

Table S1: Coordinates for 100kb region harboring *MIR172* for microsynteny analysis and coordinates for promoter and precursor for phylogenetic analysis.

Species	miRNA	Chromosome location	100 Kb region coordinates		coordinates for phylogenetic analysis	
			Start position	End position	Start position	End position
<i>Oryza sativa</i>	miR172A	Chr 9	21638003	21738111	21687503	21688111
	miR172B	Chr 1	46903572	47003809	46953072	46953809
	miR172C	Chr 7	12238035	12338145	12287535	12288145
	miR172D	Chr 2	37248091	37348220	37297591	37298220
		Chr 2	37278665	37378794	37328165	37328794
<i>Oryza barthii</i>	miR172A	Chr 2	30933600	31033623	30983100	30983623
	miR172B	Chr 1	36508471	36608708	36557971	36558708
	miR172C	Chr 7	10661579	10761689	10711079	10711689
	miR172D	Chr 2	30933582	31033711	30983082	30983711
<i>Oryza glaberrima</i>	miR172A	Chr 2	28423276	28523296	28472775	28473298
	miR172B	Chr 1	32281490	32381727	32330990	32331727
	miR172C	Chr 7	10582540	10682650	10632040	10632650
	miR172D	Chr 2	28423257	28523386	28472757	28473386
<i>Oryza glumaepatula</i>	miR172A	Chr 9	23357188	23457296	23406688	23407296
	miR172B	Chr 1	46157906	46258139	46207406	46208139
	miR172C	Chr 7	12284350	12384460	12333850	12334460
	miR172D	Chr 2	37235412	37335541	37284912	37285541
<i>Oryza punctata</i>	miR172A	Chr9	26180640	26280686	26230140	26230686
	miR172B	Chr1	45741747	45841791	45791247	45791791
	miR172C	Chr2	38771836	38871861	38821336	38821861
	miR172D	Chr2	38771883	38871953	38821383	38821953
<i>Oryza rufipogon</i>	miR172A	Chr 9	20367006	20467114	20416506	20417114
	miR172B	Chr 1	39528018	39628255	39577518	39578255
	miR172C	Chr 7	11393165	11493275	11442665	11443275
	miR172D	Chr 2	33132612	33232741	33182112	33182741
<i>Oryza brachyantha</i>	miR172A	Chr9	13982760	14082800	14032260	14032800
	miR172B	Chr1	33588435	33688477	33587935	33638477
	miR172C	Chr7	7329288	7429325	7378788	7379325
	miR172D	Chr2	26329138	26429195	26378638	26429195
<i>Sorghum bicolor</i>	miR172A	Chr 9	58724558	58824659	58774058	58774659
	miR172B	Chr 3	74138339	74238508	74187839	74188508
	miR172C	Chr 4	67595991	67696109	67645491	67646109
	miR172D	Chr 2	22151215	22251302	22200715	22201302
	miR172E	Chr 2	14072957	14173071	14122457	14123071

	miR172F	Chr 5	19245951	19346068	19295451	19296068
<i>Zea mays</i>	miR172A	Chr 7	54226707	54326789	54276207	54276789
	miR172B	Chr 5	221671349	221771474	221720849	221721474
	miR172C	Chr 4	174104928	174205050	174154428	174155050
	miR172D	Chr 6	171979786	172079859	172029286	172029859
	miR172E	Chr 3	145751592	145851765	145801092	145801765
<i>Arabidopsis thaliana</i>	miR172A	Chr2	11892914	11993015	11942414	11943015
	miR172B	Chr5	1138207	1238301	1187707	1188301
	miR172C	Chr3	3549776	3649908	3599276	3599908
	miR172D	Chr3	20537904	20638027	20587404	20588027
	miR172E	Chr5	23938472	24038596	23987972	23988596

Table S2: Forward and reverse primer sequence for amplification of *MIR172A, B, C* and *D* from different poaceae members and *Arabidopsis*.

Primer name	Forward	Reverse	Amplicon size	Tm
Os-miR172A	TGGATGGAACGGTAGAGTCG	TGAAACGGAGGGAGTGACAAG	224	59
Os-miR172B	CACAGAAAGAGGGAGGGAGG	AGTAGAGAGTGTGATGCCGC	336	59.5
Os-miR172C	CCTGCACGTAGACAACCATG	GCGGGCCCTATAAATTCTGC	316	59
Os-miR172D (i)	ATCAAAGCAGGCCATGGATC	TCGATCTCCCTCTAGCTCCA	299	59
Os-miR172D(ii)	ATCAAAGCAGGCCATGGATC	GCACAAATTGGCGAGGATG	210	59
Ob-miR172A	ATCAAAGCAGGCCATGGATC	AAACAGTCGGTGCTTGACAG	155	58
Ob-miR172B	CACAGAAAGAGGGAGGGAGG	CCGGCAGTAGAGAGTGTGAT	341	59
Ob-miR172C	AAAGCTAATCCTGCCTGCC	TCGTTGTAGGGTCGGAATC	294	60
Ob-mir172D	AAAGCAGGCCATGGATCGAG	CAAATTGGCGAGGATGAGAGG	204	60
Og-miR172A	AAAGCAGGCCATGGATCGAG	CAAATTGGCGAGGATGAGAGG	204	60
Og-miR172B	CACAGAAAGAGGGAGGGAGG	CCGGCAGTAGAGAGTGTGAT	341	59
Og-miR172C	AAAGCTAATCCTGCCTGCC	TGTAGGGTCGGAATCCAAC	290	60
Og-mir172D	ATCAAAGCAGGCCATGGATC	CAAATTGGCGAGGATGAGAG	207	59
Ou-miR172A	TGGATGGAACGGTAGAGTCG	AACGGAGGGAGTAACAAGG	222	58
Ou-miR172B	CACAGAAAGAGGGAGGGAGG	AGTAGAGAGTGTGATGCCGC	332	60
Ou-miR172C	AAAGCTAATCCTGCCTGCC	TGTAGGGTCGGAATCCAAC	290	59
Ou-mir172D	ATCAAAGCAGGCCATGGATC	CCCTCTAGCTCCATTCTCCA	296	58
Op-miR172A	TATAGTCGGTGTTTGCGGGT	TTATGTATTTGGGGACGG	257	59
Op-miR172B	ACCTGCTAGCCAATGTGTCA	GACCTGGCATTGCATACCTG	224	59
Op-miR172C	AGGAAGGGGAAAGCTAGGAAC	GCAGCCGCGGTTATATATGG	234	58
Op-mir172D	CCATGGCGACGAGTAGTAGT	CCGAATCTCCCTCTAGCTCC	268	59
Or-miR172A	AACCCCTAGCTAGAAGAGGC	CGGAGGGAGTAACAAGGATG	347	58
Or-miR172B	CACAGAAAGAGGGAGGGAGG	CCGGCAGTAGAGAGTGTGAT	341	59
Or-miR172C	CCTGCACGTAGACAACCATG	GTAGGGTCGGAATCCAACA	268	59
Or-mir172D	ATCAAAGCAGGCCATGGATC	TCGATCTCCCTCTAGCTCCA	299	59
Oa-miR172A	GGACTCTCCCTTTTCCCTCC	TGGGCTGTTGAGAGAAGAAG	227	59
Oa-miR172B	AGCTGCTAGGATGAACTCGA	ATCTGAGAATAGACGGATCGAAG	157	58
Oa-miR172C	TCAGTAGAGGAGTGCTTGCC	GATTCCATCCAATCCAGCGAG	216	59
Oa-mir172D	GGCCAGGGGAAGCTATAACT	AGACGAAGCAGCAAACAGTC	244	58
Sb-miR172A	ATTCGGCGTCTCTCACTGTC	ACAACCTTAGCTTCCACATC	284	58
Sb-miR172B	GCACTGCTAGCTGATCTGAG	TATAGCAGCTGGAGACGACG	343	58.5
Sb-miR172C	CGGGTGATGAGTGAGTGTCT	CGTCTTGCCGGATCTCATTG	271	59
Sb-mir172D	GCCGTTACCTCTTTCTCAC	GGATGGCACGATCTTTCACC	331	58
Zm-miR172A	CACCAAGCACCCAAACAAGA	TGCAGTTGATTACCATGGCG	250	58
Zm-miR172B	CCATGTACCTCTCACCCAG	ACTACGAACCCTTCCACAA	274	59
Zm-miR172C	TTTCCGACTTAAGGCATCCG	CCGTAGTGCATGCTCTCAAG	211	59
Zm-mir172D	CTGTTGACACGGACTTGCTC	AGCTCTTCCGGGACAGAAG	259	59

At-miR172A	GGGAGAGAGAGAGAGAGGGA	TGGGTTTGAGTTTGAGTTTGAG	247	58
At-miR172B	TTGTAGCCGTCGATTGTTGA	GATCTCTTGTGCGTGCGTAA	185	58.5
At-miR172C	ACCTCCGATCTGTGAATTCCT	ATGGTGCCGTCTTGAGTCTT	279	59
At-mir172D	GGGTTAGCATGTTGATGACTTCA	TCGGAGGATTCTACATATGAGGA	243	58

Table S3. Forward primer sequence for Rt-qPCR used for generating the expression profile of *MIR172* in different members of poaceae and Arabidopsis.

MIRNA	Forward Primer
Os-miR172	GAATCTTGATGATGCTGC

Supplementary Data 1

Nucleotide sequence of PCR amplified and Sanger sequenced *MIR172 A-D* from different poaceae members

>Os-miR172A

TGGATGGAACGGTAGAGTCGGTGTGTTGCGGGCGTGGCATCATCAAGATTCACATCCATGCATATA
TCACAAGACGCACATATACATCCGATTGGCTGAGAATCTTGATGATGCTGCATCCGCAGACAAG
CGCCTTTTTTCTTTCAAAGGTAAGCTCCTCTGCTATTCAAAGACCATAACATTAGTTGTTTCATCAT
CTTCATCCTTGTCACTCCCTCCGTTTCA

>Os-miR172B

CACAGAAAGAGGGAGGGAGGATCACTCTCGCCGGCGGCGTTGGTACAATTAAGCTGATGCTTAG
TCATTAATTTCCGATGCAGCATCATCAAGATTTCCACACATATATACACATGCGCTTAATTAGCTT
CGATCTCTCTCTCTCTCTCCATGCGTGCAACCATGCATCATGCAGGTGAGGGCCAGGAGAGAAA
TATTAGCTAGCTAGGTTGTTGAGATCAGAACAAAGCTCAAAGATGCATAGACATATGCATGC
ATGCAATGTAATGTGTGAATCTTGATGATGCCACGTCAGAAATCACCGACTGCTAGCTGCGGCAT
CACACTCTCTACT

>Os-miR172C

CCTGCACGTAGACAACCATGCACACATATGCTTCCTGAAACAATACTAATAGAACAATATATAT
ACGGCCGGCTCTTTGCTGGTGACGATCATCAAGATTCACGCACGATGACTACACTTGAAAACCG
ATACGTGTGCCGTGCGGCACACGTGAATCTTGATGACGCTGCACCCGCAACAAGTCGGGCTCAGCT
CGCATCCACCGCGCGCGCCGATGACGAATTGGCGACGGCGGCGGCGCGGCGGCTGTTGGATT
CCCGACCCTACAACGAACGGGCTGTGGCCTGTGGGGGCAGCAGAATTTATAGGGCCCCG

>Os-miR172Di

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CTCATCACATATAGTCAGCCAACCTCGATCTCGTTTAGGGATGAACTCGATGTGAATCTTGATGGT
GCTGCACCTGCAAGCACCGACTGTTTGCTACTAGCTCCATATATGCATCGATCCATGCCTCTCATC
CTCGCCAATTTGTGCCAATTTGTGAGATCGATGCATATATATGGTGCATACACTACCAGAAGAAT
GGATAGTATATATGGAGAATGGAGCTAGAGGGAGATCGA

>Os-miR172Dii

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CTCATCACATATAGTCAGCCAACCTCGATCTCGTTTAGGGATGAACTCGATGTGAATCTTGATGGT
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CTCGCCAATTTGTGC

>Ob-miR172A

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>Ob-miR172B

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>Ob-miR172C

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CCGCAACAAGTCGGCTCAGCTCGCATCCACCGCGCGCGCCGATGACGAATTGGCGACGGCGG
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>Ob-miR172D

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CGCCAATTTG

>Og-miR172A

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CGCCAATTTG

>Og-miR172B

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>Og-miR172C

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>Og-miR172D

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CTCGCCAATTTG

>Ou-miR172A

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>Ou-miR172B

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>Ou-miR172C

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>Ou-miR172D

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GCTGCACCTGCAAGCACCGACTGTTTGCTACTAGCTCCATATATGCATCGATCCATGCCTCTCATC
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>Op-miR172A

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>Op-miR172B

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>Op-miR172C

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>Op-miR172D

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>Or-miR172A

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ACAAGACGCACATATACATCCGATTTGGCTGAGAATCTTGATGATGCTGCATCCGCAGACAAGC
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>Or-miR172B

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>Or-miR172C

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>Or-miR172D

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>Oa-miR172A

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>Oa-miR172B

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CACCAGGCCGGCGGCGCACACGTGAATCTTGGTGATGCCGCACCCGCAACAAGTCGGCCTCGCG
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GGCCAGGGGAAGCTATAACTGTATATAAGTAAAAGCGTACCTGAGTCTCCAATTAAGCCGGCCA
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[illegible]

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GCCGTTACCTCTTTCTACCGATGCCACATATATATAGCACCACCACAGACTCCTAGCCCCGAT
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 GCCATCC

CAGAGAAAGGAAATAATATAGAAATGGTCGTTGTTTCGAATAAAAAATTTGCAAAGCTAGCTTTAG
GCGGATGGGATGACGATCTTTCACCTTAGCTAAACGTGAAGATACAAAATCTCGATTGATGGCG
AAGATGAGCACACAAACGTTCTGATGGCGCTTGTGGCGGATGCAGCATCATCAAGATTCTCATG
CATGCATTCCAAATCAGTGGTTCGGATTGATGGGTTGTGAATCTTGATGATGCCACGC

>Zm-miR172B

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GTACCAGAGCTAGTAGCTGCATGGTCGTTAATTCAATTCATCTCTTATTACTTGGAGGTGATGCAT
GAGCTAGTGAGTGTCTGCTGATGCAGCATCATCAAGATTCTCATCTCATCATATATATATACACA
CACATGCGAGGCACGCATCATTGAAGATGCATATATGCATGATGCATGAGTTGGACGATGTGAA
TCTTGATGGTGCTGCAC

>Zm-miR172C

TTTGTTAATGCATACATTCATATATATATTCCCATGAATGAATGCTTTAAGCATGAGGCAAGCAA
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CAGTGATGCATGCATGCTCTGTGATGTCTCGCAGCAGCTATATGCATATGTGATGAGATGAGAAT
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>Zm-miR172D

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GTATACAGATCATGAGGAAGCAAGAAATTATGCAAAACAGTCGGTGCTTGAGGTGCAGCACCACCA
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>At-miR172A

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>At-miR172B

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>At-miR172C

ACCTCCGATCTGTGAATTCCTACAAAAAGATTGGACTATGAAATTTCCAATCAACACAAACCTGT
TTCTATGTGTAAGCCACTGATTGCAGCTGCAGCATCATCAAGATTCTCATACATACATCAAAAAT
CTAATCATAAATGGGTTTATTTACACGAATACTTGATGATTTGTGAATCTTGATGATGCTCCAACA
GCGAACAGTAGCTGGTTGATGATAGGGATGTATGTAGTGATTTGGTTTTGTCTTGATCTTTCAA
GACTCAAGACGGCACCAT

>At-miR172D

GGGTTAGCATGTTGATGACTTCAGATTCTGAAGTTAGTGGCAGTCATTGTTTGCTATTGCAACATC
TTCAAGATTCAGAAATCAGATTCTCTTATGGGTTTTCTTTTGGCCTTTATTTTTTGGTTTGAGAAT
CTTGATGATGCTGCAGCGGCAATTAAATGGCTTACTTATCTAGGGTCTTTTTTTCCATTTTCATCAT
GTGGTTAATCAGAAATCCAGATCCTCATATGTAGAATCCTCCGA

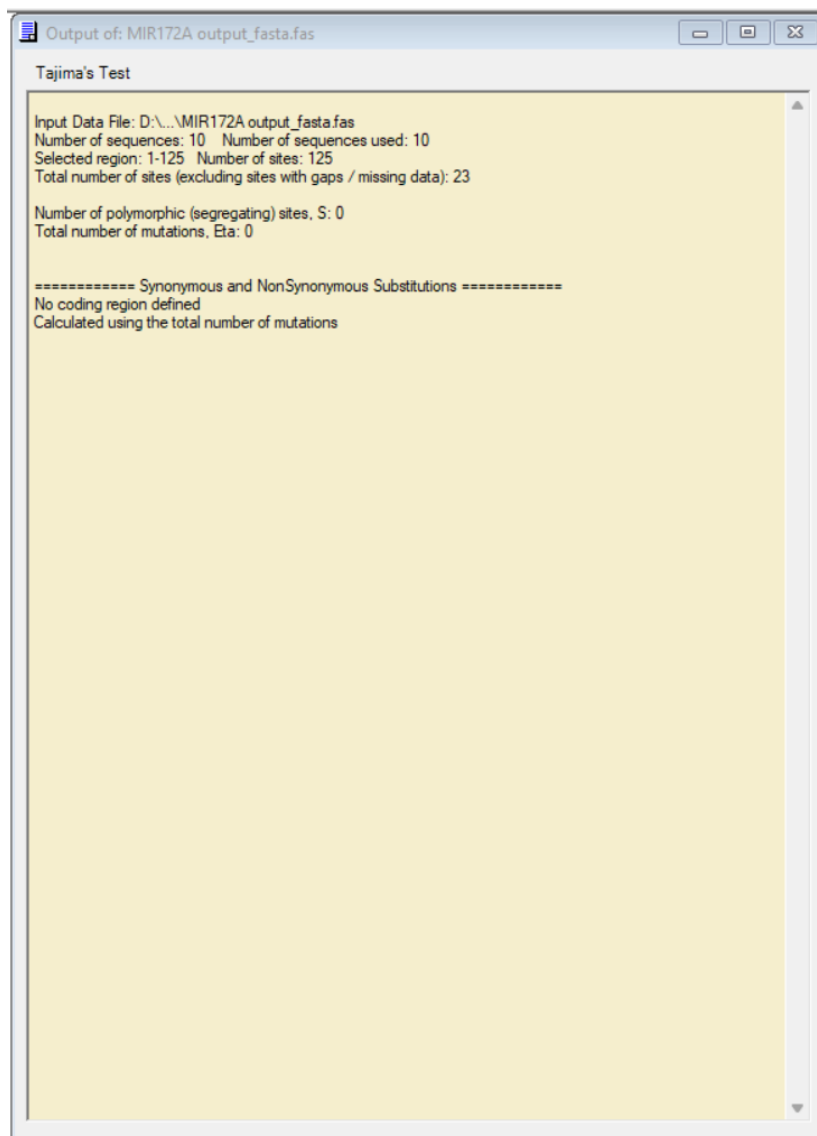


Figure S1. Screenshot of Tajima's test conducted on *MIR172A* sequences from *Oryza* spp, other poaceae members and Arabidopsis. A total of 10 sequences were included in the study.

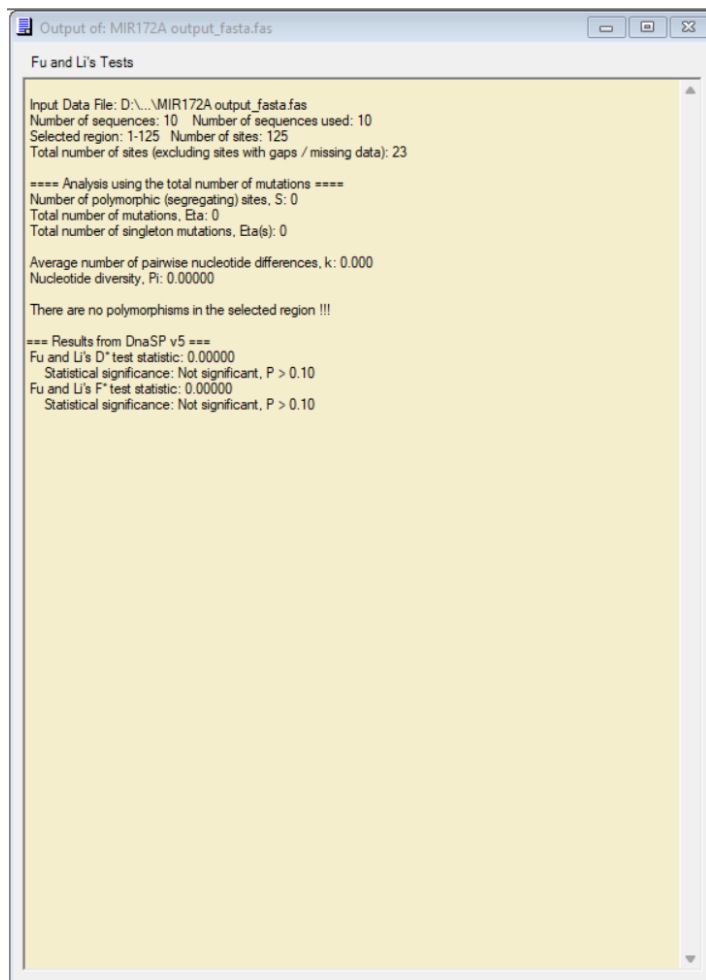


Figure S2. Screenshot of Fu and Li's test conducted on *MIR172A* sequences from *Oryza* spp, other poaceae members and *Arabidopsis*. A total of 10 sequences were included in the study.

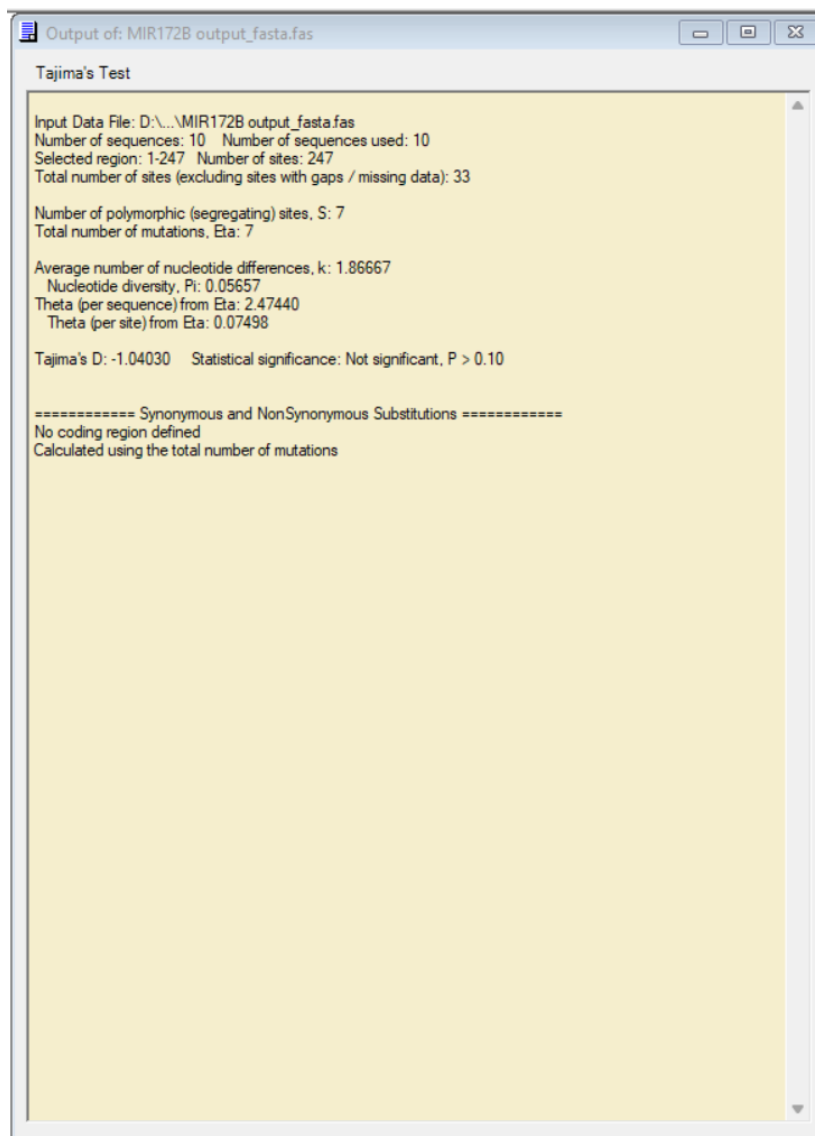


Figure S3. Screenshot of Tajima's test conducted on *MIR172B* sequences from *Oryza* spp, other poaceae members and Arabidopsis. A total of 10 sequences were included in the study.

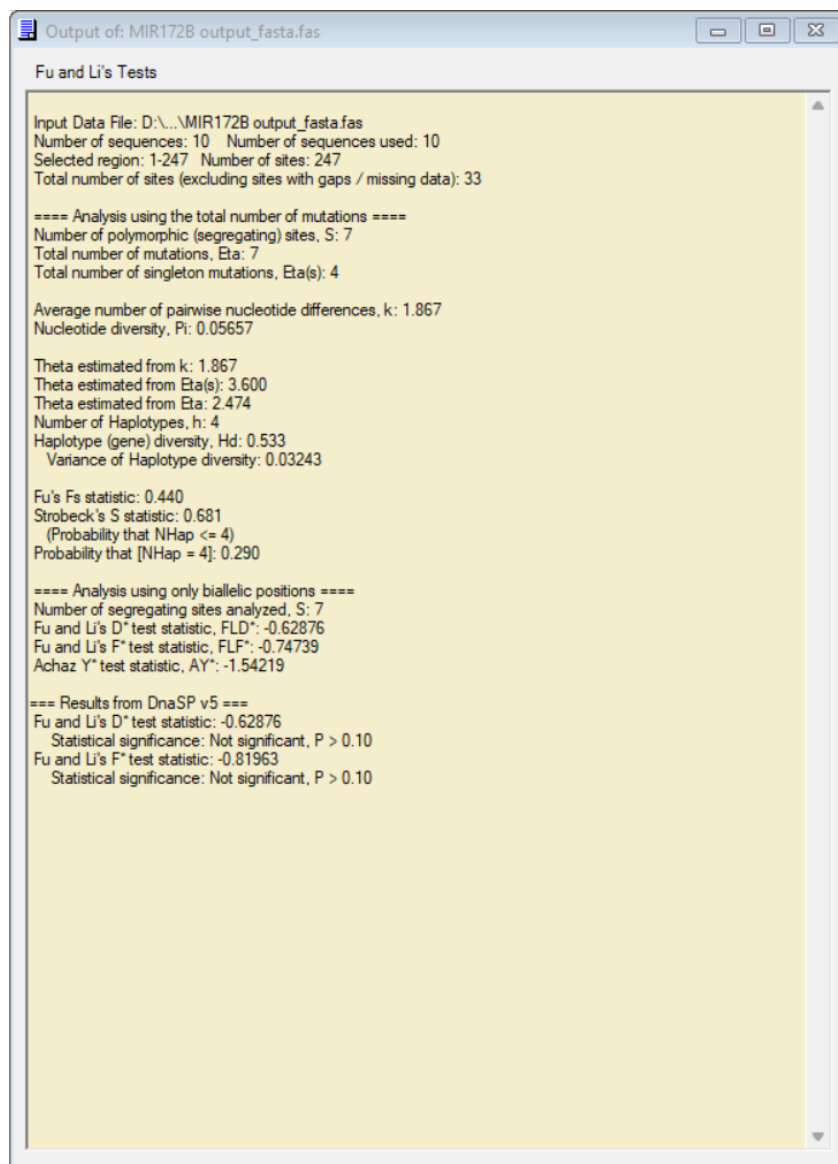


Figure S4. Screenshot of Fu and Li's test conducted on *MIR172B* sequences from *Oryza* spp, other poaceae members and Arabidopsis. A total of 10 sequences were included in the study.

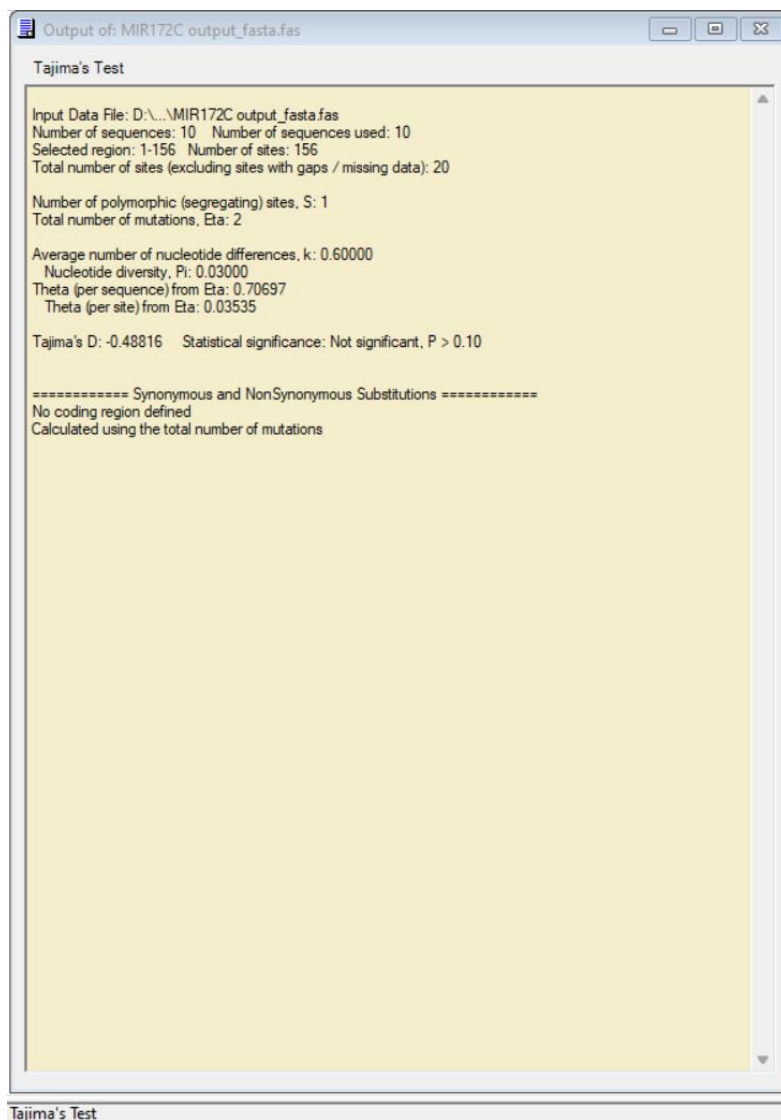


Figure S5. Screenshot of Tajima's test conducted on *MIR172C* sequences from *Oryza* spp, other poaceae members and Arabidopsis. A total of 10 sequences were included in the study.

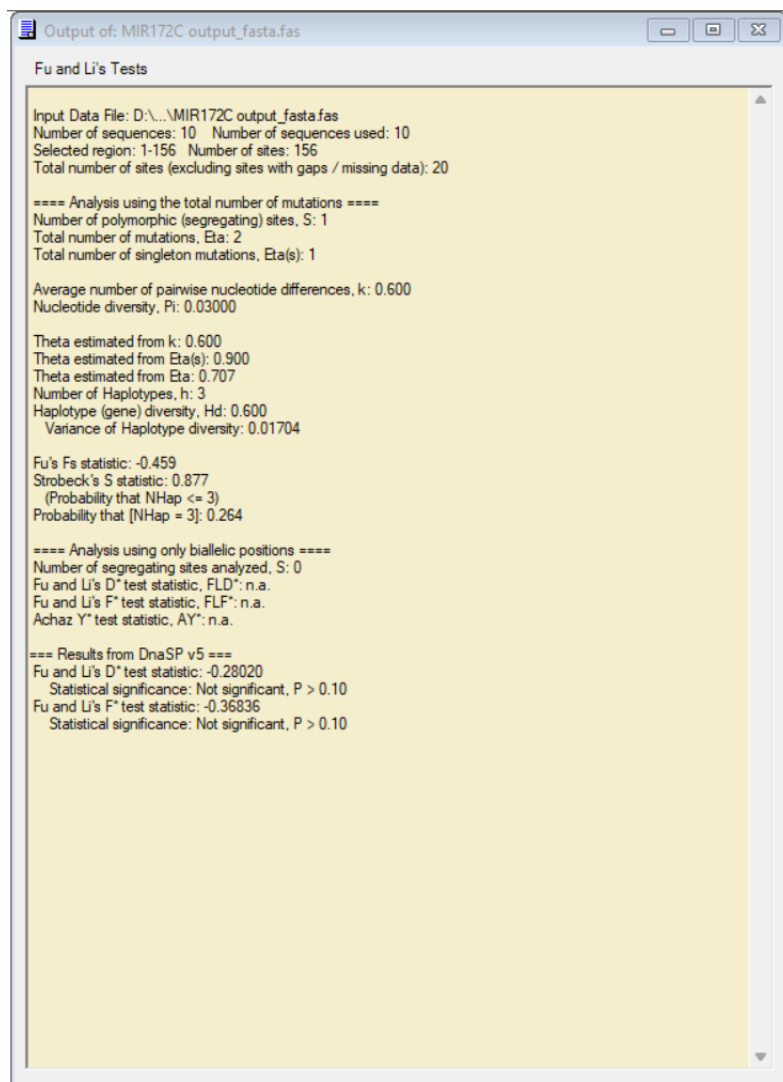


Figure S6. Screenshot of Fu and Li's test conducted on *MIR172C* sequences from *Oryza* spp, other poaceae members and *Arabidopsis*. A total of 10 sequences were included in the study.

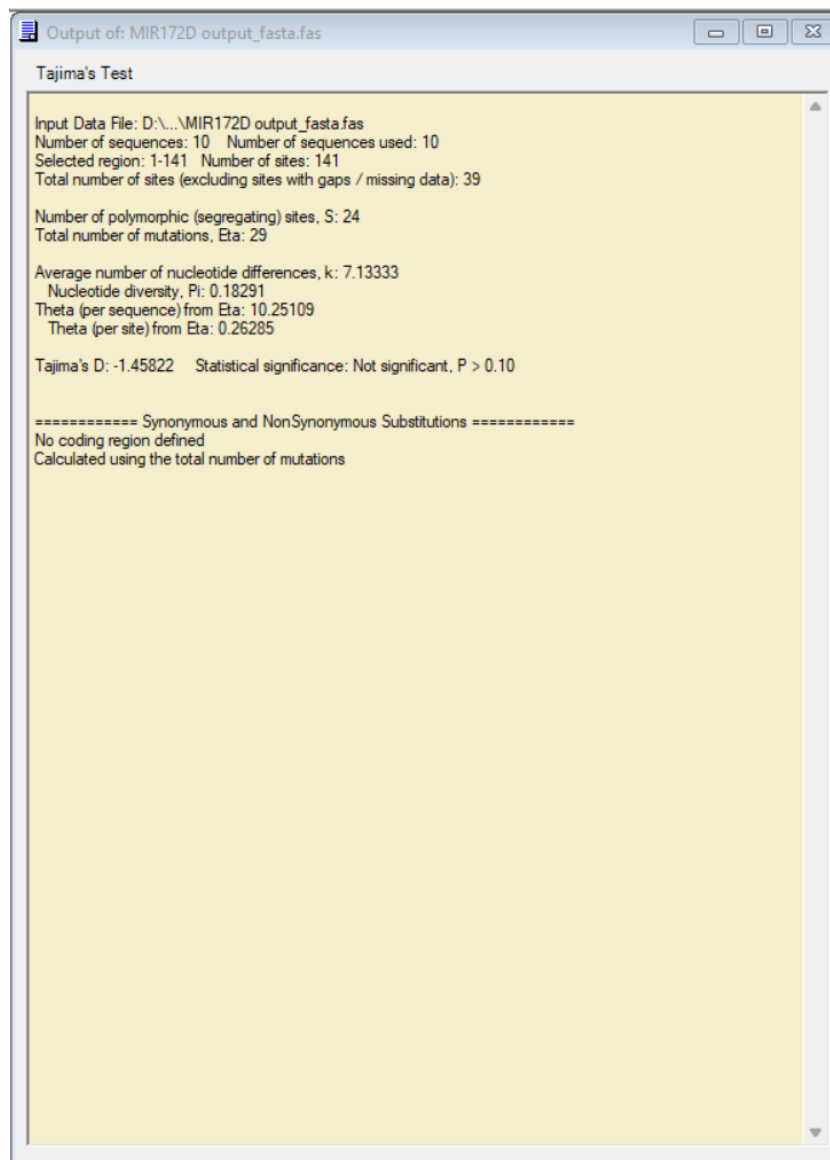


Figure S7. Screenshot of Tajima's test conducted on *MIR172D* sequences from *Oryza* spp, other poaceae members and Arabidopsis. A total of 10 sequences were included in the study.

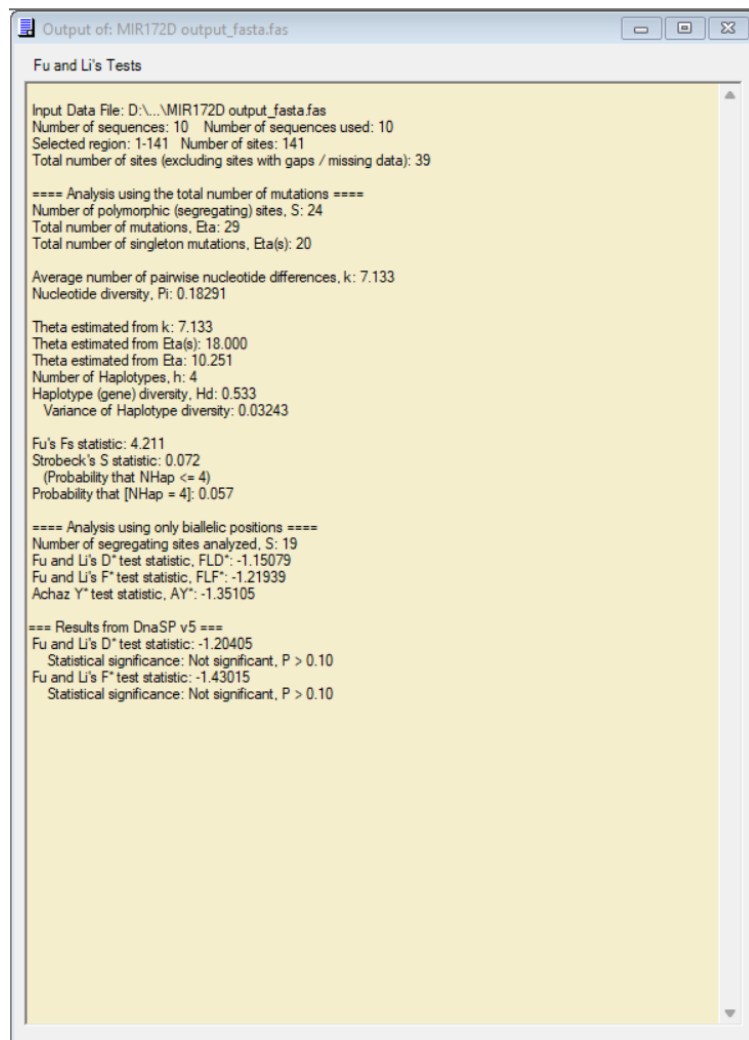


Figure S8. Screenshot of Fu and Li's test conducted on *MIR172D* sequences from *Oryza* spp, other poaceae members and *Arabidopsis*. A total of 10 sequences were included in the study.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence24Ob2g	
1	Sequence25Ob2g	Sequence46Og2g
1	Sequence26Ob2g	Sequence47Og2g
1	Sequence27Ob2g	Sequence48Og2g
1	Sequence28Ob2g	Sequence49Og2g
1	Sequence29Ob2g	Sequence50Og2g
1	Sequence30Ob2g	Sequence51Og2g
1	Sequence31Ob2g	
1	Sequence32Ob2g	Sequence53Og2g
1	Sequence33Ob2g	Sequence55Og2g
1	Sequence34Ob2g	Sequence57Og2g
1	Sequence35Ob2g	Sequence58Og2g
1	Sequence36Ob2g	Sequence59Og2g
1	Sequence37Ob2g	Sequence60Og2g
1	Sequence38Ob2g	Sequence61Og2g
1	Sequence39Ob2g	Sequence62Og2g
1	Sequence40Ob2g	Sequence63Og2g
1	Sequence41Ob2g	Sequence64Og2g
1	Sequence42Ob2g	Sequence65Og2g
1	Sequence43Ob2g	Sequence66Og2g
1	Sequence44Ob2g	Sequence67Og2g
1	Sequence45Ob2g	Sequence68Og2g

Figure S9: Synteny block diagram for *MIR172A* with *Oryza barthii* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. Ob2- *Oryza barthii* chr 2, Og2- *Oryza glaberrima* chr 2.

Duplication depth	Reference chromosome	Collinear blocks
1	Sequence46Og2g	Sequence25Ob2g
1	Sequence47Og2g	Sequence26Ob2g
1	Sequence48Og2g	Sequence27Ob2g
1	Sequence49Og2g	Sequence28Ob2g
1	Sequence50Og2g	Sequence29Ob2g
1	Sequence51Og2g	Sequence30Ob2g
1	Sequence52Og2g	
1	Sequence53Og2g	Sequence32Ob2g
1	Sequence54Og2g	
1	Sequence55Og2g	Sequence33Ob2g
1	Sequence56Og2g	
1	Sequence57Og2g	Sequence34Ob2g
1	Sequence58Og2g	Sequence35Ob2g
1	Sequence59Og2g	Sequence36Ob2g
1	Sequence60Og2g	Sequence37Ob2g
1	Sequence61Og2g	Sequence38Ob2g
1	Sequence62Og2g	Sequence39Ob2g
1	Sequence63Og2g	Sequence40Ob2g
1	Sequence64Og2g	Sequence41Ob2g
1	Sequence65Og2g	Sequence42Ob2g
1	Sequence66Og2g	Sequence43Ob2g
1	Sequence67Og2g	Sequence44Ob2g
1	Sequence68Og2g	Sequence45Ob2g

Figure S10: Synteny block diagram for *MIR172A* with *Oryza glaberrima* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. ob2- *Oryza barthii* chr 2, og2- *Oryza glaberrima* chr 2.

Duplication depth	Reference chromosome	Collinear blocks			
1	Sequence69Ou9g	Sequence89Or9g			
1	Sequence70Ou9g	Sequence90Or9g			
2	Sequence71Ou9g		Sequence5Os9g		
2	Sequence72Ou9g				
4	Sequence73Ou9g	Sequence91Or9g	Sequence7Os9g	Sequence119Oa9g	Sequence147Op9g
4	Sequence74Ou9g	Sequence92Or9g	Sequence8Os9g	Sequence121Oa9g	Sequence148Op9g
4	Sequence75Ou9g	Sequence93Or9g	Sequence9Os9g	Sequence122Oa9g	Sequence149Op9g
4	Sequence76Ou9g	Sequence94Or9g	Sequence12Os9g	Sequence124Oa9g	Sequence150Op9g
4	Sequence77Ou9g				
4	Sequence78Ou9g				
4	Sequence79Ou9g	Sequence99Or9g	Sequence15Os9g	Sequence125Oa9g	Sequence151Op9g
4	Sequence80Ou9g	Sequence100Or9g	Sequence17Os9g	Sequence126Oa9g	Sequence152Op9g
4	Sequence81Ou9g	Sequence101Or9g	Sequence18Os9g		
4	Sequence82Ou9g	Sequence102Or9g	Sequence19Os9g	Sequence129Oa9g	Sequence154Op9g
4	Sequence83Ou9g	Sequence103Or9g	Sequence20Os9g	Sequence130Oa9g	Sequence155Op9g
4	Sequence84Ou9g	Sequence104Or9g	Sequence21Os9g	Sequence131Oa9g	Sequence156Op9g
4	Sequence85Ou9g	Sequence105Or9g	Sequence22Os9g	Sequence132Oa9g	Sequence157Op9g

Figure S11: Synteny block diagram for *MIR172A* with *Oryza glumaepatula* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Os9- *Oryza sativa* chr 9, Ou9- *Oryza glumaepatula* chr 9, Or9- *Oryza rufipogon* chr 9, Oa9- *Oryza brachyantha* chr 9, Op9- *Oryza punctata* chr 9.

Duplication depth	Reference chromosome	Collinear blocks			
1	Sequence86Or9g	Sequence4Os9g			
1	Sequence87Or9g				
1	Sequence88Or9g	Sequence5Os9g			
2	Sequence89Or9g	Sequence6Os9g	Sequence69Ou9g		
2	Sequence90Or9g		Sequence70Ou9g		
4	Sequence91Or9g	Sequence7Os9g	Sequence73Ou9g	Sequence147Op9g	Sequence119Oa9g
4	Sequence92Or9g	Sequence8Os9g	Sequence74Ou9g	Sequence148Op9g	Sequence121Oa9g
4	Sequence93Or9g	Sequence9Os9g	Sequence75Ou9g	Sequence149Op9g	Sequence122Oa9g
4	Sequence94Or9g		Sequence76Ou9g		
4	Sequence95Or9g				
4	Sequence96Or9g	Sequence10Os9g		Sequence150Op9g	Sequence124Oa9g
4	Sequence97Or9g	Sequence12Os9g			
4	Sequence98Or9g	Sequence13Os9g			
4	Sequence99Or9g	Sequence15Os9g	Sequence79Ou9g	Sequence151Op9g	Sequence125Oa9g
4	Sequence100Or9g	Sequence17Os9g	Sequence80Ou9g	Sequence152Op9g	Sequence126Oa9g
4	Sequence101Or9g	Sequence18Os9g	Sequence81Ou9g		
4	Sequence102Or9g	Sequence19Os9g	Sequence82Ou9g	Sequence154Op9g	Sequence129Oa9g
4	Sequence103Or9g	Sequence20Os9g	Sequence83Ou9g	Sequence155Op9g	Sequence130Oa9g
4	Sequence104Or9g	Sequence21Os9g	Sequence84Ou9g	Sequence156Op9g	Sequence131Oa9g
4	Sequence105Or9g	Sequence22Os9g	Sequence85Ou9g	Sequence157Op9g	Sequence132Oa9g
2	Sequence106Or9g	Sequence23Os9g			Sequence133Oa9g
0	Sequence107Or9g				
0	Sequence108Or9g				

Figure S12: Synteny block diagram for *MIR172A* with *Oryza rufipogon* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Os9- *Oryza sativa* chr 9, Ou9- *Oryza glumaepatula* chr 9, Or9- *Oryza rufipogon* chr 9, Oa9- *Oryza brachyantha* chr 9, Op9- *Oryza punctata* chr 9.

Duplication depth	Reference chromosome	Collinear blocks			
1	Sequence109Oa9g	Sequence136Op9g			
1	Sequence110Oa9g	Sequence137Op9g			
1	Sequence111Oa9g	Sequence138Op9g			
1	Sequence112Oa9g	Sequence139Op9g			
1	Sequence113Oa9g				
1	Sequence114Oa9g	Sequence141Op9g			
1	Sequence115Oa9g	Sequence142Op9g			
2	Sequence116Oa9g	Sequence143Op9g	Sequence1Os9g		
2	Sequence117Oa9g	Sequence145Op9g	Sequence3Os9g		
2	Sequence118Oa9g				
4	Sequence119Oa9g			Sequence91Or9g	Sequence73Ou9g
4	Sequence120Oa9g				
4	Sequence121Oa9g	Sequence148Op9g	Sequence8Os9g	Sequence92Or9g	Sequence74Ou9g
4	Sequence122Oa9g	Sequence149Op9g	Sequence9Os9g	Sequence93Or9g	Sequence75Ou9g
4	Sequence123Oa9g				
4	Sequence124Oa9g	Sequence150Op9g	Sequence10Os9g	Sequence96Or9g	Sequence76Ou9g
4	Sequence125Oa9g	Sequence151Op9g	Sequence15Os9g	Sequence99Or9g	Sequence79Ou9g
4	Sequence126Oa9g	Sequence152Op9g	Sequence17Os9g	Sequence100Or9g	Sequence80Ou9g
4	Sequence127Oa9g				
4	Sequence128Oa9g				
4	Sequence129Oa9g	Sequence154Op9g	Sequence19Os9g	Sequence102Or9g	Sequence82Ou9g
4	Sequence130Oa9g	Sequence155Op9g	Sequence20Os9g	Sequence103Or9g	Sequence83Ou9g
4	Sequence131Oa9g	Sequence156Op9g	Sequence21Os9g	Sequence104Or9g	Sequence84Ou9g
4	Sequence132Oa9g	Sequence157Op9g	Sequence22Os9g	Sequence105Or9g	Sequence85Ou9g
2	Sequence133Oa9g		Sequence23Os9g	Sequence106Or9g	
0	Sequence134Oa9g				
0	Sequence135Oa9g				

Figure S13: Synteny block diagram for *MIR172A* with *Oryza brachyantha* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Os9- *Oryza sativa* chr 9, Ou9- *Oryza glumaepatula* chr 9, Or9- *Oryza rufipogon* chr 9, Oa9- *Oryza brachyantha* chr 9, Op9- *Oryza punctata* chr 9.

Duplication depth	Reference chromosome	Collinear blocks				
1	Sequence136Op9g	Sequence109Oa9g				
1	Sequence137Op9g	Sequence110Oa9g				
1	Sequence138Op9g	Sequence111Oa9g				
1	Sequence139Op9g	Sequence112Oa9g				
1	Sequence140Op9g					
1	Sequence141Op9g	Sequence114Oa9g				
1	Sequence142Op9g	Sequence115Oa9g				
2	Sequence143Op9g	Sequence116Oa9g	Sequence1Os9g			
2	Sequence144Op9g					
2	Sequence145Op9g	Sequence117Oa9g	Sequence3Os9g			
2	Sequence146Op9g					
4	Sequence147Op9g			Sequence73Ou9g	Sequence91Or9g	
4	Sequence148Op9g	Sequence121Oa9g	Sequence8Os9g	Sequence74Ou9g	Sequence92Or9g	
4	Sequence149Op9g	Sequence122Oa9g	Sequence9Os9g	Sequence75Ou9g	Sequence93Or9g	
4	Sequence150Op9g	Sequence124Oa9g	Sequence10Os9g	Sequence76Ou9g	Sequence96Or9g	
4	Sequence151Op9g	Sequence125Oa9g	Sequence15Os9g	Sequence79Ou9g	Sequence99Or9g	
4	Sequence152Op9g	Sequence126Oa9g	Sequence17Os9g	Sequence80Ou9g	Sequence100Or9g	
4	Sequence153Op9g					
4	Sequence154Op9g	Sequence129Oa9g	Sequence19Os9g	Sequence82Ou9g	Sequence102Or9g	
4	Sequence155Op9g	Sequence130Oa9g	Sequence20Os9g	Sequence83Ou9g	Sequence103Or9g	
4	Sequence156Op9g	Sequence131Oa9g	Sequence21Os9g	Sequence84Ou9g	Sequence104Or9g	
4	Sequence157Op9g	Sequence132Oa9g	Sequence22Os9g	Sequence85Ou9g	Sequence105Or9g	

Figure S14: Synteny block diagram for *MIR172A* with *Oryza punctata* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. Os9- *Oryza sativa* chr 9, Ou9- *Oryza glumaepatula* chr 9, Or9- *Oryza rufipogon* chr 9, Oa9- *Oryza brachyantha* chr 9, Op9- *Oryza punctata* chr 9.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence158Sb9g	
0	Sequence159Sb9g	
0	Sequence160Sb9g	
0	Sequence161Sb9g	
0	Sequence162Sb9g	
0	Sequence163Sb9g	
0	Sequence164Sb9g	
0	Sequence165Sb9g	
0	Sequence166Sb9g	
0	Sequence167Sb9g	
0	Sequence168Sb9g	
0	Sequence169Sb9g	
0	Sequence170Sb9g	
0	Sequence171Sb9g	
0	Sequence172Sb9g	
0	Sequence173Sb9g	
0	Sequence174Sb9g	
0	Sequence175Sb9g	
0	Sequence176Sb9g	
0	Sequence177Sb9g	

Figure S15: Synteny block diagram for *MIR172A* with *Sorghum bicolor* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Sb9- *Sorghum bicolor* chr 9.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence178Zm7g	
0	Sequence179Zm7g	
0	Sequence180Zm7g	
0	Sequence181Zm7g	
0	Sequence182Zm7g	
0	Sequence183Zm7g	
0	Sequence184Zm7g	
0	Sequence185Zm7g	
0	Sequence186Zm7g	
0	Sequence187Zm7g	
0	Sequence188Zm7g	
0	Sequence189Zm7g	
0	Sequence190Zm7g	
0	Sequence191Zm7g	

Figure S16: Synteny block diagram for *MIR172A* with *Zea mays* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. Zm7-*Zea mays* chr 7.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence192At2g	
0	Sequence193At2g	
0	Sequence194At2g	
0	Sequence195At2g	
0	Sequence196At2g	
0	Sequence197At2g	
0	Sequence198At2g	
0	Sequence199At2g	
0	Sequence200At2g	
0	Sequence201At2g	
0	Sequence202At2g	
0	Sequence203At2g	
0	Sequence204At2g	
0	Sequence205At2g	
0	Sequence206At2g	
0	Sequence207At2g	
0	Sequence208At2g	
0	Sequence209At2g	
0	Sequence210At2g	
0	Sequence211At2g	
0	Sequence212At2g	
0	Sequence213At2g	
0	Sequence214At2g	
0	Sequence215At2g	
0	Sequence216At2g	
0	Sequence217At2g	
0	Sequence218At2g	

Figure S17: Synteny block diagram for *MIR172A* with *Arabidopsis thaliana* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. At2- *Arabidopsis thaliana* chr 2.

Duplication depth	Reference chromosome	Collinear blocks					
2	Sequence24Ob1g	Sequence45Og1g	Sequence107Op1g				
3	Sequence25Ob1g	Sequence46Og1g		Sequence81Or1g			
4	Sequence26Ob1g	Sequence47Og1g	Sequence109Op1g	Sequence82Or1g	Sequence1Os1g		
4	Sequence27Ob1g						
4	Sequence28Ob1g	Sequence48Og1g	Sequence112Op1g	Sequence83Or1g	Sequence2Os1g		
5	Sequence29Ob1g	Sequence49Og1g		Sequence84Or1g	Sequence5Os1g	Sequence63Ou1g	
5	Sequence30Ob1g	Sequence50Og1g	Sequence115Op1g	Sequence85Or1g	Sequence6Os1g	Sequence64Ou1g	
5	Sequence31Ob1g				Sequence7Os1g	Sequence65Ou1g	
5	Sequence32Ob1g	Sequence52Og1g	Sequence117Op1g	Sequence87Or1g		Sequence66Ou1g	
5	Sequence33Ob1g				Sequence9Os1g		
5	Sequence34Ob1g			Sequence88Or1g	Sequence10Os1g		
5	Sequence35Ob1g	Sequence54Og1g	Sequence118Op1g	Sequence89Or1g	Sequence14Os1g	Sequence70Ou1g	
5	Sequence36Ob1g	Sequence55Og1g		Sequence90Or1g	Sequence15Os1g	Sequence71Ou1g	
5	Sequence37Ob1g						
5	Sequence38Ob1g						
5	Sequence39Ob1g				Sequence17Os1g	Sequence74Ou1g	
5	Sequence40Ob1g	Sequence57Og1g	Sequence124Op1g	Sequence93Or1g	Sequence18Os1g	Sequence75Ou1g	
5	Sequence41Ob1g	Sequence58Og1g	Sequence125Op1g	Sequence94Or1g		Sequence76Ou1g	
5	Sequence42Ob1g	Sequence59Og1g	Sequence129Op1g	Sequence95Or1g	Sequence21Os1g	Sequence78Ou1g	
1	Sequence43Ob1g	Sequence60Og1g					
0	Sequence44Ob1g						

Figure S18: Synteny block diagram for *MIR172B* with *Oryza barthii* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘|’ in the multi-alignment of gene orders. Os1- *Oryza sativa* chr 1, Ob1- *Oryza barthii* chr 1, Og1- *Oryza glaberrima* chr 1, Ou1- *Oryza glumaepatula* chr 1, Or1- *Oryza rufipogon* chr 1, Op1- *Oryza punctata* chr 1.

Duplication depth	Reference chromosome	Collinear blocks					
2	Sequence45Og1g	Sequence107Op1g	Sequence24Ob1g				
3	Sequence46Og1g		Sequence25Ob1g	Sequence81Or1g			
4	Sequence47Og1g	Sequence109Op1g	Sequence26Ob1g	Sequence82Or1g	Sequence1Os1g		
4	Sequence48Og1g	Sequence112Op1g	Sequence28Ob1g	Sequence83Or1g	Sequence2Os1g		
5	Sequence49Og1g	Sequence113Op1g	Sequence29Ob1g	Sequence84Or1g	Sequence5Os1g	Sequence63Ou1g	
5	Sequence50Og1g	Sequence115Op1g	Sequence30Ob1g	Sequence85Or1g	Sequence6Os1g	Sequence64Ou1g	
5	Sequence51Og1g						
5	Sequence52Og1g	Sequence117Op1g	Sequence32Ob1g	Sequence87Or1g			Sequence66Ou1g
5	Sequence53Og1g				Sequence11Os1g	Sequence67Ou1g	
5	Sequence54Og1g	Sequence118Op1g	Sequence35Ob1g	Sequence89Or1g	Sequence14Os1g	Sequence70Ou1g	
5	Sequence55Og1g	Sequence119Op1g	Sequence36Ob1g	Sequence90Or1g	Sequence15Os1g	Sequence71Ou1g	
5	Sequence56Og1g						
5	Sequence57Og1g	Sequence124Op1g	Sequence40Ob1g	Sequence93Or1g	Sequence18Os1g	Sequence75Ou1g	
5	Sequence58Og1g	Sequence125Op1g	Sequence41Ob1g	Sequence94Or1g	Sequence19Os1g	Sequence76Ou1g	
5	Sequence59Og1g	Sequence129Op1g	Sequence42Ob1g	Sequence95Or1g	Sequence21Os1g	Sequence78Ou1g	
1	Sequence60Og1g		Sequence43Ob1g				
0	Sequence61Og1g						
0	Sequence62Og1g						

Figure S19: Synteny block diagram for *MIR172B* with *Oryza glaberrima* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. Os1- *Oryza sativa* chr 1, Ob1- *Oryza barthii* chr 1, Og1- *Oryza glaberrima* chr 1, Ou1- *Oryza glumaepatula* chr 1, Or1- *Oryza rufipogon* chr 1, Op1- *Oryza punctata* chr 1.

Duplication depth	Reference chromosome	Collinear blocks					
5	Sequence63Ou1g	Sequence49Og1g	Sequence113Op1g	Sequence29Ob1g	Sequence84Or1g	Sequence5Os1g	
5	Sequence64Ou1g	Sequence50Og1g	Sequence115Op1g	Sequence30Ob1g	Sequence85Or1g	Sequence6Os1g	
5	Sequence65Ou1g			Sequence31Ob1g		Sequence7Os1g	
5	Sequence66Ou1g	Sequence52Og1g	Sequence117Op1g	Sequence32Ob1g	Sequence87Or1g		
5	Sequence67Ou1g	Sequence53Og1g				Sequence11Os1g	
5	Sequence68Ou1g						
5	Sequence69Ou1g						
5	Sequence70Ou1g	Sequence54Og1g	Sequence118Op1g	Sequence35Ob1g	Sequence89Or1g	Sequence14Os1g	
5	Sequence71Ou1g	Sequence55Og1g	Sequence119Op1g	Sequence36Ob1g	Sequence90Or1g	Sequence15Os1g	
5	Sequence72Ou1g						
5	Sequence73Ou1g						
5	Sequence74Ou1g			Sequence39Ob1g		Sequence17Os1g	
5	Sequence75Ou1g	Sequence57Og1g	Sequence124Op1g	Sequence40Ob1g	Sequence93Or1g	Sequence18Os1g	
5	Sequence76Ou1g	Sequence58Og1g	Sequence125Op1g	Sequence41Ob1g	Sequence94Or1g	Sequence19Os1g	
5	Sequence77Ou1g						
5	Sequence78Ou1g	Sequence59Og1g	Sequence129Op1g	Sequence42Ob1g	Sequence95Or1g	Sequence21Os1g	
2	Sequence79Ou1g				Sequence96Or1g		
2	Sequence80Ou1g		Sequence131Op1g		Sequence97Or1g		

Figure S20: Synteny block diagram for *MIR172B* with *Oryza glumaepatula* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Os1- *Oryza sativa* chr 1, Ob1- *Oryza barthii* chr 1, Og1- *Oryza glaberrima* chr 1, Ou1- *Oryza glumaepatula* chr 1, Or1- *Oryza rufipogon* chr 1, Op1- *Oryza punctata* chr 1.

Duplication depth	Reference chromosome	Collinear blocks					
2	Sequence81Or1g	Sequence25Ob1g	Sequence46Og1g				
4	Sequence82Or1g	Sequence26Ob1g	Sequence47Og1g	Sequence1Os1g	Sequence109Op1g		
4	Sequence83Or1g	Sequence28Ob1g	Sequence48Og1g	Sequence2Os1g	Sequence112Op1g		
5	Sequence84Or1g	Sequence29Ob1g	Sequence49Og1g	Sequence5Os1g	Sequence113Op1g	Sequence63Ou1g	
5	Sequence85Or1g	Sequence30Ob1g	Sequence50Og1g	Sequence6Os1g	Sequence116Op1g	Sequence64Ou1g	
5	Sequence86Or1g						
5	Sequence87Or1g	Sequence32Ob1g	Sequence52Og1g	Sequence8Os1g		Sequence66Ou1g	
5	Sequence88Or1g	Sequence34Ob1g					
5	Sequence89Or1g	Sequence35Ob1g	Sequence54Og1g	Sequence14Os1g		Sequence70Ou1g	
5	Sequence90Or1g	Sequence36Ob1g	Sequence55Og1g	Sequence15Os1g	Sequence119Op1g	Sequence71Ou1g	
5	Sequence91Or1g						
5	Sequence92Or1g						
5	Sequence93Or1g	Sequence40Ob1g	Sequence57Og1g	Sequence18Os1g	Sequence124Op1g	Sequence75Ou1g	
5	Sequence94Or1g	Sequence41Ob1g	Sequence58Og1g	Sequence19Os1g	Sequence125Op1g	Sequence76Ou1g	
5	Sequence95Or1g	Sequence42Ob1g	Sequence59Og1g	Sequence21Os1g		Sequence78Ou1g	
2	Sequence96Or1g				Sequence127Op1g	Sequence79Ou1g	
2	Sequence97Or1g				Sequence131Op1g	Sequence80Ou1g	

Figure S21: Synteny block diagram for *MIR172B* with *Oryza rufipogon* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Os1- *Oryza sativa* chr 1, Ob1- *Oryza barthii* chr 1, Og1- *Oryza glaberrima* chr 1, Ou1- *Oryza glumaepatula* chr 1, Or1- *Oryza rufipogon* chr 1, Op1- *Oryza punctata* chr 1.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence98Oa1g	
0	Sequence99Oa1g	
0	Sequence100Oa1g	
0	Sequence101Oa1g	
0	Sequence102Oa1g	
0	Sequence103Oa1g	
0	Sequence104Oa1g	
0	Sequence105Oa1g	
0	Sequence106Oa1g	

Figure S22: Synteny block diagram for *MIR172B* with *Oryza brachyantha* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. Oa1- *Oryza brachyantha* chr 1.

Duplication depth	Reference chromosome	Collinear blocks				
2	Sequence107Op1g	Sequence24Ob1g	Sequence45Og1g			
2	Sequence108Op1g					
3	Sequence109Op1g	Sequence26Ob1g	Sequence47Og1g	Sequence82Or1g		
3	Sequence110Op1g					
4	Sequence111Op1g				Sequence1Os1g	
4	Sequence112Op1g	Sequence28Ob1g	Sequence48Og1g	Sequence83Or1g	Sequence2Os1g	
5	Sequence113Op1g		Sequence49Og1g	Sequence84Or1g	Sequence5Os1g	Sequence63Ou1g
5	Sequence114Op1g					
5	Sequence115Op1g	Sequence30Ob1g	Sequence50Og1g		Sequence6Os1g	Sequence64Ou1g
5	Sequence116Op1g			Sequence85Or1g		
5	Sequence117Op1g	Sequence32Ob1g	Sequence52Og1g		Sequence8Os1g	Sequence66Ou1g
5	Sequence118Op1g	Sequence35Ob1g	Sequence54Og1g		Sequence14Os1g	Sequence70Ou1g
5	Sequence119Op1g		Sequence55Og1g	Sequence90Or1g	Sequence15Os1g	Sequence71Ou1g
5	Sequence120Op1g					
5	Sequence121Op1g					
5	Sequence122Op1g					
5	Sequence123Op1g					
5	Sequence124Op1g	Sequence40Ob1g	Sequence57Og1g	Sequence93Or1g		Sequence75Ou1g
5	Sequence125Op1g	Sequence41Ob1g	Sequence58Og1g	Sequence94Or1g	Sequence19Os1g	Sequence76Ou1g
5	Sequence126Op1g					
5	Sequence127Op1g			Sequence96Or1g		
5	Sequence128Op1g					
5	Sequence129Op1g	Sequence42Ob1g	Sequence59Og1g		Sequence21Os1g	Sequence78Ou1g
2	Sequence130Op1g					
2	Sequence131Op1g			Sequence97Or1g		Sequence80Ou1g

Figure S23: Synteny block diagram for *MIR172B* with *Oryza punctata* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘|’ in the multi-alignment of gene orders. Os1- *Oryza sativa* chr 1, Ob1- *Oryza barthii* chr 1, Og1- *Oryza glaberrima* chr 1, Ou1- *Oryza glumaepatula* chr 1, Or1- *Oryza rufipogon* chr 1, Op1- *Oryza punctata* chr 1.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence132Sb3g	
0	Sequence133Sb3g	
0	Sequence134Sb3g	
0	Sequence135Sb3g	
0	Sequence136Sb3g	
0	Sequence137Sb3g	
0	Sequence138Sb3g	
0	Sequence139Sb3g	
0	Sequence140Sb3g	
0	Sequence141Sb3g	
0	Sequence142Sb3g	
0	Sequence143Sb3g	
0	Sequence144Sb3g	
0	Sequence145Sb3g	
0	Sequence146Sb3g	
0	Sequence147Sb3g	
0	Sequence148Sb3g	
0	Sequence149Sb3g	
0	Sequence150Sb3g	
0	Sequence151Sb3g	
0	Sequence152Sb3g	

Figure S24: Synteny block diagram for *MIR172B* with *Sorghum bicolor* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Sb3 - *Sorghum bicolor* chr 3.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence153Zm5g	
0	Sequence154Zm5g	
0	Sequence155Zm5g	
0	Sequence156Zm5g	
0	Sequence157Zm5g	
0	Sequence158Zm5g	
0	Sequence159Zm5g	
0	Sequence160Zm5g	
0	Sequence161Zm5g	
0	Sequence162Zm5g	
0	Sequence163Zm5g	
0	Sequence164Zm5g	
0	Sequence165Zm5g	
0	Sequence166Zm5g	
0	Sequence167Zm5g	

Figure S25: Synteny block diagram for *MIR172B* with *Zea mays* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Zm5 - *Zea mays* chr 5.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence168At5g	
0	Sequence169At5g	
0	Sequence170At5g	
0	Sequence171At5g	
0	Sequence172At5g	
0	Sequence173At5g	
0	Sequence174At5g	
0	Sequence175At5g	
0	Sequence176At5g	
0	Sequence177At5g	
0	Sequence178At5g	
0	Sequence179At5g	
0	Sequence180At5g	
0	Sequence181At5g	
0	Sequence182At5g	
0	Sequence183At5g	
0	Sequence184At5g	
0	Sequence185At5g	
0	Sequence186At5g	
0	Sequence187At5g	
0	Sequence188At5g	
0	Sequence189At5g	
0	Sequence190At5g	
0	Sequence191At5g	
0	Sequence192At5g	
0	Sequence193At5g	
0	Sequence194At5g	
0	Sequence195At5g	

Figure S26: Synteny block diagram for *MIR172B* with *Arabidopsis thaliana* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. At5- *Arabidopsis thaliana* chr 5.

Duplication depth	Reference chromosome	Collinear blocks				
0	Sequence22Ob7g					
0	Sequence23Ob7g					
0	Sequence24Ob7g					
0	Sequence25Ob7g					
1	Sequence26Ob7g	Sequence83Or7g				
3	Sequence27Ob7g	Sequence84Or7g	Sequence69Ou7g	Sequence1Os7g		
4	Sequence28Ob7g	Sequence86Or7g	Sequence70Ou7g	Sequence3Os7g	Sequence52Og7g	
4	Sequence29Ob7g	Sequence89Or7g	Sequence72Ou7g	Sequence9Os7g	Sequence53Og7g	
4	Sequence30Ob7g	Sequence90Or7g	Sequence73Ou7g	Sequence10Os7g	Sequence54Og7g	
4	Sequence31Ob7g	Sequence91Or7g	Sequence74Ou7g	Sequence11Os7g	Sequence55Og7g	
4	Sequence32Ob7g	Sequence92Or7g	Sequence75Ou7g		Sequence56Og7g	
4	Sequence33Ob7g		Sequence76Ou7g		Sequence57Og7g	
4	Sequence34Ob7g	Sequence94Or7g	Sequence77Ou7g	Sequence13Os7g	Sequence58Og7g	
4	Sequence35Ob7g	Sequence95Or7g	Sequence78Ou7g	Sequence14Os7g	Sequence59Og7g	
4	Sequence36Ob7g	Sequence96Or7g	Sequence79Ou7g	Sequence16Os7g	Sequence60Og7g	
4	Sequence37Ob7g	Sequence97Or7g				
4	Sequence38Ob7g		Sequence80Ou7g	Sequence17Os7g	Sequence62Og7g	
4	Sequence39Ob7g		Sequence81Ou7g	Sequence18Os7g	Sequence63Og7g	
3	Sequence40Ob7g					
3	Sequence41Ob7g				Sequence65Og7g	
3	Sequence42Ob7g			Sequence20Os7g	Sequence66Og7g	
2	Sequence43Ob7g				Sequence67Og7g	
2	Sequence44Ob7g	Sequence105Or7g			Sequence68Og7g	
0	Sequence45Ob7g					
0	Sequence46Ob7g					

Figure S27: Synteny block diagram for *MIR172C* with *Oryza barthii* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. Os7- *Oryza sativa* chr 7, Ob7- *Oryza barthii* chr 7, Og7- *Oryza glaberrima* chr 7, Ou7- *Oryza glumaepatula* chr 7, Or7- *Oryza rufipogon* chr 7, Oa7- *Oryza brachyantha* chr 7, Op2- *Oryza punctata* chr 2, Sb4- *Sorghum bicolor* chr 4, Zm4- *Zea mays* chr 4, At3- *Arabidopsis thaliana* chr 3.

Duplication depth	Reference chromosome	Collinear blocks			
0	Sequence47Og7g				
0	Sequence48Og7g				
0	Sequence49Og7g				
0	Sequence50Og7g				
0	Sequence51Og7g				
4	Sequence52Og7g	Sequence3Os7g	Sequence70Ou7g	Sequence28Ob7g	Sequence86Or7g
4	Sequence53Og7g	Sequence9Os7g	Sequence72Ou7g	Sequence29Ob7g	Sequence89Or7g
4	Sequence54Og7g	Sequence10Os7g	Sequence73Ou7g	Sequence30Ob7g	Sequence90Or7g
4	Sequence55Og7g	Sequence11Os7g	Sequence74Ou7g	Sequence31Ob7g	Sequence91Or7g
4	Sequence56Og7g		Sequence75Ou7g	Sequence32Ob7g	Sequence92Or7g
4	Sequence57Og7g		Sequence76Ou7g	Sequence33Ob7g	
4	Sequence58Og7g	Sequence13Os7g	Sequence77Ou7g	Sequence34Ob7g	Sequence94Or7g
4	Sequence59Og7g	Sequence14Os7g	Sequence78Ou7g	Sequence35Ob7g	Sequence95Or7g
4	Sequence60Og7g	Sequence16Os7g	Sequence79Ou7g	Sequence36Ob7g	Sequence96Or7g
4	Sequence61Og7g				
4	Sequence62Og7g	Sequence17Os7g	Sequence80Ou7g	Sequence38Ob7g	
4	Sequence63Og7g	Sequence18Os7g	Sequence81Ou7g	Sequence39Ob7g	
3	Sequence64Og7g				
3	Sequence65Og7g			Sequence41Ob7g	
3	Sequence66Og7g	Sequence20Os7g		Sequence42Ob7g	
2	Sequence67Og7g			Sequence43Ob7g	
2	Sequence68Og7g			Sequence44Ob7g	Sequence105Or7g

Figure S28: Synteny block diagram for *MIR172C* with *Oryza glaberrima* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Os7- *Oryza sativa* chr 7, Ob7- *Oryza barthii* chr 7, Og7- *Oryza glaberrima* chr 7, Ou7- *Oryza glumaepatula* chr 7, Or7- *Oryza rufipogon* chr 7.

Duplication depth	Reference chromosome	Collinear blocks				
3	Sequence69Ou7g	Sequence27Ob7g	Sequence84Or7g	Sequence1Os7g		
4	Sequence70Ou7g	Sequence28Ob7g	Sequence86Or7g	Sequence3Os7g	Sequence52Og7g	
4	Sequence71Ou7g					
4	Sequence72Ou7g	Sequence29Ob7g	Sequence89Or7g	Sequence9Os7g	Sequence53Og7g	
4	Sequence73Ou7g	Sequence30Ob7g	Sequence90Or7g	Sequence10Os7g	Sequence54Og7g	
4	Sequence74Ou7g	Sequence31Ob7g	Sequence91Or7g	Sequence11Os7g	Sequence55Og7g	
4	Sequence75Ou7g	Sequence32Ob7g	Sequence92Or7g		Sequence56Og7g	
4	Sequence76Ou7g	Sequence33Ob7g			Sequence57Og7g	
4	Sequence77Ou7g	Sequence34Ob7g	Sequence94Or7g	Sequence13Os7g	Sequence58Og7g	
4	Sequence78Ou7g	Sequence35Ob7g	Sequence95Or7g	Sequence14Os7g	Sequence59Og7g	
4	Sequence79Ou7g	Sequence36Ob7g	Sequence96Or7g	Sequence16Os7g	Sequence60Og7g	
3	Sequence80Ou7g	Sequence38Ob7g		Sequence17Os7g	Sequence62Og7g	
3	Sequence81Ou7g	Sequence39Ob7g		Sequence18Os7g	Sequence63Og7g	

Figure S29: Synteny block diagram for *MIR172C* with *Oryza glumaepatula* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Os7- *Oryza sativa* chr 7, Ob7- *Oryza barthii* chr 7, Og7- *Oryza glaberrima* chr 7, Ou7- *Oryza glumaepatula* chr 7, Or7- *Oryza rufipogon* chr 7.

Duplication depth	Reference chromosome	Collinear blocks			
0	Sequence82Or7g				
1	Sequence83Or7g	Sequence26Ob7g			
3	Sequence84Or7g	Sequence27Ob7g	Sequence1Os7g	Sequence69Ou7g	
3	Sequence85Or7g		Sequence2Os7g		
4	Sequence86Or7g	Sequence28Ob7g	Sequence3Os7g	Sequence70Ou7g	Sequence52Og7g
4	Sequence87Or7g		Sequence4Os7g		
4	Sequence88Or7g		Sequence6Os7g		
4	Sequence89Or7g	Sequence29Ob7g	Sequence9Os7g	Sequence72Ou7g	Sequence53Og7g
4	Sequence90Or7g	Sequence30Ob7g	Sequence10Os7g	Sequence73Ou7g	Sequence54Og7g
4	Sequence91Or7g	Sequence31Ob7g	Sequence11Os7g	Sequence74Ou7g	Sequence55Og7g
4	Sequence92Or7g	Sequence32Ob7g		Sequence75Ou7g	Sequence56Og7g
4	Sequence93Or7g		Sequence12Os7g		
4	Sequence94Or7g	Sequence34Ob7g	Sequence13Os7g	Sequence77Ou7g	Sequence58Og7g
4	Sequence95Or7g	Sequence35Ob7g	Sequence15Os7g	Sequence78Ou7g	Sequence59Og7g
4	Sequence96Or7g	Sequence36Ob7g	Sequence16Os7g	Sequence79Ou7g	Sequence60Og7g
2	Sequence97Or7g	Sequence37Ob7g			
2	Sequence98Or7g				
2	Sequence99Or7g				
2	Sequence100Or7g				
2	Sequence101Or7g				
2	Sequence102Or7g				
2	Sequence103Or7g				
2	Sequence104Or7g				
2	Sequence105Or7g	Sequence44Ob7g			Sequence68Og7g
0	Sequence106Or7g				
0	Sequence107Or7g				
0	Sequence108Or7g				
0	Sequence109Or7g				

Figure S30: Synteny block diagram for *MIR172C* with *Oryza rufipogon* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Os7- *Oryza sativa* chr 7, Ob7- *Oryza barthii* chr 7, Og7- *Oryza glaberrima* chr 7, Ou7- *Oryza glumaepatula* chr 7, Or7- *Oryza rufipogon* chr 7.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence110Oa7g	
0	Sequence111Oa7g	
0	Sequence112Oa7g	
0	Sequence113Oa7g	
0	Sequence114Oa7g	
0	Sequence115Oa7g	
0	Sequence116Oa7g	
0	Sequence117Oa7g	
0	Sequence118Oa7g	
0	Sequence119Oa7g	
0	Sequence120Oa7g	
0	Sequence121Oa7g	
0	Sequence122Oa7g	
0	Sequence123Oa7g	
0	Sequence124Oa7g	
0	Sequence125Oa7g	
0	Sequence126Oa7g	
0	Sequence127Oa7g	
0	Sequence128Oa7g	
0	Sequence129Oa7g	
0	Sequence130Oa7g	

Figure S31: Synteny block diagram for *MIR172C* with *Oryza brachyantha* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. Oa7 - *Oryza brachyantha* chr 7.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence131Op2g	
0	Sequence132Op2g	
0	Sequence133Op2g	
0	Sequence134Op2g	
0	Sequence135Op2g	
0	Sequence136Op2g	
0	Sequence137Op2g	
0	Sequence138Op2g	
0	Sequence139Op2g	
0	Sequence140Op2g	
0	Sequence141Op2g	
0	Sequence142Op2g	
0	Sequence143Op2g	
0	Sequence144Op2g	
0	Sequence145Op2g	
0	Sequence146Op2g	
0	Sequence147Op2g	
0	Sequence148Op2g	
0	Sequence149Op2g	
0	Sequence150Op2g	
0	Sequence151Op2g	
0	Sequence152Op2g	

Figure S32: Synteny block diagram for *MIR172C* with *Oryza punctata* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Oa7 - *Oryza punctata* chr 2.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence153Sb4g	
0	Sequence154Sb4g	
0	Sequence155Sb4g	
0	Sequence156Sb4g	
0	Sequence157Sb4g	
0	Sequence158Sb4g	
0	Sequence159Sb4g	
0	Sequence160Sb4g	
0	Sequence161Sb4g	
0	Sequence162Sb4g	
0	Sequence163Sb4g	
0	Sequence164Sb4g	
0	Sequence165Sb4g	
0	Sequence166Sb4g	
0	Sequence167Sb4g	
0	Sequence168Sb4g	
0	Sequence169Sb4g	
0	Sequence170Sb4g	

Figure S33: Synteny block diagram for *MIR172C* with *Sorghum bicolor* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Sb4 - *Sorghum bicolor* chr 4.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence171Zm4g	
0	Sequence172Zm4g	
0	Sequence173Zm4g	
0	Sequence174Zm4g	
0	Sequence175Zm4g	
0	Sequence176Zm4g	
0	Sequence177Zm4g	
0	Sequence178Zm4g	
0	Sequence179Zm4g	
0	Sequence180Zm4g	
0	Sequence181Zm4g	
0	Sequence182Zm4g	

Figure S34: Synteny block diagram for *MIR172C* with *Zea mays* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Zm4-*Zea mays* chr 4.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence183At3g	
0	Sequence184At3g	
0	Sequence185At3g	
0	Sequence186At3g	
0	Sequence187At3g	
0	Sequence188At3g	
0	Sequence189At3g	
0	Sequence190At3g	
0	Sequence191At3g	
0	Sequence192At3g	
0	Sequence193At3g	
0	Sequence194At3g	
0	Sequence195At3g	
0	Sequence196At3g	
0	Sequence197At3g	
0	Sequence198At3g	
0	Sequence199At3g	
0	Sequence200At3g	
0	Sequence201At3g	
0	Sequence202At3g	
0	Sequence203At3g	
0	Sequence204At3g	
0	Sequence205At3g	
0	Sequence206At3g	
0	Sequence207At3g	
0	Sequence208At3g	
0	Sequence209At3g	
0	Sequence210At3g	
0	Sequence211At3g	

Figure S35: Synteny block diagram for *MIR172C* with *Arabidopsis thaliana* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. At3 - *Arabidopsis thaliana* chr 3.

Duplication depth	Reference chromosome	Collinear blocks						
1	Sequence43Ob2g	Sequence2Osi2g						
4	Sequence44Ob2g	Sequence3Osi2g	Sequence65Og2g	Sequence143Op2g	Sequence107Or2g			
5	Sequence45Ob2g	Sequence4Osi2g	Sequence66Og2g	Sequence144Op2g	Sequence108Or2g	Sequence88Ou2g		
5	Sequence46Ob2g		Sequence67Og2g					
6	Sequence47Ob2g	Sequence7Osi2g		Sequence146Op2g	Sequence110Or2g	Sequence90Ou2g	Sequence24Osi2g	
6	Sequence48Ob2g	Sequence8Osi2g	Sequence68Og2g	Sequence149Op2g		Sequence94Ou2g	Sequence25Osi2g	
6	Sequence49Ob2g	Sequence13Osi2g	Sequence69Og2g	Sequence150Op2g	Sequence111Or2g	Sequence95Ou2g	Sequence30Osi2g	
6	Sequence50Ob2g		Sequence70Og2g					
6	Sequence51Ob2g		Sequence73Og2g					
6	Sequence52Ob2g		Sequence74Og2g	Sequence151Op2g	Sequence113Or2g	Sequence96Ou2g	Sequence32Osi2g	
6	Sequence53Ob2g	Sequence15Osi2g		Sequence152Op2g	Sequence114Or2g			
6	Sequence54Ob2g	Sequence16Osi2g	Sequence76Og2g		Sequence115Or2g		Sequence33Osi2g	
6	Sequence55Ob2g		Sequence77Og2g			Sequence98Ou2g		
6	Sequence56Ob2g	Sequence18Osi2g	Sequence78Og2g		Sequence117Or2g	Sequence99Ou2g	Sequence35Osi2g	
6	Sequence57Ob2g	Sequence19Osi2g	Sequence79Og2g	Sequence154Op2g	Sequence118Or2g	Sequence100Ou2g	Sequence36Osi2g	
6	Sequence58Ob2g	Sequence20Osi2g	Sequence80Og2g		Sequence119Or2g	Sequence101Ou2g	Sequence37Osi2g	
6	Sequence59Ob2g	Sequence21Osi2g	Sequence81Og2g	Sequence155Op2g	Sequence120Or2g	Sequence102Ou2g	Sequence38Osi2g	
5	Sequence60Ob2g		Sequence82Og2g	Sequence157Op2g	Sequence121Or2g	Sequence103Ou2g	Sequence39Osi2g	
5	Sequence61Ob2g		Sequence83Og2g					
5	Sequence62Ob2g		Sequence84Og2g	Sequence158Op2g	Sequence122Or2g	Sequence104Ou2g	Sequence40Osi2g	
5	Sequence63Ob2g		Sequence85Og2g	Sequence159Op2g	Sequence123Or2g	Sequence105Ou2g	Sequence41Osi2g	
5	Sequence64Ob2g		Sequence86Og2g	Sequence160Op2g	Sequence124Or2g	Sequence106Ou2g	Sequence42Osi2g	
2	Sequence65Ob2g		Sequence87Og2g	Sequence163Op2g				

Figure S36: Synteny block diagram for *MIR172D* with *Oryza barthii* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. Osi2- *Oryza sativa* homeolog i chr 2, Osi2- *Oryza sativa* homeolog ii chr 2, Ob2- *Oryza barthii* chr 2, Og2- *Oryza glaberrima* chr 2, Ou2- *Oryza glumaepatula* chr 2, Or2- *Oryza rufipogon* chr 2, Op2- *Oryza punctata* chr 2.

Duplication depth	Reference chromosome	Collinear blocks
4	Sequence65Og2g	Sequence44Ob2g
5	Sequence66Og2g	Sequence45Ob2g
5	Sequence67Og2g	Sequence46Ob2g
6	Sequence68Og2g	Sequence47Ob2g
6	Sequence69Og2g	Sequence48Ob2g
6	Sequence70Og2g	Sequence49Ob2g
6	Sequence71Og2g	Sequence50Ob2g
6	Sequence72Og2g	Sequence51Ob2g
6	Sequence73Og2g	Sequence52Ob2g
6	Sequence74Og2g	Sequence53Ob2g
6	Sequence75Og2g	Sequence54Ob2g
6	Sequence76Og2g	Sequence55Ob2g
6	Sequence77Og2g	Sequence56Ob2g
6	Sequence78Og2g	Sequence57Ob2g
6	Sequence79Og2g	Sequence58Ob2g
6	Sequence80Og2g	Sequence59Ob2g
6	Sequence81Og2g	Sequence60Ob2g
6	Sequence82Og2g	Sequence61Ob2g
5	Sequence83Og2g	Sequence62Ob2g
5	Sequence84Og2g	Sequence63Ob2g
5	Sequence85Og2g	Sequence64Ob2g
5	Sequence86Og2g	Sequence65Ob2g
3	Sequence87Og2g	Sequence66Ob2g
		Sequence3Osi2g
		Sequence4Osi2g
		Sequence107Or2g
		Sequence108Or2g
		Sequence143Op2g
		Sequence144Op2g
		Sequence88Ou2g
		Sequence70Si2g
		Sequence80Si2g
		Sequence109Or2g
		Sequence146Op2g
		Sequence149Op2g
		Sequence90Ou2g
		Sequence94Ou2g
		Sequence95Ou2g
		Sequence24Osi2g
		Sequence25Osi2g
		Sequence30Osi2g
		Sequence150Op2g
		Sequence151Op2g
		Sequence96Ou2g
		Sequence32Osi2g
		Sequence160Si2g
		Sequence115Or2g
		Sequence116Or2g
		Sequence117Or2g
		Sequence153Op2g
		Sequence98Ou2g
		Sequence99Ou2g
		Sequence33Osi2g
		Sequence34Osi2g
		Sequence35Osi2g
		Sequence190Si2g
		Sequence118Or2g
		Sequence154Op2g
		Sequence100Ou2g
		Sequence101Ou2g
		Sequence36Osi2g
		Sequence200Si2g
		Sequence119Or2g
		Sequence155Op2g
		Sequence102Ou2g
		Sequence37Osi2g
		Sequence220Si2g
		Sequence121Or2g
		Sequence156Op2g
		Sequence103Ou2g
		Sequence38Osi2g
		Sequence39Osi2g
		Sequence122Or2g
		Sequence158Op2g
		Sequence104Ou2g
		Sequence123Or2g
		Sequence159Op2g
		Sequence105Ou2g
		Sequence41Osi2g
		Sequence160Op2g
		Sequence106Ou2g
		Sequence42Osi2g
		Sequence124Or2g
		Sequence163Op2g

Figure S37: Synteny block diagram for *MIR172D* with *Oryza glaberrima* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Osi2- *Oryza sativa* homeolog i chr 2, Osi2- *Oryza sativa* homeolog ii chr 2, Ob2- *Oryza barthii* chr 2, Og2- *Oryza glaberrima* chr 2, Ou2- *Oryza glumaepatula* chr 2, Or2- *Oryza rufipogon* chr 2, Op2- *Oryza punctata* chr 2.

Duplication depth	Reference chromosome	Collinear blocks					
4	Sequence88Ou2g	Sequence66Og2g	Sequence108Or2g	Sequence4Osi2g	Sequence45Ob2g		
4	Sequence89Ou2g		Sequence109Or2g				
6	Sequence90Ou2g	Sequence68Og2g			Sequence47Ob2g	Sequence146Op2g	Sequence27Osi2g
6	Sequence91Ou2g						
6	Sequence92Ou2g		Sequence110Or2g	Sequence7Osi2g			
6	Sequence93Ou2g						
6	Sequence94Ou2g	Sequence69Og2g		Sequence11Osi2g	Sequence48Ob2g	Sequence149Op2g	Sequence28Osi2g
6	Sequence95Ou2g	Sequence70Og2g	Sequence111Or2g	Sequence13Osi2g	Sequence49Ob2g	Sequence150Op2g	Sequence30Osi2g
6	Sequence96Ou2g	Sequence74Og2g	Sequence113Or2g	Sequence15Osi2g	Sequence51Ob2g	Sequence151Op2g	Sequence32Osi2g
6	Sequence97Ou2g						
6	Sequence98Ou2g	Sequence77Og2g	Sequence116Or2g	Sequence17Osi2g	Sequence54Ob2g		Sequence34Osi2g
6	Sequence99Ou2g	Sequence78Og2g	Sequence117Or2g	Sequence18Osi2g	Sequence55Ob2g		Sequence35Osi2g
6	Sequence100Ou2g	Sequence79Og2g	Sequence118Or2g	Sequence19Osi2g	Sequence56Ob2g	Sequence154Op2g	Sequence36Osi2g
6	Sequence101Ou2g	Sequence80Og2g	Sequence119Or2g	Sequence20Osi2g	Sequence57Ob2g		Sequence37Osi2g
6	Sequence102Ou2g	Sequence81Og2g	Sequence120Or2g		Sequence58Ob2g	Sequence155Op2g	
6	Sequence103Ou2g	Sequence82Og2g	Sequence121Or2g	Sequence22Osi2g	Sequence59Ob2g	Sequence156Op2g	Sequence39Osi2g
5	Sequence104Ou2g	Sequence84Og2g	Sequence122Or2g		Sequence61Ob2g	Sequence158Op2g	Sequence40Osi2g
5	Sequence105Ou2g	Sequence85Og2g	Sequence123Or2g		Sequence62Ob2g	Sequence159Op2g	Sequence41Osi2g
4	Sequence106Ou2g	Sequence86Og2g	Sequence124Or2g		Sequence63Ob2g		Sequence42Osi2g

Figure S38: Synteny block diagram for *MIR172D* with *Oryza glumaepatula* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Osi2- *Oryza sativa* homeolog i chr 2, Osi2- *Oryza sativa* homeolog ii chr 2, Ob2- *Oryza barthii* chr 2, Og2- *Oryza glaberrima* chr 2, Ou2- *Oryza glumaepatula* chr 2, Or2- *Oryza rufipogon* chr 2, Op2- *Oryza punctata* chr 2.

Duplication depth	Reference chromosome	Collinear blocks						
4	Sequence107Or2g	Sequence65Og2g	Sequence3Osi2g	Sequence44Ob2g	Sequence143Op2g			
5	Sequence108Or2g	Sequence66Og2g	Sequence4Osi2g	Sequence45Ob2g	Sequence144Op2g	Sequence88Ou2g		
5	Sequence109Or2g	Sequence69Og2g				Sequence89Ou2g		
6	Sequence110Or2g		Sequence8Osi2g	Sequence47Ob2g	Sequence146Op2g	Sequence92Ou2g	Sequence25Osi2g	
6	Sequence111Or2g		Sequence13Osi2g	Sequence49Ob2g		Sequence95Ou2g	Sequence30Osi2g	
6	Sequence112Or2g							
6	Sequence113Or2g	Sequence74Og2g		Sequence51Ob2g	Sequence151Op2g	Sequence96Ou2g	Sequence32Osi2g	
6	Sequence114Or2g			Sequence52Ob2g				
6	Sequence115Or2g	Sequence76Og2g	Sequence16Osi2g	Sequence53Ob2g			Sequence33Osi2g	
6	Sequence116Or2g	Sequence77Og2g	Sequence17Osi2g		Sequence153Op2g	Sequence98Ou2g	Sequence34Osi2g	
6	Sequence117Or2g	Sequence78Og2g	Sequence18Osi2g	Sequence55Ob2g		Sequence99Ou2g	Sequence35Osi2g	
6	Sequence118Or2g	Sequence79Og2g	Sequence19Osi2g	Sequence56Ob2g	Sequence154Op2g	Sequence100Ou2g	Sequence36Osi2g	
6	Sequence119Or2g	Sequence80Og2g	Sequence20Osi2g	Sequence57Ob2g		Sequence101Ou2g	Sequence37Osi2g	
6	Sequence120Or2g	Sequence81Og2g	Sequence21Osi2g	Sequence58Ob2g	Sequence155Op2g	Sequence102Ou2g	Sequence38Osi2g	
6	Sequence121Or2g	Sequence82Og2g	Sequence22Osi2g	Sequence59Ob2g	Sequence156Op2g	Sequence103Ou2g	Sequence39Osi2g	
5	Sequence122Or2g	Sequence84Og2g		Sequence61Ob2g	Sequence158Op2g	Sequence104Ou2g	Sequence40Osi2g	
5	Sequence123Or2g	Sequence85Og2g		Sequence62Ob2g		Sequence105Ou2g	Sequence41Osi2g	
5	Sequence124Or2g	Sequence87Og2g		Sequence63Ob2g	Sequence163Op2g	Sequence106Ou2g	Sequence42Osi2g	

Figure S39: Synteny block diagram for *MIR172D* with *Oryza rufipogon* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Osi2- *Oryza sativa* homeolog i chr 2, Osi2- *Oryza sativa* homeolog ii chr 2, Ob2- *Oryza barthii* chr 2, Og2- *Oryza glaberrima* chr 2, Ou2- *Oryza glumaepatula* chr 2, Or2- *Oryza rufipogon* chr 2, Op2- *Oryza punctata* chr 2.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence125Oa2g	
0	Sequence126Oa2g	
0	Sequence127Oa2g	
0	Sequence128Oa2g	
0	Sequence129Oa2g	
0	Sequence130Oa2g	
0	Sequence131Oa2g	
0	Sequence132Oa2g	
0	Sequence133Oa2g	
0	Sequence134Oa2g	
0	Sequence135Oa2g	
0	Sequence136Oa2g	
0	Sequence137Oa2g	
0	Sequence138Oa2g	
0	Sequence139Oa2g	
0	Sequence140Oa2g	
0	Sequence141Oa2g	

Figure S40: Synteny block diagram for *MIR172D* with *Oryza brachyantha* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Oa2- *Oryza brachyantha* chr 2.

Duplication depth	Reference chromosome	Collinear blocks						
0	Sequence142Op2g							
4	Sequence143Op2g	Sequence3Osi2g	Sequence107Or2g	Sequence65Og2g	Sequence44Ob2g			
4	Sequence144Op2g	Sequence4Osi2g	Sequence108Or2g	Sequence66Og2g	Sequence45Ob2g			
4	Sequence145Op2g	Sequence5Osi2g						
6	Sequence146Op2g	Sequence7Osi2g	Sequence110Or2g	Sequence68Og2g	Sequence47Ob2g	Sequence24Osi2g	Sequence90Ou2g	
6	Sequence147Op2g							
6	Sequence148Op2g							
6	Sequence149Op2g			Sequence69Og2g	Sequence48Ob2g		Sequence94Ou2g	
6	Sequence150Op2g	Sequence13Osi2g		Sequence72Og2g	Sequence49Ob2g	Sequence30Osi2g	Sequence95Ou2g	
6	Sequence151Op2g		Sequence113Or2g	Sequence74Og2g	Sequence51Ob2g		Sequence96Ou2g	
6	Sequence152Op2g	Sequence15Osi2g			Sequence52Ob2g	Sequence32Osi2g		
6	Sequence153Op2g	Sequence17Osi2g	Sequence116Or2g	Sequence77Og2g		Sequence34Osi2g		
5	Sequence154Op2g		Sequence118Or2g	Sequence79Og2g	Sequence56Ob2g		Sequence100Ou2g	
5	Sequence155Op2g		Sequence120Or2g	Sequence81Og2g	Sequence58Ob2g		Sequence102Ou2g	
5	Sequence156Op2g		Sequence121Or2g	Sequence82Og2g		Sequence39Osi2g	Sequence103Ou2g	
5	Sequence157Op2g				Sequence59Ob2g			
5	Sequence158Op2g		Sequence122Or2g	Sequence84Og2g	Sequence61Ob2g	Sequence40Osi2g	Sequence104Ou2g	
5	Sequence159Op2g			Sequence85Og2g	Sequence62Ob2g	Sequence41Osi2g	Sequence105Ou2g	
4	Sequence160Op2g			Sequence86Og2g	Sequence63Ob2g	Sequence42Osi2g		
3	Sequence161Op2g							
3	Sequence162Op2g							
3	Sequence163Op2g		Sequence124Or2g	Sequence87Og2g	Sequence64Ob2g			

Figure S41: Synteny block diagram for *MIR172D* with *Oryza punctata* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Osi2- *Oryza sativa* homeolog i chr 2, Osi2- *Oryza sativa* homeolog ii chr 2, Ob2- *Oryza barthii* chr 2, Og2- *Oryza glaberrima* chr 2, Ou2- *Oryza glumaepatula* chr 2, Or2- *Oryza rufipogon* chr 2, Op2- *Oryza punctata* chr 2.

Duplication depth	Reference chromosome	Collinear blocks					
4	Sequence24Osi2g	Sequence146Op2g	Sequence7Osi2g	Sequence68Og2g	Sequence47Ob2g		
5	Sequence25Osi2g		Sequence8Osi2g	Sequence69Og2g	Sequence48Ob2g	Sequence110Or2g	
5	Sequence26Osi2g		Sequence9Osi2g				
6	Sequence27Osi2g		Sequence10Osi2g				Sequence90Ou2g
6	Sequence28Osi2g		Sequence11Osi2g				Sequence94Ou2g
6	Sequence29Osi2g		Sequence12Osi2g				
6	Sequence30Osi2g	Sequence150Op2g	Sequence13Osi2g	Sequence70Og2g	Sequence49Ob2g	Sequence111Or2g	Sequence95Ou2g
6	Sequence31Osi2g		Sequence14Osi2g				
6	Sequence32Osi2g	Sequence152Op2g	Sequence15Osi2g	Sequence74Og2g	Sequence51Ob2g	Sequence113Or2g	Sequence96Ou2g
6	Sequence33Osi2g		Sequence16Osi2g	Sequence76Og2g	Sequence53Ob2g	Sequence115Or2g	
6	Sequence34Osi2g	Sequence153Op2g	Sequence17Osi2g	Sequence77Og2g		Sequence116Or2g	Sequence98Ou2g
6	Sequence35Osi2g		Sequence18Osi2g	Sequence78Og2g	Sequence55Ob2g	Sequence117Or2g	Sequence99Ou2g
6	Sequence36Osi2g		Sequence19Osi2g	Sequence79Og2g	Sequence56Ob2g	Sequence118Or2g	Sequence100Ou2g
6	Sequence37Osi2g		Sequence20Osi2g	Sequence80Og2g	Sequence57Ob2g	Sequence119Or2g	Sequence101Ou2g
6	Sequence38Osi2g		Sequence21Osi2g	Sequence81Og2g	Sequence58Ob2g	Sequence120Or2g	
6	Sequence39Osi2g	Sequence156Op2g	Sequence22Osi2g	Sequence82Og2g	Sequence59Ob2g	Sequence121Or2g	Sequence103Ou2g
5	Sequence40Osi2g	Sequence158Op2g			Sequence61Ob2g	Sequence122Or2g	Sequence104Ou2g
5	Sequence41Osi2g	Sequence159Op2g		Sequence85Og2g	Sequence62Ob2g	Sequence123Or2g	Sequence105Ou2g
5	Sequence42Osi2g	Sequence160Op2g		Sequence86Og2g	Sequence63Ob2g	Sequence124Or2g	Sequence106Ou2g

Figure S42: Synteny block diagram for *MIR172D* with *Oryza sativa* (ii) as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Osi2- *Oryza sativa* homeolog i chr 2, Osi2- *Oryza sativa* homeolog ii chr 2, Ob2- *Oryza barthii* chr 2, Og2- *Oryza glaberrima* chr 2, Ou2- *Oryza glumaepatula* chr 2, Or2- *Oryza rufipogon* chr 2, Op2- *Oryza punctata* chr 2.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence164Sb2g	
0	Sequence165Sb2g	
0	Sequence166Sb2g	
0	Sequence167Sb2g	
0	Sequence168Sb2g	
0	Sequence169Sb2g	
0	Sequence170Sb2g	
0	Sequence171Sb2g	
0	Sequence172Sb2g	
0	Sequence173Sb2g	
0	Sequence174Sb2g	
0	Sequence175Sb2g	
0	Sequence176Sb2g	
0	Sequence177Sb2g	
0	Sequence178Sb2g	
0	Sequence179Sb2g	
0	Sequence180Sb2g	
0	Sequence181Sb2g	
0	Sequence182Sb2g	
0	Sequence183Sb2g	
0	Sequence184Sb2g	
0	Sequence185Sb2g	
0	Sequence186Sb2g	
0	Sequence187Sb2g	
0	Sequence188Sb2g	
0	Sequence189Sb2g	
0	Sequence190Sb2g	

Figure S43: Synteny block diagram for *MIR172D* with *Sorghum bicolor* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by ‘||’ in the multi-alignment of gene orders. Sb2 - *Sorghum bicolor* chr 2.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence191Zm6g	
0	Sequence192Zm6g	
0	Sequence193Zm6g	
0	Sequence194Zm6g	
0	Sequence195Zm6g	
0	Sequence196Zm6g	
0	Sequence197Zm6g	
0	Sequence198Zm6g	
0	Sequence199Zm6g	
0	Sequence200Zm6g	
0	Sequence201Zm6g	
0	Sequence202Zm6g	
0	Sequence203Zm6g	
0	Sequence204Zm6g	
0	Sequence205Zm6g	
0	Sequence206Zm6g	
0	Sequence207Zm6g	
0	Sequence208Zm6g	
0	Sequence209Zm6g	

Figure S44: Synteny block diagram for *MIR172D* with *Zea mays* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. Zm6 - *Zea mays* chr 6.

Duplication depth	Reference chromosome	Collinear blocks
0	Sequence210At3g	
0	Sequence211At3g	
0	Sequence212At3g	
0	Sequence213At3g	
0	Sequence214At3g	
0	Sequence215At3g	
0	Sequence216At3g	
0	Sequence217At3g	
0	Sequence218At3g	
0	Sequence219At3g	
0	Sequence220At3g	
0	Sequence221At3g	
0	Sequence222At3g	
0	Sequence223At3g	
0	Sequence224At3g	
0	Sequence225At3g	
0	Sequence226At3g	
0	Sequence227At3g	
0	Sequence228At3g	
0	Sequence229At3g	
0	Sequence230At3g	
0	Sequence231At3g	
0	Sequence232At3g	
0	Sequence233At3g	
0	Sequence234At3g	
0	Sequence235At3g	

Figure S45: Synteny block diagram for *MIR172D* with *Arabidopsis thaliana* as reference. The first column shows duplication depth at each gene locus, second column shows the genes in reference chromosomes and the following is aligned collinear blocks where only match genes are displayed. The alignment among non-anchor genes is discarded in the output and denoted by '||' in the multi-alignment of gene orders. At3 - *Arabidopsis thaliana* chr 3.