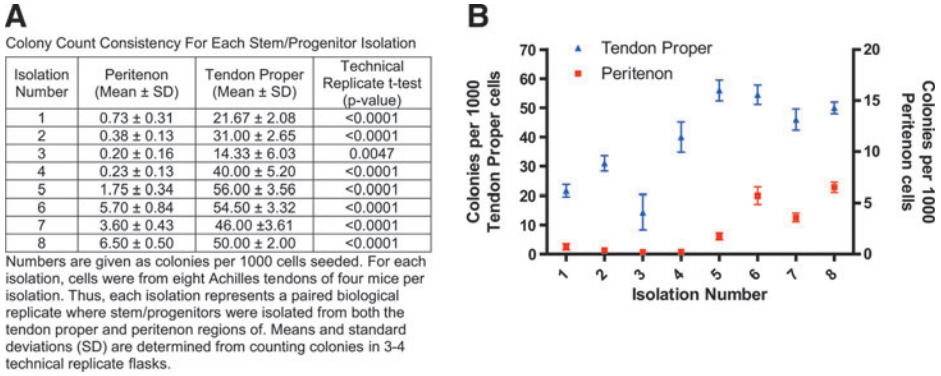

Colony Count Consistency For Each Stem/Progenitor Isolation

Isolation Number	Peritenon (Mean ± SD)	Tendon Proper (Mean ± SD)	Technical Replicate t-test (p-value)
1	0.73 ± 0.31	21.67 ± 2.08	<0.0001
2	0.38 ± 0.13	31.00 ± 2.65	<0.0001
3	0.20 ± 0.16	14.33 ± 6.03	0.0047
4	0.23 ± 0.13	40.00 ± 5.20	<0.0001
5	1.75 ± 0.34	56.00 ± 3.56	<0.0001
6	5.70 ± 0.84	54.50 ± 3.32	<0.0001
7	3.60 ± 0.43	46.00 ±3.61	<0.0001
8	6.50 ± 0.50	50.00 ± 2.00	<0.0001

Numbers are given as colonies per 1000 cells seeded. For each isolation, cells were from eight Achilles tendons of four mice per isolation. Thus, each isolation represents a paired biological replicate where stem/progenitors were isolated from both the tendon proper and peritenon regions of. Means and standard deviations (SD) are determined from counting colonies in 3-4 technical replicate flasks.

SUPPLEMENTARY FIG. S1. Sequential enzymatic isolation consistently resulted in differences in abundance of stem/progenitors by region. Each sequential enzymatic dissociation of tendon proper versus paratenon resulted in the consistent finding that more stem/progenitor cells (per 1000 cells seeded) were found in the tendon proper relative to the peritenon. **(A)** To further analyze the technical replicates, a *t*-test was done for each individual isolation. For all eight isolations, the difference was significant. There was no incidence of overlap between values intra- and interisolation. **(B)** This consistency is clearly depicted in a plot of the means and standard deviations of colony counts by isolation (Tendon Proper, ▲; Peritenon, ■).