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Figure 1.
TAZ is upregulated in PAX3-FOXO1–expressing primary human skeletal muscle myoblasts, aRMS cell lines, and tumors. A, Expression profile of human skeletal muscle myoblast (HSMM) vector control cells (Vpre) compared with PAX3-FOXO1 (P3F)–expressing HSMM cells presenescence bypass (PFpre) or postsenescence bypass (PFpost). This image is modified with permission from the Journal of Clinical Investigation. Portions of these data and validation of internal controls (WNT5A, DUSP4, MYOD, FGFR4, CXCR4) were previously reported (8, 44). qRT-PCR verifies increased WWTR1 (TAZ) expression (B), unchanged YAP expression (C), and validation of IL4R as a low-expressing internal control gene induced by P3F (refs. 45, 46; D). As measured by qRT-PCR (E) and immunoblot (F), P3F and P7F human aRMS cell lines express high levels of TAZ compared with human skeletal muscle. G, From microarray data in the Oncogenomics database (47), TAZ expression is higher in fusion-positive and fusion-negative primary human aRMS tumors than in human skeletal muscle. Representative images of RMS TMA cores immunostained for TAZ (H) and YAP protein (I). Scale bars, 100 μm. Quantification of TAZ (J) and YAP staining (K) in RMS shows increased expression of both proteins. For TAZ staining, muscle, N = 11; P3F, N = 34; P7F, N = 13; PF-neg, N = 13. For YAP staining, muscle, N = 11; P3F, N = 36; P7F, N = 10; PF-neg, N = 15. While the gene name for TAZ is WWTR1, for simplicity the label TAZ is used throughout the remainder of the figures.