

- 1 -

piece 1, NC\_000913, nudH\_mutH-, config: linear, direction: -, begin: 2967713, end: 2966980

\*2967710 \* \*2967700 \* \*2967690 \* \*2967680 \* \*2967670 \* \*2967660 \* \*2967650 \* \*2967640 \*  
 5' a g g a g g a g c a g t g g c g a g g t t g g a c a t g t c a t g a t a c c t g a t t a a a a a a c a a a c a g c a a t t a t g t g c c g a a t t a t t c g 3'  
 - arg - arg - glu - gln - trp - ala - arg - leu - gly - his - val - met - ile - pro - . . .  
 - gly - glu - ser - ser - gly - arg - gly - trp - asp - met - ser - . . .  
 - glu - arg - ala - val - gly - glu - val - gly - thr - cys - his - asp - thr - leu - ile - lys - lys - gln - thr - ala - ile - met - cys - arg - ile - phe - ala  
 ... ] NC\_000913.mutH

{ p35-(23)-p10 2967590 Gap 1.4 bits  
| p35-p10 2967590 total 6.3 bits }

This figure displays a genomic sequence from position \*2967470 to \*2967390. The top line shows the sequence with codons and amino acids. The bottom line shows the sequence with gene annotations. Two genes are identified: *nudH* (from \*2967470 to \*2967460) and *mutH* (from \*2967460 to \*2967450). The *nudH* gene is associated with a red box containing 'nudH' and 'mutH' with arrows pointing to the gene. The *mutH* gene is associated with a green box containing 'mutH'. Below the sequence, several other genes are labeled with arrows and boxes: 'ir' (pink box), 'orf 13 codons' (red box), 'p10' (blue box), and '2.4 bits' (green box). A purple box highlights a small gene at the bottom.

... | sd-ir 2967470 nudH mutH- total 6.3 bits

p10

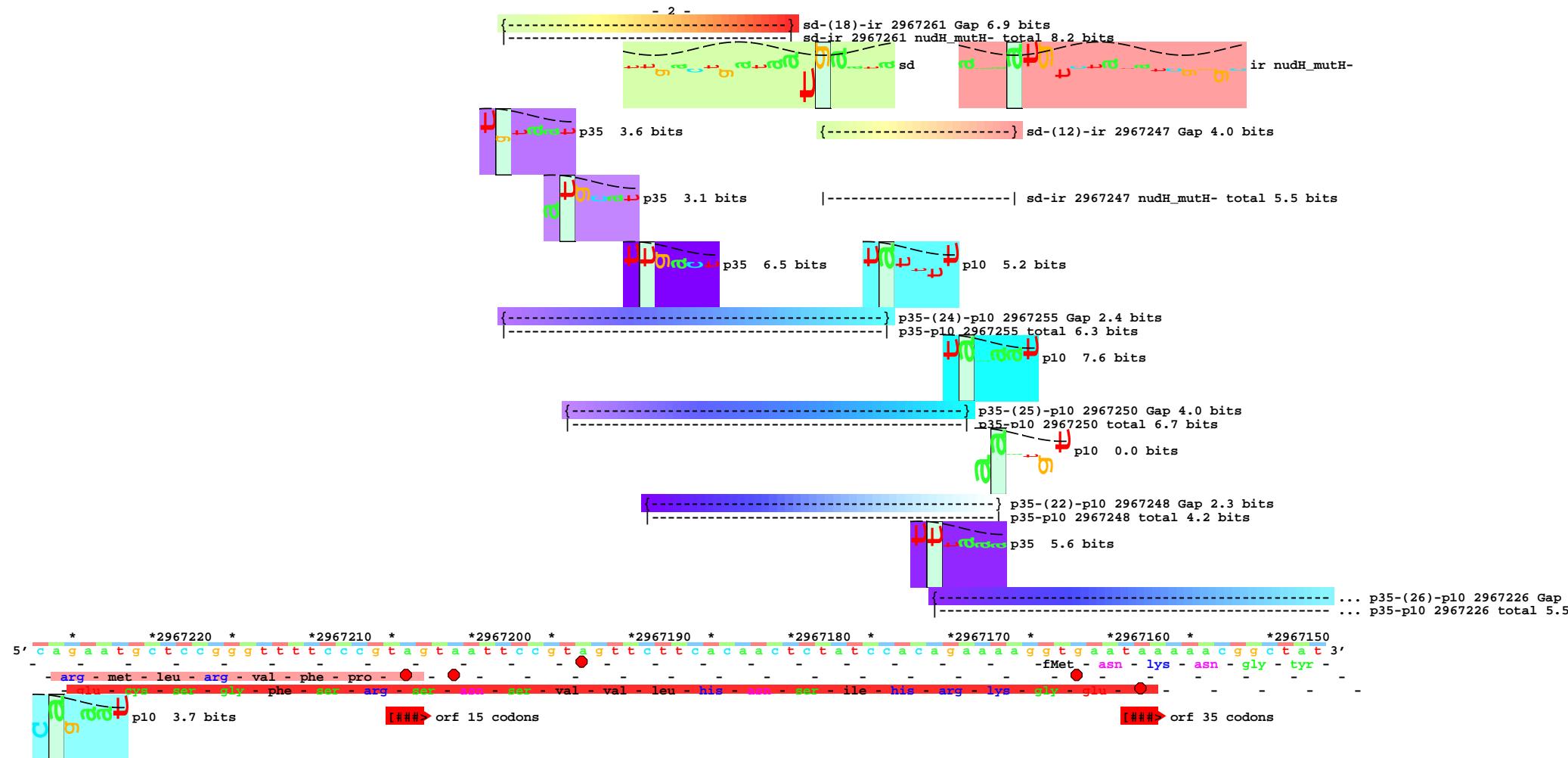
 p10 2.0 bits

 p35 5.5 bits

5' t a g t g g c a c a t t c t g t g g a t a a a a t a c g g c a t t g g t t g a t c t t t c g c c a a c c c g t a a a t g a g a g g t g t g a c c t t g g g t c a c g a 3'

-fMet - val - asp - leu - ser - pro - thr - arg - lys - fMet - ile - phe - arg - gln - pro - val - asn - glu - arg - cys - asp - leu - gly - his - glu -  
-val - ala - his - ser - val - asp - lys - tyr - gly - ile - gly -

The diagram illustrates the *nudH\_mutH* operon. It features two genes: *nudH* (green box) and *mutH* (red box). The *nudH* gene contains a Shine-Dalgarno (sd) sequence and a ribosome binding site (RBS). The *mutH* gene also has a RBS. Transcription start sites are indicated by red dots above the genes. The mature mRNA is shown as a dashed line connecting the two genes. The deduced amino acid sequences for both genes are listed below their respective genes.



```
... --> p35-(26)-p10 2967226 Gap 3.7 bits  
... --> p35-p10 2967226 total 5.5 bits
```

Sequence logo showing the conservation of amino acids at each position of the protein sequence. The x-axis represents positions 1 to 20. The y-axis lists amino acids: \* (stop), pro, leu, pro, leu, phe, ile, thr, leu, his, ile, thr, val, ser, tyr, ser, ile, val, ile, ser, val, fMet, leu, leu, val, cys, asn, ala, leu, gln, arg, val, fMet, pro, cys, arg, glu, trp. Red dots indicate positions where the amino acid is conserved across all 14 homologs.

- 3 -

