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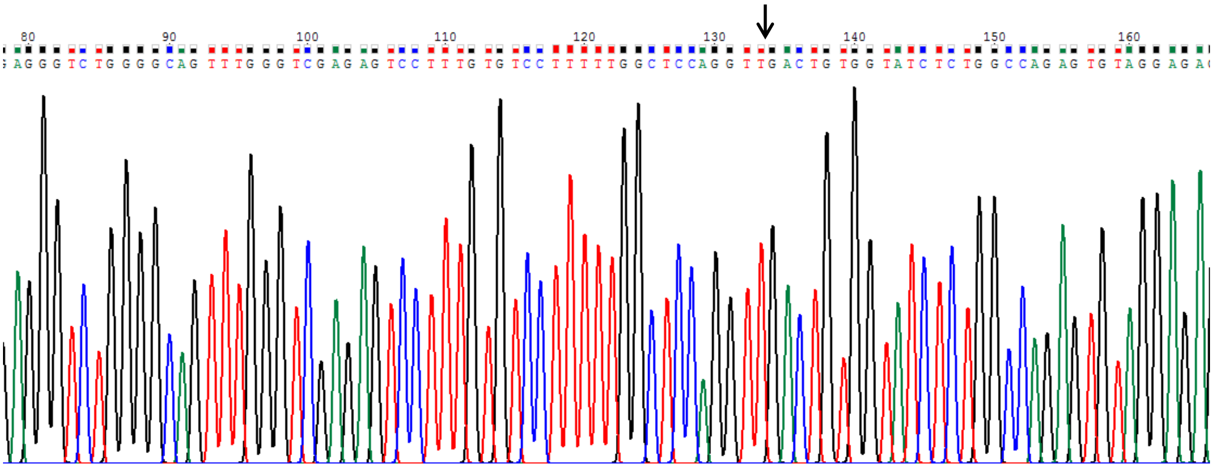

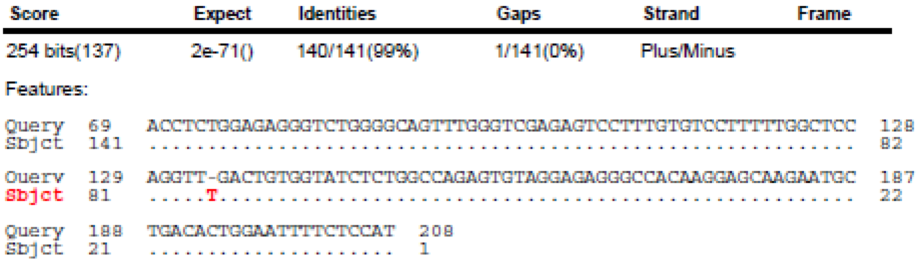

Score	Expect	Identities	Gaps	Strand	Frame
254 bits(137)	2e-71()	140/141(99%)	1/141(0%)	Plus/Minus	

Features:

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Query  129  AGGTT-GACTGTGGTATCTCTGGCCAGAGTGTAGGAGAGGGCCACAAGGAGCAAGAATGC  187
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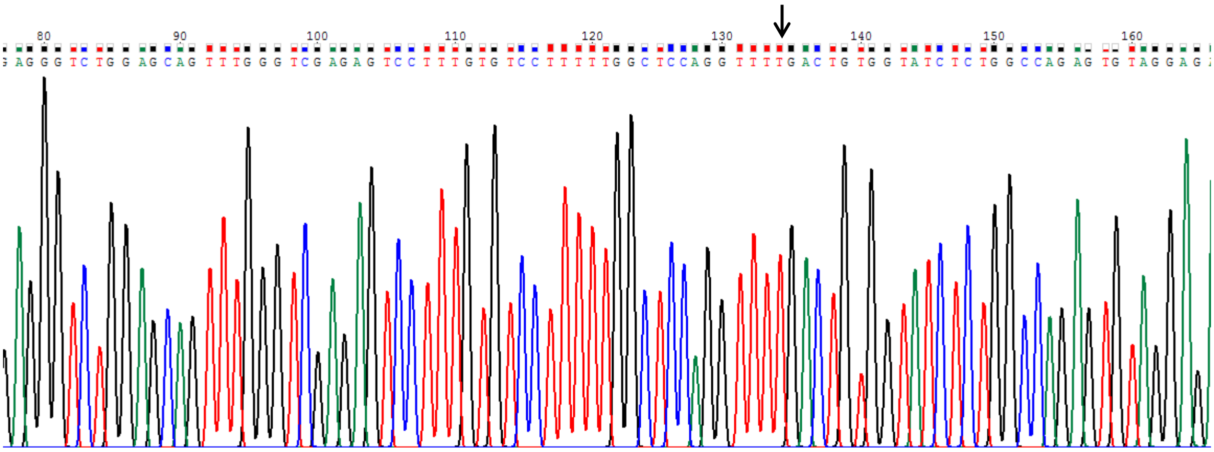
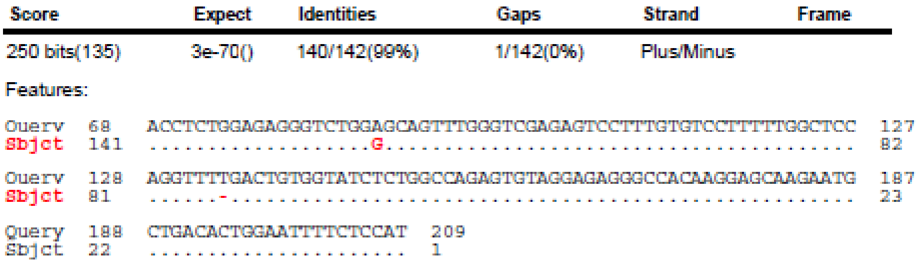
B





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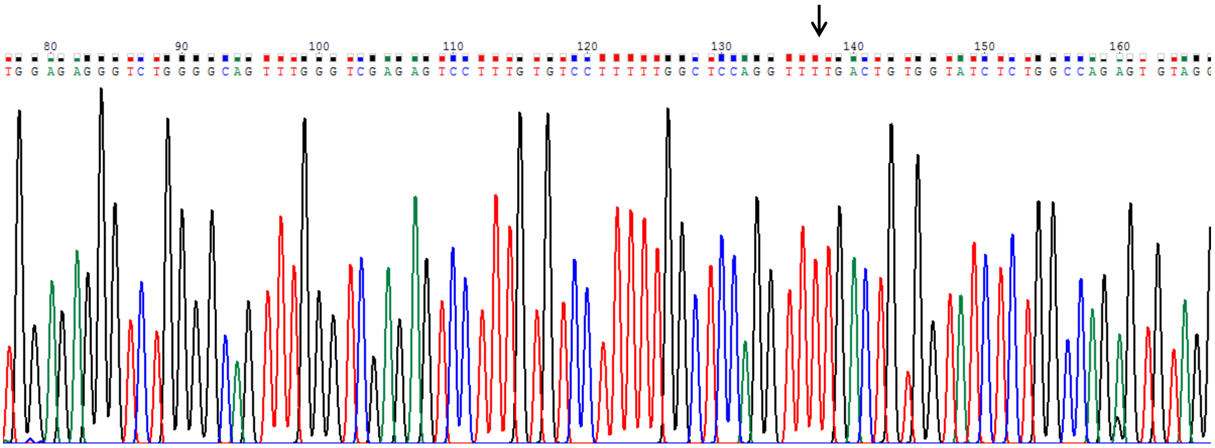
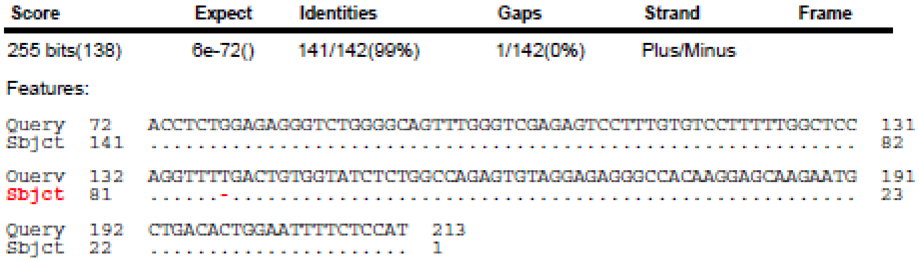
C





Score	Expect	Identities	Gaps	Strand	Frame
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Features:

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Sbjct  141  ............................................................  82

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Sbjct  81   ......-.....................................................  23

Query  192  CTGACACTGGAATTTTCTCCAT  213
Sbjct  22   ......................  1
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Figure S1: **Sequencing analysis to identify mutations prepared by CRISPR/Cas9 that are responsible for *AGR2* gene knockout.**

(A) Deletion 76T was observed in A549 AGR2KO clone G9; **(B)** Insertion 75T was detected in both A549 AGR2KO clones G9 and G2; **(C)** Insertion 75T was also detected in the second allele of A549 AGR2KO G2 clone.