

Supplemental Table 1: Strain list

| Strain | Identifier (see Tables 1, 2) | Genotype | Species | Notes | Strain background |
|---------|------------------------------------|--|---------|--|-------------------|
| YMD139 | | <i>lys2Δ0/+ +/ura3-167 MATa/MATα</i> | cer | Ancestor of <i>S. cerevisiae</i> evolved diploids (high Ty) | GRF167 x S288C |
| YMD140 | | <i>lys2Δ0/+ +/ura3-167 MATa/MATα</i> | cer | Ancestor of <i>S. cerevisiae</i> evolved diploids | GRF167 x S288C |
| YMD129 | | <i>HOΔ::kanMX/HOΔ::kanMX lys2-1/+ +/ura3-167 MATa/MATα</i> | hybrid | Ancestor of evolved hybrids | GRF167 x CBS7001 |
| YMD130 | | <i>HOΔ::kanMX/HOΔ::kanMX lys2-1/+ +/ura3-167 (high Ty) MATa/MATα</i> | hybrid | Ancestor of evolved hybrids (high Ty) | GRF167 x CBS7001 |
| YMD366 | | <i>HOΔ::kanMX /HOΔ::kanMX lys2-1/+ ura3Δ::cloNAT/+ MATa/MATα</i> | uva | Ancestor of <i>S. uvarum</i> evolved diploids | CBS7001 |
| YMD35 | Pu1 | | uva | Phosphate limitation | YMD366 |
| YMD92 | Pu2 | | uva | Phosphate limitation | YMD366 |
| YMD18 | Pc3 | | cer | Phosphate limitation | YMD140 |
| YMD77 | Pc1 | | cer | Phosphate limitation | YMD140 |
| YMD66 | Pc4 | | cer | Phosphate limitation | YMD139 |
| YMD98 | Pc2 | | cer | Phosphate limitation | YMD139 |
| YMD30 | Ph1 | | hybrid | Phosphate limitation | YMD130 |
| YMD39 | Ph2 | | hybrid | Phosphate limitation | YMD130 |
| YMD90 | Ph3 | | hybrid | Phosphate limitation | YMD129 |
| YMD101 | Ph5 | | hybrid | Phosphate limitation | YMD130 |
| YMD741 | Ph4 | | hybrid | Phosphate limitation | YMD129 |
| YMD744 | Ph6 | | hybrid | Phosphate limitation | YMD129 |
| YMD723 | Gu1 | | uva | Glucose limitation | YMD366 |
| YMD725 | Gu2 | | uva | Glucose limitation | YMD366 |
| YMD34 | Gc2 | | cer | Glucose limitation | YMD140 |
| YMD23 | Gc1 | | cer | Glucose limitation | YMD139 |
| YMD726 | Gh1 | | hybrid | Glucose limitation | YMD129 |
| YMD737 | Gh2 | | hybrid | Glucose limitation | YMD130 |
| YMD739 | Gh3 | | hybrid | Glucose limitation | YMD130 |
| YMD720 | Su1 | | uva | Sulfate limitation | YMD366 |
| YMD721 | Su2 | | uva | Sulfate limitation | YMD366 |
| YMD31 | Sc3 | | cer | Sulfate limitation | YMD140 |
| YMD83 | Sc2 | | cer | Sulfate limitation | YMD140 |
| YMD105 | Sc1 | | cer | Sulfate limitation | YMD139 |
| YMD21 | Sc4 | | cer | Sulfate limitation | YMD139 |
| YMD751 | Sh2 | | hybrid | Sulfate limitation | YMD130 |
| YMD752 | Sh3 | | hybrid | Sulfate limitation | YMD130 |
| YMD754 | Sh4 | | hybrid | Sulfate limitation | YMD130 |
| YMD747 | Sh1 | | hybrid | Sulfate limitation | YMD129 |
| YMD749 | Sh7 | | hybrid | Sulfate limitation | YMD129 |
| YMD858 | Sh5 | | hybrid | Sulfate limitation | YMD129 |
| YMD861 | Sh6 | | hybrid | Sulfate limitation | YMD129 |
| YMD3348 | | <i>ura3-167/+ MATa/MATα</i> | cer | 2 preferred <i>S. cerevisiae</i> alleles at <i>PHO84</i> | |
| YMD3349 | | <i>PHO84Δ::ScPHO84</i> (un-preferred allele)/ <i>PHO84Δ::ScPHO84</i> (un-preferred allele) <i>ura3-167/+ MATa/MATα</i> | cer | 2 un-preferred <i>S. cerevisiae</i> alleles at <i>PHO84</i> | |
| YMD3350 | | <i>PHO84Δ::ScPHO84</i> (un-preferred | cer | 1 preferred, 1 un- | |

| | | | | | |
|---------|--|---|--------|--|--|
| | | allele)/+ <i>ura3-167/+ MATa/MATα</i> | | preferred <i>S. cerevisiae</i> allele at <i>PHO84</i> | |
| YMD3351 | | <i>ura3-167/ura3-167 MATa/MATα +pIL37-PHO84-URA3</i> | cer | 3+ preferred <i>S. cerevisiae</i> alleles at <i>PHO84</i> | |
| YMD3352 | | <i>ura3-167/ura3-167 MATa/MATα +pIL37-URA3</i> | cer | 2 preferred <i>S. cerevisiae</i> alleles at <i>PHO84</i> (empty plasmid control for YMD3351) | |
| YMD3353 | | <i>HOΔ::HYGb/HOΔ::kanMX lys2-1/+ ura3Δ::cloNAT/ura3-167 PHO84Δ::kanMX/+ MATa/MATα +pIL37-PHO84-URA3</i> | hybrid | 2+ preferred <i>S. cerevisiae</i> alleles at <i>PHO84</i> | |
| YMD3354 | | <i>HOΔ::HYGb/HOΔ::kanMX lys2-1/+ ura3Δ::cloNAT/ura3-167 PHO84Δ::kanMX/+ MATa/MATα +pIL37-URA3</i> | hybrid | 1 preferred <i>S. cerevisiae</i> allele (empty plasmid control for YMD3353) | |
| YMD3355 | | <i>HOΔ::HYGb/HOΔ::kanMX lys2-1/+ ura3Δ::cloNAT/ura3-167 MATa/MATα +pIL37-PHO84-URA3</i> | hybrid | 2+ preferred <i>S. cerevisiae</i> , 1 <i>S. uvarum</i> alleles at <i>PHO84</i> | |
| YMD3356 | | <i>HOΔ::HYGb/HOΔ::kanMX lys2-1/+ ura3Δ::cloNAT/ura3-167 MATa/MATα +pIL37-URA3</i> | hybrid | 1 preferred <i>S. cerevisiae</i> , 1 <i>S. uvarum</i> allele at <i>PHO84</i> (empty plasmid control for YMD3355) | |
| YMD3357 | | <i>HOΔ::natMX-GFP/+ lys2-1/+ +ura3-167 MATa/MATα</i> | hybrid | GFP competitor strain for hybrids | |
| YMD3358 | | <i>HOΔ::natMX-GFP/+ lys2-1/+ +ura3-167 MATa/MATα (high Ty)</i> | hybrid | GFP competitor strain for hybrids (high Ty) | |
| YMD1459 | | <i>HOΔ::kanMX-GFP/+ MATa/MATα</i> | cer | GFP competitor strain for <i>S. cerevisiae</i> | |

Clones are identified by nutrient (G: glucose-limitation, P: phosphate-limitation, and S: sulfate-limitation), by species (“h” denotes a hybrid, “c” denotes *S. cerevisiae*, “u” denotes *S. uvarum*), and the number indicates its derivation from independent populations. The strain number in the Dunham lab strain database is listed for each.

Supplemental Table 2: Sequencing coverage

| Strain | Clone (see Table 1, 2) | Average Coverage |
|--------|---------------------------------|---------------------|
| YMD139 | | 58.44 |
| YMD140 | | 174.1 |
| YMD129 | | 36.6 |
| YMD130 | | 84.24 |
| YMD366 | | 176.7 |
| YMD35 | Pu1 | 288.3 |
| YMD92 | Pu2 | 60.2 |
| YMD18 | Pc3 | 389.8 |
| YMD77 | Pc1 | 82.0 |
| YMD66 | Pc4 | 57.1 |
| YMD98 | Pc2 | 100.5 |
| YMD30 | Ph1 | 32.4/28.15 |
| YMD39 | Ph2 | 39.9/34.1 |
| YMD90 | Ph3 | 38.4/32.4 |
| YMD101 | Ph5 | 19.13/17.8 |
| YMD741 | Ph4 | 63.2/57.5 |
| YMD744 | Ph6 | 37.4/69.4 |
| YMD723 | Gu1 | 94.3 |
| YMD725 | Gu2 | 80.5 |
| YMD34 | Gc2 | 72.2 |
| YMD23 | Gc1 | 104.0 |
| YMD726 | Gh1 | 25.6/47.8 |
| YMD737 | Gh2 | 35.4/30.9 |
| YMD739 | Gh3 | 21.2 |
| YMD720 | Su1 | 43.6 |
| YMD721 | Su2 | 74.3 |
| YMD31 | Sc3 | 77.4 |
| YMD83 | Sc2 | 90.9 |
| YMD105 | Sc1 | 81.6 |
| YMD21 | Sc4 | 133.7 |
| YMD751 | Sh2 | 59.8 |
| YMD752 | Sh3 | 31.7/29.4 |
| YMD754 | Sh4 | 33.7/33.0 |
| YMD747 | Sh1 | 100.1 |
| YMD749 | Sh7 | 27.6 |
| YMD858 | Sh5 | 33.5/34.9 |
| YMD861 | Sh6 | 39.2/35.1 |

Mean sequencing coverage is reported from GATK DepthOfCoverage for each evolved clone and ancestor.

| Primer name | Primer sequence | Purpose |
|----------------------------|--|--|
| ScPHO84_URA3homF | CGGAGACAATCATATGGGAGAAGCAATTGGAAGATAGAAAAAAGGTACTCGGTACATAAA GTAACCTGACAGTATTTATA | Replace <i>S. cerevisiae</i> PHO84 with <i>K. lactis</i> URA3 |
| ScPHO84_URA3homR | TGGAGGAAGTTTGAGAGGGCTTATCGCAATGGTTGTAATGGTTTAAAACTCTTTTCGAT CCATATTATTATGAAAAGAC | Replace <i>S. cerevisiae</i> PHO84 with <i>K. lactis</i> URA3 |
| SCER_chr13_23602_PHO84F | TGTCCACAGGTGCCATTGGTTG | Confirm loss of <i>S. cerevisiae</i> PHO84, gain of URA3 |
| SCER_chr13_24217_PHO84R | CGCCTTATTCATGTTGTTGGGTATCTTCAC | Confirm loss of <i>S. cerevisiae</i> PHO84 |
| SCER_URA3gain_5primeR | GGCCCAATCACAACCACATCTTAGATAGTTG | Confirm gain of <i>K. lactis</i> URA3 |
| SCER_chr13_26112_PHO84F | GCCTTTCACACGACATTTGGTGCATAAC | Confirm loss of <i>S. cerevisiae</i> PHO84 |
| SCER_chr13_26652_PHO84R | GACTTCAAACGACTCGGTATACTCTGCC | Confirm loss of <i>S. cerevisiae</i> PHO84, gain of URA3 |
| SCER_URA3gain_3primeF | GAAATGCTGGATGGGAAGCGTACC | Confirm gain of <i>K. lactis</i> URA3 |
| SCER_PHO84amp_chr13_23928F | GTAACCTGACAGTATTTATAGATTATGTAAGGGGTTT | Amplify the <i>S. cerevisiae</i> PHO84 allele |
| SCER_PHO84amp_chr13_26478R | CCATATTATTATGAAAAGACACAACCGGAAGGGG | Amplify the <i>S. cerevisiae</i> PHO84 allele |
| SUVA_PHO84amp_SCERhomF | ACAGGATGGCAGAGAGATGTGAGGAAATAATGAAATTAAGAAATTATCGAATAAATAT GTATAATAAATATGTAGCCT | Replace <i>S. cerevisiae</i> PHO84 with <i>S. uvarum</i> PHO84 |
| SUVA_PHO84amp_SCERhomR | GAAACTAATTTATCAGCCGCTCGTTTATCAACCGTTATACCAAATTATGAATAAAAAA CTATAGAGCAGAATAATAGA | Replace <i>S. cerevisiae</i> PHO84 with <i>S. uvarum</i> PHO84 |
| SUVA_lossPHO84_5primeF | CGCAATCAAACATACCGTTGATACTGATGAC | Confirm loss of <i>S. uvarum</i> PHO84 |
| SUVA_new_lossPHO84_5primeR | GAACGATGTCGAATCTTCTCTCCATCTC | Confirm loss of <i>S. uvarum</i> PHO84 |
| SUVA_new_lossPHO84_3primeF | CGTGGGCTATAACGACGCTACTG | Confirm loss of <i>S. uvarum</i> PHO84 |
| SUVA_lossPHO84_3primeR | ATCACCAATCACGTGATCTAGTTACCC | Confirm loss of <i>S. uvarum</i> PHO84 |
| SUVA_PHO84ampF | GTATAATAAATATGTAGCCTGACAGTATTTATAGATTATGTACGT | Amplify the <i>S. uvarum</i> PHO84 allele |
| SUVA_PHO84ampR | CTATAGAGCAGAATAATAGACACAACCGGCG | Amplify the <i>S. uvarum</i> PHO84 allele |
| Suva_PHO84_KANMX_F | AGTTTCTCATTGAACTTTTTGAAATTGATTCAGTAAGC CGACATGGAGGCCAGAATA | Replace <i>S. uvarum</i> PHO84 with kanMX |
| Suva_PHO84_KANMX_R | CAGTAAGCCACAACAAACAACAAGAATACATCAAAG CAGTATAGCGACCAGCATTC | Replace <i>S. uvarum</i> PHO84 with kanMX |
| pIL37_cerPHO84F | GCCCGGGGATCTCGTAACCTGACAGTATTTATAGATTATG | Cloning <i>S. cerevisiae</i> PHO84 into pIL37 plasmid |
| pIL37_cerPHO84R | GAAGTAGTGGATCTCGCCATATTATTATGAAAAGACACAAC | Cloning <i>S. cerevisiae</i> PHO84 into pIL37 plasmid |
| IL429 | GTGAGCGCGTAATACGACTC | Confirm insertion in pIL37 plasmid |
| IL430 | CACACAGGAAACAGCTATGACCATG | Confirm insertion in pIL37 plasmid |
| 30_chrIV_1055864F | CAAGAGGCAGTGGCAGACTTGC | Confirm SNP in evolved hybrid |

| | | |
|------------------------|------------------------------|-------------------------------|
| 30_chrIV_1055864R | CCGTGGAACGGGATTTGGCAG | Confirm SNP in evolved hybrid |
| 39_chrV_432778F | GGACTACAACCAGTTGACGTTG | Confirm SNP in evolved hybrid |
| 39_chrV_432778R | CGGCTATCTCGACATATGAGTAGGC | Confirm SNP in evolved hybrid |
| 741_chrVII_555885F | GGATGGGTTGTCAGTAGACGGTG | Confirm SNP in evolved hybrid |
| 741_chrVII_555885R | GTCGCCCTATGCCTGGATTG | Confirm SNP in evolved hybrid |
| 741_chrX_246208F | GTGGTATTCAAGAATGGCGCACC | Confirm SNP in evolved hybrid |
| 741_chrX_246208R | GACTCCGAGTGAGCTTCGACATC | Confirm SNP in evolved hybrid |
| 744_chrVII_972813F | GCGGTGGCATCAATGTAGTCAACC | Confirm SNP in evolved hybrid |
| 744_chrVII_972813R | GATTCTCCAGGTATGAATGCCGCTG | Confirm SNP in evolved hybrid |
| 726_chrXIII_852028F | CGGGTAACGAAGAATCGACTCTCGC | Confirm SNP in evolved hybrid |
| 726_chrXIII_852028R | GCGGAATAACCTAACACGTGGAGG | Confirm SNP in evolved hybrid |
| 737_chrIV_111919F | GATACGACAGGTAGCATACGAACCCC | Confirm SNP in evolved hybrid |
| 737_chrIV_111919R | GTGATTCTCTCCAGCACCTACCTG | Confirm SNP in evolved hybrid |
| 737_chrIII_51593F | GGATGTCGTGCAATTGTACCAGGAG | Confirm SNP in evolved hybrid |
| 737_chrIII_51593R | GCTTGAGCTCATTATCGAAGGACCC | Confirm SNP in evolved hybrid |
| 749_chrII_238875F | GCAAGAAGATCTGGCAAGCTACAAGG | Confirm SNP in evolved hybrid |
| 749_chrII_238875R | CGTCGCTACAGAAGGCTTTGGTTG | Confirm SNP in evolved hybrid |
| 749_chrXVI_490631F | CCAATGCAGTGCGCTTATTGGTTG | Confirm SNP in evolved hybrid |
| 749_chrXVI_490631R | GGCGAAAGTAAGTCCAGCACTGAG | Confirm SNP in evolved hybrid |
| 749_chrXVI_86106F | CTGGTAGTCAACCATCCCAGATG | Confirm SNP in evolved hybrid |
| 749_chrXVI_86106R | GGGCAGCAACCCTAAACTGCTG | Confirm SNP in evolved hybrid |
| 751_chrVII_936384F | CATGCTCGTTTCCATATGACCAGG | Confirm SNP in evolved hybrid |
| 751_chrVII_936384R | GCATAGAACTTCGGAGGTCAATGGG | Confirm SNP in evolved hybrid |
| 752_chrVI_162998F | GGAATTGACCCGGTGATACGTCCAAG | Confirm SNP in evolved hybrid |
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| 754_chrXIV_666675R | CTGGGACGATATCAACGAGCAATCC | Confirm SNP in evolved hybrid |
| 754_chrXV_800832F | CTGCTGTTGGCACTGATATGCC | Confirm SNP in evolved hybrid |
| 754_chrXV_800832R | CCCAGCAAGGCGATGATTCTAACTTC | Confirm SNP in evolved hybrid |
| 754_chrIV_259517F | CCTTAGCCTGCTCACTACTTAGAAGTTG | Confirm SNP in evolved hybrid |
| 754_chrIV_259517R | CCAGCTCTGTTTGAATGTGCCTCC | Confirm SNP in evolved hybrid |
| 861_chrV_269392F | TACGTCGTCTACAGTTGGACAGGC | Confirm SNP in evolved hybrid |
| 861_chrV_269392R | GTGGTTCCAGATGTGCCAACTGTG | Confirm SNP in evolved hybrid |
| 861_chrXIV_746688F | AACTGGTCTTTGGCAAATGGCTCC | Confirm SNP in evolved hybrid |
| 861_chrXIV_746688R | CAGACACAGTTTTTCAGCGATGCCC | Confirm SNP in evolved hybrid |
| 39_uva_chrVII_9524F | GGCGCCTAATGTGGAAGAAGATGAC | Confirm SNP in evolved hybrid |
| 39_uva_chrVII_9524R | GTCTTGATGCTGGTAGGCAGGTG | Confirm SNP in evolved hybrid |
| 39_uva_chrXVI_232879F | CTAAGACCGTTCCCCTCCTAAGC | Confirm SNP in evolved hybrid |
| 39_uva_chrXVI_232879R | GCCACCAGTTAGCTATATCTTTCGCTG | Confirm SNP in evolved hybrid |
| 39_uva_chrXIII_194496F | GATTCACCACGCCTAAGCTCTTGAG | Confirm SNP in evolved hybrid |
| 39_uva_chrXIII_194496R | GTTGTCAAGGAATTGCCAAAGCC | Confirm SNP in evolved hybrid |

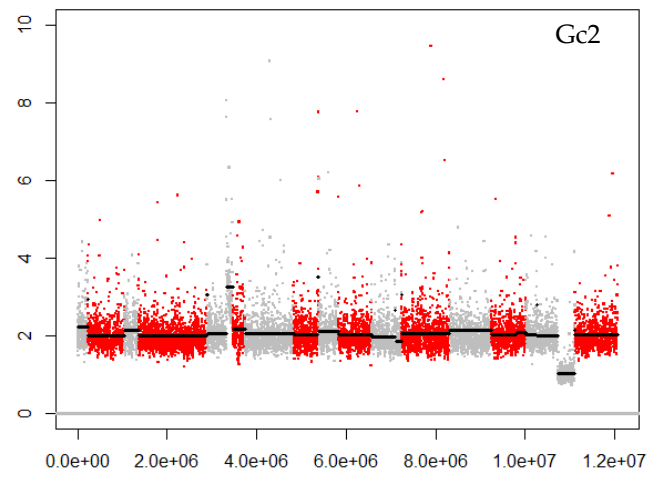
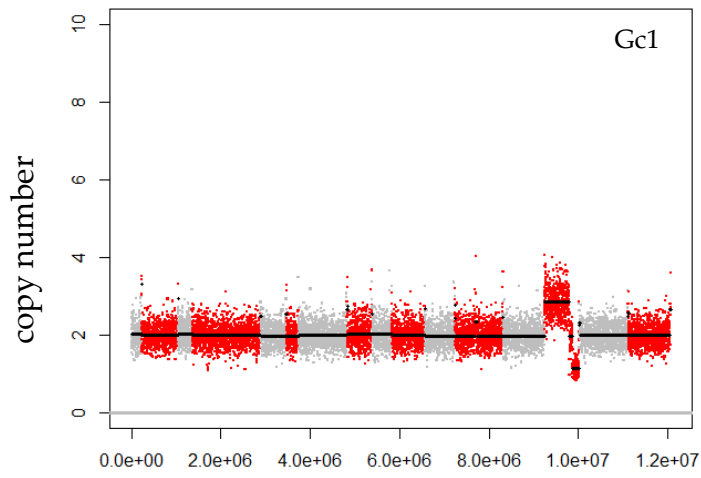
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|-------------------------|------------------------------|-------------------------------|
| 39_uva_chrIV_244399F | GAACCGACCTAGCTTCAACCCTTC | Confirm SNP in evolved hybrid |
| 39_uva_chrIV_244399R | ATACGATGTCAGCCTCGCAGGAG | Confirm SNP in evolved hybrid |
| 101_uva_chrXIII_231731F | GGATCATCGAAGGCGGTAGATCG | Confirm SNP in evolved hybrid |
| 101_uva_chrXIII_231731R | CACAAACCCTCCTGCACACCTTTC | Confirm SNP in evolved hybrid |
| 741_uva_chrXIII_324121F | GTCCATAGCACGCTGTGCTTCTG | Confirm SNP in evolved hybrid |
| 741_uva_chrXIII_324121R | GAGCATGGTAGACTGAACCAGTTTCAG | Confirm SNP in evolved hybrid |
| 749_uva_chrII_273296F | GTGGCTTGTCCATGAGATGCAACAG | Confirm SNP in evolved hybrid |
| 749_uva_chrII_273296R | CCACTCCGTGAGACCCAATCTTC | Confirm SNP in evolved hybrid |
| 752_uva_chrXIV_495890F | GTGACGGTACATGTGGTACGAACC | Confirm SNP in evolved hybrid |
| 752_uva_chrXIV_495890R | CGCGACTATGATTACACAGGCCATAC | Confirm SNP in evolved hybrid |
| 754_uva_chrV_342563F | GCCAATTCGGTACTTCCTTCTGAGC | Confirm SNP in evolved hybrid |
| 754_uva_chrV_342563R | GAATCGAGTGCCTAGCCGAGAGC | Confirm SNP in evolved hybrid |
| 754_uva_chrX_769768F | CTGTCCTGGAGACTTTCAGATTCGG | Confirm SNP in evolved hybrid |
| 754_uva_chrX_769768R | GCTGTCTTCGCCTTCGTCTGTAC | Confirm SNP in evolved hybrid |
| 754_uva_chrX_990873F | CACCATGACTGTCGCTATGTCAAACG | Confirm SNP in evolved hybrid |
| 754_uva_chrX_990873R | CACATTGGTACATGGTTCGGTGCTC | Confirm SNP in evolved hybrid |
| 754_uva_chrXII_192491F | AAAGCAGTACTCGACATGCGGC | Confirm SNP in evolved hybrid |
| 754_uva_chrXII_192491R | CTGACAGGGATGCTGGTGACAAG | Confirm SNP in evolved hybrid |
| 754_uva_chrXIV_19697F | CGGGTCGTTCCCTCAAGAGTC | Confirm SNP in evolved hybrid |
| 754_uva_chrXIV_19697R | GGGACAGATTGACAGGTTTCATTGAAGG | Confirm SNP in evolved hybrid |
| 858_uva_chrIV_310881F | CAACAGGGGAAGGTTGCCTATGAC | Confirm SNP in evolved hybrid |
| 858_uva_chrIV_310881R | CAATGTCGGTAAGTGAACAGGACCC | Confirm SNP in evolved hybrid |
| 858_uva_chrVIII_16911F | GCCTCCTTCATAGCCCTGCTTTC | Confirm SNP in evolved hybrid |
| 858_uva_chrVIII_16911R | CCCGAATCCACCCTCTTACCATAC | Confirm SNP in evolved hybrid |
| 861_uva_chrIV_413046F | GTTAGACCGATCCAGCAGGAGC | Confirm SNP in evolved hybrid |
| 861_uva_chrIV_413046R | GAACCTATTCCTAAGCAGGGTCCG | Confirm SNP in evolved hybrid |
| 739_uva_chrII_889421F | GAAGGTCGAGGCAGATCTATCCACC | Confirm SNP in evolved hybrid |
| 739_uva_chrII_889421R | GCGTAGGTGCAGAAACCACCC | Confirm SNP in evolved hybrid |

Supplemental Table 3: Primers used

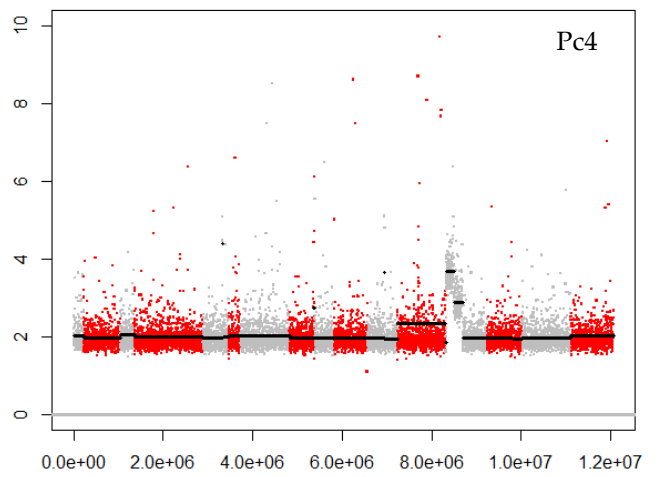
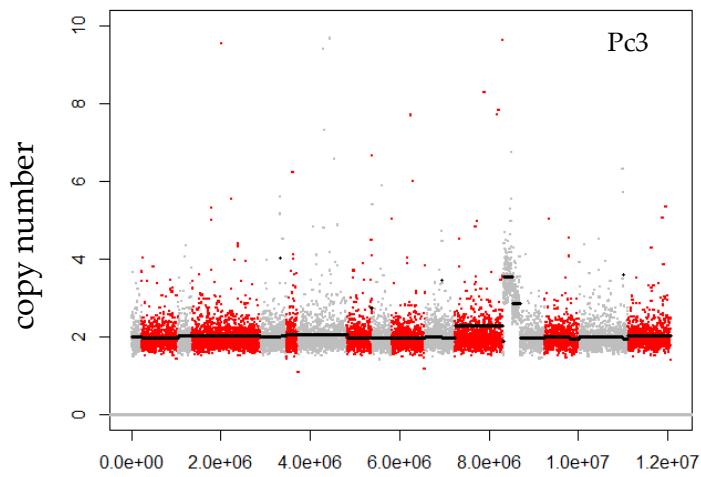
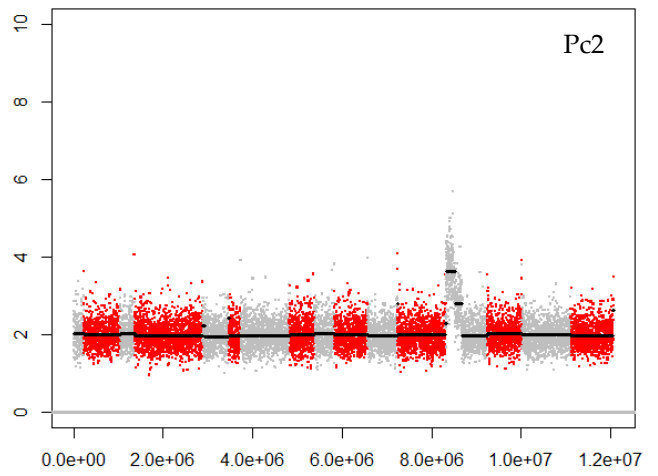
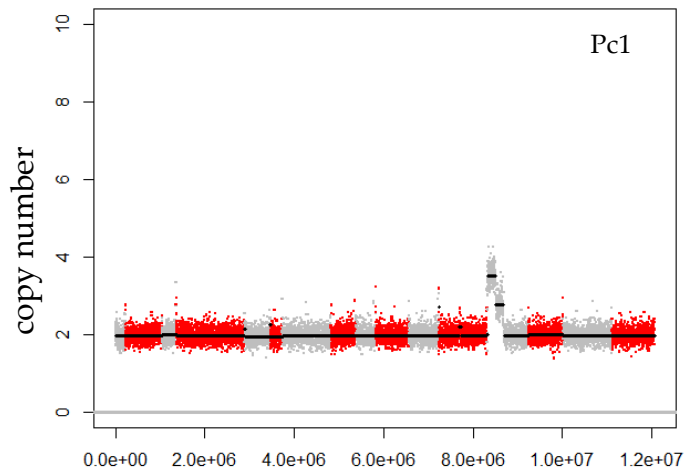
Primers used for allele replacements and SNP confirmation in evolved hybrid clones.

Supplementary Figure 1

A

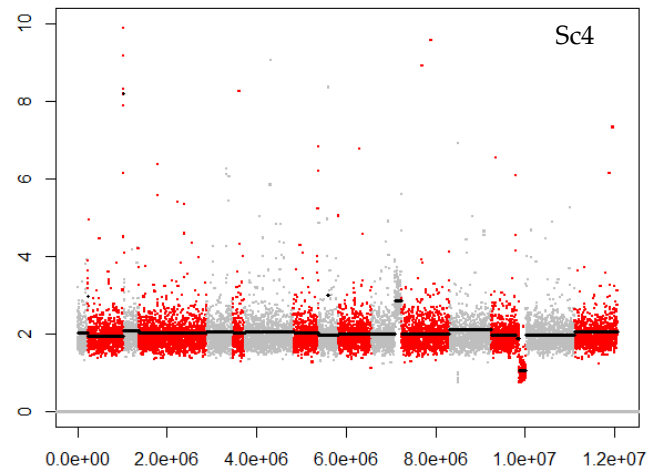
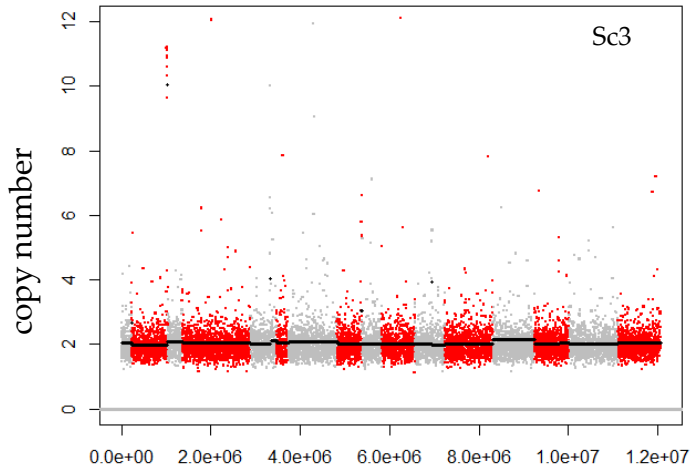
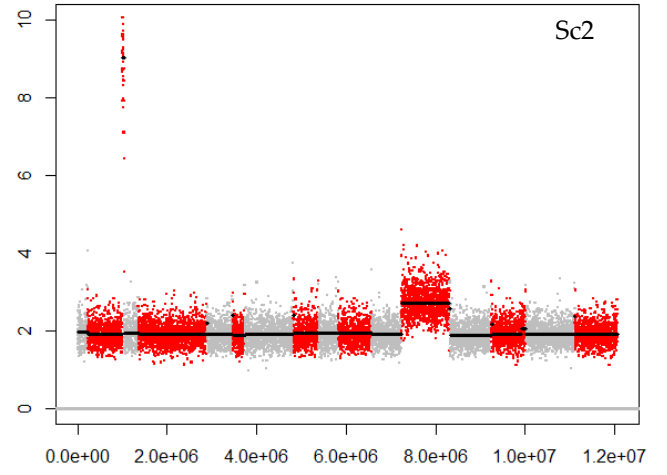
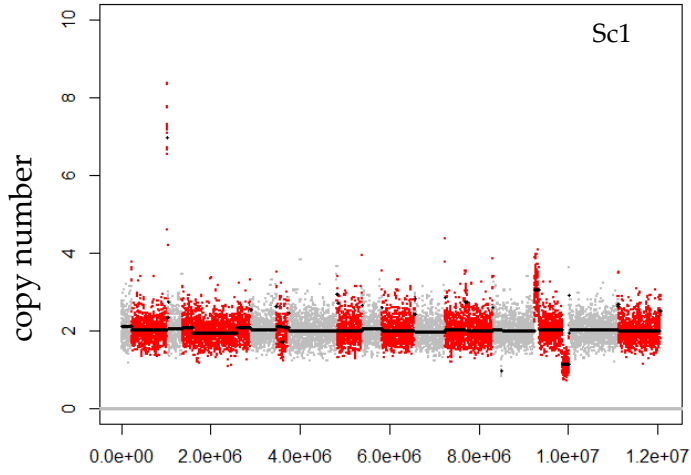


B



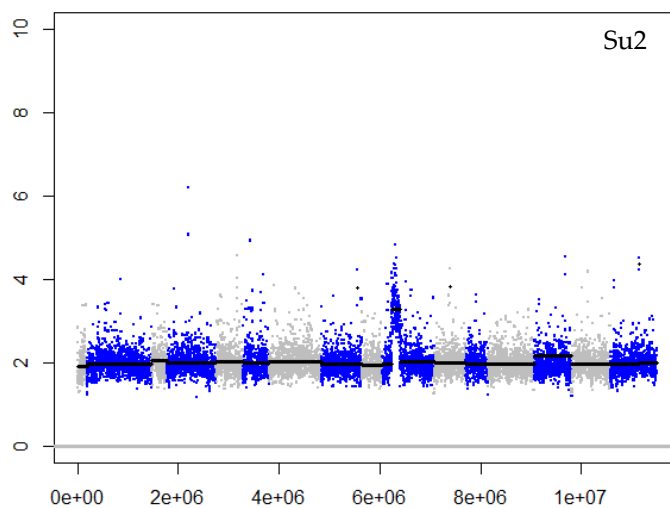
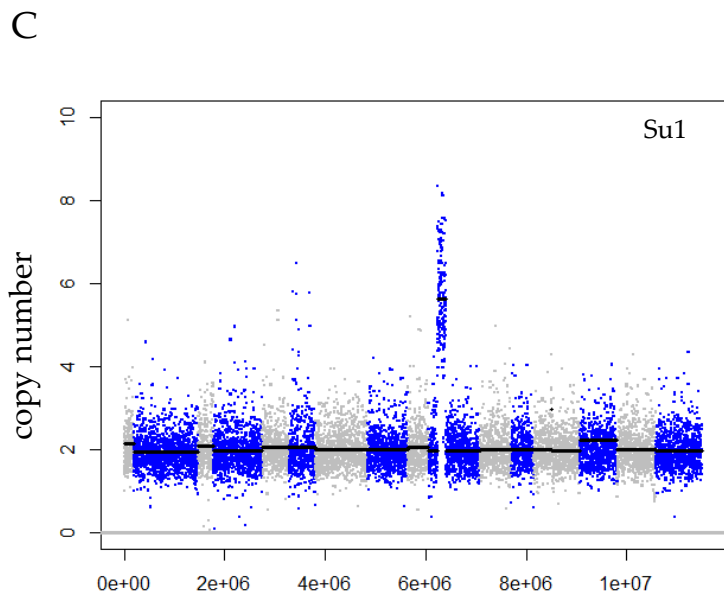
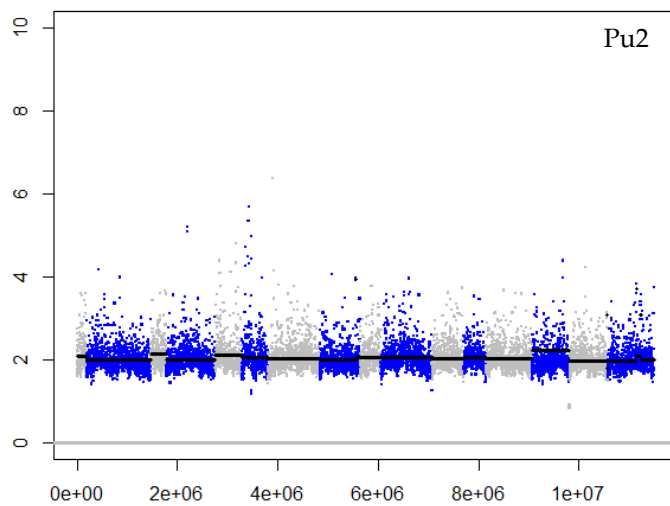
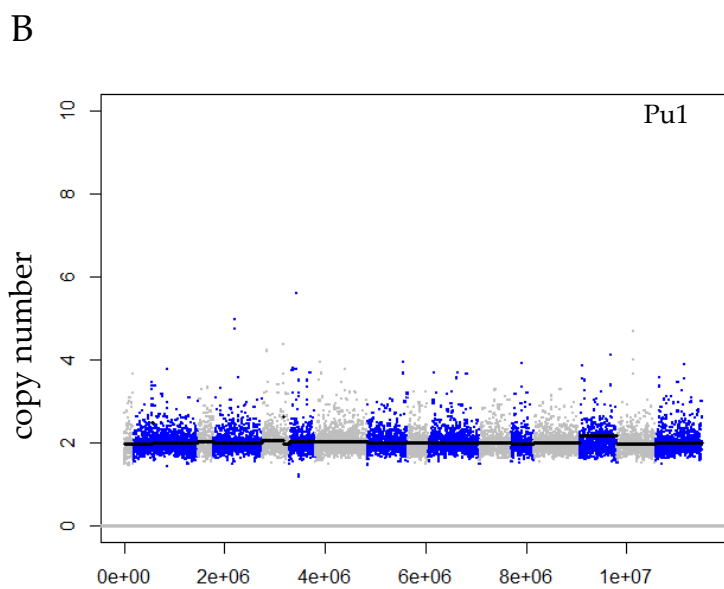
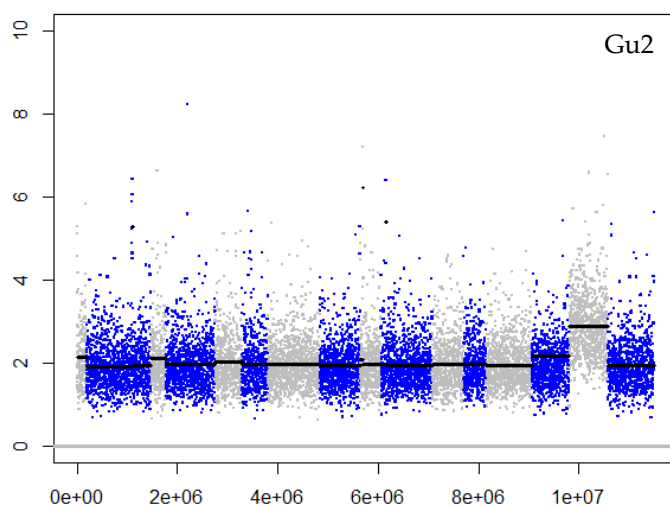
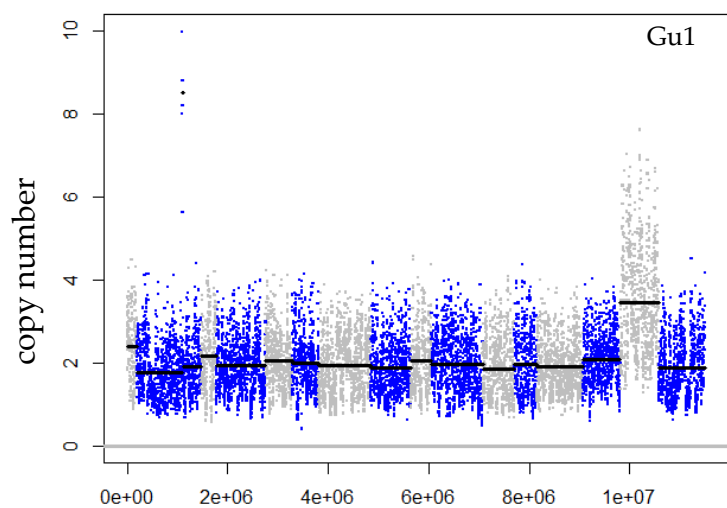
Genomic Position (bp)

C



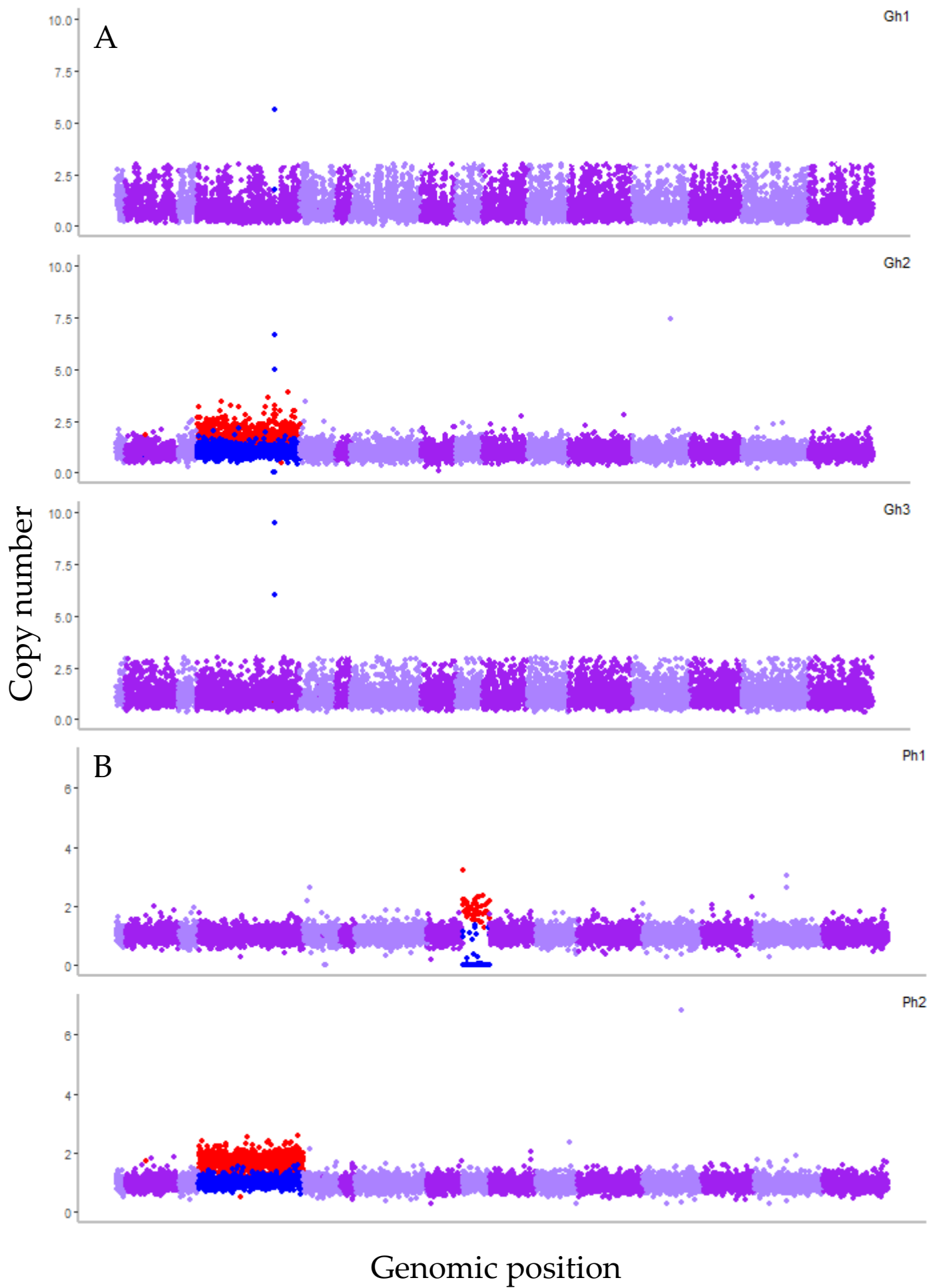
Genomic Position (bp)

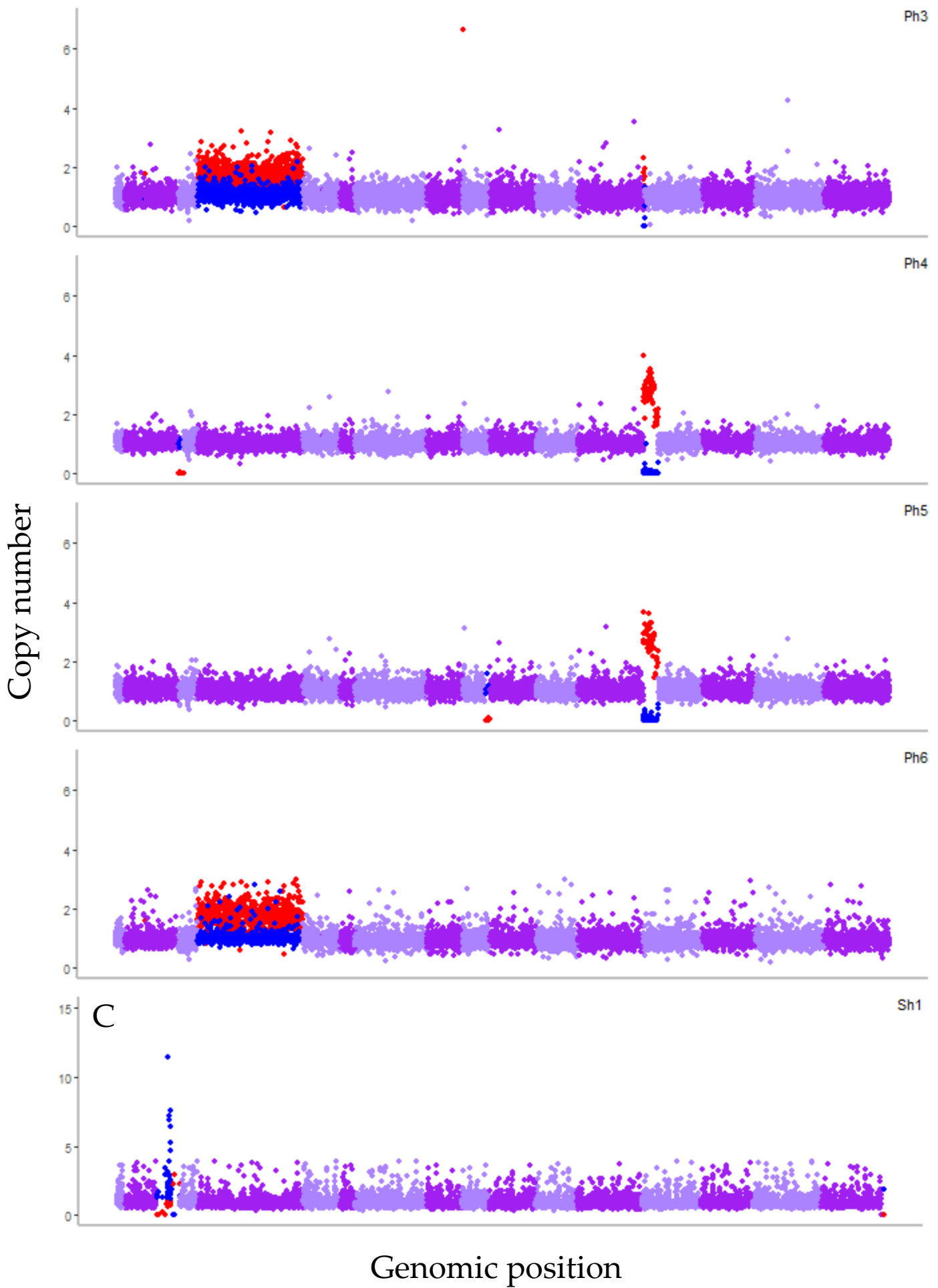
A Supplementary Figure 2

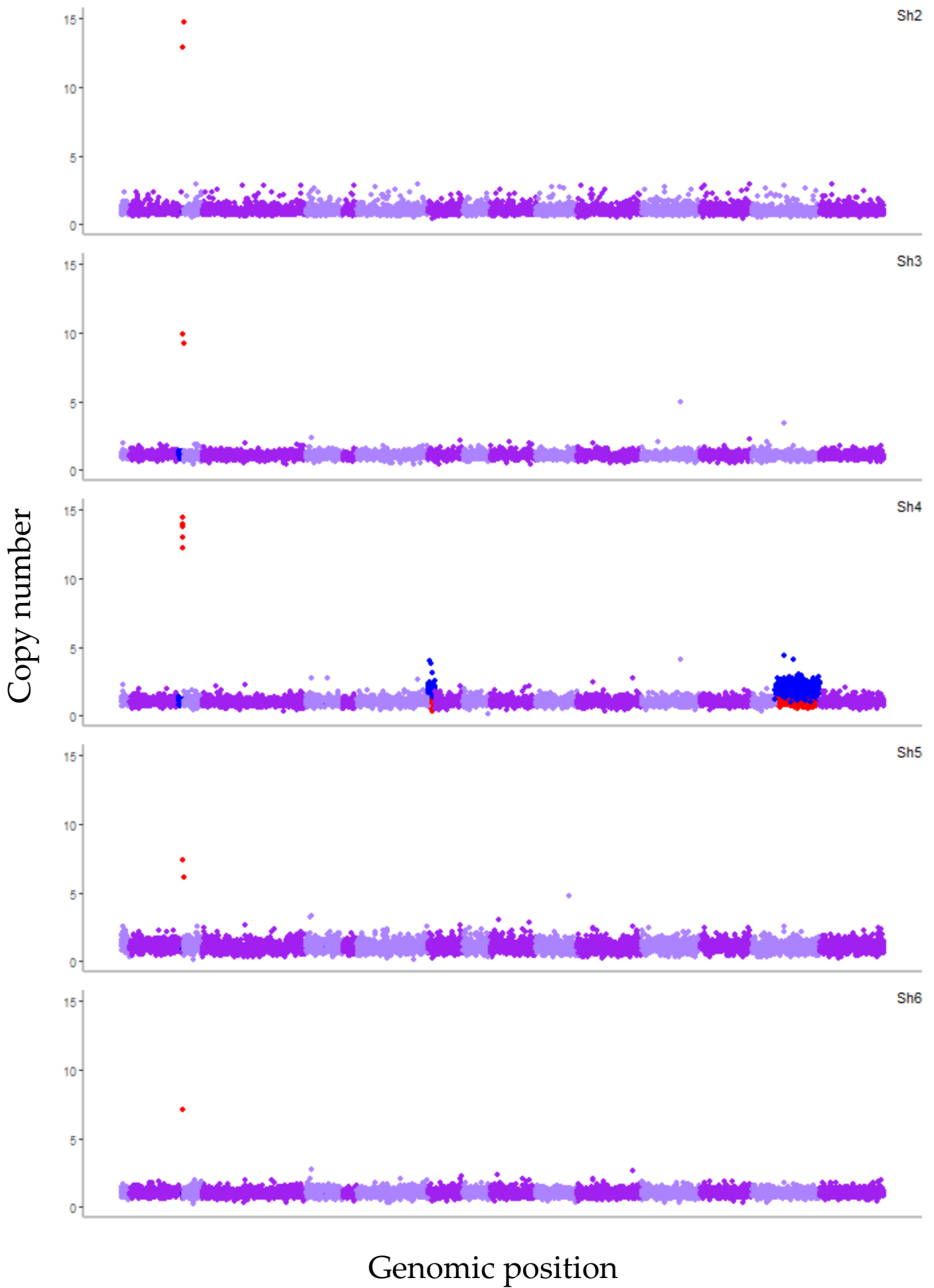


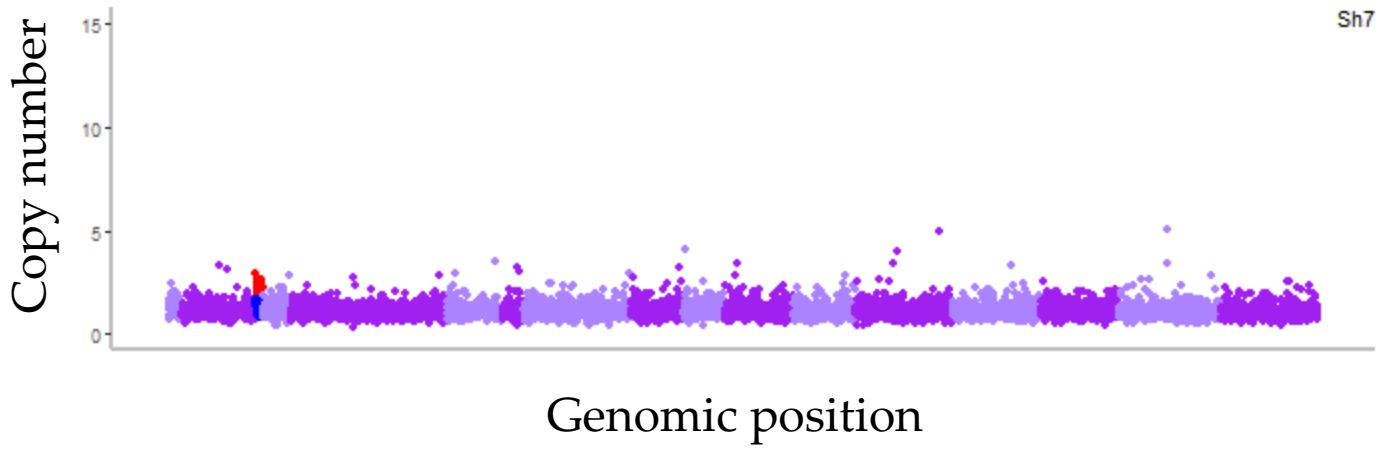
Genomic Position (bp)

Supplementary Figure 3

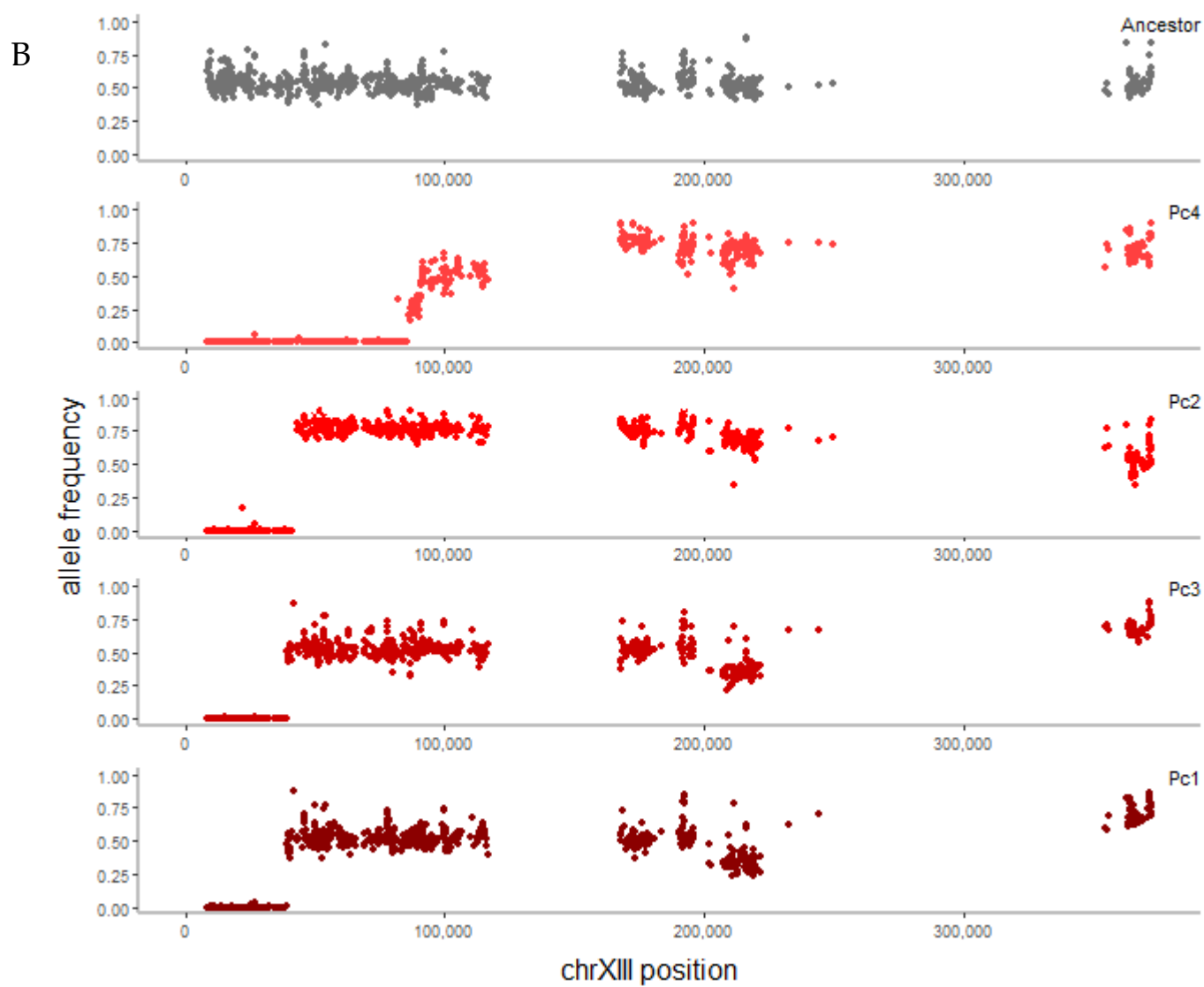
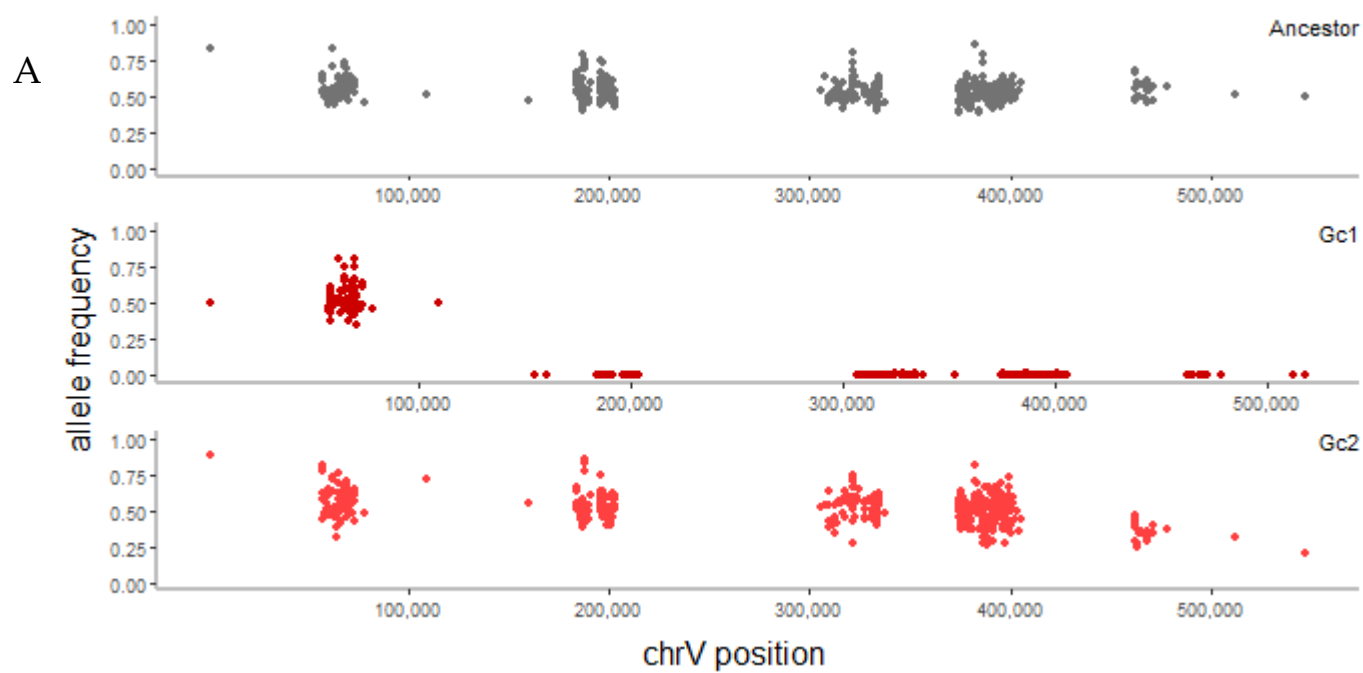


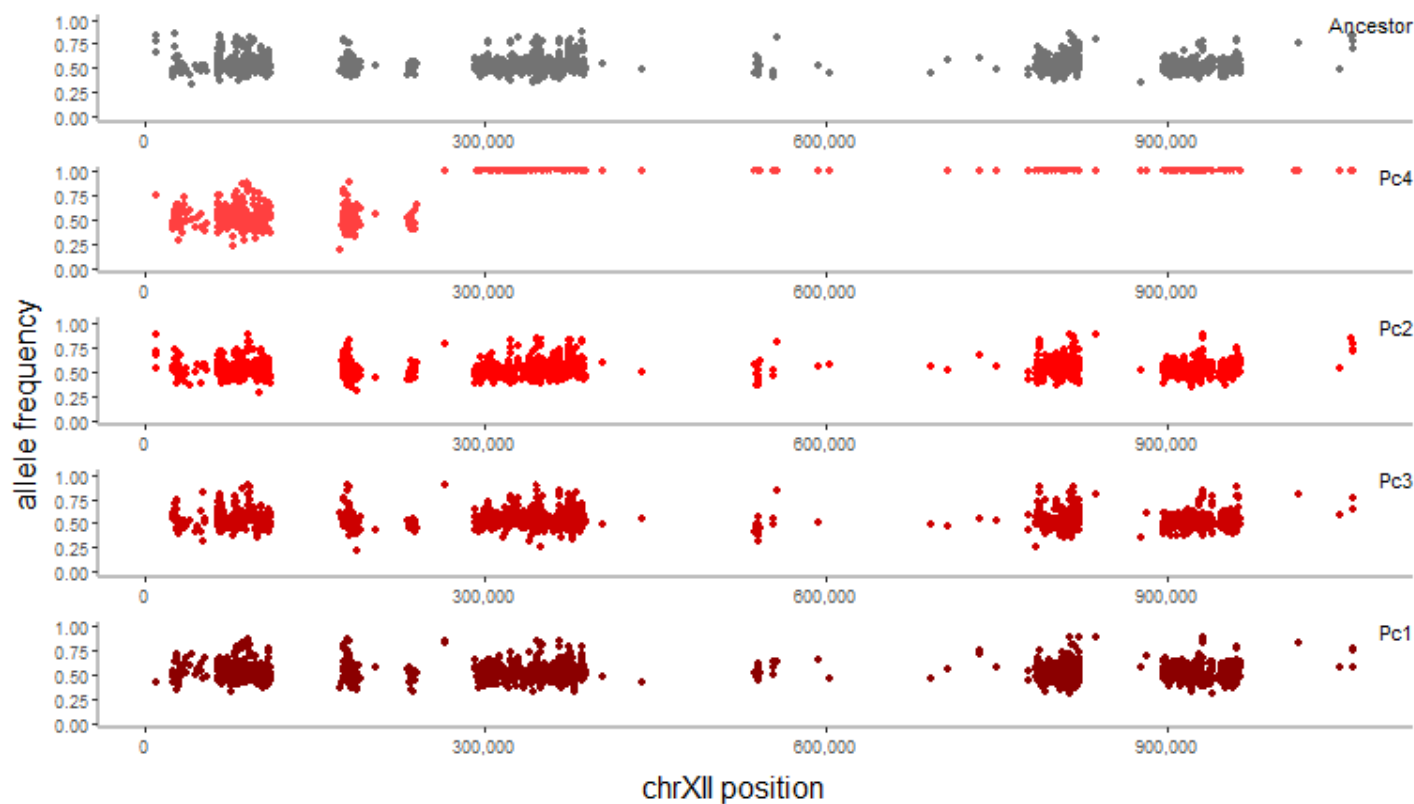




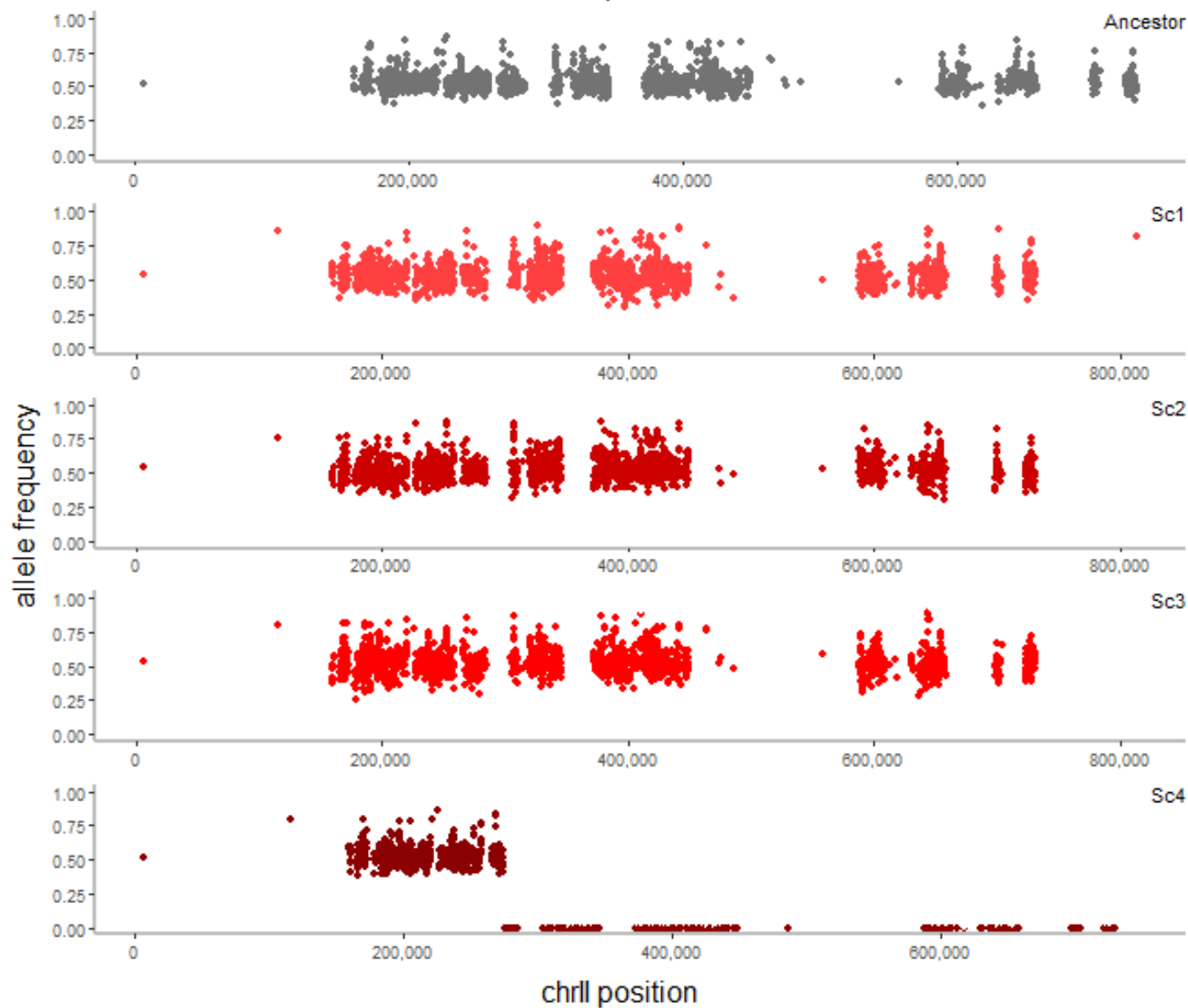


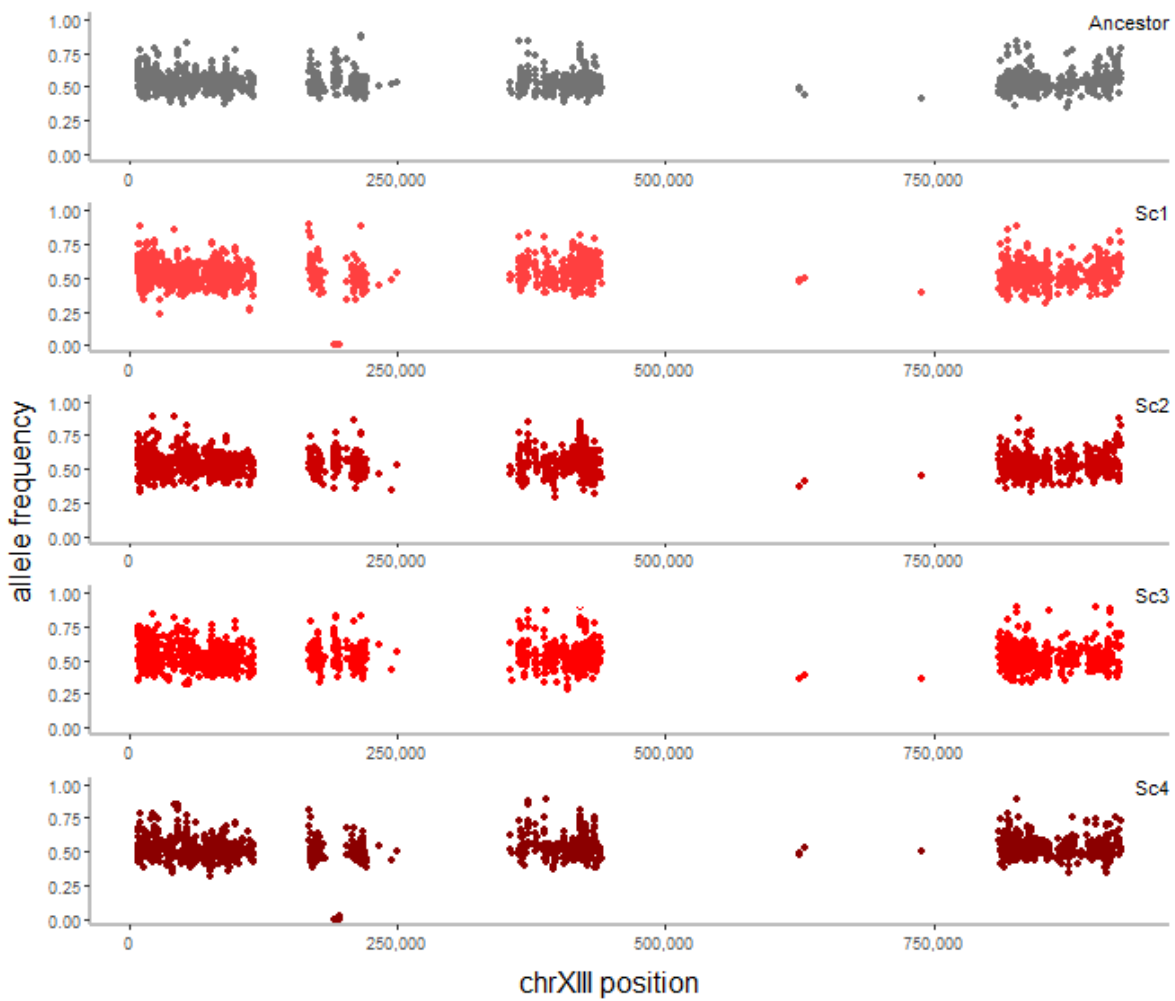
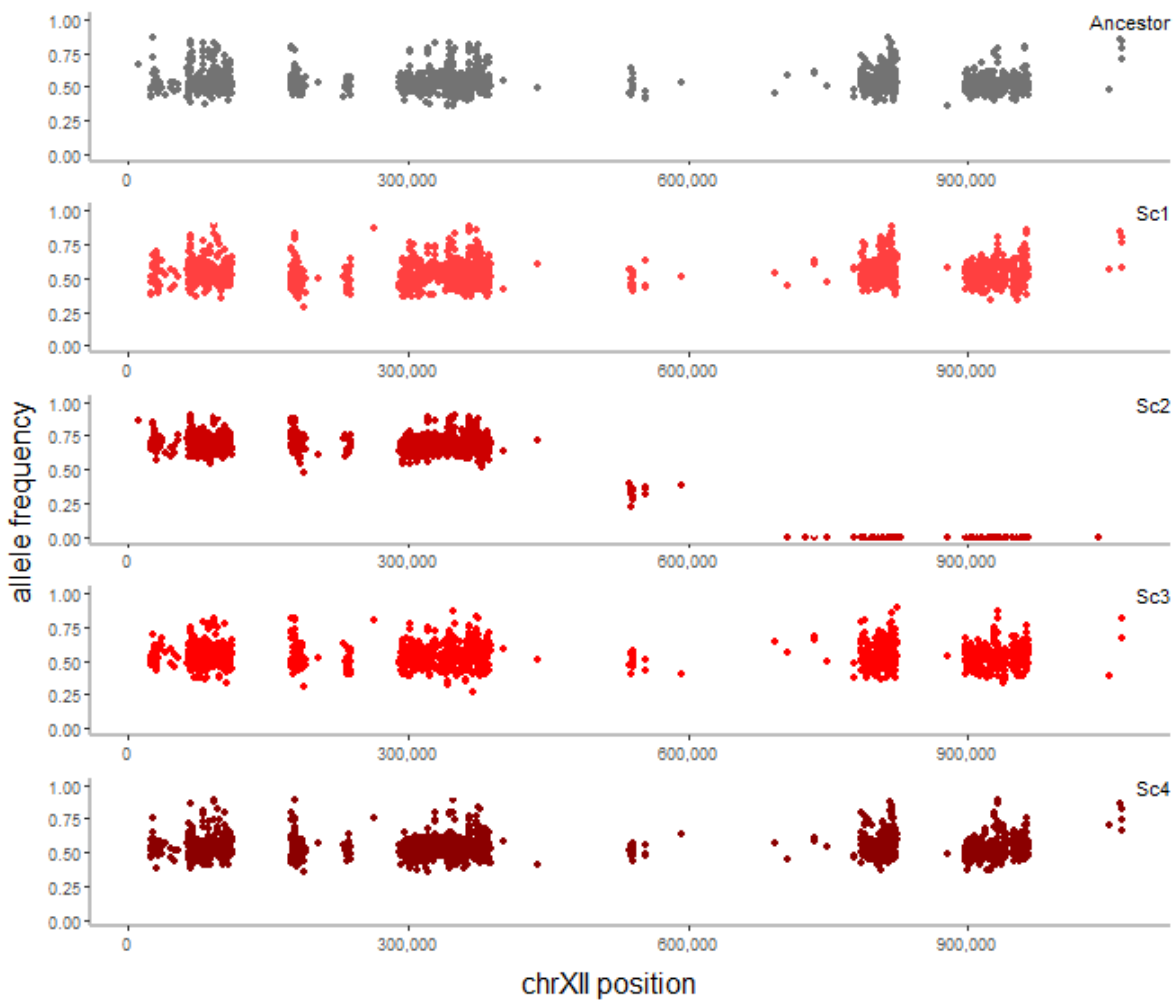
Supplementary Figure 4

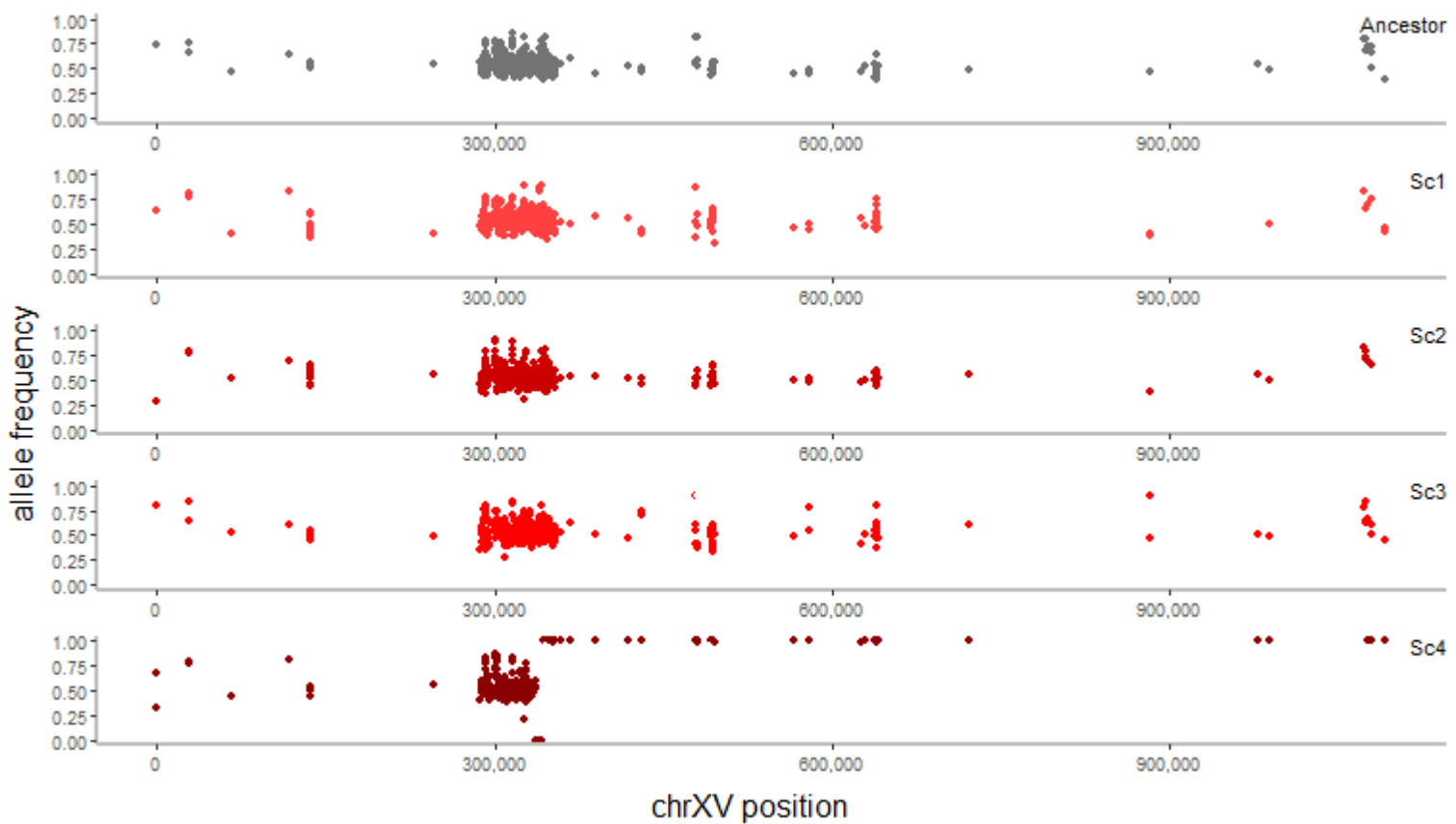
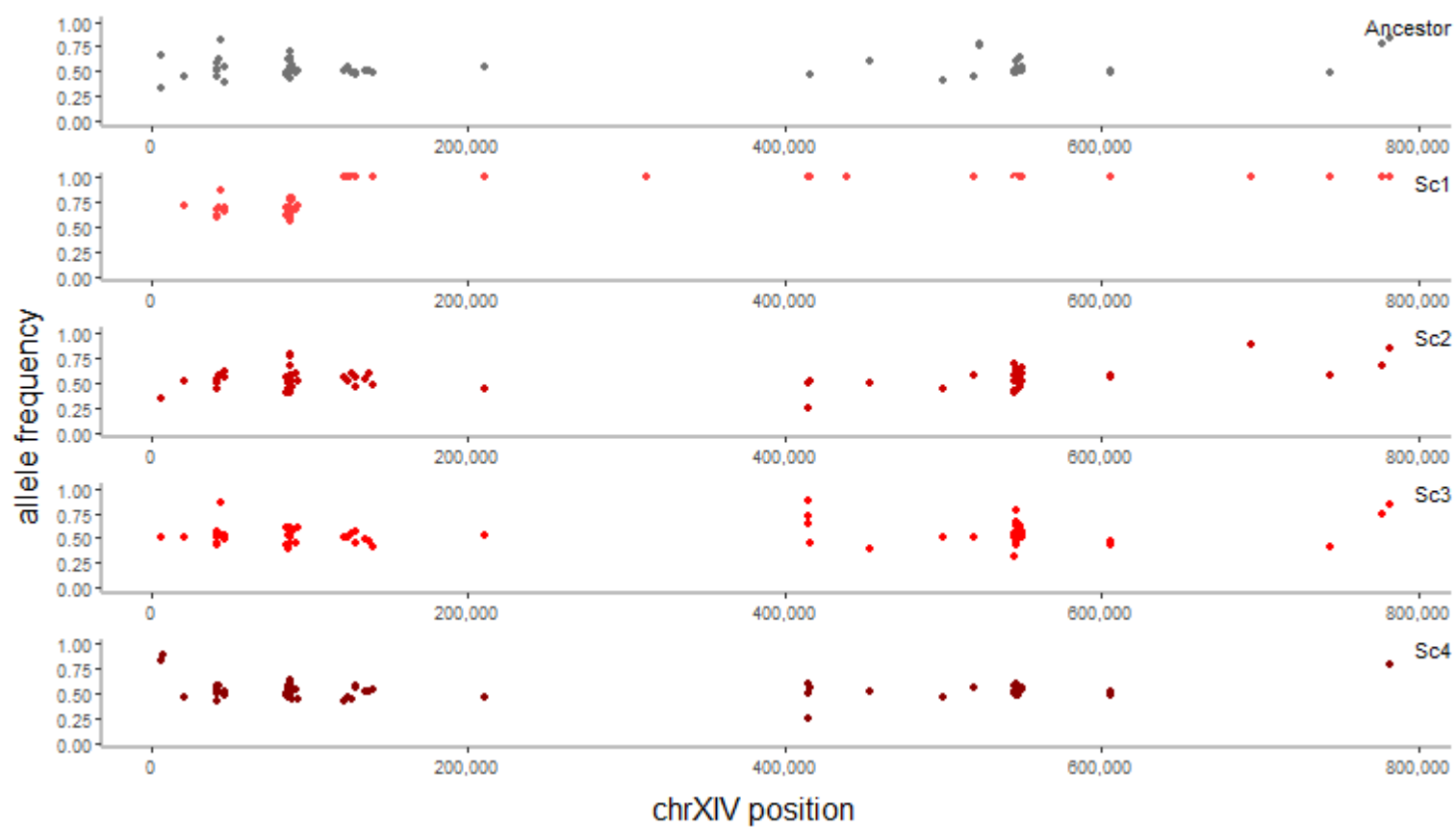




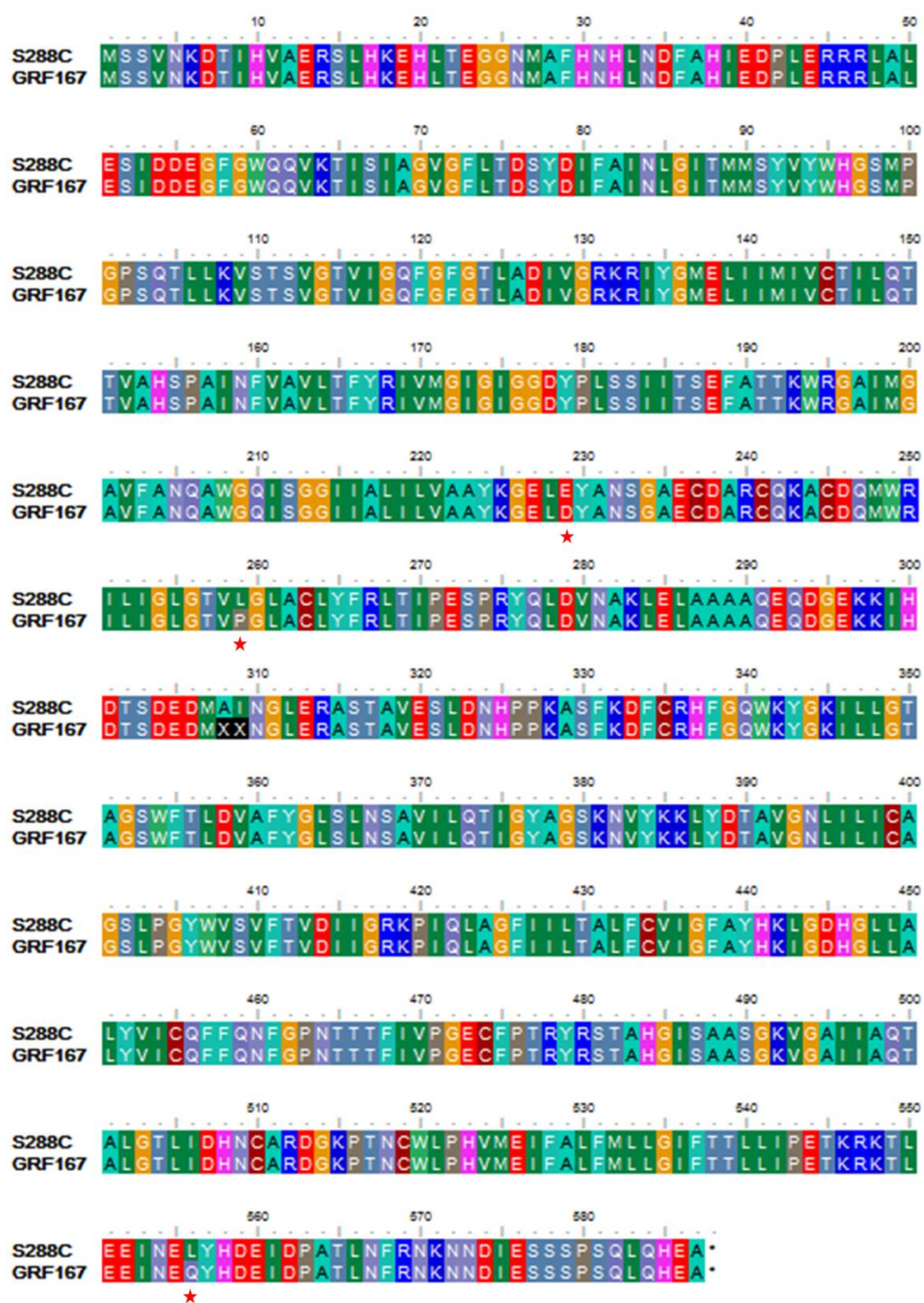
C







Supplementary Figure 5



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      10      20      30      40      50      60      70      80
S288C  ATGAGTTCCGTCAAATAAAGATACATTCATGTTGCTGAAAGAAGCTTTCATAAAAGAACCTTACCGAAGGTGGTAAACAT
GRF167  ATGAGTTCCGTCAAATAAAGATACATTCATGTTGCTGAAAGAAGCTTTCATAAAAGAACCTTACCGAAGGTGGTAAACAT
UVA     ATGAGTTCCGTTGCTAAAAGATAATATTAGTATTGCTGAAAGAAGCTTTCACAGGGAAAACCTGACTGAAGGTGGTAAACCT
      M S S V N K D T I H V A E R S L H K E H L T E G G N M
      M S S V N K D T I H V A E R S L H K E H L T E G G N M
      M S S V A K D N I S I A E R S L H R E N L T E G G N L

      90      100     110     120     130     140     150     160
S288C  GGCCTTCCACAACCAATTTGAATGATTTTGCATATTGAAGATCCTCTGGAAAAGAAGAGATTGGCTTTGGAGTCCATCCG
GRF167  GGCCTTCCACAACCAATTTGAATGATTTTGCATATTGAAGATCCTCTGGAAAAGAAGAGATTGGCTTTGGAGTCCATCCG
UVA     GGCCTTCCACAATTCATTTGAATGATTTGCCCCATATCGAAGATCCTTTGGAAAAGAAGAGATTGGCTTTGCAATCCATTCG
      A F H N H L N D F A H I E D P L E R R R L A L E S I
      A F H N H L N D F A H I E D P L E R R R L A L E S I
      A F H N H L N D F A H I E D P L E R R R L A L E S I

      170     180     190     200     210     220     230     240
S288C  ATGACGAAAGGTTTGGTGGCAACAAGTTAAGACCATCTCCATTGCTGGTGGTTGGTTTCTTGACAGATTCTTATGATATT
GRF167  ATGACGAAAGGTTTGGTGGCAACAAGTTAAGACCATCTCCATTGCTGGTGGTTGGTTTCTTGACAGATTCTTATGATATT
UVA     ATAAACGAAAGGTTTGGTGGCAACAAGTTCAAGACCATCTCCATTGCTGGTGGTTGGTTTCTTGACAGATTCTGATGATATC
      D D E G F G W Q Q V K T I S I A G V G F L T D S Y D I
      D D E G F G W Q Q V K T I S I A G V G F L T D S Y D I
      D N E G F G W Q Q V K T I S I A G V G F L T D S Y D I

      250     260     270     280     290     300     310     320
S288C  TTTGCCATTAATTTGGGTATCACTATGATGTCCTACGTTTACTGGCACGGTAGTATGCCAGGTCCAAGTCAAACCTTGTGT
GRF167  TTTGCCATTAATTTGGGTATCACTATGATGTCCTACGTTTACTGGCACGGTAGTATGCCAGGTCCAAGTCAAACCTTGTGT
UVA     TTCGCCATCAACTTGGGTATCTCCATGATGTCCTACTGGCACGGTAGCATGCCAGTTCAGTCAAACCTTGTGT
      F A I N L G I T M M S Y V Y W H G S M P G P S Q T L L
      F A I N L G I T M M S Y V Y W H G S M P G P S Q T L L
      F A I N L G I S M M S Y V Y W H G D M P A S S Q T L L

      330     340     350     360     370     380     390     400
S288C  GAAAGTTTCCACTTCGTTGGTACTGTTATTTGGTCAATTTGGTGGTGGTACTTATGATATTGTTGGTGGTAAAGAGAA
GRF167  GAAAGTTTCCACTTCGTTGGTACTGTTATTTGGTCAATTTGGTGGTGGTACTTATGATATTGTTGGTGGTAAAGAGAA
UVA     GAAAGTTTCCACTTCGTTGGTACTGTTATTTGGTCAAGTGGTGGTGGTACTTATGGCCGATATCGTTGGTGGTAAAGAGA
      K V S T S V G T V I G Q V G F G T L A D I V G R K R
      K V S T S V G T V I G Q V G F G T L A D I V G R K R
      K V S T S V G T V I G Q V G F G T L A D I V G R K K

      410     420     430     440     450     460     470     480
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GRF167  TTTATGGTATGGAACTTATTATCATGATTGCTGTACCATTTCTGAAAACCACTGTTGCTCATTCTCCTGCTATTAACTTC
UVA     TTTATGGTTTGGAACTTATTATCATGATTGTTGTACCATTTTGAACCAACCTGCGTCACTCTCCTGCCATCAACTTC
      I Y G M E L I I M I V C T I L Q T T V A H S P A I N F
      I Y G M E L I I M I V C T I L Q T T V A H S P A I N F
      I Y G L E L I I M I V C T I L Q T T V A H S P A I N F

      490     500     510     520     530     540     550     560
S288C  GTTGGTGTTTTAACTTCTACCGTATTGTCATGGGTATTGGTATCGGTGGTGACTACCCAGTATCTTCTATTATTAATTC
GRF167  GTTGGTGTTTTAACTTCTACCGTATTGTCATGGGTATTGGTATCGGTGGTGACTACCCAGTATCTTCTATTATTAATTC
UVA     GTTGCCGTTTGAACCTTCTACCGTATTGTCATGGGTATTGGTGGTGACTACCCCTATCTTCTATTATTAATTC
      V A V L T F Y R I V M G I G I G G D Y P L S S I I T S
      V A V L T F Y R I V M G I G I G G D Y P L S S I I T S
      V A V L T F Y R I V M G I G I G G D Y P L S S I I T S

      570     580     590     600     610     620     630     640
S288C  TGAATTTGCCACTACCAAAAGGAGAGGTCGCATCATGGGTGCTCTTTGCTAAACCAAGCTTGGGGTCAAATTCACGGTTC
GRF167  TGAATTTGCCACTACCAAAAGGAGAGGTCGCATCATGGGTGCTCTTTGCTAAACCAAGCTTGGGGTCAAATTCACGGTTC
UVA     TGAATTTGCTACTACCAAAAGGAGAGGTCGCATCATGGGTGCCCTCTTCGCCAACCAAGCTTGGGGTCAAATTCACGGTTC
      E F A T T K W R G A I M G A V F A N Q A W G Q I S G
      E F A T T K W R G A I M G A V F A N Q A W G Q I S G
      E F A T T K W R G A I M G A V F A N Q A W G Q I S G

      650     660     670     680     690     700     710     720
S288C  CTATCATCGCCTTATCTTGGTTCCTGCTTCAAGGGCGAACTAGAAATACGCAAACTCTGCTGCTGAATGTGATGCTAGA
GRF167  CTATCATCGCCTTATCTTGGTTCCTGCTTCAAGGGCGAACTAGAAATACGCAAACTCTGCTGCTGAATGTGATGCTAGA
UVA     CTATCATCGCCTTATTTTGGTTCCTGCTTCAAGAAATGACTTAAACTATGCTAACTCCCGTCCGCAATGTGACGCCAGA
      G I I A L I L V A A Y K G E L E Y A N S G A E C D A R
      G I I A L I L V A A Y K G E L D Y A N S G A E C D A R
      G I I A L I L V A A Y K N D L N Y A N S G A E C D A R

      730     740     750     760     770     780     790     800

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S288C TGTCAAAAAGGCTTGTGACCAAAATGTGGAGAAATCCCTTATTGGGTTGGGTACCGTTCTAGGGTTGGCATGTTTGTATTTTCAG
C Q K A C D Q M W R I L I G L G T V L G L A C L Y F R
GRF167 TGTCAAAAAGGCTTGTGACCAAAATGTGGAGAAATCCCTTATTGGGTTGGGTACCGTTCCAGGTTTGGCATGTTTGTATTTTCAG
C Q K A C D Q M W R I L I G L G T V P G L A C L Y F R
UVA TGTCAAAAAGGCTTGTGACCAAAATGTGGAGAGTGCCTTATTGGTTTAGGTACCGTCCAGGTTTGGCTATGCTGTACTTCAG
C Q K A C D Q M W R V L I G L G T V P G L L C L Y F R

810 820 830 840 850 860 870 880
S288C ATTAACTATTCCAGAAATCTCCTAGATATCAATTGGATGTTAACGCTAAGTTGGAACTTGC TGCTGCCGCACAAGAAACA
L T I P E S P R Y Q L D V N A K L E L A A A A Q E Q
GRF167 ATTGACTATTCCAGAAATCTCCTAGATATCAATTGGATGTTAACGCTAAGTTGGAACTTGC TGCTGCCGCACAAGAAACA
L T I P E S P R Y Q L D V N A K L E L A A A A Q E Q
UVA ATTGACCATTCCAGAAATCCCAAGATATCAATTAGAGCTTAATGCTGAATTG --- TTGGCTGTTGAAAAGAAAGAAACA
L T I P E S P R Y Q L D V N A E L L R V E K K E Q

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S L D N H P P K A S F K D F C R H F G Q W K Y G K I
GRF167 ATCTCTTGACAATCATCCTCCAAAAGGCTTCTCAAGATTTCTGCAGACATTTTGGTCAATGGAAGTACGGTAAAGATTT
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UVA ATCCATGACATGCAATCCTCCAAAAGGCTTCAATCAAGATTTCTGCAGACATTTTGGTCAATGGAAGTAAAGATTT
S I D M H P P K A S F K D F C K H F G Q W K Y G K I

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L L G T A G S W F T L D V A F Y G L S L N S A V I L Q
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 S T A H G I S A A S G K I G A I I A Q T A L G T L I

1530 1540 1550 1560 1570 1580 1590 1600

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 D H N C A R D G K P T N C W L P H V M E I F A L F M L
UVA ACCAACTGTGCCAAGGACGGTAAGGCCAATAACTGTGGTTACCTCACGTCATGGAAAATTTTCGCCTTTTATGTTA
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1610 1620 1630 1640 1650 1660 1670 1680

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 L G I F T T L L I P E T K R K T L E E I N E Q Y H D E
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 L G I F T T L L I P E T K R K T L E E I N E K Y H D E

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 I D P G T L N Y R N K M N D V E S S S P S Q I Q H *

S288C CATAA ---
 A *

GRF167 CATAA ---
 A *

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 A Y *