

Supplementary figure 3

Figure 3a Category 1

1. The [NAALADase/PSMA1]₁ gene is known to produce multiple [mRNA splice forms]₂ ([PSMA1a and PSMA1b]₁).
2. It had been assumed that the [human]₃ [brain and prostate]₄ express transcript variants of the enzyme generated by [differential promoter usage]₂.
3. One of these genes encodes [two]₆ different enzyme forms, alpha and beta, due to [the differential usage of first exons]₂.
4. The newly defined region contains [an intron that may be alternatively spliced and seven polyadenylation signal sequences]₂.
5. [EDNRDelta3]₁ generates the same amino acid sequence at the C terminus, but utilizes [the polyadenylation signal within the open reading frame]₂, resulting [in a shorter 3' UTR]₅.
6. The larger clone has 5' and 3' ends that are identical to the smaller clone but also has [an alternatively spliced 1.9-kilobase internal segment]₂.

Category 2

7. A [HPFK-M]₁ cDNA clone lacking [the sequences corresponding to exon IX]₅ was isolated from [human]₃ [fibroblast]₄ (IMR-90) library, suggesting that [HPFK-M]₁ transcript may be [alternatively spliced]₂.
8. Soluble [Fc gamma receptors]₁ are produced by [cleavage of the membrane receptors or by alternative splicing]₂.
9. [Northern hybridization analysis and RT-PCR]₇ suggests that the soluble and membrane bound forms of [human]₃ [AmP]₁ are products of [twodistinct genes or, through alternative splicing]₃, have different [C-terminal sequences]₅.

Category 3

10. In this study, we have identified [three]₆ [Skn-1]₁ isoforms, which encode [peptides with various N termini]₅.
11. These [two]₆ [hRPB3]₁ mRNA species differed in [3' UTR region length]₅, the longer transcript containing the AU-rich sequence motif that mediates mRNA degradation.
12. If this question is correct, the observed differences in [amino acid sequences]₅ could be explained by the existence of different mRNAs for gamma and gamma' chains.

13. [Northern blot analysis]₇ detected 2.4 kb and 3.2 kb mRNA transcripts in all tissues examined.
14. [Gene expression analysis using cph genomic fragments from normal and neoplastic cells]₇ identifies a number of transcripts including a major mRNA of 2.5 kb as well as several smaller transcripts.
15. There were [tissue-specific]₈ differences in the size of mRNA transcripts in [human]₃ [brain]₄ tissues as well.
16. All [six]₆ mRNAs were present in the samples analyzed.

figure 3b

17. A G to T mutation in exon 6 results in an in-frame termination codon in eight Hispanic patients from Colorado and New Mexico.
18. Northern analysis and RT-PCR detected aberrant splicing and mutations of TEG101 in human breast cancer cell lines.
19. We report on molecular cloning of a novel human cDNA by its interaction with the splice factor SRp30c in a yeast two-hybrid screen.
20. All exon-intron boundaries agree with GT-AG rule.
21. Using RT-PCR analysis, we show that human 20alpha-HSD, and PGFS mRNAs express ubiquitously, while DD4 mRNA is restricted to the liver.
22. Regions of strong divergence between chicken fast C-protein and human slow C-protein may represent differences in C-protein isoforms.
23. Identification of I-plastin, a human fimbrin isoform that is expressed in intestine and kidney.