Table S2. An average level of expression of known miRNAs identified in the tested seed samples [Rc - renewed seeds; Hv - seeds with high viability; Lv - seeds with low viability]

miRNA	sequence	averaged level of expression [RPM]		
		Rc	Lv	Hv
miR1120 family		**22.45**	**45.07**	**59.43**
miR1120.1	TTCTTATATTATGGGACGG	0	15.5	0
miR1120.2	TTCTTATATTATGGGACGGAG	22.45	29.57	59.43
miR156 family		**21539.61**	**15723.15**	**17281.67**
miR156a.1	ACAGAAGAGAGTGAGCACA	0	0	11.34
miR156a.2	GACAGAAGAGAGTGAGCAC	0	16.01	0
miR156a.3	TGACAGAAGAGAGTGAGC	9894.55	7297.93	8551.61
miR156a.4	TGACAGAAGAGAGTGAGCA	1524.98	958.67	959.61
miR156a.5	TGACAGAAGAGAGTGAGCAC	9740.25	7286.67	7434.18
miR156a.6	TGACAGAAGAGAGTGAGCACA	379.83	163.87	324.93
miR159 family		**42273.78**	**48560.66**	**40435.63**
miR159a.1	TGGATTGAAGGGAGCTCTG	0	0	13.25
miR159a.2	TTGGATTGAAGGGAGCTCTG	46.84	31.37	9.56
miR159a.3	TTTGGATTGAAGGGAGCT	8042.17	11496.05	9802.06
miR159a.4	TTTGGATTGAAGGGAGCTC	2161.7	2497.01	1774.04
miR159a.5	TTTGGATTGAAGGGAGCTCT	4390.36	6442.64	5159.53
miR159a.6	TTTGGATTGAAGGGAGCTCTG	27632.71	28093.59	23677.19
miR166 family		**21086.86**	**22964.34**	**18909.03**
miR166a.1	CGGACCAGGCTTCATTCC	0	0	9.7
miR166a.2	CGGACCAGGCTTCATTCCCC	0	17.22	0
miR166a.3	GGACCAGGCTTCATTCCCC	0	15.42	0
miR166a.4	TCGGACCAGGCTTCATTC	1023.67	931.61	840.17
miR166a.5	TCGGACCAGGCTTCATTCC	1864.28	1694.53	1850.68
miR166a.6	TCGGACCAGGCTTCATTCCC	1342.04	1920.68	1438.32
miR166a.7	TCGGACCAGGCTTCATTCCCC	16856.87	18384.88	14770.16
miR168 family		**3172,43**	**2088,39**	**2224,99**
miR168_3p.1	CCCGCCTTGCACCAAGTG	0	13.16	19.19
miR168_3p.2	CCCGCCTTGCACCAAGTGAA	0	13.18	0
miR168_3p.3	CCCGCCTTGCACCAAGTGAAT	194.11	85.51	55.21
miR168_3p.4	CCGCCTTGCACCAAGTGAAT	14.96	13.15	0
miR168_5p.5	CGCTTGGTGCAGATCGGGAC	0	17.55	0
miR168_5p.6	CTTGGTGCAGATCGGGAC	0	0	11.15
miR168_5p.7	GCTTGGTGCAGATCGGGAC	16.28	0	0
miR168_5p.8	TCGCTTGGTGCAGATCGGG	262.67	161.82	189.52
miR168_5p.9	TCGCTTGGTGCAGATCGGGA	1049	528.64	616.96
miR168_5p.10	TCGCTTGGTGCAGATCGGGAC	1635.41	1255.38	1332.96
miR171 family		**118**	**301.89**	**116.16**
miR171_3p.1	TGATTGAGCCGTGCCAATA	16.85	41.95	23.28
miR171_3p.2	TGATTGAGCCGTGCCAATATC	30.57	135.63	69.6

miR171_3p.3	TTGAGCCGTGCCAATATC	14.03	0	0
miR171_5p.4	TGTTGGCTCGACTCACTC	15	29.05	0
miR171_5p.5	TGTTGGCTCGACTCACTCAG	0	29.17	0
miR171_5p.6	TGTTGGCTCGACTCACTCAGA	41.55	66.09	23.28
miR397 family		**0**	**0**	**13.25**
miR397b_3p.1	ATCAACGCTGCACTCAACGGC	0	0	13.25
miR444 family		**70.07**	**76.04**	**51.94**
miR444b.1	TGCAGTTGCTGTCTCAAGC	14.24	30.6	19.95
miR444b.2	TGCAGTTGCTGTCTCAAGCT	0	15.42	0
miR444b.3	TGCAGTTGCTGTCTCAAGCTT	55.83	30.02	31.99
miR5048 family		**1739.1**	**1812.47**	**1518.54**
miR5048a.1	TATTTGCAGGTTTTAGGT	53.74	154.47	48.46
miR5048a.2	TATTTGCAGGTTTTAGGTC	362.74	334.34	380.42
miR5048a.3	TATTTGCAGGTTTTAGGTCT	244.76	173.97	222.25
miR5048a.44	TATTTGCAGGTTTTAGGTCTA	202.74	92.03	92.4
miR5048a.5	TATTTGCAGGTTTTAGGTCTAA	496.67	492.16	392.17
miR5048a.6	TTGCAGGTTTTAGGTCTA	8.42	0	9.5
miR5048a.7	TTTGCAGGTTTTAGGTCT	105.5	90.18	16.4
miR5048a.8	TTTGCAGGTTTTAGGTCTA	264.53	475.32	356.94
miR5049 family		**8.46**	**15.9**	**19.39**
miR5049e.1	AATTATTTAGGTACAGAGG	0	0	9.7
miR5049e.2	AATTATTTAGGTACAGAGGGA	8.46	15.9	9.7
miR5051 family		**641.65**	**560.27**	**476.2**
miR5051.1	TTTGGCACCTTGAAACTG	0	0	13.25
miR5051.2	TTTGGCACCTTGAAACTGG	16.84	13.16	0
miR5051.3	TTTGGCACCTTGAAACTGGG	115.21	55.39	42.76
miR5051.4	TTTGGCACCTTGAAACTGGGA	509.6	491.72	420.2
miR6200 family		**0**	**0**	**21.59**
miR6200.1	TTGGCCAACTAGATCTAT	0	0	10.25
miR6200.2	TTGGCCAACTAGATCTATG	0	0	11.34
miR6201 family		**111.35**	**78.47**	**88.36**
miR6201.1	TGACCCTGAGGCACTCATA	0	0	9.56
miR6201.2	TGACCCTGAGGCACTCATAC	25.05	0	10.25
miR6201.3	TGACCCTGAGGCACTCATACC	15	49.9	0
miR6201.4	TGACCCTGAGGCACTCATACCG	71.3	28.57	68.55