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Supplemental Data

Limited Clinical Utility of Non-invasive Prenatal Testing for Subchromosomal Abnormalities

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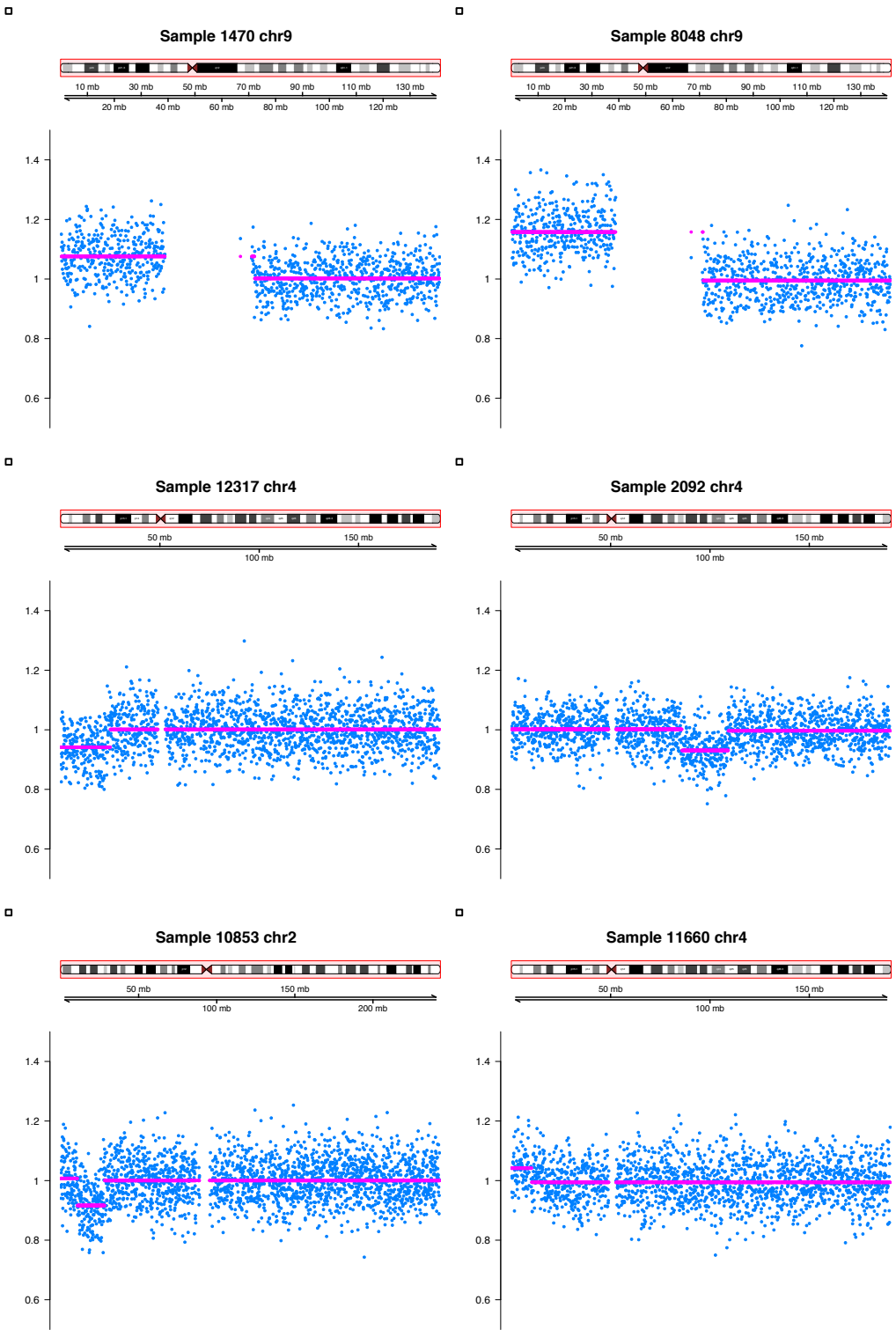
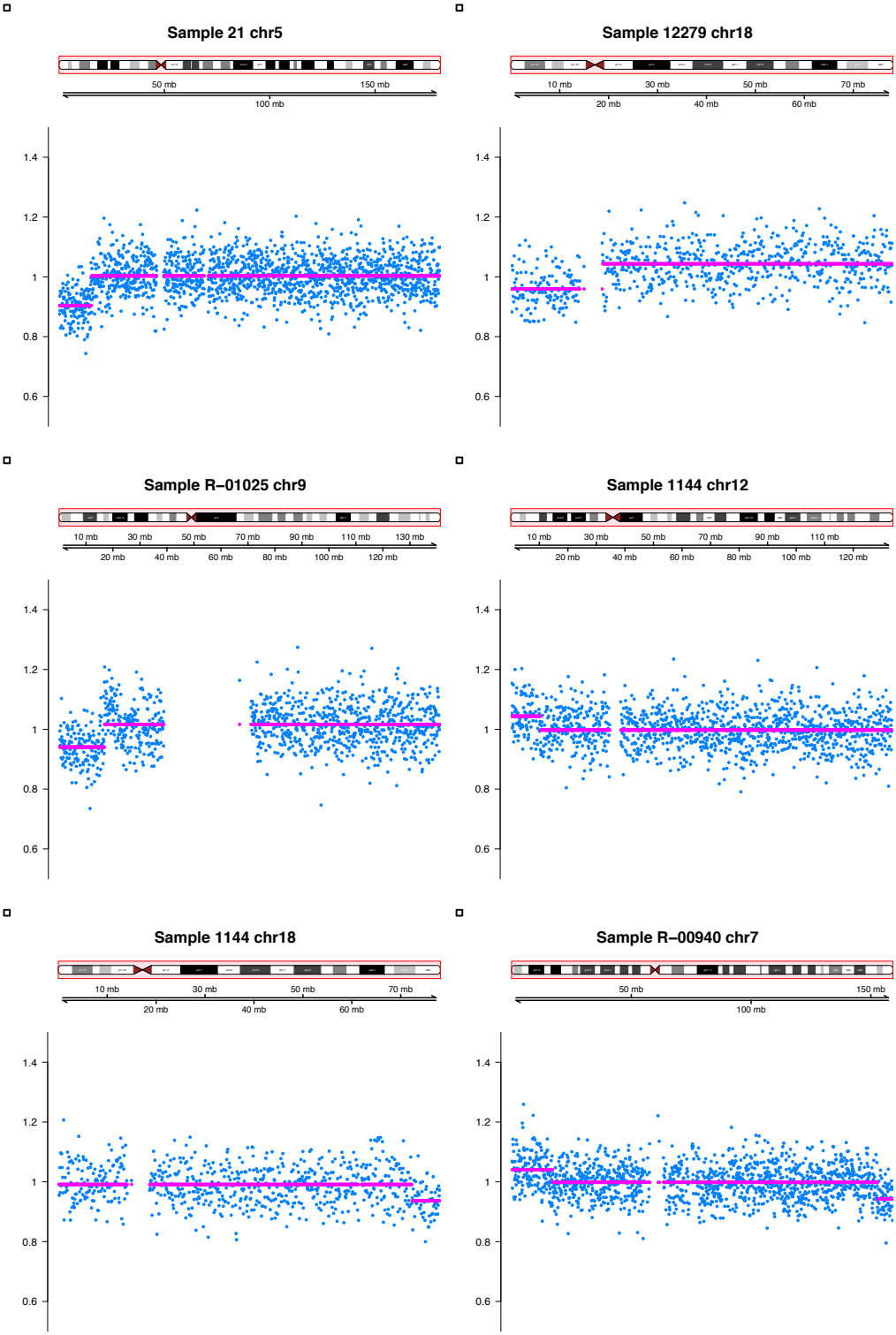
Figure S1

Normalized counts ratio for samples sequenced at 12-plex with CNVs that were detected by our analysis pipeline.




Sample 21 chr5
50 mb
150 mb
100 mb
1.4
1.2
1
0.8
0.6
Sample 12279 chr18
10 mb
30 mb
50 mb
70 mb
20 mb
40 mb
60 mb
1.4
1.2
1
0.8
0.6
Sample R−01025 chr9
10 mb
30 mb
50 mb
70 mb
90 mb
110 mb
130 mb
20 mb
40 mb
60 mb
80 mb
100 mb
120 mb
1.4
1.2
1
0.8
0.6
Sample 1144 chr12
10 mb
30 mb
50 mb
70 mb
90 mb
110 mb
20 mb
40 mb
60 mb
80 mb
100 mb
120 mb
1.4
1.2
1
0.8
0.6
Sample 1144 chr18
10 mb
30 mb
50 mb
70 mb
20 mb
40 mb
60 mb
1.4
1.2
1
0.8
0.6
Sample R−00940 chr7
50 mb
150 mb
100 mb
1.4
1.2
1
0.8
0.6

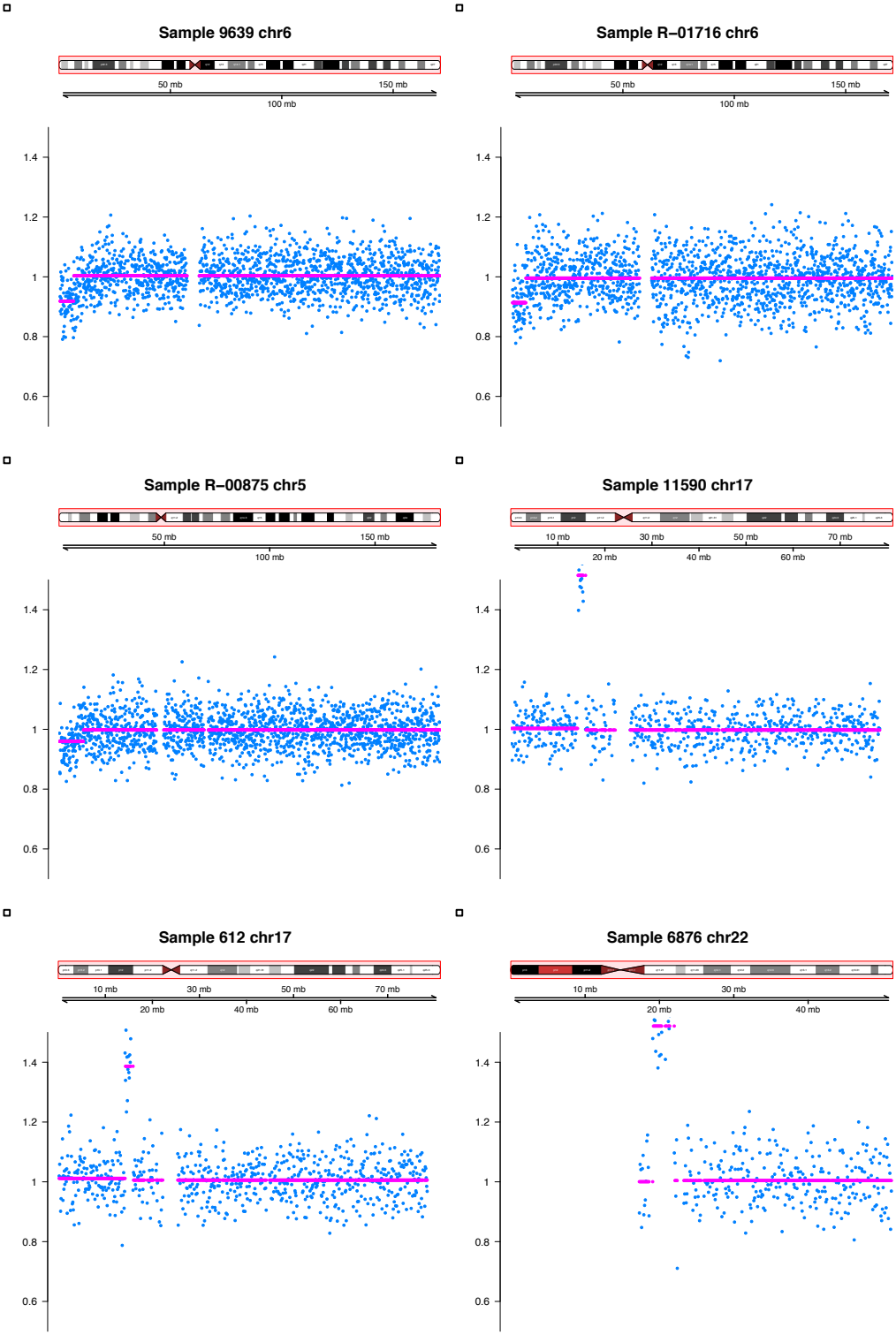
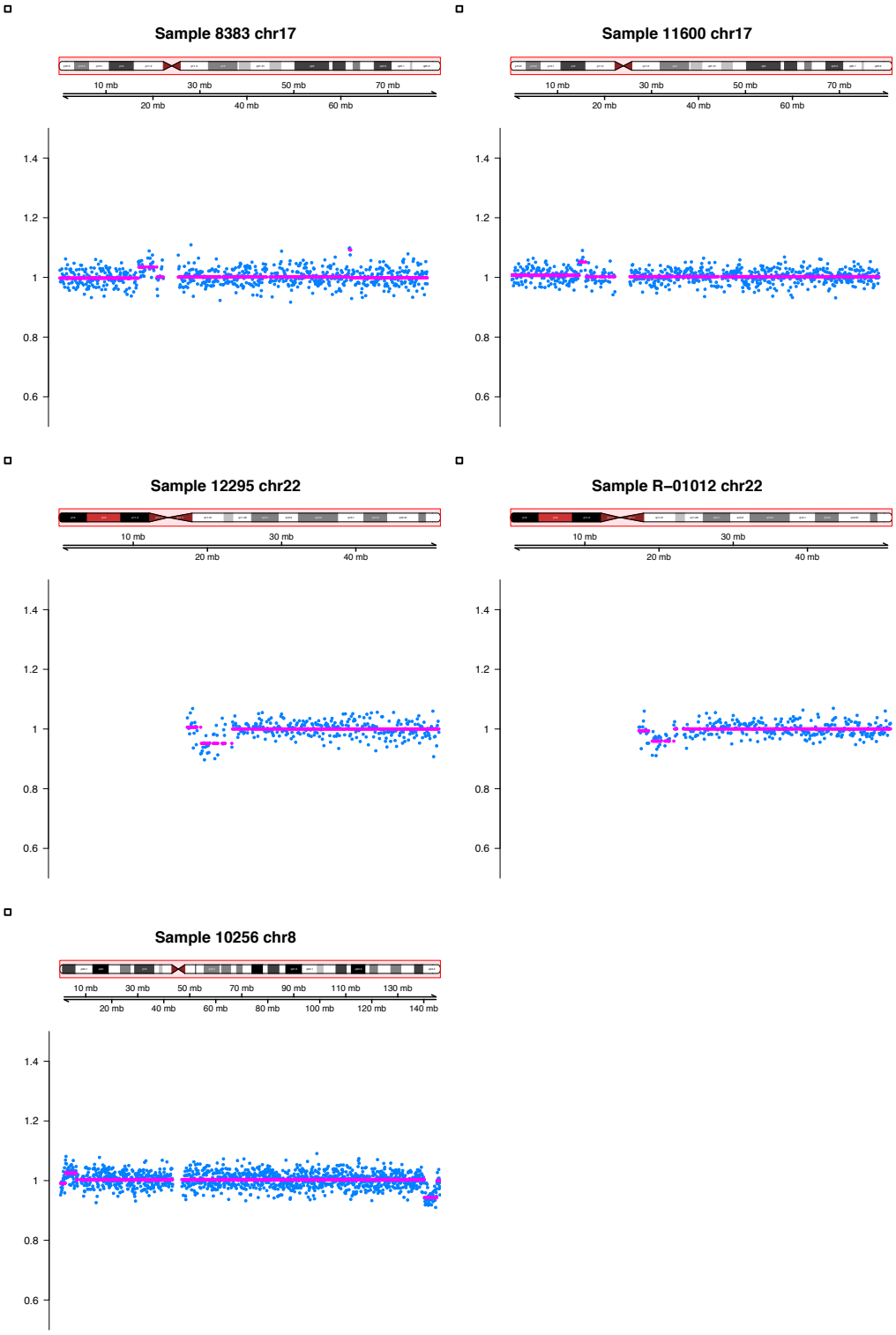
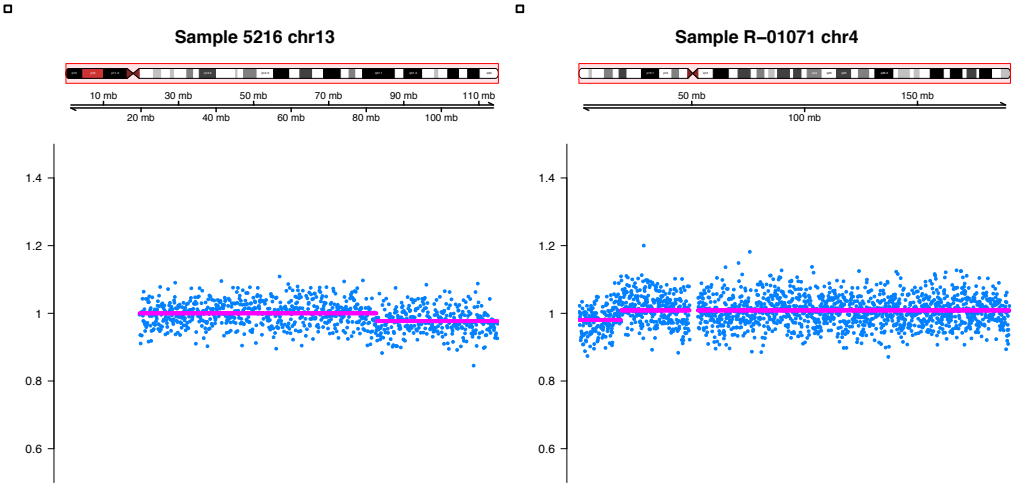

Sample 9639 chr6
50 mb
100 mb
150 mb
1.4
1.2
1
0.8
0.6
Sample R−01716 chr6
50 mb
100 mb
150 mb
1.4
1.2
1
0.8
0.6
Sample R−00875 chr5
50 mb
100 mb
150 mb
1.4
1.2
1
0.8
0.6
Sample 11590 chr17
10 mb
20 mb
30 mb
40 mb
50 mb
60 mb
70 mb
1.4
1.2
1
0.8
0.6
Sample 612 chr17
10 mb
20 mb
30 mb
40 mb
50 mb
60 mb
70 mb
1.4
1.2
1
0.8
0.6
Sample 6876 chr22
10 mb
20 mb
30 mb
40 mb
1.4
1.2
1
0.8
0.6

Figure S2

Normalized counts ratios for samples that were detected after deeper sequencing




Sample 5216 chr13
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20 mb
30 mb
40 mb
50 mb
60 mb
70 mb
80 mb
90 mb
100 mb
110 mb
1.4
1.2
1
0.8
0.6

Sample R−01071 chr4
50 mb
100 mb
150 mb
1.4
1.2
1
0.8
0.6