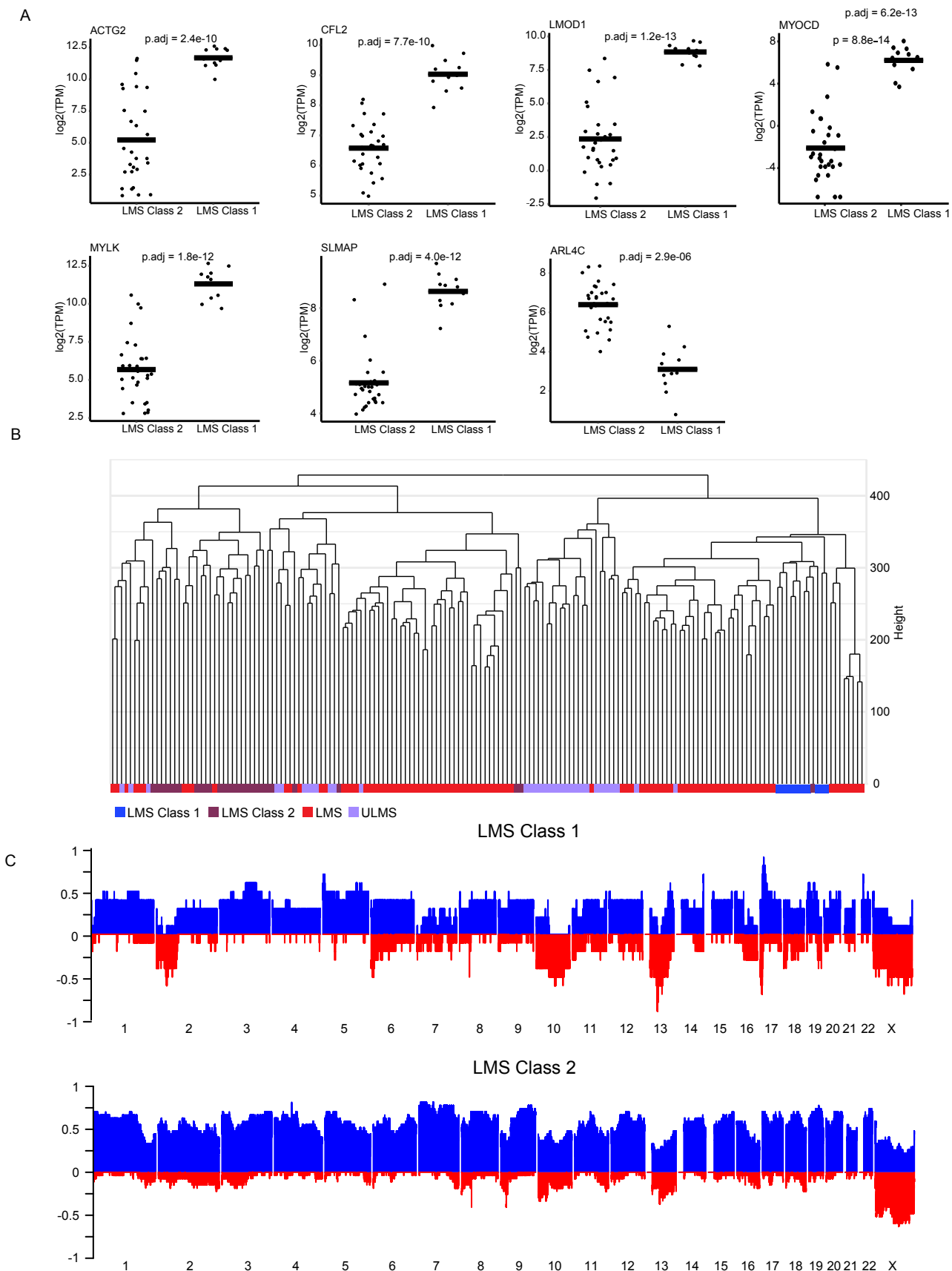




Supplementary Figure S6: Soft tissue leiomyosarcoma can be divided into two distinct classes

(A) Column scatter plots showing expression of the leiomyosarcoma Class 1 (ACTG2, CFL2, LMOD1, MYLK, SLMAP and MYOCD) and Class 2 (ARL4C) marker genes in the two leiomyosarcoma subgroups detected here (LMS Class 1, LMS Class 2). Statistical significance was assessed using an unpaired t-test with Bonferroni adjusted P-values. (B) Unsupervised hierarchical clustering of the top 25% most variably expressed protein coding genes. The clustering includes the original leiomyosarcomas (LMS Class 1 and 2) as well as validation cohort ($n = 130$) of soft tissue (LMS) and uterine leiomyosarcomas (ULMS). (C) Whole genome copy number frequency plot showing the proportion of samples harboring either gains (red) or losses (blue) among the two leiomyosarcoma subgroups LMS Class 1 (upper) and LMS Class 2 (lower).