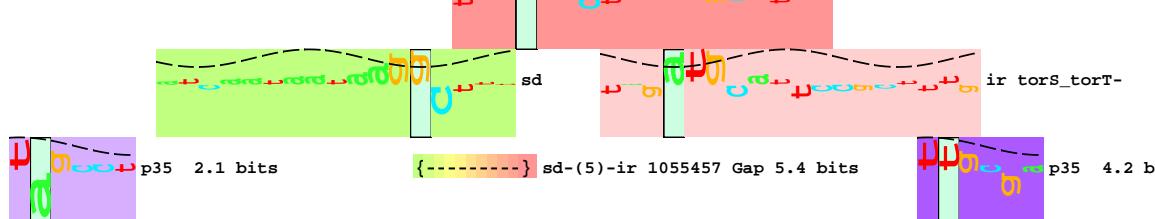


- 1 -

piece 1, NC_000913, tors_torT-, config: linear, direction: -, begin: 1055513, end: 1055382

[NC_000913.t0r]



```
|-----| sd-ir 1055457 torS_torT- total 6.8 bits
{-----| sd-(12)-ir 1055450 Gap 4.0 bits
|-----| sd-ir 1055450 torS_torT- total 5.0 bits
```

```
{-----} p35-(23)-p10 1055457 Gap 1.4 bits | ----- ... p35-p10 1055415 total 7.0  
|----- p35-p10 1055457 total 6.0 bits
```

Detailed description: This figure displays a sequence alignment between a DNA template and five different protein sequences. The DNA template is at the top, with its 5' end on the left. It features several restriction enzyme recognition sites: 1055430 (SphI), 1055420 (PstI), 1055410 (EcoRI), 1055400 (XbaI), and 1055390 (KpnI). Each site is preceded by a star (*) indicating a potential cleavage site. Below the DNA template, five protein sequences are aligned. The first four proteins share a common leader sequence: '-leu -asn -leu -phe -his -leu -lys -cys -thr -asp -arg -glu -phe -asn -pro -asp -pro -'. The fifth protein begins with a different leader: '-ser -thr -phe -phe -thr -'. Red dots are placed above the amino acid 'ser' in the first four proteins and above the amino acid 'phe' in the fifth protein, highlighting specific residues of interest.

45

[###> orf 20 codons

```
... } p35-(22)-p10 1055415 Gap 2.3 bits  
... } p35-p10 1055415 total 7.0 bits
```