# Supplementary information: Genomic prediction of cotton fibre quality and yield traits using Bayesian regression methods.

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## Supplementary Tables

Table S1. Summary of the biparental families collected since 2014.

| Family ID | Experiment ID | Year | Sample size |
|---|---|---|---|
| CSX69004 | 1402 | 2014 | 17 |
| CSX69017 | 1402 | 2014 | 22 |
| CSX69901 | 1402 | 2014 | 18 |
| CSX69009 | 1402 | 2014 | 12 |
| CSX69018 | 1403 | 2014 | 20 |
| CSX69014 | 1403 | 2014 | 11 |
| CSX69015 | 1403 | 2014 | 14 |
| CSX69008 | 1404 | 2014 | 13 |
| CSX10013 | 1404 | 2014 | 13 |
| CSX10015 | 1404 | 2014 | 17 |
| CSX10021 | 1404 | 2014 | 14 |
| CSX69022 | 1502 | 2015 | 19 |
| CSX10024 | 1502 | 2015 | 20 |
| CSX11015 | 1502 | 2015 | 21 |
| CSX10104 | 1513 | 2015 | 38 |
| CSX11102 | 1513 | 2015 | 41 |
| CSX69110 | 1519 | 2015 | 36 |
| CSX69111 | 1519 | 2015 | 18 |
| CSX69119 | 1519 | 2015 | 2 |
| CSX69120 | 1519 | 2015 | 4 |
| CSX10114 | 1519 | 2015 | 9 |
| CSX10221 | 1522 | 2015 | 18 |
| CSX11221 | 1522 | 2015 | 18 |
| CSX11813 | 1543 | 2015 | 15 |
| CSX11847 | 1543 | 2015 | 10 |
| CSX12809 | 1543 | 2015 | 21 |
| CSX12815 | 1543 | 2015 | 16 |
| CSX12816 | 1543 | 2015 | 8 |
| CSX11849 | 1545 | 2015 | 9 |
| CSX11850 | 1545 | 2015 | 11 |
| CSX10007 | 1602 | 2016 | 19 |
| CSX12017 | 1602 | 2016 | 18 |
| CSX12026 | 1602 | 2016 | 18 |
| CSX10014 | 1603 | 2016 | 19 |
| CSX10028 | 1603 | 2016 | 16 |
| CSX12028 | 1603 | 2016 | 17 |

| | | | |
|---|---|---|---|
| CSX10017 | 1604 | 2016 | 20 |
| CSX10018 | 1604 | 2016 | 16 |
| CSX12019 | 1604 | 2016 | 17 |
| CSX11207 | 1605 | 2016 | 10 |
| CSX11213 | 1605 | 2016 | 11 |
| CSX11219 | 1605 | 2016 | 10 |
| CSX11213 | 1605 | 2016 | 10 |
| CSX12011 | 1605 | 2016 | 15 |
| CSX10008 | 1702 | 2017 | 20 |
| CSX12008 | 1702 | 2017 | 21 |
| CSX12013 | 1702 | 2017 | 20 |
| CSX12018 | 1703 | 2017 | 18 |
| CSX12027 | 1703 | 2017 | 18 |
| CSX12029 | 1703 | 2017 | 17 |
| CSX69019 | 1704 | 2017 | 20 |
| CSX10011 | 1704 | 2017 | 21 |
| CSX12005 | 1704 | 2017 | 16 |
| CSX12010 | 1705 | 2017 | 14 |
| CSX12022 | 1705 | 2017 | 22 |
| CSX12022 | 1705 | 2017 | 20 |
| CSX12241 | 1706 | 2017 | 16 |
| CSX12243 | 1706 | 2017 | 10 |
| CSX12244 | 1706 | 2017 | 21 |
| CSX14504 | 1763 | 2017 | 29 |
| CSX14505 | 1763 | 2017 | 31 |

Table S2. The prediction accuracies (and standard errors in brackets) of the scenario 1: five-fold Cross validation. Methods under evaluation are Bayesian G-BLUP, Bayesian LASSO, Bayes C, Bayesian additive regression tree (BART), and these four models further adding pedigree or structure information as random effects. Traits being analysed included fibre length (LEN), uniformity (UNI), short fibre index (SFI), fibre strength (STR), fibre elongation (EL), fibre micronaire (MIC), lint yield (LY) and lint percentage (LP).

| | **LEN** | **UNI** | **SFI** | **STR** | **EL** | **MIC** | **LY** | **LP** |
|---|---|---|---|---|---|---|---|---|
| BG-BLUP | 0.75 (0.05) | 0.59 (0.07) | 0.47 (0.06) | 0.70 (0.10) | 0.61 (0.06) | 0.56 (0.03) | 0.64 (0.05) | 0.66 (0.11) |
| BG-BLUP + pedigree | 0.77 (0.03) | 0.59 (0.07) | 0.47 (0.05) | 0.70 (0.10) | 0.62 (0.07) | 0.57 (0.03) | 0.65 (0.05) | 0.68 (0.11) |
| BLASSO | 0.75 (0.05) | 0.59 (0.07) | 0.47 (0.06) | 0.70 (0.10) | 0.60 (0.06) | 0.56 (0.03) | 0.64 (0.05) | 0.66 (0.11) |
| BLASSO + pedigree | 0.77 (0.04) | 0.59 (0.07) | 0.47 (0.05) | 0.70 (0.10) | 0.62 (0.07) | 0.58 (0.02) | 0.65 (0.05) | 0.68 (0.11) |
| Bayes C | 0.75 (0.05) | 0.59 (0.07) | 0.47 (0.06) | 0.70 (010) | 0.60 (0.06) | 0.56 (0.03) | 0.64 (0.05) | 0.66 (0.11) |
| Bayes C + pedigree | 0.77 (0.03) | 0.60 (0.07) | 0.48 (0.04) | 0.70 (0.10) | 0.62 (0.08) | 0.58 (0.02) | 0.64 (0.05) | 0.68 (0.11) |
| BART | 0.72 (0.05) | 0.47 (0.10) | 0.43 (0.07) | 0.65 (0.13) | 0.60 (0.10) | 0.54 (0.02) | 0.59 (0.06) | 0.66 (0.13) |
| BART + pedigree | 0.73 (0.06) | 0.47 (0.09) | 0.44 (0.07) | 0.67 (0.12) | 0.61 (0.09) | 0.50 (0.02) | 0.62 (0.05) | 0.67 (0.12) |

Table S3. The prediction accuracies (and standard errors in brackets) of the scenario 1: leave-one-out-fold Cross validation. Methods under evaluation are Bayesian G-BLUP, Bayesian LASSO, Bayes C, BART, and these four models further adding pedigree or structure information as random effects. Traits being analysed included fibre length (LEN), uniformity (UNI), short fibre index (SFI), fibre strength (STR), fibre elongation (EL), fibre micronaire (MIC), lint yield (LY) and lint percentage (LP).

| | **LEN** | **UNI** | **SFI** | **STR** | **EL** | **MIC** | **LY** | **LP** |
|---|---|---|---|---|---|---|---|---|
| BG-BLUP | 0.79 (0.07) | 0.60 (0.16) | 0.53 (0.18) | 0.71 (0.11) | 0.55 (0.14) | 0.65 (0.11) | 0.58 (0.14) | 0.63 (0.15) |
| BG-BLUP + pedigree | 0.80 (0.07) | 0.60 (0.17) | 0.51 (0.18) | 0.71 (0.11) | 0.58 (0.14) | 0.67 (0.09) | 0.60 (0.16) | 0.64 (0.16) |
| BLASSO | 0.79 (0.07) | 0.60 (0.16) | 0.53 (0.18) | 0.71 (0.11) | 0.55 (0.14) | 0.66 (0.10) | 0.58 (0.15) | 0.63 (0.14) |
| BLASSO + pedigree | 0.80 (0.07) | 0.60 (0.17) | 0.51 (0.18) | 0.72 (0.11) | 0.58 (0.14) | 0.67 (0.09) | 0.60 (0.16) | 0.64 (0.16) |
| Bayes C | 0.80 (0.07) | 0.60 (0.17) | 0.53 (0.17) | 0.71 (0.12) | 0.55 (0.14) | 0.66 (0.10) | 0.58 (0.14) | 0.63 (0.16) |
| Bayes C + pedigree | 0.81 (0.07) | 0.60 (0.16) | 0.52 (0.18) | 0.71 (0.11) | 0.57 (0.15) | 0.67 (0.09) | 0.60 (0.16) | 0.64 (0.18) |
| BART | 0.78 (0.07) | 0.49 (0.16) | 0.53 (0.17) | 0.67 (0.14) | 0.58 (0.14) | 0.65 (0.12) | 0.60 (0.14) | 0.59 (0.13) |
| BART + pedigree | 0.79 (0.09) | 0.50 | 0.54 | 0.70 (0.12) | 0.60 (0.13) | 0.65 (0.10) | 0.61 | 0.62 |

Table S4. The prediction accuracies of the scenario 2: the lines phenotyped at seasons 1993-2016 were used as the training population, and the data collected in the 2017/18 season were used as the test population. Methods under evaluation are Bayesian G-BLUP, Bayesian LASSO and Bayes C, and the three models further adding pedigree or structure information as random effects. Traits being analysed included fibre length (LEN), uniformity (UNI), short fibre index (SFI), fibre strength (STR), fibre elongation (EL), fibre micronaire (MIC), lint yield (LY) and lint percentage (LP).

| | **LEN** | **UNI** | **SFI** | **STR** | **EL** | **MIC** | **LY** | **LP** |
|---|---|---|---|---|---|---|---|---|
| BG-BLUP | 0.41 | 0.14 | 0.18 | 0.35 | 0.43 | 0.23 | 0.17 | 0.30 |
| BG-BLUP + pedigree | 0.42 | 0.08 | 0.14 | 0.38 | 0.41 | 0.19 | 0.18 | 0.36 |
| BLASSO | 0.39 | 0.11 | 0.19 | 0.36 | 0.43 | 0.25 | 0.14 | 0.31 |
| BLASSO + pedigree | 0.42 | 0.10 | 0.20 | 0.37 | 0.43 | 0.23 | 0.15 | 0.32 |
| Bayes C | 0.42 | 0.09 | 0.20 | 0.36 | 0.43 | 0.22 | 0.17 | 0.31 |
| Bayes C + pedigree | 0.42 | 0.11 | 0.18 | 0.38 | 0.41 | 0.19 | 0.14 | 0.35 |
| BART | 0.42 | 0.10 | 0.16 | 0.35 | 0.48 | 0.28 | 0.25 | 0.32 |
| BART+pedigree | 0.42 | 0.11 | 0.15 | 0.38 | 0.46 | 0.23 | 0.25 | 0.33 |

Table S5. The prediction accuracies of the scenario 3. This approach used each biparental family from season 2017/18 as the separate test population. The training population was either all the lines phenotyped before 2017, or the families phenotyped before 2017 which are closely relevant to the target population (i.e. the related coefficient no less than 0.125 or 0.25). Numbers highlighted in bold represent the highest prediction accuracies among different approaches.

| Trait/test population | All accessions phenotyped before 2017 as training data | | Relationship coefficient≥0.125 | | | Relationship coefficient≥0.25 | | |
|---|---|---|---|---|---|---|---|---|
| | BLASSO | BLASSO + pedigree | Training sample size | BLASSO | BLASSO + pedigree | Training sample size | BLASSO | BLASSO + pedigree |
| LEN | | | | | | | | |
| CSX10008 | 0.55 | **0.59** | 686 | 0.58 | 0.57 | 356 | 0.40 | 0.38 |
| CSX12008 | 0.14 | 0.26 | 667 | 0.31 | **0.37** | 256 | 0.25 | 0.28 |
| CSX12013 | 0.00 | **0.17** | 667 | 0.14 | **0.17** | 256 | 0.00 | 0.00 |
| CSX12018 | 0.00 | 0.00 | 707 | 0.00 | 0.00 | 483 | 0.00 | 0.00 |
| CSX12027 | 0.00 | 0.00 | 712 | 0.00 | 0.00 | 481 | 0.00 | **0.30** |
| CSX12029 | **0.59** | 0.51 | 728 | 0.41 | 0.39 | 450 | 0.32 | 0.41 |
| CSX69019 | 0.13 | 0.26 | 703 | 0.06 | 0.17 | 264 | **0.30** | 0.14 |
| CSX10011 | 0.49 | 0.47 | 712 | 0.26 | 0.24 | 331 | 0.12 | 0.09 |
| CSX12010 | 0.15 | **0.26** | 681 | 0.16 | 0.17 | 327 | 0.11 | 0.19 |
| Mean | 0.23 | **0.28** | | 0.21 | 0.23 | | 0.17 | 0.20 |
| SD | 0.25 | 0.21 | | 0.20 | 0.19 | | 0.15 | 0.15 |
| UNI | | | | | | | | |
| CSX10008 | 0.03 | **0.05** | 686 | 0.04 | 0.03 | 356 | 0 | 0.01 |
| CSX12008 | 0.50 | 0.56 | 667 | 0.58 | **0.61** | 256 | 0.66 | 0.65 |
| CSX12013 | **0.22** | 0.11 | 667 | 0 | 0 | 256 | 0 | 0 |
| CSX12018 | 0.33 | **0.44** | 707 | 0.39 | 0.29 | 483 | 0.34 | 0.27 |
| CSX12027 | 0 | 0 | 712 | 0.07 | **0.17** | 481 | 0.05 | 0.14 |
| CSX12029 | **0.25** | 0.19 | 728 | 0.23 | 0.23 | 450 | 0.16 | 0.17 |
| CSX69019 | 0.30 | 0.25 | 703 | 0.30 | 0.32 | 264 | 0.31 | **0.35** |
| CSX10011 | 0.18 | 0.15 | 712 | 0.22 | 0.20 | 331 | **0.27** | 0.22 |
| CSX12010 | **0.46** | 0.55 | 681 | 0.48 | 0.50 | 327 | **0.63** | 0.61 |
| **Mean** | **0.25** | **0.26** | | **0.27** | **0.26** | | **0.27** | **0.27** |
| **SD** | **0.17** | **0.21** | | **0.20** | **0.20** | | **0.25** | **0.23** |
| SFI | | | | | | | | |
| CSX10008 | 0.20 | 0.33 | 686 | 0.34 | **0.36** | 356 | 0.31 | 0.30 |
| CSX12008 | 0.40 | 0.41 | 667 | 0.43 | 0.45 | 256 | 0.39 | **0.46** |
| CSX12013 | 0 | **0.08** | 667 | 0 | 0 | 256 | 0 | 0 |
| CSX12018 | 0 | 0 | 707 | 0 | 0 | 483 | 0 | 0 |
| CSX12027 | 0 | 0 | 712 | 0 | 0 | 481 | 0 | 0 |
| CSX12029 | 0.19 | 0.23 | 728 | **0.24** | 0.23 | 450 | 0.22 | 0.21 |
| CSX69019 | 0.02 | 0.13 | 703 | 0.13 | 0.16 | 264 | **0.24** | **0.24** |
| CSX10011 | 0.10 | 0.04 | 712 | 0 | 0 | 331 | **0.17** | 0.16 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| CSX12010 | 0.32 | 0.41 | 681 | 0.40 | **0.42** | 327 | 0.33 | 0.37 |
| **Mean** | **0.14** | **0.18** | | **0.17** | **0.18** | | **0.18** | **0.19** |
| **SD** | **0.15** | **0.17** | | **0.18** | **0.19** | | **0.15** | **0.17** |
| **STR** | | | | | | | | |
| CSX10008 | 0.49 | 0.50 | 686 | 0.31 | 0.32 | 356 | **0.54** | 0.50 |
| CSX12008 | 0.38 | 0.38 | 667 | 0.42 | **0.44** | 256 | 0.43 | 0.43 |
| CSX12013 | 0.60 | **0.62** | 667 | 0.58 | 0.57 | 256 | 0.39 | 0.39 |
| CSX12018 | 0.00 | 0.00 | 707 | 0.06 | 0.16 | 483 | **0.29** | 0.25 |
| CSX12027 | 0.41 | 0.42 | 712 | 0.36 | 0.34 | 481 | **0.45** | 0.42 |
| CSX12029 | 0.31 | **0.38** | 728 | 0.26 | 0.27 | 450 | 0.28 | 0.29 |
| CSX69019 | 0.40 | 0.46 | 703 | 0.33 | 0.27 | 264 | 0.58 | **0.59** |
| CSX10011 | 0.59 | 0.63 | 712 | 0.66 | 0.70 | 331 | 0.71 | **0.73** |
| CSX12010 | 0.44 | 0.47 | 681 | 0.56 | 0.59 | 327 | 0.58 | **0.60** |
| **Mean** | **0.40** | **0.43** | | **0.39** | **0.41** | | **0.47** | **0.47** |
| **SD** | **0.18** | **0.18** | | **0.19** | **0.18** | | **0.14** | **0.15** |
| **EL** | | | | | | | | |
| CSX10008 | **0.47** | 0.43 | 686 | 0.33 | 0.33 | 356 | 0.29 | 0.28 |
| CSX12008 | **0.43** | 0.29 | 667 | 0.10 | 0.13 | 256 | 0.17 | 0.19 |
| CSX12013 | 0.33 | **0.34** | 667 | 0 | 0 | 256 | 0 | 0 |
| CSX12018 | 0.06 | **0.12** | 707 | 0 | 0 | 483 | 0 | 0 |
| CSX12027 | 0 | 0.02 | 712 | 0 | 0 | 481 | **0.08** | 0.06 |
| CSX12029 | 0.48 | 0.36 | 728 | **0.57** | 0.54 | 450 | 0.44 | 0.38 |
| CSX69019 | 0.46 | 0.48 | 703 | 0.53 | **0.54** | 264 | 0.28 | 0.35 |
| CSX10011 | 0.27 | **0.34** | 712 | 0.11 | 0.13 | 331 | 0.07 | 0.13 |
| CSX12010 | 0.23 | 0.25 | 681 | 0.26 | 0.26 | 327 | **0.38** | 0.37 |
| **Mean** | **0.30** | **0.29** | | **0.21** | **0.21** | | **0.19** | **0.20** |
| **SD** | **0.18** | **0.15** | | **0.22** | **0.22** | | **0.16** | **0.16** |
| **MIC** | | | | | | | | |
| CSX10008 | 0.12 | 0.20 | 686 | 0.34 | 0.35 | 356 | **0.37** | 0.35 |
| CSX12008 | 0.44 | **0.46** | 667 | 0.44 | **0.46** | 256 | 0.23 | 0.25 |
| CSX12013 | 0 | **0.01** | 667 | 0 | 0 | 256 | 0 | 0 |
| CSX12018 | 0.28 | 0.42 | 707 | 0.44 | 0.49 | 483 | 0.49 | **0.50** |
| CSX12027 | 0.41 | 0.43 | 712 | 0.56 | 0.57 | 481 | 0.62 | **0.63** |
| CSX12029 | 0 | 0 | 728 | 0 | 0 | 450 | 0 | 0 |
| CSX69019 | 0.05 | 0.05 | 703 | 0 | 0 | 264 | 0.1 | **0.08** |
| CSX10011 | 0.40 | 0.42 | 712 | 0.41 | **0.45** | 331 | 0.26 | 0.28 |
| CSX12010 | 0.31 | 0.30 | 681 | 0.47 | 0.49 | 327 | 0.64 | **0.62** |
| **Mean** | **0.22** | **0.25** | | **0.30** | **0.31** | | **0.30** | **0.30** |
| **SD** | **0.17** | **0.18** | | **0.21** | **0.23** | | **0.23** | **0.23** |
| **LY** | | | | | | | | |
| CSX10008 | 0.33 | 0.27 | 686 | **0.32** | 0.30 | 356 | 0.21 | 0.21 |
| CSX12008 | 0.02 | 0.17 | 667 | 0.12 | 0.18 | 256 | 0.25 | **0.29** |
| CSX12013 | 0.41 | 0.40 | 667 | 0.42 | 0.40 | 256 | 0.48 | **0.50** |
| CSX12018 | 0 | 0.11 | 707 | 0.34 | **0.35** | 483 | 0.32 | 0.33 |
| CSX12027 | **0.22** | 0.19 | 712 | 0.07 | 0.06 | 481 | 0.17 | 0.13 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| CSX12029 | **0.18** | 0.17 | 728 | **0.18** | 0.12 | 450 | 0.16 | 0.11 |
| CSX69019 | 0.02 | 0 | 703 | 0 | 0 | 264 | 0.02 | **0.05** |
| CSX10011 | 0 | 0 | 712 | 0.02 | 0.04 | 331 | **0.40** | 0.38 |
| CSX12010 | 0.32 | 0.37 | 681 | **0.50** | 0.42 | 327 | 0.33 | 0.33 |
| **Mean** | **0.13** | **0.19** | | **0.22** | **0.21** | | **0.26** | **0.26** |
| **SD** | **0.16** | **0.14** | | **0.18** | **0.16** | | **0.14** | **0.15** |
| **LP** | | | | | | | | |
| CSX10008 | 0.58 | 0.61 | 686 | 0.62 | **0.67** | 356 | 0.49 | 0.52 |
| CSX12008 | 0.27 | 0.37 | 667 | 0.33 | **0.40** | 256 | 0.22 | 0.26 |
| CSX12013 | 0.61 | 0.60 | 667 | **0.62** | 0.59 | 256 | 0.42 | 0.42 |
| CSX12018 | 0.27 | 0.27 | 707 | 0.28 | 0.26 | 483 | 0.42 | **0.45** |
| CSX12027 | 0.32 | 0.51 | 712 | 0.52 | **0.58** | 481 | 0.51 | 0.43 |
| CSX12029 | 0.17 | 0.22 | 728 | 0.28 | 0.26 | 450 | 0.36 | **0.36** |
| CSX69019 | 0.73 | 0.70 | 703 | **0.76** | 0.70 | 264 | 0.68 | 0.58 |
| CSX10011 | 0.44 | 0.49 | 712 | **0.53** | 0.48 | 331 | 0.17 | 0.16 |
| CSX12010 | 0 | 0.06 | 681 | **0.25** | 0.15 | 327 | 0 | 0 |
| **Mean** | **0.38** | **0.43** | | **0.47** | **0.45** | | **0.36** | **0.35** |
| **SD** | **0.23** | **0.21** | | **0.19** | **0.20** | | **0.20** | **0.18** |

Table S6. The standard deviation (SD) of fibre length (LEN) and strength (STR) (after standardization of the phenotypes by checks in each trial) in each biparental family collected in the season 2017/18. The SDs of LEN is systematically lower than the ones of STR, which may partially explain why the prediction accuracies in LEN is considerably lower than the STR in Scenario 3.

| Crosses | Number of lines | LEN | STR |
|---|---|---|---|
| CSX10008 | 20 | 0.028 | 0.035 |
| CSX12008 | 21 | 0.024 | 0.028 |
| CSX12013 | 20 | 0.023 | 0.038 |
| CSX12018 | 18 | 0.028 | 0.026 |
| CSX12027 | 18 | 0.015 | 0.028 |
| CSX12029 | 17 | 0.032 | 0.032 |
| CSX69019 | 20 | 0.024 | 0.040 |
| CSX10011 | 21 | 0.020 | 0.046 |
| CSX12010 | 14 | 0.034 | 0.038 |

# Supplementary Figures

Figure S1. The pedigree chart of 1385 lines being used in genomic prediction analysis. In the figure, Circles in grey, dark blue, light blue, light Green, and dark green represent lines and/or families collected from the pre-2014 trials, year 2014, 2015, 2016 and 2017, respectively.

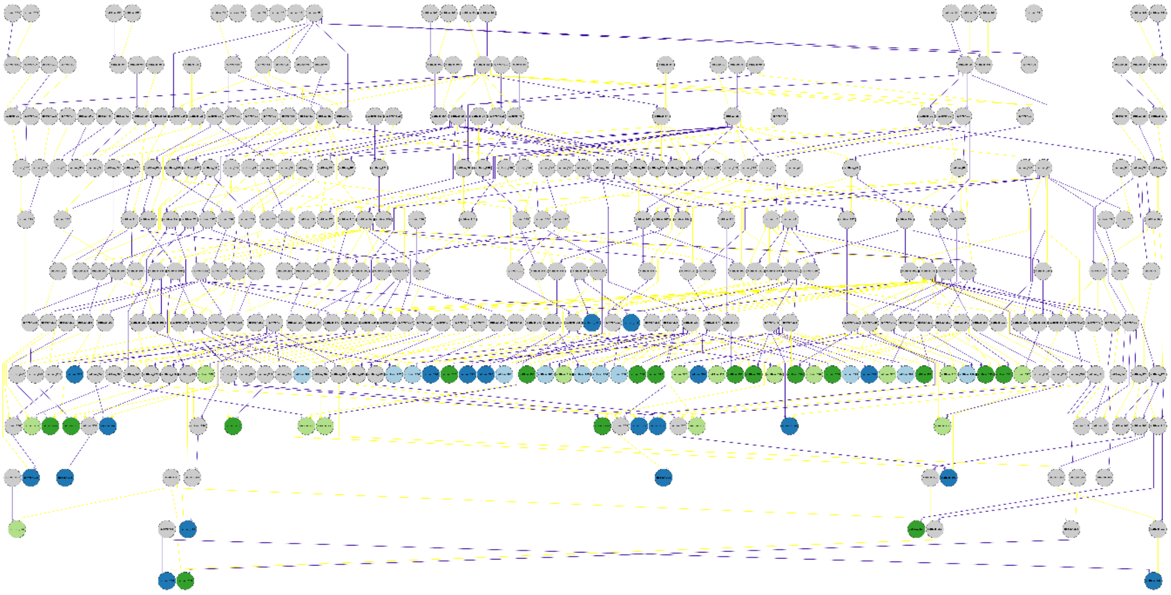
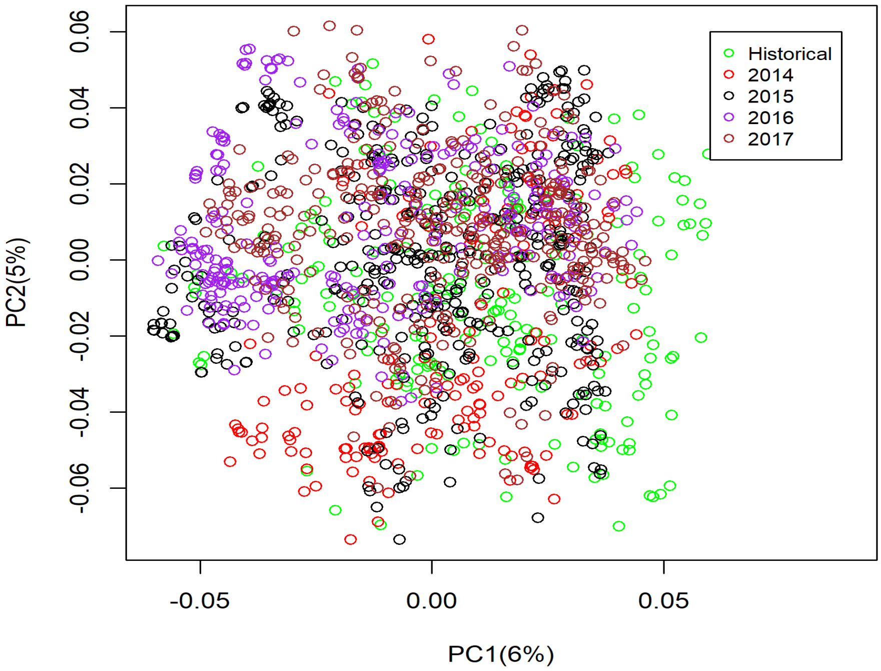


Figure S2. Principal component analysis on the genotype data of 1385 lines.


Historical
PC2(5%)
PC1(6%)