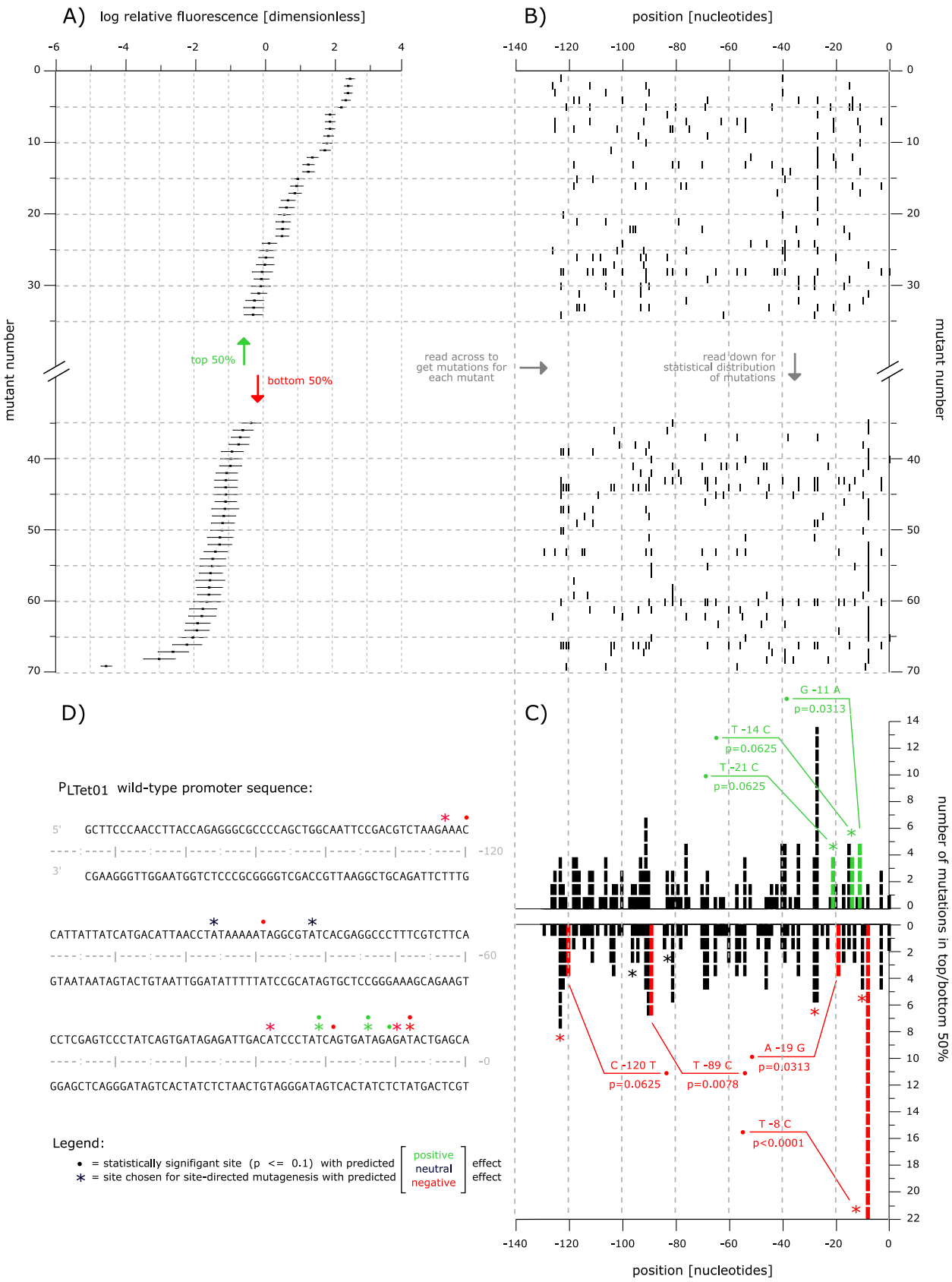
A)
log relative fluorescence [dimensionless]
mutant number
top 50%
bottom 50%
B)
position [nucleotides]
read across to get mutations for each mutant
read down for statistical distribution of mutations
mutant number
C)
G -11 A
p=0.0313
T -14 C
p=0.0625
T -21 C
p=0.0625
C -120 T
p=0.0625
T -89 C
p=0.0078
A -19 G
p=0.0313
T -8 C
p<0.0001
number of mutations in top/bottom 50%
position [nucleotides]
D)
PLTet01 wild-type promoter sequence:
5' GCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGACGTCTAAGAAAC -120
3' CGAAGGGTTGGAATGGTCTCCCGCGGGGTCGACCGTTAAGGCTGCAGATTCTTTG
CATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCA -60
GTAATAATAGTACTGTAATTGGATATTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGT
CCTCGAGTCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCA -0
GGAGCTCAGGGATAGTCACTATCTCTAACTGTAGGGATAGTCACTATCTCTATGACTCGT
Legend:
• = statistically signifigant site (p <= 0.1) with predicted positive effect
neutral effect
negative effect
* = site chosen for site-directed mutagenesis with predicted