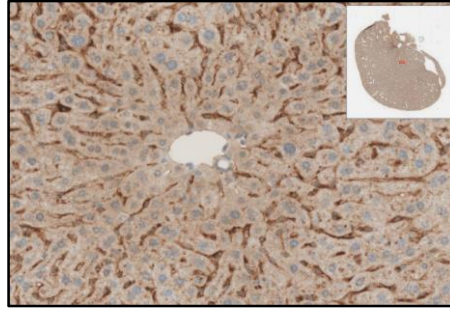
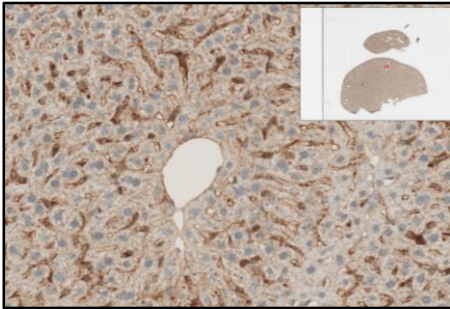


Supplemental Figure 1.

A. Liver

VWF KO

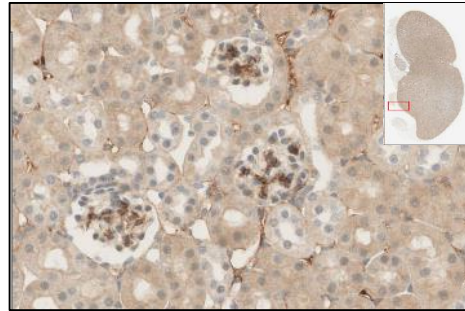
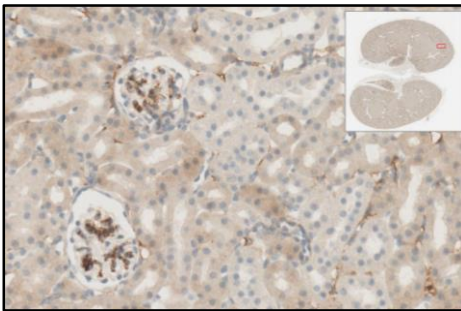
VWF/SCARA5 DKO



B. Kidney

VWF KO

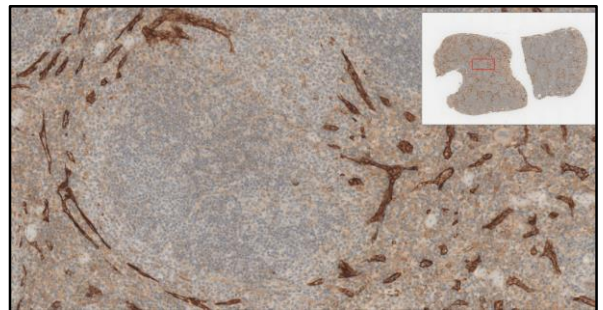
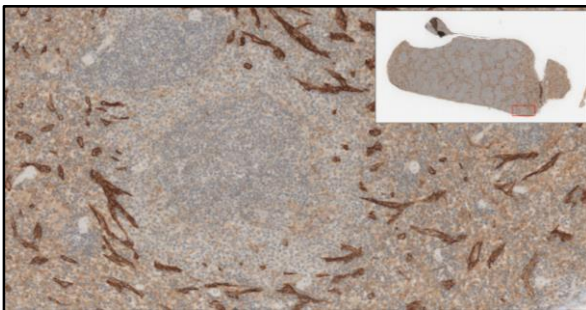
VWF/SCARA5 DKO



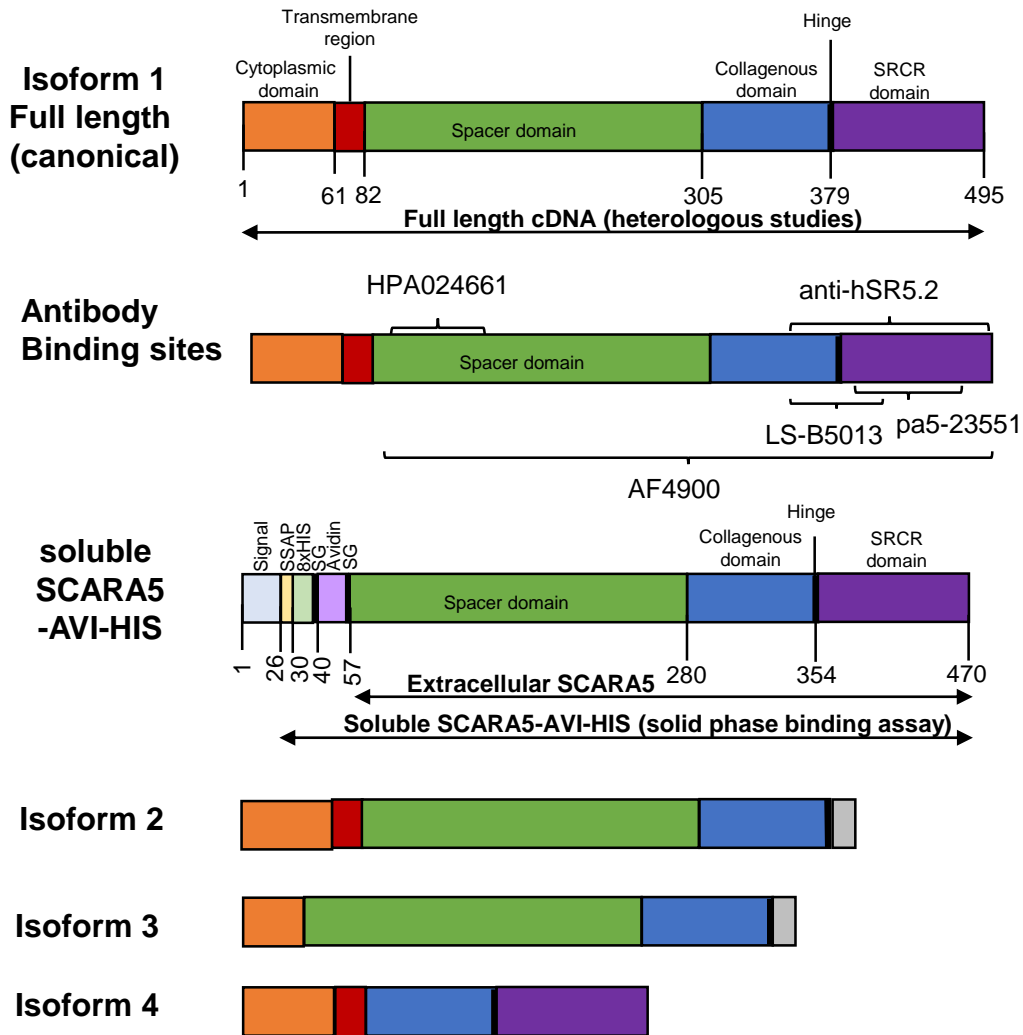
C. Spleen

VWF KO

VWF/SCARA5 DKO



Supplemental Figure 2.



Supplemental Figure 3.

>soluble SCARA5-AVI-HIS cDNA sequence – 1430 bp

gtcaGCTAGCCCACCatggggcgccgggcccgcaccctgcggtggcgctcggcctcctgctgctggcgacgctgcttgcgccg
ccgacgccccaagcgctcctCATCACCATCACCATCACCATCACAGCGGTGGCCTGAACGACATCTTC
GAGGCTCAGAAAATCGAATGGCACGAAAGCGGTAGGCCGCGCAGCTCCCCTGACGACCTGA
AGGCCCTGACTCGCAATGTGAACCGGCTGAATGAGAGCTTCCGGGACTTGCAGCTGCGGCT
GCTGCAGGCTCCGCTGCAAGCGGACCTGACGGAGCAGGTGTGGAAGGTGCAGGACGCGCT
GCAGAACCAGTCAGACTCGTTGCTGGCGCTGGCGGGCGCAGTGCAGCGGCTGGAGGGCGC
GCTGTGGGGGCTGCAGGCGCAGGCGGTGCAGACCGAGCAGGCGGTGGCCCTGCTGCGGG
ACCGCACGGGCCAGCAGAGCGACACGGCGCAGCTGGAGCTCTACCAGCTGCAGGTGGAGA
GCAACAGTAGCCAGCTGCTGCTGAGGCGCCACGCGGGCCTGCTGGACGGGCTGGCGCGCA
GGGTGGGCATCCTGGGCGAGGAGCTGGCCGACGTGGGCGGCGTGTGCGCGGCCCTCAACC
ACAGCCTGTCTACGACGTGGCCCTCCACCGCACGCGGCTGCAGGACCTGCGGGTGTGGT
GAGCAACGCCAGCGAGGACACGCGCCGCCTGCGCCTGGCGCACGTAGGCATGGAGCTGCA
GCTGAAGCAGGAGCTGGCCATGCTCAACGCGGTACCCGAGGACCTGCGCCTCAAGGACTGG
GAGCACTCCATCGCACTGCGGAACATCTCCCTCGCGAAAGGGCCACCGGGACCCAAAGGTG
ATCAGGGGGATGAAGGAAAGGAAGGCAGGCCTGGCATCCCTGGATTGCCTGGACTTCGAGG
TCTGCCCGGGGAGAGAGGTACCCAGGATTGCCCGGGCCCAAGGGCGATGATGGGAAGCT
GGGGGCCACAGGACCAATGGGCATGCGTGGGTTCAAAGGTGACCGAGGCCCAAAAGGAGA
GAAAGGAGAGAAAGGAGACAGAGCTGGGGATGCCAGTGGCGTGGAGGCCCCGATGATGATC
CGCCTGGTGAATGGCTCAGGTCCGCACGAGGGCCGCGTGGAAAGTGTACCACGACCGGCGC
TGGGGCACCGTGTGTGACGACGGCTGGGACAAGAAGGACGGAGACGTGGTGTGCCGCATG
CTCGGCTTCCGCGGTGTGGAGGAGGTGTACCGCACAGCTCGATTCCGGCAAGGCACTGGGA
GGATCTGGATGGATGACGTTGCCTGCAAGGGCACAGAGGAAACCATCTTCCGCTGCAGCTTC
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CTGAGGATCCacg

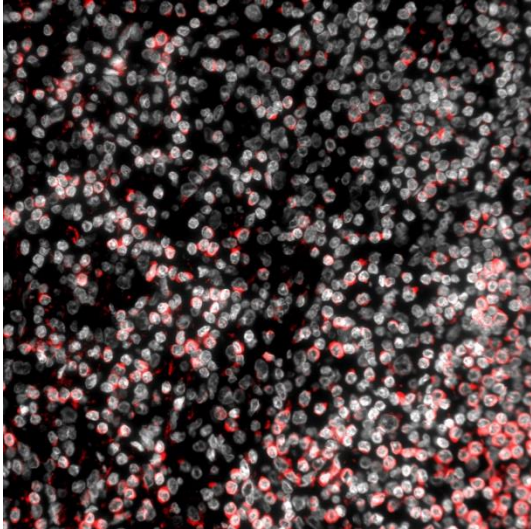
>soluble SCARA5-AVI-HIS amino acid sequence – 470 aa

MGAAARTLRLALGLLLLATLLRPADASSAPHHHHHHHHSGGLNDIFEAQKIEWHESGRPRSSPDD
LKALTRNVNRLNESFRDLQLRLLQAPLQADLTEQVWKVQDALQNSDLSLLALAGAVQRLEGALW
GLQAQAVQTEQAVALLRDRTGQQSDTAQLELYQLQVESNSSQLLLRRHAGLLDGLARRVGLGEE
LADVGGVLRGLNHSLSYDVALHRTRLQDLRVLVSNAEDTRRLRLAHVGMELQLKQELAMLNAV
EDLRLKDWEHSIALRNISLAKGPPGPKGDQDEGKEGRPGIPGLPGLRGLPGERGTPGLPGPKG
DDGKLGATGPMGMRGFKGDRGPKGKEKGDRAAGDASGVEAPMMIRLVNGSGPHEGRVEVYH
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SFSKWGVTNCGHAEDASVTCNRH

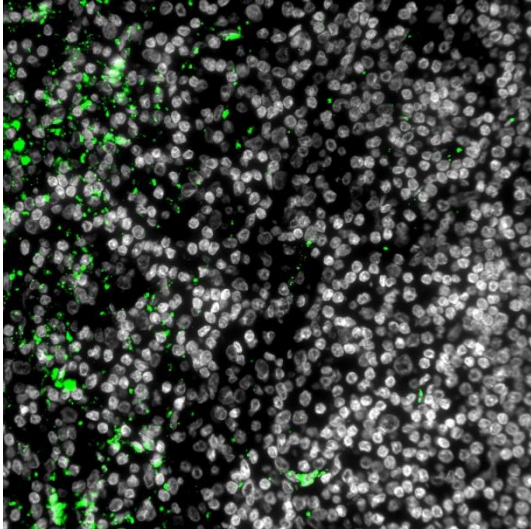
Legend: Underline = restriction site; Red = CCACC Kozak sequence; Blue = TIMP2-
signal peptide; Yellow = SSAP linker; Green = 8-His-tag; Purple = avidin-tag; Grey = SG
linker; White = SCARA5 sequence

Supplemental Figure 4.

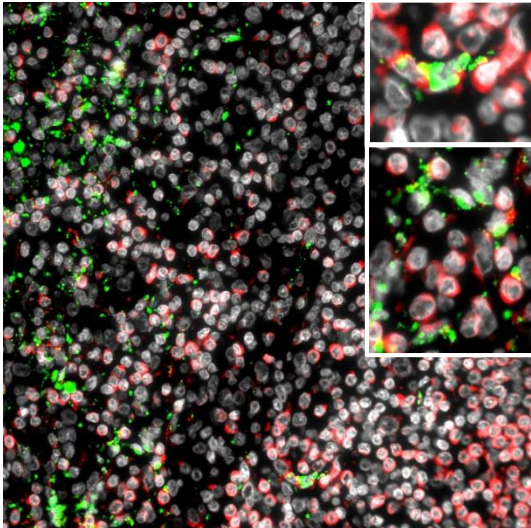
SCARA5 + DAPI



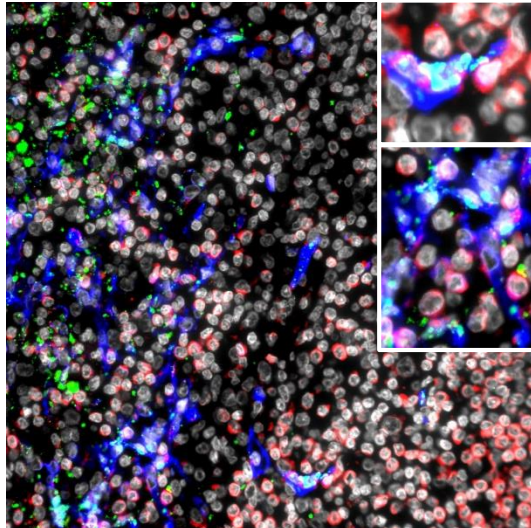
VWF + DAPI



SCARA5 + VWF + DAPI

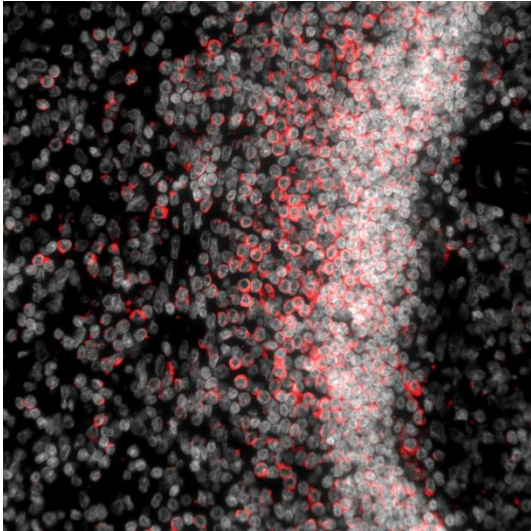


SCARA5 + VWF + CD8α + DAPI

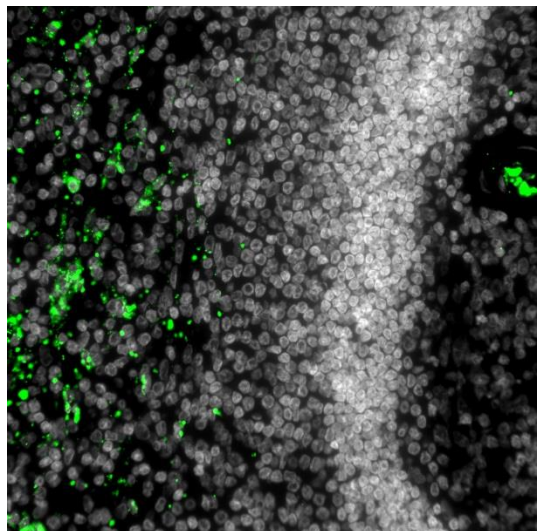


Supplemental Figure 5.

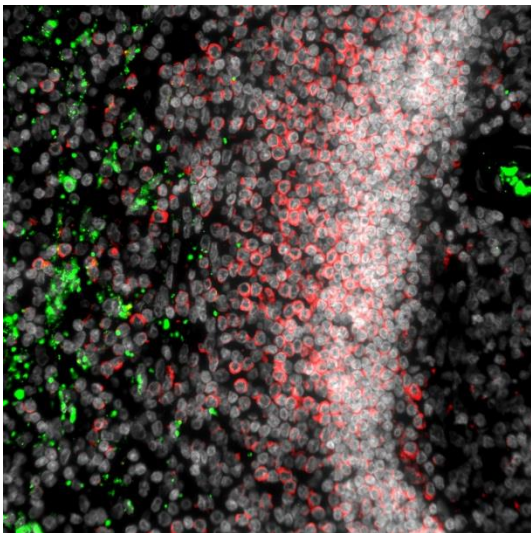
SCARA5 + DAPI



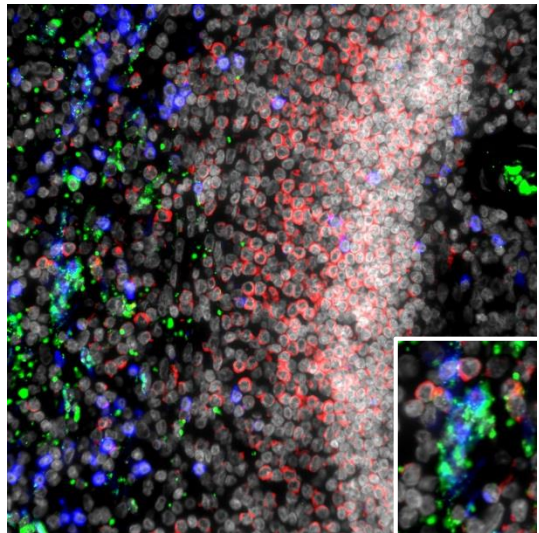
VWF + DAPI



SCARA5 + VWF + DAPI



SCARA5 + VWF + CD8 α + DAPI



Supplemental Table 1.

Gene	SNP ID	MAF	R2	D'	Distance (nt)	Variant nomenclature
SCARA5	rs4276643	0.273775	0.819704	0.991409	-2294	c.241+20332G>A
SCARA5	8:27804449	0.242075	0.953134	0.984015	-3144	8:27804449: G:GTTTTTTTTC
SCARA5	rs2685422	0.207493	0.801629	0.981124	-4079	c.241+18547C>T
SCARA5	rs2685421	0.25072	0.909175	0.983693	-4193	c.241+18433C>T
SCARA5	rs2726950	0.270893	0.80328	0.974317	-5459	c.241+17167T>C

Supplemental Table 2.

Gene	SNP ID	MAF	R2	D'	Distance	Variant nomenclature
SCARA5	rs73568968	0.206052	0.973793	0.991154	3770	c.241+13218C>A
SCARA5	rs73568971	0.206052	0.973793	0.991154	-1032	c.241+8416C>T
SCARA5	rs11783561	0.210375	0.931218	0.973446	-5532	c.241+3916G>T
SCARA5	rs10087301	0.206052	0.973793	0.991154	-6309	c.241+3139T>C
SCARA5	rs2685404	0.231988	0.866765	1	-6999	c.241+2449C>T
SCARA5	rs2685402	0.229107	0.848799	0.981577	-8277	c.241+1171T>C
SCARA5	rs11780263	0.206052	0.973793	0.991154	-9349	c.241+99C>T
SCARA5	rs73568976	0.207493	0.982529	0.991226	-9682	c.113-106A>C
SCARA5	rs2726939	0.231988	0.866765	1	-9987	c.113-411T>C
SCARA5	rs2685399	0.226225	0.895518	1	-10415	c.113-839C>A
SCARA5	rs11779320	0.190202	0.87974	0.990281	-11291	c.113-1715G>A
SCARA5	rs58732749	0.198847	0.930581	0.990775	-11506	c.113-1930G>C
SCARA5	rs11786033	0.198847	0.930581	0.990775	-11516	c.113-1940C>A

Supplemental Table 3.

	rs2726953	rs9644133
HGVS nomenclature	c.242-21543C>T	c.241+9448G>A
MAF	0.262	0.267
VWF:Ag (%): β (CI), p-value	-0.006 (-0.036 - 0.024), p=0.683	0.009 (-0.020 - 0.038), p=0.534
VWF:RCo: β (CI), p-value	0.003 (-0.028 - 0.035), p=0.835	0.018 (-0.013 - 0.05), p=0.255
FVIII:C: β (CI), p-value	-0.009 (-0.064 - 0.046) p=0.741	-0.012 (-0.066 - 0.042), p=0.654