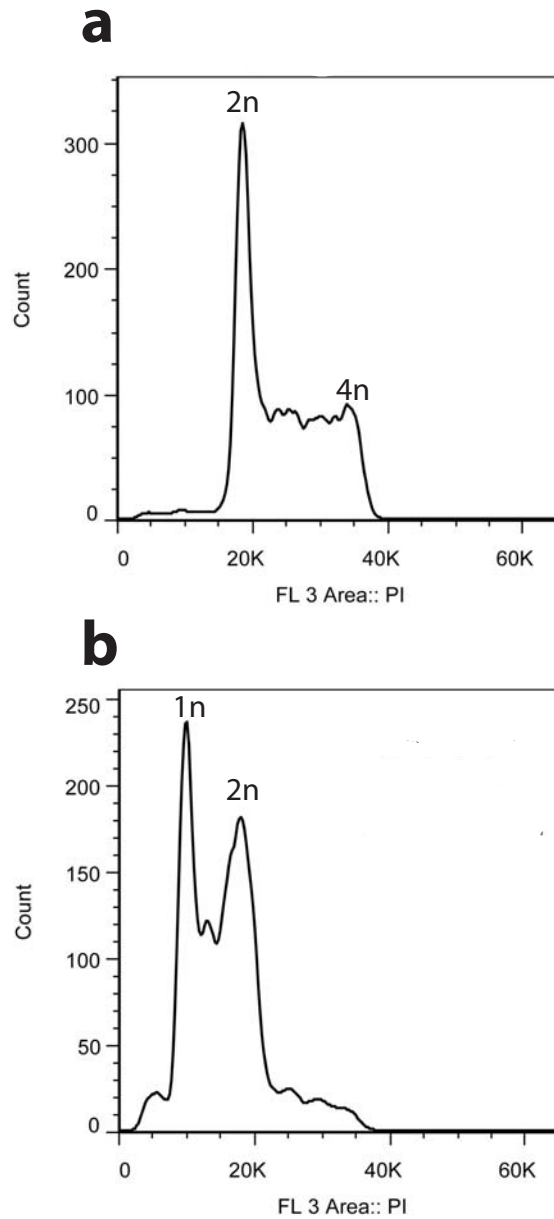


### Supplementary Figure 1 - Derivation of CBA/B6 hybrid haploid ES cells in KSR

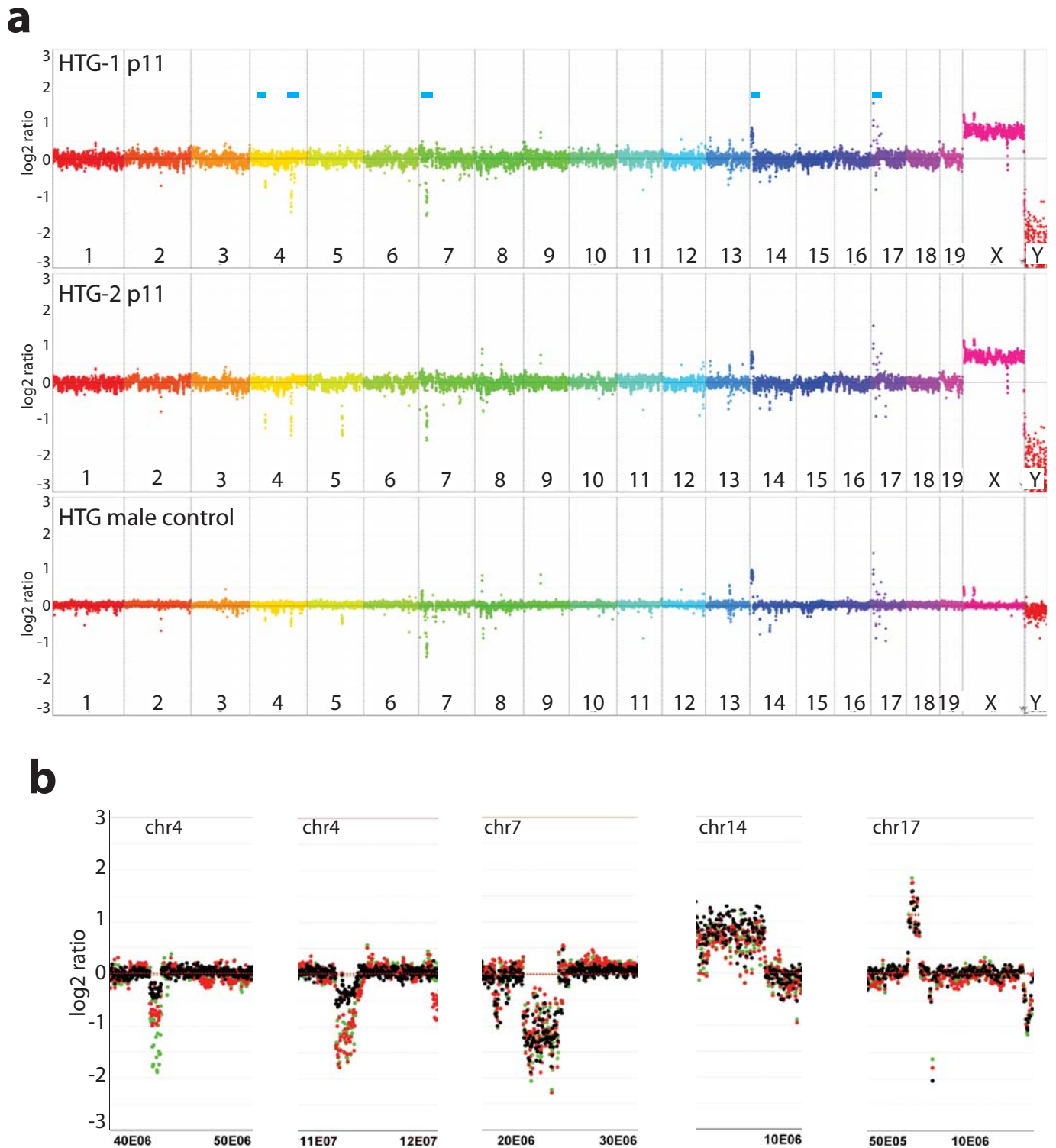
**(a)** A flow profile of DNA content after PI staining recorded from diploid control shows a 2n and 4n peak.  
**(b)** A flow profile of DNA content of an ES cell line (HAP-9, p8) derived from haploid blastocysts using Knockout Serum Replacement shows an additional 1n peak.



### 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.

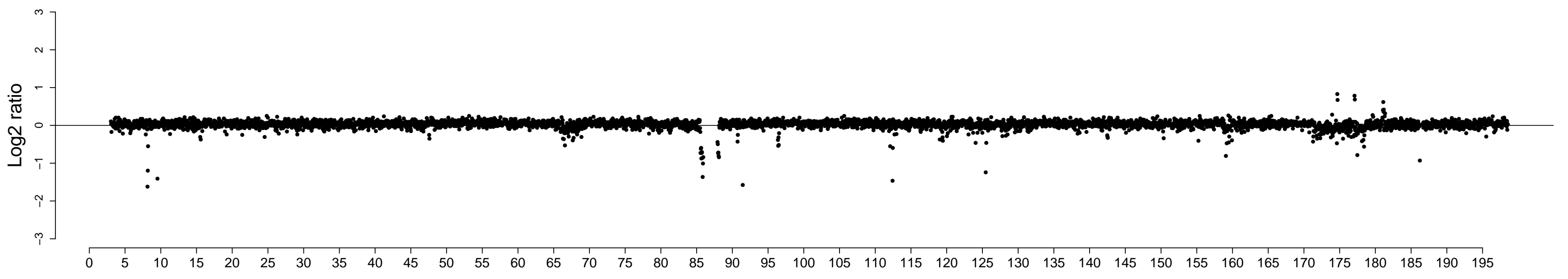
(a) Genomic overview of copy number variations (CNVs) in 200kb resolution in HTG-1 and HTG-2 haploid ES cells and control male kidney DNA from the mixed strain background of which the ES cells were derived. Average values of log<sub>2</sub> ratios are plotted using somatic C57BL6 DNA as a reference. 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.

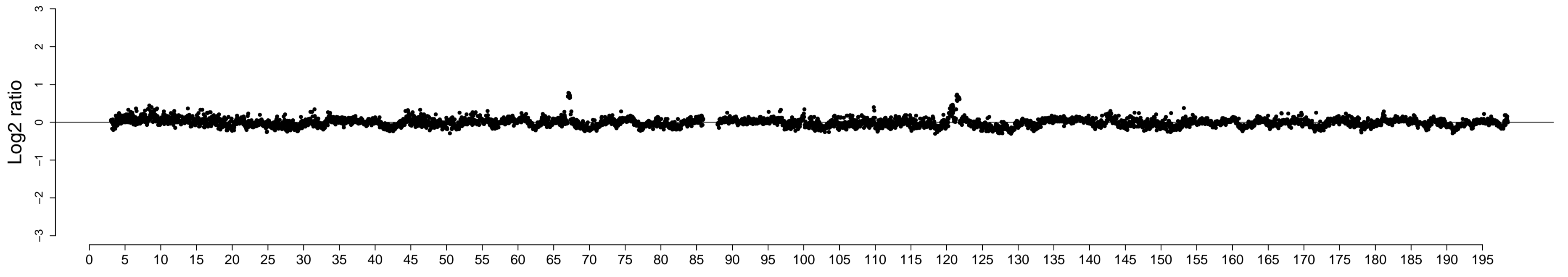
**Supplementary Figure 4 - CGH analysis of haploid ES cells**

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 log<sub>2</sub> ratios are plotted at a 40 kb resolution.

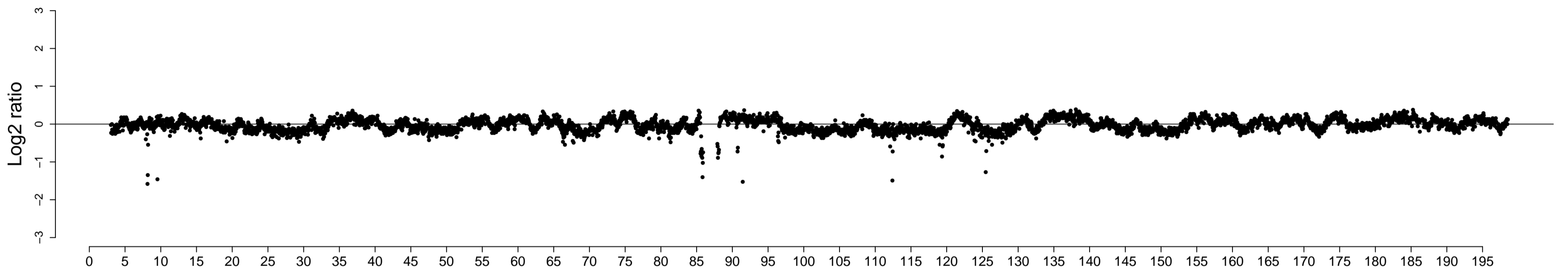
chr1:CBA control kidney



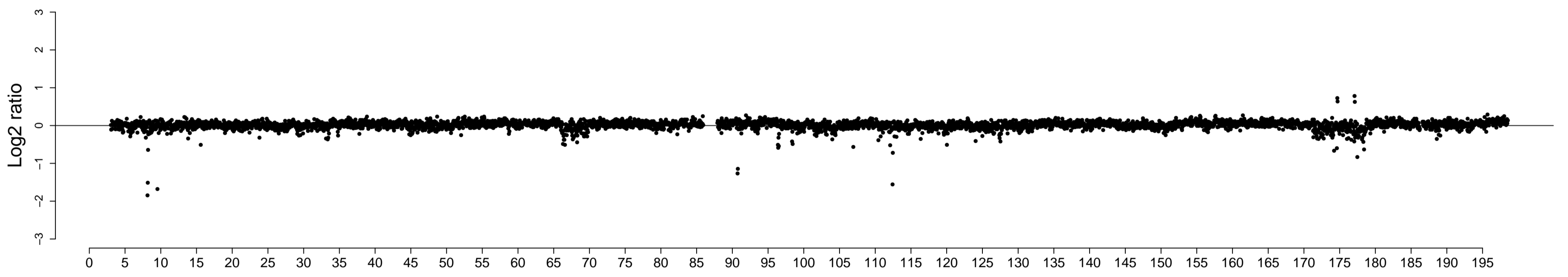
chr1:HAP1 p25



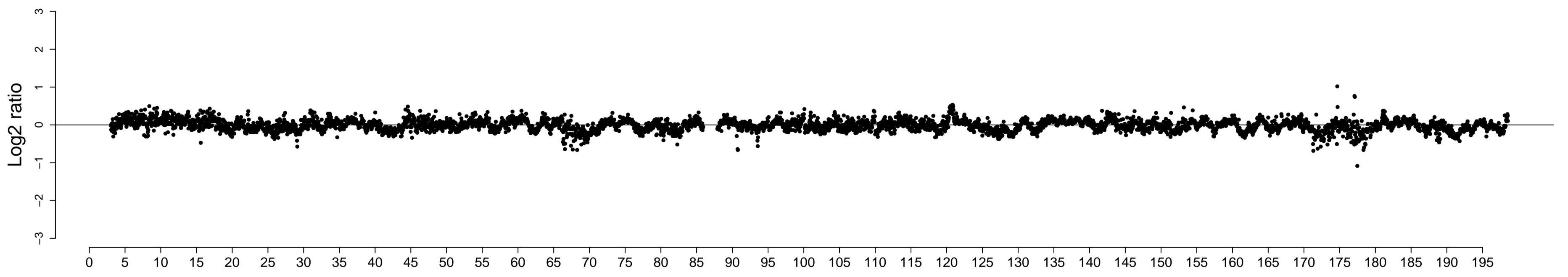
chr1:HAP2 p18



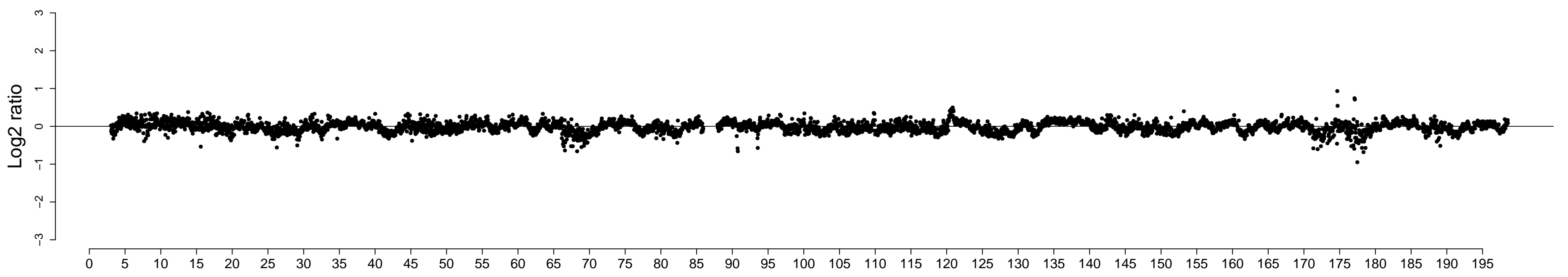
chr1:HTG\_control male kidney



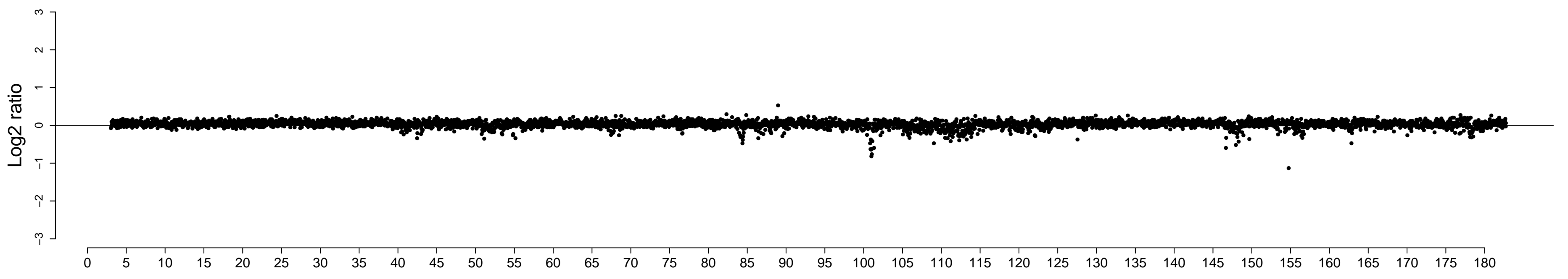
chr1:HTG1 p11



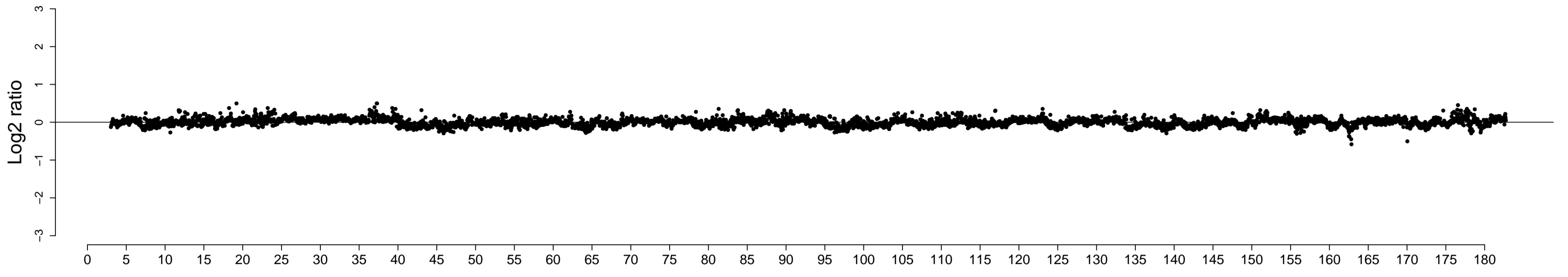
chr1:HTG2 p11



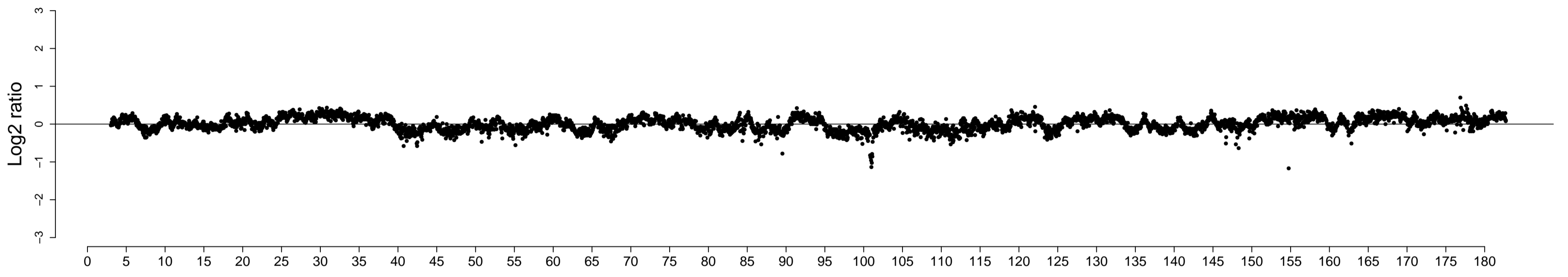
chr2:CBA control kidney



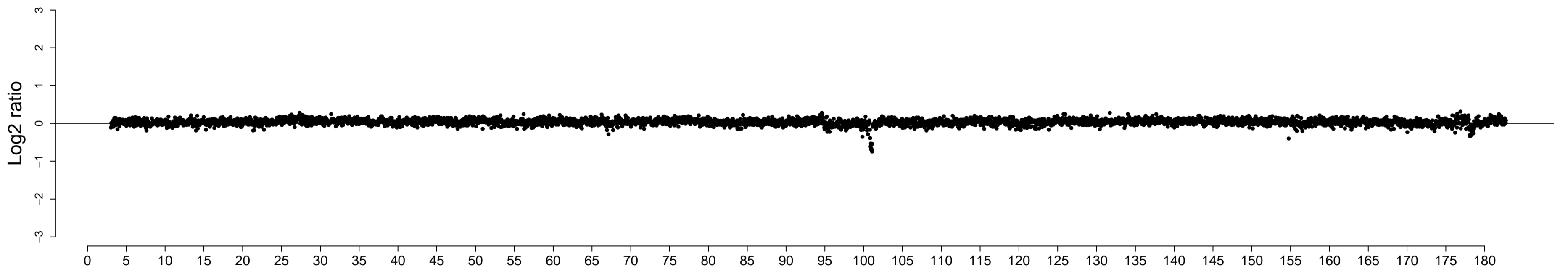
chr2:HAP1 p25



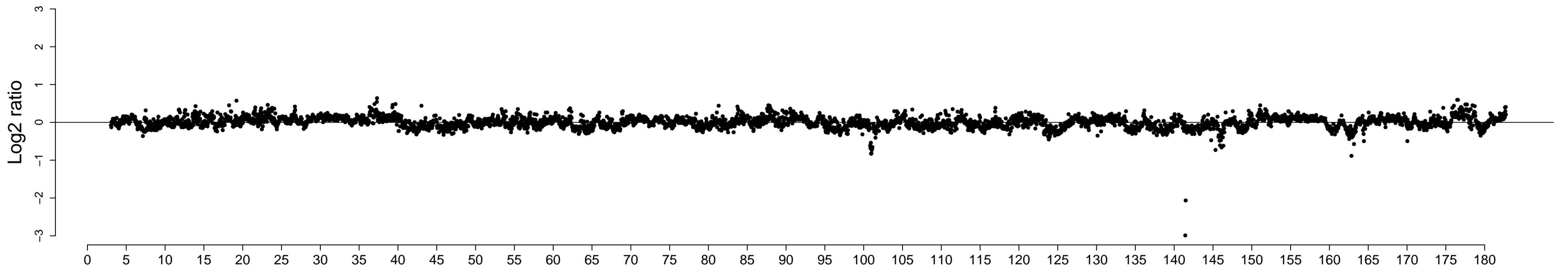
chr2:HAP2 p18



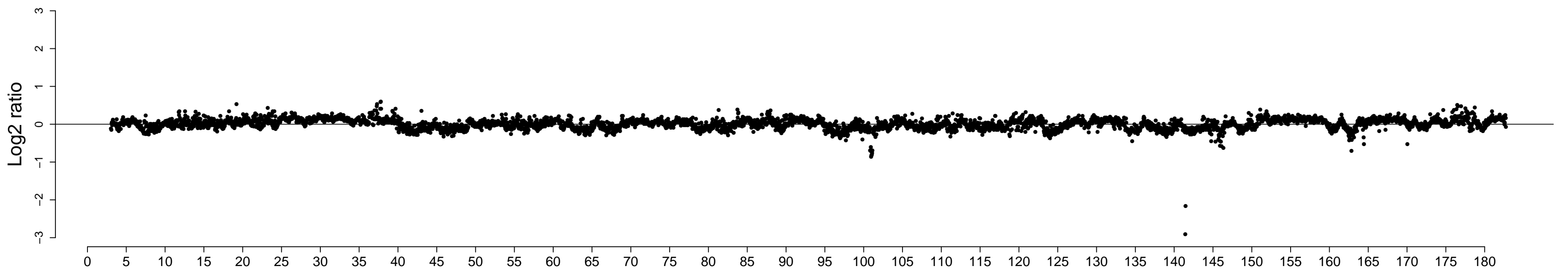
chr2:HTG\_control male kidney



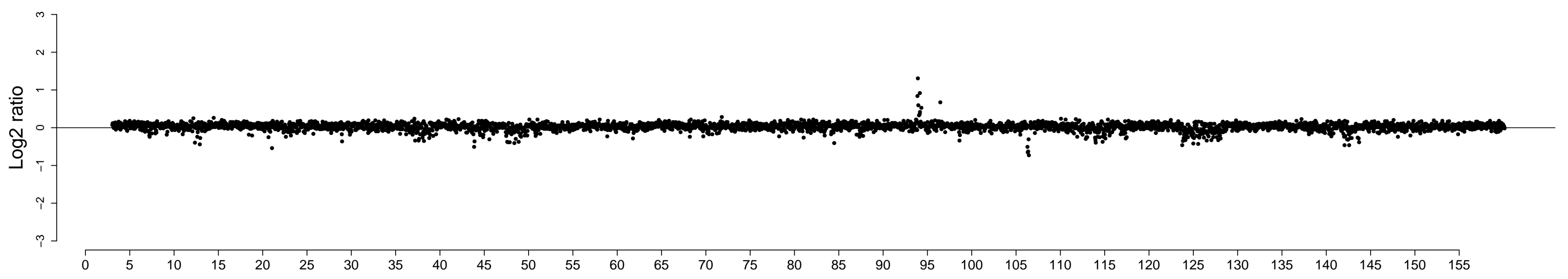
chr2:HTG1 p11



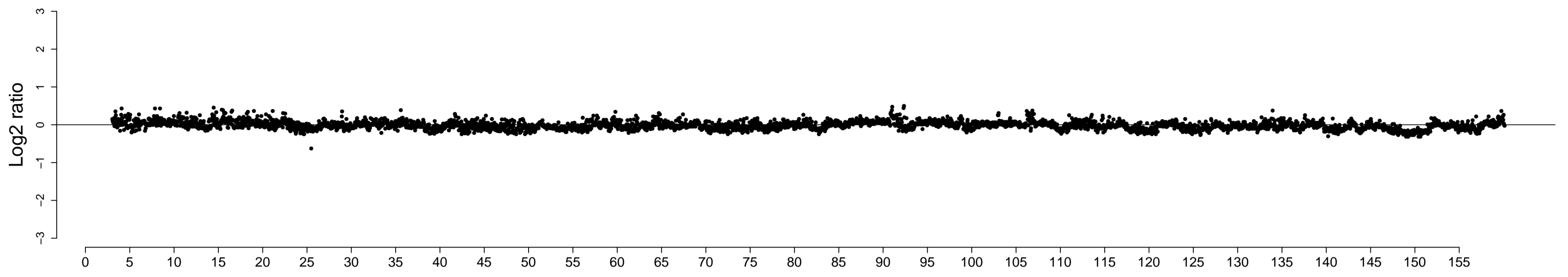
chr2:HTG2 p11



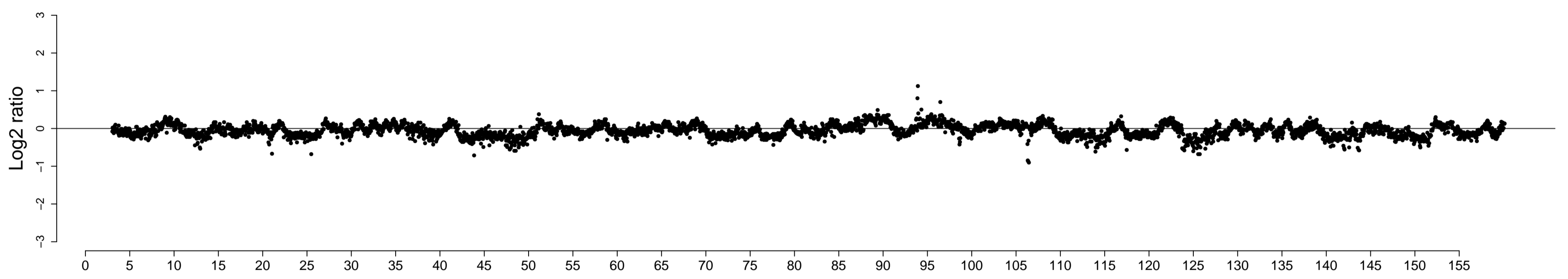
chr3:CBA control kidney



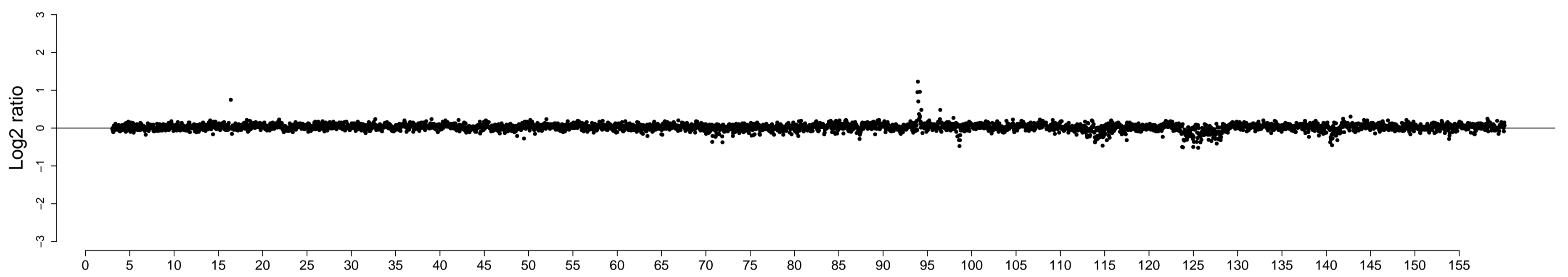
chr3:HAP1 p25



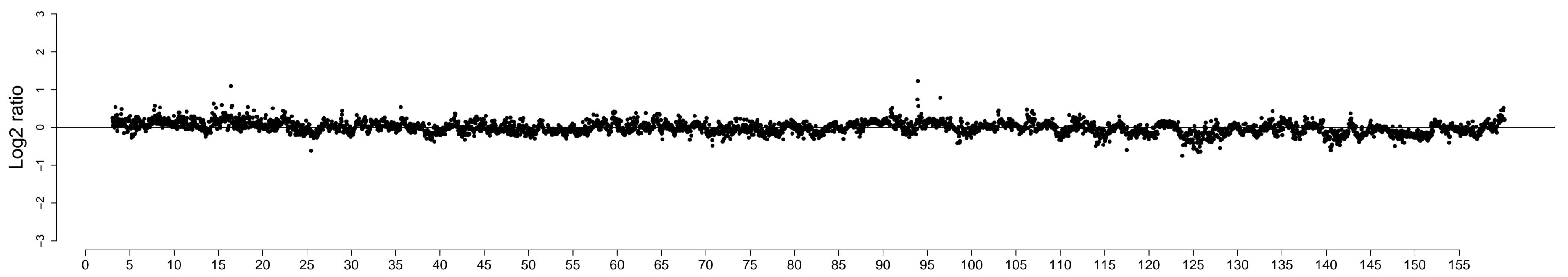
chr3:HAP2 p18



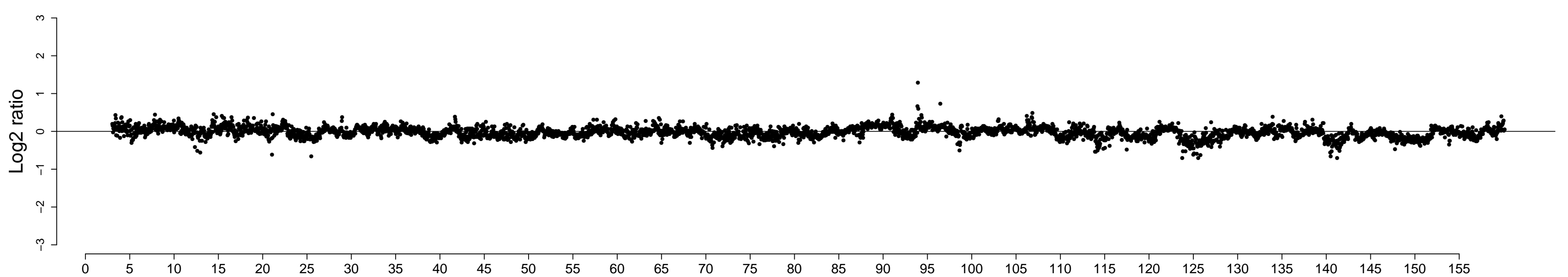
chr3:HTG\_control male kidney



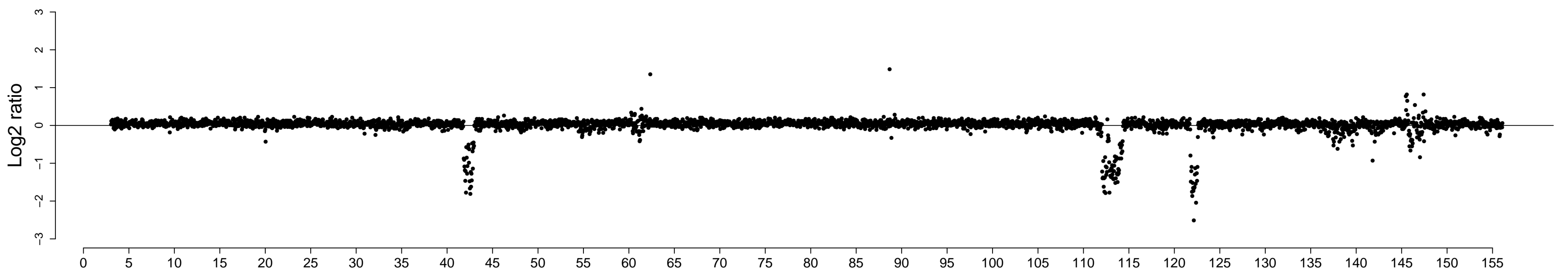
chr3:HTG1 p11



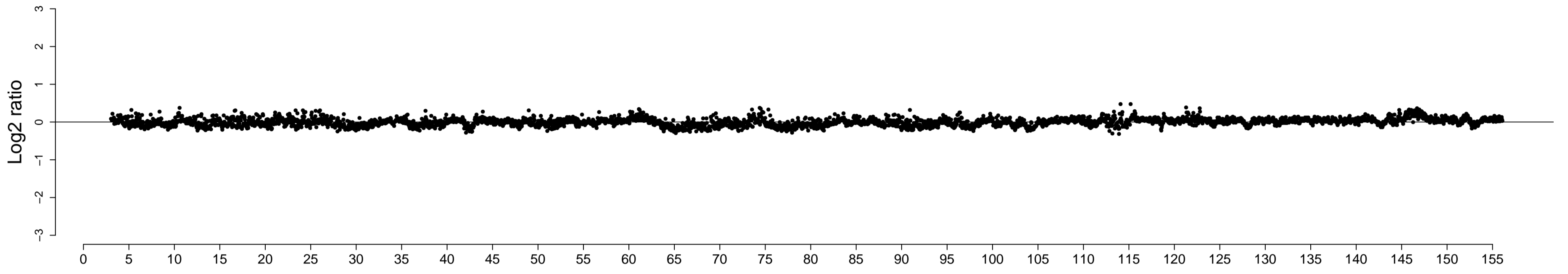
chr3:HTG2 p11



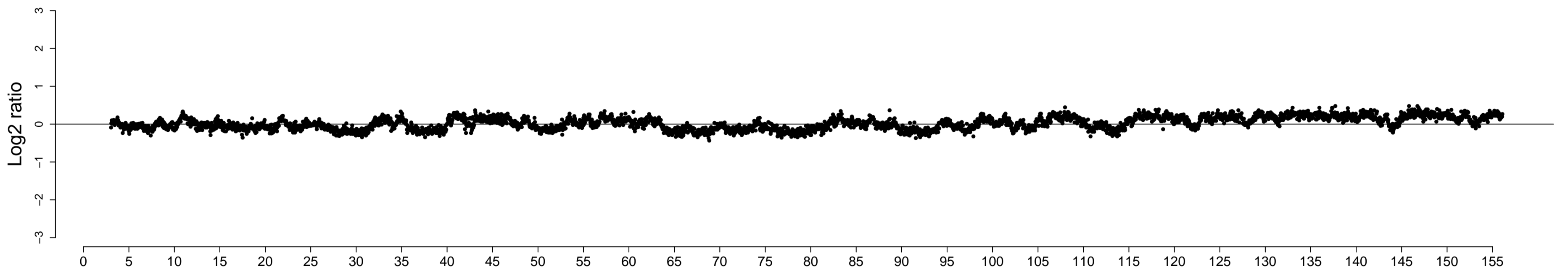
chr4:CBA control kidney



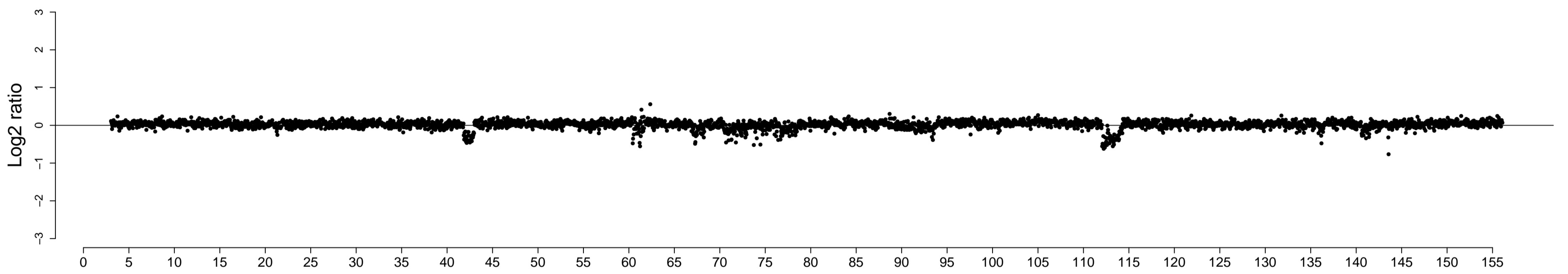
chr4:HAP1 p25



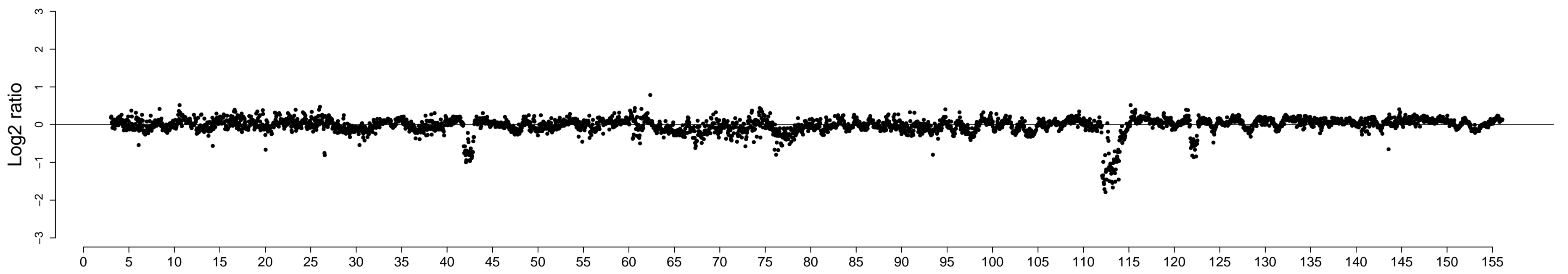
chr4:HAP2 p18



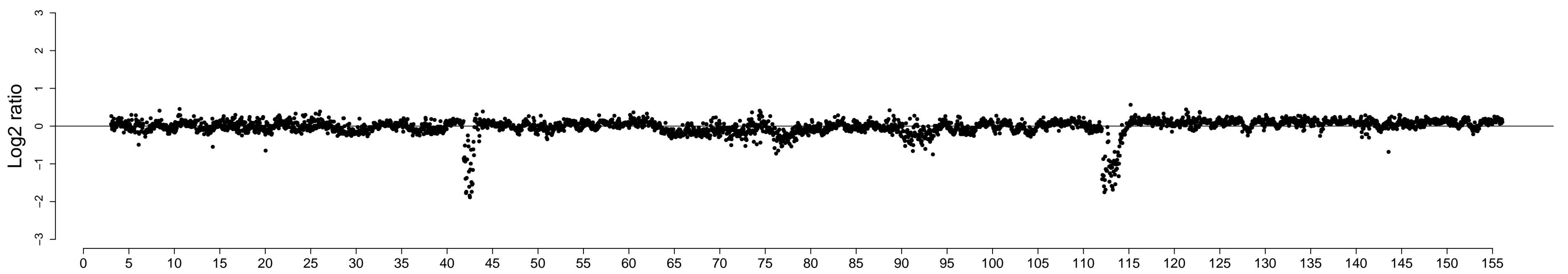
chr4:HTG\_control male kidney



chr4:HTG1 p11

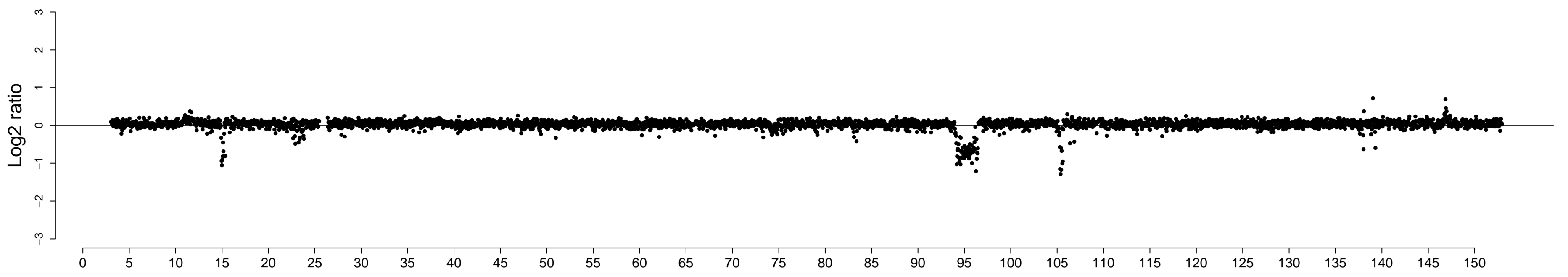


chr4:HTG2 p11

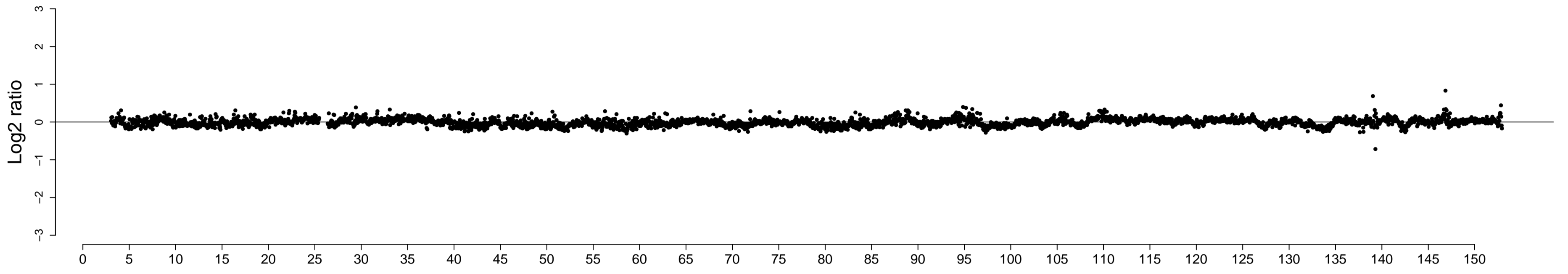




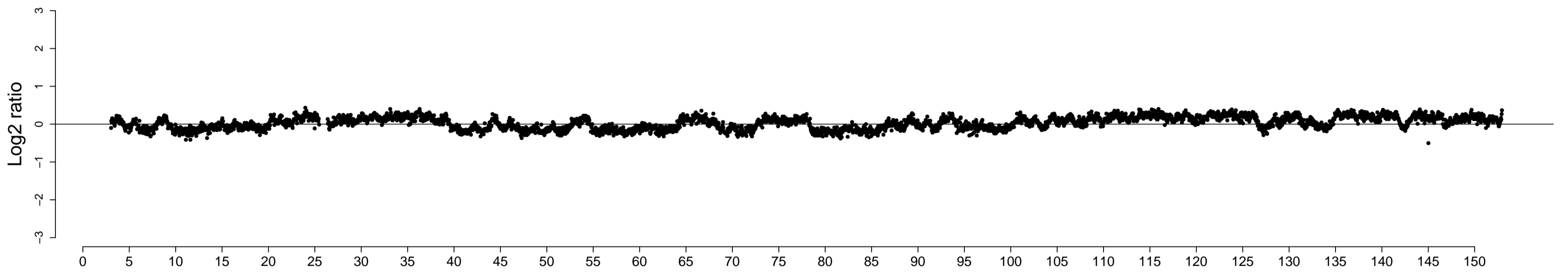
chr5:CBA control kidney



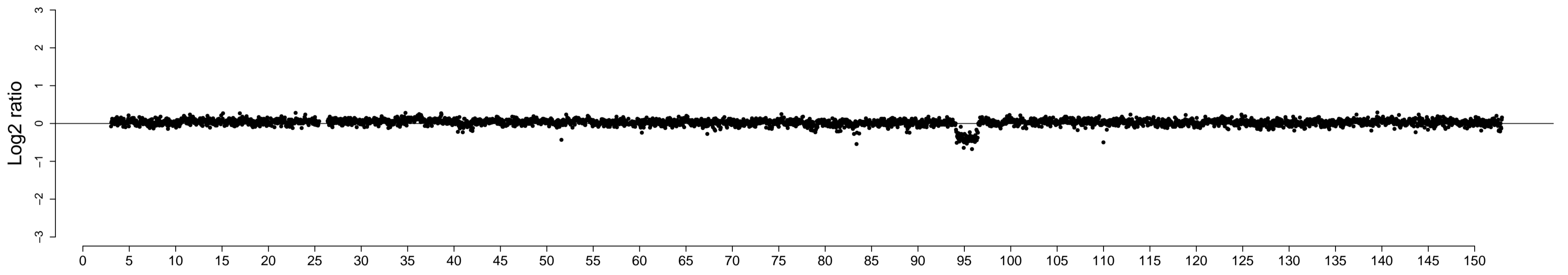
chr5:HAP1 p25



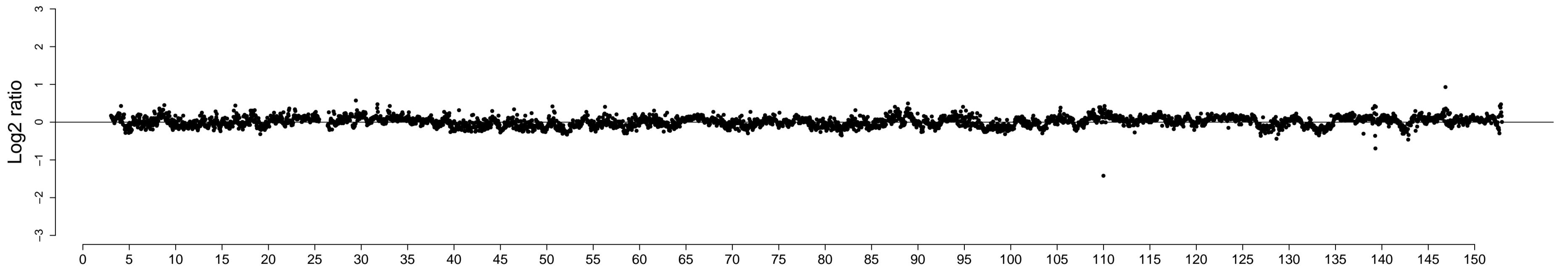
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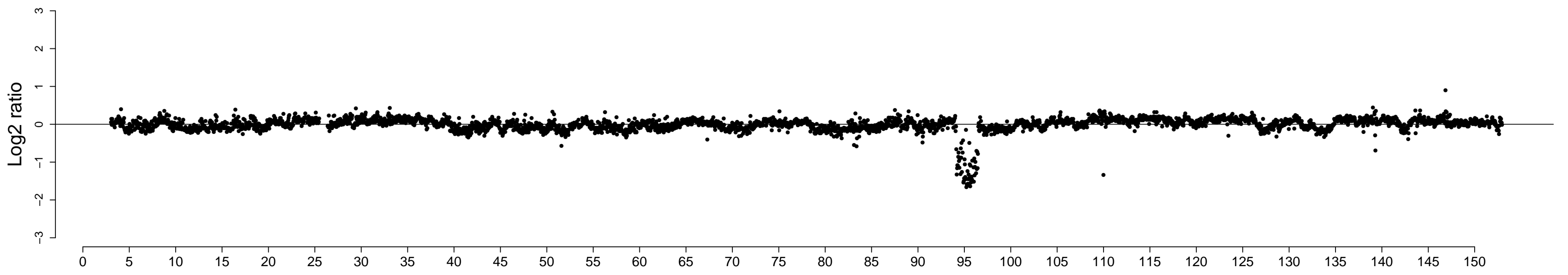
chr5:HTG\_control male kidney



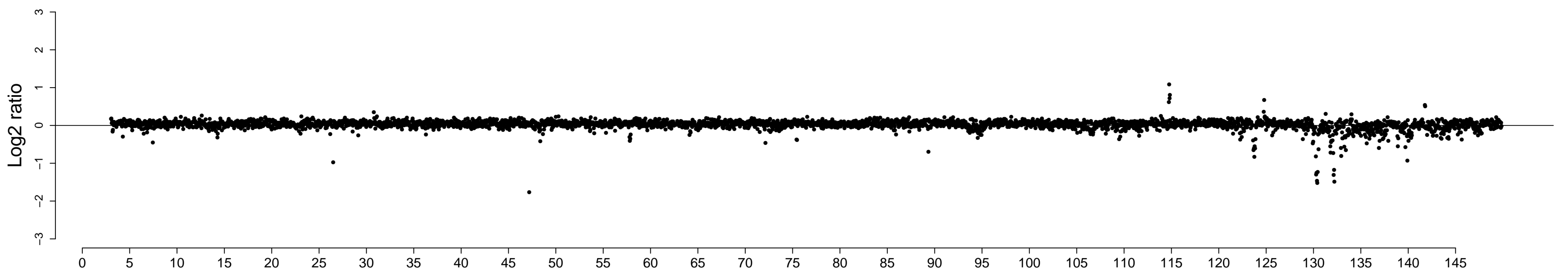
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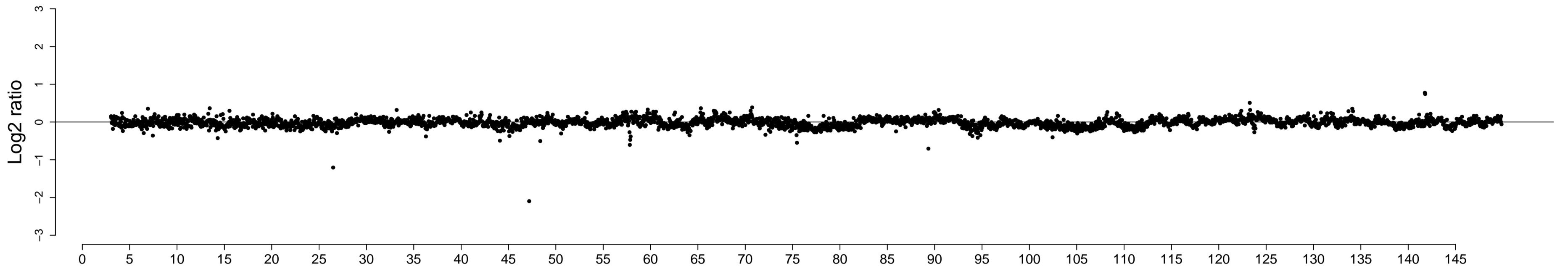
chr5:HTG2 p11



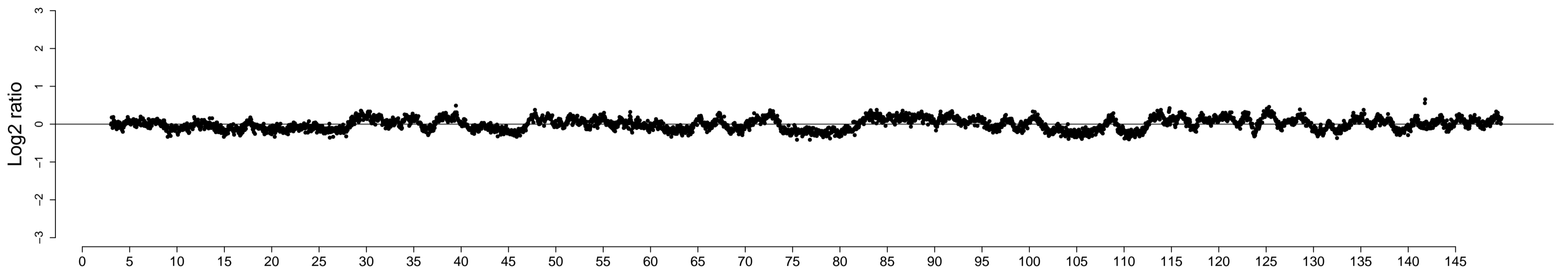
chr6:CBA control kidney



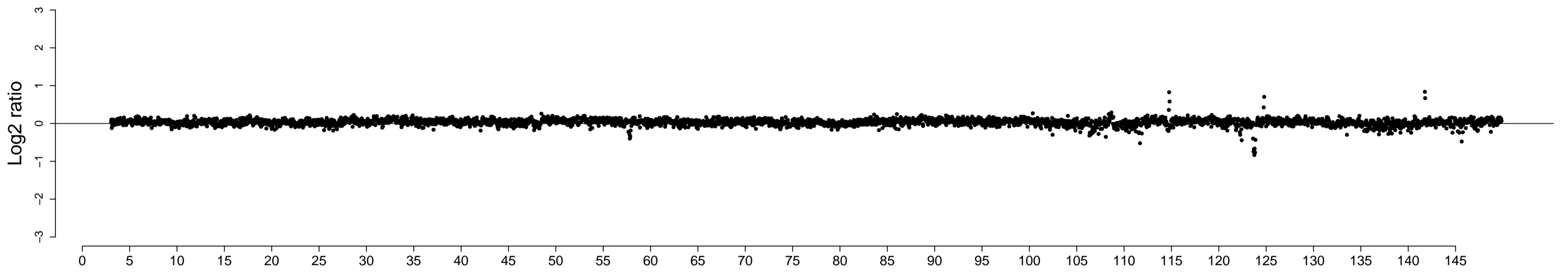
chr6:HAP1 p25



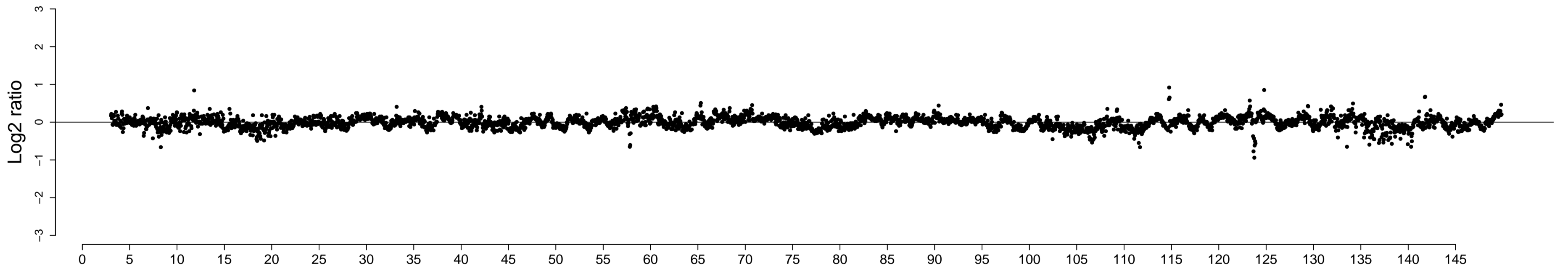
chr6:HAP2 p18



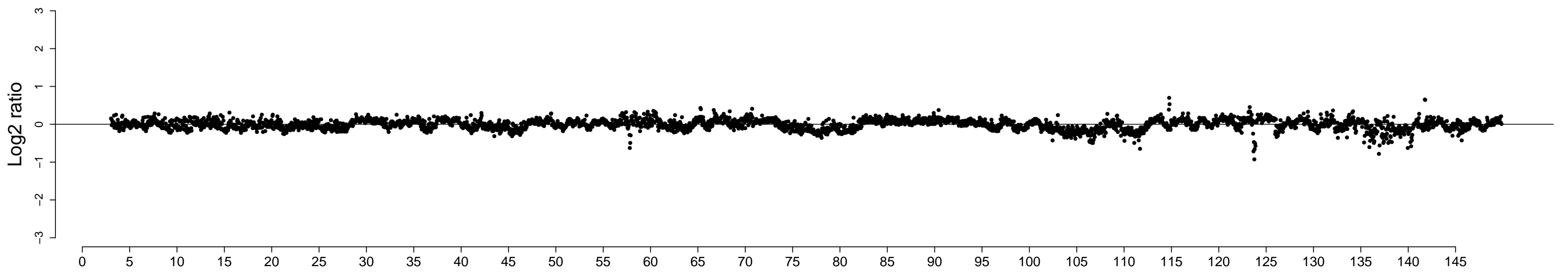
chr6:HTG\_control male kidney



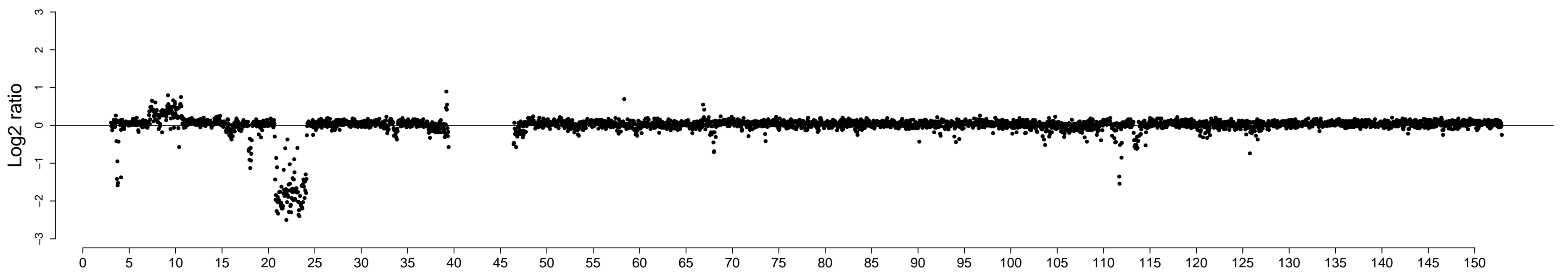
chr6:HTG1 p11



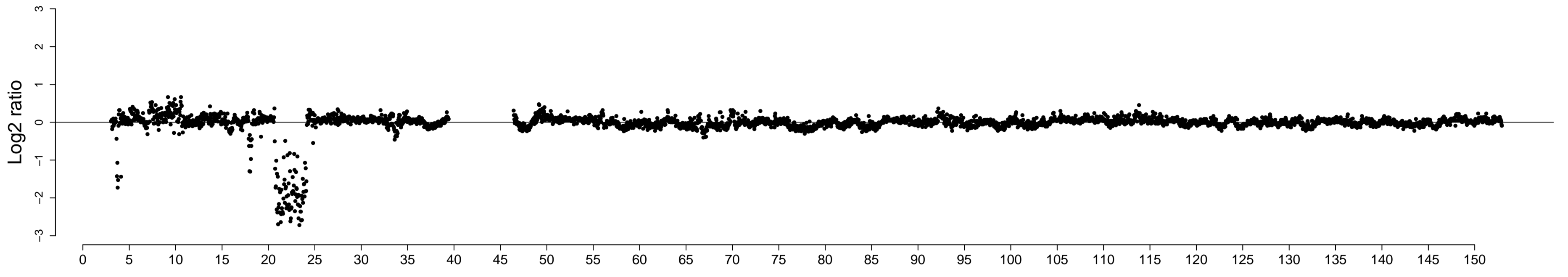
chr6:HTG2 p11



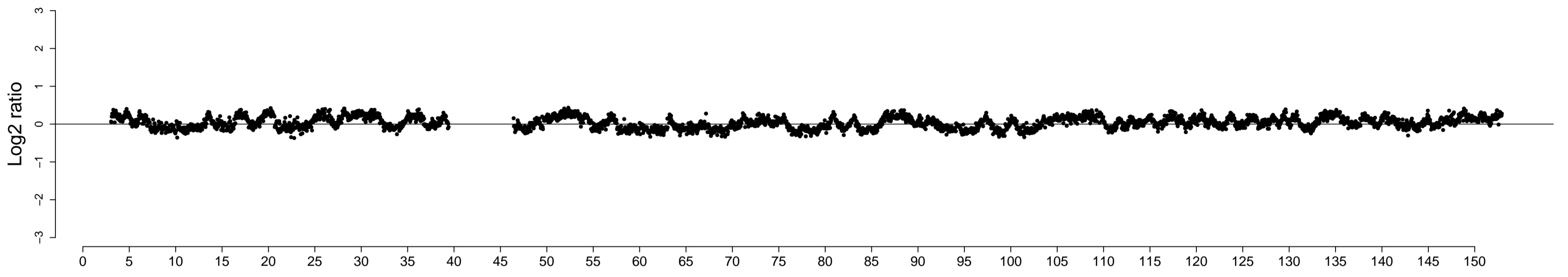
chr7:CBA control kidney



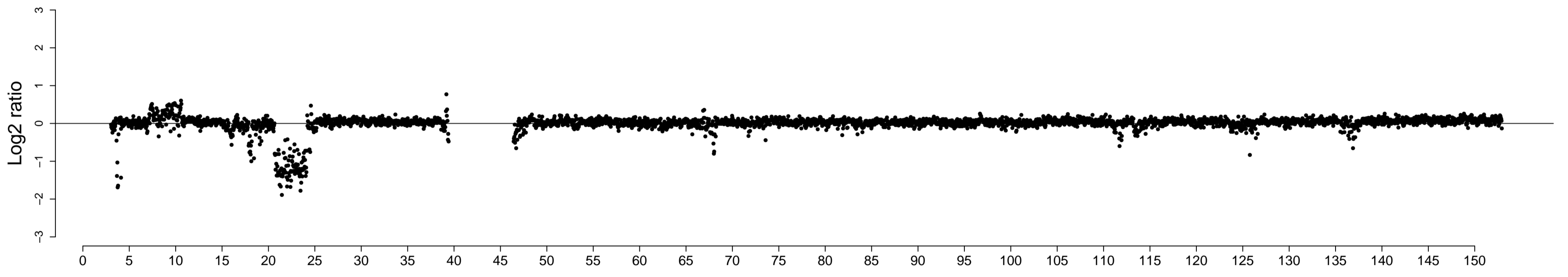
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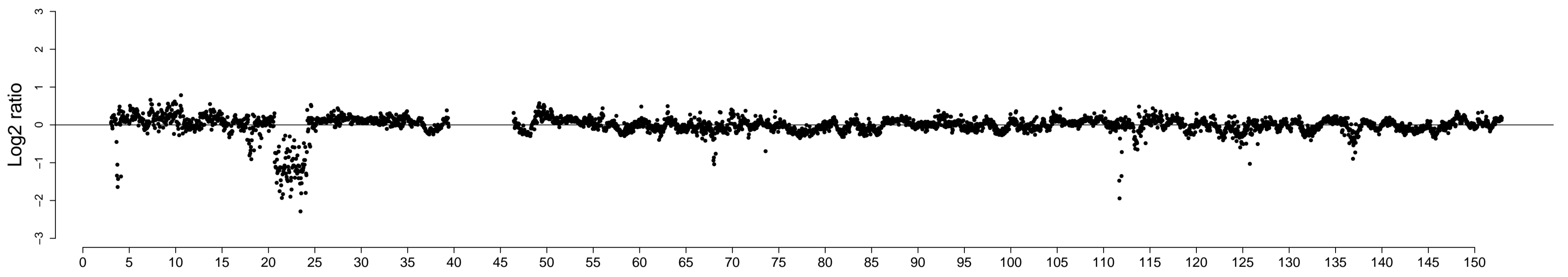
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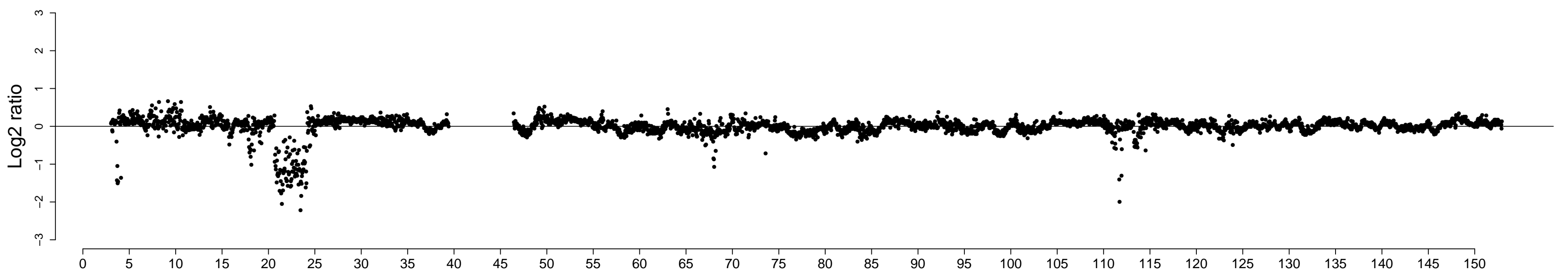
chr7:HTG\_control male kidney



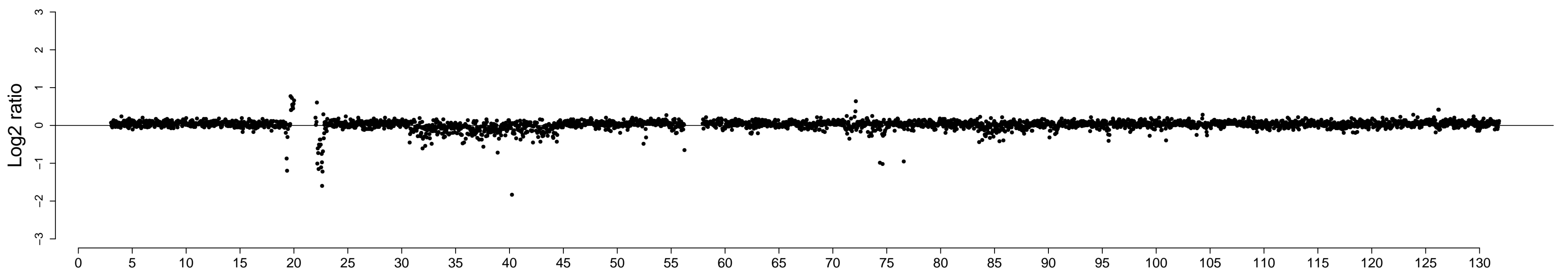
chr7:HTG1 p11



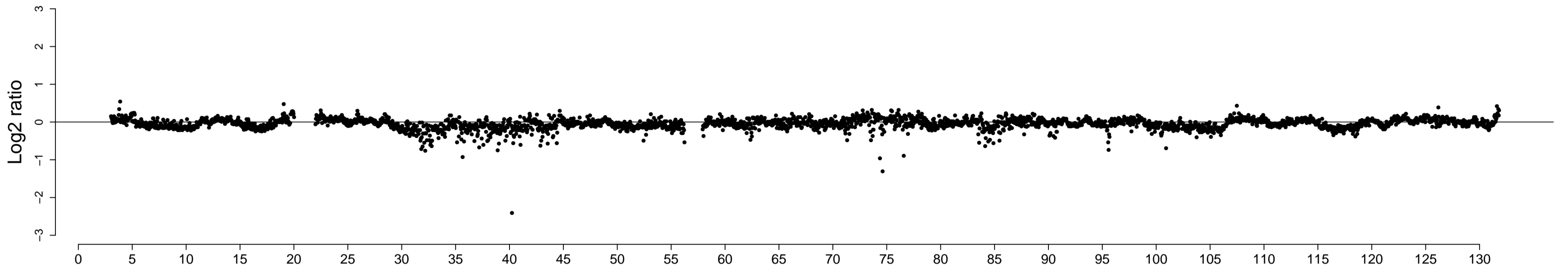
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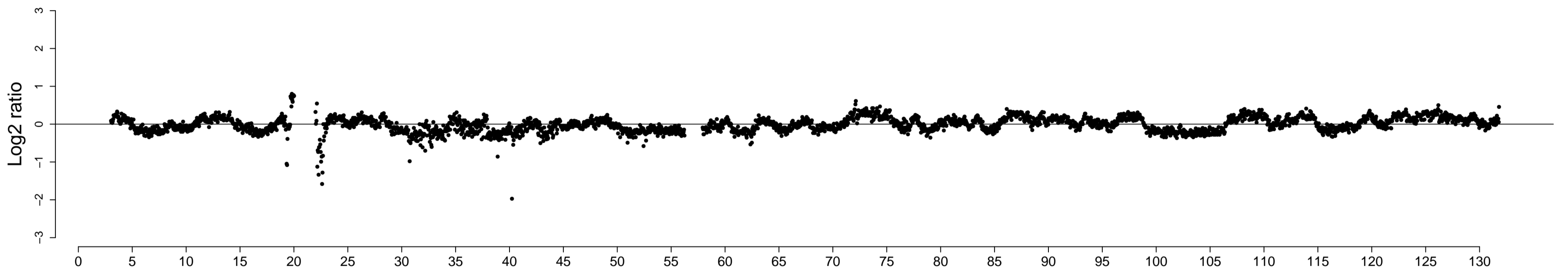
chr8:CBA control kidney



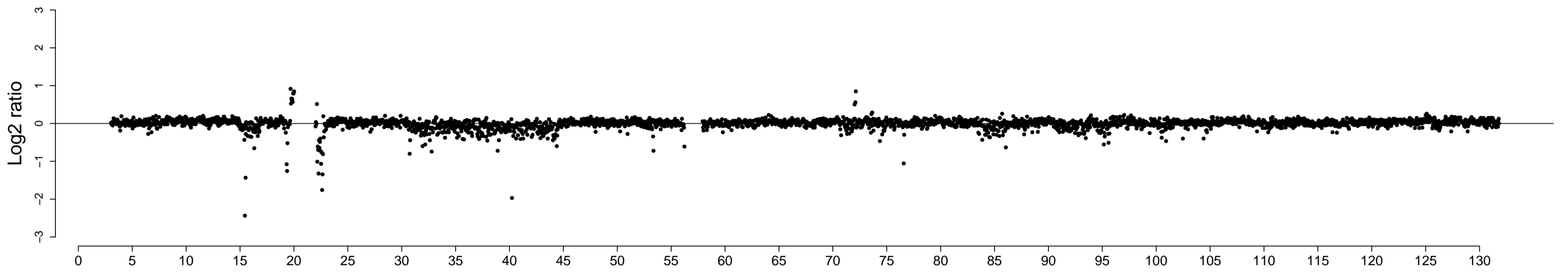
chr8:HAP1 p25



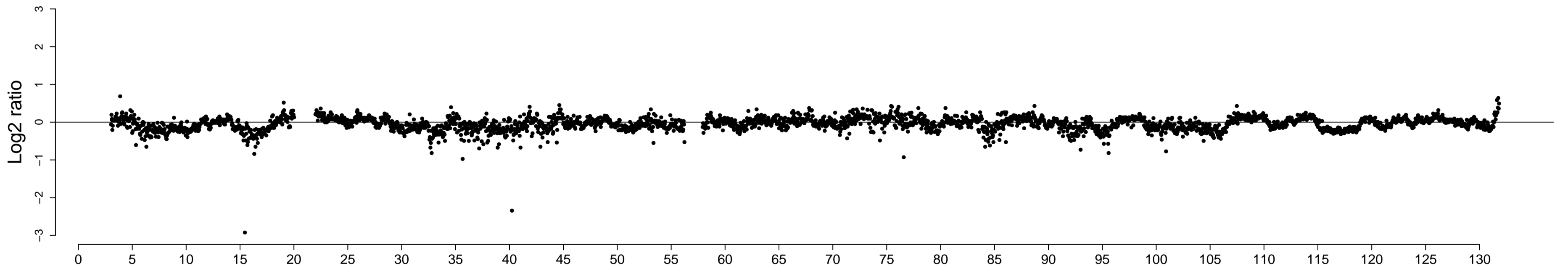
chr8:HAP2 p18



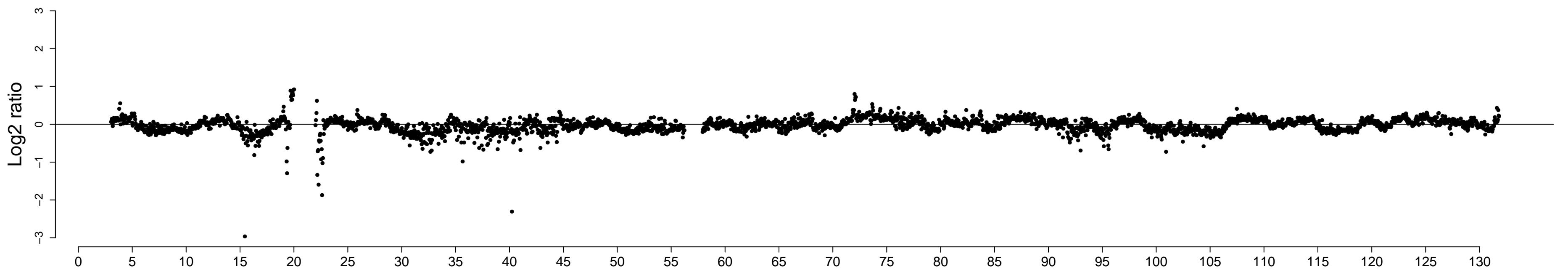
chr8:HTG\_control male kidney



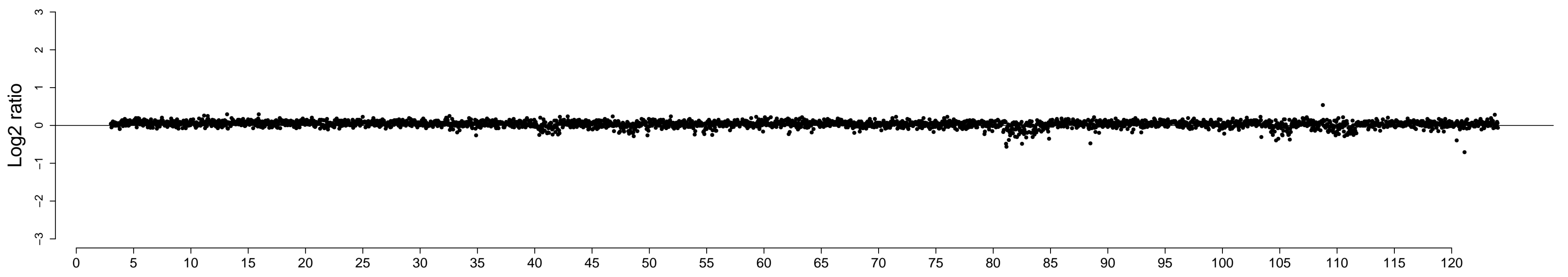
chr8:HTG1 p11



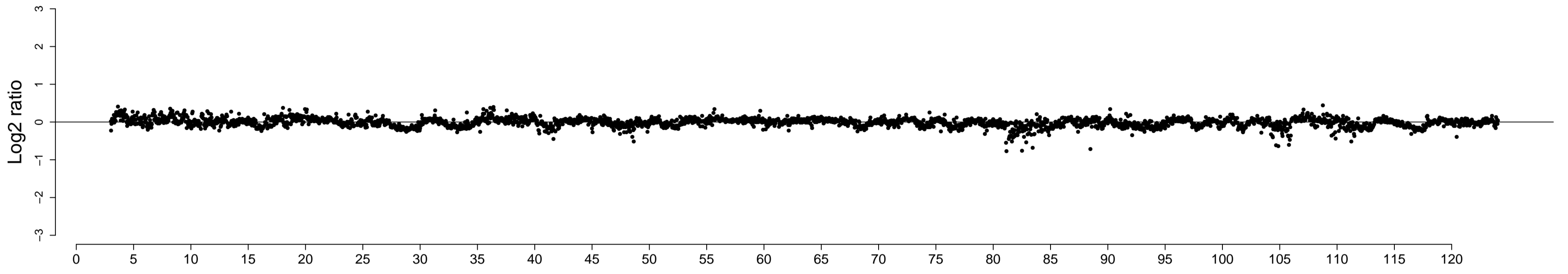
chr8:HTG2 p11



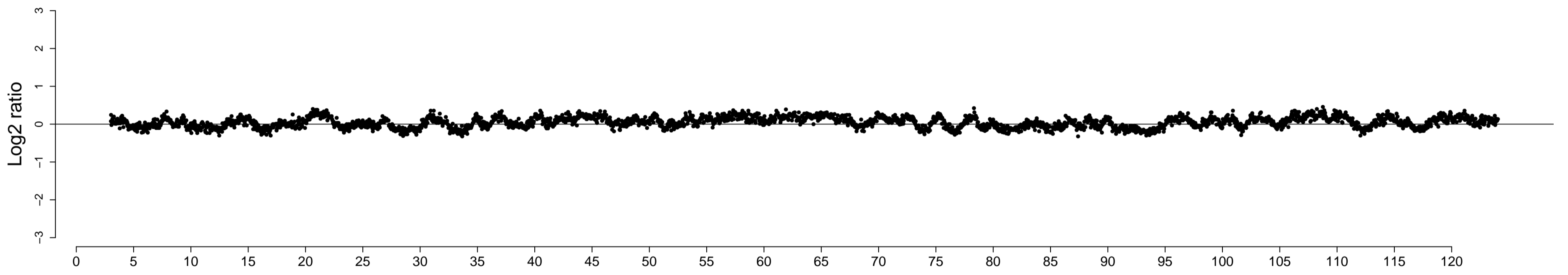
chr9:CBA control kidney



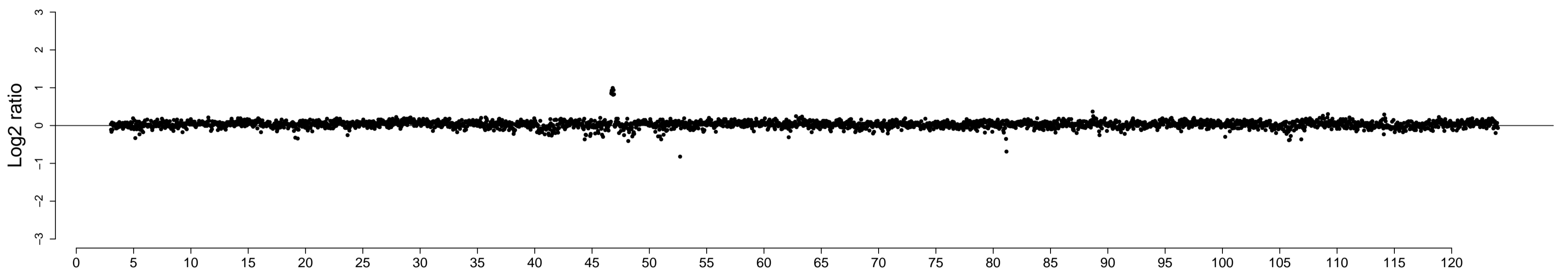
chr9:HAP1 p25



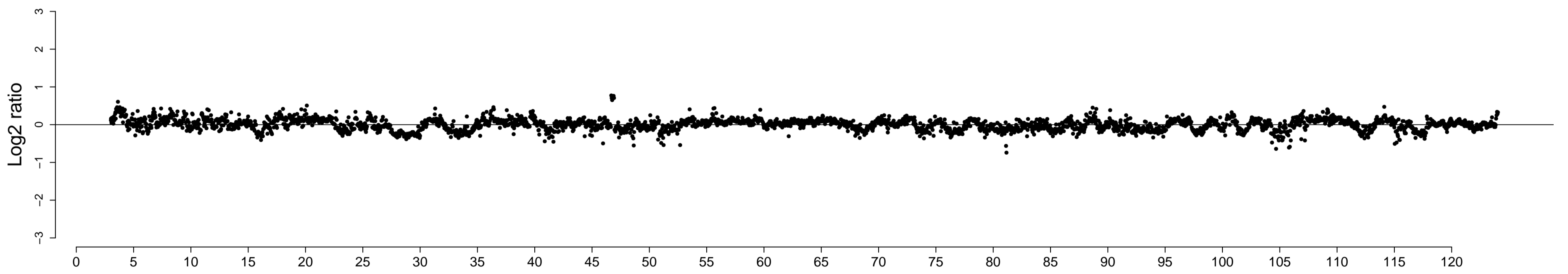
chr9:HAP2 p18



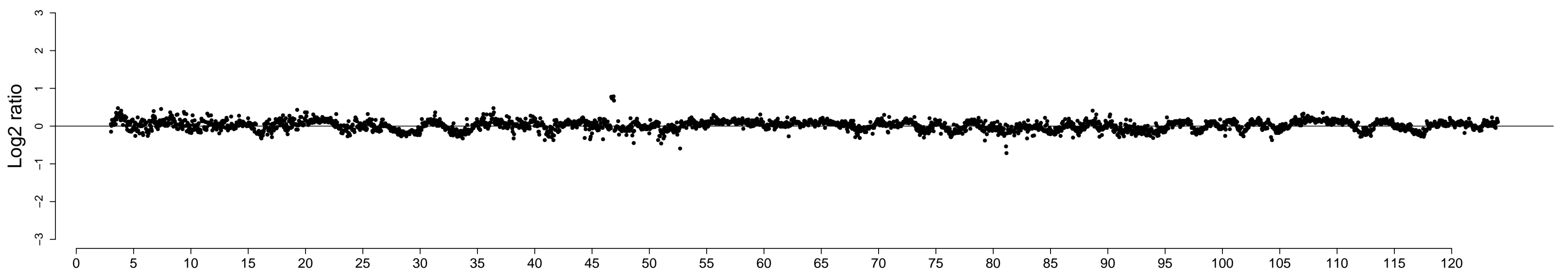
chr9:HTG\_control male kidney



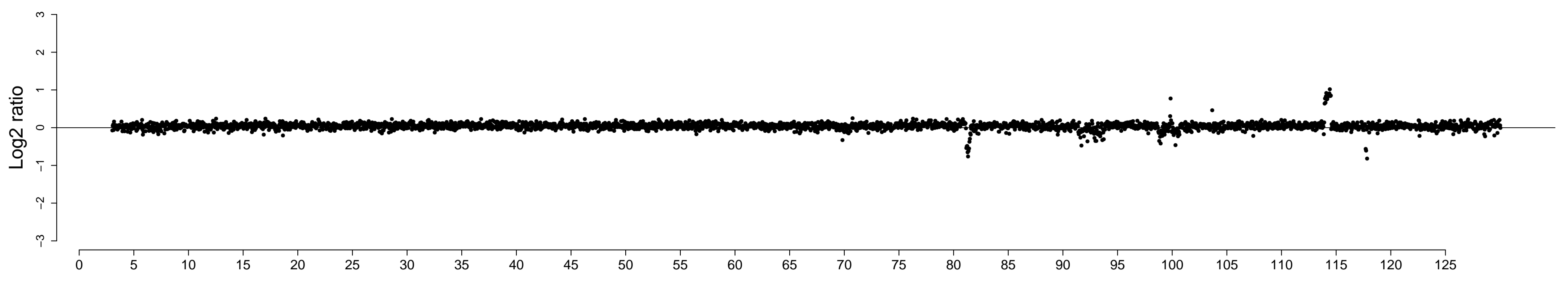
chr9:HTG1 p11



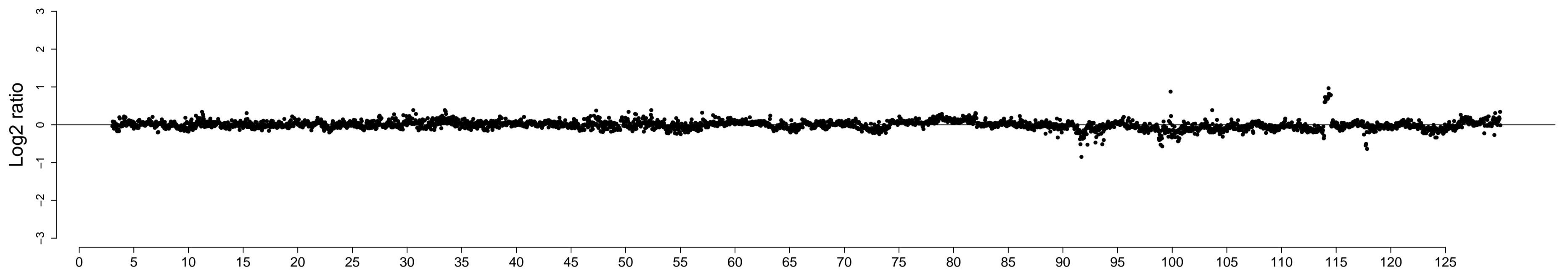
chr9:HTG2 p11



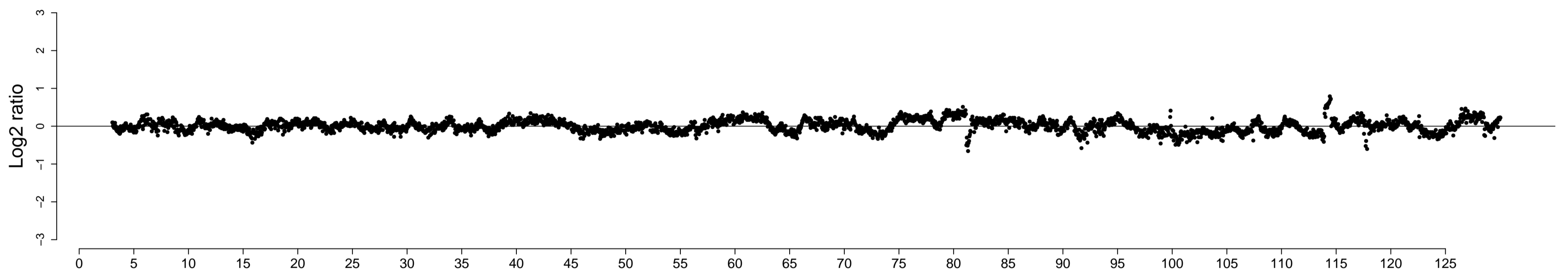
chr10:CBA control kidney



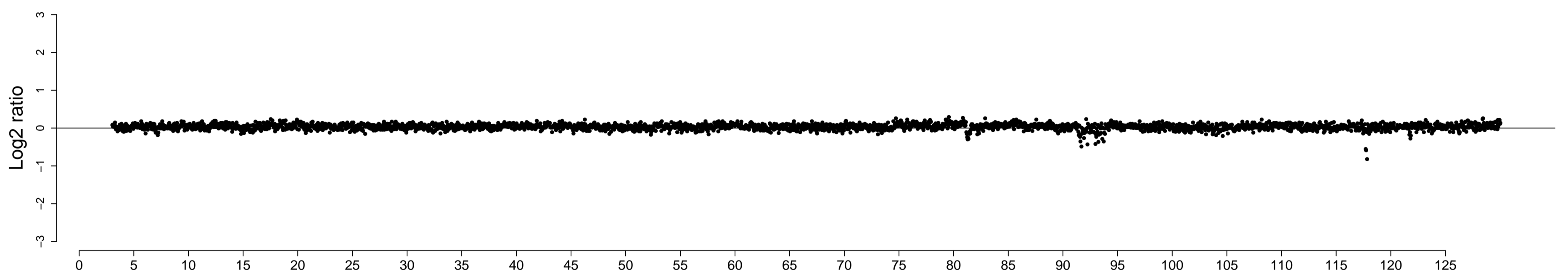
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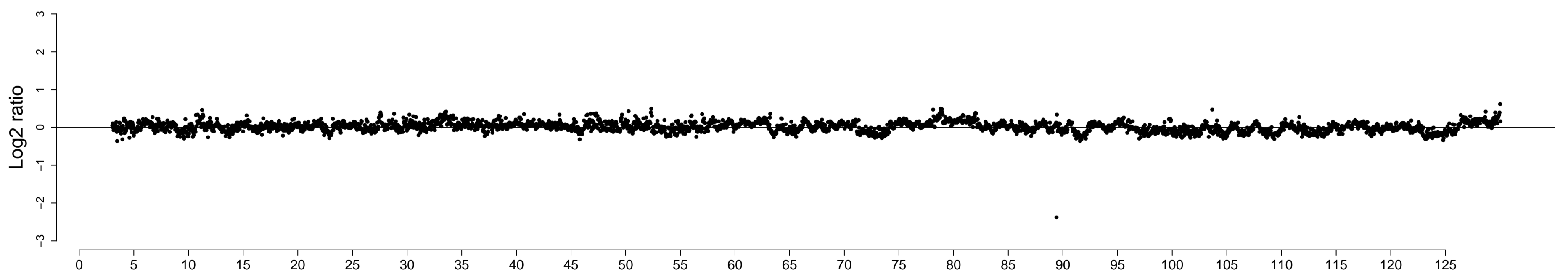
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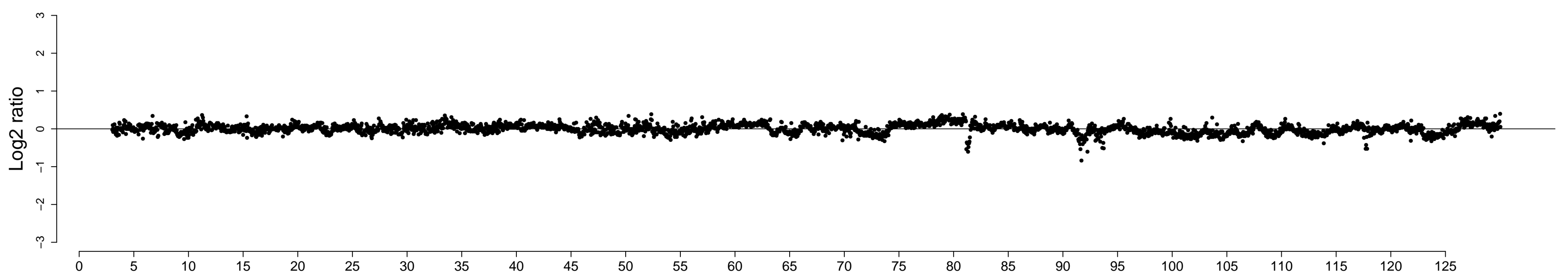
chr10:HTG\_control male kidney



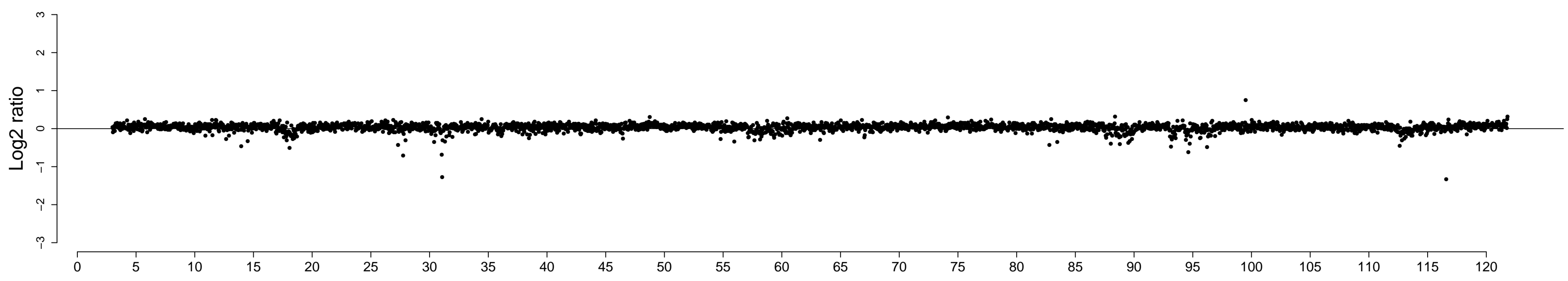
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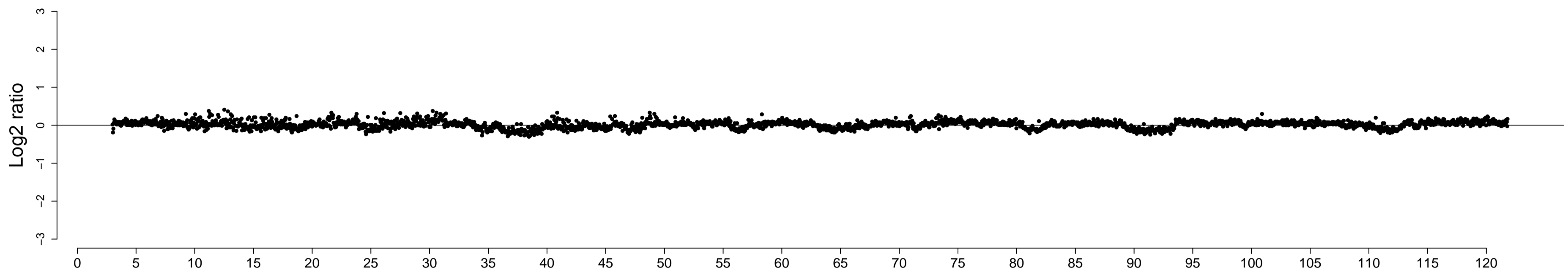
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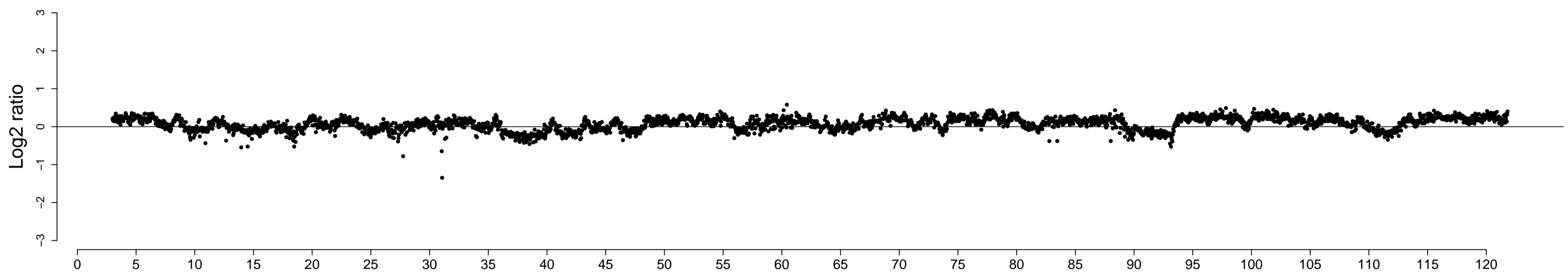
chr11:CBA control kidney



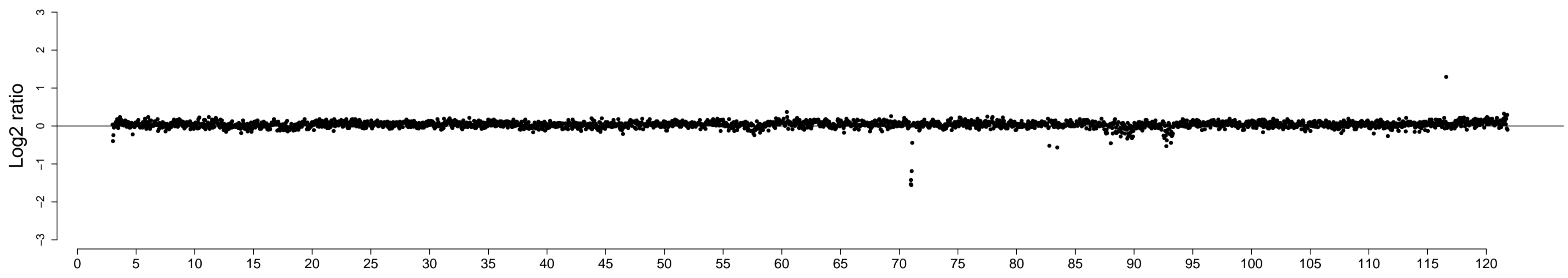
chr11:HAP1 p25



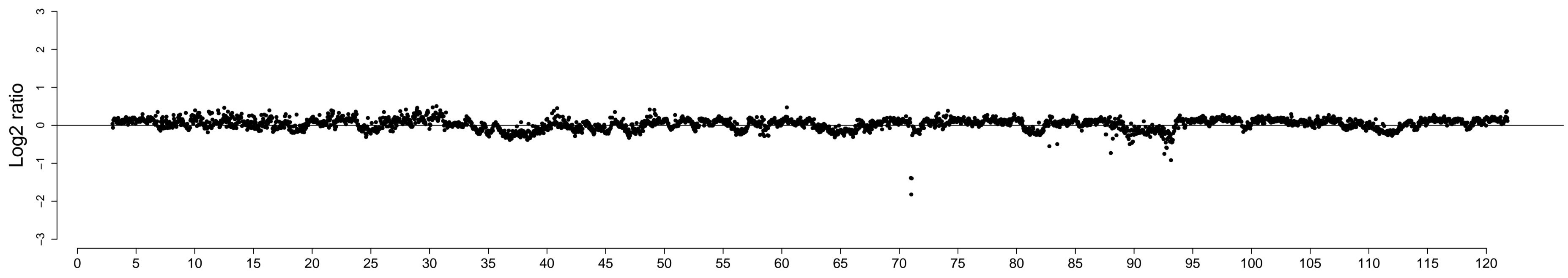
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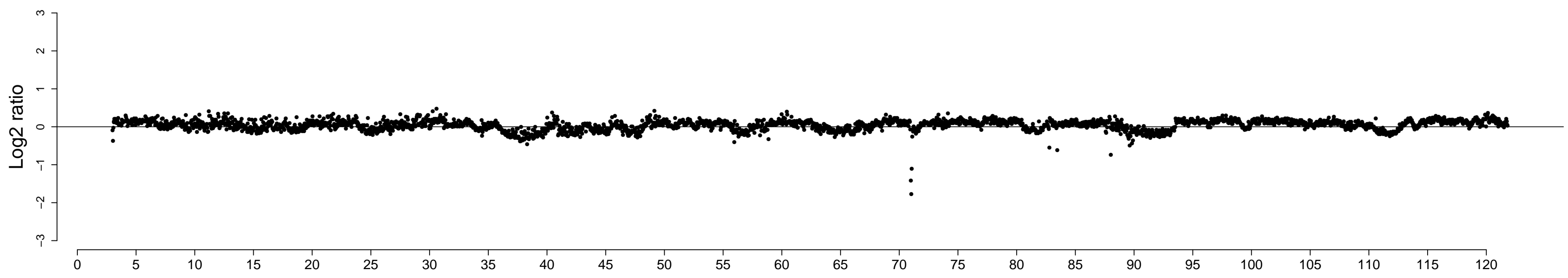
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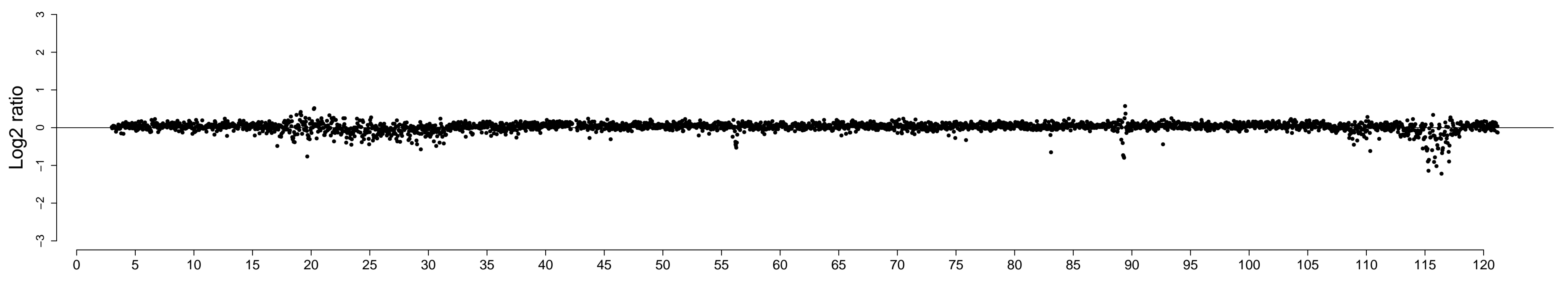
chr11:HTG1 p11



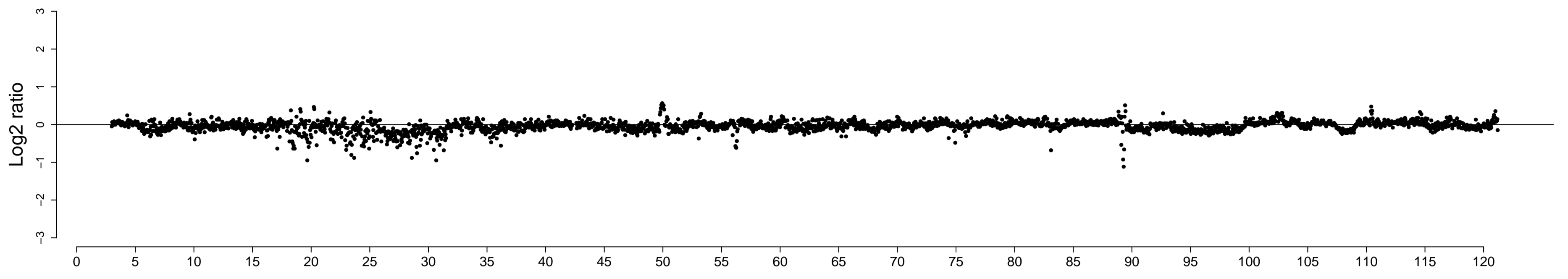
chr11:HTG2 p11



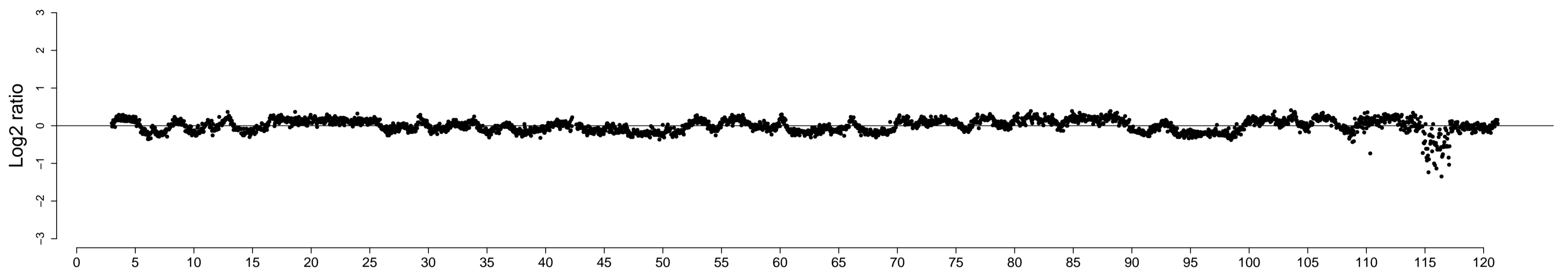
chr12:CBA control kidney



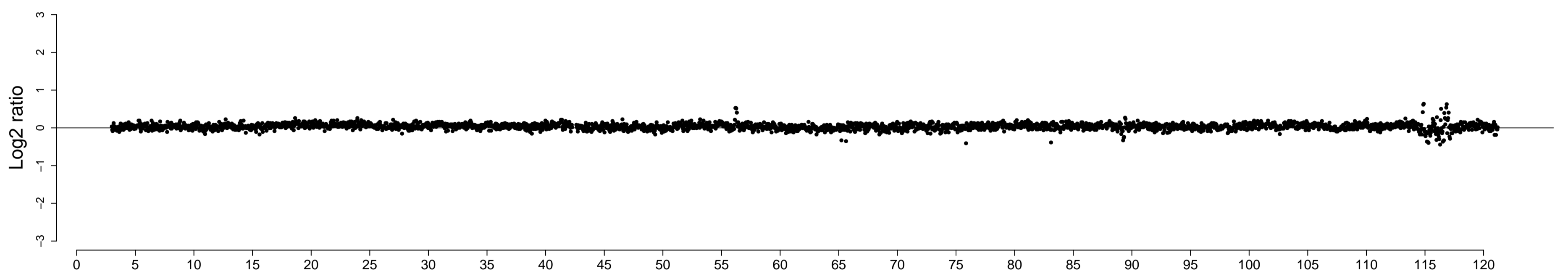
chr12:HAP1 p25



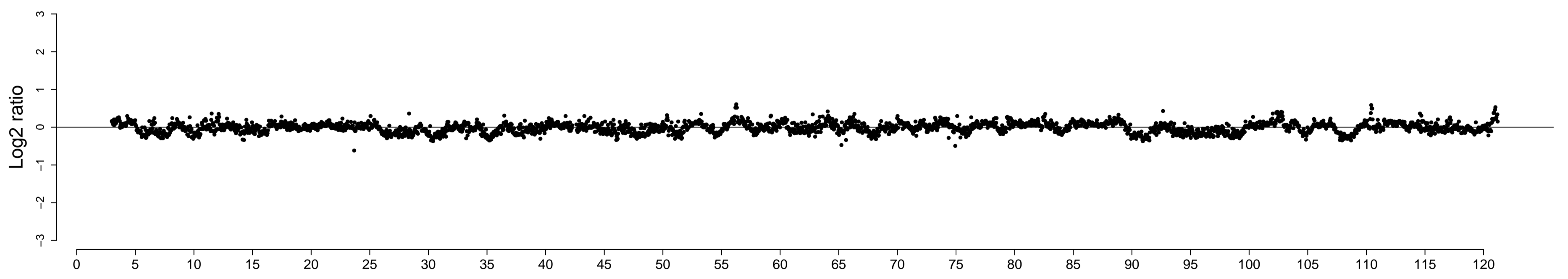
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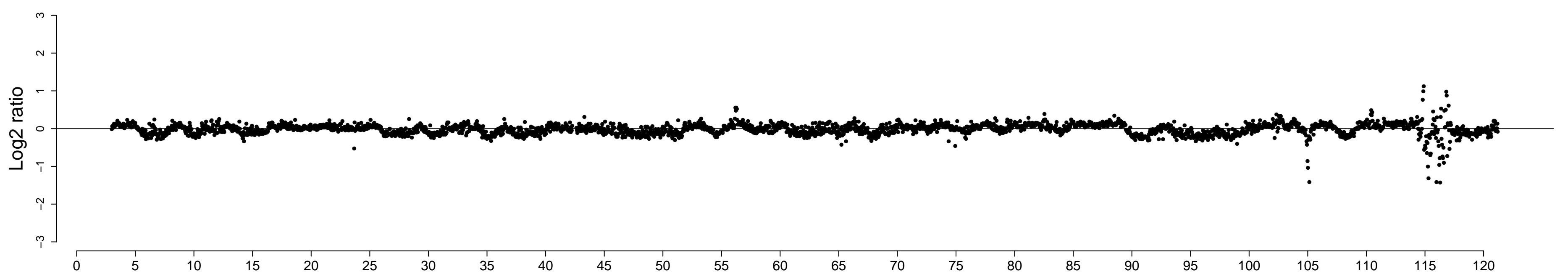
chr12:HTG\_control male kidney



chr12:HTG1 p11

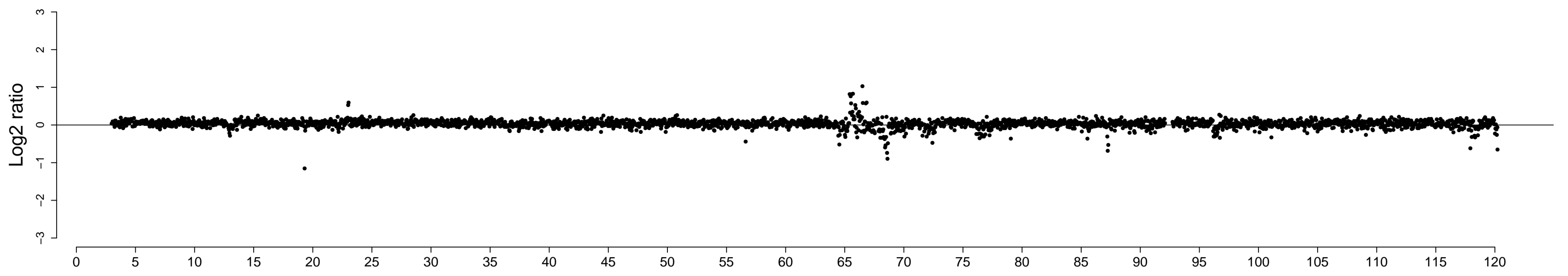


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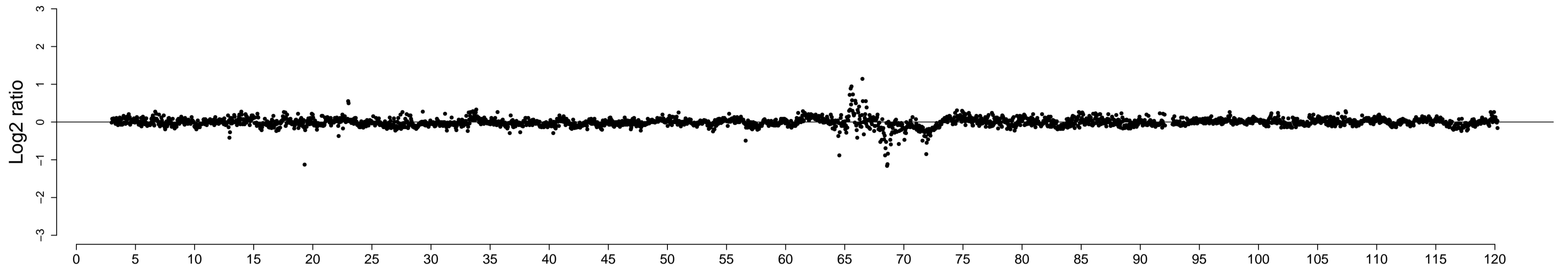




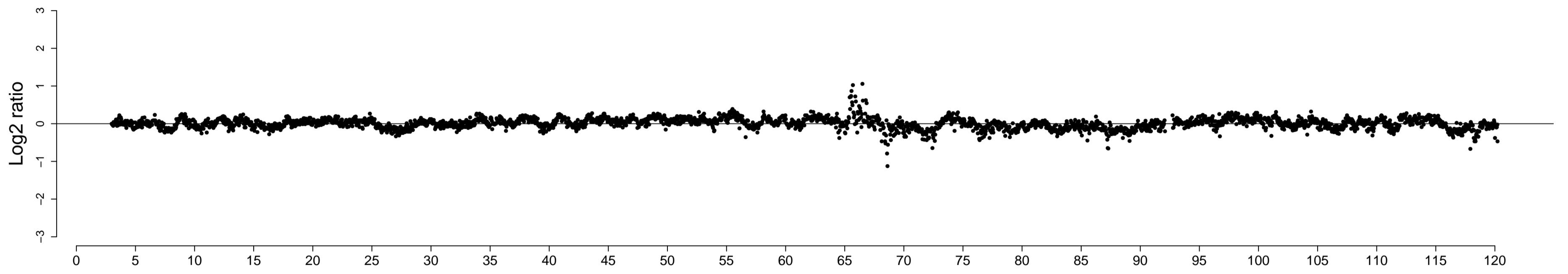
chr13:CBA control kidney



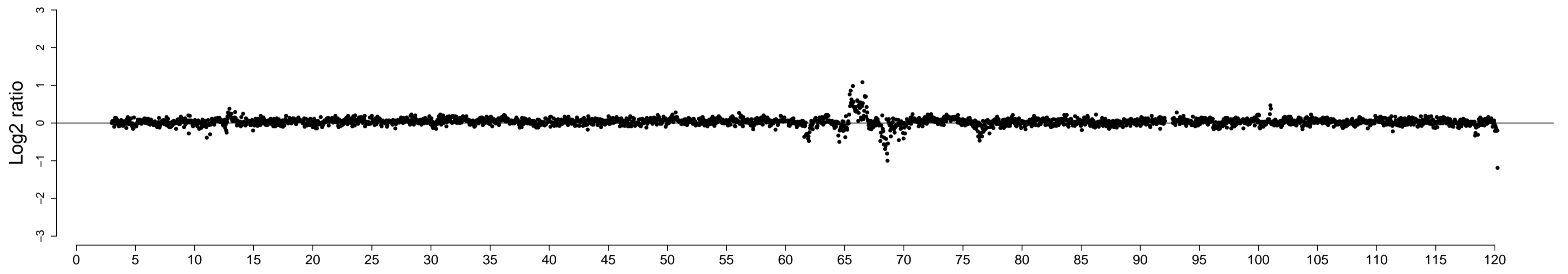
chr13:HAP1 p25



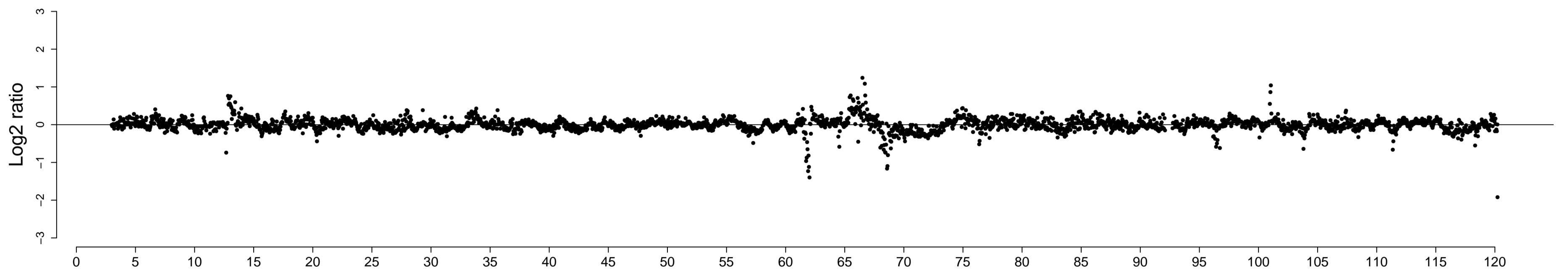
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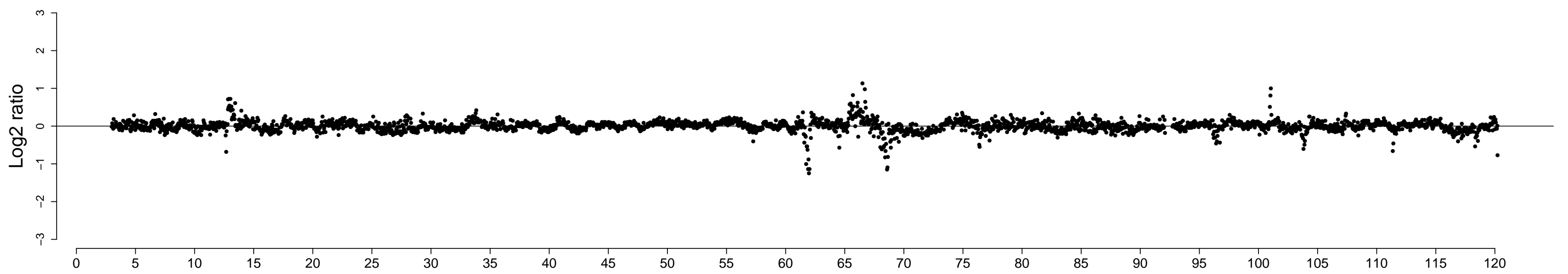
chr13:HTG\_control male kidney



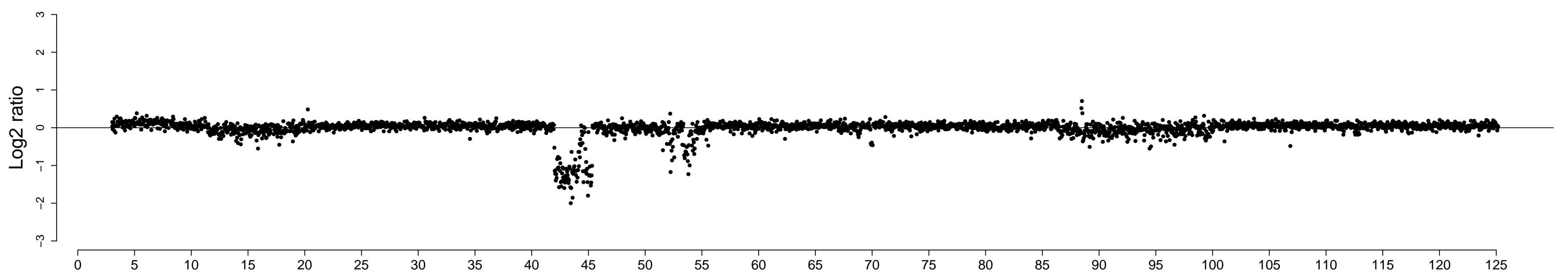
chr13:HTG1 p11



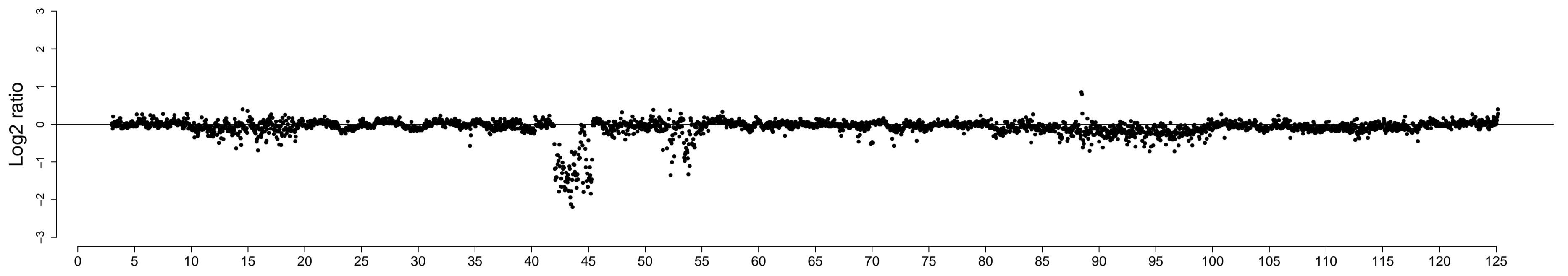
chr13:HTG2 p11



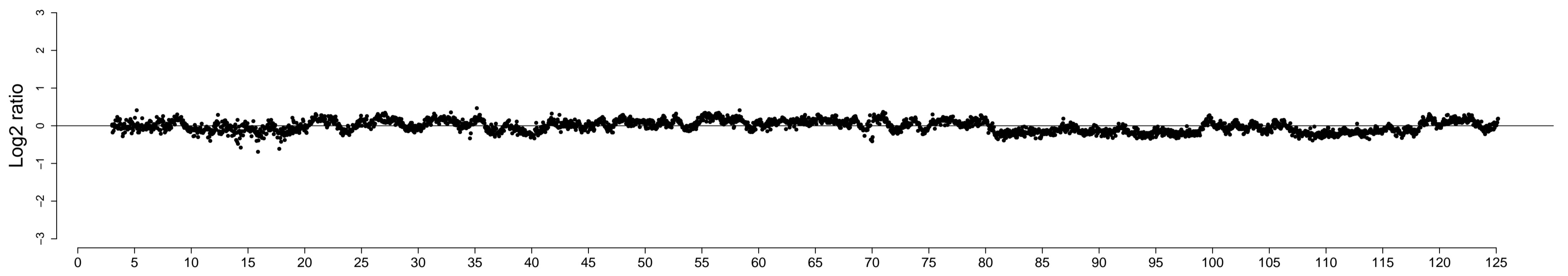
chr14:CBA control kidney



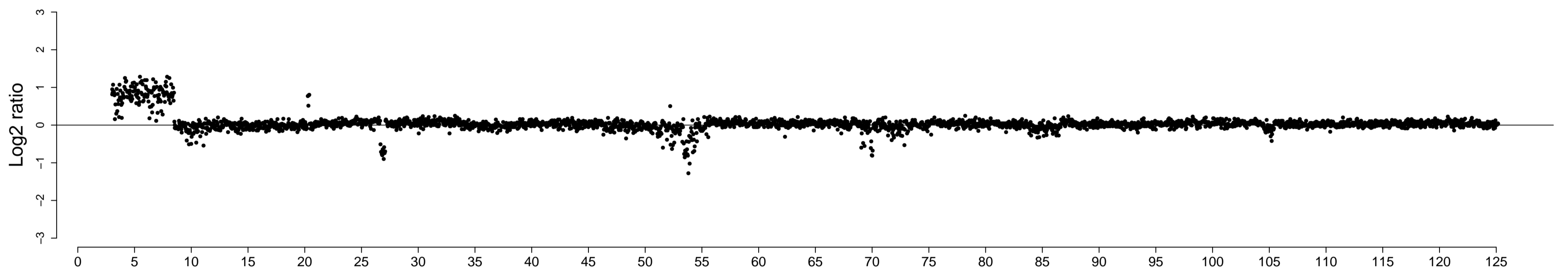
chr14:HAP1 p25



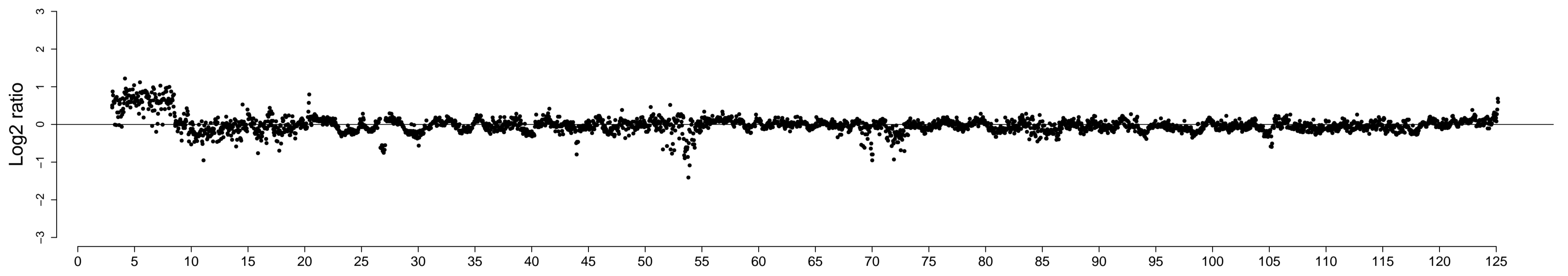
chr14:HAP2 p18



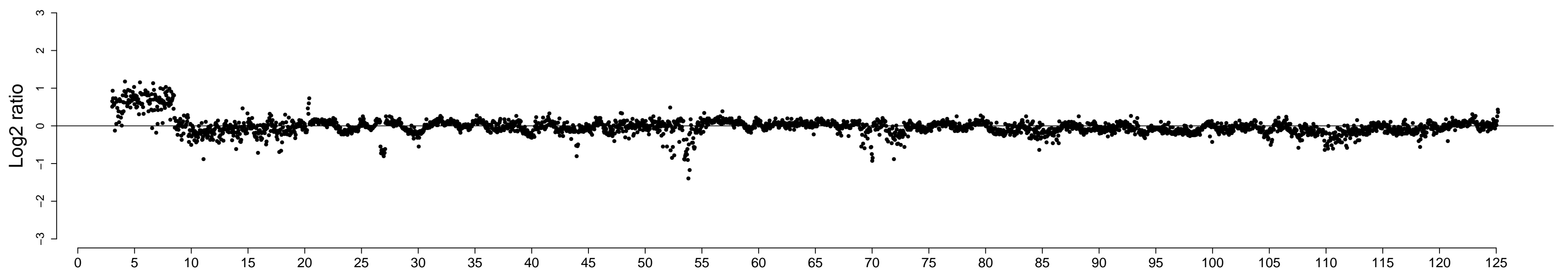
chr14:HTG\_control male kidney



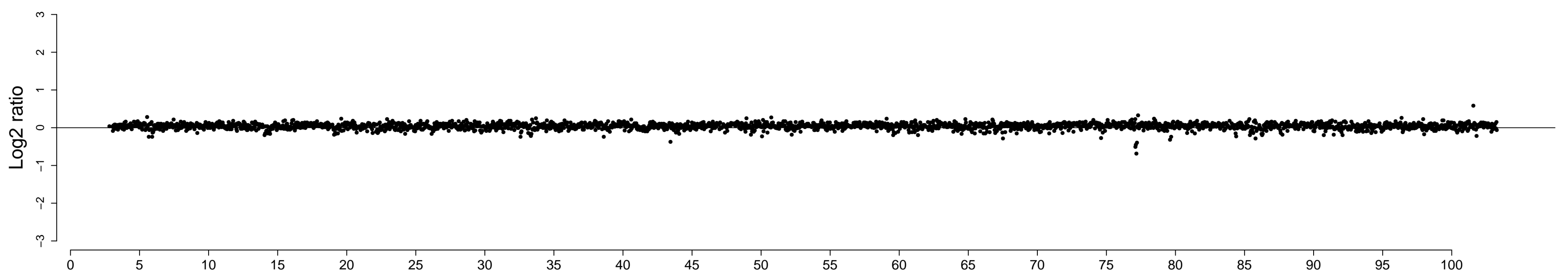
chr14:HTG1 p11



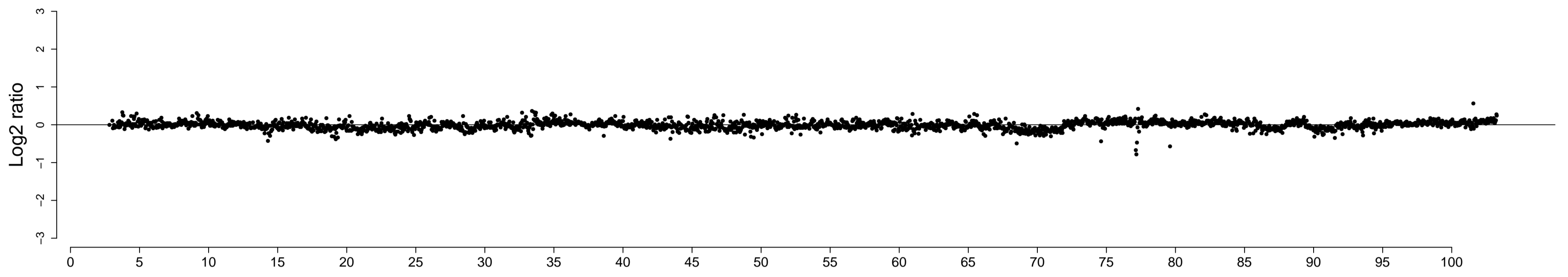
chr14:HTG2 p11



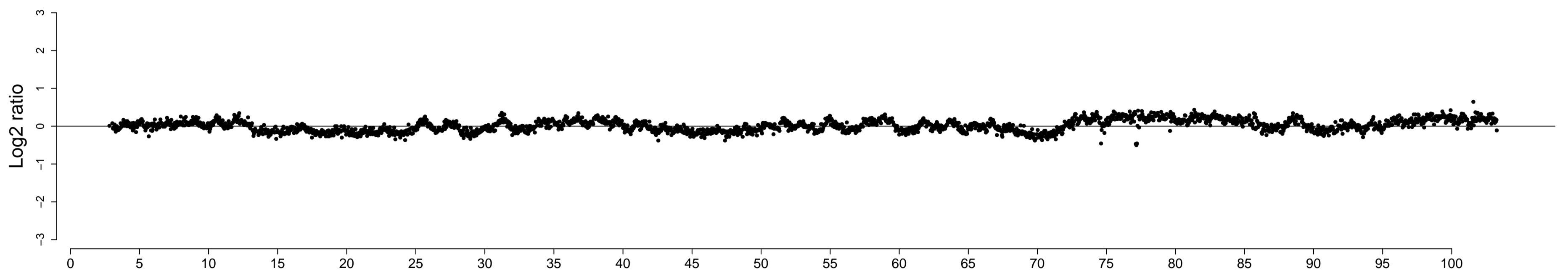
chr15:CBA control kidney



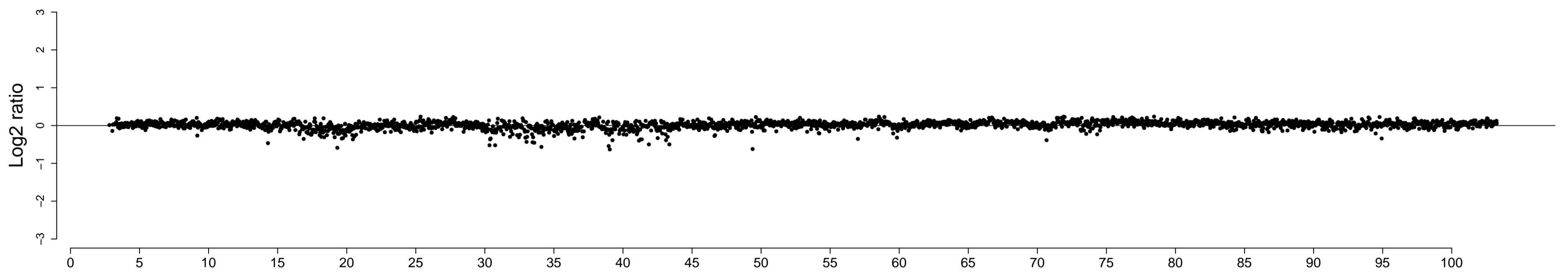
chr15:HAP1 p25



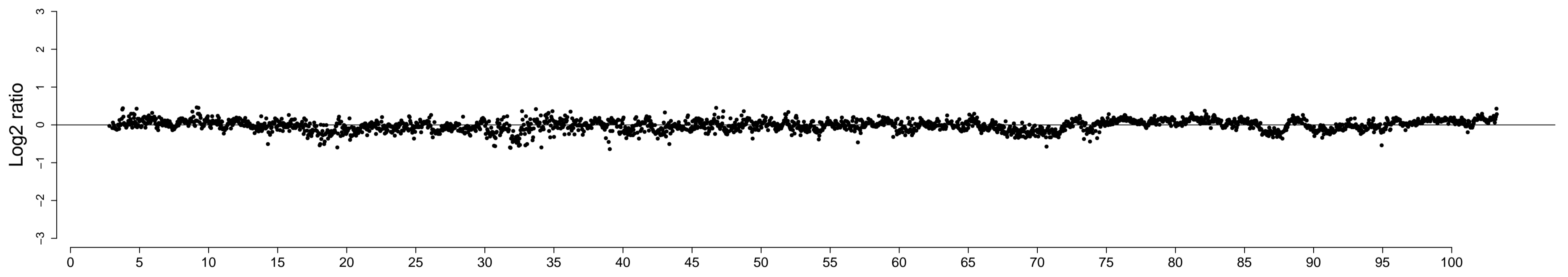
chr15:HAP2 p18



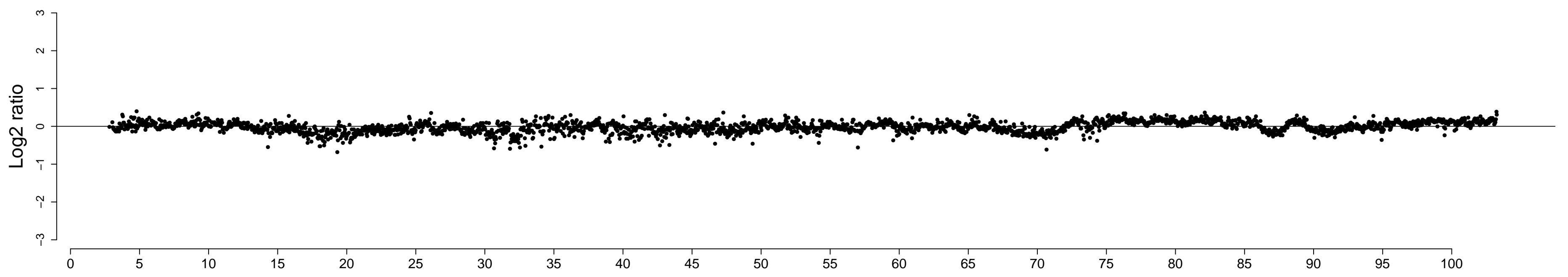
chr15:HTG\_control male kidney



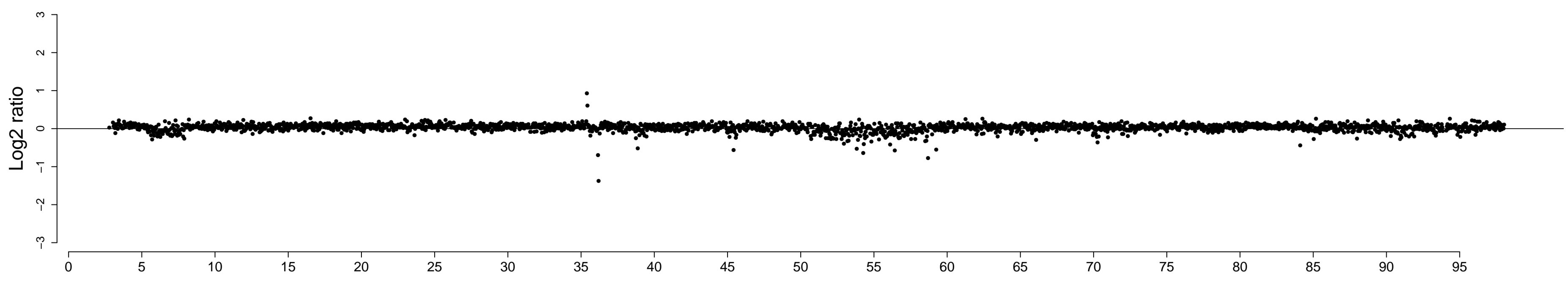
chr15:HTG1 p11



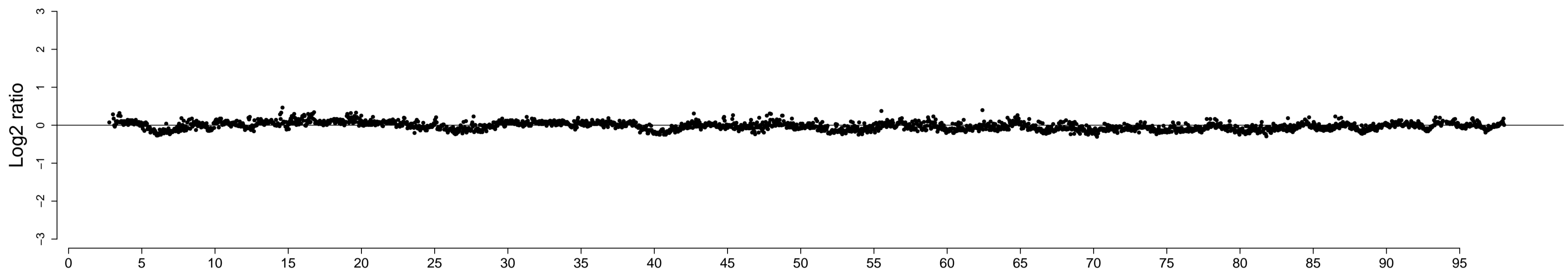
chr15:HTG2 p11



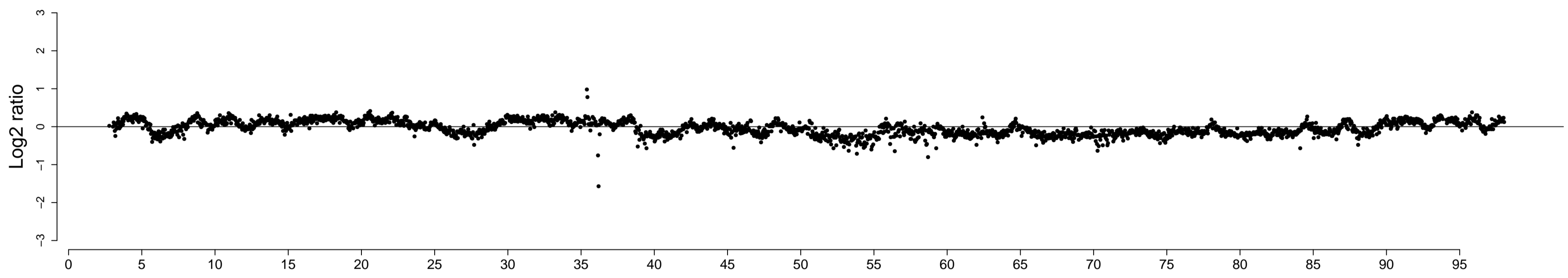
chr16:CBA control kidney



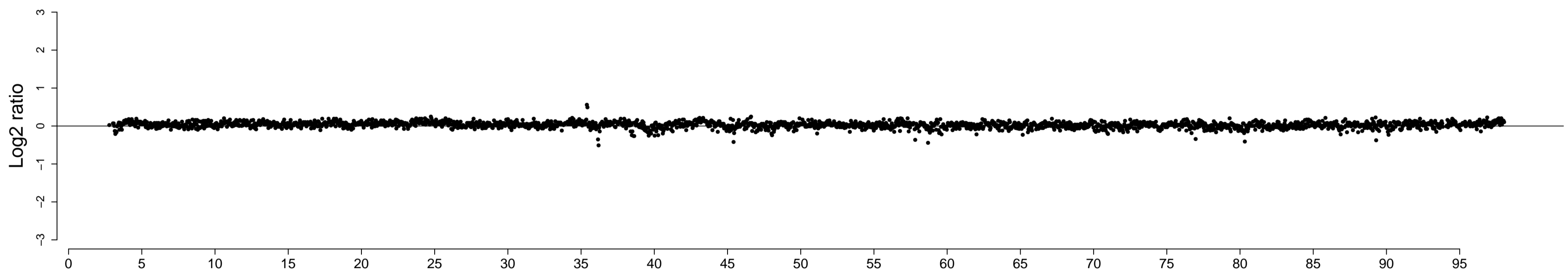
chr16:HAP1 p25



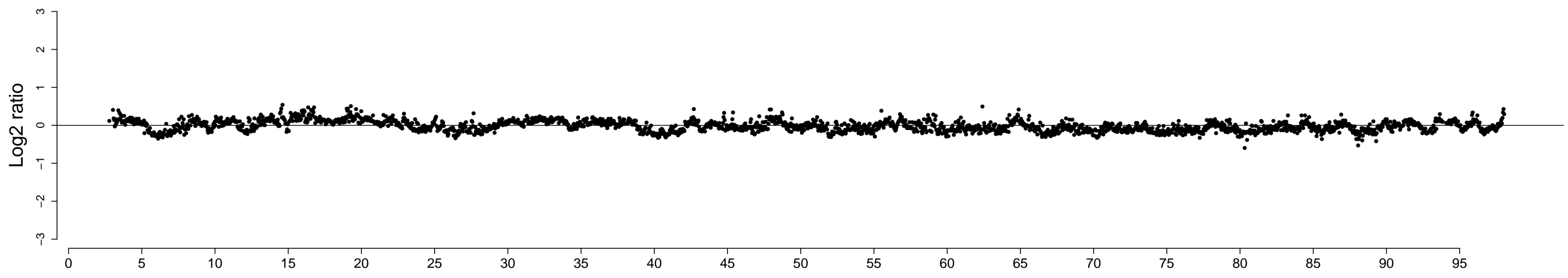
chr16:HAP2 p18



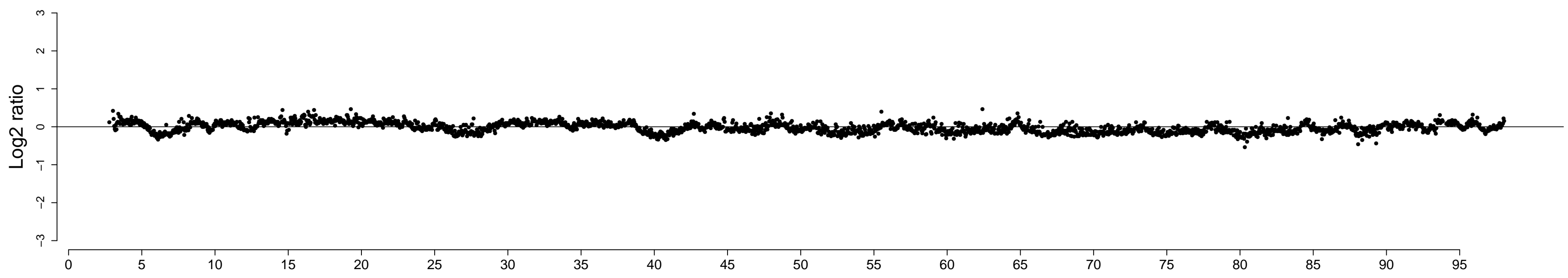
chr16:HTG\_control male kidney



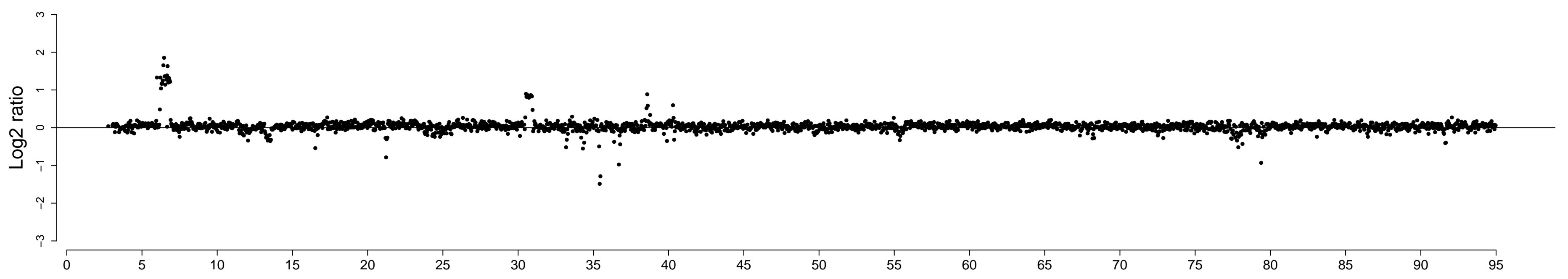
chr16:HTG1 p11



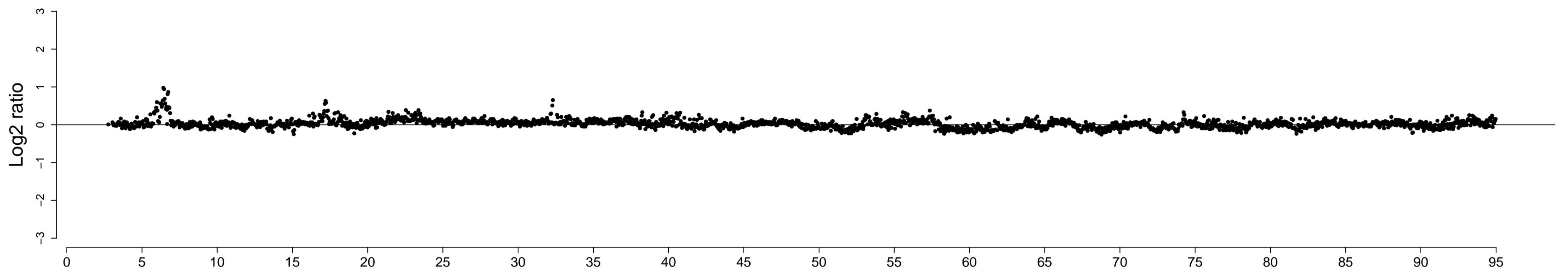
chr16:HTG2 p11



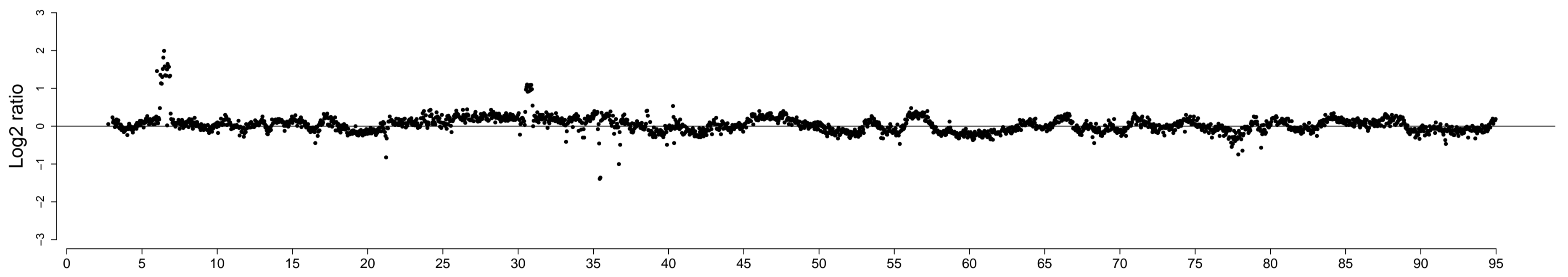
chr17:CBA control kidney



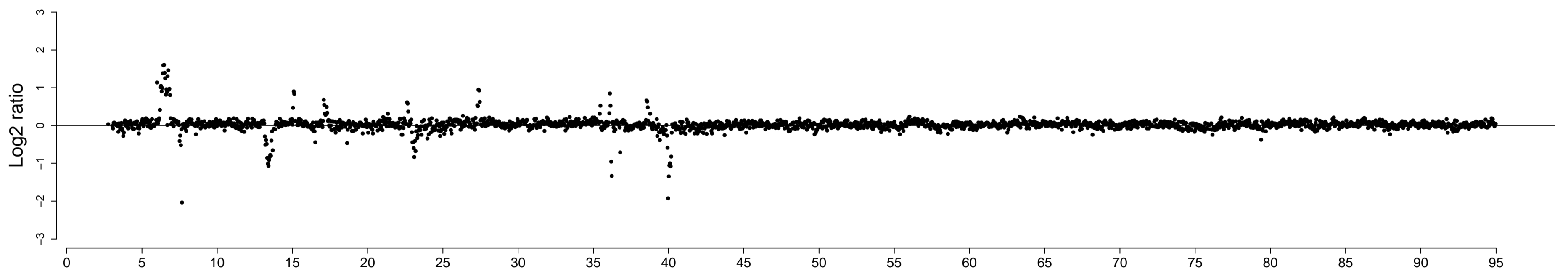
chr17:HAP1 p25



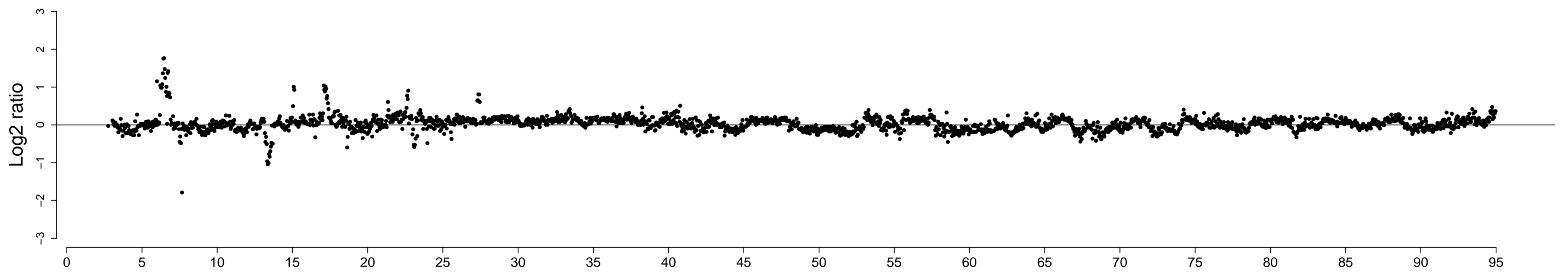
chr17:HAP2 p18



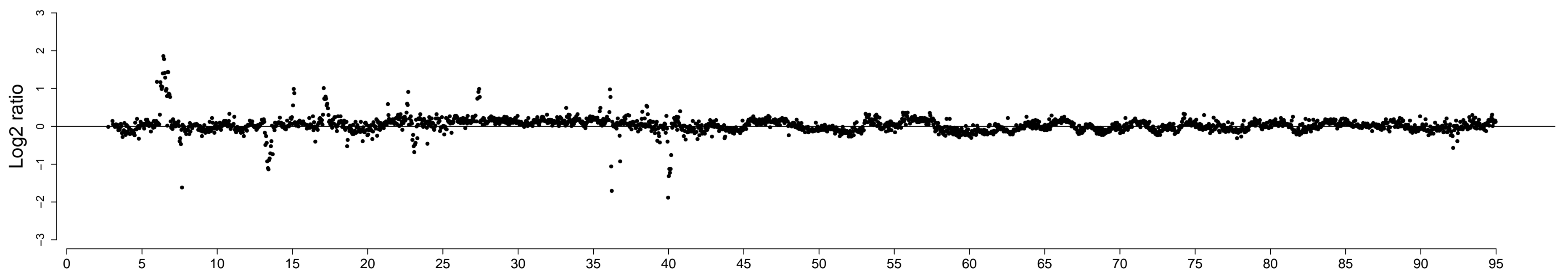
chr17:HTG\_control male kidney



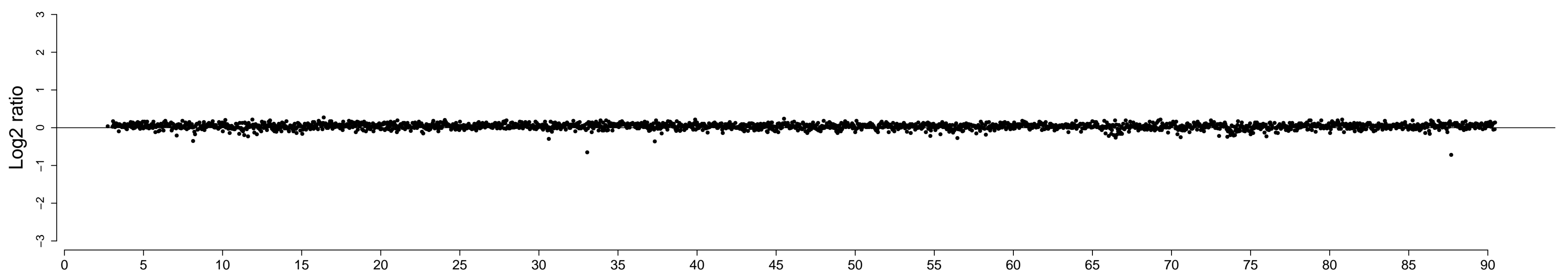
chr17:HTG1 p11



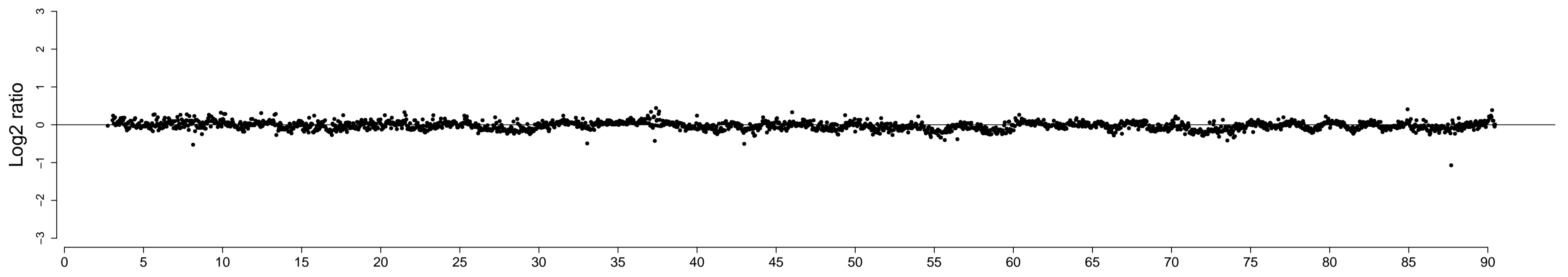
chr17:HTG2 p11



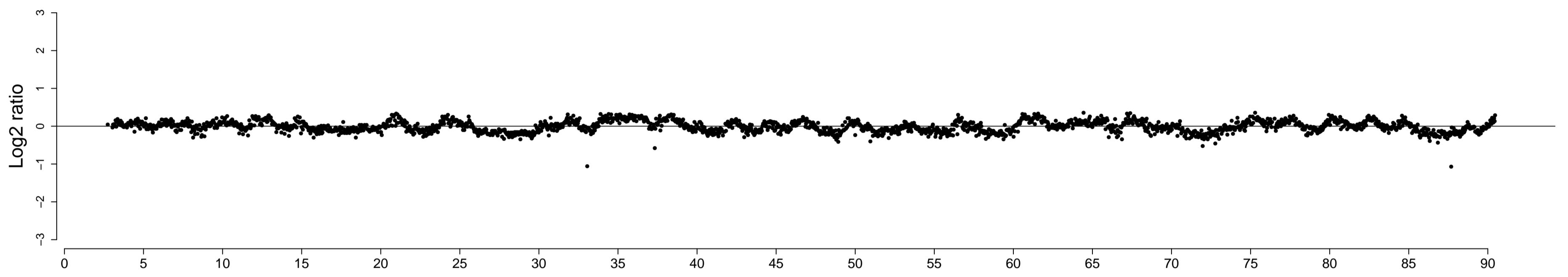
chr18:CBA control kidney



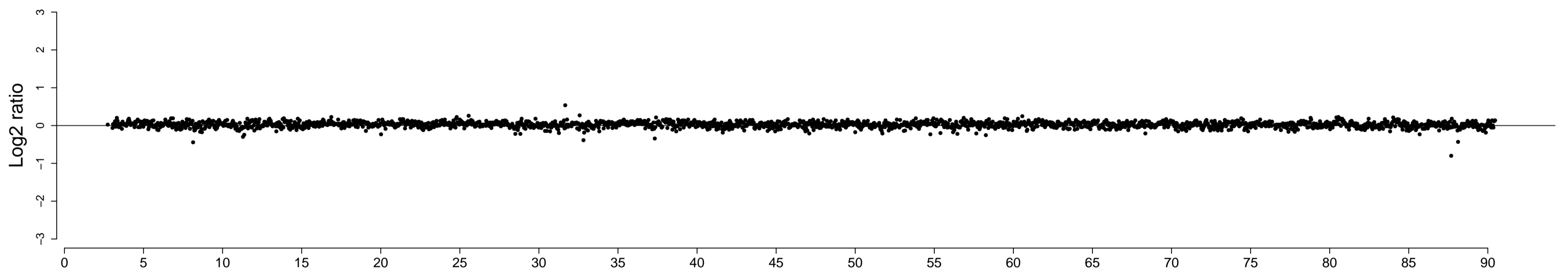
chr18:HAP1 p25



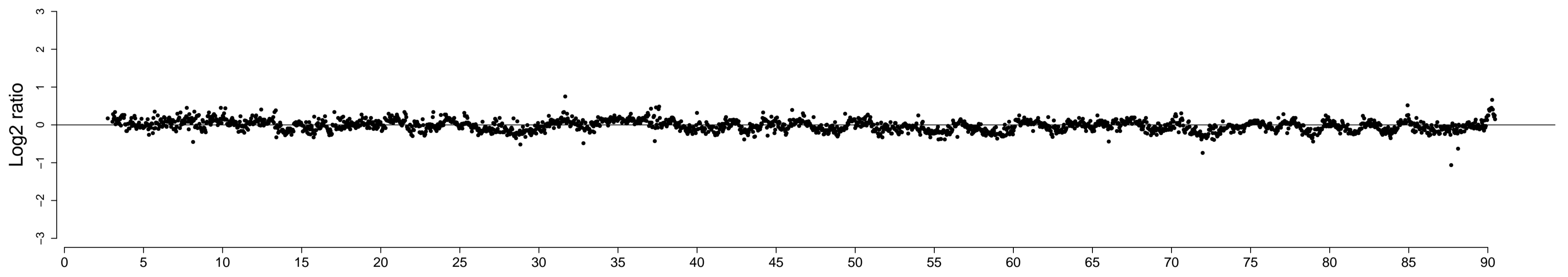
chr18:HAP2 p18



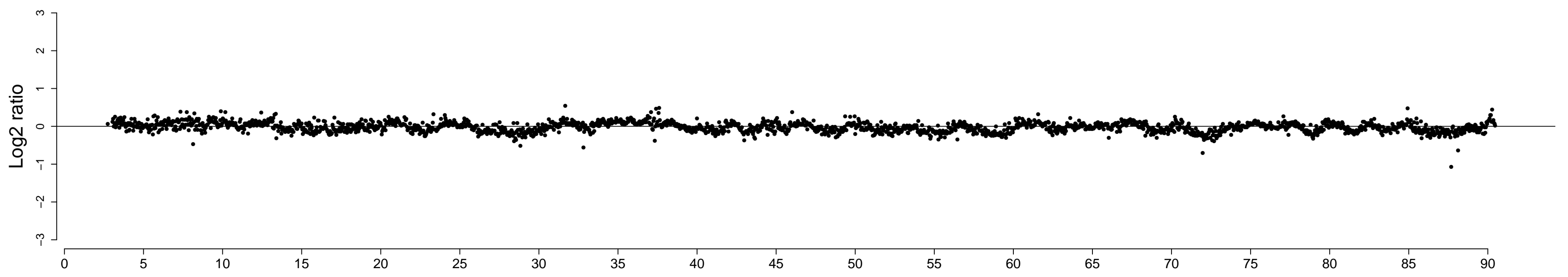
chr18:HTG\_control male kidney



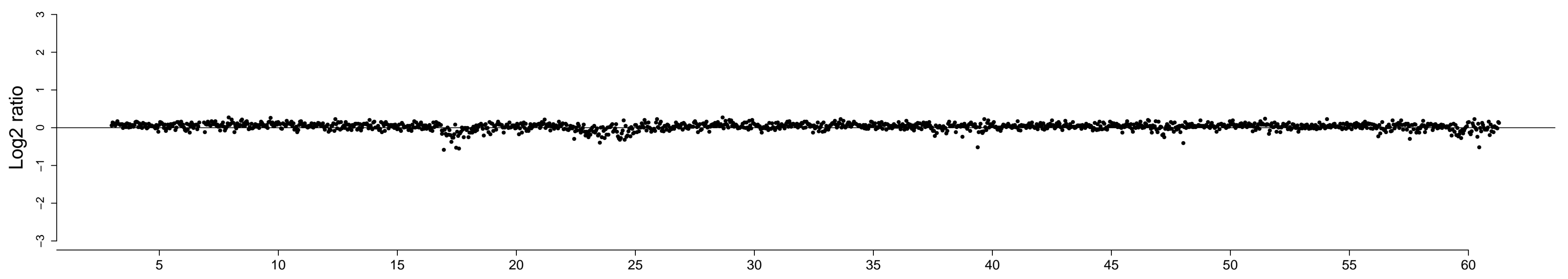
chr18:HTG1 p11



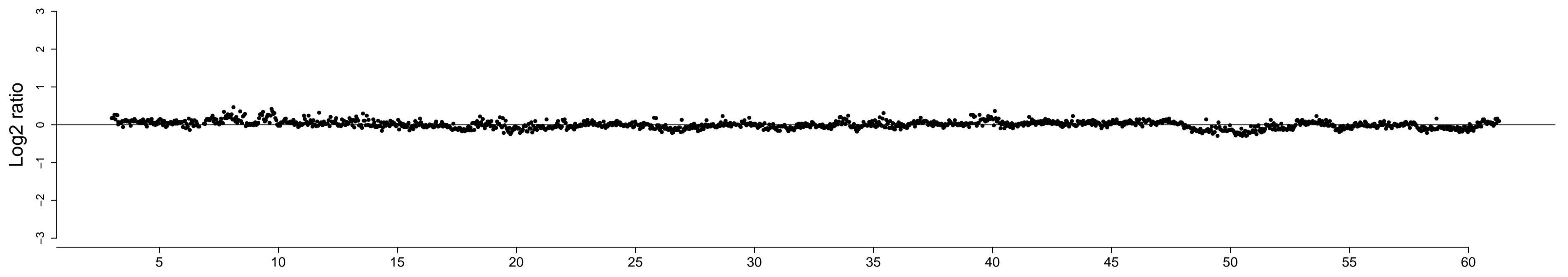
chr18:HTG2 p11



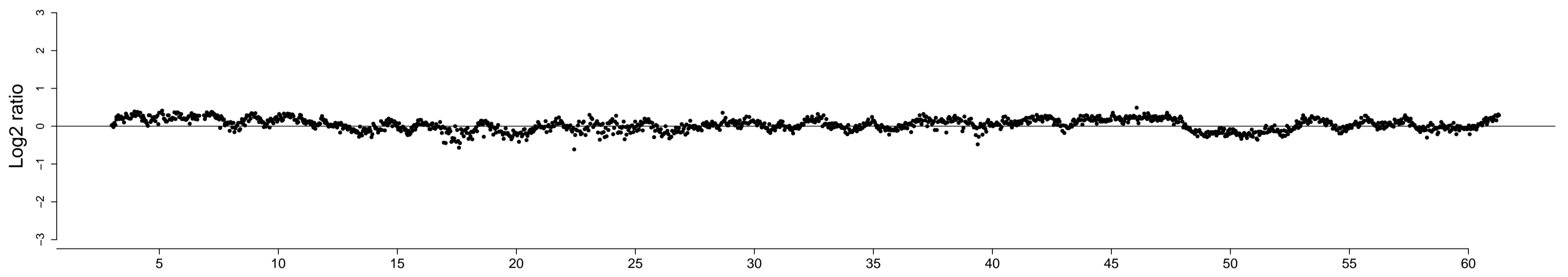
chr19:CBA control kidney



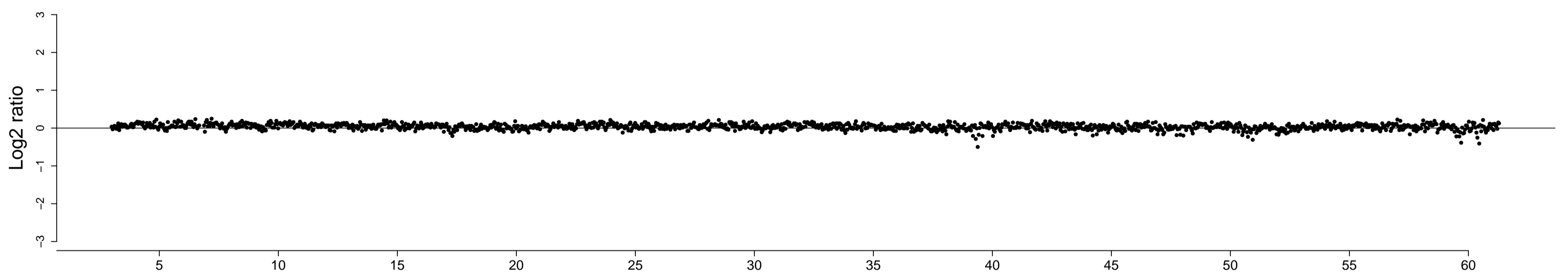
chr19:HAP1 p25



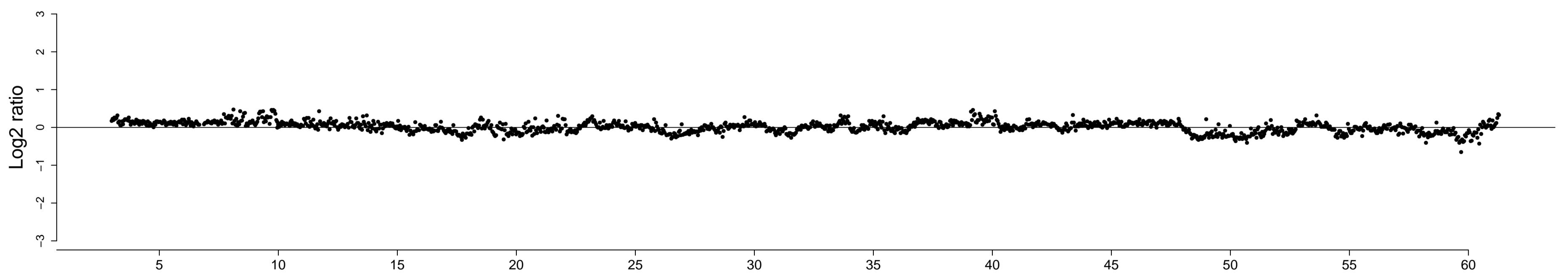
chr19:HAP2 p18



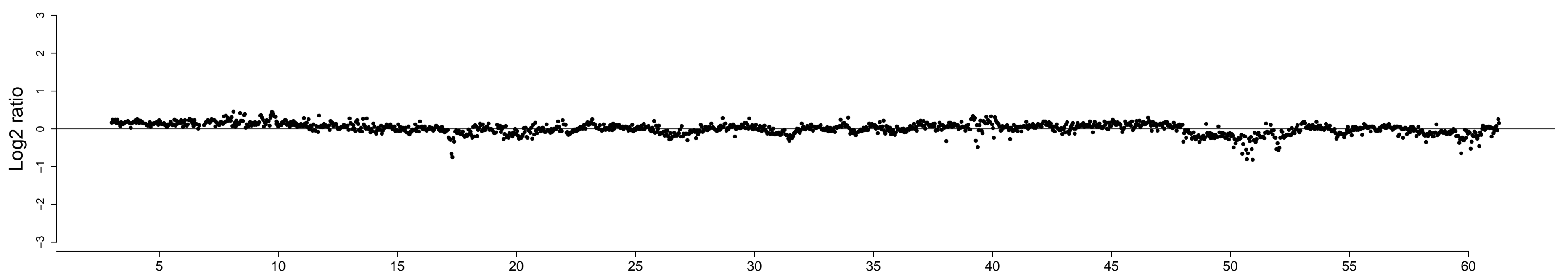
chr19:HTG\_control male kidney



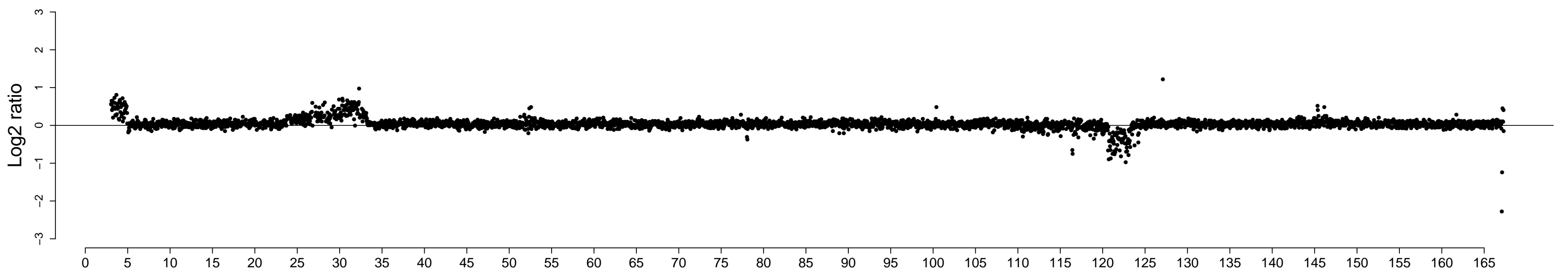
chr19:HTG1 p11



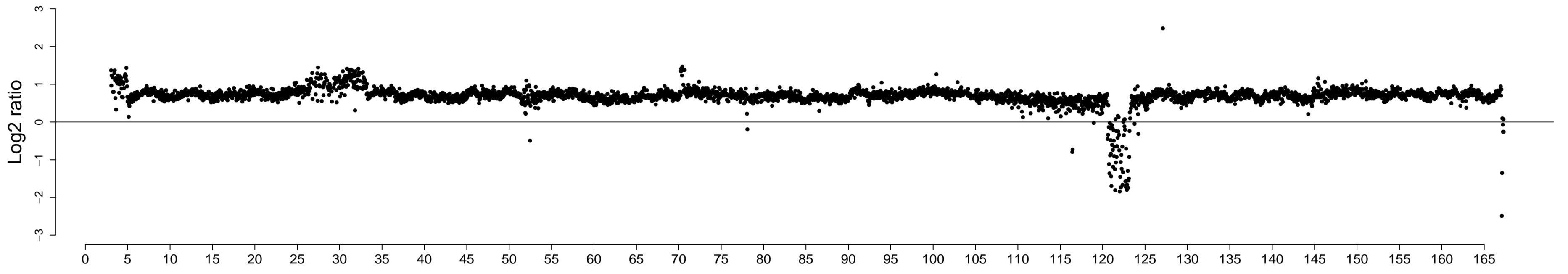
chr19:HTG2 p11



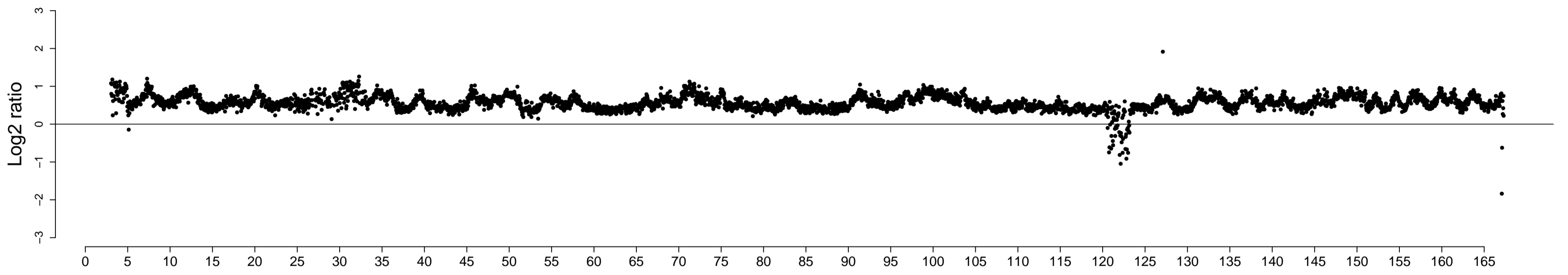
chrX:CBA control kidney



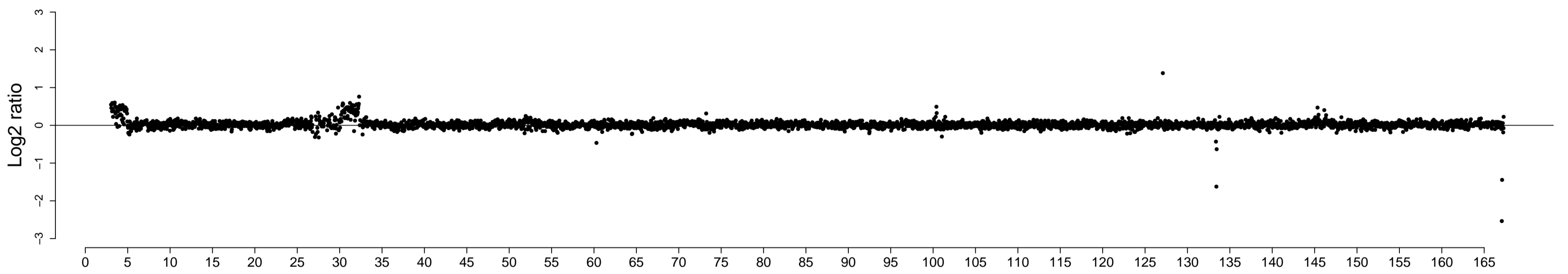
chrX:HAP1 p25



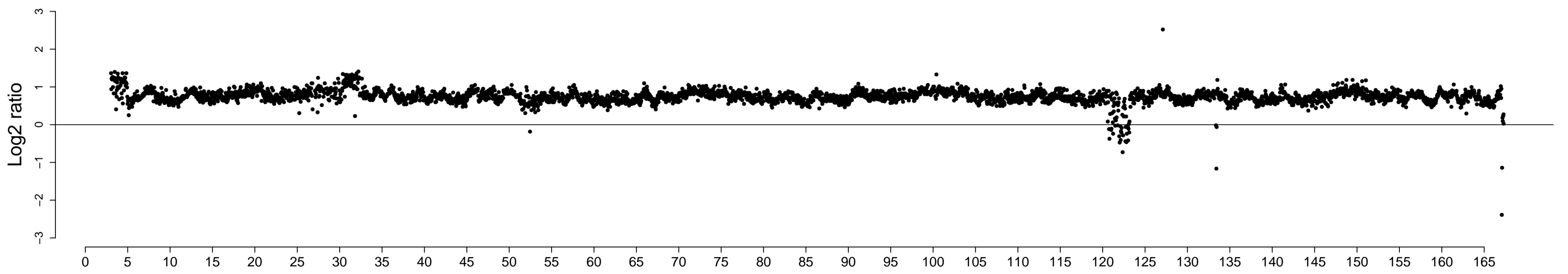
chrX:HAP2 p18



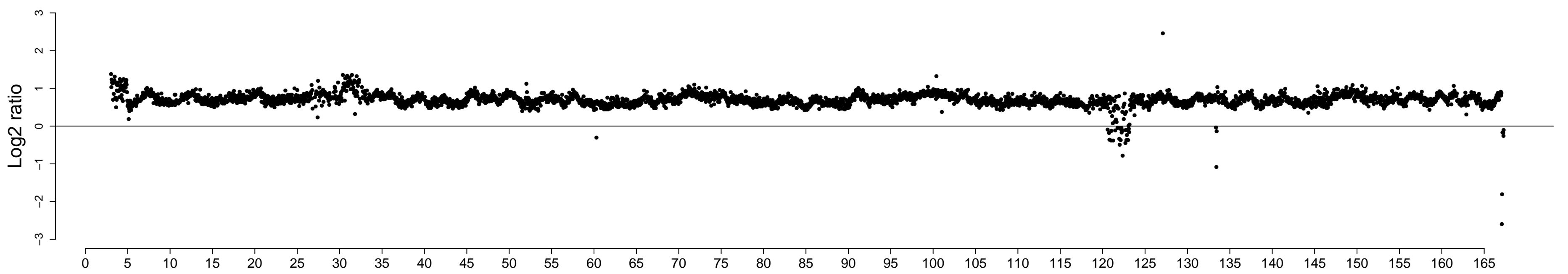
chrX:HTG\_control male kidney



chrX:HTG1 p11

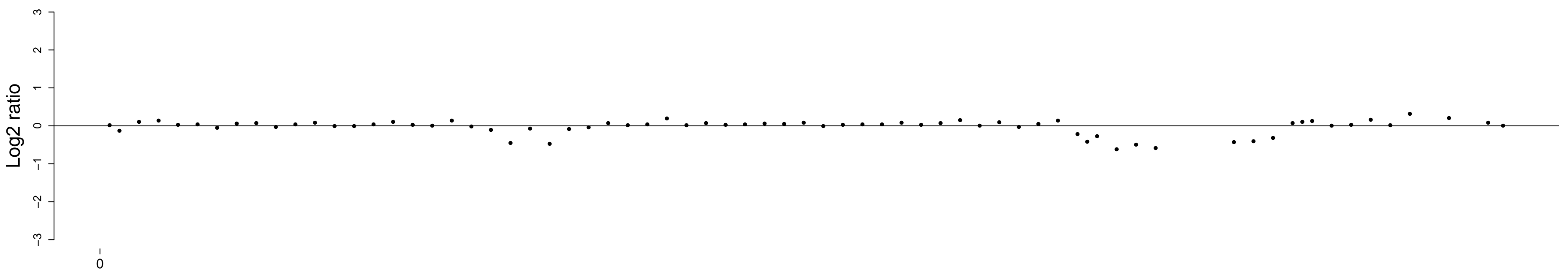


chrX:HTG2 p11





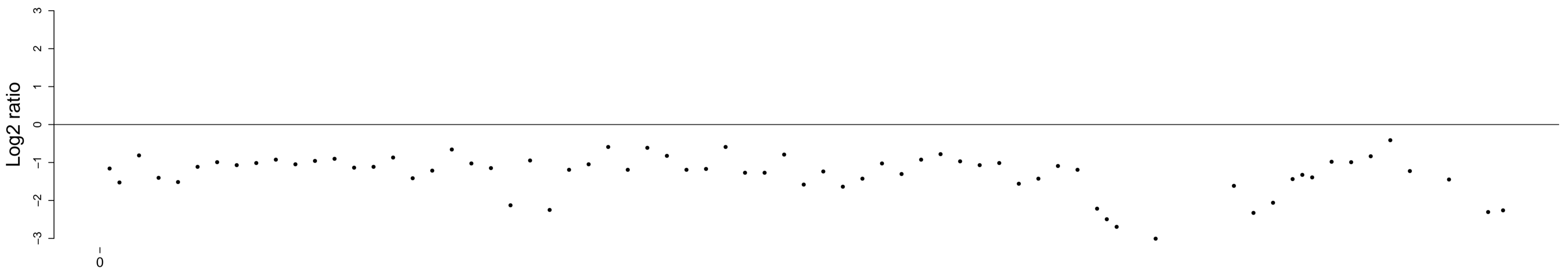
chrY:CBA control kidney



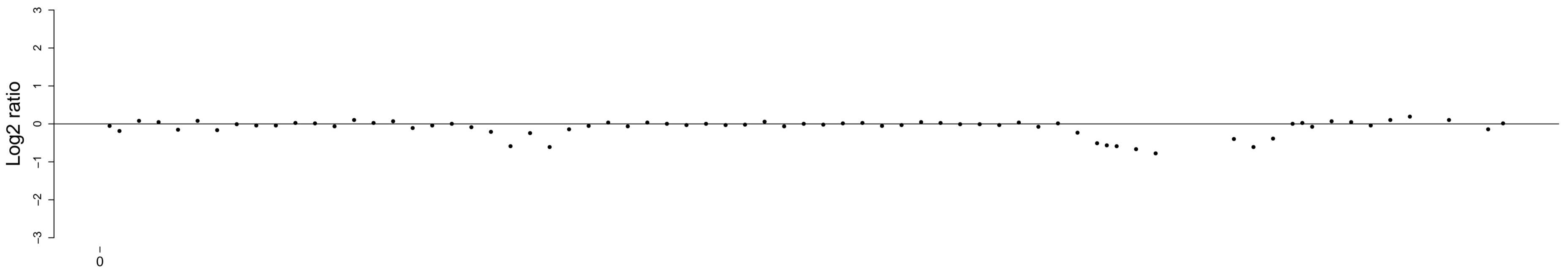
chrY:HAP1 p25



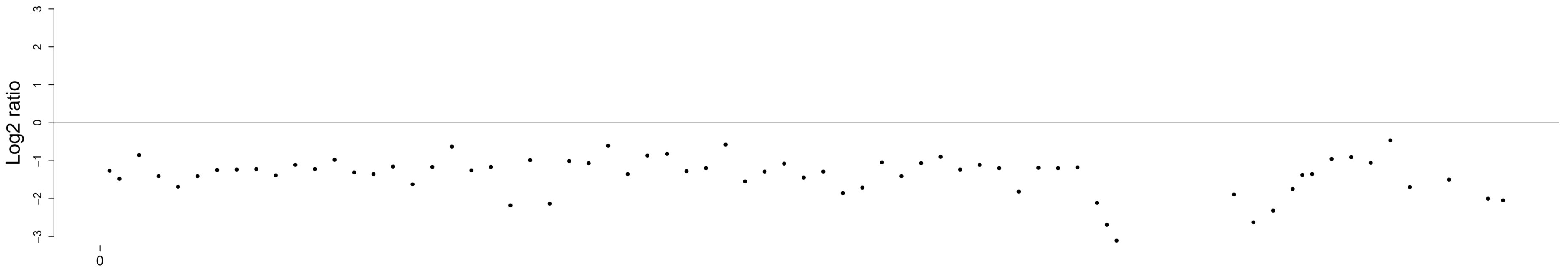
chrY:HAP2 p18



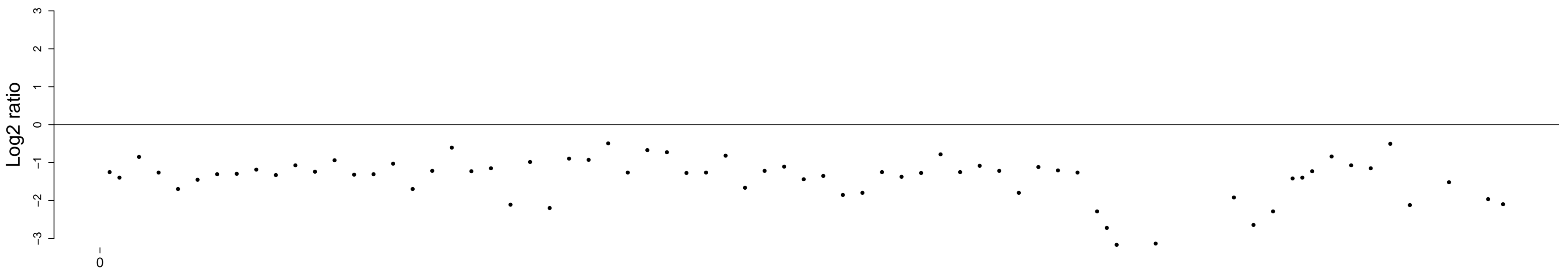
chrY:HTG\_control male kidney



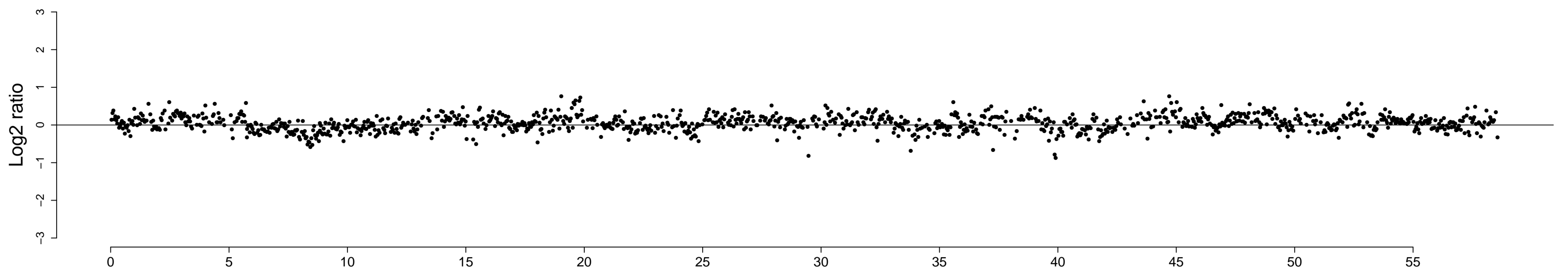
chrY:HTG1 p11



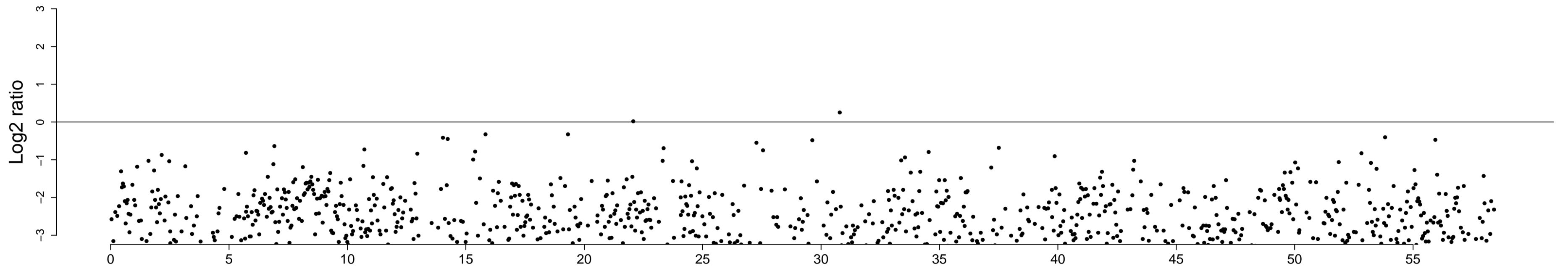
chrY:HTG2 p11



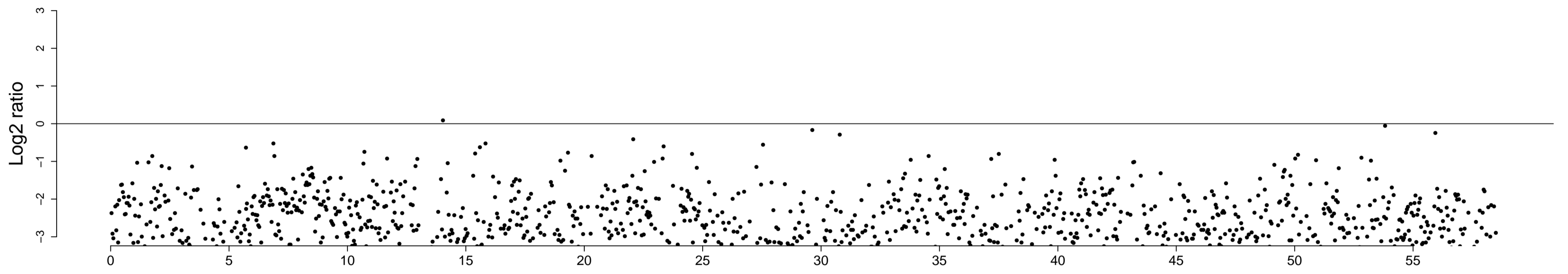
chrY\_random:CBA control kidney



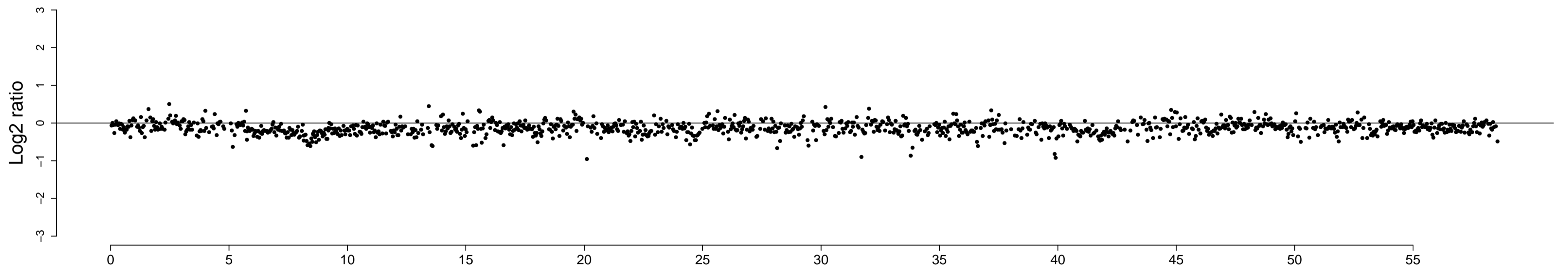
chrY\_random:HAP1 p25



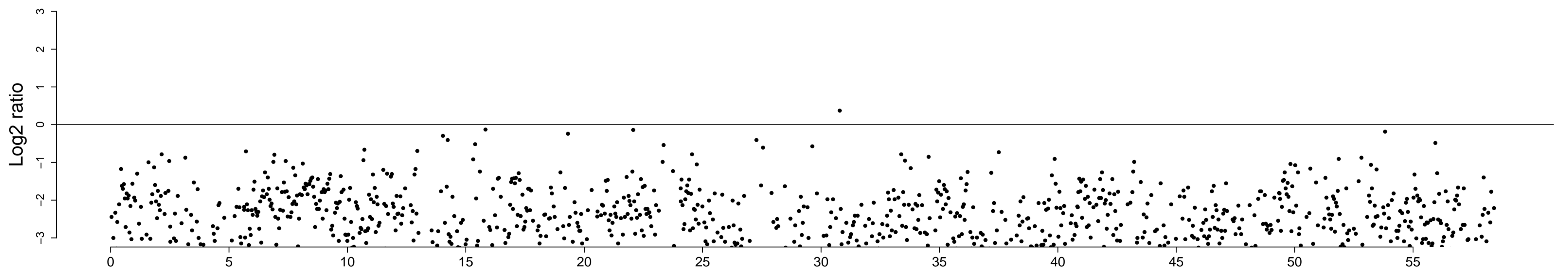
chrY\_random:HAP2 p18



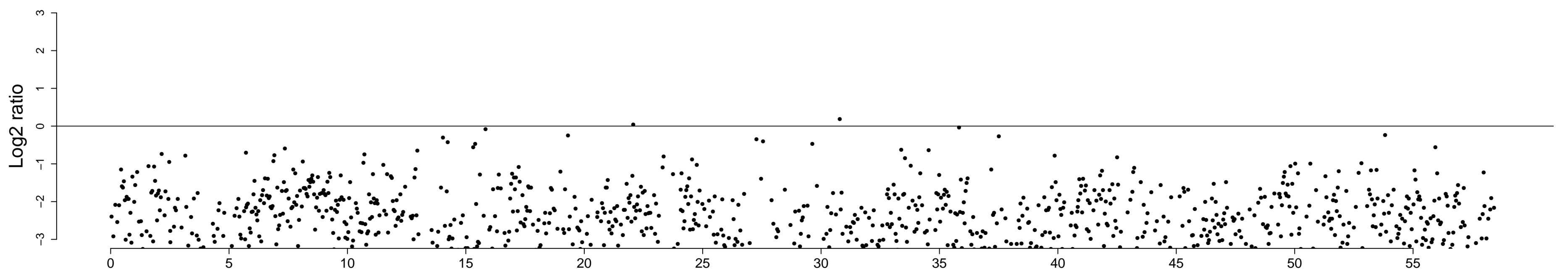
chrY\_random:HTG\_control male kidney

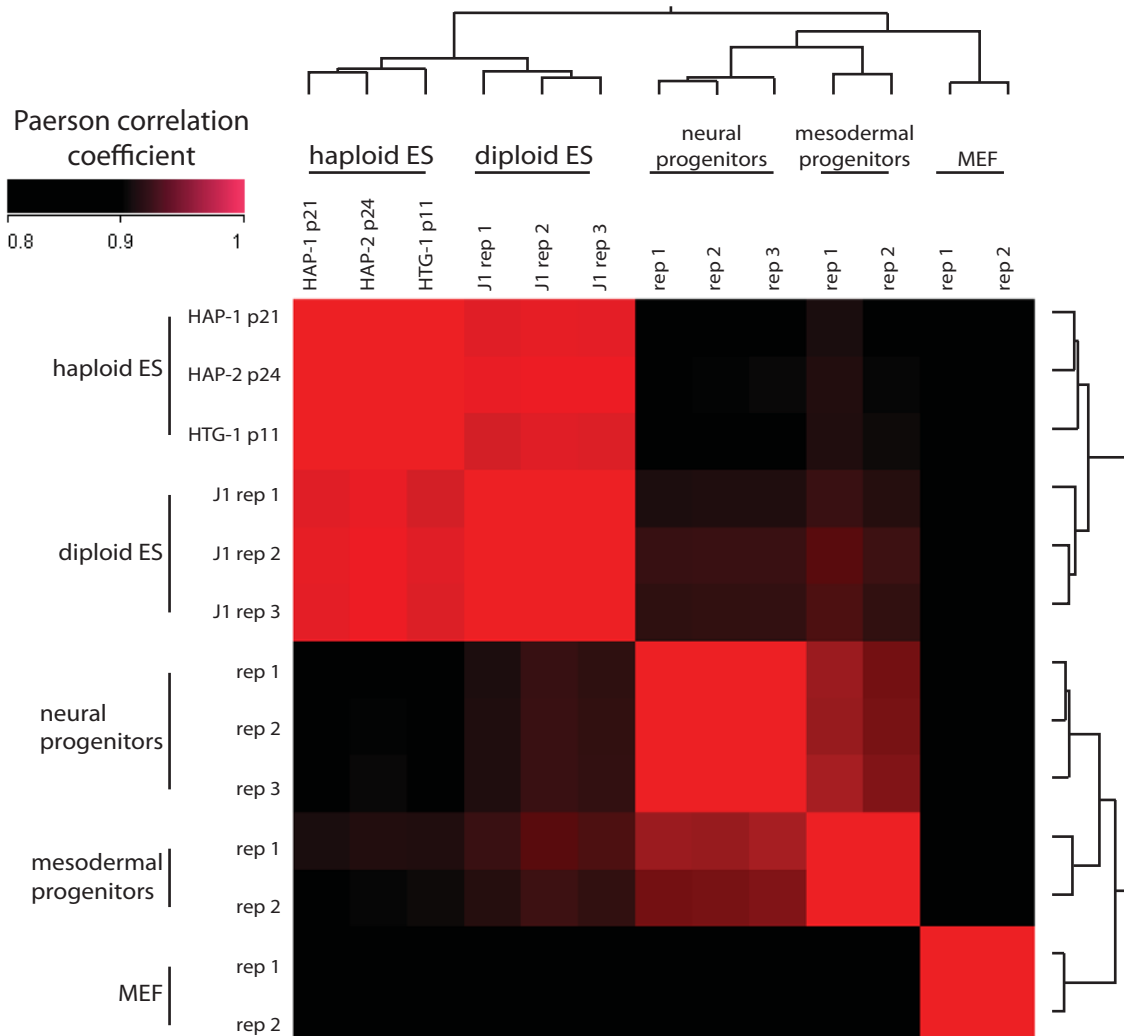


chrY\_random:HTG1 p11



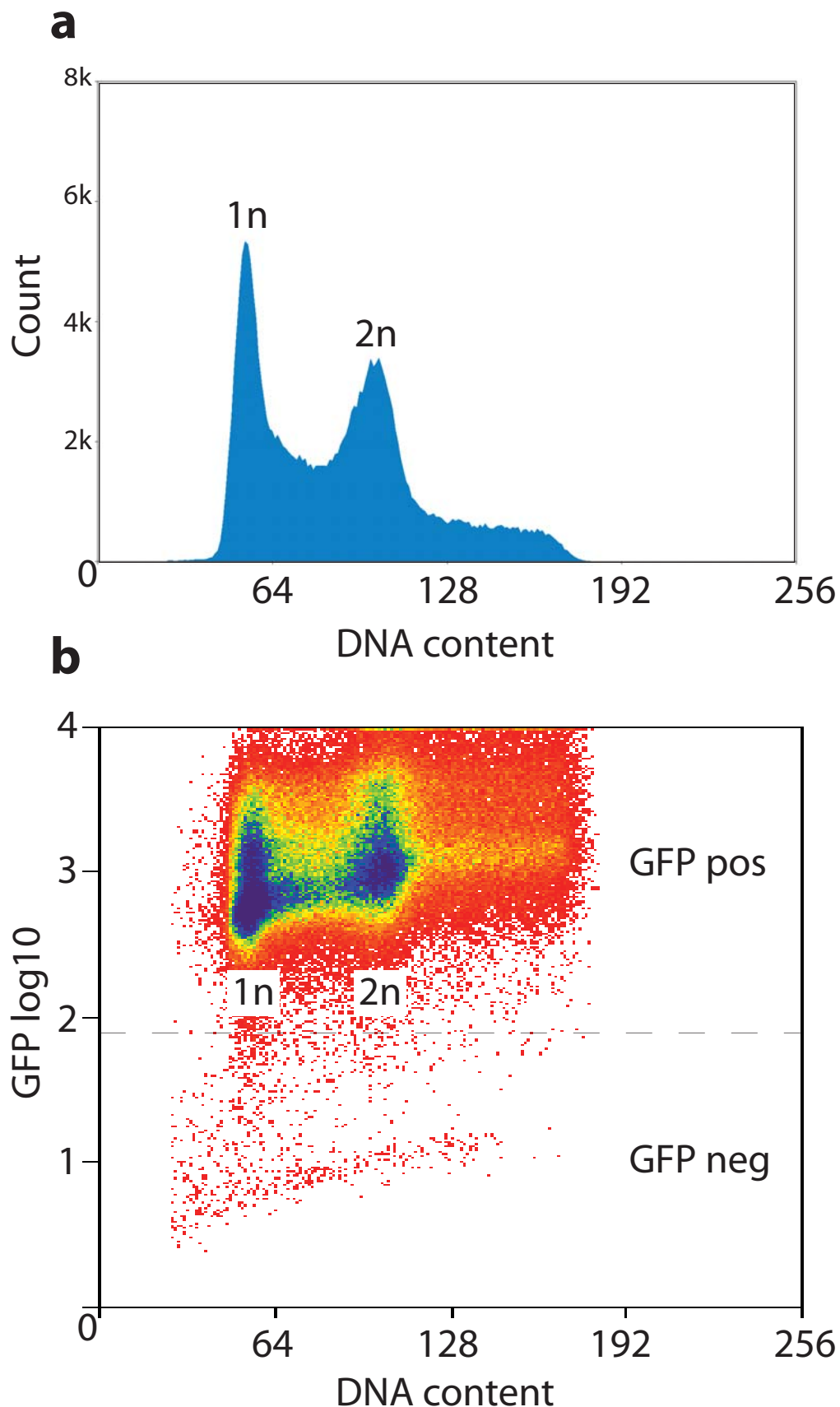
chrY\_random:HTG2 p11





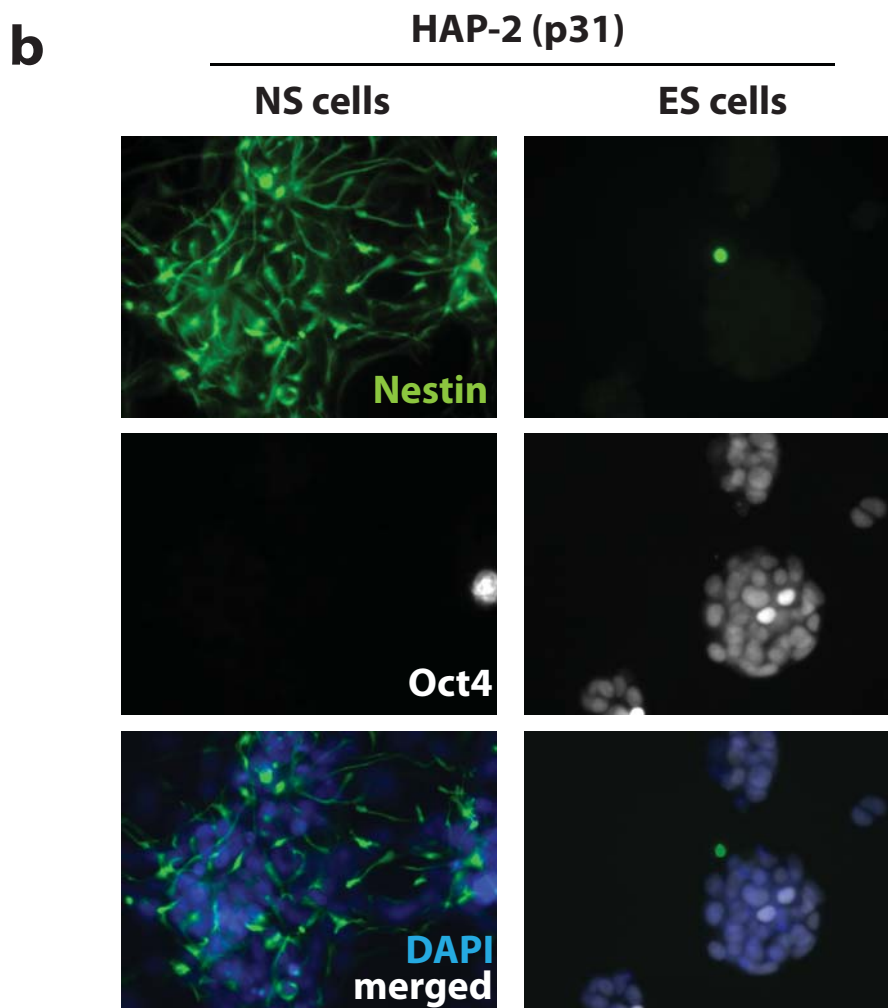
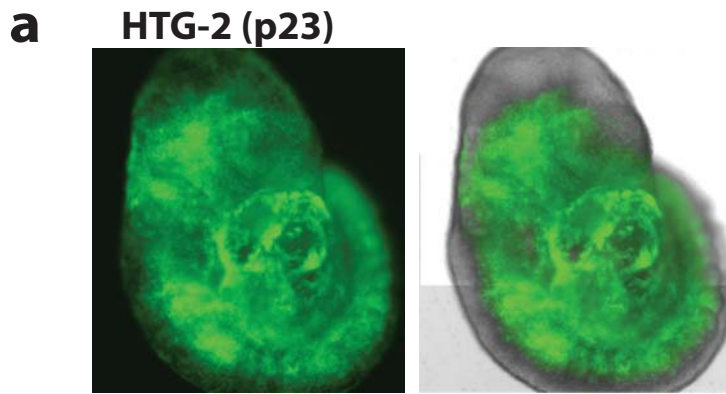
### Supplementary Figure 5 - Analysis of similarity between haploid and diploid ES cells

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 haploiid 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**

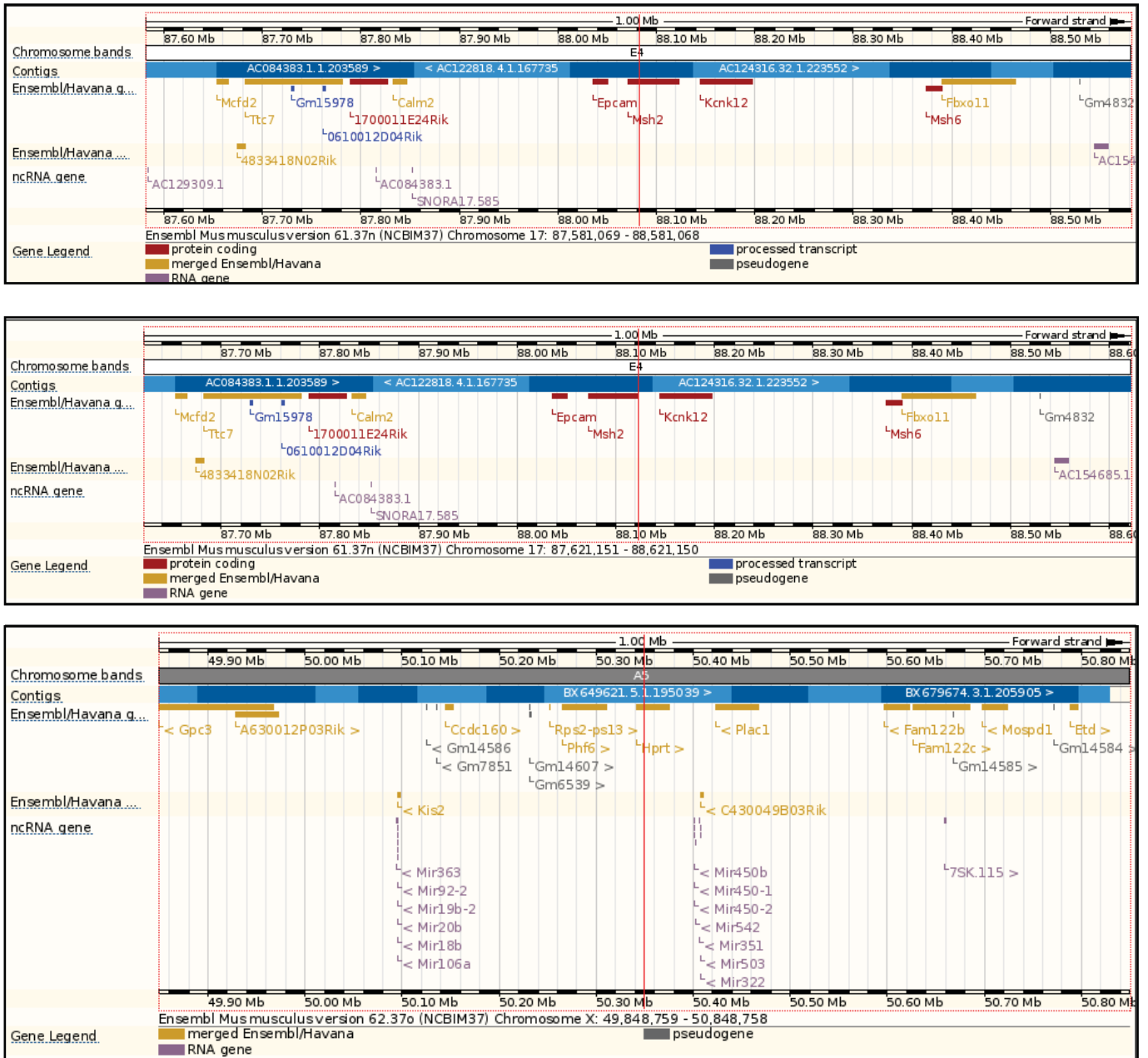
Flow profiles show the **(a)** DNA content and **(b)** DNA content combined with GFP intensity of HAP-2 ES cells transfected with a piggyBac vector for expressing GFP. The 1n / GFP positive population was purified for analysis of the developmental potential of haploid ES cells.



### 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.

**a****b**

## Supplementary Figure 8 - Genetrapp insertions recovered in mismatch repair screen

**(a)** A schematic representation of the piggyBac genetrapp 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 mismatch 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 log<sub>2</sub> value of 0.8 were determined and listed with chromosome and genomic position.





Supplementary Table 2 - differentially regulated genes in haploid ES cells (&gt; 2 fold; p&lt;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	Al662270	103814	expressed sequence Al662270
2 1416749_at	10.76	Htra1	56213	HtrA serine peptidase 1
3 1419540_at	8.46	EG434726 /// Fth17	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 1448696_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 /// LOC63263ε	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	Rps6k1	238323	ribosomal protein S6 kinase-like 1
66 1418318_at	3.16	Rnf128	66889	ring finger protein 128
67 1435514_at	3.14	Lztf1	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	D7Erd128e	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/aprimidinic 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	microchidia 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 (/
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 choroideremia; choroideremia
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	Ikbg	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	Yip6	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 pyrophosphi
162 1435452_at	2.38	LOC100047579 /// T	100047579 /// 24066C	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 /// 27066S	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 pyrophosphi
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 /// Pptr	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	Fancc	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	4930526115Rik	75135	RIKEN cDNA 4930526115 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	angiomin-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 1 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	Al846148	68229	expressed sequence Al846148
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 /// \	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	Dsty	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	Tgfb1	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, beta
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 Grp1	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 <sup>+</sup> /H <sup>+</sup> 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 9430069107Rik	77358	RIKEN cDNA 9430069107 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 NmrA1	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 NmrA1	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	Nrn11	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	Zfp361l	12192	zinc finger protein 36, C3H type-like 1