Table S1: Datasets used for Rice Blast analysis.

GEO ID	Genotype	Tissue	Stage	Strain
GSE7256	Nipponbare (S)	Leaf	Seedling Stage	FR13
GSE18361	Nipponbare (S)	Root/leaf	Seedling Stage	Guy11
GSE28308	Non-transgenic Taipei 309 (S)	Seedling	Seedling Stage	PLP-1
	Transgenic line OX-Pi54 (R)			
GSE30941	Nipponbare (S)	Leaf	Seedling Stage	FR13
				CL367
				BR29
GSE39635	Nipponbare [Pia] (R)	Leaf	Fourth Leaf Stage	Ina86-137
	Transgenic line OX-OsWRKY28 (S)			
GSE41798	IRBL18 (Pi9 NIL of LTH) (R)	Leaf	Seedling Stage	CH63
	IRBL22 (Pi9 NIL of LTH) (R)			
	LTH (S)			
GSE62893	Nipponbare (Pia) (R)	Leaf	Fourth Leaf Stage	P91-15B
	Nipponbare (S)			
GSE62894	Nipponbare (Pish) (R)	Leaf	Fourth Leaf Stage	Kyu77
	Nipponbare (S)			
GSE62895	Nipponbare (Pia) (R)	Root	Fourth Leaf Stage	P91-15B
	Nipponbare (S)			
GSE62422	Nipponbare (Pia) (R)	Leaf	Fourth Leaf Stage	P91-15B
	Nipponbare (S)			

Table S2: Datasets used for Bacterial blight analysis.

GEO ID	Genotype	Tissue	Stage	Strain
GSE36272	Nipponbare (S)	Leaf	14 Days	PXO99A
				PXO99AME7
				PXO99AME5
				T7174
				PXO86
				BLS303
				PXO99AME1
				PXO99AME2
				PXO99A-2
				MOCK
	IR24 (S)	Leaf	14 Days	PXO99A
				PXO99AME7
				PXO99AME5
				T7174
				PXO86
				BLS303
				PXO99AME1
				PXO99AME2
				PXO99A-2
				MOCK
GSE33411	IR24 (S)	Whole plants	2 Weeks	PXO86
	IRBB5 (R)			
	IRBB7 (R)			
GSE16793	Nipponbare (S)	Shoot	2 Weeks	PXO99A
GSE43050	IR24 (R)	Leaf	35 Days	PXO71
GSE63337	Osaba1-1 (R)	Leaf	6.5 Leaf Stage	PXO99
	Nipponbare (S)			

Table S3: List of primers used for quantitative real time PCR.

Locus id	WRKY name	Primer sequence
LOC_Os01g40260	OsWRKY77_qF	GAGGAAGTACGGCAAGAAGAT
	OsWRKY77_qR	CTCCACCCGCTTCTTCAC
LOC_Os01g51690	OsWRKY26_qF	GAGGTCGGACGATGAGATACT
	OsWRKY26_qR	CCGGTAGTAGTTCCTCGGATTA
LOC_Os01g53260	OsWRKY23_qF	GCAACGTGAAGAAGCAAGTG
	OsWRKY23_qR	AACTGGGAGAGGAACTGGA
LOC_Os03g21710	OsWRKY79_qF	GTTCATGCAGTGGGACGA
	OsWRKY79_qR	GTTTCCGCCGTCGTTCT
LOC_Os05g39720	OsWRKY70_qF	TACTCTTACACGAGCCAGCA
	OsWRKY70_qR	GGCTGCTCAAAGAACGACAT
LOC_Os05g45230	OsWRKY58_qF	CAGAAGGCCGTCAAGAACA
	OsWRKY58_qR	CAGGTTCTCTGTTGCAGTTTG
LOC_Os05g49620	OsWRKY19_qF	AGGTAGTGGCAGAGCCTAT
	OsWRKY19_qR	AGAAGTCGCTGCTGAACTG
LOC_Os06g44010	OsWRKY28_qF	TACGAGGGCGAGCACAA
	OsWRKY28_qR	CTGGTGCTGTGAGTGCTTG
LOC_Os09g25070	OsWRKY62_qF	GAGGAGGTGGTGCAAGTG
	OsWRKY62_qR	GTGGGATTTGATCCACAACTCTA
LOC_Os12g02450	OsWRKY64_qF	TCGTCGAAGCATCACAGATTAG
	OsWRKY64_qR	AACAGGTGACGGAGATGTTG
LOC_Os05g46020	OsWRKY07_qF	TCCGGACGAAGTCAGAGAT
	OsWRKY07_qR	CGGTAGTAGTTCCTTGGGTTG
LOC_Os09g25060	OsWRKY76_qF	GTGCTCCATCTCCATCAACT
	OsWRKY76_qR	CGGCACACCTCCTTGAG
LOC_Os03g50885	OsActin_qF	GATCTGGCATCACACCTTCTAC
	OsActin_qR	CTGGGTCATCTTCTCACGATTG

Table S4: Structural variations at nucleotide level in Tetep and HP2216 in comparison with Nipponbare.

Gene name	Position	Nipponbare	HP2216	Tetep
WRKY7	116	T	T	C
	500	G	G	A
	507	G	G	A
	511-522	CCGTGTTCAATG	deletion	CCGTGTTCAATG
	584	C	T	T
	900	T	T	C
	935	T	T	C
	1006-1192	*	*	ATATACTATGGCTGTGTTCGTTCCAGTGACATTGGGTGAGAAAGGTCCTCGTTTTCCGCGCGCACGCTTCCCAAACTACTAAACGGTGCGTTTTTTGNNAAATAGTTAATACTCAATTAATCATATGCTAATGGCCCACCTCGTTTTGCGTATCTTCCCAATCTCCCTACTCCCCTTCTCCTCAAACACACCCTAT
	1516	T	T	C
	1895	C	C	T
WRKY19	88	C	C	G
	558	A	A	T
	559	A	A	C
	623	C	C	T
	625-632	CCGCCGCCG	CCGCCGCCG	deletion
	799	G	G	A
WRKY23	514	C	C	A
	524	G	G	A
	731	G	G	A
	947	T	T	C
	1190	A	A	*
	1246	G	G	A
	1326	*	*	A
	1578	G	G	T
	1945-1947			AAA INSERTION
	2161-2162			GG INSERTION
	2442	T	T	C
	2655	G	G	A
	2762	*	*	C
	2791	*	*	A
	2859-2864	ACTTGA	ACTTGA	deletion
	2999	T	T	C
	3022	A	A	*
	3024	A	A	T
	3074			TA INSERTION
	3186-3189			TATA INSERTION
WRKY26	78	A	A	G

	114-116	*	*	ACG INSERTION
	188	G	G	T
	189-230	GCTCCGGCAGCGGCTACGGCGCCGCCTCGTACGTTGCTCCA	GCTCCGGCAGCGGCTACGGCGCCGCCTCGTACGTTGCTCCA	DELETION
	241	G	G	C
	314-316			CCA INSERTION
	363	C	C	G
	410-412			GGC INSERTION
	455	T	T	A
	499	C	C	G
	516	T	T	*
	523-525	ATA	ATA	DELETION
WRKY28	95	C	C	T
	205-206	TC	TC	AA
	1043-1056	ACAACCCGTGCCCG	DELETION	ACAACCCGTGCCCG
WRKY58	257	A	A	C
	277	C	C	A
	825	C	C	T
	837-839	TCT	TCT	DELETION
WRKY62	902	T	T	A
	1117	C	C	A
	1124	A	A	*
	1158	T	T	C
	1175	A	A	G
	1331	A	A	G
	1359-1368	*	*	GTTGGTTTTT
	1385	G	G	A
	1917	G	G	A
WRKY64	99	G	C	C
	111	A	G	G
	142	A	G	G
	154	C	T	T
	163	T	C	C
	168	T	C	C
	169	C	T	T
	187-190	TAGC	*	*
	222	A	G	G
	231	T	G	G
	246-247	TC	AT	AT
	256-258	*	CAT	CAT
	281	C	T	T
	289	T	T	A
	354	G	G	A
	419	G	G	T
	430	C	C	T
	463	C	C	G

	469	A	A	G
	473	A	A	G
	479	G	G	C
	484	A	A	G
	492	A	A	T
	503-507	GATTC	GATTC	CCACA
	509-512	CCGC	CCGC	GATG
	521	G	G	C
	524-526	GGC	GGC	CAT
	530	C	C	G
	559-560	TG	TG	CA
	570-572	CTT	CTT	*
	590	A	A	T
	700	G	G	T
	749	G	G	A
	753	T	T	*
	766	A	A	C
	785-787	CAA	CAA	*
	794	G	G	A
	803	T	T	C
	878	C	C	A
	902	A	A	G
	905	*	*	T
	924	T	T	C
	1005-1010	*	ATATAT	*
	1043	T	C	C
	1079	T	A	T
	1112	C	C	A
	1115	T	C	T
	1139	T	C	T
	1143	G	A	G
	1157	G	T	G
	1175	C	T	C
	1195	C	C	T
	1201	C	T	C
	1488	G	G	T
	1498	C	T	C
WRKY70	57	T	T	G
	107	T	T	C
	483	T	T	G
	509	T	T	C
	534	A	A	G
	764	A	A	T
	1250	C	C	A
	1825	G	G	T

	1860	T	T	C
	2243	C	C	T
	2484	G	G	A
	2789	T	T	*
WRKY76	569	G	G	A
	895-944	CGAGCGCGGACAGCTCGCTGCTGGTGGCGACGTACGAGGGCGAGCAC	deletion	CGAGCGCGGACAGCTCGCTGCTGGTGGCGACGTACGAGGGCGAGCAC
	901	C	C	T
WRKY77	824-826	CAC	deletion	CAC
WRKY79	86	T	T	C
	492	A	A	T
	898	*	*	T
	1363	A	A	C
	1365	C	C	T

Table S5: Variations at amino acid level in HP2216 and Tetep in comparison with Nipponbare

Gene name	Position	Nipponbare	HP2216	Tetep
WRKY7	80	A	A	T
	81-84	AVFN	*	AVFN
WRKY19	85-97	QVMPPGHGGLISG		QVMPPGHGGLISG
	184	A	A	T
WRKY23	155	T	T	K
WRKY26	15	N	S	N
	27	*	D	*
	52-65	GSGSGYGAASYVAP	*	GSGSGYGAASYVAP
	66	T	S	T
	94	*	P	*
	110	A	G	A
	126	*	G	*
	147	T	M	T
	184	N	N	*
	186	Y	Y	F
	187	R	R	G
	188	C	C	T
	190-209	TEGCNVKKRVERDKNDPRYVV	TEGCNVKKRVERDKNDPRYVV	*
	210	T	T	F
	211	M	T	V
	214	G	G	L
	215	I	I	V
	216	H	H	F
	217	N	N	K
	218	H	H	F
	219	V	V	G
	221	P	P	F
WRKY28	13	P	P	S
	50	P	P	T
WRKY58	72	A	A	E
	153	L	L	*
WRKY62	29-31	*	*	CVQ
WRKY64	9	P	S	S
	33	R	R	K
	55	G	G	C
	73	I	I	V
	75	E	E	Q
	79	Q	Q	L
	83	D	D	P
	84	S	S	H
	85	P	P	D

	86	H	H	D
	89	D	D	H
	90	G	G	H
	92	L	L	V
	102	V	V	I
	106	S	S	*
	112	S	S	C
	160	N	N	K
	192	H	H	Q
	220	A	A	V
	222	S	L	S
	318	A	A	S
	321	A	V	A
WRKY70	90	I	I	M
	99	I	I	T
	178	T	T	N
	370	A	A	S
	477	P	P	L
WRKY76	73	L	*	M
	74	T	*	D
	75	E	*	A
	76	V	*	A
	77	I	*	W
	78	A	*	R
	79	R	*	G
	80	L	*	G
	81	Y	*	V
	82	G	*	G
	83	G	*	C
	84	Q	*	S
	85	I	*	P
	86	P	*	V
	87	R	*	C
	88	L	*	L
	89	G	*	D
	90	L	*	L
	91	D	*	C
	92	G	*	V
	93	S	*	G
	94	A	A	L
	97	P	P	V
	99	P	P	E
	100-134	*	*	PSAARHELLDRPAGCRGGGDSKSMTNDEAKILEAK

	136	S	S	T
	137	P	P	Q
	138	L	L	M
	140	G	G	E
	141	K	K	E
	142-147	*	*	NRRLTE
	220-311	TRDNPSPRAYFRCAF APSCPVKKKVQRSAE DSSLLVATYEGEHNH PHPSPRAGELPAAAG GAGGSLPCSISINSSGP TITLDLTKNGGAVQV	*	TRDNPSPRAYFRCAFAP SCPVKKKVQRSAEDSS LLVATYEGEHNHPHPS PRAGELPAAAGGAGGS LPCSISINSSGPTITLDLT KNGGAVQV
WRKY77	93	H	H	*
WRKY79	29	V	V	A
	216	N	N	H

Table S6: Selected known Transcription factor (TF) binding elements in the promoters of DEG WRKYs.

Sl. No.	Pro ID	Nipponbare		HP2216		Tetep	
		Binding sequence	TF family	Binding sequence	TF family	Binding sequence	TF family
	pW07	acGTCGGtgt	AP2	acGTCGGtgt	AP2	acGTCGGtgt	AP2
		acgccCACGTcggtgtc	bHLH	acgccCACGTcggtgtc	bHLH		
		cCCACGtcg	bZIP	cCCACGtcg	bZIP	cCCACGtcg	bZIP
		cTTGACta	WRKY	cTTGACta	WRKY	tGTCAA	WRKY
		ccAACCAact	MYB	ccAACCAact	MYB	ccAACCAact	MYB
		aaaatTTTCT	HSF	aaaatTTTCT	HSF		
		CTCGG	Dehydrin	CTCGG	Dehydrin	CTCGG	Dehydrin
		agCGGCT	ERF	agCGGCT	ERF	agCGGCT	ERF
	pW19	aACGTGc	bHLH	aACGTGc	bHLH		
		aaaACGTGct	bZIP	aaaACGTGct	bZIP	aaaACGTGct	bZIP
		cgGTCAAagt	WRKY	cgGTCAAagt	WRKY	cgGTCAAagt	WRKY
		tggTAGGTtg	MYB	tggTAGGTtg	MYB	tggTAGGTtg	MYB
		caaCCTTAgt	AP2	caaCCTTAgt	AP2	caaCCTTAgt	AP2
		AGAAAgtttt	HSF	AGAAAgtttt	HSF	AGAAAgtttt	HSF
		CCGAG	Dehydrin	CCGAG	Dehydrin		
	pW23	tcCGGCCgcc	AP2	tcCGGCCgcc	AP2	tcCGGCCgcc	AP2
		gtggcgCACGTccggccg	bHLH	gtggcgCACGTccggccg	bHLH		
		taaCGTGGc	bZIP	taaCGTGGc	bZIP		
		ttTTGACttc	WRKY	ttTTGACttc	WRKY	ttTTGACttc	WRKY
		aaACCTAtct	MYB	aaACCTAtct	MYB	gggTGGTTgt	MYB
		TCGAC	Dehydrin	TCGAC	Dehydrin	AGAACttttt	HSF
	pW26	ccaCCGACgt	AP2	ccaCCGACgt	AP2	ccaCCGACgt	AP2
		cGAAGCttca	HSF	cGAAGCttca	HSF	cGAAGCttca	HSF
		gCACGTg	bHLH	gCACGTg	bHLH	gCACGTg	bHLH
		acatgCACGTgta	bZIP	acatgCACGTgta	bZIP	acatgCACGTgta	bZIP
		actTTGACca	WRKY	actTTGACca	WRKY	CCAAC	Dehydrin
		GTAGG	Dehydrin	GTGGG	Dehydrin	TGACC	WRKY
		ggCGGCT	ERF	ggCGGCT	ERF	AGCCGca	ERF
	pW28	GCATGtgg	bHLH	GCATGtgg	bHLH	GCATGtgg	bHLH
		tacCAGCTgg	bZIP	tacCAGCTgg	bZIP	tacCAGCTgg	bZIP
		gaGTCAAcaa	WRKY	gaGTCAAcaa	WRKY	gaGTCAAcaa	WRKY
		gcAACCAgcc	MYB	gcAACCAgcc	MYB	gcAACCAgcc	MYB
		AGAACttttt	HSF	AGAACttttt	HSF	AGAACttttt	HSF
		GTCGT	Dehydrin	GTCGT	Dehydrin	GTCGT	Dehydrin
	pW58	ccgACGTCac	bZIP	ccgACGTCac	bZIP	ccgACGTCac	bZIP
		gcaCCGACac	AP2	gcaCCGACac	AP2	gcaCCGACac	AP2
		ctgcccCACGTgttcctg	bHLH	ctgcccCACGTgttcctg	bHLH	ctgcccCACGTgttcctg	bHLH
		ccgTTGACga	WRKY	ccgTTGACga	WRKY	ccgTTGACga	WRKY
		gcAACCActa	MYB	gcAACCActa	MYB	gcAACCAcca	MYB
		CCGAG	Dehydrin	CCGAG	Dehydrin	CCGAG	Dehydrin

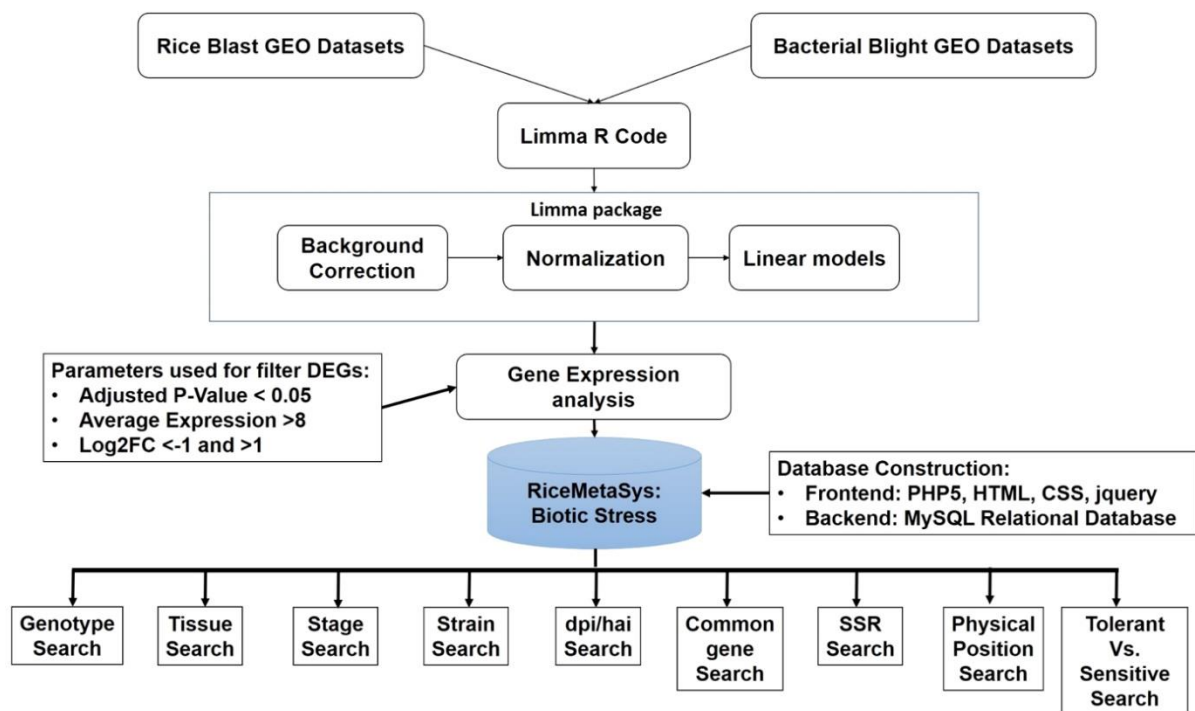| Sl. No.	Pro ID	Nipponbare		HP2216		Tetep	
		Binding sequence	TF family	Binding sequence	TF family	Binding sequence	TF family
	pW62	ctcggtCACGTaagcacg	bHLH	ctcggtCACGTaagcacg	bHLH	ctcggtCACGTaagcacg	bHLH
		ttCACGTttt	bZIP	ttCACGTttt	bZIP	ttCACGTttt	bZIP
		cgGTCAAg	WRKY	cgGTCAAg	WRKY	cgGTCAAg	WRKY
		gaAACCAacg	MYB	gaAACCAacg	MYB	gaAACCAacg	MYB
		ccTACGAggc	AP2	ccTACGAggc	AP2	ccTACGAggc	AP2
		CCAAC	Dehydrin	CCAAC	Dehydrin	CCAAC	Dehydrin
		AGCCGcg	ERF	AGCCGcg	ERF	AGCCGcg	ERF
		ACGGCgcc	NAC	ACGGCgcc	NAC	ACGGCgcc	NAC
	pW64	GAACGtac	bHLH	GAACGtac	bHLH		
		atgCGTCAca	bZIP	atgCGTCAca	bZIP		
		tagTGGTTgc	MYB	tagTGGTTgc	MYB	tagTGGTTgc	MYB
		tgaagGTTCT	HSF	tgaagGTTCT	HSF	tgaagGTTCT	HSF
		ATCGG	Dehydrin	CCTAC	Dehydrin		
	pW70	tccACGTCac	bZIP	tccACGTCac	bZIP	tccACGTCac	bZIP
		cCACGTc	bHLH	cCACGTc	bHLH	cCACGTc	bHLH
		gctTTGACca	WRKY	gctTTGACca	WRKY	gctTTGACca	WRKY
		ccAACCAtct	MYB	ccAACCAtct	MYB	ccAACCAtct	MYB
		agtatATTCT	HSF	agtatATTCT	HSF	aaaCCTTAat	AP2
		CTGAC	Dehydrin	CTGAC	Dehydrin	agtatATTCT	HSF
						CTGAC	Dehydrin
	pW76	gTGACGtaag	bZIP	gTGACGtaag	bZIP		
		attcgtgACGTGcgctcc	bHLH	attcgtgACGTGcgctcc	bHLH	attcgtgACGTGcgctcc	bHLH
		cTTGACcg	WRKY	cTTGACcg	WRKY	cTTGACcg	WRKY
		tcACCTAgcc	MYB	tcACCTAgcc	MYB	tcACCTAgcc	MYB
		AGAATattat	HSF	AGAATattat	HSF	AGAACatgct	HSF
		CACGCgtgccgaac	AP2	CACGCgtgccgaac	AP2	CACGCgtgccgaac	AP2
		CCGAA	Dehydrin	CCGAA	Dehydrin	CCGAA	Dehydrin
	pW77	gtGACGTact	bZIP	gtGACGTact	bZIP		
		GCGCGcgc	bHLH	GCGCGcgc	bHLH	GCGCGcgc	bHLH
		tCCGTTgagt	MYB	tCCGTTgagt	MYB	tCCGTTgagt	MYB
		CCGTC	Dehydrin	CCGTC	Dehydrin		
		TGACT	WRKY	TGACT	WRKY		
	pW79	gtgtgaCACGTcgtcccg	bHLH	gtgtgaCACGTcgtcccg	bHLH		
		ctaCGTGGa	bZIP	ctaCGTGGa	bZIP	ctaCGTGGa	bZIP
		cgGTCAAagg	WRKY	cgGTCAAagg	WRKY		
		gCCGTTcggt	MYB	gCCGTTcggt	MYB	gCCGTTcggt	MYB
		cgaaaTTTCT	HSF	cgaaaTTTCT	HSF	cgaaaTTTCT	HSF
		GTCTG	Dehydrin	GTCTG	Dehydrin		

Fig. S1: Metadata Analysis and Database Design: Schematic Diagram of RiceMetaSys (Biotic Stress) Database. Expression datasets were downloaded from the NCBI Gene expression Omnibus (GEO) Database. The datasets were analyzed by using limma package in R platform. Different kinds of search options were enabled for users to retrieve responsive genes from the Database.
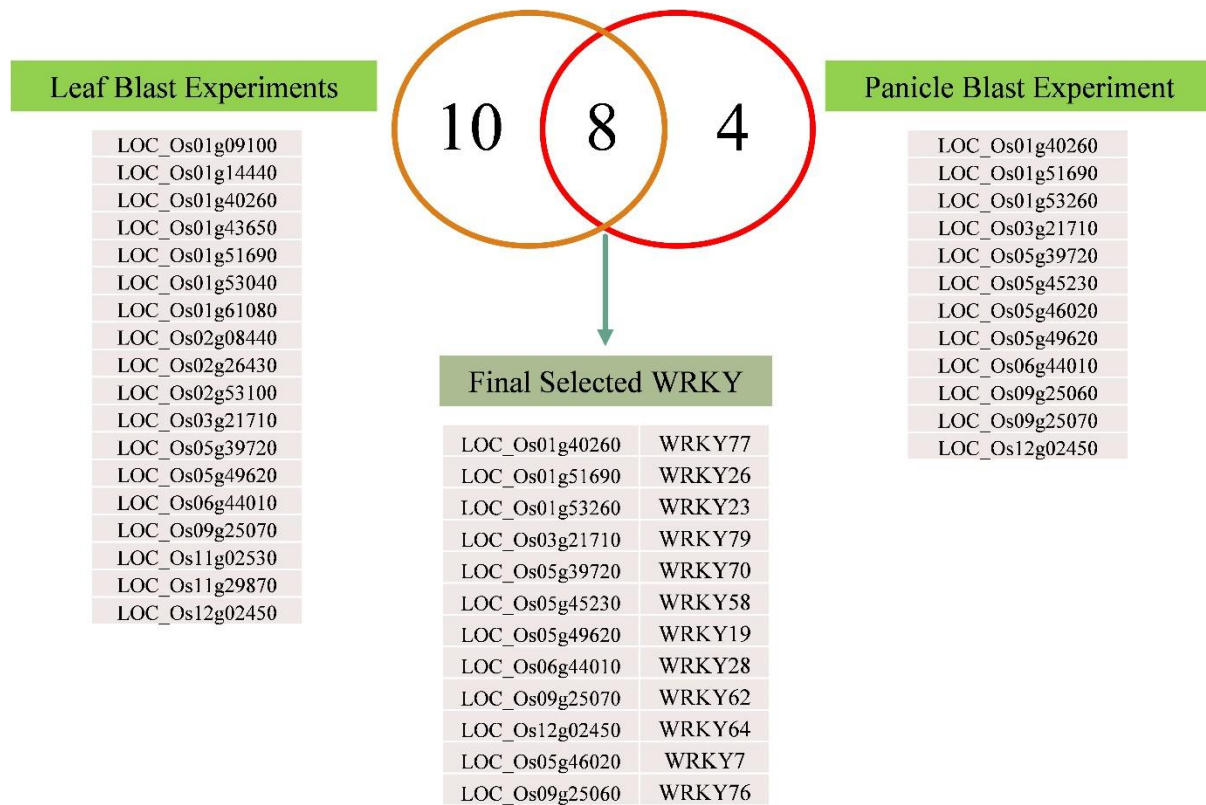
Leaf Blast Experiments

LOC_Os01g09100
LOC_Os01g14440
LOC_Os01g40260
LOC_Os01g43650
LOC_Os01g51690
LOC_Os01g53040
LOC_Os01g61080
LOC_Os02g08440
LOC_Os02g26430
LOC_Os02g53100
LOC_Os03g21710
LOC_Os05g39720
LOC_Os05g49620
LOC_Os06g44010
LOC_Os09g25070
LOC_Os11g02530
LOC_Os11g29870
LOC_Os12g02450

Panicle Blast Experiment

LOC_Os01g40260
LOC_Os01g51690
LOC_Os01g53260
LOC_Os03g21710
LOC_Os05g39720
LOC_Os05g45230
LOC_Os05g46020
LOC_Os05g49620
LOC_Os06g44010
LOC_Os09g25060
LOC_Os09g25070
LOC_Os12g02450

10   8   4

Final Selected WRKY

LOC_Os01g40260	WRKY77
LOC_Os01g51690	WRKY26
LOC_Os01g53260	WRKY23
LOC_Os03g21710	WRKY79
LOC_Os05g39720	WRKY70
LOC_Os05g45230	WRKY58
LOC_Os05g49620	WRKY19
LOC_Os06g44010	WRKY28
LOC_Os09g25070	WRKY62
LOC_Os12g02450	WRKY64
LOC_Os05g46020	WRKY7
LOC_Os09g25060	WRKY76

Fig. S2: Differentially expressed WRKY genes selected from RiceMetaSysB database and from panicle blast transcriptome.

```
                                          10        20        30        40        50        60        70
                                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os12g02450_WRKY64            ---------------------------------------------------------------------- 1
HWRKY64                          ---------------------------------------------------------------------- 1
T_WRKY64                         ---------------------------------------------------------------------- 1
LOC_Os03g21710_WRKY79            ---------------------------------------------------------------------- 1
H_WRKY79                         ---------------------------------------------------------------------- 1
T_WRKY79                         ---------------------------------------------------------------------- 1
LOC_Os05g49620_WRKY19            ---------------------------------------------------------------------- 1
H_WRKY19                         ---------------------------------------------------------------------- 1
T_WRKY19                         ---------------------------------------------------------------------- 1
LOC_Os05g46020_WRKY07            ---------------------------------------------------------------------- 1
T_WRKY07                         ---------------------------------------------------------------------- 1
H_WRKY07                         ---------------------------------------------------------------------- 1
LOC_Os01g51690_WRKY26            ---------------------------------------------------------------------- 1
H_WRKY26                         ---------------------------------------------------------------------- 1
T_WRKY26                         ---------------------------------------------------------------------- 1
H_WEKY77                         ---------------------------------------------------------------------- 1
T_WRKY77                         ---------------------------------------------------------------------- 1
LOC_Os01g40260_WRKY77            ---------------------------------------------------------------------- 1
LOC_Os05g39720_WRKY70            MTAAPGSLPLVNSRPVSLSLAASRSSFSSLLSGGAGSSLNLMTPPSSLPPSSPSSYFGGVSSSGFLDSPI 70
H_WRKY70                         MTAAPGSLPLVNSRPVSLSLAASRSSFSSLLSGGAGSSLNLMTPPSSLPPSSPSSYFGGVSSSGFLDSPI 70
T_WRKY70                         MTAAPGSLPLVNSRPVSLSLAASRSSFSSLLSGGAGSSLNLMTPPSSLPPSSPSSYFGGVSSSGFLDSPI 70
LOC_Os01g53260_WRKY23            ---------------------------------------------------------------------- 1
H_WRKY23                         ---------------------------------------------------------------------- 1
T_WRKY23                         ---------------------------------------------------------------------- 1
T_WRKY58                         ---------------------------------------------------------------------- 1
H_WRKY58                         ---------------------------------------------------------------------- 1
LOC_Os05g45230_WRKY58            ---------------------------------------------------------------------- 1
LOC_Os06g44010_WRKY28            ---------------------------------------------------------------------- 1
H_WRKY28                         ---------------------------------------------------------------------- 1
T_WRKY28                         ---------------------------------------------------------------------- 1
T_WRKY62                         ---------------------------------------------------------------------- 1
H_WRKY62                         ---------------------------------------------------------------------- 1
LOC_Os09g25070_WRKY62            ---------------------------------------------------------------------- 1
LOC_Os09g25060_WRKY76            ---------------------------------------------------------------------- 1
H_WRKY76                         ---------------------------------------------------------------------- 1
T_WRKY76                         ---------------------------------------------------------------------- 1


                                          80        90       100       110       120       130       140
                                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os12g02450_WRKY64            ---------------------------------------------------------------------- 1
HWRKY64                          ---------------------------------------------------------------------- 1
T_WRKY64                         ---------------------------------------------------------------------- 1
LOC_Os03g21710_WRKY79            ---------------------------------------------------------------------- 1
H_WRKY79                         ---------------------------------------------------------------------- 1
T_WRKY79                         ---------------------------------------------------------------------- 1
LOC_Os05g49620_WRKY19            ---------------------------------------------------------------------- 1
H_WRKY19                         ---------------------------------------------------------------------- 1
T_WRKY19                         ---------------------------------------------------------------------- 1
LOC_Os05g46020_WRKY07            ---------------------------------------------------------------------- 1
T_WRKY07                         ---------------------------------------------------------------------- 1
H_WRKY07                         ---------------------------------------------------------------------- 1
LOC_Os01g51690_WRKY26            ---------------------------------------------------------------------- 1
H_WRKY26                         ---------------------------------------------------------------------- 1
T_WRKY26                         ---------------------------------------------------------------------- 1
H_WEKY77                         ---------------------------------------------------------------------- 1
T_WRKY77                         ---------------------------------------------------------------------- 1
LOC_Os01g40260_WRKY77            ---------------------------------------------------------------------- 1
LOC_Os05g39720_WRKY70            LLTPSLFPSPTTTGALFSWITTATATAAIAPESQVQGGVKDEQQQYSDFTFLPTASTAPATTMAGATATT 140
H_WRKY70                         LLTPSLFPSPTTTGALFSWITTATATAAIAPESQVQGGVKDEQQQYSDFTFLPTASTAPATTMAGATATT 140
T_WRKY70                         LLTPSLFPSPTTTGALFSWMTTATATAATAPESQVQGGVKDEQQQYSDFTFLPTASTAPATTMAGATATT 140
LOC_Os01g53260_WRKY23            ---------------------------------------------------------------------- 1
H_WRKY23                         ---------------------------------------------------------------------- 1
T_WRKY23                         ---------------------------------------------------------------------- 1
T_WRKY58                         ---------------------------------------------------------------------- 1
H_WRKY58                         ---------------------------------------------------------------------- 1
LOC_Os05g45230_WRKY58            ---------------------------------------------------------------------- 1
LOC_Os06g44010_WRKY28            ----------------------------------MAKMLPPPSQSVPSRPPSWLYIPPRRRHGTFTSSCAF 37
H_WRKY28                         ----------------------------------MAKMLPPPSQSVPSRPPSWLYIPPRRRHGTFTSSCAF 37
T_WRKY28                         ----------------------------------MAKMLPPPSQSVSSRPPSWLYIPPRRRHGTFTSSCAF 37
T_WRKY62                         ---------------------------------------------------------------------- 1
H_WRKY62                         ---------------------------------------------------------------------- 1
LOC_Os09g25070_WRKY62            ---------------------------------------------------------------------- 1
LOC_Os09g25060_WRKY76            ---------------------------------------------------------------------- 1
H_WRKY76                         ---------------------------------------------------------------------- 1
T_WRKY76                         ---------------------------------------------------------------------- 1
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                    150       160       170       180       190       200       210
              ....|....|....|....|....|....|....|....|....|....|....|....|....|....|

LOC_Os12g02450_WRKY64  ------------------------------------------------MKNSSNKRPLVADQWHPSS 19
HWRKY64                ------------------------------------------------MKNSSNKRSLVADQWHPSS 19
T_WRKY64               ------------------------------------------------MKNSSNKRSLVADQWHPSS 19
LOC_Os03g21710_WRKY79  -------------------------------------------------MAFSSEGGVPAE 12
H_WRKY79               -------------------------------------------------MAFSSEGGVPAE 12
T_WRKY79               -------------------------------------------------MAFSSEGGVPAE 12
LOC_Os05g49620_WRKY19  -------------------------------------------------MVELCGGEGEGQI 13
H_WRKY19               -------------------------------------------------MVELCGGEGEGQI 13
T_WRKY19               -------------------------------------------------MVELCGGEGEGQI 13
LOC_Os05g46020_WRKY07  -------------------------------------------------MAAVGAHAAV- 10
T_WRKY07               -------------------------------------------------MAAVGAHAAV- 10
H_WRKY07               -------------------------------------------------MAAVGAHAAV- 10
LOC_Os01g51690_WRKY26  -------------------------------------------------MYMAAAAGASTP 13
H_WRKY26               -------------------------------------------------MYMAAAAGASTP 13
T_WRKY26               -------------------------------------------------MYMAAAAGASTP 13
H_WEKY77               -------------------------------------------------MSSLYPSLL 9
T_WRKY77               -------------------------------------------------MSSLYPSLL 9
LOC_Os01g40260_WRKY77  -------------------------------------------------MSSLYPSLL 9
LOC_Os05g39720_WRKY70  SNSFMQDSMLMAPLGGDPYNGEQQQPWSYQEPTMDADTRPAEFTSSAAAGDVAGNGSYSQVAAPAAAGGF 210
H_WRKY70               SNSFMQDSMLMAPLGGDPYNGEQQQPWSYQEPTMDADTRPAEFTSSAAAGDVAGNGSYSQVAAPAAAGGF 210
T_WRKY70               SNSFMQDSMLMAPLGGDPYNGEQQQPWSYQEPTMDADNRPAEFTSSAAAGDVAGNGSYSQVAAPAAAGGF 210
LOC_Os01g53260_WRKY23  -------------------------------------MENLQLQGDD--HDDEALPHFPYFAVPSPP 28
H_WRKY23               -------------------------------------MENLQLQGDD--HDDEALPHFPYFAVPSPP 28
T_WRKY23               -------------------------------------MENLQLQGDD--HDDEALPHFPYFAVPSPP 28
T_WRKY58               -------------------------------------MDGLEAAAGDQQHGRLLIPQLPAAYLASSS 30
H_WRKY58               -------------------------------------MDGLEAAAGDQQHGRLLIPQLPAAYLASSS 30
LOC_Os05g45230_WRKY58  -------------------------------------MDGLEAAAGDQQHGRLLIPQLPAAYLASSS 30
LOC_Os06g44010_WRKY28  RLSPSSPSSPPPPVLDFQYIQFMDSWIEQTSLSLDLNVGLPSTARRSSAPAAPIKVLVEENFLSFKKDHE 107
H_WRKY28               RLSPSSPSSPPPPVLDFQYIQFMDSWIEQTSLSLDLNVGLPSTARRSSAPAAPIKVLVEENFLSFKKDHE 107
T_WRKY28               RLSPSSPSSPPPTVLDFQYIQFMDSWIEQTSLSLDLNVGLPSTARRSSAPAAPIKVLVEENFLSFKKDHE 107
T_WRKY62               ------------------------------------------MDDDGDGSSSPTDDSAAAGLLPLFSRSPCVQ 31
H_WRKY62               ------------------------------------------------------------------------ 1
LOC_Os09g25070_WRKY62  ------------------------------------------MDDDGDGSSSPTDDSAAAGLLPLFSRSP--- 28
LOC_Os09g25060_WRKY76  -------------------------------------MDAAWRGGVGCSPVCLDLCVGLSPVREPSAARH 33
H_WRKY76               ------------------------------------------------------------------------ 1
T_WRKY76               -------------------------------------MDAAWRGGVGCSPVCLDLCVGLSPVREPSAARH 33


                    220       230       240       250       260       270       280
              ....|....|....|....|....|....|....|....|....|....|....|....|....|....|

LOC_Os12g02450_WRKY64  VCCDHRAALREIARGQSLVTQLRAIVLPALHSDERGDLAAQ--------------MLEGILDCSRKAISE 75
HWRKY64                VCCDHRAALREIARGQSLVTQLRAIVLPALHSDERGDLAAQ--------------MLEGILDCSRKAISE 75
T_WRKY64               VCCDHRAALREIAKGQSLVTQLRAIVLPALHSDERCDLAAQ--------------MLEGILDCSRKAVSQ 75
LOC_Os03g21710_WRKY79  RVAAAVNDLVEVRDG---LVRLRGFLPPPPQAEQSSSRPPC--------------AAELMDATMSKLMSA 65
H_WRKY79               RVAAAVNDLVEVRDG---LVRLRGFLPPPPQAEQSSSRPPC--------------AAELMDATMSKLMSA 65
T_WRKY79               RVAAAVNDLVEVRDG---LARLRGFLPPPPQAEQSSSRPPC--------------AAELMDATMSKLMSA 65
LOC_Os05g49620_WRKY19  MLATELAQLRAMARE------LEAKMDPDRVAAR--ELCRA--------------LASSVDRSIRLAASC 61
H_WRKY19               MLATELAQLRAMARE------LEAKMDPDRVAAR--ELCRA--------------LASSVDRSIRLAASC 61
T_WRKY19               MLATELAQLRAMARE------LEAKMDPDRVAAR--ELCRA--------------LASSVDRSIRLAASC 61
LOC_Os05g46020_WRKY07  YHHPVSGLSAPAGDAAYS---MS---SYFSHGGSSTSSS----------ASSFSAALAAATTPPLPDPS 63
T_WRKY07               YHHPVSGLSAPAGDAAYS---MS---SYFSHGGSSTSSS----------ASSFSAALAAATTPPLPDPS 63
H_WRKY07               YHHPVSGLSAPAGDAAYS---MS---SYFSHGGSSTSSS----------ASSFSAALAAATTPPLPDPS 63
LOC_Os01g51690_WRKY26  FNFCRHGSHAEYD-AVFSGSWMARRPSAAPHGGGASGSGSGSGYGAASYVAPTFGAAFRQQHLDLLDYLS 82
H_WRKY26               FNFCRHGSHAEYD-AVFSGSWMARRPSAAPHGGGASGSGSGSGYGAASYVAPTFGAAFRQQHLDLLDYLS 82
T_WRKY26               FSFCRHGSHAEYDDAVFSGSWMARRPSAAPHGGGASGS--------------SFGAAFRQQHLDLLDYLS 69
H_WEKY77               SLSESPAEYRQVGGGRYAGEDVVDDDDDMAAVADAVSSY------------LSFDMDDVEYYTPEVGFHS 67
T_WRKY77               SLSESPAEYRQVGGGRYAGEDVVDDDDDMAAVADAVSSY------------LSFDMDDVEYYTPEVGFHS 67
LOC_Os01g40260_WRKY77  SLSESPAEYRQVGGGRYAGEDVVDDDDDMAAVADAVSSY------------LSFDMDDVEYYTPEVGFHS 67
LOC_Os05g39720_WRKY70  RQQSRRSSDDGYNWRKYGQKQMKGSENPRSYYKCTFPGCPTKKKVEQSPDGQVTEIVYKGAHSHPKPPQN 280
H_WRKY70               RQQSRRSSDDGYNWRKYGQKQMKGSENPRSYYKCTFPGCPTKKKVEQSPDGQVTEIVYKGAHSHPKPPQN 280
T_WRKY70               RQQSRRSSDDGYNWRKYGQKQMKGSENPRSYYKCTFPGCPTKKKVEQSPDGQVTEIVYKGAHSHPKPPQN 280
LOC_Os01g53260_WRKY23  PLAVAPAASATTSDGHQHGPLEVLEQPPCSNNLHPDGLVDGPQLAAT---TAVPMMLPAMTSLDWQSLLQ 95
H_WRKY23               PLAVAPAASATTSDGHQHGPLEVLEQPPCSNNLHPDGLVDGPQLAAT---TAVPMMLPAMTSLDWQSLLQ 95
T_WRKY23               PLAVAPAASATTSDGHQHGPLEVLEQPPCSNNLHPDGLVDGPQLAAT---TAVPMMLPAMTSLDWQSLLQ 95
T_WRKY58               MAALSPAGDDWAAS------LILPDGGSAAAGVGEDDLGGG----------------VMAAAAEESSCG 77
H_WRKY58               MAALSPAGDDWAAS------LILPDGGSAAAGVGEDDLGGG----------------VMAAAAEESSCG 77
LOC_Os05g45230_WRKY58  MAALSPAGDDWAAS------LILPDGGSAAAGVGEDDLGGG----------------VMAAAAEESSCG 77
LOC_Os06g44010_WRKY28  VEALEAELRRASEENKKLTEMLRAVVAKYTELQGQVNDMMSAAAAAAVNAGNHQSSTSEGGSVSPSRKRI 177
H_WRKY28               VEALEAELRRASEENKKLTEMLRAVVAKYTELQGQVNDMMSAAAAAAVNAGNHQSSTSEGGSVSPSRKRI 177
T_WRKY28               VEALEAELRRASEENKKLTEMLRAVVAKYTELQGQVNDMMSAAAAAAVNAGNHQSSTSEGGSVSPSRKRI 177
T_WRKY62               AEDLEEKLRRAMEENARLTRALDAILAGHHAHQR--------------------ALLAPSLSPPPPSAT 80
H_WRKY62               ------------------------------------------------------------------------ 1
LOC_Os09g25070_WRKY62  AEDLEEKLRRAMEENARLTRALDAILAGHHAHQR--------------------ALLAPSLSPPPPSAT 77
LOC_Os09g25060_WRKY76  ELLDRPAGCRGGGDSKSMTNDEAKIVEAKVTQMSEENRRLTEVIARLYGG---QIPRLGLDGSASPPRPV 100
H_WRKY76               ----------------------------------------------------------------ASPPRPV 7
T_WRKY76               ELLDRPAGCRGGGDSKSMTNDEAKILEAKVTQMS-----------------------------EENRRL 73
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                                   290       300       310       320       330       340       350
                              ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os12g02450_WRKY64         LQLQLSSDSPHDDDGHLDDKRRVRKIVSSSSDDDDHSSSKAAEDHNAKPLRQHKRRRFGD---------- 135
HWRKY64                       LQLQLSSDSPHDDDGHLDDKRRVRKIVSSSSDDDDHSSSKAAEDHNAKPLRQHKRRRFGD---------- 135
T_WRKY64                      LQLLLSSPHDDDDHHHVDDKRRVRKIISSS-DDDDHCSSKAAEDHNAKPLRQHKRRRFGD---------- 134
LOC_Os03g21710_WRKY79         MATLGGSG---DIAGEVDAAGRWTSVAESADPMVVRREGESSAGRTRRRRGGGSRSGRGR---------- 122
H_WRKY79                      MATLGGSG---DIAGEVDAAGRWTSVAESADPMVVRREGESSAGRTRRRRGGGSRSGRGR---------- 122
T_WRKY79                      MATLGGSG---DIAGEVDAAGRWTSVAESADPMVVRREGESSAGRTRRRRGGGSRSGRGR---------- 122
LOC_Os05g49620_WRKY19         FPPP-------------EHPPPAAGNAGRDAAFKKR------------KGMAKVRRQVR---------- 95
H_WRKY19                      FPPP-------------EHPPPAAGNAGRDAAFKKRQVMVPGHGGLISGKGMAKVRRQVR---------- 108
T_WRKY19                      FPPP-------------EHPPPAAGNAGRDAAFKKRQVMVPGHGGLISGKGMAKVRRQVR---------- 108
LOC_Os05g46020_WRKY07         GSQFDISEFFFDDAPPAAVFNGAPTAA-----LPDGAAANAT---RSAAEAVPAPAPAAV 115
T_WRKY07                      GSQFDISEFFFDDAPPTAVFNGAPTAA-----LPDGAAANAT---RSAAEAVPAPAPAAV 115
H_WRKY07                      GSQFDISEFFFDDAPP----AGAPTAA-----LPDGAAANAT---RSAAEAVPAPAPAAV 111
LOC_Os01g51690_WRKY26         DDQGVPAPPP-AAVPSASYVTPAPAMAPAEPVVPDAVAAAGG-YPRSVAAAAAAVAGEGR---------- 140
H_WRKY26                      DDQGVPAPPP-AAVPSASYVTPAPAMAPAEPVVPDAVAAAGG-YPRSVAAAAAAVAGEGR---------- 140
T_WRKY26                      DDQGVPAPPPPAAVPSASYVTPAPAMGPAEPVVPDAVAAAGGGYPRSVAAAAAAVAGEGR---------- 129
H_WEKY77                      KQH---NPPPVAAAPLEAGGGREQSRR--------EAAVNLGKMDRGPAPVSGGAATGGV---------- 116
T_WRKY77                      KQH---NPPPVAAAPLEAGGGREQSRR--------EAAVNLGKMDRGPAPVSGGAATGGV---------- 116
LOC_Os01g40260_WRKY77         KQH---NPPPVAAAPLEAGGGREQSRR--------EAAVNLGKMDRGPAPVSGGAATGGV---------- 116
LOC_Os05g39720_WRKY70         GRGRGGSGYALHGGAASDAYSSADALSGTPVATPENSSASFGDDEAVNGVSSSLRVASSVGGGEDLDDDE 350
H_WRKY70                      GRGRGGSGYALHGGAASDAYSSADALSGTPVATPENSSASFGDDEAVNGVSSSLRVASSVGGGEDLDDDE 350
T_WRKY70                      GRGRGGSGYALHGGAASDAYSSADALSGTPVATPENSSASFGDDEAVNGVSSSLRVASSVGGGEDLDDDE 350
LOC_Os01g53260_WRKY23         TCLQVPPPVLEQQQPAAAAQADQYSGENDHGDLQAAESSGAGNKEKQVMAKGGAGRPSGT---------- 155
H_WRKY23                      TCLQVPPPVLEQQQPAAAAQADQYSGENDHGDLQAAESSGAGNKEKQVMAKGGAGRPSGT---------- 155
T_WRKY23                      TCLQVPPPVLEQQQPAAAAQADQYSGENDHGDLQAAESSGAGNKEKQVMAKGGAGRPSGK---------- 155
T_WRKY58                      GSSTVTSSGVTEAAAAATTTR----------------RGRGNGKK----AGGGGR------------- 113
H_WRKY58                      GSSTVTSSGVTEAAAAATTTR----------------RGRGNGKK----AGGGGR------------- 113
LOC_Os05g45230_WRKY58         GSSTVTSSGVTEAAAAATTTR----------------RGRGNGKK----AGGGGR------------- 113
LOC_Os06g44010_WRKY28         RSVDSLDDAAHHRKPSPPFVAAAAAAAYASPDQMECTSAAAAAAAKRVVREDCKPKVSKR---------- 237
H_WRKY28                      RSVDSLDDAAHHRKPSPPFVAAAAAAAYASPDQMECTSAAAAAAAKRVVREDCKPKVSKR---------- 237
T_WRKY28                      RSVDSLDDAAHHRKPSPPFVAAAAAAAYASPDQMECTSAAAAAAAKRVVREDCKPKVSKR---------- 237
T_WRKY62                      ARAPSVSTSCAAREDAAPAVAAAAASTACPSRQQPPTAEPRPKVRTVRVRADAADAT------------- 137
H_WRKY62                      -------------------------------------------VRTVRVRADAADAT------------- 14
LOC_Os09g25070_WRKY62         ARAPSVSTSCAAREDAAPAVAAAAASTACPSRQQPPTAEPRPKVRTVRVRADAADAT------------- 134
LOC_Os09g25060_WRKY76         SPLSGKKRSRESMETANSCDANSNRHQGGDADHAESFAADDGTCRRIKVSR-VCRRI------------- 156
H_WRKY76                      SPLSGKKRSRESMETANSCDANSNRHQGGDADHAESFAADDGTCRRIKVSR-VCRRI------------- 63
T_WRKY76                      T----EKRSRESMETANSCDANSNRHQGGDADHAESFAADDGTCRRIKVSR-VCRRI------------- 125


                                   360       370       380       390       400       410       420
                              ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os12g02450_WRKY64         ------------------------------SVSLETPVPHYDGHQWRKYGQKHINNSKHPRSYYRCTYR 174
HWRKY64                       ------------------------------SVSLETPVPHYDGHQWRKYGQKHINNSKHPRSYYRCTYR 174
T_WRKY64                      ------------------------------SVSLETPVPHYDGHQWRKYGQKHIKNSKHPRSYYRCTYR 173
LOC_Os03g21710_WRKY79         ------------------------------SSNKRVAATLEDGHVWRKYGQKDIQNSPYPRSYYRCTHK 161
H_WRKY79                      ------------------------------SSNKRVAATLEDGHVWRKYGQKDIQNSPYPRSYYRCTHK 161
T_WRKY79                      ------------------------------SSNKRVAATLEDGHVWRKYGQKDIQNSPYPRSYYRCTHK 161
LOC_Os05g49620_WRKY19         ------------------------------VTSVQDTASLDDGLSWRKYGQKDILGAKYPRAYFRCTHR 134
H_WRKY19                      ------------------------------VTSVQDTASLDDGLSWRKYGQKDILGAKYPRAYFRCTHR 147
T_WRKY19                      ------------------------------VTSVQDTASLDDGLSWRKYGQKDILGAKYPRAYFRCTHR 147
LOC_Os05g46020_WRKY07         --------------------ERPR-TERIAFRTKSEIEILDDGYKWRKYGKKSVKNSPNPRNYYRCSTE 163
T_WRKY07                      --------------------ERPR-TERIAFRTKSEIEILDDGYKWRKYGKKSVKNSPNPRNYYRCSTE 163
H_WRKY07                      --------------------ERPR-TERIAFRTKSEIEILDDGYKWRKYGKKSVKNSPNPRNYYRCSTE 159
LOC_Os01g51690_WRKY26         --------------------DRTT-TDKIAFRTRSDDEILDDGYKWRKYGKKSVKNSPNPRNYYRCSTE 188
H_WRKY26                      --------------------DRTT-TDKIAFRTRSDDEILDDGYKWRKYGKKSVKNSPNPR-YFGTS-- 185
T_WRKY26                      --------------------DRTM-TDKIAFRTRSDDEILDDGYKWRKYGKKSVKNSPNPRNYYRCSTE 177
H_WEKY77                      --------------------PRSKNGSKIAFKTRSEVDVLDDGYRWRKYGKKMVKNSPNPRNYYRCSSE 165
T_WRKY77                      --------------------PRSKNGSKIAFKTRSEVDVLDDGYRWRKYGKKMVKNSPNPRNYYRCSSE 165
LOC_Os01g40260_WRKY77         --------------------PRSKNGSKIAFKTRSEVDVLDDGYRWRKYGKKMVKNSPNPRNYYRCSSE 165
LOC_Os05g39720_WRKY70         PDSKRWRRDGGDGEGVSLVAGNRTVREPRVVVQTMSDIDILDDGYRWRKYGQKVVKGNPNPRSYYKCTTA 420
H_WRKY70                      PDSKRWRRDGGDGEGVSLVAGNRTVREPRVVVQTMSDIDILDDGYRWRKYGQKVVKGNPNPRSYYKCTTA 420
T_WRKY70                      PDSKRWRRDGGDGEGVSLVSGNRTVREPRVVVQTMSDIDILDDGYRWRKYGQKVVKGNPNPRSYYKCTTA 420
LOC_Os01g53260_WRKY23         --------------------KKKASRPRFAFQTRSDNDILDDGYRWRKYGQKAVKNSKHPRSYYRCTHH 204
H_WRKY23                      --------------------KKKASRPRFAFQTRSDNDILDDGYRWRKYGQKAVKNSKHPRSYYRCTHH 204
T_WRKY23                      --------------------KKKASRPRFAFQTRSDNDILDDGYRWRKYGQKAVKNSKHPRSYYRCTHH 204
T_WRKY58                      ----------------------------TPRFAFHTRSENDILDDGYRWRKYGQKAVKNSDFP--------- 148
H_WRKY58                      ----------------------------TPRFAFHTRSENDILDDGYRWRKYGQKAVKNSDFP--------- 148
LOC_Os05g45230_WRKY58         ----------------------------TPRFAFHTRSENDILDDGYRWRKYGQKAVKNSDFP--------- 148
LOC_Os06g44010_WRKY28         ----------------------------FVHADPSDLSLVVKDGYQWRKYGQKVTKDNPCPRAYFRCSFA 279
H_WRKY28                      ----------------------------FVHADPSDLSLVVKDGYQWRKYGQK---------------- 262
T_WRKY28                      ----------------------------FVHADPSDLSLVVKDGYQWRKYGQKVTKDNPCPRAYFRCSFA 279
T_WRKY62                      ----------------------------DANSMAETVKDGYQWRKYGQKVTRDNPYPRAYFRCAFA 175
H_WRKY62                      ----------------------------DANSMAETVKDGYQWRKYGQKVTRDNPYPRAYFRCAFA 52
LOC_Os09g25070_WRKY62         ----------------------------DANSMAETVKDGYQWRKYGQKVTRDNPYPRAYFRCAFA 172
LOC_Os09g25060_WRKY76         ----------------------------DPSDTSLVVKDGYQWRKYGQKVTRDNPSPRAYFRCAFA 194
H_WRKY76                      ----------------------------DPSDTSLVVKDGYQWRKYGQKV---------------- 85
T_WRKY76                      ----------------------------DPSDTSLVVKDGYQWRKYGQKVTRDNPSPRAYFRCAFA 163
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                              430       440       450       460       470       480       490
                         ....|....|....|....|....|....|....|....|....|....|....|....|....|....|

LOC_Os12g02450_WRKY64    QEEKCKATKTVQQRED--LHHANSYNGDHP------VMYTVVYYGQHTCCKGP-----AASADDHVVVEA 231
HWRKY64                  QEEKCKATKTVQQRED--LHHANSYNGDHP------IMYTVVYYGQHTCCKGP-----AALADDHVVVEA 231
T_WRKY64                 QEEKCKATKTVQQRED--LQHANSYNGDHP------VMYTVVYYGQHTCCKGP-----VASADDHVVVEA 230
LOC_Os03g21710_WRKY79    LDQGCGARRQTQRCEADPSNYDITYYGEHTCRDPSTIIPTAIANAAGAASDGPNNNIISFATGGVVVANS 231
H_WRKY79                 LDQGCGARRQTQRCEADPSNYDITYYGEHTCRDPSTIIPTAIANAAGAASDGPNNNIISFATGGVVVANS 231
T_WRKY79                 LDQGCGARRQTQRCEADPSNYDITYYGEHTCRDPSTIIPTAIANAAGAASDGPNHNIISFATGGVVVANS 231
LOC_Os05g49620_WRKY19    HTQGCNATKQVQRADGDPLLFDVVYLGDHTCG---QAAVAAAAQSAPPEHAGQ-----EQQRQSSLLAAG 196
H_WRKY19                 HTQGCNATKQVQRADGDPLLFDVVYLGDHTCG---QAAVAAAAQSAPPEHAGQ-----EQQRQSSLLAAG 209
T_WRKY19                 HTQGCNATKQVQRADGDPLLFDVVYLGDHTCG---QAAVTAAAQSAPPEHAGQ-----EQQRQSSLLAAG 209
LOC_Os05g46020_WRKY07    ---GCNVKKRVERDKDDPSYVVTTYEGTHNHVSPSTVYYASQDAA---------SGRFFVAGTQPPGSLN 221
T_WRKY07                 ---GCNVKKRVERDKDDPSYVVTTYEGTHNHVSPSTVYYASQDAA---------SGRFFVAGTQPPGSLN 221
H_WRKY07                 ---GCNVKKRVERDKDDPSYVVTTYEGTHNHVSPSTVYYASQDAA---------SGRFFVAGTQPPGSLN 217
LOC_Os01g51690_WRKY26    ---GCNVKKRVERDKNDPRYVVTMYEGIHNHVCPGTVYYAAQDAA---------SGRFFVAGISHP-DLN 245
H_WRKY26                 --------------------FVYELVFKFGCF------------------------------------- 197
T_WRKY26                 ---GCNVKKRVERDKNDPRYVVTTYEGIHNHVCPGTVYYAAQDAA---------SGRFFVAGISHP-DLN 234
H_WEKY77                 ---GCRVKKRVERARDDARFVVTTYDGVHN-PAPLHLR--PQLPP---------PGGYSIAGAPVVAPH 220
T_WRKY77                 ---GCRVKKRVERARDDARFVVTTYDGVHNHPAPLHLR--PQLPP---------PGGYSIAGAPVVAPH 221
LOC_Os01g40260_WRKY77    ---GCRVKKRVERARDDARFVVTTYDGVHNHPAPLHLR--PQLPP---------PGGYSIAGAPVVAPH 221
LOC_Os05g39720_WRKY70    ---GCPVRKHVERASNDLRAVITTYEGKHNHDVPAARGSAAAALYRATPPPQASNAGMMPTTAQPSSYLQ 487
H_WRKY70                 ---GCPVRKHVERASNDLRAVITTYEGKHNHDVPAARGSAAAALYRATPPPQASNAGMMPTTAQPSSYLQ 487
T_WRKY70                 ---GCPVRKHVERASNDLRAVITTYEGKHNHDVPAARGSAAAALYRATPPPQASNAGMMLTTAQPSSYLQ 487
LOC_Os01g53260_WRKY23    ---TCNVKKQVQRLAKDTSIVVTTYEGVHNHPCEKLMEALTPILK----------QLQFLSQF------- 254
H_WRKY23                 ---TCNVKKQVQRLAKDTSIVVTTYEGVHNHPCEKLMEALTPILK----------QLQFLSQF------- 254
T_WRKY23                 ---TCNVKKQVQRLAKDTSIVVTTYEGVHNHPCEKLMEALTPILK----------QLQFLSQF------- 254
T_WRKY58                 -------SDDE-LLFSDVDNTQTATENLRFIPLGRVYITG------------------------------ 180
H_WRKY58                 -------SDDELLLFSDVDNTQTATENLRFIPLGRVYITG------------------------------ 181
LOC_Os05g45230_WRKY58    -------SDDELLLFSDVDNTQTATENLRFIPLGRVYITG------------------------------ 181
LOC_Os06g44010_WRKY28    P--ACPVKKKVQRSADDNTVLVATYEGEHNHAQPP------------------------HHDAGSK 319
H_WRKY28                 ----------------------------------------------------------------- 262
T_WRKY28                 P--ACPVKKKVQRSADDNTVLVATYEGEHNHAQPP------------------------HHDAGSK 319
T_WRKY62                 P--SCPVKKKLQRCAEDRSMLVATYEGEHNHALSTQTTEFVASGCTTSQHAGGSSSSPLPCSISINSSGR 243
H_WRKY62                 P--SCPVKKKLQRCAEDRSMLVATYEGEHNHALSTQTTEFVASGCTTSQHAGGSSSSPLPCSISINSSGR 120
LOC_Os09g25070_WRKY62    P--SCPVKKKLQRCAEDRSMLVATYEGEHNHALSTQTTEFVASGCTTSQHAGGSSSSPLPCSISINSSGR 240
LOC_Os09g25060_WRKY76    P--SCPVKKKVQRSAEDSSLLVATYEGEHNHPHPSPRAGELPA-------AAGGAGGSLPCSISINSSGP 255
H_WRKY76                 --------------------------------------------------------------------- 85
T_WRKY76                 P--SCPVKKKVQRSAEDSSLLVATYEGEHNHPHPSPRAGELPA-------AVGGAGGSLPCSISINSSGP 224


                              500       510       520       530       540       550       560
                         ....|....|....|....|....|....|....|....|....|....|....|....|....|....|

LOC_Os12g02450_WRKY64    SQISTDSHCQSPGSSSSELQA---------------------------AAHAGDSSQCSNISVTCSSSV 273
HWRKY64                  SQISTDSHCQSPGSSSSELQA---------------------------AAHAGDSSQCSNISVTCSSSV 273
T_WRKY64                 SQISTDSHCQSPGSSSSELQA---------------------------AAHAGDSSQCSNISVTCSSSV 272
LOC_Os03g21710_WRKY79    SRLAREGTTATTTSAATQLSSSWGTSGGGGGGDDVFSSSGERFMQWDELAAAVGHVSSVGVTSSTVGSAP 301
H_WRKY79                 SRLAREGTTATTTSAATQLSSSWGTSGGGGGGDDVFSSSGERFMQWDELAAAVGHVSSVGVTSSTVGSAP 301
T_WRKY79                 SRLAREGTTATTTSAATQLSSSWGTSGGGGGGDDVFSSSGERFMQWDELAAAVGHVSSVGVTSSTVGSAP 301
LOC_Os05g49620_WRKY19    TEGIHQQVVAEPMAAPFLFTS------------------------TAAGGVDDGYFSFISPANSDC 238
H_WRKY19                 TEGIHQQVVAEPMAAPFLFTS------------------------TAAGGVDDGYFSFISPANSDC 251
T_WRKY19                 TEGIHQQVVAEPMAAPFLFTS------------------------TAAGGVDDGYFSFISPANSDC 251
LOC_Os05g46020_WRKY07    --------------------------------------------------------------------- 221
T_WRKY07                 --------------------------------------------------------------------- 221
H_WRKY07                 --------------------------------------------------------------------- 217
LOC_Os01g51690_WRKY26    --------------------------------------------------------------------- 245
H_WRKY26                 --------------------------------------------------------------------- 197
T_WRKY26                 --------------------------------------------------------------------- 234
H_WEKY77                 GRLGLEEAEVIALFRGTTATS----------------LLLP--------------- 245
T_WRKY77                 GRLGLEEAEVIALFRGTTATS----------------LLLP--------------- 246
LOC_Os01g40260_WRKY77    GRLGLEEAEVIALFRGTTATS----------------LLLP--------------- 246
LOC_Os05g39720_WRKY70    GGGGVLPAGGYGASYGGAPTT----------------TQPANGGGFAALSGRFDDDAT 529
H_WRKY70                 GGGGVLPAGGYGASYGGAPTT----------------TQPANGGGFAALSGRFDDDAT 529
T_WRKY70                 GGGGVLPAGGYGASYGGAPTT----------------TQPANGGGFAALSGRFDDDAT 529
LOC_Os01g53260_WRKY23    --------------------------------------------------------------------- 254
H_WRKY23                 --------------------------------------------------------------------- 254
T_WRKY23                 --------------------------------------------------------------------- 254
T_WRKY58                 --------------------------------------------------------------------- 180
H_WRKY58                 --------------------------------------------------------------------- 181
LOC_Os05g45230_WRKY58    --------------------------------------------------------------------- 181
LOC_Os06g44010_WRKY28    TAAAAKHSQHQPPPSAAAAVV---------------------RQQQEQAAAAGPSTEVAARKN 361
H_WRKY28                 --------------------------------------------------------------------- 262
T_WRKY28                 TAAAAKHSQHQPPPSAAAAVV---------------------RQQQEQAAAAGPSTEVAARKN 361
T_WRKY62                 TITLDLTNQAGSGSIASCGVE---------------------AAAVSGELVT--VLSPELRRH 283
H_WRKY62                 TITLDLTNQAGSGSIASCGVE---------------------AAAVSGELVT--VLSPELRRH 160
LOC_Os09g25070_WRKY62    TITLDLTNQAGSGSIASCGVE---------------------AAAVSGELVT--VLSPELRRH 280
LOC_Os09g25060_WRKY76    TITLDLTKNGGAVQVVEAAHP---------------------PPPPDLKEVCREVASPEFRTA 297
H_WRKY76                 --------------VEAAHP---------------------PPPPDLKEVCREVASPEFRTA 112
T_WRKY76                 TITLDLTKNGGAVQVVEAAHP---------------------PPPPDLKEVCREVASPEFRTA 266
```

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                                          570        580        590        600        610
                              ....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os12g02450_WRKY64         VVEDCNKLLDMLPAADELTTDVLLFDMTAYAP----LDLDINWEMDTNALWA--- 321
HWRKY64                       VVEDCNKLLDMLPAADELTTDVLLFDMTAYAP----LDLDINWEMDTNALWV--- 321
T_WRKY64                      VVEDCNKLLDMLPAADELTTDVLLFDMTAYAP----LDLDINWEMDTNSLWA--- 320
LOC_Os03g21710_WRKY79         AAENDGGNGDTAAGGGGDGGGAGSFPSSPSAGSLGFVVGPLGSIEDVDDFFPFDP 356
H_WRKY79                      AAENDGGNGDTAAGGGGDGGGAGSFPSSPSAGSLGFVVGPLGSIEDVDDFFPFDP 356
T_WRKY79                      AAENDGGNGDTAAGGGGDGGGAGSFPSSPSAGSLGFVVGPLGSIEDVDDFFPFDP 356
LOC_Os05g49620_WRKY19         QFSSDFSAGSVGVDMDHEARFEDLFSST----------LEFFQSEIQNL----- 277
H_WRKY19                      QFSSDFSAGSVGVDMDHEARFEDLFSST----------LEFFQSEIQNL----- 290
T_WRKY19                      QFSSDFSAGSVGVDMDHEARFEDLFSST----------LEFFQSEIQNL----- 290
LOC_Os05g46020_WRKY07         ------------------------------------------------------ 221
T_WRKY07                      ------------------------------------------------------ 221
H_WRKY07                      ------------------------------------------------------ 217
LOC_Os01g51690_WRKY26         ------------------------------------------------------ 245
H_WRKY26                      ------------------------------------------------------ 197
T_WRKY26                      ------------------------------------------------------ 234
H_WEKY77                      ------------------------------------------------------ 245
T_WRKY77                      ------------------------------------------------------ 246
LOC_Os01g40260_WRKY77         ------------------------------------------------------ 246
LOC_Os05g39720_WRKY70         GASYSYTSQQQQQPNDAVYYASRAKDEPRDDGIMSFFEQPLLF----------- 572
H_WRKY70                      GASYSYTSQQQQQPNDAVYYASRAKDEPRDDGIMSFFEQPLLF----------- 572
T_WRKY70                      GASYSYTSQQQQQPNDAVYYASRAKDEPRDDGIMSFFEQPLLF----------- 572
LOC_Os01g53260_WRKY23         ------------------------------------------------------ 254
H_WRKY23                      ------------------------------------------------------ 254
T_WRKY23                      ------------------------------------------------------ 254
T_WRKY58                      ------------------------------------------------------ 180
H_WRKY58                      ------------------------------------------------------ 181
LOC_Os05g45230_WRKY58         ------------------------------------------------------ 181
LOC_Os06g44010_WRKY28         LAEQMAATLTRDPGFKAALVTALSGRILELSPTKN------------------- 396
H_WRKY28                      ------------------------------------------------------ 262
T_WRKY28                      LAEQMAATLTRDPGFKAALVTALSGRILELSPTKN------------------- 396
T_WRKY62                      LVEEVVQVLKNDAEFVEAVTNAVAARVVDQIPHIPVHL---------------- 321
H_WRKY62                      LVEEVVQVLKNDAEFVEAVTNAVAARVVDQIPHIPVHL---------------- 198
LOC_Os09g25070_WRKY62         LVEEVVQVLKNDAEFVEAVTNAVAARVVDQIPHIPVHL---------------- 318
LOC_Os09g25060_WRKY76         LVEQMASALTSDPKFTGALAAAILQKLPEF------------------------ 327
H_WRKY76                      LVEQMASALTSDPKFTGALAAAILQKLPEF------------------------ 142
T_WRKY76                      LVEQMASALTSDPKFTGALAAAILQKLPEF------------------------ 296
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Fig. S3: Structural variations at amino acid level in the three genotypes.

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                    10        20        30        40        50        60        70
                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os01g51690_pW26    -----TTATA-TTCTGAGATGAATATAGTATAGCTTATTTCGTATACAACATTATTGGCCCATCTTCAAAATA 67
H289702_pW26           ------------------------------------------------------------------------- 1
T3056296_pW26          -----TTATA-AAAACATAACCCAACGAGACAATAAATTTAAAAACTAAAAGTTTTAA---AATTTCTGAGGA 64
LOC_Os01g53260_pW23    CTTCATACTGAATATAAAAATCACGATTAATTTAATGTAGAGACCAGATTAATTTCTACTTTTTCCGTTT 70
H1961965_pW23          CTTCATACTGAATATAAAAATCACGATTAATTTAATGTAGAGACCAGATTAATTTCTACTTTTTCCGTTT 70
T3027906_pW23          CTTCATACTGAATATAAAAATCACGATTAATTTAATGTAGAGACAAGATTAATTTCTACTTTTTCCGTTT 70
LOC_Os06g44010_pW28    ------------------------------------------------------------------------- 1
H1976995_pW28          ------------------------------AAAATGATTTTGAACATGTAAGTTCTGTTCATTAGTGCTAAACTGGTCC 49
T3063501_pW28          -------------------------------AAATGATTTTGAACATGTAAGTTCTGTTCATTAGTGCTAAACTGGTCC 48
LOC_Os05g46020_pW07    -------------------------------------TAACTTTCCTGTCAATAGGTTTGATTAGACTCGGGCAAA 39
H2000561_pW07          -------------------------------------TAACTTTCCTGTCAATAGGTTTGATTAGACTCGGGCAAA 39
T3066720_pW07          -------------------------------------TAACTTTCCTGTCAATAGGTTTGATTAGGCTCGGGCAAA 39
H2023318_pW64          ------------------------------------------------------------------------- 1
T3095730_pW64          ------------------------------------------------------------------------- 1
LOC_Os12g02450_pW64    ----------------------------------AATTAGTGGTCTAAAACTGAACCGCGTAAAAAGCTC 36
LOC_Os01g40260_pW77    ----------------------------------CTATGTCATTAAAATAGTTATAAAAGAA 28
T3097007_pW77          ----------------------------------CTATGTCATTAAAATAGTTATAAAAGAA 28
H1950043_pW77          -----------------------------------TATGTCATTAAAATAGTTATAAAAGAA 27
LOC_Os09g25070_pW62    ----------------------------AACACATAGCACCACACTCATATATCCGCAAATTCCTC-TAAAAGGC 46
H1972014_pW62p         ----------------------------AACACATAGCACCACACTCATATATCCGCAAATTCCTC-TAAAAGGC 46
T3091546_pW62          ----------------------------AACACATAGCACCACACTCATATATCCGCAAATTCCTC-TAAAAGGC 46
LOC_Os05g39720_pW70    -----------------------------TACAACTGTCACTGACATACA-GTCCGAGCAGAC--ACCTGAA 40
H334389_pW70           -----------------------------TACAACTGTCACTGACATACA-GTCCGAGCAGAC--ACCTGAA 40
T3094952_pW70          -----------------------------TACAACTGTCACTGACATACA-GTCCGAGCAGAC--ACCTGAA 40
LOC_Os05g45230_pW58    ----------------------------GAAACGGTCCCGAGGCAGTCCTGCGTCGCCGTTGCGCAT-CACCGAG 46
H1850565_pW58p         ----------------------------GAAACGGTCCCGAGGCAGTCCTGCGTCGCCGTTGCGCAT-CACCGAG 46
T3075919_pW58          ----------------------------GAAACGGTCCCGAGGCAGTCCTGCGTCGCCGTTGCGCAT-CACCGAG 46
LOC_Os03g21710_pW79    -----------------------------TCTCTCTGTCTGGTACTTTATTAATCACCCTCGT-TGATATA 41
H1952278_pW79          -----------------------------TCTCTCTGTCTGGTACTTTATTAATCACCCTCGT-TGATATA 41
T3070072_pW79          -----------------------------TCTCTCTGTCTGGTACTTTATTAATCACCCTCGT-TGATATA 41
LOC_Os05g49620_pW19    -----------------------------CAATCAGGCTGGCAAGAAAGAACACTGT--GCCAAG 34
H2014700_pW19          ------------------------------AATCAGGCTGGCAAGAAAGAACACTGT--GCCAAG 33
T3058779_pW19          -----------------------------CGTTCCAAATGTAACAACCTTAGTGGT---CCTGTT 34
LOC_Os09g25060_pW76    ----------------------------GTCTTAGAATATTATAATTTGTTTTAAAAGTTTCACTCATC 41
T3076120_pW76          ----------------------------------------------TTTTAAAAGTTTCACTCATC 20
H1974322_pW76p         ----------------------------GTCTTAGAATATTATAATTTGTTTTAAAAGTTTCACTCATC 41


                    80        90        100       110       120       130       140
                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os01g51690_pW26    ACAAAAATATGGAAT-TTTCAAAAAAGAAAGGTTCATCTAAAATATAT-CGATGATAAATGACAATTAAG 135
H289702_pW26           ------------------------------------------------------------------------- 1
T3056296_pW26          CAATGAATAAAAGCG-GTGACAAAATGATAGATCGAACAAATAAATAA-AGAAGGGGATAACAAAAAAAA 132
LOC_Os01g53260_pW23    CAGGTTATAAGACTT-TCTAACAAATTGTATCTAGATTCATTAATAATTATATAAATATGGATAATGTTA 139
H1961965_pW23          CAGGTTATAAGACTT-TCTAACAAATTGTATCTAGATTCATTAATAATTATATAAATATGGATAATGTTA 139
T3027906_pW23          CAAGTTATAAGACTT-TCTAACAAATTATATCTAGATTCATTAACAATTATATAAATATGAATAATGTTA 139
LOC_Os06g44010_pW28    --------------------------------------------------TAACATTTCTATAAAAAAAAA--GA 23
H1976995_pW28          TAGAATACAGTGTTT-TCTTAATATAAAAACTTATTACACTGTACTAACATTTCTATAAAAAAAAA--GA 116
T3063501_pW28          TAGAATACAGTGTTT-TCTTAATATAAAAACTTATTACACTGTACTAACATTTCTATAAAAAAAAAA-GA 116
LOC_Os05g46020_pW07    GCAGGAACACACCTGATCCAAGACCCGATACCTCTTGGACAATCGGAGCACGATAGTATTAGCAGGCAAA 109
H2000561_pW07          GCAGGAACACACCTGATCCAAGACCCGATACCTCTTGGACAATCGGAGCACGATAGTATTAGCAGGCAAA 109
T3066720_pW07          GCAGGAACACACCTGATCCAAGACCCGATACCTCTTGGACAATCGGAGCACGATAGTATTAGCAGGCAAA 109
H2023318_pW64          ------------------------------------------------------------------------- 1
T3095730_pW64          ------------------------------------------------------------------------- 1
LOC_Os12g02450_pW64    AGGTGATTAATTAGAACTTGGTGTTGAACGTACTACCTGATGATCTATCAAGCTAGCACTAAGAAACTGA 106
LOC_Os01g40260_pW77    CTGAAAAAAATTGAAAGAT--GAATTAATATGTGTGATATATCATTCCACAAGTATGCAACTTAAATTCA 94
T3097007_pW77          CTGAAAAAAATTGAAAGAT--GAATTAATATGTGTGATATATCATTCCACAAGTATGCAACTTAAATTCA 94
H1950043_pW77          CTGAAAAAAATTGAAAGAT--GAATTAATATGTGTGATATATCATTCCACAAGTATGCAACTTAAATTCA 93
LOC_Os09g25070_pW62    TAAAACACACTAGAAGGACGAAACCAACGACACATTCTTAATCTCATTAAAATTCTATGAAAGCCCCCT 116
H1972014_pW62p         TAAAACACACTAGAAAGGACGAAACCAACGACACATTCTTAATCTCATTAAAATTCTATGAAAGCCCCT 116
T3091546_pW62          TAAAACACACTAGAAAGGACGAAACCAACGACACATTCATAATCTCATTAAAATTCTATGAAAGCCCCT 116
LOC_Os05g39720_pW70    ATG--CAAATTTCAACAGTAGAATCAGTCAGCTGATTTAA-ATATAAACAGGGGTAAGAATTTAAGCA-- 105
H334389_pW70           ATG--CAAATTTCAACAGTAGAATCAGTCAGCTGATTTAA-ATATAAACAGGGGTAAGAATTTAAGCA-- 105
T3094952_pW70          ATG--CAAATTTCAACAGTAGAATCAGTCAGCTGATTTAA-ATATAAACAGGGGTAAGAATTTAAGCA-- 105
LOC_Os05g45230_pW58    GCGGCCCGACGTCACCGTTGCACGCCATTGACGCGTTCCT-GTGTAGCCGTTGTGCGGCACCGACACT-- 113
H1850565_pW58p         GCGGCCCGACGTCACCGTTGCACGCCATTGACGCGTTCCT-GTGTAGCCGTTGTGCGGCACCGACACT-- 113
T3075919_pW58          GCGGCCCGACGTCACCGTTGCACGCCACTGACGCGTTCCT-GTGTAGCCGTTGTGCGGCACCGACACT-- 113
LOC_Os03g21710_pW79    CTTGTTCTTATATCGATTCTAATATTTCTGTCCTACGTGGAGGAAAG-AGACACCTGTGTGACACGTCG 109
H1952278_pW79          CTTGTTCTTATATCGATTCTAATATTTCTGTCCTACGTGGAGGAAAG--AGACACCTGTGTGACACGTCG 109
T3070072_pW79          CTTGTTCTTATATCGATTCTAATATTTCTGTCCTACGTGGAGGAAAG--AGACACCTGTGTGACACGTCG 109
LOC_Os05g49620_pW19    CTAATTCAC-TGTCCAAGCTGATAATACTTATCATTTTGAAAAAAACACAGTCTTTAAAAAATAATTTTG 103
H2014700_pW19          CTAATTCAC-TGTCCAAGCTGATAATACTTATCATTTTGAAAAAAACACAGTCTTTAAAAAATAATTTTG 102
T3058779_pW19          CGAATCTAC-CGCAAGGATGAAGATTAAGTGTGCGCGCAAAACGAGATAAGTCATTAGCATATGATTAAT 103
LOC_Os09g25060_pW76    TTCCTTTATCGATCTAAACAAGAACATGCTTTTTTTTTTTTTTTACTTTGGTAAGTATTTGTGATAATCATGG 111
T3076120_pW76          TTCCTTTATCGATCTAAACAAGAACATGCTTTTTTTTTT--TACTTTGGTAAGTATTTGTGATAATCATGG 88
H1974322_pW76p         TTCCTTTATCGATCTAAACAAGAACATGCTTTTTTTTTTTTTTTACTTTGGTAAGTATTTGTGATAATCATGG 111
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                              150       160       170       180       190       200       210
                       ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os01g51690_pW26    AGGGGAGAAGCAACATGCTTATAATGGAGTAAGCGTAGGCCTATAAACCCCAATGATAATCATATTTGA- 204
H289702_pW26           --------------------------------------------------------------------- 1
T3056296_pW26          TAAGGGTTAGCAACTGGTGCGACTTTTAAAAACTATAAAATTAGAAATATGTGGATGATAAGGTTTGGT- 201
LOC_Os01g53260_pW23    AAAAGTCTTATAACCTGAAACAGAGGTAATAGTAAATATCGACGATGCACGTATAATCTCTAGCTCGTA- 208
H1961965_pW23          AAAAGTCTTATAACCTGAAACAGAGGTAATAGTAAATATCGACGATGCACGTATAATCTCTAGCTCGTA- 208
T3027906_pW23          AAAATCTTATAACCTGAAACGGAGGTAGTAGTAAATATCGACGATGCACGTATAATCTCTAGCTCGTA- 208
LOC_Os06g44010_pW28    GAAGAACTTTTTCTCAGAGACAGCATCAATAAGACAAAAAAAAGTTACATGGGAAAAAGAGAAAACACA- 92
H1976995_pW28          GAAGAACTTTTTCTCAGAGACAGCATCAATAAGACAAAAAAAAGTTACATGGGAAAAAGAGAAAACACA- 185
T3063501_pW28          GAAGAACTTTTTCTCAGAGACAGCATCAATAAGACAAAAAAAAGTTACATGGGAAAAAGAGAAAACACA- 185
LOC_Os05g46020_pW07    AATCAACGCCCACGTCGGTGTCGGGTGCGTATTTAAAAACATCGATA---ATATATGCATGGCTAGATA- 175
H2000561_pW07          AATCAACGCCCACGTCGGTGTCGGGTGCGTATTTAAAAACATCGATA---ATATATGCATGGCTAGATA- 175
T3066720_pW07          AATCAACGCCCACGTCGGTGTCGGGTGCGTATTTAAAAACATCGATA---ATATATGCATGGCTAGATA- 175
H2023318_pW64          ------------------------------------TACTCCCATCCTACATAGACAACTATGTAGTACAATGTGTGG 42
T3095730_pW64          --------------------------------------------------------------------- 1
LOC_Os12g02450_pW64    GGCCCTGTTTAGATGGGACTAAAACTTTTAAGTCCCTATCACATCGGATGTTTGAAAATTAATTATAAAT 176
LOC_Os01g40260_pW77    -ACTTAAAATTTGTTTTTTCCTGTGACATATAGAAGTTGAATTTTCAGTTGCATAATTATGCAGTGATAT 163
T3097007_pW77          -ACTTAAAATTTGTTTTTTCCTGTGACATATAGAAGTTGAATTTTCAGTTGCATAATTATGCAGTGATAT 163
H1950043_pW77          -ACTTAAAATTTGTTTTTTCCTGTGACATATAGAAGTTGAATTTTCAGTTGCATAATTATGCAGTGATAT 162
LOC_Os09g25070_pW62    TGCTTGTGACCAATATTCAGGTACAGAATCAATGATGTACATCCACA-TCACCTTAACCTTCTTAGATTT 185
H1972014_pW62p         TGCTTGTGACCAATATTCAGGTACAGAATCAATGATGTACATCCACA-TCACCTTAACCTTCTTAGATTT 185
T3091546_pW62          TGCTTGTGACCAATATTCAGGTACAGAATCAATGATGTACATCCACA-TCACCTTAACCTTCTTAGATTT 185
LOC_Os05g39720_pW70    -GCTAAAAAGCGATACAAACCCTAATTAACTATACTCTACTAATTAAGCTACCCAACCAT-CTGACATGG 173
H334389_pW70           -GCTAAAAAGCGATACAAACCCTAATTAACTATACTCTACTAATTAAGCTACCCAACCAT-CTGACATGG 173
T3094952_pW70          -GCTAAAAAGCGATACAAACCTTAATTAACTATACTCTACTAATTAAGCTACCCAACCAT-CTGACATGG 173
LOC_Os05g45230_pW58    -GCCCCAC-GTGTTCCTGCCCTCCATCA-CGTTGCCGCAC-ACCCGGGTCATGGCGCCGCACTTCCATGC 179
H1850565_pW58p         -GCCCCAC-GTGTTCCTGCCCTCCATCA-CGTTGCCGCAC-ACCCGGGTCATGGCGCCGCACTTCCATGC 179
T3075919_pW58          -GCCCCAC-GTGTTCCTGCCCTCCATCA-CGTTGCCGCAC-ACCCGGGTCATGGCGCCGCACTTCCACGC 179
LOC_Os03g21710_pW79    TCCCGTGTAGCCA--AAACCACTGGCCGTTCGGTCTCGGTGTTTCCAGTTTCCATCAACCGTAAGCGTGT 177
H1952278_pW79          TCCCGTGTAGCCA--AAACCACTGGCCGTTCGGTCTCGGTGTTTCCAGTTTCCATCAACCGTAAGCGTGT 177
T3070072_pW79          TCCCGTGTAGCCA--AAACCACTGGCCGTTCGGTCTCGGTGTTTCCAGTTTCCATCAACCGTAAGCGTGT 177
LOC_Os05g49620_pW19    ACCATTTTT-TTATTATAATAT-AAAAATATCAATAAATATCCTATTCCAGTGAAGCATTTTTAACACTT 171
H2014700_pW19          ACCATTTT-TTATTATAATA-ANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTTTTAACACTT 170
T3058779_pW19          TAAATTTTAATTATTAAAATCTTAAAAATGGATTTATTAGAATTTTTATAGTAACTTTTATATAGAAAGT 173
LOC_Os09g25060_pW76    CGATGATGTGAACACGCGTGCCGAACGTAAAACTATCATTTTTTTTACTTAGTAAAGACAACAAAACCAT 181
T3076120_pW76          CGATGATGTGAACACGCGTGCCGAACGTAAAACTATCATTTTTTTTACTTAGTAAAGACAACAAAACCAT 158
H1974322_pW76p         CGATGATGTGAACACGCGTGCCGAACGTAAAACTATCATTTTTTTTACTTAGTAAAGACAACAAAACCAT 181


                              220       230       240       250       260       270       280
                       ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os01g51690_pW26    TTTTAAAA-TCTTAAGGA---ATTCAAGCAATTTAAAATTCGAATTTCGACCGCTGAAATGGTG-AGAAT 269
H289702_pW26           --------------------------------------------------------------------- 1
T3056296_pW26          TTTTCAAA-GTATTAAGA---TAATAAGATAGCTATTTAACAAATTTTAAATAAAATCATATTA-AAAAA 266
LOC_Os01g53260_pW23    AATAAATTTGCATGAACA---GTTGGATATATTAATTAACCTGCTGCTGAGTGCTGGCATTTTGCACGAA 275
H1961965_pW23          AATAAATTTGCATGAACA---GTTGGATATATTAATTAACCTGCTGCTGAGTGCTGGCATTTTGCACGAA 275
T3027906_pW23          AATAAATTTGCATGAACA---GTTGGATATATTAATTAACCTGCTGCTGAGTGCTGGCATTTTGCACGAA 275
LOC_Os06g44010_pW28    ACTAAAAAGAGAAAAACACATATTACCACAATTAACTATTCTCTCTGTTCCTGAAGACATACTTCATTTT 162
H1976995_pW28          ACTAAAAAGAGAAAAACACATATTACCACAATTAACTATTCTCTCTGTTCCTGAAGACATACTTCATTTT 255
T3063501_pW28          ACTAAAAAGAGAAAAACACATATTACCACAATTAACTATTCTCTCTGTTCCTGAAGACATACTTCATTTT 255
LOC_Os05g46020_pW07    ACTAAACAGAGATTATGA---ATCAGCACATATGATTTGGGAGCATCATGTCAGACATGTCGAACACATG 242
H2000561_pW07          ACTAAACAGAGATTATGA---ATCAGCACATATGATTTGGGAGCATCATGTCAGACATGTCGAACACATG 242
T3066720_pW07          ACTAAACAGAGATTATGA---ATCAGCACATATGATTTGGGAGCATCATGTCAGACATGTCGAACACATG 242
H2023318_pW64          AGTGGAGTTGAATATACAACTGTAGAATTCACTAGTAGCTAGTATAGTTCTAGTAGAGAATTAATAGTAG 112
T3095730_pW64          --------------------------------------------------------------------- 1
LOC_Os12g02450_pW64    ATTAAACGTAGACTATTAATAAAACCCATCCATAATCTTGGACTAATTTACGAGACGAATCTAATGAGCC 246
LOC_Os01g40260_pW77    ATCA-TAT------ACTATATCTTAATACATTTTTCTCTCTTTTTTT-TAATTTTTTCATAACTATTTGT 225
T3097007_pW77          ATCA-TAT------ACTATATCTTAATACATTTTTCTCTCTTTTTTT-TAATTTTTTCATAACTATTTGT 225
H1950043_pW77          ATCA-TAT------ACTATATCTTAATACATTTTTCTCTCTTTTTTT-TAATTTTTTCATAACTATTTGT 224
LOC_Os09g25070_pW62    ACCGCTCT------AACATCCCACATACCGGATTAAAGTCATCATTT-AAAAGTGTATTGCGGGGATTGA 248
H1972014_pW62p         ACCGCTCT------AACATCCCACATACCGGATTAAAGTCATCATTT-AAAAGTGTATTGCGGGGATTGA 248
T3091546_pW62          ACCGCTCT------AACATCCCACATACCGGATTAAAGTCATCATTT-AAAAGTGTATTGCGGGGATTGA 248
LOC_Os05g39720_pW70    TTTACTACTTCAGAAGGCAGCTCCCCAATTCATTAAAAAAACCACTAGTAATTTAATTATAGCAAATTTT 243
H334389_pW70           TTTACTACTTCAGAAGGCAGCTCCCCAATTCATTAAAAAAACCACTAGTAATTTAATTATAGCAAATTTT 243
T3094952_pW70          TTTACTACTTCAGAAGGCAGCTCCCCAATTCATTAAAAAAACCACTAGTAATTTAATTATAGCAAATTTT 243
LOC_Os05g45230_pW58    CGCAGGAC--CAAAGCGGTGCCGCACGGCCGTCCTGCGCAACCACTAGTCCCACGGTATGGAAGAGCGGC 247
H1850565_pW58p         CGCAGGAC--CAAAGCGGTGCCGCACGGCCGTCCTGCGCAACCACTAGTCCCACGGTATGGAAGAGCGGC 247
T3075919_pW58          CGCGGGAC--CAAAGCGGTGCCGCACGGTCGTCCTGCGCAACCACCAGTCCCGCGGT----------C 235
LOC_Os03g21710_pW79    CATTCAACGCGCCAATGTATACTAATGAATCTTTATTTTGTGTCTGCATCATGCATTCATGCTTGTGTAC 247
H1952278_pW79          CATTCAACGCGCCAATGTATACTAATGAATCTTTATTTTGTGTCTGCATCATGCATTCATGCTTGTGTAC 247
T3070072_pW79          CATTCAACGCGCCAATGTATACTAATGAATCTTTATTTTGTGTCTGCATCATGCATTCATGCTTGTGTAC 247
LOC_Os05g49620_pW19    GTTCAAA-ACAACAAC-TAGTATTATCAACCCGCATGAAGTAGC-AAGAATCCTATG-ATCAATAC---T 234
H2014700_pW19          GTTCAAA-ACAACAAC-TAGTATTATCAACCCGCATGAAGTAGC-AAGAATCCTATG-ATCAATAC---T 233
T3058779_pW19          TTTCAAACACACCATT-TAGTTTGAAAAACGTGCTAACGGAAACCAAGAAAAAAATGTATCTTAAT---T 239
LOC_Os09g25060_pW76    CCGTGGGTATTAAGAGCAAGTACAATTGTAAAGATATAGCTTAGCTACAAGCACATATGAAAAAGGAAGA 251
T3076120_pW76          CCGTGGGTATTAAGAGCAAGTACAATTGCAAAGATATAGCTTAGCTACAAGCACATATGAAAAAGGGAGA 228
H1974322_pW76p         CCGTGGGTATTAAGAGCAAGTACAATTGTAAAGATATAGCTTAGCTACAAGCACATATGAAAAAGGAAGA 251
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                            290        300        310        320        330        340        350
                     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os01g51690_pW26  CTTACCCTTTAACCTTAAT--ACTCCCTC-CCTTTCAAATTATAAGAC-GTTTTAACTTTGGTT--CAAG 333
H289702_pW26         ---------------------------------------------------------------------- 1
T3056296_pW26        TAGATAATTTCGTATGGGT--ACTAGCCG-CAATATTGCGCTGGCTAC-CAGCTAGTTTTTTTAGATAAT 332
LOC_Os01g53260_pW23  CGTGTGCATGCACCTGACCCCACCAAACG-CAAAGCTACCATTGCATC-GACC--GCCTCCATCGGCCAT 341
H1961965_pW23        CGTGTGCATGCACCTGACCCCACCAAACG-CAAAGCTACCATTGCATC-GACC--GCCTCCATCGGCCAT 341
T3027906_pW23        CGTGTGCATGCACCTGACCCCACCAAACG-CAAAGCTACCATTGCATC-GACC--GCCTCCATCGGCCAT 341
LOC_Os06g44010_pW28  TTTCATATTTTAAGTCGTTTTAGTTTTTT-CTAATTAAACTTTTTTAA-GTTTGATGAATTTTGAAGAAA 230
H1976995_pW28        TTTCATATTTTAAGTCGTTTTAGTTTTTT-CTAATTAAACTTTTTTAA-GTTTGATGAATTTTGAAGAAA 323
T3063501_pW28        TTTCATATTTTAAGTCGTTTTAGTTTTTT-CTAATTAAACTTTTTTAA-GTTTGATGAATTTTGAAGAAA 323
LOC_Os05g46020_pW07  CCCGTGCCTATCGAACACAGTATCCGTGGGTAAAATCGCTATCGCTGCTCAGTCCAAAGTAGACGGAGCT 312
H2000561_pW07        CCCGTGCCTATCGAACACAGTATCCGTGGGTAAAATCGCTATCGCTGCTCAGTCCAAAGTAGACGGAGCT 312
T3066720_pW07        CCCGTGCCTATCGAACACAGTATCCGTGGGTAAAATCGCTATCGCTGCTCAGTCCAAAGTAGACGGAGCT 312
H2023318_pW64        TAAT-AGTTTAGGTGCAATCTATATA---TATACCACACGGTTG--GAGTATAATCTGCGTAGCGATTC 175
T3095730_pW64        --------------TATATA----TATACCACACGGTTG--GAGTATAATCTGCGTAGTGATTC 44
LOC_Os12g02450_pW64  TAATTAATCCATGATTAGCCTATGTGATGCTACAGTAAACATTCTCTAATTATAGATTAATTAGGCTTAA 316
LOC_Os01g40260_pW77  GTGACGTACTCCCTCCGTC--C----AAAAAAAGACAAACCCTGAGTTTT-CGTGTCCAACGTTTGATTG 288
T3097007_pW77        GTGACGTACTCCCTCCGTC--C----AAAAAAAGACAAACCCTGAGTTTT-CGTGTCCAACGTTTGATTG 288
H1950043_pW77        GTGACGTACTCCCTCCGTC--C----AAAAAAAGACAAACCCTGAGTTTT-CGTGTCCAACGTTTGATTG 287
LOC_Os09g25070_pW62  ACTAAATCCTGATTTGGTA--T----TGACACAAACATATACGAAAAAGAACATATTGGACATCACGTTG 312
H1972014_pW62p       ACTAAATCCTGATTTGGTA--T----TGACACAAACATATACGAAAAAGAACATATTGGACATCACGTTG 312
T3091546_pW62        ACTAAATCCTGATTTGGTA--T----TGACACAAACATATACGAAAAAGAACATATTGGACATCACGTTG 312
LOC_Os05g39720_pW70  GCTACGCTACTTCGTGGTT--C----TATATGTAAGACACCACGAAGTAAATTTTAAGAAAAAAAATA 307
H334389_pW70         GCTACGCTACTTCGTGGTT--C----TATATGTAAGACACCACGAAGTAAATTTTAAGAAAAAAAATA 307
T3094952_pW70        GCTACGCTACTTCGTGGTT--C----TATATGTAAGACACCGCATGAAGTAAATTTTAAGAAAAAAAATA 307
LOC_Os05g45230_pW58  ACCACCTTAATTCTGCGTC--CCTGTTATACAGTAGAGGTATATTTATGCAAATATTTTTCATGCAGGTA 315
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T3075919_pW58        ACCATCTTAATTCTGCGTC--CCTATTATACAGTAGAGGTATATTTGTGCAAATATTTTTCATGTAGGTA 303
LOC_Os03g21710_pW79  AGGAGGAGACCGATCCATTACGTACGTATAAAGAGAAGATGAAGCTACAAT---ATATGCAGCTCGATCG 314
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LOC_Os05g49620_pW19  AAAT-AATATTCCTTCGTT-CTAAAATATA-ACAACCTTAGTGGTCCTATTCGAATCTACCGTAAGAATG 301
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T3058779_pW19        AGTTTAGAACGGGGCCATTATTAGATTAGATATAATACTAAGGGTG-TGTTCGGACCTCT----AGGTTC 304
LOC_Os09g25060_pW76  AAAAAAACAGACCATAAATT--TGTAGTGTGAGAGATGAGCCAAGTATTAATGATTCAATGTAT------- 312
T3076120_pW76        AAAAAAACAGACCATAAATT--TGTAGTGTGAGAGATGAGCCAAGTATTAATGATTCAATGTATGTTTATA 296
H1974322_pW76p       AAAAAAACAGACCATAAATT--TGTAGTGTGAGAGATGAGCCAAGTATTAATGATTCAATGTAT------- 312


                            360        370        380        390        400        410        420
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LOC_Os01g51690_pW26  TCAAACTGT---TTCAAATTTGTAGAAAATAATAATAATATTTTTAGCTCAACACAAATTTATTATGAAA 400
H289702_pW26         --------------------------------------------------------------------- 1
T3056296_pW26        GAGAAGTAT--TTTTCAATCGGTAGATACATGCCGCTCCCTCTGTTTCAACATATAAACATTTCTAGGAT 399
LOC_Os01g53260_pW23  TCAACCTGC--AAGCGCTCGACCGGTCATCATTCATCAGCTAAAAACTGCAAAAGACGACCCAAGAGAAA 408
H1961965_pW23        TCAACCTGC--AAGCGCTCGACCGGTCATCATTCATCAGCTAAAAACTGCAAAAGACGACCCAAGAGAAA 408
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LOC_Os06g44010_pW28  AATATAGCA---ATGTTTTCAATATAAAACAAATATGCTATCAAAA--TATATTTAATATTTAATGAAAC 295
H1976995_pW28        AATATAGCA---ATGTTTTCAATATAAAACAAATATGCTATCAAAA--TATATTTAATATTTAATGAAAC 388
T3063501_pW28        AATATAGCA---ATGTTTTCAATATAAAACAAATATACTATCAAAA--TATATTTAATATTTAATGAAAC 388
LOC_Os05g46020_pW07  AAAATAAAA---TAAAGAGAGATGCCACTCATTTAATTTGTTTTATTTTAGATCGAATTTAAACTGATAT 379
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T3095730_pW64        ATGACAAAT-TAGTGGTCTAAAACTGAACCGCGTAAAAAGCTCAGGTGATTAATTAGAACTTGGTGTTG- 112
LOC_Os12g02450_pW64  AAAATTTGTCTCGTGAATTAGCTTTCATTTATGTAATTAGTTTTG-TAAGTAGTCTATATTTAATACTCT 385
LOC_Os01g40260_pW77  TTCGTTTTAT--------ATGAAATTTTTTATAATTAGTATTTTCATTGTTGTTAGATAATAAAACATGA 350
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T3091546_pW62        TAAGCTCGATGTCAATGAATTAAGTTTTCTGTAAACGTCAGTCT-GTCATCTTTAAAGCACACAGCACAG 381
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T3094952_pW70        CCCTATAAATAT-GATTATTTACTAGATGTACAATATCGTTTGTGTTACCATAAAAATACCAGGAGCAA 376
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T3075919_pW58        ---TATAAACGC-AAAATATTAATGAAAATATATATTTTCTTTTTTTTTCTTGTTAAGTACTCGACAGGG 369
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T3070072_pW79        ATCGCTAGCTGCTATCGGCGCAGCGACAGGGCTCGAGTTCGATGTCATCAGTGA----TCCAATGTTAGAT 380
LOC_Os05g49620_pW19  AAGATTAAGTGTGCGCGCAAAACGAG-ATAAGTCATTAGCATATGATTAATTAAATTTTAATTATTAAAA 370
H2014700_pW19        AAGATTAAGTGTGCGCGCAAAACGAG-ATAAGTCATTAGCATATGATTAATTAAATTTTAATTATTAAAA 369
T3058779_pW19        CCAATCCAAATCCCTCGTTTTTCGCGCGCACGTTTTTCAAAC-TGCTAAACGGTGCGTTTTTTATAAAAA 373
LOC_Os09g25060_pW76  -------------AGTAGACTATTAAAGTGACTGTAGATGATGTATTAATTTTGAAAGGTAGCAGTGGGT 369
T3076120_pW76        TAAACTATTGTATAGTAGACTATTAAAGTGACTGTAGATGATGTATTAATTTTGAAAGGTAGCAGTGGGT 366
H1974322_pW76p       -------------AGTAGACTATTAAAGTGACTGTAGATGATGTATTAATTTTGAAAGGTAGCAGTGGGT 369
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                            430       440       450       460       470       480       490
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LOC_Os01g51690_pW26  ATATATTCAATTATTAATTTAA-----TGAAACTAT-TT-ATAAA-TATTACTATA-----TTTATGCA  456
H289702_pW26         ------------------------------------ATAAA-TATTACTATA-----TTTATGCA      23
T3056296_pW26        TAAATTTTATACATAATACAAG---TATTTCTATGTC--ACCAA-TTCCAATATACGAAATCTATACA   461
LOC_Os01g53260_pW23  GAAACGATCTAGAACGAACC-G---TGCCGTCCTGCC--GTGAA-TCAGAACTTTTCCTAGTTA-ACT   468
H1961965_pW23        GAAACGATCTAGAACGAACC-G---TGCCGTCCTGCC--GTGAA-TCAGAACTTTTCCTAGTTA-ACT   468
T3027906_pW23        GAAACGATCTAGAACGAACC-G---TGCCGTCCTGCC--GTGAA-TCAGAACTTTTCCTAGTTA-ACT   468
LOC_Os06g44010_pW28  TAATTTTATTTTGTAGATGTTG---CTAATTTTCTCT--GTAAA-CTTAATTAAAT----CTTAAAAA  353
H1976995_pW28        TAATTTTATTTTGTAGATGTTG---CTAATTTTCTCT--GTAAA-CTTAATTAAAT----CTTAAAAA  446
T3063501_pW28        TAATTTTATTTTGTAGATGTTG---CTAATTTTTCT--GTAAA-CTTAATTAAAT----CTTAAAAA   446
LOC_Os05g46020_pW07  AAGCGTCTGAGTTTAAATTAAG---TGAGTGCATATTTAATGAA-AATAAATAAACTATATCTAAAAA  443
H2000561_pW07        AAGCGTCTGAGTTTAAATTAAG---TGAGTGCATATTTAATGAA-AATAAATAAACTATATCTAAAAA  443
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H2023318_pW64        AACGTACTACCTGATGATCTA---TCAAGCTAGCACTAAGGA---AGAAACTGAGTCCATGCATATA   304
T3095730_pW64        AACGTACTACCTGATGATCTA---TCAAGCTAGCACTAAGGA---AGAAACTGAGTCCATGCATATA   173
LOC_Os12g02450_pW64  AAATTAGTGTCTAAAGACAGGGA--CTAAAGTTAAGTCCCTGGATCTAAACACCACCTGAGTCCATATA 452
LOC_Os01g40260_pW77  TTAA-TACTTTAT---------GCGTGACTTGTCTT----TTTAATTTTTTTTCATAGTT--          396
T3097007_pW77        TTAA--TACTTTAT---------GCGTGACTTGTCTT----TTTAATTTTTTTTCATAGTT--         396
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T3091546_pW62        TAAAGATATTCCTCTCTTTTAAAAAAAAAGGCAAATCCTGACTAAATATATAAACATAATACATGCCTAA 451
LOC_Os05g39720_pW70  TTTGGTCACACCATGT---TATAAAGCAGGTCCTATCTTGTATCCTAGAAACACTAAATTAAT--       436
H334389_pW70         TTTGGTCACACCATGT---TATAAAGCAGGTCCTATCTTGTATCCTAGAAACACTAAATTAAT--       436
T3094952_pW70        TTTGGTCACACCATGT---TATAAAGCAGGTCCTATCTTGTATCCTAGAAACACTAAATTAAT--       436
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H1850565_pW58p       TCAAACGGACGCAATT---GACCACGCATGACACATATAAAACCAACACTACGTGAACAAAAA--       441
T3075919_pW58        TCAAACGGACGCAATT---GACCACGCATGACACATATAAAACCAACACTACGTGAACAAAAA--       429
LOC_Os03g21710_pW79  GCAACGAAAGCAAC---ATGTGTACACTAAAAGAGACGAAATTTCTATCCAAAGTAG--ATGCGGACAAC 445
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LOC_Os09g25060_pW76  TACTTGACTATATTATCAAACTTGCTCTAACACTGCGGTCTTCAATTTATAAGTAATTAAGTACGGCCCT 439
T3076120_pW76        TACTTGGCTATATTATCAAACTTGCTCTAACACTGCGGTCTTCAATTTATAAGTAATTAAGTACGGCCCT 436
H1974322_pW76p       TACTTGACTATATTATCAAACTTGCTCTAACACTGCGGTCTTCAATTTATAAGTAATTAAGTACGGCCCT 439


                            500       510       520       530       540       550       560
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LOC_Os01g51690_pW26  TAAAC--CTAGTTAAAT---T---TGAAGTAGTTTGACTTTGACCAAAGTCAAAACATCTTATAACCTGA 518
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T3056296_pW26        TTTTCAGCCAATTAGATGGTT---TAAAGGAACTCAAGCAATTTAAAATTCGAA---TTTCGACCGCTGA 525
LOC_Os01g53260_pW23  TTACGTACCAGTAGAGTACGTACGTATACGTACTGTAACTTTTACAGACAGGAA-CACCTTTTGACTTCG 537
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H1976995_pW28        TAATG--GCAAATAAATGACTTGTAATATAGAACGGGAGAGTATCTTTTTTTAA---GCTAAGGATCGAG 511
T3063501_pW28        TAATG--GCAAATAAATGACTTGTAATATAGAACGGGAGAGTATCTTTTTT-AA---GCTAAGGATCGAG 510
LOC_Os05g46020_pW07  ATTTT--CTTAACCGGTTCTTGACTATCCTATCTCCTAGCTTCACCCCCTCCCAAAATTTCTTGGTTTAG 511
H2000561_pW07        ATTTT--CTTAACCGGTTCTTGACTATCCTATCTCCTAGCTTCACCCCCTCCCAAAATTTCTTGGTTTAG 511
T3066720_pW07        AATTT--TTTAACCGGTTCTTGGCTACCCTATCTCCTAGCTTCACCCCCTCCCAAAATTTCTTGGTTTAG 511
H2023318_pW64        TATGAGCTCCATTCAGCATGC----GTGTGGTATAGGAGTTTAATTTAGT-------TTTTATGCGTCAC 363
T3095730_pW64        TATGAGCTCCATTCAGCATGC----GTGTGGTATAGGAGTTTAATTTAGT-------TTTTATGCGTCAC 232
LOC_Os12g02450_pW64  TATGAGCTCCATTCAGCATGC----GTGTGGTA--GGAGTTTAATTTAGT-------TTTTATGCGTCAC 509
LOC_Os01g40260_pW77  -TTTATAA-AAGAGTTTGTCTTTTTTTTTTGGGACGGAGGGAGTAT-AAGCAACTAGGGAAACGTTCCGT 463
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LOC_Os09g25070_pW62  ATATATAGCAAGGATTTGTCTTTTTTGACGCGGAGTTAGTAAGTCTCGAGAGAAGGAAGAAACGT-CCAA 520
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T3091546_pW62        ATATATAGCAAGGATTTGTCTTTTTTGACACGGAGTTAGTAAGTCTCGAGAGAAGGAAGAAACGT-CCAA 520
LOC_Os05g39720_pW70  GTATGCAATGTCCATT-----GGTAAATAACTCAGAGTATATTCTCCTAAAAATTACTCTATGT-TGTG  499
H334389_pW70         GTATGCAATGTCCATT-----GGTAAATAACTCAGAGTATATTCTCCTAAAAATTACTCTATGT-TGTG  499
T3094952_pW70        GTATGTAATGTCCGTT-----GGTAAATAACTCAGAGTATATTCTCCTAAAAATTACTCTATGT-TGTG  499
LOC_Os05g45230_pW58  CTATACTACAACGATTACGACGGTTTGATATCTCTCCCTCGTTCGGCGAACAAACCTGCCTGAAC-CCTA 510
H1850565_pW58p       CTATACTACAACGATTACGACGGTTTGATATCTCTCCCTCGTTCGGCGAACAAACCTGCCTGAAC-CCTA 510
T3075919_pW58        CTATACTACAACGATTACGACGGTTTGATATCTCTCCCTCGTTCGGCGAACAAACCTGCCTGAAC-CCTA 498
LOC_Os03g21710_pW79  CTGATTGAAAACTGCAGGTCTCAGAGCACGTAATCTAACGGTCCGTGTGTGTGCCAAGTAAGCGAGTACT 515
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T3058779_pW19        TTAATT--AATCATGTGCTAATGGAACGCTCCG--------TTTTYCGTGCGGAGGCACTGTGTTCCCATC 500
LOC_Os09g25060_pW76  GGTAATTCTCACAATCTCACCTAGCCAATCTCTCC[---ACA]CACCCTTGAGGCCTTGACGTAGACCCTG 506
T3076120_pW76        GGTAATTCTCACAATCTCACCTAGCCAATCTCT[CCTCCAC]ACACCCTTGAGGCCTTGACGTAGACCCTG 506
H1974322_pW76p       GGTAATTCTCACAATCTCACCTAGCCAATCTCT[CC---ACA]CACCCCTTGAGGCCTTGACGTAGACCCTG 506
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T3056296_pW26        AATGGTGAGAATCTTACCCTTTAACCTTAATATACT-ACTAT-TTG--CTAAGCTATATAGACATGCATA 591
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H1961965_pW23        TCTCCAAAC----CTATCTGAAACGGTCGAGGCGATAGCTCTCTTA--TTAATCCAC----GAGTAGTATA 598
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T3063501_pW28        AGCAGAGTGAAAGTAAAATAATAGGGCCGGAGTAATAATTAC-CAG--CTGGTTCATCCCAAAAGGTA 575
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LOC_Os01g40260_pW77  TGAGTTTAAAATCCATTCTCCTAAGCTAGCATGGATCGATGAGGACCCCACAGCTTTTTTAAAAAAATATC 533
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T3091546_pW62        AGGTTTTCCGATTAGCTCTAC-AAGGTGGTG-AGCCAGATGA----CCTAAA----TTTAAAGTCTCATC 580
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LOC_Os09g25060_pW76  AATCAACCCAAGTGGAAAAACTATCAACAGTCCATTAGCTGAACTGAACTGAAACTGCTAACCAGTAACT 576
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                              640        650        660        670        680        690        700
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LOC_Os01g51690_pW26  AA-TTCAGGAACAGTGGGAACTACTAGGATTTACTGCAACTTTCGTGGCTCCAC-TGGCCCCGGATCCCA 644
H289702_pW26         AA-TTCAGGAACAGTGGGAACTACTAGGATTTACTGCAACTTTCGTGGCTCCAC-TGGCCCCGGATCCCA 211
T3056296_pW26        AA-TTCAGGAACAGTGGGAACTACTAGGATTTACTGCAACTGTCGTGGCTCCAC-TGACCCCAGATCCCA 659
LOC_Os01g53260_pW23  TA-TATTATCATGGAGACATCAGACAAGGCTAATTAACAGAGAGGGGACAATATGCAACAACGTATCCCA 667
H1961965_pW23        TA-TATTATCATGGAGACATCAGACAAGGCTAATTAACAGAGAGGGGACAATATGCAACAACGTATCCCA 667
T3027906_pW23        TA-TATTATCATGGAGACATCAGACAAGGCTAATTAACAGAGAGGGGACAATATGCAACAACGTATCCCA 667
LOC_Os06g44010_pW28  ----GTAGTGAAGGAGTCAACAAATGAATCCAAATTAGCTAGCCTAAATTCTTT----CAGGAGGGCCA 545
H1976995_pW28        ----GTAGTGAAGGAGTCAACAAATGAATCCAAATTAGCTAGCCTAAATTCTTT----CAGGAGGGCCA 638
T3063501_pW28        ----GTAGTGAAGGAGTCAACAAATGAATCCAAATTAGCTAGCCTAAATTCTTT----CAGGAGGGCCA 637
LOC_Os05g46020_pW07  AG--AAGGCCCCCACGGCAACTACGTGGCGAAGAGGCGAAGACCGCACCCCGTCGAAGTCTTTCCCCCGG 649
H2000561_pW07        AG--AAGGCCCCCACGGCAACTACGTGGCGAAGAGGCGAAGACCGCACCCCGTCGAAGTCTTTCCCCCGG 649
T3066720_pW07        AG--AAGGCCCCCACGGCAACTACGTGGCGAAGAGGCGAAGACCGCACCCCGTCGAAGTCTTTCCCCCGG 649
H2023318_pW64        GA-GAGAGAGCTAGTGGTTGCAACTTG--CAAATTAGTCTAAGTCCAACTTATTCTACTGATAGTCCAAT 497
T3095730_pW64        GA-GAGAG--CTAGTGGTTGCAACTTG--CAAATTAGTCTAAGTCCAACTTATTCTACTGATAGTCCAAT 364
LOC_Os12g02450_pW64  GA-GAGAGAGCTAGTGGTTGCAACTTG--CAAATTAGTCTAAGTCCAACTTATTCTACTGATAGTCCAAT 643
LOC_Os01g40260_pW77  TC-TATGGACCTTATTTTTATGTATAAATAAAAATAAATAAATGACACCACTTAAATACATAGTAGTAAT 602
T3097007_pW77        TC-TATGGACCTTATTTTTATGTATAAATAAAAATAAATAAATGACACCACTTAAATACATAGTAGTAAT 601
H1950043_pW77        TC-TATGGACCTTATTTTTATGTATAAATAAAAATAAATAAATGACACCACTTAAATACATAGTAGTAAT 601
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T3091546_pW62        TC-TTTTAA--TTATTTG-ATAT-TAGGTATTTCTCTAATATTCGTGTCTTTTTTTAAGTCTTATAATAGA 645
LOC_Os05g39720_pW70  AC-G-AGAACATTGT-GTTTCTTTTTTTGGTTTTTTGCCTGTAATAGTATACGGGTATACGGTA----- 627
H334389_pW70         AC-G-AGAACATTGT-GTTTCTTTTTTTGGTTTTTTGCCTGTAATAGTATACGGGTATACGGTA----- 627
T3094952_pW70        AC-G-AGAACATTGT-GTTTCTTTTTTTGGTTTTTTGCCTGTAATAGTATACGGGTATACGGTA----- 627
LOC_Os05g45230_pW58  AT-GCAAACGTAGTA-GTTTTCGTAAACAATCTTTTAATTGCGGTCTCGTGCCGTTG-ACG--A----- 640
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LOC_Os03g21710_pW79  CCGGTCAAAGGCCGTGAATTTGTCGTGACATCACATCGCCTGTGTCATGGCGATGACGACGACGACT--- 652
H1952278_pW79        CCGGTCAAAGGCCGTGAATTTGTCGTGACATCACATCGCCTGTGTCATGGCGATGACGACGACGACT--- 652
T3070072_pW79        CCGGTCAAAGGCCGTGAATTTGTCGTGACATCACATCGCCTGTGTCATGGCGATGACGACGACGACT--- 652
LOC_Os05g49620_pW19  TCAGTTGAGCAATGCGCAGCTGCACAAGTGTGTC--CGTCTGTGGTAGGTTGAGAGTTGAGACCATTC-- 641
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T3058779_pW19        TCAGTTGAGCAATGCGCAGCTGCACAAGTGTGTC--CGTCTGTGGTAGGTTGAGAGTTGAGACCATTC-- 636
LOC_Os09g25060_pW76  AACCTCCTCACACCTCCCAATCTCGTCCACAGCATACACACGTCTACGCATGACGTACGCTTCGTGACGT 646
T3076120_pW76        AACCTCCTCACACCTCCCAATCTCGTCCACAGCATACACACGTCTACGCATGACGTACGCTTCGTGACGT 646
H1974322_pW76p       AACCTCCTCACACCTCCCAATCTCGTCCACAGCATACACACGTCTACGCATGACGTACGCTTCGTGACGT 646
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                    710       720       730       740       750       760       770
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LOC_Os01g51690_pW26 TCATCCCAGCCCCACGC-CGCCCCCAAAGTCCAAAACACCTTA--CCACACGAGGGCAAATACCAAAGGC 711
H289702_pW26        TCATCCCAGCCCCACGC-CGCCCCCAAAGTCCAAAACACCTTA--CCACACGAGGGCAAATACCAAAGGC 278
T3056296_pW26       TCATCCCAGCCCCACGC-CGCCCCCAAAGTCCAAAACACCTTA--CCACACGAGGGCAAATACCAAAGGC 726
LOC_Os01g53260_pW23 CAAGCTTCCATCCATGCATGCATGCATGGATCGGCGAAGTTAA--AATTTCTATGACTCGT-TGAGGGAC 734
H1961965_pW23       CAAGCTTCCATCCATGCATGCATGCATGGATCGGCGAAGTTAA--AATTTCTATGACTCGT-TGAGGGAC 734
T3027906_pW23       CAAGCTTCCATCCATGCATGCATGCATGGATCGGCGAAGTTAA--AATTTCTATGACTCGT-TGAGGGAC 734
LOC_Os06g44010_pW28 AATTGTAACCCTCCTGGTTGTTGGCATGTGGTGTTTTTCCTTG--AC-CCTGCTTGCAGATGCAACCAGC 612
H1976995_pW28       AATTGTAACCCTCCTGGTTGTTGGCATGTGGTGTTTTTCCTTG--AC-CCTGCTTGCAGATGCAACCAGC 705
T3063501_pW28       AATTGTAACCCTCCTGGTTGTTGGCATGTGGTGTTTTTCCTTG--AC-CCTGCTTGCAGATGCAACCAGC 704
LOC_Os05g46020_pW07 AGACATTTCCGCCATGC-TGCTAAAATAAGTGGGCACGCCGTG--CG-CGCGTGCGTGCGTTCGAGCGGC 715
H2000561_pW07       AGACATTTCCGCCATGC-TGCTAAAATAAGTGGGCACGCCGTG--CG-CGCGTGCGTGCGTTCGAGCGGC 715
T3066720_pW07       AGACATTTCCGCCATGC-TGCTAAAATAAGTGGGCACGCCGTG--CG-CGCGTGCGTGCGTTCGAGCGGC 715
H2023318_pW64       AAGCATGTGCTACATGCATCATATCAATCCATGAGATCTATTG--ATCTTCCCCTGCAATTGCCTTAGCC 565
T3095730_pW64       AAGCATGTGCTACATGCATCATATCAATCCATGAGATCTATTG--ATCTTCCCCTGCAATTGCCTGAGCC 432
LOC_Os12g02450_pW64 AAGCATGTGCTACATGCATCATATCAATCCATGAGATCTATCG--ATCTTCCCCTGCAGTTGCCTGAGCC 711
LOC_Os01g40260_pW77 TGATTTAAATTTCTGGCTCCGTCTGGACAGGAGCCGGGCCACT-TGTACTGCACAGTTCTGGACTTCTG- 670
T3097007_pW77       TGATTTAAATTTCTGGCTCCGTCTGGACAGGAGCCGGGCCACT-TGTACTGCACAGTTCTGGACTTCTG- 669
H1950043_pW77       TGATTTAAATTTCTGGCTCCGTCTGGACAGGAGCCGGGCCACT-TGTACTGCACAGTTCTGGACTTCTG- 669
LOC_Os09g25070_pW62 AGG--TAAAACATTAATTCCGTAGAAGAAAAAGTAGAATTTTGATATCCTACGAGGCCATGAGTCACAT- 712
H1972014_pW62p      AGG--TAAAACATTAATTCCGTAGAAGAAAAAGTAGAATTTTGATATCCTACGAGGCCATGAGTCACAT- 712
T3091546_pW62       AGG--TAAAAATTAATTCCGTAGAAGAAAAAGTAGAATTTTGATATCCTACGAGGCCATGAGTCACAT- 712
LOC_Os05g39720_pW70 CGCCCGGAACTAGTCAGACAAACGA--------TTCGCGACCGTCACTCCGCACGCTCCGAACCCCCGC 688
H334389_pW70        CGCCCGGAACTAGTCAGACAAACGA--------TTCGCGACCGTCACTCCGCACGCTCCGAACCCCCGC 688
T3094952_pW70       CGCCCGGAACTAGTCAGACAAACGA--------TTCGCGACCGTCACTCCGCACGCTCCGAACCCCCGC 688
LOC_Os05g45230_pW58 CGCCTTAATCTGCACACGCTTAT GGGGAGAGAGAG AGAGAGAGAGAGAGAGAGAGAGAGATCAGTA 710
H1850565_pW58p      CGCCTTAATCTGCACACGCTTAT GGGGAGAGAGAG AGAGAGAGAGAGAGAGAGAGAGAGAGATCAGTA 710
T3075919_pW58       CGCCTTAATCTGCACACGCTTA GG          AGAGAGAGAGAGAGAGAGAGAGAGAGATCAGTA 690
LOC_Os03g21710_pW79 TAGTTTAG-TATAGTATTAGTACCATATATGTATATATGT---GTAATGTAATCCATGTC-------- 708
H1952278_pW79       TAGTTTAG-TATAGTATTAGTACCATATATGTATATATGT----GTAATGTAATCCATGTC-------- 708
T3070072_pW79       TAGTTTAG-TATAGTATTAGTACCATATATGTATATATGT----GTAATGTAATCCATGTC-------- 708
LOC_Os05g49620_pW19 TATTCTAA--CAAATGGTCAGTCAGACACAAGTTTTTTTTTT--CCGAACGGTCAGTCAGACAGACAGAAG 708
H2014700_pW19       TATTCTAA--CAAATGGTCAGTCAGACACAAGTTTTTTTTTTT--CCGAACGGTCAGTCAGACAGACAGAAG 707
T3058779_pW19       TATTCTAA--CAAATGGTCAGTCAGACACAAGTTTTTTTTTTTT--CCGAACGGTCAGTCAGACAGACAGAAG 704
LOC_Os09g25060_pW76 AAGGCCTCATGCCCTATACGCGATTCGTGACGTGCGCTCCGTGACGTCGTCTTGACCGGGGCGGGACGAC 716
T3076120_pW76       AAGGCCTCATGCCCTATACGCGATTCGTGACGTGCGCTCCGTGACGTCGTCTTGACCGGGGCGGGACGAC 716
H1974322_pW76p      AAGGCCTCATGCCCTATACGCGATTCGTGACGTGCGCTCCGTGACGTCGTCTTGACCGGGGCGGGACGAC 716


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                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os01g51690_pW26 AAATAG---GCAAA-AGGCGA-CGTCC--ACGAGTCCATGTCATGA---CACACCCCAAGTTGCTGTAA 770
H289702_pW26        AAATAG---GCAAA-AGGCGA-CGTCC--ACGAGTCCATGTCATGA---CACACCCCAAGTTGCTGTAA 337
T3056296_pW26       AAATAG---GCAAA-AGGCGA-CGTCC--ACGAGTCCATGTCATGA---CACACCCCAAGTTGCTGTAA 785
LOC_Os01g53260_pW23 GAGACG---ACGGGCAGGTGAGCGACC--TTAGATACAGGGTGGTT---GTGATCTGGTTGTGCTCTAT 795
H1961965_pW23       GAGACG---ACGGGCAGGTGAGCGACC--TTAGATACAGGGTGGTT---GTGATCTGGTTGTGCTCTAT 795
T3027906_pW23       GAGACG---ACGGGCAGGTGAGCGACC--TTAGATACAGGGTGGTT---GTGATCTGGTTGTGCTCTAT 795
LOC_Os06g44010_pW28 CAGCCA---GAAGACTCTTCTATCCTC---TTAATTTGACAGAATAATCCCAGATCTAATAAAAAA-CAC 675
H1976995_pW28       CAGCCA---GAAGACTCTTCTATCCTC---TTAATTTGACAGAATAATCCCAGATCTAATAAAAAA-CAC 768
T3063501_pW28       CAGCCA---GAAGACTCTTCTATCCTC---TTAATTTGACAGAATAATCCCAGATCTAATAAAAAAACAC 768
LOC_Os05g46020_pW07 GGCGCGCGCGCGGCAACTCCCGCACCCGCTCCGAACCTTCTCCCTCCTCACGAAGCTCACCGCGAAGCCG 785
H2000561_pW07       GGCGCGCGCGCGGCAACTCCCGCACCCGCTCCGAACCTTCTCCCTCCTCACGAAGCTCACCGCGAAGCCG 785
T3066720_pW07       GGCGCGCGCGCGGCAACTCCCGCACCCGCTCCGAACCTTCTCCCTCCTCACGAAGCTCACCGCGAAGCCG 785
H2023318_pW64       GATTAT----ATTAGGATACAAGTTGTCTTAGCTGAGGTTAAGTGTAGGGCCATATTGAACAGCACTGTAT 632
T3095730_pW64       GATTAT----ATTAGGATACAAGTTGTCTTAGCTGAGGTTAAGTGTAGGGCCATATTGAACAGCACTGTAT 499
LOC_Os12g02450_pW64 GATTAT---ATTAGGGTACAAGTTGTCTTAGCTGAGGT-AATTGTAGGGCCATATTGAACAGCACTGCAT 777
LOC_Os01g40260_pW77 GTTTAGCAGAGACTCGC---CGCGCGCG-CGCGGGTGGCCGTCGCGTTGCCGGCCGTAGCTGTCGCATAT 736
T3097007_pW77       GTTTAGCAGAGACTCGC---CGCGCGCG-CGCGGGTGGCCGTCGCGTTGCCGGCCGTAGCTGTCGCATAT 735
H1950043_pW77       GTTTAGCAGAGACTCGC---CGCGCGCG-CGCGGGTGGCCGTCGCGTTGCCGGCCGTAGCTGTCGCATAT 735
LOC_Os09g25070_pW62 GAGTA--AGACGCTCGGTCACGTAAGCA-CGGGGGCGTCAGCCGCGTCACTG-CTGATGCCAACTTGCTG 778
H1972014_pW62p      GAGTA--AGACGCTCGGTCACGTAAGCA-CGGGGGCGTCAGCCGCGTCACTG-CTGATGCCAACTTGCTG 778
T3091546_pW62       GAGTA--AGACGCTCGGTCACGTAAGCA-CGGGGGCGTCAGCCGCGTCACTG-CTGATGCCAACTTGCTG 778
LOC_Os05g39720_pW70 GACCAGAAACCGTACCCGCCTTCTCCCG-CACCGGGCCCCACCATAGTCCACGTCACCTGCTCAGCGCTC 757
H334389_pW70        GACCAGAAACCGTACCCGCCTTCTCCCG-CACCGGGCCCCACCATAGTCCACGTCACCTGCTCAGCGCTC 757
T3094952_pW70       GACCAGAAACCGTACCCGCCTTCTCCCG-CACCGGGCCCCACCATAGTCCACGTCACCTGCTCAGCGCTC 757
LOC_Os05g45230_pW58 GATCGGCAGTAGTTGAGGTGGTTGATCG-GTCTATGGCTGCTCACTCTTCTC----TCAGCTTGGTGTAC 775
H1850565_pW58p      GATCGGCAGTAGTTGAGGTGGTTGATCG-GTCTATGGCTGCTCACTCTTCTC----TCAGCTTGGTGTAC 775
T3075919_pW58       GATCGGCAGTAGTTGAGGTGGTTGATCG-GTCTATGGCTGCTCACTCTTCTC----TCAGCTTGGTGTAC 755
LOC_Os03g21710_pW79 ---CGGTTTTCTTTGCCTTGCTTTGAT--CAATTCATCTGGATATGTACATCTAGGGCCACAGGGGTCGG 773
H1952278_pW79       ---CGGTTTTCTTTGCCTTGCTTTGAT--CAATTCATCTGGATATGTACATCTAGGGCCACAGGGGTCGG 773
T3070072_pW79       ---CGGTTTTCTTTGCCTTGCTTTGAT--CAATTCATCTGGATATGTACATCTAGGGCCACAGGGGTCGG 773
LOC_Os05g49620_pW19 TAGTGATTAGATTAGAGCTGGATTAGT--CTCTGCACATCTCCATGATGGCCAAGAAACCAAAAGACCGG 776
H2014700_pW19       TAGTGATTAGATTAGAGCTGGATTAGT--CTCTGCACATCTCCATGATGGCCAAGAAACCAAAAGACCGG 775
T3058779_pW19       TAGTGATTAGATTAGAGCTGGATTAGT--CTCTGCACATCTCCATGATGGCCAAGAAACCAAAAGACCGG 772
LOC_Os09g25060_pW76 GCCACGCGCGCGTGGCGCGTCCTTGTCATGGCGGGCGTCGACAGCCAGCTCGCGCGCGCCCCCGTTTTTC 786
T3076120_pW76       GCCACGCGCGCGTGGCGCGTCCTTGTCATGGCGGGCGTCGACAGCCAGCTCGCGCGCGCCCCCGTTTTTC 786
H1974322_pW76p      GCCACGCGCGCGTGGCGCGTCCTTGTCATGGCGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 786
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                              850       860       870       880       890       900       910
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LOC_Os01g51690_pW26   GTGG----CAGGGCCGTGCGGGGCATCAAAGCAAAACAATTCGAAA-CGGGGCGGCTCGCG-CACGGTCG 834
H289702_pW26          GTGG----CAGGGCCGTGCGGGGCATCAAAGCAAAACAATTCGAAA-CGGGGCGGCTCGCG-CACGGTCG 401
T3056296_pW26         GTGG----CACGGCCGCGCGGGGCATCAAAGCAAAACAATTCGAAA-CGGGGCGGCTCGCG-CACGGTCG 849
LOC_Os01g53260_pW23   CTCT----CGCCCTCTCTCCAATCTCCATCTCT---CTGTCTGATT-TGTAATCTTTTCC--CTTGGCTT 855
H1961965_pW23         CTCT----CGCCCTCTCTCCAATCTCCATCTCT---CTGTCTGATT-TGTAATCTTTTCC--CTTGGCTT 855
T3027906_pW23         CTCT----CGCCCTCTCTCCAATCTCCATCTCT---CTGTCTGATT-TGTAATCTTTTCC--CTTGGCTT 855
LOC_Os06g44010_pW28   AGTT----TAATCCTCCTTATTTTCTAAAATGAAAATAGTAGTACT-ACTACTAATTATCATCACAAATG 740
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T3063501_pW28         AGTT----TAATCCTCCTTATTTTCTAAAATGAAAATAGTAGTACT-ACTACTAATTATCATCACAAATG 833
LOC_Os05g46020_pW07   GCAA----AATCCTCCCGGAGAGAGAGACACAAACACAACACAACC-AGC-TCCCCCGCGCCCCGCGTG 848
H2000561_pW07         GCAA----AATCCTCCCGGAGAGAGAGACACAAACACAACACAACC-AGC-TCCCCCGCGCCCCGCGTG 848
T3066720_pW07         GCAA----AATCCTCCCGGAGAGAGAGACACAAACACAACACAACC-AGC-TCCCCCGCGCCCCGCGTG 848
H2023318_pW64         ACAC----CATCATCGCGTGTAT----ATATAGCCACATTAAAGTA-GGCACCAATCAAGTACACACTTC 693
T3095730_pW64         ACAC----CATCATCGCGTGTAT----ATATAGCCACATTAAAGTA-GGCACCAATCAAGTACACACTTC 560
LOC_Os12g02450_pW64   ACACGCACCATCATCCTGCATATC-TCGTTTAATTGTGTATATATAGCCACATTAAAGTACACACTTG 846
LOC_Os01g40260_pW77   CCGGGATCGAGACGTGCGTGTATGT-GCTACTGCTGCATGCGGCGATGTTTCCTGCCGCGATTTTCCAGG 805
T3097007_pW77         CCGGGATCGAGACGTGCGTGTATGT-GCTACTGCTGCATGCGGCGATGTTTCCTGCCGCGATTTTCCAGG 804
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LOC_Os09g25070_pW62   TCGTAGTGAGCACAATCGGTCAAGTCAATGGGGGAGAATGCCAAAATCTCCTTTGTGGGCTTAATTTATA 848
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T3091546_pW62         TCGTAGTGAGCACAATCGGTCAAGTCAATGGAGGAGAATGCCAAAATCTCCTTTGTGGGCTTAATTTATA 848
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LOC_Os05g45230_pW58   ACAGT-TTGAGACGCGGGAGAG-GT--G-AAGGCAGCTTGCACGCTTGCCCACCCCCACCTTCCCCGC-- 838
H1850565_pW58p        ACAGT-TTGAGACGCGGGAGAG-GT--G-AAGGCAGCTTGCACGCTTGCCCACCCCCACCTTCCCCGC-- 838
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LOC_Os03g21710_pW79   TCGGGAACCGGGACCCACCTCCGCTCTTCCATGCAGCTTCCTCATTT-TAGCCTTTTTCCGAGTTCCGAC 842
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LOC_Os05g49620_pW19   TCCAAGTGTTTGAATGACACTCGGGTAGTGATATTCTCTGCTTAGTCATAATCTTTTCCCTCGGTCCGGT 846
H2014700_pW19         TCCAAGTGTTTGAATGACACTCGGGTAGTGATATTCTCTGCTTAGTCATAATCTTTTCCCTCGGTCCGGT 845
T3058779_pW19         TCCAAGTGTTTGAATGACACTCGGGTAGTGATATTCTCTGCTTAGTCATAATCTTTTCCCTCGGTCCGGT 842
LOC_Os09g25060_pW76   CCACT-CAATTGCGTTACAGTTTTCTCCCACAGATCCATGCAAATTAAAGATCACACGGTCTCGTTCTCG 855
T3076120_pW76         CCACT-CAATTGCGTTACAGTTTTCTCCCACAGATCCATGCAAGTTAAAGATCACACGGTCTCGTTCTCG 855
H1974322_pW76p        NNNNN-NNNNNNNNNNNNNNNNNNNNNCCCACAGATCCATGCAAATTAAAGATCACACGGTCTCGTTCTCG 855


                              920       930       940       950       960       970       980
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LOC_Os01g51690_pW26   CGCGCGCCGAAGCTTCATCCAACGACTCGAGCCAGGAAGCTCGGTGCGAAGCCCA-CCGACGTCGCCCGC 903
H289702_pW26          CGCGCGCCGAAGCTTCATCCAACGACTCGAGCCAGGAAGCTCGGTGCGAAGCCCA-CCGACGTCGCCCGC 470
T3056296_pW26         CGCGCGCCGAAGCTTCATCCAACGACTCGAGCCAGGAAGCTCGGTGCGAAGCCCA-CCGACGTCGCCCGC 918
LOC_Os01g53260_pW23   TGAGCGTGCACGCTT-GCCCAACTTCCC---CTTGGCTTCTAGCGTCTTATTCCA-CACGCGCACTCCAG 920
H1961965_pW23         TGAGCGTGCACGCTT-GCCCAACTTCCC---CTTGGCTTCTAGCGTCTTATTCCA-CACGCGCACTCCAG 920
T3027906_pW23         TGAGCGTGCACGCTT-GCCCAACTTCCC---CTTGGCTTCTAGCGTCTTATTCCA-CACGCGCACTCCAG 920
LOC_Os06g44010_pW28   ACATGATTGATGCTACCTTTAGTCTTTAGACCCTAATTATCCTCCACATGCTGAAATGAAAACCACACTG 810
H1976995_pW28         ACATGATTGATGCTACCTTTAGTCTTTAGACCCTAATTATCCTCCACATGCTGAAATGAAAACCACACTG 903
T3063501_pW28         ACATGATTGATGCTACCTTTAGTCTTTAGACCCTAATTATCCTCCACATGCTGAAATGAAAACCACACTG 903
LOC_Os05g46020_pW07   CGATCGATCACGATCGATCTCATCCCTCTCGATCGCCTACTACTACCAGTACAAATCCACCCCGCCACCA 918
H2000561_pW07         CGATCGATCACGATCGATCTCATCCCTCTCGATCGCCTACTACTACCAGTACAAATCCACCCCGCCACCA 918
T3066720_pW07         CGATCGATCACGATCGATCTCATCCCTCTCGATCGCCTACTACTACCAGTACAAATCCACCCCGCCACCA 918
H2023318_pW64         TGACAAACCTGGTTAACCACACTGCCACAAAGCCAGGTGATCGTCTC---CCTTAATTAGCTTCCACTAA 760
T3095730_pW64         TGACAAACCTGGTTAACCACACTGCCACAAAGCCAGGTGATCGTCTC---CCTTAATTAGCTTCCACTAA 627
LOC_Os12g02450_pW64   TGACAAACCTGATTAACCACACTGCCACAAAGCCAGGTGATCATCTC---CCTTAATCAGCTTCCATTAA 913
LOC_Os01g40260_pW77   CAAAGTCCCCCCGCGCACACCC-CACTGGCACATGTACTACGTC-GCCGTCGGTTTGAACGCGGCCGTG 873
T3097007_pW77         CAAAGTCCCCCCGCGCACACCC-CACTGGCACATGTACTACGTC-GCCGTCGGTTTGAACGCGGCCGTG 872
H1950043_pW77         CAAAGTCCCCCCGCGCACACCC-CACTGGCACATGTACTACGTC-GCCGTCGGTTTGAACGCGGCCGTG 872
LOC_Os09g25070_pW62   TGTGGATCACCATTATCCTCGC-ACAA-AGTTCACGTTTTGGTCC-CCCTCCTGTTCGGCGACGGGCGAC 915
H1972014_pW62p        TGTGGATCACCATTATCCTCGC-ACAA-AGTTCACGTTTTGGTCC-CCCTCCTGTTCGGCGACGGGCGAC 915
T3091546_pW62         TGTGGATCACCATTATCCTCGC-ACAA-AGTTCACGTTTTGGTCC-CCCTCCTGTTCGGCGACGGGCGAC 915
LOC_Os05g39720_pW70   TCGAGGGAGCTTTGACCAGTCA-ACGG---TCAAACGTTCAAAG-GTCTATATAATGATCACCGGAGGC 883
H334389_pW70          TCGAGGGAGCTTTGACCAGTCA-ACGG----TCAAACGTTCAAAG-GTCTATATAATGATCACCGGAGGC 883
T3094952_pW70         TCGAGGGAGCTTTGACCAGTCA-ACGG----TCAAACGTTCAAAG-GTCTATATAATGATCACCGGAGGC 883
LOC_Os05g45230_pW58   TCACACCGCCCTTCACCT-TCC-ACTT----CCAGTCGCAGCTAA-CCCT-CGCAGCTGCACCTGCACAC 900
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T3075919_pW58         TCACACCGCCCTTCACCT-TCC-ACTT----CCAGTCGCAGCTAA-CCCT-CGCAGCTGCACCTGCACAC 880
LOC_Os03g21710_pW79   TGCTTTTCGGCTTTTTTCCCCG-GCGATATATAAGACGCGGATTGGCACGGCGAATTTTGCTTCATTTGC 911
H1952278_pW79         TGCTTTTCGGCTTTTTTCCCCG-GCGATATATAAGACGCGGATTGGCACGGCGAATTTTGCTTCATTTGC 911
T3070072_pW79         TGCTTTTCGGCTTTTTTCCCCG-GCGATATATAAGACGCGGATTGGCACGGCGAATTTTGCTTCATTTGC 911
LOC_Os05g49620_pW19   CAAAGTTTGGATCTGAACATGACGCAACGAATCACATTTTGCT---CCCTATAAATACTCCTCTCCCTG 912
H2014700_pW19         CAAAGTTTGGATCTGAACATGACGCAACGAATCACATTTTGCT---CCCTATAAATACTCCTCTCCCTG- 911
T3058779_pW19         CAAAGTTTGGATCTGAACATGACGCAACGAATCACATTTTGCT---CCCTATAAATACTCCTCTCCCTG- 908
LOC_Os09g25060_pW76   CCGCCTATATGTAGCGCCACCGATTCC----CCATGAACCATTCAAGTGTTTGTACTTGGCTTTGCTGGC 921
T3076120_pW76         CCGCCTATATGTAGCGCCACCGATTCC----CCATGAACCATTCAAGTGTTTGTACTTGGCTTTGCTGGC 921
H1974322_pW76p        CCGCCTATATGTAGCGCCACCGATTCC----CCATGAACCATTCAAGTGTTTGTACTTGGCTTTGCTGGC 921
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                          990      1000      1010      1020      1030      1040      1050
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LOC_Os01g51690_pW26  CCGCCCACGCGCTCTATAAGTA--GACGGCTCTTCGGCGCGTGTCACGTAA-GAGAGTCGGCCAACCCAC 970
H289702_pW26         CCGCCCACGCGCTCTATAAGTA--GACGGCTCTTCGGCGCGTGTCACGTAA-GAGAGTCGGCCAACCCAC 537
T3056296_pW26        CCGCGCACGCGCTCTATAAGTA--GACGGCTCTTCGGCGCGCGTCACGTAAAGAGAGTCGGCCAACCCAC 986
LOC_Os01g53260_pW23  CTGTTCGATCGATTCACCAGGT--ATAAAATCGCCGG------TAACGTGGCGCACGTCCGGCCGCCTGA 982
H1961965_pW23        CTGTTCGATCGATTCACCAGGT--ATAAAATCGCCGG------TAACGTGGCGCACGTCCGGCCGCCTGA 982
T3027906_pW23        CTGTTCGATCGATTCACCAGGT--ATAAAATCGCCGG------TAACGTGGCGCACGTCCGGCCGCCTGA 982
LOC_Os06g44010_pW28  ACATTAAAAAAATAAACAATTG--ATGCCTTTTCCGGAGC---AGAAATGGTAGTAGTACTACTAGTAGT 875
H1976995_pW28        ACATTAAAAAAATAAACAATTG--ATGCCTTTTCCGGAGC---AGAAATGGTAGTAGTACTACTAGTAGT 968
T3063501_pW28        ACATTAAAAAAATAAACAATTG--ATGCCTTTTCCGGAGC---AGAAATGGTAGTAGTACTACTACTAGT 968
LOC_Os05g46020_pW07  CTACATCATCCCCTCATATCCAT-GCAGATTTAGCGCCAATCCTTATAAATACGGAGCTTTCGCGCCGGC 987
H2000561_pW07        CTACATCATCCCCTCATATCCAT-GCAGATTTAGCGCCAATCCTTATAAATACGGAGCTTTCGCGCCGGC 987
T3066720_pW07        CTACATCATCCCCTCATATCCAT-GCAGATTTAGCGCCAATCCTTATAAATACGGAGCTTTCGCGCCGGC 987
H2023318_pW64        TCTTTCCACAACTATCTAGC----ACCGATTAAGAACAGCAGCTATCTTAATCAGGGAGCTTGAGATCTT 826
T3095730_pW64        TCTTTCCACAACTATCTAGC----ACCGATTAAGAACAGCAGCTATCTTAATCAGGGAGCTTGAGATCTT 693
LOC_Os12g02450_pW64  TTCTTCCACAACTATCTAGCTAGCACCGATTAAGAACAGCAGCTATCTTAATCAGAGAGCTTGATATCTT 983
LOC_Os01g40260_pW77  GTCACCGCACGCGCGCGTGCAGCATGTCGCCATGCATTCACAGC--TACTAGCTACTATACAGTATACAC 941
T3097007_pW77        GTCACCGCACGCGCGCGTGCAGCATGTCGCCATGCATTCACAGC--TACTAGCTACTATACAGTATACAC 940
H1950043_pW77        GTCACCGCACGCGCGCGTGCAGCATGTCGCCATGCATTCACAGC--TACTAGCTACTATACAGTATACAC 940
LOC_Os09g25070_pW62  GT-ACGGCGCCACTATAAGAAACGTGCCCTATTGCTGTCACGCCG-TACTTCCTCCCGCCCACCGGGCAG 983
H1972014_pW62p       GT-ACGGCGCCACTATAAGAAACGTGCCCTATTGCTGTCACGCCG-TACTTCCTCCCGCCCACCGGGCAG 983
T3091546_pW62        GT-ACGGCGCCACTATAAGCAACGTGCCCTATTGCTGTCACGCCG-TACTTCCTCCCGCCCACCGGGCAG 983
LOC_Os05g39720_pW70  GTCGTCGTTGGAAGAAGCAGTAGCCACACCCACACGCACACCCGA-TCGATCCTGGCATCCTACTCTGCT 952
H334389_pW70         GTCGTCGTTGGAAGAAGCAGTAGCCACACCCACACGCACACCCGA-TCGATCCTGGCATCCTACTCTGCT 952
T3094952_pW70        GTCGTCGTTGGAAGAAGCAGTAGCCACACCCACACGCACACCCGA-TCGATCCTGGCATCCTACGCTGCT 952
LOC_Os05g45230_pW58  GTACGCCTATATATACTCACCGCGCGCCGCCGC-CGTGCACCTG--TCCGTCCGTCCGTCC---ACTGAT 964
H1850565_pW58p       GTACGCCTATATATACTCACCGCGCGCCGCCGC-CGTGCACCTG--TCCGTCCGTCCGTCC---ACTGAT 964
T3075919_pW58        GTACGCCTATATATACTCACCGCGCGCCGCCGC-CGTGCACCTG--TCCGTCCGCCCGTCC---ACTGAT 944
LOC_Os03g21710_pW79  ACGGTATATATCCCAGTCTGTGTGTGAGTGTGTGTGGTCTGTGTGGAGTGTATGGTTGATTTGGTTGGTAAT 981
H1952278_pW79        ACGGTATATATCCCAGTCTGTGTGTGAGTGTGTGTGGTCTGTGGAGTGTATGGTTGATTTGGTTGGTAAT 981
T3070072_pW79        ACGGTATATATCCCAGTCTGTGTGTGAGTGTGTGTGGTCTGTGGAGTGTATGGTTGATTTGGTTGGTAAT 981
LOC_Os05g49620_pW19  ----TCACTACCACACTCGCCATCCTACCTCACACGCTCTCACCAACACAAGAAACCACACGCTTACGAG 978
H2014700_pW19        ----TCACTACCACACTCGCCATCCTACCTCACACGCTCTCACCAACACAAGAAACCACACGCTTACGAG 977
T3058779_pW19        ----TCACTACCACACTCGCCATCCTACCTCACACGCTCTCACCAACACAAGAAACCACACGCTTACGAG 974
LOC_Os09g25060_pW76  CTGTTTCTGTTTTGATTACTCG--AGCTCCAGAGCACAGCAGCAGAGAGACGCGAGCTGTTCGTGGTCGT 989
T3076120_pW76        CTGTTTCTGTTTTGATTACTCG--AGCTCCAGAGCACAGCAGCAGAGAGACGCGAGCTGTTCGTGGTCGT 989
H1974322_pW76p       CTGTTTCTGTTTTGATTACTCG--AGCTCCAGAGCACAGCAGCAGAGAGACGCGAGCTGTTCGTGGTCGT 989


                          1060      1070      1080      1090      1100      1110
                     ....|....|....|....|....|....|....|....|....|....|....|....|....|
LOC_Os01g51690_pW26  A-TGCACGTGTACCG-------------------------------------------------- 984
H289702_pW26         A-TGCACGTGTACCG-------------------------------------------------- 551
T3056296_pW26        A-TGCACGTGTACCG-------------------------------------------------- 1000
LOC_Os01g53260_pW23  A-CCTGCGCCGATCGAGAT---------------------------------------------- 1000
H1961965_pW23        A-CCTGCGCCGATCGAGAT---------------------------------------------- 1000
T3027906_pW23        A-CCTGCGCCGATCGAGAT---------------------------------------------- 1000
LOC_Os06g44010_pW28  AGTATTCTACTGTCAAGACCAAGACGGCGACA-------------------------------- 907
H1976995_pW28        AGTATTCTACTGTCAAGACCAAGACGGCGACA-------------------------------- 1000
T3063501_pW28        AGTATTCTACTGTCAAGACCAAGACGGCGACA-------------------------------- 1000
LOC_Os05g46020_pW07  CTCGTACTCGGCC---------------------------------------------------- 1000
H2000561_pW07        CTCGTACTCGGCC---------------------------------------------------- 1000
T3066720_pW07        CTCGTACTCGGCC---------------------------------------------------- 1000
H2023318_pW64        AATTAGGAAATAAGGAGATC-------------------------------------------- 846
T3095730_pW64        AATTAGGAAATAAGGAGATC-------------------------------------------- 713
LOC_Os12g02450_pW64  AATTAGGAATCAAGGAG------------------------------------------------ 1000
LOC_Os01g40260_pW77  ACACAATTCCGGTTGATAAAGCGCTCTGCGTGAGCTGAGCTGAGCTAGGCGTCGCGCGCG 1001
T3097007_pW77        ACACAATTCCGGTTGATAAAGCGCTCTGCGTGAGCTGAGCTGAGCTAGGCGTCGCGCGCG 1000
H1950043_pW77        ACACAATTCCGGTTGATAAAGCGCTCTGCGTGAGCTGAGCTGAGCTAGGCGTCGCGCGCG 1000
LOC_Os09g25070_pW62  CTAGCTTAGCTGCCGCC------------------------------------------------ 1000
H1972014_pW62p       CTAGCTTAGCTGCCGCC------------------------------------------------ 1000
T3091546_pW62        CTAGCTTAGCTGCCGCC------------------------------------------------ 1000
LOC_Os05g39720_pW70  CGATCGAATCGCTAGCTTTCTTCTTCTTCTTCTTCTCCTCCGTCTCCG----------------- 1000
H334389_pW70         CGATCGAATCGCTAGCTTTCTTCTTCTTCTTCTTCTCCTCCGTCTCCG----------------- 1000
T3094952_pW70        CGATCGAATCGCTAGCTTTCTTCTTCTTCTTCTTCTCCTCCGTCCCCG----------------- 1000
LOC_Os05g45230_pW58  CGACGACGACGTTAACCTCGCCGGCCGGCGCTAACA---------------------------- 1000
H1850565_pW58p       CGACGACGACGTTAACCTCGCCGGCCGGCGCTAACA---------------------------- 1000
T3075919_pW58        CGACGACGACGTTAACCTCGCCGGCCGGCGCTAACA---------------------------- 980
LOC_Os03g21710_pW79  TGGCTAAGCTAGCTATAGC---------------------------------------------- 1000
H1952278_pW79        TGGCTAAGCTAGCTATAGC---------------------------------------------- 1000
T3070072_pW79        TGGCTAAGCTAGCTATAGC---------------------------------------------- 1000
LOC_Os05g49620_pW19  ACGCCACGGCGGCGGCGGCGGCG------------------------------------------ 1001
H2014700_pW19        ACGCCACGGCGGCGGCGGCGGCG------------------------------------------ 1000
T3058779_pW19        ACGCCACGGCGGCGGCGGCGGCGGCG-------------------------------------- 1000
LOC_Os09g25060_pW76  CGTCGTCGTCG----------------------------------------------------- 1000
T3076120_pW76        CGTCGTCGTCG----------------------------------------------------- 1000
H1974322_pW76p       CGTCGTCGTCG----------------------------------------------------- 1000
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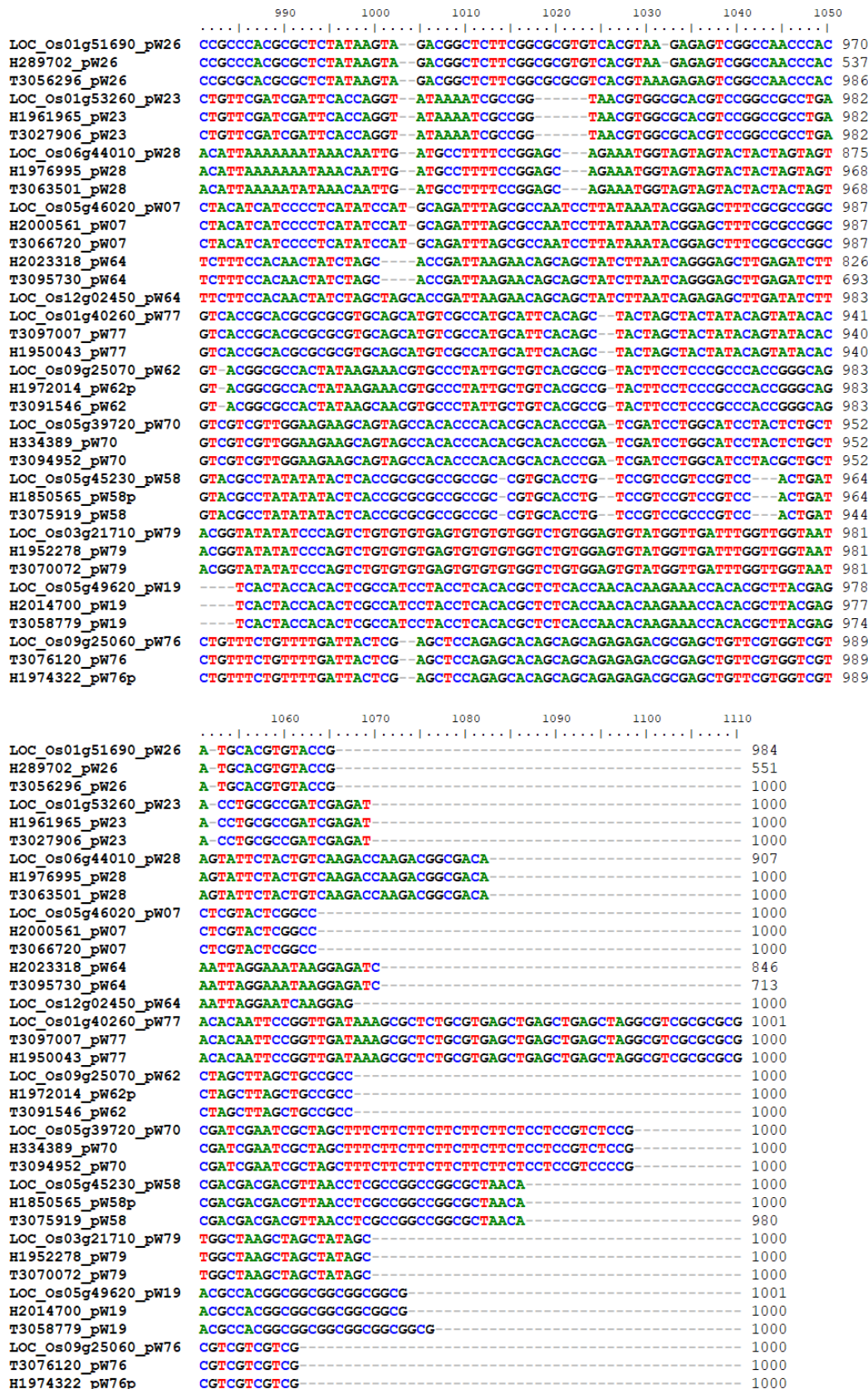
Fig. S4: Structural variation at promoter regions in Tetep and HP2216 in comparison with Nipponbare. The black boxes are showing variations and the brown arrows showing sequence dissimilarity.
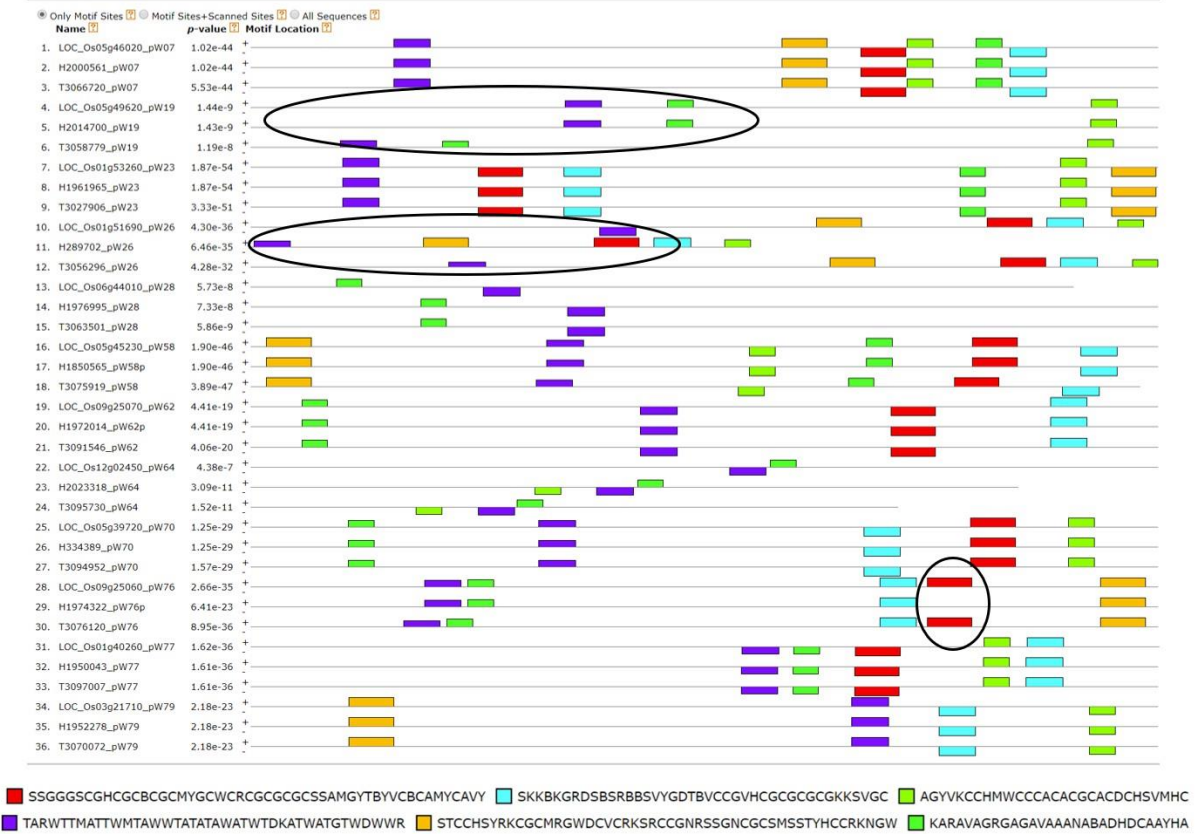
Fig. S5: 1 kb promoter analysis of DEG WRKY for conserved domains search using MEME software. Black circles depict variations in domains.