

Supplementary File 2 Differentially expressed genes (p-value < 0.05, no adjustment for multiple testing), with FC < -1.5 or FC > 1.5 (logFC 0.58) between groups CDM3, M0, and CDM0.

CDM3vsM0

Gene ID	Length	Entrez ID	Name	logFC	AveExpr	t	p-value
LRRC37A4P	6924	55073	leucine rich repeat containing 37 member A4, pseudogene	1,69	2,94	3,02	0,0052
TNNT1	2171	7138	troponin T1, slow skeletal type	1,59	0,69	2,72	0,011
SIGLEC1	7886	6614	sialic acid binding Ig like lectin 1	1,58	1,86	2,20	0,035
ISG15	942	9636	ISG15 ubiquitin-like modifier	1,56	3,36	2,10	0,044
IFI44L	10240	10964	interferon induced protein 44 like	1,42	6,87	2,15	0,040
OAS3	8251	4940	2'-5'-oligoadenylate synthetase 3	1,37	5,74	2,70	0,011
USP18	2129	11274	ubiquitin specific peptidase 18	1,36	0,97	2,16	0,039
IFITM3	1348	10410	interferon induced transmembrane protein 3	1,35	3,98	2,33	0,027
LY6E	2640	4061	lymphocyte antigen 6 family member E	1,33	3,09	2,78	0,0093
JUP	4942	3728	junction plakoglobin	1,25	1,37	2,43	0,021
D2HGDH	5279	728294	D-2-hydroxyglutarate dehydrogenase	1,12	1,59	3,27	0,0027
CATSPERG	9190	57828	cation channel sperm associated auxiliary subunit gamma	1,09	1,61	4,34	0,00015
TCN2	3122	6948	transcobalamin 2	1,09	1,05	2,33	0,027
ZDHC8	5542	29801	zinc finger DHHC-type containing 8	1,08	1,20	2,28	0,030
HELZ2	12066	85441	helicase with zinc finger 2	1,07	4,50	2,35	0,026
RASSF7	2492	8045	Ras association domain family member 7	1,05	2,00	2,29	0,029
PARP10	6033	84875	poly(ADP-ribose) polymerase family member 10	1,04	5,14	2,41	0,022
NTNG2	7845	84628	netrin G2	1,03	3,26	3,06	0,0046
MX1	8616	4599	MX dynamin like GTPase 1	1,02	7,27	2,15	0,040
FAAH	2776	2166	fatty acid amide hydrolase	1,02	1,77	3,77	0,00072
SCO2	1361	9997	SCO2, cytochrome c oxidase assembly protein	1,01	3,54	2,19	0,037
AIFM3	5401	150209	apoptosis inducing factor, mitochondria associated 3	1,01	1,00	2,93	0,0064
ARHGEF10L	7817	55160	Rho guanine nucleotide exchange factor 10 like	1,01	3,31	2,96	0,0059
SPNS3	2684	201305	sphingolipid transporter 3 (putative)	1,00	0,95	2,11	0,043
KCNC4	25042	3749	potassium voltage-gated channel subfamily C member 4	0,95	1,23	3,47	0,0016
NFIC	9347	4782	nuclear factor I C	0,94	1,14	2,42	0,022
CARD9	6699	64170	caspase recruitment domain family member 9	0,94	3,09	2,48	0,019
THEM6	3055	51337	thioesterase superfamily member 6	0,93	1,79	2,61	0,014
ABCD1	4233	215	ATP binding cassette subfamily D member 1	0,93	1,16	2,36	0,025
FAAP100	5354	80233	Fanconi anemia core complex associated protein 100	0,93	1,60	2,46	0,020

BCL9L	10470	283149	B cell CLL/lymphoma 9 like	0,93	3,22	2,34	0,026
XAF1	6615	54739	XIAP associated factor 1	0,92	7,84	2,34	0,026
TSPAN4	5841	7106	tetraspanin 4	0,91	0,99	2,60	0,014
ASPSCR1	12097	79058	ASPSCR1, UBX domain containing tether for SLC2A4	0,89	1,68	2,76	0,010
SSBP4	2974	170463	single stranded DNA binding protein 4	0,88	1,42	2,30	0,029
GPR162	3295	27239	G protein-coupled receptor 162	0,88	1,17	2,21	0,035
S1PR3	8754	1903	sphingosine-1-phosphate receptor 3	0,87	2,40	2,33	0,027
ZC3H3	3731	23144	zinc finger CCCH-type containing 3	0,87	1,73	2,64	0,013
HNRNPA1P70	1087	341333	heterogeneous nuclear ribonucleoprotein A1 pseudogene 70	0,87	1,73	2,72	0,011
ZBP1	5405	81030	Z-DNA binding protein 1	0,86	5,28	2,47	0,019
COL9A2	4151	1298	collagen type IX alpha 2 chain	0,86	1,05	2,64	0,013
MTCYBP23	1102	107075131	mitochondrially encoded cytochrome b pseudogene 23	0,86	1,24	2,48	0,019
ARHGDI1	2903	396	Rho GDP dissociation inhibitor alpha	0,86	2,15	2,47	0,019
TELO2	4239	9894	telomere maintenance 2	0,85	1,89	2,26	0,031
NDUFB7	531	4713	NADH:ubiquinone oxidoreductase subunit B7	0,85	2,00	2,07	0,047
CAP2P1	1390	353163	cyclase associated actin cytoskeleton regulatory protein 2 pseudogene 1	0,85	0,82	2,29	0,029
SLC9A1	5974	6548	solute carrier family 9 member A1	0,84	2,01	2,37	0,024
CEP295NL	2758	100653515	CEP295 N-terminal like	0,84	1,25	2,75	0,010
ECH1	2467	1891	enoyl-CoA hydratase 1	0,83	3,79	2,67	0,012
B4GALT7	4927	11285	beta-1,4-galactosyltransferase 7	0,83	2,42	2,93	0,0064
PLXNB2	7257	23654	plexin B2	0,81	4,58	2,29	0,029
C7orf50	4961	84310	chromosome 7 open reading frame 50	0,80	2,00	2,40	0,023
HLA-DQB2	2028	3120	major histocompatibility complex, class II, DQ beta 2	0,80	2,60	2,44	0,021
C1QA	1272	712	complement C1q A chain	0,80	0,78	2,24	0,033
C11orf24	3406	53838	chromosome 11 open reading frame 24	0,80	1,93	2,12	0,042
DPP7	2820	29952	dipeptidyl peptidase 7	0,79	3,38	2,04	0,050
LRRRC45	3606	201255	leucine rich repeat containing 45	0,79	2,25	2,68	0,012
LRP1	20839	4035	LDL receptor related protein 1	0,78	6,66	2,61	0,014
NELFA	5935	7469	negative elongation factor complex member A	0,78	1,73	2,32	0,027
IGSF9B	5753	22997	immunoglobulin superfamily member 9B	0,77	0,72	2,44	0,021
FLYWCH1	8419	84256	FLYWCH-type zinc finger 1	0,76	2,46	2,13	0,041
STAB1	10588	23166	stabilin 1	0,75	4,99	2,27	0,031
PPP1R26	5276	9858	protein phosphatase 1 regulatory subunit 26	0,75	1,50	2,70	0,011
FAM129B	4629	64855	family with sequence similarity 129 member B	0,75	3,28	2,40	0,023
DHX58	3843	79132	DExH-box helicase 58	0,75	4,80	2,18	0,037

DLGAP4	8789	22839	DLG associated protein 4	0,75	1,74	2,57	0,015
TNRC18	12572	84629	trinucleotide repeat containing 18	0,75	3,82	2,27	0,030
BRICD5	2083	283870	BRICHOS domain containing 5	0,74	1,55	2,67	0,012
GPBAR1	2692	151306	G protein-coupled bile acid receptor 1	0,74	1,96	2,13	0,041
NR1H3	4533	10062	nuclear receptor subfamily 1 group H member 3	0,74	0,94	2,97	0,0058
CHKB-CPT1B	5022	386593	CHKB-CPT1B readthrough (NMD candidate)	0,74	0,99	2,33	0,027
ANO8	4979	57719	anoctamin 8	0,74	1,44	2,86	0,008
LENG8	6469	114823	leukocyte receptor cluster member 8	0,74	4,52	2,30	0,029
POLRMTP1	3668	284167	RNA polymerase mitochondrial pseudogene 1	0,74	1,05	2,59	0,015
TTC21A	7735	199223	tetratricopeptide repeat domain 21A	0,73	2,51	2,46	0,020
POMGNT2	2668	84892	protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-)	0,72	1,32	2,40	0,023
MIR4697HG	5164	283174	MIR4697 host gene	0,72	1,77	2,58	0,015
ST14	4350	6768	suppression of tumorigenicity 14	0,72	2,54	2,17	0,038
ZNF444	7239	55311	zinc finger protein 444	0,72	1,59	2,71	0,011
HIST1H2AI	503	8329	histone cluster 1 H2A family member i	0,72	2,31	2,17	0,038
WIZ	7965	58525	widely interspaced zinc finger motifs	0,72	1,17	2,07	0,047
SLC12A7	5984	10723	solute carrier family 12 member 7	0,71	3,24	2,32	0,027
TTC16	6370	158248	tetratricopeptide repeat domain 16	0,71	2,27	2,44	0,021
MIR142	1625	406934	microRNA 142	0,71	3,61	2,14	0,041
ZNF618	10384	114991	zinc finger protein 618	0,71	0,86	2,93	0,0064
C3AR1	2145	719	complement C3a receptor 1	0,71	4,01	2,65	0,013
HERC6	5793	55008	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	0,71	5,32	2,40	0,023
DUS3L	3642	56931	dihydrouridine synthase 3 like	0,71	2,53	2,18	0,037
LRP5L	4555	91355	LDL receptor related protein 5 like	0,70	2,73	3,05	0,0047
FBXW5	3252	54461	F-box and WD repeat domain containing 5	0,70	4,07	2,17	0,038
STMN3	3032	50861	stathmin 3	0,70	3,85	2,35	0,026
AATBC	4874	284837	apoptosis associated transcript in bladder cancer	0,70	4,17	2,73	0,010
RABGGTA	3545	5875	Rab geranylgeranyltransferase alpha subunit	0,70	2,10	2,82	0,0085
MLST8	4323	64223	MTOR associated protein, LST8 homolog	0,70	1,92	2,34	0,026
SYNGAP1	12695	8831	synaptic Ras GTPase activating protein 1	0,69	2,35	2,26	0,031
MROH1	10903	727957	maestro heat like repeat family member 1	0,69	2,69	2,30	0,029
CLEC6A	1682	93978	C-type lectin domain containing 6A	0,69	1,10	2,09	0,046
IQSEC2	6962	23096	IQ motif and Sec7 domain 2	0,69	0,73	2,04	0,050
PRAM1	3763	84106	PML-RARA regulated adaptor molecule 1	0,69	3,02	2,77	0,0096
NCOR2	13975	9612	nuclear receptor corepressor 2	0,69	3,47	2,39	0,023

DRAP1	1737	10589	DR1 associated protein 1	0,68	3,82	2,15	0,040
CDC42BPG	6112	55561	CDC42 binding protein kinase gamma	0,68	0,80	2,08	0,046
TNFSF13	2276	8741	TNF superfamily member 13	0,68	1,50	2,12	0,042
GADD45GIP1	1782	90480	GADD45G interacting protein 1	0,68	2,55	2,07	0,047
PARP12	6285	64761	poly(ADP-ribose) polymerase family member 12	0,67	6,44	2,55	0,016
SLC25A29	7451	123096	solute carrier family 25 member 29	0,67	2,84	2,37	0,025
LLGL1	6638	3996	LLGL1, scribble cell polarity complex component	0,67	2,58	2,17	0,038
BST2	1119	684	bone marrow stromal cell antigen 2	0,67	4,99	2,05	0,050
HLA-DRB6	1326	3128	major histocompatibility complex, class II, DR beta 6 (pseudogene)	0,66	4,48	2,17	0,038
UNC93B1	3548	81622	unc-93 homolog B1, TLR signaling regulator	0,66	4,72	2,15	0,039
C9orf139	4990	401563	chromosome 9 open reading frame 139	0,66	2,66	2,21	0,035
RFNG	3865	5986	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0,66	1,23	2,15	0,040
HK3	3290	3101	hexokinase 3	0,66	6,51	2,14	0,041
SUMO2P6	288	100127922	SUMO2 pseudogene 6	0,66	0,92	2,16	0,039
GALNS	8402	2588	galactosamine (N-acetyl)-6-sulfatase	0,65	3,34	2,98	0,0057
PILRB	5764	29990	paired immunoglobulin-like type 2 receptor beta	0,65	3,81	2,50	0,018
TNK2	11297	10188	tyrosine kinase non receptor 2	0,65	4,68	2,09	0,045
TP53I3	2312	9540	tumor protein p53 inducible protein 3	0,65	1,48	2,25	0,032
USP35	5233	57558	ubiquitin specific peptidase 35	0,64	1,39	2,32	0,027
KCTD17	2786	79734	potassium channel tetramerization domain containing 17	0,64	1,29	2,10	0,044
MYO15B	12761	80022	myosin XVB	0,63	5,57	2,27	0,031
TTYH2	5375	94015	tweety family member 2	0,63	2,54	3,00	0,0054
ACAP3	8809	116983	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	0,63	3,28	2,17	0,038
NRROS	2910	375387	negative regulator of reactive oxygen species	0,63	1,74	2,44	0,021
ATP13A1	8376	57130	ATPase 13A1	0,63	3,04	2,54	0,017
SLC27A5	8025	10998	solute carrier family 27 member 5	0,63	0,92	2,60	0,014
RPL7AP64	663	728486	ribosomal protein L7a pseudogene 64	0,63	2,06	2,89	0,0070
GRAMD1B	13946	57476	GRAM domain containing 1B	0,62	3,38	2,43	0,021
ARFGAP1	6613	55738	ADP ribosylation factor GTPase activating protein 1	0,62	3,12	2,12	0,042
PRKD2	5446	25865	protein kinase D2	0,61	4,80	3,20	0,0032
TRMT112P6	372	391358	tRNA methyltransferase subunit 11-2 pseudogene 6	0,61	0,92	2,12	0,043
CTIF	8100	9811	cap binding complex dependent translation initiation factor	0,61	0,90	2,21	0,035
EEFSEC	2421	60678	eukaryotic elongation factor, selenocysteine-tRNA specific	0,61	1,79	2,76	0,010
PSRC1	2855	84722	proline and serine rich coiled-coil 1	0,60	2,07	2,39	0,023
FAM102A	6100	399665	family with sequence similarity 102 member A	0,60	3,78	2,24	0,033

CROCCP3	6813	114819	ciliary rootlet coiled-coil, rootletin pseudogene 3	0,60	2,21	3,06	0,0046
DHRS1	5002	115817	dehydrogenase/reductase 1	0,60	2,39	2,62	0,014
HPS6	2649	79803	HPS6, biogenesis of lysosomal organelles complex 2 subunit 3	0,60	2,60	2,42	0,022
ASTN2	8290	23245	astrotactin 2	0,60	1,02	2,47	0,019
MVB12B	7884	89853	multivesicular body subunit 12B	0,59	1,52	2,57	0,015
TIAF1	5337	9220	TGFB1-induced anti-apoptotic factor 1	0,59	1,44	2,54	0,017
PPARGC1B	12889	133522	PPARG coactivator 1 beta	0,59	3,06	2,66	0,012
KMT5C	4775	84787	lysine methyltransferase 5C	0,59	0,83	2,33	0,026
TPRG1	9535	285386	tumor protein p63 regulated 1	0,59	1,65	2,19	0,036
PRDX6	2367	9588	peroxiredoxin 6	-0,59	8,49	-2,11	0,044
CFAP53	1851	220136	cilia and flagella associated protein 53	-0,59	0,77	-2,16	0,038
MYLK	22167	4638	myosin light chain kinase	-0,59	6,02	-2,23	0,033
USP12	5195	219333	ubiquitin specific peptidase 12	-0,59	8,84	-2,09	0,045
MEST	4631	4232	mesoderm specific transcript	-0,59	2,78	-3,19	0,0033
F13A1	4690	2162	coagulation factor XIII A chain	-0,63	9,21	-2,55	0,016
ITGA9	8277	3680	integrin subunit alpha 9	-0,63	1,02	-2,31	0,028
NCR1	1893	9437	natural cytotoxicity triggering receptor 1	-0,63	2,86	-2,50	0,018
RNF14	4987	9604	ring finger protein 14	-0,64	7,85	-2,51	0,018
GRAMD1C	7814	54762	GRAM domain containing 1C	-0,64	4,05	-2,18	0,037
TRAPPC3L	2757	100128327	trafficking protein particle complex 3 like	-0,64	3,06	-2,20	0,036
FAM46C	5751	54855	family with sequence similarity 46 member C	-0,65	11,8	-2,20	0,036
PHEX	6384	5251	phosphate regulating endopeptidase homolog X-linked	-0,66	2,29	-2,26	0,031
PLEK2	1603	26499	pleckstrin 2	-0,66	4,79	-2,51	0,0177
MAP7	5447	9053	microtubule associated protein 7	-0,67	1,92	-2,26	0,031
GOLGA8N	7602	643699	golgin A8 family member N	-0,67	1,36	-2,14	0,041
RBMS3	18339	27303	RNA binding motif single stranded interacting protein 3	-0,67	0,76	-2,13	0,042
PCMTD1P3	472	100422595	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1 pseudogene 3	-0,67	1,25	-2,81	0,0086
TRAV22	464	28661	T cell receptor alpha variable 22	-0,69	0,85	-2,53	0,017
ZNF667-AS1	3629	100128252	ZNF667 antisense RNA 1 (head to head)	-0,69	0,75	-2,17	0,038
FKBP1B	1677	2281	FK506 binding protein 1B	-0,69	2,44	-2,27	0,030
RPS4XP7	780	442162	ribosomal protein S4X pseudogene 7	-0,69	0,61	-2,28	0,030
GZMB	1411	3002	granzyme B	-0,71	5,26	-2,40	0,023
SLC6A4	6983	6532	solute carrier family 6 member 4	-0,72	1,34	-2,26	0,031
PAGE2B	507	389860	PAGE family member 2B	-0,73	1,70	-2,27	0,030

ELL2P1	1906	646270	elongation factor for RNA polymerase II 2 pseudogene 1	-0,75	0,80	-2,43	0,021
ABCA13	19074	154664	ATP binding cassette subfamily A member 13	-0,75	3,63	-2,12	0,043
SNCA	4014	6622	synuclein alpha	-0,76	11,8	-2,26	0,031
GYPB	1566	2994	glycophorin B (MNS blood group)	-0,76	5,19	-2,76	0,0096
TCN1	1586	6947	transcobalamin 1	-0,77	2,90	-2,95	0,0061
SPATA20	5337	64847	spermatogenesis associated 20	-0,80	2,57	-2,39	0,023
UBB	1621	7314	ubiquitin B	-0,82	10,9	-2,51	0,017
IGKV3D-20	445	28874	immunoglobulin kappa variable 3D-20	-0,86	0,89	-2,23	0,034
EPB42	5574	2038	erythrocyte membrane protein band 4.2	-0,87	7,14	-2,60	0,014
NFIB	12765	4781	nuclear factor I B	-0,87	1,11	-2,76	0,010
DPCD	1718	25911	deleted in primary ciliary dyskinesia homolog (mouse)	-0,87	2,26	-2,13	0,041
HAVCR1	2151	26762	hepatitis A virus cellular receptor 1	-0,87	1,39	-3,07	0,004
EREG	5717	2069	epiregulin	-0,87	1,69	-2,09	0,045
TRIM40	2497	135644	tripartite motif containing 40	-0,89	0,91	-2,12	0,043
SH2D1B	2797	117157	SH2 domain containing 1B	-0,89	3,35	-2,45	0,020
NCAM1	12737	4684	neural cell adhesion molecule 1	-0,89	3,68	-3,01	0,0052
PITHD1	2186	57095	PITH domain containing 1	-0,91	8,28	-2,99	0,0054
KLRF1	1260	51348	killer cell lectin like receptor F1	-0,94	4,65	-2,58	0,015
AKR1C3	4532	8644	aldo-keto reductase family 1 member C3	-0,98	2,23	-2,88	0,0072
HLA-DQB1	4904	3119	major histocompatibility complex, class II, DQ beta 1	-1,01	6,17	-2,63	0,013
SLC8A3	8444	6547	solute carrier family 8 member A3	-1,02	1,41	-2,39	0,023
ANO2	6255	57101	anoctamin 2	-1,04	0,87	-2,42	0,022
ADAMTS1	7063	9510	ADAM metalloproteinase with thrombospondin type 1 motif 1	-1,07	1,91	-2,40	0,023
SLPI	596	6590	secretory leukocyte peptidase inhibitor	-1,07	2,16	-2,30	0,029
MAGI2-AS3	11625	100505881	MAGI2 antisense RNA 3	-1,14	2,16	-2,21	0,035
KANSL1-AS1	976	644246	KANSL1 antisense RNA 1	-1,18	1,60	-3,06	0,0046
FAT4	16439	79633	FAT atypical cadherin 4	-1,27	1,48	-3,50	0,0015
RPS4XP22	780	100131614	ribosomal protein S4X pseudogene 22	-1,45	3,13	-2,11	0,043
CRISP3	2247	10321	cysteine rich secretory protein 3	-1,69	1,96	-3,36	0,0021
XKR3	1690	150165	XK related 3	-1,69	-0,19	-2,18	0,037
DAAM2	12955	23500	dishevelled associated activator of morphogenesis 2	-1,73	0,69	-3,41	0,0019
CEACAM8	2551	1088	carcinoembryonic antigen related cell adhesion molecule 8	-1,74	1,12	-2,84	0,0081

CDM3vsCDM0

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NACA3P	648	389240	NACA family member 3 pseudogene	1,53	3,70	2,68	0,012
IFI44L	10240	10964	interferon induced protein 44 like	1,42	6,87	2,20	0,036
RSAD2	4834	91543	radical S-adenosyl methionine domain containing 2	1,40	6,70	2,07	0,047
IDO1	3261	3620	indoleamine 2,3-dioxygenase 1	1,36	3,66	2,91	0,0066
VSTM1	1111	284415	V-set and transmembrane domain containing 1	1,27	3,02	3,33	0,0023
IFIT3	2640	3437	interferon induced protein with tetratricopeptide repeats 3	1,18	8,32	2,11	0,043
IFI44	2038	10561	interferon induced protein 44	1,15	6,43	2,14	0,041
HERC5	4766	51191	HECT and RLD domain containing E3 ubiquitin protein ligase 5	1,13	6,42	2,06	0,048
OAS3	8251	4940	2'-5'-oligoadenylate synthetase 3	1,08	5,74	2,20	0,036
SLC16A14	4946	151473	solute carrier family 16 member 14	1,06	0,68	2,63	0,013
RNASE2	755	6036	ribonuclease A family member 2	1,00	3,72	2,43	0,021
KIAA1024	6800	23251	KIAA1024	0,99	0,54	2,20	0,035
MARCO	2079	8685	macrophage receptor with collagenous structure	0,96	2,05	2,37	0,024
ZBP1	5405	81030	Z-DNA binding protein 1	0,87	5,28	2,51	0,018
NTNG2	7845	84628	netrin G2	0,86	3,26	2,63	0,013
XAF1	6615	54739	XIAP associated factor 1	0,85	7,84	2,23	0,033
FBN1	16057	2200	fibrillin 1	0,85	1,56	2,33	0,027
SAMD9L	7135	219285	sterile alpha motif domain containing 9 like	0,80	8,97	2,20	0,035
DDX58	4353	23586	DExD/H-box helicase 58	0,77	8,14	2,19	0,037
DHX58	3843	79132	DExH-box helicase 58	0,71	4,80	2,09	0,045
EIF2AK2	10753	5610	eukaryotic translation initiation factor 2 alpha kinase 2	0,71	7,19	2,24	0,033
C9orf66	2918	157983	chromosome 9 open reading frame 66	0,70	1,13	2,05	0,049
CD101	3828	9398	CD101 molecule	0,68	4,64	3,05	0,0048
TRIM22	6020	10346	tripartite motif containing 22	0,68	9,19	2,14	0,041
RNF213	28570	57674	ring finger protein 213	0,66	10,6	2,65	0,013
SNORA22	540	677807	small nucleolar RNA, H/ACA box 22	0,66	1,17	2,72	0,011
HERC6	5793	55008	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	0,65	5,32	2,25	0,032
CATSPERG	9190	57828	cation channel sperm associated auxiliary subunit gamma	0,65	1,61	2,78	0,0093
SNORA73B	204	26768	small nucleolar RNA, H/ACA box 73B	0,65	6,69	3,12	0,0039
HNRNPA1P70	1087	341333	heterogeneous nuclear ribonucleoprotein A1 pseudogene 70	0,64	1,73	2,13	0,042
CCDC170	5419	80129	coiled-coil domain containing 170	0,64	3,39	2,89	0,0071
PARP12	6285	64761	poly(ADP-ribose) polymerase family member 12	0,63	6,44	2,44	0,021
MRPL36	1394	64979	mitochondrial ribosomal protein L36	0,63	1,46	2,66	0,012

CBWD5	12708	220869	COBW domain containing 5	0,62	2,56	2,61	0,014
SNORA49	136	677829	small nucleolar RNA, H/ACA box 49	0,62	3,24	2,12	0,042
LINC00174	5627	285908	long intergenic non-protein coding RNA 174	0,61	0,98	2,51	0,018
KIAA1958	13119	158405	KIAA1958	0,60	3,40	2,17	0,038
IL15	7860	3600	interleukin 15	0,60	3,65	2,47	0,019
SAT1	2498	6303	spermidine/spermine N1-acetyltransferase 1	0,59	9,10	2,08	0,046
MAP2K6	6125	5608	mitogen-activated protein kinase kinase 6	0,59	4,74	2,62	0,013
VEGFA	14431	7422	vascular endothelial growth factor A	0,59	2,79	3,04	0,0048
TRAPPC3L	2757	100128327	trafficking protein particle complex 3 like	-0,60	3,06	-2,06	0,048
CLEC1B	3670	51266	C-type lectin domain family 1 member B	-0,60	4,09	-2,34	0,026
GPR15	1252	2838	G protein-coupled receptor 15	-0,61	2,36	-2,66	0,012
EPB41	10739	2035	erythrocyte membrane protein band 4.1	-0,61	12,0	-2,36	0,025
ST20-AS1	4223	283687	ST20 antisense RNA 1	-0,61	0,94	-2,22	0,034
FAM46C	5751	54855	family with sequence similarity 46 member C	-0,62	11,8	-2,18	0,037
RAB2B	3610	84932	RAB2B, member RAS oncogene family	-0,64	8,14	-2,33	0,026
HEMGN	2394	55363	hemogen	-0,64	10,4	-2,17	0,038
MYCT1	3030	80177	MYC target 1	-0,65	2,80	-2,49	0,018
PRDX6	2367	9588	peroxiredoxin 6	-0,65	8,49	-2,41	0,022
GSPT1	8018	2935	G1 to S phase transition 1	-0,65	10,2	-2,43	0,021
FKBP1B	1677	2281	FK506 binding protein 1B	-0,66	2,44	-2,19	0,036
DDX6P1	1436	442192	DEAD-box helicase 6 pseudogene 1	-0,66	1,01	-2,22	0,034
IFIT1B	1972	439996	interferon induced protein with tetratricopeptide repeats 1B	-0,67	7,15	-2,22	0,034
TBCEL	7020	219899	tubulin folding cofactor E like	-0,68	8,59	-2,51	0,018
GLRX5	2845	51218	glutaredoxin 5	-0,68	8,20	-2,36	0,025
MAP7	5447	9053	microtubule associated protein 7	-0,68	1,92	-2,32	0,027
TCN1	1586	6947	transcobalamin 1	-0,68	2,90	-2,61	0,014
BPGM	2539	669	bisphosphoglycerate mutase	-0,69	9,34	-2,20	0,035
DYRK3	4218	8444	dual specificity tyrosine phosphorylation regulated kinase 3	-0,70	2,96	-2,83	0,0082
UBXN10	5571	127733	UBX domain protein 10	-0,70	1,93	-2,36	0,025
RTCA-AS1	423	100506007	RTCA antisense RNA 1	-0,71	0,95	-2,43	0,021
DNAJA4	6591	55466	DnaJ heat shock protein family (Hsp40) member A4	-0,71	6,23	-2,96	0,0059
HAVCR1	2151	26762	hepatitis A virus cellular receptor 1	-0,71	1,39	-2,49	0,018
NFIB	12765	4781	nuclear factor I B	-0,75	1,11	-2,35	0,025
ARHGEF37	5324	389337	Rho guanine nucleotide exchange factor 37	-0,75	2,22	-2,24	0,033
RAB6B	6005	51560	RAB6B, member RAS oncogene family	-0,76	1,50	-3,28	0,0026

SPATA20	5337	64847	spermatogenesis associated 20	-0,78	2,57	-2,33	0,026
C9orf153	1932	389766	chromosome 9 open reading frame 153	-0,79	1,59	-2,06	0,048
SNCA	4014	6622	synuclein alpha	-0,80	11,8	-2,47	0,019
UBBP4	1459	23666	ubiquitin B pseudogene 4	-0,80	2,98	-2,07	0,047
UBE2O	6472	63893	ubiquitin conjugating enzyme E2 O	-0,82	5,69	-2,33	0,027
GYPB	1566	2994	glycophorin B (MNS blood group)	-0,82	5,19	-3,02	0,0052
ELL2P1	1906	646270	elongation factor for RNA polymerase II 2 pseudogene 1	-0,84	0,80	-2,77	0,0095
NINJ2	2048	4815	ninjurin 2	-0,84	4,38	-2,22	0,034
NAT8B	765	51471	N-acetyltransferase 8B (putative, gene/pseudogene)	-0,85	0,79	-2,73	0,010
DPCD	1718	25911	deleted in primary ciliary dyskinesia homolog (mouse)	-0,85	2,26	-2,10	0,045
UBB	1621	7314	ubiquitin B	-0,86	10,9	-2,74	0,010
EPB42	5574	2038	erythrocyte membrane protein band 4.2	-0,89	7,14	-2,73	0,011
PAGE2B	507	389860	PAGE family member 2B	-0,89	1,70	-2,84	0,0080
FAXDC2	7222	10826	fatty acid hydroxylase domain containing 2	-0,90	6,67	-2,42	0,022
ANO2	6255	57101	anoctamin 2	-0,90	0,87	-2,09	0,045
PAQR9	4169	344838	progesterin and adipoQ receptor family member 9	-0,91	2,95	-2,40	0,023
SLC8A3	8444	6547	solute carrier family 8 member A3	-0,92	1,41	-2,17	0,038
SLC6A4	6983	6532	solute carrier family 6 member 4	-0,93	1,34	-3,02	0,0051
PITHD1	2186	57095	PITH domain containing 1	-0,95	8,28	-3,23	0,0029
OSBP2	6700	23762	oxysterol binding protein 2	-0,96	5,78	-2,15	0,040
CA1	4068	759	carbonic anhydrase 1	-0,98	8,03	-2,23	0,033
FADS2	11026	9415	fatty acid desaturase 2	-1,01	3,78	-2,11	0,043
XCL2	565	6846	X-C motif chemokine ligand 2	-1,04	1,09	-3,11	0,0040
E2F2	5457	1870	E2F transcription factor 2	-1,06	5,73	-3,35	0,0022
MAGI2-AS3	11625	100505881	MAGI2 antisense RNA 3	-1,11	2,16	-2,15	0,040
ADAMTS1	7063	9510	ADAM metalloproteinase with thrombospondin type 1 motif 1	-1,14	1,91	-2,60	0,014
NLRP2	6313	55655	NLR family pyrin domain containing 2	-1,16	1,83	-2,27	0,030
PIGC	5225	5279	phosphatidylinositol glycan anchor biosynthesis class C	-1,21	7,03	-2,52	0,017
NKX3-1	3271	4824	NK3 homeobox 1	-1,78	2,48	-2,07	0,047

CDM0vsM0

Gene ID	Length	Entrez ID	Name	logFC	AveExpr	t	p-value
TUBB2A	1727	7280	tubulin beta 2A class IIa	2,53	1,15	2,05	0,049
LRR37A4P	6924	55073	leucine rich repeat containing 37 member A4, pseudogene	1,87	2,94	3,35	0,0022
PF4V1	522	5197	platelet factor 4 variant 1	1,60	1,47	2,46	0,020
COL5A3	6750	50509	collagen type V alpha 3 chain	1,48	0,38	2,08	0,046
LGALS2	828	3957	galectin 2	1,06	3,29	2,90	0,0068
PLA2G4C	6613	8605	phospholipase A2 group IVC	0,94	1,38	2,35	0,026
THEM6	3055	51337	thioesterase superfamily member 6	0,88	1,79	2,43	0,021
VWF	10391	7450	von Willebrand factor	0,88	0,99	2,14	0,040
ARHGEF10L	7817	55160	Rho guanine nucleotide exchange factor 10 like	0,82	3,31	2,36	0,025
NECTIN3	6184	25945	nectin cell adhesion molecule 3	0,81	0,79	2,07	0,047
FAAP100	5354	80233	Fanconi anemia core complex associated protein 100	0,80	1,60	2,07	0,047
LRR345	3606	201255	leucine rich repeat containing 45	0,79	2,25	2,68	0,012
SUMO2P6	288	100127922	SUMO2 pseudogene 6	0,79	0,92	2,60	0,014
PHLDB3	4553	653583	pleckstrin homology like domain family B member 3	0,77	1,21	2,25	0,032
G6PC3	4551	92579	glucose-6-phosphatase catalytic subunit 3	0,76	0,84	2,69	0,012
ASPSCR1	12097	79058	ASPSCR1, UBX domain containing tether for SLC2A4	0,75	1,68	2,27	0,030
FLYWCH1	8419	84256	FLYWCH-type zinc finger 1	0,75	2,46	2,09	0,045
BOP1	3716	23246	block of proliferation 1	0,74	1,30	2,09	0,046
LINC01410	3038	103352539	long intergenic non-protein coding RNA 1410	0,74	2,62	2,05	0,049
GADD45GIP1	1782	90480	GADD45G interacting protein 1	0,69	2,55	2,10	0,045
PLA2G15	4464	23659	phospholipase A2 group XV	0,68	1,26	2,52	0,017
TRMT112P6	372	391358	tRNA methyltransferase subunit 11-2 pseudogene 6	0,67	0,92	2,31	0,028
POMGNT2	2668	84892	protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-)	0,67	1,32	2,19	0,036
SLC12A7	5984	10723	solute carrier family 12 member 7	0,67	3,24	2,15	0,040
SEPT10	4131	151011	septin 10	0,66	1,34	2,76	0,010
INTS5	3285	80789	integrator complex subunit 5	0,65	2,68	3,16	0,0036
C3orf18	3248	51161	chromosome 3 open reading frame 18	0,63	2,47	3,31	0,0024
B4GALT7	4927	11285	beta-1,4-galactosyltransferase 7	0,62	2,42	2,14	0,040
MORN1	11337	79906	MORN repeat containing 1	0,61	1,30	2,44	0,021
NCKIPSD	3431	51517	NCK interacting protein with SH3 domain	0,60	1,62	2,47	0,019
BANF1	1645	8815	barrier to autointegration factor 1	0,60	1,34	2,24	0,033
ANO8	4979	57719	anoctamin 8	0,60	1,44	2,27	0,031
DEXI	1722	28955	Dexi homolog	0,59	1,75	2,85	0,0079

PDK2	5481	5164	pyruvate dehydrogenase kinase 2	0,59	2,44	2,66	0,012
NEB	30567	4703	nebulin	-0,62	3,65	-2,10	0,044
TIAM2	11532	26230	T cell lymphoma invasion and metastasis 2	-0,62	4,07	-2,17	0,038
PLK2	4768	10769	polo like kinase 2	-0,63	0,88	-2,19	0,036
KIAA1324L	8115	222223	KIAA1324 like	-0,64	3,70	-2,67	0,012
C7orf25	3248	79020	chromosome 7 open reading frame 25	-0,66	1,11	-2,33	0,027
CCDC144B	9762	284047	coiled-coil domain containing 144B (pseudogene)	-0,67	3,38	-2,08	0,046
TPST1	2871	8460	tyrosylprotein sulfotransferase 1	-0,70	3,30	-3,12	0,0040
FSIP2	23761	401024	fibrous sheath interacting protein 2	-0,70	1,27	-2,05	0,049
DSC1	4271	1823	desmocollin 1	-0,70	2,68	-2,29	0,029
IL18RAP	2966	8807	interleukin 18 receptor accessory protein	-0,70	6,90	-2,20	0,035
LRRRC37A2	6756	474170	leucine rich repeat containing 37 member A2	-0,74	2,20	-2,92	0,007
KLRF1	1260	51348	killer cell lectin like receptor F1	-0,76	4,65	-2,10	0,044
GZMB	1411	3002	granzyme B	-0,77	5,26	-2,60	0,014
APOLD1	7243	81575	apolipoprotein L domain containing 1	-0,78	1,72	-2,27	0,030
SMC1B	4253	27127	structural maintenance of chromosomes 1B	-0,79	1,27	-2,10	0,044
FAT4	16439	79633	FAT atypical cadherin 4	-0,83	1,48	-2,42	0,022
RGS1	4117	5996	regulator of G protein signaling 1	-0,87	2,31	-3,11	0,004
HLA-DQB1	4904	3119	major histocompatibility complex, class II, DQ beta 1	-0,87	6,17	-2,27	0,030
CNTNAP3	9521	79937	contactin associated protein like 3	-0,90	4,00	-2,23	0,033
ABCA13	19074	154664	ATP binding cassette subfamily A member 13	-0,91	3,63	-2,49	0,019
RNASE2	755	6036	ribonuclease A family member 2	-0,92	3,72	-2,20	0,036
SLC16A14	4946	151473	solute carrier family 16 member 14	-1,04	0,68	-2,55	0,016
EREG	5717	2069	epiregulin	-1,11	1,69	-2,54	0,016
MYZAP	2561	100820829	myocardial zonula adherens protein	-1,12	1,63	-2,36	0,025
KANSL1-AS1	976	644246	KANSL1 antisense RNA 1	-1,26	1,60	-3,21	0,003
GSTM3	4750	2947	glutathione S-transferase mu 3	-1,30	1,90	-2,42	0,022
DAAM2	12955	23500	dishevelled associated activator of morphogenesis 2	-1,31	0,69	-2,73	0,010
HLA-J	1946	3137	major histocompatibility complex, class I, J (pseudogene)	-1,33	4,39	-2,14	0,040