

LG1/Chr9or23

0.00 HAU-DJ-S165**
 6.75 HAU-DJ-S235
 10.23 ACGGT-300
 11.82 CGAGGT-420
 13.38 ATGTTA-500
 14.87 Gh539
 16.01 CACGTC-800
 17.49 HAU-DJ-S166
 18.82 HAU-J6230
 20.39 NAU3159*
 21.57 BNL3383
 22.13 CGAGGT-200
 24.61 CAACAA-1000
 25.38 AGTGCA-800
 27.07 ACCGAT-800
 32.04 TCAGTC-300
 32.90 HAU-D5528
 34.98 HAU-DJ-S253
 36.81 AGCGAT-750
 39.24 TMB0670
 45.68 AACGTC-400 AACGTC-700
 50.70 HAU1792
 52.55 MON_CGR6576
 52.96 HAU1918
 61.90 MON_CGR5110*
 68.15 NAU2658
 70.86 MON_CGR6252
 73.60 HAU-DJ-I058**
 74.60 HAU-D526877
 76.33 HAU-D5159**
 76.90 GRP1934
 77.86 HAU-DJ-S254
 78.42 NBRI_HQ524340**
 79.40 NAU6984
 80.04 AAGTAT-220**
 80.81 HAU2146*
 81.03 JESPR248**
 82.14 HAU-D5208*
 82.21 HAU3241**
 82.23 TMB0382*
 82.40 HAU-D5412*
 83.00 GATCAT-400
 83.17 HAU-D5323
 83.28 MON_CGR5218a*
 83.83 DPL0012
 83.88 NAU6764
 85.42 HAU2553
 85.58 MON_SHIN-0154
 86.15 HAU-DJ-S265
 87.20 MON_CGR5494*
 88.12 HAU3576a*
 88.82 MON_DC40085
 89.42 TMB1758
 90.69 Gh551*
 93.27 AACGTC-850**
 94.57 GTCGCC-300**
 98.52 MON_DPL0044
 103.60 HAU0270
 106.19 MGHE56
 106.91 MUCS133
 110.90 CAGCGC-300
 114.17 CAGAAA-400
 121.62 DPL0218
 123.90 JESPR114
 126.87 HAU-J6181
 129.82 AACGTC-200
 140.30 NAU864
 153.12 HAU0190
 154.65 HAU4027
 167.04 HAU1661**
 170.69 DPL0395**
 180.26 HAU3414**
 193.30 MON_CGR6806**

LG2/Chr19

0.00 Gh381**
 20.50 Gh109*
 24.85 NAU3217
 29.55 NAU2126
 30.57 NAU5330
 32.68 NAU3497
 34.75 HAU4819
 38.86 TMB0176
 44.45 MON_DPL0064
 50.47 BNL3875
 54.64 MON_CGR5539
 55.69 DPL0071
 65.59 NAU911
 68.02 MON_DPL0001
 78.38 MON_DC30008
 84.65 HAU4781**
 94.99 NAU2274
 101.89 BNL2786
 102.28 NAU3096
 109.41 HAU-D5211
 114.40 HAU-DJ-S406
 121.61 BNL4069
 125.05 Gh447
 125.89 GTACAT-170
 127.46 CTCGTC-850
 136.95 TGATTA-450
 141.19 NAU3110
 166.19 GAAATA-1030
 169.31 NAU4907
 178.50 MON_CGR5022

LG3/Chr1or15

0.00 TMB0375
 16.15 CTACCC-250
 18.45 NBRI_HQ527566*
 19.83 CACTCT-750
 21.76 MON_CGR5875
 22.09 MUSB1267
 23.23 NAU2165
 24.96 DPL0300
 25.99 NBRI_HQ527317
 28.16 HAU2102b
 28.41 HAU-D5388
 28.63 NAU4044
 29.16 MON_DPL0437
 29.39 BNL2599
 30.17 NAU3083
 31.65 HAU2102a
 32.48 ACCAGC-300
 32.91 CIR307
 33.09 ACCCTG-600
 33.46 MON_COT059
 33.82 CIR234
 34.46 BNL2920
 35.10 HAU-DJ-S003
 36.66 HAU-J6039
 37.51 ACCAAC-350
 38.42 BNL3345
 40.04 HAU-DJ-I089
 41.61 HAU-DJ-S035
 43.84 BNL2827
 45.48 MON_CGR6529
 50.23 HAU3923
 50.96 NBRI_HQ526730
 53.64 NAU1001
 54.48 BNL830
 57.99 HAU-J6126
 58.83 NAU5107
 58.83 MON_DPL0052
 65.72 NAU1001
 66.44 TMB0409
 68.03 HAU-DJ-I038a*
 74.29 MON_CGR5826
 76.38 MON_CGR5853*
 77.96 MON_DPL0419**
 79.85 S282-800
 80.56 NAU4891
 81.36 ATTACA-1250
 82.24 GAAACA-1060*
 82.78 ACAACA-1250*
 83.25 GACACA-350
 83.92 ACTACA-1250**
 84.80 HAU-D5005
 85.76 HAU4220
 85.92 ACCAGT-900*
 86.70 TMB0791
 87.62 CTCGTA-800
 92.70 Gh216
 94.72 HAU-DJ-S233
 94.89 BNL2921
 97.44 MON_DPL0407*
 99.99 TTGTA-900*
 101.01 AAAGATG-800
 102.48 HAU-D5039
 102.74 NAU2741
 103.85 HAU-DJ-I038b**
 104.53 HAU2139
 106.55 HAU-DJ-I027
 107.32 NAU5163
 109.98 MON_CGR6129
 110.74 MON_CGR5056
 113.40 HAU-DJ-S081
 114.67 CCATTC-1400
 117.00 DPL0752
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 135.57 MON_CGR5282
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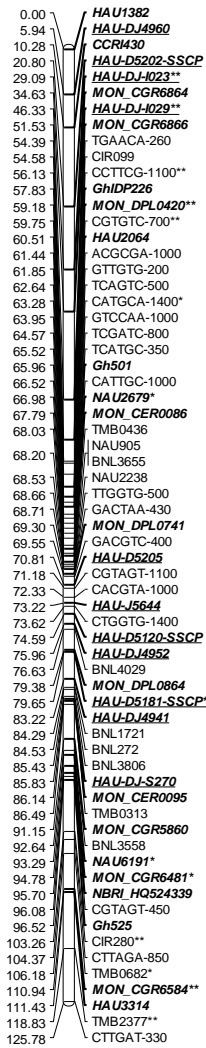
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 17.05 HAU3611
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 35.33 TMB0889
 36.88 GTGTTG-800
 39.31 BNL3948
 41.21 HAU-DJ-S174
 41.99 TTCAGC-800
 42.61 HAU-D5428
 43.59 HAU-DJ-I071
 46.23 TACGCC-600
 46.61 BNL946
 47.67 DPL0135
 48.65 TMB1939
 50.21 HAU-DJ-S077
 54.08 BNL3071
 54.95 GACTTG-250
 55.70 HAU0230
 56.98 NAU3665
 58.30 NAU2869
 60.52 HAU-DJ-I086
 62.52 HAU-J6117
 73.30 TGATTT-520
 74.98 DPL0442
 77.27 TMB0644
 79.50 TATAGC-760
 81.69 HAU-DJ-I102
 83.66 NAU2991
 84.78 Gr-Gh012
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 93.40 DPL0028
 95.30 JESPR190
 96.32 MON_COT119
 107.67 HAU1224
 131.51 MON_CGR6110

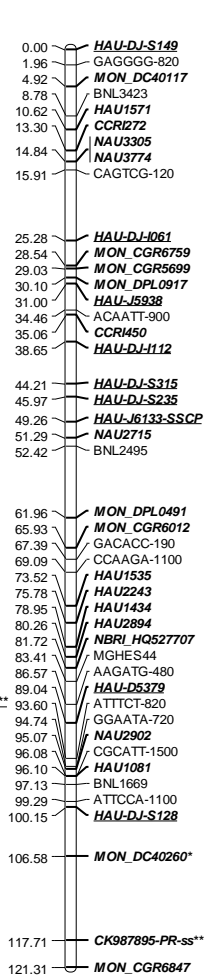
LG5/Chr7

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 7.11 TMB1838**
 11.97 HAU4589
 15.75 MON_CGR5851a
 16.51 GACGGG-180**
 19.57 NAU3639**
 22.52 TTGCA-300**
 31.52 MON_CGR6528**
 33.97 DPL0448**
 34.60 HAU-DJ-S004**
 38.23 HAU-DJ-S078**
 45.22 GTTGTG-780**
 46.20 TCCTGG-900
 48.47 ACCGAC-400**
 50.56 TCATGG-280
 51.78 MGHE575**
 56.87 ACATGC-1100
 60.95 NAU1190a**
 68.11 HAU-D5478**
 70.63 HAU-J5712**
 82.12 NBRI_HQ527867
 83.74 MON_CGR5372
 84.01 NAU1190a**
 85.43 HAU2138**
 85.66 MON_CGR6586
 100.95 MON_CGR5001
 105.52 HAU3319
 106.55 MGHE558
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 112.96 HAU4228
 121.54 CAATGT-850
 128.95 HAU-DJ-S281

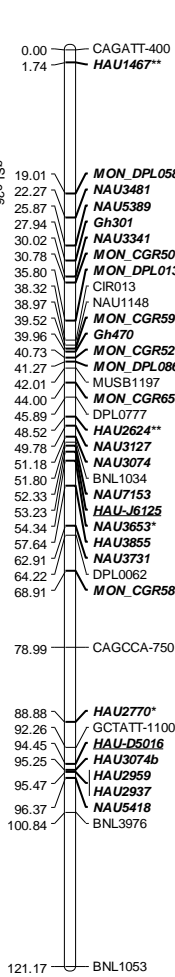
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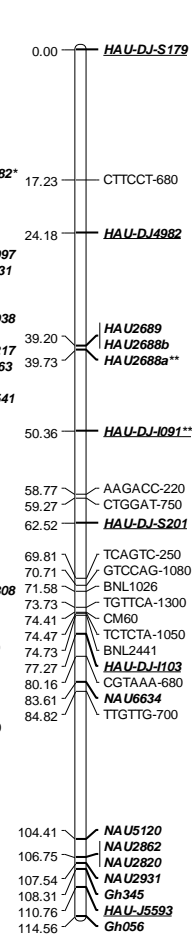
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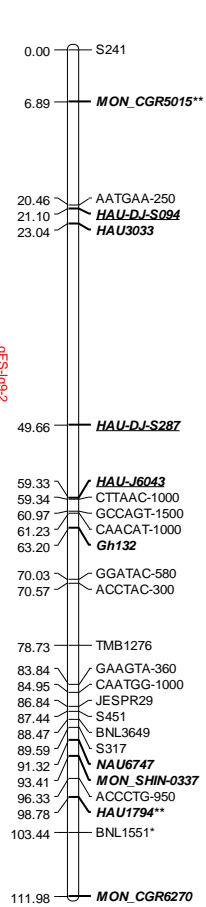
LG8/Chr21



LG9/Chr7or16



LG10/Chr21



qF1-c21

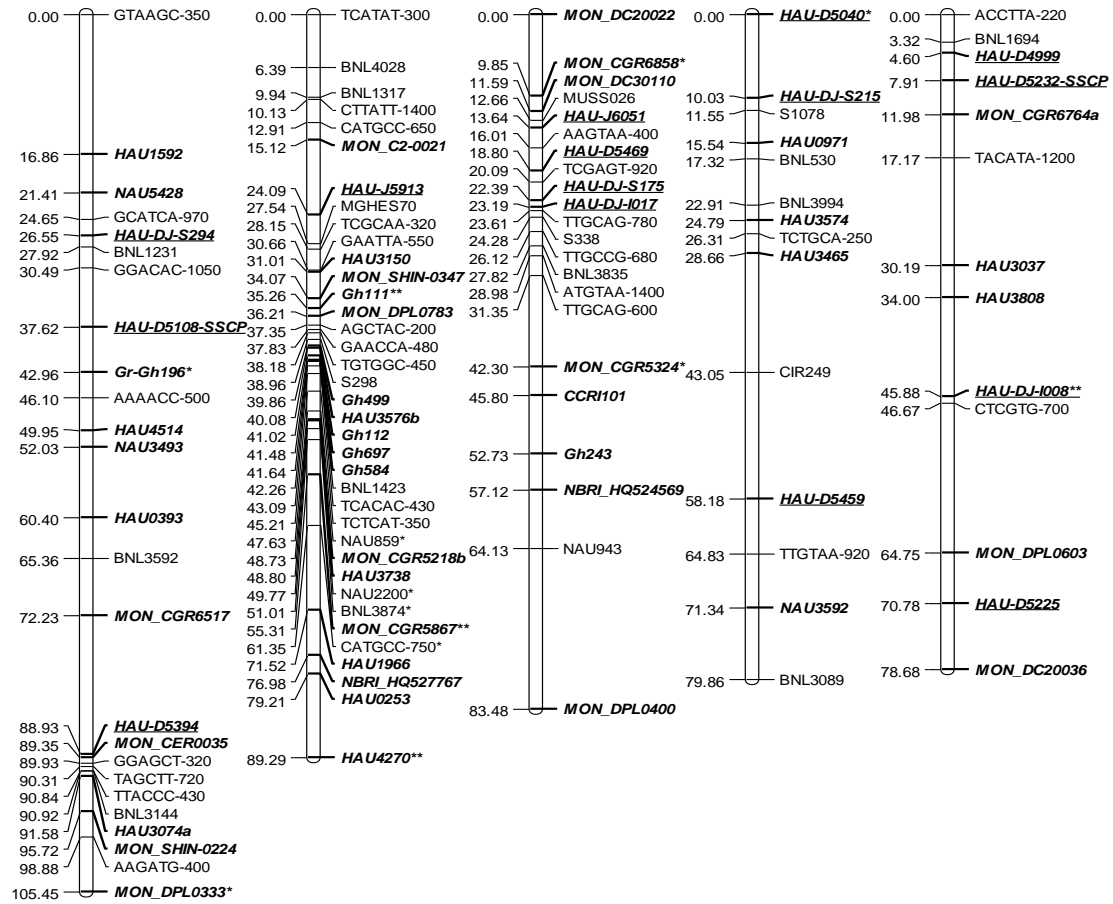
LG11/Chr11

LG12/Chr9

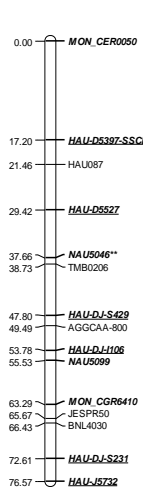
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LG14/Chr4

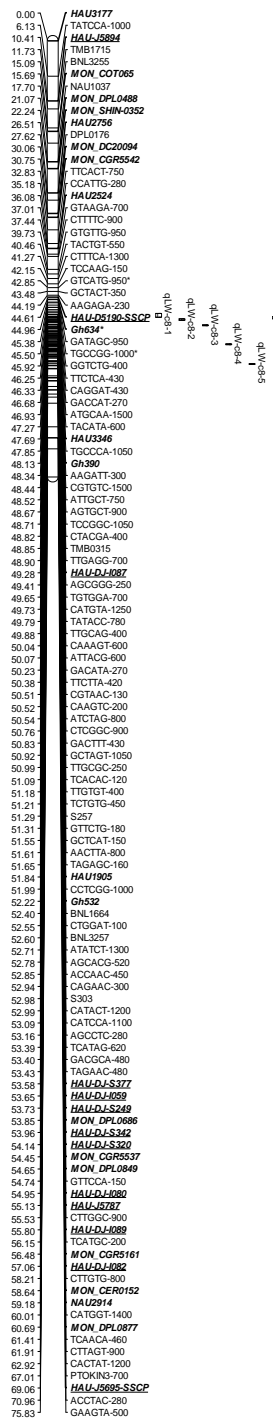
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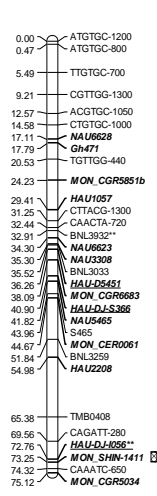
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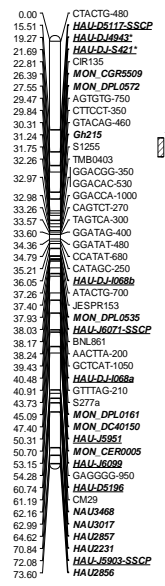
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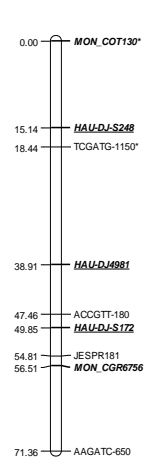
LG18/Chr14



LG19/Chr13



LG20/Chr5



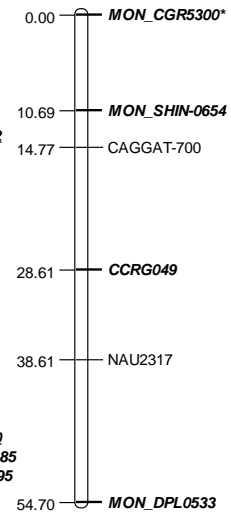
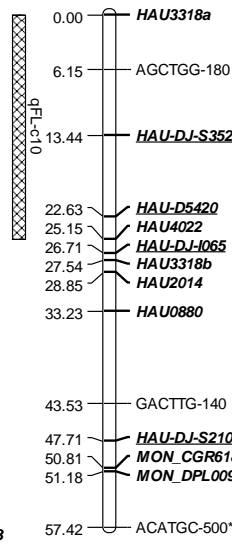
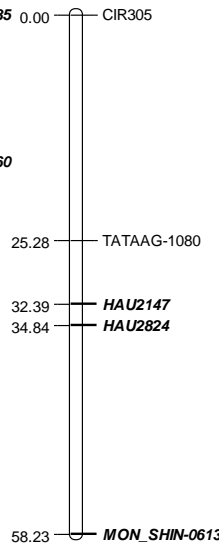
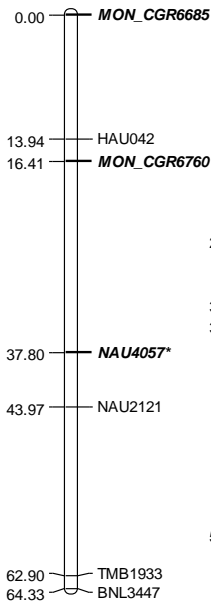
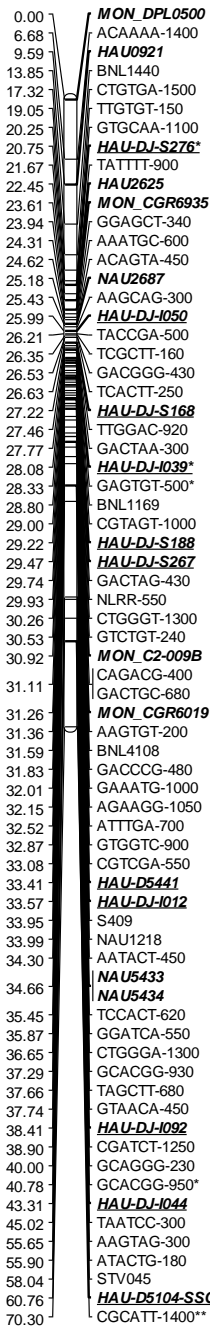
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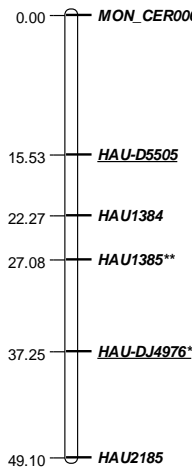
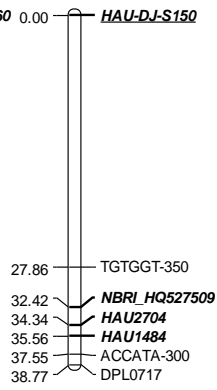
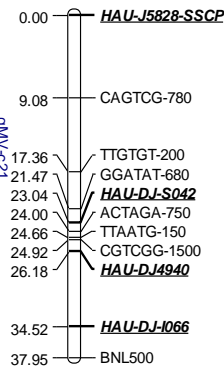
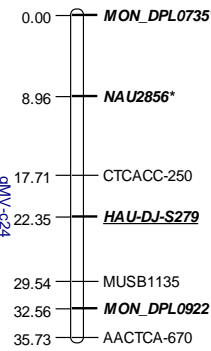
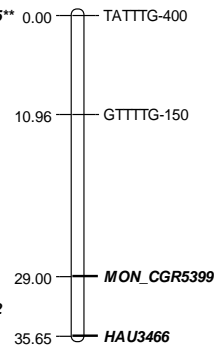
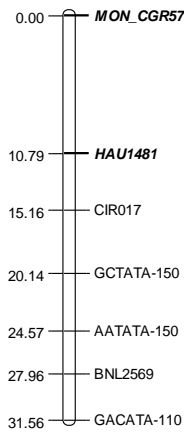
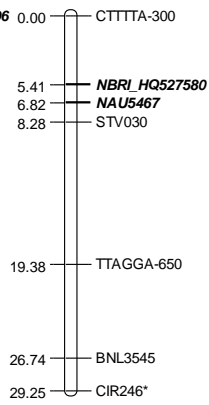
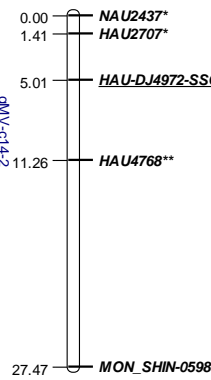
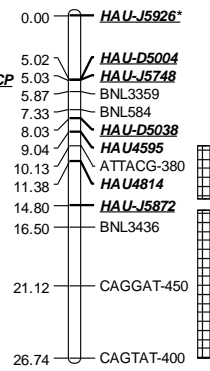
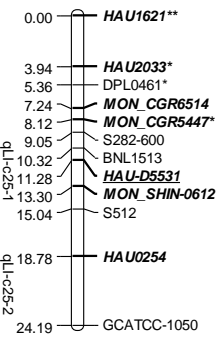
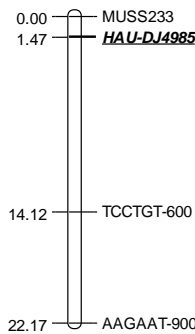
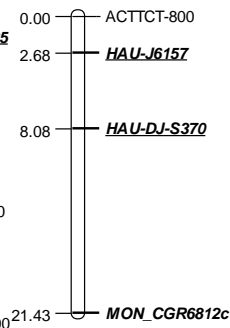
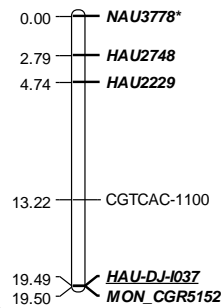
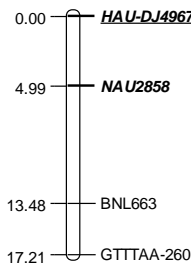
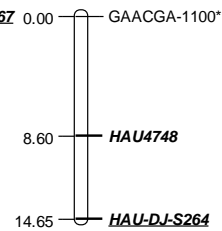
LG22/Chr5

LG23/Chr10

LG24/Chr17

LG25/Chr10



LG26/Chr5**LG27/Chr21****LG28/Chr24****LG29/Chr18****LG30/Chr10****LG31****LG32/Chr14****LG33/Chr15****LG34/Chr25****LG35/Chr24****LG36****LG37/Chr13****LG38/Chr12****LG39/Chr2****LG40/Chr13**

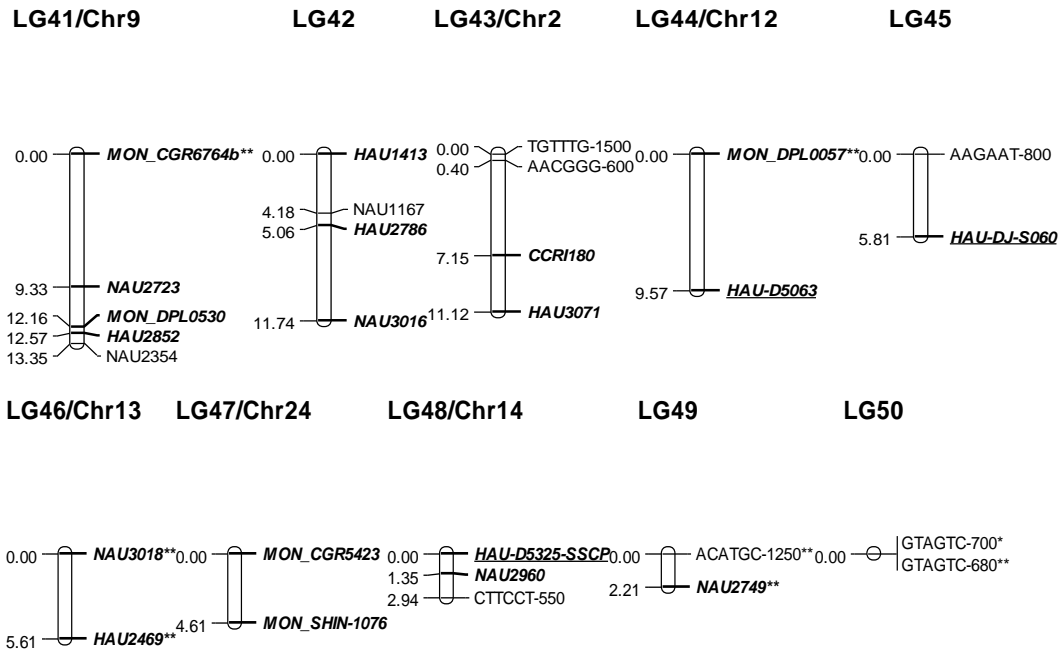


Figure S1. A genetic map of the cotton genome developed in 137 plants of the F₂ population derived from *G. hirsutum* accession DH962 and *G. hirsutum* cultivar Jimian5. A total of 1013 loci were mapped on 50 linkage groups. The locations of 21 QTLs for yield components, 12 QTLs for fiber quality are shown. Markers showing segregation distortion are indicated by asterisks (*P < 0.05; ** P < 0.01). The marker development from RAD-seq are underlined, italic, and in bold, other new added markers are italic, in bold.