```
        1         11        21        31        41        50
        |         |         |         |         |         |
HSMAR1: TTAGGTTGGTGCAAAAGTAATTGCGGTTTTTGCATTGTTGGAATTTGCCG

        51        61        71        81        91        100
        |         |         |         |         |         |
HSMAR1: TTTGATATTGGAATACATTCTTAAATAAATGTGGTTATGTTATACATCAT

        101       111       121       131       141       150
        |         |         |         |         |         |
HSMAR1: TTTAATGCGCATTTCTCGCTTTACGTTTTTTTGCTAATGACTTATTACTT

        151       161       171       181       191       200
        |         |         |    ^    |         |         |
HSMAR1: GCTGTTTATTTTATGTTTATTTTAG^ACTATGGAAATGATGTTAGACAAAA
SETMAR: GCTGTTTA-----TGTTTATTTTAG^ACTATGAAAATG...
U80773: GCTGTTTATTTTGTGTTTATTTTAG^ATGATGGAAATG...
U80769: GCTGTTCATTTCATG----TTTTAG^ACTATGAAAATG...
U80764: GCTGTTTTGTTTATGTTTATTTTAG^ACTATGGAAATG...
```

Fig. 6. A cryptic acceptor splice site in *Hsmar1* allows the recurrent transcriptional capture of *Hsmar1* transposase sequences by splicing. Alignment of the intron/exon junction of four different human genomic loci producing a chimeric transcript involving the junction of an *Hsmar1*-unrelated exon to an *Hsmar1* transposase sequence located downstream. The conserved position of the intron/exon 3' junction (indicated by "^") highlights the fact that the acceptor splice site is located at the exact same position in the four different *Hsmar1* sequences. The first line is the consensus *Hsmar1* sequence. The second sequence is from the *SETMAR* locus (intron/exon junction supported by multiple human EST, e.g., U80776). The accession numbers for EST supporting the three other junctions are given. The putative start codon of the *Hsmar1* transposase gene is boxed.