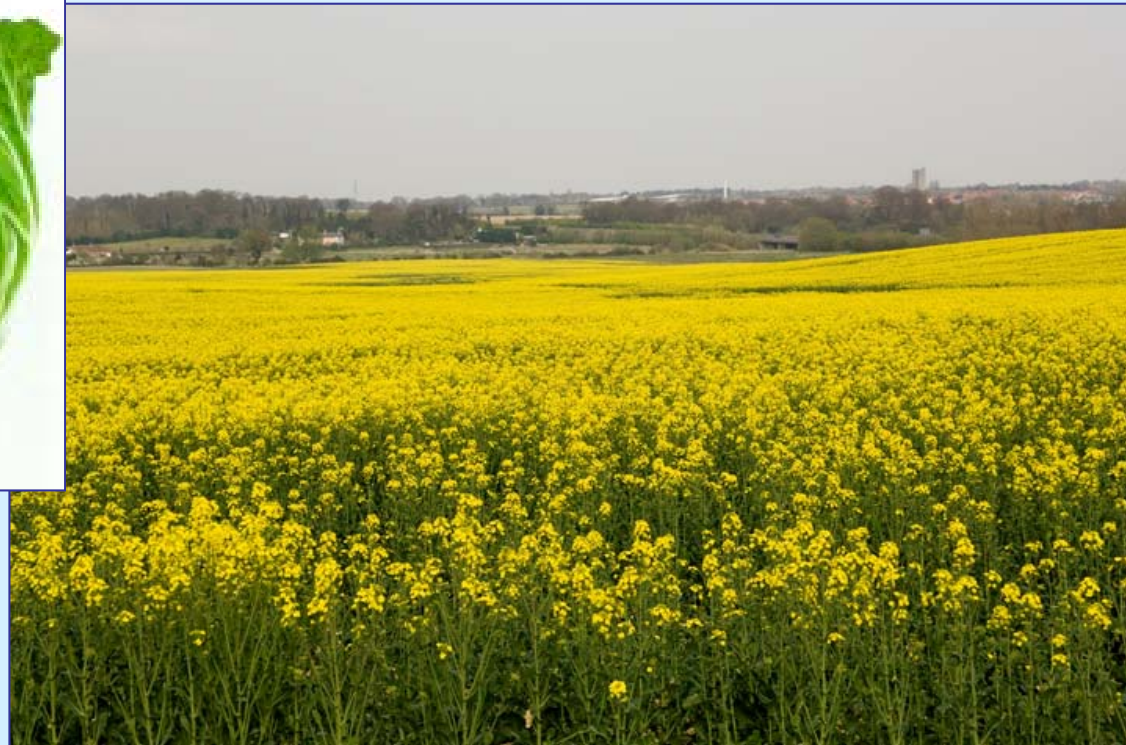


OREGIN update:

B. napus map integration with the *Brassica rapa* Genome Sequence

Ian Bancroft

27th November 2009



OREGIN map integration: Anchoring the TNDH linkage map to the *B. rapa* genome sequence

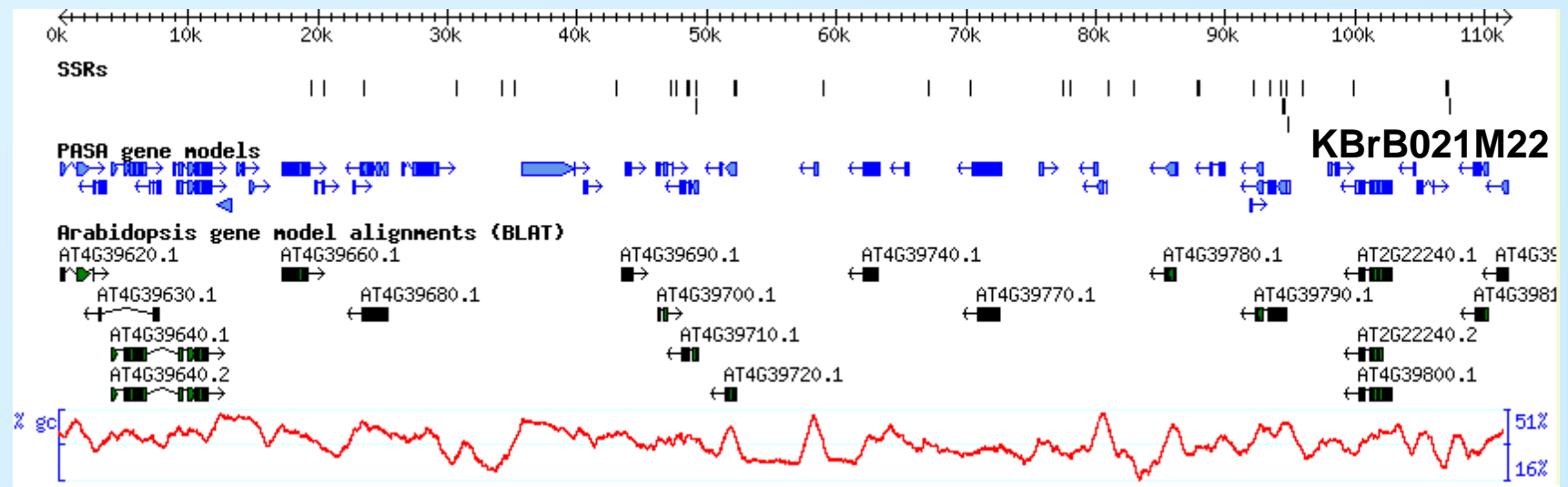
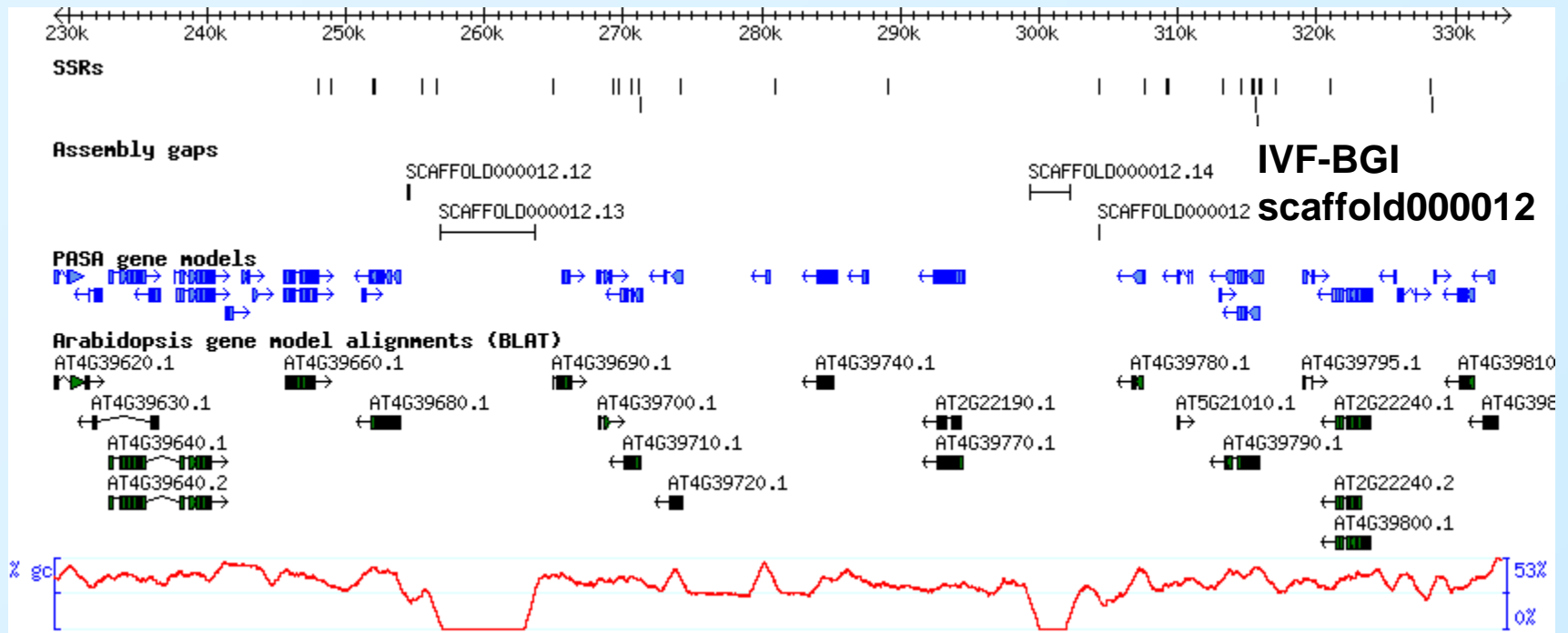
83 BAC-derived markers mapped to date (project objective: 100)

http://www.oregin.info/information/reports/markers/oregin_markers1.xls

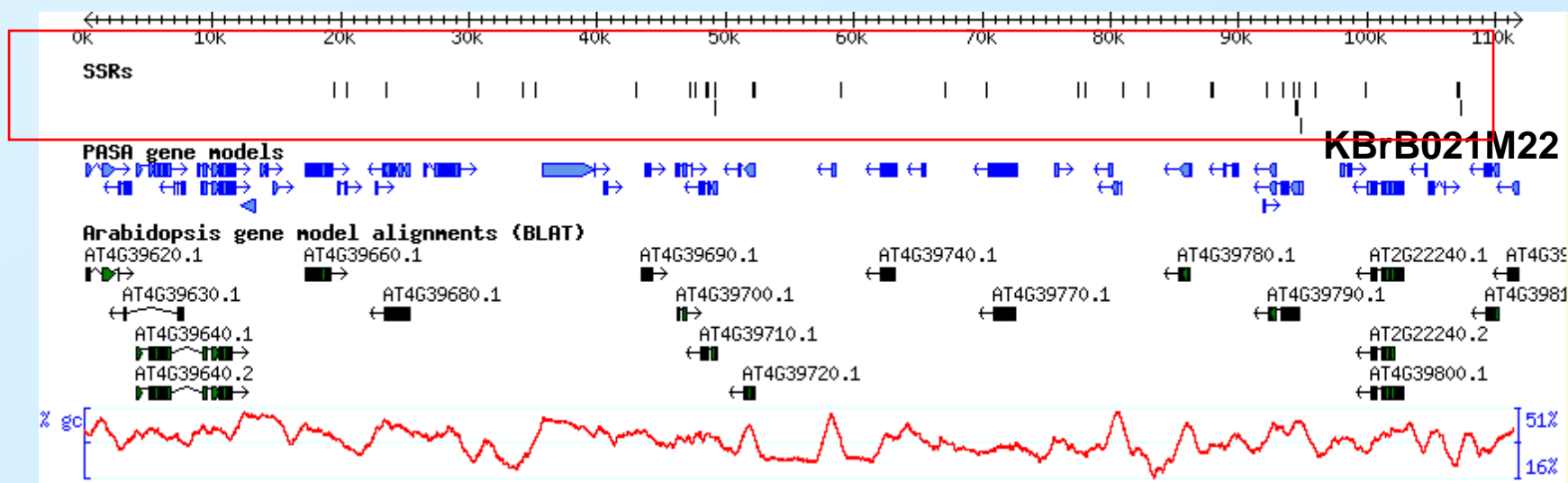
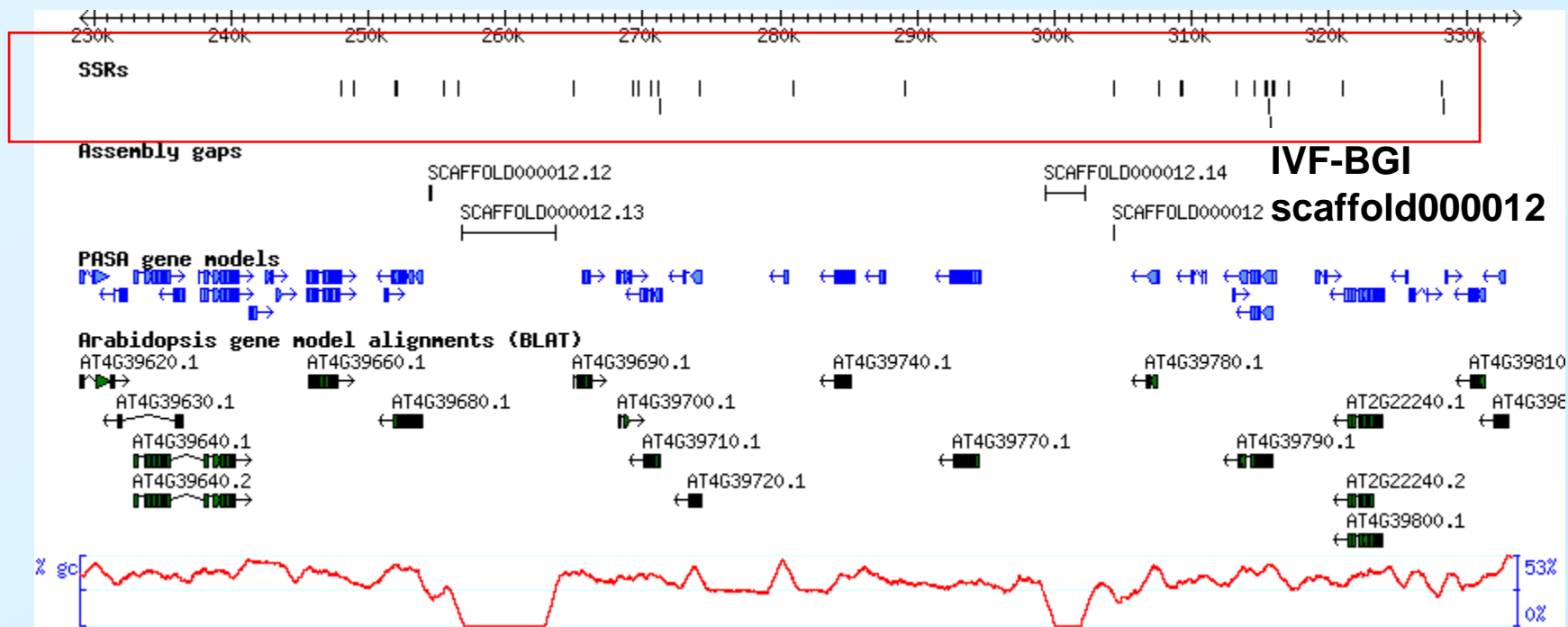
- Conducted in collaboration with CNU and HAU

Linkage Group	Marker Name	BAC Name	Left primer	Right primer	cM
A1	niab113	KBrB022O03	CAAAAAGTTGCGGTCAATCT	CCTCCAAAGCTCAATCACTG	7.06
A1	CNU142	KBrB036M17	GACCTTCGGTTCAGGGTATGG	CTGAACGGTCAATTTGTTGG	22.31
A1	CNU139	KBrS004O21	TCAAGCGCAACAAACATTGG	TGGTGTAGGGTTTAAAGTTGTGG	27.43
A1	niab096	KBrB066A08	CAAAAAGAGCGTTACCTCCA	GATGAAGCTCTGAAGACCGA	31.59
A1	CNU235	KBrB091M11	CAACCACATGAGATTGGTTAGTT	GAAATGGTTTTGGAGCGGTA	56.62
A1	CNU132	KBrB036M22	CCATGGCCTCTCGTATTGCT	CCAACGGAGTGTCCCAATC	63.91
A2	CNU389	KBrB043L02	TCCAAAATCCAATTGCTAAAAA	AAAGCATGCAACTTAAGCCATA	91.55
A3	niab115	KBrB055N13	CGGTGTATACCGAACGAGAA	AAACCAATCAACCCCTTTA	7.07
A3	niab116	KBrH006C14	CTGAACCGAATTGGCTAAAA	TAAACAGGGGAAGTGAAGCTG	10.51
A3	niab102	KBrB008I08	GAGGCCAATTCTTCAACAGA	TGCTTCATTCCGGTATTCAT	16.28
A3	CNU250	KBrB080O07	CAGATTTTCGAAAGGTGGTTGG	CCATCACCCGAAAATCCAAA	40.61
A3	CNU253	KBrS012M03	CCCCAAAACATCCAAACTCCTCA	CCCCAAAGAGATACAGAACAAGC	41.89
A3	CNU384	KBrB056I08	TGAAGGTGATGATGACGATGA	TCATGGTCTACAAAGACATACGG	45.81
A3	CNU288	KBrB032C14	GCGTTTTCTGCTCTTCTCAC	TTACCCACCTTGGCTTCATC	46.95
A3	KBrB001H24-13	KBrB001H24	CTAGCGAGGATTCCGATGAG	CCATCAATGGGCTCTACAGG	59.07
A3	CNU098	KBrB049D17	TGCGACCCAAGTAGGTGAAAC	TGTCTCTCGCTCATTATCCAA	59.18
A3	KBrB043L02-12	KBrB043L02	CGGATGCATTTTCAAGTAGG	TTCTGACAAGTCCAAGAGAACG	61.52
A3	CNU270	KBrB047D06	TCGATGATTAGTTTAGTTATTTACG	CCTCAAACCAAGGAAGATTTCA	73.07
A3	CNU321	KBrB042O05	TTGAATAATGACCCCAAATATCA	TCAATAGGTATTAACCAATTCTACCG	74.92
A3	CNU002	KBrH070D09	CAAATGCAGCAGCGATTAATA	CGGGGGTTGCAGAAAGATA	75.31
A3	CNU215	KBrB059A03	CCAACCATTTCTGTAGTCAACC	TTACGCATGTACCTGCACTAAAAA	82.15
A3	CNU370	KBrB013J16	CAAATCGGGCATTGTTCCAT	CAATCAAGGAAAAATCTGTACCAATC	91.09
A3	CNU371	KBrS012D09	TTTTTGGGTTTCTTCTCAAATGC	ACTCCAGCGAATTTGGCTTT	94.37
A3	CNU223	KBrS012D09	ACCCGAAAAGAGAATATGGCCT	ACAGTGGCGTTAGGTGGGG	95.32
A3	CNU316	KBrS003O10	TCAAGCATGTCTTAAAACTCTGA	GCGTTCACGTTTCCCATATC	97.72
A3	CNU306	KBrB084K23	GTGCCCTTTTTGCATTTGTC	GCCAAAGACCAACTTTTTAACG	98.19
A3	CNU435	KBrB084K23	AATTGAACCAAACGGAGCAC	GCTTTGCAACTAAGAGTCTTTCAA	98.46

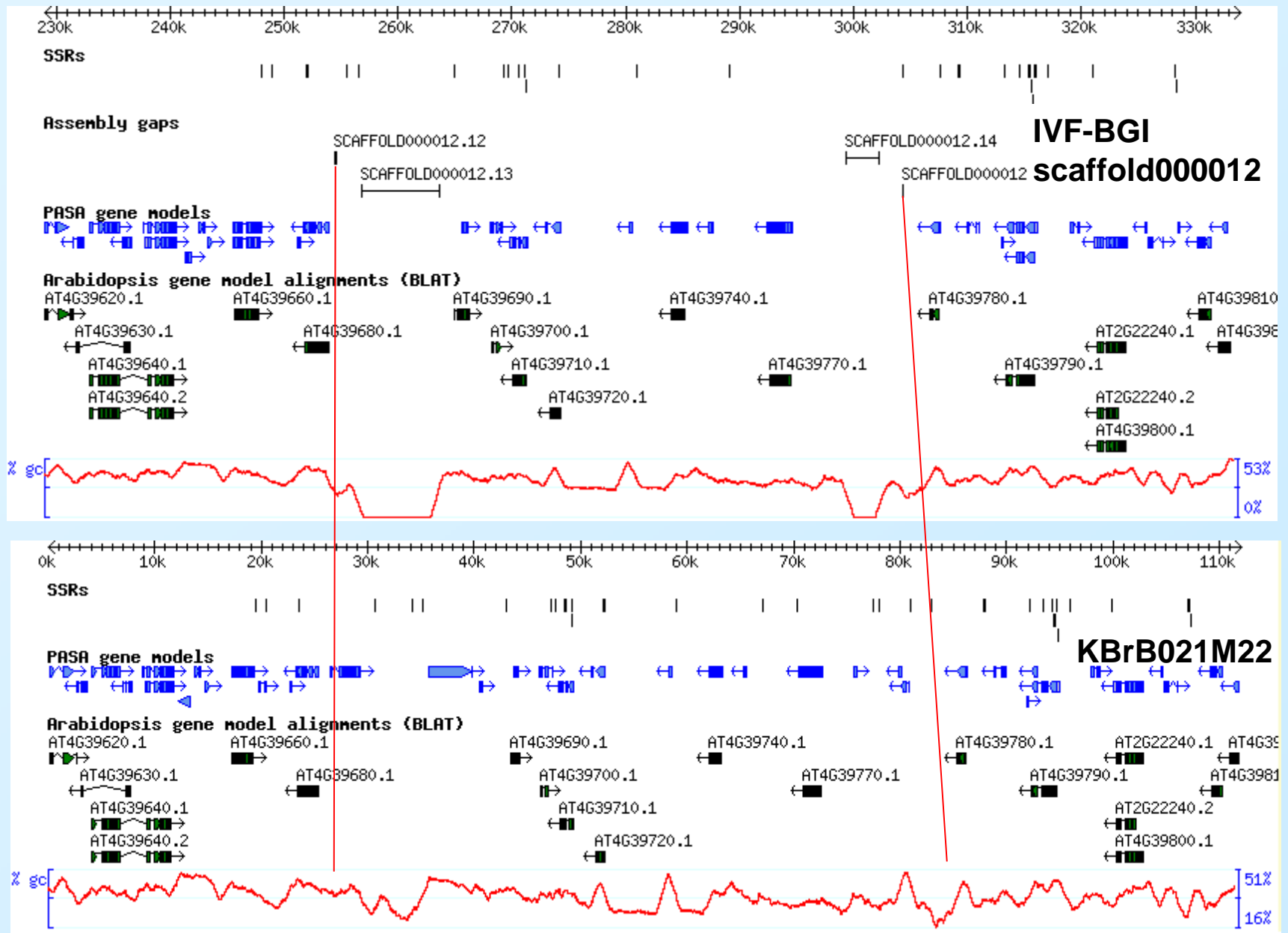
Annotation of scaffold000012 compared with KBrB021M22



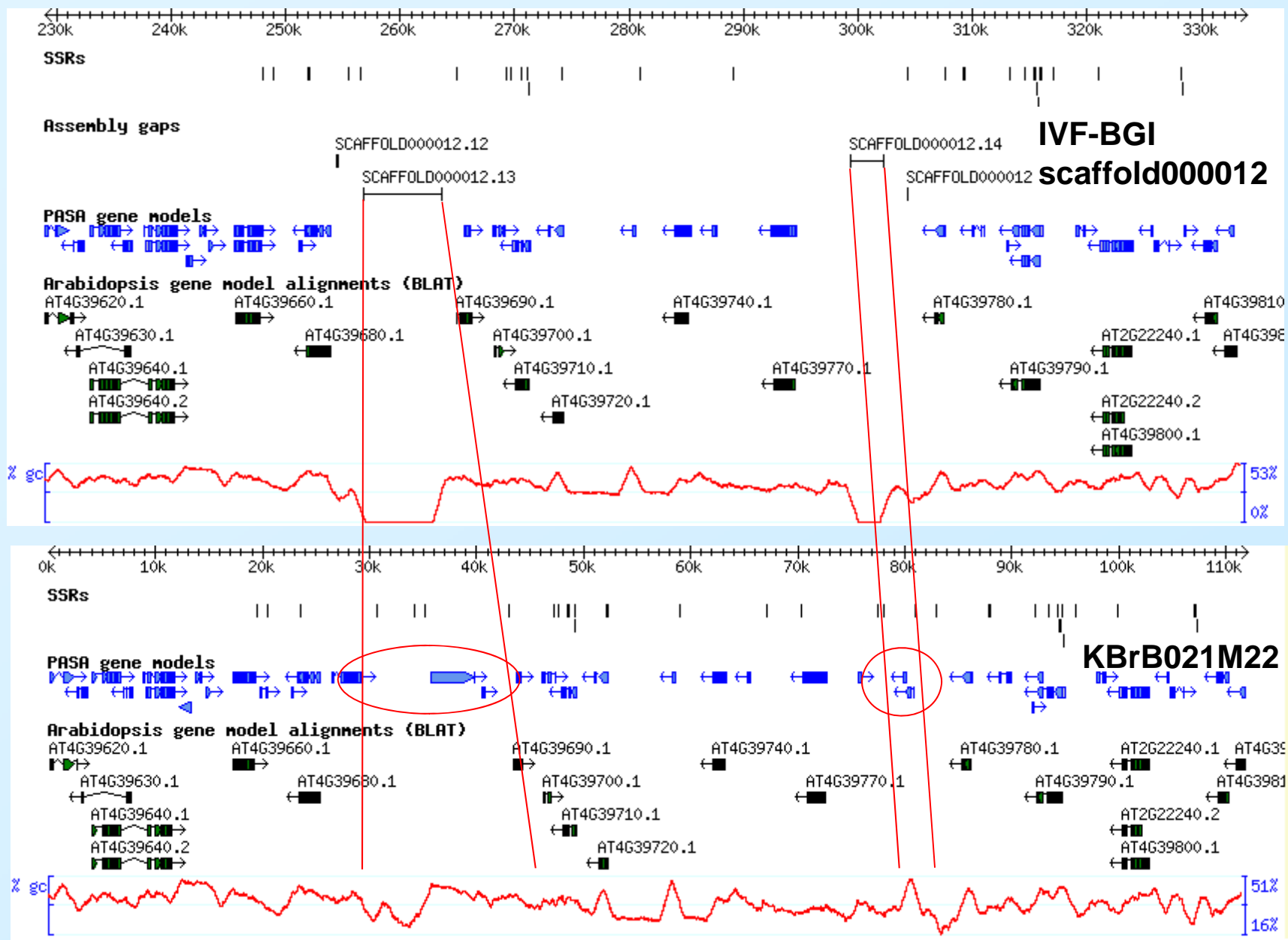
Identification of SSR regions is good



Many assembly gaps, but few affect collinear gene models



Gene models affected by assembly gaps are largely transposon-related



Ongoing *Brassica* genome sequencing efforts

Several public whole genome sequencing projects ongoing for *B. rapa* and *B. oleracea*, using 454 and/or Solexa sequencing

Several public genome re-sequencing projects for *B. napus*

Private “genome sequences” announced in press release by Bayer

UK-China genome sequencing project to contribute transcriptome sequences from a range of OREGIN DFFS, in addition to contributing to *B. oleracea* and *B. napus* genome sequencing projects.

TNDH map integration in OREGIN will be extended into genome sequence of *B. napus*, in addition to *B. rapa*