

1 **Supplemental table 3:** List of primers
2

Primer name	Target	Sequence (5'--->3')
SDM_Kpn1_F	pBGWL7	GTACAAAGTGGTACCAAAAAAATGGAAGACGCCAAAAACATAAAGAAAGG
SDM_Kpn1_R	pBGWL7	CCATTTTTTTGGTACCCTTTGTACAAGAAAGCTGAACGAGAAACGTAA
SDM_PshA1_F	pBGWL7	AAGTCCAAATTGTAACCGCGGCCAGACTAGAGTCCGCAAAAA
SDM_PshA1_R	pBGWL7	CGGTTACAATTTGGACTTTCCGCCCTTCTTGGCCTTTAT
ASP_LUC+_PshA1	LUC+	GAGACTCTAGTCTGGCCGCGTTACACGGCGATCTTTCCG
SP_PromPECP1	AT1G17710	CACCGTTGGGAAGAGAGAGAGA
ASP_PromPECP1	AT1G17710	TCTATCAGATACAATGTTTTATAG
SP_PromPPsPase1	AT1G73010	CACCTTACAGTATTAATTCCCA
ASP_PromPPsPase1	AT1G73010	GACTCAGGAAATTTCTAAAGA
SP_PromMGD3	AT2G11810	GATCGCTAGCTGTGACCCACATTAGTCTTAATTTCTTTG
ASP_PromMGD3	AT2G11810	GATCCCATGGACTATTTGGTGTGAAGAAAG
SP_PromPPsPase1_V2	AT1G17710	GGTACCGGCTACCGAATAAGTGTATGTGTC
ASP_PromPPsPase1_V2	AT1G17710	CTCGAGGACTCAGGAAATTTCTAAAGAAATTAGTG
SP_PromPECP1_V2	AT1G73010	GGTACCGAGACGATTGGGAGGGATGTGC
ASP_PromPECP1_V2	AT1G73010	CTCGAGCTATCAGATACAATGTTTTATAGGTA CTG
ATTG_protospacer	AT1G17710	ATTGTTGATGGCTGGGATGACACG
AAAC_protospacer	AT1G17710	AAACCGTGT CATCCAGCCATCAA
HRM_PECP1_F	AT1G17710	TCGGTTTCTCTAGGGCTTTGTT
HRM_PECP1_R1	AT1G17710	CATGAGCAGATTTGATGGCTGG
HRM_PECP1_R2	AT1G17710	GAGCAGATTTGATGGCTGGGAT
HRM_fugu5.1_F	AT1G15690	ATGCTCATCGATGCTCTCTGT
HRM_fugu5.1_R	AT1G15690	ATCACAGCTGCCTTGTGTGG
SP_CDS_PPsPase1	AT1G73010	CACCATGGCTTACAATAGCAAT
ASP_CDS_PPsPase1_stop	AT1G73010	CTAACTAGACTGAGACACACG
SP_CDS_PECP1	AT1G17710	CACCATGGCTAAGAATAACAAC
ASP_CDS_PECP1_stop	AT1G17710	TCACTTGACCAAATTTAAA
ASP_PPsPase1-3e	AT1G73010	GTGCCACAAGAGCAGCTATG
SP_PECP1-4e	AT1G17710	AGGGAAGACGAGCAAGATGA

ASP_PECP1-4e	AT1G17710	TCGGTCCAATCTCTAACGGT	
SP_CDS_ThMPase1	AT4G29530	ATGGCAAAAATCGTGATATTATTG	
SP_ACT2	SP_ACT2	CTTCCCTCAGCACATTCCAG	
ASP_ACT2	ASP_ACT2	AACATTGCAAAGAGTTTCAAGGT	
qPCR PRIMERS	Target	Sequence (5'--->3')	Amplification efficiency
q_SP_PPsPase1	AT1G73010	TCATGATCAAGGCAAAACCA	1,84
q ASP_PPsPase1	AT1G73010	GACGACACGTGGATGAATTG	
q_SP_PECP1	AT1G17710	TTAGGGTGCAGCTGAGAAT	1,83
q ASP_PECP1	AT1G17710	CAACGAGAGCAACCATGAGA	
q_SP_ThMPase1	AT4G29530	GAACTTGC GGATCTTGCCTT	1,73
q ASP_ThMPase1	AT4G29530	GCAGAAGTCACCTCCTCCAT	
q_SP_SPX1	AT5G20150	CGGGTTTTGAAGGAGATCAG	1,93
q ASP_SPX1	AT5G20150	GCGGCAATGAAAACACACTA	
q_SP_PHT1;4	AT2G38940	CCTCGGTCGTATTTATTACCACG	1,87
q ASP_PHT1;4	AT2G38940	CCATCACAGCTTTTGGCTCATG	
q_SP_MGD2	AT5G20410	ACAAGAAATTGGCATCTGCAT	1,77
q ASP_MGD2	AT5G20410	TGGTCCAGCTTTTGTGATGA	
q_SP_MGD3	AT2G11810	AGAGGCCGGTTTAATGGAGT	2,09
q ASP_MGD3	AT2G11810	CATCAGAGGATGCACGCTAA	
q_SP_SQD1	AT4G33030	AGCTTGGGCTAGACGTGAAA	1,92
q ASP_SQD1	AT4G33030	AGGCTCAAGTCCAAGTTCCA	
q_SP_SQD2	AT5G01220	TACCTGAAGCTCGGATTGCT	1,89
q ASP_SQD2	AT5G01220	TGTGAGAGTTCATCGCCTTG	
q_SP_NPC4	AT3G03530	TGGTTTGC GTCGGTTCCAGC	1,94
q ASP_NPC4	AT3G03530	CGTTGCTCCATGTGATGTTGCCG	
q_SP_PLDζ1	At3g16785	TGGATGGCAACCGCAAAGACAA	1,94
q ASP_PLDζ1	At3g16785	ATCGTTGTGTGTCCAGCTTCT	
q_SP_PLDζ2	At3g05630	TTTGAGGACGGTCCAATTGCCA	1,94
q ASP_PLDζ2	At3g05630	ACAACACCGATCTCAGAGTCTCGT	
q_SP_PAH1	AT3G09560	GTGTCGACGAAGGAGAACCC	2,00
q ASP_PAH1	AT3G09560	GTCCCATACCCTGACGAAGC	

q_SP_PAH2	AT5G42870	CACAACAGGTAGACGCAAGG	1,96
q ASP_PAH2	AT5G42870	CCAACCAAAGGCATAAACTGGC	
q_SP_GDPD1	AT3g02040	ACGGGCCACAGAGGGATACAGGCA	1,91
q ASP_GDPD1	AT3g02040	GTCGTCGGTTGCGACGCTCCACTT	
q_SP_GDPD2	AT5G41080	AGTGTTTCAGGAACCCAGCAGCC	1,94
q ASP_GDPD2	AT5G41080	TTGCATGTACTGCTCTCCG	
q_SP_GDPD3	AT5G43300	GCTCAAATTCGATGATAATACCG	1,96
q ASP_GDPD3	AT5G43300	CGGTTCTTGAATGTTCAATTTAC	
q_SP_GDPD5	AT1G74210	ACCAGATCGCCATGATTCTT	1,97
q ASP_GDPD5	AT1G74210	AGGGAGAGGGTGCAATGTC	
q_SP_GDPD6	AT5G08030	AACATGACCGGCTTCTTCAC	1,93
q ASP_GDPD6	AT5G08030	ACCTCTGCTTTGCACCAAGT	
q_SP_SCAMP	AT1G32050	TCTGGCTTTTCGCTAGTTGGT	1,80
q ASP_SCAMP	AT1G32050	TCCTCATGGCTCGGTAGAGT	
q_SP_ROC3	AT2G16600	ATCGTGATGGAGCTTTACGC	1,96
q ASP_ROC3	AT2G16600	TCGGTGAAAGCTTGATCCTT	
q_SP_GAPC1	AT3G04120	TGGGCCGAGGCTGGAGCTGACTACG	1,89
q ASP_GAPC1	AT3G04120	TGGAGCGTCTTTGCTGGGGGCAGA	
q_SP_GF14phi	AT1G35160	TCTGACATGCAGGACGAAAG	1,90
q ASP_GF14phi	AT1G35160	TAGAAGCTTCGGGGATAGCA	