Supplementary information for

Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas

Jinghui Zhang[1], Gang Wu[1], Claudia P. Miller[2], Ruth G. Tatevossian[3], James D. Dalton[3], Bo Tang[3], Wilda Orisme[3], Chandanamali Punchihewa[3], Matthew Parker[1], Ibrahim Qaddoumi[4], Fredrick A. Boop[5], Charles Lu[6], Cyriac Kandoth[6], Li Ding[7], Ryan Lee[3], Robert Huether[1], Xiang Chen[1], Erin Hedlund[1], Panduka Nagahawatte[1], Michael Rusch[1], Kristy Boggs[8], Jinjun Cheng[3], Jared Becksfort[1], Jing Ma[3], Guangchun Song[3], Yongjin Li[1], Lei Wei[3], Jianmin Wang[9], Sheila Shurtleff[3], John Easton[8], David Zhao[1], Robert S. Fulton[6], Lucinda L. Fulton[6], David J. Dooling[6], Bhavin Vadodaria[8], Heather L. Mulder[8], Chunlao Tang[1], Kerri Ochoa[6], Charles G. Mullighan[3], Amar Gajjar[4], Richard Kriwacki[10], Denise Sheer[11], Richard J. Gilbertson[2], Elaine R. Mardis[6], Richard K. Wilson[6], James R. Downing[3], Suzanne J. Baker[2], David W. Ellison[3]; for the St. Jude Children's Research Hospital – Washington University Pediatric Cancer Genome Project.

1. Department of Computational Biology, St. Jude Children's Research Hospital, Memphis, TN 38105, USA
2. Department of Developmental Neurobiology, St. Jude Children's Research Hospital, Memphis, TN 38105, USA
3. Department of Pathology, St. Jude Children's Research Hospital, Memphis, TN 38105, USA
4. Department of Oncology, St. Jude Children's Research Hospital, Memphis, TN 38105, USA
5. Department of Surgery, St. Jude Children's Research Hospital, Memphis, TN 38105, USA

6. The Genome Institute, Washington University School of Medicine, St Louis, MO 63108, USA
7. Department of Genetics, Washington University School of Medicine, St Louis, MO 63108, USA
8. Pediatric Cancer Genome Project Laboratory, St. Jude Children's Research Hospital, Memphis, TN 38105, USA
9. Hartwell Center for Biotechnology & Bioinformatics, St. Jude Children's Research Hospital, Memphis, TN 38105, USA
10. Department of Structural Biology, St. Jude Children’s Research Hospital, Memphis, TN 38105, USA
11. Queen Mary University of London Centre for Neuroscience and Trauma, The Blizard Institute, Barts and the London School of Medicine and Dentistry, London E1 2AT, UK

Corresponding author – Dr. David Ellison MD PhD, Dept. of Pathology, St. Jude Children's Research Hospital, 262 Danny Thomas Place, Memphis, TN 38105, USA.
tel: 001-901-595-5438; fax: 001-901-595-3100
e-mail: david.ellison@stjude.org

TABLE OF CONTENTS

Supplementary Figures

Supplementary Figure 1. Study patient cohort

Three series of tumor samples made up the study cohort of 151 tumors from 149 patients. A discovery series of 39 tumors analyzed by whole genome sequencing (WGS) and 46 tumors analyzed by mRNA-seq (27 also studied by WGS) comprised Series 1. Series 2 consisted of 84 tumor samples representative of the entire disease, in which the frequency of non-silent somatic alterations detected by WGS was tested. Series 3 consisted of 28 non-cerebellar tumors without matching germline DNA samples.

Series 1: Next Generation Sequencing

*Whole Genome Sequencing (WGS) – 39 tumors from 38 patients**
Pilocytic or pilomyxoid astrocytomas = 26, diffuse gliomas = 10(9)*, PXA or glioneuronal tumors = 3

mRNA-seq – 46 tumors from 44 patients§ (27 also with WGS)
Pilocytic or pilomyxoid astrocytomas = 16, diffuse gliomas = 27(25)§, PXA or glioneuronal tumors = 3

Total (WGS ± mRNA-seq or mRNA-seq only) – 58 tumors from 56 patients§
Pilocytic or pilomyxoid astrocytomas = 27, diffuse gliomas = 27(25)§, PXA or glioneuronal tumors = 4

Tumor resection at diagnosis and at relapse for one* or two§ patients

PXA = pleomorphic xanthoastrocytoma; PA = pilocytic astrocytoma; PMA = pilomyxoid astrocytoma

Series 2: 84 tumors from 83 patients, including 13 tumors from series 1, analyzed by high throughput sequencing, iFISH and RT-PCR to evaluate frequency of non-silent somatic aberrations detected by WGS

PAs / PMAs =54, diffuse gliomas =18, PXAs / GNTs =12

Series 3: 22 non-cerebellar tumors from 22 patients analyzed by iFISH and RT-PCR and included to augment those tumor types in which novel genetic aberrations were being detected by WGS

PAs / PMAs =12, diffuse gliomas =4, PXAs / GNTs =6

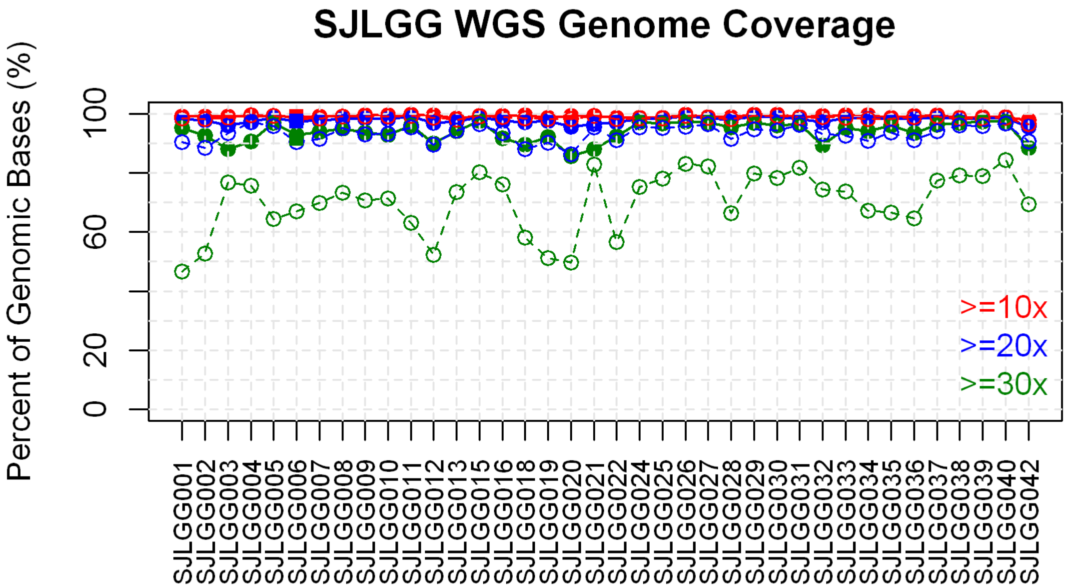
PXA = pleomorphic xanthoastrocytoma; PA = pilocytic astrocytoma; PMA = pilomyxoid astrocytoma; GNT = glioneuronal tumor

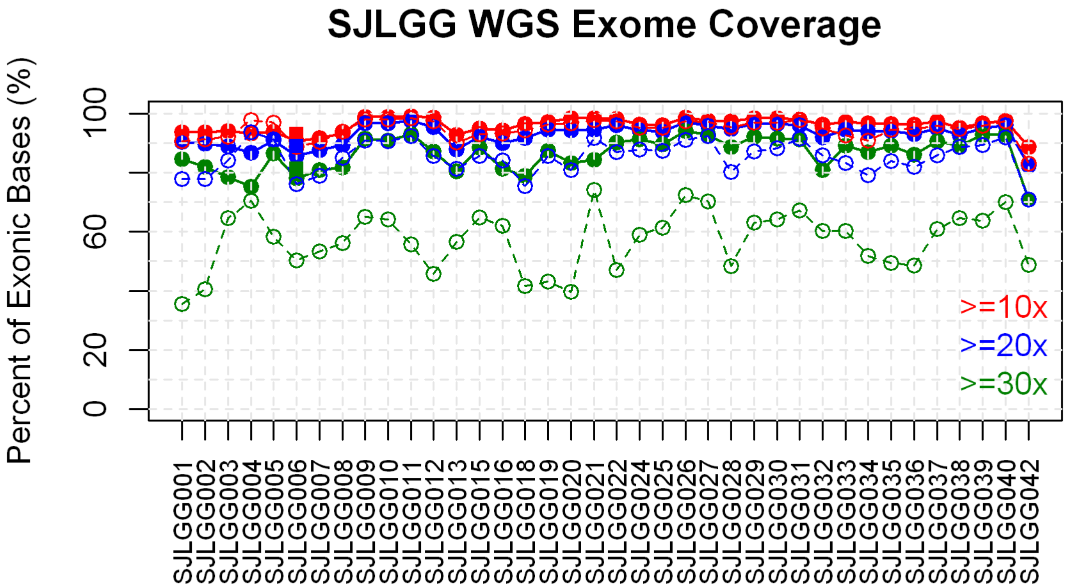
Clinicopathological characteristics of study cohort patients

	Number of patients	Mean age at surgery: years (range)	Male:Female	Cerebral cortex	Diencephalon	Cerebellum	Brain stem	Spinal cord
Pilocytic / pilomyxoid astrocytoma	92	7.7 (0.5 - 18)	45:47	10	29	38	10	5
Diffuse glioma	36	7.2 (1 - 15)	22:14	34	2	0	0	0
Glioneuronal tumor / PXA	21	10.3 (0.4 - 17)	5:16	18	0	1	2	0
Total	149							

Supplementary Figure 2. Sequence Coverage

Percentage of whole genome (top) and whole exome (bottom) covered by high-quality re
10x, 20x and 30x for each of 38 WGS tumor / germline sample pairs in the discovery set.
Diagnostic tumor samples (solid circle), relapse tumor sample (solid square) and germlin
samples (open circle).



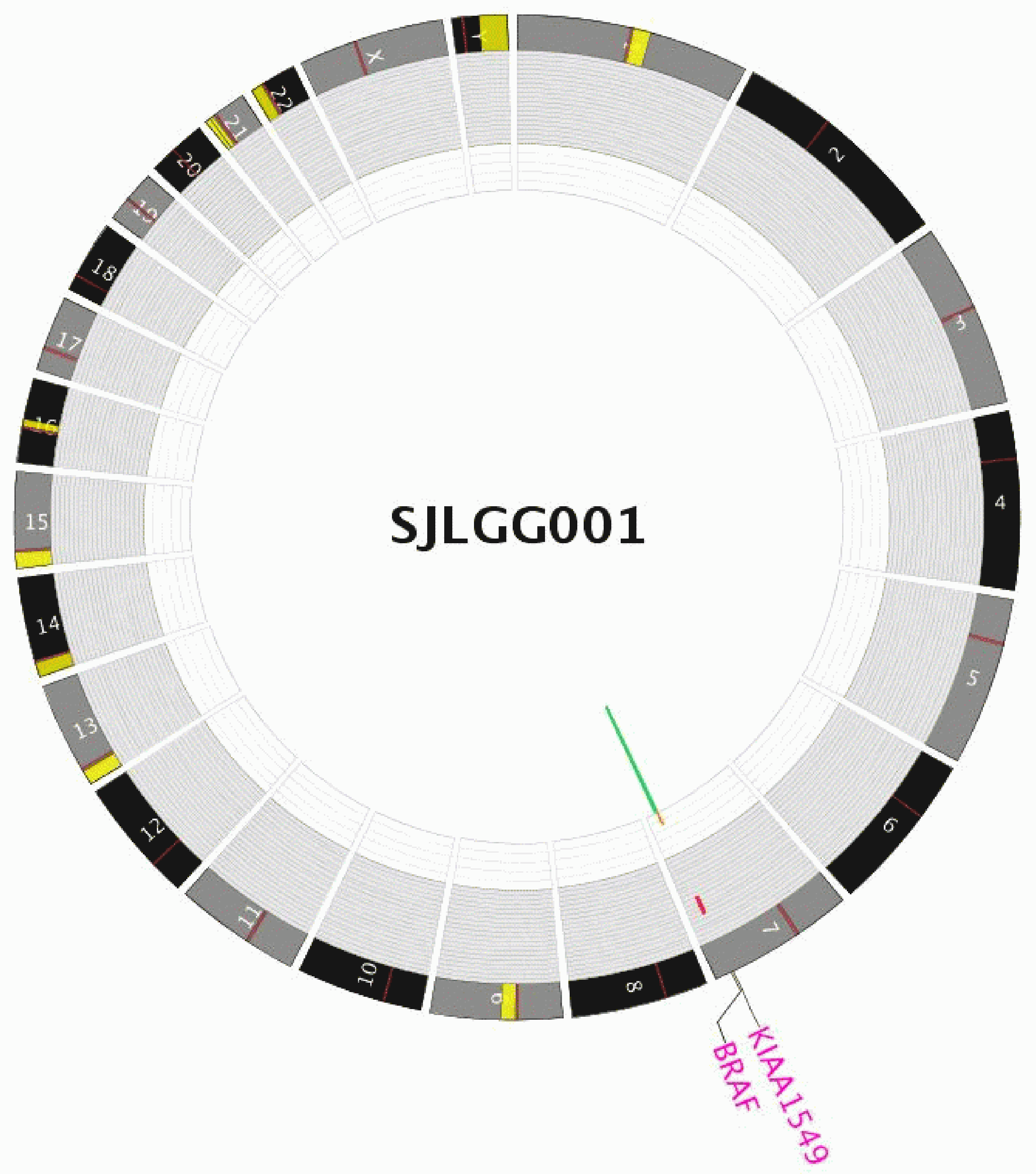


WGS = whole genome sequencing

Supplementary Figure 3. CIRCOS plots of 39 tumors analyzed by WGS

CIRCOS plots depict structural genetic variants, including DNA copy number alterations, intra- chromosomal and inter-chromosomal translocations, and mutations.

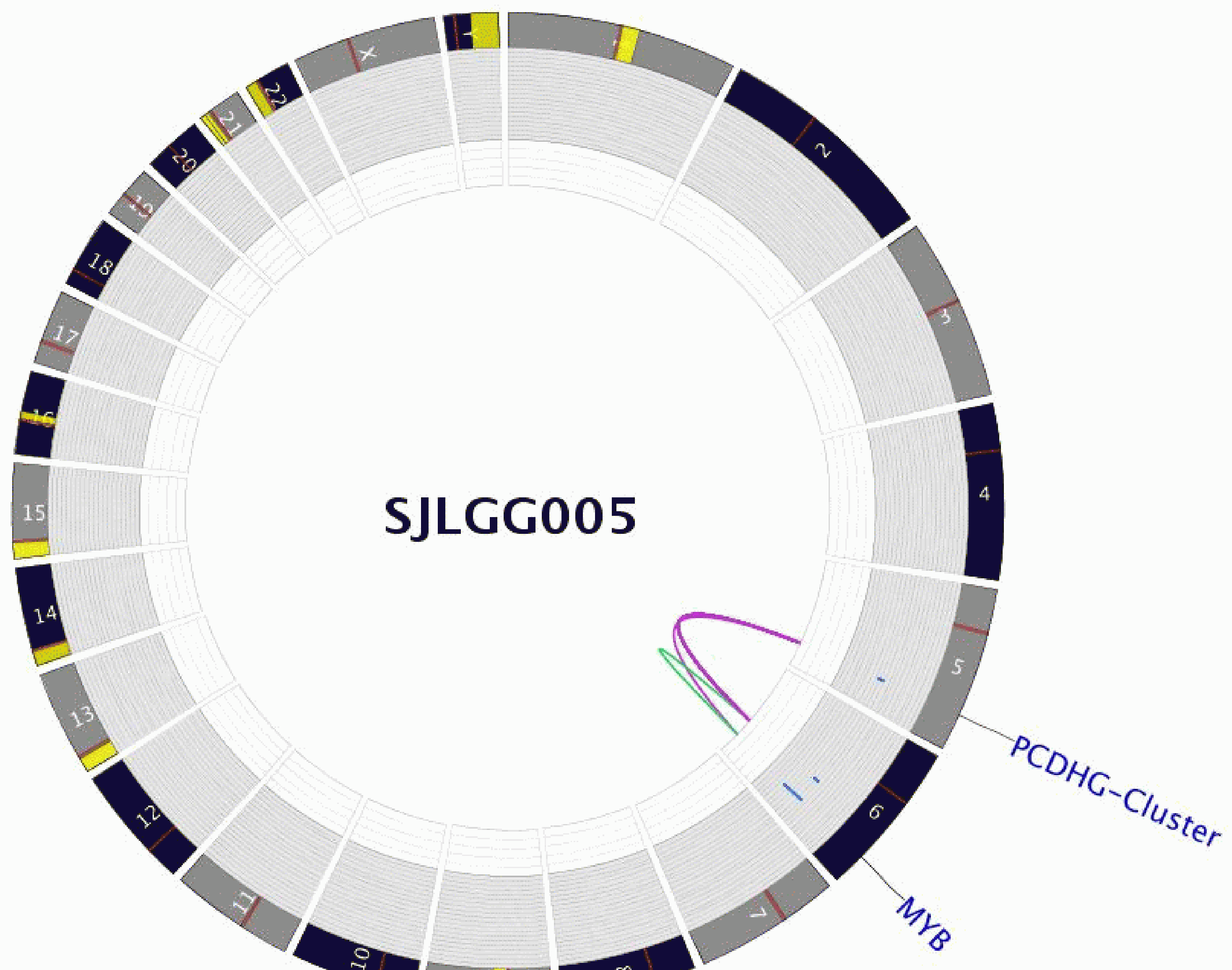
Loss of heterozygosity – orange; amplification – red; deletion – blue
Sequence mutations in RefSeq genes: missense SNVs – brown; indels – red; splice site SNVs – blue
Genes at SV breakpoints: genes involved in in-frame fusions – pink; others – blue.

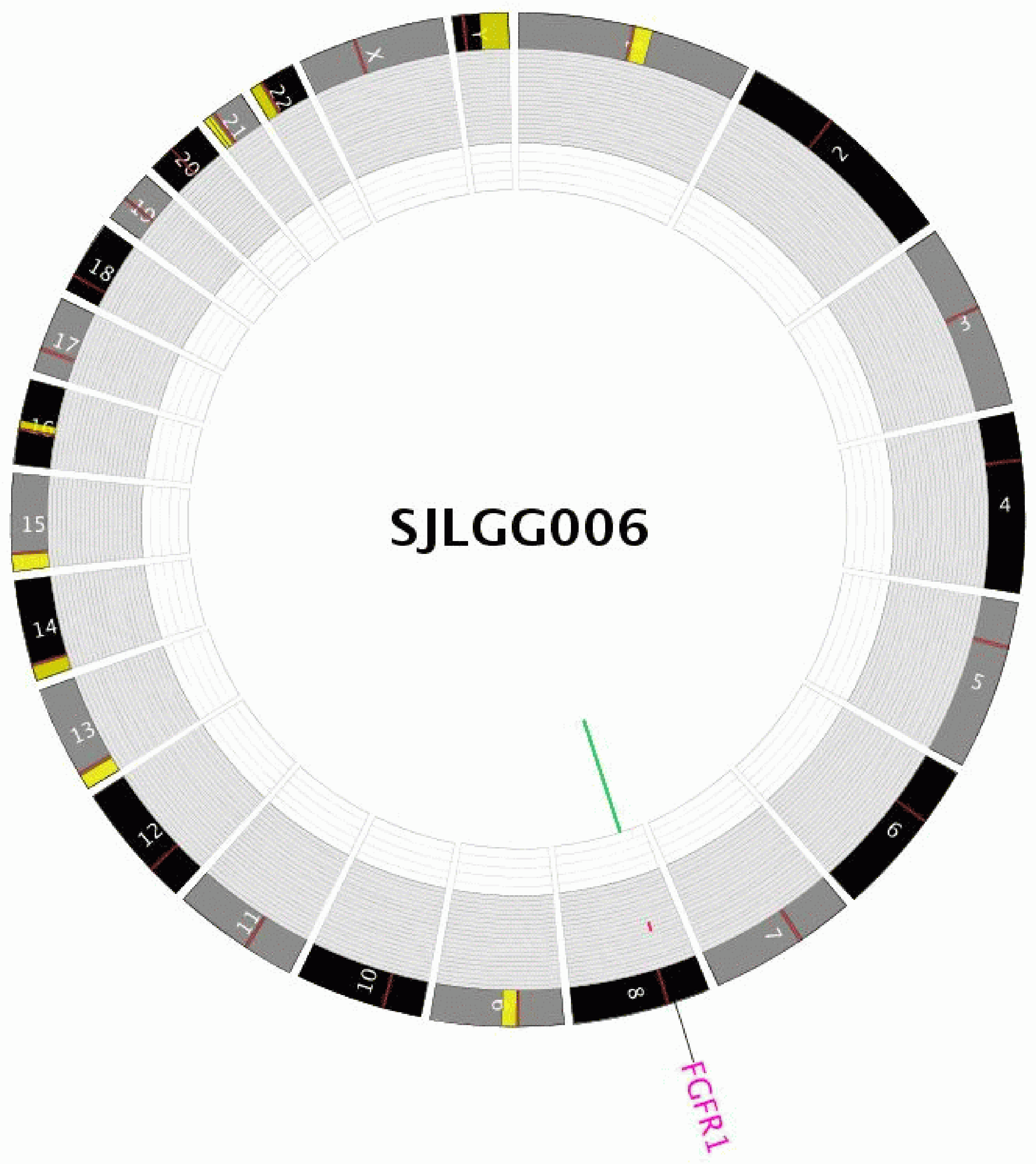

SJLGG001
KIAA1549
BRAF


SJLGG002
KIAA1549
BRAF

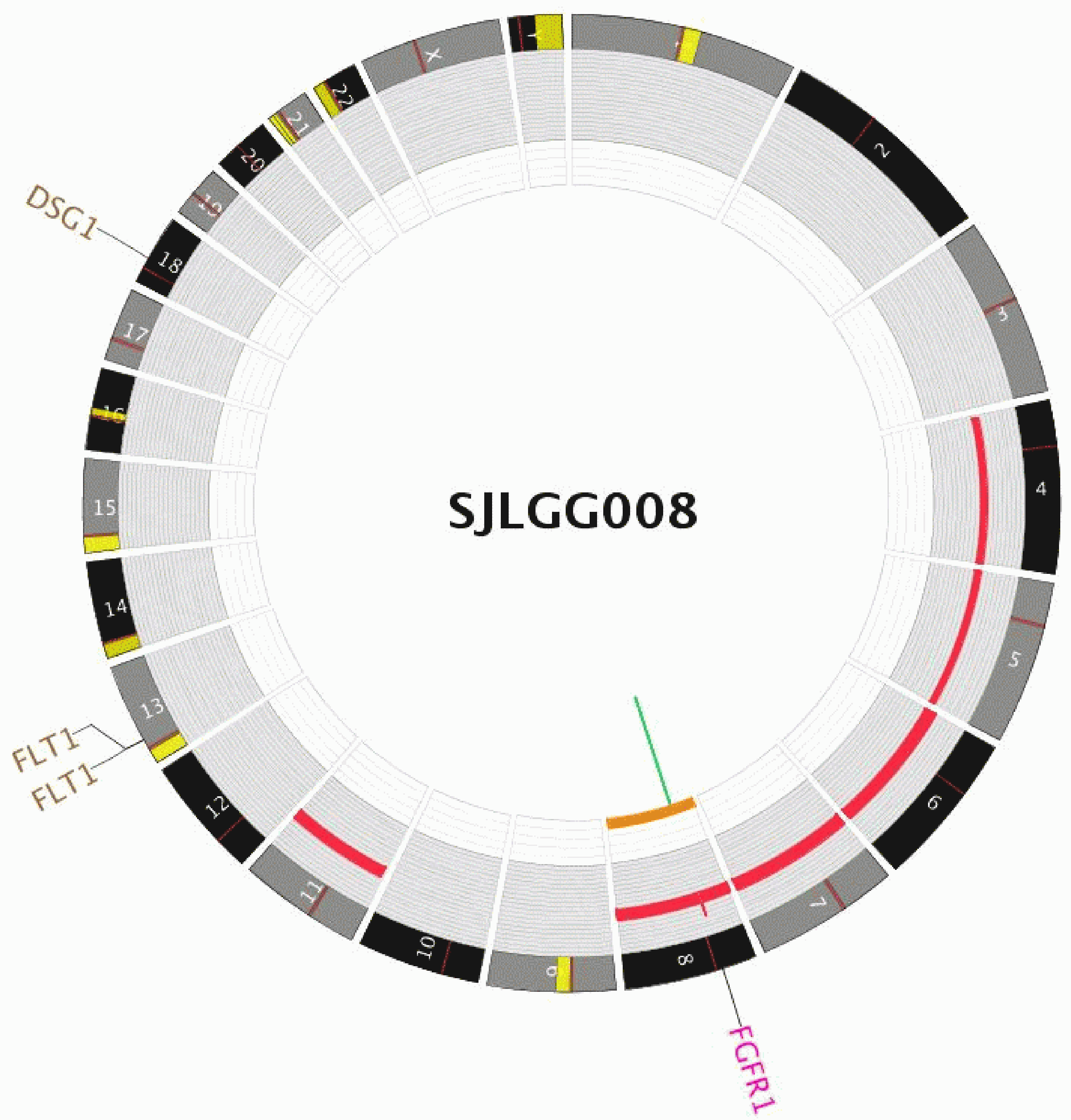

SJLGG003
KIAA1549
BRAF

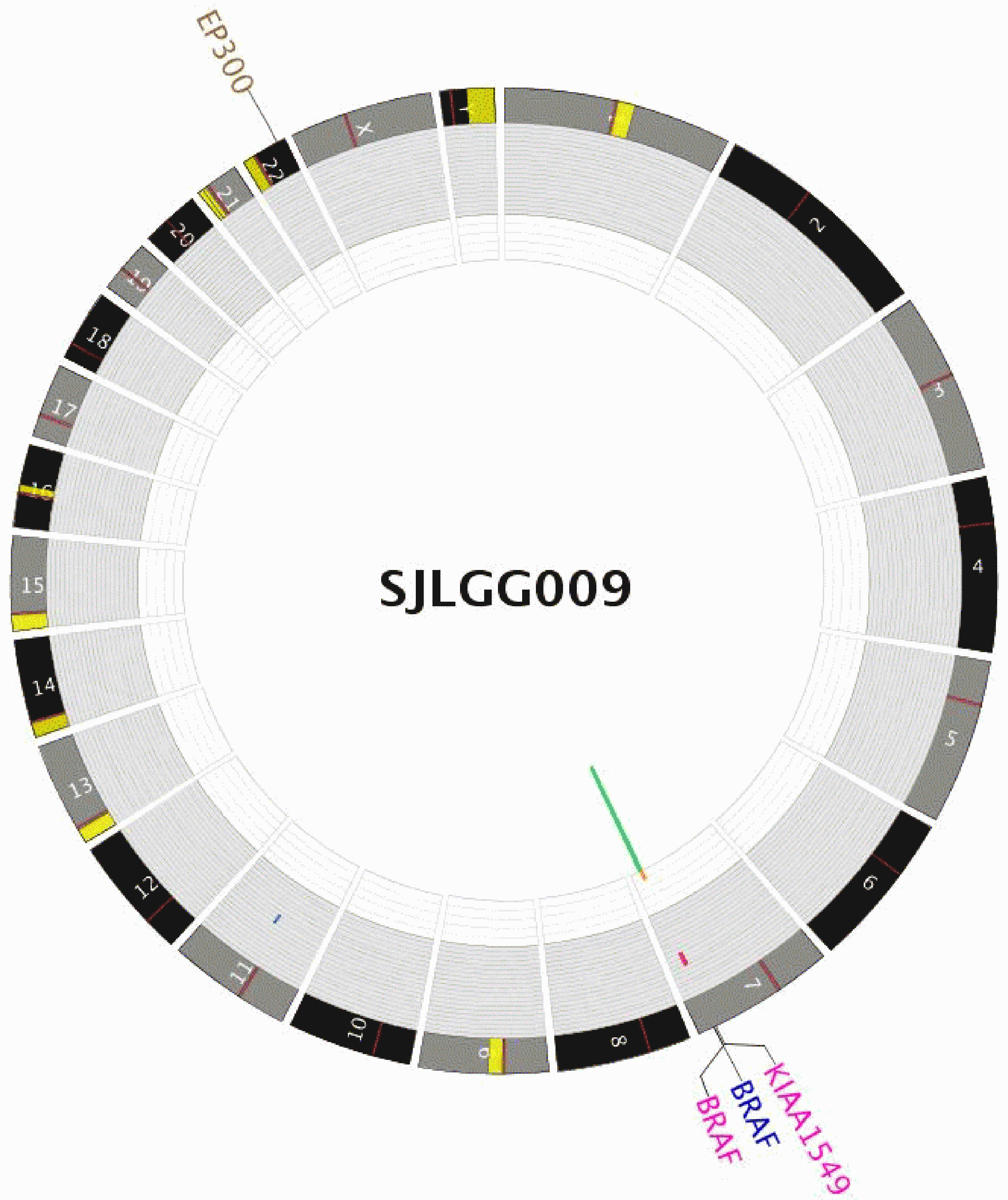

SJLGG004
NEURL4
KIAA1549
BRAF

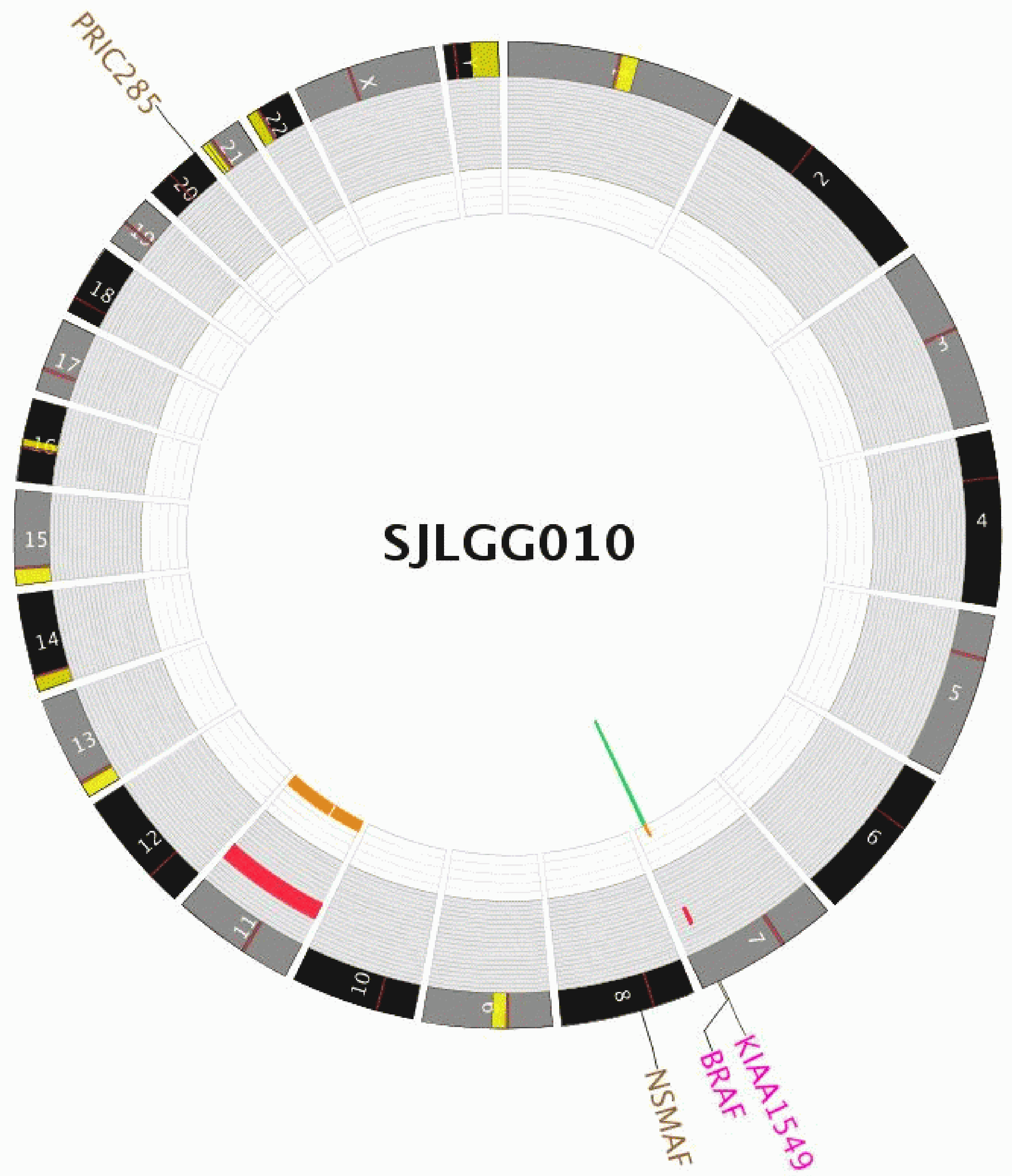

SJLGG005
PCDHG-Cluster
MYB


SJLGG006
FGFR1


SJLGG007
KIAA1549
BRAF

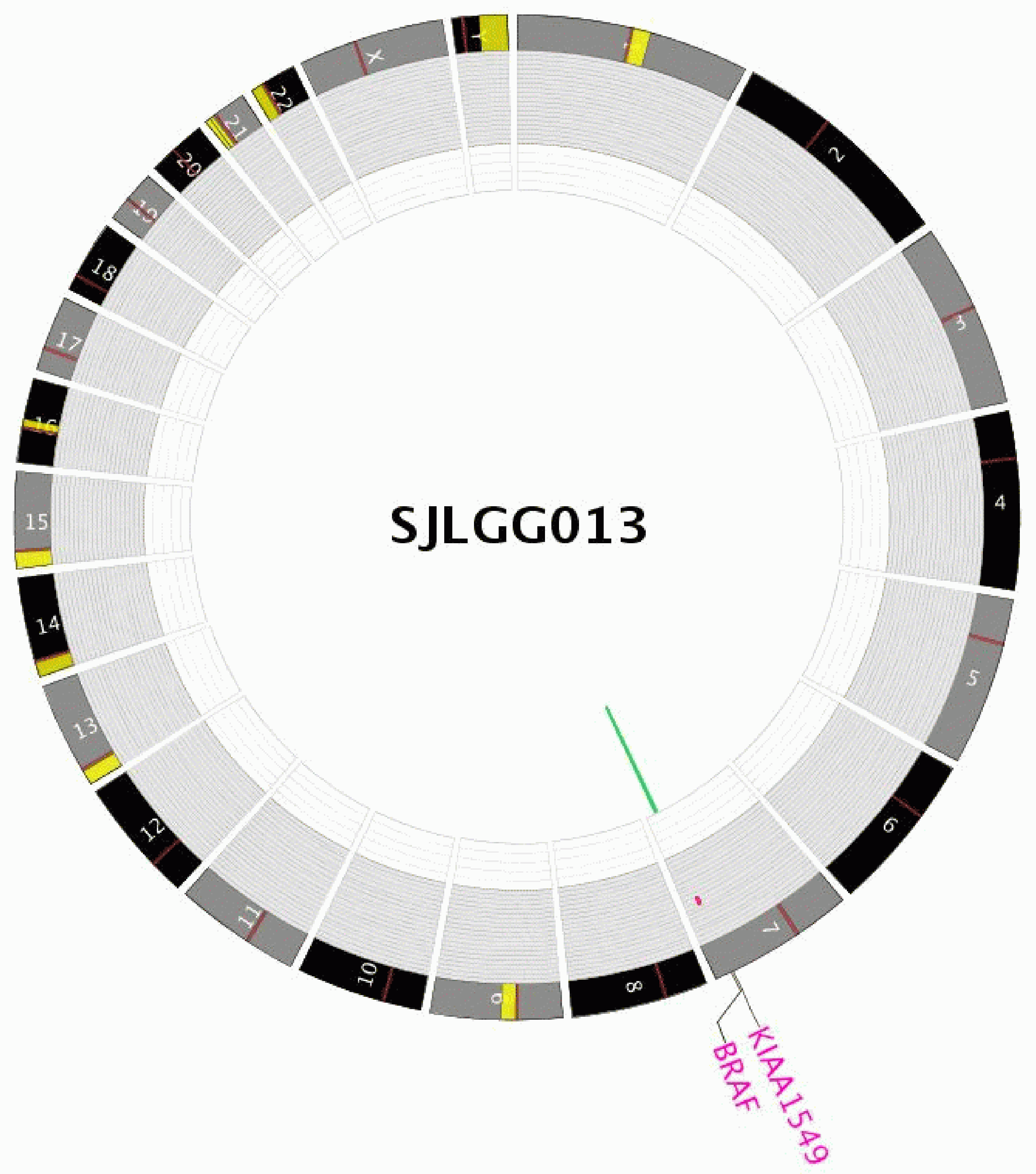

SJLGG008
DSG1
FLT1
FLT1
FGFR1

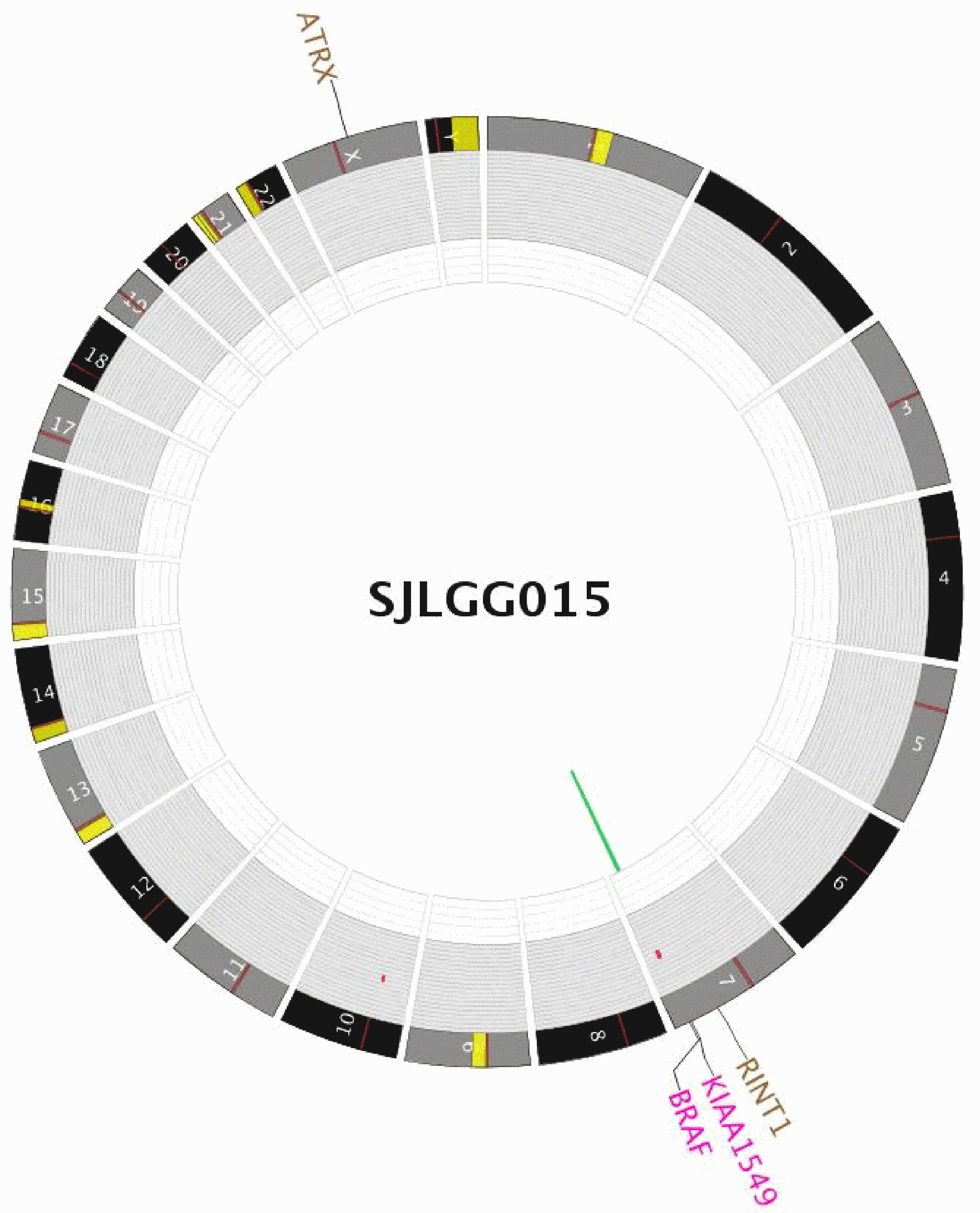

EP300
SJLGG009
KIAA1549
BRAF
BRAF

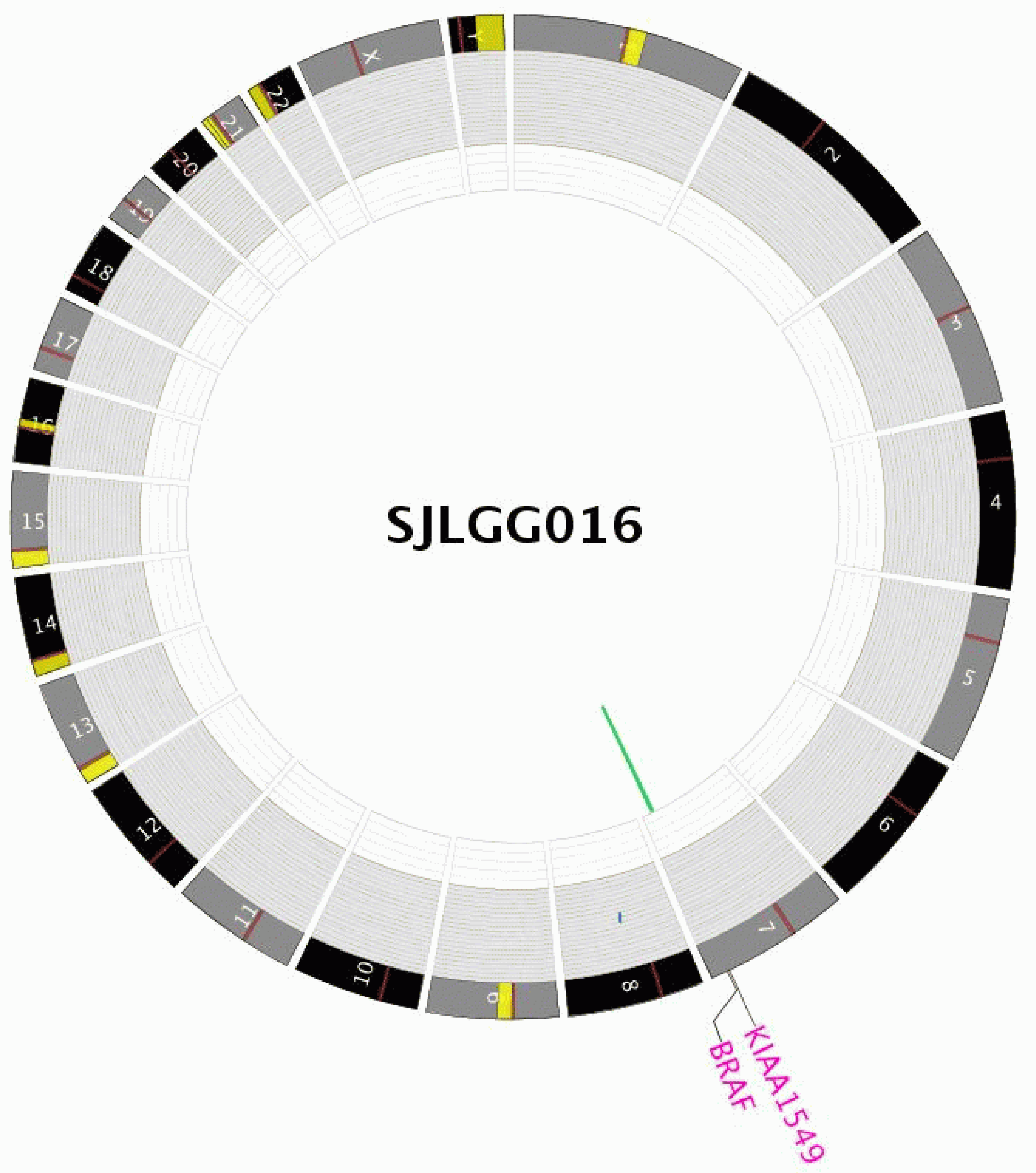

PRIC285
SJLGG010
NSMAF
BRAF
KIAA1549

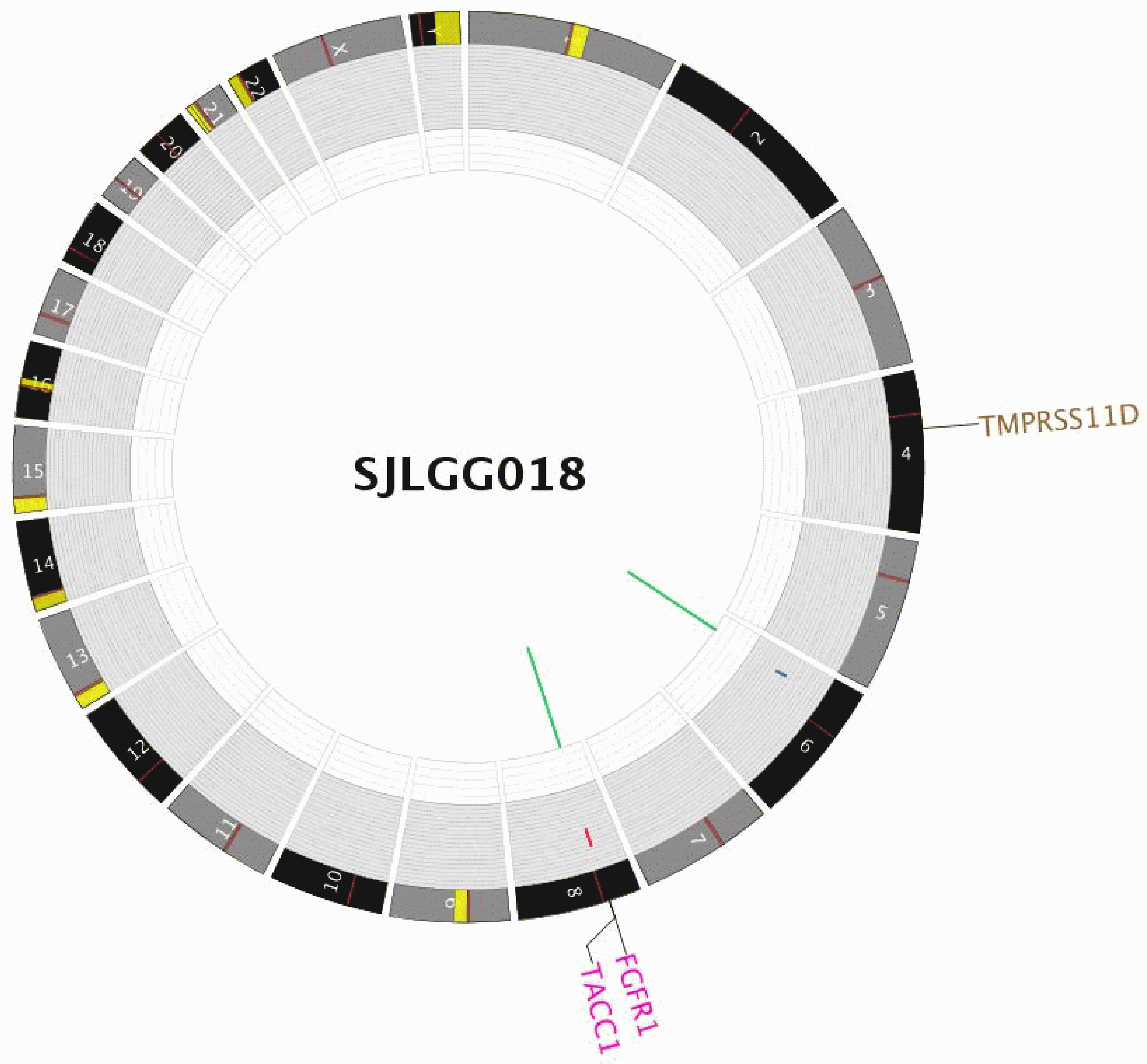

SJLGG011
KIAA1549
BRAF

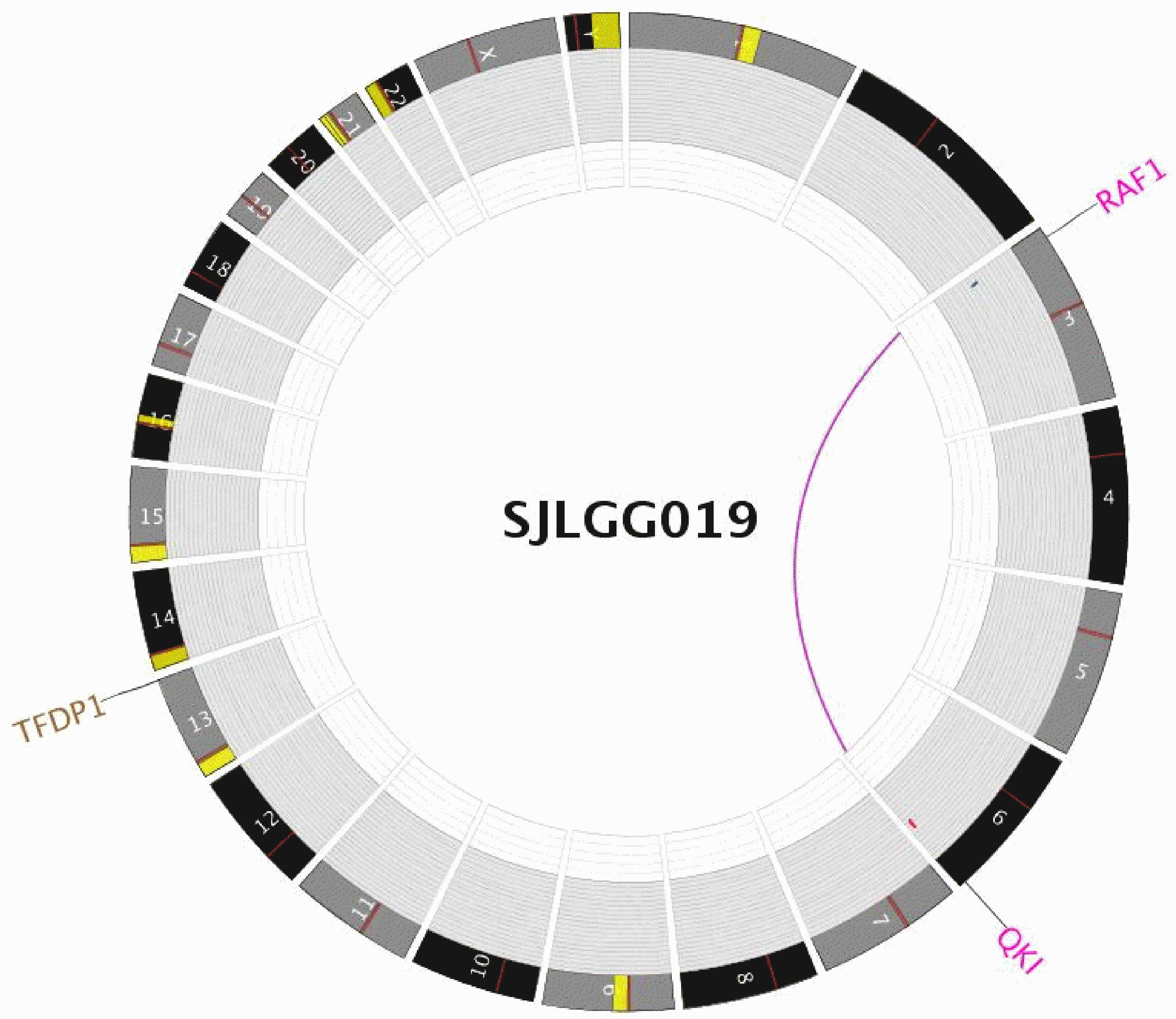

KIAA1239
SJLGG012
KIAA1549
BRAF


SJLGG013
KIAA1549
BRAF

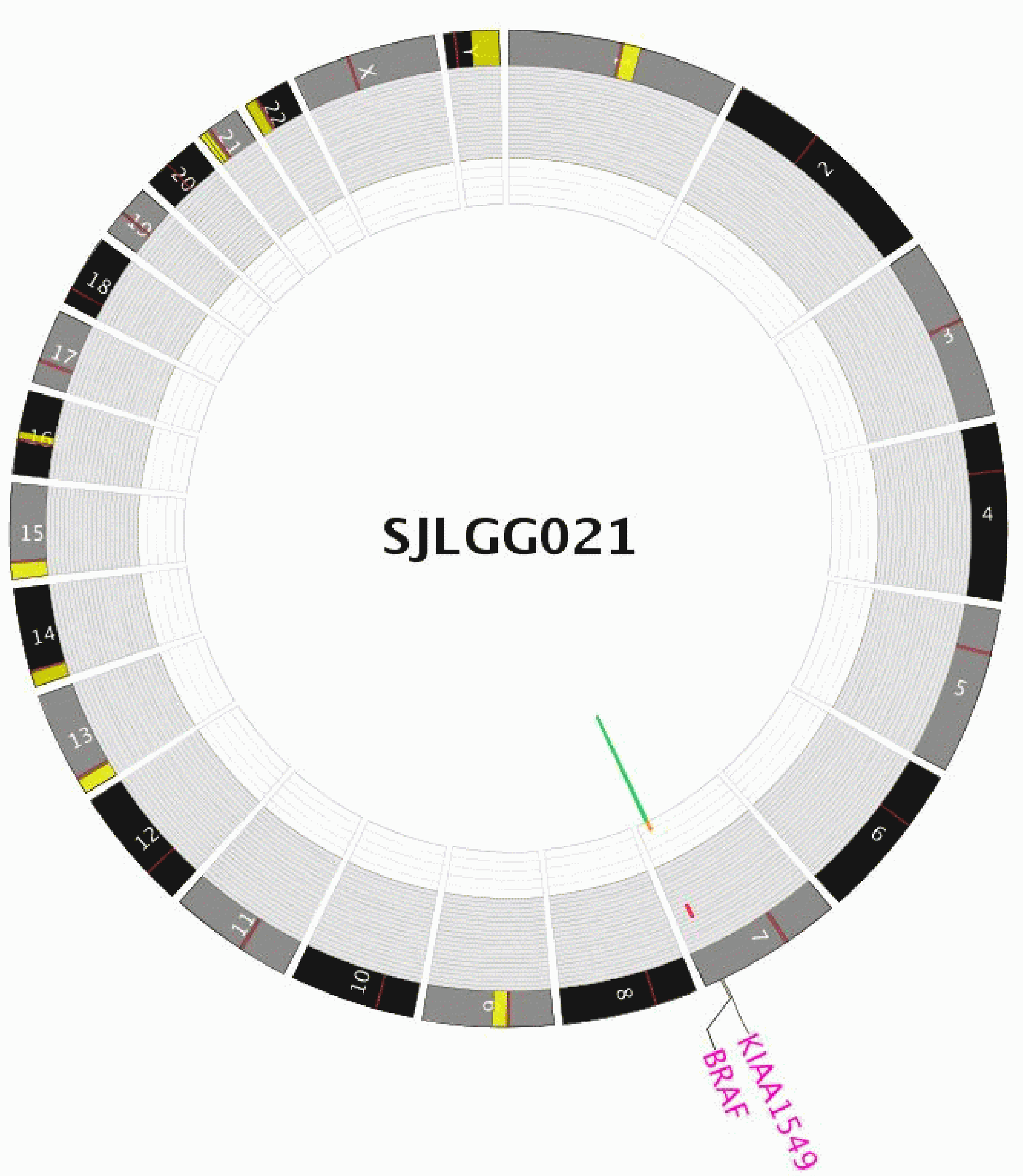

ATRX
SJLGG015
RINT1
KIAA1549
BRAF

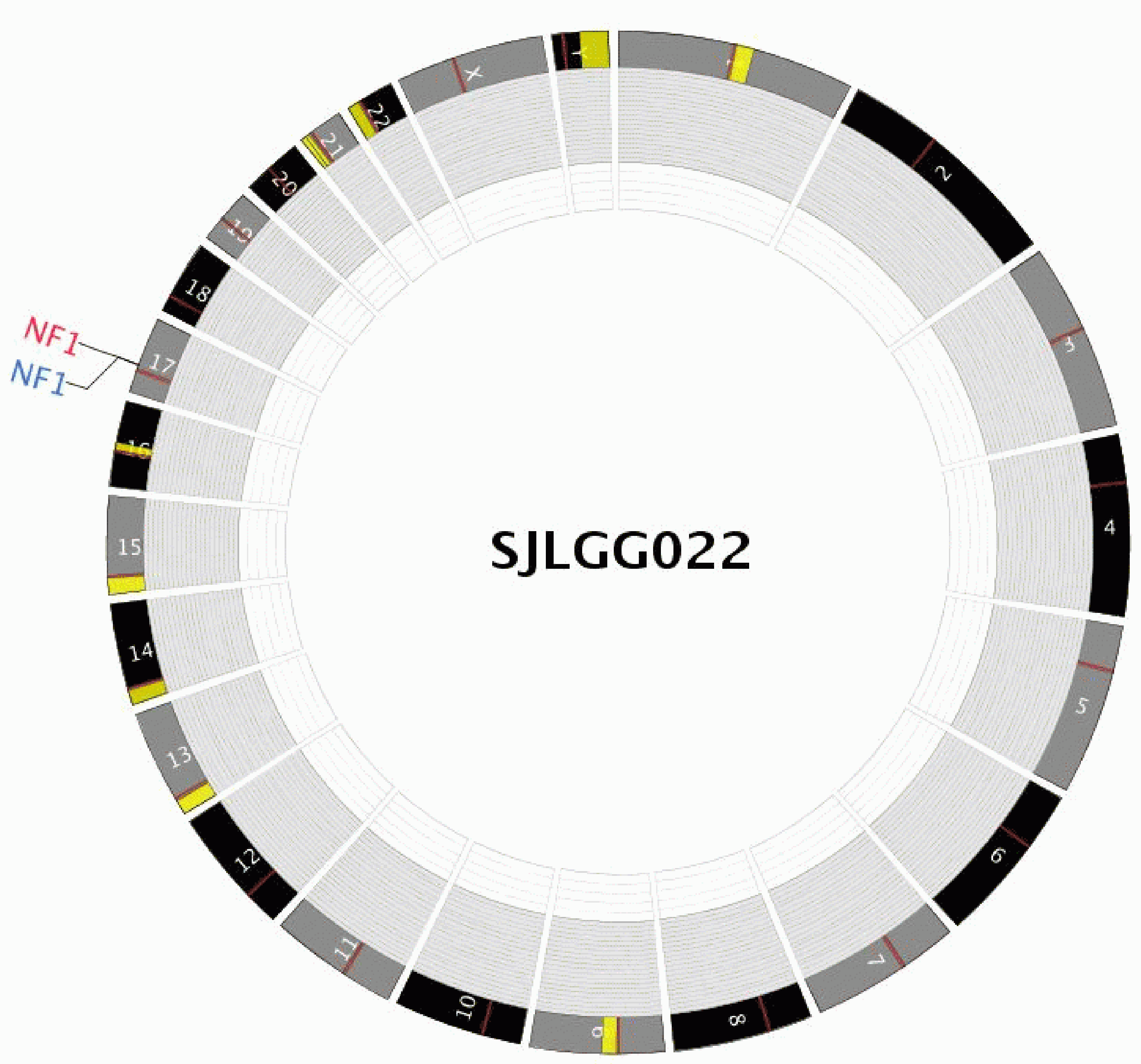

SJLGG016
KIAA1549
BRAF

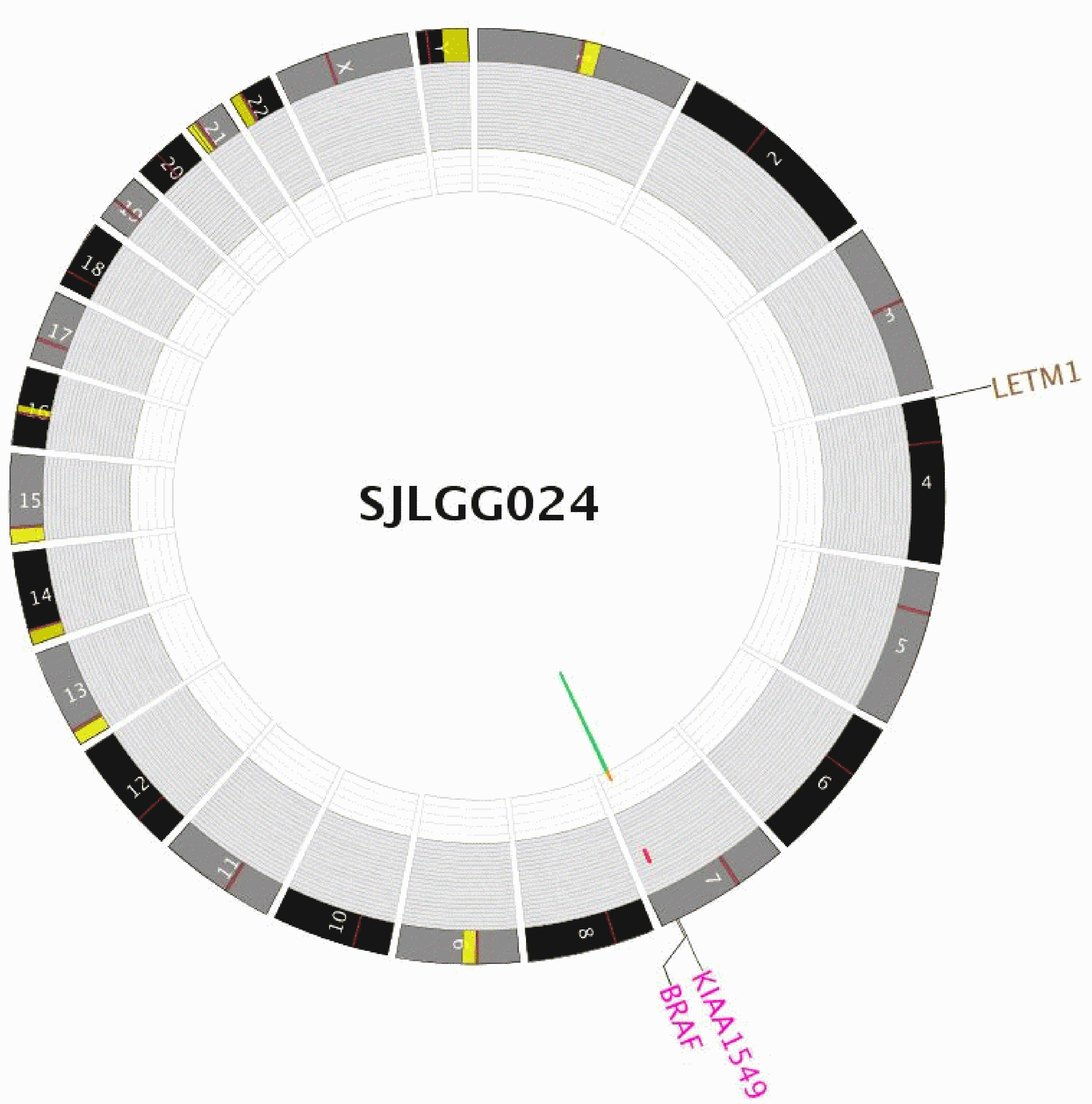

TMPRSS11D
SJLGG018
FGFR1
TACC1

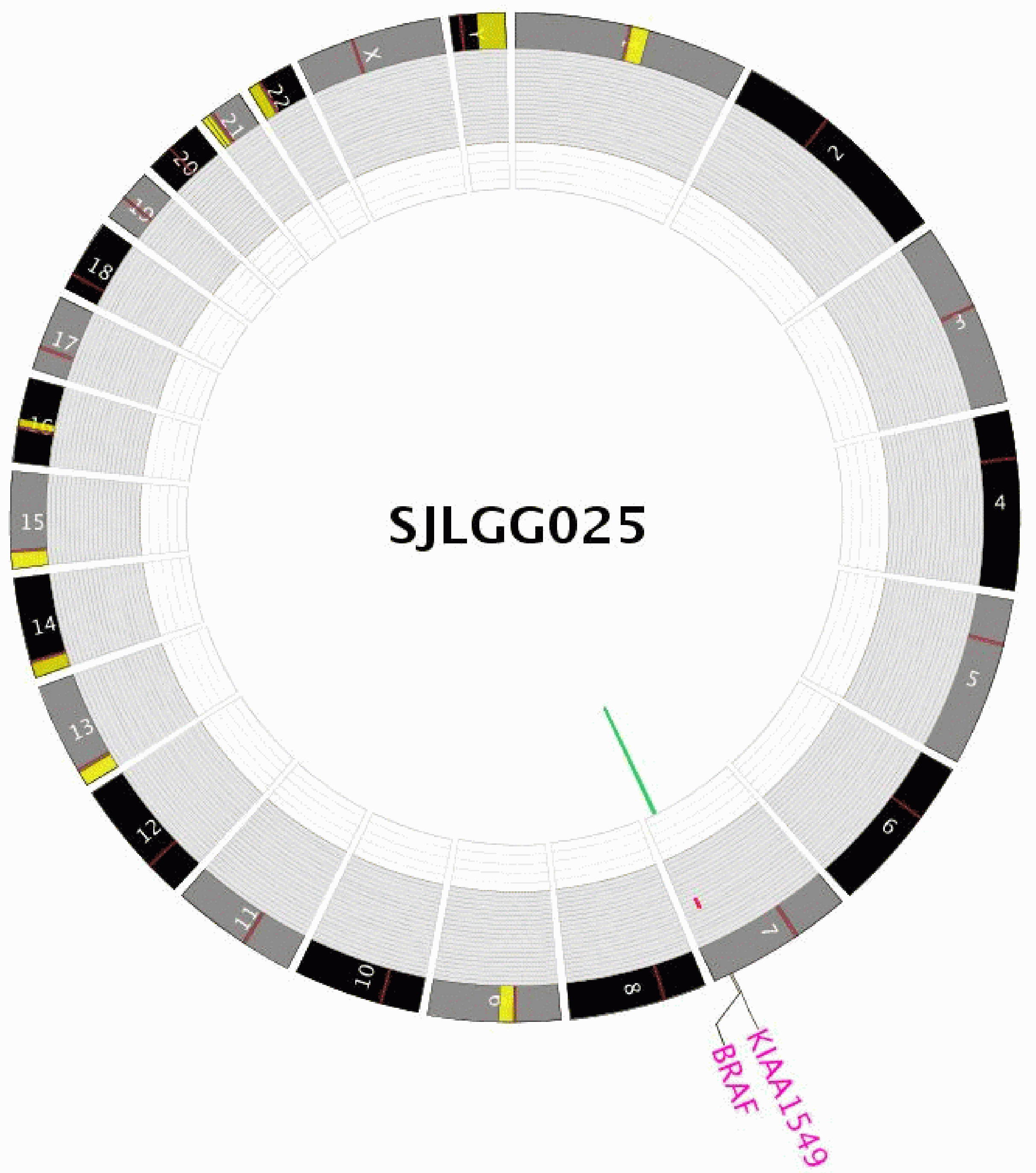

RAF1
SJLGG019
TFDP1
QKI

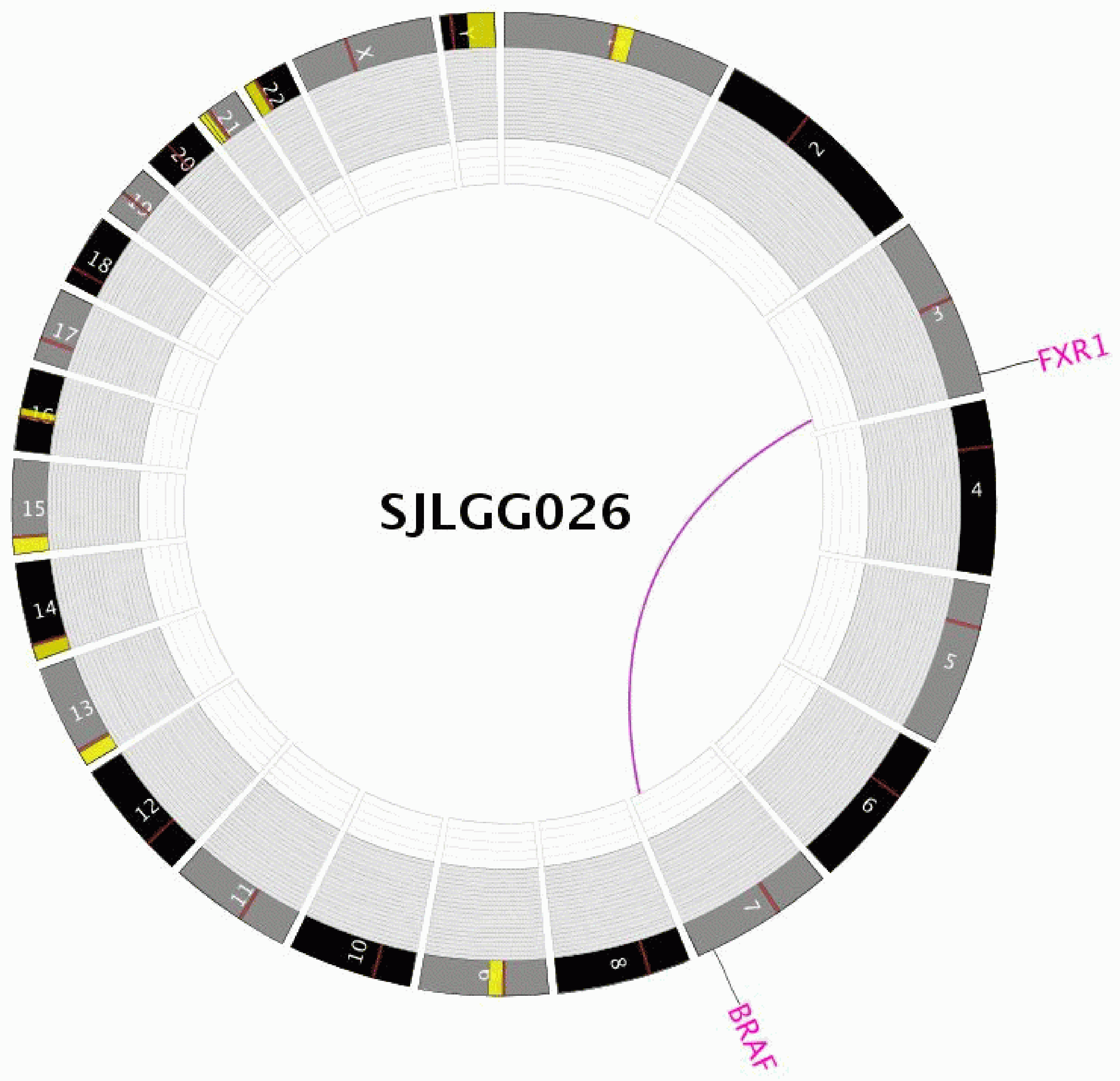

SJLGG020
KIAA1549
BRAF

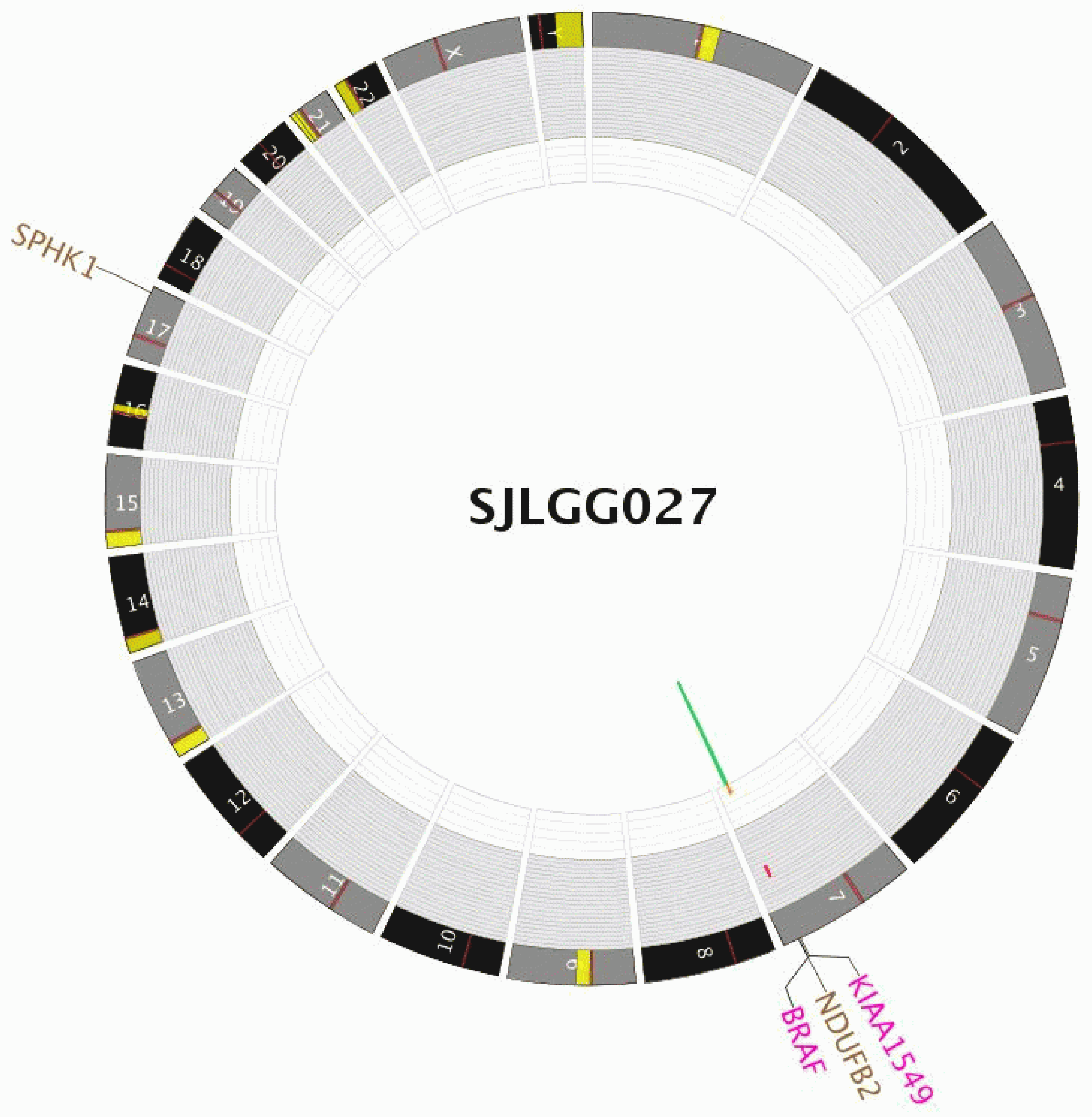

SJLGG021
KIAA1549
BRAF

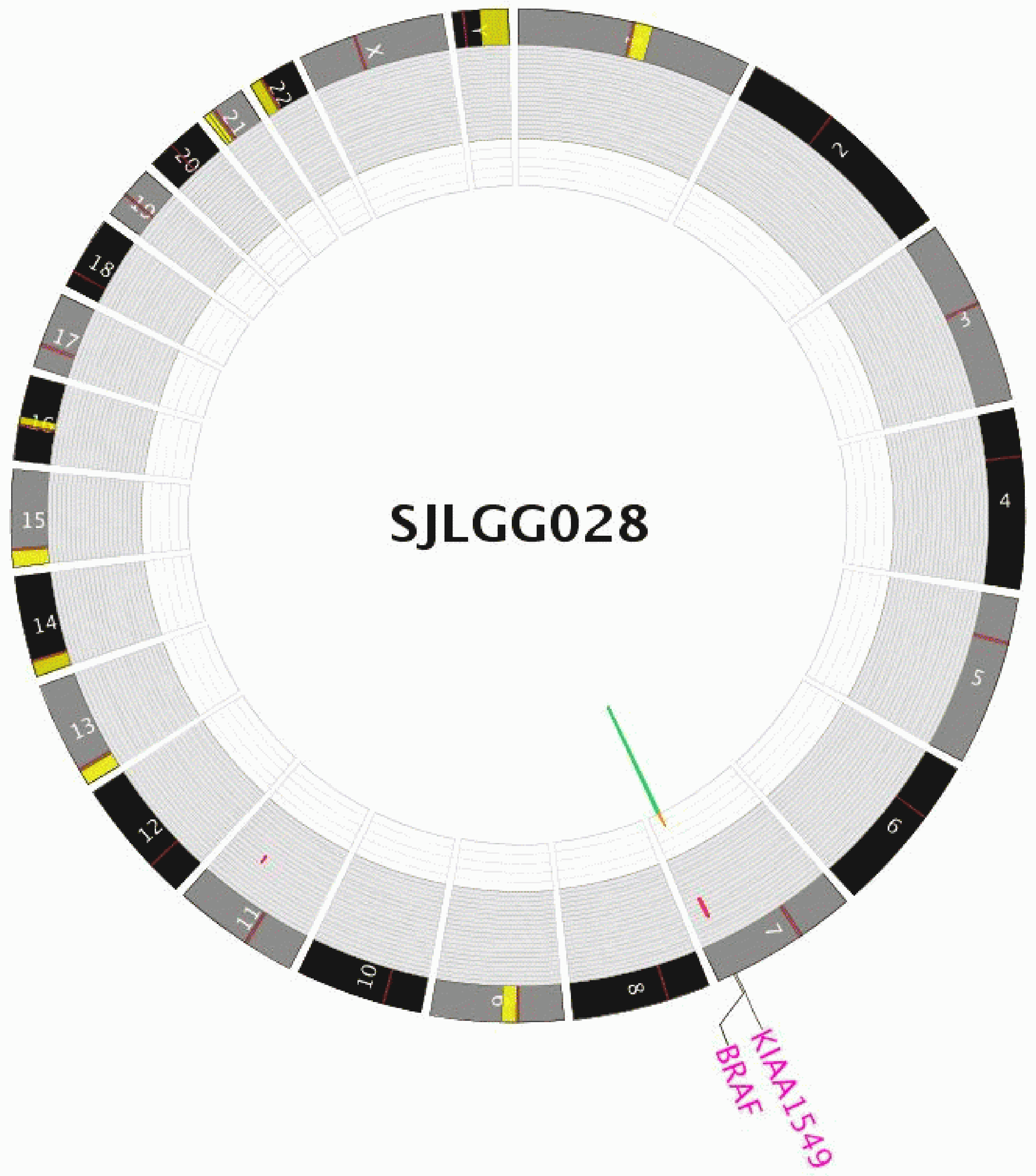

SJLGG022
NF1
NF1


SJLGG024
LETM1
KIAA1549
BRAF

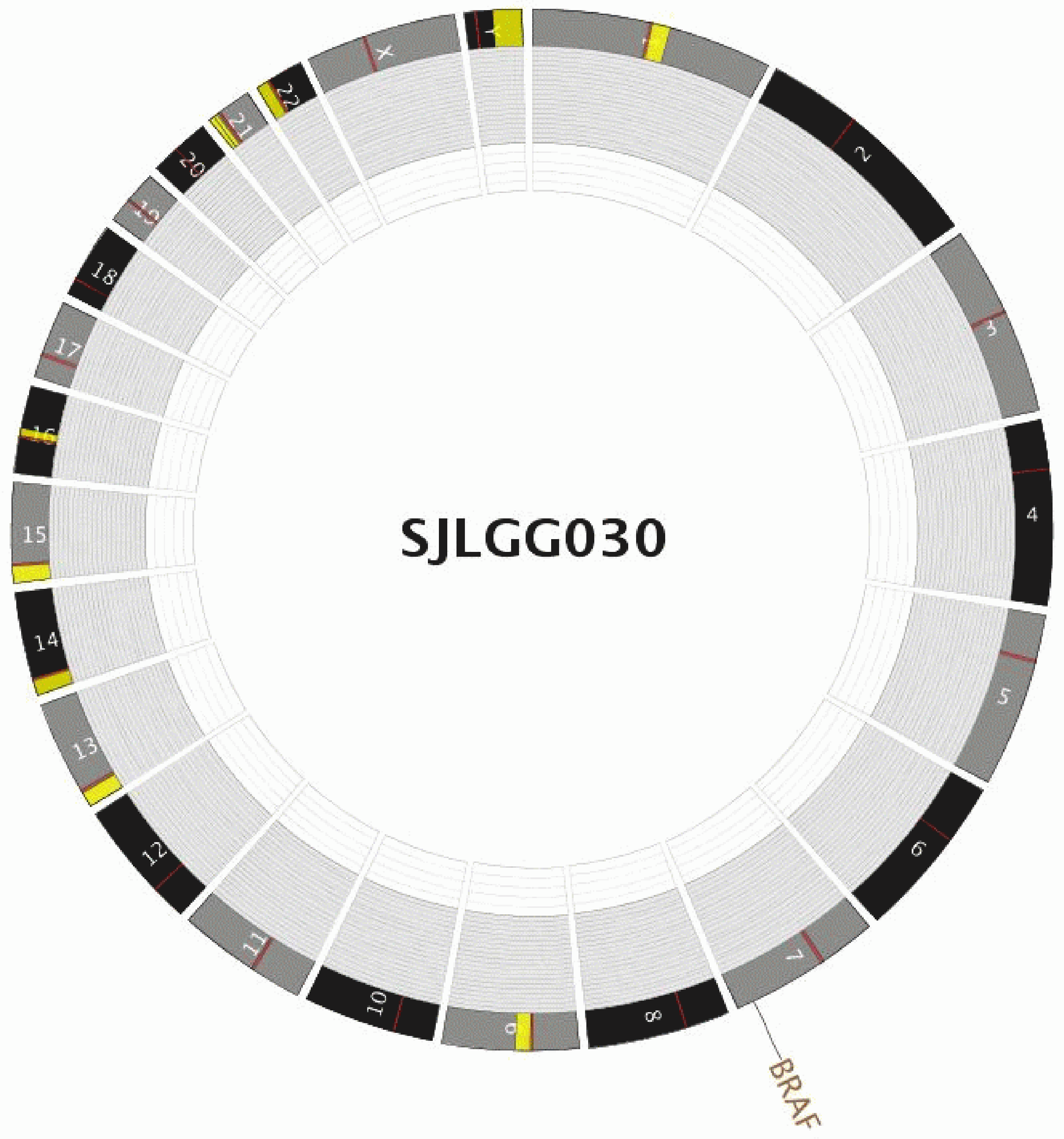

SJLGG025
KIAA1549
BRAF

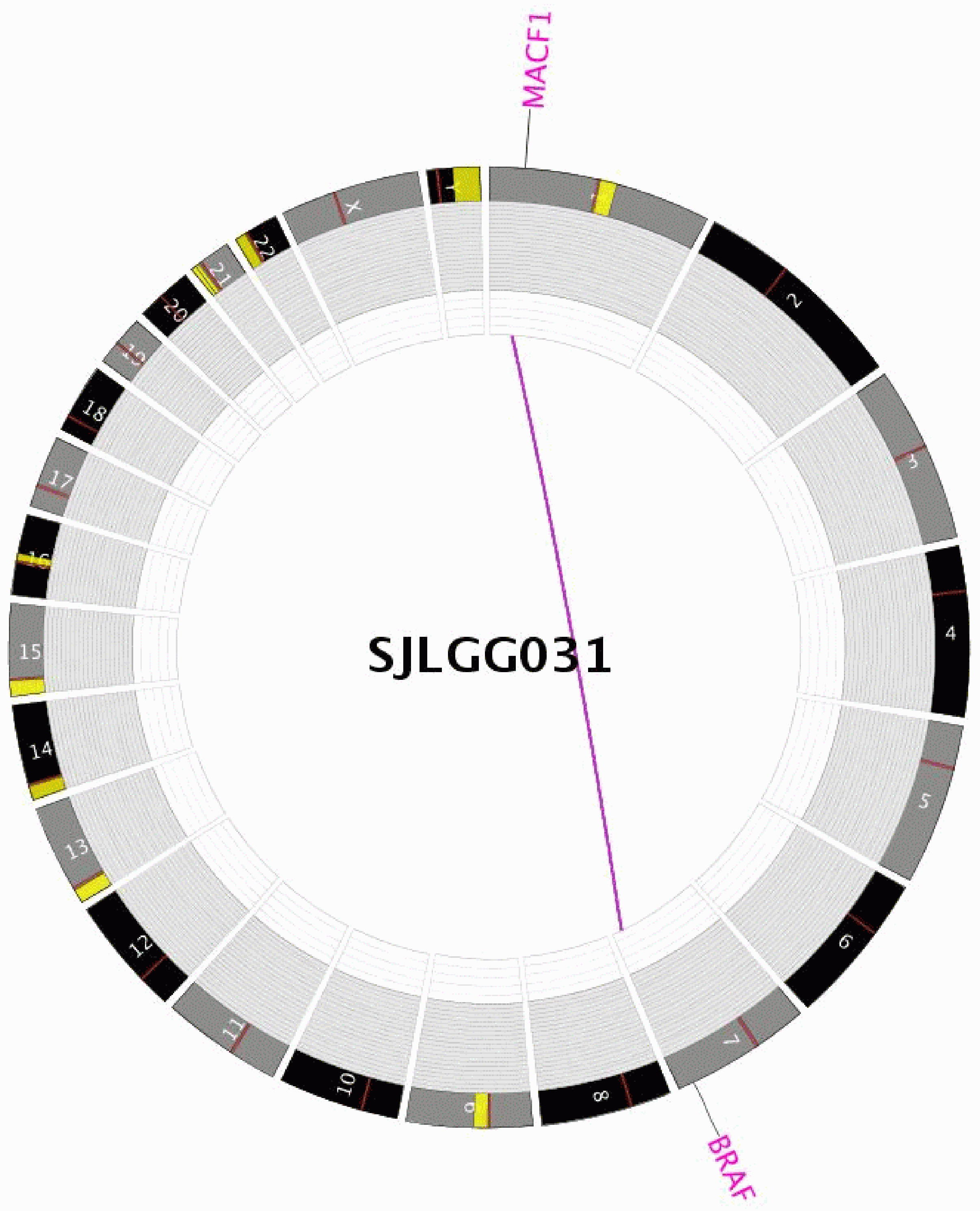

SJLGG026
FXR1
BRAF

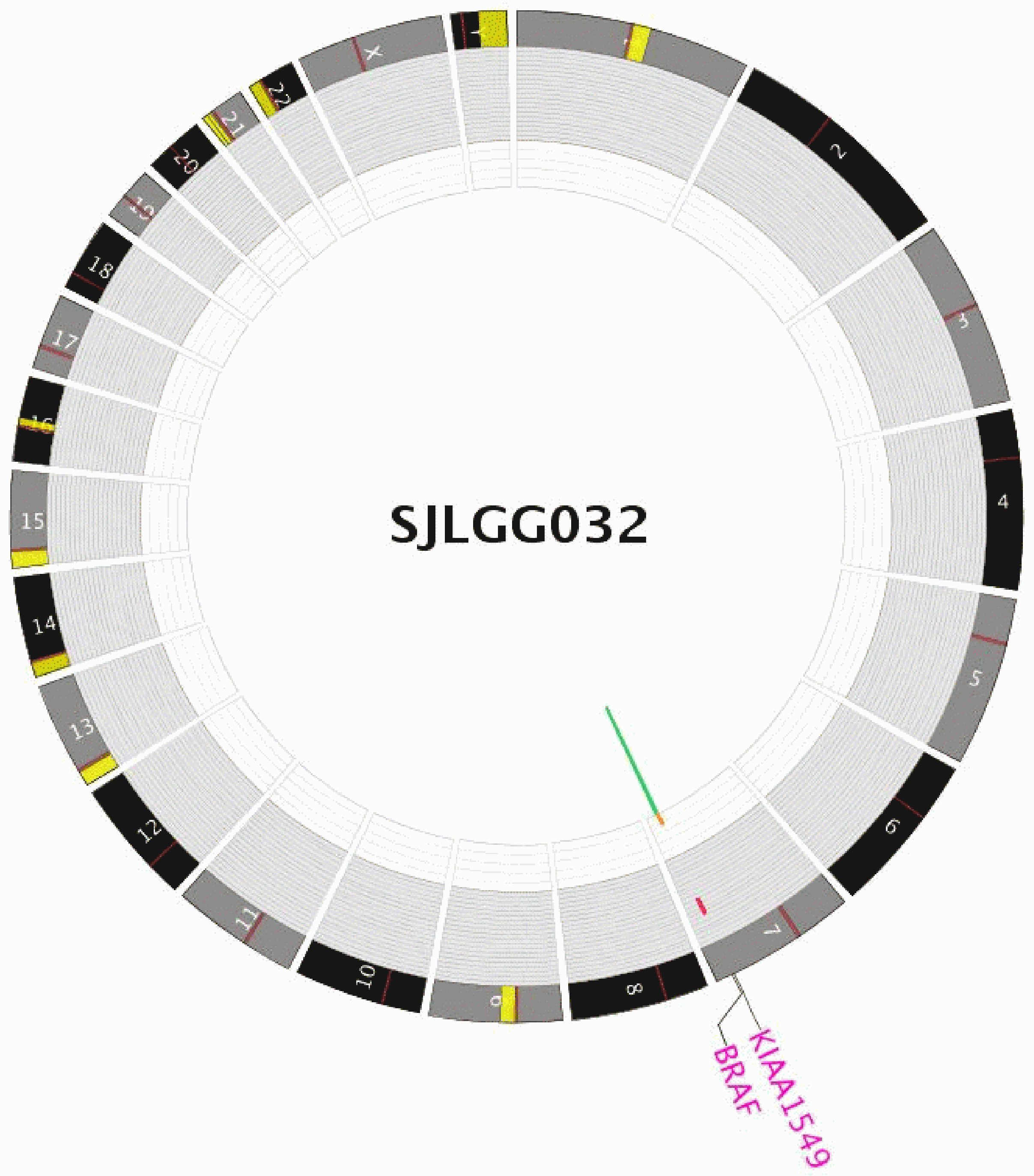

SJLGG027
SPHK1
KIAA1549
NDUFB2
BRAF

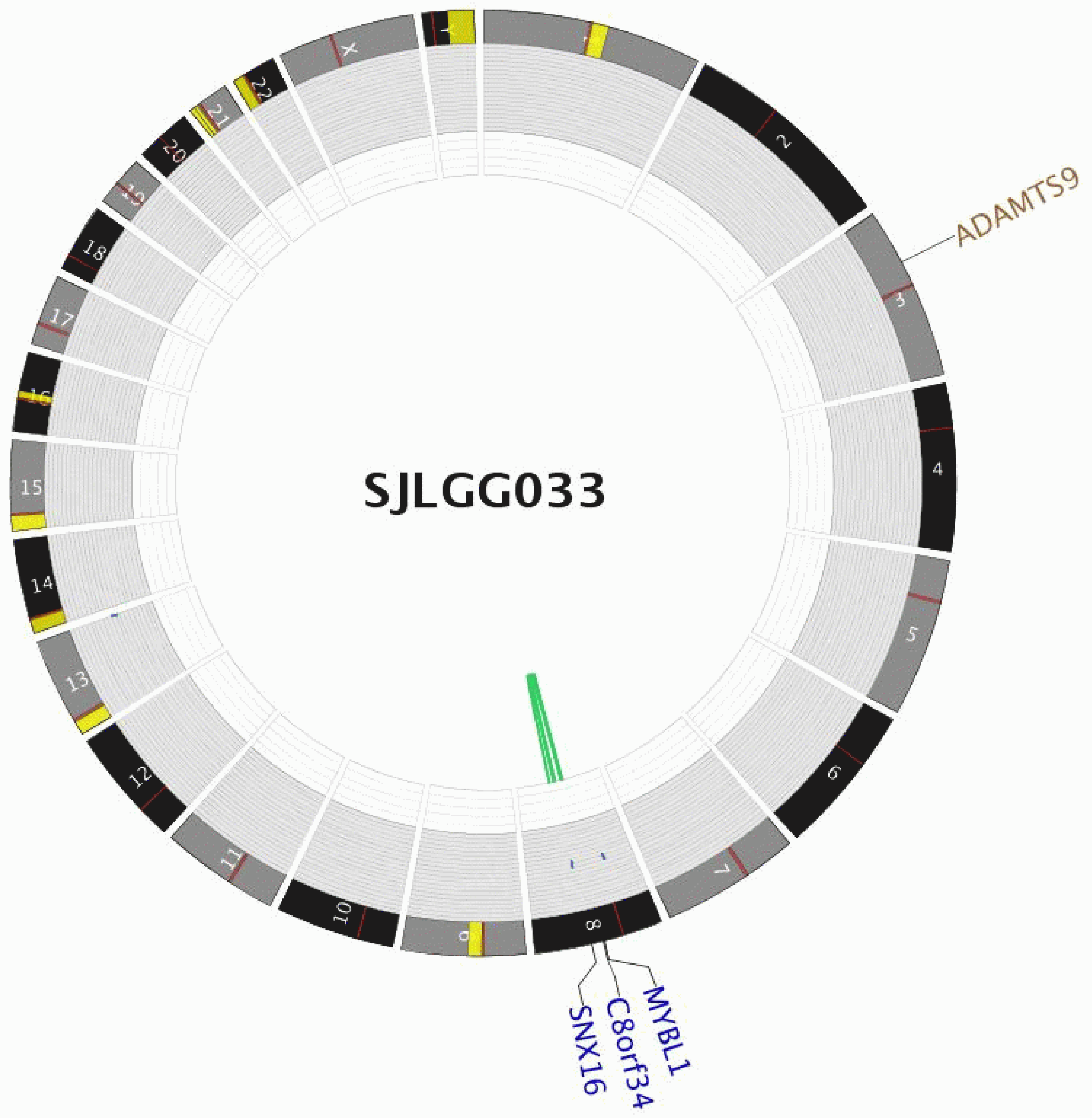

SJLGG028
KIAA1549
BRAF

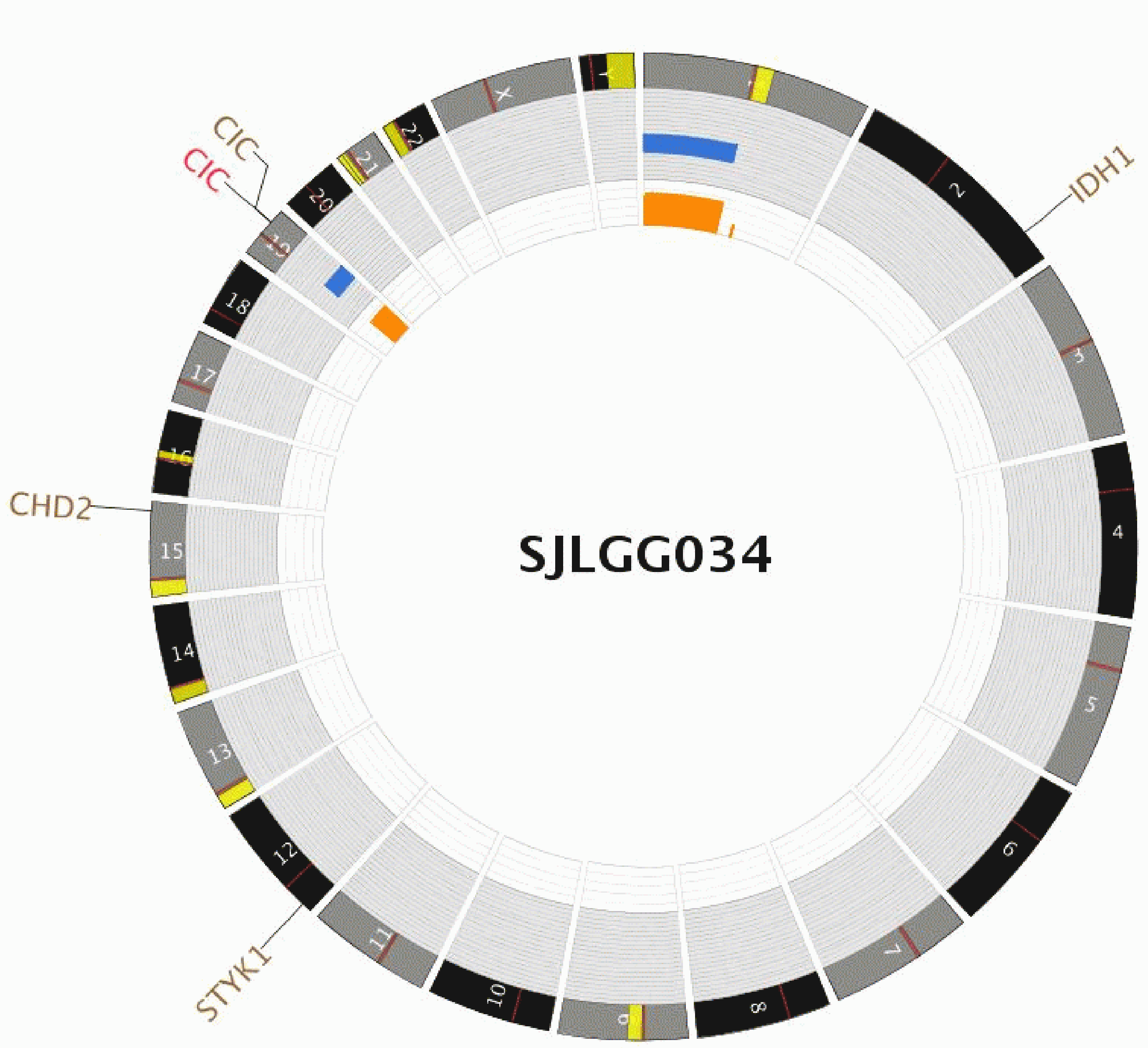

SJLGG029
BRAF

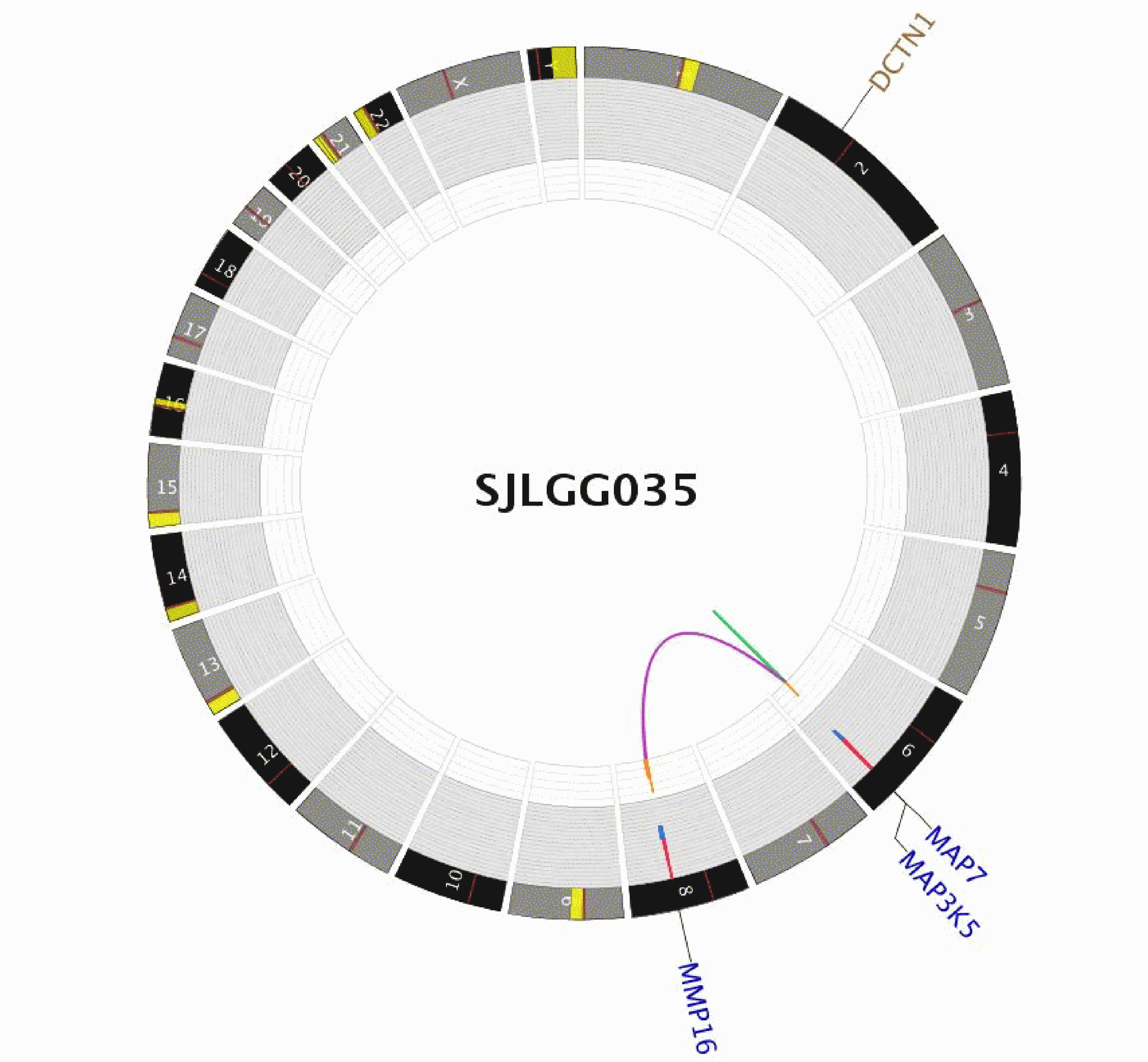

SJLGG030
BRAF

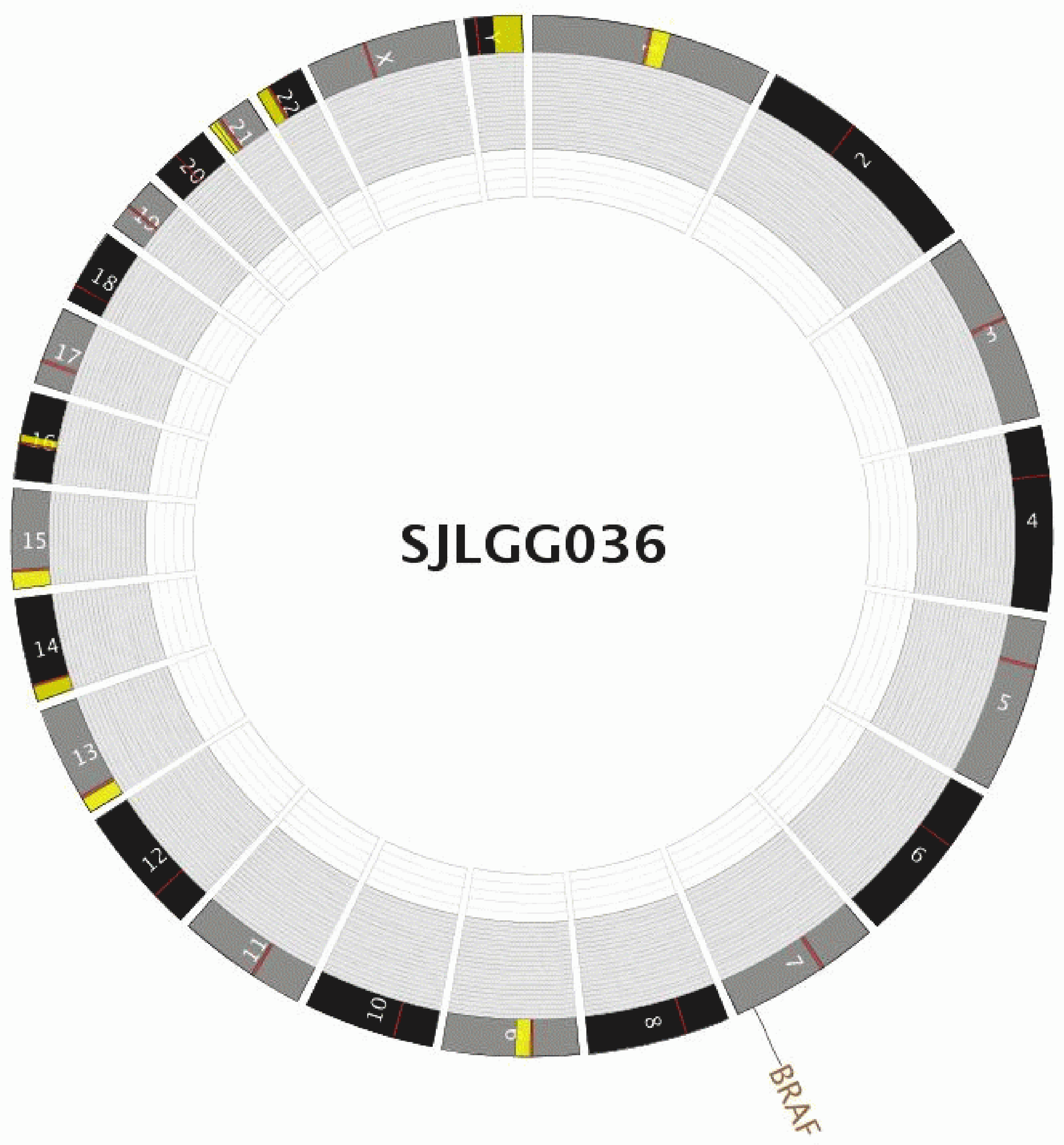

MACF1
SJLGG031
BRAF

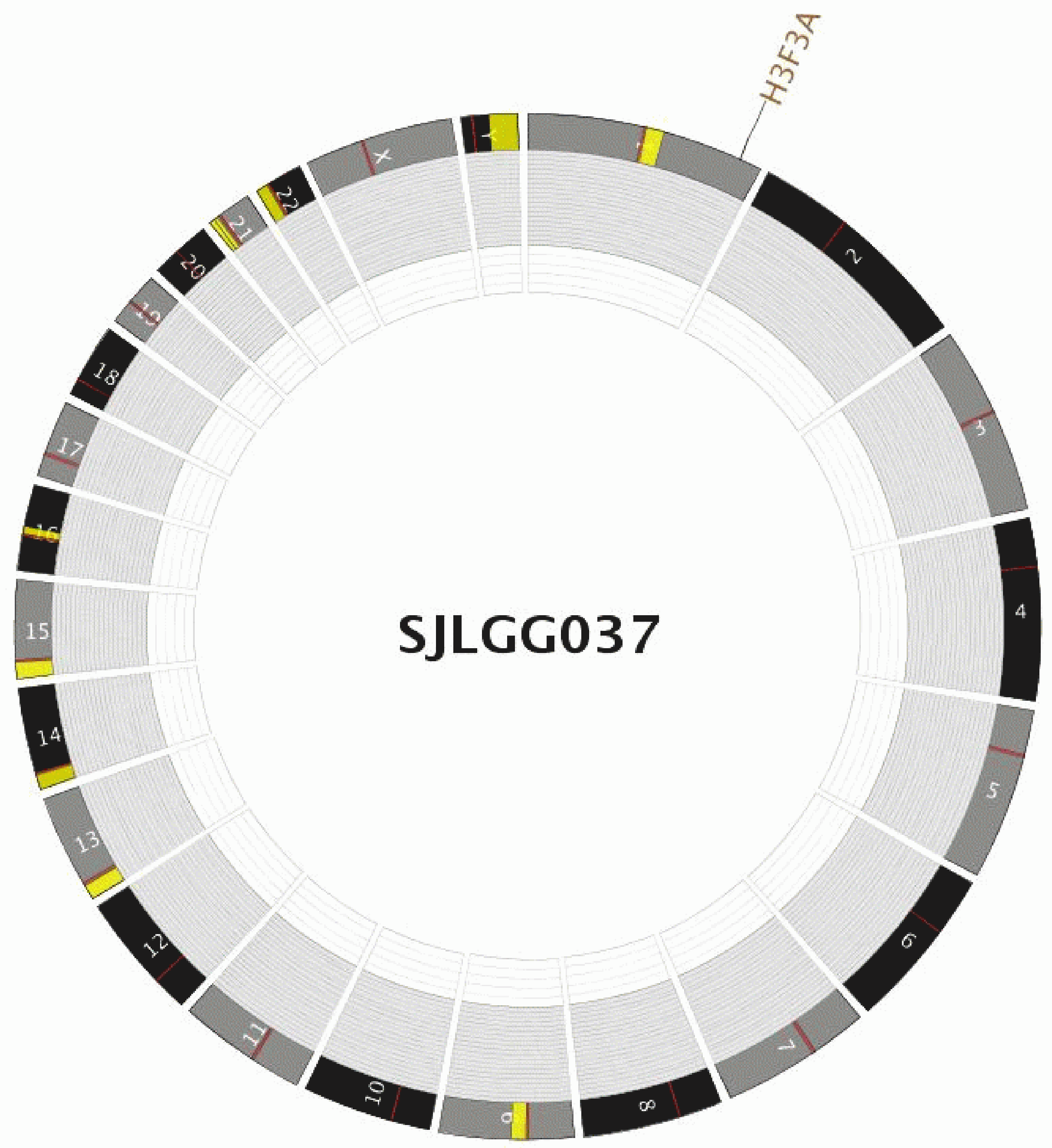

SJLGG032
KIAA1549
BRAF

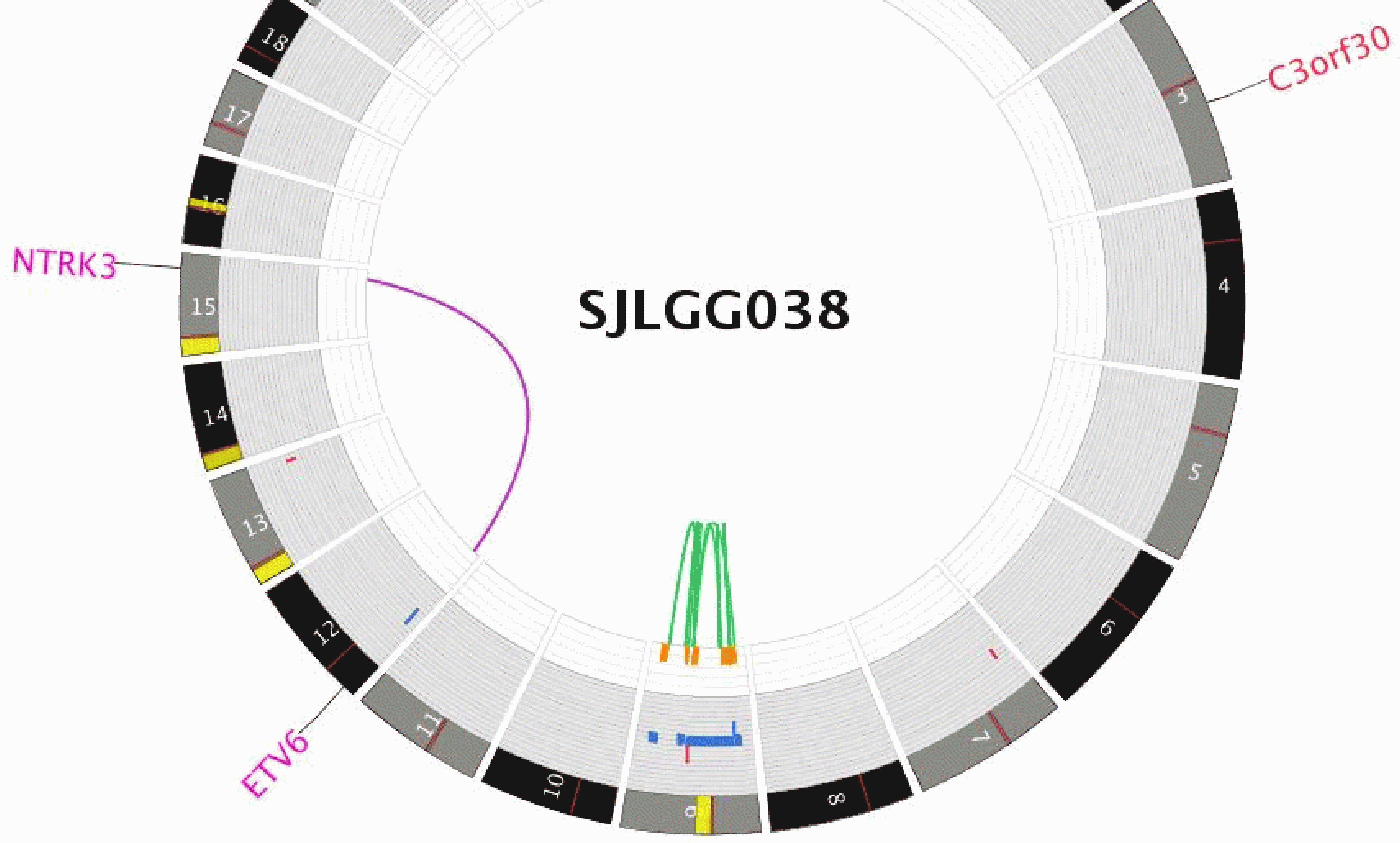

ADAMTS9
SJLGG033
MYBL1
C8orf34
SNX16

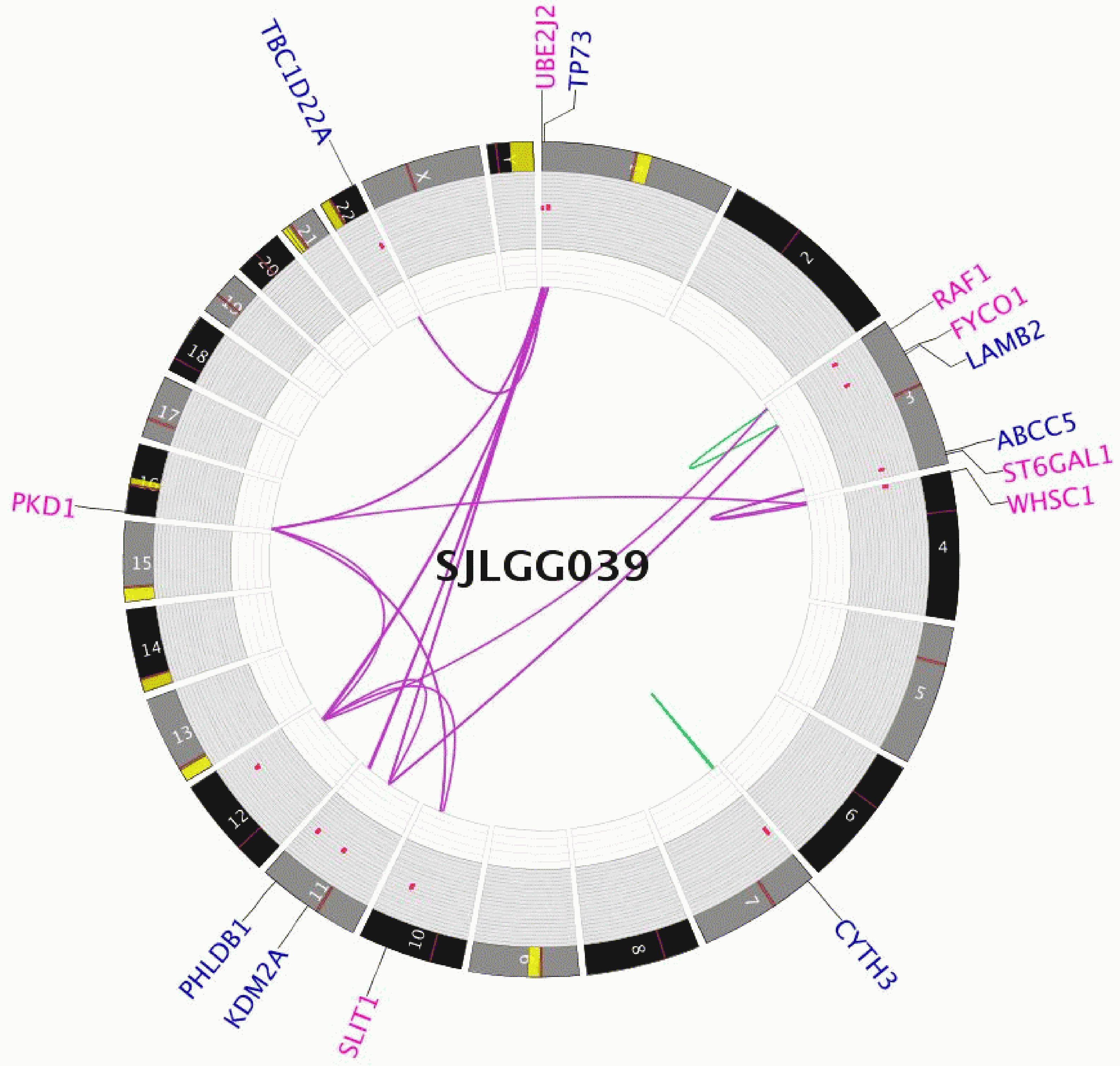

SJLGG034
CIC
CIC
IDH1
CHD2
STYK1

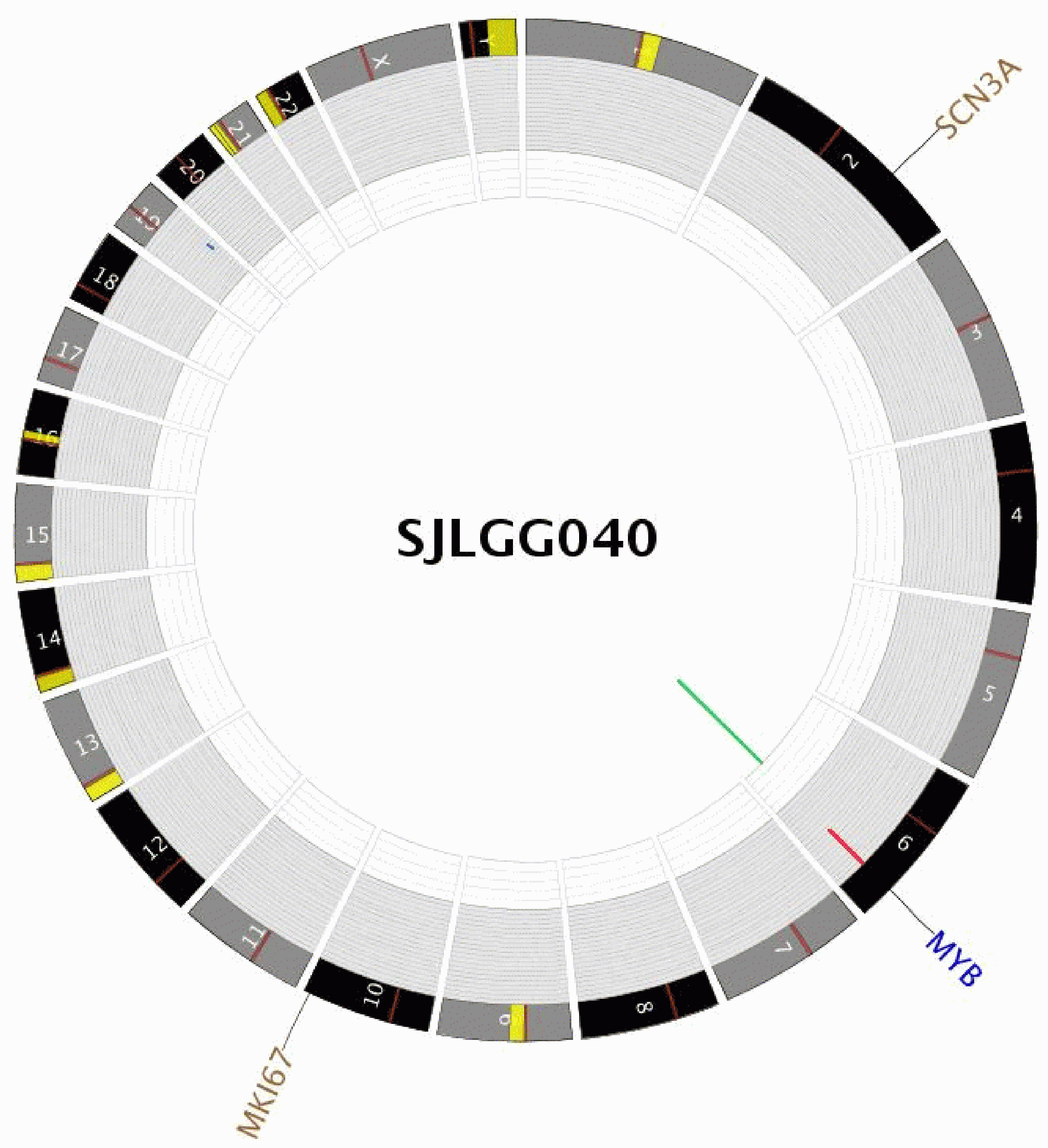

SJLGG035
DCTN1
MAP7
MAP3K5
MMP16

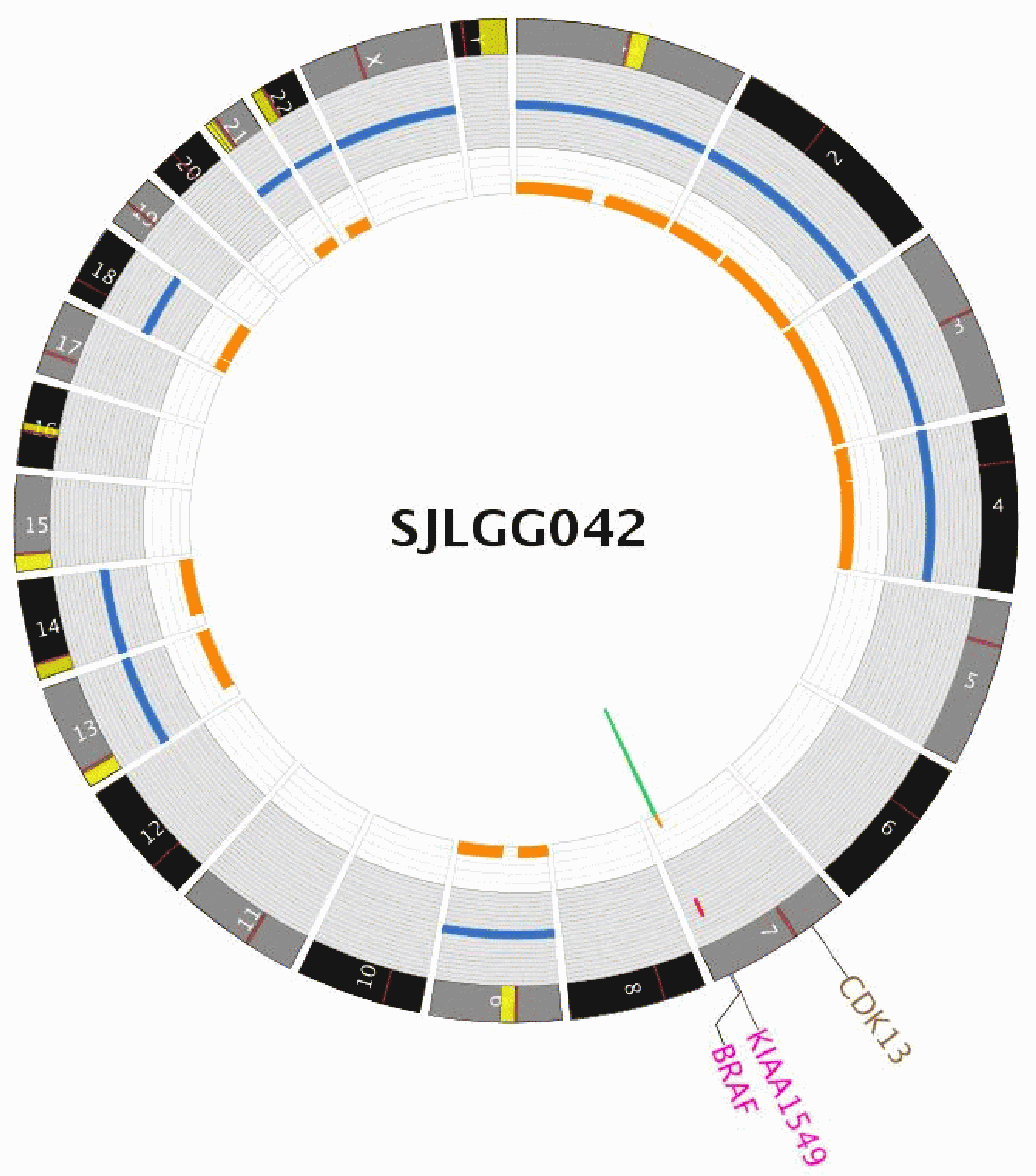

SJLGG036
BRAF


SJLGG037
H3F3A


SJLGG038
C3orf30
NTRK3
ETV6


SJLGG039
TBC1D22A
UBE2J2
TP73
RAF1
FYCO1
LAMB2
ABCC5
ST6GAL1
WHSC1
PKD1
CYTH3
PHLDB1
KDM2A
SLIT1

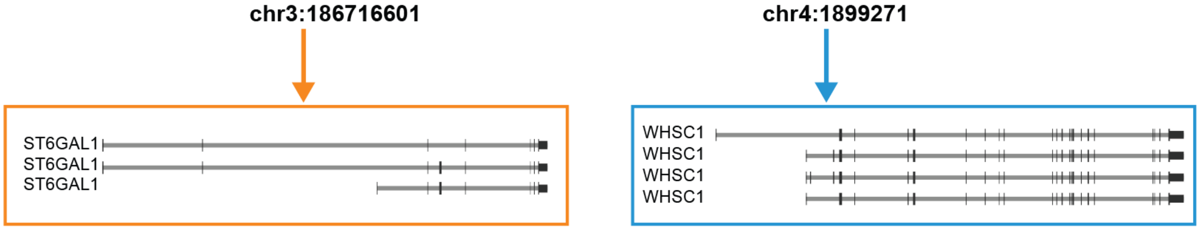

SJLGG040
SCN3A
MYB
MKI67
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X


SJLGG042
CDK13
KIAA1549
BRAF
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X

Supplementary Figure 4. Fusion of *ST6GAL1* 5’ UTR to *WHSC1* in SJLGG039

a. An SV identified by WGS indicated translocation breakpoints at intron 2 of *ST6GAL1* (chr3:186716601) and intron 3 of *WHSC1* (chr4:1899271). **b.** Split reads derived from mRNA-seq at position chr4:1902353. Subsequences at left are soft-clipped reads that match the second exon of *ST6GAL1* (chr3:18661714), while subsequences at right match exon 4 of *WHSC1*. **c.** iFISH image from the tumor demonstrating an unbalanced fusion (one yellow signal) between probes to *WHSC1* (red probe) and *ST6GAL1* (green probe) amid copy number gain.

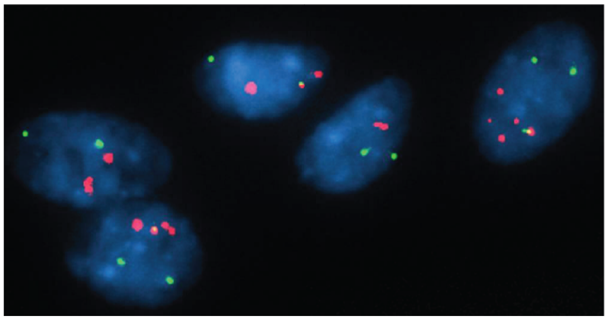
a.



b.

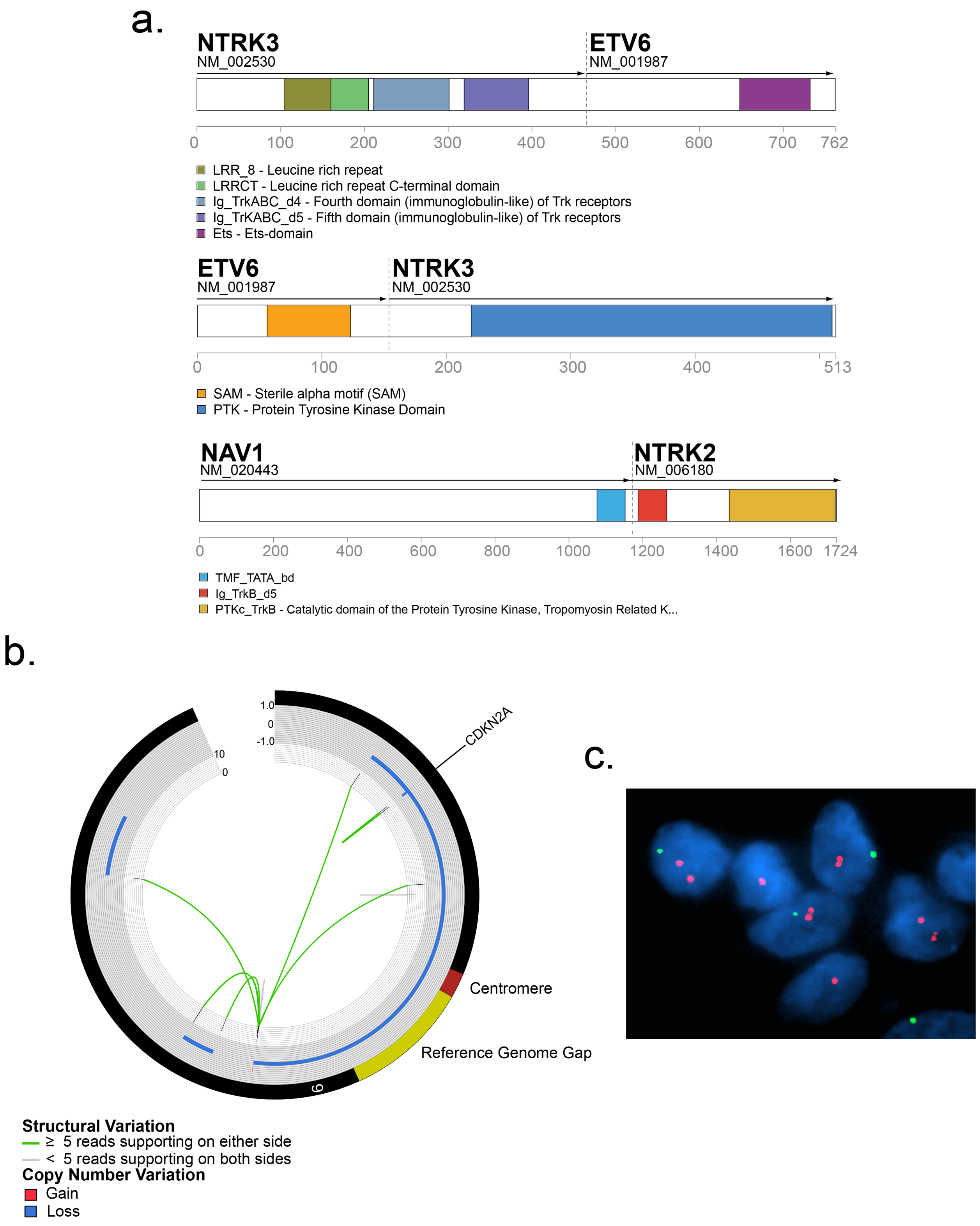
```
GGCCCCCTTGAGCCTGTCCCAAGCCCTGGTGCCAGGTGTCCATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGC
GGCCCCCTTGAGCCTGTCCCAAGCCCTGGTGCCAGGTGTCCATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGCATCA
                              ATCTGTGGAAGGACCTACCAACCAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGCATCAAGCAGAGTCCCCTTTCTGTT
                                        CATCCCCGTGCTGAGTGTTCTAAGAACAGAAGCATCTGGGCTGGATGGAATTTAGCATCAAGCAGAGTCCCCTTTCTGTT
GGCCCCCTTGAGCCTGTCCCAAGCCCTGGTGCCAGGTGTCCATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGAT
GGCCCCCTTGAGCCTGTCCCAAGCCCTGGTGCCAGGTGTCCATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGA
                                        CATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGCATCAAGCAGAGTCCCCTTTCTGTT
GGCCCCCTTGAGCCTGTCCCAAGCCCTGGTGCCAGGTGTCCATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCAT
GGCCCCCTTGAGCCTGTCCCAAGCCCTGGTGCCAGGTGTCCATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGCATT
                                CAGGTGTCCATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGCATCAAGCAGAGTCCCCTTTCTGTT
                                     GTCCATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGCATCAAGCAGAGTCCCCTTTCTGTT
                                  GGTGTCCATCCCCGTGCTGAGTGTTCTAAGAACGGAAGCATCTGGGCTGGATGGAATTTAGCATCAAGCAGAGTCCCCTTTCTGTT
```

c.



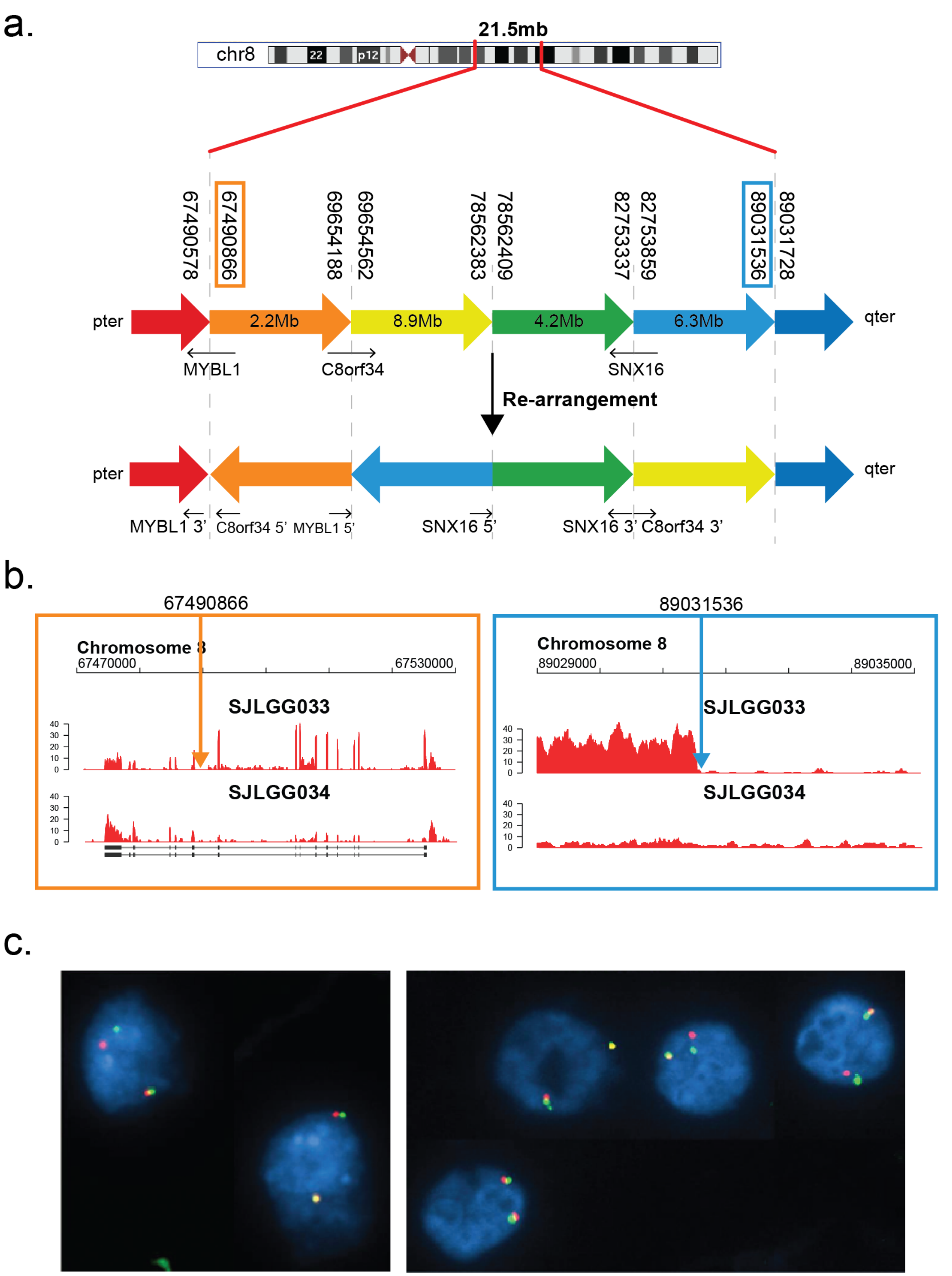
Supplementary Figure 5. SVs and CNVs identified for SJLGG038

a Reciprocal translocation of chr4-chr12 resulting in two fusion proteins, ETV6-NTRK3 and NTRK3-ETV6. Another tumor, SJLGG061, contained an isolated NAV1-NTRK2 fusion (bottom). **b** CIRCOS plot for chromosome 9 showing both CNV and SVs. All deletion segments identified by WGS were connected with SVs, except for the end point of an 8.8Mb deletion at 116Mb-125Mb. The missing SV at this site (position 125,028,999 on chromosome 9) was caused by a highly repetitive soft-clipped subsequence, TGGAATGGAATCTTCCGGAATGGAATGGAATGGAATGGAATGGAATGGAATGA, that cannot be mapped to the reference human genome. This soft-clipped sequence can only be mapped to an unassembled genome scaffold NW_001839627, which suggests that the SV partner at chr9:125,028,999 resides in a sequencing gap of the reference human genome. A 266kb homozygous deletion encompassing *CDKN2A*, *CDKN2B* and *MTAP* contrasts with other SVs on chromosome 9, which are inter-connected and probably arise through a complex rearrangement termed “chromothripsis”. **c** iFISH targeting *CDKN2A* (green probe) and a control locus on 9q (red probe) and demonstrating homozygous or hemizygous loss of *CDKN2A*.


a.
NTRK3
NM_002530
ETV6
NM_001987
0
100
200
300
400
500
600
700
762
LRR_8 - Leucine rich repeat
LRRCT - Leucine rich repeat C-terminal domain
Ig_TrkABC_d4 - Fourth domain (immunoglobulin-like) of Trk receptors
Ig_TrKABC_d5 - Fifth domain (immunoglobulin-like) of Trk receptors
Ets - Ets-domain
ETV6
NM_001987
NTRK3
NM_002530
0
100
200
300
400
513
SAM - Sterile alpha motif (SAM)
PTK - Protein Tyrosine Kinase Domain
NAV1
NM_020443
NTRK2
NM_006180
0
200
400
600
800
1000
1200
1400
1600
1724
TMF_TATA_bd
Ig_TrkB_d5
PTKc_TrkB - Catalytic domain of the Protein Tyrosine Kinase, Tropomyosin Related K...
b.
1.0
0
-1.0
10
0
CDKN2A
Centromere
Reference Genome Gap
9
Structural Variation
≥ 5 reads supporting on either side
< 5 reads supporting on both sides
Copy Number Variation
Gain
Loss
c.

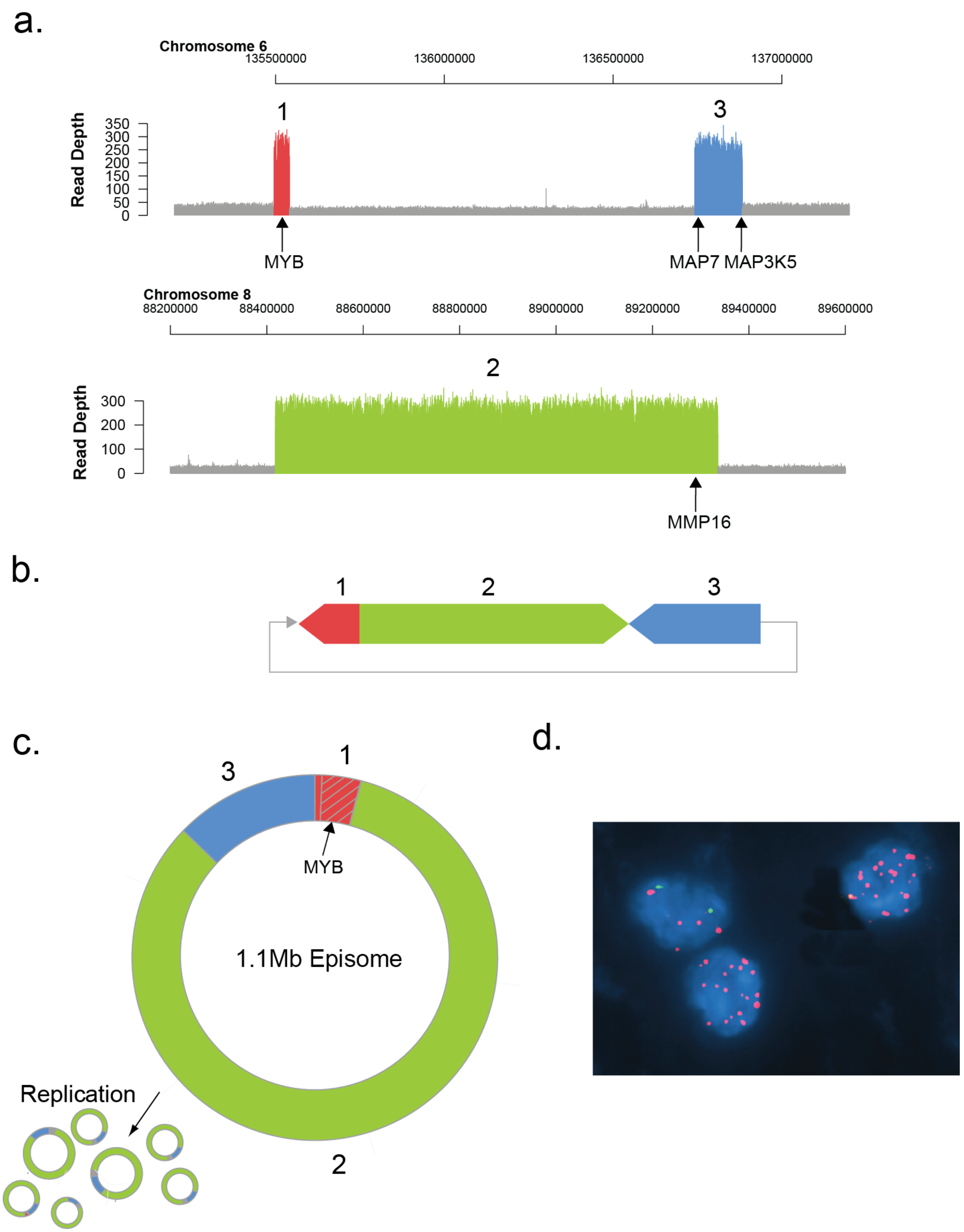
Supplementary Figure 6. Complex rearrangement involving 5 SVs and 4 genomic segments and spanning a 21.5Mb region on chromosome 8 in SJLGG033

a. Genomic locations of altered chromosomal structure and SV breakpoints involved by the rearrangement, which shows a pattern of 'closed chain' chromosomal breakage and rejoining with no concomitant copy number alteration. The coding regions of *MYBL1*, C8orf34 and *SNX16* were disrupted. C8orf34 is not expressed, but abnormal expression of *MYBL1* and *SNX16* was confirmed by mRNA-seq and RT-PCR of cDNA. WGS predicted that the last 7 exons of *MYBL1* are split from the 5' end of the *MYBL1* transcript in this rearrangement. Differential expression and break apart of the 5' and 3' regions of *MYBL1* were confirmed by RT-PCR and iFISH, respectively. **b.** Coverage graph of mRNA-seq data showing that SJLGG033 has abnormal expression of *MYBL1*, when compared to a control sample (SJLGG034) without *MYBL1* rearrangement; at left, the last 7 exons of *MYBL1* have reduced expression compared with the 5' end of the gene, while at right abnormal transcription in a non-genic region initiated from the 'partner' breakpoint for *MYBL1* rearrangement. **c.** *MYBL1* iFISH using 'break-apart' probes; fused probes (yellow) indicate an intact *MYBL1* gene, while separated green and red probes indicate rearrangement of the 5' and 3' regions of *MYBL1*.


a.
21.5mb
chr8
22
p12
67490578
67490866
69654188
69654562
78562383
78562409
82753337
82753859
89031536
89031728
pter
2.2Mb
8.9Mb
4.2Mb
6.3Mb
qter
MYBL1
C8orf34
SNX16
Re-arrangement
pter
qter
MYBL1 3'
C8orf34 5'
MYBL1 5'
SNX16 5'
SNX16 3'
C8orf34 3'
b.
67490866
Chromosome 8
67470000
67530000
SJLGG033
SJLGG034
40
30
20
10
0
89031536
Chromosome 8
89029000
89035000
SJLGG033
SJLGG034
c.

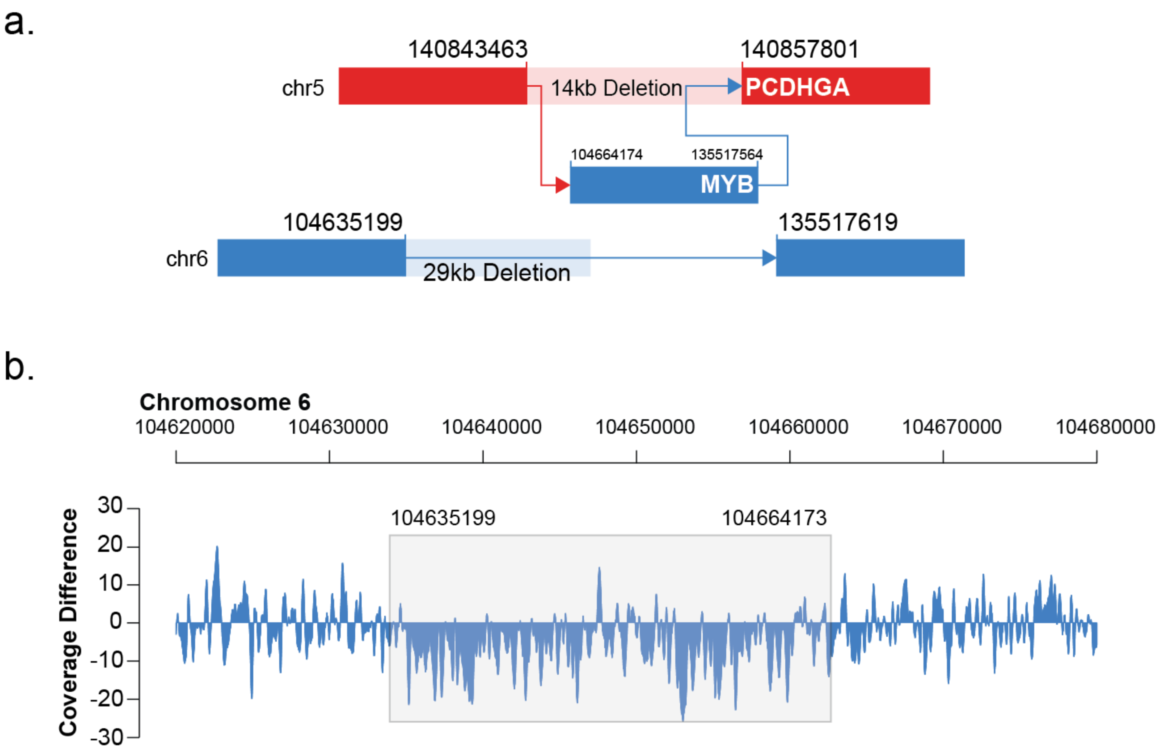
Supplementary Figure 7. Complex rearrangement resulting in formation of a *MYB* episome in SJLGG035

Four SVs have formed a 1.1Mb episome, consisting of two segments on chromosome 6 and one on chromosome 8 and resulting in loss of a 1.4Mb region between the two chromosome 6 segments. All three segments show >10x amplification, suggesting that replication of the episome occurs after rearrangement. One segment on chromosome 6 (chr6:135495476-135540965) contains the *MYB* oncogene, which is likely to be the target gene. The segment ends 654bp downstream of the *MYB* 3' UTR. **a.** Read-depth of chromosome 6 and chromosome 8 regions connected by SVs. **b.** Orientation of elements from chromosomes 6 and 8 that will form the episome by inter-chromosomal rearrangement (**c.**). **d.** iFISH verification of predicted episome replication to cause amplification; multiple signals are seen with a (red) *MYB* probe versus a green (copy number control) chromosome 6p probe.


a.
Chromosome 6
135500000
136000000
136500000
137000000
Read Depth
350
300
250
200
150
100
50
0
1
3
MYB
MAP7
MAP3K5
Chromosome 8
88200000
88400000
88600000
88800000
89000000
89200000
89400000
89600000
Read Depth
300
200
100
0
2
MMP16
b.
1
2
3
c.
3
1
MYB
1.1Mb Episome
2
Replication
d.

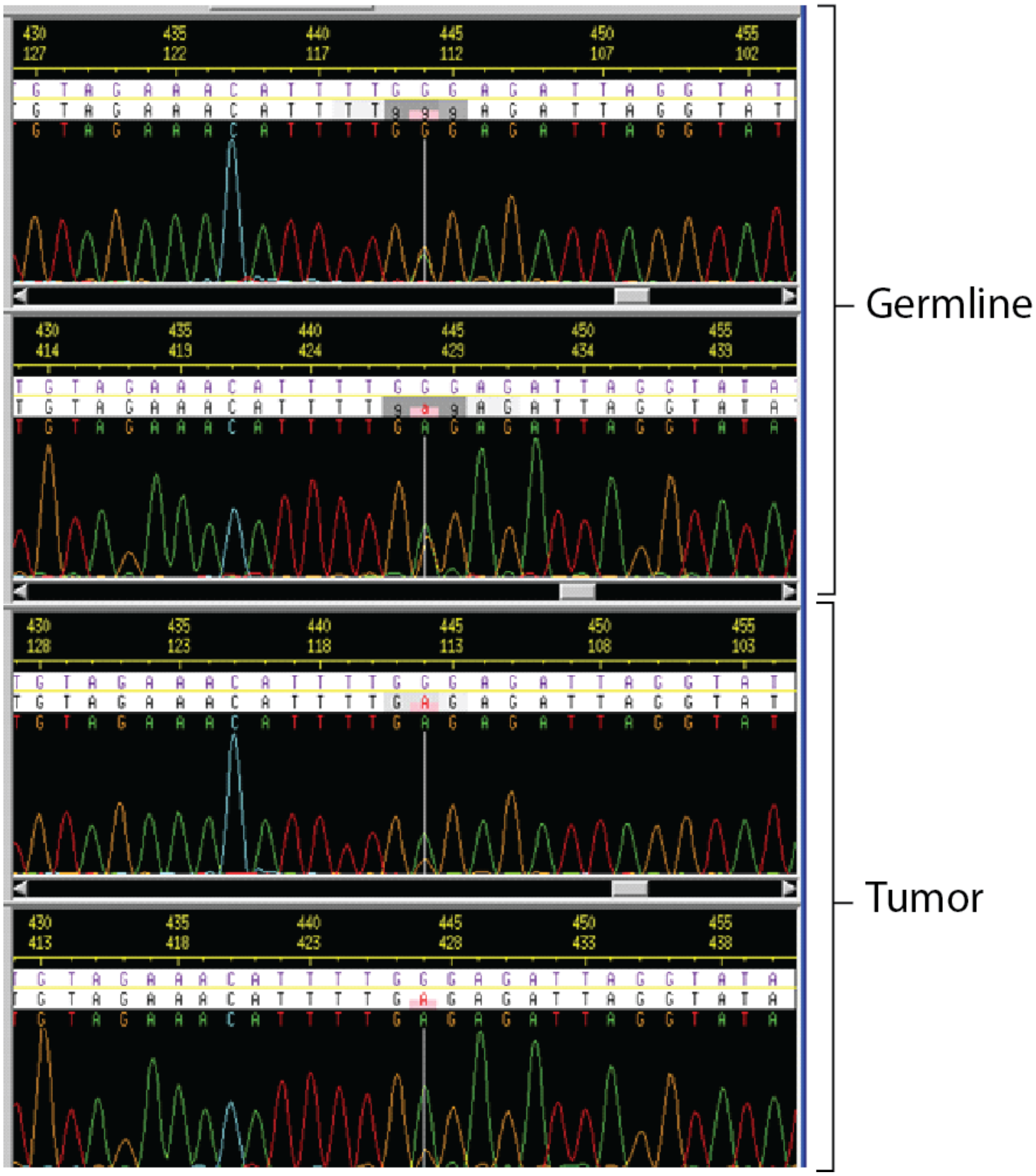
Supplementary Figure 8. Translocation of 31Mb segment from chromosome 6 to chromosome 5 producing an in-frame fusion of *MYB* and *PCDHGA* in SJLGG005

a. Three SVs were identified, including two chr5-chr6 SVs and one intra-chromosomal SV. The rearrangement predicts a 14kb deletion on chromosome 5 and a 29kb deletion on chromosome 6. **b.** Coverage plot of normalized (tumor minus normal) read-depth for a 39kb region centered on the 29kb deletion projected from the rearrangement. Reduced read depth in the box confirms the deletion indicated by SV analysis.



Supplementary Figure 9. Sanger chromatogram for SJLGG001225 centered on the NF1 W571* locus

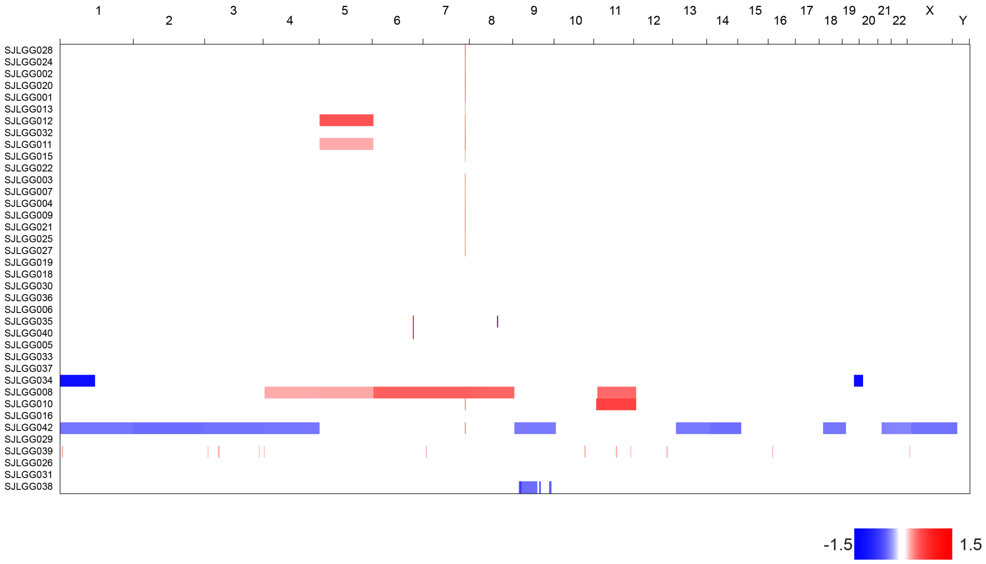
Wild-type allele is G and mutant allele is A. Top two panels are forward and reverse reads from germline DNA, while bottom two panels are forward and reverse reads from tumor DNA. Note the difference in peak heights for the mutant and wild-type alleles in the tumor sample reflecting loss of heterozygosity at this locus.



Supplementary Figure 10. Copy number heatmaps generated for WGS tumor series and non-WGS tumors using SNP array data

a. Copy number estimated from WGS data using CONSERTING. Scale from -1.5 to 1.5.
b. Copy number (non-WGS cases) estimated from SNP6 array data. Scale from -1.5 to 1.5.
Tumors are grouped on the basis of clinicopathological features labeled according to color code (see legend box).

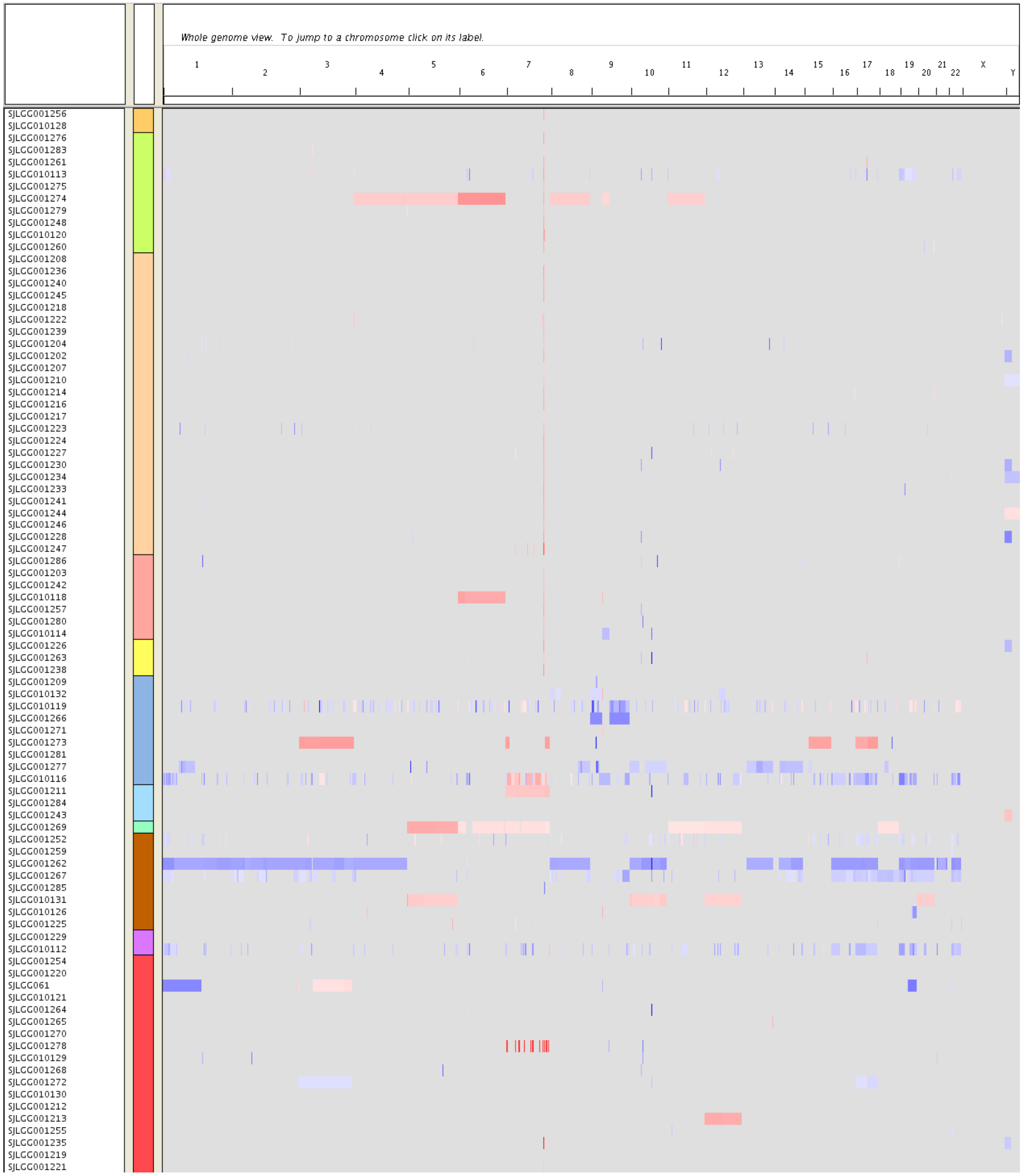
a.



Legend for Patient Subgroups

🟨 KIAA1549-BRAF - Cerebral Cortex	🟦 BRAF ^{V600E}- Cerebral Cortex
🟩 KIAA1549-BRAF - Diencephalon	🟦 BRAF ^{V600E}- Diencephalon
🟧 KIAA1549-BRAF - Cerebellum	🟩 BRAF ^{V600E}- Brainstem
🟥 KIAA1549-BRAF - Brainstem	🟫 Other RAS/RAF Aberration
🟨 KIAA1549-BRAF - Spinal Cord	🟪 FGFR1 Duplication
	🟥 Other Aberration

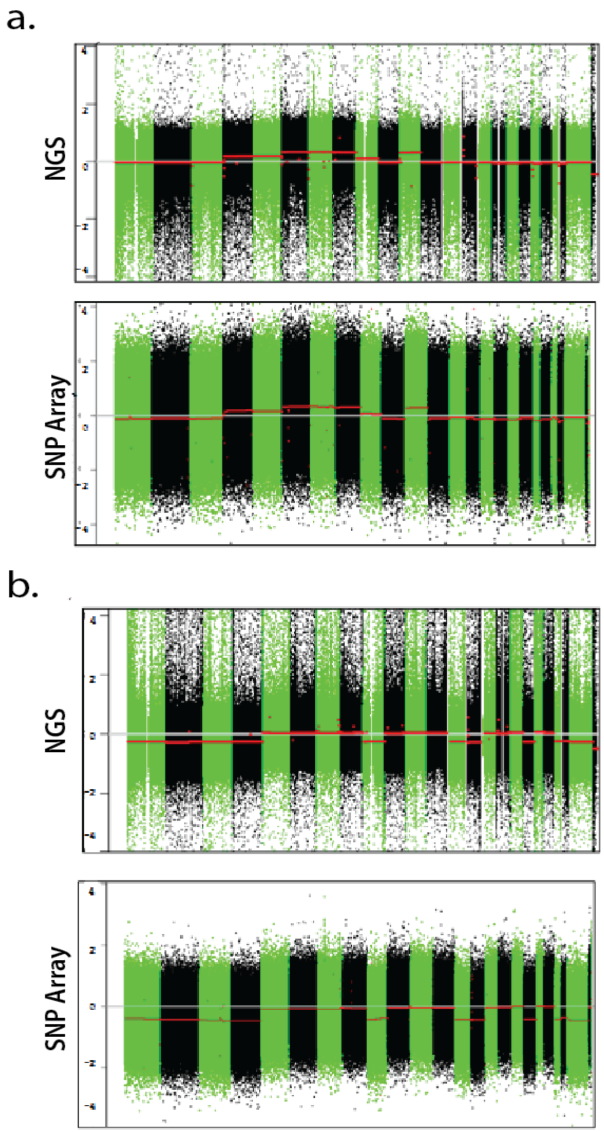
b.



Whole genome view. To jump to a chromosome click on its label.
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y
SJLGG001256
SJLGG010128
SJLGG001276
SJLGG001283
SJLGG001261
SJLGG010113
SJLGG001275
SJLGG001274
SJLGG001279
SJLGG001248
SJLGG010120
SJLGG001260
SJLGG001208
SJLGG001236
SJLGG001240
SJLGG001245
SJLGG001218
SJLGG001222
SJLGG001239
SJLGG001204
SJLGG001202
SJLGG001207
SJLGG001210
SJLGG001214
SJLGG001216
SJLGG001217
SJLGG001223
SJLGG001224
SJLGG001227
SJLGG001230
SJLGG001234
SJLGG001233
SJLGG001241
SJLGG001244
SJLGG001246
SJLGG001228
SJLGG001247
SJLGG001286
SJLGG001203
SJLGG001242
SJLGG010118
SJLGG001257
SJLGG001280
SJLGG010114
SJLGG001226
SJLGG001263
SJLGG001238
SJLGG001209
SJLGG010132
SJLGG010119
SJLGG001266
SJLGG001271
SJLGG001273
SJLGG001281
SJLGG001277
SJLGG010116
SJLGG001211
SJLGG001284
SJLGG001243
SJLGG001269
SJLGG001252
SJLGG001259
SJLGG001262
SJLGG001267
SJLGG001285
SJLGG010131
SJLGG010126
SJLGG001225
SJLGG001229
SJLGG010112
SJLGG001254
SJLGG001220
SJLGG061
SJLGG010121
SJLGG001264
SJLGG001265
SJLGG001270
SJLGG001278
SJLGG010129
SJLGG001268
SJLGG001272
SJLGG010130
SJLGG001212
SJLGG001213
SJLGG001255
SJLGG001235
SJLGG001219
SJLGG001221

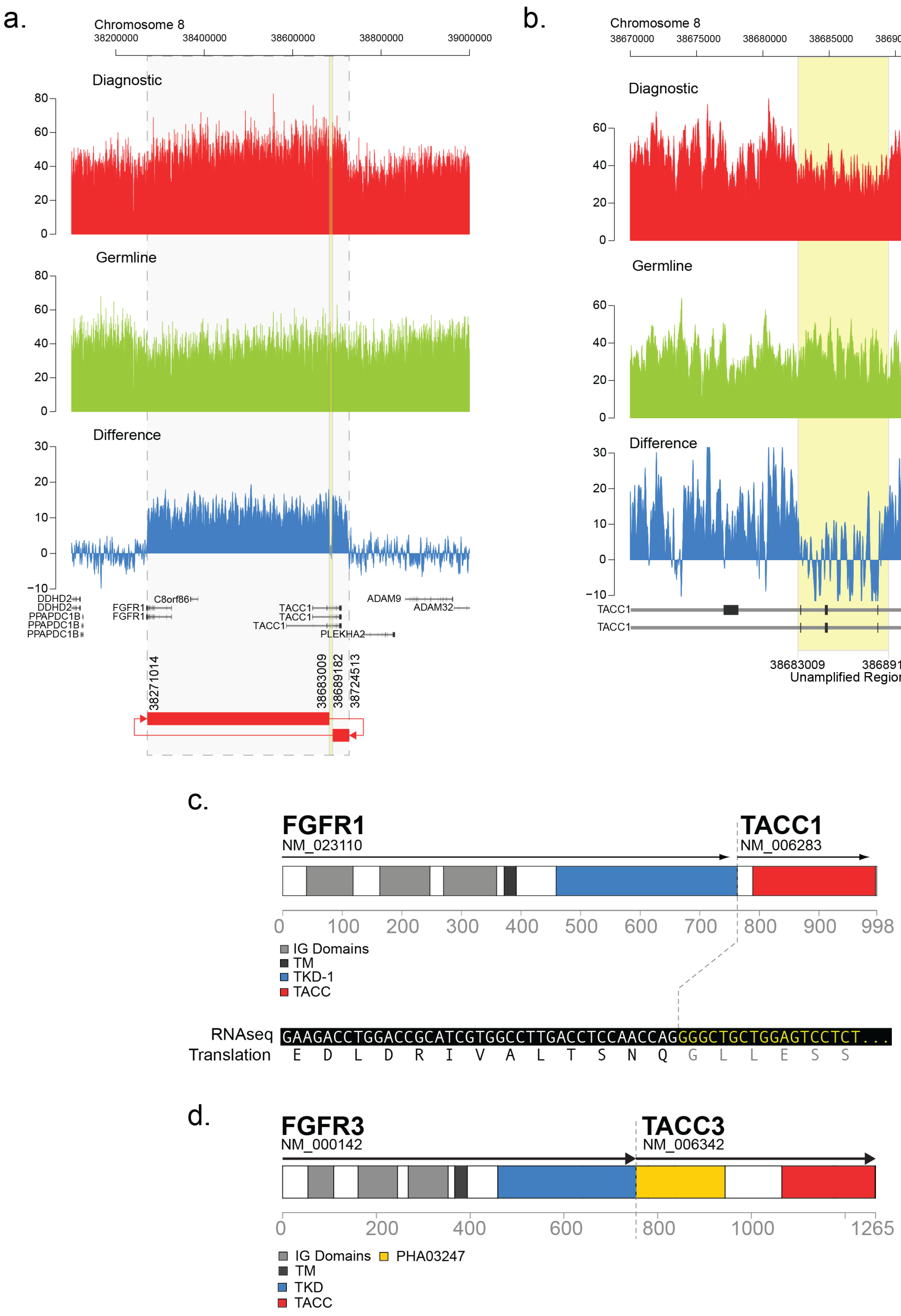
Supplementary Figure 11. Subclonal multi-chromosome copy number alterations (CNAs) detected by both WGS (top) and SNP array (bottom)

Alternating green and black blocks represent chromosomes 1-22, X. The y-axis is the $\log_2$ ratio of the tumor / normal signal derived from (top) the read-depth of WGS data and (bottom) from SNP array probe hybridization signals. **a.** CNA profile for SJLGG008. **b.** CNA profile for SJLGG042. Six chromosomes (4, 5, 6, 7, 8, 11) in SJLGG008 show low-amplitude copy number gain, while 11 chromosomes (1, 2, 3, 4, 9, 13, 14, 18, 21, 22, X) have low-level copy number loss in SJLGG042. Low-level copy number abnormalities were also corroborated by the $\log_2$ ratio of SNP array data, indicating the presence of subclonal aneuploidy in these tumors.



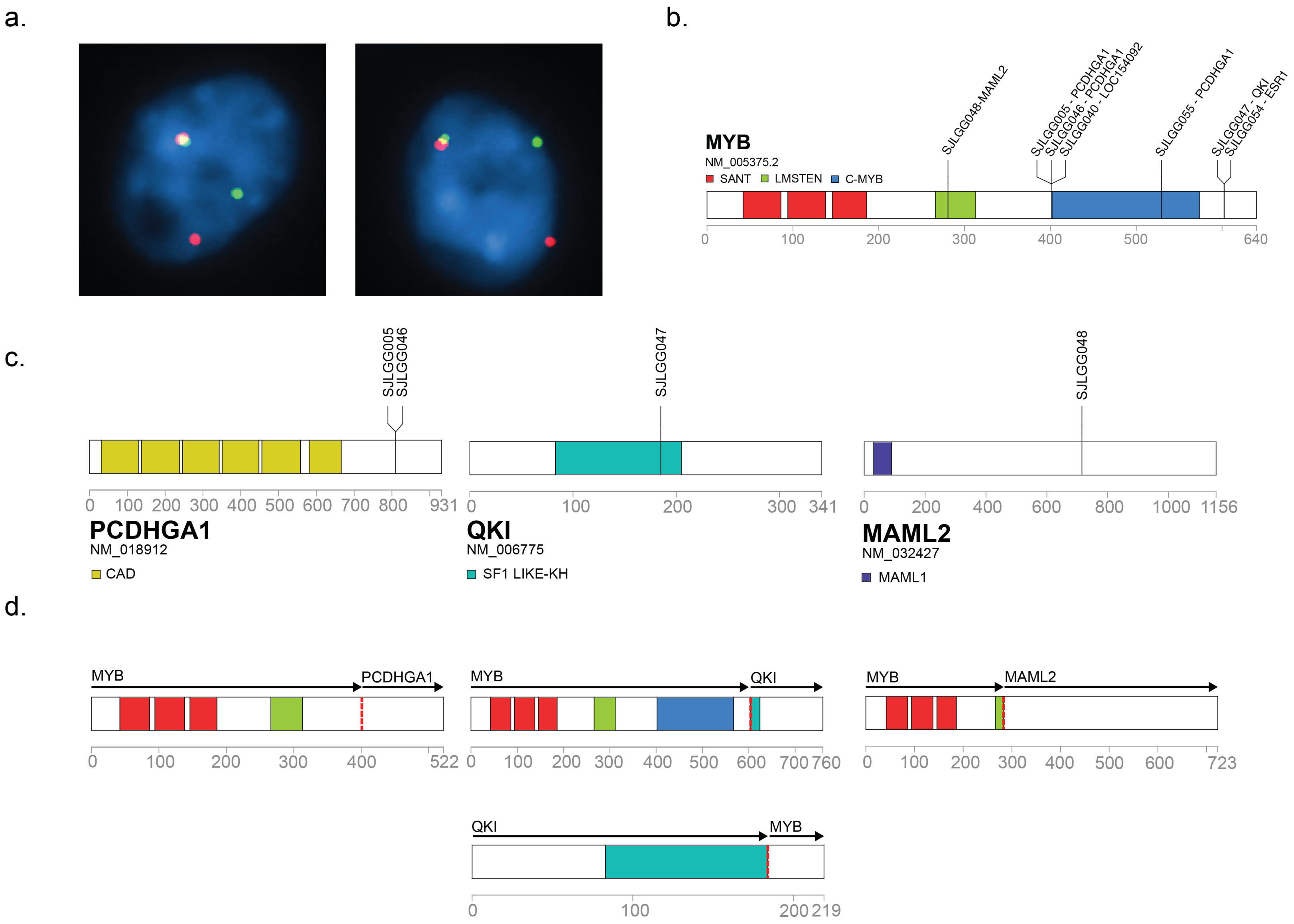
Supplementary Figure 12. Fusions between FGFR1 and TACC1 (SJLGG018) and FGFR3 and TACC3 (SJLGG001206)

a. Normalized read count of tumor genome (diagnostic sample – red), of matching germline genome (green), and the difference between them (blue) at chr8: 38,100,000-39,000,000 where a rearrangement caused by two SVs was identified. The ends of the amplicon are indicated by dashed lines, while a solid strip marks a 6kb unamplified segment within the amplicon. The breakpoints of the two SVs are indicated diagrammatically in an episome involving *FGFR1* and *TACC1*. **b.** Detail of the genomic read count around the 6kb unamplified segment. **c.** FGFR1-TACC1 fusion protein constructed from the SV junction reads of mRNA-seq data. **d.** FGFR3-TACC3 fusion in tumor SJLGG001206.


a.
Chromosome 8
38200000
38400000
38600000
38800000
39000000
Diagnostic
0
20
40
60
80
Germline
0
20
40
60
80
Difference
−10
0
10
20
30
DDHD2
DDHD2
PPAPDC1B
PPAPDC1B
PPAPDC1B
FGFR1
FGFR1
C8orf86
TACC1
TACC1
TACC1
PLEKHA2
ADAM9
ADAM32
38271014
38683009
38689182
38724513
b.
Chromosome 8
38670000
38675000
38680000
38685000
38690000
38695000
38700000
Diagnostic
0
20
40
60
Germline
0
20
40
60
Difference
−10
0
10
20
30
TACC1
TACC1
38683009
38689182
Unamplified Region
c.
FGFR1
NM_023110
TACC1
NM_006283
0
100
200
300
400
500
600
700
800
900
998
IG Domains
TM
TKD-1
TACC
RNAseq
GAAGACCTGGACCGCATCGTGGCCTTGACCTCCAACCAGGGGCTGCTGGAGTCCTCT...
Translation
E D L D R I V A L T S N Q G L L E S S
d.
FGFR3
NM_000142
TACC3
NM_006342
0
200
400
600
800
1000
1265
IG Domains
PHA03247
TM
TKD
TACC

Supplementary Figure 13. *MYB* rearrangements identified by WGS and mRNA-seq

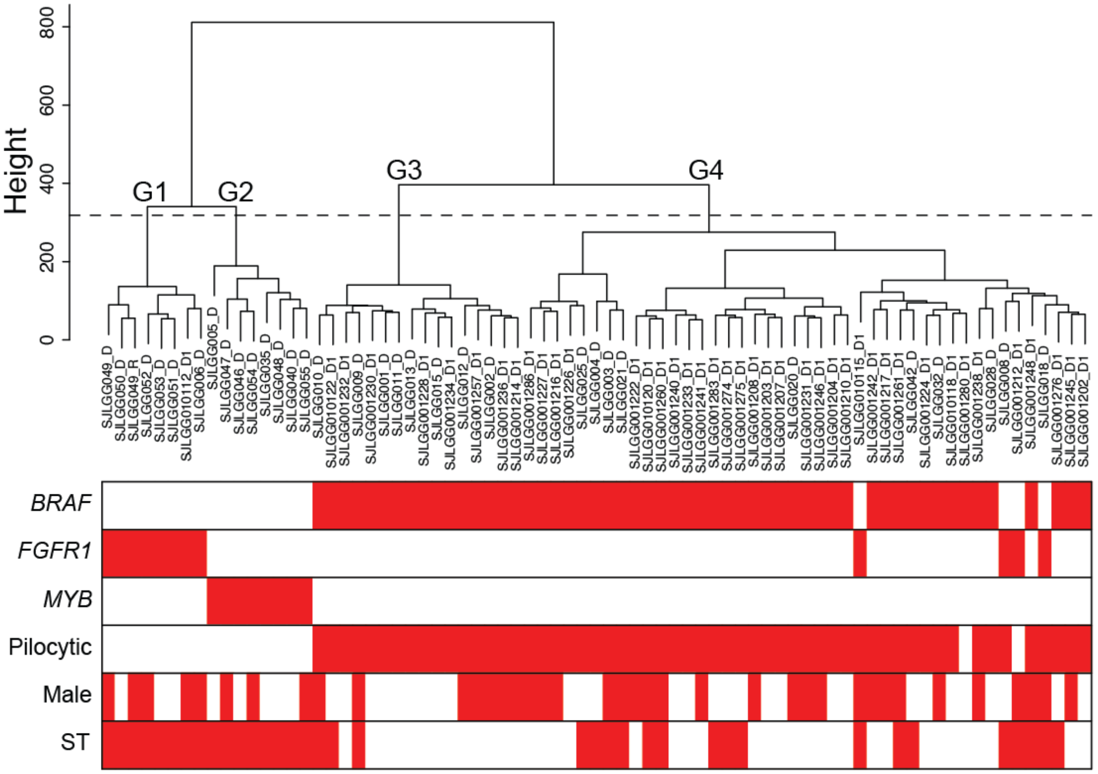
a. *MYB* rearrangement indicated by the splitting of green and red signals with ‘break apart’ iFISH probes. **b.** Start positions of breakpoints across a schematic of the MYB protein; the breakpoint for each tumor is indicated by its SJ sample number. **c.** *MYB* fusion partner genes; the breakpoint for each tumor is indicated by its SJ sample number. The *MYB-PCDHGA1* fusion was found in two samples. **d.** Fusion proteins resulting from MYB rearrangement; the MYB-QKI translocation is reciprocal, resulting in both MYB-QKI and QKI-MYB gene products.


a.
b.
MYB
NM_005375.2
SANT
LMSTEN
C-MYB
SJLGG048-MAML2
SJLGG005 - PCDHGA1
SJLGG046 - PCDHGA1
SJLGG040 - LOC154092
SJLGG055 - PCDHGA1
SJLGG047 - QKI
SJLGG054 - ESR1
0
100
200
300
400
500
640
c.
SJLGG005
SJLGG046
0
100
200
300
400
500
600
700
800
931
PCDHGA1
NM_018912
CAD
SJLGG047
0
100
200
300
341
QKI
NM_006775
SF1 LIKE-KH
SJLGG048
0
200
400
600
800
1000
1156
MAML2
NM_032427
MAML1
d.
MYB
PCDHGA1
0
100
200
300
400
522
MYB
QKI
0
100
200
300
400
500
600
700
760
MYB
MAML2
0
100
200
300
400
500
600
723
QKI
MYB
0
100
200
219

Supplementary Figure 14. Gene expression profiling using arrays and mRNA-seq

a. Unsupervised hierarchical clustering of tumors with gene expression array (Affymetrix U133 plus 2) profiling using top 10% most variable probe sets. The dotted line shows the threshold for determining subgroups. Status (positive: red) of each tumor for genetic alterations (*BRAF, FGFR1, MYB*), pathological phenotype (pilocytic), sex and anatomic site (ST: supratentorial). **b.** Analysis of association between variables and gene expression subgroups. Raw p values (two-sided Fisher's exact test) were calculated using 2X4 contingency tables. Variables significantly enriched or depleted in each subgroup are marked in red and green, respectively. Significance was determined by FWER (Familywise Error Rate) <0.05. **c.** Gene expression profiling using top 10% most variable exons based on read-depth in mRNA-seq. The dotted line shows the threshold for determining subgroups. Status (positive: red) of each tumor for genetic alterations (*BRAF*, *FGFR including FGFR3-TACC3 fusion, MYB including MYBL1 rearrangement*), pathological phenotype (pilocytic), sex and anatomic site (ST: supratentorial). **d.** Analysis of association between variables and gene expression subgroups. Raw p values (two-sided Fisher's exact tests) were calculated using 2X3 contingency tables. Variables significantly enriched or depleted in each subgroup are marked in red and green, respectively. Significance was determined by FWER (Familywise Error Rate) <0.05.

a.

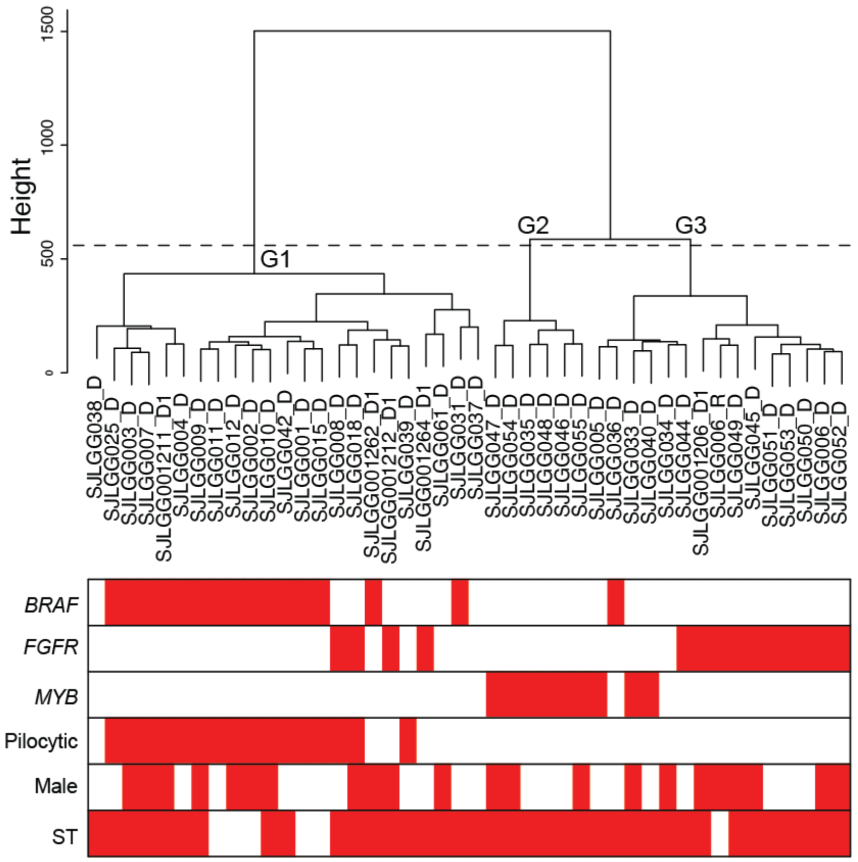


Sample clustering with top 10% most variable probesets

b.

Group	G1 (n = 8)	G2 (n = 8)	G3 (n = 16)	G4 (n = 43)	Total
BRAF	0 (0%) *p* = 7.47E-06	0 (0%) *p* = 7.47E-06	16 (100%) *p* = 4.18E-03	39 (91%) *p* = 1.35E-04	55
FGFR	8 (100%) *p* = 2.93E-08	0 (0%) *p* = 3.41E-01	0 (0%) *p* = 5.91E-02	4 (9%) *p* = 1.09E-01	12
MYB	0 (0%) *p* = 5.88E-01	8 (100%) *p* = 5.93E-11	0 (0%) *p* = 1.90E-01	0 (0%) *p* = 6.23E-04	8
Pilocytic	0 (0%) *p* = 2.59E-06	0 (0%) *p* = 2.59E-06	16 (100%) *p* = 8.48E-03	41 (95%) *p* = 5.94E-06	57
Male	5 (62%) *p* = 7.11E-01	3 (38%) *p* = 4.80E-01	7 (44%) *p* = 5.83E-01	23 (53%) *p* = 6.44E-01	38
ST	8 (100%) *p* = 1.79E-03	8 (100%) *p* = 1.79E-03	3 (19%) *p* = 1.08E-02	17 (40%) *p* = 1.06E-01	36

c.



Sample clustering with top 10% most variable exons

d.

Group	**G1 (n = 23)**	**G2 (n = 6)**	**G3 (n = 15)**	**Total**
BRAF	15 (65%) *p* = 2.83E-05	0 (0%) *p* = 7.18E-02	1 (7%) *p* = 3.37E-03	16
**FGFR*	4 (17%) *p* = 5.16E-02	0 (0%) *p* = 1.55E-01	10 (67%) *p* = 6.65E-04	14
MYB	0 (0%) *p* = 4.15E-04	6 (100%) *p* = 1.19E-05	3 (20%) *p* = 1.00	9
Pilocytic	16 (70%) *p* = 6.37E-07	0 (0%) *p* = 7.18E-02	0 (0%) *p* = 1.90E-04	16
Male	11 (48%) *p* = 1.00	3 (50%) *p* = 1.00	8 (53%) *p* = 1.00	22
ST	18 (78%) *p* = 1.88E-01	6 (100%) *p* = 5.73E-01	14 (93%) *p* = 6.47E-01	38

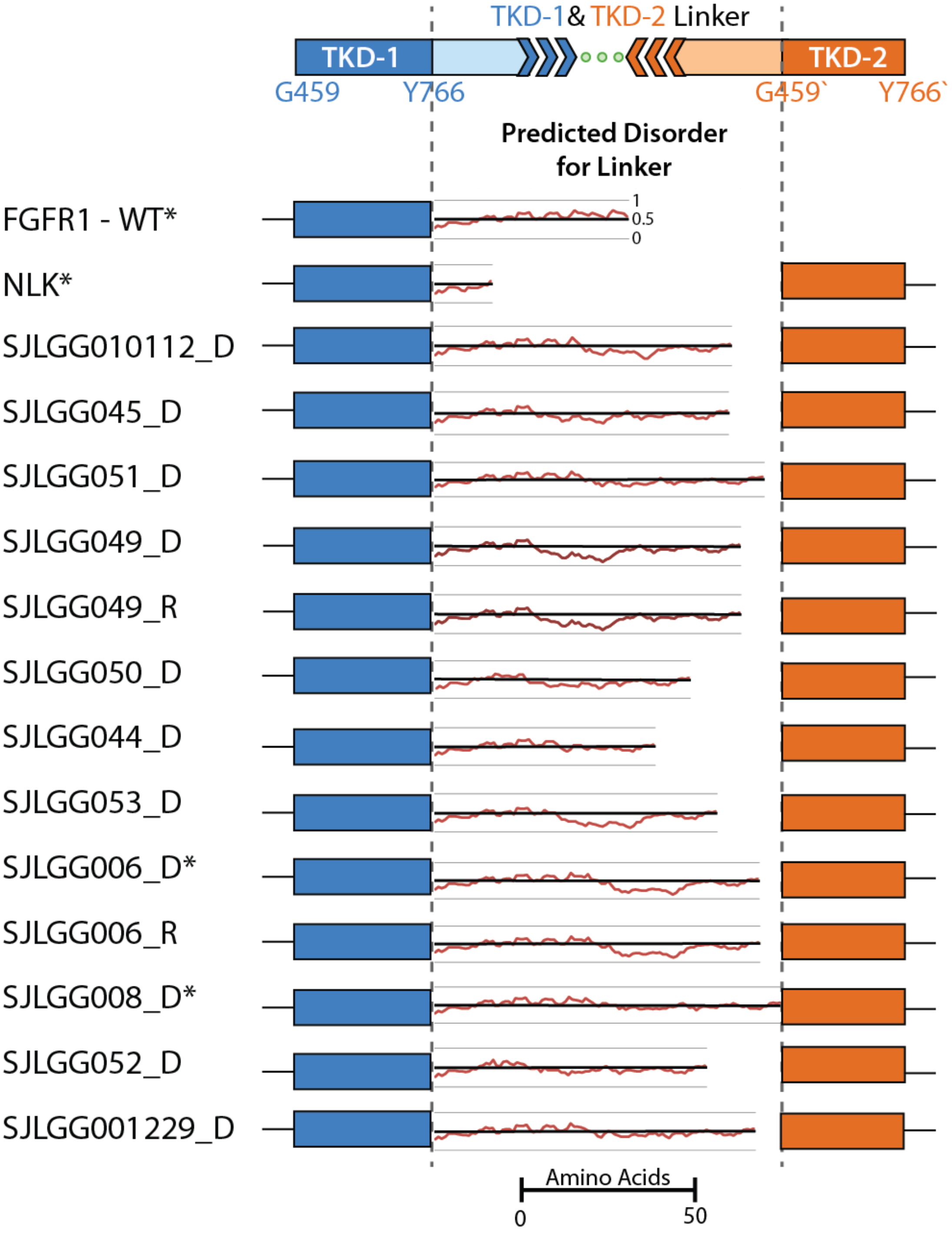
*Includes *FGFR1* lesions as well as *FGFR3-TACC3* fusion.

Supplementary Figure 15. TKD-duplicated FGFR1 proteins

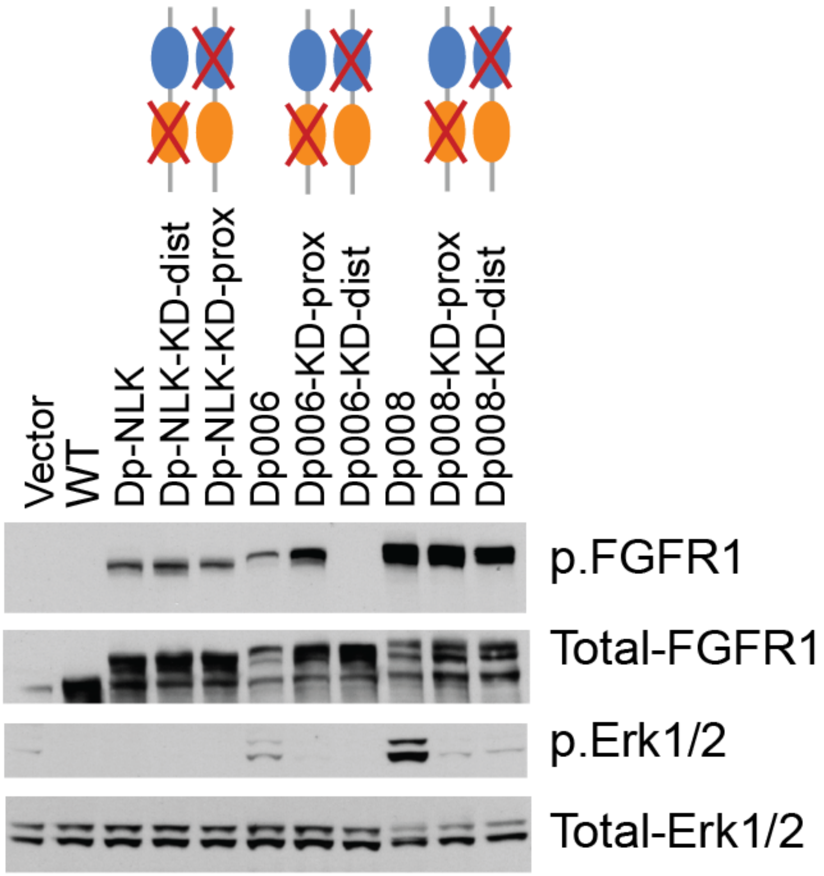
a. The program IUPred was used to analyze disorder, which reflects polypeptide flexibility within the natural N- and C-termini of wild-type (WT) FGFR1, as well as within the linker segments observed in the dual TKD fusion constructs. The C- terminal and N-terminal boundaries of the linkers between the proximal (TKD-1) and distal (TKD-2) TKDs were defined as Y766 and G459 (based on numbering of the WT domain). The IUPred per residue scores (graph between TKD-1 and TKD-2) range from 0 to 1 (light gray bars), with the value of 0.5 as a black bar. Values less than 0.5 are associated with order (foldedness) and those greater than 0.5 are associated with disorder (flexibility). The results indicate that linker peptides are predominantly disordered, consistent with a high degree of flexibility. Samples marked * were those tested for activity in HEK293T cells.

b. HEK293T cells transfected with expression vectors for wt FGFR1 (WT), a dual-TKD FGFR1 variant with no linker (Dp-NLK), and variants of Dp-NLK, Dp006, and Dp008 in which either the proximal or distal TKD was inactivated by mutation (e.g. Dp-NLK-KD-prox or Dp-NLK-KD-dist; KD = kinase-dead). Western blot analysis showed: (i) that Dp-NLK without any inactivating mutation could auto-phosphorylate, but not activate the MAPK pathway, (ii) that ligand-independent auto-phosphorylation was observed with most, but not all, partially kinase-dead mutants, and (iii) that kinase-dead mutants did not activate the MAPK pathway.

a.


TKD-1 & TKD-2 Linker
TKD-1
TKD-2
G459
Y766
G459`
Y766`
Predicted Disorder for Linker
FGFR1 - WT*
NLK*
SJLGG010112_D
SJLGG045_D
SJLGG051_D
SJLGG049_D
SJLGG049_R
SJLGG050_D
SJLGG044_D
SJLGG053_D
SJLGG006_D*
SJLGG006_R
SJLGG008_D*
SJLGG052_D
SJLGG001229_D
1
0.5
0
Amino Acids
0
50

b.



🔵 Proximal Tyrosine Kinase domain 1 (TKD-1)
🟠 Distal Tyrosine Kinase domain 2 (TKD-2)
⊗ Kinase Domain with inactivating mutation (KD)

Supplementary Table 1

Coverage and mapping status of WGS data

Genomic Coverage: the average coverage of all non-ambiguous bases in hg19.
Exon Coverage: the average coverage at all exonic bases (including all noncoding RNAs annotated in RefSeq).
% genomic bases covered: the percentage of all non-ambiguous bases covered at least 10x.
% exonic bases covered: the percentage of all bases in RefSeq annotated exons covered at least 10x.
% coding bases covered: the percentage of all RefSeq protein coding bases covered at least 10x.
% SNP detection: concordance of genotype calls derived by WGS and those of Affymetrix SNP 6.0

Patient	Sample	Lanes	% Reads Mapped	Nucleotides Sequenced	Genome Coverage	Haploid Coverage	Exon Coverage	% Genomic bases covered	% Exonic bases covered	% Coding bases coveres	% SNP Detection
SJLGG001	Diagnosis	5	95.18	166,408,914,800	46.2	41.93	42.4	99	93	93	99.23
SJLGG001	Germline	4	95.4	100,849,617,400	29	34.6	26.2	98	90	89	99.22
SJLGG002	Diagnosis	8	94.96	186,395,497,400	51.2	38.21	45.8	99	93	93	99.38
SJLGG002	Germline	8	94.96	104,221,185,000	29.8	34.23	27	98	91	90	99.51
SJLGG003	Diagnosis	5	95.31	149,292,812,200	41.2	41.85	38.1	99	94	93	99.12
SJLGG003	Germline	4	94.98	128,421,658,800	35.5	36.06	32.6	98	92	91	99.4
SJLGG004	Diagnosis	5	95.21	146,398,835,200	41.9	42.62	37.1	99	93	92	99.14
SJLGG004	Germline	4	95.31	128,902,756,600	34.6	35.15	33.4	99	97	97	99.59
SJLGG005	Diagnosis	5	95.42	193,918,962,400	50.8	51.16	46.4	99	93	93	99.14
SJLGG005	Germline	4	95.21	128,242,772,800	32.2	32.29	30.8	99	97	97	99.54
SJLGG006	Diagnosis	5	95.2	203,604,103,600	55.8	57.79	47.8	98	90	89	99.28
SJLGG006	Germline	3	93.65	118,647,418,400	33.3	34.04	29	98	88	86	99.17
SJLGG006	Relapse	5	94.97	167,357,521,600	47.6	48.42	43.3	99	93	92	99.45
SJLGG007	Diagnosis	5	94.25	202,384,639,000	56.3	57.4	49.2	99	91	90	99.29
SJLGG007	Germline	3	94.54	116,042,216,000	33.9	34.42	29.9	98	90	89	99.26
SJLGG008	Diagnosis	5	95.72	191,580,567,800	52.1	52.88	45.1	99	93	92	99.47
SJLGG008	Germline	3	94.48	119,935,146,000	35	35.56	30.9	99	93	93	99.51
SJLGG009	Diagnosis	5	95.8	206,164,401,200	51	52.17	48.6	99	98	99	99.59
SJLGG009	Germline	3	95.83	124,671,895,400	33.4	34.04	32.1	99	97	98	99.58
SJLGG010	Diagnosis	5	95.41	194,699,337,600	48.6	49.3	46.8	99	98	99	99.57
SJLGG010	Germline	3	95.16	124,693,263,800	33.8	34.31	32.1	99	97	98	99.56
SJLGG011	Diagnosis	5	95.96	190,182,982,400	46.8	47.14	44.9	99	99	99	99.55
SJLGG011	Germline	3	95.56	117,541,885,000	32	32.22	30.5	99	98	98	99.53
SJLGG012	Diagnosis	5	95.76	171,595,046,600	43.3	43.68	41.5	99	98	98	99.59
SJLGG012	Germline	3	95.56	112,886,966,600	29.7	29.93	28.4	98	97	97	99.56
SJLGG013	Diagnosis	5	95.61	192,615,886,800	47.8	48.09	41.8	98	92	92	99.5
SJLGG013	Germline	3	95.73	116,031,634,800	34.8	35.04	30.4	97	90	88	99.34
SJLGG015	Diagnosis	5	96.24	207,816,677,400	61.4	62.16	54.1	99	95	94	99.55
SJLGG015	Germline	3	93.62	127,812,011,200	36.3	36.59	32.4	99	93	92	99.49
SJLGG016	Diagnosis	5	95.45	183,555,139,400	48.9	49.63	43.5	99	94	93	99.51
SJLGG016	Germline	3	95.58	121,900,720,600	35.9	36.53	32.1	98	93	92	99.48
SJLGG018	Diagnosis	5	95.25	161,350,454,600	46.3	47.63	41.1	99	96	96	99.57
SJLGG018	Germline	3	93.28	110,778,253,800	31.4	32.37	27.3	98	94	94	99.47
SJLGG019	Diagnosis	5	92.83	160,018,056,000	46.2	47.61	43	98	97	97	99.55
SJLGG019	Germline	3	94.51	103,983,775,000	29.8	31.54	28.1	98	96	96	99.5
SJLGG020	Diagnosis	5	94.26	147,912,380,800	43.5	44.24	41.3	99	98	98	99.56
SJLGG020	Germline	3	93.64	98,277,317,400	29.2	29.62	27.1	98	96	96	99.5
SJLGG021	Diagnosis	5	94.41	156,384,864,600	45.6	46.19	42.7	99	98	98	99.57
SJLGG021	Germline	3	94.63	136,805,499,600	40.1	27.74	36.8	99	97	97	99.44
SJLGG022	Diagnosis	5	94.67	165,283,001,600	49.5	50.03	46.6	98	98	98	99.59
SJLGG022	Germline	3	94.72	101,757,995,600	30.8	31.04	28.9	98	97	97	99.56
SJLGG024	Diagnosis	5	94.81	194,310,538,600	57.2	58.01	52.1	98	96	96	99.58
SJLGG024	Germline	3	93.23	120,657,136,800	35.4	35.85	31.6	98	95	95	99.56
SJLGG025	Diagnosis	5	93.18	216,844,979,600	61.4	65.02	53.8	98	96	96	99.51
SJLGG025	Germline	3	91.56	133,551,266,800	37.1	38.73	32.8	98	95	95	99.44
SJLGG026	Diagnosis	5	93.41	231,236,306,400	65.3	68.06	60.2	99	98	98	99.53
SJLGG026	Germline	3	94.34	135,915,628,600	39.7	41.27	36	99	97	97	99.53
SJLGG027	Diagnosis	5	89.73	216,501,556,600	60.1	62.26	54.3	98	97	97	99.6
SJLGG027	Germline	3	92.53	130,078,719,800	37.8	39.04	34.4	98	97	97	99.6
SJLGG028	Diagnosis	5	91.13	205,241,413,000	55.5	59.31	49.4	98	97	97	99.56
SJLGG028	Germline	3	89.59	125,184,478,800	33.9	36.14	29.4	98	95	95	99.42
SJLGG029	Diagnosis	5	93.96	233,216,345,400	66	69.27	58.3	99	98	98	99.57
SJLGG029	Germline	3	92.81	139,871,360,000	39.8	41.31	34.5	99	96	97	99.55
SJLGG030	Diagnosis	5	93.31	220,768,809,200	61	64.55	54.6	99	98	98	99.52
SJLGG030	Germline	3	92.76	133,882,264,600	37.6	39.53	33.5	99	96	97	99.52
SJLGG031	Diagnosis	5	92.62	206,461,133,400	57.7	60.46	50.8	98	98	98	99.59
SJLGG031	Germline	3	93.99	132,379,685,200	38.2	39.77	34.2	98	97	98	99.58
SJLGG032	Diagnosis	5	90.51	173,483,837,000	46.7	49.59	41.9	99	96	96	99.49
SJLGG032	Germline	3	91.2	127,724,489,400	35.7	37.35	32	99	95	95	99.48
SJLGG033	Diagnosis	5	90.21	214,166,032,400	58.4	61.71	52.1	99	97	97	99.55
SJLGG033	Germline	3	90.95	130,830,833,000	35.2	36.78	31.7	98	92	91	99.42
SJLGG034	Diagnosis	5	91.58	212,051,387,600	58.4	61.45	51.9	99	96	96	99.55
SJLGG034	Germline	3	90.45	123,804,138,200	33.5	34.85	29.6	98	90	89	99.33
SJLGG035	Diagnosis	5	91.79	195,096,456,800	53.6	55.47	47.7	98	96	96	99.57
SJLGG035	Germline	3	92.54	115,639,977,200	33.3	34.29	29.3	98	94	94	99.51
SJLGG036	Diagnosis	5	91.83	194,104,117,200	52.8	55.18	47.2	99	96	96	99.52
SJLGG036	Germline	3	91.71	116,085,183,000	32.7	33.89	29	98	94	94	99.48
SJLGG037	Diagnosis	5	94.92	215,432,203,600	61.8	63.78	55.6	99	97	97	99.58
SJLGG037	Germline	3	94.29	130,660,147,000	38	39.03	33.2	99	95	95	99.56
SJLGG038	Diagnosis	5	94.44	208,642,455,600	60.4	61.79	53.5	98	95	95	99.53
SJLGG038	Germline	3	92.94	127,394,657,800	36.8	37.56	33	98	94	94	99.53
SJLGG039	Diagnosis	5	94.98	216,169,462,000	63.5	64.97	57.9	98	96	96	99.59
SJLGG039	Germline	3	93.38	123,418,128,400	36.6	37.25	32.8	98	95	95	99.58
SJLGG040	Diagnosis	5	93.92	226,340,769,400	64.2	66.59	56.9	98	97	97	99.55
SJLGG040	Germline	3	94.16	133,771,368,600	39.2	40.16	35	98	97	97	99.55
SJLGG042	Diagnosis	5	91.9	158,260,673,800	44.8	45.9	38.7	97	88	86	99.07
SJLGG042	Germline	3	92.16	120,511,902,400	34.6	35.86	28.8	96	83	79	98.49

Supplementary Table 2

Summary of somatic sequence mutations, SVs and copy number abnormalities identified in 39 LGG cases analyzed by WGS

* The majority (87%) of tier 1 mutations, including all non-silent mutations, were validated.
^ Tiers 2-3 include only high-quality or validated mutations. The average validation rate for these is 95%. Numbers of SVs and DNA CNVs in each case are not the same because (i) some SVs are copy-neutral rearrangements, (ii) CNVs from chromosomal gain or loss extending to the telomere will not be detected by WGS SV identification algorithms, and (iii) some CNV breakpoints are in repetitive or unmappable regions and will not be detected by SV algorithms.
\# The background mutation rate (BMR) was derived from the number of bases in non-repetitive genomic regions covered by WGS at >10x depth. Three samples (SJLGG016, SJLGG036, SJLGG039) with low tumor content were excluded from the calculation.

Sample	Sequence mutations					Copy number alterations (CNA)				SV	Combined CNV/SV (N)
	*tier1	non-silent tier1	^tier2	^tier3	#BMR	Amp (N)	Amp (Mb)	Del (N)	Del (Mb)		
SJLGG001	1	0	8	43	4.2203E-08	1	1.94	0	0	1	1
SJLGG002	1	0	3	36	3.2365E-08	1	1.95	1	0.01	1	2
SJLGG003	1	0	2	16	1.5346E-08	2	1.94	1	0	1	3
SJLGG004	2	1	2	24	2.2597E-08	1	1.94	0	0	1	1
SJLGG005	1	0	1	28	2.4183E-08	0	0	3	0.04	3	3
SJLGG006	0	0	1	7	6.5184E-09	1	0.01	0	0	1	1
SJLGG006R	0	0	1	7	6.5135E-09	0	0	0	0	1	1
SJLGG007	1	0	3	18	1.7847E-08	1	1.94	0	0	1	1
SJLGG008	12	3	13	146	1.3812E-07	8	977.22	0	0	1	8
SJLGG009	5	1	7	33	3.6056E-08	1	1.95	1	0	2	2
SJLGG010	4	2	1	48	4.2455E-08	2	136.96	0	0	1	2
SJLGG011	4	0	8	75	6.9714E-08	2	182.86	0	0	1	2
SJLGG012	4	1	9	91	8.3405E-08	2	182.85	0	0	1	2
SJLGG013	1	0	1	11	5.6801E-09	1	1.94	0	0	1	1
SJLGG015	2	2	2	22	2.0984E-08	2	1.98	0	0	1	2
SJLGG016	0	0	1	1	1.6131E-09	0	0	1	0	1	1
SJLGG018	1	1	5	22	2.2558E-08	2	0.45	1	0	2	3
SJLGG019	2	1	0	8	8.0353E-09	1	0.04	1	0.04	1	2
SJLGG020	0	0	8	37	3.6172E-08	1	1.96	0	0	1	1
SJLGG021	0	0	2	13	1.2021E-08	1	1.94	0	0	1	1
SJLGG022	1	1	2	1	3.2129E-09	0	0	0	0	0	0
SJLGG024	2	1	5	27	2.7337E-08	1	1.95	0	0	1	1
SJLGG025	0	0	1	22	1.8492E-08	1	1.95	0	0	1	1
SJLGG026	0	0	0	6	4.8074E-09	0	0	0	0	1	1
SJLGG027	3	2	5	31	3.1272E-08	1	1.94	0	0	1	1
SJLGG028	1	0	5	30	2.8972E-08	2	1.99	0	0	1	2
SJLGG029	2	1	3	42	3.7689E-08	0	0	0	0	0	0
SJLGG030	1	1	2	17	8.4189E-09	0	0	0	0	0	0
SJLGG031	1	0	1	4	4.8095E-09	0	0	0	0	2	2
SJLGG032	3	0	4	39	3.6992E-08	1	1.95	0	0	1	1
SJLGG033	2	1	3	27	2.5829E-08	0	0	3	0	5	6
SJLGG034	12	5	10	191	1.7257E-07	0	0	2	152.59	0	2
SJLGG035	1	1	4	21	2.0926E-08	4	1.1	5	4.49	4	9
SJLGG036	1	1	0	0	8.0473E-10	0	0	0	0	0	0
SJLGG037	5	1	3	22	2.4095E-08	0	0	0	0	0	0
SJLGG038	1	1	4	59	5.1495E-08	3	0.04	10	77.3	13	13
SJLGG039	0	0	1	11	9.6412E-09	13	37.84	0	0	19	19
SJLGG040	7	2	3	48	4.6502E-08	2	0.47	1	0	2	3
SJLGG042	6	1	15	110	1.0865E-07	1	1.95	11	1578.14	1	12
All	91	31	149	1394		59	1551	41	1813	76	113
mean	2	1	4	36	3.351E-08	2	40	1	46	2	3
standard deviation	3	1	4	40	3.673E-08	2	161	2	253	4	4
median	1	1	3	24	2.2597E-08	1	2	0	0	1	2
min	0	0	0	0	3.2129E-09	0	0	0	0	0	0
max	12	5	15	191	1.7257E-07	13	977	11	1578	19	19

Supplementary Table 3

Comparison of coverage and somatic coding mutation detection by exome sequencing and WGS

Sample	Exome sequencing			WGS	
	Average coverage	**Coding mutation(s)**	**Source**	**Average coverage**	**Coding mutation(s)**
SJLGG005_D	303	*RANBP6*$^{\text{P917L}}$	UK	48	*CACNA1A*$^{\text{Y1446Y}}$
SJLGG008_D	38	*DSG1*$^{\text{N286Y}}$ *FLT1*$^{\text{L29I}}$ *FLT1*$^{\text{T48A}}$ *SLC28A2*$^{\text{A335A}}$	BGI	44	*DSG1*$^{\text{N286Y}}$ *FLT1*$^{\text{L29I}}$ *FLT1*$^{\text{T48A}}$ *SLC28A2*$^{\text{A335A}}$ *MUC4*$^{\text{F4995F}}$ *CDH13*$^{\text{V16\_E2splice}}$
SJLGG030_D	63	*BRAF*$^{\text{V600E}}$ *ALDH18A1*$^{\text{I153V}}$	BGI	54	*BRAF*$^{\text{V600E}}$
SJLGG035_D	334	*DCTN1*$^{\text{R149*}}$	UK	47	*DCTN1*$^{\text{R149*}}$
SJLGG036_D	310	*BRAF*$^{\text{V600E}}$	UK	47	*BRAF*$^{\text{V600E}}$
SJLGG037_D	324	*COL14A1*$^{\text{P1482P}}$ *H3F3A*$^{\text{K27M}}$ *HUWE1*$^{\text{E2345E}}$	UK	56	*COL14A1*$^{\text{P1482P}}$ *H3F3A*$^{\text{K27M}}$ *HUWE1*$^{\text{E2345E}}$
SJLGG039_D	343	none	UK	58	none

Mutations detected by only one method are shown in red.

Supplementary Table 4

Clinical, pathological and genetic abnormalities of all 151 tumors in study cohort

Suffix '_D' or '_D1' denotes a biopsy from first diagnostic surgery. Two recurrent tumors have the suffix ' _R'.
Genetic abnormalities were identified by multiple approaches, including WGS, RNA-seq, iFISH, and RT-PCR / Sanger sequencing.

SJ Sample Name	Series	Age @ Sx	Sex	Site	Dx	FGFR abnormality	MYB / MYBL1 abnormality	BRAF abnormality	NF1 mutation	KRAS mutation	RAF1 fusion	Histone-related genes	Miscellaneous SNV #1	Miscellaneous SNV #2	Miscellaneous SNV #3	Miscellaneous SNV #4	Miscellaneous SV #1
SJLGG008_D	discovery_#1	17	F	CX	PA	FGFR1 TK duplication							DSG1:p.N286Y	FLT1:p.T48A & FLT1:p.L29I			
SJLGG045_D	discovery_#1	11	M	CX	DA	FGFR1 TK duplication											
SJLGG006_D	discovery_#1	1	M	CX	OA	FGFR1 TK duplication											
SJLGG006_R	discovery_#1	recurrent tumor			OA	FGFR1 TK duplication											
SJLGG044_D	discovery_#1	6	F	CX	OA	FGFR1 TK duplication											
SJLGG053_D	discovery_#1 & series #2	5	F	CX	DA	FGFR1 TK duplication											
SJLGG050_D	discovery_#1 & series #2	13	F	CX	DNET	FGFR1 TK duplication											
SJLGG049_D	discovery_#1 & series #2	4	M	CX	O	FGFR1 TK duplication											
SJLGG049_R	discovery_#1 & series #2	recurrent tumor			O	FGFR1 TK duplication											
SJLGG052_D	discovery_#1 & series #2	5	M	CX	O	FGFR1 TK duplication											
SJLGG051_D	discovery_#1 & series #2	6	F	CX	OA	FGFR1 TK duplication											
SJLGG001229_D1	series #2	2	M	SC	PA	FGFR1 TK duplication											
SJLGG010112_D1	series #3	5	M	CX	DA	FGFR1 TK duplication											
SJLGG018_D	discovery_#1	15	M	DE	PA	*FGFR1-TACC1*							TMPRSS11D:p.R6S				
SJLGG001212_D1	discovery_#1 & series #2	13	M	CX	DA	*FGFR1-TACC1*											
SJLGG001264_D1	discovery_#1 & series #2	2	F	CX	OA	*FGFR1-TACC1*											
SJLGG001206_D1	discovery_#1 & series #2	6	M	CX	DA	*FGFR3-TACC3*											
SJLGG001259_D1	series #2	14	M	CX	OA	FGFR1:p.N544K			NF1:p.T653fs	KRAS:p.G12D							
SJLGG010115_D1	series #3	17	M	DE	PA	FGFR1:p.N544K											
SJLGG001213_D1	series #2	5	F	DE	PA	FGFR1:p.N544K & p.V559M											
SJLGG035_D	discovery_#1	5	F	CX	DA		MYB episome						DCTN1:p.R149*				
SJLGG040_D	discovery_#1	8	F	CX	DA		MYB episome						MKI67:p.R1998*	SCN3A:p.A488S			
SJLGG054_D	discovery_#1 & series #2	3	M	CX	AG		*MYB-ESR1*										
SJLGG048_D	discovery_#1	4	F	CX	O		*MYB-MAML2*										
SJLGG005_D	discovery_#1	5	F	CX	DA		*MYB-PCDHGA1*						RANBP6:p.P917L				
SJLGG046_D	discovery_#1	4	F	CX	DA		*MYB-PCDHGA1*										
SJLGG055_D	discovery_#1 & series #2	4	M	CX	DA		*MYB-PCDHGA1*										
SJLGG047_D	discovery_#1	11	M	CX	AG		*MYB-QKI*										
SJLGG033_D	discovery_#1	9	M	CX	DA		*MYBL1* rearrangement						ADAMTS9:p.G569A				
SJLGG026_D	discovery_#1	0.4	M	CX	DIGG			*FXR1-BRAF*									
SJLGG031_D	discovery_#1	11	F	CX	GG			*BRAF-MACF1*									
SJLGG001262_D1	discovery_#1 & series #2	14	M	CX	OA			BRAF:p.G503>EYSG									
SJLGG001284_D1	series #2	10	F	DE	DA			BRAF:p.V600E				H3F3A:p.K27M					
SJLGG030_D	discovery_#1	3	M	CX	DA			BRAF:p.V600E					ALDH18A1:p.I153V				
SJLGG036_D	discovery_#1	3	M	CX	DA			BRAF:p.V600E									
SJLGG029_D	discovery_#1	5	M	CX	PA			BRAF:p.V600E									
SJLGG001281_D1	series #2	3	F	CX	DA			BRAF:p.V600E									
SJLGG001269_D1	series #2	17	F	CB	GG			BRAF:p.V600E									
SJLGG001271_D1	series #2	15	F	CX	GG			BRAF:p.V600E									
SJLGG001211_D1	discovery_#1 & series #2	3	M	DE	PA			BRAF:p.V600E									
SJLGG001243_D1	series #2	12	F	DE	PA			BRAF:p.V600E									
SJLGG001209_D1	series #2	8	M	CX	PXA			BRAF:p.V600E									
SJLGG001266_D1	series #2	16	F	CX	PXA			BRAF:p.V600E									
SJLGG001273_D1	series #2	8	F	CX	PXA			BRAF:p.V600E									
SJLGG001277_D1	series #2	9	F	CX	PXA			BRAF:p.V600E									
SJLGG010117_D1	series #3	9	M	CX	DA			BRAF:p.V600E									
SJLGG010124_D1	series #3	8	F	BS	GG			BRAF:p.V600E									
SJLGG010123_D1	series #3	2	M	BS	PA			BRAF:p.V600E									
SJLGG010133_D1	series #3	13	F	DE	PA			BRAF:p.V600E									
SJLGG010116_D1	series #3	6	F	CX	PXA			BRAF:p.V600E									
SJLGG010119_D1	series #3	8	M	CX	PXA			BRAF:p.V600E									
SJLGG010132_D1	series #3	12	F	CX	PXA			BRAF:p.V600E									
SJLGG001285_D1	series #2	14	F	CX	DA			*FAM131B-BRAF*									
SJLGG015_D	discovery_#1	10	F	CB	PA			*KIAA1549-BRAF*				ATRX:p.E991K		RINT1:p.R325W			
SJLGG009_D	discovery_#1	6	M	DE	PA			*KIAA1549-BRAF*				EP300:p.R1356*					
SJLGG042_D	discovery_#1	9	F	CX	PA			*KIAA1549-BRAF*					CDK13:p.R986H				
SJLGG012_D	discovery_#1	13	M	CB	PA			*KIAA1549-BRAF*					KIAA1239:p.N1170T				
SJLGG024_D	discovery_#1	3	F	BS	PA			*KIAA1549-BRAF*					LETM1:p.S580R				
SJLGG027_D	discovery_#1	10	F	DE	PA			*KIAA1549-BRAF*					NDUFB2:p.W74*	SPHK1:p.G111S			
SJLGG004_D	discovery_#1	0.5	F	DE	PA			*KIAA1549-BRAF*					NEURL4:p.T1239M				
SJLGG010_D	discovery_#1	3	M	CX	PA			*KIAA1549-BRAF*					NSMAF:p.V870I	PRIC285:p.A1017V			
SJLGG001_D	discovery_#1	4	F	CB	PA			*KIAA1549-BRAF*									
SJLGG002_D	discovery_#1	6	M	CB	PA			*KIAA1549-BRAF*									
SJLGG003_D	discovery_#1	1	M	DE	PA			*KIAA1549-BRAF*									
SJLGG011_D	discovery_#1	12	F	CB	PA			*KIAA1549-BRAF*									
SJLGG013_D	discovery_#1	7	F	CB	PA			*KIAA1549-BRAF*									
SJLGG016_D	discovery_#1	14	M	CX	PA			*KIAA1549-BRAF*									
SJLGG020_D	discovery_#1	5	M	CB	PA			*KIAA1549-BRAF*									
SJLGG021_D	discovery_#1	4	M	DE	PA			*KIAA1549-BRAF*									
SJLGG025_D	discovery_#1	5	F	DE	PA			*KIAA1549-BRAF*									
SJLGG028_D	discovery_#1	1	F	SC	PA			*KIAA1549-BRAF*									
SJLGG032_D	discovery_#1	9	M	CB	PA			*KIAA1549-BRAF*									
SJLGG007_D	discovery_#1	1	M	DE	PMA			*KIAA1549-BRAF*									
SJLGG001280_D1	series #2	13	F	BS	GG			*KIAA1549-BRAF*									
SJLGG001202_D1	series #2	18	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001203_D1	series #2	5	F	BS	PA			*KIAA1549-BRAF*									

SJLGG001204_D1	series #2	14	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001207_D1	series #2	3	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001208_D1	series #2	11	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001210_D1	series #2	2	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001214_D1	series #2	14	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001216_D1	series #2	3	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001217_D1	series #2	12	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001218_D1	series #2	16	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001222_D1	series #2	12	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001223_D1	series #2	6	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001224_D1	series #2	11	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001226_D1	series #2	16	F	SC	PA			*KIAA1549-BRAF*									
SJLGG001227_D1	series #2	16	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001228_D1	series #2	15	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001230_D1	series #2	2	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001231_D1	series #2	10	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001232_D1	series #2	2	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001233_D1	series #2	4	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001234_D1	series #2	3	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001236_D1	series #2	7	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001238_D1	series #2	2	M	SC	PA			*KIAA1549-BRAF*									
SJLGG001239_D1	series #2	7	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001240_D1	series #2	10	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001241_D1	series #2	6	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001242_D1	series #2	12	M	BS	PA			*KIAA1549-BRAF*									
SJLGG001244_D1	series #2	1	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001245_D1	series #2	12	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001246_D1	series #2	6	M	CB	PA			*KIAA1549-BRAF*									
SJLGG001247_D1	series #2	13	F	CB	PA			*KIAA1549-BRAF*									
SJLGG001248_D1	series #2	8	M	DE	PA			*KIAA1549-BRAF*									
SJLGG001256_D1	series #2	1	M	CX	PA			*KIAA1549-BRAF*									
SJLGG001257_D1	series #2	3	M	BS	PA			*KIAA1549-BRAF*									
SJLGG001260_D1	series #2	6	M	DE	PA			*KIAA1549-BRAF*									
SJLGG001261_D1	series #2	4	M	DE	PA			*KIAA1549-BRAF*									
SJLGG001263_D1	series #2	10	F	SC	PA			*KIAA1549-BRAF*									
SJLGG001274_D1	series #2	8	F	DE	PA			*KIAA1549-BRAF*									
SJLGG001275_D1	series #2	10	F	DE	PA			*KIAA1549-BRAF*									
SJLGG001276_D1	series #2	5	F	DE	PA			*KIAA1549-BRAF*									
SJLGG001279_D1	series #2	14	M	DE	PA			*KIAA1549-BRAF*									
SJLGG001283_D1	series #2	8	F	DE	PA			*KIAA1549-BRAF*									
SJLGG001286_D1	series #2	6	M	BS	PA			*KIAA1549-BRAF*									
SJLGG010114_D1	series #3	9	F	BS	PA			*KIAA1549-BRAF*									
SJLGG010118_D1	series #3	12	F	BS	PA			*KIAA1549-BRAF*									
SJLGG010120_D1	series #3	3	M	DE	PA			*KIAA1549-BRAF*									
SJLGG010122_D1	series #3	5	F	DE	PA			*KIAA1549-BRAF*									
SJLGG010127_D1	series #3	7	F	BS	PA			*KIAA1549-BRAF*									
SJLGG010128_D1	series #3	2	F	CX	PA			*KIAA1549-BRAF*									
SJLGG010113_D1	series #3	1	F	DE	PMA			*KIAA1549-BRAF*									
SJLGG001267_D1	series #2	16	F	CX	PA				NF1:p.N1721fs								
SJLGG001225_D1	series #2	11	M	CB	PA				NF1 W571* germline + LOH								
SJLGG022_D	discovery_#1	6	F	CB	PA				NF1:p.T2263 Y2264fs & p.R2214_E42 splice								
SJLGG010126_D1	series #3	8	F	DE	DA					KRAS:p.Q61H		H3F3A:p.K27M					
SJLGG010131_D1	series #3	12	M	DE	PA					KRAS:p.Q61H							
SJLGG019_D	discovery_#1	5	F	DE	PA						*QKI-RAF1*		TFDP1:p.A144V				
SJLGG001252_D1	series #2	7	M	CX	PA						*SRGAP3-RAF1*						
SJLGG037_D	discovery_#1	2	M	CX	DA							H3F3A:p.K27M					
SJLGG039_D	discovery_#1	10	F	CX	PA							ST6GAL1-WHSC1					*UBE2J2-PKD1*; *TP73-TBC1D22A*
SJLGG038_D	discovery_#1	13	F	CX	PXA								C3orf30:p.P12fs				*ETV6-NTRK3*
SJLGG034_D	discovery_#1	15	M	CX	O							CHD2:p.D1722V	IDH1:p.R132H	CIC:p.V676_R677fs & p.S726R	STYK1:p.P101L	BAI3:pI869_E18splice_region	
SJLGG061_D	discovery_#1 & series #3	4	M	CX	OA												*NAV1-NTRK2*
SJLGG001268_D1	series #2	15	F	CX	DA												
SJLGG001220_D1	series #2	7	M	CX	DA												
SJLGG001270_D1	series #2	6	M	CX	DA												
SJLGG001272_D1	series #2	13	M	CX	GG												
SJLGG001278_D1	series #2	16	M	CX	GG												
SJLGG001219_D1	series #2	9	M	CB	PA												
SJLGG001221_D1	series #2	1	M	BS	PA												
SJLGG001235_D1	series #2	6	F	DE	PA												
SJLGG001255_D1	series #2	4	M	DE	PA												
SJLGG001254_D1	series #2	10	F	CX	PXA												
SJLGG001265_D1	series #2	5	F	CX	PXA												
SJLGG010121_D1	series #3	14	M	CX	DA												
SJLGG010129_D1	series #3	11	F	CX	GG												
SJLGG010130_D1	series #3	3	F	CX	GG												
SJLGG010125_D1	series #3	10	F	DE	PA												

Anatomic sites: CX - cerebral cortex; DE - diencephalon; CB - cerebellum; BS - brainstem; SC - spinal cord

Pathologic diagnosis (Dx): PA - pilocytic astrocytoma; PMA - pilomyxoid astrocytoma; PXA - pleomorphic xanthoastrocytoma; DA - diffuse astrocytoma; OA - oligoastrocytoma; O - oligodendroglioma; GG - ganglioglioma; AG - angiocentric glioma; DIGG - desmoplastic infantile ganglioglioma; DNET - dysembryoplastic neuroepithelial tumor

Supplementary Table 5a

Gene coding sequence mutations (including both substitution variants and indels) for tumors analyzed by WGS

Sequence mutations (including both SNVs and indels) identified for 39 WGS cases.

Tiers 1, 2, 3 variations are reported in three separate tabs.

Gene	Sample	Chromosome	Position	Class	AA Change	Protein ID	mRNA Accession	Mut Reads Tumor	Total Reads Tumor	Mut Reads Normal	Total Reads Normal	Val Mut Reads Tumor	Val Total Reads Tumor	Val Mut Reads Normal	Val Total Reads Normal	Reference Allele	Non-reference Allele	Genotype	Flanking Region	Origin	Status	Validation Method
JAM3	SJLGG001_D	11	134021570	UTR_3	E9_UTR_3	21361905	NM_032801	15	48	0	25	90	284	0	194	A	G	A/G	GGATGGATGTTGCTGTACAC[A/G]GATGCTACAGACTTGTACTA	SOMATIC	VALID	454_SNP_DETECT
UGT3A1	SJLGG002_D	5	35961135	UTR_3	E6_UTR_3	288541304	NM_001171873	7	51	0	30	399	2218	0	1819	T	A	T/A	GAGTACAGGAGAGGGGCGTG[T/A]GGAGAGCCAAAAGGCAACTT	SOMATIC	VALID	454_SNP_DETECT
BICD1	SJLGG003_D	12	32260373	SILENT	E36E	51039802	NM_001714	5	33	0	32	164	662	0	498	G	A	G/A	GAGAAGATCCAGGCTGCCGA[G/A]TACGGGCTGGTGGTGCTGGA	SOMATIC	VALID	454_SNP_DETECT
CCDC105	SJLGG004_D	19	15132166	SILENT	A292A	226492892	NM_173482	8	22	0	32	648	2462	0	1814	G	A	G/A	GCATCCTGGGCATTTGCAGC[G/A]TGCGCCTTGGCGCTAAACGA	SOMATIC	VALID	454_SNP_DETECT
NEURL4	SJLGG004_D	17	7221962	MISSENSE	T1239M	53829370	NM_032442	12	31	0	31	28	112	0	84	G	A	G/A	GGATGGTGCCTTCAGGGCAC[G/A]TGTCCAGATTGGGCCCAAAC	SOMATIC	VALID	454_SNP_DETECT
CACNA1A	SJLGG005_D	19	13370440	SILENT	Y1446Y	148536846	NM_023035	12	58	0	27	115	603	0	488	G	A	G/A	AGAGCCCACAGCACATTGTC[G/A]TAATGGAATTCATACTTCTT	SOMATIC	VALID	454_SNP_DETECT
OR5J2	SJLGG007_D	11	55944727	SILENT	L212L	53828705	NM_001005492	15	62	0	38	202	1152	0	950	T	C	T/C	TCATTGCCATGGCCACCTTC[T/C]TGACTGTGATCATTTCCTAC	SOMATIC	VALID	454_SNP_DETECT
ARFRP1	SJLGG008_D	20	62331548	UTR_3	E7_UTR_3	197927203	NM_001134758	3	10	0	19					C	A	C/A	AGGGCCTCGAAAGGCCGCCG[C/A]TGCGCCCTGTGGAAAGGCTG	SOMATIC	PUTATIVE	
CDH13	SJLGG008_D	16	82891965	SPLICE_REGION	V16_E2splice_region	4502719	NM_001257	7	45	0	39	235	1158	0	923	A	G	A/G	TTGATGGCTTTGGTTTTCTC[A/G]GGTGCTGCTGCTAACATCTG	SOMATIC	VALID	454_SNP_DETECT
DSG1	SJLGG008_D	18	28914016	MISSENSE	N286Y	119703744	NM_001942	10	56	0	43					A	T	A/T	AAGAAAATACTCTAAATTCA[A/T]ATTTGCTCGAGATTAGAGTA	SOMATIC	VALID	SangerSequencing
FLT1	SJLGG008_D	13	29041734	MISSENSE	L29I	156104876	NM_002019	13	39	0	29					A	T	A/T	ACTCAGTTCAGGATCTTTTA[A/T]TTTTGAACCTGAACTAGATC	SOMATIC	VALID	SangerSequencing
FLT1	SJLGG008_D	13	29041677	MISSENSE	T48A	156104876	NM_002019	8	43	0	28					T	C	T/C	CCTGCATTGGAGATGCAGTG[T/C]CTGGCCTGCTTGCATGATGT	SOMATIC	VALID	SangerSequencing
LOC91948	SJLGG008_D	15	98286672	EXON	E3_exon	-1	Unknown	6	47	0	35					G	C	G/C	CCAGCAGAATTTTCCACATC[G/C]CAGGGAATGCTCTACAAAAT	SOMATIC	PUTATIVE	
MUC4	SJLGG008_D	3	195485996	SILENT	F4995F	257471027	NM_018406	4	23	0	26	73	613	0	540	A	G	A/G	GCCAGCCAAATAGTCCTACC[A/G]AAGAGCTCCAAGTCGGTGCA	SOMATIC	VALID	454_SNP_DETECT
PNPLA2	SJLGG008_D	11	825337	UTR_3	E10_UTR_3	32698724	NM_020376	10	37	0	22	122	474	0	352	G	A	G/A	GCTGCAGGCCAGGTCTCCCA[G/A]CGTCGCACTCCTGGGCCTGG	SOMATIC	VALID	454_SNP_DETECT
SLC28A2	SJLGG008_D	15	45559715	SILENT	A335A	227116277	NM_004212	7	39	0	32	148	903	0	755	G	A	G/A	ACACTCTCTGAAATCCATGC[G/A]GTGATGACTGGAGGGTTTGC	SOMATIC	VALID	454_SNP_DETECT
SNX8	SJLGG008_D	7	2294092	UTR_3	E11_UTR_3	23943858	NM_013321	11	34	0	25	101	408	0	307	T	C	T/C	AGGCACACATGGGGTCATCA[T/C]ATGGGCACAGGGCATGAGGC	SOMATIC	VALID	454_SNP_DETECT
TAF9B	SJLGG008_D	X	77385959	UTR_3	E7_UTR_3	20070280	NM_015975	4	32	0	37					T	G	T/G	CAAGTTACATCACATTAATT[T/G]GTTTTCTTTGTTGGCCTTAT	SOMATIC	PUTATIVE	
TCEA1	SJLGG008_D	8	54879301	UTR_3	E10_UTR_3	5803191	NM_006756	32	60	0	52	171	357	0	186	G	A	G/A	AGTGGGCCAATTCTTAACAC[G/A]GACATTTAAAAATGCTGCTT	SOMATIC	VALID	454_SNP_DETECT
C12orf12	SJLGG009_D	12	91346897	UTR_3	E1_UTR_3	22749303	NM_152638	14	41	0	31	162	490	0	328	C	T	C/T	GCGTTAGAATGTGCTTCTTA[C/T]GCATGTAATAAACTATCTCT	SOMATIC	VALID	454_SNP_DETECT
EP300	SJLGG009_D	22	41564765	NONSENSE	R1356*	50345997	NM_001429	10	46	0	38	572	3917	0	3345	C	T	C/T	TGGCAGAATCCTTTCCATAC[C/T]GAACCAAAGCCCTCTTTGCC	SOMATIC	VALID	454_SNP_DETECT
IGLON5	SJLGG009_D	19	51832972	UTR_3	E8_UTR_3	157819143	NM_001101372	5	39	0	46					A	G	A/G	GCAGCTGGCCCACAGGTGTG[A/G]GCTTGCTGGTCTATCACTTC	SOMATIC	PUTATIVE	
MACC1	SJLGG009_D	7	20177500	UTR_3	E7_UTR_3	157502191	NM_182762	10	46	0	33					G	C	G/C	AAATTCCTCTGGAAGGCTGG[G/C]AGCAGTGGCTCATGCCTGTA	SOMATIC	PUTATIVE	
SYNJ2BP	SJLGG009_D	14	70834140	UTR_3	E4_UTR_3	157388993	NM_018373	5	30	0	33					G	A	G/A	AATACAAAAATTAGCCAGGC[G/A]TTGTGGCACACACCTGTAAT	SOMATIC	PUTATIVE	
KCNJ2	SJLGG010_D	17	68172503	UTR_3	E2_UTR_3	4504835	NM_000891	21	40	0	24	593	1730	0	1137	C	T	C/T	GGAATAGTTACTTTACAACA[C/T]GGTCTGTTGGTCAGAGGCCC	SOMATIC	VALID	454_SNP_DETECT
LIMK2	SJLGG010_D	22	31662125	INTRON	intron	-1	Unknown	7	39	0	36	254	735	0	481	G	A	G/A	GGCAGGCTATCAAGGTGAGC[G/A]CAGGCAACAATTGCTTTGCT	SOMATIC	VALID	454_SNP_DETECT
NSMAF	SJLGG010_D	8	59498262	MISSENSE	V870I	31543297	NM_003580	21	50	0	28	199	560	0	361	C	T	C/T	TGCTCCAAGGAGGTCCCAAA[C/T]GAGCAGTTCACCAGACTGAC	SOMATIC	VALID	454_SNP_DETECT
PRIC285	SJLGG010_D	20	62197125	MISSENSE	A1017V	156105693	NM_001037335	18	39	0	22	9	22	0	13	G	A	G/A	CTGCCGCAGCCTCCGTCTGC[G/A]CTGTGGTTGCCGTGATGTCA	SOMATIC	VALID	454_SNP_DETECT
DOT1L	SJLGG011_D	19	2213961	SILENT	A591A	22094135	NM_032482	9	27	0	38	84	321	0	237	G	A	G/A	CTGGAGCAGGACAACCGCGC[G/A]CTCCGCGGCCAGAGCTTGCA	SOMATIC	VALID	454_SNP_DETECT
MAGEB16	SJLGG011_D	X	35820436	SILENT	S41S	153791873	NM_001099921	7	55	0	35	87	545	0	458	C	T	C/T	GAGAAGACCCTCCTCTCCTC[C/T]TCCCATCCTCTAGTGCCTGG	SOMATIC	VALID	454_SNP_DETECT
MLST8	SJLGG011_D	16	2258623	INTRON	intron	-1	Unknown	9	26	0	27	131	286	0	155	C	T	C/T	ACATCGTCACTGGTGAGCCC[C/T]GCCCTGGCCTCCCCCATCCC	SOMATIC	VALID	454_SNP_DETECT
PTP4A1	SJLGG011_D	6	64282387	UTR_5	E1_UTR_5	4506283	NM_003463	4	20	0	16	15	166	0	151	C	T	C/T	GGCTTGTGACGCAAGGGCGC[C/T]TCGGCGCGTGTATTGGCTCC	SOMATIC	VALID	454_SNP_DETECT
GCFC1	SJLGG012_D	21	34106210	UTR_3	E18_UTR_3	22035565	NM_016631	11	41	0	34	56	208	0	152	T	C	T/C	CAGGAAAATACAACAAAGGA[T/C]ATATTTAAAAATTAATTTAA	SOMATIC	VALID	454_SNP_DETECT
KIAA1239	SJLGG012_D	4	37447119	MISSENSE	N1170T	222418587	NM_001144990	6	40	0	31	13	1030	0	1017	A	C	A/C	AGGAAGTCTTTCTGTTTGGA[A/C]TACTGAGGACATTTCCAGCC	SOMATIC	VALID	454_SNP_DETECT
USP25	SJLGG012_D	21	17250980	UTR_3	E24_UTR_3	50312666	NM_013396	9	44	0	29	527	2119	0	1592	C	T	C/T	TAAAGCTGAAAATCGCATGG[C/T]GCTCAGACATTTTAACCGGA	SOMATIC	VALID	454_SNP_DETECT
USP26	SJLGG012_D	X	132161649	SILENT	S200S	13994268	NM_031907	12	24	0	16					A	C	A/C	TTGGATTTCTTGTATTCTAC[A/C]GAATTATTTTCTTTCAAGAA	SOMATIC	PUTATIVE	
LOC441869	SJLGG013_D	1	1353957	UTR_3	E4_UTR_3	223634006	NM_001145210	6	47	0	41					C	G	C/G	ATTTGAGCAAGCAGGCGGTA[C/G]GTGACAGGGGCTGCATGCAC	SOMATIC	PUTATIVE	
ATRX	SJLGG015_D	X	76937777	MISSENSE	E991K	20336209	NM_000489	18	63	0	30	7	88	0	81	C	T	C/T	GTCTGAAGGTTTCTTTTTTT[C/T]TTCAGTTCCCTTTTTGCTCT	SOMATIC	VALID	454_SNP_DETECT
RINT1	SJLGG015_D	7	105189134	MISSENSE	R325W	62899047	NM_021930	15	60	0	41	65	338	0	273	C	T	C/T	GGTATCACTTCAGAGGGAAC[C/T]GGCAGACTAATGTGTTAAGC	SOMATIC	VALID	454_SNP_DETECT
TMPRSS11D	SJLGG018_D	4	68725389	MISSENSE	R6S	4758508	NM_004262	21	51	0	30					G	T	G/T	TCTTGAAGTCGAAGTTACAC[G/T]TGCTGGCCTTACAAGAGAGA	SOMATIC	VALID	SangerSequencing
GIMAP2	SJLGG019_D	7	150390473	UTR_3	E3_UTR_3	28416431	NM_015660	12	60	0	36					A	G	A/G	AAAATGTGGTACCTGAAGTC[A/G]TATTTGAGATTCTATGAAAT	SOMATIC	VALID	MiSeq
TFDP1	SJLGG019_D	13	114287557	MISSENSE	A144V	6005900	NM_007111	5	31	0	24					C	T	C/T	AGTGGCAGACGAGCTGGTTG[C/T]GGAGTTCAGTGCTGCCGACA	SOMATIC	VALID	SangerSequencing
NF1	SJLGG022_D	17	29664899	splice	R2214_E43splice	4557793	NM_000267	8	31	7	16					G	A	G/A	TGGACAGAACTAGCTCAAAG[G/A]TATGTCCTAAATTAAATATA	GERMLINE	PUTATIVE	
NF1	SJLGG022_D	17	29665754	FRAMESHIFT	T2263_Y2264fs	4557793	NM_000267	10	42	0	35					TTAC	----	TTAC/----	GACCTGACAC[TTAC>----]AACAGTCAAG	SOMATIC	VALID	SangerSequencing
LETM1	SJLGG024_D	4	1821068	MISSENSE	S580R	6912482	NM_012318	13	42	0	29					G	T	G/T	GAGCAAATCCCACCCACCTC[G/T]CTGTAGTCCTGCACATCCTC	SOMATIC	VALID	SangerSequencing
LRFN5	SJLGG024_D	14	42356845	SILENT	N339N	31542244	NM_152447	18	61	0	40					C	T	C/T	AGATCTCTGGTGTATGATAA[C/T]GGAACACTTGACATTCTTAT	SOMATIC	VALID	MiSeq
ADAM6	SJLGG027_D	14	106436139	EXON	E2_exon	-1	NR_002224	7	40	0	32					C	T	C/T	GAGCAGTGCAATTATGAAGG[C/T]GTAAATACGACCAAAGACCA	SOMATIC	VALID	MiSeq
NDUFB2	SJLGG027_D	7	140402788	NONSENSE	W74*	4758778	NM_004546	13	63	0	36					G	A	G/A	CTGGATTCTCTGGCGCTTTT[G/A]GCATGACTCAGAAGAGGTGC	SOMATIC	VALID	SangerSequencing
SPHK1	SJLGG027_D	17	74382128	MISSENSE	G111S	217272880	NM_182965	8	17	0	27					G	A	G/A	TGGTGCTGCTGAACCCGCGC[G/A]GCGGCAAGGGCAAGGCCTTG	SOMATIC	VALID	SangerSequencing
IQGAP3	SJLGG028_D	1	156509309	SILENT	A971A	39753961	NM_178229	14	35	0	26					G	A	G/A	GGCATCTGAAAGATCAGCTT[G/A]GCCAGGTAGATGGGCTGAGT	SOMATIC	VALID	MiSeq
BRAF	SJLGG029_D	7	140453136	MISSENSE	V600E	33188459	NM_004333	21	74	0	45					A	T	A/T	ACCCACTCCATCGAGATTTC[A/T]CTGTAGCTAGACCAAAATCA	SOMATIC	VALID	SangerSequencing
LDB3	SJLGG029_D	10	88485964	SILENT	I573I	122056614	NM_001080114	10	41	0	33					C	T	C/T	GAGGCTGGCGACAAGTTTAT[C/T]GAAGCCCTGGGCCACACTTG	SOMATIC	VALID	MiSeq
BRAF	SJLGG030_D	7	140453136	MISSENSE	V600E	33188459	NM_004333	15	70	0	52					A	T	A/T	ACCCACTCCATCGAGATTTC[A/T]CTGTAGCTAGACCAAAATCA	SOMATIC	VALID	SangerSequencing
GCNT2	SJLGG031_D	6	10629111	UTR_3	E5_UTR_3	21717810	NM_145649	7	34	0	43					C	T	C/T	TAAAAAATATAAAAATTAGC[C/T]GGGCTTTGTGGCATGTGCCT	SOMATIC	PUTATIVE	
LOC440518	SJLGG032_D	19	22779180	EXON	E1_exon	-1	NR_033899	5	20	0	24					G	A	G/A	CCTTCCCGCCCTGCCATGTC[G/A]GAAGAAACCCGACGAGCAAA	SOMATIC	VALID	MiSeq
RDH8	SJLGG032_D	19	10132713	UTR_3	E6_UTR_3	7657478	NM_015725	9	34	0	36					C	T	C/T	GGGAGGCTTCCTGGAGGAAG[C/T]GGCATTGTTATGAGCCTTGA	SOMATIC	VALID	MiSeq
TBRG1	SJLGG032_D	11	124503339	UTR_3	E9_UTR_3	170650705	NM_032811	5	28	0	48					T	C	T/C	GGGACAAAAGGACCCAGAAG[T/C]AGAAGAATGGGGATGGAGTG	SOMATIC	VALID	MiSeq
ADAMTS9	SJLGG033_D	3	64633620	MISSENSE	G569A	33624896	NM_182920	10	54	0	31					C	G	C/G	ACAGGGCATTACTTGCCTTT[C/G]CAGGCTCGCACTCCGTCCCA	SOMATIC	VALID	SangerSequencing
SLC19A1	SJLGG033_D	21	46934966	UTR_3	E7_UTR_3	34808710	NM_194255	8	35	0	29					C	T	C/T	TGGGAGAGAGGAACCAGCTC[C/T]GAGGACCAGAGCCGCTGCTC	SOMATIC	VALID	MiSeq
ADAM11	SJLGG034_D	17	42855228	SILENT	H689H	4585710	NM_002390	18	37	0	27					C	T	C/T	CGCCGGATTTGCTCCCACCA[C/T]GGGGTGACTGCCTGGAGCCT	SOMATIC	VALID	MiSeq
BAI3	SJLGG034_D	6	69943313	SPLICE_REGION	I869_E18splice_region	4502359	NM_001704	25	67	0	29					GTAA	----	GTAA/----	GAAATAGTAA[GTAA>----]CAAAGGGAAA	SOMATIC	VALID	MiSeq
CHD2	SJLGG034_D	15	93567613	MISSENSE	D1722V	118421089	NM_001271	13	29	0	37					A	T	A/T	CTATTTCAGGCACCATCATG[A/T]CTCCAAGCGGAGGAGATCCG	SOMATIC	VALID	SangerSequencing
CIC	SJLGG034_D	19	42794946	FRAMESHIFT	V676_R677fs	112421108	NM_015125	15	4	0	17					GTGCG	-----	GTGCG/-----	CACCAATGTG[GTGCG>-----]GCCTGTCAGC	SOMATIC	VALID	SangerSequencing
CIC	SJLGG034_D	19	42795096	MISSENSE	S726R	112421108	NM_015125	13	15	0	14					A	C	A/C	GGGGCTCCCCGCTGGGTGTC[A/C]GCTTAGTGTATTCGGACAAG	SOMATIC	VALID	SangerSequencing
CIC	SJLGG034_D	19	42793092	SILENT	T328T	112421108	NM_015125	12	22	0	26					C	G	C/G	ACACTCCTGAGCTCAGACAC[C/G]AAGGCTCCGGGGAGCAGCTC	SOMATIC	VALID	MiSeq
DNAH2	SJLGG034_D	17	7699979	SPLICE_REGION	V2622_E49splice_region	75677365	NM_020877	11	29	0	22					C	T	C/T	GACATCTCCAAGGTGACTCG[C/T]GGCCTGACCTTGCCCCTTCT	SOMATIC	VALID	MiSeq
IDH1	SJLGG034_D	2	209113112	MISSENSE	R132H	28178825	NM_005896	24	44	0	35					C	T	C/T	CTTGATCCCCATAAGCATGA[C/T]GACCTATGATGATAGGTTTT	SOMATIC	VALID	SangerSequencing
LEPROTL1	SJLGG034_D	8	29963684	UTR_3	E4_UTR_3	189571652	NM_015344	20	60	0	45					A	G	A/G	GTTGATTTTTTTTGGAATCA[A/G]TATGCAATGTTAAACACTTT	SOMATIC	VALID	MiSeq
MS4A10	SJLGG034_D	11	60552828	UTR_5	E1_UTR_5	167466260	NM_206893	17	40	0	18					G	A	G/A	TTTCCCAGCGCTGTCTCTGG[G/A]GAGCTCCGGCAGCGCAAGAG	SOMATIC	VALID	MiSeq
STYK1	SJLGG034_D	12	10783793	MISSENSE	P101L	222352145	NM_018423	26	46	0	26					G	A	G/A	CCTGCAGCTTAGCCAGGGCA[G/A]GTGTGGTAGCTCCCAGAAAG	SOMATIC	VALID	SangerSequencing
TMEM155	SJLGG034_D	4	122680619	UTR_3	E6_UTR_3	112181171	NM_152399	27	57	0	46					T	C	T/C	CCCATTTGGCTATCTGAATT[T/C]AAATTAATTACAATTAAACA	SOMATIC	VALID	MiSeq
DCTN1	SJLGG035_D	2	74600063	NONSENSE	R149*	13259510	NM_004082	5	30	0	36					G	A	G/A	CTGTTTTCTCACCTTGGGTC[G/A]CCGAGTTGTGGTCTGGACAG	SOMATIC	VALID	SangerSequencing
BRAF	SJLGG036_D	7	140453136	MISSENSE	V600E	33188459	NM_004333	3	67	0	48					A	T	A/T	ACCCACTCCATCGAGATTTC[A/T]CTGTAGCTAGACCAAAATCA	SOMATIC	VALID	SangerSequencing
COL14A1	SJLGG037_D	8	121322292	SILENT	P1482P	55743096	NM_021110	6	52	0	44					G	A	G/A	AAGGGCCAGCAAGGTGAACC[G/A]GGTCCAAAGGTAATGCGCAT	SOMATIC	VALID	MiSeq

H3F3A	SJLGG037_D	1	226252135	MISSENSE	K28M	4504279	NM_002107	24	67	0	23					A	T	A/T	GGCTACAAAAGCCGCTCGCA[A/T]GAGTGCGCCCTCTACTGGAG	SOMATIC	VALID	SangerSequencing
HUWE1	SJLGG037_D	X	53590777	SILENT	E2345E	61676188	NM_031407	16	26	0	16					C	T	C/T	ATCAGGTCCTCCAGCTCATT[C/T]TCAACCTGGAGAGAAATAGA	SOMATIC	VALID	MiSeq
JPH2	SJLGG037_D	20	42740854	UTR_3	E6_UTR_3	21704281	NM_020433	11	37	0	22					A	G	A/G	CACAGAAATGAAGGGAGGAC[A/G]GCAGCAGTTCCCTCTGGCTC	SOMATIC	VALID	MiSeq
TBX18	SJLGG037_D	6	85444386	UTR_3	E8_UTR_3	122937456	NM_001080508	9	63	0	44					T	C	T/C	ATACTCATATTGTGGTATCA[T/C]CTGAAATGATCAACGGCAAG	SOMATIC	VALID	MiSeq
C3orf30	SJLGG038_D	3	118865071	FRAMESHIFT	P12fs	282847424	NM_152539	13	64	0	29					--------	GGCTGAA	--------/GGC	CTGGCTGAAC[-------->GGCTGAAC]CCTTGAAACA	SOMATIC	VALID	SangerSequencing
MKI67	SJLGG040_D	10	129904112	NONSENSE	R1998*	103472005	NM_002417	9	47	0	45					G	A	G/A	CCCCAAGGATATCTTGAGTC[G/A]TTGCTTGGAGCTTGTTGGGG	SOMATIC	VALID	SangerSequencing
MORC1	SJLGG040_D	3	108829638	SPLICE_REGION	R40_E3splice_region	221625538	NM_014429	12	64	0	48					C	G	C/G	AGCCCCTGCATCTCTGGAAA[C/G]AATACAAAAATATTATTTCT	SOMATIC	VALID	MiSeq
NEBL	SJLGG040_D	10	21073603	UTR_3	E7_UTR_3	47087157	NM_213569	19	57	0	41					G	T	G/T	CCAGCTTCCATTGCTTCACT[G/T]GCTTCTGTTACATTTTCTTC	SOMATIC	VALID	MiSeq
SCN3A	SJLGG040_D	2	166003458	MISSENSE	A488S	126362947	NM_001081676	17	58	0	52					C	A	C/A	TTTGGAACTCAACTTTGATG[C/A]TTCTGAAGAACTTTCCAACA	SOMATIC	VALID	SangerSequencing
SLC26A7	SJLGG040_D	8	92407399	UTR_3	E19_UTR_3	16306483	NM_052832	16	59	1	54					C	A	C/A	TATGCTGGCATTTTGCACAA[C/A]TTTTTGGTTGTTTAGATCCT	SOMATIC	VALID	MiSeq
SLC30A8	SJLGG040_D	8	118187125	UTR_3	E11_UTR_3	64762489	NM_173851	7	60	0	50					G	A	G/A	GTTTATATGGCAAAATGCAA[G/A]ACAATCTACAAGGGAGATTT	SOMATIC	VALID	MiSeq
ZNF493	SJLGG040_D	19	21590539	UTR_5	UTR_5	115511042	NM_175910	24	77	0	44					A	G	A/G	TCAATGTACTGTGGTTTTTT[A/G]TGTGTAAGATTATATGTTCC	SOMATIC	VALID	MiSeq
CDK13	SJLGG042_D	7	40118378	MISSENSE	R986H	145309302	NM_003718	14	38	0	28					G	A	G/A	TGCCTTGGATCCTAGTAAGC[G/A]CTGCACTGCTGAACAGGCTC	SOMATIC	VALID	SangerSequencing
KIAA1033	SJLGG042_D	12	105516023	SPLICE_REGION	A263_E10splice_region	40018629	NM_015275	9	52	0	42					A	T	A/T	GAATGATATTCCAGGTAAGT[A/T]GGTCTGTATCAGACTGTAAC	SOMATIC	VALID	MiSeq
LOC678655	SJLGG042_D	12	6552721	EXON	E5_exon	-1	NR_015382	11	31	0	25					G	A	G/A	TTTACCACAACCTGGAAATG[G/A]CTGGTGACAGAAAAGTCCTC	SOMATIC	VALID	MiSeq
OTC	SJLGG042_D	X	38267988	SPLICE_REGION	G222_E7splice_region	38788445	NM_000531	22	43	0	53					C	A	C/A	ATAAGATTTAAATTCTTCCT[C/A]CTTTAGGGTTATGAGCCGGA	SOMATIC	VALID	MiSeq
RASL10B	SJLGG042_D	17	34068967	UTR_3	E4_UTR_3	15277321	NM_033315	10	24	0	18					T	A	T/A	GAGGGGAGAAGGTTGAGCTC[T/A]CCGGCTTCCAGGGAGACCTC	SOMATIC	VALID	MiSeq
ZMAT3	SJLGG042_D	3	178737580	UTR_3	E6_UTR_3	11968019	NM_022470	10	35	0	37					A	T	A/T	CAATTAATAATTATTGTGCC[A/T]GTCTCTTCGCTTTAGCTGCA	SOMATIC	VALID	MiSeq

Column definition for tier 1 (extrapolate for tiers 2 & 3) listed below:

A. GeneName: HUGO gene symbol
B. Sample: name of the sample
C. Chromosome: chromosome
D. Position: chromosome position in hg19 coordinates.
E. Class: classification based on amino acid change pattern. ‘exon’ refers to mutations in non-coding RNA genes; ‘splice_region’ refers to mutations not directly affecting the canonical splice sites but located within 10bp of the canonical splice sites.
F. AAChange: predicted amino acid change for the mutation
G. ProteinGI: NCBI protein GI number
H. mRNA Accession: RefSeq accession number
I. # Mutant_In_Tumor: number of WGS reads containing mutant allele (tumor)
J. # Total_In_Tumor: number of WGS reads covering the site (tumor)
K. # Mutant_In_Normal: number of WGS reads containing mutant allele (normal)
L. # Total_In_Normal: number of WGS reads covering the site (normal)
M. # Mutant_In_Tumor_Validation: number of reads containing mutant allele in 454 validation sequencing (tumor)
N. # Total_In_Tumor_Validation: number of reads covering the site in 454 validation sequencing (tumor)
O. # Mutant_In_Normal_Validation: number of reads containing mutant allele in 454 validation sequencing (normal)
P. # Total_In_Normal_Validation: number of reads covering the site in 454 validation sequencing (normal)
Q. Reference Allele: the allele represented in the reference human genome. Reference allele is marked as ‘–’ for an insertion.
R. Non-reference Allele
S. Genotype of the tumor sample
T. Flanking: 20bp [reference allele/mutant allele] 20bp
U. Origin: somatic or germline mutation
V. Status: is this a putative mutation or a experimentally validated mutation
W. Validation Method: one of 454 or MySEQ or Sanger sequencing

Supplementary Table 5b

Single nucleotide substitutions in conserved regions for tumors analyzed by WGS

Name	SJQuality	Sample	Chromosome	Position	Mut Reads Tumor	Total Reads Tumor	Mut Reads Normal	Total Reads Normal	Reference Allele	Non-reference Allele	Flanking Region
chr1_163776629_163776897	SJHQ	SJLGG001	chr1	163776690	8	33	0	20	C	T	GACAGGTACCCCAGGAATTT[C/T]GATAGATGCCTGACAGGCCA
chr13_65191339_65191723	SJHQ	SJLGG001	chr13	65191512	17	40	0	37	C	G	TATGTCTGTAACAGATGTAT[C/G]CAAGTGATAGGAGTGAAAGG
chr2_119191407_119191523	SJHQ	SJLGG001	chr2	119191421	9	31	0	17	A	G	GGGGCGGGGAAGGGCAAGTG[A/G]ACATGGCACATTTCTGAGCA
chr6_110157149_110157465	SJHQ	SJLGG001	chr6	110157436	7	47	0	44	G	T	CCTTTTGAATCATTGTTTCA[G/T]GTCAATTAAACTTGTGTAAA
chrX_128461194_128461326	SJHQ	SJLGG001	chrX	128461258	18	44	0	35	C	T	GTCACCCCATTTGGAACTCA[C/T]TTCCTCTGCAAATCTTTGCT
chrX_129164032_129164239	SJHQ	SJLGG001	chrX	129164182	8	51	0	34	G	A	ATAACCATAAAGTGCTCTCC[G/A]AGGGTTGCTGTGCATCATTG
V$CEBP_C	SJHQ	SJLGG001	chr21	24762805	13	54	0	37	G	A	CAACTGAAGTAAAATCTGTC[G/A]AAATGCACCATGAAGCTTTG
chr7_69563014_69563545	SJHQ	SJLGG002	chr7	69563511	15	68	0	42	G	C	GCCATGCAGCTGTTGCCATG[G/C]CTAGCTGTGGGGTACCGGTG
chrX_73381103_73381237	SJHQ	SJLGG002	chrX	73381138	17	28	0	14	C	A	ATGTTCCCACTTTCTGTCTC[C/A]GTGGCTCCTCTCTCCTCCTC
V$POU3F2_01	SJHQ	SJLGG003	chr13	40854817	14	52	0	40	C	T	TAATAAAATAAATGTATGCA[C/T]GAATAAAAATAAATCAAAGA
V$RORA1_01	SJHQ	SJLGG003	chr2	232983699	6	45	0	39	C	T	CCTTAATTCACTTGGTAGTC[C/T]TCCTGTTTTCAGGTCACACC
chr5_167231777_167231877	SJHQ	SJLGG004	chr5	167231769	10	49	0	32	G	T	ATCACGGCATGGCGATCAAG[G/T]GACAGCTTAATTGTCAGAGG
chrX_139380963_139381915	SJHQ	SJLGG004	chrX	139381840	12	42	0	26	C	A	CATTTATCTCATTGTAGGAA[C/A]TGTCATCCTGGTTTTGTACC
chr6_135516249_135516393	SJHQ	SJLGG005	chr6	135516392	13	61	0	32	G	C	TCTGCTTTCCTAACCACGTT[G/C]ATTTGGCAGTGCTTCACTGC
chr3_87122977_87123456	SJHQ	SJLGG007	chr3	87123426	12	83	0	38	A	T	ATCATTAAAAAATAATCATA[A/T]GCACAACCAAAATGTCAATT
chr3_90190823_90191161	SJHQ	SJLGG007	chr3	90191138	8	47	0	40	C	T	AGCTCCTCGTTACATCACTG[C/T]CAGAGGGGGTGGAAAGAGTA
chr5_166075134_166075254	SJHQ	SJLGG007	chr5	166075151	17	77	0	31	A	G	GCATTCACAGACTTTTACCT[A/G]CAACTGAAAGAATGCTCAAG
chr10_111188977_111189105	SJHQ	SJLGG008	chr10	111189059	10	53	0	38	A	C	CAAGCCTTTCCACACTAGAA[A/C]GGATTTACCAGTCTCCTGAG
chr11_78521249_78521381	SJHQ	SJLGG008	chr11	78521250	21	52	0	28	C	G	ACACAAGGACAACGCAATGA[C/G]GCTTCACCAGAGAAACAGAA
chr11_92422575_92422678	SJHQ	SJLGG008	chr11	92422597	16	62	0	33	C	T	TAAATAGCACCTAAAGATGG[C/T]ATCATTTCATACGACATCCT
chr12_86147258_86147417	SJHQ	SJLGG008	chr12	86147415	8	50	0	40	T	C	AATAAATATGAATCATTTTG[T/C]ATTATCACAATAATAAAAGA
chr4_80461441_80461618	SJHQ	SJLGG008	chr4	80461513	14	40	0	39	T	C	GTGGCTGGAAACTGTCCAGG[T/C]GATAAGCATCAGGATGCTGT
chr8_29886831_29886955	SJHQ	SJLGG008	chr8	29886830	18	59	0	36	G	C	TGGGCATACTTTCTCTCTGA[G/C]TAGGAGGGAGCTTTTTGTGA
chr8_38515478_38515681	SJHQ	SJLGG008	chr8	38515624	9	60	0	30	T	C	GGAGCCAGGGGGCAATGTAA[T/C]ATAACAAAGCATTTTTCACA
chrX_78020252_78020354	SJHQ	SJLGG008	chrX	78020243	8	52	0	44	G	A	AATTGGACTCAGTGATCTCT[G/A]AGGTCAAACTTTTTGGAAAA
CpG_DEPTOR_0	SJHQ	SJLGG008	chr8	120885829	10	29	0	21	G	A	TAGCAGCGCCCCGCCCAGAT[G/A]TTTATATTTTCCTCCATCGG
CpG_PRKD1_0	SJHQ	SJLGG008	chr14	30396237	4	12	0	18	T	C	ACTGGAGAGAAATCGGTGAA[T/C]AGAGGAAGATGGGGCGAGAG
V$HEN1_02	SJHQ	SJLGG008	chr15	93153494	5	34	0	38	C	T	GGCCCTCGTTTGACAGGCTC[C/T]CCGTGGGCAGCAGCTGCCTT
V$PAX4_02	SJHQ	SJLGG008	chrX	86873968	7	53	0	50	T	C	AGGTGGTAATTATTTAAATG[T/C]TGCATATGATAAGATAGAGC
chr10_95083974_95084199	SJHQ	SJLGG009	chr10	95083998	9	60	0	49	T	A	TTTTTGAGTGTTCTGTAGAC[T/A]CTGTCTTCAGACAAAAACAA
chr13_88940658_88941046	SJHQ	SJLGG009	chr13	88940805	7	46	0	35	C	T	CAGCTGTAGTACTTCATAAT[C/T]TGCCCCTCCCAAGACTGAAT
chr2_144827672_144828232	SJHQ	SJLGG009	chr2	144828206	12	49	0	41	T	C	AGTGAGCTGTGTTAACACAA[T/C]AGACCATCTCAGGGAGAGCA
chr5_166713874_166714566	SJHQ	SJLGG009	chr5	166713910	8	56	0	32	C	A	TGTTTAGTCTTGTTCCCCTC[C/A]ATTGATAATAATGGAGGTTG
V$RFX1_02	SJHQ	SJLGG009	chr19	51017982	8	26	0	32	C	T	CCCAGCCACCACCTGGTACC[C/T]GCTGCAGTGTTTCCATGGCA
CpG_WDR85_0	SJHQ	SJLGG010	chr9	140473002	7	29	0	32	G	C	ATCCCCTCTTCATCTCCTGG[G/C]CGATTCGGTGCGCCTTTCGG
chr12_119895523_119895791	SJHQ	SJLGG011	chr12	119895528	6	35	0	30	G	A	ACTTGGTGGTTGGCGGGGGG[G/A]AGAATAATACAACACATCCT
chr1_3057065_3057211	SJHQ	SJLGG011	chr1	3057175	18	44	0	27	G	A	GGCTATTTATCTTTTGCAGC[G/A]ATATTTTACCCTCAGAGCTG
chr16_64235741_64235891	SJHQ	SJLGG011	chr16	64235802	7	47	0	35	A	T	TGTGATCTCTTTTACTAAAA[A/T]GGTCTCCCAAGCTTGGTCCC
chr8_21480877_21481184	SJHQ	SJLGG011	chr8	21481113	23	52	0	31	G	A	GGGAAATATCAGACAGCTTT[G/A]CTAGAAGTGAAGTTTCCACC
chr9_120820403_120820726	SJHQ	SJLGG011	chr9	120820645	22	48	1	24	A	G	GCAAAGAAAATAACCCAATA[A/G]GGTGTATGAGCCTGGAATAG
V$HNF1_C	SJHQ	SJLGG011	chr6	92991729	5	26	0	30	G	C	TCAAATCAGAATGGGAAAAT[G/C]AGTTATTCACTGACACATGA
V$NKX22_01	SJHQ	SJLGG011	chr14	57253200	8	33	0	30	A	T	GGCGTTTCCAAATGCATATA[A/T]TTAAACATTAAGTGGTCTCT
chr10_120001038_120001184	SJHQ	SJLGG012	chr10	120001108	11	38	0	28	A	G	GAAGAACCACTGAGGAAAGC[A/G]TGCCACAGTCTTTCCCAAAA
chr12_63149021_63150071	SJHQ	SJLGG012	chr12	63149804	8	41	0	32	C	T	AAGGTGGTGAAGCAGGCGTC[C/T]GAGACCCCCTCAAGGGCATC
chr2_156987724_156988147	SJHQ	SJLGG012	chr2	156987906	13	43	0	39	G	C	GGTACTTATATTACAAGATA[G/C]ATAAGAGGGGAAAAAAGGAG
chr8_31941899_31942035	SJHQ	SJLGG012	chr8	31942039	10	41	0	41	G	A	CTTCCCATGGTTTATTTTAA[G/A]TCTGAATTTGCATACAAACA
chrX_128382209_128382761	SJHQ	SJLGG012	chrX	128382293	14	24	0	13	C	T	AGGCGGCAAAGCTGCAGCTG[C/T]GCTATCAATTAGAACATTCT
CpG_NELF_0	SJHQ	SJLGG012	chr9	140349840	6	25	0	27	G	T	GGGACAGTGGTGCGAGCAGA[G/T]GGCCCAGCAGGGCGTCTGGG
V$LMO2COM_02	SJHQ	SJLGG012	chr7	110082825	14	48	0	37	G	A	TTTACAAAAGAAGGAACTCC[G/A]TATCAGTGTTTCTTCTCAGT
V$PBX1_02	SJHQ	SJLGG012	chr12	60365511	22	62	0	39	C	T	CTTTGATTGATATATTTTAA[C/T]GTGAGCAAAGTGATACCTCA
chr12_110522399_110522515	SJHQ	SJLGG015	chr12	110522459	7	58	0	39	A	G	GCGCCAACAGGGAAAACAGG[A/G]ATTCCCGGGTGGTGGTAAGA
chr8_74363813_74364286	SJHQ	SJLGG015	chr8	74363941	16	65	0	37	G	C	TGACAGACCTTGCTGGAGGA[G/C]AACAAGGGCTGTTTGTGCAG
chr6_44095961_44096359	SJHQ	SJLGG016	chr6	44096343	5	11	0	14	C	G	TGGGTCCCCTGGGCAGAGGT[C/G]TGGCCGCTCGGGGCAAGCCT
chr2_174440927_174441088	SJHQ	SJLGG018	chr2	174441042	6	37	0	29	C	T	AGCAAAAGTCTCCACCTCTT[C/T]CTTTCCCTGGTACACTTCCT
chr4_22711471_22712394	SJHQ	SJLGG018	chr4	22711892	19	52	0	47	C	T	GAAGAAAGTCAATTAGTTTC[C/T]GTGACTTTACCAGTAGGTTA
chr5_73737453_73737656	SJHQ	SJLGG018	chr5	73737617	14	43	0	30	G	A	AGCTTATGCCCAAGGGAGAC[G/A]GAGCCATAAGCCAATTTACA
chr7_41505176_41505538	SJHQ	SJLGG018	chr7	41505476	4	29	0	33	C	T	ATGTGGACATTAGAAGGTTA[C/T]GGACTGTGTGGCATTTTCAC
CpG_OR4Q3_600694	SJHQ	SJLGG018	chr14	19614672	10	16	0	16	G	A	TGGCCTGCAGCCCGCACTGC[G/A]GAGTGCTGGAGGTCCTTGAG
chr10_20466218_20466360	SJHQ	SJLGG020	chr10	20466238	5	16	0	15	G	A	CTGTTAGTCTTGGTGAATCT[G/A]TTCTTTCCTCTTCCCTAGCA
chr5_84012887_84013205	SJHQ	SJLGG020	chr5	84013146	19	60	0	45	G	A	CATTTCTGTAGAGGATTAGC[G/A]CCATTTATCAAGTAGTGACT
chr5_87030133_87030240	SJHQ	SJLGG020	chr5	87030202	15	34	0	38	T	C	AAAAGGTTTTCAGGGATGTC[T/C]TTTATCTTTAGAATTCATTC
chr7_139376443_139376570	SJHQ	SJLGG020	chr7	139376550	14	73	0	25	G	T	TGAAACGGAGCTGCTCTGAT[G/T]ATTAAATGAAACTGTATACA
CpG_CHRNA4_0	SJHQ	SJLGG020	chr20	61979359	15	30	0	24	G	A	GGGGACGCGGCCGCCCTCTC[G/A]CCCTTTCCTATGTGCCTTTA
CpG_MLN_171812	SJHQ	SJLGG020	chr6	33944016	9	35	0	18	C	T	CAGGATGGGGGTCGCCTCTC[C/T]GAAAGGCTGCGCTTCCTCAT
CpG_XKR5_0	SJHQ	SJLGG020	chr8	6692247	9	27	0	17	G	A	GCTTCCGCAGGGAGCCCGGC[G/A]GAAGTGGGCGGAGACGCTCC
CpG_XKR5_0	SJHQ	SJLGG020	chr8	6692248	9	27	0	16	G	C	CTTCCGCAGGGAGCCCGGCG[G/C]AAGTGGGCGGAGACGCTCCT
chr7_140419082_140419833	SJHQ	SJLGG021	chr7	140419500	8	62	0	53	T	C	TCCATTTGACTGAAAATAAA[T/C]GTCTTTTTTATGAATTGAAA
V$FOXD3_01	SJHQ	SJLGG021	chr13	67639147	13	57	0	43	T	C	TGAATGAACCTAAGGGATTA[T/C]TTGATTTAAGAGAGAATGCC
CpG_FAM19A5_0	SJHQ	SJLGG022	chr22	49141136	8	29	0	25	A	G	CGTCGGCGGCTGGCCTGTCC[A/G]GGGTTCACCCTGAGCATGGG
CpG_RIMBP2_123439	SJHQ	SJLGG022	chr12	131125952	6	37	0	26	G	A	ATGGTGACTGCCGGACACTC[G/A]GCCCGGCATCACGGGCTGGA
chr11_2724618_2725033	SJHQ	SJLGG024	chr11	2724726	15	47	0	26	C	G	TGTGCACCCGAGAGCACGCA[C/G]GCACACACGCACTCACAGCT
chr4_65758897_65759345	SJHQ	SJLGG024	chr4	65759237	7	67	0	46	G	C	TCGTGATATATGAACCTTTT[G/C]TCCTTGTCAGATTGTCCAAG
chr7_140481193_140481290	SJHQ	SJLGG024	chr7	140481226	19	57	0	41	T	G	TTATTTCCCATAATTTTTGT[T/G]AGAAACTTTTGGAGGAGTCC
chrX_54501045_54501170	SJHQ	SJLGG024	chrX	54501155	14	45	0	40	C	T	CACCTGGAGGGTGGCACAGG[C/T]GGAGATGTGGTTGGAGAGAC
V$S8_01	SJHQ	SJLGG024	chr14	84592290	17	54	0	34	C	A	TGAGATCTCGCGCTGAAAAT[C/A]TGTAAGTTTAAAAGGCAATT
chrX_117851769_117851897	SJHQ	SJLGG025	chrX	117851843	14	57	0	52	C	A	CACCAGAAAACAGAAAAGCA[C/A]CCAAAACTCCACCAAGTGCC
chr2_7845179_7845522	SJHQ	SJLGG027	chr2	7845287	19	70	0	34	G	C	ATGAATATAAACTTATTTTT[G/C]TATTTTATGCTGCTTATTTA
chr6_43045726_43045833	SJHQ	SJLGG027	chr6	43045816	16	43	0	35	G	T	TGTCCTGGTTGGGTTTTGGT[G/T]TGTGGGTCTGCCCAATGAGG
chr7_96517972_96518073	SJHQ	SJLGG027	chr7	96518026	21	55	0	46	T	C	TTTTTGCCTTCTGAATGGTT[T/C]CCCTGAGTTTTCTTTCTGAG
chrX_114882154_114882358	SJHQ	SJLGG027	chrX	114882202	10	46	0	40	T	A	AATTCTCAGATTTGTTCTCC[T/A]TTCACACTAGGACAAGACGA

V$E4BP4_01	SJHQ	SJLGG027	chr7	114536490	13	67	0	42	T	C	AAAACAATTTTCATGTCACA[T/C]AATGTCAACCCTATCTCAAT
chr6_30550829_30551003	SJHQ	SJLGG028	chr6	30550989	7	49	0	32	C	T	AGGTCTCAAGGGGCCCCTTC[C/T]AGTCCACTTACCTAGGGAAG
chr6_83520897_83521006	SJHQ	SJLGG028	chr6	83520943	23	62	0	45	T	A	TCATCAGAAAAGTCTTTATG[T/A]ATTGGAAAGTTATGAAGTTC
chr9_83992245_83992562	SJHQ	SJLGG028	chr9	83992564	12	31	0	24	C	A	AATTTGGCAAACAGAAGACG[C/A]CTCCCTTCTCTTCTCTGCAT
V$FREAC7_01	SJHQ	SJLGG028	chr15	60618418	22	51	0	39	G	A	TCTCTATTAAAAATTTAGAA[G/A]TGCTGCCTGGGTATAAACAT
V$NKX25_02	SJHQ	SJLGG028	chrX	39147644	5	41	0	54	T	A	TGTGCTTTGCAATAAACCCA[T/A]AATTGATAATGCCACGGAGC
chr2_181186460_181186728	SJHQ	SJLGG029	chr2	181186723	12	67	0	34	C	T	GTTAGGCATAGAAACCATTT[C/T]AGTTATTGACAGGACCCATA
chr2_225849043_225849189	SJHQ	SJLGG029	chr2	225849129	6	49	0	38	G	A	AAGTCTTTAGGGAGACAAAT[G/A]AGATGCTTTCTAGCTATTAC
chr4_187555825_187556039	SJHQ	SJLGG029	chr4	187555982	7	45	0	37	C	T	CACAGCCAAAAAGAAGCAAG[C/T]GCGCATGGAAAGCAAGCACA
chr11_120845172_120845325	SJHQ	SJLGG030	chr11	120845166	7	45	0	36	G	T	AGACCTCTGAAACTGAGAGT[G/T]GCTGCAGTTTTAATTAGAAT
CpG_ACTRT2_61238	SJHQ	SJLGG030	chr1	2876680	3	11	0	20	G	C	CCGCGACTGGAGTGAAGCCT[G/C]GGACCTGCCCCGCGACTGGA
chr6_78168846_78169901	SJHQ	SJLGG031	chr6	78169830	7	62	0	39	C	T	TAACATAAAAACAAACACCA[C/T]GCTCTATGCACATTCCTCCA
chr2_226361727_226361936	SJHQ	SJLGG032	chr2	226361798	21	56	0	50	C	T	CTTAGGGCTACAGCATAAAG[C/T]GGATAATCCAAGTGCCTTCA
chr4_180715584_180715925	SJHQ	SJLGG032	chr4	180715790	8	36	0	30	A	G	GTCTATTCCTACCCTTAATG[A/G]TGCTCAGATTAAGTCCCCGA
chr5_70668865_70669362	SJHQ	SJLGG032	chr5	70669076	6	24	0	27	C	G	GGCTGCATCTTAATCACGTT[C/G]GAGCTGGAGAGCCATCAGTT
V$GATA1_03	SJHQ	SJLGG032	chr7	26624376	14	34	0	39	C	T	TCCCACTTACCTACCTCTCG[C/T]GCAGATTACAGAGGGAATGC
chr11_4730764_4731757	SJHQ	SJLGG033	chr11	4731223	9	44	0	30	G	A	CACAATCTTAACCAATTCAC[G/A]GATTATTAAAGTGGGCTTTG
chr3_89727114_89727302	SJHQ	SJLGG033	chr3	89727286	9	62	0	34	C	T	CTAAATGTTCCCTTCATTCT[C/T]TTCCTGTAACTGAAATCTGG
chr6_140361398_140361652	SJHQ	SJLGG033	chr6	140361497	8	57	0	58	G	C	GTAGTTAATTCATGGTGTCT[G/C]GTATGGATCCAGCAGTTTAA
chr1_166104093_166104379	SJHQ	SJLGG034	chr1	166104235	30	70	0	39	T	G	AGCCTTTAACATCTTTCACC[T/G]GAAGAATTATTTTTAAAGAA
chr16_68685027_68685448	SJHQ	SJLGG034	chr16	68685376	16	30	0	27	G	A	AGCCCGATGACGCACTGGCC[G/A]GCCTTCATGGTGTTCTAGTC
chr2_34502369_34502623	SJHQ	SJLGG034	chr2	34502361	23	65	1	46	T	C	TTTTAAAAGTTTCAACTGTT[T/C]CTCCTGTTTATTCCTTCACC
chr4_104721550_104721714	SJHQ	SJLGG034	chr4	104721597	27	63	0	30	A	G	GAGAAAATAAGAAAAAAGGG[A/G]AGATGTTCATTGACTTGTGA
chr4_19348068_19348798	SJHQ	SJLGG034	chr4	19348536	34	66	0	34	G	A	CTGGAATGTGTAAGTTTTAC[G/A]TCAAGTGACTTTGAAATGTA
chr5_93586493_93587388	SJHQ	SJLGG034	chr5	93586761	26	47	0	42	G	A	CTGCTGACCCTAATATGGAC[G/A]AACCAATTAGACATCTCTAT
chr6_109065592_109065931	SJHQ	SJLGG034	chr6	109065777	28	54	0	35	C	T	TCAAGGTTACAGGAATTTTC[C/T]TTGGAAGCTGTTTGGATTTG
chr9_131858236_131858478	SJHQ	SJLGG034	chr9	131858472	11	31	0	22	C	T	GGACCCCCGGGGTATCCCTG[C/T]CCTCTTCAGCCTGTGGCAGC
V$BRACH_01	SJHQ	SJLGG034	chr11	43270913	28	53	0	41	A	G	TTTTGGAAGCTGGCACCCAC[A/G]CCCAGCTGTTAATTTGGAAT
V$NKX3A_01	SJHQ	SJLGG034	chr6	25512351	28	69	0	42	T	C	TAATATTACATAATTATACT[T/C]AAAATTCACCCCAAGATGTT
chr1_193693200_193693469	SJHQ	SJLGG035	chr1	193693242	19	57	0	44	A	G	TCCACAGGATTCGTTAAATG[A/G]CCTTATTAAATTTCTAAAGT
chr1_63078521_63078775	SJHQ	SJLGG035	chr1	63078785	19	62	0	44	T	C	TTACCTAACTTTCAGATGAT[T/C]TCAAATATCCAATAAAAGAT
chr2_162569782_162570224	SJHQ	SJLGG035	chr2	162569887	9	71	0	37	G	A	AGAATGAAAATTAAATTCCT[G/A]AGTAGATTTAGTAGTTAGTA
chr9_86708720_86708854	SJHQ	SJLGG035	chr9	86708809	13	59	0	31	G	T	ATCTAAATAATTGAAGACAC[G/T]TGGAGAAACATTTTAATAAA
chr1_105945311_105945767	SJHQ	SJLGG037	chr1	105945472	8	69	0	41	A	G	TAAGTAAAAGCAAGCAAAAT[A/G]TCTCTCCATGCTTTCAGAGA
chr21_20430960_20431453	SJHQ	SJLGG037	chr21	20431112	9	77	0	45	G	T	CTTGCTTTAAAGAGTGTGGG[G/T]GCAGCCATTTTGCTTCTCAG
CpG_GMPS_560622	SJHQ	SJLGG037	chr3	155027543	9	18	0	20	G	A	GCCTCGGTCACGTCGGGGTG[G/A]AGGTCCCCCACGTAGAGCGA
chr15_97245014_97245218	SJHQ	SJLGG038	chr15	97245175	11	56	0	35	A	G	ATATGACACACATATTTTGG[A/G]CTATGCATTGCTTCGAGTAT
chr5_129414622_129414806	SJHQ	SJLGG038	chr5	129414812	15	64	0	36	G	A	TGTATTTGAAGGAAAACATC[G/A]TTCTTCTCTGCTTTTTTCTC
CpG_FGF13_0	SJHQ	SJLGG038	chrX	138287253	5	11	0	17	A	G	GCGGAGGGTGGGGGCTGGCG[A/G]AGGCGGGGCCTCACAAAGCC
V$ZIC3_01	SJHQ	SJLGG038	chr18	46262355	11	46	0	33	T	C	ACACCCGGGTGGTCTGGTGG[T/C]TAGGATGGCCCCGTTCCTGG
chr3_4619672_4619845	SJHQ	SJLGG039	chr3	4619816	10	65	0	50	G	A	TACTTTCAGATTGCTATAAC[G/A]CTTGACACCATTGGGCTTTT
chr1_10782813_10783247	SJHQ	SJLGG040	chr1	10782882	8	43	0	32	G	T	GGCCTCTAGGAAGAGCTGGC[G/T]CCAGGGCTGCATGGGGCAGA
chr1_87821125_87821449	SJHQ	SJLGG040	chr1	87821279	25	64	0	44	C	T	GTATGTTAGAGGTCAAAAAC[C/T]GGCTTTCTAGAAACCACATA
CpG_CDK5R2_50295	SJHQ	SJLGG040	chr2	219773547	15	28	0	27	C	T	ATGTCTGAGTCCTTATCACT[C/T]GTGCGCAGCACAACACGACC
chr12_72353253_72353510	SJHQ	SJLGG042	chr12	72353345	18	43	0	42	T	C	TGGCTCTACCTCTCCACCTT[T/C]CCAGAAATTTCAGTTGACCT
chr15_37308313_37308429	SJHQ	SJLGG042	chr15	37308324	16	50	0	42	C	T	TGATGGGAGGGGGCAGAATC[C/T]AAAGTTAGCCAAGTCAGCTA
chr16_33791941_33792073	SJHQ	SJLGG042	chr16	33791983	5	10	0	10	G	A	TGCTCCTACTGCAAGCGGTC[G/A]TACTCCTTGGTGAGGCCCTC
chr17_12371811_12372173	SJHQ	SJLGG042	chr17	12372041	19	34	0	33	G	T	TCAATTTTTTTTTCTTGATT[G/T]TTGAGGAATGTTCATTGCCA
chr1_86848586_86848696	SJHQ	SJLGG042	chr1	86848706	31	53	0	55	G	T	CTTGAGCAAATATAAAATAA[G/T]AATTAGGAATTTCACAACTT
chr19_14974623_14974747	SJHQ	SJLGG042	chr19	14974709	11	31	0	30	G	A	ACAGTGTACATCACCGAGGC[G/A]ACAGCAGTTGAGTGTAAGTT
chr20_45986327_45987008	SJHQ	SJLGG042	chr20	45986927	5	6	0	15	C	T	ATTTGGCAGCCCCCCCACCC[C/T]CCCATCTCTGGCACCGCTCC
chr2_189210596_189210743	SJHQ	SJLGG042	chr2	189210597	9	45	0	35	C	A	TCATTCAAATACTTATTAAA[C/A]AATAACCCCTAATATTTCTT
chr3_55877945_55878128	SJHQ	SJLGG042	chr3	55878039	7	37	0	39	C	A	TGTGAGTTCTCAGATAAAAG[C/A]AAATAATGGAAACCATGCCA
chr8_106590673_106590825	SJHQ	SJLGG042	chr8	106590789	25	73	1	55	C	T	GTGATTCATCTGAAAATCTA[C/T]ATAATTCATGTTGACCAATT
chr8_59757973_59758130	SJHQ	SJLGG042	chr8	59758016	16	57	0	45	A	C	CCATCTAAAATCCCCTTATG[A/C]GAATAAATTCAAATAAGCAT
chrX_129274432_129274665	SJHQ	SJLGG042	chrX	129274481	8	40	0	45	A	T	TTGAATGAGCTGTATCAGGG[A/T]AGAAAGCCATCTCCAGAAAT
chrX_45629117_45629542	SJHQ	SJLGG042	chrX	45629284	4	32	0	40	A	T	TTGATAAATCTGATTATAAA[A/T]CGTCTTTGTTCCAGATCACA
chrX_97907161_97907459	SJHQ	SJLGG042	chrX	97907291	6	18	0	31	T	C	AGCTGCCACATATTCCCTGG[T/C]GGCTGTCCTTCTTGACTACC
V$PPARG_02	SJHQ	SJLGG042	chr12	4586434	14	39	0	41	A	G	CCACAAATGGTTCATTGTCC[A/G]CCACTTTTGGCATTTGTAAC
chr1_61649921_61650423	SJLQ	SJLGG009	chr1	61649941	5	32	0	32	C	T	GCCAGTGAAGGGCGACGTTC[C/T]GCTCCTTACATGGCGGCTGT
chr1_72635415_72635584	SJHLQ	SJLGG011	chr1	72635570	6	42	0	36	C	A	AGACTTAACACACTAATGTT[C/A]TGTGGAAAATGAGTAAGATA
chr10_131691137_131692143	SJLQ	SJLGG012	chr10	131691872	5	31	0	19	T	C	TGAAGAAAATTTTTACCAGC[T/C]CTGACAATTTCCCCTGGCAT
chr11_55093855_55094098	SJHLQ	SJLGG009	chr11	55093915	12	71	0	25	G	A	TCCCTTAAAACTTACAGTCA[G/A]GAAGGGAGGCATAAAGCCCT
chr13_21835025_21835380	SJLQ	SJLGG002	chr13	21835372	7	30	0	10	G	A	GCCTGGGGGAACTGGGGACT[G/A]CCCTGCTGCAACTGGTGCGG
chr14_59602414_59602713	SJLQ	SJLGG008	chr14	59602475	5	27	0	25	T	A	CCTCCAGGAGGGAAGGGTCC[T/A]CAGCCTTGGCCCAGAGGCTG
chr17_12399278_12399551	SJHLQ	SJLGG006	chr17	12399403	8	56	0	33	G	A	TGGAAATGAATGGATTTTCC[G/A]TAATGTAGGACCTCATCACA
chr17_12399278_12399551	SJHLQ	SJLGG006R	chr17	12399403	5	53	0	33	G	A	TGGAAATGAATGGATTTTCC[G/A]TAATGTAGGACCTCATCACA
chr9_126251077_126251361	SJHLQ	SJLGG013	chr9	126251267	6	35	0	38	G	T	CTCAAAACATTTCCTATAGC[G/T]AAGGCTTCAAAGGTAGAGAA
CpG_MAOA_616	SJLLQ	SJLGG001	chrX	43514793	5	31	0	18	G	A	CGAACTCCTCCGATGGGGCC[G/A]TCACAGCCTCCAATCAGGAC

Supplementary Table 5c

Single nucleotide substitutions in non-repetitive regions for tumors analyzed by WGS

SJQuality	Sample	Chromosome	Position	Mut Reads Tumor	Total Reads Tumor	Mut Reads Normal	Total Reads Normal	Reference Allele	Non-reference Allele	Flanking Region
SJHQ	SJLGG001	chr11	21673456	18	42	0	35	G	T	ACTTGCCCCGGGATGTTCTT[G/T]AATTTTTTCTTATTCTTGTG
SJHQ	SJLGG001	chr1	143651193	20	34	0	27	G	A	TATGATGGTTAAACTGAGAC[G/A]TGTGCCAGGAAGGTTAGGGT
SJHQ	SJLGG001	chr1	1558087	13	38	0	23	C	T	CCTGCCTCTGCTCGAGTATC[C/T]GGCCTCTGTCGTGAGTGCCT
SJHQ	SJLGG001	chr12	101416249	11	58	0	32	G	A	GAACCACTCATAACATTTGC[G/A]TACTGAATAATTTAAATGTT
SJHQ	SJLGG001	chr12	3118755	21	33	0	27	G	A	CCCTACTTCATTCACCCACC[G/A]GTGATGACTTAGACCCGAGA
SJHQ	SJLGG001	chr13	19739594	11	34	0	25	C	T	CCAATGACATATAAGCTAGA[C/T]GGGTGGGGCTAGATGGGTGG
SJHQ	SJLGG001	chr13	28902039	12	26	0	25	G	A	CAGACCCTTGCGAGTAGAGC[G/A]GCTTCTGGTTACTGTCACAC
SJHQ	SJLGG001	chr13	57352502	10	47	0	47	A	T	CAAGGATCAGATCTGCAATG[A/T]ATTATTTTCTGACTTACCCC
SJHQ	SJLGG001	chr13	57352532	10	49	0	44	A	T	TGACTTACCCCTGCCCCACT[A/T]GCAGTCTGGCATAATTTTTA
SJHQ	SJLGG001	chr13	93058699	18	47	0	23	C	T	TCTTCCACTACCAAAATATA[C/T]GTGGAGCTATATCAACTTGG
SJHQ	SJLGG001	chr15	71248469	13	47	0	28	T	C	TAGGGGAGGAAAATTTCTAA[T/C]TGGAGAAATTTGACTGATAT
SJHQ	SJLGG001	chr15	77612936	10	43	0	24	A	G	GGAGTTAAATGACCTTATCT[A/G]GAGCAGCTAACTGAGCCTCA
SJHQ	SJLGG001	chr1	80464092	6	36	0	30	T	C	CCATTTGACCAAAAGAATGG[T/C]AAAATATAAGAATCAGATGA
SJHQ	SJLGG001	chr18	7528567	7	51	0	31	C	T	TCTATCTTACTTTTAATATT[C/T]CATTCAAGTCCAATGGATTT
SJHQ	SJLGG001	chr1	97269938	14	45	0	29	A	T	CAAGTGTGAGTTTATGAAGA[A/T]GATAGCACTTGCGGAAAAAA
SJHQ	SJLGG001	chr2	192071618	6	28	0	31	C	T	TTCCATCCTCCTTCATGAAA[C/T]GGCCTTTTGTTCCTTTAGCT
SJHQ	SJLGG001	chr22	49987482	17	40	0	26	C	T	CCTTGAAGCCAAGAGGAGCT[C/T]ACCGCTCCAGGCAGCAGAAG
SJHQ	SJLGG001	chr2	40734424	13	39	0	20	C	T	ACATTTCAACATACGTTGAT[C/T]GAAACATGATTAATATGATA
SJHQ	SJLGG001	chr2	47584051	27	67	0	40	G	A	TTATAGTTTGATAATTCATT[G/A]AAACAGAATCATTTTATATC
SJHQ	SJLGG001	chr3	111249777	10	46	0	21	T	A	GATTCAACACTGTGGGAAAC[T/A]TGTGCCATCCCAGGATTGCT
SJHQ	SJLGG001	chr3	56321102	15	34	0	30	C	G	CCCTCAACCTACATGCCTAA[C/G]TGGAAACCCAAATAAAGTAG
SJHQ	SJLGG001	chr4	130446492	12	40	0	35	G	C	ACTAATGGTGATTAATTCCT[G/C]CCAACAAAGCAGACGTATTT
SJHQ	SJLGG001	chr4	136490997	17	57	0	23	G	C	TTTCCACAGAGGTATAGTTT[G/C]TTCAGCTCTATCTTGACAAA
SJHQ	SJLGG001	chr4	141642990	20	54	0	36	G	A	TCTCCTGTGACTGAATGCCC[G/A]TCTTGATAACTTGCCCAACA
SJHQ	SJLGG001	chr4	181804435	16	42	0	35	C	T	ATTTCATTTAGTAGAAACCA[C/T]TGAACTGTTCTTACCAAACT
SJHQ	SJLGG001	chr4	30144548	12	50	0	35	T	C	TAAAACTCCAGGGTTTGTAA[T/C]ATTTATAATTGGTTTCTTAC
SJHQ	SJLGG001	chr4	35339778	16	55	0	49	A	T	AGATTAAAAGCTTTTAATAA[A/T]ACTGTTTTATGTAGAGATTG
SJHQ	SJLGG001	chr4	52996906	20	63	0	43	G	A	TTGAGCATGTATCAATGAAC[G/A]TTTATTCAGAATGAGCTACA
SJHQ	SJLGG001	chr4	85529722	12	43	0	22	C	T	CTTCCATCTGTCTTTATCCT[C/T]AGTGGCTGACCTCTTAGGTA
SJHQ	SJLGG001	chr5	129650866	20	47	0	32	G	A	AATTCCATTGTTATTCTCAC[G/A]TTTTTACATAAGTACATGCA
SJHQ	SJLGG001	chr6	165850000	8	39	0	39	A	G	GCTTTAACCTTGGGTACTTG[A/G]AATTAATAACAATTATAAAT
SJHQ	SJLGG001	chr6	49807768	6	42	0	33	G	T	AGACTTATGTGTTAATCTAA[G/T]AAATACATGTAGCTGAAGGA
SJHQ	SJLGG001	chr6	64126231	10	39	0	29	T	C	TGGTCCAAGGAAACATCAGA[T/C]GGCATTGAGGGCCAAACTGA
SJHQ	SJLGG001	chr6	6966316	11	68	0	32	G	A	TAATTTTTAGTTAAAAATGC[G/A]TAGCCTTCCCAAGTACATTA
SJHQ	SJLGG001	chr7	138558520	16	56	0	25	G	T	CACAGACTGCAACCAGAGGA[G/T]GGGATGCACAAACCCTGGGC
SJHQ	SJLGG001	chr7	138558525	16	59	0	21	T	A	ACTGCAACCAGAGGAGGGGA[T/A]GCACAAACCCTGGGCCACTC
SJHQ	SJLGG001	chr8	24049616	12	39	0	15	T	C	GAGAGCTTTGGGGGAATTTC[T/C]CAGCAGGACTCCTTGCATGA
SJHQ	SJLGG001	chr9	12908564	23	50	0	43	G	A	CCTTTTCCTTTTTAAAACTT[G/A]GAGTCCAAGAGCTTTTCATC
SJHQ	SJLGG001	chr9	32348319	18	50	0	24	A	T	TAATGGGTCTTTAAAAAAAA[A/T]TTGCCACAATAGAAAATAAA
SJHQ	SJLGG001	chrX	113932183	11	37	0	31	T	A	TCATTACTTCTTCTTGTACC[T/A]CTTACATTAACTGTATTGAC
SJHQ	SJLGG001	chrX	117065405	16	45	0	22	A	T	GCCTCCAGGTCTTAAGGATG[A/T]AAGGGATGTTTTCAACTGGC
SJHQ	SJLGG001	chrX	142936981	18	54	0	35	A	G	TAAATATACATATATAGTAT[A/G]TATTATCTTGAAAGTTGTAA
SJHQ	SJLGG001	chrX	5116551	7	50	0	40	G	A	GACGACTCTGAATATAAATG[G/A]AAATATTTAGAAGTGAACAT
SJHQ	SJLGG002	chr1	104340801	16	54	0	45	A	G	GTTCCTCATATATACTTCTT[A/G]CAAAATCCCTAAATATGCCT
SJHQ	SJLGG002	chr1	185755522	8	51	0	28	A	T	TCTGTCATTTATGTCTTTGC[A/T]GGGAGCTCATTATTTGGCCA
SJHQ	SJLGG002	chr12	14035275	12	42	0	24	G	A	TGGAATTTGTCTGGATAAAC[G/A]GAAGGCACCAAAGCAGGAAT
SJHQ	SJLGG002	chr1	227141495	19	45	0	25	G	T	ATAGAAGCCGGGAGTTGCCC[G/T]AGATGTTTGAGTGATGCTCC
SJHQ	SJLGG002	chr12	27780321	21	64	0	30	G	A	TGACCACAGAATACTGTGGC[G/A]TTCTACCAGCATAGTCGAAT
SJHQ	SJLGG002	chr12	29328912	16	77	0	44	A	T	AAAATAAAGCAAAATACCAA[A/T]ATTTAATATCAAAAGTAAAA
SJHQ	SJLGG002	chr13	19910677	22	60	0	39	C	T	CCAACACACTTGGTATAATA[C/T]TTACAACATTCATATTTGAA
SJHQ	SJLGG002	chr15	22334208	14	124	0	83	C	T	TATTACCTCTGAGTCTCAAA[C/T]ATGTTTGAGGAATAAATTTA
SJHQ	SJLGG002	chr16	62621802	12	72	0	26	T	C	CTTTTAGCCTAACCCCTAAA[T/C]CTGGATAGTCAGTAGGAACA
SJHQ	SJLGG002	chr16	63361516	8	52	0	39	T	C	CATGTAAACATAATTTCTGT[T/C]AATCAAATGCTTGCCAGGAG
SJHQ	SJLGG002	chr17	45794564	17	46	0	23	C	T	GTCCTTCTACCCGTTCCTCC[C/T]TTGAGCAAGAGGCCTGCAGG
SJHQ	SJLGG002	chr1	81492614	15	66	0	28	T	C	ATCAGGCTTGCTTCTGTTTG[T/C]ACAGTGATAAATAAGACAGG
SJHQ	SJLGG002	chr20	3217708	12	33	0	26	C	T	AGGTCACTCATGGGGCTAGG[C/T]ACAGGACACAGCCTGAAGCC
SJHQ	SJLGG002	chr2	124534334	13	71	0	44	C	A	GAAAAATAATACTCAAAGAT[C/A]TCATAATTCAGAAGTTTCTA
SJHQ	SJLGG002	chr2	135281056	18	58	0	27	T	A	AGAAAAAATGCTTAAAAAGC[T/A]ATTACTGATGTCTTTCAAAA
SJHQ	SJLGG002	chr2	141720117	21	68	0	34	C	G	ACGGTGTTCTGTAGCTTCTT[C/G]TCTGAAGAGGAGGTTGGCTC
SJHQ	SJLGG002	chr2	168760734	19	50	0	31	T	G	TTCTTTTCCTTCACAGGTTT[T/G]GATGGCTTTGGTTTTCAAAG
SJHQ	SJLGG002	chr2	180724821	9	49	0	30	A	G	TTTGTTCCTTCTATAGGAAC[A/G]TCTTTTGCTACTACATCTTG
SJHQ	SJLGG002	chr2	212222914	10	49	0	36	A	G	TAATCAAGAAAATGATCAAG[A/G]AAGACATTATAAAAAAGATG
SJHQ	SJLGG002	chr3	70642818	28	70	0	34	G	A	ATATTAGAAACATCATATCC[G/A]TTTCGCTTTCTGTGAATATA
SJHQ	SJLGG002	chr3	88453160	21	45	0	26	C	T	GGGGAGACAAGTTCCACATA[C/T]TTGGTATATTTCTTTTCTTG
SJHQ	SJLGG002	chr4	179660420	22	55	0	32	G	A	ATCTTACATTTAGTTTGTTC[G/A]GAATTGCACTGTTTTATTCT
SJHQ	SJLGG002	chr5	21093477	6	43	0	44	G	T	AATTGTTGACATTTAATTTT[G/T]ATTATAATGTCACCATATAT
SJHQ	SJLGG002	chr5	28285884	22	58	0	32	A	G	TAAATGTTGTGCCTAATAGT[A/G]GGATTATAAAATGCTTAAAT
SJHQ	SJLGG002	chr5	51217917	9	62	0	45	A	G	CTAGAAAATACCTAGATCTA[A/G]CTACATTCTTATTATTTAAT
SJHQ	SJLGG002	chr5	88392956	32	75	0	49	A	G	TTTTGACCAAAAAAATTCAA[A/G]ATCAACCTCTGTGCTCTAAT

SJHQ	SJLGG002	chr5	91379540	20	67	0	32	G	A	CAGGTTTCTGATTCTGATAT[G/A]TAAATCACTGTACTGTCATA
SJHQ	SJLGG002	chr6	164992035	14	46	0	28	C	A	AAGGTTTATGTCGTTGCTCG[C/A]GTGATGGAATTACGTCTCTT
SJHQ	SJLGG002	chr6	87139641	10	58	0	42	C	G	TTATTTTCCATCTTTCCAGT[C/G]TTTCCCTTCCCATTCCACAG
SJHQ	SJLGG002	chr7	138831656	24	80	0	28	A	C	GGAAGGGTCAAATAGTATTA[A/C]CTGTAACCTAAGGGCTTTCC
SJHQ	SJLGG002	chr7	83861043	15	44	0	31	C	A	TCCTGTAAAATAAATTAGCA[C/A]CCTGAGGACATCCTTTGGCT
SJHQ	SJLGG002	chr8	49925456	8	39	0	28	G	A	TTTATCTTTGGGATCACGTC[G/A]TTGTTATCTTTAGGGTCACA
SJHQ	SJLGG002	chr8	68319496	18	49	0	30	C	A	TGACCACCAATTACTGTCTG[C/A]ACTTAACACAGGAGGCAAGG
SJHQ	SJLGG002	chrX	70030849	23	33	0	15	G	A	TAAAATTTACAGAACATGTC[G/A]TTACAAATATTCCAATGAGT
SJHQ	SJLGG002	chrX	92931352	7	24	0	25	C	A	TACATTTGTAATCAACATCT[C/A]CAAATTAATTTATCAATATT
SJHQ	SJLGG002	chrX	93313112	16	21	0	19	C	T	TAATGGCTTTAAAGACAAAC[C/T]TTTAATTTTTTGCAAAGACT
SJHQ	SJLGG003	chr10	37237851	6	36	0	40	T	C	TATGGGCATAATGGAACTTC[T/C]AAAATTTCTGAAAAATCCCA
SJHQ	SJLGG003	chr11	2888783	5	27	0	39	G	A	GAGACCTTCTCTGACTGAGC[G/A]CATGAAGCTGGCTCTTCCTG
SJHQ	SJLGG003	chr13	114253281	9	35	0	33	C	T	ATGGAAAGTTTATTTAAAAA[C/T]GTAGGGTGCAGAAAGGTGTC
SJHQ	SJLGG003	chr13	29585773	9	51	0	45	T	C	TAACTGAATAATATGGTTTT[T/C]CCTTTTTAATTTATTTTCAT
SJHQ	SJLGG003	chr13	56627395	6	38	0	32	T	G	TATTCCAAATATATTATTAT[T/G]TTTCATGGCATCACAAAGAA
SJHQ	SJLGG003	chr13	93902566	10	38	0	36	C	T	AAAGGAGTGACTCTTTCTCA[C/T]GAAAGAAAACTGAGGGTCCT
SJHQ	SJLGG003	chr13	94413478	10	40	0	41	A	G	AATTAGGCACTGCATTATAA[A/G]CTCTGATTTTAAAAAGCAGT
SJHQ	SJLGG003	chr16	52242685	14	42	0	47	G	A	TTTCAAACTCTAGTTCAAAC[G/A]TTCTGAAATCCCTATGAGGC
SJHQ	SJLGG003	chr18	57520826	13	37	0	38	T	C	AGAGTTCCCATGGGGTTCTG[T/C]TGTTCTGCTTAAGTAATGCT
SJHQ	SJLGG003	chr3	34733250	6	29	0	40	T	C	ATAGTTATTGATATGCATCA[T/C]CAACTCTTTTGACATTTGTG
SJHQ	SJLGG003	chr4	53689686	11	29	0	42	G	A	CAAATTAAACTTTAGGAGGA[G/A]AGAAGGAGTCCATATCACTG
SJHQ	SJLGG003	chr6	162021358	8	35	0	38	A	G	TTCCTTTTCTATCCTCATTC[A/G]TCTGGGTGGACTTCTTCCAA
SJHQ	SJLGG003	chr6	89159941	11	33	0	42	T	G	CCACAGTTTTAAAAATAGGA[T/G]ACATTTCCAAAGATGTGAGC
SJHQ	SJLGG003	chr7	98144403	10	48	0	51	C	T	GTTTTTCTCTAGTCCCCCTT[C/T]CTGTGATGATGAATGTCTGG
SJHQ	SJLGG003	chr8	99232972	10	43	0	29	A	G	TTTCGCAACCATTTTACCAA[A/G]CCGGTTCTTGGTTAAATACT
SJHQ	SJLGG003	chr9	29161784	14	38	0	39	A	G	TTCCTGTGTAACAAGCCACT[A/G]TATAGTAACAATAAAAACTA
SJHQ	SJLGG004	chr10	98059142	11	47	0	34	G	T	CCTGTTATAACTAAAATATA[G/T]AAATTTCTTGTACTTGTTAG
SJHQ	SJLGG004	chr1	192542717	14	36	0	37	T	A	AATTAATAGGGAACTTTCAA[T/A]GCCCTGCCATGCACTTGTCA
SJHQ	SJLGG004	chr1	195397308	12	37	0	33	T	A	GAAGAGGAAACTTTAAGCAA[T/A]TTTTTAAGTGGGAAGGGTAC
SJHQ	SJLGG004	chr12	40533284	7	35	0	38	A	G	CACAAAAAAAAGTCATTTGC[A/G]ACACGATTTAATATGCTTAG
SJHQ	SJLGG004	chr1	245214406	11	38	0	26	C	T	ACCTTCTGTAATACTTTAAA[C/T]TGTAGCAACCTGGCCAGGCT
SJHQ	SJLGG004	chr14	73614921	5	35	0	41	C	A	GGCAGGCTTTCTCTACTTTA[C/A]CACATTTATAATATATTTGG
SJHQ	SJLGG004	chr16	34416541	10	31	0	35	C	G	CATATTCATTCCACAAAGAC[C/G]TTTGTCTGCACAAGCACATC
SJHQ	SJLGG004	chr19	45408793	7	30	0	28	T	C	TCTGGGCGGCAGCCTCCACA[T/C]TCCCCTTCCACGCTTGGCCC
SJHQ	SJLGG004	chr2	18459634	5	28	0	32	C	A	TTATGAGTGTCCCCACATAG[C/A]TTGTGTGCCTTTGGGTAAAT
SJHQ	SJLGG004	chr2	207494481	7	36	0	29	C	A	TGCAATATTTTGATAGTTAG[C/A]TAAGTAGCTTTGCAACTCGT
SJHQ	SJLGG004	chr3	167036103	16	44	0	47	T	C	AGCCTTCTCAGTGATATTTG[T/C]AGTTAATATGGATACAAAAT
SJHQ	SJLGG004	chr4	111786553	8	55	0	40	C	T	TTTTATAAAGTTCCTGTTTT[C/T]ATGGCATAGATAATTTTTTT
SJHQ	SJLGG004	chr4	183012805	9	32	0	38	C	T	GCTGGTGCTGAGAATGTCAA[C/T]GAAGCTTGATGGGGAGCCTT
SJHQ	SJLGG004	chr4	26959013	12	41	0	24	T	C	AAACATTGACTAAGTACTTC[T/C]ACTGCTGTTGCTGGTGGTGG
SJHQ	SJLGG004	chr5	112548492	10	46	0	43	C	A	GGGAGGCATTCCTGTACTTT[C/A]TAAATTGCACAAGATGTCAC
SJHQ	SJLGG004	chr5	11327568	14	43	0	37	T	C	AATCTAAAAGGTAAATTGTC[T/C]TCACAAACTCTATTACAACC
SJHQ	SJLGG004	chr5	51990441	9	43	0	23	T	C	AGATACTCCACGGAGGCATC[T/C]TCTACTTTACTATAATTATC
SJHQ	SJLGG004	chr5	53231159	11	33	0	27	G	A	ACAAGCAGATACATGTTTGT[G/A]CAGGATGGAAGTAGTGATAA
SJHQ	SJLGG004	chr6	140479581	6	40	0	28	T	C	AAACTTAAATTGGAAGAAGC[T/C]ATAACATTAATATAGAAAAG
SJHQ	SJLGG004	chr7	40560567	10	51	0	31	A	T	TCAACTCAAAACTAGTAAAT[A/T]ATTTTATTGCAAATGTGGTT
SJHQ	SJLGG004	chr8	3717642	8	30	0	31	C	T	GTTTGCCTTCATATTGATCC[C/T]CTTTGAAGCTTAGAATCTAA
SJHQ	SJLGG004	chr9	8287786	10	42	0	40	G	A	ACAATACAACCTCACTTGGC[G/A]TTAGTATTGATTCTAGCCTC
SJHQ	SJLGG004	chr9	85566999	13	40	0	36	C	T	TGTTGTACAAGGGGAGGTTA[C/T]CATCAAAATAGAATGAAATA
SJHQ	SJLGG004	chrX	96272437	8	47	0	29	C	T	ACAACATGAATTCACATATG[C/T]ATTGAATGGGGAGGAAGAGT
SJHQ	SJLGG005	chr10	115664145	13	51	0	27	C	T	TGAAAAACTGGTAATTTGCA[C/T]GGTATATTTTTAAAAGAAAC
SJHQ	SJLGG005	chr10	2774404	20	45	0	34	C	T	CAGCCCGCCCAGCAGTCATT[C/T]GTATGCTACAAGTGGGCCTG
SJHQ	SJLGG005	chr10	72136713	6	37	0	35	G	A	CATTGGGAAGGAGGTAGGGC[G/A]CAGCCAACTGCAGGAGAAAG
SJHQ	SJLGG005	chr10	83187921	6	32	0	33	C	A	CCACTCCACTGTGACACTAT[C/A]CCTGTGAAAGCTTCCATAAG
SJHQ	SJLGG005	chr1	190675532	12	42	0	19	G	A	GCAAGGAATACTCAAGGAGC[G/A]TTGGTATTAAGGACAAATAA
SJHQ	SJLGG005	chr1	245230982	11	36	0	32	G	A	GTTAGTAGAACAAGATCCAC[G/A]TAATCTACACCCTGGTGAAG
SJHQ	SJLGG005	chr12	54839093	13	54	0	22	A	T	GGTGAGTTCGCCATGGCTAG[A/T]CTATGAATAGGATGGGGAGA
SJHQ	SJLGG005	chr14	62460886	7	40	0	34	A	G	AACGGAGTTTGGAATGGAAG[A/G]AGGTAGTGTTGAAGAGAGAA
SJHQ	SJLGG005	chr1	70386933	6	49	0	36	G	A	TGGGTTTAAAAGGAGAGTTC[G/A]TTTTCAGGTAGAGTAGATAA
SJHQ	SJLGG005	chr17	26374441	14	58	0	31	T	G	AAGCCAAGGGGAAAATACTC[T/G]GTGCTGTCCTGTCAACTAAT
SJHQ	SJLGG005	chr18	31851119	10	60	0	43	G	A	CTGCAAGCGTGATAACAAAC[G/A]ATTAACTTTTCCGCTAATTA
SJHQ	SJLGG005	chr20	62766267	18	58	0	41	G	A	CGGTCCTTGACAGTGATTCC[G/A]TGCATCACAAACACACACGC
SJHQ	SJLGG005	chr21	45160246	7	35	0	26	G	A	TGGCGCGTGGGCGCAGAGCC[G/A]GCCGTGACCCACAAGTGCGT
SJHQ	SJLGG005	chr2	43874759	9	33	0	18	G	A	TGTATTTTTCAATGCAAACC[G/A]TATGGCATTGCTTCTAAGTG
SJHQ	SJLGG005	chr2	59197351	4	38	0	43	C	A	AAGACTAATTATATTAACTT[C/A]TATTACCTAAAGTGCAGTTT
SJHQ	SJLGG005	chr4	135925160	7	45	0	31	C	A	TATGAAATTTTCATTAAATG[C/A]CAATCAAAATATCTAAATGA
SJHQ	SJLGG005	chr5	17315455	11	37	0	43	A	T	CATATGAGAGCAATACACAG[A/T]TTGGGGTAAAACAGCCAGAA
SJHQ	SJLGG005	chr5	45287715	14	51	0	38	A	G	CTCACAATTCAATTTTGTTT[A/G]TAGTGAGGAAATTAGAATTT
SJHQ	SJLGG005	chr5	76058741	11	54	0	43	G	A	TTTTCCAGTTTCATCTTTTA[G/A]AAGATTGAATCCAGCTACAG
SJHQ	SJLGG005	chr6	123713131	14	45	0	20	C	T	ATGGAGGATTTGCAAAGACG[C/T]GAATGATATGCAGTTCTGCT
SJHQ	SJLGG005	chr6	135466150	10	38	0	25	G	A	AAGTAATGGCAAATGAATTC[G/A]ATGTTTTAAACAATATTTTT
SJHQ	SJLGG005	chr6	135518947	12	55	0	37	G	A	TTCCAATTCATCTTTAAATG[G/A]AAGAGTTTGGGAAGAGGATG
SJHQ	SJLGG005	chr7	57792624	8	51	0	34	C	A	AATACCGTACAAATATCAAA[C/A]TTAGAAGAAGCATAAACAAT
SJHQ	SJLGG005	chr7	85510801	7	47	0	39	T	C	TATTTAAGCAAGAAATAGTC[T/C]AGTTGTTTCATCATTAAAAA

SJHQ	SJLGG005	chr8	135991722	6	59	0	45	T	G	TAGATACTTTTTCCTACCAT[T/G]TATTTTTCCTGTAATGAACA
SJHQ	SJLGG005	chr8	25867300	8	54	0	33	C	A	AAAACTGTTTTGCAGGGAAA[C/A]ACCCCAGTTAGAAATTCAGT
SJHQ	SJLGG005	chr9	103750607	12	45	0	41	C	T	CTTTTGTCTTCCAAAATGGA[C/T]TCTTGTAGCCCAATTCAGAG
SJHQ	SJLGG005	chrX	73600657	13	58	0	40	C	T	GGTGCTCTAATAAATTCATG[C/T]AAATGAGCCCAGGCTTTGTA
SJHQ	SJLGG006R	chr10	31655854	6	60	0	47	C	A	TATAGTTCAGTCCCCTTTAG[C/A]ATTCCACATACAGTTAGTGC
SJHQ	SJLGG006	chr10	31655854	15	76	0	47	C	A	TATAGTTCAGTCCCCTTTAG[C/A]ATTCCACATACAGTTAGTGC
SJHQ	SJLGG006	chr1	103759863	23	74	0	41	G	A	ACAAAATATGAAGCAAATTC[G/A]GGTATAGGGTTATTGAGAAG
SJHQ	SJLGG006R	chr1	103759863	1	53	0	41	G	A	ACAAAATATGAAGCAAATTC[G/A]GGTATAGGGTTATTGAGAAG
SJHQ	SJLGG006	chr15	66369870	12	42	0	30	C	T	ATCTTCCCTAGTCCCACCTC[C/T]ACCTCCAGAAGGAACGAAAG
SJHQ	SJLGG006R	chr15	66369870	2	36	0	30	C	T	ATCTTCCCTAGTCCCACCTC[C/T]ACCTCCAGAAGGAACGAAAG
SJHQ	SJLGG006	chr2	99279218	12	64	0	48	T	C	GGTTTCAGGACTCCCAAAGA[T/C]CATCAGTGCAAATCTCCAAA
SJHQ	SJLGG006R	chr2	99279218	2	50	0	48	T	C	GGTTTCAGGACTCCCAAAGA[T/C]CATCAGTGCAAATCTCCAAA
SJHQ	SJLGG006	chr5	167935873	9	43	0	26	G	A	TGCAGGTACACGGAACATGA[G/A]CTCCTCTCTGAAAGAGGCTA
SJHQ	SJLGG006R	chr5	167935873	6	38	0	26	G	A	TGCAGGTACACGGAACATGA[G/A]CTCCTCTCTGAAAGAGGCTA
SJHQ	SJLGG006	chr6	55413428	11	80	0	48	T	C	CTTAAATAAATTCCATTTTT[T/C]TAAAAGTAGCTTCAGCAATA
SJHQ	SJLGG006R	chr6	55413428	4	62	0	48	T	C	CTTAAATAAATTCCATTTTT[T/C]TAAAAGTAGCTTCAGCAATA
SJHQ	SJLGG007	chr10	132188426	12	50	0	26	C	A	ACATGCTCAGGATGCTGTGG[C/A]TACAACAAAGCTTCCTTTCC
SJHQ	SJLGG007	chr1	195482878	16	73	0	40	G	A	GTGTTATTTTTTTCTGAAAC[G/A]TATAAGGTACAAAGTGGAAT
SJHQ	SJLGG007	chr17	66687785	12	54	0	35	C	T	TTGCAGGTCCTAATTTATTT[C/T]ACCTTCTCCGAAATGTTCAC
SJHQ	SJLGG007	chr2	840407	9	61	0	33	A	C	GTATTGCTTTTGGCAGAAAT[A/C]ACACAAATACAGATTTTGAT
SJHQ	SJLGG007	chr3	133488450	11	38	0	29	G	A	TGTGGCACAATAGGTACCCC[G/A]TCTTCTCAGCTAGCTACCCC
SJHQ	SJLGG007	chr3	25219789	10	55	0	42	C	T	CTTAGAACACAGGGAACATA[C/T]GAAAAAAGGGGGAGTTAAAA
SJHQ	SJLGG007	chr4	174589322	8	46	0	32	C	A	CAGAGTGTAATAGGCTCTGA[C/A]CTAAGAGGATAATCTTCATC
SJHQ	SJLGG007	chr5	158037051	15	45	0	33	C	A	AGGCTTCTCTCAGCACTTGG[C/A]AAGACTCCTCTTCATTTTGC
SJHQ	SJLGG007	chr5	27407098	10	70	0	34	A	T	GCTTCTAGTTTAGACAGAGA[A/T]GGCACTTGGTATATATAATA
SJHQ	SJLGG007	chr5	35774535	13	58	0	42	C	G	AGTAAGAATAATTTAGGTAC[C/G]TAATTAGGAAAATAAATTTT
SJHQ	SJLGG007	chr5	78996169	6	54	0	43	C	T	GCCTTGGGTTCCAGAATCTT[C/T]GCCAGTTAGTTTTGATTTGC
SJHQ	SJLGG007	chr6	169497461	6	47	0	35	G	C	CCATTCTTCCCCTTGTCTGC[G/C]TCAGTATTATTAGTGCACAT
SJHQ	SJLGG007	chr6	74208128	12	70	0	39	T	C	TATGCAAGATAGTACACGTG[T/C]ATGGCTTAAAGGAAACCATA
SJHQ	SJLGG007	chr7	140277043	14	55	0	52	G	T	TATCTGAGAATAGTGGTGAG[G/T]GAGAGTAAATTAGATCAAAA
SJHQ	SJLGG007	chr7	147718283	4	38	0	43	T	A	TTGTTGGTGGAGGTTTTTTG[T/A]TTTTGTTTTGTTTTTGGACT
SJHQ	SJLGG007	chr7	45261545	7	57	0	34	A	G	TCCCTTCCAGGCCATAAAAC[A/G]GCTGCCATGTCCCTTTCCAC
SJHQ	SJLGG007	chr8	118809075	12	68	0	47	T	C	GTATTAATGTATTTGTAAGC[T/C]TTGATATTTATAACACTTTC
SJHQ	SJLGG007	chr8	91813220	9	50	0	46	C	T	CATCAAGACAATTTAAAATA[C/T]GTCCAAGATAATATGATTAA
SJHQ	SJLGG008	chr10	110981766	8	57	0	42	C	T	CTCCTTTCAAAACCCTTCCC[C/T]GCACTCCCTATTTTTCACAA
SJHQ	SJLGG008	chr10	120678202	8	44	0	51	A	G	GAGTTTATATGTTGAAAAGA[A/G]CAACCAATCTCCCTTAGGGA
SJHQ	SJLGG008	chr10	28022177	20	69	0	32	G	A	TGAATCTTTGTAGATCATTT[G/A]TCTCATATATATTTGTAAAC
SJHQ	SJLGG008	chr10	32280861	6	47	0	38	C	T	AAGTGGTTAGAATACACATG[C/T]ATGTATACATGAGTATTATG
SJHQ	SJLGG008	chr10	58273208	9	37	0	24	G	A	TCCATGTTAACTAAAAACTC[G/A]CAGGAAGAAAGGAAGTCATA
SJHQ	SJLGG008	chr11	23857166	11	80	0	49	T	G	TTATTATTATCTGCTATTAT[T/G]TCTGAGAAGTTGCTATATTG
SJHQ	SJLGG008	chr11	33937779	12	62	0	31	G	T	TCTGTCTTTTAGGATTAAAA[G/T]CTTCTAAGAAAAAAACACTG
SJHQ	SJLGG008	chr11	6242085	10	71	0	41	A	G	TGTCTCTAAACATGAACAGG[A/G]CAATATGAGGCCAATCATGG
SJHQ	SJLGG008	chr1	175497615	5	44	0	47	G	A	CCTTTAAAATAAATTTGTAG[G/A]TGCACCATGTGAATTTCCAA
SJHQ	SJLGG008	chr1	187205072	6	48	0	41	C	T	AATTTGACATGAAATAAAAA[C/T]AAAAAGCTTCTTTCAAACTC
SJHQ	SJLGG008	chr1	188967797	17	56	0	61	C	T	TCATATGACAGAATCCTTGA[C/T]GTGAATGGAAAAAGTACTAT
SJHQ	SJLGG008	chr11	90890947	12	76	0	40	T	C	CTGAAAATGTAGGTCTTTCT[T/C]GAAAAGTTAATATTGTGAAA
SJHQ	SJLGG008	chr1	198190092	7	50	0	34	G	C	AGAAGGAATATTGAGTTTTT[G/C]AATAACCTTGAAGATTGAAA
SJHQ	SJLGG008	chr12	129969018	19	52	0	47	G	A	TTGCTATAAAATATCATCTC[G/A]TGCTCTAGAAAGGTCGCAAA
SJHQ	SJLGG008	chr1	215159969	9	48	0	34	G	T	TAAGTAGCATGGTACTGTCA[G/T]TGGTAGTGGGACTTTGGAGG
SJHQ	SJLGG008	chr12	20575338	7	40	0	35	C	G	TTTAAAAAGATAATCTATGC[C/G]TTGAAGTGCCATTTTTATTT
SJHQ	SJLGG008	chr12	67579852	12	52	0	42	C	T	TGGTGGCATCATGACCTAAA[C/T]ATGGCAAGAGTTTTCAATTA
SJHQ	SJLGG008	chr12	85815951	8	52	0	32	C	T	CCAACTGTGTATTTTCAATA[C/T]ACTGAAAAGCAGTGTATTAG
SJHQ	SJLGG008	chr13	104627913	8	42	0	38	C	A	TTCATGGGAATTATCAATTT[C/A]TTTTACTATATCTCTGGCTT
SJHQ	SJLGG008	chr13	111691609	9	34	0	32	T	C	TGTGTGTGTTTGAGAACTTA[T/C]GTATTCCTATGATCTTTTGT
SJHQ	SJLGG008	chr13	31070300	6	54	0	46	C	T	GCACCTGAAGATGGGGGTGC[C/T]CAAAGGAAGGAAAAGGAAAA
SJHQ	SJLGG008	chr1	35212521	6	26	0	26	C	T	GAGGCATACTGCTGGGGGTG[C/T]GGAGGGGCGGGACGCAGAGG
SJHQ	SJLGG008	chr13	56159078	7	45	0	34	G	A	TTCAACATAGTAGAGGGCAC[G/A]GAGATGAAACCAGCTCTGTT
SJHQ	SJLGG008	chr13	64946462	6	57	0	46	G	A	AAAAGAAAAGTGGAGGAAAC[G/A]TGAAAGAGAAGAATGACTGA
SJHQ	SJLGG008	chr13	70047547	8	48	0	31	T	A	GAGGCAGACTCACATATCCA[T/A]GGTCACAATGTTGAAAGATG
SJHQ	SJLGG008	chr13	86277261	5	41	0	43	A	G	AAGTATGTACAGTGTCAATT[A/G]TGTTCTCATTTAGTTTTAAT
SJHQ	SJLGG008	chr13	88221575	11	43	0	39	C	T	ATCTGAAATTCAGCTTCCTA[C/T]GTTACCCAAAGTTAGAAAGC
SJHQ	SJLGG008	chr14	41921858	11	50	0	39	A	G	AGGCATCTTTACATCAAAAT[A/G]TTTTAAGATAAAAATCAAAT
SJHQ	SJLGG008	chr14	44572681	6	46	0	43	C	T	AAGTATGTGGTTTCAGACTA[C/T]CATAAGTAATCAATGGGGAA
SJHQ	SJLGG008	chr14	51105854	7	46	0	48	G	C	AGCATTATAGACTTTTGTGA[G/C]CAGACACAGGAACATAACTT
SJHQ	SJLGG008	chr14	68102648	11	55	0	52	G	A	ATCTGCCATGTAAAATATTT[G/A]AGTCTGTAACTTTAAAAGCC
SJHQ	SJLGG008	chr14	71569526	15	50	0	42	C	A	TTTTATATATGCAATTTGGG[C/A]AGCATCTCTTTTTAAAAAGT
SJHQ	SJLGG008	chr15	27496357	9	38	0	36	T	C	TCGGCCCAGATTTCCTCTGC[T/C]GTGAGGTCTTGAACTTAGTT
SJHQ	SJLGG008	chr1	55716865	7	46	0	35	G	T	CTAAGAGAACTGATGAAAAG[G/T]GATTCTGGAAGTGCAGGGTC
SJHQ	SJLGG008	chr15	67837527	8	46	0	35	A	T	TCTCTGTGTCATTCTTGGTT[A/T]TGTGCCCCACCTCTGTGTCG
SJHQ	SJLGG008	chr15	72576586	7	52	0	41	A	C	TCAAAATGATGCAGCTGTCT[A/C]AATGGCTTTGTCCAAATGTC
SJHQ	SJLGG008	chr15	77747962	6	47	0	43	A	G	GACCTGTTTGTATAAAGTGC[A/G]GTGAAGAGCCAAACTTGTAT
SJHQ	SJLGG008	chr16	54871790	14	48	0	34	G	A	GCACGTAGTAGGTGCTGCAC[G/A]CAGTTTTTATTCTCTTTCTC
SJHQ	SJLGG008	chr16	66024983	7	44	0	33	G	A	GCAGAAGATAAAAACTTACA[G/A]CCTTTTGGTATGTTTTCCTT
SJHQ	SJLGG008	chr16	80248612	7	44	0	34	T	C	ACATAATCAGTTCTGTTACG[T/C]CACTCTCTTCTAACTTTTGA

SJHQ	SJLGG008	chr18	14075906	6	54	0	40	T	C	TCCATTTTCTATTGCTGAAC[T/C]ACACACCACACACCACACAC
SJHQ	SJLGG008	chr18	22320124	6	42	0	32	A	T	CAAAGCCGCCAGTCTCCTGC[A/T]GGTATTTCCCACTTTTTCCT
SJHQ	SJLGG008	chr18	41142672	6	57	0	52	A	G	AAAATGTTAAATAGCTTTTT[A/G]TGCCAGCCAACTCTTGATTA
SJHQ	SJLGG008	chr18	44249151	5	31	0	33	G	C	CAGGGTGAAGCCCAGGCCTG[G/C]AGCAGACTCCAGATCAGCCT
SJHQ	SJLGG008	chr18	57465533	13	50	0	23	C	T	ATCCTTCAACCAACTGAAGA[C/T]GTTTTGGCAGGACCTGCAAA
SJHQ	SJLGG008	chr18	59460740	8	50	0	52	T	C	ATTTTCTTTTTTAGAAAATA[T/C]GGAACTTTCTGGCATGCCTA
SJHQ	SJLGG008	chr19	32694120	5	29	0	32	C	T	ATGAGCAGCATTGCCTCTTC[C/T]CCATGGATGCCTGGTGCGTA
SJHQ	SJLGG008	chr20	44676841	11	35	0	28	G	A	TTGCTTTGTTTTGCTGAGTC[G/A]TGCCCTAAAAGCCCAGCCTT
SJHQ	SJLGG008	chr2	1019904	7	46	0	35	G	A	AGATATTTATTTGAAAAATC[G/A]TAATACTAAAAGTGAGGGAC
SJHQ	SJLGG008	chr2	114831133	6	30	0	29	G	T	GAGGAGCAGCAGGGAGAACG[G/T]GATAGGGTGGGCCTGAAGTG
SJHQ	SJLGG008	chr2	119798166	11	53	0	53	G	C	GATTATGGAAATATTACGTA[G/C]ATATATAAAATTGTTTGACT
SJHQ	SJLGG008	chr21	30315464	7	58	0	47	G	C	ATCTTACAGATAACTAAAAA[G/C]ATCTATCTGTAGAATGAATA
SJHQ	SJLGG008	chr2	130659258	6	41	0	41	A	G	GATCTTAAACTTGGAATTGT[A/G]TGAAGACCACACAGGGATTT
SJHQ	SJLGG008	chr2	137826436	9	57	0	52	C	A	ACAGGAAGAGCTTGTCTTTA[C/A]TTCTATAATGTAAACTCCTG
SJHQ	SJLGG008	chr2	13977073	9	43	0	57	C	T	GTTCCCCAAACATATGGATA[C/T]GATAAGCACAGCCATATACC
SJHQ	SJLGG008	chr21	40600925	7	39	0	39	T	C	AGCACAGGTGTAGGAAATTA[T/C]TTATTCTGAATTTTTTCAAA
SJHQ	SJLGG008	chr2	157546533	7	56	0	37	G	C	GTACTGTGCAAAATCTTTCT[G/C]AATAACGGGTGACCATCAGG
SJHQ	SJLGG008	chr2	181225958	7	41	0	49	T	A	CAGAAATGGCATATATTGGA[T/A]TGAAAACTAAAGTGGTCAGT
SJHQ	SJLGG008	chr2	189354828	8	52	0	55	G	T	ACATTTCAGTATTTACTATA[G/T]TATCATTTTATTTTTTTAAA
SJHQ	SJLGG008	chr2	207973835	6	50	0	46	C	T	TTATCTAAAATATGCAAATG[C/T]AGTAGTACTGAGATACCACT
SJHQ	SJLGG008	chr2	210807319	13	47	0	34	C	T	GTTTTGATAAAAATTATGAT[C/T]ACAACACATACAAAGTTAAG
SJHQ	SJLGG008	chr22	18342558	10	29	0	21	G	A	GGCTCTATGTCCCTATGGTT[G/A]ACCAGGCTCTGTGTGGCATT
SJHQ	SJLGG008	chr2	218434319	7	38	0	31	G	A	TAGATTTCTTAAGAAGTCAA[G/A]GTGTAGTCTTCTTGCTTCCT
SJHQ	SJLGG008	chr2	219159853	8	32	0	29	G	A	GAGCCCTTTTTCTGACTATA[G/A]GGTCAAAAATAACACCTGAA
SJHQ	SJLGG008	chr2	226084293	9	44	0	35	G	A	AACAGAAACAAGGAAAAACA[G/A]GTCATGGGAACATTGGAAAC
SJHQ	SJLGG008	chr2	38731789	7	62	0	48	C	T	GAAAATAAATTGTTAGCAAA[C/T]GACTCTTCCCCATCTGTTTT
SJHQ	SJLGG008	chr2	46080464	8	55	0	42	C	A	GTGTTCTTCCAAGATGAGAA[C/A]AAGAAGCAATTATACCAGGA
SJHQ	SJLGG008	chr2	52134934	6	44	0	49	G	A	ATTTCTCTGTATTTGGACAT[G/A]CTTCCTGGATCCAAAGTCTT
SJHQ	SJLGG008	chr2	58480353	7	47	0	34	A	G	TATTCCTTATTTCTAAGGTC[A/G]ATAATTCTGAACATCTAAAA
SJHQ	SJLGG008	chr2	62840942	6	56	0	41	G	A	AATGGTTGGGAACCAAGACA[G/A]GGTGAAATCAAGGATGGCTG
SJHQ	SJLGG008	chr2	64818620	15	43	0	30	G	A	CAGGCTGAGGTAGTTTTAGC[G/A]GGTGGAGGGGCAGGGAAAAA
SJHQ	SJLGG008	chr2	97021021	14	37	0	33	G	A	GGTCTTCAATGGGCCTGGGG[G/A]TAGGAGATTTCATGAGATTA
SJHQ	SJLGG008	chr3	103048463	9	57	0	30	C	T	TTGATATTTTGTTAAGTGTG[C/T]TAAAACATTAAGGTTTGCAA
SJHQ	SJLGG008	chr3	105964941	7	49	0	49	C	A	TTACTAGAATCGGCTTATGT[C/A]CATTTTTTAATGTTAGCTCT
SJHQ	SJLGG008	chr3	156010263	5	35	0	44	A	T	TGTTCTATTTTATGATAAAG[A/T]CAGTAGTTTCTGGGATTATA
SJHQ	SJLGG008	chr3	158758064	11	58	0	38	T	A	TTAAGTAAACTTTTAAAAAA[T/A]TAGATCTAGGCATGGTTCTA
SJHQ	SJLGG008	chr3	159899795	8	67	0	39	A	C	TTTTCTCATCTGGTTAAAAA[A/C]TAATTCAGAGGATTTTTTTC
SJHQ	SJLGG008	chr3	176845496	7	37	0	50	C	A	GACAAGGAAGAATTCACTGT[C/A]TGAAACACTATTGAGTCACT
SJHQ	SJLGG008	chr3	21174464	8	54	0	38	T	C	ATTTGGAGAAAGCTTTTAGC[T/C]TTTTCCTTTTGTAGGACTTC
SJHQ	SJLGG008	chr3	21662810	6	44	0	35	G	A	AAAGTAAATGGAATTAATGG[G/A]CTGTCGCTGGCAATCTTTAG
SJHQ	SJLGG008	chr3	25417651	7	52	0	54	T	C	AAAGTTGGGCTATTACTAAC[T/C]GGTGTAGAATCAGTCACATA
SJHQ	SJLGG008	chr3	88726638	10	50	0	49	G	C	TTTCGCCAGACACCTGATTA[G/C]AAAGAACAAGCAAACCTTAT
SJHQ	SJLGG008	chr3	96170179	7	51	0	45	G	A	GGATGTAATAAATGATCTTG[G/A]ATTATAAAAATAAGATTATT
SJHQ	SJLGG008	chr4	102814666	9	69	0	46	T	G	ACACAAATTTTAAAGAAAAT[T/G]TACAAACTAATGTTATGATT
SJHQ	SJLGG008	chr4	118734568	7	53	0	39	T	G	AGACTTCAAGGTGGCACCAT[T/G]TTCAAAAATCTCCGATTGTC
SJHQ	SJLGG008	chr4	163068810	7	64	0	43	A	T	TTTGAAGAGGCTTTCCAGAA[A/T]GTTTTTATTGTTTGCATTGT
SJHQ	SJLGG008	chr4	170355004	10	59	0	61	C	T	TAGTTCAGTTATTTCTGAAA[C/T]GACAGACTACTTCTTTTGCC
SJHQ	SJLGG008	chr4	172020292	7	56	0	39	G	C	TTGGTATAGTGATAAGAATC[G/C]TCTTACTGTTTAGCCTTTGA
SJHQ	SJLGG008	chr4	74540407	5	40	0	42	G	A	TCTTGAAATCTTTCCTGACT[G/A]GAAGTCCAGAGCATGAACTT
SJHQ	SJLGG008	chr4	8352761	5	24	0	26	C	T	ACAGGCTCCTGTGACCCTGA[C/T]GCCAGGGGAAACTCGAGTCT
SJHQ	SJLGG008	chr4	85855769	17	64	0	39	C	A	GCAGAATTAATGACATGTCT[C/A]CTAAATTATGACTTCAGATT
SJHQ	SJLGG008	chr4	86512738	7	39	0	26	T	C	TACAAGTCACAGTCATTAGT[T/C]ACAAGTCACAAGCCATTAGT
SJHQ	SJLGG008	chr4	99957585	11	56	0	48	G	A	ATTTTAGAAAAACAATCATA[G/A]ACAAGGTAAATTCTAACAAA
SJHQ	SJLGG008	chr5	101594210	17	57	0	44	G	A	CTATGAGCAGAGATGAGAAT[G/A]GTCTCTAAGTATCAAATTAA
SJHQ	SJLGG008	chr5	112516689	6	45	0	43	C	G	CAACTCTAATTTTGAAGAAT[C/G]AAAAGATTCCAACCTCCCAA
SJHQ	SJLGG008	chr5	129457912	8	57	0	32	A	C	AATCAGCCTGTGATAACAGC[A/C]GATTTAGACATCCTTCAATT
SJHQ	SJLGG008	chr5	153856179	6	29	0	27	A	G	TGAGCTTTCGTCAGTTTACC[A/G]CAGGCCCCCGCAGGTTGGAT
SJHQ	SJLGG008	chr5	23071725	10	57	0	42	C	T	TATGCATGTTCACCATCTCT[C/T]ATGGCCTCCTACGTCAATGA
SJHQ	SJLGG008	chr5	24498073	6	55	0	40	C	G	GCCCTGATGCAAAACCGTAT[C/G]TGCACACATCAGAAAAGTGA
SJHQ	SJLGG008	chr5	51065122	9	64	0	35	C	T	CCAGGTTAATTACAGCTGTG[C/T]GAGTCTTTATTATTTTATGA
SJHQ	SJLGG008	chr5	52307966	17	55	0	28	A	G	AGAGTGGAGATTCCCTCAGG[A/G]TGAGGACTGTATTTTAAATT
SJHQ	SJLGG008	chr5	85968579	9	77	0	42	C	T	TGCTTTTTGCATTTCCAGCC[C/T]AGAGGATAATATATTAGCTT
SJHQ	SJLGG008	chr5	87061747	18	53	0	40	A	G	TTCTGTGTAAGCATCCTGCT[A/G]TTACCGATGCTGTGATTGTC
SJHQ	SJLGG008	chr6	105520501	14	64	0	47	T	C	GTATCACCAACTAACTATTT[T/C]TGAAAACTCAGTGTTTTTAC
SJHQ	SJLGG008	chr6	122278752	11	76	0	44	A	T	TGAAAAACCACGACCTTTTC[A/T]TTGACTGGTATGTGTTTTGT
SJHQ	SJLGG008	chr6	131179597	10	78	0	42	T	C	CCCAATTCTTCAGTCCACTT[T/C]CAAATAATGACACGTAGAGG
SJHQ	SJLGG008	chr6	133324411	13	65	0	51	C	T	TTTTACAAAAAGCACTGTAG[C/T]TATTTCCTAAAGAGGATTAA
SJHQ	SJLGG008	chr6	153523049	8	64	0	41	A	G	CTTTTGGTATTCCTTTATGA[A/G]GAGTTGAAGCTTAAGATGTC
SJHQ	SJLGG008	chr6	68333793	11	81	0	46	T	A	TGAACAAAGATATTATAAAA[T/A]GATTTAATACCTAAATATTC
SJHQ	SJLGG008	chr6	83232107	8	69	0	56	T	C	ATGAGTGATTCATCCAGATT[T/C]GGGGTAAACTGTTAATGCAT
SJHQ	SJLGG008	chr6	8846757	15	60	0	46	G	T	TCATAATGTCTCCTTCTAGT[G/T]CTTTAATAGCTTTTGTGTCA
SJHQ	SJLGG008	chr7	115708250	9	55	0	37	G	T	ATATGTTTTTTTGTATTTTT[G/T]TCGGGGGTTGGGAGACTTGG
SJHQ	SJLGG008	chr7	142588890	9	40	0	33	T	C	TGAAACTCTCCAATGTCCTT[T/C]TGTACTCAAACATCCAGCGC
SJHQ	SJLGG008	chr7	146557775	9	80	0	47	C	G	TTAAAATGTATTGTCTTAAC[C/G]TAAAGAAAGCATCTACATTC

SJHQ	SJLGG008	chr7	22026079	11	45	0	25	G	A	AACGCAGCTTGCTGCTCTGC[G/A]TCTCCCCATCCTAGGCCCAA
SJHQ	SJLGG008	chr7	41827931	16	80	0	54	A	C	TTTCATTAATTGCTTTCCCT[A/C]TTTACTGTTAACTACTCACT
SJHQ	SJLGG008	chr7	52190879	10	61	0	35	C	T	GAAGAAGTAAAAATGCAAGC[C/T]GTTCTAATGGTAATTTAGCA
SJHQ	SJLGG008	chr7	53829853	11	90	0	66	G	C	TATCTTAGTAGACATTTTTG[G/C]TATTTTGGTTCAAATTTTTG
SJHQ	SJLGG008	chr7	85156985	9	51	0	39	T	C	GCACTATTAATAGTACTTAA[T/C]AGGTACTCTTATAGCCCTTT
SJHQ	SJLGG008	chr8	111569066	18	76	0	35	A	T	CAAAAAATAAGTAAATAAAT[A/T]ATTTAAATACTCCTATTTTT
SJHQ	SJLGG008	chr8	137823894	12	72	0	47	A	G	AATAAAAATGATAACATGCC[A/G]AAGGTCTCTATTCTAGTCAT
SJHQ	SJLGG008	chr8	20975286	7	59	0	39	T	A	TCAATCAATGAATAAAGCAA[T/A]TAATAAAAGATGGATTTCTT
SJHQ	SJLGG008	chr8	27152181	15	60	0	35	C	T	ATCATAGAAATGAATGGCTG[C/T]GAATAGCAATGATTTTTTTT
SJHQ	SJLGG008	chr8	34163324	9	47	0	36	G	A	TGAATGACACACTCTGTAGG[G/A]AGGGGACAAATGTTCTGAAT
SJHQ	SJLGG008	chr8	36408766	17	61	0	44	T	C	ACATTGGTCAGTCATTCTAA[T/C]TGGAAATGCTATTTTTTAAC
SJHQ	SJLGG008	chr8	80342901	12	52	0	48	T	C	AAGAGAATATTCCACCAACA[T/C]TTTTCCCATGGTCAGAAAGA
SJHQ	SJLGG008	chr8	84588468	11	66	0	51	A	C	TATTAAATATTATCCTACAA[A/C]CTTAGGTTAGCATATCTTAG
SJHQ	SJLGG008	chr9	112759693	7	52	0	38	T	A	GATAGTCTCGCTGTCATTAC[T/A]GCTACTATTGCAGCCCCGCT
SJHQ	SJLGG008	chr9	12632753	8	60	0	43	G	A	TTGTCCTCTTCATTAGAGTG[G/A]AGGTTCTTTATGAGCAGAAA
SJHQ	SJLGG008	chr9	32947395	9	43	0	34	G	A	TCGCCCTGAACCCTGCAAAC[G/A]TCGTCATCGAAGGGAAGGGT
SJHQ	SJLGG008	chr9	9587548	11	59	0	51	C	A	AATGGCAGCCCAAAAAAGAC[C/A]AGTTTGCTTCCTTCTAAGTA
SJHQ	SJLGG008	chrX	104573299	8	46	0	37	C	A	TGCGTTTACCTGCAGCAAAA[C/A]CCTACAGAATTCACCTGAGG
SJHQ	SJLGG008	chrX	120485826	9	55	0	29	G	T	CAAAGATAGGGAGGAACATG[G/T]TCACATTGATTCTTGGTTGT
SJHQ	SJLGG008	chrX	127638278	9	71	0	44	C	T	GAATAAGGTAGTTAAAAGAA[C/T]GGCCTAAGTGTGCTAGATTA
SJHQ	SJLGG008	chrX	134228378	7	36	0	28	G	C	CCTTCCCTCTCCCACCTTTT[G/C]CCTGCTTGCCAACCCTTACA
SJHQ	SJLGG008	chrX	149796814	14	53	0	39	T	A	CAGACACCTCTCCCTCTTTT[T/A]TTTGAAACCTAACTTTCCCC
SJHQ	SJLGG008	chrX	26311805	7	49	0	38	G	C	TTCTTTATCTGGTTTGAGCT[G/C]TTCATTAAATTATCCTCCAA
SJHQ	SJLGG008	chrX	26313269	9	60	0	43	A	T	TTCAAGATGAAATTAGTAAT[A/T]TCTTTGGAGTTTCTCAAAAG
SJHQ	SJLGG008	chrX	4009997	10	46	0	40	C	T	GGGATAAGAGGTAAAATACA[C/T]GTGTTTTATATTTAATCAAC
SJHQ	SJLGG008	chrX	40274147	9	47	0	25	G	A	GAGTTAGTGACTGTTACTGC[G/A]AAGAAGGCAGTGGGTAAGGA
SJHQ	SJLGG008	chrX	43340235	6	54	0	51	T	C	CTTGTCCACTGCAGTTCTTG[T/C]GTCATTTCAGCTAATACTAT
SJHQ	SJLGG008	chrX	55286473	8	65	0	54	G	A	GGAAAAAACATGTGTAAAAC[G/A]TACTTAAGTTGATTACTCAA
SJHQ	SJLGG008	chrX	68021339	8	38	0	24	G	A	CAGTTGGTTGGCTGGCAGAG[G/A]GTGAAGTTGGCTGTGAGACC
SJHQ	SJLGG008	chrX	75569853	8	45	0	30	A	C	TTTATTTTTCAGTAATAATA[A/C]TAAAAGCACTTTAACTCTCT
SJHQ	SJLGG008	chrX	81080406	14	45	0	43	T	C	CCCCAAGAAAAGCTCTAAGT[T/C]TGTTTTTCCGTTCTACTTCT
SJHQ	SJLGG008	chrX	98357510	11	37	0	27	C	A	TCCAGCAGAGTAGAAACAAT[C/A]AAAACACCATTTGAGTGCCT
SJHQ	SJLGG009	chr10	37108468	9	39	0	32	G	A	AGCATAGGCAGAAAAATACT[G/A]TGAAGTTGAAGTTATTATTA
SJHQ	SJLGG009	chr10	37825036	12	48	0	40	A	G	ATGAGGACATAGCCACAGGA[A/G]TCTGTGGCATCTGTGCTCAC
SJHQ	SJLGG009	chr10	99283347	7	42	0	32	C	A	CTGAGCCCAGCACCTGGCAT[C/A]AACATGAAGCGATGGTTGTA
SJHQ	SJLGG009	chr1	10762648	7	43	0	27	C	T	CCAGAGGCCTGGCAATGACC[C/T]GGGCCAGGGAGCTTGGAGAG
SJHQ	SJLGG009	chr11	18042805	8	45	0	36	A	G	TATATTTCACATACTAGGCA[A/G]AAAACAAATTCTTGTTAGAT
SJHQ	SJLGG009	chr1	215147513	9	59	0	45	G	A	ATTTAATTGAAGGGCTGAAG[G/A]CATTTTTGGCTCCCCATGGG
SJHQ	SJLGG009	chr12	43657595	9	52	0	32	A	G	TTTATTTTCTTTTAAACTCC[A/G]CAAGAATTTGGTAGTTGCAT
SJHQ	SJLGG009	chr12	72200585	11	43	0	42	A	T	TTAAGTTCCAAAACAAAAGC[A/T]TTAAACACAAGTTGACTTTA
SJHQ	SJLGG009	chr12	84664911	8	52	0	29	C	T	CCTTCTGACAGGAAAAGCCT[C/T]TCCCCAGGCTTTTACTTCTA
SJHQ	SJLGG009	chr17	33119262	8	44	0	28	G	A	TGATGAATGGAGATGCCTTG[G/A]GCTGGGTGAAACAGGAGCAT
SJHQ	SJLGG009	chr18	59549099	13	46	0	39	C	A	TCTCAGAGAAGACATTTTTC[C/A]TTGTTAATTAACAGTCTTCT
SJHQ	SJLGG009	chr20	58060708	16	59	1	47	C	T	ATATTTCAGGGGCTCTGAAA[C/T]GATAGCCCCCATTACTTTCT
SJHQ	SJLGG009	chr21	17714370	6	33	0	33	T	C	AGCGAACGTCTAATCACTTA[T/C]CTGTGATGGTGATTACATGA
SJHQ	SJLGG009	chr2	121617865	15	52	0	41	G	A	CCTGAGGATGGCTTCGGTCA[G/A]TTCCAGTACCCCCAAGGAGC
SJHQ	SJLGG009	chr2	123114965	4	28	0	41	G	A	AACAGCAATGGCAGCAAGAG[G/A]TGTCATTTACTGAGTGCACT
SJHQ	SJLGG009	chr2	175450695	11	36	0	28	C	T	CACTGAAAACAAATTCACTT[C/T]AAGTGGCTTCTCCTCTTCGC
SJHQ	SJLGG009	chr2	194252519	16	46	0	45	C	T	AGGACTTCAATAAAGAAAAG[C/T]GTAGGATTAGTTCAAAAAAA
SJHQ	SJLGG009	chr2	222934748	8	55	0	35	G	T	AATGCCAATTTCTACAGAAA[G/T]AAATATTTCTTAGCCATCCA
SJHQ	SJLGG009	chr3	35954934	14	50	0	31	A	G	TTATTTTTGTGTTTATGTTT[A/G]CACCTCAGTATCACATGGAC
SJHQ	SJLGG009	chr4	22895051	16	54	0	38	G	A	CTAAGTTTCTAAATTTATAC[G/A]TCTTAATTATCTGTAAGGAA
SJHQ	SJLGG009	chr4	34870326	11	46	0	38	A	G	CGTTTAATTTCTATAACTTG[A/G]GTAAAACTGTTTACTCCCAA
SJHQ	SJLGG009	chr5	139672297	7	48	0	33	A	G	CATTTGAACTTAAATTATAT[A/G]AATGAAATAAGGATACACTC
SJHQ	SJLGG009	chr5	161600880	9	48	0	53	A	T	ACAAAAAATCACTCATGTTC[A/T]AAACAAATCATTATTTGCAA
SJHQ	SJLGG009	chr5	19651847	15	54	0	35	G	A	TTTCATTTGAAGGGATAAAT[G/A]TCTATGATAAGCAGGTATAG
SJHQ	SJLGG009	chr5	98333070	21	63	0	35	C	T	CTTGAATGGAGTGAGGGGAA[C/T]GTAAAGATGAATACAAGGAA
SJHQ	SJLGG009	chr6	82660522	9	59	0	34	A	G	AGCTCTTGATATTCATCAGA[A/G]TTTCCTACCCTGGCCTCAGG
SJHQ	SJLGG009	chr7	119867524	15	53	0	33	G	A	ATTGTGCTAGCCTTTCTGAC[G/A]TCACAATATCTGCTTGTTAC
SJHQ	SJLGG009	chr7	24595833	8	52	0	25	C	G	GTTCACAATTCTTTTTTAAT[C/G]AGGAACTCTGGCTTCTTCTG
SJHQ	SJLGG009	chr8	133802618	10	38	0	26	G	A	TACCATTTAATGCATTTCAC[G/A]GGTATTGCAAAGATCTCGAT
SJHQ	SJLGG009	chr9	30588595	7	48	0	35	G	T	ATTCCCAGCCTCCAATGTTG[G/T]TATTCCTGAAAACTTTGTCC
SJHQ	SJLGG009	chr9	34575313	10	41	0	27	G	A	AGGCTAAGTCTGTGGGGAGC[G/A]GGGTACTGCTCCTCTTGTAG
SJHQ	SJLGG009	chr9	39110944	4	28	0	30	C	T	AAATTGCCCAGTTCTCAAAC[C/T]TTCTTTTGTATGCATTTGTG
SJHQ	SJLGG009	chrY	3338677	14	24	0	20	G	A	TTGATTGATAAAATTTAATC[G/A]CAGTTATTTTATGAGTTGCT
SJHQ	SJLGG010	chr10	133118134	11	39	0	24	C	T	TGGTGGGGACACCTGGTGAC[C/T]GAGGACATATCCGTACTAGC
SJHQ	SJLGG010	chr10	1624462	20	43	0	30	C	T	TGGGAAGTGACGTGACCCTG[C/T]GTTACCTGCTGGTGGCAGAG
SJHQ	SJLGG010	chr10	96919980	14	40	0	34	C	T	CCCATCTACACTGAAAATTT[C/T]GACTACTGGTCGTGAGACCA
SJHQ	SJLGG010	chr1	191839968	7	31	0	28	C	G	TCAAGTTTGCGGAAATTGAA[C/G]TTTTCCCAGAGGGTAGTGTC
SJHQ	SJLGG010	chr12	127173121	6	42	0	34	T	A	CCAATCCTAGAAACACCTGT[T/A]GCTTGTTGGGTGAGAAGTTT
SJHQ	SJLGG010	chr12	25983302	12	45	0	48	G	A	TAAGCTCAATGAGGTTTTCC[G/A]GAATTCAGGTTTTGTTGGAG
SJHQ	SJLGG010	chr13	32088692	13	44	0	38	G	T	GAGAAAAAAGGGTCCAGGAA[G/T]AGTTGGAATAAACAGGGAGT
SJHQ	SJLGG010	chr13	62890188	21	60	0	33	T	C	CATTAAGTGAATATGCTTAG[T/C]TGATCAATATATTAACTATA
SJHQ	SJLGG010	chr13	88921749	17	45	0	35	C	T	TAACTTTGTTTACCCAAATT[C/T]TAATTTGTCTACACTATTTC

SJHQ	SJLGG010	chr14	53408824	8	40	0	31	C	A	GCTGGAACTTATTAAATATA[C/A]TAGATTATATTTTAACCTAC
SJHQ	SJLGG010	chr14	81733878	13	47	0	39	A	G	ATGCCTCAGGTATTATGTAT[A/G]TTTGTTTCAGGAATCAGAAG
SJHQ	SJLGG010	chr17	32765701	11	35	0	32	T	C	AGGGGGACAGGGCTGGGAAG[T/C]CCCTTTTAACTTCTGACATC
SJHQ	SJLGG010	chr17	60040431	4	33	0	37	G	A	CCCCTCCTCCCTCTTTTTTG[G/A]TGAAAGGTGTCAGAAAGCCT
SJHQ	SJLGG010	chr18	14632198	17	44	0	29	C	A	ACTTCAGCACTGGGGCTGTG[C/A]ACAGCAGGATGTGGGGCAGT
SJHQ	SJLGG010	chr1	82282382	18	38	1	28	A	G	GTTAAAAAGATGTTTACAGT[A/G]CTTTCATGTTTGGCATTATT
SJHQ	SJLGG010	chr19	30587951	16	46	0	35	C	T	TTCAACAGATGGAGGGGTCG[C/T]GGCCCCCAGAGCTGGGGAGC
SJHQ	SJLGG010	chr20	51342344	15	45	0	31	G	C	AAAGTCTTCATGGAAAGGCA[G/C]CTATTTGCACTAATGGTATT
SJHQ	SJLGG010	chr20	7621281	26	47	0	26	C	T	TAATAATTTACTCGTCTTCC[C/T]GTAGTATTAGTGAAATTGCT
SJHQ	SJLGG010	chr21	10399670	8	69	0	42	C	A	AATTGATAGGAAAGACATGA[C/A]AAATGTAATGAAATCAATGG
SJHQ	SJLGG010	chr2	122952047	15	56	0	40	C	T	AATGCTGTCAGATGCAAGCA[C/T]GTGGTAAACCCATGCTGGTT
SJHQ	SJLGG010	chr21	25301294	7	56	0	51	G	T	CCAGTTAATACCTGCAAAAT[G/T]CTAAAAATATAATCCTTTAA
SJHQ	SJLGG010	chr21	26130023	13	46	0	43	C	T	TGTATTTATTTCAGAACAGA[C/T]GGCAATGTAATTTGTCATGC
SJHQ	SJLGG010	chr21	36847422	14	49	0	28	C	T	AATGAAGAGCATTTCCAAAG[C/T]TGTTTGAGGAAGCTGGGCTG
SJHQ	SJLGG010	chr2	194972007	12	40	0	27	G	A	ACAGGTAATTTTATCTATTC[G/A]TATGAGTTTGATAACACACC
SJHQ	SJLGG010	chr2	218495496	7	56	0	33	G	C	GACTCTTTGAGAAAATACTA[G/C]AAGTCTACATCTGCAGGCCT
SJHQ	SJLGG010	chr2	34083392	4	35	0	38	A	G	GTGGATTCTTATTTCAGGAT[A/G]CAACTATTACAAATAATATC
SJHQ	SJLGG010	chr2	73835433	16	44	0	26	G	A	CCTTCCAGATTGTGAGCCCC[G/A]GGCTAGGGTTTTCTGTGCTG
SJHQ	SJLGG010	chr3	162673386	16	44	0	54	G	T	AGTCCCTGGGAATAAATATA[G/T]TTTGTAGTCGAAAATAATTT
SJHQ	SJLGG010	chr3	176510280	9	51	0	34	C	T	CAAAATTCTTTCTACAATAC[C/T]CCCAAATGATTCCAGGTATC
SJHQ	SJLGG010	chr3	183429508	10	56	0	40	C	G	GACTTCCATATGTAACATTA[C/G]ATAATGAGCCACTCTCCTAG
SJHQ	SJLGG010	chr4	11674301	19	54	0	45	G	A	ACCACTGTCCTGAATCACAA[G/A]CCTACCTGTAGGATCGACTT
SJHQ	SJLGG010	chr4	60085607	7	50	0	32	C	T	CTATTACTTTTAACCCCTCA[C/T]TTGTTCTGTCCTGAGAAGCA
SJHQ	SJLGG010	chr4	64615568	12	53	0	28	C	A	TATTTTTGGATTATTAAATT[C/A]ACTATATTTATTTTATTATA
SJHQ	SJLGG010	chr4	69491973	7	39	0	53	A	T	CAGCTTTTTCCTGCATACTA[A/T]TTAGAAATCTTAGGAACTGC
SJHQ	SJLGG010	chr4	88261328	16	52	0	54	C	A	ACTCTGGTCTCCTTTAATAT[C/A]ATTGTTCTATGATTCCATTA
SJHQ	SJLGG010	chr5	22811515	4	37	0	42	C	T	AGGCCCCTAAGCAGATTAGA[C/T]GATATTCAGTGGCGGAAGTT
SJHQ	SJLGG010	chr5	28438140	14	41	0	23	C	T	AATAATTCCCAATACTAACA[C/T]TTTCTGTCAGTACTAATCCA
SJHQ	SJLGG010	chr5	28439090	21	65	0	43	T	C	CTCAGAGAGTAAAATGAATG[T/C]AATGTTAAGATACAGTTAAG
SJHQ	SJLGG010	chr6	104502240	15	45	0	23	G	A	GACATTTTGTGTTAAATACC[G/A]TATATGAAACTTATATGTAA
SJHQ	SJLGG010	chr6	13386102	16	50	0	38	T	C	AGGATAAAGCCAGTGAATTA[T/C]TCCCCTTCAGTTCCCTCTCT
SJHQ	SJLGG010	chr6	158015339	7	47	0	36	A	G	GGTTTTCTTAACATAGATAA[A/G]TTACTTTCAGCCTTGCCTCC
SJHQ	SJLGG010	chr6	48722658	19	51	0	32	G	A	GTGATCTCTGCTCCTCGGGA[G/A]TTCACCTTCCAAAACAGAAA
SJHQ	SJLGG010	chr6	50062380	10	27	0	32	G	A	ATCTTGAAATATGAAGGGTA[G/A]GCAATTATTTCACTATACAT
SJHQ	SJLGG010	chr7	115692363	8	57	0	47	A	G	TATTTATTTACATTTATCAA[A/G]ATGTGTTAAATATAAGCCAT
SJHQ	SJLGG010	chr7	79270796	16	37	0	45	G	C	CTGTCATTATAAAACATGTA[G/C]TCTATCACTGCTAATGTCAA
SJHQ	SJLGG010	chr7	98859419	27	54	0	34	G	A	AGCCAATTGAAGTGAGCTCC[G/A]CTCACACTTCCTCATCACTT
SJHQ	SJLGG010	chr8	109087160	22	57	0	24	G	A	GTGGTCTCTTCATACTTACA[G/A]AACTTGTTCTAAAATACACA
SJHQ	SJLGG010	chrX	85553030	6	24	0	24	T	A	CCTCCTTGCCTTCTGCCTTC[T/A]ATTGAAGTGACATTTGTATA
SJHQ	SJLGG011	chr10	132013707	17	56	0	21	C	A	GGGGTCAGCTGCAAGATTAC[C/A]ACTTAAAACAGAATCCTGCT
SJHQ	SJLGG011	chr10	33523676	6	46	0	33	T	C	TGCCTGAATTAATGCCTTTT[T/C]CCATAGTTAAATTAAAGGAG
SJHQ	SJLGG011	chr10	82720982	9	39	0	31	T	C	CAGAAATCATCAAATTTCCC[T/C]CCAGATGAGCCTTTACCAAG
SJHQ	SJLGG011	chr10	83736302	16	47	0	32	G	T	ACTCTAGGATAGATTGCTGA[G/T]ATATTTTTCATCAATGGAAA
SJHQ	SJLGG011	chr11	25721067	18	44	0	45	G	A	CTGAGTACAGCACACAGCAG[G/A]GGGACCTGGGCCTGTCTGGA
SJHQ	SJLGG011	chr11	92024566	11	54	0	29	T	A	GAGAAGACAGGGTAAGAATG[T/A]TATAGATCACATTTTTAATG
SJHQ	SJLGG011	chr11	96956270	5	40	0	46	C	T	TTTTAGTCCTGGCTTGAAAA[C/T]TCTTCGAAATTTGAACATTT
SJHQ	SJLGG011	chr11	96958741	6	41	0	47	A	T	TTGTCTTTAAGGGGAACAAA[A/T]CTAAAAAGAGTGCTGCTAGA
SJHQ	SJLGG011	chr12	20184629	7	50	0	36	C	A	CATGTATACAATACCTGATA[C/A]TTTACTGTTACAGATCATGT
SJHQ	SJLGG011	chr13	102870134	6	37	0	30	C	A	TGTGAGGTCCACCGGTGAAG[C/A]GCTACAGCTGAGATGGCCCC
SJHQ	SJLGG011	chr13	47614675	8	43	0	28	C	T	ATTCCTCTAGCACATACTGA[C/T]GAAAGGGGAAAAAAATAACT
SJHQ	SJLGG011	chr13	69493800	6	38	0	28	A	C	ATAAAAAGGACATAACCTTA[A/C]AATTATAAACCTAGTGACAG
SJHQ	SJLGG011	chr13	76492321	6	35	0	40	A	G	GTACTTAATGCCCTAAAGAA[A/G]GAGTGAGGAACATCAATTTC
SJHQ	SJLGG011	chr13	89275440	5	20	0	36	G	A	CAGAAACTGGAAAAGTATAA[G/A]GGAAAGGAGCCATAATCCTT
SJHQ	SJLGG011	chr13	90799751	18	51	0	31	A	T	TGAAGAAAAATAAACAAATG[A/T]AGGCAAATTTTTAAGCACTT
SJHQ	SJLGG011	chr14	43054225	8	42	0	45	T	C	AAGTAAAAGTGATAACCTCA[T/C]TGGTTCCTTTGAAAAAAATA
SJHQ	SJLGG011	chr15	30328513	9	45	0	29	A	G	CAAAATGTGTATAGAAAATC[A/G]GCAGTCACTCACTAATGAAA
SJHQ	SJLGG011	chr15	39040298	4	38	0	51	A	G	CAGAAACTCCCTTTGCAGAA[A/G]ATCTTTAAGCCAAGGAATTA
SJHQ	SJLGG011	chr15	57282626	9	55	0	42	A	G	TATAGACTTGTAGTTATAGG[A/G]TAAATGTATGCCAAAGCTTT
SJHQ	SJLGG011	chr1	63572646	8	43	0	32	T	C	ATAGGAATATAATGATCTCA[T/C]AGTGTAGATGATTTAACATA
SJHQ	SJLGG011	chr16	5842134	10	44	0	29	C	T	GTGGATAAGTGATTTTAAAG[C/T]CCGGGACCCCAGTCTAAGGG
SJHQ	SJLGG011	chr16	6376062	10	48	0	29	C	T	CATATGCATTGGCAGAAAAT[C/T]GGTTAACTCTTATTGAACCT
SJHQ	SJLGG011	chr16	80392734	7	50	0	38	C	G	ACGCTCAGCAGTGCAAGGCA[C/G]CACCAGGTGATTCTGATGTG
SJHQ	SJLGG011	chr16	85814946	13	42	0	35	G	A	TTCAACACTGTTTACAAAAG[G/A]CACAGTCAACACCACTGAGA
SJHQ	SJLGG011	chr1	72638236	9	49	0	38	A	C	AAAAATCCATTTTTCATCAT[A/C]AAAAATGGATTTCAAAAAAA
SJHQ	SJLGG011	chr1	72641055	7	41	0	26	C	T	GTCATATCTAGAAGTTATCA[C/T]TGGTCTCCAGATTCCAATTA
SJHQ	SJLGG011	chr17	33062928	7	48	0	34	G	A	TTGGGTCTGGAGTATGTGAG[G/A]AAGAGTAGACCAGACCTTGG
SJHQ	SJLGG011	chr18	55609287	7	42	0	38	G	C	ACAAAAGGCGTGTACCCAGT[G/C]CAAGATTTTTCAAAGAGCAC
SJHQ	SJLGG011	chr18	6606733	4	29	0	32	A	C	TAACAGATATACTGAGCACA[A/C]TTATCAATGATTTCTGGAGT
SJHQ	SJLGG011	chr20	22215651	7	51	0	32	G	A	AAGACACATTTTCTGGAGCA[G/A]CTGCTATTGCTCAATATTGA
SJHQ	SJLGG011	chr20	61719369	6	40	0	30	G	A	CCTGGGCAGCGTCCTCTTCC[G/A]TTTCTTACGAGGTGGCTCCA
SJHQ	SJLGG011	chr2	117561378	4	32	0	38	T	A	GATGAGCCTACAGGATACAG[T/A]GGAGCTCTGGTGCCAAATGG
SJHQ	SJLGG011	chr21	25916590	11	51	0	25	C	T	TCAACTCTATGCATTTAACA[C/T]ATTCCAGAGCTCCCATTATA
SJHQ	SJLGG011	chr2	208521298	7	39	0	36	A	C	GTGGGATCTGACTGCTTTGC[A/C]TTGTGCTATATACATCAATC
SJHQ	SJLGG011	chr22	22758577	8	30	0	31	G	A	GAGCACAGAAGGCAGGACTC[G/A]GGACAATCTTCATCATGACC

SJHQ	SJLGG011	chr2	236866491	6	37	0	47	C	T	CTTGAGTTCACAGGGGGCTT[C/T]AGCCCTCAACTGATTTCCTC
SJHQ	SJLGG011	chr2	40621337	8	39	0	22	C	A	AGTGAGCTTAAGTTGAGAAA[C/A]CCTGCACTAACATTAAGAAC
SJHQ	SJLGG011	chr2	40972634	8	41	0	25	G	A	CCTCCAGTTTTTCGAGGACC[G/A]TAGGCTACATCTTCAGCTCC
SJHQ	SJLGG011	chr2	77241155	7	54	0	36	T	C	CATATGGGAACTAAAGTGAA[T/C]AAATTCTTCACTGTGTGTTT
SJHQ	SJLGG011	chr3	153128669	8	55	0	32	A	G	TTATTCTGTGAAGGCCAATG[A/G]AAGATAACCATGTTTGTGAG
SJHQ	SJLGG011	chr3	164272044	6	32	0	30	A	T	GAATTTTAATTACTACTATC[A/T]AGACATTTTTCACCTTTAAA
SJHQ	SJLGG011	chr3	95531613	5	37	0	43	T	C	GAGATAGTGACAGAGTGGCT[T/C]TGTATGCTTTGGCCTAGTCA
SJHQ	SJLGG011	chr3	96876236	7	57	0	39	T	G	TGTTTTCTTTTGGTATAATT[T/G]GCTAGAAGAGTCAATATATA
SJHQ	SJLGG011	chr4	109710803	8	57	0	34	G	A	TTCTCCCCAAATGCAAACAC[G/A]GAGCCAGTTTCCCTCAAGGC
SJHQ	SJLGG011	chr4	188461219	9	60	0	37	T	C	AATGTCGTTAGTCTAGAAAT[T/C]GAAGAAATGAAGAAAATCTG
SJHQ	SJLGG011	chr4	35404897	4	29	0	34	C	G	AGAATTTGGGAAAATATTGA[C/G]TATTACAAAATGTCATAATT
SJHQ	SJLGG011	chr4	47515333	14	50	0	40	A	G	TTCATGGACAATCTCCTGTG[A/G]GTTTAGGCACTGAAGGAAAT
SJHQ	SJLGG011	chr5	20302396	7	39	0	33	G	C	AGTTCTTCATCTTTTTAAAA[G/C]TTGAATAAACTTAACGTCAA
SJHQ	SJLGG011	chr5	23670872	17	43	0	34	C	T	TTACAATGATATAATAGCAG[C/T]TCAGTTAGCTAATCTTCACA
SJHQ	SJLGG011	chr5	26371638	8	53	0	30	A	T	TTTCTCATGAACTCCTCAAA[A/T]TATCTGTTTTTCTGACATCA
SJHQ	SJLGG011	chr5	51311475	7	38	0	33	G	T	CAAGACAATGTCACCAGTAT[G/T]CCCACTACAATTACCACATG
SJHQ	SJLGG011	chr5	58218810	7	44	0	33	C	A	TGTGGAAAATGCCTGTCGTT[C/A]ATGTTCCTGGCAGATCTGCA
SJHQ	SJLGG011	chr5	84632932	8	37	0	21	C	T	ACTCCTATTCTTTATAACCA[C/T]GCTTTACTTTCAATAGTACA
SJHQ	SJLGG011	chr6	103715025	8	46	0	38	C	A	GCAAATGTGGTTTCTCTCAA[C/A]CTCAGATATCTTCAACTTTT
SJHQ	SJLGG011	chr6	121258072	10	58	0	47	A	G	TTGATCTTTTCTATTCTTCC[A/G]TCATATTCTTATTTTCTGGT
SJHQ	SJLGG011	chr6	124037239	12	56	0	35	T	A	AAAAGAGCTGCTAATACAAA[T/A]TCATACTGCATTACAAGGAG
SJHQ	SJLGG011	chr6	124498711	5	34	0	39	T	G	TACAAAAAAATTAATCCCTA[T/G]TTAGAAATCTCTGCATAGCA
SJHQ	SJLGG011	chr6	28982652	17	40	0	32	C	T	CCTAGGGACTTGTTTTGTTA[C/T]GACCCTGTAGCGGTTGCCGC
SJHQ	SJLGG011	chr6	51409077	9	48	0	34	G	T	TGTAATTTATACATTCTATA[G/T]TTTAAGATACTTTACCTTCA
SJHQ	SJLGG011	chr6	63275606	7	27	0	27	G	A	GGAACATATCACAATTTTTC[G/A]TATGCATTTTCAAAAAATTC
SJHQ	SJLGG011	chr6	81765593	8	50	0	33	G	T	GTGGCTTCTCTTAAGAGGCA[G/T]TATGGTTTGGAATCTTAAGA
SJHQ	SJLGG011	chr6	87490214	7	37	0	33	A	T	CAAGTTTCTAGCTGATACTT[A/T]ACATGCAAAAATACCAGATG
SJHQ	SJLGG011	chr6	96625004	7	56	0	36	C	G	TACTCCTCACTTAGATCAAA[C/G]CCAGAGAACTTCCCTCAATC
SJHQ	SJLGG011	chr6	98144887	11	42	0	30	T	A	GCTAGAAAACTAGAAGCCCC[T/A]GAATGATGAAGTGGAATGTC
SJHQ	SJLGG011	chr7	81069796	7	42	0	26	C	A	GTATCTGTCTAAGATATATT[C/A]ATATAAATTAGGATACAGCA
SJHQ	SJLGG011	chr8	123551807	9	28	0	25	G	A	AGGCAATCCTAAGCAGCTGC[G/A]TCACCCTCCAGCCACTTTAC
SJHQ	SJLGG011	chr8	1364958	5	22	0	28	C	T	CCTGGGGGCGGAATGTGGCT[C/T]GCGAGCACCCGTGCCGGCCT
SJHQ	SJLGG011	chr8	92243092	8	40	0	34	C	T	CAAGCAAGGAGGAAAAAGAC[C/T]AAATTGAATTTATAAGACTA
SJHQ	SJLGG011	chr9	16354308	11	53	0	41	C	T	CCATAGTCAAATGGAACTAC[C/T]GACTGTCTCCAGGTATATGC
SJHQ	SJLGG011	chr9	4427158	9	37	0	29	G	A	TTTATGCATGGGTGAGAGGC[G/A]ATGGAACAGTAAGTTGGATG
SJHQ	SJLGG011	chr9	76503844	9	52	0	40	G	T	GGATTAAAATGAAAAGAAAA[G/T]TTTAAGTTAACAACTCTGGT
SJHQ	SJLGG011	chr9	84849138	10	50	0	37	C	T	CACTGAATTTCTAGGCACCT[C/T]GGTAGACTTGAACAATGAGG
SJHQ	SJLGG011	chrX	128457168	11	58	0	31	G	A	CTTCGTCCATGCAGTATGTC[G/A]CAAGCTTCCCCCAGCCCCAT
SJHQ	SJLGG011	chrX	51985180	4	35	0	41	T	C	AGTTTTTTAAAGCACAGACA[T/C]GTTCTTAATTATTCTTGAAG
SJHQ	SJLGG011	chrX	79501704	7	35	0	29	T	A	CCTGGAAGGCAATACAAACT[T/A]CTTCCTCACAAGCAAGGCTA
SJHQ	SJLGG012	chr10	10089272	15	55	0	31	C	T	TAGTCATGTCCTCCACCTTT[C/T]GTTGTTAGTGGTACCTCTTC
SJHQ	SJLGG012	chr10	10192903	13	46	0	30	C	T	GGTCTTTCACCTGAGGTCTC[C/T]GAAGACCACTGAGGCAAATA
SJHQ	SJLGG012	chr10	109250424	8	26	0	32	A	G	GAATGAGCAGACCAAGATTT[A/G]TCTGCACTGATTGTAAGCAG
SJHQ	SJLGG012	chr10	117918401	13	39	0	22	A	T	TGAGGCCTCAACACAGTCTC[A/T]GCCCCTATGAGCCATGCACA
SJHQ	SJLGG012	chr10	120179064	5	26	0	27	A	G	TCTCAATATGGGCTTTTGAA[A/G]TGATTTTCATCCTATTCCTT
SJHQ	SJLGG012	chr10	35082852	13	55	0	37	A	G	GATACCTTCAATTAGAGGTA[A/G]AGTATCTCATTTTAAGAAAA
SJHQ	SJLGG012	chr10	45729230	12	40	0	29	G	A	TATATATTACAGCTTAACGC[G/A]GCACTGGATTAAATGGCAAT
SJHQ	SJLGG012	chr10	52982359	5	45	0	59	G	A	TTGTTTCATAAATAACTCTC[G/A]CCCAAAGTTTAAGTAATGGA
SJHQ	SJLGG012	chr10	66592045	6	33	0	33	G	A	AAGTTATTTGATAAAATATA[G/A]GAACATGTGAGCTAACTCAG
SJHQ	SJLGG012	chr1	113707119	11	45	0	31	T	G	TAAGTATGTCTGTTTTGAAG[T/G]GGGACAAGGAGCAGCCTCAG
SJHQ	SJLGG012	chr11	13814353	14	34	0	33	C	T	GCAGGGTCGTAAATAGGGAA[C/T]GAAGCCAAGGGTCAGGAGGA
SJHQ	SJLGG012	chr11	39347053	9	42	0	40	G	A	CTTTTCTTGCCATTTATTAC[G/A]TTTCAAGCAAATTAATGTTA
SJHQ	SJLGG012	chr11	50117415	9	37	0	29	T	A	TCATGTAAAGATAGATTAGA[T/A]TTGATAGCTTCAAATTCATT
SJHQ	SJLGG012	chr1	179317166	8	44	0	32	C	T	TTCATTCATTTGAAATGGAC[C/T]GTCTAGTTCTGTAGGAATGA
SJHQ	SJLGG012	chr11	7971380	9	40	0	36	G	T	GCTAAGTGTATTCCCATTTG[G/T]AGTTTAGAATCTGATGGTTC
SJHQ	SJLGG012	chr1	187676095	12	42	0	28	G	T	AAAGGTAATGATATCACCAA[G/T]GATTTGCCACTGCTTCAGTG
SJHQ	SJLGG012	chr1	197958748	24	73	0	28	C	T	ATCCTGAGCCTCTTGACCTG[C/T]AATATTAATTCCAACTGTCA
SJHQ	SJLGG012	chr12	119769515	16	47	0	18	G	A	GCCCCCCAAAGCACTAAATC[G/A]TTCTAGAAAATACTTCTGTT
SJHQ	SJLGG012	chr12	133126901	4	20	0	26	C	T	GGGAGAGCAGAGAGGCCTGG[C/T]GGGGCGGGGACGGAGAAGGC
SJHQ	SJLGG012	chr12	18844927	20	52	0	34	T	C	AAAGTGGCTAGGTCCTGAAG[T/C]AGACGTGGAGTGTAGCTTCC
SJHQ	SJLGG012	chr12	2236524	6	43	0	30	T	C	GCAGTGAACTGTGTTTTCTT[T/C]TATTATCAGGTTTGCCTAAG
SJHQ	SJLGG012	chr1	232436681	8	34	0	35	G	A	GAACCTTGTGTTGGAAAAAC[G/A]TCAAGGAGGAAAAAAAAGTG
SJHQ	SJLGG012	chr12	73822208	13	41	0	28	C	T	GCCAGCTAAATTATCTTTTA[C/T]ATCATAAATCTGTAATGATG
SJHQ	SJLGG012	chr1	29772118	12	44	0	29	G	T	GGAACCTGGGGAATCGGCAA[G/T]AAAAATTCCTGCCTGACTCT
SJHQ	SJLGG012	chr13	34728233	9	30	0	52	G	A	ATTGAAAAACTCCCCCCACC[G/A]GCCAATTCTGAAACAAGTGC
SJHQ	SJLGG012	chr13	38157406	13	47	0	16	C	T	TATTTATTTATAATTTGACA[C/T]CCTTACTGTCCAAATTTTGA
SJHQ	SJLGG012	chr14	20318056	10	59	0	44	G	A	GTCTACTTAAAATGACTGAC[G/A]TATATAAAAAGAGTTCTGGA
SJHQ	SJLGG012	chr14	65183436	6	30	0	34	C	T	CGGACCCCGACCCTGGCACC[C/T]ACCACTTCATAGTTCAGAGC
SJHQ	SJLGG012	chr15	41252224	16	42	0	26	G	A	AGTGGCTGACGCTCTGGGGC[G/A]CTGGGGAGGAGGCAGGAAGC
SJHQ	SJLGG012	chr15	86415981	9	41	0	27	G	A	AATATAAGACTGGTCAGCCC[G/A]CCAAACTAGAGGGATAGAGT
SJHQ	SJLGG012	chr15	96573886	16	52	0	39	C	T	TAATGGAAAATACAGTAAAA[C/T]GGAGACAAAGATACTATTTT
SJHQ	SJLGG012	chr17	72270722	5	24	0	27	C	G	GACCCTGCAGCCTCTGTACA[C/G]CCTGCCTCATACCCTCCTAC
SJHQ	SJLGG012	chr17	8552772	17	56	0	25	G	A	ACAGTTTTGGTACTTGCCTC[G/A]TCTGTCTCCCTAGACCTGGC
SJHQ	SJLGG012	chr18	44204280	9	30	0	18	A	C	ACGGCAAGGGAGAGAGATTC[A/C]GCGGGGGCTGCCCTGGGGGT

SJHQ	SJLGG012	chr18	60233771	9	43	0	31	T	G	TTTCCATACTGCTGCCGTGT[T/G]TGTTTTCTAAAATACCATTT
SJHQ	SJLGG012	chr18	69744245	14	46	0	32	C	T	CACCATAATTTCTACCACTA[C/T]GTTTACTTCTATCTGCTATG
SJHQ	SJLGG012	chr20	12514662	11	44	0	27	G	T	GTACATACAATTCAAGCCTT[G/T]TCCTCACCAGTAATGAGGCC
SJHQ	SJLGG012	chr20	24303447	13	53	0	38	G	A	AGAACAAAGATCTGTGAAGC[G/A]GGTCCAGATGTGAGGTGTGG
SJHQ	SJLGG012	chr20	5356933	14	41	0	36	G	A	GGTAAGTCAGTGAAAGTATC[G/A]TGCATAAGGATTTGTAAGGA
SJHQ	SJLGG012	chr20	6459134	9	27	0	32	C	A	GGCTGGCATGAGAGAAAAAG[C/A]AAAAGAGAAAGAGAGACAGG
SJHQ	SJLGG012	chr2	103015384	7	35	0	33	T	C	CACCTCTCTCTTTTTAAATG[T/C]CAAATTGCCTTGCACCTACC
SJHQ	SJLGG012	chr21	24026591	8	37	0	22	C	G	TGTAGCAGTTTGCCATAGAT[C/G]AAGCATAAAGGCTGGAAGGG
SJHQ	SJLGG012	chr21	24914692	14	48	0	31	C	A	TGTGAAATTTGTAACAAAGA[C/A]CACACAGTAAACTTTATCCA
SJHQ	SJLGG012	chr2	15424862	10	46	0	41	C	G	GATTTCTAATACTATGTTAC[C/G]AAGTTAGATTAAATAGTAAA
SJHQ	SJLGG012	chr2	169613210	14	47	0	34	C	T	CCTCCATCATAATGTGGGGA[C/T]GGATCGGCTCTGAGCATAAG
SJHQ	SJLGG012	chr2	217655273	6	32	0	27	G	A	CCTCCTGCCCCCCGCCTCCC[G/A]CCTCCCACCTCCCGAGGTCT
SJHQ	SJLGG012	chr22	35715116	6	29	0	40	G	A	GGAAGGAGTGGTGGGCAGAG[G/A]TCAGAAGAAAGAAAGCAGGA
SJHQ	SJLGG012	chr2	51984614	15	33	0	35	T	C	TTGGAGTTTTAGGAACATTC[T/C]GGTTTAAGGCTACTGTATGA
SJHQ	SJLGG012	chr2	80190963	9	39	0	27	G	T	GCACAGCCAAACCCCTGCCA[G/T]GTAGACCTTTGGAAATTTGA
SJHQ	SJLGG012	chr3	13251096	10	31	0	19	G	C	CTCCCATGTGCCTGGGGCTA[G/C]GCTCTCCCTGCAGCACACCC
SJHQ	SJLGG012	chr3	157223187	7	42	0	29	C	T	GGCAGAATGGCAACAGCAAC[C/T]AGATATTACACCTGTTTGTC
SJHQ	SJLGG012	chr3	175281466	10	58	0	29	C	T	GAGACAAAAGAAATTCTCTG[C/T]CTTCAAAAACATGTAGGAGA
SJHQ	SJLGG012	chr3	184222075	13	50	0	37	G	A	ATGTGGCAATTTCTGTCTAC[G/A]CTTTTTTGTATTTTTCAAAT
SJHQ	SJLGG012	chr3	27357650	7	26	0	37	C	T	ACCGTGATACCCAATGAAAA[C/T]GTGTGAGCAAGGGACTGGCC
SJHQ	SJLGG012	chr3	38813116	9	46	0	28	A	T	AATAGATGGAGTGGGGAGGG[A/T]TGTGTGTGGCTGGGACAGCC
SJHQ	SJLGG012	chr3	77041768	12	48	0	31	C	T	TATATGAAATGTTGGCATAA[C/T]GTCAATTTTTTCCTAAAAAT
SJHQ	SJLGG012	chr3	95451447	13	40	0	32	G	T	AAAAAATATAATAAATCAAA[G/T]AAATAAGAAAAAGTAAAAAT
SJHQ	SJLGG012	chr4	13462651	4	25	0	29	A	G	CATTCAAGATAAATCCAGCA[A/G]CTAAGATGCAATGCAAGCTA
SJHQ	SJLGG012	chr4	162503394	8	34	0	42	C	A	TTGTTTTTATTATGAATTGA[C/A]AAATTGTTAAGATAAATATT
SJHQ	SJLGG012	chr4	190075813	13	50	0	24	C	T	TATTCTACACCCTGGGAGTC[C/T]GTGGAGGCCCCTGGAGAAAG
SJHQ	SJLGG012	chr5	101069290	11	39	0	29	C	A	GCAAAATAATGTTGGTAAAA[C/A]CTTATTCCCATCCTTCCAAG
SJHQ	SJLGG012	chr5	102667515	14	54	0	28	T	C	AGTTAACCACCGCCCCTAAT[T/C]CCCAATTCCTTGCTTCAATC
SJHQ	SJLGG012	chr5	162540619	18	43	0	31	C	T	ATCACTCCTGTTTTGAAGAC[C/T]TGTGCTAAAGAATTAAGTGA
SJHQ	SJLGG012	chr5	169476922	15	55	0	27	C	T	ACATGGCCCATTACAGGCAA[C/T]GGGGAAATGTTGTGGCCATG
SJHQ	SJLGG012	chr5	27988228	19	47	0	27	T	A	CATTTCTCTCCTGTTCATTG[T/A]TTTTATTACAACAAACCTAA
SJHQ	SJLGG012	chr5	50487457	15	58	0	43	G	T	TTAGCAGTCACTTAGCCCTT[G/T]TGCTATATTTCATTGTATTA
SJHQ	SJLGG012	chr6	123316272	12	36	0	31	A	G	TCCTACATTAATTTGCATTA[A/G]TTTAATTAATAAATGCTCTA
SJHQ	SJLGG012	chr6	132332819	18	44	0	26	T	C	ATTTTTGGAAACTGTAGGTT[T/C]GTACATTTGGTAAGGGCATG
SJHQ	SJLGG012	chr6	132968287	11	32	0	35	T	C	GCACACAACCTTTTTAGTTT[T/C]TAAGTTCTGAAATCCAATAA
SJHQ	SJLGG012	chr6	142954429	11	48	0	30	T	C	AAATTTGGACTATGTATCTA[T/C]TATTAACTAACATTTCTGGA
SJHQ	SJLGG012	chr6	169363684	11	47	0	27	T	C	GTCAACCAAACATAGAGGCA[T/C]GGAAGAGTTATAGAAGAAGT
SJHQ	SJLGG012	chr6	98725506	13	49	0	28	T	C	ACAACCCCAAGATGTGTAAA[T/C]ATTTATCATTCAGGCCATTT
SJHQ	SJLGG012	chr7	135521483	11	49	0	30	C	T	AGGAACATGTGTCGTGTAGG[C/T]GCAGGGCCATGACACAGAGA
SJHQ	SJLGG012	chr7	145349415	12	36	0	34	G	A	TCAGGGACACCGCCTGTCTC[G/A]TACTCTTTTTCCTGTCTAGA
SJHQ	SJLGG012	chr7	30643261	21	56	0	34	G	A	TTCAGTGTTTAATGACTGTT[G/A]CATTTCCCATTATGCTGACC
SJHQ	SJLGG012	chr7	50367611	7	30	0	30	C	T	AGCAATCCTGCCCAGGGACG[C/T]GTCTCTGTCACTGTCCTCTG
SJHQ	SJLGG012	chr7	68501822	11	47	0	29	C	G	CTTATTCCATAGACATAAAA[C/G]AACTTGTGTTTTGCTTGGTA
SJHQ	SJLGG012	chr7	8487325	14	52	0	34	T	A	GAAAAGTGAATGATTTGCCC[T/A]GAGGTGTTTAATCCTGCCTT
SJHQ	SJLGG012	chr7	93639634	6	42	0	33	G	A	TGTTAGCAAGGAGTTATGCG[G/A]AGATAAGAATTGTTACAAGG
SJHQ	SJLGG012	chr8	105038448	8	39	0	38	A	T	TAATGTGCTAATACATTTCT[A/T]CATATTTCAATGCATGTGTA
SJHQ	SJLGG012	chr8	11871649	10	37	0	40	C	G	ACCCCAGGAGGCCAGCCTGG[C/G]TACGCAGCCCCATCCCACAC
SJHQ	SJLGG012	chr8	32408060	8	40	0	27	C	T	ATGAATTAAGAAGGGGCCAG[C/T]GGTCTGAAGTAGCATCCTGT
SJHQ	SJLGG012	chr8	70492156	9	41	0	34	C	T	AAACCTAAGAAAAATAATGA[C/T]GGAAACTGAAATATGTACTA
SJHQ	SJLGG012	chr8	71962037	12	55	0	31	G	A	TTACATAAAGAGAGAAAAAT[G/A]GGAGGGCCTCCCAGGCAAGA
SJHQ	SJLGG012	chr9	24382489	16	46	0	28	A	T	GAGAACTAAAAGATTGAGTT[A/T]ATAGTCAGAGGAATAAATAA
SJHQ	SJLGG012	chr9	25908089	8	39	0	20	G	C	TCTAACACTATATATGTAGG[G/C]ATGTGTTTGTTGCAGTTAGG
SJHQ	SJLGG012	chr9	71089212	10	35	0	21	A	G	TATAGTTTTCCTAATTGACA[A/G]ATTTAGAATTTCCTTATCTG
SJHQ	SJLGG012	chr9	72915727	11	37	0	40	G	A	TAAGTTTTGGGCACATAAAA[G/A]GATGAAAGAGTAAAAAACTA
SJHQ	SJLGG012	chr9	73288458	7	44	0	32	C	T	ACACAGTAATGTCCTAGGCA[C/T]TTTTATGTCTAAAATAGATG
SJHQ	SJLGG012	chrX	124942276	14	29	0	16	T	A	TCCTCACTTTCTCTCTTTAG[T/A]TTTCAAAAGGCTTTAGGTGA
SJHQ	SJLGG012	chrX	142621258	9	15	0	12	G	A	CCCTCATGTGCTCACTGCTC[G/A]GACTCTGTCTCAGCACTGTG
SJHQ	SJLGG013	chr1	169262569	4	29	0	32	T	G	AAAAAAAAATTGTAGTCAGT[T/G]CAGTTTCAAATGTATTATTT
SJHQ	SJLGG013	chr14	39917320	13	66	0	34	C	T	AGGCTGCAGGTTTTCCATGA[C/T]GTTTCATAGTGGAATTTCAT
SJHQ	SJLGG013	chr15	71766207	11	40	0	31	C	T	CATAGTCAGTATCACCTGGG[C/T]ACATTCTTACTTACCAGCCC
SJHQ	SJLGG013	chr22	47166853	4	26	0	28	C	T	CCTTCCTGTGACGGGGGCCG[C/T]GGAAGAGCTGGTGGGTGAGA
SJHQ	SJLGG013	chr7	137548694	4	31	0	41	A	T	GGAAATGCTTACATGAGTCA[A/T]AATGTGAGTGAATGTCTCAA
SJHQ	SJLGG013	chr7	52959796	4	39	0	43	T	C	ACTGGTTATACACCTGTTCT[T/C]AGGGAGAGACACTGCTGAGA
SJHQ	SJLGG013	chr8	106590902	7	51	0	37	T	C	ACTTCACCTGGATATTAATA[T/C]TAATACTATCTTGGTAAGAG
SJHQ	SJLGG013	chr8	29996969	10	44	0	30	C	T	GTGTCAAGGATCTAGAAGAG[C/T]GCCCTAGGCATCCTCTCAAG
SJHQ	SJLGG013	chr8	76628513	11	48	0	32	A	T	ATTGGCCCCTGTGATCACAA[A/T]GCTGATTAGAATGTGTTAGA
SJHQ	SJLGG013	chr9	28463284	16	55	0	36	C	T	TTTAGTGTGAAGAAATTTAT[C/T]AAATCTCTTTTGTCTGATGC
SJHQ	SJLGG013	chrX	3529265	10	55	0	41	C	T	TGGAGGGCTCTCATTCACCA[C/T]GTCTTTCAGCAGGTTGGTTC
SJHQ	SJLGG015	chr1	106654928	7	67	0	41	C	T	TCTTTATTCTCCGAAGAAGA[C/T]GCAGTTCTAAAGTAATCATA
SJHQ	SJLGG015	chr13	55478649	18	71	0	47	T	C	TTTTCCCCATATTGATATGA[T/C]ATAGCAGAAAGTTGGATTTA
SJHQ	SJLGG015	chr13	86355735	12	63	0	49	G	A	CAAGATCTTTGAAACTGATG[G/A]TTTGAAATATATTAGGAAAA
SJHQ	SJLGG015	chr14	81256642	21	69	0	42	A	T	TATTAAAAAAGAATATGAAA[A/T]AAAATGGAAACATTCAGAAA
SJHQ	SJLGG015	chr17	54680891	14	66	0	43	C	T	GTTCTATCTGGGGCTCCAAG[C/T]ATACCAAGAGTTCAGAGTCC
SJHQ	SJLGG015	chr17	74749241	15	62	0	50	C	T	GCCAATCGAGAGTACAGTAC[C/T]TGTCAAAGTCTCTTGGTTCT

SJHQ	SJLGG015	chr18	34472293	12	55	0	34	G	A	AGTCTTTGAAATAGTTTTGG[G/A]AAAGTAAAAAACCTAAAGTT
SJHQ	SJLGG015	chr20	13703787	16	81	0	45	T	C	GACTTGTTCCCATAATAAAC[T/C]TCCTCCAGAGGGTTTAGTTG
SJHQ	SJLGG015	chr21	25671958	12	62	0	29	A	G	TAAACTGAGAACCTAGTAAG[A/G]TTATGGAAGAGCCTCCTGTT
SJHQ	SJLGG015	chr21	31214723	7	60	0	43	G	A	ATGGAGAAATAAAAGGAAGC[G/A]AAGAAAAGATCTCTGTACTA
SJHQ	SJLGG015	chr21	31938986	19	65	0	31	A	T	AATTGTTGAAAAGACCTGTG[A/T]TTAAGAACATTTCTGTTTTT
SJHQ	SJLGG015	chr2	154149105	10	49	0	30	G	A	AGGTTGCAGGAGCAGTTGGG[G/A]GTACAGTGGCAGCAGATCAG
SJHQ	SJLGG015	chr2	209930193	11	52	0	41	C	T	ATTGAGATCTTTTTTAAAAC[C/T]AAAATACCAGAATTCTTTGC
SJHQ	SJLGG015	chr2	84427901	7	41	0	29	G	A	GCTTCATTTGCTGTTTTGCA[G/A]ACTCTTGGCATCTGGTAATA
SJHQ	SJLGG015	chr5	106710905	8	48	0	41	C	T	GTGCAGCACTGCTCATTGTC[C/T]CATCTCTGGTCCAGTCAGCT
SJHQ	SJLGG015	chr6	101914008	11	66	0	41	C	T	TGTCATTGCCAGTGTTGTGG[C/T]AACGTCAAAGTGTTTCTTTC
SJHQ	SJLGG015	chr6	139681291	9	74	0	55	C	T	TTCTTTTTGGCTTTGTCATA[C/T]GGACCAGTGCATTTATTATG
SJHQ	SJLGG015	chr6	27404788	11	51	0	38	C	T	TAGAGACAGGACTATATAAA[C/T]ATTCTGTGTTAACCTTCAGG
SJHQ	SJLGG015	chr8	122809823	8	51	0	44	C	T	TTGTTAGATAAAAGATAATA[C/T]GGTCTCTTTTTTCACATTTT
SJHQ	SJLGG015	chr9	137541345	14	69	0	41	G	A	ATTTTCTGTTTCCTAGACCC[G/A]TGTTCTTGTAGGGAAATTAG
SJHQ	SJLGG015	chrX	24965000	13	59	0	37	C	G	TTTCCTATTATGTCCTTCAA[C/G]TGTGTCATAAAAAATTTTCT
SJHQ	SJLGG015	chrX	38222800	12	54	0	30	T	C	GACTGTTAGTCAGTGCTTAC[T/C]CCTTAACATTATCAGTACTT
SJHQ	SJLGG016	chr6	156679995	6	40	0	36	C	T	TTTCTGTATGATGTGTTACA[C/T]GAATGCCTAGGAGACTCAAT
SJHQ	SJLGG018	chr10	59804549	12	51	0	42	C	A	GCAGGAGAACCTAAAATAAG[C/A]AACAGGCATGGGTCCCACAG
SJHQ	SJLGG018	chr10	9780514	8	46	0	33	A	T	TATTTTTTTTTTAACTTTCA[A/T]CCTACAACACTCACAGCATG
SJHQ	SJLGG018	chr12	126827659	6	41	0	33	G	T	GAGGACTGGTGCTCAAAGCT[G/T]GGGGGGTCAGATAGGGAGGC
SJHQ	SJLGG018	chr1	29610658	13	37	0	26	C	T	CATGTGCCCTACCTCAAGGG[C/T]GCCTTCTCCCAGGGTGACAG
SJHQ	SJLGG018	chr14	60062155	20	50	0	45	C	T	TCTCCAACTGCTACTCCTTT[C/T]ATTCACTTCTACCTCTTCGT
SJHQ	SJLGG018	chr14	98672325	14	36	0	39	T	C	CAGTATGTCTTCAATTTCCA[T/C]GGTGGAAATAGAGCTGCCCA
SJHQ	SJLGG018	chr16	67640237	20	53	0	27	G	A	TGCTCACGTTTCAGGGTTCC[G/A]TTCAAATTCCACATTTATGA
SJHQ	SJLGG018	chr18	38483003	19	51	0	45	C	T	CAGATTGGGAAGTGACCTGG[C/T]GAGTCCTAGAGATGATTTGA
SJHQ	SJLGG018	chr18	69811619	6	58	0	41	G	C	TAATCCTAGTGGCTGATTTA[G/C]ATTCAGAATGGTTTAATTCA
SJHQ	SJLGG018	chr20	1531356	19	52	0	33	C	T	CTAATATAGAACATACTGGA[C/T]TGGGCCCAGACCAACCCCAC
SJHQ	SJLGG018	chr2	19673007	21	48	0	34	C	A	AAAAAACACAGCTGAGAGTT[C/A]AATATGAAGAAGGGGTCTGA
SJHQ	SJLGG018	chr2	51747098	16	48	0	31	A	T	TGTTAGCTAGGAGCCAGCTG[A/T]TTGAGACTGGGCTTGACCGT
SJHQ	SJLGG018	chr3	119557315	25	58	0	32	C	G	ATCCATACCCACTAATTTAG[C/G]ACAACAGTTTACAGTTTTGT
SJHQ	SJLGG018	chr6	141310663	19	44	0	33	T	A	TTTATTTTCATGAATCTTAT[T/A]AAATGTCCTCCGGCCCAGTT
SJHQ	SJLGG018	chr6	15367529	16	43	0	37	C	G	TCATCTTTGTTTCCTTCTCC[C/G]AAATCAAGATGGCCTGAATT
SJHQ	SJLGG018	chr6	99507186	4	38	0	45	G	A	AGGTATAAGCTGTGACCTCC[G/A]TCTTCACCTTGTTCTATTAT
SJHQ	SJLGG018	chr7	108872354	23	52	0	56	T	C	TGCTATATTCCATGCAATAT[T/C]TTGATTATTTCTATTTCATG
SJHQ	SJLGG018	chr7	53319771	14	56	0	34	G	A	GAAAGAAAATATATGAAACC[G/A]CAATAACATAGTCACTCCTC
SJHQ	SJLGG018	chr8	139508060	14	38	0	31	G	A	CACATCACTTAACATCAAGA[G/A]CATCATAACCTGATGGAAAA
SJHQ	SJLGG018	chr8	2209240	9	65	0	48	G	A	AGTCCAGGTGTGCTGTGATG[G/A]AGAGGCCTCCATGTGGCCTT
SJHQ	SJLGG018	chr8	23682062	20	48	0	33	C	T	TTCATTTCACTCCATGAATT[C/T]GGGAAATTTTAGAATAATGT
SJHQ	SJLGG018	chr8	7332273	21	29	0	17	G	C	TTACCGTGTGTGGCCAGGGT[G/C]CCAAGGACATCTAGGACTCC
SJHQ	SJLGG019	chr12	61839289	6	44	0	31	G	A	AATTAGCCACTTTAGATTTC[G/A]GGAGAGAAATACAACTCTAT
SJHQ	SJLGG019	chr15	58987316	6	44	0	35	T	C	CTATTTTCTCTTTTCCTTCA[T/C]TTCACGTCAGTCTTGGCACC
SJHQ	SJLGG019	chr4	80597658	8	61	0	37	A	C	TCTGAATTACATTTGGAAAC[A/C]GATCTACCACCATCCTAATG
SJHQ	SJLGG019	chr5	6973864	8	38	0	38	C	T	TCCCCGTCTATTTTTTGGCT[C/T]TGCCAGGCTGCTTGCTTCTT
SJHQ	SJLGG019	chr5	86403894	8	49	0	32	G	C	AGTCAGGAATCAAAAAAGCA[G/C]GAAATATATTTTTTCCCTTA
SJHQ	SJLGG019	chr6	166446625	5	33	0	38	C	T	GGAACACTCTCCCCGAACCA[C/T]GTACTGACCTATTGGCTCAG
SJHQ	SJLGG019	chr7	308033	5	41	0	43	G	C	AGCGTGCTGTGAGTCTTAAC[G/C]AGGATAGCAAGTGCCACTCC
SJHQ	SJLGG019	chr9	138300070	7	37	0	33	A	G	CCCCCACTCATTGCAAAAAA[A/G]CCCCACTGAAAGCAAAAGGA
SJHQ	SJLGG020	chr10	50685246	20	50	0	27	C	A	AATAAAAACAAAATGAAAAT[C/A]AAACCTGAACCTACCAGGAT
SJHQ	SJLGG020	chr11	122887754	6	32	0	31	C	T	AACAGAAGGCGAGTACGGAG[C/T]GAGTTCTAGCTGCATGTGAA
SJHQ	SJLGG020	chr11	61610580	21	42	0	43	T	C	ATTCTGAGGTTAAAACTCTT[T/C]CGTAGTTCAGCACTGTACTT
SJHQ	SJLGG020	chr1	176297585	10	32	0	19	C	T	TACCCATGATTTTGAGGTTC[C/T]GTTAGCCTCAAAGCATTGAT
SJHQ	SJLGG020	chr11	83558802	15	41	0	36	C	T	CGTTCCCATTTCTAAAACCA[C/T]AATTCCACTTGATGATTTAA
SJHQ	SJLGG020	chr12	104374495	11	33	0	23	C	T	AATAAAGAAAATCTCTTTCC[C/T]ATATATGAAATACTTTGTTC
SJHQ	SJLGG020	chr12	108228831	12	31	0	31	G	T	AGATCATAGGTTGGGTGAAA[G/T]TATATAATTAATAGCTCTGT
SJHQ	SJLGG020	chr12	14628961	17	48	0	39	C	T	CCATTTTTTTTGTCTTAATA[C/T]GGTACAGTATTCTACAAAGA
SJHQ	SJLGG020	chr1	223097389	20	46	0	34	A	G	TTCTGTTGTAAAAATTGTAG[A/G]TTTTAGAGGTAGAATTTTCA
SJHQ	SJLGG020	chr1	238094915	19	49	0	38	A	G	CTGATCTTATCTTGTCCTCT[A/G]GAAGTGGAAGAGTGGTTTAG
SJHQ	SJLGG020	chr12	52464860	16	44	0	27	A	G	CTCTGCCCTATAAGCAGAAT[A/G]TAGGAATTGTTTGCCTAGTG
SJHQ	SJLGG020	chr12	83568996	6	41	0	32	C	A	AAAAACAAAGTCGGGAAACA[C/A]AAAGTGACACCCTCAGTAGA
SJHQ	SJLGG020	chr12	83568997	6	43	0	32	A	G	AAAACAAAGTCGGGAAACAC[A/G]AAGTGACACCCTCAGTAGAG
SJHQ	SJLGG020	chr12	83568998	6	44	0	32	A	C	AAACAAAGTCGGGAAACACA[A/C]AGTGACACCCTCAGTAGAGG
SJHQ	SJLGG020	chr13	100125989	18	47	0	28	C	T	ATAAAACAATTTAAAAATTT[C/T]GCCCAGTGTAACTTTGTTTA
SJHQ	SJLGG020	chr13	39962050	13	34	0	42	G	C	CACTGCTGCCTGTGACTAAC[G/C]ACAAGGGATGGGCTCTTGGA
SJHQ	SJLGG020	chr1	66984221	11	36	0	34	T	A	AAATTCCATTTATTTGAAGA[T/A]GCAATTCACTAACAATTTTG
SJHQ	SJLGG020	chr16	83376554	19	36	0	33	C	A	TACATAAAATTGCCTCAGAG[C/A]TTTATTTTGATTGATTTCCT
SJHQ	SJLGG020	chr17	12798583	14	55	0	29	G	A	GAAGTTTTTTTGTCTTTTAC[G/A]ACAGTACTTTGCATGATGAA
SJHQ	SJLGG020	chr17	31786730	15	40	0	33	G	A	GCAGGGGAGAATGTTGGCAG[G/A]GCTGGCCGTGCCTGTGGGGA
SJHQ	SJLGG020	chr18	31559903	4	36	0	41	A	G	AGCAATTTTAATGAATTACA[A/G]GTATTTAAATGCCACAAAAT
SJHQ	SJLGG020	chr20	26148520	17	155	0	116	G	T	CACATGAGGAGGGCCGGCTG[G/T]GTCTTTCTCCATTCTTTGGG
SJHQ	SJLGG020	chr20	36034539	9	26	0	26	G	A	CTGGGTGGCATCTGGAGATC[G/A]CAGGGGGCGGGTGTGTGTGT
SJHQ	SJLGG020	chr2	172542066	11	36	0	42	A	G	GCACCCTCTTAAAATCTACC[A/G]GTGGATTCACATCATCTGTA
SJHQ	SJLGG020	chr2	216002259	9	53	0	46	A	G	AAGACGTTGCAATGAGCAAG[A/G]GAAGATAGATTGTAGTAGTA
SJHQ	SJLGG020	chr3	172824982	16	46	0	21	G	A	CCCAATGTCACTCTTACAGT[G/A]ACATTGTAGTGACTTAATAA
SJHQ	SJLGG020	chr3	2897554	10	50	0	34	G	A	AGTCAGAAATAAATGGAAAG[G/A]GAAGGATTTTTAACGAAAGG

SJHQ	SJLGG020	chr4	117995244	11	34	0	29	A	G	TAGAAATGAAAATATTCTGC[A/G]AATGAAAAACATGCATTTCG
SJHQ	SJLGG020	chr5	102715332	11	40	0	23	A	G	TTATTCCACATCATAAGCCC[A/G]TCAAGTGGGTTATTAACTCA
SJHQ	SJLGG020	chr5	25320099	4	40	0	43	C	T	AGAGTCTGGGTAAATTTAAC[C/T]AGTAAGTAAAAACTTAAAGT
SJHQ	SJLGG020	chr5	51117843	17	46	0	14	T	G	GAATATGACCCTCTCATTTT[T/G]ATATGCCTCTTATGGTAGCC
SJHQ	SJLGG020	chr6	143460327	13	49	0	28	A	G	AAGTGGTGGCCTTTTTGTTT[A/G]GTTATTTGTTTTAGTACATC
SJHQ	SJLGG020	chr6	54713637	8	50	0	48	G	T	CTGGTTGGAGGAGACCTTTT[G/T]AAAAGAGGCCACTTAGCTTA
SJHQ	SJLGG020	chr7	138537907	18	65	0	40	G	A	TGGGCAGAGTCTGTCCAGCG[G/A]CAGTCAGTTGGAACCAATGG
SJHQ	SJLGG020	chr7	144250413	8	49	0	45	G	A	TATTTATCCCAGAAGTAAGC[G/A]TTACTGACAGCAGAAACAGG
SJHQ	SJLGG020	chr8	33816685	19	49	0	32	A	G	AATGTAAATAACCTTAAGAT[A/G]TGAGCTCTACATTAACACTT
SJHQ	SJLGG020	chr9	30235598	11	29	0	30	T	C	CAAACAATTATCTAAAATTC[T/C]ATTATTTAATTTTTGAGTTT
SJHQ	SJLGG021	chr12	17021392	10	43	0	43	C	T	ACATGGAACAATGGGGTCTT[C/T]GAGTCTACCGGGAAGGGCCC
SJHQ	SJLGG021	chr18	68668277	13	50	0	43	A	C	TTAAATCTAATTAGAATCAT[A/C]AAGTTTCAGTTCCTATAAAT
SJHQ	SJLGG021	chr20	991774	16	49	0	42	C	T	AATTGCCCATCTTCCCCAGG[C/T]TTTGGTCCATCTACCTGAAA
SJHQ	SJLGG021	chr21	25315813	10	27	0	36	G	A	TTGCCTTTTATTTGTATGTC[G/A]GTATGATTTCTCTATAGGTA
SJHQ	SJLGG021	chr21	25943517	6	29	0	44	A	T	GAATGTTTCCCAACTAAATC[A/T]TGTTTTTAAATTTTAAATAG
SJHQ	SJLGG021	chr2	194296326	3	10	0	28	A	G	TTAATCCAATTTTAATATAA[A/G]TACACATTGATACTTTAATA
SJHQ	SJLGG021	chr3	156740618	16	59	0	43	A	G	GAATAATTCTGTAATTCTGT[A/G]ATGTTGCTAATAAATCATCA
SJHQ	SJLGG021	chr3	95151164	14	58	0	40	G	A	TGACAAGAATTCAATCCTAA[G/A]CTGCTATGTTAAGAAGTCTG
SJHQ	SJLGG021	chr4	30758328	14	58	0	44	T	G	TTCATTACTCATTCTCTTCC[T/G]GTCTTTTGTTCAGTCTCTCT
SJHQ	SJLGG021	chr5	43348234	7	41	0	46	T	C	ATGTCTAACTATGTCTATGG[T/C]TGCACCTTTTGAAATTTCCG
SJHQ	SJLGG021	chr5	88720939	5	33	0	37	A	G	TCCTGTACTTTCAATAAGAG[A/G]GAAACACAGAACCAGGTAAA
SJHQ	SJLGG021	chr7	63377816	18	50	0	47	T	A	TAAAAGTTTGGGAGAACTTA[T/A]TATTATTGACTTGAGTTTTT
SJHQ	SJLGG021	chr9	76223447	8	43	0	33	G	T	GGCATGTAACTGAATTCATA[G/T]CTAATACATTTGATTTTACC
SJHQ	SJLGG022	chr18	73770707	9	43	0	26	C	T	GGACCTGCTGGCCTAGTAGC[C/T]GGGAGGAAACAGCGGCCGAG
SJHQ	SJLGG024	chr11	24752878	21	69	0	42	A	G	GTTCCCTACCAGTCACAACT[A/G]TTCTTTTGCAAACAATATTC
SJHQ	SJLGG024	chr11	57653135	17	42	0	28	C	T	CCCTCTCACTCAAATCTCCA[C/T]GTCCCACCCCATCTTCCCTT
SJHQ	SJLGG024	chr12	84022210	14	59	0	56	A	G	CCTATTTTTTGAGTATGGCC[A/G]TCTGTTGAACATTATCTAAT
SJHQ	SJLGG024	chr13	103480217	8	47	0	35	G	A	GTAAAGCAGACGTCTCTTCC[G/A]TTCTCTCCCATTGTGGAAGA
SJHQ	SJLGG024	chr13	27516447	14	51	0	32	C	T	GCCACACTAGTATTGCCAGG[C/T]GCAGCAAATCAGTGTCAGGC
SJHQ	SJLGG024	chr13	39054358	12	58	0	46	A	G	TATTTTCTTAAAACTCATTT[A/G]AACTTTCAATGGGATTGGAC
SJHQ	SJLGG024	chr14	22753364	9	37	0	29	C	A	GATATTGTATTTTTGAAATA[C/A]ACCTCATTTTACCCAATAAC
SJHQ	SJLGG024	chr14	37613501	17	71	0	39	A	G	TATTACTTATCTCAATTAAT[A/G]ATGATTGATCAAATTTGTTT
SJHQ	SJLGG024	chr14	85799847	14	49	0	38	C	A	GTCACCCAAATTGGAGCCAG[C/A]TGGAGGAGTGGTTTCTTGTA
SJHQ	SJLGG024	chr18	34274370	6	51	0	36	C	G	CTCATTCTGCTGGAGCGGGC[C/G]GGCTCCTCCACAGCTTCCCG
SJHQ	SJLGG024	chr1	84212584	15	54	0	31	A	G	CTTCCACATAACTTCTGAAA[A/G]TCCAAATATGCCATGATTTC
SJHQ	SJLGG024	chr1	96141586	24	68	0	37	G	A	TAATGCAGGATAATTTCATA[G/A]GTTAATGCTTATTATTTACA
SJHQ	SJLGG024	chr2	113561019	11	48	0	24	G	A	ATGGAACTGTAACTCTATTC[G/A]GTAGGGGAACAGAATTCACA
SJHQ	SJLGG024	chr2	143852700	21	49	0	38	G	A	AGTGGCATAGTTTTTTGGGG[G/A]GATGAAGTAGGAGTAATACT
SJHQ	SJLGG024	chr2	21351012	19	48	0	40	G	A	TATGAACTTTCATTCTCCAC[G/A]TATTTGTTTGTTCTGGATAT
SJHQ	SJLGG024	chr3	168316789	6	40	0	37	G	T	TTCTCTCTCTCTCTCGGCTT[G/T]TGTCCTTCGGAATATTTCCT
SJHQ	SJLGG024	chr3	35155443	18	64	0	40	G	C	CTGACAATCTTATAGAGTCT[G/C]TATAATGCTGAACTTTGTCA
SJHQ	SJLGG024	chr4	102669563	15	56	0	44	T	C	AAGGAAGCTTCTTTCATTTC[T/C]AACAGCAAAGTGTGCTGTGA
SJHQ	SJLGG024	chr4	136978499	22	57	0	35	C	T	TACATATATCTTAAGCCATA[C/T]GTTTTGTAATTCATTAATTT
SJHQ	SJLGG024	chr4	143925506	10	65	0	40	G	A	TGATCAAAGATGTAACCTTC[G/A]AGAGTTCTTCCACTTATCTC
SJHQ	SJLGG024	chr4	41739186	13	53	0	36	A	T	TTAACAGCACCCGGGCTTCC[A/T]GTGACAAGGTAGGAAAACTT
SJHQ	SJLGG024	chr7	21606930	12	65	0	46	C	A	AATTGTATTTCCTCTTGTCA[C/A]CTACATGTTCTTTGCGTTCA
SJHQ	SJLGG024	chr8	42585174	9	47	0	47	T	A	TTGGGAGCTCCAAAAATAAA[T/A]TCAGATTAAAACTTAAAAGA
SJHQ	SJLGG024	chr9	1168921	11	52	0	50	C	T	TCTGAAGGCAACACAATTGA[C/T]GAAAATTGTTTTCAAAAAAA
SJHQ	SJLGG024	chrX	63809466	15	43	0	40	C	A	GCTCCTTGAATTCATCCCTT[C/A]AACACTTTGAACTCATATAG
SJHQ	SJLGG024	chrX	82243983	10	51	0	50	G	A	CTATTCAGGCAGTTATCTAT[G/A]GCCATCTTTCATCAGTTTTT
SJHQ	SJLGG024	chrX	82243984	10	51	0	47	G	T	TATTCAGGCAGTTATCTATG[G/T]CCATCTTTCATCAGTTTTTC
SJHQ	SJLGG025	chr10	36098730	10	66	0	49	C	T	GTGACTCAGCTGTGTGCCAA[C/T]GTAACTATTTTTCATTTGTC
SJHQ	SJLGG025	chr10	55752449	16	64	0	34	C	T	TGTCAAATTTGGGAATGAAA[C/T]GTCTCTGGTGAAAAGAAATA
SJHQ	SJLGG025	chr12	95073731	6	58	0	43	C	T	ACTTGTTGCAGTCAATGTTT[C/T]TTCAGACTCGGTTTTCAGTC
SJHQ	SJLGG025	chr13	71238075	8	18	0	23	A	T	CTGGTATTCTGCAGAATGAC[A/T]TTTTTTTTTTTTTTCTGACTG
SJHQ	SJLGG025	chr13	72488366	13	54	0	31	T	A	GGAAAGGCAATGTCCCCTAA[T/A]TTCTTTATGTCAGTAATATT
SJHQ	SJLGG025	chr13	82247076	8	63	0	37	T	G	GGGATTACATTTGTGTGTGT[T/G]TTTTTCCCCCCCAAGCACTG
SJHQ	SJLGG025	chr17	72047747	13	39	0	33	C	T	GGGGAAGCCCTAGGGCCCCG[C/T]GAGAGCAAAGGGCCTGTGGG
SJHQ	SJLGG025	chr18	45216008	10	45	0	38	G	A	AACTCCCAGGAAAATCAGAG[G/A]GCTGTGCCTAGGCTCCAGGG
SJHQ	SJLGG025	chr2	126523313	12	74	0	48	G	T	CTTTTTAAATTCTGTTATTT[G/T]TACATAACGCACTCTTACAG
SJHQ	SJLGG025	chr2	201060386	7	58	0	33	G	A	CGAGGTAAACTGGAAACTAC[G/A]TGTCTTTTACTCAACTCCAA
SJHQ	SJLGG025	chr3	11202242	7	68	0	40	G	T	CTTCTCACATACTTAACCAA[G/T]GTCCTCATCCTGTTCCCCTT
SJHQ	SJLGG025	chr4	84887809	13	63	0	41	C	A	AAGATTTGACAGGTAAATGT[C/A]AGCTAAATGGTTTATTGGCT
SJHQ	SJLGG025	chr5	105823804	14	78	0	33	A	G	TTTTTCTACTAGGTTAAACA[A/G]TAAAACCTGAAATAAATTAG
SJHQ	SJLGG025	chr6	110833165	11	53	0	32	C	T	ACAATGAAAAATCACCTTTC[C/T]AATTCTATTCTCCTACATCT
SJHQ	SJLGG025	chr7	138586845	12	83	0	43	G	T	TCTAATTTTTATTCTTTGTT[G/T]ATACTTATTCGTTTAATGAT
SJHQ	SJLGG025	chr7	140431408	17	77	0	41	A	G	TAGCCAATGTTTTAGAGAGG[A/G]CAATTTTAACTATTGGTTTA
SJHQ	SJLGG025	chr8	146072650	15	60	0	38	C	T	GTTCACACTGCACTGCAATT[C/T]GGGCTTCGGTAAGCTCATCT
SJHQ	SJLGG025	chr9	121402792	12	51	0	25	C	T	ACCCACAATTTTAAGGGTCT[C/T]CCTGAGGGCCCGAGTTGGTG
SJHQ	SJLGG025	chrX	123988576	17	76	0	57	C	A	TGGGAAAGAAATTTCAAAAT[C/A]TTAAGACATAACTTCAAGTA
SJHQ	SJLGG025	chrX	135710743	9	36	0	34	G	A	ATGTGCATTGGGTACAAGAT[G/A]GCGCCTCCTCTTCCTGGGAA
SJHQ	SJLGG025	chrX	137935610	7	41	0	30	C	A	TTACAAATATACCCCCTTAC[C/A]ATTTAGCATGTAATTTTGCT
SJHQ	SJLGG025	chrX	56580176	7	61	0	37	G	A	TTCCCATTGCCTCTTTTCTC[G/A]GAATCCTAAAGCTATCCTAA
SJHQ	SJLGG026	chr17	58335561	9	59	0	38	A	T	ACATGAAATGATGCAAATGA[A/T]AAACATGAAATGATGCAAAT

SJHQ	SJLGG026	chr21	25983643	8	63	0	45 T	A	TGTCTCTAAGAAAGCCATAC[T/A]TTTTTGTTAATATATCTATA
SJHQ	SJLGG026	chr22	32960947	6	30	0	22 C	T	CAAACAGTGCTCCTGGACTG[C/T]ACCCAAACAGTGCTCCTGGA
SJHQ	SJLGG026	chr4	141519691	7	43	0	31 C	T	TTGGGGTGTCTTGGTACCTC[C/T]GCCATGAGCAAGGCGCAGGG
SJHQ	SJLGG026	chr7	97576962	6	60	0	46 G	A	GGATGAAGAAAGACATCTGC[G/A]TCAGACAGCCCGCATGAGAG
SJHQ	SJLGG026	chr8	142345872	8	35	0	24 C	T	GTGTTGAGGCCAGGGCTCAA[C/T]GTGTATCAGGAGTGACCAGG
SJHQ	SJLGG027	chr10	51741656	12	21	0	27 G	A	AGTTCAGACTCAAACCTTGT[G/A]AAAAACAGGTTCTAGAAAGG
SJHQ	SJLGG027	chr10	71429045	6	30	0	33 C	G	CAGCTGCATATTCCGAGTCT[C/G]CCCCAGCCTGCCTGGTTTGC
SJHQ	SJLGG027	chr10	86711648	6	48	0	48 G	A	TTTTCCCCATGCTCTCATCT[G/A]TCTTCAAGGCTGTTTATCAT
SJHQ	SJLGG027	chr11	131567082	18	63	0	38 C	T	GGATGTGAATATAATAAGCA[C/T]AGAGATTACAGTCATTACAA
SJHQ	SJLGG027	chr11	34387583	16	53	0	32 A	C	ATTATCTGCTTAAAAAAAAA[A/C]CAAAATCAACAATTGTGCTC
SJHQ	SJLGG027	chr13	113677476	14	46	0	41 T	G	GACGCCCCTCGGCTCAGCCC[T/G]CTAAGAGACTCGGCAGCCAG
SJHQ	SJLGG027	chr13	88405034	15	73	0	37 A	C	TTCACTGTGGTCACTCAATC[A/C]TTCTGTGTGAGTTATTGTGT
SJHQ	SJLGG027	chr1	51935497	9	39	0	41 G	A	GATTAGCTAGAAAAACTACC[G/A]CCTATGTCACAGATAATCTC
SJHQ	SJLGG027	chr16	28053346	16	52	0	34 G	A	GGAATTGTGGTTTTACATTC[G/A]CCATTTCTGTTATGAAAGGA
SJHQ	SJLGG027	chr19	13383614	11	36	0	32 G	A	AGAGAGGGGTGGAGAAACCC[G/A]TAGGTTATTTCCATAGGAGA
SJHQ	SJLGG027	chr1	96907286	6	42	0	46 T	C	CATATTGTTCACTTCCGAAT[T/C]TTATCACTTGCCTAATTTTT
SJHQ	SJLGG027	chr2	118609367	17	63	0	24 G	T	CTAAGGCAAGGCCTTAGAAG[G/T]ATCCTTTGTTTCTGATGGGA
SJHQ	SJLGG027	chr21	26075588	12	50	0	34 T	C	TAAAGGACAAGTGTAAGACC[T/C]CTAGAAGAGATATTTTATAG
SJHQ	SJLGG027	chr2	226415712	17	61	0	41 T	C	ATAGAAGACTCAGGCTATTA[T/C]CCATTATAGATATGACTACA
SJHQ	SJLGG027	chr22	49407724	4	14	0	16 C	T	ACCCAGGCAGGCCCCTCTCC[C/T]ATCCCTCCCATCCTCCCGCA
SJHQ	SJLGG027	chr2	67408064	11	45	0	39 T	A	GTCATAATGAGTCCGATTGA[T/A]TTGTGAAACCTTAATATACA
SJHQ	SJLGG027	chr3	85883438	19	56	0	36 C	T	CCCTTAAGAATTATAAATCT[C/T]GAAAATGCAAGCCAAACACA
SJHQ	SJLGG027	chr3	93585178	7	49	0	41 C	T	GGAAGACTTAGGATTGGATG[C/T]CATGCTTCATGGCATCCATG
SJHQ	SJLGG027	chr3	95359906	16	59	0	45 A	T	TGGGACAGGATTTCACCAAA[A/T]GTAGTTAATATTCCAATTTC
SJHQ	SJLGG027	chr4	131419325	11	42	0	42 C	T	ACTTTCAGATGGGACAGGTT[C/T]GGTAGATCAAGAGACTGCAG
SJHQ	SJLGG027	chr4	28400424	12	48	0	42 G	A	CATTCATTCATTAGCCTCCC[G/A]GAAGTTGGGCAGGCCTTAAA
SJHQ	SJLGG027	chr4	45926139	17	55	0	32 C	T	CAATGGGTAACATGGAATAC[C/T]TCTGAGGAAGTGGCACCTTT
SJHQ	SJLGG027	chr4	81695422	13	60	0	37 A	T	CAGGCACATAAGTTACCCTG[A/T]AGTCACCAAAACTTTGCATA
SJHQ	SJLGG027	chr5	174910264	17	60	0	52 A	G	AACAGTTCCAGGTAGCCGAC[A/G]TCATTGTGAGAATGTCTTTA
SJHQ	SJLGG027	chr5	21768135	13	50	0	51 G	T	GATGAAATTCATTTAACCTT[G/T]ATTCAGCATGAGTATTATTA
SJHQ	SJLGG027	chr7	140335102	18	67	0	46 T	A	ATAAATAAATAAGTAAATGT[T/A]TTATGACAAATATAACTTTC
SJHQ	SJLGG027	chr7	70629664	14	45	0	33 C	T	AGAACCAACACATTTTCAAA[C/T]AGTGTGGTAACCTGGTGAGT
SJHQ	SJLGG027	chr8	38824279	12	48	0	22 T	A	CACAACTCTTTAAATTTTTT[T/A]AAAAGTTTTATTCACAATAG
SJHQ	SJLGG027	chr9	98854825	15	65	0	46 G	A	TAGCATATTATCATGCCAGC[G/A]TTTTCCTGACTCTGAGCTGA
SJHQ	SJLGG027	chrX	19222401	6	53	0	40 A	G	TCTAAATCTCTTCATTTTGC[A/G]TTTAAACCATTTTGGGCTCT
SJHQ	SJLGG027	chrX	41806980	18	61	0	44 C	T	CAGAGGATGGTTATTTACTA[C/T]GTTATAGTTAAAAGTATAAA
SJHQ	SJLGG028	chr10	26416871	39	81	0	46 C	A	TTCTTTAAAATAATTAAGAT[C/A]TTTTTAGTAAGATTTTCAAA
SJHQ	SJLGG028	chr10	28218220	19	47	0	28 C	T	ACAGATGAATAGATGAGAGA[C/T]GATTGATAGATAAAATAATG
SJHQ	SJLGG028	chr10	37442189	8	76	0	45 A	G	TTGATGAGGACTAGAACATA[A/G]GTTAGATATTTTTAAGAGAG
SJHQ	SJLGG028	chr10	56343113	20	51	0	45 T	A	ATTTACTTGTGCTACTTGGA[T/A]AATTGTTATTTTCCTCCATT
SJHQ	SJLGG028	chr10	75202644	13	39	0	39 T	A	AATTGTTTACAGGAAAAAAA[T/A]TTTTTTTATTGAAAAGCAAT
SJHQ	SJLGG028	chr1	146905271	13	47	0	46 G	A	TGAGTTAAATGCATGTCACC[G/A]TGTAATTGATGGAGAAAACA
SJHQ	SJLGG028	chr1	181312951	12	29	0	21 T	G	TGGTGATGCCCTGTCTCCTC[T/G]CAGAATCGTCCCTATCACCC
SJHQ	SJLGG028	chr12	24068686	24	56	0	49 T	C	TAGGAGATGCTGAATCTCCT[T/C]AAAATCAAGGACAGTAGGAC
SJHQ	SJLGG028	chr13	90908627	16	47	0	37 C	T	AATTTGTAGAAAATTATTTA[C/T]AAGAGGCAATTTGTGTAGAA
SJHQ	SJLGG028	chr15	53695739	4	29	0	38 G	T	CAGAGCGTGAATGACACAGG[G/T]TATCCGATGTCACATGGCTG
SJHQ	SJLGG028	chr1	57483315	15	42	0	34 G	A	TCTTGCTGATTAATCTCGCA[G/A]TGTTAAACACTTCTGCGGAA
SJHQ	SJLGG028	chr16	35029534	11	26	0	24 C	A	CAGACATCCGACACTTGCAA[C/A]ACTCCCATAGAAACACACAG
SJHQ	SJLGG028	chr17	69019500	17	37	0	25 C	T	GATTATAGCAAACTTTAATG[C/T]ACTCTCATCGGCTGACTACA
SJHQ	SJLGG028	chr17	76288370	16	38	0	25 G	A	GGCTTTCCCTGCGTGGGGGC[G/A]ACACTGTTGCCAGTTACAGA
SJHQ	SJLGG028	chr18	27205748	7	56	0	42 G	T	ACAAATAAGATATATATTTC[G/T]TTAATATCATCAAATGACAA
SJHQ	SJLGG028	chr1	8286852	4	19	0	25 G	A	GACACAGGGGGGCCCAGGGA[G/A]AAGCCACAGCTTCTGGAGAC
SJHQ	SJLGG028	chr2	180166821	18	46	0	51 A	T	AAAGCCTATAGTTGTAACAC[A/T]TATAGTAATTCTACTAAAGA
SJHQ	SJLGG028	chr2	41752780	15	48	0	58 C	T	TGTTTCTTCACCTTGGATGA[C/T]GGTATGGCACCATGGTGTGG
SJHQ	SJLGG028	chr2	57484444	9	68	0	48 C	T	TAATACTCCCTTGTCTGAAA[C/T]GTTTAAATTGATGTGAACAG
SJHQ	SJLGG028	chr3	187764998	22	60	1	38 C	A	ATATTGCAAAAGGTAGAATA[C/A]CTACAGGCAGCTTTTTCTTT
SJHQ	SJLGG028	chr4	27056084	16	34	0	30 C	T	GAAACTTACATATACACTAA[C/T]GTTGGCGGTCACCCGGGGAT
SJHQ	SJLGG028	chr4	29208568	23	53	0	38 G	C	CAGGGACATGTCTATAAATA[G/C]AATAGAATAAAAGGTATACA
SJHQ	SJLGG028	chr5	45229024	31	65	0	41 T	C	CAGAAGAAGAAAAATATCAC[T/C]ATACCATTAATGTCTTTTAC
SJHQ	SJLGG028	chr5	94038409	18	45	0	49 C	G	CACTTCTTTGTAAAATTTTT[C/G]CAAGAGCTTATTAGTTCTTG
SJHQ	SJLGG028	chr6	71282290	30	61	0	50 T	C	ACTATATTGAAAGTTATTTT[T/C]ACATTGTAAATTATGTTTTT
SJHQ	SJLGG028	chr7	151966898	6	57	0	43 A	G	AGCAAGGTTCTTATGGCAGG[A/G]GAAAAGTGAGAGGAAACAAA
SJHQ	SJLGG028	chr7	20584204	32	62	0	43 G	A	TTAAGAAAACTCATAGCTTT[G/A]TGAAGAATTCTATTCTTGAA
SJHQ	SJLGG028	chr8	107940901	15	60	0	45 A	C	TCTCTAATTTGTATCTATAC[A/C]GTGTTAAAAGAGCATCAGTT
SJHQ	SJLGG028	chr8	79230743	11	56	0	46 T	C	ACAAAAGGGGACCAAAGTTA[T/C]GTTCACCTTGGAAATTATAT
SJHQ	SJLGG028	chrX	66267492	33	63	0	51 A	T	GTCACTTTTCTGTAACTCTC[A/T]TAAGACATTTTATTTGCATT
SJHQ	SJLGG029	chr10	82246324	6	43	0	35 A	G	GGTTGGGTTAAATGAGGTCA[A/G]AGGAGCACTCTGTAGGATCC
SJHQ	SJLGG029	chr10	83000048	8	55	0	44 A	G	TTTGTCCATCCCAAGGTTGG[A/G]ACTTTGACTACATCTTTGTC
SJHQ	SJLGG029	chr10	86024192	9	71	0	39 G	T	TTCCCTGTTAAAGGGAAAAG[G/T]GATCCCACAAATTTTCTATA
SJHQ	SJLGG029	chr1	106467199	11	75	0	53 G	A	GCAATTAGTCTTACAGATAC[G/A]ATTTTGAAGATACTCTATTT
SJHQ	SJLGG029	chr12	119573220	11	70	0	46 G	A	CAAAAACCTGTACAAATGTC[G/A]AAACCAAAAACAATAATAAT
SJHQ	SJLGG029	chr12	15385394	9	60	0	38 G	T	TCCTGAGTCCACAACATAAT[G/T]CAGCCATTCTTAGATTCTAT
SJHQ	SJLGG029	chr13	45861802	7	59	0	34 C	T	GTCTACTTTCCCAGAATTCT[C/T]TCTCCCCACCCCATCTCACC
SJHQ	SJLGG029	chr13	47072833	19	85	0	43 A	G	TGTACAGATTTATCTTAGCT[A/G]AATATAGTTCTATCAGACTT

SJHQ	SJLGG029	chr13	70099629	17	82	0	45	T	C	AGAATTAGTACCCAAAAATG[T/C]ATGGTAAGACACTAAGCTTG
SJHQ	SJLGG029	chr13	89195335	21	86	0	47	G	T	TCTATTTGCATTGTCATTAT[G/T]TATGTGAGCAATATCTTAGG
SJHQ	SJLGG029	chr14	55031538	15	72	0	39	A	G	GGAAAACAAAAGTGTTAATT[A/G]GTGGAATAATATCTCAGATA
SJHQ	SJLGG029	chr16	16731933	11	89	0	61	T	C	AAAGCACAACATGAGACCTA[T/C]TCTAAGGTGATTAGAAGACT
SJHQ	SJLGG029	chr16	60801248	9	82	0	49	C	G	TTTTCTGTAAGAATTTGTAT[C/G]TAATTTCTAAAAAAATCAAG
SJHQ	SJLGG029	chr18	42866517	11	65	0	43	G	A	ATAGAGGACTAAAGGTGGCT[G/A]CATTAATTTTAGATCGAATA
SJHQ	SJLGG029	chr1	97501684	13	63	0	63	C	G	CCTACTAGTATTTTCTTATG[C/G]ATTACATTTGTTTCATTTGT
SJHQ	SJLGG029	chr20	38745043	15	80	0	50	C	T	CTGGCAACCAGGAGTCAGAG[C/T]ACATTATCTGTTATTAGCAC
SJHQ	SJLGG029	chr2	132914817	10	70	0	65	T	C	TTATATTTCAATGAGATAGA[T/C]TCATTTTTATTCTATGTATT
SJHQ	SJLGG029	chr2	153879633	9	70	0	42	G	T	ATGCAAAAGTATTTGCTATT[G/T]TACTATCAAGTGATAAGTTA
SJHQ	SJLGG029	chr2	234237286	6	39	0	33	G	A	ACCTACCATCGCTACTACCC[G/A]CAGGGCAGCAGGCCTAGGGG
SJHQ	SJLGG029	chr2	40803036	12	71	0	57	C	A	TTCACTGTATAGTATATATT[C/A]TTTTTTGTGTGAATAATTTT
SJHQ	SJLGG029	chr2	51743840	10	67	0	48	G	T	GAATTTTTTTATCATAGGTT[G/T]GCTTCCCTGGGAAGCAAGTT
SJHQ	SJLGG029	chr2	53027645	14	72	0	60	G	A	CAAAATGGTTGTGTTTGATC[G/A]AAAGATCACAAGCAGTTTTC
SJHQ	SJLGG029	chr2	63823180	10	60	0	32	A	G	TTGTCCTTACCATATGCTCT[A/G]TAGTTTGAAAAAACCCAGAA
SJHQ	SJLGG029	chr3	139684287	8	38	0	38	G	T	CCAGGGGTAATGTGGGAGTG[G/T]TATTCTCCACTTCTGGGGCC
SJHQ	SJLGG029	chr4	181415748	18	90	0	43	G	C	TTTGTATGAAGAACTATCAG[G/C]GTGAAAAAGGTTATAGCTAG
SJHQ	SJLGG029	chr4	32908994	21	83	0	42	A	G	TAAATGTAGTGTAAAGAAAA[A/G]GAAACTTTTAATAAAAGCAG
SJHQ	SJLGG029	chr4	71108852	7	60	0	65	C	T	TGGATAATTCTACCATTTCA[C/T]GAATTATTTCTTCTTACCAA
SJHQ	SJLGG029	chr4	87275566	7	48	0	34	G	A	TGATTTTCACTTCTGTAGTC[G/A]AAATTATTTGGAGCAGTATT
SJHQ	SJLGG029	chr5	103464375	10	74	0	41	C	G	ATTGGCTTCCTGGCAGCTCG[C/G]GAGCACCCTTGACATTTAAA
SJHQ	SJLGG029	chr5	25822558	23	87	0	51	A	C	TCAACTTTTCTTTTACTGAA[A/C]GTGGTCTGGTTAATTCTTAC
SJHQ	SJLGG029	chr6	54138384	9	47	0	32	A	G	CCCAATGTACTTCCCAATAC[A/G]TACACCCTCCTGACACACAC
SJHQ	SJLGG029	chr7	123122128	9	63	0	52	G	T	CAATATTAAAACATAAAACT[G/T]GGGGGGAGAACCTCAAAACT
SJHQ	SJLGG029	chr7	145545037	23	87	0	35	G	A	TGAAGAAATAAATGTGTCAT[G/A]GTTGCAAAAATTAGAAAAAT
SJHQ	SJLGG029	chr7	55201652	6	47	0	33	C	T	AGTAAGCAAAAGTCTCAGCG[C/T]AGAGATTAGACAAGTAGAAT
SJHQ	SJLGG029	chr8	13665131	8	61	0	61	G	A	ATTTTTAAATTATAGACACC[G/A]TACTAGTCTTTAAAAAATGG
SJHQ	SJLGG029	chr8	20222660	15	62	0	41	C	G	TTCAATATAGCCAATTCTCC[C/G]TTTTTTGTCTCCATCTTTCC
SJHQ	SJLGG029	chr8	36772049	17	63	0	35	G	A	GTAATGATAAACATAAATGC[G/A]AAGCCAAGCTAGGACCATCA
SJHQ	SJLGG029	chr8	84410079	12	91	0	55	A	T	TTTCATTGATGAAACATTTA[A/T]CTTGTACCGAAGTACCAGTC
SJHQ	SJLGG029	chr9	112388285	12	82	0	44	A	G	GAATGAGCTACAGGTATGTT[A/G]AAATCAAAACTATCTGGATT
SJHQ	SJLGG029	chr9	16077526	11	40	0	49	G	T	GATTATGCTCACCCCCTTGT[G/T]CTCCTGCCTTTTTTCATGAG
SJHQ	SJLGG029	chrX	91363380	13	38	0	22	C	T	GACACTGTACTTCAAATCAG[C/T]GTGCATCCATTTTGAATATT
SJHQ	SJLGG029	chrY	8483496	13	25	0	26	G	A	CCTGCACCCAACCTCTTTCA[G/A]GAATGGAGTCAGAAAAGCAG
SJHQ	SJLGG030	chr11	109526305	6	44	0	46	C	T	AAAGTGTGTGTGCCAGAAAA[C/T]GCGTCCCTGTCCTAGCAAGG
SJHQ	SJLGG030	chr1	119548521	13	45	0	39	C	T	ATGAAATGCTCAGACTCTCT[C/T]CCTAGCGGAGCTAGTGGAAG
SJHQ	SJLGG030	chr12	13253854	15	43	0	27	C	A	CCCGAGTTTTGGGAACACTT[C/A]AATTCAGTGGGAAGGACCCT
SJHQ	SJLGG030	chr1	31504187	13	70	0	45	C	T	AACCAGAAATATTAAAAATT[C/T]TATTTATATGTCCCAAGGAA
SJHQ	SJLGG030	chr13	33276383	10	53	0	43	C	T	TTTTGGTCATTGACCCCTTG[C/T]AAATAGAGAGACCCTACTTT
SJHQ	SJLGG030	chr13	88658686	15	81	0	48	G	A	TTTTTTGTTGCACATTTTAC[G/A]TATTAAATATATGTGCTATA
SJHQ	SJLGG030	chr16	15263188	8	50	0	38	C	T	GCTAGCTTGTTCCATCAGGA[C/T]CCCTTCTTTCACTGTGCAAA
SJHQ	SJLGG030	chr2	177092934	7	57	0	36	T	C	AAGGAAGCACCTGGTAGTTA[T/C]GCTATAAAGGAAAGTGATTG
SJHQ	SJLGG030	chr2	82617273	19	55	0	57	G	A	CCTTTTCTCTGCAATAATCT[G/A]CCTCAAATATCAATGCAAGC
SJHQ	SJLGG030	chr3	134057922	11	47	0	30	G	A	GCTTGGTGTACCAAGCCCCC[G/A]AGAGGGTGCCTGTCACTCAA
SJHQ	SJLGG030	chr3	146331270	9	64	0	56	A	G	TTATGAGTTTGTTTAAATAT[A/G]AGTGTTTGAAAATAATTTTG
SJHQ	SJLGG030	chr3	60367449	8	62	0	57	G	A	TTAACTTTCTAGTATCAACT[G/A]GTATATACAATCATTACTCT
SJHQ	SJLGG030	chr4	139671011	14	73	0	44	A	G	AAAAAATTGACTTGAGAGGG[A/G]AAAAAGTTCTTGCCATTCTC
SJHQ	SJLGG030	chr4	181553829	6	57	0	44	C	T	GTAGAGAAATGTTAATAATA[C/T]GACCACCTCTGCTTCTGATA
SJHQ	SJLGG030	chr4	24929190	9	53	0	47	A	G	ATAGTTGTAACGTTGATTAA[A/G]GCAGGTGCTGAAACCTTCTC
SJHQ	SJLGG030	chr5	28538734	11	62	0	46	A	G	CAACTCCAACAAACCTAAAG[A/G]CCTTATCTAACTAGCCAAGC
SJHQ	SJLGG030	chr6	134972392	13	46	0	34	G	A	TAGGGAATAGTAGATGACTC[G/A]TAGGTGCCCAAACCATTTTG
SJHQ	SJLGG031	chr13	26650190	7	45	0	32	C	T	GGAATTTTTCTGGGAATTGA[C/T]AAGACTCTGTAAAAACAAAT
SJHQ	SJLGG031	chr17	32381249	6	50	0	35	C	T	ATCAGTGTTTTCATTACATG[C/T]GTCCCTTTCCCTCATTGCTC
SJHQ	SJLGG031	chr3	74679683	7	64	0	42	C	T	AAGAATATTGCTGCGCTATG[C/T]TTACTAAATATAAGATTAGA
SJHQ	SJLGG031	chrX	26594603	9	74	0	52	C	T	AAAAAAGCAAATGCAGATGA[C/T]ATGGGGGAGAATATAATTTA
SJHQ	SJLGG032	chr10	5697899	9	33	0	39	C	T	TAGCGTCTTCCGCTGCCACA[C/T]GCAAAGATGACTAAGATGCA
SJHQ	SJLGG032	chr11	22918712	7	42	0	37	C	T	TTCTTCCTCAGCCTCATTAG[C/T]TAGCTGCGCCGGGTTGTAAG
SJHQ	SJLGG032	chr12	118472378	7	24	1	39	C	T	AGACACCTGTGATACCAAAG[C/T]GCTCTCTCTGTCTCTCTCTC
SJHQ	SJLGG032	chr12	82458658	4	40	0	51	C	A	TTATTCTCTTCTGGAATATG[C/A]TAAACCTCTGCAGAGATATT
SJHQ	SJLGG032	chr13	66069427	18	50	0	58	A	T	TTCTGTAAATTCTTATGAAA[A/T]ATTTTAAGAATAATAGGTTA
SJHQ	SJLGG032	chr13	93502273	16	47	0	30	C	T	AAGATTCAGTGGCAAGACCC[C/T]GGAAATGTTCAGTAAGTTGA
SJHQ	SJLGG032	chr14	94574973	14	30	0	25	G	A	TCTGAATATACTGCCTCCCC[G/A]GGGGCCCTTCCCAGAGAGAA
SJHQ	SJLGG032	chr15	75993176	6	24	0	30	G	A	TGGTGACTGTGGGTCTGGAC[G/A]GCTGCCTGGACCTGAAATCT
SJHQ	SJLGG032	chr1	62593909	13	35	0	17	G	T	AAGATGCATTAGATAAACTT[G/T]ATACCTTTAGAAATTCATTA
SJHQ	SJLGG032	chr16	59697054	4	36	0	45	G	T	CATGCAGTGTTAACAAGAAG[G/T]GCTTACTGTCTTTATTGTAA
SJHQ	SJLGG032	chr17	38989749	15	43	0	47	C	T	ATTTCCTGCTTCCCTCCCTC[C/T]CCTGCTTCCTTCCTTCCATC
SJHQ	SJLGG032	chr17	40429238	4	20	0	22	G	A	ACTCTCCTTTCCTCTGCTAC[G/A]TCTATCTCCCGGAGCTGGCC
SJHQ	SJLGG032	chr1	83877684	7	28	0	51	A	T	GAGAGCTGACTAAAGAAGAT[A/T]GAATGAAAAGGAAACATTGC
SJHQ	SJLGG032	chr18	45372310	4	40	0	47	C	A	AGATAATGTCTTTCTGAAGT[C/A]TAACTTTAAATATACTACTG
SJHQ	SJLGG032	chr1	89457108	14	39	0	38	C	T	GGCTACAGCTAATAATGCGC[C/T]GCCCACACTGTTACAAGAGT
SJHQ	SJLGG032	chr1	97392903	4	28	0	30	C	T	GTTTGGAGGCCATTATGAGT[C/T]AGGCAACAGCTTTCTCATTG
SJHQ	SJLGG032	chr20	13000662	12	51	0	45	G	T	CTGACTTCCTCAGATCCCCA[G/T]ATTAGAAACTTTGGCTCTGA
SJHQ	SJLGG032	chr2	116042957	20	51	0	34	G	T	AAAGGCCGGTAATAATGAAC[G/T]TAAAATAGGGAAGAAAAGAC
SJHQ	SJLGG032	chr21	17551055	4	34	0	41	T	G	TATTTCATTTTCCCATCTCC[T/G]GATGGCAAGGACTCTATCAT

SJHQ	SJLGG032	chr2	154230002	8	44	0	33	T	G	TGTTTGTGTTGCTTCTGACC[T/G]GAGGATCCCTATATACAATT
SJHQ	SJLGG032	chr2	217719446	8	20	0	37	G	A	TTACAGAGCAGGCGGGCACC[G/A]CCAGGGACATCTGTCTTCAA
SJHQ	SJLGG032	chr2	4631233	6	47	0	37	A	G	TTGAAGATATTCACGATAGG[A/G]GAGAGACCAAGCAGTTAGAG
SJHQ	SJLGG032	chr2	53426355	13	41	0	38	G	A	GCCCTGACATATAAAGGTAC[G/A]GAAATGGAAATTGTCCATAT
SJHQ	SJLGG032	chr4	182268572	7	26	0	41	G	A	CCTTATAGCTATGGTAAGGG[G/A]AAAAGATTCTATCCTTATTA
SJHQ	SJLGG032	chr5	21353967	4	38	0	42	A	C	TATAAGCAGTCCGATTATTA[A/C]AAAAATATGTGCCTGATTCT
SJHQ	SJLGG032	chr6	90218700	15	29	0	23	G	T	GAGGAGGGTGCTTCCAAAAG[G/T]TGTGTGGAGCTGTTTGTTGA
SJHQ	SJLGG032	chr7	139042118	12	59	0	49	T	A	CACTCCTCAATTTTGATCAT[T/A]ATGTATTGTATAGACTATTT
SJHQ	SJLGG032	chr7	77762972	13	35	0	37	A	C	TTCTTTGCTAATAACATCAA[A/C]TTTTCAACTGAAATTGACTC
SJHQ	SJLGG032	chr7	85652306	4	31	0	40	G	A	CAATCAGGCAGGACCAAAAT[G/A]TAAGTGTTCCCAAGATAGCT
SJHQ	SJLGG032	chr8	128111019	5	32	0	51	A	G	TGATTTGTTCCAAGCCCCAA[A/G]TTTAAGCAGTTTGAGAGGTA
SJHQ	SJLGG032	chr8	49294619	4	21	0	26	G	A	AGAAGCCAATGGGAGGTAGA[G/A]AAGCAGGGAAGGCAAGTGGA
SJHQ	SJLGG032	chr8	87744145	14	38	0	42	A	C	ATGTGGGGCATGATACAAAA[A/C]CTTCCATTTACTTAACAGAG
SJHQ	SJLGG032	chr8	95479118	4	35	0	41	C	T	AGGTACTTACTTATCATTAC[C/T]AAAAGTTTATTTTATAGACT
SJHQ	SJLGG032	chr9	10066282	6	53	0	40	C	T	TCTGAACTTTAACCACTATC[C/T]TGAAAATATGTTTATCTATT
SJHQ	SJLGG032	chr9	10366174	4	34	0	37	G	T	TGTAGTGCTGCTGATATATG[G/T]CTCTGCGATGTATGCTTCCC
SJHQ	SJLGG032	chr9	104576807	4	38	0	50	T	C	CCTACCAAGTTATTAATAGT[T/C]TGGCCTGACCAAAGCCAAAA
SJHQ	SJLGG032	chr9	78167561	6	42	0	44	T	C	TCAGATTTCCTTTGACAATC[T/C]GTGGGAGAAGGAAGAATCTG
SJHQ	SJLGG032	chrX	32157938	7	24	0	24	T	G	CTTAAAACATTCTTAAAACT[T/G]TATAGAAATTTTGCCTGCCT
SJHQ	SJLGG032	chrY	23976150	3	9	0	16	C	A	GCCGTTTCCAGTGACCACTT[C/A]AGAGTGTCGAAAAGCCTCCT
SJHQ	SJLGG033	chr10	48325301	10	36	0	29	C	T	CAATGTGTTCTCAGCCCAGC[C/T]GCAGACACGTGCTGCCCCAG
SJHQ	SJLGG033	chr10	78663341	13	51	0	35	C	T	CACTGCTAGCTCCTCTGCCT[C/T]GGGACGGCCATGTGCCCTCT
SJHQ	SJLGG033	chr11	38303765	8	52	0	42	G	C	ATCCCTCTTAAAAGATCTTT[G/C]TCAAATTCACAGTGATGGAC
SJHQ	SJLGG033	chr1	213936838	8	66	0	36	C	T	CATGGACCCAAGGTCAATTC[C/T]GAGCAGGAAGAGCTCTATTC
SJHQ	SJLGG033	chr12	64777529	15	56	0	41	G	T	AAAAAAAATGATTAAAAAAA[G/T]AAGTCCACAACTATAAATCA
SJHQ	SJLGG033	chr12	85451022	18	81	0	28	A	T	AATTAGCTCTTTAAAGTATA[A/T]CTTTTCAGATCTTAGAAAAA
SJHQ	SJLGG033	chr12	86667529	20	56	0	29	C	T	GCCAGTGTATACACTGCATA[C/T]GATAACAGAGTGAATATATA
SJHQ	SJLGG033	chr13	36561924	9	47	0	35	G	A	ACACTTGCTTCTTTTCCCTC[G/A]GACTTGAGGTAACCCAATAC
SJHQ	SJLGG033	chr13	69457534	10	77	0	42	C	T	TGTTAGCGAGAACGAGAACA[C/T]TGTCAAGGTGAAAATAATTT
SJHQ	SJLGG033	chr15	34059622	5	40	0	49	G	A	GTGTGTTCTCTTAAGCTATA[G/A]GCCAGGGGGTCCCAACTCTT
SJHQ	SJLGG033	chr16	29952730	6	43	0	31	C	A	TATGTCCTTCATTCTGTTCT[C/A]CAAAAAGCCATTGCCTTCCT
SJHQ	SJLGG033	chr16	81443035	5	20	0	24	C	T	CCATGTCCAGTGGCCACCAC[C/T]GAGCTGGCCCTGGTCCAGCT
SJHQ	SJLGG033	chr1	92435166	10	68	0	42	G	A	ATTTAAATTGTAAAACCAGC[G/A]TGCTAATTGTTGCTGACTTA
SJHQ	SJLGG033	chr20	34233781	8	37	0	41	G	A	CTAATGTGTGGAGTATAGTG[G/A]AGTGTGGCATTAACAAACTT
SJHQ	SJLGG033	chr2	227746667	14	56	0	42	A	C	TGTTAATGAGTGGTGATCAC[A/C]AATACCAAGTAGTTCTTATT
SJHQ	SJLGG033	chr2	57958493	29	81	0	35	G	A	ATATATGTTGTCTATCCATT[G/A]AGACTAAGTTTTAACACAAG
SJHQ	SJLGG033	chr4	161740034	14	62	0	41	A	G	ATCTGTGAAAAAGAATACTC[A/G]AAATATTGTTTTATGTTTAT
SJHQ	SJLGG033	chr4	4432342	8	53	0	41	G	A	GTGTCTTTAGACAATGACTC[G/A]GGACAGTGGAATGAAACAGA
SJHQ	SJLGG033	chr4	64637350	16	61	0	56	A	T	TGCTATTCTCCCTGGTTTTA[A/T]AAATCTATCAGTCAGTGTCA
SJHQ	SJLGG033	chr5	26650446	8	58	0	38	T	C	CCCTTTCTCTTACTCTTTTA[T/C]CTTTCACAGTGGTTAAGAGA
SJHQ	SJLGG033	chr5	97969729	18	58	0	35	A	C	TATGTGCTACTCAAAAAAAA[A/C]CATTTTTGCTTGTCTCAGCT
SJHQ	SJLGG033	chr7	42785110	7	49	0	39	T	G	TCTGTGATCTATTCTTTGGG[T/G]CTCTCATCCCTATGAAGCAG
SJHQ	SJLGG033	chr8	115599785	8	49	0	45	A	G	TGGTCATTCCAGAAGCTACT[A/G]TTGAGACATAATATTATGGT
SJHQ	SJLGG033	chr8	41317240	9	59	0	42	G	C	ACTTTTTACCTTTGCAACAA[G/C]ATAACGAAAACAAATAGGTA
SJHQ	SJLGG033	chr8	41317257	11	56	0	37	G	C	CAAGATAACGAAAACAAATA[G/C]GTAATCAAACCACGACTATT
SJHQ	SJLGG033	chr8	69654136	8	65	0	45	C	T	CATTTAGGTTTATAGAATTT[C/T]AATTTAGCACTCACACTCCT
SJHQ	SJLGG033	chr8	79990340	12	49	0	34	C	T	TGGGGTTCGCTCGATGACCC[C/T]GGATGGGGGGTCACACATGC
SJHQ	SJLGG034	chr10	116041409	11	34	0	33	C	T	TGTCTTGACCTGCAGAGCCT[C/T]GTGTGGACACTTGTTGTGTG
SJHQ	SJLGG034	chr10	30659172	17	37	0	26	C	A	ATCTCCCAGCCACCCTGTTG[C/A]TCTCTGCTGAATTTTTTACA
SJHQ	SJLGG034	chr10	37587234	32	57	0	24	C	T	AGAAGTAAACAAGAGGTTGA[C/T]GTGCAATAAGCGTTCAAAAA
SJHQ	SJLGG034	chr10	48490176	17	48	0	27	A	G	GGCACAGTTTTGCTCCTGTC[A/G]TCCTCTTTATTTACCCCTTT
SJHQ	SJLGG034	chr10	53098777	14	43	0	31	A	G	TATATCCATTTCACTGTCAC[A/G]TGTAAGTATTCATTAAATTG
SJHQ	SJLGG034	chr10	75547730	21	45	0	37	T	G	AGCAATTTTGTGAGATGTAG[T/G]TTGTCATGTTATCACTACTT
SJHQ	SJLGG034	chr11	103421922	22	58	0	22	T	C	ACATTTATTTTGAGCCAGCA[T/C]GACAAATTTAGGAGAAAACA
SJHQ	SJLGG034	chr11	109322626	29	63	0	46	C	A	AGAGTTTCTTTCCAGAATGG[C/A]TTAGTCAAACCTTACCAGAC
SJHQ	SJLGG034	chr11	125012325	10	26	0	16	C	T	CTTCCTGAAATTCCGCTTCA[C/T]CCCAGGCCTGGCACTGCTCA
SJHQ	SJLGG034	chr11	37720324	7	54	0	39	T	C	ATATTGCTAAGAAATCTTTA[T/C]ACCTAACTCATATCTATTCC
SJHQ	SJLGG034	chr1	147002106	19	48	0	49	T	C	AACAATAATAATTTATCTAA[T/C]GCCTCCTCAATTAAACTAGC
SJHQ	SJLGG034	chr11	58404759	28	57	0	38	G	T	AGCACCTATCTCAGAGTTCT[G/T]TCTGATGCTCTGAGGCTGAG
SJHQ	SJLGG034	chr1	168984667	15	39	0	29	C	T	ACCCATACAGCCCTCTCTCT[C/T]CCTCTACTCCACCTCCAGAG
SJHQ	SJLGG034	chr1	173632171	9	26	0	21	A	G	TTATAATTCTTCAGTGTCTG[A/G]CATCCAACTCCCCACCCTTC
SJHQ	SJLGG034	chr11	8149261	28	59	0	41	A	G	AGCAGGATTTAATGGAGGCT[A/G]CTTATTCTCTTCTTAAAACC
SJHQ	SJLGG034	chr1	187222558	15	44	0	32	T	C	TGCGTTTTTGAGACCTGACA[T/C]TTTCTCTGCTCTAGCCTAAG
SJHQ	SJLGG034	chr12	126193407	17	43	0	30	T	C	GGCTCATTCTTCCTCATGGC[T/C]CATTGCTCTTCCCAGCTCTG
SJHQ	SJLGG034	chr12	128711362	20	57	0	42	A	G	CTTAGCATTTAACTCCCCCG[A/G]GTATAATCACCCTCCACTTA
SJHQ	SJLGG034	chr1	216493378	40	76	0	40	T	G	ACTAACATATAAGCCCATAT[T/G]TATGTAACAAAATGATAGAA
SJHQ	SJLGG034	chr1	216493401	38	78	0	36	A	T	TGTAACAAAATGATAGAAAT[A/T]TAAGCATTTTATATAGTTTG
SJHQ	SJLGG034	chr12	25891803	15	39	0	27	C	T	TCTGCCTGATGGAAGGAGGG[C/T]CCACAGTCCACCAGTGGGGC
SJHQ	SJLGG034	chr1	226715262	7	29	0	30	G	T	GAGCCAGAGCCAGGGACGCT[G/T]GGACGACCACTCCTGGGGGC
SJHQ	SJLGG034	chr12	33976184	28	64	1	38	A	G	AAATATCTTTTTAAAAAGGG[A/G]AAAAATTATAGCTTAAAGAA
SJHQ	SJLGG034	chr12	42299650	27	50	0	28	C	T	ATCCCGCCACCTAATGCTGT[C/T]GCAAACAGGGGAAGCAGGTG
SJHQ	SJLGG034	chr12	4678410	26	67	0	42	A	T	TTATAGGTGCAATTTTTAAT[A/T]CCTAAAACAAACTTATTTTG
SJHQ	SJLGG034	chr12	66858326	25	60	0	58	T	C	TTTATGGTAGCAGGATTTAA[T/C]TGTCAACAATTCAGGAAAAC
SJHQ	SJLGG034	chr12	71219231	16	39	0	35	A	T	GCAAACTGCATCCAAATCCA[A/T]ACACATACCTCTTGATACCA

SJHQ	SJLGG034	chr12	74152826	36	79	0	54	G	T	TAGTATTCACATAAGAATTT[G/T]TAAAAGATATGCTATCCATT
SJHQ	SJLGG034	chr12	74228426	26	52	0	33	T	A	AAGACAGGTGGTGGAAAGTA[T/A]AAACCAAGCAGAAAGAATTG
SJHQ	SJLGG034	chr12	87924693	23	52	0	32	C	T	AATAAAGGTAAATATTTTAT[C/T]GGGAAAAAAGCCACCAAATA
SJHQ	SJLGG034	chr12	96987586	32	77	0	42	A	G	CCTTAACTTTACATTTTACT[A/G]TCATTTAAATTTAAGTAGCA
SJHQ	SJLGG034	chr13	104508681	23	64	0	42	T	A	ATTAAAACAAAATAATCAAA[T/A]TCAGAGTTAACTAAACAATT
SJHQ	SJLGG034	chr13	106663563	23	54	0	44	A	T	CAAAAAGAAGAATATCCCAC[A/T]AAATGGATGGTGTATGTCTT
SJHQ	SJLGG034	chr13	110549784	18	51	0	45	A	G	TTTGTGACCTTCCATGATAC[A/G]GCTGTATTTTTCTGAATTTA
SJHQ	SJLGG034	chr13	19700061	23	48	0	39	C	T	TTCAAGATTTCTGTACAGTA[C/T]GTTCATTGTCTGCTTTATCT
SJHQ	SJLGG034	chr13	23556449	14	36	0	35	C	T	AGGAGTTAATGATTAAGAGG[C/T]GCCTTGAGTTCGGTCCCACT
SJHQ	SJLGG034	chr13	57602456	31	77	0	38	C	T	TTGCATATTGCATAAAAGAA[C/T]GTGAGAATAGATTAAAAAGC
SJHQ	SJLGG034	chr13	59930510	8	58	0	36	C	G	TAAAATACCCAAGTTAGCAT[C/G]CACTACAGTATCCTGTACAT
SJHQ	SJLGG034	chr13	69565141	24	68	0	37	A	G	CTGGCATCTCTGTATCACAG[A/G]AATTTCTTACTATTTTGGAC
SJHQ	SJLGG034	chr13	71341198	27	52	0	32	T	C	TATTATATTGAACATTTGGA[T/C]AGAAAATCTTCCAAAAATGT
SJHQ	SJLGG034	chr13	90800862	20	54	0	49	A	T	GGTAAATTAGTAAGAAACTA[A/T]TTTTATATACAATTATTTTC
SJHQ	SJLGG034	chr14	19117195	22	127	0	86	G	C	AATGCAAATTCAGTTGATAA[G/C]TTTAAATGGTATAGTAGTTT
SJHQ	SJLGG034	chr1	42619771	16	18	0	31	G	A	ATGGGAGAGTGGCAGTAGTC[G/A]TCACAGCAGGGCCTGTCTGC
SJHQ	SJLGG034	chr14	58724817	6	45	0	33	C	T	CATACTTAAAAATAGAAACT[C/T]GTCGATAAGTATTAGGGCAA
SJHQ	SJLGG034	chr14	80888766	30	64	0	23	G	A	TTATGTACCTTTTCTTTAGC[G/A]TCTTGTCCTTTTTCTTTGAG
SJHQ	SJLGG034	chr15	24638235	20	55	0	44	T	A	GATTCCTGCTTACAGAGACC[T/A]GAAATGAACCTTTAGACACC
SJHQ	SJLGG034	chr15	47480578	31	70	0	52	G	A	TCATTTATATTTCCTGTAAC[G/A]TGAAGACTAACATTAATGGG
SJHQ	SJLGG034	chr15	82080279	17	55	0	24	A	G	GGTGTTTTTTAGACAGATCA[A/G]TTTCACCATGAGAGCTAAAG
SJHQ	SJLGG034	chr15	98435197	27	60	0	28	G	C	GGGTGATGCGAGCCACCCTT[G/C]AACAGGTGGACTGATTGGTA
SJHQ	SJLGG034	chr15	98988109	11	26	0	22	G	C	GCTGAGCTGAGAAGCGCTGA[G/C]CTGAGAAGCGCCTGCCATGG
SJHQ	SJLGG034	chr16	10398194	17	62	0	48	C	T	ATAAAGAAAAGCAATTGATT[C/T]CATGCCACCAATTTCAGTAA
SJHQ	SJLGG034	chr16	24015331	30	65	0	36	G	A	TGCTATTTTATTGTTGTCAC[G/A]GACATTATGCATTCAAATAA
SJHQ	SJLGG034	chr16	59183438	25	45	0	36	A	G	CTTTAAAGACAAAACTTGGG[A/G]TTGTGTAAATTCTTAGGTCT
SJHQ	SJLGG034	chr16	60597694	22	65	0	30	C	T	GAAAGGGTCTGTCATAAAGA[C/T]AAGTTACTGAGAGATGTGTG
SJHQ	SJLGG034	chr16	64018617	28	63	0	30	C	A	TATTTTCATCTGATTTAGAT[C/A]ATATTACTTATTGACAAAGA
SJHQ	SJLGG034	chr16	6586984	23	56	0	29	C	G	CTAAGGGGATTCCTTCCTAT[C/G]CATTGTCTTTTCTGGGGAAA
SJHQ	SJLGG034	chr16	74216697	18	51	0	31	G	A	AACTACTTCTTCCATATTCC[G/A]AATAACTTTAATCCTCCCAG
SJHQ	SJLGG034	chr16	83030202	25	48	0	30	T	A	AACAACAAAAACGACCTTGT[T/A]TAAGTTTTACGCCTTATAAG
SJHQ	SJLGG034	chr17	20148708	9	36	0	35	T	G	TGAATGCCCGGTGCCCTGCC[T/G]CTCTTCCTCTGATTCAGGTC
SJHQ	SJLGG034	chr17	21757898	19	42	0	21	C	T	TTTGGCCAAGCGTGGCCAGG[C/T]GCGGTGGCTCACGAAATCAT
SJHQ	SJLGG034	chr17	36499857	17	35	0	29	G	C	CTCTCTAACGTCACCAGCTG[G/C]CTTCTGGATGTAGGTATGAG
SJHQ	SJLGG034	chr1	73940058	14	25	0	37	C	T	GAGAATTCTGTGCTGTGTTC[C/T]CAATGGGATCCTGGGAAAAT
SJHQ	SJLGG034	chr1	74118877	23	38	0	27	T	A	ACCTGAAAGAAAGTTAGCAT[T/A]AGCTTAAACCTTCCCCTAAA
SJHQ	SJLGG034	chr17	50590473	21	44	0	36	C	T	TAATAATTTCTCAAATGTGC[C/T]TGAATATTTATTTTACTTTT
SJHQ	SJLGG034	chr18	26357397	19	52	0	45	A	C	TTGAATTCAGGGTTCTAGAA[A/C]CTAAAAAAAAAATAATACTA
SJHQ	SJLGG034	chr18	28163529	25	55	0	42	C	T	AGTATTTTTGTTTAGAAAAA[C/T]GAGAATTCTGCATCTTTCTC
SJHQ	SJLGG034	chr18	57856654	27	68	1	29	G	T	ACATTCATGTCTAACTGCAT[G/T]TATGTGCTGTCTCTTGGTTT
SJHQ	SJLGG034	chr1	89022839	27	37	0	34	G	A	GCATTCAGCTGGAGCTGGGC[G/A]CAAAGCTTCAGATAAGCTTT
SJHQ	SJLGG034	chr18	9453242	39	77	0	47	G	A	GTTCTCAGCAACCATTTTGC[G/A]AAAATAAGTTACTACTTATA
SJHQ	SJLGG034	chr1	92254405	22	34	0	49	A	C	CAGAGAGTGCTCTTGTAAAA[A/C]CATTGTCTAACAACACTTTC
SJHQ	SJLGG034	chr19	28803412	26	39	0	39	A	G	GCACCCTGATTAATAGCCCC[A/G]CCAAAATGGTCCTCAAGGGC
SJHQ	SJLGG034	chr20	13895646	23	49	0	28	G	A	ATTTTTACTTTTATAACTTC[G/A]TTTTGAAGGTAAAGACCAGA
SJHQ	SJLGG034	chr20	42200817	11	31	0	35	G	A	GAGAGGGGAGGTCATGAGTG[G/A]GTGAGGCCACAGCTCCTGAT
SJHQ	SJLGG034	chr2	100372473	22	42	0	37	A	G	TGGGCTCCTTAGGAAAGGTA[A/G]CTGTGCACAATGGTGGGATA
SJHQ	SJLGG034	chr2	109540931	19	32	0	19	C	T	AGTCGATTAAATAACGTGAG[C/T]GGTGCCAACACTTTCCCTAT
SJHQ	SJLGG034	chr21	24943566	17	56	0	52	A	G	TCATCCTAGAGAACTGAAAC[A/G]TTTTGGCAAAAAATGTTTTT
SJHQ	SJLGG034	chr21	26693702	32	59	0	45	T	C	GAACAAGGTCAGAGAAGTTA[T/C]CTTGGATGGTAGAAGAGAAG
SJHQ	SJLGG034	chr2	139107884	23	63	0	29	T	G	TTTTTAAACCACTTTTTTTT[T/G]GCAAATCAGTGGGACAAAAT
SJHQ	SJLGG034	chr2	144690081	25	59	0	43	C	T	AAGAAATCTTACTCTACTCG[C/T]TCTTTTCTATGGCTAAAGGA
SJHQ	SJLGG034	chr2	154871676	27	65	0	44	T	C	AAAAGATATGGTACTTCTTT[T/C]CTAATACCAGAGTTTGAAGT
SJHQ	SJLGG034	chr2	159517077	7	51	0	33	C	A	TAGTCACAGTTTTGCAAATT[C/A]TCAATTTGCATAATTTTACA
SJHQ	SJLGG034	chr2	163740740	13	41	0	39	T	A	GGAGTCATTAACAGGACATA[T/A]GATAGGAAGTTTGGGTTTAT
SJHQ	SJLGG034	chr2	174461102	30	60	0	43	T	C	TTTAGTCAGGATTTTGTCTC[T/C]GGTCTAATCAGCTGTGGTCA
SJHQ	SJLGG034	chr2	202251902	27	62	0	39	C	T	GATAATATCAGAGAATCATT[C/T]AATGATTGTCATTGTTCCAG
SJHQ	SJLGG034	chr22	19345510	16	42	0	26	G	A	CGGGCAACAAGGAGCTCTCT[G/A]CAGTGCTGTGACTGAATTCT
SJHQ	SJLGG034	chr2	222715122	15	45	0	31	T	C	ATGCCTCTGGCTGCACCTGG[T/C]GCAAATAGCACACGTTCTCA
SJHQ	SJLGG034	chr2	242857121	9	23	0	25	G	A	CCCAGGGTATGACCCCCGTC[G/A]TCCAAACCCCGGCCCAACGT
SJHQ	SJLGG034	chr2	30011396	18	51	0	27	C	T	CTTGGGTATTCATGAGAAAG[C/T]GAAAGGGAGGGAACTAGACA
SJHQ	SJLGG034	chr2	33941840	24	74	0	44	T	C	TCTTATCTATCAAGGACATG[T/C]CAGTATCTTTATTATTTTTC
SJHQ	SJLGG034	chr2	57416428	25	58	0	30	T	C	TAATAATTTGAGATAGCATC[T/C]GAAAAAGAATGTCTGGAATA
SJHQ	SJLGG034	chr2	60525168	9	41	0	26	T	C	CTTTAAATCCATTTCGCACG[T/C]TATTGCACATTCCTTTGTGC
SJHQ	SJLGG034	chr2	65993090	12	56	0	31	C	T	CAGCAATGGACCCATGACAG[C/T]GAGAATAACATGGAAGCAGC
SJHQ	SJLGG034	chr2	68699940	29	60	0	29	C	T	TCACATTATGTCAATGATCC[C/T]GTTTAACTTTTACAAACATT
SJHQ	SJLGG034	chr2	78601695	31	77	0	31	A	G	GATTGCCTTATATGTATGAA[A/G]CACAGTTAATGTAAAACTAG
SJHQ	SJLGG034	chr2	78947486	21	49	0	36	A	T	CATCTGCTTGTTTTTTTTCC[A/T]GTGTACAATCATGGCAAGTG
SJHQ	SJLGG034	chr3	107726701	11	35	1	25	C	T	AATGGGAATGAGGAAAGGTC[C/T]CTCTGTGGTTTAGGGAAATG
SJHQ	SJLGG034	chr3	137552502	24	61	0	30	T	C	TCTCTCTACACTATTTGTCA[T/C]CAAAAAGGCCCCTTCATTCC
SJHQ	SJLGG034	chr3	147471986	29	61	0	34	A	G	ACAGCTCAGTAACTATAGTG[A/G]AAAAAAAGGGGGTGGGTTTC
SJHQ	SJLGG034	chr3	162942408	27	54	0	31	G	A	TACTATACTACATAAGGCAG[G/A]TATTTTATAGTCATGTATCA
SJHQ	SJLGG034	chr3	188473684	17	42	0	25	C	G	AAAACCCATATCACGCTATG[C/G]CACTTCTCTTGTTCAACCTG
SJHQ	SJLGG034	chr3	191410671	26	62	0	46	G	A	AGATAAGCAATATTCTCATC[G/A]TCTAGGCTGATGATTCCCAA

SJHQ	SJLGG034	chr3	192887338	22	60	0	45	C	T	GGCATTAATTAGAAATACTG[C/T]AATGATTATATAAAAATATT
SJHQ	SJLGG034	chr3	21903916	34	73	0	45	G	A	CCTGAGATTCTTATATCACA[G/A]TACGATTGTAAGAAATAGGA
SJHQ	SJLGG034	chr3	25540546	12	65	0	45	C	G	TATGTGACAGGACTTGCAAC[C/G]TTAAACAAGATTTCCAGGCA
SJHQ	SJLGG034	chr3	30995014	23	63	0	36	C	T	TCCCTCCAGCTCAGTGTGTC[C/T]AGGACTAATCTGTTAGGGGT
SJHQ	SJLGG034	chr3	418811	20	56	0	42	G	T	TTAATAGTTATCTCAACAAT[G/T]GTACGGGGTAAAAGGTGAAG
SJHQ	SJLGG034	chr3	57924647	8	23	0	31	C	T	CTGTGTAAGCATGCTTAAAG[C/T]ATGATATAGGGAGTCTTGAA
SJHQ	SJLGG034	chr3	60775417	25	59	0	40	C	T	TATTAAACACCTGACTCTGT[C/T]CCTTGAATAACAGACATTTC
SJHQ	SJLGG034	chr3	7360289	19	42	0	44	G	A	TTTAACAAAAATCAGATGCT[G/A]GTTAATCTCTTTTCATTTGG
SJHQ	SJLGG034	chr3	77825885	21	48	0	38	G	C	CTTCTTTTTTTAATAGTTTG[G/C]AGAAGCAACTAAATTCTCAG
SJHQ	SJLGG034	chr3	84680773	28	61	0	40	G	A	GTGTCTAGTGTTGACTTGAG[G/A]CAGTTCTTCCACTAATACAC
SJHQ	SJLGG034	chr3	85002606	10	38	0	45	A	T	TGCTTGTGGCTGAAAAAGTC[A/T]GGAACAGTTAAGAAATGGTG
SJHQ	SJLGG034	chr3	99811872	19	60	0	36	C	T	TTTGTGGGGTTTCATAAATA[C/T]GTTGAAGGAGTAGAGGTTAC
SJHQ	SJLGG034	chr4	101409766	33	73	0	37	A	G	GAGCCCATATTCAATACGTT[A/G]GCTAATTCCCTTTTAAAGTG
SJHQ	SJLGG034	chr4	108678987	23	53	0	38	T	C	TCTTTATTTACCCTAAATGA[T/C]CCTGGGCATTTGCTACTTTC
SJHQ	SJLGG034	chr4	132932169	21	56	0	40	A	G	TTCATACAATCAAGCATTAT[A/G]AAGTGATATGCAGTATCATA
SJHQ	SJLGG034	chr4	137388369	28	68	0	40	G	C	ATTTGATACATAGTTCAAAC[G/C]TTTTCCAAACATATATTGAA
SJHQ	SJLGG034	chr4	157349706	28	66	0	51	G	T	TTAAAACTTAATCCCCTTAA[G/T]TATAATTTAAATGTCAGGGA
SJHQ	SJLGG034	chr4	175560833	14	59	0	41	T	C	TAATTGGAGTACCAGGTGTC[T/C]CCCTATGGAAGTTCACTTTT
SJHQ	SJLGG034	chr4	186914992	27	62	0	33	G	A	TAAGATTCAGGTACTGCCAT[G/A]GACAGCAATAGAGCACACAC
SJHQ	SJLGG034	chr4	189785476	20	46	0	17	G	A	CTATGCAACGTCACCCCATC[G/A]TCTTCTTCCCTGTGCAGGGT
SJHQ	SJLGG034	chr4	34118200	30	64	0	51	C	A	ATTATAAATTTATCTCTAAA[C/A]ATTTCTATAAGTTTGAATTC
SJHQ	SJLGG034	chr4	55621529	17	38	0	28	C	T	AAATGCACTGCATAGGCTTG[C/T]GGCTTACTGTGGGCATTGAA
SJHQ	SJLGG034	chr4	73072660	25	67	0	39	A	T	TTCACGAGCCCAAAATTCCA[A/T]ATCTATGTACTCCTAAAATT
SJHQ	SJLGG034	chr4	74368131	12	45	0	38	A	G	ACATCCTGCAGTTGAGAATA[A/G]TGAGGGAGTGGAGGGTAAGG
SJHQ	SJLGG034	chr4	77699817	18	47	0	56	C	G	TATAAGGATAATCTGATTTT[C/G]AAAAAGTTAGCCTCCTTACT
SJHQ	SJLGG034	chr5	106279630	20	56	0	35	T	C	ATGAAAGCAAATCTCATCTG[T/C]GGAAAGTAAAAGAGAGAGGT
SJHQ	SJLGG034	chr5	108319508	6	37	0	30	G	A	CAGCTAAAATGCACTACCCA[G/A]ATTCTTCTTCCAAAAATGCA
SJHQ	SJLGG034	chr5	113142301	10	39	0	28	T	C	TTTTACAGGGAAGTGTCAGA[T/C]ATTAGCCTCAGCTAAGGAGG
SJHQ	SJLGG034	chr5	135376862	19	40	0	37	C	T	GGCTGAAGGCGTGGCTAACC[C/T]CTGCACACCTAGAGAGTGAC
SJHQ	SJLGG034	chr5	148631473	27	60	0	29	G	A	ATAGAGGATCTTGTCCATGC[G/A]TTTCAGATCTCAGATTCTTC
SJHQ	SJLGG034	chr5	157506355	21	42	0	23	A	T	CACTTCCCCATTTCTCCATT[A/T]TGTTTCTTTAGACAGCCAAG
SJHQ	SJLGG034	chr5	161237044	25	63	0	47	A	G	AGAGTCGTTCTTTCATTTTT[A/G]CTTTCATATCTCTCCTTCAT
SJHQ	SJLGG034	chr5	161421271	41	77	0	42	C	A	TCAAACATAATTACCCTTTG[C/A]CTTTCTATTGAACTTCAGAA
SJHQ	SJLGG034	chr5	164025805	7	62	0	48	T	A	GTCTACTGAGGGAAGTTTTT[T/A]GTTTTTGTTTTTGTAATTGC
SJHQ	SJLGG034	chr5	174200508	20	49	0	23	C	T	TTTTTCAAGAAGGCATAGGT[C/T]CTTATTGTGTCAGCTGAGCA
SJHQ	SJLGG034	chr5	35946214	15	45	0	29	G	C	TATCCAGCACTGAGGAAGGA[G/C]GCCCGGGGCGAACGTATTGG
SJHQ	SJLGG034	chr5	54684873	21	58	0	36	C	T	ACTGTAACATTTTTAAATGA[C/T]GATTTAAATGTTTATTTATA
SJHQ	SJLGG034	chr5	62410240	27	67	0	35	T	C	GAAAGATGACCTTGTGTTTT[T/C]AAACTCATCTGTAACTGTCC
SJHQ	SJLGG034	chr5	66297598	19	69	0	38	C	T	AACCACCTACAGGTTGTGTT[C/T]TACTCACTGTATCTCCTTCA
SJHQ	SJLGG034	chr5	88596959	26	74	0	45	C	T	CCTTATAAGCAACTATACCT[C/T]TTCCTACTATTTTCTATATG
SJHQ	SJLGG034	chr5	91113676	9	61	0	49	G	A	TTTTATTTCCGGCCACAAAG[G/A]CCATAATTGCAAAAAGAATT
SJHQ	SJLGG034	chr5	93642501	31	72	0	42	G	A	TGCAGCCCTCATTTCTTTCC[G/A]TAATTGTCCATGTGATTAAT
SJHQ	SJLGG034	chr6	125516721	19	56	0	34	T	A	AGATCTATGGAAAAGGCACT[T/A]ACGTGAAATTCTCTGATGAT
SJHQ	SJLGG034	chr6	129462494	23	52	0	44	G	A	CTGCTAGGTGCCAGAAATGC[G/A]GATCTTGAGGAATATACAAG
SJHQ	SJLGG034	chr6	135410377	26	48	0	26	A	G	GGAGAAAAAATAACCTGGGG[A/G]CATGGGTTCTCATTTTAGAA
SJHQ	SJLGG034	chr6	143947936	25	45	0	32	A	T	AGCGTGTCAATTAAAGAAAG[A/T]CAGGGAAGGGTTTTAGCAAA
SJHQ	SJLGG034	chr6	19001585	26	53	0	39	G	T	TACCAGAGAAAAGAATCAAG[G/T]ATCATACTTATTTTCTAAGT
SJHQ	SJLGG034	chr6	35756080	19	49	0	32	C	A	TTGGGGCATGAATGAAAGTC[C/A]CCCAGAAGAGACCAAAGCTC
SJHQ	SJLGG034	chr6	49373831	21	51	0	46	A	G	ATTCTGTGCCTCAGGATGTG[A/G]CAATGCTTATAAATCCCACA
SJHQ	SJLGG034	chr6	54783905	30	59	0	34	A	G	ACTGAGGAAGTTAGAACATG[A/G]AAGATTATTGAATTGTTGAA
SJHQ	SJLGG034	chr6	6197078	30	55	0	42	C	T	GATGATCTATAATTATTTTT[C/T]GAGTTCTCTATTTTCTCTCC
SJHQ	SJLGG034	chr6	66289314	29	69	0	37	G	A	TGGAAATATATATCAGAGAC[G/A]GCAAAGGTCTTTGTGTATTA
SJHQ	SJLGG034	chr6	76498128	13	40	0	35	C	T	ACGTTCTAGCATCATCTTTC[C/T]CTGAGCTTCTTCTGCCTCAG
SJHQ	SJLGG034	chr6	80803843	23	58	0	30	T	G	ATTGATTTAGAAAATTTAAA[T/G]TGCAACTTTTCTTAAATATG
SJHQ	SJLGG034	chr6	82515201	27	61	0	48	G	A	GATTGATATTATTTCCTTTG[G/A]GAACTCTCTGGAGGAGGTTA
SJHQ	SJLGG034	chr6	82977893	14	41	0	29	A	G	GCTCTATCTGCACGACATTG[A/G]CAAGAGCAGAGGCCAAACGT
SJHQ	SJLGG034	chr6	84976368	11	48	0	39	A	G	TTTTTTTTTTTAAACAAAGG[A/G]AAGAACAATCGCATTTCTTT
SJHQ	SJLGG034	chr7	115571219	22	59	0	42	T	C	CTTTACGTATAATTCCAATA[T/C]GCATTTAGGCTTATCTATGT
SJHQ	SJLGG034	chr7	132037403	23	45	0	23	G	A	TTCACACACTATGGGGAAGC[G/A]AACACTCTCCGGGCTGGTGG
SJHQ	SJLGG034	chr7	147792092	23	57	0	30	G	A	TAAGAGGCAGTGGAACCAAT[G/A]AAATGATGAACCGAGAGTAA
SJHQ	SJLGG034	chr7	23514928	22	65	0	47	A	G	TCTTTGGTGAGTTTGTAATT[A/G]TATAAATAAATTGCTGTTGG
SJHQ	SJLGG034	chr7	3964205	24	45	0	27	G	A	ATTCTGTTTGGGTCTCGTAC[G/A]TTATCATCTGTTACCAGTGA
SJHQ	SJLGG034	chr7	40356070	14	43	1	47	C	T	TGAGGATAAAGGCCAGACCA[C/T]GGTTCCATCTGCTTGGTCAA
SJHQ	SJLGG034	chr7	48695053	20	42	0	35	C	T	ATCCCACTAATCCTAATCAC[C/T]CAGCTAATCCCTTTGAGAAG
SJHQ	SJLGG034	chr7	69273668	15	49	0	30	C	T	AGCCTGTGGTATCTGACCAG[C/T]TGCTCTCAGTGCATATAGCC
SJHQ	SJLGG034	chr7	7707062	27	63	0	28	C	A	ACCGCATACTAGGCTTGGGG[C/A]AGCAGGATTATACAGGTCCC
SJHQ	SJLGG034	chr7	88698489	16	46	0	31	T	A	GCTTTATGAAAGAAGAAAAC[T/A]TGTAAGGCCTACCTGTCATA
SJHQ	SJLGG034	chr8	100664002	25	55	0	45	C	T	CTCAAAAAGTCATTTTTCTT[C/T]TTGTTTGTTTGGGGCTTTTT
SJHQ	SJLGG034	chr8	110116870	9	62	0	32	C	T	AAAACCCCTGAAGAACAGGA[C/T]ATTTTCCCATCAGTAGCAGA
SJHQ	SJLGG034	chr8	12959057	20	54	0	34	A	G	TCTCTAGACACTAAAAATGT[A/G]TAAGGTCTCCCACTGGAGTA
SJHQ	SJLGG034	chr8	134045763	17	39	0	27	T	C	CAAGTCTGCATTCCTCAGGG[T/C]GAACTCCTGACCTCAGGAAT
SJHQ	SJLGG034	chr8	138667185	23	54	0	24	G	A	TATGAAAAAGGTGTTGTGAA[G/A]GATAGTTACAATTATAAGAG
SJHQ	SJLGG034	chr8	140767348	5	22	0	23	G	T	AGAGGTCGTTGTAATTGGGG[G/T]AGCCATGAGCTCCGAGCCTC
SJHQ	SJLGG034	chr8	145584998	20	42	0	37	C	T	TCCCTGAACTAGAGCCATGG[C/T]CTGGCCTGTTTAACAGGCTG

SJHQ	SJLGG034	chr8	32768057	24	66	0	45	T	A	CATCTATTTAATAAGTTCCT[T/A]AAGGTCAGCAATTATATAAT
SJHQ	SJLGG034	chr8	3844931	22	44	0	38	G	T	TAACGACTAATGGATACAGG[G/T]GTTGTCTGTCTCCGTTCCTG
SJHQ	SJLGG034	chr8	40869078	26	61	0	32	T	C	TTTTCAGATATTCAGATATA[T/C]ATCTCATATGTATATTTCCT
SJHQ	SJLGG034	chr8	5777770	32	76	0	35	G	A	TCACCTGGGCACTAGCCCGG[G/A]TCTACTTTTGCTTGAGTATT
SJHQ	SJLGG034	chr8	61292204	21	44	0	38	C	T	TTGTTAACTATTTTGGCAGA[C/T]GGGAATGTTTCTTTGGTGAC
SJHQ	SJLGG034	chr9	104866271	13	53	0	34	C	T	TTAACAAAGCACCCCTCTCA[C/T]GTATACACTTAATTTAAAAA
SJHQ	SJLGG034	chr9	1687870	24	62	0	30	A	G	TGGCTTTGACACTTCACTAC[A/G]TCTGTATTCCCCAGTCCTTG
SJHQ	SJLGG034	chr9	24220675	22	47	0	27	C	A	CATGGCTCCTGCCGTTAGTA[C/A]TCATGGCTCTAATGACTGAA
SJHQ	SJLGG034	chr9	25814872	16	47	0	35	G	A	GCCTGAACAAATTAATAATC[G/A]CAAGACAGAATTCTGACCTT
SJHQ	SJLGG034	chr9	84313777	15	53	0	45	G	A	GCTCATGCAGAATCATAAGG[G/A]CATGTATTCATGATGTGCTA
SJHQ	SJLGG034	chr9	92242817	22	51	0	26	T	G	GTCACTTGAATATTGGGCTA[T/G]TCTGAGAACAACCCAGTGGA
SJHQ	SJLGG034	chrX	130171425	19	22	0	16	G	A	CATATTAATACCAGTGCTTC[G/A]TTTTTCATGCATTTAGCCTC
SJHQ	SJLGG034	chrX	65523423	18	22	0	19	G	T	CTGAGCAACAGAAAATCTTG[G/T]GGGTAAATTTCCCCTAAGGA
SJHQ	SJLGG034	chrY	18835347	19	29	0	31	T	A	TAATCAGCACTTTGGTCAAC[T/A]CAGAATCTCAACAAGAATAA
SJHQ	SJLGG034	chrY	18926409	21	25	0	24	T	C	CCTTTGAGCAAGCTTATTTG[T/C]GCCACATCCAATTATACCTT
SJHQ	SJLGG034	chrY	18958667	31	36	0	23	A	G	ACTGTAATTCAGAGCCTTCA[A/G]ATTCCCAGTTCACAATATGT
SJHQ	SJLGG035	chr10	126355625	10	26	0	22	G	A	CCCCCCACACTCTTATACCC[G/A]TACCCCAAAGCCCCACTCAG
SJHQ	SJLGG035	chr10	135070947	16	53	0	27	C	T	CCTCATCCTGCAGGTTTCCT[C/T]CCGAGTCCTGGAATTCTAAA
SJHQ	SJLGG035	chr12	111141812	16	41	0	27	T	C	TTTTTCTCTTTTTTAAAATG[T/C]ATTGTTTCTCTTATTAAAAA
SJHQ	SJLGG035	chr12	7059502	12	45	0	25	T	G	TGTATCCCCTGTTGAGCTGC[T/G]TTTCCTCGTTTTGGTTTGGC
SJHQ	SJLGG035	chr14	87176938	15	55	0	42	T	C	CATTCGCAAAAACAGAGCAT[T/C]TGGGATTAGCATCAGTCAGA
SJHQ	SJLGG035	chr16	26201280	11	41	0	29	G	A	CCCCCCATGGCCCCTGCCCT[G/A]GTAAAGACCATCTGACGTCC
SJHQ	SJLGG035	chr16	74720491	18	51	0	33	C	A	ACTACGTCTCCACACACACA[C/A]AAAAAAAGATATTTATTAAG
SJHQ	SJLGG035	chr17	72801377	16	42	0	14	G	A	GCAGCTGTCAAGGGCTTCCC[G/A]TGCCTGCCTTTTGCAGGGAA
SJHQ	SJLGG035	chr19	9318397	17	44	0	30	C	T	TTGTCTTTCTGTTCCCTTCC[C/T]GCCTTTCTCTACTCAGCTCT
SJHQ	SJLGG035	chr2	134337633	11	42	0	31	A	C	ACCAGTGGCCCGTCATTAGC[A/C]CATCAATCCAAAGGTACAGG
SJHQ	SJLGG035	chr2	41562399	16	57	0	34	C	T	ACAAAACTATGGGGAAGGAA[C/T]GCCTGTGAAACAGAAAATAG
SJHQ	SJLGG035	chr3	185773979	12	54	0	34	C	T	GTGTATTTCTGTTCTGGGCA[C/T]AAAAACAGTAACAGTGTTTT
SJHQ	SJLGG035	chr3	27531481	16	26	0	26	G	A	CCGGGAGTATACCAGCCTAG[G/A]TATTTTGTTGTCTCCACTGA
SJHQ	SJLGG035	chr4	75217404	7	57	0	39	G	T	CATTCTGACGAACTGATAAA[G/T]TCTAATTTTCCTTTCGACTA
SJHQ	SJLGG035	chr5	21048860	10	76	0	42	A	G	TGCATTTTATAATCCTCTTA[A/G]GATCATTTAATTCCTTTCTT
SJHQ	SJLGG035	chr6	147961143	16	37	0	34	C	T	GAATTGTTCAGCTGCCGTCA[C/T]ACACATTATGGCTAAAAAGC
SJHQ	SJLGG035	chr7	40942299	20	63	0	39	T	A	ATAATGTTAAAATCTTAATA[T/A]AAATGAAATCATATTTTCAA
SJHQ	SJLGG035	chr7	53427495	6	37	0	30	G	A	ATTCACAGGGCTGTGTTCTC[G/A]AGGTTCTGCAGGATGAGTCC
SJHQ	SJLGG035	chr8	142630783	10	37	0	20	G	A	TGGGGCTCACTCCAGGAACT[G/A]TTTTCCTATCTGGGAAGTGA
SJHQ	SJLGG035	chrX	122360131	23	66	0	55	A	G	GAGGATATGGGTTTATCTAA[A/G]ACTCCACTACCCACATAAAA
SJHQ	SJLGG035	chrX	129802776	17	56	0	44	G	C	CACTTTATTACTTAGATATA[G/C]ACTTTATGTTGATGCTCAGT
SJHQ	SJLGG037	chr1	101641318	23	85	0	49	C	A	AGTTCTGATTTTGTAATTTT[C/A]ATTTCAATGAGCATGAAAAC
SJHQ	SJLGG037	chr12	75554929	13	80	0	44	C	T	TTAATGGAGGTTTAGATATC[C/T]TAATATAAAAACTCAGGAGT
SJHQ	SJLGG037	chr15	58756362	6	57	0	42	C	T	TGTCACCCTCCCAACCCCCT[C/T]TATACTTGCCCCTTTCTATC
SJHQ	SJLGG037	chr15	98507333	10	53	0	45	C	T	TGTGTCACTTTTTTATCCCC[C/T]TTGATGTTAACACATTAAAA
SJHQ	SJLGG037	chr16	4066623	8	79	0	42	T	A	GAGAAAGGAAAAACTAAATT[T/A]AAAATCTGAGACTAGGTAGC
SJHQ	SJLGG037	chr16	87716836	7	36	0	28	C	T	ACAGCACAGCGGGCCGGCAC[C/T]GCCGGGGTGGGTTGTCTGGG
SJHQ	SJLGG037	chr21	21026714	11	66	0	31	T	A	GGCTTTTGAAGCAAAGCTAA[T/A]TTCTCACACGTTCCTCTCCT
SJHQ	SJLGG037	chr2	125673992	12	93	0	43	T	C	AAAGGCTATATAAATCAGCC[T/C]TTTGCTTGGCTATATATTCC
SJHQ	SJLGG037	chr2	12865775	15	46	0	34	C	T	GAAGTTACGTTTGACTTTCG[C/T]GAAAGAGCATGACCCTGTCC
SJHQ	SJLGG037	chr21	29236729	8	58	0	40	C	A	TGCACAAGCTTTTCTCTGCC[C/A]AACTCCTCTTTGTCCACAAC
SJHQ	SJLGG037	chr2	189368800	7	63	0	40	C	T	TTCAGTACTACAGAGTATCT[C/T]AAAAGTAATGCTAAAAATGA
SJHQ	SJLGG037	chr2	89101618	11	53	0	40	G	A	TAGCTATCTGTGATTTATTA[G/A]TTTGACACTGGATCCCCGTT
SJHQ	SJLGG037	chr3	14405386	11	43	0	28	G	A	GAACCTCTAAACCTTGCCCC[G/A]CTCAAGGATGGAGTGACCAT
SJHQ	SJLGG037	chr3	166362074	22	68	0	41	A	C	TCAATTAGTAAATCCATGCT[A/C]ATGTGGATACTAAGTTGTTT
SJHQ	SJLGG037	chr3	88038496	8	56	0	40	C	A	TGAGTGCCATTAGGGGCTGT[C/A]CTTACTAGTAAGTTTCTTTG
SJHQ	SJLGG037	chr5	162111858	8	66	0	56	G	A	CCAGTGGTAATGAGAAATCC[G/A]CTCCAGAGAATTGACAGAGT
SJHQ	SJLGG037	chr6	6057115	10	55	0	40	G	A	ACTGACATTTTTAGTGCTAC[G/A]CGGAGAGGACTCTTACAGTG
SJHQ	SJLGG037	chr8	106185813	22	68	0	52	T	C	AATCAGAATTTTTAAAATTC[T/C]ATATATTTATGTAGGTTTTT
SJHQ	SJLGG037	chr8	2610004	8	69	0	49	A	G	ATTAAGTCTTTACATATGTG[A/G]GCATATAACATGTGAAATTT
SJHQ	SJLGG037	chr8	85047552	7	68	0	59	T	C	ATCAATTAGTCAATCAACAA[T/C]AATATTTAGTAGTATCTTAT
SJHQ	SJLGG037	chr9	113460856	8	72	0	50	T	A	GATTATTTTTATTTCCTTGA[T/A]GGACATTCCTGTCACAGCTT
SJHQ	SJLGG037	chr9	75436917	20	71	0	37	G	A	TATCATTCAAGTCAGGAATC[G/A]AGAGTCACAACGGCTCCTTG
SJHQ	SJLGG038	chr10	133580610	11	41	0	34	C	T	TGATGTGGAGGACAGGGCTG[C/T]GGCCGCCTGGCCCACTGCTG
SJHQ	SJLGG038	chr10	61803919	12	57	0	37	G	T	AAGTAATGGTGAAAAGTAGA[G/T]ATTTTTCTGTTTTAGGAGAT
SJHQ	SJLGG038	chr10	8242224	12	36	0	40	T	G	CTCATAATTACAGAACTATG[T/G]GGTAAGGACTGCAGTGAATA
SJHQ	SJLGG038	chr11	128578045	9	67	0	47	C	T	TGCCTTGGTTTCCCCATTGC[C/T]GTGCATGGGGGAGGAAGCTT
SJHQ	SJLGG038	chr11	60849244	9	44	0	28	C	T	CAGCCCTTGTCCCCAGCATG[C/T]AGCCTCCCTCTTTGGGATCC
SJHQ	SJLGG038	chr1	196201128	10	55	0	49	G	A	ACTAATTAAAAAGTGAGAAC[G/A]CTAATAAAGTTTGCACTTTT
SJHQ	SJLGG038	chr1	196676908	15	70	0	53	A	T	AGATAAGTAACTTTAATGAA[A/T]TTAGACAAAACATATGTCTT
SJHQ	SJLGG038	chr12	131028515	12	67	0	44	C	G	TAGGATTGTCACCGTTTTAA[C/G]CTGTTTTTGTTTTCCTATGC
SJHQ	SJLGG038	chr12	71398505	10	49	0	34	G	A	CACACCTGCCCAATTCTCTC[G/A]CTCCAACTTGTATTCACTCT
SJHQ	SJLGG038	chr12	99435150	9	72	0	44	A	G	AGACAGATACTTTGCAATTT[A/G]ATTTTCTAAAATAGCTGAGT
SJHQ	SJLGG038	chr13	86644145	25	87	0	43	G	A	TTGTGAAATAAGGAAAAGTA[G/A]ATTTATCTTTCATGAATGCC
SJHQ	SJLGG038	chr14	89966112	18	64	0	32	C	A	TCTAGTCAGACTAAAGTGTG[C/A]AAACTGCTTCTCACATGTTC
SJHQ	SJLGG038	chr17	26630144	20	76	0	47	C	T	ATACATATATTTATGTATTT[C/T]GGAAGTAAATTTTCATTAGA
SJHQ	SJLGG038	chr17	51547546	14	57	0	42	C	T	CTAACCTTGATAGTGCCTTG[C/T]CTTCCCCTTATGTTATGCTG
SJHQ	SJLGG038	chr19	4695797	9	33	0	37	C	T	ATTTCATGATCCAAGTGTTC[C/T]GGAAACAATGGCCTAAGTCT

SJHQ	SJLGG038	chr20	14511379	15	58	0	41	C	T	TTCCAAGATGATTAAGAGCG[C/T]GGAAAAATAATTTATCTTAA
SJHQ	SJLGG038	chr20	34102329	6	23	0	19	C	T	TTCCGGGGAGTGCTGAGGTC[C/T]GGCGGGTGCTGCCCCTGTTC
SJHQ	SJLGG038	chr21	29699110	14	60	0	49	G	A	AGCTGCTCACTTTAATTCTG[G/A]ATGTTCGACTAGTAAAAAAG
SJHQ	SJLGG038	chr2	156029748	20	55	0	35	G	T	AAAATCTTAAACTAGAGGTT[G/T]AATAAAGAGAACAGATTTTC
SJHQ	SJLGG038	chr2	168243208	13	66	0	37	T	G	TACAGTATCAGTGTCTGACA[T/G]GCAAATTCAGCTTTCCAGTC
SJHQ	SJLGG038	chr2	18646851	16	70	0	49	A	G	CTAAATGGCTTGAAAGCTAA[A/G]TACGACTTTTTCTCTAAGCG
SJHQ	SJLGG038	chr2	193537207	16	60	0	36	C	A	ACGGGGCCTCTTGATGACCA[C/A]GAGCTTCCCTTGGTTCCTTG
SJHQ	SJLGG038	chr2	226322081	18	69	0	45	G	T	TTCACCTTCATTGAAGGGCA[G/T]ATTTCACCAGCCCTTCAATG
SJHQ	SJLGG038	chr22	29598485	12	43	0	27	C	T	AGGGGAAGGAGGCTGCCGCC[C/T]AGGTTGTTTGTTAAGAGGAT
SJHQ	SJLGG038	chr2	241838980	11	41	0	23	G	A	TGGTGTGGCCTGAGCAAGTC[G/A]CTGCCCCGCCTGGGCTCCAG
SJHQ	SJLGG038	chr3	1069798	12	57	0	46	C	T	AAACTTCCTTCTGAAATATT[C/T]GGAAGAAAATAAAAAGATAT
SJHQ	SJLGG038	chr3	122385311	14	60	0	30	G	A	TTTGGGGGTAAGAAATGGGG[G/A]TAGTATTTCTAGAGTAGAAG
SJHQ	SJLGG038	chr3	165359624	19	59	0	34	G	A	CTGGCCAAAATATGAATTTC[G/A]TTTCTGTATTGCTATGTTTT
SJHQ	SJLGG038	chr3	33987339	17	63	0	44	C	T	CATCATGCCAAAAAACCCCC[C/T]GATAGCTTCCCACTGATGGA
SJHQ	SJLGG038	chr3	80674377	8	50	0	42	A	T	CACACTTTCCCATAGACATG[A/T]GTACCTGGACAAGAAAAGAC
SJHQ	SJLGG038	chr4	11687404	11	51	0	36	C	G	TGCCTTGACAATGTTCCCAG[C/G]CTCCCCTCTTTGTGTGATGT
SJHQ	SJLGG038	chr4	132293921	9	71	0	38	A	G	GTATTTGGCAATAATAGGAG[A/G]TTGAGCTTCAAATGTGAATT
SJHQ	SJLGG038	chr4	135202394	21	67	0	43	C	T	TAGCAAAAAATCTTTAATGA[C/T]GAGAAATATTTTTCCTACGT
SJHQ	SJLGG038	chr4	136164317	15	71	0	48	G	T	CAACAACTTCTTCAATTTTA[G/T]CTTTATTTTTAGCTCATCAT
SJHQ	SJLGG038	chr4	43759564	19	62	0	50	G	A	AAATCAGGTCATATACTTTC[G/A]GATTTGACTTCTAGGTAAGA
SJHQ	SJLGG038	chr4	64218230	19	74	0	42	C	A	CTGCTCTTCAATGGTATCTT[C/A]ATCACAATCCAAATACACTG
SJHQ	SJLGG038	chr4	90657364	13	70	0	33	C	T	CATGATAAAATTACACTTAA[C/T]GAACCCAACCTCCTTTTCCA
SJHQ	SJLGG038	chr5	165547892	12	49	0	48	G	A	CAACATCCCAATGGCTCTAC[G/A]GTCCCCTCTATGCATGCACT
SJHQ	SJLGG038	chr5	179567231	10	45	0	26	G	A	CCACAGGGATGCCCAGAGAG[G/A]GGCTGGGCTGCCAGTGGTCC
SJHQ	SJLGG038	chr5	4425514	17	64	0	32	G	A	AGAGAAATGGATTGTTAACC[G/A]CAGAAATAAATATATACCTT
SJHQ	SJLGG038	chr5	84111188	19	69	0	43	T	G	TGTGATATGCCTTGTAGAAC[T/G]TTTAACTCAAACTATTTTAT
SJHQ	SJLGG038	chr6	103179966	23	86	0	41	T	G	AAATATTATTTTTGACTTGT[T/G]GCTGTACAGAATACATAGAG
SJHQ	SJLGG038	chr6	107707548	7	45	0	48	G	C	AAGTAACTTCATGTTTATTA[G/C]ATGTAAATAGTTTTACATTG
SJHQ	SJLGG038	chr6	122327469	20	68	0	45	C	T	AAGTAGGGTGCAAGATATTC[C/T]GTTAAGAAGAAAATAAGAGG
SJHQ	SJLGG038	chr6	132966005	13	58	0	42	C	T	AATTTAACTCACCATACATA[C/T]TTTGACTCAAGTAACTGATT
SJHQ	SJLGG038	chr6	72271025	20	65	0	41	C	T	ACTTCCATTTACAATGTATA[C/T]GAAATATAAGAAAGGTAGCA
SJHQ	SJLGG038	chr7	156219508	11	59	0	39	C	T	CTGCCTGTTTCAGGCTGTTA[C/T]GTTTTAATAGTATGATATTT
SJHQ	SJLGG038	chr7	43338444	14	48	0	34	G	A	GTCTGCCGCCCCCACATCTC[G/A]AGGCTCCTTTCACAGCTCTT
SJHQ	SJLGG038	chr7	56850970	9	41	0	30	A	T	CAGCAATAAACTACATTAAA[A/T]CAATATTCAAATATATACAC
SJHQ	SJLGG038	chr8	110374245	14	48	0	37	C	T	GCCCTAAGTCTACTGATTGT[C/T]AATTAAAGAGAGAGCACAAT
SJHQ	SJLGG038	chr8	138463732	19	52	0	42	G	A	TCAGGGTATCTGGCTCATAA[G/A]TTTAACAAATAGCTATCATT
SJHQ	SJLGG038	chr9	125135459	8	30	0	24	G	A	GTAATGTGGAGCAGGAGGCT[G/A]AGGTTGGATGCGTAATGTGG
SJHQ	SJLGG038	chr9	21748890	15	48	0	34	G	A	ACATTATTGGTATCTAATAA[G/A]AACCTATGGTTGGCCCTTTT
SJHQ	SJLGG038	chr9	78650939	16	61	0	35	G	A	AGCTACCAGAAGAGCATGCT[G/A]AAAAAAATAAATAAAACCTC
SJHQ	SJLGG038	chr9	78652700	18	57	0	35	G	T	CGTACGTGGGGAATTGTGGT[G/T]AATTTTCTTGCCTATACAAC
SJHQ	SJLGG038	chr9	78654436	20	75	0	48	G	A	GAAAAATGTGTATGAGGAAG[G/A]GAGGCCCAAGTAACTGCTAG
SJHQ	SJLGG038	chrX	132404386	17	51	0	33	G	T	ACAGGGCTTTAGCACTGGAT[G/T]CTTATGAACGTAGTGCCGTC
SJHQ	SJLGG038	chrX	33655031	16	60	0	30	T	G	AGCAACTATTTTATTAGGGC[T/G]CAATTTATTATATCGACTCA
SJHQ	SJLGG038	chrX	73968012	26	70	0	44	T	A	ATGTATAATTAATTACCTCA[T/A]AAGTTTGGTTCTATTAGAGT
SJHQ	SJLGG039	chr1	119495660	9	49	0	33	C	T	ATGTTTTTTAAATGTATAAA[C/T]CCAATACTGACATTTTTCCA
SJHQ	SJLGG039	chr1	151656648	13	72	0	43	A	G	CTGCAGTTGCTTAAACATTT[A/G]TGCTCCGTAGTGCTCTTGGT
SJHQ	SJLGG039	chr12	6899842	10	68	0	32	C	T	CTGTGCCATCTCAGCCTTTC[C/T]GCCCTCAGACCTTTCCAGCC
SJHQ	SJLGG039	chr4	10318600	9	56	0	37	G	A	ATTCTTTTTGTACTGCAGAC[G/A]TGTACCTTGGTGCTTGAGGC
SJHQ	SJLGG039	chr4	104427776	8	70	0	35	T	C	TTTGGACAATATTAAACATT[T/C]TTATTTTATGTTGCATACTA
SJHQ	SJLGG039	chr4	11223914	6	58	0	44	G	A	GGATCCTGAGAATGTGACTC[G/A]TTGTATTGGAAGGACAAATG
SJHQ	SJLGG039	chr5	5107350	11	51	0	46	G	A	GTTTGTTCTCCAAACCTGGA[G/A]AGTCAGACCACTCACTTTAT
SJHQ	SJLGG039	chr5	62731609	6	55	0	47	C	T	AATGCACGTTGAATCAAGTC[C/T]GAAAGGAAATTTCAGGAAGT
SJHQ	SJLGG039	chrX	100805662	4	28	0	31	G	A	AGGTTTGTGTGTGGATGGGC[G/A]TTGCCAGGGGATCCCTGCGG
SJHQ	SJLGG039	chrX	30426660	5	39	0	40	A	G	ATAGAGAGAGAGAAAGAAAG[A/G]AAAGAGAAAAAGTAGATTAC
SJHQ	SJLGG039	chrX	32287709	8	59	0	39	G	A	AGGAGAGAGAGTTATTCAAC[G/A]AATTATTATATACCGACTAT
SJHQ	SJLGG040	chr10	44563720	25	58	0	27	G	A	CAAACCCAGGATTGCCTAAA[G/A]TTTCTGGCTCTGTGGGGCCT
SJHQ	SJLGG040	chr1	105830315	15	61	0	28	G	A	TAGTCAGAACAGGGTGTTTC[G/A]TGCCCTTCCACCATGGTTTG
SJHQ	SJLGG040	chr11	88686144	6	59	0	51	C	T	TGGATAATGGAGGATTTTCC[C/T]CTCTCTTTTCTAAACTTTCT
SJHQ	SJLGG040	chr1	192503596	11	83	0	51	G	A	TAAATGTAAAGAAAATATCC[G/A]TCTATAAAATCTATGATATC
SJHQ	SJLGG040	chr1	197739180	34	87	0	47	G	A	TATTATAGTTACTGATTATA[G/A]TTATTACTTGTTAGATCCTA
SJHQ	SJLGG040	chr12	126893017	18	56	0	49	C	T	TGTACCAGCATCTTCCTGGA[C/T]GAGCAGGAACTCACAAAATG
SJHQ	SJLGG040	chr12	130658850	30	74	0	40	C	T	ATGTCTTCTTAGCATGACAT[C/T]AAAGCTAAAGCCATTTTTTA
SJHQ	SJLGG040	chr1	238524421	6	56	0	47	A	G	ATATAGACACTCTCATTTAT[A/G]TGTGTGTATATATATATATA
SJHQ	SJLGG040	chr12	83967852	14	51	0	37	G	A	GAACGTGGTAAGGAGGTCAA[G/A]ATTATTTTCAATGGGTTCTA
SJHQ	SJLGG040	chr13	77082735	22	77	0	39	C	T	TTGCTTAATAAATGATTATT[C/T]GTAAGACTGTTCTGAATGGT
SJHQ	SJLGG040	chr15	32081437	26	57	0	30	C	T	TTCCTCATGCAGGGTAGAAA[C/T]CAGGAGAAACTGCTGGGCCT
SJHQ	SJLGG040	chr15	92915958	14	47	0	33	C	T	CTCTGCAAAGGTAGCCCTTC[C/T]GTTTGGATCTTACTTACCTC
SJHQ	SJLGG040	chr16	56360687	17	38	0	33	G	A	CAGAGGCAGGAGGGCGGCCC[G/A]GGGCAGCACCTGCTCTGCTC
SJHQ	SJLGG040	chr1	70312130	14	64	0	38	A	T	CTGATGATTAGTTTACCAAA[A/T]GATAAAAACTGCCTGCAGTA
SJHQ	SJLGG040	chr20	49975230	20	53	0	36	G	A	GTGTCTAGAAAGGAAGATGC[G/A]GAGGAAAGGGCCATGGCAGT
SJHQ	SJLGG040	chr2	242153017	18	43	0	46	C	T	GCCCTCAAAACTGTTCCCGA[C/T]GCACAGCCCCTCCTGGGTGA
SJHQ	SJLGG040	chr2	34582155	25	60	0	38	G	C	GGTAGCACGCTATCACCAAA[G/C]CATCAACCTGCTTTGGTCAT
SJHQ	SJLGG040	chr2	37996416	11	74	0	51	A	G	GAAACAGCCATTTTGTTTTT[A/G]AAAGATCTGGTCATTGACAG
SJHQ	SJLGG040	chr3	102950785	20	65	0	47	A	T	TCACATTTCAGCTGTTTAAC[A/T]TTTGGGGCCAGTTAAACTAT

SJHQ	SJLGG040	chr3	145619521	25	62	0	44	T	C	GATCTGAAACGAGTTTGCAT[T/C]CTAAAACCAAACTGAATCTG
SJHQ	SJLGG040	chr3	175768035	19	71	0	33	T	C	ACAAACATGGGGAGGAGTTA[T/C]TGATATAGTGACAAAGTCTG
SJHQ	SJLGG040	chr3	94868255	27	93	0	37	T	C	AAATAGTCATAAAGGACTTG[T/C]GAAGAGCAATAAATCAAACA
SJHQ	SJLGG040	chr4	168514790	16	72	0	47	G	T	GTTTAAAATTTTGCAGAGAG[G/T]GGTATCATGTCTGAATGCAT
SJHQ	SJLGG040	chr4	179087123	16	67	0	45	C	T	ATTATGCAGGGTCAGGAAAA[C/T]GTTAAAAACGTTGAACACCT
SJHQ	SJLGG040	chr4	64650230	7	69	0	54	A	T	CTTTTATCTGAAAAAAATAA[A/T]GATTCCAAACTATTTTTAAT
SJHQ	SJLGG040	chr4	68933455	7	55	0	40	G	C	ATAATCACCTTAGTATCTTG[G/C]AACCATCTGGGATGTTACCC
SJHQ	SJLGG040	chr4	70095803	41	98	0	52	A	T	ACATGATATATCATAGTTAT[A/T]TTTCTATATTTACTTTAAAA
SJHQ	SJLGG040	chr4	74174126	26	70	0	52	G	C	ACTGAGTCAGTTTAGTGCTA[G/C]TCTGCACCTCCCTCTAGAGT
SJHQ	SJLGG040	chr4	97583115	34	91	0	61	C	T	ACCCCAAACTAATAAGGTAG[C/T]GTTAACTATGAGAGAGAAAA
SJHQ	SJLGG040	chr5	104517311	21	67	0	57	A	T	GCTAAGTATACATCCTGAAA[A/T]TAAAAAAAAAATGTTAAAGT
SJHQ	SJLGG040	chr5	117747223	7	63	0	48	A	C	ACTTTAATCTGTCACCCCCC[A/C]AAAAAAGAAAAATTAGACCA
SJHQ	SJLGG040	chr5	119815799	16	67	0	43	C	A	ATTGTATGCCCTTGGGGAAA[C/A]TAACATTTGTTAAAATACAG
SJHQ	SJLGG040	chr5	25683735	12	44	0	31	C	A	GCCTCCCTTAGGAAAACATG[C/A]CACATTTCAATCGCTGGAAG
SJHQ	SJLGG040	chr6	108072126	23	56	0	49	C	T	CTCATCTATATCTTCACTTT[C/T]GTCCTGGATTTTTAGGATAG
SJHQ	SJLGG040	chr6	146313258	25	72	0	46	C	T	AGCCGTTCTCCCTGAAAAAA[C/T]GTGTATCTTTTGACTAACTC
SJHQ	SJLGG040	chr6	154941774	14	73	0	61	T	C	TTATTCAATAATACTGTTCA[T/C]ACCCTACTTCAAGTAATTCT
SJHQ	SJLGG040	chr6	42335005	9	46	0	35	G	C	ACTCTTACTAACAGAAACAA[G/C]CACAGAGGCCACAGAGCATT
SJHQ	SJLGG040	chr7	23810158	24	79	0	44	T	G	ATTTAGCATATTAGTATCCC[T/G]GATTTCCATTAATGCTCTTA
SJHQ	SJLGG040	chr7	81497723	16	73	0	47	C	T	TTCAAAGTTTTTCCAATGGA[C/T]GTACACATGTGTTACTTTTA
SJHQ	SJLGG040	chr8	22578397	16	51	0	43	G	A	TCACATGGTGACTTCTTACA[G/A]CACCCAAAACAGCGCCAAGT
SJHQ	SJLGG040	chr8	60013695	24	56	0	37	T	C	TGCACAAGTGAATGCAGGGG[T/C]ATTCAGAGCTCAATAGTAAT
SJHQ	SJLGG040	chr8	71155661	31	78	0	47	C	T	TTACTGAGGCTGGATTCCAA[C/T]GCCAGTTATAAGTTAACTTA
SJHQ	SJLGG040	chr8	74797388	12	66	0	46	A	G	CCACATTGACGAGAAGCGAT[A/G]TCTAGTTTTCCTTCCTCATT
SJHQ	SJLGG040	chr8	85214876	22	65	0	48	C	T	AGTCAGTGGAAAGCCATTTA[C/T]GGGTTATATGTAGTAGGCAG
SJHQ	SJLGG040	chr9	131719657	8	55	0	49	T	C	TATGCATATAAGCTGAGATC[T/C]GTCTTCATACTTGGAGGAGT
SJHQ	SJLGG040	chr9	22861253	11	60	0	44	G	C	TAAAAGACAGTCTAAAAAAG[G/C]GGTCCTAGAGAATGATAAAA
SJHQ	SJLGG040	chrX	121701587	14	54	0	30	A	C	TTTAAAATTCCCACATTTTG[A/C]CTCTTGCTCTATAGCAGTTT
SJHQ	SJLGG040	chrX	132669214	15	42	0	38	G	A	TCACCTGAGGCCAAGAGTGA[G/A]AGTTGCTCCCTATAAATCAT
SJHQ	SJLGG042	chr10	63452751	11	60	0	49	A	G	ATCAAGAAAAAATTTCAGAA[A/G]GAACTCCCTTTTCCTTTGTT
SJHQ	SJLGG042	chr10	87795777	15	31	0	30	C	T	GCAGGGCTGTGAGGGCACAT[C/T]GCCAAATGCATTACAATCAG
SJHQ	SJLGG042	chr11	117485046	9	30	0	33	C	T	AGCCCTATGTAGGTAGAGTG[C/T]TATATACACCACTGGTTCTT
SJHQ	SJLGG042	chr11	131493877	12	37	0	22	G	A	CAAAGGCAGTTGCTCTGACC[G/A]AGGTCACTAAAGGCTCTTAA
SJHQ	SJLGG042	chr11	134501022	12	36	0	23	A	G	CGCTTTGCTGGGTGCTCACT[A/G]CCTACGTGCTGAGCACTCTG
SJHQ	SJLGG042	chr1	147017128	4	23	0	30	G	A	CCCAAGTGTGTTACTCACCG[G/A]GGAGCTGCCTCTTGGGGAGG
SJHQ	SJLGG042	chr1	157386814	7	31	0	40	A	G	GCACTTTAGAAGAATTCATG[A/G]GCAGTGCCTGTCAATGGGTA
SJHQ	SJLGG042	chr11	83344623	9	29	0	22	T	C	CCCAACTTGTAAAAAGTCCA[T/C]GGGGGCTGGGAGAGGGAGGA
SJHQ	SJLGG042	chr1	194727884	11	36	0	47	C	A	AAAGTTTAATTCATTACATT[C/A]ACTCCACAGGATCCCTTTTC
SJHQ	SJLGG042	chr12	103358188	11	34	0	33	C	A	AACTAATGACTATATCAATG[C/A]AAGAGATACGTGCTTCTTAA
SJHQ	SJLGG042	chr12	23708942	16	55	0	36	G	A	TATTGAAAGGCTGACATACA[G/A]AGTGATGGATGGTGATGACA
SJHQ	SJLGG042	chr12	24365435	9	27	0	20	G	A	GGAAGCAGTAACACGGGAGG[G/A]GTTACAAGGAAGGAAGGATT
SJHQ	SJLGG042	chr1	237781250	17	35	0	27	C	T	TACCCCCAAAGTCAGGTCTC[C/T]TGAGGGTACAACAGAACAAA
SJHQ	SJLGG042	chr12	5842883	10	28	0	30	C	T	ATAACTAAAACAACTGCAGG[C/T]GGTGCCATTCTATCCTCACC
SJHQ	SJLGG042	chr12	72951774	20	46	0	33	A	G	CACACATACATGCTCTTATT[A/G]CTGCATTTTAAATACATATA
SJHQ	SJLGG042	chr12	90382608	17	45	0	41	C	A	GGCCACAGGGACACAGTAAT[C/A]AGCTCTAATACTTTTCTCTC
SJHQ	SJLGG042	chr12	95930850	19	38	0	44	A	C	AGAGCTCTGGAGAAGGGACG[A/C]GTGATTAAGAGAGACTAGCA
SJHQ	SJLGG042	chr13	50353634	12	44	0	31	T	C	CTCTCCACATCTCACACATC[T/C]CTTATATTTCTTATTCCCTT
SJHQ	SJLGG042	chr13	66663803	17	38	0	37	C	T	TGGTAATTTATCTTAAATAA[C/T]GACTGGCATTTTCCAAATAG
SJHQ	SJLGG042	chr13	69312831	23	55	0	51	A	G	GATTTAGAAAAATAATATAT[A/G]TAATGACCATAACAGTGTTT
SJHQ	SJLGG042	chr13	82697335	5	35	0	57	T	A	ATTGCTATATACATTATTAT[T/A]TTTTGACTCACTATGCTCTA
SJHQ	SJLGG042	chr14	43185055	13	49	0	38	T	C	ATTTATGCCTTGTTGTGTTT[T/C]TATTTATCAAGTTCCCAAGA
SJHQ	SJLGG042	chr14	44106752	11	39	0	48	G	T	GTTACTAGTCTTAAAGAAAG[G/T]TTTGCCCATAATGTATGAAA
SJHQ	SJLGG042	chr15	28088867	14	42	0	29	T	A	ACCAGGTATTACTAGTTTCT[T/A]ACGAACCATGGAAATGGCCA
SJHQ	SJLGG042	chr15	61306999	12	44	0	43	T	C	CAAAGGGGTAGAAAGACAAA[T/C]GGGTGGTCAAAATTAACAGC
SJHQ	SJLGG042	chr15	68998593	17	38	0	22	A	G	CTGCCTCCTCACCGCTTCCA[A/G]CATCCCAACTTGTCTTTTTA
SJHQ	SJLGG042	chr16	34260217	22	60	0	34	C	A	TTACTTCTGTTGGAAATTAA[C/A]GTTGAGCTCTAAAAGTTTTC
SJHQ	SJLGG042	chr16	34473615	20	61	0	46	C	T	GGGCAGGGTGACAGTGAAGG[C/T]AGGAAGATCACATAACAATG
SJHQ	SJLGG042	chr16	34619744	14	44	0	44	T	C	GGGGCACAGAAATCAGATGA[T/C]AGGGGAATCATTTTTTCTAA
SJHQ	SJLGG042	chr16	71008340	16	36	0	26	C	T	AAGAATCCTTTTAGCTGATC[C/T]CAGAGGCACAAAAGCTGCTC
SJHQ	SJLGG042	chr16	7270107	19	47	0	30	A	T	GTGTGTATCAGACCAAACAA[A/T]ATTCACCATATTCAACAATT
SJHQ	SJLGG042	chr17	13109548	20	40	1	47	T	C	CACTCCAATTATCTAGCTTA[T/C]CTTTCATATCTATAAGGAAT
SJHQ	SJLGG042	chr17	39733188	6	30	0	22	G	A	CATGTAGCTGGCTGCTGGGA[G/A]AGGGAGCACCCGCTGAGTCA
SJHQ	SJLGG042	chr1	74441728	4	38	0	46	C	A	TACCTACTTCTAAAAATAAT[C/A]AATTATTTATAATGCCTTGG
SJHQ	SJLGG042	chr1	82642976	17	36	0	53	C	T	TTTCAAGAGGTCAATTTCTA[C/T]CTAACAGGAAGCATTATGGA
SJHQ	SJLGG042	chr18	28225379	20	34	0	35	G	A	TCTTCTATTGTTGATTGTGC[G/A]ATATCAGGTGGTTTAGATGT
SJHQ	SJLGG042	chr18	37724780	25	50	0	37	A	G	TTCATCTACAGAAAAAAAAA[A/G]TCAGTAAAAATATTGCCAGA
SJHQ	SJLGG042	chr18	58143049	21	38	0	39	A	G	ATATTAAGTCAAAAAAGAAA[A/G]TGACATTTAAATTTATTGAT
SJHQ	SJLGG042	chr20	44184061	23	55	0	39	C	T	AAGGGGGCACACCTGGCTTT[C/T]GGGTCACATTGGCCAAGATC
SJHQ	SJLGG042	chr2	115868085	5	43	0	48	T	A	CATTATCTAAATTAAAGGAT[T/A]TAAGTTATTTTACTATAAGT
SJHQ	SJLGG042	chr2	128166491	8	23	0	15	G	C	GTTGGCCCTTAGGCGCTAGG[G/C]CTGAGAAGACTTAGGCGGAC
SJHQ	SJLGG042	chr2	139098547	11	25	0	39	G	T	CAGAGCAGTACAATAAATAG[G/T]TTACTCAAAATAATGGGGTT
SJHQ	SJLGG042	chr2	167758369	21	39	0	45	A	G	TTTTCCTGACTGTTCAGTCT[A/G]TGGCTTTGTGTCTTAAAATA
SJHQ	SJLGG042	chr2	167928226	10	35	0	38	C	T	AAACATGAGAACTATGAAAA[C/T]GGGGAAAGTATTATGGACCC
SJHQ	SJLGG042	chr2	183982465	19	56	0	44	C	T	GTTGATTTTGTATTTATATA[C/T]AAACACTGCATATTGTTGGA

SJHQ	SJLGG042	chr2	189223568	27	56	0	52	C	T	ATAGTCATTAGTTTAATTAA[C/T]GTTATTAACATTGGACATCC
SJHQ	SJLGG042	chr2	27791546	12	26	0	30	G	A	ACGGAAGATACAAAATCTGC[G/A]GAGTTGGCCCCAAAGCCATG
SJHQ	SJLGG042	chr3	103418758	25	50	0	33	A	T	GTAATGCATGAAGGGAAATA[A/T]AATAATCTGTAAACATAATC
SJHQ	SJLGG042	chr4	114129617	8	43	0	45	A	G	ATAGATGGTAATGCAACACT[A/G]TAATATAAAACAGTGCATAA
SJHQ	SJLGG042	chr4	118804695	10	52	0	44	A	G	GTACTAATTTAGAGACACCA[A/G]TAAAGGTAATGATGGCACAA
SJHQ	SJLGG042	chr4	137905203	17	36	0	51	G	A	ATGCTGTAATGTATGTTTGC[G/A]CGAGATTGGAACTCCTTTTT
SJHQ	SJLGG042	chr4	161502284	16	47	0	38	G	A	GTATATGGCCATGTTTTAAA[G/A]CTACTGTTTTAGAGAGAATT
SJHQ	SJLGG042	chr4	163029819	7	39	0	48	T	C	AATGAATAAGAGAAAATTAA[T/C]TTGTATGATGCTATTAAAAT
SJHQ	SJLGG042	chr4	18101297	9	41	0	44	C	T	AATAAAATAGAGCAAGTCAG[C/T]TTTCCAGGATAATCAAGAAG
SJHQ	SJLGG042	chr4	29028281	17	40	0	37	T	G	AAAGTTACATTTGGAGAACC[T/G]TGGAATTTGAGCATTTGACT
SJHQ	SJLGG042	chr4	67001322	23	46	0	47	T	A	AGCATATTTGATGTATGATA[T/A]TTTTTAGCTTCATACCTATT
SJHQ	SJLGG042	chr4	67826777	19	42	0	37	A	G	CTTTGCAAGGTACTTCTTTC[A/G]TACATGCTTTACATGCTTCT
SJHQ	SJLGG042	chr4	70082922	5	37	0	50	G	A	AAATGCCTACTCCTGAACTT[G/A]TTTCACAGATTGTCTTGTAA
SJHQ	SJLGG042	chr4	77232501	18	55	0	44	C	T	GACTGGAGGGAAATTCAGCA[C/T]GCCTGTACTTGAAAATGAAT
SJHQ	SJLGG042	chr5	101915115	20	63	0	46	T	C	TACTACATTTTTCTATGATT[T/C]CTGGATCACTGTTGTTTAAT
SJHQ	SJLGG042	chr5	106338223	18	50	0	36	A	G	TGACATTAGAAAAGTAACTC[A/G]CCTAAGTGAATTTCTTACGT
SJHQ	SJLGG042	chr5	116124258	17	41	0	32	C	G	AGAGTATATTATGTGGAACC[C/G]ATATGTAGTGACCCTGATCT
SJHQ	SJLGG042	chr5	120415161	19	41	0	45	A	T	TCCTTTAGTGACTAGTAAAA[A/T]AATTTCCTTTGAATAAAAGA
SJHQ	SJLGG042	chr5	2418763	13	27	0	15	G	A	CGAGGGCCGCGGCGTCTCCC[G/A]TCCTGCTGGGGAGTTTTAGC
SJHQ	SJLGG042	chr5	49737838	12	54	0	38	C	A	GGAATATTCAGTGCTCTGAA[C/A]CAAATTAAATAAATTAGTGC
SJHQ	SJLGG042	chr5	91631249	21	58	0	56	T	A	ATTATGTATTAAGATAAGAA[T/A]TTTTAGCTTTCTGTTTCTTC
SJHQ	SJLGG042	chr6	104513070	19	48	0	27	C	T	GCAATGTCCATGGTGACATT[C/T]GATATGTCCCAAAATCAGGA
SJHQ	SJLGG042	chr6	123440466	16	49	0	47	T	C	TAGATGTCATTGTGGAGATG[T/C]TTATGGAACTACTTGTATCT
SJHQ	SJLGG042	chr6	124585072	10	69	0	53	A	G	TCTGATGTGCAAACTATGGA[A/G]AATGGCAATTTTGAAGCACC
SJHQ	SJLGG042	chr6	127312317	27	72	0	41	G	A	TAACCCAAAGTACCTTAAAC[G/A]TGGTTTTCTTATACAACTTA
SJHQ	SJLGG042	chr6	129370848	25	60	0	36	A	G	AAAATTAAAAAGAGGCTTAA[A/G]GTCCATACTTAAGACCCAGA
SJHQ	SJLGG042	chr6	140865799	18	55	0	36	T	C	GAGATTCATGACTGATGCGC[T/C]TGAACTTGTCTGATTCAAGA
SJHQ	SJLGG042	chr6	147982623	17	41	0	32	C	T	TCTCTGAAGAAATTGCCAGC[C/T]CCCAAATTATTAGTCACTCT
SJHQ	SJLGG042	chr6	167707048	8	23	0	16	C	T	GCCCCAGCATGCTGAGGAGC[C/T]GAGCCCACCTCTCTCCAAGA
SJHQ	SJLGG042	chr6	39690845	15	33	0	39	A	T	CCCATGTAGATAAGCTCAAC[A/T]GTTTAAGCTAAGAATCTGGG
SJHQ	SJLGG042	chr6	44465356	14	30	0	25	C	T	CAGTGGCAGGTTCCTTACAC[C/T]CAGTGCAAACACCACCAAAA
SJHQ	SJLGG042	chr6	4468155	7	45	0	32	T	A	GAATCAGCAGCTTAGAGATT[T/A]TTATTACCTATTAATAAAAA
SJHQ	SJLGG042	chr6	48829667	8	33	0	48	G	A	ACAGCCCCAGCTGATCACAA[G/A]CTTTATGTTTTTGGGTAACA
SJHQ	SJLGG042	chr6	50654102	20	44	0	31	A	C	TCCCCTGATTCTGGTCACGA[A/C]TTTTATTTGTTCTTTCTTGT
SJHQ	SJLGG042	chr6	62402231	30	61	0	55	T	C	AGAAATGTAATATTTAAATG[T/C]TAATAGTAACCAATTGAAAA
SJHQ	SJLGG042	chr6	62492528	7	26	0	23	G	T	AGCTATTATTGCATAGCAAA[G/T]ACCGTAAAATTTTAATAGCA
SJHQ	SJLGG042	chr6	63352206	17	37	0	41	T	A	GTTCCCACTGTGTCTTTAGA[T/A]CTCTAGTTCTCAGTCTTCTT
SJHQ	SJLGG042	chr6	85687786	12	35	0	27	T	A	TCACTGGAAGCTTCTGATGA[T/A]CTACCCTGTAACTGACTACT
SJHQ	SJLGG042	chr7	105843293	16	43	0	38	C	T	ATCAAACACTATTGTACACC[C/T]AGTATCTGTTCAAAACTGCA
SJHQ	SJLGG042	chr7	122388492	7	43	0	39	T	G	TATTTGCAAGAAACAGTGAC[T/G]TTATGTTTATCACAAAGTAT
SJHQ	SJLGG042	chr7	153602784	24	52	0	43	T	A	GAAACCTGGGTATCTATAAC[T/A]TGTGAAGGCTGAGGAATAGA
SJHQ	SJLGG042	chr7	158778196	17	40	0	34	G	A	TCCCTCTTTTCCTCTGTCTC[G/A]TCCACCTTGGCTGCATGGCC
SJHQ	SJLGG042	chr7	40944926	25	59	0	36	T	C	TAAAACATTCTCTCTTTTGA[T/C]TACAACCTGAAGAATTTATG
SJHQ	SJLGG042	chr7	5667974	17	43	0	26	T	C	TACAATTTTATCATAAATCA[T/C]GAGCCAACTGTCAGTTATAC
SJHQ	SJLGG042	chr7	57574240	19	62	0	38	G	T	AAATTTTCCCTTTAAACTCT[G/T]GAATCTTTTTTAGATAATGT
SJHQ	SJLGG042	chr7	67984440	8	46	0	36	A	G	ATAAGCATTTGGCTTTCTCC[A/G]AGTGGTGTTCCTGGAGCTAC
SJHQ	SJLGG042	chr7	88626387	26	68	0	42	A	T	CATAATGCTTTTAAGGCAAT[A/T]TGTTTAACTGATACACACTT
SJHQ	SJLGG042	chr7	95377491	17	46	0	38	G	A	TCACCCCAAAACTGCCAAGC[G/A]CTCAGCTAGGCATAACATAA
SJHQ	SJLGG042	chr7	97406557	10	37	0	30	G	T	GATGTGGGCAAAATACCATA[G/T]CTAGAAAAGCTATGATTGTC
SJHQ	SJLGG042	chr8	125162648	23	62	0	38	C	T	GAATCAAAATCTCAGTTCAT[C/T]GAGTGAAAAACAGATCAGGA
SJHQ	SJLGG042	chr8	126947124	19	62	0	39	A	T	CTAAAATGTATGTTTTGTAT[A/T]ACCACAACAGAAGGAAGAAT
SJHQ	SJLGG042	chr8	15776815	17	55	0	48	A	G	TAGAAATAAACACTCCCTAG[A/G]AAGGCTACCTAAAACTTATT
SJHQ	SJLGG042	chr8	16135288	28	59	0	46	T	C	ATTTTTCTTTGATTGATTTT[T/C]CTTTTTTTCTGATTTTTTGC
SJHQ	SJLGG042	chr8	21003445	15	46	1	44	G	A	CTTTGATCCTTAAATGATGA[G/A]ATCTCAAAAACTTCTCAAGG
SJHQ	SJLGG042	chr8	61612793	8	60	0	35	G	A	ATACTAAATTAGTACTTGGT[G/A]ATTGCTTGCCTTAGGCTCTT
SJHQ	SJLGG042	chr8	73951541	14	48	0	37	C	G	TTATTTCTGTTCAACCTCCC[C/G]AAAATTTTGAGTGTAAAATA
SJHQ	SJLGG042	chr9	85196455	23	43	0	33	C	A	TTAGGCCTACCCACTAGTGC[C/A]AAAAAGGGGTAGCTGCAGGT
SJHQ	SJLGG042	chr9	87205980	7	44	0	27	T	C	CTTCAAATTGGGAGACTTTG[T/C]TTTCTGTTTTCTTTCTGATG
SJHQ	SJLGG042	chrX	123245177	11	35	0	36	C	T	GCTTTAAAAATGAAAAAAGA[C/T]ATTCACAAGTGATACCTTTG
SJHQ	SJLGG042	chrX	139153660	13	39	0	30	G	A	TTTTTTCTCTGCAGCACATA[G/A]GGGTAGGGTTGGTAGGGGGA
SJHQ	SJLGG042	chrX	26492742	8	41	0	36	C	G	TGGGGGATATGCCCAAAGCA[C/G]TGACAATTCTGTGACTACAT
SJHQ	SJLGG042	chrX	36071021	4	35	0	41	T	C	AGTGCTTTAAAATGTATATT[T/C]AGCATGCCTCTTTCAGATAC
SJHQ	SJLGG042	chrX	72359724	14	34	0	53	G	A	CTGAGTACCCTAGTGCAAAG[G/A]AATCCTCCCTTTTCTAGGAA
SJHQ	SJLGG042	chrX	78469019	16	37	0	32	T	A	TGTGTATGTGTGTCTCTGAG[T/A]GTTAAAATTTTATTTTATTT
SJHQ	SJLGG042	chrX	92593457	12	29	0	43	C	T	TTGTATCTTCATGTGCTCAG[C/T]TTGAGTTAGTTTACCATATC

Supplementary Table 6

Copy number alterations identified in WGS data

Seg_mean is the mean of the difference (adjusted for GC content) between the normalized read depth in paired Diagnosis (D) and Germline (G) samples in each genomic segment. Gene List records the first five and the last five genes in a genomic interval if the total number of genes exceed 10.
Log2Ratio is the mean of the GC-corrected log2 (read depth of normalized D/G) in each genomic segment.

Sample	Chromosome	loc.start	loc.end	seg.mean	Log2Ratio	Size	Gene List
SJLGG001_D	7	138547083	140488022	0.39	0.47	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG002_D	7	138543819	140490296	0.365	0.453	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG002_D	X	124405701	124414900	-0.253	-1.154	CURATED	
SJLGG003_D	10	104547760	104547957	-0.207	-0.535	CURATED_FOCAL	C10orf26
SJLGG003_D	17	62280503	62280668	0.213	0.218	CURATED_FOCAL	TEX2
SJLGG003_D	7	138549568	140489475	0.253	0.314	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG004_D	7	138546757	140487585	0.262	0.331	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG005_D	5	140843463	140857800	-0.157	-0.222	CURATED	PCDHGA1,PCDHGA2,PCDHGA3,PCDHGB1,PCDHGA4,PCDHGA10,PCDHGB7,PCDHGA11,PCDHGA12,PCDHGC3
SJLGG005_D	6	104635199	104664173	-0.155	-0.258	CURATED	
SJLGG005_D	6	138273347	138273507	-0.55	-0.599	CURATED	
SJLGG006_D	8	38271155	38276284	0.198	0.336	CURATED_FOCAL	FGFR1
SJLGG007_D	7	138548949	140490793	0.2	0.272	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG008_D	11	2954001	135006516	0.25	0.31	CURATED	NAP1L4,CARS,OSBPL5,MRGPRG,MRGPRE,THYN1,ACAD8,GLB1L3,GLB1L2,B3GAT1
SJLGG008_D	4	3521101	191154276	0.15	0.175	CURATED	LRPAP1,ADRA2C,OTOP1,TMEM128,LYAR,DUX4L4,DUX4L5,DUX4L6,DUX4L2,DUX4
SJLGG008_D	5	1	180915260	0.149	0.177	CURATED	PLEKHG4B,LRRC14B,CCDC127,SDHA,PDCD6,GNB2L1,TRIM52,OR4F16,OR4F29,OR4F3
SJLGG008_D	6	1	171115067	0.285	0.332	CURATED	GPX5,SCAND3,TRIM27,ZNF311,DUSP22,DLL1,FAM120B,PSMB1,TBP,PDCD2
SJLGG008_D	7	1	159138663	0.275	0.332	CURATED	LOC389831,FAM20C,LOC100288524,PDGFA,PRKAR1B,PTPRN2,NCAPG2,ESYT2,WDR60,VIPR2
SJLGG008_D	8	1	38271148	0.264	0.321	CURATED	OR4F21,ZNF596,FBXO25,C8orf42,ERICH1,DDHD2,PPAPDC1B,WHSC1L1,LETM2,FGFR1
SJLGG008_D	8	38271149	38277105	0.578	0.828	CURATED_FOCAL	FGFR1
SJLGG008_D	8	38277106	146364022	0.269	0.316	CURATED	FGFR1,C8orf86,TACC1,PLEKHA2,HTRA4,ZNF7,COMMD5,ZNF250,ZNF16,C8orf33
SJLGG009_D	11	65285605	65285793	-0.221	-0.358	CURATED	
SJLGG009_D	7	138541101	140489604	0.284	0.359	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG010_D	11	1	135006516	0.362	0.439	CURATED	LOC653486,SCGB1C1,ODF3,BET1L,RIC8A,THYN1,ACAD8,GLB1L3,GLB1L2,B3GAT1
SJLGG010_D	7	138539401	140493100	0.391	0.474	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG011_D	5	1	180915260	0.135	0.171	CURATED	PLEKHG4B,LRRC14B,CCDC127,SDHA,PDCD6,GNB2L1,TRIM52,OR4F16,OR4F29,OR4F3
SJLGG011_D	7	138543701	140488667	0.405	0.485	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG012_D	5	1	180915260	0.303	0.373	CURATED	PLEKHG4B,LRRC14B,CCDC127,SDHA,PDCD6,GNB2L1,TRIM52,OR4F16,OR4F29,OR4F3
SJLGG012_D	7	138552320	140490511	0.28	0.35	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG013_D	7	138550301	140488000	0.163	0.214	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG015_D	10	37491201	37529600	0.141	0.186	CURATED_FOCAL	ANKRD30A
SJLGG015_D	7	138543473	140481674	0.164	0.215	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG016_D	8	67574935	67575315	-0.188	-0.32	CURATED_FOCAL	VCPIP1
SJLGG018_D	6	31922345	31922471	-0.292	-0.508	CURATED_FOCAL	RDBP
SJLGG018_D	8	38271014	38683008	0.382	0.479	CURATED_FOCAL	FGFR1,C8orf86,TACC1
SJLGG018_D	8	38689182	38724513	0.419	0.494	CURATED_FOCAL	TACC1
SJLGG019_D	3	12645604	12685300	-0.142	-0.234	CURATED_FOCAL	RAF1
SJLGG019_D	6	163899501	163940903	0.215	0.271	CURATED_FOCAL	QKI
SJLGG020_D	7	138537132	140494105	0.42	0.501	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG021_D	7	138548153	140490561	0.3	0.373	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG024_D	7	138540541	140491303	0.324	0.411	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG025_D	7	138547246	140493653	0.219	0.284	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG027_D	7	138548658	140488745	0.26	0.342	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG028_D	11	89838401	89883600	0.17	0.203	CURATED_FOCAL	NAALAD2
SJLGG028_D	7	138553001	140493800	0.439	0.537	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG032_D	7	138541228	140492950	0.352	0.436	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG033_D	13	113994377	113994727	-0.149	-0.334	CURATED_FOCAL	GRTP1
SJLGG033_D	8	40079668	40081746	-0.128	-0.202	CURATED	
SJLGG033_D	8	82753337	82753858	-0.151	-0.387	CURATED_FOCAL	SNX16
SJLGG034_D	1	1	121351600	-0.409	-0.787	CURATED	SRSF10,OR4F5,OR4F16,OR4F29,OR4F3,NBPF7,ADAM30,NOTCH2,FAM72B,FCGR1B
SJLGG034_D	19	27890301	59128983	-0.4	-0.819	CURATED	UQCRFS1,VSTM2B,POP4,PLEKHF1,C19orf12,ZBTB45,TRIM28,CHMP2A,UBE2M,MZF1
SJLGG035_D	6	135491705	135495475	-0.297	-0.477	CURATED	
SJLGG035_D	6	135495476	135540964	6.32	2.911	CURATED_FOCAL	MYB
SJLGG035_D	6	135540965	136741488	-0.311	-0.52	CURATED	AHI1,PDE7B,FAM54A,BCLAF1,MAP7
SJLGG035_D	6	136741489	136882616	6.447	2.86	CURATED_FOCAL	MAP7,MAP3K5
SJLGG035_D	6	136882617	136884679	-0.261	-0.431	CURATED_FOCAL	MAP3K5
SJLGG035_D	8	87411636	87411711	0.325	0.33	CURATED_FOCAL	WWP1
SJLGG035_D	8	87411712	88417777	-0.324	-0.53	CURATED_FOCAL	WWP1,FAM82B,CPNE3,CNGB3,CNBD1
SJLGG035_D	8	88417778	89335431	6.861	2.872	CURATED_FOCAL	DCAF4L2,MMP16
SJLGG035_D	8	89335432	91617806	-0.32	-0.522	CURATED	MMP16,RIPK2,OSGIN2,NBN,DECR1,CALB1
SJLGG038_D	12	12018549	12018558	-0.408	-0.488	CURATED_FOCAL	ETV6
SJLGG038_D	13	105810501	105826300	0.19	0.247	CURATED	
SJLGG038_D	7	17355201	17377100	0.211	0.26	CURATED_FOCAL	AHR
SJLGG038_D	9	14731424	21749090	-0.212	-0.342	CURATED	FREM1,TTC39B,SNAPC3,PSIP1,C9orf93,IFNA13,IFNA2,IFNA8,IFNA1,IFNE
SJLGG038_D	9	21749091	22015572	-0.496	-0.968	CURATED_FOCAL	MTAP,CDKN2A,CDKN2B
SJLGG038_D	9	22015573	78518259	-0.182	-0.291	CURATED	DMRTA1,ELAVL2,TUSC1,LOC100506422,C9orf82,C9orf40,C9orf41,C9orf95,OSTF1,PCSK5
SJLGG038_D	9	78559926	78562969	-0.154	-0.255	CURATED_FOCAL	PCSK5
SJLGG038_D	9	78566224	78583404	-0.191	-0.31	CURATED_FOCAL	PCSK5
SJLGG038_D	9	78654643	78663079	-0.161	-0.251	CURATED_FOCAL	PCSK5
SJLGG038_D	9	78666783	78671456	0.359	0.419	CURATED_FOCAL	PCSK5
SJLGG038_D	9	84653505	89337632	-0.21	-0.341	CURATED	RASEF,FRMD3,C9orf103,UBQLN1,GKAP1,NAA35,GOLM1,C9orf153,ISCA1,ZCCHC6
SJLGG038_D	9	89340180	89348567	-0.232	-0.364	CURATED	
SJLGG038_D	9	116237623	125028999	-0.198	-0.329	CURATED	RGS3,ZNF618,AMBP,KIF12,COL27A1,NDUFA8,MORN5,LHX6,RBM18,MRRF
SJLGG039_D	1	1196437	3649437	0.105	0.174	CURATED	UBE2J2,SCNN1D,ACAP3,PUSL1,CPSF3L,ARHGEF16,MEGF6,TPRG1L,WRAP73,TP73
SJLGG039_D	1	9555201	12584120	0.129	0.185	CURATED	SLC25A33,TMEM201,PIK3CD,CLSTN1,CTNNBIP1,MFN2,MIIP,TNFRSF8,TNFRSF1B,VPS13D
SJLGG039_D	10	95588803	98887881	0.139	0.181	CURATED	TMEM20,PLCE1,NOC3L,TBC1D12,HELLS,TM9SF3,PIK3AP1,LCOR,C10orf12,SLIT1
SJLGG039_D	11	66966686	69541460	0.123	0.183	CURATED	KDM2A,ADRBK1,ANKRD13D,SSH3,POLD4,TPCN2,MYEOV,CCND1,ORAOV1,FGF19
SJLGG039_D	11	115411801	118491726	0.133	0.186	CURATED	BUD13,ZNF259,APOA5,APOA4,APOC3,TTC36,TMEM25,IFT46,ARCN1,PHLDB1
SJLGG039_D	12	103110023	106295960	0.135	0.174	CURATED	PAH,ASCL1,C12orf42,STAB2,NT5DC3,C12orf45,ALDH1L2,KIAA1033,APPL2,C12orf75
SJLGG039_D	16	410315	2172065	0.093	0.16	CURATED	MRPL28,TMEM8A,NME4,DECR2,RAB11FIP3,NPW,SLC9A3R2,NTHL1,TSC2,PKD1
SJLGG039_D	22	44632201	47557135	0.127	0.195	CURATED	KIAA1644,LDOC1L,PRR5,PRR5-ARHGAP8,ARHGAP8,TRMU,CELSR1,GRAMD4,CERK,TBC1D22A
SJLGG039_D	3	9662023	12649233	0.136	0.188	CURATED	MTMR14,CPNE9,BRPF1,OGG1,CAMK1,PPARG,TSEN2,LOC100129480,MKRN2,RAF1
SJLGG039_D	3	46001511	49169000	0.13	0.182	CURATED	FYCO1,XCR1,CCR1,CCR3,CCR2,IMPDH2,QRICH1,QARS,USP19,LAMB2
SJLGG039_D	3	183723574	186716600	0.132	0.178	CURATED	ABCC5,HTR3D,HTR3C,HTR3E,EIF2B5,KNG1,EIF4A2,RFC4,ADIPOQ,ST6GAL1
SJLGG039_D	4	1899271	5039610	0.131	0.188	CURATED	WHSC1,WHSC2,C4orf48,NAT8L,POLN,ZBTB49,D4S234E,STX18,MSX1,CYTL1
SJLGG039_D	7	6300098	9539556	0.204	0.255	CURATED	CYTH3,C7orf70,RAC1,DAGLB,KDELR2,MIOS,RPA3,GLCCI1,ICA1,NXPH1
SJLGG040_D	19	50565726	50566416	-0.14	-2.03	CURATED_FOCAL	
SJLGG040_D	6	134735463	135107969	4.623	2.461	CURATED_FOCAL	
SJLGG040_D	6	135420365	135517292	4.571	2.464	CURATED_FOCAL	MYB
SJLGG042_D	1	1	249250621	-0.168	-0.265	CURATED	SRSF10,OR4F5,OR4F16,OR4F29,OR4F3,LOC646627,SH3BP5L,ZNF672,ZNF692,PGBD2
SJLGG042_D	13	1	115169878	-0.175	-0.261	CURATED	TUBA3C,TPTE2,MPHOSPH8,PSPC1,ZMYM5,GAS6,RASA3,CDC16,UPF3A,ZNF828
SJLGG042_D	14	1	107349540	-0.178	-0.282	CURATED	OR11H12,POTEG,POTEM,OR11H2,OR4Q3,MTA1,CRIP2,CRIP1,C14orf80,TMEM121
SJLGG042_D	18	1	78077248	-0.173	-0.268	CURATED	USP14,THOC1,COLEC12,CETN1,CLUL1,HSBP1L1,TXNL4A,RBFA,ADNP2,PARD6G
SJLGG042_D	2	1	243199373	-0.181	-0.29	CURATED	FAM110C,SH3YL1,ACP1,FAM150B,TMEM18,D2HGDH,GAL3ST2,NEU4,PDCD1,C2orf85
SJLGG042_D	21	1	48129895	-0.166	-0.245	CURATED	TPTE,BAGE2,BAGE3,BAGE4,BAGE5,C21orf58,PCNT,DIP2A,S100B,PRMT2
SJLGG042_D	22	1	51304566	-0.124	-0.235	CURATED	POTEH,OR11H1,CCT8L2,XKR3,GAB4,MAPK8IP2,ARSA,SHANK3,ACR,RABL2B
SJLGG042_D	3	1	198022430	-0.174	-0.271	CURATED	CHL1,CNTN6,CNTN4,IL5RA,TRNT1,LRCH3,IQCG,RPL35A,LMLN,FAM157A
SJLGG042_D	4	1	191154276	-0.184	-0.265	CURATED	YTHDC1,ZNF595,ZNF718,MAFIP,TMPRSS11E,DUX4L4,DUX4L5,DUX4L6,DUX4L2,DUX4
SJLGG042_D	7	138540270	140488759	0.405	0.47	CURATED	KIAA1549,ZC3HAV1L,ZC3HAV1,TTC26,UBN2,MKRN1,DENND2A,ADCK2,NDUFB2,BRAF
SJLGG042_D	9	1	141213431	-0.161	-0.257	CURATED	WASH1,FOXD4,CBWD1,C9orf66,DOCK8,ARRDC1,C9orf37,EHMT1,CACNA1B,FAM157B
SJLGG042_D	X	1	155270560	-0.179	-0.273	CURATED	PLCXD1,GTPBP6,PPP2R3B,SHOX,CRLF2,H2AFB2,TMLHE,SPRY3,VAMP7,IL9R

Supplementary Table 7

Structural Variations identified in WGS samples

See glossary of terms below table

Sample	ChrA	PosA	OrientationA	ChrB	PosB	OrientationB	Type	Usage	Gene	Chromosomes	Tx	Valid CDS	In-Frame CDS	Modified In-Frame CDS	mutA	mutB	Validation Status
SJLGG001_D	7	140488023	+	7	138547083	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	10	5	VALID
SJLGG002_D	7	140490297	+	7	138543819	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	10	5	VALID
SJLGG003_D	7	140489476	+	7	138549568	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	5	4	VALID
SJLGG004_D	7	140487586	+	7	138546757	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	2	8	VALID
SJLGG005_D	5	140843463	+	6	104664174	+	CTX	TRUNCATING	PCDHGB1	chr5,chr5,chr5,chr5,chr	20	0	0	0	6	3	VALID
SJLGG005_D	6	104635199	+	6	135517619	+	DEL	TRUNCATING	MYB	chr6	4	0	0	0	3	1	VALID
SJLGG005_D	6	135517564	+	5	140857801	+	CTX	TRUNCATING	MYB	chr6	5	0	0	0	2	1	VALID
SJLGG006_D	8	38276282	+	8	38271155	+	INS	GENIC	FGFR1_FGFR1	chr8,chr8	9	9	9	9	0	4	VALID
SJLGG006_R	8	38276282	+	8	38271155	+	INS	GENIC	FGFR1_FGFR1	chr8,chr8	9	9	9	9	0	4	VALID
SJLGG007_D	7	140490794	+	7	138548949	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	8	3	VALID
SJLGG008_D	8	38277106	+	8	38271149	+	INS	GENIC	FGFR1_FGFR1	chr8,chr8	9	9	0	0	6	4	VALID
SJLGG009_D	7	140489200	+	7	138541101	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	6	1	VALID
SJLGG009_D	7	140489605	+	7	140504330	-	ITX	TRUNCATING	BRAF	chr7	2	0	0	0	3	2	VALID
SJLGG010_D	7	140493176	+	7	138539500	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	3	0	VALID
SJLGG011_D	7	140488668	+	7	138543648	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	6	1	VALID
SJLGG012_D	7	140490512	+	7	138552320	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	6	3	VALID
SJLGG013_D	7	140487437	+	7	138550782	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	10	5	VALID
SJLGG015_D	7	140481674	+	7	138543473	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	6	4	VALID
SJLGG016_D	7	140488340	+	7	138547386	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	1	0	VALID
SJLGG018_D	6	31922345	+	6	31922472	+	DEL	GENIC	RDBP_RDBP	chr6,chr6	1	1	1	1	0	4	PUTATIVE
SJLGG018_D	8	38689182	-	8	38271014	+	ITX	GENIC	FGFR1_TACC1	chr8,chr8	9	9	9	9	6	10	VALID
SJLGG019_D	3	12645604	+	6	163940904	-	CTX	GENIC	QKI_RAF1	chr6,chr3	1	1	1	1	4	2	VALID
SJLGG020_D	7	140494106	+	7	138537132	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	4	10	VALID
SJLGG021_D	7	140490562	+	7	138548153	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	0	3	VALID
SJLGG024_D	7	140491304	+	7	138540541	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	2	4	VALID
SJLGG025_D	7	140493649	+	7	138547246	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	1	6	VALID
SJLGG026_D	3	180685038	+	7	140483012	-	CTX	GENIC	FXR1_BRAF	chr3,chr7	2	2	2	2	3	3	VALID
SJLGG027_D	7	140488746	+	7	138548658	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	1	9	VALID
SJLGG028_D	7	138551226	+	7	140493693	+	INS	GENIC	BRAF_KIAA1549	chr7,chr7	2	2	2	2	3	6	VALID
SJLGG031_D	1	39757516	-	7	140492181	+	CTX	GENIC	BRAF_MACF1	chr7,chr1	1	1	1	1	0	4	VALID
SJLGG031_D	1	39757537	+	7	140492254	-	CTX	GENIC	MACF1_MACF1	chr1,chr1	1	1	1	0	2	1	VALID
SJLGG032_D	7	140492951	+	7	138541228	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	4	7	VALID
SJLGG033_D	8	67490866	+	8	89031536	+	INS	TRUNCATING	MYBL1	chr8	2	0	0	0	3	0	VALID
SJLGG033_D	8	69654188	+	8	67490578	-	INS	GENIC	C8orf34_MYBL1	chr8,chr8	2	2	2	2	8	0	VALID
SJLGG033_D	8	78562383	+	8	89031728	+	DEL	INTERGENIC							5	5	VALID
SJLGG033_D	8	78562409	-	8	82753859	+	ITX	TRUNCATING	SNX16	chr8	1	0	0	0	3	4	VALID
SJLGG033_D	8	82753337	+	8	69654563	+	INS	TRUNCATING	C8orf34	chr8,chr8	4	3	3	0	9	4	VALID
SJLGG035_D	6	135491705	+	6	136884680	+	DEL	TRUNCATING	MAP3K5	chr6	1	0	0	0	7	3	VALID
SJLGG035_D	6	135540965	+	8	89335432	-	CTX	TRUNCATING	MMP16	chr8	1	0	0	0	128	108	VALID
SJLGG035_D	6	136882615	+	6	135495476	+	INS	TRUNCATING	MAP3K5	chr6	1	0	0	0	1	107	VALID
SJLGG035_D	8	88417780	-	6	136741489	+	CTX	TRUNCATING	MAP7	chr6	6	0	0	0	1	147	VALID
SJLGG038_D	9	14731424	+	9	78562970	+	DEL	TRUNCATING	PCSK5	chr9	2	0	0	0	8	3	PUTATIVE
SJLGG038_D	9	21749091	+	9	22015572	+	DEL	TRUNCATING	CDKN2B-AS1	chr9	1	0	0	0	5	0	VALID
SJLGG038_D	9	22024624	+	9	22025145	+	DEL	INTRONIC							4	6	VALID
SJLGG038_D	9	37804215	+	9	37804296	+	DEL	INTRONIC							0	4	PUTATIVE
SJLGG038_D	9	78559926	+	9	78663080	+	DEL	GENIC	PCSK5_PCSK5	chr9,chr9	2	2	0	0	4	3	PUTATIVE
SJLGG038_D	9	78566224	+	9	116237623	-	ITX	TRUNCATING	PCSK5	chr9,chr9	3	0	0	0	8	5	PUTATIVE
SJLGG038_D	9	78654643	+	9	36070277	+	INS	GENIC	PCSK5_RECK	chr9,chr9	1	1	0	0	0	11	PUTATIVE
SJLGG038_D	9	78671457	+	9	89348568	+	DEL	TRUNCATING	PCSK5	chr9	1	0	0	0	5	6	PUTATIVE
SJLGG038_D	9	84653505	+	9	78666783	+	INS	TRUNCATING	PCSK5	chr9	2	0	0	0	7	5	PUTATIVE
SJLGG038_D	9	89337633	-	9	78583405	+	ITX	TRUNCATING	PCSK5	chr9	2	0	0	0	4	3	PUTATIVE
SJLGG038_D	9	89340180	+	9	78518260	+	INS	TRUNCATING	PCSK5	chr9	2	0	0	0	12	1	PUTATIVE
SJLGG038_D	12	12018549	+	15	88646889	-	CTX	GENIC	ETV6_NTRK3	chr12,chr15	3	3	3	3	4	6	VALID
SJLGG038_D	12	12018559	-	15	88646886	+	CTX	GENIC	NTRK3_ETV6	chr15,chr12	1	1	1	1	1	2	VALID
SJLGG039_D	1	3643330	-	11	115411715	+	CTX	TRUNCATING	TP73	chr1	6	0	0	0	0	3	VALID
SJLGG039_D	1	3643581	+	11	69538645	+	CTX	TRUNCATING	TP73	chr1	3	0	0	0	0	5	VALID
SJLGG039_D	1	3649438	+	22	47557135	-	CTX	TRUNCATING	TP73	chr22,chr1	14	2	2	0	4	2	VALID
SJLGG039_D	1	12582471	+	12	103110023	+	CTX	INTERGENIC							1	3	VALID
SJLGG039_D	1	12584121	+	11	118491727	-	CTX	TRUNCATING	PHLDB1	chr11	2	0	0	0	4	5	VALID
SJLGG039_D	3	12649234	+	3	46001511	+	DEL	GENIC	FYCO1_RAF1	chr3,chr3	1	1	1	1	2	3	VALID
SJLGG039_D	3	49168971	+	11	66966686	+	CTX	TRUNCATING	KDM2A	chr11,chr3	3	0	0	0	2	2	VALID
SJLGG039_D	3	186716601	+	4	1899271	+	CTX	GENIC	ST6GAL1_WHSC1	chr3,chr4	3	3	3	0	3	1	VALID
SJLGG039_D	4	5039611	+	3	183723574	+	CTX	TRUNCATING	ABCC5	chr3	1	0	0	0	0	3	VALID
SJLGG039_D	7	9539557	+	7	6300098	+	INS	TRUNCATING	CYTH3	chr7	1	0	0	0	6	4	VALID
SJLGG039_D	10	98887882	+	16	2158836	+	CTX	GENIC	PKD1_SLIT1	chr16,chr10	1	1	0	0	3	0	VALID
SJLGG039_D	11	69540077	+	1	9555182	+	CTX	INTERGENIC							0	2	VALID
SJLGG039_D	11	69541460	+	12	103111315	+	CTX	INTERGENIC							1	3	VALID
SJLGG039_D	12	103110079	-	10	95588803	+	CTX	INTERGENIC							3	3	VALID
SJLGG039_D	12	103112184	+	3	9662023	+	CTX	INTERGENIC							0	3	VALID
SJLGG039_D	12	106295961	+	1	12581667	+	CTX	INTERGENIC							3	2	VALID
SJLGG039_D	16	410315	-	4	5037703	+	CTX	INTERGENIC							1	2	VALID
SJLGG039_D	16	2170637	+	12	103110956	-	CTX	TRUNCATING							2	2	VALID
SJLGG039_D	16	2172065	+	1	1196437	+	CTX	GENIC	UBE2J2_PKD1	chr1,chr16	8	8	0	0	4	2	VALID
SJLGG040_D	6	135107970	+	6	135420365	+	DEL	INTERGENIC							95	94	PUTATIVE
SJLGG040_D	6	135517293	+	6	134735463	+	INS	TRUNCATING	MYB	chr6	5	0	0	0	78	66	VALID
SJLGG042_D	7	140488760	+	7	138540270	+	INS	GENIC	KIAA1549_BRAF	chr7,chr7	1	1	1	1	3	11	VALID

Column Title	Column Definition	
Sample	Sample name	
ChrA	Chromosome for breakpoint A	
PosA	Position of breakpoint A	
OrientationA	+	Region to the left of PosA is included in mutant genotype
	-	Region to the right of PosA is included in mutant genotype
ChrB	Chromosome for breakpoint B	
PosB	Position of breakpoint B	
OrientationB	+	Region to the right of PosA is included in mutant genotype
	-	Region to the left of PosA is included in mutant genotype
	INS	Insertion
	DEL	Deletion

Type	INV	Inversion
	ITX	Intrachromosomal translocation
	CTX	Interchromosomal translocation
Usage	GENIC	Both endpoints were in genes: checked for fusion
	HALF_INTERGENIC	One endpoint was in a gene: checked for truncation
	CO_GENIC	Both endpoints were in genes: checked for and found fusion that involved multiple events
	INTERGENIC / INTRONIC	Neither endpoint was in a gene or both were in the same intron of a gene; no gene fusion or truncation
	INVERTED_REPEAT	Both endpoints were in the same gene, but in opposite orientations: checked for truncation
Gene	Fusion or truncated gene that would result from structural variation	
Chromosomes	Chromosomes involved in the rearrangement	
Tx	Number of predicted fusion transcripts	
Valid CDS	Number of predicted fusion transcripts with an annotated CDS start and stop	
In-Frame CDS	Number of “Valid CDS” transcripts with a CDS length divisible by three.	
Mod. In-Frame CDS	Number of “In-Frame CDS” transcripts that are not identical to an existing annotated transcript.	
mutA	Number of reads supporting the structural variation at breakpoint A	
mutB	Number of reads supporting the structural variation at breakpoint B	
Validation Status	Valid	The SV has been experimentally validated
	Putative	The SV has yet to be validated

Supplementary Table 8

Non-silent SNVs and indels identified in tumor series 1 & 2

All variants are validated somatic mutations, except for the NF1 germline truncation mutations (one splice variation and one nonsense mutation - yellow highlights).
The column definition is the same as Supplementary Table 5. The two additional columns, ‘SIFT Result’ and ‘PPH2 Result’, refer to ‘deleterious status’ assigned by SIFT and ‘deleterious status’ assigned by polyPHEN2, respectively.

The origin of one novel non-silent variant, *TMPRSS1*^{E90A}, which was found in tumor SJLGG001259_D in recurrence screening, cannot be determined due to lack of matching normal sample.

Cohort	Gene	Sample	Chromosome	Position	Class	AA Change	Protein ID	mRNA Accession	SIFT Result	PPH2 Result	Reference	Non-refere	Genotype	Flanking Region
Discovery	NEURL4	SJLGG004_D	17	7221962	MISSENSE	T1239M	53829370	NM_032442	DELETERIOUS	POSSIBLY_DAMAGING	G	A	G/A	GGATGGTGCCTTCAGGGCAC[G/A]TGTCCAGATTGGGCCCAAAC
Discovery	DSG1	SJLGG008_D	18	28914016	MISSENSE	N286Y	119703744	NM_001942	DELETERIOUS	POSSIBLY_DAMAGING	A	T	A/T	AAGAAAATACTCTAAATTCA[A/T]ATTTGCTCGAGATTAGAGTA
Discovery	FLT1	SJLGG008_D	13	29041677	MISSENSE	T48A	156104876	NM_002019	DELETERIOUS	PROBABLY_DAMAGING	T	C	T/C	CCTGCATTGGAGATGCAGTG[T/C]CTGGCCTGCTTGCATGATGT
Discovery	FLT1	SJLGG008_D	13	29041734	MISSENSE	L29I	156104876	NM_002019	DELETERIOUS	POSSIBLY_DAMAGING	A	T	A/T	ACTCAGTTCAGGATCTTTTA[A/T]TTTTGAACCTGAACTAGATC
Discovery	EP300	SJLGG009_D	22	41564765	NONSENSE	R1356*	50345997	NM_001429			C	T	C/T	TGGCAGAATCCTTTCCATAC[C/T]GAACCAAAGCCCTCTTTGCC
Discovery	NSMAF	SJLGG010_D	8	59498262	MISSENSE	V870I	31543297	NM_003580	TOLERATED	BENIGN	C	T	C/T	TGCTCCAAGGAGGTCCCAAA[C/T]GAGCAGTTCACCAGACTGAC
Discovery	PRIC285	SJLGG010_D	20	62197125	MISSENSE	A1017V	156105693	NM_001037335	TOLERATED	BENIGN	G	A	G/A	CTGCCGCAGCCTCCGTCTGC[G/A]CTGTGGTTGCCGTGATGTCA
Discovery	KIAA1239	SJLGG012_D	4	37447119	MISSENSE	N1170T	222418587	NM_001144990	TOLERATED	BENIGN	A	C	A/C	AGGAAGTCTTTCTGTTTGGA[A/C]TACTGAGGACATTTCCAGCC
Discovery	ATRX	SJLGG015_D	X	76937777	MISSENSE	E991K	20336209	NM_000489	TOLERATED	BENIGN	C	T	C/T	GTCTGAAGGTTTCTTTTTTT[C/T]TTCAGTTCCCTTTTTGCTCT
Discovery	RINT1	SJLGG015_D	7	105189134	MISSENSE	R325W	62899047	NM_021930	DELETERIOUS	PROBABLY_DAMAGING	C	T	C/T	GGTATCACTTCAGAGGGAAC[C/T]GGCAGACTAATGTGTTAAGC
Discovery	TMPRSS11D	SJLGG018_D	4	68725389	MISSENSE	R6S	4758508	NM_004262	TOLERATED	POSSIBLY_DAMAGING	G	T	G/T	TCTTGAAGTCGAAGTTACAC[G/T]TGCTGGCCTTACAAGAGAGA
Discovery	TFDP1	SJLGG019_D	13	114287557	MISSENSE	A144V	6005900	NM_007111	DELETERIOUS	POSSIBLY_DAMAGING	C	T	C/T	AGTGGCAGACGAGCTGGTTG[C/T]GGAGTTCAGTGCTGCCGACA
Discovery	NF1	SJLGG022_D	17	29665754	FRAMESHIFT	T2263_Y2264fs	4557793	NM_000267			TTAC	----	TTAC/----	GACCTGACAC[TTAC>----]AACAGTCAAG
Discovery	NF1	SJLGG022_D	17	29664899	splice	R2214_E43splice	4557793	NM_000267	-		G	A	G/A	TGGACAGAACTAGCTCAAAG[G/A]TATGTCCTAAATTAAATATA
Discovery	LETM1	SJLGG024_D	4	1821068	MISSENSE	S580R	6912482	NM_012318	TOLERATED	POSSIBLY_DAMAGING	G	T	G/T	GAGCAAATCCCACCCACCTC[G/T]CTGTAGTCCTGCACATCCTC
Discovery	NDUFB2	SJLGG027_D	7	140402788	NONSENSE	W74*	4758778	NM_004546			G	A	G/A	CTGGATTCTCTGGCGCTTTT[G/A]GCATGACTCAGAAGAGGTGC
Discovery	SPHK1	SJLGG027_D	17	74382128	MISSENSE	G111S	217272880	NM_182965	TOLERATED	PROBABLY_DAMAGING	G	A	G/A	TGGTGCTGCTGAACCCGCGC[G/A]GCGGCAAGGGCAAGGCCTTG
Discovery	BRAF	SJLGG029_D	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	ACCCACTCCATCGAGATTTC[A/T]CTGTAGCTAGACCAAAATCA
Discovery	BRAF	SJLGG030_D	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	ACCCACTCCATCGAGATTTC[A/T]CTGTAGCTAGACCAAAATCA
Discovery	ADAMTS9	SJLGG033_D	3	64633620	MISSENSE	G569A	33624896	NM_182920	DELETERIOUS	PROBABLY_DAMAGING	C	G	C/G	ACAGGGCATTACTTGCCTTT[C/G]CAGGCTCGCACTCCGTCCCA
Discovery	CHD2	SJLGG034_D	15	93567613	MISSENSE	D1722V	118421089	NM_001271	DELETERIOUS	PROBABLY_DAMAGING	A	T	A/T	CTATTTCAGGCACCATCATG[A/T]CTCCAAGCGGAGGAGATCCG
Discovery	CIC	SJLGG034_D	19	42794946	FRAMESHIFT	V676_R677fs	112421108	NM_015125			GTGCG	-----	GTGCG/----	CACCAATGTG[GTGCG>-----]GCCTGTCAGC
Discovery	CIC	SJLGG034_D	19	42795096	MISSENSE	S726R	112421108	NM_015125	DELETERIOUS	BENIGN	A	C	A/C	GGGGCTCCCCGCTGGGTGTC[A/C]GCTTAGTGTATTCGGACAAG
Discovery	IDH1	SJLGG034_D	2	209113112	MISSENSE	R132H	28178825	NM_005896	DELETERIOUS	PROBABLY_DAMAGING	C	T	C/T	CTTGATCCCCATAAGCATGA[C/T]GACCTATGATGATAGGTTTT
Discovery	STYK1	SJLGG034_D	12	10783793	MISSENSE	P101L	222352145	NM_018423	TOLERATED	BENIGN	G	A	G/A	CCTGCAGCTTAGCCAGGGCA[G/A]GTGTGGTAGCTCCCAGAAAG
Discovery	DCTN1	SJLGG035_D	2	74600063	NONSENSE	R149*	13259510	NM_004082			G	A	G/A	CTGTTTTCTCACCTTGGGTC[G/A]CCGAGTTGTGGTCTGGACAG
Discovery	BRAF	SJLGG036_D	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	ACCCACTCCATCGAGATTTC[A/T]CTGTAGCTAGACCAAAATCA
Discovery	H3F3A	SJLGG037_D	1	226252135	MISSENSE	K28M	4504279	NM_002107	DELETERIOUS	BENIGN	A	T	A/T	GGCTACAAAAGCCGCTCGCA[A/T]GAGTGCGCCCTCTACTGGAG
Discovery	C3orf30	SJLGG038_D	3	118865071	FRAMESHIFT	P12fs	282847424	NM_152539			--------	GGCTGAA	--------/GGC	CTGGCTGAAC[-------->GGCTGAAC]CCTTGAAACA
Discovery	MKI67	SJLGG040_D	10	129904112	NONSENSE	R1998*	103472005	NM_002417			G	A	G/A	CCCCAAGGATATCTTGAGTC[G/A]TTGCTTGGAGCTTGTTGGGG
Discovery	SCN3A	SJLGG040_D	2	166003458	MISSENSE	A488S	126362947	NM_001081676	TOLERATED	BENIGN	C	A	C/A	TTTGGAACTCAACTTTGATG[C/A]TTCTGAAGAACTTTCCAACA
Discovery	CDK13	SJLGG042_D	7	40118378	MISSENSE	R986H	145309302	NM_003718	DELETERIOUS	PROBABLY_DAMAGING	G	A	G/A	TGCCTTGGATCCTAGTAAGC[G/A]CTGCACTGCTGAACAGGCTC
Recurrence	BRAF	SJLGG001209_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	BRAF	SJLGG001211_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	BRAF	SJLGG001243_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	BRAF	SJLGG001262_D1	7	140477800	PROTEININS	G503>EYSG	33188459	NM_004333	-		---------	CTGAGTACT		ACAAGCTCACCTGAGTACT[---------/CTGAGTACT]CCTACTTCAT
Recurrence	BRAF	SJLGG001266_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	BRAF	SJLGG001269_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	BRAF	SJLGG001271_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	BRAF	SJLGG001273_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	BRAF	SJLGG001277_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	BRAF	SJLGG001281_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	BRAF	SJLGG001284_D1	7	140453136	MISSENSE	V600E	33188459	NM_004333	DELETERIOUS	BENIGN	A	T	A/T	TCGAGATTTC[A/T]CTGTAGCTAG
Recurrence	FGFR1	SJLGG001213_D1	8	38273561	MISSENSE	V559M	13186251	NM_015850	DELETERIOUS	PROBABLY_DAMAGING	C	T	C/T	GCATACTCCA[C/T]GATGACATAC
Recurrence	FGFR1	SJLGG001213_D1	8	38274849	MISSENSE	N544K	13186251	NM_015850	DELETERIOUS		G	T	G/T	CCCCCAGCAG[G/T]TTGATGATAT
Recurrence	FGFR1	SJLGG001259_D1	8	38274849	MISSENSE	N544K	13186251	NM_015850	DELETERIOUS		G	C	G/C	CCCCCAGCAG[G/C]TTGATGATAT
Recurrence	KRAS	SJLGG001259_D1	12	25398284	MISSENSE	G12D	15718763	NM_033360	DELETERIOUS	POSSIBLY_DAMAGING	C	T	C/T	GCCTACGCCA[C/T]CAGCTCCAAC
Recurrence	NF1	SJLGG001259_D1	17	29552226	FRAMESHIFT	T653fs	4557793	NM_000267	-		-------	TACGTAC	-------/TACG	GAAGAATTACTACGTAC[-------/TACGTAC]TCCTGGAGCC
Recurrence	NF1	SJLGG001267_D1	17	29653227	FRAMESHIFT	N1721fs	4557793	NM_000267	-		A	-	A/-	GGTATTCCACA[A/-]TGCTCTCAAG
Recurrence	NF1	SJLGG001225_D1	17	29548939	nonsense	W571*	4557793	NM_000267	-		G	A	A/A	AAACATTTTG[G/A]GAGATTAGGT

Supplementary Table 9

Significantly mutated gene analysis for mutations identified in tumors from series 1 and 2

Only non-silent mutations are included in the analysis using the MuSiC package.
Significantly mutated genes that pass the FDR test (<0.2) are shown in bold letters. Only *BRAF*, *NF1*, *H3F3A*, and *FGFR1* are mutated in more than one tumor.

#Gene	Indels	SNVs	# Mutations	#Cases	P-value			FDR		
					FCPT	LRT	CT	FCPT	LRT	CT
BRAF	**1**	**12**	**13**	**14**	**0**	**0**	**0**	**0**	**0**	**0**
NF1	**3**	**1**	**4**	**4**	**3.52E-06**	**8.05E-11**	**1.05E-10**	**0.04087**	**9.34E-07**	**1.21E-06**
H3F3A	**0**	**2**	**2**	**2**	**8.48E-04**	**5.55E-09**	**7.42E-08**	**1**	**4.29E-05**	**0.00057**
FGFR1	**0**	**3**	**3**	**2**	**3.09E-03**	**7.51E-07**	**8.88E-07**	**1**	**0.00436**	**0.00515**
FLT1	**0**	**2**	**2**	**1**	**1.25E-02**	**4.92E-06**	**4.39E-06**	**1**	**0.02283**	**0.02038**
CIC	**1**	**1**	**2**	**1**	**3.53E-02**	**2.76E-05**	**2.03E-05**	**1**	**0.09140**	**0.07841**
KRAS	0	1	1	1	0.27166	0.00012	0.00019	1	0.35616	0.61268
TMPRSS11D	0	1	1	1	0.29479	0.00015	0.00033	1	0.35616	0.73804
LETM1	0	1	1	1	0.42150	0.00043	0.00035	1	0.59021	0.73804
IDH1	0	1	1	1	0.41710	0.00042	0.00190	1	0.52499	1
STYK1	0	1	1	1	0.37987	0.00031	0.00121	1	0.52125	1
SPHK1	0	1	1	1	0.66326	0.00229	0.00363	1	1	1
ADAMTS9	0	1	1	1	0.67955	0.00247	0.00429	1	1	1
ATRX	0	1	1	1	0.77079	0.00463	0.00749	1	1	1
DSG1	0	1	1	1	0.73624	0.00381	0.00872	1	1	1
NSMAF	0	1	1	1	0.67769	0.00251	0.01055	1	1	1
EP300	0	1	1	1	0.75161	0.00421	0.01143	1	1	1
CDK13	0	1	1	1	0.77343	0.00497	0.01676	1	1	1
TFDP1	0	1	1	1	0.78217	0.00537	0.01827	1	1	1
DCTN1	0	1	1	1	0.79062	0.00569	0.02513	1	1	1
CHD2	0	1	1	1	0.89086	0.01393	0.04679	1	1	1
NEURL4	0	1	1	1	0.90382	0.01612	0.04855	1	1	1
PRIC285	0	1	1	1	0.92910	0.02223	0.05555	1	1	1

FCPT: Fisher's combined P-value test
CT: Convolution test
LRT: Likelihood ratio test.

Supplementary Table 10

WHO classification of low-grade gliomas and low-grade glioneuronal tumors in this study cohort

Low-grade gliomas				Low-grade glioneuronal tumors	
circumscribed *		diffuse *			
diagnosis	grade	diagnosis	grade	diagnosis	grade
pilocytic astrocytoma	I	**astrocytoma**	II	**ganglioglioma**	I
pilomyxoid astrocytoma	II	oligodendroglioma	II	desmoplastic infantile ganglioglioma	I
		oligoastrocytoma	II	dysembryoplastic neuroepithelial tumor	I
pleomorphic xanthoastrocytoma §	n/a	angiocentric glioma	I		

* architectural arrangement by radiology and pathology

§ has a glioneuronal immunophenotype

n/a - not assigned

Tumors in **bold** are relatively common.

Supplementary Table 11a

Primers for Tier 1 non-silent Single Nucleotide Variation validation

Primer Name	Primer Sequence (Forward)	Primer Sequence (Reverse)
GPX1	TCTCGAAGAGCATGAAGTTGGGCTC	TTATCGAGAATGTGGCGTCCCTCTG
NEURL4	AGGTCACAGGAGCTGGGCTAGAAGG	ACCAGGCCTGTGAGTAGAGAAGGGC
USP6	TTCCTTCCTTCCCGAAGTGCTGACT	TGTCTCCTCAGGATCCTCCTGGGTT
DSG1	ATGTCAGCGGAATGTGAGTG	CCAATTTCCTTCATTTCCAGA
FLT1-T48A	ACTATTTGGGCATCCCTTCC	AGTTTAAAAGGCACCCAGCA
FLT1-L29I	CTGCATTGGAGATGCAGTGT	ATGAAATTCAGAGCCCAGGA
KCNT1	GTCCCTGAGTCCTCTCAGCCTTGGT	CAGTCCACCTAGATGGTCCACCCTG
EP300	CTGAGGCGACAGAATCACCCTGAGT	GTGGAGGGCAGTCAGAGCCATACTC
SOX1	ATGATGATGGAGACCGACCTGCACT	TCATGTAGCCCTGCGAGTTGGAGAT
NSMAF	AGGCTCCAGGGACATGTTTACGACA	TGTGTTGCAGATAGTCGCCATGTCC
PRIC285	AGGTCTCTGGCACGAAAGAGCAGTG	TCTGGGAGAGCTTCATCCGTGAGTG
PRRG2	GTTCACTGCAGCCTCAATTTCCTGG	CTCGAAAGCAGCTCTTCAGTGAGGC
LPHN1	CTGGTGGGAAACCCTGTCTGTGAAC	ACCGGGCCGAGATTGAACTTCTCTA
KIAA1239	TGCTCCCTGGATGGTCTGTATGCTT	TGAAAGCTCAATGCTGACCACCTCA
HRNR	AGAAGAGTGACCCGAGCGAGACTCA	GCAACATGGTTCTGCATCAGGACAG
PDZD4	GTGATGTCGGTCTGAGTGCCACTGT	GCTGCAGACAGCAGATTCCTTGCTT
CDK10	CACCTGGAGGACCTTCTTACCTGGG	GAACTCTGGGACTGTCGTTCCCG
CDK10	CACCTGGAGGACCTTCTTACCTGGG	GAACTCTGGGACTGTCGTTCCCG
ATP8B3	CTTGATCATGTTGATGTCGTTGGCA	AACGGAGACTTCCTGGTCAGTGTCG
ATRX	TCCTTTCCCTGTTGACTTCTCAGCAT	TGATGGTGTCGATAAGCTTTCTGGGA
CC2D1A	TGCAGTCCCTTATCCTTCCTCCACC	CCACCAGATATGCATCCCTGAGCAC
RINT1	GCCTAGGCACGTCTCAAATTCCTGT	TCAGCAATATCTGATGCCCAAGAGC
TMPRSS11D	GAGCTATGGTGACTGCCAGGA	GGCAGAAAGGAAAGCAACTCC
TFDP1	ACGGCATTTCTCCATGAAGGT	GTGGGCATTTGTGCATTTCTG
NF1	GCTACCAAGATCACCATAGCATGA	CTTTCCTTTAGCACTGATGAGACC
LETM1	GGGCAACAGAGCAAGACCTTC	AGGAAATCGACATCCTCAGCG
NDUFB2	ACGCTGTCTGCCATGTTGTTT	CCTGCCTGGTGACAGAGTGAA
SPHK1	GTGGACGATCGGGAGAAACAT	GTGAGCATCAGCGTGAAGGAG
DCTN1	TGCTCATACACGTGCCCTCAT	TGGACTTCTGGGATTTCTGGG
CIC	ACTGGGCTCAGGAACCTTCAA	CTGGCACCTGCTGTGTCATTT
CIC	ACATCCTGCAGACACTGGTGC	GGGTGCCCACCAGTAGGTTAGT
CHD2	GGCTGGGTCCAGGAATATGGT	TAATGGTCTGAGGGTCCCTGG
BAI3	TCCCACTCTCGCTTTGCATTA	GCTAAGGAGGAGACGAACCCA
C3orf30	GCCTCTTTCTCACACACTGCG	CTTCCTTTCGGCCTGGTTCTT
BRAF	ACTCAGCAGCATCTCAGGGC	GGAAAGCATCTCACCTCATCC
OTC	GGGAAGGAGACGCGATATTGA	CCTGGTAACCTTGGAAAGCCT
ADAMTS9	ATAGCTTTCCAGTGCCATCCC	TTGAGCAGATGCAGTGCAGAC
CDK13	TGTTTGGTTTGGTGCTTACGTG	TCACTTACTCTGGTGGAGGCA
MKI67	AAGCCGGCCAGGTCTTCTAGT	AGCAAGAGACGGCCACAAACT
SCN3A	TGACGCTGTCTTCAGATTCGG	GATAAGCAACCACCACGAAGAA
STYK1	TCTCAATGTTCGCAAAGCCTG	CCTTGCCAATTTGTTTCAGGG
AIM1L	CTTTTGGGGTGGTGGACAAG	ATGTCCCTGTCCTCCCCTTT
FGFR1-D623A	ATACACCGAGCCCTGGCAGCCA	TGCCAGGGCTCGGTGTATGCA

Supplementary Table 11b

Primers for structural variant analysis

Sample ID #	Primer Name	Primer Sequence (Forward)	Primer Sequence (Reverse)
All samples screened	*KIAA1549* Ex.10 / *BRAF* Ex.12	GGTGGTGATGGTGATTGTTG	AGGCTTGTAACTGCTGAGGTG
All samples screened	*SRGAP3* Ex.9 / *RAF1* Ex.12	ATGCCACCATGCAGACATTA	CATTCCCTGAGCCGTCTG
All samples screened	*FGFR1* Ex.18 / *FGFR1* Ex.10	CATGCCCCTGGACCAGTA	TCTTCGGGAAGCTCATACTCA
All samples screened	*QKI* Ex.1 / *RAF1* Ex. 14	GCAGCTGATGAACGACAAGA	AGAACCACTCCAGCGTGACT
All samples screened	*FXR1* Ex.4 / *BRAF* Ex.14	CAAGAGCAAATGACCAAGAGC	GGATGATTGACTTGGCGTGT
All samples screened	*ETV6* Ex.1 / *NTRK3* Ex. 18	TGTCTGAGACTCCTGCTCAGTG	GTAGATTGGGGTGGCCTTC
SJLGG0048	*MYB* Ex.6 / *MAML2* Ex.4	CTCCGCCTACAGCTCAACTC	GCCTTGACAAATGTCGGTTT
SJLGG0047	*MYB* Ex.9 / *QKI* Ex. 6	GAACCACACATGCAGCTACC	TGTCTGATCAAAGGCATTATGG
SJLGG0047	*QKI* Ex. 2 / *MYB* Ex. 16	CCTGATGCTGTGGGACCTAT	CGAGCTTGACTGGAAGATGTC
SJLGG0055	*MYB* Ex.9 / *PCDH* Ex. 3	GAACCACACATGCAGCTACC	TGCAGCATCTCTGTGTCAAA
SJLGG0005	*MYB* Ex.9 / *PCDH* Ex. 3	GAACCACACATGCAGCTACC	TGCAGCATCTCTGTGTCAAA
SJLGG0046	*MYB* Ex.9 / *PCDH* Ex. 2	GAACCACACATGCAGCTACC	CTCTGGGCCTGAGAGAAACG
SJLGG0040	*MYB* Ex. 9 / *LOC154092 Ex.2*	CACCAGACCTCATGGAGACA	GCACCTCTCCCTGCTTGTAA
SJLGG0019	*QKI* Ex. 2 / *RAF1* Ex. 9	CCTGATGCTGTGGGACCTAT	GCTACTGGACAGGGCTGAAG
SJLGG0026	*FXR1* Ex.12-13 / *BRAF* Ex.11	AGCTGCGACAGATTGGTTCT	CTCGAGTCCCGTCTACCAAG
SJLGG0018	*FGFR1* Ex. 18 / *TACC1* Ex. 12	CATGCCCCTGGACCAGTA	GAGCTGCACTCTCAGCCTTT
SJLGG1212	*FGFR1* Ex. 17 / *TACC1* Ex. 7	GTGTCTGCTGACTCCAGTGC	GAGCTGCACTCTCAGCCTTT
SJLGG001264	*FGFR1* Ex. 19 / *TACC1* Ex. 8	AGC CCA GTA ACT GCA CCA AC	TCT TGT CTG ATT CGC TGA GG
SJLGG001206	*FGFR3* Ex.17 / *TACC3* Ex. 4	AGG AGC TCT TCA AGC TGC TG	GCG CCA TCA GAT ACA TCA AA
SJLGG0038	*ETV6* Ex. 3 / *NTRK3* Ex. 14	AAAGCTCTCCTGCTGCTGAC	AGTTCTCGCTTCAGCACGAT
SJLGG0038	*NTRK3* Ex. 10 / *ETV6* Ex.5	CTCATTGCCAAAAACCCACT	CTGGTGGTTGTTCTCCTGGT
SJLGG061	*NAV1* Ex. 15-16 / *NTRK2* Ex. 11	CCG AGG AGA AGG ACA CTG AG	ACA GTG AAT GGA ATG CAC CA
SJLGG0039	*ST6GAL1* Ex1-2 / *WHSC*1 Ex.4	AGCAAGGGGAGAGCCAGT	GGGGTAGTGTTAGGGGGTGT
SJLGG0033	*MYBL* Ex.8-9 / Chr.8 (reverse complemented)	CCATCACAGCCTGGAAGTTT	CTCCAGGCAACGTCAAGATT
SJLGG0033	*SNX16* Chr.8 / *C8orf34* Chr.8^{g}	CCGTTCTTCACAGCTTACAGG	AGAGGGGCTGCTTACACAGA
SJLGG0033	*SNX16* Chr.8 / Chr. 8	GGTCGAACTGTGCCTGGTAT	AAGCAAGGACCTGAGGAACA
SJLGG0033	*PKIA Chr.8 / DCAF4L2* Chr.8^{g}	TTCGACCGAGGAGTCATACC	ACTGATGCATGCGTACCAAA
SJLGG0033	*C8orf34* Chr.8 */ MYBL1* Chr.8^{g}	GACTGTAGTCACCCTGTTGTGC	GGAACAGAACAGAGCCCTCA
SJLGG0054	*MYB* Ex.9 / *ESR1* Int. (reverse complemented)	GAACCACACATGCAGCTACC	GTATTGGCAAATGGGGTTTG
SJLGG0054	*MYB* Int. 14 */ ESR1* Int. 5^{g} (reverse complemented)	GCGAGACCCTGTCTCTACCA	ACCTGGCCCATCAGTTCTTA
SJLGG0039	*TP73* Chr.1 / *TBC1D22A* Chr.22	GTGTGGCCAGACCTCCAG	TCAATACATGCCCTTGTGAAA
SJLGG0039	*TP73* Chr. 1 / Chr11^{g}	GATGGGTAGATAATAAATGGGGG	TGTTAACAGCAGGGATACTGAGA
SJLGG0039	*UBE2J2* Chr.1 / *PKD1* Chr. 16	CCGGTGCCTTACATCTGTG	GGTCAAGGCTCTCGTCACTC
SJLGG0039	*PKD1 / SLIT1*^{g}	AAGAAAGCACAGCGGAGAA	CCTACGCCTGGTACTTCTCG
SJLGG0035	*MYB* 3'UTR / *MMP16*	TTGATGAGACCACTGCCATC	CATAGCTTTGGGCCCTTATG
SJLGG0035	MYB Ex.14 / MMP16^{g}	CTGCTCACACCACTGGGAAG	CGGCGAATAGCTTTACGAGT
SJLGG0035	MAP3K5 Chr.6 / MYB promoter^{g}	AACAACCTTCCCCAACCTCT	AGCAGCTTTCAAAGTTAGTCAACA
SJLGG0035	MAP3K5 Ex.26 / Chr.6	CATTTCAGCCTTGCATCTGA	CTGCAGCAAGAGGCACTGTA
SJLGG0035	*MAP7* Chr.8 / Chr.6	CCAGGGTGTATTAGCCACAGA	TCCACCTTCCAGCTACCATC
SJLGG0031	*BRAF* Ex.7 / *MACF1* Ex. 19	ACCACCCAATACCACAGGAA	TTATGCAGGCTCTGAAGGTG
SJLGG0031	*MACF1* Ex. 16 / *BRAF* Ex. 11	AGCTGGTCACCTTGCGTCTA	TCCAAATGATCCAGATCCAA

Under Sample ID # 'All samples screened' primers were used to screen tumor across the study cohort for each respective structural variant. Remaining primers were used to validate specific structural variants identified in specific cases, as listed. Validation was performed by sequencing in genomic DNA for samples annotated by 'g'.

Supplementary Table 11c

Primers used to verify full-length cDNA of FGFR1 duplications and the FGFR1-D623A mutant

Primer Name	**Primer Sequence**
FGFR1-5’	ATGGATCCACCATGTGGAGCTGGA
FGFR1-3’	AGCTCGAGTCAGCGGCGTTTGCGTC
FGFR1-ex6-forward	CCCTCTGACAAGGGCAACTA
FGFR1-ex9-forward	CCCCTGTACCTGGAGATCAT
FGFR1-ex11-reverse	GTTGGGTTTGTCCTTGTCCA
FGFR1-ex18-forward	CATGCCCCTGGACCAGTA
FGFR1-D623A-forward	ATACACCGAGCCCTGGCAGCCA
FGFR1-D623A-reverse	TGCCAGGGCTCGGTGTATGCA

Supplementary Table 11d

Gene list for recurrence screening of somatic sequence variations

Gene Name	Gene Accession Number
FGFR1	NM_023110.2
MYB	NM_001130173.1
BRAF	NM_004333.4
RAF1	NM_002880.3
KRAS	NM_004985.3
TP53	NM_000546.4
PTEN	NM_000314.4
NEURL4	NM_000314.4
DSG1	NM_001942.2
FLT1	NM_002019.3
NSMAF	NM_003580.3
PRIC285	NM_001037335.2
EP300	NM_001429.3
ATRX	NM_000489.3
MAML2	NM_032427.1
QKI	NM_006775.2
NF1	NM_000267.1
MYBL1	NM_001080416.2
FXR1	NM_005087.3
TFDP1	NM_007111.4
FGFR2	NM_022970
FGFR3	NM_001163213
CIC	NM_015125
CDK13	NM_003718
STYK1	NM_018423
CHD2	NM_001271
BAI3	NM_001704
ADAMTS9	NM_182920
LETM1	NM_012318
DCTN1	NM_004082
SPHK1	NM_021972
TMPRSS11D	NM_004262

Supplementary Table 11e

iFISH probes

Gene Name	Purpose	BAC(s)	Control probe BAC(s)
FGFR1	Copy number abnormality	RP11-148D21	RP11-962B15 & RP11-803N20
FGFR1	Fusion (break apart)	RP11-246A12 & RP11-118H9	
MYB	Fusion (break apart)	RP11-63K22 and RP11-170P19	
MYB-PCDHGA1	Fusion	RP11-203P20 & RP11-96J7	
MYB-QKI	Fusion	RP11-1054F19 & RP11-944B14	
MYB-MAML2	Fusion	RP11-13L14 & 77A22	
MYB-ESR1	Fusion	RP11-665K24 & RP11-485E20	
BRAF	Fusion (break apart)	RP11-837G3 & RP11-948O19	
ETV6	Fusion (break apart)	RP11-297N18 & RP11-265F21	
FXR1	Fusion (break apart)	CTD-2549I21 & RP11-1115J16	
MACF1	Fusion (break apart)	RP11-15J6 & RP11-445L12	
MYBL1	Fusion (break apart)	RP11-110J18 & RP11-117K19	
MYBL2	Fusion (break apart)	RP11-35G1 & CTC-820M21	
NTRK3	Fusion (break apart)	RP11-96B23 & PR11-948I15	
RAF1	Fusion (break apart)	RP11-767C1 & RP11-455K5	
ST6GAL1	Fusion (break apart)	RP11-358N22 & RP11-1012P8	
WHSC1	Fusion (break apart)	CTD-2309G22 & RP11-21N18	

Supplementary Note

Capture validation of SNVs in 16 tumors analyzed by WGS

WGS analysis of 16 tumors (SJLGG001-016) predicted a total of 3,546 putative SNVs (tiers 1-3). A custom capture array was designed to enrich each target site for Illumina sequencing of tumor DNA and normal DNA, in order to validate the presence of the non-reference allele and to confirm its somatic origin, i.e. absence of the non-reference allele in matching germline [1].

After mapping the reads to the reference genome, 36% of the target sites either failed in custom capture design or lacked sufficient coverage to determine whether a target variant was somatic or germline. Of the 2,283 sites with sufficient coverage in custom capture (101x average coverage), 716 were classified as a high quality (HQ) somatic variant and 1,567 were classified as a low quality (LQ) somatic variant by WGS analysis using a quality classification matrix, as previously described [1]. Of 716 WGS HQ variants, 584 were validated as somatic mutations, at an overall validation rate of 82%, while only 22 WGS LQ variants were validated as somatic mutations, at an overall validation rate of 1%. These results show that only a very small fraction (3.7%) of validated somatic mutations were derived from LQ variants, despite an extensive validation assay targeting 1,567 LQ variants.

Analysis of background mutation rate (BMR) in 39 WGS cases

Mutations (tiers 1-3) that had been experimentally validated or classified as HQ variants by WGS were selected for BMR analysis. Since capture validation had been undertaken for tumors SJLGG001-016, almost all somatic variants (97.5%) used for calculating BMR in these tumors had been experimentally validated. We obtained the total number of effectively covered bases (i.e. depth >10x in both tumor and matching normal samples) in tiers 1, 2 and 3 for each case. The BMR for the 16 tumors subjected to exhaustive capture validation, ranging from 6.52×10^{-9} in sample SJLGG006 to 1.38×10^{-7} in sample SJLGG008 (Supplementary Table 2), was very similar to the BMR ascertained from validated tier 1 mutations and HQ mutations (tiers 2,3) in remaining tumors, which ranged from 3.21×10^{-9} to 1.73×10^{-7}.

Analysis of 7 LGG samples by both whole-genome and whole exome sequencing

To assess potential false negative calls caused by insufficient coverage, we ran whole exome sequencing (WES) at a high coverage (245x average coverage) for 7 pairs of matching tumor DNA / normal DNA samples previously analyzed by WGS. Samples SJLGG005, SJLGG035, SJLGG036, SJLGG037 and SJLGG039 were sequenced at the UK Wellcome Trust high-throughput genomics center at an average coverage of 303-343x, while samples SJLGG008 and SJLGG030 were sequenced at BGI with an average coverage of 38x and 63x, respectively. Resulting data are presented in Supplementary Table 3.

WGS had identified a total of 13 experimentally validated somatic coding mutations in these 7 samples (Supplementary Table 3). WES detected two additional somatic SNVs (*RANBP6*$^{\text{P917L}}$ in SJLGG005 and *ALDH18A1*$^{\text{I153V}}$ in SJLGG030) that were missed by WGS. On the other hand, WES missed three validated coding variants detected by WGS (*CACNA1A*$^{\text{Y1446Y}}$ in SJLGG005, *MUC4*$^{\text{F4995F}}$ and *CDH13*$^{\text{V16\_E2splice\_region}}$ in SJLGG008). The two SNVs missed by WGS analysis had >40x read coverage, but the mutant alleles were present in 11-13% of the NGS reads, suggesting that they are likely to be subclonal. By contrast, the 3 SNVs missed by WES were caused by poor coverage (0-6x).

Complex SVs in four cerebral tumors

Of the 13 SVs in SJLGG038, two are reciprocal chr4-chr12 translocations producing in-frame fusion proteins, *ETV6-NTRK3* and *NTRK3-ETV6*. This fusion has the same structure as those first reported in congenital fibrosarcoma; it has both the capacity to transform and to activate the MAPK/ERK and PI3K pathways [2,3]. Remaining SVs are all on chromosome 9, where each SV breakpoint is the end point of one of ten chromosome 9 CNV segments (Supplementary Fig. 15). In SJLGG033, five SVs detected across a 21.5Mb region on chromosome 8q showed a different pattern, disrupting *MYBL1* and forming a ‘closed chain’ of chromosomal breakage / rejoining with no concomitant CNV (Supplementary Fig. 9). A similar pattern has previously been reported in prostate cancer [4]. Four SVs in SJLGG035 formed a 1.1Mb episome that consisted of two segments on chromosome 6 encompassing *MYB* and one segment on chromosome 8 (Supplementary Fig. 10).

Gene expression profiling of LGG tumors

Gene expression profiling was performed using Affymetrix U133 plus 2 microarrays and mRNA-seq.

Tumors (n=75) assessed on U133 plus2 microarrays consisted of 55 with *BRAF* alterations, 8 with *MYB* rearrangement and 12 with *FGFR1* abnormalities. Robust Multi-array Average scores were used to normalize and to estimate expression levels. Using R package WGCNA and the top 10% most variable probesets, hierarchical clustering identified two major groups, each containing two subgroups (Supplementary Figure 14a). The first group consists exclusively of supratentorial non-pilocytic tumors with *FGFR1* or *MYB* abnormalities and divides into two subgroups (G1 & G2) that contain the tumors with *FGFR1* alterations (G1) or those with *MYB* rearrangements (G2). The second group includes all tumors with *BRAF* alterations and four tumors with *FGFR1* aberrations and also divides into two subgroups (G3 & G4). The four subgroups show significant enrichment with genetic alteration and pathological classification (pilocytic versus non-pilocytic tumors), but not gender (Supplementary Figure 14b). While the array data indicate that tumors cluster according to genetic alteration, pathology and anatomic site, because of strong associations between these variables, the first group of solely supratentorial tumors with non-pilocytic pathology clearly divides according to genotype into subgroups G1 and G2.

RNA-seq was carried out on 44 tumors, 16 with *BRAF* alterations, 9 with *MYB* or MYBL1 rearrangement, 14 with *FGFR1* or *FGFR3* abnormalities, and 5 with miscellaneous genetic alterations. Average coverage of each exon was extracted from the BAM files and normalized by quantile normalization [1]. Hierarchical clustering using the 10% most variable exons revealed three subgroups designated G1, G2 and G3 in Supplementary Figure 14c. Significant enrichment of *BRAF* alterations, *MYB* / *MYBL1* rearrangements and *FGFR* aberrations was found in G1, G2 and G3, respectively. G1 was also found to have significant enrichment for pilocytic morphology, while no association was found with gender (Supplementary Figure 14d).

Supplementary References

1. Zhang, J. *et al.* A novel retinoblastoma therapy from genomic and epigenetic analyses. *Nature* 481, 329-34 (2012).
2. Tognon, C. *et al.* Expression of the ETV6-NTRK3 gene fusion as a primary event in human secretory breast carcinoma. *Cancer Cell* 2, 367-76 (2002).
3. Wai, D.H. *et al.* The ETV6-NTRK3 gene fusion encodes a chimeric protein tyrosine kinase that transforms NIH3T3 cells. *Oncogene* 19, 906-15 (2000).
4. Berger, M.F. *et al.* The genomic complexity of primary human prostate cancer. *Nature* 470, 214-20 (2011).