**Genome-wide Analyses Identify Recurrent Amplifications of Receptor Tyrosine Kinases and Cell Cycle Regulatory Genes in Diffuse Intrinsic Pontine Glioma**

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Supplementary Figures

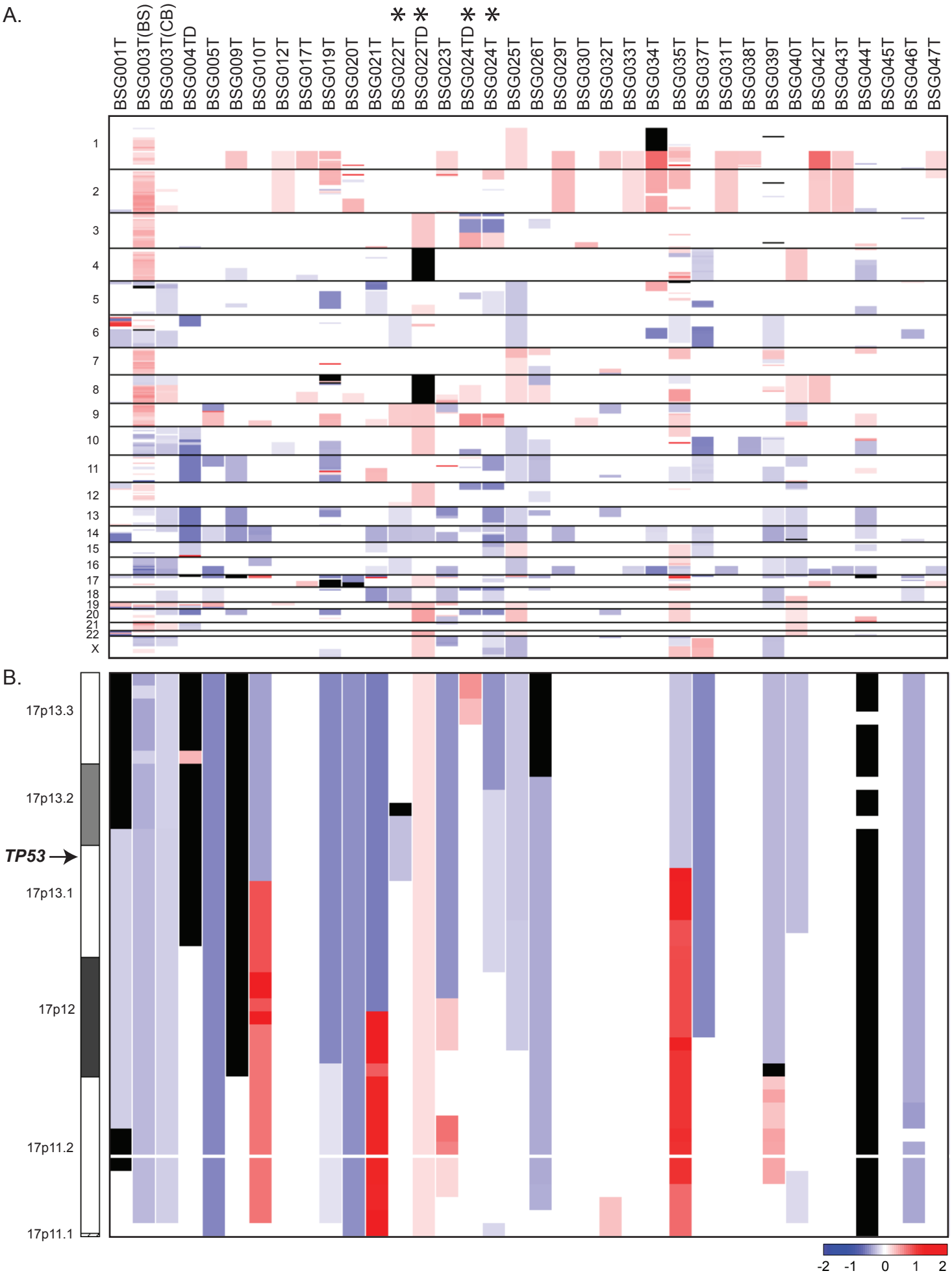
**Figure S1. The majority of LOH is associated with copy number losses**. A. Heat map showing copy number gains (red) and losses (blue), and copy neutral LOH (black) for (A) the whole genome, (B) chromosome 17p, from 36 DIPG compared with matched normal samples.
There are shared and distinct imbalances in paired samples from diagnostic and autopsy cases, indicated by asterisks. Diagnostic cases are designated "TD".

**Figure S2: Focal gains of BRAF are found in 7/8 exophytic low-grade brainstem gliomas, and none of 43 DIPGs**. Heat map of segmented copy number data showing chromosome 7. Specific focal gains of a region on chromosome 7q34 extending from *KIAA 1549* to *BRAF was only seen in LGGs. The genes contained in the specific region of focal gain shown by the boxed region on the chromosome ideogram are shown at the bottom of the figure.* Copy number gains (red) and losses (blue) are shown in 43 DIPG (BSG) and 8 low-grade exophytic brainstem gliomas (LGG-BSG).

**Figure S3: Focal gains of RTKs are associated with overexpression.** Maps of regions of gain and associated expression are shown for (A) PDGFRA, (B) MET and (C) IGF1R. The chromosome region containing focal amplifications, and the extent of amplification for each tumor is shown. The minimal common region of amplification is shown with a gray box, and genes within the minimal common region along with chromosomal position are shown below. Heatmap shows expression of all probes within the maximal region of amplification. The

minimal common region of amplification is shown with a gray bar in all panels. For the expression heatmap, expression of all genes within the maximum region of focal gain is shown for all tumors with available expression data. Genes contained in the common minimal region of gain are shaded in gray at the bottom of the heatmap. Tumors with focal gains identified by SNP analysis are labeled in red, tumors with scattered amplification identified only by FISH are labeled in purple, and tumors without evidence of copy number gain in this region are labeled in black. Overexpression of *PDGFRA* and *IGF1R* was seen in tumors with and without amplification. For *PDGFRA*, tumors with SNP-detected amplification showed 1.7-fold higher expression than tumors without amplification ($p=0.1$). For *IGF1R*, tumors with SNP-detected amplification showed 1.4-fold higher expression than tumors without amplification ($p=0.2$). *MET* overexpression was more specifically associated with amplification; tumors with SNP-detected amplification of *MET* showed 5.9-fold higher expression than tumors without amplification ($p=0.001$). (B) Tumor BSG001T contained a focal gain within a small region of *MET* that did not contain the probe sets used to detect *MET* expression. This very focal gain may indicate a genomic rearrangement of *MET* in this tumor.

Figure S1


A.
BSG001T
BSG003T(BS)
BSG003T(CB)
BSG004TD
BSG005T
BSG009T
BSG010T
BSG012T
BSG017T
BSG019T
BSG020T
BSG021T
BSG022T
BSG022TD
BSG023T
BSG024TD
BSG024T
BSG025T
BSG026T
BSG029T
BSG030T
BSG032T
BSG033T
BSG034T
BSG035T
BSG037T
BSG031T
BSG038T
BSG039T
BSG040T
BSG042T
BSG043T
BSG044T
BSG045T
BSG046T
BSG047T
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
B.
17p13.3
17p13.2
TP53
17p13.1
17p12
17p11.2
17p11.1
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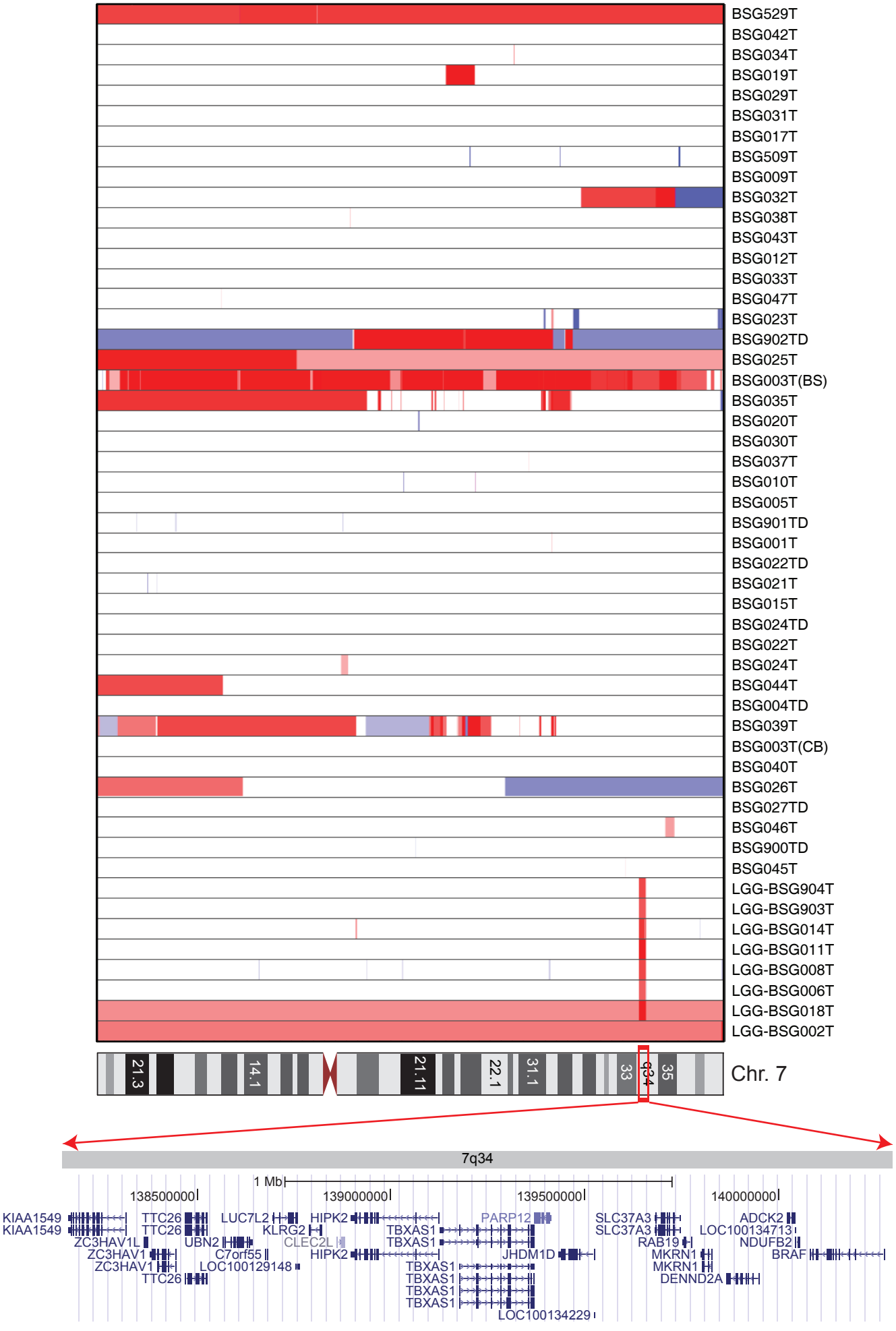
-1
0
1
2

Figure S2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BSG038T
BSG043T
BSG012T
BSG033T
BSG047T
BSG023T
BSG902TD
BSG025T
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BSG035T
BSG020T
BSG030T
BSG037T
BSG010T
BSG005T
BSG901TD
BSG001T
BSG022TD
BSG021T
BSG015T
BSG024TD
BSG022T
BSG024T
BSG044T
BSG004TD
BSG039T
BSG003T(CB)
BSG040T
BSG026T
BSG027TD
BSG046T
BSG900TD
BSG045T
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LGG-BSG018T
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21.11
22.1
31.1
33
q34
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Chr. 7
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KIAA1549
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TTC26
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KLRG2
HIPK2
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TBXAS1
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PARP12
JHDM1D
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SLC37A3
ADCK2
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UBN2
CLEC2L
RAB19
NDUFB2
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C7orf55
MKRN1
BRAF
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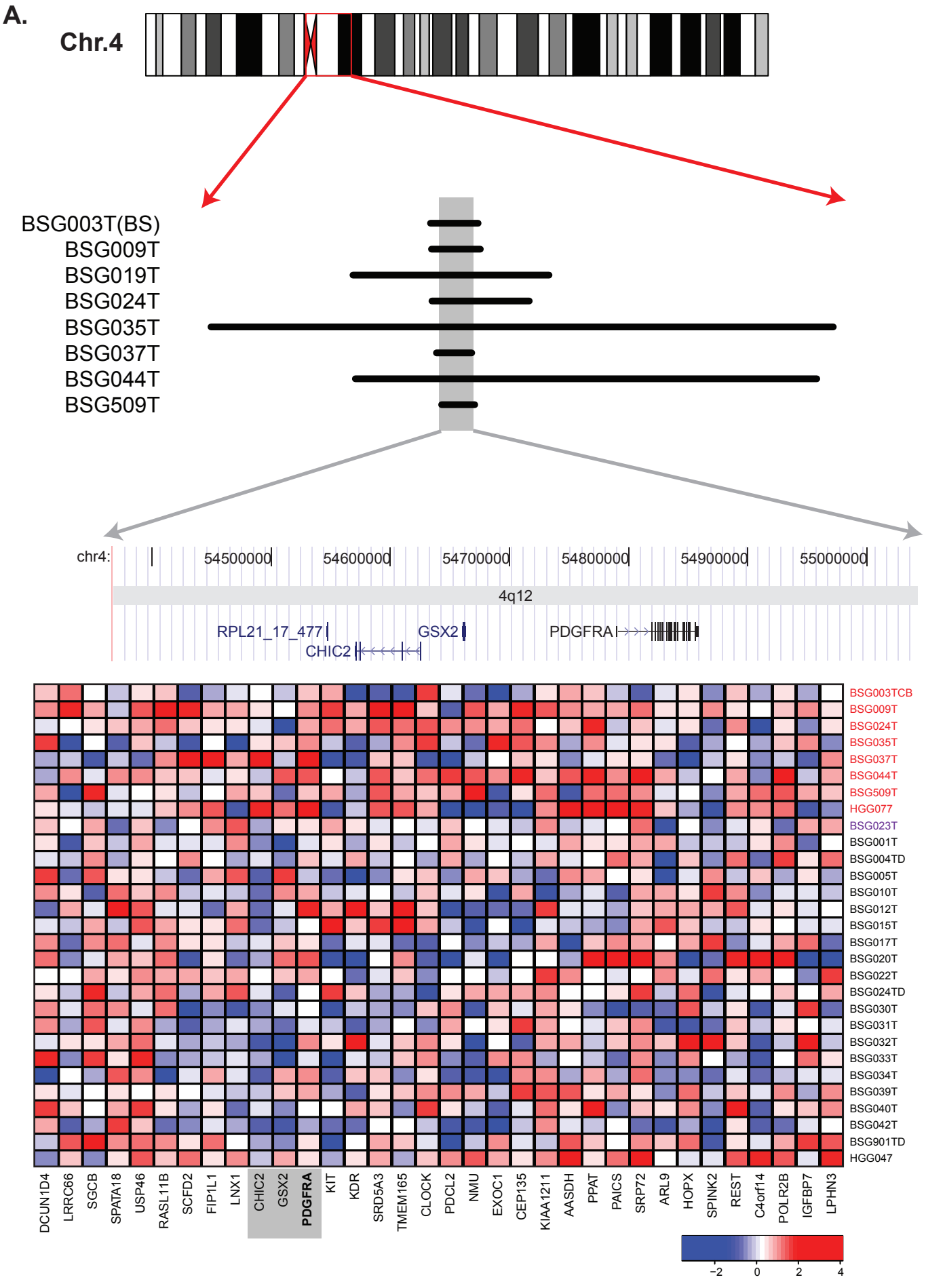
Figure S3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BSG024T
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BSG037T
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BSG509T
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54600000
54700000
54800000
54900000
55000000
4q12
RPL21_17_477
GSX2
PDGFRA
CHIC2
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BSG024T
BSG035T
BSG037T
BSG044T
BSG509T
HGG077
BSG023T
BSG001T
BSG004TD
BSG005T
BSG010T
BSG012T
BSG015T
BSG017T
BSG020T
BSG022T
BSG024TD
BSG030T
BSG031T
BSG032T
BSG033T
BSG034T
BSG039T
BSG040T
BSG042T
BSG901TD
HGG047
DCUN1D4
LRRC66
SGCB
SPATA18
USP46
RASL11B
SCFD2
FIP1L1
LNX1
CHIC2
GSX2
PDGFRA
KIT
KDR
SRD5A3
TMEM165
CLOCK
PDCL2
NMU
EXOC1
CEP135
KIAA1211
AASDH
PPAT
PAICS
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POLR2B
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LPHN3
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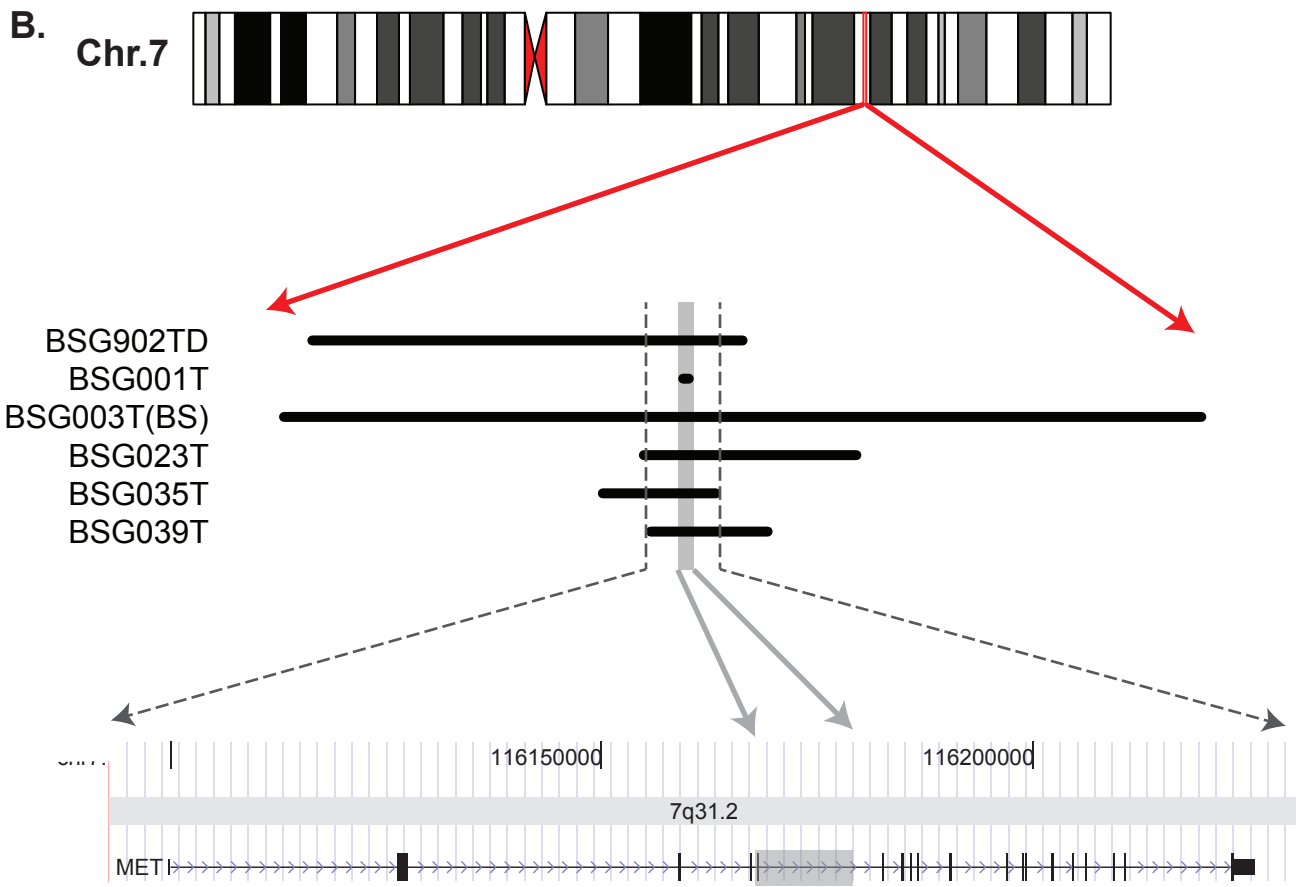
0
2
4


B.
Chr.7
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BSG003T(BS)
BSG023T
BSG035T
BSG039T
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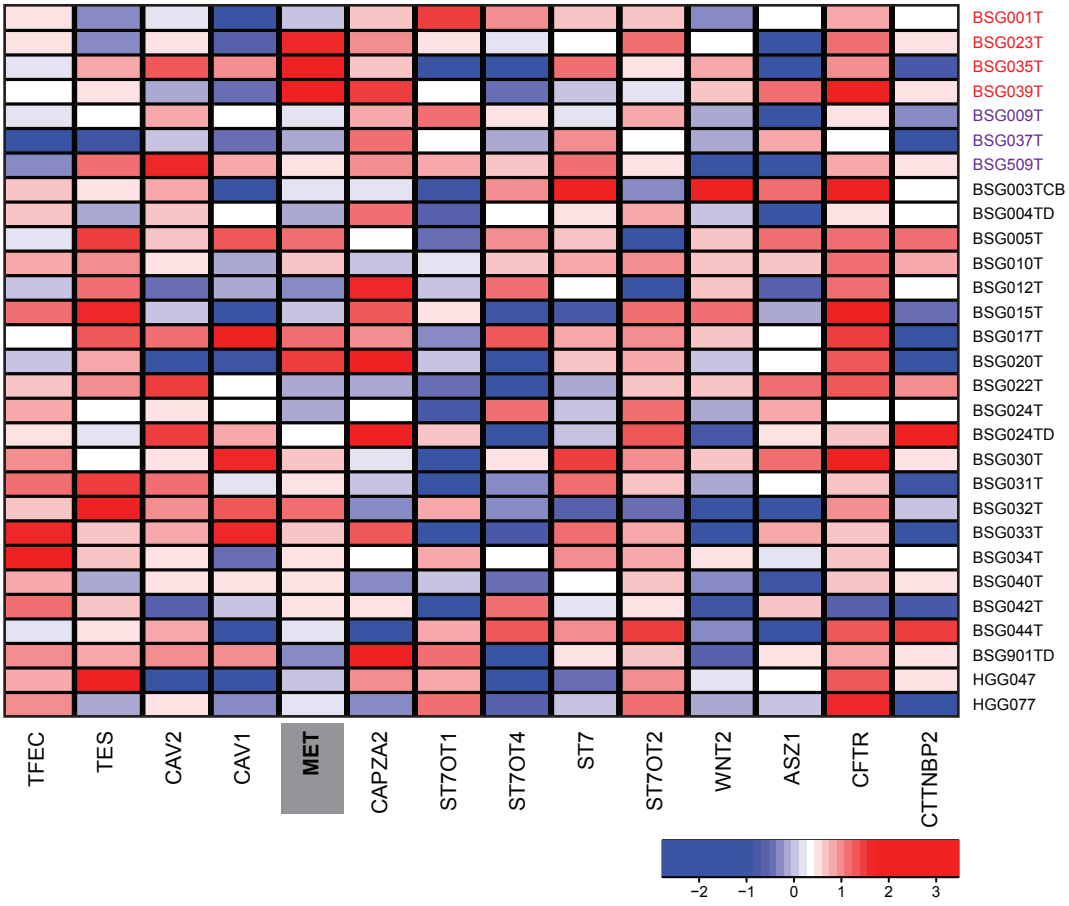
116200000
7q31.2
MET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BSG022T
BSG024T
BSG024TD
BSG030T
BSG031T
BSG032T
BSG033T
BSG034T
BSG040T
BSG042T
BSG044T
BSG901TD
HGG047
HGG077
TFEC
TES
CAV2
CAV1
MET
CAPZA2
ST7OT1
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ASZ1
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CTTNBP2
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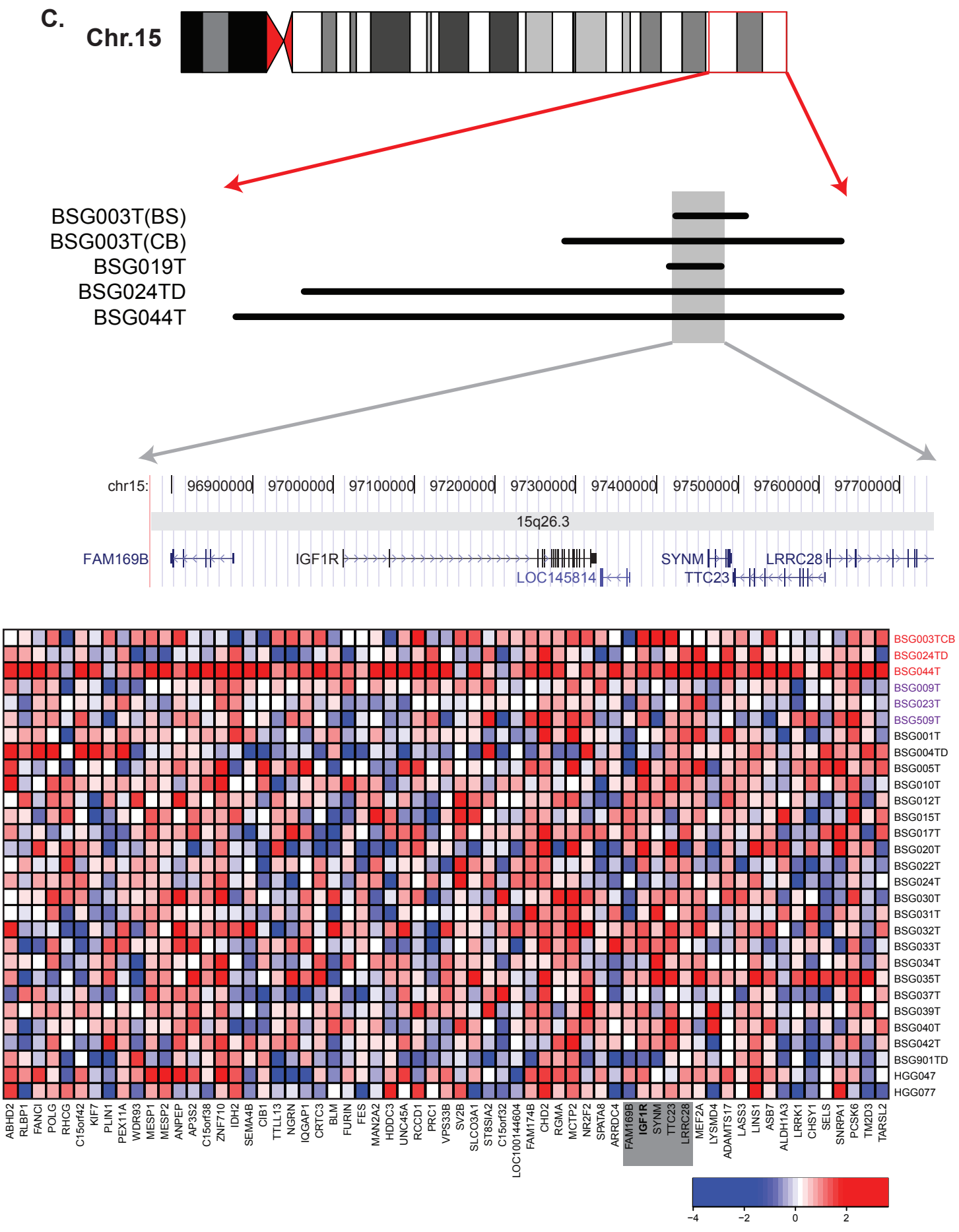
−1
0
1
2
3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BSG003T(CB)
BSG019T
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chr15:
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BSG023T
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BSG022T
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BSG032T
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BSG034T
BSG035T
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BSG039T
BSG040T
BSG042T
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HGG047
HGG077
ABHD2
RLBP1
FANCI
POLG
RHCG
C15orf42
KIF7
PLIN1
PEX11A
WDR93
MESP1
MESP2
ANPEP
AP3S2
C15orf38
ZNF710
IDH2
SEMA4B
CIB1
TTLL13
NGRN
IQGAP1
CRTC3
BLM
FURIN
FES
MAN2A2
HDDC3
UNC45A
RCCD1
PRC1
VPS33B
SV2B
SLCO3A1
ST8SIA2
C15orf32
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FAM174B
CHD2
RGMA
MCTP2
NR2F2
SPATA8
ARRDC4
FAM169B
IGF1R
SYNM
TTC23
LRRC28
MEF2A
LYSMD4
ADAMTS17
LASS3
LINS1
ASB7
ALDH1A3
LRRK1
CHSY1
SELS
SNRPA1
PCSK6
TM2D3
TARSL2
−4
−2
0
2