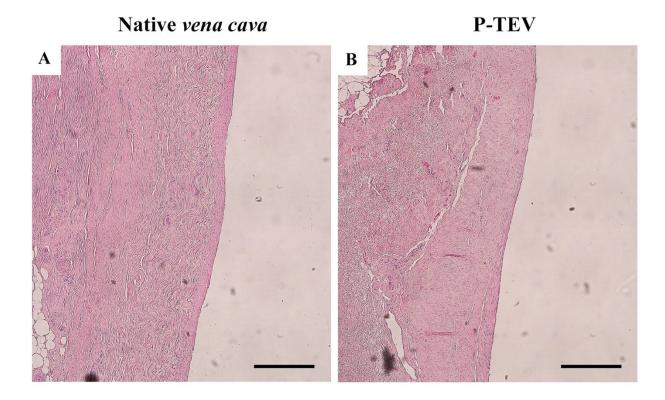
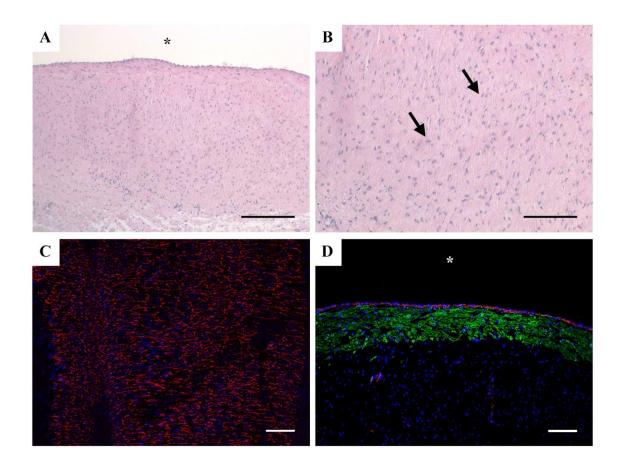
Electronic Supplementary Material (ESI) for Biomaterials Science. This journal is © The Royal Society of Chemistry 2023

Supplementary Materials "Personalized tissue-engineered veins – Long term safety, functionality and cellular transcriptome analysis in large animals "

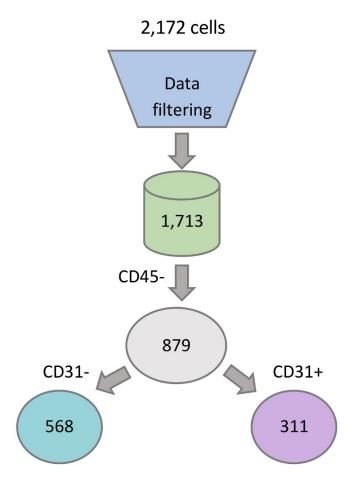


Supplementary figure 1. Cellular morphology of native *vena cava* tissue and P-TEV on year after transplantation

Low magnification tissue morphology illustrated with Hematoxylin and Eosin staining. A) Tissue from native *vena cava* shows the normal tissue morphology. B) Tissue morphology of P-TEV after 12 months *in vivo* Scale bars are 200 μm.



Supplementary figure 2 Histology images of P-TEV 6 months after surgery in the GLP study. A and B) Hematoxylin and Eosin staining showing the recellularized vein tissue. Arrows indicate cell nuclei. C) *En face* image of the luminal side of the graft with DAPI (blue) and antibody against CD31 (red). D) Antibodies against CD31 (red) and alpha smooth muscle actin (green), and DAPI (blue). \* = luminal side. Scale bars are 200 μm in A; 50 μm in B; 20 μm in C and D.



**Supplementary Figure 3. Filtering of cells for RNA sequencing data analysis.** Filtering of low-quality cells, blood cells and split into CD31 (PECAM) positive and negative cells for subsequent data analysis. The number of cells in each filtering step are shown in the figure.

## Supplementary table I

Vessel Nr	Luminal diameter (mm)	Graft length (cm)
Surgeries in Sweden		
1	6.4	2.5
2	5.1	2.5
3	4.4-7.0	2.3
4	4.5	2.5
5	7.6	2.5
6	7.0	3.0
7	7.6	2.5
Surgeries in Spain		
1	5.1	3.3
2	4.5	3.0
3	6.4	2.2

Supplementary Table II. oper and information	le II. aPCR accevi	information					
Assay name	II igu	Efficiency	건	Slope	Y-intercept	Amplicon length	Context sequence
CD31 (PECAM)	re	960	0 998	-3 474	40.07	100	CAGTCGAGGAACAAGACCGTGTTATATTCTCCTGTCAAGCTAATGTCATATTTGGGACCGCGGGGGATCTCTGATTCCC CCGTGAGGAAATCTTCTCTAAATCCCAAGTTCCAAAGAGCTAAAGGAGTAATC
CD54 (ICAM-1)	863 MM	0,87	866'0	3.673	41,7	105	TITITGAACTGAGTAATGTGGAAAACGATGGCACTCTACTCT
VFGF	NN 214084		666 ()	-3 531	39 48	<u></u>	TGCTCTTGGGGTGCATTGGAGCCTTGCCTGCTCTACCTCCACCAGGCCAGGGCTGCAGGGTGCCAGGCTGCAGAGAGAG
FLT-1 (VEGFR1)	XM 021065525.1	0.92	68660	-3.519	40.37	= =	TGGGCAGCAGCAGGTCCTGACTTGGACCATTTATGGTGTCCCTCCACCTGCCGTCACATGGCTCTGGCGACCCTGTGGCCATAAGAAGTTTTGCTCCCGTAACGAAGAGTCCTTTG
FLK-2 (VEGFR2)	XM 003128987.6	1,01	766'0	-3.309	39,1	110	CAGAGCCACGTGGTATCTCTGGTTGTGAATGTCCCACCCCAGATTGGTGAGAAATCTCTGATCTCCCCGTGGACTCTTACCACCTCACTGACAGTCTATGCTGTTCTCCCCCGAGCTACATCCACTGGT
CD144 (VE-Cadherin)	NM_001001649.2	0,92	666'0	-3.528	39,37	120	TCTCCCTGAGCACTGAGGACAGCAACTTCACCCTCACGGATAATCACGATAACACGGCCAACATCACAGTCAAGCACGGGTAAAGGTCCACCACCTTCCCATACTCTCGGA
CD105 (Endoglin)	NM_214031.1	0,93	666'0	-3.494	39,46	167	CAACCCTGGAGCTGACTGTCCAGATGACCAACCCAAACGGCGCCCGGGCCCCAAGAGGTGCTCCTGATCCTCAGTGTGAACAA CAAGTTC
KLF2 (Krippel-like Factor 2)	NM 001134351.2	6.0	766'0	-3.574	39,83	250	AGAGCTCGCACCTCAAGGCGCACCTGCGCACGCATACAGGCGAGAAGCCCTACCACTGCAACTGGGACGGCTGCGGCTGGAA ACTCA
vWF	NM 001246221.1	68'0	666'0	-3.612	40,55	124	CATCTCGTGCAACATCTCCTCTGAAATGCAGAAGGGCCTGTGGGAGCAGTGCCAGCTTCTGAAGAGTGCCTCGGTGTTCGCCCCCCCGAGCTTCTTCGTGGCCTCTGTGAAAGATGCTGTGTGCCATGTGC
Tie2	XM 021062678.1	0,93	666'0	-3.496	38,97	134	GCCCCAGGATGCTGGAGTGTACTCGGCCAGGTACATAGGAGGAAACCTCTTCACCTCGGCCTTCACCAGGCTGATAGTCCGGC GGGGACCTGAATGTAACCGTGTGGACGGCTTGCATGAACAATGGGATCTGCCATGAAGATACTGGAGAATGCATTT
bFGFR	XM 005671767	0,94	866'0	-3.479	38,78	108	CCCACCTTGCGCTGGCTGAAAAATGGCAAAGAATTCAAGCCTGACCACAGAATCGGAGGCTACAAGGTCCGTTATGCCACCT CGTGGTGCCCTCCGACAAGGGCAACTACACCTGCGTGGAGAACGAGTAT
PDGFA	XM_021085925	0,92	666'0	-3.535	39,66	171	CACGTCCGCCAACTTTCTGATCTGGCCGCCGTGCGTGGAGGTGAAACGCTGTACTGGCTGCAGCAACACACGCTGCAAGGTCCAAGGTGCAGCGTGCAGGTGCAAGGTGCAAGGTGCAAGGTGCAAGGTGCGAAAGAGAAGAAGAAAGA
abha-SMA	NM 001164650	0,91	666'0	-3.571	39,64	152	CCCATGAGACATACAAAAAGGTAATGCCGCCGTGAAGCACCAGCCAG
SMARHC	XVX 021086165	900	000	-3 437	39.47	13.	TGGCAAAGATGACATCCAGAAGATGAACCGCCCAAGTTCTCCAAGGTGGAGGACATGGCAGGGCTGACGTGTCTCAATGAA CTGAGGGAAGGTACTTCTCGGGACTCATCTACACGTACTCGGGCCTCTTCTGCGTGGTGGTAAACCCCTACAAGCAGCTGCCC ATTGACATGTACAAGGGCAAGAAGCGGAAGATGCCGCCCCACATCTACGCCATCGCCGACACGCCTACCGGAGCATGC AGTCCATTCTTGTGCACAGGCGAGTCTGGAGCCGGAAAACGGAAAACCACAAGAAAAGTCATCACGGTTTTGGCCATGGTGGCGAGGCATGC
MYOCD (Myocardin)	NM_213745	0,91	666'0	-3.536	40,36	135	GARGEGGGAGAGGAGCAGCCGCCGTGGACTGTGCCCGTGAAGGGCCCATAAAGGGGAACCAAGTGAGTCTCTCCCAAAT TGAAGAGGACGACGAGCAGCGACGGCTTTCTCCAGATCAGACGCGAAGT AAGATCATGAGTCATCTCGGGCCTCATCTGAACGTGGTCAACCTGCTGGGGGCCCTCCAAAGAGGAGGTCCCATCTACATCT

Supplementary Table Gene names in heatmap,

FOXP1 WTAP GJA1 TXNRD1 CSDE1 LARP1 missing: 14639 missing: 15188 missing: 15087 missing:7151 missing: 15088 missing: 12518 missing:3153 RAMP2 SELENOS RANBP1 missing:3573 MT1X SRSF3 ADGRG1 missing:4395 EMP2 LIMA1 HNRNPA3 missing: 13002 PRSS23 TSPAN12 HSPA9 TIMP1 CLEC14A CDH5 BTF3 RHOJ RGS4 STOM KTN1 OLR1 SRRMI TMED5 DCLK1 RHOB SGK1 S0O2 ADGRL4 missing:8035 LMNA RNPS1 NFKBIZ CLDN5 missing:2769 CEBPZ RGS2 S1PR1 STX11 COPS4 AOPEP ITM2B ISG15 EMP1 missing: 13263 FGF2 MAFF SGCE GLT8O2 PTGES LGALS3BP

GMFB FAM180B

## **Supplementary Table IV**

## Gene names in heatmap, Figure 9C

NSA2

PROX1

missing:14549

AXL

EEF10

RAB7A

PRKAA1A

PDIA3

BUB3

HNRNPA.3

missing:14639

missing:12517

missing:15088

missing:15188

missing:12518

missing:7151

missing: 15087

missing:12520

missing:15324

missing: 15236

FGF2

NCL

**SFPQ** 

GSN

missing: 10206

EIF3J

VIM

C3

missing:13263

KLF4

PTGS2

FBLN1

SERPINE1

missing:1294

AMCF-II

S100A10

**BGN** 

RPS3

MT1X

PGRMC1

**SOCBP** 

IMP3

missing: 13095 **SELENOM** 

MIS12

TWF1

F2RL2

missing:7887

COV3