Supplemental Table S1. Information about oligonucleotides used for the small RNA blot and qPCR

Primer/Probe			Sequence (5' to 3')
For small-RNA Northern			
Figure 2	miR156		GTGCTCACTCTCTTCTGTCA
	miR172		ATGCAGCATCATCAAGATTCT
Figure 3	miR164a		TGCACGTGCCCTGCTTCTCCA
	miR164c		CGCACGTGCCCTGCTTCTCCA
	miR319a		GGGAGCTCCCTTCAGTCCAA
Figure 5	miR166a		GGGGAATGAAGCCTGGTCCGA
	miR824		TCCCTTCTCACAAATGGTCTA
	miR168		TTCCCGACCTGCACCAAGCGA
	miR390a		GGCGCTATCCCTCCTGAGCTT
	miR167a		TAGATCATGCTGGCAGCTTCA
	miR403		CGAGTTTGTGCGTGAATCTAA
	miR395		GAGTTCCCCCAAACACTTCAG
	siR255		TACGCTATGTTGGACTTAGAA
	siR752		AACGCTATGTTGGACTTAGGA
	siR289		TATGCTATGTTGGACTTAGAA
	siR850		GTCGATATGTTGAACTTAGAA
	miR393		GATCAATGCGATCCCTTTGGA
	miR399b		CAGGGCAACTCTCCTTTGGCA
	miR408		GCCAGGGAAGAGGCAGTGCAT
	miR396		CAGTTCAAGAAAGCTGTGGAA
	miR161		CCCCGATGTAGTCACTTTCAA
	miR159b		AAGAGCTCCCTTCAATCCAAA
	miR165a		GGGGGATGAAGCCTGGTCCGA
	miR163		ATCGAAGTTCCAAGTCCTCTTCAA
	5S rRNA		GAGGGATGCAACACGAGGACTT
For qPCR			
Figure 2	miR156a	F	GGACAAGAGAAACGCAAAGAAAC
		R	AGTGAGCACGCAAGAGAAGCAAG
	miR156b	F	AGAGGGAGAGATGGTGATTGAGGAATG

		R	GAGAGGTCAAGCAGGCAGAGATAGG
	miR157c	F	GAGAGCACTAAGGATGACATGCAA
		R	TCATCCACATGCGGTGTGA
	miR172a	F	ATCTGTTGATGGACGGTGGTGATTC
		R	GAGAGGGAAAGAATAGTCGTTGATTGC
	miR172b	F	TAGGCGCAGCACCATTAAGATTCAC
		R	GGTATTTGTAGCCGTCGATTGTTGATG
	SPL3	F	TGAGTTTGATGAAGCCAAGC
		R	TCACACGTTTCACCGTCTTT
	SPL4	F	CACAATGAGCGAAGAAGGAA
		R	TTGATTCTGCATCACCACCT
	SPL9	F	AGAACATTGGATACAAGAGTGATGAGG
		R	GTTTGAGTCGCCAATTCCCTTGTAGC
	SPL11	F	CCAGCAGGAAAGTCCAAGTT
		R	AGAGAGAGAGCACGGTGGAT
	TOE1	F	CTCAGCGTGGAGTTAGCTTG
		R	CCGAGGATCCATAAGGAAGA
	TOE2	F	ACCACCACCATAGCTTCCTC
		R	GGCCTTCCAACTTATTCCAA
Figure 3/4	miR164a	F	CGAAATCCGTCTCATTTGCTTATTTGC
		R	AGCTCATGTTGGAGAAGTTAAGTACG
	miR164b	F	TCTCACCACAAATGCGTGTATATATGC
		R	GAAGATGGGCACATGAAGAACTAACTC
	miR164c	F	GAGTAACACTTGATGGAGAAGCAGGG
		R	CTGTTCTATCCATTGACGATTGCATCC
	miR319a	F	GAGAGCTTCCTTGAGTCCATTCACAG
		R	CCGCATCATTCATTCATTTAACGAGTC
	miR319c	F	GCCGACTCATCCATCCAAACACTC
		R	AATATCTCCCGCATCATTCACACAGTC
	CUC1	F	GCACGTGTCCTGTTTCTCCAATAA
		R	ATCTGTCCCGATGATCCCAAA
	CUC2	F	ACCACTACCCTCGGCTACAC
		R	AGGGACAGTGGAGAAACAGG
	NAC1	F	TTTGATGAGACAGCCTCTGC
		R	AATTGGAGAAGCAGGGTACG
	TCP3	F	GAGCTAAACATTGTAAAACAG
		R	CAAGTGGGGTTAAAGGTTTCC

	TCP4	F	GGCTCCTTCGAATCATAACCT
		R	GGAGGCGGAAGCAGAGGTGTG
Figure 5	miR159a	F	TTCAAACATGAGTTGAGCAGGGTAAAG
		R	AGGGCAAGTTAAAGCTCCTGAGATATC
	miR167c	F	GCCAGCATGATCTTGTCTTCCTCTC
		R	ATTAGCAGGTGAAACTACCAGCATGAC
	miR168a	F	CGGGAACCAATTCGGCTGACAC
		R	CCAATCCCTGCTCACAAACCAATAAAG
	miR165a	F	TTATCATGAGGGTTAAGCTATTT
		R	CGAGGATACTCTCTATGATCACT
	miR165b	F	AGGCTATTTCTGTTGTGGGGAATGTTG
		R	GGATGAAGCCTGGTCCGACGATAC
	miR166a	F	GACTCTGGCTCGCTCTATTCATGTTG
		R	GCCTGGTCCGAAGACGCTAAAAC
	miR396a	F	TTCCACAGCTTTCTTGAACTG
		R	CCCACAGCTTTATTGAACCGCAAATC
	miR403a	F	AGAGTCGTATTACATGTTTTGTGCTTG
		R	CGAGTTTGTGCGTGAATCTAATCCAAC
	miR408a	F	AGAGAGACAGGGAACAAGCAGAGC
		R	AAGAGGCAGTGCATGGGTAGAGAC
	miR824a	F	CCAATACCCCCCAGTCTCTAAATT
		R	CCCTGCTGCACCATGAGAAC
	MYB33	F	ATGCAGATGAAACTCCACCA
		R	TCGCTCATGCTACCTGTCTC
	MYB65	F	CATCGCAGGTAGAGGAGTCA
		R	ATCAACAAACTGTGCTTCGC
	ARF3	F	TTCCCGCCTACTCAATAACC
		R	CCACACCAAATGTTCCTCTG
	ARF4	F	TCAGGTGTTATGGACCTGGA
		R	ATTGCGGGAATGATTTAAGC
	AGO1	F	AAGGAGGTCGAGGAGGGTAT
		R	AGCTCGGGAACTGATTGTCT
	PHB	F	AACAGGGCTATGCTCATCTGC
		R	AACGAACGACCAATTCACGAAC
	PHV	F	GATGGTCTCCAATGAGTAGTGA
		R	GGACACCACTTCCAAAACTTG
	REV	F	GCCAAGCTAATGCAACAGGGA

		R	AGGAGAAGGCAAGACAATGCA
	GRF1	F	CAACAATGTCGATTCTTGGC
		R	AGATGGAGCCATAGGGATTG
	GRF3	F	CAGATGGAGGACACATCCTG
		R	TGGAGAGACAAGTGGCTGAG
	AGO2	F	GAGCGGTGGTGAAATCATTG
		R	CGCACAACTCTCCCTCTCTC
	ARPN	F	ACCTTTAACGCTGTGGGTTG
		R	CCTTCACTACGTTGTGCATCC
	AGL16	F	AGGTTTCAGAGGTCGAGGGT
		R	ATGATCATGCTGCGGTTG
	DCL1	F	CCATTCCTAAGCGAAGTTTCA
		R	CCGAGCAACATAAAGATCCA
	SE	F	TATGGTGATGAAAGGCCTCA
		R	ACCATAACCTCCACGTCCTC
	HYL1	F	TGTTTCCTCTGGTGTTTCCA
		R	CTCATAAACAGGCGTTGGG
	ABH1	F	TGCTGGAAAGTTTCATGAGC
		R	CCCTCGAATGATCAGAAGGT
	CBP20	F	CAGGTTCGTGATGAATACCG
		R	AGCTTGAGGATAAGCTCCCA
	RDR6	F	AAGAGTTTAGGCCGTGCTGT
		R	GCTCATTCGCCAAGTTTCTT
	SDN1	F	GAATCAACTAACATGGTAGCTGT
		R	TCTACCACAGAGAGACTAGCAT
	SDN2	F	GAAGATGGAACCGACAAAGATCG
		R	GATCTTGAGCAGTAAGTCCAGTA
	SDN3	F	GATTGTGAGATGGTTACCTGTGA
		R	TGAATATCTGCAACAGAAAGAGTA
	SDN5	F	AAGCGAAAGCAGAACTCGAT
		R	CCAATCCAGGAAGGTAGAGC
	DDL	F	GAAAGAAGGATTGCCGACAT
		R	TTTCCCGGTACTGAATGACA
For ChIP-qPCR			
Figure 5	miR156a	F	TTGGCTAACAATTTGCCACT
		R	TTAGGGCTTGTTGATGTTGG
	miR164a	F	TCATGATGATAAATGCCGAAG

		R	AGTCTTTGACGACCCACCTT
	miR164c	F	GGTGATGAGTTTGGGTCAGTT
		R	CGCATTTACATATACGCATGG
	miR166a	F	TGAGCCTATTTCCAACGTTCT
		R	TTGAACATGGCCATAATTTGTT
	miR168a	F	TGCTCTTTATCTCGGAATATTTG
		R	GTGAAAATTTGGTGGGCATT
	miR172b	F	AGAGACACGCAATGACTTCG
		R	TGGTATTAAGGACTTGTAGGACTCA
	TOE1	F	TGGACCAATATCCATCAAGC
		R	TTAGGAATGTACGTTGGTGTGTT
Figure 5/1	FLC	F	TTTGTGTTAATCTCCCGAACA
		R	GTGTTACCAAAGTCGTGCCTAC
For MNase-qPCR			
Figure 8	MIR156A C	F	AAAGAATCAAAGAGAGGGAGGGA
		R	AAAGGGTCTCAAATGGAATCTCT
	MIR156A B	F	TGGCTCTTGTCGCTTTCTTT
		R	TTCAATTCAATGCGTCGCCA
	MIR156A A	F	TGGCGACGCATTGAATTGAA
		R	AGACCATTCATTGTTCACTCTCA
	MIR156A D	F	AAGCTTTGTGTTAGATCTGAGTTTT
		R	TCCCTCCCTCTCTTTGATTCTTTG
	MIR164A C	F	GCGATCGTTTAGCTCTCTTCA
		R	ATGATGGCATCTCACGCAAA
	MIR164A B	F	AAGGTCTTGCTTGTCAACGC
		R	TGCTAGGTTGCTAGGCGTAC
	MIR164A A	F	TTAGGACAACACGCAAAGCC
		R	GAAGGGTCAAAAGGGCAAGG
	MIR164A D	F	TCATGTGCTTGGAAATGCGG
		R	TGTTTGTTGGTTTGCACGTG
	FLC B	F	GCTACTTTTGCATTGCCTTAGT
		R	CCGTATCGTAGGGGAGGAAA
	FLC A	F	TGAACTCTTCCGACTTCTCAAA
		R	AGGCGAGTGGTTCTTTGTTT
	FLC C	F	GGATGCGTCACAGAGAACAG
		R	CGACAAGTCACCTTCTCCAA
	ACT2 P	F	GGATCGATGCCAAAAGTCCC

		R	CGTTCTAAATTTTGTCGACGTGA
	ACT2 GB	F	GCTGGAATCCACGAGACAAC
		R	CCACCACTGAGCACAATGTT
	FWA GB	F	CATCCACCAACTCTACCAGC
		R	AGCCATCTCTTTGCACCTAG
	EVD GB	F	CGACATGTTCTCTTGCCCTT
		R	TGTTTGAGGAATCCGATGCT
RT-qPCR			
Figure 1	JAZ9	F	AGAAGAGTTTAGGCCGTGCTG
		R	TCGCCTTGTTTCTTGCTTGTG
	JAZ10	F	AGAAGAGTTTAGGCCGTGCTG
		R	TCGCCTTGTTTCTTGCTTGTG
	JAZ1	F	AGAAGAGTTTAGGCCGTGCTG
		R	TCGCCTTGTTTCTTGCTTGTG
	UBQ6	F	AGAAGAGTTTAGGCCGTGCTG
		R	TCGCCTTGTTTCTTGCTTGTG
	HSP70	F	TTCCAAACCCAAGGACAGAG
		R	ATGGAGCCAGTGGAGAAGTG
Figure 2-4, 6/8	RDR6	F	AGAAGAGTTTAGGCCGTGCTG
		R	TCGCCTTGTTTCTTGCTTGTG
	SE	F	GTGTACAAGCATCTCAAGC
		R	CCTGTCTTGTCTACAAGC
	ABH1	F	GAAAGCTTCAGCCAATGC
		R	ACATCTTCACCCGAGAAC
	TUB	F	CTCAAGAGGTTCTCAGCAGTA
		R	TCACCTTCTTCATCCGCAGTT

Supplemental Table S2. Numbers of lateral root in WT and *arp6*

	WT (12 d)		*arp6* (12 d)		WT (8 d)		*arp6* (8 d)	
plant	LR	LR/cm	LR	LR/cm	LR	LR/cm	LR	LR/cm
#1	12	2.22	9	2.13	12	2.22	9	2.13
#2	14	2.08	12	3.04	14	2.08	12	3.04
#3	16	2.62	12	3.63	16	2.62	12	3.63
#4	12	2.04	10	3.29	12	2.04	10	3.29
#5	11	1.95	12	2.72	11	1.95	12	2.72
#6	18	2.83	9	2.36	18	2.83	9	2.36
#7	12	1.94	10	2.2	12	1.94	10	2.20
#8	11	1.92	10	3.76	11	1.92	10	3.76
#9	15	2.52	13	2.7	15	2.52	13	2.70
#10			8	2.08			8	2.08
av.	13.44	2.23	10.5	2.79		1.38		2.02
s.d.	2.38	0.33	1.61	0.6		0.45		0.65

LR indicates lateral root number.

Supplemental Table S3. Root lengths of WT and *arp6*

	WT(8 d)	*arp6* (8 d)	WT(11 d)	*arp6* (11 d)
#1	3.89	1.55	5.42	4.23
#2	3.44	1.34	6.73	3.95
#3	3.29	2.00	6.12	3.31
#4	2.39	2.42	5.88	3.04
#5	3.24	2.48	5.64	4.42
#6	3.78	2.48	6.37	3.81
#7	3.01	2.15	6.19	4.54
#8	2.59	1.41	5.71	2.66
#9	4.11	1.68	5.95	4.82
#10	3.69	1.85		3.85
#11	3.11	1.62		
#12	3.36	1.47		
#13	4.34	2.48		
#14		2.61		
#15		2.36		
av.	3.40	2.00	6.00	3.86
s.d.	0.55	0.45	0.39	0.67

Supplemental Table 4. Comparison of individual miRNA abundance in small RNA librari

	sequence	width	is.miRNA	miRNA	arp6_1_mu	arp6_2_mu	arp6_3_mu
2009963	ACTCATA	21	TRUE	ath-miR50	5	11	10
11236188	TGAGATG	21	TRUE	ath-miR18	1	0	0
9708740	TAAGTTA	21	TRUE	ath-miR18	0	0	0
12514020	TTGTGCG	21	TRUE	ath-miR56	0	0	0
12221521	TTCGATGT	20	TRUE	ath-miR77	0	2	0
11928588	TGTTTGTT	22	TRUE	ath-miR83	0	0	0
12700368	TTTGACGT	21	TRUE	ath-miR39	151	145	151
11146951	TGAAGCT	22	TRUE	ath-miR16	11	10	12
12587351	TTTAGGTC	21	TRUE	ath-miR84	7	5	3
1555553	ACATATG	21	TRUE	ath-miR55	29	21	18
12247696	TTCGTTGT	21	TRUE	ath-miR85	13	8	8
9831861	TACGCATT	22	TRUE	ath-miR77	1	0	2
11602163	TGGGTTG	24	TRUE	ath-miR56	1	1	0
2399955	AGAGAGT	22	TRUE	ath-miR81	0	2	1
8534003	GGAATCTT	21	TRUE	ath-miR17	1	1	1
10158788	TATGATCA	21	TRUE	ath-miR56	1	3	0
12338890	TTGAAGA	24	TRUE	ath-miR16	686	601	546
7769283	GATCCCC	20	TRUE	ath-miR81	4	4	2
11178664	TGACAGA	20	TRUE	ath-miR15	4	8	8
2827479	AGGCTTTT	21	TRUE	ath-miR56	2	0	3
12263198	TTCTCAAG	21	TRUE	ath-miR82	78	60	78
11178675	TGACAGA	20	TRUE	ath-miR15	4885	4276	5284
12028489	TTAGATTC	21	TRUE	ath-miR40	3177	2830	2786
11384618	TGCCAAA	21	TRUE	ath-miR39	178	173	160
11300501	TGATCTCT	22	TRUE	ath-miR83	3	3	6
10154888	TATGAGA	21	TRUE	ath-miR40	15	14	19
12433576	TTGGACT	21	TRUE	ath-miR31	59	64	61
2834933	AGGGACT	21	TRUE	ath-miR56	12	10	15
3475912	ATCATGCT	21	TRUE	ath-miR39	22	19	16
9999426	TAGTCCG	21	TRUE	ath-miR82	3	2	9
3475826	ATCATGC	21	TRUE	ath-miR39	289	227	236
11178689	TGACAGA	20	TRUE	ath-miR15	4	3	2
12788414	TTTTACTG	21	TRUE	ath-miR50	27	26	27
12349009	TTGACAG	21	TRUE	ath-miR15	1237	1055	984
3691737	ATGAATTT	21	TRUE	ath-miR86	19	12	14
12448447	TTGGCATT	20	TRUE	ath-miR39	86	93	78
2657183	AGCTAAG	21	TRUE	ath-miR56	9	7	8
12025189	TTAGAGTT	21	TRUE	ath-miR78	99	88	75
12433569	TTGGACT	21	TRUE	ath-miR31	898	737	726
12171987	TTCCACA	21	TRUE	ath-miR39	2100	1769	1840

6632395	CTGAAGT	21	TRUE	ath-miR39	80	74	70
9682280	TAAGATC	22	TRUE	ath-miR85	11	16	15
809842	AAGCTCA	21	TRUE	ath-miR39	277	218	211
11146943	TGAAGCT	21	TRUE	ath-miR16	1318	1239	1254
11335382	TGATTGG	21	TRUE	ath-miR77	90	82	91
12737151	TTTGGATT	21	TRUE	ath-miR15	12342	10612	10927
10716267	TCGGACC	21	TRUE	ath-miR16	9256	9366	8244
12822051	TTTTCTTC	21	TRUE	ath-miR83	4	6	3
11402788	TGCCTGG	21	TRUE	ath-miR16	103	63	82
12545875	TTGTTTTG	21	TRUE	ath-miR56	90	75	88
10889118	TCTCGCG	20	TRUE	ath-miR56	12	10	16
10711155	TCGCTTG	21	TRUE	ath-miR16	120	133	123
10236078	TATTGGC	21	TRUE	ath-miR17	325	340	260
5456912	CCCCAAA	20	TRUE	ath-miR15	181	165	145
11115469	TGAAAGT	21	TRUE	ath-miR16	11514	9955	10618
5774248	CCTTCTCA	21	TRUE	ath-miR82	148	145	125
11333895	TGATTGA	21	TRUE	ath-miR17	307	290	298
748539	AAGATAA	21	TRUE	ath-miR85	27	22	13
11843991	TGTGTTCT	21	TRUE	ath-miR39	200	137	94
3749554	ATGCACT	21	TRUE	ath-miR40	949	737	874
11107952	TGAAACC	21	TRUE	ath-miR59	6	3	2
10494048	TCCAATA	21	TRUE	ath-miR86	12	6	12
11480930	TGGAAGA	23	TRUE	ath-miR56	75	56	67
11506489	TGGAGAA	21	TRUE	ath-miR16	130	122	110
11506498	TGGAGAA	21	TRUE	ath-miR16	88	78	80
10460098	TCATGGT	21	TRUE	ath-miR84	9	2	6
2296023	AGAATCTT	21	TRUE	ath-miR17	3	11	7
12346641	TTGAATTG	21	TRUE	ath-miR84	3008	2874	2620
164895	AAACGAA	21	TRUE	ath-miR83	39	35	39
10320009	TCAATAG	21	TRUE	ath-miR86	10	10	4
12040446	TTAGGCT	21	TRUE	ath-miR18	2	1	6
4175645	ATTTCTAG	21	TRUE	ath-miR84	5	8	3
12227372	TTCGCTTG	22	TRUE	ath-miR17	967	854	844
12223998	TTCGCAG	21	TRUE	ath-miR39	6	6	3
10363755	TCACTCCT	21	TRUE	ath-miR84	15	10	22
11843988	TGTGTTCT	21	TRUE	ath-miR39	21380	21356	19169
10471665	TCATTGAG	21	TRUE	ath-miR39	22	25	10

ies between WT and arp6.

arp6_4_mu	wt_1_multi	wt_2_multi	wt_3_multi	wt_4_multi	Likelihood	ordering	FDR.DE
10	7557	5954	5876	5922	1	2>1	0
1	118	109	111	81	1	2>1	6.87E-13
1	17	26	19	24	1	2>1	5.94E-10
1	14	24	25	19	1	2>1	7.19E-10
0	47	43	38	35	1	2>1	6.22E-10
0	6	15	8	2	1	2>1	5.52E-08
132	1035	1165	850	1164	1	2>1	1.67E-11
6	62	46	49	38	1	2>1	8.98E-08
3	26	14	13	11	0.995	2>1	0.000216
19	87	66	75	62	1	2>1	1.71E-07
11	49	28	33	20	1	2>1	4.18E-05
0	2	2	2	3	1	2>1	2.62E-07
3	7	5	2	0	1	2>1	2.28E-05
2	3	1	9	1	1	2>1	2.55E-05
0	2	2	3	1	1	2>1	1.34E-07
1	3	1	7	2	1	2>1	3.52E-06
422	1720	1561	1241	1277	1	2>1	1.99E-06
3	4	10	7	4	0.999	2>1	6.25E-05
1	8	13	9	10	0.978	2>1	0.00098
3	3	6	4	2	1	2>1	1.11E-05
95	116	137	123	140	0.998	2>1	9.89E-05
5004	8382	8695	7370	7481	0.974	2>1	0.00137
2789	4649	5189	4373	4385	0.989	2>1	0.000511
135	315	276	227	219	0.994	2>1	0.00027
5	14	5	2	6	0.982	2>1	0.000801
18	35	22	21	22	0.903	2>1	0.004249
41	110	85	71	74	0.949	2>1	0.002955
10	16	23	13	19	0.757	2>1	0.016363
19	38	37	21	11	0.833	2>1	0.006407
2	9	8	1	2	0.957	2>1	0.002214
280	382	290	259	269	0.199	2>1	0.09011
4	5	5	3	2	1	2>1	2.83E-05
33	32	30	38	28	0.37	2>1	0.046313
1219	1332	1256	1317	1178	0.058	2>1	0.128092
20	9	15	24	25	0.406	2>1	0.034419
96	110	109	93	79	0.238	2>1	0.076437
6	12	5	8	7	0.967	2>1	0.001883
64	74	90	94	88	0.191	2>1	0.094688
666	903	820	664	817	0.031	2>1	0.13319
1706	2607	1736	1671	1795	0.018	2>1	0.138302

62	74	89	68	65	0.165	2>1	0.108379
17	7	18	20	16	0.287	2>1	0.067468
234	291	250	224	183	0.075	2>1	0.118084
1158	1479	1239	1169	1061	0.017	1>2	0.143359
99	101	76	72	104	0.173	1>2	0.103806
8298	12937	10435	7846	9116	0.002	1>2	0.153457
7266	7999	9664	6455	6615	0.004	1>2	0.148432
2	3	3	5	2	1	1>2	3.79E-05
77	96	66	63	53	0.255	1>2	0.071928
79	82	86	52	53	0.531	1>2	0.026882
15	10	17	9	7	0.319	1>2	0.058943
134	102	109	97	93	0.816	1>2	0.01033
267	231	267	188	236	0.635	1>2	0.023724
166	112	147	108	136	0.822	1>2	0.007721
9647	10768	7459	6936	6737	0.064	1>2	0.123101
141	124	121	94	88	0.821	1>2	0.009014
270	266	214	227	153	0.878	1>2	0.005165
22	13	21	14	12	0.643	1>2	0.018832
161	201	35	71	100	0.188	1>2	0.099228
745	728	629	463	438	0.787	1>2	0.013192
2	2	1	2	3	1	1>2	1.78E-05
11	6	3	9	7	0.977	1>2	0.001166
73	48	43	24	47	0.99	1>2	0.000424
104	74	62	72	66	0.999	1>2	4.73E-05
76	55	38	59	35	0.998	1>2	0.000139
6	6	2	3	2	0.998	1>2	0.000119
6	5	4	2	4	0.996	1>2	0.00017
2495	1531	1361	1037	1263	1	1>2	5.62E-06
29	16	24	12	12	0.999	1>2	7.92E-05
6	0	1	8	4	0.992	1>2	0.000339
3	0	1	3	1	1	1>2	3.42E-05
4	1	2	3	2	1	1>2	1.56E-05
843	388	376	318	300	1	1>2	1.90E-07
3	2	2	3	0	1	1>2	1.34E-05
14	6	5	3	9	0.983	1>2	0.000654
19502	9071	6759	6093	5527	1	1>2	2.10E-07
31	4	4	4	4	0.999	1>2	7.06E-05

FWER.DE	arp6 avera	wt averag	fold chang	mean leve	ratio ((arp6/wt**100, %)
0	9	6327.25	-9.46	7.9	0.14
1.37E-12	0.5	104.75	-7.71	2.86	0.48
2.08E-08	0.25	21.5	-6.43	1.21	1.16
2.73E-08	0.25	20.5	-6.36	1.18	1.22
2.24E-08	0.5	40.75	-6.35	2.17	1.23
3.53E-06	1	7.75	-2.95	1.48	12.9
5.01E-11	144.75	1053.5	-2.86	8.61	13.74
6.01E-06	9.75	48.75	-2.32	4.45	20
0.023945	4.5	16	-1.83	3.08	28.13
1.23E-05	21.75	72.5	-1.74	5.31	30
0.004257	10	32.5	-1.7	4.17	30.77
1.99E-05	0.75	2.25	-1.58	0.38	33.33
0.002184	1.25	3.5	-1.49	1.06	35.71
0.002473	1.25	3.5	-1.49	1.06	35.71
9.38E-06	0.75	2	-1.42	0.29	37.5
0.000302	1.25	3.25	-1.38	1.01	38.46
0.000167	563.75	1449.75	-1.36	9.82	38.89
0.006542	3.25	6.25	-0.94	2.17	52
0.110713	5.25	10	-0.93	2.86	52.5
0.001014	2	3.75	-0.91	1.45	53.33
0.010625	77.75	129	-0.73	6.65	60.27
0.153964	4862.25	7982	-0.72	12.6	60.92
0.05776	2895.5	4649	-0.68	11.84	62.28
0.030082	161.5	259.25	-0.68	7.68	62.3
0.090684	4.25	6.75	-0.67	2.42	62.96
0.427486	16.5	25	-0.6	4.34	66
0.314912	56.25	85	-0.6	6.11	66.18
0.913394	11.75	17.75	-0.6	3.85	66.2
0.581308	19	26.75	-0.49	4.49	71.03
0.242626	4	5	-0.32	2.16	80
1	258	300	-0.22	8.12	86
0.002774	3.25	3.75	-0.21	1.8	86.67
0.999869	28.25	32	-0.18	4.91	88.28
1	1123.75	1270.75	-0.18	10.22	88.43
0.997736	16.25	18.25	-0.17	4.11	89.04
1	88.25	97.75	-0.15	6.54	90.28
0.208712	7.5	8	-0.09	2.95	93.75
1	81.5	86.5	-0.09	6.39	94.22
1	756.75	801	-0.08	9.6	94.48
1	1853.75	1952.25	-0.07	10.89	94.95

1	71.5	74	-0.05	6.18	96.62
1	14.75	15.25	-0.05	3.91	96.72
1	235	237	-0.01	7.88	99.16
1	1242.25	1237	0.01	10.28	100.42
1	90.5	88.25	0.04	6.48	102.55
1	10544.75	10083.5	0.06	13.33	104.57
1	8533	7683.25	0.15	12.98	111.06
0.003817	3.75	3.25	0.21	1.8	115.38
1	81.25	69.5	0.23	6.23	116.91
0.987937	83	68.25	0.28	6.23	121.61
0.999995	13.25	10.75	0.3	3.58	123.26
0.769426	127.5	100.25	0.35	6.82	127.18
0.977288	298	230.5	0.37	8.03	129.28
0.656025	164.25	125.75	0.39	7.17	130.62
1	10433.5	7975	0.39	13.16	130.83
0.717428	139.75	106.75	0.39	6.93	130.91
0.497548	291.25	215	0.44	7.97	135.47
0.944319	21	15	0.49	4.15	140
1	148	101.75	0.54	6.94	145.45
0.853753	826.25	564.5	0.55	9.42	146.37
0.00167	3.25	2	0.7	1.35	162.5
0.131519	10.25	6.25	0.71	3	164
0.047706	67.75	40.5	0.74	5.71	167.28
0.004865	116.5	68.5	0.77	6.48	170.07
0.015153	80.5	46.75	0.78	5.94	172.19
0.012855	5.75	3.25	0.82	2.11	176.92
0.018679	6.75	3.75	0.85	2.33	180
0.000495	2749.25	1298	1.08	10.88	211.81
0.008442	35.5	16	1.15	4.57	221.88
0.037952	7.5	3.25	1.21	2.3	230.77
0.00341	3	1.25	1.26	0.95	240
0.001447	5	2	1.32	1.66	250
1.39E-05	877	345.5	1.34	9.1	253.84
0.00123	4.5	1.75	1.36	1.49	257.14
0.073954	15.25	5.75	1.41	3.23	265.22
1.55E-05	20351.75	6862.5	1.57	13.53	296.56
0.007458	22	4	2.46	3.23	550