

Sample ID	Age (Dmyr)	Sex	Histopathological subtype	Location
19-229	3m1D	F	Proliferating IH	Frontal scalp
22-010 I	2m20D	F	Proliferating IH	Sternum
16-125 I	8m8D	F	Proliferating IH	Scalp
17-183	6m6D	F	Proliferating IH	Lower lip
17-092	4m26D	F	Proliferating IH	Right ear
15-375	5m21D	F	Proliferating IH	Left ear
18-017	9m18D	M	Proliferating IH	Right ear
17-436	7m22D	M	Proliferating IH	Posterior neck
22-052	5m1D	M	Proliferating IH	Left thigh
20-108	4m4D	M	Proliferating IH	Right flank
17-251	3m24D	M	Proliferating IH	Left periauricular
16-004	9m13D	M	Proliferating IH	Left cheek
17-370 III	14m13D	F	Plateau IH	Right abdomen
16-013 I	14m26D	F	Plateau IH	Left forehead
15-032	17m1D	F	Plateau IH	Chest
15-031	13m16D	F	Plateau IH	Scalp
17-411	14m11D	M	Plateau IH	Forehead
16-319	12m6D	M	Plateau IH	Scrotum
17-410	18m18D	M	Plateau IH	Chin
15-002	15m24D	M	Plateau IH	Scalp
15-217	60m	F	Involuting IH	Nose
15-169	47m22D	F	Involuting IH	Sternum
16-222	61m5D	F	Involuting IH	Lower lip
17-166	68m	F	Involuting IH	Right upper arm
22-081	22m	M	Involuting IH	Scalp
17-285	58m15D	M	Involuting IH	Nasal dorsum
17-094	56m18D	M	Involuting IH	Nose
14-003	61m22D	M	Involuting IH	Right thigh
22-023	8yrs	F	Normal skin	Ear
23-074	8yrs	F	Normal skin	Ear
23-077	8yrs	F	Normal skin	Ear
23-078	13yrs	F	Normal skin	Ear
23-007	9yrs	M	Normal skin	Ear
21-178	11yrs	M	Normal skin	Ear
20-110	9yrs	M	Normal skin	Ear
23-069	7yrs	M	Normal skin	Ear

Supplementary Table.1: Clinical and histological details of patient samples from Infantile Haemangioma (IH) and healthy normal skin.

Pathway	-log(p-value)	zScore	Ratio	Molecules
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Response to elevated platelet cytosolic Ca ²⁺	23.6	- 2.236068	0.341	A1BG, AHSG, ALB, APLP2, APOA1, APOOL, CALU, CFL1, CLEC3B, CLU, CYB5R1, FGA, FGB, FGG, FN1, HRG, HSPA5, IGF2, ITIH3, ITIH4, KNG1, MAGED2, MANF, ORM1, PECAM1, PFN1, PHACTR2, PLG, PROS1, QSOX1, RARRES2, SELENOP, SERPINA1, SERPINA3, SERPINA4, SERPING1, SOD1, SPARC, STX4, TF, TGFB1, TMX3, TOR4A, VWF
Acute Phase Response Signalling	22.7		0.281	AGT, AHSG, ALB, AMBP, APCS, APOA1, C1QA, C1QC, C3, C4BPA, C5, C9, CP, F2, FGA, FGB, FGG, FN1, HNRNPK, HPX, HRG, IL1RAP, IL33, IRAK1, ITIH2, ITIH3, ITIH4, KLKB1, LBP, MAP2K1, MAP2K6, MYD88, NFKB2, ORM1, PLG, RBP4, RBP7, RRAS2, SAA4, SERPINA1, SERPINA3, SERPIND1, SERPINF1, SERPING1, SHC1, SOD2, TAB1, TF, TTR, VWF
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by IGFBPs	19.1	- 0.800640 8	0.315	AHSG, ALB, APLP2, APOA1, APOB, APOL1, C3, CALU, CP, DNAJC3, F2, FGA, FGG, FN1, FSTL1, FUCA2, HSP90B1, IGF2, IGFALS, IGFBP7, ITIH2, KNG1, LAMB1, MEN1, MMP2, NUCB1, P4HB, PDIA6, PLG, PROC, QSOX1, RCN1, SERPINA1, SERPINC1, SERPIND1, SPARCL1, TF, TGOLN2, VWA1
DHCR24 Signalling Pathway	17.4	- 5.604485 4	0.285	A1BG, AGT, AHSG, ALB, AMBP, APOA1, APOA4, APOB, APOC1, APOC3, APOD, APOL1, C3, C9, CASP3, CLU, FGA, GC, GSK3B, HPR, HPX, ITIH4, KNG1, NFKB2, ORM1, PCYOX1, PIK3C2A, PLTP, PON1, RBP4, RRAS2, SAA4, SCARB1, SERPINA1, SERPINF1, TF, TM7SF2, TTR, VTN
LXR/RXR Activation	17.4	- 5.666666 7	0.301	A1BG, AGT, AHSG, ALB, AMBP, APOA1, APOA4, APOB, APOC1, APOC3, APOD, APOL1, C3, C9, CLU, FGA, GC, HADH, HPR, HPX, IL1RAP, IL33, ITIH4, KNG1, LBP, NFKB2, ORM1, PCYOX1, PLTP, PON1, RBP4, SAA4, SERPINA1, SERPINF1, TF, TTR, VTN
Post-translational protein phosphorylation	16.9	- 0.342997 2	0.318	AHSG, ALB, APLP2, APOA1, APOB, APOL1, C3, CALU, CP, DNAJC3, FGA, FGG, FN1, FSTL1, FUCA2, HSP90B1, IGFBP7, ITIH2, KNG1, LAMB1, MEN1, NUCB1, P4HB, PDIA6, PROC, QSOX1, RCN1, SERPINA1, SERPINC1, SERPIND1, SPARCL1, TF, TGOLN2, VWA1
Neutrophil degranulation	13	0.361157 56	0.145	A1BG, AHSG, ALDOC, ANO6, ANXA2, APAF1, ARHGAP45, ARSB, ATP11A, C3, CAT, CD93, CEACAM1, CMTM6, COMMD3, CPNE3, CTSA, CTSZ, CYB5R3, DEGS1, DNAJC13, DNAJC3, DYNLL1, ERP44, FUCA1, FUCA2, GALNS, GLB1, GMFG, GNS, GSN, HBB, HLA-B, HSP90AB1, IDH1, IQGAP2, LGALS3, LPCAT1, LTA4H, MAN2B1, MGST1, MOSPD2, ORM1, OSTF1, PDXK, PECAM1, PGM1, PGM2, PNP, PRCP, PRDX6, PYGB, PYGL, QSOX1, RAB31, RAP2C, SERPINA1, SERPINA3, SERPINB1, SRP14, STK10, STOM, TIMP2, TMBIM1, TOLLIP, TTR, TXNDC5
Formation of Fibrin Clot (Clotting Cascade)	12.5	- 3.299831 6	0.462	F10, F12, F2, FGA, FGB, FGG, KLKB1, KNG1, PRCP, PROC, PROS1, SERPINC1, SERPIND1, SERPINE2, SERPING1, VWF
Coagulation System	12.3	0.242535 63	0.486	F10, F12, F2, FGA, FGB, FGG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINA1, SERPINC1, SERPIND1, VWF
Complement cascade	12	- 4.898979 5	0.237	C1QA, C1QC, C3, C4BPA, C5, C6, C7, C8A, C8B, C8G, C9, CFH, CFI, CLU, CPB2, CPN1, CPN2, F2, FCN3, IGHV3-33, IGKV4-1, IGLC3, IGLV1-47, IGLV1-51, IGLV3-21, IGLV3-25, IGLV5-45, PROS1, SERPING1, VTN
Processing of Capped Intron-Containing Pre-mRNA	12	7	0.171	AQR, CCDC12, CDC40, CHERP, CLP1, DDX5, GLE1, HNRNPA2B1, HNRNPK, ISY1, LSM3, LSM4, LSM6, LUC7L3, MFAP1, NCBP1, NCBP2, NUP35, NUP50, NUP58, PAPOLA, POLR2C, POLR2G, PPIL4, PPP1R8, PPWD1, PQBP1, RBM10, RBM39, RBM8A, SF3B4, SF3B6, SNRNP70, SNRPB2, SNRPC, SNW1, SRRM2, SRSF1, SRSF10, SRSF11, SRSF2, SRSF4, SRSF6, TCERG1, THOC1, THOC3, TRA2B, YBX1
Extracellular matrix organization	11.8	- 1.133893 4	0.264	AGRN, ASPN, BGN, CEACAM1, COL4A1, COL4A2, COL5A3, COL6A1, COL6A2, COL6A3, DAG1, DCN, DMD, FGF2, FMOD, FN1, ITGA1,

				ITGA6, ITGB4, LAMB1, LUM, NCAM1, NID1, PTPRS, SPARC, TGFB1, TTR, VTN
Integrin cell surface interactions	10	- 0.208514 4	0.271	AGRN, BSG, COL4A1, COL4A2, COL5A3, COL6A1, COL6A2, COL6A3, FGA, FGB, FGG, FN1, ICAM2, ITGA1, ITGA4, ITGA6, JAM2, JAM3, LUM, PECAM1, VTN, VWF
Complement System	9.52	- 0.333333 3	0.405	C1QA, C1QC, C3, C4BPA, C5, C6, C7, C8A, C8B, C8G, C9, CFH, CFI, SERPING1
Collagen biosynthesis and modifying enzymes	8.78	2.064741 6	0.284	COL14A1, COL28A1, COL4A1, COL4A2, COL5A3, COL6A1, COL6A2, COL6A3, COLGALT1, CRTAP, P3H1, P3H3, P4HA1, P4HB, PLOD1, PLOD2, PLOD3, PPIB, SERPINH1
Aryl Hydrocarbon Receptor Signalling	8.68	- 1.290994 4	0.189	ALDH2, ALDH4A1, ALDH5A1, ALDH6A1, APAF1, BAX, CDK6, CDKN1B, HSP90AB1, HSP90B1, HSPB1, MCM7, MGST1, NFIA, NFIB, NFIC, NFKB2, NQO1, NQO2, RB1, SMARCA4, SP1, TGFB1, TRIP11
Mitochondrial Dysfunction	8.22	2.771434 84	0.137	AIFM1, ATP1A2, ATP5F1A, ATP5F1B, ATP5MG, ATP5PB, BAX, BCL2, BID, CAMK2G, CASP3, CLIC2, COX4I2, COX7A2L, CREB1, CYB5R3, CYC1, GPD2, GPX3, GPX4, GPX7, HTRA2, MAOA, MAOB, MAPK10, MGST1, NDUFA4L2, OGDH, OPA1, PDHA1, PDHB, PDHX, PIK3C2A, PPIF, PPP3CC, PRDX6, SDHA, SDHB, SNCA, SOD1, SOD2, UQCR10, UQCRB, UQCRC2
Binding and Uptake of Ligands by Scavenger Receptors	8.21	- 2.041241 5	0.214	ALB, AMBP, APOA1, APOB, APOL1, COL4A1, COL4A2, HBB, HPR, HPX, HSP90B1, HSPH1, IGHV3-33, IGKV4-1, IGLC3, IGLV1-47, IGLV1-51, IGLV3-21, IGLV3-25, IGLV5-45, JCHAIN, SCARB1, SPARC, STAB1
Superoxide Radicals Degradation	7.98	- 0.377964 5	0.875	CAT, CYGB, GPX7, NQO1, SOD1, SOD2, SOD3
Extrinsic Prothrombin Activation Pathway	7.48		0.562	F10, F12, F2, FGA, FGB, FGG, PROC, PROS1, SERPINC1
Apoptosis Signalling	6.8	0.447213 6	0.202	AIFM1, APAF1, BAX, BCL2, BCL2L1, BID, BIRC6, CASP10, CASP3, CASP6, CASP7, CDK1, CYC1, DFFA, HTRA2, LMNA, MAP2K1, NFKB2, PLCG1, PLCG2, RRAS2
Erythrocytes take up oxygen and release carbon dioxide	6.77	- 2.449489 7	0.857	AQP1, CA1, CA2, HBB, RHAG, SLC4A1
Protein Ubiquitination Pathway	6.53	4.438772 66	0.136	ANAPC1, ANAPC5, BIRC6, CBL, CDC23, CRYAB, DNAJB11, DNAJC1, DNAJC10, DNAJC13, DNAJC3, ELOC, HLA-B, HSP90AB1, HSP90B1, HSPA12A, HSPA13, HSPA14, HSPA5, HSPB1, HSPH1, IFT25, NEDD4, NEDD4L, PSMB2, PSMD10, STUB1, UBE2E3, UBE2G1, UBE2H, UBE2I, UBE2K, UBE2N, UBE2R2, UBE4B, UCHL1, USP11
Clathrin-mediated Endocytosis Signalling	6.48		0.149	AAK1, ALB, AP3S1, APOA1, APOA4, APOB, APOC1, APOC3, APOD, APOL1, ARPC2, ARPC3, CBL, CLTA, CLU, DAB2, DNM1, F2, FGF2, ITGB4, ORM1, PCYOX1, PIK3C2A, PON1, PPP3CC, RBP4, SAA4, SERPINA1, SH3GLB2, TF, TFRC
Detoxification of Reactive Oxygen Species	6.48	- 1.154700 5	0.324	CAT, ERO1A, GPX3, GPX7, P4HB, PRDX1, PRDX2, PRDX6, SOD1, SOD2, SOD3, TXN2

Supplementary Table 2: Differentially expressed proteins in the top 25 enriched canonical pathways (female proliferating vs involuting IH) through core analysis in Ingenuity Pathway Analysis.

Pathway	-log(p-value)	zScore	Ratio	Molecules
Processing of Capped Intron-Containing Pre-mRNA	64.6	10.48809	0.383	ACIN1, CCAR1, CCDC12, CDC40, CHERP, CHTOP, CLP1, CPSF4, CPSF6, CSTF3, CWC22, DDX39A, DDX46, DHX15, DHX9, EIF4A3, EIF4E, FUS, GPKOW, HNRNPA1, HNRNPA2B1, HNRNPA3, HNRNPC, HNRNPF, HNRNPK, HNRNPM, HNRNPU, IK, LOC102724594/U2AF1, LSM3, LSM4, LSM6, LSM7, LUC7L3, MFAP1, NCBP1, NCBP2, NUDT21, NUP155, NUP160, NUP188, NUP205, NUP43, NUP54, NUP58, NUP62, NUP88, NUP93, NUP98, PABPN1, PCBP2, PLRG1, POLDIP3, POLR2C, POLR2G, PPIL4, PPP1R8, PPWD1, PQBP1, PRCC, PRPF38A, PRPF4, PTBP1, RANBP2, RBM10, RBM39, RBM42, RBM5, RBM8A, RBMX, SARNP, SF1, SF3A1, SF3A3, SF3B1, SF3B3, SF3B4, SNRNP40, SNRPA, SNRPA1, SNRPB, SNRPD1, SNRPD2, SNRPD3, SNRPG, SNU13, SNW1, SRRM1, SRRM2, SRRT, SRSF1, SRSF10, SRSF2, SRSF3, SRSF4, SRSF7, SYMPK, TCERG1, TFIP11, THOC1, THOC2, THOC3, THOC5, THOC7, TRA2B, U2AF2, U2SURP, UPF3B, USP39, YBX1
RHO GTPase cycle	25.6	9.112957	0.193	AKAP13, ARHGAP1, ARHGAP18, ARHGAP25, ARHGAP4, ARHGAP45, ARHGAP9, ARHGDIB, ARHGEF1, ARHGEF12, ARHGEF17, ARHGEF2, ARHGEF40, ARHGEF6, ARHGEF7, CAPZB, CDC37, CDC42BPA, CDC42BPB, CKB, CLTC, CPNE8, CSK, CYBB, DOCK1, DOCK10, DOCK4, DOCK6, DOCK8, DOCK9, EFHD2, ELMO2, EPHA2, FARP1, FGD5, FMNL3, GFOD1, GIT1, GIT2, HNRNPC, HSP90AB1, ITGB1, ITS2N2, KTN1, LBR, LMNB1, MOSPD2, NCF1, NCF2, NCF4, NCK2, NCKAP1, PAK2, PAK4, PEAK1, PICALM, PKN1, PKN2, PLD1, PLXND1, RAC1, RBMX, RHOC, RHOG, ROCK2, SHMT2, SNAP23, SOWAHC, SRGAP2, SRRM1, STARD13, STK10, SWAP70, TAOK3, TMOD3, TMPO, TPM4, TRA2B, TWF1, UACA, VAV1, VAV2, WAS, WASF2, WDR91, WIPF2, ZNF512B
RNA Polymerase II Transcription	23.5	6.855655	0.315	AFF4, CDC40, CDC73, CDK9, CHTOP, CLP1, CPSF4, CPSF6, CSTF3, CTR9, DDX39A, EIF4A3, ERCC2, ERCC3, GTF2B, GTF2E1, LOC102724594/U2AF1, NCBP1, NCBP2, NUDT21, PABPN1, POLDIP3, POLR2C, POLR2G, RBM8A, SARNP, SNRPB, SNRPD3, SNRPG, SRRM1, SRSF1, SRSF2, SRSF3, SRSF4, SRSF7, SUPT5H, SUPT6H, SYMPK, TAF4, TCEA1, THOC1, THOC2, THOC3, THOC5, THOC7, U2AF2, UPF3B
Neutrophil degranulation	15.2	8.013877	0.151	ACTR2, ADAM10, ALDOC, ANPEP, AP2A2, APAF1, ARHGAP45, ARHGAP9, ARPC5, ARSA, ARSB, ASAH1, ATP11B, BST2, C1orf35, C3, CD53, CD93, CNN2, COMMD3, COTL1, CPNE1, CTSC, CTSZ, CYBB, DBNL, DDOST, DDX3X, DEGS1, DNAJC13, DPP7, DYNLT1, ENPP4, ERP44, FUCA1, GALNS, GCA, GLB1, GMFG, GNS, GUSB, HLA-B, HSP90AB1, HVCN1, ILF2, IST1, ITGAV, KCMF1, LPCAT1, MAN2B1, MNDA, MOSPD2, MVP, NME2, OSTF1, PECAM1, PGM2, PLD1, PRCP, RAB31, RAC1, RAP2C, RHOG, SERPINB6, SNAP23, STK10, TSPAN14, TXNDC5, XRCC5, XRCC6
Signalling by VEGF	14.4	5.385165	0.287	BCAR1, CDH5, CRK, CTNNA1, CTNNB1, CTNND1, CYBB, DOCK1, ELMO1, ELMO2, FLT1, FYN, ITGAV, ITPR1, ITPR2, NCF1, NCF2, NCF4, NCK2, NCKAP1, NOS3, NRP1, PAK2, PLCG1, PTK2, PXN, RAC1, ROCK2, VAV1, VAV2, WASF2
RHOA Signalling	14.2	4.003786	0.266	ACTR2, ACTR3, ARHGAP1, ARHGAP4, ARHGAP9, ARHGEF1, ARHGEF12, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, ARPC5L, KTN1, MPRIP, MSN, NEDD4, PFN1, PI4KA, PIKFYVE, PKN1, PLD1, PPP1R12A, PTK2, RAPGEF2, RDX, ROCK2, SEPTIN11, SEPTIN2, SEPTIN4, SEPTIN7, SEPTIN8, SEPTIN9
ISG15 antiviral mechanism	14	5	0.352	EIF2AK2, EIF4A2, EIF4A3, EIF4E, EIF4G2, EIF4G3, FLNB, KPNA2, NEDD4, NUP155, NUP160, NUP188, NUP205, NUP43, NUP54, NUP58, NUP62, NUP88, NUP93, NUP98, PLCG1, RANBP2, RIGI, UBA7, UBE2N
Integrin Signalling	13.7	5.059644	0.203	ACTR2, ACTR3, ARHGEF7, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, ARPC5L, ASAP1, BCAR1, CRK, DOCK1, FYN, GIT1, GSK3B, ILKAP, ITGA1, ITGA4, ITGAV, ITGB1, ITGB5, MAP2K1, MPRIP, NCK2, PAK2, PAK4, PFN1, PIK3C2A, PIK3CD, PIKFYVE, PLCG1, PPP1R12A, PTEN, PTK2, PXN, RAC1, RAP2A, RHOC, RHOG, SHC1, VASP, WAS

Signalling by Rho Family GTPases	13.7	6.111919	0.184	ACTR2, ACTR3, ARHGEF1, ARHGEF12, ARHGEF17, ARHGEF2, ARHGEF6, ARHGEF7, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, ARPC5L, CDH5, CYBB, ITGA1, ITGA4, ITGAV, ITGB1, ITGB5, MAP2K1, MSN, NCF1, NCF2, NEDD4, PAK2, PAK4, PI4KA, PIK3C2A, PIK3CD, PIKFYVE, PKN1, PLD1, PPP1R12A, PTK2, RAC1, RDX, RHOC, RHOG, ROCK2, SEPTIN11, SEPTIN2, SEPTIN4, SEPTIN7, SEPTIN8, SEPTIN9, STMN1, WAS
EPH-Ephrin signalling	13.5	5.291503	0.298	ACTR2, ACTR3, ADAM10, AP2A1, AP2A2, ARHGEF7, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, CLTA, CLTC, CLTCL1, EFNB1, EFNB2, EPHA2, EPHB4, FYN, GIT1, MYH9, NCK2, PAK2, PTK2, RAC1, ROCK2, VAV2, YES1
Fcy Receptor-mediated Phagocytosis in Macrophages and Monocytes	13.5	4.913538	0.298	ACTR2, ACTR3, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, ARPC5L, CBL, CRK, DOCK1, FYN, LCP2, NCF1, NCK2, PLCG1, PLD1, PLD3, PRKCH, PTEN, PXN, RAC1, VASP, VAV1, VAV2, WAS, YES1
SUMOylation of RNA binding proteins	13.4	4.472136	0.435	HNRNPC, HNRNPK, NOP58, NUP155, NUP160, NUP188, NUP205, NUP43, NUP54, NUP58, NUP62, NUP88, NUP93, NUP98, PHC2, RANBP2, RNF2, SUMO1, SUMO2, UBE2I
Metabolism of non-coding RNA	12.7	4.582576	0.382	GEMIN4, NCBP1, NCBP2, NUP155, NUP160, NUP188, NUP205, NUP43, NUP54, NUP58, NUP62, NUP88, NUP93, NUP98, PHAX, RANBP2, SNRPB, SNRPD1, SNRPD2, SNRPD3, SNRPG
Actin Cytoskeleton Signalling	12.7	5.778429	0.184	ACTR2, ACTR3, ARHGEF1, ARHGEF12, ARHGEF6, ARHGEF7, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, ARPC5L, BCAR1, CRK, CSK, DOCK1, GIT1, ITGA1, ITGA4, ITGAV, ITGB1, ITGB5, MAP2K1, MPRIP, MSN, MYH9, NCKAP1, PAK2, PAK4, PFN1, PIK3C2A, PIK3CD, PPP1R12A, PTK2, PXN, RAC1, RAP2A, RDX, ROCK2, SHC1, TMSB10/TMSB4X, VAV1, VAV2, WAS, WASF2
SUMOylation of chromatin organization proteins	12.5	4.582576	0.375	CBX5, HDAC1, HDAC2, NUP155, NUP160, NUP188, NUP205, NUP43, NUP54, NUP58, NUP62, NUP88, NUP93, NUP98, PHC2, RANBP2, RNF2, SUMO1, SUMO2, SUMO3, UBE2I
MicroRNA Biogenesis Signalling Pathway	12.2	4.866643	0.203	AGO2, ATM, DDX17, DICER1, EWSR1, EXOSC10, EXOSC2, FUS, HNRNPA1, HNRNPA2B1, HSP90AB1, HSP90B1, ILF2, ILF3, KHSRP, NUP155, NUP160, NUP188, NUP205, NUP43, NUP54, NUP58, NUP62, NUP88, NUP93, NUP98, PIK3C2A, PIK3CD, POLR2C, POLR2G, QKI, RAP2A, SF3A1, SMAD1, SRSF1, SRSF3, XPO5, XRN1
GP6 Signalling Pathway	11.5	2.886751	0.236	ADAM10, COL12A1, COL15A1, COL18A1, COL1A2, COL28A1, COL2A1, COL3A1, COL4A1, COL4A2, FYN, GSK3B, ITPR1, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMC1, LCP2, PIK3C2A, PIK3CD, PLCG1, PRKCH, PTK2, RAC1, RHOG, VAV1, VAV2
Clathrin-mediated Endocytosis Signalling	11.4		0.188	AAK1, ACTR2, ACTR3, AP1S2, AP2A1, AP2A2, AP3B1, AP3D1, AP3M1, AP3M2, AP3S1, APOA1, APOB, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, ARPC5L, ARRB1, ARRB2, CBL, CD2AP, CLTA, CLTC, CLTCL1, CLU, DAB2, HIP1, ITGB1, ITGB5, MYO1E, PICALM, PIK3C2A, PIK3CD, PON1, RAC1, SH3KBP1, TSG101
SUMOylation of DNA damage response and repair proteins	11.4	4.795832	0.303	NUP155, NUP160, NUP188, NUP205, NUP43, NUP54, NUP58, NUP62, NUP88, NUP93, NUP98, PARP1, PHC2, PML, RANBP2, RNF2, SMC5, SMC6, STAG2, SUMO1, SUMO2, SUMO3, UBE2I
SUMOylation of DNA replication proteins	11.4	4.242641	0.4	NUP155, NUP160, NUP188, NUP205, NUP43, NUP54, NUP58, NUP62, NUP88, NUP93, NUP98, RANBP2, SUMO1, SUMO2, SUMO3, TOP1, TOP2B, UBE2I

Leukocyte Extravasation Signalling	11.1	3.086975	0.192	AFDN, ARHGAP1, ARHGAP4, ARHGAP9, BCAR1, CDH5, CRK, CTNNA1, CTNNB1, CTNND1, CYBB, ICAM1, ITGA4, ITGB1, JAM2, JAM3, MSN, NCF1, NCF2, NCF4, PECAM1, PIK3C2A, PIK3CD, PLCG1, PRKCH, PTK2, PXN, RAC1, RDX, ROCK2, SIPA1, THY1, TIMP3, VASP, VAV1, VAV2, WAS
RHO GDI Signalling	10.6	-4.56383	0.177	ACTR2, ACTR3, ARHGAP1, ARHGAP4, ARHGAP9, ARHGDIB, ARHGEF1, ARHGEF12, ARHGEF17, ARHGEF2, ARHGEF6, ARHGEF7, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, ARPC5L, CDH5, CREBBP, EP300, ITGA1, ITGA4, ITGAV, ITGB1, ITGB5, MSN, MYH9, PAK2, PAK4, PI4KA, PIKFYVE, PPP1R12A, RAC1, RDX, RHOC, RHOG, ROCK2, WASF2
SUMOylation of SUMOylation proteins	10.3	3.872983	0.441	NUP155, NUP160, NUP188, NUP205, NUP43, NUP54, NUP58, NUP62, NUP88, NUP93, NUP98, RANBP2, SUMO1, SUMO2, UBE2I
Sertoli Cell-Germ Cell Junction Signalling Pathway (Enhanced)	10.2	0.632456	0.169	ACTR2, ACTR3, AFDN, ARPC1B, ARPC2, ARPC3, ARPC4, ARPC5, ARPC5L, BCAR1, CD2AP, CTNNA1, CTNNB1, CTNND1, EPS8, GSK3B, GUCY1A1, GUCY1B1, ICAM1, IL1RAP, ITGB1, JAM2, JAM3, LAMA2, LAMA3, LAMA4, LAMA5, LAMB1, LAMB2, LAMC1, MAP2K1, NECTIN2, PIK3C2A, PIK3CD, PRKAB1, PTK2, RAC1, RAP2A, SP1, TAB1
Protein Sorting Signalling Pathway	10.2	5.830952	0.191	AP1S2, AP3B1, AP3D1, AP3M1, AP3M2, AP3S1, ARFGEF1, CLINT1, CLTA, CLTC, CLTCL1, COPG1, COPZ1, CTBP1, FYN, GGA2, GUCY1A1, GUCY1B1, KDELR2, PLD1, PLD3, RER1, SEC24A, SEC24B, SEC31A, SERPINH1, SNX18, SNX6, TMED2, TMED5, WASHC2A/WASHC2C, WASHC4, WASHC5, YES1
Sumoylation Pathway	10	-1.41421	0.243	ARHGDIB, CREBBP, CTBP1, CTBP2, EP300, FAS, HDAC1, HDAC2, KDM1A, PML, RAC1, RANBP2, RCC1, RFC1, RFC3, RFC4, RHOC, RHOG, SAE1, SP1, SUMO1, SUMO2, SUMO3, UBA2, UBE2I

Supplementary Table 3: Differentially expressed proteins in the top 25 enriched canonical pathways (female plateau vs involuting IH) through core analysis in Ingenuity Pathway Analysis.

Pathway	-log(p-value)	zScore	Ratio	Molecules
Response to elevated platelet cytosolic Ca ²⁺	24.4	-5.04825	0.25	A1BG, ABCC4, ACTN1, AHSG, ALB, APOH, CD109, CD9, CLEC3B, CLU, ECM1, FGB, FGG, HRG, ITIH4, KNG1, ORM1, PLG, PROS1, QSOX1, RARRES2, SELENOP, SERPINA1, SERPINA3, SERPINA4, SERPING1, SOD1, SPARC, STXBP3, TF, THBS1, TMSB10/TMSB4X, VWF
Acute Phase Response Signalling	22.5	-2.06474	0.195	AHSG, ALB, AMBP, APCS, APOH, C3, C4BPA, C5, C9, CP, F2, FGB, FGG, HPX, HRG, ITIH2, ITIH4, KLKB1, KRAS, LBP, MAP3K5, NGFR, ORM1, PLG, RBP4, RRAS, RRAS2, SERPINA1, SERPINA3, SERPIND1, SERPINF1, SERPING1, TF, TTR, VWF
DHCR24 Signalling Pathway	19.3	-5.38516	0.212	A1BG, AHSG, ALB, AMBP, APOB, APOC3, APOD, APOH, APOL1, C3, C9, CLU, GC, HPR, HPX, ITIH4, KNG1, KRAS, ORM1, PON1, RBP4, RRAS, RRAS2, SERPINA1, SERPINF1, TF, TTR, VCAM1, VTN
LXR/RXR Activation	18.5	-4.81125	0.22	A1BG, AHSG, ALB, AMBP, APOB, APOC3, APOD, APOH, APOL1, C3, C9, CLU, GC, HPR, HPX, ITIH4, KNG1, LBP, NGFR, ORM1, PON1, RBP4, SERPINA1, SERPINF1, TF, TTR, VTN
Coagulation System	18.5	-0.24254	0.486	F10, F12, F13B, F2, FGB, FGG, KLKB1, KNG1, PLG, PROC, PROS1, SERPINA1, SERPINA5, SERPINC1, SERPIND1, THBD, VWF
Complement cascade	18.4	-4.79583	0.207	C3, C4BPA, C5, C6, C7, C8A, C8B, C8G, C9, CD81, CFH, CFHR1, CFI, CLU, CPB2, CPN1, CPN2, F2, FCN3, IGKV3D-20, IGKV4-1, IGLV1-47, IGLV1-51, IGLV3-19, PROS1, SERPING1, VTN
Formation of Fibrin Clot (Clotting Cascade)	17.5	-3.63803	0.436	F10, F12, F13B, F2, FGB, FGG, KLKB1, KNG1, PRCP, PROC, PROS1, SERPINA5, SERPINC1, SERPIND1, SERPING1, THBD, VWF
Extracellular matrix organization	16.8	-2.44949	0.226	ASPEN, BGN, COL4A1, COL4A2, COL5A3, COL6A1, COL6A2, COL6A3, DAG1, DCN, DMD, FGF2, FMOD, ITGA3, ITGA6, ITGB4, LAMB1, LUM, NCAM1, PTPRS, SH3PXD2A, SPARC, TTR, VTN
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by IGF-BPs	15.2	-3.67423	0.194	AHSG, ALB, APOB, APOL1, C3, CP, CTSG, DNAJC3, F2, FGG, IGFALS, ITIH2, KNG1, LAMB1, MFGE8, NUCB1, PLG, PROC, QSOX1, SERPINA1, SERPINC1, SERPIND1, TF, VWA1
Extrinsic Prothrombin Activation Pathway	12.6		0.625	F10, F12, F13B, F2, FGB, FGG, PROC, PROS1, SERPINC1, THBD
Post-translational protein phosphorylation	12.4	-3.1305	0.187	AHSG, ALB, APOB, APOL1, C3, CP, DNAJC3, FGG, ITIH2, KNG1, LAMB1, MFGE8, NUCB1, PROC, QSOX1, SERPINA1, SERPINC1, SERPIND1, TF, VWA1
Complement System	12.1	0.377964	0.351	C3, C4BPA, C5, C6, C7, C8A, C8B, C8G, C9, CFH, CFI, SERPING1
Neutrophil degranulation	11.8	-3.16228	0.084	A1BG, AHSG, ANO6, ANXA2, ARHGAP45, ARSA, BST1, C3, CAT, CD44, CD47, CD68, CD93, CPNE3, CTSG, CYB5R3, DNAJC3, FGL2, GSN, HLA-B, IQGAP2, LGALS3, LTA4H, MAN2B1, ORM1, PAFAH1B2, PNP, PRCP, PYGB, QSOX1, RAP2C, SERPINA1, SERPINA3, STK10, TIMP2, TMBIM1, TMT1A, TTR, TXNDC5, VAT1
Intrinsic Prothrombin Activation Pathway	11.3	-1.26491	0.31	COL5A3, F10, F12, F13B, F2, FGB, FGG, KLKB1, KNG1, PROC, PROS1, SERPINC1, THBD

Integrin cell surface interactions	11.2	-2.18282	0.2	CD44, CD47, COL4A1, COL4A2, COL5A3, COL6A1, COL6A2, COL6A3, FGB, FGG, ITGA3, ITGA6, LUM, THBS1, VCAM1, VTN, VWF
Collagen biosynthesis and modifying enzymes	8.51	0.83205	0.194	COL28A1, COL4A1, COL4A2, COL5A3, COL6A1, COL6A2, COL6A3, CRTAP, P3H1, P3H3, PCOLCE, PLOD1, SERPINH1
Binding and Uptake of Ligands by Scavenger Receptors	8.28	-2.5	0.143	ALB, AMBP, APOB, APOL1, COL4A1, COL4A2, HPR, HPX, IGKV3D-20, IGKV4-1, IGLV1-47, IGLV1-51, IGLV3-19, JCHAIN, SCARA5, SPARC
Assembly of collagen fibrils and other multimeric structures	7.97	-1.1547	0.197	CD151, COL4A1, COL4A2, COL5A3, COL6A1, COL6A2, COL6A3, ITGA6, ITGB4, PCOLCE, PLEC, PXDN
Erythrocytes take up carbon dioxide and release oxygen	7.25	-2.44949	0.545	AQP1, CA1, CA2, CYB5R2, RHAG, SLC4A1
Clathrin-mediated Endocytosis Signalling	7.17		0.0962	ACTG1, ALB, APOB, APOC3, APOD, APOL1, ARF6, CLTA, CLU, DNM1, F2, FGF2, ITGB4, ORM1, PON1, PPP3R1, RBP4, SERPINA1, SH3GLB2, TF
Cell surface interactions at the vascular wall	7.06	-4.47214	0.0948	APOB, ATP1B1, CD44, CD47, F2, GPC1, IGKV3D-20, IGKV4-1, IGLV1-47, IGLV1-51, IGLV3-19, ITGA3, ITGA6, JCHAIN, KRAS, L1CAM, PROC, PROS1, THBD, TSPAN7
NCAM signalling for neurite out-growth	6.94	-1.50756	0.18	COL4A1, COL4A2, COL5A3, COL6A1, COL6A2, COL6A3, KRAS, NCAM1, PTPRA, SPTA1, SPTB
Erythrocytes take up oxygen and release carbon dioxide	6.92	-2.23607	0.714	AQP1, CA1, CA2, RHAG, SLC4A1
L1CAM interactions	6.77	-1.29099	0.12	ACTG1, ALCAM, ANK1, CLTA, CNTN1, CNTNAP1, DCX, DLG3, DNM1, EGFR, L1CAM, LAMB1, NCAM1, SPTA1, SPTB
Atherosclerosis Signalling	6.42	-2.84019	0.113	ALB, APOB, APOC3, APOD, APOL1, CLU, CMA1, COL5A3, ORM1, PLA2G4A, PON1, RBP4, SERPINA1, TPSAB1/TPSB2, VCAM1

Supplementary Table 4: Differentially expressed proteins in the top 25 enriched canonical pathways (male proliferating vs involuting IH) through core analysis in Ingenuity Pathway Analysis.

Pathway	-log(p-value)	zScore	Ratio	Molecules
Complement cascade	6.86	-2.44949	0.0519	C1S, C5, C8A, C8B, CLU, IGHV3-33, VTN
Collagen biosynthesis and modifying enzymes	5.81	2.236068	0.0746	CRTAP, P3H1, P3H3, PLOD1, SERPINH1
LXR/RXR Activation	5.79	-2.44949	0.0488	AMBP, APOC3, APOD, CLU, SAA4, VTN
DHCR24 Signalling Pathway	5.51	-2.44949	0.0438	AMBP, APOC3, APOD, CLU, SAA4, VTN
Complement System	5.38		0.108	C1S, C5, C8A, C8B
DNA Damage/Telomere Stress Induced Senescence	4.66	1	0.0714	H1-1, H1-2, H1-5, H2AC20
Apoptotic execution phase	3.32		0.0577	H1-1, H1-2, H1-5
IL-12 Signalling and Production in Macrophages	3.26	1.341641	0.0219	APOC3, APOD, CLU, FCGR2B, SAA4
Atherosclerosis Signalling	3.2	-2	0.0301	APOC3, APOD, CLU, SAA4
Granzyme A Signalling	2.87		0.0405	H1-1, H1-2, H1-5
Acute Phase Response Signalling	2.67		0.0216	AMBP, C1S, C5, SAA4
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	2.62	-2	0.0209	APOC3, APOD, CLU, SAA4
Clathrin-mediated Endocytosis Signalling	2.49		0.0192	APOC3, APOD, CLU, SAA4
Antimicrobial peptides	2.35		0.0588	ATOX1, CAMP
Coagulation System	2.33		0.0571	F10, SERPINA5
Formation of Fibrin Clot (Clotting Cascade)	2.23		0.0513	F10, SERPINA5
Hematoma Resolution Signalling Pathway	2.16	2	0.0155	C5, C8A, C8B, CA1
Response to elevated platelet cytosolic Ca ²⁺	2.16		0.0227	CLU, ECM1, SERPINA4
Protein Kinase A Signalling	2.15	1	0.0122	GNG12, H1-1, H1-2, H1-5, PTEN
SUMOylation of DNA replication proteins	2.11		0.0444	AAAS, TOP1
Ascorbate Recycling (Cytosolic)	2.06		0.333	GLRX
NAD Signalling Pathway	2		0.0199	H1-1, H1-2, H1-5
Histone Modification Signalling Pathway	1.96	1	0.0136	H1-1, H1-2, H1-5, H2AC20
Glutathione Redox Reactions II	1.93		0.25	GLRX
MicroRNA Biogenesis Signalling Pathway	1.76		0.016	AAAS, DBR1, EXOSC9
Major pathway of rRNA processing in the nucleolus and cytosol	1.76		0.0161	EXOSC9, RPL39, RRP1
Telomere Maintenance	1.71		0.0274	H2AC20, RFC3
Erythrocytes take up oxygen and release carbon dioxide	1.69		0.143	CA1
Role of JAK family kinases in IL-6-type Cytokine Signalling	1.65		0.0253	SERPINA4, SERPINA5

Supplementary Table 5: Differentially expressed proteins in the top 25 enriched canonical pathways (male plateau vs involuting IH) through core analysis in Ingenuity Pathway Analysis.

	Fold regulation (normalised to β -actin)								
	Proliferating IH					Involuting IH			
MAOA (male IH)	0.40	0.53	0.59	0.07	0.27	1.00	1.11	3.60	3.21
MAOA (female IH)	0.98	0.38	0.83	0.75	0.47	1.20	1.32	1.46	5.59
Complex I (male IH)	0.25	0.29	0.13	0.12	0.29	0.13	0.16	1.46	0.54
Complex I (female IH)	0.18	1.06	0.09	0.56	0.76	0.08	0.08	0.34	0.96
Complex II (male IH)	0.47	0.43	0.49	0.26	0.45	0.43	0.22	0.76	1.20
Complex II (female IH)	0.55	0.53	0.15	0.26	0.50	0.19	0.17	0.49	0.48
Complex III (male IH)	0.36	0.53	0.37	0.30	0.18	0.33	0.14	1.17	1.59
Complex III (female IH)	0.27	0.61	0.06	0.23	0.57	0.18	0.37	0.42	6.97
Complex IV (male IH)	0.49	0.69	0.77	0.43	0.40	0.54	0.29	0.24	1.33
Complex IV (female IH)	0.56	0.71	0.16	0.41	0.52	0.04	0.43	1.46	
Complex V (male IH)	0.52	0.69	0.44	0.30	0.23	0.40	0.09	1.27	1.26
Complex V (female IH)	0.42	0.71	0.21	0.47	0.56	0.34	0.90	1.61	0.57
Na+K+ATPase (male IH)	1.75	1.75	0.62	0.61		1.75	0.10	1.70	3.86
Na+K+ATPase (female IH)	0.41	0.40	0.03	0.30	0.60	0.18	0.08	0.63	0.24
FAS (male IH)	0.46	0.72	0.86	0.15	0.11	0.70	0.47	0.53	1.23
FAS (female IH)	0.74	0.75	0.72	0.24	0.23	0.22	0.26	0.54	0.22
VDAC (male IH)	0.26	0.53	0.42	0.43	0.67	0.40	0.48	0.34	0.67
VDAC (female IH)	0.40	0.75	0.08	0.38	0.51	0.05	0.07	0.67	9.22
AMPK (male IH)	0.43	0.95	0.61	0.38	0.58	0.58	0.73	1.39	0.70
AMPK (female IH)	0.73	0.98	0.17	0.47	0.39	0.39	0.28	0.55	0.27

Supplementary Table 6: Western Blot quantification: Protein expression values normalized to β -actin in proliferating and involuting IH.

Symbol	Proliferating IH (Grouped)		Involuting IH (Grouped)		Proliferating IH (Female)		Involuting IH (Female)		Proliferating IH (Male)		Involuting IH (Male)	
	Fold change	p-value	Fold change	p-value	Fold change	p-value	Fold change	p-value	Fold change	p-value	Fold change	p-value
ABCA1	1.04	0.799912	1.51	0.241403	1.31	0.476121	1.82	0.385818	0.83	0.395965	1.25	0.432841
ABCG1	0.30	0.000010	1.04	0.584563	0.31	0.011864	0.80	0.275997	0.28	0.000698	1.35	0.004107
ACAA2	1.08	0.408665	2.41	0.043713	1.24	0.068132	3.71	0.092534	0.94	0.668140	1.56	0.276827
AKR1D1	1.47	0.195482	0.99	0.827549	0.92	0.840384	0.79	0.530310	2.35	0.023759	1.23	0.435821
ANGPTL3	0.72	0.714674	2.53	0.012874	0.38	0.477014	3.02	0.023029	1.37	0.247033	2.11	0.173414
ANKRA2	1.01	0.179063	2.26	0.049185	1.42	0.591792	4.46	0.074065	0.72	0.064279	1.15	0.542347
APOA1	2.33	0.125726	8.81	0.339866	2.50	0.376667	42.32	0.373051	2.17	0.106901	1.83	0.194902
APOA2	0.88	0.317964	0.86	0.406014	0.36	0.275384	0.45	0.390613	2.16	0.030303	1.64	0.197945
APOA4	1.36	0.254379	0.98	0.987664	0.92	0.840384	0.91	0.876824	2.02	0.042741	1.06	0.744339
APOB	1.25	0.310546	1.72	0.344223	0.85	0.461332	3.66	0.367267	1.85	0.110205	0.81	0.577153
APOC3	1.47	0.195482	1.46	0.351249	0.92	0.840384	1.74	0.420806	2.35	0.023759	1.23	0.435821
APOD	0.29	0.000308	2.48	0.037373	0.33	0.071926	2.11	0.322798	0.25	0.001336	2.92	0.069671
APOE	1.07	0.124813	0.75	0.324886	2.53	0.833786	3.41	0.594064	0.45	0.038308	0.16	0.018233
APOF	1.47	0.195482	3.32	0.340920	0.92	0.840384	0.79	0.530310	2.35	0.023759	13.99	0.373439
APOL1	4.21	0.001067	3.62	0.011014	5.82	0.016257	2.80	0.174241	3.04	0.015558	4.68	0.057111
APOL2	0.89	0.650869	1.37	0.130049	1.02	0.725379	1.04	0.621223	0.79	0.136161	1.79	0.020548
APOL5	8.21	0.015559	3.65	0.058265	6.92	0.156782	1.51	0.425626	9.75	0.062079	8.83	0.059091
CDH13	1.75	0.020474	1.53	0.160276	2.64	0.006680	1.01	0.727007	1.16	0.474554	2.31	0.154490
CEL	0.33	0.000020	1.24	0.251922	0.36	0.020596	1.49	0.330579	0.30	0.000539	1.04	0.765580
CELA3A	1.46	0.192022	1.48	0.339854	1.06	0.785137	1.34	0.521978	2.00	0.045503	1.64	0.044524
CELA3B	1.47	0.195482	1.01	0.908451	0.92	0.840384	0.79	0.530310	2.35	0.023759	1.28	0.423233
CETP	38.31	0.000565	5.13	0.078052	57.19	0.018139	3.95	0.276224	25.67	0.035818	6.67	0.141730
CNBP	0.63	0.001204	1.37	0.059599	0.63	0.067884	1.30	0.264358	0.64	0.001667	1.45	0.221887
COLEC12	1.55	0.055283	1.90	0.039914	1.75	0.241013	1.93	0.282289	1.39	0.139843	1.87	0.099796
CXCL16	0.40	0.003757	0.40	0.011589	0.65	0.217322	0.77	0.329129	0.24	0.003694	0.21	0.010974
CYB5R3	0.58	0.002565	0.69	0.409726	0.71	0.234184	0.77	0.936948	0.47	0.003371	0.62	0.202785

CYP11A1	1.41	0.231794	1.99	0.157333	1.14	0.908297	2.62	0.221033	1.74	0.151783	1.51	0.356563
CYP39A1	0.13	0.000051	0.35	0.197568	0.12	0.000513	0.68	0.974700	0.14	0.028089	0.18	0.002237
CYP46A1	1.14	0.585443	2.00	0.159401	0.78	0.429596	1.78	0.399361	1.67	0.070958	2.24	0.050995
CYP51A1	0.71	0.034813	0.61	0.053041	0.76	0.292564	0.82	0.487756	0.67	0.019268	0.46	0.007420
CYP7A1	1.25	0.391044	4.40	0.340663	0.81	0.630487	10.68	0.374096	1.95	0.070462	1.82	0.246247
CYP7B1	2.65	0.054952	1.85	0.568328	4.21	0.400992	3.96	0.553247	1.67	0.038645	0.87	0.968569
DHCR24	0.10	0.000004	0.11	0.003020	0.12	0.001347	0.45	0.339575	0.09	0.000335	0.03	0.000124
DHCR7	0.19	0.000001	0.26	0.078455	0.27	0.001200	0.74	0.982020	0.14	0.000122	0.09	0.000007
FDFT1	0.95	0.510470	1.33	0.137807	1.06	0.575532	2.10	0.019597	0.86	0.291820	0.85	0.589704
FDPS	0.66	0.029712	1.44	0.270569	0.89	0.803618	2.44	0.247174	0.49	0.002674	0.84	0.574832
HDLBP	0.54	0.004896	1.05	0.535442	0.64	0.329283	1.26	0.482605	0.45	0.001231	0.88	0.995081
HMGCR	0.32	0.000001	0.42	0.332109	0.31	0.000157	0.83	0.796365	0.32	0.005799	0.21	0.000891
HMGCS1	0.38	0.000006	0.51	0.877661	0.44	0.009895	1.14	0.531462	0.33	0.000621	0.23	0.001527
HMGCS2	0.13	0.000002	0.27	0.587573	0.15	0.003630	0.31	0.294081	0.12	0.001569	0.24	0.957292
IDI1	0.82	0.151356	1.00	0.996836	0.84	0.405521	0.96	0.913191	0.79	0.042707	1.05	0.130913
IDI2	1.05	0.948136	2.74	0.012843	0.63	0.186295	2.36	0.112819	1.73	0.216804	3.16	0.074982
IL4	1.47	0.195482	0.99	0.828392	0.92	0.840384	0.79	0.530911	2.35	0.023759	1.23	0.435821
INSIG1	1.27	0.296293	1.61	0.141775	1.03	0.963406	1.45	0.344592	1.56	0.046929	1.78	0.334148
INSIG2	0.74	0.002556	1.50	0.046194	0.79	0.175348	1.90	0.092435	0.70	0.007220	1.18	0.282173
LCAT	0.61	0.135934	2.26	0.048383	0.64	0.533705	1.59	0.420835	0.59	0.046450	3.21	0.047649
LDLR	2.02	0.015753	1.17	0.376962	1.62	0.252515	0.98	0.717380	2.52	0.058119	1.39	0.326919
LDLRAP1	0.43	0.003294	0.62	0.045718	0.49	0.152152	0.74	0.390884	0.37	0.001765	0.51	0.041419
LEP	0.17	0.003698	0.39	0.985238	0.20	0.151128	0.58	0.647402	0.15	0.018885	0.27	0.004352
LIPE	0.16	0.032835	0.69	0.389822	0.37	0.865059	1.26	0.392067	0.07	0.000335	0.37	0.062949
LRP10	0.34	0.000750	0.74	0.421556	0.52	0.169992	1.49	0.351448	0.23	0.000003	0.37	0.010914
LRP12	0.83	0.266863	1.24	0.257125	1.14	0.688785	1.44	0.225098	0.61	0.003077	1.07	0.665107
LRP1B	0.85	0.477217	1.84	0.108979	0.74	0.490333	2.71	0.104923	0.98	0.743104	1.24	0.790831
LRP6	6.22	0.000056	5.19	0.011780	10.85	0.006027	6.06	0.022862	3.56	0.016717	4.44	0.059084
LRPAP1	0.93	0.312513	0.91	0.552502	1.05	0.797462	1.09	0.683080	0.83	0.055829	0.76	0.140859

MBTPS1	0.75	0.009100	0.72	0.171389	0.75	0.126494	0.67	0.427096	0.76	0.001407	0.78	0.227423
MVD	0.48	0.007178	0.93	0.725646	0.74	0.514764	2.00	0.164076	0.31	0.000303	0.43	0.014573
MVK	0.20	0.000008	0.72	0.914131	0.26	0.011508	1.71	0.330245	0.15	0.000448	0.30	0.002795
NPC1L1	1.47	0.195482	1.44	0.362612	0.92	0.840384	1.54	0.474532	2.35	0.023759	1.34	0.282760
NR0B2	1.47	0.195482	0.99	0.827549	0.92	0.840384	0.79	0.530310	2.35	0.023759	1.23	0.435821
NR1H4	1.47	0.195482	0.99	0.827549	0.92	0.840384	0.79	0.530310	2.35	0.023759	1.23	0.435821
NSDHL	0.42	0.000053	1.10	0.406056	0.54	0.020881	2.29	0.105978	0.33	0.002238	0.53	0.015243
OLR1	1.47	0.195482	0.99	0.840063	0.92	0.840384	0.80	0.540676	2.35	0.023759	1.23	0.435821
OSBPL1A	1.08	0.400100	1.61	0.108254	1.25	0.082056	1.50	0.398653	0.93	0.787713	1.72	0.247834
OSBPL5	0.54	0.009768	0.80	0.383894	0.68	0.392432	0.94	0.859913	0.44	0.000083	0.68	0.272665
PCSK9	0.20	0.000000	0.16	0.000013	0.16	0.000018	0.25	0.022558	0.25	0.000182	0.11	0.000225
PMVK	0.49	0.000027	0.70	0.532267	0.48	0.005332	1.15	0.553665	0.49	0.007095	0.42	0.000143
PPARD	0.45	0.002110	0.96	0.992774	0.58	0.146521	1.75	0.072691	0.35	0.003047	0.53	0.040722
PRKAA1	1.13	0.414301	1.9	0.002837	0.96	0.773208	1.56	0.165465	1.33	0.024062	2.32	0.012562
PRKAA2	0.19	0.000129	2.43	0.311697	0.25	0.063883	1.36	0.413999	0.14	0.000799	4.35	0.367130
PRKAG2	0.48	0.000107	1.40	0.148867	0.42	0.011446	1.22	0.539604	0.54	0.004056	1.60	0.060969
SCAP	0.42	0.005576	0.64	0.120554	0.51	0.108473	0.71	0.356201	0.35	0.001118	0.58	0.140335
SCARF1	3.84	0.000824	3.77	0.023752	5.33	0.019787	2.51	0.343461	2.77	0.033974	5.67	0.035897
SNX17	1.01	0.850068	0.95	0.934862	1.14	0.463905	1.03	0.797690	0.89	0.205138	0.87	0.538530
SOAT1	0.35	0.000172	0.57	0.766531	0.46	0.019789	1.10	0.512640	0.27	0.000100	0.29	0.000562
SORL1	0.10	0.000000	0.19	0.000000	0.09	0.000001	0.23	0.000224	0.11	0.001955	0.16	0.000568
SREBF1	0.17	0.000012	0.49	0.035802	0.25	0.020744	0.93	0.923449	0.11	0.000027	0.26	0.002161
SREBF2	0.51	0.001180	0.65	0.070201	0.64	0.225819	1.04	0.851071	0.41	0.000028	0.41	0.000656
STAB1	7.22	0.000241	4.54	0.025994	10.62	0.031512	4.64	0.184061	4.91	0.001244	4.45	0.110371
STAB2	0.20	0.000000	0.41	0.047543	0.21	0.000194	1.00	0.915940	0.20	0.000207	0.16	0.001989
STARD3	0.60	0.065664	1.02	0.976230	0.80	0.749359	1.38	0.579431	0.45	0.001738	0.75	0.496592
TM7SF2	0.14	0.000142	0.59	0.565445	0.18	0.000328	2.87	0.251596	0.11	0.004480	0.12	0.000302
TRERF1	0.58	0.014647	0.47	0.001871	0.59	0.244416	0.54	0.066172	0.58	0.016463	0.40	0.042868
VLDLR	0.51	0.518783	2.13	0.205972	0.89	0.662142	2.80	0.160527	0.29	0.000042	1.62	0.420248

ACTB	1.29	0.41189 9	0.62	0.11568 3	2.09	0.19033 7	0.97	0.85871 8	0.80	0.24298 3	0.40	0.04502 6
B2M	1.31	0.06225 8	1.78	0.04688 7	1.15	0.51271 2	1.36	0.02823 1	1.50	0.01267 8	2.33	0.14048 2
GAPDH	0.49	0.00001 4	1.06	0.44375 5	0.51	0.01107 4	0.88	0.34580 1	0.48	0.00262 1	1.28	0.45609 7
HPRT1	1.32	0.24479 7	1.13	0.66914 5	1.08	0.99218 2	0.75	0.39234 2	1.63	0.00721 4	1.70	0.18990 3
RPLP0	0.92	0.74648 9	0.73	0.41970 9	0.75	0.34630 1	1.05	0.78903 8	1.14	0.46195 3	0.51	0.05329 9

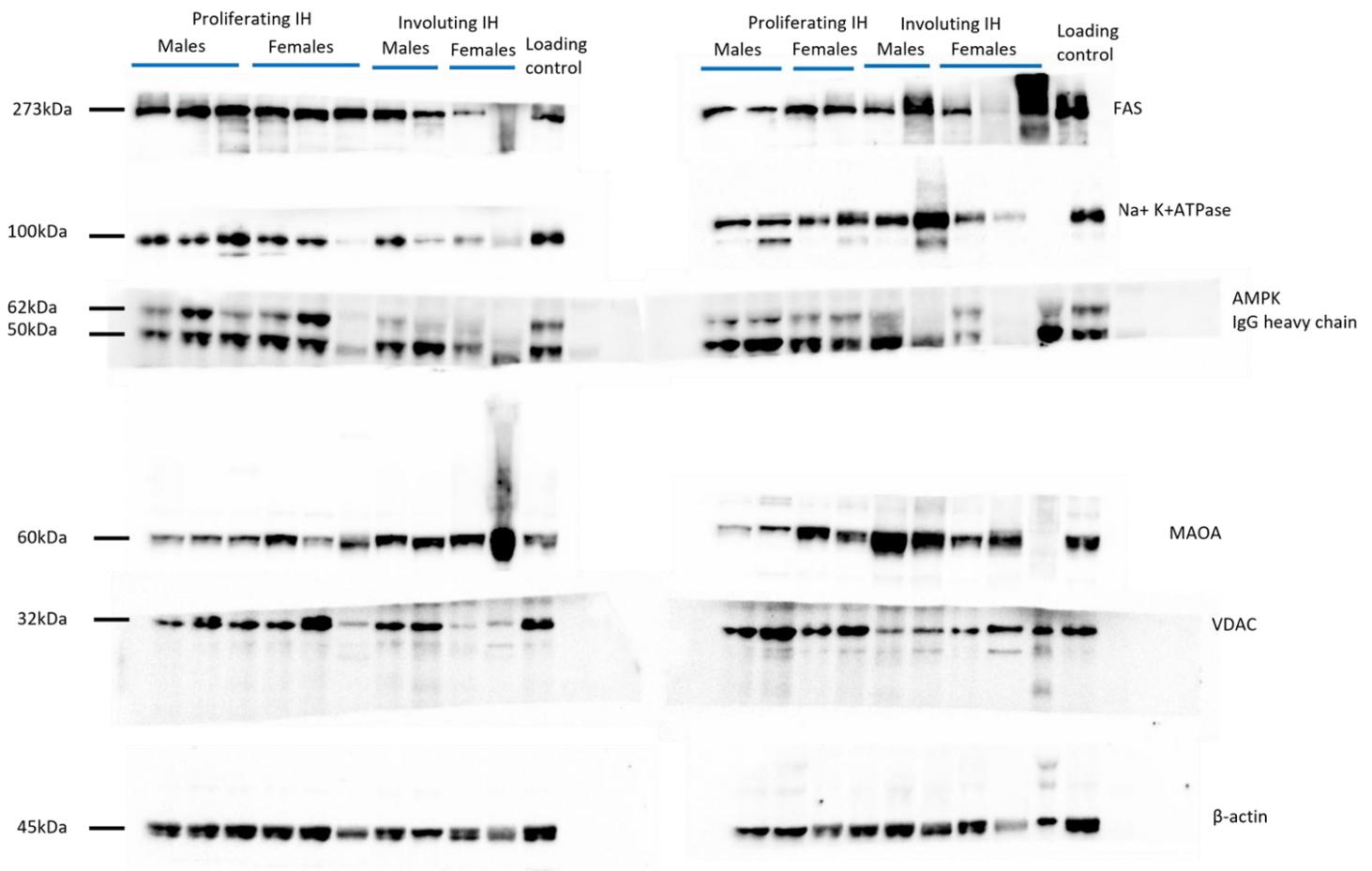
Supplementary Table 7: Gene expression profiling in proliferating and involuting IH (compared to normal skin) using the human apolipoprotein signalling and cholesterol metabolism PCR array.

Symbol	Involuting v Proliferating IH (Grouped)		Involuting v Proliferating IH (Female)		Involuting v Proliferating IH (Male)	
	Fold change	p-value	Fold change	p-value	Fold change	p-value
ABCA1	1.45	0.196288	1.39	0.378612	1.50	0.226179
ABCG1	3.47	0.000770	2.54	0.057299	4.73	0.000155
ACAA2	2.24	0.023683	3.01	0.058751	1.67	0.166333
AKR1D1	0.67	0.081417	0.86	0.555290	0.52	0.096000
ANGPTL3	3.53	0.004655	8.03	0.012008	1.55	0.216322
ANKRA2	2.24	0.000596	3.13	0.002413	1.61	0.073570
APOA1	3.78	0.264224	16.94	0.285279	0.84	0.602597
APOA2	0.98	0.802999	1.28	0.394617	0.76	0.514969
APOA4	0.72	0.243200	0.99	0.993994	0.52	0.096000
APOB	1.37	0.285453	4.30	0.273047	0.44	0.058503
APOC3	1.00	0.603352	1.89	0.295729	0.52	0.096000
APOD	8.59	0.003286	6.32	0.161990	11.67	0.010031
APOE	0.70	0.924361	1.34	0.416582	0.36	0.081385
APOF	2.26	0.265555	0.86	0.555290	5.95	0.286440
APOL1	0.86	0.971682	0.48	0.307567	1.54	0.221332
APOL2	1.53	0.069480	1.03	0.666590	2.28	0.003502
APOL5	0.44	0.154051	0.22	0.177415	0.91	0.768707
CDH13	0.87	0.833739	0.38	0.022369	1.98	0.134644
CEL	3.74	0.001237	4.08	0.050984	3.43	0.006913
CELA3A	1.02	0.623617	1.26	0.526383	0.82	0.358883
CELA3B	0.68	0.109034	0.86	0.555290	0.54	0.141485
CETP	0.13	0.008826	0.07	0.026081	0.26	0.265884
CNBP	2.17	0.000240	2.07	0.007651	2.26	0.031263
COLEC12	1.22	0.304231	1.10	0.682957	1.35	0.268659
CXCL16	1.01	0.913577	1.18	0.647701	0.87	0.934202
CYB5R3	1.20	0.358443	1.09	0.641773	1.32	0.356596
CYP11A1	1.42	0.176667	2.31	0.143690	0.87	0.715872
CYP39A1	2.70	0.259557	5.88	0.172413	1.24	0.731519
CYP46A1	1.75	0.131734	2.29	0.245716	1.34	0.280735
CYP51A1	0.86	0.554764	1.08	0.611747	0.68	0.166592
CYP7A1	3.51	0.264292	13.26	0.285692	0.93	0.863189

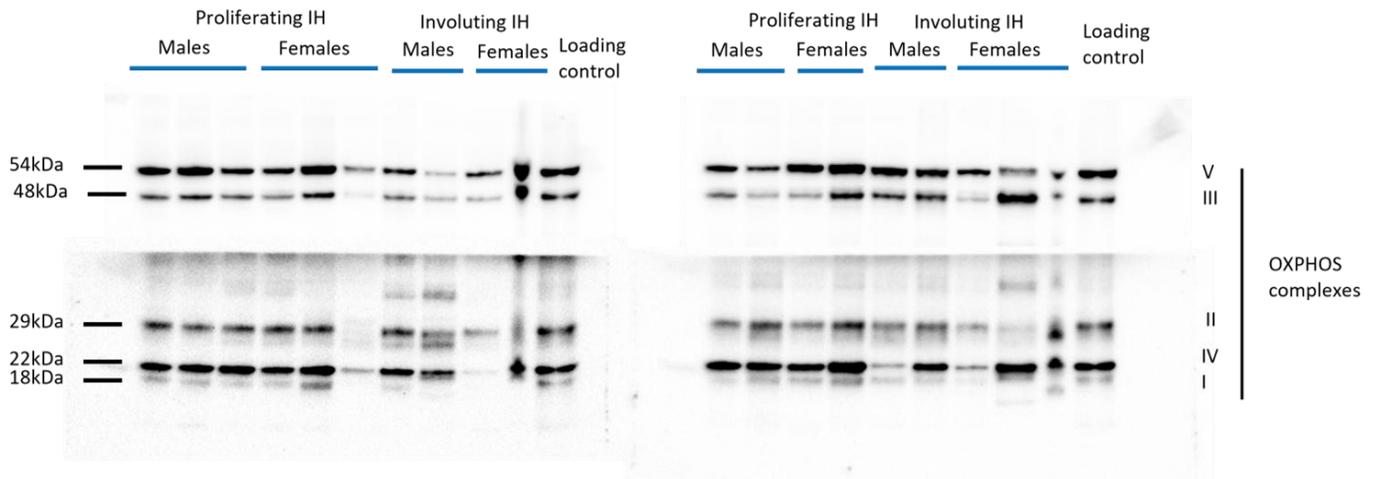
CYP7B1	0.70	0.117126	0.94	0.623948	0.52	0.137666
DHCR24	1.08	0.415807	3.87	0.173955	0.30	0.274526
DHCR7	1.34	0.296132	2.74	0.192985	0.66	0.368076
FDFT1	1.40	0.050697	1.98	0.006515	0.99	0.925186
FDPS	2.17	0.083050	2.76	0.161009	1.71	0.065962
HDLBP	1.95	0.028042	1.95	0.225916	1.95	0.098224
HMGCR	1.32	0.209380	2.66	0.090333	0.66	0.345056
HMGCS1	1.36	0.252071	2.61	0.190067	0.71	0.137847
HMGCS2	2.01	0.158080	2.01	0.352334	2.01	0.327430
IDI1	1.23	0.114406	1.14	0.457026	1.32	0.019769
IDI2	2.62	0.004329	3.76	0.035798	1.82	0.095821
IL4	0.67	0.081547	0.86	0.556176	0.52	0.096000
INSIG1	1.27	0.188213	1.40	0.172335	1.14	0.515233
INSIG2	2.02	0.002518	2.41	0.028073	1.70	0.008878
LCAT	3.67	0.011587	2.49	0.277421	5.40	0.012021
LDLR	0.58	0.532325	0.60	0.938953	0.55	0.424905
LDLRAP1	1.45	0.273466	1.51	0.484727	1.39	0.165202
LEP	2.32	0.317516	2.95	0.353304	1.82	0.876070
LIPE	4.25	0.253835	3.45	0.300978	5.23	0.078322
LRP10	2.15	0.028074	2.87	0.062679	1.61	0.191713
LRP12	1.49	0.036899	1.27	0.381778	1.75	0.083607
LRP1B	2.16	0.024850	3.66	0.038604	1.27	0.326744
LRP6	0.83	0.641619	0.56	0.048686	1.25	0.483202
LRPAP1	0.97	0.999631	1.04	0.706819	0.91	0.553953
MBTPS1	0.96	0.890628	0.90	0.988976	1.03	0.730452
MVD	1.94	0.074252	2.71	0.064081	1.39	0.228498
MVK	3.57	0.060646	6.50	0.070687	1.96	0.223128
NPC1L1	0.98	0.698888	1.68	0.339830	0.57	0.107849
NR0B2	0.67	0.081417	0.86	0.555290	0.52	0.096000
NR1H4	0.67	0.081417	0.86	0.555290	0.52	0.096000
NSDHL	2.60	0.035857	4.26	0.025373	1.59	0.150424
OLR1	0.67	0.083961	0.87	0.570195	0.52	0.096000
OSBPL1A	1.49	0.091173	1.20	0.461488	1.84	0.158566
OSBPL5	1.47	0.123938	1.38	0.507287	1.55	0.160624
PCSK9	0.82	0.986141	1.58	0.354546	0.43	0.057589
PMVK	1.43	0.169324	2.40	0.084816	0.85	0.433102
PPARD	2.14	0.007584	3.04	0.007266	1.50	0.264955
PRKAA1	1.68	0.000673	1.62	0.057495	1.74	0.015039
PRKAA2	12.95	0.202457	5.44	0.136411	30.82	0.257345
PRKAG2	2.94	0.003271	2.93	0.118582	2.95	0.004801
SCAP	1.52	0.206091	1.38	0.471817	1.68	0.119873
SCARF1	0.98	0.424093	0.47	0.627740	2.05	0.091510
SNX17	0.94	0.833719	0.91	0.824702	0.97	0.990641
SOAT1	1.63	0.200669	2.38	0.226804	1.11	0.728021

SORL1	1.88	0.302526	2.54	0.042209	1.39	0.931319
SREBF1	2.94	0.019505	3.73	0.048557	2.31	0.090125
SREBF2	1.28	0.243683	1.63	0.217327	1.00	0.919853
STAB1	0.63	0.479147	0.44	0.256015	0.91	0.733213
STAB2	2.01	0.036195	4.84	0.002143	0.83	0.863355
STARD3	1.70	0.089395	1.73	0.409404	1.68	0.148653
TM7SF2	4.13	0.127255	15.73	0.101735	1.09	0.775262
TRERF1	0.80	0.500477	0.92	0.781466	0.69	0.502473
VLDLR	4.20	0.112465	3.16	0.326312	5.56	0.231263
ACTB	0.48	0.031734	0.47	0.154307	0.51	0.123277
B2M	1.36	0.141869	1.18	0.634481	1.55	0.189525
GAPDH	2.14	0.197779	1.70	0.024889	2.69	0.281615
HPRT1	0.86	0.608371	0.70	0.031428	1.05	0.641889
RPLP0	0.79	0.536366	1.41	0.282587	0.45	0.023392

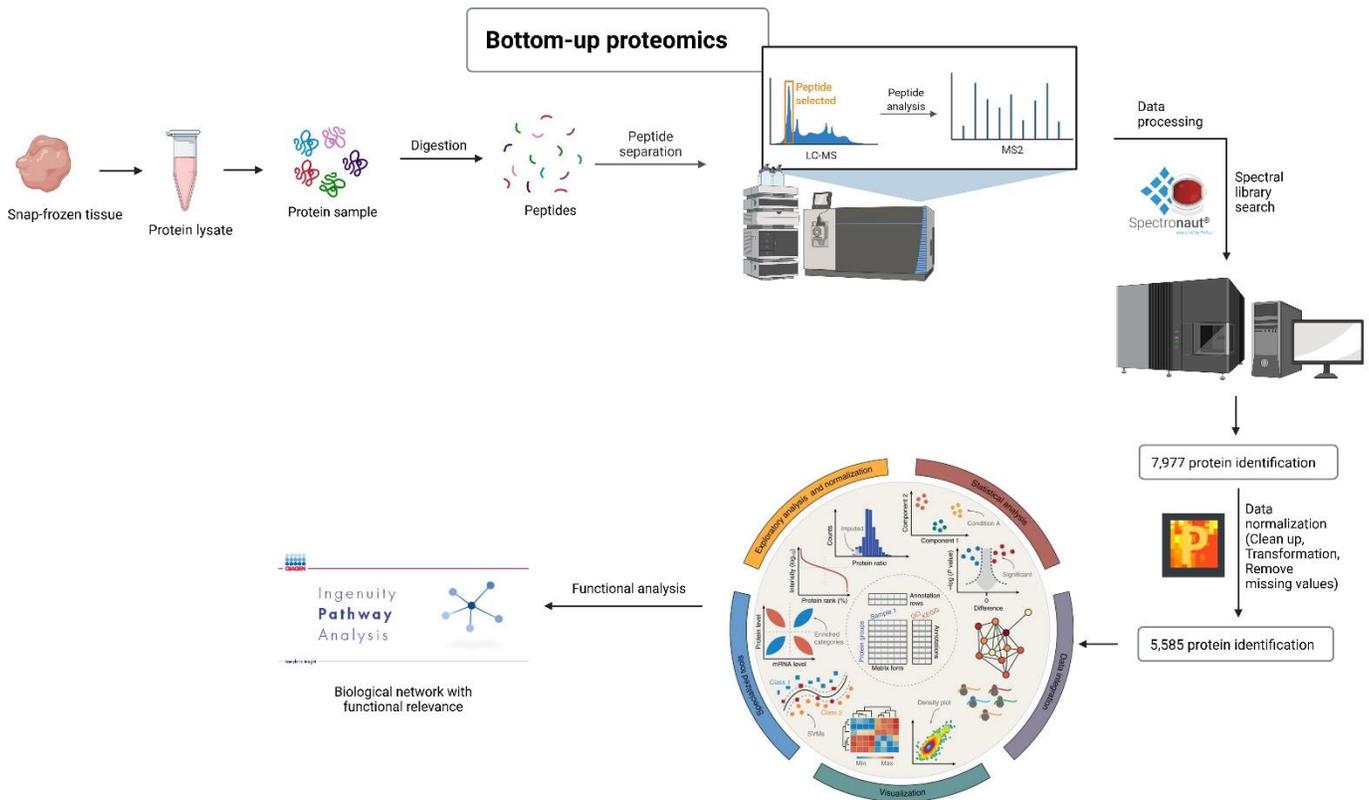
Supplementary Table 8: Gene expression profiling in proliferating and involuting IH using the human apolipoprotein signalling and cholesterol metabolism PCR array.



Supplementary Figure 1: Complete western blot data for FAS, Na+K+ATPase, AMPK, MAOA, VDAC, β -actin in proliferating and involuting IH.



Supplementary Figure 2: Complete western blot data for OXPHOS complexes (I-V) in proliferating and involuting IH.



Supplementary Figure 3: Untargeted (bottom-up) proteomics in Infantile Haemangioma; (a) Schematic representation of the workflow for bottom-up proteomics from sample processing, protein extraction, followed by mass spectrometry analysis and bioinformatics based functional annotation using Perseus MaxQuant and Ingenuity Pathway analysis.