

Extracted from FastA Library HamCheese.fasta

Tag	Name	5' End	3' End	Length
DNAM_1	1	102	410	309
DNAM_2	2	370	1992	1623
DNAM_3	3	2010	2318	309
DNAM_4	4	2335	4254	1920
DNAM_5	5	4280	5032	753
DNAM_6	6	5085	6428	1344
DNAM_7	7	6510	6692	183
DNAM_8	8	6714	7301	588
DNAM_9	9	7312	7650	339
DNAM_10	10	7655	7909	255
DNAM_11	11	7902	8342	441
DNAM_12	12	8378	8959	582
DNAM_13	13	9060	9413	354
DNAM_14	14	9060	9784	726
DNAM_15	15	9788	12076	2288
DNAM_16	16	12076	12921	846
DNAM_17	17	12931	14175	1245
DNAM_18	18	14180	15139	960
DNAM_19	19	15149	15772	624
DNAM_20	20	15772	16194	423

Description	Sequence	Product	Regions	Blast	Context
			Start Stop Length		
			9060 9386 327		
			9386 9784 399		

Six Frame Translation of Extracted from FastA Library HamCheese.fasta

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P G R T Q S R R T C M R S A P C R L S C S T S I R R A W W T C W T M S N S
R R A G P K A G G P A C A R L F A D * A A Q Q V F A G P G G F A G R * A T R
A G Q D P K Q E D I H A I G S S L Q T E L L N K Y S P G L V D L L D D E Q L
9227 C C C G G G C A G G C C A A A G C A G G A G G C C T G C A T G C G C T C G G C T C C C T G C A G A T T G A G C T G C T C A C A A G T A T T C G C C G G G C C T G G T G G A C C T G C T G G A C G A T G A G C A A C T C
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29228 G C G C C C G T C C T G G T T T C G T C C T C T G G A C G T A C G G A G C C G A G G G A C G T C T A A C T C G A C G A T T G T T C A T A G C G G C C C G A C C A C C T G G A C G A C C T G C T A C T C G T T G A G
V G P L V W L L L V Q M R E A G Q L N L Q E V L I R R A Q H V Q Q V I L L E
R R A P G L A P P G A H A R S G A S Q A A * C T N A P G P P G A P R H A V
A P C S G F C S S R C A S P E R C I S S S L L Y E G P R T S R S S S C S

R S S W H G R R R R E S T W G N R K P L P P P P R G A F G G Y S V R P P F G H
A P R G M A G G V G N Q R G (G) I A S L C L L L E E H S E A I Q Y D L L V M
I L V A H Q E A S S S S * R S I R R L F S T T F W S N
9342 G C G C T C C T C G T G C A T G G C A G G A G G C G T C G G G A T C A A C G T G G G A A T C G C A A G C C T C G C C T C C T A G A G G A G C A T T C G G A G G C T A T T C A G T A C G A C C T T T G G T C A T
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29113 C C G A G G A G C A C C G T A C C G T C C T C C G A G C C C T T A G T T G C A C C C C T T A G C G T T C G G A G C G G A G G A T C T C C T C G T A A G C C T C C G A T A A G T C A T G C T G G A A A C C A G T A
R E E H C P L L R R S D V H P F R L G R G G G L P A N P P * E T R G K P *
R A G R P M A P P T P F * R P P I A L R Q R R R S S C E S A I * Y S R K T M
A S R T A H C S A D P I L T P S D C A E A E E * L L M R L S N L V V K Q D

P A S R A T R D A G F V V V G P A R G R Q A F R A L V R A G A R A A A G P C
R R L E O L G T P A L S W W D L L V V V K H S G P S S A L A R E L O P D L
  
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Position: 9485 Font: 10

I think that the frameshift is at position 9386 (the nucleotide that both regions share). I am different than your call by 3. I can't tell why your error message says you are wrong. But I call the frameshift in the middle of the slippery sequence. Go the amino acids go from glycine to glycine (the circles) and share on the rectangled nucleotide "G".