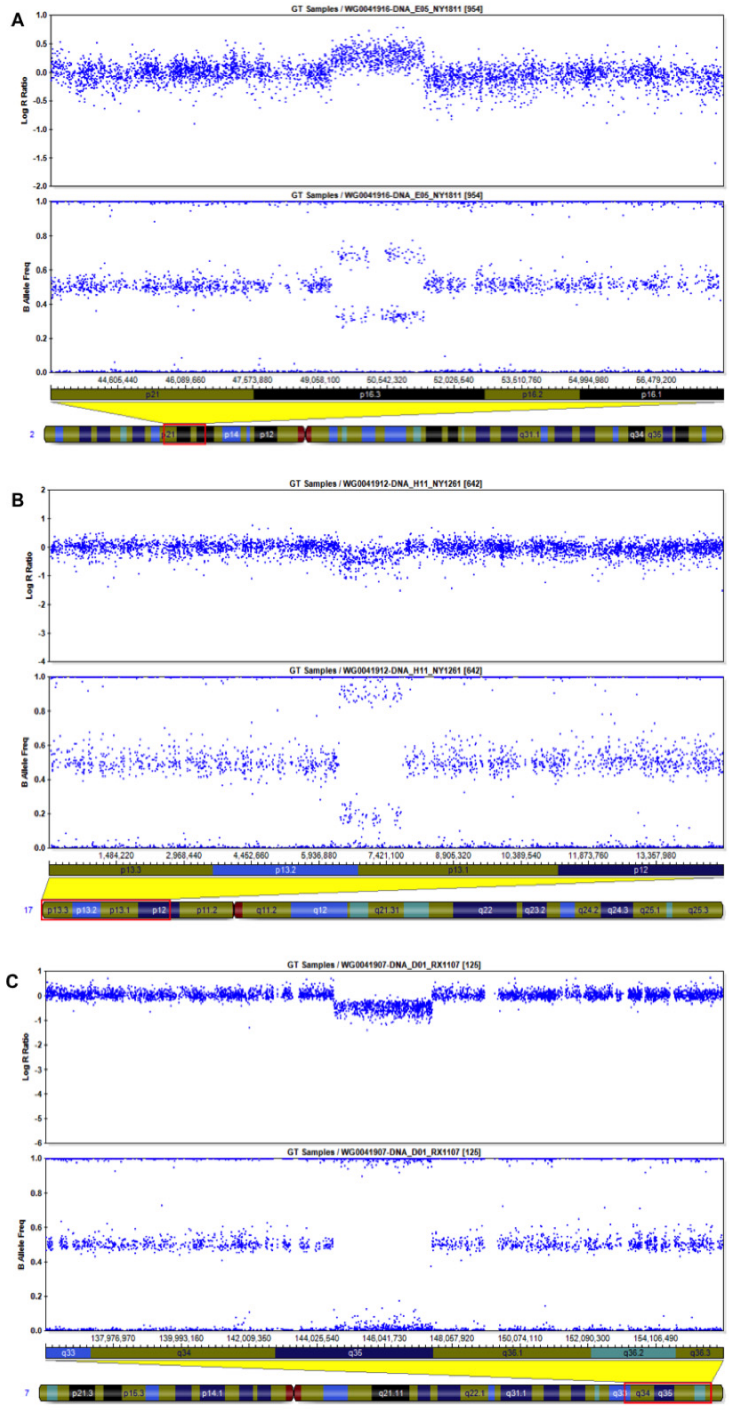
A
GT Samples / WG0041916-DNA_E05_NY1811 [954]
Log R Ratio
GT Samples / WG0041916-DNA_E05_NY1811 [954]
B Allele Freq
44,606,440
46,089,660
47,573,880
49,058,100
50,542,320
52,026,540
53,510,760
54,994,980
56,479,200
B
GT Samples / WG0041912-DNA_H11_NY1261 [642]
Log R Ratio
GT Samples / WG0041912-DNA_H11_NY1261 [642]
B Allele Freq
1,484,220
2,968,440
4,452,660
5,936,880
7,421,100
8,905,320
10,389,540
11,873,760
13,357,980
C
GT Samples / WG0041907-DNA_D01_RX1107 [125]
Log R Ratio
GT Samples / WG0041907-DNA_D01_RX1107 [125]
B Allele Freq
137,976,970
139,993,160
142,009,360
144,025,540
146,041,730
148,057,920
150,074,110
152,090,300
154,106,490

Figure S2 The examples of CNVs found only in AD patients but not in normal controls. (A) Increase in the log R ratio (top) and split in the B-allele frequency (bottom) are consistent with a partial duplication of chromosome 2p16.3. (B) Decrease in the log R ratio (top) and “0 or 1” frequency of the B-allele (bottom) are consistent with a partial deletion of chromosome 17p13.1-p13.2. (C) Decrease in the log R ratio (top) and “0 or 1” frequency of the B-allele (bottom) are consistent with a partial deletion of chromosome 7q35-q36.1.