

Table 4. List of loci from the *TAS* gene prediction algorithm ($P < 0.005$) using Col-0 MPSS small RNA data

Locus*	Name [†]	<i>n</i>	<i>k</i>	<i>P</i> value	Small RNA sequence [‡]	Hits [§]	Predicted target
At1g50055	TAS1b	14	8	1.10E-08	UUCUAAGUCCAACAUAGCGUA	4	At1g51670 At4g29760 At4g29770 At5g18040 At5g18065
					UUCUAAGUCCAACAUAGCAUA	4	At5g18040 At5g18065
					AACAAGCGAAUGAGUCAUUCA	1	At4g05420
At2g27400	TAS1a	15	6	1.62E-05	UUCUAAGUCCAACAUAGCGUA	4	At1g51670 At4g29760 At4g29770 At5g18040 At5g18065
					UCCUAAGUCCAACAUAGCGUU	1	At5g18040 At5g18065
At1g63070	PPR	21	6	1.48E-04	UUCUCCAUCUUGUUGAGCAGA	3	At1g62590 At1g62910 At1g63070 At1g63080 At1g63150 At1g63330 At1g63400 At1g64580 At4g25180
					UUGUGUUGAAAAAGCCCAUGA(siR3as)	2	At1g63070 At1g63080
					UUUAAAGCCAAAUCAGGUUCA	2	At1g62590 At1g62910 At1g63070 At1g63080
					ACAUCAGCCUCUAUUUUGCCU	4	At1g62910 At1g62930 At1g63070 At1g63080 At1g63130 At2g07360 At3g61780
					AGAUCUGGUUGACAACCUUUC	4	At1g62670 At1g62910 At1g62930 At1g63070 At1g63080 At1g63130 At1g63150 At5g23150
					UUGUGUUGAAAAAGCCCAUGA(siR3as)	2	At1g62670 At1g62910 At1g62930 At1g63070
At1g63080	PPR	21	6	1.48E-04	AGAUCUGGUUGACAACCUUUC	4	At1g63080 At1g63130 At1g63150 At5g23150
					UUGUGUUGAAAAAGCCCAUGA(siR3as)	2	At1g63070 At1g63080

									At1g62590 At1g62910
									At1g63070 At1g63080
							UUCUCCAUCUUGUUGAGCAGA	3	At1g63150 At1g63330
									At1g63400 At1g64580
									At4g25180
							UUUAAAGCCAAAUCAGGUUCA	2	At1g62590 At1g62910
									At1g63070 At1g63080
									At1g62910 At1g62930
							ACAUCAGCCUCUAUUUUGCCU	4	At1g63070 At1g63080
									At1g63130 At2g07360
									At3g61780
At1g63130	PPR		21	6	1.48E-04	CACCAGGCUCUAUUUUGCCU		1	At1g62670 At4g00950
									At1g62930 At1g63130
							UCAAAGCCAAAUCAUAUCAC(siR9as)	4	At1g63150 At1g63330
									At1g63400
							GGGAAAAUAGAGCCUGGUGUU	1	At3g17780
									At1g62910 At1g63070
							AAUCGGGCUGAUAUCCCAUUU	1	At1g63080 At1g63130
									At5g04250
							AGAGCUUCAGAAGCAGUGGCU	1	At5g15400
									At1g62910 At1g62930
							CCACUGCUUCUGAAGCUCUGU	4	At1g63130 At1g63150
At2g39681	TAS2		9	4	3.49E-04	GAUGGUAGUUCAAGUAUCCA		1	At2g39680
									GUAUCAUCAUUCGCUUGGAGA
									At5g60050
									At1g51670 At4g29760
At2g39675	TAS1c		17	5	5.18E-04	UUCUAAGUCCAACAUAAGCGUA		4	At4g29770 At5g18040
									At5g18065
							UUCUAAGUCCAACAUAUCGAC	2	At4g29770
Chr4:5560355	IGR between At4g08692 and At4g08695	19	5	9.17E-04	GCUUCUUUUGGCUAACAGAGU			1	At1g74850 At5g48340
At4g08710	Hypothetical protein	12	4	1.25E-03	AGUCUCCUUCGUUGCCGUCGC			4	At4g35985
Chr2:8111556	IGR between At2g18690 and At2g18700	13	4	1.75E-03	UUUCUAACUUCGCCAGACUAC			1	At4g16890
Chr4:2559720	IGR between At4g04990 and At4g05000	22	5	1.90E-03	GGUUUGCUUACUUGUUUCGAU			1	At2g26000

						GAAUAAUCAGUCUUUGC UUUA	4	At3g18780
						GUUCAGAAUCUCAUUCGAUAC	1	At1g10220 At2g46660 At4g34310 At5g55860
Chr5:16033101	IGR between At5g40000 and At5g40010	22	5	1.90E-03		UUUCCAUGC UAACUAUGAACG	1	At4g32700
Chr1:11839123	IGR between At1g32720 and At1g32730	2	2	1.98E-03		GUUCCAUCGUGUUUCUAAAC	2	At1g33170
At1g44930	Hypothetical protein	2	2	1.98E-03		UCCGCCGCCAGUUGCAACAG	1	At1g35110 At1g44930 At1g71840
Chr1:24277774	IGR between At1g65345 and At1g65347	2	2	1.98E-03		ACCCAGUUCAGUGAGACGCUC	4	At2g07705
						ACGAUCUAAGUAAGGAGGUAG	3	At2g07705 At3g55270
At2g07705	Hypothetical protein	2	2	1.98E-03		ACCCAGUUCAGUGAGACGCUC	4	At2g07705
						ACGAUCUAAGUAAGGAGGUAG	3	At2g07705 At3g55270
At3g13370	Hypothetical protein	2	2	1.98E-03		GGUCCACUUUAUAACCUCCG	4	At3g13370
Chr3:9418974	IGR between At3g25790 and At3g25800	2	2	1.98E-03		UGAAGGAUCGAGGUCGAGGCA	2	At1g56650 At1g66370 At1g66390
Chr3:9577407	IGR between At3g26170 and At3g26180	2	2	1.98E-03		UGUGGUUGGUCCUGGGUUUCC	1	At1g27980
At3g31900	Hypothetical protein	2	2	1.98E-03				
At4g01980	Hypothetical protein	2	2	1.98E-03		CACGGGGUCUUUGC UAUGUU	2	At2g22710 At5g28890 At1g37080 At2g22710
						AGCUUUUUGCUCAUUUCGGAC	4	At2g38940 At4g35540 At5g28890 At5g45230
						CAUCUUUGCCCAUCUUUGCUU	2	At2g22710 At3g27240 At5g28890 At5g40810
At4g03760	Hypothetical protein	2	2	1.98E-03		AAUUGAGUUCGGUGGUCCGGA	2	At1g40133
Chr5:14644470	IGR between At5g37010 and At5g37020	2	2	1.98E-03		AAUUGUCCGUGUUAGAAUUGU	1	At3g21450
At3g29033	Glycine-rich protein	23	5	2.35E-03		UCUCCGAGUACCGCCGUCCAC	1	At1g44085
						GGACUGUAACCAUCUGGAUUC	1	At1g44085
Chr2:689346	IGR between At2g02550 and At2g02560	7	3	2.55E-03		CUGACUACCCCGGCAUUAG	6	At5g45030
Chr2:6982074	IGR between At2g16030 and At2g16040	7	3	2.55E-03		AGAGUUUUGGUAACAAUCAAC	1	At1g77830
Chr2:8829532	IGR between At2g20460 and At2g20465	24	5	2.88E-03				
At3g42550	Aspartyl protease family protein	15	4	3.15E-03		CUGCUCGGCAUGGAAGGUUGU	2	At1g50200
						CGAGCCAUGAACUCGACCUCA	2	At5g52850
						AGAACCGUCGCCUCGUAGCCG	2	At3g42550

Chr4:2346821	IGR between At4g04630 and At4g04635	15	4	3.15E-03	AGAUACAACCGCACAGAUUGC AGAUAGCGGUGUACAGACAAC AGAUUACGCUGUACAGAUUGU	4 3 1	At4g21480 At2g47980 At5g61970
Chr2:641230	IGR between At2g02440 and At2g02450	8	3	3.95E-03			
Chr4:728380	IGR between At4g01680 and At4g01690	8	3	3.95E-03			
Chr5:5217351	IGR between At5g15980 and At5g15990	8	3	3.95E-03			
At3g06435	Expressed protein	64	8	4.16E-03	CAACGUCUACAAAAAGUUC AGUUCUCUCGUCAAUGGACAA AAGGAAUGCUUCUGAUUCAUU AACUUUUUUGUAGACGUUGAC CCUAUGAUACUCAUUUUCGAC UUGAGGUCCCUACUGAAUUGU	2 2 2 2 2 2	At3g06435 At3g06435 At5g67130 At4g25570 At5g65810 At3g06435 At1g36920 At3g06435
Chr2:4114132	IGR between At2g10555 and At2g10560	26	5	4.20E-03	GGAAAUCAGGUUUAGUGAUG CUCAAGACAAAAGCAGACGCA UGAGACUCGGGCUCAUAUUGU UCACUAAACCUGAUUUUCCAC	2 2 1 2	At4g37880 At4g37210 At5g49820 At1g71870
At3g44580	Hypothetical protein	26	5	4.20E-03	AGAAGUUCUUGCAGCGUUGUU GAU AACAGGACGCUUGUAGG UGGCCUCACAUCAAUAUGCUU CAAAGCUGCCAGUAGCUUUGU	1 1 2 2	At3g10690 At3g11070 At5g55070 At3g44580 At2g14000 At2g14000 At3g44580

*The locus name or the first base position of the small RNA cluster

†Gene annotation or intergenic region (IGR)

‡Phased small RNAs listed are either inferred from the coordinates of 17-nt MPSS signatures (bolded) or validated by Northern blot analyses (this study). Only the ones with predicted target genes were shown. TAS2-derived ta-siR2140 is not represented in Col-0 MPSS database thus is not included in the current list.

§The number of genomic hits for each corresponding 17-nt MPSS signature

¶miRU was used for predicting small RNA target genes (score ≤ 2 , G:U ≤ 4 , indels ≤ 1 , other mismatches ≤ 2). PPR genes are in bold.