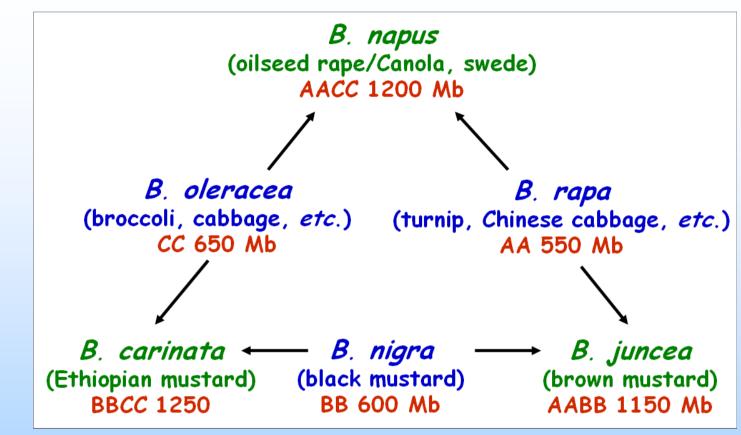
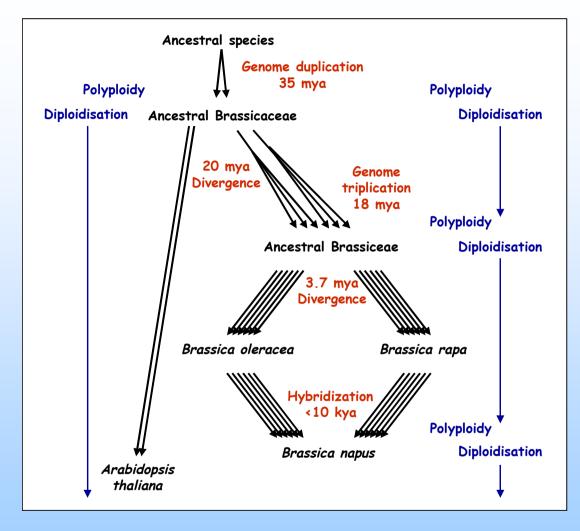
Identifying the functional bases of trait variation in *Brassica napus* using Associative Transcriptomics

- Brassica genome structure and evolution
- Genome framework for association genetics
- Establishing marker-trait associations



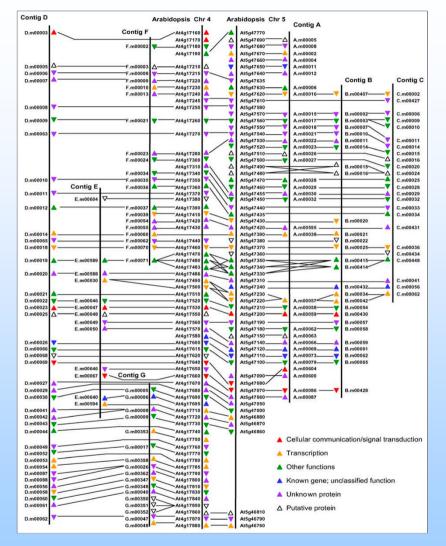
GENOME RELATIONSHIPS BETWEEN SPECIES - "U's TRIANGLE"

MULTIPLE ROUNDS OF POLYPLOIDY/DIPLOIDIZATION



- Model system for the impacts of polyploidy on the structure of plant genomes
- Molecular genetic analyses, particularly comparative, will be problematic

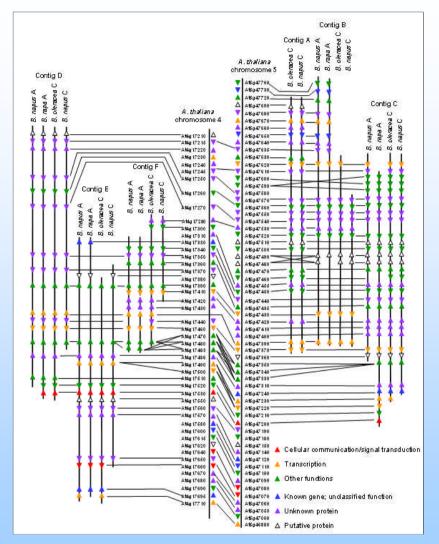
GENOME MICROSTRUCTURE IN "DIPLOID" BRASSICA SPECIES



Example (Brassica oleracea)

- Triplicated genome paralogues
- Extensive collinearity between protein-coding genes in *Brassica* and *Arabidopsis*
- Extensive interspersed gene loss
- Evidence for transduplication of genes/gene fragments

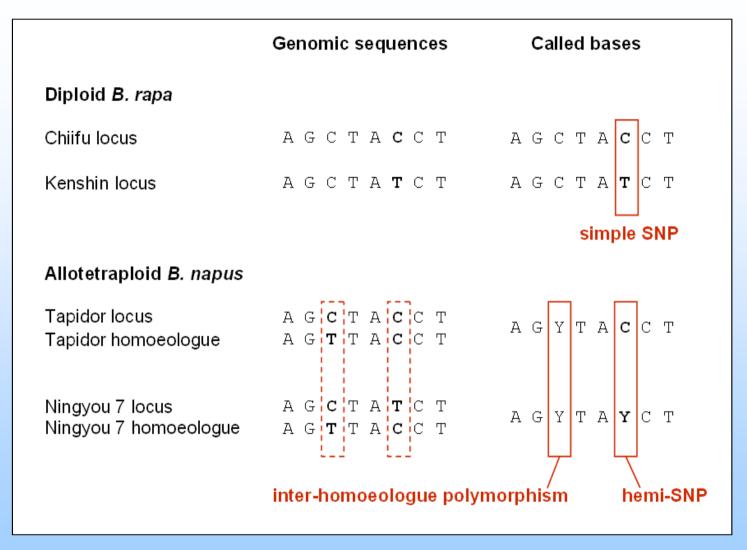
COMPARATIVE ANALYSIS BETWEEN BRASSICA SPECIES



Comparison of genome microstructure across orthologous genome segments in *B. oleracea*, *B. rapa* and both genomes of *B. napus*

- High collinearity between proteincoding genes in A and C genomes, as represented in diploids and B. napus, but some breakdown
- Considerably more interspersion of transposon-related sequences in gene space of C genome

POLYMORPHISM TYPES IN A POLYPLOID

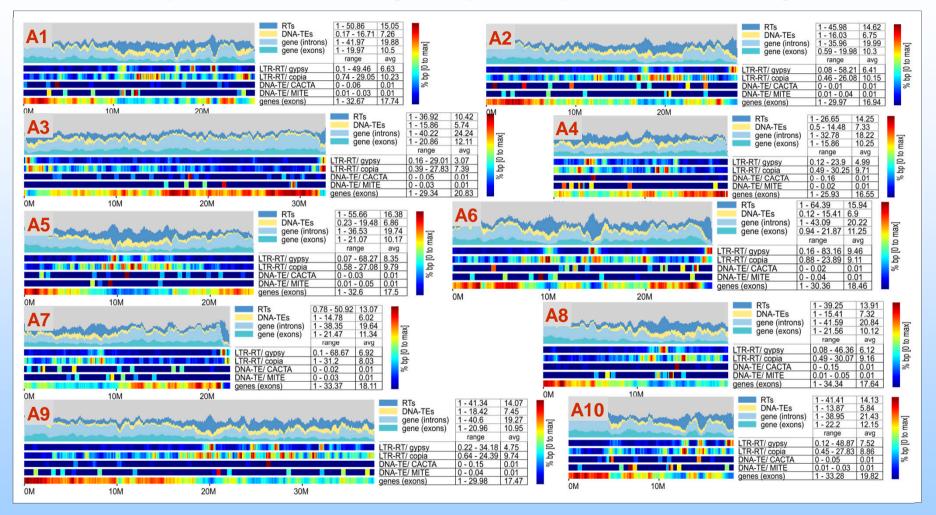


GENOME SEQUENCING

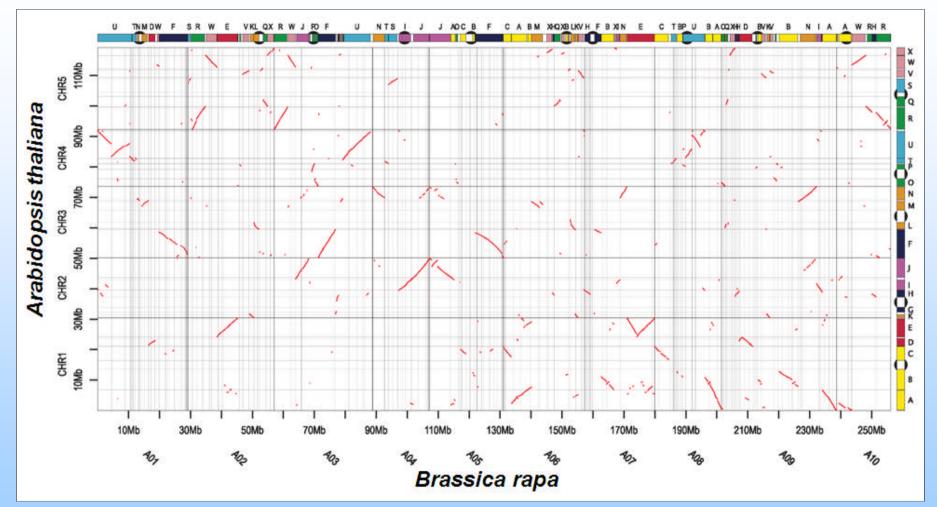
Brassica rapa:

284 Mb gene space sequenced

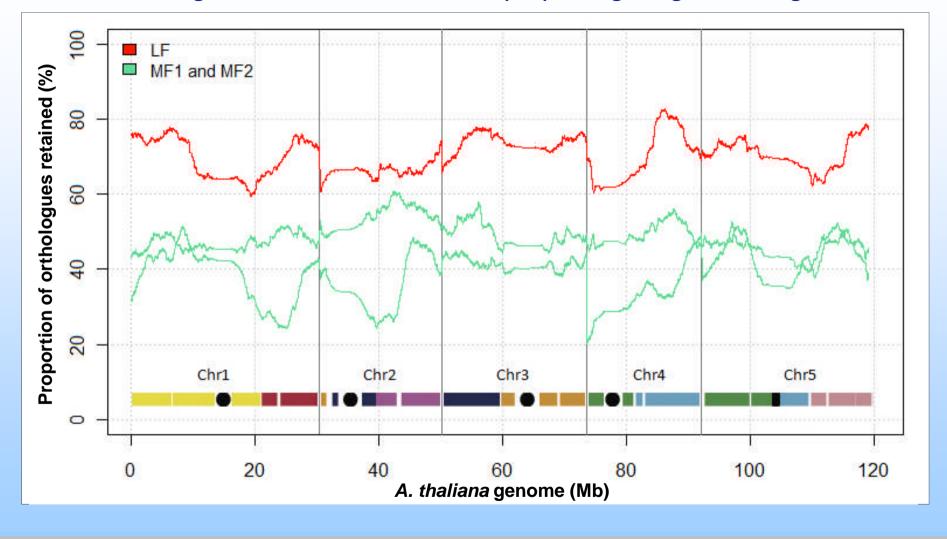
41,174 gene models

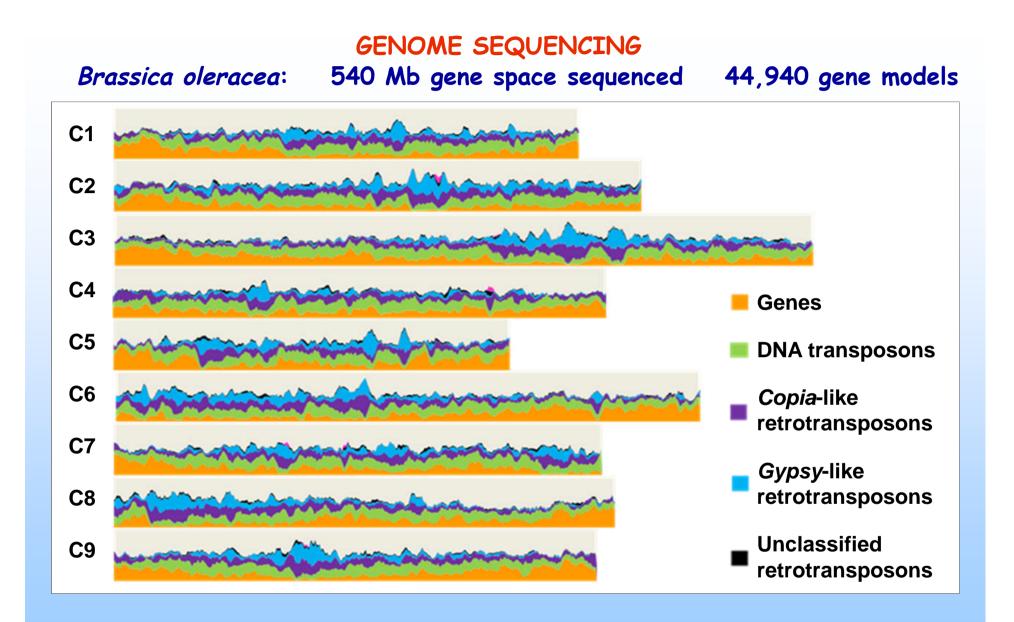






GENOME - SCALE COMPARATIVE ANALYSIS Differential gene loss from *Brassica rapa* paralogous genome segments



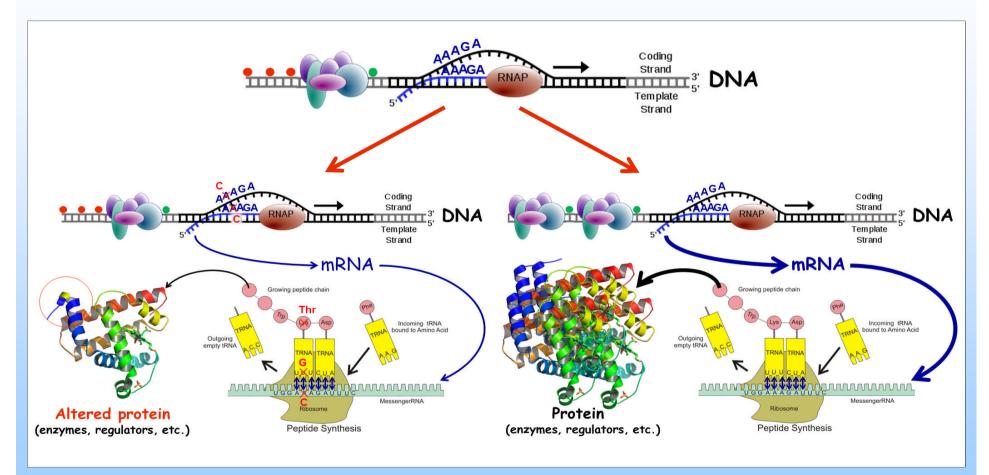


Identifying the functional bases of trait variation in *Brassica napus* using Associative Transcriptomics

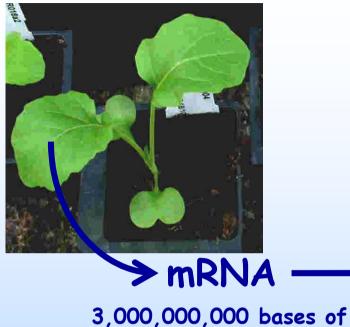
- Brassica genome structure and evolution
- Genome framework for association genetics
- Establishing marker-trait associations

GENETIC VARIATION

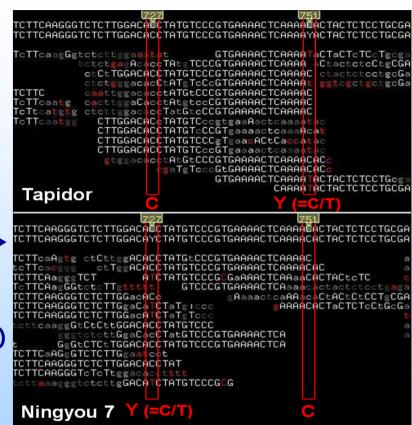
- Genetic variation controls productivity and quality of crops
- Both gene sequence variation and gene expression variation are important



USE "FUNCTIONAL GENOTYPES" FOR MAPPING



3,000,000,000 bases of sequence per plant (~ one complete human genome)



Unigene reference sequence

SNP DETECTION USING ILLUMINA SEQUENCING

- Established reference sequence based on the 94k unigenes (EST assemblies) used for the community *Brassica* microarray
- Conducted Illumina sequencing runs on two cultivars (Tapidor & Ningyou 7)
- Used components of M.A.Q. for sequence alignment and SNP calling
- Bioinformatics processing of data for the detection of putative SNPs

INTEGRATED SNP DISCOVERY AND ASSAY

Transcriptome SNPs distributed throughout gene space

Can be converted to DNA-based assays for marker-assisted selection

NOT dependent upon having to first discover polymorphisms before analysis of sequence variation

Adapted bioinformatics pipeline to simultaneously identify polymorphic loci (positions within *Brassica* unigene reference sequences), assess suitability for use as markers across panels of lines and produce scoring strings

UNIGENE-BASED ALIGNMENTS BASED ON BLAST SIMILARITY

Unigene: SNP coordinate

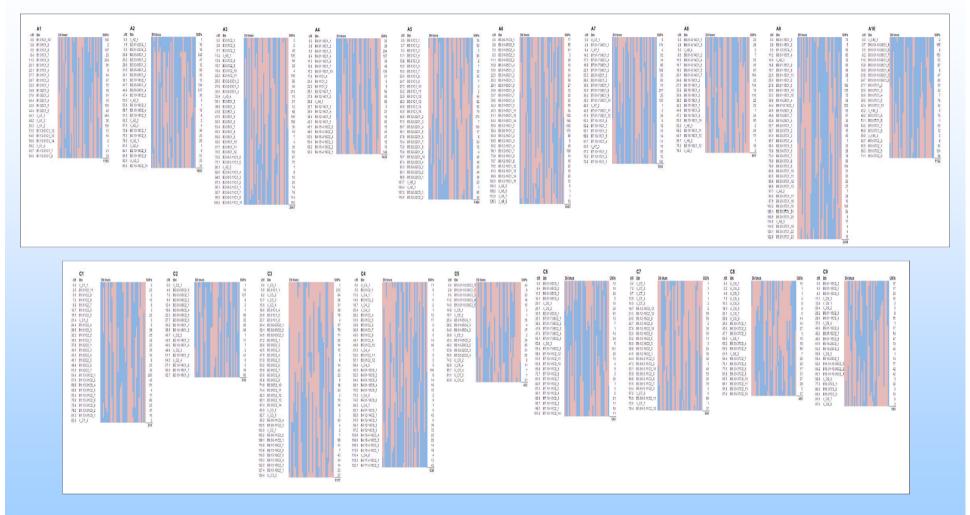
Alignment to AGI models

Alignment to genome sequences

Allele scoring strings

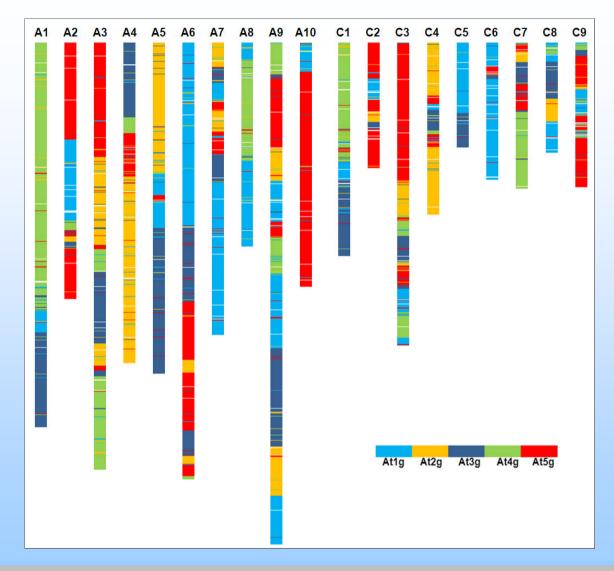
1					2														1	/													
	•	B. rapa		그 널	you	2742 22				a <i>mere</i> r		an area		202	725		152/1 (2)	55 6000	K	_ \$	ົ້	<u>ი</u> თ	ы	4 4	8 8	6	38	64 F9	8	0	a 2	مي ا	~
SNP ID	AGI code	Scaffold	Position	Order Tapidor	Ningyou	TN04	TN08	TN10	TN24	TN28	TN31	TN33	TN44	TN48	TN57	TN72	TN76	TN85	TN88	TN90		TN109	TN12	TN124	TN128	TN129	TN13	TN169	TN16	TN170		TN176	LIN.
JCVI_6069:704	AT4G34200.1	Scattold000097	505973	8.14 C	Y	BB		AU		A	BA		B /		B	B	A A	A	B		- U	B	B	<mark>Б В</mark>			A A		A	AE		B	A
JCVI_6069:710	AT4G34200.1	Scattold000097	505973	8.14 C	М	В В	А	A L	JB	Α	B A	B	в /	A A	в	В	U A	A	BI	B U	U	в	в	в в	В	в	A A	A	A	AE	A	В	А
JCVI_34283:459	AT4G34430.1	Scattold000097	593251	8.14 C	Y	В В	U	UE	S B	A	B A	B	В /	A U	в	В	A A	A	BI	B A	U	в	в	в в	В	в	A A	A	A	AE	A	В	U
JCVI_34283:343	AT4G34430.1	Scaffold000097	593251	8.14 R	А	B B	A	AE	5 B	A	UA	V U	B /	A A	В	В	A A	A	BI	B A	A	В	U	B B	В	В	UA	A A	A	AE	A	В	U
JCVI_7890:204	AT4G34640.1	Scaffold000097	697187	8.14 T	γ	B A	В	BA	A	В	B A	A	AI	3 B	В	В	A B	A	AI	B A	A	В	В	A A	В	Α	UA	U	В	A A	A	В	A
JCVI_4009:345	AT4G34670.1	Scaffold000097	702318	8.14 C	М	B B	Α	A E	5 B	Α	B A	B	B /	A A	U	В	A A	A	BI	B A	A	В	в	B B	В	В	A A	V U	A	AE	A	В	А
JCVI_4009:255	AT4G34670.1	Scaffold000097	702318	8.14 Y	Т	B B	A	AE	S B	Α	B A	B	В /	A A	В	В	A A	A	B	U A	A	В	В	B B	В	В	A A	A U	A .	A E	A	В	Α
JCVI_4009:156	AT4G34670.1	Scaffold000097	702318	8.14 C	М	B B	В	A E	A	В	A B	A	AI	3 A	А	В	A B	A	A	A B	В	В	Α	A A	В	А	BE	3 U	A	A E	A	В	Α
JCVI_4009:669	AT4G34670.1	Scaffold000097	702318	8.14 R	А	UB	A	AE	S B	A	B A	B	U /	A A	В	В	A A	A	UI	B A	A	В	В	B A	В	U	A A	AA	A	AE	U	в	Α
JCVI_5729:517		Scaffold000097	759664	8.14 T	W	B B	A	BE	S B	В	A B	S B	BI	3 B	В	U	B B	В	A	A A	A	В	A	B A	В	В	ΒL	JB	В	A E	В	A	Α
JCVI_5729:748		Scaffold000097	759664	8.14 A	R	B B	Α	ΒE	S B	В	A B	B	BI	3 B	в	U	B B	в	A	A A	A	в	A	B A	В	В	UA	B	В	AE	В		Α
JCVI_5729:290		Scaffold000097	759664	8.14 T	K	B B	U	BE	S U	В	A B	5 B	BI	3 B	в	A	B B	В	A	A A	A	В	A	B A	В	В	B A	A B	В	A E	В	A	Α
JCVI_5729:750		Scattold000097	759664	8.14 A	W	B B	Α	ΒE	S B	В	A B	S B	BI	3 B	в	U	B B	U	A	A A	A	в	U	B A	В	в	B A	A B	В	AE	В		А
JCVI_5729:326		Scattold000097	759664	8.14 A	R	В В	в	BE	S U	В	UB	5 B	BI	3 B	в	U	в в	В	UI	UA	A	В	U	B A	В	в	B A	A B	A	AE	В		U
JCVI_12696:940	AT4G35090.1	Scattold000097	876853	8.14 C	Y	A B	U	B A	A	В	UB	S B	A /	A B	в	В	B A	A	A	A B	A	В	в	BB	В	A	BE	S A	В	AE	A		В
JCVI_12696:1324	AT4G35090.1	Scattold000097	876853	8.14 R	G	В В	A	BA	A	В	A B	5 B	A /	A A	В	в	в в	В	в	A A	В	в	U	A B	В	в	BE	3 B	A	A A	A		Α
JCVI_28018:639	AT4G32140.1	Scattold000187	10821	8.15 R	G	в в	A	AE	U	A	B A	V U	U /	A A	в	в	A A	A	BI	B A	A	в	U	ΒU	в	U	UA	A	A	AE	A		Α
JCVI_28018:1138	AT4G32140.1	Scattold000187	10821	8.15 Y	С	BU	A	AE	S B	A	UA	B	U	A A	в	В	A A	A	В	B A	A	В	U	UB	U	U	A A	AA	A	AE	A		Α
JCVI_639:789	AT4G32150.1	Scattold000187	18324	8.15 G	К	B B	A	AE	5 B	A	BA	B	В /	A A	В	В	A A	A	В	B A	A	В	в	B B	В	В	A A	A	A	AE	A		Α
JCVI_16397:622	AT4G32180.1	Scattold000187	25484	8.15 T	Y	BA	в	BA	A	В	BA	AA	AI	3 B	в	В	A B	A	AI	B A	A	В	в	BA	В	A	A A	AB	В	A A	A		A
JCVI_16397:94	AT4G32180.1	Scattold000187	25484	8.15 T	Y	B A	В	B A	A	в	B A	A	AI	3 B	в	в	A B	A	A	B A	A	в	в	BA	В	A	A A	A B	В	A A	A		A
EV119370:596	AT4G32180.1	Scattold000187	28497	8.15 G	R	в в	A	AE	S B	A	BA	AB	в	A A	В	В	A A	A	В	BA	A	В	в	в в	В	В	ΑL	JA	U	AE	A		A
EV119370:230	AT4G32180.1	Scattold000187	28497	8.15 R	A	BB	A	AE	5 B	A	BA	N B	в /	AA	В	В	A A	A	В	BA	A	В	в	в в	В	В	A A	A	A	AE	A		A
EV119370:263	AT4G32180.1	Scattold000187	28497	8.15 M	С	в в	A	AE	в в	A	BA	A B	в	AA	В	В	A A	A	В	BA	A	В	В	в в	В	В	A A	AA	A .	AE	A		A
EV119370:233	AT4G32180.1	Scattold000187	28497	8.15 S	G	BU	A	AE	в В	A	BA	B	В /	AA	В	В	A A	A	В	BA	A	В	В	BB	В	В	AA	AA	A .	AE	A		A
EV119370:614	AT4G32180.1	Scattold000187	28497	8.15 Y	C	ВВ	A	AL	5 0	A	BA	В	0 /	AA	В	U	AA	A	В	BA	A	В	В	вв	В	U	AA	AA	A	AL	A	В	A
EE531667:217	AT4G32330.2	Scattold000187	61525	8.15 C	Y	вв	A	AL	5 B	A	BA	В	в /	AA	В	В	UA	A	в	BA	U	В	в	вв	В	В	AL	A	A	UE	A		A
EE531667:230	AT4G32330.2	Scattold000187	61525	8.15 Y	C	BA	В	BA	AA	В	BA	A	AI	3 B	В	В	AB	A	A	BA	A	В	в	BA	В	A	AL	JB	в	AA	A		A
JCVI_3408:264	AT4G32330.1	Scattold000187	110479	8.15 Y	1	вв	A	AL	5 В	A	BA	В	в	AA	В	В	AA	A	в	BA	A	В	в	BB	В	в	AP	AA	A	AL	A		A
JCVI_3408:646	AT4G32330.1	Scattold000187	110479	8.15 A	M	BA	в	BF	AA	В	BA	AA	AI	5 B	В	в	AB	A	A	BA	A	В	в	БА	В	A	AU	JB	В	AF	A		U
JCVI_7045:298	AT4G32470.1	Scattold000187 Scattold000187	136533 136533	8.15 T 8.15 C	r		A	A	BB	A	D A	D	В /		P	B	AA	A			A	D	2		P	D	AP	AA	A	0 0	A	1.1	A
JCVI_7045:164 JCVI_27824:419	AT4G32470.1 AT4G32600.1	Scattold000187	176160	8.15 C 8.15 A	R	BA	B	D F		Б		A	UI	5 D	B	B	AB	A	A		A	B	Б		U	A	AP		B	AA	A		A
					, V		A	A		A			8 (B	AA	A			0	D	2		B	0			0		A		A
JCVI_18068:737 JCVI_18068:810	AT2G25670.1 AT2G25670.1	Scattold000187 Scattold000187	179249 179249	8.15 C 8.15 R	G	D D	A	A D		A	BA	D			D	D	AA	A			A	D	D		D	D	AA	A	A .		A		AA
JCVI_18068:556	AT2G25670.1	Scattold000187	179249	8.15 R 8.15 R	A	D A	0		A			A	A			D		A	A		A	0	0		D	A	AA		8	A	A		A
EV091869:255	AT4G32610.1	Scattold000187	180476	8.15 K 8.15 Y	C	D A	D	D /	A	P	D A	A	A		D	D		A	A		A	D	D		D	A	AA		P	AF	A	U	
EV091869:235	AT4G32610.1	Scattold000187	180476	8.15 K	G	BA	B	B	A	u	BA	A	~		B	ū		A	~		A	B	ü	UA	B	~		B	U U		A		A
JCVI_17976:182	AT4G32610.1	Scattold000010	58380	8.16 M	0		D	B		0			A 1			P		~	~		A	P				~	A A		P		A		A
JCVI_1/976:182	AT4G31730.1	Scattold000010	65401	8.16 G	ĸ	BB		UE		0	BA	R	B		B	В		A	B	BA	A	B	B	BB	B	B			~		A		A
JCVI_4028:284 JCVI_6862:987	AT4G31720.2	Scattold000010	122952	8.16 C	M	B D	B			B	BD	B	8		B	^	R P	P			P	B	^		B	0			~		A	-	B
JCVI_6862:1077	AT4G31480.1	Scattold000010	122952	8.16 M	C	BB	B		B	B	B		B		B	2	BB	P	2		P	B	~		B	2			A		A	1.1	В
JCVI_6862:1077	AT4G31480.1	Scattold000010	122952	8.16 A	M	BU	B	B		B	BA				B	B			A 1	ви	D	B	B	BA	B	A		JB	B		A		D U
JCVI_6862:246	AT4G31480.1	Scattold000010	122952	8.16 A 8.16 R		BA	В	BA	A	В	BA		A	з в	В	В	AB	A	A		A	В	В	BA	В	A	AA		B	AA		100	-
101_0002:240	A14051400.1	300000000000000000000000000000000000000	122952	0.10 K	A	DA	D	DF	A	D	DA	A	AI		D	D	M D	A	A	A	A	D	D	DA	D	A	AP	1 0	D	AL	A	D	A

LINKAGE MAP CONSTRUCTION USING mRNA-seq TNDH linkage map with 21,323 SNP markers in 527 recombination bins



GENOME ANALYSIS USING mRNA-seq

Analysis of collinearity with the genome of *Arabidopsis thaliana* via 9,169 anchoring unigenes



UNMAPPED UNIGENES ORDERED BY MAPPED SEQUENCE SCAFFOLDS

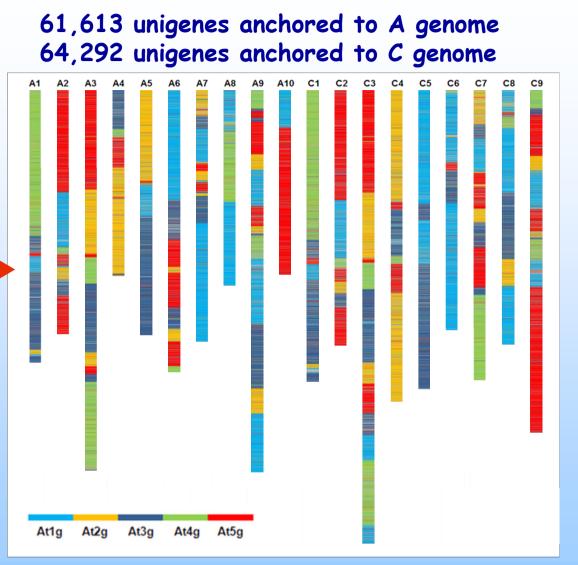
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	CX192070	AS	9153474	A Scaffold000097	794210	
	JCVI 5729	AS	9176822		759664	
	JCVI 3918	AS	9177527	A Scaffold000097	759714	
	EV075943	AS	9182978	A Scaffold000103	470339	AT1G43570.1
	DY023723	AS	9197232	-	740289	A11645570.1
				-		
	JCVI_1057	A8	9212467	-	725113	AT4G34720.1
	CV546751	A8	9219387	A_Scaffold000097	718170	
	JCVI_10034	A8	9219799	A_Scaffold000097	716806	AT4G34710.1
	JCVI_12180	A8	9221365	A_Scaffold000097	716121	AT4G34710.1
	EX120610	A8	9222032	A_Scaffold000097	715694	
	EE470793	A8	9227903	A_Scaffold000097	709576	AT4G34700.1
5253	EX066713	A8	9230322	A_Scaffold000097	707204	AT4G34680.1
5254	JCVI_8753	A8	9230420	A_Scaffold000097	706938	AT4G34680.1
5255	BG543396	A8	9231064	A_Scaffold000097	706628	AT4G34680.1
5256	JCVI_4009	A8	9235433	A_Scaffold000097	702318	AT4G34670.1
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5258	JCVI_26743	A8	9238438	A Scaffold000011	2652027	AT4G34660.1
	JCVI_16353	A8	9238913	A Scaffold000097	698854	AT4G34660.1
	EE542458	A8	9239928	A Scaffold000097	697689	AT4G34660.1
	JCVI 17975	A8	9240040		697678	
	JCVI 7890	AS	9240469		697187	AT4G34640.1
	EE536108	AS	9243526		694157	AT4G34640.1
	JCVI_12520	AS	9243526	A Scaffold000097	694040	AT4G34640.1
				-		
	JCVI_18916	A8	9254489	-	683046	
	ES907398	A8	9261123	A_Scaffold000097	676452	AT4G34580.1
	JCVI_25534	A8	9271398	A_Scaffold000099	755577	
	JCVI_32337	A8	9271400	A_Scaffold000099	755576	
	JCVI_22797	A8	9281778	A_Scaffold000097	654550	
	JCVI_36670	A8	9285016		652016	AT4G34510.1
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	EV039315	A8	9333674	A Scaffold000162	28424	
	EE518255	AS	9335725	A Scaffold000181	51322	
	ES269389	AS	9341763	A_Scaffold000097	595943	AT4G34440.1
	JCVI 34283	AS	9344371	A Scaffold000097	593251	
	-			-		
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	ES898531	A8	9346197	A_Scaffold000097	591269	AT4G34430.4
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	EX127275	A8	9359192	-	578204	
	EV085789	A8	9360121	A_Scaffold000097	577295	
5290	EV106406	A8	9367444	A_Scaffold000097	569822	AT4G34390.1
5291	EV106450	A8	9367446	A_Scaffold000097	569785	AT4G34390.1
5292	EX079894	A8	9367763	A_Scaffold000097	569795	AT4G34390.1
5293	EV106761	A8	9367791	A_Scaffold000097	569777	AT4G34390.1
	EX058924	A8	9370511	A_Scaffold000097	566973	AT4G34390.1
	ES984770	AS	9373170	A Scaffold000097	564202	
					201202	

Use BLAST to identify *B. rapa* and *B. oleracea* genome sequence scaffolds corresponding to linkage-mapped unigenes, assemble into preudomolecules representing the *B. napus* genome.

Use BLAST to identify best match between sequence of every unigene and the pseudomolecules representing the *B. napus* genome.

UNMAPPED UNIGENES ORDERED BY MAPPED SEQUENCE SCAFFOLDS

1	unigene	A Chr	Start	B. rapa scaffolds	Start	AGI	Γ
5240	EV141692	A8	9151176	A_Scaffold000097	796364		Г
	JCVI_15733	A8	9151537	-	795749		F
	CX192070	A8		A_Scaffold000097		AT4G34840.1	
	JCVI_5729	A8		A Scaffold000097	759664		
	JCVI_3918	A8	9177527	-	759714		
	EV075943	A8	9182978		470339	AT1G43570.1	E
	DY023723	AS		A Scaffold000097	740289	A11045570.1	-
	JCVI_1057	AS	9212467	-		AT4G34720.1	L
	CV546751	AS	9219387	-	718170	A14654720.1	H
	JCVI 10034	AS	9219387			AT4G34710.1	H
							H
	JCVI_12180	A8	9221365		716121	AT4G34710.1	-
	EX120610	A8		A_Scaffold000097	715694		
	EE470793	A8	9227903		709576		L
	EX066713	A8	9230322	-	707204		L
	JCVI_8753	A8		A_Scaffold000097		AT4G34680.1	L
	BG543396	A8		A_Scaffold000097		AT4G34680.1	L
	JCVI_4009	A8		A_Scaffold000097	702318		
	CV432227	A8		A_Scaffold000097	702318		
	JCVI_26743	A8	9238438	A_Scaffold000011	2652027	AT4G34660.1	
5259	JCVI_16353	A8	9238913	A_Scaffold000097	698854	AT4G34660.1	
5260	EE542458	A8	9239928	A_Scaffold000097	697689	AT4G34660.1	
5261	JCVI_17975	A8	9240040	A_Scaffold000097	697678	AT4G34660.1	Г
15262	JCVI_7890	A8	9240469	A Scaffold000097	697187	AT4G34640.1	
	EE536108	A8	9243526	A Scaffold000097	694157		
5264	JCVI_12520	A8		A_Scaffold000097	694040	AT4G34640.1	F
	JCVI_18916	AS		A_Scaffold000097	683046		F
	ES907398	A8		A_Scaffold000097	676452		F
	JCVI 25534	AS		A_Scaffold000099	755577	2111021200.1	١.
	JCVI 32337	AS		A Scaffold000099	755576		t.
	JCVI_22797	AS		A Scaffold000097	654550	AT4G34520.1	H
	_	AS		A Scaffold000097	652016		⊢
	JCVI_36670			-			⊢
	EV163038	A8		A_Scaffold000097	651611	AT4G34510.1	-
	CX271024	A8		A_Scaffold000097	631967		
	JCVI_15279	A8		A_Scaffold000097	619381		L
	JCVI_21808	A8		A_Scaffold000097	615712		
	JCVI_18088	A8		A_Scaffold000097	614719		L
	EE451883	A8		A_Scaffold000097	612711		L
	EV221548	A8	9326235	-	611453		L
15278	JCVI_31968	A8	9327663	A_Scaffold000097	610093	AT4G34450.1	
5279	EV039315	A8	9333674	A_Scaffold000162	28424		
5280	EE518255	A8	9335725	A_Scaffold000181	51322		
5281	ES269389	A8	9341763	A_Scaffold000097	595943	AT4G34440.1	
5282	JCVI_34283	A8	9344371	A_Scaffold000097	593251	AT4G34430.1	
15283	ES912981	A8	9345298	A_Scaffold000097	592291	AT4G34430.3	
	ES898531	A8		A Scaffold000097	591269		
	EX091671	A8	9348079	-	589535		
	JCVI 23541	AS		A Scaffold000097	581044		F
	JCVI_19991	AS		A_Scaffold000097	580865		F
	EX127275	AS		A_Scaffold000097	578204	A14654410.1	
	EV085789	AB					
			9360121	-	577295		H
	EV106406	A8		A_Scaffold000097		AT4G34390.1	
	EV106450	A8		A_Scaffold000097	569785		
	EX079894	A8		A_Scaffold000097	569795		
	EV106761	A8	9367791		569777		
	EX058924	A8		A_Scaffold000097	566973		
	ES984770	A8		A_Scaffold000097	564202		
	ES912902	A8	0277250	A Scaffold000097	560074	AT1G35920.1	

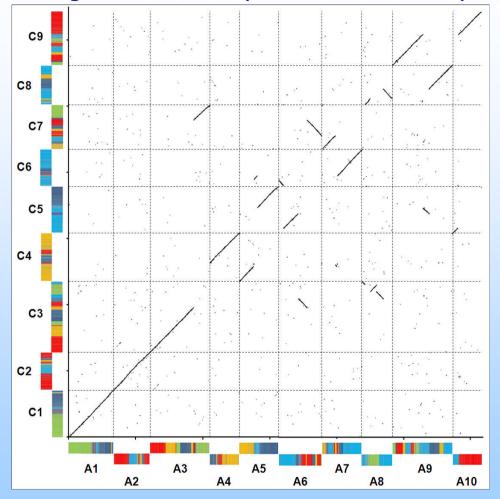


BEST UNIGENE SEQUENCE MATCHES TO A AND C GENOMES

Rearrangements between A and C genomes (as represented in B. napus)

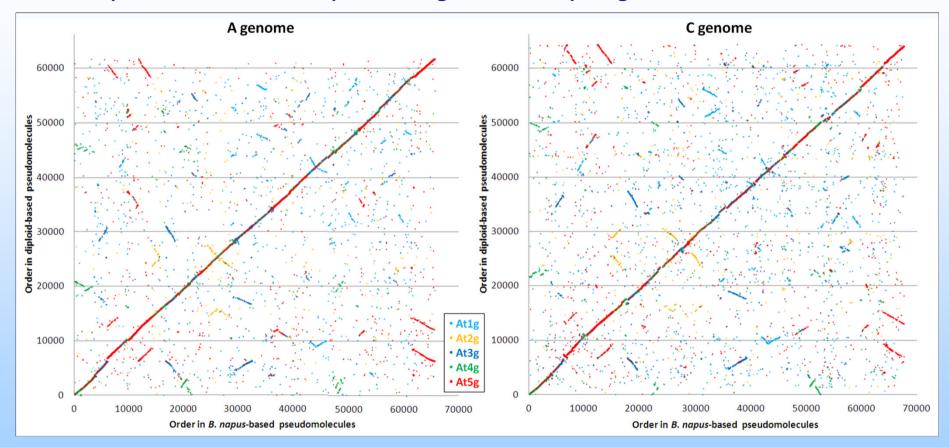
48,442 unigenes collinear between genomes

(BLAST-mapped 1E-30 to both genomes, filtered to exclude those with inconsistent cross-genome matches for both flanking unigenes)



BEST UNIGENE SEQUENCE MATCHES TO RAPESEED GENOME

Good (but not perfect) collinearity between diploid-based and *B. napus*based pseudomolecules representing the *B. napus* genome

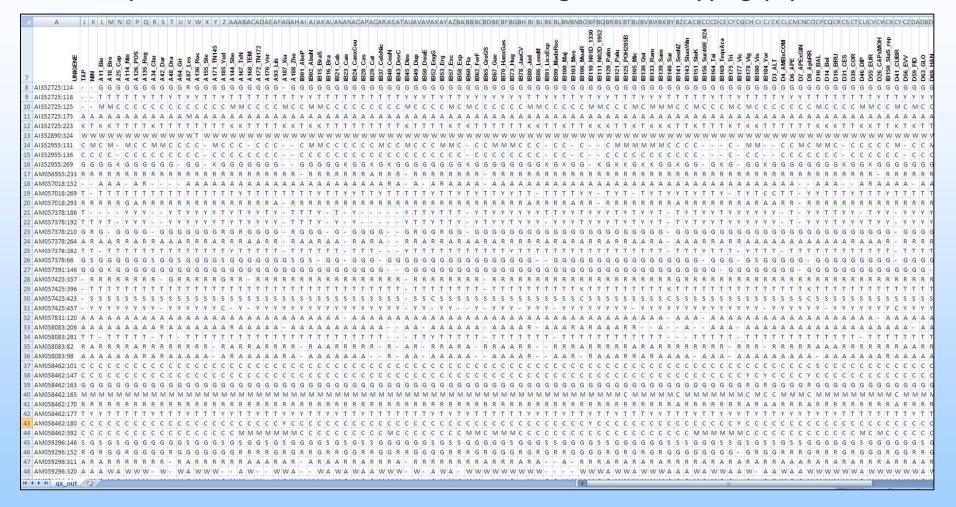


Identifying the functional bases of trait variation in *Brassica napus* using Associative Transcriptomics

- Brassica genome structure and evolution
- Genome framework for association genetics
- Establishing marker-trait associations

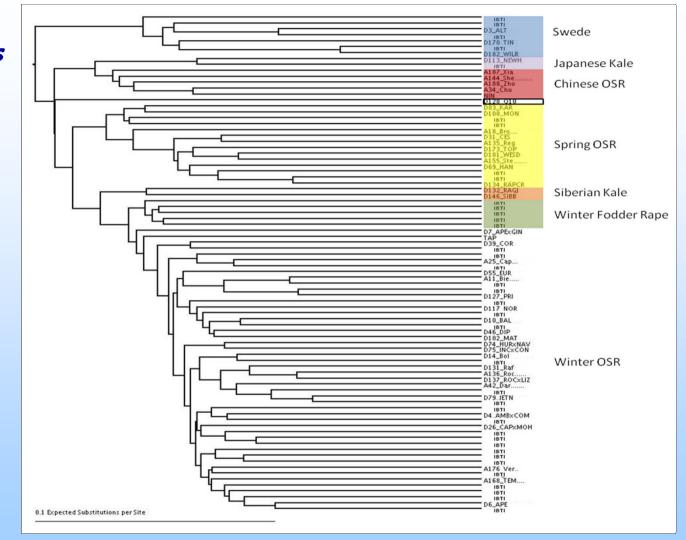
ASSAY OF SNPs ACROSS DIVERSITY PANELS

Transcriptome SNPs identification and scoring as for mapping populations



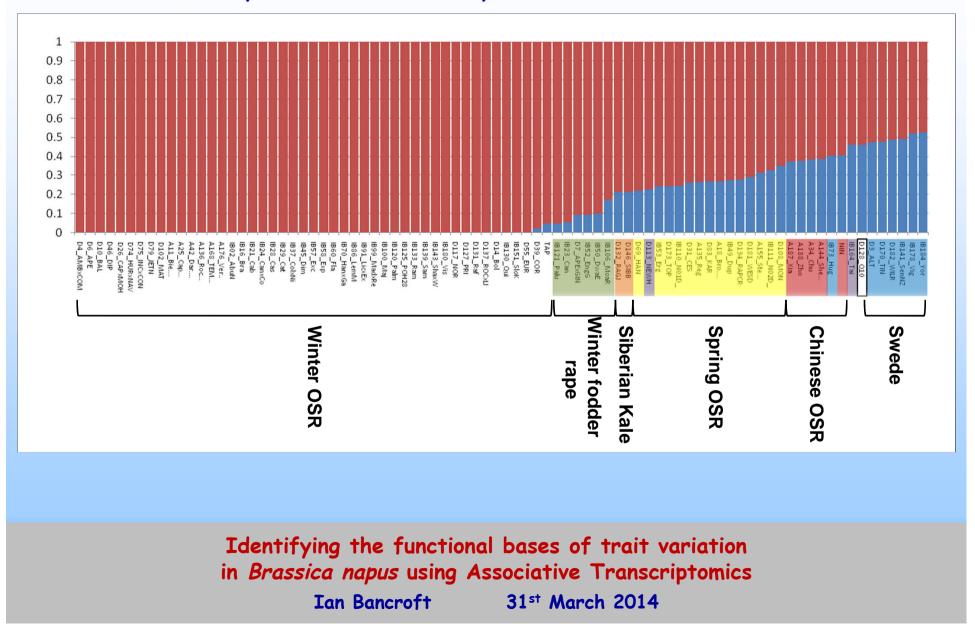
RELATEDNESS ANALYSIS

Tree construction across 83 *B. napus* accessions with 101,644 transcriptome SNPs.



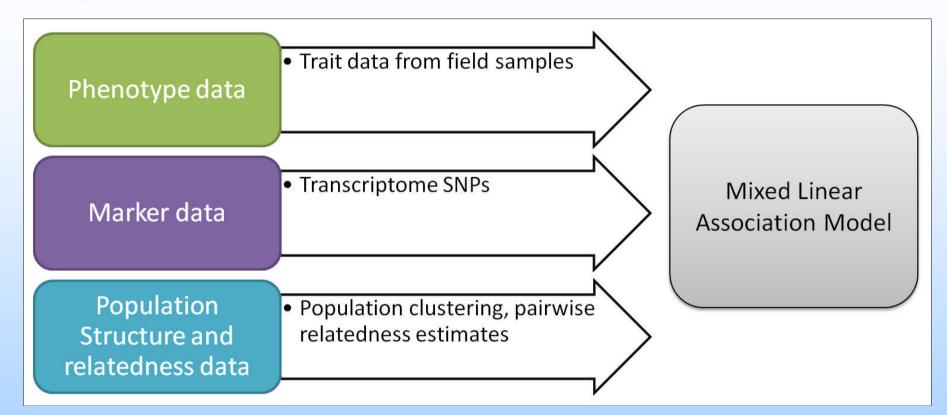
POPULATION STRUCTURE ANALYSIS

STRUCTURE analysis across 83 B. napus accessions



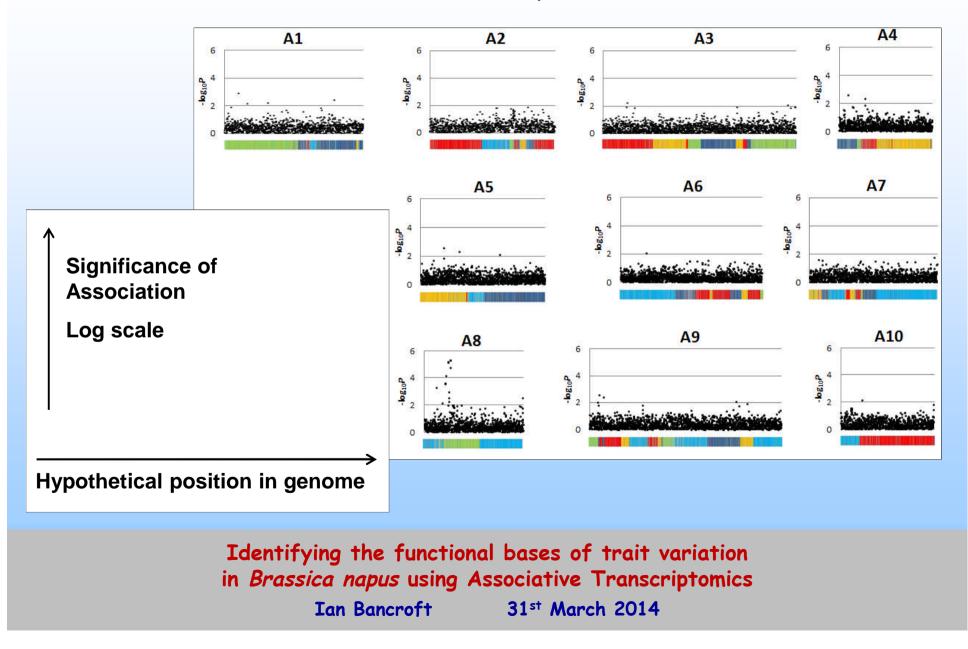
ASSOCIATION GENETICS

Linkage Disequilibrium analysis

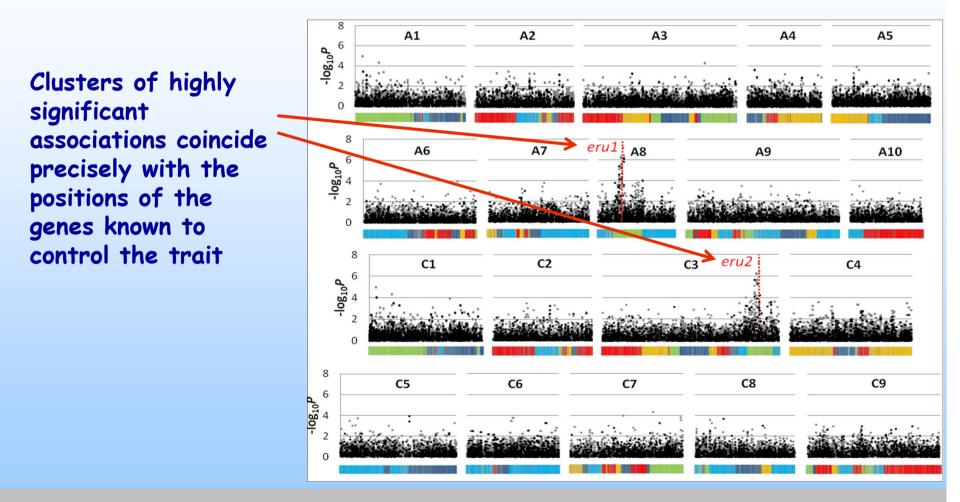


VISUALISING MARKER-TRAIT ASSOCIATIONS

Genome-Wide Association Scans: "Manhattan plots"



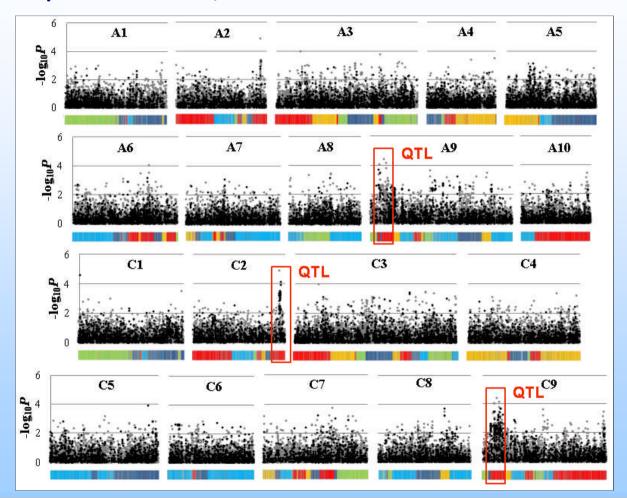
EXAMPLE OF ASSOCIATION GENETICS USING TRANSCRIPOME SNPs Validation experiment: Linkage Disequilibrium analysis for erucic acid content of seed oil (53 *B. napus* accessions)



ASSOCIATION GENETICS USING TRANSCRIPOME SNPs: GLUCOSINOLATES

Trait of unknown basis: Linkage Disequilibrium analysis for glucosinolate content of seeds (53 *B. napus* accessions)

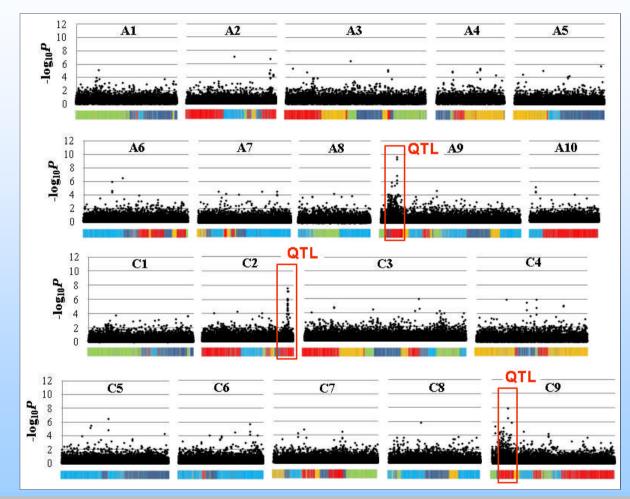
Genome-wide association scan for SNP markers in 125,905 hypothetically ordered unigenes



CORRELATE GENE EXPRESSION VARIATION WITH TRAIT VARIATION

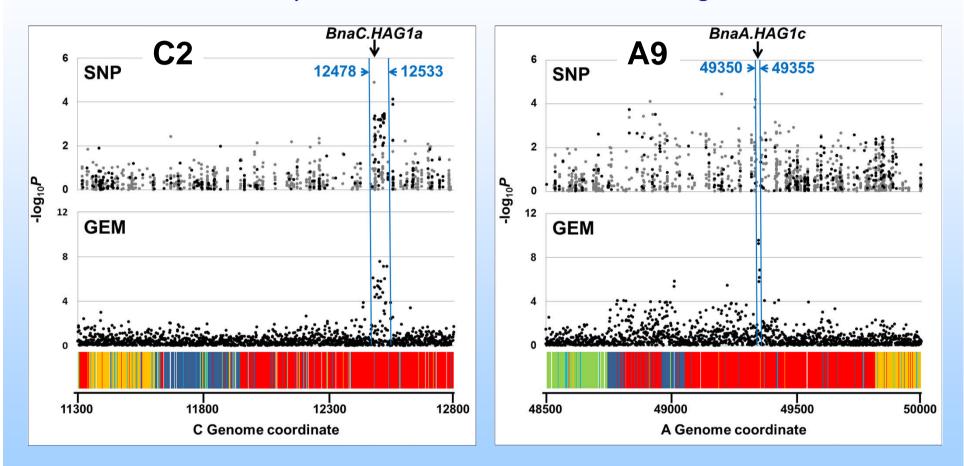
Trait of unknown basis: Regression analysis for glucosinolate content of seeds (53 *B. napus* accessions)

Genome-wide regression for expression variation in 125,905 hypothetically ordered unigenes



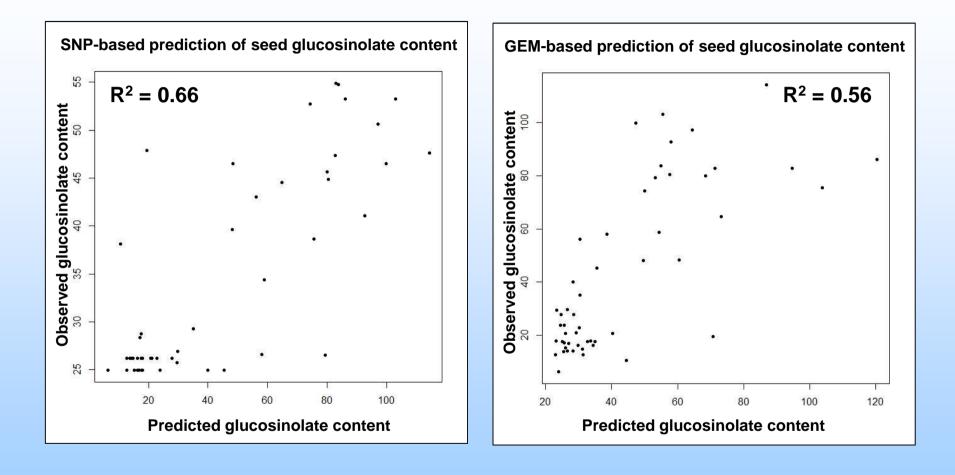
IDENTIFICATION OF CANDIDATE GENES

- Association analyses provide molecular markers to support breeding
- Associative Transcriptomics often identifies causative gene variants



TRAIT PREDICTION

Markers associated with variation are predictive of quantitative trait values



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