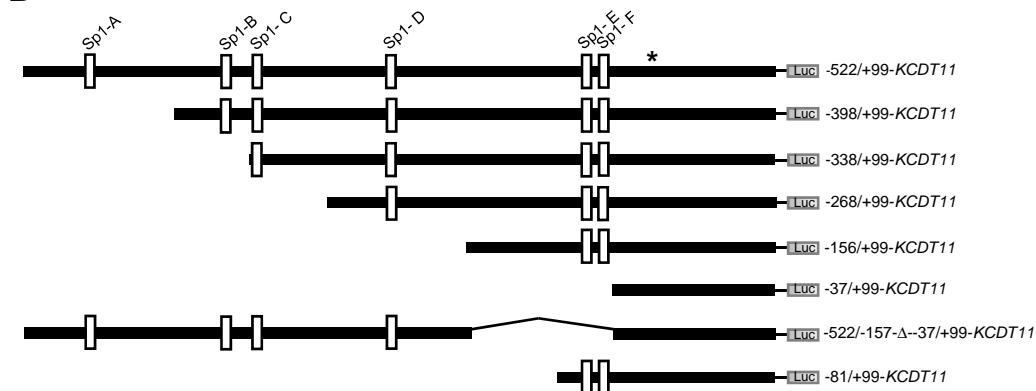
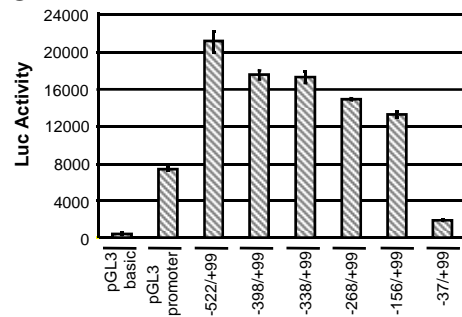


A

-522 CGCTGCGGGG CGGGGGCTCT CGGGCTGGGG CGACGTGGCC AGCCCAGTCC TGCCGAGGGG TGGGGCTGCG CCTGGGGCTC₈
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 Spl-B
 -442 GCTGGCCCGG CGCCGCCGCG GAGAGAGCGC GCCCGGGCCA CCCCGGCTGG AAGGCATCCC CGGAATGCGG CGGCTCAGCA
Spl-B 9 10 11 12 13 14 15 16 Spl-C 17 18 19 20
 -362 CCCCCCCCCT CGGGAATTC CCGGGGGAGC CGCTGGGAGG GACTCGGCTC CCGGGCTGGG CCGGCCGGGC CTCGGGCTCT
 21 22 23 24 25 26 27 28 Spl-D 29
 -282 GAGCGGTGGG ATTAGAGGCT CCAGCCCCGC CGACTTGCG ACGTGAGATC GGGCACACCT GAGCGGGCCG GGGGCCCTCG
 30 31 32 33 34 35 36 37 38 39
 -202 TGGCCACATC CGGGGCGGACG TGCGTAGTCT ACCCCGTCCC GCCAGCGTCT GCCAGTCCAG CCAGTCCGCC CAGTCTCTCG₄₇
 40 41 42 43 44 45 46 47
 -122 CGTCCGAGAC TGGCTCCAG CCTCCCACCT CCGCCCGGGC CGCGCGAGCC TCCGGGGGCC GGGGCCGGG CGCCAGGGG
 48 Spl-F49 50 51 52 53 54 55 56 57 58 59 60 Spl-F
 -42 CGGGGCTGTC TCTTAAAGGG CCCCGGGCGG CTGCCCTTAG GCCACTTCT GGGGCGGAG AGGACCTCAG CGGCTGCGGC
 61 62 63 64 65 66 67
 +38 GACACCCAGG GAAGGCGGGC CGGCGGGGTC CCGAAACTCC TGGTGTTTC CATCAGAGCC CTC

B**C****D**