SUPPLEMENTARY INFORMATION

Derivation of haploid embryonic stem cells from mouse embryos

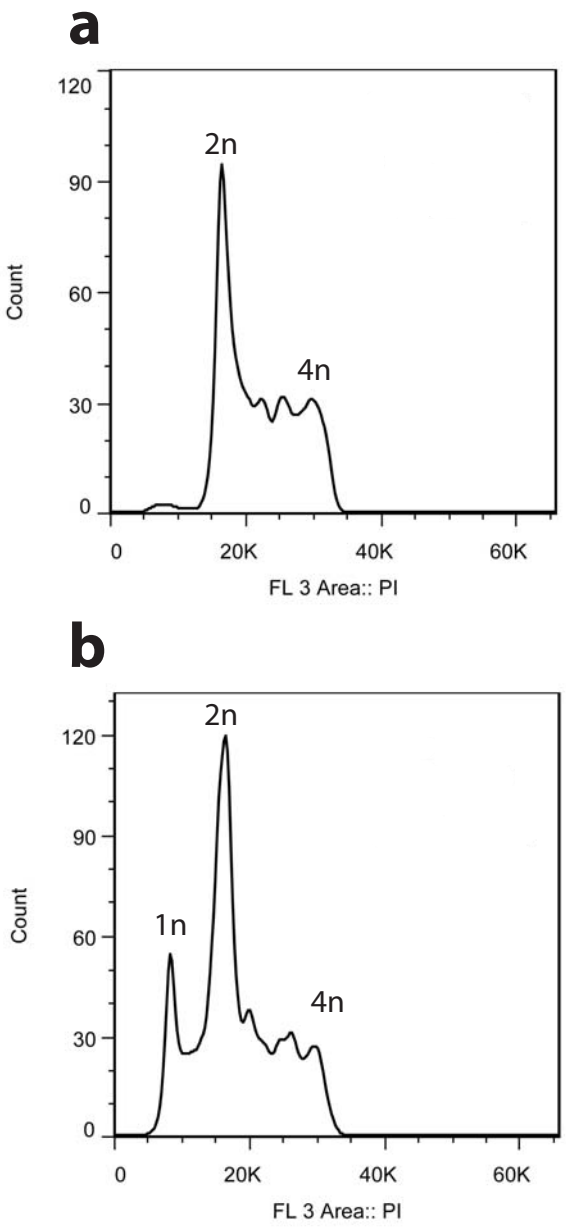
Martin Leeb & Anton Wutz

Wellcome Trust Centre for Stem Cell Research

University of Cambridge

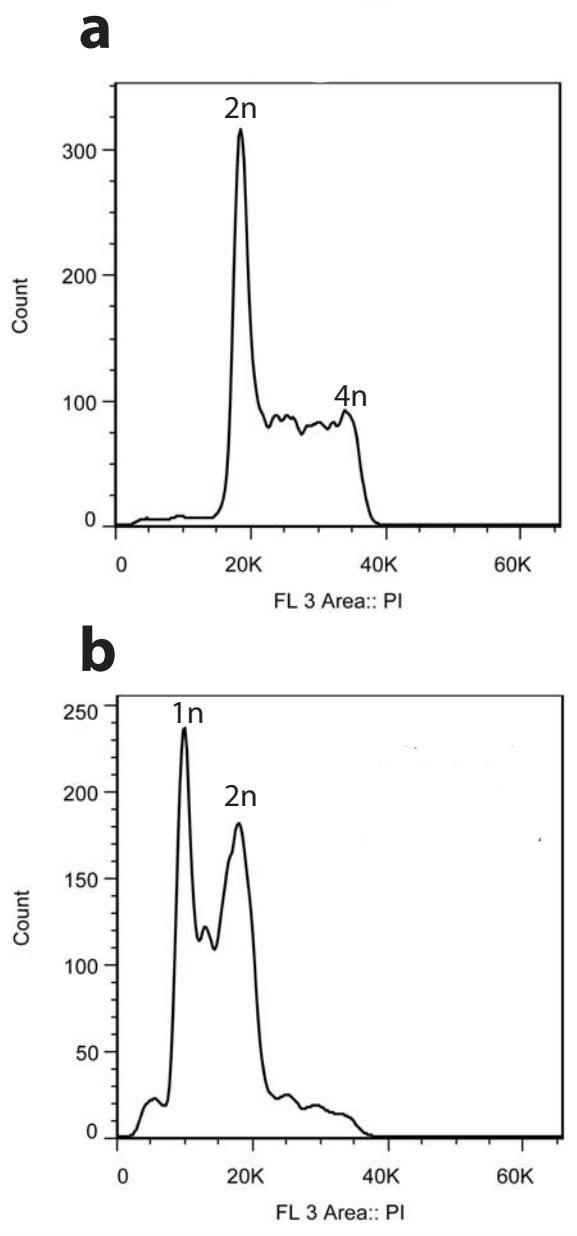
Tennis Court Road, Cambridge CB2 1QR, UK

Phone: +44-1223760234 ; FAX: +44-1223760241 ; email: aw512@cam.ac.uk



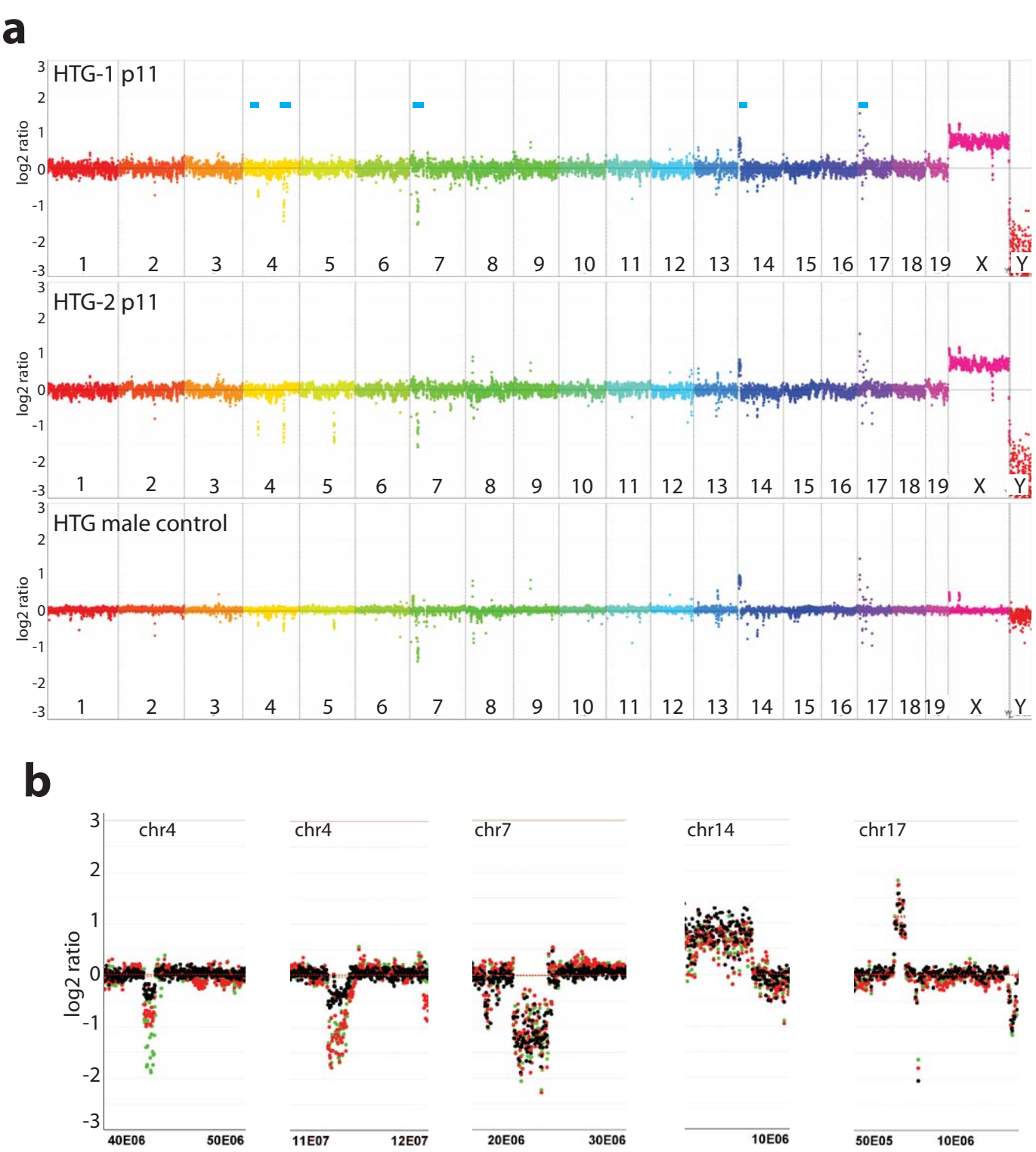
Supplementary Figure 1 - Derivation of CBA/B6 hybrid haploid ES cells in KSR

(a) A flow profile of DNA content after PI staining recorded from diploid control shows a 2n and 4n peak. **(b)** A flow profile of DNA content of an ES cell line (HAP-9, p8) derived from haploid blastocysts using Knockout Serum Replacement shows an additional 1n peak.



Supplementary Figure 2 - Derivation of haploid ES cells from a mixed genetic background in 2i medium

(a) A flow profile shows the DNA content of a diploid control ES cell line after PI staining.
(b) A flow profile of a haploid ES cell line (HTG-1, p8) derived from blastocysts with a mixed genetic background shows a nearly pure haploid cell population with 1n and 2n peaks but no 4n peak.

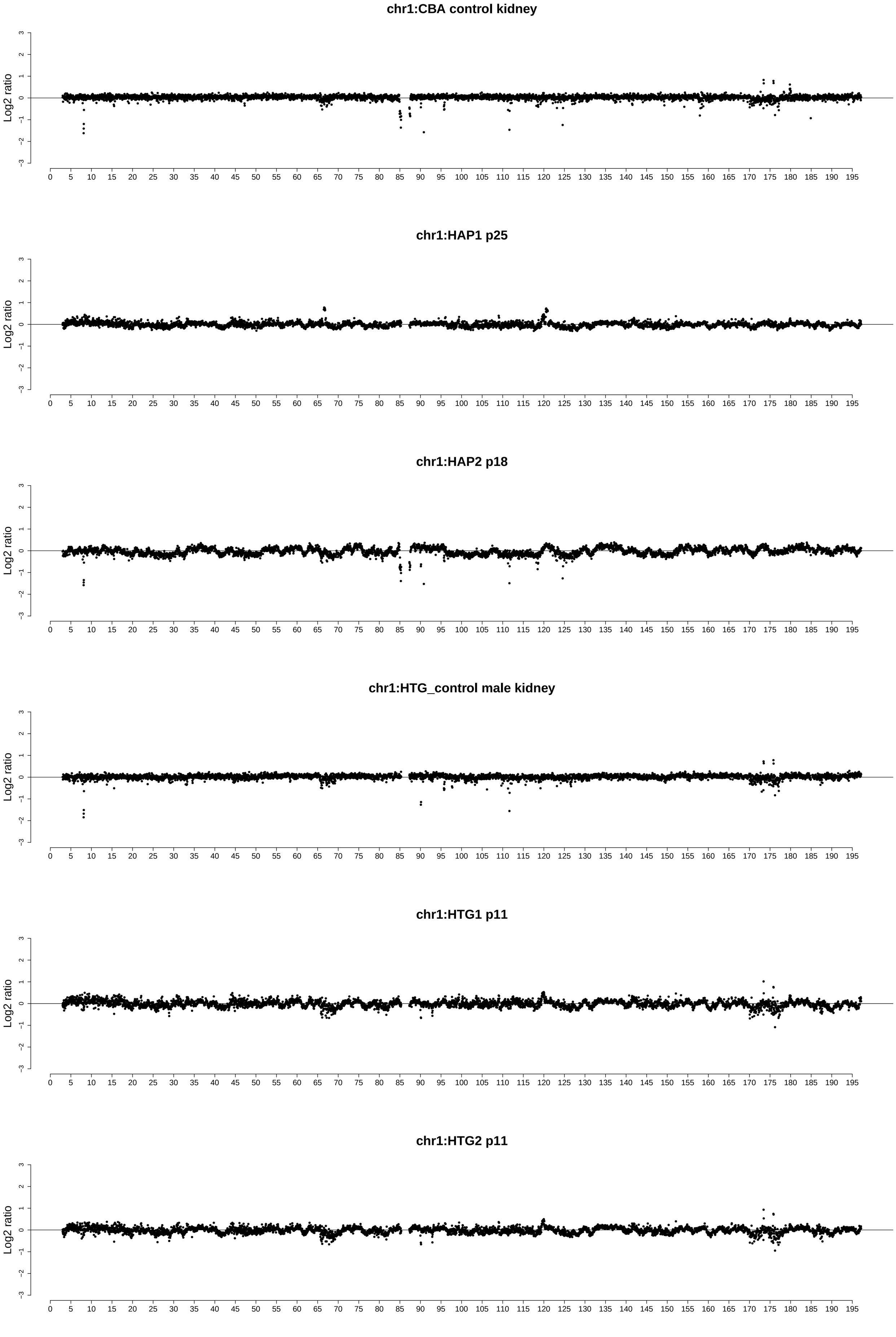


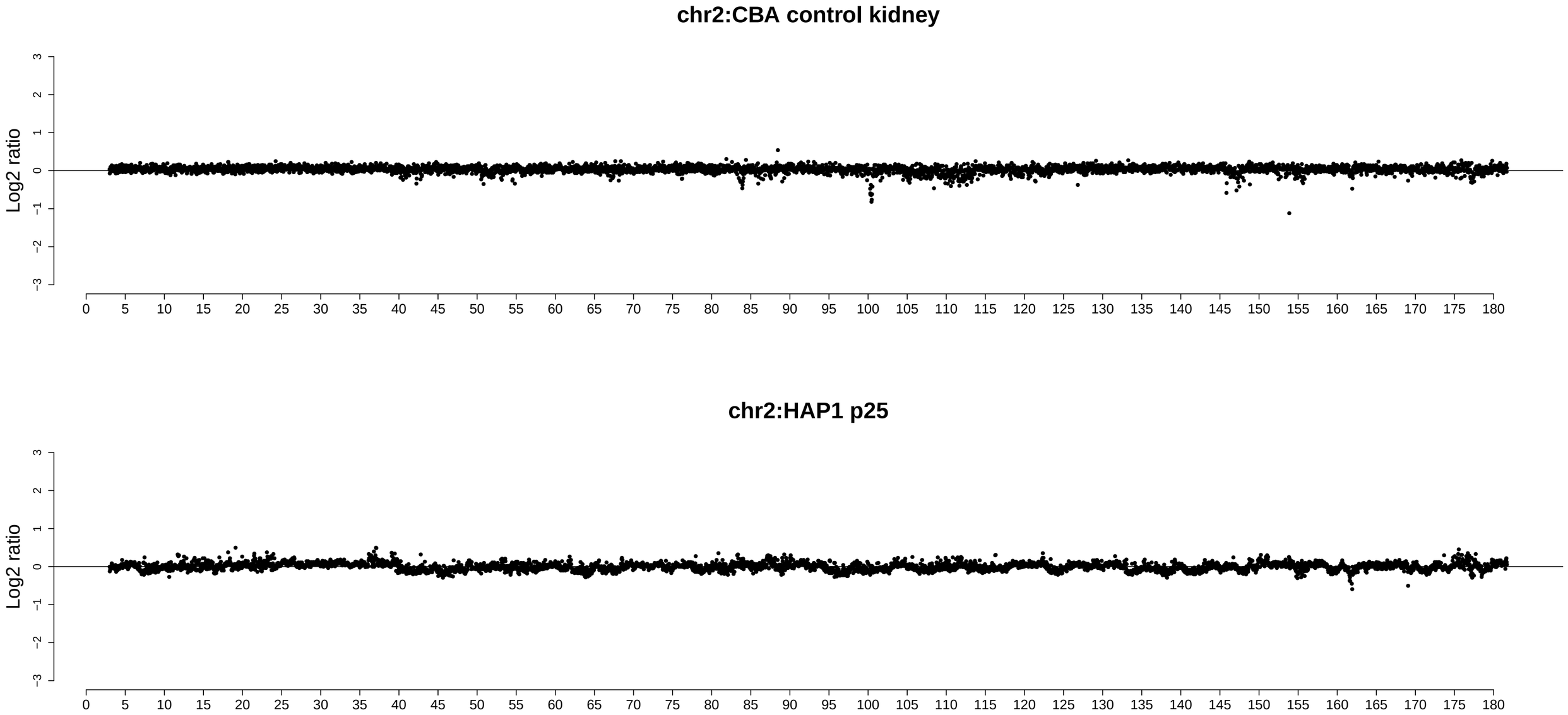
Supplementary Figure 3 - CGH analysis of HTG haploid ES cells.

(**a**) Genomic overview of copy number variations (CNVs) in 200kb resolution in HTG-1 and HTG-2 haploid ES cells and control male kidney DNA from the mixed strain background of which the ES cells were derived. Average values of log2 ratios are plotted using somatic C57BL6 DNA as a reference. Blue bars on top indicate the positions of regions enlarged in panel b.
(**b**) Zoom in views of regions with CNVs on chromosomes 4, 7, 14 and X are shown.
Signals from somatic kidney DNA from HTG genetic background mouse strain (black), HTG-1 (green) and HTG-2 (red) ES cells are overlaid and shown at 40 kb resolution. The positions of CNVs overlap indicating they are likely resulting from genomic variation between the strain of origin and C57BL6 mouse strains.

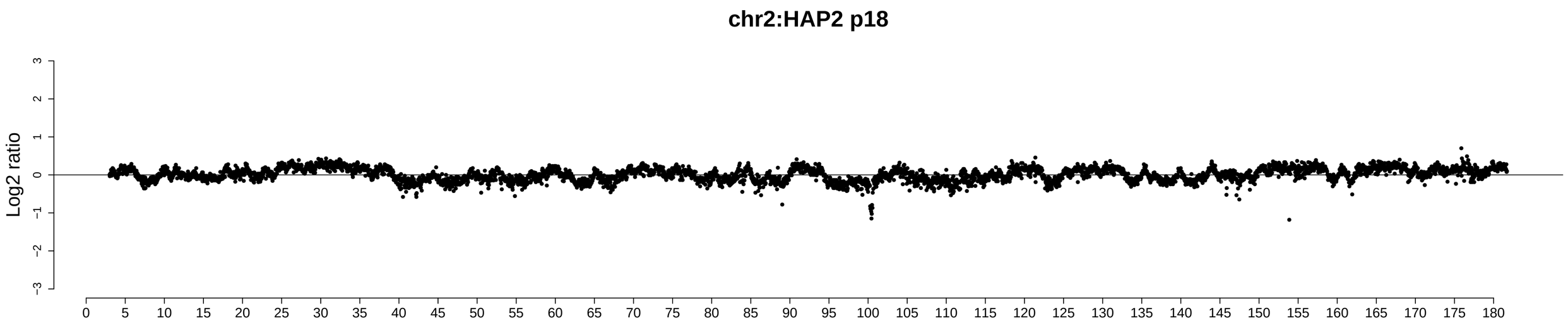
Supplementary Figure 4 - CGH analysis of haploid ES cells

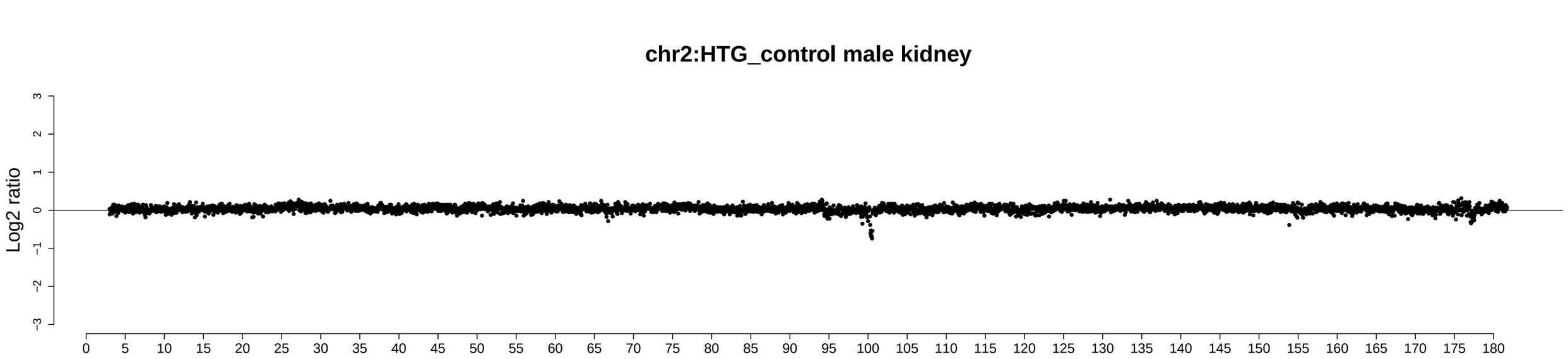
CGH profiles of HAP-1, HAP-2, HTG-1 and HTG-2 haploid mouse ES cells are shown along genomic coordinates. Kidney DNA from a CBA male mouse and from a male of the transgenic mixed background strain from which HTG ES cells were derived were analysed as controls. All hybridizations were performed using a C57BL6 male DNA reference. Average values of log2 ratios are plotted at a 40 kb resolution.

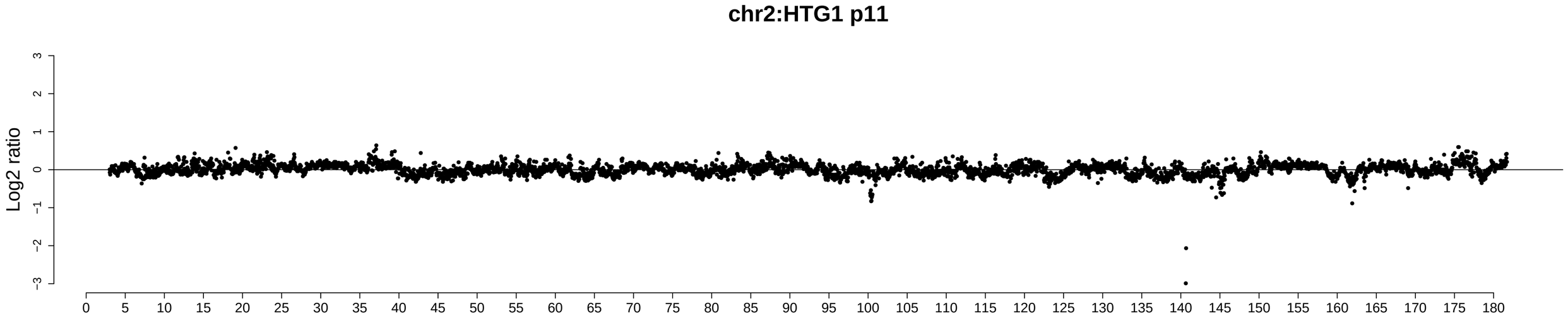

chr1:CBA control kidney
chr1:HAP1 p25
chr1:HAP2 p18
chr1:HTG_control male kidney
chr1:HTG1 p11
chr1:HTG2 p11
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195

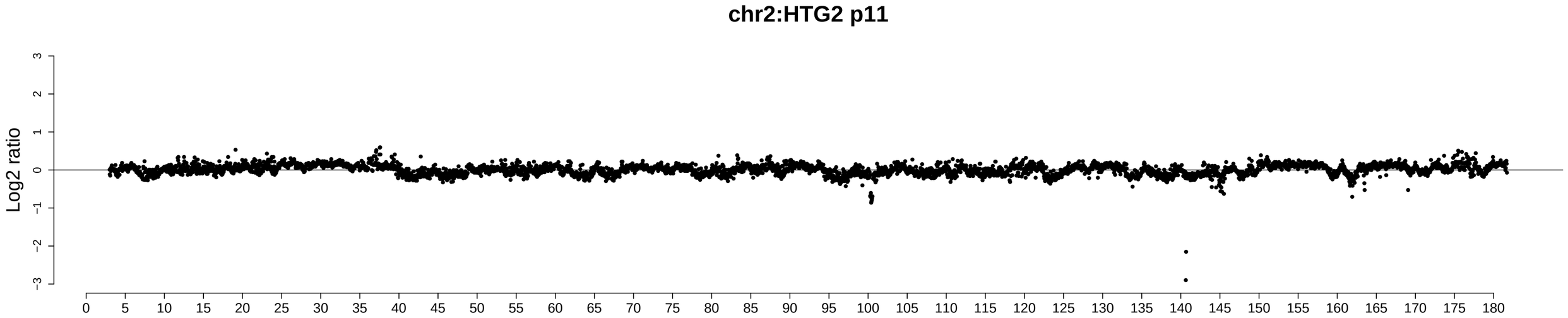

chr2:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180

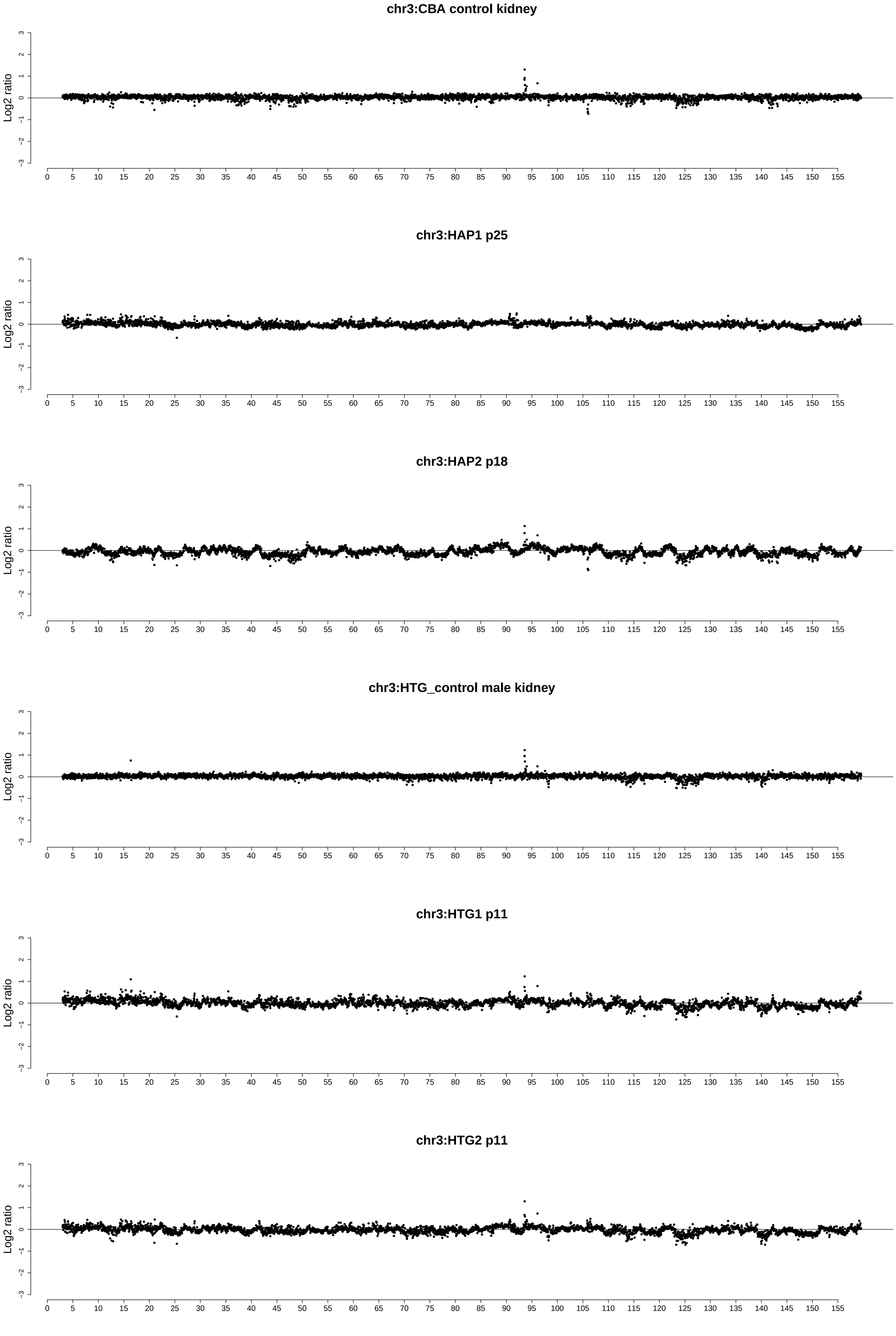
chr2:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180

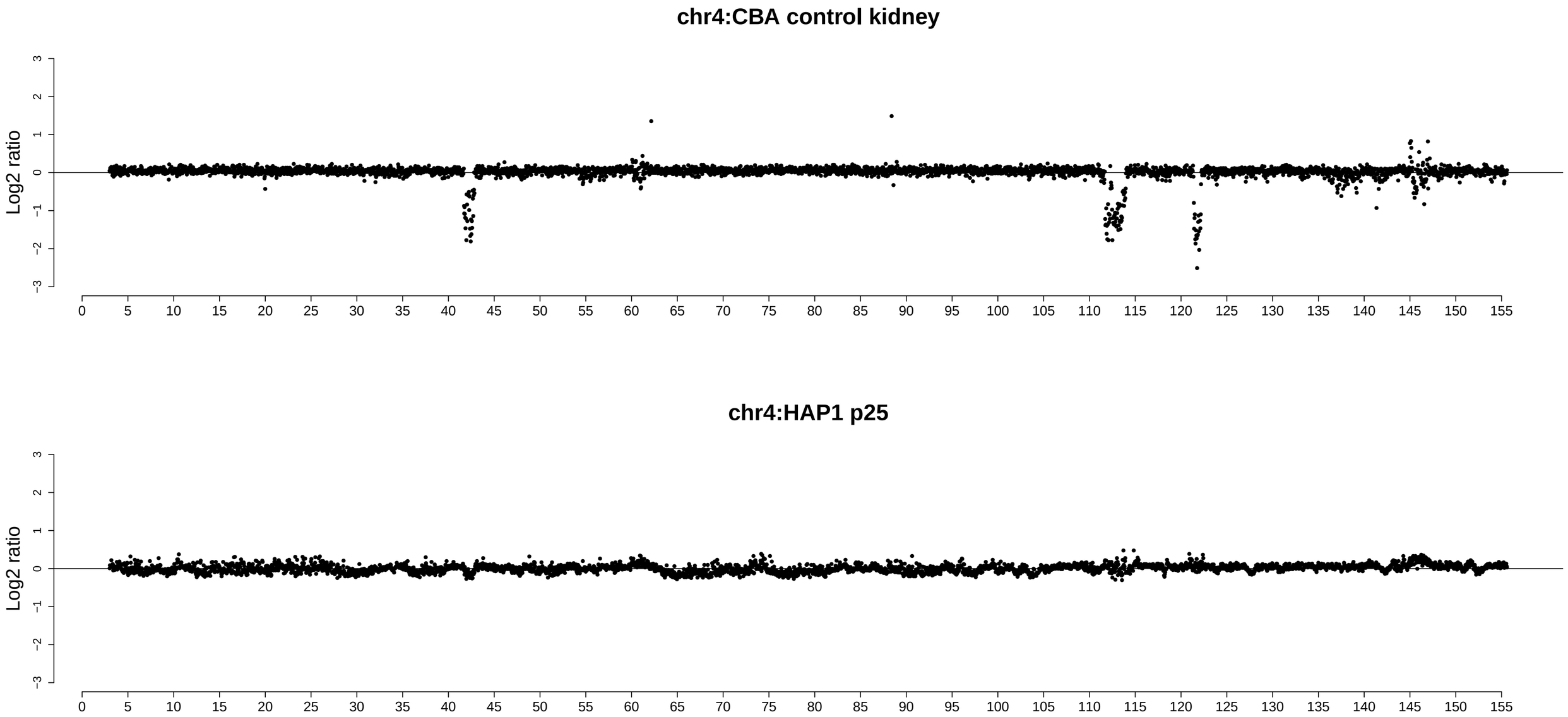

chr2:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180


chr2:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180

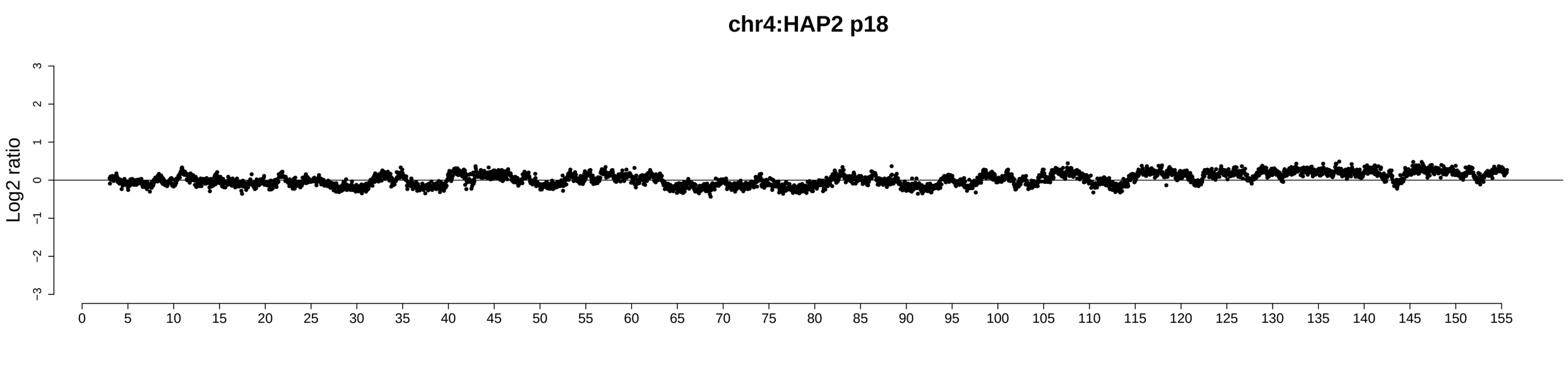

chr2:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180

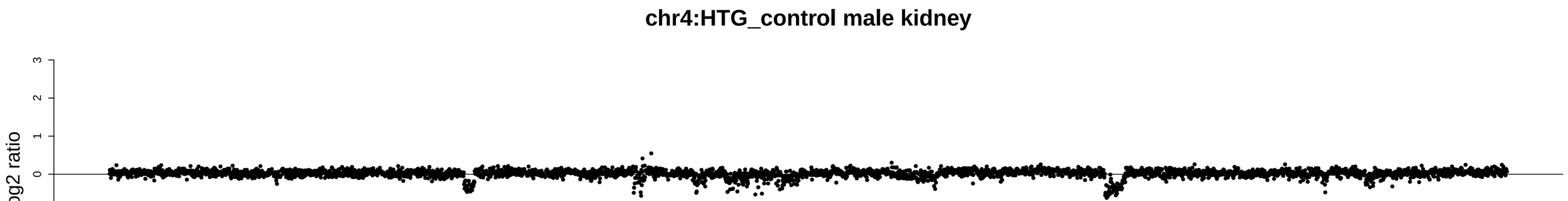

chr2:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180

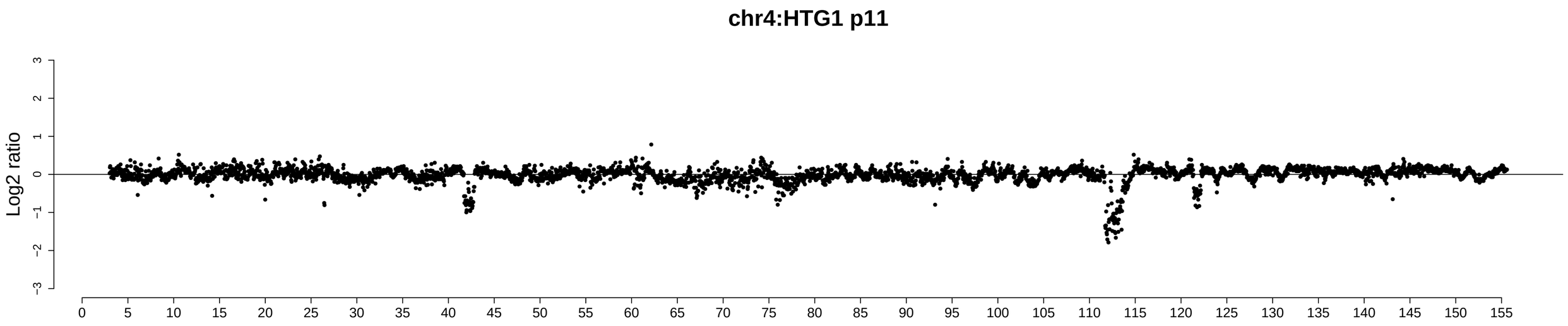

chr3:CBA control kidney
chr3:HAP1 p25
chr3:HAP2 p18
chr3:HTG_control male kidney
chr3:HTG1 p11
chr3:HTG2 p11
Log2 ratio
−3
−2
−1
0
1
2
3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
105
110
115
120
125
130
135
140
145
150
155

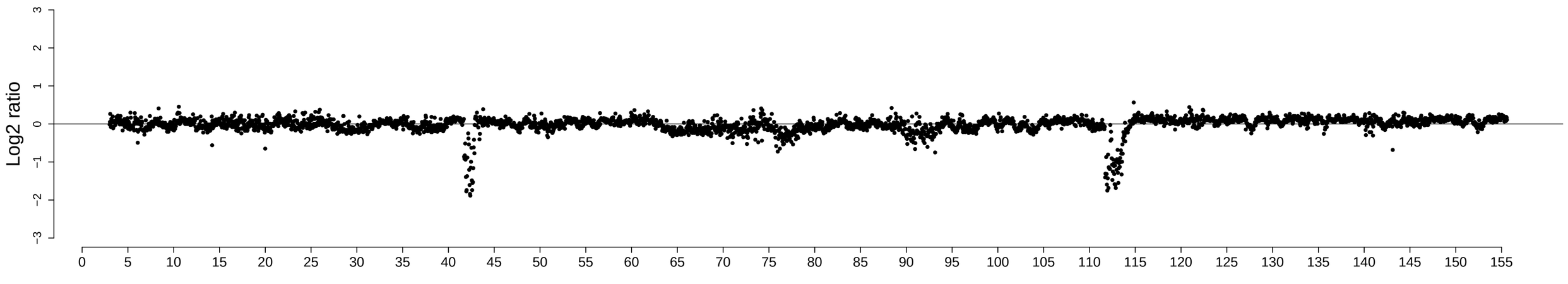

chr4:CBA control kidney
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155

chr4:HAP1 p25
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155

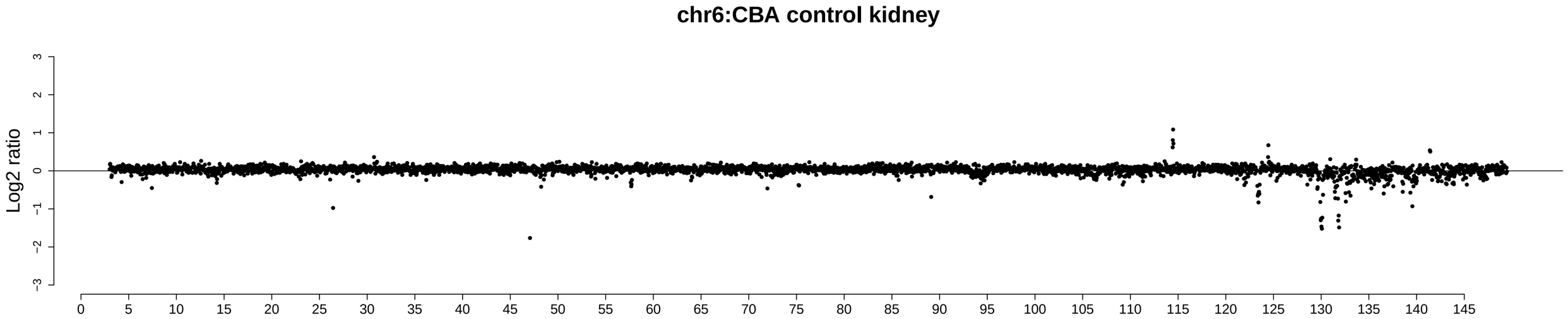

chr4:HAP2 p18
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155

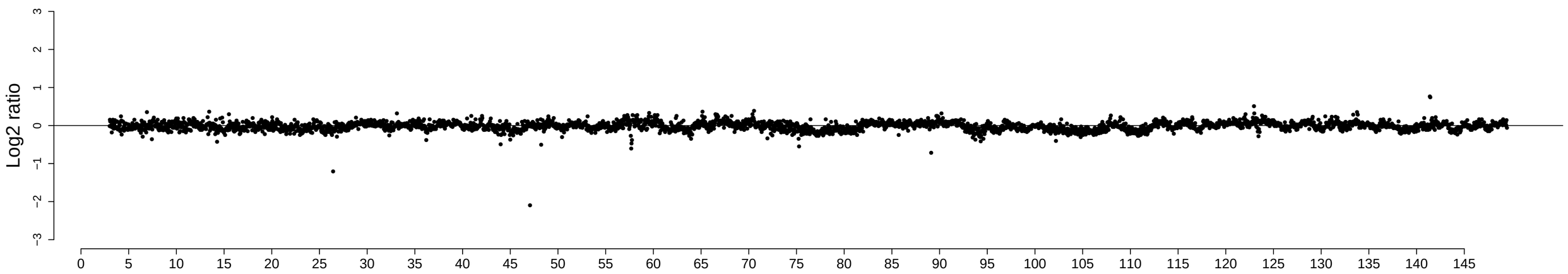

chr4:HTG_control male kidney
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155

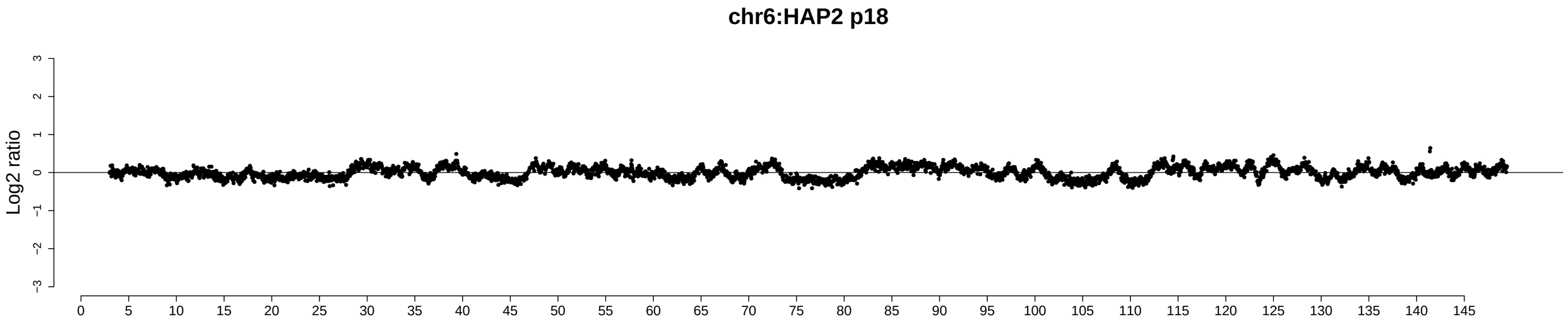

chr4:HTG1 p11
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155

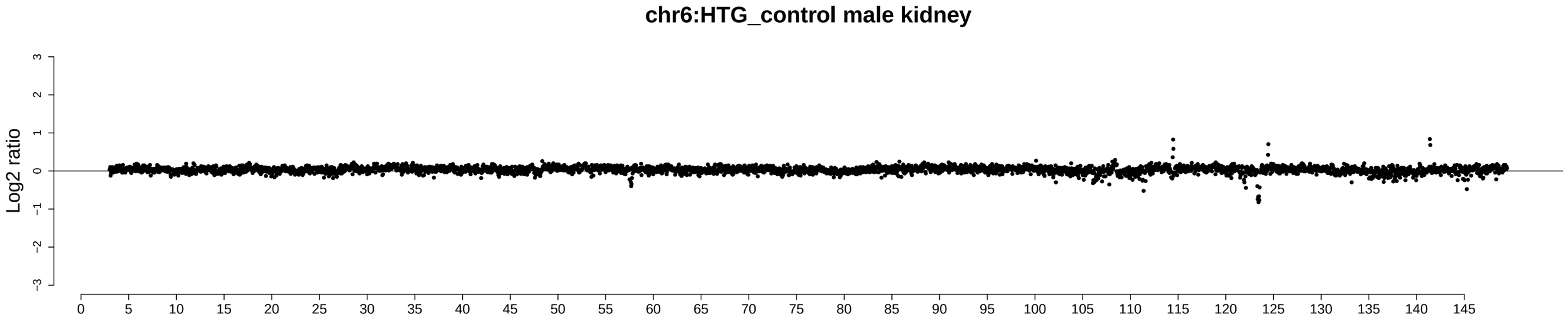

chr4:HTG2 p11
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155

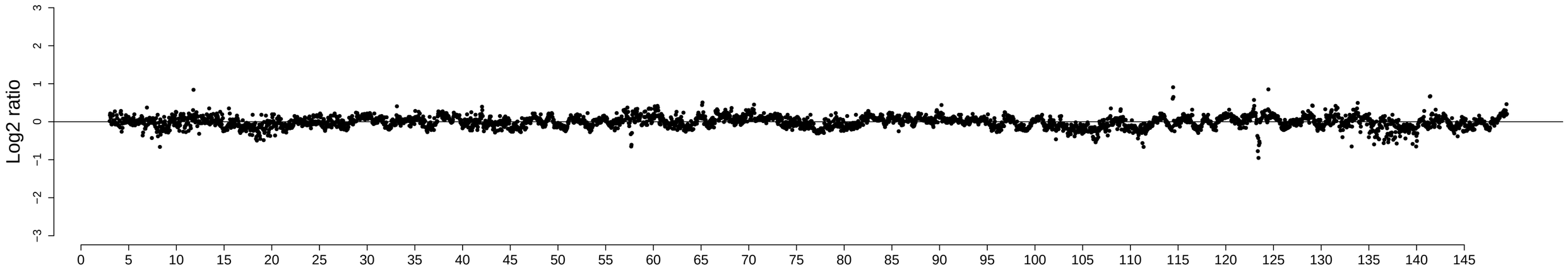
chr5:CBA control kidney
chr5:HAP1 p25
chr5:HAP2 p18
chr5:HTG_control male kidney
chr5:HTG1 p11
chr5:HTG2 p11
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150

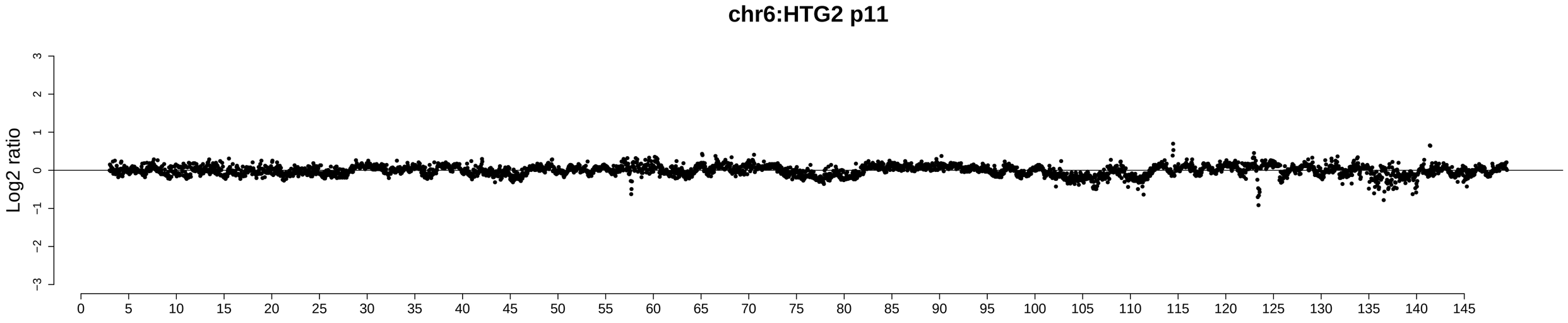

chr6:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145

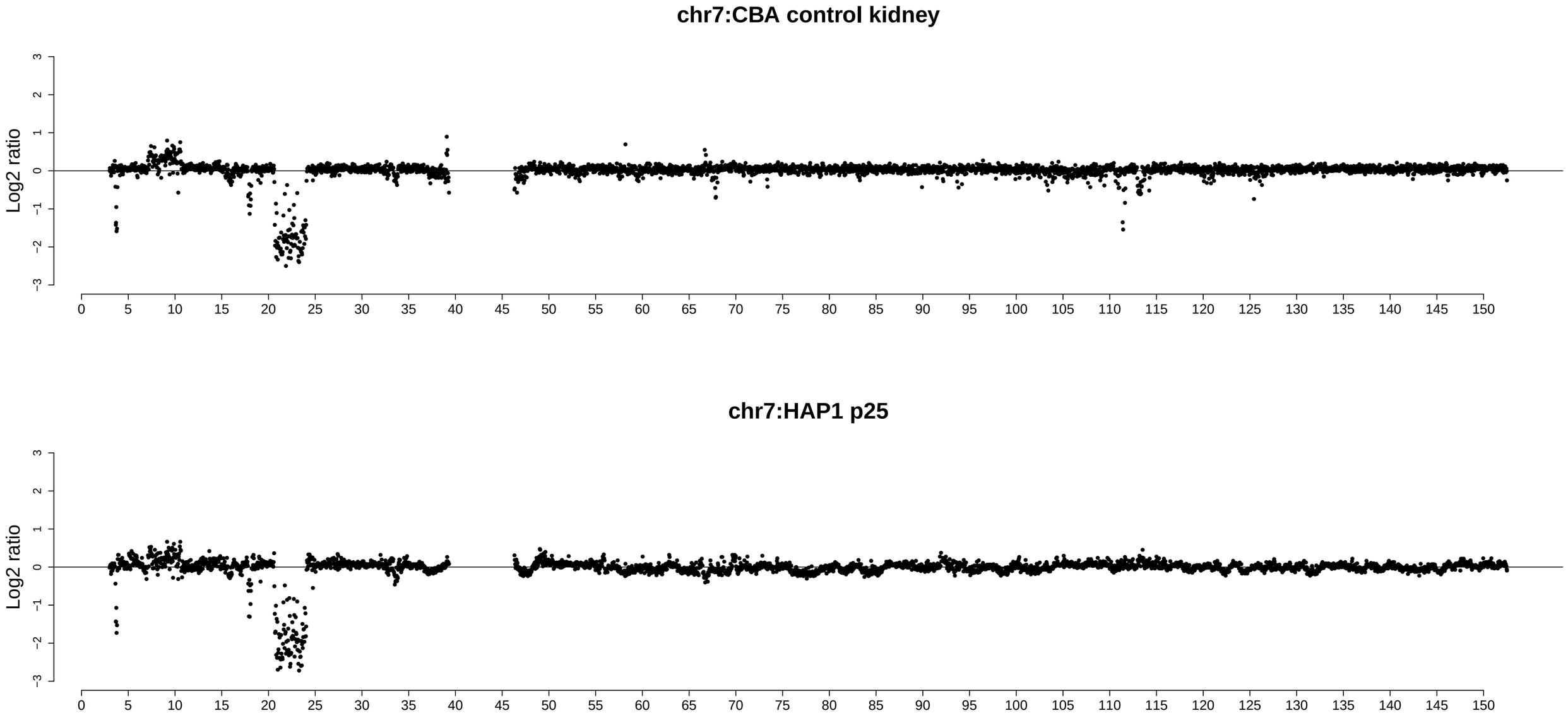

chr6:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145


chr6:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145

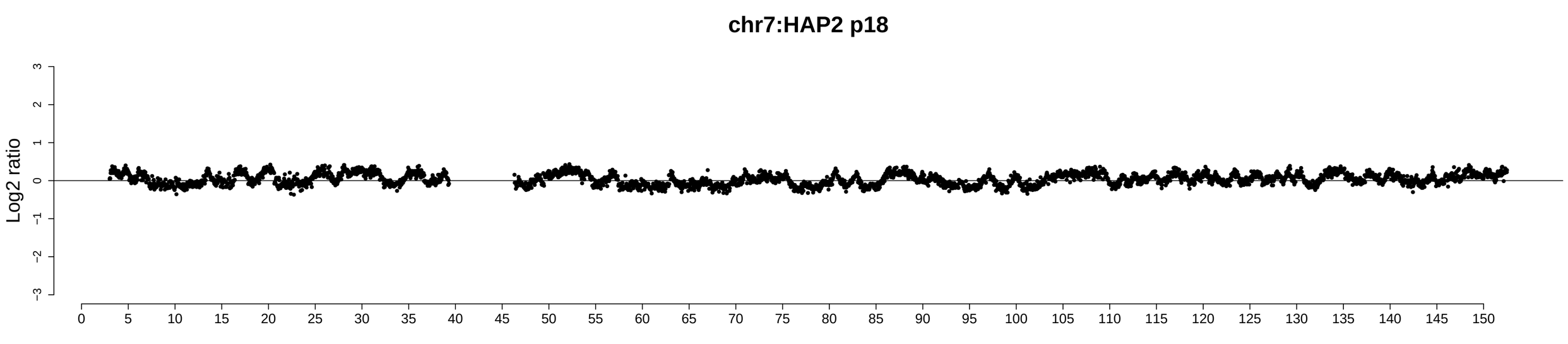

chr6:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145

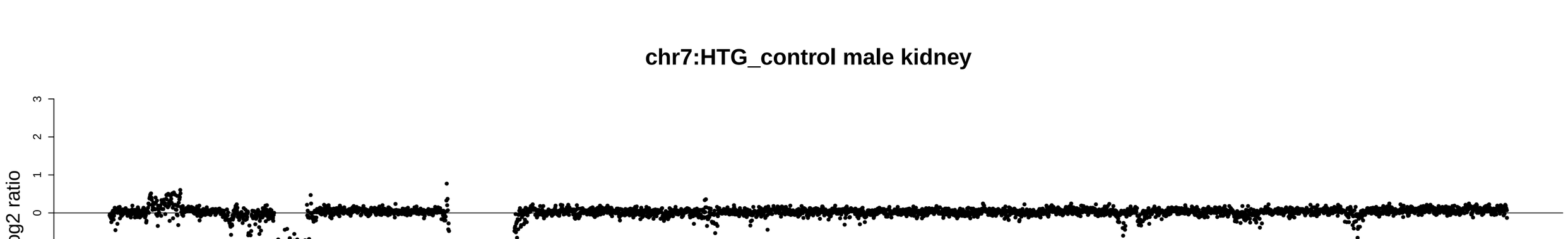

chr6:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145

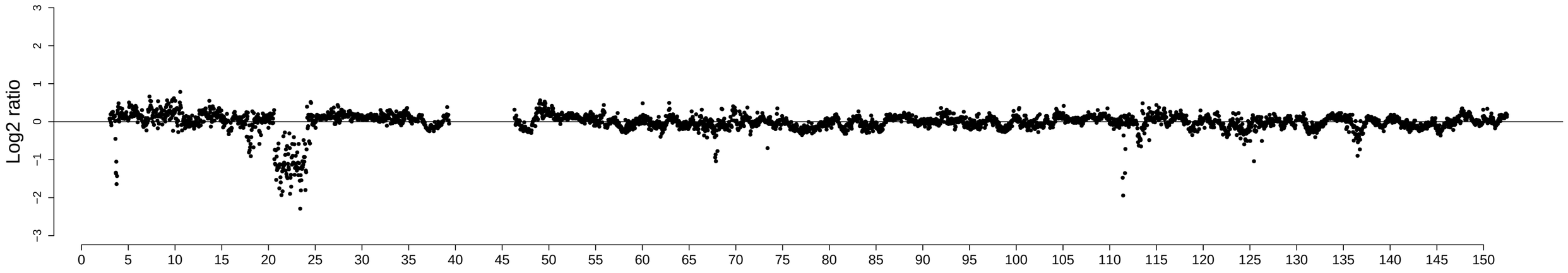

chr6:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145

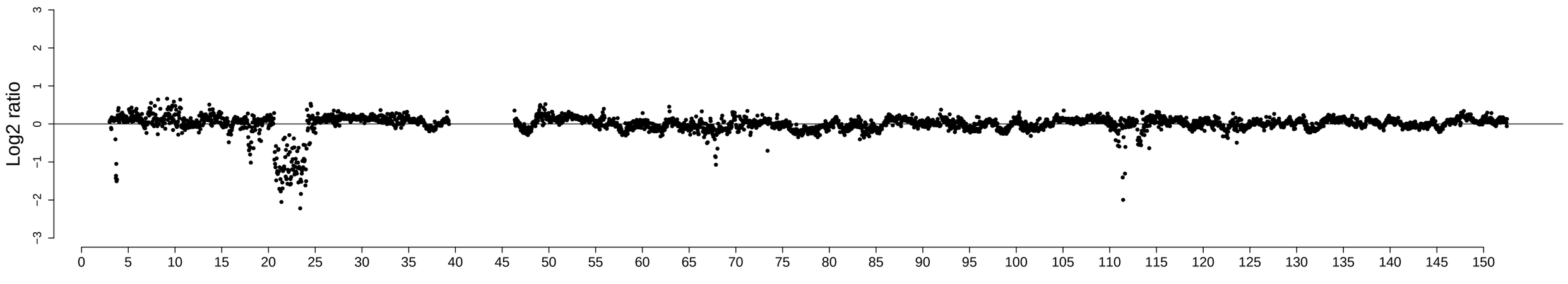

chr7:CBA control kidney
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150

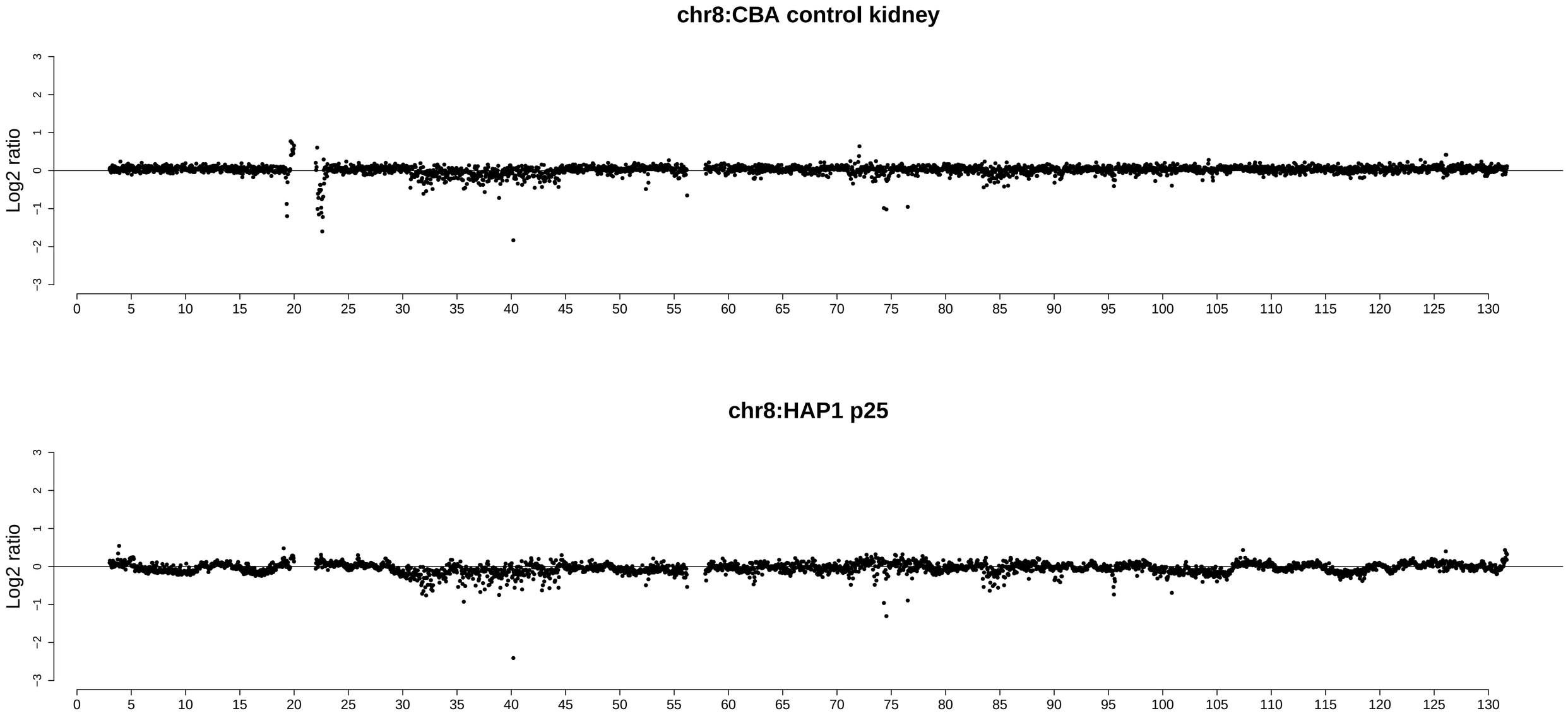
chr7:HAP1 p25
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150

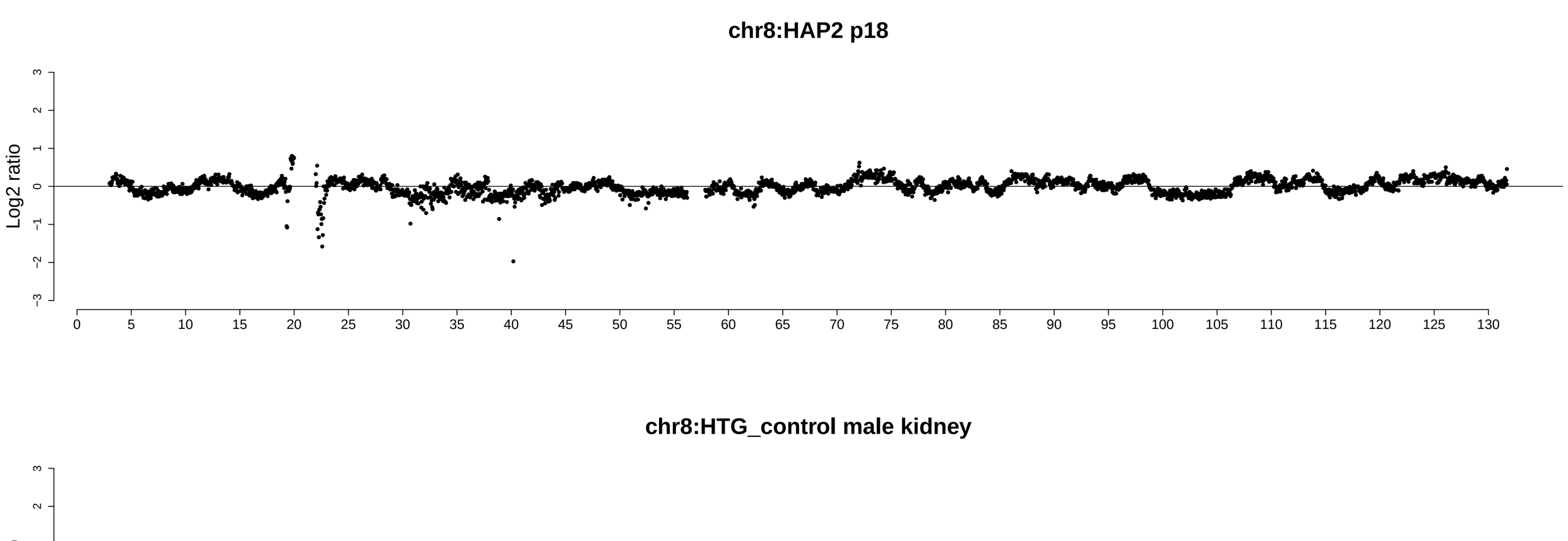

chr7:HAP2 p18
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150

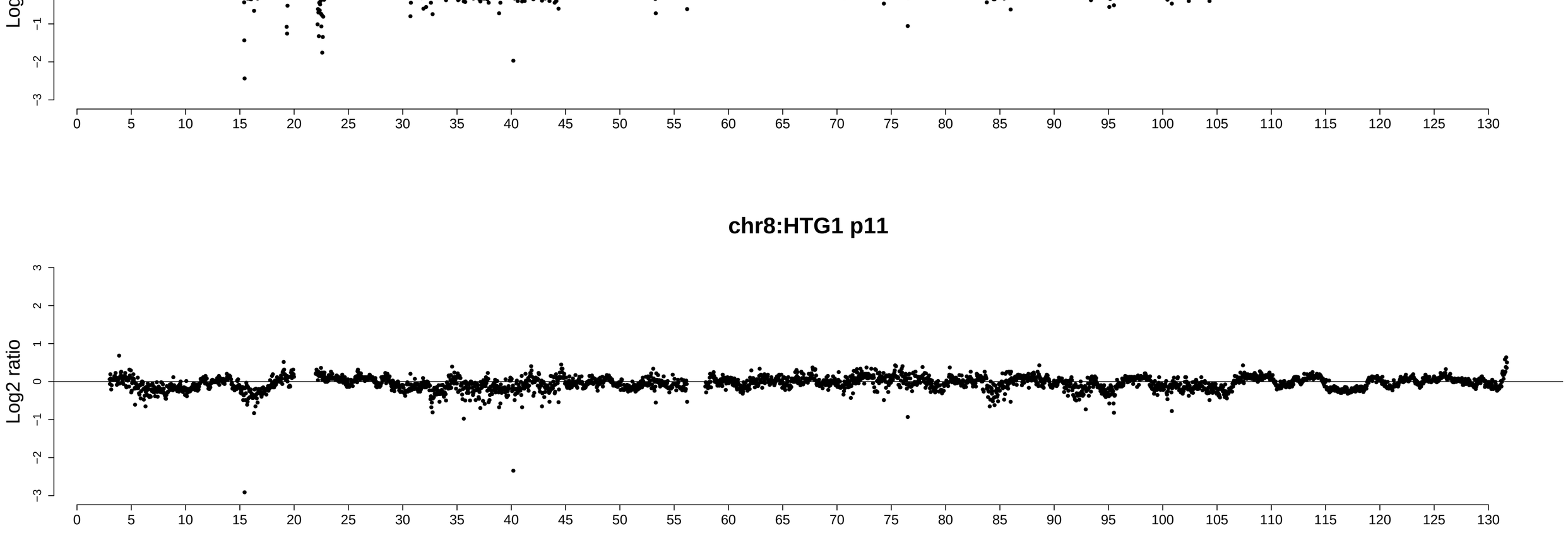

chr7:HTG_control male kidney
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150

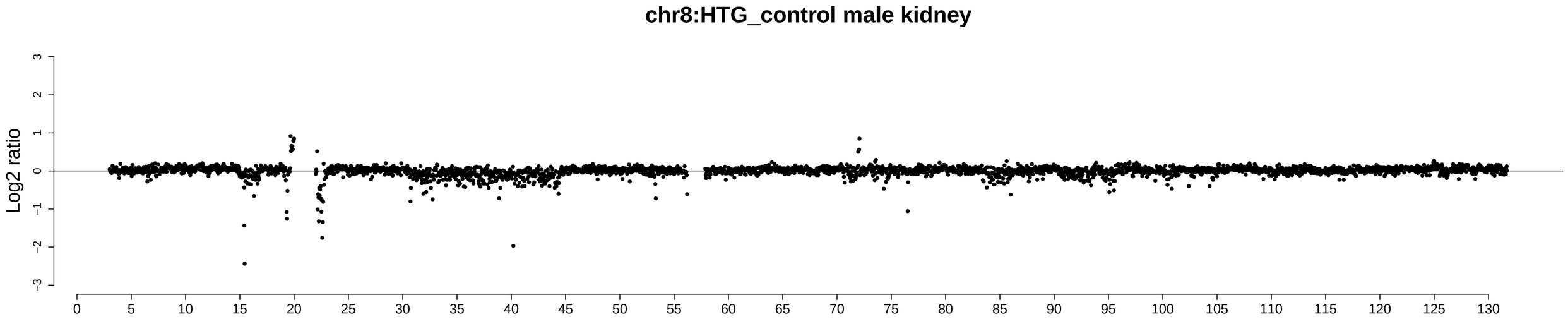

chr7:HTG1 p11
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150


chr7:HTG2 p11
Log2 ratio
−3
−2
−1
0
1
2
3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150

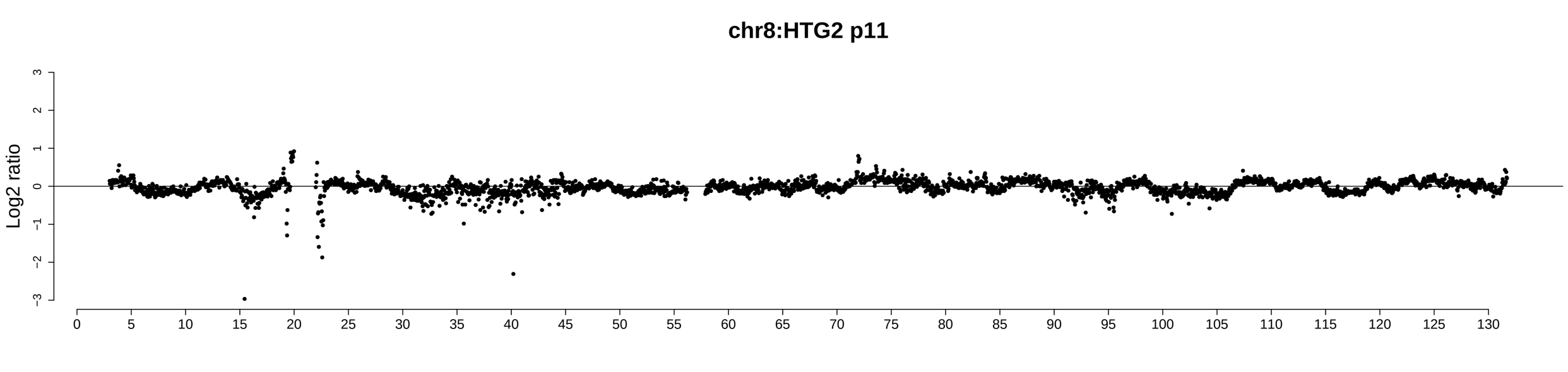

chr8:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130

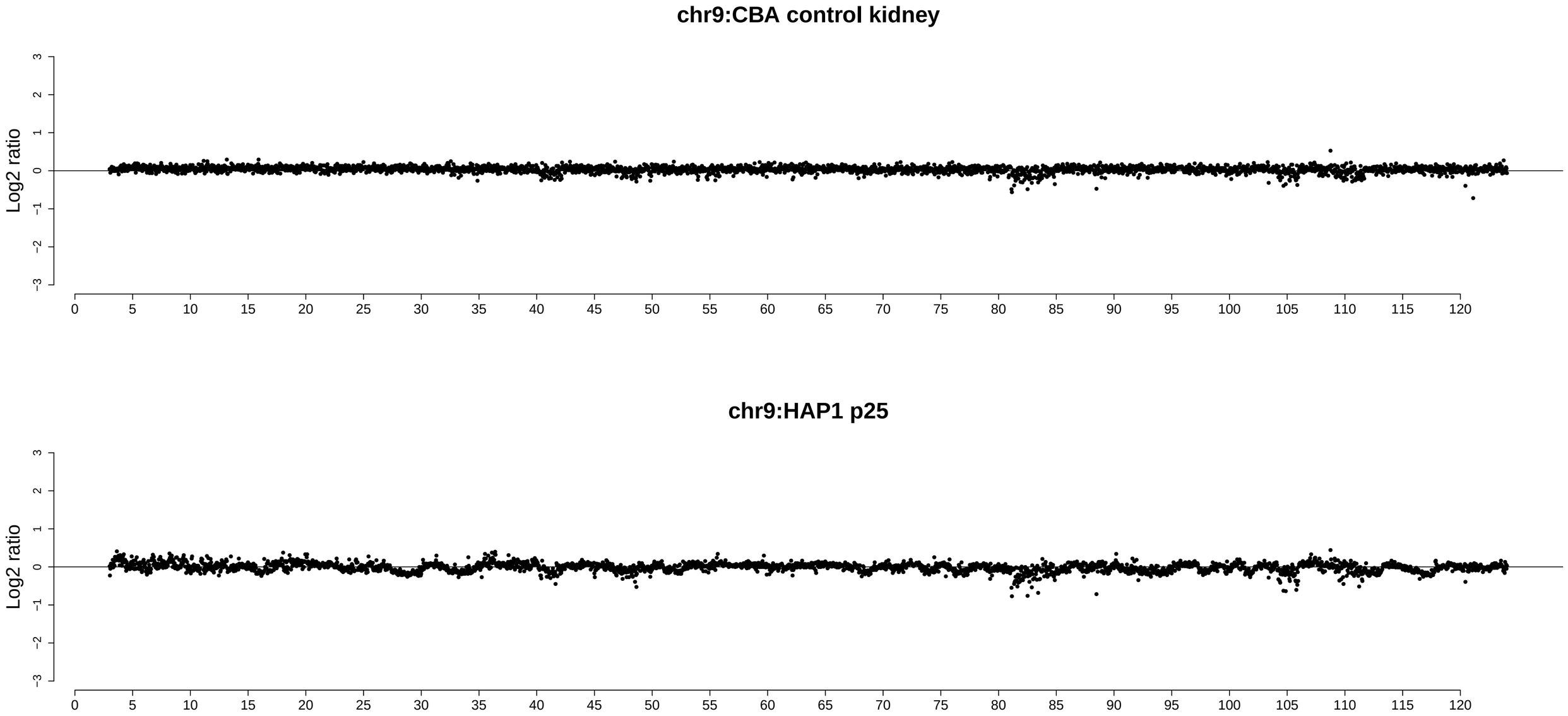

chr8:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130


chr8:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130

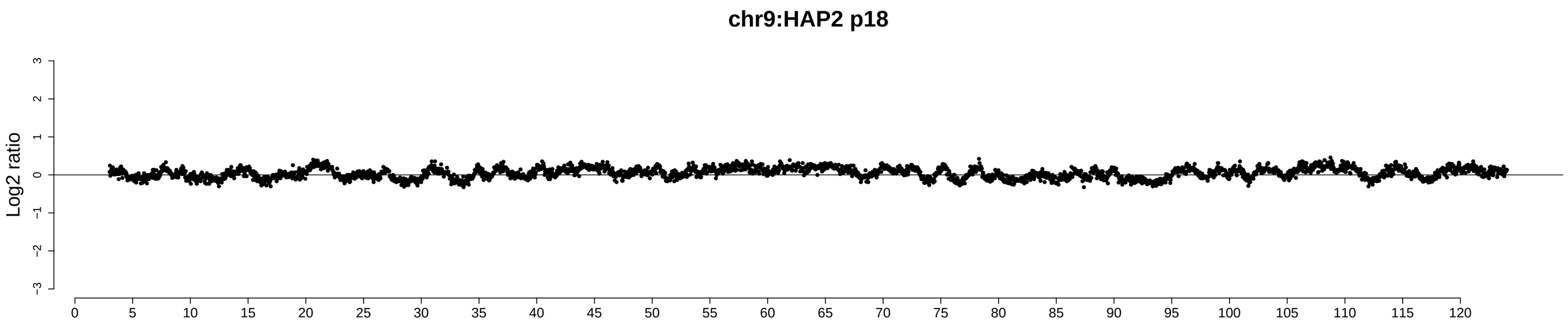

chr8:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130

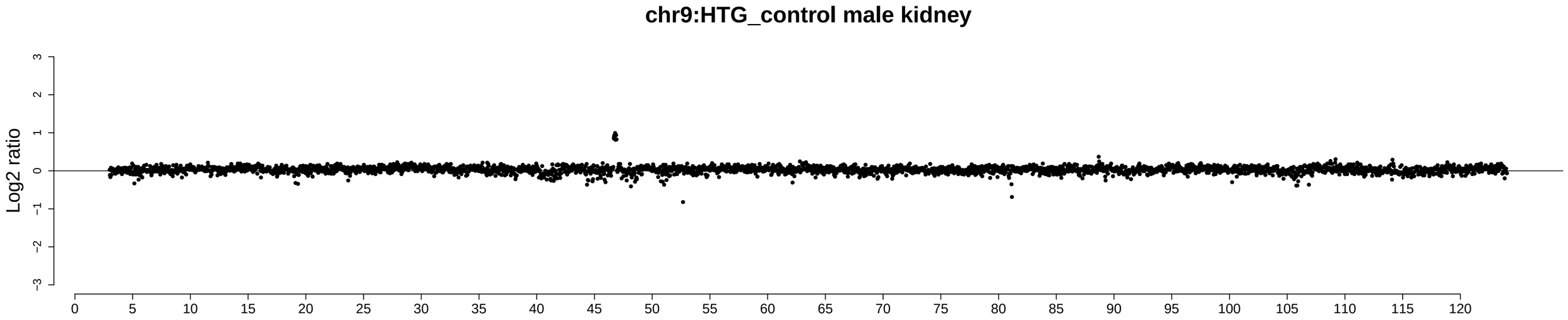
chr8:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130

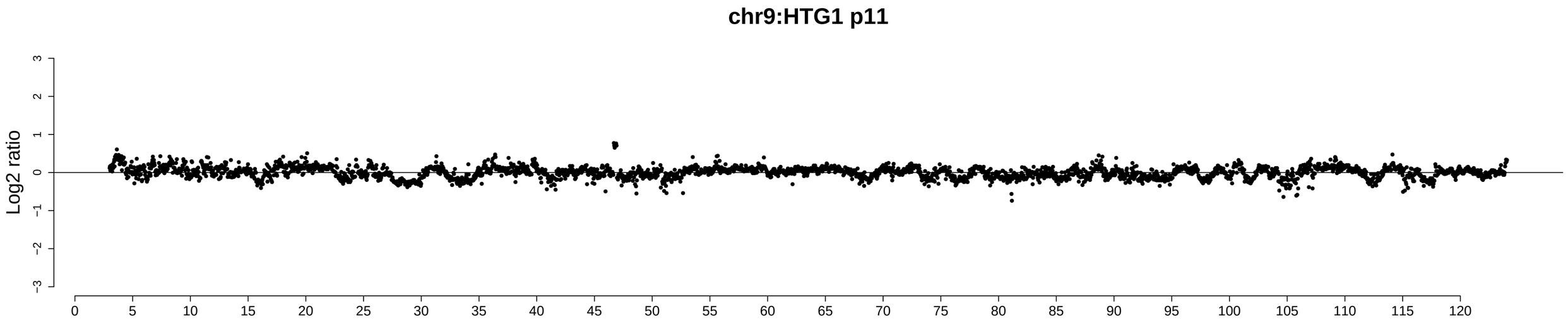

chr8:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130

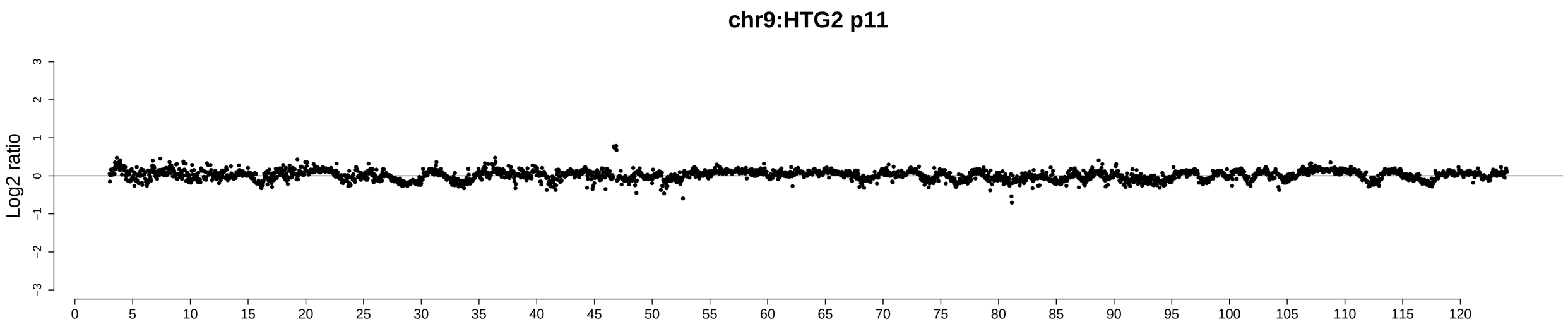

chr9:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

chr9:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

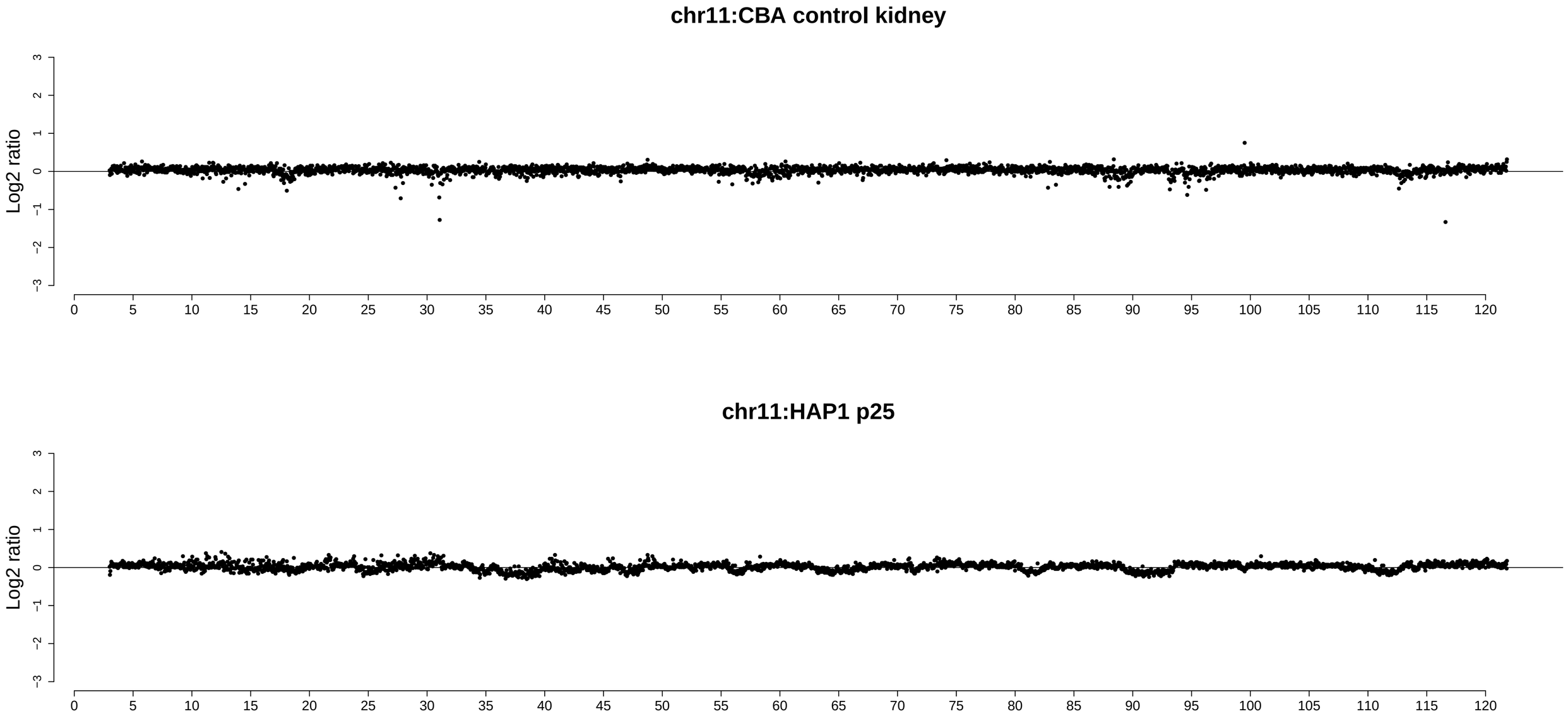

chr9:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120


chr9:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

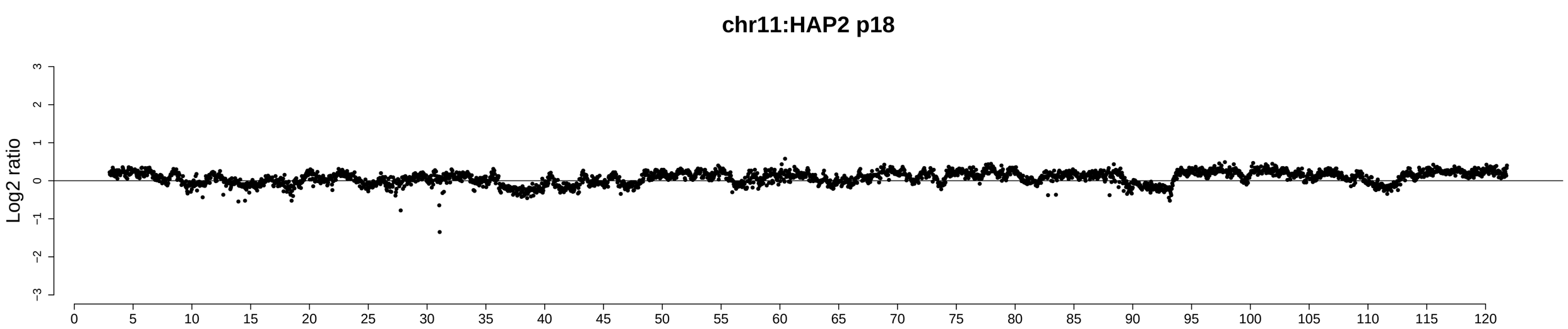

chr9:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

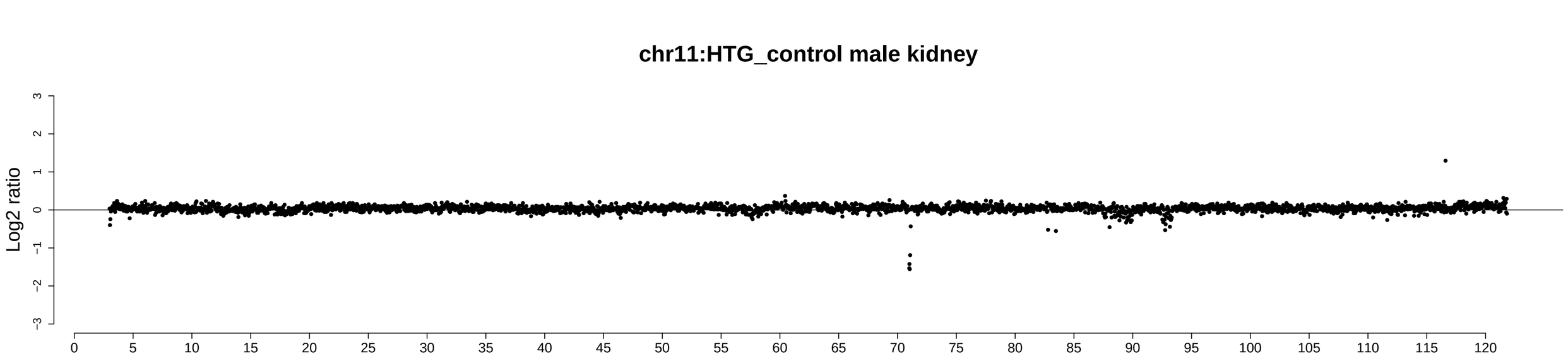

chr9:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

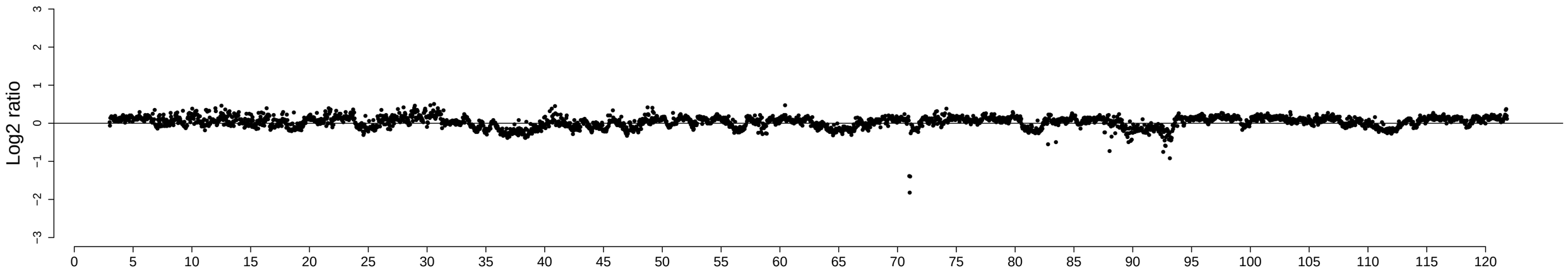
chr10:CBA control kidney
chr10:HAP1 p25
chr10:HAP2 p18
chr10:HTG_control male kidney
chr10:HTG1 p11
chr10:HTG2 p11
Log2 ratio
−3
−2
−1
0
1
2
3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
105
110
115
120
125

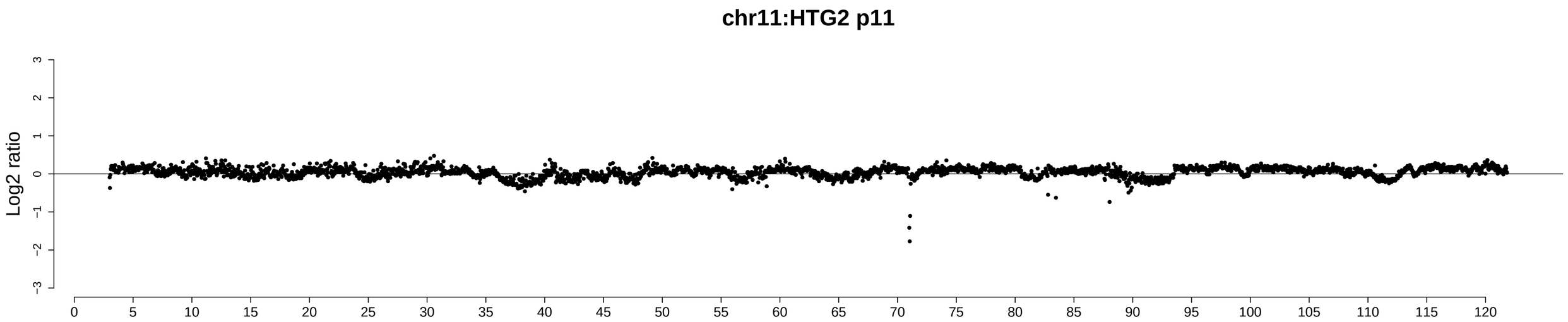

chr11:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

chr11:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

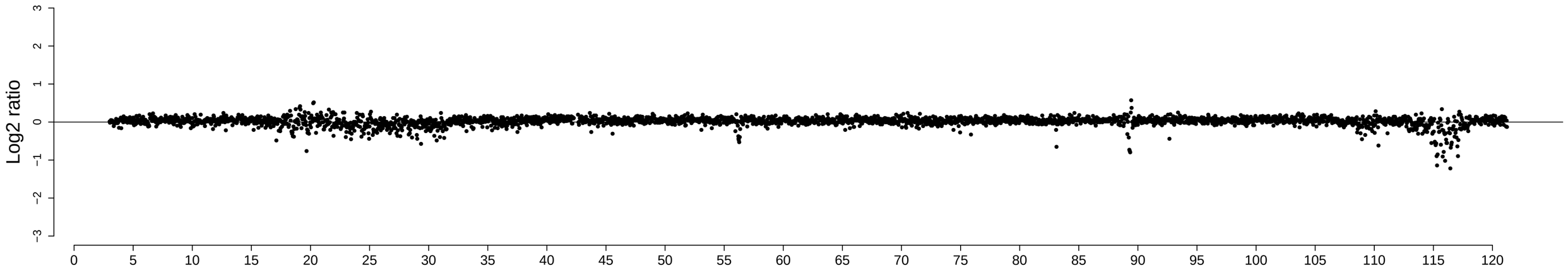

chr11:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120


chr11:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

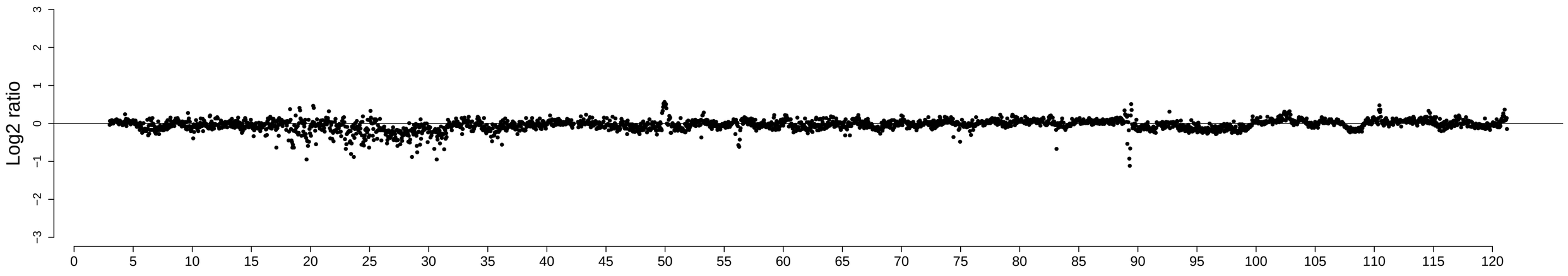

chr11:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120


chr11:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

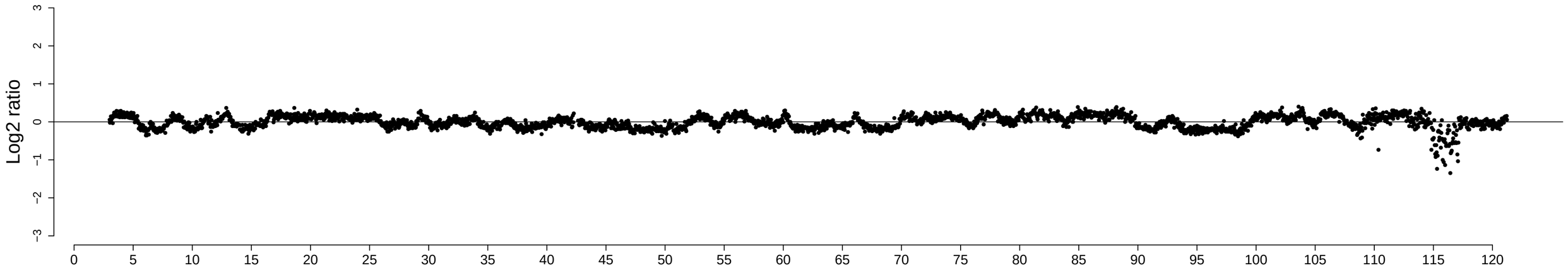
chr12:CBA control kidney



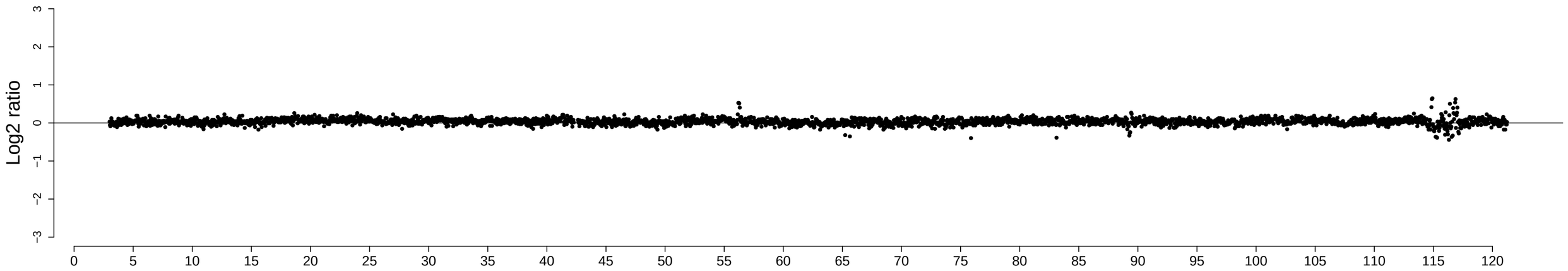
chr12:HAP1 p25



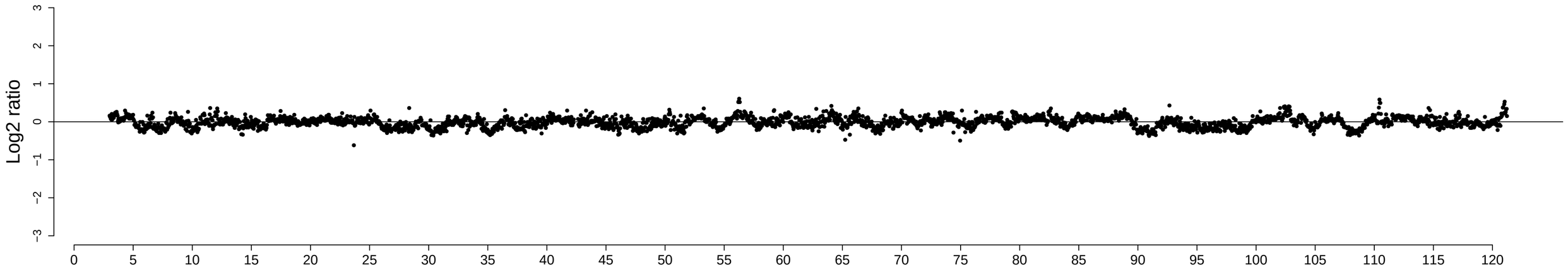
chr12:HAP2 p18



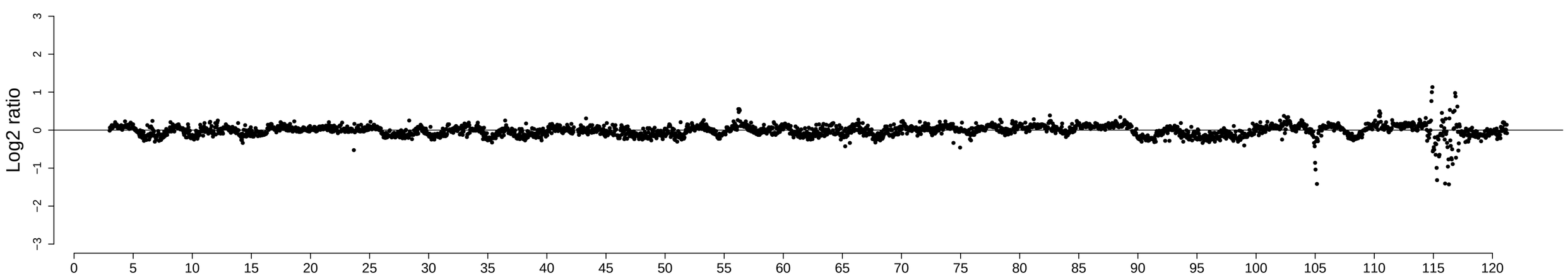
chr12:HTG_control male kidney

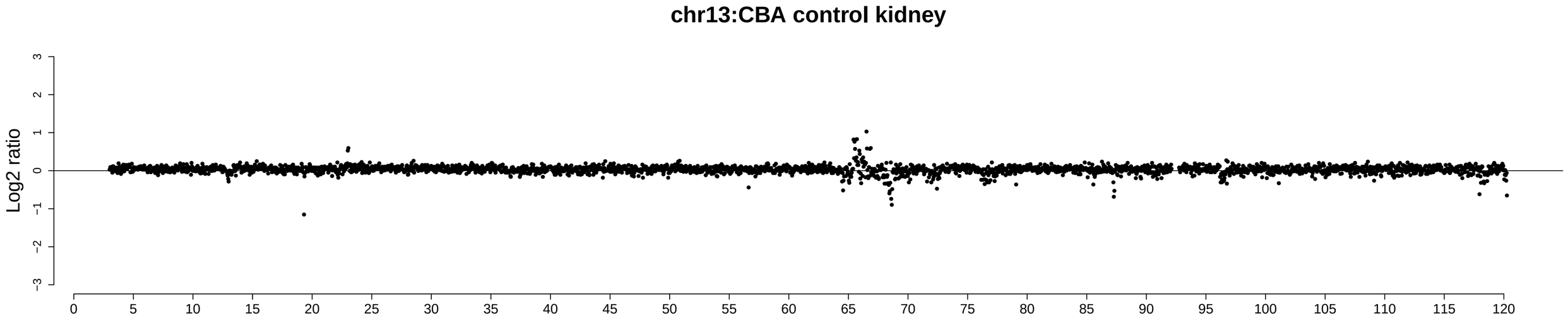


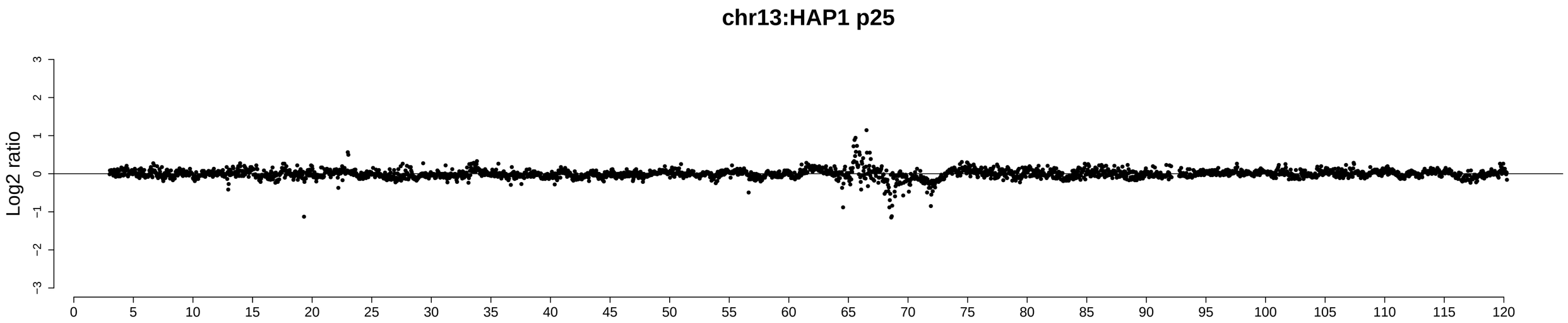
chr12:HTG1 p11

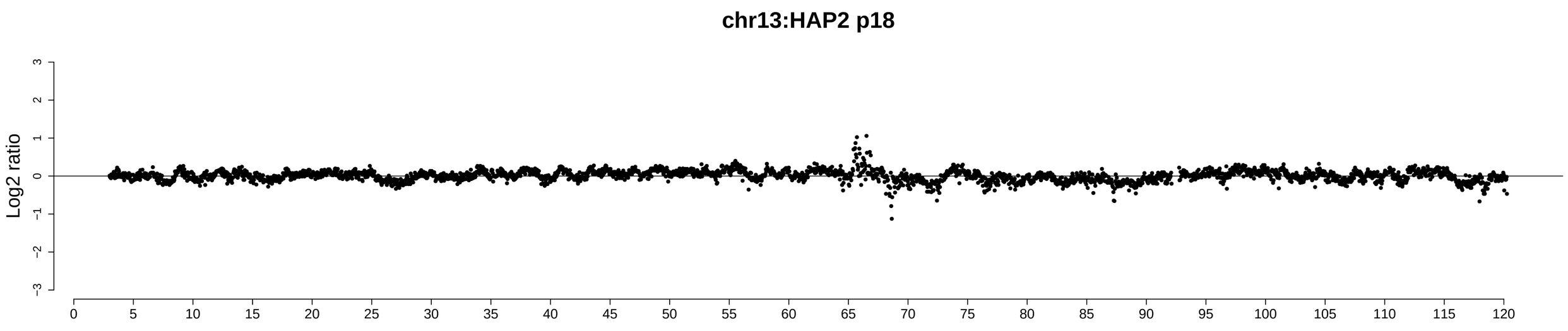


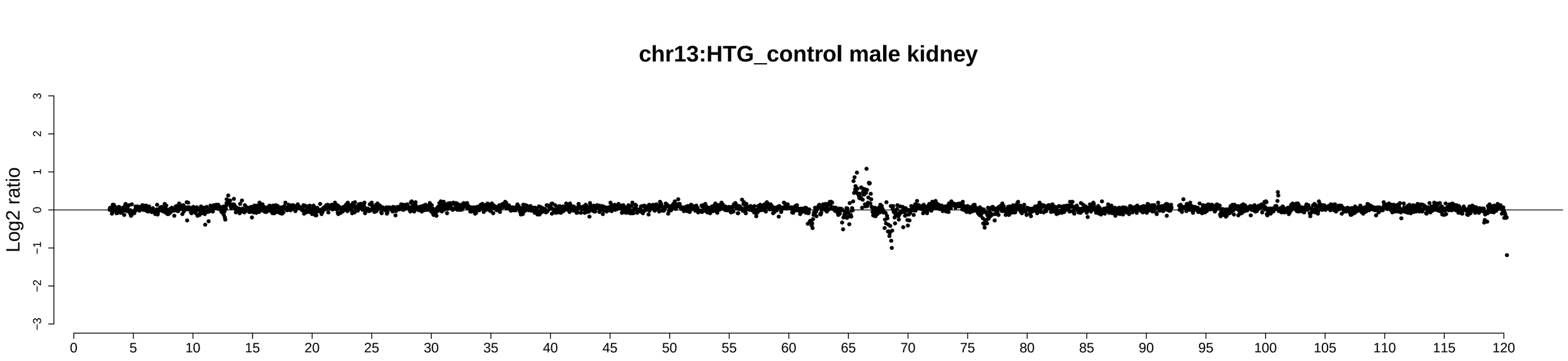
chr12:HTG2 p11

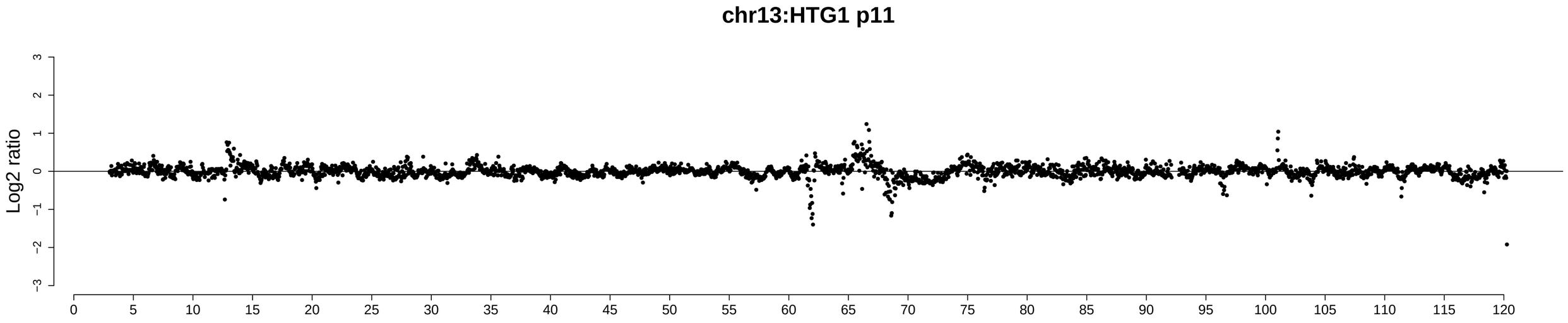


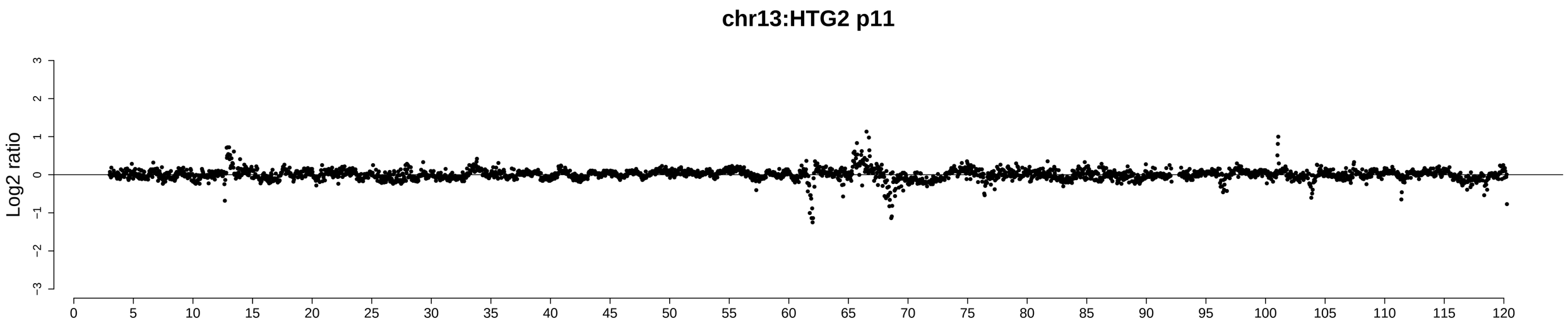

chr13:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

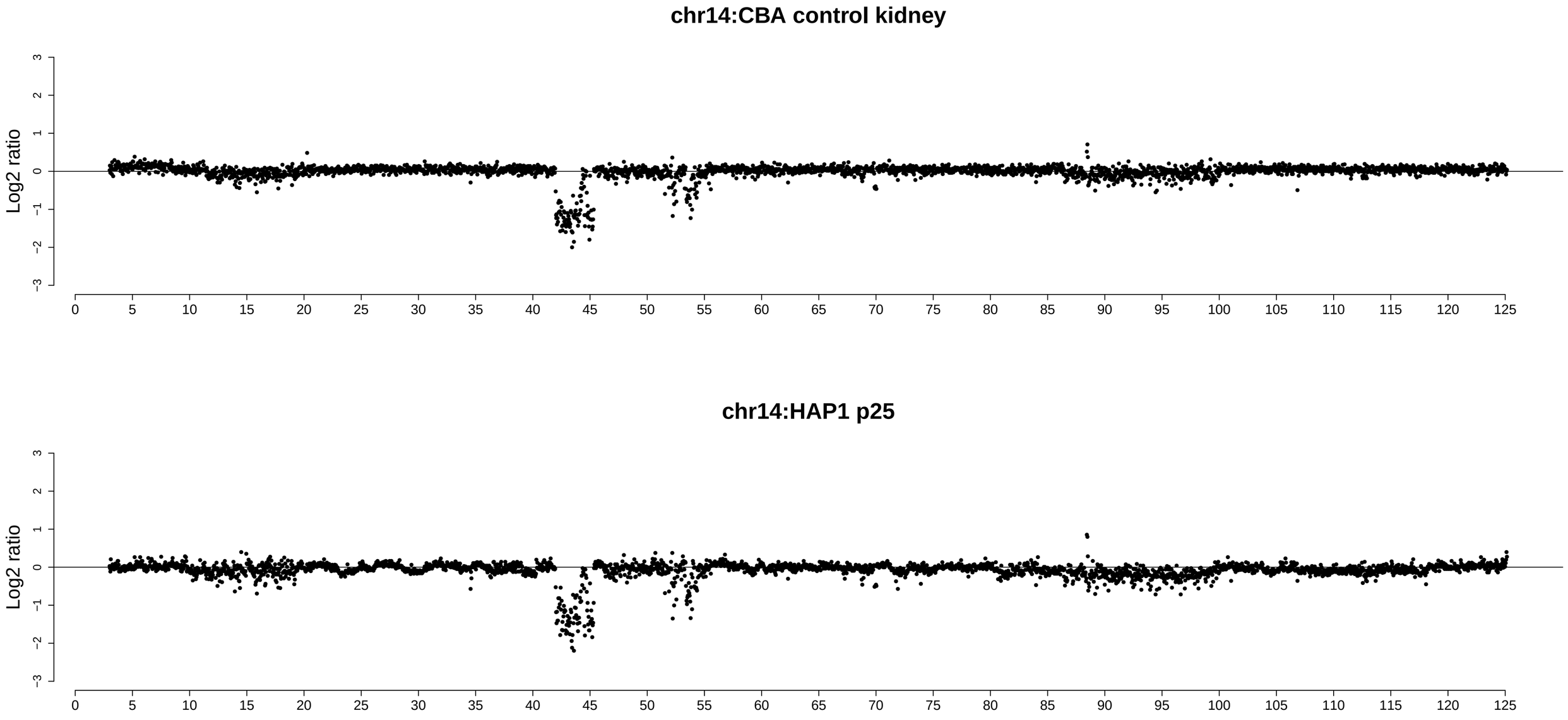

chr13:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

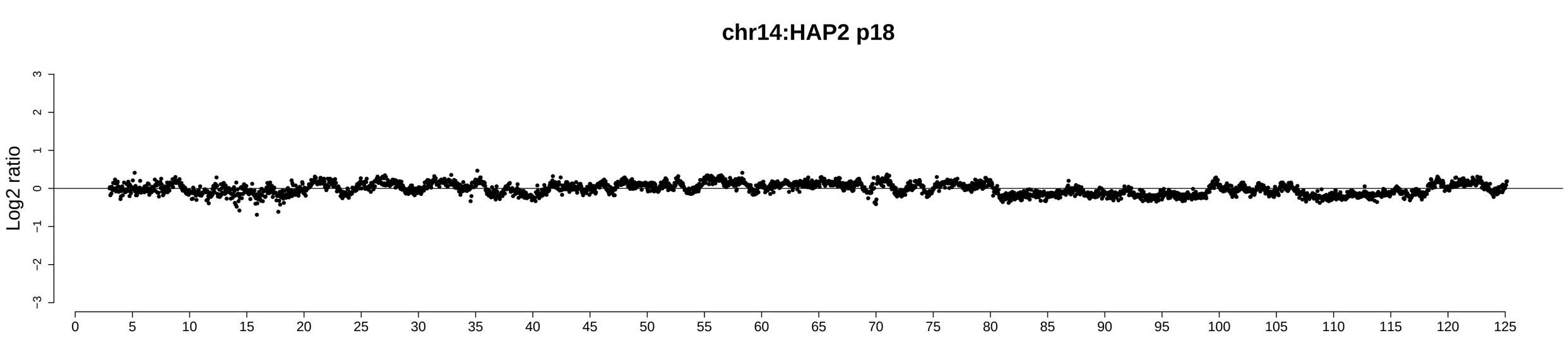

chr13:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120


chr13:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

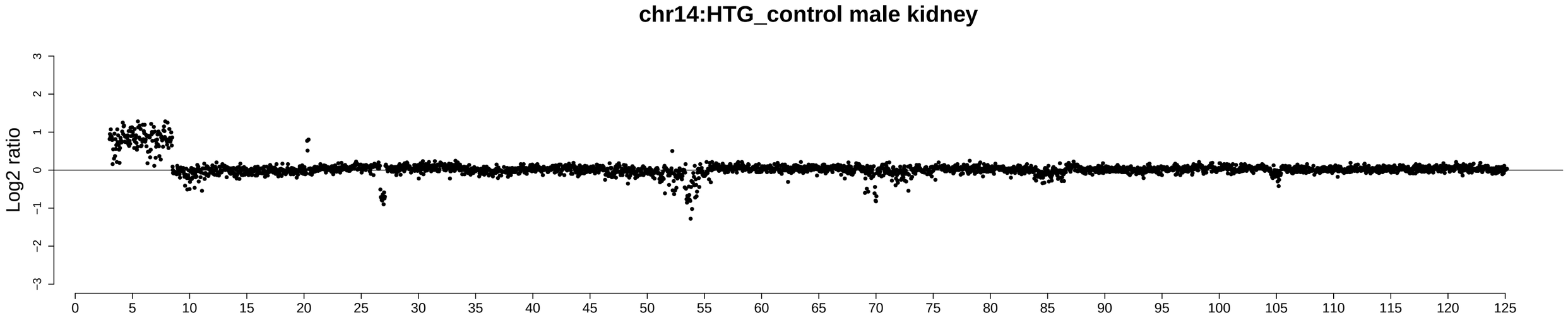

chr13:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

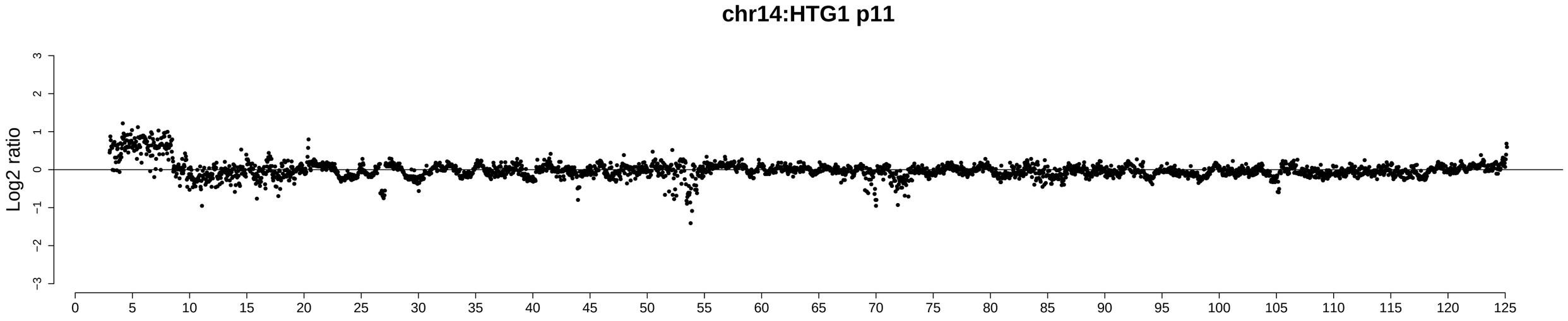

chr13:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120

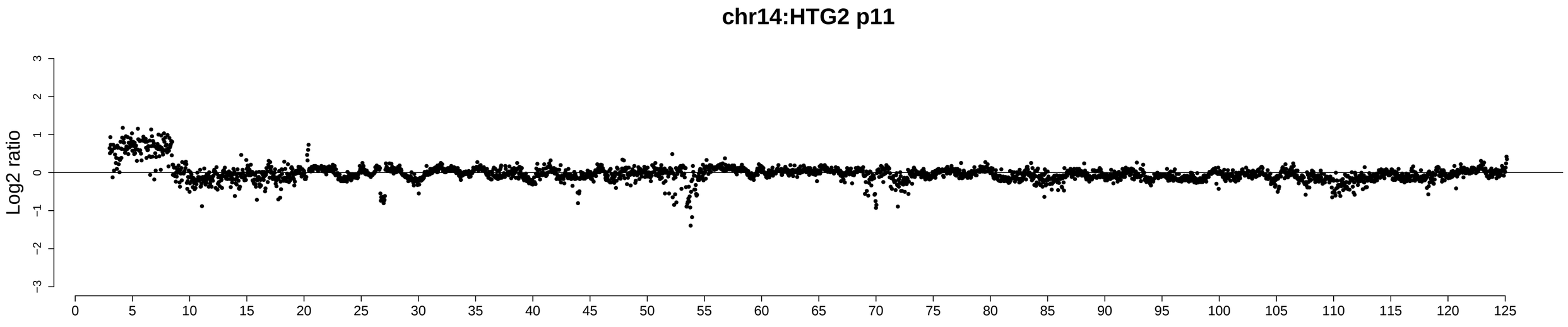

chr14:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125

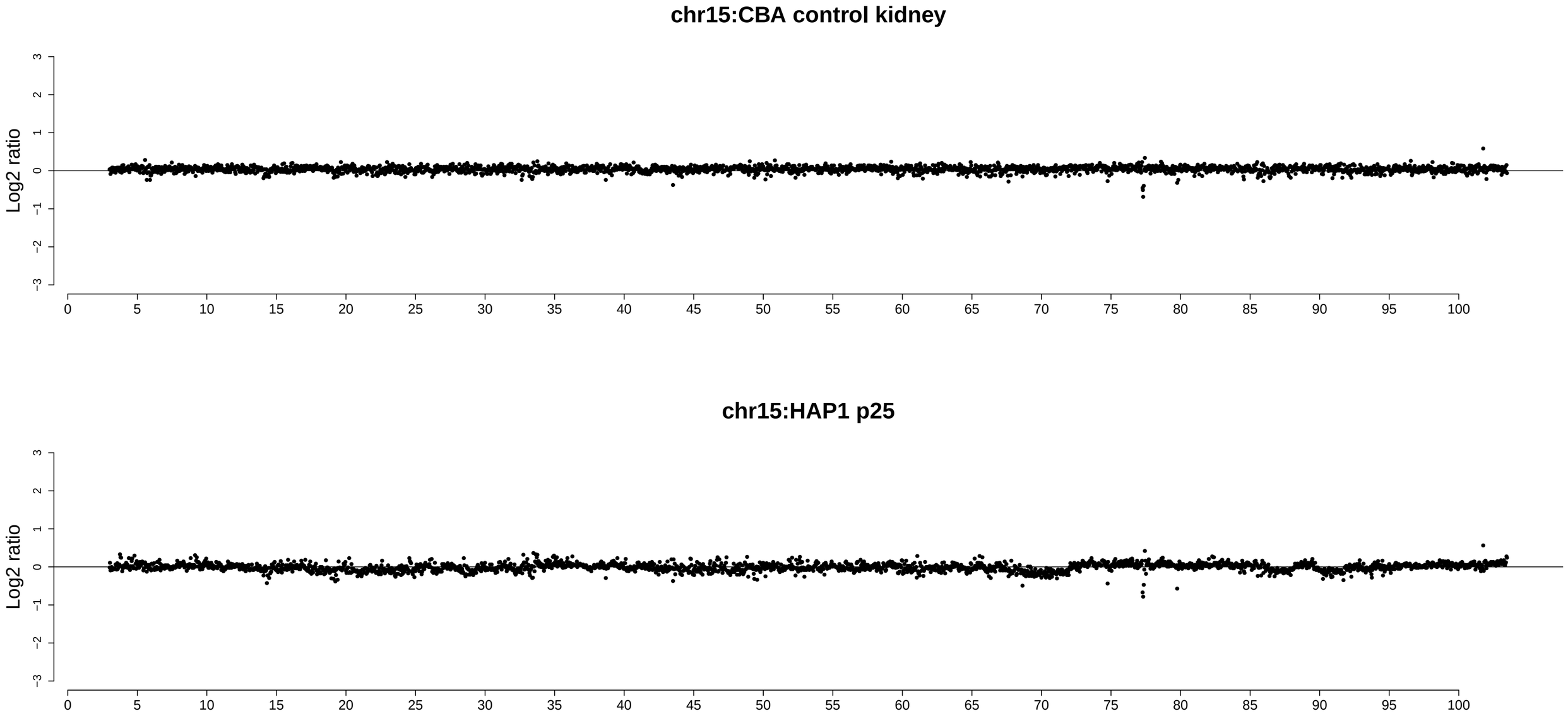

chr14:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125

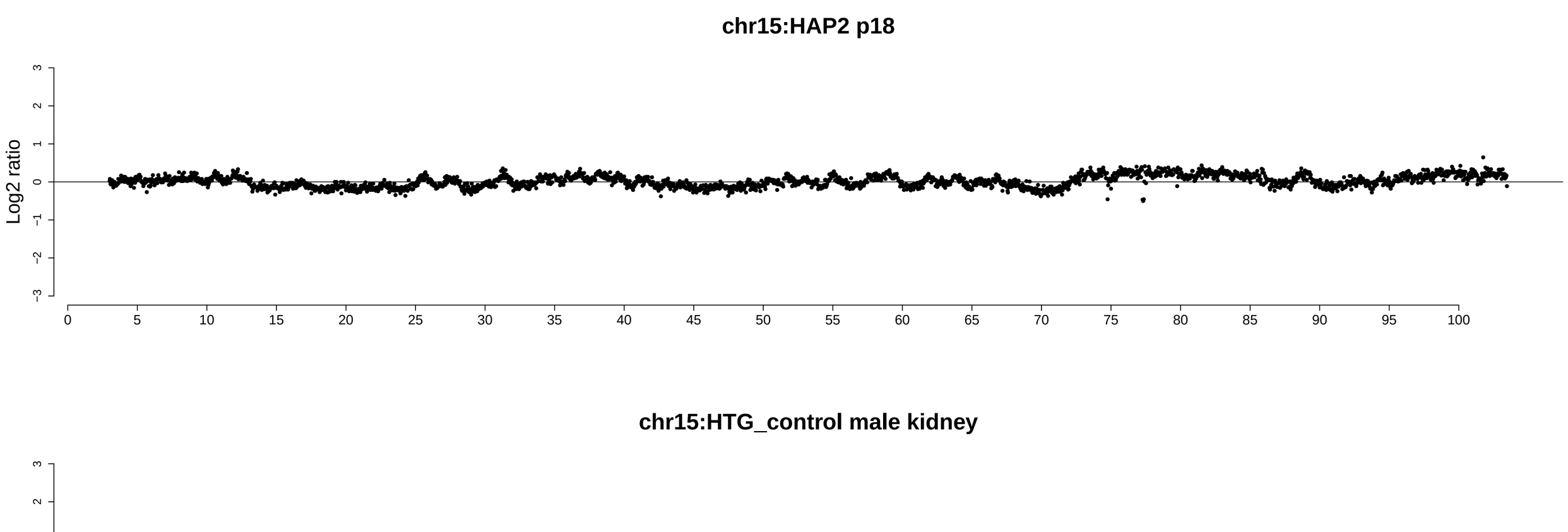
chr14:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125


chr14:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125

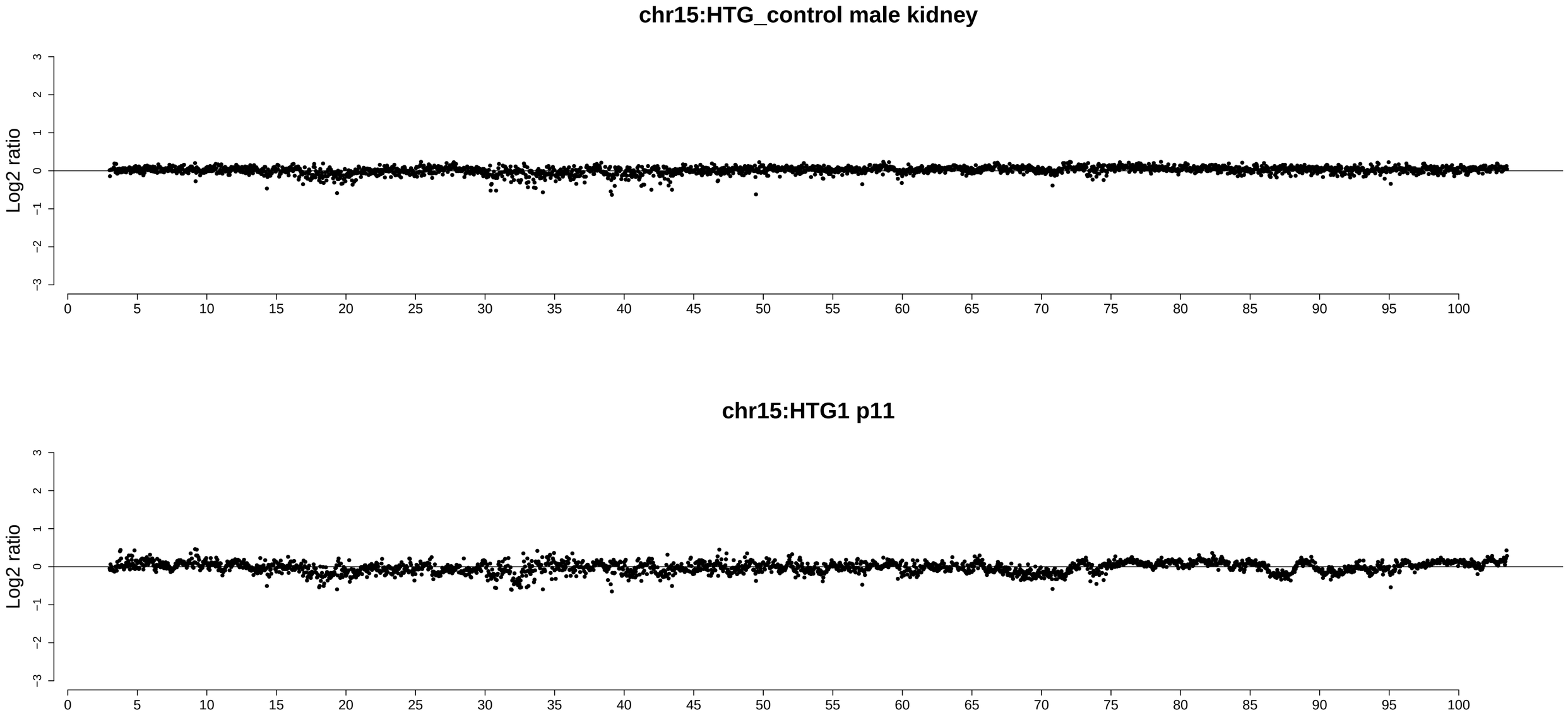

chr14:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125


chr14:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125


chr15:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100

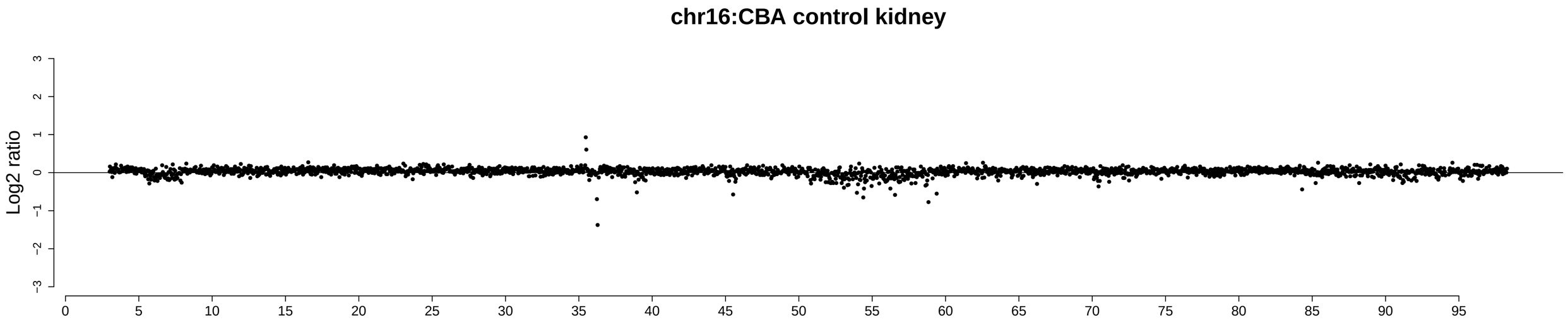

chr15:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100

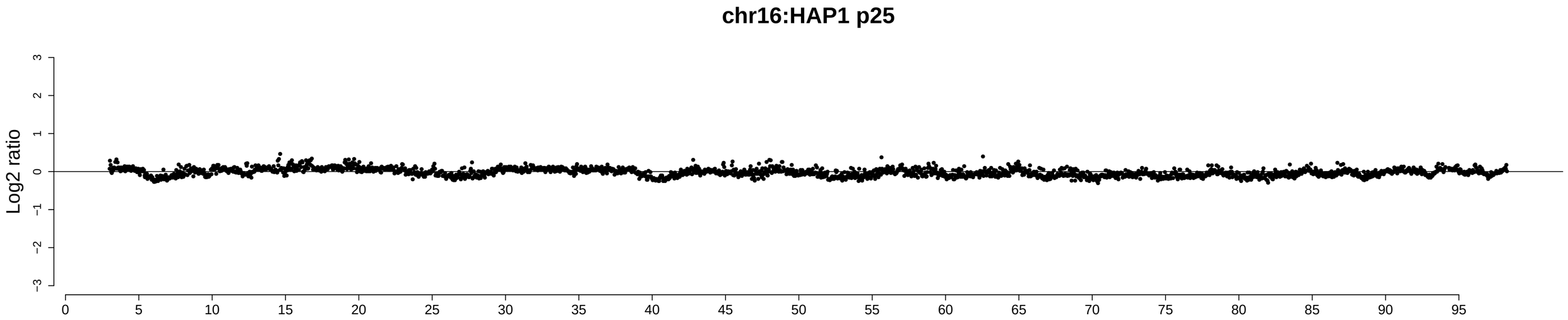
chr15:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100

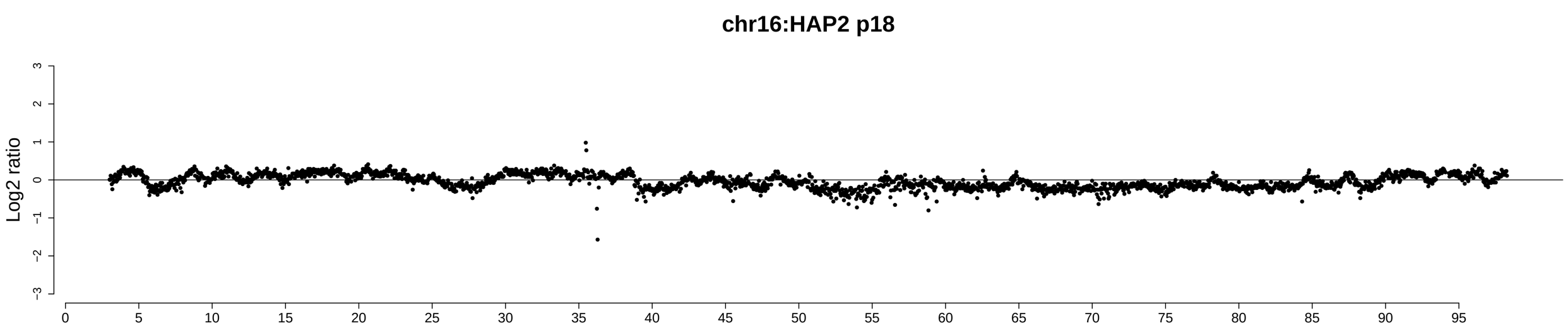

chr15:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100

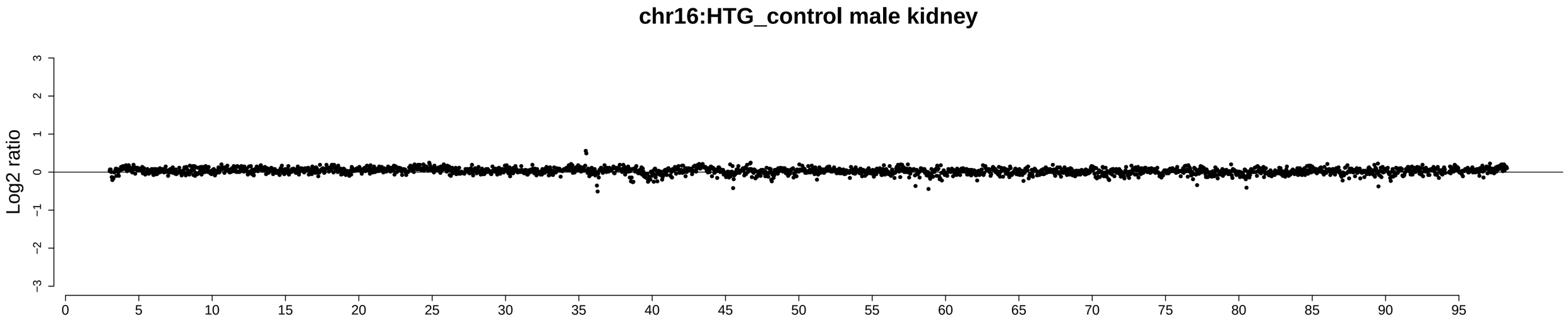
chr15:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100

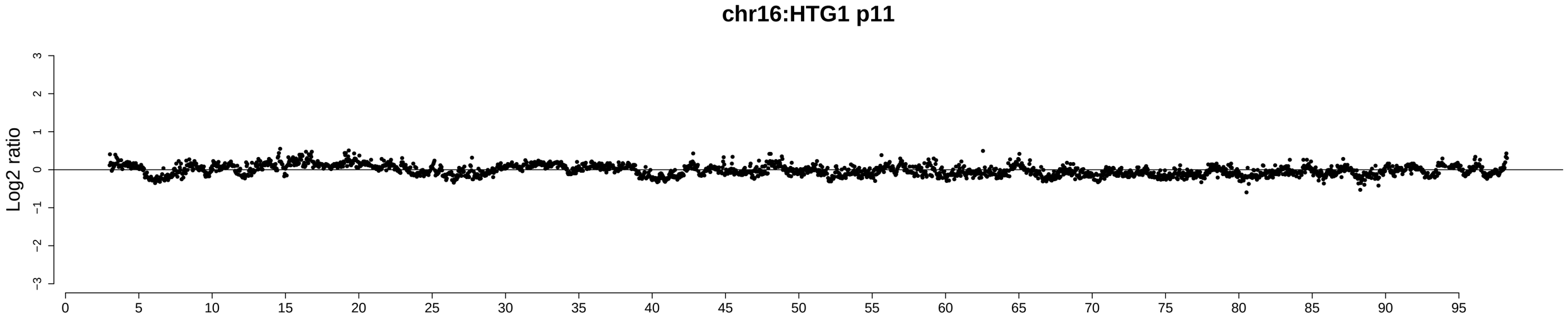
chr15:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100

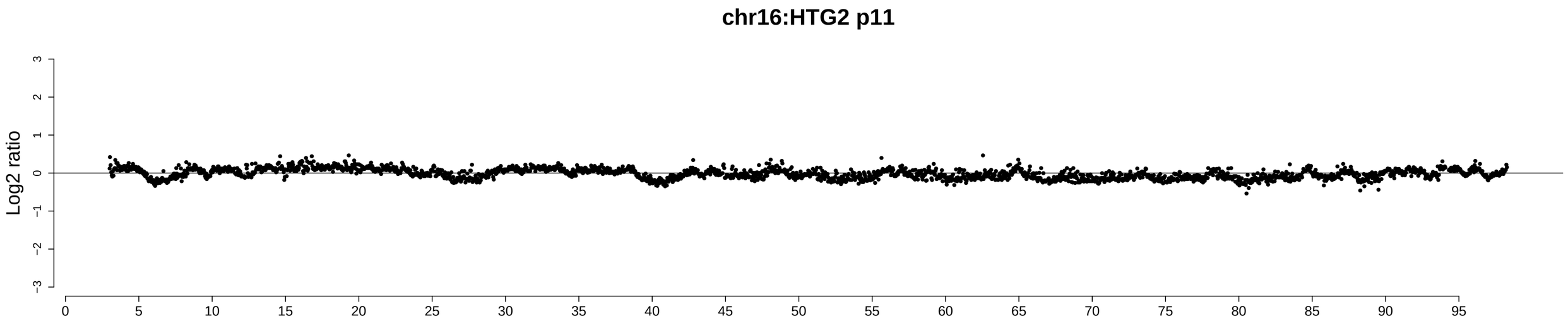

chr16:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95

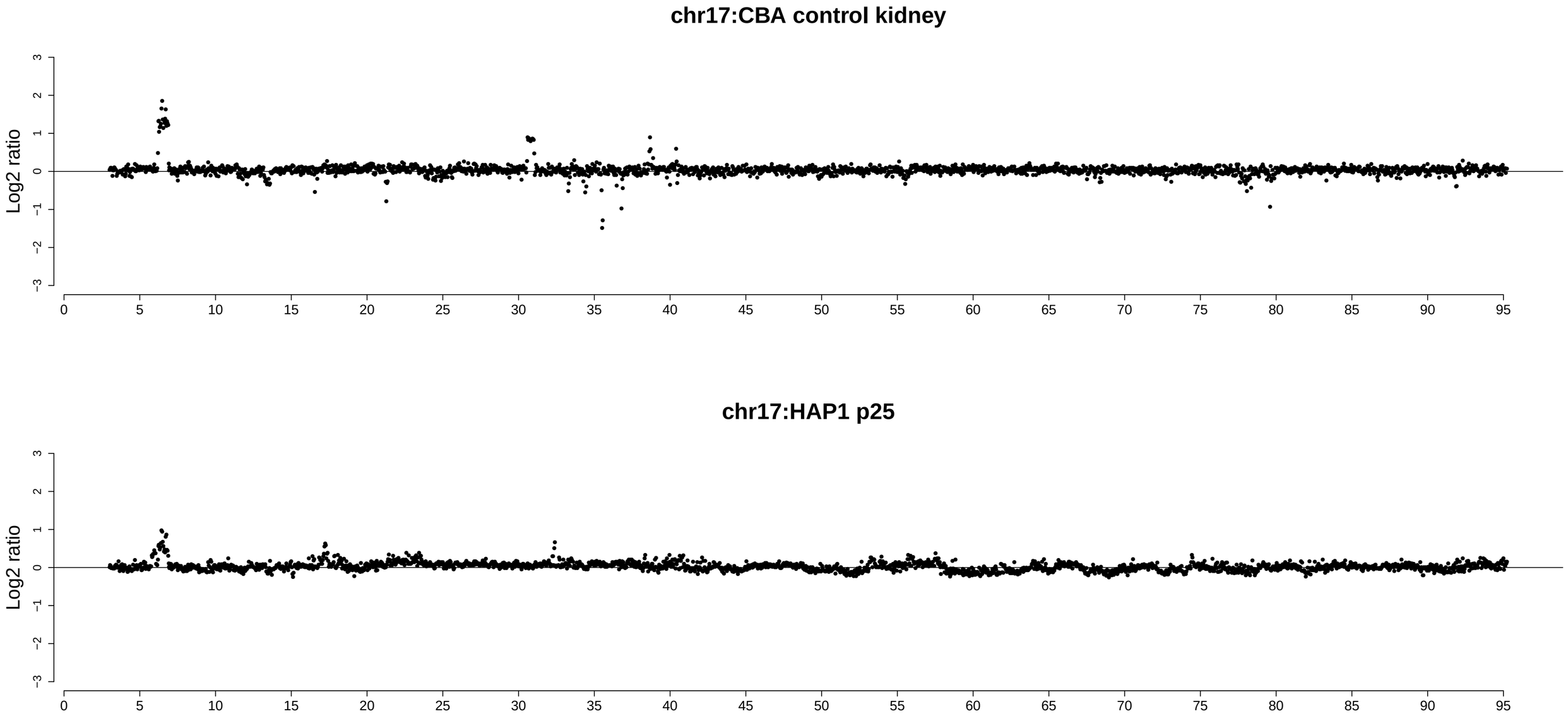

chr16:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95


chr16:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95

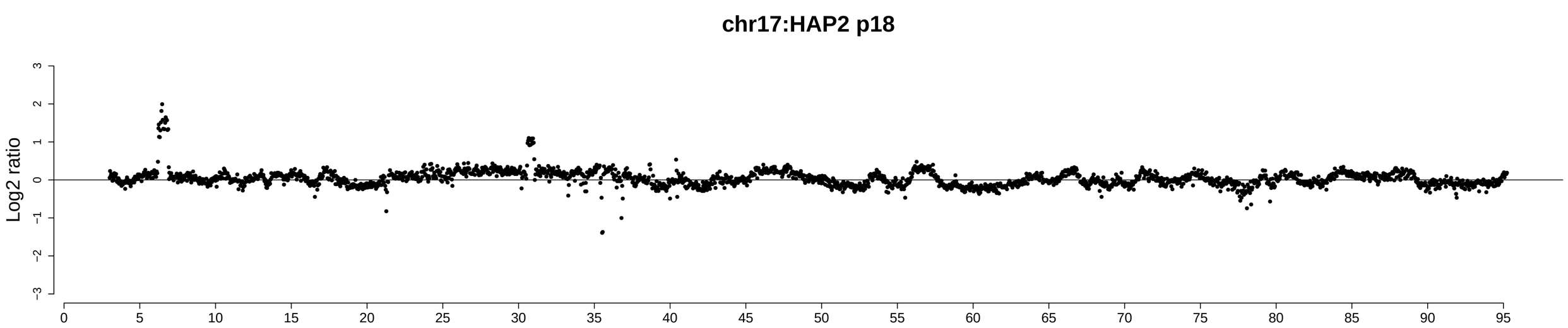

chr16:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95

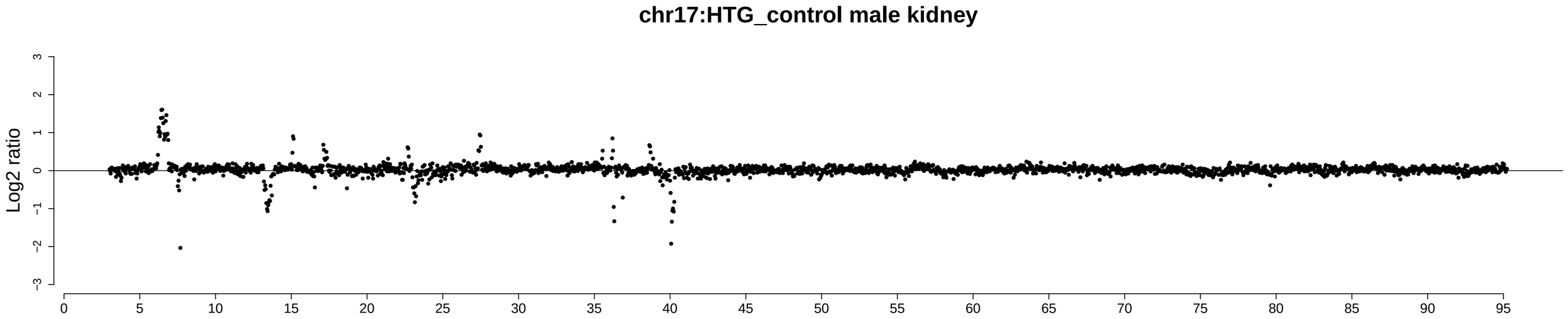

chr16:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95

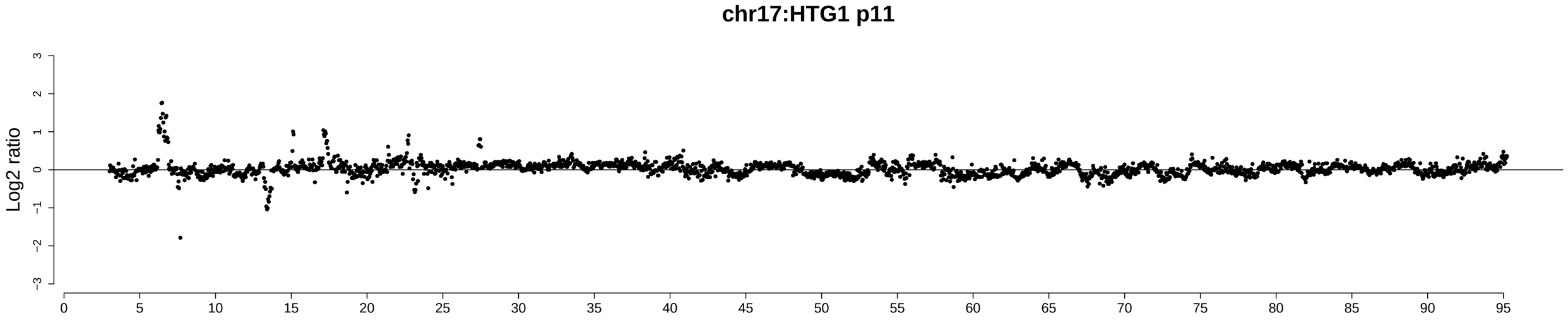

chr16:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95

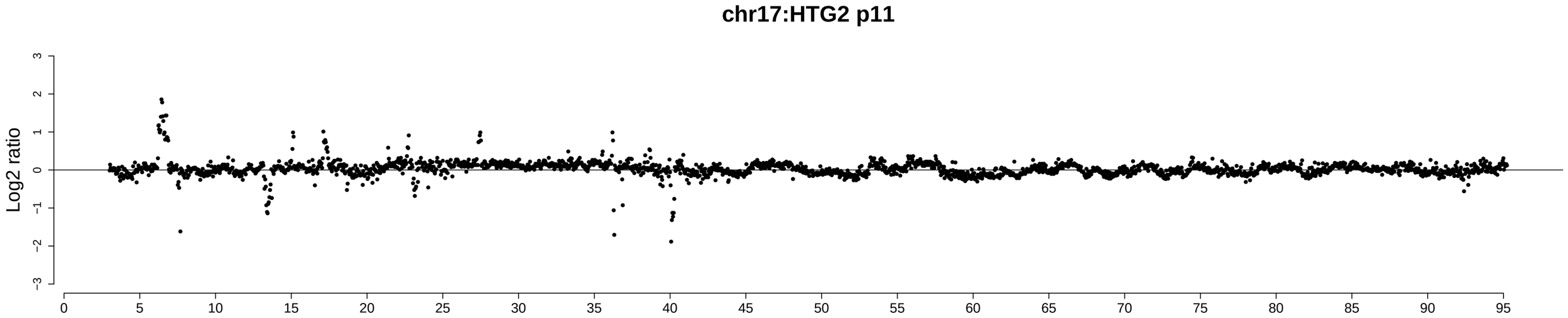

chr17:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95

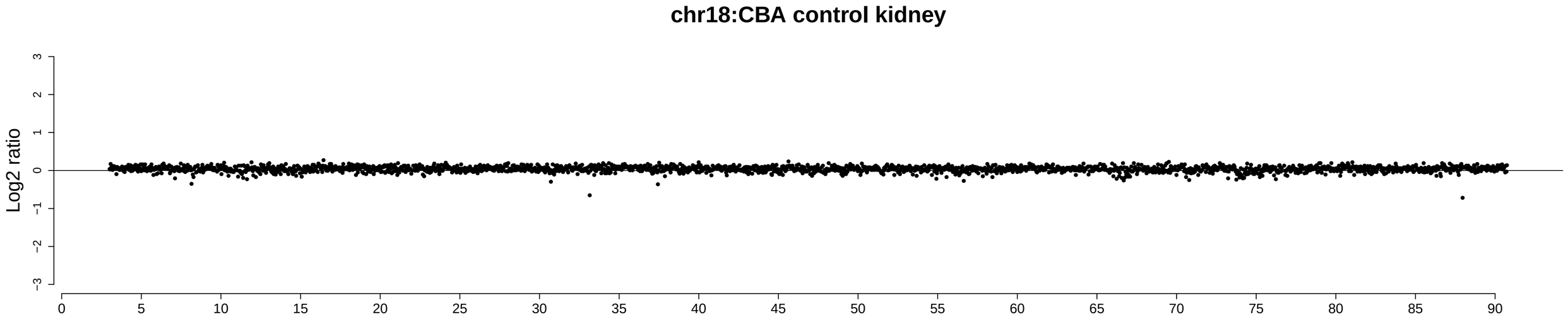
chr17:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95

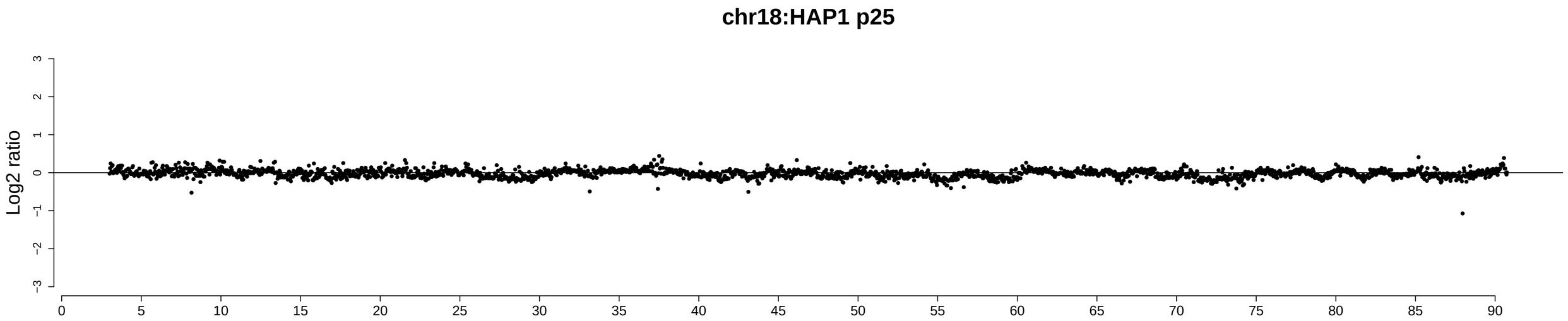

chr17:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95

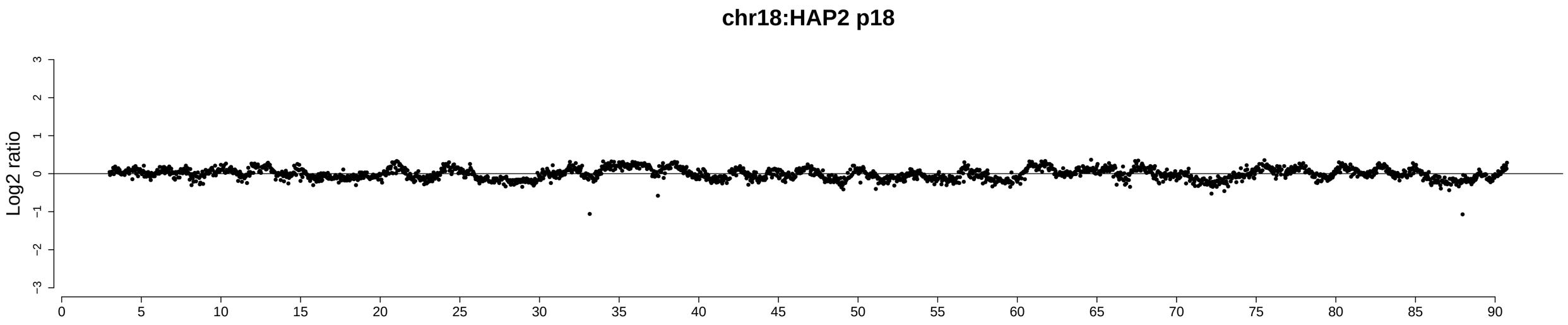

chr17:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95

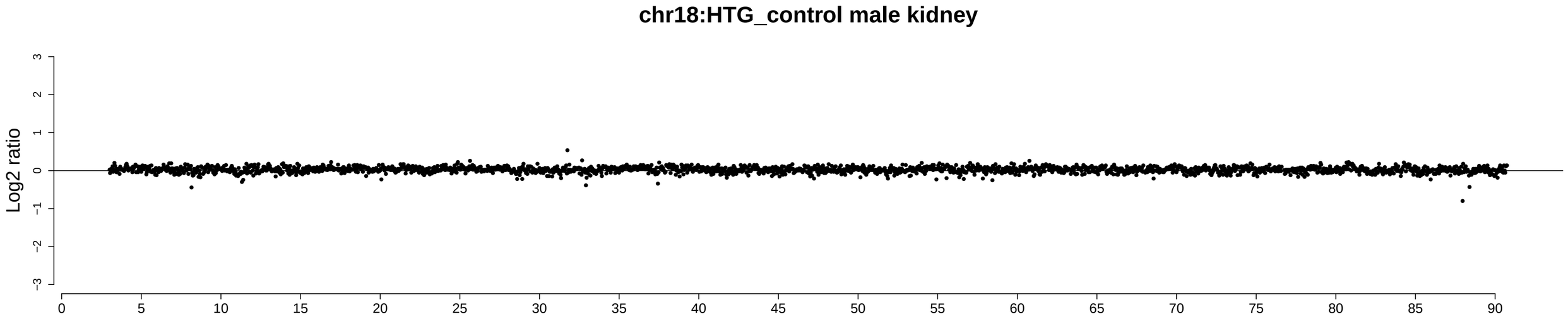

chr17:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95

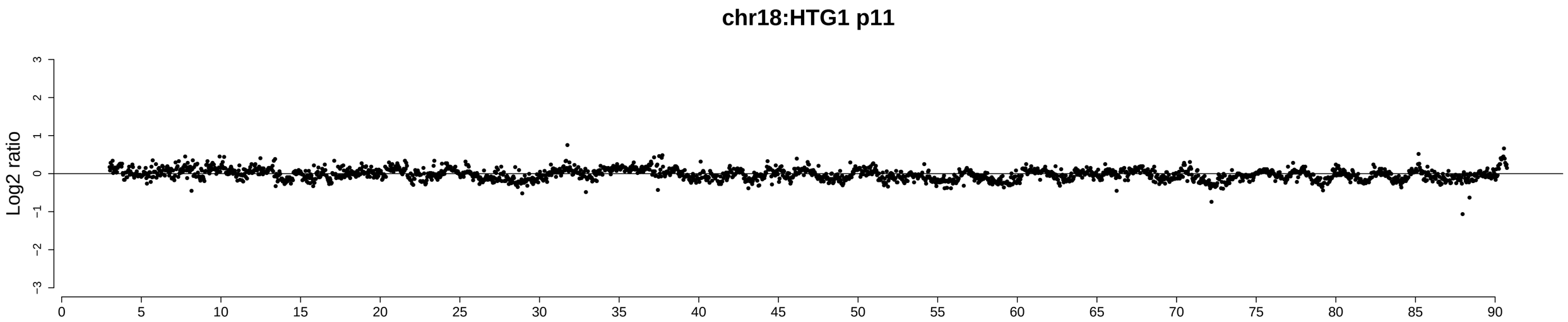

chr17:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95

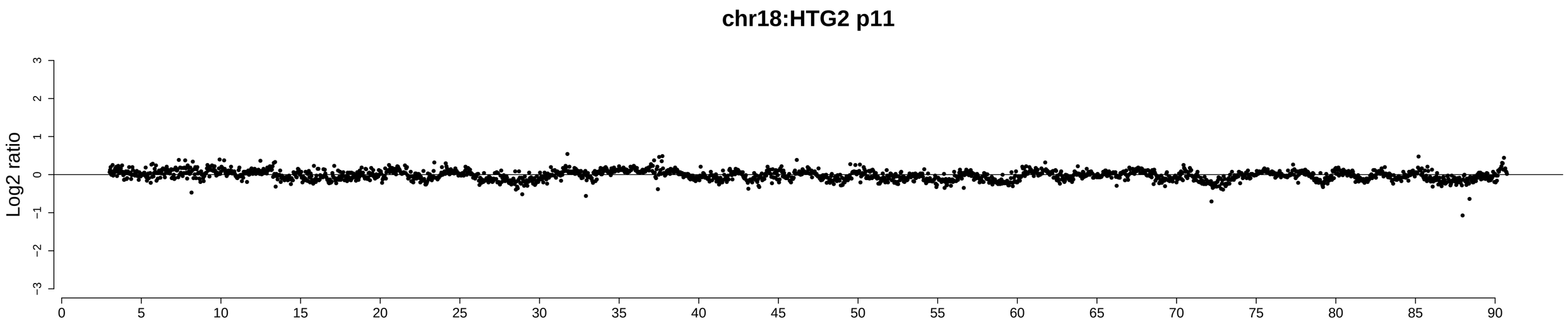

chr18:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90


chr18:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90

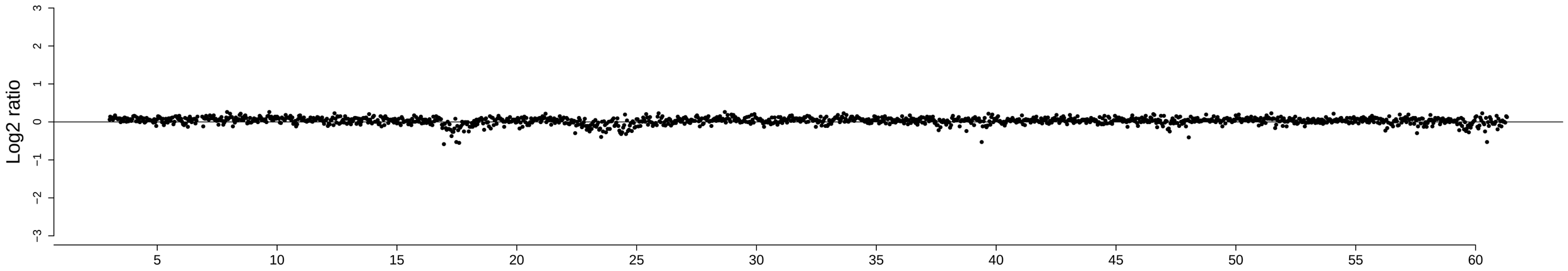

chr18:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90


chr18:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90

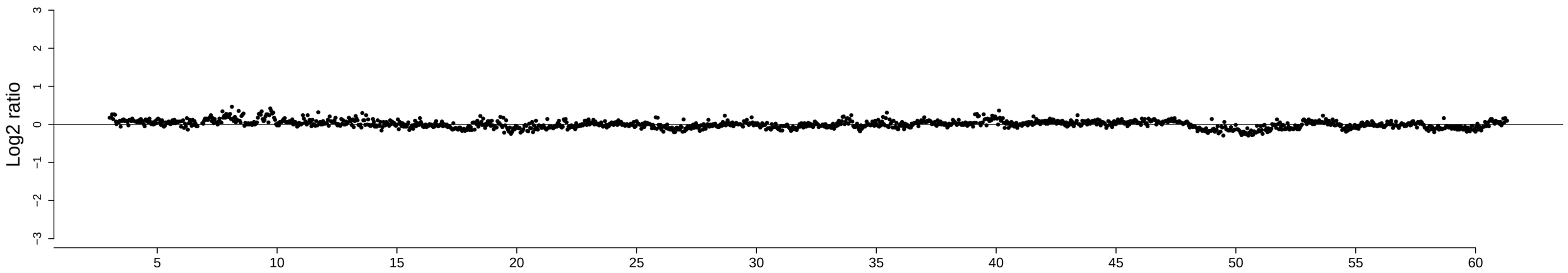

chr18:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90


chr18:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90

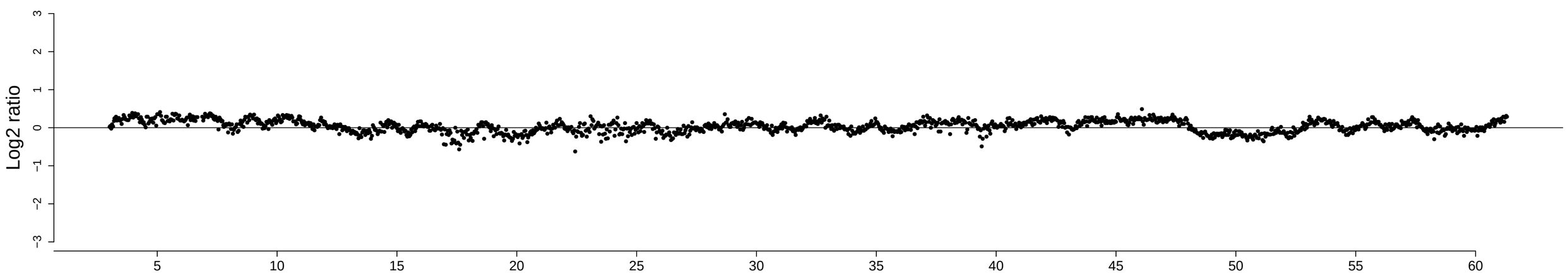
chr19:CBA control kidney



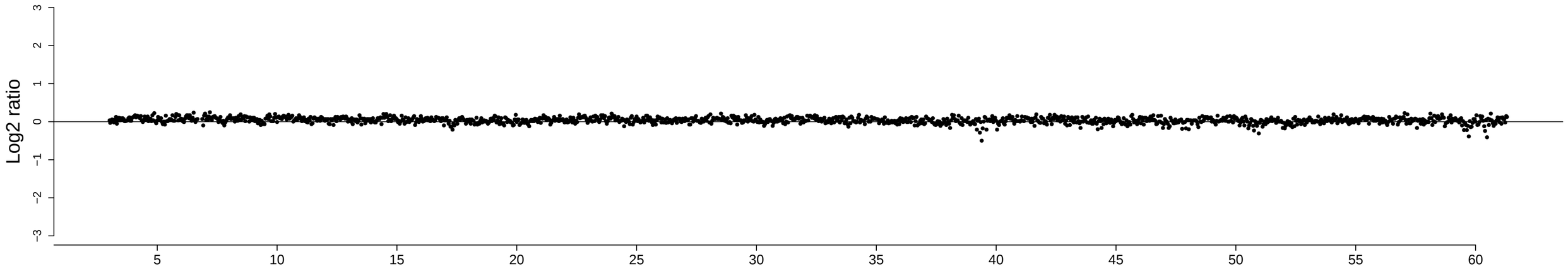
chr19:HAP1 p25



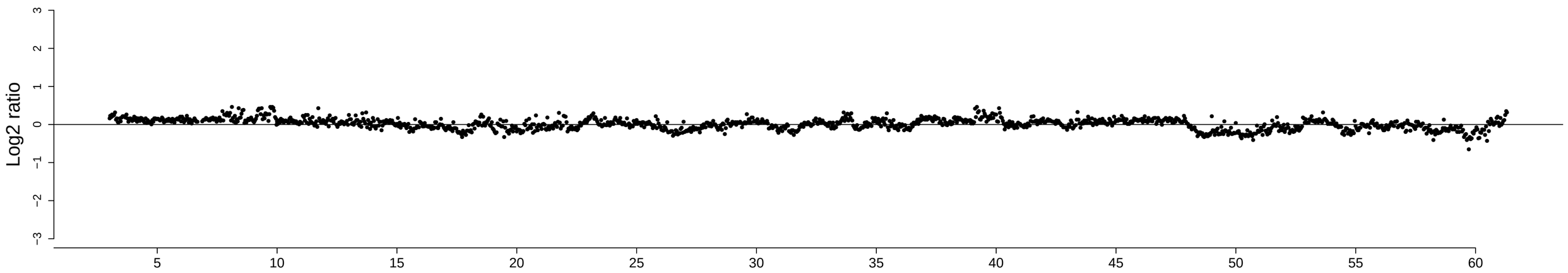
chr19:HAP2 p18



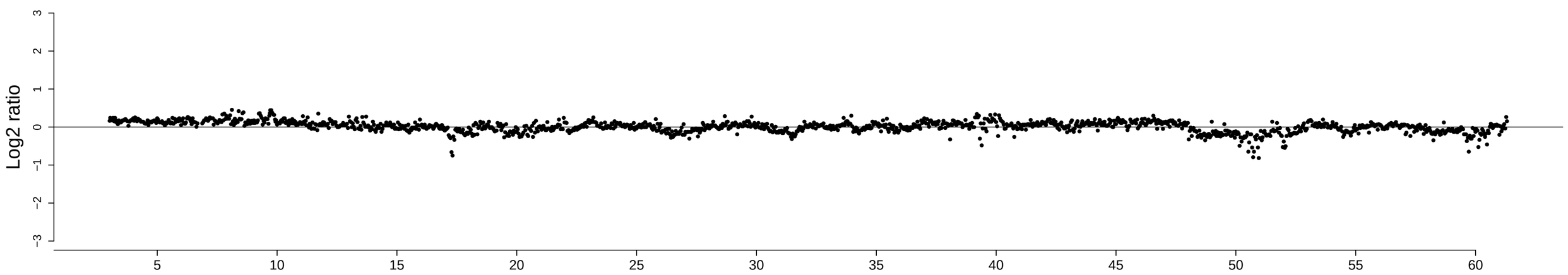
chr19:HTG_control male kidney

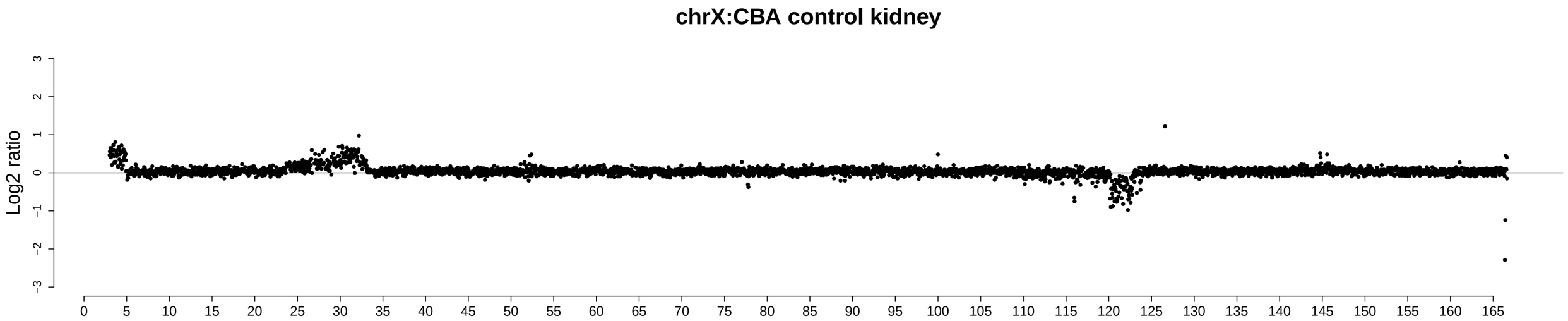


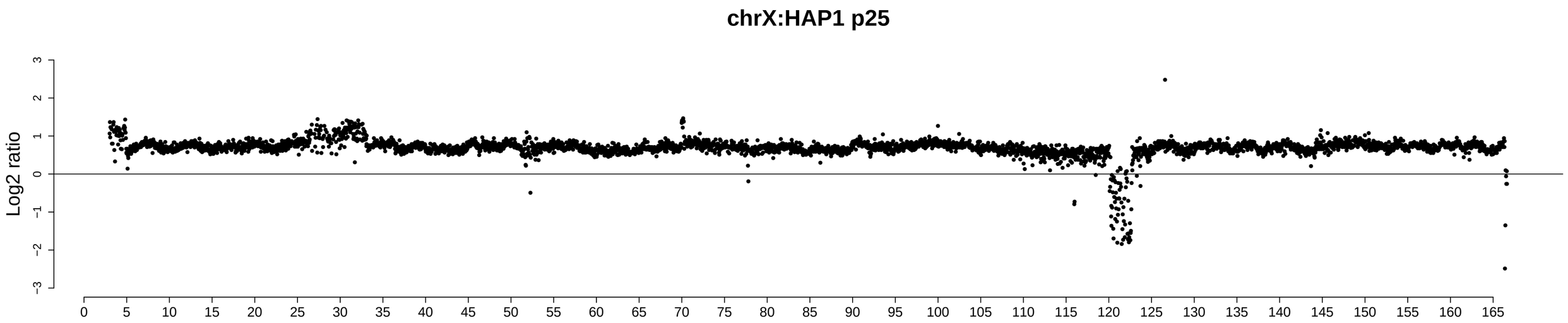
chr19:HTG1 p11

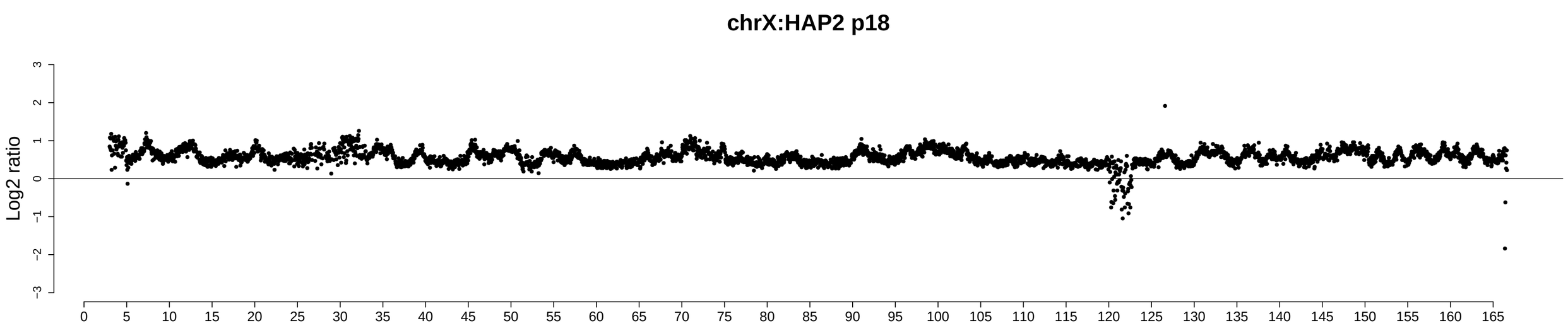


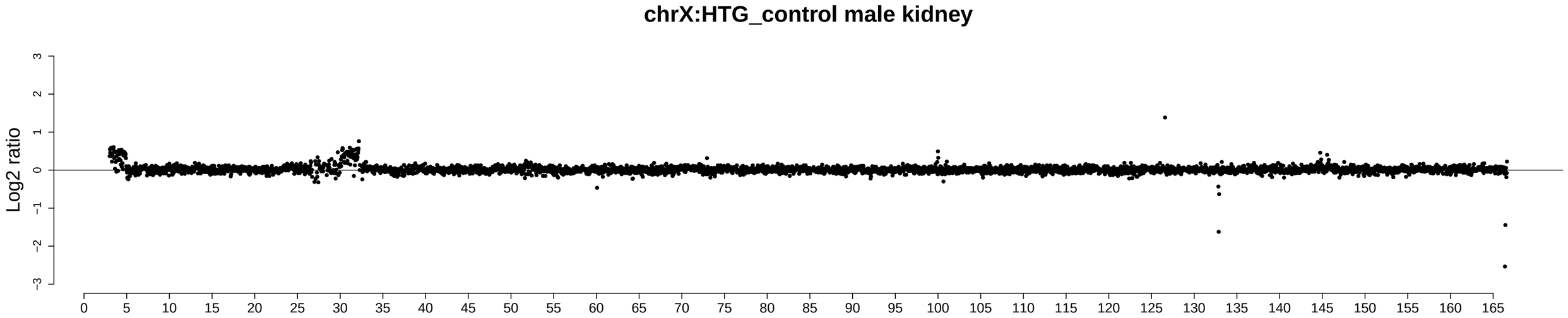
chr19:HTG2 p11

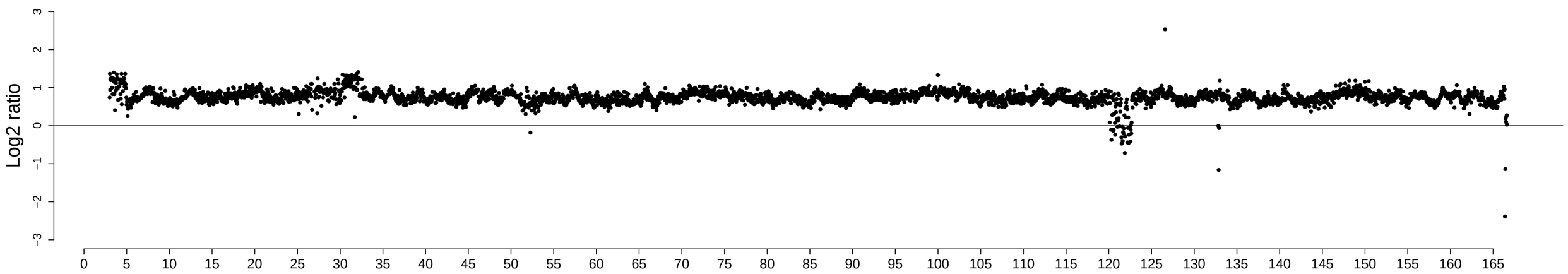


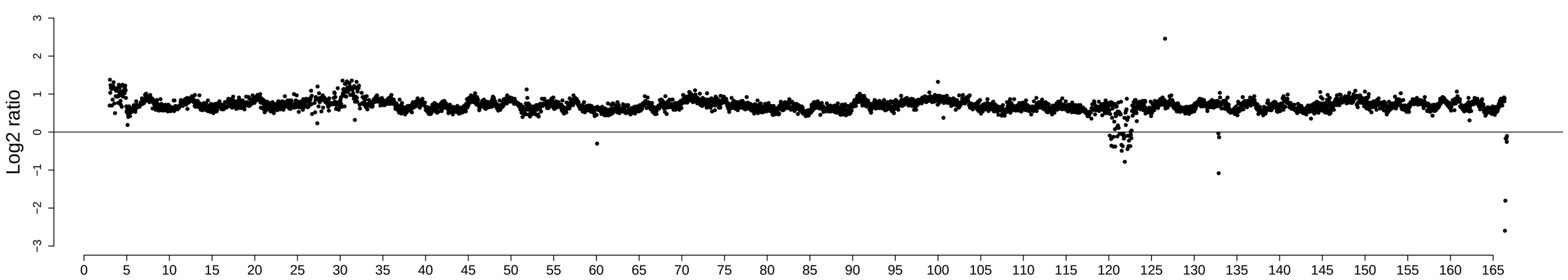

chrX:CBA control kidney
Log2 ratio
−3 −2 −1 0 1 2 3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165

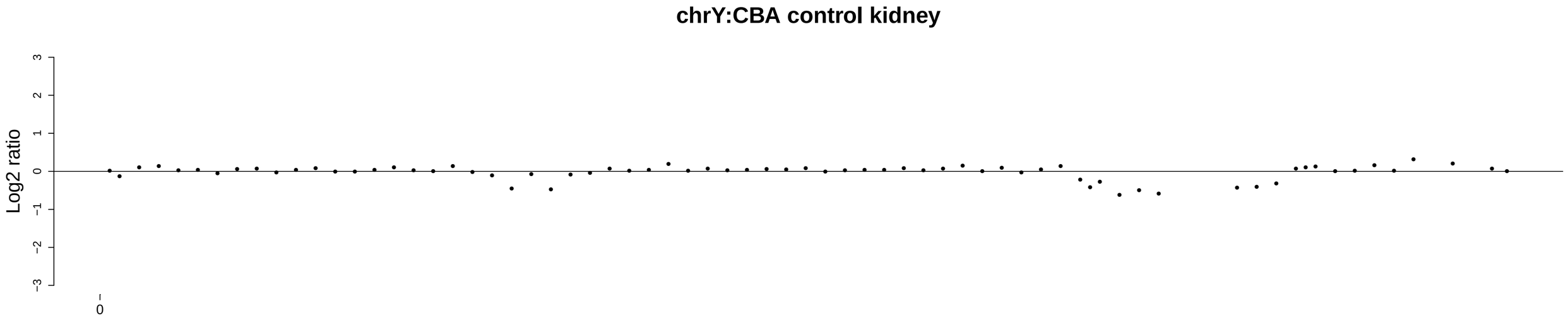

chrX:HAP1 p25
Log2 ratio
−3 −2 −1 0 1 2 3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165

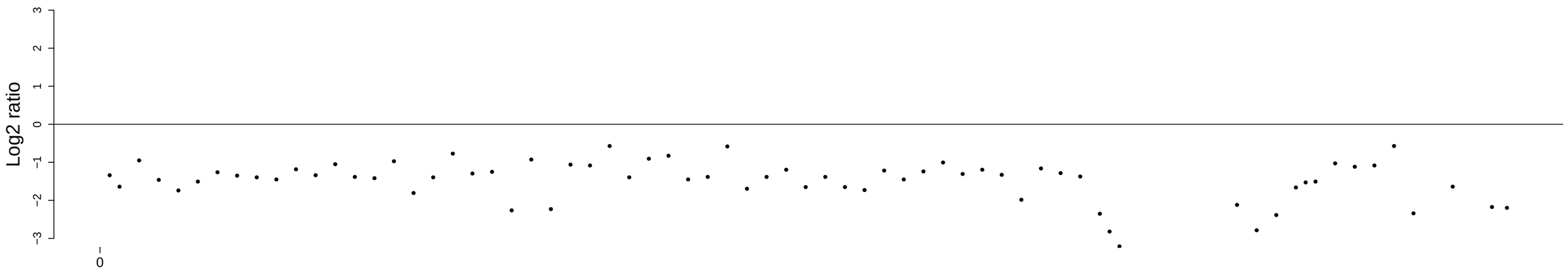

chrX:HAP2 p18
Log2 ratio
−3 −2 −1 0 1 2 3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165

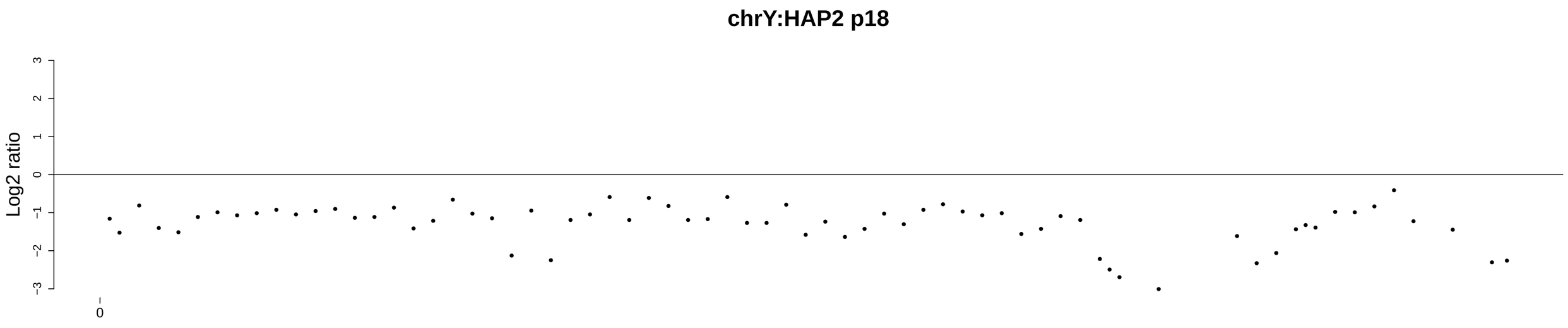

chrX:HTG_control male kidney
Log2 ratio
−3 −2 −1 0 1 2 3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165

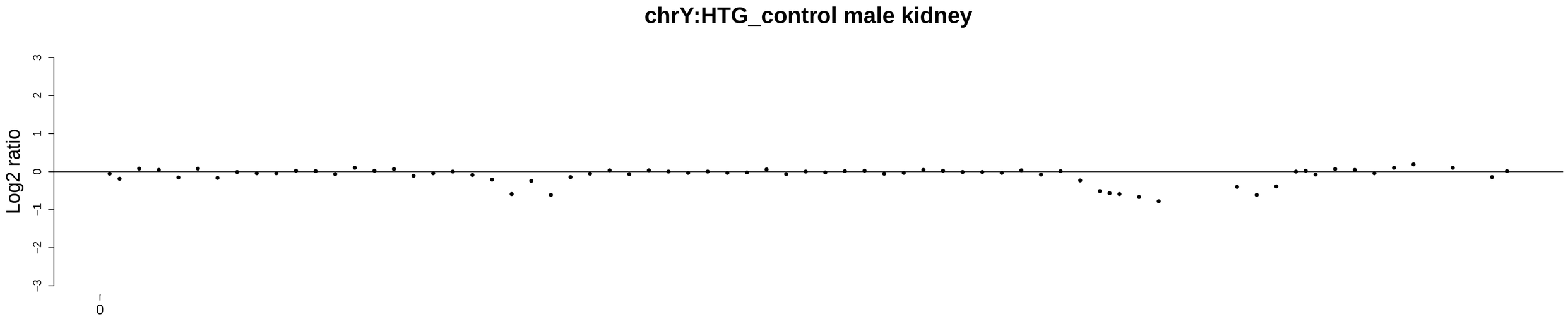

chrX:HTG1 p11
Log2 ratio
−3 −2 −1 0 1 2 3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165

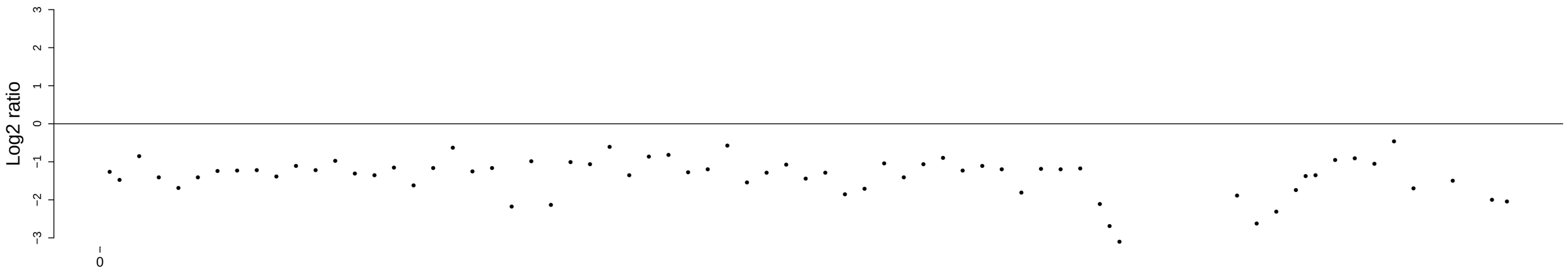

chrX:HTG2 p11
Log2 ratio
−3 −2 −1 0 1 2 3
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165

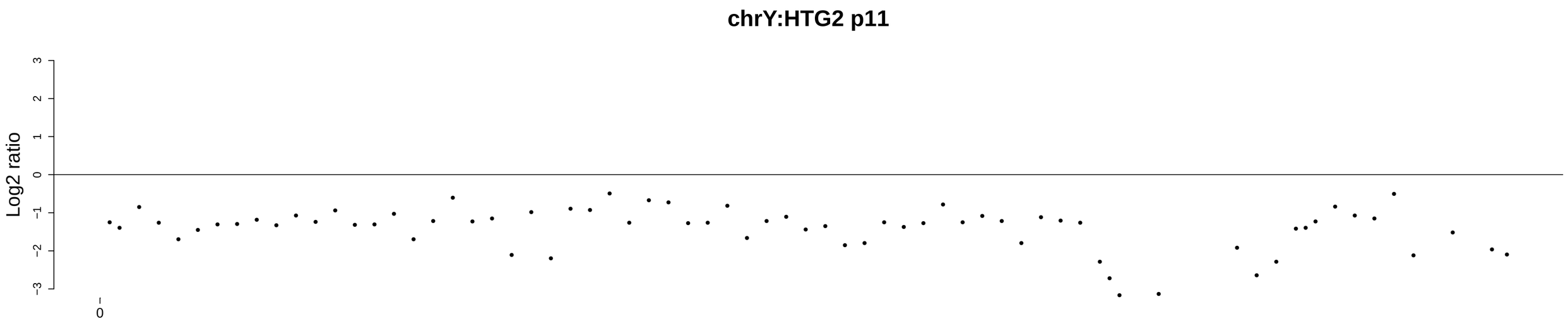

chrY:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0

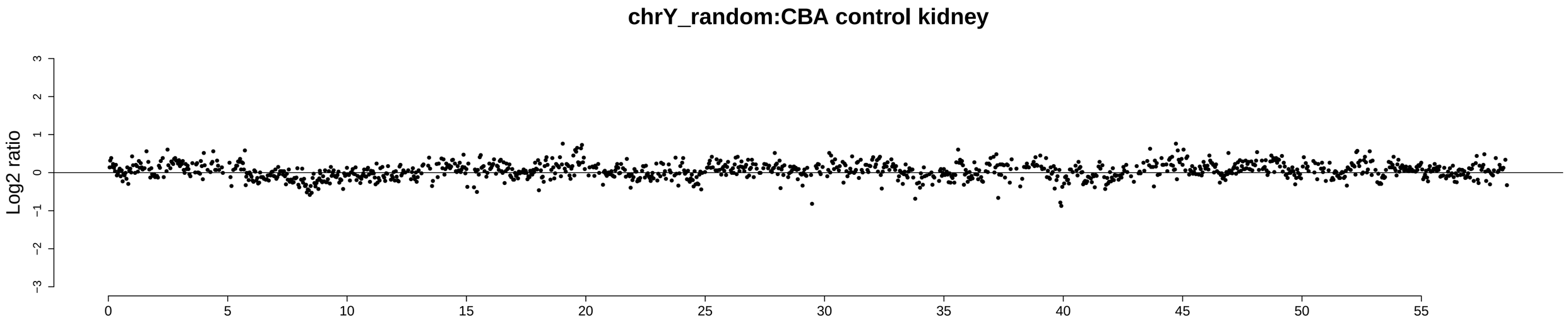

chrY:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0

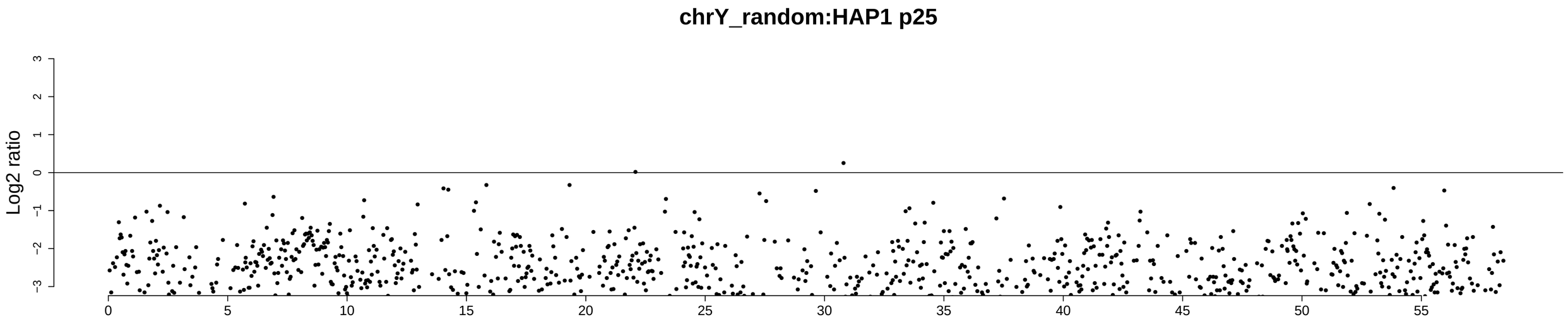

chrY:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0

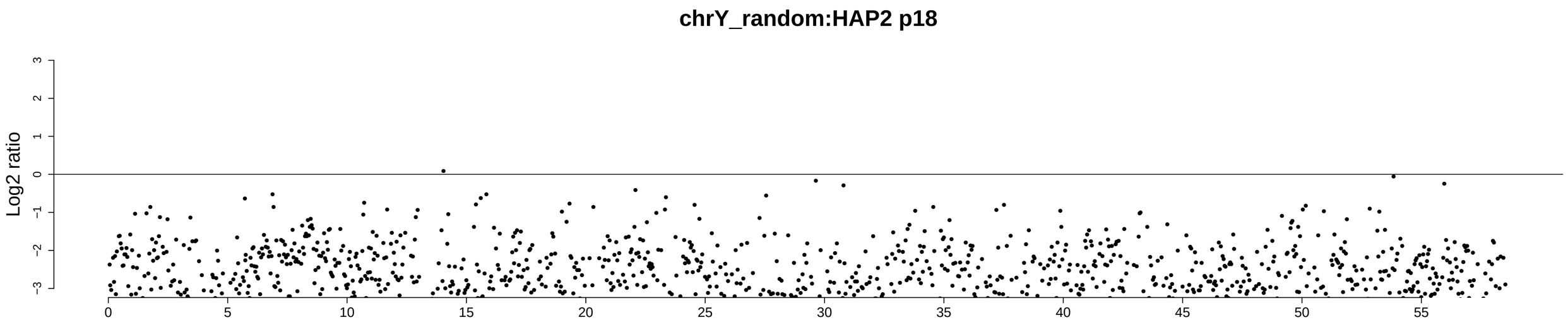

chrY:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0

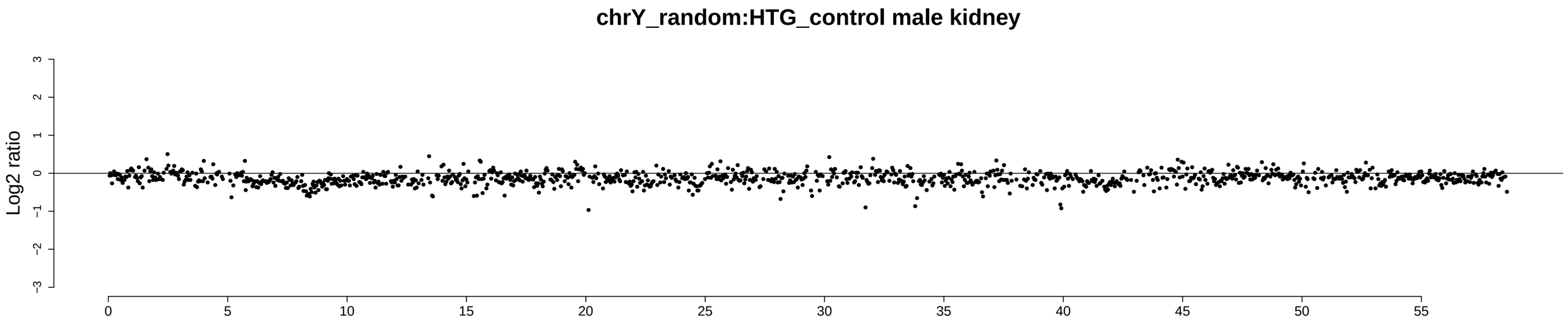

chrY:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0

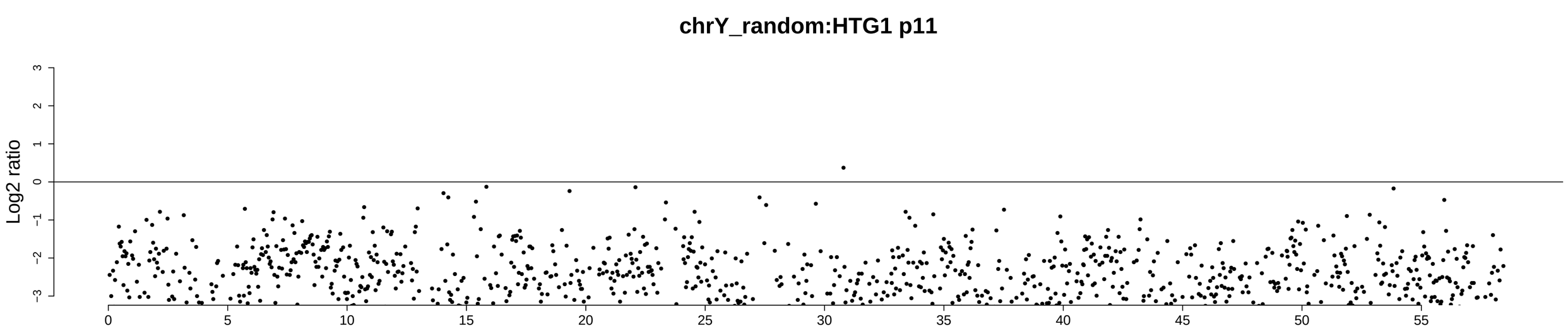

chrY:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0

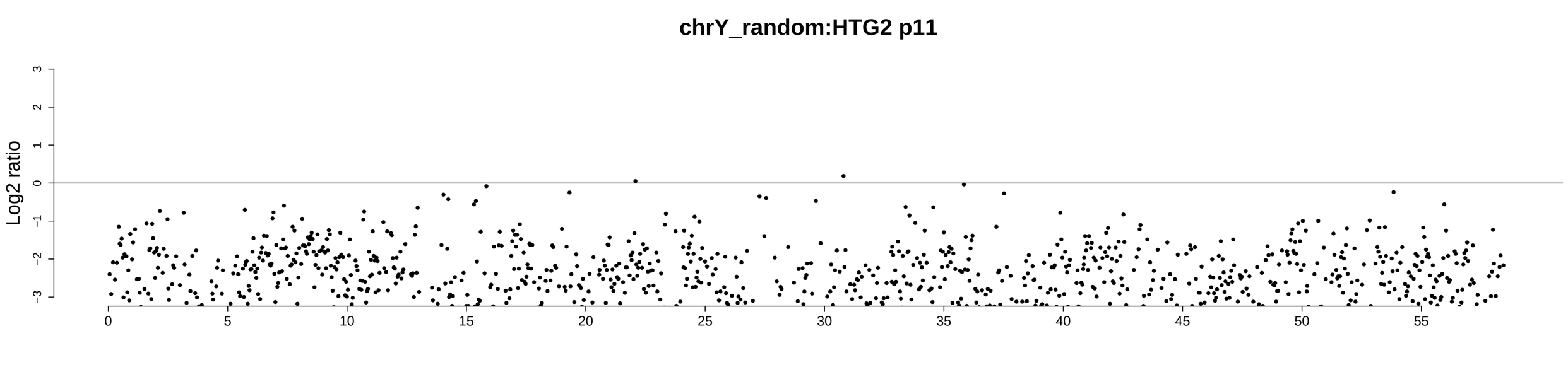

chrY_random:CBA control kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55

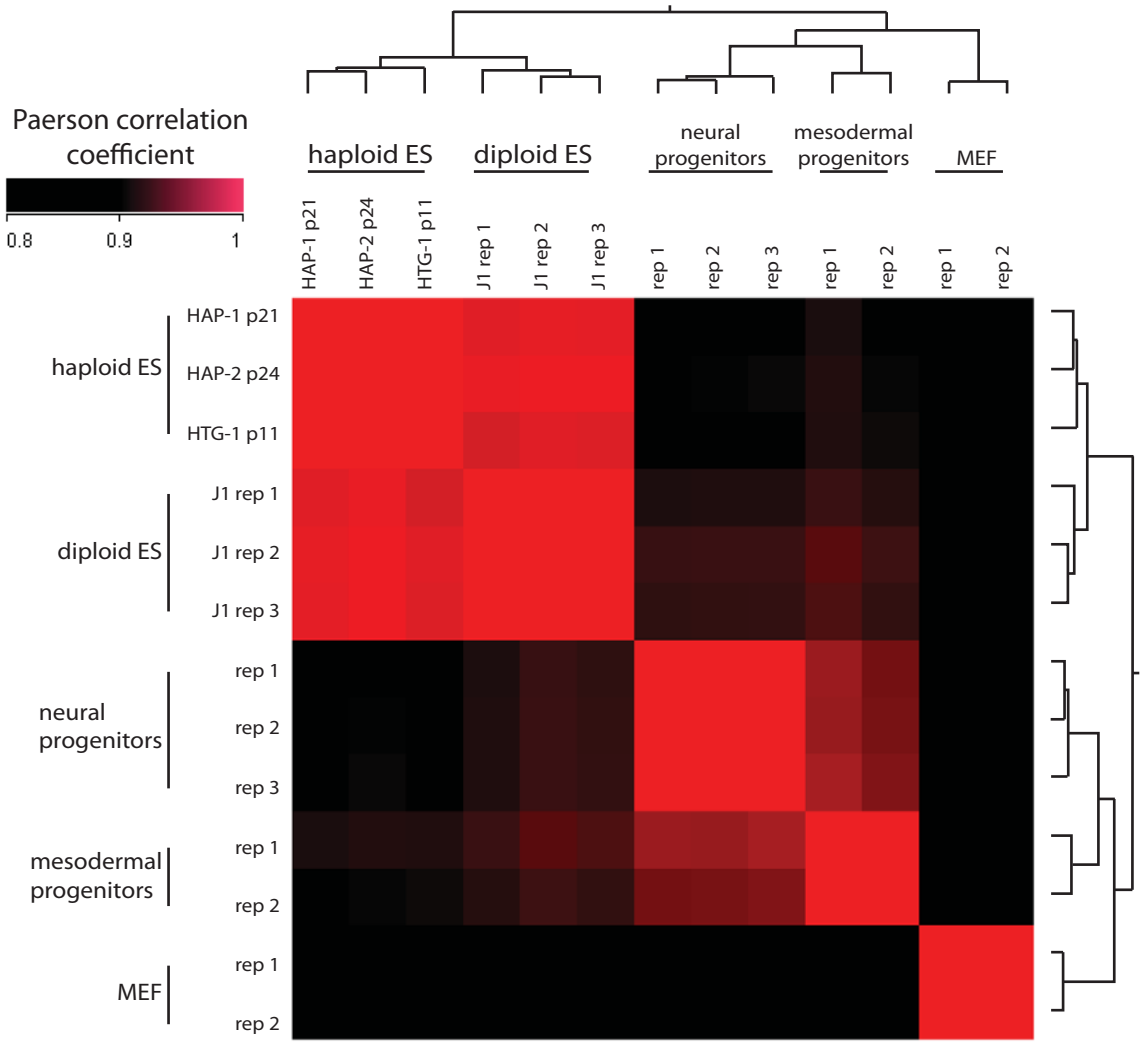

chrY_random:HAP1 p25
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55


chrY_random:HAP2 p18
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55


chrY_random:HTG_control male kidney
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55

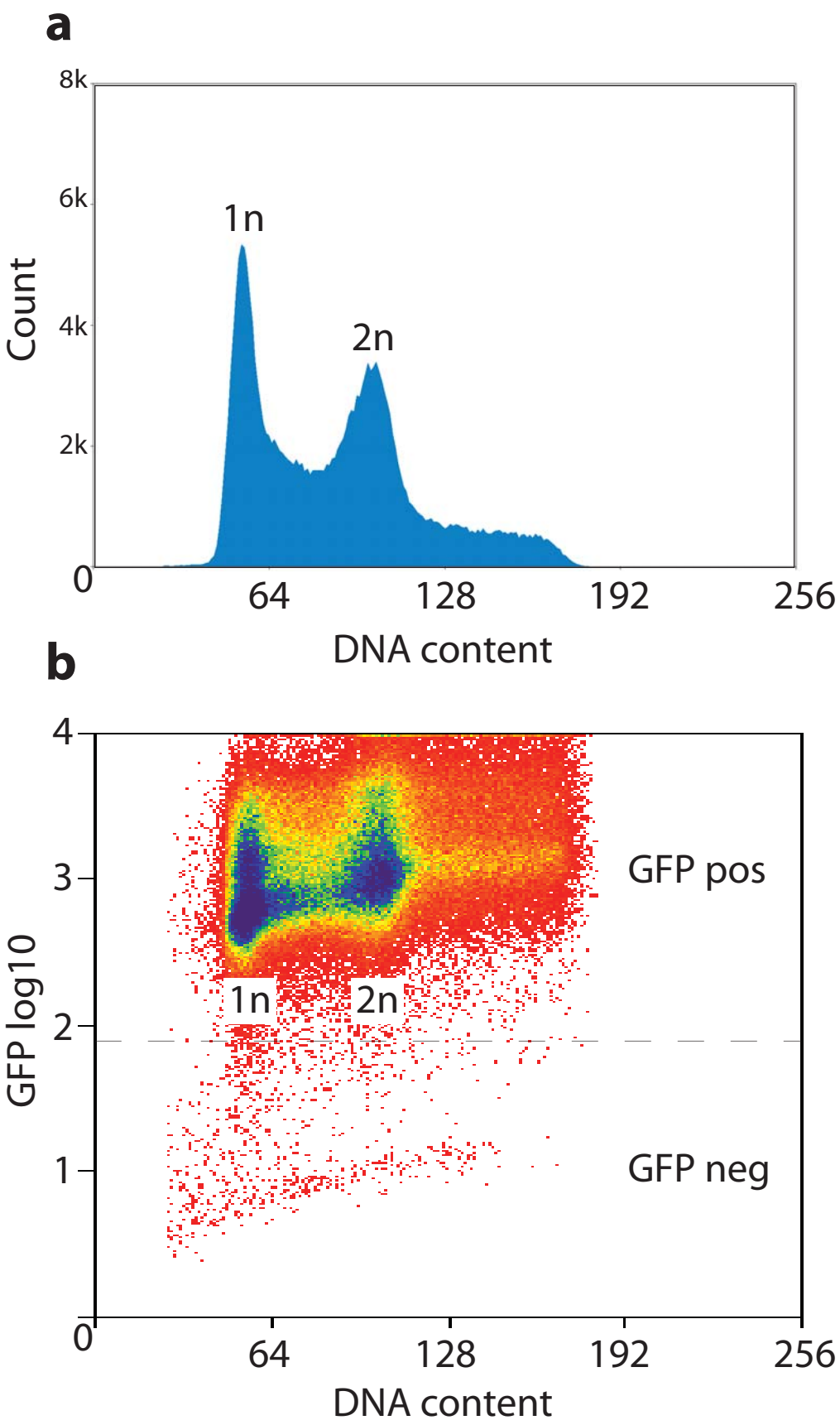

chrY_random:HTG1 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55


chrY_random:HTG2 p11
Log2 ratio
3
2
1
0
−1
−2
−3
0
5
10
15
20
25
30
35
40
45
50
55



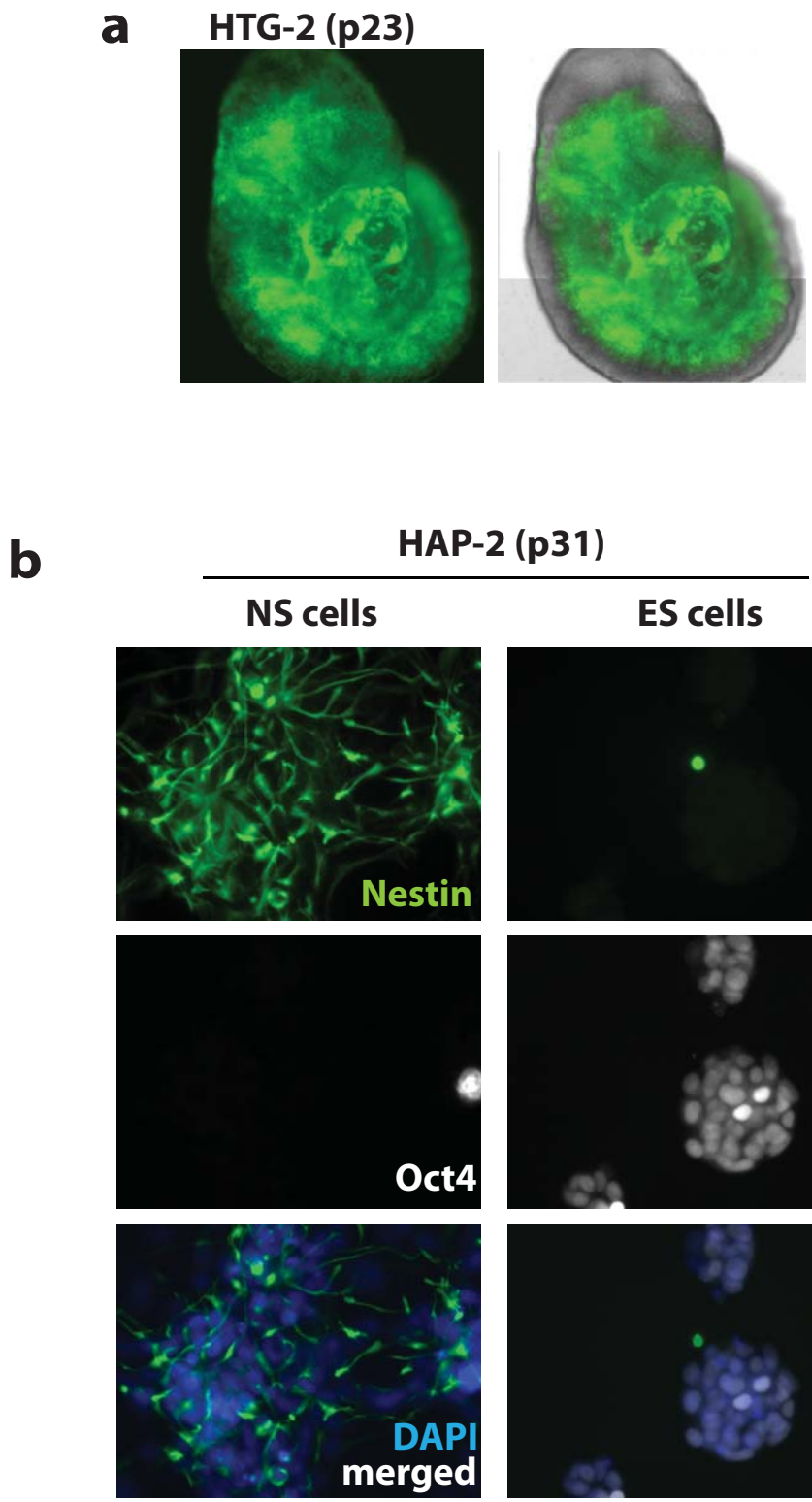
Supplementary Figure 5 - Analysis of similarity between haploid and diploid ES cells

An overview of the gene expression profiles of haploid and diploid ES cells is shown. Gene expression profiles were clustered using all genes and the Paerson correlation coefficient was calculated (indicated by red color). Three different haploid ES cell lines (HAP-1, HAP-2, and HTG-1) cluster together showing highly similar expression profiles. Gene expression of haplioid ES cells is highly similar to control diploid J1 ES cells but different from mouse embryonic fibroblasts (MEF) or neural and mesodermal progenitors. The dendrogram (top and right) was generated by hierarchical clustering by Euclidean distance and complete linkage analysis (rep1, rep2, rep3 indicate biological replicates).



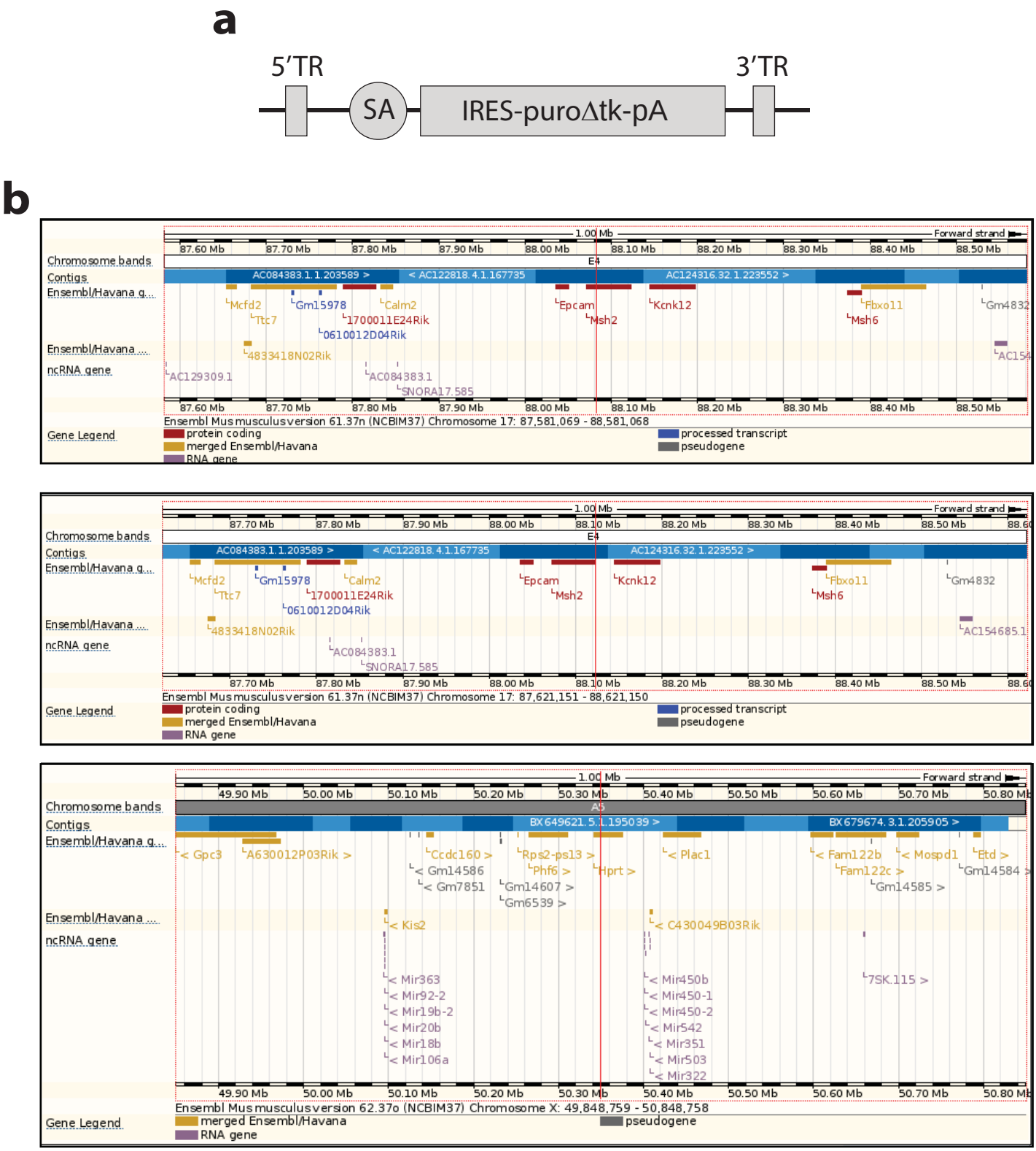
Supplementary Figure 6 - Stable integration of a GFP transgene into haploid ES cells

Flow profiles show the **(a)** DNA content and **(b)** DNA content combined with GFP intensity of HAP-2 ES cells transfected with a piggyBac vector for expressing GFP. The 1n / GFP positive population was purified for analysis of the developmental potential of haploid ES cells.



Supplementary Figure 7 - Developmental potential of haploid ES cells.

(**a**) A GFP image and merged GFP brightfield image of a chimeric E9.5 embryo from injection of GFP labeled HTG-2 ES cells (p23) into C57BL6 host blastocysts.
(**b**) Immunofluorescence analysis of Nestin (green) and Oct4 (white) expression in HAP-2 (p31) ES cells and HAP-2 derived neural stem (NS) cells. A merged image with DNA stained with DAPI (blue) is shown below.



Supplementary Figure 8 - Genetrap insertions recovered in missmatch repair screen

(a) A schematic representation of the piggyBac genetrap vector is shown (SA, splice acceptor).
(b) Genome browser view shows BLAST hits for sequences recovered by Splinkerette PCR from 6-TG resistant clones obtained from a missmatch repair screen using haploid mouse ES cells (see text). Seven clones were analysed and three insertions into genes previously identified to mediate 6-TG sensitivity were identified. Two independent insertions in the *Msh2* and one insertion in the *Hprt* gene are shown. The integration sites were mapped to intron three and fifteen of *Msh2* on chromosome 17 at base position 88,081,425 and 88,121,546, respectively. A further insertion was identified in intron 1 of the *Hprt* gene at base position 50,349,004 on the X chromosome. All gene trap insertions were in forward orientation trapping the gene transcripts as expected. Genomic positions and gene structure are based on the NCBI37/mm9 assembly of the mouse genome.

Supplementary Table 1 - Segmentation table of the CGH analysis of haploid ES cells
Segmentation analysis of the CGH profiles of HAP-1, HAP-2, HTG-1 and HTG-2 haploid mouse ES cells and CBA and HTG control male somatic samples was performed using the NimbleScan software (Roche). Copynumber deviations with a cut-off log2 value of 0.8 were determined and listed with chromosome and genomic position.

HAP1

CHROMOSOME	START	STOP	SIZE	DATAPOINTS	LOG2_RATIO_N
chr7	3699999	3819999	120000	43	-1.4371
chr7	20699999	24059999	3360000	637	-1.88153
chr12	89299999	89379999	80000	34	-0.89872
chr13	68619999	68699999	80000	32	-1.03683
chr14	42059999	42219999	160000	54	-1.32819
chr14	42259999	42339999	80000	29	-0.89743
chr14	42379999	42419999	40000	14	-1.37748
chr14	42459999	42539999	80000	28	-0.84389
chr14	42579999	42659999	80000	33	-1.58313
chr14	42699999	42859999	160000	49	-1.15406
chr14	42899999	43019999	120000	40	-1.66039
chr14	43059999	43379999	320000	92	-1.39357
chr14	43419999	43619999	200000	48	-1.70756
chr14	43659999	43859999	200000	63	-1.0446
chr14	43899999	44099999	200000	66	-1.44165
chr14	44139999	44259999	120000	38	-0.81347
chr14	44539999	44579999	40000	22	-1.67539
chr14	44739999	44819999	80000	33	-0.90922
chr14	44859999	45179999	320000	84	-1.32847
chr14	45219999	45259999	40000	22	-1.68286
chr14	45299999	45339999	40000	21	-1.2028
chr14	52259999	52379999	120000	43	-0.83266
chrX	1.22E+08	1.22E+08	400000	26	-1.31437
chrX	1.22E+08	1.23E+08	440000	37	-1.45574

HAP2

CHROMOSOME	START	STOP	SIZE	DATAPOINTS	LOG2_RATIO_N
chr1	8139999	8219999	80000	32	-1.15655
chr2	1E+08	1.01E+08	280000	89	-0.91674
chr8	19339999	19379999	40000	20	-1.06806
chr8	22179999	22299999	120000	41	-0.97395
chr8	22539999	22699999	160000	47	-1.10896
chr13	68619999	68699999	80000	32	-0.82539
chr16	35499999	35539999	40000	24	0.88028
chr17	6259999	6899999	640000	180	1.45984
chr17	30619999	31019999	400000	124	1.01428
chr17	35539999	35579999	40000	22	-1.37624
chrX	3019999	4939999	1920000	288	0.84469
chrX	6659999	8019999	1360000	391	0.85511
chrX	19699999	20699999	1000000	291	0.80541
chrX	70699999	71699999	1000000	295	0.91882

CBA

CHROMOSOME	START	STOP	SIZE	DATAPOINTS	LOG2_RATIO_N
chr1	8139999	8219999	80000	32	-1.12563
chr3	93579999	93659999	80000	34	0.91478
chr4	41739999	42779999	1040000	218	-1.07415
chr4	1.12E+08	1.12E+08	520000	152	-1.31422
chr4	1.12E+08	1.14E+08	1080000	302	-1.22262
chr4	1.21E+08	1.22E+08	760000	190	-1.51206
chr5	14939999	15179999	240000	65	-0.81371
chr5	1.05E+08	1.05E+08	320000	98	-0.83343
chr6	1.14E+08	1.15E+08	80000	21	0.80806
chr6	1.3E+08	1.3E+08	200000	67	-1.26461
chr6	1.32E+08	1.32E+08	120000	42	-1.17524
chr7	3699999	3819999	120000	43	-1.36942
chr7	20699999	24059999	3360000	637	-1.7698
chr7	1.11E+08	1.11E+08	40000	22	-1.44423
chr8	19339999	19379999	40000	20	-1.03835
chr8	22179999	22299999	120000	41	-0.87322
chr8	22539999	22699999	160000	47	-1.0725
chr10	1.14E+08	1.14E+08	560000	166	0.82654
chr14	42059999	42219999	160000	54	-1.2489
chr14	42259999	42539999	280000	71	-1.0259
chr14	42579999	43379999	800000	214	-1.30787
chr14	43419999	43499999	80000	18	-1.72834
chr14	43539999	43579999	40000	20	-0.91193
chr14	43619999	43659999	40000	20	-1.53924
chr14	43699999	44099999	400000	119	-1.14346
chr14	44539999	44579999	40000	22	-1.29833
chr14	44779999	45339999	560000	149	-1.1872
chr16	36259999	36299999	40000	23	-1.03884
chr17	6259999	6899999	640000	180	1.33058
chr17	30619999	31059999	440000	135	0.81562
chr17	35539999	35579999	40000	22	-1.38383

HTG1

CHROMOSOME	START	STOP	SIZE	DATAPOINTS	LOG2_RATIO_N
chr2	1.41E+08	1.41E+08	40000	22	-2.52593
chr4	1.12E+08	1.12E+08	520000	152	-1.35882
chr4	1.12E+08	1.14E+08	1120000	314	-1.10913
chr7	3699999	3819999	120000	43	-1.36731
chr7	20659999	24099999	3440000	657	-1.13375
chr7	1.11E+08	1.11E+08	40000	22	-1.71019
chr11	71019999	71099999	80000	33	-1.53765
chr13	61779999	62059999	280000	88	-0.94
chr13	1.01E+08	1.01E+08	80000	33	0.81669
chr17	6259999	6899999	640000	180	1.14906
chr17	15099999	15179999	80000	34	0.81085
chr17	17139999	17419999	280000	86	0.85432
chrX	3019999	4939999	1920000	288	1.0814
chrX	30259999	32539999	2280000	323	1.13215

HTG2

CHROMOSOME	START	STOP	SIZE	DATAPOINTS	LOG2_RATIO_N
chr2	1.41E+08	1.41E+08	40000	22	-2.5294
chr4	41739999	41899999	160000	46	-0.81093
chr4	41939999	42059999	120000	31	-1.57142
chr4	42299999	42419999	120000	35	-1.63516
chr4	42459999	42539999	80000	19	-0.91833
chr4	42579999	42739999	160000	37	-1.49251
chr4	1.12E+08	1.12E+08	520000	152	-1.30365
chr4	1.12E+08	1.14E+08	1120000	314	-1.12804
chr5	93899999	96219999	2320000	436	-1.13902
chr7	3699999	3819999	120000	43	-1.36012
chr7	20659999	24099999	3440000	657	-1.13761
chr7	1.11E+08	1.11E+08	40000	22	-1.699
chr8	19339999	19419999	80000	31	-0.9636
chr8	22179999	22699999	520000	134	-0.82898
chr11	71019999	71099999	80000	33	-1.43011
chr12	1.15E+08	1.15E+08	80000	32	0.96374
chr12	1.16E+08	1.16E+08	80000	34	-1.05337
chr13	61779999	62059999	280000	88	-0.88837
chr13	68619999	68699999	80000	32	-1.01729
chr17	6259999	6419999	160000	57	1.13188
chr17	6459999	6499999	40000	23	1.81624
chr17	6539999	6579999	40000	21	1.35198
chr17	6619999	6699999	80000	31	0.91102
chr17	6739999	6779999	40000	14	1.43104
chr17	6819999	6899999	80000	34	0.82523
chr17	13379999	13579999	200000	55	-0.93881
chr17	15099999	15179999	80000	34	0.80715
chr17	27379999	27539999	160000	56	0.83116
chr17	36219999	36259999	40000	21	0.87917
chr17	36299999	36339999	40000	23	-1.3855
chr17	40099999	40219999	120000	44	-1.38925
chr17	40259999	40299999	40000	21	-0.94208
chrX	3019999	4939999	1920000	288	1.03411
chrX	30259999	32219999	1960000	317	1.07972
chrX	1.66E+08	1.66E+08	40000	14	-2.19935

HTG

CHROMOSOME	START	STOP	SIZE	DATAPOINTS	LOG2_RATIO_N
chr1	8139999	8179999	40000	21	-1.68233
chr1	90139999	90179999	40000	23	-1.2043
chr3	93579999	93659999	80000	34	0.95819
chr7	3699999	3819999	120000	43	-1.44193
chr7	20659999	24099999	3440000	657	-1.15177
chr8	19339999	19379999	40000	20	-1.16629
chr8	22539999	22699999	160000	47	-1.14805
chr9	46699999	46939999	240000	78	0.88481
chr11	71019999	71099999	80000	33	-1.42496
chr14	3019999	3139999	120000	25	1.05951
chr14	3979999	8499999	4520000	876	0.83956
chr17	6259999	6899999	640000	180	1.13787
chr17	36299999	36339999	40000	23	-1.14227
chr17	40059999	40299999	240000	77	-1.11641

Supplementary Table 2 - differentially regulated genes in haploid ES ells (> 2 fold; p<0.05)

Upregulated genes in haploid vs diploid ES cells

	Probe Set ID	Fold change	Gene Symbol	Entrez Gene	Gene Description
1	1434068_s_at	11.99	AI662270	103814	expressed sequence AI662270
2	1416749_at	10.76	Htra1	56213	HtrA serine peptidase 1
3	1419540_at	8.46	EG434726 /// Fthl17	434726 /// 434727 ///	predicted gene 14458
4	1460670_at	8.39	Riok3	66878	RIO kinase 3 (yeast)
5	1419134_at	7.66	Rhbg	58176	Rhesus blood group-associated B glycoprotein
6	1436107_at	7.51	Lsm8	76522	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)
7	1427512_a_at	7.47	Lama3	16774	laminin, alpha 3
8	1450001_a_at	7.34	Ush1c	72088	Usher syndrome 1C homolog (human)
9	1456036_x_at	7.24	Gsto1	14873	glutathione S-transferase omega 1
10	1454799_at	7.01	Agpat9	231510	1-acylglycerol-3-phosphate O-acyltransferase 9
11	1424692_at	6.90	2810055F11Rik	67217	RIKEN cDNA 2810055F11 gene
12	1436355_at	6.73	Fads6	328035	fatty acid desaturase domain family, member 6
13	1454869_at	6.60	Wdr40b	245404	WD repeat domain 40B
14	1453977_at	6.54	Exoc4	20336	exocyst complex component 4
15	1437152_at	6.40	Mex3b	108797	mex3 homolog B (C. elegans)
16	1454737_at	6.27	Dusp9	75590	dual specificity phosphatase 9
17	1437867_at	5.95			
18	1416531_at	5.83	Gsto1	14873	glutathione S-transferase omega 1
19	1426988_at	5.80	Klhdc5	232539	kelch domain containing 5
20	1450460_at	5.53	Aqp3	11828	aquaporin 3
21	1422008_a_at	5.53	Aqp3	11828	aquaporin 3
22	1421385_a_at	5.33	Myo7a	17921	myosin VIIA
23	1445281_a_at	5.28	B230311B06Rik	381914	RIKEN cDNA B230311B06 gene
24	1444416_at	5.26	Cenpa	12615	centromere protein A
25	1429308_at	5.23	Prdm16	70673	PR domain containing 16
26	1433845_x_at	5.15	Dusp9	75590	dual specificity phosphatase 9
27	1438251_x_at	4.82	Htra1	56213	HtrA serine peptidase 1
28	1449031_at	4.79	Cited1	12705	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1
29	1437409_s_at	4.78	Gpr126	215798	G protein-coupled receptor 126
30	1438238_at	4.72	2010315B03Rik	630836	RIKEN cDNA 2010315B03 gene
31	1426223_at	4.66	Ttc39c	72747	tetratricopeptide repeat domain 39C
32	1435948_at	4.40	Tmem181 /// Tmem	100040525 /// 77106	transmembrane protein 181C, pseudogene
33	1448596_at	4.13	Slc6a8	102857	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
34	1438842_at	4.09	Mtch2	56428	mitochondrial carrier homolog 2 (C. elegans); predicted gene, 100039384; predi
35	1417120_at	4.08	Miip	28010	migration and invasion inhibitory protein
36	1449036_at	4.05	Rnf128	66889	ring finger protein 128
37	1439422_a_at	4.04	Fam132a	67389	family with sequence similarity 132, member A
38	1429169_at	4.03	Rbm3	19652	predicted gene 15453; RNA binding motif protein 3
39	1424082_at	4.03	Tbc1d13	70296	TBC1 domain family, member 13
40	1429504_at	3.97	Rnpc3	67225	RNA-binding region (RNP1, RRM) containing 3
41	1444226_at	3.78	Foxo3	56484	forkhead box O3
42	1418681_at	3.75	Alg13	67574	asparagine-linked glycosylation 13 homolog (S. cerevisiae)
43	1451754_a_at	3.71	Wdr45	54636	WD repeat domain 45
44	1433844_a_at	3.60	Dusp9	75590	dual specificity phosphatase 9
45	1456804_at	3.57	EG627821	627821	predicted gene 6792
46	1437302_at	3.56	Adrb2	11555	adrenergic receptor, beta 2
47	1450843_a_at	3.55	Serpinh1	12406	serine (or cysteine) peptidase inhibitor, clade H, member 1
48	1459740_s_at	3.55	Ucp2	22228	uncoupling protein 2 (mitochondrial, proton carrier)
49	1428933_at	3.53	Hdac8	70315	histone deacetylase 8
50	1451148_at	3.52	LOC100047214 /// F	100047214 /// 68943	similar to PTEN induced putative kinase 1
51	1422743_at	3.48	Phka1	18679	phosphorylase kinase alpha 1
52	1454009_at	3.45	1700008O03Rik	69349	RIKEN cDNA 1700008O03 gene
53	1438750_at	3.42	Atrx	22589	alpha thalassemia/mental retardation syndrome X-linked homolog (human)
54	1448599_s_at	3.39	Miip	28010	migration and invasion inhibitory protein
55	1426241_a_at	3.38	Scmh1	29871	sex comb on midleg homolog 1
56	1435069_at	3.35	BC064078	408064	cDNA sequence BC064078
57	1425601_a_at	3.34	Rtkn	20166	rhotekin
58	1430538_at	3.28	2210013O21Rik	70123	RIKEN cDNA 2210013O21 gene
59	1417116_at	3.26	Slc6a8	102857	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
60	1422823_at	3.26	Eps8 /// LOC63263	13860 /// 632638	epidermal growth factor receptor pathway substrate 8
61	1434092_at	3.22	Atg9b	213948	ATG9 autophagy related 9 homolog B (S. cerevisiae)
62	1416239_at	3.20	Ass1	11898	argininosuccinate synthetase 1
63	1455721_at	3.20	Gspt2	14853	G1 to S phase transition 2
64	1436200_at	3.19	Lonrf3	74365	LON peptidase N-terminal domain and ring finger 3

	Probe Set ID	Fold change	Gene Symbol	Entrez Gene	Gene Description
65	1426466_s_at	3.19	Rps6kl1	238323	ribosomal protein S6 kinase-like 1
66	1418318_at	3.16	Rnf128	66889	ring finger protein 128
67	1435514_at	3.14	Lztfl1	93730	leucine zipper transcription factor-like 1; predicted gene 6776
68	1449476_at	3.14	Rage	26448	renal tumor antigen
69	1447957_at	3.09	D7Ertd128e	52222	DNA segment, Chr 7, ERATO Doi 128, expressed
70	1422711_a_at	3.08	Pnck	93843	pregnancy upregulated non-ubiquitously expressed CaM kinase
71	1417850_at	3.04	Rb1	19645	retinoblastoma 1
72	1422744_at	3.02	Phka1	18679	phosphorylase kinase alpha 1
73	1427564_at	3.02	Diap2	54004	diaphanous homolog 2 (Drosophila)
74	1451169_at	3.02	Nomo1	211548	nodal modulator 1
75	1448330_at	3.01	Gstm1	14862	similar to Glutathione S-transferase Mu 1 (GST class-mu 1) (Glutathione S-trans
76	1455817_x_at	3.00	Zxdb	668166	zinc finger, X-linked, duplicated B
77	1451269_at	2.99	Pdzd11	72621	PDZ domain containing 11
78	1446583_at	2.97			
79	1449119_at	2.97	Arih2	23807	ariadne homolog 2 (Drosophila); predicted gene 12263
80	1437369_at	2.97	Fgd1	14163	FYVE, RhoGEF and PH domain containing 1
81	1460600_at	2.96	AA414768	245350	expressed sequence AA414768
82	1453040_at	2.96	Mcart6	67062	mitochondrial carrier triple repeat 6
83	1424838_at	2.95	A330049M08Rik	230822	RIKEN cDNA A330049M08 gene
84	1450919_at	2.93	Mpp1	17524	membrane protein, palmitoylated
85	1425068_a_at	2.91	Tex264	21767	testis expressed gene 264
86	1444057_at	2.91			UBX domain protein 4
87	1434493_at	2.91	1810022K09Rik	69126	predicted gene 4540; RIKEN cDNA 1810022K09 gene
88	1421896_at	2.91	Elk1	13712	ELK1, member of ETS oncogene family
89	1422327_s_at	2.90	G6pd2 /// G6pdx	14380 /// 14381	glucose-6-phosphate dehydrogenase 2
90	1437449_at	2.90	Rsad1	237926	radical S-adenosyl methionine domain containing 1
91	1444837_at	2.89			Scm-like with four mbt domains 2
92	1417393_a_at	2.88	Fam132a	67389	family with sequence similarity 132, member A
93	1418901_at	2.86	Cebpb	12608	CCAAT/enhancer binding protein (C/EBP), beta
94	1438065_at	2.83	Rprd1a	225283	regulation of nuclear pre-mRNA domain containing 1A
95	1437435_at	2.83	1700061G19Rik	78625	RIKEN cDNA 1700061G19 gene
96	1424322_at	2.81	Apex2	77622	apurinic/apyrimidinic endonuclease 2
97	1436347_a_at	2.81	5530601H04Rik	71445	RIKEN cDNA 5530601H04 gene
98	1433741_at	2.81	Cd38	12494	CD38 antigen
99	1434436_at	2.81	Morc4	75746	microrchidia 4
100	1427844_a_at	2.76	Cebpb	12608	CCAAT/enhancer binding protein (C/EBP), beta
101	1448524_s_at	2.76	Ssr4	20832	signal sequence receptor, delta
102	1428705_at	2.75	1700007K13Rik	69327	RIKEN cDNA 1700007K13 gene
103	1426863_at	2.75	Rbmx	19655	RNA binding motif protein, X chromosome
104	1417412_at	2.74	F8a	14070	factor 8-associated gene A
105	1457313_at	2.73	Ocrl	320634	oculocerebrorenal syndrome of Lowe
106	1455028_at	2.72	Mapt	17762	microtubule-associated protein tau
107	1444585_at	2.70	Adc	242669	arginine decarboxylase
108	1435218_at	2.69	Rasgef1a	70727	RasGEF domain family, member 1A
109	1439753_x_at	2.69	Six4	20474	sine oculis-related homeobox 4 homolog (Drosophila)
110	1423436_at	2.68	Gsta3	14859	glutathione S-transferase, alpha 3
111	1417357_at	2.67	Emd	13726	emerin
112	1438671_at	2.66	Ppp2r2c	269643	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isofo
113	1416416_x_at	2.66	Gstm1	14862	similar to Glutathione S-transferase Mu 1 (GST class-mu 1) (Glutathione S-trans
114	1441229_at	2.66	D230019N24Rik	399607	RIKEN cDNA D230019N24 gene
115	1434681_at	2.66	4932441K18Rik	353170	predicted gene 8258; similar to factor inhibiting activating transcription factor 4 (A
116	1451751_at	2.66	Ddit4l	73284	DNA-damage-inducible transcript 4-like
117	1436780_at	2.65	Ogt	108155	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine
118	1436509_at	2.64	Mlec	109154	malectin
119	1439824_at	2.64	Chm	12662	similar to choroidermia; choroidermia
120	1419763_at	2.63	Nkap	67050	reproductive homeobox 3B; UPF3 regulator of nonsense transcripts homolog B
121	1448188_at	2.59	Ucp2	22228	uncoupling protein 2 (mitochondrial, proton carrier)
122	1450161_at	2.59	Ikbkg	16151	inhibitor of kappaB kinase gamma
123	1426025_s_at	2.58	Laptm5	16792	lysosomal-associated protein transmembrane 5
124	1428654_at	2.57	1200016B10Rik	66875	RIKEN cDNA 1200016B10 gene
125	1439476_at	2.56	Dsg2	13511	desmoglein 2; similar to Dsg2 protein
126	1417732_at	2.55	Anxa8	11752	annexin A8
127	1416032_at	2.54	Tmem109	68539	transmembrane protein 109
128	1418237_s_at	2.54	Col18a1	12822	collagen, type XVIII, alpha 1
129	1417721_s_at	2.53	Laptm5	16792	lysosomal-associated protein transmembrane 5
130	1453375_at	2.53	4930422N03Rik	76871	RIKEN cDNA 4930422N03 gene
131	1424286_at	2.53	Prkx	19108	protein kinase, X-linked
132	1456504_at	2.52	Zfp182	319535	zinc finger protein 182
133	1420922_at	2.52	Usp9x	22284	ubiquitin specific peptidase 9, X chromosome
134	1420433_at	2.51	Taf7l	74469	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor

	Probe Set ID	Fold change	Gene Symbol	Entrez Gene	Gene Description
135	1460471_at	2.50	Ooep	67968	oocyte expressed protein homolog (dog)
136	1432026_a_at	2.50	Herc5	67138	hect domain and RLD 5
137	1427235_at	2.49	Kdm6a	22289	4lysine (K)-specific demethylase 6A
138	1455111_at	2.49	Yipf6	77929	similar to Yip1 domain family, member 6; Yip1 domain family, member 6
139	1441937_s_at	2.49	LOC100047214 /// F	100047214 /// 68943	similar to PTEN induced putative kinase 1
140	1431856_a_at	2.48	C1qtnf6	72709	C1q and tumor necrosis factor related protein 6
141	1451884_a_at	2.48	Lsm2	27756	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)
142	1455198_a_at	2.48	Ppp2r3a	19054	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha; RIKEN cDNA
143	1416397_at	2.48	Mesdc1	80889	mesoderm development candidate 1
144	1430975_at	2.47	8430416G17Rik	71469	RIKEN cDNA 8430416G17 gene
145	1456716_s_at	2.47	3110002H16Rik	76482	RIKEN cDNA 3110002H16 gene
146	1449046_a_at	2.47	Josd2	66124	Josephin domain containing 2
147	1448645_at	2.46	Msl3	17692	male-specific lethal 3 homolog (Drosophila)
148	1435458_at	2.46	Pim1	18712	proviral integration site 1
149	1444500_at	2.46	Ahsa1	217737	AHA1, activator of heat shock protein ATPase homolog 1 (yeast)
150	1460579_at	2.45	Dnpep	13437	aspartyl aminopeptidase
151	1456609_at	2.44	Camk2n1	66259	calcium/calmodulin-dependent protein kinase II inhibitor 1
152	1434424_at	2.43	Mfsd7b	226844	major facilitator superfamily domain containing 7B
153	1452859_at	2.43	1200016B10Rik	66875	RIKEN cDNA 1200016B10 gene
154	1453091_s_at	2.43	Letmd1	68614	LETM1 domain containing 1
155	1445634_at	2.42			microtubule-associated protein tau
156	1431774_a_at	2.41	Lyrm1	73919	LYR motif containing 1
157	1419309_at	2.40	Pdpn	14726	podoplanin
158	1416155_at	2.40	Hmgb3	15354	predicted gene 11805; predicted gene 8850; high mobility group box 3; similar to
159	1445241_at	2.40	Rab11fip4	268451	RAB11 family interacting protein 4 (class II)
160	1438857_x_at	2.40	Irak1	16179	interleukin-1 receptor-associated kinase 1
161	1448192_s_at	2.38	AU021838 /// Prps1	19139 /// 328099	mirror-image polydactyly gene 1 homolog (human); phosphoribosyl pyrophospha
162	1435452_at	2.38	LOC100047579 /// T	100047579 /// 24066(	similar to transmembrane protein 20; transmembrane protein 20
163	1436917_s_at	2.37	Gpsm1	67839	G-protein signalling modulator 1 (AGS3-like, C. elegans)
164	1455727_at	2.37	Zrsr2	22184	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2
165	1417099_at	2.36	Ftsj1 /// LOC100044	100044636 /// 54632	similar to Ftsj homolog; FtsJ homolog 1 (E. coli)
166	1435567_at	2.36	Phka1	18679	phosphorylase kinase alpha 1
167	1457394_at	2.35	2900002K06Rik	70226	RIKEN cDNA 2900002K06 gene
168	1435051_at	2.35	Wdr44	72404	WD repeat domain 44
169	1458684_at	2.35			similar to Ss18 protein; synovial sarcoma translocation, Chromosome 18
170	1421499_a_at	2.35	Ptpn14	19250	protein tyrosine phosphatase, non-receptor type 14
171	1423228_at	2.34	B4galt6	56386	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6; similar to B
172	1455784_at	2.34	Sec1	56546	secretory blood group 1
173	1434263_at	2.34	F630110N24Rik	73822	RIKEN cDNA F630110N24 gene
174	1419206_at	2.34	Cd37	12493	CD37 antigen
175	1448354_at	2.34	G6pdx	14381	glucose-6-phosphate dehydrogenase X-linked
176	1416865_at	2.34	Fgd1	14163	FYVE, RhoGEF and PH domain containing 1
177	1446234_at	2.34			4lysine (K)-specific demethylase 6A
178	1423660_at	2.33	Ctdsp2 /// ENSMUS	100043719 /// 52468	predicted gene 9770
179	1434061_at	2.33	Rp2h	19889	retinitis pigmentosa 2 homolog (human)
180	1437495_at	2.33	Mbtps2 /// Yy2	100073351 /// 27066	membrane-bound transcription factor peptidase, site 2; similar to zinc finger, X-li
181	1434849_at	2.33	Tspyl2	52808	TSPY-like 2
182	1448419_at	2.33	Pop4	66161	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)
183	1451611_at	2.33	Pla2g16	225845	phospholipase A2, group XVI
184	1416052_at	2.32	Prps1	19139	mirror-image polydactyly gene 1 homolog (human); phosphoribosyl pyrophospha
185	1426955_at	2.32	Col18a1	12822	collagen, type XVIII, alpha 1
186	1426484_at	2.31	Ubxn4	67812	UBX domain protein 4
187	1423451_at	2.31	Pgrmc1	53328	progesterone receptor membrane component 1
188	1417637_a_at	2.31	Hmg20b	15353	high mobility group 20 B
189	1432205_a_at	2.30	C130038G02Rik	77521	RIKEN cDNA C130038G02 gene
190	1439201_at	2.30	Usp14	59025	ubiquitin specific peptidase 14
191	1436541_at	2.29	2310008H09Rik	66356	RIKEN cDNA 2310008H09 gene
192	1425516_at	2.29	Ogt	108155	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine
193	1434360_s_at	2.29	LOC632664 /// Ptpr	19270 /// 632664	protein tyrosine phosphatase, receptor type, G; similar to protein tyrosine phospl
194	1449740_s_at	2.28	Dsg2	13511	desmoglein 2; similar to Dsg2 protein
195	1454082_a_at	2.28	Giyd2	75764	GIY-YIG domain containing 2
196	1448371_at	2.28	Mylpf	17907	myosin light chain, phosphorylatable, fast skeletal muscle
197	1424236_at	2.27	Tbc1d10b	68449	TBC1 domain family, member 10b
198	1433913_at	2.27	C80913	19777	expressed sequence C80913
199	1448908_at	2.27	Ppap2b	67916	phosphatidic acid phosphatase type 2B
200	1460177_at	2.27	Cndp2	66054	CNDP dipeptidase 2 (metallopeptidase M20 family)
201	1460649_at	2.27	Irak1	16179	interleukin-1 receptor-associated kinase 1
202	1456279_a_at	2.26	Bcap31	27061	B-cell receptor-associated protein 31
203	1428357_at	2.25	2610019F03Rik	72148	RIKEN cDNA 2610019F03 gene
204	1437780_at	2.25	Fancb	237211	Fanconi anemia, complementation group B

	Probe Set ID	Fold change	Gene Symbol	Entrez Gene	Gene Description
205	1454787_at	2.25	Zdhhc9	208884	similar to zinc finger, DHHC domain containing 9; zinc finger, DHHC domain con
206	1418397_at	2.23	Zfp275	27081	zinc finger protein 275
207	1451302_at	2.23	1110012L19Rik	68618	RIKEN cDNA 1110012L19 gene; predicted gene 8512
208	1431228_s_at	2.22	4930526I15Rik	75135	RIKEN cDNA 4930526I15 gene
209	1450995_at	2.22	Folr1	14275	folate receptor 1 (adult)
210	1439064_at	2.22	BC030046	277154	cDNA sequence BC030046
211	1422616_s_at	2.22	Wdr54	75659	WD repeat domain 54
212	1448269_a_at	2.21	Klhl13	67455	kelch-like 13 (Drosophila)
213	1423122_at	2.20	Avpi1	69534	arginine vasopressin-induced 1
214	1445693_at	2.20	Araf	11836	v-raf murine sarcoma 3611 viral oncogene homolog
215	1448772_at	2.20	Ube2a	22209	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)
216	1460169_a_at	2.20	Pctk1	18555	PCTAIRE-motif protein kinase 1
217	1444390_at	2.20	Prdm14	383491	PR domain containing 14
218	1448118_a_at	2.19	Ctsd	13033	cathepsin D
219	1424124_at	2.19	Mospd2	76763	motile sperm domain containing 2
220	1420725_at	2.19	Tmlhe	192289	trimethyllysine hydroxylase, epsilon
221	1450264_a_at	2.18	Chka	12660	choline kinase alpha
222	1434518_at	2.18	Phka2	110094	phosphorylase kinase alpha 2
223	1440344_at	2.18	Snord89	100217461	small nucleolar RNA, C/D box 89
224	1431044_at	2.18	Thoc1	225160	THO complex 1
225	1438843_x_at	2.17	Mtch2	56428	mitochondrial carrier homolog 2 (C. elegans); predicted gene, 100039384; predi
226	1454816_at	2.17	Rp2h	19889	retinitis pigmentosa 2 homolog (human)
227	1415956_a_at	2.17	Pctk1	18555	PCTAIRE-motif protein kinase 1
228	1429400_at	2.16	Clcn5	12728	chloride channel 5
229	1424224_at	2.16	Asb8	78541	ankyrin repeat and SOCS box-containing 8
230	1453895_at	2.16	C330026N13Rik	78531	RIKEN cDNA C330026N13 gene
231	1426734_at	2.15	Fam43a	224093	family with sequence similarity 43, member A
232	1426497_at	2.15	Kdm5c	20591	lysine (K)-specific demethylase 5C
233	1423978_at	2.14	Sbk1	104175	SH3-binding kinase 1
234	1451070_at	2.14	Gdi1	14567	guanosine diphosphate (GDP) dissociation inhibitor 1
235	1456981_at	2.14	Tmc7	209760	transmembrane channel-like gene family 7; similar to Tmc7 protein
236	1455247_at	2.13	Amotl1	75723	angiomotin-like 1
237	1452800_a_at	2.13	Apoo	68316	similar to Novel transmembrane domain containing protein; apolipoprotein O
238	1451299_at	2.13	Prkx	19108	protein kinase, X-linked
239	1430449_at	2.13	Kidins220	77480	kinase D-interacting substrate 220
240	1430215_at	2.13	2610020H08Rik	434234	RIKEN cDNA 2610020H08 gene
241	1450107_a_at	2.12	Renbp	19703	renin binding protein
242	1435860_at	2.12	Slc5a6	330064	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
243	1422965_at	2.11	Agtrap	11610	angiotensin II, type I receptor-associated protein
244	1424167_a_at	2.11	Pmm1	29858	phosphomannomutase 1
245	1423662_at	2.11	Atp6ap2	70495	ATPase, H+ transporting, lysosomal accessory protein 2
246	1420909_at	2.11	Vegfa	22339	vascular endothelial growth factor A
247	1438270_at	2.11	AI846148	68229	expressed sequence AI846148
248	1427573_at	2.11	Chic1	12212	cysteine-rich hydrophobic domain 1
249	1458358_at	2.11	Pank2	74450	pantothenate kinase 2 (Hallervorden-Spatz syndrome)
250	1436905_x_at	2.11	Laptm5	16792	lysosomal-associated protein transmembrane 5
251	1421797_a_at	2.10	Snx12	55988	sorting nexin 12
252	1428334_at	2.10	Ostm1	14628	osteopetrosis associated transmembrane protein 1
253	1450038_s_at	2.10	Usp9x	22284	ubiquitin specific peptidase 9, X chromosome
254	1439631_at	2.09	Zcchc11	230594	zinc finger, CCHC domain containing 11
255	1448668_a_at	2.09	Irak1	16179	interleukin-1 receptor-associated kinase 1
256	1426410_at	2.08	Pdk3	236900	pyruvate dehydrogenase kinase, isoenzyme 3
257	1441391_at	2.07			guanine nucleotide binding protein (G protein), beta polypeptide 1-like; similar to
258	1449622_s_at	2.07	Atp6ap1	54411	ATPase, H+ transporting, lysosomal accessory protein 1
259	1426306_a_at	2.07	LOC100046560 /// M	100046560 /// 80884	similar to melanoma antigen family D, 2; melanoma antigen, family D, 2
260	1457316_at	2.07	Mtap6	17760	microtubule-associated protein 6
261	1417442_a_at	2.06	Pex3	56535	peroxisomal biogenesis factor 3
262	1451049_at	2.05	Bcap31	27061	B-cell receptor-associated protein 31
263	1435008_at	2.05	Slc9a6	236794	solute carrier family 9 (sodium/hydrogen exchanger), member 6
264	1424106_at	2.05	1200003C05Rik	104771	RIKEN cDNA 1200003C05 gene
265	1423661_s_at	2.04	Ctdsp2 /// ENSMUS	100043719 /// 52468	predicted gene 9770
266	1435566_s_at	2.04	Araf	11836	v-raf murine sarcoma 3611 viral oncogene homolog
267	1451400_at	2.04	Gemin8	237221	similar to gem (nuclear organelle) associated protein 8; predicted gene 5455; ge
268	1428773_s_at	2.04	Bcor	71458	BCL6 interacting corepressor
269	1432158_a_at	2.04	Trappc2	66226	similar to Chain A, The Crystal Structure Of The Bet3-Trs31-Sedlin Complex; tra
270	1449916_at	2.02	Pbx4	80720	pre-B-cell leukemia homeobox 4
271	1432011_at	2.02	2900052L18Rik	76835	predicted gene 4407; RIKEN cDNA 2900052L18 gene
272	1434908_at	2.02	Scaf1	233208	SR-related CTD-associated factor 1
273	1441970_at	2.02	E430010N07Rik	399572	RIKEN cDNA E430010N07 gene
274	1429776_a_at	2.02	Dnajb6	23950	DnaJ (Hsp40) homolog, subfamily B, member 6; predicted gene 5917; predictec
275	1425525_a_at	2.01	P2rx4	18438	purinergic receptor P2X, ligand-gated ion channel 4
276	1436300_at	2.01	Dstyk	213452	dual serine/threonine and tyrosine protein kinase
277	1430780_a_at	2.01	Pmm1	29858	phosphomannomutase 1

Downregulated genes in haploid vs diploid ES cells

	Probe Set ID	Fold change	Gene Symbol	Entrez Gene	Gene Description
1	1417210_at	-46.94	Eif2s3y	26908	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked
2	1443621_at	-34.01	Xaf1	327959	XIAP associated factor 1
3	1426438_at	-32.17	Ddx3y	26900	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
4	1445226_at	-23.48	BC023969	407828	cDNA sequence BC023969
5	1452077_at	-21.18	Ddx3y	26900	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
6	1427302_at	-12.31	Enpp3	209558	ectonucleotide pyrophosphatase/phosphodiesterase 3
7	1416371_at	-10.48	Apod	11815	apolipoprotein D
8	1437721_at	-9.30	Coro1c	23790	coronin, actin binding protein 1C; predicted gene 5790
9	1438833_at	-9.18	Casc5	76464	cancer susceptibility candidate 5
10	1415949_at	-8.97	Cpe /// LOC100046	100046434 /// 12876	carboxypeptidase E; similar to carboxypeptidase E
11	1438933_x_at	-7.94	Rasgrp2	19395	RAS, guanyl releasing protein 2
12	1415897_a_at	-7.72	Mgst1	56615	microsomal glutathione S-transferase 1
13	1437671_x_at	-6.76	Prss23	76453	protease, serine, 23
14	1450857_a_at	-6.55	Col1a2	12843	collagen, type I, alpha 2
15	1423110_at	-6.45	Col1a2	12843	collagen, type I, alpha 2
16	1417461_at	-6.33	Cap1	12331	CAP, adenylate cyclase-associated protein 1 (yeast)
17	1426598_at	-6.23	Uty	22290	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome
18	1439757_s_at	-6.02	Epha4	13838	Eph receptor A4
19	1452384_at	-5.96	Enpp3	209558	ectonucleotide pyrophosphatase/phosphodiesterase 3
20	1417462_at	-5.72	Cap1	12331	CAP, adenylate cyclase-associated protein 1 (yeast)
21	1439555_at	-5.52	Rlf	109263	rearranged L-myc fusion sequence
22	1433542_at	-5.44	Inpp5f	101490	inositol polyphosphate-5-phosphatase F
23	1451260_at	-5.18	Aldh1b1	72535	aldehyde dehydrogenase 1 family, member B1
24	1460616_at	-5.11	Slco4c1	227394	solute carrier organic anion transporter family, member 4C1
25	1433783_at	-5.07	Ldb3	24131	LIM domain binding 3
26	1425538_x_at	-4.56	Ceacam1	26365	carcinoembryonic antigen-related cell adhesion molecule 1; carcinoembryonic a
27	1432075_a_at	-4.49	Tekt1	21689	tektin 1
28	1431057_a_at	-4.47	Prss23	76453	protease, serine, 23
29	1416008_at	-4.24	Satb1	20230	special AT-rich sequence binding protein 1
30	1448123_s_at	-4.16	Tgfbi	21810	transforming growth factor, beta induced
31	1421929_at	-4.10	Epha4	13838	Eph receptor A4
32	1426108_s_at	-4.09	Cacnb1	12295	calcium channel, voltage-dependent, beta 1 subunit
33	1423505_at	-4.05	Tagln	21345	transgelin
34	1435836_at	-3.90	Pdk1	228026	pyruvate dehydrogenase kinase, isoenzyme 1
35	1427630_x_at	-3.74	Ceacam1	26365	carcinoembryonic antigen-related cell adhesion molecule 1; carcinoembryonic a
36	1438403_s_at	-3.72	Malat1	72289	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
37	1429509_at	-3.72	Lsm12	268490	LSM12 homolog (S. cerevisiae)
38	1449071_at	-3.69	Myl7	17898	myosin, light polypeptide 7, regulatory
39	1421100_a_at	-3.62	Dab1	13131	disabled homolog 1 (Drosophila)
40	1418188_a_at	-3.52	Malat1	72289	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
41	1420989_at	-3.51	4933411K20Rik	66756	RIKEN cDNA 4933411K20 gene
42	1418189_s_at	-3.50	Malat1	72289	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
43	1423162_s_at	-3.45	Spred1	114715	sprouty protein with EVH-1 domain 1, related sequence
44	1418617_x_at	-3.44	Clgn	12745	calmegin
45	1423184_at	-3.35	Itsn2	20403	intersectin 2
46	1444616_x_at	-3.33			C-type lectin domain family 2, member e
47	1434447_at	-3.25	Met	17295	met proto-oncogene
48	1450494_x_at	-3.24	Ceacam1	26365	carcinoembryonic antigen-related cell adhesion molecule 1; carcinoembryonic a
49	1424130_a_at	-3.23	Ptrf	19285	polymerase I and transcript release factor
50	1429021_at	-3.23	Epha4	13838	Eph receptor A4
51	1417780_at	-3.21	Lass4	67260	LAG1 homolog, ceramide synthase 4
52	1427311_at	-3.17	Bptf	207165	bromodomain PHD finger transcription factor
53	1416612_at	-3.17	Cyp1b1	13078	cytochrome P450, family 1, subfamily b, polypeptide 1
54	1417141_at	-3.16	Igtp	16145	interferon gamma induced GTPase
55	1456120_at	-3.15	Secisbp2l	70354	SECIS binding protein 2-like
56	1429778_at	-3.12	Optn	71648	optineurin
57	1427998_at	-3.10	Lsm12	268490	LSM12 homolog (S. cerevisiae)
58	1435679_at	-3.08	Optn	71648	optineurin
59	1421129_a_at	-3.05	Atp2a3	53313	ATPase, Ca++ transporting, ubiquitous
60	1458539_at	-2.95	R3hdm1	226412	R3H domain 1 (binds single-stranded nucleic acids)
61	1457936_at	-2.93	Mapk8	26419	mitogen-activated protein kinase 8
62	1439882_at	-2.92	Sec23ip	207352	Sec23 interacting protein
63	1424598_at	-2.87	Ddx6	13209	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
64	1450647_at	-2.87	Hps3	12807	Hermansky-Pudlak syndrome 3 homolog (human)
65	1438200_at	-2.87	Sulf1	240725	sulfatase 1
66	1450839_at	-2.85	D0H4S114	27528	DNA segment, human D4S114

	Probe Set ID	Fold change	Gene Symbol	Entrez Gene	Gene Description
67	1429183_at	-2.84	Pkp2	67451	plakophilin 2
68	1447680_at	-2.83	Anp32e	66471	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
69	1456697_x_at	-2.80	Dmtf1	23857	cyclin D binding myb-like transcription factor 1
70	1440146_at	-2.78	Vps13a	271564	vacuolar protein sorting 13A (yeast)
71	1450068_at	-2.77	Baz1b	22385	bromodomain adjacent to zinc finger domain, 1B
72	1417220_at	-2.76	Fah	14085	fumarylacetoacetate hydrolase
73	1424657_at	-2.74	Taok1	216965	TAO kinase 1
74	1448300_at	-2.73	Mgst3	66447	microsomal glutathione S-transferase 3
75	1449799_s_at	-2.72	Pkp2	67451	plakophilin 2
76	1433809_at	-2.70	Ddx5	13207	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5; predicted gene 12183
77	1458332_x_at	-2.69	Sox4	20677	SRY-box containing gene 19; SRY-box containing gene 4
78	1418197_at	-2.66	Ucp1	22227	uncoupling protein 1 (mitochondrial, proton carrier)
79	1436319_at	-2.65	Sulf1	240725	sulfatase 1
80	1452330_a_at	-2.63	Mxra8	74761	matrix-remodelling associated 8
81	1427456_at	-2.63	Wdfy3	72145	WD repeat and FYVE domain containing 3
82	1436311_at	-2.61	Gemin5	216766	gem (nuclear organelle) associated protein 5
83	1437117_at	-2.61	Centb1	216859	centaurin, beta 1
84	1430240_a_at	-2.60	Clgn	12745	calmegin
85	1443778_at	-2.57	Sox4	20677	SRY-box containing gene 19; SRY-box containing gene 4
86	1424703_at	-2.53	Hemk1	69536	HemK methyltransferase family member 1
87	1423066_at	-2.53	Dnmt3a	13435	DNA methyltransferase 3A
88	1416105_at	-2.52	Nnt	18115	nicotinamide nucleotide transhydrogenase
89	1436020_at	-2.52	Zfp828	101994	zinc finger protein 828
90	1438708_x_at	-2.51	Ywhab	54401	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, bet
91	1448632_at	-2.50	Psmb10	19171	proteasome (prosome, macropain) subunit, beta type 10
92	1427261_at	-2.49	Wwc1	211652	WW, C2 and coiled-coil domain containing 1
93	1439150_x_at	-2.49	Grtp1	66790	GH regulated TBC protein 1
94	1434140_at	-2.49	Mcf2l	17207	mcf.2 transforming sequence-like
95	1453293_a_at	-2.48	2810408A11Rik	70419	RIKEN cDNA 2810408A11 gene
96	1421005_at	-2.48	Cep110	26920	centrosomal protein 110
97	1427231_at	-2.46	Robo1	19876	roundabout homolog 1 (Drosophila)
98	1443787_x_at	-2.45	Casp14	12365	caspase 14
99	1455608_at	-2.44	Sclt1	67161	sodium channel and clathrin linker 1
100	1433730_at	-2.44	Elmod2	244548	ELMO domain containing 2
101	1439995_at	-2.41	Nhedc2	97086	Na+/H+ exchanger domain containing 2
102	1421928_at	-2.40	Epha4	13838	Eph receptor A4
103	1449311_at	-2.38	Bach1	12013	BTB and CNC homology 1
104	1424658_at	-2.37	Taok1	216965	TAO kinase 1
105	1452115_a_at	-2.36	Plk4	20873	polo-like kinase 4 (Drosophila)
106	1425205_at	-2.34	Ddx19b	234733	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b
107	1427950_at	-2.34	Rnf160	78913	ring finger protein 160
108	1437248_at	-2.34	2700049A03Rik	76967	RIKEN cDNA 2700049A03 gene
109	1431215_at	-2.30	Dnajc6	72685	DnaJ (Hsp40) homolog, subfamily C, member 6
110	1418524_at	-2.28	Pcm1	18536	pericentriolar material 1
111	1455604_at	-2.27	Fzd5	14367	frizzled homolog 5 (Drosophila)
112	1443971_x_at	-2.27	Mpp7	75739	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
113	1453172_at	-2.27	Hspa13	110920	heat shock protein 70 family, member 13
114	1451117_a_at	-2.27	Tom1l1	71943	target of myb1-like 1 (chicken)
115	1420410_at	-2.27	Nr5a2	26424	nuclear receptor subfamily 5, group A, member 2
116	1431672_at	-2.27	9430069I07Rik	77358	RIKEN cDNA 9430069I07 gene
117	1418947_at	-2.27	Nek3	23954	NIMA (never in mitosis gene a)-related expressed kinase 3
118	1444749_at	-2.26			apolipoprotein D
119	1456863_at	-2.25	Epha4	13838	Eph receptor A4
120	1452497_a_at	-2.25	Nfatc3	18021	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
121	1460291_at	-2.25	Cdk6	12571	cyclin-dependent kinase 6
122	1419642_at	-2.24	Purb	19291	purine rich element binding protein B
123	1453562_a_at	-2.23	Nmral1	67824	NmrA-like family domain containing 1
124	1435155_at	-2.23	Cgn	70737	cingulin; cDNA sequence BC021767
125	1432282_a_at	-2.23	Tlcd2	380712	TLC domain containing 2
126	1450093_s_at	-2.23	Zbtb7a	16969	zinc finger and BTB domain containing 7a
127	1419240_at	-2.23	Tex14	83560	testis expressed gene 14
128	1455905_at	-2.21	2610507B11Rik	72503	RIKEN cDNA 2610507B11 gene
129	1449058_at	-2.21	Gli1	14632	GLI-Kruppel family member GLI1
130	1452670_at	-2.21	Myl9	98932	myosin, light polypeptide 9, regulatory
131	1419350_at	-2.19	Hook2	170833	hook homolog 2 (Drosophila)
132	1422546_at	-2.19	Ilf3	16201	interleukin enhancer binding factor 3
133	1430530_s_at	-2.15	Nmral1	67824	NmrA-like family domain containing 1
134	1416688_at	-2.15	Snap91	20616	synaptosomal-associated protein 91
135	1447752_x_at	-2.15	Drg1	13494	developmentally regulated GTP binding protein 1
136	1426753_at	-2.14	Phf17	269424	PHD finger protein 17
137	1454849_x_at	-2.14	Clu /// LOC1000461	100046120 /// 12759	similar to clusterin; clusterin
138	1425608_at	-2.12	Dusp3	72349	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)
139	1449126_at	-2.11	Zfp90	22751	zinc finger protein 90
140	1416517_at	-2.10	Pnpla6	50767	patatin-like phospholipase domain containing 6
141	1437224_at	-2.10	Rtn4	68585	reticulon 4
142	1416740_at	-2.10	Col5a1	12831	collagen, type V, alpha 1
143	1428835_at	-2.09	Myh14	71960	myosin, heavy polypeptide 14

	Probe Set ID	Fold change	Gene Symbol	Entrez Gene	Gene Description
144	1456819_at	-2.09	Nrn1l	234700	neuritin 1-like
145	1430287_s_at	-2.08	Hemk1	69536	HemK methyltransferase family member 1
146	1428563_at	-2.08	Ddx10	77591	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
147	1455998_at	-2.08	LOC667118	667118	similar to Zinc finger BED domain containing protein 4
148	1434279_at	-2.08			Fas (TNF receptor superfamily member 6)
149	1437213_at	-2.07	Nudt21	68219	nudix (nucleoside diphosphate linked moiety X)-type motif 21
150	1415973_at	-2.06	Marcks	17118	myristoylated alanine rich protein kinase C substrate
151	1434362_at	-2.06			sterol O-acyltransferase 1
152	1458361_at	-2.05	Dclre1c	227525	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae)
153	1436302_at	-2.05	Slc10a7	76775	solute carrier family 10 (sodium/bile acid cotransporter family), member 7
154	1434177_at	-2.05	Ece1	230857	endothelin converting enzyme 1
155	1436134_at	-2.05	Scn2b	72821	sodium channel, voltage-gated, type II, beta
156	1436893_a_at	-2.05	Mar-07	57438	membrane-associated ring finger (C3HC4) 7; similar to axotrophin
157	1428583_at	-2.04	Nufip2	68564	nuclear fragile X mental retardation protein interacting protein 2
158	1416610_a_at	-2.03	Clcn3	12725	chloride channel 3
159	1429886_at	-2.02	Rnf160	78913	ring finger protein 160
160	1447766_x_at	-2.01	Limd2	67803	similar to epithelial protein lost in neoplasm; LIM domain containing 2
161	1421142_s_at	-2.01	Foxp1	108655	forkhead box P1
162	1450644_at	-2.00	Zfp36l1	12192	zinc finger protein 36, C3H type-like 1