Figure S5. Genotyping Structural Variation. Frequency spectrum for 130 deletion events identified through ESP, validated and breakpoint-refined using sequence or arrayCGH, and present in at least 1% of unrelated chromosomes. Each deletion event is indicated with tick marks along the X-axis, with the global allele frequency for that event indicated by the total height of the corresponding vertical bar (a). The allele proportions within the three distinct populations are indicated in blue (YRI), red (CEU), or green (CHB+JPT), respectively. b-d) Frequency of deletion event within each population plotted separately.


A
ASN/Total
CEU/Total
YRI/Total
Frequency
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
1
10
19
28
37
46
55
64
73
82
91
100
109
118
127
Deletion Event
B
ASN_Del_Freq
Frequency
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
1
10
19
28
37
46
55
64
73
82
91
100
109
118
127
Deletion Event
C
CEU_Del_Freq
Frequency
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
1
10
19
28
37
46
55
64
73
82
91
100
109
118
127
Deletion Event
D
YRI_Del_Freq
Frequency
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
1
10
19
28
37
46
55
64
73
82
91
100
109
118
127
Deletion Event