

Complex Alternative Splicing of the Smarca2 Gene Suggests the Importance of Smarca2-B Variants (Min Yang, et al.)

ACCCTGAACCAGATGATTGCTCGCCGGGAGGAAGAATTTGATCTTTTTATGCGCATGGACATGGACC GGCGGAGGGAGGA
 TGCCCGGAACCCGAAGCGCAAACCCCGCTTGATGGAGGAAGATGAGCTGCCCTCCTGGATTATCAAGGATGACGCCGAAG
 TGGAAAGGCTCACCTGTGAAGAAGAGGAGGAGAAGATATTTGGGAGGGGCTCTCGCCAGCGCCGGGATGTGGACTACAGT
 GATGCCCTCACCCGAGAAGCAATGGCTCAGGGCCATCGAAGACGGCAATTTGGAAGAAATGGAAGAGGAGGTACGGCTTAA
 GAAGAGAAAAAGACGAAGAAATGTGGATAAAGACCCCGTGAAGGAAGATGTGGAAAAAGCGAAGAAAAGAAGAGGCCGCC
 CTCCGGCTGAGAAGTTGTACCAAATCCCCAAAACCTAACGAAGCAGATGAACGCCATCATTTGATACTGTGATAAACTAC
 AAAGACAGGTGTAACGTGGAGAAGGTGCCCTGTAATTTCTCAGTTGGAAATAGAAGGAAACAGTTTCAGGGCGACAGCTCAG
 TGAAGTCTTCATTACGTTACCTTCCAGGAAAGACTTACCAGAATACTATGAATTAATTAGGAAGCCAGTGGATTTCAAAA
 AGATAAAGGAGCGAATCCGTAATCATAAGTAT

Fig. S1. Sequence of the region between exon 26 and exon 31 of the mSmarca2-a1 cDNA. Exon 26 and exon 31 are incomplete. Every other exon is presented in grey color to show the boundary of the neighbor exons. The underlined part is the 54-bp exon 29 that is skipped in the mSmarca2-a2 (NM_011416.2) in the NCBI database.

mSmarca2-b3	CCCCACTAACTGTGATTTCCGATAGCCGGCCTGCTGATAGTGGTAAGGCCATCGAAGACG
mSmarca2-b4	CCCCACTAACTGTGATTTCCGATAGCCGGCCTGCTGATAGTGGTAAGGCCATCGAAGACG
mSmarca2-b3	GCAATTTGGAAGAAATGGAAGAGGAGGTACGGCTTAAGAAGAGAAAAAGACGAAGAAATG
mSmarca2-b4	GCAATTTGGAAGAAATGGAAGAGGAGGTACGGCTTAAGAAGAGAAAAAGACGAAGAAATG
mSmarca2-b3	TGGATAAAGACCCCGTGAAGGAAGATGTGGAAAAAGCGAAGAAAAGAAGAGGCCGCCCTC
mSmarca2-b4	TGGATAAAGACCCCGTGAAGGAAGATGTGGAAAAAGCGAAGAAAAGAAGAGGCCGCCCTC
mSmarca2-b3	CGGCTGAGAAGTTGTACCAAATCCCCAAAACCTAACGAAGCAGATGAACGCCATCATTTG
mSmarca2-b4	CGGCTGAGAAGTTGTACCAAATCCCCAAAACCTAACGAAGCAGATGAACGCCATCATTTG
mSmarca2-b3	ATACTGTGATAAACTACAAAGgtgtaacgtggagaaggtgcccctgtaattctcagttgga
mSmarca2-b4	ATACTGTGATAAACTACAAAG-----
mSmarca2-b3	aatagaaggaacagACAGTTCAGGGCGACAGCTCAGTGAAGTCTTCATTACGTTACCTT
mSmarca2-b4	-----ACAGTTCAGGGCGACAGCTCAGTGAAGTCTTCATTACGTTACCTT
mSmarca2-b3	CCAGGAAAGACTTACCAGAATACTATGAATTAATTAGGAAGCCAGTGGATTTCAAAAAGA
mSmarca2-b4	CCAGGAAAGACTTACCAGAATACTATGAATTAATTAGGAAGCCAGTGGATTTCAAAAAGA
mSmarca2-b3	TAAAGGAGCGAATCCGTAATCATAAGTA
mSmarca2-b4	TAAAGGAGCGAATCCGTAATCATAAGTATCGGAGC

mSmarca2-b10:

CTGTATGTTGAATTAGGGCTCGCTCTCTTGCCAACACGTCACCAGTCCGAAACTGGGGTTTGCTTCTGTGATTTATTTTCATTATTGTGCTGGTA
 AAAGgtttggaaggaattctttctggggtagtacttttagcattgtgtgcaagttttttttttgttttggtttggtttcttttctt
 cttcttcttcttttttaatctccccccccccccagctaagttgtccggtgagctagcttaacaaataatatttttaaatcagagaagcccca
 taatttcccttacaagcaagagaaatcttaagtctaaactcttgaagtgcgaaaagcatcgggaaataggaggaattgatttccattagaaaaag
 ccccttagaaaccacagaacatgaagccctgcatatagatgtgttcccggtctttggggaggaggaagatttcggtagctctctgcatcctgca
 taaaaaccttaacttaaggggaataatgCTGATG¹AAGAGACTAGCAGCTCGCTGCTTTGCCGGCTTGTTAATTTTATCCCCACTAACTGTGATTTTC
 CGATAGCCGGCCTGCTGATAGTGGTAAGGCCATCGAAGACGGCAATTTGGAAGAAATGGAAGAGGAGGTACGGCTTAAGAAGAGAAAAAGACGAAG
 AAATGTGGATAAAGACCCCGTGAAGGAAGATGTGGAAAAAGCGAAGAAAAGAAGAGGCCGCCCTCCGGCTGAGAAGTTGTACCAAATCCCCAAA
 ACTAACGAAGCAGATGAACGCCATCATTTGATACTGTGATAAACTACAAAGACAGTTTCAGGGCGACAGCTCAGTGAAGTCTTCATTACGTTACCTTC
 CAGGAAAGACTTACCAGAATACTATGAATTAATTAGGAAGCCAGTGGATTTCAAAAAGATAAAGGAGCGAATCCGTAATCATAAGTATCGGAGCCT
 GGGAGACCTGGAGAAAGACGTCATGCTTCTCTGTCCAAACGCAC

Fig. S2: Part of the sequences of the three novel mSmarca2-b variants. **Top panel:** Sequences of the region between exon 2 and exon 7 of the mSmarca2-b3 and mSmarca2-b4. The exon 2 and exon 7 is incomplete. The exon 2 is presented in grey color to show the boundary between the 96-bp exon 2 and the 218-bp exon 4. Different from the mSmarca2-b2 documented in the NCBI database (NM_026003.2), both mSmarca2-b3 and mSmarca2-b4 lack the 35-bp exon 3 and the mSmarca2-b3 retains the 54-bp exon 5. **Bottom panel:** part of the mSmarca2-b10 sequence. The sequences underlined at the 5'- and 3'- ends are forward primer mSmarca2F'43 and reverse primer mSmarca2R4524, respectively. The lowercase letters are the 408 nucleotides of intron 1 retained by exon 1, within which the underlined atg is the start codon that adds two amino acids to the proteins starting from the ATG1 at exon 2.

Fig. S3: Sequences of the nine hSmarca2-b variants and two of the original 5'RACE sequences. These sequences are aligned to project out the differences among the variants. Every other exon is presented in grey color to show the boundary of the neighbor exons. The lowercase letters in the hSmarca2-b1 indicate the parts that may be involved in alternative splicing.
