# *The Br* GSP: Progress on first-pass annotation and seed BAC selection

UK-BRC 23rd May 2007

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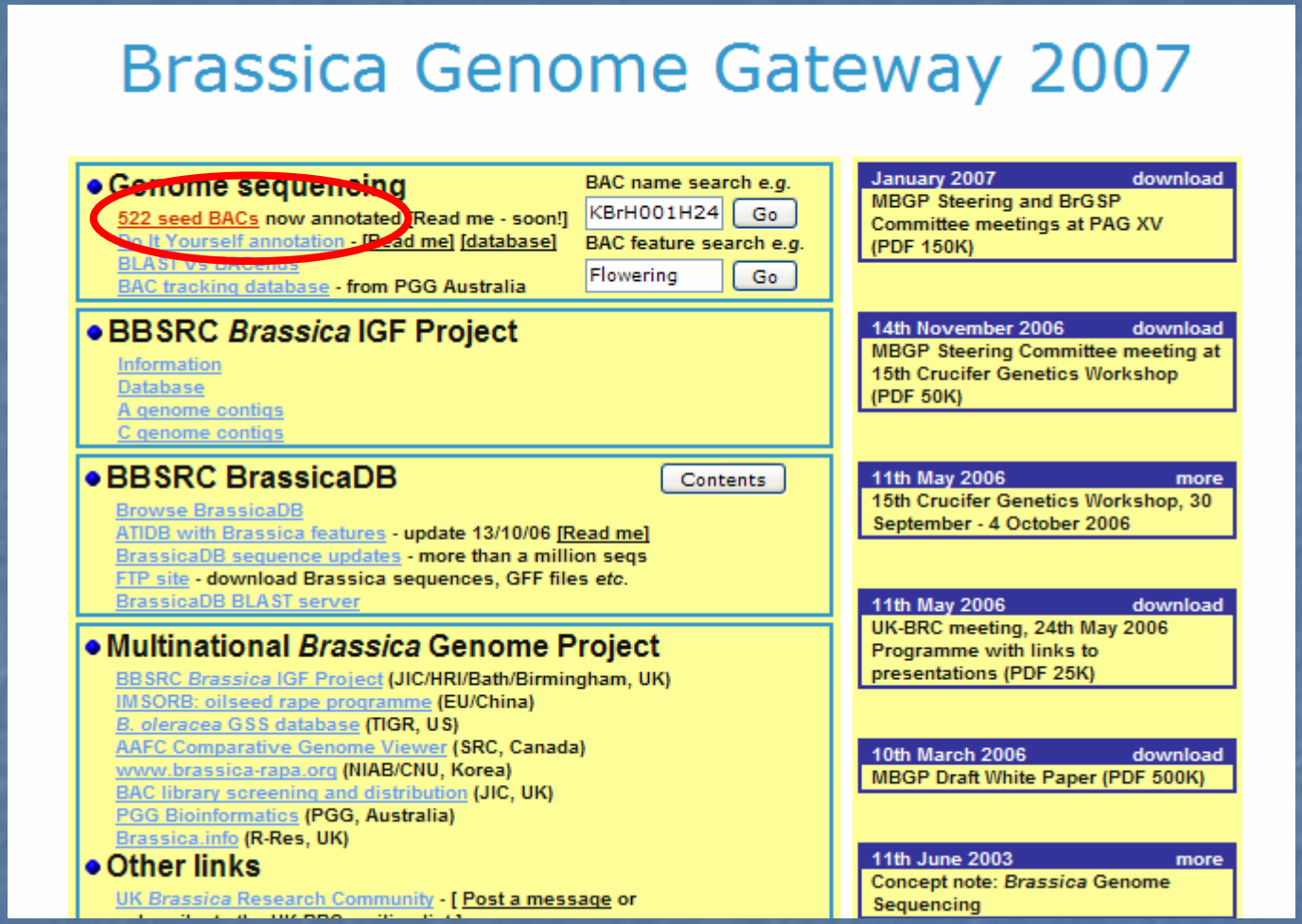


**http://brassica.bbsrc.ac.uk**

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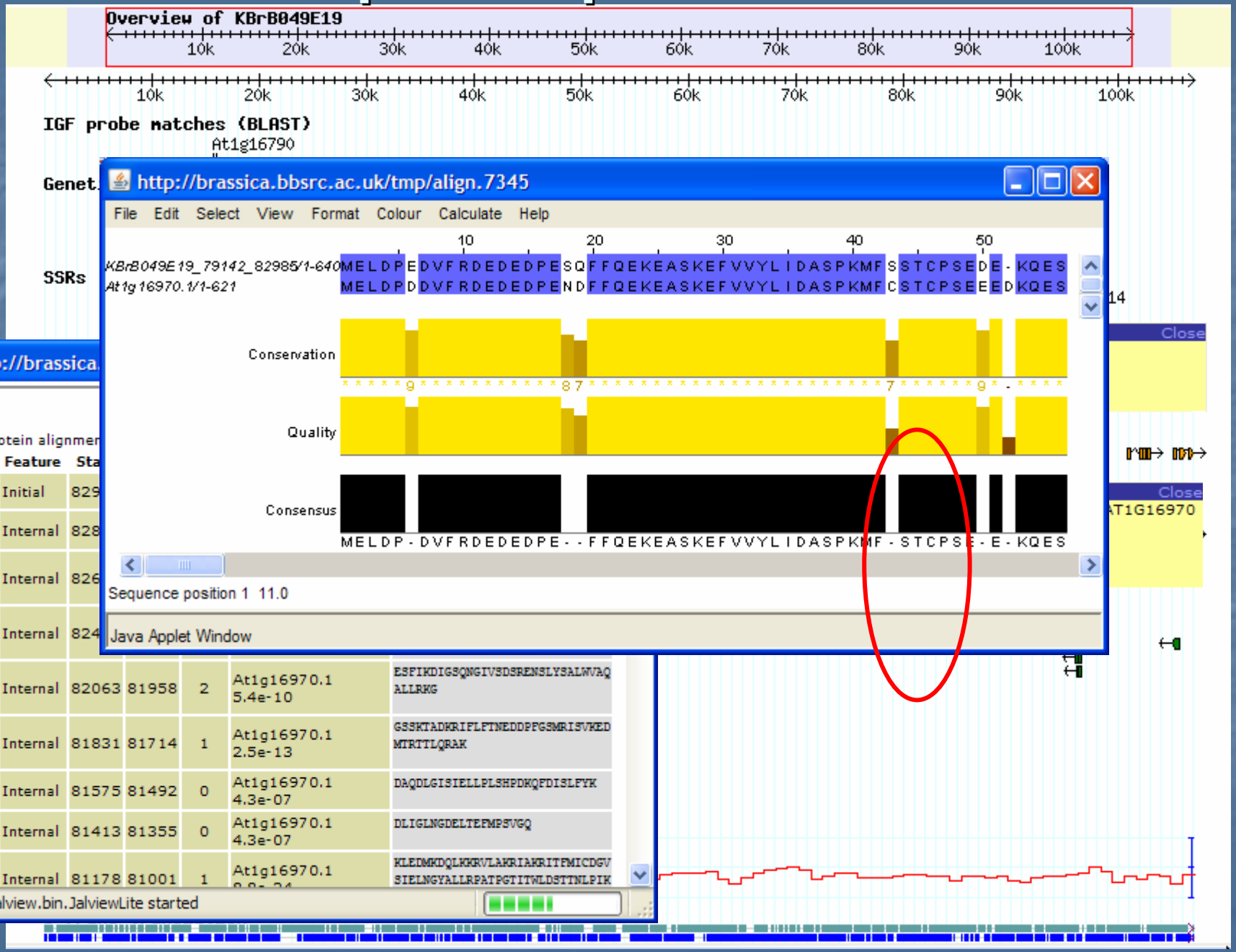
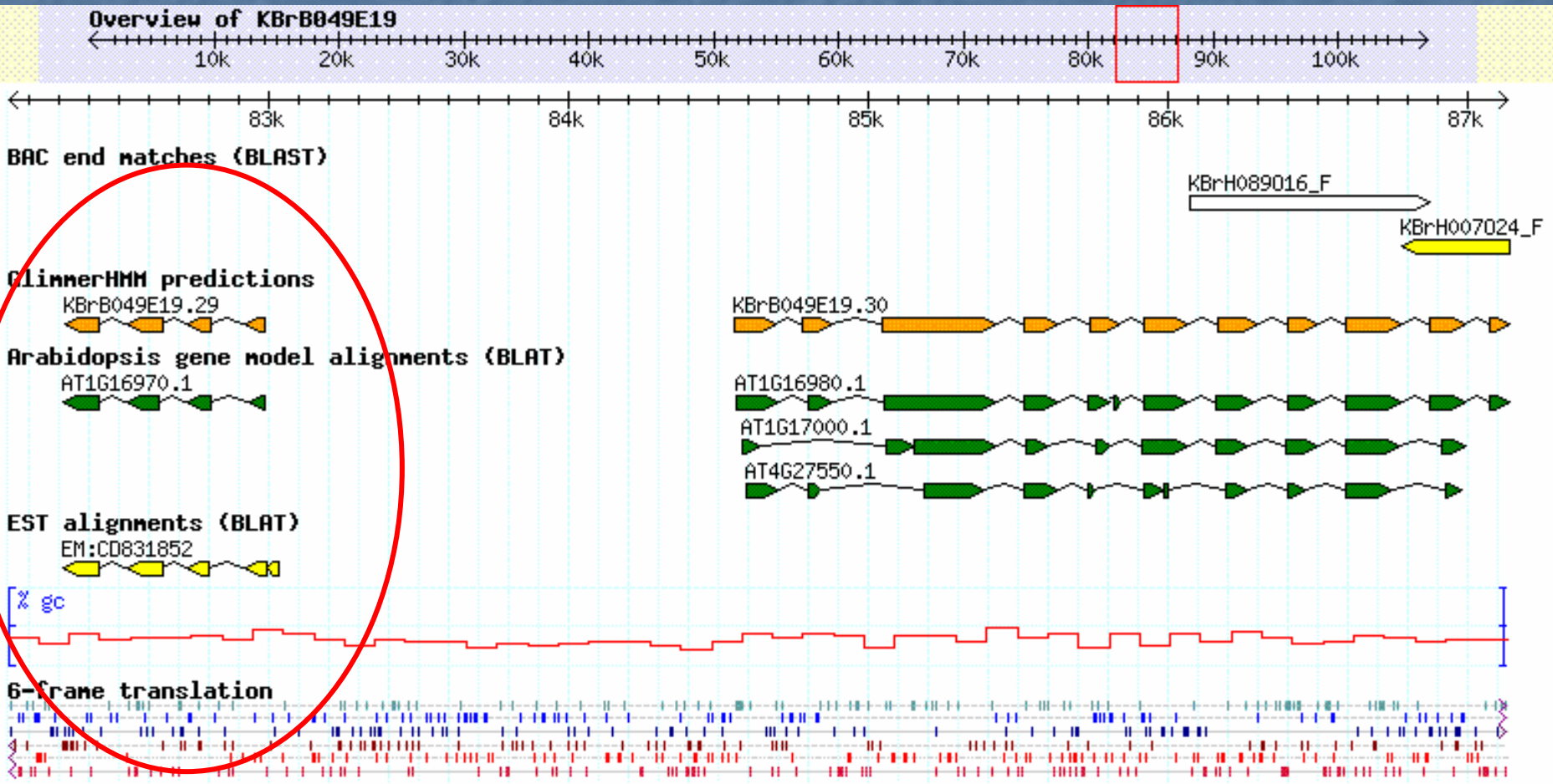
# Example first pass annotation



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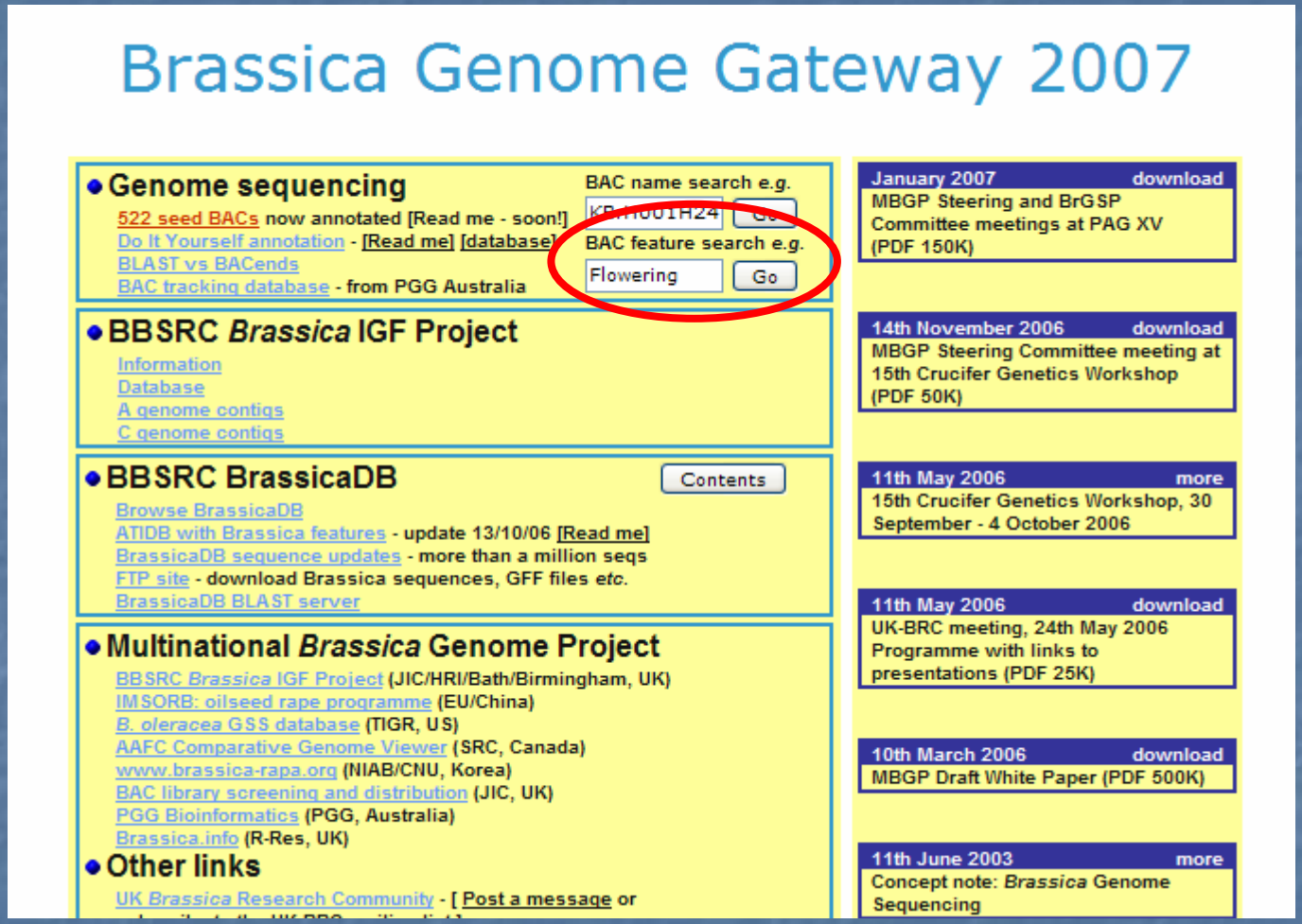


**http://brassica.bbsrc.ac.uk**

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Brassica BAC annotation - Mozilla Firefox

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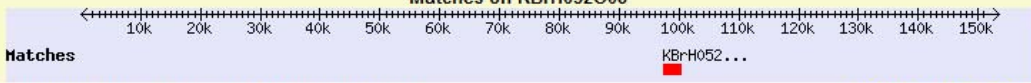
http://brassica.bbsrc.ac.uk/cgi-bin/gbrowse/jic_brassica

Gateway IGF IMSORB ATIDB Annotation DB Brassica-ATIDB jilin4 WAN Agrenet jicbio status Weather F1 FIA timing Intranet Charge

**Matches on KBrH004D11**

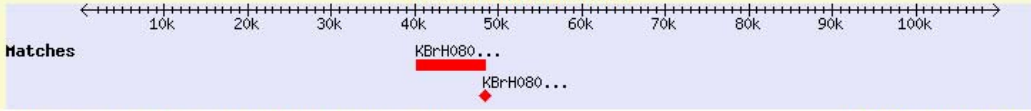

| | | | |
|---|---|---|---|
| KBrH004D11.14 | At5g10140.1 (E=1.7e-25) FLC (**FLOWERING** LOCUS C) | KBrH004D11:43,541..46,799 (3259 bp) | score=7.46 |
| KBrH004D11.14 | At5g10140.1 (E=4.0e-06) FLC (**FLOWERING** LOCUS C) | KBrH004D11:43,541..46,799 (3259 bp) | score=7.46 |

**Matches on KBrH052O08**



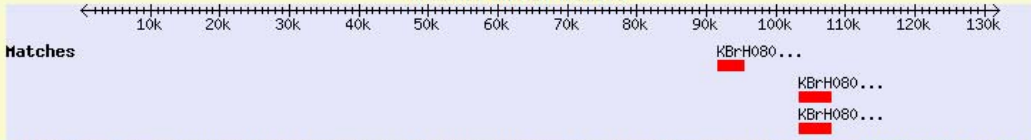

| | | | |
|---|---|---|---|
| KBrH052O08.27 | At5g10140.1 (E=5.7e-25) FLC (**FLOWERING** LOCUS C) | KBrH052O08:97,426..100,370 (2945 bp) | score=7.46 |

**Matches on KBrH080A08**




| | | | |
|---|---|---|---|
| KBrH080A08.10 | At5g10140.1 (E=3.8e-26) FLC (**FLOWERING** LOCUS C) | KBrH080A08:40,166..48,456 (8291 bp) | score=7.46 |
| KBrH080A08.23 | At5g10140.1 (E=6.5e-17) T31P16.130, MADS-box protein **flowering** locus F (FLF), GO:0016566 [specific transcriptional repressor activity] GO:0008372 [cellular_component unknown] GO:0009910 [negative regulation of flower development] GO:0003700 [transcription factor activity] | KBrH080A08:48,241..48,654 (414 bp) | score=5.97 |

**Matches on KBrH080C09**

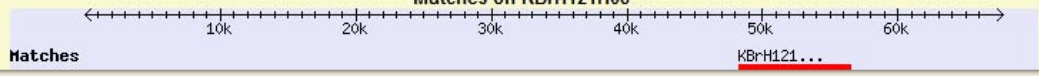



| | | | |
|---|---|---|---|
| KBrH080C09.26 | At1g77080.5 (E=9.6e-23) MAF1 (MADS AFFECTING **FLOWERING** 1) , AGL27 MAF1 AT1G77080.4 AT1G77080.2 AT1G77080.3 AT1G77080 AT1G77080 FLM **FLOWERING** LOCUS M MADS AFFECTING **FLOWERING** 1 AT1G77080 AT1G77080 AT1G77080 [ biological_process, regulation of transcription, DNA-dependent (GO:0006355) ] [ molecular_function, transcription factor activity (GO:0003700) ] [ biological_process, regulation of flower development (GO:0009909) ] [ biological_process, negative regulation of flower development (GO:0009910) ] | KBrH080C09:91,587..95,296 (3710 bp) | score=8.94 |
| KBrH080C09.27 | At5g65070.1 (E=1.9e-06) MAF4 (MADS AFFECTING **FLOWERING** 4) | KBrH080C09:103,328..107,787 (4460 bp) | score=7.30 |
| KBrH080C09.27 | At5g65080.1 (E=6.8e-22) MAF5 (MADS AFFECTING **FLOWERING** 5 VARIANT I) | KBrH080C09:103,328..107,787 (4460 bp) | score=7.22 |

**Matches on KBrH117M18**

| | | | |
|---|---|---|---|
| KBrH117M18.16 | At5g10140.1 (E=5.7e-25) T31P16.130, MADS-box protein **flowering** locus F (FLF), GO:0016566 [specific transcriptional repressor activity] GO:0008372 [cellular_component unknown] GO:0009910 [negative regulation of flower development] GO:0003700 [transcription factor activity] | KBrH117M18:46,939..49,858 (2920 bp) | score=5.97 |

**Matches on KBrH121H08**




Done

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Brassica BAC annotation - Mozilla Firefox

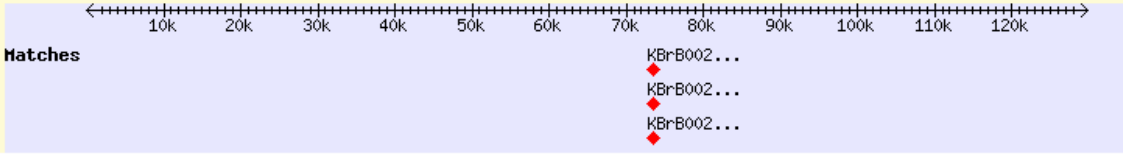
File Edit View Go Bookmarks Tools Help

http://brassica.bbsrc.ac.uk/cgi-bin/gbrowse/jic_brassica?name=GO%3A0006355

Gateway IGF IMSORB ATIDB Annotation DB Brassica-ATIDB jiilin4 WAN Agrenet jicbio status Weather F1 FIA timing Intranet Charge

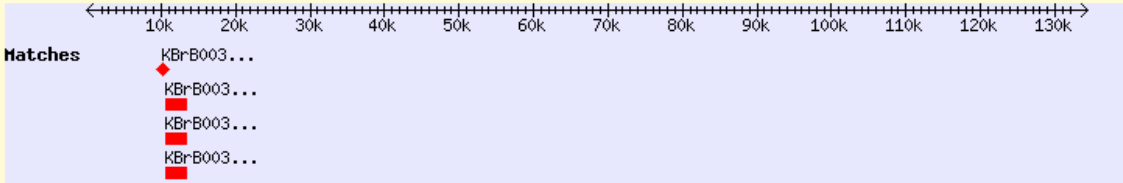
(GO:0006355) ]

**Matches on KBrB002K01**




| | | | |
|---|---|---|---|
| KBrB002K01.20 | At5g18000.1 (E=1.6e-38) DNA binding / transcription factor , AT5G18000.1 AT5G18000 MCM23.7 MCM23_7 [ cellular_component, cellular component unknown (**GO**:0008372) ] [ molecular_function, DNA binding (**GO**:0003677) ] [ molecular_function, transcription factor activity (**GO**:0003700) ] [ biological_process, regulation of transcription, DNA-dependent (**GO**:**0006355**) ] | **KBrB002K01**:72,959..74,423 (1465 bp) | score=3.00 |
| KBrB002K01.20 | At5g18000.1 (E=1.3e-18) DNA binding / transcription factor , AT5G18000.1 AT5G18000 MCM23.7 MCM23_7 [ cellular_component, cellular component unknown (**GO**:0008372) ] [ molecular_function, DNA binding (**GO**:0003677) ] [ molecular_function, transcription factor activity (**GO**:0003700) ] [ biological_process, regulation of transcription, DNA-dependent (**GO**:**0006355**) ] | **KBrB002K01**:72,959..74,423 (1465 bp) | score=3.00 |
| KBrB002K01.20 | At5g18000.1 (E=4.9e-26) DNA binding / transcription factor , AT5G18000.1 AT5G18000 MCM23.7 MCM23_7 [ cellular_component, cellular component unknown (**GO**:0008372) ] [ molecular_function, DNA binding (**GO**:0003677) ] [ molecular_function, transcription factor activity (**GO**:0003700) ] [ biological_process, regulation of transcription, DNA-dependent (**GO**:**0006355**) ] | **KBrB002K01**:72,959..74,423 (1465 bp) | score=3.00 |

**Matches on KBrB003A10**




| | | | |
|---|---|---|---|
| KBrB003A10.5 | At3g05670.1 (E=1.6e-19) DNA binding / protein binding / ubiquitin-protein ligase/ zinc ion binding , AT3G05670.1 AT3G05670 F18C1.6 F18C1_6 [ molecular_function, DNA binding (**GO**:0003677) ] [ biological_process, regulation of transcription, DNA-dependent (**GO**:**0006355**) ] | **KBrB003A10**:10,186..10,491 (306 bp) | score=3.15 |
| KBrB003A10.6 | At3g05670.1 (E=4.8e-39) DNA binding / protein binding / ubiquitin-protein ligase/ zinc ion binding , AT3G05670.1 AT3G05670 F18C1.6 F18C1_6 [ molecular_function, DNA binding (**GO**:0003677) ] [ biological_process, regulation of transcription, DNA-dependent (**GO**:**0006355**) ] | **KBrB003A10**:10,586..13,343 (2758 bp) | score=3.15 |
| KBrB003A10.6 | At3g05670.1 (E=3.7e-126) DNA binding / protein binding / ubiquitin-protein ligase/ zinc ion binding , | **KBrB003A10**:10,586..13,343 | score=3.15 |

Done

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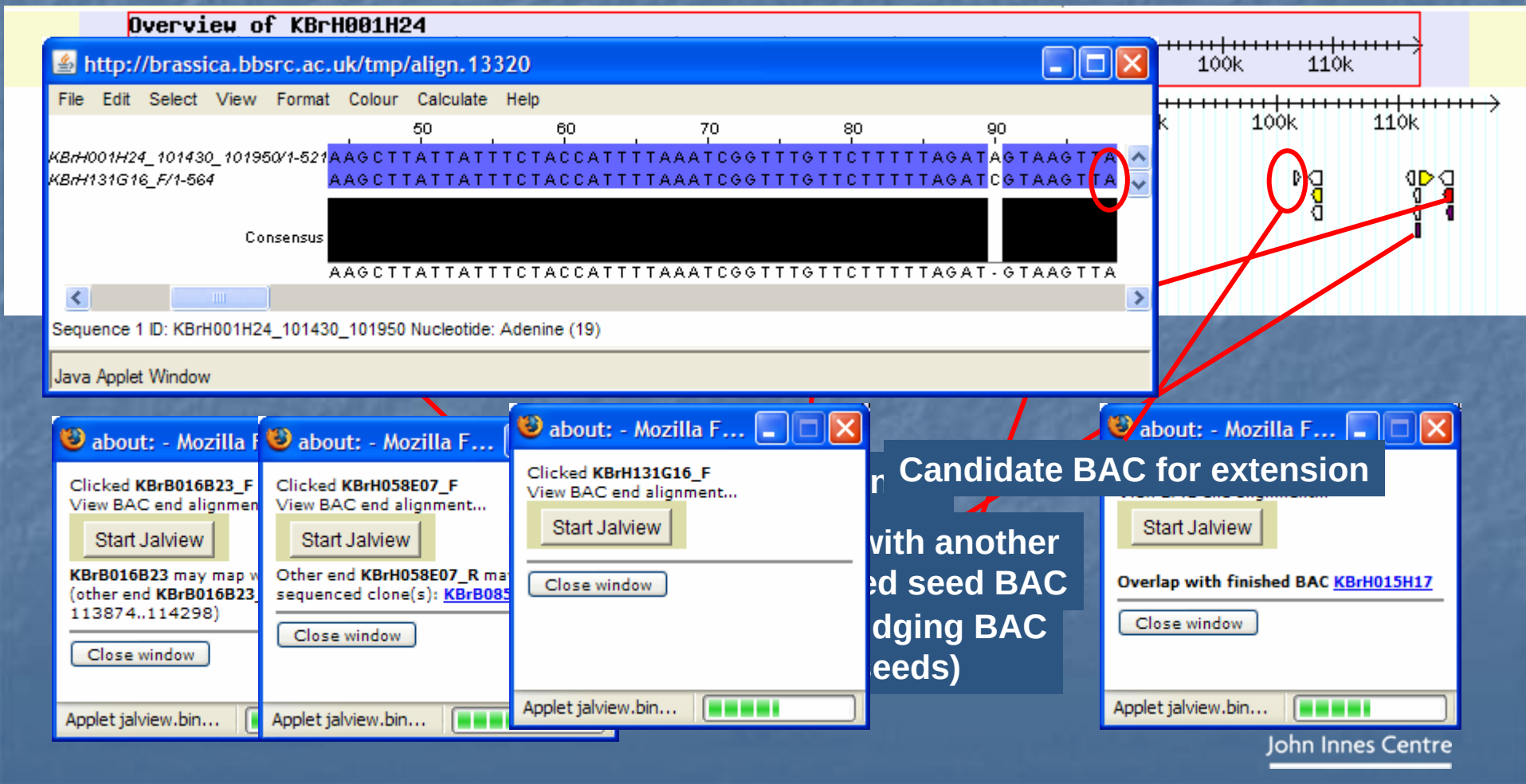
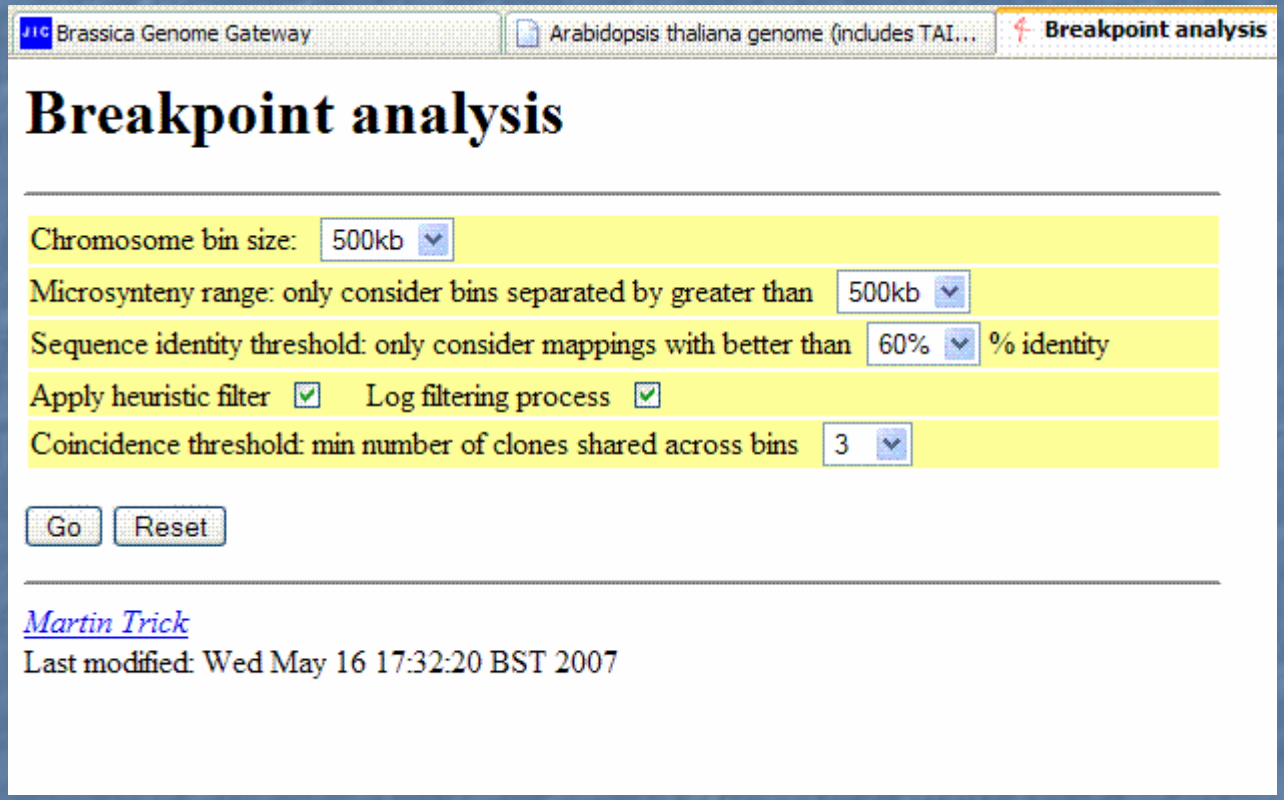
# Extending from existing seed BACs



# Selection of new seeds

- Problem: the ~500 seed BACs selected show clustering and, already, many overlaps are suspected or demonstrated
- Premise: clones inferred to span breakpoints with respect to the Arabidopsis sequence will be a useful new source of seed BACs for extension
- The Parkin *et al.* map contains about 80 such breakpoints – there are likely to be many more revealed at the microscale
- Method: programmatically interrogate database recording all BAC end-mappings, to discover significant associations between non-contiguous chromosome bins

# The breakpoint sniffer

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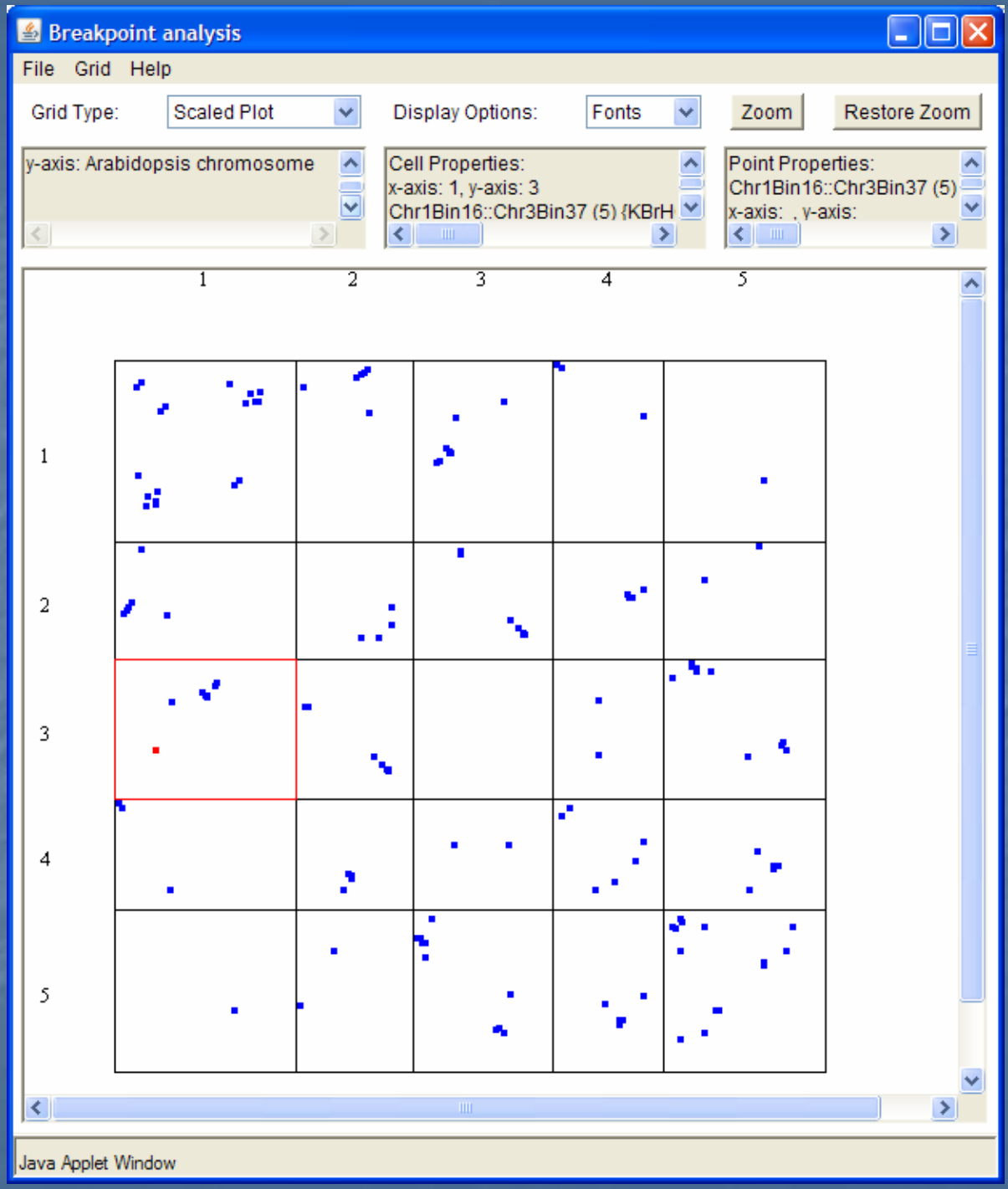

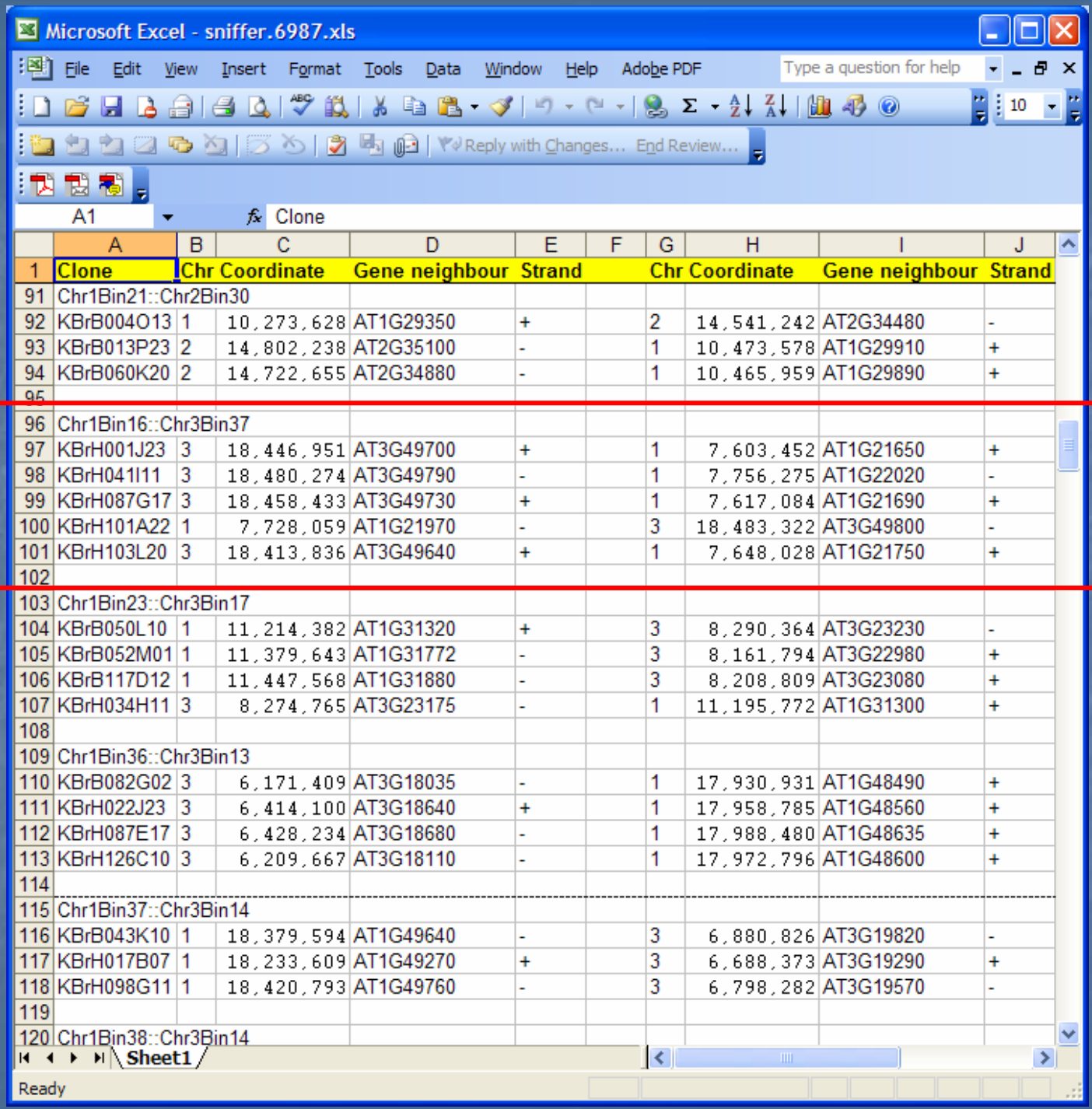


| | A | B | C | D | E | F | G | H | I | J |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Clone | Chr | Coordinate | Gene neighbour | Strand | | Chr | Coordinate | Gene neighbour | Strand |
| 91 | Chr1Bin21::Chr2Bin30 | | | | | | | | | |
| 92 | KBrB004O13 | 1 | 10,273,628 | AT1G29350 | + | | 2 | 14,541,242 | AT2G34480 | - |
| 93 | KBrB013P23 | 2 | 14,802,238 | AT2G35100 | - | | 1 | 10,473,578 | AT1G29910 | + |
| 94 | KBrB060K20 | 2 | 14,722,655 | AT2G34880 | - | | 1 | 10,465,959 | AT1G29890 | + |
| 95 | | | | | | | | | | |
| 96 | Chr1Bin16::Chr3Bin37 | | | | | | | | | |
| 97 | KBrH001J23 | 3 | 18,446,951 | AT3G49700 | + | | 1 | 7,603,452 | AT1G21650 | + |
| 98 | KBrH041I11 | 3 | 18,480,274 | AT3G49790 | - | | 1 | 7,756,275 | AT1G22020 | - |
| 99 | KBrH087G17 | 3 | 18,458,433 | AT3G49730 | + | | 1 | 7,617,084 | AT1G21690 | + |
| 100 | KBrH101A22 | 1 | 7,728,059 | AT1G21970 | - | | 3 | 18,483,322 | AT3G49800 | - |
| 101 | KBrH103L20 | 3 | 18,413,836 | AT3G49640 | + | | 1 | 7,648,028 | AT1G21750 | + |
| 102 | | | | | | | | | | |
| 103 | Chr1Bin23::Chr3Bin17 | | | | | | | | | |
| 104 | KBrB050L10 | 1 | 11,214,382 | AT1G31320 | + | | 3 | 8,290,364 | AT3G23230 | - |
| 105 | KBrB052M01 | 1 | 11,379,643 | AT1G31772 | - | | 3 | 8,161,794 | AT3G22980 | + |
| 106 | KBrB117D12 | 1 | 11,447,568 | AT1G31880 | - | | 3 | 8,208,809 | AT3G23080 | + |
| 107 | KBrH034H11 | 3 | 8,274,765 | AT3G23175 | - | | 1 | 11,195,772 | AT1G31300 | + |
| 108 | | | | | | | | | | |
| 109 | Chr1Bin36::Chr3Bin13 | | | | | | | | | |
| 110 | KBrB082G02 | 3 | 6,171,409 | AT3G18035 | - | | 1 | 17,930,931 | AT1G48490 | + |
| 111 | KBrH022J23 | 3 | 6,414,100 | AT3G18640 | + | | 1 | 17,958,785 | AT1G48560 | + |
| 112 | KBrH087E17 | 3 | 6,428,234 | AT3G18680 | - | | 1 | 17,988,480 | AT1G48635 | + |
| 113 | KBrH126C10 | 3 | 6,209,667 | AT3G18110 | - | | 1 | 17,972,796 | AT1G48600 | + |
| 114 | | | | | | | | | | |
| 115 | Chr1Bin37::Chr3Bin14 | | | | | | | | | |
| 116 | KBrB043K10 | 1 | 18,379,594 | AT1G49640 | - | | 3 | 6,880,826 | AT3G19820 | - |
| 117 | KBrH017B07 | 1 | 18,233,609 | AT1G49270 | + | | 3 | 6,688,373 | AT3G19290 | + |
| 118 | KBrH098G11 | 1 | 18,420,793 | AT1G49760 | - | | 3 | 6,798,282 | AT3G19570 | - |
| 119 | | | | | | | | | | |
| 120 | Chr1Bin38::Chr3Bin14 | | | | | | | | | |

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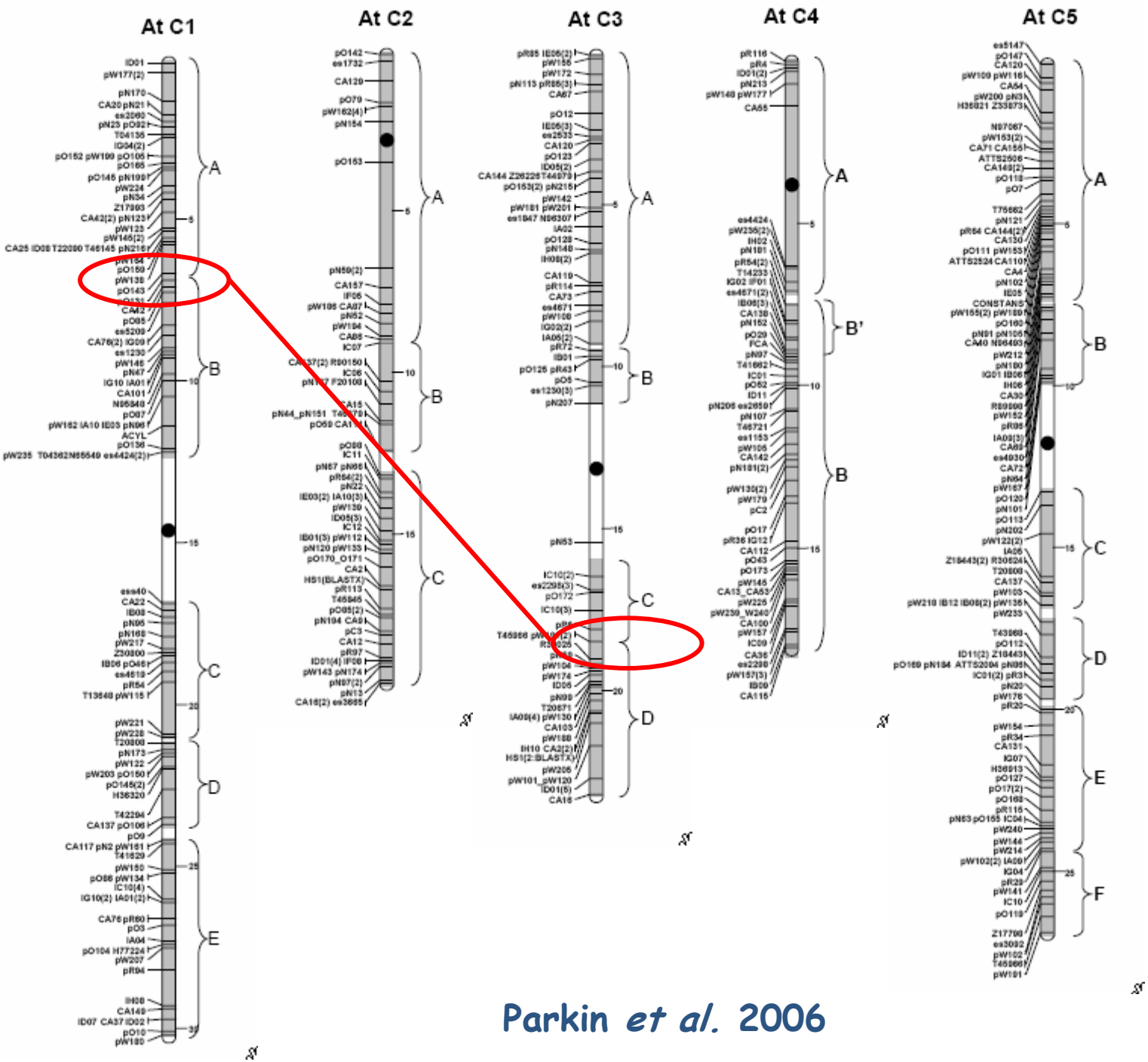


Parkin *et al.* 2006

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