Gene	Forward 5′→3′	Reverse 5′→3′
ABCC4	CATTGAGAGGGTGTCAGAGG	GCCTTGTAGAGTTGGGGTCT
ACSS3	ACGATGTGATGTAGAGACCCTG	GACGCTTTTTCCTGCTTGCC
ANGPT1	TGGGACAGCAGGAAAACAGAG	GCCACAAGCATCAAACCACC
ANGPT2	TGGGAAGGGAATGAGGCTTAC	TCCTGGTTGGCTGATGCTG
ANKRD22	CAAAGACAAAGCAGAATGAGGC	GCAGAGGGATAAGAGACTGGTT
E2F7	CAGTCTTGGTGTGGAAAGGAGA	CTCAGGGTTTTTGGCAGGC
NRP2	CCCCGAACCCAACCAGAAGA	CAGTGTTTGCCCAGGAGGTC
RGS4	ACATCGGCTAGGTTTCCTGCT	TGACTTCCTCTTGGCTCACTC
RYR2	TGAAAGCATCAAACGCAGCA	CAATGAATGTGAGCAGCCCG
THBS1	CCAACCGCATTCCAGAGTC	GTCATCAGGCACAGGGGG
B2M	GGCTATCCAGCGTACTCCAAA	CGGATGGATGAAACCCAGACA
GAPDH	CAAATTCCATGGCACCGTCA	GACTCCACGACGTACTCAGC

Supplementary Table S1. Primer sequences for RT-qPCR validation. Forward and reverse primer sequences (5′→3′) for the ten target genes and two reference genes (B2M, GAPDH) used in this study.

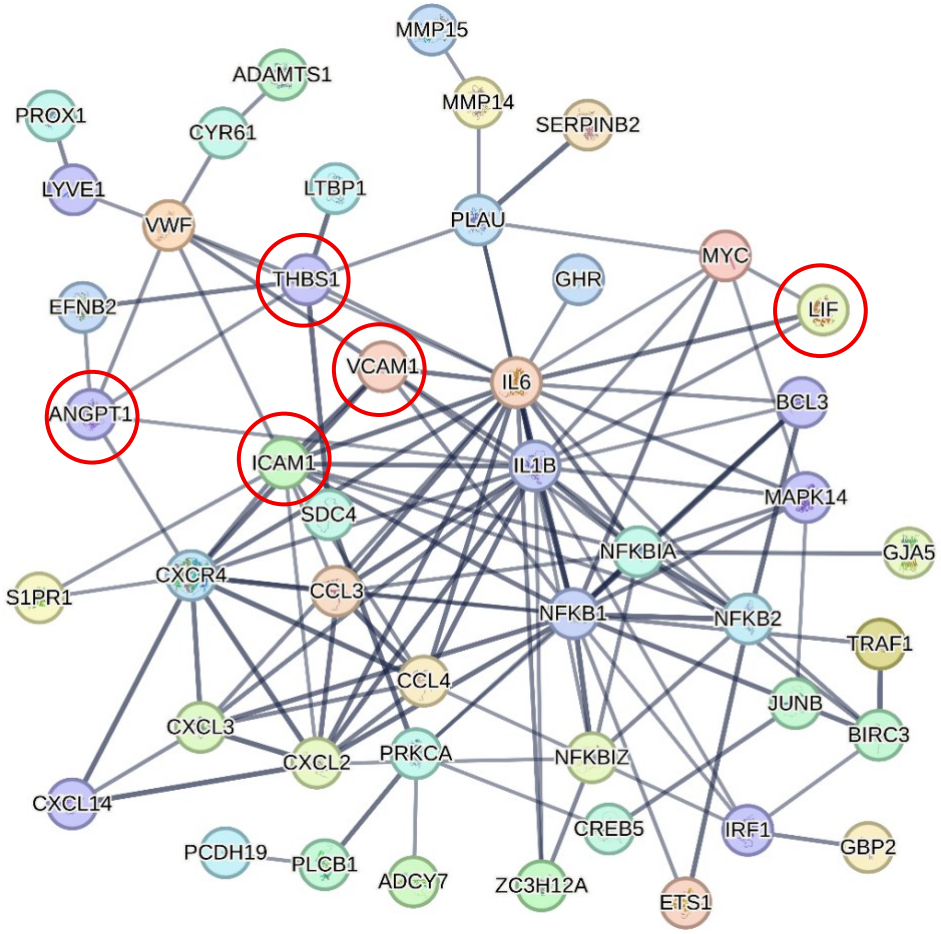
Pool	Group	Nº of readings	Pipeline 1	Pipeline 2	Pipeline 3
			% Aligned		
Pool_D1	Donor	71295392	98.94	88.9	96.69
Pool_D2	Donor	79865035	99.22	90.3	97.08
Pool_PM1	Patient	66047275	99.15	88.9	96.81
Pool_PM2	Patient	59152441	99.02	90	96.78

Supplementary Table S2. RNA-seq alignment statistics per pool. Total reads and percentage of reads aligned to the GRCh38.p13 reference genome for each of the four pooled samples (Pool_D1, Pool_D2, Pool_PM1, Pool_PM2) across the three bioinformatic pipelines.

Gene	Forward 5′→3′	Reverse 5′→3′
Positive regulation of cell motility (GO:2000147)	ANGPT1, CFAP20, CXCR4, EPB41L4B, HAS2, LYVE1, MMP14, PROX1, WISP1	ADAMTS1, BMP2, BMP4, CCL3, CCL4, CHD13, EDN2, ETS1, GLIPR2, ICAM1, IL1B, IL6, NRP2, PLAU, PPAP2B, PRKCA, S1PR1, SEMA3B, THBS1, ZC3H12A
Tube morphogenesis (GO:0035239)	ANGPT1, CALCRL, CITED1, EFNB2, GJA5, GLI3, GLUL, HAS2, MAPK14, MMP14, PROX1	ADAMTS16, ADM, BMP2, BMP4, CDH13, E2F7, EDN2, JUNB, MTSS1, MYC, NFIB, NINJ1, NRP2, NRXN3, PRKCA, RYR2, S1PR1, SDC4, THBS1, ZC3H12A, ZMIZ1
Regulation of cell adhesion (GO:0030155)	ANGPT1, CXCR4, EFNB2, EPB41L4B, GLI3, HAS2, HLA-DQB2, MAPK14, MMP14, PCK1, PRKAA1	BMP2, BMP4, CDH13, EDIL3, ETS1, FRMD5, FSTL3, HLA-DRB1, HLA-DRB5, IL1B, IL6, IRF1, LIF, NFKBIZ, PLAU, PPAP2B, PRKCA, S1PR1, SDC4, THBS1, VCAM1, ZC3H12A, ZMIZ1
Positive regulation of cell migration (GO:0030335)	ANGPT1, CXCR4, EPB41L4B, HAS2, LYVE1, MMP14, PROX1, WISP1	ADAMTS1, BMP2, BMP4, CCL3, CCL4, CHD13, EDN2, ETS1, GLIPR2, ICAM1, IL1B, IL6, NRP2, PLAU, PPAP2B, PRKCA, S1PR1, SEMA3B, THBS1, ZC3H12A
Positive regulation of locomotion (GO:0040017)	ANGPT1, CFAP20, CXCR4, EPB41L4B, HAS2, LYVE1, MMP14, PROX1, WISP1	ADAMTS1, BMP2, BMP4, CCL3, CCL4, CHD13, EDN2, ETS1, GLIPR2, ICAM1, IL1B, IL6, NRP2, PLAU, PPAP2B, PRKCA, S1PR1, SEMA3B, THBS1, ZC3H12A
Vasculature development (GO:0001944)	ANGPT1, CALCRL, CITED1, EFNB2, GJA5, GLI3, GLUL, HAS2, MAPK14, MMP14, PROX1	ADM, BMP2, BMP4, CDH13, E2F7, EDN2, JUNB, LIF, NINJ1, NRP2, NRXN3, PPAP2B, PRKCA, S1PR1, THBS1, ZCEH12A, ZMIZ1
Regulation of locomotion (GO:0040012)	ANGPT1, ARHGAP18, CFAP20, CXCR4, EFNB2, EPB41L4B, GLUL, HAS2, LYVE1, MMP14, MPP1, PLCB1, PROX1, SSX2IP, WISP1	ADAMTS1, BMP2, BMP4, CCL3, CCL4, CD200, CDH13, EDN2, ETS1, FRMD5, GLIPR2, ICAM1, IL1B, IL6, NINJ1, NRP2, PLAU, PPAP2B, PRKCA, S1PR1, SDC4, SEMA3B, THBS1, ZC3H12A
Regulation of cell motility (GO:2000145)	ANGPT1, ARHGAP18, CFAP20, CXCR4, EPB41L4B, GLUL, HAS2, LYVE1, MMP14, MPP1, PLCB1, PROX1, SSX2IP, WISP1	ADAMTS1, BMP2, BMP4, CCL3, CCL4, CD200, CDH13, EDN2, ETS1, FRMD5, GLIPR2, ICAM1, IL1B, IL6, NINJ1, NRP2, PLAU, PPAP2B, PRKCA, S1PR1, SDC4, SEMA3B, THBS1, ZC3H12A
Blood vessel morphogenesis (GO:0048514)	ANGPT1, CALCRL, CITED1, EFNB2, GJA5, GLI3, GLUL, HAS2, MAPK14, MMP14, PROX1	ADM, BMP4, CDH13, E2F7, EDN2, JUNB, NINJ1, NRP2, NRXN3, PRKCA, S1PR1, THBS1, ZC3H12A, ZMIZ1
Tube development (GO:0035295)	ANGPT1, CALCRL, CCKBR, CITED1, EFNB2, GJA5, GLI3, GLUL, HAS2, HDC, MAPK14, MMP14, PROX1,	ADAMTS16, ADM, BMP2, BMP4, CDH13, E2F7, EDN2, JUNB, MTSS1, MYC, NFIB, NINJ1, NRP2, NRXN3, PRKCA, RYR2, S1PR1, SDC4, THBS1, ZC3H12A, ZMIZ1
Blood vessel development (GO:0001568)	ANGPT1, CALCRL, CITED1, EFNB2, GJA5, GLI3, GLUL, HAS2, MAPK14, MMP14, PROX1	ADM, BMP4, CDH13, E2F7, EDN2, JUNB, NINJ1, NRP2, NRXN3, PPAP2B, PRKCA, S1PR1, THBS1, ZC3H12A, ZMIZ1
Circulatory system development (GO:0072359)	ANGPT1, CALCRLC CITED1, EFNB2, GJA5, GLI3, GLUL, HAS2, MAPK14, MMP14, PROX1,	ADAMTS1, ADM, BICC1, BMP2, BMP4, CDH13, DNAH11, E2F7, EDN2, HSPB7, INHBA, JUNB, LIF, NINJ1, NRP2, NRXN3, PPAP2B, PRKCA, RYR2, S1PR1, THBS1, VCAM1, ZC3H12A, ZMIZ1

Regulation of cell migration (GO:0030334)	ANGPT1, CXCR4, EPB41L4B, GLUL, HAS2, LYVE1, MMP14, MPP1, PLCB1, PROX1, WISP1	ADAMTS1, BMP2, BMP4, CCL3, CCL4, CD200, CDH13, EDN2, ETS1, FRMD5, GLIPR2, ICAM1, IL1B, IL6, NINJ1, NRP2, PLAU, PPAP2B, PRKCA, S1PR1, SDC4, SEMA3B, THBS1, ZC3H12A
Response to cytokine (GO:0034097)	ABCA1, ALAD, CITED1, CXCR4, GHR, HAS2, MAPK14, PLCB1	BIRC3, CCL3, CCL4, CD200, CDC42EP2, EDN2, GBP2, ICAM1, IL1B, IL6, INHBA, IRF1, MYC, NFKB1, NFKB2, NFKBIA, NFKBIZ, NRP2, PRKCA, THBS1, TRAF1, TUBA1A, VCAM1, ZC3H12A
Positive regulation of cell adhesion (GO:0045785)	ANGPT1, EFNB2, EPB41L4B, GLI3, HAS2, HLA-DQB2, PCK1, PRKAA1	CDH13, EDIL3, ETS1, FRMD5, FSTL3, HLA-DRB1, HLA-DRB5, IL1B, IL6, LIF, NFKBIZ, PPAP2B, PRKCA, SDC4, VCAM1, ZMIZ1
Response to peptide (GO:1901652)	ABCA1, ALAD, CITED1, CXCR4, GHR, HAS2, MAPK14, PLCB1	BIRC3, CCL3, CCL4, CD200, CDC42EP2, EDN2, GBP2, ICAM1, IL1B, IL6, INHBA, IRF1, MYC, NFKB1, NFKB2, NFKBIA, NFKBIZ, NRP2, PRKCA, THBS1, TRAF1, TUBA1A, VCAM1, ZC3H12A
Response to bacterium (GO:0009617)	ABCA1, ALAD, CITED1, EFNB2, HDC, KLHL6, MAPK14, PCK1, SLC9A9	ADM, BCL3, BMP2, CD200, CXCL2, GBP2, HLA-DRB1, HMCN1, IL1B, IL6, NFIB, NFKB1, NFKB2, NFKBIA, NFKBIZ, PTGFR, RNASE1, VCAM1, ZC3H12A
Response to lipid (GO:0033993)	ABCA1, ALAD, CITED1, EFNB2, GHR, MAPK14, MMP15, PCK1, PLCB1, PRKAA1, TRIM16	CA9, CCL3, CD200, FABP3, GBP2, IL1B, IL6, INHBA, JUNB, NFKB1, NFKB2, NFKBIA, NFKBIZ, PRKCA, PTGFR, THBS1, VCAM1, ZC3H12A, ZMIZ1
Positive regulation of cell differentiation (GO:0045597)	CXCR4, EFNB2, GHR, GLI3, GLUL, ID4, MAPK14, MMD, MMP14, PCK1, PLCB1, PROX1, TRIM16, WISP1	ADM, BMP2, BMP4, ETS1, GLIPR2, HLA-DRB1, IL1B, IL6, INHBA, JUNB, LIF, NFKB1, NFKBIZ, PRKCA, ZC3H12A, ZMIZ1
Angiogenesis (GO:0001525)	ANGPT1, CALCRL, EFNB2, GJA5, GLUL, MAPL14, MMP14	BMP4, CDH13, E2F7, EDN2, NINJ1, NRP2, NRXN3, PRKCA, S1PR1, THBS1, ZC3H12A

Supplementary Table S3. Gene lists for the top 20 enriched GO biological processes. For each significantly enriched term, the associated upregulated and downregulated genes from the consensus DEG set are listed. Key angiogenesis-related genes are highlighted.



Supplementary Figure S1. Protein-protein interaction network of consensus DEGs. STRING analysis of the 234 consensus DEGs, showing interactions with a confidence threshold >0.7. Key angiogenesis-related genes (ANGPT1, THBS1, BMP4, GLUL) and endothelial factors (VCAM1, ICAM1, LIF) form central hubs in the network.