

## Transcriptome profiling identifies a recurrent *CRYL1-IFT88* chimeric transcript in hepatocellular carcinoma

### Supplementary Materials

#### Supplementary File: the full-length *CRYL1-IFT88* fusion sequence obtained by 3' and 5' RACE experiments

#### The full-length *CRYL1-IFT88* fusion transcript (779 bp)

> *CRYL1-IFT88*

GGCGCCGCGTCCCCGGCCCAACCATGGC  
 GTCCTCCGCGCCGGCTGCGTGGTGCATCGTTG  
 GCAGTGGAGTCATTGGGCGAAGCTGGGCCATG  
 CTGTTTGCCAGTGGAGGCTTCCAGGTGAAACT  
 CTATGACATTGAGCAACAGCAGATAAGGAACG  
 CCCTGGAAAACATCAGAAAGGAGATGAAGTTG  
 CTGGAGCAGGCAGGTTCTCTGAAAGGCTCCCT  
 GAGTGTGGAAGAGCAGCTGTCACTCATCAGTG  
 GTTGTCCCAATATCCAAGAAGCAGTAGAGGGT  
 GCCATGCACATTCAGTAACATCAGAGATTTTCATT  
 AAACCTGGAGGTTGAATTCATTTTCGGAGTTCAAT  
 GATATGTCCAAAGAATCAGGTACTATAATCGTATAG  
 ACAACTCCTGTAATATATCCACAGTGCAAAATTAT  
 CCCCCTTCTCTGTCATTCCCTAGTGAGAAAAATCC  
 AACTGCAGACTTGACTGCCTTCGGTGAAGGCACA  
 CGGCAAATTCTTCTGAAAAATAATACCCTTCAAGA  
 TTGACTCTTCCCGTTTTACACAGCAATTGTCTCAG  
 CTTGGGACCAAAGTATTTACAAAGCAAGCAAACA  
 ACAGACTAGCGAACAGGGACACTTCTGAAGCTGG  
 TGATGCAGAAATCCACTGCCAAGCAGGGTGGGGG  
 GCCAGTCACCTCTCCTGGAATGTTCCATATGTAAG

CTGACACAACCTTAACATCTTAAATACAGAATTCCA  
 ATCAAAAAGAAAAGCAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAA

Note: Bold sequence was from *CRYL1*, and light sequence was from *IFT88*. The red sequence was the primer of 5' and 3' RACE experiments. Underline ATG and TAA were the start codon and stop codon. The breakpoint occurred in TAA

#### The longest ORF predicted by NCBI ORF-finder (279 bp)

> *CRYL1-IFT88* ORF

ATGGCGTCTCCGCGCCGGCTGCGTGGTGA  
 TCGTTGGCAGTGGAGTCATTGGGCGAAGCTGGGC  
 CATGCTGTTTGCCAGTGGAGGCTTCCAGGTGAAA  
 CTCTATGACATTGAGCAACAGCAGATAAGGAACG  
 CCCTGGAAAACATCAGAAAGGAGATGAAGTTGC  
 TGGAGCAGGCAGGTTCTCTGAAAGGCTCCCTGA  
**GTGTGGA**AGAGCAGCTGTCACTCATCAGTGGTTG  
 TCCCAATATCCAAGAAGCAGTAGAGGGTGCCATG  
 CACATTCAGTAA

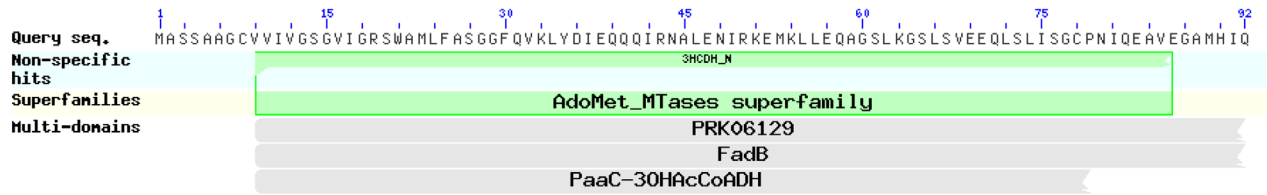
#### The predicted AA sequence (92 aa)

> *CRYL1-IFT88* aa

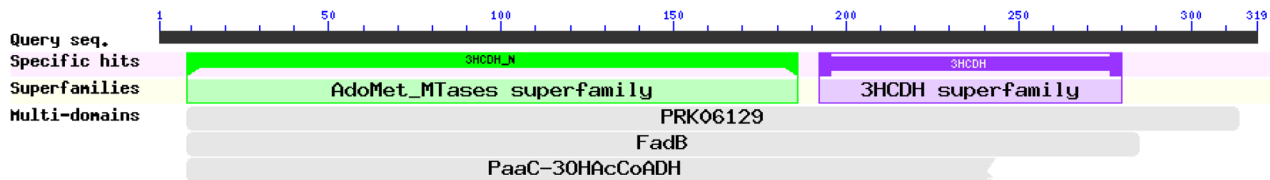
MASSAAGCVVIVGSGVIGRSWAMLFASGGFQ  
 VKLYDIEQQQIRNALENIRKEMKLLLEQAGSLKGSLS  
 VEEQLSLISGCPNIQEAVEGAMHIQ

The CRYL1-IFT88 function domain predicted by NCBI CD-Search

The CRYL1-IFT88 function domain predicted by NCBI CD-Search



The CRYL1 function domain predicted by NCBI CD-Search



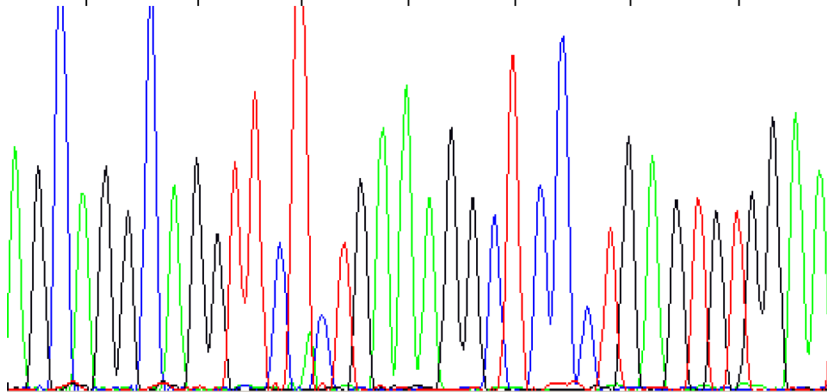
The CRYL1 function domain predicted by NCBI CD-Search

5' RACE PCR production

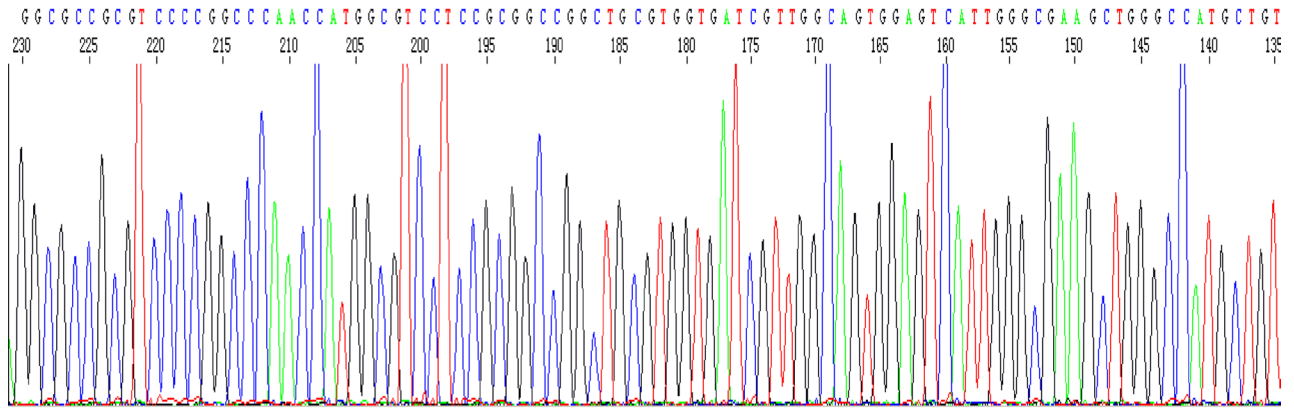
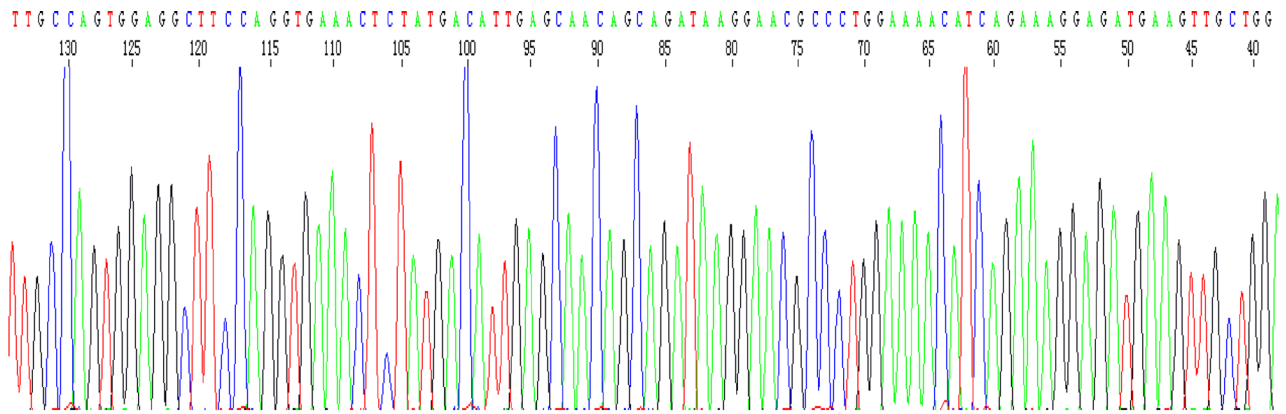
A G C A G G C A G G T T C T C T G A A A G G C T C C C T G A G T G T G A A

35 30 25 20 15 10 5

sequences:



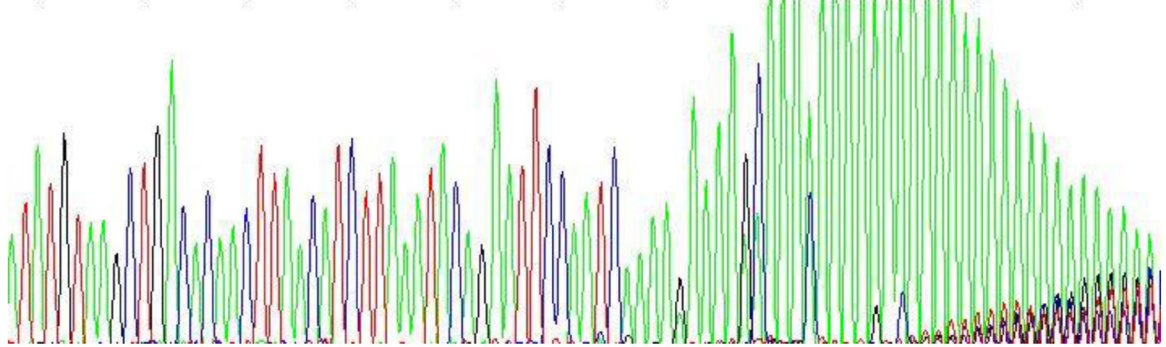
5' RACE PCR production sequences:



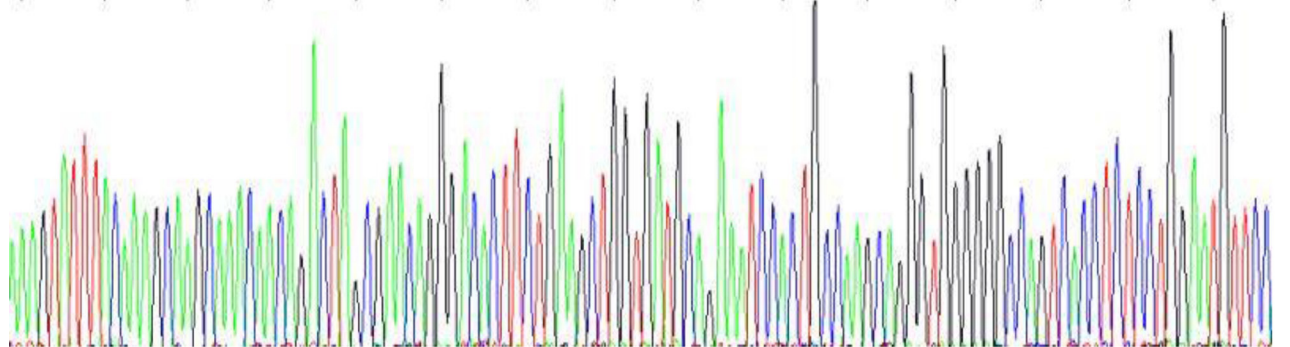
3' RACE production sequences:

3' RACE production sequences:

ATATGTAAGCTGACACAACTTAACTCTTAAATACAGAAATTCAAATCAAAGAAAA GCAAAAA  
241 249 257 265 273 281 289 297 305 313 321



AAA GTATTTACAAAGCAAGCAAAACAGACTAGCGAACAGGGACACTTCTGAAAGCTGGTGATGCAGAAATCCATG CCAAGCAGGGTGGGGGCCAGTCACCTCTCCTGGAAATGTTCC  
121 129 137 145 153 161 169 177 185 193 201 209 217 225 233



CTG CAGACTTGACTGCCITCGGTGA GGCACAGGC AAATTCTTCTGAAAAATAATCCCTTCAAGATTGACTCTTCCGGTTTTACACAGCAATTGTCTCAGCTTGGGACC  
17 25 33 41 49 57 65 73 81 89 97 105 113

