Smooth Muscle Transcriptome Browser: offering genome-wide references and expression profiles of transcripts expressed in intestinal SMC, ICC, and PDGFRα^{+} cells

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Supplementary Figures

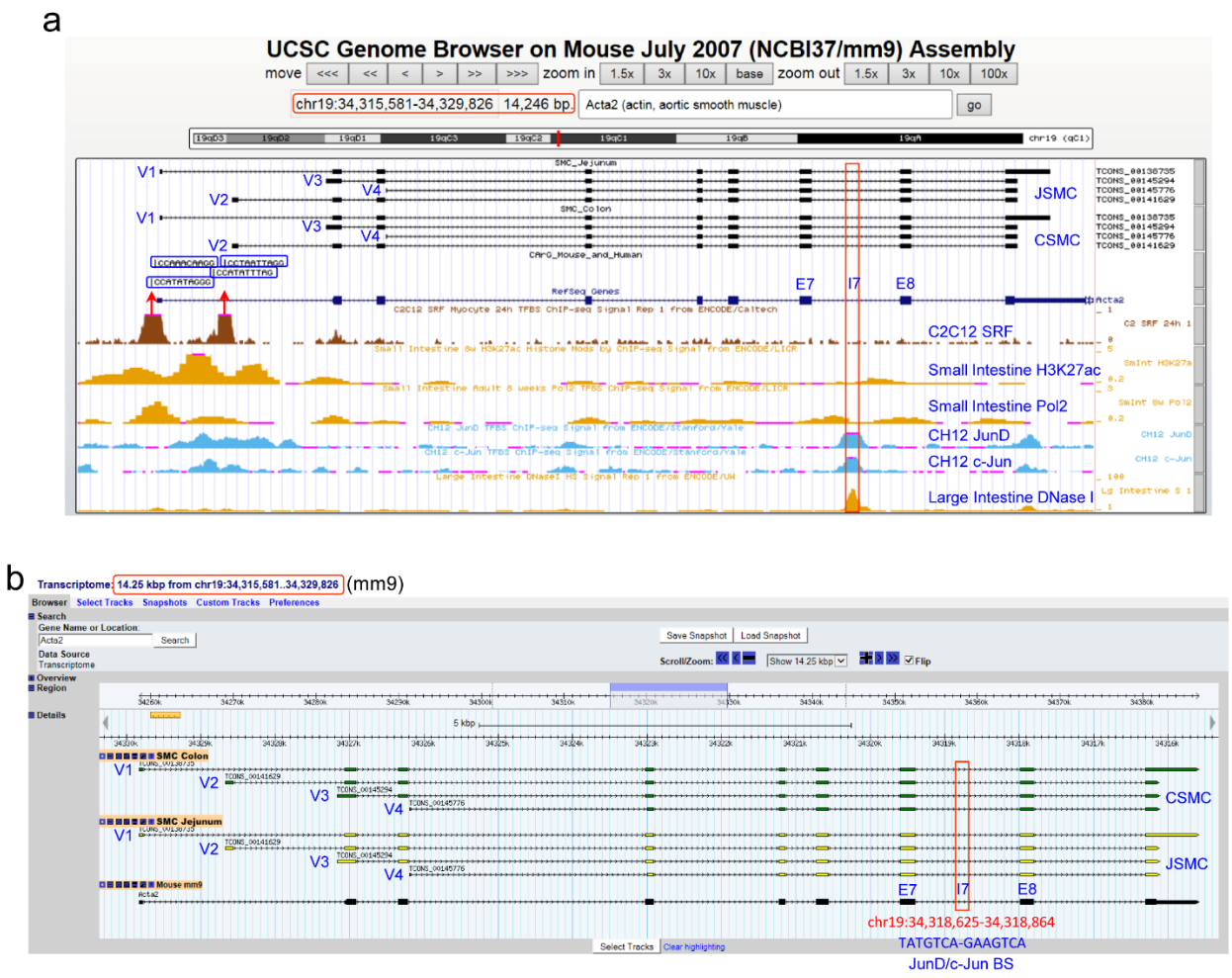

Figure S1. Complementary analysis of *Acta2* using both the Smooth Muscle Genome Browser (SMGB) and Smooth Muscle Transcriptome Browser (SMTB). (**a**) A map view of *Acta2* transcripts in the SMGB. Four transcriptional variants (V1-4) identified in CSMC and JSMC are shown within chr19:34,315,581-34,329,826 in the mouse mm9 genome. Four CArG boxes that are conserved between mice and humans are boxed in blue. Two SRF binding sites match with the CArG boxes proximate to V1 and V2 first exons. The promoter region coincides with H3K27ac modification sites and Pol2 binding sites in the small intestine genome. JunD and c-Jun binding sites are shown within intron 7. These Jun binding sites coincide with the DNase I hypersensitive region in the large intestine genome. (**b**) A map view of *Acta2* transcripts in the SMTB. The same four transcriptional variants (V1-4) identified in CSMC and JSMC are shown contained within a 14.25 kb segment (chr19:34,315,581-34,329,826 in mm9). The two JunD and c-Jun binding sites, TATGTCA and GAAGTCA, are found at chr19:34,318,625-34,318,864. For all ENCODE data displays (Maximum display mode, full; Peaks, hide; Signal, full), the following data sets were selected in Expression and Regulation: for C2C12 SRF, Caltech TFBS; for Small Intestine H3K27ac, LICR Histone; for Small Intestine Pol2, LICR TFBS; for CH12 JunD and CH12 c-Jun, Stan/Yale TFBS; for Large Intestine DNase I, UW DNase I HS.

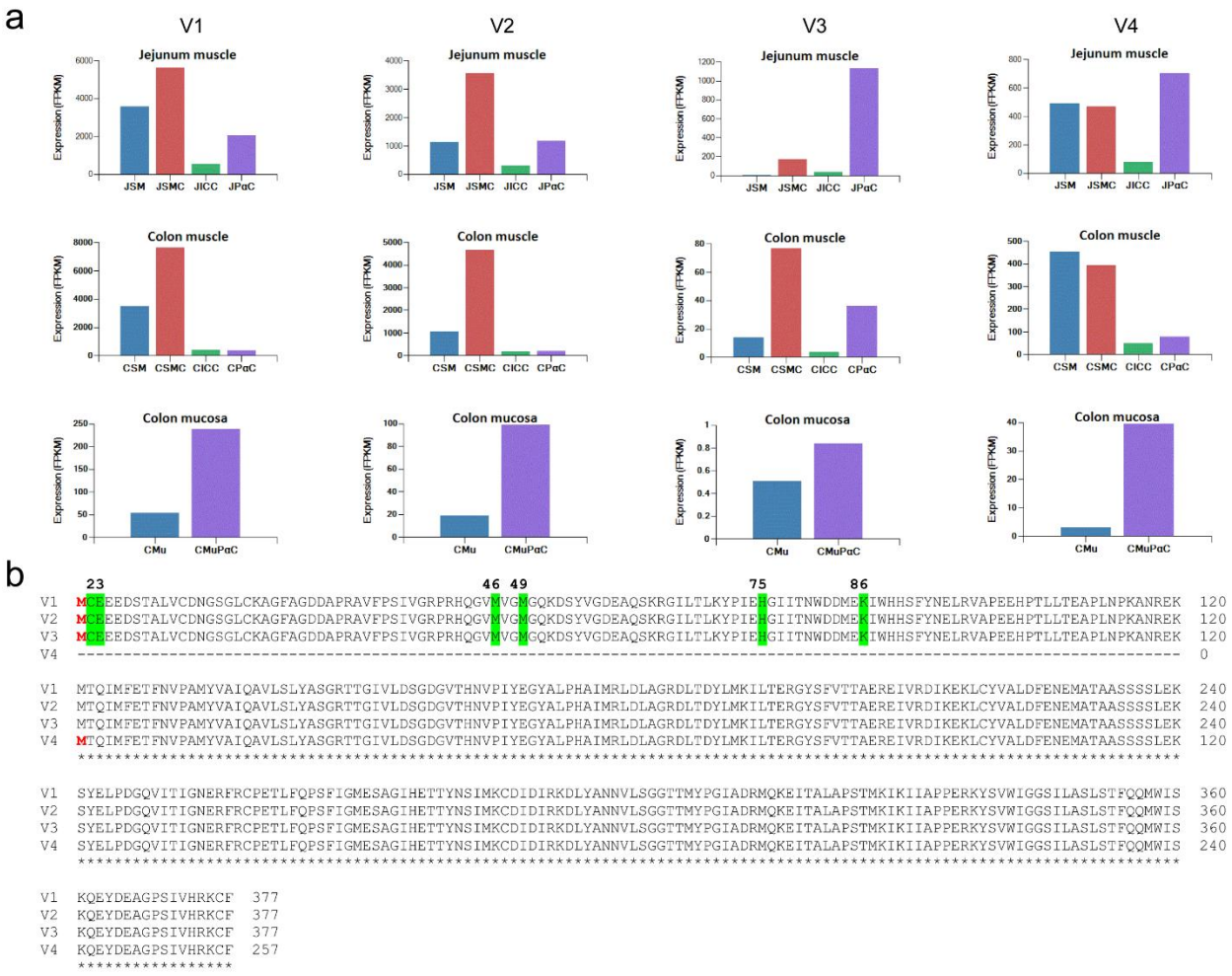

Figure S2. Comparison of mRNA expression and *in silico* translated amino acid sequence of *Acta2* variants in intestinal tissue and cells. (**a**) mRNA expression of *Acta2* variants V1-V4 in Jejunal smooth muscle tissue (JSM), isolated jejunal cells (JSMC, JICC, and JPαC), colonic smooth muscle tissue (CSM) and isolated colonic cells (CSMC, CICC, and CPαC), as well as colonic mucosa tissue (CMu) and isolated cells (CMuPαC). (**b**) Alignment of *in silico* translated primary amino acid sequence of variant open reading frames. Sequence beginning methionines (M) found at the origin of V1-4 are indicated in red. Post-translationally modified residues (2, 3, 46, 49, 75, and 86 from UniProt are highlighted in green.