

Table SI. List of common upregulated genes defined as the genes with logFC > 0.8 in all comparisons and with F-test FDR value less than 0.05.

Gene symbol	Gene name	Illumina Probe ID	Average expression log2-intensity	Log2 fold change SCCF - HF_der	Log2 fold change MEBF - HF_der	Log2 fold change BCCF - HF_der	F-test P-value	F-test FDR
GPR177	Wnt ligand secretion mediator	ILMN_1671260	9,62	4,78	4,84	0,81	1,90x10 ⁻¹⁶	3x10 ⁻¹³
TMTC1	transmembrane O-mannosyltransferase targeting cadherins 1	ILMN_1811426	7,54	4,94	5,48	1,05	7,2x10 ⁻¹⁶	9,5x10 ⁻¹³
IGFBP7	insulin like growth factor binding protein 7	ILMN_2062468	12,34	3,55	3,79	2,79	2,4x10 ⁻¹⁵	2,5x10 ⁻¹²
OSBPL10	oxysterol binding protein like 10	ILMN_1669497	6,56	2,42	3,58	0,93	3,2x10 ⁻¹³	1,8x10 ⁻¹⁰
CDH6	cadherin 6	ILMN_1766675	8,69	5,72	5,46	1,75	4,30x10 ⁻¹¹	1,5x10 ⁻⁸
TBX2	T-box transcription factor 2	ILMN_1792256	6,67	3,23	2,79	1,12	4,2x10 ⁻¹⁰	1,1x10 ⁻⁷
EFEMP1	EGF containing fibulin extracellular matrix protein 1	ILMN_2350634	10,62	4,85	5,54	3,97	1,6x10 ⁻⁹	3,4x10 ⁻⁷
C19orf4	transmembrane protein 59 like	ILMN_1730945	7,03	2,63	5,04	1,5	2,8x10 ⁻⁷	2,6x10 ⁻⁵
KCNK6	potassium two pore domain channel subfamily K member 6	ILMN_1701173	7,8	1,02	1,22	1,88	3,7x10 ⁻⁷	3,4x10 ⁻⁵
RDH10	retinol dehydrogenase 10	ILMN_1714335	9,63	3,45	3,36	1,85	4x10 ⁻⁷	3,5x10 ⁻⁵
ARHGAP20	Rho GTPase activating protein 20	ILMN_1782761	5,77	1,83	2,23	0,93	8,2x10 ⁻⁷	5,9x10 ⁻⁵
PTGFRN	prostaglandin F2 receptor inhibitor	ILMN_1743130	8,35	1,89	1,9	0,96	8,3x10 ⁻⁷	6x10 ⁻⁵
CRLF1	cytokine receptor like factor 1	ILMN_1681515	8,56	2,32	5,15	2,4	8,5x10 ⁻⁷	6x10 ⁻⁵
MFGE8	milk fat globule EGF and factor V/VIII domain containing	ILMN_1756071	13,92	1,47	2,31	1,66	8,7x10 ⁻⁷	6,2x10 ⁻⁵
TPD52L1	TPD52 like 1	ILMN_1714383	6,63	1,54	1,27	2,53	1,3x10 ⁻⁶	8,4x10 ⁻⁵
GRAMD3	GRAM domain containing 2B	ILMN_2065690	10,23	1,35	2,19	1,92	1,4x10 ⁻⁶	9x10 ⁻⁵

LEPREL1	prolyl 3-hydroxylase 2	ILMN_1657373	9,55	3,51	4,01	0,89	1,4x10 ⁻⁶	9,20x10 ⁻⁵
RAMP1	receptor activity modifying protein 1	ILMN_1764754	6,56	2,46	3,72	1,67	2x10 ⁻⁶	0,00012
FLJ10916	threonine synthase like 2	ILMN_2173294	8,2	2,3	2,63	2,59	2,2x10 ⁻⁶	0,00013
RARRES3	phospholipase A and acyltransferase 4	ILMN_1701613	6,9	2,09	1,55	1,14	2,6x10 ⁻⁶	0,00015
PRSS23	serine protease 23	ILMN_1797776	9,08	1,65	1,45	1,91	3,6x10 ⁻⁶	2x10 ⁻⁴
FOXC2	forkhead box C2	ILMN_1705201	6,05	1,96	1,5	0,9	4,1x10 ⁻⁶	0,00022
IL6	interleukin 6	ILMN_1699651	8,18	3	1,35	3,88	5,5x10 ⁻⁶	0,00028
IGFBP4	insulin like growth factor binding protein 4	ILMN_1665865	12,94	1,87	1,44	0,86	7x10 ⁻⁶	0,00034
RPS6KA2	ribosomal protein S6 kinase A2	ILMN_1702501	10,41	0,97	1,34	1,61	7,1x10 ⁻⁶	0,00034
TFG	trafficking from ER to golgi regulator	ILMN_2341815	10,5	1,87	2,3	2,15	7,2x10 ⁻⁶	0,00034
LAMC1	laminin subunit gamma 1	ILMN_1810852	12,45	1,19	1,17	1,15	7,5x10 ⁻⁶	0,00035
VLDLR	very low density lipoprotein receptor	ILMN_2361862	6,51	1,23	2,81	0,82	7,8x10 ⁻⁶	0,00036
JAG1	jagged canonical Notch ligand 1	ILMN_1691376	6,61	1,96	3,38	2,01	8,3x10 ⁻⁶	0,00039
RGS4	regulator of G protein signaling 4	ILMN_1758067	9,27	2,37	1,86	1,51	9x10 ⁻⁶	0,00041
CHIC2	cysteine rich hydrophobic domain 2	ILMN_1679428	10,61	1,04	1,06	0,82	1x10 ⁻⁵	0,00045
MGST1	microsomal glutathione S-transferase 1	ILMN_2355168	11,43	1,87	1,92	1,65	1,4x10 ⁻⁵	0,00057
ITGAV	integrin subunit alpha V	ILMN_2169439	9,8	1,12	1,68	0,93	1,7x10 ⁻⁵	0,00067
SFRP4	secreted frizzled related protein 4	ILMN_1810172	6,7	1,39	3,47	3,95	1,8x10 ⁻⁵	0,00073
NTN4	netrin 4	ILMN_2113490	7	2,6	3,6	0,84	1,9x10 ⁻⁵	0,00075
SUSD2	sushi domain containing 2	ILMN_1693270	7,86	3,86	3,62	2,23	2,2x10 ⁻⁵	0,00085
LOC284023	ring finger protein 227	ILMN_1739325	7,4	1,45	1,99	1,13	2,4x10 ⁻⁵	0,00089
CXCL16	C-X-C motif chemokine ligand 16	ILMN_1728478	6,68	1,74	2,43	1,17	2,6x10 ⁻⁵	0,00098
CCPG1	NA	ILMN_1794190	8,61	0,92	1,43	1,42	3,1x10 ⁻⁵	0,0011
MSC	musculin	ILMN_1741404	7,75	1,94	2,64	1,69	3,1x10 ⁻⁵	0,0011
NOV	cellular communication network factor 3	ILMN_1787186	7,46	1,83	2,85	1,07	3,7x10 ⁻⁵	0,0013

PDGFRL	platelet derived growth factor receptor like	ILMN_1680339	7,08	2,47	4,27	0,98	$4,2 \times 10^{-5}$	0,0014
IGFBP2	insulin like growth factor binding protein 2	ILMN_1725193	8,01	2,46	2,75	3,58	$4,3 \times 10^{-5}$	0,0014
F2R	coagulation factor II thrombin receptor	ILMN_1742866	9,16	1,51	1,02	0,9	5×10^{-5}	0,0016
PNMA2	PNMA family member 2	ILMN_1790778	6,25	2,48	1,59	1,44	$5,1 \times 10^{-5}$	0,0017
DEPDC6	DEP domain containing MTOR interacting protein	ILMN_1756685	6,61	2,64	3,5	2,1	$5,3 \times 10^{-5}$	0,0017
MFAP5	microfibril associated protein 5	ILMN_1733415	10,44	1,67	0,99	3,64	$5,9 \times 10^{-5}$	0,0018
SLC1A1	solute carrier family 1 member 1	ILMN_1658917	6,78	2,03	1,75	0,85	$6,5 \times 10^{-5}$	0,002
HAPLN3	hyaluronan and proteoglycan link protein 3	ILMN_1654319	6,71	0,9	1,94	2,48	$7,8 \times 10^{-5}$	0,0023
DIO2	iodothyronine deiodinase 2	ILMN_1737650	6,78	3,23	4,18	1,7	$8,5 \times 10^{-5}$	0,0025
FZD4	frizzled class receptor 4	ILMN_1743367	8,51	2,4	1,67	0,96	1×10^{-4}	0,0029
VEGFA	vascular endothelial growth factor A	ILMN_2375879	7,51	0,89	1,06	2,05	0,00012	0,0032
COL4A1	collagen type IV alpha 1 chain	ILMN_1653028	10,19	0,84	1,3	1,92	0,00015	0,004

Table SII. List of common downregulated genes defined as the genes with logFC < -0.8 in all comparisons and with F-test FDR value less than 0.05.

Gene symbol	Gene name	Illumina Probe ID	Average expression log2-intensity	Log2 fold change SCCF - HF_der	Log2 fold change MEBF - HF_der	Log2 fold change BCCF - HF_der	F-test P-value
PODXL	podocalyxin like	ILMN_2413158	8,7	-5,66	-7,41	-1,09	1,20x10 ⁻²¹
HOXB8	homeobox B8	ILMN_1798496	6,32	-5,04	-5,1	-1,85	1,3x10 ⁻²⁰
C4orf31	neuron derived neurotrophic factor	ILMN_1689176	6,52	-4,5	-4,95	-2,04	1,2x10 ⁻¹²
AKR1C2	aldo-keto reductase family 1 member C2	ILMN_2412336	8,58	-2,66	-1,33	-0,89	1,5x10 ⁻¹¹
CD24	CD24 molecule	ILMN_2060413	6,08	-4,7	-5,02	-3,11	2x10 ⁻¹¹
QPRT	quinolinate phosphoribosyltransferase	ILMN_1700268	6,81	-3,27	-3,53	-2,17	6,9x10 ⁻¹¹
BAALC	BAALC binder of MAP3K1 and KLF4	ILMN_1687751	7,85	-3,45	-2,38	-1,17	6x10 ⁻¹⁰
GNG2	G protein subunit gamma 2	ILMN_1807925	5,91	-3,14	-3,12	-1,66	7,4x10 ⁻¹⁰
MATN2	matrilin 2	ILMN_1694840	8,58	-2,94	-3,02	-1,71	9,3x10 ⁻¹⁰
MMP12	matrix metalloproteinase 12	ILMN_2073758	5,06	-2,22	-2,34	-1,74	2x10 ⁻⁹
PIK3R1	phosphoinositide-3-kinase regulatory subunit 1	ILMN_1760303	8,05	-1,39	-2,02	-0,8	2,9x10 ⁻⁹
CGB5	chorionic gonadotropin beta 5 subunit	ILMN_2163790	5,05	-2,15	-2,11	-1,79	6,2x10 ⁻⁹
PTPRN	protein tyrosine phosphatase receptor type N	ILMN_1658576	5,31	-2,59	-2,77	-1,88	3,4x10 ⁻⁸
MMP3	matrix metalloproteinase 3	ILMN_1784459	8,39	-4,45	-6,43	-1,96	4,8x10 ⁻⁸

C11orf87	chromosome 11 open reading frame 87	ILMN_1810376	5,29	-2,23	-2,43	-1,17	5,9x10 ⁻⁸
ANPEP	alanyl aminopeptidase, membrane	ILMN_1763837	10,9	-1,61	-1,58	-0,88	1,2x10 ⁻⁷
MOXD1	monooxygenase DBH like 1	ILMN_1687501	9,71	-2,2	-1,75	-1,15	1,7x10 ⁻⁷
TRNP1	TMF1 regulated nuclear protein 1	ILMN_1695946	11,36	-2,02	-2,13	-1,48	4,4x10 ⁻⁷
LRP4	LDL receptor related protein 4	ILMN_1675268	6,26	-2,62	-1,55	-0,88	7,1x10 ⁻⁷
CGB1	chorionic gonadotropin subunit beta 1	ILMN_2044645	4,9	-1,44	-1,5	-1,41	8,4x10 ⁻⁷
PRLR	prolactin receptor	ILMN_1669781	5	-1,67	-1,8	-1,42	8,9x10 ⁻⁷
KCNS3	potassium voltage-gated channel modifier subfamily S member 3	ILMN_2175112	7,04	-1,3	-2,02	-1,81	9,9x10 ⁻⁷
HAND1	heart and neural crest derivatives expressed 1	ILMN_1680987	5,27	-2,12	-2,52	-1,78	1,1x10 ⁻⁶
ZNF536	zinc finger protein 536	ILMN_1772155	6,29	-2,48	-1,61	-2	2,1x10 ⁻⁶
EDG1	sphingosine-1-phosphate receptor 1	ILMN_1653504	5,82	-1,8	-1,41	-1,12	2,1x10 ⁻⁶
TSPAN13	tetraspanin 13	ILMN_1669881	7,79	-2,58	-3,69	-1,86	2,8x10 ⁻⁶
CPEB1	cytoplasmic polyadenylation element binding protein 1	ILMN_2369603	5,25	-1,58	-1,19	-1,5	3,1x10 ⁻⁶
HOMER2	homer scaffold protein 2	ILMN_1671486	6,29	-2,47	-1,24	-1,2	3,5x10 ⁻⁶
GRP	gastrin releasing peptide	ILMN_2413323	4,85	-2,1	-2,14	-1,99	5,5x10 ⁻⁶
TSPAN10	tetraspanin 10	ILMN_1656194	7,11	-1,03	-1,25	-1,79	7,5x10 ⁻⁶

CNIH3	cornichon family AMPA receptor auxiliary protein 3	ILMN_1749071	6,11	-1,72	-2,7	-0,86	8,6x10 ⁻⁶
SOX11	SRY-box transcription factor 11	ILMN_1773459	4,7	-0,99	-1,14	-0,9	1,3x10 ⁻⁵
TRPV2	transient receptor potential cation channel subfamily V member 2	ILMN_2049536	8,06	-3,38	-1,85	-1,87	1,6x10 ⁻⁵
CCDC85A	coiled-coil domain containing 85A	ILMN_1669982	6,96	-2,73	-3,96	-1,28	1,6x10 ⁻⁵
NETO2	neuropilin and tolloid like 2	ILMN_1760849	6,69	-2,2	-3,43	-1,63	2,1x10 ⁻⁵
TRIM55	tripartite motif containing 55	ILMN_2347622	4,94	-1,29	-1,73	-1,57	2,2x10 ⁻⁵
SSX2IP	SSX family member 2 interacting protein	ILMN_1720844	6,44	-2,07	-2,72	-1,62	2,2x10 ⁻⁵
CGNL1	cingulin like 1	ILMN_1730229	5,69	-1,74	-1,7	-1,18	2,4x10 ⁻⁵
HOXA5	homeobox A5	ILMN_1753613	5,07	-2,04	-2,06	-1,25	2,9x10 ⁻⁵
ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	ILMN_1758461	5,29	-1,96	-2,17	-0,94	3,1x10 ⁻⁵
HEY1	hes related family bHLH transcription factor with YRPW motif 1	ILMN_1788203	5,54	-1,76	-2,15	-1,89	3,3x10 ⁻⁵
DTNA	dystrobrevin alpha	ILMN_1730201	6,29	-1,35	-1,93	-1,39	3,4x10 ⁻⁵
CXCL12	C-X-C motif chemokine ligand 12	ILMN_1791447	10,95	-3,42	-2,66	-1,13	3,6x10 ⁻⁵
TYRO3	TYRO3 protein tyrosine kinase	ILMN_1740169	7,69	-0,86	-1,61	-0,83	3,7x10 ⁻⁵

CLEC12A	C-type lectin domain family 12 member A	ILMN_2292178	4,74	-1,38	-1,37	-1,14	4,9x10 ⁻⁵
IFI44	interferon induced protein 44	ILMN_1760062	6,75	-2,02	-1,41	-0,87	6,1x10 ⁻⁵
ZNF536	zinc finger protein 536	ILMN_2150586	4,93	-1,28	-0,92	-1,05	6,2x10 ⁻⁵
AMPH	amphiphysin	ILMN_1685834	8,4	-1,54	-1,33	-1,06	8,2x10 ⁻⁵
NKX2-6	NK2 homeobox 6	ILMN_1766678	4,8	-1,05	-1,16	-1,01	0,00011

Table SIII. Results of the functional enrichment analysis performed by Enricher web server on upregulated genes (shown in Table SI).

Term	P-value	Adjusted P-value	Odds Ratio	Combined Score	Assigned Genes
NOTCH Signaling in Multiple Myeloma	<0.0001	0.001	108.7	1302.8	<i>IL6</i> JAG1 <i>VEGFA</i>
VEGFA/NOTCH1/WNT Cross-talk in Blood Vessel Sprouting and Branching in Cancer	<0.0001	0.001	47.8	607.5	FOXC2 JAG1 FZD4 <i>VEGFA</i>
Coagulation Factors and PAR1/2 Receptors (F2R/F2RL1) in Endometriosis	< 0.0001	0.009	41.2	387.5	<i>IL6</i> F2R <i>VEGFA</i>
Tumor Infiltrating Macrophages in Cancer Progression and Immune Escape	0.0001	0.009	36.2	327.5	<i>IL6</i> <i>MFGE8</i> VEGFA
Mast-Cell Activation without Degranulation	0.0003	0.015	26.0	210.8	<i>IL6</i> F2R

					<i>VEGFA</i>
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