

Table S1: R-genes conservation in plants. For each species investigated (lines), the number of annotated genes and super-R-genes as well as the number and percentage of orthologs (using as reference genomes rice for monocots and grape for eudicots) are indicated in columns. Fisher's Exact tests for the significant conservation of super-R-genes compared to the total number of annotated genes are provided in the last column (right).

Species	All genes		Resistance genes		P-value
	Genes #	Orth #	R-genes #	Orth #	
Sorghum	34008	6147	1717	413	2.52E-05
Maize	32540	4454	1867	319	5.23E-04
<i>Brachypodium</i>	25504	8533	1662	495	2.73E-02
□	□	□	□	□	□
<i>Arabidopsis</i>	33198	2389	1559	74	3.54E-04
Populus	30260	4555	1297	122	2.68E-07
Papaya	19205	3199	703	101	1.81E-01
Soybean	46164	4013	3310	148	2.08E-17
Apple	58979	3498	4252	125	4.49E-17
Lotus	15470	1720	668	46	1.32E-03
Strawberry	34809	3289	1452	108	1.85E-02
Cacao	27814	4472	1439	149	1.47E-07

Table S2: R-genes domains/family diversity in plants. The numbers of different R-domain (lines) combinations are provided for each species (monocots and eudicots) investigated (columns) as well as for the R gene families structured into: ¹PRR/PTI (LRR-RLK, LRR, LysM, and LysM kinase, in blue), ²ETI (NBS-LRR, in red), ³other 'R-combination' (gene including NBS domain alone without LRR domains and RGA genes, in green), ⁴and 'R-pathway' (WRKYs, protein-kinases, in purple).

DOMAINS	Monocots				Eudicots									
	Oryza sativa	Brachypodium distachyon	Sorghum bicolor	Zea mays	Vitis vinifera	Arabidopsis thaliana	Carica papaya	Fragaria vesca	Glycine max	Lotus japonicus	Malus domestica	Populus trichocarpa	Theobromacacao	
LRR ¹	328	173	125	299	151	145	82	246	351	85	732	126	225	
LRR-Pkinase ¹	315	163	211	211	116	156	91	145	381	62	331	190	174	
LRR-Pkinase-Ser/Thr Kinase ¹	9	□	3	□	□	3	□	□	8	□	□	□	□	
TIR-LRR-Pkinase ¹	□	□	□	□	□	□	□	1	□	□	□	□	□	
TIR-LRR ¹	□	□	□	1	□	□	□	24	□	1	4	□	□	
TIR-LRR-WRKY ¹	□	□	□	□	□	□	□	3	□	□	□	□	□	
LRR-WRKY ¹	□	□	□	□	□	□	□	□	□	□	□	□	2	
LysM ¹	14	11	14	□	7	9	9	3	31	□	9	16	3	
LysM-Pkinase ¹	2	□	6	2	3	3	2	□	18	□	□	8	1	
NBS-LRR ²	235	98	176	45	121	53	19	52	215	9	420	76	86	
NBS-LRR-Pkinase ²	□	1	□	□	□	□	□	1	□	□	3	□	□	
TIR-NBS-LRR-Pkinase ²	□	□	□	□	1	□	□	□	□	□	2	□	□	
NBS-LRR-Pkinase-WRKY ²	□	□	1	□	□	1	□	□	□	□	□	□	□	
TIR-NBS-LRR ²	2	□	□	2	32	78	8	11	142	8	145	21	5	
NBS-LRR-WRKY ²	□	□	□	□	□	□	□	□	□	□	1	□	□	
NBS ³	298	100	105	91	65	19	23	75	50	43	224	23	122	
NBS-WRKY ³	□	□	1	□	□	1	□	□	□	□	□	□	□	
NBS-Pkinase ³	1	□	1	1	□	□	□	□	□	□	1	□	2	
TIR-NBS-Pkinase ³	□	□	□	□	□	□	□	□	□	□	1	□	□	
TIR-NBS ³	3	□	□	1	10	16	□	15	4	17	63	2	5	
TIR-Pkinase ³	□	□	□	□	□	□	□	3	□	□	1	□	□	
RG ³	102	104	39	45	91	126	□	□	146	5	117	32	□	
TIR ³	5	2	2	9	7	31	5	91	20	23	124	8	4	
Pkinase ⁴	1018	930	872	1041	437	847	422	733	1603	381	1952	732	757	
Pkinase-Ser/Thr Kinase ⁴	205	□	65	□	□	□	□	□	162	□	□	□	□	
Pkinase-WRKY ⁴	1	□	□	□	□	□	□	1	□	□	1	□	□	
WRKY ⁴	99	80	96	106	37	71	42	48	179	34	121	63	53	
Total	2637	1662	1717	1854	1078	1559	703	1452	3310	668	4252	1297	1439	

Table S3: Number of R-genes in the ancestral duplicated chromosomes in grasses. The table provides the number of R genes and associated P-values (calculated by the permutation test method, see the material and methods) for the n=5/12 paleoancestor (AGK), rice (OS) Brachypodium (BD), sorghum (SB) and maize (ZM) genomes.

	N=5 AGK	N=12 AGK	<i>P-value</i>	OS	<i>P-value</i>	BD	<i>P-value</i>	SB	<i>P-value</i>	ZM	<i>P-value</i>
A1	108	72	8.09E-06	38	8.85E-03	32	3.54E-03	40	8.48E-03	49	6.85E-04
A5		40		21		14		23		25	
A8	46	25	5.38E-01	16	3.81E-01	11	6.14E-01	17	3.70E-02	16	2.66E-01
A9		22		12		9		8		19	
A11	70	39	4.85E-01	21	1.14E+00	12	7.55E-02	19	5.41E-01	18	1.78E-01
A12		43		22		5		16		23	
A2	85	46	4.41E-01	22	1.31E+00	13	9.18E-02	29	2.33E-01	29	4.13E-01
A6		41		24		20		22		24	
A2	47	13	4.00E-06	8	1.78E-05	8	4.57E-02	8	1.98E-02	9	4.06E-03
A4		36		27		15		17		21	
A3	32	18	4.75E-01	17	5.31E-03	10	3.38E-01	10	3.85E-01	12	2.33E-01
A10		15		8		7		7		8	
A3	77	44	2.02E-01	26	9.78E-01	21	3.04E-01	26	4.94E-01	25	4.25E-01
A7		36		26		24		22		26	

Table S4: Number of R-genes in the recent duplicated maize chromosomes. The table provides the number of R genes and associated *P-values* (calculated by the permutation test method, see the material and methods) for the maize duplicated regions deriving from the n=12 paleoancestor (AGK).

AGK (<i>n</i> = 12) Chromosomes	Maize Chromosome	Maize R genes #	AGK (<i>n</i> = 12) R-genes #	Permutation <i>P-value</i>
A1	m3	40	49	1.34E-05
	m8	18		
A5	m6	16	25	2.70E-01
	m8	12		
A8	m1	14	16	6.99E-03
	m4	6		
A9	m7	17	19	1.10E-02
	m2	10		
A11	m4	13	18	5.05E-02
	m2	7		
A12	m3	16	23	7.46E-02
	m10	7		
	m1	3		
A2	m5	22	29	2.55E-03
	m4	10		
A6	m9	16	24	1.61E-07
	m5	6		
	m6	4		
A2	m4	6	9	6.25E-01
	m5	5		
A4	m2	15	21	3.39E-01
	m10	12		
A3	m1	9	12	4.70E-02
	m9	4		
A10	m1	2	8	1.21E-02
	m5	7		
A3	m1	18	25	2.42E-02
	m5	5		
	m9	5		
A7	m2	8	26	1.02E-05
	m7	24		

Table S5: Number of R-genes clusters in ancient duplicated grass chromosomes. The table provides for n=12 ancestral chromosomes (Chromosomes A1 to A12 in lines) the number of R genes (GN #, number of genes) and clusters (CLS #, number of clusters) observed in the paleoancestor (AGK), rice (OS) *Brachypodium* (BD), sorghum (SB) and maize (ZM) genomes.

Chr	AGK	GN #	CLS #	OS	GN #	CLS #	BD	GN #	CLS #	SB	GN #	CLS #	ZM	GN #	CLS #
A1	72	24	10	38	6	3	32	8	4	40	14	7	49	11	4
A5	40	16	5	21	4	2	14	6	3	23	11	3	25	8	3
A8	25	10	3	16	4	2	11	0	0	17	5	2	16	2	1
A9	22	13	5	12	4	2	9	6	3	8	4	2	19	6	3
A11	39	12	5	21	2	1	12	4	2	19	6	3	18	7	3
A12	43	13	6	22	4	2	5	2	1	16	6	3	23	6	3
A2	46	25	10	22	8	3	13	12	6	29	20	8	29	8	4
A6	41	12	4	24	4	2	20	5	2	22	9	4	24	8	4
A2	13	0	0	8	0	0	8	0	0	8	0	0	9	0	0
A4	36	7	3	27	2	1	15	3	1	17	0	0	21	4	2
A3	18	6	3	17	4	2	10	2	1	10	4	2	12	2	1
A10	15	8	4	8	2	1	7	2	1	7	2	1	8	6	3
A3	44	13	5	26	4	2	21	7	3	26	8	4	25	0	0
A7	36	14	6	26	2	1	24	10	5	22	6	3	26	8	4

Table S6: Number of R-genes clusters in recent duplicated maize chromosomes. The table provides for n=12 ancestral chromosomes (Chromosomes A1 to A12 in lines) the number of R-genes (GN #, number of genes), R-genes in cluster (GNC #, number of genes in clusters) and clusters (CLS #, number of clusters) observed in maize (ZM) duplicated chromosomes genomes.

AGK	chromosome	GN #	GNC #	CLS #
A1	m3	40	14	7
	m8	18	3	3
A5	m6	16	6	3
	m8	12	5	3
A8	m1	14	3	2
	m4	6	0	0
A9	m7	17	2	1
	m2	10	2	1
A11	m4	13	10	5
	m2	7	4	4
A12	m3	16	9	6
	m10	7	7	6
	m1	3		
A2	m5	22	9	6
	m4	10	3	2
A6	m9	16	15	10
	m5	6		
	m6	4	0	0
A2	m4	6	1	1
	m5	5	0	0
A4	m2	15	3	2
	m10	12	4	3
A3	m1	9	2	1
	m9	4	2	1
A10	m1	2	0	0
	m5	7	6	3
A3	m1	18	5	4
	m5	5	1	1
	m9	5		
A7	m2	8	2	2
	m7	24	12	8

Table S7: R-genes clusters distribution in plants. OS, BD, SB, ZM, VV, TC, CP, FV, MD, PT, LJ, AT, and GM represent Rice, *Brachypodium*, Sorghum, Maize, Grape, Cacao, Papaya, Strawberry, Poplar, Lotus, *Arabidopsis*, and Soybean, respectively (columns). The number of clusters (Cluster #), the number of super-R-gene in clusters (super-R-gene clusters #), the total number of super-R-genes (Total super-R-genes #) and percentages are provided in lines. R-genes in cluster here also are divided into four categories including PTI, ETI, ‘R-combination’, and ‘R-pathway’.

	OS	BD	SB	ZM	VV	AT	PT	CP	GM	MD	LJ	FV	TC
Cluster #	486	366	374	405	179	328	172	142	665	857	137	292	255
# R-gene in clusters #	1951	1214	1160	1139	776	1062	417	396	2397	3464	377	886	1011
# PTI in clusters	486	231	240	301	208	196	105	98	543	890	88	272	299
# ETI in clusters	205	77	144	36	146	117	42	24	317	500	12	38	77
# R-combination in clusters	333	179	126	98	126	55	20	26	168	446	64	117	121
# R-pathway in clusters	927	727	650	704	296	694	250	248	1369	1629	213	460	514
Total R-genes #	2637	1717	1867	1662	1078	1559	1297	703	3310	4252	668	1452	1439
Percentage (%)	73.99	70.70	62.13	68.53	71.99	68.12	32.15	56.33	72.42	81.47	56.44	61.02	70.26

Table S8: R-genes duplication frequency in maize. **A**-The number of R-genes in singletons and clusters (columns) are indicated in lines for rice (OS), *Brachypodium* (BD), sorghum (SB), maize (ZM) characterized in R-loci, R-loci with Single R-gene duplication (corresponding to single-gene or small-scale duplication SSD), Single R-gene duplication Hotspots (where one R-loci region can be duplicated in other loci at least two times), % R-loci with single R-gene duplication (corresponding to the frequency of single R-gene duplication loci vs total R-loci), % Single R-gene duplication hotspots (corresponding to the frequency of hotspot loci vs total number single R-gene duplication loci) shown in lines. **B**-The relationship among the singleton R-locus, clustered R-locus, and hotspot R-locus was illustrated in the paleo-duplicated blocks mediated by whole genome duplication and transposed duplication events among the ancestral WGD chromosome pairs (R1 & R5) and non-paralogous chromosomes (R7). Blue, purple, and red rectangles represent genes, R-genes and duplicated genes respectively.

A

	OS (Singletons+Clusters)	BD (Singletons+Clusters)	SB (Singletons+Clusters)	ZM (Singletons+Clusters)
R-loci	1173 (687+486)	815 (449+366)	931 (557+374)	1134 (729+405)
R-loci with Single R-gene duplication	153	74	115	404
Single R-gene duplication Hotspots	36	28	36	209
% R-loci with single R-gene duplication	13.04	9.08	12.35	35.63
% Single R-gene duplication hotspots	23.53	37.84	31.3	51.73

B

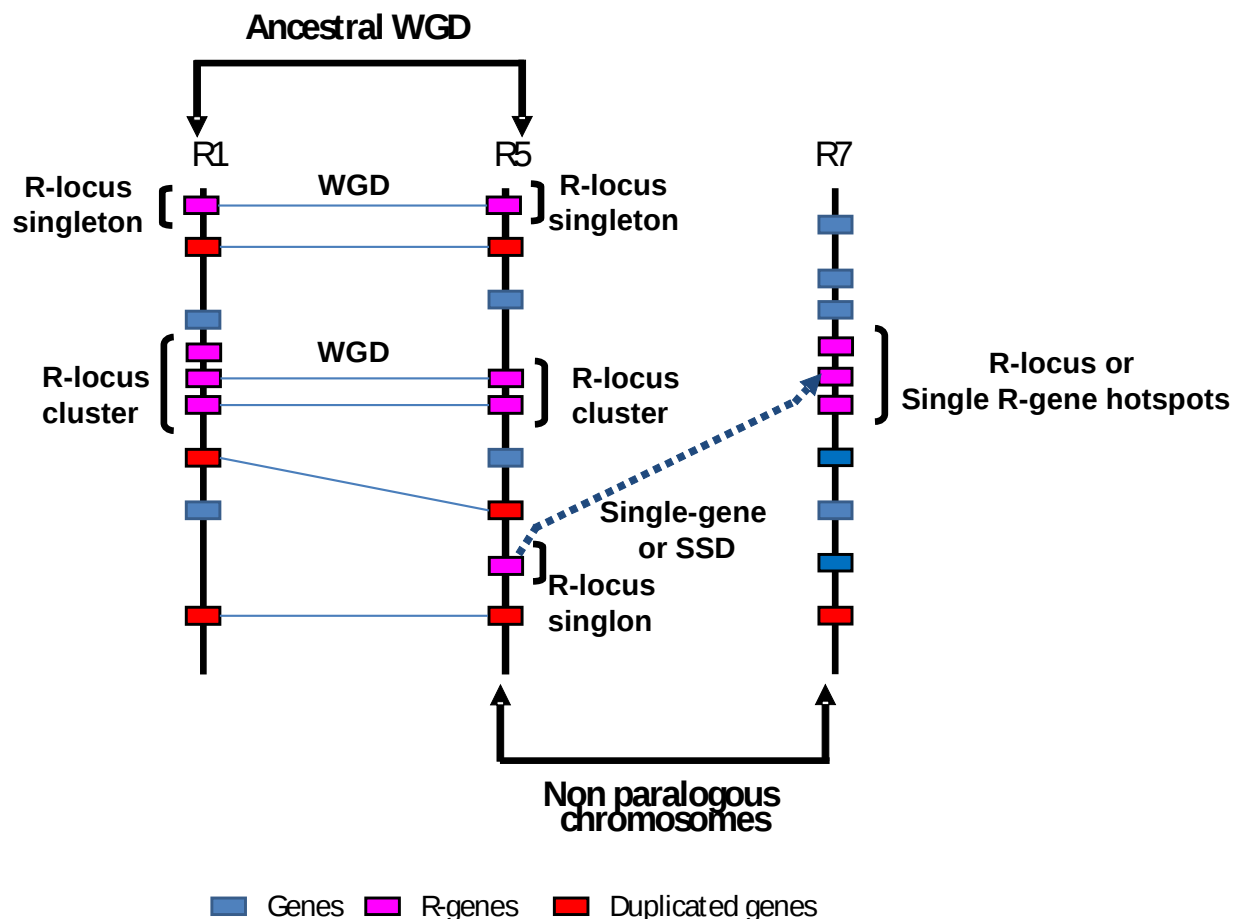


Table S9: R-genes duplication frequency in maize compared to other grasses The number of R-loci (singletons + clusters one cluster considered as one loci independently from the number of R-genes detected); Single R-gene duplication (number of non ortholog duplicated R-loci), % Single R-gene duplication % (Single R-gene duplication percentage) are provided in columns for rice (OS), *Brachypodium* (BD), sorghum (SB), maize (ZM). *P-values* (Fisher's Exact Test) are provided as last column for the comparison of ZM/OS, ZM/BD and ZM/SB.

Species	R-loci	Single R-gene duplication	% Single R-gene duplication	Fisher's Exact Test
ZM	1134	404	35.63	6.32E-24
OS	1173	153	13.04	
ZM	1134	404	35.63	2.28E-29
BD	815	74	9.08	
ZM	1134	404	35.63	1.71E-22
SB	931	115	12.35	

Table S10: R-genes targeted by miRNAs in plants. OS, BD, SB, ZM, VV, TC, CP, FV, MD, PT, LJ, AT, and GM represent Rice, *Brachypodium*, Sorghum, Maize, Grape, Cacao, Papaya, Strawberry, Poplar, Lotus, *Arabidopsis*, and Soybean, respectively; ¹Number of R-genes can be targeted by miRNAs; ²Percentage of resistant genes can be targeted by miRNAs; ³randomly selected 600 non-resistant genes ten times. ⁴Paired student t-test was performed on the percentage of genes targeted by miRNAs observed to the total R-gene vs non-R-genes.

Species	Total_R-genes			NON_R-genes ³		
	targets ¹	R-genes	% ²	targets ¹	R-genes	% ²
OS	949	2637	35.99	676	6000	11.27
BD	476	1662	28.64	742	6000	12.37
SB	647	1717	37.68	662	6000	11.03
ZM	554	1867	29.67	676	6000	11.27
Average	656.50	1970.75	33.31	689	6000	11.48
VV	154	1078	14.29	892	6000	14.87
TC	631	1439	43.85	580	6000	9.67
CP	139	703	19.77	773	6000	12.88
FV	314	1452	21.63	1011	6000	16.85
MD	1565	4252	36.81	163	6000	2.72
PT	448	1297	34.54	420	6000	7
LJ	242	668	36.23	210	6000	3.5
AT	737	1559	47.27	799	6000	13.32
GM	1380	3310	41.69	2203	6000	36.72
Average	623.33	1750.89	35.60	783.44	6000	13.06

$${}^4P = 7.34E-06$$

Table S11: R-domains targeted by miRNAs in eudicots. Number and percentages of NBS, LRR, TIR, WRKY and Pkinase domains (columns) are provided for the nine eudicots species investigated. T-test (paired student t-test) was performed between the percentage of domain vs total R-gene regulated by miRNAs for NBS and LRR, TIR and LRR, LRR and WRKY, and LRR and Pkinase.

Species	NBS	% NBS regulated by miRNA	TIR	% TIR regulated by miRNA	LRR	% LRR regulated by miRNA	WRKY	% WRKY regulated by miRNA	Pkinase	% Pkinase regulated by miRNA
VV	229	25.76	50	24	421	19.24	37	5.41	557	12.03
AT	168	70.24	125	64	436	58.26	73	36.99	1010	46.93
PT	122	63.11	31	58.06	413	44.79	63	31.75	930	32.15
CP	50	32	13	23.08	200	19	42	14.29	515	18.64
GM	411	73.72	166	84.94	1097	54.79	179	34.64	2172	37.66
MD	860	70.58	340	71.76	1638	47.01	123	19.51	2292	28.1
LJ	77	74.03	49	71.43	165	40.61	34	23.53	443	31.38
FV	154	17.53	148	16.89	483	20.5	52	23.08	884	23.53
TC	220	81.36	14	71.43	492	50.2	55	32.73	934	37.58
Average	254.56	56.48	104.00	53.95	593.89	39.38	73.11	24.66	1081.89	29.78

$P = 2.17E-03$

$P = 8.04E-03$

$P = 1.21E-03$

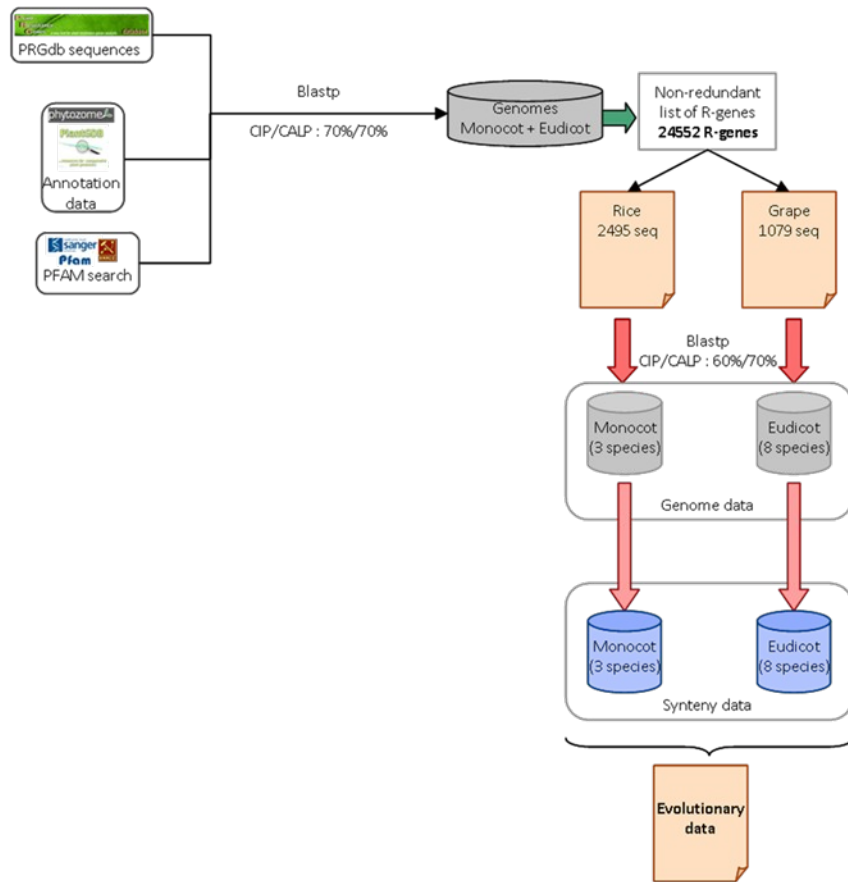
$P = 3.97E-03$

Table S12: R-genes cluster loci targeted by miRNAs in plants. Cluster-loci, if several R-genes (at least two) are clustered distributing on the chromosome, this clustered location as one cluster loci; Cluster miRNA, At least one R-gene in Cluster loci can be targeted by miRNAs; %cluster-miRNA, percentage of cluster-loci regulated by miRNAs in the total cluster loci.

	Species	Cluster-loci #	Cluster-miRNA #	Cluster-miRNA %	Non-cluster #	Non-cluster-miRNA #	Non-cluster-miRNA %	<i>P</i> -value (Fisher's Exact Test)
Eudicots	<i>Arabidopsis</i>	139	119	85.61	398	218	54.77	3.74E-03
	Cacao	110	89	80.91	229	99	43.23	7.45E-06
	Soybean	292	227	77.74	650	250	38.46	1.19E-09
	Poplar	63	48	76.19	424	173	40.8	3.68E-03
	Apple	460	327	71.09	550	240	43.64	3.85E-06
	Lotus	47	33	70.21	537	177	32.96	2.98E-03
	Papaya	48	26	54.17	150	22	14.67	9.75E-05
	Stawberry	128	57	44.53	340	59	17.35	1.17E-05
	Grape	102	44	43.14	195	22	11.28	1.80E-06
Monocots	Rice	231	173	74.89	436	183	41.97	1.68E-05
	Sorghum	159	109	68.55	485	216	44.54	4.82E-03
	Maize	31	18	58.06	769	233	30.3	4.91E-02
	<i>Brachypodium</i>	132	69	52.27	315	96	30.48	4.89E-03

Figure S1: R-genes and miRNA detection pipelines. (A) Method for R-genes characterization and mapping in plant genomes. **(B)** miRNAs target prediction for R-genes in plants. Calculation of CIP/CALP was performed according to Salse 2012 . miRNA targets were predicted using Targetfinder software (see method section).

A



B

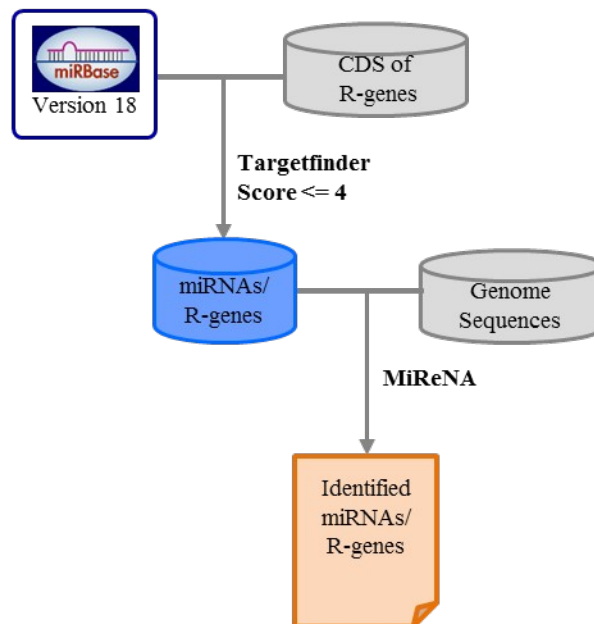


Figure S2: R-domains distribution in plant genomes. Three results of different methods in detecting R-gens including Annotation (Annot), Plant Resistance Gene database (PRGDB), and PFAM domain (Pfam) are as shown as colored bars. NR, total non-redundant R-genes content in integrating the three methods, LRR, NBS, TIR, LysM, RG contents are highlighted with the color code legend at the bottom of the figure.

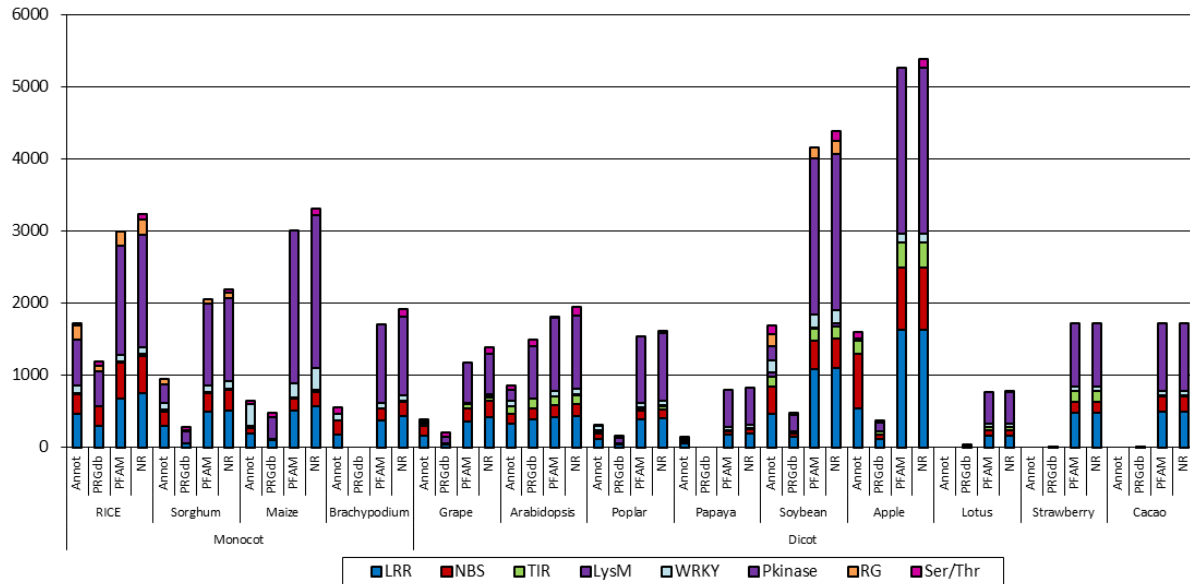


Figure S3: R-genes family distribution in plant genomes. The color code illustrates the R-gene families PTI/ETI/R-combination/R-pathway characterized for the from 13 plant genomes including monocots (rice, *Brachypodium*, sorghum, and maize) and eudicots (*Arabidopsis*, Grape, Cacao, Papaya, Strawberry, Poplar, Lotus, Apple, and Soybean).

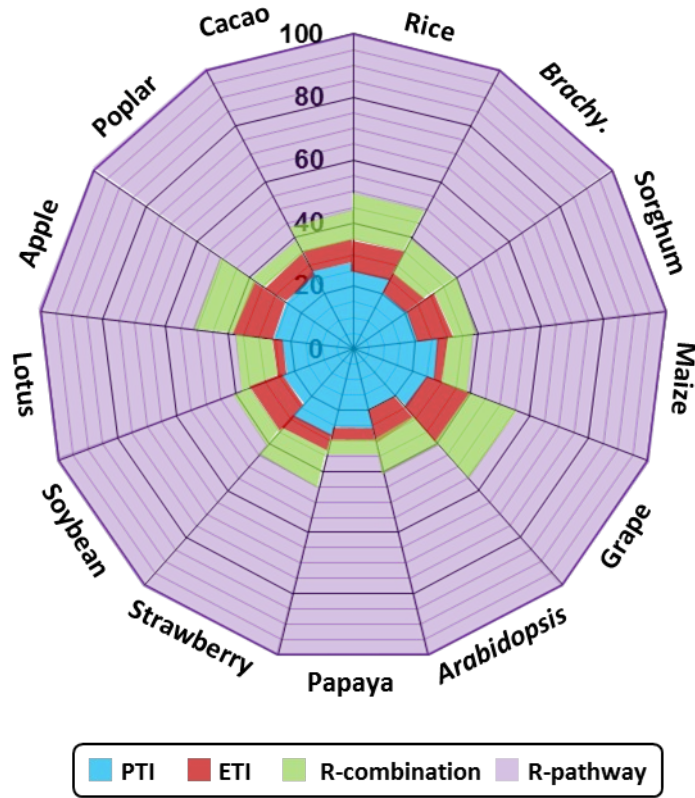


Figure S4: R-genes paleohistorical evolution in eudicots. The modern genome structures of eudicots are depicted with a seven color code that illuminate their relationships with $n = 7$ AGK (top) in respectively. The percentages of resistant domains (reference as color code legend at the bottom) are shown with circular distributions for the nine eudicot genomes (bottom) investigated.

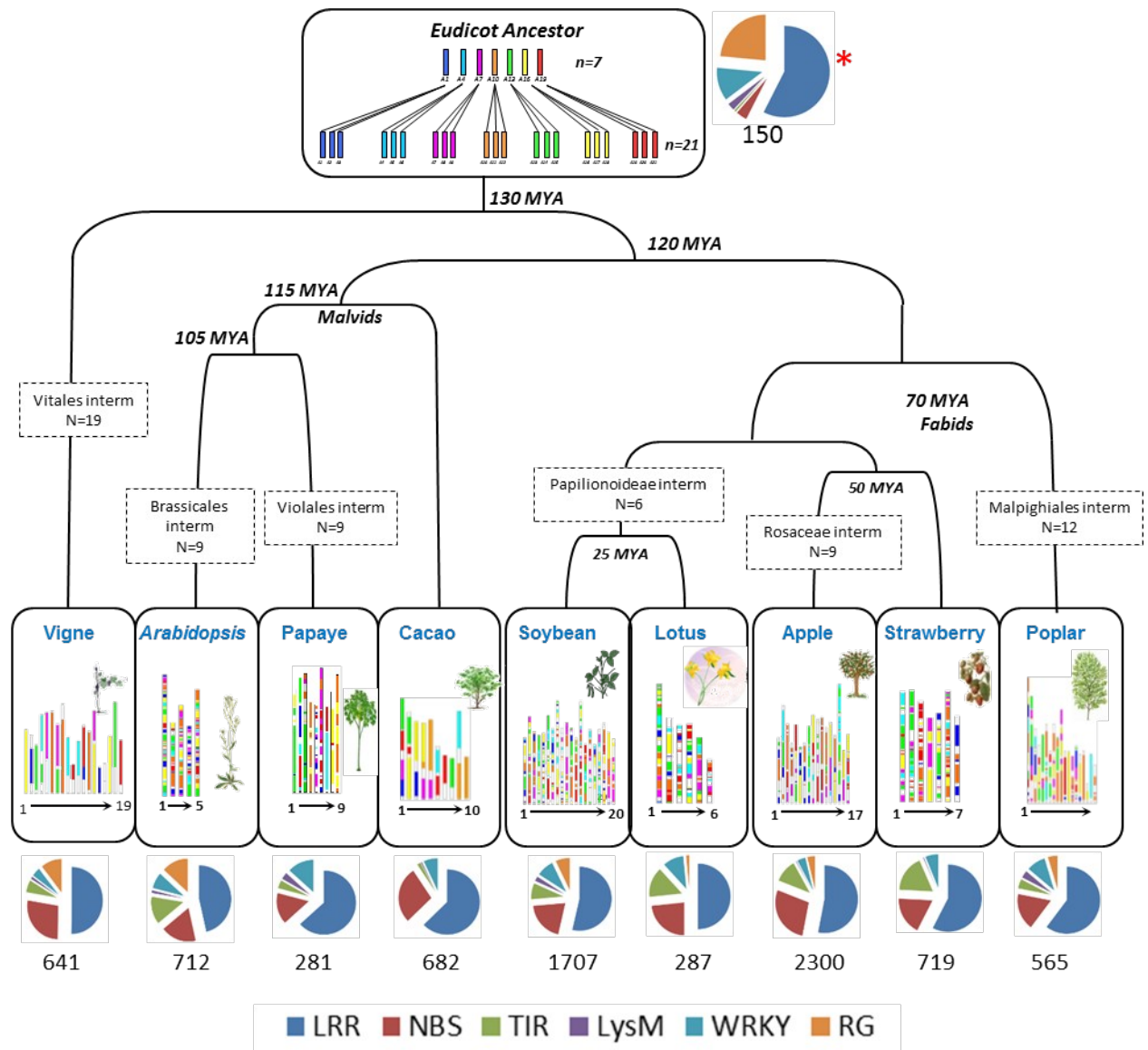


Figure S5: Evolutionary scenario of R-gene families in monocots. The modern grass genome structures (bottom) are depicted with a five-color code that illuminates their relationship with the $n = 5$ (A5, A7, A11, A8, A4) and $n=12$ (A1 to A12) ancestors (top), according to Murat et al. . The characterized R-genes are illustrated as vertical bars on the chromosomes of modern and ancestral genomes. The percentages of R-gene classes (LRR, NBS, TIR, LysM, RG, highlighted with the color code legend at the bottom) are shown with circular distributions for the four monocot genomes (bottom), the rice/*Brachypodium* and sorghum/maize ancestral genome intermediates (center), as well as for the ancestral genomes (top). Statistically enriched and impoverished R-gene families (PTI/ETI/R-combination/R-pathway depicted with a four-color code) are illustrated with red and blue stars on the circular distributions, respectively.

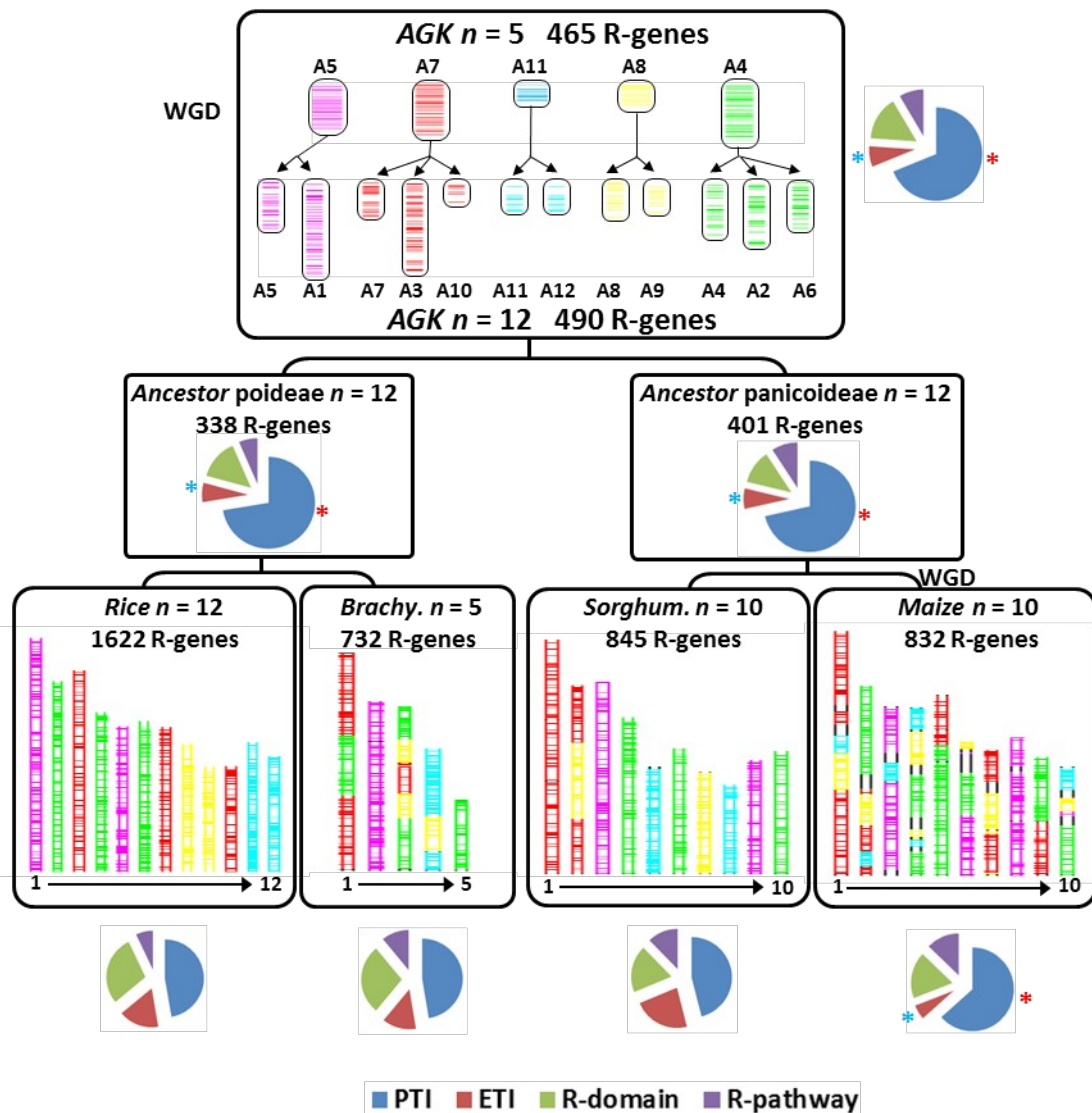


Figure S6: R-genes distribution and content in clusters. The X-axis represents gene number of R-genes in clusters; the Y-axis represents the percentage of observed clusters with OS for rice BD for *Brachypodium*, SB for sorghum and ZM for maize.

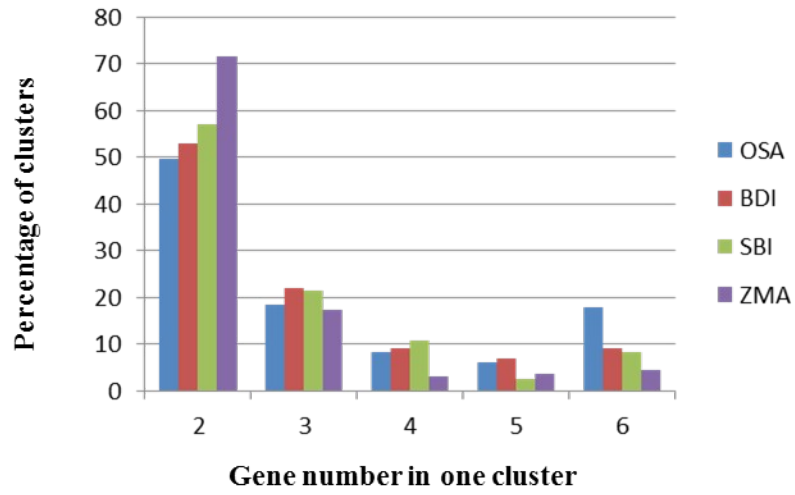


Figure S7: R-domains combination in clusters. (A) Illustration of the different domain (color code) combinations observed in the characterized R-gene clusters. (B) Domain distribution in the combined R-genes. Y axis represents the percentage of domains and X axis represents the different domains. (C) Using LRR domain as a reference, the distribution of the other domains combined with LRR are shown for O, B, S, Z, V, A, C, F, G, L, M, P, T representing rice, *Brachypodium*, Sorghum, Maize, Grape, *Arabidopsis*, Papaya, Strawberry, Soybean, Lotus, Apple, Poplar and Cacao respectively.

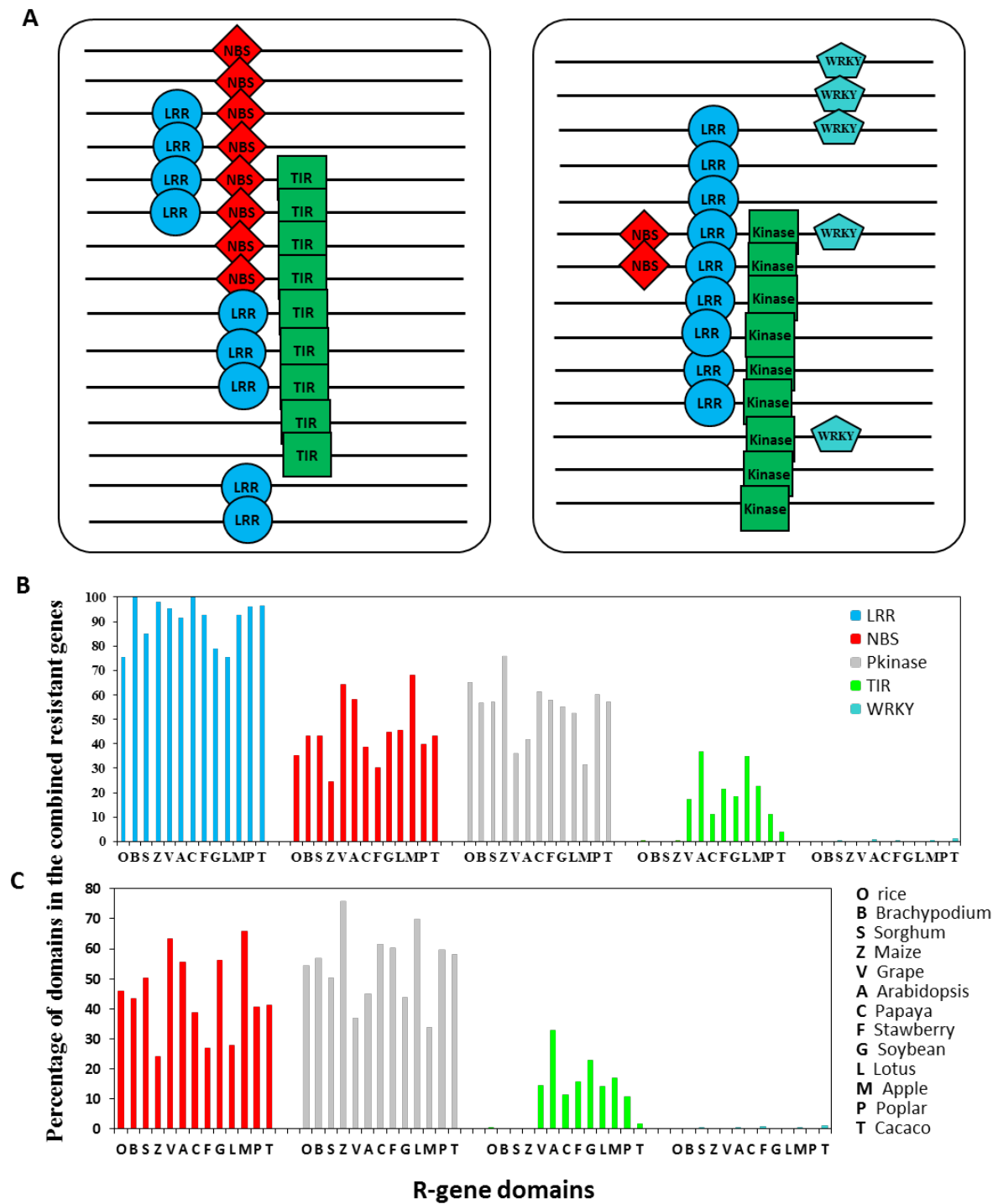
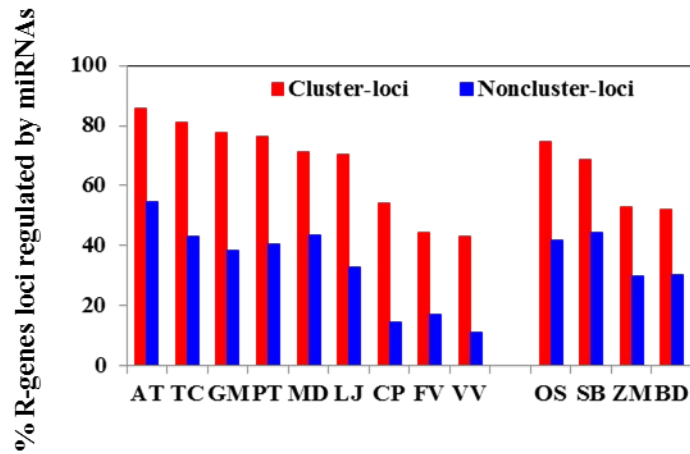


Figure S8: R-genes clusters targeted by miRNAs in plants. X-axis represents the investigated species including eudicots (*Arabidopsis*/AT, Cacao/TC, Soybean/GM, Poplar/PT, Apple/MD, Lotus/LJ, Papaya/CP, Strawberry/FV, and grape/VV), and monocots (Rice/OS, Sorghum/SB, Maize/ZM, and *Brachypodium*/BD); Y-axis represents the percentage of R-genes loci regulated by miRNAs (either cluster or non cluster).



Eudicots: AT, *Arabidopsis*; TC, Cacao; GM, Soybean; PT, Poplar; MD, Apple; LJ, Lotus; CP, Papaya; FV, Strawberry; VV, grape/VV,

Monocots: OS, Rice; SB, Sorghum; ZM, Maize; BD, *Brachypodium*