Supplementary Table S1. Consistent Differences in Expression of Tendon Versus Vascular and Pericyte Markers Demonstrate a Differential Enrichment for Cell Origin in the Tendon Proper Versus Peritenon

Tnmd/Actb			*Emcn/Actb*		
Isolation number	*Peritenon*	*Tendon proper*	*Isolation number*	*Peritenon*	*Tendon proper*
1	3.077	**16.166**	1	**913.147**	1.0354
2	0.373	**35.177**	2	**99.772**	74.949
3	0.159	**2.957**	3	**100.541**	73.789
4	6.046	**8.014**	4	**58.641**	46.639
5	1.720	**22.602**	5	**156.249**	3.878
6	2.303	**56.801**	6	**1245.690**	45.235
7	**8.153**	6.489	7	**41.178**	31.135

Scx/Actb			*Cd133/Actb*		
Isolation number	*Peritenon*	*Tendon proper*	*Isolation number*	*Peritenon*	*Tendon proper*
1	**24.715**	16.168	1	**7.862**	1.079
2	4.626	**18.556**	2	**19.0375**	1.924
3	4.823	**23.757**	3	**43.258**	11.223
4	4.615	**10.700**	4	9.997	**13.533**
5	13.703	**59.119**	5	**6.183**	1.050
6	20.157	**127.672**	6	**33.779**	3.900
7	4.932	**92.049**	7	6.249	**6.353**

Gene expression for tendon markers Tenomodulin (Tnmd) and Scleraxis (Scx) is consistently higher in stem/progenitors of the tendon proper, while gene expression for vascular marker, Endomucin (Emcn), and pericyte marker (Cd133) is consistently greater for peritenon-derived stem/progenitor cells. The values given for each paired biological replicate are mean transcript abundance for each target gene relative to Actb. **Bold numbers** represent the greater values of the pairs. Each mean is determined from three technical replicates via qPCR. All values $\times 10^{-4}$.