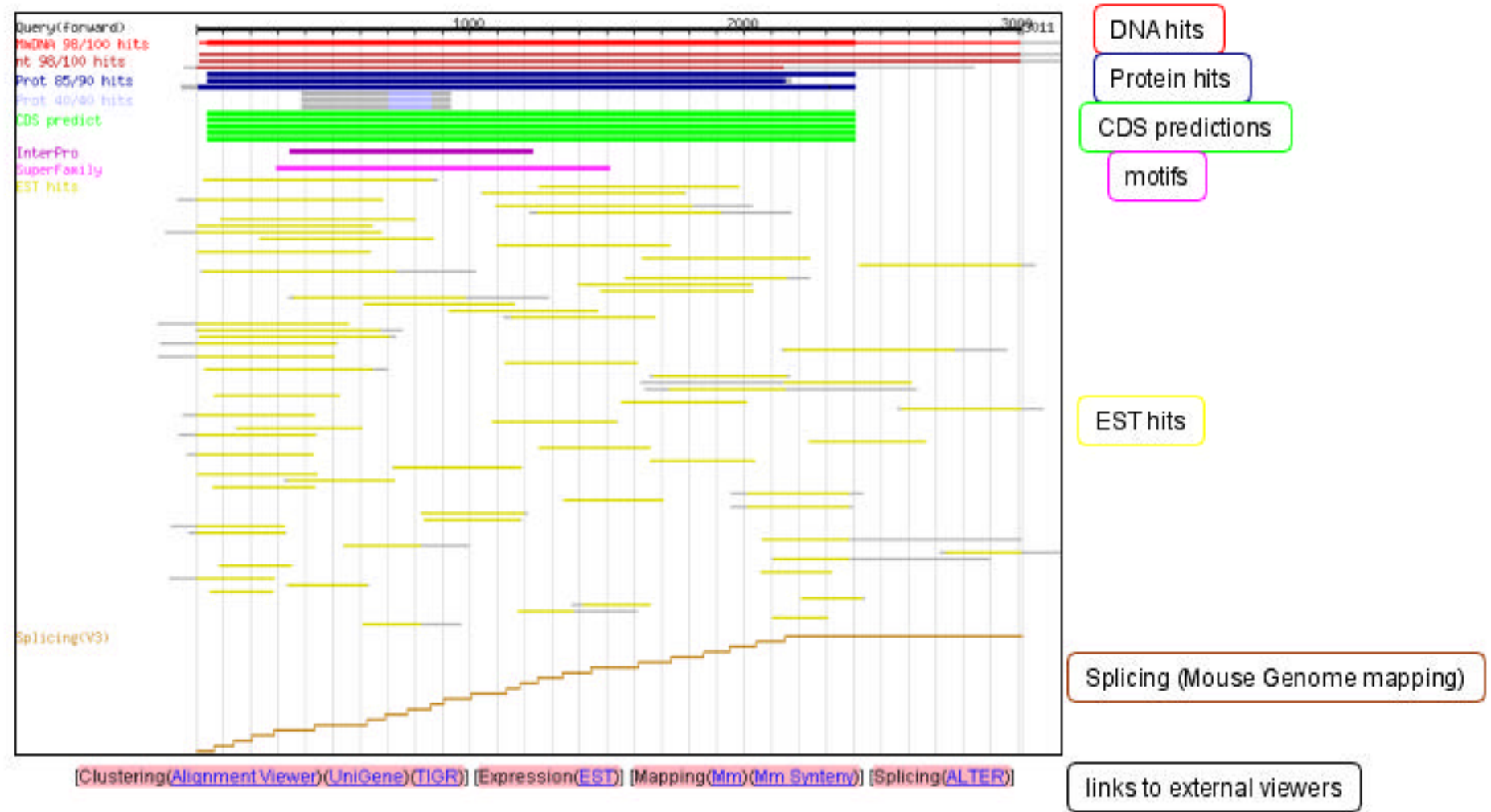


# Supplementary Information 7A

## FANTOM 2 Viewer



# Supplementary Information 7B

## cDNA Annotation system (CAS)

### Integrated Summary Image

The image displays the cDNA Annotation system (CAS) interface. The main window shows a cDNA record with various annotations. A callout box labeled 'Detailed view' points to a 'Reflect information' window. Another callout box labeled 'Click mouse' points to a 'Curation frame' window. The 'Reflect information' window contains a table with the following data:

accession	annotation text	reflect
Candida Gene Name	HYPOTHETICAL_G73312A.PROTEIN homolog (Mus musculus)	present in / add this
Candida Gene Symbol		present in / add this
Synonyms		present in / add this
Match Status 1	<input type="checkbox"/> complete <input type="checkbox"/> partial <input type="checkbox"/> problem	present in / add this
Match Status 2	<input type="checkbox"/> same as seq <input type="checkbox"/> different	present in / add this
Match Status 3	<input type="checkbox"/> same as ref <input type="checkbox"/> unaligned <input type="checkbox"/> wrong	present in / add this

The 'Curation frame' window shows a form for editing gene information, including fields for 'Candida Gene Name', 'Candida Gene Symbol', 'Synonyms', 'Match Status 1', 'Match Status 2', and 'Match Status 3'. The 'Alignment 1' window displays a FASTA alignment between a cDNA sequence and a protein sequence:

```
FASTA compares a TSA sequence to a protein sequence data base
sequence 3 3109 May 28, 2001
Please cite:
Penczek et al. Genome (1997) 44:26-36

/taq/taq1 14497: 1823 aa
/taq1 533343807/PP88854999/3013 contig=91 seq=1 seqid=3018
vs /taq/taq1 14417 library
seqid=taq /taq=taq1 14417 library

787 residues in 1 sequence

FASTA (3 39 May 28(2) function: optimized, BLO88 matrix (15 -5) itup: 2
junk: 48, opt: 42, gap-pen: -15, -2 shift: -28, sub: -28, wdl: 16
Size: 1560
The best scores are:
>CITE/C99811 (787) [1] 5188 (787 aa)
<=3278/089001
>intra 1140 insel: 5188 opt: 5168
Smith-Waterman score: 5160.99 492: identical (39 492: unappd) in 787 aa overlc0 (41-2482 1-787)
ri1511 #S1I01LACPLAKP8HLEAPPIE8P8TEE8H88PPEDIPVLGG8V8P8P8
<SPTP# #S1I01LACPLAKP8HLEAPPIE8P8TEE8H88PPEDIPVLGG8V8P8P8
10 20 38 48 60
ri1511 CULVYI88KKEE8E8P8I8L8P8I8G8G8K8LL8B8L8G8K8T8L8K8H8P8L8T8I8I8
```