Genome-wide detection of intervals of genetic heterogeneity underlying complex traits

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S1 Supplementary Tables

Phenotype Name	#Samples	%Cases	#SNPs	$\delta^*_{ m Bonferroni}$	$\delta_{ extsf{fais}}$	$\delta_{ t fais-wy}$
Chlorosis 16	176	47.73	214051	2.18e-12	2.09e-08	1.70e-07
Chlorosis 10	177	15.82	214051	2.18e-12	1.52e-08	1.96e-07
Leaf roll 22	176	17.61	214051	2.18e-12	1.52e-08	1.85e-07
Emco5	86	80.23	214044	2.18e-12	2.41e-08	3.81e-07
Emoy	76	53.95	213981	2.18e-12	3.26e-08	3.13e-07
Hiks1	84	60.71	213988	2.18e-12	2.65e-08	2.56e-07
Noco2	87	55.17	214043	2.18e-12	2.96e-08	3.18e-07
Anthocyanin 16	176	39.77	214051	2.18e-12	1.90e-08	1.54e-07
Anthocyanin 10	177	18.64	214051	2.18e-12	1.52e-08	1.86e-07
Anthocyanin 22	177	36.16	214051	2.18e-12	1.85e-08	1.56e-07
Emwa1	85	62.35	214042	2.18e-12	2.64e-08	2.71e-07
avrRpt2	89	80.9	214032	2.18e-12	2.40e-08	3.44e-07
avrB	87	63.22	214032	2.18e-12	2.48e-08	2.68e-07
Leaf roll 16	176	21.02	214051	2.18e-12	1.57e-08	1.77e-07
avrRpm1	84	66.67	214022	2.18e-12	2.42e-08	2.99e-07
Chlorosis 22	176	62.5	214051	2.18e-12	1.85e-08	1.55e-07
Leaf roll 10	177	55.93	214051	2.18e-12	1.99e-08	1.74e-07
avrPphB	90	51.11	214032	2.18e-12	3.16e-08	2.86e-07
LES	95	22.11	214051	2.18e-12	2.04e-08	3.32e-07
LY	95	30.53	214051	2.18e-12	2.17e-08	2.80e-07
YEL	95	8.42	214051	2.18e-12	4.64 e-08	9.67 e-07

Table S1: Corrected significance threshold of FAIS (δ_{FAIS}), FAIS-WY ($\delta_{\text{FAIS-WY}}$) and the exhaustive Bonferroni significance threshold ($\delta^*_{\text{Bonferroni}}$).

Description	Phenotype	\mathbf{Chr}	Position	Ref	Alt	MAF	snpEFF Effect	Codon Change	AA Change	Gene ID	P-Value
	avrB	3	2288913	G	Т	0.046	5 Prime UTR Variant			AT3G07195	2.92E-01
		3	2289178	Т	Α	0.23	Intron Variant			AT3G07195	3.05E-05
		3	2289559	T	A	0.356	Synonymous Variant	cgT/cgA	Arg58Arg	AT3G07195	1.94E-02
	avrPphB	1	4139802	-T -	C	0.167	Synonymous Variant	agT/agC	Ser455Ser	AT1G12200	1.62E-05
Hypersensitive Response		3	4140044 2310055	T	G	0.250	Missense Variant	Tag/Cag	Trp118Cly	AT3C07260	2.88E-07
	avrRnm1	3	2311035	т	G	0.155	Intergenic	1 gg/ Ggg	11p1100ly	A13G07200	2.78E-00 8.26E-02
	uoniipmi	3	2311574	Ċ	Т	0.179	Intergenic				1.28E-01
	D 10	4	13231162	T	С	0.247	Intergenic				1.02E-04
	avrRpt2	4	13231999	G	Т	0.056	Intergenic				1.49E-04
		2	14018996	А	С	0.079	Synonymous Variant	gcT/gcG	Ala320Ala	AT2G33040	4.73E-02
		2	14019038	А	G	0.085	Synonymous Variant	tcT/tcC	Ser306Ser	AT2G33040	5.88E-01
		2	14019977	G	C	0.096	Missense Variant	atC/atG	Ile120Met	AT2G33040	3.71E-02
		2	14020898	G	Т	0.124	Intergenic				3.60E-01
		2	14021720	т	1	0.079	Synopymous Variant	atT /at A	Lou60Lou	AT2C 33050	1.00E-01 5.26F 03
		2	14022070	A	т	0.124	Synonymous Variant	tcA/tcT	Ser531Ser	AT2G33050	1.60E-01
	Leaf roll 10	2	14023726	A	Ť	0.294	Synonymous Variant	atA/atT	Ile619Ile	AT2G33050	8.19E-03
Leaf roll presence		2	14023855	C	G	0.09	Missense Variant	agC/agG	Ser662Arg	AT2G33050	6.18E-02
A.		2	14023969	С	Α	0.085	Synonymous Variant	ctC/ctA	Leu700Leu	AT2G33050	1.01E-01
		2	14024162	С	Т	0.09	Missense Variant	Ctt/Ttt	Leu765Phe	AT2G33050	6.18E-02
		2	14024485	С	Α	0.09	Intergenic				6.18E-02
		2	14025154	Т	G	0.085	Intergenic				1.01E-01
		2	14025341	A	G	0.147	Intergenic			ATTO COORDO	5.76E-02
		2	14025518	1	G	0.356	5 Prime UTR Variant			A12G33060	4.88E-04
	Leaf roll 16	5 5	18040300	A C	т	0.130	Intergenic				0.14E-04 1.75E-03
	LES	4	8307440	T	G	0.188	Missense Variant	Aaa/Caa	Lys75Gln	AT4G14440	2.26E=04
		4	8307761	A	т	0.147	Intergenic	maa/ Caa	Lysroom	11401440	1.82E-01
		4	8307910	Т	Ā	0.232	Intergenic				1.42E-01
Presence or absence of le-		4	8308076	Α	G	0.368	Intergenic				4.02E-03
sioning		4	8308306	Т	Α	0.074	Intergenic				3.42E-01
		4	8308768	Т	Α	0.042	Intergenic				5.72E-01
		4	8308977	C	A	0.295	Intergenic	~ / .			2.88E-01
		1	18192753	G	A	0.253	Missense Variant	gGc/gAc	Gly406Asp	AT1G49190	3.87E-02
Presence or absence of el-	LY	1	18192950	<u> </u>	A C	0.263	Intron Variant			AT1G49190	7.99E-02
ther lesioning of yenowing		1	18196934	C	G	0.211	Introli variant			A11G49190	2.83E-04 4.80E-02
	YEL	3	20137884	C	A	0.495	3 Prime UTB Variant			AT3G54390	5.69E-03
		3	20139860	Ť	G	0.358	Intergenic			1110001000	2.52E-01
Presence or absence of yel-		3	20142484	А	G	0.211	Missense Variant	cTa/cCa	Leu39Pro	AT3G54400	1.97E-01
lowing		3	20143997	Т	G	0.421	Intergenic				1.33E-01
		3	20144047	\mathbf{C}	G	0.053	Intergenic				1.00E+00
		3	20144480	A	С	0.411	Intergenic	~ / .			1.93E-02
	Anthocyanin 10	1	5951857	G	Т	0.085	Synonymous Variant	ctC/ctA	Leu415Leu	AT1G17370	7.71E-02
		1	5952292	A	G	0.362	Synonymous Variant	ttT/ttC	Phe301Phe	AT1G17370 AT1C17270	3.21E-05 7.60E-01
		2	1702970	A	G	0.057	Synonymous Variant	otT/otC	Val106Val	AT2G04845	6.46E=03
Visual anthocyanin pres- ence	Anthocyanin 16	2	1703341	A	т	0.091	Intron Variant	801/800	Varioovar	AT2G04845	2.96E-03
		2	1703427	G	Ā	0.136	Synonymous Variant	gtC/gtT	Val70Val	AT2G04845	1.35E-02
	Anthocyanin 22	2	1703930	Т	Α	0.091	Missense Variant	Atg/Ttg	Met22Leu	AT2G04845	2.96E-03
		1	14037978	А	G	0.254	Intergenic	·			1.14E-02
		1	14039321	Т	С	0.35	Intergenic				7.43E-01
		1	14040254	C	A	0.232	Intergenic				1.52E-02
		1	14040529	G	A	0.237	Intergenic Mission Venient	Tt=/Ct=	T 400 V-1	ATT2C196720	9.68E-03
Visual Chlorosis precense	Chlorosis 22	3 3	9825206 0825206	т Т	C	0.170	Synonymous Variant	1 tg/Gtg Ttg/Ctg	Leu400 Val	AT3G20730	1.98E-04 6.86F-04
		3	9825506	Ă	Ť	0.034	Synonymous Variant	tcA/tcT	Ser495Ser	AT3G26730	1.99E-04
		3	9825646	G	Ā	0.176	Intron Variant		201 100001	AT3G26730	1.98E-04
		3	9825765	Α	Т	0.188	Intron Variant			AT3G26730	1.15E-03
		3	9826159	Α	\mathbf{C}	0.176	Intron Variant			AT3G26730	1.98E-04
		3	9826344	G	\mathbf{C}	0.244	Intron Variant			AT3G26730	2.05E-01
		3	9827153	Т	A	0.239	Missense Variant	$\rm ttT/ttA$	Phe734Leu	AT3G26730	1.45E-01
		3	9829739	A	Т	0.25	Intergenic				1.10E-01
		3 9	9829837	G	A T	0.415	Intergenic 5 Duine UTD V			AT2C106742	0.38E-01 0.52E-00
		ა 1	5770265	A T	1 C	0.29	Symposium Variant	an A /acC	L mc5701 mc	A13G20/42	2.55E-02 2.07E-02
Visual Chlorosis precense	Emwa1	1	5779815	Ċ	т	0.071	Synonymous Variant	tcG/tcA	Ser447Ser	AT1G16900	2.07E-05 3.66E-02
		1	5780043	č	Ť	0.141	Missense Variant	Gca/Aca	Ala429Thr	AT1G16900	5.37E-05

Table S2: snpEFF annotation of the most significant intervals that do not contain a significant SNP found by an univariate Fisher exact test. For each individual SNP, the *p*-value obtained from the univariate Fisher exact test is displayed in the right-most column.

$ \begin{array}{c} & = 3 & 228913 & G & T & 0.66 & 5 \\ & = 3 & 228913 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.36 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.37 & 5 \\ & = 3 & 228953 & T & A & 0.278 & 5 \\ & = 4 & 219953 & A & T & 0.294 & 5 \\ & = 4 & 219953 & A & T & 0.294 & 5 \\ & = 4 & 2199573 & A & T & 0.294 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 4 & 219953 & T & G & 0.096 & 5 \\ & = 1 & 101002 & T & 0 & 0.096 & 5 \\ & = 1 & 101002 & T & 0 & 0.096 & 5 \\ $	Description	Phenotype	\mathbf{Chr}	Position	Ref	Alt	MAF	snpEFF Effect	Codon Change	AA Change	Gene ID	P-Value
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$		avrB	3	2288913	G	Т	0.046	5 Prime UTR Variant			AT3G07195	2.92E-01
Bits 3 229550 T A 0.456 Synanymores Variant cs/1/cs/2 AT36(7):56 14.00:16 Hypersensitive Response			3	2289178	Т	Α	0.23	Intron Variant			AT3G07195	3.05E-05
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$			3	2289559	Т	Α	0.356	Synonymous Variant	cgT/cgA	Arg58Arg	AT3G07195	1.94E-02
Itypescensitive Response \$\$ - 1 \$ 10000 \$\$ - 1 \$ 0000 \$\$ 10000 \$\$ - 1000000 \$\$ - 1000000 \$\$ - 10000000000		avrPphB	1	4129510	Т	C	0.189	Synonymous Variant	tcA/tcG	Ser64Ser	AT1G12170	1.00E-06
$ \left \begin{array}{c} \operatorname{arr} Rpm1 & 3 & 231073 & C & T & 0 & 0.20 & 0$	Hypersensitive Response		1	4130384	A	T	0.078	Intergenic Mission Venient	T/C	T	172007960	5.13E-03
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$		aw Pom 1	3	2310035	T	C	0.155	Intergonia	1gg/Ggg	Irpii8Gly	A15G07200	2.78E-00 8.26F 02
$ \frac{4}{22798} = \frac{122792}{1} T = C = 0.133 Misseav Variant at 32/26/2 Me87th AT4C2550 9.499-04 AT4C25$		uonipmi	3	2311055	Ċ	т	0.202	Intergenic				1.28E-01
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$			4	12279427	Ť	C	0.133	Missense Variant	aTg/aCg	Met86Thr	AT4G23530	9.40E-03
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		avrRpt2	4	12280837	G	Č	0.133	3 Prime UTR Variant			AT4G23530	1.12E-04
Leaf roll presence 2 14019308 A G 0.085 Synonymous Variant ictT/AC Bir2Met AT2G3804 5.888-01 Leaf roll presence 2 1402080 G T 0.121 Intergenic 1.002-01			2	14018996	А	С	0.079	Synonymous Variant	gcT/gcG	Ala320Ala	AT2G33040	4.73E-02
$ \begin{tabular}{ c c c c c c c c c c c c c c c c c c c$			2	14019038	Α	G	0.085	Synonymous Variant	tcT/tcC	Ser306Ser	AT2G33040	5.88E-01
$ \begin{array}{c} 1 402089 & G & T & 0.124 \\ 2 & 14021726 & C & T & 0.075 \\ 14022176 & T & A & 0.124 \\ 2 & 14023727 & A & T & 0.294 \\ 2 & 14023727 & A & T & 0.294 \\ 2 & 14023727 & A & T & 0.294 \\ 2 & 14023727 & A & T & 0.294 \\ 2 & 14023727 & A & T & 0.294 \\ 2 & 14023727 & A & T & 0.294 \\ 2 & 14023726 & A & T & 0.294 \\ 2 & 14023762 & A & T & 0.294 \\ 2 & 14023762 & A & T & 0.294 \\ 2 & 14023762 & A & T & 0.294 \\ 2 & 14023762 & A & T & 0.294 \\ 2 & 14023762 & A & T & 0.294 \\ 2 & 1402486 & C & T & 0.09 \\ 2 & 1402486 & C & T & 0.09 \\ 2 & 1402485 & C & A & 0.09 \\ 2 & 1402485 & C & A & 0.09 \\ 2 & 14025414 & T & G & 0.035 \\ 2 & 14025415 & T & G & 0.035 \\ 2 & 14025415 & T & G & 0.035 \\ 2 & 14025415 & T & G & 0.035 \\ 2 & 14025415 & T & G & 0.035 \\ 2 & 14025415 & T & G & 0.035 \\ 2 & 14025413 & T & G & 0.365 \\ 2 & 14025413 & T & G & 0.365 \\ 2 & 14025413 & T & G & 0.366 \\ 2 & 14025413 & T & G & 0.366 \\ 2 & 14025413 & T & G & 0.366 \\ 2 & 14025413 & T & G & 0.366 \\ 2 & 1300400 & C & T & 0.188 \\ 2 & 167690 & 187690 & 187690 \\ 2 & 1300400 & C & T & 0.188 \\ 2 & 167690 & 187690 & 187690 \\ 2 & 1300400 & C & T & 0.188 \\ 2 & 167690 & 187690 & 187690 & 187690 \\ 2 & 1202541 & T & G & 0.356 \\ 2 & 157610 & 187690 & 187690 & 177610 \\ 2 & 1202541 & C & C & 0.035 \\ 2 & 1107 & 118182256 & C & 0 & 0.358 \\ 2 & 013588 & C & C & 0.035 \\ 2 & 013588 & C & C & 0.036 \\ 2 & 013588 & C & C & 0.036 \\ 2 & 013588 & C & C & 0.037 \\ 3 & 2014399 & T & G & 0.211 \\ 1 & 1819125 & C & C & 0.038 \\ 2 & 013588 & C & C & 0.038 \\ 2 & 01$			2	14019977	G	С	0.096	Missense Variant	atC/atG	Ile120Met	AT2G33040	3.71E-02
$ \begin{array}{c} 1 4402176 & T & 0.070 \\ 2 & 1402176 & G & T & 0.070 \\ 2 & 1402346 & A & T & 0.77 \\ 2 & 1402346 & A & T & 0.77 \\ 2 & 1402346 & A & T & 0.77 \\ 2 & 1402346 & A & T & 0.77 \\ 2 & 1402345 & C & G & 0.07 \\ 2 & 1402355 & C & G & 0.09 \\ 2 & 1402355 & C & G & 0.09 \\ 2 & 1402355 & C & G & 0.09 \\ 2 & 1402355 & C & G & 0.09 \\ 2 & 1402355 & C & G & 0.08 \\ 2 & 1402366 & C & T & 0.08 \\ 2 & 1402356 & C & T & 0.09 \\ 2 & 1402354 & C & T & 0.09 \\ 2 & 1402354 & C & T & 0.09 \\ 2 & 1402354 & C & T & 0.09 \\ 2 & 1402354 & C & T & 0.09 \\ 2 & 1402354 & C & T & 0.09 \\ 2 & 1402354 & C & T & 0.09 \\ 2 & 1402354 & C & T & 0.09 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402554 & C & 0 & 0.08 \\ 2 & 1402556 & C & 0 & 0.16 \\ 2 & 140256 & C & 0 & 0.16 \\ 2 & 1500400 & C & 0 & 0.18 \\ 2 & 1500400 & C & 0 & 0.18 \\ 2 & 1500400 & C & 0 & 0.18 \\ 2 & 1500400 & C & 0 & 0.08 \\ 2 & 18102753 & C & 0 & 0.05 \\ 2 & 18102753 & C & 0 & 0.05 \\ 2 & 18102753 & C & 0 & 0.05 \\ 2 & 11810152 & A & 0.023 \\ 2 & 0137884 & C & G & 0.024 \\ 2 & 104387 & T & G & 0.025 \\ 2 & 0137884 & C & G & 0.024 \\ 2 & 0137884 & C & G & 0.024 \\ 2 & 0148897 & T & G & 0.025 \\ 2 & 0137884 & C & G & 0.025 \\ 2 & 0137884 & C & G & 0.026 \\ 2 & 013784 & T & G & 0.026 \\ 2 & 013784 & C & G & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & G & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 013784 & C & 0 & 0.026 \\ 2 & 01484 & C & C & 0.026 \\ 2 & 01484 & C & C & 0.026 \\ 2 & 01484 & C & C & 0.026 \\ 2 & 01484 & C & C & 0.026 \\ 2 & 01484 & C & $			2	14020898	G	Т	0.124	Intergenic				3.60E-01
$ \begin{array}{c} 1 \\ \text{Leaf roll presence} \\ \text{Leaf roll presence} \\ \text{Leaf roll presence} \\ \begin{array}{c} 1 \\ \text{Leaf roll presence} \\ 1 \\ \text{Leaf roll presence} \\ \begin{array}{c} 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ 1 $			2	14021726	G	Т	0.079	Intergenic		T 00T		1.60E-01
Leaf roll presence $\begin{array}{cccccccccccccccccccccccccccccccccccc$			2	14022076	T	A	0.124	Synonymous Variant	ctT/ctA	Leu69Leu	AT2G33050	5.26E-03
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		Loof roll 10	2	14023402	A	T	0.079	Synonymous Variant	tCA/tCI	Jef10Ile	A12G55050 AT2C33050	1.00E-01 8.10F-03
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	Leaf roll presence	Lear Ion 10	2	14023855	Ĉ	G	0.294	Missense Variant	arr/arr	Ser662Arg	AT2G33050	6.18E-02
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Lear for presence		2	14023969	č	Ă	0.085	Synonymous Variant	ctC/ctA	Leu700Leu	AT2G33050	1.01E-01
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $			2	14024162	č	Т	0.09	Missense Variant	Ctt/Ttt	Leu765Phe	AT2G33050	6.18E-02
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $			2	14024485	С	Α	0.09	Intergenic	,			6.18E-02
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$			2	14025154	Т	G	0.085	Intergenic				1.01E-01
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$			2	14025341	Α	G	0.147	Intergenic				5.76E-02
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$			2	14025518	Т	G	0.356	5 Prime UTR Variant			AT2G33060	4.88E-04
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		Leaf roll 16	5	18040355	A	G	0.136	Intergenic				6.14E-04
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		I DO	5	18040400	C	T	0.188	Intergenic	A /0	I 10401	ATTE (10200	1.75E-03
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	Presence or absence of le-		Э Б	6520722		G	0.105	Introp Variant	Aaa/Caa	Lys164Gin	A15G19380	0.70E-00 2.05E-01
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	sioning	LES	5	6531656	C	Δ	0.055	5 Prime UTR Verient			AT5C19390	5.05E-01 6.98E-03
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		LY	1	18192753	G	A	0.253	Missense Variant	gGc/gAc	Glv406Asp	AT1G49190	3.87E-02
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	Presence or absence of ei-		1	18192956	č	A	0.263	Intron Variant	800/8110	019 100110p	AT1G49190	7.99E-02
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	ther lesioning or yellowing		1	18193152	Ã	С	0.211	Intron Variant			AT1G49190	2.83E-04
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $			1	18196934	С	G	0.284	Intergenic				4.80E-02
Presence or absence of yel- lowing YEL 3 20139860 T G 0.358 Intergenic CTa/cCa Leu39Pro AT3G5400 1.97E-01 1 20143997 T G 0.421 Intergenic 1.33E-01 1.00E+00 3 20144480 A C 0.0411 Intergenic 1.33E-01 3 20144480 A C 0.0411 Intergenic 1.00E+00 3 2014480 A C 0.0411 Intergenic 1.00E+00 4 5951829 A G 0.362 Synonymous Variant ctC/ctA Leu415Len AT1G17370 7.1E-02 1 5954613 T A 0.091 Intron Variant CtC/ctA Leu415Len AT1G14370 7.69E-01 ence 1 703341 A T 0.091 Intron Variant CtC/gtT Val70Val AT2G04845 2.96E-03 1 104037978 A G 0.232 Intergenic 1.32E-02<			3	20137884	С	А	0.495	3 Prime UTR Variant			AT3G54390	5.69E-03
Presence or absence of yel- lowing YEL 3 20142484 A G 0.211 Missense Variant (mergenic) CTa/cCa Leu39Pro AT3G54400 1.97E-01 3 20144047 C G 0.421 Intergenic 1.33E-01 1.00E+00 3 20144480 A C 0.411 Intergenic 1.00E+00 1 5951857 G T 0.085 Synonymous Variant ctC/ctA Leu415Leu AT1G17370 7.71E-02 Visual anthocyanin pres- ence Anthocyanin 16 1 5954613 T A 0.119 Intron Variant ctC/ctA Leu415Leu AT1G17370 7.69E-01 Visual anthocyanin pres- ence Anthocyanin 16 2 1703341 A T 0.091 Missense Variant gtC/gtC Val106Val AT2G04845 2.96E-03 1 14037978 A G 0.237 Intergenic 7.33E-01 1.14E-02 1 14040529 G A 0.232 Intergenic 7.33E-			3	20139860	Т	G	0.358	Intergenic				2.52E-01
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Presence or absence of yel-	YEL	3	20142484	A	G	0.211	Missense Variant	cTa/cCa	Leu39Pro	AT3G54400	1.97E-01
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	lowing		3	20143997	Т	G	0.421	Intergenic				1.33E-01
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $			3	20144047	C	G	0.053	Intergenic				1.00E+00
$ \begin{array}{c} \mbox{Anthocyanin 10} & 5951391 & G & 1 & 0.363 & Synonymous Variant & CC/CA & Detribute & Alt Part 1050 & 1.1 E-02 \\ \mbox{Anthocyanin 10} & 595292 & A & G & 0.362 & Synonymous Variant & TT/tC & Phe301Phe & AT1G17370 & 7.69E-01 \\ \mbox{Anthocyanin 16} & 2 & 170331 & A & 0.119 & Intron Variant & TT/tC & Val106Val & AT2G04845 & 6.46E-03 \\ \mbox{2 & 1703431 & A & T & 0.091 & Intron Variant & gtT/gtC & Val106Val & AT2G04845 & 2.96E-03 \\ \mbox{2 & 170330 T } A & 0.091 & Missense Variant & Atg/Ttg & Met2Leu & AT2G04845 & 2.96E-03 \\ \mbox{2 & 1703930 T } A & G & 0.254 & Intergenic &$		Anthocyanin 10	3 1	20144460	A C	<u>т</u>	0.411	Synonymous Variant	at C / at A	Lou415Lou	AT1C17370	7.71E.02
			1	5952292	A	G	0.085	Synonymous Variant	ttT/ttC	Phe301Phe	AT1G17370	3.21E-02
			1	5954613	Т	Ă	0.119	Intron Variant	001/000	1 nego11 ne	AT1G17370	7.69E-01
		Anthocyanin 16	2	1702970	А	G	0.057	Synonymous Variant	gtT/gtC	Val106Val	AT2G04845	6.46E-03
$ \begin{array}{c} \mbox{Visual antnocyanin pres-} \\ \mbox{ence} \\ \mbox{ant ant bocyanin pres-} \\ \mbox{ant bocyanin pres-} \\ $	37. 1 (1 .		2	1703341	Α	Т	0.091	Intron Variant	0 ,0		AT2G04845	2.96E-03
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	Visual anthocyanin pres-		2	1703427	G	Α	0.136	Synonymous Variant	gtC/gtT	Val70Val	AT2G04845	1.35E-02
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	ence		2	1703930	Т	А	0.091	Missense Variant	Atg/Ttg	Met22Leu	AT2G04845	2.96E-03
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		Anthocyanin 22	1	14037978	Α	G	0.254	Intergenic				1.14E-02
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$			1	14039321	Т	Ċ	0.35	Intergenic				7.43E-01
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $			1	14040254	C	A	0.232	Intergenic				1.52E-02
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Visual Chlorosis precense	Chlorosis 22	1 2	14040529	<u>- G</u> - т	A C	0.237	Missonso Variant	Ttg/Ctg	Lou400Vol	AT3C26730	9.08E-05
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$			3	9825306	т	c	0.170	Synonymous Variant	Ttg/Gtg Ttg/Ctg	Leu400 var Leu429Leu	AT3G26730	6.86E-04
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$			3	9825506	Ā	Ť	0.034	Synonymous Variant	tcA/tcT	Ser495Ser	AT3G26730	1.99E-01
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$			3	9825646	G	А	0.176	Intron Variant	. ,		AT3G26730	1.98E-04
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$			3	9825765	А	Т	0.188	Intron Variant			AT3G26730	1.15E-03
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$			3	9826159	Α	\mathbf{C}	0.176	Intron Variant			AT3G26730	1.98E-04
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$			3	9826344	G	\mathbf{C}	0.244	Intron Variant			AT3G26730	2.05E-01
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$			3	9827153	Т	Α	0.239	Missense Variant	$\rm ttT/ttA$	Phe734Leu	AT3G26730	1.45E-01
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$			3	9829739	A	Т	0.25	Intergenic				1.10E-01
3 9831240 A 1 0.29 5 Prime U1R Variant Al13G26/42 2.33E-02 1 5779265 T C 0.071 Synonymous Variant aaA/aaG Lys570Lys Al13G26/42 2.33E-02 Visual Chlorosis precense Emwal 1 5779815 C T 0.118 Synonymous Variant tcG/tcA Ser447Ser Al13G16900 3.66E-02 1 5780043 C T 0.141 Missense Variant Gca/Aca Ala429Thr AT1G16900 5.37E-05			3	9829837	G	A	0.415	Intergenic				6.38E-01
$\begin{array}{cccccccccccccccccccccccccccccccccccc$			う 1	9831240 5770965	A T	1 C	0.29	Synonymous Variant	an A /sof	Luc5701	A13G20/42	2.55E-02
1 5780043 C T 0.143 Missense Variant Gca/Aca Ala429Thr ATIG16900 5.37E-05	Vigual Chlorosis processo	Emwa1	1	5779815	Ċ	Т	0.071	Synonymous Variant	tcG/tcA	Lysor0Lys Ser447Ser	AT1G10900 AT1G16900	2.07E-05 3.66E-02
	, and enorosis precense		1	5780043	č	Ť	0.141	Missense Variant	Gca/Aca	Ala429Thr	AT1G16900	5.37E-05

Table S3: snpEFF annotation of the most significant intervals that do not contain or are in close proximity $(\pm 10kb)$ to a significant SNP found by an univariate Fisher exact test or a linear mixed model. For each individual SNP, the *p*-value obtained from the univariate Fisher exact test is displayed in the right-most column. Rows in blue are different intervals then identified using the filtering Scenario 2.

S2 Supplementary Figures



Figure S1: A schematic representation of the filtering procedure. In each cluster of overlapping intervals, the interval with smallest p-value is the result.



Figure S2: Proportion of novel intervals among all intervals found by **FAIS-WY** for the phenotype YEL with the highest degree of population structure. The green part shows the proportion of novel intervals found by **FAIS-WY**. The red part (UFE \pm 10kb \LMM \pm 10kb) are intervals containing an UFE hit or are in close proximity (\pm 10kb) to one and the hit could not be found with a LMM. The blue part (LMM \pm 10kb \UFE \pm 10kb) are intervals containing a LMM hit or are in close proximity (\pm 10kb) to one and the hit could not be found with a LMM. The blue part (LMM \pm 10kb \UFE \pm 10kb) are intervals containing a LMM hit or are in close proximity (\pm 10kb) to one and the hit could not be found with an UFE. The purple part (LMM \pm 10kb \cap UFE \pm 10kb) are intervals that contain both, a hit (\pm 10kb) found with an UFE and a LMM.

S3 Simulation study: additional results

The supplementary figures in this section may aid in our discussion of the performance of FAIS and FAIS-WY. In all figures in this section, $\alpha = 0.05$.

S3.1 Speed, as the number of permutations varies

Figure S3 shows how the speed of FAIS-WY varies as the number of permutations J increases. Of course, FAIS does not vary, since it does not use Westfall-Young permutations, but is displayed for comparison purposes. The relationship appears to be approximately linear (speed vs number of permutations, J). This shows that if the simulation that produced Figure 4 (in the main text) used a larger number of permutations, there would be a larger difference in the (raw) times between FAIS and FAIS-WY.



Figure S3: A figure comparing the speed of FAIS and FAIS-WY as the number of permutations varies. Of course, FAIS does not vary, but is displayed for comparison purposes. Note that the axes are log-scaled (base 10). Other parameter values: n=100, L=11000.

S3.2 Speed, as the number of individuals varies

Figure S4 shows how the speeds of FAIS and FAIS-WY vary as n, the number of individuals, increases. Their speeds both appear to increase (approximately) linearly as n increases (but with different slopes).



Figure S4: A figure comparing the speed of FAIS and FAIS-WY as the number of individuals varies. Note that the axes are NOT log-scaled. Other parameter values: L=1100, J=100.

S3.3 Accuracy

Figure S5 shows the proportion of correctly detected significant intervals for FAIS, FAISWY, BRUTE and UFE, for different values of p_{case} , as the length of the significant interval increases, averaged over M = 1000 trials. It appears that the length of the significant interval does not appear to play too much of a role for the first three methods - for example, see panel $p_{case} = 0.5$, where the detection rates are fairly constant per method for FAIS, FAISWY and BRUTE. However, note that UFE performs poorly for longer intervals, for $p_{case} < 0.9$.



Figure S5: A figure comparing the accuracies of FAIS, FAIS-WY, BRUTE and UFE for different values of p_{case} , as the length of the significant interval increases. Other parameter values: n=100, J=1000, number of M=1000.

Figure S6 (on the next page) shows the same information, with the roles of p_{case} and l, the length of the significant interval, exchanged. This figure more clearly shows that FAIS and FAISWY are significantly more accurate than BRUTE, and that UFE performs progressively worse as the length of significant intervals increases. This is to be expected, since UFE is only attempting to detect a significant difference in single SNPs. However, this figure decisively shows that, for detecting significant *intervals*, UFE is far inferior to interval-search methods.

Finally, Figure S7 shows the resulting False Discovery Rate (FDR) when FAIS and FAIS-WY are set to control the FWER at $\alpha = 0.05$. As expected, the FDR decreases with increasing p_{case} . This figure should be compared to Figure 4 in the main text which illustrates the difference in power between these four methods.

All simulations were performed on an iMac with CPU 2.9 Ghz Intel Core i5, and 16 GB of RAM (1600 MHz DDR3). Figures were produced in R using ggplot2.



Figure S6: A figure comparing the accuracies of FAIS and FAIS-WY BRUTE and UFE for significant intervals of different lengths, as caseP varies. Other parameter values: n=100, J=1000, M=1000.



Figure S7: A figure showing the FDR of FAIS, FAISWY and BRUTE, as p_{case} varies. Other parameter values: n=100, J=1000, M=1000.