1G55140 AT1G55140 AT1G55152 AT4G12980 AT1G31300 AT1G31310	PHOTOSYSTEM II REACTION CENTER FOTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (GAD GLYCEROL-3-PHOSPHATASE 1 (GPP1) LYSOPHOSPHATIDYL ACYLTRANSFER/ MITOCHONDRIAL SUCCINATE-FUMARA na na na na na na na na	unknown proteir 4, 12421515 Chloroplast-locs 2_8887576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes RCS1: 2_12277436 Encodes a prot 3_22652199 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily co 3_4184548 glutamate decai 1_24553237 glycerol-3-phosi 4_13138062 Encodes an enc 3_21349461 Mitochondrial st 5_141816 Pseudouridine s 1_7054356 Ribonuclease III 1_20577471 unknown proteir 1_20577596 Auxin-responsiv 4_7589964 TRAM, LAG1 ai 1_11197828	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic innovimal promoter promoter promoter promoter intergenic proximal promoter promoter promoter three_prime_UTR intergenic intergenic intergenic
AT2G20890 AT2G30070 AT1G80670 AT1G80670 AT2G28630 AT3G61190 AT5G20650 AT5G22640 AT3G313060 AT4G25840 AT3G57650 AT4G25840 AT1G55140 AT1G55140 AT1G5140 AT1G31300 AT1G31300 AT1G31310 AT2G35750	PHOTOSYSTEM II REACTION CENTER FOTASSIUM TRANSPORTER 1 (KT1) RNA EXPORT FACTOR 1 (RAE1) 3-KETOACYL-COA SYNTHASE 12 (KCS1 BON ASSOCIATION PROTEIN 1 (BAP1) COPPER TRANSPORTER 5 (COPPT5) EMBRYO DEFECTIVE 1211 (emb1211) EVOLUTIONARILY CONSERVED C-TERI GLUTAMATE DECARBOXYLASE 2 (GAD GLYCEROL-3-PHOSPHATASE 1 (GPP1) LYSOPHOSPHATIDYL ACYLTRANSFER MITOCHONDRIAL SUCCINATE-FUMARA na	unknown proteir 4_12421515 Chloroplast-locs 2_8987576 Encodes a high 2_12834990 This gene is pre 1_30323872 Encodes KCS1: 2_12277436 Encodes COS1: 2_12277436 Encodes COPT 5_6986071 EMB1211 is a N 5_7528560 evolutionarily cs 3_4184548 glutamate decai 1_24553237 glycerol-3-phos; 4_13138062 Encodes an enc 3_21349461 Mitochondrial st 5_141816 Pseudouridine s 1_7054356 Ribonuclease IIII 1_20574471 unknown proteir 1_20577596 Auxin-responsiv 4_7589964 TRAM, LAG1 at 1_11197828 unknown proteir 1_11197828 unknown proteir 1_11197828	3.87 3.87 3.86 3.86 3.86 3.86 3.86 3.86 3.86 3.86	promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter intergenic intron proximal promoter pro

AT3G13062	na	Polyketide cycla 3_4184548	3.86	promoter
AT2G26720	na	Cupredoxin sup 2 11386090	3.86	intergenic
AT3G15480	na	Protein of unknc 3_5227988	3.86	promoter
AT3G19235	na	pre-tRNA; tRNA 3_6664212	3.86	intergenic
AT3G19240	na	Vacuolar import 3_6664212	3.86	promoter
AT3G19250 AT3G28480	na na	Protein of unknr 3_6664212 Oxoglutarate/irc 3_10678368	3.86 3.86	intergenic five_prime_UTR
AT3G28695	na	pre-tRNA; tRNA 3_10759363	3.86	downstream
AT3G28700	na	Protein of unknc 3_10759363	3.86	promoter
AT3G48440	na	Zinc finger C-x8 3_17941195	3.86	promoter
AT5G01335	na	transposable el 5_141816	3.86	intergenic
AT5G20660	na	Zn-dependent e 5_6986071	3.86	promoter
AT5G40180 AT5G51300	na na	BEST Arabidop: 5_16067843 splicing factor-rc 5_20853057	3.86 3.86	promoter
AT5G51300	na	Mutants exhibit 5_20853057	3.86	proximal promoter exon
AT3G19050	PHRAGMOPLAST ORIENTING KINESIN :		3.86	promoter
AT3G46830	RAB GTPASE HOMOLOG A2C (RABA2c)	RAB GTPase h: 3_17248815	3.86	promoter
AT5G40170	RECEPTOR LIKE PROTEIN 54 (RLP54)		3.86	promoter
AT3G48430	RELATIVE OF EARLY FLOWERING 6 (RI		3.86	intergenic
AT1G55150 AT1G55150	RNA HELICASE 20 (RH20) RNA HELICASE 20 (RH20)	DEA(D/H)-box F 1_20574471 DEA(D/H)-box F 1_20577596	3.86 3.86	promoter intergenic
AT2G37080		Encodes RIP3 (2_15586221	3.86	proximal promoter
AT5G21170	(AKINBETA1)	Encodes AKINb 5_7208584	3.85	downstream
AT1G20440	COLD-REGULATED 47 (COR47)	Belongs to the c 1_7085704	3.85	five_prime_UTR
AT1G63710	CYTOCHROME P450, FAMILY 86, SUBF		3.85	exon
AT1G10130	ENDOPLASMIC RETICULUM-TYPE CALC		3.85	proximal promoter
AT2G47520 AT1G13020	ETHYLENE RESPONSE FACTOR 71 (ER EUKARYOTIC INITIATION FACTOR 4B2 (3.85 3.85	intergenic promoter
AT1G72500	na	LOCATED IN: p 1_27298695	3.85	promoter
AT3G16851	na	unknown proteir 3_5753953	3.85	intergenic
AT1G20410	na	Pseudouridine s 1_7085704	3.85	intergenic
AT1G20420	na	pre-tRNA; tRNA 1_7085704	3.85	intergenic
AT1G20430 AT2G18030	na na	unknown proteir 1_7085704 Peptide methior 2_7840053	3.85 3.85	proximal promoter promoter
AT4G12005	na	unknown proteir 4 7196413	3.85	promoter
AT5G21222	na	protein kinase ft 5_7208584	3.85	promoter
AT2G19170	SUBTILISIN-LIKE SERINE PROTEASE 3		3.85	promoter
AT2G24570	WRKY DNA-BINDING PROTEIN 17 (WRK		3.85	proximal promoter
AT1G48260	CBL-INTERACTING PROTEIN KINASE 1		3.84	intron
AT2G28190 AT1G51700	COPPER/ZINC SUPEROXIDE DISMUTAS DOF ZINC FINGER PROTEIN 1 (DOF1)	Encodes a chioi 2_12017730 Encodes dof zin 1_19171170	3.84 3.84	intergenic proximal promoter
AT5G09410	ETHYLENE INDUCED CALMODULIN BIN		3.84	intron
AT1G52520	FAR1-RELATED SEQUENCE 6 (FRS6)	FAR1-related se 1_19565666	3.84	promoter
AT5G48030	GAMETOPHYTIC FACTOR 2 (GFA2)	encodes a mitor 5_19469975	3.84	promoter
AT2G17540	na	unknown proteir 2_7630127	3.84	intergenic
AT3G13190	na	Plant protein of 3_4240423	3.84	five_prime_UTR
AT3G49070 AT5G63380	na na	Protein of unknr 3_18193383 Encodes a pero 5_25390274	3.84 3.84	exon promoter
AT5G07340	na	Calreticulin fami 5_2317067	3.84	promoter
AT2G06025	na	Acyl-CoA N-acy 2_2350124	3.84	intron
AT2G46290	na	Transducin/WD 2_19005615	3.84	downstream
AT3G25720	na	RNA-directed D 3_9381769	3.84	intergenic
AT4G17810	na	C2H2 and C2H(4_9905821	3.84	proximal promoter
AT5G09513 AT1G77740	na PHOSPHATIDYLINOSITOL-4-PHOSPHAT	pseudogene of 5_2958327 Encodes PIP5K 1_29223355	3.84 3.84	promoter intron
AT5G09520	PRO-GLU-LEU ILE VAL-PRO-LYS 2 (PEL		3.84	three_prime_UTR
AT1G51690	PROTEIN PHOSPHATASE 2A 55 KDA RE		3.84	intergenic
AT5G25610	RESPONSIVE TO DESSICATION 22 (RD2		3.84	promoter
AT2G46280	TGF-BETA RECEPTOR INTERACTING P		3.84	promoter
AT1G12240 AT4G29160	(ATBETAFRUCT4) (SNF7.1)	Encodes a vac. 1_4157486 SNF7.1; CONT. 4_14380673	3.83 3.83	three_prime_UTR promoter
AT5G47580	ALTERED SEED GERMINATION 7 (ASG7		3.83	promoter
AT1G61810	BETA-GLUCOSIDASE 45 (BGLU45)	beta-glucosidas 1_22829771	3.83	promoter
AT4G29150	IQ-DOMAIN 25 (IQD25)	IQ-domain 25 (l 4_14380673	3.83	downstream
AT2G16240	na	pre-tRNA; tRNA 2_7039267	3.83	downstream
AT3G49550 AT1G12244	na na	unknown proteir 3_18367674 Polynucleotidyl 1 4157486	3.83 3.83	promoter promoter
AT1G20380	na	Prolyl oligopepti 1 7062033	3.83	intron
AT2G30050	na	transducin famil 2_12824315	3.83	promoter
AT1G66870	na	Carbohydrate-b 1_24947967	3.83	proximal promoter
AT1G66880	na	Protein kinase s 1_24947967	3.83	intron
AT3G22133 AT3G13700	na	transposable el 3_7798020 RNA-binding (R 3 4492828	3.83 3.83	proximal promoter
AT3G13700 AT3G49400	na na	Transducin/WD 3_18324556	3.83	three_prime_UTR intron
AT4G18060	na	SH3 domain-col 4_10030011	3.83	promoter
AT4G18070	na	unknown proteir 4_10030011	3.83	proximal promoter
AT5G47590	na	Heat shock prot 5_19297451	3.83	intergenic
AT3G07560	PEROXIN 13 (PEX13)	Encodes peroxi 3_2413452	3.83	five_prime_UTR
AT3G13710 AT1G13440	PRENYLATED RAB ACCEPTOR 1.F4 (PF GLYCERALDEHYDE-3-PHOSPHATE DEF		3.83 3.82	five_prime_UTR promoter
AT5G54070	HEAT SHOCK TRANSCRIPTION FACTOR		3.82	downstream
AT5G54080	HOMOGENTISATE 1,2-DIOXYGENASE (I		3.82	promoter
AT2G46685	MICRORNA166A (MIR166A)	Encodes a micr 2_19171609	3.82	intergenic
AT2G37750	na	unknown proteir 2_15831221	3.82	exon
AT4G40011	na	unknown proteir 4_18551275	3.82	exon
AT1G72250 AT4G01040	na na	Di-glucose bind 1_27192653 Glycosyl hydrol(4 455664	3.82 3.82	promoter downstream
AT1G22720	na	Protein kinase s 1_8039829	3.82	intergenic
AT1G32650	na	unknown proteir 1_11807043	3.82	intergenic
AT3G06470	na	GNS1/SUR4 me 3_1984912	3.82	exon
AT3G23170	na	unknown proteir 3_8268814	3.82	promoter
AT3G28923 AT3G20300	na na	Pseudogene of 3_10949516 Protein of unknc 3_7082680	3.82 3.82	intergenic proximal promoter
AT3G20300 AT3G55240	na na	Overexpression 3_20476687	3.82	proximal promoter
			-	,

ATEC00000		Main facilitates 5 05474000	2.00	
AT5G62680 AT5G56630	na PHOSPHOFRUCTOKINASE 7 (PFK7)	Major facilitator 5_25171622 phosphofructoki 5_22923098	3.82 3.82	intergenic
AT2G05070	PHOTOSYSTEM II LIGHT HARVESTING		3.82	proximal promoter promoter
AT1G09530	PHYTOCHROME INTERACTING FACTOR		3.82	five_prime_UTR
AT4G01050	THYLAKOID RHODANESE-LIKE (TROL)	-	3.82	promoter
AT5G54075	U3 SMALL NUCLEOLAR RNAD (U3D)	U3 small nuclec 5_21945806	3.82	promoter
AT2G46400	WRKY DNA-BINDING PROTEIN 46 (WRK		3.82	proximal promoter
AT1G66140	ZINC FINGER PROTEIN 4 (ZFP4)	Encodes a zinc 1 24621095	3.82	intron
AT1G08680	ARF GAP-LIKE ZINC FINGER-CONTAINII	A member of AF 1 2762609	3.81	five_prime_UTR
AT4G23990	CELLULOSE SYNTHASE LIKE G3 (CSLG		3.81	promoter
AT5G40890	CHLORIDE CHANNEL A (CLC-A)	Encodes a merr 5_16385301	3.81	five_prime_UTR
AT1G14900	HIGH MOBILITY GROUP A (HMGA)	Encodes a prote 1_5139521	3.81	promoter
AT3G57150	HOMOLOGUE OF NAP57 (NAP57)	Encodes a puta 3_21153865	3.81	downstream
AT1G19870	IQ-DOMAIN 32 (iqd32)	IQ-domain 32 (i: 1_6894791	3.81	downstream
AT1G68480	JAGGED (JAG)	Encodes a puta 1_25688501	3.81	proximal promoter
AT2G32510	MITOGEN-ACTIVATED PROTEIN KINASE	member of MEk 2_13798985	3.81	exon
AT1G19860	na	Zinc finger C-x8 1_6894791	3.81	promoter
AT1G21780	na	BTB/POZ doma 1_7654115	3.81	downstream
AT1G21790	na	TRAM, LAG1 ar 1_7654115	3.81	promoter
AT1G62310	na	transcription fac 1_23039916	3.81	promoter
AT3G55780	na	Glycosyl hydrol: 3_20705413	3.81	promoter
AT5G16140	na	Peptidyl-tRNA h 5_5272046	3.81	promoter
AT4G02940	na	oxidoreductase, 4_1308566	3.81	intron
AT5G47020	na	unknown proteir 5_19090272	3.81	intergenic
AT5G47030	na	Encodes the mil 5_19090272	3.81	promoter
AT1G09150	na	pseudouridine s 1_2946095	3.81	promoter
AT1G26620	na	Plant protein of 1_9202352	3.81	proximal promoter
AT1G29715	na	pseudogene, pt 1_10393014	3.81	promoter
AT1G62600	na	Flavin-binding n 1_23179378	3.81	promoter
AT2G25890	na	Oleosin family p 2_11037100	3.81	promoter
AT1G14910	na	ENTH/ANTH/VI 1_5139521	3.81	downstream
AT3G03270	na	Adenine nucleol 3_761630	3.81	intron
AT3G62735	na	pre-tRNA; tRNA 3_23210699	3.81	promoter
AT5G65480	na	unknown proteir 5_26175912	3.81	promoter
AT5G61770	PETER PAN-LIKE PROTEIN (PPAN)	PETER PAN-lik 5_24818375	3.81	intergenic
AT3G44735	PHYTOSULFOKINE 3 PRECURSOR (PSI	Phytosulfokine (3_16292596	3.81	promoter
AT3G57140	SUGAR-DEPENDENT 1-LIKE (SDP1-LIKE	sugar-depender 3_21153865	3.81	promoter
AT4G36710	(HAM4)	GRAS family tra 4_17307446	3.8	exon
AT1G33560	ACTIVATED DISEASE RESISTANCE 1 (A	Encodes a NB\$ 1_12168143	3.8	proximal promoter
AT1G46264	HEAT SHOCK TRANSCRIPTION FACTOR	Encodes SCHIZ 1_17226486	3.8	downstream
AT4G36720	HVA22-LIKE PROTEIN K (HVA22K)	HVA22-like prot 4_17307446	3.8	promoter
AT1G21880	LYSM DOMAIN GPI-ANCHORED PROTE		3.8	promoter
AT2G45412	na	unknown proteir 2_18714579	3.8	exon
AT2G32020	na	Acyl-CoA N-acy 2_13632004	3.8	promoter
AT1G10865	na	FUNCTIONS IN 1_3616207	3.8	promoter
AT1G30200	na	F-box family prc 1 10625091	3.8	five_prime_UTR
AT1G63855	na	Putative methyll 1_23701068	3.8	promoter
AT1G80170	na	Pectin lyase-lik€ 1_30156552	3.8	proximal promoter
AT2G26695	na	Ran BP2/NZF z 2_11363486	3.8	proximal promoter
AT2G35637	na	Potential natura 2_14984398	3.8	promoter
AT2G35640	na	Homeodomain-l 2_14984398	3.8	downstream
AT1G56020	na	unknown proteir 1_20952004	3.8	promoter
AT1G63860	na	Disease resista 1_23701068	3.8	intergenic
AT3G13480	na	unknown proteir 3_4394110	3.8	promoter
AT2G31080	na	transposable ele 2_13222225	3.8	intergenic
AT3G21890	na	B-box type zinc 3_7711980	3.8	proximal promoter
AT3G43580	na	Beta-galactosid 3_15502719	3.8	five_prime_UTR
AT4G08151	na	This gene enco 4_5155676	3.8	intergenic
AT4G21970	na	Protein of unknc 4_11652695	3.8	proximal promoter
AT5G11680	na	FUNCTIONS IN 5_3761052	3.8	downstream
AT4G28600	NO POLLEN GERMINATION RELATED 2	encodes a calm 4_14129237	3.8	promoter
AT3G57520	SEED IMBIBITION 2 (SIP2)	SIP2 encodes a 3_21293190	3.8	promoter
AT5G66920	SKU5 SIMILAR 17 (sks17)	SKU5 similar 1: 5_26722417	3.8	promoter
AT5G04040	SUGAR-DEPENDENT1 (SDP1)	Encodes a triac 5_1089674	3.8	five_prime_UTR
AT2G31070	TCP DOMAIN PROTEIN 10 (tcp10)	TCP family prot 2_13222225	3.8	five_prime_UTR
AT5G11690	TRANSLOCASE INNER MEMBRANE SUI	mitochondrial in 5_3761052	3.8	promoter
AT3G26420	(ATRZ-1A)	Zinc finger-cont 3_9671460	3.79	promoter
AT5G16590	(LRR1)	Leucine-rich rer 5_5431677	3.79	promoter
AT5G61000	(RPA70D)	RPA70D; FUNC 5_24552908	3.79	promoter
AT1G75010	ACCUMULATION AND REPLICATION OF		3.79	intergenic
AT5G65390	ARABINOGALACTAN PROTEIN 7 (AGP7)		3.79	proximal promoter
AT5G56870	BETA-GALACTOSIDASE 4 (BGAL4)	beta-galactosid: 5_23001305	3.79	proximal promoter
AT5G62180	CARBOXYESTERASE 20 (CXE20)	carboxyesterasi 5_24978585	3.79	intergenic
AT5G10930	CBL-INTERACTING PROTEIN KINASE 5		3.79	intergenic
AT4G22910	FIZZY-RELATED 2 (FZR2)	FIZZY-related 2 4_12012528	3.79	promoter
AT1G48620	HIGH MOBILITY GROUP A5 (HON5)	This gene is pre 1_17976460	3.79	promoter
AT1G35515	HIGH RESPONSE TO OSMOTIC STRESS		3.79	three_prime_UTR
AT4G22970	HOMOLOG OF SEPARASE (ESP)	Encodes a sepa 4_12043873	3.79	promoter
AT1G76135	MICRORNA394B (MIR394B)	Encodes a micr 1_28567152	3.79	proximal promoter
AT1G35516	na	myb-like transcr 1_13079534	3.79	three_prime_UTR
AT5G18310	na	unknown proteir 5_6061876	3.79	intron
AT1G63140	na	O-methyltransfe 1_23416257	3.79	proximal promoter
AT1G75000	na	GNS1/SUR4 mt 1_28164464	3.79	exon
AT1G13940	na	Plant protein of 1_4768978	3.79	proximal promoter
AT2G44198	20	unknown proteir 2_18276146	3.79	exon
AT2G31140	na		3.79	promoter
AT2G44200	na	Peptidase S24/: 2_13269787		
	na na	CBF1-interactin 2_18276146	3.79	promoter
AT3G26430	na na na	CBF1-interactin 2_18276146 GDSL-like Lipas 3_9671460	3.79 3.79	promoter promoter
AT3G57370	na na na na	CBF1-interactin 2_18276146 GDSL-like Lipas 3_9671460 Cyclin family prc 3_21228679	3.79 3.79 3.79	promoter promoter promoter
AT3G57370 AT3G57380	na na na na na	CBF1-interactin 2_18276146 GDSL-like Lipas 3_9671460 Cyclin family prc 3_21228679 Glycosyltransfei 3_21228679	3.79 3.79 3.79 3.79	promoter promoter promoter proximal promoter
AT3G57370 AT3G57380 AT4G22980	na na na na na na	CBF1-interactin 2_18276146 GDSL-like Lipas 3_9671460 Cyclin family prr 3_21228679 Glycosyltransfei 3_21228679 FUNCTIONS IN 4_12043873	3.79 3.79 3.79 3.79 3.79	promoter promoter promoter proximal promoter downstream
AT3G57370 AT3G57380 AT4G22980 AT5G57120	na na na na na na na	CBF1-interactin 2_18276146 GDSL-like Lipas 3_9671460 Cyclin family pro 3_21228679 Glycosyltransfei 3_21228679 FUNCTIONS IN 4_12043873 FUNCTIONS IN 5_23124605	3.79 3.79 3.79 3.79 3.79 3.79	promoter promoter promoter proximal promoter downstream promoter
AT3G57370 AT3G57380 AT4G22980 AT5G57120 AT3G26410	na na na na na na TRNA MODIFICATION 11 (TRM11)	CBF1-interactin 2_18276146 GDSL-like Lipas 3_9671460 Cyclin family pr 3_21228679 Glycosyltransfei 3_21228679 FUNCTIONS IN 4_12043873 FUNCTIONS IN 5_23124605 Encodes a prott 3_9671460	3.79 3.79 3.79 3.79 3.79 3.79 3.79	promoter promoter promoter proximal promoter downstream promoter promoter
AT3G57370 AT3G57380 AT4G22980 AT5G57120	na na na na na na na	CBF1-interactin 2_18276146 GDSL-like Lipas 3_9671460 Cyclin family pro 3_21228679 Glycosyltransfei 3_21228679 FUNCTIONS IN 4_12043873 FUNCTIONS IN 5_23124605	3.79 3.79 3.79 3.79 3.79 3.79	promoter promoter promoter proximal promoter downstream promoter

AT3G55130	ATP-BINDING CASSETTE G19 (ABCG19)	Encodes a vac. 3_20437425	3.78	proximal promoter
AT1G78882	CONSERVED PEPTIDE UPSTREAM OPE		3.78	promoter
AT3G26330	CYTOCHROME P450, FAMILY 71, SUBFA	putative cytochr 3_9649914	3.78	proximal promoter
AT5G44210	ERF DOMAIN PROTEIN 9 (ERF9)	encodes a mem 5_17807645	3.78	downstream
AT3G53760	GAMMA-TUBULIN COMPLEX PROTEIN 4		3.78	promoter
AT5G56030	HEAT SHOCK PROTEIN 81-2 (HSP81-2)		3.78	promoter
AT5G39760	HOMEOBOX PROTEIN 23 (HB23)	homeobox prote 5_15911148	3.78	promoter
AT1G66760	na	MATE efflux fan 1_24904610	3.78	downstream
AT5G18920 AT2G25520	na na	Cox19-like CHC 5_6309931 Drug/metabolite 2_10860185	3.78 3.78	promoter
AT1G13640	na	Phosphatidylino 1_4680248	3.78	proximal promoter promoter
AT1G72950	na	Disease resista 1_27444269	3.78	promoter
AT1G78880	na	Ubiquitin-specifi 1_29656217	3.78	promoter
AT1G78890	na	unknown proteir 1_29656217	3.78	promoter
AT2G37050	na	Leucine-rich reg 2_15568873	3.78	promoter
AT3G48140	na	B12D protein; C 3_17778294	3.78	promoter
AT3G49800	na	BSD domain-co 3_18473839	3.78	promoter
AT4G39930	na	unknown proteir 4_18518874	3.78	exon
AT5G36925	na	unknown proteir 5_14566454	3.78	promoter
AT3G02730	THIOREDOXIN F-TYPE 1 (TRXF1)	thioredoxin F-ty 3_589841	3.78	promoter
AT2G17790	VPS35 HOMOLOG A (VPS35A)	Encodes a prote 2_7733603	3.78	promoter
AT3G18035	(HON4)	A linker histone 3_6171843	3.77	promoter
AT4G14720 AT4G14716	(PPD2) ACIREDUCTONE DIOXYGENASE 1 (ARE	PPD2 (and its p 4_8431938	3.77 3.77	downstream five_prime_UTR
AT2G02000	GLUTAMATE DECARBOXYLASE 3 (GAD		3.77	intergenic
AT2G25295	LOW-MOLECULAR-WEIGHT CYSTEINE-		3.77	intergenic
AT1G11550	na	pre-tRNA; tRNA 1_3881491	3.77	promoter
AT1G31355	na	60S ribosomal r 1_11226382	3.77	proximal promoter
AT1G49580	na	Calcium-depend 1_18351380	3.77	promoter
AT1G80360	na	Pyridoxal phosp 1_30211768	3.77	proximal promoter
AT2G01990	na	unknown proteir 2_469071	3.77	proximal promoter
AT3G11600	na	unknown proteir 3_3666320	3.77	proximal promoter
AT3G56820	na	unknown proteir 3_21041838	3.77	promoter
AT5G24570	na	unknown proteir 5_8406112	3.77	five_prime_UTR
AT5G18140	na	Chaperone Dna 5_5998161	3.77	promoter
AT3G57670	NO TRANSMITTING TRACT (NTT)	Encodes a a C2 3_21367014	3.77	intergenic
AT3G53232 AT1G68540	ROTUNDIFOLIA LIKE 1 (RTFL1)	ROTUNDIFOLI/ 3_19728130	3.77 3.77	intergenic
AT1G66540 AT3G56825	TETRAKETIDE ALPHA-PYRONE REDUC U2 SMALL NUCLEOLAR RNA4 (U2.4)	U2.4; snRNA; q 3 21041838	3.77	proximal promoter exon
AT1G11545	XYLOGLUCAN ENDOTRANSGLUCOSYL		3.77	proximal promoter
AT3G11900	AROMATIC AND NEUTRAL TRANSPORT		3.76	promoter
AT5G03540	EXOCYST SUBUNIT EXO70 FAMILY PRO	-	3.76	proximal promoter
AT5G56860	GATA, NITRATE-INDUCIBLE, CARBON N		3.76	proximal promoter
AT2G25950	na	CONTAINS Inte 2_11070810	3.76	downstream
AT2G25964	na	unknown proteir 2_11070810	3.76	three_prime_UTR
AT1G09750	na	Eukaryotic aspa 1_3158802	3.76	exon
AT3G04860	na	Plant protein of 3_1341089	3.76	promoter
AT2G43530	na	Encodes a defe 2_18070990	3.76	intergenic
AT2G43535	na	Encodes a defe 2_18070990	3.76	five_prime_UTR
AT5G21280	na	hydroxyproline-ı 5_7265803	3.76	promoter
AT2G20410	na	RNA-binding A\$ 2_8802299	3.76	promoter
AT2G34050 AT2G34060	na na	INVOLVED IN: 2_14384276	3.76 3.76	five_prime_UTR
AT3G59850	na	Peroxidase sup 2_14384276 Pectin lyase-like 3 22112579	3.76	proximal promoter proximal promoter
AT5G39830	na	unknown proteir 5_3514275	3.76	intergenic
AT5G04170	na	Calcium-binding 5 1145489	3.76	five_prime_UTR
AT4G28610	PHOSPHATE STARVATION RESPONSE		3.76	promoter
AT1G57990	PURINE PERMEASE 18 (PUP18)	Member of a far 1_21444546	3.76	proximal promoter
AT5G03530	RAB GTPASE HOMOLOG C2A (RABC2A	Encodes a merr 5_889054	3.76	proximal promoter
AT4G04220	RECEPTOR LIKE PROTEIN 46 (RLP46)	receptor like prc 4_2033250	3.76	promoter
AT4G17230	SCARECROW-LIKE 13 (SCL13)	Encodes a scar 4_9665042	3.76	proximal promoter
AT4G01470	TONOPLAST INTRINSIC PROTEIN 1;3 (T		3.76	intergenic
AT2G43520	TRYPSIN INHIBITOR PROTEIN 2 (TI2)	Encodes putativ 2_18070990	3.76	intergenic
AT1G09760	U2 SMALL NUCLEAR RIBONUCLEOPRO		3.76	intergenic
AT5G03455 AT5G61790	(CDC25) CALNEXIN 1 (CNX1)	Encodes a hom 5_864186 calnexin 1 (CN) 5_24829910	3.75 3.75	downstream promoter
AT1G70782	CONSERVED PEPTIDE UPSTREAM OPE			proximal promoter
AT2G29090	CYTOCHROME P450, FAMILY 707, SUBF			intron
AT2G29080	FTSH PROTEASE 3 (ftsh3)	encodes an Ftsl 2_12495956	3.75	proximal promoter
AT1G78220	GENERAL REGULATORY FACTOR 13 (C		3.75	proximal promoter
AT3G20670	HISTONE H2A 13 (HTA13)	Encodes HTA1: 3_7229346	3.75	promoter
AT1G15060	na	Uncharacterise(1_5186929	3.75	five_prime_UTR
AT3G27420	na	unknown proteir 3_10148491	3.75	promoter
AT3G51000			3.75	promoter
	na	alpha/beta-Hydr 3_18946702		in
AT3G51010	na	unknown proteir 3_18946702	3.75	three_prime_UTR
AT3G51010 AT2G38980	na na	unknown proteir 3_18946702 pseudogene, sir 2_16278619	3.75 3.75	intron
AT3G51010 AT2G38980 AT5G43960	na na na	unknown proteir 3_18946702 pseudogene, sii 2_16278619 Nuclear transpc 5_17691978	3.75 3.75 3.75	intron promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120	na na na na	unknown proteir 3_18946702 pseudogene, sir 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042	3.75 3.75 3.75 3.75	intron promoter promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120 AT2G24290	na na na	unknown proteir 3_18946702 pseudogene, sir 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042 Protein of unknc 2_10338548	3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120	na na na na na	unknown proteir 3_18946702 pseudogene, sir 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042	3.75 3.75 3.75 3.75	intron promoter promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120 AT2G24290 AT5G03460	na na na na na na	unknown proteir 3_18946702 pseudogene, sir 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042 Protein of unknc 2_10338548 unknown proteir 5_864186 Thioredoxin sup 5_3847016	3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120 AT2G24290 AT5G03460 AT5G11930	na n	unknown proteir 3, 18946702 pseudogene, sii 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042 Protein of unknc 2_10338548 unknown proteir 5_864186 Thioredoxin sup 5_3847016 This gene is pre 1_9963602 Encodes a low ₹ 1_26314349	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter promoter promoter proximal promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120 AT2G24290 AT5G03460 AT5G11930 AT1G28380 AT1G69870 AT2G45790	na NECROTIC SPOTTED LESIONS 1 (NSL1 NITRATE TRANSPORTER 1.7 (NRT1.7) PHOSPHOMANNOMUTASE (PMM)	unknown proteir 3, 18946702 pseudogene, sir 2,16278619 Nuclear transpo 5,17691978 Major facilitator 1,27132042 Protein of unkno 2,10338548 Unknown proteir 5,864186 Thioredoxin sup 5,3847016 This gene is pre 1,9963602 Encodes a low 1,26314349 encodes a phos 2,18855588	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter proximal promoter five_prime_UTR proximal promoter promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120 AT2G24290 AT5G03460 AT5G11930 AT1G28380 AT1G69870 AT2G45790 AT2G05620	na NECROTIC SPOTTED LESIONS 1 (NSL1 NITRATE TRANSPORTER 1.7 (NRT1.7) PHOSPHOMANNOMUTASE (PMM) PROTON GRADIENT REGULATION 5 (PC	unknown proteir 3_18946702 pseudogene, sir 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042 Protein of unknc 2_10338548 unknown proteir 5_864186 Thioredoxin sup 5_3347016 This gene is pre 1_9963602 Encodes a low 1_26314349 encodes a phos 2_18855588 Involved in elec 2_2081994	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter prominal promoter five_prime_UTR proximal promoter promoter promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120 AT2G24290 AT5G03460 AT5G11930 AT1G28380 AT1G69870 AT2G45790 AT2G05620 AT2G40830	na NECROTIC SPOTTED LESIONS 1 (NSL1 NITRATE TRANSPORTER 1.7 (NRT1.7) PHOSPHOMANNOMUTASE (PMM) PROTON GRADIENT REGULATION 5 (PC RING-H2 FINGER C1A (RHC1A)	unknown proteir 3, 18946702 pseudogene, sii 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042 Protein of unknc 2_10338548 unknown proteir 5_864186 Thioredoxin sup 5_3847016 This gene is pre 1_9963602 Encodes a low 1_26314349 encodes a phos 2_18855588 Involved in elec 2_2081994 Encodes a puta 2_17042543	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter proximal promoter five_prime_UTR proximal promoter promoter promoter promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120 AT2G24290 AT5G03460 AT5G11930 AT1G69870 AT2G45790 AT2G05620 AT2G46830 AT1G66580	na ne NECROTIC SPOTTED LESIONS 1 (NSL1 NITRATE TRANSPORTER 1.7 (NRT1.7) PHOSPHOMANNOMUTASE (PMM) PROTON GRADIENT REGULATION 5 (PI RING-H2 FINGER C1A (RHC1A) SENESCENCE ASSOCIATED GENE 24 (unknown proteir 3, 1846/702 pseudogene, sir 2_162/78619 Nuclear transpo 5, 17691978 Major facilitator 1_27132042 Protein of unkno 2, 10338548 Unknown proteir 5, 864186 Thioredoxin sup 5_3847016 This gene is pre 1_9963602 Encodes a low 1_26314349 encodes a phos 2_18855588 Involved in elec 2_2081994 Encodes a put 2_17042543 senescence ass 1_24839085	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter promoter proximal promoter five_prime_UTR proximal promoter promoter promoter promoter promoter promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120 AT2G24290 AT5G03460 AT5G11930 AT1G68870 AT2G45790 AT2G45620 AT2G40830 AT1G65880 AT1G65880 AT2G23010	na NECROTIC SPOTTED LESIONS 1 (NSL1 NITRATE TRANSPORTER 1.7 (NRT1.7) PHOSPHOMANNOMUTASE (PMM) PROTON GRADIENT REGULATION 5 (PC RING-H2 FINGER C1A (RHC1A) SENESCENCE ASSOCIATED GENE 24 (C SERINE CARBOXYPEPTIDASE-LIKE 9 (S	unknown proteir 3_18946702 pseudogene, sir 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042 Protein of unknc 2_10338548 unknown proteir 5_864186 Thioredoxin sup 5_3847016 This gene is pre 1_9963602 Encodes a low a_126314349 encodes a phos 2_18855588 Involved in elec 2_2081994 Encodes a puta 2_17042543 senescence ass 1_24839085 serine carboxyp 2_9798178	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter proximal promoter five_prime_UTR proximal promoter promoter promoter promoter promoter promoter promoter promoter promoter
AT3G51010 AT2G38980 AT1G43960 AT1G72120 AT2G24290 AT5G03460 AT5G11930 AT1G28380 AT1G28380 AT2G45790 AT2G05620 AT2G46830 AT1G66580 AT1G66580 AT2G23010 AT5G43970	na NECROTIC SPOTTED LESIONS 1 (NSL1 NITRATE TRANSPORTER 1.7 (NRT1.7) PHOSPHOMANNOMUTASE (PMM) PROTON GRADIENT REGULATION 5 (PR RING-H2 FINGER C1A (RHC1A) SENESCENCE ASSOCIATED GENE 24 (SERINE CARBOXYPEPTIDASE-LIKE 9 (STRANSLOCASE OF OUTER MEMBRANE	unknown proteir 3, 18946702 pseudogene, sii 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042 Protein of unknc 2_10338548 Unknown proteir 5_864186 Thioredoxin sup 5_3847016 This gene is pre 1_9963602 Encodes a low 1_26314349 encodes a phos 2_18855588 Involved in elec 2_2081994 Encodes a puta 2_17042543 senescence ass 1_24839085 serine carboxyp 2_9798178 Subunit of the T 5_17691978	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter proximal promoter five_prime_UTR proximal promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter
AT3G51010 AT2G38980 AT5G43960 AT1G72120 AT2G24290 AT5G03460 AT5G11930 AT1G28380 AT1G28380 AT2G45790 AT2G05620 AT2G05680 AT2G23010 AT1G6580 AT2G23010 AT1G61275	na n	unknown proteir 3, 18446702 pseudogene, sir 2,16278619 Nuclear transpo 5,17691978 Major facilitator 1,27132042 Protein of unkn 2,10338548 Unknown proteir 5,864186 Thioredoxin sup 5,3847016 This gene is pre 1,9963602 Encodes a low 1,26314349 encodes a phos 2,18855588 Involved in elec 2,2081994 Encodes a put 2,17042543 senescence ass 1,24839085 serine carboxyp 2,9798178 Subunit of the T 5,17691978 U12; snRNA; gir 1,22603191	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter promoter proximal promoter five_prime_UTR proximal promoter promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter exon
AT3G51010 AT2G38980 AT1G72120 AT2G24290 AT5G41930 AT1G1930 AT1G28380 AT1G69870 AT2G45790 AT2G4580 AT2G40830 AT1G6580 AT2G23010 AT5G43970 AT1G643970 AT1G78440	na NECROTIC SPOTTED LESIONS 1 (NSL1 NITRATE TRANSPORTER 1.7 (NRT1.7) PHOSPHOMANNOMUTASE (PMM) PROTON GRADIENT REGULATION 5 (PC RING-H2 FINGER C1A (RHC1A) SENESCENCE ASSOCIATED GENE 24 (C SERINE CARBOXYPEPTIDASE-LIKE 9 (S TRANSLOCASE OF OUTER MEMBRANE U12 SMALL NUCLEOLAR RNA (U12) ARABIDOPSIS THALIANA GIBBERELLIN	unknown proteir 3_18946702 pseudogene, sir 2_16278619 Nuclear transpc 5_17691978 Major facilitator 1_27132042 Protein of unkno 2_10338548 unknown proteir 5_864186 Thioredoxin sup 5_3847016 This gene is pre 1_9963602 Encodes a low 1_26314349 encodes a phos 2_18855588 Involved in elec 2_2081994 Encodes aputa 2_17042543 senescence ass 1_24839085 serine carboxyp 2_9798178 Subunit of the T 5_17691978 U12; snRNA; gi 1_22603191 Encodes a gibb 1_29514407	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter promoter proximal promoter five_prime_UTR proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter exon proximal promoter
AT3G51010 AT2G38980 AT1G43960 AT1G72120 AT2G24290 AT5G03460 AT5G01930 AT1G28380 AT1G28380 AT1G68870 AT2G45790 AT2G45790 AT2G45830 AT1G66580 AT1G66580 AT1G64830 AT1G6423010 AT5G43970 AT1G64175 AT1G78440 AT3G60250	na n	unknown proteir 3, 18946702 pseudogene, si 2, 16278619 Nuclear transpc 5, 17691978 Major facilitator 1, 27132042 Protein of unkno 2, 10338548 Unknown proteir 5, 864186 Thioredoxin sup 5, 3847016 This gene is pre 1, 9963602 Encodes a low 1, 26314349 encodes a phos 2, 18855588 Involved in elec 2, 2081994 Encodes a puta 2, 17042543 senescence ass 1, 24839085 serine carboxyp 2, 9798178 Subunit of the T 5, 17691978 U12; snRNA; gi 1, 22603191 Encodes a gibb 1, 29514407 Regulatory (bet 3, 2227229	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter promoter proximal promoter five_prime_UTR proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter exon proximal promoter proximal promoter proximal promoter proximal promoter
AT3G51010 AT2G38980 AT1G72120 AT2G24290 AT5G41930 AT1G1930 AT1G28380 AT1G69870 AT2G45790 AT2G4580 AT2G40830 AT1G6580 AT2G23010 AT5G43970 AT1G643970 AT1G78440	na NECROTIC SPOTTED LESIONS 1 (NSL1 NITRATE TRANSPORTER 1.7 (NRT1.7) PHOSPHOMANNOMUTASE (PMM) PROTON GRADIENT REGULATION 5 (PC RING-H2 FINGER C1A (RHC1A) SENESCENCE ASSOCIATED GENE 24 (C SERINE CARBOXYPEPTIDASE-LIKE 9 (S TRANSLOCASE OF OUTER MEMBRANE U12 SMALL NUCLEOLAR RNA (U12) ARABIDOPSIS THALIANA GIBBERELLIN	unknown proteir 3, 1846/702 pseudogene, si 2 162/78619 Nuclear transpo 5, 17691978 Major facilitator 1,27132042 Protein of unkn 2, 10338548 Unknown proteir 5, 864186 Thioredoxin sup 5,3847016 This gene is pre 1,9963602 Encodes a low 1, 26314349 encodes a phos 2,18855588 Involved in elec 2, 2081994 Encodes a put 2, 17042543 senescence as: 1,24839085 serine carboxyp 2,9798178 Subunit of the T 5,17691978 U12; snRNA; gi 1,22603191 Encodes a gibb 1,29514407 Regulatory (bet 3,22272299 Encodes a prote 5,18377799	3.75 3.75 3.75 3.75 3.75 3.75 3.75 3.75	intron promoter promoter promoter promoter promoter proximal promoter five_prime_UTR proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter exon proximal promoter

AT2G38530	LIPID TRANSFER PROTEIN 2 (LTP2)	Involved in lipid 2_16127768	3.74	proximal promoter
AT2G28405	LOW-MOLECULAR-WEIGHT CYSTEINE		3.74	proximal promoter
AT3G06520	na	agenet domain- 3_2019927	3.74	promoter
AT1G29660	na	GDSL-like Lipas 1_10371087	3.74	proximal promoter
AT2G04795	na	unknown proteir 2_1682728	3.74	promoter
AT1G30600	na	Subtilase family 1_10845575	3.74	proximal promoter
AT3G02080	na	Ribosomal prote 3_365363	3.74	promoter
AT3G09850	na	D111/G-patch d 3_3025937	3.74	promoter
AT3G09860	na	unknown proteir 3_3025937	3.74	promoter
AT3G57470	na	Insulinase (Pepi 3_21269106	3.74	downstream
AT3G57460	na	catalytics;metal 3_21269106	3.74	intergenic
AT4G03030	na	Galactose oxida 4_1337618	3.74	promoter
AT4G35240	na	Protein of unkno 4_16764570	3.74	intron
AT5G38096	na	Pseudogene of 5_15204243	3.74	intron
AT5G55530	na	Calcium-depend 5_22496058	3.74	downstream
AT5G11490	na	adaptin family p 5_3671701	3.74	promoter
AT5G57720	na	AP2/B3-like trar 5_23391942	3.74	promoter
AT5G07470	PEPTIDEMETHIONINE SULFOXIDE RED		3.74	five_prime_UTR
AT3G06510 AT3G26030	SENSITIVE TO FREEZING 2 (SFR2) SERINE/THREONINE PROTEIN PHOSPI	Encodes a prote 3_2019927	3.74 3.74	downstream
AT5G54380	THESEUS1 (THE1)	Encodes THESI 5_22081800	3.74	promoter proximal promoter
AT3G34380	3-KETOACYL-COA SYNTHASE 14 (KCS		3.73	promoter
AT3G10260 AT3G62290	ADP-RIBOSYLATION FACTOR A1E (ARE		3.73	•
AT3G02290 AT3G13970	AUTOPHAGY 12 B (APG12B)	AUTOPHAGY 1 3 4615428	3.73	promoter proximal promoter
AT3G13970	DNA GYRASE B1 (GYRB1)	Protein targeting 3_3179892	3.73	promoter
AT4G02350	EXOCYST COMPLEX COMPONENT SEC		3.73	•
AT1G09420	GLUCOSE-6-PHOSPHATE DEHYDROGI		3.73	intergenic
AT1G64390	GLYCOSYL HYDROLASE 9C2 (GH9C2)		3.73	three_prime_UTR proximal promoter
AT5G49230	HYPERSENSITIVE TO RED AND BLUE (3.73	
				promoter
AT4G18010	INOSITOL(1,4,5)P3 5-PHOSPHATASE II		3.73	intergenic
AT1G53790	na	F-box and asso 1_20081572 unknown proteir 1_20081572	3.73	promoter
AT1G53800	na		3.73	promoter
AT4G02360	na	Protein of unknr 4_1041039	3.73	promoter
AT3G62285	na	pre-tRNA; tRNA 3_23051448	3.73	downstream
AT2G28130	na	unknown proteir 2_11987912	3.73	proximal promoter
AT1G09995	na	DNA repair DE/ 1_3263774	3.73	promoter
AT1G10000	na	Ribonuclease H 1_3263774	3.73	downstream
AT1G21580	na	Zinc finger C-x8 1_7565894	3.73	promoter
AT1G33110	na	MATE efflux fan 1_12005887	3.73	intron
AT1G55604	na	Pseudogene of 1_20779264	3.73	intergenic
AT2G27315	na	Protein of unknc 2_11689344	3.73	intergenic
AT1G21590	na	Protein kinase r 1_7565894	3.73	intergenic
AT1G26940	na	Cyclophilin-like 1_9343023	3.73	promoter
AT3G06660	na	PAPA-1-like fan 3_2102268	3.73	promoter
AT2G18690	na	unknown proteir 2_8102294	3.73	intergenic
AT4G17680	na	SBP (S-ribonuc 4_9842847	3.73	downstream
AT4G09620	na	Mitochondrial tr: 4_6079186	3.73	promoter
AT4G38640	na	Plasma-membra 4_18059676	3.73	three_prime_UTR
AT5G01890	na	Leucine-rich rec 5_346568	3.73	proximal promoter
AT5G23665	na	pre-tRNA; tRNA 5_7981462	3.73	exon
AT5G49215	na	Pectin lyase-lik€ 5_19953062	3.73	promoter
AT1G09415	NIM1-INTERACTING 3 (NIMIN-3)	encodes a kinas 1_3038505	3.73	promoter
AT3G21865	PEROXIN 22 (PEX22)	Interacts with PI 3_7703429	3.73	promoter
AT4G38630	REGULATORY PARTICLE NON-ATPASE		3.73	promoter
AT1G05460	SILENCING DEFECTIVE (SDE3)	Encodes a prote 1_1605068	3.73	promoter
AT3G56400	WRKY DNA-BINDING PROTEIN 70 (WR		3.73	proximal promoter
AT1G70490	(ARFA1D)	A member of AF 1_26565846	3.72	promoter
AT2G17870	COLD SHOCK DOMAIN PROTEIN 3 (CSI		3.72	promoter
AT5G43060	ESPONSIVE TO DEHYDRATION 21B (RI		3.72	intron
AT3G50760	GALACTURONOSYLTRANSFERASE-LIK		3.72	promoter
AT5G56740	HISTONE ACETYLTRANSFERASE OF T		3.72	promoter
AT5G25220	KNOTTED1-LIKE HOMEOBOX GENE 3 (3.72	downstream
AT5G41900	na	alpha/beta-Hydr 5_16769360	3.72	exon
AT2G36090	na	F-box family prc 2_15159399	3.72	exon
AT5G06540	na	Pentatricopeptic 5_1998664	3.72	intergenic
AT5G39790	na	Encodes a chlor 5_15935334	3.72	promoter
AT3G17930	na	unknown proteir 3_6143385	3.72	promoter
AT4G27395	na	pre-tRNA; tRNA 4_13704781	3.72	promoter
AT1G03760	na	Prefoldin chape 1_943666	3.72	promoter
AT4G10820	na	F-box family prc 4_6649694	3.72	proximal promoter
AT5G25230	na	Ribosomal prote 5_8738654	3.72	proximal promoter
AT1G52750	na	alpha/beta-Hydr 1_19649419	3.72	promoter
AT1G63490	na	transcription fac 1_23553334	3.72	proximal promoter
AT2G38870	na	Predicted to enc 2_16237928	3.72	proximal promoter
AT2G43110	na	unknown proteir 2_17921840	3.72	promoter
AT5G13810	na	Glutaredoxin far 5_4455211	3.72	promoter
AT5G56745	na	pre-tRNA; tRNA 5_22955778	3.72	promoter
AT5G60580	na (OEDO)	RING/U-box suj 5_24353775	3.72	promoter
AT1G17890	(GER2)	GER2; FUNCTI 1_6155860	3.71	promoter
AT1G06290	ACYL-COA OXIDASE 3 (ACX3)	Encodes an acy 1_1922191	3.71	promoter
AT4G25960	ATP-BINDING CASSETTE B2 (ABCB2)	P-glycoprotein 2 4_13175947	3.71	proximal promoter
AT5G53290	CYTOKININ RESPONSE FACTOR 3 (CR		3.71	intergenic
AT3G02410	ISOPRENYLCYSTEINE METHYLESTERA		3.71	intron
AT3G14431	na	unknown proteir 3_4825616	3.71	intergenic
AT5G41100	na	FUNCTIONS IN 5_16447172	3.71	promoter
AT1G64450	na	Glycine-rich pro 1_23941873	3.71	exon
AT3G28220	na	TRAF-like family 3_10524106	3.71	promoter
AT5G45350	na	proline-rich fami 5_18383982	3.71	promoter
AT2G45100	na	Cyclin/Brf1-like 2_18598528	3.71	promoter
AT4G18650	na	A maternally ex ₁ 4_10266573	3.71	proximal promoter
AT2G41705	na	camphor resista 2_17396718	3.71	proximal promoter
AT1G25510	na	Eukaryotic aspa 1_8959208	3.71	three_prime_UTR
AT3G07570		1 MOChromo hb(2 2/20127		exon
	na	Cytochrome b5(3_2420137	3.71	
AT3G24150	na na	unknown proteir 3_8725948	3.71	promoter

AT3G21690	na	MATE efflux fan 3_7640847	3.71	exon
AT3G57750	na	Protein kinase s 3_21395497	3.71	downstream
AT3G57760	na	Protein kinase s 3_21395497	3.71	promoter
AT4G34412	na	CONTAINS Inte 4_16454697	3.71	promoter
AT4G21745	na	PAK-box/P21-R 4_11549680	3.71	intron
AT4G34415	na	pre-tRNA; tRNA 4_16454697	3.71	intron
AT3G24160	PUTATIVE TYPE 1 MEMBRANE PROTEIN		3.71	promoter
AT5G13170	SENESCENCE-ASSOCIATED GENE 29 (3.71	intergenic
AT3G19570	SNOWY COTYLEDON 3 (SCO3)	Encodes SCO3 3_6801872	3.71 3.71	downstream
AT4G18390 AT3G19580	TEOSINTE BRANCHED 1, CYCLOIDEA A ZINC-FINGER PROTEIN 2 (ZF2)	Encodes zinc fir 3_6801872	3.71	promoter intergenic
AT4G34700	B22 SUBUNIT OF EUKARYOTIC MITOCH		3.7	downstream
AT4G28540	CASEIN KINASE I-LIKE 6 (CKL6)	casein kinase I- 4_14106785	3.7	promoter
AT1G28430	CYTOCHROME P450, FAMILY 705, SUBF		3.7	intergenic
AT3G02990	HEAT SHOCK TRANSCRIPTION FACTOR		3.7	promoter
AT3G50890	HOMEOBOX PROTEIN 28 (HB28)	homeobox prote 3_18916044	3.7	promoter
AT1G05100	MITOGEN-ACTIVATED PROTEIN KINASI	member of MEk 1_1469282	3.7	promoter
AT3G13530	MITOGEN-ACTIVATED PROTEIN KINASI	MAP3K epsilon 3_4419648	3.7	promoter
AT3G23250	MYB DOMAIN PROTEIN 15 (MYB15)	Member of the F 3_8307997	3.7	proximal promoter
AT3G30170	na	transposable el 3_11798742	3.7	intergenic
AT1G01350	na	Zinc finger (CC(1_136005	3.7	promoter
AT1G55960	na	Polyketide cycla 1_20930056	3.7	promoter
AT1G55964	na	pseudogene of 1_20930056	3.7	proximal promoter
AT2G16250	na	Leucine-rich reg 2_7043541	3.7	proximal promoter
AT3G14200	na na	Chaperone Dna 3_4715264	3.7	proximal promoter
AT3G44610 AT4G14740	na	Protein kinase s 3_16191477 FUNCTIONS IN 4_8454024	3.7 3.7	intron five_prime_UTR
AT4G14740	na	This gene encor 4 14117850	3.7	intergenic
AT5G19090	na	Heavy metal tra 5_6385674	3.7	proximal promoter
AT4G36090	na	oxidoreductase, 4_17080871	3.7	promoter
AT3G16140	PHOTOSYSTEM I SUBUNIT H-1 (PSAH-1		3.7	proximal promoter
AT2G32660	RECEPTOR LIKE PROTEIN 22 (RLP22)		3.7	promoter
AT5G43470	RECOGNITION OF PERONOSPORA PAR		3.7	intron
AT4G11150	VACUOLAR ATP SYNTHASE SUBUNIT E	Encodes a vacu 4_6799830	3.7	promoter
AT1G69310	WRKY DNA-BINDING PROTEIN 57 (WRK	member of WRł 1_26058265	3.7	promoter
AT5G07500	(PEI1)	Encodes an em 5_2372810	3.69	exon
AT3G48990	ACYL-ACTIVATING ENZYME 3 (AAE3)	Encodes an oxa 3_18161465	3.69	promoter
AT4G21530	ANAPHASE PROMOTING COMPLEX 4 (A		3.69	downstream
AT2G38120	AUXIN RESISTANT 1 (AUX1)	Encodes an aux 2_15974281	3.69	exon
AT1G02730	CELLULOSE SYNTHASE-LIKE D5 (CSLD		3.69	promoter
AT4G14510	CRM FAMILY MEMBER 3B (CFM3B)	Encodes a CRN 4_8341260	3.69	promoter
AT1G09350	GALACTINOL SYNTHASE 3 (GolS3)	Predicted to enc 1_3018366	3.69	proximal promoter
AT4G09500	na	UDP-Glycosyltri 4_6017982	3.69	promoter
AT5G57060	na	FUNCTIONS IN 5_23092244	3.69	intergenic
AT5G64710 AT5G59770	na na	Putative endon 5_25869174 Protein-tyrosine 5_24079138	3.69 3.69	promoter
AT5G63145	na	pre-tRNA; tRNA 5 25330140	3.69	intergenic downstream
AT5G63150	na	unknown proteir 5_25330140	3.69	promoter
AT1G16820	na	vacuolar ATP st 1_5758445	3.69	exon
AT1G33050	na	unknown proteir 1_11971110	3.69	intron
AT1G57840	na	pseudogene, pt 1_21425608	3.69	intron
AT1G57850	na	Toll-Interleukin-l 1_21425608	3.69	intron
AT1G78860	na	curculin-like (ma 1_29647931	3.69	promoter
AT1G78865	na	na 1_29647931	3.69	exon
AT2G31141	na	unknown proteir 2_13272113	3.69	exon
AT2G31150	na	ATP binding;AT 2_13272113	3.69	promoter
AT2G33585	na	unknown proteir 2_14224108	3.69	exon
AT2G33590	na	NAD(P)-binding 2_14224108	3.69	promoter
AT2G36650 AT1G33055	na na	unknown proteir 2_15359476	3.69 3.69	promoter
AT3G01590	na	unknown proteir 1_11971110 Galactose muta 3 225848	3.69	downstream promoter
AT3G08780	na	unknown proteir 3_2667549	3.69	promoter
AT2G31140	na	Peptidase S24/; 2 13272113	3.69	intergenic
AT2G37220	na	Encodes a chloi 2_15633027	3.69	intergenic
AT3G23700	na	Nucleic acid-bin 3_8533854	3.69	promoter
AT3G53730	na	Histone superfa 3_19912379	3.69	downstream
AT3G53740	na	Ribosomal prote 3_19912379	3.69	intergenic
AT4G11177	na	pre-tRNA; tRNA 4_6819426	3.69	downstream
AT4G14520	na	Protein of unknr 4_8341260	3.69	promoter
AT4G24920	na	secE/sec61-gar 4_12820855	3.69	promoter
AT5G16030	na	unknown proteir 5_5235955	3.69	proximal promoter
AT4G34400	na	AP2/B3-like trar 4_16448511	3.69	intergenic
AT4G35670	na na	Pectin lyase-like 4_16914030 Quinone reduct: 4_17324445	3.69 3.69	proximal promoter
AT4G36750 AT3G19180	na PARALOG OF ARC6 (PARC6)	Encodes a chloi 3_6632572	3.69	promoter promoter
AT5G20360	PHOX3 (Phox3)	Encodes a chiol 3_6632572 Encodes one of 5_6881198	3.69	intergenic
AT3G20300	PURPLE ACID PHOSPHATASE 17 (PAP1		3.69	proximal promoter
AT2G42800	RECEPTOR LIKE PROTEIN 29 (RLP29)	receptor like prc 2_17809919	3.69	promoter
AT4G21534	SPHINGOSINE KINASE 2 (SPHK2)	Diacylglycerol k 4_11456015	3.69	promoter
AT4G12040	STRESS-ASSOCIATED PROTEIN 7 (SAP		3.69	promoter
AT1G71880	SUCROSE-PROTON SYMPORTER 1 (SL	Sucrose transpt 1_27046320	3.69	intergenic
AT5G20350	TIP GROWTH DEFECTIVE 1 (TIP1)	Encodes a prote 5_6881198	3.69	three_prime_UTR
AT1G63780	(IMP4)	Small nucleolar 1_23667401	3.68	promoter
AT3G21250	ATP-BINDING CASSETTE C8 (ABCC8)	member of MRF 3_7463811	3.68	promoter
AT3G01640	GLUCURONOKINASE G (GLCAK)	AtGlcAK is a su 3_239291	3.68	promoter
AT3G21260	GLYCOLIPID TRANSFER PROTEIN 3 (GI		3.68	downstream
AT4G16143	IMPORTIN ALPHA ISOFORM 2 (IMPA-2)		3.68	intergenic
AT3G03310 AT4G11330	LECITHIN: CHOLESTEROL ACYLTRANSF MAP KINASE 5 (MPK5)	MAP kinase 4_6890682	3.68 3.68	promoter proximal promoter
AT5G14565	MICRORNA398C (MIR398C)	Encodes a micr 5_4694185	3.68	promoter
AT1G12030	na	Protein of unknr 1_4066925	3.68	proximal promoter
AT3G03320	na	RNA-binding A\$ 3_781655	3.68	promoter
AT4G37180	na	myb family trans 4_17504491	3.68	promoter
AT5G09876	na	unknown proteir 5_3080574	3.68	downstream

AT2G22200	na	encodes a mem 2 9444463	3.68	promoter
AT2G22201	na	unknown proteir 2_9444463	3.68	promoter
AT4G31330	na	Protein of unknc 4_15203600	3.68	downstream
AT1G15885	na	unknown proteir 1_5460458	3.68	promoter
AT1G63790	na	pre-tRNA; tRNA 1_23667401	3.68	downstream
AT1G67460	na	Minichromosom 1_25272129	3.68	promoter
AT1G67470	na	Protein kinase s 1_25272129	3.68	promoter
AT1G03520	na	Core-2/I-branch 1_880203	3.68	promoter
AT3G15548	na	unknown proteir 3_5266703	3.68	promoter
AT3G50850	na	Putative methyll 3_18905078	3.68	proximal promoter
AT4G16141	na	GATA type zinc 4_9133262	3.68	promoter
AT5G14550	na	Core-2/I-branch 5_4694185	3.68	promoter
AT5G46170	na	F-box family prc 5_18718108	3.68	proximal promoter
AT4G39230	na	encodes a prote 4_18267875	3.68	promoter
AT5G14560	na	unknown proteir 5_4694185	3.68	downstream
AT5G37010	na	unknown proteir 5_14623133	3.68	promoter
AT5G46180	ORNITHINE-DELTA-AMINOTRANSFERA		3.68	intergenic
AT2G05100	PHOTOSYSTEM II LIGHT HARVESTING		3.68	promoter
AT1G80480	PLASTID TRANSCRIPTIONALLY ACTIVE		3.68	promoter
AT1G80490	TOPLESS-RELATED 1 (TPR1)	TOPLESS-relat 1_30260773	3.68	downstream
AT5G59300	UBIQUITIN CARRIER PROTEIN 7 (UBC7)		3.68	promoter
AT1G63800	UBIQUITIN-CONJUGATING ENZYME 5 (I		3.68	downstream
AT3G50740	UDP-GLUCOSYL TRANSFERASE 72E1 (3.68	three_prime_UTR
AT3G51820	(G4)	Encodes a prot 3_19219109	3.67	promoter
AT5G13490	ADP/ATP CARRIER 2 (AAC2)	Encodes mitoch 5_4337764	3.67	downstream
AT3G22370	ALTERNATIVE OXIDASE 1A (AOX1A)	Encodes AOX1; 3_7908730	3.67	three_prime_UTR
AT3G51920	CALMODULIN 9 (CAM9)	encodes a diver 3_19269530	3.67	promoter
AT1G64390		glycosyl hydrola 1_23905671	3.67	intergenic
AT1G31140	GORDITA (GOA)	Encodes a B-six 1_11119698	3.67	three_prime_UTR
AT2G18960	H(+)-ATPASE 1 (HA1)	Encodes a plasi 2_8219934	3.67	proximal promoter
AT2G18550	HOMEOBOX PROTEIN 21 (HB21)	Encodes a hom 2_8053452	3.67	proximal promoter
AT3G08770	LIPID TRANSFER PROTEIN 6 (LTP6)	Predicted to end 3_2664926	3.67	promoter
AT4G23850	LONG-CHAIN ACYL-COA SYNTHETASE	, –	3.67	five_prime_UTR
AT3G46580	METHYL-CPG-BINDING DOMAIN PROTE		3.67	intergenic
AT2G38325	MICRORNA390A (MIR390A)	Encodes a micr 2_16062580	3.67	intergenic
AT1G32730	na	unknown proteir 1_11840872	3.67	promoter
AT3G05160	na	Major facilitator 3_1457160	3.67	promoter
AT5G38005	na	Unknown gene 5_15151689	3.67	intergenic
AT5G10730	na	NAD(P)-binding 5_3393207	3.67	promoter
AT5G04500	na	a member of the 5_1283252	3.67	promoter
AT1G19485	na	Transducin/WD 1_6746714	3.67	promoter
AT1G05380	na	Acyl-CoA N-acy 1_1576743	3.67	promoter
AT1G31150	na	FUNCTIONS IN 1_11119698	3.67	promoter
AT3G46585	na	pre-tRNA; tRNA 3_17149829	3.67	downstream
AT3G59870	na	unknown proteir 3_22118334	3.67	promoter
AT4G23882	na	Heavy metal tra 4_12419266	3.67	intergenic
AT4G23885	na	unknown proteir 4_12419266	3.67	promoter
AT5G25615	na	transposable el 5_8927285	3.67	proximal promoter
AT5G04840	na	bZIP protein; FL 5_1405175	3.67	promoter
AT5G13500	na	unknown proteir 5_4337764	3.67	promoter
AT5G13500 AT5G15260	na na	unknown proteir 5_4337764 Ribosomal prote 5_4955167	3.67 3.67	promoter promoter
AT5G13500 AT5G15260 AT5G41920	na na na	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tra 5_16781030	3.67 3.67 3.67	promoter promoter exon
AT5G13500 AT5G15260 AT5G41920 AT5G66790	na na na na	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tra 5_16781030 Protein kinase s 5_26667690	3.67 3.67 3.67 3.67	promoter promoter exon downstream
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380	na na na na NAD+ TRANSPORTER 2 (NDT2)	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tra 5_16781030 Protein kinase s 5_26667690 Encodes a mito: 1_8903423	3.67 3.67 3.67 3.67 3.67	promoter promoter exon downstream promoter
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT5G06690	na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1)	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tra 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061989	3.67 3.67 3.67 3.67 3.67 3.67	promoter promoter exon downstream promoter promoter
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT5G06690 AT2G40950	na na na na na nAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17)	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family frz 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328	3.67 3.67 3.67 3.67 3.67 3.67 3.66	promoter promoter exon downstream promoter promoter intergenic
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT5G06690 AT2G40950 AT5G16390	na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME A	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tra 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter promoter intergenic downstream
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT5G06690 AT2G40950 AT5G16390 AT2G23980	na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tra 5_16781030 Protein kinase s 5_26667690 Encodes a mitor 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter promoter intergenic downstream promoter
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT5G06690 AT2G40950 AT5G16390 AT2G23980 AT3G47500	na na na na na na nAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3)	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter promoter intergenic downstream promoter promoter
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT5G06690 AT2G40950 AT5G16390 AT2G23980 AT3G47500 AT3G21270	na na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2)	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tra 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a mito 1_8903423 Encodes at hior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter intergenic downstream promoter promoter intergenic
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT5G06690 AT2G40950 AT5G16390 AT2G23980 AT3G47500 AT3G21270 AT2G40940	na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS	unknown proteit 5_4337764 Ribosomal prote 5_4955167 GRAS family trs 5_16781030 Protein kinase s 5_26667890 Encodes a mito 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter intergenic downstream promoter intergenic downstream promoter
AT5G13500 AT5G15260 AT5G641920 AT5G66790 AT1G25380 AT5G066990 AT2G40950 AT5G16390 AT2G23980 AT3G47500 AT3G21270 AT2G40940 AT4G37840	na na na na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS HEXOKINASE-LIKE 3 (HKL3)	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061898 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_1024907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792887	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter promoter intergenic downstream promoter intergenic moter promoter
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT5G06690 AT2G40950 AT5G16390 AT2G23980 AT3G47500 AT3G21270 AT3G40940 AT4G37840 AT3G21220	na na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS HEXOKINASE-LIKE 3 (FIKL3) MAP KINASE KINASE 5 (MKK5)	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fire 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a mito 1_2903423 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter intergenic downstream promoter intergenic downstream promoter intergenic promoter
ATSG13500 ATSG41920 ATSG41920 ATSG46790 ATIG25380 ATSG66990 AT2G40950 AT2G23980 AT3G21270 AT3G21270 AT4G37840 AT4G37840 AT4G37840 AT3G21220 AT2G35630	na na na na na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS HEXOKINASE-LIKE 3 (HKL3) MAP KINASE KINASE 5 (MKK5) MICROTUBULE ORGANIZATION 1 (MOR	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a puta 4_17792687 Member of the f 2_14966626	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter intergenic downstream promoter intergenic downstream promoter
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT5G06690 AT2G40950 AT5G16390 AT2G23980 AT3G47500 AT3G21270 AT3G40940 AT4G37840 AT3G21220	na na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS HEXOKINASE-LIKE 3 (FIKL3) MAP KINASE KINASE 5 (MKK5)	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061898 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a mito 3_7445675 Member of the 1_2_14966626 SNARE-like sup 1_224449887	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter promoter intergenic downstream promoter
AT5G13500 AT5G41920 AT5G66790 AT5G66790 AT1G25380 AT5G66990 AT2G40950 AT2G23980 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G21220 AT3G21220 AT3G21220 AT3G21220 AT3G21220 AT3G21220	na na na na na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS HEXOKINASE-LIKE 3 (HKL3) MAP KINASE KINASE 5 (MKK5) MICROTUBULE ORGANIZATION 1 (MOR na	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes at mito 1_8903423 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the 1 2_14966626 SNARE-like sur 1_22449687 other RNA	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter intergenic downstream promoter promoter intergenic downstream promoter intergenic promoter
AT5G13500 AT5G15260 AT5G41920 AT5G66790 AT1G25380 AT2G40950 AT2G40950 AT3G23980 AT3G21270 AT3G21270 AT2G40940 AT3G21220 AT3G37840 AT3G21220 AT2G35630 AT1G6970 AT1G64618	na na na na na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS HEXOKINASE-LIKE 3 (HKL3) MAP KINASE KINASE 5 (MKK5) MICROTUBULE ORGANIZATION 1 (MOR na	unknown proteit 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a puta 4_17792687 Member of the f 2_14966626 SNARE-like sur 1_22449687 other RNA 1_24005833 LOCATED IN: e 1_27031293	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter promoter intergenic downstream promoter
ATSG13500 ATSG41920 ATSG41920 ATSG466790 ATIG25380 ATSG66690 ATZG40950 ATZG23980 AT3G21270 ATZG40940 ATAG37840 ATAG37840 ATAG37840 ATGG6970 ATGG6970 ATGG6971 ATGG6971 ATGG6971 ATGG6971 ATGG77866	na na na na na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS HEXOKINASE-LIKE 3 (HKL3) MAP KINASE KINASE 5 (MKK5) MICROTUBULE ORGANIZATION 1 (MOR na na na	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes at mito 1_8903423 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the 1 2_14966626 SNARE-like sur 1_22449687 other RNA	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter promoter intergenic downstream promoter five_prime_UTR
ATSG13500 ATSG41920 ATSG41920 ATSG66790 ATSG666790 ATGG66890 ATGG16390 ATGG16390 ATGG23980 ATGG23980 ATGG21270 ATGG40940 AT4G37840 ATGG37840 ATGG6970 ATGG64618 ATGG64618 ATGG18750	na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS HEXOKINASE-LIKE 3 (HKL3) MAP KINASE KINASE 5 (MKK5) MICROTUBULE ORGANIZATION 1 (MOR na na na	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061898 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a mito 3_7447504 Ethylene recept 2_17087328 Encodes a mito 3_7445675 Member of the 1_2_1496626 SNARE-like sup 1_22449687 other RNA 1_24005833 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter promoter intergenic downstream promoter p
AT5G13500 AT5G41920 AT5G46790 AT1G25380 AT5G66690 AT2G40950 AT2G23980 AT3G23980 AT3G21270 AT3G21270 AT3G21220 AT3G37840 AT3G37840 AT3G37840 AT1G6970 AT1G64618 AT1G71866 AT2G18750 AT2G23985	na na na na na na na na na NAD+ TRANSPORTER 2 (NDT2) WCRKC THIOREDOXIN 1 (WCRKC1) (BZIP17) CHLOROPLASTIC ACETYLCOENZYME / CYCLIC NUCLEOTIDE-GATED CHANNEI CYCLING DOF FACTOR 3 (CDF3) DOF ZINC FINGER PROTEIN 2 (DOF2) ETHYLENE RESPONSE SENSOR 1 (ERS HEXOKINASE-LIKE 3 (HKL3) MAP KINASE KINASE 5 (MKK5) MICROTUBULE ORGANIZATION 1 (MOR na na na na	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes at hito 5_2061898 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the 1 2_14966626 SNARE-like sur 1_22449687 other RNA	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter intergenic downstream promoter promoter promoter intergenic promoter
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ATSG13500 ATSG41920 ATSG46790 ATSG46790 ATGG66790 ATGG46990 ATGG40950 ATGG40950 ATGG40940 ATGG40940 ATGG5880 ATGG21270 ATGG6780 ATGG4780 ATGG4780 ATGG4780 ATGG4780 ATGG4780 ATGG4780 ATGG4780 ATGG4780 ATGG4818 ATGG4780 ATGG4818 ATGG4780 ATGG4818 ATGG4780 ATGG4818 ATGG4780 ATGG4818 ATGG4780 ATGG48180 ATGG4780 ATGG48180 ATGG4780 ATGG48180 ATGG4780 ATGG7870 ATGG7870 ATGG7870 ATGG7870 ATGG7870 ATGG7870 ATGG7870 ATGG7870 ATGG7870	na n	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thio 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the 1_2_1496626 SNARE-like sur 1_22449687 other RNA 1_24005833 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508 unknown proteir 2_10204907 Protein kinase s 2_12430332 ARM repeat sur 3_172042 RING/U-box sur 3_4367130 unknown proteir 1_516758036 unknown proteir 5_16758036 This gene is pre 1_4328548 Encodes a plan 1_3658668 Encodes a ubiq 3_7477504 BES1/BZR1 hor 1_29602118 Beta glucosidas 1_9179346 RNA-binding pri 1_11877408	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter exon downstream promoter intergenic downstream promoter pro
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ATSG13500 ATSG41920 ATSG46790 ATIG25380 ATSG66790 ATIG25380 ATSG66990 ATZG40950 ATZG40950 AT3G21270 AT3G21280 AT3G21280 AT3G21280 AT3G21280 AT3G3630 AT1G66618 ATZG23985 AT3G23885 AT3G23881 AT3G14850 AT3G14850 AT3G14850 AT3G14860 AT1G12710 AT1G10940 AT1G10950 AT3G21280 AT1G278700 AT1G28560 AT1G32790	na n	unknown proteit 5_4337764 Ribosomal prote 5_4955167 GRAS family fire 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the! 2_14866626 SNARE-like suy 1_22449687 other RNA 1_24005833 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508 unknown proteit 2_1024907 Protein kinase s 2_12430332 ARM repeat suy 3_172042 RING/U-box suy 3_4367130 unknown proteit 3_5464623 Protein of unkn 5_5360763 Unknown proteit 5_16758036 unknown proteit 5_16758036 unknown proteit 5_16758036 This gene is pre 1_4328548 Encodes a plan 1_3658668 Encodes a plan 1_3658668 Encodes a plan 1_3658668 Encodes a unita 3_7477504 BES1/BZR1 hor 1_29602118 beta qlucosidas 1_9179346 RNA-binding pn 1_11877408 encodes a nem 4_6797665 EXORDIUM like 5_2941678 Encodes HopW 4_15367944 member of MAF 1_27640466	3.67 3.67 3.67 3.67 3.67 3.66 3.66 3.66	promoter promoter exon downstream promoter exon downstream promoter intergenic downstream promoter proximal promoter intergenic intron promoter intergenic proximal promoter intergenic proximal promoter intergenic proximal promoter intergenic
ATSG13500 ATSG41920 ATSG41920 ATSG66790 ATSG466790 ATGG6690 AT2G40950 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G40940 AT4G37840 AT3G21270 AT1G64618 AT1G64618 AT1G18750 AT2G23985 AT3G47500 AT3G47866 AT2G18750 AT2G23985 AT3G641850 AT3G13430 AT3G16117 AT5G16380 AT3G1617 AT5G16380 AT3G14170 AT1G10940 AT1G78700 AT1G78	na n	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thio 1_8903423 Encodes a thio 1_52061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_1024907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the 1_2_1496626 SNARE-like sur 1_22449687 other RNA 1_24005833 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508 unknown proteir 2_10204907 Protein kinase s 2_12430332 ARM repeat sur 3_172042 RING/U-box sur 3_4367130 unknown proteir 3_5464623 Protein of unkn 5_5360763 alpha/beta-Hydr 5_16758036 Unknown proteir 5_16758036 This gene is pre 1_4328548 Encodes a plan 1_3658668 Encodes a ubiq 3_7477504 BES1/BZR1 hor 1_29602118 BES1/BZR1 hor 1_29602118 ENAD-bindling pri 1_11877408 encodes a mem 4_6797665 EXORDIUM like 5_2941678 ENCOME STARE STAR	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter exon downstream promoter intergenic downstream promoter pro
ATSG13500 ATSG15260 ATSG41920 ATSG66790 ATIG25380 ATSG66990 ATZG409500 ATZG409500 ATZG23980 AT3G21270 AT3G21270 AT3G21270 AT3G21220 AT3G3630 AT1G60970 AT3G31220 AT2G35630 AT1G66970 AT3G312420 AT3G312420 AT3G314500 AT3G31	na n	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family fre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a mito 1_8903423 Encodes a mito 1_52061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the 1_21496626 SNARE-like sur 1_22449687 other RNA 1_24005833 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508 unknown proteir 2_10204907 Protein kinase s 2_12430332 ARM repeat sur 3_172042 RING/U-box sur 3_4367130 unknown proteir 3_5464623 Protein of unkn 5_5360763 alpha/beta-Hydr 5_16758036 Unknown proteir 5_16758036 This gene is pre 1_4328548 Encodes a plan 1_3658668 Encodes a ubiq 3_7477504 BES1/BZR1 hor 1_29602118 ENA-binding pri 1_11877408 encodes a mem 4_6797665 EXORDIUM like 5_2941678 Encodes HopW 4_15367944 unknown proteir 1_2760466	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter intergenic downstream promoter intergenic downstream promoter five_prime_UTR
ATSG13500 ATSG41920 ATSG46790 ATIG25380 ATSG66790 ATIG25380 ATSG66990 AT2G40950 AT2G40950 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G3630 AT3G21270 AT3G46940 AT3G21220 AT3G3630 AT1G6970 AT1G64618 AT2G18750 AT2G23985 AT3G14850 AT1G17500 AT4G37750 AT4G37750 AT4G37750 AT4G37750 AT4G37750 AT4G37750	na n	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family trs 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the l 2_14966626 SNARE-like suy 1_22449687 other RNA 1_24005633 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508 unknown proteir 2_1024907 Protein kinase s 2_12430332 ARM repeat suy 3_172042 RING/U-box suy 3_4367130 unknown proteir 3_5464623 Protein of unknc 5_5360763 Lins gene is pre 1_4328548 Encodes a plan 1_3658668 Encodes a nem 4_6797665 EXORDIUM like 5_2941678 ENA-binding pn 1_11877408 encodes a nem 4_6797665 EXORDIUM like 5_2941678 Encodes BoyW 4_15367944 member of MAF 1_27640466 Peroxidase sup 4_15367944 unknown proteir 1_23101134 Phototropic-resi 3_18530048	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter exon downstream promoter intergenic downstream promoter pro
ATSG13500 ATSG41920 ATSG66790 ATIG25380 ATSG66790 ATIG25380 ATSG66990 AT2G40950 AT2G40950 AT3G21270 AT3G21280 AT3G21280 AT3G21280 AT3G218750 AT2G23985 AT3G218750 AT3G313430 AT3G16117 ATSG16380 AT3G141800 AT3G141800 AT1G12710 AT1G10940 AT1G10950 AT3G21280 AT1G2750 AT3G21280 AT1G32790 AT3G3141140 AT5G09440 AT4G31750 AT4G31750 AT4G31760 AT4G31760 AT4G31760 AT4G31760 AT1G62422 AT3G49970 AT3G53640	na n	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tre 5_16781030 Protein kinase s 5_26667690 Encodes a mitor 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encydes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a puta 4_17792687 Encodes a puta 4_17792687 Member of the 1_214966626 SNARE-like sur 1_22449687 Other RNA 1_24005833 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508 unknown proteir 2_10204907 Protein kinase s 2_12430332 ARM repeat sur 3_172042 RING/U-box sur 3_4367130 unknown proteir 3_5464623 Protein of unknc 5_5360763 alpha/beta-Hydr 5_16758036 Unknown proteir 5_16758036 This gene is pre 1_4328548 Encodes an Jan 1_3658668 Encodes an Ara 1_3658668 Encodes an Ara 1_3658668 Encodes an Ara 1_3658668 Encodes an Ara 1_3658668 Encodes an Hara 1_37408 Encystal Sur 3_4777504 ESS1/BZR1 hor 1_29602118 beta glucosidas 1_9179346 RNA-binding pr 1_11877408 encystal Sur 3_48537944 unknown proteir 1_23101134 Protein kinase s 3_18830048 Protein kinase s 3_18889162	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter exon downstream promoter intergenic downstream promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter pro
ATSG13500 ATSG135260 ATSG41920 ATSG66790 ATSG66790 ATGG66990 AT2G40950 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G47500 AT3G21280 AT3G21280 AT3G3630 AT1G60970 AT1G64618 AT1G78700 AT3G13430 AT3G13430 AT3G16117 AT5G16380 AT3G14850 AT3G21280 AT1G19710 AT1G19940 AT1G19710 AT1G19710 AT1G19710 AT1G78700 AT1G73500 AT1G73500 AT1G73500 AT1G62422 AT3G49970 AT1G6353640 AT1G633030	na n	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a mito 1_8903423 Encodes a thio 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the 1_2 1496626 SNARE-like sur 1_22449687 other RNA 1_24005833 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508 unknown proteir 2_10204907 Protein kinase s 2_12430332 ARM repeat sur 3_172042 RING/U-box sur 3_4367130 unknown proteir 3_5464623 Protein of unknc 5_5360763 alpha/beta-Hydr 5_16758036 Unknown proteir 5_16758036 This gene is pre 1_4328548 Encodes a plan 1_3658668 Encodes a ubiq 3_7477504 BES1/BZR1 hor 1_29602118 BENADIUM like 5_2941678 Encodes a mem 4_6797665 EXORDIUM like 5_2941678 Encodes HopW 4_15367944 unknown proteir 1_27604666 Encodes up 1_127604667 ENCOMENTAL STANDIUM like 5_2941678 Encodes HopW 4_15367944 unknown proteir 1_23101134 Phototropic-resi 3_18530048 Protein kinase s 3_19889162 Galactose oxide 4_1338672	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter exon downstream promoter intergenic downstream promoter pro
ATSG13500 ATSG15260 ATSG41920 ATSG66790 ATIG25380 ATSG66990 ATZG40950 ATZG40950 ATZG23980 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G21270 AT3G3630 AT1G60970 AT3G21280 AT3G313430 AT3G16117 AT5G16380 AT3G13430 AT3G1170 AT1G12710 AT1G10940 AT1G12710 AT1G10940 AT1G10950 AT3G13760 AT1G32790 AT1G26560 AT1G32790 AT1G26560 AT1G32790 AT4G11140 AT5G09440 AT4G31750 AT4G31750 AT4G31760 AT1G62422 AT3G49970 AT3G53640 AT4G31760 AT1G62422 AT3G49970 AT3G53640 AT4G31290	na n	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family trs 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a thior 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the 1_214966626 SNARE-like sup 1_22449687 other RNA 1_24405633 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508 unknown proteir 2_1024907 Protein kinase s 2_12430332 ARM repeat sup 3_172042 RING/U-box sup 3_4367130 unknown proteir 3_5464623 Protein of unknc 5_5360763 Lis gene is pre 1_4328548 Encodes a palan 1_3658668 Encodes a palan 1_3658668 Encodes a palan 1_3658668 Encodes a palan 1_3658668 Encodes a mem 4_6797665 EXCRDIUM like 5_2941678 ENCOMED 1_1337944 member of MAF 1_27640466 Peroxidase sup 4_15367944 member of MAF 1_27640466 Peroxidase sup 4_15367944 unknown proteir 1_23101134 Protetrio kinase s 3_19889162 Galactose oxida 4_1338672 ChaC-like famili, 4_15185952	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter intergenic downstream promoter p
ATSG13500 ATSG135260 ATSG41920 ATSG66790 ATSG66790 ATGG66990 AT2G40950 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G47500 AT3G21270 AT3G47500 AT3G21280 AT3G21280 AT3G3630 AT1G60970 AT1G64618 AT1G78700 AT3G13430 AT3G13430 AT3G16117 AT5G16380 AT3G14850 AT3G21280 AT1G19710 AT1G19940 AT1G19710 AT1G19710 AT1G19710 AT1G78700 AT1G73500 AT1G73500 AT1G73500 AT1G62422 AT3G49970 AT1G6353640 AT1G633030	na n	unknown proteir 5_4337764 Ribosomal prote 5_4955167 GRAS family tre 5_16781030 Protein kinase s 5_26667690 Encodes a mito 1_8903423 Encodes a mito 1_8903423 Encodes a thio 5_2061989 bZIP17 appears 2_17087328 Encodes for the 5_5360763 member of Cycl 2_10204907 Dof-type zinc fir 3_17506131 Encodes Dof zir 3_7477504 Ethylene recept 2_17087328 Encodes a puta 4_17792687 Encodes a mito 3_7445675 Member of the 1_2 1496626 SNARE-like sur 1_22449687 other RNA 1_24005833 LOCATED IN: e 1_27031293 Calmodulin-binc 2_8125508 unknown proteir 2_10204907 Protein kinase s 2_12430332 ARM repeat sur 3_172042 RING/U-box sur 3_4367130 unknown proteir 3_5464623 Protein of unknc 5_5360763 alpha/beta-Hydr 5_16758036 Unknown proteir 5_16758036 This gene is pre 1_4328548 Encodes a plan 1_3658668 Encodes a ubiq 3_7477504 BES1/BZR1 hor 1_29602118 BENADIUM like 5_2941678 Encodes a mem 4_6797665 EXORDIUM like 5_2941678 Encodes HopW 4_15367944 unknown proteir 1_27604666 Encodes up 1_127604667 ENCOMENTAL STANDIUM like 5_2941678 Encodes HopW 4_15367944 unknown proteir 1_23101134 Phototropic-resi 3_18530048 Protein kinase s 3_19889162 Galactose oxide 4_1338672	3.67 3.67 3.67 3.67 3.67 3.67 3.66 3.66	promoter promoter exon downstream promoter exon downstream promoter intergenic downstream promoter pro

AT4G31280	na	unknown proteir 4_15185952	3.65	five_prime_UTR
AT5G05795	na	pre-tRNA; tRNA 5_1742677	3.65	promoter
AT5G07800	na	Flavin-binding n 5_2487398	3.65	exon
AT5G09443	na	Potential natura 5_2941678	3.65	proximal promoter
AT5G09445	na	unknown proteir 5_2941678	3.65	intergenic
AT3G56710	SIGMA FACTOR BINDING PROTEIN 1 (S		3.65	proximal promoter
AT1G78710	TRICHOME BIREFRINGENCE-LIKE 42 (T	Encodes a merr 1_29602118	3.65	intron
AT3G13300	VARICOSE (VCS)	Encodes VCS (' 3_4303712	3.65	promoter
AT2G39190	(ATATH8)	member of ATH 2_16349999	3.64	five_prime_UTR
AT4G10920	(KELP)	Transcriptional (4_6696287	3.64	intergenic
AT3G52090	(NRPB11)	Non-catalytic su 3_19319233	3.64	promoter
AT5G66690	(UGT72E2)	UGT72E2 is an 5_26628555	3.64	intergenic
AT5G65800	ACC SYNTHASE 5 (ACS5)	1-aminocyclopr(5_26333913	3.64	proximal promoter
AT2G13360	ALANINE:GLYOXYLATE ÁMINOTRANSFI		3.64	promoter
AT2G28350	AUXIN RESPONSE FACTOR 10 (ARF10)	Involved in root 2_12112782	3.64	proximal promoter
AT2G27220	BEL1-LIKE HOMEODOMAIN 5 (BLH5)	BEL1-like home 2_11644215	3.64	intergenic
AT2G26980	CBL-INTERACTING PROTEIN KINASE 3	encodes a serin 2 11518573	3.64	intron
AT2G20190	CLIP-ASSOCIATED PROTEIN (CLASP)	Encodes a micr 2_8711757	3.64	three_prime_UTR
AT2G44810	DEFECTIVE ANTHER DEHISCENCE 1 (D		3.64	intergenic
AT1G21390	EMBRYO DEFECTIVE 2170 (emb2170)	embryo defectiv 1_7491360	3.64	proximal promoter
AT4G04020	FIBRILLIN (FIB)	Fibrillin precurs: 4_1931817	3.64	promoter
AT3G26640	LIGHT-REGULATED WD 2 (LWD2)	Encodes LIGHT 3_9793096	3.64	promoter
AT4G30074	LOW-MOLECULAR-WEIGHT CYSTEINE-	Encodes a merr 4_14701704	3.64	proximal promoter
AT5G62470	MYB DOMAIN PROTEIN 96 (MYB96)	Encodes a R2R 5_25084960	3.64	intergenic
AT1G16180	na	Serinc-domain c 1_5543096	3.64	downstream
AT2G10940	na	Bifunctional inhi 2_4312150	3.64	promoter
AT3G22550	na	Protein of unknc 3_7990376	3.64	intergenic
AT5G17650	na	glycine/proline-r 5_5818667	3.64	promoter
AT5G17660	na	tRNA (guanine- 5_5818667	3.64	three_prime_UTR
AT5G27730	na	Protein of unknc 5_9820018	3.64	promoter
AT5G58510	na	unknown proteir 5_23654638	3.64	promoter
AT1G32620	na	pre-tRNA; tRNA 1_11797316	3.64	promoter
AT1G32630	na	unknown proteir 1_11797316	3.64	promoter
AT3G10035	na	pre-tRNA; tRNA 3_3096240	3.64	exon
AT3G15115	na	unknown proteir 3_5088200	3.64	proximal promoter
AT3G26630	na	Tetratricopeptid 3_9793096	3.64	promoter
AT3G10040	na	sequence-speci 3_3096240	3.64	downstream
AT3G15120	na	P-loop containir 3_5088200	3.64	downstream
AT3G52100	na	RING/FYVE/PH 3_19319233	3.64	promoter
AT3G60480	na	unknown proteir 3_22348478	3.64	promoter
AT3G60490	na	encodes a mem 3_22348478	3.64	proximal promoter
AT3G62528	na	This gene enco 3_23131374	3.64	downstream
AT3G62529	na	pseudogene of 3_23131374	3.64	promoter
AT4G10910	na	unknown proteir 4_6696287	3.64	promoter
AT4G18725	na	pre-tRNA; tRNA 4_10302090	3.64	downstream
AT4G36270	na	ATP binding; BE 4_17165289	3.64	promoter
AT4G35730	na	Regulator of Vp 4_16930910	3.64	promoter
AT4G36280	na	Histidine kinase 4_17165289	3.64	downstream
AT5G55220	na	trigger factor tyr 5_22397477	3.64	promoter
AT5G57790	na	unknown proteir 5_23413997	3.64	promoter
AT5G12460	na	Protein of unknc 5_4042198	3.64	proximal promoter
AT5G16110	na	unknown proteir 5_5262565	3.64	exon
AT5G25010	na	Protein of unknc 5_8616064	3.64	exon
AT5G37550	na	unknown proteir 5_14916779	3.64	intergenic
AT5G47250	na	LRR and NB-AF 5_19188854	3.64	promoter
AT5G55210	na	unknown proteir 5_22397477	3.64	promoter
AT2G20180	PHYTOCHROME INTERACTING FACTOR	Encodes a nov€ 2_8711757	3.64	intergenic
AT1G16190	RADIATION SENSITIVE23A (RAD23A)	Encodes a merr 1_5543096	3.64	promoter
AT4G18730	RIBOSOMAL PROTEIN L16B (RPL16B)	encodes a cytos 4_10302090	3.64	promoter
AT5G43880	TON1 RECRUITING MOTIF 21 (TRM21)	Protein of unknc 5_17643671	3.64	promoter
AT3G26520	TONOPLAST INTRINSIC PROTEIN 2 (TIP		3.64	intergenic
AT1G04820	TUBULIN ALPHA-4 CHAIN (TUA4)	Encodes an alpl 1_1358436	3.64	promoter
AT5G57160	(ATLIG4)	Encodes the Ar. 5_23154224	3.63	intergenic
AT5G26340	(MSS1)	Encodes a prote 5_9245287	3.63	intron
AT4G25650	ACD1-LIKE (ACD1-LIKE)	Similar to ACD1 4_13083283	3.63	promoter
AT2G37550	ARF-GAP DOMAIN 7 (AGD7)	A member of AF 2_15757612	3.63	promoter
AT1G48790	ASSOCIATED MOLECULE WITH THE SH			
AT3G30180			3.63	five_prime_UTR
AT4000400	BRASSINOSTEROID-6-OXIDASE 2 (BR6)	Encodes a cyto 3_11812870	3.63	intron
AT4G23180	BRASSINOSTEROID-6-OXIDASE 2 (BR6) CYSTEINE-RICH RLK (RECEPTOR-LIKE	Encodes a cyto 3_11812870 Encodes a rece 4_12138159	3.63 3.63	intron five_prime_UTR
AT4G23190	BRASSINOSTEROID-6-OXIDASE 2 (BR6) CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE	Encodes a cyto 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159	3.63 3.63 3.63	intron five_prime_UTR intergenic
AT4G23190 AT4G31820	BRASSINOSTEROID-6-OXIDASE 2 (BR6) CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP)	Encodes a cytoi 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of the 4_15393075	3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron
AT4G23190 AT4G31820 AT3G13060	BRASSINOSTEROID-6-OXIDASE 2 (BR6) CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI	Encodes a cytoi 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of the 4_15393075 evolutionarily cc 3_4180338	3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460	BRASSINOSTEROID-6-OXIDASE 2 (BR6) CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1)	Encodes a cytoi 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thi 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478	3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080	BRASSINOSTEROID-6-OXIDASE 2 (BR6I CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4)	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putatir 4_12138159 A member of thr 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842	3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680	BRASSINOSTEROID-6-OXIDASE 2 (BR6: CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14)	Encodes a cytoi 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thi 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (II 2_18108193	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130	BRASSINOSTEROID-6-OXIDASE 2 (BR6) CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IGD14) LACCASE 2 (LAC2)	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cz 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (I) 2_18108193 putative laccase 2_12525667	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G37555	BRASSINOSTEROID-6-OXIDASE 2 (BR6I CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putatir 4_12138159 A member of thr 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (Ir 2_18108193) putative laccase 2_12525667 Potential natura 2_15757612	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G37555 AT1G10640	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na	Encodes a cytoi 3_11812870 Encodes a rece 4_12138159 Encodes putati 4_12138159 A member of thi 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (II 2_18108193 putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter promoter exon exon proximal promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G37555 AT1G10640 AT4G21910	BRASSINOSTEROID-6-OXIDASE 2 (BR6/CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of the 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (II 2_521842 IQ-domain 14 (II 2_521667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter promoter exon exon proximal promoter downstream
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G37555 AT1G10640 AT4G21910 AT4G21903	BRASSINOSTEROID-6-OXIDASE 2 (BR6I CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (Ir 2_18108192) putative laccase 2_12526667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream proximal promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G29130 AT4G21910 AT4G21910 AT4G21903 AT2G23650	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na	Encodes a cytoi 3_11812870 Encodes a rece 4_12138159 Encodes putati 4_12138159 A member of thi 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(It 2_521842 IQ-domain 14 (Ir 2_18108193 putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 pre-IRNA; tRNA 2_10059437	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream proximal promoter downstream
AT4G23190 AT4G31820 AT3G313060 AT4G34460 AT2G02080 AT2G29130 AT2G37555 AT1G10640 AT4G21903 AT4G21903 AT2G23650 AT3G14800	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of the 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (I) 2_18108193 putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 me-tRNA; tRNA 2_10059437 transposable els 3_4970325	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream proximal promoter downstream promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G29130 AT4G21910 AT4G21903 AT4G21903 AT3G14800 AT5G04390	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(IE 2_521842 IQ-domain 14 (lr 2_18108193 putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 pre-tRNA; tRNA 2_10059437 transposable eli 3_4970325 C2H2-type zinc 5_1240585	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream proximal promoter downstream promoter downstream
AT4G23190 AT4G31820 AT3G313060 AT4G34460 AT2G02080 AT2G29130 AT2G37555 AT1G10640 AT4G21903 AT4G21903 AT2G23650 AT3G14800	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putatir 4_12138159 A member of thr 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (Ir 2_18108193) putative laccase 2_12525667 Potential natura 2_15757612 Pectin Iyase-like 1_3519132 MATE efflux fan 4_11625225 pre-IRNA; tRNA 2_10059437 transposable eli 3_4970325 C2H2-type zinc 5_1240585 Pseudogene of 5_22706079	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream proximal promoter downstream promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G37555 AT1G10640 AT4G21903 AT2G23650 AT3G14800 AT5G56061	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 Encodes putativ 4_12138159 A member of the 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (II 2_521842 IQ-domain 14 (II 2_521840) Encodes 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 C2H2-type zinc 5_1240585 Pseudogene of 5_22706079 basic helix-loop 5_23154224	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream promoter downstream promoter downstream promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G29130 AT4G21903 AT4G21903 AT3G23650 AT3G14800 AT5G604390 AT5G56061 AT5G57150	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (EMP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na na na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(IE 2_521842 IQ-domain 14 (lr 2_521842 IQ-domain 14 (lr 2_18108193 putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 pre-tRNA; tRNA 2_10059437 transposable eli 3_4970325 C2H2-type zinc 5_1240585 Pseudogene of 5_22706079 basic helix-loop 5_23154224 NAC domain co 5_1240585	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream proximal promoter downstream promoter downstream promoter downstream promoter intron
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G43680 AT2G29130 AT2G37555 AT1G10640 AT4G21910 AT4G21910 AT4G21960 AT5G04390 AT5G04390 AT5G56061 AT5G56061 AT5G04400	BRASSINOSTEROID-6-OXIDASE 2 (BR6I CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (Ir 2_18108193 putative laccase 2_12525667 Potential natura 2_15757612 Pectin Iyase-like 1_3519132 MATE efflux fan 4_111625225 pre-tRNA; tRNA 2_10059437 transposable el 3_4970325 CZH2-type zinc 5_1240585 Pseudogene of 5_22706079 basic helix-loop 5_23154224 NAC domain co 5_1240585 serine carboxyp 4_15003066	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream proximal promoter downstream promoter downstream promoter intron proximal promoter
AT4G23190 AT4G31820 AT3G13060 AT3G13060 AT4G34460 AT2G202080 AT2G29130 AT2G29130 AT2G29130 AT4G21903 AT4G21903 AT3G23650 AT3G14800 AT5G56061 AT5G57150 AT5G504400 AT4G30810	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na na na na na na na na na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (Ir 2_18108193 putative laccase 2_12525667 Potential natura 2_15757612 Pectin Iyase-like 1_3519132 MATE efflux fan 4_111625225 pre-tRNA; tRNA 2_10059437 transposable el 3_4970325 CZH2-type zinc 5_1240585 Pseudogene of 5_22706079 basic helix-loop 5_23154224 NAC domain co 5_1240585 serine carboxyp 4_15003066	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream promoter downstream promoter intron proximal promoter intron proximal promoter promoter promoter
AT4G23190 AT4G31820 AT3G13060 AT3G13060 AT4G34460 AT2G02080 AT2G29130 AT2G29130 AT4G21903 AT4G21903 AT3G14800 AT5G504390 AT5G56061 AT5G57150 AT3G04400 AT4G30810 AT4G30810 AT1G60940	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na	Encodes a cytor 3_11812870 Encodes a rore 4_12138159 Encodes putativ 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(IE 2_521842 IQ-domain 14 (Ir 2_521842 IQ-domain 14 (Ir 2_18108193 putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 pre-tRNA; tRNA 2_10059437 transposable eli 3_4970325 C2H2-type zinc 5_1240585 Pseudogene of 5_22706079 basic helix-loop 5_23154224 NAC domain co 5_1240585 serine carboxyp 4_15003066 encodes a mem 1_22442311 Encodes a sphil 4_11459465	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon proximal promoter downstream proximal promoter downstream promoter downstream promoter intron proximal promoter promoter intron proximal promoter promoter promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G37555 AT1G10640 AT4G21910 AT4G21910 AT4G21960 AT5G04390 AT5G04390 AT5G04400 AT5G04400 AT4G30810 AT4G08410 AT4G0840 AT4G0840 AT4G0840 AT4G21540	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na na na na na na na na na	Encodes a cytor 3_11812870 Encodes a rore 4_12138159 Encodes putativ 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (Ir 2_521842 IQ-domain 14 (Ir 2_18108193 putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 pre-tRNA; tRNA 2_10059437 transposable eli 3_4970325 C2H2-type zinc 5_1240585 Pseudogene of 5_22706079 basic helix-loop 5_23154224 NAC domain co 5_1240585 serine carboxyp 4_15003066 encodes a mem 1_22442311 Encodes a sphil 4_11459465	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter five_prime_UTR promoter exon exon proximal promoter downstream proximal promoter downstream promoter downstream promoter intron proximal promoter promoter promoter promoter promoter promoter promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G237555 AT1G10640 AT4G21910 AT4G21903 AT2G23650 AT3G14800 AT5G56061 AT5G56061 AT5G56061 AT5G560440 AT4G30810 AT4G6940 AT4G21540 AT4G21540 AT2G28520	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na na na na na NAC DOMAIN CONTAINING PROTEIN 77 SERINE CARBOXYPEPTIDASE-LIKE 29 (SHF1-RELATED PROTEIN KINASE 2.10 (SPHINGOSINE KINASE 1 (SPHK1) VACUOLAR PROTON ATPASE A1 (VHA-BMBRYO DEFECTIVE 2761 (EMB2761) EVOLUTIONARILY CONSERVED C-TERI	Encodes a cytor 3_11812870 Encodes a rore 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(IE 2_521842 IQ-domain 14 (It 2_521842 IQ-domain 14 (It 2_18108193) putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 pre-IRNA; IRNA 2_10059437 transposable elt 3_4970325 C2H2-type zinc 5_1240585 Pseudogene of 5_22706079 basic helix-loop 5_23154224 NAC domain co 5_1240585 serine carboxyp 4_15003066 encodes a mem 1_22442311 Encodes a sphil 4_11459465 Vacuolar proton 2_12205811 Encodes a dual 2_1701416 evolutionarily cc 5_24559872	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter five_prime_UTR promoter exon exon proximal promoter downstream proximal promoter downstream promoter downstream promoter promoter intron proximal promoter promoter promoter promoter promoter intergenic promoter five_prime_UTR
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G202080 AT2G43680 AT2G29130 AT2G29130 AT4G21903 AT4G21903 AT3G3650 AT3G14800 AT5G56061 AT5G504400 AT4G30810 AT4G30810 AT4G21540 AT4G21540 AT2G28520 AT2G04842 AT2G04842 AT2G04824 AT2G04842 AT2G04842 AT2G04842	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE EVSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na na na na na na na na na	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (II 2_18108193) putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 pre-1RNA; tRNA 2_10059437 transposable elv 3_4970325 C2H2-type zinc 5_1240585 Pseudogene of 5_22706079 basic helix-loop 5_23154224 NAC domain co 5_1240585 serine carboxyp 4_15003066 encodes a mem 1_22442311 Encodes a sphii 4_111459465 Vacuolar proton 2_12205811 Encodes a dual 2_17014116 evolutionarily cc 5_24559872 Zinc finger hom 2_681439	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter promoter exon exon exon proximal promoter downstream proximal promoter downstream promoter intron proximal promoter intron proximal promoter intron proximal promoter intron proximal promoter
AT4G23190 AT4G31820 AT3G13060 AT4G34460 AT2G02080 AT2G43680 AT2G29130 AT2G237555 AT1G10640 AT4G21910 AT4G21903 AT2G23650 AT3G14800 AT5G56061 AT5G56061 AT5G56061 AT5G560440 AT4G30810 AT4G6940 AT4G21540 AT4G21540 AT2G28520	BRASSINOSTEROID-6-OXIDASE 2 (BR6i CYSTEINE-RICH RLK (RECEPTOR-LIKE CYSTEINE-RICH RLK (RECEPTOR-LIKE ENHANCER OF PINOID (ENP) EVOLUTIONARILY CONSERVED C-TERI GTP BINDING PROTEIN BETA 1 (AGB1) INDETERMINATE(ID)-DOMAIN 4 (IDD4) IQ-DOMAIN 14 (IQD14) LACCASE 2 (LAC2) na na na na na na na na na NAC DOMAIN CONTAINING PROTEIN 77 SERINE CARBOXYPEPTIDASE-LIKE 29 (SHF1-RELATED PROTEIN KINASE 2.10 (SPHINGOSINE KINASE 1 (SPHK1) VACUOLAR PROTON ATPASE A1 (VHA-BMBRYO DEFECTIVE 2761 (EMB2761) EVOLUTIONARILY CONSERVED C-TERI	Encodes a cytor 3_11812870 Encodes a rece 4_12138159 Encodes putativ 4_12138159 A member of thv 4_15393075 evolutionarily cc 3_4180338 Encodes the he 4_16479478 indeterminate(II 2_521842 IQ-domain 14 (II 2_18108193) putative laccase 2_12525667 Potential natura 2_15757612 Pectin lyase-like 1_3519132 MATE efflux fan 4_11625225 MATE efflux fan 4_11625225 pre-1RNA; tRNA 2_10059437 transposable elv 3_4970325 C2H2-type zinc 5_1240585 Pseudogene of 5_22706079 basic helix-loop 5_23154224 NAC domain co 5_1240585 serine carboxyp 4_15003066 encodes a mem 1_22442311 Encodes a sphii 4_111459465 Vacuolar proton 2_12205811 Encodes a dual 2_17014116 evolutionarily cc 5_24559872 Zinc finger hom 2_681439	3.63 3.63 3.63 3.63 3.63 3.63 3.63 3.63	intron five_prime_UTR intergenic intron promoter five_prime_UTR promoter five_prime_UTR promoter exon exon proximal promoter downstream proximal promoter downstream promoter downstream promoter promoter intron proximal promoter promoter promoter promoter promoter intergenic promoter five_prime_UTR

AT4G32551	LEUNIC (LUC)	LEUNIG regulat 4 15707190	3.62	promotor
AT2G47190	LEUNIG (LUG) MYB DOMAIN PROTEIN 2 (MYB2)	Encodes a MYE 2_19377308	3.62	promoter three_prime_UTR
AT3G23910	na	BEST Arabidop: 3_8640338	3.62	proximal promoter
AT1G07940	na	GTP binding Ek 1_2462220	3.62	intergenic
AT2G20050	na	protein serine/th 2 8656435	3.62	proximal promoter
AT1G24350	na	Acid phosphata: 1_8640639	3.62	five_prime_UTR
AT1G24360	na	NAD(P)-binding 1_8640639	3.62	five_prime_UTR
AT2G02600	na	pre-tRNA; tRNA 2_706881	3.62	downstream
AT2G23090	na	Uncharacterise(2_9830430	3.62	promoter
AT3G22810	na	FUNCTIONS IN 3_8067823	3.62	proximal promoter
AT3G59660	na	C2 domain-cont 3_22038736	3.62	promoter
AT3G60805	na	pre-tRNA; tRNA 3_22470393	3.62	promoter
AT4G22666	na	Bifunctional inhi 4_11918002	3.62	downstream
AT5G01670 AT5G65030	na na	NAD(P)-linked c 5_251611 unknown proteir 5_25976869	3.62 3.62	promoter proximal promoter
AT3G03030	NINE-CIS-EPOXYCAROTENOID DIOXYG		3.62	intergenic
AT1G30100	NINE-CIS-EPOXYCAROTENOID DIOXYG	_	3.62	intergenic
AT1G30100	NITRATE REDUCTASE 1 (NIA1)	Encodes the cyl 1_29239495	3.62	promoter
AT1G80770	PIGMENT DEFECTIVE 318 (PDE318)	pigment defectiv 1_30355035	3.62	promoter
AT2G22190	TREHALOSE-6-PHOSPHATE PHOSPHA		3.62	promoter
AT5G05860	UDP-GLUCOSYL TRANSFERASE 76C2 (Encodes a cytol 5_1765374	3.62	promoter
AT3G11730	(ATFP8)	Encodes a merr 3_3708693	3.61	intergenic
AT4G22780	ACT DOMAIN REPEAT 7 (ACR7)	Member of a far 4_11968539	3.61	three_prime_UTR
AT4G26570	CALCINEURIN B-LIKE 3 (CBL3)	member of AtCE 4_13411249	3.61	promoter
AT3G10600	CATIONIC AMINO ACID TRANSPORTER		3.61	intron
AT1G66160	CYS, MET, PRO, AND GLY PROTEIN 1 (C		3.61	proximal promoter
AT4G33240	FORMS APLOID AND BINUCLEATE CELI		3.61	proximal promoter
AT1G15550 AT5G18170	GIBBERELLIN 3-OXIDASE 1 (GA3OX1)		3.61	exon
AT1G79530	GLUTAMATE DEHYDROGENASE 1 (GDF GLYCERALDEHYDE-3-PHOSPHATE DEF		3.61	five_prime_UTR
AT4G03190	GRR1-LIKE PROTEIN 1 (GRH1)	Encodes one of 1_29919626 Encodes an F b 4_1407272	3.61 3.61	promoter
AT3G61590	HAWAIIAN SKIRT (HWS)	HAWAIIAN SKII 3 22794416	3.61	promoter downstream
AT3G61890	HOMEOBOX 12 (HB-12)	Encodes a hom 3_22915460	3.61	promoter
AT2G46680	HOMEOBOX 7 (HB-7)	encodes a putal 2_19168856	3.61	proximal promoter
AT1G06148	na	Unknown gene 1 1877777	3.61	promoter
AT5G19060	na	CONTAINS Inte 5 6372653	3.61	promoter
AT2G15170	na	Plant basic secr 2_6587443	3.61	promoter
AT1G49520	na	SWIB complex I 1 18328984	3.61	proximal promoter
AT1G76460	na	RNA-binding (R 1_28689229	3.61	promoter
AT1G76720	na	eukaryotic trans 1_28800428	3.61	promoter
AT2G01330	na	nucleotide bindi 2_160966	3.61	promoter
AT1G22403	na	other RNA 1_7910690	3.61	proximal promoter
AT2G43370	na	RNA-binding (R 2_18013330	3.61	promoter
AT3G03960	na	TCP-1/cpn60 cl 3_1024110	3.61	promoter
AT3G11720	na	Polyketide cycla 3_3708693	3.61	intron
AT3G15260	na	Protein phospha 3_5142821	3.61	downstream
AT3G14830	na	unknown proteir 3_4982557	3.61	promoter
AT5G05140	na na	Transcription el 5_1519763	3.61	promoter
AT5G26990 AT4G28530	NAC DOMAIN CONTAINING PROTEIN 74	Drought-respon 5_9490919	3.61 3.61	promoter intron
AT4G39390	NUCLEOTIDE SUGAR TRANSPORTER-		3.61	proximal promoter
AT4G28660	PHOTOSYSTEM II REACTION CENTER F		3.61	promoter
AT3G61600	POZ/BTB CONTAININ G-PROTEIN 1 (PO		3.61	proximal promoter
AT5G13170	SENESCENCE-ASSOCIATED GENE 29 (3.61	intergenic
AT4G25520	SEUSS-LIKE 1 (SLK1)	SEUSS-like 1 (\$ 4_13036568	3.61	promoter
AT3G15270	SQUAMOSA PROMOTER BINDING PRO		3.61	proximal promoter
AT3G14350	STRUBBELIG-RECEPTOR FAMILY 7 (SR	STRUBBELIG-r 3_4789358	3.61	proximal promoter
AT5G26980	SYNTAXIN OF PLANTS 41 (SYP41)	member of SYP 5_9490919	3.61	promoter
AT1G66150	TRANSMEMBRANE KINASE 1 (TMK1)	receptor-like tra 1_24634646	3.61	three_prime_UTR
AT5G18680	TUBBY LIKE PROTEIN 11 (TLP11)	Member of TLP 5_6231409	3.61	proximal promoter
AT3G24810	(ICK3)	Kip-related prot 3_9058622	3.6	proximal promoter
AT2G28800	ALBINO 3 (ALB3)	member of Chlo 2_12359371	3.6	promoter
AT3G18980	EIN2 TARGETING PROTEIN1 (ETP1)	EIN2 targeting r 3_6546250	3.6	promoter
AT1G08510 AT2G37380	FATTY ACYL-ACP THIOESTERASES B (I		3.6	promoter
AT2G37360 AT2G02160	MEMBRANE-ASSOCIATED KINASE REG		3.6 3.6	intergenic
AT3G45638	na	CCCH-type zinc 2_556242 Unknown gene 3_16755620	3.6	promoter exon
AT4G05018	na	unknown proteir 4 2572595	3.6	intergenic
AT5G63700	na	zinc ion binding: 5_25497854	3.6	promoter
AT3G11180	na	2-oxoglutarate (3_3504039	3.6	promoter
AT3G62200	na	Putative endon: 3_23025949	3.6	promoter
AT1G30680	na	toprim domain-c 1_10881464	3.6	promoter
AT1G64120	na	pre-tRNA; tRNA 1_23802317	3.6	promoter
AT1G64130	na	Polyketide cycla 1_23802317	3.6	promoter
AT1G79390	na	unknown proteir 1_29864381	3.6	promoter
AT3G18790	na	FUNCTIONS IN 3_6477595	3.6	promoter
AT2G45810	na	DEA(D/H)-box I 2_18859486	3.6	promoter
AT4G27870	na	Vacuolar iron tr: 4_13883105	3.6	downstream
AT4G24805	na	S-adenosyl-L-m 4_12785373	3.6	exon
AT4G27875 AT5G48900	na na	pre-tRNA; tRNA 4_13883105 Pectin lyase-like 5_19826016	3.6 3.6	promoter intron
AT5G46900 AT5G54170	na	Polyketide cycla 5_21987152	3.6	five_prime_UTR
AT4G05020	NAD(P)H DEHYDROGENASE B2 (NDB2)		3.6	promoter
AT4G03020	RECEPTOR-LIKE PROTEIN KINASE 4 (R		3.6	promoter
AT1G79380	RING DOMAIN LIGASE 4 (RGLG4)	Encodes a ubiq 1_29864381	3.6	intergenic
AT5G42820	(U2AF35B)	U2 auxiliary fact 5_17171788	3.59	promoter
AT4G36870	BEL1-LIKE HOMEODOMAIN 2 (BLH2)	Encodes a merr 4_17373064	3.59	intron
AT2G44480	BETA GLUCOSIDASE 17 (BGLU17)	beta glucosidas 2_18358821	3.59	proximal promoter
AT4G36880	CYSTEINE PROTEINASE1 (CP1)	cysteine protein 4_17373064	3.59	intergenic
AT2G46590	DOF AFFECTING GERMINATION 2 (DAG		3.59	proximal promoter
AT3G09350		Encodes one of 3_2870881	3.59	promoter
	FES1A (Fes1A)			
AT1G61800	GLUCOSE-6-PHOSPHATE/PHOSPHATE	glucose6-Phosr 1_22822710	3.59	proximal promoter
AT5G63800	GLUCOSE-6-PHOSPHATE/PHOSPHATE MUCILAGE-MODIFIED 2 (MUM2)	glucose6-Phosr 1_22822710 Involved in muc 5_25531802	3.59 3.59	proximal promoter intron
	GLUCOSE-6-PHOSPHATE/PHOSPHATE	glucose6-Phosr 1_22822710	3.59	proximal promoter

AT1G15600	na	unknown proteir 1 5370095	3.59	three_prime_UTR
AT1G15610	na	unknown proteir 1_5370095	3.59	proximal promoter
AT3G06070	na	unknown proteir 3_1830163	3.59	intergenic
AT2G07000	na	unknown proteir 2 2901851	3.59	downstream
AT1G66345	na	Pentatricopeptic 1_24742641	3.59	intergenic
AT3G13940	na	DNA binding;DN 3_4602556	3.59	promoter
AT3G23880	na	F-box and asso 3 8623387	3.59	promoter
AT3G22550	na	Protein of unknc 3_7992538	3.59	exon
AT5G41580	na	RING/U-box suj 5_16631332	3.59	proximal promoter
AT5G42825	na	unknown proteir 5_17171788	3.59	promoter
AT5G51600	PLEIADE (PLE)	Mutant has defe 5_20964615	3.59	promoter
AT2G36420	TON1 RECRUITING MOTIF 27 (TRM27)	unknown proteir 2_15286234	3.59	promoter
AT3G06060	TSC10A (TSC10A)	Encodes one of 3_1830163	3.59	five_prime_UTR
AT1G10550	XYLOGLUCAN:XYLOGLUCOSYL TRANS		3.59	promoter
AT5G02470	(DPA)	core cell cycle c 5_545007	3.58	promoter
AT4G39660	ALANINE:GLYOXYLATE AMINOTRANSF		3.58	promoter
AT5G66200	ARMADILLO REPEAT ONLY 2 (ARO2)	Armadillo repea 5_26453239	3.58	downstream
AT2G23080	CASEIN KINASE II, ALPHA CHAIN 3 (CKA		3.58	promoter
AT5G19180	E1 C-TERMINAL RELATED 1 (ECR1)	Encodes a subt 5_6452273	3.58	proximal promoter
AT2G41070	ENHANCED EM LEVEL (EEL)	Transcription fa 2 17130296	3.58	promoter
AT1G04370	ETHYLENE-RESPONSIVE ELEMENT BIN		3.58	proximal promoter
AT5G66190	FERREDOXIN-NADP(+)-OXIDOREDUCT		3.58	promoter
AT4G23100	GLUTAMATE-CYSTEINE LIGASE (GSH1		3.58	intron
AT1G51950	INDOLE-3-ACETIC ACID INDUCIBLE 18 (3.58	promoter
AT1G11735	MICRORNA171B (MIR171B)	Encodes a micr 1_3960369	3.58	intergenic
AT3G48201	MICRORNA861A (MIR861A)	Encodes a micr 3_17837985	3.58	downstream
AT1G71350	na	eukaryotic trans 1_26891397	3.58	promoter
AT3G07030	na	Alba DNA/RNA- 3_2225554	3.58	promoter
AT3G53370	na	S1FA-like DNA- 3 19788912	3.58	•
AT3G53380	na	Concanavalin A 3 19788912	3.58	promoter downstream
AT5G33380	na na	Ubiquitin-like su 5_3522442	3.58	proximal promoter
AT1G02290	na	unknown proteir 1_453064	3.58	
AT1G02230 AT1G12120	na na	Plant protein of 1_4117918	3.58	promoter promoter
AT1G28375	na	unknown proteir 1_9960358	3.58	proximal promoter
AT2G23070 AT1G67350	na	Protein kinase s 2_9826956	3.58	promoter
	na	unknown proteir 1_25233737	3.58	proximal promoter
AT3G48200	na	unknown proteir 3_17837985	3.58	promoter
AT4G23090	na	unknown proteir 4_12102873	3.58	proximal promoter
AT5G01910	na	unknown proteir 5_357932	3.58	three_prime_UTR
AT5G06050	na	Putative methyll 5_1823035	3.58	intron
AT5G06060	na	NAD(P)-binding 5_1823035	3.58	intergenic
AT5G53205	na	unknown proteir 5_21585457	3.58	downstream
AT5G03240	POLYUBIQUITIN 3 (UBQ3)	encodes ubiquit 5_773454	3.58	intron
AT5G24470	PSEUDO-RESPONSE REGULATOR 5 (P		3.58	exon
AT3G07040	RESISTANCE TO P. SYRINGAE PV MAC		3.58	intergenic
AT2G20310	RPM1 INTERACTING PROTEIN 13 (RIN1		3.58	proximal promoter
AT1G62180	5'ADENYLYLPHOSPHOSULFATE REDU		3.57	promoter
AT1G24657	na	unknown pseud 1_8739468	3.57	proximal promoter
AT1G58235	na	unknown proteir 1_21579865	3.57	three_prime_UTR
AT3G49950	na	GRAS family tra 3_18518502	3.57	intergenic
AT1G62181	na	unknown proteir 1_22977730	3.57	exon
AT1G21010	na	unknown proteir 1_7344768	3.57	proximal promoter
AT4G03340	na	Core-2/I-branch 4_1470258	3.57	promoter
AT1G16960	na	Ubiquitin domaii 1_5799824	3.57	promoter
AT1G70185	na	other RNA 1_26429864	3.57	exon
AT1G70949	na	unknown proteir 1_26752489	3.57	exon
AT1G76810	na	eukaryotic trans 1_28836584	3.57	five_prime_UTR
AT2G03750	na	P-loop containir 2_1149243	3.57	promoter
AT3G25660	na	Amidase family 3_9343620	3.57	proximal promoter
AT3G23840	na	HXXXD-type ac 3_8611859	3.57	exon
AT4G32920	na	glycine-rich prot 4_15895256	3.57	exon
AT4G23000	na	Calcineurin-like 4_12053652	3.57	proximal promoter
AT4G30970	na	unknown proteir 4_15069121	3.57	downstream
AT4G36520	na	Chaperone Dna 4_17236132	3.57	proximal promoter
AT4G36840	na	Galactose oxida 4_17351290	3.57	promoter
AT5G49665	na	Zinc finger (C3F 5_20167162	3.57	exon
AT2G06050	OXOPHYTODIENOATE-REDUCTASE 3 (3.57	five_prime_UTR
AT2G18660	PLANT NATRIURETIC PEPTIDE A (PNP-		3.57	promoter
AT2G16850	PLASMA MEMBRANE INTRINSIC PROTE		3.57	promoter
AT1G16470	PROTEASOME SUBUNIT PAB1 (PAB1)	Encodes 20S pi 1_5622720	3.57	promoter
AT1G16460	RHODANESE HOMOLOGUE 2 (RDH2)	encodes a cytor 1_5622720	3.57	promoter
AT4G30960	SOS3-INTERACTING PROTEIN 3 (SIP3)		3.57	downstream
AT2G03760	SULPHOTRANSFERASE 12 (SOT12)	Encodes a bras 2_1149243	3.57	downstream
AT1G75500	WALLS ARE THIN 1 (WAT1)	An Arabidopsis 1_28341702	3.57	proximal promoter
AT2G25080	GLUTATHIONE PEROXIDASE 1 (GPX1)		3.56	proximal promoter
AT4G01950	GLYCEROL-3-PHOSPHATE ACYLTRANS		3.56	proximal promoter
AT1G22990	HEAVY METAL ASSOCIATED ISOPREN		3.56	proximal promoter
AT4G14550	INDOLE-3-ACETIC ACID INDUCIBLE 14 (3.56	three_prime_UTR
AT3G45640	MITOGEN-ACTIVATED PROTEIN KINASI		3.56	downstream
AT3G10330	na	Cyclin-like famil: 3_3199600 F-box/RNI-like/F 5 7553621	3.56	promoter
AT5G22730 AT4G11860	na	F-box/RNI-like/F5_7553621 FUNCTIONS IN 4 7139550	3.56	promoter
	na		3.56	proximal promoter
AT5G24990	na	Protein of unkno 5_8610526	3.56	promoter
AT1G05950	na	unknown proteir 1_1807735	3.56	promoter
AT1G17490	na	unknown proteir 1_6008484	3.56	promoter
AT1G27120	na	Galactosyltrans 1_9420479	3.56	proximal promoter
AT1G05960	na	ARM repeat sur 1_1807735	3.56	intergenic
AT2G40130	na	Double Clp-N m 2_16764807	3.56	proximal promoter
AT4G14548	na	other RNA 4_8347874	3.56	downstream
AT4G39140	na	RING/U-box sui 4_18232096	3.56	promoter
AT4G34272	na	This gene encor 4_16406398	3.56	downstream
AT3G25882	NIM1-INTERACTING 2 (NIMIN-2)	encodes a kinas 3_9472550	3.56	proximal promoter
AT3G45650	NITRATE EXCRETION TRANSPORTER1		3.56	promoter
AT5G01730	SCAR FAMILY PROTEIN 4 (SCAR4)	Encodes a merr 5_277724	3.56	promoter

AT3G20630	UBIQUITIN-SPECIFIC PROTEASE 14 (UE	Encodes a ubiq 3_7208562	3.56	promoter
AT5G14070	(ROXY2)	Encodes glutare 5_4542774	3.55	intergenic
AT5G53190	(SWEET3)	Nodulin MtN3 fa 5_21572356	3.55	three_prime_UTR
AT2G30970	ASPARTATE AMINOTRANSFERASE 1 (A		3.55	promoter
AT4G00140	EMBRYO SAC DEVELOPMENT ARREST		3.55	proximal promoter
AT3G23400	FIBRILLIN 4 (FIB4)	Encodes FIBRIL 3_8378352	3.55	promoter
AT1G72520	LIPOXYGENASE 4 (LOX4)	PLAT/LH2 dom: 1_27309503	3.55	intron
AT3G55850 AT3G55840	LONG AFTER FAR-RED 3 (LAF3)	Encodes a prod 3_20721583	3.55	downstream
AT1G11230	na na	Hs1pro-1 protei 3_20721583 Protein of unknr 1_3764824	3.55 3.55	proximal promoter promoter
AT1G56300	na	Chaperone Dna 1_21079149	3.55	exon
AT3G29170	na	Eukaryotic prote 3_11139133	3.55	proximal promoter
AT4G01400	na	FUNCTIONS IN 4_577878	3.55	proximal promoter
AT4G01410	na	Late embryoger 4_577878	3.55	promoter
AT1G03740	na	Protein kinase s 1_937712	3.55	intergenic
AT1G23100	na	GroES-like fami 1_8193606	3.55	proximal promoter
AT1G55840	na	Sec14p-like phc 1_20873030	3.55	proximal promoter
AT1G61790	na	Oligosaccharyltı 1_22816513	3.55	intergenic
AT2G38995	na	O-acyltransfera: 2_16281673	3.55	promoter
AT3G01300	na na	Protein kinase s 3_93570	3.55	five_prime_UTR
AT2G27090 AT2G30960	• • • • • • • • • • • • • • • • • • • •	Protein of unknc 2_11572441	3.55 3.55	proximal promoter
AT3G01310	na na	unknown proteir 2_13178407 Phosphoglycera 3_93570	3.55	promoter intergenic
AT3G07350	na	Protein of unknc 3_2350395	3.55	intergenic
AT3G51130	na	unknown proteir 3_18994121	3.55	promoter
AT4G13040	na	Integrase-type [4_7613333	3.55	five_prime_UTR
AT4G25707	na	This gene encor 4_13096989	3.55	intergenic
AT4G26240	na	unknown proteir 4_13289086	3.55	promoter
AT4G36130	na	Ribosomal prote 4_17097482	3.55	promoter
AT5G53180	POLYPYRIMIDINE TRACT-BINDING PRO		3.55	promoter
AT1G07530	SCARECROW-LIKE 14 (SCL14)	Encodes a merr 1_2316444	3.55	five_prime_UTR
AT2G27100	SERRATE (SE)	Identified as a le 2_11572441	3.55	promoter
AT1G03750	SWITCH 2 (SWI2)	switch 2 (SWI2) 1_937712	3.55	promoter
AT2G27400	TRANS-ACTING SIRNA1A (TAS1A)	Trans-acting siF 2_11722521	3.55	promoter
AT1G09940 AT1G32640	(HEMA2) (MYC2)	Encodes glutarr 1_3239452 Encodes a MYC 1_11804382	3.54 3.54	five_prime_UTR intergenic
AT3G21160	ALPHA-MANNOSIDASE 2 (MNS2)	Encodes an alpl 3_7412751	3.54	intergenic
AT3G21150	B-BOX DOMAIN PROTEIN 32 (BBX32)	Encodes a prote 3 7412751	3.54	exon
AT3G07370	CARBOXYL TERMINUS OF HSC70-INTE		3.54	five_prime_UTR
AT1G48110	EVOLUTIONARILY CONSERVED C-TERI		3.54	intergenic
AT3G09530	EXOCYST SUBUNIT EXO70 FAMILY PRO	A member of E) 3_2928412	3.54	downstream
AT5G47040	LON PROTEASE 2 (LON2)	Encodes a merr 5_19092810	3.54	intergenic
AT3G05790	LON PROTEASE 4 (LON4)	Encodes a merr 3_1725445	3.54	promoter
AT2G22910	N-ACETYL-L-GLUTAMATE SYNTHASE 1		3.54	promoter
AT3G63052	na	This gene enco 3_23298832	3.54	downstream
AT2G39210	na	Major facilitator 2_16366000	3.54	downstream
AT1G48100	na	Pectin lyase-like 1_17769703	3.54	three_prime_UTR
AT5G18200 AT2G22905	na na	encodes an ade 5_6015055 Expressed prote 2_9749799	3.54 3.54	promoter intergenic
AT3G21140	na	Pyridoxamine 5' 3_7412751	3.54	proximal promoter
AT1G09575	na	Protein of unkno 1_3100854	3.54	intergenic
AT2G40450	na	BTB/POZ doma 2_16894281	3.54	proximal promoter
AT3G07340	na	basic helix-loop 3_2344557	3.54	proximal promoter
AT2G32090	na	Lactoylglutathio 2_13644287	3.54	promoter
AT2G41890	na	curculin-like (ma 2_17477619	3.54	intergenic
AT3G21690	na	MATE efflux fan 3_7638646	3.54	promoter
AT3G62280	na	GDSL-like Lipas 3_23050066	3.54	intron
AT4G22790	na	MATE efflux fan 4_11976808	3.54	promoter
AT5G47030	na	Encodes the mil 5_19092810	3.54	intergenic
AT5G47510 AT1G09570	na PHYTOCHROME A (PHYA)	Sec14p-like phc 5_19274855 Light-labile cyto 1 3100854	3.54 3.54	promoter promoter
AT2G32080	PURIN-RICH ALPHA 1 (PUR ALPHA-1)	similar to the co 2_13644287	3.54	promoter
AT1G14360	UDP-GALACTOSE TRANSPORTER 3 (UT		3.54	promoter
AT2G20825	ULTRAPETALA 2 (ULT2)	ULTRAPETALA 2_8967447	3.54	proximal promoter
AT4G18170	WRKY DNA-BINDING PROTEIN 28 (WRK		3.54	intergenic
AT5G40395	(U6acat)	U6acat; snRNA 5_16166275	3.53	exon
AT2G31200	ACTIN DEPOLYMERIZING FACTOR 6 (AI		3.53	promoter
AT1G05610	ADP-GLUCOSE PYROPHOSPHORYLASI		3.53	promoter
AT2G45880	BETA-AMYLASE 7 (BAM7)	Encodes a beta 2_18878469	3.53	downstream
AT1G52927	BRI1-LIKE 2 (BRL2)	Encodes a leuci 2_439318	3.53	intergenic
AT1G52827 AT1G20450	CADMIUM TOLERANCE 1 (CDT1) EARLY RESPONSIVE TO DEHYDRATION	Cysteine-rich pr 1_19672005 Encodes a gent 1_7089188	3.53 3.53	promoter five_prime_UTR
AT1G20450 AT1G34550	EMBRYO DEFECTIVE 2756 (EMB2756)	EMBRYO DEFE 1_12651063	3.53	intron
AT4G13494	MICRORNA863A (MIR863A)	Encodes a micr 4_7847019	3.53	downstream
AT3G16010	na	Pentatricopeptic 3_5433948	3.53	promoter
AT4G14730	na	Bax inhibitor-1 f 4_8448309	3.53	promoter
AT3G17110	na	pseudogene, gl 3_5837288	3.53	proximal promoter
AT5G06370	na	NC domain-con 5_1948610	3.53	five_prime_UTR
AT2G45870	no.	Bestrophin-like 2_18878469	3.53	intergenic
	na		3.53	promoter
AT1G19020	na	unknown proteir 1_6568024		
AT1G72270	na na	CONTAINS Inte 1_27211240	3.53	promoter
AT1G72270 AT1G74320	na na na	CONTAINS Inte 1_27211240 encodes a choli 1_27940782	3.53 3.53	five_prime_UTR
AT1G72270 AT1G74320 AT1G76520	na na na na	CONTAINS Inte 1_27211240 encodes a choli 1_27940782 Auxin efflux carı 1_28715194	3.53 3.53 3.53	five_prime_UTR five_prime_UTR
AT1G72270 AT1G74320 AT1G76520 AT2G01220	na na na na na	CONTAINS Inte 1_27211240 encodes a choli 1_27940782 Auxin efflux carı 1_28715194 Nucleotidylyl tra 2_123123	3.53 3.53 3.53 3.53	five_prime_UTR five_prime_UTR promoter
AT1G72270 AT1G74320 AT1G76520 AT2G01220 AT2G21220	na na na na na na	CONTAINS Inte 1_27211240 encodes a choli 1_27940782 Auxin efflux carı 1_28715194 Nucleotidylyl tra 2_123123 SAUR-like auxir 2_9088047	3.53 3.53 3.53 3.53 3.53	five_prime_UTR five_prime_UTR promoter proximal promoter
AT1G72270 AT1G74320 AT1G76520 AT2G01220 AT2G21220 AT3G13120	na na na na na	CONTAINS Inte 1_27211240 encodes a choli 1_27940782 Auxin efflux carl 1_28715194 Nucleotidylyl tra 2_123123 SAUR-like auxir 2_9088047 Ribosomal prote 3_4221823	3.53 3.53 3.53 3.53 3.53 3.53	five_prime_UTR five_prime_UTR promoter proximal promoter promoter
AT1G72270 AT1G74320 AT1G76520 AT2G01220 AT2G21220	na na na na na na na	CONTAINS Inte 1_27211240 encodes a choli 1_27940782 Auxin efflux carı 1_28715194 Nucleotidylyl tra 2_123123 SAUR-like auxir 2_9088047	3.53 3.53 3.53 3.53 3.53	five_prime_UTR five_prime_UTR promoter proximal promoter
AT1G72270 AT1G74320 AT1G76520 AT2G01220 AT2G21220 AT3G13120 AT3G50685	na na na na na na na na	CONTAINS Inte 1_27211240 encodes a choil 1_27940782 Auxin efflux carı 1_28715194 Nucleotidylyl tra 2_123123 SAUR-like auxir 2_9088047 Ribosomal prote 3_4221823 unknown proteir 3_18834893	3.53 3.53 3.53 3.53 3.53 3.53 3.53	five_prime_UTR five_prime_UTR promoter proximal promoter promoter promoter
AT1G72270 AT1G74320 AT1G76520 AT2G01220 AT2G21220 AT3G13120 AT3G50685 AT3G52527 AT3G50690 AT4G21910	na na na na na na na na	CONTAINS Inte 1_27211240 encodes a choil 1_27940782 Auxin efflux car 1_28715194 Nucleotidylyl tra 2_123123 SAUR-like auxir 2_9088047 Ribosomal prote 3_12834893 transposable els 3_19478106 Leucine-rich rer 3_18834893 MATE efflux fan 4_11628834	3.53 3.53 3.53 3.53 3.53 3.53 3.53 3.53	five_prime_UTR five_prime_UTR promoter proximal promoter promoter promoter exon downstream intron
AT1G72270 AT1G74320 AT1G76520 AT2G01220 AT2G21220 AT3G513120 AT3G55688 AT3G52527 AT3G50690 AT4G21910 AT4G17900	na n	CONTAINS Inte 1_27211240 encodes a choil 1_27940782 Auxin efflux carl 1_28715194 Nucleotidylyl tra 2_123123 SAUR-like auxir 2_9088047 Ribosomal prote 3_4221823 unknown proteir 3_18834893 transposable els 3_19478106 Leucine-rich rer 3_18834893 MATE efflux fan 4_11628834 PLATZ transcrif 4_9943501	3.53 3.53 3.53 3.53 3.53 3.53 3.53 3.53	five_prime_UTR five_prime_UTR promoter proximal promoter promoter promoter exon downstream intron proximal promoter
AT1G72270 AT1G74320 AT1G76520 AT2G01220 AT2G21220 AT3G13120 AT3G50685 AT3G50685 AT3G50690 AT4G21910 AT4G17900 AT5G19090	na n	CONTAINS Inte 1_27211240 encodes a choil 1_27940782 Auxin efflux carı 1_28715194 Nucleotidyly tra 2_123123 SAUR-like auxir 2_9088047 Ribosomal prote 3_4221823 unknown proteir 3_18834893 transposable els 3_19478106 Leucine-rich rer 3_18834893 MATE efflux fan 4_11628834 PLATZ transcrir 4_9943501 Heavy metal tra 5_6387597	3.53 3.53 3.53 3.53 3.53 3.53 3.53 3.53	five_prime_UTR five_prime_UTR promoter proximal promoter promoter promoter exon downstream intron proximal promoter five_prime_UTR
AT1G72270 AT1G74320 AT1G76520 AT2G01220 AT2G21220 AT3G13120 AT3G50685 AT3G52527 AT3G50690 AT4G21910 AT4G17900	na n	CONTAINS Inte 1_27211240 encodes a choil 1_27940782 Auxin efflux carl 1_28715194 Nucleotidylyl tra 2_123123 SAUR-like auxir 2_9088047 Ribosomal prote 3_4221823 unknown proteir 3_18834893 transposable els 3_19478106 Leucine-rich rer 3_18834893 MATE efflux fan 4_11628834 PLATZ transcrif 4_9943501	3.53 3.53 3.53 3.53 3.53 3.53 3.53 3.53	five_prime_UTR five_prime_UTR promoter proximal promoter promoter promoter exon downstream intron proximal promoter

AT3G04070	NAC DOMAIN CONTAINING PROTEIN 47	NAC domain co 3 1063975	3.53	proximal promoter
AT5G08740	NAD(P)H DEHYDROGENASE C1 (NDC1)		3.53	promoter
AT1G31330	PHOTOSYSTEM I SUBUNIT F (PSAF)	Encodes subun 1 11216042	3.53	promoter
AT1G58470	RNA-BINDING PROTEIN 1 (RBP1)	encodes an RN 1_21724910	3.53	proximal promoter
AT2G26570	WEAK CHLOROPLAST MOVEMENT UND		3.53	proximal promoter
AT3G52310	ATP-BINDING CASSETTE G27 (ABCG27)	ABC-2 type tran 3_19399044	3.52	intron
AT5G41410	BELL 1 (BEL1)	Homeodomain r 5_16581788	3.52	intron
AT5G54590	CALCIUM/CALMODULIN-REGULATED R	Splice variant A 5_22179113	3.52	proximal promoter
AT1G17455	ELF4-LIKE 4 (ELF4-L4)	ELF4-like 4 (ELI 1_5998681	3.52	downstream
AT1G30040	GIBBERELLIN 2-OXIDASE (GA2OX2)	Encodes a gibb 1_10537336	3.52	promoter
AT1G28300	LEAFY COTYLEDON 2 (LEC2)	Transcription fa 1_9896169	3.52	intergenic
AT1G12805	na	nucleotide bindi 1_4367167	3.52	downstream
AT1G12810	na	proline-rich fami 1_4367167	3.52	promoter
AT3G52302	na	This gene encor 3_19399044	3.52	promoter
AT2G26780	na	ARM repeat sur 2_11409832	3.52	promoter
AT1G15670	na	Galactose oxida 1_5388195	3.52	proximal promoter
AT3G02100	na	UDP-Glycosyltr; 3_371293	3.52	proximal promoter
AT3G11285	na	pre-tRNA; tRNA 3_3535061	3.52	promoter
AT3G19000	na	2-oxoglutarate (3_6556048	3.52	proximal promoter
AT3G19002	na	Potential natura 3_6556048	3.52	intergenic
AT3G19010	na	2-oxoglutarate (3_6556048	3.52	downstream
AT5G20840	na	Phosphoinositid 5_7069259	3.52	promoter
AT5G21535	na	transposable eli 5_7234480	3.52	intergenic
AT5G58950	na	Protein kinase s 5_23803813	3.52	promoter
AT4G21680	NITRATE TRANSPORTER 1.8 (NRT1.8)	Encodes a nitra 4_11520438	3.52	proximal promoter
AT3G02110	SERINE CARBOXYPEPTIDASE-LIKE 25 (serine carboxyp 3_371293	3.52	intron
AT1G17460	TRF-LIKE 3 (TRFL3)	Arabidopsis tha 1_5998681	3.52	promoter
AT4G15210	BETA-AMYLASE 5 (BAM5)	cytosolic beta-a 4_8669602	3.51	promoter
AT5G01630	BRCA2-LIKE B (BRCA2B)	Ortholog of brea 5_241224	3.51	promoter
AT1G64980	CADMIUM 2+ INDUCED (CDI)	Encodes a puta 1_24139379	3.51	promoter
AT1G77630	LYSIN-MOTIF (LYSM) DOMAIN PROTEIN		3.51	downstream
AT3G56220	na	transcription rec 3_20857355	3.51	proximal promoter
AT4G01270	na	RING/U-box su _l 4_535192	3.51	downstream
AT4G01280	na	Homeodomain-I 4_535192	3.51	promoter
AT5G03490	na	UDP-Glycosyltr: 5_872548	3.51	exon
AT5G19025	na	Ribosomal prote 5_6357133	3.51	promoter
AT1G10120	na	basic helix-loop 1_3306283	3.51	five_prime_UTR
AT1G66870	na	Carbohydrate-b 1 24948703	3.51	proximal promoter
AT1G66880	na	Protein kinase s 1_24948703	3.51	intron
AT3G56140	na	Protein of unknc 3 20829249	3.51	promoter
AT3G56130	na	biotin/lipoyl attar 3_20829249	3.51	three_prime_UTR
AT4G29610	na	Cytidine/deoxyc 4_14517271	3.51	promoter
AT5G17000	na	Zinc-binding del 5_5587289	3.51	promoter
AT5G17010	na	Major facilitator 5_5587289	3.51	downstream
AT5G21070	na	unknown proteir 5_7155999	3.51	promoter
AT5G25451	na	Pseudogene of 5_8860061	3.51	proximal promoter
AT1G08380	PHOTOSYSTEM I SUBUNIT O (PSAO)	Encodes subun 1 2641974	3.51	promoter
AT2G24220	PURINE PERMEASE 5 (PUP5)	Member of a far 2_10300043	3.51	promoter
AT3G54990	SCHLAFMUTZE (SMZ)	Encodes a AP2 3_20378242	3.51	proximal promoter
AT2G46330	ARABINOGALACTAN PROTEIN 16 (AGP		3.5	five_prime_UTR
AT3G48560	CHLORSULFURON/IMIDAZOLINONE RE		3.5	promoter
AT5G27320	GA INSENSITIVE DWARF1C (GID1C)	Encodes a gibb 5_9631421	3.5	downstream
AT3G53950	na	glyoxal oxidase 3_19976237	3.5	exon
AT1G14518	na	Unknown gene 1_4966001 Mitochondrial st 2_19019248	3.5 3.5	intergenic
AT2G46320 AT3G13410	na na		3.5	intergenic
AT5G57790	na	unknown proteir 3_4364377	3.5	promoter
		unknown proteir 5_23415514		proximal promoter
AT5G18230	na NITROCEN EIVATION & (NIES) LIKE 4 (N	transcription rec 5_6027224	3.5	five_prime_UTR
AT5G65720	NITROGEN FIXATION S (NIFS)-LIKE 1 (N		3.5 3.5	promoter
AT3G05690	NUCLEAR FACTOR Y, SUBUNIT A2 (NF-	small GTP bindi 5 18244273		promoter
AT5G45130 AT5G38470	RAB HOMOLOG 1 (RHA1)		3.5 3.5	five_prime_UTR
	RADIATION SENSITIVE23D (RAD23D) UBIQUITIN EXTENSION PROTEIN 1 (UBO	Encodes a merr 5_15404524		promoter
AT3G52590 AT4G02590			3.5	promoter
	UNFERTILIZED EMBRYO SAC 12 (UNE1:		3.5	three_prime_UTR
AT3G56400	WRKY DNA-BINDING PROTEIN 70 (WRK		3.5	promoter
AT3G12110 AT2G39350	ACTIN-11 (ACT11) ATP-BINDING CASSETTE G1 (ABCG1)	Encodes an act 3_3860025 ABC-2 type tran 2_16432800	3.49	downstream promoter
AT2G39350 AT5G14870	ATT PURPLING CASSETTE GT (ABCGT)		3 10	
	CYCLIC MUCLECTIDE GATED CHANNE		3.49	
	CYCLIC NUCLEOTIDE-GATED CHANNEL	Encodes a merr 5_4811178	3.49	promoter
AT4G37890	EMBRYO SAC DEVELOPMENT ARREST	Encodes a merr 5_4811178 embryo sac dev 4_17815659	3.49 3.49	promoter proximal promoter
AT4G37890 AT3G12120	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2)	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme r 3_3860025	3.49 3.49 3.49	promoter proximal promoter intergenic
AT4G37890 AT3G12120 AT3G01290	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme rr 3_3860025 SPFH/Band 7/P 3_87912	3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream
AT4G37890 AT3G12120 AT3G01290 AT4G23060	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22)	Encodes a mer 5_4811178 embryo sac dev 4_17815659 Major enzyme ri 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940	3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron
AT4G37890 AT3G12120 AT3G01290 AT4G23060 AT4G31877	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C)	Encodes a mer 5_4811178 embryo sac dev 4_17815659 Major enzyme r 3_3860625 SPFH/Band 7/P 3_87912 IQ-domain 22 (I 4_12088940 Encodes a micr 4_15415998	3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter
AT4G37890 AT3G12120 AT3G01290 AT4G23060 AT4G31877 AT3G11440	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65)	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme r 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (I+_12088940 Encodes a micr 4_15415998 Member of the f 3_3601140	3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter
AT4G37890 AT3G12120 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme rr 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (I 4_12088940 Encodes a micr 4_1541599 Member of the F 3_3601140 GDSL-like Lipas 1_11297491	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter promoter
AT4G37890 AT3G12120 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G52310	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme r 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (I 4_12088940 Encodes a micr 4_15415998 Member of the f 3_3601140 GDSL-like Lipas 1_11297491 protein kinase ft 1_19478088	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter promoter promoter
AT4G37890 AT3G12120 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G52310 AT1G63835	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na na na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme rr 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940 Encodes a micr 4_15415998 Member of the f 3_3601140 GDSL-like Lipas 1_11297491 protein kinase ft 1_19478088 transposable elit 1_23688605	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter promoter promoter intergenic
AT4G37890 AT3G12120 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G52310 AT1G63835 AT1G74120	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme rr 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940 Encodes a micrr 4_15415998 Member of the F 3_3601140 GDSL-like Lipas 1_11297491 protein kinase fs 1_19478088 transposable elt 1_2368605 Mitochondrial trr 1_27873403	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter promoter promoter promoter promoter intergenic promoter
AT4G37890 AT3G11210 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G52310 AT1G63835 AT1G74120 AT3G07025	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme r 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (I 4_12088940 Encodes a micr 4_15415998 Member of the f 3_3601140 GDSL-like Lipas 1_11297491 protein kinase ft 1_19478088 transposable elt 1_23688605 Mitochondrial tr: 1_27873403 pre-IRNA; IRNA 3_2221856	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter promoter promoter promoter promoter promoter promoter promoter promoter promoter
AT4G37890 AT3G12120 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G52310 AT1G63835 AT1G74120 AT3G07025 AT2G39710	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IGD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme rs 3_860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940 Encodes a micr 4_15415998 Member of the fs_3601140 GDSL-like Lipas t_11297491 protein kinase fs 1_19478018 transposable eli 1_23688605 Mitochondrial trs 1_27873403 pre-tRNA; tRNA 3_2221856 Encodes a Cyst 2_16560031	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter proximal promoter promoter promoter intergenic promoter intergenic promoter intergenic intergenic
AT4G37890 AT3G12120 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G63835 AT1G74120 AT3G07025 AT2G39710 AT3G26085	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme n 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940 Encodes a micn 4_15415998 Member of the f 3_3601140 GDSL-like Lipas 1_11297491 protein kinase fs 1_19478088 transposable elt 1_23688605 Mitochondrial tri 1_27873403 pre-IRNA; IRNA 3_2221856 Encodes a Cyst 2_16560031 CAAX amino ter 3_9532628	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter promoter promoter promoter promoter promoter promoter promoter intergenic promoter downstream
AT4G37890 AT3G012190 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G52310 AT1G63835 AT1G74120 AT3G07025 AT2G39710 AT3G26085 AT3G25700	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme r 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (I 4_12088940 Encodes a micr 4_15415998 Member of the f 3_3601140 GDSL-like Lipas 1_11297491 protein kinase ft 1_19478088 transposable el 1_23688605 Mitochondrial tr 1_27873403 pre-tRNA; tRNA 3_2221856 Encodes a Cyst 2_16560031 CAAX amino te 13_9532628 Eukaryotic aspa 3_9363796	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter promoter promoter promoter intergenic promoter promoter intergenic promoter intergenic downstream intergenic
AT4G37890 AT3G01290 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G52310 AT1G52310 AT1G52310 AT3G7025 AT3G7025 AT3G26085 AT3G26085 AT3G25700 AT3G55590	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IGD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme r 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940 Encodes a micr 4_15415998 Member of the f 3_3601140 GDSL-like Lipas t_11297491 protein kinase f t_19478088 transposable eli 1_23688605 Mitochondrial trs 1_27873403 pre-tRNA; tRNA 3_2221856 Encodes a Cyst 2_16560031 CAAX amino tes 3_9532628 Eukaryotic aspa 3_9363796 hydroxyproline-i 3_20964252	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter proximal promoter promoter promoter intergenic promoter intergenic downstream intergenic downstream intergenic proximal promoter proximal promoter
AT4G37890 AT3G012190 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G52310 AT1G52310 AT1G52310 AT1G74120 AT3G07025 AT2G39710 AT3G26085 AT3G25700 AT3G56590 AT3G56590	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme n 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940 Encodes a micn 4_15415998 Member of the f 3_3601140 GDSL-like Lipas 1_11297491 protein kinase f: 1_19478088 transposable eli 1_23688605 Mitochondrial tri 1_27873403 pre-tRNA; tRNA 3_2221856 Encodes a Cyst 2_16560031 CAAX amino ter 3_9532628 Eukaryotic aspa 3_9363796 hydroxyproline-i 3_20964252 unknown proteir 3_21241460	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter proximal promoter promoter promoter intergenic promoter intergenic downstream intergenic downstream intergenic proximal promoter intergenic
AT4G37890 AT3G012190 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G52310 AT1G63835 AT1G74120 AT3G07025 AT2G39710 AT3G26085 AT3G25700 AT3G565990 AT3G557400 AT4G37895	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme r 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (I 4_12088940 Encodes a micr 4_15415998 Member of the f 3_3601140 GDSL-like Lipas 1_11297491 protein kinase ft 1_19478088 transposable el 1_23688605 Mitochondrial tr 1_27873403 pre-IRNA; IRNA 3_2221856 Encodes a Cyst 2_16560031 CAAX amino te 13_9532628 Eukaryotic aspa 3_9363796 hydroxyproline-i 3_20964252 unknown proteir 3_21241460 Potential natura 4_17815659	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter promoter promoter promoter promoter promoter promoter promoter promoter intergenic promoter intergenic downstream intergenic proximal promoter intergenic intergenic intergenic intergenic intergenic intergenic
AT4G37890 AT3G01290 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G52310 AT1G52310 AT1G63835 AT1G74120 AT3G07025 AT2G39710 AT3G26085 AT3G25700 AT3G55590 AT3G57400 AT4G37895 AT4G37895	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IGD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme n 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940 Encodes a micr 4_15415998 Member of the f 3_3601140 GDSL-like Lipas 1_11297491 protein kinase f 1_19478018 transposable els 1_23688605 Mitochondrial trs 1_27873403 pre-IRNA; IRNA 3_2221856 Encodes a Cyst 2_16560031 CAAX amino tes 3_9532628 Eukaryotic aspa 3_9363796 hydroxyproline-i 3_20964252 unknown proteir 3_21241460 Potential natura 4_17815659 early-responsivi 4_16992958	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter proximal promoter promoter promoter promoter intergenic promoter intergenic downstream intergenic proximal promoter intergenic downstream intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic intergenic downstream
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ATAG37890 AT3G12120 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G52310 AT1G52310 AT1G52310 AT3G63835 AT1G74120 AT3G67025 AT2G39710 AT3G25700 AT3G56590 AT3G57400 AT4G37895 AT4G35880 AT3G5616340 AT5G51380 AT3G561340 AT5G51380	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme ri 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940 Encodes a micri 4_15415998 Member of the fi 3_3601140 GDSL-like Lipas 1_11297491 protein kinase fi 1_19478088 transposable eli 1_23688605 Mitochondrial tri 1_27873403 pre-tRNA; tRNA 3_2221856 Encodes a Cyst 2_16560031 CAAX amino tei 3_9532628 Eukaryotic aspa 3_9363796 hydroxyproline-i 3_20964252 unknown proteir 3_21241460 Potential natura 4_17815659 early-responsivi 4_16992958 Eukaryotic aspa 4_16992958 Eukaryotic aspa 4_16992958 ENLARYOTIC ALTORETIC SUSTINESSES ENLARYOTIC SUSTINESSES ENL	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter proximal promoter promoter promoter promoter intergenic promoter intergenic downstream intergenic downstream intergenic intergenic downstream promoter intergenic material promoter intergenic downstream promoter intergenic downstream promoter exon promoter promoter
AT4G37890 AT3G01290 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G52310 AT1G63835 AT1G74120 AT3G07025 AT2G39710 AT3G65690 AT3G56590 AT3G57400 AT4G35870 AT4G35870 AT5G51380 AT5G16340 AT5G51380 AT3G565380 AT5G16340	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme rn 3_3860025 SPFH/Band 7/P 3_87912 Q-domain 22 (I 4_12088940 Encodes a micr 4_15415998 Member of the f 3_3601140 GDSL-like Lipas 1_11297491 protein kinase ft 1_19478088 transposable elt 1_23688605 Mitochondrial trn 1_27873403 pre-IRNA; tRNA 3_2221856 Encodes a Cyst 2_16560031 CAAX amino ten 3_9532628 Eukaryotic aspa 3_9363796 hydroxyproline-i 3_20964252 unknown proteir 3_21241460 Potential natura 4_17815659 early-responsivi 4_16992958 Eukaryotic aspa 4_59536261 RNI-like superft 5_20875822 Encodes AtRG\$ 3_9532628 putative transm 3_19220016	3.49 3.49 3.49 3.49 3.49 3.49 3.49 3.49	promoter proximal promoter intergenic downstream intron promoter intergenic promoter intergenic downstream intergenic intergenic downstream promoter intergenic downstream promoter intergenic downstream promoter intergenic downstream promoter promoter promoter promoter promoter promoter promoter promoter promoter intergenic downstream promoter
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ATAG37890 AT3G01290 AT3G01290 AT4G23060 AT4G31877 AT3G11440 AT1G31550 AT1G52310 AT1G52310 AT3G63835 AT1G74120 AT3G6085 AT3G25700 AT3G56590 AT3G57400 AT4G37895 AT4G35880 AT3G56590 AT4G35880 AT5G51380 AT3G5618340 AT3G5618340 AT3G5618340 AT3G5618340 AT3G5618340 AT3G7895 AT3G7897 AT4G35880 AT3G7897 AT4G35880 AT3G7897 AT4G35880	EMBRYO SAC DEVELOPMENT ARREST FATTY ACID DESATURASE 2 (FAD2) HYPERSENSITIVE INDUCED REACTION IQ-DOMAIN 22 (IQD22) MICRORNA156C (MIR156C) MYB DOMAIN PROTEIN 65 (MYB65) na	Encodes a merr 5_4811178 embryo sac dev 4_17815659 Major enzyme ri 3_3860025 SPFH/Band 7/P 3_87912 IQ-domain 22 (li 4_12088940 Encodes a micri 4_15415998 Member of the fi 3_3601140 GDSL-like Lipas 1_11297491 protein kinase fi 1_19478088 transposable eli 1_23688605 Mitochondrial tri 1_27873403 pre-IRNA; IRNA 3_2221856 Encodes a Cyst 2_16560031 CAAX amino tei 3_9532628 Eukaryotic aspa 3_9363796 hydroxyproline-i 3_20964252 unknown proteir 3_21241460 Potential natura 4_17815659 early-responsivi 4_16992958 Eukaryotic aspa 4_16992958	3.49 3.49	promoter proximal promoter intergenic downstream intron promoter proximal promoter proximal promoter promoter promoter promoter promoter intergenic promoter intergenic downstream intergenic downstream intergenic intergenic downstream promoter intergenic downstream promoter proximal promoter proximal promoter
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AT3G01280	VOLTAGE DEPENDENT ANION CHANNE	Encodes a volta 3_87912	3.49	downstream
AT2G46720	3-KETOACYL-COA SYNTHASE 13 (KCS1		3.48	downstream
AT3G30180	BRASSINOSTEROID-6-OXIDASE 2 (BR6	Encodes a cyto 3_11802388	3.48	intergenic
AT1G29930	CHLOROPHYLL A/B BINDING PROTEIN		3.48	promoter
AT5G05690	CONSTITUTIVE PHOTOMORPHOGENIC		3.48	exon
AT3G19270	CYTOCHROME P450, FAMILY 707, SUBI		3.48	downstream
AT2G18020	EMBRYO DEFECTIVE 2296 (EMB2296)	embryo defectiv 2_7837016	3.48	promoter
AT2G42280	FLOWERING BHLH 4 (FBH4)	basic helix-loop 2_17613551	3.48	promoter
AT3G19260 AT4G32551	LAG1 HOMOLOGUE 2 (LOH2)	LAG1 homolog 3_6673600	3.48 3.48	proximal promoter downstream
AT1G07900	LEUNIG (LUG) LOB DOMAIN-CONTAINING PROTEIN 1	LEUNIG regulat 4_15713763	3.48	downstream
AT4G30410	na	sequence-speci 4_14873672	3.48	proximal promoter
AT1G04425	na	other RNA 1_1193976	3.48	promoter
AT1G23040	na	hydroxyproline-ı 1_8166549	3.48	intergenic
AT1G71110	na	unknown proteir 1_26817520	3.48	proximal promoter
AT5G51740	na	Peptidase family 5_21016705	3.48	promoter
AT2G42240	na	RNA-binding (R 2_17596740	3.48	promoter
AT4G23470	na	PLAC8 family pi 4_12249080	3.48	five_prime_UTR
AT5G28410	na	unknown proteir 5_10356784	3.48	proximal promoter
AT1G07901	na	unknown proteir 1_2443657	3.48	intergenic
AT1G10660	na	unknown proteir 1_3532377	3.48	promoter
AT1G29500 AT1G62190	na na	SAUR-like auxir 1_10320966 Kua-ubiquitin cc 1_22980386	3.48 3.48	promoter
AT1G02190 AT2G46730	na	pseudogene, sir 2_19200346	3.48	proximal promoter proximal promoter
AT3G03920	na	H/ACA ribonucli 3_1010591	3.48	promoter
AT1G79640	na	Protein kinase s 1_29972210	3.48	proximal promoter
AT3G14172	na	FUNCTIONS IN 3_4705828	3.48	promoter
AT3G05910	na	Pectinacetyleste 3_1767625	3.48	promoter
AT4G25433	na	peptidoglycan-b 4_13000679	3.48	intergenic
AT4G32560	na	paramyosin-rela 4_15713763	3.48	intron
AT5G05550	na	sequence-speci 5_1640828	3.48	promoter
AT5G12890	na	UDP-Glycosyltr: 5_4071288	3.48	promoter
AT5G12900	na	unknown proteir 5_4071288	3.48	intergenic
AT5G38400	na	unknown proteir 5_15377095	3.48	intergenic
AT5G55050 AT4G29230	na NAC DOMAIN CONTAINING PROTEIN 75	GDSL-like Lipas 5_22335858	3.48 3.48	proximal promoter
AT1G37130	NITRATE REDUCTASE 2 (NIA2)	Identified as a rr 1_14158524	3.48	proximal promoter promoter
AT1G37130	RADIATION SENSITIVE23B (RAD23B)	Encodes a merr 1 29972210	3.48	three_prime_UTR
AT5G38410	RUBISCO SMALL SUBUNIT 3B (RBCS3E		3.48	downstream
AT3G07880	SUPERCENTIPEDE1 (SCN1)	SUPERCENTIP 3 2513955	3.48	promoter
AT4G20890	TUBULIN BETA-9 CHÀIN (TÚB9)	tubulin 9 4_11182062	3.48	promoter
AT1G51710	UBIQUITIN-SPECIFIC PROTEASE 6 (UBI	Ubiquitin-specifi 1_19180044	3.48	promoter
AT5G14060	(CARAB-AK-LYS)	lysine-sensitive 5_4535416	3.47	five_prime_UTR
AT1G77180	(SKIP)	Encodes a puta 1_29002179	3.47	promoter
AT4G18600	(WAVE5)	Encodes a merr 4_10247566	3.47	promoter
AT2G34690	ACCELERATED CELL DEATH 11 (ACD1:		3.47	promoter
AT4G00730	ANTHOCYANINLESS 2 (ANL2)	Encodes a hom 4_307544	3.47	intergenic
AT3G10570 AT3G21550	CYTOCHROME P450, FAMILY 77, SUBF. DUF679 DOMAIN MEMBRANE PROTEIN		3.47 3.47	promoter proximal promoter
AT3G23400	FIBRILLIN 4 (FIB4)	Encodes FIBRIL 3_8376539	3.47	three_prime_UTR
AT3G28340	GALACTURONOSYLTRANSFERASE-LIK		3.47	promoter
AT1G22770	GIGANTEA (GI)	Together with C 1_8061799	3.47	promoter
AT2G23770	LYSM-CONTAINING RECEPTOR-LIKE K		3.47	intergenic
AT1G49032	na	unknown proteir 1_18138859	3.47	three_prime_UTR
AT1G62780	na	unknown proteir 1_23251276	3.47	promoter
AT1G73120	na	unknown proteir 1_27498179	3.47	promoter
AT5G64780	na	Uncharacterisec 5_25902104	3.47	five_prime_UTR
AT4G01340	na	CHP-rich zinc fi 4_556669	3.47	exon
AT1G49850	na	RING/U-box sui 1_18456620	3.47	promoter
AT1G63480 AT1G68735	na	AT hook motif D 1_23543451	3.47	proximal promoter
AT1G66735 AT1G75295	na na	Encodes a defe 1_25812180 Potential natura 1_28258662	3.47 3.47	intron proximal promoter
AT1G73293	na	pre-tRNA; tRNA 1 29002179	3.47	downstream
AT1G25570	na	Di-glucose bind 1_8991264	3.47	intergenic
AT3G09030	na	BTB/POZ doma 3_2754756	3.47	promoter
AT2G28200	na	C2H2-type zinc 2_12025495	3.47	downstream
AT3G23390	na	Zinc-binding rib: 3_8376539	3.47	downstream
AT3G46370	na	Leucine-rich rer 3_17050748	3.47	proximal promoter
AT3G43720	na	Bifunctional inhi 3_15616139	3.47	intron
AT4G02010	na	Protein kinase s 4_880898	3.47	promoter
AT4G02530	na	chloroplast thyle 4_1114484	3.47	promoter
AT4G17100 AT4G17098	na na	EXPRESSED If 4_9609188 Potential natura 4_9609188	3.47 3.47	intergenic intron
AT4G17098 AT5G14050	na na	Transducin/WD 5 4535416	3.47	downstream
AT4G37553	na	Potential natura 4_17649244	3.47	promoter
AT5G51340	na	Tetratricopeptid 5_20862918	3.47	promoter
AT4G00740	QUASIMODO 3 (QUA3)	Encodes a Golg 4_307544	3.47	three_prime_UTR
AT3G05210	(ERCC1)	encodes a hom 3_1483950	3.46	intergenic
AT1G77850	AUXIN RESPONSE FACTOR 17 (ARF17)	Posttranscriptio 1_29272199	3.46	promoter
AT5G56870	BETA-GALACTOSIDASE 4 (BGAL4)	beta-galactosid: 5_23004114	3.46	promoter
AT4G11050	GLYCOSYL HYDROLASE 9C3 (GH9C3)	glycosyl hydrola 4_6753041	3.46	proximal promoter
AT3G19260	LAG1 HOMOLOGUE 2 (LOH2)	LAG1 homolog 3_6672376	3.46	proximal promoter
AT1G27920	MICROTUBULE-ASSOCIATED PROTEIN		3.46	proximal promoter
AT3G01530	MYB DOMAIN PROTEIN 57 (MYB57)	Member of the F 3_210391	3.46	exon
AT5G59780 AT3G12700	MYB DOMAIN PROTEIN 59 (MYB59) na	Encodes a puta 5_24085951 Eukaryotic aspa 3_4035384	3.46 3.46	proximal promoter proximal promoter
AT1G14710	na	hydroxyproline-i 1_5065131	3.46	five_prime_UTR
AT1G29070	na	Ribosomal prote 1_10149741	3.46	promoter
AT1G29060	na	Target SNARE : 1_10149741	3.46	downstream
AT1G30320	na	Remorin family 1_10680027	3.46	promoter
AT3G01316	na	snoRNA; snoRN 3_105252	3.46	promoter
AT1G76878	na	Potential natura 1_28869606	3.46	proximal promoter
AT3G13275	na	unknown proteir 3_4289891	3.46	promoter
AT3G22540	na	Protein of unknr 3_7986424	3.46	proximal promoter

AT3G01520	na	Adenine nucleo 3 210391	3.46	intergenic
AT3G08610	na	unknown proteir 3_2616881	3.46	promoter
AT3G56050	na	Protein kinase f: 3_20802774	3.46	proximal promoter
AT3G56060 AT3G62490	na na	Glucose-methai 3_20802774 transposable eli 3_23116425	3.46 3.46	intergenic proximal promoter
AT4G32340	na	Tetratricopeptid 4_15614300	3.46	five_prime_UTR
AT5G08190	NUCLEAR FACTOR Y, SUBUNIT B12 (NI	nuclear factor Y 5_2635888	3.46	promoter
AT3G55330	PSBP-LIKE PROTEIN 1 (PPL1)	PsbP-like protei 3_20515521	3.46	promoter
AT4G14220 AT1G58100	RING-H2 GROUP F1A (RHF1A) TCP DOMAIN PROTEIN 8 (TCP8)	encodes a RIN(4_8195693 Encodes TCP8, 1_21513945	3.46 3.46	promoter five_prime_UTR
AT3G53540	TON1 RECRUITING MOTIF 19 (TRM19)	unknown proteir 3_19851075	3.46	promoter
AT1G78690	(At1g78690p)	Encodes a lysor 1_29596565	3.45	promoter
AT1G01520	ALTERED SEED GERMINATION 4 (ASG		3.45	promoter
AT5G04930 AT1G01510	AMINOPHOSPHOLIPID ATPASE 1 (ALA1 ANGUSTIFOLIA (AN)	Encodes a puta 5_1444948 Encodes a hom 1_190414	3.45 3.45	five_prime_UTR intergenic
AT1G19800	ATP-BINDING CASSETTE I14 (ABCI14)		3.45	proximal promoter
AT5G61900	BONZAI 1 (BON1)	Encodes a plasi 5_24859340	3.45	five_prime_UTR
AT3G28740	CYTOCHROME P450, FAMILY 81, SUBF CYTOCHROME P450, FAMILY 87, SUBF		3.45 3.45	promoter promoter
AT3G03470 AT2G45420	LOB DOMAIN-CONTAINING PROTEIN 18		3.45	proximal promoter
AT5G66850	MITOGEN-ACTIVATED PROTEIN KINAS		3.45	proximal promoter
AT3G09480	na	Histone superfa 3_2915442	3.45	promoter
AT3G09470 AT3G19790	na na	Major facilitator 3_2915442 unknown proteir 3_6875996	3.45 3.45	proximal promoter promoter
AT3G19800	na	Protein of unknc 3_6875996	3.45	promoter
AT3G50030	na	ARM-repeat/Tel 3_18546616	3.45	exon
AT5G18650	na	CHY-type/CTCF 5_6216802	3.45	proximal promoter
AT1G14580 AT5G28300	na na	C2H2-like zinc f 1_4987679 Duplicated hom 5_10295789	3.45 3.45	proximal promoter proximal promoter
AT5G14230	na	CONTAINS Inte 5_4589609	3.45	proximal promoter
AT1G56233	na	Encodes a defe 1_21051759	3.45	proximal promoter
AT1G69860	na	Major facilitator 1_26306732 Transducin/WD 2_15608682	3.45	proximal promoter
AT2G37160 AT1G29160	na na	Dof-type zinc fir 1 10182892	3.45 3.45	promoter intergenic
AT2G26730	na	Leucine-rich reg 2_11391441	3.45	three_prime_UTR
AT3G03460	na	unknown proteir 3_826633	3.45	proximal promoter
AT3G23760	na	FUNCTIONS IN 3_8562703	3.45 3.45	downstream
AT4G19150 AT4G34180	na na	Ankyrin repeat f 4_10474129 Cvclase family r 4_16371438	3.45	proximal promoter promoter
AT5G05830	na	RING/FYVE/PH 5_1755738	3.45	promoter
AT5G15500	na	Ankyrin repeat f 5_5033701	3.45	promoter
AT5G22608 AT5G61910	na na	unknown proteir 5_7512965 DCD (Developn 5_24859340	3.45 3.45	promoter five_prime_UTR
AT1G29150	NON-ATPASE SUBUNIT 9 (ATS9)	specifically inter 1_10182892	3.45	downstream
AT1G48480	RECEPTOR-LIKE KINASE 1 (RKL1)	Arabidopsis tha 1_17917657	3.45	proximal promoter
AT3G08710	THIOREDOXIN H-TYPE 9 (TH9)	Associated to pl 3_2645159	3.45	promoter
AT3G15360 AT2G37260	THIOREDOXIN M-TYPE 4 (TRX-M4) TRANSPARENT TESTA GLABRA 2 (TTG	encodes a prok 3_5188341	3.45 3.45	promoter promoter
AT2G22500	UNCOUPLING PROTEIN 5 (UCP5)	Encodes one of 2_9562951	3.45	intergenic
AT5G11100	(SYTD)	SYTD; FUNCTI 5_3531450	3.44	proximal promoter
AT5G05730	ANTHRANILATE SYNTHASE ALPHA SUI		3.44	promoter
AT1G79110 AT3G03220	BOI-RELATED GENE 2 (BRG2) EXPANSIN A13 (EXPA13)	Encodes one of 1_29762806 member of Alph 3_744125	3.44 3.44	intergenic promoter
AT5G17020	EXPORTIN 1A (XPO1A)	Encodes a merr 5_5594731	3.44	intron
AT3G13810	INDETERMINATE(ID)-DOMAIN 11 (IDD11		3.44	promoter
AT5G64813 AT2G21180	LIGHT INSENSITIVE PERIOD1 (LIP1) na	The LIP1 gene (5_25910180 unknown proteir 2_9074833	3.44 3.44	promoter three_prime_UTR
AT1G09690	na	Translation prot 1_3137635	3.44	promoter
AT1G14650	na	SWAP (Suppre: 1_5027604	3.44	promoter
AT1G14780	na	MAC/Perforin di 1_5091548	3.44	exon
AT1G76405 AT1G80950	na na	unknown proteir 1_28661798 Phospholipid/ql\ 1 30415242	3.44 3.44	promoter promoter
AT2G33550	na	Homeodomain-I 2_14211525	3.44	five_prime_UTR
AT3G28940	na	AIG2-like (aviru 3_10969379	3.44	five_prime_UTR
AT3G12700	na	Eukaryotic aspa 3_4038113	3.44 3.44	intron
AT3G55050 AT3G59680	na na	Protein phospha 3_20402515 unknown proteir 3_22043968	3.44	intron promoter
AT4G22770	na	AT hook motif D 4_11964802	3.44	intron
AT4G34110	POLY(A) BINDING PROTEIN 2 (PAB2)	Putative poly-A 4_16336233	3.44	promoter
AT1G10470 AT3G58040	RESPONSE REGULATOR 4 (ARR4) SEVEN IN ABSENTIA OF ARABIDOPSIS	Encodes a two- 1_3442560	3.44 3.44	three_prime_UTR promoter
AT4G34640	SQUALENE SYNTHASE 1 (SQS1)	Encodes a Kilk 3_21466497 Encodes squale 4 16542244	3.44	intergenic
AT4G34650	SQUALENE SYNTHASE 2 (SQS2)	Encodes a prote 4_16542244	3.44	promoter
AT5G08150	SUPPRESSOR OF PHYTOCHROME B 5		3.44	proximal promoter
AT1G03110 AT1G52340	TRNA MODIFICATION 82 (TRM82) ABA DEFICIENT 2 (ABA2)	Encodes a gene 1_749138 Encodes a cyto: 1_19491004	3.44 3.43	promoter intron
AT1G80070	ABNORMAL SUSPENSOR 2 (SUS2)	a genetic locus 1_30117730	3.43	promoter
AT3G60620	CYTIDINEDIPHOSPHATE DIACYLGLYCE	cytidinediphospl 3_22406318	3.43	promoter
AT4G12400	HOP3 (Hop3)	Encodes one of 4_7341469	3.43	promoter
AT1G51760 AT4G30064	IAA-ALANINE RESISTANT 3 (IAR3) LOW-MOLECULAR-WEIGHT CYSTEINE	encodes a mem 1_19198751 - Encodes a mem 4_14694567	3.43 3.43	proximal promoter exon
AT5G58465	MICRORNA390B (MIR390B)	Encodes a micr 5_23636367	3.43	proximal promoter
AT1G31358	MICRORNA404 (MIR404)	Encodes a micr 1_11231219	3.43	proximal promoter
AT3G27820 AT2G35795	MONODEHYDROASCORBATE REDUCT na	Encodes a pero 3_10315025 Chaperone Dna 2_15043503	3.43 3.43	promoter three_prime_UTR
AT5G39530	na na	Protein of unknr 5_15827746	3.43	five_prime_UTR
AT2G41750	na	DTW domain-cc 2_17422536	3.43	promoter
AT1G01210	na	DNA-directed R 1_88773	3.43	promoter
AT1G49130 AT1G49140	na na	B-box type zinc 1_18176504 Complex I subu 1_18176504	3.43 3.43	promoter intergenic
AT1G68680	na	unknown proteir 1_25785327	3.43	promoter
AT1G75460	na	ATP-dependent 1_28327566	3.43	promoter
AT1G79710 AT1G80060	na na	Major facilitator 1_29994904 Ubiquitin-like su 1_30117730	3.43 3.43	promoter promoter
		22.44 24 1_00111100	50	F. 0010.

AT3G06433	na	pseudogene of : 3_1959953	3.43	intron
AT3G45210	na	Protein of unknc 3_16557155	3.43	downstream
AT3G62570	na	Tetratricopeptid 3_23142492	3.43	five_prime_UTR
AT3G62010	na	unknown proteir 3_22963909	3.43	proximal promoter
AT4G12405	na	pre-tRNA; tRNA 4_7341469	3.43	exon
AT5G03140	na	Concanavalin A 5_737464	3.43	downstream
AT5G57480	na	P-loop containir 5_23281341	3.43	promoter
AT4G39580	na	Galactose oxida 4_18387050	3.43	promoter
AT5G03130 AT5G51055	na na	unknown proteir 5_737464 pre-tRNA; tRNA 5_20756313	3.43 3.43	intergenic promoter
AT5G56960	na	basic helix-loop 5_23038021	3.43	intergenic
AT2G41850	POLYGALACTURONASE ABSCISSION Z		3.43	proximal promoter
AT2G20140	REGULATORY PARTICLE AAA-ATPASE		3.43	promoter
AT2G35800	S-ADENOSYL METHIONINE TRANSPOR		3.43	proximal promoter
AT5G01820	SERINE/THREONINE PROTEIN KINASE		3.43	promoter
AT3G01390	VACUOLAR MEMBRANE ATPASE 10 (VI		3.43	promoter
AT5G24380	YELLOW STRIPE LIKE 2 (YSL2)	closest Arabidol 5_8323427	3.43	promoter
AT2G32930 AT2G21590	ZINC FINGER NUCLEASE 2 (ZFN2) (APL4)	Encodes a zinc 2_13969082 Encodes the lar 2_9238266	3.43 3.42	promoter
AT1G31860	(AT-IE)	encodes a bifun 1_11436664	3.42	promoter promoter
AT4G34250	3-KETOACYL-COA SYNTHASE 16 (KCS1		3.42	downstream
AT4G11080	3XHIGH MOBILITY GROUP-BOX1 (3xHM		3.42	promoter
AT5G10860	CBS DOMAIN CONTAINING PROTEIN 3		3.42	intergenic
AT5G45390	CLP PROTEASE P4 (CLPP4)	One of several 5_18396250	3.42	promoter
AT5G36120	COFACTOR ASSEMBLY, COMPLEX C (E		3.42	five_prime_UTR
AT5G10840	ENDOMEMBRANE PROTEIN 1 (EMP1)	Endomembrane 5_3427975	3.42	promoter
AT1G56600	GALACTINOL SYNTHASE 2 (GoIS2)	GolS2 is a galar 1_21206337	3.42	proximal promoter
AT1G65040 AT1G68460	HOMOLOG OF YEAST HRD1 (Hrd1B) ISOPENTENYLTRANSFERASE 1 (IPT1)	Encodes one of 1_24163768	3.42 3.42	promoter intergenic
AT5G53760	MILDEW RESISTANCE LOCUS O 11 (ML		3.42	proximal promoter
AT5G17795	na	This gene encor 5_5875137	3.42	exon
AT1G32710	na	Cytochrome c o 1_11832994	3.42	promoter
AT1G31870	na	unknown proteir 1_11436664	3.42	promoter
AT1G80130	na	Tetratricopeptid 1_30143520	3.42	proximal promoter
AT1G80133	na	unknown proteir 1_30143520	3.42	downstream
AT2G21580	na na	Ribosomal prote 2_9238266 SPT2 chromatir 2_9657452	3.42 3.42	intergenic
AT2G22720 AT3G01980	na	NAD(P)-binding 3_329011	3.42	intron five_prime_UTR
AT3G15120	na	P-loop containir 3 5095958	3.42	promoter
AT5G64270	na	splicing factor, r 5_25706504	3.42	promoter
AT5G53460	NADH-DEPENDENT GLUTAMATE SYNTI	NADH-depende 5_21700280	3.42	intron
AT3G19840	PRE-MRNA-PROCESSING PROTEIN 400		3.42	promoter
AT5G37260	REVEILLE 2 (RVE2)	Encodes a MYE 5_14753281	3.42	promoter
AT3G56850 AT2G28470	ABA-RESPONSIVE ELEMENT BINDING F BETA-GALACTOSIDASE 8 (BGAL8)	putative beta-ga 2_12175611	3.41 3.41	promoter
AT5G65940	BETA-HYDROXYISOBUTYRYL-COA HYD		3.41	proximal promoter proximal promoter
AT5G44800	CHROMATIN REMODELING 4 (CHR4)	chromatin remo 5_18093597	3.41	promoter
AT5G12170	CRT (CHLOROQUINE-RESISTANCE TRA		3.41	intron
AT3G47500	CYCLING DOF FACTOR 3 (CDF3)	Dof-type zinc fir 3_17504077	3.41	three_prime_UTR
AT5G08170	EMBRYO DEFECTIVE 1873 (EMB1873)	EMBRYO DEFE 5_2631336	3.41	promoter
AT4G34200	EMBRYO SAC DEVELOPMENT ARREST		3.41	promoter
AT3G20770	ETHYLENE-INSENSITIVE3 (EIN3)	Encodes EIN3 (3_7260359	3.41	downstream
AT2G30470 AT1G10210	HIGH-LEVEL EXPRESSION OF SUGAR-I MITOGEN-ACTIVATED PROTEIN KINASE		3.41 3.41	proximal promoter proximal promoter
AT2G41730	na	unknown proteir 2_17409598	3.41	exon
AT2G30480	na	unknown proteir 2_12987307	3.41	three_prime_UTR
AT1G25420	na	Regulator of Vp 1_8915990	3.41	promoter
AT4G19520	na	disease resistar 4_10648234	3.41	proximal promoter
AT5G59700	na	Protein kinase s 5_24051484	3.41	intergenic
AT5G59690	na	Histone superfa 5_24051484	3.41	promoter
AT3G20760 AT2G28480	na na	Nse4, compone 3_7260359 RNA-binding CF 2_12175611	3.41 3.41	proximal promoter intergenic
AT2G23480 AT2G32795	na	Unknown gene 2_13911777	3.41	intergenic
AT3G44630	na	Disease resistal 3_16195885	3.41	promoter
AT3G44620	na	protein tyrosine 3_16195885	3.41	downstream
AT3G59150	na	F-box/RNI-like s 3_21872640	3.41	promoter
AT5G11000	na	Plant protein of 5_3480598	3.41	promoter
AT5G59000	na	RING/FYVE/PH 5_23817679	3.41	proximal promoter
AT1G02060	na SDIDDIG (SDI)	FUNCTIONS IN 5_26380167 Encodes a WD/ 1_728286	3.41 3.41	five_prime_UTR
AT1G03060 AT3G15990	SPIRRIG (SPI) SULFATE TRANSPORTER 3;4 (SULTR3;		3.41	proximal promoter intron
AT2G02180	TOBAMOVIRUS MULTIPLICATION PROT		3.41	proximal promoter
AT3G12060	TRICHOME BIREFRINGENCE-LIKE 1 (TE		3.41	promoter
AT3G56860	UBP1-ASSOCIATED PROTEIN 2A (UBA2	encodes a nucle 3_21048521	3.41	downstream
AT1G10200	WLIM1 (WLIM1)	Encodes a merr 1_3347838	3.41	five_prime_UTR
AT1G28320	(DEG15)	Mutants in this (1_9924479	3.4	five_prime_UTR
AT5G47370	(HAT2)	homeobox-leuci 5_19216457	3.4	three_prime_UTR
AT1G59590	(ZCF37)	ZCF37 mRNA, (1_21886945	3.4 3.4	proximal promoter downstream
AT2G03730 AT5G11160	ACT DOMAIN REPEAT 5 (ACR5) ADENINE PHOSPHORIBOSYLTRANSFE	Member of a srr 2_1137485 adenine phosph 5_3552960	3.4	intergenic
AT4G21940	CALCIUM-DEPENDENT PROTEIN KINAS		3.4	promoter
AT3G14690	CYTOCHROME P450, FAMILY 72, SUBFA		3.4	promoter
AT4G33010	GLYCINE DECARBOXYLASE P-PROTEIN	glycine decarbo 4_15931326	3.4	five_prime_UTR
AT5G11170	HOMOLOG OF HUMAN UAP56 A (UAP56		3.4	promoter
AT2G37380	MEMBRANE-ASSOCIATED KINASE REG		3.4	intergenic
AT1G19460	na	Galactose oxida 1_6737952	3.4	proximal promoter
AT1G20250 AT3G53611	na na	pre-tRNA; tRNA 1_7016483 This gene encoi 3_19878608	3.4 3.4	promoter exon
AT1G05390	na	pre-tRNA; tRNA 1 1583865	3.4	promoter
AT1G47980	na	unknown proteir 1_17695621	3.4	proximal promoter
AT2G04378	na	Beta-galactosid: 2_1526818	3.4	five_prime_UTR
AT2G04380	na	unknown proteir 2_1526818	3.4	downstream
AT2G04390	na	Ribosomal S17 2_1526818 unknown proteir 1_7343975	3.4 3.4	promoter
AT1G21010	na	ananown proteil 1_7343973	J. T	proximal promoter

AT1G72510	na	Protein of unknc 1_27301211	3.4	proximal promoter
AT3G21330	na	basic helix-loop 3_7505122	3.4	proximal promoter
AT3G12700	na	Eukaryotic aspa 3_4039223	3.4	downstream
AT4G01455	na	pre-tRNA; tRNA 4_612260	3.4	promoter
AT4G16563	na	Eukaryotic aspa 4_9332917	3.4	proximal promoter
AT4G21926	na	unknown proteir 4_11640324	3.4	promoter
AT4G21930	na	Protein of unknc 4_11640324	3.4	exon
AT5G08200	na	peptidoglycan-b 5_2637543	3.4	promoter
AT5G47360	na	Tetratricopeptid 5_19216457	3.4	proximal promoter
AT5G50915	na	basic helix-loop 5_20713049	3.4	proximal promoter
AT5G08190	NUCLEAR FACTOR Y, SUBUNIT B12 (NE		3.4	downstream
AT5G02190	PROMOTION OF CELL SURVIVAL 1 (PC		3.4	proximal promoter
AT3G53610 AT4G35800	RAB GTPASE HOMOLOG 8 (RAB8) RNA POLYMERASE II LARGE SUBUNIT	GTPase AtRAB 3_19878608	3.4 3.4	promoter promoter
AT3G22680	RNA-DIRECTED DNA METHYLATION 1 (3.4	promoter
AT1G20260	V-ATPASE B SUBUNIT 3 (VAB3)	One of three ge 1_7016483	3.4	promoter
AT4G39210	(APL3)	Encodes the lar 4_18259483	3.39	promoter
AT3G51970	ACYL-COA STEROL ACYL TRANSFERA		3.39	five_prime_UTR
AT3G25780	ALLENE OXIDE CYCLASE 3 (AOC3)	Encodes allene 3 9409049	3.39	promoter
AT3G22890	ATP SULFURYLASE 1 (APS1)	encodes ATP st 3_8111200	3.39	proximal promoter
AT1G32500	ATP-BINDING CASSETTE I7 (ABCI7)	Encodes a merr 1_11749902	3.39	three_prime_UTR
AT3G51960	BASIC LEUCINE ZIPPER 24 (BZIP24)	bZIP transcriptic 3_19284381	3.39	promoter
AT3G57180	BRASSINAZOLE(BRZ) INSENSITIVE PAL		3.39	promoter
AT4G11920	CELL CYCLE SWITCH PROTEIN 52 A2 (3.39	promoter
AT5G67260	CYCLIN D3;2 (CYCD3;2)	Encode CYCD3 5_26838116	3.39	intergenic
AT5G67190	DREB AND EAR MOTIF PROTEIN 2 (DEA		3.39	proximal promoter
AT1G32490	ENHANCED SILENCING PHENOTYPE 3		3.39	promoter
AT5G05740 AT2G44150	ETHYLENE-DEPENDENT GRAVITROPIS		3.39	promoter
AT5G06300	HISTONE-LYSINE N-METHYLTRANSFER		3.39 3.39	promoter
AT1G22610	LONELY GUY 7 (LOG7) na	Putative lysine (5_1924623 C2 calcium/lipid 1 7993966	3.39	intron promoter
AT1G22010 AT2G14790	na na	transposable el 2_6346356	3.39	proximal promoter
AT1G29160	na	Dof-type zinc fir 1_10184446	3.39	promoter
AT1G63640	na	P-loop nucleosic 1_23596004	3.39	promoter
AT2G44140	na	Peptidase family 2_18258464	3.39	promoter
AT3G27865	na	snoRNA; snoRN 3_10328346	3.39	promoter
AT3G46850	na	Subtilase family 3_17255429	3.39	proximal promoter
AT3G53430	na	Ribosomal prote 3 19810614	3.39	promoter
AT4G16162	na	Leucine-rich reg 4_9161694	3.39	promoter
AT4G25400	na	basic helix-loop 4_12979775	3.39	proximal promoter
AT5G58787	na	RING/U-box su; 5_23744843	3.39	downstream
AT5G67411	na	GRAS family tra 5_26898143	3.39	intergenic
AT5G10110	na	unknown proteir 5_3168356	3.39	promoter
AT5G36980	na	BEST Arabidop: 5_14609934	3.39	proximal promoter
AT5G58790	na	FUNCTIONS IN 5_23744843	3.39	promoter
AT5G67265	na	unknown proteir 5_26838116	3.39	intergenic
AT5G67410	na	unknown proteir 5_26898143	3.39	proximal promoter
AT4G28530	NAC DOMAIN CONTAINING PROTEIN 74		3.39	proximal promoter
AT1G64280	NONEXPRESSER OF PR GENES 1 (NPF		3.39	promoter
AT1G19300 AT4G12800	PARVUS (PARVUS) PHOTOSYSTEM I SUBUNIT L (PSAL)	The PARVUS/G 1_6670509 Encodes subun 4 7521367	3.39 3.39	intergenic
AT2G16850	PLASMA MEMBRANE INTRINSIC PROTE		3.39	five_prime_UTR intergenic
AT3G04240	SECRET AGENT (SEC)	Has O-linked N- 3_1121038	3.39	promoter
AT4G21790	TOBAMOVIRUS MULTIPLICATION 1 (TO		3.39	promoter
AT5G64530	XYLEM NAC DOMAIN 1 (XND1)	xylem NAC dorr 5_25793935	3.39	proximal promoter
AT5G67030	ABA DEFICIENT 1 (ABA1)	Encodes a singl 5 26757328	3.38	promoter
AT5G01340	MITOCHONDRIAL SUCCINATE-FUMARA	Mitochondrial st 5_145033	3.38	promoter
AT3G27920	MYB DOMAIN PROTEIN 0 (MYB0)	Encodes a Myb 3_10365258	3.38	proximal promoter
AT5G26600	na	Pyridoxal phosp 5_9377281	3.38	promoter
AT1G67300	na	Major facilitator 1_25197054	3.38	five_prime_UTR
AT1G74088	na	FUNCTIONS IN 1_27859561	3.38	proximal promoter
AT4G01810	na	Sec23/Sec24 pi 4_780478	3.38	promoter
AT5G66070	na	RING/U-box su ₁ 5_26421754	3.38	promoter
AT5G59830	na	unknown proteir 5_24105032	3.38	promoter
AT1G76660 AT2G01690	na na	FUNCTIONS IN 1_28772649 ARM repeat sur 2_313832	3.38 3.38	proximal promoter promoter
AT2G01690 AT2G24160	na na	pseudogene, lei 2_10271453	3.38	proximal promoter
AT2G24160	na	transposable el 2_10490437	3.38	exon
AT2G24000 AT2G28510	na	Dof-type zinc fir 2_12202044	3.38	proximal promoter
AT1G56020	na	unknown proteir 1_20953478	3.38	three_prime_UTR
AT1G76670	na	Nucleotide-suga 1_28772649	3.38	three_prime_UTR
AT3G17090	na	Protein phosphe 3 5826726	3.38	promoter
AT2G38070	na	Protein of unknc 2_15928556	3.38	promoter
AT3G61790	na	Protein with RIN 3_22873854	3.38	promoter
AT5G01350	na	unknown proteir 5_145033	3.38	intergenic
AT5G17900	na	microfibrillar-as: 5_5924533	3.38	promoter
AT1G21640	NAD KINASE 2 (NADK2)	Encodes a prote 1_7588564	3.38	intron
AT3G20970	NFU DOMAIN PROTEIN 4 (NFU4)	Encodes a prote 3_7348207	3.38	five_prime_UTR
AT3G25165	RALF-LIKE 25 (RALFL25)	Member of a div 3_9164975	3.38	proximal promoter
AT1G10470	RESPONSE REGULATOR 4 (ARR4) UROPHORPHYRIN METHYLASE 1 (UPM	Encodes a two- 1_3444776	3.38	proximal promoter five prime UTR
AT5G40850 AT2G06925	(PLA2-ALPHA)	Encodes a urop 5_16366528 Encodes a secr 2_2843249	3.38 3.37	five_prime_UTR five_prime_UTR
AT3G54690	(SETH3)	Sugar isomeras 3_20246414	3.37	promoter
AT4G15480	(UGT84A1)	Encodes a prot 4_8851315	3.37	proximal promoter
AT1G04220	3-KETOACYL-COA SYNTHASE 2 (KCS2)		3.37	intron
AT5G58890	AGAMOUS-LIKE 82 (AGL82)	AGAMOUS-like 5_23782966	3.37	intergenic
AT5G60790	ATP-BINDING CASSETTE F1 (ABCF1)	member of GCN 5_24456082	3.37	promoter
AT3G44340	CLONE EIGHTY-FOUR (CEF)	homologous to 13_16020327	3.37	promoter
AT5G51070	EARLY RESPONSIVE TO DEHYDRATION		3.37	promoter
AT5G50950	FUMARASE 2 (FUM2)	Encodes a fuma 5_20728211	3.37	proximal promoter
AT4G32890	GATA TRANSCRIPTION FACTOR 9 (GAT		3.37	five_prime_UTR
AT1G50900	GRANA DEFICIENT CHLOROPLAST 1 (C		3.37	promoter
AT4G00950	MATERNAL EFFECT EMBRYO ARREST		3.37	proximal promoter
AT5G60890	MYB DOMAIN PROTEIN 34 (MYB34)	Myb-like transcr 5_24495702	3.37	exon

AT4C10420		unknown proteir 4 10600097	3.37	provimal promotor
AT4G19430 AT1G50890	na na	ARM repeat sur 1_18866028	3.37	proximal promoter five prime UTR
AT1G77660	na	Histone H3 K4-: 1_29187923	3.37	promoter
AT2G40435	na	BEST Arabidop: 2_16885842	3.37	proximal promoter
AT2G43460	na	Ribosomal L38€ 2_18045788	3.37	downstream
AT3G04640	na	glycine-rich prot 3_1261040	3.37	three_prime_UTR
AT3G10970	na	Haloacid dehalc 3_3436351	3.37	promoter
AT3G54680	na	proteophosphor 3_20246414	3.37	intergenic
AT5G58900	na	Homeodomain-I 5_23782966	3.37	downstream
AT5G59790	na	CONTAINS Inte 5_24090736	3.37	five_prime_UTR
AT5G02450	na	Ribosomal prote 5_535080	3.37 3.37	intergenic
AT5G41670	na	6-phosphoglucc 5_16667346		promoter
AT5G41675 AT4G21350	na PLANT U-BOX 8 (PUB8)	pre-tRNA; tRNA 5_16667346 Encodes a U-bc 4 11357512	3.37 3.37	downstream promoter
AT3G18830	POLYOL/MONOSACCHARIDE TRANSPO		3.37	five_prime_UTR
AT1G79670	RESISTANCE TO FUSARIUM OXYSPOR		3.37	exon
AT5G53970	TYROSINE AMINOTRANSFERASE 7 (TA		3.37	proximal promoter
AT3G04630	WVD2-LIKE 1 (WDL1)	Member of a srr 3_1261040	3.37	downstream
AT2G37250	ADENOSINE KINASE (ADK)	encodes adenyl 2_15641917	3.36	five_prime_UTR
AT1G79440	ALDEHYDE DEHYDROGENASE 5F1 (ALI		3.36	promoter
AT5G07300	BONZAI 2 (BON2)	Encodes a copii 5_2303241	3.36	three_prime_UTR
AT5G04870	CALCIUM DEPENDENT PROTEIN KINAS		3.36	promoter
AT4G31380	FPF1-LIKE PROTEIN 1 (FLP1)	encodes a smal 4_15228797	3.36	proximal promoter
AT1G80340 AT4G35860	GIBBERELLIN 3-OXIDASE 2 (GA3OX2)	Encodes a proti 1_30201125	3.36 3.36	exon
AT4G35660 AT4G01680	GTP-BINDING 2 (GB2) MYB DOMAIN PROTEIN 55 (MYB55)	GTP-binding prc 4_16989297 Encodes a puta 4_718194	3.36	promoter
AT2G16720	MYB DOMAIN PROTEIN 33 (MYB33)	Encodes a merr 2_7258962	3.36	proximal promoter proximal promoter
AT1G24330	na	ARM repeat sur 1_8631329	3.36	promoter
AT1G66553	na	unknown proteir 1_24831337	3.36	downstream
AT3G17680	na	Kinase interactii 3_6044617	3.36	promoter
AT3G26750	na	CONTAINS Inte 3_9842185	3.36	promoter
AT4G12790	na	P-loop containir 4_7519512	3.36	promoter
AT1G73900	na	pre-tRNA; tRNA 1_27789048	3.36	exon
AT5G25600	na	BEST Arabidop: 5_8912097	3.36	intergenic
AT1G12064	na	unknown proteir 1_4078167	3.36	promoter
AT1G15650	na	pre-tRNA; tRNA 1_5380995	3.36	downstream
AT1G56045	na	Ribosomal prote 1_20962550	3.36	promoter
AT1G60590 AT1G72940	na	Pectin lyase-lik€ 1_22319494 Toll-Interleukin-l 1 27442149	3.36 3.36	proximal promoter promoter
AT1G72940 AT1G26208	na na	Potential natura 1_9066526	3.36	downstream
AT1G26930	na	Galactose oxida 1_9340078	3.36	proximal promoter
AT1G30340	na	transposable el 1_10694597	3.36	proximal promoter
AT3G04760	na	Pentatricopeptic 3_1305922	3.36	promoter
AT3G10970	na	Haloacid dehalc 3_3431722	3.36	intergenic
AT3G60286	na	This gene enco 3_22281844	3.36	exon
AT5G04880	na	pseudogene of . 5_1420464	3.36	intergenic
AT5G07310	na	encodes a mem 5_2303241	3.36	proximal promoter
AT5G15700	na	Nucleus encod 5_5122411	3.36	proximal promoter
AT5G15710	na	Galactose oxida 5_5122411	3.36	promoter
AT5G39320	na	UDP-glucose 6- 5_15742670	3.36	promoter
AT5G53340 AT4G21680	na NITRATE TRANSPORTER 1.8 (NRT1.8)	Galactosyltrans 5_21643731 Encodes a nitra 4_11522176	3.36 3.36	promoter proximal promoter
AT4G21080 AT4G30210	P450 REDUCTASE 2 (ATR2)	Encodes NADP 4_14795917	3.36	proximal promoter
AT1G78540	SH2 DOMAIN PROTEIN B (SHB)	Encodes a prote 1_29544855	3.36	promoter
AT1G26210	SOB FIVE-LIKE 1 (SOFL1)	AtSOFL1 acts r 1_9066526	3.36	proximal promoter
AT3G51895	SULFATE TRANSPORTER 3;1 (SULTR3;		3.36	proximal promoter
AT5G26910	TON1 RECRUITING MOTIF 8 (TRM8)	unknown proteir 5_9470392	3.36	five_prime_UTR
AT5G50810	TRANSLOCASE INNER MEMBRANE SUI	Encodes a smal 5_20676745	3.36	promoter
AT5G58180	(ATYKT62)	member of YKT 5_23545472	3.35	intron
AT3G10800	(BZIP28)	Encodes bZIP2l 3_3379309	3.35	five_prime_UTR
AT5G02470	(DPA)	core cell cycle c 5_542269	3.35	downstream
AT1G62380	ACC OXIDASE 2 (ACO2)	Encodes a proti 1_23083535	3.35	exon
AT5G65890 AT2G37940	ACT DOMAIN REPEAT 1 (ACR1) ARABIDOPSIS INOSITOL PHOSPHORYL	Member of ACT 5_26358078	3.35 3.35	downstream proximal promoter
AT1G71800	CLEAVAGE STIMULATING FACTOR 64 (3.35	exon
AT5G09463	CONSERVED PEPTIDE UPSTREAM OPE		3.35	promoter
AT5G09462	CONSERVED PEPTIDE UPSTREAM OPE		3.35	promoter
AT5G09461	CONSERVED PEPTIDE UPSTREAM OPE	Upstream open 5_2946857	3.35	promoter
AT5G16715		embryo defectiv 5_5493318	3.35	three_prime_UTR
AT3G12080	EMBRYO DEFECTIVE 2738 (emb2738)	embryo defectiv 3_3847702	3.35	promoter
AT1G10910	EMBRYO DEFECTIVE 3103 (EMB3103)	Pentatricopeptic 1_3639709	3.35	promoter
AT5G58190	EVOLUTIONARILY CONSERVED C-TERI		3.35	proximal promoter
AT1G46264	HEAT SHOCK TRANSCRIPTION FACTOR HISTONE ACETYLTRANSFERASE OF TH		3.35	proximal promoter
AT5G64610 AT3G58030	na	RING/U-box su; 3 21484401	3.35 3.35	promoter intron
AT5G33030	na	Dof-type zinc fir 5_542269	3.35	proximal promoter
AT1G64650	na	Major facilitator 1 24026620	3.35	promoter
AT1G74860	na	unknown proteir 1 28123163	3.35	promoter
AT1G77560	na	pre-tRNA; tRNA 1_29143167	3.35	promoter
AT2G22180	na	hydroxyproline-ı 2_9431281	3.35	intergenic
AT3G14710	na	RNI-like superfa 3_4943297	3.35	intergenic
AT4G11450	na	Protein of unkno 4_6962118	3.35	promoter
AT5G09460	na	sequence-speci 5_2946857	3.35	promoter
AT5G16720	na	Protein of unkno 5_5493318	3.35	proximal promoter
AT4G35080	na	high-affinity nick 4_16696928	3.35	proximal promoter
AT4G35985 AT5G65900	na na	Senescence/del 4_17034011 DEA(D/H)-box F 5 26358078	3.35 3.35	promoter promoter
AT2G43020	POLYAMINE OXIDASE 2 (PAO2)	Encodes a poly: 2_17891042	3.35	promoter
AT5G16400	THIOREDOXIN F2 (TRXF2)	Encodes an f-ty 5_5365401	3.35	promoter
AT2G18700	TREHALOSE PHOSPHATASE/SYNTHAS		3.35	proximal promoter
AT1G26570	UDP-GLUCOSE DEHYDROGENASE 1 (U		3.35	promoter
AT5G64940		Encodes a merr 5_25948807	3.34	promoter
AT0007000	ABC2 HOMOLOG 13 (ATH13)			
AT2G27228	CONSERVED PEPTIDE UPSTREAM OPE	Upstream open 2_11650287	3.34	promoter
AT5G43430		Upstream open 2_11650287		promoter promoter

AT5G57685	GLUTAMINE DUMPER 3 (GDU3)	Encodes a merr 5_23365805	3.34	downstream
AT2G45480	GROWTH-REGULATING FACTOR 9 (GR		3.34	promoter
AT2G27230	LONESOME HIGHWAY (LHW)	Encodes a nucl 2_11650287	3.34	promoter
AT1G13370	na	Histone superfa 1_4585463	3.34	intergenic
AT4G24970	na	Histidine kinase 4_12831131	3.34	exon
AT4G20310	na	Peptidase M50 4_10964867	3.34	intergenic
AT5G12850	na	CCCH-type zinc 5_4056093	3.34	promoter
AT2G35410	na	RNA-binding (R 2_14898289	3.34	promoter
AT1G11125	na	unknown proteir 1_3719539	3.34	exon
AT1G48745	na	unknown proteir 1_18030571	3.34	promoter
AT2G27229	na	Pentatricopeptic 2_11650287	3.34	intergenic
AT3G10760	na	Homeodomain-I 3_3371649	3.34	intergenic
AT3G10770	na	Single-stranded 3_3371649	3.34	intergenic
AT3G12910	na	NAC (No Apical 3_4107233	3.34	proximal promoter
AT4G10080	na	unknown proteir 4_6302695	3.34	promoter
AT4G13265	na	pre-tRNA; tRNA 4_7731121	3.34	downstream
AT4G13270	na	Late embryoger 4_7731121	3.34	promoter
AT4G14200	na	Pentatricopeptic 4_8188760	3.34	five_prime_UTR
AT4G27270	na	Quinone reduct: 4_13661269	3.34	downstream
AT4G37180	na	myb family trans 4_17506898	3.34	intergenic
AT4G33640	na	unknown proteir 4_16160350	3.34	promoter
AT5G40450	na	unknown proteir 5_16197233	3.34	proximal promoter
AT4G37190	na	LOCATED IN: c 4_17506898	3.34	promoter
AT5G47860	na	Protein of unknr 5_19381364	3.34	promoter
AT1G69295	PLASMODESMATA CALLOSE-BINDING		3.34	proximal promoter
AT5G60690	REVOLUTA (REV)	REVOLUTA reg 5_24397031	3.34	five_prime_UTR
AT5G48880	3-KETO-ACYL-COENZYME A THIOLASE		3.33	proximal promoter
AT3G18690	MAP KINASE SUBSTRATE 1 (MKS1)	Encodes a nucl 3_6430520	3.33	promoter
AT1G48095	na	unknown proteir 1_17763722	3.33	intergenic
AT2G03290	na	emp24/gp25L/p 2_999356	3.33	promoter
AT2G34620	na	Mitochondrial tr. 2_14577069	3.33	promoter
AT3G54390	na	sequence-speci 3_20140791	3.33	proximal promoter
AT3G54400	na	Eukaryotic aspa 3_20140791	3.33	intron
AT5G66780	na	unknown proteir 5_26663253	3.33	promoter
AT2G07170	na	ARM repeat sur 2_2974948	3.33	promoter
AT2G17160	na	Interleukin-1 rec 2_7472434	3.33	promoter
AT2G02780	na	Leucine-rich reg 2_784836	3.33	promoter
AT2G11140	na	transposable el 2_4416600	3.33	downstream
AT1G52905	na	unknown proteir 1_19705866	3.33	promoter
AT1G71710	na	DNAse I-like su _l 1_26978569	3.33	intron
AT2G25800	na	CONTAINS Inte 2_11009713	3.33	exon
AT3G56200	na	Encodes a puta 3_20849891	3.33	promoter
AT5G02680	na	LOCATED IN: e 5_608349	3.33	downstream
AT5G02690	na	unknown proteir 5_608349	3.33	intergenic
AT5G39030	na	Protein kinase s 5_15619928	3.33	promoter
AT5G66180	na	S-adenosyl-L-m 5_26448896	3.33	promoter
AT2G28610	PRESSED FLOWER (PRS)	Encodes a hom 2_12263155	3.33	exon
AT3G05030	SODIUM HYDROGEN EXCHANGER 2 (N	Encodes a vacu 3_1396033	3.33	intron
AT1G04750	VESICLE-ASSOCIATED MEMBRANE PR	Encodes vesicle 1_1333663	3.33	promoter
AT1G66140	ZINC FINGER PROTEIN 4 (ZFP4)	Encodes a zinc 1_24622017	3.33	promoter
AT1G28290	ARABINOGALACTAN PROTEIN 31 (AGP	Encodes an aty 1_9895265	3.32	intergenic
AT4G19210	ATP-BINDING CASSETTE E2 (ABCE2)	member of RLI : 4_10501145	3.32	promoter
AT5G41410	BELL 1 (BEL1)	Homeodomain r 5_16578949	3.32	proximal promoter
AT3G14680	CYTOCHROME P450, FAMILY 72, SUBFA	putative cytochr 3_4933042	3.32	proximal promoter
AT4G38170	FAR1-RELATED SEQUENCE 9 (FRS9)	FAR1-related st 4_17904297	3.32	promoter
AT5G49730	FERRIC REDUCTION OXIDASE 6 (FRO6		3.32	intergenic
AT5G49720	GLYCOSYL HYDROLASE 9A1 (GH9A1)	Encodes a merr 5_20200487	3.32	promoter
AT4G31560	HIGH CHLOROPHYLL FLUORESCENCE	Encodes HCF1! 4_15295137	3.32	promoter
AT5G47010	LOW-LEVEL BETA-AMYLASE 1 (LBA1)	Required for no 5_19071821	3.32	promoter
AT2G43790	MAP KINASE 6 (MPK6)	Encodes a MAF 2_18137684	3.32	proximal promoter
AT1G06180	MYB DOMAIN PROTEIN 13 (MYB13)	member of MYE 1_1890385	3.32	intron
AT3G58640	na	Mitogen activate 3_21693922	3.32	promoter
AT1G11175	na	other RNA 1_3745534	3.32	exon
AT1G20875	na	unknown proteir 1_7261650	3.32	exon
AT3G22290	na	Endoplasmic rel 3_7880568	3.32	proximal promoter
AT4G26130	na	unknown proteir 4_13239015	3.32	intergenic
AT1G18415	na	Potential natura 1_6345752	3.32	promoter
AT1G18420	na	Aluminium activ 1_6345752	3.32	downstream
AT1G18430	na	pre-tRNA; tRNA 1_6345752	3.32	promoter
AT2G43780	na	unknown proteir 2_18137684	3.32	promoter
AT1G14450	na	NADH dehydrog 1_4946081	3.32	downstream
AT1G54670	na	pre-tRNA; tRNA 1_20413041	3.32	promoter
AT2G22220	na	pre-tRNA; tRNA 2_9449908	3.32	promoter
AT2G22230	na	Thioesterase su 2_9449908	3.32	promoter
AT2G27480	na	Calcium-binding 2_11746567	3.32	promoter
AT1G01320	na	Tetratricopeptid 1_128457	3.32	intron
AT2G45023	na	other RNA 2_18572204	3.32	promoter
AT1G68410	na	Protein phospha 1_25652954	3.32	intron
AT3G52460	na	hydroxyproline-ı 3_19445818	3.32	proximal promoter
AT3G57340	na	FUNCTIONS IN 3_21217943	3.32	proximal promoter
AT3G57360	na	unknown proteir 3_21225489	3.32	promoter
AT4G01960	na	unknown proteir 4_853582	3.32	promoter
AT4G17070	na	peptidyl-prolyl c 4_9598186	3.32	five_prime_UTR
AT4G17390	na	Ribosomal prote 4_9715672	3.32	promoter
AT4G17410	na	DWNN domain, 4_9715672	3.32	promoter
AT4G19200	na	proline-rich fami 4_10501145	3.32	intergenic
AT5G16030	na	unknown proteir 5_5236701	3.32	proximal promoter
AT5G01445		unknown proteir 5_182551	3.32	five_prime_UTR
	na			
AT5G24230	na na	Lipase class 3-r 5_8229682	3.32	exon
		Lipase class 3-r 5_8229682 chaperone bind 5_23515105	3.32 3.32	exon promoter
AT5G24230 AT5G58110 AT5G64090	na	Lipase class 3-r 5_8229682 chaperone bind 5_23515105 FUNCTIONS IN 5_25647915	3.32 3.32	promoter promoter
AT5G24230 AT5G58110 AT5G64090 AT5G67140	na na	Lipase class 3-r 5_8229682 chaperone bindi 5_23515105 FUNCTIONS IN 5_25647915 F-box/RNI-like s 5_26797336	3.32 3.32 3.32	promoter promoter proximal promoter
AT5G24230 AT5G58110 AT5G64090 AT5G67140 AT5G67150	na na na na na	Lipase class 3-r 5_8229682 chaperone bind 5_23515105 FUNCTIONS IN 5_25647915 F-box/RNI-like s 5_26797336 HXXXD-type ac 5_26797336	3.32 3.32 3.32 3.32	promoter promoter proximal promoter promoter
AT5G24230 AT5G58110 AT5G64090 AT5G67140	na na na na	Lipase class 3-r 5_8229682 chaperone bind 5_23515105 FUNCTIONS IN 5_25647915 F-box/RNI-like s 5_26797336 HXXXD-type ac 5_26797336	3.32 3.32 3.32	promoter promoter proximal promoter

AT5G60040	NUCLEAR RNA POLYMERASE C1 (NRP	Encodes a subi 5_24173217	3.32	promoter
AT1G56250	PHLOEM PROTEIN 2-B14 (PP2-B14)	Encodes an F-b 1_21060682	3.32	intergenic
AT4G38160	PIGMENT DEFECTIVE 191 (pde191)	pigment defectiv 4_17904297	3.32	intron
AT5G55190	RAN GTPASE 3 (RAN3)	A member of R/ 5_22392143	3.32	promoter
AT1G11180	SECRETORY CARRIER MEMBRANE PR	Secretory carrie 1_3745534	3.32	promoter
AT3G16290	EMBRYO DEFECTIVE 2083 (EMB2083)	embryo defectiv 3_5525225	3.31	promoter
AT1G08720	ENHANCED DISEASE RESISTANCE 1 (E		3.31	promoter
AT1G69410	EUKARYOTIC ELONGATION FACTOR 5/	_	3.31	promoter
AT1G13250	GALACTURONOSYLTRANSFERASE-LIK		3.31	intergenic
AT3G45210	na	Protein of unknc 3_16559642	3.31	proximal promoter
AT1G13370	na	Histone superfa 1_4587497	3.31	intergenic
AT1G65560	na	Zinc-binding del 1_24373797	3.31	five_prime_UTR
AT2G30230	na	unknown proteir 2_12898484	3.31	intergenic
AT4G23930	na	Late embryoger 4_12436855	3.31	promoter
AT5G65440 AT5G08600	na	unknown proteir 5_26157381	3.31 3.31	intergenic
AT5G08600	na na	U3 ribonucleopr 5_2790089 pre-tRNA; tRNA 5_26157381	3.31	intron
	NONPHOTOCHEMICAL QUENCHING 6 (promoter promoter
AT5G43050 AT5G23090	NUCLEAR FACTOR Y, SUBUNIT B13 (NF		3.31 3.31	
AT3G25030	PHOTOSYSTEM I SUBUNIT H-1 (PSAH-1		3.31	promoter promoter
AT5G08610	PIGMENT DEFECTIVE 340 (PDE340)	P-loop containir 5_2790089	3.31	promoter
AT2G01570	REPRESSOR OF GA1-3 1 (RGA1)	Member of the \ 2 257419	3.31	five_prime_UTR
AT1G05680	URIDINE DIPHOSPHATE GLYCOSYLTRA		3.31	promoter
AT2G21150	XAP5 CIRCADIAN TIMEKEEPER (XCT)	XAP5 family prc 2_9064501	3.31	proximal promoter
AT5G05690	CONSTITUTIVE PHOTOMORPHOGENIC		3.3	proximal promoter
AT1G61210	DWD HYPERSENSITIVE TO ABA 3 (DWA		3.3	promoter
AT1G47128	ESPONSIVE TO DEHYDRATION 21A (RE		3.3	intergenic
AT1G80790	FACTOR OF DNA METHYLATION 5 (FDM		3.3	promoter
AT5G47770	FARNESYL DIPHOSPHATE SYNTHASE		3.3	downstream
AT5G08640	FLAVONOL SYNTHASE 1 (FLS1)	Encodes a flavc 5_2803861	3.3	promoter
AT5G47780	GALACTURONOSYLTRANSFERASE 4 (3.3	promoter
AT3G13222	GBF-INTERACTING PROTEIN 1 (GIP1)	Encodes a prote 3 4254475	3.3	promoter
AT3G58680	MULTIPROTEIN BRIDGING FACTOR 1B		3.3	downstream
AT3G24640	na	lyases; BEST A 3_8993993	3.3	intergenic
AT4G36370	na	unknown proteir 4_17187436	3.3	intron
AT3G04485	na	Unknown gene 3_1198743	3.3	intron
AT1G04501	na	unknown proteir 1_1224638	3.3	exon
AT5G08630	na	DDT domain-co 5 2803861	3.3	proximal promoter
AT1G10110	na	F-box family prc 1_3302454	3.3	promoter
AT1G10110	na	basal transcripti 1_6311397	3.3	downstream
AT1G66130	na	NAD(P)-binding 1_24615493	3.3	exon
AT1G76350	na	Plant regulator I 1_28639540	3.3	promoter
AT1G70330	na	Polynucleotidyl 1_30359573	3.3	intron
AT2G18770	na	P-loop containir 2_8134520	3.3	promoter
AT1G18335	na	Acyl-CoA N-acy 1_6311397	3.3	promoter
AT3G13223	na	pre-tRNA; tRNA 3_4254475	3.3	promoter
AT3G13223	na	Pectin lyase-like 3 19712632	3.3	proximal promoter
AT3G58690	na	Protein kinase s 3_21709065	3.3	promoter
AT4G33380	na	unknown proteir 4_16071838	3.3	intron
AT5G59150	RAB GTPASE HOMOLOG A2D (RABA2D		3.3	promoter
AT5G58590	RAN BINDING PROTEIN 1 (RANBP1)	Encodes a Ran 5_23679869	3.3	downstream
AT4G36380	ROTUNDIFOLIA 3 (ROT3)	Encodes a cyto 4_17187436	3.3	downstream
AT2G40160	(TBL30)	Encodes a cytor 4_17107450 Encodes a merr 2_16779250	3.29	three_prime_UTR
AT3G14370	(WAG2)	The WAG2 and 3 4800770	3.29	proximal promoter
AT3G46090	(ZAT7)	ZAT7; FUNCTIC 3_16927488	3.29	proximal promoter
AT5G13160	AVRPPHB SUSCEPTIBLE 1 (PBS1)	Mutant is defect 5 4176593	3.29	five_prime_UTR
AT2G23760	BEL1-LIKE HOMEODOMAIN 4 (BLH4)	Encodes a merr 2 10113066	3.29	intron
AT5G64050	GLUTAMATE TRNA SYNTHETASE (ERS	_	3.29	promoter
AT2G40170	LATE EMBRYOGENESIS ABUNDANT 6 (3.29	intergenic
AT5G09690	MAGNESIUM TRANSPORTER 7 (MGT7)		3.29	promoter
AT5G03552	MICRORNA822A (MIR822A)	Encodes a micr 5 898063	3.29	proximal promoter
AT1G28180	na	P-loop containir 1_9846108	3.29	proximal promoter
AT1G46554	na	other RNA 1 17253737	3.29	exon
AT1G77680	na	Ribonuclease II/ 1_29196308	3.29	promoter
AT2G22482	na	na 2_9552890	3.29	proximal promoter
AT1G03180	na	unknown proteir 1_773318	3.29	promoter
AT1G03290	na	unknown proteir 1_807288	3.29	promoter
AT1G33415	na	Potential natura 1_12123608	3.29	intron
AT1G33420	na	RING/FYVE/PH 1_12123608	3.29	promoter
AT1G35110	na	transposable el 1_12840294	3.29	exon
AT2G23820	na	Metal-depender 2_10140400	3.29	promoter
AT3G06680	na	Ribosomal L29€ 3_2114902	3.29	intron
AT3G28690	na	Protein kinase s 3_10754955	3.29	promoter
AT4G02940	na	oxidoreductase, 4_1306508	3.29	five_prime_UTR
AT5G01650	na	Tautomerase/M 5_244191	3.29	promoter
AT5G11310	na	Pentatricopeptic 5_3606350	3.29	promoter
AT5G38155	na	pre-tRNA; tRNA 5_15225314	3.29	promoter
AT5G03555	NUCLEOBASE CATION SYMPORTER 1		3.29	downstream
AT1G35112	SADHU NON-CODING RETROTRANSPO		3.29	exon
AT1G32050	SECRETORY CARRIER MEMBRANE PR		3.29	promoter
AT1G66140	ZINC FINGER PROTEIN 4 (ZFP4)	Encodes a zinc 1_24624108	3.29	proximal promoter
AT5G08530	51 KDA SUBUNIT OF COMPLEX I (CI51)		3.28	promoter
AT2G33310	AUXIN-INDUCED PROTEIN 13 (IAA13)	Auxin induced c 2_14116017	3.28	five_prime_UTR
AT4G33580	BETA CARBONIC ANHYDRASE 5 (BCA5		3.28	intron
AT4G08920	CRYPTOCHROME 1 (CRY1)	Encodes CRY1, 4_5718637	3.28	intergenic
AT5G52320	CYTOCHROME P450, FAMILY 96, SUBFA		3.28	proximal promoter
AT1G03170	FANTASTIC FOUR 2 (FAF2)	A member of the 1_768045	3.28	proximal promoter
AT4G13940	HOMOLOGY-DEPENDENT GENE SILEN		3.28	downstream
AT4G14750	IQ-DOMAIN 19 (IQD19)	IQ-domain 19 (I 4_8469418	3.28	proximal promoter
AT1G69610	na	FUNCTIONS IN 1_26187597	3.28	exon
AT4G16380	na	Heavy metal tra 4_9254481	3.28	promoter
AT2G37540	na	NAD(P)-binding 2_15753987	3.28	promoter
AT5G61520	na	Major facilitator 5_24738919	3.28	downstream
AT5G61510	na	GroES-like zinc 5_24738919	3.28	exon

AT1G07310	na	Calcium-depend 1_2249033	3.28	promoter
AT1G29470	na	S-adenosyl-L-m 1_10314156	3.28	promoter
AT1G30730	na	FAD-binding Be 1_10900253	3.28	proximal promoter
AT2G01680	na	Ankyrin repeat f 2_302810	3.28	intergenic
AT1G30720	na	FAD-binding Be 1_10900253	3.28	intergenic
AT2G30960	na	unknown proteir 2_13177544	3.28	exon
AT3G15900	na	unknown proteir 3_5377066	3.28	five_prime_UTR
AT3G52565	na	pre-tRNA; tRNA 3_19499941	3.28	proximal promoter
AT4G33565	na	RING/U-box su ₁ 4_16139141	3.28	intergenic
AT4G39780	na	encodes a mem 4_18457062	3.28	intergenic
AT5G24210	na	alpha/beta-Hydr 5_8216222	3.28	proximal promoter
AT5G08535	na	D111/G-patch d 5_2762000	3.28	promoter
AT5G46080	na	Protein kinase s 5_18690557	3.28	exon
AT5G57300	na	S-adenosyl-L-m 5_23211230	3.28	promoter
AT5G57310	na	unknown proteir 5_23211230	3.28	intron
AT5G64880	na	unknown proteir 5_25932288	3.28	promoter
AT4G13950	RALF-LIKE 31 (RALFL31)	Member of a div 4_8057258	3.28	intergenic
AT3G09270	GLUTATHIONE S-TRANSFERASE TAU 8		3.27	proximal promoter
AT5G12930 AT4G39600	na	unknown proteir 5_4086013	3.27	proximal promoter
AT1G02080	na na	Galactose oxida 4_18390673	3.27 3.27	promoter
	• • • • • • • • • • • • • • • • • • • •	transcription rec 1_373441		intron
AT1G79529	na	Potential natura 1_29915470	3.27	promoter
AT1G19835	na	Plant protein of 1_6865815	3.27	intergenic
AT1G79520	na	Cation efflux far 1_29915470	3.27	proximal promoter
AT3G01513	na	unknown proteir 3_204394	3.27	proximal promoter
AT3G61028	na	Putative endoni 3_22582664	3.27	intron
AT4G23740	na	Leucine-rich rer 4_12369523	3.27	downstream
AT5G14230	na	CONTAINS Inte 5_4591686	3.27	promoter
AT5G12010	na	unknown proteir 5_3880829	3.27	proximal promoter
AT4G19170	NINE-CIS-EPOXYCAROTENOID DIOXYG		3.27	promoter
AT2G40380	PRENYLATED RAB ACCEPTOR 1.B2 (PR		3.27	five_prime_UTR
AT2G21790	RIBONUCLEOTIDE REDUCTASE 1 (RNF		3.27	promoter
AT4G33210	SLOW MOTION (SLOMO)	Encodes SLOM 4_16021249	3.27	promoter
AT4G32660	(AME3)	Encodes proteir 4_15756016	3.26	promoter
AT5G65050	AGAMOUS-LIKE 31 (AGL31)	Originally publis 5_25982161	3.26	promoter
AT5G18120	APR-LIKE 7 (APRL7)	Encodes a prote 5_5990871	3.26	promoter
AT5G17290	AUTOPHAGY 5 (APG5)	Autophagy prote 5_5689917	3.26	promoter
AT3G49670	BARELY ANY MERISTEM 2 (BAM2)	Encodes a CLA 3_18417153	3.26	promoter
AT1G69370	CHORISMATE MUTASE 3 (CM3)	Encodes choris 1_26080003	3.26	five_prime_UTR
AT3G61130	GALACTURONOSYLTRANSFERASE 1 (0	Encodes a prote 3_22621982	3.26	five_prime_UTR
AT1G06520	GLYCEROL-3-PHOSPHATE ACYLTRANS	Encodes a men 1_1998420	3.26	proximal promoter
AT1G05550	na	Protein of unknc 1_1642979	3.26	intron
AT1G65820	na	microsomal glut 1_24484994	3.26	promoter
AT2G37440	na	DNAse I-like su 2_15721819	3.26	exon
AT2G37450	na	nodulin MtN21-l 2_15721819	3.26	intergenic
AT3G62580	na	Late embryoger 3_23145579	3.26	proximal promoter
AT4G22320	na	unknown proteir 4_11794911	3.26	promoter
AT4G29440	na	Regulator of Vp 4_14477893	3.26	intron
AT5G62910	na	RING/U-box su ₁ 5_25250525	3.26	intron
AT1G61330	na	FBD, F-box and 1_22625699	3.26	intergenic
AT1G70350	na	unknown proteir 1_26508423	3.26	promoter
AT1G70810	na	Calcium-depend 1_26704029	3.26	promoter
AT2G20060	na	Ribosomal prote 2_8658903	3.26	promoter
AT3G50520	na	Phosphoglycera 3_18750154	3.26	intergenic
AT3G56050	na	Protein kinase f: 3_20797753	3.26	downstream
AT4G05060	na	PapD-like super 4_2592135	3.26	five prime UTR
AT5G22390	na	Protein of unknc 5 7416323	3.26	intergenic
AT5G02870	na	Ribosomal prote 5_657692	3.26	promoter
AT5G18110	NOVEL CAP-BINDING PROTEIN (NCBP)		3.26	promoter
AT2G28930	PROTEIN KINASE 1B (PK1B)	protein kinase 1 2 12421485	3.26	proximal promoter
AT5G17300	REVEILLE 1 (RVE1)	Myb-like transcr 5_5693474	3.26	proximal promoter
AT5G17300	REVEILLE 1 (RVE1)	Myb-like transcr 5_5689917	3.26	intergenic
AT3G57920	SQUAMOSA PROMOTER BINDING PRO		3.26	promoter
AT3G56040	UDP-GLUCOSE PYROPHOSPHORYLAS		3.26	
AT4G29140	ACTIVATED DISEASE SUSCEPTIBILITY		3.25	promoter proximal promoter
AT1G19220	AUXIN RESPONSE FACTOR 19 (ARF19)		3.25	promoter
AT3G14010	CTC-INTERACTING DOMAIN 4 (CID4)	hydroxyproline-i 3_4636254	3.25	promoter
AT2G47220	DOMAIN OF UNKNOWN FUNCTION 724		3.25	promoter
AT1G18840	IQ-DOMAIN 30 (IQD30)	IQ-domain 30 (I 1_6504320	3.25	five_prime_UTR
AT4G29840	METHIONINE OVER-ACCUMULATOR 2		3.25	promoter
AT5G57910	na	unknown proteir 5_23451073	3.25	downstream
AT3G59923	na	pre-tRNA; tRNA 3 22138920	3.25	downstream
AT3G59925 AT3G59926	na	pre-tRNA; tRNA 3 22138920	3.25	promoter
AT3G59920 AT3G59930	na	Encodes a defe 3_22138920	3.25	intergenic
AT5G59930 AT5G64450	na	BEST Arabidop: 5_25771841	3.25	promoter
AT5G03668	na na	Potential natura 5_946357	3.25	intergenic
AT1G12330	na na	unknown proteir 1_4196239	3.25	intergenic
AT1G12330 AT2G36220	na na	unknown proteir 1_4196239 unknown proteir 2_15191148	3.25	proximal promoter
AT3G59020	na na	ARM repeat sur 3 21818269	3.25	proximal promoter
AT4G15975		RING/U-box suj 4_9052141	3.25	proximal promoter promoter
AT4G15975 AT4G24050	na na	NAD(P)-binding 4 12495203	3.25	promoter proximal promoter
AT4G24050 AT4G32760		ENTH/VHS/GA 4 15804663	3.25	intergenic
AT4G32760 AT4G32765	na na			downstream
	na	pre-tRNA; tRNA 4_15804663	3.25	
AT4G36510	na	unknown proteir 4_17228973	3.25	intron
AT5G61490	na	Uncharacterise: 5_24732489	3.25	promoter
AT4G25130	PEPTIDE MET SULFOXIDE REDUCTASE		3.25	five_prime_UTR
AT3G26570	PHOSPHATE TRANSPORTER 2;1 (PHT2		3.25	promoter
AT2G01660	PLASMODESMATA-LOCATED PROTEIN		3.25	exon
AT5G57900	SKP1 INTERACTING PARTNER 1 (SKIP1		3.25	promoter
AT5G03670	TON1 RECRUITING MOTIF 28 (TRM28)		3.25	proximal promoter
AT2G45660	AGAMOUS-LIKE 20 (AGL20)	Controls flowerii 2_18811177	3.24	promoter
AT2G32480	ARABIDOPSIS SERIN PROTEASE (ARAS		3.24	promoter
AT3G23210	BASIC HELIX-LOOP-HELIX 34 (bHLH34)		3.24	promoter
	BASIC LEUCINE-ZIPPER 2 (bZIP2)	Encodes a b-ZII 2_7899268	3.24	promoter
AT2G18160	5/10/0 2200//12 2// / 2// (b2// 2)			

AT4G18700	CBL-INTERACTING PROTEIN KINASE 12	Encodes CBI -ir 4 10293443	3.24	proximal promoter
AT2G18162	CONSERVED PEPTIDE UPSTREAM OPE		3.24	promoter
AT3G26200	CYTOCHROME P450, FAMILY 71, SUBF		3.24	promoter
AT3G26260 AT3G14650	CYTOCHROME P450, FAMILY 72, SUBF		3.24	promoter
AT5G66460			3.24	•
	ENDO-BETA-MANNASE 7 (MAN7)	Encodes a end: 5_26538238		downstream
AT2G47600	MAGNESIUM/PROTON EXCHANGER (M		3.24	promoter
AT1G79720	na	Eukaryotic aspa 1_29999096	3.24	promoter
AT5G44590	na	S-adenosyl-L-m 5_17987245	3.24	promoter
AT1G05020	na	ENTH/ANTH/VI 1_1437566	3.24	five_prime_UTR
AT4G36470	na	S-adenosyl-L-m 4_17217379	3.24	proximal promoter
AT5G02610	na	Ribosomal L29 5_587487	3.24	promoter
AT1G03270	na	CBS domain-co 1_799064	3.24	promoter
AT1G33475	na	SNARE-like sur 1_12148358	3.24	promoter
AT1G35220	na	unknown proteir 1_12908784	3.24	promoter
AT2G31730	na	basic helix-loop 2_13490110	3.24	promoter
AT2G31740	na	S-adenosyl-L-m 2_13490110	3.24	intergenic
AT3G04850	na	Tesmin/TSO1-lil 3_1336064	3.24	promoter
AT3G16510				
	na	Calcium-depend 3_5618575	3.24	promoter
AT2G41810	na	FUNCTIONS IN 2_17443848	3.24	proximal promoter
AT3G52765	na	pre-tRNA; tRNA 3_19554887	3.24	promoter
AT4G38760	na	Protein of unknc 4_18096302	3.24	promoter
AT4G22620	na	SAUR-like auxir 4_11907967	3.24	exon
AT4G22990	na	Major Facilitator 4_12051854	3.24	promoter
AT4G30750	na	unknown proteir 4_14982469	3.24	promoter
AT4G30760	na	Putative endon: 4_14982469	3.24	promoter
AT5G54145	na	unknown proteir 5_21971208	3.24	proximal promoter
AT5G59010	na	Protein kinase r 5_23824661	3.24	proximal promoter
AT5G01030	na	Protein of unkno 5 9798	3.24	promoter
AT5G25520		SPOC domain / 5 8884984		
	na	_	3.24	promoter
AT5G37750	na	Chaperone Dna 5_14994349	3.24	proximal promoter
AT5G47170	na	unknown proteir 5_19159194	3.24	promoter
AT5G60980	na	Nuclear transpc 5_24543340	3.24	promoter
AT5G66455	na	pseudogene of 5_26538238	3.24	promoter
AT2G27350	OTUBAIN-LIKE DEUBIQUITINASE 1 (OTL	Encodes an otu 2 11704317	3.24	promoter
AT4G38770	PROLINE-RICH PROTEIN 4 (PRP4)	Encodes one of 4 18096302	3.24	intergenic
AT3G16520	UDP-GLUCOSYL TRANSFERASE 88A1 (_	3.24	three_prime_UTR
AT4G30290	XYLOGLUCAN ENDOTRANSGLUCOSYL		3.24	promoter
AT1G01720	(ATAF1)	Belongs to a lar 1_266367	3.23	proximal promoter
AT1G15220	(CCMH)	Encodes a prote 1_5241520	3.23	five_prime_UTR
AT5G09320	(VPS9B)	VPS9B; CONT/ 5_2892883	3.23	proximal promoter
AT3G17590	BUSHY GROWTH (BSH)	Encodes the Ari 3_6019808	3.23	promoter
AT5G07070	CBL-INTERACTING PROTEIN KINASE 2	Encodes CBL-ir 5_2198563	3.23	promoter
AT4G16590	CELLULOSE SYNTHASE-LIKE A01 (CSL)	encodes a gene 4_9347858	3.23	intron
AT4G26500	CHLOROPLAST SULFUR E (CPSUFE)	Sulfur acceptor 4_13383714	3.23	promoter
AT3G42670	CHROMATIN REMODELING 38 (CHR38)		3.23	proximal promoter
AT1G15380	GLYOXYLASE I 4 (GLYI4)	Lactoylglutathio 1_5291714	3.23	intron
AT2G46180	GOLGIN CANDIDATE 4 (GC4)		3.23	
		This gene is pre 2_18971452		promoter
AT4G02670	INDETERMINATE(ID)-DOMAIN 12 (IDD12		3.23	exon
AT1G04550	INDOLE-3-ACETIC ACID INDUCIBLE 12 (3.23	five_prime_UTR
AT3G50310	MITOGEN-ACTIVATED PROTEIN KINASE	Encodes a men 3_18648865	3.23	exon
AT2G30362	na	Potential natura 2_12939488	3.23	exon
AT4G14300	na	RNA-binding (R 4_8230812	3.23	promoter
AT1G53370	na	F-box and asso 1_19913352	3.23	intergenic
AT2G32415	na	Polynucleotidyl 2 13765567	3.23	promoter
AT1G53380	na	Plant protein of 1_19913352	3.23	exon
AT4G23895	na	Pleckstrin home 4_12426390	3.23	three prime UTR
AT4G23910	na		3.23	
		unknown proteir 4_12426390		promoter
AT4G23900	na	Nucleoside diph 4_12426390	3.23	three_prime_UTR
AT5G09655	na	pre-tRNA; tRNA 5_2993260	3.23	promoter
AT3G07120	na	RING/U-box su _i 3_2254911	3.23	exon
AT5G23690	na	Polynucleotide ¿ 5_7987547	3.23	five_prime_UTR
AT4G36470	na	S-adenosyl-L-m 4_17214577	3.23	intergenic
AT4G36460	na	unknown proteir 4 17214577	3.23	proximal promoter
AT1G08115	na	U1A small nucle 1_2538254	3.23	promoter
AT1G26490	na	pre-tRNA; tRNA 1 9158182	3.23	promoter
AT1G64563	na	other RNA 1_23978508	3.23	promoter
AT1G79980	na	pre-tRNA; tRNA 1_30084114	3.23	promoter
AT1G79990 AT1G79990	na	structural molec 1 30084114	3.23	promoter
AT1G79990 AT2G14660	na	unknown proteir 2_6272372	3.23	promoter
AT1G01710	na	Acyl-CoA thioes 1_266367	3.23	three_prime_UTR
AT1G78840	na	F-box/RNI-like/F 1_29641272	3.23	promoter
AT3G08880	na	unknown proteir 3_2702810	3.23	promoter
AT3G16565	na	alanine-tRNA lic 3_5642767	3.23	promoter
AT3G42150	na	unknown proteir 3_14309304	3.23	promoter
AT3G56130	na	biotin/lipoyl atta 3_20826668	3.23	five_prime_UTR
AT4G02720	na	unknown proteir 4_1205947	3.23	promoter
AT4G02660				
	na	Beige/BEACH d 4_1176252	3.23	proximal promoter
AT4G02725				proximal promoter promoter
AT4G02725 AT4G16600	na na	unknown proteir 4_1205947	3.23	promoter
AT4G16600	na na na	unknown proteir 4_1205947 Nucleotide-diph 4_9347858	3.23 3.23	promoter proximal promoter
AT4G16600 AT5G44680	na na na na	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208	3.23 3.23 3.23	promoter proximal promoter downstream
AT4G16600 AT5G44680 AT5G60190	na na na na na	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prot 5_24234424	3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter
AT4G16600 AT5G44680 AT5G60190 AT5G35970	na na na na na na	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prote 5_24234424 P-loop containir 5_14123424	3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330	na na na na na NAC DOMAIN CONTAINING PROTEIN 82	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_1802428 Encodes a prote 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883	3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter exon
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330 AT5G09660	na na na na na na NAC DOMAIN CONTAINING PROTEIN 82 PEROXISOMAL NAD-MALATE DEHYDRO	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prote 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micre 5_2993260	3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter exon downstream
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330	na na na na na NAC DOMAIN CONTAINING PROTEIN 82	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_1802428 Encodes a prote 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883	3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter exon
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330 AT5G09660	na na na na na na NAC DOMAIN CONTAINING PROTEIN 82 PEROXISOMAL NAD-MALATE DEHYDRO	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prote 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micre 5_2993260	3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter exon downstream
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330 AT5G09660 AT5G65158	na na na na na na na na na NAC DOMAIN CONTAINING PROTEIN 82 PEROXISOMAL NAD-MALATE DEHYDRO PLAT DOMAIN PROTEIN 3 (PLAT3)	unknown proteir 4_1205947 Nucleotide-diph 4_9347885 DNA glycosylas 5_18024208 Encodes a prote 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micre 5_2993260 Lipase/lipooxygi 5_26027920	3.23 3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter exon downstream proximal promoter
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330 AT5G09660 AT5G65158 AT3G06300	na PEROXISOMAL NAD-MALATE DEHYDR(PLAT DOMAIN PROTEIN 3 (PLAT3) PROLYL 4-HYDROXYLASE 2 (PH2) PYROPHOSPHORYLASE 6 (PPa6)	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prot 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micrr 5_2993260 Lipase/lipcoxyg 5_26027920 Encodes a prot 5_2993260 Encodes a prot 5_2993260	3.23 3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter exon downstream proximal promoter intergenic promoter
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330 AT5G09660 AT5G65158 AT3G06300 AT5G09650 AT4G39890	na na na na na na na na na NAC DOMAIN CONTAINING PROTEIN 8: PEROXISOMAL NAD-MALATE DEHYDRO PLAT DOMAIN PROTEIN 3 (PLAT3) PROLYL 4-HYDROXYLASE 2 (P4H2) PYROPHOSPHORYLASE 6 (PPa6) RAB GTPASE HOMOLOG H1C (RABH1c)	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prote 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micre 5_2993260 Lipase/lipooxyg 5_26027920 Encodes a prote 5_2993260 RAB GTPase hr 4_18505984	3.23 3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter exon downstream proximal promoter intergenic promoter five_prime_UTR
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330 AT5G09660 AT5G65158 AT3G06300 AT5G09650 AT4G39890 AT3G07040	na na na na na na na na na NAC DOMAIN CONTAINING PROTEIN 82 PEROXISOMAL NAD-MALATE DEHYDRC PLAT DOMAIN PROTEIN 3 (PLAT3) PROLYL 4-HYDROXYLASE 2 (P4H2) PYROPHOSPHORYLASE 6 (PPa6) RAB GTPASE HOMOLOG H1C (RABH1c) RESISTANCE TO P. SYRINGAE PV MAC	unknown proteit 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prot 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micr 5_2993260 Lipase/lipocxyg 5_26027920 Encodes a prot 3_1910886 Encodes a prot 5_2993260 RAB GTPase ht 4_18505984 Contains an N+1_3_2229169	3.23 3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter exon downstream proximal promoter intergenic promoter five_prime_UTR promoter
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09630 AT5G09665 AT3G06300 AT5G09650 AT4G39880 AT3G07040 AT3G56380	na NAC DOMAIN CONTAINING PROTEIN 82 PEROXISOMAL NAD-MALATE DEHYDR(PLAT DOMAIN PROTEIN 3 (PLAT3) PROLYL 4-HYDROXYLASE 2 (P4H2) PYROPHOSPHORYLASE 6 (PPa6) RAB GTPASE HOMOLOG H1C (RABH1c; RESISTANCE TO P. SYRINGAE PV MAC RESPONSE REGULATOR 17 (RR17)	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA qlycosylas 5_18024208 Encodes a prot 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micrr 5_2993260 Lipase/lipooxyg 5_26027920 Encodes a prot 3_1910886 Encodes a prot 5_2993260 RAB GTPase hr 4_18505984 Contains an N-1 3_2229169 response regulz 3_20904673	3.23 3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter exon downstream proximal promoter intergenic promoter five_prime_UTR promoter proximal promoter proximal promoter
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330 AT5G65158 AT3G06300 AT5G09650 AT4G39890 AT3G07040 AT3G656380 AT3G03600	na NAC DOMAIN CONTAINING PROTEIN 8: PEROXISOMAL NAD-MALATE DEHYDRO PLAT DOMAIN PROTEIN 3 (PLAT3) PROLYL 4-HYDROXYLASE 2 (P4H2) PYROPHOSPHORYLASE 6 (PPa6) RAB GTPASE HOMOLOG H1C (RABH1C; RESISTANCE TO P. SYRINGAE PV MAC RESPONSE REGULATOR 17 (RR17) RIBOSOMAL PROTEIN S2 (RPS2)	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prote 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micre 5_2993260 Lipase/lipcoxyg 5_26027920 Encodes a prote 5_2993260 RAB GTPase hi 4_18505984 Contains an N-t 3_2229169 response reguls 3_20904673 Structural comp 3_868645	3.23 3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter promoter exon downstream proximal promoter intergenic promoter five_prime_UTR promoter proximal promoter proximal promoter promoter promoter promoter
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330 AT5G09660 AT5G65158 AT3G06300 AT5G09650 AT4G39890 AT3G07040 AT3G56380 AT3G03600 AT4G11370	na na na na na na na na na NAC DOMAIN CONTAINING PROTEIN 82 PEROXISOMAL NAD-MALATE DEHYDRC PLAT DOMAIN PROTEIN 3 (PLAT3) PROLYL 4-HYDROXYLASE 2 (P4H2) PYROPHOSPHORYLASE 6 (PPa6) RAB GTPASE HOMOLOG H1C (RABH1c) RESISTANCE TO P. SYRINGAE PV MAC RESPONSE REGULATOR 17 (RR17) RIBOSOMAL PROTEIN S2 (RPS2) RING-H2 FINGER A1A (RHA1A)	unknown proteit 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prott 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micrt 5_2993260 Lipase/lipocxyg 5_26027920 Encodes a prott 5_2993260 Encodes a prott 5_2993260 RAB GTPase ht 4_18505984 Contains an N-t 3_2229169 response reguls 3_20904673 Structural comp 3_868645 Encodes a put 4_6908137	3.23 3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter exon downstream promoter intergenic promoter five_prime_UTR promoter five_prime_UTR promoter proximal promoter proximal promoter proximal promoter exon
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09660 AT5G09660 AT5G65158 AT3G06300 AT5G09650 AT4G39890 AT3G07040 AT3G56380 AT3G03600 AT4G11370 AT2G30360	na NAC DOMAIN CONTAINING PROTEIN 82 PEROXISOMAL NAD-MALATE DEHYDRO PLAT DOMAIN PROTEIN 3 (PLAT3) PROLYL 4-HYDROXYLASE 2 (P4H2) PYROPHOSPHORYLASE 6 (PPa6) RAB GTPASE HOMOLOG H1C (RABH1c', RESISTANCE TO P. SYRINGAE PV MAC RESPONSE REGULATOR 17 (RR17) RIBOSOMAL PROTEIN S2 (RPS2) RING-H2 FINGER A1A (RHA1A) SOS3-INTERACTING PROTEIN 4 (SIP4)	unknown proteir 4_1205947 Nucleotide-diph 4_9347858 DNA qlycosylas 5_18024208 Encodes a prot 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892833 encodes a micrr 5_2993260 Lipase/lipooxyg 5_26027920 Encodes a prot 3_1910886 Encodes a prot 5_2993260 RAB GTPase hr 4_18505984 Contains an N+1 3_2229169 response regula 3_20904673 Structural comp 3_868645 Encodes a put 4_6908137 Encodes a SOS 2_12939488	3.23 3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter exon downstream proximal promoter intergenic promoter five_prime_UTR promoter proximal promoter proximal promoter proximal promoter exon proximal promoter
AT4G16600 AT5G44680 AT5G60190 AT5G35970 AT5G09330 AT5G09660 AT5G65158 AT3G06300 AT5G09650 AT4G39890 AT3G07040 AT3G56380 AT3G03600 AT4G11370	na na na na na na na na na NAC DOMAIN CONTAINING PROTEIN 82 PEROXISOMAL NAD-MALATE DEHYDRC PLAT DOMAIN PROTEIN 3 (PLAT3) PROLYL 4-HYDROXYLASE 2 (P4H2) PYROPHOSPHORYLASE 6 (PPa6) RAB GTPASE HOMOLOG H1C (RABH1c) RESISTANCE TO P. SYRINGAE PV MAC RESPONSE REGULATOR 17 (RR17) RIBOSOMAL PROTEIN S2 (RPS2) RING-H2 FINGER A1A (RHA1A)	unknown proteit 4_1205947 Nucleotide-diph 4_9347858 DNA glycosylas 5_18024208 Encodes a prott 5_24234424 P-loop containir 5_14123424 NAC domain co 5_2892883 encodes a micrt 5_2993260 Lipase/lipocxyg 5_26027920 Encodes a prott 5_2993260 Encodes a prott 5_2993260 RAB GTPase ht 4_18505984 Contains an N-t 3_2229169 response reguls 3_20904673 Structural comp 3_868645 Encodes a put 4_6908137	3.23 3.23 3.23 3.23 3.23 3.23 3.23 3.23	promoter proximal promoter downstream promoter exon downstream promoter intergenic promoter five_prime_UTR promoter five_prime_UTR promoter proximal promoter proximal promoter proximal promoter exon

4.70007070	(00111 4)	00111 4 511110 0 45000775	0.00	
AT2G37970	(SOUL-1)	SOUL-1; FUNC 2_15890775	3.22	promoter
AT1G69440	ARGONAUTE7 (AGO7)	Encodes ARGC 1_26105698	3.22	proximal promoter
AT4G26140	BETA-GALACTOSIDASE 12 (BGAL12) CELLULOSE SYNTHASE LIKE A14 (CSL/	putative beta-ga 4_13249793	3.22 3.22	proximal promoter
AT3G56000 AT1G80790			3.22	promoter
AT1G60790 AT3G61890	FACTOR OF DNA METHYLATION 5 (FDN HOMEOBOX 12 (HB-12)	Encodes a hom 3_22913465	3.22	three_prime_UTR
AT1G14380	IQ-DOMAIN 28 (IQD28)	IQ-domain 28 (I-1_4921659	3.22	intergenic promoter
AT4G16260	na	Glycosyl hydrol: 4_9199927	3.22	downstream
AT1G26920	na	unknown proteir 1_9328706	3.22	proximal promoter
AT1G52590	na	Putative thiol-di: 1_19590373	3.22	promoter
AT1G32390 AT1G79510	na	Uncharacterize(1_29912020	3.22	proximal promoter
AT1G79950	na	RAD3-like DNA 1_30073553	3.22	promoter
AT1G80800	na	pseudogene, 40 1_30363294	3.22	proximal promoter
AT2G36200	na	P-loop containir 2_15185494	3.22	promoter
AT1G61900	na	unknown proteir 1 22879915	3.22	intergenic
AT1G79520	na	Cation efflux far 1 29912020	3.22	downstream
AT3G57120	na	Protein kinase s 3_21139059	3.22	five_prime_UTR
AT4G02100	na	Heat shock prot 4_928767	3.22	proximal promoter
AT4G17680	na	SBP (S-ribonuc 4_9844301	3.22	promoter
AT4G30010	na	unknown proteir 4_14674485	3.22	intergenic
AT4G34730	na	ribosome-bindin 4_16569395	3.22	intron
AT5G08310	na	Tetratricopeptid 5_2675413	3.22	promoter
AT5G20810	na	SAUR-like auxir 5_7043758	3.22	promoter
AT5G61950	na	Ubiquitin carbox 5_24873204	3.22	promoter
AT5G09350	PHOSPHATIDYLINOSITOL 4-OH KINASE		3.22	promoter
AT4G16250	PHYTOCHROME D (PHYD)	Encodes a phyt 4_9199927	3.22	promoter
AT2G31680	RAB GTPASE HOMOLOG A5D (RABA5d)	RAB GTPase h: 2_13475061	3.22	promoter
AT1G58470	RNA-BINDING PROTEIN 1 (RBP1)	encodes an RN 1_21727013	3.22	promoter
AT1G31600	TRNA METHYLTRANSFERASE 9 (TRM9)	RNA-binding (R 1_11316632	3.22	promoter
AT1G70560	TRYPTOPHAN AMINOTRANSFERASE O	TAA1 is involve 1_26601969	3.22	proximal promoter
AT4G16160	(ATOEP16-2)	Homologous to 4_9157289	3.21	promoter
AT2G38120	AUXIN RESISTANT 1 (AUX1)	Encodes an aux 2_15964326	3.21	intergenic
AT1G51070	BASIC HELIX-LOOP-HELIX 115 (bHLH11)		3.21	proximal promoter
AT4G31840	EARLY NODULIN-LIKE PROTEIN 15 (EN		3.21	promoter
AT3G26650	GLYCERALDEHYDE 3-PHOSPHATE DEF		3.21	promoter
AT4G00150	HAIRY MERISTEM 3 (HAM3)	Belongs to one 4_59295	3.21	promoter
AT1G51060	HISTONE H2A 10 (HTA10)	Encodes HTA1(1_18926785	3.21	promoter
AT2G42880	MAP KINASE 20 (MPK20)	member of MAF 2_17845071	3.21	proximal promoter
AT1G15165	na	RING/FYVE/PH 1_5220263	3.21	promoter
AT2G20480	na	unknown proteir 2_8831622	3.21	promoter
AT1G15670	na	Galactose oxida 1_5391063	3.21	exon
AT2G46930	na	Pectinacetyleste 2_19283135	3.21	promoter
AT1G64470	na	Ubiquitin-like su 1_23946220	3.21	promoter
AT4G16155	na	dihydrolipoyl del 4_9157289	3.21	exon
AT5G04060	na	S-adenosyl-L-m 5_1099028	3.21	promoter
AT1G18550	na	ATP binding mic 1_6384592	3.21	promoter
AT1G66910	na	Protein kinase s 1_24965278	3.21	proximal promoter
AT1G66920	na	Protein kinase s 1_24965278	3.21	downstream
AT1G69550 AT2G06860	na na	disease resistar 1_26153727 transposable el 2_2764947	3.21 3.21	promoter proximal promoter
AT2G17305	na	CONTAINS Inte 2_7525986	3.21	proximal promoter
AT2G42955	na	unknown proteir 2_17867749	3.21	promoter
AT1G29450	na	SAUR-like auxir 1_10306640	3.21	promoter
AT2G43590	na	Chitinase family 2_18081568	3.21	three_prime_UTR
AT1G68872	na	Unknown gene 1_25891835	3.21	promoter
AT3G63290	na	2-oxoglutarate (3_23381594	3.21	promoter
AT3G63280	NIMA-RELATED KINASE 4 (NEK4)	Encodes AtNek 3_23381594	3.21	downstream
AT4G22540	OSBP(OXYSTEROL BINDING PROTEIN)		3.21	intron
AT4G12110	STEROL-4ALPHA-METHYL OXIDASE 1-1		3.21	promoter
AT2G02760	UBIQUITING-CONJUGATING ENZYME 2		3.21	promoter
AT2G28840	XB3 ORTHOLOG 1 IN ARABIDOPSIS THA		3.21	promoter
AT2G06850	XYLOGLUCAN ENDOTRANSGLUCOSYL		3.21	intron
AT1G76410	(ATL8)	ATL8; FUNCTIC 1_28668129	3.2	proximal promoter
AT4G26420	(GAMT1)	A member of the 4_13350532	3.2	intergenic
AT3G21870	CYCLIN P2;1 (CYCP2;1)	cyclin p2;1 (CY(3_7704954	3.2	promoter
AT2G46840	DOMAIN OF UNKNOWN FUNCTION 724		3.2	promoter
AT5G41370 AT3G21420	HOMOLOG OF XERODERMA PIGMENTO LATERAL BRANCHING OXIDOREDUCTA		3.2 3.2	promoter
AT3G21420 AT3G06140	LOG2-LIKE UBIQUITIN LIGASE4 (LUL4)		3.2	intergenic
AT5G39240	na	Encodes a atyp 5_15713148	3.2	three_prime_UTR promoter
AT1G03240		unknown proteir 1 793213	3.2	
AT1G03240 AT1G30310	na na	transposable eli 1_10677127	3.2	promoter proximal promoter
AT1G30310 AT1G74440	na na	Protein of unknr 1_27980512	3.2	proximal promoter promoter
AT2G18320	na	F-box associate 2 7958019	3.2	intergenic
AT1G30590	na	RNA polymeras 1_10840004	3.2	five_prime_UTR
AT2G37220	na	Encodes a chlor 2_15631919	3.2	intergenic
AT3G06130	na	Heavy metal tra 3_1856728	3.2	proximal promoter
AT3G28080	na	nodulin MtN21-I 3_10451441	3.2	promoter
AT3G55880	na	A gain-of-functic 3 20737782	3.2	three_prime_UTR
AT3G58060	na	Cation efflux far 3_21503381	3.2	intergenic
AT4G28400	na	Protein phospha 4_14047885	3.2	promoter
AT5G37540	na	Eukaryotic aspa 5_14912079	3.2	proximal promoter
AT4G39050	na	Kinesin motor fa 4_18193040	3.2	promoter
AT1G56430	NICOTIANAMINE SYNTHASE 4 (NAS4)	Encodes a prote 1_21133683	3.2	intergenic
AT2G39970	PEROXISOMAL NAD CARRIER (PXN)	Encodes peroxi 2_16686749	3.2	promoter
AT3G12250	TGACG MOTIF-BINDING FACTOR 6 (TGA		3.2	promoter
AT1G64230	UBIQUITIN-CONJUGATING ENZYME 28		3.2	promoter
AT3G25620	ATP-BINDING CASSETTE G21 (ABCG21)		3.19	five_prime_UTR
AT5G20540	BREVIS RADIX-LIKE 4 (BRXL4)	Belongs to five- 5_6947329	3.19	proximal promoter
AT5G40200	DEGP PROTEASE 9 (DegP9)	Encodes a puta 5_16070162	3.19	promoter
AT4G17060	FRIGIDA INTERACTING PROTEIN 2 (FIP.		3.19	promoter
AT4G21860	METHIONINE SULFOXIDE REDUCTASE		3.19	intergenic
AT1G48830				promoter
	na	Ribosomal prote 1_18061474	3.19	
AT1G48840	na na	Plant protein of 1_18061474	3.19	promoter

AT2G35208	na	unknown proteir 2 14835193	3.19	proximal promoter
AT2G18560	na	UDP-Glycosyltri 2 8059839	3.19	exon
AT3G47240	na	transposable eli 3_17397741	3.19	proximal promoter
AT5G49440	na	unknown proteir 5_20049605	3.19	downstream
AT3G06210 AT5G12940	na na	ARM repeat sur 3_1880687 Leucine-rich rer 5_4088407	3.19 3.19	exon exon
AT1G67480	na	Galactose oxida 1_25276205	3.19	promoter
AT2G34590	na	Transketolase f: 2_14571038	3.19	promoter
AT2G40460	na	Major facilitator 2_16897978	3.19	intron
AT3G25805 AT4G17070	na na	unknown proteir 3_9428365	3.19 3.19	promoter
AT4G17070	na	peptidyl-prolyl c 4_9595257 alpha/beta-Hydr 4_9046146	3.19	downstream proximal promoter
AT4G15960	na	alpha/beta-Hydr 4_9046146	3.19	exon
AT4G22170	na	CONTAINS Inte 4_11736376	3.19	promoter
AT4G26860	na	Predicted pyrid: 4_13505244	3.19	promoter
AT4G26870 AT5G09880	na na	Class II aminoa 4_13505244 Splicing factor, (5_3085308	3.19 3.19	promoter promoter
AT5G09890	na	Protein kinase f: 5_3085308	3.19	intergenic
AT5G21130	na	Late embryoger 5_7186729	3.19	exon
AT5G51170	na	unknown proteir 5_20795418	3.19	promoter
AT5G55340	na PDLLIKE 4.3 (PDII 4.3)	MBOAT (memb 5_22441163	3.19	promoter
AT3G54960 AT2G29650	PDI-LIKE 1-3 (PDIL1-3) PHOSPHATE TRANSPORTER 4;1 (PHT4)	Encodes a prote 3_20366944 Encodes an ino 2_12676128	3.19 3.19	promoter promoter
AT1G70730	PHOSPHOGLUCOMUTASE 2 (PGM2)	Encodes a cyto: 1_26672988	3.19	intron
AT1G28230	PURINE PERMEASE 1 (PUP1)	Encodes a trans 1_9864713	3.19	promoter
AT3G57860	UV-B-INSENSITIVE 4-LIKE (UVI4-LIKE)	Encodes a prote 3_21426123	3.19	promoter
AT2G45190 AT3G46970	ABNORMAL FLORAL ORGANS (AFO) ALPHA-GLUCAN PHOSPHORYLASE 2 (F	Encodes a men 2_18632204 Encodes a cyto 3_17306513	3.18 3.18	proximal promoter promoter
AT2G16500	ARGININE DECARBOXYLASE 1 (ADC1)		3.18	five_prime_UTR
AT5G52570	BETA-CAROTENE HYDROXYLASE 2 (BE		3.18	intron
AT3G56940	COPPER RESPONSE DEFECT 1 (CRD1)		3.18	promoter
AT5G14320	EMBRYO DEFECTIVE 3137 (EMB3137)	Ribosomal prote 5_4618963	3.18	promoter
AT5G10140 AT2G44950	FLOWERING LOCUS C (FLC) HISTONE MONO-UBIQUITINATION 1 (HL	MADS-box proti 5_3179554	3.18 3.18	promoter promoter
AT4G29150	IQ-DOMAIN 25 (IQD25)	IQ-domain 25 (I 4_14376693	3.18	proximal promoter
AT2G17130	ISOCITRATE DEHYDROGENASE SUBUN		3.18	promoter
AT3G56930	na	DHHC-type zinc 3_21076367	3.18	downstream
AT5G55640 AT5G09800	na na	unknown proteir 5_22534150 ARM repeat sur 5_3043471	3.18 3.18	promoter exon
AT3G09800 AT3G02840	na	ARM repeat sur 3_618842	3.18	exon
AT5G02730	na	CAP (Cysteine- 5_615846	3.18	exon
AT1G66820	na	glycine-rich prot 1_24930903	3.18	intergenic
AT1G66830	na	Leucine-rich rer 1_24930903	3.18	exon
AT3G14130 AT1G04790	na na	Aldolase-type T 3_4688303 RING/U-box suj 1_1344979	3.18 3.18	five_prime_UTR promoter
AT1G06650	na	encodes a prote 1 2035703	3.18	promoter
AT1G22110	na	structural consti 1_7802555	3.18	five_prime_UTR
AT1G49420	na	Heavy metal tra 1_18288073	3.18	exon
AT1G80870	na	Protein kinase s 1_30391112	3.18	proximal promoter
AT2G02960 AT2G03250	na na	RING/FYVE/PH 2_864472 EXS (ERD1/XP 2_982183	3.18 3.18	promoter exon
AT2G30120	na	unknown proteir 2_12863201	3.18	proximal promoter
AT1G06645	na	2-oxoglutarate (1_2035703	3.18	downstream
AT2G39300	na	unknown proteir 2_16413705	3.18	promoter
AT2G44970 AT1G74088	na na	alpha/beta-Hydr 2_18548612 FUNCTIONS IN 1_27861112	3.18 3.18	downstream promoter
AT3G11130	na	Clathrin, heavy 3_3491961	3.18	promoter
AT2G23171	na	unknown proteir 2_9868858	3.18	proximal promoter
AT2G25800	na	CONTAINS Inte 2_11010585	3.18	proximal promoter
AT2G28200	na	C2H2-type zinc 2_12021523	3.18	proximal promoter
AT3G16740 AT4G18570	na na	F-box and asso 3_5699281 Tetratricopeptid 4 10233670	3.18 3.18	promoter intron
AT4G18580	na	unknown proteir 4_10233670	3.18	intergenic
AT4G31351	na	This gene encor 4_15216290	3.18	proximal promoter
AT5G40720	na	CONTAINS Inte 5_16297239	3.18	proximal promoter
AT4G35905	na na	unknown proteir 4_17008214 pre-tRNA; tRNA 5_26195576	3.18 3.18	promoter downstream
AT5G65535 AT3G46980	PHOSPHATE TRANSPORTER 4;3 (PHT4		3.18	intergenic
AT2G38670	PHOSPHORYLETHANOLAMINE CYTIDY	Encodes a mito 2_16168681	3.18	promoter
AT3G02850	STELAR K+ OUTWARD RECTIFIER (SKC		3.18	intergenic
AT5G60970	TEOSINTE BRANCHED 1, CYCLOIDEA A		3.18	proximal promoter
AT3G15355 AT5G48230	UBIQUITIN-CONJUGATING ENZYME 25 ACETOACETYL-COA THIOLASE 2 (ACAT		3.18 3.17	promoter five prime UTR
AT2G37300	ATP-BINDING CASSETTE I16 (ABCI16)		3.17	downstream
AT5G52060	BCL-2-ASSOCIATED ATHANOGENE 1 (E	A member of Ar 5_21156257	3.17	proximal promoter
AT5G53130	CYCLIC NUCLEOTIDE GATED CHANNEL		3.17	five_prime_UTR
AT3G11170	FATTY ACID DESATURASE 7 (FAD7) GOLGI SNARE 12 (GOS12)	Chloroplastic er 3_3499327 Encodes a mer 2 18639907	3.17	promoter
AT2G45200 AT2G22496	MICRORNA779A (MIR779A)	Encodes a micr 2_9561712	3.17 3.17	intron intergenic
AT5G67080	MITOGEN-ACTIVATED PROTEIN KINASE		3.17	proximal promoter
AT1G11430	MULTIPLE ORGANELLAR RNA EDITING	Encodes a prote 1_3849243	3.17	downstream
AT1G12190	na	F-box and asso 1_4132454	3.17	intergenic
AT1G73870	na na	B-box type zinc 1_27781008	3.17	intergenic
AT1G73875 AT3G10780	na na	DNAse I-like su 1_27781008 emp24/gp25L/p. 3_3374970	3.17 3.17	five_prime_UTR promoter
AT3G10700	na	Single-stranded 3_3374970	3.17	proximal promoter
AT5G57340	na	unknown proteir 5_23222956	3.17	intergenic
AT1G67570	na	Protein of unknot 1_25325197	3.17	five_prime_UTR
AT1G07380 AT1G11440	na na	Neutral/alkaline 1_2266579 BEST Arabidop: 1_3849243	3.17 3.17	exon promoter
AT1G11440 AT1G17570	na na	pre-tRNA; tRNA 1_6038795	3.17	exon
AT1G48325	na	Expressed prote 1_17860431	3.17	intergenic
AT1G73580	na	Calcium-depend 1_27656273	3.17	intergenic
AT2G17787	na	unknown proteir 2_7731066	3.17	promoter

AT2G23330	na	transposable ek 2_9932801	3.17	promoter
AT1G11300	na	protein serine/th 1_3794124	3.17	promoter
AT2G37290	na	Ypt/Rab-GAP d 2_15662476	3.17	proximal promoter
AT2G41770 AT2G45750	na na	Protein of unknc 2_17427292 S-adenosyl-L-m 2_18842086	3.17 3.17	promoter promoter
AT3G09010	na	Protein kinase s 3_2749423	3.17	proximal promoter
AT3G11165	na	unknown proteir 3_3499327	3.17	promoter
AT2G32760	na	unknown proteir 2_13894841	3.17	downstream
AT3G22770 AT3G50590	na na	F-box associate 3_8048663 Transducin/WD 3_18770893	3.17 3.17	exon promoter
AT4G22530	na	S-adenosyl-L-m 4_11859531	3.17	exon
AT4G39380	na	FUNCTIONS IN 4_18312892	3.17	promoter
AT4G39820	na	Tetratricopeptid 4_18478384	3.17	promoter
AT5G02340 AT5G22090	na na	Cysteine/Histidii 5_494994 Protein of unknc 5_7318595	3.17 3.17	proximal promoter intron
AT5G37740	na	Calcium-depend 5_14992763	3.17	intron
AT4G30996	NA(+)- AND K(+)-SENSITIVE 1 (NKS1)	NKS1, a plant-s 4_15101278	3.17	promoter
AT4G22540 AT5G58360	OSBP(OXYSTEROL BINDING PROTEIN) OVATE FAMILY PROTEIN 3 (OFP3)	OSBP(oxystero 4_11859531 ovate family pro 5_23588233	3.17 3.17	intergenic intergenic
AT2G45740	PEROXIN 11D (PEX11D)	member of the r 2_18842086	3.17	intergenic
AT2G32765	SMALL UBIQUITINRELATED MODIFIER		3.17	promoter
AT5G13750	ZINC INDUCED FACILITATOR-LIKE 1 (ZI		3.17	promoter
AT3G12400 AT5G13490	(ELC) ADP/ATP CARRIER 2 (AAC2)	Mutants of this (3_3945877 Encodes mitoch 5_4335334	3.16 3.16	promoter promoter
AT3G01770	BROMODOMAIN AND EXTRATERMINAL		3.16	promoter
AT5G41610	CATION/H+ EXCHANGER 18 (CHX18)	member of Puta 5_16638247	3.16	downstream
AT5G50250	CHLOROPLAST RNA-BINDING PROTEIN		3.16	promoter
AT1G08130 AT3G03810	DNA LIGASE 1 (LIG1) EMBRYO SAC DEVELOPMENT ARREST	Encodes the Ar. 1_2548336 embryo sac dev 3_976526	3.16 3.16	promoter promoter
AT2G20680	ENDO-BETA-MANNASE 2 (MAN2)	Glycosyl hydrol: 2_8919968	3.16	promoter
AT2G44840	ETHYLENE-RESPONSIVE ELEMENT BIN		3.16	five_prime_UTR
AT1G73250 AT5G15570	GDP-4-KETO-6-DEOXYMANNOSE-3,5-E na	Bromodomain tr 5_5066168	3.16 3.16	promoter
AT3G56330	na	N2,N2-dimethyl: 3_20890167	3.16	promoter promoter
AT3G54830	na	Transmembrane 3_20316906	3.16	proximal promoter
AT4G04692	na	pseudogene of 4_2375746	3.16	intron
AT2G31990 AT3G09470	na na	Exostosin family 2_13612903 Major facilitator 3 2911349	3.16 3.16	intron intron
AT5G09470	na	ARM repeat sur 5 3045224	3.16	proximal promoter
AT1G28600	na	GDSL-like Lipas 1_10053260	3.16	promoter
AT1G28610	na	GDSL-like Lipas 1_10053260	3.16	intergenic
AT1G43997 AT1G63410	na na	Pseudogene of 1_16705482 Protein of unknc 1_23509844	3.16 3.16	proximal promoter downstream
AT1G69250	na	Nuclear transpc 1_26035578	3.16	downstream
AT2G36402	na	transposable eli 2_15275245	3.16	intergenic
AT1G69252	na	other RNA 1_26035578	3.16	proximal promoter
AT3G14075 AT3G32917	na na	Mono-/di-acylgly 3_4667074 transposable ele 3_13480788	3.16 3.16	intron proximal promoter
AT3G44400	na	Disease resista 3_16049778	3.16	promoter
AT4G10130	na	DNAJ heat shor 4_6321664	3.16	promoter
AT4G18820 AT4G20320	na na	AAA-type ATPa 4_10329901 CTP synthase f: 4_10970983	3.16 3.16	promoter intergenic
AT5G13240	na	transcription rec 5_4229566	3.16	proximal promoter
AT4G31170	na	Protein kinase s 4_15156566	3.16	proximal promoter
AT4G31180	na	Class II aminoa: 4_15156566	3.16	intron
AT4G38401 AT4G38405	na na	unknown proteir 4_17979887 unknown proteir 4_17979887	3.16 3.16	promoter intergenic
AT5G41605	na	pre-tRNA; tRNA 5_16638247	3.16	exon
AT5G41612	na	Potential natura 5_16638247	3.16	promoter
AT5G66240 AT4G35790	na PHOSPHOLIPASE D DELTA (PLDDELTA	Transducin/WD 5_26466112	3.16 3.16	promoter promoter
AT1G14870	PLANT CADMIUM RESISTANCE 2 (PCR		3.16	exon
AT4G29720	POLYAMINE OXIDASE 5 (PAO5)	polyamine oxida 4_14558694	3.16	intergenic
AT4G35800	RNA POLYMERASE II LARGE SUBUNIT		3.16	intergenic
AT5G41600 AT1G80920	VIRB2-INTERACTING PROTEIN 3 (BTI3) (J8)	A nuclear encor 1_30404593	3.16 3.15	intergenic five_prime_UTR
AT1G13280	ALLENE OXIDE CYCLASE 4 (AOC4)	Encodes allene 1_4548628	3.15	three_prime_UTR
AT1G08080	ALPHA CARBONIC ANHYDRASE 7 (ACA		3.15	proximal promoter
AT1G60260 AT1G60270	BETA GLUCOSIDASE 5 (BGLU5) BETA GLUCOSIDASE 6 (BGLU6)	beta glucosidas 1_22221535 beta glucosidas 1_22221535	3.15 3.15	promoter downstream
AT4G28860	CASEIN KINASE I-LIKE 4 (ckl4)	casein kinase I- 4_14246225	3.15	promoter
AT1G55620	CHLORIDE CHANNEL F (CLC-F)	Encodes a chloi 1_20791249	3.15	promoter
AT3G55040	GLUTATHIONE TRANSFERASE LAMBDA	Encodes a merr 3_20400324 Encodes a jasm 2_19033685	3.15	five_prime_UTR
AT2G46370 AT1G77860	JASMONATE RESISTANT 1 (JAR1) KOMPEITO (KOM)	mutant has Alte 1_29282026	3.15 3.15	promoter intergenic
AT1G11000	MILDEW RESISTANCE LOCUS O 4 (MLC	A member of a I 1_3671248	3.15	intergenic
AT2G23290	MYB DOMAIN PROTEIN 70 (MYB70)	Member of the F 2_9905899	3.15	five_prime_UTR
AT5G12980 AT3G09500	na na	Cell differentiati 5_4108154 Ribosomal L29 3 2916862	3.15 3.15	five_prime_UTR promoter
AT3G09500 AT3G15290	na na	3-hydroxyacyl-C 3_5144872	3.15	promoter
AT3G25400	na	CONTAINS Inte 3_9213031	3.15	promoter
AT1G55625	na	pre-tRNA; tRNA 1_20791249	3.15	promoter
AT1G17145 AT3G55960	na na	RING/U-box su; 1_5862704 Haloacid dehalc 3 20763209	3.15 3.15	promoter promoter
AT5G21326	na	Ca2+regulated : 5_7222150	3.15	downstream
AT5G21378	na	pre-tRNA; tRNA 5_7222150	3.15	promoter
AT1G10900	na	RNA polymeras 1_2089884	3.15	downstream
AT1G10990 AT1G56230	na na	unknown proteir 1_3671248 Protein of unknc 1 21048675	3.15 3.15	promoter intron
AT1G72855	na	Potential natura 1_27416135	3.15	promoter
AT1G79190	na	ARM repeat sur 1_29788443	3.15	promoter
AT2G17030 AT1G80930	na na	CONTAINS Inte 2_7399017 MIF4G domain- 1_30404593	3.15 3.15	promoter intergenic
AT3G17830	na	Molecular chape 3_6101756	3.15	promoter

AT3G26511				
	na	unknown proteir 3 9717158	3.15	intergenic
AT3G55050		Protein phosph: 3_20400324	3.15	downstream
AT3G60320		Protein of unknc 3_22296802	3.15	proximal promoter
AT4G00585	na	unknown proteir 4_252684	3.15	promoter
AT4G00590	na	N-terminal nucle 4_252684	3.15	promoter
AT4G31200		SWAP (Suppre: 4_15164992	3.15	promoter
AT4G39020		SH3 domain-coi 4_18183192	3.15	intron
AT5G21430	NADH DEHYDROGENASE-LIKE COMPLI		3.15	promoter
AT1G06800	PHOSPHOLIPASE A I GAMMA 1 (PLA-I{g		3.15	intron
AT1G61520 AT5G65830	PHOTOSYSTEM I LIGHT HARVESTING (3.15 3.15	intron
AT5G05080	RECEPTOR LIKE PROTEIN 57 (RLP57) UBIQUITIN-CONJUGATING ENZYME 22		3.15	promoter promoter
AT5G63860		UV-B-specific si 5_25559901	3.15	promoter
AT5G61840	(GUT1)	GUT1; CONTAI 5_24842095	3.14	promoter
AT5G67520	ADENOSINE-5'-PHOSPHOSULFATE (AP		3.14	downstream
AT1G28290	ARABINOGALACTAN PROTEIN 31 (AGP:		3.14	proximal promoter
AT5G22740	CELLULOSE SYNTHASE-LIKE A02 (CSL)	encodes a beta 5_7559240	3.14	intron
AT3G27160	GLUCOSE HYPERSENSITIVE 1 (GHS1)		3.14	promoter
AT2G17480	MILDEW RESISTANCE LOCUS O 8 (MLC		3.14	intergenic
AT4G39120	MYO-INOSITOL MONOPHOSPHATASE L		3.14	exon
AT3G30300		O-fucosyltransfe 3_11924386	3.14	five_prime_UTR
AT4G29103		unknown proteir 4_14346735	3.14	promoter
AT1G16100		pre-tRNA; tRNA 1_5518265	3.14	promoter
AT2G37035 AT1G12390		unknown proteir 2_15556838 Cornichon famil ¹ 1_4220044	3.14 3.14	promoter
AT1G12390 AT5G27770		Ribosomal L22e 5_9835827	3.14	promoter promoter
AT1G34220		Regulator of Vp 1_12466169	3.14	promoter
AT1G27285		transposable ele 1 9478783	3.14	exon
AT1G27290		unknown proteir 1_9478783	3.14	proximal promoter
AT3G05675		BTB/POZ doma 3_1657478	3.14	intergenic
AT3G18620	na	DHHC-type zinc 3_6408067	3.14	promoter
AT3G05670	na	RING/U-box prc 3_1657478	3.14	intergenic
AT3G44430	na	unknown proteir 3_16068850	3.14	exon
AT3G57950		unknown proteir 3_21460314	3.14	promoter
AT4G17620		glycine-rich prot 4_9821861	3.14	promoter
AT4G26400		RING/U-box sui 4_13346586	3.14	five_prime_UTR
AT4G17616		Pentatricopeptic 4_9821861	3.14	downstream
AT4G33960		unknown proteir 4_16275129	3.14	proximal promoter
AT4G26410 AT5G02385		Uncharacterise: 4_13346586 pre-tRNA; tRNA 5_508138	3.14 3.14	promoter intergenic
AT5G02560		Tetratricopeptid 5 902820	3.14	promoter
AT5G38300		unknown proteir 5_15307632	3.14	intergenic
AT5G42880		Plant protein of 5_17191394	3.14	promoter
AT5G44568		unknown proteir 5_17962201	3.14	five_prime_UTR
AT5G55600		agenet domain- 5_22525700	3.14	promoter
AT4G33950	OPEN STOMATA 1 (OST1)	Encodes calciur 4_16275129	3.14	intergenic
AT5G67530	PLANT U-BOX 49 (PUB49)	plant U-box 49 (5_26941101	3.14	promoter
AT2G37080		Encodes RIP3 (2_15585273	3.14	promoter
AT5G56760	SERINE ACETYLTRANSFERASE 1;1 (SE		3.14	promoter
AT1G06110	SKP1/ASK-INTERACTING PROTEIN 16 (\$		3.14	promoter
AT4G08810		Calcium binding 4_5618820	3.13	proximal promoter
AT4G08930		Encodes a prot 4_5729434	3.13	five_prime_UTR
AT2G06255 AT1G79830		ELF4-like 3 (ELI 2_2458818 This gene is pre 1_30027643	3.13 3.13	intron
AT3G57550		guanylate kinas 3_21305106	3.13	downstream proximal promoter
AT2G18170		MAP kinase 7 (I 2 7905563	3.13	intergenic
AT2G39200	MILDEW RESISTANCE LOCUS O 12 (ML		3.13	proximal promoter
AT4G16770		2-oxoglutarate (4_9440846	3.13	intergenic
AT2G38610		RNA-binding KF 2_16150056	3.13	
AT5G43870	na	FUNCTIONS IN 5_17636847		promoter
AT5G02860	na		3.13	promoter proximal promoter
	Ila	Pentatricopeptic 5_653867	3.13 3.13	
AT2G33140	na	Pentatricopeptic 5_653867 pre-tRNA; tRNA 2_14047423	3.13 3.13	proximal promoter promoter exon
AT2G38180	na na	Pentatricopeptic 5_653867 pre-tRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734	3.13 3.13 3.13	proximal promoter promoter exon proximal promoter
AT2G38180 AT3G23510	na na na	Pentatricopeptic 5_653867 pre-tRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734 Cyclopropane-f; 3_8428440	3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter intron
AT2G38180 AT3G23510 AT3G45030	na na na na	Pentatricopeptic 5_653867 pre-tRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734 Cyclopropane-f: 3_8428440 Ribosomal prot: 3_16472500	3.13 3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter intron promoter
AT2G38180 AT3G23510 AT3G45030 AT3G51500	na na na na na	Pentatricopeptic 5_653867 pre-tRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734 Cyclopropane-f: 3_8428440 Ribosomal prote 3_16472500 unknown proteir 3_19108062	3.13 3.13 3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter intron promoter promoter
AT2G38180 AT3G23510 AT3G45030	na na na na na na	Pentatricopeptic 5_653867 pre-tRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734 Cyclopropane-f: 3_8428440 Ribosomal prott 3_16472500 unknown proteir 3_19108062 transposase-likt 3_14318369	3.13 3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter intron promoter promoter promoter proximal promoter proximal promoter
AT2G38180 AT3G23510 AT3G45030 AT3G51500 AT3G42170	na na na na na na na	Pentatricopeptic 5_653867 pre-tRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734 Cyclopropane-f: 3_8428440 Ribosomal prote 3_16472500 unknown proteir 3_19108062	3.13 3.13 3.13 3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter intron promoter promoter
AT2G38180 AT3G23510 AT3G45030 AT3G51500 AT3G42170 AT3G45040	na na na na na na na	Pentatricopeptic 5_653867 pre-IRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734 Cyclopropane-ft: 3_8428440 Ribosomal prott 3_16472500 unknown proteii 3_19108062 transposase-likt 3_14318369 encodes a puta 3_16472500 CONTAINS Inte 3_17565524	3.13 3.13 3.13 3.13 3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter intron promoter promoter proximal promoter downstream
AT2G38180 AT3G23510 AT3G45030 AT3G51500 AT3G42170 AT3G47630 AT3G5795 AT5G18490	na n	Pentatricopeptic 5_653867 pre-tRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734 Cyclopropane-f: 3_8428440 Ribosomal prote 3_16472500 unknown proteir 3_19108062 transposase-likt 3_14318369 Encodes a puta 3_16472500 CONTAINS Inte 3_17565524 pre-tRNA; tRNA 3_20709398 Plant protein of 5_6133937	3.13 3.13 3.13 3.13 3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter intron promoter promoter proximal promoter downstream promoter
AT2G38180 AT3G23510 AT3G45030 AT3G51500 AT3G42170 AT3G45040 AT3G47630 AT3G55795 AT5G18490 AT5G15120	na n	Pentatricopeptic 5_653867 pre-tRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734 Cyclopropane-ft: 3_8428440 Ribosomal prott 3_16472500 unknown proteii 3_19108062 transposase-likt 3_14318369 encodes a puta 3_16472500 CONTAINS Inte 3_17565524 pre-tRNA; tRNA 3_20709398 Plant protein of 5_6133937 Protein of unknt 5_4898658	3.13 3.13 3.13 3.13 3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter intron promoter promoter proximal promoter downstream promoter downstream downstream promoter
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AT2G38180 AT3G23510 AT3G45030 AT3G51500 AT3G45040 AT3G47630 AT3G47630 AT5G15120 AT5G15120 AT5G15120 AT5G15130 AT2G33150 AT2G33150 AT3G34640 AT3G55800 AT1G79820 AT2G27760 AT2G27760 AT2G27760 AT2G27760 AT2G27760 AT3G456400 AT4G37790 AT4G3558000 AT5G55600 AT5G55600 AT3G5760 AT2G27760 AT2G27760 AT2G27760 AT2G27760 AT2G27760 AT3G13510 AT3G13510 AT3G13510 AT3G13510 AT3G1350000 AT5G49910 AT5G12170 AT3G11220 AT5G03280	na n	Pentatricopeptit 5_653867 pre-tRNA; tRNA 2_14047423 SGNH hydrolas 2_15995734 Cyclopropane-f: 3_8428440 Ribosomal prote 3_16472500 unknown proteil 3_19108062 transposase-lik: 3_14318369 Encodes a puta 3_16472500 CONTAINS Inte 3_17656524 pre-tRNA; tRNA 3_20709398 Plant protein of 5_6133937 Protein of unkn 5_4898658 Galactose oxid: 5_24350795 Encodes a prot 1_19050330 Encodes an org 2_14047423 plant glycogenir 5_6133937 Present in trans 2_14587841 Encodes a prot 6_22416479 Encodes the ch 3_20709398 SUPPRESSOR 1_30027643 Encodes a trans 3_17556098 Encodes a rans 3_17556098 Encodes a rans 3_17556098 Encodes a prot 6_22432012 Encodes home 4_17767912 Encodes a plasi 4_7858086 Encodes the ca 3_18534447 Stromal heat sh 5_20303224 Encodes one of 5_3931551 A subunit of Elio 3_3513844 Involved in ethy 5_785582	3.13 3.13 3.13 3.13 3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter exon promoter promoter promoter promoter promoter promoter downstream promoter intergenic promoter downstream promoter intergenic promoter five_prime_UTR promoter proximal promoter downstream promoter proximal promoter prom
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AT2G38180 AT3G23510 AT3G45030 AT3G51500 AT3G45040 AT3G47630 AT3G47630 AT5G15120 AT5G15120 AT5G15120 AT5G15130 AT2G33150 AT2G33150 AT3G34640 AT3G55800 AT1G79820 AT2G27760 AT2G27760 AT2G27760 AT2G27760 AT2G27760 AT3G456400 AT4G37790 AT4G3558000 AT5G55600 AT5G55600 AT3G5760 AT2G27760 AT2G27760 AT2G27760 AT2G27760 AT2G27760 AT3G13510 AT3G13510 AT3G13510 AT3G13510 AT3G1350000 AT5G49910 AT5G12170 AT3G11220 AT5G03280	na n	Pentatricopeptis 5, 653867 pre-IRNA; tRNA 2, 14047423 SGNH hydrolas 2, 15995734 Cyclopropane-ft; 3, 8428440 Ribosomal prott 3, 16472500 unknown proteii 3, 19108062 transposase-likt; 3, 14318369 Encodes a puta 3, 16472500 CONTAINS Inte 3, 17565524 pre-IRNA; IRNA 3, 20709388 Plant protein of 5, 6133937 Protein of unknt; 5, 4898658 Galactose oxide 5, 24350795 Encodes an ora 2, 14047423 plant glycogenir 5, 6133937 Present in trans 2, 14587841 Encodes a prott 1, 19050330 Encodes the ch 3, 20709388 SUPPRESSOR 1, 30027643 Encodes a trans 3, 17556098 Encodes tRNA i 2, 11827742 Encodes a multi 2, 800851 Cncodes home: 4, 17767912 Encodes home: 4, 17767912 Encodes the ch 3, 2352012 Encodes one of 5, 3931551 A subunit of Elo 3, 3513484 Involved in ethy 5, 785582 gamma-tocophe; 1, 24136141 LIGHT SENSITI 3, 8325709	3.13 3.13 3.13 3.13 3.13 3.13 3.13 3.13	proximal promoter promoter exon proximal promoter exon promoter promoter promoter promoter promoter promoter downstream promoter intergenic promoter downstream promoter intergenic promoter five_prime_UTR promoter proximal promoter downstream promoter proximal promoter prom

AT5G54260	MEIOTIC RECOMBINATION 11 (MRE11)	DNA repair and 5 22038306	3.12	intergenic
AT1G70645	MICRORNA777A (MIR777A)	Encodes a micr 1_26637727	3.12	promoter
AT3G11210	na	SGNH hydrolas 3_3513484	3.12	promoter
AT3G01961	na	unknown proteir 3_326149	3.12	intergenic
AT1G65950	na	Protein kinase s 1_24551217	3.12	promoter
AT1G66070	na	Translation initia 1_24598596	3.12	promoter
AT1G11300	na	protein serine/th 1_3797635	3.12	intron
AT1G31660	na	CONTAINS Inte 1_11330766	3.12	downstream
AT1G78010	na	tRNA modificatii 1_29333405	3.12	promoter
AT3G58035	na	pre-tRNA; tRNA 3_21487426	3.12	downstream
AT4G13505	na	Potential natura 4_7858086	3.12	exon
AT5G64400	na	BEST Arabidop: 5_25750527	3.12	downstream
AT5G24890	na	unknown proteir 5_8559416	3.12	promoter
AT5G64401	na	unknown proteir 5_25750527	3.12	exon
AT1G08100	NITRATE TRANSPORTER 2.2 (NRT2.2)	Encodes a high 1_2530389	3.12	proximal promoter
AT5G64410	OLIGOPEPTIDE TRANSPORTER 4 (OPT		3.12	intergenic
AT4G06746	RELATED TO AP2 9 (RAP2.9)	encodes a mem 4_4073733	3.12	downstream
AT1G31650	RHO GUANYL-NUCLEOTIDE EXCHANG		3.12	promoter
AT1G31480	SHOOT GRAVITROPISM 2 (SGR2)	encodes a nove 1_11265794	3.12	promoter
AT2G31880	SUPPRESSOR OF BIR1 1 (SOBIR1)	Encodes a puta 2_13554969	3.12	exon
AT5G46350	WRKY DNA-BINDING PROTEIN 8 (WRK)		3.12	proximal promoter
AT3G28210	(PMZ)	Encodes a puta 3_10520287	3.11	promoter
AT4G19700	(RING)	Encodes BOI (E 4_10713021	3.11	intergenic
AT3G19190	AUTOPHAGY 2 (ATG2)	Encodes autoph 3_6639645	3.11	promoter
AT1G64990	GPCR-TYPE G PROTEIN 1 (GTG1)	Encodes a GPC 1_24146155	3.11	intron
AT2G46260	LIGHT-RESPONSE BTB 1 (LRB1)	Involvement in r 2_18995949	3.11	promoter
AT1G28395	na	unknown proteir 1_9971503	3.11	five_prime_UTR
AT5G64130	na	cAMP-regulatec 5_25666322	3.11	promoter
AT3G28200	na	Peroxidase sup 3_10520287	3.11	intergenic
AT4G25433	na	peptidoglycan-b 4_13002817	3.11	proximal promoter
AT1G11950	na	Transcription fa 1_4039487	3.11	proximal promoter
AT1G55270	na	Galactose oxida 1_20620057	3.11	five_prime_UTR
AT2G44255	na	Potential natura 2_18297645	3.11	promoter
AT2G44260	na	Plant protein of 2_18297645	3.11	exon
AT3G19184	na	AP2/B3-like trar 3_6639645	3.11	intergenic
AT3G26539	na	unknown proteir 3_9740498	3.11	intergenic
AT3G53960	na	Major facilitator 3_19980983	3.11	promoter
AT3G61810	na	Glycosyl hydrol: 3_22876984	3.11	promoter
AT4G02800	na	unknown proteir 4_1249917	3.11	promoter
AT4G03298	na	unknown proteir 4_1446425	3.11	promoter
AT4G31510	na	unknown proteir 4_15276132	3.11	downstream
AT4G34600	na	unknown proteir 4_16527838	3.11	proximal promoter
AT5G44010	na	unknown proteir 5_17709446	3.11	promoter
AT5G12950	na	FUNCTIONS IN 5_4091286	3.11	proximal promoter
AT5G17780	na	alpha/beta-Hydr 5_5869062	3.11	promoter
AT2G01650	PLANT UBX DOMAIN-CONTAINING PRO		3.11	promoter
AT3G54480	SKP1/ASK-INTERACTING PROTEIN 5 (S		3.11	promoter
AT1G49950	TELOMERE REPEAT BINDING FACTOR		3.11	promoter
AT3G13360	WPP DOMAIN INTERACTING PROTEIN	Encodes an out 3_4340476	3.11	promoter
AT3G51800	(ATG2)	putative nuclear 3_19213783	3.1	promoter
AT2G35600	BREVIS RADIX-LIKE 1 (BRXL1)	Belongs to five- 2_14943980	3.1	intron
AT1G07430	HIGHLY ABA-INDUCED PP2C GENE 2 (F	highly ABA-indu 1_2284401	3.1	proximal promoter
AT5G02770	MODIFIER OF SNC1, 11 (MOS11)	Encodes a cons 5_629379	3.1	promoter
AT3G57560	N-ACETYL-L-GLUTAMATE KINASE (NAG	encodes a N-ac 3_21312330	3.1	promoter
AT2G46230	na	PIN domain-like 2_18986034	3.1	promoter
AT4G33980	na	FUNCTIONS IN 4_16285197	3.1	promoter
AT1G63950	na	Heavy metal tra 1_23734644	3.1	promoter
AT1G05140	na	Peptidase M50 1_1482479	3.1	promoter
AT1G63730	na	Disease resista 1_23645194	3.1	downstream
AT1G63740	na	Disease resista 1_23645194	3.1	promoter
AT1G76630	na	Tetratricopeptid 1_28759433	3.1	promoter
AT1G77160	na	Protein of unknc 1_28997848	3.1	proximal promoter
AT2G02060	na	Homeodomain-I 2_497263	3.1	intron
AT2G02061	na	Nucleotide-diph 2_497263	3.1	proximal promoter
AT2G19120	na	P-loop containir 2_8292370	3.1	five_prime_UTR
AT2G38350	na	unknown proteir 2_16069220	3.1	exon
AT2G45245	na	Unknown gene 2_18661375	3.1	promoter
AT2G45250	na	Integral membra 2_18661375	3.1	promoter
AT1G76620	na	Protein of unknc 1_28759433	3.1	downstream
AT3G13335	na	pre-tRNA; tRNA 3_4330919	3.1	downstream
AT3G62220	na	Protein kinase s 3_23031217	3.1	promoter
AT4G09150	na	T-complex prote 4_5828522	3.1	intron
AT4G03180	na	CONTAINS Inte 4_1403070	3.1	promoter
AT4G37440	na	unknown proteir 4_17601188	3.1	promoter
AT5G14700	na	NAD(P)-binding 5_4740913	3.1	intron
AT5G18710	na	Domain of unkn 5_6240998	3.1	promoter
AT5G38020	na	encodes a prot∈ 5_15170359	3.1	proximal promoter
AT2G28610	PRESSED FLOWER (PRS)	Encodes a hom 2_12259537	3.1	proximal promoter
AT3G13330	PROTEASOME ACTIVATING PROTEIN 2		3.1	proximal promoter
AT1G16240	SYNTAXIN OF PLANTS 51 (SYP51)	Encodes one of 1_5556859	3.1	promoter
AT5G59340	WUSCHEL RELATED HOMEOBOX 2 (W		3.1	promoter
AT5G33290	XYLOGALACTURONAN DEFICIENT 1 (X		3.1	exon
AT5G56130	(TEX1)	Encodes a com 5_22725238	3.09	promoter
AT5G36880	ACETYL-COA SYNTHETASE (ACS)	Encodes a plast 5_14540373	3.09	promoter
AT2G38400	ALANINE:GLYOXYLATE AMINOTRANSF		3.09	five_prime_UTR
AT3G55260	BETA-HEXOSAMINIDASE 1 (HEXO1)	Encodes a prote 3_20489065	3.09	promoter
AT5G24630	BRASSINOSTEROID-INSENSITIVE4 (BIN		3.09	five_prime_UTR
AT3G20410	CALMODULIN-DOMAIN PROTEIN KINAS		3.09	promoter
AT4G28880	CASEIN KINASE I-LIKE 3 (ckl3)	casein kinase I- 4_14251111	3.09	promoter
AT2G01505	CLAVATA3/ESR-RELATED 16 (CLE16)	Member of a lar 2_229900	3.09	proximal promoter
AT1G49970			2.00	promoter
	CLP PROTEASE PROTEOLYTIC SUBUN		3.09	
AT1G17470	DEVELOPMENTALLY REGULATED G-PF	Encodes a merr 1_6002872	3.09	promoter
AT4G21200	DEVELOPMENTALLY REGULATED G-PR GIBBERELLIN 2-OXIDASE 8 (GA2OX8)	Encodes a merr 1_6002872 Encodes a prote 4_11305594	3.09 3.09	promoter intron
	DEVELOPMENTALLY REGULATED G-PF	Encodes a merr 1_6002872	3.09	promoter

AT3G17609	HY5-HOMOLOG (HYH)	Encodes a hom 3 6023716	3.09	promoter
AT1G26945	KIDARI (KDR)	Encodes a basi 1_9349026	3.09	proximal promoter
AT5G14010	KNUCKLES (KNU)	Encodes KNUC 5_4521126	3.09	proximal promoter
AT3G27220	na	Galactose oxida 3_10053848	3.09	promoter
AT3G27230	na		3.09	•
		S-adenosyl-L-m 3_10053848		promoter
AT5G21960 AT3G60260	na	encodes a mem 5_7258833 ELMO/CED-12 3 22273877	3.09 3.09	exon
AT1G32290	na	unknown proteir 1 11650988		five_prime_UTR
	na		3.09	promoter
AT1G49975	na	INVOLVED IN: 1_18504748	3.09	promoter
AT1G69980	na	unknown proteir 1_26357805	3.09	promoter
AT1G79740	na	hAT transposon 1_30007043	3.09	promoter
AT2G01510	na	Tetratricopeptid 2_229900	3.09	intergenic
AT2G29210	na	splicing factor P 2_12557967	3.09	promoter
AT2G30105	na	CONTAINS Inte 2_12849659	3.09	promoter
AT2G30180	na	pre-tRNA; tRNA 2_12881550	3.09	promoter
AT2G37190	na	Ribosomal prote 2_15620190	3.09	promoter
AT2G30100	na	pentatricopeptid 2_12849659	3.09	three_prime_UTR
AT2G36470	na	Plant protein of 2_15300808	3.09	five_prime_UTR
AT3G51720	na	Plant protein of 3_19186638	3.09	downstream
AT3G51730	na	saposin B doma 3_19186638	3.09	promoter
AT4G11300	na	CONTAINS Inte 4_6877031	3.09	intergenic
AT4G21445	na	unknown proteir 4_11424723	3.09	five_prime_UTR
AT5G41900	na	alpha/beta-Hydr 5_16771085	3.09	intron
AT5G14080	na	Tetratricopeptid 5_4545446	3.09	promoter
AT5G27710	na	unknown proteir 5_9812942	3.09	promoter
AT5G43140	na	Peroxisomal me 5_17321347	3.09	promoter
AT5G50805	na	pre-tRNA; tRNA 5_20675303	3.09	downstream
AT5G59613	na	unknown proteir 5_24016629	3.09	promoter
AT1G79750	NADP-MALIC ENZYME 4 (NADP-ME4)	The malic enzyr 1_30007043	3.09	intergenic
AT2G30170	PHOTOSYSTEM II CORE PHOSPHATAS		3.09	promoter
AT4G21210	PPDK REGULATORY PROTEIN (RP1)	Encodes a PPD 4_11305594	3.09	proximal promoter
AT4G35020	RAC-LIKE 3 (RAC3)	A member of R(4_16672451	3.09	intron
AT2G37180	RESPONSIVE TO DESICCATION 28 (RD:	a member of the 2_15620190	3.09	intergenic
AT3G14350	STRUBBELIG-RECEPTOR FAMILY 7 (SR	STRUBBELIG-r 3 4788004	3.09	proximal promoter
AT5G43130	TBP-ASSOCIATED FACTOR 4 (TAF4)	TBP-associated 5 17321347	3.09	promoter
AT1G17460	TRF-LIKE 3 (TRFL3)	Arabidopsis thal 1_6002872	3.09	downstream
AT1G24100	UDP-GLUCOSYL TRANSFERASE 74B1 (Encodes a UDF 1_8525246	3.09	downstream
AT2G47170	(ARF1A1C)	Gene encoding 2 19366498	3.08	promoter
AT4G34030	3-METHYLCROTONYL-COA CARBOXYL		3.08	downstream
AT1G27450	ADENINE PHOSPHORIBOSYL TRANSFE		3.08	intergenic
AT3G24503	ALDEHYDE DEHYDROGENASE 2C4 (AL		3.08	proximal promoter
AT5G15160	BANQUO 2 (BNQ2)	BNQ2 belongs t 5_4926004	3.08	intergenic
AT2G26900	BILE ACID:SODIUM SYMPORTER FAMIL		3.08	proximal promoter
AT1G48310	CHROMATIN REMODELING FACTOR18		3.08	promoter
AT5G01600	FERRETIN 1 (FER1)	Encodes a ferri 5_226922	3.08	intergenic
AT3G21260	GLYCOLIPID TRANSFER PROTEIN 3 (GI		3.08	intron
AT1G73360	HOMEODOMAIN GLABROUS 11 (HDG11		3.08	proximal promoter
AT3G50630	KIP-RELATED PROTEIN 2 (KRP2)	Kip-related prot 3_18800295	3.08	promoter
AT5G50050	MOB1-LIKE (MOB1-like)	Encodes a gene 5_18462121	3.08	promoter
AT2G18193	na	P-loop containir 2_7919490	3.08	•
		transposable el 5_20208976		promoter
AT5G49743	na na		3.08	promoter
AT5G49746		transposable eli 5_20208976	3.08	promoter
AT4G34040	na	RING/U-box suj 4_16304151	3.08	downstream
AT4G34035	na	pre-tRNA; tRNA 4_16304151	3.08	exon
AT1G06860	na	pre-tRNA; tRNA 1_2108030	3.08	proximal promoter
AT1G14205	na	Ribosomal L18r 1_4855447	3.08	promoter
AT1G15450	na	pre-tRNA; tRNA 1_5309576	3.08	downstream
AT2G17490	na	transposable eli 2_7604114	3.08	proximal promoter
AT1G48315	na	Potential natura 1_17853958	3.08	promoter
AT3G11580	na	AP2/B3-like trar 3_3652547	3.08	proximal promoter
AT4G16680	na	P-loop containir 4_9391745	3.08	proximal promoter
AT5G01595	na	Potential natura 5_226922	3.08	promoter
AT4G32250	na			
AT5G57580		Protein kinase s 4_15573381	3.08	promoter
	na	Calmodulin-binc 5_23314497	3.08	downstream
AT5G62680	na	Calmodulin-binc 5_23314497 Major facilitator 5_25168125	3.08 3.08	downstream promoter
AT5G01590	na na	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922	3.08 3.08 3.08	downstream promoter three_prime_UTR
AT5G01590 AT5G56520	na na na	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922 unknown proteir 5_22884392	3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter
AT5G01590 AT5G56520 AT5G57570	na na na na	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922 unknown proteir 5_22884392 GCK domain-cc 5_23314497	3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter
AT5G01590 AT5G56520 AT5G57570 AT1G27460	na na na na NO POLLEN GERMINATION RELATED 1	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922 unknown proteir 5_22884392 GCK domain-cc 5_23314497 encodes a calm 1_9534457	3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter
AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260	na na na na NO POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334)	Calmodulin-binc 5 _23314497 Major facilitator 5 _25168125 unknown proteir 5 _226922 unknown proteir 5 _22884392 GCK domain-cc 5 _23314497 encodes a calm 1 _9534457 ATPase, F0 cor 4 _1557381	3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter intergenic
AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260 AT1G73370	na na na na NO POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334) SUCROSE SYNTHASE 6 (SUS6)	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922 unknown proteir 5_22884392 GCK domain-cc 5_23314497 encodes a calm 1_95344457 ATPase, F0 cor 4_15573381 Encodes a prote 1_27584176	3.08 3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter intergenic intergenic
AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260 AT1G73370 AT2G43710	na na na na NO POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334) SUCROSE SYNTHASE 6 (SUS6) SUPPRESSOR OF SA INSENSITIVE 2 (S	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922 unknown proteir 5_22884392 GCK domain-cc 5_23314497 encodes a calm 1_9534457 ATPase, F0 cor 4_15573381 Encodes a prote 1_27584176 Encodes a stea 2_18119287	3.08 3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter intergenic intergenic proximal promoter
AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260 AT1G73370 AT2G43710 AT1G03680	na na na na NO POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334) SUCROSE SYNTHASE 6 (SUS6) SUPPRESSOR OF SA INSENSITIVE 2 (S THIOREDOXIN M-TYPE 1 (THM1)	Calmodulin-binc 5 _23314497 Major facilitator 5 _25168125 unknown proteir 5 _226922 unknown proteir 5 _22884392 GCK domain-cc 5 _23314497 encodes a calm 1 _9534457 ATPase, F0 cor 4 _15573381 Encodes a prote 1 _27584176 Encodes a prote 1 _27584176 encodes a chlor 1 _918130	3.08 3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter intergenic intergenic intergenic proximal promoter promoter
AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260 AT1G73370 AT2G43710 AT1G03680 AT2G19450	na na na na na na no POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334) SUCROSE SYNTHASE 6 (SUS6) SUPPRESSOR OF SA INSENSITIVE 2 (S THIOREDOXIN M-TYPE 1 (THM1) TRIACYLGLYCEROL BIOSYNTHESIS DE	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922 unknown proteir 5_22884392 GCK domain-cc 5_23314497 encodes a calm 1_9534457 ATPase, F0 cor 4_15573381 Encodes a prote 1_27584176 Encodes a stea 2_18119287 encodes a chlor 1_918130 Encodes Acyl-C 2_8424693	3.08 3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter
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AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260 AT1G73370 AT2G43710 AT2G19450 AT5G15170 AT3G03900 AT4G33300 AT4G33300 AT4G33300 AT4G23840 AT1G22840 AT3G63420 AT2G43900 AT2G43900 AT1G51960 AT2G19600 AT1G50260 AT1G55820 AT1G55820 AT5G07315	na na na na na na na NO POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334) SUCROSE SYNTHASE 6 (SUS6) SUPPRESSOR OF SA INSENSITIVE 2 (S THIOREDOXIN M-TYPE 1 (THM1) TRIACYLGLYCEROL BIOSYNTHESIS DE TYROSYL-DNA PHOSPHODIESTERASE ADENOSINE-5-PHOSPHOSULFATE (AP ADR1-LIKE 1 (ADR1-L1) ALBINO OR PALE GREEN MUTANT 1 (AI ATP/PHOSPHATE CARRIER 3 (APC3) CYTOCHROME C-1 (CYTC-1) GGAMMA-SUBUNIT 1 (GG1) HARMLESS TO OZONE LAYER 1 (HOL1) INOSITOL-POLYPHOSPHATE 5-PHOSPH Q-DOMAIN 27 (IGD27) K+ EFFLUX ANTIPORTER 4 (KEA4) N-TERMINAL-TRANSMEMBRANE-C2 DC na na	Calmodulin-binc 5 _23314497 Major facilitator 5 _25168125 unknown proteir 5 _226922 unknown proteir 5 _226922 unknown proteir 5 _22884392 GCK domain-cc 5 _23314497 encodes a calm 1 _9534457 ATPase, F0 cor 4 _15573381 Encodes a stea _2 _18119287 encodes a chlor 1 _918130 Encodes a stea _2 _18119287 encodes a chlor 1 _918130 Encodes a chlor 1 _918130 Encodes a chlor 1 _918130 Encodes a mer 4 _16056587 Encodes a MPE 3 _23417189 Encodes a mito 5 _2309886 Encodes a mito 5 _2309886 Encodes a finc 2 _18184166 Encodes a 5-inc 2 _18184166 Encodes a 1-inc 2 _18484166 Encodes a 1-inc 2 _1848416	3.08 3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter promoter promoter intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter promoter promoter promoter promoter intergenic promoter proximal promoter proximal promoter proximal promoter
AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260 AT1G73370 AT2G43710 AT1G03680 AT2G19450 AT5G15170 AT3G03900 AT3G63410 AT5G07320 AT3G63420 AT3G63420 AT3G63420 AT2G43910 AT2G43910 AT2G43910 AT2G43910 AT1G51960 AT1G55820 AT1G55820 AT1G55820 AT1G55820 AT1G55820 AT1G55820 AT1G55820 AT1G55820 AT5G7315 AT5G16010	na na na na na na na na na NO POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334) SUCROSE SYNTHASE 6 (SUS6) SUPPRESSOR OF SA INSENSITIVE 2 (S THIOREDOXIN M-TYPE 1 (THM1) TRIACYLGLYCEROL BIOSYNTHESIS DE TYROSYL-DNA PHOSPHODIESTERASE ADENOSINE-5-PHOSPHODIESTERASE ADENOSINE-5-PHOSPHOSULFATE (AP ADEN1-LIKE 1 (ADR1-L1) ALBINO OR PALE GREEN MUTANT 1 (A ATP/PHOSPHATE CARRIER 3 (APC3) CYTOCHROME C-1 (CYTC-1) GGAMMA-SUBUNIT 1 (GG1) HARMLESS TO OZONE LAYER 1 (HOL1) INOSITOL-POLYPHOSPHATE 5-PHOSPH IQ-DOMAIN 27 (IGD27) K+ EFFLUX ANTIPORTER 4 (KEA4) N-TERMINAL-TRANSMEMBRANE-C2 DC na na na	Calmodulin-binc 5 _23314497 Major facilitator 5 _25168125 unknown proteir 5 _226922 unknown proteir 5 _22884392 GCK domain-cc 5 _23314497 encodes a calm 1 _9534457 ATPase, F0 cor 4 _15573381 Encodes a prote 1 _27584176 Encodes a chlor 1 _918130 Encodes a chlor 1 _918130 Encodes Acyl-C 2 _8424693 tyrosyl-DNA phc 5 _4926004 Provides actival 3 _1004980 Encodes a mer 4 _16056587 Encodes a mer 4 _16056587 Encodes a mer 4 _16056587 Encodes a mer 8 _23417189 Encodes a mer 8 _23417189 Encodes a mer 9 _23417189 Encodes cytoch 1 _8080691 heterotrimeric G _2309886 Encodes cytoch 1 _8080691 heterotrimeric G _23417189 HARMLESS TC _ 18184166 Encodes a 5-inc _ 18184166 Encodes a 5-inc _ 18184166 Encodes a _17 (li _19308042 member of Puta _ 2 _8479050 N-terminal-trans 1 _18621881 CONTAINS Inte 1 _20864225 pre-tRNA; tRNA 5 _2309886 3-0x0-5-alpha-s 5 _5227514	3.08 3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter promoter promoter intergenic intergenic intergenic proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter downstream promoter intergenic promoter
AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260 AT1G3370 AT2G43710 AT2G43710 AT5G15170 AT3G03900 AT4G33300 AT3G63410 AT3G63420 AT3G63420 AT2G43910 AT1G519600 AT2G43910 AT1G51960 AT2G43900 AT1G51960 AT2G43910 AT1G51960 AT3G03701 AT3G03701	na na na na na na na na NO POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334) SUCROSE SYNTHASE 6 (SUS6) SUPPRESSOR OF SA INSENSITIVE 2 (S THIOREDOXIN M-TYPE 1 (THM1) TRIACYLGLYCEROL BIOSYNTHESIS DE TYROSYL-DNA PHOSPHODIESTERASE ADENOSINE-5'-PHOSPHOSULFATE (AP ADR1-LIKE 1 (ADR1-L1) ALBINO OR PALE GREEN MUTANT 1 (AI ATP/PHOSPHATE CARRIER 3 (APC3) CYTOCHROME C-1 (CYTC-1) GGAMMA-SUBUNIT 1 (GG1) HARMLESS TO OZONE LAYER 1 (HOL1) INOSITOL-POLYPHOSPHATE 5-PHOSPH IQ-DOMAIN 27 (IQD27) K+ EFFLUX ANTIPORTER 4 (KEA4) N-TERMINAL-TRANSMEMBRANE-C2 DC na na na na na	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922 unknown proteir 5_226922 unknown proteir 5_22884392 GCK domain-cc 5_23314497 encodes a calm 1_9534457 ATPase, F0 cor 4_15573381 Encodes a prot 1_27584176 Encodes a stea 2_1819287 encodes a chlor 1_918130 Encodes a chlor 1_918130 Encodes a chlor 1_918130 Encodes a cylor 2_8424693 tyrosyl-DNA phb 5_4926004 Provides actival 3_1004980 Encodes a mire 1_6056587 Encodes a mire 5_2309886 Encodes a mire 5_2309886 Encodes cytoch 1_8080691 heterotrimeric G_3_23417189 HARMLESS TC_2_18184166 IQ-domain 27 (il 1_19308042 member of Puta 2_8479050 N-terminal-trans 1_18621881 CONTAINS Inte 1_20864225 pre-tRNA; tRNA 5_2309886 -oxo-5-alpha-s_5_5227514 Potential natura 3_918984	3.08 3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter promoter promoter intergenic intergenic intergenic proximal promoter proximal promoter proximal promoter promoter promoter promoter promoter downstream promoter downstream promoter pr
AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260 AT1G73370 AT2G43710 AT1G03680 AT2G19450 AT5G15170 AT3G03900 AT4G33300 AT4G33300 AT4G23840 AT1G22840 AT2G43900 AT1G50260 AT2G19600 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260 AT1G50260	na na na na na na na na NO POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334) SUCROSE SYNTHASE 6 (SUS6) SUPPRESSOR OF SA INSENSITIVE 2 (S THIOREDOXIN M-TYPE 1 (THM1) TRIACYLGLYCEROL BIOSYNTHESIS DE TYROSYL-DNA PHOSPHODIESTERASE ADENOSINE-5-PHOSPHOSULFATE (AP ADR1-LIKE 1 (ADR1-L1) ALBINO OR PALE GREEN MUTANT 1 (AI ATP/PHOSPHATE CARRIER 3 (APC3) CYTOCHROME C-1 (CYTC-1) GGAMMA-SUBUNIT 1 (GG1) HARMLESS TO OZONE LAYER 1 (HOL1) INOSITOL-POLYPHOSPHATE 5-PHOSPH Q-DOMAIN 27 (IQD27) K+ EFFLUX ANTIPORTER 4 (KEA4) N-TERMINAL-TRANSMEMBRANE-C2 DC na na na na na	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922 unknown proteir 5_226922 unknown proteir 5_22884392 GCK domain-cc 5_23314497 encodes a calm 1_9534457 ATPase, F0 cor 4_15573381 Encodes a prote 1_27584176 Encodes a stea 2_18119287 encodes a chlor 1_918130 Encodes a stea 2_18119287 encodes a chlor 1_918130 Encodes a chlor 1_918130 Encodes a MPE 3_23417189 Encodes a MPE 3_23417189 Encodes a mer 4_16056587 Encodes a MPE 3_23417189 Encodes a mito 5_2309886 Encodes cytoch 1_8080691 Herbortorimeric G 3_23417189 HARMLESS TC 2_18184166 Encodes a 5-inc 2_18184166 Encodes a 5-inc 2_18184166 Encodes a 5-inc 2_18184166 Encodes a 1-18621881 CO-domain 27 (il 1_19308042 member of Puta 2_8479050 N-terminal-trans 1_18621881 CONTAINS line 1_20864225 pre-IRNA; IRNA 5_2309886 3-oxo-5-alpha-s 5_5227514 Potential natura 3_918984 Chaperone Dna 1_25964489	3.08 3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter five_prime_UTR
AT5G01590 AT5G56520 AT5G57570 AT1G27460 AT4G32260 AT1G73370 AT2G43710 AT1G03680 AT2G19450 AT5G15170 AT3G03900 AT3G63410 AT5G07320 AT3G63420 AT2G43910 AT2G43910 AT1G51960 AT1G55820 AT1G55820 AT1G55820 AT5G7315 AT5G16010 AT3G1307315 AT5G16010 AT3G13070	na na na na na na na na na NO POLLEN GERMINATION RELATED 1 PIGMENT DEFECTIVE 334 (PDE334) SUCROSE SYNTHASE 6 (SUS6) SUPPRESSOR OF SA INSENSITIVE 2 (S THIOREDOXIN M-TYPE 1 (THM1) TRIACYLGLYCEROL BIOSYNTHESIS DE TYROSYL-DNA PHOSPHODIESTERASE ADENOSINE-5-PHOSPHODIESTERASE ADENOSINE-5-PHOSPHOSULFATE (APACHA) ALBINO OR PALE GREEN MUTANT 1 (A ATP/PHOSPHATE CARRIER 3 (APC3) CYTOCHROME C-1 (CYTC-1) GGAMMA-SUBUNIT 1 (GG1) HARMLESS TO OZONE LAYER 1 (HOL1) INOSITOL-POLYPHOSPHATE 5-PHOSPH IQ-DOMAIN 27 (IGD27) K+ EFFLUX ANTIPORTER 4 (KEA4) N-TERMINAL-TRANSMEMBRANE-C2 DO na na na na na	Calmodulin-binc 5_23314497 Major facilitator 5_25168125 unknown proteir 5_226922 unknown proteir 5_226922 unknown proteir 5_22884392 GCK domain-cc 5_23314497 encodes a calm 1_9534457 ATPase, F0 cor 4_15573381 Encodes a stent 1_27584176 Encodes a stent 2_1819287 encodes a chlor 1_918130 Encodes a chlor 1_918130 tyrosyl-DNA phc 5_4926004 Provides actival 3_1004980 tyrosyl-DNA phc 5_4926004 Provides actival 3_1004980 Encodes a mer 4_16056587 Encodes a mer 4_16056587 Encodes a MPE 3_23417189 Encodes a mito 5_2309886 Encodes cytoch 1_8080691 heterotrimeric C 3_23417189 HARMLESS TC 2_18184166 Incodes a 5-inc 2_18184166 Incodes a 5-inc 2_18184166 IQ-domain 27 (I 1_19308042 member of Puta 2_8479050 hterminal-trans 1_18621881 CONTAINS Inte 1_20864225 pre-IRNA; IRNA 5_2309886 3-oxo-5-alpha-s 5_5227514 Potential natura 3_918984 Chaperone Dna 1_25964489 CBS domain-co 3_4195521	3.08 3.08 3.08 3.08 3.08 3.08 3.08 3.08	downstream promoter three_prime_UTR proximal promoter promoter promoter promoter promoter promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter proximal promoter promoter promoter promoter downstream promoter downstream promoter downstream promoter promot

AT4G33060	na	Cyclophilin-like 4_15948415	3.07	promoter
AT1G22850	na	SNARE associa 1_8080691	3.07	exon
AT2G15980	na	Tetratricopeptid 2_6952762	3.07	exon
AT1G54820	na	Protein kinase s 1_20445797	3.07	proximal promoter
AT1G76880	na	Duplicated hom 1_28865379	3.07	promoter
AT2G28390	na	SAND family prc 2_12143525	3.07	promoter
AT3G24120	na	Homeodomain-I 3_8708218	3.07	intron
AT3G27910	na	Galactose oxida 3_10358867	3.07	proximal promoter
AT4G14740	na	FUNCTIONS IN 4_8454939	3.07	proximal promoter
AT4G33310	na	unknown proteir 4_16056587	3.07	downstream
AT4G36230	na	unknown proteir 4_17144860	3.07	proximal promoter
AT5G11980	na	conserved oligo 5_3872358	3.07	promoter
AT4G22540	OSBP(OXYSTEROL BINDING PROTEIN)		3.07	proximal promoter
AT1G15110 AT1G55810	PHOSPHATIDYLSERINE SYNTHASE 1 (F		3.07	proximal promoter
AT1G55810 AT3G46010	URIDINE KINASE-LIKE 3 (UKL3) ACTIN DEPOLYMERIZING FACTOR 1 (A)	One of the hom 1_20864225	3.07 3.06	three_prime_UTR downstream
AT3G46000	ACTIN DEPOLYMERIZING FACTOR 1 (AI		3.06	
AT4G19710	ASPARTATE KINASE-HOMOSERINE DEI		3.06	promoter proximal promoter
AT1G08450	CALRETICULIN 3 (CRT3)	Encodes one of 1_2671959	3.06	promoter
AT2G02560	CULLIN-ASSOCIATED AND NEDDYLATION		3.06	promoter
AT4G31770	DEBRANCHING ENZYME 1 (DBR1)	Encodes a RNA 4_15372761	3.06	promoter
AT3G10160	DHFS-FPGS HOMOLOG C (DFC)	Encodes a prote 3_3144766	3.06	promoter
AT1G07110	FRUCTOSE-2,6-BISPHOSPHATASE (F2)		3.06	promoter
AT1G08460	HISTONE DEACETYLASE 8 (HDA08)	histone deacety 1_2671959	3.06	promoter
AT1G63005	MICRORNA399B (MIR399B)	Encodes a phos 1_23344717	3.06	intergenic
AT2G39170	na	unknown proteir 2_16336265	3.06	promoter
AT1G25460	na	NAD(P)-binding 1_8944449	3.06	downstream
AT1G22430	na	GroES-like zinc: 1_7919164	3.06	five_prime_UTR
AT3G13226	na	regulatory prote 3_4266374	3.06	promoter
AT1G75140	na	unknown proteir 1_28204524	3.06	promoter
AT1G75150	na	unknown proteir 1_28204524	3.06	three_prime_UTR
AT2G19130	na	S-locus lectin pi 2_8293656	3.06	promoter
AT2G25210	na	Ribosomal prote 2_10739791	3.06	promoter
AT1G01830	na	ARM repeat sur 1_298584	3.06	three_prime_UTR
AT1G18680	na	HNH endonucle 1_6433468	3.06	promoter
AT2G39130	na	Transmembrane 2_16327806	3.06	proximal promoter
AT3G02645	na	Plant protein of 3_567902	3.06	downstream
AT3G02650	na	Tetratricopeptid 3_567902	3.06	promoter
AT3G15160	na	unknown proteir 3_5104288	3.06	promoter
AT3G55646 AT4G36270	na na	unknown proteir 3_20642837 ATP binding; BE 4_17160865	3.06 3.06	proximal promoter downstream
AT4G36268	na	unknown proteir 4_17160865	3.06	downstream
AT5G63320	NUCLEAR PROTEIN X1 (NPX1)	Encodes NPX1 5_25373976	3.06	intergenic
AT5G63310	NUCLEOSIDE DIPHOSPHATE KINASE 2		3.06	promoter
AT1G01820	PEROXIN 11C (PEX11C)	member of the r 1_298584	3.06	promoter
AT1G75840	RAC-LIKE GTP BINDING PROTEIN 5 (AR		3.06	five_prime_UTR
AT3G49430	SERINE/ARGININE-RICH PROTEIN SPLI		3.06	five_prime_UTR
AT5G57990	UBIQUITIN-SPECIFIC PROTEASE 23 (UE		3.06	proximal promoter
AT1G78130	UNFERTILIZED EMBRYO SAC 2 (UNE2)	unfertilized emb 1_29400014	3.06	promoter
AT1G10550	XYLOGLUCAN:XYLOGLUCOSYL TRANS	Encodes a merr 1_3479493	3.06	exon
AT3G45100	(SETH2)	encodes Arabid 3_16504420	3.05	promoter
AT1G58350	(ZW18)	ZW18; INVOLV 1_21669868	3.05	proximal promoter
AT1G21710	8-OXOGUANINE-DNA GLYCOSYLASE 1	Encodes 8-oxo; 1_7624329	3.05	promoter
AT1G58080	ATP PHOSPHORIBOSYL TRANSFERASE		3.05	five_prime_UTR
AT5G57660	CONSTANS-LIKE 5 (COL5)	CONSTANS-liki 5_23353941	3.05	proximal promoter
AT3G19760	EUKARYOTIC INITIATION FACTOR 4A-III		3.05	promoter
AT5G27380	GLUTATHIONE SYNTHETASE 2 (GSH2)		3.05	promoter
AT5G42780	HOMEOBOX PROTEIN 27 (HB27)	homeobox prote 5_17154717	3.05	promoter
AT3G01100	HYPOTHETICAL PROTEIN 1 (HYP1)	unknown proteir 3_34691	3.05	downstream
AT5G09805	INFLORESCENCE DEFICIENT IN ABSCIS		3.05	intergenic
AT4G36890 AT3G58680	IRREGULAR XYLEM 14 (IRX14)	The IRX14 gene 4_17382097	3.05	promoter
AT1G74650	MULTIPROTEIN BRIDGING FACTOR 1B MYB DOMAIN PROTEIN 31 (MYB31)	Member of the F 1_28040804	3.05 3.05	promoter promoter
AT5G02320	MYB DOMAIN PROTEIN 3F (MYB3F)		3.05	promoter
AT5G17250	na	Alkaline-phosph 5_5675057	3.05	proximal promoter
AT4G21920	na	unknown proteir 4_11637815	3.05	proximal promoter
AT3G45095	na	transposable eli 3_16504420	3.05	promoter
AT5G65880	na	unknown proteir 5_26352900	3.05	promoter
AT1G06510	na	unknown proteir 1_1992293	3.05	promoter
AT1G06515	na	Protein of unknc 1_1992293	3.05	promoter
AT2G29340	na	NAD-dependen 2_12596949	3.05	promoter
AT2G33250	na	unknown proteir 2_14097333	3.05	promoter
AT3G03570	na	FUNCTIONS IN 3_856731	3.05	promoter
AT3G58676	na	This gene enco 3_21706845	3.05	exon
AT3G59950	na	Peptidase family 3_22147982	3.05	promoter
AT4G19380	na	Long-chain fatty 4_10570378	3.05	intron
AT5G09876	na	unknown proteir 5_3078952	3.05	proximal promoter
AT4G29680	na	Alkaline-phosph 4_14539911	3.05	promoter
AT4G31740	na	Sec1/munc18-lil 4_15363541	3.05	promoter
AT5G27395	na	Mitochondrial in 5_9671445	3.05	downstream
AT5G46250	na na	RNA-binding pri 5_18755244	3.05	promoter
AT5G54630	na na	zinc finger prote 5_22192061 Preprotein trans 5_24318045	3.05	intergenic
AT5G60460 AT1G52880	na NO APICAL MERISTEM (NAM)	Transcription fa 1_19692567	3.05	promoter proximal promoter
AT1G52880 AT1G65390	PHLOEM PROTEIN 2 A5 (PP2-A5)	phloem protein : 1_24292263	3.05 3.05	proximal promoter promoter
AT1G65390 AT1G70370	POLYGALACTURONASE 2 (PG2)	polygalacturona 1_26518443	3.05	intergenic
AT3G58500	PROTEIN PHOSPHATASE 2A-4 (PP2A-4)		3.05	five_prime_UTR
AT1G49600	RNA-BINDING PROTEIN 47A (RBP47A)		3.05	promoter
AT1G43850	SEUSS (SEU)	Encodes a trans 1_16617106	3.05	promoter
AT3G01090	SNF1 KINASE HOMOLOG 10 (KIN10)	encodes a SNF 3_34691	3.05	promoter
AT3G59770	SUPPRESSOR OF ACTIN 9 (SAC9)	Encodes a phos 3_22086251	3.05	promoter
AT5G16850	TELOMERASE REVERSE TRANSCRIPTA		3.05	promoter
AT1G53300	TETRATRICOPEPTIDE-REPEAT THIORE		3.05	five_prime_UTR
AT1G64040	TYPE ONE SERINE/THREONINE PROTE		3.05	five_prime_UTR

AT40::::				
AT1G14140	UNCOUPLING PROTEIN 3 (UCP3)	Mitochondrial st 1_4839747	3.05	promoter
AT1G32200	(ATS1)	Encodes a chlor 1 11604969	3.04	exon
AT3G06500	ALKALÍNE/NEUTRAL INVERTASE C (A/N		3.04	intergenic
AT5G49480	CA2+-BINDING PROTEIN 1 (CP1)	AtCP1 encodes 5_20069774	3.04	proximal promoter
AT1G22840	CYTOCHROME C-1 (CYTC-1)	Encodes cytoch 1_8079307	3.04	five_prime_UTR
AT4G12330	CYTOCHROME P450, FAMILY 706, SUBF		3.04	exon
AT4G05420	DAMAGED DNA BINDING PROTEIN 1A (3.04	promoter
AT2G40300	FERRITIN 4 (FER4)	Encodes FERR 2_16833347	3.04	promoter
AT1G74420	FUCOSYLTRANSFERASE 3 (FUT3)	Predicted fucos 1 27971241	3.04	proximal promoter
AT5G62480	GLUTATHIONE S-TRANSFERASE TAU 9		3.04	downstream
AT1G25250	INDETERMINATE(ID)-DOMAIN 16 (IDD16		3.04	proximal promoter
AT3G09710	IQ-DOMAIN 1 (IQD1)	Ca(2+)-depende 3_2979339	3.04	intron
AT1G13220	LITTLE NUCLÈI2 (LINC2)	Encodes a nucli 1_4520185	3.04	intron
AT1G68510	LOB DOMAIN-CONTAINING PROTEIN 42		3.04	downstream
AT3G23165	LOW-MOLECULAR-WEIGHT CYSTEINE-		3.04	intergenic
AT1G61732	MICRORNA776A (MIR776A)	Encodes a micr 1_22795235	3.04	promoter
AT2G36600	na	pre-tRNA; tRNA 2_15346917	3.04	intergenic
AT5G44375	na	pre-tRNA; tRNA 5_17878334	3.04	proximal promoter
AT1G67510	na	Leucine-rich reg 1_25298102	3.04	exon
AT2G33205	na	Serinc-domain (2_14074547	3.04	proximal promoter
AT4G33700	na	FUNCTIONS IN 4_16179549	3.04	promoter
AT1G10440	na	pre-tRNA; tRNA 1 3431148	3.04	downstream
AT1G38140	na	transposable eli 1_14305598	3.04	intergenic
AT1G13230	na	Encodes a leuci 1_4520185	3.04	promoter
AT1G22830	na	Tetratricopeptid 1_8079307	3.04	downstream
AT2G44640	na	FUNCTIONS IN 2_18417135	3.04	promoter
AT2G45630	na	D-isomer specif 2_18798167	3.04	intergenic
AT2G22482	na	na 2_9550179	3.04	promoter
AT4G09040	na	RNA-binding (R 4_5797407	3.04	promoter
AT4G12650	na	Endomembrane 4_7470594	3.04	promoter
AT5G61520	na	Major facilitator 5_24741328	3.04	promoter
AT5G13140	na	Pollen Ole e 1 a 5_4171901	3.04	promoter
AT5G65685	na	UDP-Glycosyltr; 5 26278352	3.04	proximal promoter
AT1G67500	RECOVERY PROTEIN 3 (REV3)	Encodes the ca 1_25298102	3.04	proximal promoter
AT4G26840	SMALL UBIQUITIN-LIKE MODIFIER 1 (SL		3.04	promoter
AT4G11780		unknown proteir 4_7088044	3.04	exon
AT2G47260	WRKY DNA-BINDING PROTEIN 23 (WRK		3.04	proximal promoter
AT4G05410	YAOZHE (YAO)	Encodes a nucli 4 2745757	3.04	promoter
AT1G69780	(ATHB13)	Encodes a hom 1_26260869	3.03	downstream
AT1G18450	ACTIN-RELATED PROTEIN 4 (ARP4)	Encodes a gene 1 6348059	3.03	promoter
AT1G67730	BETA-KETOACYL REDUCTASE 1 (KCR1		3.03	downstream
AT5G02110	CYCLIN D7;1 (CYCD7;1)	Encodes CYCLI 5_416587	3.03	promoter
AT1G60660	CYTOCHROME B5-LIKE PROTEIN (CB5L		3.03	proximal promoter
AT3G56630	CYTOCHROME P450, FAMILY 94, SUBFA		3.03	promoter
AT1G21910	DEHYDRATION RESPONSE ELEMENT-E		3.03	promoter
AT4G00550	DIGALACTOSYL DIACYLGLYCEROL DEI		3.03	promoter
AT5G24400	EMBRYO DEFECTIVE 2024 (emb2024)	Encodes a prote 5 8331899	3.03	promoter
AT5G53860	EMBRYO DEFECTIVE 2737 (emb2737)	A locus involve: 5_21865210	3.03	promoter
AT1G26120	ISOPRENYLCYSTEINE METHYLESTERA		3.03	intron
AT5G06980	na	unknown proteir 5_2169949	3.03	intergenic
AT3G45420	na	Concanavalin A 3_16660248	3.03	proximal promoter
AT1G34580	na	Major facilitator 1_12659983	3.03	proximal promoter
AT3G03680	na	C2 calcium/lipid 3_907476	3.03	promoter
AT4G17810	na	C2H2 and C2H(4 9904563	3.03	proximal promoter
AT5G38200	na	Class I glutamin 5_15256311	3.03	five_prime_UTR
AT5G50200	na	NAD(P)-binding 5_20749704	3.03	promoter
AT1G60670	na	Protein of unknot 1_22343653	3.03	promoter
AT2G27180	na	unknown proteir 2_11620853	3.03	exon
AT3G03847	iia			
AT3G05047	na	SALID-like auxir 3 082841		
	na	SAUR-like auxir 3_982841	3.03	promoter
	na	Ribosomal L29e 3_2118015	3.03 3.03	promoter promoter
AT3G08030	na na	Ribosomal L29€ 3_2118015 Protein of unknr 3_2564977	3.03 3.03 3.03	promoter promoter intron
AT3G08030 AT3G61490	na na na	Ribosomal L29€ 3_2118015 Protein of unknr 3_2564977 Pectin lyase-lik€ 3_22759094	3.03 3.03 3.03 3.03	promoter promoter intron exon
AT3G08030 AT3G61490 AT4G00560	na na na na	Ribosomal L29€ 3_2118015 Protein of unknc 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620	3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream
AT3G08030 AT3G61490	na na na na na	Ribosomal L29€ 3_2118015 Protein of unknc 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Proti 3_23316495	3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925	na na na na na na	Ribosomal L29€ 3_2118015 Protein of unknr 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686	3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter
AT3G08030 AT3G61490 AT4G00560 AT3G63095	na na na na na	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705	3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980	na na na na na na na	Ribosomal L29¢ 3_2118015 Protein of unknx 3_2564977 Pectin lyase-lik¢ 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420	na na na na na na na na	Ribosomal L29¢ 3_2118015 Protein of unknx 3_2564977 Pectin lyase-lik¢ 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prot 4_15247995 ARM repeat suţ 5_6337512	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980	na na na na na na na na	Ribosomal L29¢ 3_2118015 Protein of unknx 3_2564977 Pectin lyase-lik¢ 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G19340	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpo 4_6704886 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat su; 5_6337512 unknown protei 5_6514985	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon downstream
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G19340 AT5G66558	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Proti 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat sup 5_6337512 unknown proteir 5_6614985 Potential natura 5_26567001 Phototropic-resj 5_26567001	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon downstream promoter exon downstream promoter
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G19340 AT5G66558 AT5G66560	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Proti 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat sup 5_6337512 unknown proteir 5_6614985 Potential natura 5_26567001 Phototropic-resj 5_26567001	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon downstream promoter downstream
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G19340 AT5G66556 AT1G52890	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat sup 5_6337512 unknown proteir 5_6614985 Potential natura 5_26567001 Phototropic-resi 5_26567001 Phototropic-resi 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon downstream promoter downstream promoter downstream promoter
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G19340 AT5G66558 AT5G66560 AT1G52890 AT1G37130	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat sup 5_6337512 unknown proteir 5_6614985 Potential natura 5_26567001 Phototropic-resi 5_26567001 Phototropic-resi 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon downstream promoter downstream promoter downstream promoter intergenic
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G19340 AT5G66558 AT5G66560 AT1G52890 AT1G37130 AT5G65690	na n	Ribosomal L29s 3_2118015 Protein of unkn 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Proti 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat sup 5_6337512 unknown proteir 5_6514985 Potential natura 5_26567001 Phototropic-resi 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes a puta 5_26265014	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic proximal promoter
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G18980 AT5G66550 AT5G66560 AT1G52890 AT1G37130 AT5G665690 AT1G57740	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat sut 5_6337512 unknown proteir 5_6514985 Potential natura 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes a puta 5_26265014 Psby precursor 1_25393748	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter exon downstream promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G18980 AT5G66558 AT5G66550 AT1G52890 AT1G37130 AT5G65690 AT1G7740 AT1G18080	na n	Ribosomal L29s 3_2118015 Protein of unkn 3_2564977 Protein yase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpo 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat sup 5_6337512 unknown proteir 5_6514985 Potential natura 5_26567001 Phototropic-resp 5_26567001 encodes a NAC 1_19698537 identified as a n 1_14163706 Encodes a puta 5_26265014 PsbY precursor 1_25393748 Encodes a trans 1_23019384	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon downstream promoter downstream promoter downstream promoter intergenic proximal promoter intergenic promoter intergenic promoter
AT3G08030 AT3G61490 AT3G63095 AT4G10925 AT4G1925 AT4G25980 AT4G31420 AT5G18980 AT5G6558 AT5G66560 AT1G52890 AT1G37130 AT5G65690 AT1G67740 AT1G67740 AT1G67740	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Pectin lyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 ARM repeat suf 5_6337512 unknown proteir 5_6514985 Potential natura 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes a puta 5_26265014 PsbY precursor 1_25393748 Encodes the Ar 1_6222052 Encodes a trans 1_23019384 Encodes CTC1 4_6116655	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic proximal promoter intergenic promoter promoter promoter
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G31420 AT5G18980 AT5G18980 AT5G66560 AT1G62890 AT1G37130 AT5G665690 AT1G67740 AT1G18080 AT1G62300 AT4G09680	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Protein yase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat su; 5_6337512 unknown proteir 5_6514985 Potential natura 5_26567001 Phototropic-resi 5_26567001 Phototropic-resi 5_262657001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes a puta 5_26265014 Psby precursor 1_25393748 Encodes the Ari 1_6222052 Encodes a trans 1_23019384 Encodes CTC1 4_6116655 FASCICLIN-like 5_17762119	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter exon downstream promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic promoter promoter promoter promoter promoter
AT3G08030 AT3G61490 AT4G00560 AT4G090560 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G18980 AT5G66558 AT5G665690 AT1G37130 AT1G62300 AT1G62300 AT1G62300 AT1G62300 AT1G62300 AT4G69680 AT4G09680 AT5G44130	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Protein yase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat su; 5_6337512 unknown proteir 5_6514985 Potential natura 5_26567001 Phototropic-resi 5_26567001 Phototropic-resi 5_262657001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes a puta 5_26265014 Psby precursor 1_25393748 Encodes the Ari 1_6222052 Encodes a trans 1_23019384 Encodes CTC1 4_6116655 FASCICLIN-like 5_17762119	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter intron promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic proximal promoter promoter promoter promoter promoter promoter promoter promoter downstream
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G19340 AT5G66558 AT5G66560 AT1G52890 AT1G67740 AT1G67740 AT1G67740 AT1G67740 AT1G62300 AT1G62300 AT4G09680 AT1G623440	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Protein yase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpo 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 Potential natura 5_26567001 Phototropic-resj 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes a trans 1_23019384 Encodes CTC1 4_6116655 FASCICLIN-like 5_17762119 ferredoxin/thick 5_7902213 A member of AF 5_21204848	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter exon downstream promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic promoter promoter promoter promoter promoter promoter promoter promoter downstream intergenic intergenic promoter promoter promoter promoter downstream intergenic
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G18980 AT5G66560 AT1G62890 AT1G37130 AT5G666690 AT1G67740 AT1G18080 AT1G62300 AT4G09680 AT5G44130 AT5G44130 AT5G23440 AT5G23440 AT5G22410	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Protein yase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpo 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 Potential natura 5_26567001 Phototropic-resj 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes a trans 1_23019384 Encodes CTC1 4_6116655 FASCICLIN-like 5_17762119 ferredoxin/thick 5_7902213 A member of AF 5_21204848	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intergenic promoter intron exon downstream intergenic promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic promoter promoter downstream promoter intergenic promoter promoter promoter promoter promoter downstream intergenic promoter downstream intergenic promoter downstream intergenic promoter
AT3G08030 AT3G61490 AT4G00560 AT4G090560 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G18980 AT5G66558 AT5G665690 AT1G37130 AT1G62300 AT1G62300 AT1G62300 AT1G62300 AT5G23441 AT5G23441 AT5G23441 AT5G23441 AT1G7430	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Protein yase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 ARM repeat su; 5_6337512 unknown proteir 5_6514985 Potential natura 5_26567001 Phototropic-res; 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes aputa 5_26265014 Psby precursor 1_25393748 Encodes the Ari 1_6222052 Encodes a trans 1_23019384 Encodes CTC1 4_6116655 FASCICLIN-like 5_17762119 ferredoxin/thiors 5_7902213 A member of AF 5_21204848 highly ABA-indu 1_2280728	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter exon downstream promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic promoter promoter downstream intergenic promoter downstream
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G19340 AT5G6558 AT5G66560 AT1G52890 AT1G67740 AT1G67740 AT1G67740 AT1G62300 AT4G09680 AT1G62340 AT5G23440 AT5G52210 AT5G52210 AT1G7430 AT5G52210	na n	Ribosomal L29s 3_2118015 Protein of unkn 3_2564977 Protein fyase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpc 4_6704686 Peroxidase sup 4_13190705 Zinc finger prots 4_15247995 ARM repeat sup 5_6337512 unknown proteir 5_6614985 Potential natura 5_26567001 Phototropic-resis 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes a puta 5_26265014 Psby precursor 1_26393748 Encodes at rans 1_23019384 Encodes CTC1 4_6116655 FASCICLIN-like 5_17762119 ferredoxin/thiors 5_7902213 A member of AF 5_21204848 highly ABA-indu 1_2280728 JOSEPHIN-like 2_12670857	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter promoter intron exon downstream intergenic promoter exon downstream promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic promoter promoter promoter promoter promoter promoter promoter promoter promoter downstream intergenic promoter downstream intergenic promoter downstream promoter
AT3G08030 AT3G61490 AT4G00560 AT3G63095 AT4G10925 AT4G25980 AT4G31420 AT5G18980 AT5G68560 AT1G62890 AT1G37130 AT5G665690 AT1G67740 AT1G18080 AT1G62300 AT1G62300 AT1G62304 AT5G23440 AT5G23440 AT5G23440 AT5G2210 AT1G07430 AT2G29640 AT1G79850	na n	Ribosomal L29¢ 3_2118015 Protein of unkn 3_2564977 Protein yase-like 3_22759094 NAD(P)-binding 4_240620 Encodes a Prot 3_23316495 Nuclear transpo 4_6704686 Peroxidase sup 4_13190705 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 Zinc finger prote 4_15247995 Potential natura 5_26567001 encodes a NAC 1_19698537 Identified as a n 1_14163706 Encodes a NAC 1_19698537 Identified as a n 1_24163706 Encodes a trans 1_23019384 Encodes CTC1 4_6116655 FASCICLIN-like 5_17762119 ferredoxin/thiors 5_7902213 A member of AF 5_21204848 highly ABA-indu 1_2280728 JOSEPHIN-like 2_12670857 Encodes a trans 1_2301987	3.03 3.03 3.03 3.03 3.03 3.03 3.03 3.03	promoter promoter intron exon downstream intergenic promoter exon downstream promoter exon downstream promoter downstream promoter intergenic proximal promoter intergenic promoter downstream promoter downstream promoter promoter promoter promoter downstream intergenic promoter downstream intergenic promoter downstream promoter downstream promoter proximal promoter proximal promoter proximal promoter
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AT1G04000	na	unknown proteir 1_1030726	3.02	proximal promoter
AT1G78800	na	UDP-Glycosyltri 1_29628008	3.02	promoter
AT3G44620	na	protein tyrosine 3_16193811	3.02	promoter
AT3G55485	na	na 3_20571361	3.02	promoter
AT4G03500	na	Ankyrin repeat f 4_1553740	3.02	intron
	na	pre-tRNA; tRNA 5_6400843	3.02	
AT5G19095				promoter
AT5G44375	na	pre-tRNA; tRNA 5_17877638	3.02	downstream
AT5G04420	na	Galactose oxida 5_1250018	3.02	promoter
AT5G06110	na	DnaJ domain ;N 5_1843882	3.02	promoter
AT5G18400	na	Cytokine-induce 5 6095044	3.02	intron
AT5G40945	na	pre-tRNA; tRNA 5_16410770	3.02	downstream
	na			
AT5G61170		Ribosomal prote 5_24611056	3.02	promoter
AT5G62760	na	P-loop containir 5_25209645	3.02	promoter
AT3G15500	NAC DOMAIN CONTAINING PROTEIN 3	Encodes an AT ₁ 3_5237595	3.02	intergenic
AT5G44370	PHOSPHATE TRANSPORTER 4;6 (PHT4	Encodes an ino 5_17877638	3.02	promoter
AT1G04010	PHOSPHOLIPID STEROL ACYL TRANSF		3.02	intergenic
AT3G02800	PLANT AND FUNGI ATYPICAL DUAL-SPI		3.02	five_prime_UTR
AT5G44140	PROHIBITIN 7 (PHB7)	prohibitin 7 (PH 5_17762119	3.02	promoter
AT5G40950	RIBOSOMAL PROTEIN LARGE SUBUNIT	ribosomal protei 5_16410770	3.02	promoter
AT1G07420	STEROL 4-ALPHA-METHYL-OXIDASE 2-	Arabidopsis tha 1_2280728	3.02	intergenic
AT2G29630	THIAMINC (THIC)	Encodes a prote 2_12670857	3.02	intergenic
AT5G67360	(ARA12)	Encodes a subt 5_26874593	3.01	promoter
AT2G31970		Encodes the Ar; 2 13600371		
	(RAD50)			promoter
AT3G54340	APETALA 3 (AP3)	Floral homeotic 3_20121451	3.01	promoter
AT4G25960	ATP-BINDING CASSETTE B2 (ABCB2)	P-glycoprotein 2 4_13176565	3.01	proximal promoter
AT4G03080	BRI1 SUPPRESSOR 1 (BSU1)-LIKE 1 (BS	BRI1 suppressc 4 1365502	3.01	promoter
AT1G55490	CHAPERONIN 60 BETA (CPN60B)	encodes the bel 1_20719292	3.01	promoter
AT3G22880	DISRUPTION OF MEIOTIC CONTROL 1 (3.01	promoter
AT4G30850	HEPTAHELICAL TRANSMEMBRANE PR		3.01	promoter
AT3G21760	HYPOSTATIN RESISTANCE 1 (HYR1)	Encodes HYR1, 3_7666707	3.01	promoter
AT3G53130	LUTEIN DEFICIENT 1 (LUT1)	Lutein-deficient 3_19692747	3.01	promoter
AT1G04630	MATERNAL EFFECT EMBRYO ARREST	maternal effect 1 1291148	3.01	promoter
AT3G26980	MEMBRANE-ANCHORED UBIQUITIN-FO			five_prime_UTR
AT1G76140	na	Prolyl oligopepti 1_28571263	3.01	exon
AT2G22450	na	riboflavin biosyr 2_9530492	3.01	promoter
AT1G03570	na	pre-tRNA; tRNA 1_892517	3.01	exon
AT1G68710	na	ATPase E1-E2 1_25799652	3.01	proximal promoter
AT1G72790	na	hydroxyproline-ı 1 27396479	3.01	exon
AT1G72800	na	RNA-binding (R 1_27396479	3.01	
				proximal promoter
AT2G17970	na	2-oxoglutarate (2_7821465		promoter
AT2G34340	na	Protein of unknc 2_14488112	3.01	intergenic
AT2G36410	na	Family of unkno 2_15280734	3.01	downstream
AT3G21755	na	Potential natura 3_7666707	3.01	downstream
AT3G26990	na	ENTH/VHS fam 3_9948024	3.01	downstream
AT5G16567	na	This gene enco 5_5417383	3.01	proximal promoter
AT4G31490	na	Coatomer, beta 4_15268395	3.01	promoter
AT4G38781	na	unknown proteir 4_18111261	3.01	promoter
AT5G02050	na	Mitochondrial gl 5_404418	3.01	promoter
AT5G07980	na	dentin sialophos 5_2557888	3.01	proximal promoter
AT5G22780	na	Adaptor protein 5_7598810	3.01	proximal promoter
AT5G25920	na	BEST Arabidop: 5_9046593	3.01	promoter
AT5G28630	na	glycine-rich prot 5_10636538	3.01	promoter
AT5G39785	na	FUNCTIONS IN 5_15932093	3.01	exon
AT4G01550	NAC DOMAIN CONTAINING PROTEIN 69	Encodes a plasi 4 676451	3.01	promoter
AT5G22790	RETICULATA-RELATED 1 (RER1)	reticulata-relate 5_7598810	3.01	intergenic
AT4G12910			3.01	promoter
	SERINE CARBOXYPEPTIDASE-LIKE 20 (
AT4G30960	SOS3-INTERACTING PROTEIN 3 (SIP3)		3.01	proximal promoter
AT5G65780	(ATBCAT-5)	encodes a chlor 5_26316295	3	five_prime_UTR
AT4G31300	(PBA1)	Encodes 20S pt 4 15188666	3	promoter
AT2G23600	ACETONE-CYANOHYDRIN LYASE (ACL)	Encodes a prote 2 10043844	3	promoter
AT2G46980	ASYNAPTIC 3 (ASY3)	Encodes ASY3, 2_19304350	3	promoter
AT3G55950	CRINKLY4 RELATED 3 (CCR3)	CRINKLY4 relat 3_20752761	3	intergenic
AT5G11530	EMBRYONIC FLOWER 1 (EMF1)	Involved in regu 5_3693608	3	proximal promoter
AT3G26618	EUKARYOTIC RELEASE FACTOR 1-3 (E	eukaryotic relea 3_9788447	3	promoter
AT5G66510	GAMMA CARBONIC ANHYDRASE 3 (GAI	Encodes mitoch 5 26551684	3	promoter
AT2G32700	LEUNIG HOMOLOG (LUH)	Encodes a WD ₂ 2_13866693	3	promoter
AT1G64660	METHIONINE GAMMA-LYASE (MGL)	Encodes a func 1 24029934		intron
AT2G23620				
	METHYL ESTERASE 1 (MES1)	Encodes a prote 2_10051761	3	proximal promoter
AT2G38325	MICRORNA390A (MIR390A)	Encodes a micr 2_16059570	3	proximal promoter
AT2G47350	na	HIT zinc finger; 2_19433742	3	promoter
AT3G55410	na	2-oxoglutarate c 3_20540982	3	promoter
AT4G32785	na	CONTAINS Inte 4_15811880	3	downstream
AT4G32790	na	Exostosin family 4 15811880	3	promoter
AT4G00560	na	NAD(P)-binding 4_242881		proximal promoter
AT4G36150	na	Disease resista 4_17104618	3	promoter
AT5G48760	na	Ribosomal prote 5_19772774	3	promoter
AT1G10220	na	BEST Arabidop: 1_3351867	3	promoter
AT1G16570	na	UDP-Glycosyltr: 1_5673658	3	promoter
				•
AT1G22410	na	Class-II DAHP : 1_7911827	3	promoter
AT1G31760	na	SWIB/MDM2 dc 1_11373610		promoter
AT1G68340	na	Protein of unknc 1_25615523	3	promoter
AT1G72410	na	COP1-interactir 1_27257105	3	promoter
AT2G11890	na	adenylate cycla: 2_4802751	3	promoter
AT2G26800	na	Mutant has incr 2_11432712	3	five_prime_UTR
AT2G28710	na	C2H2-type zinc 2_12321619	3	proximal promoter
AT2G37110		PLAC8 family pi 2_15592565		five_prime_UTR
AT1CEFOCO	na		3	exon
AT1G55260	na na	Bifunctional inhi 1_20616115		
				proximal promoter
AT1G55265	na na	Protein of unknc 1_20616115	3	proximal promoter intergenic
AT1G55265 AT2G37100	na na na	Protein of unknc 1_20616115 protamine P1 fa 2_15592565	3	intergenic
AT1G55265 AT2G37100 AT2G37100	na na na na	Protein of unknr 1_20616115 protamine P1 fa 2_15592565 protamine P1 fa 2_15590463	3 3 3	intergenic proximal promoter
AT1G55265 AT2G37100 AT2G37100 AT2G44930	na na na na na	Protein of unknc 1_20616115 protamine P1 fa 2_15592565 protamine P1 fa 2_15590463 Plant protein of 2_18532047	3 3 3 3	intergenic proximal promoter promoter
AT1G55265 AT2G37100 AT2G37100	na na na na	Protein of unknr 1_20616115 protamine P1 fa 2_15592565 protamine P1 fa 2_15590463 Plant protein of 2_18532047 hypoxia-respon: 3_17728152	3 3 3	intergenic proximal promoter
AT1G55265 AT2G37100 AT2G37100 AT2G44930	na na na na na	Protein of unknc 1_20616115 protamine P1 fa 2_15592565 protamine P1 fa 2_15590463 Plant protein of 2_18532047	3 3 3 3	intergenic proximal promoter promoter promoter
AT1G55265 AT2G37100 AT2G37100 AT2G44930 AT3G48030 AT4G16105	na na na na na na na	Protein of unknc 1_20616115 protamine P1 fa 2_15592565 protamine P1 fa 2_15590463 Plant protein of 2_18532047 hypoxia-respon: 3_17728152 pre-tRNA; tRNA 4_9108876	3 3 3 3 3 3	intergenic proximal promoter promoter promoter intergenic
AT1G55265 AT2G37100 AT2G37100 AT2G44930 AT3G48030	na na na na na na	Protein of unknr 1_20616115 protamine P1 fa 2_15592565 protamine P1 fa 2_15590463 Plant protein of 2_18532047 hypoxia-respon: 3_17728152	3 3 3 3 3	intergenic proximal promoter promoter promoter

AT4G33180	na	alpha/beta-Hydr 4_16000273	3	five_prime_UTR
AT5G11640	na	Thioredoxin sup 5_3741904	3	promoter
AT5G08565	na	Transcription ini 5_2775811	3	promoter
AT5G11225	na	pre-tRNA; tRNA 5_3578368	3	promoter
AT5G11630	na	unknown proteir 5_3741904	3	intron
AT5G47740	na	Adenine nucleo 5_19337909	3	proximal promoter
AT5G65240	na	Leucine-rich rer 5_26078300	3	promoter
AT4G00570	NAD-DEPENDENT MALIC ENZYME 2 (NA	Encodes an NA 4_242881	3	exon
AT5G17770	NADH:CYTOCHROME B5 REDUCTASE 1	Encodes NADH 5_5866622	3	five_prime_UTR
AT1G70940	PIN-FORMED 3 (PIN3)	A regulator of at 1_26739782	3	intergenic
AT2G28550	RELATED TO AP2.7 (RAP2.7)	related to AP2.7 2_12225723	3	downstream
AT4G35480	RING-H2 FINGER A3B (RHA3B)	Encodes a puta 4_16852473	3	exon
AT2G39705	ROTUNDIFOLIA LIKE 8 (RTFL8)	ROTUNDIFOLI/ 2_16555606	3	proximal promoter
AT5G17240		SET domain grc 5_5666758	3	promoter
AT5G11190	SHINE2 (SHN2)	encodes a mem 5_3563901	3	proximal promoter
AT3G55120	TRANSPARENT TESTA 5 (TT5)	Catalyzes the ci 3_20432388	3	proximal promoter
AT1G70560	TRYPTOPHAN AMINOTRANSFERASE O	TAA1 is involve 1_26603414	3	proximal promoter
AT2G26580	YABBY5 (YAB5)	YABBY5 (YAB5 2_11308318	3	proximal promoter