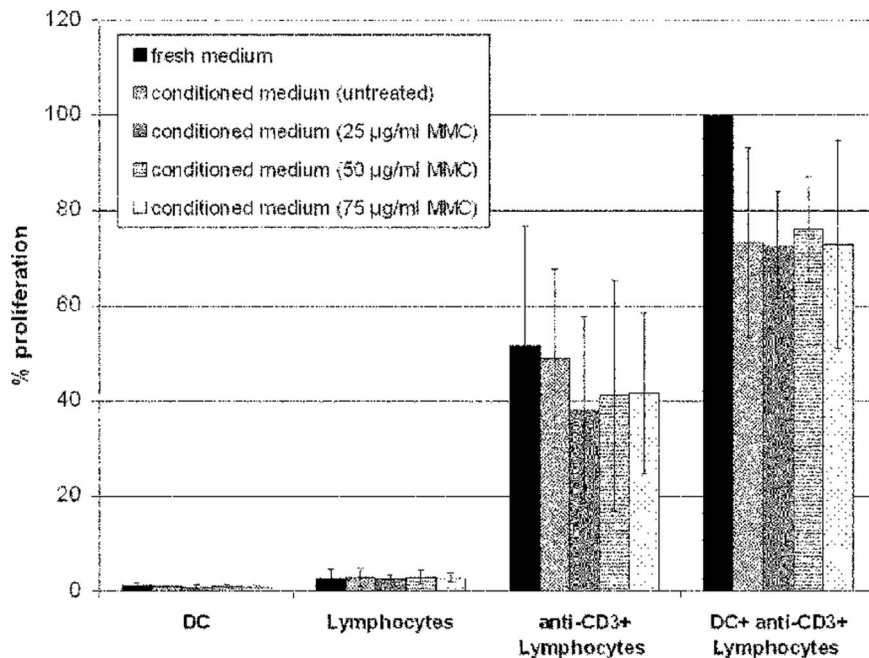
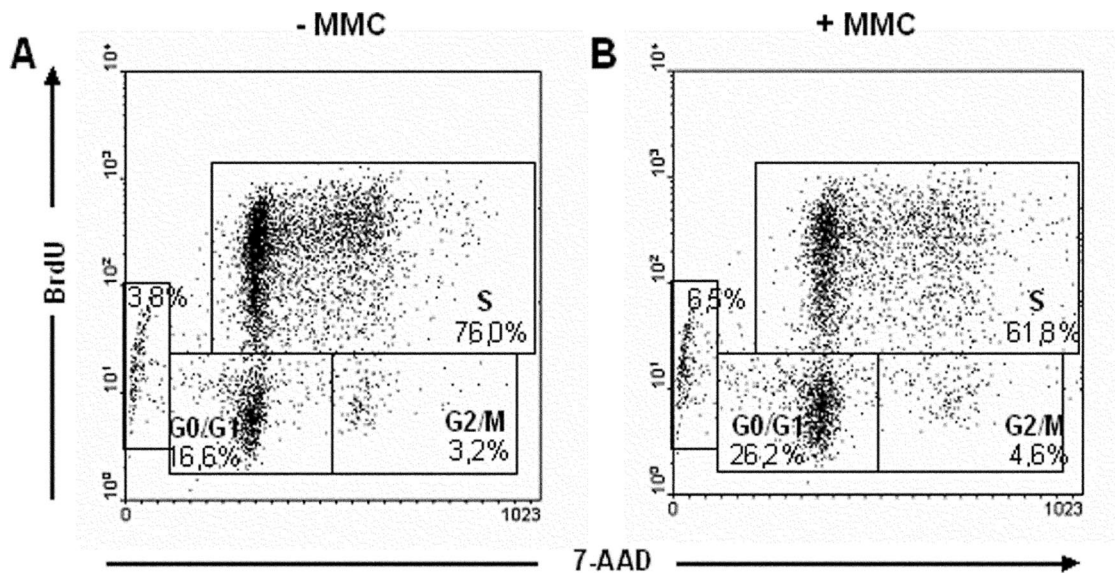


# Supporting Information

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**Fig. S1.** Influence of MMC-DCs culture medium on stimulated T cells. MMC-treated (25–75 µg/ml) or untreated DCs were cultivated for 72 h. Supernatants (conditioned medium) were collected and used for cultures of anti-CD3 antibody-stimulated T cells ( $2 \times 10^5$  per well; 4 days), with or without autologous DCs. Controls consisted of DCs and lymphocytes only. Data represent mean  $\pm$  SD and are expressed as percentage of positive control values (DC+anti-CD3+lymphocytes = 100%) (conditioned medium MMC versus conditioned medium untreated,  $P > 0.05$ ) ( $n = 4$ ).



**Fig. S2.** Cell cycle analysis of T cells exposed to MMC-DCs. Anti-CD3 antibody-stimulated T cells were cocultured with (A) untreated and (B) MMC-treated (25  $\mu$ g MMC/ml) autologous DCs for 2 days. Twenty-four hours after supplementation with 10  $\mu$ M BrdU, the cells were analyzed by flow cytometry using a BrdU-Flow-Kit (BD PharMingen). The displayed quadrants show the percentage of cells in the corresponding cell cycle (G<sub>0</sub>/G<sub>1</sub>, G<sub>2</sub>/M, S) as well as that of dead cells.

**Table S1. Gene expression of MMC-treated DCs measured by affymetrix microarray**

Down-regulated Genes	Acc. No.	Symbol	Gene	Function	Fold change	P-Value
<b>Development</b>	NM_000127	EXT1	exostoses (multiple) 1	skeletal development, glycosaminoglycan biosynthesis, cell cycle	5.28	<10 <sup>-8</sup>
	NM_032242	PLXNA1	plexin A1	development	1.32	39.09 x 10 <sup>-8</sup>
	M64445	CSF2RA	colony stimulating factor 2 receptor, $\alpha$ , low-affinity (granulocyte-macrophage)	proliferation, differentiation and functional activation of hematopoietic stem cells	2.83	<10 <sup>-8</sup>
	NM_030775	WNT5B	wingless-type MMTV integration site family, member 5B	development, frizzled-2 and Wnt receptor signaling pathway	3.03	0.01 x 10 <sup>-8</sup>
<b>Apoptosis</b>	NM_006457	PDLIM5	PDZ and LIM domain 5	organ development, cell lineage specification	2.30	1.84 x 10 <sup>-8</sup>
	NM_003879	<b>CFLAR</b>	CASP8 and FADD-like apoptosis regulator (coding for cFLIP)	anti-apoptosis, induction of apoptosis by extracellular signals	2.00	<10 <sup>-8</sup>
	*AF01545			2.00	<10 <sup>-8</sup>	
	*AF041461			2.00	0.47 x 10 <sup>-8</sup>	
	*AF009619			1.74	71.51 x 10 <sup>-8</sup>	
NM_013982	<b>NRG2</b>	neuregulin 2	anti-apoptosis, signal transduction, cell-cell signaling, embryonic development	5.66	<10 <sup>-8</sup>	
<b>Metabolism</b>	NM_001329	CTBP2	C-terminal binding protein 2	L-serine biosynthesis, metabolism, negative regulation of cell proliferation	4.29	2.50 x 10 <sup>-8</sup>
	*AF222711				4.59	0.75 x 10 <sup>-8</sup>
	*BC002486				3.25	0.1 x 10 <sup>-8</sup>
	NM_024830	AYTL2	acyltransferase like 2	metabolism	3.48	<10 <sup>-8</sup>
	NM_022172	PC	pyruvate carboxylase	gluconeogenesis, metabolism, lipid biosynthesis	3.48	1.23 x 10 <sup>-8</sup>
	NM_000167	GK	glycerol kinase	Carbohydrate-, glycerol-3-phosphate-, glycerol-metabolism	3.25	<10 <sup>-8</sup>
	M55575	BCKDHB	branched chain keto acid dehydrogenase E1, $\beta$ polypeptide	branched chain family amino acid catabolism	6.50	0.15 x 10 <sup>-8</sup>
<b>Protein Modification</b>	NM_017792	<b>MAP4K4</b>	mitogen-activated protein kinase kinase kinase 4	protein amino acid phosphorylation, response to stress	5.66	6.24 x 10 <sup>-8</sup>
	NM_003033	ST3GAL1	ST3 $\beta$ -galactoside $\alpha$ -2,3-sialyltransferase 1	protein amino acid glycosylation, protein modification	4.00	0.15 x 10 <sup>-8</sup>
	NM_000944	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, $\alpha$ isoform (calcineurin A $\alpha$ )	protein amino acid dephosphorylation	2.30	0.64 x 10 <sup>-8</sup>
	NM_005160	ADRBK2	adrenergic, $\beta$ , receptor kinase 2	protein amino acid phosphorylation, signal transduction	2.64	0.08 x 10 <sup>-8</sup>
	NM_004834	MAP4K4	mitogen-activated protein kinase kinase kinase 4	protein amino acid phosphorylation, response to stress, promotes migration of cells	3.48	2.27 x 10 <sup>-8</sup>
	NM_006904	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	double-strand break repair, DNA recombination, protein modification	4.29	16.95 x 10 <sup>-8</sup>
	NM_004667	HERC2	hect domain and RLD 2	ubiquitin cycle, intracellular protein transport, protein modification	6.50	0.33 x 10 <sup>-8</sup>
	AB034951	HSPA8	heat shock 70kDa protein 8	protein folding, response to unfolded protein	1.74	<10 <sup>-8</sup>
	AF135794	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, $\gamma$ )	protein amino acid phosphorylation, signal transduction	10.56	48.70 x 10 <sup>-8</sup>
	NM_006904	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	double-strand break repair via nonhomologous end joining, DNA recombination, protein modification	4.29	<10 <sup>-8</sup>
	NM_024064	PRKCH	protein kinase C, $\epsilon$	protein amino acid phosphorylation, intracellular signaling cascade	3.48	28.73 x 10 <sup>-8</sup>

Down-regulated Genes						
Genes	Acc. No.	Symbol	Gene	Function	Fold change	P-Value
Transport	NM_014683	ULK2	unc-51-like kinase 2 (C. elegans)	protein amino acid phosphorylation	2.14	46.71 x 10 <sup>-8</sup>
	NM_021945	C6orf85	chromosome 6 open reading frame 85	transport	5.66	20.38 x 10 <sup>-8</sup>
	NM_004853	STX8	syntaxin 8	transport	4.59	5.1 x 10 <sup>-8</sup>
	NM_006348	COG5	component of oligomeric golgi complex 5	intra-Golgi vesicle-mediated and protein transport	3.48	4.60 x 10 <sup>-8</sup>
	NM_018264	TYW1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	electron transport	3.25	19.96 x 10 <sup>-8</sup>
	NM_018303	EXOC2	exocyst complex component 2	exocytosis, protein transport	2.64	<10 <sup>-8</sup>
	NM_004565	PEX14	peroxisomal biogenesis factor 14	protein targeting and transport	2.46	16.51 x 10 <sup>-8</sup>
	NM_014251	SLC25A13	solute carrier family 25, member 13 (citric)	transport	2.83	0.6 x 10 <sup>-8</sup>
	NM_020674	CYP20A1	cytochrome P450, family 20, subfamily A, polypeptide 1	electron transport	2.46	0.93 x 10 <sup>-8</sup>
	Signal Transduction	NM_005369	MCF2	MCF.2 cell line derived transforming sequence	intracellular signaling cascade, regulation of Rho protein signal transduction	27.86
NM_019011		TRIAD3	TRIAD3 protein	ubiquitin cycle, apoptosis, ATP synthesis coupled proton transport	2.00	4.06 x 10 <sup>-8</sup>
NM_012296		GAB2	GRB2-associated binding protein 2	signaling to antigen, cytokines and growth factor receptor	3.73	<10 <sup>-8</sup>
NM_002221		ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	signal transduction	8.57	1.61 x 10 <sup>-8</sup>
NM_004145		MYO9B	myosin IXB	intracellular signaling cascade, actin filament-based movement, signal transduction	2.30	0.01 x 10 <sup>-8</sup>
Transcription	NM_015061	JMJD2C	jumonji domain containing 2C	regulation of transcription, DNA-dependent	6.06	0.07 x 10 <sup>-8</sup>
	NM_004269	CRSP8	cofactor for Sp1 transcriptional activation, subunit 8, 34kDa	transcription, regulation of transcription, DNA-dependent	2.64	8.58 x 10 <sup>-8</sup>
Unknown	NM_000332	ATXN1	ataxin 1	-	6.06	5.59 x 10 <sup>-8</sup>
	NM_013275	ANKRD11	ankyrin repeat domain 11	-	3.48	0.01 x 10 <sup>-8</sup>
	NM_015556	SIPA1L1	Signal-induced proliferation-associated 1 like 1	-	4.59	20.89 x 10 <sup>-8</sup>
	NM_002149	HPCAL1	hippocalcin-like 1	-	3.73	0.10 x 10 <sup>-8</sup>
	NM_016196	RBM19	RNA binding motif protein 19	-	2.83	1.02 x 10 <sup>-8</sup>
	NM_017794	KIAA1797	KIAA1797	-	6.50	3.39 x 10 <sup>-8</sup>
	NM_005758	HNRPA3P1	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	-	6.06	9.22 x 10 <sup>-8</sup>
	NM_032340	C6orf125	chromosome 6 open reading frame 125	-	2.46	47.08 x 10 <sup>-8</sup>
Upregulated Genes						
Genes	Acc. No.	Symbol	Gene	Function	Fold change	P-Value
Development	NM_005461	MAFB	v-maf musculoaponeurotic fibro-sarcoma oncogene homolog B (avian)	transcription, regulation of transcription, DNA-dependent, sensory organ development	11.31	<10 <sup>-8</sup>
	NM_016399	TRIAP1	TP53 regulated inhibitor of apoptosis 1	anti-apoptosis, DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	4.00	5.03 x 10 <sup>-8</sup>
Apoptosis	NM_003914	CCNA1	cyclin A1	apoptosis, regulation of cyclin dependent protein kinase activity, cell cycle, mitosis	3.48	0.46 x 10 <sup>-8</sup>
	NM_004295	TRAF4	TNF receptor-associated factor 4	signal transduction, development, apoptosis regulation	2.83	23.08 x 10 <sup>-8</sup>
	NM_022121	PERP	PERP, TP53 apoptosis effector	apoptosis, cell adhesion, protein binding	1.87	32.76 x 10 <sup>-8</sup>

Upregulated Genes	Acc. No.	Symbol	Gene	Function	Fold change	P-Value
	NM_018494 *AF274972	LRDD	leucine-rich repeats and death domain containing (coding for PIDD)	signal transduction, apoptosis	2.83 3.25	$0.5 \times 10^{-8}$ $0.5 \times 10^{-8}$
	NM_004083	DDIT3	DNA-damage-inducible transcript 3	regulation of progression through cell cycle, transcription, regulation of transcription	4.00	$28.1 \times 10^{-8}$
	NM_004110	FDXR	ferredoxin reductase	electron transport, lipid metabolism, steroid biosynthesis	8.57	$<10^{-8}$
	NM_003842	TNFRSF 10B	tumor necrosis factor receptor superfamily, member 10b (coding for TRAIL-R2)	caspase activation, signal transduction, cell surface receptor linked signal transduction	2.00	$38.12 \times 10^{-8}$
	NM_003841	TNFRSF 10C	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	apoptosis, signal transduction	16.00	$50.24 \times 10^{-8}$
<b>Metabolism</b>	NM_000067	CA2	carbonic anhydrase II	one-carbon compound metabolism	3.73	$0.23 \times 10^{-8}$
	NM_016006	ABHD5	abhydrolase domain containing 5r	proteolysis, aromatic compound metabolism	6.96	$0.01 \times 10^{-8}$
	NM_000269	NME1	non-metastatic cells 1, protein (NM23A)	GTP-, UTP-, CTP-biosynthesis	3.03	$<10^{-8}$
	NM_014059	RGC32	response gene to complement 32	regulation of cyclin dependent protein kinase activity	39.40	$0.04 \times 10^{-8}$
	NM_031459	SESN2	sestrin 2	cell cycle arrest	3.25	$79.46 \times 10^{-8}$
	NM_002061	GCLM	glutamate-cysteine ligase, modifier subunit	cysteine metabolism, glutathione biosynthesis	1.74	$1.96 \times 10^{-8}$
	NM_015423	AASDH PPT	aminoadipate-semialdehyde DH-phosphopantetheinyl transferase	fatty acid biosynthesis	1.87	$12.79 \times 10^{-8}$
	NM_002065	GLUL	glutamate-ammonia ligase (glutamine synthetase)	regulation of neurotransmitter levels, glutamine biosynthesis, nitrogen compound metabolism	2.00	$0.02 \times 10^{-8}$
	NM_001236	CBR3	carbonyl reductase 3	metabolism	2.14	$9.37 \times 10^{-8}$
	NM_004219	PTTG1	pituitary tumor-transforming 1	DNA metabolism, DNA repair, transcription from RNA polymerase II promoter	2.14	$39 \times 10^{-8}$
	NM_000270	NP	nucleoside phosphorylase	nucleotide/nucleic acid metabolism, DNA modification	1.87	$46.97 \times 10^{-8}$
	NM_014252	SLC25A15	solute carrier family 25 (mitochondrial carrier, ornithine transporter) member 15	urea cycle, mitochondrial ornithine transport, amino acid metabolism	4.29	$8.64 \times 10^{-8}$
	NM_017421 *AL136726	COQ3	coenzyme Q3 homolog, methyltransferase ( <i>S. cerevisiae</i> )	ubiquinone biosynthesis	21.11 32.00	$46.11 \times 10^{-8}$ $0.03 \times 10^{-8}$
	NM_009590	AOC2	amine oxidase, copper containing 2 (retina-specific)	catecholamine metabolism, visual perception, biogenic amine metabolism	3.73	$0.18 \times 10^{-8}$
	AF096304	TM7SF2	transmembrane 7 superfamily member 2	cholesterol-, steroid-, lipid-biosynthesis	2.83	$0.26 \times 10^{-8}$
	NM_001807	CEL	carboxyl ester lipase	triacylglycerol metabolism, cholesterol catabolism	2.64	$0.66 \times 10^{-8}$
	NM_013267	GLS2	glutaminase 2 (liver, mitochondrial)	amino acid metabolism, glutamine metabolism	12.13	$80.74 \times 10^{-8}$
<b>Protein Modification</b>	NM_031301	APH1B	anterior pharynx defective 1 homolog B ( <i>C. elegans</i> )	Notch signaling pathway, protein processing	3.74	$86.16 \times 10^{-8}$
	NM_005729	PPIF	peptidylprolyl isomerase F(cyclophilinF)	protein folding	2.64	$1.28 \times 10^{-8}$
	NM_019116	UBPH	ubiquitin-binding protein homolog	protein modification	2.39	$0.53 \times 10^{-8}$

Upregulated Genes	Acc. No.	Symbol	Gene	Function	Fold change	P-Value
	NM_006389	HYOU1	hypoxia up-regulated 1	protein folding, response to stress, glycolysis	1.32	45.64 x 10 <sup>-8</sup>
	NM_013336	SEC61A1	Sec61 $\alpha$ 1 subunit ( <i>S. cerevisiae</i> )	protein targeting, secretion, transport	1.52	0.73 x 10 <sup>-8</sup>
	BC001134	FTS	fused toes homolog (mouse)	ubiquitin cycle, protein modification, apoptosis	1.41	2.17 x 10 <sup>-8</sup>
<b>Transport</b>	NM_016072	GOLT1B	golgi transport 1 homolog B ( <i>S. cerevisiae</i> )	vesicle-mediated transport, positive regulation of I- $\beta$ B kinase/NF- $\kappa$ B cascade	1.52	3.29 x 10 <sup>-8</sup>
	NM_003764	STX11	syntaxin 11	intracellular protein and membrane fusion, transport	1.52	<10 <sup>-8</sup>
	NM_006555	YKT6	YKT6 v-SNARE homolog ( <i>S. cerevisiae</i> )	vesicle targeting and docking during exocytosis, transport	2.00	6.16 x 10 <sup>-8</sup>
	NM_006815	TMED2	transmembrane emp24 domain trafficking protein 2	intracellular protein transport, ER to Golgi vesicle-mediated transport	1.32	0.01 x 10 <sup>-8</sup>
	NM_024628	SLC12A8	solute carrier family 12 (potassium/ chloride transporters), member 8	amino acid transport	2.00	28.61 x 10 <sup>-8</sup>
<b>Signal Transduction</b>	NM_001124	ADM	adrenomedullin	cAMP and progesterone biosynthesis, signal transduction	9.85	0.04 x 10 <sup>-8</sup>
	U82979	LILRB4	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4 (coding for ILT3)	immune response, signal transduction, defense response	1.62	1.35 x 10 <sup>-8</sup>
	NM_007173	PRSS23	protease, serine, 23	proteolysis, signal transduction, G-protein coupled receptor protein signaling pathway	3.25	0.03 x 10 <sup>-8</sup>
	NM_022337	RAB38	RAB38, member RAS oncogene family	small GTPase mediated signal transduction, protein transport	3.03	41.29 x 10 <sup>-8</sup>
	NM_005903	SMAD5	SMAD, mothers against DPP homolog 5 ( <i>Drosophila</i> )	transcription, regulation of transcription, DNA-dependent, signal transduction	6.50	0.05 x 10 <sup>-8</sup>
	NM_022036	GPRC5C	G protein-coupled receptor, family C, group 5, member C	signal transduction, G-protein coupled receptor protein signaling pathway, G-protein coupled receptor	11.31	41.52 x 10 <sup>-8</sup>
<b>Processing Transcription Replication</b>	NM_006079	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	regulation of transcription from RNA polymerase II promoter	2.30	43.5 x 10 <sup>-8</sup>
	*AF109161				2.64	0.01 x 10 <sup>-8</sup>
	NM_006502	POLH	polymerase (DNA directed), $\epsilon$	DNA replication and repair, regulation of DNA repair	2.46	<10 <sup>-8</sup>
	NM_004089	TSC22D3	TSC22 domain family, member 3 (coding for GILZ)	regulation of transcription, DNA-dependent	1.87	62.57 x 10 <sup>-8</sup>
	NM_007362	NCBP2	nuclear cap binding protein subunit 2, 20kDa	mRNA processing, mRNA export from nucleus, snRNA export from nucleus	1.23	51.01 x 10 <sup>-8</sup>
	NM_003655	CBX4	chromobox homolog 4 (Pc class homolog, <i>Drosophila</i> )	chromatin assembly or disassembly, transcription, regulation of transcription, DNA-dependent	1.87	62.11 x 10 <sup>-8</sup>
	NM_002632	PGF	placental growth factor, vascular endo-thelial growth factor-related protein	regulation of progression through cell cycle, angiogenesis, signal transduction	22.63	70.73 x 10 <sup>-8</sup>
<b>Different Functions</b>	NM_003518	HIST1 H2BG	histone 1, H2bg	nucleosome assembly, chromosome organization and biogenesis (sensu Eukaryota)	3.73	0.02 x 10 <sup>-8</sup>
	NM_006449	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	regulation of cell shape	32.00	30.95 x 10 <sup>-8</sup>



Upregulated Genes	Acc. No.	Symbol	Gene	Function	Fold change	P-Value
	NM_000024	ADRB2	adrenergic, $\beta$ -2-, receptor, surface	activation of MAPK activity, receptor mediated endocytosis, transmembrane receptor protein tyrosine kinase activity	4.59	$0.02 \times 10^{-8}$
	NM_024005	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	RNA/DNA/protein binding, ATP binding	4.29	$<10^{-8}$
	NM_007071	HHLA3	HERV-H LTR-associating 3	protein binding	2.00	$4.7 \times 10^{-8}$
	AL136660	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	signal peptide processing	1.32	$74.04 \times 10^{-8}$
	BC002709	TP53AP1	TP53 activated protein 1	response to stress and to DNA damage stimulus	4.00	$0.02 \times 10^{-8}$
<b>Unknown</b>	NM_013399	C16orf5	chromosome 16 open reading frame 5	-	1.62	$4.92 \times 10^{-8}$
	NM_018112	TMEM38B	transmembrane protein 38B	-	1.23	$87.64 \times 10^{-8}$

Variants are labelled with \* and relevant genes are displayed in bold characters. Accession numbers are shown in column 1.