

Table 1 Suppl. Identification of miRNAs in two soybean genotypes.

Representative sequences	Annotation	gma (miRBase)	BX10-AI-normalized	BX10+AI-normalized	BD2-AI-normalized	BD2+AI-normalized
TCTCGGACCAGGCTTCATTCC	vun-miR166b.3	gma-miR166k	312951.1721	142270.0866	327265.8496	218172.756
TCGGACCAGGCTTCATTCCCC	zma-miR166t	gma-miR166o	69737.63578	34328.61997	84704.79722	69693.21253
GTTCAATAAAGCTGTGGGAAG	aly-miR396a*	gma-miR396i-3p	29488.52124	19766.52527	13021.86115	6523.418934
TTTCGGACCAGGCTTCATTCC	ptc-miRf10034	gma-miR166t	13491.98575	7583.032997	15291.48915	11326.51596
TTTGGATTGAAGGGAGCTCTA	vvi-miR159c	gma-miR159e-3p	10788.43528	7159.929863	10271.36438	8519.679646
TGTTGTTTTACCTATTCCACCT	gso-miR1510b	gma-miR1510b-3p	8999.468982	5611.092842	8917.876257	7965.209588
TTCACGTCGGGTTCACCA	ppt-miR894	-	7399.196771	9024.443714	5954.92353	5874.956471
AACCAGGCTCTGATACCATGG	gma-miR1511	gma-miR1511	8368.433806	5160.583142	6367.394738	4820.34444
TCTTCCCTACACCTCCCATAACC	gso-miR482b	gma-miR482d-3p	6763.006078	3503.233585	6063.741311	3092.263893
GGAATGGGCTGATTGGGAAGC	vun-miR482*	-	5717.467404	4941.35701	3852.149453	3788.152617
TTGGACTGAAGGGAGCTCCCT	vvi-miR319f	gma-miR319m	4355.383339	2629.61965	2206.412258	1393.503178
ACCTGGCTCTGATACCA	rgl-miR5139	-	2373.599633	1941.247397	2181.537423	2361.020229
CCCCACGGTGGGCGCCA	bdi-miR5054	-	2085.921832	1738.463225	1862.338598	2378.266541
CATTCCATACATCGTCTGACGA	vun-miR1507a	gma-miR1507a	2122.010445	1023.786035	2674.844697	1763.435489
TGGACTGAAGGGAGCTCCTTC	vun-miR319c.3	gma-miR319l	1072.347358	689.4661844	1612.575881	1079.619184
TTGCCGATTCCACCCATTCTA	pvu-miR2118	gma-miR2118b-3p	1285.785726	880.192919	1248.813584	893.3590054
TCGCTTGGTGCAGGTCGGGAA	vvi-miR168	gma-miR168a	1418.798043	753.0417626	876.7604083	672.606201
TTCCACAGCTTTCTTGAACCT	zma-miR396g	gma-miR396c	1409.518114	654.3900033	904.7421234	662.2584133
TAAGAGAATTGTAAGTCACTG	gma-miR4413	gma-miR4413b	794.9805895	544.7769374	1274.722579	773.4971311
TCGGACCAGGCTTCATTCCCCG	gma-miR166q	gma-miR166j-3p	982.6413771	516.2775403	1117.195887	729.5190334
GGAATGTTGTCTGGCTCGAGG	vun-miR166c*.4	gma-miR166l	1374.460604	708.1004056	497.4527139	360.4479385
TTAATCAAGGAAATCACGGTCG	gso-miR1509a	gma-miR1509a	495.9606531	480.1052285	648.7612477	593.2731619
CCCGCCTTGCACTCAACTGAAT	aly-miR168a*	-	882.6243639	362.8192481	559.6343032	372.5203575
TGTTGTTTTACCTATTCCACCC	gma-miR1510a	gma-miR1510a-3p	499.0539628	258.6868355	606.2704951	398.3898267
TCCAAAGGGATCGCATTGATTT	zma-miR393g	gma-miR393k	300.0510396	155.6505535	493.3072746	288.8757402
TGAAGCTGCCAGCATGATCTGG	rco-miR167c	gma-miR167j	287.6778009	184.1499507	413.5075684	318.194472
TTCCCAATTCCGCCCATTCCTA	gma-miR482	gma-miR482a-3p	489.7740337	322.2624137	266.3444739	124.1734525
TGCGAGTGTCTTCGCCTCTGAT	gso-miR2109	gma-miR2109	345.4195817	214.8416091	381.380414	241.4483798
TCGATAAACCTCTGCATCCAG	zma-miR162b	gma-miR162c	422.7523238	195.1112573	317.1261051	207.8180698
TATGGGGGGATTGGGAAGGAA	gma-miR482b	gma-miR482e	418.6279109	232.3796997	224.8900811	145.7313435
TGAGACCAAATGAGCAGCTGA	gso-miR3522b	gma-miR3522	293.8644202	123.8627644	277.7444319	198.3325977
TTGACAGAAGATAGAGAGCAC	vvi-miR156i	gma-miR156m	182.5052715	112.9014579	312.9806658	224.202067
AAGCTCAGGAGGGATAGCGCC	zma-miR390	gma-miR390g	186.6296844	60.28718623	251.8354364	180.2239692
TGCCTGGCTCCCTGTATGCCA	zma-miR160m	gma-miR160f	158.7920973	135.9224017	189.6549472	154.3556
TGTGTTCTCAGGTCGCCCCCTG	vvi-miR398c	gma-miR398c	279.428975	93.171106	189.6538472	70.70988267
TGAGAATTTGGCCTCTGTCCA	gma-miR5038b	gma-miR5038b	253.6513943	135.9202017	143.0176553	78.47072345
ACGGGTCGCTCTCACCTGGAG	gma-miR4416	gma-miR4416a	82.48825831	51.51814096	239.3991186	187.1224944
AGCTGCTTAGCTATGGATCCC	gma-miR159d	gma-miR159d	231.9982265	93.171106	109.854141	86.23156423
TTAATCAAGGAAATCACGGTTG	gma-miR1509b	gma-miR1509b	114.4524584	92.07497534	139.9085758	158.6660782
TTCATTTTTAAATAGGCATTG	gma-miR1514a	gma-miR1514a	141.2611424	99.74788995	167.8902909	87.95619552

AGCCAAGGGTGATTTGCCGGC	vun-miR169c.3	gma-miR169n	238.1848459	169.9002521	38.34531336	28.4564162
CCTCAAAGGCTTCCACTACTG	gma-miR5037	gma-miR5037a	90.73708414	30.69165845	212.4537632	106.9271396
TCTCGGACCAGGCTTCAATCC	zma-miR166k	gma-miR166u	109.2969423	31.7877891	169.9630106	125.0357681
TGACAGAAGAGAGTGAGCAC	zma-miR156o	gma-miR156y	66.92840019	48.22974899	103.454183	102.8909301
TGAGAGAAAAGCCATGACTTAC	gma-miR1513	gma-miR1513b	101.0481164	70.15236216	93.27238386	49.15199161
TTAAGACGGAACCTACAAAGATT	gma-miR4345	gma-miR4345	146.4166585	95.36336731	39.38167319	25.00715363
CCTCATTCCAAACATCATCTAA	mtr-miR1507	gma-miR1507c-3p	141.2611424	42.74909569	76.69062673	44.8404134
CGTTCCCCAGTGAGTCGCCA	osa-miR5072	-	65.99060665	64.67170887	78.76334637	95.7170363
TGGACTGAAGGGGAGCTCCTTC	vun-miR319c.2	gma-miR319i	52.58626467	61.38331689	103.6359821	77.60840781
GCTCAAGAAAGCTGTGGGAGA	vun-miR396b*	gma-miR396k	124.7634907	60.28718623	49.74527139	50.01430725
AGTAGTGGAACTTTGAGGCCT	gma-miR5037c	gma-miR5037c	36.08861301	18.6342212	152.3448936	75.88377652
TAGAAAGGGAAATAGCAGTTG	gso-miR1508a	gma-miR1508c	123.7323875	72.34462348	56.99979014	29.31873184
TAGAAGCTCCCCATGTTCTCA	gma-miR4996	gma-miR4996	121.670181	31.7877891	79.79970619	33.63031005
ATTGGAGTGAAGGGAGCTCCT	gma-miR159c	gma-miR159f-3p	52.58736467	19.73145186	145.0903749	46.56614468
TAAGTGGAAATCTTAAAGCAT	gma-miR1512	gma-miR1512b	88.67487769	76.72914611	56.99979014	28.4564162
TTGTTTCGATAAACTGTTGTG	gma-miR5372	gma-miR5372	70.11501957	46.03748767	74.61790709	54.32588547
TTATAGTCTGACATCTGGAAT	gma-miR5374	gma-miR5374	112.390252	78.92140743	22.79991605	17.24631285
TAATCTGCATCCTGAGGTTT	vun-miR2111a.2	gma-miR2111f	72.17722602	66.86397019	40.41803301	48.28967597
CATCGGGGGCGCAACGCCCTCGA	pta-miR1310	-	80.42605185	58.09492492	50.78163121	31.04336312
TGTCGCAGGATAGAGGGCACTG	vvi-miR3627	gma-miR5786	2.062206458	72.34462348	3.109079462	137.1081871
CCCTCAAAGGCTTCCAGTATT	vvi-miR477	-	30.93309687	10.96130659	116.0722999	53.46356982
TGAGCCAGGATGGCTTGCCGGC	mtr-miR169p	gma-miR169r	56.71067759	33.98005042	87.05422494	24.14483798
ATGCACTGCCTCTTCCCTGGC	vvi-miR408	gma-miR408c-3p	65.99060665	37.2684424	53.89071068	37.94188826
ACACGGACACCGGACACGACACG	gma-miR4403	gma-miR4403	56.71067759	21.92261318	71.50882763	38.8042039
TTTGATACACTAGCACGGGTC	lja-miR2199	-	63.92840019	36.17231174	39.38167319	22.4202067
TTAGATTCACGCACAACTTG	vun-miR403	gma-miR403b	54.64847113	26.30713581	47.67255175	24.14483798
TAGAATGTATAATATGAGAGGCCT	gma-miR4379	gma-miR4379	38.15081947	26.30713581	49.74527139	36.21725698
GCTTACTCTCTATCTGTCACC	aly-miR156f*	-	29.90199364	14.24969856	63.21794906	37.07957262
TTACTATAGAAGTACTTGTGGAGC	gma-miR5375	gma-miR5375	29.90199364	23.01874383	52.85435085	33.63031005
CTCTCCCTCAAGGGCTTCTCG	csi-miR477b	-	27.83978718	18.6342212	56.99979014	35.35494133
CTTCCATATCTGGGGAGCTTC	pvu-miR159.2	-	41.24412916	31.7877891	38.34531336	25.00715363
TTGAGCCGCGCCAATATCACT	vvi-miR171f	gma-miR171k-3p	31.9642001	17.53809054	47.67255175	37.07957262
TGGAGAAGCAGGGCACGTGCA	zma-miR164h	gma-miR164k	46.3996453	31.7877891	33.16351426	16.3839972
GTATGGTCATACGGATTGTTGATC	gma-miR4380b	gma-miR4380b	44.33743884	61.38331689	12.43631785	6.036209496
GACTCCATCGCCCAATGGA	tae-miR2008	-	47.43074853	28.49939713	16.58175713	30.18104748
TTCCATGATAAGATCTTTGACT	gma-miR5678	gma-miR5678	50.52405822	23.01874383	26.94535534	20.69557542
TGATTCTAGATGATGTTGACA	gma-miR5373	gma-miR5373	21.65316781	19.73035186	46.63619193	22.4202067
CTGGGCAGCAACACCA	bdi-miR5059	-	29.90199364	26.30713581	13.47267767	38.8042039
AATCAGAACATGACACGTGACAGT	gma-miR1520n	gma-miR1520n	49.49295499	18.6342212	18.65447677	20.69557542
GTAGTGATGCCTAGAGGTCC	gma-miR5044	gma-miR5044	22.68427104	0.0011	68.39974816	16.3839972
CGTGATATTGGTACGGCTCATC	ghr-miR479	gma-miR171b-5p	47.43074853	12.05743725	22.79991605	22.4202067
GAGCTCCTTGAAGTCCAATTG	aly-miR159b*	gma-miR159a-5p	41.24412916	27.40326647	16.58175713	12.93473463
CTAGAAAGGGAAATAGCAGTTG	gma-miR1508a	gma-miR1508a	32.99530332	30.69165845	18.65447677	12.93473463
TGACTAAAGATTGTCCAAAAG	gma-miR5370	gma-miR5370	43.30633561	29.59552779	13.47267767	7.760840781
AAGCTCAGGAGGGATAGCACC	vun-miR390a.2	gma-miR390d	15.46654843	2.192261318	32.12715444	43.97809776

GGAATGTTGTTTGGCTCGAGG	aly-miR166g*	gma-miR166j-5p	34.02640655	17.53809054	19.69083659	22.4202067
CGAGCCGAATCAATATCACTC	gma-miR171b	gma-miR171b-3p	27.83978718	14.24969856	29.01807498	19.83325977
TCATTTTGC GTGCAATGATCTG	vun-miR1515	gma-miR1515b	20.62206458	18.6342212	33.16351426	18.10862849
TTCCACAGCTTTCTTGAAGTGT	gma-miR396e	gma-miR396e	24.74647749	13.15356791	37.30895354	13.79705028
AATGAGAACATGACACGTGATAGT	gma-miR1520l	gma-miR1520l	43.30633561	7.672914611	21.76355623	8.623156423
CGAGAGTTTCGTGACTACAAC TTC	gma-miR4998	gma-miR4998	42.27523238	32.88391976	1.036359821	2.586946927
GCGTATGAGGAGCCAAGCATA	bra-miR160a*	gma-miR160a-3p	36.08861301	17.53809054	13.47267767	11.21010335
CATGGAAGTGAATCGGGTGAC	gma-miR5671	gma-miR5671	14.4354452	10.96130659	26.94535534	22.4202067
TTGTAAC TAATTTGT CGGTACC	gma-miR4411	gma-miR4411	28.87089041	19.73035186	11.39995803	12.93473463
CAGCCAAGAATGACTTGCCGG	ptc-miR169t	gma-miR169l-5p	32.99530332	12.05743725	14.50903749	6.898525138
TTATTGTAGATAACTTTGGCC	mtr-miR5261	-	10.31103229	14.24969856	16.58175713	23.28252234
TGAGAAAAGGACAGTAGAAAAGCC	gma-miR4393a	gma-miR4393a	39.1819227	15.34582922	7.254518745	1.724631285
ATCCTTGGGATGTAGATTACC	lja-miR2111*	gma-miR2111d	26.80868395	14.24969856	14.50903749	6.898525138
TGTGCTTGGACTGAAGGGAGC	ptc-miRf10629	-	16.49765166	12.05743725	13.47267767	14.65936592
TTGGCATTCTGTCCACCTCC	zma-miR394b	gma-miR394g	14.4354452	8.76904527	20.72719641	11.21010335
CAAGGATGACTTGCCGGCATT	zma-miR169r	gma-miR169s	13.40434198	12.05743725	18.65447677	8.623156423
CAGCGGAATGAGAAGACGAAAAGT	gma-miR4398	gma-miR4398	19.59096135	10.96130659	11.39995803	8.623156423
CAGCTTTCTTGAAC TA	vvi-miR396a	-	21.65316781	7.672914611	11.39995803	5.173893854
CGGGCAAGTTGTTTTGGCTAC	ptc-miRf10669	gma-miR169l-3p	15.46654843	10.96130659	11.39995803	7.760840781
ATCATGCTATCCCTTTGGATT	ptc-miRf10552	-	13.40434198	7.672914611	15.54539731	8.623156423
TGCCAAAGGAGATTTGCCCTG	mtr-miR399h	gma-miR399g	5.155516144	9.865175929	15.54539731	13.79705028
TAACAAGTGGGTTTGTG TACT	gma-miR4409	gma-miR4409	18.55985812	6.576783953	9.327238386	9.485472065
TTGACCAATCAGAACATGACAGAT	gma-miR1520q	gma-miR1520q	13.40434198	5.480653294	15.54539731	6.898525138
AATCAGAACATGACACATAACAGT	gma-miR1520k	gma-miR1520k	6.186619373	7.672914611	16.58175713	9.485472065
TTGTGTTCTCAGGTCACCCCT	vvi-miR398a	gma-miR398b	7.217722602	4.384522635	5.181799103	22.4202067
CGGGAGCCTATGAAGGT TAAC	gma-miR5037d	gma-miR5037d	6.186619373	1.096130659	24.8726357	6.898525138
AGGTCATCTTGCAGCTTCAA	aly-miR167d*	-	7.217722602	6.576783953	12.43631785	11.21010335
TGAAGATTTGAAGAATTTGGGA	gma-miR5376	gma-miR5376	18.55985812	15.34582922	1.036359821	0.0011
CGCTATCCATCCTGAGTTTCA	aly-miR390a*	gma-miR390c	1.031103229	5.480653294	11.39995803	14.65936592
TCCTGATCGTCAAGCGCGAAGA	gma-miR4997	gma-miR4997	10.31103229	15.34582922	1.036359821	5.173893854
TGTCAAAGATGTGGCGAATACT	gma-miR4397	gma-miR4397-3p	12.37323875	3.288391976	12.43631785	3.449262569
AACAAGACATGATGACGTGACACT	gma-miR4387a	gma-miR4387a	12.37323875	7.672914611	6.218158924	5.173893854
GCTCAGGTCTCTTGGCTCCT	ptc-miRf12215	-	13.40434198	5.480653294	4.145439283	7.760840781
ACATCATAGAACTGGCACT	mtr-miR5245	-	7.217722602	5.480653294	11.39995803	6.036209496
TCCAAAGGGATCGCATTGATCC	vun-miR393a.2	gma-miR393g	9.27992906	2.192261318	13.47267767	5.173893854
TTGACAGAAGAGAGTGAGCAC	sbi-miR157	gma-miR156o	2.062206458	3.288391976	13.47267767	11.21010335
GCTCTCTATACTTCTGT CATC	aly-miR157c*	-	11.34213552	3.288391976	4.145439283	11.21010335
TCGCGTCGGGATCACCA	osa-miR5077	-	2.062206458	4.384522635	6.218158924	17.24631285
TGCCAAAGGAGAGTTGCCCTG	zma-miR399h	gma-miR399h	6.186619373	5.480653294	8.290878565	9.485472065
TGAAGCTGCCAGCATGATCTT	vun-miR167f	gma-miR167f	1.031103229	4.384522635	7.254518745	14.65936592
GCTCACTTCTCTATCTGTCAGC	aly-miR156c*	-	3.093309687	3.288391976	9.327238386	10.34778771
ATCAGAACGTGACATGTGACCGTC	gma-miR1520m	gma-miR1520m	12.37323875	4.384522635	6.218158924	2.586946927
GGCAAGTTGGCCTTGGCTATA	gso-miR169g*	-	4.124412916	9.865175929	5.181799103	6.036209496
ATTGGAGTGAAGGGAGCT	ptc-miR159f	gma-miR156aa	3.093309687	3.288391976	14.50903749	2.586946927
TTTCCAAATGTAGACAAAGCA	bra-miR158	-	4.124412916	7.672914611	6.218158924	5.173893854

AGAGACTTACGGATCAACTTGATC	gma-miR4361	gma-miR4361	5.155516144	5.480653294	6.218158924	4.311578212
TTCATTTTTAAATAGACATTG	gma-miR1514b	gma-miR1514b	13.40434198	3.288391976	4.145439283	0.0011
ATGAGATCGTACAGAAGAAGGTTC	gma-miR4364a	gma-miR4364a	5.155516144	4.384522635	8.290878565	2.586946927
TTGAGCCGCGTCAATATCTCA	vun-miR171.2	gma-miR171t	1.031103229	2.192261318	8.290878565	7.311578212
AGCAATGGAATTATAGACTGC	gma-miR5668	gma-miR5668	8.248825831	6.576783953	3.109079462	0.862315642
CAATAAGAATCTGACACGTGG	gma-miR1520c	gma-miR1520c	8.248825831	2.192261318	3.109079462	5.173893854
TTAGGGACCAAATTGACAGCGCCT	gma-miR4388	gma-miR4388	3.093309687	0.0011	5.181799103	10.34778771
CGTAGATCCCCACAACAGT	gma-miR4412	gma-miR4412-3p	7.217722602	3.288391976	5.181799103	2.586946927
TAAGCTTCTCACGGATCAAGTTT	gma-miR4347	gma-miR4347	6.186619373	2.192261318	7.254518745	2.586946927
TTGAGAAGGGACAACAGAAAAGCC	gma-miR4393b	gma-miR4393b	6.186619373	4.384522635	4.145439283	3.449262569
CATCTTCAACTTGCTCAACGG	gma-miR5041	gma-miR5041	4.124412916	6.576783953	3.109079462	4.311578212
AATAAGAATGTGACATGTGACAGT	gma-miR1520e	gma-miR1520e	9.27992906	2.192261318	3.109079462	3.449262569
TTGAGCCGCGTCAATATCTTA	vun-miR171.1	gma-miR171p	5.155516144	0.0011	8.290878565	4.311578212
TATCTTGATCACAGCCCCATT	gma-miR5042	gma-miR5042	3.093309687	4.384522635	7.254518745	2.586946927
AACGAAAAAGGACTAACGATGAGT	gma-miR4399	gma-miR4399	6.186619373	4.384522635	3.109079462	3.449262569
TATGGGATAAATGTGAGCTCA	gma-miR1523	gma-miR1523a	1.031103229	0.0011	6.218158924	9.485472065
AGATCATGTGGCAGTTTCACC	ahy-miR167	-	0.0011	3.288391976	6.218158924	6.898525138
AAGCCAAGGATGACTTGCCGA	gma-miR169c	gma-miR169c	0.0011	6.288391976	8.181799103	1.862315642
TGATTGAGCCGTGCCAATATC	zma-miR171j	gma-miR171u	2.062206458	6.576783953	5.181799103	1.724631285
CGGGGGACGGACTGGGA	peu-miR2911	-	2.062206458	6.576783953	4.145439283	2.586946927
GCAGCGATGCGTTGAGC	ptc-miRf10440	-	0.0011	6.576783953	0.0011	8.623156423
AAACAGTTGACGTACGTACGGATT	gma-miR4360	gma-miR4360	5.155516144	2.192261318	4.145439283	3.449262569
GGAGGCAGCGGTTTCATCGATC	csi-miR162*	-	2.062206458	3.288391976	9.327238386	0.0011
TTAAACATACGGATCAGGTTGATC	gma-miR4343a	gma-miR4343a	2.062206458	0.0011	8.290878565	4.311578212
CTTCTAAACATTTTTTCCCTTATG	gma-miR5035	gma-miR5035	6.186619373	3.288391976	3.109079462	1.724631285
TTTGTTAACCGTTGGATCGTCT	ptc-miRf10383	-	2.062206458	1.096130659	7.254518745	3.449262569
AGAGGCCCTTGGGGAGGAGTA	gma-miR5036	gma-miR5036	3.093309687	1.096130659	6.218158924	3.449262569
CAAAGACGGTCGTGATGTCAGCACC	gma-miR4374a	gma-miR4374a	3.093309687	7.672914611	1.036359821	1.724631285
CAACAGCGAAAGAACTTTCTTCT	gma-miR4364b	gma-miR4364b	5.155516144	1.096130659	2.072719641	5.173893854
CATCTGAAGGATAGAACACATA	gma-miR5378	gma-miR5378	9.27992906	3.288391976	0.0011	0.862315642
ACCCGAACCTGAACCTGAAC	ath-miRf10452	-	3.093309687	3.288391976	3.109079462	3.449262569
AGGGACAGTCTCAGGTAGACA	gma-miR5368	gma-miR5368	4.124412916	3.288391976	2.072719641	3.449262569
TAGCTGCCGACTCATTCATCCA	smo-miR319	-	5.155516144	5.480653294	2.072719641	0.0011
ATCAGACACTGCATTCAAAGACGG	gma-miR4384	gma-miR4384	3.093309687	2.192261318	3.109079462	4.311578212
CGGCTTTCTTGAAGTG	ptc-miR396f	-	4.124412916	5.480653294	2.072719641	0.862315642
GCATGACTTGACTGAGGACATG	mtr-miR5255	-	5.155516144	4.384522635	2.072719641	0.862315642
AATGGGCTGATTGGGAAGCAA	pvu-miR482*	-	1.031103229	5.480653294	2.072719641	3.449262569
TTTAGTTGGCATGCATTTAAG	mtr-miR5248	-	4.124412916	1.096130659	3.109079462	3.449262569
ATACGCTCTGATACCATGTTAGAA	pab-miR1863	-	5.155516144	0.0011	3.109079462	3.449262569
TTACCTATTCCACCCATTCCA	mtr-miR2089	-	4.124412916	4.384522635	2.072719641	0.862315642
TCATTGAGTGCAGCGTTGATG	vvi-miR397a	gma-miR397b-5p	1.031103229	2.192261318	5.181799103	2.586946927
CACTAGTGGTCGCGCCTGGGGCCC	gma-miR4375	gma-miR4375	4.124412916	2.192261318	2.072719641	2.586946927
CAGCTTTCTTGAGCTG	ptc-miRf11357	-	6.186619373	0.0011	2.072719641	2.586946927
TCAGAACATGACACATGACAAAC	gma-miR1520f	gma-miR1520f	2.062206458	0.0011	5.181799103	3.449262569
TCAAAGGGAGTTGTAGGGGAA	vun-miR2119	gma-miR2119	1.031103229	0.0011	0.0011	9.485472065

TTAAGTGATGACGTGGTAGACA	gma-miR4371b	gma-miR4371b	4.124412916	3.288391976	1.036359821	0.862315642
ACATATTATGGGCCTCAAACGGAC	gma-miR4402	gma-miR4402	2.062206458	2.192261318	4.145439283	0.862315642
CCCGAGAAGAAGAAGAAGCT	ath-miR5021	-	2.062206458	4.384522635	1.036359821	1.724631285
ATGATGACGATGATGAAAAA	ath-miR5658	-	1.031103229	1.096130659	5.181799103	1.724631285
GACTTACAGATCAACTTGATTCGT	gma-miR4343b	gma-miR4343b	2.062206458	1.096130659	4.145439283	1.724631285
ATGTAGACATTCTAAGACGGTTCT	gma-miR4352b	gma-miR4352b	3.093309687	0.0011	4.145439283	1.724631285
TCATGTTCTTATTGGATGATGACT	gma-miR1520p	gma-miR1520p	1.031103229	2.192261318	3.109079462	2.586946927
ATTCTAAGACAGTTATCTGAGACC	gma-miR4405	gma-miR4405	2.062206458	0.0011	4.145439283	2.586946927
GCTCACTACTCTTTCTGTCCGTT	aly-miR156a*	-	1.031103229	1.096130659	3.109079462	3.449262569
TGACGTACGTACGGATTGACAATC	gma-miR4373	gma-miR4373	3.093309687	0.0011	2.072719641	3.449262569
CTCAAAAAGAGCTTATGGCTTG	gma-miR1516	gma-miR1516a-3p	2.062206458	1.096130659	3.109079462	1.724631285
CCTTGCATCAACTGAATCGGA	ath-miRf10239	-	3.093309687	1.096130659	2.072719641	1.724631285
TCAGAACATAACACGTGACAATCA	gma-miR1520g	gma-miR1520g	3.093309687	0.0011	3.109079462	1.724631285
CCTGACTGGAATGCCTTGTT	smo-miR1092	-	2.062206458	5.480653294	0.0011	0.0011
TAACTCAACCTTACAAAACCGGAT	gma-miR1527	gma-miR1527	1.031103229	3.288391976	3.109079462	0.0011
AAGAAAACGGATGCGCGAAC	osa-miR5539	-	2.062206458	3.288391976	1.036359821	0.862315642
CGAGTCCGAGGAAGGAATCC	gma-miR1524	gma-miR1524	6.186619373	0.0011	1.036359821	0.0011
GGATGGCAATACTGTGGATAT	ptc-miRf12139	-	1.031103229	3.288391976	1.036359821	1.724631285
CATGTGCCCTCTTCCCATC	aly-miR164b*	-	2.062206458	0.0011	4.145439283	0.862315642
ATCATGTTGATCCGTATGAGTCAT	gma-miR4410	gma-miR4410	2.062206458	2.192261318	1.036359821	1.724631285
ATTGGATCTCAGTTGAACCGGTCT	gma-miR4383	gma-miR4383	4.124412916	0.0011	1.036359821	1.724631285
GACAGTCATCATCGAATAAGAAC	gma-miR1520b	gma-miR1520b	1.031103229	1.096130659	2.072719641	2.586946927
CCGTGAACTGTCTTAGAATGTGCA	gma-miR4378b	gma-miR4378b	1.031103229	0.0011	3.109079462	2.586946927
AATCATCGTCCAATCAAAATGT	gma-miR1520o	gma-miR1520o	1.031103229	0.0011	2.072719641	3.449262569
AGGTGGGCATACTGTCAACTG	gma-miR394b	gma-miR394b-3p	1.031103229	3.288391976	2.072719641	0.0011
TCACCTCCACCACCAGACCCA	ptc-miRf10426	-	2.062206458	2.192261318	2.072719641	0.0011
CTCGGCAAGAATAAGAAGAAGA	gma-miR4391	gma-miR4391	3.093309687	2.192261318	1.036359821	0.0011
GCTCTCTAGGCTTCTGTATCCT	aly-miR157d*	-	0.0011	3.288391976	2.072719641	0.862315642
TTTGGTCTTTAATCAAGCTGA	gma-miR5677	gma-miR5677	2.062206458	0.0011	4.145439283	0.0011
ACTCTCCCTCAAGGGCTT	csi-miR473	-	3.093309687	0.0011	3.109079462	0.0011
GATAATTGTGTTGTACATT	gma-miR5674	gma-miR5674b	0.0011	2.192261318	3.109079462	0.862315642
AGAATCTTGATGATGCTGCAT	vvi-miR172d	gma-miR172h-3p	2.062206458	1.096130659	2.072719641	0.862315642
GATCAAGTTGATCCGGAAGTC	gma-miR4369	gma-miR4369	2.062206458	1.096130659	2.072719641	0.862315642
CGAGCCGAATCAATACCACT	ptc-miR171n	gma-miR171s	3.093309687	1.096130659	1.036359821	0.862315642
TGTCCCTTCTCTGCACCACC	gma-miR5043	gma-miR5043	2.062206458	2.192261318	0.0011	1.724631285
TAAGAACCTGACACATGACAATCA	gma-miR1520j	gma-miR1520j	3.093309687	1.096130659	0.0011	1.724631285
TGAAGCTGCCAGCATGATCTGA	vun-miR167g	gma-miR167g	1.031103229	0.0011	3.109079462	1.724631285
CGTACTCGTCGGGTATCGGGTATC	gma-miR4390	gma-miR4390	1.031103229	0.0011	3.109079462	1.724631285
AACGTGACATGTGACAGTCAACA	gma-miR1520i	gma-miR1520i	2.062206458	0.0011	2.072719641	1.724631285
CCTTCGTCCATATGGGAAGACT	gma-miR1531	gma-miR1531	0.0011	2.192261318	1.036359821	2.586946927
AAGGACGGTGCCTACGTAAGCATC	gma-miR4368b	gma-miR4368b	3.093309687	1.096130659	1.036359821	0.0011
ATAAGTGTTGCAAAATAGTCCTTC	gma-miR1519	gma-miR1519	2.062206458	0.0011	3.109079462	0.0011
CAGTGCATGACTATATCGCCT	gma-miR4358	gma-miR4358	0.0011	2.192261318	2.072719641	0.862315642
CTTAGTAGAGATTTGTTGGTTGGT	gma-miR4366	gma-miR4366	2.062206458	1.096130659	1.036359821	0.862315642
CAGTAACTGTGGCCTTCCAT	aly-miR4242	-	1.031103229	0.0011	3.109079462	0.862315642

CTTGTTTGTGGTGATGTCTAG	gma-miR1535	gma-miR1535b	1.031103229	0.0011	3.109079462	0.862315642
GCTTTGGAAGTAATAGGTTCC	mtr-miR2609c	-	2.062206458	0.0011	2.072719641	0.862315642
TTGACAGAAGATAGAGAGCAT	sly-miR157c	gma-miR156r	0.0011	0.0011	4.072719641	0.862315642
GCAGTGGCTTGGTTAAGGGA	gma-miR4995	gma-miR4995	0.0011	1.096130659	2.072719641	1.724631285
AGATATTGGTGCGGTTCATC	gma-miR171c	gma-miR171c-5p	2.062206458	1.096130659	0.0011	1.724631285
AACCCCTCAAAGGCTTCCGCCG	gma-miR5037b	gma-miR5037b	0.0011	0.0011	3.109079462	1.724631285
AAGTTGTGATGAGAATCAATG	gma-miR4415	gma-miR4415a-5p	2.062206458	0.0011	1.036359821	1.724631285
AAATGGTGTCTGCTAGGC	ptc-miRf10544	-	0.0011	2.192261318	0.0011	2.586946927
TGCATTTGCACCTGCACTTTA	tcc-miR530b	gma-miR530e	1.031103229	0.0011	1.036359821	2.586946927
CAGAGGAAGCAACACTTGTACC	gma-miR4407	gma-miR4407	2.062206458	0.0011	0.0011	2.586946927
CGTGTCACATCCTGGTTGGACATG	gma-miR1520r	gma-miR1520r	0.0011	0.0011	0.0011	4.311578212
AACCTCCGTAGCCTGTATCAAAC	gma-miR2107	gma-miR2107	2.062206458	1.096130659	1.036359821	0.0011
AGTTTTACTTGTCTGCATCCG	osa-miR413	-	3.093309687	1.096130659	0.0011	0.0011
TCCCAAATGTAGACAAAGCA	bol-miR158	-	0.0011	0.0011	4.145439283	0.0011
TGAGCCAAGGATGACTT	vun-miR169d.2	gma-miR169p	1.031103229	0.0011	3.109079462	0.0011
TGATATTGGTACGGCTCATCT	ptc-miR479	-	1.031103229	0.0011	3.109079462	0.0011
TAGTCGTGTGATTGTAAGGTTTCAT	gma-miR4357	gma-miR4357	2.062206458	1.096130659	0.0011	0.862315642
AACAACATTGGATGAGGGTTG	gma-miR4408	gma-miR4408	2.062206458	1.096130659	0.0011	0.862315642
TGATTGAGTCGTGTCAATATC	mtr-miR171	gma-miR171d	0.0011	0.0011	3.109079462	0.862315642
AACATGAAACATGACCGTCATCA	gma-miR1520a	gma-miR1520a	1.031103229	0.0011	2.072719641	0.862315642
ACAACCTGAAGGACCGATGTAGAAT	gma-miR5377	gma-miR5377	2.062206458	0.0011	1.036359821	0.862315642
TTGGACTGAAAGGAGC	gma-miR319c	gma-miR319c	3.093309687	0.0011	0.0011	0.862315642
CCCACAGCTTTATTGAACT	gcl-miR396a	-	1.031103229	1.096130659	0.0011	1.724631285
CTGGATAGGAGTATGGGCTTG	gma-miR4395	gma-miR4395	1.031103229	0.0011	1.036359821	1.724631285
TTGGTCAATGTCGTTTCGAA	gma-miR1517	gma-miR1517	0.0011	0.0011	1.036359821	2.586946927
ATATGTAGTTTCTAAGACGATGCT	gma-miR4396	gma-miR4396	0.0011	0.0011	1.036359821	2.586946927
AAACAGATCTAAATGGATTCC	gma-miR5667	gma-miR5667	1.031103229	2.192261318	0.0011	0.0011
CGTGATGACATGACACTTCGTCT	gma-miR4387c	-	1.031103229	1.096130659	1.036359821	0.0011
AAAGACCAAACGAGAAGCTGCAT	gma-miR4346	gma-miR4346	1.031103229	1.096130659	1.036359821	0.0011
TTTGGGTAAATAGTCACTTTT	gma-miR1534	gma-miR1534	0.0011	0.0011	3.109079462	0.0011
AATGTGTTGTGTTTGTTCGGA	gma-miR2108a	gma-miR2108a	0.0011	0.0011	3.109079462	0.0011
ATAATCTAGCTCTGGTACCATGTT	osa-miR1873*	-	0.0011	0.0011	3.109079462	0.0011
CCCCAAAAGAAATGTGTCTTT	ptc-miRf10971	-	0.0011	0.0011	3.109079462	0.0011
AGAATTTGTGGGAATGGGCTGA	gma-miR482a	gma-miR482a-5p	0.0011	0.0011	3.109079462	0.0011
CACGTGCTCCCCCTTCTCCAAC	aly-miR164a*	-	2.062206458	0.0011	1.036359821	0.0011
AAGTAGACATTCTAAGACGTTACT	gma-miR4344	gma-miR4344	2.062206458	0.0011	1.036359821	0.0011
CCAATTGAATCGGTCCAACCGGC	gma-miR4354	gma-miR4354	2.062206458	0.0011	1.036359821	0.0011
CATCATCATCATCATC	ghr-miR414f	-	0.0011	2.192261318	0.0011	0.862315642
TCAGCAACGTCTTTGAAAGTAGGC	gma-miR4401	gma-miR4401a	0.0011	1.096130659	1.036359821	0.862315642
CTGAGCTCTGATACCAAATGAT	ath-miR829.1	-	1.031103229	1.096130659	0.0011	0.862315642
ATTAACGTCCGATCAAAACGTGAC	gma-miR1520h	gma-miR1520h	1.031103229	1.096130659	0.0011	0.862315642
GCAGCAGCATCAAGATTCA	aly-miR172b*	gma-miR172j	0.0011	0.0011	2.072719641	0.862315642
TAAAAACGTGACATGTGACGATCA	gma-miR4372	gma-miR4372a	0.0011	0.0011	2.072719641	0.862315642
TGAAGTGTGTTGGGGGAAGTC	zma-miR395p	gma-miR395m	1.031103229	0.0011	1.036359821	0.862315642
ACATCATCGTGTTCCTGAAC	ath-miRf10183	-	0.0011	1.096130659	0.0011	1.724631285

TTGAGCCGTGCCAATATCACA	zma-miR171f	gma-miR171q	0.0011	1.096130659	0.0011	1.724631285
CTACAATTATCTGATCTAT	osa-miR5083	-	0.0011	0.0011	1.036359821	1.724631285
GAGTAGACTTGTCCGATTAGCGT	gma-miR4370	gma-miR4370	0.0011	0.0011	1.036359821	1.724631285
AAAGGAAGAGGCCGTGCATGA	ath-miRfl1042	-	1.031103229	0.0011	0.0011	1.724631285
CATTCCGGTGAGTCTGTT	ath-miRfl0251	-	0.0011	1.096130659	1.036359821	0.0011
CACACGCTAAGCGAGAGGAGCTCG	gma-miR1532	gma-miR1532	0.0011	1.096130659	1.036359821	0.0011
TTAGTGTGGATAATAATTT	mtr-miR2676f	-	0.0011	1.096130659	1.036359821	0.0011
ACTTGCAAAGACGGTGTGAACA	gma-miR4374b	gma-miR4374b	0.0011	1.096130659	1.036359821	0.0011
GGTTAGCTCAAGGATCTCACA	gma-miR4994	gma-miR4994	0.0011	1.096130659	1.036359821	0.0011
GAAGATGAAGCTGTTCTC	ath-miRfl0764	-	1.031103229	1.096130659	0.0011	0.0011
CTGAAGTGTGGGAAACTC	osa-miR395t	gma-miR395c	1.031103229	1.096130659	0.0011	0.0011
TTGTTTTGTGGAGCATGAC	osa-miR1857	-	1.031103229	1.096130659	0.0011	0.0011
TATACTCCCTCCATTCTAAATAT	osa-miRfl1316	-	1.031103229	1.096130659	0.0011	0.0011
CACCCTATGTCCCAAAACCT	osa-miRfl1624	-	1.031103229	1.096130659	0.0011	0.0011
TAGTTGGTGTAGCGATTGTC	peu-miR2910	-	1.031103229	1.096130659	0.0011	0.0011
ATTGGGATTCAGTTGGAGTTGGTT	gma-miR4351	gma-miR4351	1.031103229	1.096130659	0.0011	0.0011
CAATGTAGTGTGGTAAGTGGTC	gma-miR5669	gma-miR5669	1.031103229	1.096130659	0.0011	0.0011
TAGCATCATCAAGATTCACAT	ptc-miRfl2020	gma-miR172b-5p	0.0011	0.0011	2.072719641	0.0011
TGAAATGGTAGATTTTCTTG	osa-miR5543	-	0.0011	0.0011	2.072719641	0.0011
TATGTTAACTGATTTTCATGGAT	gma-miR4382	gma-miR4382	0.0011	0.0011	2.072719641	0.0011
AAGAGGAAAATCAAGCAAGA	gma-miR1526	gma-miR1526	1.031103229	0.0011	1.036359821	0.0011
CAATGGACTATGTAAGATT	mtr-miR5256	-	1.031103229	0.0011	1.036359821	0.0011
AGTTTGTAGAGTGATACACT	ppt-miR1223d	-	1.031103229	0.0011	1.036359821	0.0011
TGTGATGACATGACACTCTGTCTG	gma-miR4387b	gma-miR4387b	1.031103229	0.0011	1.036359821	0.0011
AAATGGACTAAAGAGAAAGGGGCC	gma-miR4394	gma-miR4394	1.031103229	0.0011	1.036359821	0.0011
AGGTACCCTTTCAGATAGTCTC	gma-miR5034	gma-miR5034	1.031103229	0.0011	1.036359821	0.0011
GGAGGCATCCAAAGGGATT	ptc-miRfl2019	-	2.062206458	0.0011	0.0011	0.0011
ACGAATTGCTGATCCGTATGTGCA	gma-miR4380a	gma-miR4380a	2.062206458	0.0011	0.0011	0.0011
CTGTGCTGTCTAGTAAGAAGA	tae-miR2028	-	2.062206458	0.0011	0.0011	0.0011
AGAAAATGAATGATGAGGATGGG	gma-miR5380b	gma-miR5380b	2.062206458	0.0011	0.0011	0.0011
AAGAAAGCTGTGGGAGAATATGGC	gma-miR396d	gma-miR396d	0.0011	1.096130659	0.0011	0.862315642
CGGAAGAACTTCTTTTGCAGATC	gma-miR4365	gma-miR4365	0.0011	0.0011	1.036359821	0.862315642
GTAGGGTCCAGCGGCAAGA	ptc-miRfl0840	-	0.0011	0.0011	1.036359821	0.862315642
AGGGCCATGTTGGGCAAAGATA	ptc-miRfl1775	-	0.0011	0.0011	1.036359821	0.862315642
GCATGCTGGATCTTCTACT	ptc-miRfl1818	-	0.0011	0.0011	1.036359821	0.862315642
AACACGTCATCGTTTAATGGAAGA	gma-miR4377	gma-miR4377	0.0011	0.0011	1.036359821	0.862315642
AGAGCTTTCTTCAGTCCACT	aly-miR319b*	-	1.031103229	0.0011	0.0011	0.862315642
TAATGGAGAATGTTGAAC	gma-miR1521	gma-miR1521a	1.031103229	0.0011	0.0011	0.862315642
GATGTGTTGAAAGTCTTACATGAC	gma-miR4341	gma-miR4341	1.031103229	0.0011	0.0011	0.862315642
TACTGAACTCAATCACTTGCTGCC	osa-miR5538	-	1.031103229	0.0011	0.0011	0.862315642
TCCGTTGTAGTCTAGAAAAA	ptc-miR1445	-	1.031103229	0.0011	0.0011	0.862315642
TCCTGAACCCTAGCGAAGTAAATC	gma-miR4367	gma-miR4367	1.031103229	0.0011	0.0011	0.862315642
AGGTCGGACCAATCCAATCGGGAT	gma-miR4389	gma-miR4389	1.031103229	0.0011	0.0011	0.862315642
AGCCAAGAATGACTCGCCT	tcc-miR169f	-	1.031103229	0.0011	0.0011	0.862315642
CCGTGGAGTCTCGCGAAAGACG	gma-miR5673	gma-miR5673	1.031103229	0.0011	0.0011	0.862315642

CCTTCTCCCCCACC	ghr-miR482b	-	0.0011	0.0011	0.0011	1.724631285
GAAGTGACGTTAACATCGGTTC	gma-miR4359a	gma-miR4359a	0.0011	0.0011	0.0011	1.724631285
GCCCGTCTAGCTAAGTTGG	tae-miR2018	-	0.0011	0.0011	0.0011	1.724631285
AGGTGGACATACTGCCAATAG	aly-miR394b*	-	0.0011	1.096130659	0.0011	0.0011
GTTTTTCCTAACCCGCCATT	ath-miR472	-	0.0011	1.096130659	0.0011	0.0011
ACTCGGATGTCTGATTGAGTGCCT	ath-miRf10142	-	0.0011	1.096130659	0.0011	0.0011
GGCCGATCTGCTGAGC	ath-miRf10241	-	0.0011	1.096130659	0.0011	0.0011
GACTCCTCCCAATGG	ghr-miR482c	-	0.0011	1.096130659	0.0011	0.0011
GGAATGGGCTGTTTGGGAAGC	mdo-miR482*	-	0.0011	1.096130659	0.0011	0.0011
TATCGAGAAGAAGATTGCTGAA	mtr-miR5227	-	0.0011	1.096130659	0.0011	0.0011
AAGAGAATGATAGTTACGGAT	mtr-miR5250	-	0.0011	1.096130659	0.0011	0.0011
TATGAGACACTTCGACCAGAC	osa-miRf10649	-	0.0011	1.096130659	0.0011	0.0011
CGTGGCATGACACGTGGACGT	osa-miRf11274	-	0.0011	1.096130659	0.0011	0.0011
AAATACTCTCTTCGTCTAAATA	osa-miRf11604	-	0.0011	1.096130659	0.0011	0.0011
GGATTTCCGCAGGCGGACC	osa-miRf12000	-	0.0011	1.096130659	0.0011	0.0011
TTCCTATTAATGATTGTGACA	ppt-miR1052	-	0.0011	1.096130659	0.0011	0.0011
CAATGTCTCCGCATATTTGTT	ptc-miRf10129	-	0.0011	1.096130659	0.0011	0.0011
TTTTGGAAAGAAAGTGACT	ptc-miRf10300	-	0.0011	1.096130659	0.0011	0.0011
CATCTGGCCTTCACTGTT	ptc-miRf10930	-	0.0011	1.096130659	0.0011	0.0011
GCTCAACACATGGCTGCGAC	ptc-miRf11750	-	0.0011	1.096130659	0.0011	0.0011
AGGCCATGAATTGTGGACT	ptc-miRf11770	-	0.0011	1.096130659	0.0011	0.0011
ACATGTCGCTGTCGGGCGCG	sbi-miR5386	-	0.0011	1.096130659	0.0011	0.0011
ACAAGGAGACAAGCATGT	aly-miR160c*	-	0.0011	0.0011	1.036359821	0.0011
AGAGCTTCCTTGAGTCCATTC	aly-miR319a*	-	0.0011	0.0011	1.036359821	0.0011
CTTTAATCTAATTTTCATTGCTTA	aly-miR4246	-	0.0011	0.0011	1.036359821	0.0011
TAAGGCACGAGAACATCAAC	aly-miR4250	-	0.0011	0.0011	1.036359821	0.0011
AATGGAGAAGATGAGCAAGAAAGA	ath-miR835	-	0.0011	0.0011	1.036359821	0.0011
TTGGTAGAGAATCGTTGAGA	ath-miRf10105	-	0.0011	0.0011	1.036359821	0.0011
TTGGCGCTATCTATCCTGAGT	ath-miRf10111	-	0.0011	0.0011	1.036359821	0.0011
AGGACGAGGAGCACCACAA	ath-miRf11036	-	0.0011	0.0011	1.036359821	0.0011
TGACAGAAGAGAGTGGGCACT	zma-miR156r	gma-miR156s	0.0011	0.0011	1.036359821	0.0011
CCATGGATCCCTAACATGTGG	mtr-miR1510b*	-	0.0011	0.0011	1.036359821	0.0011
GACTTAGAATGTAGGATGGTGGCA	gma-miR4342	gma-miR4342	0.0011	0.0011	1.036359821	0.0011
AGGCATCTCATGAAGACTGTT	mtr-miR5244	-	0.0011	0.0011	1.036359821	0.0011
TAACATGGTATCAGAGCTGGACTC	osa-miR1873	-	0.0011	0.0011	1.036359821	0.0011
TTCAAATGATTTTGTGTCGTT	gma-miR4350	gma-miR4350	0.0011	0.0011	1.036359821	0.0011
CTTGAGCTGTAATACTTGA	osa-miR5498	-	0.0011	0.0011	1.036359821	0.0011
AAGAATCTGAGAAATGTTAGAACC	osa-miR809h	-	0.0011	0.0011	1.036359821	0.0011
CTTCGACGATGACGACGT	osa-miRf10273	-	0.0011	0.0011	1.036359821	0.0011
TCTTCCTCTGGACGCCGGC	osa-miRf10819	-	0.0011	0.0011	1.036359821	0.0011
TATCCGGTTGTTAAGAACC	osa-miRf11138	-	0.0011	0.0011	1.036359821	0.0011
CAGCTGCTGAAGCTCCCCGAG	osa-miRf11188	-	0.0011	0.0011	1.036359821	0.0011
TTAGATCTCCAATGCCACTGT	ppt-miR1028b	-	0.0011	0.0011	1.036359821	0.0011
TGAGACGGGATCAAGGATACC	ppt-miR1039	-	0.0011	0.0011	1.036359821	0.0011
ATCCTCGTCTTCCTCGTCT	ppt-miR414	-	0.0011	0.0011	1.036359821	0.0011

CTCTCCCTGAAAGGCTC	ppt-miR477e	-	0.0011	0.0011	1.036359821	0.0011
CAGGACTGTCTTAGAAAGCCAGGC	gma-miR4356	gma-miR4356	0.0011	0.0011	1.036359821	0.0011
TAACGCGTGATATGTTAACATC	gma-miR4359b	gma-miR4359b	0.0011	0.0011	1.036359821	0.0011
CGATTACCAGAAGGCTTATTAG	gma-miR4363	gma-miR4363	0.0011	0.0011	1.036359821	0.0011
ATCCGCCTCGTCAACGCG	ptc-miRf10228	-	0.0011	0.0011	1.036359821	0.0011
ACTCGGGTGACTCGGCCT	ptc-miRf10232	-	0.0011	0.0011	1.036359821	0.0011
AGTTTCTGAAGGTCTTA	ptc-miRf10276	-	0.0011	0.0011	1.036359821	0.0011
TATGTGATCAAAGTGTGAC	ptc-miRf10816	-	0.0011	0.0011	1.036359821	0.0011
CATGGGCTTTGAGTTGCA	ptc-miRf11211	-	0.0011	0.0011	1.036359821	0.0011
GACGATCTCAGTGGCGGACC	ptc-miRf11916	-	0.0011	0.0011	1.036359821	0.0011
CGAACTGAACCAAACCGTT	ptc-miRf12144	-	0.0011	0.0011	1.036359821	0.0011
ACGGTTTGGTTCGGTTCGGACT	ptc-miRf12439	-	0.0011	0.0011	1.036359821	0.0011
TTATTAAACTCGGCTCGGCCCGGC	ptc-miRf12516	-	0.0011	0.0011	1.036359821	0.0011
TCGAAGGTTCTGGAGAGGACTGCCT	gma-miR4386	gma-miR4386	0.0011	0.0011	1.036359821	0.0011
GAAAAATTCGGAAGACGTCACTC	gma-miR4400	gma-miR4400	0.0011	0.0011	1.036359821	0.0011
TTTCTAAGACGGTTTTTTGTTT	gma-miR4992	gma-miR4992	0.0011	0.0011	1.036359821	0.0011
TGCGCCAAAAGAAGAGTTGTCCTGC	vvi-miR399i	-	0.0011	0.0011	1.036359821	0.0011
TTTTGAGAAAAGGAGGATGTCATC	gma-miR5369	gma-miR5369	0.0011	0.0011	1.036359821	0.0011
GACATGAAAATCATTATTATGAT	gma-miR5379	gma-miR5379	0.0011	0.0011	1.036359821	0.0011
GGTGACCCAGAAGAAGTTGATGA	gma-miR5679	gma-miR5679	0.0011	0.0011	1.036359821	0.0011
GGTCATGCTGTGACAGCCTCACT	aly-miR167b*	-	1.031103229	0.0011	0.0011	0.0011
CCCGCCTTGATCAACTGAA	aly-miR168b*	-	1.031103229	0.0011	0.0011	0.0011
GCAAGAAAATGAATTCGTTT	aly-miR3441.2*	-	1.031103229	0.0011	0.0011	0.0011
GTTGAAGGAAATGGAGGACC	ath-miRf10240	-	1.031103229	0.0011	0.0011	0.0011
TTGCTGCTTGTAACCTTACCT	ath-miRf10557	-	1.031103229	0.0011	0.0011	0.0011
TGGTTGGAGTTGGTCTGATG	ath-miRf10566	-	1.031103229	0.0011	0.0011	0.0011
AGTTGTCTGAGTCGTCAT	ath-miRf10627	-	1.031103229	0.0011	0.0011	0.0011
CCTCGTGAGGCGGATTACTTC	bra-miR2111a*	-	1.031103229	0.0011	0.0011	0.0011
TATCATCGTCAACATTATCAA	ghr-miR414d	-	1.031103229	0.0011	0.0011	0.0011
CTTGGAAGGAGGGGCCTCTT	vun-miR319c.4	gma-miR319f	1.031103229	0.0011	0.0011	0.0011
TCTAGGGATAAGCATATATTG	mtr-miR2645	-	1.031103229	0.0011	0.0011	0.0011
AGGGACCAAAAATGTAAGAATCGT	mtr-miR5284g	-	1.031103229	0.0011	0.0011	0.0011
TATTGGCTAGAGATAAGACAAAGA	gma-miR4349	gma-miR4349	1.031103229	0.0011	0.0011	0.0011
TGGCTGCTAGGCTCCT	osa-miR2094	-	1.031103229	0.0011	0.0011	0.0011
GAGAGAATGAAGAGCCGGTGG	osa-miR5507	-	1.031103229	0.0011	0.0011	0.0011
AAAGGAGATTGTGGAGATTGT	osa-miR815c	-	1.031103229	0.0011	0.0011	0.0011
GGAGAGGCTGGCACTG	osa-miRf10139	-	1.031103229	0.0011	0.0011	0.0011
GTCAAGCTCGATCGAGC	osa-miRf11074	-	1.031103229	0.0011	0.0011	0.0011
CTCATGGTGAAGTGGAGC	osa-miRf11458	-	1.031103229	0.0011	0.0011	0.0011
AGTGATGACGTGACAAACGAAGT	gma-miR4371a	gma-miR4371a	1.031103229	0.0011	0.0011	0.0011
CGGAACCATTCGTCGGAGC	ptc-miRf11822	-	1.031103229	0.0011	0.0011	0.0011
GCTGGAAAACACTTTGCTGGA	ptc-miRf12049	-	1.031103229	0.0011	0.0011	0.0011
CCCGTTTGGTTGCTGAGAA	ptc-miRf12247	-	1.031103229	0.0011	0.0011	0.0011
ACACCAAAGGCCTCTGCACTT	ptc-miRf12309	-	1.031103229	0.0011	0.0011	0.0011
CTTTCCTCTGCAGGGCACCA	ptc-miRf12375	-	1.031103229	0.0011	0.0011	0.0011

TGAATCTTGATGCTGCTGCACC	sbi-miR172e	-	1.031103229	0.0011	0.0011	0.0011
TCGATGTAGAAAAGAGATTGGTGA	gma-miR4385	gma-miR4385	1.031103229	0.0011	0.0011	0.0011
TGGACGAGGACGAGCAACT	tae-miR2012	-	1.031103229	0.0011	0.0011	0.0011
ATTCTGAGAGAACCGGTGTAGAAT	gma-miR4406	gma-miR4406	1.031103229	0.0011	0.0011	0.0011
TGAGTGACAGAGGAGAGTGG	vvi-miR156e	-	1.031103229	0.0011	0.0011	0.0011
AATTATTTACACACATGCT	vvi-miR3635*	-	1.031103229	0.0011	0.0011	0.0011
TTTAGGAATTAGTTACTCA	gma-miR5371	gma-miR5371-5p	1.031103229	0.0011	0.0011	0.0011
CGGATAGCCAAGGATGACTTGCCT	zma-miR169m	-	1.031103229	0.0011	0.0011	0.0011
CTTGAATGCTGATCATGCTGC	zma-miR172n	-	1.031103229	0.0011	0.0011	0.0011
CTTGTTGAATTGTTGGAATCC	mtr-miR5559	gma-miR5559	1.031103229	0.0011	0.0011	0.0011
CAAAGCATCTATCAAGGAAC	aly-miR3441.1	-	0.0011	0.0011	0.0011	0.862315642
ATTTGTGCCAATCATTG	aly-miR4227	-	0.0011	0.0011	0.0011	0.862315642
CATATGGGTGACTTATACT	aly-miR774.2	-	0.0011	0.0011	0.0011	0.862315642
AATAGATGAAGATTTGGAT	aly-miR774b	-	0.0011	0.0011	0.0011	0.862315642
GTGGCAAACCAAAGACGACAGTGT	aly-miR851	-	0.0011	0.0011	0.0011	0.862315642
TTCTTGTTGGATGCCTTGGACT	ath-miR5016	-	0.0011	0.0011	0.0011	0.862315642
ACGAGGAAGAAGATGTTAGAATT	ath-miR5641	-	0.0011	0.0011	0.0011	0.862315642
CTATTGAATCTGTTGGTTACC	ath-miR5649b	-	0.0011	0.0011	0.0011	0.862315642
TTAGACGATCATCAACAAACT	ath-miR827	-	0.0011	0.0011	0.0011	0.862315642
ATTTGTTGGTTCAAAAACA	ath-miRf10052	-	0.0011	0.0011	0.0011	0.862315642
CGAGATCGTCGTCGAGTGGCGC	ath-miRf10144	-	0.0011	0.0011	0.0011	0.862315642
AACAACGTCGTCGTTTCGT	ath-miRf10427	-	0.0011	0.0011	0.0011	0.862315642
ATCCAAAACGACGTCGGACG	ath-miRf10446	-	0.0011	0.0011	0.0011	0.862315642
GAAAACTCGAACCCAAACCT	ath-miRf10453	-	0.0011	0.0011	0.0011	0.862315642
ACTTAGAGTTTTCTGAATACCT	ath-miRf10648	-	0.0011	0.0011	0.0011	0.862315642
AATGTGTTGTAAAGTGAATATC	gma-miR1518	gma-miR1518	0.0011	0.0011	0.0011	0.862315642
TATAATAATAATAATAAT	gma-miR1533	gma-miR1533	0.0011	0.0011	0.0011	0.862315642
TATTGGCCTGGTTCACTCAGA	aly-miR171a*	gma-miR171j-5p	0.0011	0.0011	0.0011	0.862315642
ATTTTAAAGTTTCGTTTTGGTCC	mtr-miR2671j	-	0.0011	0.0011	0.0011	0.862315642
TCTTATAATTAGGACCGAAGGGCC	mtr-miR5281f	-	0.0011	0.0011	0.0011	0.862315642
TAGAGAAATTTGATCATGATTA	osa-miR1426	-	0.0011	0.0011	0.0011	0.862315642
TCTCTCTCTCTTGATTCTG	osa-miR3979	-	0.0011	0.0011	0.0011	0.862315642
TAGGAGGTAAGACGGAAGACA	osa-miR5494	-	0.0011	0.0011	0.0011	0.862315642
ATCTTGCAATTGCCTGGCA	osa-miRf10934	-	0.0011	0.0011	0.0011	0.862315642
ATGGCCACACTGTCCTCCAGA	osa-miRf11538	-	0.0011	0.0011	0.0011	0.862315642
CAGTCTCGTCATATATGACC	osa-miRf11571	-	0.0011	0.0011	0.0011	0.862315642
ATGGATGAGGATTTGGCAA	osa-miRf11681	-	0.0011	0.0011	0.0011	0.862315642
TGAGAGAAGACGAAGACATG	osa-miRf11861	-	0.0011	0.0011	0.0011	0.862315642
TCTAGAACACGAGATATACTA	peu-miR2912b	-	0.0011	0.0011	0.0011	0.862315642
AAGAGGAGCTAGAACTTAAAG	ppd-miR163	-	0.0011	0.0011	0.0011	0.862315642
ATGGAGTCCTGAATTAGCTG	ppt-miR1036	-	0.0011	0.0011	0.0011	0.862315642
TTGAAGGTCTGCATCGTT	ppt-miR902d	-	0.0011	0.0011	0.0011	0.862315642
CCAAGGTCTGTATCATAGTT	ppt-miR902g	-	0.0011	0.0011	0.0011	0.862315642
CCTCCCTACTACTACCATTCT	pta-miR482d	-	0.0011	0.0011	0.0011	0.862315642
CCAAGAAGGACTTGTCGGAGC	ptc-miR169aa	-	0.0011	0.0011	0.0011	0.862315642

CGAGGAGAATAGTACCCT	ptc-miRfl1264	-	0.0011	0.0011	0.0011	0.862315642
CTTGGTAGTAGTAGCAGCT	ptc-miRfl1495	-	0.0011	0.0011	0.0011	0.862315642
ACTCTGGCTGATCTGAACGA	ptc-miRfl1776	-	0.0011	0.0011	0.0011	0.862315642
ATTGAACTGATCGAACCGACTGAT	ptc-miRfl1864	-	0.0011	0.0011	0.0011	0.862315642
AGGACCTAAATCTCTTGATTT	ptc-miRfl2451	-	0.0011	0.0011	0.0011	0.862315642
TTCCACAAGCTTTCTTGAAGCTG	sbi-miR396e	-	0.0011	0.0011	0.0011	0.862315642
TTAGATGACCATCAACAAATA	tcc-miR827	-	0.0011	0.0011	0.0011	0.862315642
CCTTTTTTATTTGTTGCAG	gma-miR5039	gma-miR5039	0.0011	0.0011	0.0011	0.862315642

Table 2 Suppl. Putative target genes of all the DEMs and the annotations (--:uncharacterized protein).

miRNA	Target accession	Description
in BX10		
miR159d	GLYMA07G07870	AT hook motif DNA-binding family protein
	GLYMA02G09535	pectinesterase 10-related
	GLYMA16G34000	--
	GLYMA16G34070	--
	GLYMA16G34030	--
	GLYMA16G34078	--
miR162c	GLYMA03G42290	endoribonuclease dicer homolog 1
	GLYMA07G06590	60S Ribosomal protein l5
	GLYMA02G36110	LETM1-like protein
	GLYMA10G08801	LETM1-like protein
	GLYMA19G45060	endoribonuclease dicer homolog 1
	GLYMA13G21200	cactin
	GLYMA20G11040	MYB transcription factor
miR166k	GLYMA08G00626	--
	GLYMA07G05791	--
	GLYMA05G21726	homeobox-leucine zipper protein athb-15
	GLYMA07G01950	homeobox-leucine zipper protein athb-15
	GLYMA08G21620	homeobox-leucine zipper protein athb-15
	GLYMA08G41890	--
	GLYMA06G11370	PHD finger-containing protein
miR166o	GLYMA18G43540	ammonium transporter 2
	GLYMA07G05791	--
	GLYMA08G00626	--
	GLYMA05G21726	homeobox-leucine zipper protein ATHB-15
	GLYMA07G01950	homeobox-leucine zipper protein ATHB -15
	GLYMA08G21620	homeobox-leucine zipper protein ATHB -15
	GLYMA09G02750	homeobox-leucine zipper protein ATHB-14-related
	GLYMA06G09100	--
	GLYMA05G30000	--
	GLYMA08G13110	--
	GLYMA11G20520	--
	GLYMA12G08080	--
	GLYMA15G13640	homeobox-leucine zipper protein ATHB-14-related
miR166h-3p	GLYMA08G00626	--
	GLYMA07G05791	--
	GLYMA05G29470	DNA-binding domain-containing protein-related
	GLYMA02G18670	ATP-binding cassette
	GLYMA18G52940	eukaryotic translation initiation factor 5
miR171b-5p	GLYMA04G37830	--
miR3522	GLYMA07G31262	--
	GLYMA07G31301	--
	GLYMA07G31270	--
	GLYMA07G00640	--
	GLYMA17G07160	--
	GLYMA15G42181	--
miR390g	GLYMA09G03731	--
	GLYMA02G04010	proline-rich receptor-like protein kinase PERK12-related
	GLYMA08G47200	kinase-like protein TMKL1-related
	GLYMA10G33941	ubiquitin-protein ligase

miR396c	GLYMA12G35440	phytosulfokine receptor 2
	GLYMA20G38980	serine/threonine protein kinase
	GLYMA15G14675	--
	GLYMA13G16280	protein kinase family protein
	GLYMA18G38440	kinase-like protein TMKL1-related
	GLYMA14G03770	leucine-rich repeat receptor-like serine/threonine-protein kinase BAM3
	GLYMA02G43602	1-aminocyclopropane-1-carboxylate oxidase 3-related
	GLYMA05G20930	--
	GLYMA03G36370	F26K24.14 protein-related
	GLYMA06G46634	--
	GLYMA08G35547	phosphatidylinositol/phosphatidylcholine transfer protein SFH13-related
	GLYMA07G30200	--
	GLYMA02G36700	heat shock 70 kda protein 5
	GLYMA08G14560	--
	GLYMA09G35883	phosphatase
	GLYMA09G37000	G-protein coupled receptor
	GLYMA06G16835	--
	GLYMA04G38230	--
	GLYMA19G39020	F26K24.14 protein-related
	GLYMA17G08020	heat shock 70 kDa protein
miR396k	GLYMA18G01000	--
	GLYMA16G15580	protein XRI1
	GLYMA18G49680	G-protein coupled receptor
	GLYMA13G11614	methyltransferase
	GLYMA03G41190	phosphoenolpyruvate carboxylase kinase
miR403b	GLYMA17G12035	--
	GLYMA15G09475	LRR domain-containing protein
	GLYMA16G03560	--
	GLYMA08G41500	leucine-rich repeat receptor-like serine
	GLYMA09G28575	--
miR1507a	GLYMA11G00740	5'/3'-nucleotidase SURE
	GLYMA03G30940	transcription factor tt8
	GLYMA02G44515	--
	GLYMA11G04720	malate dehydrogenase, glyoxysomal
	GLYMA20G02820	protein argonaute 2-related
	GLYMA15G13260	protein argonaute 2-related
	GLYMA14G40580	basic-leucine zipper
	GLYMA18G14680	leucine-rich repeat receptor-like serine
	GLYMA16G33310	--
	GLYMA08G41800	--
	GLYMA03G29270	--
	GLYMA01G04241	--
	GLYMA01G35120	--
	GLYMA11G33480	NADH-ubiquinone oxidoreductase 75 kDa subunit
	GLYMA08G23272	--
	GLYMA04G29220	--
	GLYMA03G29370	--
	GLYMA18G09314	--
	GLYMA19G05600	--
	GLYMA0121S00200	--
	GLYMA18G09670	--
	GLYMA0121S00240	--
	GLYMA18G09786	--
	GLYMA18G09220	--

miR1507c-3p	GLYMA18G09980	--
	GLYMA18G09327	--
	GLYMA18G09720	--
	GLYMA18G09290	--
	GLYMA18G09140	--
	GLYMA0589S00200	--
	GLYMA18G04730	NADH-ubiquinone oxidoreductase 75 kDa subunit
	GLYMA17G20221	--
	GLYMA20G00521	transcription factor MYC3-related
	GLYMA18G29440	nucleobase-ascorbate transporter 11
	GLYMA05G08621	--
	GLYMA11G21200	--
	GLYMA04G29220	--
	GLYMA01G04241	--
	GLYMA15G35920	--
miR1520n	GLYMA19G05600	--
	GLYMA16G02100	mRNA splicing factor
	GLYMA16G34340	transcription cofactor
	GLYMA02G43880	--
	GLYMA10G05151	fasciclin-like arabinogalactan protein 1
miR4403	GLYMA11G07300	VAM6/VPS39-like protein
	GLYMA05G23530	basic helix-loop-helix transcription factor
	GLYMA09G15630	BRCA1-a complex subunit BRE
	GLYMA15G43050	BRCA1-a complex subunit BRE
	GLYMA04G36170	--
	GLYMA05G05720	SNARE protein
	GLYMA01G36646	--
	GLYMA02G01870	--
	GLYMA06G22820	UDP-glycosyltransferase 89b1
	GLYMA07G35430	F26K24.10 protein
miR5037a	GLYMA19G42730	dehydrogenase
	GLYMA12G16526	--
	GLYMA14G10850	cytosolic Fe-S cluster assembly factor NUBP1
	GLYMA14G36770	--
	GLYMA13G25590	protein zinc induced facilitator 1-related
	GLYMA20G03790	F26K24.10 protein
	GLYMA05G03020	--
	GLYMA07G18320	trihelix transcription factor GT-3a-related
	GLYMA12G13020	--
	GLYMA08G41560	--
miR5678	GLYMA07G07240	BYPASS1-related protein-related
	GLYMA08G25441	--
	GLYMA17G13680	--
	GLYMA18G43190	trihelix transcription factor gt-3a-related
	GLYMA13G30860	--
	GLYMA15G31040	--
	GLYMA09G26960	CHIP, isoform b
	GLYMA06G19825	mannose-1-phosphate guanylyltransferase alpha
	GLYMA04G34880	mannose-1-phosphate guanylyltransferase alpha
	GLYMA06G02940	ATP binding microtubule motor family protein
	GLYMA11G36980	squamosa promoter-binding-like protein 10-related
	GLYMA19G17790	--
	GLYMA19G06900	mannose-1-phosphate guanylyltransferase alpha
	GLYMA12G37050	ethylene receptor 1-related

PN-miR156f*	GLYMA14G38960	DNA helicase
	GLYMA16G32250	DNA helicase
	GLYMA18G00903	squamosa promoter-binding-like protein 10-related
	GLYMA18G47720	atypical dual-specificity phosphatase
	GLYMA09G32660	AFP homolog 2
	GLYMA04G07030	--
	GLYMA18G08000	amino acid transporter
in BD2		
miR482a-3p	GLYMA05G01650	transporter
	GLYMA06G11210	serine protease
	GLYMA07G33600	abscisic acid-insensitive 5-like protein 6
	GLYMA01G31520	--
miR5037c	GLYMA15G17956	polycomb protein PCl
	GLYMA13G31150	protein SMG7l
	GLYMA17G31900	ethylene-responsive transcription factor shine 2-related
miR1512b	GLYMA15G01650	CASC3/barentsz EIF4AIII binding protein
	GLYMA18G06300	TP53-regulating kinase
	GLYMA18G27930	AT15655P
miR169r	GLYMA18G52110	glucose-6-phosphate 1-dehydrogenase
	GLYMA08G21550	--
	GLYMA07G01870	--
	GLYMA04G40730	O-fucosyltransferase-like protein
miR164k	GLYMA06G14070	O-fucosyltransferase-like protein
	GLYMA09G01820	farnesyl pyrophosphate synthase
	GLYMA11G07720	FG-gap repeat-containing protein
	GLYMA06G35660	protein cup-shaped cotyledon 1-related
	GLYMA05G00930	NAC domain-containing protein 100-related
	GLYMA06G21020	NAC domain protein NAC5
	GLYMA08G18470	NAC domain protein
	GLYMA12G09700	OTU domain-containing protein 5
	GLYMA04G33270	NAC domain-containing protein 100-related
	GLYMA11G15010	UDP-glucuronic acid decarboxylase 5
miR4380b	GLYMA07G31840	40S ribosomal protein S6
	GLYMA13G38410	--
	GLYMA19G31280	cystathionine beta-lyase
miR5373	GLYMA18G11941	--
	GLYMA16G25795	histone-lysine N-methyltransferase SUV5
in common		
miR398c	GLYMA02G31270	--
	GLYMA06G28650	blue copper protein
	GLYMA03G40280	superoxide dismutase
	GLYMA01G15687	tRNA-dihydrouridine
	GLYMA06G19680	actin family cytoskeletal protein
miR4996	GLYMA06G42170	--
	GLYMA07G31310	--
	GLYMA05G25690	--
	GLYMA05G25701	--
	GLYMA09G00740	--
	GLYMA04G09110	NADP-dependent malic enzyme 2-related
	GLYMA13G25150	--
	GLYMA13G25260	--
	GLYMA13G25181	--
	GLYMA15G07691	--
	GLYMA15G07710	--

miR159f-3p	GLYMA15G07705	--
	GLYMA13G29160	transcription factor tcp2-related
	GLYMA06G47000	transcription factor
	GLYMA04G15150	transcription factor
	GLYMA03G24060	dehydrogenase
	GLYMA03G00740	CED-12,signaling molecule
	GLYMA04G32324	transcription factor tcp17-related
	GLYMA06G22240	transcription factor tcp17-related
	GLYMA13G04031	MYB transcription factor
	GLYMA15G35860	MYB transcription factor
	GLYMA20G11040	MYB transcription factor
	GLYMA13G25716	MYB transcription factor
	GLYMA13G10090	G2/mitotic-specific cyclin-B
	GLYMA14G24480	G2/mitotic-specific cyclin-B
	GLYMA19G39340	--
	GLYMA19G29990	CED-12,signaling molecule
	GLYMA16G03286	--
	GLYMA16G25932	--
	GLYMA15G20030	acyltransferase
PN-miR477	GLYMA06G00445	nucleotidyltransferase
	GLYMA02G14080	--
	GLYMA07G04480	lipoxygenase
	GLYMA12G05856	disco-interacting protein 2
	GLYMA04G37460	Dek domain-containing chromatin associated protein
	GLYMA06G17600	Dek domain-containing chromatin associated protein
	GLYMA12G34550	dehydration-responsive protein RD22
miR5044	GLYMA19G33700	mRNA splicing factor
	GLYMA11G01040	--
	GLYMA06G19260	serine carboxypeptidase-like 1-related
	GLYMA09G40770	--
miR5786	GLYMA20G06725	--
	GLYMA09G06890	plasma membrane calcium-transporting atpase 2
	GLYMA09G41040	cation transporter
	GLYMA12G03060	enoyl-[acyl-carrier-protein] reductase [NADH]
	GLYMA11G10770	dehydrogenase
	GLYMA13G16461	alpha/beta-hydrolases superfamily protein
	GLYMA15G18176	plasma membrane calcium-transporting ATPase 2
	GLYMA18G44550	cation transporter
	GLYMA13G37591	secretory carrier-associated membrane protein 1-related

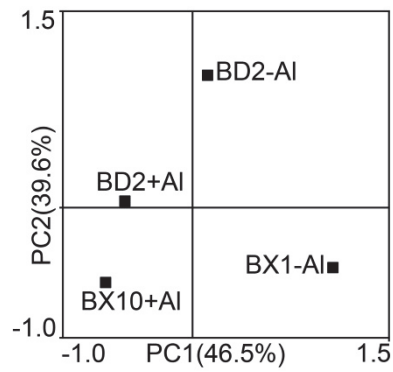


Fig.1 Suppl. Influences of genotype and AI on the expression patterns of soybean miRNAs. Principle component analysis based on normalized reads of miRNAs with combined reads over 50 in the four libraries. Two principle components were extracted, describing 86.1% of miRNA expression variations.

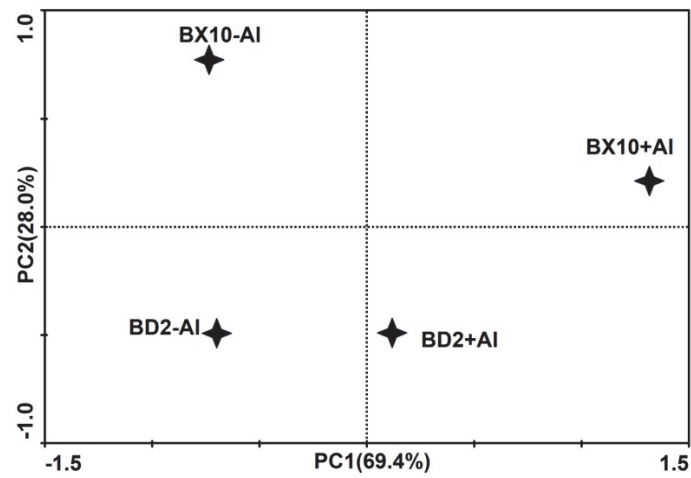


Fig.2 Suppl. Influence of AI and genotype on the expression patterns of differentially expressed miRNAs in BX10.

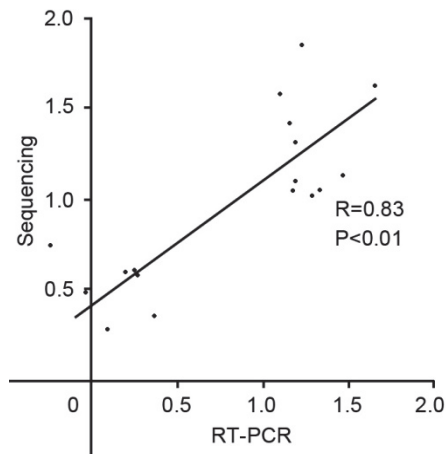


Fig.3 Suppl. Real-time qPCR (RT-PCR) and high-throughput sequencing results are significantly correlated ($r = 0.83$, $P < 0.01$).