

gene	control	control	control	control	control	control	control
GSM901319	GSM901320	GSM901321	GSM901322	GSM901323	GSM901324	GSM901325	
MMP1	4.4310344	7.60825062	3.95502899	4.55266267	4.51759346	3.63441023	4.28332445
MMP3	5.20554853	6.41245898	5.2199706	4.47055079	4.64462538	5.29732865	5.3290219
REG1B	4.14017636	3.72325432	5.81675974	4.09794883	4.01033235	4.17438303	3.88835795
REG1A	5.22742079	4.63481793	7.87665954	5.15596981	4.20234716	4.372986	4.01994235
CXCL11	2.85625781	3.03727174	2.72774595	2.52796149	2.89653926	2.80870007	2.78477323
CXCL1	6.27158794	5.75479513	5.55758984	5.98727874	7.63941163	5.35436455	5.6185685
CXCL8	4.89530796	4.2087179	4.90620927	4.4432771	5.35871752	4.82106744	5.04273785
IDO1	6.3515146	6.50328989	6.85953296	6.46816583	6.32328097	6.17633839	5.33652209
S100A8	6.18833234	5.51744946	4.82131042	6.03546531	4.95622937	5.28594455	4.23411542
IL1B	7.10971072	6.61057768	6.10741689	6.38207979	6.27461407	6.51500766	6.21237741
CXCL9	7.17878903	7.01562698	5.58623206	4.90109821	6.97095204	6.58821805	5.71925161
AQP9	4.92572163	5.57056815	5.45279447	4.97341954	5.30060759	5.06017315	5.26478341
HCAR3	3.53845667	3.596673	3.50879645	3.55323797	3.98412065	4.00105182	3.66540386
DEFA5	4.13465722	4.36824474	8.53159177	4.01033089	5.13415765	4.29068376	3.61094601
CXCL10	6.74753393	6.47212803	6.13428247	5.18457689	6.39433014	5.5732026	5.18415282
LCN2	9.861267	10.7355818	10.2213671	8.19093545	9.23970534	9.19986843	9.32761506
PTGS2	4.01763566	3.25589618	3.40163006	4.26831787	3.17539894	3.25698936	3.22624715
SLC6A14	4.47144219	3.93749803	4.60478515	2.75906941	3.05707527	4.30111282	3.45039914
MMP10	3.42571268	4.38334688	3.62880132	3.73810066	3.66304024	3.66300824	3.44316968
DMBT1	6.47492514	7.89847593	10.1440498	7.51865855	5.78150911	8.397353	8.08499673
CHI3L1	4.01763566	5.05995292	3.78352288	3.25343867	3.88623973	3.89617513	4.01846602
PLAU	7.13723238	6.96579069	6.46925838	6.90002779	6.82636962	6.39755323	6.90641064
CXCL3	6.92867822	5.32267767	5.61423414	6.38478459	5.71862064	5.53964242	4.7894686
S100A9	6.69508198	6.36424307	6.23226631	7.00762923	6.95542732	6.46407971	6.723843
FCGR3B	4.63217087	5.73712681	4.53315201	4.47485632	4.08433788	4.76764252	4.75517278
COL6A3	9.75356128	10.1035761	9.35243644	9.29144693	9.63190231	9.29199	9.19836626
COL4A1	9.35310403	9.39131289	8.83724777	8.75792076	9.19410842	8.83896829	8.73861313
SELE	3.73078968	3.31836395	3.68449809	3.41848791	3.26698735	3.30966898	3.33834901
CFI	4.79552186	4.67514274	5.9605465	4.43205518	4.38894791	4.08966297	4.69048802
TNFAIP6	4.34388422	4.8037957	4.8086433	5.00877002	4.32272484	4.5513567	4.42188497
DEFA6	5.2280442	5.28520211	7.94231707	5.11820527	5.85130336	5.47996287	4.78282116
WARS	8.10372385	8.36015444	7.67684673	7.75177203	8.03772699	7.72352628	7.8895505
DUOXA2	6.3668312	6.43149818	7.02873817	5.83265552	5.92341473	7.05553965	6.80531565
CD55	8.64063228	8.87478021	8.76110665	8.13608491	8.18638441	8.87686386	8.54037231
APOL1	6.58566871	7.05419253	7.25966069	6.08111954	6.54215782	6.49463069	6.383659
OLFM4	9.20964675	8.79053683	10.4591883	8.36019742	6.99194765	10.718437	7.94530995
CXCL6	3.52768262	3.06104387	3.34603692	3.35104937	5.24451761	2.85817993	3.15133011
DUOX2	5.4786276	9.30330928	8.57505991	5.18457689	5.15469754	8.08560274	7.92207433
MMP12	8.0309577	9.9709681	9.71536955	7.53374502	9.05372858	8.442669	9.48010498
NCF2	5.66908744	6.11938699	5.11692231	5.97420774	5.07702817	5.04565695	6.22320307
IFNG	4.0059493	3.85592174	4.40230729	4.03476246	3.99301001	4.32993848	3.94031562
STAT1	10.0462205	9.98516187	9.88859558	9.42596253	10.4045334	9.9495848	9.7625331
MNDA	6.10955986	6.41223426	5.35448179	6.22153067	5.635355	5.34820214	6.00523562
TIMP1	9.86867092	10.4886287	9.07284179	9.08891859	9.55738105	9.14254152	9.36879177
IFITM2	10.2535787	10.2904962	9.95558197	9.98331654	10.2737072	9.7247671	9.48084224
IL6	4.01357866	3.90242428	4.20286908	4.50636865	3.84158261	4.02343456	3.88191053
GNA15	5.9011865	5.94815925	5.68330253	5.84279971	5.79637485	5.5179211	6.01751913
SLC7A5	6.06226251	6.79047614	5.89844559	6.30638659	5.86479122	6.03062844	5.88463298
CTSK	8.48570807	8.60573942	7.71107128	8.35772211	8.09187704	8.30651688	8.41507245
CXCL2	3.31166779	3.10593053	3.37727954	3.41299866	3.17424402	3.40304638	3.18445417
SLC2A3	5.7533135	5.82175848	4.88308636	5.73036684	5.30303046	5.18291448	5.49759656
CCL20	9.44515484	8.77185824	7.90289895	8.33812859	8.69298468	8.28705912	7.4385143

CASP1	8.62335371	8.36361113	8.23483023	8.0076416	7.782504	8.06953785	8.58463572
SPINK4	7.51998891	10.1543089	11.7756974	7.79164645	8.15818781	10.0640449	9.76967964
PLAUR	7.47277151	7.78260077	7.73936094	7.21739165	7.06231272	7.66508879	7.69864636
ICAM1	6.68735115	6.54184545	6.1515663	6.5723486	6.45629398	6.17651313	6.48900438
NOS2	5.47471544	5.18175631	5.91078681	5.28441444	5.88426945	5.84257661	5.94180227
PI3	7.76266749	9.50757304	9.52845166	6.67328424	6.36472707	9.39061569	8.52847825
S100A12	3.4993862	3.65042998	3.39776347	3.49506583	3.30157833	3.52187902	3.38736104
TMEM158	6.8624754	6.54184488	6.29074918	5.59524383	6.5015989	5.66757734	5.52598976
WNT5A	7.01607092	6.85811685	6.39496252	6.33385847	6.24855478	6.50439318	6.19314812
GBP1	7.8775581	7.70544467	7.95028146	7.28912063	7.78372184	7.59549636	7.04972938
C4BPB	5.56295821	5.75084141	5.75179125	4.96239131	5.77092121	6.07929241	5.46247499
IFIT3	6.36870501	6.77580959	6.79522258	6.32555976	6.76410896	6.7625055	6.31236547
CEMIP	4.26879179	4.47608003	4.43292329	4.4136154	4.38615747	4.60415917	4.47202688
ANKRD22	7.88207715	8.05733779	8.33366895	7.41984151	7.8460264	8.06438999	7.47778602
REG3A	2.90503481	3.66778187	7.15787734	3.08861069	3.9602127	3.74394929	3.53996032
PLEK	7.61769781	7.36781647	6.65915466	7.34040611	7.49404016	7.31357693	7.31027719
IFITM3	10.8266945	10.9634879	10.5315396	10.5780884	11.0560201	10.3243606	10.2239522
BCL2A1	6.69621822	5.82227946	5.2377116	6.30901984	6.32782129	5.00690009	4.95817806
LAMP3	6.61164002	6.32295182	4.9166831	6.36602695	6.70413558	6.01992164	5.16347317
UBD	8.19718843	6.93347496	7.51099424	7.01005449	7.50750463	6.39119983	5.03531888
GBP5	5.22589517	5.50693777	5.0628986	5.33994094	5.63298159	5.38781661	5.30491509
ACKR4	4.01646284	4.13125827	4.46974453	4.09089437	4.11711742	4.36020509	4.23156045
ADM	8.40388273	8.59223876	8.98771072	9.26941595	8.65587463	8.94374589	9.67145494
PHLDA1	7.16632052	6.43537922	6.21233826	6.94523566	5.96663315	6.2383044	6.0377567
MMP7	5.15864737	5.10402877	4.64646092	5.18291609	4.31525847	5.25878806	4.73122721
CXCL5	2.77649866	2.70086441	2.66465285	2.69601568	2.61372312	2.52532267	2.8075173
RAB31	8.00377935	8.18506103	7.74339396	7.5418153	7.89496572	7.58210628	7.66063826
CCL3L3	6.62045527	5.69447767	6.66055136	6.57312983	5.69574003	6.15887377	5.97742639
NAMPT	6.78635174	6.82486441	7.26562738	7.10454125	6.63333971	6.71429413	7.09623206
ACSL1	6.1212987	6.72499749	6.22061996	7.23809799	6.85242196	6.16137013	6.95059454
C4BPA	4.65746331	5.95445027	5.93945785	4.68895531	5.08337742	5.27057624	5.6146096
LILRB2	6.11396768	6.70169524	5.82823544	5.97932514	5.29160115	5.75449625	6.38185822
TCN1	3.55189194	3.76132245	3.64719768	3.71655262	3.51774818	4.04727357	3.63301539
BACE2	7.99863653	8.75780719	8.80619904	7.63905227	8.44309084	8.0708198	7.45302593
RND1	5.9935574	6.03312654	6.11220014	6.38367024	5.69255229	6.01892799	6.27548604
IRF1	7.62114546	8.09538553	8.238846	7.8819877	8.0045105	7.72595744	7.81447824
TAP1	8.47845456	8.47169353	8.27792756	8.41640019	8.78687227	8.39610403	8.58154528
CXCR2	4.74602755	4.69343448	4.57753768	4.83964704	4.21595464	4.45939894	4.59513064
MAFF	5.70423429	6.15014246	5.70204476	5.67874851	5.86515073	5.70578771	6.00844957
CSF2RB	7.89355997	8.47696483	6.92360186	7.82268998	7.35752723	7.26350383	7.38458804
PDE4B	7.30298807	7.12356517	6.47119913	6.66992475	6.85678605	6.61840794	6.63496337
CCL2	7.99916883	7.8978756	7.7034296	8.13784918	7.6977228	7.93832022	8.315338
CD274	5.28414504	5.06257093	5.45692645	5.41364221	5.06529816	5.32241799	5.06926086
TFPI2	3.48603394	3.00614697	3.05202619	3.21139648	3.11909817	3.07533879	3.07594439
CYR61	9.46432157	6.55493934	5.79545504	7.02075052	6.63980043	5.47681254	5.93597088
CCL4	6.40612085	6.81663419	6.59069536	6.61103619	6.46775595	6.51748021	6.38321316
CSF3R	6.13612334	6.58766736	6.16516243	6.38634985	6.18142626	6.64952101	6.44127277
KYNU	5.67181735	5.76044854	5.26422744	5.65793467	5.72037233	5.7728161	5.84807802
MMP9	8.69666766	7.4897598	7.45060755	7.77771968	8.25708811	7.48849526	6.5312922
UBE2L6	8.78245837	8.73428369	8.64695277	8.07757203	8.89919028	8.39517464	8.30589019
MUC1	8.60457506	9.01362855	9.25676918	8.36148541	9.31123544	9.22483381	9.41933182
IL13RA2	3.72718406	3.8180244	3.54790676	3.25280301	3.3352231	3.44660133	3.52158458
PROK2	2.52465694	3.14975438	2.73707932	3.07934677	2.91628146	3.0384848	2.86666293
S100P	9.19425643	11.3243969	11.3748991	9.14571971	10.5486788	10.8608621	10.7095952

SERPINA3	5.81645446	5.28474221	4.8424569	5.24292117	5.36339566	4.83161187	4.52520459
GBP2	8.44286574	8.4374663	8.30262486	8.27211446	8.2129852	8.18586033	8.05973863
COL15A1	8.95552711	8.54247432	8.22054501	8.01122025	9.08805771	8.03833426	7.56442111
REG4	8.19797956	9.69182725	9.48548432	6.29366813	8.54480194	10.0433157	7.69381283
GZMB	5.3375387	5.28536493	4.80400991	4.62718863	4.67897661	4.48487902	4.77101496
FOXQ1	5.95912335	5.35745585	5.89243322	5.94883489	5.68731873	6.01371549	5.51960782
LPL	3.72512136	3.83040885	3.40881701	3.81549825	3.74573094	3.72829605	3.92780731
TNIP3	3.27616119	3.57180784	3.52652182	3.3233239	2.9962466	2.979469	3.06835336
C2CD4A	3.89249078	4.17589316	4.19168887	3.77342138	3.98782463	4.14397012	4.15197108
PCSK1	6.08628595	4.8126409	6.28660334	5.20378072	7.27500466	5.45096327	5.73084635
LPCAT1	6.80506777	6.77262933	6.0463667	5.97492816	6.61425827	5.86411387	6.48175686
CTHRC1	5.44759394	5.98779948	5.02711428	5.06064825	5.91553465	5.09401276	5.24671098
SRGN	3.44151714	3.3649945	3.42569464	3.37655834	3.49959415	3.14859972	3.27357693
EGFL6	3.51698543	3.60433587	3.57931854	3.58813566	3.9130528	3.68827588	3.68062533
C1R	9.33235429	9.34073628	8.47994838	8.87934726	8.91568907	8.54848447	8.54733041
DRAM1	7.13258194	7.28737268	6.88808686	6.8103997	6.79452678	5.66757734	6.6991932
PLA2G2A	10.192922	11.3600469	11.0994229	9.14802226	10.9892282	12.4637479	11.2801715
VNN1	5.01667878	5.46459605	4.88797989	4.83490575	4.55859823	5.09401276	4.38104404
FCGR1B	3.84380539	4.99403647	3.82694672	4.32452323	3.62374816	3.69219932	4.13411546
HLA-DMA	8.88834844	9.12072892	8.64837876	8.69632172	8.74848125	8.17132682	8.93957553
FCGR1CP	4.65031379	5.25467904	4.76961555	5.06499734	4.89164163	4.68970778	4.93227766
CCL11	5.70094933	7.44718821	6.18835091	7.41861372	5.34958369	7.34270665	6.66927869
PFKFB3	7.17826104	6.64917623	6.91510283	6.42689175	6.43127126	7.00993957	7.15795584
IL1RN	5.94348963	5.82547307	5.69770196	4.33727929	5.90067206	6.26021064	5.58648195
TREM1	4.03220892	4.58356325	4.48437889	4.39239902	4.48098237	4.44999882	4.2087179
FCER1G	6.57599795	7.87370651	6.64765441	7.23205517	6.60906084	6.33935484	7.6954324
COL1A2	11.3164852	11.146092	10.6246377	11.0833138	10.9434106	10.7586482	10.5532286
IFITM1	10.85546	10.6188459	10.5329127	11.0425392	10.8333577	9.98174087	10.0704152
INHBA	2.87517708	3.10706598	2.85882482	3.14796226	2.91750768	3.04411386	3.05752117
GPR84	4.28386516	4.16322924	4.2619711	4.33258733	4.09676469	3.81539337	3.89087545
GREM1	9.44038619	8.58527979	7.36153949	5.78903	8.37659419	7.24418739	6.65587872
PLA2G7	6.58116638	7.49441293	7.40093043	7.46451943	6.71035409	6.37493302	8.39867424
IER3	10.2556126	8.53049401	9.07802929	9.85332989	9.78167354	9.44321471	9.31119009
STC1	5.53976585	4.89379078	4.75587836	5.06820808	5.09802941	5.07940966	4.59698933
SLC7A11	4.5856751	4.67832011	4.50266877	4.31509328	4.42922197	4.45203516	4.44802058
TMEM45A	6.70471489	7.03777121	6.2573113	6.38578573	5.99549502	5.52857918	6.49553932
PDZK1IP1	8.95900471	8.90275709	8.79960136	8.26950993	8.31754574	8.79417968	8.81624825
TNFSF13B	8.61963898	8.09294524	6.8037897	7.78557212	8.10762154	7.300632	7.39410894
SELL	7.43744396	6.02018633	4.9455945	7.7261679	7.2334284	5.3145312	4.66157638
GOS2	8.43202908	6.80794461	6.96274612	6.51109587	7.03055572	7.32848332	7.32826239
L1TD1	4.4632786	5.94968156	6.10772645	5.91242082	5.90089296	5.89922502	5.54405589
MIR8071-2	12.4754587	13.020961	10.1186757	11.2844607	13.0690187	11.2007438	12.3030277
ADGRL4	6.34827031	6.44053041	5.90334761	6.20377979	5.95121795	5.73095441	5.88472344
MXRA5	9.16682683	8.98282707	8.38673947	8.79383766	8.67813185	8.75930051	8.25068301
CLDN8	11.6127674	10.2927129	11.1248889	9.8039585	11.2594802	11.4066679	11.4596918
GUCA2A	11.9016979	12.3798942	12.3856908	12.485007	12.123761	12.1075855	12.5868701
AQP8	10.3139241	10.9230331	11.9254452	12.9038705	12.1685912	10.803513	12.5235002
ABCG2	7.2452535	8.8814693	8.57439883	9.70317263	8.70373285	8.24336903	8.19910527
CHP2	10.157826	9.66104485	9.87060688	10.6513344	10.2179745	9.88793607	10.0084627
PCK1	11.3439995	10.8321657	11.5132545	10.9212305	10.6622235	10.7528929	11.3347811
HMGCS2	11.5771961	12.0102121	11.8939935	12.7109356	12.0142992	11.9789362	12.0132393
SLC26A2	13.3431856	12.9485179	13.2881233	13.6443326	13.5938738	13.2658493	13.6912318
GUCA2B	9.12920618	10.4531048	10.6503866	10.1138861	9.8976972	9.37682557	9.33001771

CDHR1	6.98830141	6.77499882	7.48281418	4.27966856	6.23381902	6.75487422	6.70372403
HSD17B2	9.98734345	10.3061228	10.1411832	10.8933979	10.0074687	9.87557502	10.3432076
ABCB1	8.11360725	8.24343755	8.76593822	8.46554112	8.44660553	8.59889884	8.51001533
SLC16A9	8.83621907	9.61075891	10.4063522	9.31740692	8.10762154	10.0952323	9.67855076
PNLIPRP2	9.26549111	4.52902479	9.05268946	8.59357906	9.42710035	10.0572207	8.71433935
SLC51B	8.47703651	8.50978696	9.49405679	9.86837734	8.64943849	8.39394428	9.06909643
ADIRF	9.83040004	9.20902767	9.67789342	9.61567113	8.99870777	9.13115966	9.39215153
MT1M	9.59133051	10.5052149	10.1476671	7.46132655	8.73233165	9.16215848	11.3439732
MEP1A	11.0703004	11.3085399	11.4551814	11.4108339	10.9776835	11.5001487	11.7225986
MT1F	10.3289185	11.2356947	11.2582417	10.271464	9.92613417	10.1814001	12.0307851
DHRS11	9.61507553	10.0984223	10.0947064	10.5444059	9.62718992	9.73338118	10.2586618
TRPM6	6.56341536	6.54499644	7.04343794	6.82474593	7.5934741	6.76390664	7.65814188
UGT2A3	7.57178177	7.77298666	7.96925621	8.35512006	7.77205502	8.33990326	7.95534902
SLC26A3	13.2178539	13.3609729	13.7223957	13.7302553	13.5234743	13.4652674	13.6446397

gene	control GSM270808	control GSM270809	control GSM270810	control GSM423047	control GSM423048	control GSM423049	control GSM423050
MMP1	169	199.9	504.6	283.9	273.6	339.1	114.9
MMP3	108.5	70.4	144.5	52.8	2.5	35.2	35
REG1B	77.6	554	145.1	15336.6	4483.3	2689.9	5508.8
REG1A	105.3	856	141.3	15822.6	9678.7	8020.6	13518.6
CXCL11	53.7	38.7	48	82.3	35.5	29.9	60.4
CXCL1	36.2	419.6	515.6	214.3	19.8	31.8	192.4
CXCL8	50.1	162.6	132.3	86.8	28	1.6	9
IDO1	145.7	280.6	267.8	83.7	69	6.6	57.7
S100A8	318	449.8	426.6	54.6	21.5	99	65.1
IL1B	214.3	199.3	310.6	102.3	54.4	106.3	33.2
CXCL9	96.5	322	474.1	60.2	45.8	25.4	97.5
AQP9	7.6	15.3	117	1.8	7.6	3.6	4.3
HCAR3	14.3	7	11.8	17.5	2.7	6.8	18.9
DEFA5	420.9	108.3	84.7	18055.5	16500.6	20360	19556.9
CXCL10	272.1	411.8	682.1	775	224.7	135.9	289.4
LCN2	997.9	3875.1	3147.9	1188.2	459.8	56.3	417.9
PTGS2	82.6	22.9	57.3	11.8	5	2.6	3.7
SLC6A14	47.1	104.1	92.4	29.8	18.3	8.2	33.3
MMP10	96.8	6	77.8	11	0.9	27	26.2
DMBT1	686.6	1120.4	1935.5	10079.5	3643.3	1638.4	3961.7
CHI3L1	27.9	100.2	155.5	7	3.5	1.9	76.5
PLAU	393.6	586.6	797.4	62	47.3	29.1	57.9
CXCL3	29.3	237.8	228.4	121.5	18.7	24.5	131.3
S100A9	231.9	311.7	425	25.5	22.3	65.2	31.8
FCGR3B	156.1	165	119.9	29.1	26.7	56.2	56.5
COL6A3	1349.9	1807.8	2032.9	334.6	195.2	249.4	226.5
COL4A1	1538.6	1633.8	2350.4	355.2	309	279.1	281.5
SELE	45.6	37.9	8.6	2.8	11.2	6.3	1.6
CFI	36.2	145.8	24.4	108.6	136	54	242.2
TNFAIP6	121.6	77.6	91.1	36.3	21	13.2	6.4
DEFA6	128.2	132	77.1	16071.5	10178.8	15797.7	19442.9
WARS	1112.8	754.3	1261.8	209.3	215.2	172.3	185.7
DUOXA2	402.1	322.5	396.1	76.9	16.1	7.8	10.7
CD55	2733.4	1711.8	2138.9	1891.3	1210.1	1366.8	600.3
APOL1	187.6	174.6	246.6	167.2	190.3	126	94.6
OLFM4	6408.8	3762.5	9844.5	12176.5	6502.4	7906.1	10769.4
CXCL6	43.2	90	118.6	200.9	34	16.8	30.4
DUOX2	900.8	424.9	1215.3	252.3	42	48.4	2.2
MMP12	2110.4	1298.7	2196.1	848	317.2	65.8	210.7
NCF2	334.5	446	390.8	41.7	46.2	16.8	52.7
IFNG	47.6	6.5	19.8	36.5	17.5	6.7	4.3
STAT1	3525.7	3713.9	4578.7	2021.3	1014.2	1119.9	1337.6
MNDA	227.8	520.8	264.6	20.4	32.9	32.3	49.8
TIMP1	2696.1	3710.8	2680.1	177.4	147.6	105.9	189.8
IFITM2	4774.5	4425.4	6990.9	652.5	379.9	223.1	779
IL6	70.7	24.8	70.4	26.5	17.8	15.8	20.4
GNA15	94.2	223.5	249.5	9	33.8	5.6	35.3
SLC7A5	234	285.7	161.3	109.9	19.4	30.3	51.6
CTSK	1607.4	1606	1654.7	123.1	85.2	74.1	160.9
CXCL2	11.2	4	84	10.7	1.4	1.6	1.3
SLC2A3	71.4	209.1	238	8.8	9.9	35	125.5
CCL20	546.4	1437.4	1423.6	7859.4	530.4	526.7	8141

CASP1	893.8	1475.3	2435	1704.8	981.9	750.1	1077.7
SPINK4	1893.6	3885	2612.4	3985.1	6628.9	5214.8	5039.2
PLAUR	1610.6	603.4	1406.9	274.3	126.4	126.3	125.2
ICAM1	306.2	350.3	375.3	65.8	21.9	39.7	118
NOS2	167.1	305.4	201.2	403.4	19.9	24.8	79.4
PI3	725.7	819.2	1805.6	113.8	50.5	65.2	118
S100A12	36.4	77.3	24	36.2	14.1	10.1	45.3
TMEM158	105.8	174.4	158.8	31.1	13.3	2.8	48
WNT5A	729.6	784.2	604	201.3	104	77.1	174.2
GBP1	1092.3	1150.4	2334.3	1466.6	927.7	714.5	610.5
C4BPB	166.9	30.8	118.4	101.1	57.5	42.4	50.9
IFIT3	236.6	265.9	456.1	445.7	525.3	375.1	476.8
CEMIP	12.2	8.1	9.4	2.7	6.3	2.2	3.2
ANKRD22	556.7	896.4	1551.4	90.9	64.4	82.5	93.8
REG3A	37.4	280.3	90	13559.8	10020.9	15249.7	15525.3
PLEK	374.7	700.5	221.7	78.7	82.5	27.7	196
IFITM3	8235.9	6498	11906	987.2	539.6	385.3	838.6
BCL2A1	128.5	195.1	311.9	62.9	48.6	55.5	502.2
LAMP3	163.4	260	411.6	31	76.6	23.9	43.1
UBD	140	552.2	854.8	974.3	400.2	107.7	2559.9
GBP5	100.4	105.9	156	34.3	23.1	30.7	45.7
ACKR4	13.7	6.9	89.5	728.5	383.2	198.8	341.1
ADM	1195.1	1954.9	2861.2	344.8	495.4	541.7	195.6
PHLDA1	342.8	326.7	438.1	134.5	72.2	57.9	50.5
MMP7	79.2	141.5	147.8	56.6	18.8	27.8	17.5
CXCL5	10.4	23.9	34.2	11.8	2.3	6.3	1.6
RAB31	584.4	673.9	681	146.4	73	91.8	69.2
CCL3L3	312.5	636.7	791.3	86.4	63.4	21.9	49.8
NAMPT	806	326.7	671.1	434.9	278.3	271	201.2
ACSL1	674	434.6	765.3	55.8	141.6	476.3	118.1
C4BPA	294.3	150.1	153.9	60.5	37.6	43.7	6.5
LILRB2	78	282	252.7	5.7	6.2	1.7	3.8
TCN1	100.9	16.1	135.8	38.1	35.9	44.8	33.4
BACE2	998.2	1413.1	1803.7	287.1	135.1	117.1	288.3
RND1	46.7	96.5	98	32.5	41.1	8.4	70.4
IRF1	1196.9	1291.2	2167.9	1035.7	537.9	546.3	795.1
TAP1	1204.5	1759	2494.9	1003.4	678	434.6	1015.8
CXCR2	68.2	60.7	56.5	5.1	14.9	14.7	23.7
MAFF	279.8	209.3	325.1	166.8	130.3	117.1	151.8
CSF2RB	493.7	918	900.7	83.1	76.8	41.1	274
PDE4B	282	481.9	405.7	48	22	27.4	94.3
CCL2	913.2	1450.9	2324	67.4	12.2	16.5	10.8
CD274	128.1	113.8	152.5	47.7	52.9	25.6	62.8
TFPI2	64.7	12.8	55	2.4	2	7.7	2.4
CYR61	252.9	151.4	233.1	17.5	37.9	43.6	52.9
CCL4	316.7	648.4	470.3	86.1	21.4	33.4	68.2
CSF3R	244.8	265.3	383.4	35.3	71.6	47.4	64.6
KYNU	45.2	201.4	218.3	50.7	52.6	37	40.8
MMP9	887.1	724.5	1194.9	59.4	116.2	84.7	307.9
UBE2L6	1131.3	1494	2113	686	623.9	570.7	685.9
MUC1	2579	2987.3	4413.6	154.5	90.3	101.3	115.8
IL13RA2	90.7	68.9	128.5	1	1.3	1.6	30.7
PROK2	3.2	13.2	61.9	0.6	20.8	17.2	13.3
S100P	1928	11357.9	9715.8	283.8	688.8	731.5	505

SERPINA3	117.2	149.4	109.6	64.7	14.7	9.8	38.1
GBP2	825.3	1006.2	723.4	736.3	522.9	486.9	360.7
COL15A1	1152	716.9	1125	53.6	54.1	51.6	63.2
REG4	1860.1	2083.8	3941.7	3429.2	6624	8009.5	4854.9
GZMB	90.6	178.6	138.9	316.8	9.2	49.7	41.2
FOXQ1	228.6	289.9	396.8	38.6	16.3	35.4	62.3
LPL	7.1	67.6	85.4	163.8	88.9	25.1	72.2
TNIP3	5.7	33.1	62.8	12.8	1	17.3	2.2
C2CD4A	127.8	74.5	92.1	92.8	2	2	69
PCSK1	150.8	124.6	189	103.6	90.7	160.5	222.4
LPCAT1	255.2	296.6	410.8	65.9	63.6	38.6	144.5
CTHRC1	240.9	261.6	197.2	47.2	24.7	19.6	65.8
SRGN	4.7	90.4	32.7	22	3	2.1	14.9
EGFL6	80.2	51.3	74.8	33	19	3.9	8.1
C1R	1859.9	1957.8	1732.9	247	84.9	62.6	117.4
DRAM1	442.2	591.3	644.4	98	94.5	60.9	101.7
PLA2G2A	3260.6	26195.6	43726.2	10355.9	2280.8	7961.8	13469.3
VNN1	14.7	115.3	21.7	1172.3	875.2	802.2	450.6
FCGR1B	185.2	219.9	236.1	2.6	19.6	1.9	5.7
HLA-DMA	1658	2781.9	2581.5	1555.6	1634	1636.9	1563.9
FCGR1CP	154	279.8	184.9	23.1	14.7	13.3	40.1
CCL11	3378.1	1678.8	1798.2	80.1	31.4	54.3	138.8
PFKFB3	352.5	478.5	392	451.5	138.6	236.3	207.3
IL1RN	87.9	266.2	255.9	56.9	147.2	87.8	85.2
TREM1	15.8	40.6	129.8	1.4	20.4	34.1	24.4
FCER1G	1115	1804.2	1679.3	83.1	67.4	41.3	82
COL1A2	6182.3	6919.8	7022.5	670.6	465.5	431.3	535.1
IFITM1	8396.6	6993.9	8018.5	1767.8	907.5	819	1840.1
INHBA	43.8	63	3.4	2.8	28.2	11.4	2.9
GPR84	120.4	11	32.2	12.6	13.7	0.9	25.9
GREM1	45.2	113.1	10.2	75.4	7.5	14.2	36.1
PLA2G7	469.1	1283.2	1053.3	67.8	85.4	19.3	67
IER3	1659.4	3207.3	4079.4	427.6	179.4	182	285.4
STC1	121.4	66.9	158.9	8.7	18.8	19.3	60.9
SLC7A11	10.6	82.6	86.5	19.1	5.1	19.8	37.9
TMEM45A	326	355.5	465.4	55.1	16.6	48.3	54.2
PDZK1IP1	2262.2	1830.3	1875.8	333.2	96.1	76.8	254.4
TNFSF13B	409.5	697.8	510.4	101.8	48	67.7	196.5
SELL	146.2	343.3	419.5	30.3	63.6	35.5	210.6
GOS2	389.3	517.7	323.4	268.4	200.9	103.8	283.4
L1TD1	498.1	237.4	112.5	31.8	15.4	19	25.7
MIR8071-2	7194.5	33123.2	38060.2	503	355.9	131.9	1041.6
ADGRL4	141.2	117	101.1	29.3	43.1	54.1	43
MXRA5	1443.8	1266.8	1403.2	218.8	98.3	84.4	125.8
CLDN8	4169.4	7395.5	6055.6	107.2	104.6	505.5	35.3
GUCA2A	48048.1	17450.6	40423.8	13864.7	11794.1	15664.4	12545.6
AQP8	34006.9	6731.9	15029.3	2.7	4.3	11	19.1
ABCG2	4299.6	1541.2	2547.9	4349.8	6129.8	7722.5	3535.3
CHP2	9693.5	3407.2	4868.9	3902.3	6355.5	5913.8	3521.4
PCK1	13230.6	8947.7	7206.9	5468.6	2269.1	5735.3	5410.5
HMGCS2	22166.9	7747.2	14113.2	908.4	691.7	356.5	261.3
SLC26A2	42447.2	36562.4	32257.3	2814	3057.8	3670.1	1619.8
GUCA2B	12529.7	1451.8	11546.7	6575.1	2237.4	8114.7	3743.1

CDHR1	185.4	247.7	594.6	55.9	118.6	175.2	62.6
HSD17B2	12172	4158.6	6529.1	3260.9	3623.5	5717.9	3379.4
ABCB1	3390.1	711.9	2620.4	3571	4183.9	4040	3017.7
SLC16A9	2696.4	2814.6	2298.5	20.4	295	381.2	66.3
PNLIPRP2	805.5	1847.4	1043.4	6717	3046.7	2546.2	366.3
SLC51B	5120.7	1657.4	3179.9	2106.3	4001.3	3447.1	1621.8
ADIRF	6983.4	2615.4	1688.3	6851.5	10697.3	10213.5	5112.1
MT1M	12653.1	7347.4	4156.3	93.9	146.7	796.4	4942.3
MEP1A	9001.8	6149.1	7249.6	10673.7	11370.9	15377.3	9140.4
MT1F	26264.7	14186.9	10659.7	1182.9	2400.2	3938.3	10799.8
DHRS11	8776.9	8224.1	8814.9	4803.7	4025.2	4202.7	3876.1
TRPM6	776.9	410.4	535.1	94.8	101.5	101.1	97
UGT2A3	1304.3	1637.9	1827.3	2276.2	1179.5	2008.7	2906.1
SLC26A3	53688.8	35110.5	44083.8	9627.1	10698.3	13320.3	8092.7

gene	control GSM423051	control GSM423052	control GSM364627	control GSM364628	control GSM364629	control GSM364630	control GSM364631
MMP1	146.9	75.9	17.3	0.7	851.9	33	35.4
MMP3	63.8	14.1	29.3	20.1	507.9	23.7	42.2
REG1B	849.1	4468.3	29.4	7	35.5	1167.7	17.3
REG1A	8229.9	7636.8	9.2	4.1	9.4	5999.1	5.9
CXCL11	48.4	203.2	15.3	8.1	26.9	113.2	6.9
CXCL1	33.8	59.6	85	81.9	216.1	69.8	36.7
CXCL8	27.4	2.2	26.3	19.8	1484.8	22.3	28.1
IDO1	113.2	262.6	42.2	23.8	40.5	55.9	6.2
S100A8	49.2	76.4	35.3	25.4	86.8	17.8	22.3
IL1B	65.8	84.6	64.8	86.1	82.2	83.5	74.6
CXCL9	85.3	276.2	34.7	34.5	118.6	57.1	34.8
AQP9	4	3.2	2.8	6.6	4.2	2.6	6.9
HCAR3	6.1	21.2	20.1	17.1	21.5	1	17.7
DEFA5	22650.7	13674.6	130.4	2.3	3.4	73.1	23.6
CXCL10	134.4	282.8	53.7	5.2	104.3	158.7	20.2
LCN2	69.7	109.5	2548.8	2162.9	3439.1	254.9	186
PTGS2	1.9	11	24.4	16.4	33.3	1.2	2.2
SLC6A14	25.7	27.2	20.3	61.2	146.1	29.7	15.9
MMP10	7.9	0.6	11	20.9	47.9	1.9	5
DMBT1	2106.7	670.1	486.4	540	348.1	2021.8	353.4
CHI3L1	9.2	61.4	3.7	13.5	116	6.1	1.5
PLAU	43.1	168.3	24.1	23.7	155.6	51	5.6
CXCL3	1.6	3.5	71.4	88	107.3	122.7	35.3
S100A9	17.3	46.6	36.8	5.1	39.9	25.2	31.1
FCGR3B	40.2	47.6	64.6	5	54.2	38.6	33.6
COL6A3	392.7	500.9	318.5	60.1	388.2	159.7	87.8
COL4A1	396.1	334.5	307.8	120.4	754.4	160.8	106.1
SELE	1.1	7.7	11.6	22	1.7	12	15.1
CFI	127.1	167.8	50.6	8.2	3.8	405.8	20.1
TNFAIP6	4.1	2	21.7	12.1	47.8	20.3	4.3
DEFA6	19578.4	9981.6	36.2	6.1	6.8	66.2	32.7
WARS	132.6	301.3	122.7	43.1	256.6	291.4	120.7
DUOXA2	6.6	5.9	58.1	117.2	112.2	13.7	24
CD55	746.5	590.3	807.1	425.1	384.7	2020	526.2
APOL1	92.6	139.2	83.3	79.1	74.6	91.8	38
OLFM4	9504.1	7377.7	6186.8	3856.5	930.9	3489.4	3175.8
CXCL6	45.6	43.6	17.5	12.2	21.5	12.3	30.8
DUOX2	5	59.4	556.1	1525.9	498	31.7	77.2
MMP12	278.1	1072.3	195.4	97.8	838.7	111.7	58.4
NCF2	5.3	99.4	31.2	5.9	67.9	3.1	39.2
IFNG	25.8	6.3	22.8	32.3	26.1	14.7	13.1
STAT1	1121	1556.6	1078.5	1045.3	1633.8	1445.6	1024.1
MNDA	33.4	161.2	23.2	15.9	42.5	16.3	11.8
TIMP1	241.6	561.6	166.8	495.9	1167.3	141.6	113.6
IFITM2	342.5	1193.7	597.9	220	994.9	572.6	345.1
IL6	28.3	47.2	32.6	2.9	114.4	9.4	36.4
GNA15	5	24.4	62.4	20	32.7	12.7	9.4
SLC7A5	45.6	88.3	56.6	45.6	82.4	77.1	58.6
CTSK	191.7	424.1	146.4	125.6	279.4	89.2	96.5
CXCL2	16.4	1.5	2.3	1.5	2.4	1.4	4.1
SLC2A3	51.9	208.5	40.5	8.8	85.6	7.5	3.5
CCL20	417.4	2173.3	400.1	802.9	860.4	1019.6	251.8

CASP1	934.4	584.1	569.1	452.4	384.7	372.3	291.3
SPINK4	5017.8	2698.4	769.1	868	350.1	2637.8	705
PLAUR	123.8	99.7	542.6	685.1	393.5	1369.2	495.3
ICAM1	24.9	150.3	49.8	35.5	96.2	12.4	64.1
NOS2	28	48.8	47.4	66.2	42.7	121.2	73.3
PI3	60.3	5.3	248	2746.3	1447	87.1	173.6
S100A12	20	2.3	38	33.8	20.1	32	8.6
TMEM158	13.2	71.2	39.1	40.7	151.1	18.3	7.3
WNT5A	116.8	264.8	131.8	43.7	123.2	131.4	49
GBP1	736.6	547.5	362.9	321	452.3	631.3	294.6
C4BPB	66.4	57.3	78.5	37.5	55.9	40.4	79
IFIT3	496.6	252.8	136.4	80.4	124.1	321.8	112.7
CEMIP	32	2.6	8.4	3	2	3.6	2.9
ANKRD22	94.4	101.8	398.2	211	257.6	636.9	409.3
REG3A	16013.1	9436.5	16.4	21	7.8	41	16.8
PLEK	90.2	300.7	33.2	70.6	130.9	78.6	7.6
IFITM3	627.6	1031.9	920.7	462.3	1720.5	1190.2	403.1
BCL2A1	74.1	863	40.9	22.4	57.2	24	12.6
LAMP3	78	272.5	14.2	4.1	45.5	17.6	21.5
UBD	657.5	2902.5	101	116	285.6	161.3	22.4
GBP5	22.3	47.6	44.2	28.3	32	30.2	45.3
ACKR4	360.5	254.1	50	10	37.8	92	38.6
ADM	329.5	153.5	533.3	1656.8	1045.6	804	644.2
PHLDA1	55.9	143.6	54.5	78.5	173.8	44	77.2
MMP7	47.5	17	5.6	4.3	76.6	8.2	3.2
CXCL5	14.9	11.6	0.9	5.9	15.2	1.1	1
RAB31	100	368.5	118.5	87.5	327.2	62.7	106.1
CCL3L3	35.4	69.2	83.1	35.2	51.1	30.8	39.6
NAMPT	324.8	213.5	215.4	189.5	233	667.7	358.8
ACSL1	167.3	236.3	260.6	329	199.7	393.9	377.2
C4BPA	9.5	33.1	364.9	52.6	25.4	78.2	95.3
LILRB2	3	25.3	7.8	4.3	2.4	10	12
TCN1	3	26.6	21.6	15	23.7	23.4	16.1
BACE2	159.5	178.3	512.9	451.1	280.2	415.2	279.2
RND1	6.1	66.4	110.9	72	13.6	144.5	174.3
IRF1	505.7	503.4	312.7	384.6	409.4	745.3	357
TAP1	942.3	709.5	495.1	473.9	569.9	767.1	453.1
CXCR2	13.5	26	25.1	8.7	12	2.9	16.4
MAFF	114.5	82.9	102.9	184.4	132.1	178.7	104.1
CSF2RB	100	1160.6	66.5	51.4	115	5	40.4
PDE4B	27.1	296.8	39.6	6.1	69.6	42.1	11.5
CCL2	7.4	53.6	7.9	26.1	42.6	2.4	6.4
CD274	33.7	35.4	59.8	50.5	55.7	49.2	41.6
TFPI2	2.1	1.2	9.5	14	50.7	0.6	17.2
CYR61	25.3	34.1	46.4	93.5	109	31.5	4.5
CCL4	12.3	86.9	37.5	8.1	48.9	63.8	31.9
CSF3R	9.3	55.6	83.3	63.6	67.9	39.1	65.7
KYNU	16.9	60.1	13.9	33.2	33.8	8.1	24.1
MMP9	132.6	1035.2	76.7	69	206.3	94.5	69.2
UBE2L6	628	551.2	204.8	291.3	305.4	454.7	157.5
MUC1	71.1	45.4	988.2	1243.7	1353.7	400.3	590.1
IL13RA2	23.4	5.9	4.4	4.6	27.6	83.2	14.5
PROK2	2.8	1.1	1.8	0.5	10.3	1.8	3
S100P	554.6	235.2	2409.9	2479.5	2902.2	1743.2	1606.8

SERPINA3	20.2	171.6	7.8	9.5	7.3	6.9	3.8
GBP2	579.6	375.9	409.4	265.2	215.2	292.5	352.5
COL15A1	63.8	102.2	123.6	55.7	217.7	26.3	57.9
REG4	6833.8	3965.1	756.3	690.8	519	324	270.4
GZMB	47.6	64.2	61.4	47.3	35.1	73.1	30.3
FOXQ1	26.1	63.5	248.3	37.1	58.9	100.3	34.1
LPL	107	165.6	4	17.8	1.3	8.2	2.9
TNIP3	15.1	28.5	3.2	10.7	15.1	3.1	2.4
C2CD4A	35.2	26.1	14.9	8.9	26.9	20.2	8.1
PCSK1	131.6	89.5	23	19.9	21.8	7.1	23
LPCAT1	28.6	252	31.5	22.6	131.5	36.3	17.7
CTHRC1	59.2	132.1	72.5	32.1	315.2	18.6	26.7
SRGN	9.9	13.6	6.8	27.6	5.7	20.1	12.3
EGFL6	29.9	25.4	39.4	51.4	19.9	46.9	26.2
C1R	127.3	310.3	134.8	96.3	203.8	35.8	36.8
DRAM1	48	153.6	92.4	88.9	117.4	80.8	57.2
PLA2G2A	6711	2792.1	1106.1	12010.3	11120.9	2020.2	1388.6
VNN1	441	550.3	19.4	147	40.7	1.2	5.3
FCGR1B	5.1	10.2	20.1	32.2	7.8	6.9	5.7
HLA-DMA	1383.5	1526.6	287.8	138.9	302.2	195.9	62.7
FCGR1CP	26.5	13.8	13.2	24.9	34.2	19.1	25.3
CCL11	53.5	48.2	140	64.9	52.4	44.9	47.4
PFKFB3	268.2	299	183.9	215.8	177.3	143	104.7
IL1RN	95.6	90.1	43.2	17.2	142	1104.1	64
TREM1	26	7.7	5.9	37	9.7	3.2	5.2
FCER1G	47.3	127.2	40.8	35.7	75.8	29	15.7
COL1A2	631.3	1031.7	640.1	202.4	1333.5	188.3	121.1
IFITM1	1382.5	1892.7	1410.8	306.1	2178.9	2321.7	710.6
INHBA	29.8	22	24.6	14.5	28.3	46.4	30.3
GPR84	2.6	9.7	13.5	3.3	20	2	16.1
GREM1	87.8	345.3	189.9	64.4	434.8	38.8	41.3
PLA2G7	63	138.2	77.6	43.3	88.4	41.3	23.2
IER3	204.9	245.9	425	1277.2	826.1	2604	597.5
STC1	13	25.1	22.6	27	113.2	11.6	16.2
SLC7A11	1.5	10.6	39.4	19.8	16.2	49.4	30.7
TMEM45A	72.4	371.1	55.8	43.3	71.5	20.8	40.6
PDZK1IP1	188.2	112.4	616.9	776.5	907.5	133.6	267.4
TNFSF13B	119.4	488.5	72	69.6	95.3	37.3	54.5
SELL	122.9	906.1	3.6	25.1	43.2	23.6	20.9
GOS2	136.1	169.6	96.6	264.6	143.1	47.1	80.9
L1TD1	29.2	37.7	215.3	69	40.5	157.7	182
MIR8071-2	1529.3	5352.6	653.9	784.3	1672.7	245.5	250.9
ADGRL4	55.2	68.6	56.5	5.8	48	7.3	13.3
MXRA5	167.2	280.3	104.7	83.5	203.7	74	39.3
CLDN8	165.4	22.6	254	3042.8	2322.8	78.2	1657.4
GUCA2A	17183.5	8552.4	9651.1	10972.4	10246.1	16446.6	15461.9
AQP8	2.9	6.1	12576.9	4091.4	5731.2	12248.5	13249.4
ABCG2	7049.8	3299.3	2980	710.7	847.3	4076.6	6013.8
CHP2	5628.7	2738.2	4618.7	2390.1	1041.2	3146.4	4728.3
PCK1	2503.8	2485.3	4772.2	6424.2	4021.4	5718.4	8783.2
HMGS2	905	392.2	8758.7	3365.5	4351.1	9146.9	11044.3
SLC26A2	4006.9	1399.8	12076.6	12772.3	11536	11272.4	13110.7
GUCA2B	5770	2786	5384.8	6482.2	3421.3	6472.8	9529.8

CDHR1	149.7	54.5	103.3	122.4	48.3	19.7	168.1
HSD17B2	7285.1	2645.5	4176.1	3189.5	2365.4	7642.7	4370.9
ABCB1	4206.2	2947.3	878.4	1089.6	1369.3	1021.2	1142.1
SLC16A9	346.2	70.4	1955	504.2	1367	1595.3	1340.1
PNLIPRP2	5819.3	3651.8	189.1	53.8	487.9	60	235
SLC51B	5573.9	1787.6	1962	1362.6	843.1	3745	2368.8
ADIRF	10788.9	5931.4	2117.2	371.8	334.5	2112.4	1335
MT1M	4399.1	5421.5	2308.5	3798.2	2126.8	708.2	1004.6
MEP1A	13297.8	7990.7	3505.5	5780	3898.1	5615.8	4829
MT1F	13576.1	11727.8	7520.9	7832	4900.8	4330.7	4636.9
DHRS11	3964.7	2759.4	3192.5	2792.3	2240.5	3768.2	3295.8
TRPM6	152.4	93	243.1	337.5	385.4	174.3	287
UGT2A3	2405.8	2518.4	1209.3	1312.8	750.1	1685.6	2098
SLC26A3	11044.3	7430.7	16508.3	16898	16566.4	19806.7	20270.7

gene	control	CD	CD	CD	CD	CD	CD
	GSM364632	GSM901326	GSM901327	GSM901328	GSM901329	GSM901330	GSM901331
MMP1	26.8	5.51620381	6.87602076	11.370705	10.1642462	9.04897833	6.88853177
MMP3	19.1	4.96820017	7.64508428	10.4421399	10.2464379	5.93807287	5.24636164
REG1B	9.5	7.86113587	12.6806355	10.0896191	5.66676115	3.87600069	4.45004655
REG1A	6.3	8.76334	12.5656765	11.7710526	9.20999437	6.4803331	4.30928246
CXCL11	1	2.98605407	7.89130775	3.93371939	7.15655522	3.06571133	2.62586826
CXCL1	18.7	5.4276866	10.6424682	8.81855646	8.53716424	5.75049778	5.4321077
CXCL8	1.7	3.9698834	7.43937531	7.57992222	9.82371231	4.85293677	4.15676691
IDO1	35.5	6.3772746	11.7375624	8.94727843	7.69942314	7.17396682	5.00995311
S100A8	12.7	7.11388246	9.7970682	10.2443691	12.0945203	6.46275224	5.61094374
IL1B	41.2	6.4364791	7.85507961	7.51432743	8.25673533	5.7542227	6.26784863
CXCL9	39.3	6.28945724	11.6376491	9.54562377	7.60838649	6.71456175	4.20788343
AQP9	3.9	5.74339455	6.17080654	7.02185536	7.96831308	4.96143754	5.1457384
HCAR3	16	3.80976931	6.43411535	4.86413597	7.21246518	3.7732547	3.76177729
DEFA5	26.2	12.4975664	11.3012894	12.8055721	5.46847428	8.43251871	4.85492536
CXCL10	26.1	5.84559482	10.6480611	9.16199455	7.71794059	7.07588004	4.72501475
LCN2	90.8	9.7091309	13.219721	12.3980135	10.0122036	9.34292905	9.00413689
PTGS2	24	3.24500244	4.2996405	3.65132819	4.42486624	3.33835894	3.20602235
SLC6A14	17.6	3.05576712	8.52773936	7.5295881	8.57403428	2.99570414	3.36249337
MMP10	0.7	3.84889803	4.09451359	5.02826688	6.2651777	3.62767615	3.36705264
DMBT1	349.6	10.8888274	13.1074925	12.4567098	11.5046625	8.92019625	8.69995878
CHI3L1	2.7	4.20740338	11.0337301	9.84741338	11.5646686	5.13159958	3.95769773
PLAU	29.5	6.63741726	8.00864165	7.94892861	8.10056705	7.15949902	6.49823052
CXCL3	40.2	4.50885226	10.2294872	7.39637027	6.99718763	5.49631972	4.6952887
S100A9	6.4	7.21749947	8.47079416	8.80024626	9.82807563	7.093448	6.68183841
FCGR3B	7.2	4.39822599	8.08125081	8.14056013	7.94734261	4.81990192	4.63493065
COL6A3	146.8	9.08736045	10.2446802	12.027998	11.6759905	10.4472755	9.2467967
COL4A1	248	8.58027739	9.50549719	10.9146418	10.8453794	9.24544583	8.9136442
SELE	1.5	3.3657641	3.44194338	3.77308689	5.12264972	3.37840272	3.31830099
CFI	32.9	5.75425559	7.09380613	8.2825218	7.75581363	4.9447443	4.35575056
TNFAIP6	19.4	3.90187861	5.40754243	6.86295398	6.13463405	4.230085	4.25463389
DEFA6	27.6	11.8746882	11.3695747	12.1951903	6.61958011	7.56546229	5.14886019
WARS	112.4	7.90636772	10.6262806	9.34746566	9.79537522	8.14302831	7.45360853
DUOXA2	14.3	6.51757709	10.1595705	8.2628894	7.31985466	5.90401973	6.37484334
CD55	679.6	8.86942905	9.84459997	10.3453605	10.901232	9.00493909	8.71868918
APOL1	86.8	7.16364848	8.94409705	8.67977628	8.5409179	6.44346043	6.39069186
OLFM4	2646.1	11.5045899	13.1798198	13.1433392	13.4360901	12.2205161	12.2283647
CXCL6	1.2	3.16573852	6.78278294	7.66644906	7.1825289	3.51596901	3.65945388
DUOX2	77.4	5.21956509	11.4290737	10.9703926	8.57065999	4.24580028	4.3634066
MMP12	135.6	7.66356977	11.3463686	10.37312	11.2464828	7.86680605	8.71372319
NCF2	24.9	5.52064932	7.14689388	7.35014807	7.14687635	6.07372858	5.19540848
IFNG	14	4.2393033	7.61617427	4.44169011	4.07496851	4.15000816	3.72243114
STAT1	1051.5	10.2746179	12.5812315	11.4402901	10.6484849	10.1160699	9.59089872
MNDA	0.9	5.37326367	7.53713454	7.682933	7.22510579	5.49399933	4.56901404
TIMP1	112.6	8.81239477	10.5706948	11.2890668	11.7676921	9.60060042	8.91498639
IFITM2	486.9	9.76064019	11.4149612	11.5081458	11.4561857	9.74233425	9.55547933
IL6	30.2	3.90187861	5.29585523	4.47774701	4.31771007	3.92342167	3.93644835
GNA15	5	5.52817946	6.38892627	6.81027356	6.75331983	5.45944672	5.43592258
SLC7A5	61.3	5.87056115	7.966711	7.11777093	8.05543059	6.26087801	6.44564903
CTSK	157.6	7.67866676	9.57448156	9.96215908	9.40714167	8.40845163	7.26998912
CXCL2	2.8	3.39634462	3.74297411	3.4398768	3.43442466	3.28085756	3.1999329
SLC2A3	60.1	5.78764855	6.98505781	6.19893498	6.71620042	5.63009039	5.22531413
CCL20	146.8	8.21576819	11.418539	8.54377528	6.78298811	7.00654416	6.49507561

CASP1	779.4	9.29316288	10.4819847	9.4735468	8.92548576	8.57711232	8.57327331
SPINK4	727.2	9.18698756	9.52259743	13.2734788	13.2375991	12.3814355	11.9319872
PLAUR	516.8	8.39769983	8.89149744	8.15615728	8.25136161	7.3568245	8.40591489
ICAM1	27.8	6.06657377	8.00728838	7.25999871	6.97410816	6.35803676	6.21890186
NOS2	33.7	5.47834559	8.48382261	7.18435348	5.38935284	6.07874407	5.78638844
PI3	516.2	8.69525922	10.8106701	11.019431	9.8802023	6.33661658	6.72394882
S100A12	10.5	3.5463882	3.52471627	3.98078077	8.16061275	3.4518421	3.18195952
TMEM158	66.4	5.28149452	7.41091463	7.59218513	8.11178868	5.57654945	5.76397084
WNT5A	73.5	6.5450079	6.80851582	8.97281253	8.82460859	7.09922891	6.51139639
GBP1	282.3	8.34256295	11.0094186	9.40937508	9.31442341	7.60766162	6.79419166
C4BPB	14.9	6.97530726	7.88900182	7.9461888	9.25808788	6.19423606	6.79614023
IFIT3	82.4	6.9357768	8.8617034	8.16576211	7.71938584	6.50201607	6.50192609
CEMIP	4.2	4.59566202	4.5414848	4.59408081	5.12514566	4.60512625	4.44403612
ANKRD22	319.9	8.91648315	10.3610338	9.45807769	9.33020927	8.52879601	9.18855486
REG3A	16.4	11.7816359	12.3413147	11.9671828	6.88210803	5.348459	3.65567154
PLEK	10.8	7.00896793	8.37867288	7.41941958	7.83219418	7.13068601	6.93315
IFITM3	1105.6	10.5850713	12.3440557	11.9204498	11.9418683	10.4342949	10.4207275
BCL2A1	12.7	5.2350419	8.13373271	7.20426991	7.83776594	5.65246859	4.38636815
LAMP3	16	5.49279382	8.77655573	6.8011578	7.32048476	5.6841741	4.22262402
UBD	98.5	8.28486786	11.2365467	9.23591783	9.8346791	5.75082184	4.64469417
GBP5	32.3	5.38540217	8.22767273	6.8954948	6.17460469	5.67355379	4.35165519
ACKR4	31.8	5.57823254	6.6000559	5.81046307	6.10404738	4.7222629	4.38157827
ADM	1032.9	8.34271582	10.5821737	9.50770163	10.4354606	8.35835182	8.73427431
PHLDA1	48.9	5.64477004	7.95800679	7.56070538	8.32525673	6.58628166	5.96898299
MMP7	23.1	4.67200004	5.325738	6.16805978	6.78666794	4.69473122	4.04313368
CXCL5	12	2.79340329	2.53345653	2.94417809	2.89236918	2.73975239	2.74879388
RAB31	122.9	7.3889049	9.16215079	9.73249656	9.50935941	7.83461762	7.79025924
CCL3L3	8.5	4.84318938	7.03966853	6.70819278	6.97370777	5.65941138	5.86669686
NAMPT	317	7.36474378	8.53638113	7.62236846	8.27597268	8.03662086	7.18233019
ACSL1	232.7	7.69549528	8.28132353	8.43880235	8.53199889	7.96291877	7.36012302
C4BPA	96.5	4.86146954	6.86941455	7.66942021	7.33905709	4.84769909	5.94141976
LILRB2	3.8	5.66134142	6.91081186	6.84312345	7.08952738	6.14633559	5.83817874
TCN1	39.5	3.84651045	4.542489	4.18084455	7.84559349	4.15143938	3.72733144
BACE2	225.8	9.05908634	9.84526813	10.0074112	10.2343453	8.77970081	8.74396461
RND1	22.2	6.24501652	6.83002537	6.51333212	6.40406038	6.27635028	6.57416416
IRF1	472.6	8.706053	9.98187436	9.10515396	8.60454483	8.61917725	8.2124765
TAP1	402.1	9.39026728	10.4408131	9.66235078	9.25505768	8.71486139	8.52760475
CXCR2	2.5	5.02102919	6.57947784	5.76344277	5.61324863	4.08834403	4.25809474
MAFF	116	6.38335696	6.71457306	6.2724591	6.26138344	5.7440446	6.1679247
CSF2RB	50.9	7.05159549	9.28372378	8.32005292	8.52743079	7.4736015	7.67199005
PDE4B	4	5.99381922	8.26567962	7.70758888	7.50022459	6.18668754	6.63397113
CCL2	29.6	7.00866826	9.05257768	8.94386505	7.99975347	7.66836962	6.91751588
CD274	22.1	5.36175994	6.34443649	5.38530822	5.13443674	5.52979436	4.72740361
TFPI2	1.9	3.29512041	2.8560454	2.96160862	7.41234986	3.1565742	3.74786975
CYR61	7.4	4.43313596	7.67783846	6.7812357	7.06664293	4.48366878	5.80773504
CCL4	56	6.42743253	8.22578006	7.11328214	7.41923205	6.45517284	6.18326005
CSF3R	42	6.43700951	7.04972012	6.71873864	6.82379009	6.80740028	6.28891382
KYNU	10.7	5.8234741	6.9951873	6.56283174	6.66342468	5.7650517	5.2045993
MMP9	36.9	6.97826523	9.364129	9.7530647	8.38394568	7.6756768	7.22490607
UBE2L6	217	9.14515937	10.8619446	9.8039983	9.19042246	8.74485856	7.69854714
MUC1	455.7	10.1380061	10.1143553	10.3918214	10.5574221	9.23205681	9.4262232
IL13RA2	30	3.35441691	3.66526566	4.19629087	8.41847166	3.80293006	4.56301411
PROK2	1.8	2.93669461	3.7234458	3.40528644	6.71499262	3.20172764	2.88962724
S100P	1068.4	12.2529755	12.2292375	12.6824614	13.2987769	12.5194191	10.8277926

SERPINA3	15.7	4.78475393	6.25440417	5.81837156	7.60626373	5.23520982	4.79438202
GBP2	239.9	8.88462146	10.1274259	9.37243035	8.91044302	7.6670625	7.91133327
COL15A1	96.5	7.82611834	8.28030585	10.0727446	9.92844106	8.21689727	7.62503692
REG4	161.7	8.85251116	8.75093446	11.886133	13.1466454	10.589849	8.60410049
GZMB	53.8	5.85642644	7.8163699	5.83979607	6.77882321	4.99261342	4.74956232
FOXQ1	33.6	5.4511877	7.21835303	6.87180347	7.54790283	5.56419073	6.08513709
LPL	8.6	5.32617551	6.14823525	6.7321879	6.00291384	4.20479389	4.4627156
TNIP3	1.4	3.39249684	7.72855343	4.79174052	4.02106178	3.3072299	3.23618821
C2CD4A	7	3.95074784	6.90166693	4.81991556	6.73849054	4.14578211	4.4139437
PCSK1	4.4	5.79993632	7.80105051	7.16554216	7.85972155	4.16865937	4.95118657
LPCAT1	41.3	6.06657377	8.0962199	8.11310701	8.22536675	6.08043688	6.41451582
CTHRC1	30.8	4.95849102	6.04203079	9.26413484	7.53948793	5.25567859	4.85492536
SRGN	8.8	3.29227414	3.3649945	3.29537856	3.59440571	3.21466918	3.33882038
EGFL6	3.6	3.58150024	5.27791776	6.38196009	5.5257926	4.1036874	3.29124097
C1R	57.4	8.30366009	9.93040218	10.4536388	10.2309327	8.73179964	8.23056885
DRAM1	65.5	6.39759776	7.628125	8.25631663	7.84604802	6.16459312	6.40519736
PLA2G2A	464.3	11.6034488	13.3886495	12.7258228	13.3922307	10.9272475	12.1814488
VNN1	24.3	4.74093525	5.93820305	5.88060297	6.17725089	4.57660485	4.50167539
FCGR1B	12.4	3.77740089	7.11313273	6.15653967	6.20703569	4.02366961	4.14814432
HLA-DMA	138.2	9.17848389	10.7955285	9.95793205	8.94453782	8.50989792	7.72151602
FCGR1CP	20.9	4.55671785	6.97856341	6.59422436	6.40977262	5.15240103	4.59960015
CCL11	46.1	8.10449029	8.66192693	10.4553533	9.97259888	7.9470814	7.7348055
PFKFB3	181	6.40724925	8.10709178	7.52400316	7.57131261	6.26499218	6.4626173
IL1RN	20.6	5.62707719	6.27509023	7.47538506	10.1227894	6.25641976	5.42062069
TREM1	5	4.86175329	4.72164693	4.58832237	5.6723874	4.7083453	4.42013719
FCER1G	44.2	5.84559482	8.28038185	8.0834885	7.9985933	7.12078105	5.79729608
COL1A2	362.6	10.5490099	11.2033599	13.0220244	12.034827	11.0402078	10.1638427
IFITM1	1534.5	10.7696558	12.4193958	11.9749077	11.5567405	10.5850491	10.7965512
INHBA	2.1	3.29255764	3.00138825	3.13865253	3.0652592	3.25675407	3.09780686
GPR84	1.2	4.1203945	4.96494701	4.89317048	4.87694143	3.85944528	4.20187319
GREM1	242.9	4.4063035	7.92129857	10.0102811	10.7002252	5.69246114	6.12669627
PLA2G7	36	6.18276619	9.226855	8.03577956	8.09981491	7.68060361	5.44685235
IER3	831	9.4762042	10.2491444	9.8009474	9.62149221	9.60896529	9.53630137
STC1	21.5	4.82033568	4.890657	5.94045002	7.35748488	5.36173955	4.829915
SLC7A11	29.6	4.82817984	4.5839989	4.83345332	5.49488489	4.65081432	4.67858921
TMEM45A	32.8	5.71787115	5.9671381	8.44380979	8.93218723	6.27509143	5.76104098
PDZK1IP1	708.7	8.20484092	10.2418946	9.67089166	8.41178626	7.56755959	8.12746256
TNFSF13B	58.9	6.45356753	9.69587894	8.49509415	7.51828593	6.8825367	6.35795964
SELL	32	4.97087845	7.71070959	7.54212377	7.63446676	5.0210711	4.07980782
GOS2	78.3	5.23961391	7.1170722	7.10856248	7.6609008	5.92610545	5.50634085
L1TD1	177.7	8.65541342	8.80854651	9.54002179	8.75031272	7.99986743	7.43146213
MIR8071-2	96.6	12.3285944	13.633291	13.0847033	14.4411459	11.897425	12.2590951
ADGRL4	67.7	6.02073381	6.93754976	7.88752287	8.00567881	6.24814263	5.78335415
MXRA5	117.5	8.48999687	9.78392956	10.0252843	8.97139558	9.11497279	7.84791969
CLDN8	643.3	8.07770517	4.11468501	4.59066908	4.20273686	7.34161895	10.0881303
GUCA2A	15855.6	12.9012603	8.69579036	11.2271547	11.3281417	12.3833545	12.6008742
AQP8	15077.2	12.7978407	7.58542386	10.4785782	8.91305924	12.9662286	13.1297392
ABCG2	3420.7	10.989314	4.33992827	7.47257685	9.14447446	11.0573113	11.170919
CHP2	6124.3	10.4978139	7.78708937	9.32585065	7.45660507	10.633126	10.2982927
PCK1	3906.8	10.9399094	6.93030958	8.90966257	8.83158567	10.7905514	11.0187096
HMGCS2	13668.6	12.5745324	7.90706407	9.67907385	10.2991688	12.0891478	12.9355087
SLC26A2	13689.8	13.362609	11.5399261	12.255787	10.9927052	13.5496323	13.7740768
GUCA2B	8208.9	10.5005974	5.89478761	9.33472496	9.34775631	10.0328789	10.8142606

CDHR1	69.3	6.59671	5.24603176	3.3563375	4.7673357	5.97910878	7.40614918
HSD17B2	7239.9	11.0971413	7.17844956	9.19798584	10.691568	11.1783428	10.8710169
ABCB1	1304	9.32849148	5.25459167	6.44282885	7.7198958	9.06532582	8.27721721
SLC16A9	1962.4	9.67146182	5.48723316	7.72175769	9.49538281	10.1456061	9.42533777
PNLIPRP2	34.6	7.39484916	4.02647902	5.35508681	5.15469754	8.41875234	8.10986141
SLC51B	2297	10.3027385	8.22068693	8.49152629	8.9325816	10.3447132	10.4586284
ADIRF	1880.6	9.95106621	7.89030009	8.21455303	8.88863626	9.54029619	9.68370505
MT1M	921.2	9.6772786	3.73675883	8.79982038	6.66003542	8.83280256	6.11868168
MEP1A	4808.1	11.2159312	8.74873047	10.8235441	11.0713834	11.4355795	11.2558623
MT1F	2845.8	10.6401148	7.80039802	9.99075053	9.52338791	10.1857129	8.91761254
DHRS11	2324.9	10.4187098	8.49786908	9.38508426	9.2749681	10.0804904	10.6356911
TRPM6	317.4	7.35037116	6.0163911	6.26888776	5.37629864	6.90125894	7.60636362
UGT2A3	899.3	6.13639358	5.52704385	4.5641759	4.51936159	8.91743506	8.19194501
SLC26A3	22632.6	13.8228495	13.1971463	13.4224548	13.6147759	13.979667	13.8569872

gene	CD	CD	CD	CD	CD	CD	CD
GSM901332	GSM901333	GSM901334	GSM901335	GSM901336	GSM901337	GSM901338	
MMP1	4. 78848489	7. 70862512	6. 88998268	6. 94436899	4. 68579001	4. 18249628	9. 35135628
MMP3	5. 40977041	9. 65705801	5. 20640301	5. 16537294	5. 31991443	4. 55063962	10. 3155053
REG1B	8. 67046749	10. 6832227	5. 07722838	6. 66003542	4. 13731833	3. 98379368	12. 3579914
REG1A	10. 5574184	12. 626795	9. 45134473	8. 67942536	4. 95977895	4. 39118536	12. 0099592
CXCL11	2. 97254535	6. 71863524	2. 69083401	3. 36831042	2. 56414869	2. 36322582	6. 67308123
CXCL1	7. 31283402	10. 7547688	5. 50180796	9. 30072245	5. 1570414	5. 19439035	11. 575821
CXCL8	4. 79066709	7. 50630266	4. 90066738	6. 1003399	4. 13694836	4. 84553338	9. 9629382
ID01	8. 30514215	9. 90575829	6. 53601279	7. 75239615	6. 00291384	5. 46161837	9. 72522042
S100A8	7. 51665571	11. 1953267	6. 13619682	8. 30505333	5. 70797897	5. 96923021	12. 4592373
IL1B	7. 00940724	8. 14554678	6. 55933907	7. 93679879	5. 78494425	5. 87373848	9. 72431349
CXCL9	9. 03846824	10. 9202561	6. 15156873	8. 16020269	5. 01269137	4. 84380156	9. 47269496
AQP9	5. 22263548	6. 89428362	5. 46163034	5. 48749109	5. 27292322	5. 44600676	8. 35438292
HCAR3	3. 74058265	5. 32689202	3. 54015876	4. 58683077	3. 81242983	4. 36828856	8. 3419023
DEFA5	9. 46423863	11. 7976341	7. 81026874	11. 2544592	7. 47747718	5. 64859861	13. 0964046
CXCL10	7. 47650397	10. 2727616	7. 3940804	9. 51827431	5. 40379334	4. 66796716	9. 68103537
LCN2	11. 8663539	13. 1313943	8. 91431905	11. 4383577	8. 54787866	7. 88286666	13. 5806258
PTGS2	2. 95982393	4. 45343081	3. 49430878	3. 35876123	3. 15288394	3. 45801804	5. 3398411
SLC6A14	5. 06850538	8. 78322802	2. 89933974	5. 60847846	3. 10780969	3. 3023299	10. 4497118
MMP10	3. 65840363	6. 29689094	3. 88667362	4. 2599094	3. 44094247	3. 27420219	7. 03575094
DMBT1	12. 5604667	11. 7062898	10. 208606	9. 71195634	8. 93622586	7. 15806728	12. 6185185
CHI3L1	7. 52650205	11. 7457698	3. 96313098	4. 00210199	3. 45051767	3. 55924021	11. 2851844
PLAU	6. 54075341	8. 66695498	7. 24916671	6. 87173064	6. 63591927	6. 76637644	9. 25441831
CXCL3	6. 87725562	10. 4840597	5. 1876871	8. 89327551	5. 30387391	5. 67472267	10. 5663478
S100A9	6. 8013676	9. 76877381	6. 49259068	7. 63631221	6. 30193837	6. 3616489	10. 9030587
FCGR3B	5. 55571861	8. 21787457	5. 3832185	5. 54040162	5. 37336202	4. 28136435	8. 21174681
COL6A3	9. 4524537	12. 0691455	9. 45979456	8. 86890846	8. 81944163	8. 78814525	11. 4918657
COL4A1	9. 32088878	11. 0017828	8. 92841521	8. 80085134	8. 34448803	8. 65917643	10. 990821
SELE	3. 42853095	4. 86150141	3. 53159259	3. 24049094	3. 02945642	3. 12619933	4. 0265342
CFI	6. 70705503	7. 14234002	5. 14215064	5. 61677403	4. 92283756	4. 23225266	7. 47186165
TNFAIP6	4. 66652552	5. 37465389	4. 49545121	3. 97480527	4. 10853316	4. 79971052	6. 8858096
DEFA6	8. 98312095	11. 5038658	6. 45719602	10. 598022	6. 37416844	5. 38562013	12. 3450696
WARS	8. 59496788	9. 95266828	8. 13643578	8. 1699764	7. 98571644	7. 54862734	10. 0455715
DUOXA2	8. 20119246	10. 1761951	6. 58015419	8. 65391538	6. 4583282	5. 950108	11. 4564454
CD55	9. 63723489	10. 0977228	9. 48453353	10. 436111	8. 61332906	8. 52836549	11. 646616
APOL1	8. 16330342	8. 26249657	6. 91944623	7. 74469975	6. 25141426	6. 3031546	9. 08503746
OLFM4	12. 6142372	13. 2003856	12. 1230632	12. 8226929	10. 7170103	11. 0399524	13. 0784603
CXCL6	3. 09591492	8. 20804079	3. 46252411	3. 47030801	3. 5578199	3. 27017089	8. 24533004
DUOX2	9. 72869585	11. 3885839	6. 39581675	9. 21870874	4. 37227573	5. 35781335	12. 3586697
MMP12	8. 32973667	11. 3956941	10. 1635704	10. 2465328	7. 12413701	7. 78261119	12. 2373257
NCF2	5. 48220987	7. 44830842	6. 01721553	5. 84501815	5. 44723833	5. 98301848	7. 72421293
IFNG	4. 35143025	5. 58677922	3. 94960392	5. 57772862	3. 74640491	3. 87420778	4. 47246594
STAT1	11. 0001846	11. 7310519	10. 0502851	10. 8126722	9. 66043175	9. 71415118	11. 4216148
MNDA	5. 97496212	8. 52468867	6. 02725779	5. 39264939	5. 53414343	5. 5372297	8. 55267419
TIMP1	9. 58955242	11. 6833382	9. 03525717	9. 06194245	8. 82923198	8. 83053254	11. 3290282
IFITM2	10. 3759829	11. 2969879	9. 84777697	10. 1493755	9. 66118167	9. 79518933	11. 4819242
IL6	4. 23050998	4. 99587217	3. 89958905	4. 09261475	4. 14514276	3. 7138715	4. 63141689
GNA15	6. 45332818	6. 75601595	5. 51026855	5. 9121247	5. 19990937	5. 55355617	7. 72957323
SLC7A5	6. 88336765	8. 13571358	6. 41293613	6. 93176367	6. 09953668	6. 10800416	7. 9719
CTSK	8. 59245235	10. 6717579	8. 23838986	7. 3423797	7. 76800712	8. 14231092	10. 1404514
CXCL2	3. 45257224	3. 54836591	3. 16791038	3. 48307268	3. 23592735	3. 09238302	4. 02242838
SLC2A3	6. 09782064	7. 04161882	5. 9194068	5. 88831623	4. 85241872	5. 33545648	7. 2466881
CCL20	9. 38194461	10. 4264979	8. 69039276	12. 1377283	7. 16095922	6. 55276619	11. 8212102

CASP1	9.26961142	9.45074724	7.92195121	9.65544756	8.26201251	8.44827388	10.3308371
SPINK4	12.622733	12.4392243	9.91286768	11.9334112	10.3582043	11.2577782	12.9063463
PLAUR	8.17249299	8.2762851	8.53859981	9.31385195	7.667729	7.76757846	10.2048617
ICAM1	6.18221605	8.07065719	6.69024186	6.93591958	6.23568559	6.45944989	8.59822612
NOS2	6.73085084	7.2292655	5.43817787	7.9230103	5.99191202	5.65038737	8.92824325
PI3	9.68070232	12.1012359	6.18600602	9.4423691	8.18862558	8.43969676	12.4847479
S100A12	3.38636427	5.72629598	3.49576702	3.77977036	3.43481045	3.21295937	8.32011053
TMEM158	6.13195961	7.64714099	6.22737447	5.9313674	5.82934711	5.99962937	8.63284698
WNT5A	7.72963619	8.16160707	7.7181788	7.33430222	5.94491128	7.13661575	8.27858532
GBP1	9.41827571	10.3271056	8.3331997	9.70259133	6.68181151	7.51933955	10.3972338
C4BPB	7.6691957	8.0298584	6.81008978	7.56823578	6.44275789	6.64683361	9.57046716
IFIT3	7.49322002	7.9495132	6.72444569	7.83606509	6.31337337	6.38431444	8.15337007
CEMIP	5.14663084	4.48673862	4.28556707	4.47680632	4.0941664	3.77204218	4.44469064
ANKRD22	8.91648315	9.06691817	8.98057972	9.72117053	7.58869328	7.26455749	10.0019677
REG3A	8.79199562	12.7823677	6.28848945	10.8175133	5.22757726	4.44653145	13.0603775
PLEK	6.99825544	8.94558885	7.57821857	7.48280038	7.01691044	6.25985322	8.46078566
IFITM3	11.1808164	11.8509406	10.437366	11.0378689	10.4570277	10.7695073	11.8993499
BCL2A1	5.92656317	8.15827876	6.44288281	6.36836283	4.92578319	5.07920265	9.03294749
LAMP3	6.98885674	8.4688811	6.61542276	6.6459963	5.77695747	4.90260054	8.60453357
UBD	8.88056018	10.5453184	7.19906442	9.07972072	6.0851961	6.04901794	9.97611221
GBP5	6.03022242	7.22141546	5.43025417	5.72400281	5.03055649	4.74502674	7.10620363
ACKR4	5.3283341	4.91819187	4.52804161	6.3232676	3.98687525	4.00981358	5.94085274
ADM	9.50297134	9.76007312	8.95504134	10.5318379	8.26826433	8.23382054	11.2869586
PHLDA1	5.32141163	8.63095454	6.71241373	6.17080654	5.76266497	6.12598089	8.48354413
MMP7	5.26474643	7.83541092	4.76998124	4.93916147	4.52217765	4.07276629	7.51834532
CXCL5	2.67239504	3.09966988	2.6286901	3.13469397	2.54892342	2.81694595	2.9495249
RAB31	7.8537858	9.32533241	8.05945357	7.11484907	7.48719082	7.62374548	9.65609178
CCL3L3	5.72011943	7.0706888	6.49546702	5.97846243	4.90513368	5.64242268	7.94964784
NAMPT	7.52390649	8.12107908	7.81900261	8.29199145	7.21305871	6.06390817	9.38214634
ACSL1	6.89237837	7.59555962	6.66525105	7.37901768	7.11366566	6.92259113	8.69302125
C4BPA	6.28263827	7.1854921	5.50926819	6.58365622	6.16507392	5.22877659	10.352732
LILRB2	6.67898947	7.32102638	6.27504442	6.2655218	5.6458419	6.03312654	7.33343465
TCN1	4.21355878	7.04701639	3.8458098	4.00989965	3.70179388	3.81812421	7.21599057
BACE2	9.58220001	9.2740877	8.35686805	9.25590236	8.04010713	8.99709527	10.0311716
RND1	6.6291708	6.97695696	6.92154728	7.24364607	6.55557052	5.86459697	7.80408854
IRF1	8.69505141	9.11918994	8.29640725	9.43890897	7.95536485	7.92335191	9.5393497
TAP1	9.53643715	9.87284881	8.8504955	9.6164392	8.30288502	8.30570786	9.88222991
CXCR2	4.85830945	6.22864667	4.80286	4.91310508	4.21073155	4.21622583	7.30767845
MAFF	6.2134314	6.39966249	6.50176932	7.09682607	5.64266158	5.75344616	7.49157291
CSF2RB	7.36019644	9.17913382	7.76500382	7.3093851	7.2463156	7.67664682	9.3484582
PDE4B	7.20068739	8.51973715	6.9070986	6.56494357	5.91228728	6.22169589	8.91027491
CCL2	7.52012371	10.1881218	7.7479927	7.6709601	7.00401792	8.2148404	9.50969631
CD274	5.95387877	5.7731646	5.20440805	6.03141891	5.29215007	5.24779788	6.17796751
TFPI2	3.33626976	3.06423245	3.38439151	3.22365149	3.0731051	3.07709987	3.59407621
CYR61	3.94882822	10.195975	5.47562417	4.95627018	4.34667798	6.06012248	7.40647285
CCL4	6.58117306	8.14028598	7.00873441	7.2730977	5.94981765	6.28011062	8.61180704
CSF3R	6.4255826	6.68375454	6.34522211	6.82384899	6.42632424	6.40166416	7.29310677
KYNU	5.62648316	7.25657683	5.74874645	5.34076672	5.34318062	5.77511848	7.62205708
MMP9	8.71014075	10.2794592	7.97266553	7.6088306	6.80992796	7.46972319	10.0233775
UBE2L6	9.72952427	10.0670063	8.55483716	9.58192528	8.05488486	8.40108091	10.1540528
MUC1	10.1766308	9.34184104	8.73777442	10.0012824	9.01329463	8.26044104	10.2412529
IL13RA2	4.0937498	4.85159989	3.8733081	4.36187704	3.39083696	3.45182296	5.13970078
PROK2	3.05283375	4.31897931	2.89628206	3.28911148	2.92636499	2.81042456	7.70256373
S100P	12.1272461	12.307201	10.6278655	12.0195806	8.77503022	10.1351647	12.3912556

SERPINA3	4.84699977	7.0952559	5.38750751	5.01839586	4.97534986	5.41404575	7.63567899
GBP2	9.23727951	9.91390267	8.55644762	9.21765166	8.23199157	8.24588625	9.53380256
COL15A1	7.88720678	9.87938567	8.49956969	7.75517862	7.84311109	8.25761514	9.64966973
REG4	10.9550142	11.2950596	8.55736501	9.14920916	7.06953652	6.92959047	10.8678624
GZMB	5.44338481	7.37212212	5.52012257	7.54515953	5.11343924	4.16224338	6.57013939
FOXQ1	8.05361406	7.87712121	7.20676858	6.10016068	5.67285215	5.67026572	9.2268317
LPL	4.41027264	5.5012783	4.31131088	3.98421507	3.79187634	4.20235777	7.87636189
TNIP3	4.06894077	7.56059074	3.63163352	6.57718146	2.81194893	3.46670827	9.33676037
C2CD4A	4.18827553	5.91676501	3.77325315	4.91675803	4.0959126	3.92209206	6.77350683
PCSK1	6.58373231	8.05482843	5.2608024	4.59558227	4.89621744	4.23101478	7.93222393
LPCAT1	7.43921255	8.76727372	6.57501477	6.54851574	6.10894401	6.75227868	8.5076172
CTHRC1	5.3404195	8.59661107	5.90112964	5.04540275	4.06067356	6.04984026	8.24588625
SRGN	3.21479898	3.77574352	3.20619954	3.43224263	3.3649945	3.50344865	3.95821687
EGFL6	3.99936864	6.37192116	3.69222637	3.79402573	4.43087372	4.08684127	5.8032026
C1R	9.10632589	10.8035163	8.78047105	8.0310543	8.42279733	8.2991579	10.2722073
DRAM1	7.33500359	8.53476703	7.03786146	6.79549539	6.43089937	6.54270353	8.28014699
PLA2G2A	12.2909011	12.4195657	9.73627419	11.9278516	8.94035713	10.9319171	11.4768838
VNN1	5.33950857	6.16519766	4.65439891	4.81619087	4.56813671	4.60807039	8.09513493
FCGR1B	4.84270296	6.91648176	4.00006865	3.8176603	4.42138823	3.75534852	6.12979826
HLA-DMA	9.86394764	10.1983142	8.90358875	8.46998002	7.80545628	8.28925963	10.0894375
FCGR1CP	5.82998508	6.86330779	5.1060239	4.72232227	4.72404266	4.76746101	6.06313178
CCL11	8.6663779	10.5812975	8.85948652	7.05383656	7.13508143	9.131222	9.68709457
PFKFB3	6.71016823	8.16541448	6.74692972	6.90054693	6.63793965	6.84717807	9.40767118
IL1RN	5.71387572	7.73786055	5.33316207	6.96500138	4.51200722	5.82965586	9.1238057
TREM1	4.66050017	5.24425559	4.55693273	4.5854196	3.99881111	4.25134916	5.17864198
FCER1G	6.48614331	7.91433702	7.43749148	5.00574695	6.67163301	6.88693134	8.04304051
COL1A2	10.9941808	12.58639	10.8300221	9.49781268	10.4544149	10.045926	12.3212835
IFITM1	11.3816178	11.8516093	10.667814	11.3096657	11.2120995	10.6397918	11.8668275
INHBA	3.02839157	2.80156996	3.18095538	3.39546262	2.99133269	3.27420219	3.04918174
GPR84	4.8962633	5.17474809	4.13479421	4.2594782	4.17727245	3.8821441	5.34127006
GREM1	5.27584002	11.7092002	5.95837027	5.35759375	6.15319596	5.80660764	10.3115445
PLA2G7	6.85225221	8.74560662	7.49955911	6.27987255	6.34587592	7.0617607	9.12120513
IER3	9.76557523	10.4820172	10.3387446	11.0665159	8.77672609	9.45314316	10.551427
STC1	4.60514117	5.29305969	5.27765294	5.51266471	4.98945999	4.66779026	7.4943576
SLC7A11	4.25310291	5.1002453	4.34534072	4.72651852	4.51325432	4.04333407	5.08527136
TMEM45A	5.3622206	7.87155077	6.38749828	5.63272396	5.95238038	6.17594653	7.74010492
PDZK1IP1	9.26397722	10.0102907	7.62893867	9.23993644	8.68067959	7.83185683	11.2155155
TNFSF13B	7.77015357	9.62231866	7.39111431	6.91720341	6.51614818	6.71864714	8.69500351
SELL	6.37896297	9.27438045	6.43791105	6.35569633	4.42933535	4.70671441	9.00156229
GOS2	6.26721701	7.99976141	5.80340569	6.98706839	6.64653776	6.52549132	9.11162042
L1TD1	9.27867747	8.98053466	8.51783585	7.91043141	6.31172274	5.75658385	8.71026491
MIR8071-2	13.0357735	14.4379619	11.9704698	11.0396898	11.3984811	10.3750381	14.4466861
ADGRL4	6.29757008	7.68049811	6.44751173	6.53827006	5.64605488	5.9403817	7.71765707
MXRA5	8.5946905	9.9681236	8.87011246	7.36013032	8.18721737	8.23153453	9.77834527
CLDN8	6.00345426	4.04243864	9.73713731	6.94142334	9.67458948	10.0671566	4.27473465
GUCA2A	11.602571	7.15110501	12.2900679	12.9137401	12.6776401	12.3491882	7.99258844
AQP8	10.7574407	4.13179137	12.8275649	12.2120722	13.2138159	12.1810071	8.23634843
ABCG2	7.48519626	5.12319152	10.4876175	9.3530283	10.3688547	9.5021043	6.42258438
CHP2	9.69147039	6.33630266	10.6385049	10.5701522	10.8579356	10.8287266	7.02663153
PCK1	10.568573	6.27256441	11.1220155	9.32578592	11.1370603	10.7754152	5.16425903
HMGCS2	11.5565205	7.74462714	12.7755	12.2554673	12.4825525	12.0234496	7.41824182
SLC26A2	13.2843212	9.21914904	13.4419725	13.4850408	13.8986725	13.5191179	9.26728468
GUCA2B	9.11919275	5.5827632	10.355717	10.8793962	10.588077	9.99307348	6.05291903

CDHR1	4.5290552	4.75804479	5.43059824	5.84559482	7.65513125	4.6228354	4.36182274
HSD17B2	10.3922978	7.54468854	11.4896372	10.4450537	11.1925024	10.7975824	8.68802012
ABCB1	7.99005369	5.21861011	8.7861508	7.53991033	9.07531681	8.64457284	6.05482419
SLC16A9	8.35099309	6.60106572	9.25766399	8.46794646	8.96792252	9.46297305	6.70961723
PNLIPRP2	6.13335464	4.83788099	8.00465485	4.18065139	8.15429623	8.72036213	4.26563483
SLC51B	9.6665557	7.34120931	10.3260107	10.6226158	10.2025191	10.074178	8.05386112
ADIRF	8.44080568	8.42241375	10.1055185	10.5299608	9.96901562	9.9004425	7.64491074
MT1M	10.069693	6.13206518	7.82788212	6.15275757	10.3839325	11.3885951	3.95337996
MEP1A	11.3380478	8.77383222	11.349351	11.3681287	11.962869	11.4972493	9.80749516
MT1F	11.0386	8.63310648	9.53672435	8.77787529	11.6732081	12.0918135	7.32332992
DHRS11	9.80755021	7.57329538	10.3541219	10.4000078	10.6674369	10.5843855	7.81037673
TRPM6	6.52673229	5.37114099	6.66714789	6.85567491	7.57251912	7.21978206	5.55023577
UGT2A3	4.70909657	3.26269455	7.59146421	7.35662866	7.64407933	7.4656191	3.74305946
SLC26A3	13.5197319	12.0553038	13.7491561	13.8564304	13.9108739	13.6160039	13.3493929

gene	CD	CD	CD	CD	CD	CD	CD
	GSM270786	GSM270787	GSM270788	GSM270789	GSM423010	GSM423012	GSM423013
MMP1	11502.9	5601.5	41360.3	460.7	1155.3	2654.9	1180.5
MMP3	20026.4	10273.3	43553.7	445.6	934.8	2343	1215.9
REG1B	31968.8	2182.5	31525	23981.7	1282.2	9351.2	6104.3
REG1A	31349.7	2621.5	34398.9	36038.2	6708.8	11645	6957.8
CXCL11	1877.4	101.7	5396.5	293.5	224.1	74.2	384
CXCL1	19791.4	1105.1	15620.7	2156.9	1037.1	2007	2219
CXCL8	10267	3892.4	28847.1	20624.6	481.8	356.7	2698.2
IDO1	7524	403.4	27585.8	1926.6	529.4	163.2	8705.9
S100A8	29181.4	367.2	39682.3	22352.6	567.4	260.8	873.2
IL1B	17217.6	1241.1	28821.2	8151	328.2	212.1	1587.3
CXCL9	10335.5	1899.4	17607.9	2196.3	166.3	137	2294
AQP9	3071.7	23.2	12617.4	1417.6	26.2	71.2	65.4
HCAR3	13668.9	56.5	36704.2	9401.7	65.5	61.7	168.3
DEFA5	6921.3	19559	6868.2	8964.6	7988.4	2764.5	6112
CXCL10	17171.2	1564.4	13610.5	3066.5	305	193.1	1604.9
LCN2	29257.3	7206	22464.3	9718.7	10980.6	18484.8	6915.4
PTGS2	207.5	166.8	604.2	307.2	55.7	4.4	158.1
SLC6A14	13122	56	3353.9	360.8	838.3	912.4	1354.5
MMP10	1178.4	1815.8	8310.1	183.2	116.7	194.6	369.2
DMBT1	30905.6	2463.5	22348.8	30835.1	6077.3	9605.8	13093.4
CHI3L1	4477.4	655.7	17211.4	540.1	152.2	640.8	814.2
PLAU	11285.6	1274.1	18458.4	1347.9	153	205.6	876.6
CXCL3	9942.1	474.1	6096.1	417	588.8	562.5	1886.7
S100A9	11699.1	190.9	17578.6	3701	114.2	325	271.8
FCGR3B	9795.5	162.6	21060.5	2007.5	78	59.6	179.5
COL6A3	8354.4	3432.2	23435.7	4083.7	403	2251	655.3
COL4A1	7619.4	5660	16988.5	4357.9	833.6	1245.7	675
SELE	617.8	4.6	617.8	29.4	95.7	32.5	56.1
CFI	589.6	161.9	490.3	542.9	208.5	185.4	489.8
TNFAIP6	2778	122.7	14374	988.1	45.9	90	46.3
DEFA6	2492.4	11442.6	2803.8	3374.6	4278.9	1064.2	3532
WARS	5056.2	1093.4	13424.4	1745.2	503.4	306.4	2339.1
DUOXA2	9945.7	271.1	6224.1	1015.7	1650.2	2260.7	693.6
CD55	17697.3	1782.4	9309.1	7091.2	7582	3009.2	5663.9
APOL1	2202.6	679.8	7921.5	2075.8	273.4	262.3	883.7
OLFM4	24740.4	10675.5	34868	30888.4	20268	19183.1	11622
CXCL6	2289.9	161.7	6779.3	275.4	39.5	183.4	222
DUOX2	16383.9	1697.6	13754.1	2865.1	8639.5	7407.7	2364.8
MMP12	21756.1	5993	34333.6	6866.7	1923.7	1854.7	8374.8
NCF2	2299.4	304	5622	775.5	44.5	78.4	195.6
IFNG	579.8	38.3	1924	111.1	35.7	19.4	135.1
STAT1	11949.3	7759.3	21061.2	13068.1	2108.1	1477.9	4558.2
MNDA	4616.4	336.6	7492.9	1244.1	60.8	92.6	164
TIMP1	23248.4	5993.6	29847.7	4864.5	1991.9	3636.1	891.8
IFITM2	20665.1	8097.3	29203	11082.4	1142.5	3047.6	2505.4
IL6	728.4	162.9	3047.4	105.3	63.2	36.8	108.7
GNA15	1522.7	265	1394.9	267.5	123.9	121.6	104.6
SLC7A5	1584.5	431.3	1003	391.2	73.3	116.1	78.9
CTSK	4418.1	2364	8108.9	1620.9	356.3	941.5	427.3
CXCL2	134.6	3.8	153.5	13.1	53.4	10.7	50.5
SLC2A3	1001.8	244.4	4341	735.8	22.2	97.6	145.2
CCL20	21994.1	1931.2	1107.4	8471.6	972.6	3051.9	3258.2

CASP1	5849.2	2119.6	5232.7	3864.4	1075	1166.6	3139.5
SPINK4	9513.2	1237.3	12681.1	23894.4	19314.6	7240.8	1897.5
PLAUR	11388.4	1730.2	8763.1	4407.7	614.4	614	2095.2
ICAM1	4434.6	449.4	6530.8	819.4	118.6	84.4	200.5
NOS2	6333	236.4	3393.9	889.4	444.3	516.6	569.8
PI3	19618.9	780.8	18780.5	4008.1	2473.2	10981	4380
S100A12	2616.8	65.3	4159.6	2900.9	66	22.7	40.6
TMEM158	2014.6	662.2	3036.4	429.6	171.8	398.1	171.3
WNT5A	1724.6	1163.2	4810.7	1289.9	307.3	282	365.2
GBP1	11430.8	2395	23607.7	5095.6	867.9	691.8	2541.2
C4BPB	4778.3	93.8	1344.2	784.3	332.4	550.4	730.2
IFIT3	2193.8	601.9	7759	1195.2	317.2	187.8	663.8
CEMIP	18.8	6.6	37.2	16	4.4	2.3	4.5
ANKRD22	9211.8	1031.5	4743.5	2655.9	808.7	929.1	2174.7
REG3A	15744.3	10827.9	9725	7324.1	2390.5	4393.2	5810.5
PLEK	4729.9	471.4	28562.5	3407.4	323	307	181.6
IFITM3	18535	8694	24273.9	11474.4	2165.7	3198.8	4839
BCL2A1	7768.5	320.4	18537.9	3850	274.2	294.9	287.8
LAMP3	1714.8	498.8	5009.1	513.7	119.5	94.7	342.6
UBD	9223	1814.2	13030	5252.2	2213.7	1581.8	3612.7
GBP5	960.4	225.2	6126.9	743.9	101.4	80.1	190.1
ACKR4	209.7	159.1	803.2	604.1	261.2	128.7	554
ADM	16668	2645.3	17244.9	7578.5	1256.5	1671.6	3582.1
PHLDA1	3926.1	618.5	3510.8	598.9	257.9	262.1	616.6
MMP7	1292.4	77.5	326.2	54.7	341.9	790.9	198.4
CXCL5	21.8	6.9	87.5	30.8	2.8	17.9	2.9
RAB31	4093.5	1528.4	9324.6	1949.3	191.4	617	351.2
CCL3L3	1570.2	334.2	8552.2	2168.9	44.2	55.9	184.6
NAMPT	3974.7	346.4	7256	1140.9	287.5	227.8	1069.7
ACSL1	4605.6	656.3	14987.9	3336.8	304.8	435.7	678.1
C4BPA	3169.5	91.3	640.9	1530.4	284.7	607.8	395.2
LILRB2	1603.5	139.2	2743.1	491.1	32.8	19.2	98.4
TCN1	733.8	166.2	2274.6	72	1074.4	339	54.1
BACE2	5034.1	2305.2	4828.8	4820.4	2042.8	2006.5	1226.3
RND1	818.5	191.8	365.7	255.5	58.5	88.7	159.7
IRF1	8244.8	2617.6	11538.7	4723.2	593.9	790.1	1447.4
TAP1	8482.9	3955.2	14188.7	8063.8	1503.7	1240.8	2998.9
CXCR2	1789.9	103.7	2666.6	328.5	55.4	31.7	63.6
MAFF	1185.7	506.3	919.2	810.8	127.9	179.2	201.6
CSF2RB	5852.9	1330.9	15637.5	2225.8	444.2	436.3	549.5
PDE4B	5749.9	621.1	9412.6	1418.9	202.6	179.1	259.3
CCL2	7632.1	1329.1	2174.7	1046.3	82.4	115.2	110.8
CD274	491.9	93.3	1902.2	223.3	36	58.4	110.2
TFPI2	123.2	80.6	407.4	709.8	46	12.7	25.3
CYR61	3818.4	376.1	2901.8	279.1	91.2	122.4	422.5
CCL4	4143.7	389.4	8020.2	1638.3	118.3	96.6	178.5
CSF3R	2033.2	399.7	5001.1	737	192.8	150.5	109
KYNU	972	140.5	1536.6	150.1	118.2	113.7	103.6
MMP9	5978.9	2037.1	15790	1728.4	432.1	876	1053.2
UBE2L6	4703.1	2547.9	8125.1	4696	658.2	612.3	2212.2
MUC1	11353.1	6274.4	11379	11997.5	2689	2149.3	2899.1
IL13RA2	330.6	323.2	2026.6	50.6	57.9	31.1	32
PROK2	2180.7	3	7428.5	1018.6	24.3	29.9	23.8
S100P	13729	2960	16041.8	11038.6	14472.7	3251.5	5053.6

SERPINA3	5253.8	158.5	556.7	312.5	560.4	569.4	53.5
GBP2	3977	2256.8	7970.4	4089.5	462.9	416.9	1394.8
COL15A1	1791.6	1894.2	9576.5	1273.3	551.2	642.1	163.4
REG4	5163.7	476	11562.8	8748.4	18476.4	4382.9	1673.4
GZMB	5870	183.6	3519.9	384.5	64.1	88.5	181
FOXQ1	1769.1	674.8	1758.7	524.4	704.1	552.8	147.7
LPL	254.7	173.1	319.4	34.3	122.7	203.6	82.1
TNIP3	12995.4	67.4	2122.1	193.6	87.8	541.3	580.4
C2CD4A	2410.3	93.9	538.7	422.6	363.1	183.9	293.8
PCSK1	556.5	247.5	1050.2	325.4	380.7	192.2	123
LPCAT1	2795.8	536	2741.2	979.2	482.2	427.8	285.1
CTHRC1	905.2	391.7	4253.8	159.6	199.5	715.4	76.6
SRGN	56.9	4.7	276.4	12.3	43.8	7.8	7.7
EGFL6	228.1	176	2959	126	78.6	139.4	70.5
C1R	4635.2	3356.1	8316.7	3470.3	273.1	597.1	262
DRAM1	2566.1	1032	3508.7	1008	179.6	243.1	293.2
PLA2G2A	29077.1	8694.5	35485.5	39292.1	18121.7	6637.7	15672.6
VNN1	341.7	35.8	292.8	189.7	894.1	384.5	12
FCGR1B	1280.4	181.8	2547.1	556.7	60.3	39.4	118.1
HLA-DMA	5258.3	3183	6270.8	3420.9	1192.8	729.1	2591.8
FCGR1CP	1203.2	227.9	2658.6	673.9	24.5	35.3	129.3
CCL11	1684.2	1303.7	2103.2	1636.4	115	186.4	92.3
PFKFB3	4144.7	681.6	6196.6	1683.8	304.9	255.5	479.9
IL1RN	14064.3	173.2	30788	5107	1123.7	273.1	342.7
TREM1	1420.2	17.5	4329.4	494.5	2	25	27.3
FCER1G	3870.1	1063.2	7800	1891.1	69.3	83.2	198.5
COL1A2	15632.5	9571.8	32578.9	8938.4	1791.9	6052.5	997
IFITM1	19825.4	12506.8	29566.8	21033.7	2168.9	3839.6	6194.3
INHBA	39.4	5.7	174.1	33.6	13.1	14	29.6
GPR84	1097.9	56.1	1642.3	486.8	2.7	25	16.3
GREM1	3058	496.2	1368.8	141.6	197.7	550.8	176.5
PLA2G7	3271.8	745.6	8543.7	1692	119.5	107.6	913.6
IER3	14076.4	3188	14410.1	9229.2	1671	1182.1	6277
STC1	408.8	391.8	694.7	15.5	110.5	77.4	201.5
SLC7A11	219.9	2.9	290.5	43.6	110.7	46.5	71.9
TMEM45A	475.1	562.9	1990.1	581.2	366.2	172.9	51.4
PDZK1IP1	8609.6	2207.8	6068.1	1967	3575.5	2711.6	1453
TNFSF13B	1520.8	775.6	3711.9	1049.3	170.8	156.8	341.4
SELL	3364.5	356.6	5516.7	806.5	419	299.5	60.7
GOS2	6239.4	484.5	14253.7	4055	136.9	190.4	237.9
L1TD1	1738	682.6	264.5	2345.2	306	268.5	476.1
MIR8071-2	26851.6	28201.4	50218.7	26278	27654.5	26308.7	2695.9
ADGRL4	309.6	297.9	826.7	193	105.4	154.3	86.3
MXRA5	2624.4	1737.7	7416.2	2315.6	1345	805.7	222.7
CLDN8	26.5	5781.3	43.4	478.6	42.4	29.6	203.9
GUCA2A	10770.6	23139.1	156.8	21213	602.7	1881.6	1652.7
AQP8	3052.4	17359	66.7	5652.6	95.5	1585.1	395
ABCG2	246.8	1985.2	69.6	564.3	477.6	308.8	94.2
CHP2	750.2	8481	167.6	6277	518.3	647.9	1615.4
PCK1	169.1	8738.7	97	4337.6	695.3	608.9	1486.4
HMGCS2	3546.5	14610.1	221.7	5583.5	415.9	635.4	1149.5
SLC26A2	2565.2	30333.6	967	13475.3	1876.2	5162.6	4569.7
GUCA2B	4136.3	4804.8	5.2	6019.4	120.7	551.1	247.2

CDHR1	174.3	693.2	25.2	190.6	98.2	45.8	25.7
HSD17B2	1444.2	5982.1	1521	6726.3	1867.6	1136.2	328.2
ABCB1	311.4	2716.7	154.2	2187.7	198.8	243.4	48.4
SLC16A9	351.4	1248.7	63.7	411.2	147.7	249.2	160.2
PNLIPRP2	9.2	85.5	102.3	230.4	3	59.8	60.2
SLC51B	1218.6	3054.6	210.5	4079	371.5	286.2	1125
ADIRF	662.8	2105.8	158.9	1300.8	157.6	193.3	339.2
MT1M	2866.3	3809.1	559.2	1410.3	181	90.6	624.6
MEP1A	2512.1	10260	660.7	8263.3	2158.1	1350.4	711.4
MT1F	6520.9	10812.6	2965.3	7546.7	901.4	485.5	1187.4
DHRS11	2177	7178.8	533.1	4673.1	622.1	743.1	859.4
TRPM6	117	445.6	127.9	244.6	68.3	46.6	104.7
UGT2A3	254.3	2246.9	25	766.4	23.2	175.3	519.9
SLC26A3	26222.6	39125.5	8736.5	41112.1	8877.8	21996.1	12750.1

gene	CD	CD	CD	CD	CD	CD	CD
	GSM423015	GSM423017	GSM423019	GSM423021	GSM423023	GSM423025	GSM423027
MMP1	890.2	4317.3	568.3	2532.8	1211	469.4	5608.8
MMP3	1192.2	2544.7	961.4	3856.8	2512.9	925.8	3504.4
REG1B	11604.2	1294.2	3811.7	12964.9	16440.2	11727.7	10896
REG1A	12178.9	3927	8031.6	14841.8	17048.3	11714.8	12713.6
CXCL11	626.8	131.6	2016.1	495.2	1453.3	178.6	198.3
CXCL1	1963.5	652.7	2507.1	1781.2	1543	2195.3	1046.4
CXCL8	952.7	1553.1	912	2445.6	745.6	662.9	1071.7
IDO1	6499.2	227.6	7264.2	2080.9	5244.9	2717.4	697.6
S100A8	792.3	1118.7	1281.5	1037.1	969.8	501	1812.5
IL1B	1033.7	606.3	810.8	1792.8	1513.8	797.7	401.9
CXCL9	451.6	252.2	2957.6	1072.5	720.5	635.4	490.7
AQP9	70.5	34.6	49.9	87	79.9	48	135.3
HCAR3	208.2	209.3	169.9	190.9	342	97.3	142.4
DEFA5	401.6	2148.6	474.8	1511.6	9088.3	1157	7291.3
CXCL10	589.5	219.6	3183.5	1212.6	948.6	433.6	379.4
LCN2	8870.2	3876.7	7886.5	9762.5	8541.1	11735.5	5946.6
PTGS2	41.4	4.1	10	143.4	17.2	58.8	49.7
SLC6A14	2787.9	293.6	4384.8	2147	2197.7	2525	759.4
MMP10	165.4	120.2	161.7	579.6	72.7	67.2	65.6
DMBT1	9336.7	1254.6	8015.5	10504.6	13161.6	10589.5	5957.4
CHI3L1	309.4	846	188.8	450.4	338.5	354.6	854.1
PLAU	207.4	171.9	275.4	341.4	189.6	154.6	146.6
CXCL3	971.7	201.2	2727.6	1070.3	760.5	1559.9	506.2
S100A9	365.4	296.7	352.7	456	346.5	350	563.5
FCGR3B	61.7	182.7	152.2	168.9	228.8	99.5	220
COL6A3	311.3	1046.3	409.7	433.1	382.6	274.8	1056.7
COL4A1	333.8	1497.5	569.1	526.6	353.1	354.8	814.4
SELE	20.8	56.7	56.3	138.4	38.4	60.5	114.5
CFI	535.6	75.6	180.2	196.5	547.2	257.8	311.7
TNFAIP6	79.8	247.9	104.4	155.4	77.9	68.6	224.1
DEFA6	320.3	719.2	224.5	1191	6207.3	860.7	4995.6
WARS	1995.1	384.7	2971.3	1083.6	2454.8	668.7	459
DUOXA2	1468	252.9	1179.6	1276.4	1476.3	1619.8	538.6
CD55	5725.2	1587	2928.3	5235.9	7427.8	3371.4	1670.4
APOL1	1362.1	169.7	832	345.2	1297.7	601.5	409.6
OLFM4	9821.4	8082.7	11785.8	10504.2	12018.7	11302.5	9980
CXCL6	93.7	116.2	210.1	275.5	42.5	156	375.9
DUOX2	4999.1	712.2	3419	3538.9	5102	3889.9	2401.8
MMP12	2277.9	2242.1	3792.8	2780.2	1964	2700.5	932.9
NCF2	7.4	71.2	90.5	88.2	84	54.8	97.2
IFNG	47.8	13.3	185.6	113.7	30.6	45.4	39.6
STAT1	4051.7	1993.3	5175.3	2990.4	4165.1	3278.3	3046.9
MNDA	90.2	112.5	177.6	93.1	90.5	102.1	141.5
TIMP1	1118.6	1635.9	1452.8	1052.4	1094.8	977.7	999.2
IFITM2	2513.2	1345.5	2228.9	1861.1	2445.5	2088.9	1742.8
IL6	55.7	175.2	95.5	227.6	60.2	90.5	79
GNA15	148	151.5	125.4	79.6	102.6	58.5	67.5
SLC7A5	149.3	121.5	128.9	114.8	142.3	32.2	121.8
CTSK	181.4	826	265	253.4	271	175.6	565.7
CXCL2	22	1.8	54.5	19.5	12.1	1.3	7
SLC2A3	100.5	20.3	136.3	137.6	59.5	76.7	111.8
CCL20	4908.1	2192.9	6217	4132.1	4130.3	5710.1	2285.1

CASP1	3213.6	675.2	3353.6	1772.3	2663.9	2371.3	1606.7
SPINK4	7328.4	11971.5	2214.9	6199.1	10702.7	6615.8	9649.4
PLAUR	2653.4	1224.9	1617	2356.7	2177.9	1034.3	551.9
ICAM1	194.4	149.1	432.6	382.9	283.8	110.6	131.4
NOS2	909.1	67	1018.7	626.7	1218.1	488.9	163.8
PI3	5328.9	2131.8	4911.9	5353.4	2956.3	6986.9	3556
S100A12	46	58.1	42.8	33.8	33.5	68.2	55.2
TMEM158	153.4	385.3	85.2	179.5	105.2	29.3	135.7
WNT5A	221.5	627.4	303	294.3	741.4	221.8	455.6
GBP1	2261.3	729.4	3204.8	1601.8	2308	1492.5	1512.2
C4BPB	572.6	187.5	441	699.5	624.8	446.2	286.8
IFIT3	598.9	160.2	918.5	283	576.2	391.7	330.9
CEMIP	3.6	11.6	6.7	7.3	10	5.2	5
ANKRD22	1609.4	948.6	1727.3	1473.8	1511.1	1367.3	652.1
REG3A	674.4	1097.1	110.7	1131.8	8036.5	3747.6	6226.5
PLEK	130.3	191.1	117	160.5	353.8	80.9	117
IFITM3	4348.5	2313.2	5531.2	3662	5854.1	4174.3	3118.9
BCL2A1	194.9	117.1	291.8	268	170.2	138.5	207.1
LAMP3	91.5	214.8	242.2	122.4	199.1	157.2	182.3
UBD	1937.6	1018.4	5965.4	2089.1	2521.7	1800.9	2027.6
GBP5	46.6	113.6	207.2	109.8	118	72.5	115.6
ACKR4	438.9	169.9	295	189.2	381.8	212.1	314.7
ADM	5388	807.9	4833.3	2908	5009.9	4324.5	1621.8
PHLDA1	538	202.7	303.2	553.1	261.1	212.2	219.1
MMP7	91.4	413.1	155.1	180	151.6	371.5	201.7
CXCL5	0.7	43.3	103.6	20.6	2	9.7	24.2
RAB31	239.3	406.1	543.6	490.7	344.7	325.3	592.4
CCL3L3	124.5	30.8	165.7	422	106.5	104.2	163.5
NAMPT	1016.1	126.9	1049.6	774.7	981.9	1019.8	589.1
ACSL1	636.9	586	410.7	514.2	821.7	436.2	606
C4BPA	584.4	140	235.4	412.3	1147.7	335.4	266.2
LILRB2	27.7	4.5	81.4	47.2	23.9	9.3	54.5
TCN1	240.9	194.6	69.3	90.9	421.8	218	183.3
BACE2	1934	1126.9	1448.5	1369.4	1962.8	1440.3	1115.8
RND1	196.3	114.1	173.2	224.4	376.6	168.7	53.6
IRF1	1633.8	424.5	1730.8	1106.6	1483	807.8	1103.3
TAP1	2663.4	1140.7	3001.7	2349.4	2695.7	1565.8	1676.3
CXCR2	84.4	65.1	71.5	50.3	83.1	48	87.1
MAFF	558.3	252.2	304.3	377.8	385.7	174.6	180.4
CSF2RB	150.6	316.1	520.2	240.6	201.7	210.5	343.3
PDE4B	132.3	167.9	184.7	163.5	192	140.4	130
CCL2	35.6	57.3	264.6	180	106.6	120.5	170.2
CD274	118.1	66.8	185.7	109.8	154.7	97.4	94.4
TFPI2	20.3	6.8	40.1	38.9	26	20.4	138.9
CYR61	105.1	81.5	182.5	224.6	110.1	75.7	101.8
CCL4	125.6	153.9	163.8	298.7	119.8	110.9	125
CSF3R	116.8	245.9	122.5	73.3	139.7	35.8	145.1
KYNU	114.8	152.8	108.5	121	122.1	124.4	158.6
MMP9	226.1	1024.1	472.2	275	305.2	273.8	361.8
UBE2L6	2031.6	691	2343.4	1053.7	1876.6	1352.4	1231.9
MUC1	3394.6	1383.3	2197.3	2499.5	3486	2070.8	2008.1
IL13RA2	5.5	79	59.4	56.9	1.8	46.5	46.6
PROK2	48.4	44.1	28.3	13.1	39.8	25.3	46.7
S100P	8694.5	11712.3	5980.3	7866	8307.5	7645	4962.2

SERPINA3	248.9	63.3	78.3	74.6	719.6	96	152.7
GBP2	1114.8	434	1646.3	743	1124.1	812.9	683.8
COL15A1	111.6	672	185.3	157.5	52.8	167	493.6
REG4	5688.2	3502.2	3284.1	2590.4	5794.2	3609.2	4415.3
GZMB	182.2	73.5	537.5	177.9	70.7	53.7	117.1
FOXQ1	181.7	362.5	68.4	68	327.8	65.3	275.2
LPL	24.9	149	2.3	54.4	67	16.4	146.9
TNIP3	1344.9	24	772.3	560.5	710.5	729.8	196.9
C2CD4A	582.9	122.9	654.3	514.9	813	550.6	154.8
PCSK1	375.3	313.4	126.4	195.5	611.6	985	353.5
LPCAT1	397.1	150	479.7	440.9	497	297.3	302.5
CTHRC1	57.5	402.4	115.6	92.9	103.5	61.8	358.9
SRGN	6.1	6.2	17.2	10.8	27.3	6.7	12.9
EGFL6	23.5	171.5	18.7	13.4	18.4	27.8	99.3
C1R	191.3	609.4	239.8	256	325.5	163.7	349.4
DRAM1	192.6	236.1	410.6	228	213.5	303.2	216
PLA2G2A	12868.5	4824.3	14663.3	14237.6	15850.1	14215.9	9836.6
VNN1	120.5	50.8	111.5	73.8	48.7	491.4	38
FCGR1B	61.4	36.5	124.4	72.3	55.5	40.1	103.4
HLA-DMA	1777.8	585.1	1828.2	1187.8	1996.7	1766.2	1135.1
FCGR1CP	59.5	40.7	132.1	74.3	56.4	66.2	70.4
CCL11	65.4	251.8	85.4	45.6	76.5	76.2	96.6
PFKFB3	803.3	254.2	1165.8	975.7	885.8	831.6	347.2
IL1RN	503	389.3	733.5	459.1	809.4	304.7	335.8
TREM1	62.9	41.9	29.3	45.5	22.5	8.7	47.1
FCER1G	82.8	123.3	221.8	190.9	120.7	117.6	141.4
COL1A2	317.1	6492.3	882	547.6	727.1	483.8	2786.7
IFITM1	5796.4	1871.2	5487.9	4815.9	8030.9	5565.9	3636.1
INHBA	35.1	54.5	14.7	56.5	2.8	2.1	41
GPR84	5.4	91.3	43.7	27.3	32.7	32.2	32.9
GREM1	20.7	377.1	273.4	513.6	110.9	99.1	592.2
PLA2G7	129.1	75.1	376.8	199.7	141.8	329.1	189.6
IER3	2862.5	2884.1	2806.9	4150.1	3068	2311.4	1839.1
STC1	86	71.3	61	149.4	79.4	45.3	83.2
SLC7A11	80.3	92.7	75	41	69.4	45.8	26.7
TMEM45A	103.2	191.9	86.9	102.6	56.9	108.1	132.2
PDZK1IP1	3638.9	630.7	2671.1	2248.7	3352.5	3307.6	1098.1
TNFSF13B	152.4	122.3	320.3	141.1	177.1	131.6	128
SELL	69	101.6	130.2	111.6	58.8	106.7	202.9
GOS2	215.8	263	234.7	305	278.8	147.2	233.2
L1TD1	617.4	653.7	121.1	407.4	692.5	94.9	348.4
MIR8071-2	2548.5	21016.1	7492.4	4827.1	2529.4	2075.9	11676.4
ADGRL4	72	95	61	68.1	27.8	77	150.8
MXRA5	483	815.3	208.3	290.4	1289.1	1085.9	708.8
CLDN8	550.6	90.6	302.5	707.2	19.2	964.5	94.1
GUCA2A	5365	5658.5	1793.9	5834.4	4688.8	1114.9	4341.2
AQP8	246.7	903.3	331.3	582.4	350.9	161.8	4175
ABCG2	30.7	386.2	76	56.2	163.9	137.8	849.1
CHP2	486	1269.7	754.2	1191.5	702.8	489.3	1054.7
PCK1	451.1	887.3	255.2	1285.1	1068.4	1643.8	1043.4
HMGCS2	531.1	2571.8	314.6	726.8	235.9	877.3	1980.6
SLC26A2	1894.2	12081.9	923.5	3494.8	1953.3	2732.5	7111.6
GUCA2B	1348.7	1290.2	619.5	2048.8	1591.5	143.9	1083.8

CDHR1	79.4	62.7	53.9	67.4	57.8	65.8	58.8
HSD17B2	616.4	933	601	643.5	694.7	679.2	1073.8
ABCB1	186.4	283.7	222	318.3	395.5	236.7	280.8
SLC16A9	359.7	878.7	91.1	101.3	98.3	58.7	305.3
PNLIPRP2	53	47.5	205.7	90.9	47.2	278.8	6.9
SLC51B	904.2	616.8	884.4	976.8	845.5	647.6	1087.8
ADIRF	151.7	210.3	307.2	264.1	82.8	228.2	433.5
MT1M	72.2	650.2	341.6	274.8	201.2	77.3	2116.8
MEP1A	1434.4	2175	1100.1	1078.3	1876.5	1375.8	2349.8
MT1F	474.8	2527.6	1013.9	1135.8	707.3	473.9	6391.3
DHRS11	1111.3	1211.2	1000.3	1370.5	1117.1	843.3	1727.8
TRPM6	108.4	76.3	68.7	84.4	112.4	103.3	120.5
UGT2A3	154.5	122.3	691.2	628	172.8	672.9	432.9
SLC26A3	14161.5	20329.3	11737.2	14454.9	14643.2	15250.1	13669

gene	CD	CD	CD	CD	CD	CD	CD
	GSM423029	GSM423031	GSM423033	GSM423035	GSM423037	GSM423039	GSM423041
MMP1	609.4	1342.3	7185	8961.5	12817.8	7621.6	7497.8
MMP3	749.6	2433.7	8504.1	6898.5	14051.9	8826.7	9139
REG1B	56.1	1717.1	14746.6	62	14864.9	12028.6	11096.9
REG1A	82	3246	18988.6	397.4	15353.2	13219.1	11698.8
CXCL11	22.1	145.2	916.5	562.7	1007.7	654	329.6
CXCL1	1974.9	3364.5	3288.7	4419	4092	1370.2	4258.6
CXCL8	209.2	1026.7	5796.5	8906.2	11169.8	3847.5	4235.3
IDO1	51.4	314.1	9565	326.1	6512.5	2808.8	2022.6
S100A8	150.9	692.7	6365	10380.6	10289.8	6785.2	7349
IL1B	385	364	3021.7	3089.8	6043.4	1826.4	2773.6
CXCL9	91.1	389.4	2069.5	78.6	1420.5	4441.2	169.2
AQP9	21.1	98.3	272.3	1392.1	1860.8	243.8	441.7
HCAR3	25.1	123.7	2327.9	2545.2	6146	320.5	2743.4
DEFA5	1126.9	272.8	6176.7	866.2	1810	6500.2	1724.8
CXCL10	91.9	228.8	1407.1	236.1	2991.9	2671.7	587.2
LCN2	16877.1	19458.7	6604.7	4848.9	8763.3	4365.2	14064.6
PTGS2	29.8	24.5	376.8	396	348.4	160.6	216.3
SLC6A14	2364.2	2893.8	2854.3	900.2	1483.8	337.5	4766.5
MMP10	201	1184.9	839.2	374.9	275.8	215.9	1476.8
DMBT1	969.9	2595	8369.2	255.5	4225.9	7583.9	8313.4
CHI3L1	227.8	496.4	2219.7	2806.5	2239.1	2615.7	1656.3
PLAU	182.3	396.3	470.9	1537.1	1089.9	364.9	607.9
CXCL3	485.6	2212.5	1699.8	1006.4	1098.4	820.6	2820.2
S100A9	570.3	888.7	1857.4	7123.6	4177.4	1772.4	2055.3
FCGR3B	70.4	232.1	1640.6	1893.8	1112.4	388.6	1094.6
COL6A3	576.3	1341.8	2256.7	7191.9	3445.6	765.8	2474.9
COL4A1	708.3	1219.5	2401.4	5732.7	6242.5	846.6	1387.1
SELE	69	14.2	838.8	599.2	1177.9	193.9	94.4
CFI	62.8	227.2	554.1	247.6	1055.8	211.9	958.2
TNFAIP6	33.2	32.5	632.7	1511.4	2739	1400.5	734.9
DEFA6	353.3	569.7	3169.2	809.3	1322	3481.7	824.9
WARS	142.8	448	3995.5	627	1252.1	1315.1	819.8
DUOXA2	2252	4980.9	1075.4	281	1729	343	4349.5
CD55	3065.9	8658.9	6870.8	2516.9	3620.3	1190.3	8278
APOL1	205.9	248.1	1367.9	214.5	832.9	496.2	1219.8
OLFM4	13912.5	15057.3	15631.6	9034	11619.7	9005.1	11069
CXCL6	82.8	228.8	910.6	3992.5	3251.8	661.6	1064.3
DUOX2	6927.9	6927.8	2397.6	1021	5327.2	951.4	9944.8
MMP12	2275.7	7517	5385.1	3422.9	5040.7	2612.8	4443.7
NCF2	56.4	90.2	288.5	717.2	539.4	266.7	298.8
IFNG	23.3	3.9	95.1	2.1	357.4	252.4	48
STAT1	1538	1649	4903.2	1704.5	4568.8	4212	3221.3
MNDA	80.9	86.3	735.4	1337.9	607.4	432.4	548.1
TIMP1	1666.2	3433.2	3067.8	6476.5	7037	2407.3	4867.3
IFITM2	1701	3857.9	4572	6547.5	5619	2425.3	3514.7
IL6	43.2	50.5	483.6	232.6	396.7	599.3	255
GNA15	165.2	220.8	137.8	169.5	188	111.8	235.4
SLC7A5	159.5	151.4	181.3	292.6	123.9	130	101.7
CTSK	471.4	392.9	932.8	1974.9	1458.6	553.1	655.5
CXCL2	31.4	9.1	29.7	11.7	16.3	6.2	24
SLC2A3	75	100.9	311.4	652.2	469.1	339.1	279.2
CCL20	3737.3	3447.4	555.4	1714	4784.7	1397.1	4469.9

CASP1	1096.5	1783.8	2407.4	675.3	2234.7	1377.8	1924
SPINK4	3054.7	6674.8	8108.4	6512	6233.6	8982.9	7217
PLAUR	1936.4	1318	2454.5	1272	1482.8	1022.4	1845.3
ICAM1	127.5	105.6	331.1	404.5	545.1	322.7	451.8
NOS2	446.9	295	315.1	76.6	523.5	165.1	1084.2
PI3	9295.2	13731.5	4745.1	1988.7	9473.3	1821.5	10985.4
S100A12	36.4	39.3	224.8	1453.4	404.1	808.9	426.2
TMEM158	279.1	202.4	377.7	1205.9	304.8	206.4	316.7
WNT5A	165.6	268.7	1337.7	3380.7	1679.4	528.4	1315.3
GBP1	509	851.2	3347.7	568.5	5233.3	2703.2	1986.9
C4BPB	355.5	1458.3	1275.2	291.4	401.7	209.8	1106
IFIT3	172.8	151.1	426.3	138.9	1020	326.4	637.8
CEMIP	3.2	6.1	2.9	81.1	2.9	13.3	8.1
ANKRD22	837.1	1347.4	1537.3	688.6	1433.5	1010.7	714.9
REG3A	178.9	2020.1	9565.7	138.7	3039.3	3552.5	7772.1
PLEK	132.4	140.2	904.7	1501.4	3417.5	453.5	915.2
IFITM3	2677.8	6335	6490.9	5157.4	5438.9	4066.4	4530.5
BCL2A1	24.7	168.8	1086.2	2479.9	3146.1	916.7	1285.4
LAMP3	204.9	145.1	792.3	377.9	1399.1	487.8	134.9
UBD	381.8	1172.6	3028.8	1680.9	4006.6	3369.4	2226.5
GBP5	71.3	54.1	374.6	115.5	668	366	185.7
ACKR4	25.9	89.2	374.5	119.9	398.2	179.4	472.2
ADM	1587.5	3811	3195.5	3066.6	4409.5	2171.9	4988.3
PHLDA1	592.3	589.4	1319.6	1904.5	455.2	291.9	743.7
MMP7	1553.9	2225.1	168.8	992.5	186.4	121.1	2280.8
CXCL5	10.7	39.2	16.3	96.5	34.6	36.5	77.9
RAB31	716.2	579.7	723.2	1856.6	1282.9	542.1	691.6
CCL3L3	50.4	124.1	1229	1045.6	1799.5	455.7	276.6
NAMPT	213.4	881.6	1382.7	1515.1	2235.2	662.5	1436.6
ACSL1	216.2	175.1	915.6	3122.4	1803.8	1100.2	870.2
C4BPA	425.9	980.3	1033.7	153.2	225.2	115.3	847
LILRB2	11.6	34.4	183.7	255.9	442.7	146.9	114.7
TCN1	421.2	1136.6	332.9	465	197	121.4	1806.5
BACE2	1429.5	1558.2	1321.1	1125.1	1223.4	1197.8	2521.8
RND1	96.2	240	130	33.6	144	108.1	399.4
IRF1	593.6	478.9	1196.1	528	1898	1352.5	1103
TAP1	956.1	851.7	2292.3	846.8	2808.3	2476.5	1753.4
CXCR2	10.5	33.4	313.7	710.8	269.1	95.2	329
MAFF	496.4	139.3	212.4	288.9	193.9	147.8	361.3
CSF2RB	328	245.3	887.3	1332.2	3248.8	918.1	599.4
PDE4B	191.6	238.3	360.3	719.8	1403.2	441.7	411
CCL2	117.8	60.7	937.6	769.4	1001.6	523.5	158
CD274	55.7	47.8	109	44.4	281	135.9	196.6
TFPI2	2.6	3	134.3	140.3	52.3	128.4	31.4
CYR61	237.1	251	510	426.8	705.1	303.6	216.1
CCL4	62.9	135.2	816.5	528.3	1543	381.9	273.1
CSF3R	115.8	107.4	295.8	747.9	377.8	190.7	339.2
KYNU	120.6	197.7	350.3	231.2	377.3	123.6	287.8
MMP9	465.6	587.2	869.1	1771.4	802.6	1871.5	799.8
UBE2L6	581.9	717.2	2182.1	708.9	1633.1	1595.3	1075.4
MUC1	2265.2	2508.7	2182.8	732.6	2327.5	2273.2	2685.7
IL13RA2	2.7	110.9	430.8	200.6	342.3	125.2	369.2
PROK2	2.1	51.5	342.2	1072.5	421.2	113.6	468.8
S100P	4126.8	13552.5	9973.4	6860	10268.9	3759.1	7332.3

SERPINA3	479.6	564.6	478.7	486.8	265.2	140.9	1080.7
GBP2	433.3	549.7	1236.1	435.5	1578.7	804	948.5
COL15A1	528.6	499.9	1508.5	2270.3	4935	377.7	607.9
REG4	1651.1	6840.9	11198.1	8446.2	9695.8	3843.7	11229.8
GZMB	49.1	70.7	493.4	96.9	430.7	194.4	71.4
FOXQ1	174.5	318.5	296.2	439.8	131.8	113.9	1368.6
LPL	63.3	44.9	25.2	175.3	91	60.5	145.1
TNIP3	540.2	713.8	454.6	214.6	653.9	62.4	878.9
C2CD4A	167.9	464.1	517.8	420.9	317	513.2	549.7
PCSK1	256.4	1181.7	265.3	172.8	252	506.6	197.1
LPCAT1	769.3	576.4	601	410.8	594.5	297.7	493.7
CTHRC1	115.6	246.5	851.8	2191.9	1890.9	451.5	411.7
SRGN	2.1	0.9	49.8	64.4	44.6	33.7	28.8
EGFL6	27.9	39.3	135.2	358.5	482.6	105.1	160.7
C1R	328.2	341.9	643.8	1509.6	811.7	449.5	457.3
DRAM1	286.9	196.2	355.5	275.2	370.3	444.4	298.2
PLA2G2A	4022.6	14261.3	16613.3	9879	17007.8	12890.4	8426.2
VNN1	957.4	681.7	166.7	90.3	640.1	7	1096.7
FCGR1B	30.9	31.7	176.5	97.1	176.6	275.5	126.2
HLA-DMA	695	1194.2	1605.8	735.7	1450.8	1905.5	1222.5
FCGR1CP	52.9	50.2	158.4	100.4	223.5	254.5	127.1
CCL11	175.9	62.9	316	400.5	386.5	144.4	124
PFKFB3	906.9	860.5	897.6	1728.7	1782	716	2358.9
IL1RN	300.3	519.5	2755.5	3500.1	8639.9	510.8	4123.9
TREM1	3.4	100.9	200.9	721.1	699.4	55.7	307.2
FCER1G	81.4	98.8	281.3	441.3	609.2	719.4	244.9
COL1A2	1543.9	1876.1	4714.8	9655.6	8495.9	2048.7	4785.4
IFITM1	3262.2	6302.4	6908.9	3993.2	5968.2	4808.6	4801.6
INHBA	23.9	10.5	31.2	73	55.3	24.8	71.5
GPR84	42.6	8.9	44.4	199	166.3	129.1	91.6
GREM1	540.4	204.9	3359.6	4254.9	302.8	956.5	288.5
PLA2G7	44.1	198.9	571.3	177.6	483.2	794.3	186.2
IER3	3187.6	3894.6	3007.1	3327.2	2794.8	2733.7	1634
STC1	67.9	90.2	315.9	343.6	232.2	112.2	282.5
SLC7A11	38.5	106.6	71.9	66.3	61	50.6	102.4
TMEM45A	74.3	83.9	315.1	652.5	406.7	212.2	275.5
PDZK1IP1	3466.9	5066.6	2133.7	1216.5	4108.4	935.3	7038.5
TNFSF13B	164.9	167.7	398.9	236.5	504.3	480.2	246
SELL	246.4	191.8	594.6	1101.7	830.5	709.2	448.9
GOS2	135	165.4	922.5	1200.5	1638.9	752.7	1074.2
L1TD1	174.5	171.1	1379	92.5	158.1	212.1	118.2
MIR8071-2	25558.2	14288.7	20439.3	15336.7	22080	11996.6	15986.3
ADGRL4	118.7	156.2	350.7	574.7	944	78.8	128.4
MXRA5	1180.6	611.3	2135.2	1852.4	2048.8	418.2	2429.9
CLDN8	1176.2	265.3	10.1	6.5	54.7	453.6	11.4
GUCA2A	2831.8	357.1	46.6	1080	1150.8	6802	185.2
AQP8	213.2	120.9	1.7	313.8	20.8	1484.9	9
ABCG2	109.7	83.7	14.8	316	133.8	372.8	207.9
CHP2	273.9	176.9	94.3	150.3	851.4	1104.1	347.2
PCK1	788.4	306.6	37.2	235.2	157.4	2378.6	43.8
HMGCS2	54.5	153.7	158.5	235.2	19	217.8	74.1
SLC26A2	2156.4	545.5	498.6	549.7	887.3	6807	148.7
GUCA2B	458.9	181.3	3	331.2	156.8	1496.3	93.6

CDHR1	108.9	41	34.2	17.4	12.5	49.1	22.2
HSD17B2	833.8	455.1	436.5	752.9	884.6	602.5	1489
ABCB1	264.2	80.3	48.8	115.3	216.3	322.5	137.5
SLC16A9	142.1	280.2	107.6	382.9	88.1	243.8	65.1
PNLIPRP2	69.4	51.8	30.6	2.1	92.1	111.2	23.5
SLC51B	149.3	391.2	140.1	78.6	490.6	325.1	338
ADIRF	101.1	134.2	224.1	170.7	99.9	169.9	116.4
MT1M	4.6	116.1	62.5	316.2	299.2	267.1	89.6
MEP1A	1559.3	698.6	229.6	1083.9	1780.3	1112.8	1931
MT1F	419.6	477.1	516	1006.6	1221.2	922	414.4
DHRS11	597.7	413.2	177.5	347.5	482.3	1145.1	437.4
TRPM6	62	47.3	31.3	48.3	65	93	4.2
UGT2A3	36.5	56	6.7	22.3	1.9	813.1	43.4
SLC26A3	16601.3	12197.3	2762.3	10096	14601.6	13643.9	8616.9

gene	CD	CD	CD	CD	CD	CD	CD
	GSM423043	GSM423045	GSM423053	GSM423055	GSM423057	GSM423059	GSM423061
MMP1	9744.1	14203.8	1392.2	5103.3	8010	2287.4	92.9
MMP3	11970.1	12635.9	185.1	850	5493.6	1305.8	36.3
REG1B	585.5	26535.5	20684.8	24998.1	26151.9	14330	784.3
REG1A	2328.9	24880.2	21819	24948.5	24852.4	14826.5	1296.7
CXCL11	468.6	796.2	21	202.9	1724.4	283.6	140.8
CXCL1	4089.9	2641.9	196.5	1014.9	1145.5	537.7	401.5
CXCL8	7155.9	5041.9	137.1	1655.8	5775.6	1809.9	100.4
IDO1	2367.9	2928.5	236.1	274.9	4403.8	455.7	139.8
S100A8	10294	1752.6	379.7	1114.8	4814.3	1838.1	74.4
IL1B	7377.1	1825.9	96.8	753.4	2163.1	1029.6	103.8
CXCL9	191.5	1676.4	75.1	164.7	1574	216.3	132.3
AQP9	1072.4	149.7	13.8	58.7	454.5	135.1	9.5
HCAR3	3064.6	434.8	3.1	191.8	1841.1	636.4	20
DEFA5	745	5718.5	20034.2	16472.9	21693.1	13922	5235.6
CXCL10	414.9	2170.5	206.5	527.5	3322.3	399.2	204.1
LCN2	15194.1	11313	3214.7	4462.9	11603.8	5874.6	5127.9
PTGS2	603.4	293	0.8	102.5	137.5	64.3	15.3
SLC6A14	3707.4	1345.7	216.3	319.5	844.4	762.7	251.3
MMP10	1194.3	1117.4	121.7	194.9	409	207.3	7.1
DMBT1	1984.1	16907.6	14769.2	11838.7	17762.8	11680.3	4090.9
CHI3L1	1310.9	1791	3	181.8	669.5	67.8	2.7
PLAU	1019	727.8	58.7	94.1	300	177.4	63.6
CXCL3	2823.9	768.2	128.9	655.7	749	530.4	194.6
S100A9	3536.1	787.2	126.8	409.2	1122.2	551.8	40.3
FCGR3B	2101.3	267.8	156.7	266.1	620	314.3	20.6
COL6A3	2020.2	2104.4	263.2	472.1	531.9	421.2	483
COL4A1	1375	1994.2	493.9	800	855	551.1	603.5
SELE	860.9	217.3	10.8	57.5	172.2	36.8	12.1
CFI	547.7	256.5	925	1305.5	1073.9	1090.8	77.4
TNFAIP6	831.7	1077.1	8.4	59.2	484.2	61.5	31.1
DEFA6	507.9	2382.2	17942.5	10268.1	16596.5	11552.1	2578.2
WARS	1173.7	1355.6	378.2	302.9	2103.2	710.7	190.2
DUOXA2	3240.6	1404.9	371.7	702.5	1887.1	786.2	477.2
CD55	8959.5	6111.6	2447	4819.1	8377.6	4204.1	769.9
APOL1	1150.6	329.5	201.9	145.4	356.9	213.9	197.8
OLFM4	18032.3	15210.1	14743	12652.5	16853.8	11283.2	13797.8
CXCL6	691.9	706.8	175.7	115.3	512.2	277.5	29.5
DUOX2	7756.8	3730	1894.7	2049.1	8122.6	3911.4	1079.4
MMP12	7475	15117.9	378.7	318.7	3484.7	921.4	700
NCF2	391.9	317.8	7.2	63.5	226.4	81.8	16
IFNG	39.2	89.6	34.2	66.4	267.8	52.7	19.2
STAT1	2614.1	4181.9	2244.5	1840.7	6183.3	2751	1682.8
MNDA	815.4	262.3	39.6	128.4	368.8	211.8	19.2
TIMP1	9243.5	5761.8	466.8	1048.2	1544	791.8	739
IFITM2	7066.5	2844.9	999.6	1845.5	3359.1	1948.3	1584.9
IL6	433	736.9	14.5	148.1	176.9	96.5	47.9
GNA15	328.5	170.7	12.8	76.8	139.1	49.5	40.9
SLC7A5	270.5	135.3	110.3	121.6	84.7	68.6	50.5
CTSK	1067	997.7	148.4	169.3	287.5	179.3	221.5
CXCL2	25.9	5.4	2.1	13.3	24.7	18.8	4.8
SLC2A3	393.9	178.2	73.8	100.3	165.3	183.7	20
CCL20	2775.8	2646.8	1053.8	11144.3	2828.4	1116.2	2790.6

CASP1	752	1376.7	1556.6	1169	1979.2	2347.8	1681.1
SPINK4	4788.8	7325.7	19458.7	15592	19677.5	14092.7	1831.3
PLAUR	2582.1	1887.6	286	444.3	811.5	513.2	374.4
ICAM1	677.1	280.8	75.2	193.5	297.8	128.5	63.4
NOS2	570	604.4	342.5	285.9	1124.6	644.4	142.9
PI3	12901.1	6830.6	119.7	459	333.7	292.3	2651
S100A12	766.5	104.3	50.1	97.7	106.9	42.9	16.2
TMEM158	529.4	559.4	7.5	12.9	158.3	67.3	116.3
WNT5A	1198	825	585.6	453.4	1269.5	959.7	194.6
GBP1	1141.4	2983	1206.3	1258.4	4001.3	1294.1	611.6
C4BPB	809.2	675.2	189.7	487.1	557	328.7	162.4
IFIT3	325.4	385	516.6	508	1123.5	628.2	178.3
CEMIP	73.8	4.4	3.3	2.3	2.9	1.9	2.6
ANKRD22	1400.8	1747.2	173.9	613.8	803.8	357.1	887.2
REG3A	842.4	4770.6	15192.7	15051	18679.8	11074.4	3415.7
PLEK	1305.4	501.7	76.2	96	932.5	156.3	73.5
IFITM3	7465.9	4827.6	1290.6	2601.2	4880.9	2906.4	2320.9
BCL2A1	2411.3	524	64.5	153.5	884	342.5	46.7
LAMP3	428.9	585.4	48.1	50.7	593.6	95.7	37.7
UBD	2372.4	1934	1132.5	3611	8373.8	2943.9	1003.7
GBP5	149.7	192.1	82.3	39.9	341.2	99.8	40.6
ACKR4	161.1	196	782.9	476.8	1098.1	854.7	145.1
ADM	4518.9	2906.6	552.3	1508.2	1659.6	830.5	1309.7
PHLDA1	1441.5	582	69.3	181.4	271.2	258.1	124.7
MMP7	1460.1	252.9	26.1	121.4	111.3	63.6	190.2
CXCL5	13.3	49.2	1.5	27.3	54.1	33.1	14.2
RAB31	911.4	705	87.3	159.9	572.8	160.7	244.5
CCL3L3	1048.9	335.9	69.4	153.8	684.1	177.5	50.5
NAMPT	1539.4	516	301.8	558.2	472	469.4	228.9
ACSL1	1585.3	578.1	149.8	229.4	926.1	320.3	532.4
C4BPA	427.9	1246.1	24.6	208	133.6	141.9	198
LILRB2	234.3	156.9	11.3	60	176.3	25	5.8
TCN1	1609.4	395.3	77.4	268.1	565.1	210.8	53.2
BACE2	1317.1	1456.1	780.3	887.1	1551.8	1276.9	985.4
RND1	152.5	105.2	145.6	38.5	131.1	137.1	34
IRF1	837.5	1123.6	806.4	1063.2	2044.6	1224	534.6
TAP1	1573.6	2686.6	1449.1	1308	4127.7	1923.1	1171.1
CXCR2	519.9	95.2	45	84.7	302.8	123.5	14.8
MAFF	255.2	319.8	103.6	206.8	160.2	127.1	134.4
CSF2RB	1212.1	607.8	75	189.2	1298.2	241.2	129.6
PDE4B	983.3	290.6	42.4	157.7	419.6	153.3	45.4
CCL2	675.3	347.1	47.4	86.5	138.4	39	39.2
CD274	139.7	100	78.6	44.3	149	67.1	30.8
TFPI2	118.6	182.9	10.4	139	47.5	11.9	8.9
CYR61	773.4	298.9	42.3	141.8	111.8	29.7	30
CCL4	1208.3	392.8	91	133.2	636	214.6	41.8
CSF3R	601.2	197.9	137.6	175.3	378.7	192.3	9.6
KYNU	212.1	120.8	83.9	22.5	62.1	58.4	64.8
MMP9	1003.9	3042.7	96.9	76.1	528.7	170.9	79.7
UBE2L6	838.2	1500.8	619	738.4	1909.2	892.3	560.5
MUC1	2065	1891.3	516.6	1123.9	1627.3	657.7	1349.4
IL13RA2	666.4	150.4	8.2	108.1	152.9	34.1	1.8
PROK2	1032.3	122.5	1.8	25.6	190.7	129.4	5.4
S100P	8908	3793.1	1418.9	5178.3	1664.9	948.4	3128.6

SERPINA3	799.2	972.6	415.5	482	1394.9	635	55.4
GBP2	641.6	868.8	630	712.5	1566.3	791.6	360
COL15A1	1369.8	911.9	131.9	406.6	427.7	253.2	251.3
REG4	9161.6	2222.2	11585.4	12504.4	13729.4	9254.9	1896.2
GZMB	246	206.5	72	83.2	582.6	110.4	75.2
FOXQ1	640.9	217.4	65.4	195.1	270.9	144.2	340.3
LPL	37.5	148	316	393.3	1060.6	519.2	149.6
TNIP3	664.4	539.5	20.9	24.3	64.7	28.7	64.3
C2CD4A	309.3	217.9	200.8	237.5	547.2	424.2	98.3
PCSK1	181.6	95.9	70.2	174.9	206.6	329.9	128.1
LPCAT1	436.1	331.9	134.3	175.6	243.3	307.8	255.4
CTHRC1	623.8	688.3	41.2	93.8	274.4	67.6	56
SRGN	83.9	6.9	2.6	7.1	52.3	17.6	11.3
EGFL6	101.3	157.2	29.4	49.1	75.9	27.9	48.5
C1R	784.3	693	174.9	286.8	322.2	233.7	195.6
DRAM1	282.3	324.5	96.6	94	337.9	116.7	138.2
PLA2G2A	10047.1	23135.5	13827.9	10739.2	19868.7	12193.2	3430.9
VNN1	217.9	10	2018.3	1438.5	932.2	993.8	73.5
FCGR1B	98.8	108.4	15.1	36.1	194.6	59.9	26.1
HLA-DMA	1756.8	752.1	1593.2	1368.5	2094.9	1118.2	406
FCGR1CP	76.4	141.8	41	18.4	180.2	53.6	41.2
CCL11	345	133.3	68.1	104.6	182.5	131.6	185.1
PFKFB3	1320.3	1129.5	346.7	257.3	1062.7	490.6	257.5
IL1RN	7983.1	649.3	283.3	996.2	2313.8	790.3	112
TREM1	613.5	107.8	37.8	56.7	207.8	70.6	4.1
FCER1G	402	476	64.9	48.3	228.5	119.2	48.2
COL1A2	3035.9	4423.9	515.1	887.5	1187.5	469.9	1530.5
IFITM1	6938.8	7239.1	2796.1	3845.9	8466.4	5909.7	2884.8
INHBA	33.5	32.5	28	27.8	38.7	19.9	11.3
GPR84	238.2	72.6	4.4	25.2	93.1	38.8	13
GREM1	1142.1	621.8	187.6	440.9	267.2	179.4	238.1
PLA2G7	279	617.2	65.4	26	232.1	66	53.5
IER3	5681.6	2755.4	312.9	2327.8	1360.3	642.4	1509.4
STC1	514.5	199.1	10	82.3	80.4	54	21.7
SLC7A11	201.1	66.4	25.7	54.2	90	58.1	19.9
TMEM45A	355	165.8	88.1	71.5	210.5	124.8	61.1
PDZK1IP1	5271.8	2341.6	972.6	1268.9	4546.9	2062	1452.7
TNFSF13B	259.3	331.1	309.5	187.8	695.6	340	80.8
SELL	1410.7	425.7	33.9	72.6	462.5	169.2	34.1
GOS2	3179.8	815.1	133.3	253.7	842	508	84.4
L1TD1	324	134	83.3	242.2	57.7	60.1	241.8
MIR8071-2	27945.4	5272.2	1376.1	474.2	9732.1	907.5	4600.7
ADGRL4	293.6	170.4	53.5	65.1	109	73.8	104
MXRA5	1299.8	667	930.1	803.7	2054.6	1227.1	248.6
CLDN8	4.4	86.1	4.6	16.5	22.9	26.5	17
GUCA2A	286.1	7443.6	8628.1	5731.4	2812.3	5550	3406.3
AQP8	1.7	1293.2	2.7	706	8.9	6.1	8543.9
ABCG2	170	212.6	3563.7	3239	1259.2	2261.3	2611.8
CHP2	64.2	1668	2985	2458.7	1396.4	2629.7	1918.3
PCK1	62.4	1297.8	8300.8	4090.3	1500.8	2067.1	1985.5
HMGCS2	3.8	706	287.9	2687.3	5.6	259.7	4684.1
SLC26A2	166.6	7421.5	1822.4	2719.2	1157.5	1193.3	16161.6
GUCA2B	84.7	1478.7	2141.8	1742.8	284.8	1454.4	1042.6

CDHR1	55.2	42.5	37.4	16.1	46.1	6.2	68.3
HSD17B2	791.3	881.9	3171.1	2583.2	1561.5	2705.4	1739.5
ABCB1	40.1	345.8	1893.5	1638.4	1290.1	1564.9	419.6
SLC16A9	83.4	304.6	17.5	424.5	2	28.4	553.8
PNLIPRP2	3.4	44.9	3909.7	4062	1915.1	191.7	232.5
SLC51B	179.7	906.8	2080.6	1649.8	628.5	1416.6	747.1
ADIRF	175.8	189.2	6635.8	5771.4	1932.3	3705.9	440.2
MT1M	31.3	223.6	460.2	42.1	150.3	388.2	271.3
MEP1A	229.6	2052	9848.4	12268	6696.4	7337.3	2450.1
MT1F	331.1	1709.7	3162	618.1	983.7	2196	822.5
DHRS11	198.3	1493.1	4368.7	2646.6	1501.3	3404.5	1172.3
TRPM6	8	64.3	81.8	75.3	24.5	55.7	102.1
UGT2A3	14	467.1	5075.3	1499.5	1581.2	2786	549.3
SLC26A3	7234.3	22856.1	4731	11550	3893.6	7236.5	24373.8

gene	CD	CD	CD	CD	CD	CD	CD
	GSM423063	GSM423065	GSM423067	GSM423069	GSM423071	GSM423073	GSM423075
MMP1	670.5	2589.2	3318.8	3095.5	5267.4	2709.4	2848
MMP3	131.2	1270.7	2341.8	1072.5	3372.1	3778.9	1157.8
REG1B	19597.8	13903.7	20592.6	10077.5	12405.8	10083.1	28830
REG1A	21510.3	20166.3	24522.5	30496.5	17863.9	13075.5	26759
CXCL11	249.5	492	362.7	455.2	891.7	405.8	275.4
CXCL1	330.3	339.1	1127.6	495.1	1001.8	697.2	401.6
CXCL8	209.6	632.3	8098.6	2004.4	777.2	2551.6	1449.6
IDO1	299.6	1355.1	1313.9	972.2	2146.3	1112.9	322.7
S100A8	460.9	531.9	6548.6	2081.4	2861.4	2117.6	975.9
IL1B	118.6	276.7	3971.7	665.3	546.4	869.3	805.3
CXCL9	176.3	5159.8	641.2	812	1478.9	575.4	283.4
AQP9	42.9	112	930	156.4	101.3	222.9	148.4
HCAR3	165.5	184.2	4351.9	281.5	197	1103.6	351.3
DEFA5	16252.9	19503.2	23715.3	11162.3	17027.4	11868.4	19318.2
CXCL10	465.3	2578.7	1463.7	984.3	2487.4	737.2	577.1
LCN2	5271.8	3000.1	2059.7	2715.7	9697	5201.9	7289.6
PTGS2	4.6	89.7	398.5	131.5	19	59.5	82.3
SLC6A14	251	262.5	134.4	256.4	738.9	374.1	325.1
MMP10	33.2	68.4	215.1	49.3	194.2	194.5	132.3
DMBT1	13759.3	12224.4	10202.3	17147.4	10771.2	8833.6	15740.3
CHI3L1	60.4	1171	691.6	61.9	856.3	381.4	159.9
PLAU	79.6	132.2	525.9	254.2	226.9	286.1	151.7
CXCL3	452.9	115.2	268.2	86.5	524.6	241.3	151.2
S100A9	167.8	244.3	1415.7	568.3	1054.3	499.4	249.8
FCGR3B	133.5	191.9	681.2	724.4	399	354.8	234.8
COL6A3	302.7	1007.5	708.8	1146.9	1321.1	630.8	508.7
COL4A1	584	875.4	754.8	1392.4	1137.3	873.4	424
SELE	26.6	237.8	167.9	226.9	71	206.3	49.4
CFI	1322.5	1018.6	467.6	783	1435.4	927.2	627.3
TNFAIP6	66.4	299.5	1221.5	229.4	148.8	235.9	140.3
DEFA6	15059.8	13932.9	17726	8630	14487.4	11162.2	15300.8
WARS	491	1018.6	547.1	566.8	1109.4	603.9	326.5
DUOXA2	353	230.2	350.2	276.6	710.3	185.7	599.4
CD55	1972.8	1837.3	3337.7	2451.4	3619.7	2665.5	4573
APOL1	224.1	211.4	147.5	183.1	580.2	221.4	277
OLFM4	14748	11075.9	11165.5	20233.5	12777.1	8494.2	16259.5
CXCL6	336.3	194.1	118	708	778.4	534.1	236.4
DUOX2	1979.5	1027.9	2090.8	972.7	2288.1	1038	2663.8
MMP12	143.6	1969.1	4738.3	399.1	2922.4	1091.7	1845.8
NCF2	49.6	137.7	261.3	86.5	176.4	69.1	64
IFNG	30.5	104.4	200	58.6	86.3	61.5	41.6
STAT1	2975.7	4968.3	1877.4	3351	3409.1	2720.1	2429.2
MNDA	74.8	267.9	373.9	258	349.9	158.3	181.8
TIMP1	540.9	1272.7	1393	1346.5	1524.5	991.7	962.3
IFITM2	1310.1	1882.1	2990.3	2566.8	2816.4	1906.5	1326.9
IL6	29.2	211.7	287.1	64	73.4	96.6	114.6
GNA15	11.9	45.9	93.6	76.4	117.5	61.5	105.9
SLC7A5	127.2	85.6	154.9	101.7	104.2	108.9	74.4
CTSK	195.5	637.6	242.5	514.8	800.5	309.3	191.2
CXCL2	18.3	14	2.8	25.8	7.7	2.7	2.7
SLC2A3	53.5	135.6	381.3	193.9	189.8	182.8	173.7
CCL20	3020.7	1164.7	974.8	503.5	2431.5	516.6	1816.8

CASP1	1848.5	1630.5	1009.4	1273.5	1410.1	1548.7	1324.5
SPINK4	10993.9	17291.1	12493.2	24324.8	12765	11624.4	18499.1
PLAUR	219.8	230.8	562.1	518.7	290.9	286.2	482.8
ICAM1	135.5	181.8	446.9	184	279.4	168.5	131.4
NOS2	505.4	318.2	290.5	323.3	295.5	176	373
PI3	111.2	94.1	425.1	94.2	405.4	117.4	350.4
S100A12	32.3	45.6	165.6	82.7	78.1	58.2	62.6
TMEM158	2.7	82.8	199.5	89.9	124.4	65.7	62.5
WNT5A	811.2	868.4	507.3	565.1	313.8	379	858.2
GBP1	2169.5	2835.7	2194.1	2069	1417.5	1252.6	1753.4
C4BPB	276	178.1	146.6	163.2	296.3	215.4	251.8
IFIT3	671.3	601.1	376.2	748.8	530.8	436.3	615.2
CEMIP	2.4	2.4	7.6	3.7	3.5	7.6	4.1
ANKRD22	161.5	383.6	316.2	470.8	441.6	280	327
REG3A	14945.8	14443.7	16991.5	20849.6	14500.4	9747.9	17721.6
PLEK	154.4	149.4	1801.6	291	312.4	267.4	163.6
IFITM3	1982.5	2675	3149	3409.7	4626.2	2171.2	2335.6
BCL2A1	126.6	492.7	1467	263.7	464.7	429.9	209.7
LAMP3	93.2	396.5	688.2	459.1	308.4	287.3	146
UBD	3261.6	8205.4	2277.7	1617.6	3171.2	1209.7	3446.4
GBP5	114.8	339.5	214.9	207.4	240.1	181.7	61.5
ACKR4	872.1	672.9	452.5	890.7	1258.8	840.2	568.9
ADM	363	495.9	702.5	442.2	377.2	309.9	748.5
PHLDA1	132.5	169.6	255.5	278.2	204.7	220.1	220.7
MMP7	93.2	122.8	284.7	62.9	204.1	112	144
CXCL5	15.5	38.1	18.4	2	9.6	28.1	30.3
RAB31	127	447.7	268.3	276.6	365.5	321.6	192.8
CCL3L3	106.2	89.4	1966.8	106.6	121.4	235.6	169.8
NAMPT	415.4	306.9	639.1	333.9	407.3	302.6	133.4
ACSL1	248.4	497.5	678.8	444.1	444	694.9	277.8
C4BPA	53.1	113.5	98.7	27.5	7.9	36.1	65.3
LILRB2	6.6	96.7	148.5	95.8	142.4	52.3	31.2
TCN1	80.8	153.9	119.4	175.9	1155.4	482.1	562.7
BACE2	394.2	669.5	426.8	751.5	693.8	716.2	737.2
RND1	74.1	15.2	72.5	49.7	62.9	49.5	113.3
IRF1	1098.5	968.9	1462.6	860.1	1231.3	771.4	992.6
TAP1	2185.3	2872.5	1898.3	1823.3	2340.9	1217.6	2226.9
CXCR2	63.7	74.4	264.9	155.5	137.3	93.5	76.6
MAFF	124.9	90	165.7	123.7	111.6	95.2	116.1
CSF2RB	206.6	664.7	1057.6	553.9	528.9	570.3	278.9
PDE4B	86.1	275.9	844.9	105.4	174.4	328.8	117.8
CCL2	79.2	275.2	241.7	309.1	266.2	121.3	124.7
CD274	83.6	81.2	132.6	61.7	99.6	90.6	59.8
TFPI2	2.3	46.2	674.7	506.5	42.7	121.4	12.4
CYR61	39.1	87.1	86.2	80.6	100.3	129.4	92.9
CCL4	128.1	159.5	1711.1	162.3	169	212	194.2
CSF3R	125.4	148.2	561.1	221.3	274.9	378.2	159.8
KYNU	50.6	119	111.9	113.1	98.9	40.2	54.3
MMP9	117.1	1446.5	887.2	214.1	475.5	298.9	205.4
UBE2L6	1061.7	1412	750.2	871.6	1238.8	778.9	815.6
MUC1	365.3	994.4	545.5	685.8	788	669.1	821.8
IL13RA2	11.1	33	162.6	124.4	52.9	103.6	72
PROK2	2.1	27.5	210.9	105.3	49.3	135.3	83.3
S100P	772.3	913.1	1083.9	3529	3711.2	1628.8	1912.7

SERPINA3	153.4	169.8	191.7	135.2	406.4	863.6	463.5
GBP2	952.3	968.7	591.2	457	859.8	551	577.5
COL15A1	231.9	586.8	577.2	839.9	551.3	818.4	189.7
REG4	6761.2	10450.7	8529.9	13681.9	9071.4	7332.3	6553.8
GZMB	72	168.4	223.1	173.9	257.7	164.4	114.3
FOXQ1	213.2	126	149.2	425.3	457.3	386.2	200.1
LPL	805.9	666.6	500.7	1561	370.8	414.8	512.9
TNIP3	2.3	29.2	48.4	2.9	2	11.2	61.1
C2CD4A	199.2	270.3	78.2	271	117.3	167	164.5
PCSK1	254.7	250.4	118.6	30.4	61.9	65.4	9.3
LPCAT1	184.4	308.9	240.4	89.9	164.6	164.9	152.6
CTHRC1	53.9	440.2	150.7	330.9	420.3	249.8	100.1
SRGN	18.8	20.7	1.9	27.1	11.9	26.1	7.2
EGFL6	40.1	82.4	49.5	160	91.7	50.3	57.1
C1R	256.4	633.8	257.9	555.4	741.2	470.6	262.9
DRAM1	129.3	315	183.4	229.4	299	179.7	188.2
PLA2G2A	11824.7	8272.3	8871.8	4499.1	12517.6	7898.2	11358.1
VNN1	1643.1	109.2	701	1128.4	1304.4	1289.8	1602.8
FCGR1B	55.8	219.7	132.7	152.9	131.5	72.4	46.8
HLA-DMA	1832.2	2322	1575.6	1363.8	2353	1421.6	1599.6
FCGR1CP	27.2	248.6	126.9	147.6	114.3	78.8	54.8
CCL11	156	207.6	111.4	781.1	542.2	265.4	97.3
PFKFB3	527	397.7	364.6	480.4	309.4	347.8	309.9
IL1RN	264.4	215.8	4380.6	803.3	930.8	1121.6	769
TREM1	12.2	1.7	330.7	30.5	97.3	180.1	54.3
FCER1G	80.5	363.6	369.2	113.2	375.3	155.7	124.9
COL1A2	915.7	2740.6	1529	2736.8	3139.3	1614.1	1271.6
IFITM1	3561.9	4988.7	4228	4167.6	4495.3	3149.9	4250.3
INHBA	15.4	13.1	16.3	19.1	1.4	33.1	33.4
GPR84	18.1	38.2	75.7	1.8	36.3	20.5	46.3
GREM1	160.3	1029.1	71.5	283.4	677	1657.4	79.8
PLA2G7	54.3	586.3	241.9	112.3	291.6	83.7	94.5
IER3	449.1	833.1	958	563.9	556.5	693.2	840.8
STC1	22.9	44.3	95.2	214	61.9	87.5	75.5
SLC7A11	14.1	44.9	38.6	49.8	42.8	10.9	33.7
TMEM45A	53.4	188.9	104.3	142.5	106.6	177.2	85.2
PDZK1IP1	1256.2	1180.9	647.8	910.9	2685.3	689.5	1550.7
TNFSF13B	429.3	946.7	305.6	576.3	671.7	389.7	283.1
SELL	93	539.9	352.9	204.4	421.2	173.1	102.8
GOS2	239.2	284.8	1319.8	480.7	317.2	406.1	585.8
L1TD1	31.8	87.2	87.2	42.4	17	58.5	42
MIR8071-2	2549.2	19494.7	6177.7	9678.5	13473.6	8365.8	5027.7
ADGRL4	63.6	145.4	61.7	252.4	179.2	158.5	64.8
MXRA5	1605.8	1088.9	495.5	738	987.1	890.8	1095.1
CLDN8	3.5	32	47.5	3.6	13.9	3	48.9
GUCA2A	5486	4877	18501.3	1440.9	1653.5	2313.9	10612.2
AQP8	3.4	22.1	12.4	4.5	28.8	3	5.7
ABCG2	2508.2	1678	4280.7	1781	1983	2072.5	4248.9
CHP2	2509.8	1891.6	3900.6	1550.6	2183.2	2256.3	2983
PCK1	6638.4	2969.4	6467.2	3117	2866.3	3893.9	5759.2
HMGCS2	43.3	26.3	115.8	936	172.4	957.7	279.2
SLC26A2	1399.1	1376	1998.2	1752.3	776.1	866.5	2532.4
GUCA2B	1550	521.2	5633	209.6	590.5	971.4	1423.4

CDHR1	1.9	41.3	49.8	42.8	4.6	36.5	4.5
HSD17B2	2091.2	1084.1	4377.8	2017.2	3583.7	2697.6	2943.8
ABCB1	1819.3	1334.5	2813.2	865.7	879.7	826.2	2049.4
SLC16A9	2.5	19.8	49	34.8	44.3	9.7	9.7
PNLIPRP2	2748.3	1132.7	204.3	168.2	4064.8	247.3	2389.7
SLC51B	976	726.4	1407	844	801.7	563.5	1674.7
ADIRF	3842.3	3470.6	6698.8	4394.5	4616.6	3318.9	5797.2
MT1M	5.1	37.5	35.4	782.8	393.8	649.4	226.8
MEP1A	9311.4	6192.3	13692.1	5295.2	6149	5541.6	12079
MT1F	288.3	605.9	1022.6	4039	2434.6	3490.6	1743.3
DHRS11	3824.4	1843.9	4455	2426.2	4027.2	3192.8	3483.2
TRPM6	64.6	50.9	145.3	35.9	52.8	14.8	12.2
UGT2A3	4126.3	861	1113.8	1572.6	1866.5	4443.2	1801.4
SLC26A3	4473.9	6487.6	8588.8	3622	2636.4	3084.8	7294.8

gene	CD	CD	CD	CD	CD	CD
	GSM423077	GSM423079	GSM423081	GSM423083	GSM423085	GSM423087
MMP1	2565.9	8743.7	4781.2	11199.5	15093.1	12386.4
MMP3	676.4	4636.4	1722.2	9058.3	14579.1	12098
REG1B	24744.1	26672.1	4267.1	19278.5	12126.7	12377.7
REG1A	25704.7	27765.1	11595.4	27145.7	17310.6	17158.7
CXCL11	150.9	389.4	327.7	347.1	878.4	717.3
CXCL1	599.4	1023.2	938	3520.2	5371.6	6651.7
CXCL8	436.6	3749.4	463.3	12432.5	16564.3	7160.7
ID01	390.5	739.4	316.5	649.4	5323.8	3416.9
S100A8	420.5	8286.1	2408.5	4404.4	19528.7	13798
IL1B	240.1	2748.1	359.4	5844.2	14256.7	8939.9
CXCL9	121	437.4	141.6	455.1	2518.5	1543.5
AQP9	56.5	470.3	221.7	430.1	1829.4	989.8
HCAR3	121.2	1140.6	130.6	2020.9	7375.3	3182.4
DEFA5	8565.7	12093.9	3452.2	22905.9	4189.2	10442.4
CXCL10	190.3	1587.7	605.5	1438.3	3212.7	2974.2
LCN2	14156	11081.1	10779	5200.9	7680.8	8402.9
PTGS2	27.4	214.8	30.3	582.2	951	927.2
SLC6A14	537.4	1499.5	2542.2	468.4	897.5	2532.5
MMP10	113.3	292.4	47.4	1115.5	227.5	1280.1
DMBT1	18420.7	17684	7670	14977.2	5549.5	5633.1
CHI3L1	157.4	234.9	604.1	1192.1	2053.6	3207.5
PLAU	132	187.7	124.6	758.7	740	1267.3
CXCL3	361.9	316.5	637.1	1056.6	1386.7	2838
S100A9	130.4	1594.6	746.8	1725.4	8844.1	8032.9
FCGR3B	63.1	885.6	268.4	1071.5	6157.4	3279.2
COL6A3	506.9	440.4	851.6	1591.9	3993	3808.2
COL4A1	728.3	896.4	514.7	1617.8	4539	3457
SELE	165.7	105.6	8.5	341.8	1687.4	1390
CFI	528.4	1049	1077.7	479.4	975.6	384.5
TNFAIP6	52.5	261.3	81.2	456	1657.4	1390.1
DEFA6	4679.3	8544.1	1216.3	18172.6	2040	6575.1
WARS	553.7	442.7	414.6	756.6	1798.6	2810.7
DUOXA2	1418.1	1571.3	1402.2	461.3	603.2	889
CD55	7563.2	6663.8	4515.7	2648.8	5765.9	7472.7
APOL1	481.8	455.2	1129.8	137	776	379.6
OLFM4	15911.8	18707.8	9294.6	16649.5	12921.6	13470.1
CXCL6	130.7	672.7	520.5	693.3	2518.6	1196.2
DUOX2	6426.2	4803.5	3754.1	1727.1	2337	2821.2
MMP12	1011.3	1598	872.7	9913	4745.5	5875.5
NCF2	54.9	264.9	118.6	353.4	1260.1	585.2
IFNG	28.6	239.6	30.5	148.3	348.2	155.4
STAT1	2260	2699.2	3160.8	2813	5881.4	3128
MNDA	50.9	676.7	149.8	610.2	3292.7	1742.1
TIMP1	2070.4	1759.6	1969.5	3988.1	5155.1	8535
IFITM2	1349.3	2321.8	1365.7	3812.2	8991.5	8122.7
IL6	34	271.9	51.3	1455.7	1125.9	1634.4
GNA15	86.1	119.7	152.7	188.1	236.8	267.9
SLC7A5	64.5	102.2	72.1	115.8	158.6	290.2
CTSK	262.8	192.9	377.7	626.8	2017.9	1256.1
CXCL2	1.6	2.2	46.8	2.4	19	24.7
SLC2A3	62.9	303.4	101.6	376.6	1334	1167.1
CCL20	1096.2	4641.5	2639.3	8624.2	1895	2636.4

CASP1	1117.8	2609.5	1930.2	1480.5	2113.1	1402.8
SPINK4	22378.7	24747.3	10264.3	19623.7	8195.7	11430.1
PLAUR	540.4	1001.7	558.5	1515.5	1936.1	3897.8
ICAM1	101.7	199.2	118.7	511.1	716.9	1021.4
NOS2	368.7	517.6	289.9	608.8	219.6	491.3
PI3	1845.8	469.3	1476.4	306.7	1299.8	3455
S100A12	41.7	326.2	68	227	1896.3	1533.2
TMEM158	21.8	63.1	68.7	654.4	496.3	863.2
WNT5A	448.3	1334.6	453.2	1472.3	1716.2	1437.7
GBP1	768.3	1988.1	1296.1	2010.4	5145.6	3334.1
C4BPB	649.1	630.8	385.5	292.3	571	657.1
IFIT3	370.4	551.6	330.9	475.1	1046.3	699.9
CEMIP	5.1	5.5	4.5	3.4	5.8	62.7
ANKRD22	583.1	476.6	393.7	231.5	873.7	1454.3
REG3A	14743.2	12055.4	7962	17820.7	8765	8729.5
PLEK	138.2	666.4	139.7	1265.4	4521.8	1694.7
IFITM3	2881.5	2973.7	2103	3498.4	7817.4	8728.5
BCL2A1	72.7	1132.2	271.1	1242.4	4978.4	3079.3
LAMP3	172.9	182.9	34.1	347.3	1501.7	572.5
UBD	1455.3	5201.2	2166.1	2985.9	3114.3	1415.1
GBP5	57.9	185.1	58	152.2	784.7	713.9
ACKR4	506.8	839.1	930.2	533.9	671.8	336
ADM	2174.7	1366	1420.8	825.5	2953.6	3967.2
PHLDA1	260.5	221.1	328.1	474	686.7	1311.6
MMP7	278.5	93	991.4	212.9	480.5	142.1
CXCL5	45.8	48.9	56.2	52.8	103.7	41.9
RAB31	185.2	431.6	319	761.9	2382	1086.1
CCL3L3	94.2	579.9	56.5	830.8	2869.8	2207.2
NAMPT	160	709.6	693.8	494	3153.9	1852.9
ACSL1	204.5	748.6	533.3	661.4	2874.1	2346.1
C4BPA	404.9	276.8	83.9	9.7	502.2	672
LILRB2	8.3	140.9	72.2	223.3	482.1	419.2
TCN1	439.3	957.9	2147.3	199.7	579.2	453.3
BACE2	1627.4	1081.8	1322.6	613.1	1014.9	1426.3
RND1	69.5	189.8	169.1	49.3	157.3	140.1
IRF1	629.9	1279	731.4	1281.2	2373.9	1740.3
TAP1	1709.7	2484	1531.6	2397.4	2939.7	2809.2
CXCR2	46.2	310.6	118.4	302.7	1379	567.2
MAFF	137.2	176.4	184.4	231.1	303	239.6
CSF2RB	275.9	598.6	221	651.7	2868	1656
PDE4B	81.9	276.8	82.5	498.4	3114.8	1084.9
CCL2	53	329.4	46.4	554.7	1725.7	2257.4
CD274	48.4	43.2	58.5	128.8	205.8	229.2
TFPI2	54.9	126.8	563.7	448.8	1992.3	548.8
CYR61	80.9	76.1	52.9	608	703	581.6
CCL4	65.4	498.5	102.3	1275	2209.1	2060.8
CSF3R	159.4	355.5	160.1	446.8	815.9	640
KYNU	111.4	143	232.1	101.2	585.8	169.4
MMP9	185.9	174.2	150.2	2523.9	771.7	1335.4
UBE2L6	707.9	959.6	983.6	903.6	2307.6	1252.3
MUC1	2845.1	1172.8	2598.9	509.4	1785.4	2078.3
IL13RA2	50.3	151.6	147.6	132.2	591.6	551.9
PROK2	39.3	390.3	22.3	399.7	1553.6	581.3
S100P	9601.4	3723.9	9970.6	989.4	8084.6	6767.8

SERPINA3	814.9	2361.6	796.2	305.3	447	224.4
GBP2	509	1233.6	495.3	631.3	1975.5	982.4
COL15A1	646.1	337.6	199.9	1091	4842.1	1669
REG4	15067.4	16274.2	13191.1	7521.6	9817.7	7382.1
GZMB	75.4	270.9	225.3	492.4	755.2	277.1
FOXQ1	643.8	143.2	1951.6	268.2	364.3	283.6
LPL	386.4	361.4	78.2	724.7	183.4	164.3
TNIP3	50.8	59.1	26	123	215.7	794.6
C2CD4A	184.5	492.1	123.6	150.9	201.5	217.4
PCSK1	142.6	124	198.9	75.7	400.5	508.9
LPCAT1	320.2	513.5	365.6	206.7	567.8	308.8
CTHRC1	218.6	112.9	213.9	580.4	2294	1211.2
SRGN	21.6	40.2	18	63.9	121.2	79.8
EGFL6	83	46.6	65.7	92.7	388	261.7
C1R	230.8	348.6	272.1	533.5	934.8	802.1
DRAM1	172.1	192.6	180.3	260.5	440.7	365.7
PLA2G2A	11892.3	10528.1	4964.8	10988.6	10533.8	15153.8
VNN1	1222.2	1122.3	1388.4	977.6	225.9	71.7
FCGR1B	24	113.7	40.9	98	281	408
HLA-DMA	1119.7	1371.9	1095.1	1375.6	1873.8	1398.4
FCGR1CP	21.1	128.3	31	113.1	292	347
CCL11	62.2	125.4	174.2	219	573.6	386.4
PFKFB3	446.7	1114.2	539.3	1117.8	2082.5	1802.6
IL1RN	1121.2	2073	1594.4	2912	8996.1	4990
TREM1	13	299.3	127.2	371.2	1161.5	631.2
FCER1G	52	183.2	132.8	387.2	618.1	885.7
COL1A2	1125.8	823.6	1634	3695.7	10151.7	6814.6
IFITM1	4422.4	5338.1	2614.4	3637.7	6072.6	8314.9
INHBA	3.2	15	30.8	67.9	100.1	83.9
GPR84	19.8	27.5	2.7	173.3	262.8	277.2
GREM1	85.7	362.9	194.2	1237.2	2223.2	359.6
PLA2G7	70.7	99.5	61.3	206.3	760.2	288.3
IER3	1279.1	1461.8	936.3	2391.1	4008	5963
STC1	67.1	97.5	76	471.1	243.9	689.1
SLC7A11	78.2	56.3	75.4	59.9	69	123.2
TMEM45A	780.9	107.8	462.2	142.9	709.5	232.7
PDZK1IP1	3428.1	3731.6	3138.1	698	1585.3	2030.1
TNFSF13B	185.8	306.4	290.4	356.4	802.8	465.4
SELL	108.4	321	165.6	538.7	1582.7	1358.3
GOS2	232.3	775.6	207.2	1552.8	3718.5	3085.5
L1TD1	201.6	66	198.7	6	612.5	650.5
MIR8071-2	6210.6	5973	8167.3	5593	14788.1	20421.7
ADGRL4	143.6	149.2	43.8	145.5	690.4	284.9
MXRA5	1538.8	2288.5	1052.7	521.2	1436.5	1060.3
CLDN8	0.8	8.9	22.3	1.3	9.8	19.1
GUCA2A	2916.8	5704.6	953.3	7433.5	500.1	1432.3
AQP8	283.8	7.4	8	8.1	196.5	311.7
ABCG2	1381.8	1171.8	1458.6	3171.7	300.6	67.1
CHP2	1402.4	1919.6	684	2311.8	519.5	357.2
PCK1	1504.1	569.4	3464.4	2637	221.7	390.4
HMGCS2	675	116.3	1287.1	137.8	215.9	61.5
SLC26A2	5619.3	1088.7	544.8	1858.5	929.8	1614.3
GUCA2B	289	811.2	426.2	1166.2	124.3	294.2

CDHR1	29.3	4.5	4.4	41	14	45.7
HSD17B2	3055	1968.5	2978.8	2541.3	496.1	451.7
ABCB1	762.7	2004.2	510.2	1683.3	129.6	108.8
SLC16A9	225.5	16.6	254.8	22.5	115.6	108.7
PNLIPRP2	3.3	3924.4	98.4	293.2	20	5.6
SLC51B	774.6	1142.6	433.8	773.9	398.1	337.6
ADIRF	1042.2	5518.1	3806	3640.1	513.5	205.9
MT1M	158.2	148.5	194.3	968.8	25.8	8.4
MEP1A	5129.3	9438	4078.9	9801.4	921.6	742
MT1F	1718.4	1394.1	878.6	5232.2	261.9	228.8
DHRS11	1925.4	2050.8	1836.8	3379	401.8	580.4
TRPM6	9.7	25.6	39.8	64.8	39.2	68.1
UGT2A3	92.2	1825.2	1938.5	2850.2	45.6	180.9
SLC26A3	15467.6	6410.8	7956.9	5671.3	13358.8	12786.3