

Fig. 1

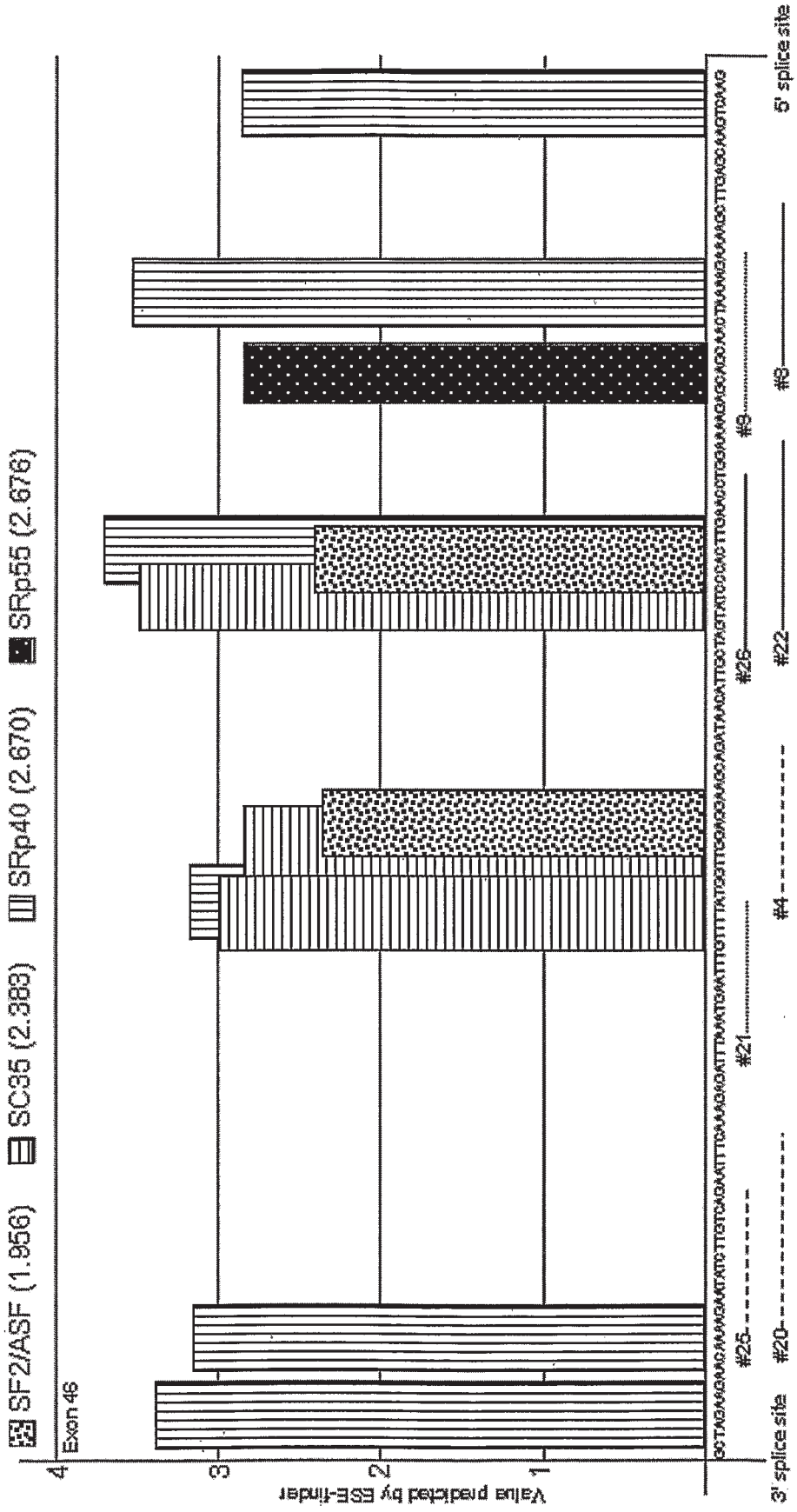

SF2/ASF (1.956)
SC35 (2.383)
SRp40 (2.670)
SRp55 (2.676)
Exon 46
Value predicted by ESE-finder
4
3
2
1
3' splice site
5' splice site
#25
#20
#21
#4
#6
#26
#22
#23
#8
#24
AONs that induce exon skipping in over 25% of control transcripts
AONs that induce exon skipping in less than 25% of control transcripts
AONs that do not induce exon skipping in control transcripts

Fig. 2

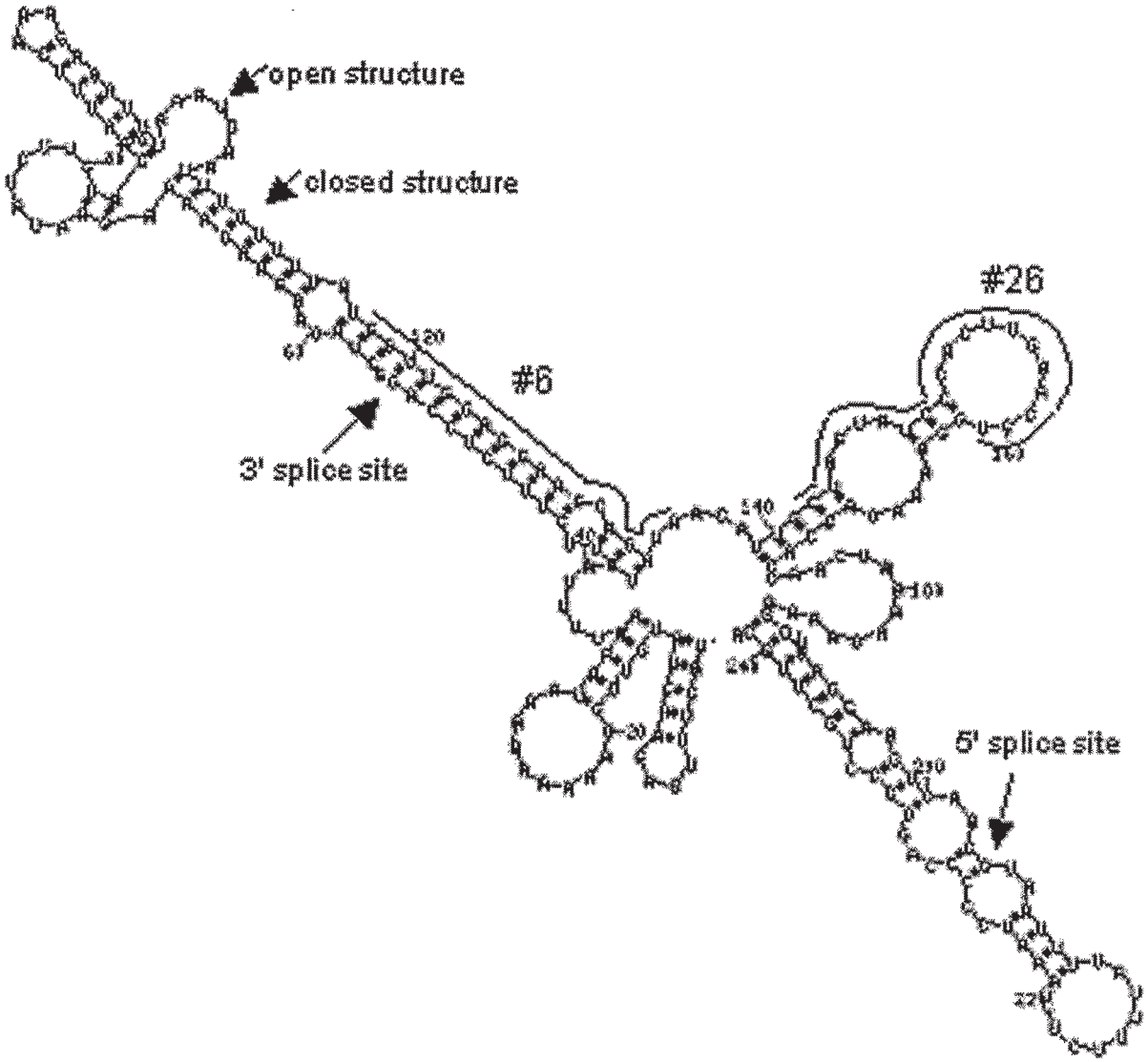

open structure
closed structure
#26
#6
3' splice site
5' splice site

Fig. 3

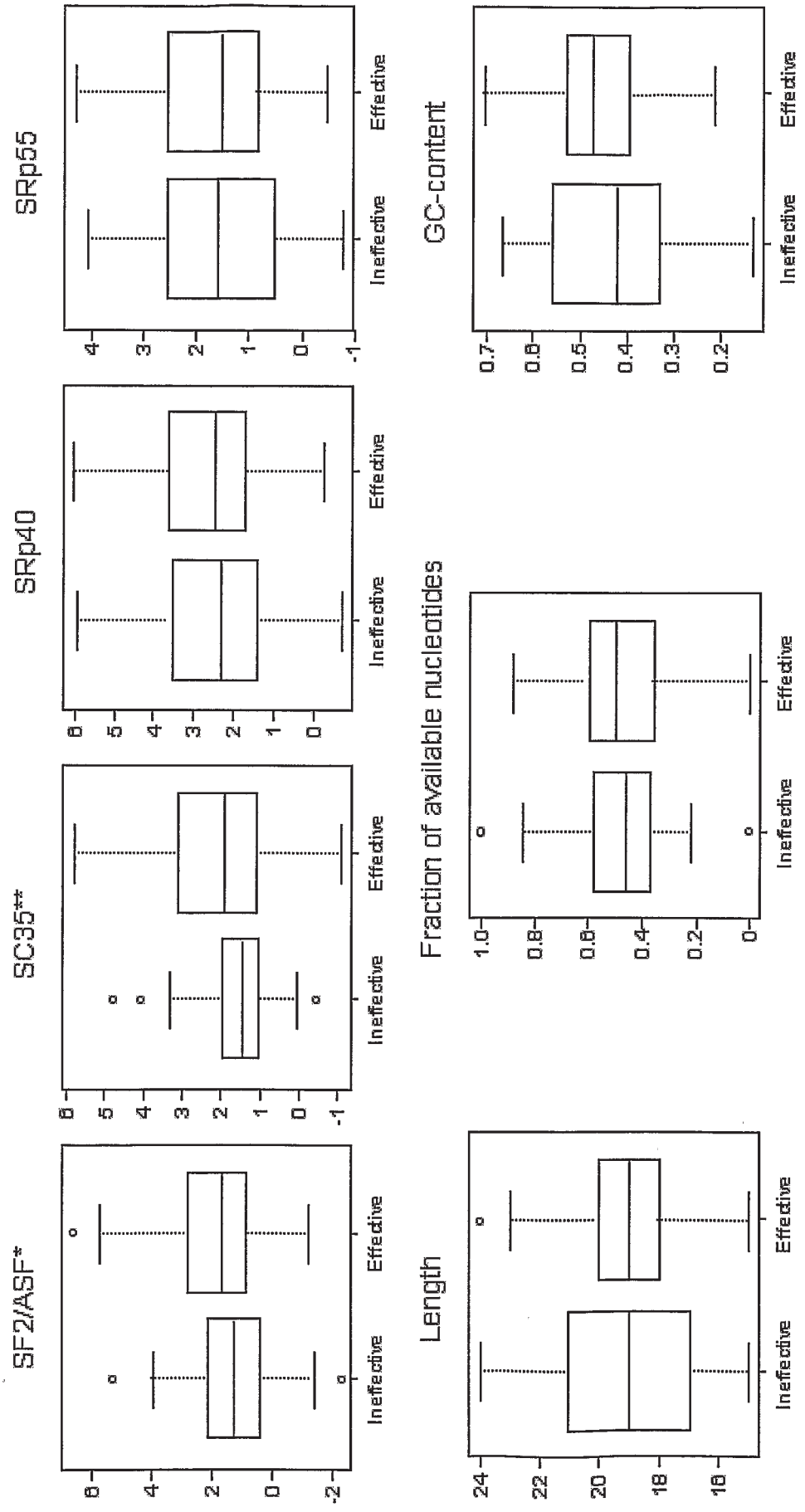

SF2/ASF*
SC35**
SRp40
SRp55
Length
Fraction of available nucleotides
GC-content
Ineffective
Effective

Fig. 4A

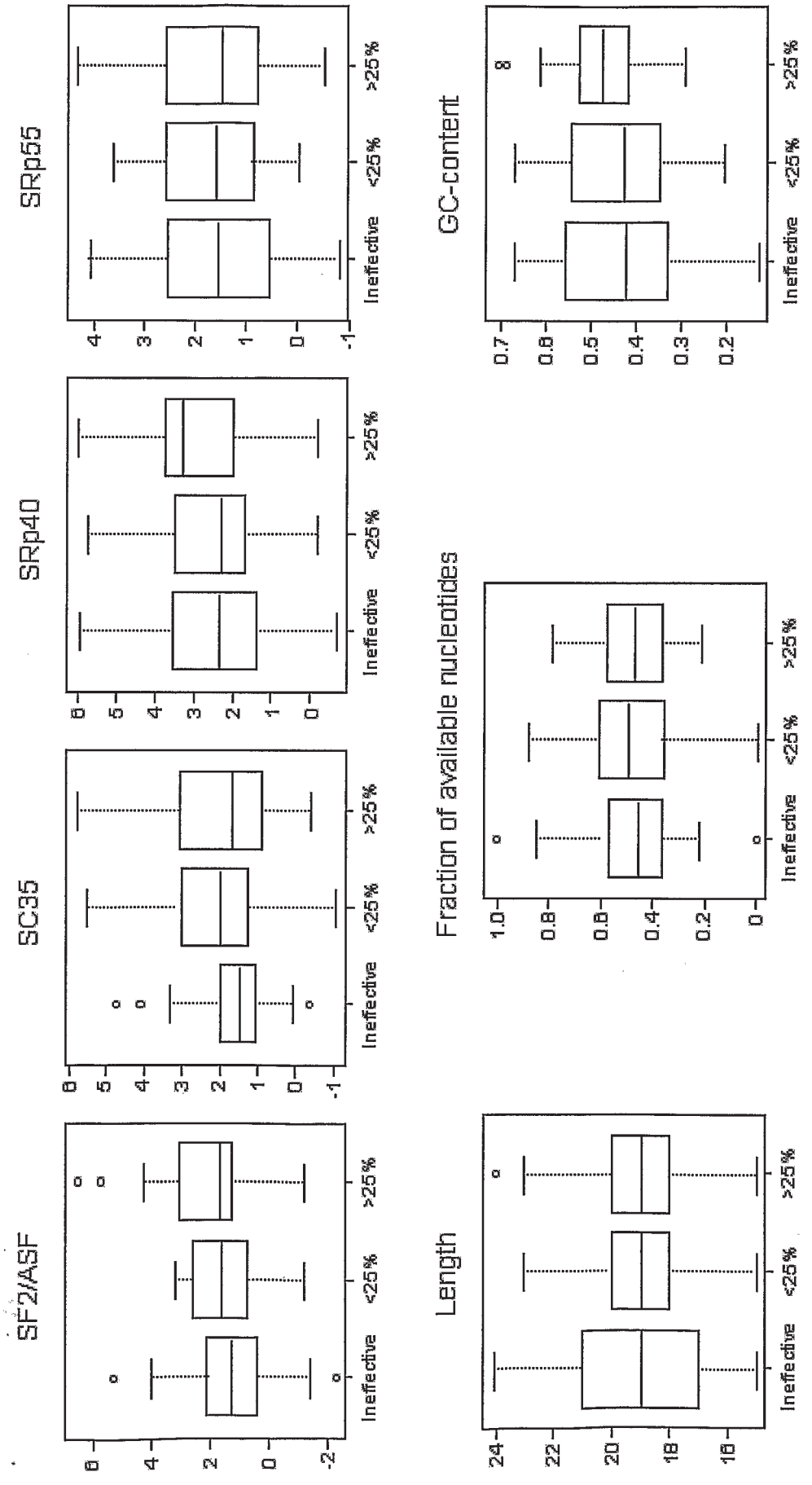

SF2/ASF
SC35
SRp40
SRp55
Fraction of available nucleotides
GC-content
Length
Ineffective
<25%
>25%

Fig. 4B