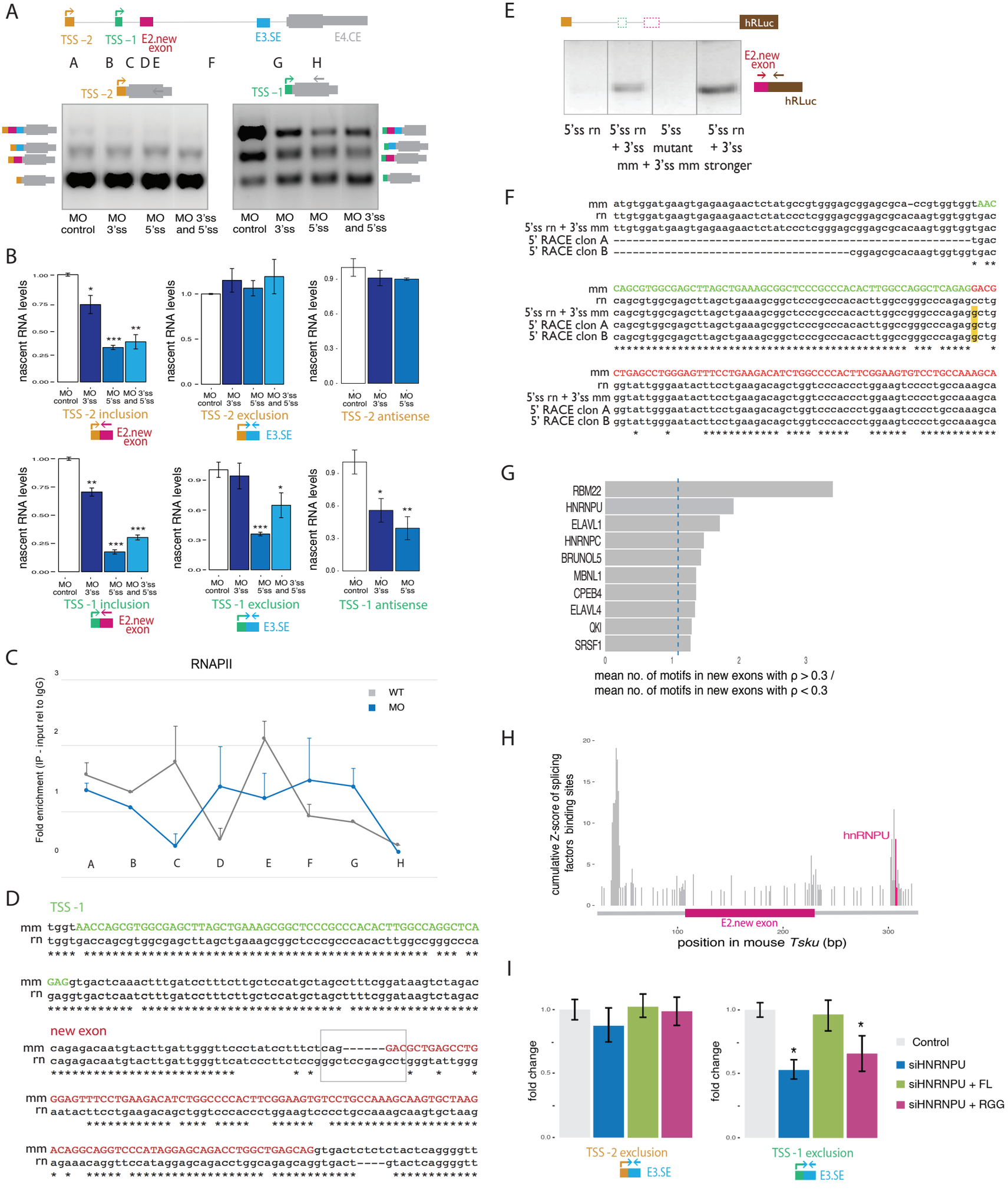
A
TSS –2
TSS –1
E2.new exon
E3.SE
E4.CE
A B C D E F G H
MO control
MO 3'ss
MO 5'ss
MO 3'ss and 5'ss
B
nascent RNA levels
TSS -2 inclusion
TSS -2 exclusion
TSS -2 antisense
TSS -1 inclusion
TSS -1 exclusion
TSS -1 antisense
E2.new exon
E3.SE
C
RNAPII
WT
MO
Fold enrichment (IP - input rel to IgG)
D
TSS -1
new exon
mm tggtAACCAGCGTGGCGAGCTTAGCTGAAAGCGGCTCCCGCCCACACTTGGCCAGGCTCA
rn tggtgaccagcgtggcgagcttagctgaaagcggctcccgcccacacttggccgggccca
mm GAGgtgactcaaactttgatcctttcttgctccatgctagcctttcggataagtctagac
rn gaggtgactcaatctttgatcctttcttgctccatgctagcttttcggataagtctagac
mm cagagacaatgtacttgattgggttccctatcctttctcag------GACGCTGAGCCTG
rn cagagacaatgtacttgattgggttcatcccttctccgggctccgagcctgggtattggg
mm GGAGTTTCCTGAAGACATCTGGCCCCACTTCGGAAGTGTCCTGCCAAAGCAAGTGCTAAG
rn aatacttcctgaagacagctggtcccaccctggaagtcccctgccaaagcaagtgctaag
mm ACAGGCAGGTCCCATAGGAGCAGACCTGGCTGAGCAGgtgactctctctactcaggggtt
rn agaaacaggttccataggagcagacctggcagagcaggtgact----gtactcaggggtt
E
hRLuc
E2.new exon
5'ss rn
5'ss rn + 3'ss
5'ss mutant
5'ss rn + 3'ss mm + 3'ss mm stronger
F
mm atgtggatgaagtgagaagaactctatgccgtgggagcggagcgca-ccgtggtggtAAC
rn ttgtggatgaagtgagaagaactctatccctcgggagcggagcgcacaagtggtggtgac
5'ss rn + 3'ss mm ttgtggatgaagtgagaagaactctatccctcgggagcggagcgcacaagtggtggtgac
5' RACE clon A ----------tgac
5' RACE clon B ----------cggagcgcacaagtggtggtgac
mm CAGCGTGGCGAGCTTAGCTGAAAGCGGCTCCCGCCCACACTTGGCCAGGCTCAGAGGACG
rn cagcgtggcgagcttagctgaaagcggctcccgcccacacttggccgggcccagagcctg
5'ss rn + 3'ss mm cagcgtggcgagcttagctgaaagcggctcccgcccacacttggccgggcccagaggctg
5' RACE clon A cagcgtggcgagcttagctgaaagcggctcccgcccacacttggccgggcccagaggctg
5' RACE clon B cagcgtggcgagcttagctgaaagcggctcccgcccacacttggccgggcccagaggctg
mm CTGAGCCTGGGAGTTTCCTGAAGACATCTGGCCCCACTTCGGAAGTGTCCTGCCAAAGCA
rn ggtattgggaatacttcctgaagacagctggtcccaccctggaagtcccctgccaaagca
5'ss rn + 3'ss mm ggtattgggaatacttcctgaagacagctggtcccaccctggaagtcccctgccaaagca
5' RACE clon A ggtattgggaatacttcctgaagacagctggtcccaccctggaagtcccctgccaaagca
5' RACE clon B ggtattgggaatacttcctgaagacagctggtcccaccctggaagtcccctgccaaagca
G
RBM22
HNRNPU
ELAVL1
HNRNPC
BRUNOL5
MBNL1
CPEB4
ELAVL4
QKI
SRSF1
mean no. of motifs in new exons with ρ > 0.3 /
mean no. of motifs in new exons with ρ < 0.3
H
cumulative Z-score of splicing factors binding sites
hnRNPU
E2.new exon
position in mouse Tsku (bp)
I
fold change
TSS -2 exclusion
TSS -1 exclusion
E3.SE
Control
siHNRNPU
siHNRNPU + FL
siHNRNPU + RGG