

Supplementary Table 1 Sample information for scRNA-seq

geo_accession	Pathology	Gender	Age	Dataset
GSM4546349	NAG	F	61	GSE150290
GSM3954946	NAG	M	58	GSE134520
GSM3954949	CAG	M	51	GSE134520
GSM3954950	CAG	F	62	GSE134520
GSM3954951	CAG	F	62	GSE134520
GSM3954957	CAG(IM)	M	67	GSE134520
GSM5573492	GC (Diffuse)	F	66	GSE183904
GSM5573497	GC (Intestinal)	F	65	GSE183904
GSM5573478	GC (Intestinal)	F	84	GSE183904
GSM5573466	CAG(IM)	M	74	GSE183904
GSM5573471	CAG(IM)	M	62	GSE183904
GSM5573474	CAG(IM)	M	73	GSE183904
GSM5573475	GC (Mixed)	M	73	GSE183904
GSM5573494	GC (Intestinal)	M	64	GSE183904
GSM5573472	GC (Intestinal)	M	62	GSE183904
GSM5573480	GC (Intestinal)	M	68	GSE183904
GSM5573483	GC (Intestinal)	F	68	GSE183904
GSM5573467	GC (Mixed)	M	74	GSE183904
GSM5573486	CAG(IM)	M	74	GSE183904
GSM5573490	CAG(IM)	F	86	GSE183904
GSM5573469	CAG(IM)	M	83	GSE183904
GSM5573489	GC (Diffuse)	F	67	GSE183904
GSM5573491	GC (Intestinal)	F	86	GSE183904
GSM5573493	GC (Diffuse)	F	70	GSE183904
GSM5573468	GC (Diffuse)	M	83	GSE183904
GSM5573495	GC (Mixed)	M	55	GSE183904
GSM5573498	GC (Intestinal)	M	80	GSE183904
GSM5573499	GC (Intestinal)	M	82	GSE183904
GSM5573504	GC (Intestinal)	F	73	GSE183904
GSM5573505	GC (Diffuse)	M	60	GSE183904
GSM5573470	GC (Diffuse)	M	83	GSE183904
GSM5573479	GC (Intestinal)	M	36	GSE183904
GSM5573481	GC (Intestinal)	M	88	GSE183904
GSM5573482	GC (Intestinal)	M	65	GSE183904

Supplementary Table 2 STRING database analysis

category	term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network
GO Process	GO:0002376	Immune system process	36	2481	0.61	9.88E-11	CEACAM6,MI F,AHCY,C1QB P,PYCARD,SL C7A5,EPCAM, TNFRSF10B,C XCL16,CXCL3, CXCL8,CPNE1 ,PKM,PMAIP1 ,PLAUR,IFI6,C TSB,DDX21,T AP1,CCL20,ST AT1,ILF2,CD5 5,ASS1,CTSA, PSMB9,ISG15, GCNT3,IFITM 3,MDK,IFITM CEACAM6,MI F,AHCY,C1QB P,PYCARD,CX CL16,CXCL3, CXCL8,CPNE1 ,PKM,PLAUR, IFI6,CTSB,DD X21,TAP1,CCL 20,STAT1,ILF2 ,CD55,ASS1,C TSA,ISG15,GC NT3,IFITM3,M DK,IFITM1,IL CEACAM6,MI F,C1QBP,PYC ARD,CPNE1,P KM,PMAIP1,P LAUR,IFI6,CT SB,DDX21,ST AT1,ILF2,CD5 5,CTSA,ISG15, GCNT3,IFITM 3,MDK,IFITM
GO Process	GO:0006955	Immune response	28	1588	0.69	2.03E-09	CEACAM6,MI F,AHCY,C1QB P,PYCARD,CX CL16,CXCL3, CXCL8,CPNE1 ,PKM,PLAUR, IFI6,CTSB,DD X21,TAP1,CCL 20,STAT1,ILF2 ,CD55,ASS1,C TSA,ISG15,GC NT3,IFITM3,M DK,IFITM1,IL CEACAM6,MI F,C1QBP,PYC ARD,CPNE1,P KM,PMAIP1,P LAUR,IFI6,CT SB,DDX21,ST AT1,ILF2,CD5 5,CTSA,ISG15, GCNT3,IFITM 3,MDK,IFITM
GO Process	GO:0002252	Immune effector process	22	969	0.8	8.46E-09	CEACAM6,MI F,AHCY,C1QB P,PYCARD,CX CL16,CXCL3, CXCL8,CPNE1 ,PKM,PLAUR, IFI6,CTSB,DD X21,TAP1,CCL 20,STAT1,ILF2 ,CD55,ASS1,C TSA,ISG15,GC NT3,IFITM3,M DK,IFITM1,IL CEACAM6,MI F,C1QBP,PYC ARD,CPNE1,P KM,PMAIP1,P LAUR,IFI6,CT SB,DDX21,ST AT1,ILF2,CD5 5,CTSA,ISG15, GCNT3,IFITM 3,MDK,IFITM

GO Process	GO:000695 2	Defense response	23	1296	0.7	2.32E-07	MIF,AHCY,TI MP1,C1QBP,P YCARD,CXCL 16,CXCL3,CX CL8,PMAIP1,I FI6,DDX21,TA P1,CCL20,ELF 3,STAT1,CD55 ,ASS1,ISG15,IF ITM3,MDK,IFI MIF,AHCY,C1 QBP,SOX9,PY CARD,GDF15, TNFRSF10B,C XCL16,CXCL3, SLC39A4,CXC
GO Process	GO:000960 5	Response to external stimulus	30	2310	0.56	2.32E-07	L8,PKM,PMAI P1,UPP1,PLA UR,IFI6,DDX2 1,REG4,CCL20 ,STAT1,CD55, EFNA1,ASS1,I SG15,TYMP,IF ITM3,MDK,IFI GPRC5A,CEA CAM6,MIF,A HCY,TIMP1,P LOD3,C1QBP, HSPE1,SOX9,P YCARD,GDF1 5,EPCAM,TNF RSF10B,CXCL 16,CXCL3,SLC 39A4,CXCL8,C
GO Process	GO:005089 6	Response to stimulus	54	8046	0.27	2.14E-06	PNE1,PKM,P MAIP1,UPP1, PLAUR,IFI6,C TSB,DDX21,R EG4,TAP1,STI P1,CCL20,ELF 3,CLDN7,STA T1,ILF2,CD55, EFNA1,ASS1, CTSA,PSMB9,I SG15,CLDN3, TYMP,GCNT3 ,IFITM3,MDK,

GO Process	GO:0052547	Regulation of peptidase activity	13	449	0.91	1.47E-05	IHMF1,HSPE1, PYCARD,TNF RSF10B,PMAI P1,PLAUR,IFI6,EFNA1,PSMB9,CLDN3,BCAP31,CLDN4,ADRM1,MIF1,FLOD3,HSPE1,SOX9,PYCARD, GDF15,CXCL16,CXCL3,CXL8,PKM,PMAI P1,IFI6,CTSB, DDX21,STIP1, CCL20,CLDN7,STAT1,ASS1,PSMB9,ISG15,CLDN3,IFITM3, MDK,IFITM1, ARPC1B,CTD MIF,AHICY,TIMP1,C1QBP,H SPE1,PYCARD, TNFRSF10B,CXCL16,CXCL3, SLC39A4,CXL8,PKM,PMAI P1,UPP1,PLAUR,IFI6,DDX21,TAP1,CCL20,ELF3,STAT1,CD55,ASS1,PSMB9,ISG15,CLDN3,IFITM3, MDK,IFITM1,HSPE1,PYCARD,TNFRSF10B,PMAIP1,EFNA1,CLDN3,BCAP31,CLDN4,ADRM1
GO Process	GO:0010033	Response to organic substance	31	3011	0.46	1.50E-05	
GO Process	GO:0006950	Response to stress	33	3485	0.42	2.66E-05	
GO Process	GO:0010952	Positive regulation of peptidase activity	9	198	1.1	6.20E-05	

GO Process	GO:003409 7	Response to cytokine	18	1101	0.66	6.20E-05	MIF,TIMP1,SOX9,PYCARD,CXCL16,CXCL3,CXCL8,IFI6,STIP1,CCL20,STAT1,ASS1,PSMB9,ISG15,IFITM3,IFITM1,IMIF,AHICY,TIMP1,PLOD3,HSP1,SOX9,PYCARD,GDF15,CXCL16,CXCL3,CXCL8,CPNE1,PKM,PMAIP1,PLAUR,IFI6,CTSB,DDX21,STIP1,CCL20,CLDN7,STAT1,EFNA1,ASS1,PSMB9,ISG15,CLDN3,TYMP,IFITM3,MDK,IFITM1,ARPCMIF,C1QBP,PYCARD,CXCL16,CXCL3,CXCL8,PMAIP1,IFI6,CTSB,DDX21,REG4,TAP1,CCL20,STAT1,CD55,ASS1,PSMB9,ISG15,IFITM3,IFITM1,B
GO Process	GO:004222 1	Response to chemical	36	4333	0.37	8.75E-05	AP1,IFI6,DDX21,REG4,TAP1,CCL20,STAT1,CD55,ASS1,PSMB9,ISG15,IFITM3,IFITM1,B
GO Process	GO:004441 9	Interspecies interaction between organisms	23	1899	0.53	8.75E-05	AP1,IFI6,DDX21,REG4,TAP1,CCL20,STAT1,CD55,ASS1,PSMB9,ISG15,IFITM3,IFITM1,B
GO Process	GO:005160 7	Defense response to virus	9	210	1.08	8.75E-05	AP1,IFI6,DDX21,STAT1,ISG15,IFITM3,IFITM1,IFITM2,IFITM3,IFITM4,IFITM5,IFITM6,IFITM7,IFITM8,IFITM9,IFITM10,IFITM11,IFITM12,IFITM13,IFITM14,IFITM15,IFITM16,IFITM17,IFITM18,IFITM19,IFITM20,IFITM21,IFITM22,IFITM23,IFITM24,IFITM25,IFITM26,IFITM27,IFITM28,IFITM29,IFITM30,IFITM31,IFITM32,IFITM33,IFITM34,IFITM35,IFITM36,IFITM37,IFITM38,IFITM39,IFITM40,IFITM41,IFITM42,IFITM43,IFITM44,IFITM45,IFITM46,IFITM47,IFITM48,IFITM49,IFITM50,IFITM51,IFITM52,IFITM53,IFITM54,IFITM55,IFITM56,IFITM57,IFITM58,IFITM59,IFITM60,IFITM61,IFITM62,IFITM63,IFITM64,IFITM65,IFITM66,IFITM67,IFITM68,IFITM69,IFITM70,IFITM71,IFITM72,IFITM73,IFITM74,IFITM75,IFITM76,IFITM77,IFITM78,IFITM79,IFITM80,IFITM81,IFITM82,IFITM83,IFITM84,IFITM85,IFITM86,IFITM87,IFITM88,IFITM89,IFITM90,IFITM91,IFITM92,IFITM93,IFITM94,IFITM95,IFITM96,IFITM97,IFITM98,IFITM99,IFITM100
GO Process	GO:007134 5	Cellular response to cytokine stimulus	17	1013	0.67	8.75E-05	AP1,IFI6,DDX21,STAT1,ISG15,IFITM3,IFITM1,IFITM2,IFITM3,IFITM4,IFITM5,IFITM6,IFITM7,IFITM8,IFITM9,IFITM10,IFITM11,IFITM12,IFITM13,IFITM14,IFITM15,IFITM16,IFITM17,IFITM18,IFITM19,IFITM20,IFITM21,IFITM22,IFITM23,IFITM24,IFITM25,IFITM26,IFITM27,IFITM28,IFITM29,IFITM30,IFITM31,IFITM32,IFITM33,IFITM34,IFITM35,IFITM36,IFITM37,IFITM38,IFITM39,IFITM40,IFITM41,IFITM42,IFITM43,IFITM44,IFITM45,IFITM46,IFITM47,IFITM48,IFITM49,IFITM50,IFITM51,IFITM52,IFITM53,IFITM54,IFITM55,IFITM56,IFITM57,IFITM58,IFITM59,IFITM60,IFITM61,IFITM62,IFITM63,IFITM64,IFITM65,IFITM66,IFITM67,IFITM68,IFITM69,IFITM70,IFITM71,IFITM72,IFITM73,IFITM74,IFITM75,IFITM76,IFITM77,IFITM78,IFITM79,IFITM80,IFITM81,IFITM82,IFITM83,IFITM84,IFITM85,IFITM86,IFITM87,IFITM88,IFITM89,IFITM90,IFITM91,IFITM92,IFITM93,IFITM94,IFITM95,IFITM96,IFITM97,IFITM98,IFITM99,IFITM100

GO Process	GO:001922	Cytokine-mediated signaling pathway	14	678	0.76	9.99E-05	MIF, TIMP1, IFI6, CARD, CXCL3, CXCL8, IFI6, CL20, STAT1, PSMB9, ISG15, IFITM3, IFITM1, IFITM2, CEACAM6, MIF, TIMP1, C1QBP, SOX9, PYCARD, EPCAM, CXCL16, CXCL8, CCL20, CLDN7, EFNA1, CLDN3, MDK, IFITM1, MIF, C1QBP, YCARD, CXCL16, IFI6, DDX21, CCL20, STAT1, CD55, ASS1, ISG15, IFITM3, IFITM1, IFITM2, CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, C1QBP, MDK, IFI6, STAT1, ISG15, IFITM3, IFITM1, IFITM2, MIF, C1QBP, PYCARD, CXCL16, CXCL3, CXCL8, PMAIP1, IFI6, DDX21, REG4, CCL20, STAT1, CD55, ASS1, ISG15, IFITM3, TIMP1, HSP1, PYCARD, TNFRSF10B, PMAIP1, PLAUR, IFI6, EFNA1, PSMORCAP31A
GO Process	GO:200014	Regulation of cell motility	16	929	0.68	0.00012	RD, EPCAM, CXCL16, CXCL8, CCL20, CLDN7, EFNA1, CLDN3, MDK, IFITM1, MIF, C1QBP, YCARD, CXCL16, IFI6, DDX21, CCL20, STAT1, CD55, ASS1, ISG15, IFITM3, IFITM1, IFITM2, CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, C1QBP, MDK, IFI6, STAT1, ISG15, IFITM3, IFITM1, IFITM2, MIF, C1QBP, PYCARD, CXCL16, CXCL3, CXCL8, PMAIP1, IFI6, DDX21, REG4, CCL20, STAT1, CD55, ASS1, ISG15, IFITM3, TIMP1, HSP1, PYCARD, TNFRSF10B, PMAIP1, PLAUR, IFI6, EFNA1, PSMORCAP31A
GO Process	GO:004508	Innate immune response	14	703	0.75	0.00014	CCL20, STAT1, CD55, ASS1, ISG15, IFITM3, IFITM1, IFITM2, CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, C1QBP, MDK, IFI6, STAT1, ISG15, IFITM3, IFITM1, IFITM2, MIF, C1QBP, PYCARD, CXCL16, CXCL3, CXCL8, PMAIP1, IFI6, DDX21, REG4, CCL20, STAT1, CD55, ASS1, ISG15, IFITM3, TIMP1, HSP1, PYCARD, TNFRSF10B, PMAIP1, PLAUR, IFI6, EFNA1, PSMORCAP31A
GO Process	GO:005090	Leukocyte migration	10	316	0.95	0.00015	AM, TNFRSF10B, CXCL16, CXCL3, CXCL8, C1QBP, MDK, IFI6, STAT1, ISG15, IFITM3, IFITM1, IFITM2, MIF, C1QBP, PYCARD, CXCL16, CXCL3, CXCL8, PMAIP1, IFI6, DDX21, REG4, CCL20, STAT1, CD55, ASS1, ISG15, IFITM3, TIMP1, HSP1, PYCARD, TNFRSF10B, PMAIP1, PLAUR, IFI6, EFNA1, PSMORCAP31A
GO Process	GO:006033	Type I interferon signaling pathway	6	67	1.4	0.00015	IFI6, STAT1, ISG15, IFITM3, IFITM1, IFITM2, MIF, C1QBP, PYCARD, CXCL16, CXCL3, CXCL8, PMAIP1, IFI6, DDX21, REG4, CCL20, STAT1, CD55, ASS1, ISG15, IFITM3, TIMP1, HSP1, PYCARD, TNFRSF10B, PMAIP1, PLAUR, IFI6, EFNA1, PSMORCAP31A
GO Process	GO:005170	Response to other organism	18	1256	0.6	0.00018	IFI6, DDX21, REG4, CCL20, STAT1, CD55, ASS1, ISG15, IFITM3, TIMP1, HSP1, PYCARD, TNFRSF10B, PMAIP1, PLAUR, IFI6, EFNA1, PSMORCAP31A
GO Process	GO:005254	Regulation of endopeptidase activity	11	418	0.87	0.00018	RSF10B, PMAIP1, PLAUR, IFI6, EFNA1, PSMORCAP31A

GO Process	GO:009854 2	Defense response to other organism	15	900	0.67	0.00026	ILF,CIQBP,IF YCARD,CXCL 16,PMAIP1,IFI 6,DDX21,CCL 20,STAT1,CD5 5,ASS1,ISG15,I FITM3,IFITM1 CEACAM6,CEACAM10,C1 QBP,SOX9,PY CARD,EPCA
GO Process	GO:200014 7	Positive regulation of cell motility	12	547	0.79	0.00026	M,CXCL16,CX CL8,CCL20,CL DN7,CLDN3, MDK,CLDN4, CEACAM6,C1 QBP,SOX9,PY CARD,EPCA
GO Process	GO:003015 5	Regulation of cell adhesion	13	712	0.71	0.00055	M,CXCL8,PLA UR,FXD5,CL DN7,CD55,EF NA1,ASS1,MD CEACAM6,MI F,TIMP1,C1QB P,HSPE1,SOX9 ,PYCARD,EPC
GO Process	GO:004298 1	Regulation of apoptotic process	19	1550	0.53	0.00057	AM,TNFRSF1 0B,PMAIP1,PL AUR,IFI6,CTS B,CLDN7,STA T1,EFNA1,MD CEACAM6,MI F,PYCARD,CX
GO Process	GO:004211 9	Neutrophil activation	11	497	0.79	0.00061	CL8,CPNE1,P KM,PLAUR,C TSB,ILF2,CD5 5,CTSA

GO Process	GO:0051179	Localization	39	5591	0.29	0.00064	CEACAM6,MI SP,MIF,TIMP1 ,PLOD3,DDX3 9A,SOX9,PYC ARD,SLC7A5, EPCAM,NOP5 8,TNFRSF10B, CXCL16,CCT3 ,CXCL3,SLC39 A4,CXCL8,CP NE1,PKM,PM AIP1,PLAUR, FXD5,CTSB, TAP1,CCL20,I LF2,CD55,EFN A1,CTSA,PSM B9,GCNT3,M DK,ARPC1B,B CAP31,FAT1, CEACAM6,MI F,TIMP1,C1QB P,SOX9,PYCA RD,CXCL16,C XCL8,CCL20,E FNA1,CLDN3, MDK,IFITM1, STAT1,ISG15,I FITM3,IFITM1 ,IL32,IFITM2 FISF11,PYCA RD,TNFRSF10 B,PMAIP1,PL AUR,IFI6,PSM B9,RCAP31, CEACAM6,MI F,C1QBP,PYC ARD,CPNE1,P KM,PLAUR,C TSB,ILF2,CD5 5,CTSA,GCNT
GO Process	GO:0030334	Regulation of cell migration	14	865	0.66	7.00E-04	
GO Process	GO:0048525	Negative regulation of viral process	6	105	1.2	0.00085	
GO Process	GO:2000116	Regulation of cysteine-type endopeptidase activity	8	240	0.97	0.00085	
GO Process	GO:0002443	Leukocyte mediated immunity	12	641	0.72	0.00088	

GO Process	GO:0007166	Cell surface receptor signaling pathway	23	2325	0.44	0.001	MIF,TIMP1,SOX9,PYCARD,GDF15,TNFRSF10B,CXCL3,CXCL8,PLAUR,IFI6,CCL20,STAT1,EFNA1,PSMB9,ISG15,IFITM3,MDK,IFITM1,ARPC1B,ILY6E.II.32,IFITHSPE1,PYCARD,TNFRSF10B,PMAIP1,EFNA1,BCAP31,ADRM1,CXCL16,CCL20,STAT1,ASS1,IFITM3,IFITM1,IFITM2,STAT1,IFITM3,IFITM1,IFITMGPRC5A,CEACAM6,MIF,TIMP1,C1QBP,HSP1,SOX9,PYCARD,GDF15,EPCAM,TNFRSF10B,CXCL16,CCT3,CXCL8,CPNE1,PKM,PMAIP1,PLAUR,DDX21,CCL20,ELF3,CLDN7,STAT1,ILF2,CD55,EFNA1,ASS1,PSMB9,CKS2,ISG15,CLDN3,MDK,IFITM1,ARPC1B
GO Process	GO:0010950	Positive regulation of endopeptidase activity	7	176	1.05	0.0011	
GO Process	GO:0034341	Response to interferon-gamma	7	182	1.03	0.0013	
GO Process	GO:0035456	Response to interferon-beta	4	31	1.56	0.0018	
GO Process	GO:0048518	Positive regulation of biological process	40	6112	0.26	0.0018	

GO Process	GO:0048584	Positive regulation of response to stimulus	22	2257	0.44	0.002	MIF,C1QBP,S OX9,PYCARD, GDF15,TNFRS F10B,CXCL8,C PNE1,PMAIP1 ,PLAUR,DDX2 1,CCL20,ELF3, CD55,EFNA1, PSMB9,CLDN 3,MDK,ARPC 1B,BCAP31,CL CEACAM6,MI F,PYCARD,CP
GO Process	GO:0043312	Neutrophil degranulation	10	484	0.76	0.0023	NE1,PKM,PL AUR,CTSB,ILF 2,CD55,CTSA, CXCL8,STAT1
GO Process	GO:0050792	Regulation of viral process	7	215	0.96	0.0031	,ISG15,IFITM3, IFITM1,IL32,IF ITM2 CEACAM6,MI F,PYCARD,CP
GO Process	GO:0002366	Leukocyte activation involved in immune response regulation or cysteine-type endopeptidase activity involved in apoptotic process	11	626	0.69	0.0032	NE1,PKM,PL AUR,CTSB,ILF 2,CD55,CTSA, MDK HSPE1,PYCA RD,TNFRSF10
GO Process	GO:0043281	Leukocyte activation involved in immune response regulation or cysteine-type endopeptidase activity involved in apoptotic process	7	216	0.96	0.0032	B,PMAIP1,PL AUR,IFI6,BCA P31 MIF,TIMP1,PL OD3,SOX9,PY CARD,GDF15, CXCL16,CXCL 3,CXCL8,CPN
GO Process	GO:0070887	Cellular response to chemical stimulus	25	2919	0.38	0.0032	E1,PKM,PMAI P1,IFI6,CTSB,S TIP1,CCL20,S TAT1,ASS1,PS MB9,ISG15,IFI TM3,MDK,IFI MIF,AHCY,II MP1,PYCARD
GO Process	GO:0006954	Inflammatory response	10	515	0.73	0.0033	,CXCL3,CXCL 8,CCL20,ELF3, ASS1 MDK

GO Process	GO:0016477	Cell migration	13	896	0.61	0.0033	CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, CCL20, EFNA1, MDK, EPCAM6, MIF, TIMP1, C1QBP, HSP, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CXCL16, CCT3, CXCL8, CPNE1, PMAIP1, PLAUR, DDITX21, CCL20, ELF3, CLDN7, STAT1, ILF2, CD55, EFNA1, ASS1, PSMB9, CKS2, ISG15, CLDN3, MDK, IFITM1, CEACAM6, C1QBP, SOX9, PYCARD, CXCL16, CXCL8, CCL20, CLDN3, MDK, CXCL8, IFITM3, IFITM1, IL32, IFITM2, CXCL8, IFITM3, IFITM1, IFITM2, CXCL8, ISG15, IFITM3, IFITM1, IL32, IFITM2, MIF, C1QBP, IPYCARD, CXCL8, DDX21, CCL20, STAT1, CD55, PSMB9, ISG15, MDK, ARPC1B, MIF, C12
GO Process	GO:0048522	Positive regulation of cellular process	37	5579	0.27	0.0033	CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, CCL20, EFNA1, MDK, EPCAM6, MIF, TIMP1, C1QBP, HSP, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CXCL16, CCT3, CXCL8, CPNE1, PMAIP1, PLAUR, DDITX21, CCL20, ELF3, CLDN7, STAT1, ILF2, CD55, EFNA1, ASS1, PSMB9, CKS2, ISG15, CLDN3, MDK, IFITM1, CEACAM6, C1QBP, SOX9, PYCARD, CXCL16, CXCL8, CCL20, CLDN3, MDK, CXCL8, IFITM3, IFITM1, IL32, IFITM2, CXCL8, IFITM3, IFITM1, IFITM2, CXCL8, ISG15, IFITM3, IFITM1, IL32, IFITM2, MIF, C1QBP, IPYCARD, CXCL8, DDX21, CCL20, STAT1, CD55, PSMB9, ISG15, MDK, ARPC1B, MIF, C12
GO Process	GO:0030335	Positive regulation of cell migration	10	522	0.73	0.0035	CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, CCL20, CLDN3, MDK, CXCL8, IFITM3, IFITM1, IL32, IFITM2, CXCL8, IFITM3, IFITM1, IFITM2, CXCL8, ISG15, IFITM3, IFITM1, IL32, IFITM2, MIF, C1QBP, IPYCARD, CXCL8, DDX21, CCL20, STAT1, CD55, PSMB9, ISG15, MDK, ARPC1B, MIF, C12
GO Process	GO:1903901	Negative regulation of viral life cycle	5	86	1.21	0.0035	CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, CCL20, CLDN3, MDK, CXCL8, IFITM3, IFITM1, IL32, IFITM2, CXCL8, IFITM3, IFITM1, IFITM2, CXCL8, ISG15, IFITM3, IFITM1, IL32, IFITM2, MIF, C1QBP, IPYCARD, CXCL8, DDX21, CCL20, STAT1, CD55, PSMB9, ISG15, MDK, ARPC1B, MIF, C12
GO Process	GO:0052372	Modulation by symbiont of entry into host	4	42	1.43	0.0039	CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, CCL20, CLDN3, MDK, CXCL8, IFITM3, IFITM1, IL32, IFITM2, CXCL8, IFITM3, IFITM1, IFITM2, CXCL8, ISG15, IFITM3, IFITM1, IL32, IFITM2, MIF, C1QBP, IPYCARD, CXCL8, DDX21, CCL20, STAT1, CD55, PSMB9, ISG15, MDK, ARPC1B, MIF, C12
GO Process	GO:1903900	Regulation of viral life cycle	6	153	1.04	0.0039	CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, CCL20, CLDN3, MDK, CXCL8, IFITM3, IFITM1, IL32, IFITM2, CXCL8, IFITM3, IFITM1, IFITM2, CXCL8, ISG15, IFITM3, IFITM1, IL32, IFITM2, MIF, C1QBP, IPYCARD, CXCL8, DDX21, CCL20, STAT1, CD55, PSMB9, ISG15, MDK, ARPC1B, MIF, C12
GO Process	GO:0002684	Positive regulation of immune system process	13	949	0.58	0.0054	CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, CCL20, CLDN3, MDK, CXCL8, IFITM3, IFITM1, IL32, IFITM2, CXCL8, IFITM3, IFITM1, IFITM2, CXCL8, ISG15, IFITM3, IFITM1, IL32, IFITM2, MIF, C1QBP, IPYCARD, CXCL8, DDX21, CCL20, STAT1, CD55, PSMB9, ISG15, MDK, ARPC1B, MIF, C12

GO Process	GO:0040011	Locomotion	15	1251	0.53	0.0055	CEACAM6, MIF, SLC7A5, EPCAM, TNFRSF10B, CXCL16, CXCL3, CXCL8, PLAUR, CXCL20, EFNA1, TYMP, GDF15, SLC39A4, PKM1, PMAIP1, UPP1, STAT1, ASS1, LDHA, CXCL8, ISG15, IFITM3, IFITM1, IFITM2, GPRC5A, IL1F7, C1QBP, SOX9, PYCARD, GDF15, TNFRSF10B, CXCL8, CPNE1, PLAUR, IFI6, STAT1, EFNA1, CEACAM6, MIF, TIMP1, PYCARD, CPNE1, PKM, PLAUR, CTSB, ILF2, CD55, CTSA, GPRC5A, CEACAM6, MIF, TIMP1, C1QBP, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CXCL16, CXCL3, SLC39A4, CXCL8, PMAIP1, UPP1, PLAUR, IFI6, CTSB, CXCL20, STAT1, EFNA1, PSMB9, ISG15, TYMP, IFITM3, MDK, IFITM1, ARPC1B, TIMP1, CLDN3, CLDN4
GO Process	GO:0031667	Response to nutrient levels	9	449	0.75	0.006	
GO Process	GO:0045069	Regulation of viral genome replication	5	99	1.15	0.006	
GO Process	GO:0009968	Negative regulation of signal transduction	15	1271	0.52	0.0064	
GO Process	GO:0045055	Regulated exocytosis	11	697	0.64	0.0064	
GO Process	GO:0007154	Cell communication	35	5320	0.26	0.007	
GO Process	GO:1905048	Regulation of metallopeptidase activity	3	17	1.69	0.0076	

GO Process	GO:0007165	Signal transduction	33	4876	0.28	0.0077	GPRC5A,CEA CAM6,MIF,TI MP1,C1QBP,S OX9,PYCARD, GDF15,EPCA M,TNFRSF10B ,CXCL16,CXC L3,SLC39A4,C XCL8,PMAIP1 ,PLAUR,IFI6,C TSB,CCL20,ST AT1,EFNA1,P SMB9,ISG15,T YMP,IFITM3, MDK,IFITM1, GPRC5A,MIF, C1QBP,HSPE1 ,SOX9,PYCAR D,GDF15,TNF RSF10B,PMAI P1,PLAUR,CC L20,EFNA1,C KS2,CLDN3,B CAP31,CLDN GPRC5A,MIF, C1QBP,SOX9, PYCARD,GDF 15,TNFRSF10B ,CXCL8,CPNE 1,PLAUR,IFI6, STAT1,CD55,E FNA1,PSMB9,
GO Process	GO:0032270	Positive regulation of cellular protein metabolic process	17	1635	0.46	0.0081	IFITM3,IFITM 1,IFITM2 PYCARD,CXC L16,CXCL8,C CL20,STAT1,A SS1.PSMB9
GO Process	GO:0048585	Negative regulation of response to stimulus	17	1636	0.46	0.0081	
GO Process	GO:0046597	Negative regulation of viral entry into host cell	3	18	1.67	0.0084	
GO Process	GO:0034612	Response to tumor necrosis factor	7	269	0.86	0.0085	

GO Process	GO:006509	Regulation of molecular function	33	4913	0.27	0.0085	GPRC5A,MIF,TIMP1,C1QBP,HSPE1,SOX9,PYCARD,GDF15,TNFRSF10B,CXCL16,CXCL3,CXCL8,CPNE1,PMAIP1,PLAUR,IFI6,FXD5,CTSB,CCL20,ELF3,STAT1,EFNA1,CTSA,PSMB9,CKS2,CLDN3,TYMP,MDK,BCMIF,TIMP1,PLOD3,SOX9,PYCARD,GDF15,CXCL3,CXCL8
GO Process	GO:0071310	Cellular response to organic substance	21	2369	0.39	0.0085	,PKM,IFI6,CTSB,STIP1,CCL20,STAT1,ASS1,PSMB9,ISG15,IFITM3,IFITM1
GO Process	GO:0030277	Maintenance of gastrointestinal epithelium	3	20	1.62	0.0103	SOX9,TFE3,MUC13
GO Process	GO:0016338	Calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules	3	21	1.6	0.0116	CLDN7,CLDN3,CLDN4

GO Process	GO:002305 2	Signaling	34	5239	0.26	0.0116	GPRC5A,CEA CAM6,MIF,TI MP1,C1QBP,S OX9,PYCARD, GDF15,EPCA M,TNFRSF10B ,CXCL16,CXC L3,SLC39A4,C XCL8,PMAIP1 ,PLAUR,IFI6,C TSB,CCL20,ST AT1,EFNA1,P SMB9,ISG15,T YMP,IFITM3, MDK,IFITM1, ARPC1B,BCA ISG15,IFITM3, IFITM1,IFITM 2
GO Process	GO:004507 1	Negative regulation of viral genome replication	4	61	1.26	0.0116	GPRC5A,CEA CAM6,MISP, MIF,AHCY,TI MP1,PLOD3,C 1QBP,HSPE1, DDX39A,SOX 9,PYCARD,G DF15,SLC7A5, EPCAM,NOP5 8,TNFRSF10B, LACTB2,CXC L16,CCT3,CX CL3,SLC39A4, CXCL8,CPNE1 ,PKM,PMAIP1 ,UPP1,PLAUR, IFI6,FXVD5,C TSB,DDX21,T AP1,STIP1,CC L20,ELF3,CLD N7,STAT1,ILF 2,CD55,EFNA 1,ASS1,CTSA,
GO Process	GO:000998 7	Cellular process	66	15024	0.09	0.0121	GPRC5A,CEA CAM6,MISP, MIF,AHCY,TI MP1,PLOD3,C 1QBP,HSPE1, DDX39A,SOX 9,PYCARD,G DF15,SLC7A5, EPCAM,NOP5 8,TNFRSF10B, LACTB2,CXC L16,CCT3,CX CL3,SLC39A4, CXCL8,CPNE1 ,PKM,PMAIP1 ,UPP1,PLAUR, IFI6,FXVD5,C TSB,DDX21,T AP1,STIP1,CC L20,ELF3,CLD N7,STAT1,ILF 2,CD55,EFNA 1,ASS1,CTSA,

GO Process	GO:0051716	Cellular response to stimulus	39	6489	0.23	0.0121	GPRC5A,CEACAM6,MIF,TIMP1,PLOD3,C1QBP,SOX9,PLYCARD,GDF15,EPCAM,TNFRSF10B,CXCL16,CXCL3,SLC39A4,CXCL8,CNE1,PKM,PMaip1,UPP1,PLAUR,IFI6,CTS,STIP1,CCL20,STAT1,EFNA1,ASS1,PSMB9,ISG15,TYMP,IFITM3,MDK,IFITM1,CEACAM6,MIF,TIMP1,PYCARD,CXCL8,C
GO Process	GO:0001775	Cell activation	13	1075	0.53	0.0137	PNE1,PKM,PLAUR,CTSB,ILF2,CD55,CTSA,
GO Process	GO:0035455	Response to interferon-alpha	3	23	1.56	0.0137	MDK,IFITM3,IFITM1,IFITM2,CEACAM6,MIF,PYCARD,CXCL8,CPNE1,PKM,PLAUR,CTS,ILF2,CD5
GO Process	GO:0045321	Leukocyte activation	12	929	0.56	0.014	5,CTSA,MDK,MIF,C1QBP,P
GO Process	GO:0002685	Regulation of leukocyte migration	6	209	0.9	0.0145	YCARD,CXCL8,CCL20,MDK,MIF,CXCL16,CXCL3,CXCL8
GO Process	GO:0006935	Chemotaxis	9	545	0.66	0.018	,PLAUR,CCL20,EFNA1,TYMP,MDK,CEACAM6,PYCARD,EPCA
GO Process	GO:0022407	Regulation of cell-cell adhesion	8	424	0.72	0.018	M,PLAUR,FXD5,CD55,ASS1,MDK

GO Process	GO:0043280	Positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	5	136	1.01	0.018	HSPE1,PYCARD,TNFRSF10B,PMAIP1,BCAP31
GO Process	GO:0090023	Positive regulation of neutrophil chemotaxis	3	26	1.51	0.018	C1QBP,CXCL8,MDK
GO Process	GO:0051336	Regulation of hydrolase activity	14	1284	0.48	0.0192	TIMP1,HSPE1,PYCARD,TNFRSF10B,PMAIP1,PLAUR,IFI6,CCL20,EFNA1,PSMB9,CLDN3,BCAP31,CTDN1A,ADP,CEACAM6,MIF,TIMP1,PYCARD,CXCL16,CXCL8,CPNE1,PKM,PLAUR,CTSB,TAP1,ILF2,CD55,CTSA,ARPC1B,BCASOX9,GCNT3,TFF3,MUC13
GO Process	GO:0016192	Vesicle-mediated transport	17	1805	0.42	0.0199	CXCL16,CXCL8,CPNE1,PKM,PLAUR,CTSB,TAP1,ILF2,CD55,CTSA,ARPC1B,BCASOX9,GCNT3,TFF3,MUC13
GO Process	GO:0022600	Digestive system process	4	74	1.18	0.0199	CXCL16,CXCL3,CXCL8,CCL20,MDK
GO Process	GO:0030595	Leukocyte chemotaxis	5	142	0.99	0.0203	3,CXCL8,CCL20,MDK
GO Process	GO:0090200	Positive regulation of release of cytochrome c from mitochondria	3	28	1.48	0.0203	PYCARD,PMAIP1,PLAUR
GO Process	GO:0002687	Positive regulation of leukocyte migration	5	144	0.99	0.0212	C1QBP,PYCARD,CXCL8,CCL20,MDK

GO Process	GO:0050790	Regulation of catalytic activity	20	2386	0.37	0.0215	GPRC5A,MIF,TIMP1,HSPE1,PYCARD,GDF15,TNFRSF10B,PMAIP1,PLAUR,IFI6,CTSB,CCL20,EFNA1,CTSA,PSMB9,CKS2,CLDN3,BCAP31,CLD
GO Process	GO:0043085	Positive regulation of catalytic activity	15	1489	0.45	0.0239	GPRC5A,MIF,HSPE1,PYCARD,GDF15,TNFRSF10B,PMAIP1,CCL20,EFNA1,CTSA,CKS2,CLDN3,BCAP31,CLDN3,GPRC5A,MIF,HSPE1,PYCARD,GDF15,TNFRSF10B,PMAIP1,CCL20,EFNA1,CTSA,CKS2,CLDN3,BCAP31,CLDN3,GPRC5A,MIF,HSPE1,PYCARD,GDF15,TNFRSF10B,PMAIP1,PLAUR,CCL20,EFNA1,CTSA,CKS2,CLDN3,BCAP31,GPRC5A,MIF,C1QBP,HSPE1,SOX9,PYCARD,GDF15,EPCAM,TNFRSF10B,CCT3,PMAIP1,PLAUR,CCL20,ELF3,STAT1,ILF2,EFNA1,ASS1,CKS2,CLDN3,MDK,BCAP31,CLD
GO Process	GO:0044093	Positive regulation of molecular function	17	1842	0.41	0.0239	GPRC5A,MIF,HSPE1,PYCARD,GDF15,TNFRSF10B,PMAIP1,PLAUR,CCL20,EFNA1,CTSA,CKS2,CLDN3,BCAP31,GPRC5A,MIF,C1QBP,HSPE1,SOX9,PYCARD,GDF15,EPCAM,TNFRSF10B,CCT3,PMAIP1,PLAUR,CCL20,ELF3,STAT1,ILF2,EFNA1,ASS1,CKS2,CLDN3,MDK,BCAP31,CLD
GO Process	GO:0051173	Positive regulation of nitrogen compound metabolic process	24	3239	0.32	0.0259	GPRC5A,MIF,HSPE1,PYCARD,GDF15,TNFRSF10B,CCT3,PMAIP1,PLAUR,CCL20,ELF3,STAT1,ILF2,EFNA1,ASS1,CKS2,CLDN3,MDK,BCAP31,CLD

GO Process	GO:0048583	Regulation of response to stimulus	28	4114	0.28	0.0261	GPRC5A,MIF, TIMP1,C1QBP,SOX9,PYCARD,GDF15,TNFRSF10B,CXCL8,CPNE1,PMAIP1,PLAUR,IFI6,DDX21,CCL20,ELF3,STAT1,CD55,EFNA1,PSMB9,CLDN3,MDK,IFITM1,ARPC1B,BCAP31,CLDN3,GPRC5A,MIF, TIMP1,C1QBP,HSPE1,SOX9, PYCARD,GDF15,TNFRSF10B, PMAIP1,PLAUR,IFI6,CCL20,EFNA1,CTSA,PSMB9,CKS2,ISG15,CLDN3,BCAP31,CLDN3,MIF,C1QBP,SOX9,PYCARD, CXCL8,DDX21, CCL20,STAT1,CD55,PSMB9, ISG15,MDK,IFITM1,ARPC1B, MIF,CLDN3, AHCY,UPP1,TYMP, PYCARD,CXCL8,CCL20,STAT1,ASS1,PSMB9, PLOD3,CLDN3,FAT1, AHCY,PKM,STAT1,ASS1,LDHA, MIF,C1QBP,SOX9,PYCARD, GDF15,TNFRSF10B,CPNE1,PMAIP1,DDX21, CCL20,EFNA1,BCAP31
GO Process	GO:0051246	Regulation of protein metabolic process	22	2828	0.34	0.0261	,PMAIP1,PLAUR,IFI6,CCL20,EFNA1,CTSA,PSMB9,CKS2,ISG15,CLDN3,BCAP31,CLDN3,MIF,C1QBP,SOX9,PYCARD, CXCL8,DDX21, CCL20,STAT1,CD55,PSMB9, ISG15,MDK,IFITM1,ARPC1B, MIF,CLDN3, AHCY,UPP1,TYMP, PYCARD,CXCL8,CCL20,STAT1,ASS1,PSMB9, PLOD3,CLDN3,FAT1, AHCY,PKM,STAT1,ASS1,LDHA, MIF,C1QBP,SOX9,PYCARD, GDF15,TNFRSF10B,CPNE1,PMAIP1,DDX21, CCL20,EFNA1,BCAP31
GO Process	GO:0002682	Regulation of immune system process	15	1514	0.44	0.0269	,CCL20,STAT1,CD55,PSMB9, ISG15,MDK,IFITM1,ARPC1B, MIF,CLDN3, AHCY,UPP1,TYMP, PYCARD,CXCL8,CCL20,STAT1,ASS1,PSMB9, PLOD3,CLDN3,FAT1, AHCY,PKM,STAT1,ASS1,LDHA, MIF,C1QBP,SOX9,PYCARD, GDF15,TNFRSF10B,CPNE1,PMAIP1,DDX21, CCL20,EFNA1,BCAP31
GO Process	GO:0009164	Nucleoside catabolic process Cellular	3	32	1.42	0.0269	MIF,CLDN3, AHCY,UPP1,TYMP, PYCARD,CXCL8,CCL20,STAT1,ASS1,PSMB9, PLOD3,CLDN3,FAT1, AHCY,PKM,STAT1,ASS1,LDHA, MIF,C1QBP,SOX9,PYCARD, GDF15,TNFRSF10B,CPNE1,PMAIP1,DDX21, CCL20,EFNA1,BCAP31
GO Process	GO:0071356	response to tumor necrosis factor	6	245	0.84	0.0271	L8,CCL20,STAT1,ASS1,PSMB9, PLOD3,CLDN3,FAT1, AHCY,PKM,STAT1,ASS1,LDHA, MIF,C1QBP,SOX9,PYCARD, GDF15,TNFRSF10B,CPNE1,PMAIP1,DDX21, CCL20,EFNA1,BCAP31
GO Process	GO:0003382	Epithelial cell morphogenesis	3	34	1.39	0.0304	AHCY,PKM,STAT1,ASS1,LDHA, MIF,C1QBP,SOX9,PYCARD, GDF15,TNFRSF10B,CPNE1,PMAIP1,DDX21, CCL20,EFNA1,BCAP31
GO Process	GO:0007584	Response to nutrient	5	160	0.94	0.0304	TAT1,ASS1,LDHA, MIF,C1QBP,SOX9,PYCARD, GDF15,TNFRSF10B,CPNE1,PMAIP1,DDX21, CCL20,EFNA1,BCAP31
GO Process	GO:1902533	Positive regulation of intracellular signal transduction	12	1041	0.51	0.0308	F10B,CPNE1,PMAIP1,DDX21, CCL20,EFNA1,BCAP31

GO Process	GO:0043066	Negative regulation of apoptotic process	11	893	0.54	0.0321	CEACAM6,MIF,TIMP1,SOX9,EPCAM,TNFRSF10B,PLAUR,IFI6,CLDN7,EFNA1,MDK
GO Process	GO:2001242	Regulation of intrinsic apoptotic signaling pathway Cell-cell	5	164	0.93	0.0326	MIF,PYCARD,PMAIP1,PLAUR,BCAP31
GO Process	GO:0098742	adhesion via plasma-membrane adhesion	6	257	0.81	0.033	CEACAM6,EPCAM,CLDN7,CLDN3,FAT1,CLDN4
GO Process	GO:0006919	Activation of cysteine-type endopeptidase activity involved in apoptotic process	4	90	1.09	0.0332	HSPE1,PYCARD,TNFRSF10B,PMAIP1
GO Process	GO:0009966	Regulation of signal transduction	23	3107	0.32	0.0332	GPRC5A,MIF,TIMP1,C1QBP,SOX9,PYCARD,GDF15,TNFRSF10B,CXCL8,CPNE1,PMAIP1,PLAUR,IFI6,DDX21,CCL20,ELF3,STAT1,CD55,EFNA1,PSMB9,MDK,CEACAM6,MIF,SP,MIF,TIMP1,DDX39A,PYCARD,SLC7A5,CXCL16,CCT3,SLC39A4,CXCL8,CPNE1,PKM,PMAIP1,PLAUR,FXYD5,CTSB,TAP1,ILF2,CD55,CTSA,PSMB9,GCNT3,ARPC1B,BCAP31,CLDN4
GO Process	GO:0051234	Establishment of localization	29	4479	0.26	0.0397	

GO Process	GO:0051345	Positive regulation of hydrolase activity	10	772	0.56	0.0397	HSPE1, PYCARD, TNFRSF10B, PMAIP1, CCL20, EFNA1, CLDN3, BCAP31, CTNNA4, ADPR, CEACAM6, MIF, SP, MIF, TIMP1, C1QBP, SOX9, PYCARD, EPCAM, CXCL16, CT3, CXCL8, PMAIP1, FXYD5, CCL20, CLDN7, EFNA1, CLDN3, MDK, IFITSOX9, PYCARD, CXCL8, CCL20, PSMB9, GPRC5A, MIF, C1QBP, HSPE1, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CCT3, PMAIP1, PLAUR, DX21, CCL20, ELF3, STAT1, ILF2, EFNA1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, ADPR, CEACAM6, MIF, SP, MIF, TIMP1, C1QBP, HSPE1, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CCT3, PMAIP1, PLAUR, CCL20, ELF3, STAT1, ILF2, EFNA1, ASS1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, MIF, TIMP1, GDF15, CXCL16, CXCL3, CXCL8, CCL20, IL32
GO Process	GO:0032879	Regulation of localization	21	2740	0.33	0.0402	AM, CXCL16, CT3, CXCL8, PMAIP1, FXYD5, CCL20, CLDN7, EFNA1, CLDN3, MDK, IFITSOX9, PYCARD, CXCL8, CCL20, PSMB9, GPRC5A, MIF, C1QBP, HSPE1, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CCT3, PMAIP1, PLAUR, DX21, CCL20, ELF3, STAT1, ILF2, EFNA1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, ADPR, CEACAM6, MIF, SP, MIF, TIMP1, C1QBP, HSPE1, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CCT3, PMAIP1, PLAUR, CCL20, ELF3, STAT1, ILF2, EFNA1, ASS1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, MIF, TIMP1, GDF15, CXCL16, CXCL3, CXCL8, CCL20, IL32
GO Process	GO:0071347	Cellular response to interleukin-1	5	174	0.9	0.0402	D, CXCL8, CCL20, PSMB9, GPRC5A, MIF, C1QBP, HSPE1, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CCT3, PMAIP1, PLAUR, DX21, CCL20, ELF3, STAT1, ILF2, EFNA1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, ADPR, CEACAM6, MIF, SP, MIF, TIMP1, C1QBP, HSPE1, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CCT3, PMAIP1, PLAUR, CCL20, ELF3, STAT1, ILF2, EFNA1, ASS1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, MIF, TIMP1, GDF15, CXCL16, CXCL3, CXCL8, CCL20, IL32
GO Process	GO:0010604	Positive regulation of macromolecule metabolic process	25	3600	0.29	0.0421	AM, TNFRSF10B, CCT3, PMAIP1, PLAUR, DX21, CCL20, ELF3, STAT1, ILF2, EFNA1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, ADPR, CEACAM6, MIF, SP, MIF, TIMP1, C1QBP, HSPE1, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CCT3, PMAIP1, PLAUR, CCL20, ELF3, STAT1, ILF2, EFNA1, ASS1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, MIF, TIMP1, GDF15, CXCL16, CXCL3, CXCL8, CCL20, IL32
GO Process	GO:0031325	Positive regulation of cellular metabolic process	24	3413	0.29	0.0471	AM, TNFRSF10B, CCT3, PMAIP1, PLAUR, CCL20, ELF3, STAT1, ILF2, EFNA1, ASS1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, ADPR, CEACAM6, MIF, SP, MIF, TIMP1, C1QBP, HSPE1, SOX9, PYCARD, GDF15, EPCAM, TNFRSF10B, CCT3, PMAIP1, PLAUR, CCL20, ELF3, STAT1, ILF2, EFNA1, ASS1, CKS2, CLDN3, MDK, BCAP31, CTNNA4, MIF, TIMP1, GDF15, CXCL16, CXCL3, CXCL8, CCL20, IL32
GO Function	GO:0005125	Cytokine activity	8	233	0.98	0.0044	DF15, CXCL16, CXCL3, CXCL8, CCL20, IL32

GO Function	GO:0005515	Protein binding	45	7026	0.25	0.0044	GPRC5A,CEA CAM6,MISP, MIF,AHCY,TI MP1,C1QBP,H SPE1,DDX39A ,SOX9,PYCAR D,GDF15,EPC AM,NOP58,T NFRSF10B,CX CL16,CCT3,C XCL3,CXCL8, CPNE1,PKM, UPP1,PLAUR, FXD5,CTSB, DDX21,TAP1, STIP1,CCL20, CLDN7,STAT1 ,EFNA1,ASS1, CKS2,ISG15,C LDN3,TYMP, MDK,ARPC1B MIF,TIMP1,G DF15,CXCL16, CXCL3,CXCL8 ,CCL20,TYMP, MDK I Y6F II MIF,TIMP1,C1 QBP,PYCARD, GDF15,CXCL1 6,CXCL3,CXC L8,PLAUR,TA P1,CCL20,STA T1,EFNA1,ISG 15,TYMP,MD CXCL16,CXCL 3,CXCL8,CCL 20,STAT1 MIF,TIMP1,G DF15,CXCL16, CXCL3,CXCL8 ,CCL20,TYMP, MDK II 32
GO Function	GO:0030545	Receptor regulator activity	11	536	0.76	0.0044	
GO Function	GO:0005102	Signaling receptor binding	18	1581	0.5	0.0057	
GO Function	GO:0042379	Chemokine receptor binding	5	70	1.3	0.0057	
GO Function	GO:0048018	Receptor ligand activity	10	490	0.76	0.0057	

GO Function	GO:004280	Identical protein binding	19	1896	0.45	0.0112	CEACAM6,MIF,AHICY,DDX39A,PYCARD,GDF15,CPNE1,PKM,UPP1,DX21,TAP1,CLDN7,STAT1,ASS1,CLDN3,TYMP,CLDN4,CXCL16,CXCL
GO Function	GO:000800	Chemokine activity	4	48	1.37	0.0127	3,CXCL8,CCL20,MIF,PYCARD,CXCL16,CXCL
GO Function	GO:000512	Cytokine receptor binding	7	264	0.87	0.0163	3,CXCL8,CCL20,STAT1,GPRC5A,CEACAM6,MIF,AHICY,TIMP1,PLOD3,C1QBP,HSPE1,PYCARD,GDF15,SLC7A5,EPCAM,CXCL16,PDZ
GO Component	GO:000557	Extracellular region	40	4166	0.43	1.32E-07	K1IP1,CCT3,CXCL3,CXCL8,CPNE1,PKM,PLAUR,CTSB,REG4,CCL20,ILF2,CD55,EFNA1,ASS1,CTSA,PPA1,PSMB9,ISG15,GCNT3,MDK,ARPC5,GPRC5A,CEACAM6,MIF,AHICY,TIMP1,PLOD3,C1QBP,HSPE1,GDF15,SLC7A5,EPCAM,CXCL16,PDZ
GO Component	GO:000561	Extracellular space	32	3195	0.45	7.70E-06	ZK1IP1,CCT3,CXCL3,CXCL8,CPNE1,PKM,CTSB,CCL20,CD55,ASS1,CTSA,PPA1,PSMB9,GCNT3,ARPC5,GPRC5A,CEACAM6,MIF,AHICY,TIMP1,PLOD3,C1QBP,HSPE1,GDF15,SLC7A5,EPCAM,CXCL16,PDZ

GO Component	GO:003198	Vesicle	33	3879	0.38	0.00015	GPRC5A,CEACAM6,MIF,AHCY,TIMP1,PLOD3,HSPE1,PYCARD,GDF15,SLC7A5,EPCAM,PDZK1IP1,CCT3,SLC39A4,CPNE1,PKM,PLAUR,CTSB,TAP1,ILF2,CD55,ASS1,CTSA,PPA1,PSMB9,GCNT3,IFITM3,ARPC3,GPRC5A,MIF,AHCY,TIMP1,PLOD3,HSPE1,GDF15,SLC7A5,EPCAM,P
GO Component	GO:007006	Extracellular exosome	23	2099	0.49	0.00026	DZK1IP1,CCT3,CPNE1,PKM,CTSB,CD55,ASS1,CTSA,PPA1,PSMB9,GCNT3,ARPC1B,IFITM3,CEACAM6,ILF1F,TIMP1,PYCARD,CPNE1,PKM,PLAUR,CTSB,ILF2,CD55,CTSA,TFF3,TMPRSS4,CEACAM6,SLC7A5,EPCAM,SLC39A4,CTSB,FAT1,CLDN4,MIIC13
GO Component	GO:003014	Secretory granule	13	845	0.63	0.0022	KM,PLAUR,CTSB,ILF2,CD55,CTSA,TFF3,TMPRSS4,CEACAM6,SLC7A5,EPCAM,SLC39A4,CTSB,FAT1,CLDN4,MIIC13
GO Component	GO:001632	Apical plasma membrane	8	350	0.81	0.0085	CLDN7,CLDN3,CLDN4
GO Component	GO:001632	Apicolateral plasma membrane	3	19	1.64	0.0109	EPCAM,CLDN7,CLDN3,CLDN4
GO Component	GO:001632	Lateral plasma membrane	4	61	1.26	0.0131	EPCAM,CLDN7,CLDN3,CLDN4

GO Component	GO:0016020	Membrane	47	9072	0.16	0.0488	GPRC5A,CEACAM6,MISP,MIF,PLOD3,C1QBP,HSPE1,DDX39A,PYCARD,SLC7A5,EPCAM,NOP58,TNFRSF10B,TMEM45B,CXCL16,PDZK1IP1,CCT3,SLC39A4,CPNE1,PMaip1,PLAUR,IFI6,FXD5,CTSB,DDX21,TAP1,CLDN7,ILF2,CD55,EFNA1,ASS1,CTSA,CLDN3,GCNT3,IFITM3,IFITM1,BCAP31,FAT1,CLDN4,CEACAM6,PLAUR,CD55,EFNA1,LY6E,CXCL16,CXCL3,CXCL8,CCL20
GO Component	GO:0031225	Anchored component of membrane Chemokine	5	169	0.92	0.0488	IFI6,ISG15,IFITM3,IFITM2
STRING clusters	CL:18273	receptors bind chemokines Interferon	4	34	1.52	0.0453	
STRING clusters	CL:19391	alpha/beta signaling, and ISG15-protein conjugation	4	36	1.49	0.0453	
KEGG	hsa05130	Pathogenic Escherichia coli infection	7	187	1.02	0.002	PYCARD,TNFRSF10B,CXCL8,CLDN7,CLDN3,ARPC1B,CLDN4,CEACAM6,MIF,TIMP1,PYCARD,CXCL8,CPNE1,PKM,PLAUR,IFI6,CTSB,TAP1,CCL20,STAT1,ILF2,CD55,CTSA,PSMB9,ISG15,IFITM3,IFITM1,ARPC1B,BCAP3
Reactome	HSA-168256	Immune System	24	1956	0.54	8.13E-05	

Reactome	HSA-909733	Interferon alpha/beta signaling	6	69	1.39	3.00E-04	IFI6,STAT1,ISG15,IFITM3,IFITM1,IFITM2,CEACAM6,MIIF,PYCARD,CP
Reactome	HSA-6798695	Neutrophil degranulation	10	473	0.77	0.0057	NE1,PKM,PLAUR,CTSB,ILF2,CD55,CTSA,CEACAM6,MIIF,PYCARD,CP
Reactome	HSA-168249	Innate Immune System	14	1025	0.58	0.0081	NE1,PKM,PLAUR,CTSB,ILF2,CD55,CTSA,PSMB9,ISG15,APP,C1B,MIIF,MIF,IMP1,CXCL8,IFI6,CC
Reactome	HSA-1280215	Cytokine Signaling in Immune system	11	681	0.65	0.0136	L20,STAT1,PSMB9,ISG15,IFITM3,IFITM1,CXCL16,CXCL
Reactome	HSA-380108	Chemokine receptors bind chemokines	4	57	1.29	0.024	3,CXCL8,CCL20
Reactome	HSA-202733	Cell surface interactions at the vascular wall	5	138	1.01	0.0429	F,SLC7A5,EPCAM,TNFRSF1
WikiPathways	WP619	Type II interferon signaling (IFNG)	5	37	1.58	0.00026	IFI6,TAP1,STAT1,PSMB9,ISG15,IMP1,PLOD3,CXCL16,CXC
WikiPathways	WP4754	IL-18 signaling pathway	8	270	0.92	0.0022	L3,CXCL8,CC
WikiPathways	WP4197	Immune response to SARS-CoV-2	3	23	1.56	0.024	L20,CLDN3,CXCL3,CXCL8,STAT1,IFITM1
WikiPathways	WP5039	innate immunity evasion and cell-specific immune response	4	66	1.23	0.024	1
WikiPathways	WP3614	Photodynamic therapy-induced HIF-1 survival signaling	3	37	1.36	0.0416	PKM,PMAIP1,LDHA
WikiPathways	WP3890	Nanomaterial-induced inflammasome activation	2	7	1.9	0.0416	PYCARD,CTSB
WikiPathways	WP4239	Epithelial to mesenchymal transition in colorectal cancer	5	160	0.94	0.0416	GDF15,CLDN7,CLDN3,CLDN4,TMPRSS4

WikiPathways	WP4877	Host-pathogen interaction of human coronaviruses - MAPK signaling	3	35	1.38	0.0416	IFITM3,IFITM1,IFITM2
Monarch HPO	HP:0002024	Malabsorption	7	171	1.06	0.0328	CEACAM6,MIF,EPCAM,SLC39A4,CD55,EFNA1,TYMP,GPRC5A,CEACAM6,MISP,PLOD3,PYCARD,GDF15,SLC7A5,EPCAM,TNFRSF10B,TMEM45B,CCT3,CXCL8,PKM,UPP1,CTSB,DX21,REG4,STIP1,ELF3,CLDN7,ASS1,CTSA,PPA1,ISG15,CLDN3,GCNT3,BCAP31,CLGPRC5A,CEACAM6,MISP,ACHY,PLOD3,PYCARD,GDF15,SLC7A5,EPCAM,TNFRSF10B,TMEM45B,CCT3,CXCL8,PKM,UPP1,CTSB,DDX21,REG4,STIP1,ELF3,CLDN7,ASS1,CTSA,PPA1,ISG15,CLDN3,GCNT3,BCAP31,CLDN4,TFF3,
TISSUES	BTO:0000511	Gastrointestinal tract	33	1680	0.74	6.40E-14	CXCL8,PKM,UPP1,CTSB,DX21,REG4,STIP1,ELF3,CLDN7,ASS1,CTSA,PPA1,ISG15,CLDN3,GCNT3,BCAP31,CLGPRC5A,CEACAM6,MISP,ACHY,PLOD3,PYCARD,GDF15,SLC7A5,EPCAM,TNFRSF10B,TMEM45B,CCT3,CXCL8,PKM,UPP1,CTSB,DDX21,REG4,STIP1,ELF3,CLDN7,ASS1,CTSA,PPA1,ISG15,CLDN3,GCNT3,BCAP31,CLDN4,TFF3,
TISSUES	BTO:0000058	Alimentary canal	34	1865	0.71	7.77E-14	CCT3,CXCL8,PKM,UPP1,CTSB,DDX21,REG4,STIP1,ELF3,CLDN7,ASS1,CTSA,PPA1,ISG15,CLDN3,GCNT3,BCAP31,CLDN4,TFF3,

TISSUES	BTO:00006 48	Intestine	28	1249	0.8	5.48E-13	GPRC5A,CEA CAM6,MISP,P LOD3,PYCAR D,SLC7A5,EP CAM,TNFRSF 10B,TMEM45B ,CCT3,CXCL8, PKM,UPP1,CT SB,DDX21,RE G4,ELF3,CLD N7,ASS1,CTS A,ISG15,CLD N3,GCNT3,CL DN1,TEF2,TD GPRC5A,CEA CAM6,MISP, MIF,AHCY,TI MP1,PLOD3,C 1QBP,HSPE1,P YCARD,GDF1 5,SLC7A5,EPC AM,TNFRSF1 0B,TMEM45B, CXCL16,PDZ K1IP1,CCT3,C XCL8,PKM,UP P1,FXYD5,CTS B,DDX21,REG 4,STIP1,CCL20 ,ELF3,CLDN7, STAT1,ILF2,C D55,EFNA1,A SS1,CTSA,PPA 1,ISG15,CLDN 3,TYMP,GCN T3,MDK,BCA
TISSUES	BTO:00014 91	Viscus	50	5020	0.44	7.86E-13	

TISSUES	BTO:00003 45	Digestive gland	37	2645	0.59	3.03E-12	CEACAM6,MI F,AHICY,TIMP 1,PLOD3,C1Q BP,HSPE1,PY CARD,SLC7A 5,EPCAM,TNF RSF10B,CCT3, CXCL8,PKM,F XYD5,CTSB,D DX21,STIP1,C CL20,STAT1,I LF2,CD55,EFN A1,ASS1,CTS A,PPA1,ISG15, CLDN3,TYMP ,IFITM3,BCAP MIF,AHICY,TI MP1,C1QBP,H SPE1,GDF15,S LC7A5,EPCA M,NOP58,TNF RSF10B,LACT B2,CCT3,SLC3
TISSUES	BTO:00030 99	Internal female genital organ	33	2593	0.55	2.45E-09	9A4,PKM,PM AIP1,UPP1,PL AUR,IFI6,CTS B,DDX21,CLD N7,STAT1,CD 55,ASS1,CTSA, PPA1,TYMP,I FITM3,MDK,I GPRC5A,MISP ,PYCARD,TNF RSF10B,TME
TISSUES	BTO:00002 69	Colon	16	577	0.89	5.83E-08	M45B,UPP1,D DX21,REG4,C LDN7,ISG15,C LDN3,GCNT3, CLDN4,TFF3,

TISSUES	BTO:00007 59	Liver	26	1882	0.59	1.53E-07	MIF,AHICY,II MP1,C1QBP,H SPE1,EPCAM, TNFRSF10B,C CT3,PKM,CTS B,DDX21,STIP 1,CCL20,STAT 1,ILF2,CD55,E FNA1,ASS1,C TSA,PPA1,ISG 15,TYMP,BCA P31.FAT1.I.D CEACAM6,MI SP,MIF,AHICY ,TIMP1,PLOD 3,C1QBP,HSP E1,DDX39A,S OX9,PYCARD, SLC7A5,EPCA M,TNFRSF10B ,CXCL16,PDZ K1IP1,CCT3,S
TISSUES	BTO:00005 22	Gland	48	6602	0.31	5.19E-07	LC39A4,CXCL 8,PKM,PMAIP 1,FXD5,CTSB ,DDX21,STIP1, CCL20,CLDN7 ,STAT1,ILF2,C D55,EFNA1,A SS1,CTSA,PPA 1,ISG15,CLDN 3,TYMP,IFITM 3,MDK,BCAP3 1,FAT1,CLDN GPRC5A,MIF, TIMP1,C1QBP ,DDX39A,CXC L16,CCT3,CX
TISSUES	BTO:00007 63	Lung	20	1162	0.68	5.19E-07	CL3,CXCL8,P KM,CTSB,STIP 1,ILF2,CD55,T YMP,BCAP31, SNRPB,TFF3,L

TISSUES	BTO:00014 89	Whole body	66	12619	0.16	6.72E-07	GPRC5A,CEA CAM6,MISP, MIF,AHCY,TI MP1,PLOD3,C 1QBP,HSPE1, DDX39A,SOX 9,PYCARD,G DF15,SLC7A5, EPCAM,NOP5 8,TNFRSF10B, LACTB2,TME M45B,CXCL16 ,PDZK1IP1,CC T3,CXCL3,SLC 39A4,CXCL8,C PNE1,PKM,P MAIP1,UPP1, PLAUR,IFI6,F XYD5,CTSB,D DX21,REG4,T AP1,STIP1,CC L20,ELF3,CLD N7,STAT1,ILF MIF,AHCY,II MP1,C1QBP,H SPE1,DDX39A ,SOX9,GDF15, SLC7A5,EPCA M,NOP58,TNF RSF10B,LACT B2,CXCL16,C CT3,SLC39A4, CPNE1,PKM,P MAIP1,UPP1, PLAUR,IFI6,C TSB,DDX21,T AP1,STIP1,CL DN7,STAT1,IL F2,CD55,ASS1, CTSA,PPA1,IS G15,TYMP,IFI TM3,MDK,IFI TM1 R C A P31
TISSUES	BTO:00000 83	Female reproductive system	44	5799	0.33	1.27E-06	

TISSUES	BTO:0001488	Endocrine gland	45	6036	0.32	1.27E-06	CEACAM6,MI F,AHICY,TIMP 1,PLOD3,C1Q BP,HSPE1,DD X39A,SOX9,PY CARD,SLC7A 5,EPCAM,TNF RSF10B,CXCL 16,CCT3,SLC3 9A4,CXCL8,P KM,PMAIP1,F XYD5,CTSB,D DX21,STIP1,C CL20,CLDN7, STAT1,ILF2,C D55,EFNA1,A SS1,CTSA,PPA 1,ISG15,CLDN 3,TYMP,IFITM 3,BCAP31,FAT 1,CLDN4,SNR GPCR5A,MIF, TIMP1,C1QBP ,DDX39A,CXC L16,CCT3,CX CL3,CXCL8,P KM,CTSB,STIP 1,ELF3,ILF2,C D55,TYMP,BC AP31,SNRPB,
TISSUES	BTO:0000203	Respiratory system	21	1436	0.61	2.21E-06	

TISSUES	BTO:00030 91	Urogenital system	47	6716	0.29	2.66E-06	MIF,ATF1,11 MP1,C1QBP,H SPE1,DDX39A ,SOX9,GDF15, SLC7A5,EPCA M,NOP58,TNF RSF10B,LACT B2,CXCL16,PD ZK1IP1,CCT3, SLC39A4,CXC L8,CPNE1,PK M,PMAIP1,UP P1,PLAUR,IFI 6,CTSB,DDX21 ,TAP1,STIP1,E LF3,CLDN7,S TAT1,ILF2,CD 55,ASS1,CTSA, PPA1,ISG15,T YMP,IFITM3, MDK,IFITM1 MIF,TIMP1,HS PE1,NOP58,T NFRSF10B,LA
TISSUES	BTO:00014 24	Uterus	17	1020	0.67	9.43E-06	CTB2,PKM,P MAIP1,DDX21 ,STAT1,CD55, ASS1,PPA1,IFI TM3,MDK,IFI CEACAM6,11 MP1,PLOD3,P YCARD,CXCL
TISSUES	BTO:00009 88	Pancreas	13	568	0.81	1.12E-05	8,PKM,FXYD5, CTSB,CCL20,B CAP31,IL32,T MDR3,ATP AHCY,HSPE1, DDX39A,SLC7 A5,EPCAM,C
TISSUES	BTO:00005 80	Blood cancer cell	17	1098	0.64	2.40E-05	CT3,CXCL3,C XCL8,PKM,D DX21,STIP1,ST AT1,IFITM1,B CAP31,FAT1,L 11MP1,1NFRS F10B,LACTB2,
TISSUES	BTO:00014 21	Uterine cervix	9	277	0.96	6.73E-05	PKM,CD55,AS S1,IFITM3,IFIT M1,1DHA

TISSUES	BTO:00012 53	Skin	16	1069	0.62	8.23E-05	MIF,AHIC1,G DF15,SLC7A5, CCT3,CXCL8, PKM,UPP1,PL AUR,IFI6,CTS B,STIP1,CTSA, SNRPB,LDHA ATPM,GDF15, SLC7A5,CCT3, CXCL8,PKM, UPP1,PLAUR, IFI6,CTSB,CL DN7,STAT1,C D55,CTSA,TY MP,CTDN4,T AHCY,C1QBP, GDF15,SLC7A 5,EPCAM,CCT 3,CXCL8,PKM ,UPP1,PLAUR, IFI6,CTSB,DD X21,CLDN7,S TAT1,ILF2,CD 55,CTSA,TYM P,CLDN4,LD AHCY,GDF15, SLC7A5,CCT3, PKM,UPP1,PL AUR,IFI6,CTS B,CLDN7,STA T1,CD55,CTS A,TYMP,CLD N4,LDHA, MIF,AHCY,II MP1,HSPE1,P YCARD,SLC7 A5,NOP58,TN FRSF10B,CXC L16,CCT3,CX CL3,CXCL8,P KM,PLAUR,F XYD5,CTSB,D DX21,TAP1,IL F2.CTSA.PPA1
TISSUES	BTO:00004 49	Fetus	17	1229	0.59	9.90E-05	
TISSUES	BTO:00001 74	Embryonic structure	22	2132	0.46	0.00024	
TISSUES	BTO:00010 78	Placenta	16	1176	0.58	0.00025	
TISSUES	BTO:00005 70	Hematopoietic system	24	2543	0.42	0.00032	

TISSUES	BTO:0001271	Leukemia cell	14	949	0.62	0.00043	AT11,DDX39A,SLC7A5,CC T3,CXCL8,PK M,DDX21,STI P1,STAT1,IFIT M1,BCAP31,F AT11,CTQB IMF1,CTQB ,SLC7A5,EPC AM,TNFRSF1 0B,SLC39A4,P KM,PMAIP1,L V6F1DHA GPRC5A,CEA CAM6,MISP, MIF,AHCY,TI MP1,PLOD3,C 1QBP,HSPE1, DDX39A,SOX 9,PYCARD,G DF15,SLC7A5, EPCAM,NOP5 8,TNFRSF10B, LACTB2,TME M45B,CXCL16 ,PDZK1IP1,CC T3,CXCL3,SLC 39A4,CXCL8,C PNE1,PKM,P MAIP1,UPP1, PLAUR,IFI6,F XYD5,CTSB,D DX21,REG4,T AP1,STIP1,CC L20,ELF3,CLD N7,STAT1,ILF EPCAM,CXCL
TISSUES	BTO:0000975	Ovary	10	482	0.76	0.00058	8,PKM,REG4,B CAP31,CLDN 4.II.32.I.DHA MIF,AHCY,PY CARD,GDF15, SLC7A5,NOP5 8,CCT3,CXCL
TISSUES	BTO:0000042	Animal	67	14895	0.1	0.00063	8,PKM,UPP1,P LAUR,IFI6,CT SB,DDX21,STI P1,CTSA,IFIT M3,SNRPB,LD
TISSUES	BTO:0001307	Stomach	8	291	0.89	0.00065	
TISSUES	BTO:0000634	Integument	20	1970	0.45	0.00073	

TISSUES	BTO:0000089	Blood	17	1675	0.45	0.0038	MIF,ATIC1,ITMP1,HSPE1,SLC7A5,NOP58,CCT3,CXCL3,CXCL8,PKM,CITSB,DDX21,TAP1,CTSA,FA
TISSUES	BTO:000051	Lung cancer cell	5	124	1.05	0.0051	T1LY6E,LDH,CEACAM6,EP
TISSUES	BTO:0000785	Lymphoma cell	6	203	0.92	0.0052	CAM,CXCL8,PKM,PLAUR,HSPE1,EPCAM,CXCL3,PKM,STIP1,LDH,C1QBP,SOX9,PYCARD,SLC
TISSUES	BTO:0000421	Connective tissue	11	871	0.55	0.0135	7A5,CXCL16,CT3,PKM,CTSB,STIP1,PPA1,SNRPR,AHCY,EPCA
TISSUES	BTO:0000586	Colonic cancer cell	6	249	0.83	0.0144	M,PKM,REG4,CLDN7,ASS1
TISSUES	BTO:0000878	Mononuclear cell	4	117	0.98	0.0427	SLC7A5,CXCL3,CXCL8,LY6E,CEACAM6,MI
COMPAR TMENTS	GOCC:0005576	Extracellular region	28	2035	0.58	2.61E-07	F,TIMP1,PLOD3,C1QBP,HSPE1,GDF15,EP
COMPAR TMENTS	GOCC:0005615	Extracellular space	18	985	0.71	1.04E-05	CAM,CXCL16,PDZK1IP1,CXCL3,CXCL8,PKM,PLAUR,CITSB,CCL20,STAT1,CD55,CTSA,ISG15,MDK,FAT1,LY6E,TEF3,IL32,LDH,CEACAM6,MI
COMPAR TMENTS	GOCC:0005615	Extracellular space	18	985	0.71	1.04E-05	F,TIMP1,C1QBP,HSPE1,GDF15,EPCAM,CXCL16,CXCL3,CXCL8,PKM,CITSB,STAT1,CD55,IL32,LDH

COMPAR TMENTS	GOCC:003 1982	Vesicle	25	2051	0.53	1.51E-05	GPRC5A,CEA CAM6,MIF,TI MP1,PLOD3,H SPE1,PYCARD ,GDF15,SLC7 A5,EPCAM,SL C39A4,CPNE1 ,PKM,PLAUR, CTSB,TAP1,IL F2,CD55,CTSA ,PPA1,GCNT3, IFITM3,I.DHA GPRC5A,CEA CAM6,MISP, MIF,AHCY,TI MP1,PLOD3,C 1QBP,HSPE1, DDX39A,SOX 9,PYCARD,G DF15,SLC7A5, EPCAM,NOP5 8,TNFRSF10B, LACTB2,CXC L16,PDZK1IP1 ,CCT3,CXCL3, SLC39A4,CXC L8,CPNE1,PK M,PMAIP1,UP P1,PLAUR,IFI 6,FXD5,CTSB ,DDX21,REG4, TAP1,STIP1,C CL20,ELF3,CL DN7,STAT1,IL F2,CD55,ASS1,
COMPAR TMENTS	GOCC:011 0165	Cellular anatomical entity	67	13853	0.13	8.18E-05	

COMPAR TMENTS	GOCC:000 5737	Cytoplasm	48	7871	0.23	0.00074	CEACAM6,MI SP,MIF,AHCY ,TIMP1,PLOD 3,C1QBP,HSP E1,PYCARD,G DF15,SLC7A5, NOP58,LACT B2,CCT3,SLC3 9A4,CPNE1,P KM,PMAIP1, UPP1,PLAUR, IFI6,CTSB,DD X21,REG4,TAP 1,STIP1,STAT1 ,ILF2,CD55,AS S1,CTSA,PPA1 ,PSMB9,ISG15, TYMP,GCNT3 ,IFITM3,IFITM 1,BCAP31,FAT 1,SNRPR,TFE3, CEACAM6,MI F,TIMP1,PYC
COMPAR TMENTS	GOCC:003 0141	Secretory granule	12	704	0.68	0.0029	ARD,CPNE1,P KM,PLAUR,C TSB,ILF2,CD5 5,CTSA,TPMR, MIF,TIMP1,HS
COMPAR TMENTS	GOCC:007 0062	Extracellular exosome	9	368	0.83	0.0029	PE1,GDF15,EP CAM,PKM,CT SB,CD55,LDH CEACAM6,MI F,TIMP1,PLO D3,PYCARD,S
COMPAR TMENTS	GOCC:003 1410	Cytoplasmic vesicle	17	1709	0.44	0.0188	LC39A4,CPNE 1,PKM,PLAU R,CTSB,TAP1,I LF2,CD55,CTS A,IFITM3,TM EPCAM,CLD
COMPAR TMENTS	GOCC:000 5923	Bicellular tight junction	4	75	1.17	0.0323	N7,CLDN3,CL DN4
COMPAR TMENTS	GOCC:190 2912	Pyruvate kinase complex	2	4	2.15	0.0323	PKM,LDHA
COMPAR TMENTS	GOCC:010 1031	Chaperone complex	3	31	1.43	0.0369	HSPE1,CCT3,S TIP1

COMPAR TMENTS	GOCC:004 3227	Membrane- bounded organelle	46	8685	0.17	0.0389	GPRC5A,CEA CAM6,MISP, MIF,TIMP1,PL OD3,C1QBP,H SPE1,DDX39A ,SOX9,PYCAR D,GDF15,SLC7 A5,EPCAM,N OP58,LACTB2 ,SLC39A4,CP NE1,PKM,PM AIP1,PLAUR,I FI6,CTSB,DDX 21,TAP1,STIP1 ,ELF3,STAT1,I LF2,CD55,ASS 1,CTSA,PPA1,I SG15,GCNT3,I FITM3,IFITM1 ,BCAP31,FAT1 SNRPR,TFE3, CEACAM6,PY CARD,CPNE1,
COMPAR TMENTS	GOCC:000 5773	Vacuole	9	612	0.61	0.0472	CTSB,CTSA,P PA1,IFITM3,IF ITM1,IFITM2, MIF,AHICY,C1 QBP,HSPE1,P YCARD,SLC7 A5,NOP58,CC T3,CPNE1,PK M,PMAIP1,UP P1,DDX21,STI P1,STAT1,ASS 1,PSMB9,ISG1 5,SNRPB,IL32, IFI6,DDX21,SI
COMPAR TMENTS	GOCC:000 5829	Cytosol	22	2919	0.32	0.0474	AT1,ISG15,IFI TM3,IFITM1,I FITM2, MIF,C1QBP,P YCARD,IFI6,D DX21,TAP1,C D55,PSMB9,IS G15,IFITM3,IF ITM1,IFITM2
UniProt Keywords	KW-0051	Antiviral defense	7	127	1.19	0.00019	
UniProt Keywords	KW-0391	Immunity	12	522	0.81	0.00019	

UniProt Keywords	KW-0399	Innate immunity	10	324	0.94	0.00019	MIF,C1QBP,P YCARD,IFI6,D DX21,CD55,IS G15,IFITM3,IF ITM1,IFITM2, CEACAM6,11 MP1,PLOD3,G DF15,SLC7A5, EPCAM,TNFR SF10B,CXCL16 ,CCT3,CXCL3, CXCL8,PLAU R,CTSB,REG4, CCL20,CD55,E FNA1,CTSA,IS G15,GCNT3,M DK,FAT1,CLD NA1,LY6E,TFE3 CXCL16,CXCL
UniProt Keywords	KW-1015	Disulfide bond	27	3304	0.36	0.0023	3,CXCL8,CCL 20,TYMP MIF,PYCARD, CXCL3,CXCL8 ,CCL20,ELF3 MIF,GDF15,C XCL16,CXCL3, CXCL8,CCL20 MIF,TIMP1,PL OD3,C1QBP,G DF15,CXCL16, CXCL3,CXCL8 ,PLAUR,CTSB, REG4,CCL20, CD55,EFNA1,I SG15,MDK,TF CEACAM6,PL AUR,CD55,EF NA1,LY6E EPCAM,CLD N7,CLDN3,CL DN4
UniProt Keywords	KW-0145	Chemotaxis	5	95	1.17	0.0039	
UniProt Keywords	KW-0395	Inflammatory response	6	162	1.02	0.0039	
UniProt Keywords	KW-0202	Cytokine	6	186	0.96	0.0054	
UniProt Keywords	KW-0964	Secreted	18	1818	0.44	0.0054	
UniProt Keywords	KW-0336	GPI-anchor	5	138	1.01	0.0119	
UniProt Keywords	KW-0796	Tight junction	4	96	1.07	0.0303	

UniProt Keywords	KW-0732	Signal	23	3233	0.3	0.0387	CEACAM6,II MP1,PLOD3,G DF15,EPCAM, TNFRSF10B,C XCL16,CXCL3, SLC39A4,CXC L8,PLAUR,FX YD5,CTSB,RE G4,CCL20,CD 55,EFNA1,CTS A.MDK.FAT1
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Supplementary Table 3**model_lasso_min**

	s0
(Intercept)	5.09E-12
CLDN7	1.019254152
TFF3	1.000614923
TYMP	1.24619318
PLOD3	1.170055599
NOP58	1.064234493
CCL20	0.996162778
IFI6	1.169272181
LACTB2	1.096064518
TNFRSF10B	1.087761117
CPNE1	1.53056928
PKM	1.144240393
EFNA1	1.246705198
GDF15	1.619387319
UPP1	1.169239565
MISP	1.123968918
TIMP1	1.772294161
EPCAM	1.014414947
CXCL3	0.932566127
MIF	1.258644836
MDK	1.049491331
CKS2	1.290050157
BCAP31	1.106590376

Supplementary Table 4 model_lasso_1se

	s0
(Intercept)	2.95E-06
CLDN7	1.145102432
TYMP	1.001470801
PLOD3	1.106499356
TNFRSF10I	1.121891779
CPNE1	1.12667366
PKM	1.000838302
GDF15	1.161949811
UPP1	1.089985727
TIMP1	1.403007979
CKS2	1.260454817
BCAP31	1.361207329
SNRPB	1.121589012
