

Figure S1. The stem-loop structures of MIR172 loci from *A. thaliana* (At) and *A. arenosa* (Aa) (MIR172a, b, d, and e) were predicted using RNA secondary structure prediction software the Vienna RNA package (http://www.tbi.univie.ac.at/~ivo/RNA/). The miR172 sequence in each locus was indicated by red lines on the structures. For each *AtMIR172*, there are two corresponding *AaMIR172* loci (Aa-1 and Aa-2).



Figure S2. Sequence alignment of *A. arenosa MIR172a* locus with the corresponding *A. thaliana MIR172a*. Multiple sequence alignment performed using MultAlin (<u>http://prodes.toulouse.inra.fr/multalin/</u>).

	1	10	20	30	40	50	50		80	30	100	110	120	130
AtniR172b BaniR172b-1 BaniR172b-2 Consensus	TRGTGR	TTCTTCACT TTTCTTCACT .ttcttcact	6CACCTCTC TGCACCTCTC TGCACCTCTC GCACCTCTC	ACTECETTIC ACTECETTIC ACTECETTIC ACTECETTIC	TCTAR-CTF TCTARARCTF TCTARARCTF TCTARARCTF	IGTETTOTOT IGTETTOTOTO IGTETTOTOTO IGTETTOTOTOTO	IGCACCCA IGCAGTACCTA IGCCGTACCCA IGC.gtACCCA	TTTATGTGT TTTATGTGT TTTATGTGT TTTATGTGT	ACGTACTATT ACGTACTATT ACGTACTATT ACGTACTATT	ATCTCATAAA GTCTCATAAA GTCTCATAAA gTCTCATAAA	TAAATATTTI TAAAATAATI TAAAATATTI TAAAAtattI	TARARTTAGA TTTRA TTTTR TTTTR	IGCATTTATT IGCATTTATT IGCATTTATT IGCATTTATT	CATATG GATATG GATATG GATATG GATATG
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
RtniR172b RaniR172b-1 RaniR172b-2 Consensus	ARAARG ARAA-G ARAA-G ARAA-G ARAA.G	TTACAAGATT TTACAAGATT TTACAAGATT TTACAAGATT	AGTITGITGI GGTITGITGI GGTITGITGI 2GTITGITGI	IGTGTGAGACT IGTTTGAGCCT IGTGTGAGCCT IGTgTGAGCCT	TTGGATCGAC TTGGATCGAC TTGGATCGAC TTGGATCGAC	AGATCGAAA AGAT AGATAGAAA AGATAGAAA	IA-ATTAACTA TAACTA IAGATTAACTA III III IIIIIIIIIIIIIIIIIIIIIIIIIIIII	ACCGGTCAG ACCGGTCAG ACCGGTCAG ACCGGTCAG	TATTGAATAT TACTGGATAT TACTGGATAT TACTGGATAT		ATATGCTC- ATCTATTCGA ATCTCTTCGA ATCT.LTCga	CCTATCATAT CCTATCATAT CCTATCATAT	SCRTTCGC SCTTCRTTGG GCTTCRTTGC GCtTcrTGC	TTATAC TTATAT TTATAT TTATAL
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
AtmiR172b AaniR172b-1 AamiR172b-2 Consensus	TTT CRI TTT CRI TTTCRI TTTCRI TTT.CRI	CACAATTTGT Catcatttgt Catcatttgt Catcatttgt Catcatttgt	TTTCTTCACC TT-CTT-ACC TT-CTT-ACC TT-CTT-ACC TT.CTT.ACC	GTCTRARAT GTCTRARATA GTCTRARARA GTCTRARARA	-CAGRAGATT GCAGRATATT GCGGRATATT gCaGRALATT	CCATATATT CCATATATT CCATATATT CCATATATT	TT-CTTAT TTTCTAATTA TTTCTTAT TTTCTTAT	GACGTAA Atgacgtaa Gacgtaa Gacgtaa	ARGGACCACT ARGGACCAGT ARGGACCART ARGGACCA, T	TATAAGTTGA TATAAATTGA TATAAATTGA TATAAATTGA TATAAATTGA	CACGTCAGCO CACGTCAGCO CACGTCAGCO CACGTCAGCO	CTTGGATTCG CTTGGATTCT CTTGGATTCT CTTGGATTCC	/GAGGTTTTT IGAGGTTTTT IGAGGTTTTT IGAGGTTTTT	CTCTCT CTCTTT CTCTCT CTCTCT CTCTCT
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
RtniR172b RaniR172b-1 RaniR172b-2 Consensus	ACTTCR ACTTCR ACTTCR ACTTCR	CCTATCTACT CCTATCTACT CCTATCTACT CCTATCTACT	TTTCCTCATA TTTCCTCATA TTTCCTCATA TTTCCTCATA	NTCCCRCTGCT NTCCCRCTGCT NTCCCRCTGCT NTCCCRCTGCT	TTTCTC0 TTTCTCTTTC TTTCTCCTTC TTTCTC_LLC	TTCTTCTTC TTCTTCTTC TTCATCTTC TTCLTCTTC	TIGITITI-C TIGITITIC TIGITITIC TIGITITIC TIGITITIC	TCGTTTTT TCGTTTTTT TCGTTTTTC TCGTTTTTL		CTCC CTCC ATTCTTCTCC CTCC	RAGARARTRO RATARARTTO RATARARTTO RALARARTLO	AGATCGRARA AAATCGGARA AAATCGGARA AAATCGGARA	SATTAGATET SATTAGATET GATTAGATET GATTAGATET	ATTTTG ATTTTG ATTTTG ATTTTG ATTTTG
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
AtniR172b AaniR172b-1 AaniR172b-2 Consensus	TETREC TITREC TITREC TETREC	AAGARATTAT AAGATATTAT AAGATATTAT AAGALATTAT	CATTTTO TATTATTTTO TATTTTO LATTTTO	CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR	TCATAT TCATATTTCT TCATATTTCT TCATATTCC	ATTGTTC TATTGTTC TATTGTTC LATTGTTC	ATTATGTTGT ATTATGTTGT ATTATGTTGT ATTATGTTGT	ACAATAATA ATAATAATA ATAATAATA ALAATAATA	GATACTCGAT GATATTCGAT GATACTCGAT GATACTCGAT	CTCTT6T6C6 CTCTT6T6T6 CTCTT6T6T6 CTCTT6T6C6	TGCGT TGTGTGTGTGTG TGTGTGTGTGTG TGLGTgLgLg	AAATT TAAGTT TGTGTAAGTT \$AAgTT	TATACAAGT TATACAAGT TATACAAGT TATACAAGT TATACAAGT	TGTCGG TGTCGG TGTCGG TGTCGG
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
AtniR172b RaniR172b-1 RaniR172b-2 Consensus	CGGATCI CGGATCI CGGATCI CGGATCI	Catggaa-ga Catggaaaga Catggaa-ga Catggaa-ga	AAGCTCATCI TAGCTCATCI NAGCTCATCI AGCTCATCI	IGTEGTTGTTT IGTEGTTGTTT IGTEGTTGTTT IGTEGTTGTTT	GTAGGCGCAC GTAGGTGCAC GTAGGTGCAC GTAGGLGCAC	icaccattaa icaccatcaa icaccatcaa icaccatcaa icaccatcaa	IGATTCACATG IGATTCACATG IGATTCACATG IGATTCACATG	CAAATTGAT AAAATTGAT AAAATTGAT AAAATTGAT	ARATACCCTA Aratctccta Aratctcctr Aratctcctr	AATTAGGGTT ARTTAGGGTT ARTTAGGGTT ARTTAGGGTT	TTGATATGTA TTGATATGTA TTGATATGTA TTGATATGTA	ITATGAGAATC Itatgagaatc Itatgagaatc Itatgagaatc Itatgagaatc	/TGATGATGC FTGATGATGC FTGATGATGC FTGATGATGC	TGCATC TGCATC TGCATC TGCATC TGCATC
	781	79 0	800	810	820	830	840	850	860	870	880	890	900	910
AtniR172b HaniR172b-1 AaniR172b-2 Consensus	ARCAATI ARCAATI ARCAATI ARCAATI	CGACGGCTAC CGACGGCTAC CGACGGCTAC CGACGGCTAC	AAA-TACCTA AAAATACCTA AAAATACCTA AAAATACCTA	HAGCTTGAGA HAGCTCGAGT GAGCTCGAGT HAGCTCGAGL	RAGARACTTO RAGARACTTO RAGARACTTO RAGARACTTO	AAGATATTG AAGAT <mark>G</mark> TTA AAGAT <mark>G</mark> TTA AAGAT <mark>g</mark> TTa	ATTGANGTCT ATTGATGTCT ATTGATGTCT ATTGALGTCT	GGATCEATC GGATC GGATC GGATC	TTTGGTARAT TTTGGTARAT TTTGGTARAT TTTGGTARAT	CTCTCTCTTG CTCTATCTTG CTCTATCTTG CTCTATCTTG CTCTATCTTG	ATTAGTTTTA ATTAGTTTGA ATTAGTTTGA ATTAGTTTgA	IAGRATCACTT IAGRATCACTT IAGRATCACTT IAGRATCACTT		GTGTTT GTGTTT GTGTTT GTGTTT GTGTTT
	911 	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
AtniR172b AaniR172b-1 AaniR172b-2 Consensus	GRACAT GRACAT GRACAT GRACAT	-GTTTACATA TGTTTACATG TGTTTACATG	TATCATCTAT TATCATATAT TATCATATAT	IGTCTCART		ACATTGGGT		TTTTCTTAR	TCTAGGGTCA	ATGACG	GATTAGGGCO	TTAATTACAA	(CRATATGGA 	AARACT AARACT BARACT
		EGTITACATS	TATCATaTAT	GTCTCLeTLL	atatatata	acattgggt	GT TATATATA SLLATATATA	TCTTCTTAR TCTTCTTAR TettCTTAR	TCTAGGGTCA TCTAGGGTCA TCTAGGGTCA	ATTAATAACG ATTAATAACG ATLaataACG	GATTAGGGCO Gattagggco Gattagggco	TTAATTACAA TTAATTACAA	TGAA-ATGGA tgaA, At GGA	AAAACT
	10 41 :	LGTTTHCHT9 1050	TATCATATAT 1060	1070	atatatata 1080	ACATTGGGT acattgggt 1090	GI ТАТАТАТА .glc ататата 1100	TCTTCTTAR TCTTCTTAR TettCTTAR 1110	TCTAGGGTCA TCTAGGGTCA TCTAGGGTCA 1120	ATTAATAACG ATTAATAACG ATLaalaACG 1130	GATTAGGGC0 GATTAGGGC0 1140	11101110CA0 11100 1150	TGAA-ATGGA tgaA,AtGGA 1160	AARACT 1170 1
AtniR172b AaniR172b-1 AaniR172b-2 Consensus	1041 : AITITG AGTITG AGTITG ASTITG	LOTTIACATS 1050 COTTIGATOT COTTIGATOT COTTIGATOT COTTIGATOT	TATCATATAT 1060 TGACTTGAGT TGGCTTGTGT TGGCTTGTGT TGgCTTGLGT	IGTCTCLCTLL 1070 IGTTGHTGAAAC IATTGAGGAAC IATTGAGGAAC IATTGAGGAAC	ALALALALALA 1080 AGATGTATAA AGATGTATAA AGATGTATAA AGATGTATAA	ACATTGGGT acattgggt 1090 HIGITATGTA HG-ATGTC HG-ATGTT HG, ATGT,	GTTATATATA SELATATATA 1100 GTATGTALTG CATGTAATATA ATGTAATATA ATGTAATATA ATGTAALATA	TCTTCTTAR TCTTCTTAR TeTTCTTAR 1110 TATTTTTC TATCTTARC TATCTTARC TATCTTARC	TCTAGGGTCA TCTAGGGTCA TCTAGGGTCA 1120 TAGAATCATT TGTATTTTT TGTATTTTTT TgLALTLLTT	ATTANTAACG ATTANTAACG ATtaataACG 1130 CITIRGICICU CIAGGAICATU CIAGGAICATU CIAGGAICATU	GATTAGGGCC GATTAGGGCC 1140 CARCTCTCCF ATGATTTC1 ATGATTTC1 atgaTtTC1	TTAATTACAA TTAATTACAA 1150 TTAATCAAAT TTAATCAAAT TTAATCAAAT TTAGTCTC TTAGTCTC	TGAA-ATGGA tgaA,AtGGA 1160 5AGGTCCTTA CATTA CATTA CaTTA	AARACT 1170 TAGGTA TAGGTG TAGGTG TAGGTg
AtniR172b BaniR172b-1 BaniR172b-2 Consensus	1041 : HTTTG AGTTTG AGTTTG AGTTTG AgTTTG 1171 :	LGTTTACATS 1050 CCTTTGATCT CCTTTGATCT CCTTTGATCT CCTTTGATCT 1180	TATCATATA1 1060 TGACTTGAG TGGCTTGTG1 TGGCTTGTG1 TGgCTTGLG1 1190	GTCTCLETEL 1070 GTTGHTGAAA ATTGAGGAAA GATTGAGGAAA GATTGAGGAAA I200	atatatata 1080 AGATGTATAA AGATGTATAA AGATGTATAA AGATGTATAA 1210	ACATTGGGT acallgggt 1090 HGTTATGTA HGATGTC HGATGTC HGATGT, HG, ATGT, 1220	GTTATATATA SCLATATATA 1100 GTATGTACTG ATGTATATA ATGTAATATA aTgTaaLaTa 1230	TCTTCTTAR TCTTCTTAR 1110 TATTTTTA TATCTTARC TATCTTARC TATCTTARC TATCTTARC 1240	TCTAGGGTCA TCTAGGGTCA 1120 TRGAATCATT TGTATTTTT TGTATTTTT TgLALTLLTT 1250	ATTANTANCO ATTANTANCO ATLAALARCO 1130 CITTAGTACC CTAGGATCAT CTAGGATCAT CTAGGATCAT CTAGGATCAT CTAGGATCAT	GATTAGGGCC GATTAGGGCC 1140 CRACTCTCCC ATCATCTCCC ATCATCTCCC ATCATCTCC ATCATCTCCC ATCATCTCCC ATCA	ITTAATTACAA ITTAATTACAA III50 ITTAATCAAATTACAA ITTAATCAAATTACAA ITTAATCAAATTACAAATTA ITTAATCAAATTAA ITTAATCAAATTAA ITTAATCAAATTAA IIIIIIIIII	TGRA-ATGGA tgaA, AtGGA 1160 586GTCCTTA CATTA CATTA CaTTA 1290	AAAACT 1170 TAGGTA TAGGTG TAGGTG TAGGTg 1300
Atnik172b Aanik172b-1 Aanik172b-2 Consensus Atnik172b-1 Aanik172b-1 Aanik172b-2 Consensus	1041 :: ATTTG AGTTG AGTTG AGTTG AGTTG AGTTG AGTTG AGTGG AGCTA ATGCTA	LGTTTACATS 1050 CCTTTGATCT CCTTTGATCT CCTTTGATCT CCTTTGATCT CCTTTGATCT 1180 TGATCAAGAA TGATCAAGAA TGATCAAGAA	TATCATATAT 1060 TGACTTGAGT TGGCTTGTGT TGGCTTGTGT TGgCTTGLGT 1190 CARCAAGATC CARCAAGATC CARCAAGATC	GTCTCLETLL 1070 IGTTGATGAAGAAC IATTGAGGAAC IATTGAGGAAC I200 SGTGAGCACAG SGTGAACACAGA SGTGAACACAG GGTGAACACAG	atatatata 1080 AGATGTATAA AGATGTATAA AGATGTATAA AGATGTATAA 1210 ATCGGCCAGG ATCGGCCGGC ATCGGCCGG ATCGGCCGG ATCGGGCCG	ACATTGGGT acattgggt 1090 HGTTATGTA HG-ATGTC HG-ATGTC HG-ATGTC 1220 HCGGTCACT GGTCACT GGTCACT	GTINTATATA gulatatata 1100 GTATGIAATATA ATGIAATATA ATGIAATATA ATGIAALATA 1230 TITTAGAAAG TITTAGAAAG TITTAGAAAG TITTAGAAAG	TCTTCTTAR TCTTCTTAR 1110 TATTTTTT TATCTTARC TATCTTARC TATCTTARC TATCTTARC 1240 GAGGATGTTA AAAGATCGA AAAGATCGA AAAGATCGA AAAGATCGA	TCTAGGGTCA TCTAGGGTCA 1120 TRGAATCATT TGTATTTTT TGTATTTTT TGTATTTTT 1250 TATTGTATATTG TGTTATATTG TGTTATATTG TGTTATATTG TGTTATATTG	ATTARTACC ATTARTACC ATTARTACC ATTARTACC 1130 CTTTAGTCC CTACCATCAT CTACCATCAT CTACCATCAT CTACCATCATCAT CTACCATCATCATCATCATCATCATCATCATCATCATCAT	GATTAGGGCC GATTAGGGCC GATTAGGGCC CARCTCTCCF ATGATTTTC1 atgaTLTLC1 1270 CAGGTCTANA CAGGTCTANA CAGGTCTANA	ITARITACAR ITARITACAR IIISO IITARITCARARI ITARITCARARI ITARITCA IITARITCA IITARITCA IITARITCA IITARITCA IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARI IITARITACAR IITARITCA IITARITTA	1689-81669 1160 5966510000 5966510000 6966510000 1160 5966510000 1160 1160 1290 1967106100 96511061000 96511061000 96511061000 96511061000 96511061000	AAAACT 1170 TAGGTA TAGGTA TAGGTA TAGGTG TAGGTG 1300
Atnik172b Aanik172b-1 Ranik172b-2 Consensus Atnik172b Aanik172b-1 Aanik172b-1 Ranik172b-2 Consensus	1041 :: AGTITG AGTITG AGTITG AGTITG AGTITG AGTITG 1171 :: ATGCTR ATGCTR ATGCTR ATGCTR ATGCTR 1301 ::	LGTTTACATS 1050 LCTTTGATCT CCTTTGATCT CCTTTGATCT CCTTTGATCT CCTTTGATCATCATCT 1180 TGATCAAGAA TGATCAAGAA TGATCAAGAA TGATCAAGAA TGATCAAGAA 1310	TATCATATAT TGACTTGAGT TGACTTGAGT TGGCTTGTGTG TGGCTTGTGTG TGGCTTGTGT TGGCTTGLGT 1190 CAACAAGAATC CAACAAGAATC CAACAAGAATC CAACAAGAATC CAACAAGAATC	GTCTCLETLL 1070 GTTGATGABC ATTGAGGAAC TTGAGGAAC 1200 2016ACACAC 2016ACACACA 2016AACACACA 2016AACACACA 2016AACACACA 2016AACACACA 2016AACACACA 2016AACACACA 2016AACACACACACACACACACACACACACACACACACACA	atatatata 1080 AGATGTATAA AGATGTATAA AGATGTATAA AGATGTATAA 1210 ATCGGCCAGG ATCGGCCAGG ATCGGCCGG ATCGGCCG ATCGGCCG ATCGGCCG 1340	ACAT TGGGT ACAT TGGGT 1090 116TATGTA 116-ATGTC 116-ATGTC 116-ATGTC 1220 11CGGTCACT GGTCACT GGTCACT GGTCACT 1350	GTINTATATA gularatara 1100 GTATGTAATATA ATGTAATATA ATGTAATATA ATGTAATATA 1230 TITTAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAA TITTAAAAAAAA	TCTTCTTAR TCTTCTTAR 1110 TATCTTRAC TATCTTRAC TATCTTRAC TATCTTRAC 1240 GAGATGTTR RANGATCGR RANGATCGR ANAGATCGR 1370	TCTAGGGTCA TCTAGGGTCA 1120 TBGARATCATT TBGARATCATT TGTATTTTT TGTATTTTT TgLALTLTT 1250 TATTGTTATATTG TGTTATATTG TGTTATATTG TGTTATATTG 1380	ATTARTACCO ATTARTACCO ATTARTACCO ATTARTACCO 1130 CITIAGICIC CIACOATCA CIACOA	6011106660 601106660 1140 CARCTCTCCC ATGATTTCT ATGATTTCT ATGATTTCT 1270 1270 1270 CAGGTCTAAT CAGGTCTAAT CAGGTCTAAT	1178117867 1178178678 1150 117817688 117867070	1689-81668 1160 6966TCCTTA CATTA CATTA 1290 186TTCGTCC -06TTCGTCC -06TTCGTCC 1420	RARACT 1170
Atnik172b Aanik172b-1 Ranik172b-2 Consensus Atnik172b-1 Aanik172b-2 Consensus Atnik172b-2 Ranik172b-1 Aanik172b-1 Aanik172b-1 Aanik172b-2 Consensus	1041 :: ATTTIG AGTTIG AGTTIG AGTTIG AGTTIG ATGCTA A	LGTTTACATS 1050 LCTTTGATCT CCTTTGATCT CCTTTGATCT CCTTTGATCT 1180 TGATCAAGAA TGATCAAGAA TGATCAAGAA TGATCAAGAA 1310 TTTTATAGTT TTTTATAGTT TTTTATAGTT TTTTATAGTT	TATCATATAT TGGCTTGAGT TGGCTTGTGTG TGGCTTGTGTG TGGCTTGTGTG TGGCTTGLG1 1190 CAACAAGATG CAACAAGATG CAACAAGATG CAACAAGATG TCAATTTTAG TCAATTTTAG TCAATTTTAG	GTCTCLCTLL 1070 IGTTGATGARGAAC GTTGAGGAAC GTTGAGGAAC GTTGAGGAAC GTTGAGGAAC CTTGAGGAACACAG CTGAACACAGA 1330 IGACAGTCTTG GACAGTCTTG GACAGTCTTG GACAGTCTTG		ACAT TGGGT 1090 IGTTATGTA IGTTAGTA IGTTAGTA IGTTAGTA IGTTAGTA IGTTAGTA IGTTAGTA IGTTAGTA IGTTAGTA	GTI HIAIAHA gula Ata Ata Ata 1100 GIAIGIAATAA AIGIAATAA AIGIAATAA AIGIAATAA 1230 TITIAGAAAA TITIAGAAAA TITIAGAAAA TITIAGAAAA IJGO GIGIGICCACC GIGIGGCCACC GIGIGGCCACC		TCTAGGGTCA TCTAGGGTCA 1120 THGGAATCATT TGTAATCATT TGTAATTTTT TGTAATTTTT TGTAATTTTT TGTAATTG TGTTATATTG TGTTATATTG TGTTATATCG 1380 TGGGTTATTA TGGGTTATTA TGGGTTATTA	ATTAGTACCG ATTAGTACCG ATTAGTACCG ATTAGTACCG 1130 CTTAGTACCC CTAGGATCAT CTAGGATCAT CTAGGATCAT CTAGGATCAT TIGTTATTAGT TIGTTATTAGT TIGTTATTAGT TIGTTATTAGT 1390 CTTGGTCCCG CTTGGTCCCG CTTGGTCCCG CTTGGTCCCG	CARCTCTCC GATTAGGGCC GATTAGGGCC 1140 CRACTCTCC ATCATTTCT ATCATTTCT ATCATTTCT 1270 CAGGTCTAN CAGGTCTAN CAGGTCTAN CAGGTCTAN CAGGTCTAN AA AA AA AA		1689-91669 1160 5966TCCTTA 	AAAACT 1170
AtniR172b AaniR172b-1 RaniR172b-2 Consensus AtniR172b-1 BaniR172b-2 Consensus AtniR172b-1 RaniR172b-1 RaniR172b-1 Consensus	1041 :: ATTIGA AGTITGA AGTITGA AGTITGA AGTITGA AGTITGA AGTITGA AGGITA ATGCTA ATGCTA ATGCTA ATGCTA ATGCTA ATGCTA AGGCCA CAGACC CAGACC CAGACC CAGACC CAGACC CAGACC	LGTTTACATS 1050 LCTTTGATCT LCTTTGATCT CCTTTGATCT LIBO TGATCAAGAA TGATCAAGAA TGATCAAGAA TGATCAAGAA TGATCAAGAA 1310 TTTAAGATT TTTAAGATT TTTTATAGTT TTTTATAGTT TTTTATAGTT 1111 ATAGTT 1111 ATAGTT 111	TATCATATAT 1060 TGACTTGAG TGGCTTGTGT TGGCTTGTGT 1190 CAACAAGAAT CAACAAGAAT CAACAAGAAT CAACTAAGAT TCAATTTTAC TCAATTTTAC TCAATTTTAC TCAATTTTAC 1450	1070 1071 1070 1071 1076 1076 1077 1078 1079 1070 1071 1070 1070 1100 1200 1200 1200 1200 1200 1200 1200 1200 1300 1330 16000000000000000000000000000000000000	atatatata 1080 AGATGTATAA ATCGGCCOG ATCGGCOGCOG ATCGGCOGCOG	ACAT TGGGT 1090 ITGTATGTA ITG-ATGT ITG-ATGT ITG-ATGT ITG-ATGT ITG-ATGT ITG-ATGT ITG-ATGT ITG-ATGT ITG-ATGT ITGGTCACT GGTCACT GGTCACT 1350 TGTTABTA IGTTABTA IGTTABTA IGTTABTA 1480	GTINTANAN gularatara 1100 GTATGTAATATA ATGTAATATA ATGTAATATA ATGTAATATA 1230 TTTTAAAAAA 1230 TTTTAAAAAAA 1230 TTTTAAAAAAA TTTTAAAAAAA TTTTAAAAAAA TTTTAAAAAA	TCTTCTTAA TCTTCTTAA 1110 TATCTTAAC TATCTTAAC TATCTTAAC TATCTTAAC TATCTTAAC 1240 GAGATGTTA AAAGATCTAAC 1370 TICTATTC TTCTATTC TTCTATTC TTCTATTC 1500	TCTAGGGTCA TCTAGGGTCA TCTAGGGTCA 1120 TRGARTCATT TGTATTTTT TGTATTTTT TGTATTTTT TGTATTTTT TGTATTTTT TGTATTTTT 1250 TGTATATTG TGTATATTG TGTATATTG TGTATATTG TGTATATTG TGTATATTG TGTGTTATTA TGGGTTATTA TGGGTTATTA TGGGTTATTA TGGGTTATTA TGGGTTATTA	ATTABTACCG ATTABTACCG ATTABTACCG ATTABTACCG 1130 CTTTAGTCCC CTACCACATA CACATA	6011106660 601106660 601106600 1140 CARCTCTCCF ATGATTTCT ATGATTTCT 1270 CAGGTGTATAR CAGGTGTARA CAGGTCTARA CAGGTCTARA CAGGTCTARA CAGGTCTARA 1400 AAATTTCTT AA AAATTTCTT	1178117867 1150 1150 1150 117861CTC 1786TCTC 1786TCTC 1280 1280 1890 1890 1990	1689-81668 1160 5066TCCTTA 5066TCCTTA CATTA CATTA 1290 1290 1290 1290 1290 1420 	AAAAACT 1170 1146616 146616 146616 146617 1300

Figure S3. Sequence alignment of *A. arenosa MIR172b* locus with the corresponding *A. thaliana MIR172b*. Multiple sequence alignment performed using MultAlin (http://prodes.toulouse.inra.fr/multalin/).

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
AtniR172d RaniR172d-1 RaniR172d-2 Consensus	ATCGAT ATTGAT ATTGAT ATTGAT	iccacaaaac iccacaaaac iccacaaaac iccacaaaac	TTAATGCTT TTAATGCTT TTAATGCTT TTAATGCTT	GTGGGCTACGC GTGGGCTACGC GTGGGCTACGC GTGGGCTACGC	ARCGCRTCT ARCGCRTCT ARCGCRTCT ARCGCRTCT	TCTCTGCTCT TCTCTGCTCT TCTCTGCTCT TCTCTGCTCT	CTTCGTTTT CTTTGTTTT- CTTTGNTTT- CTTLGLTTT,	TAACACTCTT AACACTCTT AACACTCTT AACACTCTT	GCTTGCTCCA GCTTGCTCCA GCTTGCTCCA GCTTGCTCCA	TTRATTTACT TTRATTTACT TTRATTTACT TTRATTTACT	CTATCTTCAAT CTCTTCAAT CTCTTCAAT CTCTTCAAT	TCCTTTC-T TCCTTTCCNT TCCTTTCCTT TCCTTTCe, T		CCCTCAGA CCCTCAGA CCCTCAGA CCCTCAGA
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
AtniR172d RaniR172d-1 RaniR172d-2 Consensus	TTTGCC TTTGCC TTTGCC TTTGCC	CTTTTCA-TT CTTTTCA-TT CTTTTCAATT CTTTTCAATT	AATTATGGC AATTATGGC AATTATGGC AATTATGGC	Cacagtgagtg Cacagtgagg Cacagtgagg Cacagtgagg Cacagtgagg	TTAATGAGO TTAATGAGO TTAATGAGO TTAATGAGO TTAATGAGO	CTTTGGTATA CTTTGGTATA CTTTGGTATA CTTTGGTATA CTTTGGTATA	TTTGGTATCT TTTGGTGTCT TTTGGTGTCT TTTGGTgTCT	TCGATTACGA TCGATTACGA TCGATTACGA TCGATTACGA	TGTGCAACTG TGTGTAACTG TGTGTAACTG TGTGLAACTG	TTTCCCTAAT TTTCCCTAAT TTTCCCTAAT TTTCCCTAAT		TCTCTCTCTCTC CTCTCTATAGO CTCTCTATAGO CTCTCTATAGO	TCTCTAATA 8 8	ATTCAAGA GTCAAGA GTCAAGA GTCAAGA SgTCAAGA
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
AtniR172d AaniR172d-1 AaniR172d-2 Consensus	ARATCI ARATCI ARATCI ARATCI	ICAACCGTTG ICAACCGTTG ICAACCGTTG ICAACCGTTG	ATCTCTTTC ATCTCTTTC ATCTCTTTC ATCTCTTTC		TTTAAACAO TTTAAACAO TTTAAACAO TTTAAACAO TTTAAACAO	TTTACCCTT TTTACCCTT TTTACCCTT TTTACCCTT	ICCTACTITO ICCTACTITO ICCTACTITO ICCTACTITO	TTCACCCT TTCACCACCCT TTCACCACCCCT TTCACCACCCT	ГАЛАТС Галатсатат Талатс Галатс		CETTERGATET TETTERGATET TETTERGATET LETTERGATET	CTTTACTCTT CTTTACTCAG CTTTACTCAG CTTTACTCAG	TACTI TARARTCTI TARARTCT TARARTCT TAcactCTI	ATTAGGGT ICTAGGGT ICTAGGGT ICTAGGGT
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
AtniR172d RaniR172d-1 RaniR172d-2 Consensus	TAGCAT TAGCTO TAGCTO TAGCTO	GTTGATGAC GATGATGAC GATGATGAG GaTGATGAG	TTCAGATTC TTCAGATTT TTCAGATTT TTCAGATTL	TGAAGTTAGTO TGAAGTTAGTO TGAAGTTAGTO TGAAGTTAGTO	GCAGTCATT GCAGTCATT GCAGTCATT GCAGTCATT	GTTTGCTAT GTTTGCTAT GTTTGCTAT GTTTGCTAT	FGCAACATCT FGCAACATCT FGCAACATCT FGCAACATCT	TCAAGATTCA TCAAGATTCA TCAAGATTCA TCAAGATTCA	GAAATCAGAT GAAATCAGAT GAAATCAGAT GAAATCAGAT	TCTCTTATGG TCTTTTATGG TCTTTTATGG TCTCTTTATGG	GTTTTCTTTTG GTTTTCTTTTG GTTTTCTTTTG GTTTTCTTTTG	AGCCTTTATT AGCCTATATT AGCCTATATT AGCCTATATT	TTTTGGTT AFTTGGTT ATTTGGTT aTTTGGTT	TGAGAATC Tgagaatc Tgagaatc Tgagaatc
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
AtniR172d AaniR172d-1 AaniR172d-2 Consensus	TTGATO TTGATO TTGATO TTGATO	ATGCTGCAG ATGCTGCAG ATGCTGCAG ATGCTGCAG	CGGCAATTA CGGCAATTG CGGCAATTG CGGCAATTg	AATGGCTTACT AATGGCTTATT AATGGCTTATT AATGGCTTACT	TATCTAGG TATCTAGG TATCTAGG TATCTAGG TATCTAGG	TCTTTTTT TTTTATTT TTTTATTT TTTTTTTG TCTTCTTT.	CATTITCA TCA TCA TCA TCA	CATGTGGTTA -GTGGTTTTA -GTGGTTTTA gTGgttTTA	ATCAGARATC Atcagaratc Atcagaratc Atcagaratc	CAGATECTER CAGATECTEG CAGATECTEG CAGATECTEg	TATGTAGAATO TATGTTGATTO TATGTTGATTO TATGTCGACTO	XTCCGATATG XTCCGATATG XTCCGATATG XTCCGATATG	ATRACTTG AACGCTTAT AACGCTTA AACGCTTA AacgCTTa	GGTGAAA GGTTAAA GGTTAAA GGTLAAA
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
AtniR172d AaniR172d-1 AaniR172d-2 Consensus		ITTCACAGGT ITGCACAGGT ITGCACAGGT ITgCACAGGT	TATECATATE TATTCATATE TATTCATATE TATTCATATE TATECATATE	ATTATATATA ATGATTAT ATGATTAT ATGATTAT ATgATTAT	ATARGCACA CTARGCATA CTARGCATA CTARGCALA	CATATATAT CATATATAT CATATATATA CATATATAT	TAATAGATI ICAATAGA ICAATAGA CAATAGA	TGTGTGTGTGTA GTGTGTGTGTA GTGTGTGTGTA GTGTGTGT	TARACATATT TGAACARATT TGAACARATT TGAACARATT TgAACARATT	TGT-GGACAA TTTTGGAGAA TTTTGGAGAA TTTTGGAGAA TLTLGGAgAA	AACGATGATGA AATGATGATGA AATGATGATGA AATGATGATGA AALGATGATGA	IATGATTTGAA IATGATATATT IATGATATATAT IATGATATATA IATGATaTatt	AARCGARTA RARCGARTA RARCGARTA RARCGARTA	ATGTATAT ATGTATAT ATGTATAT ATGTATAT ATGTATAT
	781	79 0	800	810	820	830	840	850	860	870	880	890	900	910
AtniR172d RaniR172d-1 RaniR172d-2 Consensus	ACTACI ATACAC ATACAC Atacas	ICTCAATT GTAAATATC GTAAATATC gTAAATATC gTAAATATC	GATTARG TAGATGARG TAGATGARG LaGATgARG	TGAACCCTTCC TGAGCCCTTAT TGAGCCCTTAC TGAgCCCTTAC	TTATAGATO TTATAGATO TTATAGATO TTATAGATO	ITTTTT ITTTTC ITTTTC ITTTTC ITTTTC	ГТАЛАЛАЛА ГТТААС ГТТААС ГТСААС	TTTTTGCTGCI TTTTTGCTGCI TTTTTGCTGCI TTTTTGCTGCI	ACGATGCATA ACGATGTATA ACGATGTATA ACGATGLATA	GATCCTGAAAI GATCCTGAAAI GATCCTGAAAI GATCCTGAAAI	ATTTCCARARF ATTTCCARARF ATTTCCARARF ATTTCCARARF	IGGTTTTAGGG IGGTTTTAGGG IGGTTTTAGGG IGGTTTTAGGG		CTRACGAC CTRACGAC CTRACGAC CTRACGAC
	91 1	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
AtniR172d RaniR172d-1 RaniR172d-2 Consensus	aragte Aragte Aragte Aragte Aragte	itataagacc itataagacc itataagacc itataagacc	TGTTTCTGT TGTCTCTAA TGTCTCTAA TGTCTCTAA	AGACTCRAGG Agactcraag Agactcraag Agactcraag Agactcraag	-GATTCATA CGATTCATA CGATTCATA CGATTCATA	IAA-TGCATA IAACTGCATAI IAACTGCATAI IAACTGCATAI	AATITGATT AATITGATT AATITGATT AATITGATT AATITGATT	ATATAATAATI ATATAATAATI ATATAATAATI ATATAATAATI ATATAATAATI	GACTGARAGG GARTTARAGG GARTTARAGG GARTTARAGG	GTTTGGAGGAI GTTTGGAGGAI GTTTGGAGGAI GTTTGGAGGAI	ATTGGACATA1 AGTTGACATA1 AGTTGACATA1 Agttgacata1 Agttgacata1	TGTATGARGGA TGTATGACGGA TGTATGACGGA TGTATGA <mark>G</mark> GGA	G-CATGTAT GCCATGTAT GCCATGTAT GCCATGTAT GCCATGTAT	IAT-GTC IATATGTC IATATGTC IATATGTC IATatGTC
AtmiR172d AaniR172d-1 AaniR172d-2 Consensus	10 104 4 TGTTG1 TGTTG1 TGTTG1 TGTTG1													

Figure S4. Sequence alignment of *A. arenosa MIR172d* locus with the corresponding *A. thaliana MIR172d*. Multiple sequence alignment performed using MultAlin (<u>http://prodes.toulouse.inra.fr/multalin/</u>).

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
AtniR172e AaniR172e-1 AaniR172e-2 Consensus	TGTCATA	ITTGAGAACT	CTTTAGCCTT TAGCCTT TAGCCTT TAGCCTT	TEGETTETE TEGETTETE TEGETTETE TEGETTETE	TTCCTGACAC TTCCTGACAC TTCCTGACAC TTCCTGACAC	TTGTATAGTG TTGTATAGTG TTGTATAGTG TTGTATAGTG	SAAGTGGGCT SAAGTGGGCT SAAGTGGGCT SAAGTGGGCT	TGTGTTATAT TGTGTTATAT TGTGTTATAT TGTGTTATAT	AGATGGGATC TGATGCGATC TGATGCGATC LGATGCGATC		ATTTAAAAAGTC Atttaaaagtc Atttaaaagtc Atttaaaagtc Atttaaaagtc	AATTAGAGA TATTAGAGAG TTTTAGAGAG LATTAGAGA8	TCTTGATGO ATCTTGATGO ATCTTGATGO ATCTTGATGO TCTTGATGO	TACTTC
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
AtniR172e AaniR172e-1 AaniR172e-2 Consensus	TGTCCCT TGTCCCT TGTCCCT TGTCCCT	TTCCAAGTG TTCCAAGTG TTCCAAGTG TTCCAAGTG	ATTTTACETC ATTTTACATC ATTTTACATC ATTTTACATC ATTTTACATC	GACCAACTA GACCAACTA GACCAACTA GACCAACTA GACCAACTA	GCTITTTTCA GCTITCTITA GCTITCTITA GCTITCTITA GCTITGTTLA	TATGAGTGTA Totgagtgta Totgagtgta Totgagtgta Totgagtgta	ITATATICAT ITATATICAT ITATATICAT ITATATICAT ITATATICAT	IGTACCTATCT IGTACCTATCT IGTACCTATCT IGTACCTATCT IGTACCTATCT	CTCTCRATTG CTCTCRATTA CTCTCRATTA CTCTCRATTA	CTTCTCACCI CTTCTCACCI CTTCTCACCI CTTCTCACCI	AAAATCATCTT AAAATCATCTT AAAATCATCTT AAAATCATCTT AAAATCATCTT	GCTGATTCAT GCTGATTCAT GCTGATTCAT GCTGATTCAT	TTECTETCTE TTECTETTTE TTECTETTTE TTECTETTE	RATCET RATCET RATCET RATCET
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
AtmiR172e RamiR172e-1 RamiR172c-2 Consensus	CITECIT CITECIT CITECIT CITECIT CITECIT		CTTTTTCATT CTTTTTCATT CTTTTTCATT CTTTTTCATT CTTTTTCATT	TGTTGATTT TGTTGATTA TGTTGATTA TGTTGATTA	RAACCATGGG RAACCATGGG RAACCATGGG RAACCATGGG	AGTTCCCAAC AGTTCCCAAC AGTTCCCAAC AGTTCCCAAC	CTTTAGACCT CTTTAGAGCT CTTTAGAGCT CTTTAGA _S CT	ICGAAACCGAT ICGAAACCGGT ICGAAACCGGT ICGAAACCGgT	AAGGATCTTT AAGGATCTTT AAGGATCTTT AAGGATCTTT AAGGATCTTT	CTCTGCGGT CTCCGCGGT CTCCGCGGT CTCCGCGGT	TGAAATAGCTA Tgaaatagctg Tgaaatagctg Tgaaatagctg Tgaaatagctg	GGTTCTCGAT GGTTCTCGAT GGTTCTCGAT GGTTCTCGAT	GAATAGG GAACAGGGAA GAACAGGGAA GAACAGGgoo	C IRAGGTC IRAGGTC NonestC
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
AtniR172e AaniR172e-1 AaniR172e-2 Consensus	TRECETT TRECETT TRECETT TRECETT	TGGTGG-AT TGGTGG-AT TGGTGGGAT TGGTGG.AT	GTTATCA-GC GTTACCA-GC GTTACCACGC GTTACCACGC GTTACCA.GC	CAGTA-GTC CAGTA-GTC CAGTATGTC CAGTA.GTC	GCAGATGCA GCAGATGCA CGCAGATGCA GCAGATGCA	GCACCATTAA GCACCATTAA GCACCATTAA GCACCATTAA GCACCATTAA	IGATTCACAA IGATTCACAA IGATTCACAA IGATTCACAA	IGAGATGTGGT IGAGATGTGGT IGAGATGTGGT IGAGATGTGGT	TCCCTTTGCT TCCCTTTGTT TCCCTTTGTT TCCCTTTGLT	TCGCCTCT TCGCCTCT TCGCCTCT TCGCCTCT	CGATCCG <mark>C</mark> AGA CGATCCG <mark>R</mark> AGA CGATCCG <mark>R</mark> AGA CGATCCG <mark>B</mark> AGA	AAAGGGTTCC AAAGGGTTCC AAAGGGTTCC AAAGGGTTCC AAAGGGTTCC	TTATCGAGTG TT-TCGAGTG TT-TCGAGTG TT-TCGAGTG	GGAATC GGAATC GGAATC GGAATC
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
AtniR172e AaniR172e-1 AaniR172e-2 Consensus	TTGATGA TTGATGA TTGATGA TTGATGA	TGCTGCATO TGCTGCATO TGCTGCATO TGCTGCATO	AGCARATACA AGCARATACA AGCARATACA AGCARATACA	ITGGCTACTC ITGGCTACTC ITGGCTACTC ITGGCTACTC	TTGTCRCTTC TATCRCTTT TATCRCTTT TATCRCTTL	TTTTTETCA TTTTTTETCA TTTTTTECA TTTTTTECA TTTTTTECA	ATTETETAGT ATTETETAGT ATTETETAGT ATTETETAGT ATTETETAGT	rgaagagagta rgaagaaagta rgaagaaagta rgaagaaagta	ATGATGTCTT GAGATGTCTTI GAGATGTCTTI gaGATGTCTTI	SGAGATETT SGAGATETT SGAGATETT SGAGATETT	ICAC ICAAAGGACTC ICAAAGGACTC ICAaaggactC	AARAACACAA AARAAACAGAA AARAAACAGAA AARAAACAGAA AARAAACAgAA	GGTARAGTCT IGGTARAGTCT IGGTARAGTC1 IGGTARAGTC1	
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
AtniR172c RaniR172c-1 RaniR172c-2 Consensus	TIGITI TIGITI TIGITI TIGITI TIGITI	CTGTCTCTT CTGTCTCAT CTGTCTCAT CTGTCTCAT	GGCAATATCT GGCAATTTCT GGCAATTTCT GGCAATTTCT	TGATCATGCI TGATCATGCI TGATCATGCI TGATCATGCI	ACATECTETE Acatettete Acatettete Acatettete	AAATATCTGT Aratatcttt Aratatcttt Aratatcttt	F-AAGTITAT IGAAGTICAT IGAAGTICAT IgAAGTICAT	IGGTGTTTCTA IGGTGTTTCTA IGGTGTTTCTA IGGTGTTTCTA	TTTTGCTTTT TTTTGCATTT TTTTGCATTT TTTTGCATTT	STTATTGGCI STTATTGGCI STTATTGGCI STTATTGGCI STTATTGGCI	ARARACATTCA ARARCCATTCA ARARCCATTCA ARARCCATTCA	CATGTGCAAG Catgtgtaag Catgtgtaag Catgtgtaag	IGATCC <mark>CA</mark> CAT IGATCCCACAT IGATCC-NCAT IGATCC-NCAT	ATGCTT ATGCTT ATGCTT ATGCTT
	781	79 0	800	810	820	830	840	850	860	870	880	890	900	910
AtniR172c AaniR172c-1 AaniR172c-2 Consensus	TRARACC TRARAC TRARAC TRARAC	CCAARCARG CCAARCARG CCAA-CARG CCAA-CARG	ATTGTARCAA ATTGTARCAA ATTGTARCAA ATTGTARCAA	CTGTATTTA CTGTATTTA CTGTATTTA CTGTATTTA	ARATARATAG ARATARATTG ARATARATTG ARATARATCG	ACTATGATAA Attatgacaa Attatgacaa Attatgacaa Attatgacaa	IGTTTCTARO IGTTTCTARO IGTTTCTARO IGTTTCTARO IGTTTCTARO	ATGAATGTGA Atgaatgtga Atgaatgtga Atgaatgtga	AATAG ATAGAGTGAG ATAGAGTGAG AtagagtgAG	IGAGAACTCI Igagaactci Igagaactci Igagaactci	IGAAGTGAGAA IGAAGTGAGAA IGAAGTGAGAA IGAAGTGAGAA	GTCTCTTGTG GTCTCTTGTG GTCTCTTGTG GTCTCTTGTG	ACTATEGTTT GTTACEGETT GTCACEGETT GCCACEGETT	TGTGGGA TGTGAGA TGTGAGA TGTGAGA
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
AtniR172c AaniR172c-1 AaniR172c-2 Consensus	ACTOROR ACTOROR ACTOROR ACTOROR	ITGGTCACAT ITGGTCACAT ITGGTCACAT ITGGTCACAT	GTGAGAATGG GTGAAAATGG GTGAANATGG GTGAAAATGG	TCCATARCTI TCCATARATI TCCATARATI TCCATARATI	GTTTGTTGGT GTTTGTTGGT GTTTGTTGGT GTTTGTTG	CA-ATTCCTT CA-ATTCTTT CAGATTCTTT CAGATTCLTT	IGCCTTTGGT IGCCTTTGGT IGCCTTTGGT IGCCTTTGGT	ICCCA-AGGTT ICCCA-AGGTT ICCCAGAGGTT ICCCA AGGTT	TATTGTGTAT TATTGCGTAT TATTGCGTAT TATTGCGTAT	TATATAGT TATATAGT TATATAGT TATATAGT TATATAGT	TTCRTTGRCC- TTCTTTGRCCC TTCTCTGRCCC TTCLLTGRCCC	GACCAAGAAA GATARAGGAT GATARAGGAT GALARAG _S AL	AA-CTARACA AATARARACA AATARARACA AALAAARACA	
	1041 1	.050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
AtniR172c RaniR172e-1 RaniR172e-2 Consensus	CCACATG CCACATG CCACATG CCACATG	IGATCA IGATCATATO IGATCATATO IGATCATATO IGATCALALO	AGTINCICGO AATI-CICGO a.tt.ctego	GACACATTT GACACATTT gacacattt	TCCTTGTTA TCC-TTGTTA LCC.LLgLLa	GRAAATATCT GAAAATATCT gaaaatatct	TTGTTRGGG TTGTTRGGG Ltgttaggg	GAGAAATTAA GAGAAATTAA ggagaaattaa	TGTATAATTG TGTATAATTG LgLaLaatLg	CRAATAATA CAAATAATA Caaataata	ATATTATTGA AATATTATTGA Batattattga	AAGTITGTIT AAGTITGTIT aagtttgttt	GAGARARATA GAGARARATA gagaaaaat?	ITATTAA ITATTAA Itattaa
	1171 1	180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
RtniR172e AaniR172e-1 AaniR172e-2 Consensus	ATTITIC	AAAGTTTAT AAAGTTTAT aaagtttat	ATAAATTGGT ATAAATTGGT ataaattggt	GGGTCTCTT GGGTCTCTT 888LcLcLL;	GTGCARTGGR GTGCARTGGR gtgcaatgga	ATATTATGAA ATATTATGAA alallalgaa	AGTAAATTO AGTAAATTO aagtaaatto	CARATTTTACT CARATTTTACT CARATTTTACT CaaaLLLLacL	TGCTATTIGT TGCTATTIGT LgcLaLLLgL	ITTACATTT ITTACATTT LLacaLLL;	GAATTGTTAGT GAATTGTTAGT gaallgtlagt	GACTITICII GACTITICII gactiticii	TGGCRARTCG TGGCRARTCG Lggcaaatcş	TACACT TACACT stacact
	1301 1	310	1320	1330	1340	1350	1360	1370	1380 138	5				
AtniR172e RamiR172e-1 RamiR172e-2 Consensus	AATGGTC AATGGTC aatggtc	CCAACTOCT CCAACTOCT CCAACTOCT	GATAATATAT GATAATATAT gataatatat	TTTAATCCG TTTAATCCG LtLaatccg	CATTTGTAAG CATTTGTAAG catttgtaag	CTTTTTAACA CTTTTTAACA CLLLLLAACA	AGTAAACAA AGTAAACAA Magtaaacaa	ICGATGGCAGA ICGATGGCAGA ICGATGGCAGA	GRARATCRCT GRAR gada	' 1				

Figure S5. Sequence alignment of *A. arenosa MIR172e* locus with the corresponding *A. thaliana MIR172e*. Multiple sequence alignment performed using MultAlin (<u>http://prodes.toulouse.inra.fr/multalin/</u>).