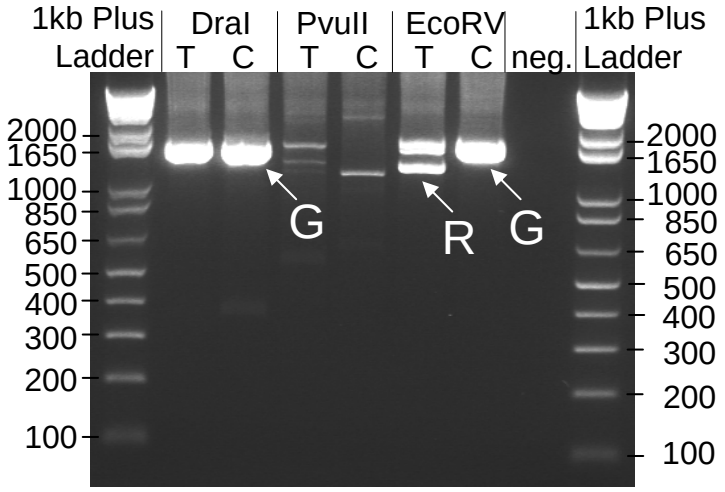
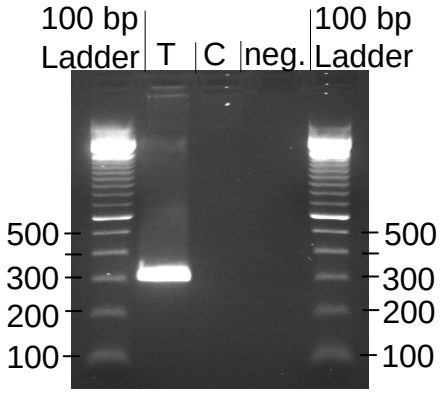
2A LM-PCR with Vδ1-for(-275)/ Vδ1(-69)



Germline:

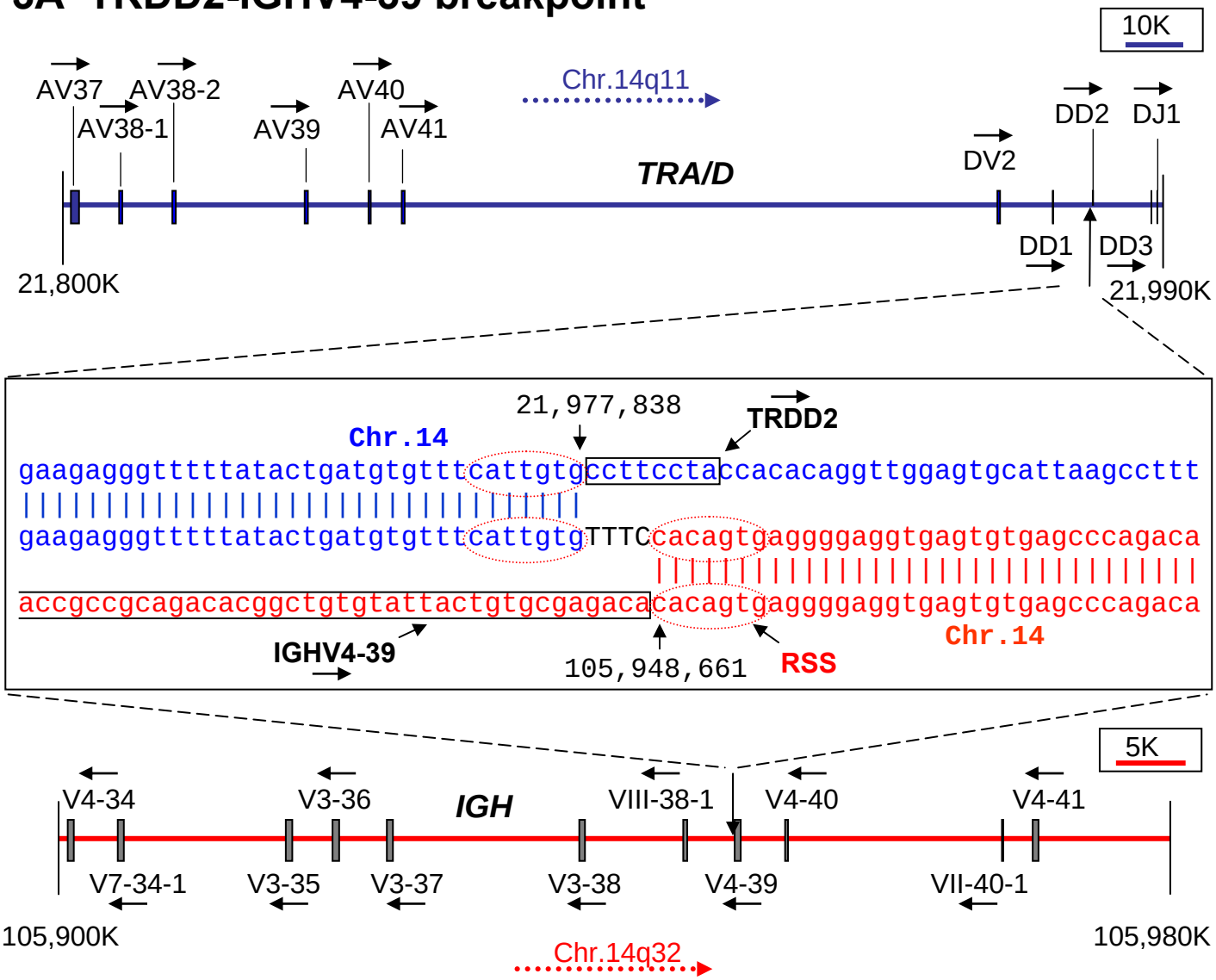
DraI:	1609 bp
PvuII:	-
EcoRV:	1658 bp

2B Confirmation gDNA PCR with Vδ1(-69)/ Jδ1(-189)

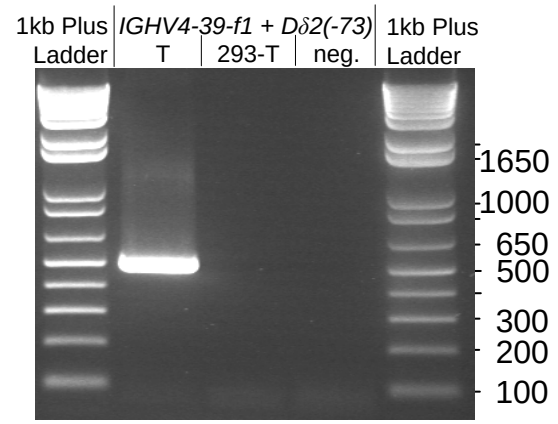


Expected size: 304 bp

3A TRDD2-IGHV4-39 breakpoint

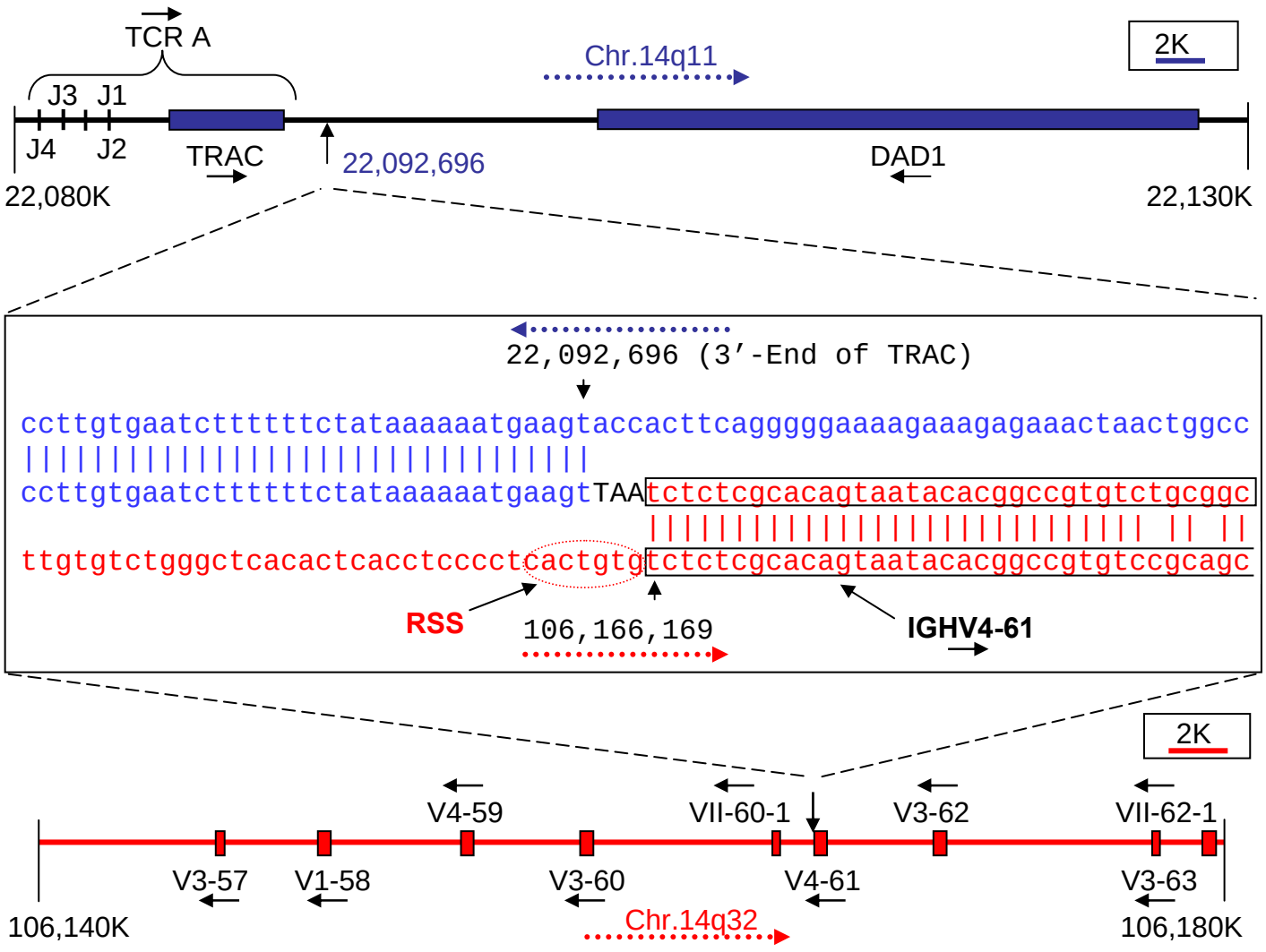


3B Confirmation gDNA PCR with IGHV4-39-f1/ Dδ2(-73)

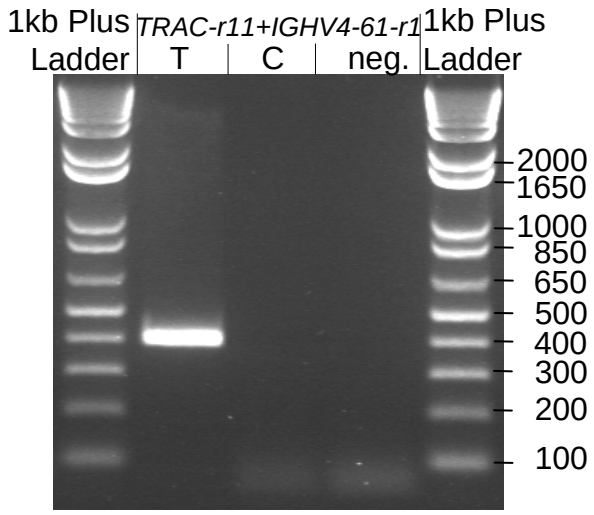


Expected size: 496 bp

4A 3´- TRAC-IGHV4-61 breakpoint

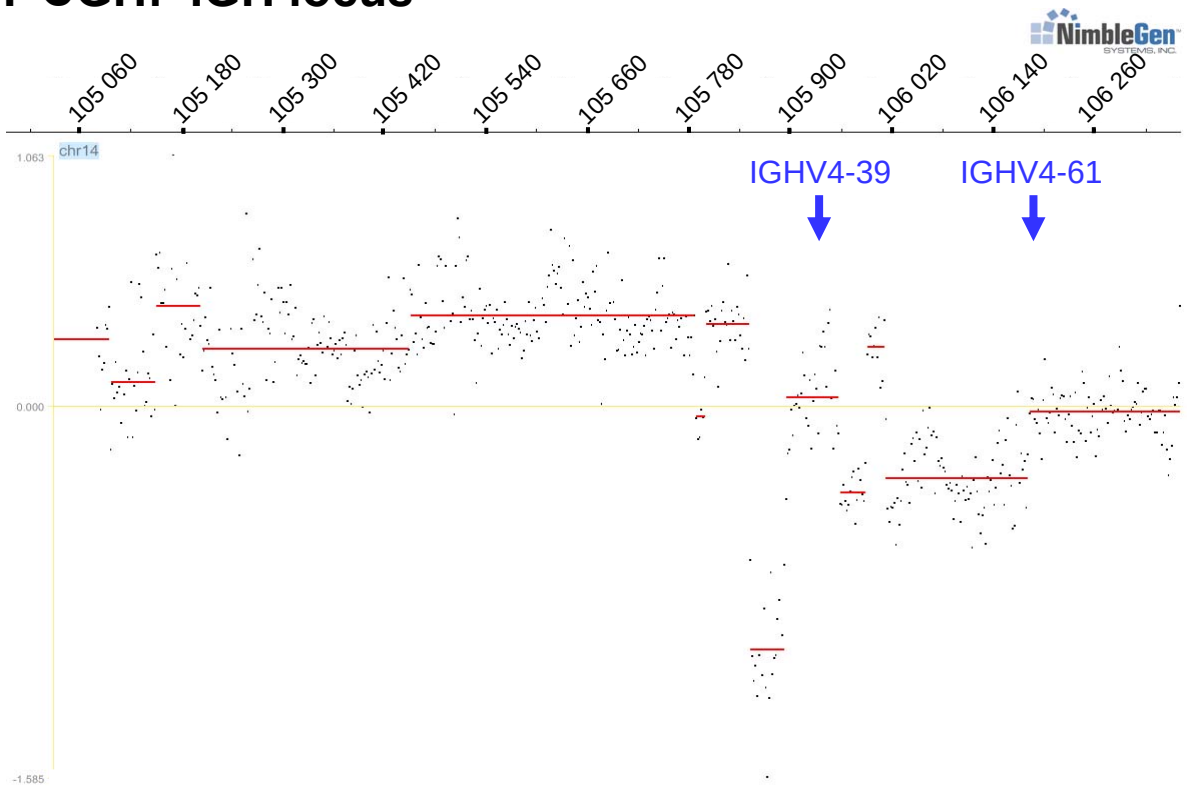


4B Confirmation gDNA PCR with TRAC-r11/ IGHV4-61-r1



Expected size: 392 bp

5 FT-CGH: IGH locus



Supplementary Figure Legends:

Figure 2A LM-PCR with Vδ1-for(-275)/ Vδ1(-69)

LM-PCR with forward primers V1-for(-275)/AP1 and V1(-69)/AP2 showed the germline configuration in *DraI* and *EcoRV*. A additional PCR product with a size of 1400 bp was visible in *EcoRV*. Sequencing of this fragment revealed the *TRDV1-TRDJ1* rearrangement within the T-cell receptor alpha/delta locus on 14q11. T: T-ALL sample and C: HEK 293-T used as a control.

Figure 2B Confirmation gDNA PCR with Vδ1(-69) / Jδ1(-189)

The T-cell receptor alpha/delta rearrangement *TRDV1-TRDJ1* was confirmed with V1(-69) and Jd1(-189) primers on genomic DNA of T-ALL sample.

Figure 3A TRDD2-IGHV4-39 breakpoint

Sequencing the atypical fragment of the LM-PCR at position 21,976K revealed a breakpoint at 5´-end of the *TRDD2*-fragment of the T-cell receptor alpha/delta locus and 3´-end of the *IGHV4-39* fragment of the *IGH*. Four nucleotides are inserted between the rearranged sequences.

Figure 3B Confirmation gDNA PCR with IGHV4-39-f1/ Dδ2(-73)

The inv(14)(q11q32) of the T-ALL sample involving the sequence of *TRDD2-IGHV4-39* was confirmed with primers on genomic DNA.

Figure 4A 3´- TRAC-IGHV4-61 breakpoint

Sequencing result of the atypical fragments revealed the inv(14)(q11q32). By this inversion *IGHV4-61* is agminate to a sequence locating 3´- end of constant region of *TRA/D*.

Figure 4B **Confirmation gDNA PCR with TRAC-r11/ IGHV4-61-r1**

The inv(14)(q11q32) involving the *IGHV4-61* fragment was confirmed with TRAC-r11 and IGHV4-61-r1 primers on genomic DNA.

Figure 5 **FT-CGH: IGH locus**

Due to a large number of repetitive sequences in the *IGH* locus the FT-CGH show not clearly the *IGH* breakpoint at the area of *IGHV4-39* of the inv(14)(q11q32). The second breakpoint of *IGHV4-61* at position 106,166K revealed a sharp break including a deletion.