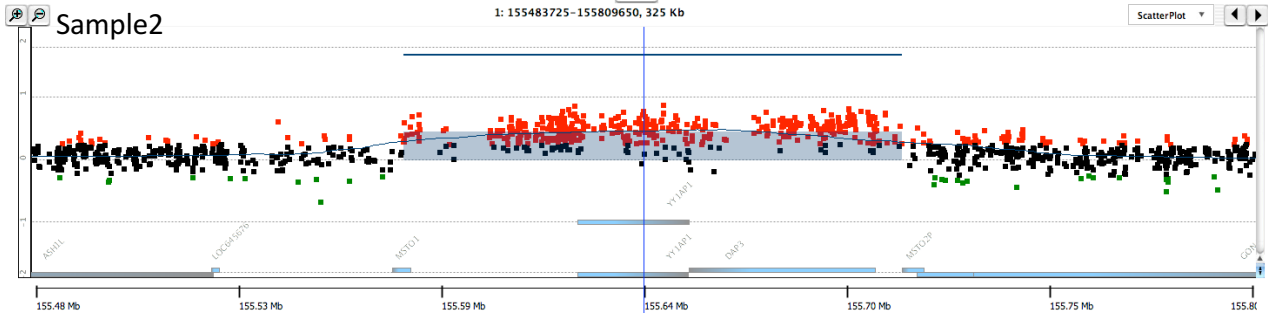
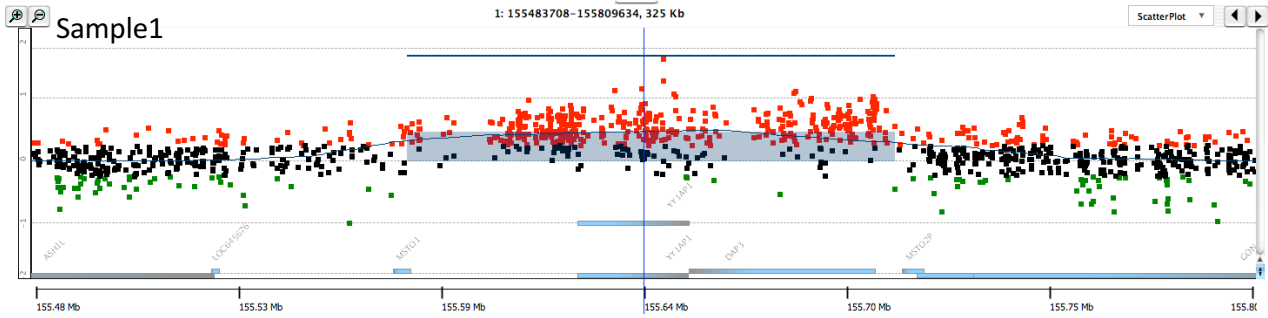
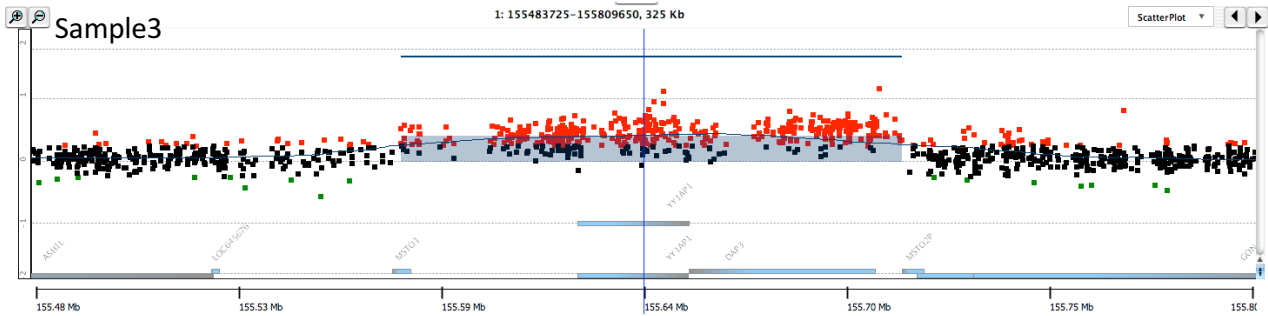


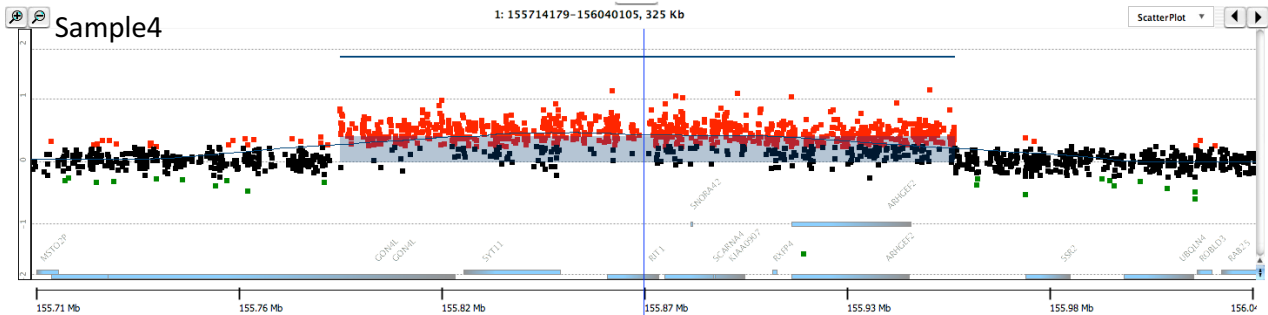
Supplemental Fig S7. A summary figure showing the results of 89 aCGHs and 53 nucleotide-level breakpoint junctions. Red dots signify relative copy number gain of that specific interrogating oligonucleotide probe and thus in aggregate indicate the genomic interval duplicated, and green dots indicate copy number loss. For each of the 53 samples with breakpoint junctions solved at nucleotide-level resolution, we showed the sequences at the junctions under the aCGH result. The first line of sequence shows the reference sequence on the 5' end; the middle line shows the sample sequence; and the bottom line shows the 3-end reference sequence. The sequences are on the plus strand. The repetitive elements covering the breakpoints and their orientation are annotated near the relative reference sequences. The sequence of microhomology at the breakpoint junction is highlighted in red. The grey sequence starts from the first mismatching base. For those with no microhomology at the breakpoints, we colored the first base near the aligned sequence in green and documented its position. The genomic coordinates of the microhomologies are annotated in hg19 assembly.



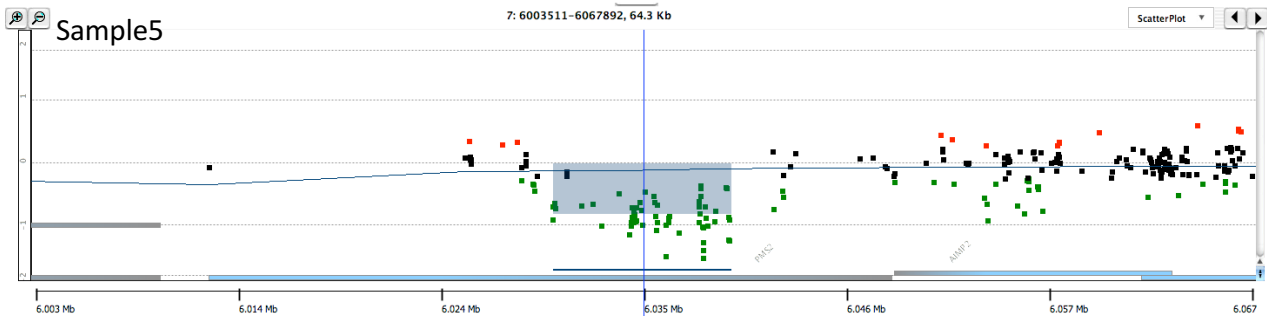
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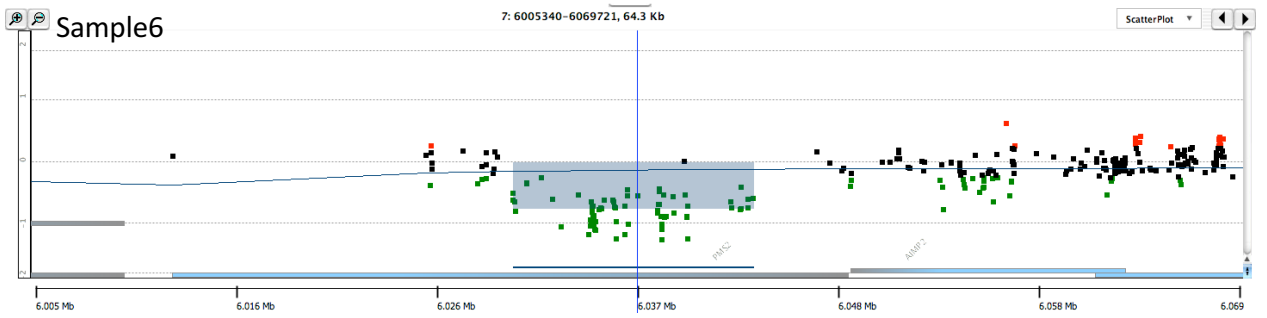
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 LCR +



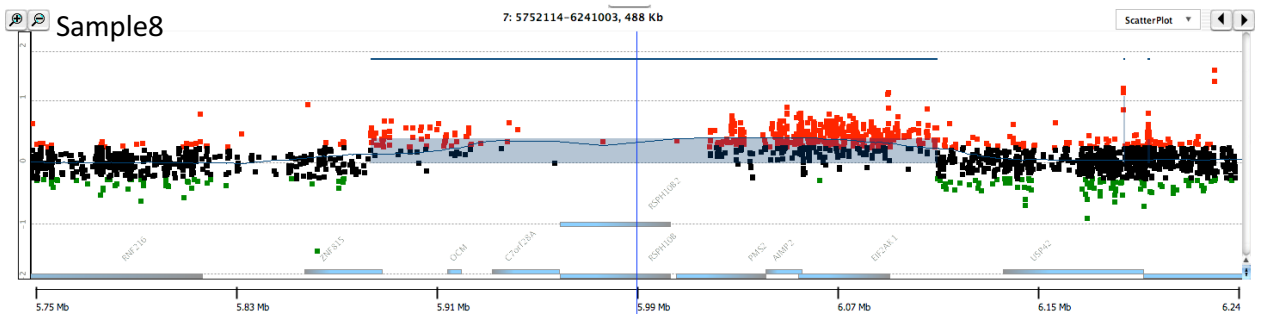
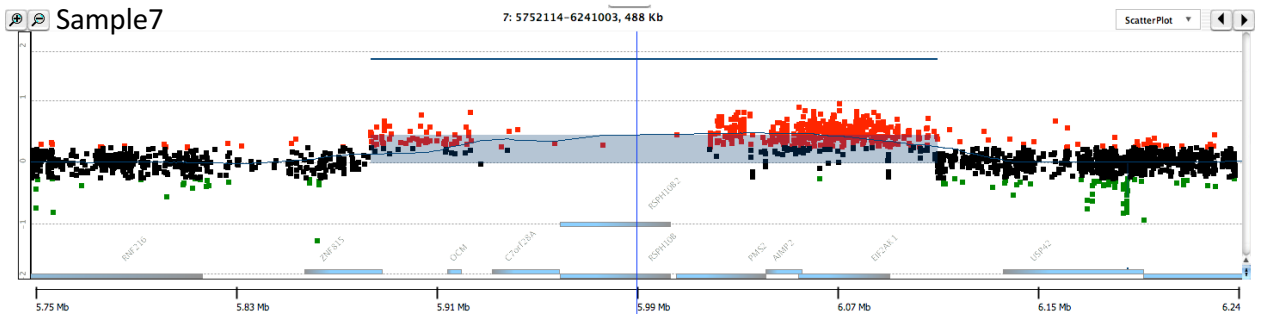
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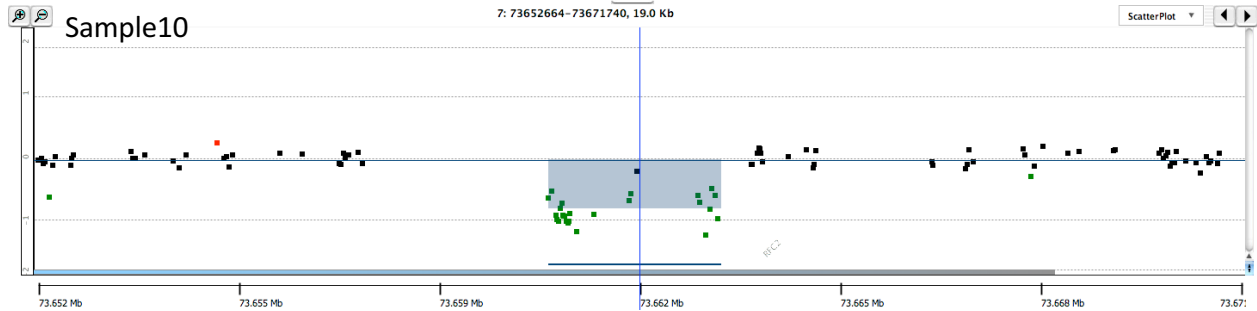
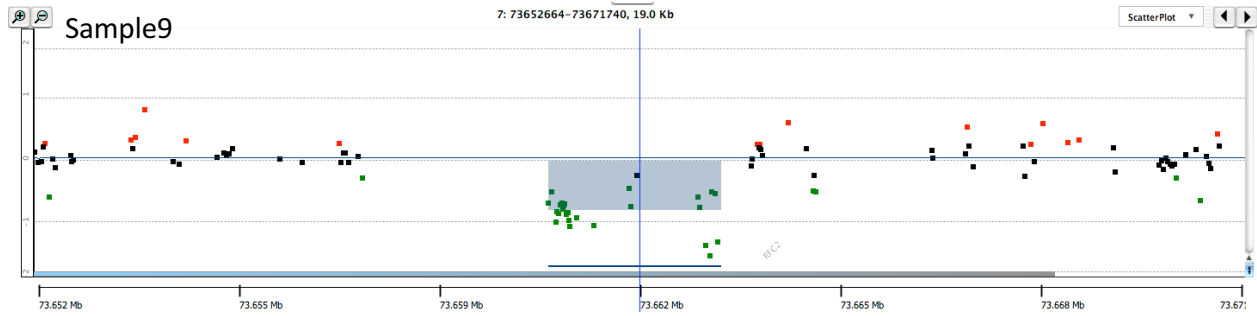


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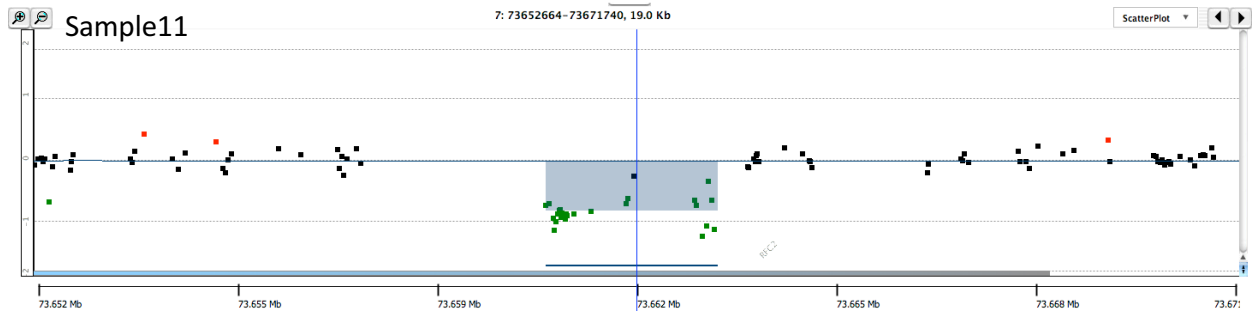


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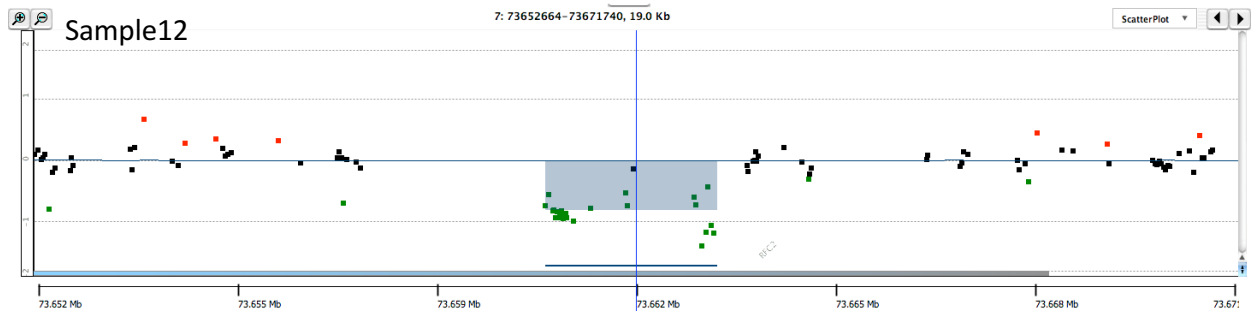




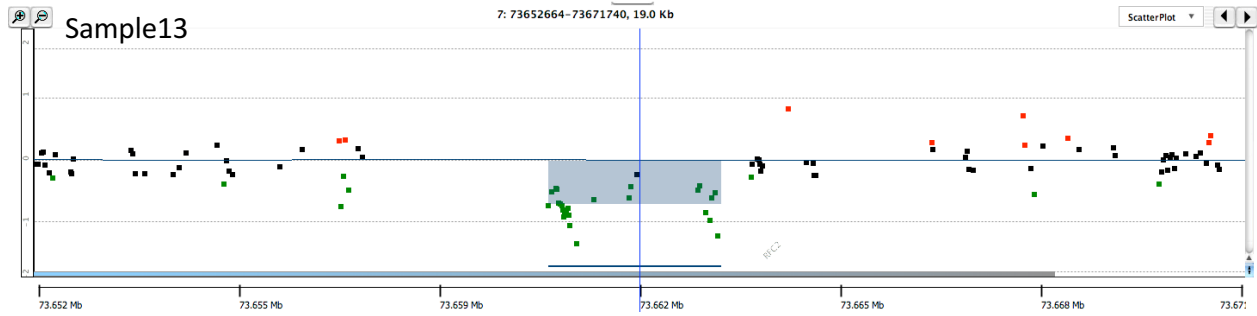
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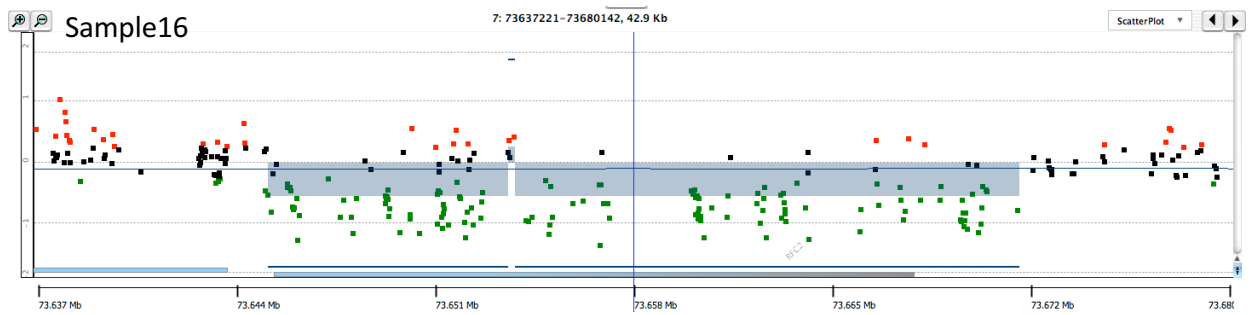
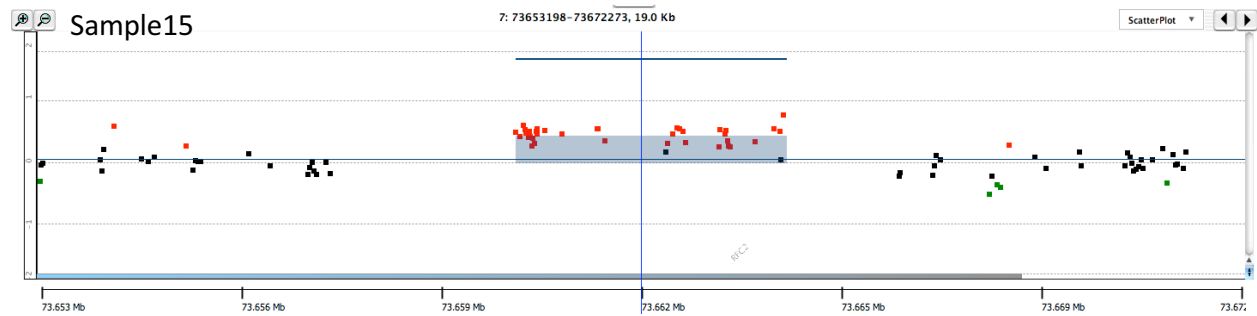
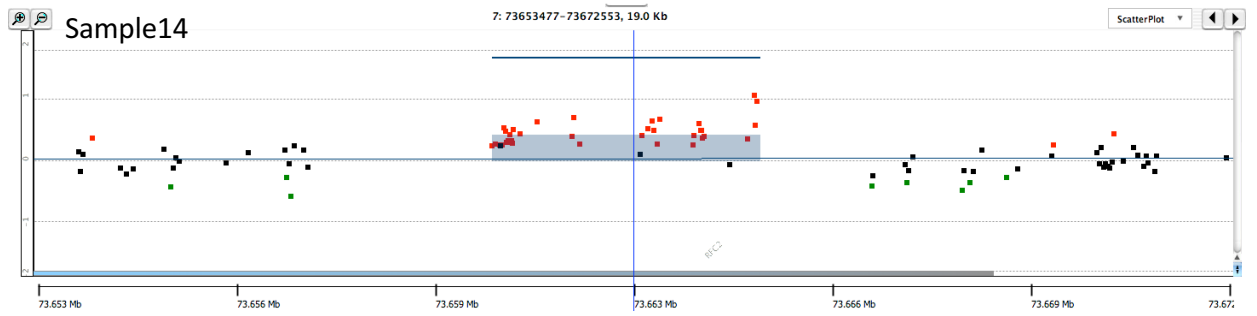
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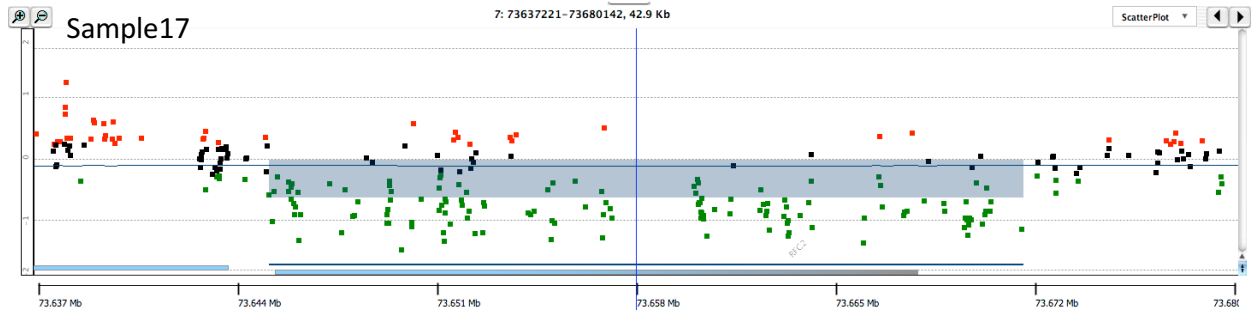
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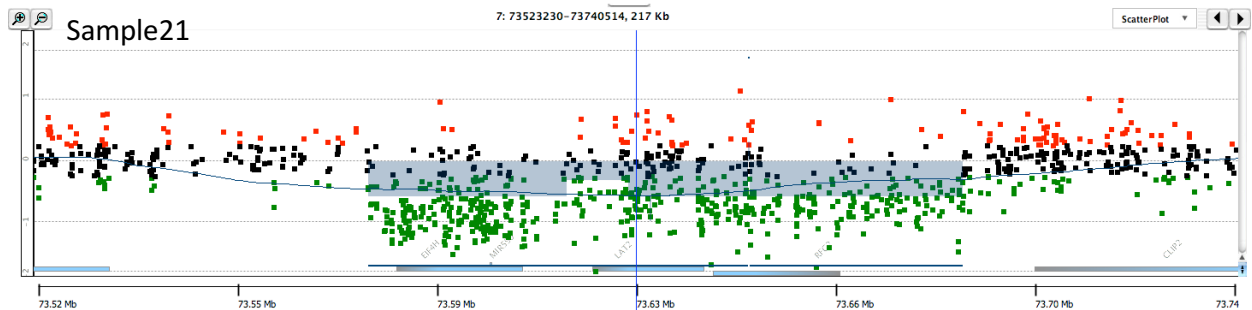
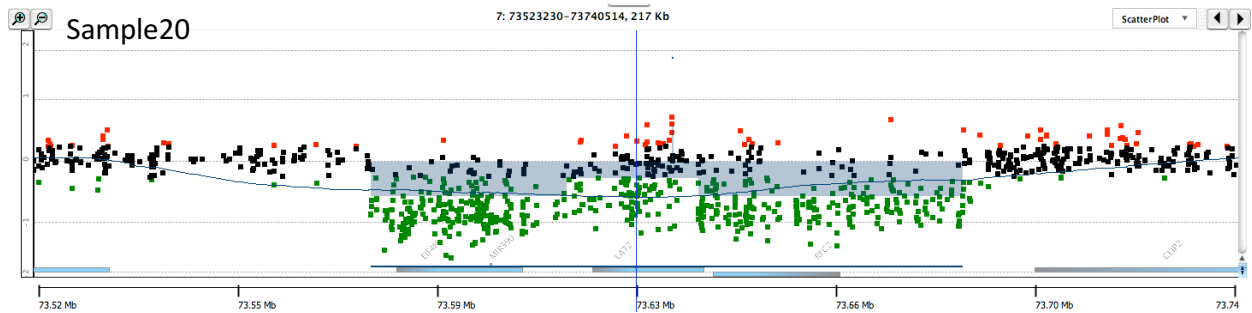
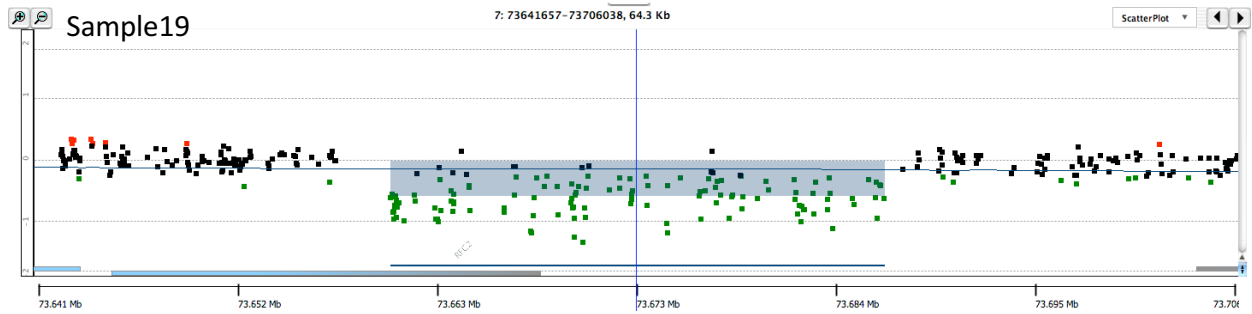
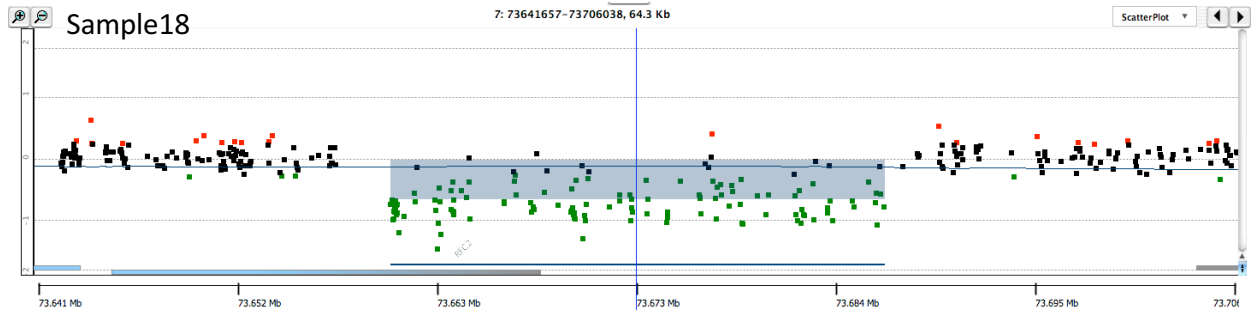
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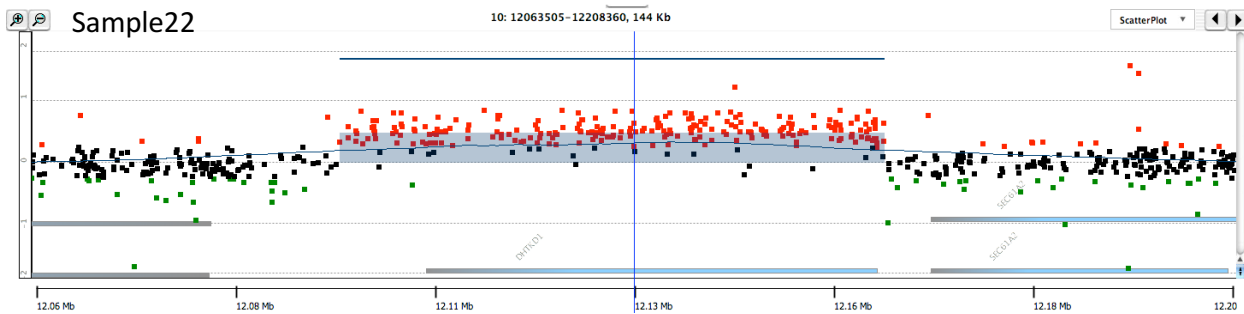


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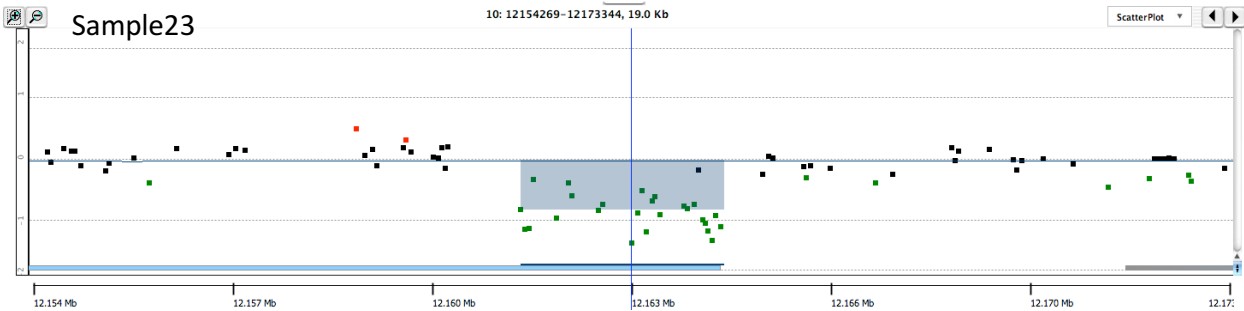


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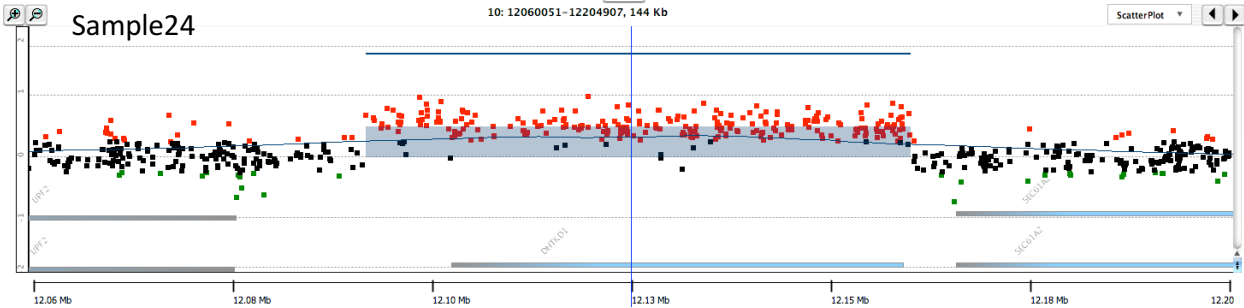




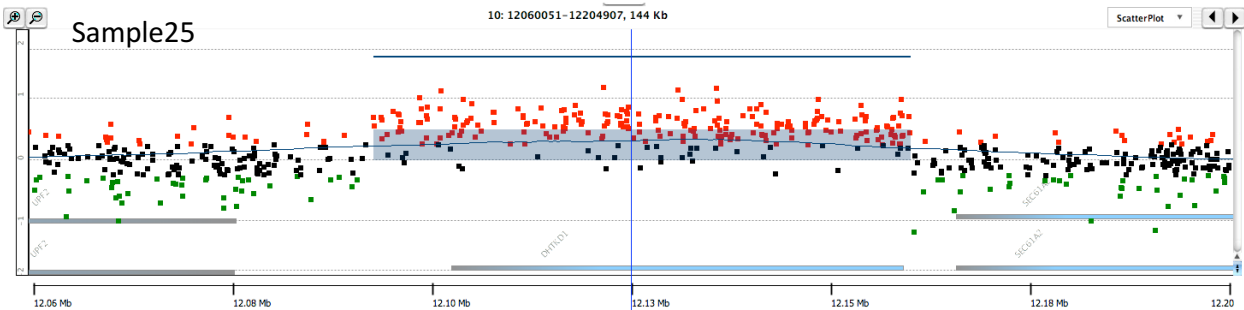
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AluY + Chr10:12100331-12100345



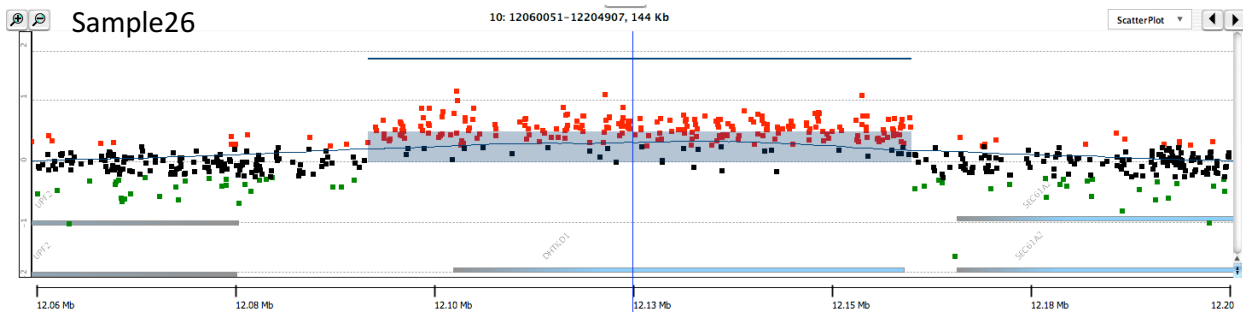
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 GCAGGAGAATCACTTGATCT**GGGAGGCGGAGG**TTCAGTGAGCCGAGATTGCACCCTGTACTCCAGCC
AluY + Chr10:12165521-12165532 C,rs12784869



AluSx + Chr10:12166163-12166177
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AluY + Chr10:12100331-12100345

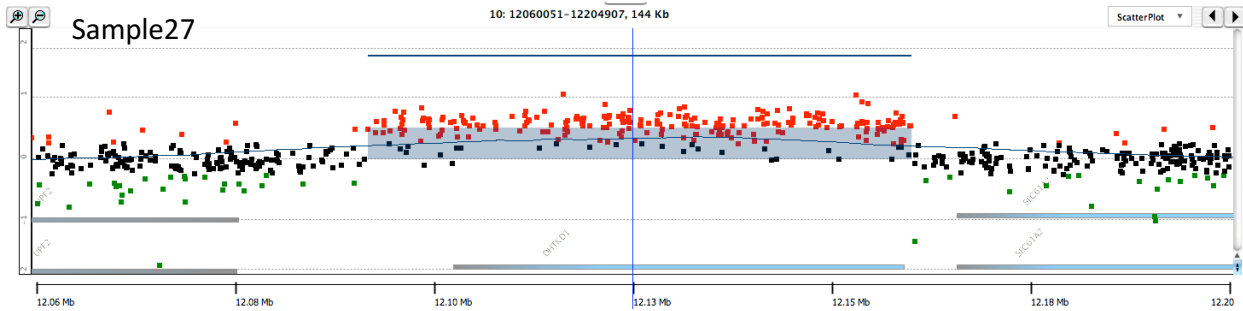


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AluY + Chr10:12100331-12100345



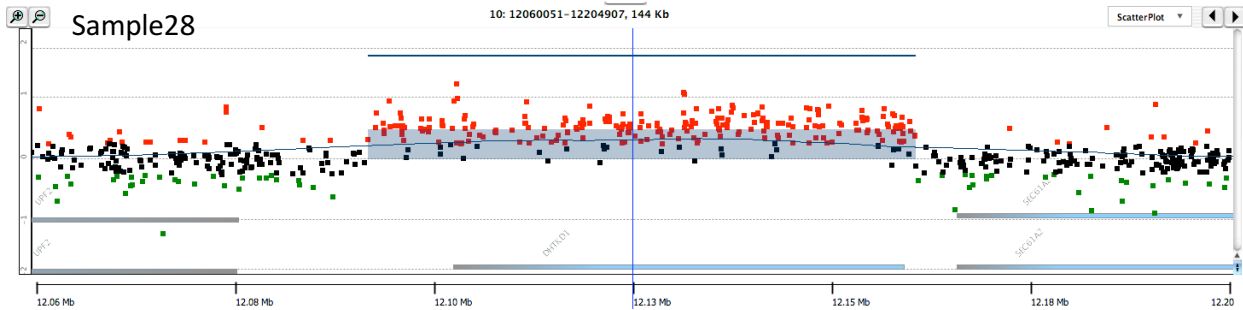
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AluY + Chr10:12100331-12100345



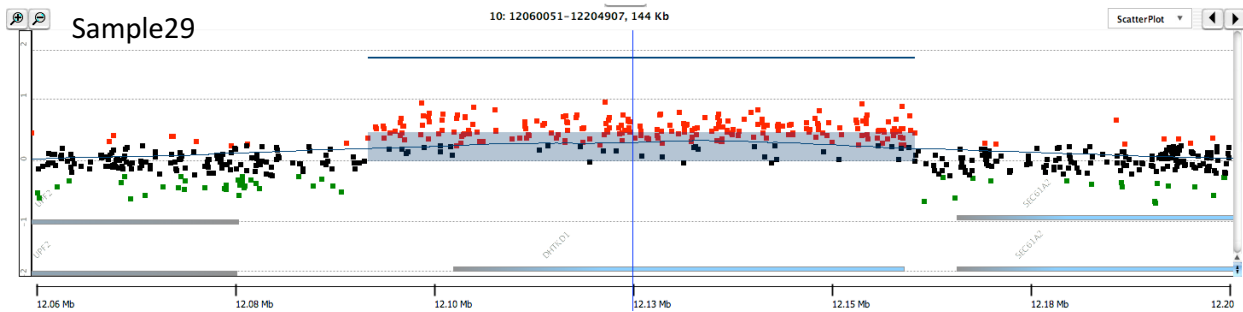
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AluY + Chr10:12100331-12100345



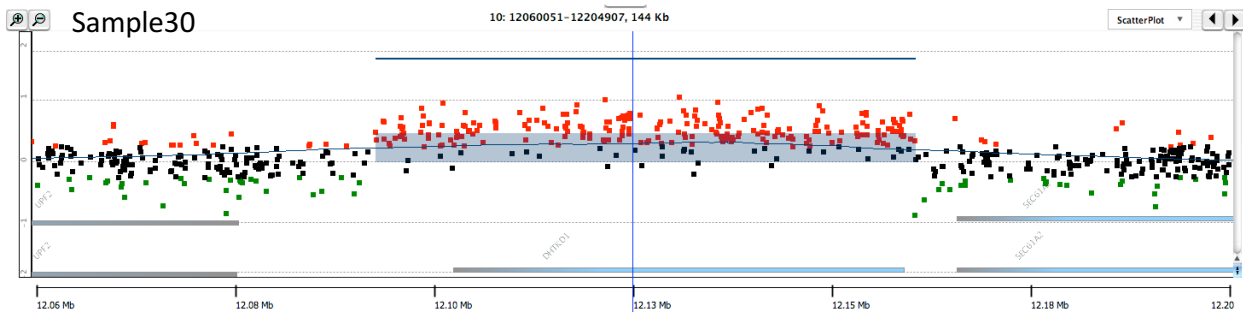
Sample28
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AluSx + Chr10:12166163-12166177
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AluY + Chr10:12100331-12100345



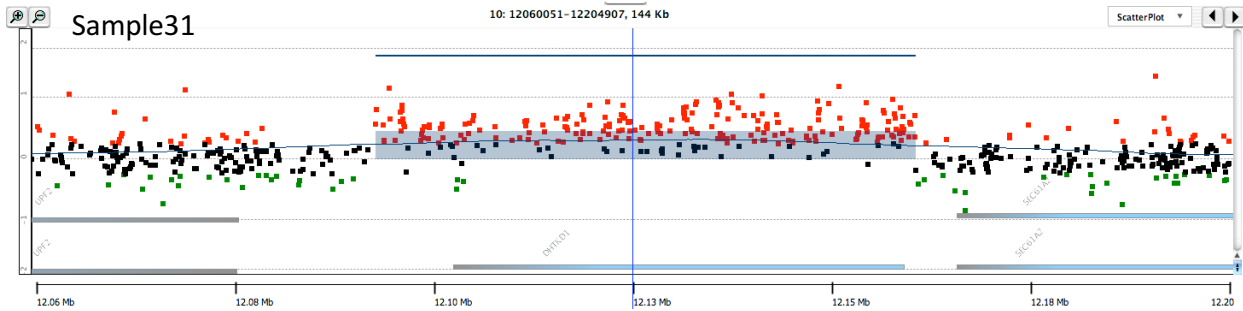
Sample29
10: 12060051-12204907, 144 Kb

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AluY + Chr10:12100331-12100345



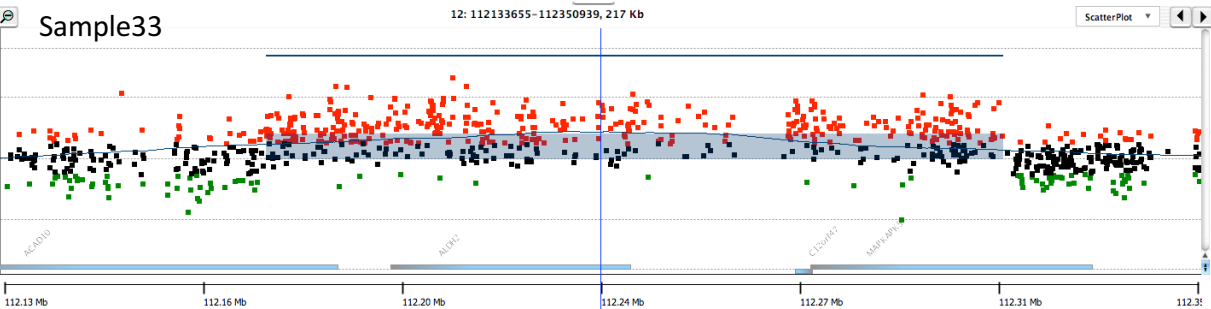
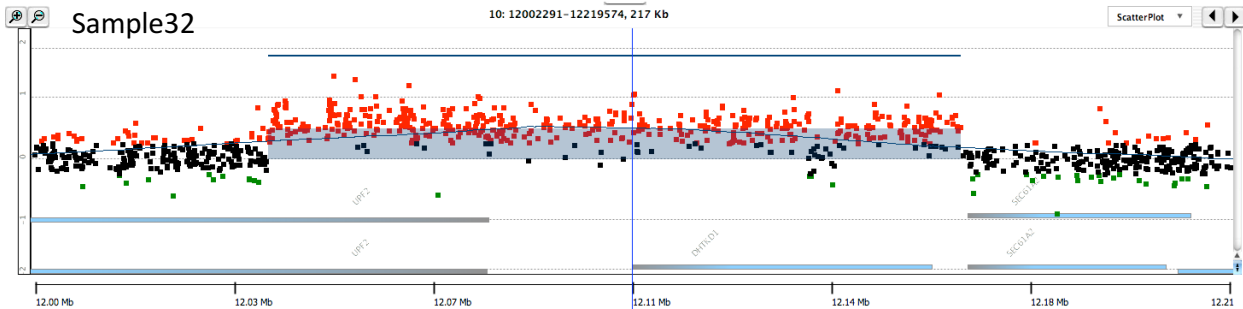
Sample30 10: 12060051-12204907, 144 Kb ScatterPlot

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 TGGCTCATGCTTGTAATCCCG**GCACTTTGGGAGGCT**GAGGCGGGCGGATCATGAGGTCAGGAGATCGAGA
 TGGCTCATGCCTGTAATCCCA**GCACTTTGGGAGGCT**GAGGCGGGCGGATCATGAGGTCAGGAGATCGAGA
AluY + Chr10:12100331-12100345



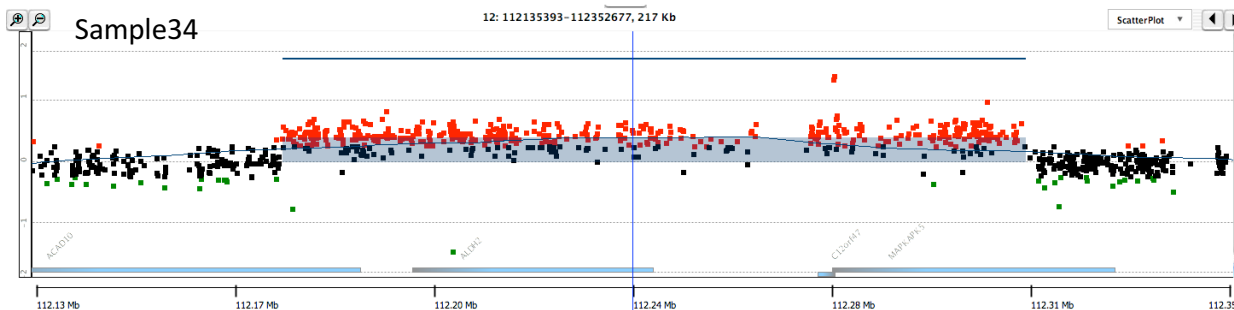
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AluY + Chr10:12100331-12100345

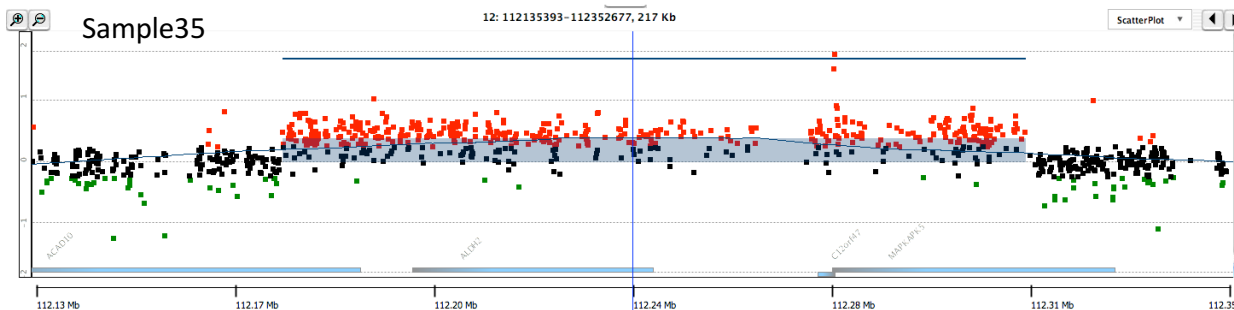


Sample33 12: 112133655-112350939, 217 Kb ScatterPlot

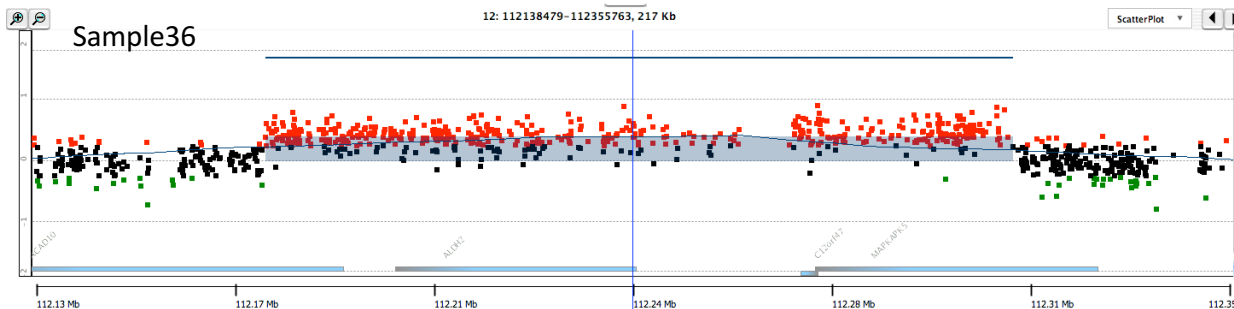
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AluSq2 - Chr12:112180759-112180769



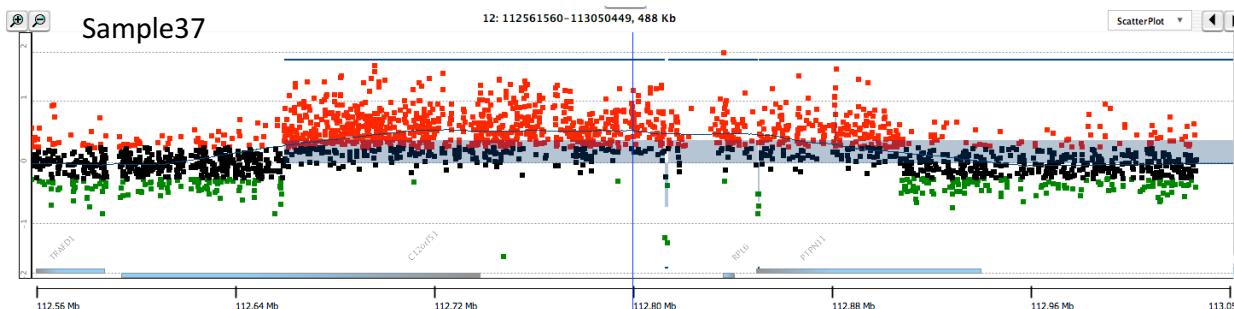
Sample34
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 AluSq2 - Chr12:112180759-112180769



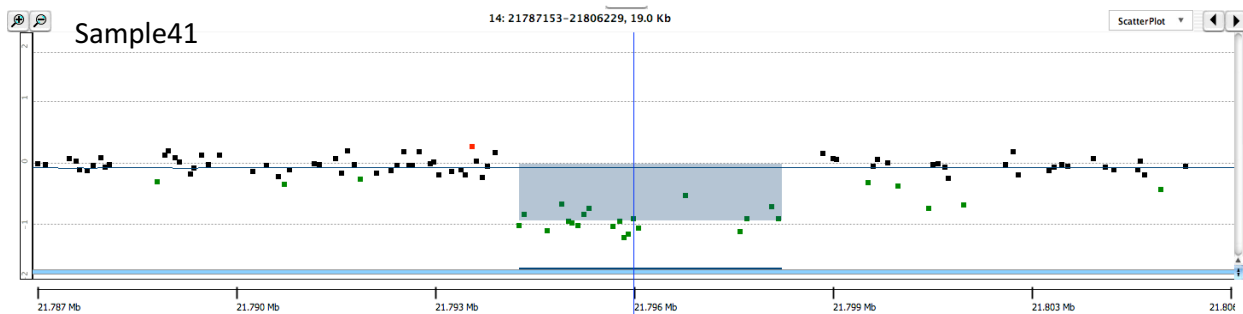
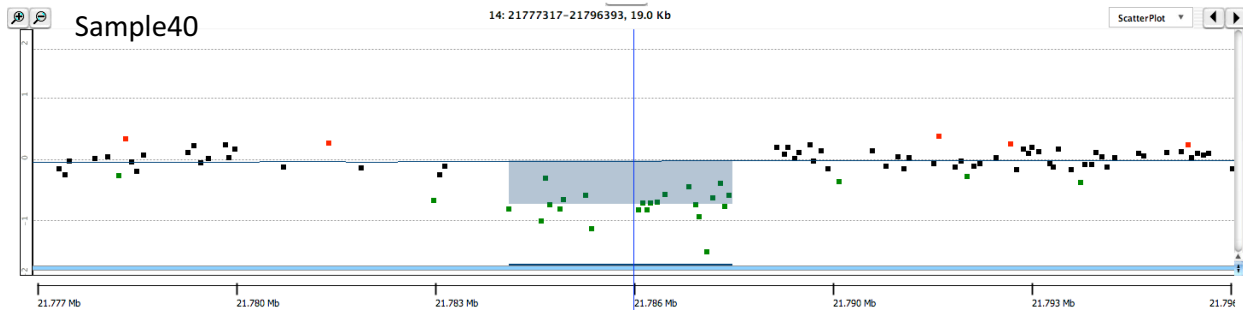
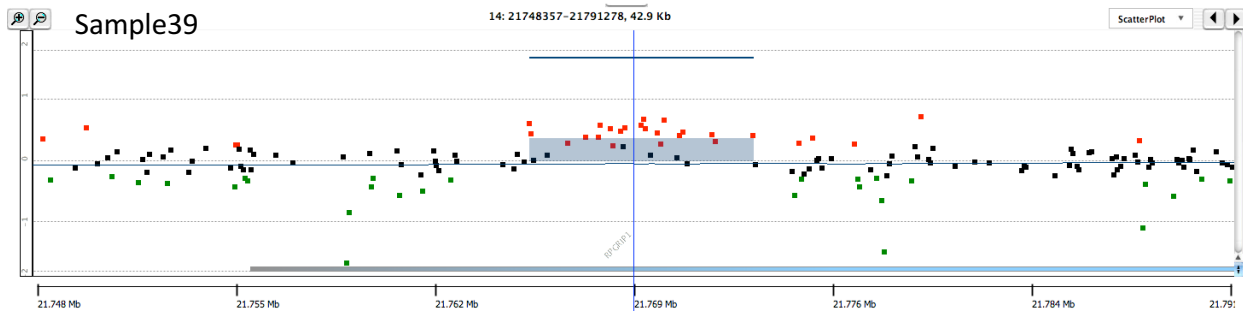
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 AluSq2 - Chr12:112180759-112180769



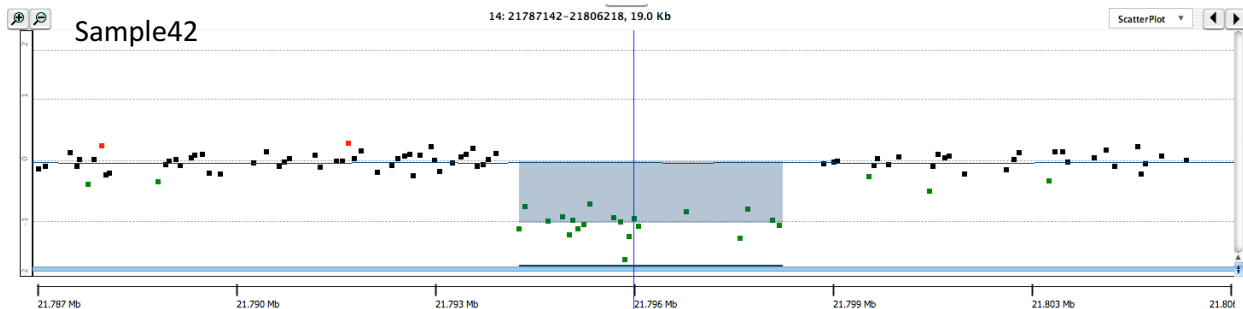
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 TCTGGGCTCAAGTGATCCTCCTG**CCTCAGCCTCC**CAAAGTGCTGGGGTTACAGGCGTGAGCCAAAGCACC
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 AluSq2 - Chr12:112180759-112180769



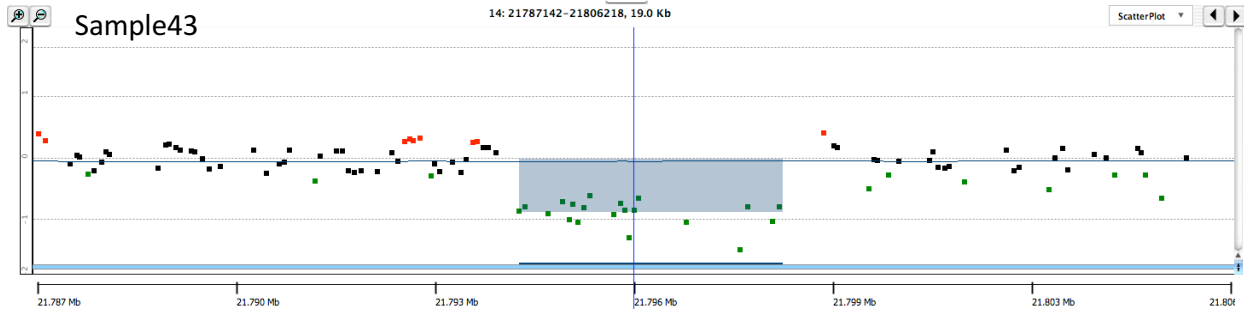
Sample37
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 AluSq2 - Chr12:112180759-112180769



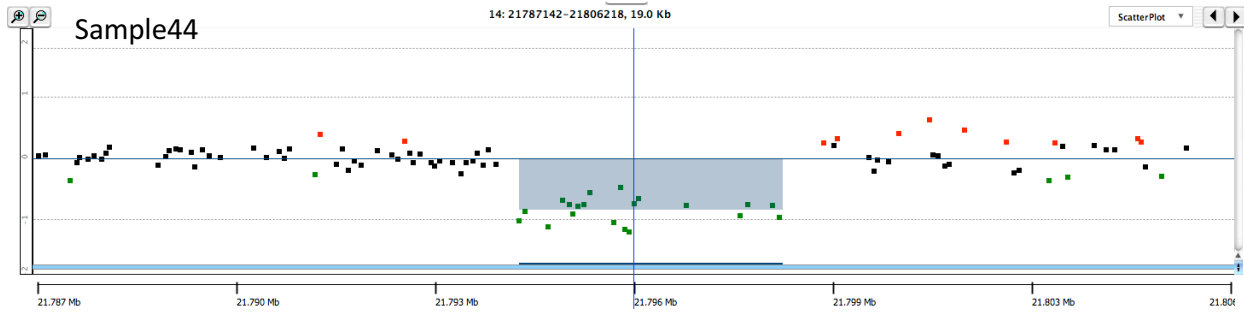
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AluSx - Chr14:21799320-21799345



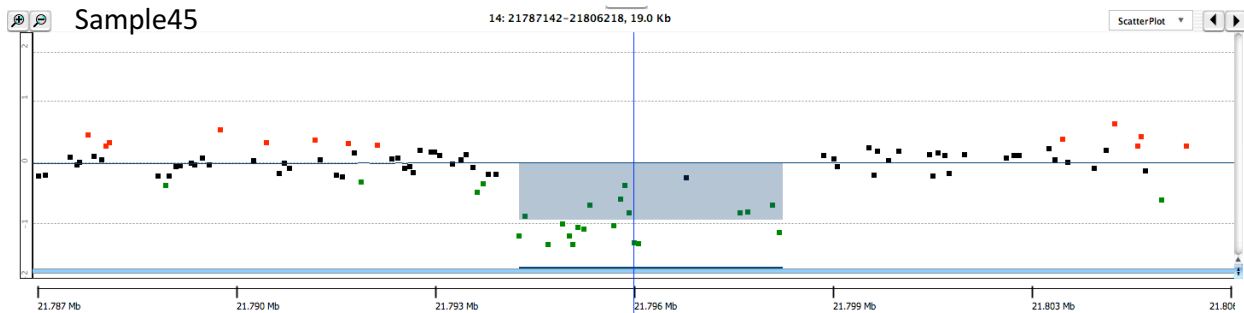
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AluSx - Chr14:21799320-21799345



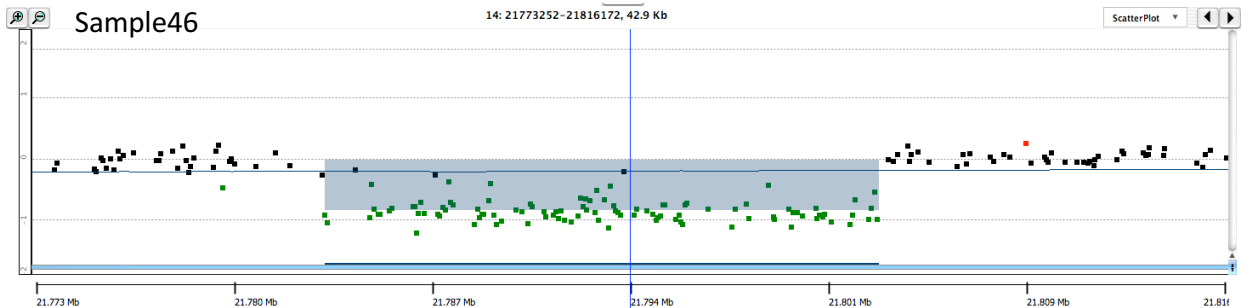
Sample43
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 AluSx - Chr14:21799320-21799345



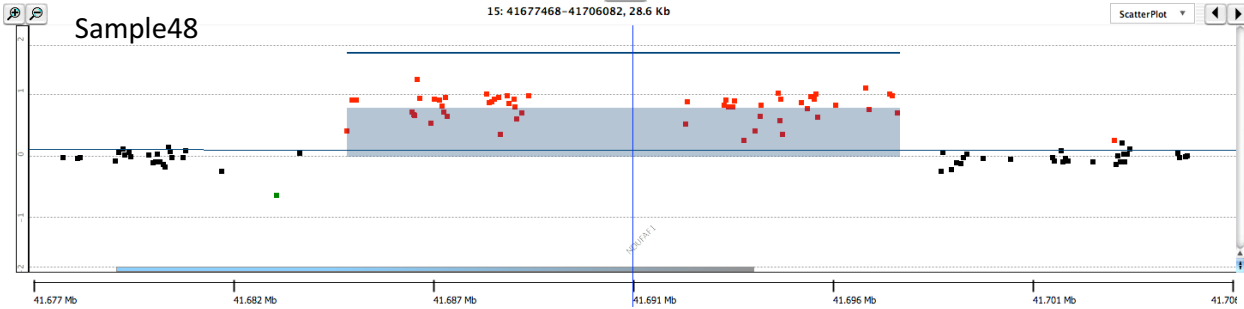
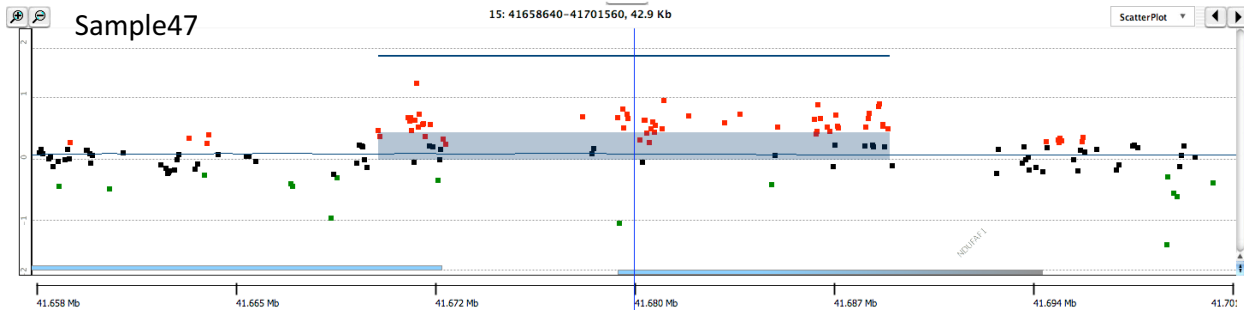
Sample44
 14: 21787142 - 21806218, 19.0 Kb
 AluSp - Chr14:21794781-21794806
 GACCTCAGGTGAACCTCCCACCTGAGCCTCCCAAAGTGCTGGGATTACAGACGTGAGCCACCGCGCCTGG
 GACCTCAGGTGAACCTCCCACCTGAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCGA
 GACCTTAGGTGATCCGCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCGA
 AluSx - Chr14:21799320-21799345



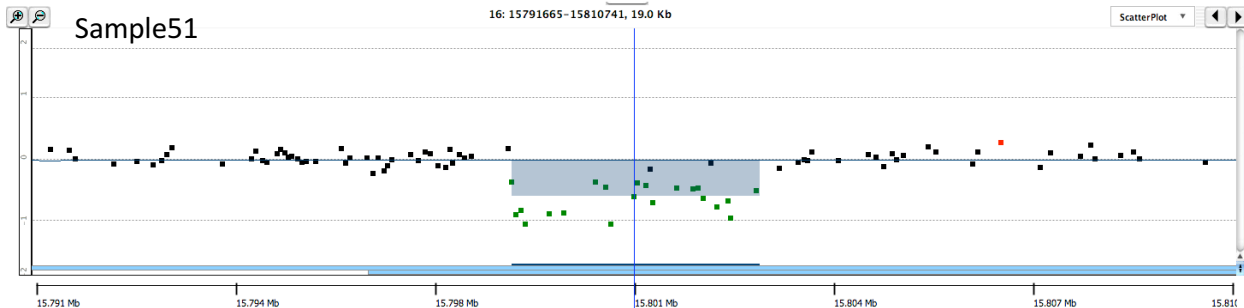
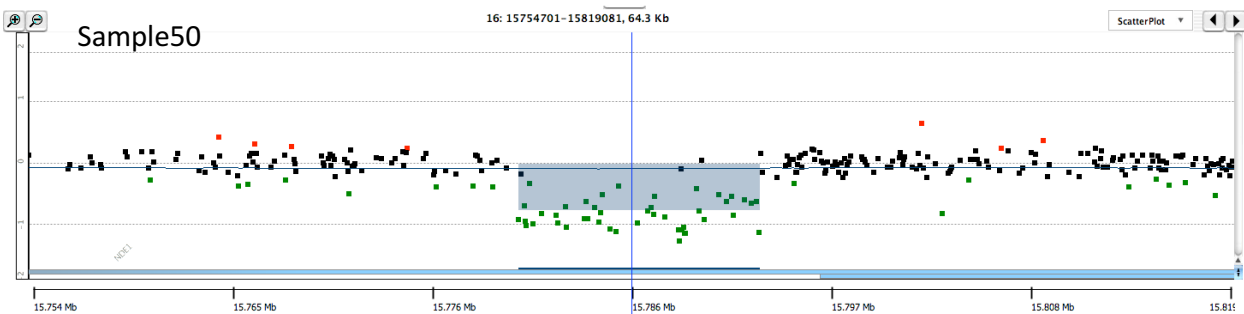
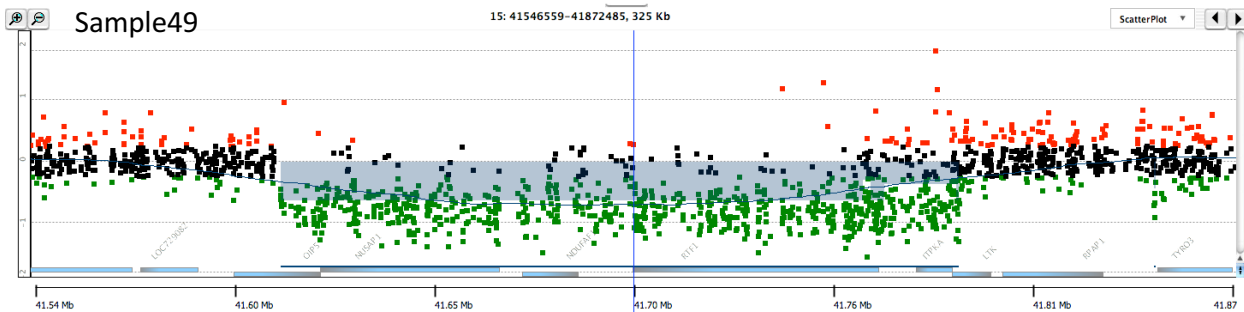
Sample45
 14: 21787142 - 21806218, 19.0 Kb
 AluSp - Chr14:21794781-21794806
 GACCTCAGGTGAACCTCCCACCTGAGCCTCCCAAAGTGCTGGGATTACAGACGTGAGCCACCGCGCCTGG
 GACCTCAGGTGAACCTCCCACCTGAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCGA
 GACCTTAGGTGATCCGCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCGA
 AluSx - Chr14:21799320-21799345



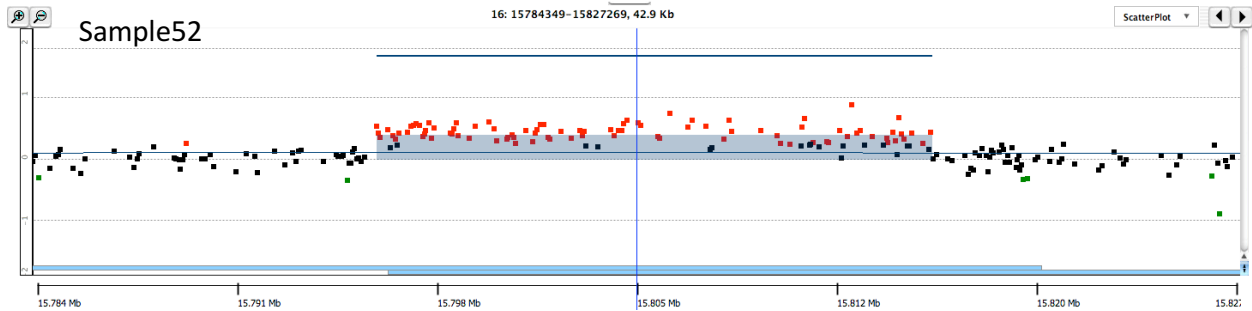
Sample46
 14: 21773252 - 21816172, 42.9 Kb



AluSq2 - Chr15:41698386-41698406
 TTGGTCAGGCTAGTCTGC **AACTCCTGACCTCAGGTGATC** CACCCGCCTCAGCCTCCCAAAGTGCTGGGAT
 TTGGTCAGGCTAGTCTGC **AACTCCTGACCTCAGGTGATC** TGCCCATCTCAGCCTCCCAAAGTGCTGGGAT
AluSx3 - Chr15:41684493-41684513
 TAGACCAGGCTGGTCTCA **AACTCCTGACCTCAAGTGATC** TGCCCATCTCAGCCTCCCAAAGTGCTGGGAT

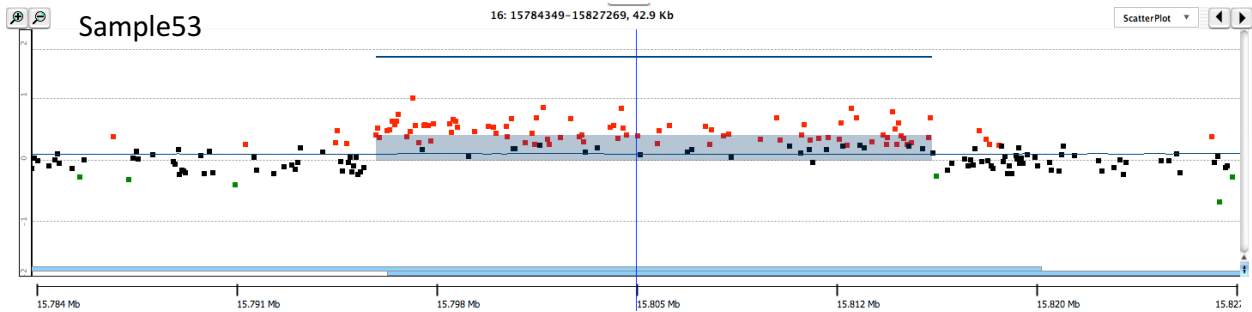


Chr16:15799291-15799291
 TGGTCACGTGAGGGGAGACTTTGGGTAGGAGGAAGA **GAGTGGGCAGAAGAAGGAAAAATCAGATCTGCCT**
 TGGTCACGTGAGGGGAGACTTTGGGTAGGAGGAAGATTACAGGGATTACAGGTGTGAGCCACTGCACCCG
 TGACCTCAAGTGATCCACCCACCTCGGCCTCCCAAAGAGC **TGGGATTACAGGTGTGAGCCACTGCACCCG**
AluSz - Chr16:15803439-15803439



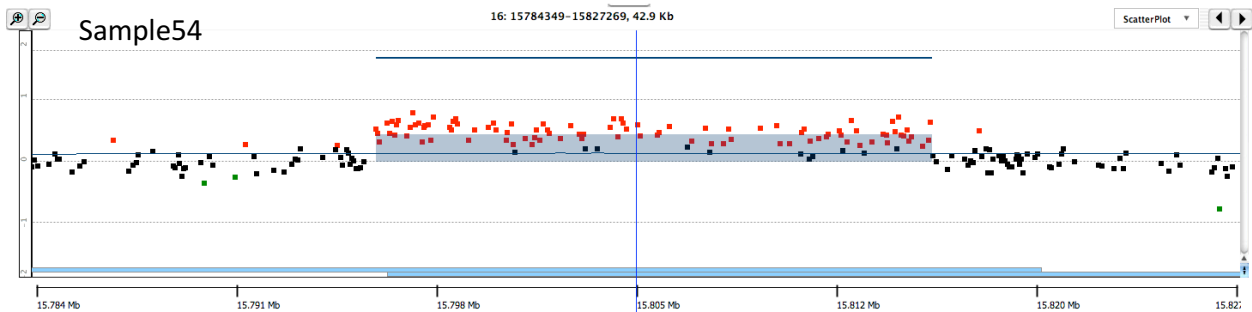
16: 15784349-15827269, 42.9 Kb

Chr16:15816331-15816331
 AGCCAAACTTCCAGTATTCAGCAAAGACAGGGACCTCTAAATGGCACAGTCAACACAAAAATCCCACACT
 AGCCAAACTTCCAGTATTCAGCAAAGTATTCAGCCAGTATTCCTGGCTCACATGATCCTCCTGCCTTAGC
 CAGTGCAGTGGCGTGATCATAGCTCACTGCAGCCTGGAACTCCTGGCTCACATGATCCTCCTGCCTTAGC
 AluJr - Chr16:15796336-15796336



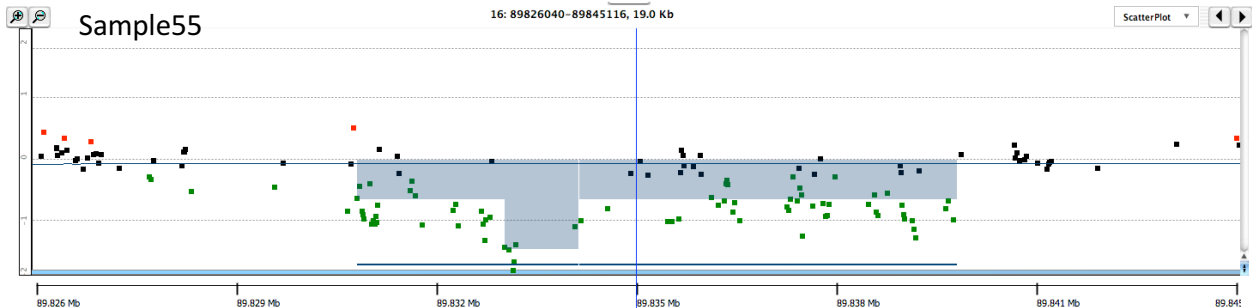
16: 15784349-15827269, 42.9 Kb

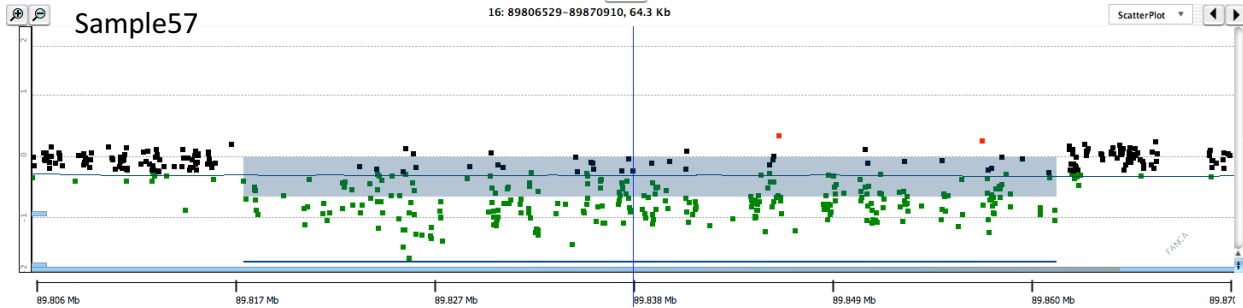
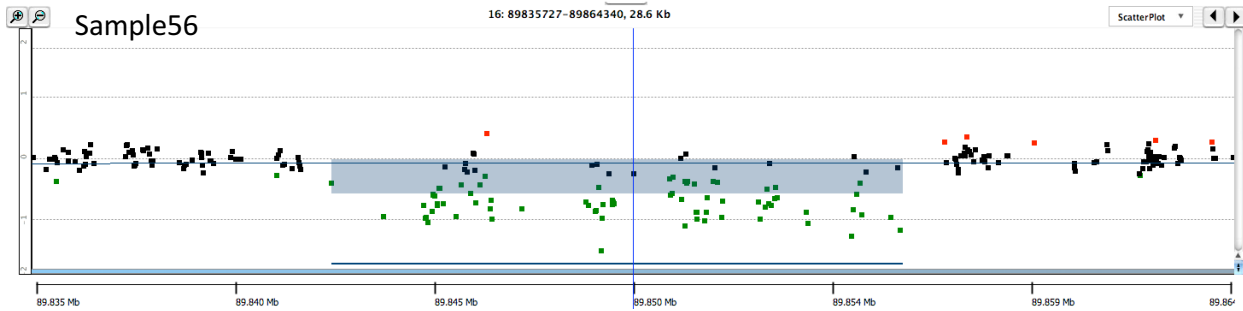
Chr16:15816331-15816331
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 AGCCAAACTTCCAGTATTCAGCAAAGTATTCAGCCAGTATTCCTGGCTCACATGATCCTCCTGCCTTAGC
 CAGTGCAGTGGCGTGATCATAGCTCACTGCAGCCTGGAACTCCTGGCTCACATGATCCTCCTGCCTTAGC
 AluJr - Chr16:15796336-15796336



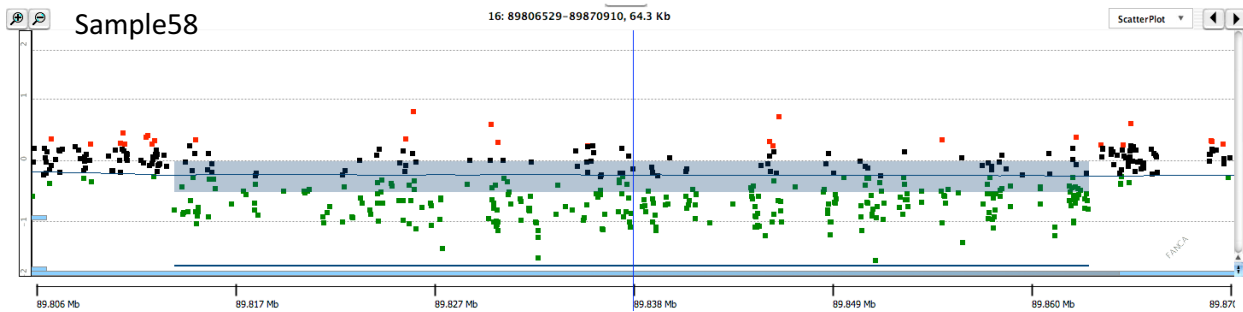
16: 15784349-15827269, 42.9 Kb

Chr16:15816331-15816331
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 AluJr - Chr16:15796336-15796336

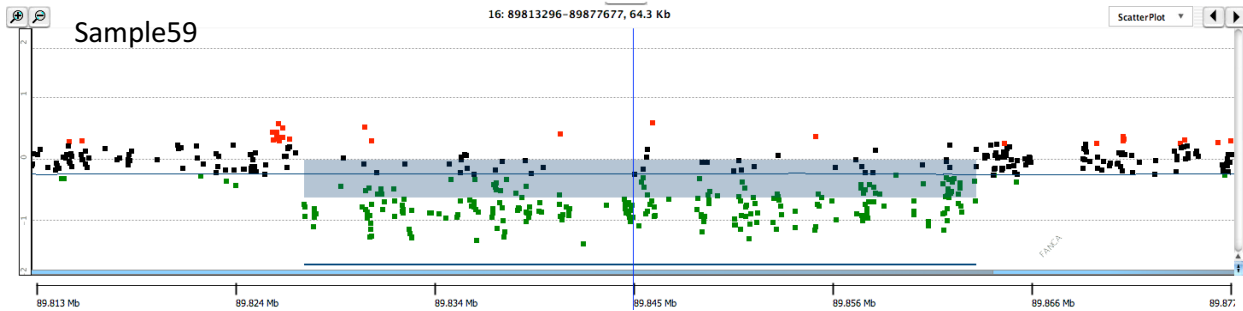




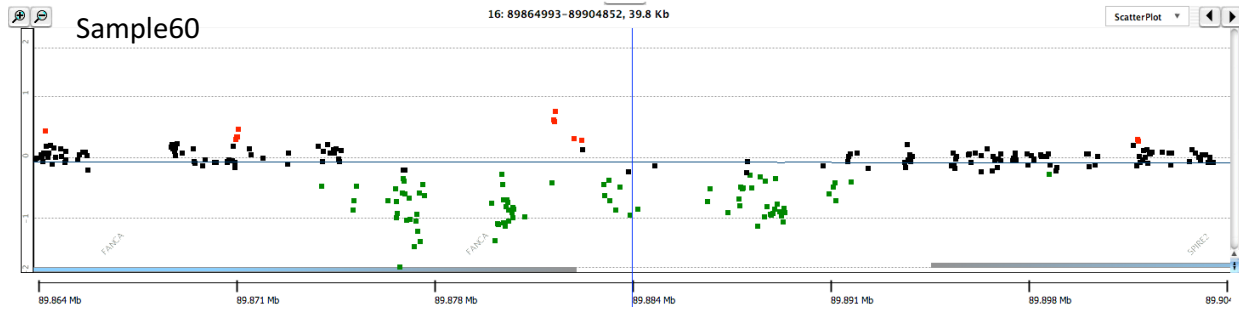
AluJb + Chr16:89817648-89817657
 AAGAAGAATAAAGATCAGGTGCAGTGGCTCACG**CCTGTAATCC**AACAATTTGGAGACCGAGATGGGTGG
 AAGAAGAATAAAGATCAGGTGCAGTGGCTCACG**CCTGTAATCC**CAACACTTCGACACTCTGGGAAGCCAA
 ATTTCTATTTTACGCTGGGTGCGGTGGCTCACA**CCTGTAATCC**CAACACTTCGACACTCTGGGAAGCCAA
AluSx3 + Chr16:89861776-89861785



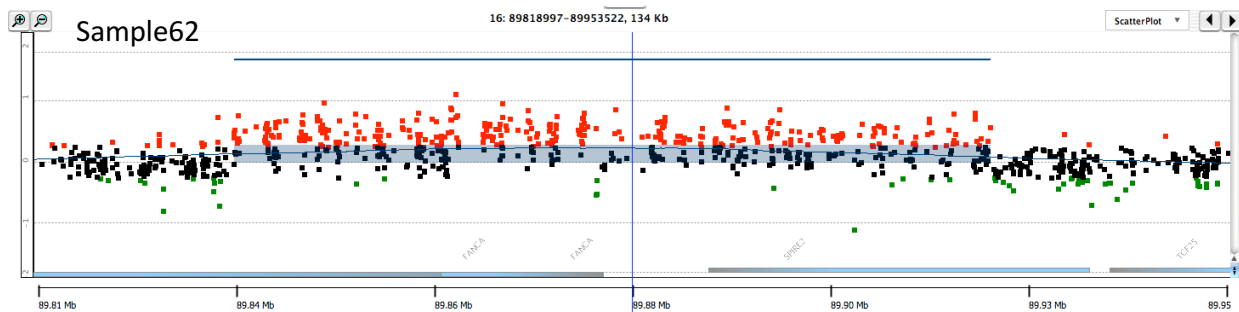
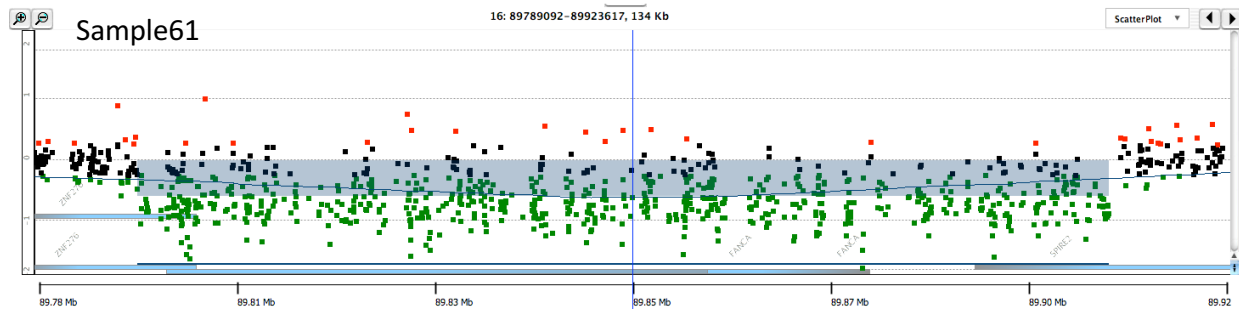
AluSg + Chr16:89814083-89814095
 GTGAGCCAAGATTTCACTGCTGCACTCCAGCC**TGGGCGACAGAGC**AAGACTCTGTCTCAAAAAATAAATA
 GTGAGCCAAGATTTCACTGCTGCACTCCAGCC**TGGGCGACAGAGC**GAAATTCGTCTCAAAAAAGAAAA
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AluY + Chr16:89863542-89863554



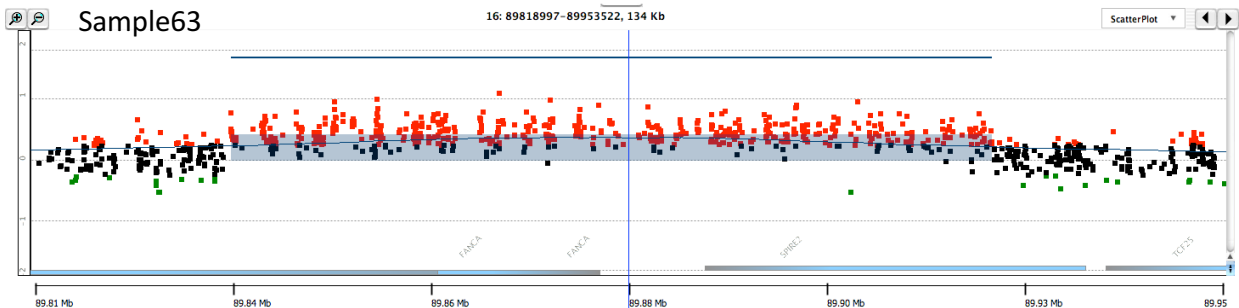
AluY + Chr16:89827581-89827592
 GCCAGGCGCGGTGGCTCACGCC**CTTTGGGAGGC**CAAGGCAAGTGGATCACGAGGTCA
 GCCAGGCGCGGTGGCTCACGCC**CTTTGGGAGGC**TGAGGTGGGTGTTATCACTTGAGG
 GCCAGGTGCGGTGGCTCACGCC**CTTTGGGAGGC**TGAGGTGGGTGTTATCACTTGAGG
AluSq + Chr16:89864039-89864050



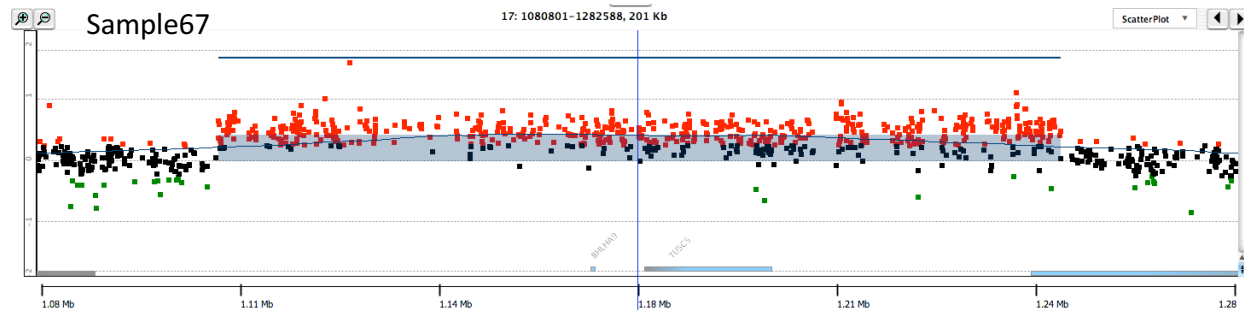
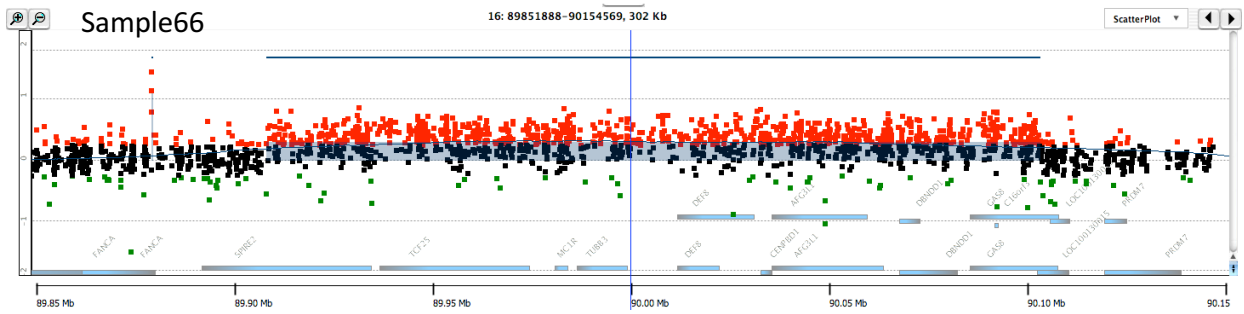
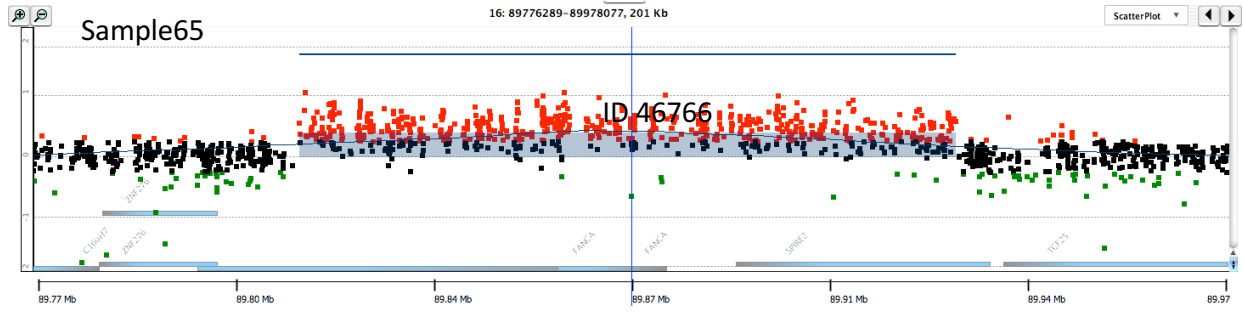
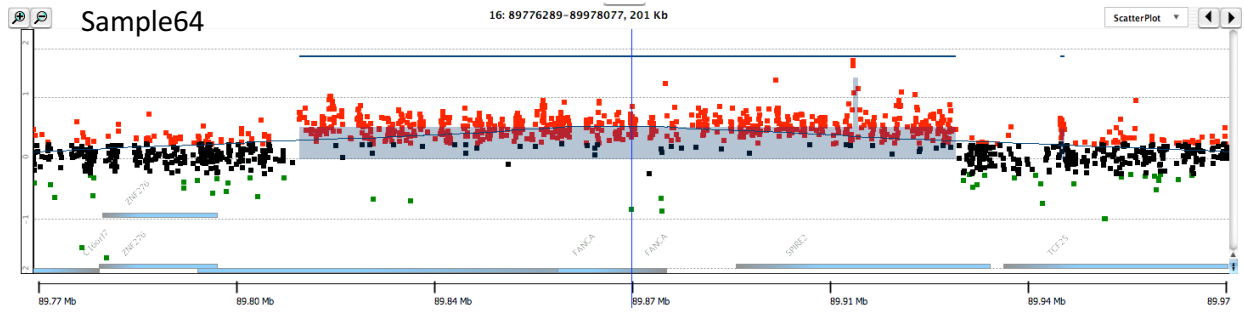
AluY - Chr16:89875354-89875376
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 GAGACAGAGTCACGCTCTGTCA**CCCAGGCTGGAGTGCAGTGGCGC**GATCTCGGCTCACTGCAAGCTCCGC
 GAGATGGAGTCTCGCTCTGTCC**CCCAGGCTGGAGTGCAGTGGCGC**GATCTCGGCTCACTGCAAGCTCCGC
AluY - Chr16:89891821-89891843



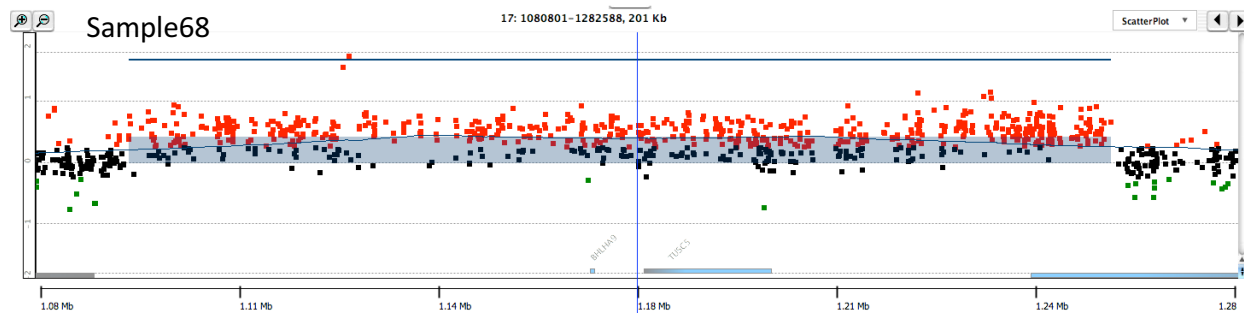
AluJr - Chr16:89926702-89926706
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 TTTTTCTTCTTTTTGAGACAAGGCTTGCTC**TGCTG**GCTTCTACTGGAGATAAAGCCACACACTTCAAGA
 TCTTCAGCTCATAGCGGCTCCACAGGGAGAT**TGCTG**GCTTCTACTGGAGATAAAGCCACACACTTCAAGA
 Chr16:89841572-89841576

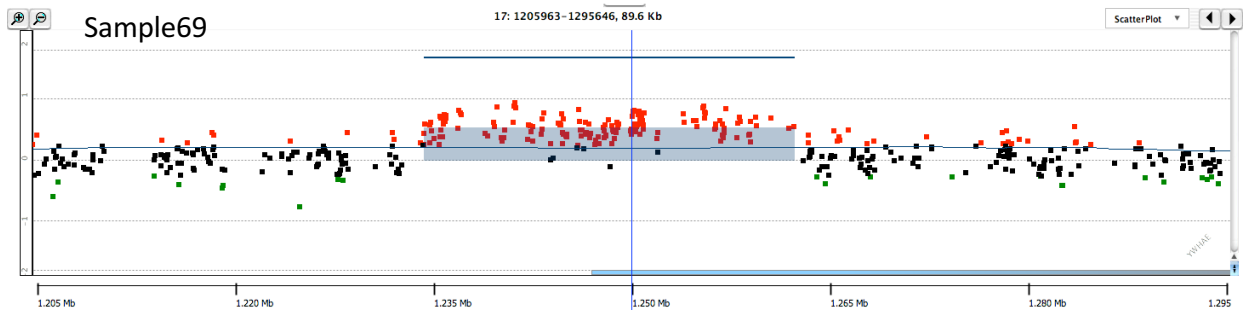


AluJr - Chr16:89926702-89926706
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 TTTTTCTTCTTTTTGAGACAAGGCTTGCTC**TGCTG**GCTTCTACTGGAGATAAAGCCACACACTTCAAGA
 TCTTCAGCTCATAGCGGCTCCACAGGGAGAT**TGCTG**GCTTCTACTGGAGATAAAGCCACACACTTCAAGA
 Chr16:89841572-89841576

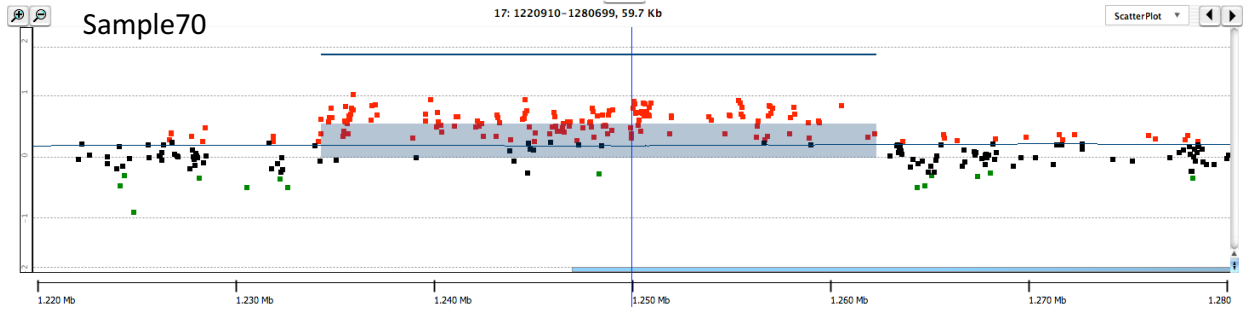


AluSp - Chr17:1253414-1253452
 CCTGGCTAA**TTTTGTATTTT**AGTAGAGATGGGG**TTCTCCATGTTGG**TCAGGCTGGTCTCGAACTCCTG
 CCTGGCTAA**TTTTGTATTTT**AGTAGAGATGGGG**TTCTCCATGTTGG**CCAGGATGGTCTCAAAC**TCCCG**
AluSx1 - Chr17:1111233-1111271
 CAGCCTAA**TTTTGTATTTT**AGTAGAGATGGGG**TTCA**CCATGTTGGCCAGGATGGTCTCAAAC**TCCCG**

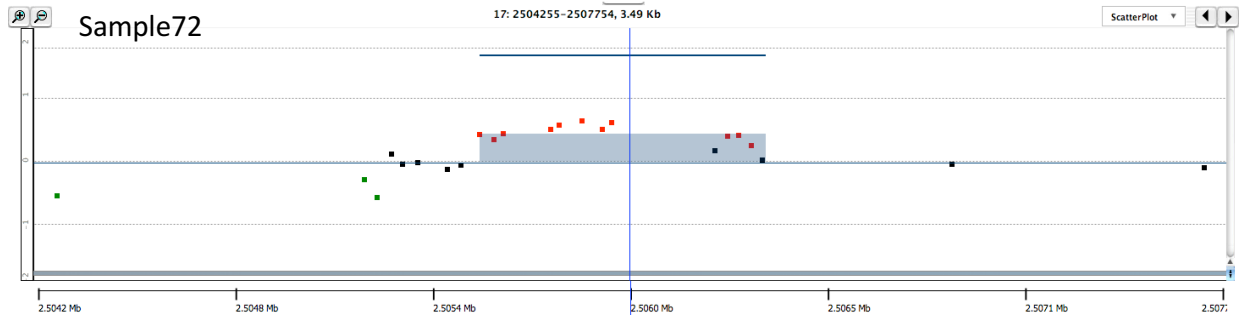
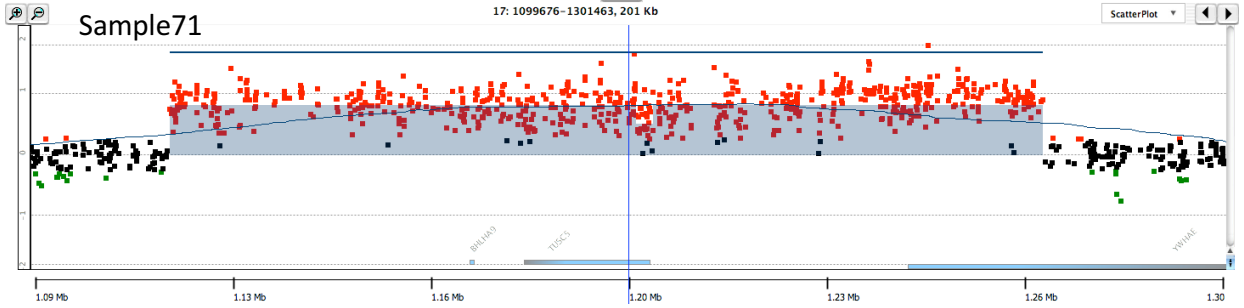


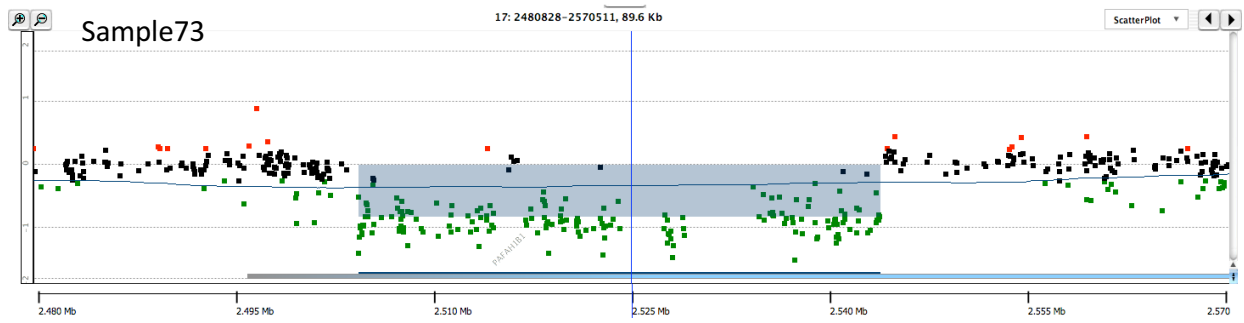


L1 +
 Chr17:1263080-1263081
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 TTTCAAATAGTGGTGATTACACAACACTGTCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGAT
 CAGCTACTCGGGAGGCTGAGGCAGGAGAA TCGCTTGAACCCGGGAGGTTGCAGTGAGCTGAGAT
 AluSq2 +
 Chr17:1234614-1234615

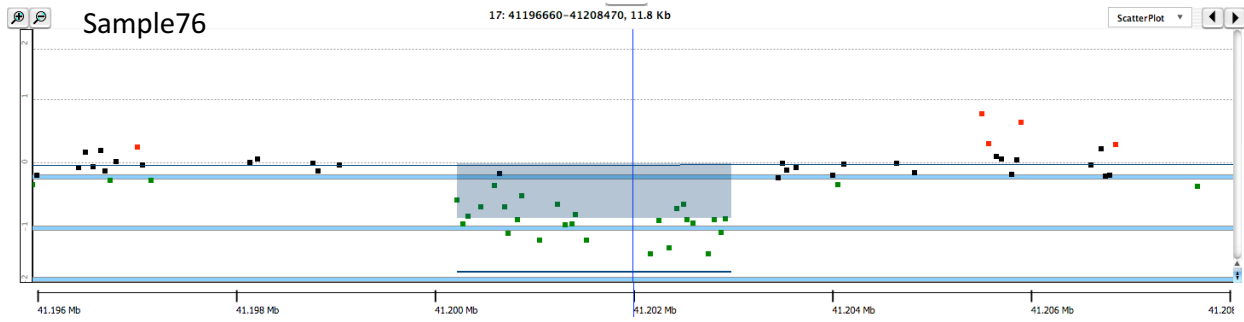
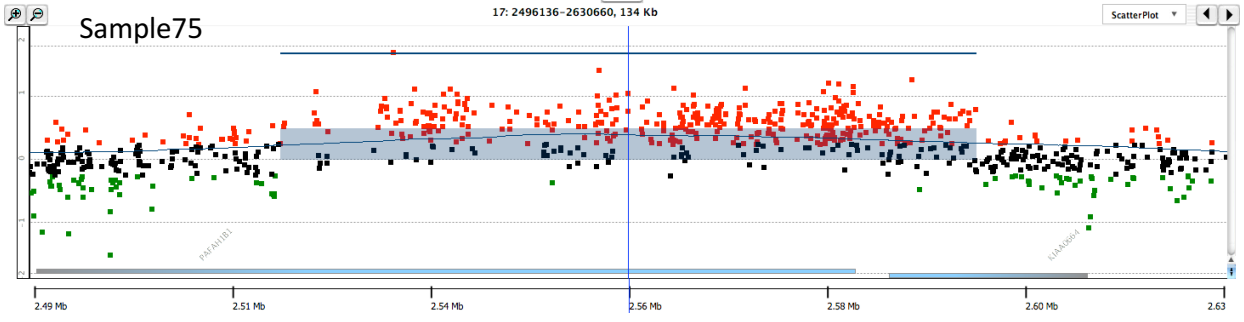
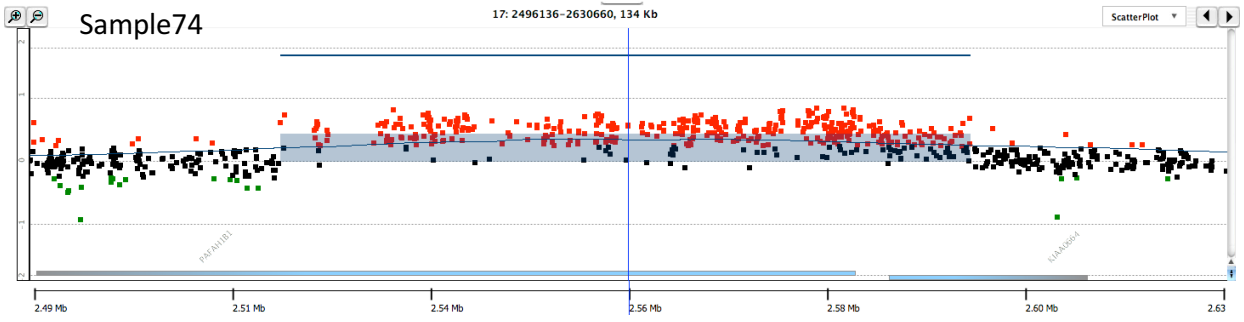


L1 +
 Chr17:1263080-1263081
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 TTTCAAATAGTGGTGATTACACAACACTGTCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGAT
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 AluSq2 +
 Chr17:1234614-1234615

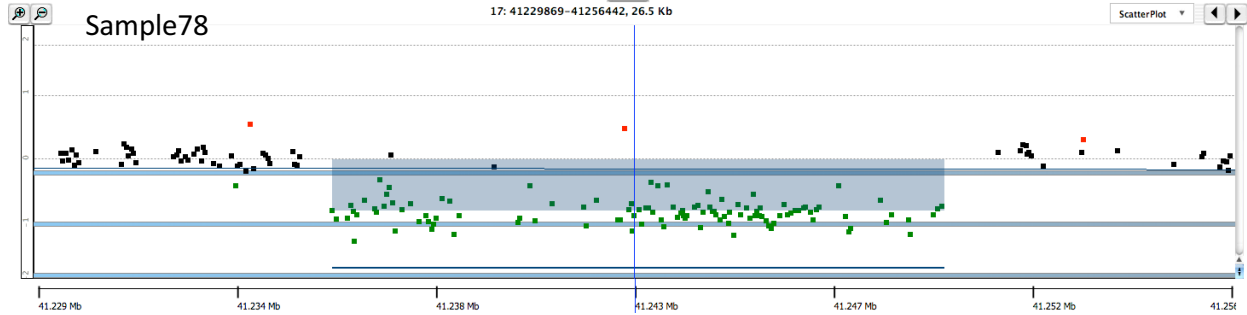
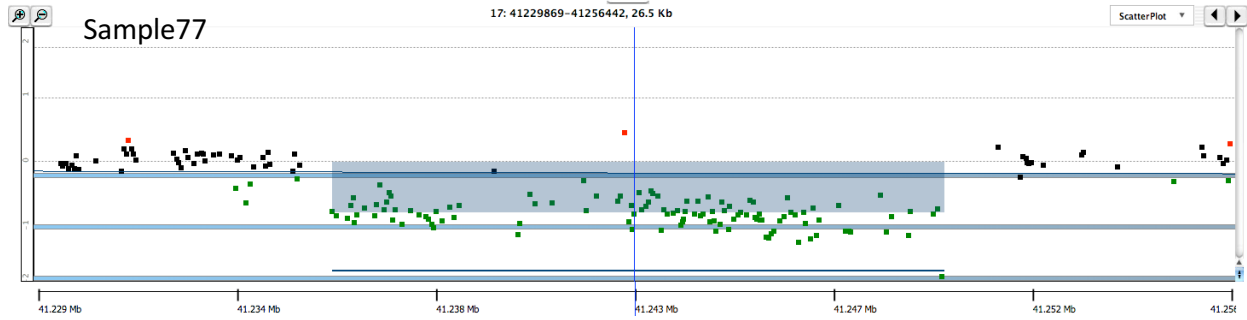




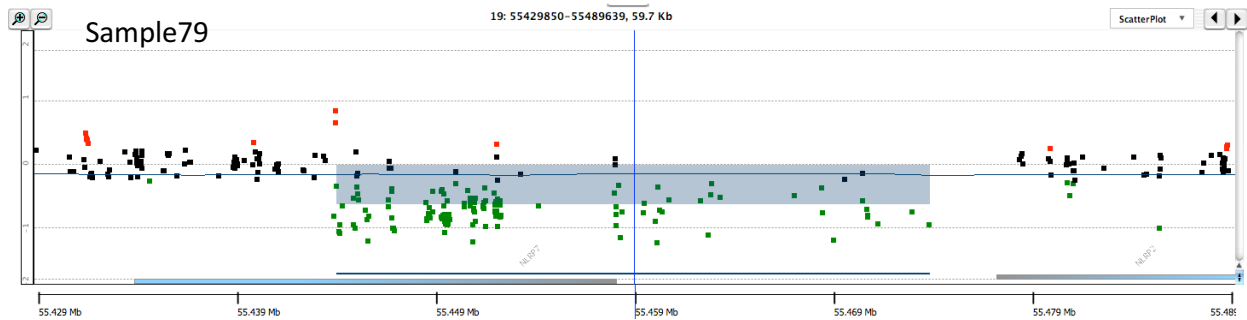
AluSq2 - Chr17:2504984-2504991
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 AGGCCTTGAACCTCCTGACCTCAGGTGATCCTCCTG**CCTCGGCC**TCCCAAAGTGCTGGGATTACAGATGTG
 TGGTCTTGAACCTCCTGACCTCAGGTGATG**CCGCCA****CCTCGGCC**TCCCAAAGTGCTGGGATTACAGATGTG
AluSx1 - Chr17:2544701-2544708



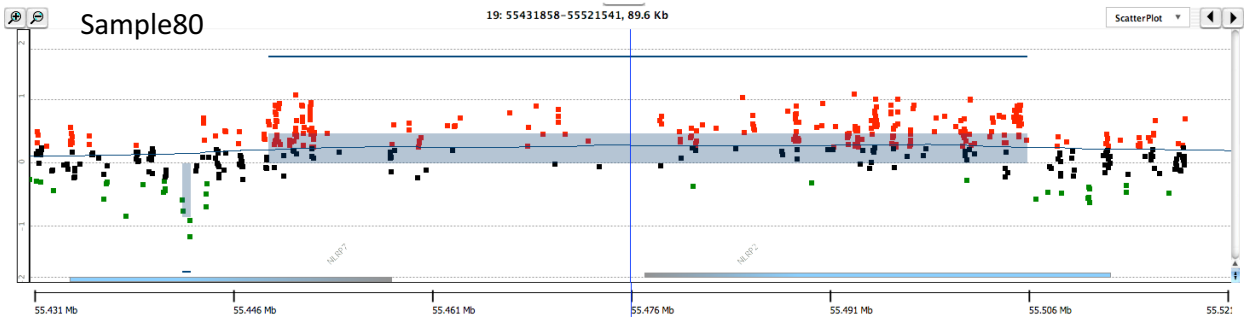
AluSc - Chr17:41200437-41200445
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 GACGGGGTTTCGCCATGTTGGTTGGCCAGGAT**TGGTCTCGA**ACTCCTGACCTCGTGATCTGCCTGTCTTGG
 TAGAGACAGGGTTTCACCATGTTGGT**CAGGC****TGGTCTCGA**ACTCCTGACCTCGTGATCTGCCTGTCTTGG
AluSg - Chr17:41203867-41203875



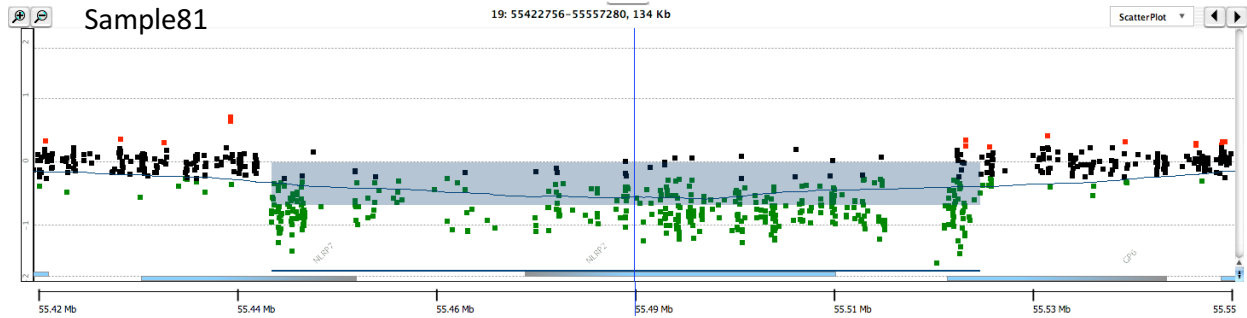
AluSx - Chr17:41236381-41236389
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 ATTTTGTATTTTGTAGTAGAGACGGGTTTCA**CCATGTTGG**CAGGCTGGTCTTGAACTCCCGACCTCAG
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AluSp - Chr17:41251038-41251046



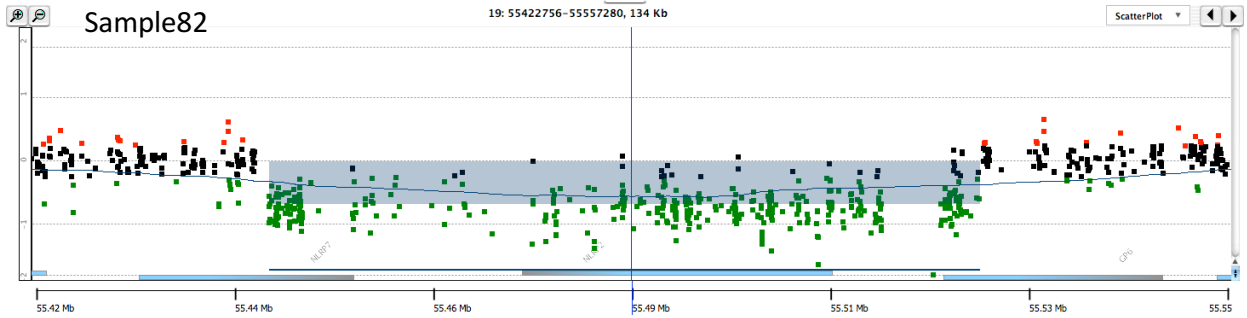
AluY - Chr19:55444778-55444793
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 CATGATCCACCCGCCTCGGCCTCCCAAAGT**GCTGGGATTACAGGCA**CCCGCCACCACGCCGACTAATTT
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AluSg7 - Chr19:55475378-55475393



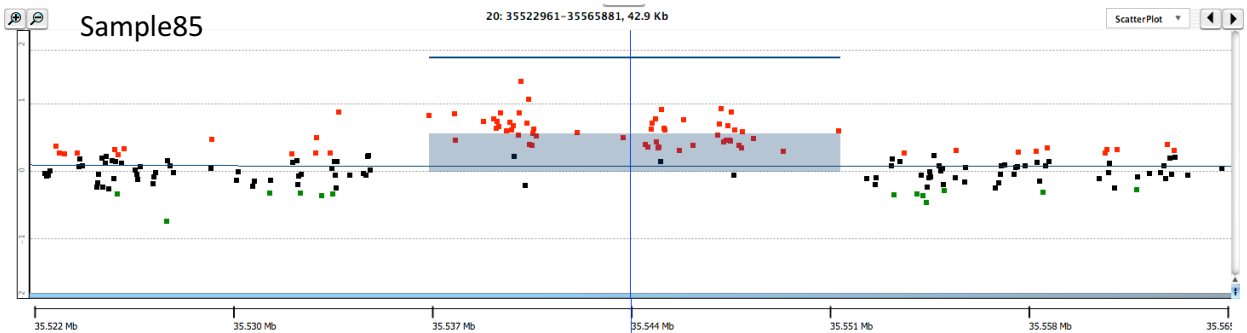
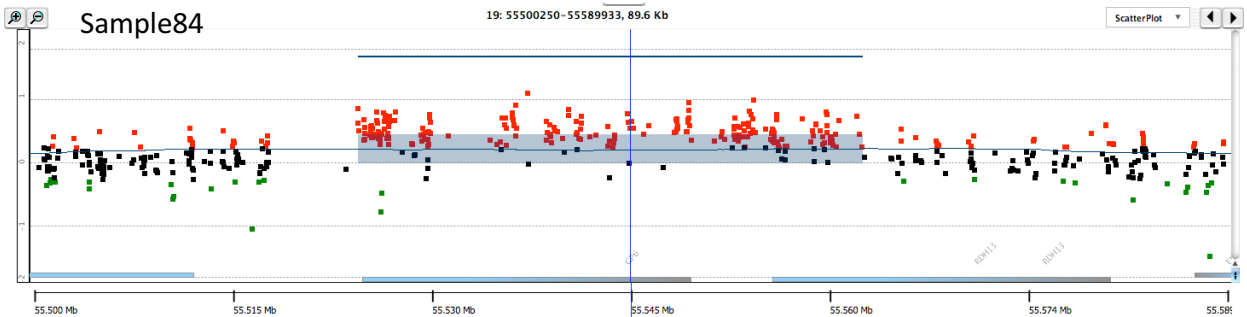
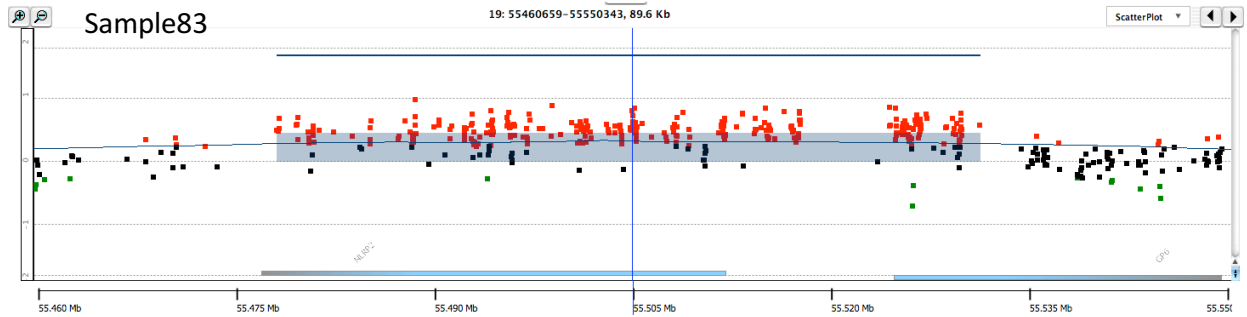
AluSq2 - Chr19:55506229-55506238
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 CCTCAGGTGATCCGCCATCTC**GGCCTCCCAA**ACGTGCTGGGATTACAGGCATGAGCCACCACCGCC
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AluY - Chr19:55445561-55445570

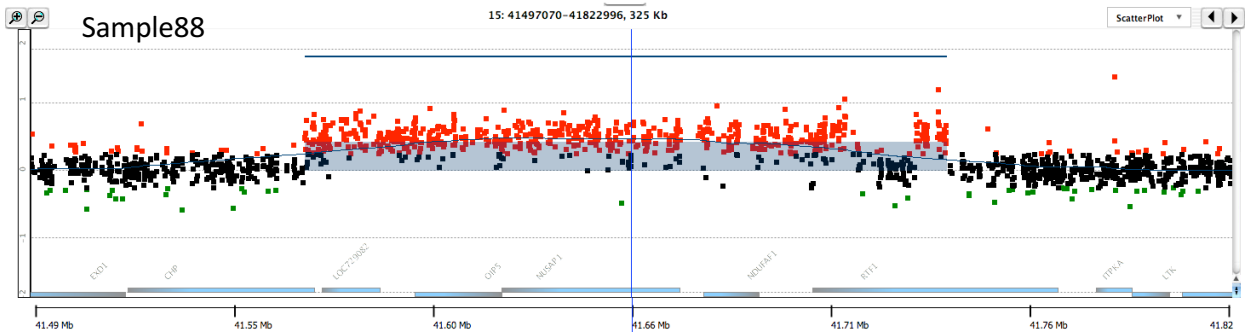
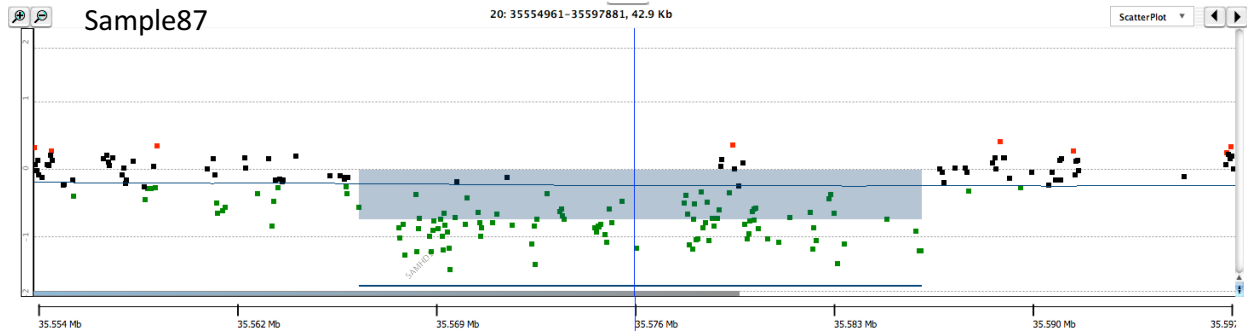
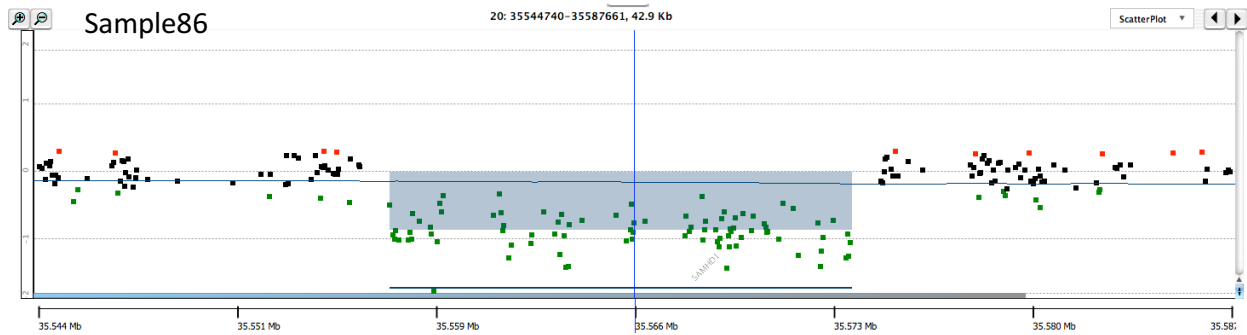


AluSq2 + Chr19:55449271-55449271
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 AGCCTGGGCAACAAGAGTAAATCTCCGTCTACCAAGGGTTGGGTGCAGAGTCAGGAGAGGTTAGGAAG
 GATGCCATGGGGAAATGGAAGAAAAGGCAGAGTGAGTGGGTTGGGTGCAGAGTCAGGAGAGGTTAGGAAG
 L2 - Chr19:55528913-55528913



AluSq2 + Chr19:55449271-55449271
 AGCCTGGGCAACAAGAGTAAATCTCCGTCTCACCAAAAAAAAAAAAAAAAAAAAAGACAGCTGGAAAATC
 AGCCTGGGCAACAAGAGTAAATCTCCGTCTACCAAGGGTTGGGTGCAGAGTCAGGAGAGGTTAGGAAG
 GATGCCATGGGGAAATGGAAGAAAAGGCAGAGTGAGTGGGTTGGGTGCAGAGTCAGGAGAGGTTAGGAAG
 L2 - Chr19:55528913-55528913





Alujr4 + Chr15:41745798-41745799
 CAAAAAATTTAAAAATTAGCTGGGTGTTATGGTATGCACCTGAGGTCCCAACTACTTAGGAGGCTGAGG
 CAAAAAATTTAAAAATTAGCTGGGTGTTATGGTATGCACGTTTTAGTGGCTGGGCGCGGTGGCTTACGC
 TGTTAAGGTTGGTCACTTACTTCTTTGTTTTGAAAAAGTTACGTTTTAGTGGCTGGGCGCGGTGGCTTACGC
 Chr15:41571119-41571120

L2a + Chr15:41721734-41721734
 GGTACTCCCCTGCTTCAAACCATTTGATGGCTTCCACTGCCTAACTTCCATGCTCCTCACCCCTGTTTT
 GGTACTCCCCTGCTTCAAACCATTTGATGGCTTCCATCAAACGTGCAGGATGGTCTTGATCTCCTGACC
 ATTTTTTTTTGTATTTTTAGTAGAGACGGGGTTCTCTGTGTTAGCCAGGATGGTCTTGATCTCCTGACC
AluY - Chr15:41737342-41737342

