

## **Additional File 2**

### **Figure A. Fragment analysis of breakpoint PCR of the familial 1325-bp deletion encompassing exon 8 of the *STK11* gene.**

Figure shows an agarose gel with the deleted allele preferentially amplified in the proband. Size ladder (Invitrogen 1 KB plus) is in the lane labeled as 1 kb+, while wild-type DNA in lane 1, proband DNA in lane 2, and water in lane 3. The two alternative forward primers used in amplification are labeled as Fa and Fb. The expected sizes of fragments generated from normal wild type alleles are written on top of the gel and the sizes of the amplicons generated from deleted alleles are highlighted with an arrow on the right. Asterisks highlight the bands sequenced.

### **Figure B. Sequence from the deletion locus of the the familial 1325-bp deletion encompassing exon 8 of the *STK11* gene.**

Sequence shows the breakpoints in relation to the adjoining sequence; repeat elements, SNPs, exons, and primers. Sequence coordinates are listed according to UCSC hg 18 build (March 2006), and the two interruptions demarcate the breakpoints. Nucleotides in bold and capitalized font represent exons. Nucleotides in bold and underlined font correspond to the primers used in breakpoint PCR. SNPs (130 build) are highlighted in red font, and microhomology at breakpoints is shown boxed.

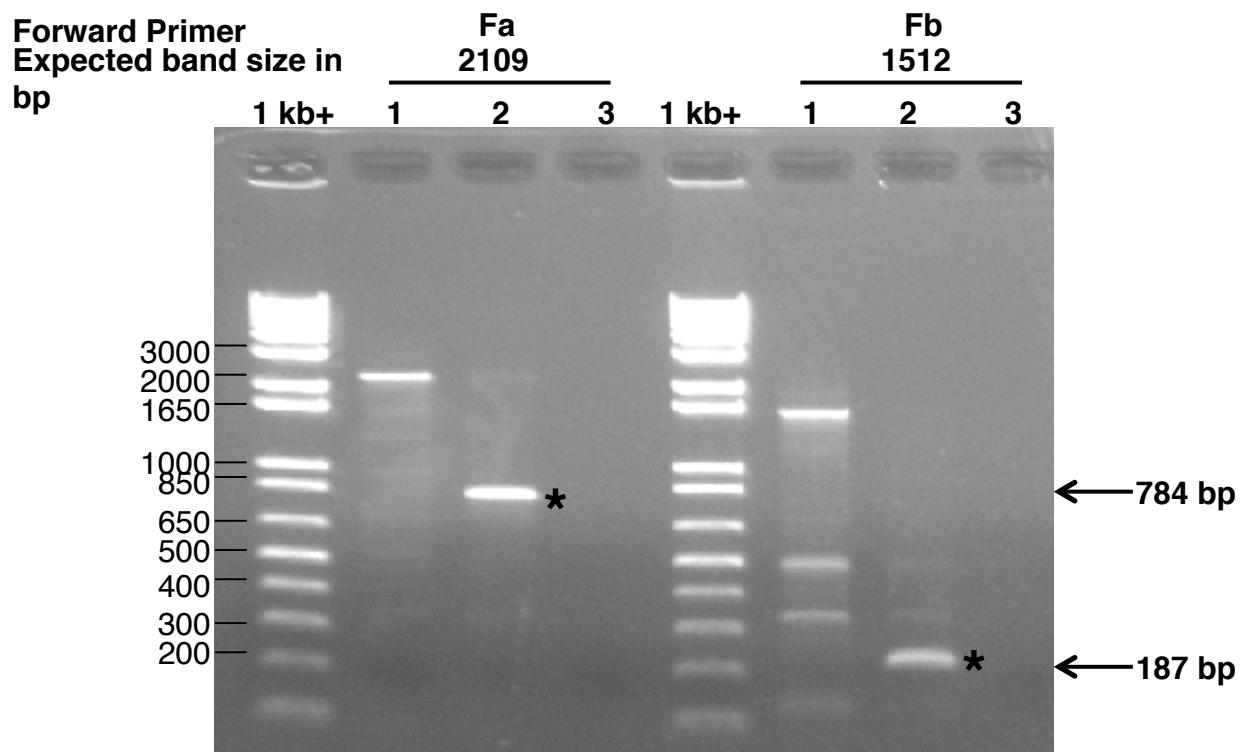
### **Figure C. Fragment analysis of breakpoint PCR of the familial 971-bp deletion encompassing exon 3 of the *STK11* gene.**

Figure shows an agarose gel with the deleted allele preferentially amplified in the proband with one of four reverse primers used. Size ladder (Invitrogen 1 KB plus) is in the lane labeled as 1 kb+, while wild-type DNA in lane 1, proband DNA in lane 2, and water in lane 3. The four alternative reverse primers used in amplification are labeled as Ra, Rb, Rc and Rd. The expected sizes of fragments generated from normal wild type alleles are written on top of the gel. The size of the amplicon generated from deleted allele, when amplified using Rd primer, is highlighted with an arrow on the right. Asterisks highlight the bands sequenced.

### **Figure D. Sequence from the deletion locus of the the familial 97-bp deletion encompassing exon 3 of the *STK11* gene.**

Sequence shows the breakpoints in relation to the adjoining sequence; repeat elements, SNPs, exons, and primers. Sequence coordinates are listed according to UCSC hg 18 build (March 2006), and the two interruptions demarcate the breakpoints. Nucleotides in bold and capitalized font represent exons. Nucleotides in bold and underlined font correspond to the primers used in breakpoint PCR. RepeatMasker are highlighted with blue font, SNPs (130 build) are highlighted in red font, and microhomology at breakpoints is shown boxed.

**Additional File 2, Figure A**



## Additional File 2, Figure B

chr19:1173251-1174850

aggcatggaqatqcqccaqqqaqqgcacagctggtccaaacactggcga **Fb**  
gagcctcttttccctcctgggctcccagcagcagggtgtggc  
tggatccagcccaggccccagctccatgacagggaaagacagagc  
Ggacggggtcagcag

(Breakpoint @ chr19:1,173,416 in intron 7)

gccccacagtgccgcctccctcacttcgtgggctc  
tgctcctctgcaccagcccctggaggcccttgagccgtctgtggagccc  
ctccgagccccgaggccaccactgagaccggcttggagatggagtg  
ccggaccctgaggcgctggctgtgattgtgccttgggggtctctgcaca  
gtcgggtcatctgggcgcctggcgggactgggctgccccccatagc  
ctcctggctggatgtgctcaggccccccagacccccctctggcctt  
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acctgggacacaggcctcagggtggaggggacatctgtcaggctggag  
caggtcagcctgcctgccttagaggacatggctgagcttctgtggcac  
agccacccttgcacggcctggtcccagctcctgagtggtggcaggtac  
cctgggcccagaggagctgggtcgaaaaactggaccgcctgggtggc  
ctgacaggcgcactgctctggcggttgcaCTGGTTCCCGGAAGAAC

**ATCCTCCGGCTGAAGCACCACTGCCATCCCACCGAGCCCCAGACACCAAG Exon 8**

GACCGGTGGCGCAGCATGACTGTGGTGCGTACTTGGAGGACCTGCACGG

CGCGGACGAGGACGAGGACCTCTTCCGACATCGAGGATGACATCATCTACA

**CTCAGGACTTCACGGTGCCCCgt**gagtgctggggggggccctggcggc

ctgctgactcggccaggatgtcccacgggagcagggtgcctgcctgtctg

caaca-----390 bp not shown-----aggcg

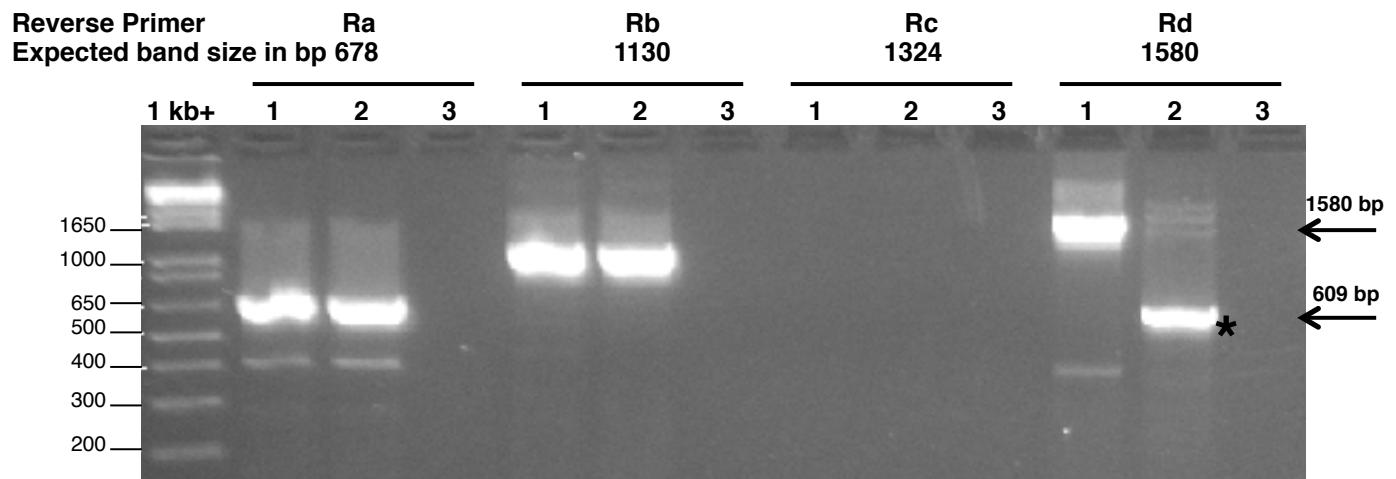
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Agaccttcaggagaggaagcctctggccggcgcggcag

(Breakpoint @ chr19:1,174,740 in intron 8)

taggcctga  
ggaggagctcaggccttagcgtagggcggcccacattggcaagccagcc R  
cctccccggccatgctccggcttggctgtttcgccaggctggccg

## Additional File 2, Figure C



## Additional File 2, Figure D

chr19:1,169,801-1,171,400

cgggctgacctttgtggccattttqqtcgtggctggcggtgtcctcgta F  
tcatctgtggacacccccatgggtcttacggcacagccctccctacgggg  
actttgcttcataaggccctgtgcccaagagaagagcagaagtggct  
gaggctgggctgtgttccctgagccacgcggtcagggccctgggaccg  
tcctgcataggcccgagcctgctggggggcgtccaggaggcaccatcc  
cccgcacatgggcagggtggg

(Breakpoint @ chr19:1,170,072 in intron 2)

ggacgtgagccccgcaggaacgtgc  
aagagttagccctgtcctcccttcggcgttaggcttcctctggac  
gtggggccctgggcctttcagaggggtggctgagggcagggtggcc  
ctggcccggaggggggcaaggtgggtcagagggtccctccagagcccc  
ttttctggccccctgtcttcgtggctgtgagtgccgcggccctgag  
ctgtgtgtccttagcgcccacGTATATGGTGTGGAGTACTGCGTGTGT Exon 3  
**GGCATGCAGGAAATGCTGGACAGCGTGCCGGAGAAGCGTTCCCAGTGTG**  
**CCAGGCCAACGG**gtgcgtgcgcggggcagggcagggtgggggcgaaaa  
cgggggccaggcaggcaggcaggctccttcgtgaggccacactgttgtcc Ra  
tgatattcattgacatgaaggccaaagttttttttttttttt  
**gtgttttttcgagatggagtctactctgtcgcccaggctgagtgca**  
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**cgtttttttgtat**tttagtagagacgggtttcaccgtgtt  
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ggcccaagtttaaaaacagttttgggtccccatgtgtggcatccac  
aggcagggtgtccaaaccccgcctccatcttqtaggctgtgc Rb  
ctgaggccagtggcctgcttcagccatcgctggcagccgcctgc  
accagatctcctggatgcaggctgtggcctcagagtca  
(Breakpoint @ chr19:1171042 in intron 3)

ccccttgc  
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cgggggccctggccagacgtggctggccggacgagggtggccactgcaggc  
gcagggtgtggctccctgtggaccttagcccttcctgtgtgc  
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gcagctgcaaaaggggaccctgtgaggggcaggaggcctggccccagg  
acgggtgtgtgctgcccgcagGTACTTCTGTCAGCTGATTGACGGCCTGG Rd