

## File S1. All Transcription factor binding sites (TFBS) identified in the prom

Seq. name	accession	gene symbol	GeneID	matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			O\$INRE	Core prom	O\$DINR.0	Drosophila		0.94
VvACS1	VvACS1			O\$INRE	Core prom	O\$DINR.0	Drosophila		0.94
VvACS6	VvACS6			O\$INRE	Core prom	O\$DINR.0	Drosophila		0.94
VvACS9	VvACS9			O\$INRE	Core prom	O\$DINR.0	Drosophila		0.94
VvACO1	VvACO1			O\$INRE	Core prom	O\$DINR.0	Drosophila		0.94
VvACO2	VvACO2			O\$INRE	Core prom	O\$DINR.0	Drosophila		0.94
VvACS4	VvACS4			O\$INRE	Core prom	O\$DINR.0	Drosophila		0.94

Seq. name	accession	gene symbol	GeneID	matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACS1	VvACS1			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACS1	VvACS1			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACS1	VvACS1			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.88
VvACS1	VvACS1			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACS2	VvACS2			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.88
VvACS2	VvACS2			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.88
VvACS6	VvACS6			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACS9	VvACS9			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACO2	VvACO2			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACO2	VvACO2			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACO2	VvACO2			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.88
VvACO2	VvACO2			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACO2	VvACO2			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACO2	VvACO2			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACO4	VvACO4			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.88
VvACO4	VvACO4			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACO4	VvACO4			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACO4	VvACO4			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACO4	VvACO4			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.9
VvACS4	VvACS4			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.88
VvACS4	VvACS4			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.88
VvACS4	VvACS4			O\$PTBP	Plant TATA	O\$PTATA.(Plant TATA			0.88

Seq. name	accession	gene symbol	GeneID	matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACO4	VvACO4			O\$TELO	Protein inv	O\$ZSCAN	Zinc finge		0.76

Seq. name	accession	gene symbol	GeneID	matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACS1	VvACS1			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACS1	VvACS1			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACS1	VvACS1			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACS1	VvACS1			O\$VTBP	Vertebrate	O\$ATATA.(Avian C-ty			0.78
VvACS2	VvACS2			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACS2	VvACS2			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACS2	VvACS2			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACS2	VvACS2			O\$VTBP	Vertebrate	O\$LTATA.(Lentivirus			0.82
VvACS2	VvACS2			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACS2	VvACS2			O\$VTBP	Vertebrate	O\$MTATA. Muscle TA			0.84
VvACS6	VvACS6			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACS6	VvACS6			O\$VTBP	Vertebrate	O\$VTATA.(Mammaliar			0.89
VvACS6	VvACS6			O\$VTBP	Vertebrate	O\$MTATA. Muscle TA			0.84
VvACS6	VvACS6			O\$VTBP	Vertebrate	O\$LTATA.(Lentivirus			0.82
VvACS6	VvACS6			O\$VTBP	Vertebrate	O\$VTATA.(Mammaliar			0.89
VvACS9	VvACS9			O\$VTBP	Vertebrate	O\$VTATA.(Cellular an			0.9
VvACO1	VvACO1			O\$VTBP	Vertebrate	O\$ATATA.(Avian C-ty			0.78

VvACO1	VvACO1	O\$VTBP	Vertebrate	O\$LTATA.C	Lentivirus	0.82
VvACO1	VvACO1	O\$VTBP	Vertebrate	O\$ATATA.C	Avian C-ty	0.78
VvACO1	VvACO1	O\$VTBP	Vertebrate	O\$LTATA.C	Lentivirus	0.82
VvACO1	VvACO1	O\$VTBP	Vertebrate	O\$VTATA.C	Mammaliar	0.89
VvACO2	VvACO2	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACO2	VvACO2	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACO2	VvACO2	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACO2	VvACO2	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACO2	VvACO2	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACO2	VvACO2	O\$VTBP	Vertebrate	O\$LTATA.C	Lentivirus	0.82
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$ATATA.C	Avian C-ty	0.78
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$ATATA.C	Avian C-ty	0.78
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$LTATA.C	Lentivirus	0.82
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$VTATA.C	Mammaliar	0.89
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$VTATA.C	Mammaliar	0.89
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACO4	VvACO4	O\$VTBP	Vertebrate	O\$VTATA.C	Cellular an	0.9
VvACS4	VvACS4	O\$VTBP	Vertebrate	O\$LTATA.C	Lentivirus	0.82
VvACS4	VvACS4	O\$VTBP	Vertebrate	O\$MTATA.	Muscle TA	0.84
VvACS4	VvACS4	O\$VTBP	Vertebrate	O\$LTATA.C	Lentivirus	0.82
VvACS4	VvACS4	O\$VTBP	Vertebrate	O\$MTATA.	Muscle TA	0.84

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS1	VvACS1	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS1	VvACS1	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS1	VvACS1	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS1	VvACS1	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS2	VvACS2	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS2	VvACS2	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS6	VvACS6	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS6	VvACS6	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACO2	VvACO2	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACO2	VvACO2	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACO4	VvACO4	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS4	VvACS4	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS4	VvACS4	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83
VvACS4	VvACS4	O\$YTBP	Yeast	TATA	O\$SPT15.	TATA-bindi		0.83

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$ABRE	ABA respo	P\$ABF2.0	Abscisic ac			0.83
VvACS1	VvACS1	P\$ABRE	ABA respo	P\$ABRE.0	ABA respo			0.82
VvACO2	VvACO2	P\$ABRE	ABA respo	P\$ABF1.0	ABA (absci			0.79

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$AGP1	Plant	GAT	P\$GATA4.	GATA trans		0.91
VvACS1	VvACS1	P\$AGP1	Plant	GAT	P\$AGP1.0	AG-motif b		0.91
VvACS1	VvACS1	P\$AGP1	Plant	GAT	P\$GATA19	GATA trans		0.85
VvACO1	VvACO1	P\$AGP1	Plant	GAT	P\$AGP1.0	AG-motif b		0.91

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$AHBP	Arabidopsi	P\$BLR.01	Transcript			0.9
VvACS1	VvACS1	P\$AHBP	Arabidopsi	P\$HAT2.0	Homeobox			0.87
VvACS1	VvACS1	P\$AHBP	Arabidopsi	P\$ATHB34	Homeobox			0.89
VvACS1	VvACS1	P\$AHBP	Arabidopsi	P\$ATHB32	Homeobox			0.92

VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB40 Homeobox	0.84
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB34 Homeobox	0.89
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB9. PHAVOLU	0.83
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB53 Homeobox	0.85
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB34 Homeobox	0.89
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB5. Homeobox	0.86
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$ATHB23 Homeobox	0.84
VvACS1	VvACS1	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$HAHB4. Sunflower	0.87
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB33 Homeobox	0.89
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB23 Homeobox	0.84
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB15 Homeobox	0.83
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB15 Homeobox	0.83
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$HAT2.0' Homeobox	0.87
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$HAHB4. Sunflower	0.87
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$WUS.01 Homeodon	0.94
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB23 Homeobox	0.84
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB34 Homeobox	0.89
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB5. Homeobox	0.86
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$WUS.01 Homeodon	0.94
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB15 Homeobox	0.83
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB53 Homeobox	0.85
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB34 Homeobox	0.89
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB40 Homeobox	0.84
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACS2	VvACS2	P\$AHBP	Arabidopsi P\$HAHB4. Sunflower	0.87
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB34 Homeobox	0.89
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB53 Homeobox	0.85
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB51 Homeobox	0.89
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB23 Homeobox	0.84
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB1. Arabidopsi:	0.9
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB5. HDZip clas	0.89
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB23 Homeobox	0.84
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB5. Homeobox	0.86
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB33 Homeobox	0.89
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB15 Homeobox	0.83

VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$ATHB51 Homeobox	0.89
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$HAHB4. Sunflower	0.87
VvACS6	VvACS6	P\$AHBP	Arabidopsi P\$WUS.01 Homeodon	0.94
VvACS9	VvACS9	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACS9	VvACS9	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACS9	VvACS9	P\$AHBP	Arabidopsi P\$WUS.01 Homeodon	0.94
VvACS9	VvACS9	P\$AHBP	Arabidopsi P\$ATHB21 Homeobox	0.84
VvACS9	VvACS9	P\$AHBP	Arabidopsi P\$WUS.01 Homeodon	0.94
VvACS9	VvACS9	P\$AHBP	Arabidopsi P\$ATHB9. PHAVOLU	0.83
VvACS9	VvACS9	P\$AHBP	Arabidopsi P\$ATHB34 Homeobox	0.89
VvACO1	VvACO1	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACO1	VvACO1	P\$AHBP	Arabidopsi P\$ATHB40 Homeobox	0.84
VvACO1	VvACO1	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACO1	VvACO1	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACO1	VvACO1	P\$AHBP	Arabidopsi P\$ATHB15 Homeobox	0.83
VvACO1	VvACO1	P\$AHBP	Arabidopsi P\$ATHB15 Homeobox	0.83
VvACO1	VvACO1	P\$AHBP	Arabidopsi P\$ATHB40 Homeobox	0.84
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB9. HD-ZIP cla	0.77
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB23 Homeobox	0.84
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB25 Homeobox	0.85
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB23 Homeobox	0.84
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB15 Homeobox	0.83
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB23 Homeobox	0.84
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$WUS.01 Homeodon	0.94
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB6. Homeobox	0.95
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB34 Homeobox	0.89
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB20 Homeobox	0.83
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB5. Homeobox	0.86
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB23 Homeobox	0.84
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB1. Arabidopsi:	0.9
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB13 Homeobox	0.89
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$ATHB6. Homeobox	0.95
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACO2	VvACO2	P\$AHBP	Arabidopsi P\$WUS.01 Homeodon	0.94
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB1. Arabidopsi:	0.9
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB34 Homeobox	0.89
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB5. Homeobox	0.86
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB5. Homeobox	0.86
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB5. HDZip clas	0.89
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB24 Homeobox	0.84
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$REVOLI Homeobox	0.93
VvACO4	VvACO4	P\$AHBP	Arabidopsi P\$ATHB32 Homeobox	0.92
VvACS4	VvACS4	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS4	VvACS4	P\$AHBP	Arabidopsi P\$ATHB5. Homeobox	0.86
VvACS4	VvACS4	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9
VvACS4	VvACS4	P\$AHBP	Arabidopsi P\$BLR.01 Transcript	0.9

VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB34	Homeobox	0.89
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB32	Homeobox	0.92
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$BLR.01	Transcript	0.9
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$BLR.01	Transcript	0.9
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB51	Late Merist	0.83
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB24	Homeobox	0.84
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB24	Homeobox	0.84
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$BLR.01	Transcript	0.9
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB24	Homeobox	0.84
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB23	Homeobox	0.84
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$WUS.01	Homeodon	0.94
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB24	Homeobox	0.84
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$HAHB4.	Sunflower	0.87
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$HAHB4.	Sunflower	0.87
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$HAHB4.	Sunflower	0.87
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$WUS.01	Homeodon	0.94
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB25	Homeobox	0.85
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$WUS.01	Homeodon	0.94
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB6.	Homeobox	0.95
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB34	Homeobox	0.89
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB20	Homeobox	0.83
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB23	Homeobox	0.84
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB34	Homeobox	0.89
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$BLR.01	Transcript	0.9
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$BLR.01	Transcript	0.9
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB34	Homeobox	0.89
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB23	Homeobox	0.84
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB34	Homeobox	0.89
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB1.	Arabidopsi:	0.9
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB25	Homeobox	0.85
VvACS4	VvACS4	P\$AHBP	Arabidopsi	P\$ATHB32	Homeobox	0.92

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix Info	Opt.
VvACS1	VvACS1	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS1	VvACS1	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS1	VvACS1	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS2	VvACS2	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS2	VvACS2	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS2	VvACS2	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACO1	VvACO1	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACO2	VvACO2	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACO2	VvACO2	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACO4	VvACO4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACO4	VvACO4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86
VvACS4	VvACS4	P\$AHLF	AT-hook	cc	P\$AHL20.	(AT-hook m	0.86

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix Info	Opt.
VvACS2	VvACS2	P\$AP2L	APETALA2	P\$TOE2.0	Target of e	0.8	
VvACS2	VvACS2	P\$AP2L	APETALA2	P\$TOE2.0	Target of e	0.8	
VvACS6	VvACS6	P\$AP2L	APETALA2	P\$TOE2.0	Target of e	0.8	
VvACS9	VvACS9	P\$AP2L	APETALA2	P\$SMZ.01	Ethylene-r	0.85	

VvACS9	VvACS9		P\$AP2L	APETALA2	P\$SMZ.01	Ethylene-r	0.85	
VvACO1	VvACO1		P\$AP2L	APETALA2	P\$SMZ.01	Ethylene-r	0.85	
<b>Seq. name</b>	<b>accession</b>	<b>Gene symbl</b>	<b>GeneID</b>	<b>Family</b>	<b>Family Info</b>	<b>Matrix</b>	<b>Matrix Info</b>	<b>Opt.</b>
VvACS6	VvACS6		P\$AREF	Auxin resp	P\$ARE.01	Auxin Resp	0.93	
<b>Seq. name</b>	<b>accession</b>	<b>Gene symbl</b>	<b>GeneID</b>	<b>Family</b>	<b>Family Info</b>	<b>Matrix</b>	<b>Matrix Info</b>	<b>Opt.</b>
VvACS6	VvACS6		P\$ARF3	Auxin Resp	P\$ETT.01	ETTIN (Au:	0.83	
VvACO2	VvACO2		P\$ARF3	Auxin Resp	P\$ETT.02	ETTIN (sec	0.83	
VvACO4	VvACO4		P\$ARF3	Auxin Resp	P\$ETT.01	ETTIN (Au:	0.83	
<b>Seq. name</b>	<b>accession</b>	<b>Gene symbl</b>	<b>GeneID</b>	<b>Family</b>	<b>Family Info</b>	<b>Matrix</b>	<b>Matrix Info</b>	<b>Opt.</b>
VvACS2	VvACS2		P\$ARID	ARID/BRIC	P\$AT1G20	ARID/BRIC	0.93	
VvACO2	VvACO2		P\$ARID	ARID/BRIC	P\$AT1G20	ARID/BRIC	0.93	
VvACO2	VvACO2		P\$ARID	ARID/BRIC	P\$AT1G20	ARID/BRIC	0.93	
VvACS4	VvACS4		P\$ARID	ARID/BRIC	P\$AT1G20	ARID/BRIC	0.93	
VvACS4	VvACS4		P\$ARID	ARID/BRIC	P\$AT1G20	ARID/BRIC	0.93	
<b>Seq. name</b>	<b>accession</b>	<b>Gene symbl</b>	<b>GeneID</b>	<b>Family</b>	<b>Family Info</b>	<b>Matrix</b>	<b>Matrix Info</b>	<b>Opt.</b>
VvACS1	VvACS1		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
VvACS1	VvACS1		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
VvACS2	VvACS2		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
VvACS2	VvACS2		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
VvACS9	VvACS9		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
VvACO1	VvACO1		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
VvACO1	VvACO1		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
VvACO2	VvACO2		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
VvACO4	VvACO4		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
VvACS4	VvACS4		P\$ASRC	AS1/AS2 r	P\$AS1_AS	AS1/AS2 r	0.86	
<b>Seq. name</b>	<b>accession</b>	<b>Gene symbl</b>	<b>GeneID</b>	<b>Family</b>	<b>Family Info</b>	<b>Matrix</b>	<b>Matrix Info</b>	<b>Opt.</b>
VvACS1	VvACS1		P\$BRRE	Brassinost	P\$BZR1.0	Brassinazo	0.83	
VvACS6	VvACS6		P\$BRRE	Brassinost	P\$BZR1.0	Brassinazo	0.95	
<b>Seq. name</b>	<b>accession</b>	<b>Gene symbl</b>	<b>GeneID</b>	<b>Family</b>	<b>Family Info</b>	<b>Matrix</b>	<b>Matrix Info</b>	<b>Opt.</b>
VvACS1	VvACS1		P\$C3HF	CCCH dor	P\$AT3G12	KH and zin	0.99	
VvACS1	VvACS1		P\$C3HF	CCCH dor	P\$AT3G12	KH and zin	0.99	
VvACS1	VvACS1		P\$C3HF	CCCH dor	P\$AT3G12	KH and zin	0.99	
VvACS2	VvACS2		P\$C3HF	CCCH dor	P\$AT3G12	KH and zin	0.99	
VvACS6	VvACS6		P\$C3HF	CCCH dor	P\$AT3G12	KH and zin	0.99	
VvACS9	VvACS9		P\$C3HF	CCCH dor	P\$ZF67.01	Zinc finge	0.96	
VvACO2	VvACO2		P\$C3HF	CCCH dor	P\$AT3G12	KH and zin	0.99	
VvACO2	VvACO2		P\$C3HF	CCCH dor	P\$AT3G12	KH and zin	0.99	
VvACO4	VvACO4		P\$C3HF	CCCH dor	P\$ZF67.01	Zinc finge	0.96	
<b>Seq. name</b>	<b>accession</b>	<b>Gene symbl</b>	<b>GeneID</b>	<b>Family</b>	<b>Family Info</b>	<b>Matrix</b>	<b>Matrix Info</b>	<b>Opt.</b>
VvACS2	VvACS2		P\$CAAT	CCAAT bin	P\$CAAT.0	CCAAT-bo:	0.97	
VvACS2	VvACS2		P\$CAAT	CCAAT bin	P\$CAAT.0	CCAAT-bo:	0.97	
VvACO1	VvACO1		P\$CAAT	CCAAT bin	P\$CAAT.0	CCAAT-bo:	0.97	
VvACO2	VvACO2		P\$CAAT	CCAAT bin	P\$CAAT.0	CCAAT-bo:	0.97	
<b>Seq. name</b>	<b>accession</b>	<b>Gene symbl</b>	<b>GeneID</b>	<b>Family</b>	<b>Family Info</b>	<b>Matrix</b>	<b>Matrix Info</b>	<b>Opt.</b>
VvACO1	VvACO1		P\$CARM	CA-rich mc	P\$CARIC-	CA-rich el	0.78	
VvACS4	VvACS4		P\$CARM	CA-rich mc	P\$CARIC-	CA-rich el	0.78	
<b>Seq. name</b>	<b>accession</b>	<b>Gene symbl</b>	<b>GeneID</b>	<b>Family</b>	<b>Family Info</b>	<b>Matrix</b>	<b>Matrix Info</b>	<b>Opt.</b>
VvACS1	VvACS1		P\$CCAF	Circadian c	P\$EE.01	Evening el	0.84	
VvACS1	VvACS1		P\$CCAF	Circadian c	P\$EE.01	Evening el	0.84	

VvACS1	VvACS1	P\$CCAF	Circadian cP\$RVE1.0 Myb family	0.83
VvACS1	VvACS1	P\$CCAF	Circadian cP\$LHY.01 LATE ELO	0.85
VvACS1	VvACS1	P\$CCAF	Circadian cP\$RVE1.0 Myb family	0.83
VvACS2	VvACS2	P\$CCAF	Circadian cP\$LHY1.0' Late elong;	0.84
VvACS2	VvACS2	P\$CCAF	Circadian cP\$CCA1.0 Circadian c	0.85
VvACS2	VvACS2	P\$CCAF	Circadian cP\$EPR1.0 Early-phyt	0.83
VvACS2	VvACS2	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACS2	VvACS2	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACS2	VvACS2	P\$CCAF	Circadian cP\$AT3G10 Myb family	0.84
VvACS2	VvACS2	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACS6	VvACS6	P\$CCAF	Circadian cP\$EPR1.0 Early-phyt	0.83
VvACS6	VvACS6	P\$CCAF	Circadian cP\$LHY1.0' Late elong;	0.84
VvACS9	VvACS9	P\$CCAF	Circadian cP\$AT3G10 Myb family	0.84
VvACS9	VvACS9	P\$CCAF	Circadian cP\$CCA1.0 Circadian c	0.8
VvACO1	VvACO1	P\$CCAF	Circadian cP\$CCA1.0 Circadian	0.92
VvACO1	VvACO1	P\$CCAF	Circadian cP\$CCA1.0 Circadian	0.92
VvACO1	VvACO1	P\$CCAF	Circadian cP\$LHY1.0' Late elong;	0.84
VvACO1	VvACO1	P\$CCAF	Circadian cP\$LHY1.0' Late elong;	0.84
VvACO2	VvACO2	P\$CCAF	Circadian cP\$CCA1.0 Circadian c	0.85
VvACO2	VvACO2	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACO2	VvACO2	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACO2	VvACO2	P\$CCAF	Circadian cP\$AT3G10 Myb family	0.84
VvACO2	VvACO2	P\$CCAF	Circadian cP\$LHY1.0' Late elong;	0.84
VvACO4	VvACO4	P\$CCAF	Circadian cP\$AT3G10 Myb family	0.84
VvACO4	VvACO4	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACO4	VvACO4	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACO4	VvACO4	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACO4	VvACO4	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACO4	VvACO4	P\$CCAF	Circadian cP\$CCA1.0 Circadian	0.92
VvACS4	VvACS4	P\$CCAF	Circadian cP\$CCA1.0 Circadian c	0.85
VvACS4	VvACS4	P\$CCAF	Circadian cP\$CCA1.0 Circadian c	0.85
VvACS4	VvACS4	P\$CCAF	Circadian cP\$LHY1.0' Late elong;	0.84
VvACS4	VvACS4	P\$CCAF	Circadian cP\$EPR1.0 Early-phyt	0.83
VvACS4	VvACS4	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACS4	VvACS4	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACS4	VvACS4	P\$CCAF	Circadian cP\$CCA1.0 Circadian c	0.85
VvACS4	VvACS4	P\$CCAF	Circadian cP\$CCA1.0 Circadian c	0.85
VvACS4	VvACS4	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACS4	VvACS4	P\$CCAF	Circadian cP\$EE.01 Evening el	0.84
VvACS4	VvACS4	P\$CCAF	Circadian cP\$CCA1.0 Circadian c	0.85
VvACS4	VvACS4	P\$CCAF	Circadian cP\$CCA1.0 Circadian c	0.85
VvACS4	VvACS4	P\$CCAF	Circadian cP\$AT3G10 Myb family	0.84
VvACS4	VvACS4	P\$CCAF	Circadian cP\$LHY.01 LATE ELO	0.85

Seq. name	accession	GeneID	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS2	VvACS2		P\$CE1F	Coupling e	P\$SBOX.0	Sugar and	0.87

Seq. name	accession	GeneID	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$CGCG	Calmodulir	P\$ATSR1.	Arabidopsi:	0.84
VvACS6	VvACS6		P\$CGCG	Calmodulir	P\$OSCBT.	Oryza sativ	0.78

Seq. name	accession	GeneID	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS2	VvACS2		P\$CNAC	Calcium re	P\$CBNAC	Calmodulir	0.85
VvACS9	VvACS9		P\$CNAC	Calcium re	P\$CBNAC	Calmodulir	0.85
VvACO2	VvACO2		P\$CNAC	Calcium re	P\$CBNAC	Calmodulir	0.85
VvACO2	VvACO2		P\$CNAC	Calcium re	P\$CBNAC	Calmodulir	0.85
VvACO4	VvACO4		P\$CNAC	Calcium re	P\$CBNAC	Calmodulir	1
VvACS4	VvACS4		P\$CNAC	Calcium re	P\$CBNAC	Calmodulir	0.85

Seq. name	accession	gene symbol	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACS1	VvACS1			P\$DOFF	DNA bindir	P\$HCA2.0	High Camb		0.99
VvACS1	VvACS1			P\$DOFF	DNA bindir	P\$OBP1.0	Dof zinc fi		0.99
VvACS1	VvACS1			P\$DOFF	DNA bindir	P\$OBP3.0	Zinc finger		0.96
VvACS1	VvACS1			P\$DOFF	DNA bindir	P\$DOF3.5	Dof zinc f		0.96
VvACS1	VvACS1			P\$DOFF	DNA bindir	P\$DOF1.0	Dof1 / MNE		0.98
VvACS1	VvACS1			P\$DOFF	DNA bindir	P\$DOF3.5	Dof zinc f		0.96
VvACS2	VvACS2			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACS2	VvACS2			P\$DOFF	DNA bindir	P\$PBOX.0	Prolamin b		0.75
VvACS6	VvACS6			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACS6	VvACS6			P\$DOFF	DNA bindir	P\$DOF4.2	Dof zinc fi		0.88
VvACS6	VvACS6			P\$DOFF	DNA bindir	P\$DOF1.0	Dof1 / MNE		0.98
VvACS6	VvACS6			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACS9	VvACS9			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACS9	VvACS9			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACS9	VvACS9			P\$DOFF	DNA bindir	P\$DOF2.0	Dof2 - sing		0.98
VvACS9	VvACS9			P\$DOFF	DNA bindir	P\$PBOX.0	Prolamin b		0.75
VvACS9	VvACS9			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACS9	VvACS9			P\$DOFF	DNA bindir	P\$PBOX.0	Prolamin b		0.75
VvACO1	VvACO1			P\$DOFF	DNA bindir	P\$PBOX.0	Prolamin b		0.75
VvACO1	VvACO1			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACO1	VvACO1			P\$DOFF	DNA bindir	P\$PBOX.0	Prolamin b		0.75
VvACO2	VvACO2			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACO2	VvACO2			P\$DOFF	DNA bindir	P\$DOF5.1	Dof zinc f		0.98
VvACO2	VvACO2			P\$DOFF	DNA bindir	P\$PBF.01	PBF (MPBI		0.97
VvACO2	VvACO2			P\$DOFF	DNA bindir	P\$OBP1.0	Dof zinc fi		0.99
VvACO2	VvACO2			P\$DOFF	DNA bindir	P\$OBP4.0	Dof zinc fi		0.97
VvACO2	VvACO2			P\$DOFF	DNA bindir	P\$DOF3.0	Dof3 - sing		0.99
VvACO2	VvACO2			P\$DOFF	DNA bindir	P\$PBOX.0	Prolamin b		0.75
VvACO2	VvACO2			P\$DOFF	DNA bindir	P\$DOF1.6	Dof zinc f		0.93
VvACO4	VvACO4			P\$DOFF	DNA bindir	P\$PBOX.0	Prolamin b		0.75
VvACO4	VvACO4			P\$DOFF	DNA bindir	P\$DOF1.6	Dof zinc f		0.93
VvACO4	VvACO4			P\$DOFF	DNA bindir	P\$DOF3.5	Dof zinc f		0.96
VvACO4	VvACO4			P\$DOFF	DNA bindir	P\$DOF3.0	Dof3 - sing		0.99
VvACO4	VvACO4			P\$DOFF	DNA bindir	P\$DOF2.0	Dof2 - sing		0.98
VvACO4	VvACO4			P\$DOFF	DNA bindir	P\$DOF2.0	Dof2 - sing		0.98
VvACO4	VvACO4			P\$DOFF	DNA bindir	P\$DOF4.2	Dof zinc fi		0.88
VvACO4	VvACO4			P\$DOFF	DNA bindir	P\$DOF3.0	Dof3 - sing		0.99
VvACS4	VvACS4			P\$DOFF	DNA bindir	P\$DOF3.0	Dof3 - sing		0.99
VvACS4	VvACS4			P\$DOFF	DNA bindir	P\$PBOX.0	Prolamin b		0.75
VvACS4	VvACS4			P\$DOFF	DNA bindir	P\$DAG2.0	DOF Affect		0.92
VvACS4	VvACS4			P\$DOFF	DNA bindir	P\$DOF1.0	Dof1 / MNE		0.98

Seq. name	accession	gene symbol	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS9	VvACS9			P\$DPBF	Dc3 promo	P\$DPBF.0	bZIP factor		0.89

Seq. name	accession	gene symbol	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$DREB	Dehydratio	P\$DDF2.0	Dwarf and		0.81
VvACS6	VvACS6			P\$DREB	Dehydratio	P\$DDF2.0	Dwarf and		0.81
VvACS6	VvACS6			P\$DREB	Dehydratio	P\$DDF2.0	Dwarf and		0.81
VvACS6	VvACS6			P\$DREB	Dehydratio	P\$DDF2.0	Dwarf and		0.81
VvACS6	VvACS6			P\$DREB	Dehydratio	P\$DEAR3.	DREB and		0.85
VvACS6	VvACS6			P\$DREB	Dehydratio	P\$ERF039	Ethylene-r		0.89
VvACS6	VvACS6			P\$DREB	Dehydratio	P\$AT1G12	Dehydratio		0.87
VvACS9	VvACS9			P\$DREB	Dehydratio	P\$RAP2.1.	Ethylene-re		0.77
VvACO2	VvACO2			P\$DREB	Dehydratio	P\$CRT_DF	C-repeat/d		0.89

VvACO2	VvACO2		P\$DREB	Dehydratio	P\$DDF1.0	Dwarf and	0.86
VvACO2	VvACO2		P\$DREB	Dehydratio	P\$DDF1.0	Dwarf and	0.86
VvACO4	VvACO4		P\$DREB	Dehydratio	P\$ERF023	Ethylene-r	0.8

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACO2	VvACO2		P\$EINL	Ethylen ins	P\$EIN3.01	Protein eth	0.82	
VvACO2	VvACO2		P\$EINL	Ethylen ins	P\$EIN3.01	Protein eth	0.82	

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS1	VvACS1		P\$EPFF	EPF-type z	P\$STZ.01	Salt tolera	0.99	
VvACS2	VvACS2		P\$EPFF	EPF-type z	P\$STZ.01	Salt tolera	0.99	
VvACS6	VvACS6		P\$EPFF	EPF-type z	P\$ZPT22.0	Member of	0.75	
VvACS4	VvACS4		P\$EPFF	EPF-type z	P\$STZ.01	Salt tolera	0.99	

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACO1	VvACO1		P\$EREF	Ethylen re	P\$ANT.01	ANT (Arabi	0.81	

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS1	VvACS1		P\$FLO2	Floral hom	P\$AP2.01	APETALA2	0.87	
VvACS2	VvACS2		P\$FLO2	Floral hom	P\$AP2.01	APETALA2	0.87	
VvACS9	VvACS9		P\$FLO2	Floral hom	P\$AP2.01	APETALA2	0.87	
VvACO2	VvACO2		P\$FLO2	Floral hom	P\$AP2.01	APETALA2	0.87	
VvACO4	VvACO4		P\$FLO2	Floral hom	P\$AP2.01	APETALA2	0.87	
VvACS4	VvACS4		P\$FLO2	Floral hom	P\$AP2.01	APETALA2	0.87	

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACO1	VvACO1		P\$FORC	Fungal anc	P\$FORCA	Promoter n	0.85	
VvACO2	VvACO2		P\$FORC	Fungal anc	P\$FORCA	Promoter n	0.85	
VvACO2	VvACO2		P\$FORC	Fungal anc	P\$FORCA	Promoter n	0.85	

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS6	VvACS6		P\$GAGA	GAGA eler	P\$BPC.01	Basic pent	1	

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS2	VvACS2		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	
VvACO1	VvACO1		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	
VvACO1	VvACO1		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	
VvACO1	VvACO1		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	
VvACO2	VvACO2		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	
VvACO2	VvACO2		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	
VvACO2	VvACO2		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	
VvACO4	VvACO4		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	
VvACO4	VvACO4		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	
VvACS4	VvACS4		P\$GAPB	GAP-Box (	P\$GAP.01	Cis-elemer	0.88	

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS1	VvACS1		P\$GARP	Myb-relate	P\$ARR14.	Two-compr	0.87	
VvACS9	VvACS9		P\$GARP	Myb-relate	P\$ARR11.	Two-compr	0.85	
VvACS9	VvACS9		P\$GARP	Myb-relate	P\$ARR10.	Type-B res	0.97	
VvACO1	VvACO1		P\$GARP	Myb-relate	P\$ARR10.	Type-B res	0.97	
VvACO1	VvACO1		P\$GARP	Myb-relate	P\$ARR10.	Type-B res	0.97	
VvACO2	VvACO2		P\$GARP	Myb-relate	P\$ARR10.	Type-B res	0.97	

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACO1	VvACO1		P\$GAZL	GA- and AI	P\$GAL3.0	GAZ-like 3	0.88	

Seq. name	accession	niene symb	GenID	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS1	VvACS1		P\$GBOX	Plant G-bo	P\$OSBZ8.	Oryza sativ	0.84	

VvACS1	VvACS1	P\$GBOX	Plant G-bo	P\$GBF1.0	bZIP protei	0.94
VvACS1	VvACS1	P\$GBOX	Plant G-bo	P\$ABZ1.0	Anaerobic	0.91
VvACS9	VvACS9	P\$GBOX	Plant G-bo	P\$ABZ1.0	Anaerobic	0.91
VvACO2	VvACO2	P\$GBOX	Plant G-bo	P\$GBF1.0	bZIP protei	0.94

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix Info	Opt.
VvACS6	VvACS6	P\$GCCF	GCC box f:	P\$ERE_JE	Ethylene-r		0.85
VvACS9	VvACS9	P\$GCCF	GCC box f:	P\$RAP2-6	Ethylene-re		0.87
VvACO2	VvACO2	P\$GCCF	GCC box f:	P\$RAP2-6	Ethylene-re		0.87

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix Info	Opt.
VvACS1	VvACS1	P\$GLKF	Golden2-lit	P\$AT2G40	G2-like fan		0.92
VvACS1	VvACS1	P\$GLKF	Golden2-lit	P\$AT2G40	G2-like fan		0.92
VvACS1	VvACS1	P\$GLKF	Golden2-lit	P\$PHL2.0	PHR1-like		0.95
VvACS1	VvACS1	P\$GLKF	Golden2-lit	P\$AT3G12	Myb family		0.9
VvACS2	VvACS2	P\$GLKF	Golden2-lit	P\$AT2G40	G2-like fan		0.92
VvACS6	VvACS6	P\$GLKF	Golden2-lit	P\$AT2G40	G2-like fan		0.92
VvACS6	VvACS6	P\$GLKF	Golden2-lit	P\$PHL2.0	PHR1-like		0.95
VvACS6	VvACS6	P\$GLKF	Golden2-lit	P\$AT2G40	G2-like fan		0.92
VvACS9	VvACS9	P\$GLKF	Golden2-lit	P\$PHL2.0	PHR1-like		0.95
VvACS9	VvACS9	P\$GLKF	Golden2-lit	P\$AT2G40	G2-like fan		0.92
VvACS9	VvACS9	P\$GLKF	Golden2-lit	P\$AT3G12	Myb family		0.9
VvACO2	VvACO2	P\$GLKF	Golden2-lit	P\$AT3G12	Myb family		0.9
VvACO2	VvACO2	P\$GLKF	Golden2-lit	P\$UIF1.01	ULT1 inter		0.88
VvACS4	VvACS4	P\$GLKF	Golden2-lit	P\$AT2G40	G2-like fan		0.92
VvACS4	VvACS4	P\$GLKF	Golden2-lit	P\$PHL2.0	PHR1-like		0.95

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix Info	Opt.
VvACS9	VvACS9	P\$GRFF	Growth reg	P\$ATGRF5	Growth-reg		0.93
VvACS9	VvACS9	P\$GRFF	Growth reg	P\$ATGRF5	Growth-reg		0.93

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix Info	Opt.
VvACS1	VvACS1	P\$GTBX	GT-box ele	P\$S1F.01	S1F, site 1		0.79
VvACS1	VvACS1	P\$GTBX	GT-box ele	P\$GT1.01	GT1-Box b		0.85
VvACS1	VvACS1	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS1	VvACS1	P\$GTBX	GT-box ele	P\$GT1.01	GT1-Box b		0.85
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$ASIL1.0	Arabidopsi		0.93
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$GTL1.0	Trihelix tr		0.88
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$GTL1.0	Trihelix tr		0.88
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$GTL1.0	Trihelix tr		0.88
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$GT1.02	Trihelix tra		0.81
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$GT1.01	GT1-Box b		0.85
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$S1F.01	S1F, site 1		0.79
VvACS2	VvACS2	P\$GTBX	GT-box ele	P\$S1F.01	S1F, site 1		0.79
VvACS6	VvACS6	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS6	VvACS6	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS6	VvACS6	P\$GTBX	GT-box ele	P\$S1F.01	S1F, site 1		0.79
VvACS6	VvACS6	P\$GTBX	GT-box ele	P\$S1F.01	S1F, site 1		0.79
VvACS9	VvACS9	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS9	VvACS9	P\$GTBX	GT-box ele	P\$GT3A.0	Trihelix DN		0.83
VvACS9	VvACS9	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS9	VvACS9	P\$GTBX	GT-box ele	P\$SBF1.0	SBF-1		0.87
VvACS9	VvACS9	P\$GTBX	GT-box ele	P\$GT2L.0	Trihelix tr		0.87
VvACO1	VvACO1	P\$GTBX	GT-box ele	P\$GT1.01	GT1-Box b		0.85
VvACO1	VvACO1	P\$GTBX	GT-box ele	P\$GT1.01	GT1-Box b		0.85
VvACO1	VvACO1	P\$GTBX	GT-box ele	P\$GTL1.0	Trihelix tr		0.88

VvACO2	VvACO2	P\$GTBX	GT-box ele P\$S1F.01	S1F, site 1	0.79
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$S1F.01	S1F, site 1	0.79
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$GT1.01	GT1-Box b	0.85
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$GT1.02	Trihelix tra	0.81
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$GT2.01	Trihelix tra	0.89
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$GTL1.0	Trihelix tr	0.88
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$S1F.01	S1F, site 1	0.79
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO2	VvACO2	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO4	VvACO4	P\$GTBX	GT-box ele P\$GT1.01	GT1-Box b	0.85
VvACO4	VvACO4	P\$GTBX	GT-box ele P\$GTL1.0	Trihelix tr	0.88
VvACO4	VvACO4	P\$GTBX	GT-box ele P\$S1F.01	S1F, site 1	0.79
VvACO4	VvACO4	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACO4	VvACO4	P\$GTBX	GT-box ele P\$GT1.01	GT1-Box b	0.85
VvACO4	VvACO4	P\$GTBX	GT-box ele P\$S1F.01	S1F, site 1	0.79
VvACO4	VvACO4	P\$GTBX	GT-box ele P\$GT1.01	GT1-Box b	0.85
VvACO4	VvACO4	P\$GTBX	GT-box ele P\$GT2_G1	GT2-box a	0.92
VvACO4	VvACO4	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACS4	VvACS4	P\$GTBX	GT-box ele P\$GTL1.0	Trihelix tr	0.88
VvACS4	VvACS4	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACS4	VvACS4	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACS4	VvACS4	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACS4	VvACS4	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACS4	VvACS4	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACS4	VvACS4	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87
VvACS4	VvACS4	P\$GTBX	GT-box ele P\$GTL1.0	Trihelix tr	0.88
VvACS4	VvACS4	P\$GTBX	GT-box ele P\$SBF1.0	SBF-1	0.87

Seq. name	Accession	Gene symbol	GenelD	Matrix	Family Info	Matrix Info	Opt.
VvACS1	VvACS1	P\$HEAT	Heat shock	P\$HSE.01	Heat shock	0.81	
VvACS1	VvACS1	P\$HEAT	Heat shock	P\$HSE.01	Heat shock	0.81	
VvACS1	VvACS1	P\$HEAT	Heat shock	P\$HSFA6E	Heat stress	0.81	
VvACS1	VvACS1	P\$HEAT	Heat shock	P\$HSFB2/	Heat shock	0.85	
VvACS1	VvACS1	P\$HEAT	Heat shock	P\$HSFB2/	Heat stress	0.81	
VvACS1	VvACS1	P\$HEAT	Heat shock	P\$HSFC1.	Heat shock	0.84	
VvACS2	VvACS2	P\$HEAT	Heat shock	P\$HSFB3.	Heat stress	0.83	
VvACS2	VvACS2	P\$HEAT	Heat shock	P\$HSE.01	Heat shock	0.81	
VvACS2	VvACS2	P\$HEAT	Heat shock	P\$HSFB2/	Heat shock	0.85	
VvACS2	VvACS2	P\$HEAT	Heat shock	P\$HSFA6E	Heat stress	0.81	
VvACS2	VvACS2	P\$HEAT	Heat shock	P\$HSE.01	Heat shock	0.81	
VvACS2	VvACS2	P\$HEAT	Heat shock	P\$HSFA4/	Heat stress	0.81	
VvACS6	VvACS6	P\$HEAT	Heat shock	P\$HSFB3.	Heat stress	0.83	
VvACS6	VvACS6	P\$HEAT	Heat shock	P\$HSFB3.	Heat stress	0.83	
VvACS6	VvACS6	P\$HEAT	Heat shock	P\$HSFB3.	Heat stress	0.83	
VvACS6	VvACS6	P\$HEAT	Heat shock	P\$HSFB3.	Heat stress	0.83	
VvACS9	VvACS9	P\$HEAT	Heat shock	P\$HSFB3.	Heat stress	0.83	
VvACS9	VvACS9	P\$HEAT	Heat shock	P\$HSFA4/	Heat stress	0.81	
VvACS9	VvACS9	P\$HEAT	Heat shock	P\$HSFA6E	Heat stress	0.81	
VvACS9	VvACS9	P\$HEAT	Heat shock	P\$HSFA1/	Arabidopsi	0.75	
VvACS9	VvACS9	P\$HEAT	Heat shock	P\$HSFA1E	Heat stress	0.8	
VvACS9	VvACS9	P\$HEAT	Heat shock	P\$HSFA6E	Heat stress	0.81	

VvACS9	VvACS9		P\$HEAT	Heat shock P\$HSFA6E	Heat stress	0.81
VvACS9	VvACS9		P\$HEAT	Heat shock P\$HSFA1A	Arabidopsi	0.75
VvACS9	VvACS9		P\$HEAT	Heat shock P\$HSFB3.	Heat stress	0.83
VvACO1	VvACO1		P\$HEAT	Heat shock P\$HSE.01	Heat shock	0.81
VvACO1	VvACO1		P\$HEAT	Heat shock P\$HSFC1.	Heat shock	0.86
VvACO1	VvACO1		P\$HEAT	Heat shock P\$HSFB3.	Heat stress	0.83
VvACO1	VvACO1		P\$HEAT	Heat shock P\$HSFC1.	Heat shock	0.86
VvACO1	VvACO1		P\$HEAT	Heat shock P\$HSE.01	Heat shock	0.81
VvACO2	VvACO2		P\$HEAT	Heat shock P\$HSE.01	Heat shock	0.81
VvACO4	VvACO4		P\$HEAT	Heat shock P\$HSFB3.	Heat stress	0.83
VvACS4	VvACS4		P\$HEAT	Heat shock P\$HSFB2A	Heat shock	0.85

Seq. name	accession	gene symb	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		1
VvACS1	VvACS1		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		1
VvACS2	VvACS2		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		1
VvACS2	VvACS2		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89
VvACS2	VvACS2		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89
VvACS2	VvACS2		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89
VvACS2	VvACS2		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89
VvACS2	VvACS2		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89
VvACS6	VvACS6		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89
VvACO2	VvACO2		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		1
VvACS4	VvACS4		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89
VvACS4	VvACS4		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89
VvACS4	VvACS4		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89
VvACS4	VvACS4		P\$HMGF	High mobil	P\$HMG_1Y	High mobili		0.89

Seq. name	accession	gene symb	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$HOCT	Octamer m	P\$HOCT.0	Octamer m		0.76

Seq. name	accession	gene symb	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACS2	VvACS2		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACS2	VvACS2		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACS2	VvACS2		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACS6	VvACS6		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACS6	VvACS6		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACS9	VvACS9		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO1	VvACO1		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO1	VvACO1		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO2	VvACO2		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO2	VvACO2		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO2	VvACO2		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO2	VvACO2		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO4	VvACO4		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO4	VvACO4		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO4	VvACO4		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACO4	VvACO4		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACS4	VvACS4		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACS4	VvACS4		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93
VvACS4	VvACS4		P\$IBOX	Plant I-Box	P\$GATA.0	Class I GA		0.93

Seq. name	accession	gene symb	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$IDDF	ID domain	P\$ID1.01	Maize INDI		0.92
VvACS1	VvACS1		P\$IDDF	ID domain	P\$ID1.01	Maize INDI		0.92
VvACS1	VvACS1		P\$IDDF	ID domain	P\$ID1.01	Maize INDI		0.92
VvACS9	VvACS9		P\$IDDF	ID domain	P\$ID1.01	Maize INDI		0.92
VvACO2	VvACO2		P\$IDDF	ID domain	P\$ID1.01	Maize INDI		0.92

Seq. name	accession	gene symbol	GeneID	matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$JARE	Jasmonate	P\$JARE.0	Jasmonate		0.75
VvACS1	VvACS1			P\$JARE	Jasmonate	P\$JARE.0	Jasmonate		0.75
VvACS1	VvACS1			P\$JARE	Jasmonate	P\$JARE.0	Jasmonate		0.75
VvACO1	VvACO1			P\$JARE	Jasmonate	P\$JARE.0	Jasmonate		0.75
VvACO1	VvACO1			P\$JARE	Jasmonate	P\$JARE.0	Jasmonate		0.75
VvACO4	VvACO4			P\$JARE	Jasmonate	P\$JARE.0	Jasmonate		0.75

Seq. name	accession	gene symbol	GeneID	matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$KAN1	Transcript	P\$AT5G45	G2-like fan		0.87
VvACS1	VvACS1			P\$KAN1	Transcript	P\$EFM.01	Early Flow		0.85
VvACS1	VvACS1			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS1	VvACS1			P\$KAN1	Transcript	P\$AT2G20	Myb-like H		0.82
VvACS1	VvACS1			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS1	VvACS1			P\$KAN1	Transcript	P\$AT5G45	G2-like fan		0.87
VvACS2	VvACS2			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS2	VvACS2			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS2	VvACS2			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS2	VvACS2			P\$KAN1	Transcript	P\$EFM.01	Early Flow		0.85
VvACS2	VvACS2			P\$KAN1	Transcript	P\$EFM.01	Early Flow		0.85
VvACS6	VvACS6			P\$KAN1	Transcript	P\$EFM.01	Early Flow		0.85
VvACS6	VvACS6			P\$KAN1	Transcript	P\$EFM.01	Early Flow		0.85
VvACS6	VvACS6			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS6	VvACS6			P\$KAN1	Transcript	P\$EFM.01	Early Flow		0.85
VvACS6	VvACS6			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS6	VvACS6			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS6	VvACS6			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS6	VvACS6			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS9	VvACS9			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS9	VvACS9			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS9	VvACS9			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS9	VvACS9			P\$KAN1	Transcript	P\$AT5G45	G2-like fan		0.87
VvACS9	VvACS9			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS9	VvACS9			P\$KAN1	Transcript	P\$AT5G45	G2-like fan		0.87
VvACO1	VvACO1			P\$KAN1	Transcript	P\$KAN4.0	KANADI 4		0.83
VvACO1	VvACO1			P\$KAN1	Transcript	P\$EFM.01	Early Flow		0.85
VvACO1	VvACO1			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACO1	VvACO1			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACO2	VvACO2			P\$KAN1	Transcript	P\$AT5G45	G2-like fan		0.87
VvACO2	VvACO2			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACO2	VvACO2			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACO2	VvACO2			P\$KAN1	Transcript	P\$KAN4.0	KANADI 4		0.78
VvACO2	VvACO2			P\$KAN1	Transcript	P\$AT5G45	G2-like fan		0.87
VvACO4	VvACO4			P\$KAN1	Transcript	P\$AT2G20	Myb-like H		0.82
VvACO4	VvACO4			P\$KAN1	Transcript	P\$KAN4.0	KANADI 4		0.83
VvACS4	VvACS4			P\$KAN1	Transcript	P\$KAN4.0	KANADI 4		0.78
VvACS4	VvACS4			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92
VvACS4	VvACS4			P\$KAN1	Transcript	P\$KBX.01	KANADI bc		0.92

Seq. name	accession	gene symbol	GeneID	matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$L1BX	L1 box, mc	P\$HDG1.0	Homeodon		0.85
VvACS1	VvACS1			P\$L1BX	L1 box, mc	P\$HDG9.0	Homeodon		0.77
VvACS1	VvACS1			P\$L1BX	L1 box, mc	P\$PDF2.0	Protoderm:		0.82
VvACS1	VvACS1			P\$L1BX	L1 box, mc	P\$HDG1.0	Homeodon		0.85
VvACS1	VvACS1			P\$L1BX	L1 box, mc	P\$PDF2.0	Protoderm:		0.82
VvACS1	VvACS1			P\$L1BX	L1 box, mc	P\$HDG1.0	Homeodon		0.85
VvACS1	VvACS1			P\$L1BX	L1 box, mc	P\$PDF2.0	Protoderm:		0.82
VvACS2	VvACS2			P\$L1BX	L1 box, mc	P\$HDG1.0	Homeodon		0.85
VvACS2	VvACS2			P\$L1BX	L1 box, mc	P\$ATML1.	Arabidopsi:		0.76

VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$HDG1.0 Homeodon	0.85
VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$HDG9.0 Homeodon	0.77
VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$HDG1.0 Homeodon	0.85
VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$ATML1. Arabidopsi:	0.76
VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.82
VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$HDG9.0 Homeodon	0.77
VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.82
VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$HDG9.0 Homeodon	0.77
VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$HDG9.0 Homeodon	0.77
VvACS2	VvACS2	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.85
VvACS6	VvACS6	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.82
VvACS6	VvACS6	P\$L1BX	L1 box, mc P\$HDG1.0 Homeodon	0.85
VvACS6	VvACS6	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.82
VvACS6	VvACS6	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.82
VvACS6	VvACS6	P\$L1BX	L1 box, mc P\$HDG9.0 Homeodon	0.77
VvACS9	VvACS9	P\$L1BX	L1 box, mc P\$ATML1. L1-specifi	0.82
VvACS9	VvACS9	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.85
VvACO1	VvACO1	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.82
VvACO1	VvACO1	P\$L1BX	L1 box, mc P\$HDG1.0 Homeodon	0.85
VvACO1	VvACO1	P\$L1BX	L1 box, mc P\$ATML1. Arabidopsi:	0.76
VvACO2	VvACO2	P\$L1BX	L1 box, mc P\$ATML1. Arabidopsi:	0.76
VvACO2	VvACO2	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.85
VvACO2	VvACO2	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.85
VvACO2	VvACO2	P\$L1BX	L1 box, mc P\$PDF2.0; Protoderm:	0.82
VvACO2	VvACO2	P\$L1BX	L1 box, mc P\$HDG1.0 Homeodon	0.85
VvACO4	VvACO4	P\$L1BX	L1 box, mc P\$ATML1. L1-specifi	0.82
VvACO4	VvACO4	P\$L1BX	L1 box, mc P\$ATML1. L1-specifi	0.82
VvACS4	VvACS4	P\$L1BX	L1 box, mc P\$HDG1.0 Homeodon	0.85
VvACS4	VvACS4	P\$L1BX	L1 box, mc P\$HDG9.0 Homeodon	0.77
VvACS4	VvACS4	P\$L1BX	L1 box, mc P\$HDG9.0 Homeodon	0.77
VvACS4	VvACS4	P\$L1BX	L1 box, mc P\$ATML1. Arabidopsi:	0.76
VvACS4	VvACS4	P\$L1BX	L1 box, mc P\$ATML1. L1-specifi	0.82
VvACS4	VvACS4	P\$L1BX	L1 box, mc P\$HDG9.0 Homeodon	0.77
VvACS4	VvACS4	P\$L1BX	L1 box, mc P\$ATML1. L1-specifi	0.82

Seq. name	Accession	GeneID	Matrix	Family Info	Matrix Info	Opt.
VvACS1	VvACS1	P\$L1BDF	LOB doma	P\$ASL18.(Asymmetri		0.86
VvACS9	VvACS9	P\$L1BDF	LOB doma	P\$LBD19.(LOB doma		0.87
VvACO2	VvACO2	P\$L1BDF	LOB doma	P\$ASL18.(Asymmetri		0.86

Seq. name	Accession	GeneID	Matrix	Family Info	Matrix Info	Opt.
VvACS2	VvACS2	P\$L1LEGB	Legumin B	P\$FUSCA; B3 domain		0.95
VvACS9	VvACS9	P\$L1LEGB	Legumin B	P\$IDE1.01 Iron-defici		0.77
VvACO1	VvACO1	P\$L1LEGB	Legumin B	P\$FUSCA; B3 domain		0.95
VvACO2	VvACO2	P\$L1LEGB	Legumin B	P\$FUSCA; B3 domain		0.95

Seq. name	Accession	GeneID	Matrix	Family Info	Matrix Info	Opt.
VvACS6	VvACS6	P\$L1LFYB	LFY bindin	P\$LFY.01 Plant speci		0.93
VvACO1	VvACO1	P\$L1LFYB	LFY bindin	P\$LFY.01 Plant speci		0.93

Seq. name	Accession	GeneID	Matrix	Family Info	Matrix Info	Opt.
VvACS9	VvACS9	P\$L1LICM	Leaf and ti	P\$OSLIC.(Oriza sativ;		1
VvACS4	VvACS4	P\$L1LICM	Leaf and ti	P\$OSLIC.(Oriza sativ;		1

Seq. name	Accession	GeneID	Matrix	Family Info	Matrix Info	Opt.
VvACS2	VvACS2	P\$L1REM	Light resp	P\$RAP22. RAP2.2, in		0.85
VvACO4	VvACO4	P\$L1REM	Light resp	P\$RAP22. RAP2.2, in		0.85
VvACS4	VvACS4	P\$L1REM	Light resp	P\$RAP22. RAP2.2, in		0.85

VvACS4	VvACS4	P\$LREM	Light resp	P\$RAP22. RAP2.2, in	0.85
VvACS4	VvACS4	P\$LREM	Light resp	P\$RAP22. RAP2.2, in	0.85
VvACS4	VvACS4	P\$LREM	Light resp	P\$RAP22. RAP2.2, in	0.85
VvACS4	VvACS4	P\$LREM	Light resp	P\$RAP22. RAP2.2, in	0.85

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$MADS	MADS	box P\$SOC1.0	Suppresso		0.9
VvACS1	VvACS1		P\$MADS	MADS	box P\$AGL3.0	AGL3, MAI		0.83
VvACS1	VvACS1		P\$MADS	MADS	box P\$AGL3.0	AGL3, MAI		0.83
VvACS1	VvACS1		P\$MADS	MADS	box P\$AGL15.0	(Floral hom		0.79
VvACS1	VvACS1		P\$MADS	MADS	box P\$MADS.C	Binding sit		0.75
VvACS1	VvACS1		P\$MADS	MADS	box P\$SQUA.0	MADS-box		0.9
VvACS1	VvACS1		P\$MADS	MADS	box P\$AGL15.0	(AGL15, Arz		0.8
VvACS2	VvACS2		P\$MADS	MADS	box P\$SVP.01	Short Vege		0.77
VvACS6	VvACS6		P\$MADS	MADS	box P\$FLC.01	Flowering		0.82
VvACS6	VvACS6		P\$MADS	MADS	box P\$AGL3.0	AGL3, MAI		0.83
VvACS6	VvACS6		P\$MADS	MADS	box P\$AP1.01	Floral hom		0.86
VvACS6	VvACS6		P\$MADS	MADS	box P\$AGL15.0	(Floral hom		0.79
VvACS9	VvACS9		P\$MADS	MADS	box P\$AGL15.0	(AGL15, Arz		0.79
VvACS9	VvACS9		P\$MADS	MADS	box P\$AGL15.0	(Floral hom		0.79
VvACS9	VvACS9		P\$MADS	MADS	box P\$AGL3.0	AGL3, MAI		0.83
VvACS9	VvACS9		P\$MADS	MADS	box P\$SVP.01	Short Vege		0.77
VvACS9	VvACS9		P\$MADS	MADS	box P\$SQUA.0	MADS-box		0.9
VvACO1	VvACO1		P\$MADS	MADS	box P\$MADS.C	Binding sit		0.75
VvACO1	VvACO1		P\$MADS	MADS	box P\$AGL3.0	AGL3, MAI		0.83
VvACO1	VvACO1		P\$MADS	MADS	box P\$AGL3.0	AGL3, MAI		0.83
VvACO2	VvACO2		P\$MADS	MADS	box P\$MADS.C	Binding sit		0.75
VvACO2	VvACO2		P\$MADS	MADS	box P\$FLC.01	Flowering		0.82
VvACO2	VvACO2		P\$MADS	MADS	box P\$SQUA.0	MADS-box		0.9
VvACO2	VvACO2		P\$MADS	MADS	box P\$SQUA.0	MADS-box		0.9
VvACO2	VvACO2		P\$MADS	MADS	box P\$SQUA.0	MADS-box		0.9
VvACO2	VvACO2		P\$MADS	MADS	box P\$AP1.01	Floral hom		0.86
VvACO2	VvACO2		P\$MADS	MADS	box P\$AG.01	Agamous,		0.8
VvACO4	VvACO4		P\$MADS	MADS	box P\$AGL15.0	(AGL15, Arz		0.79
VvACO4	VvACO4		P\$MADS	MADS	box P\$AG.01	Agamous,		0.8
VvACO4	VvACO4		P\$MADS	MADS	box P\$SQUA.0	MADS-box		0.9
VvACO4	VvACO4		P\$MADS	MADS	box P\$SQUA.0	MADS-box		0.9
VvACO4	VvACO4		P\$MADS	MADS	box P\$AGL3.0	AGL3, MAI		0.83
VvACO4	VvACO4		P\$MADS	MADS	box P\$AGL15.0	(AGL15, Arz		0.8
VvACO4	VvACO4		P\$MADS	MADS	box P\$AGL15.0	(AGL15, Arz		0.79
VvACS4	VvACS4		P\$MADS	MADS	box P\$AGL15.0	(AGL15, Arz		0.8
VvACS4	VvACS4		P\$MADS	MADS	box P\$SQUA.0	MADS-box		0.9

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$MIIG	MYB	IIG-ty P\$MYB62.	Myb domai		0.84
VvACS1	VvACS1		P\$MIIG	MYB	IIG-ty P\$MYB27.	Myb domai		0.8
VvACS1	VvACS1		P\$MIIG	MYB	IIG-ty P\$PALBO.	Putative ci		0.81
VvACS1	VvACS1		P\$MIIG	MYB	IIG-ty P\$MYB62.	Myb domai		0.84
VvACS1	VvACS1		P\$MIIG	MYB	IIG-ty P\$MYBC1.	Maize C1 r		0.92
VvACS1	VvACS1		P\$MIIG	MYB	IIG-ty P\$MYB67.	Myb domai		0.91
VvACS1	VvACS1		P\$MIIG	MYB	IIG-ty P\$P_ACT.	(Maize activ		0.93
VvACS1	VvACS1		P\$MIIG	MYB	IIG-ty P\$PALBO.	Putative ci		0.81
VvACS2	VvACS2		P\$MIIG	MYB	IIG-ty P\$BOS1.0	Botrytis-s		0.87
VvACS2	VvACS2		P\$MIIG	MYB	IIG-ty P\$MS188.	Male steri		0.88
VvACS2	VvACS2		P\$MIIG	MYB	IIG-ty P\$MYBC1.	Maize C1 r		0.92
VvACS6	VvACS6		P\$MIIG	MYB	IIG-ty P\$MYB107.	Myb domai		0.92
VvACS6	VvACS6		P\$MIIG	MYB	IIG-ty P\$SMRE.C	Secondary		0.93
VvACS6	VvACS6		P\$MIIG	MYB	IIG-ty P\$MS188.	Male steri		0.88

VvACS6	VvACS6	P\$MIIG	MYB IIG-ty P\$MYB99.	Myb domai	0.9
VvACS6	VvACS6	P\$MIIG	MYB IIG-ty P\$MYB49.	Myb domai	0.89
VvACS6	VvACS6	P\$MIIG	MYB IIG-ty P\$MS188.	Male steri	0.88
VvACS9	VvACS9	P\$MIIG	MYB IIG-ty P\$MYB121	Myb domai	0.85
VvACS9	VvACS9	P\$MIIG	MYB IIG-ty P\$MYB59.	Myb domai	0.83
VvACS9	VvACS9	P\$MIIG	MYB IIG-ty P\$MYBC1.	Maize C1 r	0.92
VvACS9	VvACS9	P\$MIIG	MYB IIG-ty P\$MS188.	Male steri	0.88
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$MYB107	Myb domai	0.92
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$MYB93.	Myb domai	0.93
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$PALBO	Putative ci	0.81
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$MYB99.	Myb domai	0.9
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$MS188.	Male steri	0.88
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$SMRE.C	Secondary	0.93
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$MYB107	Myb domai	0.92
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$MYB93.	Myb domai	0.93
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$ACTYP.	AC-type m	0.87
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$PALBO	Putative ci	0.81
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$MYB99.	Myb domai	0.9
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$MS188.	Male steri	0.88
VvACO1	VvACO1	P\$MIIG	MYB IIG-ty P\$MYB55.	Myb domai	0.91
VvACO2	VvACO2	P\$MIIG	MYB IIG-ty P\$MYB57.	Myb domai	0.77
VvACO2	VvACO2	P\$MIIG	MYB IIG-ty P\$MYB99.	Myb domai	0.9
VvACO2	VvACO2	P\$MIIG	MYB IIG-ty P\$MYB49.	Myb domai	0.89
VvACO2	VvACO2	P\$MIIG	MYB IIG-ty P\$MYB57.	Myb domai	0.77
VvACO2	VvACO2	P\$MIIG	MYB IIG-ty P\$MYB49.	Myb domai	0.89
VvACO2	VvACO2	P\$MIIG	MYB IIG-ty P\$MS188.	Male steri	0.88
VvACO2	VvACO2	P\$MIIG	MYB IIG-ty P\$BOS1.0	Botrytis-s	0.87
VvACO2	VvACO2	P\$MIIG	MYB IIG-ty P\$MYB59.	Myb domai	0.83
VvACO4	VvACO4	P\$MIIG	MYB IIG-ty P\$MYB99.	Myb domai	0.9
VvACO4	VvACO4	P\$MIIG	MYB IIG-ty P\$MYB49.	Myb domai	0.89
VvACO4	VvACO4	P\$MIIG	MYB IIG-ty P\$MYB62.	Myb domai	0.84
VvACO4	VvACO4	P\$MIIG	MYB IIG-ty P\$MYB99.	Myb domai	0.9
VvACO4	VvACO4	P\$MIIG	MYB IIG-ty P\$MYB49.	Myb domai	0.89
VvACS4	VvACS4	P\$MIIG	MYB IIG-ty P\$MYB121	Myb domai	0.85
VvACS4	VvACS4	P\$MIIG	MYB IIG-ty P\$MS188.	Male steri	0.88
VvACS4	VvACS4	P\$MIIG	MYB IIG-ty P\$BOS1.0	Botrytis-s	0.87
VvACS4	VvACS4	P\$MIIG	MYB IIG-ty P\$BOS1.0	Botrytis-s	0.87
VvACS4	VvACS4	P\$MIIG	MYB IIG-ty P\$MS188.	Male steri	0.88

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS6	VvACS6		P\$MSAE	M-phase-s	P\$MYB3R	Myb-relate		0.82
VvACS9	VvACS9		P\$MSAE	M-phase-s	P\$MYB3R	Myb-relate		0.82
VvACS9	VvACS9		P\$MSAE	M-phase-s	P\$MYB3R	Myb-relate		0.82
VvACO2	VvACO2		P\$MSAE	M-phase-s	P\$MYB3R	Myb-relate		0.82

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$MYBL	MYB-like p	P\$MYBPH	Myb-like pr		0.8
VvACS1	VvACS1		P\$MYBL	MYB-like p	P\$MYB33.	Myb domai		0.88
VvACS1	VvACS1		P\$MYBL	MYB-like p	P\$AS1_AS	AS1/AS2 r		0.99
VvACS2	VvACS2		P\$MYBL	MYB-like p	P\$MYB65.	Myb domai		0.92
VvACS2	VvACS2		P\$MYBL	MYB-like p	P\$MYBPH	Myb-like pr		0.76
VvACS2	VvACS2		P\$MYBL	MYB-like p	P\$ATY13.C	Myb domai		0.93
VvACS2	VvACS2		P\$MYBL	MYB-like p	P\$MYB96.	Myb domai		0.9
VvACS2	VvACS2		P\$MYBL	MYB-like p	P\$NTMYB.	Anther-spe		0.96
VvACS6	VvACS6		P\$MYBL	MYB-like p	P\$CARE.0	CAACTC r		0.83
VvACS6	VvACS6		P\$MYBL	MYB-like p	P\$GAMYB	GA-regulat		0.91
VvACS6	VvACS6		P\$MYBL	MYB-like p	P\$MYB52.	Myb domai		0.87
VvACS6	VvACS6		P\$MYBL	MYB-like p	P\$GAMYB	GA-regulat		0.91

VvACS6	VvACS6	P\$MYBL	MYB-like p P\$GAMYB GA-regulat	0.91
VvACS9	VvACS9	P\$MYBL	MYB-like p P\$WER.01 Myb-domai	0.87
VvACS9	VvACS9	P\$MYBL	MYB-like p P\$CARE.0 CAACTC r	0.83
VvACS9	VvACS9	P\$MYBL	MYB-like p P\$MYB33. Myb domai	0.88
VvACO1	VvACO1	P\$MYBL	MYB-like p P\$NTMYB. Anther-spe	0.96
VvACO1	VvACO1	P\$MYBL	MYB-like p P\$GAMYB GA-regulat	0.91
VvACO1	VvACO1	P\$MYBL	MYB-like p P\$ATY13.0 Myb domai	0.93
VvACO1	VvACO1	P\$MYBL	MYB-like p P\$MYB52. Myb domai	0.87
VvACO1	VvACO1	P\$MYBL	MYB-like p P\$MYB52. Myb domai	0.87
VvACO1	VvACO1	P\$MYBL	MYB-like p P\$MYB96. Myb domai	0.91
VvACO1	VvACO1	P\$MYBL	MYB-like p P\$ATY13.0 Myb domai	0.93
VvACO1	VvACO1	P\$MYBL	MYB-like p P\$ATY13.0 Myb domai	0.93
VvACO2	VvACO2	P\$MYBL	MYB-like p P\$MYB96. Myb domai	0.91
VvACO4	VvACO4	P\$MYBL	MYB-like p P\$MYBPH Myb-like pr	0.8
VvACO4	VvACO4	P\$MYBL	MYB-like p P\$MYB96. Myb domai	0.9
VvACO4	VvACO4	P\$MYBL	MYB-like p P\$AS1_AS AS1/AS2 r	0.99
VvACO4	VvACO4	P\$MYBL	MYB-like p P\$AS1_AS AS1/AS2 r	0.99
VvACO4	VvACO4	P\$MYBL	MYB-like p P\$ATMYB; R2R3-MYE	0.88
VvACO4	VvACO4	P\$MYBL	MYB-like p P\$AS1_AS AS1/AS2 r	0.99
VvACO4	VvACO4	P\$MYBL	MYB-like p P\$ATMYB; R2R3-MYE	0.88
VvACS4	VvACS4	P\$MYBL	MYB-like p P\$MYB101 Myb domai	0.88
VvACS4	VvACS4	P\$MYBL	MYB-like p P\$ATY13.0 Myb domai	0.93
VvACS4	VvACS4	P\$MYBL	MYB-like p P\$ATMYB; R2R3-type	0.87

Seq. name	Accession	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$MYBS	MYB protei	P\$ATDIV1. DIVARICA			0.93
VvACS1	VvACS1	P\$MYBS	MYB protei	P\$PHR1.0 Phosphate			0.84
VvACS1	VvACS1	P\$MYBS	MYB protei	P\$ATDIV1. DIVARICA			0.93
VvACS1	VvACS1	P\$MYBS	MYB protei	P\$ZMMRP Zea mays l			0.79
VvACS1	VvACS1	P\$MYBS	MYB protei	P\$MYBS1. Myb/SANT			0.87
VvACS1	VvACS1	P\$MYBS	MYB protei	P\$TAMYB; MYB protei			0.83
VvACS1	VvACS1	P\$MYBS	MYB protei	P\$TAMYB; MYB protei			0.83
VvACS2	VvACS2	P\$MYBS	MYB protei	P\$PHR1.0 Phosphate			0.84
VvACS2	VvACS2	P\$MYBS	MYB protei	P\$MYBST MybSt1 (M			0.9
VvACS2	VvACS2	P\$MYBS	MYB protei	P\$HVMCB Hordeum v			0.93
VvACS6	VvACS6	P\$MYBS	MYB protei	P\$ATDIV6. DIVARICA			0.9
VvACS6	VvACS6	P\$MYBS	MYB protei	P\$ATDIV1. DIVARICA			0.93
VvACS6	VvACS6	P\$MYBS	MYB protei	P\$ATDIV1. DIVARICA			0.93
VvACS9	VvACS9	P\$MYBS	MYB protei	P\$ATDIV1. DIVARICA			0.93
VvACS9	VvACS9	P\$MYBS	MYB protei	P\$PHR1.0 Phosphate			0.84
VvACS9	VvACS9	P\$MYBS	MYB protei	P\$ATDIV1. DIVARICA			0.93
VvACS9	VvACS9	P\$MYBS	MYB protei	P\$PHR1.0 Phosphate			0.84
VvACO1	VvACO1	P\$MYBS	MYB protei	P\$MYBST MybSt1 (M			0.9
VvACO1	VvACO1	P\$MYBS	MYB protei	P\$TAMYB; MYB protei			0.83
VvACO1	VvACO1	P\$MYBS	MYB protei	P\$MYBH.0 Myb hypoc			0.83
VvACO1	VvACO1	P\$MYBS	MYB protei	P\$ATDIV6. DIVARICA			0.9
VvACO2	VvACO2	P\$MYBS	MYB protei	P\$MYBST MybSt1 (M			0.9
VvACO2	VvACO2	P\$MYBS	MYB protei	P\$PHR1.0 P1BS, PHF			0.82
VvACO2	VvACO2	P\$MYBS	MYB protei	P\$HVMCB Hordeum v			0.93
VvACO4	VvACO4	P\$MYBS	MYB protei	P\$PHR1.0 P1BS, PHF			0.82
VvACS4	VvACS4	P\$MYBS	MYB protei	P\$ATDIV1. DIVARICA			0.93

Seq. name	Accession	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$MYCL	Myc-like b	P\$MYCRS Myc recogn			0.93
VvACS1	VvACS1	P\$MYCL	Myc-like b	P\$PIL5.01 Phytochr			0.89
VvACS6	VvACS6	P\$MYCL	Myc-like b	P\$ICE.01 ICE (induc			0.95
VvACS9	VvACS9	P\$MYCL	Myc-like b	P\$PIF4.01 Phytochr			0.97
VvACS9	VvACS9	P\$MYCL	Myc-like b	P\$PIF4.01 Phytochr			0.97

VvACS9	VvACS9		P\$MYCL	Myc-like bε	P\$MYCRS	Myc recogn	0.93
VvACO1	VvACO1		P\$MYCL	Myc-like bε	P\$PIF4.01	Phytochr	0.97
VvACO2	VvACO2		P\$MYCL	Myc-like bε	P\$PIL5.01	Phytochr	0.89
VvACO4	VvACO4		P\$MYCL	Myc-like bε	P\$ICE.01	ICE (induc	0.95

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$MYCS	Cis-regulat	P\$MYCS.C	Mycorrhiza		0.86
VvACS4	VvACS4		P\$MYCS	Cis-regulat	P\$MYCS.C	Mycorrhiza		0.86

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$NACD	NAC doma	P\$ANAC07	Transcripti		0.84
VvACS1	VvACS1		P\$NACD	NAC doma	P\$ANAC07	Transcripti		0.84
VvACS2	VvACS2		P\$NACD	NAC doma	P\$ANAC08	NAC doma		0.79
VvACS2	VvACS2		P\$NACD	NAC doma	P\$ANAC08	NAC doma		0.79
VvACS2	VvACS2		P\$NACD	NAC doma	P\$ANAC09	NAC doma		0.83
VvACS2	VvACS2		P\$NACD	NAC doma	P\$ANAC09	NAC doma		0.99
VvACS2	VvACS2		P\$NACD	NAC doma	P\$ANAC10	NAC doma		0.94
VvACS6	VvACS6		P\$NACD	NAC doma	P\$ANAC10	NAC doma		0.94
VvACS6	VvACS6		P\$NACD	NAC doma	P\$ANAC10	NAC doma		0.94
VvACS9	VvACS9		P\$NACD	NAC doma	P\$ANAC08	NAC doma		0.79
VvACS9	VvACS9		P\$NACD	NAC doma	P\$ANAC08	NAC doma		0.79
VvACS9	VvACS9		P\$NACD	NAC doma	P\$ANAC07	Transcripti		0.84
VvACS9	VvACS9		P\$NACD	NAC doma	P\$ANAC09	NAC doma		0.98
VvACS9	VvACS9		P\$NACD	NAC doma	P\$ANAC07	Transcripti		0.84
VvACS9	VvACS9		P\$NACD	NAC doma	P\$ANAC10	NAC doma		0.94
VvACO1	VvACO1		P\$NACD	NAC doma	P\$ANAC08	NAC doma		0.79
VvACO1	VvACO1		P\$NACD	NAC doma	P\$ANAC09	NAC doma		0.98
VvACO4	VvACO4		P\$NACD	NAC doma	P\$ANAC07	Transcripti		0.84

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$NACF	Plant speci	P\$ANAC09	NAC doma		0.81
VvACS1	VvACS1		P\$NACF	Plant speci	P\$TANAC6	Wheat NAC		0.75
VvACS1	VvACS1		P\$NACF	Plant speci	P\$ANAC09	NAC doma		0.81
VvACS2	VvACS2		P\$NACF	Plant speci	P\$ANAC07	NAC doma		0.75
VvACS2	VvACS2		P\$NACF	Plant speci	P\$ANAC08	NAC doma		0.75
VvACS2	VvACS2		P\$NACF	Plant speci	P\$ANAC07	NAC doma		0.75
VvACS2	VvACS2		P\$NACF	Plant speci	P\$ANAC09	NAC doma		0.75
VvACS6	VvACS6		P\$NACF	Plant speci	P\$ANAC09	Arabidopsi		0.94
VvACS9	VvACS9		P\$NACF	Plant speci	P\$ANAC09	Arabidopsi		0.94
VvACS9	VvACS9		P\$NACF	Plant speci	P\$ANAC07	NAC doma		0.75
VvACS9	VvACS9		P\$NACF	Plant speci	P\$ANAC08	NAC doma		0.75
VvACS9	VvACS9		P\$NACF	Plant speci	P\$ANAC07	NAC doma		0.75
VvACO1	VvACO1		P\$NACF	Plant speci	P\$ANAC07	NAC doma		0.75
VvACO2	VvACO2		P\$NACF	Plant speci	P\$IDEF2.0	Transcripti		0.96
VvACS4	VvACS4		P\$NACF	Plant speci	P\$ANAC09	Arabidopsi		0.94
VvACS4	VvACS4		P\$NACF	Plant speci	P\$TANAC6	Wheat NAC		0.75
VvACS4	VvACS4		P\$NACF	Plant speci	P\$ANAC09	Arabidopsi		0.92

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co		0.85
VvACS1	VvACS1		P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co		0.85
VvACS1	VvACS1		P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co		0.85
VvACS1	VvACS1		P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co		0.85
VvACS1	VvACS1		P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co		0.85
VvACS2	VvACS2		P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co		0.85
VvACS2	VvACS2		P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co		0.85
VvACS2	VvACS2		P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co		0.85
VvACS2	VvACS2		P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co		0.85

VvACS9	VvACS9	P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co	0.85
VvACS9	VvACS9	P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co	0.85
VvACO1	VvACO1	P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co	0.85
VvACO1	VvACO1	P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co	0.85
VvACO2	VvACO2	P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co	0.85
VvACO2	VvACO2	P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co	0.85
VvACO4	VvACO4	P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co	0.85
VvACS4	VvACS4	P\$NCS1	Nodulin co	P\$NCS1.0	Nodulin co	0.85

Seq. name	Accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$NCS2	Nodulin co	P\$NCS2.0	Nodulin co			0.79
VvACS6	VvACS6	P\$NCS2	Nodulin co	P\$NCS2.0	Nodulin co			0.79

Seq. name	Accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS2	VvACS2	P\$NIGS	NACL-indu	P\$NIG1.01	NACL-indu			0.81
VvACS2	VvACS2	P\$NIGS	NACL-indu	P\$NIG1.01	NACL-indu			0.81

Seq. name	Accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$NTMF	NAC factor	P\$NTL6.01	NAC WITH			0.97
VvACS1	VvACS1	P\$NTMF	NAC factor	P\$ANAC00	(NAC doma			0.81
VvACS1	VvACS1	P\$NTMF	NAC factor	P\$NTL8.02	NAC with t			0.97
VvACS1	VvACS1	P\$NTMF	NAC factor	P\$NTL6.01	NAC WITH			0.97
VvACS1	VvACS1	P\$NTMF	NAC factor	P\$NTL8.01	NAC WITH			0.97
VvACS1	VvACS1	P\$NTMF	NAC factor	P\$ANAC00	(NAC doma			0.81
VvACS2	VvACS2	P\$NTMF	NAC factor	P\$NTL8.01	NAC WITH			0.97
VvACS2	VvACS2	P\$NTMF	NAC factor	P\$NTL8.01	NAC WITH			0.97
VvACS2	VvACS2	P\$NTMF	NAC factor	P\$NTL6.02	NTM1-LIKE			0.91
VvACS2	VvACS2	P\$NTMF	NAC factor	P\$NTL8.01	NAC WITH			0.97
VvACS6	VvACS6	P\$NTMF	NAC factor	P\$NTM1.0	NAC with t			0.8
VvACS6	VvACS6	P\$NTMF	NAC factor	P\$NTM1.0	NAC with t			0.8
VvACS6	VvACS6	P\$NTMF	NAC factor	P\$NTL8.01	NAC WITH			0.97
VvACS9	VvACS9	P\$NTMF	NAC factor	P\$NTL8.01	NAC WITH			0.97
VvACS9	VvACS9	P\$NTMF	NAC factor	P\$NTL6.01	NAC WITH			0.97
VvACS9	VvACS9	P\$NTMF	NAC factor	P\$NTL6.01	NAC WITH			0.97
VvACS9	VvACS9	P\$NTMF	NAC factor	P\$NTL8.02	NAC with t			0.97
VvACO1	VvACO1	P\$NTMF	NAC factor	P\$ANAC00	(NAC doma			0.81
VvACO1	VvACO1	P\$NTMF	NAC factor	P\$NTL8.02	NAC with t			0.97
VvACO2	VvACO2	P\$NTMF	NAC factor	P\$NTM1.0	NAC with t			0.8
VvACO2	VvACO2	P\$NTMF	NAC factor	P\$NTM1.0	NAC with t			0.8
VvACO2	VvACO2	P\$NTMF	NAC factor	P\$NTL6.01	NAC WITH			0.97
VvACO4	VvACO4	P\$NTMF	NAC factor	P\$NTM1.0	NAC with t			0.8
VvACO4	VvACO4	P\$NTMF	NAC factor	P\$NTM1.0	NAC with t			0.8
VvACO4	VvACO4	P\$NTMF	NAC factor	P\$NTL8.01	NAC WITH			0.97
VvACO4	VvACO4	P\$NTMF	NAC factor	P\$NTL6.01	NAC WITH			0.97
VvACS4	VvACS4	P\$NTMF	NAC factor	P\$NTL8.01	NAC WITH			0.97

Seq. name	Accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS4	VvACS4	P\$OCSE	Enhancer €	P\$OCSL.0	OCS-like e			0.75

Seq. name	Accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$OPAQ	Opaque-2	P\$O2_GCI	Recognition			0.81
VvACS2	VvACS2	P\$OPAQ	Opaque-2	P\$O2_GCI	Recognition			0.81
VvACS6	VvACS6	P\$OPAQ	Opaque-2	P\$O2_GCI	Recognition			0.81
VvACO1	VvACO1	P\$OPAQ	Opaque-2	P\$GCN4.0	GCN4, con			0.81
VvACO2	VvACO2	P\$OPAQ	Opaque-2	P\$O2.02	Opaque-2 i			0.87
VvACO4	VvACO4	P\$OPAQ	Opaque-2	P\$O2.01	Opaque-2			0.87

Seq. name	Accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
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VvACS6	VvACS6		P\$PAHD	Paired amf	P\$AT1G24	Paired amf	0.88	
VvACO4	VvACO4		P\$PAHD	Paired amf	P\$AT1G24	Paired amf	0.88	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACS1	VvACS1		P\$PALA	Conserved	P\$PALBO	Putative c	0.84	
VvACS4	VvACS4		P\$PALA	Conserved	P\$PALBO	Putative c	0.84	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACS1	VvACS1		P\$PCDR	Factors in	P\$GMNAC	Heterodime	1	
VvACO1	VvACO1		P\$PCDR	Factors in	P\$GMNAC	Heterodime	1	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACS2	VvACS2		P\$PNRE	Plant nitra	P\$NRE43-	Motif simil	0.84	
VvACS9	VvACS9		P\$PNRE	Plant nitra	P\$NBS.01	NIN-bindin	0.81	
VvACS9	VvACS9		P\$PNRE	Plant nitra	P\$NBS.01	NIN-bindin	0.81	
VvACO1	VvACO1		P\$PNRE	Plant nitra	P\$NRE43-	Motif simil	0.84	
VvACO1	VvACO1		P\$PNRE	Plant nitra	P\$NRE43-	Motif simil	0.84	
VvACO4	VvACO4		P\$PNRE	Plant nitra	P\$NBS.01	NIN-bindin	0.81	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACS9	VvACS9		P\$PSPE	Protein se	P\$TL1.01	Cis-elemer	0.91	
VvACO1	VvACO1		P\$PSPE	Protein se	P\$TL1.01	Cis-elemer	0.91	
VvACO4	VvACO4		P\$PSPE	Protein se	P\$TL1.01	Cis-elemer	0.91	
VvACS4	VvACS4		P\$PSPE	Protein se	P\$TL1.01	Cis-elemer	0.91	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACS1	VvACS1		P\$PSRE	Pollen-spe	P\$GAAA.0	GAAA moti	0.83	
VvACO1	VvACO1		P\$PSRE	Pollen-spe	P\$GAAA.0	GAAA moti	0.83	
VvACO1	VvACO1		P\$PSRE	Pollen-spe	P\$GAAA.0	GAAA moti	0.83	
VvACO4	VvACO4		P\$PSRE	Pollen-spe	P\$GAAA.0	GAAA moti	0.83	
VvACO4	VvACO4		P\$PSRE	Pollen-spe	P\$GAAA.0	GAAA moti	0.83	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACS9	VvACS9		P\$RAV5	5'-part of b	P\$RAV1-5.	5'-part of	0.96	
VvACS9	VvACS9		P\$RAV5	5'-part of b	P\$RAV1.0	AP2/ERF a	0.93	
VvACO2	VvACO2		P\$RAV5	5'-part of b	P\$RAV1.0	AP2/ERF a	0.93	
VvACO4	VvACO4		P\$RAV5	5'-part of b	P\$RAV1.0	AP2/ERF a	0.93	
VvACO4	VvACO4		P\$RAV5	5'-part of b	P\$RAV1.0	AP2/ERF a	0.93	
VvACS4	VvACS4		P\$RAV5	5'-part of b	P\$RAV1-5.	5'-part of	0.96	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACS1	VvACS1		P\$REMF	B3 domain	P\$REM1.0	Reproducti	0.92	
VvACS6	VvACS6		P\$REMF	B3 domain	P\$REM1.0	Reproducti	0.83	
VvACO4	VvACO4		P\$REMF	B3 domain	P\$REM1.0	Reproducti	0.92	
VvACO4	VvACO4		P\$REMF	B3 domain	P\$REM1.0	Reproducti	0.92	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACO2	VvACO2		P\$RKDS	RWP-RK d	P\$RKD2.0	RWP-RK d	0.93	
VvACS4	VvACS4		P\$RKDS	RWP-RK d	P\$RKD2.0	RWP-RK d	0.93	
VvACS4	VvACS4		P\$RKDS	RWP-RK d	P\$RKD2.0	RWP-RK d	0.93	
VvACS4	VvACS4		P\$RKDS	RWP-RK d	P\$RKD2.0	RWP-RK d	0.93	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACS6	VvACS6		P\$ROOT	Root hair-s	P\$RHE.02	Root hair-s	0.77	
<b>Seq. name</b>	<b>accession</b>	<b>GeneID</b>	<b>Matrix</b>	<b>Family</b>	<b>Family Inf</b>	<b>Matrix</b>	<b>Matrix Inf</b>	<b>Opt.</b>
VvACS2	VvACS2		P\$SBPD	SBP-doma	P\$SPL14.0	Squamosa	0.83	
VvACS2	VvACS2		P\$SBPD	SBP-doma	P\$SPL1.0	Squamosa	0.84	

VvACS6	VvACS6	P\$SBPD	SBP-doma	P\$SPL14.0	Squamosa	0.83
VvACS6	VvACS6	P\$SBPD	SBP-doma	P\$SBP.01	SQUA pror	0.88
VvACS9	VvACS9	P\$SBPD	SBP-doma	P\$SPL14.0	Squamosa	0.83
VvACS9	VvACS9	P\$SBPD	SBP-doma	P\$SPL9.01	Squamosa	0.95
VvACS9	VvACS9	P\$SBPD	SBP-doma	P\$SPL9.01	Squamosa	0.95
VvACO2	VvACO2	P\$SBPD	SBP-doma	P\$SPL9.01	Squamosa	0.95

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS4	VvACS4		P\$SEF3	Soybean	e P\$SEF3.0	SEF3, Soy		0.87

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS2	VvACS2		P\$SEF4	Soybean	e P\$SEF4.0	Soybean e		0.98
VvACO2	VvACO2		P\$SEF4	Soybean	e P\$SEF4.0	Soybean e		0.98
VvACS4	VvACS4		P\$SEF4	Soybean	e P\$SEF4.0	Soybean e		0.98

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$SPF1	Sweet pot	e P\$SP8BF.0	DNA-bindir		0.87
VvACS9	VvACS9		P\$SPF1	Sweet pot	e P\$SP8BF.0	DNA-bindir		0.87
VvACO4	VvACO4		P\$SPF1	Sweet pot	e P\$SP8BF.0	DNA-bindir		0.87
VvACO4	VvACO4		P\$SPF1	Sweet pot	e P\$SP8BF.0	DNA-bindir		0.87
VvACO4	VvACO4		P\$SPF1	Sweet pot	e P\$SP8BF.0	DNA-bindir		0.87
VvACS4	VvACS4		P\$SPF1	Sweet pot	e P\$SP8BF.0	DNA-bindir		0.87
VvACS4	VvACS4		P\$SPF1	Sweet pot	e P\$SP8BF.0	DNA-bindir		0.87

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACO1	VvACO1		P\$SRSF	SHI relate	P\$STY1.0	SHI relate		0.86
VvACO4	VvACO4		P\$SRSF	SHI relate	P\$STY1.0	SHI relate		0.86

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$STKL	Storekeep	e P\$ATSTKL	DNA-bindir		0.81
VvACS6	VvACS6		P\$STKL	Storekeep	e P\$ATSTKL	DNA-bindir		0.81
VvACS6	VvACS6		P\$STKL	Storekeep	e P\$ATSTKL	DNA-bindir		0.81
VvACO1	VvACO1		P\$STKL	Storekeep	e P\$ATSTKL	DNA-bindir		0.81
VvACS4	VvACS4		P\$STKL	Storekeep	e P\$ATSTKL	DNA-bindir		0.81

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$STKM	Storekeep	e P\$STK.01	Storekeep		0.85
VvACS1	VvACS1		P\$STKM	Storekeep	e P\$STK.01	Storekeep		0.85
VvACS2	VvACS2		P\$STKM	Storekeep	e P\$STK.01	Storekeep		0.85
VvACO2	VvACO2		P\$STKM	Storekeep	e P\$STK.01	Storekeep		0.85
VvACO2	VvACO2		P\$STKM	Storekeep	e P\$STK.01	Storekeep		0.85
VvACO4	VvACO4		P\$STKM	Storekeep	e P\$STK.01	Storekeep		0.85
VvACS4	VvACS4		P\$STKM	Storekeep	e P\$STK.01	Storekeep		0.85

Seq. name	accession	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACS1	VvACS1		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACS2	VvACS2		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACS6	VvACS6		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACS6	VvACS6		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACS6	VvACS6		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACS6	VvACS6		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACO2	VvACO2		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACO2	VvACO2		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACO2	VvACO2		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACO4	VvACO4		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACO4	VvACO4		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81
VvACS4	VvACS4		P\$SUCB	Sucrose bc	P\$SUCRO	Sequence		0.81

VvACS4	VvACS4	P\$SUCB	Sucrose bc P\$SUCRO	Sequence	0.81
VvACS4	VvACS4	P\$SUCB	Sucrose bc P\$SUCRO	Sequence	0.81
VvACS4	VvACS4	P\$SUCB	Sucrose bc P\$SUCRO	Sequence	0.81
VvACS4	VvACS4	P\$SUCB	Sucrose bc P\$SUCRO	Sequence	0.81

Seq. name	accession	GeneID	Family	Matrix	Matrix Info	Opt.
VvACO4	VvACO4	P\$SURE	Sugar resp	P\$SURE.0	Sugar resp	0.99

Seq. name	accession	GeneID	Family	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$SWNS	Secondary	P\$ANAC0	(NAC doma	0.83
VvACS1	VvACS1	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACS1	VvACS1	P\$SWNS	Secondary	P\$ANAC0	(NAC doma	0.83
VvACS2	VvACS2	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACS2	VvACS2	P\$SWNS	Secondary	P\$ANAC0	(NAC doma	0.98
VvACS2	VvACS2	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACS6	VvACS6	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACS6	VvACS6	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACS6	VvACS6	P\$SWNS	Secondary	P\$ANAC0	(NAC doma	0.83
VvACS6	VvACS6	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACS9	VvACS9	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACS9	VvACS9	P\$SWNS	Secondary	P\$ANAC0	(NAC doma	0.98
VvACO1	VvACO1	P\$SWNS	Secondary	P\$ANAC0	(NAC doma	0.83
VvACO1	VvACO1	P\$SWNS	Secondary	P\$ANAC0	(NAC doma	0.83
VvACO2	VvACO2	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACO4	VvACO4	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACO4	VvACO4	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACO4	VvACO4	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92
VvACO4	VvACO4	P\$SWNS	Secondary	P\$ANAC0	(NAC doma	0.83
VvACO4	VvACO4	P\$SWNS	Secondary	P\$ANAC0	(NAC doma	0.83
VvACS4	VvACS4	P\$SWNS	Secondary	P\$SNBE.0	Secondary	0.92

Seq. name	accession	GeneID	Family	Matrix	Matrix Info	Opt.
VvACO2	VvACO2	P\$TCPF	DNA-bindir	P\$ATTCP2	TCP class	0.94
VvACO2	VvACO2	P\$TCPF	DNA-bindir	P\$PCF2.0	TCP class	0.89

Seq. name	accession	GeneID	Family	Matrix	Matrix Info	Opt.
VvACS1	VvACS1	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS1	VvACS1	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS1	VvACS1	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS1	VvACS1	P\$TCXF	CRC doma	P\$SOL1.0	CXC doma	0.84
VvACS2	VvACS2	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS2	VvACS2	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS2	VvACS2	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS2	VvACS2	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACS6	VvACS6	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACS6	VvACS6	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS6	VvACS6	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACS9	VvACS9	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACO1	VvACO1	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACO2	VvACO2	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO2	VvACO2	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO2	VvACO2	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO2	VvACO2	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACO2	VvACO2	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO2	VvACO2	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACO2	VvACO2	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO2	VvACO2	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACO2	VvACO2	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81

VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACO4	VvACO4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$SOL1.0	CXC doma	0.84
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$SOL1.0	CXC doma	0.84
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$SOL1.0	CXC doma	0.84
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$SOL1.0	CXC doma	0.84
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX2.0	TESMIN/T	0.81
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$SOL1.0	CXC doma	0.84
VvACS4	VvACS4	P\$TCXF	CRC doma	P\$TCX6.0	TESMIN/T	0.88

Seq. name	accession	niene symb	GenelD	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS2	VvACS2			P\$TEFB	TEF-box	P\$TEF1.0	TEF cis ac	0.76
VvACO1	VvACO1			P\$TEFB	TEF-box	P\$TEF1.0	TEF cis ac	0.76
VvACO4	VvACO4			P\$TEFB	TEF-box	P\$TEF1.0	TEF cis ac	0.76

Seq. name	accession	niene symb	GenelD	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS2	VvACS2			P\$TELO	Telo box (p	P\$TBP3.0	Telomere b	0.81
VvACS2	VvACS2			P\$TELO	Telo box (p	P\$RPBX.0	Ribosomal	0.84
VvACS6	VvACS6			P\$TELO	Telo box (p	P\$TBP3.0	Telomere b	0.81
VvACS9	VvACS9			P\$TELO	Telo box (p	P\$TBP3.0	Telomere b	0.81
VvACS9	VvACS9			P\$TELO	Telo box (p	P\$TBP3.0	Telomere b	0.81
VvACO2	VvACO2			P\$TELO	Telo box (p	P\$ATPUR/	Arabidopsi	0.85
VvACO4	VvACO4			P\$TELO	Telo box (p	P\$TBP3.0	Telomere b	0.81
VvACS4	VvACS4			P\$TELO	Telo box (p	P\$TBP3.0	Telomere b	0.81
VvACS4	VvACS4			P\$TELO	Telo box (p	P\$TBP3.0	Telomere b	0.81
VvACS4	VvACS4			P\$TELO	Telo box (p	P\$RPBX.0	Ribosomal	0.84
VvACS4	VvACS4			P\$TELO	Telo box (p	P\$ATPUR/	Arabidopsi	0.85
VvACS4	VvACS4			P\$TELO	Telo box (p	P\$TRP1.0	Telomere r	0.78
VvACS4	VvACS4			P\$TELO	Telo box (p	P\$TRP1.0	Telomere r	0.78

Seq. name	accession	niene symb	GenelD	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS9	VvACS9			P\$TERE	Tracheary-	P\$TERE.0	Tracheary-	0.79
VvACO4	VvACO4			P\$TERE	Tracheary-	P\$TERE.0	Tracheary-	0.79

Seq. name	accession	niene symb	GenelD	latrix Famil	Family Inf	Matrix	Matrix Inf	Opt.
VvACS1	VvACS1			P\$TGAF	Basic/leuci	P\$TGA4.0	Transcript	0.84
VvACS1	VvACS1			P\$TGAF	Basic/leuci	P\$TGA6.0	TGACG (T	0.85
VvACS9	VvACS9			P\$TGAF	Basic/leuci	P\$TGA4.0	Transcript	0.84
VvACS9	VvACS9			P\$TGAF	Basic/leuci	P\$TGA4.0	Transcript	0.84
VvACS4	VvACS4			P\$TGAF	Basic/leuci	P\$TGA2.0	Transcripti	0.87

Seq. name	Accession	Gene Symbol	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS6	VvACS6			P\$TODS	Time-of-da	P\$ME.01	Morning el	1
VvACS9	VvACS9			P\$TODS	Time-of-da	P\$HUD.01	Hormone u	1

Seq. name	Accession	Gene Symbol	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$TOEF	Target of e	P\$TOE2.0	Target of e	0.87
VvACS1	VvACS1			P\$TOEF	Target of e	P\$TOE2.0	Target of e	0.87
VvACS2	VvACS2			P\$TOEF	Target of e	P\$TOE1.0	Target of e	0.82
VvACS9	VvACS9			P\$TOEF	Target of e	P\$TOE2.0	Target of e	0.87
VvACO2	VvACO2			P\$TOEF	Target of e	P\$TOE1.0	Target of e	0.82
VvACO2	VvACO2			P\$TOEF	Target of e	P\$TOE1.0	Target of e	0.82
VvACO2	VvACO2			P\$TOEF	Target of e	P\$TOE1.0	Target of e	0.82
VvACS4	VvACS4			P\$TOEF	Target of e	P\$TOE1.0	Target of e	0.82
VvACS4	VvACS4			P\$TOEF	Target of e	P\$TOE1.0	Target of e	0.82
VvACS4	VvACS4			P\$TOEF	Target of e	P\$TOE1.0	Target of e	0.82
VvACS4	VvACS4			P\$TOEF	Target of e	P\$TOE1.0	Target of e	0.82

Seq. name	Accession	Gene Symbol	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS6	VvACS6			P\$TRIH	Trihelix do	P\$VFP5.0	Trihelix-do	0.85
VvACO2	VvACO2			P\$TRIH	Trihelix do	P\$ASIL2.0	Arabidopsi	0.84

Seq. name	Accession	Gene Symbol	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$URNA	Upstream s	P\$USE.01	Upstream s	0.75

Seq. name	Accession	Gene Symbol	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS9	VvACS9			P\$VRES	VIP1 resp	P\$BZIP52.	Basic leuci	0.91

Seq. name	Accession	Gene Symbol	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$WBXF	W Box fam	P\$WRKY1	Calmodulin	0.94
VvACS1	VvACS1			P\$WBXF	W Box fam	P\$WRKY1	WRKY DN,	0.93
VvACS2	VvACS2			P\$WBXF	W Box fam	P\$WRKY2	WRKY DN,	0.9
VvACS6	VvACS6			P\$WBXF	W Box fam	P\$WRKY1	WRKY DN,	0.93
VvACS6	VvACS6			P\$WBXF	W Box fam	P\$ZAP1.0	Zinc-deper	1
VvACS6	VvACS6			P\$WBXF	W Box fam	P\$WRKY4	WRKY DN,	0.87
VvACO1	VvACO1			P\$WBXF	W Box fam	P\$ERE.01	Elicitor re	0.89
VvACO1	VvACO1			P\$WBXF	W Box fam	P\$WRKY2	WRKY DN,	0.9
VvACO1	VvACO1			P\$WBXF	W Box fam	P\$ZAP1.0	Zinc-deper	1
VvACO4	VvACO4			P\$WBXF	W Box fam	P\$WRKY.0	WRKY plar	0.92
VvACO4	VvACO4			P\$WBXF	W Box fam	P\$WRKY1	WRKY DN,	0.93
VvACO4	VvACO4			P\$WBXF	W Box fam	P\$WRKY1	WRKY DN,	0.93
VvACO4	VvACO4			P\$WBXF	W Box fam	P\$WRKY.0	WRKY plar	0.92
VvACS4	VvACS4			P\$WBXF	W Box fam	P\$WRKY.0	WRKY plar	0.92
VvACS4	VvACS4			P\$WBXF	W Box fam	P\$WRKY4	WRKY DN,	0.83
VvACS4	VvACS4			P\$WBXF	W Box fam	P\$ZAP1.0	Zinc-deper	1

Seq. name	Accession	Gene Symbol	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$WOXF	WUS home	P\$WOX13	WUSCHEL	0.87
VvACS1	VvACS1			P\$WOXF	WUS home	P\$WOX13	WUSCHEL	0.87
VvACS2	VvACS2			P\$WOXF	WUS home	P\$WOX13	WUSCHEL	0.87
VvACO1	VvACO1			P\$WOXF	WUS home	P\$WOX13	WUSCHEL	0.87
VvACO1	VvACO1			P\$WOXF	WUS home	P\$WOX13	WUSCHEL	0.87
VvACO2	VvACO2			P\$WOXF	WUS home	P\$WOX13	WUSCHEL	0.87

Seq. name	Accession	Gene Symbol	GeneID	Matrix	Family Info	Matrix	Matrix Info	Opt.
VvACO1	VvACO1			P\$WTBX	WT-Box	P\$WRKY7	WRKY DN,	0.79

Seq. name	accession	gene symbol	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS1	VvACS1			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS1	VvACS1			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS2	VvACS2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS2	VvACS2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS2	VvACS2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS2	VvACS2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS2	VvACS2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS2	VvACS2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS2	VvACS2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS6	VvACS6			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS6	VvACS6			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS9	VvACS9			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACS9	VvACS9			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO1	VvACO1			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO1	VvACO1			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO1	VvACO1			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO2	VvACO2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO2	VvACO2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO2	VvACO2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO2	VvACO2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO2	VvACO2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO2	VvACO2			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO4	VvACO4			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92
VvACO4	VvACO4			P\$YABB	Yabby fami	P\$CRC.01	Yabby tran		0.92

Seq. name	accession	gene symbol	GeneID	Matrix	Family	Family Info	Matrix	Matrix Info	Opt.
VvACS6	VvACS6			P\$ZFAT	Zinc finger	P\$ZAT6.01	Zinc finger		0.8
VvACS6	VvACS6			P\$ZFAT	Zinc finger	P\$ZAT6.01	Zinc finger		0.8
VvACS9	VvACS9			P\$ZFAT	Zinc finger	P\$ZAT6.01	Zinc finger		0.8
VvACO1	VvACO1			P\$ZFAT	Zinc finger	P\$ZAT6.01	Zinc finger		0.8
VvACS4	VvACS4			P\$ZFAT	Zinc finger	P\$ZAT6.01	Zinc finger		0.8

oter region of the *VvACS* and *VvACO* genes.

Start position	End position	Core position	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
69	79	74	+	0.969	0.94	0	ttTCATttatt
994	1004	999	+	1	0.948	0.008	gaTCAGttctt
508	518	513	+	0.969	0.955	0.015	ttTCATtcctt
983	993	988	+	1	0.94	0	taTCAGtttct
603	613	608	+	1	0.987	0.047	taTCAGttgtg
1	11	6	+	0.969	0.94	0	ttTCATttaat
684	694	689	+	0.969	0.955	0.015	ttTCATtcctt

Start position	End position	Core position	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
8	22	15	+	1	0.933	0.033	ctacTATAaatTTta
149	163	156	+	1	0.934	0.034	aaaaTATAataaaaa
151	165	158	+	1	0.912	0.012	aataTATAataaaaa
153	167	160	+	1	0.955	0.075	tataTATAaaaaaaa
259	273	266	+	1	0.93	0.03	gaaaTATAatattt
101	115	108	+	1	0.95	0.07	ggaaTATAaaaataa
181	195	188	+	1	0.96	0.08	acaaTATAaaaaaat
426	440	433	+	1	0.913	0.013	tactTATAaatcgat
814	828	821	+	1	0.922	0.022	gagcTATAaagatta
68	82	75	+	1	0.996	0.096	tcccTATAaatatcat
545	559	552	+	1	0.914	0.014	gaatTATAaaat
547	561	554	+	1	1	0.12	attaTATAaatataa
553	567	560	+	1	0.93	0.03	taaaTATAaaaaata
604	618	611	+	1	0.94	0.04	aaaaTATAaaaaaacg
1051	1065	1058	+	1	0.912	0.012	ttgcTATAatatttac
366	380	373	+	1	0.941	0.061	aaaaTATAaaaaaat
419	433	426	+	1	0.93	0.03	ccttTATAaaaaata
481	495	488	+	1	0.952	0.052	ttctTATAaataatt
1085	1099	1092	+	1	0.927	0.027	ctgtTATAaaaaatg
1360	1374	1367	+	1	0.907	0.007	aagaTATAaatgaaa
293	307	300	+	1	0.902	0.022	ttcaTATAaacttaa
1022	1036	1029	+	0.826	0.899	0.019	tttaTTTAAAAaaat
1338	1352	1345	+	0.826	0.899	0.019	attaTTTAAAAaaaa

Start position	End position	Core position	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
906	920	913	+	1	0.765	0.005	aGCACccaccgagag

Start position	End position	Core position	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
9	25	17	+	1	0.93	0.03	tactaTAAAttttattt
152	168	160	+	0.892	0.916	0.016	atataTATAaaaaaaa
154	170	162	+	1	0.968	0.068	atataTAAAAaaaaaaag
191	207	199	+	1	0.953	0.053	agttaTAAAtttcttct
612	628	620	+	1	0.809	0.029	ttttaagTAAGtattta
57	73	65	+	0.892	0.937	0.037	ttgtaTATAagacaagt
102	118	110	+	1	0.967	0.067	gaataTAAAaataataa
182	198	190	+	1	0.968	0.068	caataTAAAAaaatataa
747	763	755	+	1	0.832	0.012	atgTATAaccataatta
948	964	956	+	1	0.956	0.056	tggtataTAAAtttttt
961	977	969	+	1	0.847	0.007	ttttTAAAaatatcacc
427	443	435	+	1	0.935	0.035	acttaTAAAtcgatcac
524	540	532	+	1	0.913	0.023	ttctTAAAtcatttg
566	582	574	+	1	0.854	0.014	ttctTAAAtcaagta
720	736	728	+	1	0.833	0.013	cccTATAatcacattgt
801	817	809	+	1	0.913	0.023	ttctTAAAtttatttg
815	831	823	+	1	0.931	0.031	agctaTAAAgattatga
79	95	87	+	1	0.875	0.095	cgggtttTAAGttcagc

113	129	121 +	1	0.864	0.044	gagTATAaggacatgaa
277	293	285 +	1	0.825	0.045	ttttgtTAAgtatgta
625	641	633 +	1	0.84	0.02	acaTATAatcctccttt
1107	1123	1115 +	1	0.904	0.014	ccctgTAAAagatcgac
69	85	77 +	1	0.966	0.066	ccctaTAAatcatagt
546	562	554 +	0.892	0.911	0.011	aattaTATAaatataaa
548	564	556 +	1	0.944	0.044	ttataTAAAtataaaaa
554	570	562 +	1	0.962	0.062	aaataTAAAaaataatt
605	621	613 +	1	0.976	0.076	aaataTAAAaaacgggt
1107	1123	1115 +	1	0.843	0.023	acaTATAattattagaa
29	45	37 +	1	0.783	0.003	ttatacaTAAGaattat
104	120	112 +	1	0.781	0.001	tgtaataTAAGtctaca
106	122	114 +	1	0.853	0.033	taaTATAagtctacatt
367	383	375 +	1	0.968	0.068	aaataTAAAaaatatt
420	436	428 +	1	0.958	0.058	ctttaTAAAaaatatt
482	498	490 +	1	0.934	0.034	tcttaTAAAtaattgaa
712	728	720 +	1	0.901	0.011	taacaTAAAgctaaat
1004	1020	1012 +	1	0.957	0.067	gaccaTAAAagacagat
1086	1102	1094 +	1	0.958	0.058	tgtaataTAAAaaatgatt
1361	1377	1369 +	1	0.945	0.045	agataTAAAtgaaagaa
294	310	302 +	1	0.849	0.029	tcaTATAaacttaaat
455	471	463 +	1	0.847	0.007	ttttTAAAaagccttc
643	659	651 +	1	0.849	0.029	acaTATAaatatatt
840	856	848 +	1	0.843	0.003	tcattTAAAaacttaag

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
146	162	154 +	1	0.921	0.091	gaaaaaTATAataaa	
148	164	156 +	1	0.91	0.08	aaaaataTATAaaaa	
256	272	264 +	1	0.963	0.133	tgagaaaTATAtatatt	
258	274	266 +	1	0.943	0.113	agaaataTATAatttt	
260	276	268 +	1	0.858	0.028	aaataataTATAtttaa	
894	910	902 +	1	0.955	0.125	tatgtaaTATAatttt	
896	912	904 +	1	0.846	0.016	tgtaataTATAtttag	
664	680	672 +	1	0.919	0.089	ggttaaTATAatcca	
1075	1091	1083 +	1	0.847	0.017	ccatcatTATAattga	
542	558	550 +	1	0.841	0.011	aaagaatTATAaaata	
1050	1066	1058 +	1	0.889	0.059	attgctaTATAttaca	
988	1004	996 +	1	0.835	0.005	agaaaaTATAgtatg	
27	43	35 +	1	0.837	0.007	caaacaTATAgtaaa	
414	430	422 +	1	0.834	0.004	catattaTATAttcct	
647	663	655 +	1	0.851	0.021	ataataaTATAtttatt	

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
769	785	777 +	1	0.837	0.007	aaaataaACGTgactca	
1077	1093	1085 +	1	0.9	0.08	aatttatACGTgtaatg	
1294	1310	1302 +	1	0.795	0.005	gacgaACACgagtcgat	

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
852	866	859 +	1	0.912	0.002	gcgccaGATCagaga	
968	982	975 +	1	0.912	0.002	tgggtaGATCtttct	
988	1002	995 +	1	0.871	0.021	acataaGATCagttc	
1379	1393	1386 +	1	0.925	0.015	tggaagGATCtgcaa	

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
31	49	40 +	0.826	0.936	0.036	tttccaaTTTAttgctcat	
171	189	180 +	1	0.882	0.012	aaattaaaTGATAagaaaa	
206	224	215 +	1	0.975	0.085	ctttgtTAATtaccct	
209	227	218 +	1	0.931	0.011	ttgttaaTTATcctgaa	

297	315	306 +	0.826	0.936	0.036	gaagaaaTTTAttgtgac
418	436	427 +	1	0.849	0.009	atgggtttgATTAtaatt
424	442	433 +	1	0.858	0.018	tttgattataATTGagttt
446	464	455 +	1	0.999	0.159	agtcatattaATTAattat
450	468	459 +	1	0.996	0.106	atattaatTAATtctct
621	639	630 +	1	0.877	0.047	agtatttaTCATttaaaca
809	827	818 +	1	0.966	0.036	accatggATGAttagattc
863	881	872 +	1	0.854	0.004	gagatCAATatttcaatc
881	899	890 +	1	0.927	0.007	caaataaaTTATgttccat
1333	1351	1342 +	1	0.94	0.05	agctcattTAATAaataat
1340	1358	1349 +	0.831	0.949	0.089	taatAAATaattttttt
1381	1399	1390 +	1	0.847	0.007	ttgacttaaATTAataaa
1384	1402	1393 +	1	1	0.1	gacttaaATTAataaattt
73	91	82 +	1	0.942	0.072	tgagtctattATTAccatc
105	123	114 +	1	0.894	0.004	tataaaaaTAATAacaaac
184	202	193 +	1	0.858	0.018	atataaaaaATTAatgaa
187	205	196 +	1	1	0.1	taaaaaaATTAatgaatat
191	209	200 +	1	0.848	0.018	aaaattaATGAatgatgatt
197	215	206 +	1	0.969	0.039	aatgaatATGAttggaat
291	309	300 +	1	0.902	0.002	aatcaacATTAattgtgat
348	366	357 +	1	0.85	0.02	ggtatgaATGAtaaacaac
568	586	577 +	1	0.945	0.025	tgtaaaaaTTATgtacatt
661	679	670 +	1	0.861	0.021	tttttatttATTAaatga
669	687	678 +	1	0.885	0.015	ttattaaaTGATgaatttg
692	710	701 +	1	0.861	0.021	tctcgtatttATTAaatcc
708	726	717 +	1	0.975	0.045	tccttttATGAttgaggat
750	768	759 +	1	0.935	0.065	tataaccataATTAccaag
765	783	774 +	1	1	0.06	caagacATTAagtaaaaag
855	873	864 +	1	0.981	0.141	tgtaagaataATTAataat
859	877	868 +	1	0.947	0.057	agaataatTAATAattgaa
862	880	871 +	0.866	0.961	0.101	ataatTAATAattgaatca
876	894	885 +	1	1	0.06	aatcacATTAaaatctctt
1114	1132	1123 +	1	0.998	0.098	taaaaaaATTAttacaaaa
1144	1162	1153 +	1	0.886	0.056	taaaagaATGAatgaatttt
1168	1186	1177 +	1	0.857	0.007	gaaacCAATagttttttat
1205	1223	1214 +	1	0.929	0.029	ttttaatATTAtaatcct
1250	1268	1259 +	1	0.949	0.059	aaggtagtTAATcaagttt
1260	1278	1269 +	1	0.844	0.004	atcaagttttATTAattta
1263	1281	1272 +	1	0.933	0.013	aagttttaTTATttataa
1271	1289	1280 +	1	0.879	0.039	ttatttataATTGatattg
1330	1348	1339 +	1	0.998	0.098	attaaaaATTAtttaaatta
1338	1356	1347 +	1	0.92	0	ttattaaaTTATAataata
1350	1368	1359 +	1	0.869	0.029	aataatatttATTAaattt
1367	1385	1376 +	1	0.904	0.034	tttctagattATTAcctta
126	144	135 +	1	0.998	0.098	cttaaaaATTAtttaataa
131	149	140 +	1	0.934	0.044	aaattattTAATAaaacaa
225	243	234 +	1	0.856	0.006	atcaaCAATatttgaatt
249	267	258 +	1	0.934	0.044	tgcaaaaaTAATtgcacac
360	378	369 +	1	0.842	0.002	tgaatcttttATTAacatt
406	424	415 +	1	0.989	0.059	aaattgaATGAttggttct
493	511	502 +	1	0.936	0.096	ctaatttgaATTAttttc
496	514	505 +	1	0.989	0.089	atttgaATTAttttcatt
526	544	535 +	0.936	0.936	0.046	ctttaaaATCAtttgatgg
637	655	646 +	1	0.84	0	caaatcttttATTAacatt
682	700	691 +	0.811	0.939	0.079	gaattGAATAattcattct
717	735	726 +	1	0.901	0.011	caccctaTAATcacattg
803	821	812 +	1	0.998	0.098	ctttaaaATTAtttggtgg
819	837	828 +	1	0.878	0.048	tgaataATGAtcgtgata

923	941	932 +	1	0.99	0.1	cactacaaTAATtcccaaa
955	973	964 +	1	0.931	0.031	ggtccatATTAatftttaga
1070	1088	1079 +	1	0.959	0.089	gatggccatcATTAtatat
1382	1400	1391 +	1	0.963	0.023	tctccgATTAaatttgtgt
302	320	311 +	1	0.971	0.041	aatgcacATGAttgccgct
818	836	827 +	1	0.926	0.006	tataaagaTTATgagttca
847	865	856 +	1	1	0.06	tcagtcATTAaaccgagag
970	988	979 +	1	0.863	0.023	tatctCAATgatctatcag
1098	1116	1107 +	1	0.963	0.023	tggcagATTAatatacacc
1274	1292	1283 +	1	0.877	0.047	cccctcaTCATgacttaa
1324	1342	1333 +	1	0.945	0.055	atcatttTAATcaacctg
482	500	491 +	1	0.842	0.002	aggaattttATTAagatg
506	524	515 +	1	0.845	0.005	gattacatttATTGagtat
554	572	563 +	1	0.955	0.035	caagtctaTTATgccacaa
713	731	722 +	1	0.972	0.042	agaatacATGAttatcagc
811	829	820 +	1	0.88	0.05	ggaatgaATGAtgatgaa
814	832	823 +	1	0.883	0.053	atgaatgATGAtgaaaatt
1039	1057	1048 +	1	0.868	0.028	ttttcagataATTGttgat
281	299	290 +	1	0.775	0.005	gaaagacATGAaaccctc
410	428	419 +	1	0.862	0.022	agtcatttATTAattgt
414	432	423 +	1	0.853	0.003	atatttatTAATtgttttc
466	484	475 +	1	0.953	0.113	atactgataATTAaaaaa
520	538	529 +	1	0.884	0.054	tattttATGAtgatttta
523	541	532 +	1	0.972	0.042	ttttatgATGAttttaaaa
540	558	549 +	1	0.93	0.01	aaaaagaaTTATataaata
558	576	567 +	1	0.969	0.129	ataaaaaataATTAaaaat
667	685	676 +	1	1	0.06	caaacATTAaaaaatggt
843	861	852 +	1	0.968	0.018	catttCAATaatattgtgt
943	961	952 +	1	0.939	0.049	atagaagtTAATAataaaaa
946	964	955 +	0.884	0.832	0.002	gaagtTAATAataaaaatta
961	979	970 +	0.811	0.929	0.069	attaaGAATAaatttgaaa
1062	1080	1071 +	1	0.847	0.007	ttacatcaaaATTAattgt
1065	1083	1074 +	1	1	0.1	catcaaaATTAattgtgga
1104	1122	1113 +	1	0.933	0.093	ccgacatataATTAttaga
1107	1125	1116 +	1	0.989	0.089	acatataATTAttagaaaa
1224	1242	1233 +	1	0.972	0.042	tgggtctATGAtttcaaaa
1260	1278	1269 +	1	0.912	0.022	tatttgaTTATgaaagt
1276	1294	1285 +	0.9	0.96	0.01	agtcaTAATcattcataag
1317	1335	1326 +	1	0.972	0.042	attaggtATGAttaaaaag
1321	1339	1330 +	1	0.963	0.023	ggtatgATTAaaaagatgc
21	39	30 +	1	0.926	0.006	ttatgcaTTATacataag
34	52	43 +	1	0.99	0.09	cataagaATTAtactatt
212	230	221 +	1	0.934	0.044	ttttttcTAATtatgaaa
215	233	224 +	1	0.94	0.02	ttttctaaTTATgaaaaca
251	269	260 +	0.831	0.932	0.072	atggaAAATAaattttttc
266	284	275 +	0.826	0.936	0.036	tttcaaaTTTAttctaaaa
483	501	492 +	0.831	0.951	0.091	cttatAAATAaattgaaaat
720	738	729 +	1	0.976	0.076	aagctaaATTAactaatcgt
768	786	777 +	0.826	0.936	0.036	catgaaaGTTAtgtgggc
928	946	937 +	1	1	0.11	tttgacaATTAttttctca
948	966	957 +	1	0.844	0.004	aaacaattttATTAtacac
951	969	960 +	1	0.929	0.009	caattttaTTATacacaac
1090	1108	1099 +	1	0.994	0.064	ataaaaaATGAttatgaaa
1093	1111	1102 +	1	0.935	0.015	aaaaatgaTTATgaaaaa
41	59	50 +	1	0.998	0.098	aaaaaaaATTAttttcttt
113	131	122 +	0.831	0.94	0.08	gacaaAAATAaattttgaa
181	199	190 +	1	0.998	0.098	atctaaaATTAttggtttg
219	237	228 +	1	1	0.1	tattcaaaATTAatgttttt

229	247	238 +	1	0.984	0.094	aatgtttTAATtatgaaa
232	250	241 +	1	0.939	0.019	gttttaaTTATgaaagat
246	264	255 +	0.826	0.938	0.038	aagataaTTTAatctattc
314	332	323 +	0.826	0.936	0.036	tttcaaTTAAttattgt
318	336	327 +	1	0.839	0.009	caattattTATTgtgaca
339	357	348 +	1	0.991	0.151	acataattaATTAaatta
344	362	353 +	1	0.84	0	atthaataaATTAaatt
354	372	363 +	0.826	0.936	0.036	atataaaTTAAttcacta
363	381	372 +	1	0.963	0.123	tattcactaATTAaattc
382	400	391 +	1	0.852	0.012	tatgtattgATTAactta
386	404	395 +	1	0.963	0.023	tattgATTAacttacacc
527	545	536 +	1	0.842	0.002	gcattctttATTAttatt
530	548	539 +	1	0.923	0.053	ttctttattATTAttatt
533	551	542 +	1	0.923	0.053	tttattattATTAttatt
536	554	545 +	1	0.923	0.053	tattattattATTAttttc
572	590	581 +	1	1	0.06	gcacacATTAagataaca
664	682	673 +	1	0.851	0.001	tactcattTAATttttaa
787	805	796 +	1	0.963	0.023	aatagATTAaccctagct
866	884	875 +	1	0.962	0.012	atctCAATAataaatcaa
934	952	943 +	1	0.945	0.055	actaacctTAATcaatttt
941	959	950 +	1	0.835	0.005	ttaatCAATtttttttga
976	994	985 +	1	0.973	0.133	ttcaaaactaATTAataaa
980	998	989 +	1	0.948	0.058	aaactaatTAATAaatata
996	1014	1005 +	1	0.931	0.031	ataatatATTAatttagga
1138	1156	1147 +	1	0.998	0.098	acataaaATTAttaattgt
1168	1186	1177 +	1	0.916	0.026	ttcacctTAATAagttta
1177	1195	1186 +	1	0.99	0.15	aataagtttaATTAattat
1181	1199	1190 +	1	0.999	0.109	agtttaataATTAattttg
1184	1202	1193 +	1	0.989	0.089	ttaattaATTAattttgtaa
1217	1235	1226 +	1	0.852	0.002	tcaagaatTAATtttgggc
1331	1349	1340 +	1	0.929	0.009	atcatataTTATtataaaa

**tart positioend positiochor positi Strand Core sim. Matrix simat. sim. - o Sequence**

868	878	873 +	1	0.866	0.006	cAATAttttca
882	892	887 +	1	0.906	0.046	aAATAaattat
1393	1403	1398 +	1	0.894	0.034	tAATAaattta
955	965	960 +	1	0.882	0.022	aAATAttttt
1303	1313	1308 +	1	0.899	0.039	aAATAaatttt
1394	1404	1399 +	1	0.988	0.128	tAATAtattta
329	339	334 +	1	0.875	0.015	gAATAtagtat
435	445	440 +	1	0.899	0.039	aAATAaatttt
462	472	467 +	1	0.881	0.021	aAATAtacttg
377	387	382 +	1	0.889	0.029	aAATAttttag
498	508	503 +	1	0.882	0.022	aAATAttttta
279	289	284 +	1	0.894	0.034	tAATAaatttc
619	629	624 +	1	0.876	0.016	aAATAtttcc
651	661	656 +	1	0.988	0.128	tAATAtattta
765	775	770 +	1	0.87	0.01	cAATAttttga
787	797	792 +	1	0.89	0.03	aAATAgattaa
903	913	908 +	1	0.875	0.015	tAATAttttga
992	1002	997 +	1	0.902	0.042	aAATAtaatat
997	1007	1002 +	1	0.994	0.134	tAATAtattaa

**tart positioend positiochor positi Strand Core sim. Matrix simat. sim. - o Sequence**

234	248	241 +	1	0.814	0.014	aagctTCGTatgct
688	702	695 +	1	0.802	0.002	ctttcTCGTattta
1324	1338	1331 +	1	0.817	0.017	atttctTCGTatttt
759	773	766 +	1	0.873	0.023	acttcatgGTACaat

1141	1155	1148 +	1	0.871	0.021	aggttcttGTACTaa
765	779	772 +	1	0.872	0.022	aatttctgGTACatg

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>1</sub>	Sequence
885	897	891 +		1	0.932	0.002	aatTGTCtcaatc

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>1</sub>	Sequence
1222	1232	1227 +		1	0.913	0.083	ctGTCGgccga
1014	1024	1019 +		1	0.961	0.131	cggTCGAcaga
699	709	704 +		1	0.965	0.135	ttGTCGgtaaa

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>1</sub>	Sequence
1298	1318	1308 +		1	0.947	0.017	aaaaAAATaaatatttc
430	450	440 +		1	0.935	0.005	ttcaaAAATaaatatttt
568	588	578 +		1	0.941	0.011	attaaAAATaaaatattaa
343	363	353 +		0.93	0.936	0.006	aatttAATaaattaaat
347	367	357 +		1	0.937	0.007	taattAAATaaaatatttt

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>1</sub>	Sequence
220	228	224 +		1	0.867	0.007	tccTTGAaa
252	260	256 +		1	0.918	0.058	tcgTTGAga
285	293	289 +		1	0.867	0.007	gccTTGAat
870	878	874 +		1	0.867	0.007	taaTTGAat
691	699	695 +		1	0.92	0.06	ttgTTGAat
222	230	226 +		1	0.867	0.007	tagTTGAag
1303	1311	1307 +		1	0.894	0.034	tagTTGAaa
274	282	278 +		1	0.865	0.005	tagTTGAga
662	670	666 +		1	0.906	0.046	tccTTGAct
1100	1108	1104 +		1	0.867	0.007	tttTTGAat

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>1</sub>	Sequence
671	689	680 +		1	0.83	0	gtcaaaCGTGaggaaatt
1231	1249	1240 +		1	0.954	0.004	gatctcCGTGtgctggcct

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>1</sub>	Sequence
163	173	168 +		1	0.992	0.002	aaaaAAAGaaa
185	195	190 +		1	0.993	0.003	gaaaAAAGtta
520	530	525 +		1	0.992	0.002	caaaAAAGttg
739	749	744 +		1	0.992	0.002	ataaAAAGatg
279	289	284 +		1	0.997	0.007	aaaaAAAGgtg
412	422	417 +		1	0.969	0.009	caaaAAAGtgt
538	548	543 +		1	0.992	0.002	aaaaAAAGaat
805	815	810 +		1	0.991	0.001	ttaaAAAGtat
127	137	132 +		1	0.968	0.008	aaaaAAAGtct

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>1</sub>	Sequence
615	623	619 +		1	0.993	0.023	atCCAAtca
1170	1178	1174 +		1	0.979	0.009	aaCCAAtag
187	195	191 +		1	0.976	0.006	ccCCAAtca
1366	1374	1370 +		1	0.974	0.004	acCCAAttg

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>1</sub>	Sequence
615	633	624 +		1	0.808	0.028	gttatcgAACAcataataat
22	40	31 +		1	0.784	0.004	catttcaACAatatatgt

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>1</sub>	Sequence
145	161	153 +		1	0.904	0.064	ggaaaaAATatataaa
255	271	263 +		1	0.871	0.031	ttgagaAATatataat

454	470	462 +	1	0.844	0.014	taattaatTATCtctat
479	495	487 +	0.808	0.869	0.019	tgcccaaAAATcaaacc
573	589	581 +	1	0.848	0.018	cgtttcaaTATCattct
493	509	501 +	1	0.984	0.144	ttttaaGATAtttgatt
879	895	887 +	1	0.919	0.069	cacattaaAATCtctta
881	897	889 +	1	0.872	0.042	cattaAAATcctctatg
950	966	958 +	1	0.894	0.054	gtataaAATAtttttt
1002	1018	1010 +	1	0.893	0.053	aaataaAATAtttgttt
1071	1087	1079 +	1	0.948	0.108	caattaAATAtcacttt
1347	1363	1355 +	1	0.85	0.01	tataatAATAtttatta
323	339	331 +	1	0.832	0.002	tatagAAATcctcaca
1338	1354	1346 +	1	0.907	0.067	tggctGATAtttgaac
605	621	613 +	1	0.944	0.104	tcgccaAATAtcatttt
962	978	970 +	1	0.851	0.051	tctacagaTATCtcaat
152	168	160 +	1	0.939	0.019	aagcaaGATAttgagtg
468	484	476 +	1	0.921	0.001	agaacaGATAagagagg
1039	1055	1047 +	1	0.844	0.004	ttttcaGATAattgttg
1392	1408	1400 +	1	0.928	0.088	aacctGATAttttct
584	600	592 +	1	0.867	0.017	taaatacaAATCttaat
620	636	628 +	1	0.9	0.06	gttaaaAATAtttcaaa
629	645	637 +	1	0.866	0.026	atttcaAATAtttaaac
760	776	768 +	1	0.97	0.13	accaaaAATAtcctatt
1252	1268	1260 +	1	0.911	0.071	tcaaacGATAtttgtat
362	378	370 +	1	0.841	0.001	atataaAATAtaaaaaa
372	388	380 +	1	0.901	0.061	taaaaaAATAttttaga
424	440	432 +	1	0.896	0.056	ataaaaAATAtgtagag
493	509	501 +	1	0.894	0.054	attgaaAATAttttaa
987	1003	995 +	1	0.903	0.063	tagaaaAATAtatgtat
1356	1372	1364 +	1	0.994	0.074	gtggaaGATAtaaatga
57	73	65 +	1	0.892	0.042	ttttgcaaAATCtgtat
124	140	132 +	1	0.897	0.047	ttttgaaAATCtacta
242	258	250 +	1	0.869	0.029	atgaaaGATAatftaat
278	294	286 +	1	0.848	0.018	ataatAAATtctaat
614	630	622 +	1	0.896	0.056	aaaaaaAATAtttcca
646	662	654 +	1	0.858	0.018	tataatAATAtatttat
806	822	814 +	1	0.947	0.097	taaatcaaAATCtttta
882	898	890 +	1	0.881	0.031	caaccatAATCttaa
957	973	965 +	1	0.929	0.089	tgaaagAATAtctagcg
992	1008	1000 +	1	0.861	0.021	aatatAATAtattaat
1026	1042	1034 +	1	0.936	0.086	tttaaaaaAATCtgaat
1118	1134	1126 +	1	0.938	0.088	aagaggaaAATCtaatt
1359	1375	1367 +	1	0.842	0.002	aaaaaaAATAgcaaata
1371	1387	1379 +	0.808	0.89	0.04	aaataaaAAATcatatt

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
122 134 128 + 0.826 0.905 0.035 agaaCACTtctat

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
1212 1228 1220 + 1 0.966 0.126 atcCGCGtgctaacgct  
6 22 14 + 0.817 0.795 0.015 tgtCGAGgttgatagca

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
683 703 693 + 1 0.863 0.013 atttGCTTtctcgtatttat  
739 759 749 + 1 0.853 0.003 cttGCTTgagaccgagg  
346 366 356 + 1 0.87 0.02 atttGCTTtatggcatttt  
987 1007 997 + 1 0.856 0.006 aactGCTTgaaagatgg  
831 851 841 + 1 1 0 gtttGCTTccctacaccggt  
799 819 809 + 1 0.863 0.013 cctaGCTTaatcaaaatc

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
130	152	141 +		1	0.989	0.019	ggggtgagaAAAAGaggg;
154	176	165 +		1	0.994	0.004	atataaaaaaaaaAAAGa;
156	178	167 +		1	0.993	0.003	ataaaaaaAAAAagaaa
158	180	169 +		1	0.97	0.01	ataaaaaaAAAAGaaatt;
180	202	191 +		1	0.995	0.035	gataagaaaAAAGttatae
225	247	236 +		1	0.994	0.014	gaaaaaattAAAGaaaac
515	537	526 +		1	0.978	0.018	ccggacaaaAAAGttgag
334	356	345 +		1	0.991	0.021	taaaaaataAAAGaggtai
579	601	590 +		1	0.772	0.022	tgtacattacatgcAAAGgc
258	280	269 +		1	0.987	0.017	aattgcacaAAAGagaga
274	296	285 +		1	0.979	0.099	gaaaaaaaaAAAAGgtga;
1058	1080	1069 +		1	0.982	0.002	tattggcttAAAGatggcca
1123	1145	1134 +		1	0.972	0.002	cgccaactaAAAGtgaag
231	253	242 +		1	0.987	0.017	tgatgtttaAAAGagactta
407	429	418 +		1	0.989	0.019	ggcaccaaaaAAAGtgtcc;
492	514	503 +		1	0.995	0.015	agctacaatAAAGctagca
659	681	670 +		1	0.843	0.093	agctcatcatgtgaAAAGtc
664	686	675 +		1	0.985	0.015	atcatgtgaAAAGtggact;
807	829	818 +		1	0.792	0.042	tatgtaggagctatAAAGal
697	719	708 +		1	0.761	0.011	gtaggatgaaattcAAAGa
1323	1345	1334 +		1	0.97	0	attttgagtAAAGtgtggag;
1368	1390	1379 +		1	0.758	0.008	caagctaggagtggAAAG
241	263	252 +		1	0.977	0.007	ggaatcacaAAAGgggga;
256	278	267 +		1	0.981	0.001	gaatgaaaaaAAAAGag;
258	280	269 +		1	0.989	0.019	atgaaaaaaaaAAAGagata
531	553	542 +		1	0.993	0.003	tgattttaaAAAAGAaattat
800	822	811 +		1	0.982	0.012	tggacttaaAAAGtatccct
1156	1178	1167 +		1	0.996	0.006	gtcttggctAAAGcaatgg;
1368	1390	1379 +		1	0.764	0.014	ccaattgggtgtgaAAAGta
1373	1395	1384 +		1	0.972	0.042	tgggtgtgaAAAGtaagatt
3	25	14 +		1	0.781	0.031	tatttttttttAAAGtttat
78	100	89 +		1	0.935	0.005	aaaatttttAAAGtaattttae
122	144	133 +		1	0.971	0.011	tttgtaaaaAAAGtctgaag
273	295	284 +		1	0.995	0.005	tttattctaAAAGcatatttta
710	732	721 +		1	0.986	0.006	cctaacataAAAGctaata
1228	1250	1239 +		1	0.993	0.013	catgaacatAAAGctaact
1285	1307	1296 +		1	0.895	0.015	tgaaggctAAAAGgctaa;
1293	1315	1304 +		1	0.995	0.005	aaaaggctaAAAGcatag
454	476	465 +		1	0.996	0.006	tttttttaaAAAGcctctctc
1032	1054	1043 +		1	0.781	0.031	aaaatctgaattttAAAGtct
1087	1109	1098 +		1	0.934	0.014	ttggttgatAAAGttttgaat;
1100	1122	1111 +		1	0.985	0.005	ttttgaatAAAGaagagae

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
600	610	605 +		1	0.92	0.03	gACACtcgcca

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
1284	1304	1294 +		1	0.84	0.03	ttcttcacaCGACatgtagg
11	31	21 +		1	0.833	0.023	aggttgataCGACatggttt
38	58	48 +		1	0.88	0.07	aagaattaaCGACattgat
1100	1120	1110 +		1	0.858	0.048	tgtaggttgCGACatctcac
1249	1269	1259 +		1	0.874	0.024	ttggctaACCGtctccgac
1256	1276	1266 +		0.801	0.899	0.009	accgtccTCCGacggggc
1271	1291	1281 +		1	0.937	0.067	gggtctccCGACaatga;
851	871	861 +		1	0.779	0.009	tcattaaaCCGAgagcg;
25	45	35 +		1	0.946	0.056	caattgggCCGActtcatgl

1009	1029	1019 +	1	0.881	0.021	ccacacggtCGACagagt
1096	1116	1106 +	1	0.993	0.133	ataaagagcCGACatata
906	926	916 +	1	0.854	0.054	agcaccACCgagagag

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
53	67	60 +		0.811	0.878	0.058	ccatgcATTGcattt
1388	1402	1395 +		1	0.833	0.013	agattcAATGttggt

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
768	790	779 +		1	0.992	0.002	aaaaataaacgtgactCAC
776	798	787 +		1	0.997	0.007	gtaaaagatgaaccttCAC
829	851	840 +		1	0.832	0.082	atcgtgataatCAGTccac
352	374	363 +		1	0.99	0	aaattaaaatttttCACTa

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
1066	1084	1075 +		1	0.837	0.027	gccatattTCCcatggat

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
198	216	207 +		1	0.904	0.034	aaattctcttTTGTtaa
1002	1020	1011 +		1	0.967	0.097	aaataaaatatTTGTtta
554	572	563 +		1	0.906	0.036	gggcaacatatTTGTtca
640	658	649 +		1	0.912	0.042	ttaacaaattTTGTtaa
1033	1051	1042 +		1	0.884	0.014	aaaacagtttTTGTtctt
822	840	831 +		1	0.904	0.034	aaagatttttTTGTttt

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
1358	1374	1366 +		1	0.864	0.014	tgagatGGGCcaagcta
24	40	32 +		1	0.861	0.011	tcaattGGGCcgacttc
158	174	166 +		1	0.891	0.041	tttttGGGCatgggt

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
265	297	281 +		1	1	0	caaaagAGAGaaaaaa

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
194	208	201 +		1	0.904	0.024	attaATGAatatgat
820	834	827 +		1	0.908	0.028	gatgATGAaaattag
889	903	896 +		1	0.898	0.018	tttgATGAataaaac
1052	1066	1059 +		1	0.9	0.02	gttgATGAagatgag
254	268	261 +		1	0.927	0.047	gggaATGAaaaaaaa
932	946	939 +		0.808	0.889	0.009	aaaaATTAaaaaatg
1238	1252	1245 +		0.808	0.889	0.009	caaaATTAagaaaaat
1099	1113	1106 +		1	0.918	0.038	gattATGAaaaaatg
1140	1154	1147 +		1	0.951	0.071	ccagATGAacataat
574	588	581 +		0.808	0.892	0.012	acacATTAagataac

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
971	981	976 +		1	0.907	0.037	gtaGATCtttc
102	112	107 +		1	0.854	0.004	aaAGATttgta
1294	1304	1299 +		1	0.997	0.027	gtAGATccgga
674	684	679 +		1	0.97	0	aaAGATccttg
1382	1392	1387 +		1	0.976	0.006	aaAGATctgca
342	352	347 +		1	0.972	0.002	gaAGATttgct

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
337	349	343 +		0.968	0.899	0.019	taTCGAtgtccat

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
769	787	778 +		1	0.88	0.04	aaaataaACGTgactcac

1066	1084	1075 +	1	0.986	0.046	aattcaCACGtaatttata
1077	1095	1086 +	1	0.911	0.001	aatttatACGTgtaatgtg
1349	1367	1358 +	1	0.913	0.003	agtggaAACGTgtaaca:
742	760	751 +	1	0.988	0.048	taggccCACGtcatggag:

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
1114	1132	1123 +		1	0.906	0.056	tctcacatcCGCCaactaa
26	44	35 +		1	0.898	0.028	acagtttGCCGtctggtag
1096	1114	1105 +		1	0.931	0.061	ataaagaGCCGacatata

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
191	207	199 +		1	0.984	0.064	agttataaaATTCttct
327	343	335 +		1	0.953	0.033	ctgttgatATTCtttt
815	831	823 +		1	0.967	0.017	gatgattagATTCatag
929	945	937 +		1	0.975	0.075	aatcagaatATTCcttt
1234	1250	1242 +		1	0.959	0.039	tatatttatATTCttaa
114	130	122 +		1	0.946	0.026	ttcttcacATTCttaa
514	530	522 +		1	0.954	0.004	tccttcatATTCttta
791	807	799 +		1	0.953	0.033	ttattcacATTCttta
708	724	716 +		1	0.957	0.007	aaagcagagATTCacct
1019	1035	1027 +		1	0.992	0.072	atgttaaaaATTCttat
1360	1376	1368 +		1	0.915	0.015	gtaacaacATTCaata
873	889	881 +		1	0.925	0.025	accttaatATTCagaa
1381	1397	1389 +		1	0.977	0.097	aaaagtaagATTCaatg
369	385	377 +		1	0.964	0.044	actaattaaATTCtatg
745	761	753 +		1	0.967	0.017	acaatttagATTCataa

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
455	465	460 +		1	0.948	0.018	atccTGACatg
1058	1068	1063 +		1	0.942	0.012	tgccTGACatt

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
91	109	100 +		1	0.828	0.038	ttttacATGGcaatgtag
609	627	618 +		0.969	0.877	0.027	ccattttaaGTAAtattt
972	990	981 +		1	0.878	0.008	tagatcttcTTAAaaca
1352	1370	1361 +		0.844	0.858	0.008	ttttttggGTCAattcct
126	144	135 +		1	0.977	0.047	cacttctatGTGAAttgaa
560	578	569 +		1	0.978	0.098	gtttgtaggTAAAaatta
767	785	776 +		1	0.937	0.057	agacattaagTAAAagatg
856	874	865 +		1	0.878	0.008	gtaagaataaTTAAaatt
906	924	915 +		1	0.951	0.081	attttagtgTTAAatga
1035	1053	1044 +		1	0.925	0.045	tgaaaagatgTAAAacaal
1247	1265	1256 +		1	0.816	0.006	ttaaaggtaGTTAatcaag
1280	1298	1289 +		1	0.857	0.007	aattgatatGTTAatttca
1331	1349	1340 +		1	0.887	0.017	ttaaaaattaTTAAattat
1351	1369	1360 +		1	0.894	0.024	ataatattaTTAAatttt
117	135	126 +		1	0.886	0.016	ttcacattcTTAAaatt
518	536	527 +		1	0.873	0.003	ttcatattctTTAAaatca
535	553	544 +		1	0.874	0.084	catttgATGGaataacaat
1353	1371	1362 +		1	0.868	0.078	actttgATGGatcagagt
227	245	236 +		1	0.876	0.006	catgtgatgTTAAaagag
829	847	838 +		1	0.889	0.059	tgagttcaaGTAActtct
844	862	853 +		1	0.884	0.014	ttctcagtcTTAAaccga
1012	1030	1021 +		1	0.9	0.03	aatttgaatgTTAAaaatt
1072	1090	1081 +		1	0.88	0.01	tccaagtcaGTAAtgcag
318	336	327 +		0.844	0.875	0.025	atcaatgaaGTGAatatac
372	390	381 +		0.844	0.87	0.02	ccctcatagGTCAatagt
1102	1120	1111 +		1	0.92	0.04	gagggccctgTAAAagatc

109	127	118 +	1	0.833	0.043	aaactcATGGcaaaacttt
233	251	242 +	1	0.795	0.005	ctaaccATGGaatcacaa:
350	368	359 +	0.844	0.867	0.017	gcttttatgGTCAttttt
374	392	383 +	1	0.811	0.001	ttcttttagGTTAtagcaa
467	485	476 +	1	0.914	0.044	tacttgataaTTAAaaaaa
526	544	535 +	1	0.873	0.003	tatgatgattTTAAaaaaa
559	577	568 +	1	0.892	0.022	taaaaaataaTTAAaata
592	610	601 +	1	0.881	0.011	aatcttaattTTAAaatat
611	629	620 +	0.826	0.905	0.015	aaaaaacggGTTAaaaa:
679	697	688 +	1	0.926	0.046	aatgtttgTAAAttgt
748	766	757 +	1	0.805	0.015	cacgtcATGGagacccaa
795	813	804 +	1	0.876	0.006	gagaatggacTTAAaaag
920	938	929 +	1	0.884	0.014	tgataaggagTTAAaaatt
927	945	936 +	1	0.884	0.014	gagtaaaaaTTAAaata
940	958	949 +	1	0.895	0.025	aaaatagaagTTAAaata
1318	1336	1327 +	1	0.932	0.062	ttaggtatgaTTAAaaaga
81	99	90 +	0.969	0.867	0.017	attttaaaGTAAAtttaa
116	134	125 +	1	0.969	0.089	ctacatttgTAAAaaaag
245	263	254 +	1	0.866	0.076	gtttgATGGaaaataatt
306	324	315 +	1	0.875	0.005	ttaggtgtttTAAActtt
565	583	574 +	1	0.877	0.027	taatagaagGTTAttctca
577	595	586 +	1	0.913	0.123	attctcATGGattcatcta
594	612	603 +	1	0.87	0.02	taattctaGTTActgtta
696	714	705 +	1	1	0.08	agattgctgGTAAacctaa
1040	1058	1049 +	1	0.967	0.097	tttttgctcTTAAaata
30	48	39 +	1	0.97	0.09	acaatatatgTAAAaaaaa
226	244	235 +	1	0.877	0.007	attaatgtttTAAAttatg
449	467	458 +	1	0.886	0.016	ttttttttTTAAaaagc
598	616	607 +	1	0.875	0.005	ttttttttTTAAaaaaa
668	686	677 +	1	0.919	0.049	catttaattTTAAaattt
906	924	915 +	1	0.938	0.068	tatttgataTTAAaaaga
1017	1035	1026 +	1	0.87	0	aggatttatTTAAaaaaa
1146	1164	1155 +	1	0.934	0.054	ttattaatgTAAAggat
1377	1395	1386 +	1	0.892	0.022	aaaatcatatTTAAaaat

**Start position, end position, core position, Strand, Core sim., Matrix sim., sim. - o1, Sequence**

224	246	235 +	1	0.824	0.014	tgaaaaaattaaAGAAaa:
284	306	295 +	0.826	0.821	0.011	aaagaaaatttaGGAAga
788	810	799 +	0.807	0.879	0.069	gttgaacaATCTggaaag:
931	953	942 +	1	0.986	0.136	tcagaataTTCCttttcgaa:
971	993	982 +	1	0.829	0.019	gtagatctTCTtaaaaac:
1163	1185	1174 +	1	0.851	0.011	ataGAAGcatcaaatggg:
159	181	170 +	1	0.832	0.002	aaactattTCTatacattat
310	332	321 +	1	0.85	0.04	caagaagggaaAGAAg:
782	804	793 +	0.861	0.946	0.096	gatgaaccTTCActatcat:
823	845	834 +	1	0.873	0.063	ttagtggaTCTTgaatttcg
1094	1116	1105 +	1	0.881	0.071	taagaattgtttAGAAtaga:
1360	1382	1371 +	1	0.907	0.097	attaaattTCTagattatta:
178	200	189 +	1	0.877	0.047	gtcaatccTCTTacaagta:
388	410	399 +	0.801	0.867	0.037	gtttataTTCAagaatcaa:
669	691	680 +	0.801	0.865	0.035	aatatataTTCAagaattg:
1205	1227	1216 +	0.845	0.837	0.007	ctaacattTCCataacctg
70	92	81 +	1	0.879	0.049	ctgtttcTCTTaaaaggatt
121	143	132 +	1	0.845	0.035	accatggcTCTTggaattg
262	284	273 +	1	0.841	0.031	gatgtctgTCTTggagta:
274	296	285 +	1	0.857	0.107	ggagtaaTTTCaggaaag:
647	669	658 +	1	0.82	0.02	accgattTCTTagctcat:
914	936	925 +	1	0.854	0.044	tttcagaaTCTTggaactct

982	1004	993 +		1	0.824	0.014	ctatcagtTTCTggaccttc
1136	1158	1147 +		0.857	0.754	0.004	agaaaagGTTCTgtgacta
1362	1384	1373 +		0.801	0.836	0.006	taacaacaTTCAataaca
701	723	712 +		1	0.822	0.012	gatgaaattcaaAGAAtac
945	967	956 +		1	0.872	0.012	atgagtggctCTAGaatcc
1155	1177	1166 +		0.845	0.834	0.004	accaattcTTCcaciaaagf
1190	1212	1201 +		1	0.864	0.004	tgttgcctttCTAGgagcctt
1305	1327	1316 +		1	0.861	0.051	gttgaaatggtGAGAAcca
478	500	489 +		1	0.829	0.019	taaaaaaatatAGAAaaa
269	291	280 +		1	0.847	0.017	caaatttaTTCtaaagca
717	739	728 +		1	0.968	0.118	ttgaattTTCtattttcatca

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
17	31	24 +		1	1	0	atTTATTttttatt
84	98	91 +		1	1	0	tattTATTtttacct
145	159	152 +		1	1	0	gattTATTtttttaa
812	826	819 +		1	0.926	0.036	ctttTATTttattag
954	968	961 +		1	0.904	0.014	aaaaTATTtttttaa
1268	1282	1275 +		1	0.958	0.068	ttatTATTttataat
1351	1365	1358 +		1	0.899	0.009	ataaTATTtattaaa
131	145	138 +		1	0.979	0.089	aatTATTtaataaa
442	456	449 +		1	1	0	ttttTATTttttaa
46	60	53 +		1	0.918	0.028	aatTATTttctttt
319	333	326 +		1	0.898	0.008	aattTATTtattgtg
544	558	551 +		1	0.898	0.008	ttatTATTttcta
1189	1203	1196 +		1	0.904	0.014	taatTATTtghtaat

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
1205	1221	1213 +		1	0.76	0	ctccccacATCCgcggtgc

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
175	191	183 +		1	0.989	0.059	taaatGATAagaaaaaa
352	368	360 +		1	0.935	0.005	tgaatGATAaacaata
733	749	741 +		1	0.943	0.013	caagaGATAaaaagatg
1107	1123	1115 +		1	0.954	0.024	gaataGATAaaaaaatt
152	168	160 +		1	0.932	0.002	actatGATAatcagtc
734	750	742 +		1	0.932	0.002	tggtgGATAaattgact
1223	1239	1231 +		1	0.957	0.027	gggatGATAatggtgat
133	149	141 +		1	0.932	0.002	cggtgGATAaattccatt
469	485	477 +		1	0.964	0.034	gaacaGATAagagaggg
285	301	293 +		1	0.935	0.005	gacatGATAaccctct
916	932	924 +		1	0.953	0.023	tcggtGATAaggagtta
1090	1106	1098 +		1	0.95	0.02	aattaGATAaagagccg
1013	1029	1021 +		1	0.94	0.01	agacaGATAacagataa
1020	1036	1028 +		1	0.94	0.01	taacaGATAacagaaaa
1266	1282	1274 +		1	0.951	0.021	tggccGATAagagaaa
1382	1398	1390 +		1	0.961	0.031	ggatGATAataagtaa
243	259	251 +		1	0.958	0.028	tgaaaGATAaattaatc
578	594	586 +		1	0.975	0.045	attaaGATAacacaac
1088	1104	1096 +		1	0.939	0.009	tggtGATAaagttttt

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
895	913	904 +		1	0.952	0.032	tccatTTGTcccaaatttt
1005	1023	1014 +		1	0.925	0.005	gtctcTTGTccatttgatg
1092	1110	1101 +		1	0.934	0.014	tggtTTGTctatgtgggt
1064	1082	1073 +		1	0.967	0.047	acattTTGTccaagtcatg
121	139	130 +		1	0.93	0.01	aaactTTGTcttccactag

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
489	513	501 +		1	0.752	0.002	tcaaaccattcatagGTGT
726	750	738 +		1	0.769	0.019	actctccaacctacGTGT
1078	1102	1090 +		1	0.787	0.037	atftatacgtgtaatGTGT
66	90	78 +		1	0.755	0.005	ttcgacaatgtgccgGTGT
785	809	797 +		1	0.872	0.122	gttgtttaaggcaaGTGT
295	319	307 +		1	0.809	0.059	aagagaaaatfttagGTGT

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
194	206	200 +		1	0.921	0.051	tataaaATTCttc
330	342	336 +		1	0.886	0.036	gttgatATTCttt
359	371	365 +		1	0.935	0.015	gaGAATAactaaa
932	944	938 +		1	0.999	0.179	cagaATATcctt
1035	1047	1041 +		1	0.932	0.012	tcGAATAagagct
1304	1316	1310 +		1	0.888	0.018	cactatATTCcac
100	112	106 +		1	0.965	0.045	agGAATataaaaa
198	210	204 +		1	0.931	0.011	atGAATatgattg
858	870	864 +		1	0.944	0.024	aaGAATAattaat
929	941	935 +		1	0.864	0.014	ggtgatATTCaat
1237	1249	1243 +		1	0.891	0.041	atftatATTCtta
389	401	395 +		1	0.867	0.017	tttcatATTCaag
517	529	523 +		1	0.885	0.035	tttcatATTCttt
542	554	548 +		1	0.954	0.034	tgGAATAacaatt
670	682	676 +		1	0.872	0.022	atatatATTCaag
685	697	691 +		1	0.93	0.01	ttGAATAattcat
819	831	825 +		1	0.961	0.041	tgGAATAatgatc
1285	1297	1291 +		1	0.94	0.02	atGAATattgccc
154	166	160 +		1	0.934	0.014	gaGAATAacgggt
202	214	208 +		1	0.92	0	gtGAATAagggtg
802	814	808 +		1	0.945	0.025	aaGAATatgtagg
1022	1034	1028 +		1	0.917	0.047	ttaaaaATTCtta
1307	1319	1313 +		1	0.992	0.072	tgGAATatccccgc
1363	1375	1369 +		1	0.911	0.041	aacaacATTCaat
136	148	142 +		1	0.871	0.041	tgataATTCcat
173	185	179 +		1	0.857	0.007	aacgatATTCgcc
327	339	333 +		1	0.932	0.012	gtGAATatagtat
893	905	899 +		1	0.923	0.003	atGAATAaaactg
876	888	882 +		1	0.931	0.061	tttaatATTCaga
964	976	970 +		1	0.944	0.024	aaGAATAattgg
1080	1092	1086 +		1	0.955	0.035	tgGAATAaaaaat
1136	1148	1142 +		1	0.793	0.013	gaGAATgatcttc
1384	1396	1390 +		1	0.932	0.062	agtaagATTCaat
283	295	289 +		1	0.825	0.005	aagcATATtttta
571	583	577 +		1	0.893	0.063	aaggttATTCtca
718	730	724 +		1	0.861	0.081	ttGAATttccta
960	972	966 +		1	0.946	0.026	aaGAATatctagc
1103	1115	1109 +		1	0.922	0.002	ttGAATAaagaag

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
169	185	177 +		1	0.878	0.028	agaaattaAATGataag
242	258	250 +		1	0.795	0.025	gaaaatTAAAtcgttga
327	343	335 +		1	0.858	0.038	ctgttgatATTCttt
841	857	849 +		1	0.854	0.004	ftgaattgAATGcgcca
929	945	937 +		1	0.991	0.171	aatcagaatATTCctt
1186	1202	1194 +		1	0.889	0.039	aaaaaatgAATGccccat
1301	1317	1309 +		1	0.873	0.053	aggcactatATTCcacc
189	205	197 +		1	0.987	0.137	aaaaaattAATGaataat
580	596	588 +		1	0.842	0.082	gtaCATTatcatgcaaag

667	683	675 +	1	0.886	0.036	at ttattaAATGatgaa
698	714	706 +	1	0.84	0.07	at ttatTAAAtcctttt
845	861	853 +	1	0.9	0.05	tatattttAATGtaaga
878	894	886 +	1	0.808	0.048	tcaCATTaaaatctctt
926	942	934 +	1	0.844	0.024	atgggtgatATTCaatt
1069	1085	1077 +	1	0.796	0.026	ctcaatTAAAtatcact
1234	1250	1242 +	1	0.861	0.041	tatattttatATTCttaa
1336	1352	1344 +	1	0.782	0.012	aattatTAAAtataat
1356	1372	1364 +	1	0.829	0.059	at ttatTAAAttttcta
1378	1394	1386 +	1	0.894	0.044	ttacctTAAAtccttt
386	402	394 +	1	0.832	0.012	tggttttatATTCaaga
404	420	412 +	1	0.862	0.012	tcaaattgAATGattgg
514	530	522 +	1	0.857	0.037	tcctttcatATTCttta
667	683	675 +	1	0.85	0.03	ttaatataATTCaaga
1384	1400	1392 +	1	0.815	0.045	tccgatTAAAtttgtgt
294	310	302 +	1	0.943	0.123	aacttgTAAAtgcacat
1076	1092	1084 +	1	0.944	0.094	agtcagTAAAtgcaggf
170	186	178 +	1	0.85	0.03	atgaacgatATTCgcca
809	825	817 +	1	0.89	0.04	agggaatgAATGatgat
1135	1151	1143 +	1	0.771	0.011	tagCATTgcatgacaat
1	17	9 +	1	0.764	0.004	tttCATTtaattttgtg
68	84	76 +	1	0.888	0.038	tccctaTAAAtacatag
578	594	586 +	1	0.866	0.016	aaatatTAAAtacaaat
873	889	881 +	1	0.865	0.045	accttaatATTCagaa
1386	1402	1394 +	1	0.854	0.004	taagattcAATGttggt
274	290	282 +	1	0.828	0.008	ttattcTAAAtagcatat
1360	1376	1368 +	1	0.898	0.078	aagataTAAAtgaaaga
221	237	229 +	1	0.977	0.127	ttcaaattAATGttttt
345	361	353 +	1	0.785	0.015	tttaatTAAAttaaaat
369	385	377 +	1	0.854	0.084	actaatTAAAttctatg
665	681	673 +	1	0.77	0.01	actCATTtaatttttaa
871	887	879 +	1	0.823	0.003	caataaTAAAtcaacc
921	937	929 +	1	0.858	0.088	aagaatTAAAtaaacta
985	1001	993 +	1	0.869	0.049	aattaaTAAAtataata

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
512	532	522 +		1	0.916	0.056	ttacCGGAcaaaaaagttc
1297	1317	1307 +		1	0.984	0.114	gatCCGGaaatggaatatr
789	809	799 +		1	0.942	0.082	tcccCGGAgaatggactta

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
580	606	593 +		1	0.996	0.046	gtacattaCATGcaaaggc
62	88	75 +		0.81	0.772	0.002	ccattgtGCTTgtttctctae
448	474	461 +		1	0.967	0.017	at ttttccCATGcaacaagc
46	72	59 +		1	0.972	0.022	ctcaattcCATGcattgcatt

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
997	1009	1003 +		0.914	0.934	0.004	aCCCActgcgtag
839	851	845 +		0.914	0.938	0.008	gACCAatgtgatg

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
604	610	607 +		1	1	0	cTCGCca
1294	1300	1297 +		1	1	0	cTCGCcc

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
212	222	217 +		1	0.936	0.086	aaATCTaatac
589	599	594 +		1	0.911	0.061	tcATCTaattt
131	141	136 +		1	0.884	0.034	aaATCTactat

179	189	184 +	1	0.99	0.14	ttATCTaaaat
555	565	560 +	1	0.926	0.076	taATCTaatag
703	713	708 +	1	0.921	0.071	tcATCTaataa
1125	1135	1130 +	1	0.926	0.076	aaATCTaat

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>j</sub>	Sequence
156	176	166 +		1	0.924	0.024	atataaaaaaaaaGAAA
489	509	499 +		1	0.863	0.033	tcaaaCCATtcataggtgta
604	624	614 +		1	0.908	0.078	tctttCCATttaaagtaagta
787	807	797 +		1	0.82	0.03	tgtgaacaatctgGAAAg
891	911	901 +		1	0.814	0.064	atgttCCATtgtcccaaatt
1142	1162	1152 +		1	0.936	0.036	tcagtccaaAAATtgcctgt
1152	1172	1162 +		0.801	0.82	0.02	aattgcctgtaataGAAGc
357	377	367 +		1	0.836	0.066	gataaacaataaGAAAg
260	280	270 +		1	0.836	0.016	ttgcacaaaagagaGAAA
313	333	323 +		1	0.942	0.112	tctttCCATgtatagaaatct
842	862	852 +		1	0.865	0.005	gtccacCAAAtaagtca
1028	1048	1038 +		1	0.847	0.057	ttttgtacaaaagGAAAc
72	92	82 +		0.925	0.815	0.025	tgtTTCTtctaaaaggattc
278	298	288 +		1	0.801	0.011	taatttcaggaaagGAAAc
905	925	915 +		0.973	0.873	0.043	cggtgCCAAttcagaattc
1295	1315	1305 +		1	0.819	0.049	tagatccggaatGAAAt
1382	1402	1392 +		1	0.941	0.041	gaaactcaaAAATgggatt
140	160	150 +		1	0.753	0.003	taattCCATtgaagcaag
1259	1279	1269 +		1	0.866	0.036	gcattCCATtccagaatgt
1316	1336	1326 +		1	0.86	0.03	gagaaCCATtttgagtaaa
48	68	58 +		1	0.763	0.013	caattCCATgcattgcattt
241	261	251 +		0.831	0.833	0.013	ggaatcacaaaaggGGA
485	505	495 +		1	0.902	0.002	aatatagaaAAATggtttta
756	776	766 +		1	0.915	0.015	ggagaccaaAAATatccta
932	952	942 +		1	0.939	0.039	aaaaattaaAAATagaagf
1233	1253	1243 +		0.814	0.896	0.036	gatttcAAAAtaagaaaat
1362	1382	1372 +		1	0.841	0.041	attTACCcaattggtgtgag
726	746	736 +		1	0.807	0.017	aatTACTaatcgtagaaga
835	855	845 +		0.902	0.821	0.021	gctTCCctacaccggtttg
975	995	985 +		1	0.95	0.05	aagaacaaaAAATagaa
1099	1119	1109 +		1	0.914	0.014	gattatgaaAAATagttttg
1159	1179	1169 +		0.973	0.843	0.013	aacacCCAAGtacaggag
1264	1284	1274 +		1	0.802	0.002	aatggccgataagaGAAA
1345	1365	1355 +		1	0.817	0.027	tgcTACTgtaggtggaaga
259	279	269 +		1	0.845	0.045	ctattcctgttttaGAAAat
1355	1375	1365 +		1	0.925	0.025	aaaaaaaaAAATagca

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>j</sub>	Sequence
282	302	292 +		1	0.886	0.046	ttaaagaaaattTAGGaag
286	306	296 +		1	0.834	0.034	agaaaattTAGGaagaa
534	554	544 +		1	0.898	0.088	agacGGGtTgtgggtta
539	559	549 +		1	0.894	0.054	gggtTgtgggtTAGGcca
1042	1062	1052 +		1	0.933	0.013	agagctgGTAGTtttctac
1123	1143	1133 +		1	0.964	0.054	ctgttataggggTAGGtggf
1127	1147	1137 +		1	0.991	0.061	tataggGTAgtgtgtcag
1134	1154	1144 +		0.936	0.824	0.014	gtagGTGGtcagtcacaa
829	849	839 +		0.809	0.872	0.002	gattctgaatTTCGgtatat
833	853	843 +		0.806	0.885	0.005	cttgaattCGGTatatttta
1246	1266	1256 +		1	0.946	0.026	cttaaagGTAGttaatca
803	823	813 +		1	0.95	0.03	ctttaaattatTTGGTgga
807	827	817 +		1	1	0.07	aaaattatTTGGTggaata
945	965	955 +		0.807	0.883	0.003	atgagaattGGGTccatatl

1090	1110	1100 +	1	0.907	0.007	gaaaatcaaagtTAGGttg
1094	1114	1104 +	1	0.922	0.032	atcaaatgTAGGttgcgac
1329	1349	1339 +	0.869	0.896	0.016	ttcgtattTGGTctgatatt
237	257	247 +	1	0.93	0.08	ttaaagagactTAGGtatg
241	261	251 +	1	0.955	0.125	aagagactTAGGtatgca
483	503	493 +	1	0.954	0.034	tgaccagTAGctacaata
1179	1199	1189 +	0.806	0.895	0.015	tatgaaattCGGTgctgttc
394	414	404 +	1	0.955	0.035	agttctaagggtTTGGtgta
398	418	408 +	1	0.977	0.047	ctaagggtTGGTgtagga
690	710	700 +	0.83	0.835	0.025	acaaGAGGtaggatgaa
820	840	830 +	1	0.965	0.065	gatgatgaaaatTAGGgtg
824	844	834 +	1	0.98	0.1	atgaaaatAGGTgtgacc
902	922	912 +	1	1	0.07	actgtgatTTGGtcaggaa
920	940	930 +	1	0.962	0.042	aattgtgagggtTTGGtgta
924	944	934 +	1	0.979	0.049	gttgagggtTGGTgtaagg
990	1010	1000 +	1	0.945	0.075	ttctggtGTTGttggtttac
1177	1197	1187 +	0.83	0.817	0.007	cattGAGGttgtgtgcct
1268	1288	1278 +	1	0.937	0.037	ttccagaatgtTAGGtggg
1272	1292	1282 +	1	0.926	0.046	agaatgttAGGTgggtgg
1276	1296	1286 +	0.972	0.965	0.055	tgtttaggtGGTGgatacc
327	347	337 +	1	0.77	0	tcttttagctTTAGgaagal
368	388	378 +	1	0.909	0.009	tttcttctttTAGGttata
372	392	382 +	1	0.932	0.042	cttctttTAGGttatagcaa
1081	1101	1091 +	1	0.827	0.057	ggaataaaaaTTAGata
1206	1226	1216 +	1	0.891	0.001	ttaaataTAGGtttaattgg
1216	1236	1226 +	0.807	0.893	0.013	ggttaattGGTctatgatt
1307	1327	1317 +	1	0.955	0.085	catggtctaaaTTAGgtatg
1311	1331	1321 +	1	0.982	0.152	gtctaaatTAGGtatgatta
295	315	305 +	1	0.929	0.029	aagagaaaattTAGGgtt
299	319	309 +	1	0.937	0.047	gaaaattTAGGgtttttaa
341	361	351 +	1	0.849	0.009	tgtagaatgttTAGGcaac
1341	1361	1351 +	1	0.924	0.024	tctctgctactgTAGGtgga
1345	1365	1355 +	1	0.896	0.006	tgctactgTAGGtggaaga
203	223	213 +	1	0.934	0.084	atcctaaaattTAGGtattc
207	227	217 +	1	0.936	0.056	taaaatttAGGTattcaaat
998	1018	1008 +	1	0.873	0.003	aatatattaatTTAGgatta
1075	1095	1085 +	0.856	0.883	0.013	acgactataatTTTGgttga
1079	1099	1089 +	0.869	0.91	0.03	ctataattTGGTgataaaa

start position	end position	strand	Core sim.	Matrix sim.	sim. - o1	Sequence
289	309	299 +	1	0.909	0.089	gaaagAACGgtctggact
155	175	165 +	1	0.877	0.057	agaatAACGggtttaagtc
624	644	634 +	1	0.862	0.042	atctcAACGgattttgaag
610	630	620 +	1	0.851	0.031	taaaaAACGggttaaaaa

start position	end position	strand	Core sim.	Matrix sim.	sim. - o1	Sequence
182	202	192 +	1	0.815	0.015	taagaaaaaaGTTAataa
580	600	590 +	0.88	0.941	0.061	atatcattctGTTTtactca
1115	1135	1125 +	1	1	0.01	atttccatCTGTtatagggg
46	66	56 +	0.853	0.921	0.001	acatattaccGTTGtatata
497	517	507 +	1	0.801	0.041	aagatattTAGTgctgcttt
515	535	525 +	1	0.948	0.018	ttgcttggtGTTGacatgg
1188	1208	1198 +	1	0.909	0.009	ttaatattAGTTtttatttt
1246	1266	1256 +	1	0.977	0.017	cttaaaggtaGTTAatcaa
199	219	209 +	1	0.836	0.006	cggtcgtagAGTTgtcata
345	365	355 +	1	0.919	0.009	atatggtttGTTAttgaatc
378	398	388 +	0.801	0.87	0	tgaagtGTTGgttttatattc
622	642	632 +	1	0.91	0	atatagtcttGTTAatcaatc

1299	1319	1309 +	1	0.914	0.004	tgaacattttGTTAtacttta
19	39	29 +	0.833	0.873	0.003	aaagcaacaGTTTgccg
434	454	444 +	1	0.839	0.009	aggatttgAGTTgctaaa
680	700	690 +	0.832	0.927	0.047	actactttctGTTGttgaatc
351	371	361 +	0.949	0.964	0.004	tgaggagggtGTTGaggc
605	625	615 +	1	0.942	0.032	tcagttgtgtGTTAtcgaac
990	1010	1000 +	1	0.933	0.003	ttctgggtgtGTTGgttttac
994	1014	1004 +	0.801	0.87	0	ggtgttGTTGgttttactgat
1178	1198	1188 +	0.817	0.918	0.048	attgagGTTTggtgtgcctt
1181	1201	1191 +	1	0.912	0.002	gaggtttgtGTTGcctttct
1295	1315	1305 +	1	0.946	0.016	cagctttgaGTTGaaatgt
1341	1361	1351 +	1	0.941	0.011	agagtattgGTTGtgatga
266	286	276 +	1	0.913	0.003	aaaagagataGTTGaga
160	180	170 +	1	0.808	0.008	ttgaaaattGTTAttgaaa
593	613	603 +	1	0.982	0.082	ctaatttctAGTTactgttag
599	619	609 +	1	1	0.01	tctagttaCTGTtagcttgtg
641	661	651 +	1	1	0.01	tgagcttaCTGTtagcttgc
1029	1049	1039 +	0.829	0.896	0.016	acagaaaacaGTTTttgtt
1077	1097	1087 +	1	1	0.01	tttagaaaCTGTataaaaa
1116	1136	1126 +	0.829	0.896	0.016	tttagaaaacaGTTTttaca
257	277	267 +	0.829	0.897	0.017	atctattcCTGTtttagaaa
1080	1100	1090 +	1	0.933	0.003	tataatttgGTTGataaagi
1227	1247	1237 +	1	0.915	0.045	atttgggCAGTgcagatg

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
211	229	220 +		1	0.941	0.011	gtttaatTATCcttgaaaa
397	415	406 +		1	0.848	0.008	caaaaaATATgccatggg
455	473	464 +		1	0.944	0.014	aattaatTATCtctattgt
574	592	583 +		1	0.795	0.005	gtttcaaTATCattctgtt
620	638	629 +		1	0.877	0.007	aagtattTATCatttaaac
930	948	939 +		1	0.972	0.142	atcagaATATtccttttcg
1302	1320	1311 +		1	0.855	0.025	ggcactATATtccaccctt
196	214	205 +		1	0.848	0.008	taatgaATATgattggaaa
607	625	616 +		1	0.921	0.021	gtggagctATCCaatcagt
801	819	810 +		1	0.947	0.017	aactttcATCCttttatt
217	235	226 +		1	0.94	0.04	aatcccTTATcaacaatat
627	645	636 +		1	0.933	0.003	gtctgtTATCaaatcttt
1311	1329	1320 +		1	0.966	0.036	tatacttTATCttatttct
724	742	733 +		1	0.933	0.003	tacagatTATCatagctta
800	818	809 +		1	0.848	0.008	gcaagaATATgtaggagct
1156	1174	1165 +		1	0.966	0.036	acagtgtTATCttatataca
1305	1323	1314 +		1	0.984	0.144	aatggaATATcccgcgtgaa
7	25	16 +		1	0.979	0.079	aatgctttATCCcagtatt
171	189	180 +		1	0.84	0.01	tgaacgATATtcgccacc
610	628	619 +		1	0.831	0.001	tgtgtgtTATCgaacacat
718	736	727 +		1	0.908	0.008	acatgaTTATcagcagca
194	212	203 +		1	0.953	0.053	attaccctATCCtccctca
458	476	467 +		1	0.876	0.056	caaaaaATATacttgataa
761	779	770 +		1	0.964	0.034	ccaaaaatATCCtatttct
281	299	290 +		1	0.881	0.061	aaaagcATATtttaagag
173	191	182 +		1	0.94	0.01	tactattTATCtaaaatta

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
669	687	678 +		1	0.936	0.006	gtgtcaaACGTgaggaaa
1066	1084	1075 +		1	0.909	0.019	aattcaCACGtaatttata
459	477	468 +		1	0.953	0.003	gttggACATttgaccata
221	239	230 +		1	0.992	0.022	gaactgcaTGTGatgttta
660	678	669 +		1	0.989	0.019	gctcatcaTGTGaaaagt

1349	1367	1358 +	1	0.968	0.038	agtggaaACGTgtaaca:
341	359	350 +	1	0.995	0.025	gatgtccaTGTGaggagg
742	760	751 +	1	0.92	0.03	taggccCACGtcatggag:
1323	1341	1332 +	1	0.97	0.02	cagaaACATctgatagggt

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
324	334	329 +		1	0.882	0.022	ttTCTTgttga
425	435	430 +		1	0.896	0.036	ttTCTTcttct

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
1055	1083	1069 +		0.874	0.859	0.019	ttctacatgtaattcaCACG
1274	1302	1288 +		0.874	0.885	0.045	ttgaaacatcttctcaCACG
52	80	66 +		1	0.821	0.031	taccgtgtatataagaCAA
571	599	585 +		0.807	0.811	0.021	aaaaattatgtacattaCAT
748	776	762 +		1	0.83	0	tgtataaccataattacCAA
1004	1032	1018 +		1	0.998	0.008	ataaaatattgttttaCAAG
1245	1273	1259 +		1	0.951	0.011	tcttaaaggtagttaatCAAC
559	587	573 +		1	0.956	0.016	taatcagttctttaaataCAAG
575	603	589 +		1	0.949	0.009	tcaagtcaatccttttaCAAC
377	405	391 +		1	0.798	0.008	gcagatttctttgatgCAAG
382	410	396 +		1	0.804	0.014	tttctttgatgcaagaCAAG
771	799	785 +		0.803	0.885	0.045	aatagctttgtgaactCATC
818	846	832 +		1	0.999	0.019	tataaagattatgagtCAA
865	893	879 +		1	0.842	0.002	gcgattgatagaacaCA
1057	1085	1071 +		1	0.948	0.008	ctgcctgacattttgtcCAAC
138	166	152 +		1	0.863	0.073	gataattccattggaagCAA
281	309	295 +		1	0.988	0.008	gtttaagtatgtaaataCAAC
751	779	765 +		0.803	0.881	0.041	ggagaagcagaatgtccCA

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
1057	1083	1070 +		1	0.995	0.185	tctacatgtaattcaCACGt:
1068	1094	1081 +		1	0.762	0.012	ttcacacgtaatttatACGT
1276	1302	1289 +		1	0.816	0.006	gaaacatcttctcaCACG:
54	80	67 +		1	0.766	0.016	ccgtgtatataagaCAAGf
513	539	526 +		1	0.753	0.003	gctttgCTTGtggtgacat
573	599	586 +		0.853	0.812	0.062	aaattatgtacattaCATGc
1006	1032	1019 +		1	0.804	0.054	aaaatattgttttaCAAGa:
3	29	16 +		1	0.95	0.01	ttttgtcgaggttgaTACGac
78	104	91 +		1	0.995	0.055	ttctaaaaggatttcTACGg
384	410	397 +		1	0.752	0.002	ttctttgatgcaagaCAAGg
738	764	751 +		1	0.777	0.027	gcttagCTTGagaccgag:
1059	1085	1072 +		1	0.809	0.059	gcctgacattttgtcCAAGtc
140	166	153 +		1	0.801	0.051	taattccattggaagCAAG:
733	759	746 +		1	0.984	0.024	aattttgttaggccCACGt:
69	95	82 +		1	0.943	0.003	tgtattaattccctTACGtca
467	493	480 +		0.969	0.76	0.01	ccttctctagtgcaTACGtc
509	535	522 +		1	0.97	0.05	tcctctctagtgcacACGC

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
175	185	180 +		0.878	0.909	0.059	tAAATgataag
225	235	230 +		1	0.856	0.006	gAAAAaattaa
380	390	385 +		1	0.913	0.063	aAAAAgatggg
522	532	527 +		1	0.859	0.009	aAAAAgttgag
948	958	953 +		1	0.916	0.066	gAAAAgatagt
673	683	678 +		0.878	0.916	0.066	tAAATgatgaa
741	751	746 +		1	0.913	0.063	aAAAAgatgta
777	787	782 +		1	0.957	0.107	tAAAAgatgaa
1036	1046	1041 +		1	0.922	0.072	gAAAAgatgta

82	92	87 +	0.805	0.883	0.033	aAAAGgatttc
360	370	365 +	0.878	0.871	0.021	aAAATgatgtc
529	539	534 +	0.878	0.874	0.024	gAAATgatatg
1112	1122	1117 +	1	0.928	0.078	tAAAAGatcga
976	986	981 +	1	0.852	0.002	gAAAAGgtttt
1330	1340	1335 +	1	0.907	0.057	aAAAAGatgca
1094	1104	1099 +	0.878	0.949	0.099	aAAATgattat
1157	1167	1162 +	0.805	0.877	0.027	aAAAGgattct

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
1001	1015	1008 +		1	0.898	0.108	tcttgtCTCTgtcc
74	88	81 +		1	0.912	0.122	tttgaCTCTtaact

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
272	284	278 +		1	0.813	0.003	catGTACgaggag
537	549	543 +		1	0.845	0.035	tggGTACgtattc

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
168	190	179 +		1	1	0.03	aagaaattaaatgaTAAGa
273	295	284 +		1	0.831	0.021	ttaaACTTtttaaagaaat
283	305	294 +		1	0.976	0.006	taaagaaaatttagGAAGa
601	623	612 +		1	0.995	0.025	atttcttccatttTAAGtaagf
666	688	677 +		1	0.98	0.01	ggcgtgtcaaactgtaGGf
755	777	766 +		1	0.858	0.048	tcatACTTgtattaaaaata
310	332	321 +		1	1	0.03	caagaaggaatagaaGC
354	376	365 +		1	1	0.03	aatgataaacaataaGGf
759	781	770 +		1	0.996	0.086	aattaccaagacatTAAGt
982	1004	993 +		1	0.98	0.01	atattacatctcaggaGGAf
82	104	93 +		1	0.835	0.035	cttaACTTtgatacaatttgi
757	779	768 +		1	0.855	0.055	cataACTTtataccaatttgi
1025	1047	1036 +		1	1	0.03	gctttttggtacaaaaGGAA
275	297	286 +		1	1	0.03	gagtaatttcaggaaaGGA
783	805	794 +		1	0.985	0.015	gaactcatgaaaccTAAGc
919	941	930 +		1	1	0.03	gaattctggaactcTAAGa
992	1014	1003 +		1	0.972	0.002	ctggacctcagatGAAGc
231	253	242 +		1	0.822	0.012	ttcaACTTgtgacttaaagt
237	259	248 +		1	0.991	0.021	tttgacttaaagtGAAGa
464	486	475 +		1	0.812	0.012	atatACTTgataaataaa
1028	1050	1039 +		1	0.827	0.027	aataACTTtattgaaactg
1230	1252	1241 +		1	1	0.03	tatgattcaaaatTAAGaa
740	762	751 +		1	0.842	0.042	gaagACTTcatggagaag
863	885	874 +		1	0.82	0.02	tttACTTctcctaccagtcc
1199	1221	1210 +		1	0.98	0.01	aagtgtagcactagaGGf
1378	1400	1389 +		1	0.995	0.025	agagggtatgataaTAAGt
1106	1128	1117 +		1	0.98	0.01	aataaagaagagaagaGC

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
469	489	479 +		1	0.757	0.007	ttcctctagtgcatACGTctc

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
1379	1395	1387 +		0.829	0.822	0.012	aatttgACTTaaattaa
918	934	926 +		1	0.955	0.145	aatatgACATgggtgat
16	32	24 +		1	0.831	0.021	gatacgACATgggtttt
1058	1074	1066 +		1	0.893	0.083	gaagaTGAGccatattt
743	759	751 +		1	0.902	0.032	aggcCCACgtcatggag
1177	1193	1185 +		1	0.986	0.116	aggttcatgTCATcaag

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
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144	160	152 +	1	0.887	0.007	aaaCAACgactatgata
963	979	971 +	1	0.91	0.03	acaCAACaacaanaagaa

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
1192	1210	1201 +		0.825	0.849	0.009	tgaatgcCCATccctccca
460	478	469 +		0.8	0.844	0.004	taaaaagCCTTcctctagt

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
1092	1098	1095 +		1	1	0	TGTGttt
612	618	615 +		1	1	0	TGTGtta

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
779	811	795 +		1	0.844	0.004	aaagatgaaCCTTcactat
61	93	77 +		1	0.811	0.001	gccattgtgctgtttctctaa
1268	1300	1284 +		1	0.846	0.036	ctgaacccccctcatcatgac
671	703	687 +		1	0.868	0.028	tggaaagatCCTTgacaa
854	886	870 +		1	0.86	0.02	tagggagacCCTTaccatt
875	907	891 +		1	0.845	0.035	taccagtcctctgttcaaaact

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
1036	1050	1043 +		1	0.914	0.004	tttGAAGAagatccc
248	262	255 +		1	0.919	0.009	agtGAAGaaagactt
751	765	758 +		1	0.937	0.027	ggaGAAGcagaatgt
1114	1128	1121 +		1	0.92	0.01	agaGAAGaggaaaat

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
282	298	290 +		1	0.838	0.008	ttaaGAAAttagga
249	265	257 +		1	0.831	0.001	gtgaaGAAAgacttgaa
524	540	532 +		1	0.876	0.046	taagaGAAAtgatatgt
382	398	390 +		1	0.862	0.032	ttttaGAAAttttata
1273	1289	1281 +		1	0.862	0.032	taagaGAAAggtgaag

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
555	567	561 +		1	0.971	0.011	ggcAACAtatttg
1128	1140	1134 +		1	0.948	0.018	gtcAACAgagaaa
662	674	668 +		1	0.969	0.039	aacAACAAAacat
196	208	202 +		1	0.944	0.014	tacAACAAatttt
967	979	973 +		1	0.966	0.036	aacAACAAAagaa
335	347	341 +		1	0.964	0.004	cacAACATAattt

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
656	666	661 +		1	0.96	0.04	gtcTACAacag
699	709	704 +		1	0.887	0.057	ctatACACgaa
839	849	844 +		1	0.921	0.001	cccTACAccgg
1243	1253	1248 +		1	0.962	0.042	aacTACAacat

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
817	831	824 +		0.983	0.952	0.022	cCTTCaccttccctt
424	438	431 +		1	0.979	0.049	aTTTCttcttctct
427	441	434 +		0.983	0.987	0.057	tCTTCttcttcttct
430	444	437 +		0.983	0.931	0.001	tCTTCttcttcttct

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
689	713	701 +		1	0.771	0.001	ataattcattctataCACGa

tart positio	nd positio	chor positi	Strand	Core sim.	Matrix simat.	sim. - o	Sequence
270	286	278 +		1	0.88	0.05	accatgTACGaggaggc
535	551	543 +		1	0.889	0.049	gatggGTACgtattccc

191	207	199 +	1	0.868	0.038	caagtaTACGgtcgtag
1139	1155	1147 +	1	0.929	0.049	agtcgGTACcatgtaca
87	103	95 +	1	0.864	0.034	gatttcTACGgaatcaa
105	121	113 +	1	0.975	0.025	gatttGTACtgcctcta
1144	1160	1152 +	1	0.965	0.015	ttctGTACtaaacagt
38	54	46 +	1	0.95	0	ttcatGTACtcaattcc

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
879 893 886 + 1 0.88 0.01 aatcaACCCataatc

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
1197 1207 1202 + 1 0.987 0.007 agTTTTtattt  
440 450 445 + 1 0.984 0.004 aaTTTTtattt  
897 907 902 + 1 0.981 0.001 aaTTTTtaata

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
7 19 13 + 1 0.92 0.05 acTACTataaatt  
52 64 58 + 1 0.969 0.099 atTACTattgcca  
44 56 50 + 1 0.991 0.121 atTACTatttttc  
603 615 609 + 1 0.873 0.003 gtTACTgttagct  
645 657 651 + 1 0.873 0.003 ctTACTgttagct  
134 146 140 + 1 0.923 0.053 tcTACTattcacc  
171 183 177 + 1 0.995 0.125 atTACTatttadc

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
1365 1377 1371 + 1 0.863 0.003 ggccaAGCTagga  
1187 1199 1193 + 1 0.881 0.021 catcaAGCTagca

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
212 228 220 + 1 0.866 0.056 ttaaatTATCcttgaaa  
218 234 226 + 1 0.847 0.037 atccctTATCaacaata  
628 644 636 + 1 0.82 0.01 tcttgtTATCaaatctt  
8 24 16 + 1 0.867 0.057 atgcttTATCccagtat  
174 190 182 + 1 0.823 0.013 actattTATCtaaaatt

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
1181 1195 1188 + 1 0.867 0.017 accTAAAaaaatgaa  
1341 1355 1348 + 1 0.915 0.065 taaTAAAataatttt  
356 370 363 + 1 0.864 0.014 tgaTAAAc aaataag  
638 652 645 + 1 0.863 0.013 attTAAAc aaatttt  
1082 1096 1089 + 1 0.89 0.04 gaaTAAAaaattaga  
484 498 491 + 1 0.892 0.042 ttaTAAAaattgaa  
98 112 105 + 1 0.854 0.004 tccTAAAaaactttg

**tart positiochor positi Strand Core sim. Matrix simat. sim. - o1Sequence**  
227 245 236 + 1 0.811 0.001 aaAAATaaagaaaaga  
484 502 493 + 1 0.885 0.075 aaAAATcaaaccattcata  
108 126 117 + 1 0.828 0.018 aaAAATaataacaaagaa  
129 147 138 + 1 0.843 0.033 aaAAATatttaataaaaac  
252 270 261 + 1 0.838 0.028 aaAAATaattgcacaaaac  
529 547 538 + 1 0.923 0.113 taAAATcatttgatggaat  
806 824 815 + 1 0.81 0 taAAATtatttggtggaat  
561 579 570 + 1 0.835 0.025 aaAAATaattaaaaataaa  
589 607 598 + 1 0.841 0.031 acAAATcttaattttaaaa  
1238 1256 1247 + 1 0.812 0.002 caAAATaagaaaaatcaa  
254 272 263 + 1 0.856 0.046 gaAAATaattttttcaaa  
1093 1111 1102 + 1 0.815 0.005 aaAAATgattatgaaaaat  
116 134 125 + 1 0.83 0.02 aaAAATaattttggaaaat

222	240	231 +	1	0.823	0.013	tcAAATtaatgtttta
1031	1049	1040 +	1	0.853	0.043	aaAAATctgaatttaaag
1141	1159	1150 +	1	0.825	0.015	taAAATtattaattgtaa
1376	1394	1385 +	1	0.946	0.136	aaAAATcatatttaaaaa

start	end	start	end	strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
1054	1066	1060	+		1	1	0.01	aaataAAAAaaa

start	end	start	end	strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
273	293	283	+		0.819	0.839	0.009	ttaaCTTTtaaagaaaa
601	621	611	+		0.907	0.94	0.02	atttcttccattTAAGtaa
755	775	765	+		1	0.861	0.031	tcataCTTGtattaaaaata
1007	1027	1017	+		0.938	0.962	0.042	aaatattgttttaCAAGaa
1011	1031	1021	+		1	0.991	0.011	attgttttaCAAGaaaaaa
1080	1100	1090	+		0.907	0.943	0.023	atcacttttaaatTAAGaat
23	43	33	+		0.938	0.932	0.012	catggttttgtatCAAGaat
384	404	394	+		0.938	0.932	0.012	gttggtttatattCAAGaat
757	777	767	+		0.819	0.831	0.001	cataaCTTTtataccaattg
1024	1044	1034	+		1	0.937	0.017	cgcttttggtaacaAAAGga
69	89	79	+		1	0.921	0.001	gctgttcttctaAAAGgat
825	845	835	+		1	0.986	0.006	attatgagttCAAGtaacct
36	56	46	+		1	0.836	0.006	agaggCTTGagcaagaa
231	251	241	+		1	0.846	0.016	tcaaCTTGtgactaaagt
1230	1250	1240	+		0.907	0.967	0.047	tatgattcaaaatTAAGaa
3	23	13	+		1	0.93	0.01	tatttttttttAAAGttt
117	137	127	+		1	0.937	0.017	tacattttgtaaaaAAAGtct
268	288	278	+		1	0.929	0.009	tcaaatttattctaAAAGcat
740	760	750	+		0.884	0.855	0.025	gaagaCTTCatggagaa
919	939	929	+		1	0.854	0.024	agaggCTTGttgacaatt
945	965	955	+		1	0.941	0.021	tcaatttttttgAAAGaat

start	end	start	end	strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
739	753	746	+		1	0.944	0.004	gtgtagGCCCacgtc
1001	1015	1008	+		1	0.998	0.108	tatgggcCCCAcacg

start	end	start	end	strand	Core sim.	Matrix sim.	sim. - o <sub>1</sub>	Sequence
260	290	275	+		1	0.93	0.05	aaatatataTTTTaaact
269	299	284	+		1	0.921	0.041	tattttaaactTTTTaaaga
429	459	444	+		0.962	0.883	0.003	ttataattgagTTTGaaagt
862	892	877	+		1	0.846	0.006	agagatcaataTTTTcaat
143	173	158	+		1	0.918	0.038	aagatttattTTTTaaaact
952	982	967	+		1	0.901	0.021	ataaaatattTTTTaaaaa
1074	1104	1089	+		1	0.915	0.035	ttaaatacacTTTTaaatt
1283	1313	1298	+		1	0.896	0.086	tgatatgtaatttCAAaaa
391	421	406	+		1	0.816	0.006	ttatattcaagaatCAAAttg
763	793	778	+		0.962	0.914	0.034	tttataccaTTTGaaattg
1082	1112	1097	+		1	0.815	0.005	tatatattgaaatCAAAtg
165	195	180	+		1	0.866	0.056	gttaagtcaaattCAAAGA
696	726	711	+		1	0.877	0.067	gtaggatgaaattCAAAG
418	448	433	+		0.841	0.893	0.013	ttataattgtTTTCaaaaat
439	469	454	+		1	0.944	0.064	aaattttattTTTTaaaaca
523	553	538	+		1	0.91	0.03	ttttatgatgaTTTTaaaaa
576	606	591	+		1	0.844	0.034	taaaatattaataCAAAtc
589	619	604	+		1	0.94	0.06	acaaatcttaaTTTTaaaai
619	649	634	+		1	0.901	0.091	ggttaaaaatatttCAAAta
961	991	976	+		0.962	0.883	0.003	attaagaataaTTTGgaac
1224	1254	1239	+		1	0.887	0.077	tgggtctatgattCAAAtt
1345	1375	1360	+		1	0.836	0.026	gtcttcgggtgtCAAAtta

2	32	17 +	1	0.898	0.018	ttattttttTTTaaagttatg
63	93	78 +	0.843	0.88	0	taatgcattgaTTTAAAAat
72	102	87 +	1	0.945	0.065	gatttaaaaatTTTaaagt
83	113	98 +	1	0.939	0.059	tttaaaagtaaTTTaaaaa
149	179	164 +	0.962	0.884	0.004	ttggactctaTTTGaaaat
255	285	270 +	0.841	0.889	0.009	aaaataatTTTCaaatt
372	402	387 +	0.843	0.886	0.006	taaaaaaatTTTAgaaa
453	483	468 +	1	0.883	0.003	tccactcaagcTTTaaat
506	536	521 +	1	0.825	0.015	ttaagaactgtttCAAaa
520	550	535 +	0.962	0.884	0.004	caaaaactattTTTGaaa
1105	1135	1120 +	0.962	0.889	0.009	gaaaaatagttTTTGaaa
13	43	28 +	1	0.853	0.043	acaattacacattCAAac
114	144	129 +	0.962	0.89	0.01	acaaaaataatTTTGaa
209	239	224 +	1	0.883	0.073	aaattaggtattCAAAta
222	252	237 +	1	0.856	0.016	tcaaattaatgTTTTaatta
303	333	318 +	1	0.868	0.028	ctaaatttaTTTcaattai
446	476	461 +	1	0.895	0.015	ttttttttTTTaaaaagcc
595	625	610 +	1	0.915	0.035	cctttttttTTTaaaaaaa
665	695	680 +	1	0.944	0.064	actcatttaatTTTaaaatt
705	735	720 +	1	0.915	0.075	atctaataaaaTTTTgaatt
772	802	787 +	1	0.932	0.052	ttgacctaaaaTTTTaata
807	837	822 +	1	0.891	0.011	aatcaaaatcTTTaaag
889	919	904 +	1	0.9	0.02	taatctaaatTTTaatatt
964	994	979 +	1	0.854	0.044	atatctagcgtattCAAac
1031	1061	1046 +	1	0.887	0.007	aaaaatcgaaTTTTaaag
1090	1120	1105 +	1	0.852	0.012	gttgataaagtTTTTgaata
1331	1361	1346 +	0.843	0.888	0.008	atcatatattaTTAaaaaa

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
312	332	322 +		0.957	0.773	0.013	agAAGGgaatagaagga
55	75	65 +		0.957	0.762	0.002	gcAAGGccatgttcgacac
1285	1305	1295 +		0.957	0.79	0.03	tgAAGGctaaaaggctaa

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
1208	1234	1221 +		1	0.869	0.059	taatattattaatCCTAaatt
1312	1338	1325 +		1	0.885	0.045	ttattcacacaaCCCTatatt
1191	1217	1204 +		1	0.932	0.122	gccccaccacaacCCTAaa
782	808	795 +		1	0.835	0.025	tgaactcatgaaaCCTAag
1109	1135	1122 +		1	0.863	0.053	tatacacctcggcCCTAaaa
219	245	232 +		1	0.995	0.145	ttttgtgcaaaaACCCtaacc
697	723	710 +		1	0.833	0.023	gattgtcggtaaaaCCTAaac
86	112	99 +		1	0.829	0.019	cgtaaaaagaagtCCTAaa
192	218	205 +		1	0.826	0.016	ttggtttgacaatCCTAaaaa
582	608	595 +		1	0.852	0.012	agataacacaaaCCCTttt
786	812	799 +		1	0.897	0.047	taaatagattaACCCtagct
1045	1071	1058 +		1	0.823	0.043	taaagctgAAACtctaaac
1052	1078	1065 +		1	0.787	0.007	tgaaactctAAACcttcagti

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
704	714	709 +		1	0.799	0.009	catcAAAGcag
715	725	720 +		1	0.853	0.063	cataAAAGcta

tart positio	nd positio	chor positio	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
706	724	715 +		1	0.845	0.005	gagaaaaTGACttaacctc
1227	1245	1236 +		1	0.877	0.027	tctgaaaTGACctcatctt
512	530	521 +		1	0.855	0.015	tgatgaTGACattgggga
1278	1296	1287 +		1	0.846	0.006	ttcatcaTGACttaaggta
76	94	85 +		1	0.875	0.005	atcccttACGTcaaaa

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>j</sub>	Sequence
1196	1204	1200 +		1	1	0	aCCACaacc
304	312	308 +		1	1	0	tgACATga

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>j</sub>	Sequence
733	743	738 +		1	0.956	0.086	caACCTacgtg
986	996	991 +		0.813	0.881	0.011	aaACATAagat
1378	1388	1383 +		1	0.944	0.124	ttacCTTAaat
792	802	797 +		1	0.904	0.034	aaACCTaagca
591	601	596 +		1	0.842	0.022	aatCTTAatt
825	835	830 +		1	0.828	0.008	ttccCTTAatt
1201	1211	1206 +		1	0.827	0.007	atgcCTTAaaa
299	309	304 +		1	0.861	0.041	taaaCTTAaat
847	857	852 +		1	0.834	0.014	aaaaCTTAaga
889	899	894 +		1	0.865	0.045	taatCTTAaat
936	946	941 +		1	0.989	0.169	taacCTTAatc

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>j</sub>	Sequence
1259	1273	1266 +		0.81	0.875	0.025	gtcctCCGAcggggg
787	801	794 +		1	0.901	0.061	ttccCCGgagaatg

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>j</sub>	Sequence
1202	1218	1210 +		1	0.784	0.034	tcctcCCACatccgcg

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>j</sub>	Sequence
183	197	190 +		1	0.934	0.024	gaagcCAGCttttga

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>j</sub>	Sequence
682	698	690 +		1	0.95	0.01	ggaaaTTGAcgaaagct
1377	1393	1385 +		1	0.95	0.02	caaatTTGActtaaatt
521	537	529 +		1	0.903	0.003	tgtggTTGAcatgggat
71	87	79 +		1	0.942	0.012	gtgtTTGActcttaac
463	479	471 +		1	1	0	gacatTTGAcccataag
740	756	748 +		1	0.91	0.04	ataattTGACTcataaa
1147	1163	1155 +		1	0.922	0.032	acaataTGACcaattct
1168	1184	1176 +		1	0.914	0.014	caaagTTGAcattgagg
1204	1220	1212 +		1	1	0	gagccTTGAccatggcg
232	248	240 +		1	0.939	0.019	catatTTGAcAAagttt
618	634	626 +		1	0.962	0.032	tgcccTTGActataatt
660	676	668 +		1	0.962	0.032	tgtccTTGActataatt
924	940	932 +		1	0.952	0.032	cttgtTTGAcAattatt
192	208	200 +		1	0.952	0.032	ttgtTTGAcAaatccta
713	729	721 +		1	0.85	0.02	aaattTTGAatttcct
767	783	775 +		1	1	0	atattTTGAcctaaaat

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>j</sub>	Sequence
874	884	879 +		1	0.972	0.102	tttCAATcaaa
925	935	930 +		1	0.965	0.095	tttCAATcaga
615	625	620 +		1	0.909	0.039	atcCAATcagt
187	197	192 +		1	0.897	0.027	cccCAATcaga
317	327	322 +		1	0.877	0.007	catCAATgaag
101	111	106 +		1	0.964	0.094	cttCAATcaaa

tart positi	nd positi	ochor positi	Strand	Core sim.	Matrix simat.	sim. - o <sub>j</sub>	Sequence
269	285	277 +		1	0.876	0.086	ctttaGACTtttgttta

tart positi	nd positi	chor positi	Strand	Core sim.	Matrix sim.	sim. - o	Sequence
175	187	181 +		1	0.944	0.024	taaaTGATAagaa
813	825	819 +		1	0.948	0.028	tggaTGATtagat
201	213	207 +		1	0.946	0.026	aataTGATtggaa
250	262	256 +		1	0.939	0.019	tctaTGATcaagg
352	364	358 +		1	0.942	0.022	tgaaTGATAaaca
673	685	679 +		1	0.929	0.009	taaaTGATgaatt
712	724	718 +		1	0.957	0.037	ttaTGATtgagg
1148	1160	1154 +		1	0.923	0.003	agaaTGATgaatt
152	164	158 +		1	0.965	0.045	actaTGATAatca
410	422	416 +		1	0.922	0.002	tgaaTGATtgggt
512	524	518 +		1	0.933	0.013	tgtaTGATgacat
1223	1235	1229 +		1	0.93	0.01	gggaTGATAatgg
717	729	723 +		1	0.957	0.037	tacaTGATtatca
815	827	821 +		1	0.922	0.002	tgaaTGATgatga
818	830	824 +		1	0.921	0.001	atgaTGATgaaaa
285	297	291 +		1	0.92	0	gacaTGATAaccc
524	536	530 +		1	0.956	0.036	ttaTGATgattt
527	539	533 +		1	0.929	0.009	atgaTGATtttaa
1228	1240	1234 +		1	0.94	0.02	tctaTGATttcaa
1321	1333	1327 +		1	0.98	0.06	ggtaTGATtaaaa
1094	1106	1100 +		1	0.97	0.05	aaaaTGATtatga
1382	1394	1388 +		1	0.962	0.042	ggtaTGATAataa

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919	929	924 +		1	0.912	0.112	ttaCACTaca
1168	1178	1173 +		1	0.893	0.093	atgaCACTacc
1211	1221	1216 +		1	0.885	0.085	caaaCACTaaa
742	752	747 +		1	0.879	0.079	gaaaCACTatg
364	374	369 +		1	0.804	0.004	atttCACTaat

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atagtt  
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ātaacctc  
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ātaaatcgg  
\TGaaagttat

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jtaatgt  
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āaaaaa  
āatggtt  
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jcaaggca  
gtcactca  
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aaataaattt  
aatgattggt  
gtctcattta  
taggttgcgac  
agccagcttt  
aatatcatgatta  
aaattttat  
aaaaatatac  
aagaattatat  
taattttaaa  
tataaaaaacgg  
ttaaacaat  
aaggtttaactg  
aagaaaatca  
ccaattgg

jcattat  
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aatfttaaaaa  
atgtaataaa  
tgttattgaaa  
attctaaaag  
ittttatatagt  
aaaattttattc  
ctattttgaa  
icgtgtcaaaca  
acagtttttaca  
iatatatgtaa  
aatctactattca  
atgttttaa  
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tttattgtg  
ttcctcta  
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tcattcctta  
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igattaacccta  
jattttttgtt  
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taattaataaa  
jctgaaactcta  
iaagaagagaag  
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icattttcca  
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gtcaacag  
:atggaat  
ataaaaagc  
aaaactttg  
ttttagg  
.ttttttt  
ttaaataca  
>cttcagt  
catacga

	<b>Matrix Family</b>	<b>p-value</b>	<b>Match Total</b>	<b>Common to #sequences</b>	<b>VvACS1</b>	<b>VvACS6</b>	<b>VvACO2</b>	<b>VvACO4</b>
1	P\$DREB	0.819037	12	5	1	6	3	1
2	P\$SUCB	0.418866	17	6	2	4	3	2
3	P\$PNRE	0.253327	6	4	0	0	0	1
4	P\$AP2L	0.914425	6	4	0	1	0	0
5	P\$ARF3	0.827874	3	3	0	1	1	1
6	P\$ABRE	0.969899	3	2	2	0	1	0
7	P\$BRRE	0.810462	2	2	1	1	0	0
8	P\$CGCG	0.986233	2	2	1	1	0	0
9	P\$NCS2	0.446747	2	2	1	1	0	0
10	O\$TELO	0.281565	1	1	0	0	0	1
11	P\$AREF	0.824885	1	1	0	1	0	0
12	P\$CE1F	0.422214	1	1	0	0	0	0
13	P\$DPBF	0.559366	1	1	0	0	0	0
14	P\$EINL	0.417803	2	1	0	0	2	0
15	P\$EREF	0.488788	1	1	0	0	0	0
16	P\$GAGA	0.4764	1	1	0	1	0	0
17	P\$GAZL	0.965416	1	1	0	0	0	0
18	P\$GRFF	0.771363	2	1	0	0	0	0
19	P\$HOCT	0.740728	1	1	1	0	0	0
20	P\$NIGS	0.98582	2	1	0	0	0	0
21	P\$OCSE	0.868674	1	1	0	0	0	0
22	P\$ROOT	0.649763	1	1	0	1	0	0
23	P\$SEF3	0.453306	1	1	0	0	0	0
24	P\$SURE	0.001708	1	1	0	0	0	1
25	P\$URNA	0.251697	1	1	1	0	0	0
26	P\$VRES	0.410371	1	1	0	0	0	0
27	P\$WTBX	0.469041	1	1	0	0	0	0
28	P\$AGP1	0.998922	4	2	3	0	0	0
29	P\$CARM	0.335232	2	2	0	0	0	0
30	P\$FORC	0.389629	3	2	0	0	2	0
31	P\$LFYB	0.678304	2	2	0	1	0	0
32	P\$LICM	0.896724	2	2	0	0	0	0
33	P\$MYCS	0.551056	2	2	1	0	0	0
34	P\$PAHD	0.39664	2	2	0	1	0	1
35	P\$PALA	0.499616	2	2	1	0	0	0
36	P\$PCDR	0.871859	2	2	1	0	0	0
37	P\$RKDS	0.268074	4	2	0	0	1	0
38	P\$SRSF	0.740728	2	2	0	0	0	1
39	P\$TCPF	0.987603	2	2	0	0	2	0
40	P\$TERE	0.426046	2	2	0	0	0	1
41	P\$TODS	0.930441	2	2	0	1	0	0
42	P\$TRIH	0.979168	2	2	0	1	1	0
43	P\$ARID	0.079838	5	3	0	0	2	0
44	P\$CAAT	0.205669	4	3	0	0	1	0
45	P\$GBOX	0.987107	5	3	3	0	1	0
46	P\$GCCF	0.977191	3	3	0	1	1	0
47	P\$IDDF	0.163289	5	3	3	0	1	0
48	P\$JARE	0.957489	6	3	3	0	0	1
49	P\$LBDP	0.99358	3	3	1	0	1	0
50	P\$LREM	0.036169	7	3	0	0	0	1
51	P\$MSAE	0.974456	4	3	0	1	1	0
52	P\$PSRE	0.154811	5	3	1	0	0	2
53	P\$REMF	0.230546	4	3	1	1	0	2
54	P\$SEF4	0.235841	3	3	0	0	1	0
55	P\$TEFB	0.677433	3	3	0	0	0	1

56	P\$TGAF	0.896962	5	3	2	0	0	0
57	P\$EPFF	0.426046	4	4	1	1	0	0
58	P\$GARP	0.93707	6	4	1	0	1	0
59	P\$LEGB	0.519148	4	4	0	0	1	0
60	P\$PSPE	0.235861	4	4	0	0	0	1
61	P\$RAV5	0.729987	6	4	0	0	1	2
62	P\$SBPD	0.947802	8	4	0	2	1	0
63	P\$SPF1	0.936413	7	4	1	0	0	3
64	P\$STKL	0.75837	5	4	1	2	0	0
65	P\$WOXF	0.169127	6	4	2	0	1	0
66	P\$CNAC	0.006792	6	5	0	0	2	1
67	P\$GAPB	0.011258	10	5	0	0	3	2
68	P\$HMGF	0.138067	13	5	2	1	1	0
69	P\$STKM	0.053993	7	5	2	0	2	1
70	P\$TOEF	0.48873	11	5	2	0	3	0
71	P\$ZFAT	0.760194	5	5	0	2	0	0
72	O\$INRE	0.288822	7	6	2	1	1	0
73	O\$PTBP	0.001695	23	6	5	1	6	5
74	O\$YTBP	0.010326	15	6	5	2	2	1
75	P\$AHLF	0.28187	19	6	3	0	2	2
76	P\$C3HF	0.216058	9	6	3	1	2	1
77	P\$FLO2	0.371991	6	6	1	0	1	1
78	P\$GLKF	0.041891	15	6	4	3	2	0
79	P\$MYCL	0.836571	9	6	2	1	1	1
80	P\$OPAQ	0.782895	6	6	1	1	1	1
81	P\$TELO	0.041201	13	6	0	1	1	1
82	P\$WBXF	0.033171	16	6	2	3	0	4
83	P\$NACD	0.904052	18	6	2	2	0	1
84	P\$NACF	0.020416	17	7	3	1	1	0
85	P\$ASRC	0.333184	10	7	2	0	1	1
86	P\$NCS1	0.032711	17	7	5	0	2	1
87	P\$YABB	0.025867	22	7	2	2	5	2
88	O\$VTBP	0.043271	42	8	5	5	6	10
89	P\$AHBP	0.007502	151	8	17	18	22	14
90	P\$CCAF	0.017015	45	8	5	2	5	6
91	P\$DOFF	0.013292	42	8	7	4	8	8
92	P\$GTBX	0.003874	60	8	4	4	16	9
93	P\$HEAT	0.035643	33	8	6	4	1	1
94	P\$IBOX	0.043303	19	8	1	2	3	4
95	P\$KAN1	0.02837	38	8	6	7	5	2
96	P\$L1BX	0.014821	43	8	7	5	5	2
97	P\$MADS	0.014821	36	8	7	4	7	7
98	P\$MIIG	0.005718	52	8	8	6	8	5
99	P\$MYBL	0.000992	35	8	3	5	1	7
100	P\$MYBS	0.005718	26	8	7	3	3	1
101	P\$SWNS	0.043298	21	8	3	4	1	5
102	P\$TCXF	0.037999	49	8	4	3	9	11
103	P\$NTMF	0.031134	27	8	6	3	3	4

VvACS2	VvACS9	VvACO1	VvACS4
0	1	0	0
1	0	0	5
1	2	2	0
2	2	1	0
0	0	0	0
0	0	0	0
0	0	0	0
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0	1	0	0
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0	0	2	0
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1	0	0	5
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1	0	0	1
1	0	1	0

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1	1	1	0
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0	2	0	1
2	3	0	0
0	1	0	2
0	0	1	1
1	0	2	0
1	1	0	1
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3	0	1	8
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5	6	2	0
4	4	1	3
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4	2	2	1
6	2	3	0
6	1	5	4
31	7	7	35
7	2	4	14
2	6	3	4
10	5	3	9
6	9	5	1
3	1	2	3
5	6	4	3
12	2	3	7
1	5	3	2
3	4	13	5
5	3	8	3
3	4	4	1
3	2	2	1
4	1	1	16
4	4	2	1

**Table 1. Transcription factor binding site (TFBS) analysis of the pro**

Matrix Family	Detailed Family Information	p-value	VvACSI
<b>DREB</b>	Dehydration responsive element binding factors	0.82	<b>1</b>
<b>SUCB</b>	Sucrose box	0.42	<b>2</b>
<b>ARF3</b>	Auxin Response Factor 3	0.83	0
<b>PNRE</b>	Plant nitrate-responsive cis-elements	0.25	0
<b>AP2L</b>	APETALA2-like transcription factors	0.91	0
<b>ABRE</b>	ABA response elements	0.97	<b>2</b>
<b>BRRE</b>	Brassinosteroid (BR) response element	0.81	<b>1</b>
<b>CGCG</b>	Calmodulin binding / CGCG box binding proteins	0.99	<b>1</b>
<b>NCS2</b>	Nodulin consensus sequence 2	0.45	<b>1</b>

	Seq. name	Detailed Family Information	Matrix Info	Opt.
<b>P\$DREB</b>	VvACS1	Dehydration responsive element binding factors	Dwarf and D	0.81
	VvACS6	Dehydration responsive element binding factors	Dwarf and D	0.81
	VvACS6	Dehydration responsive element binding factors	Dwarf and D	0.81
	VvACS6	Dehydration responsive element binding factors	Dwarf and D	0.81
	VvACS6	Dehydration responsive element binding factors	DREB and E	0.85
	VvACS6	Dehydration responsive element binding factors	Ethylene-res	0.89
	VvACS6	Dehydration responsive element binding factors	Dehydration-	0.87
	VvACS9	Dehydration responsive element binding factors	Ethylene-resp	0.77
	VvACO2	Dehydration responsive element binding factors	C-repeat/deh	0.89
	VvACO2	Dehydration responsive element binding factors	Dwarf and D	0.86
	VvACO2	Dehydration responsive element binding factors	Dwarf and D	0.86
	VvACO4	Dehydration responsive element binding factors	Ethylene-res	0.8

	Seq. name	Detailed Family Information	Matrix Info	Opt.
<b>P\$SUCB</b>	VvACS1	Sucrose box	Sequence mo	0.81
	VvACS1	Sucrose box	Sequence mo	0.81
	VvACS2	Sucrose box	Sequence mo	0.81
	VvACS6	Sucrose box	Sequence mo	0.81
	VvACS6	Sucrose box	Sequence mo	0.81
	VvACS6	Sucrose box	Sequence mo	0.81
	VvACS6	Sucrose box	Sequence mo	0.81
	VvACO2	Sucrose box	Sequence mo	0.81
	VvACO2	Sucrose box	Sequence mo	0.81
	VvACO2	Sucrose box	Sequence mo	0.81
	VvACO4	Sucrose box	Sequence mo	0.81
	VvACO4	Sucrose box	Sequence mo	0.81
	VvACS4	Sucrose box	Sequence mo	0.81
	VvACS4	Sucrose box	Sequence mo	0.81
	VvACS4	Sucrose box	Sequence mo	0.81
	VvACS4	Sucrose box	Sequence mo	0.81
	VvACS4	Sucrose box	Sequence mo	0.81

	Seq. name	Detailed Family Information	Matrix Info	Opt.
<b>P\$ARF3</b>	VvACS6	Auxin Response Factor 3	ETTIN (Aux)	0.83
	VvACO2	Auxin Response Factor 3	ETTIN (seco	0.83

VvACO4 Auxin Response Factor 3 ETTIN (Auxin) 0.83

<b>P\$PNRE</b>	<b>Seq. name</b>	<b>Detailed Family Information</b>	<b>Matrix Info</b>	<b>Opt.</b>
	VvACS2	Plant nitrate-responsive cis-elements	Motif similar	0.84
	VvACS9	Plant nitrate-responsive cis-elements	NIN-binding	0.81
	VvACS9	Plant nitrate-responsive cis-elements	NIN-binding	0.81
	VvACO1	Plant nitrate-responsive cis-elements	Motif similar	0.84
	VvACO1	Plant nitrate-responsive cis-elements	Motif similar	0.84
	VvACO4	Plant nitrate-responsive cis-elements	NIN-binding	0.81

<b>P\$AP2L</b>	<b>Seq. name</b>	<b>Detailed Family Information</b>	<b>Matrix Info</b>	<b>Opt.</b>
	VvACS2	APETALA2-like transcription factors	Target of ear	0.8
	VvACS2	APETALA2-like transcription factors	Target of ear	0.8
	VvACS6	APETALA2-like transcription factors	Target of ear	0.8
	VvACS9	APETALA2-like transcription factors	Ethylene-res	0.85
	VvACS9	APETALA2-like transcription factors	Ethylene-res	0.85
	VvACO1	APETALA2-like transcription factors	Ethylene-res	0.85

<b>P\$ABRE</b>	<b>Seq. name</b>	<b>Detailed Family Information</b>	<b>Matrix Info</b>	<b>Opt.</b>
	VvACS1	ABA response elements	Abscisic acid	0.83
	VvACS1	ABA response elements	ABA respons	0.82
	VvACO2	ABA response elements	ABA (abscisi	0.79

<b>P\$BRRE</b>	<b>Seq. name</b>	<b>Detailed Family Information</b>	<b>Matrix Info</b>	<b>Opt.</b>
	VvACS1	Brassinosteroid (BR) response element	Brassinazole-	0.83
	VvACS6	Brassinosteroid (BR) response element	Brassinazole-	0.95

<b>P\$CGCG</b>	<b>Seq. name</b>	<b>Detailed Family Information</b>	<b>Matrix Info</b>	<b>Opt.</b>
	VvACS1	Calmodulin binding / CGCG box binding proteins	Arabidopsis t	0.84
	VvACS6	Calmodulin binding / CGCG box binding proteins	Oryza sativa	0.78

<b>P\$NCS2</b>	<b>Seq. name</b>	<b>Detailed Family Information</b>	<b>Matrix Info</b>	<b>Opt.</b>
	VvACS1	Nodulin consensus sequence 2	Nodulin cons	0.79
	VvACS6	Nodulin consensus sequence 2	Nodulin cons	0.79

**noter sequences of the *VvACS* and *VvACO* genes.**

<i>VvACS6</i>	<i>VvACO2</i>	<i>VvACO4</i>	<i>VvACS2</i>	<i>VvACS9</i>	<i>VvACO1</i>	<i>VvACS4</i>
6	3	1	0	1	0	0
4	3	2	1	0	0	5
1	1	1	0	0	0	0
0	0	1	1	2	2	0
1	0	0	2	2	1	0
0	1	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0

Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	at. sim.	- o]
1284	1304	1294	+	1	0.84	0.03	
11	31	21	+	1	0.833	0.023	
38	58	48	+	1	0.88	0.07	
1100	1120	1110	+	1	0.858	0.048	
1249	1269	1259	+	1	0.874	0.024	
1256	1276	1266	+	0.801	0.899	0.009	
1271	1291	1281	+	1	0.937	0.067	
851	871	861	+	1	0.779	0.009	
25	45	35	+	1	0.946	0.056	
1009	1029	1019	+	1	0.881	0.021	
1096	1116	1106	+	1	0.993	0.133	
906	926	916	+	1	0.854	0.054	

Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	at. sim.	- o]
227	245	236	+	1	0.811	0.001	
484	502	493	+	1	0.885	0.075	
108	126	117	+	1	0.828	0.018	
129	147	138	+	1	0.843	0.033	
252	270	261	+	1	0.838	0.028	
529	547	538	+	1	0.923	0.113	
806	824	815	+	1	0.81	0	
561	579	570	+	1	0.835	0.025	
589	607	598	+	1	0.841	0.031	
1238	1256	1247	+	1	0.812	0.002	
254	272	263	+	1	0.856	0.046	
1093	1111	1102	+	1	0.815	0.005	
116	134	125	+	1	0.83	0.02	
222	240	231	+	1	0.823	0.013	
1031	1049	1040	+	1	0.853	0.043	
1141	1159	1150	+	1	0.825	0.015	
1376	1394	1385	+	1	0.946	0.136	

Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	at. sim.	- o]
1222	1232	1227	+	1	0.91	0.083	
1014	1024	1019	+	1	0.96	0.131	

699	709	704 +		1	0.97	0.135
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Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	at. sim. - o]
779	811	795 +		1	0.84	0.004
61	93	77 +		1	0.81	0.001
1268	1300	1284 +		1	0.85	0.036
671	703	687 +		1	0.87	0.028
854	886	870 +		1	0.86	0.02
875	907	891 +		1	0.85	0.035

Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	at. sim. - o]
234	248	241 +		1	0.81	0.014
688	702	695 +		1	0.80	0.002
1324	1338	1331 +		1	0.82	0.017
759	773	766 +		1	0.87	0.023
1141	1155	1148 +		1	0.87	0.021
765	779	772 +		1	0.87	0.022

Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	at. sim. - o]
769	785	777 +		1	0.84	0.007
1077	1093	1085 +		1	0.90	0.08
1294	1310	1302 +		1	0.80	0.005

Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	at. sim. - o]
671	689	680 +		1	0.83	0
1231	1249	1240 +		1	0.95	0.004

Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	at. sim. - o]
1212	1228	1220 +		1	0.97	0.126
6	22	14 +		0.817	0.80	0.015

Start position	End position	Anchor position	Strand	Core sim.	Matrix sim.	at. sim. - o]
1001	1015	1008 +		1	0.90	0.108
74	88	81 +		1	0.91	0.122

**Sequence**

ttctcacaCGACatgtaggc  
aggttgataCGACatggttt  
aagaattaaCGACattgataa  
ttaggttgCGACatctcaca  
ttggctaACCGtctccgacg  
accgtccTCGGacgggggtcc  
gggtcctccCGACaatgaata  
tcattaaCCGAgagcgcatt  
caattgggCCGActtcatgta  
ccacacggtCGACagagtcaa  
ataaagagcCGACatataatt  
agcaccACCgagagaggctt

**Sequence**

aaAAATtaaagaaaagaaa  
aaAAATcaaaccattcata  
aaAAATaataacaaagaac  
aaAAATtattaataaaac  
aaAAATaattgcacaaaag  
taAAATcatttgatggaat  
taAAATtattggtggaat  
aaAAATaattaaaataaa  
acAAATcttaatttataaa  
caAAATtaagaaatcaaa  
gaAAATaattttttcaaa  
aaAAATgattatgaaaaat  
aaAAATaattttgaaaat  
tcAAATtaatgttttaaat  
aaAAATctgaattttaaag  
taAAATtattaattgtaaa  
aaAAATcatatttaaaaaa

**Sequence**

ctGTCGgccga  
cggTCGAcaga

ttGTCGgtaaa

**Sequence**

aaagatgaaCCTTcactatcataacttttcac  
gccattgtgctgtttcttctaaAAGGatttct  
ctgaaccccttcatcatgacttAAGGtagatc  
tgaaaagatCCTTgacaaaacaagagtaggat  
tagggagacCCTTaccattcccacgaagactt  
taccagtcctggttcaaacAAGGccagag

**Sequence**

aagtctTCGTatgct  
ctttcTCGTattta  
atttctTCGTattt  
acttcatGTACaat  
aggttctGTACtaa  
aatttctGTACatg

**Sequence**

aaaataaACGTgactca  
aatttatACGTgtaatg  
gacgaACACgagtcag

**Sequence**

gtcaaaCGTGaggaaattg  
gatctcCGTGtgetggcct

**Sequence**

atcCGCGtgetaacgct  
tgtCGAGggtgatacga

**Sequence**

tcttgtCTCTgtcc  
tttgaCTCTtaact