SUPPLEMENTARY DATA

Regulation of Inflammatory Phenotype in Macrophages by a Diabetes-Induced Long Noncoding RNA

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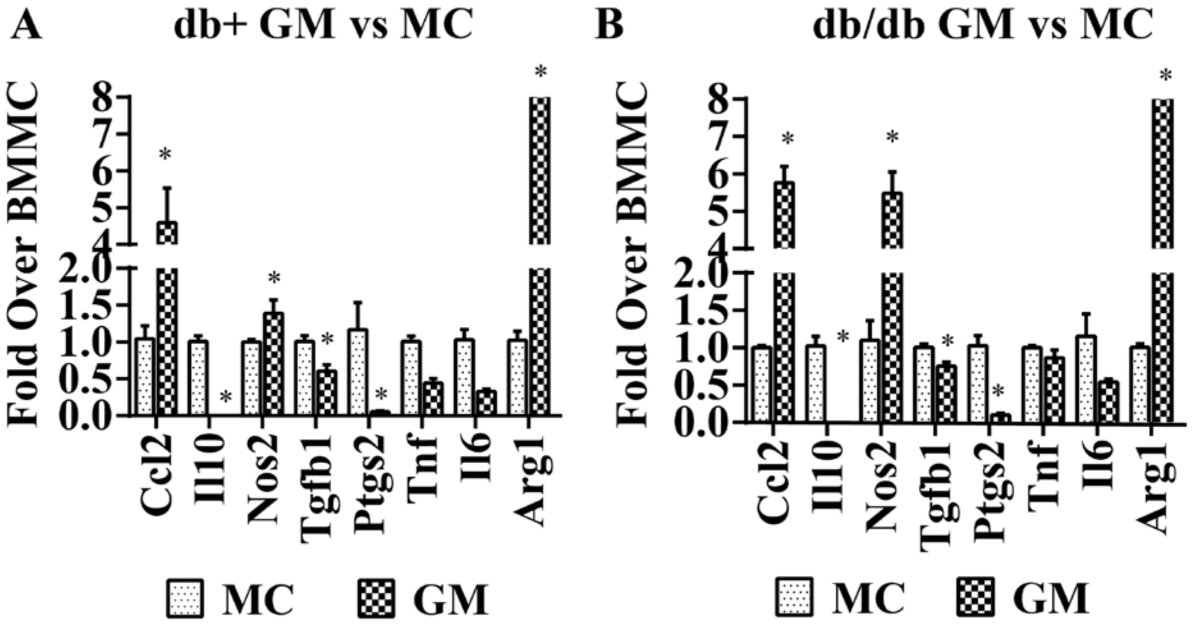
Supplementary Figure 1. Expression of pro-inflammatory genes and those associated with alternatively activated macrophages in BMMC(MC) and BMGM (GM). A-B. Bar graphs showing gene expression in BMGM from db/+ (A) and db/db (B) mice relative to respective BMMC. BMMs from db/+ and db/db mice were cultured in 10 ng/ml MCSF (BMMC) or 20 ng/ml GM-CSF (BMGM) for 7 days and expression of indicated genes were analyzed by RT-QPCR. Results were expressed as Fold over BMMC. Data showed elevated levels of inflammatory genes and reduced levels of alternatively activated genes in BMGM from both db/+ (A) and db/db (B) mice, consistent with M1 and M2 phenotypes of GM-CSF and MCSF differentiated cells respectively. Bar graph for Arg1 is shown truncated because its levels were >100 fold in BMGM vs BMMC. Mean±SEM (*, p<0.05, n=4).



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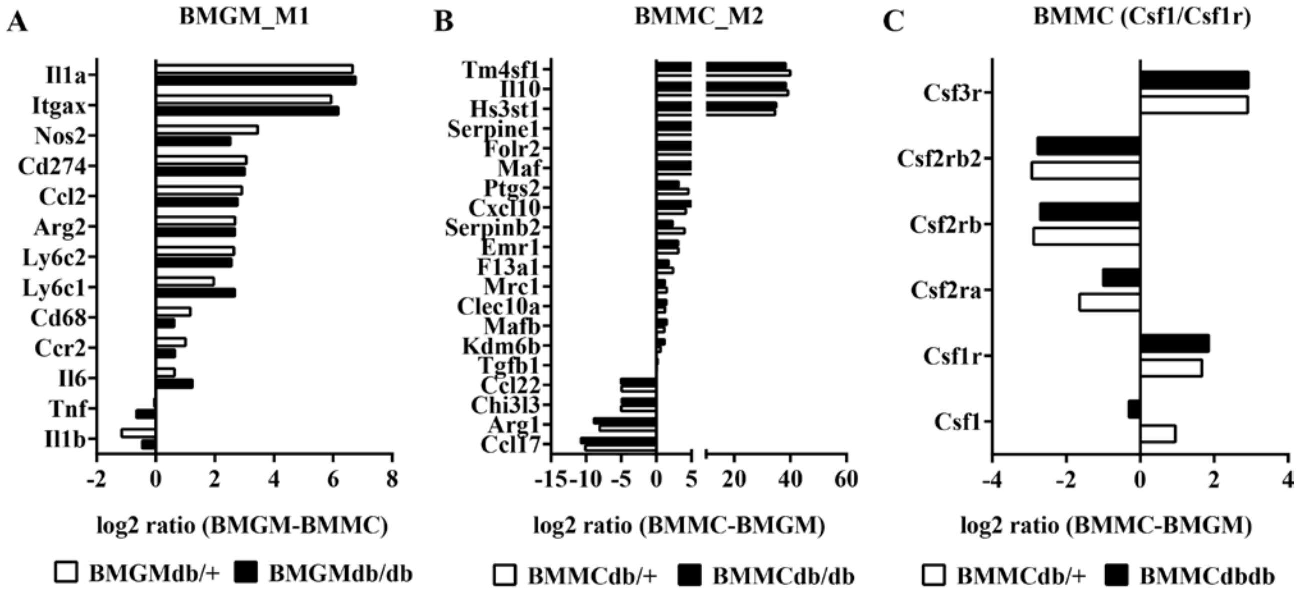
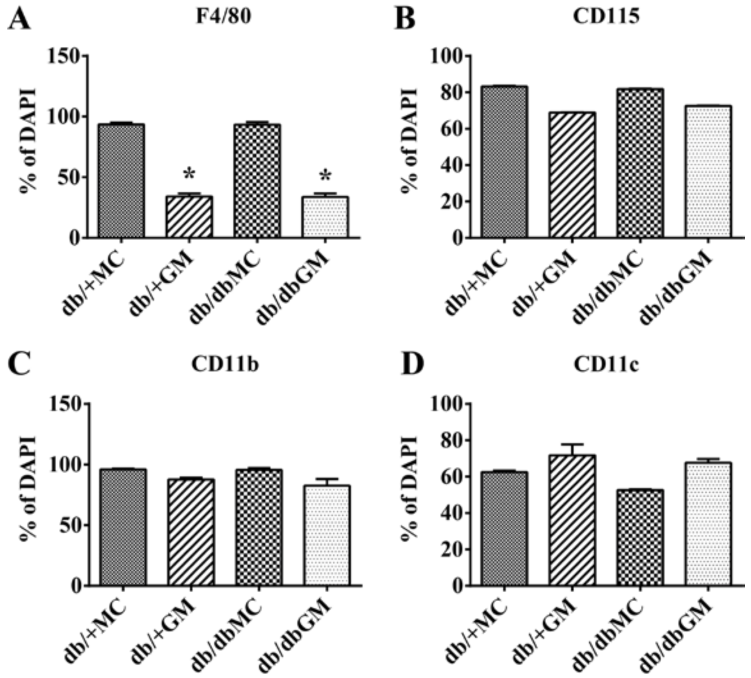
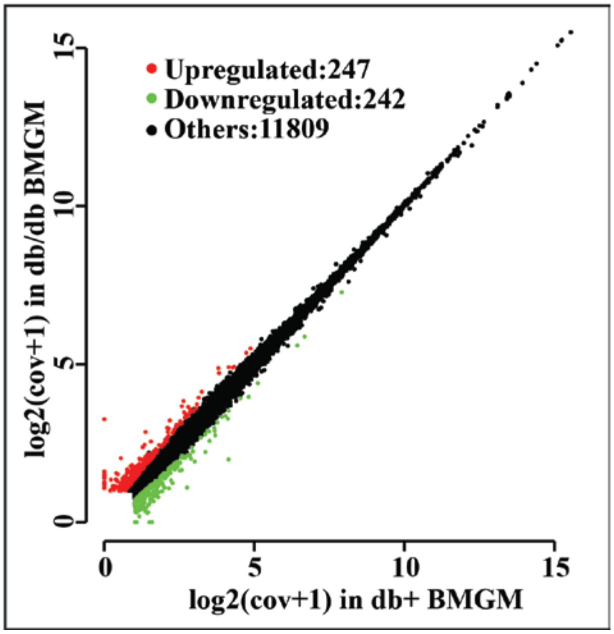
Supplementary Figure 2. Results of RNA-seq analysis showing expression of Macrophage M1/M2 markers in BMMC, and differentially expressed genes in BMGM. A. Typical M1 gene expression levels in BMGM relative to BMMC. B. Typical M2 gene expression levels in BMMC relative to BMGM. C. *Csf1* and *Csf1R* expression levels are elevated in BMMC relative to BMGM. In contrast, expression of GM-CSF receptors (*Csf2rb* and *Csf2rb2*) was markedly reduced in BMMC. Global gene expression in BMMC and BMGM isolated from db/+ and db/db mice was analyzed by RNA-seq as indicated in the Methods section. Results shown further support the M1 and M2 phenotypes of BMGM and BMMC respectively. Relative levels of indicated genes are shown. Data represents log2 ratio as indicated on the ‘X’ axis.



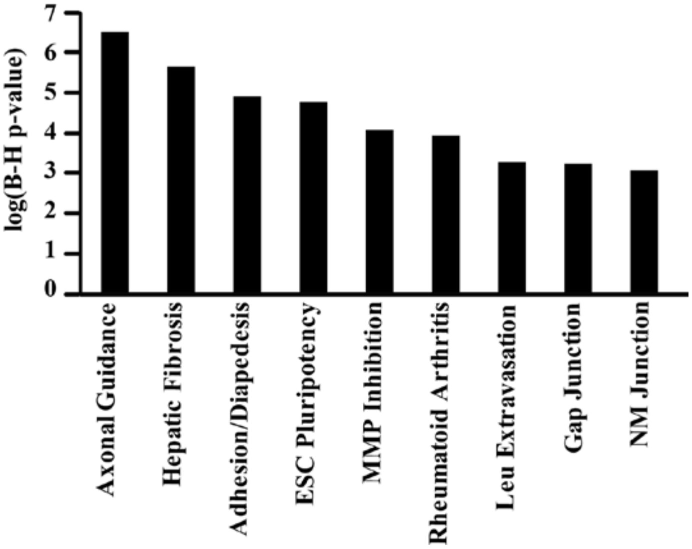
Supplementary Figure 3. Flow cytometry data showing protein levels of macrophage markers in BMM. BMMC and BMGM from db/+ and db/db mice were stained with F4/80 (A), CD115 (B), CD11b (C) and CD11c (D) antibodies and FACS analyses were performed. Data represents % of cells positive for the indicated antibodies relative to total number of DAPI stained cells. A *, $p<0.05$ (n=4). B-D (n=2). Flow cytometry experiments revealed that majority of BMMC were positive for F4/80, CD115 (CSF1R), CD11b and CD11c. Whereas in BMGM, cells positive for F4/80 and CD115 were reduced, but those positive for CD11c were moderately increased. BMMs were detached using Accutase, washed and resuspended in 100 ul of PBS containing 0.5% BSA (FACS buffer, FB). BMMs were blocked with anti-mouse CD16/32 Antibody (TruStain fcX™, Biolegend, San Diego, CA) for 20 min, then incubated for 30 min at 4^0C with the indicated fluorescently labeled antibodies (purchased from Biolegend). Cells were then washed three times with FB, stained with DAPI and FACS analysis was performed by the Analytical Flow Cytometry core facility on an LSR Fortessa X-20 (BD Bioscience, San Diego, CA), with color compensation without dye, and single color stained cells. Data was analyzed using FlowJo software and results are shown as the % of DAPI stained cells.



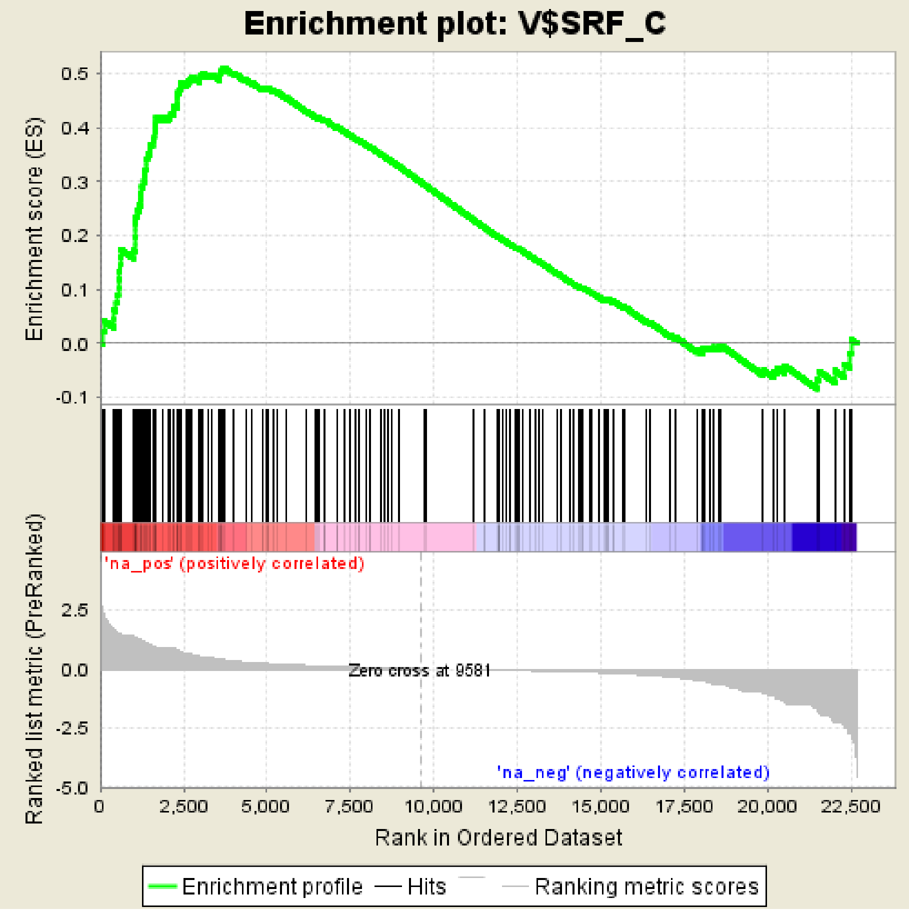
Supplementary Figure 4. Scatter plot of differentially expressed RefSeq genes in db/dbBMGM vs db/+BMGM. RNA-seq data of BMGM from db/+ and db/db mice were analyzed as decribed in Methods section. Data represents log2 ratio (db/dbBMGM-db/+BMGM).



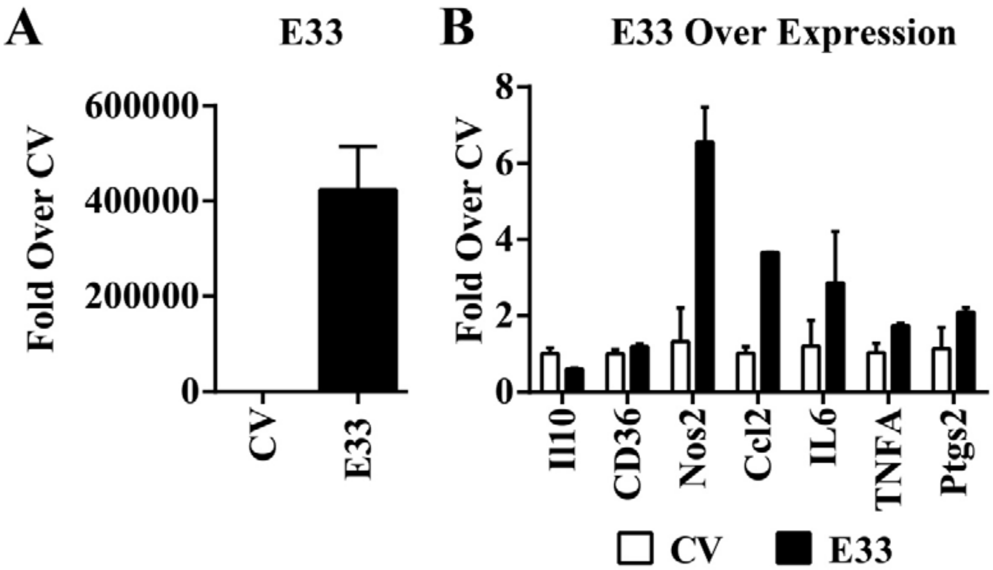
Supplementary Figure 5. Canonical Signaling Pathways enriched among differentially expressed genes (DEG) in db/dbBMMC. DEG (with minimum coverage of 1 and ≥ 1.5 fold change) were analyzed by Ingenuity Pathway Analysis (IPA). Bar graph shows top 9 significantly enriched pathways.



Supplementary Figure 6. Enriched motifs (FDR < 5%) identified by GSEA among differentially expressed genes (DEG) in db/dbBMMC. All RefSeq genes were ranked based on fold change (log2 ratio) in each gene's expression between db/dbBMMC and db/+BMMC and analyzed by pre-ranked GSEA for enriched transcription factor binding sites. Results showed that the promoters (± 2 kb from transcription start sites) of upregulated genes were significantly enriched (FDR < 5%) with Serum Response Factor (SRF) motifs.



Supplementary Figure 7. Regulation of inflammatory genes by E330013P06 in BMMC. (A-B) BMMC from normal C57BL/6 mice were transiently transfected with E33 or GFP control (CV) expression vectors. Expression of E33 mRNA (A) and mRNAs of the indicated inflammatory genes (B) was determined by RT-QPCR 48 h post transfection. Results were expressed as fold over GFP transfected cells (CV). Data are represented as Mean±SEM (n=2).



Supplementary Table 1. Alignment Summary of RNA-seq Data Analysis.

	db/+BMGM	db/dbBMGM	db/+BMMC	db/dbBMMC
Total Reads	50,280,104	49,644,878	54,959,198	49,598,692
Aligned Reads	39,869,517	39,800,076	42,441,619	39,777,530
Exon Reads	14,382,802	15,150,865	13,524,428	14,580,453
rRNA Reads	13,928,610	12,049,716	14,176,581	11,977,409
% Aligned	79.29%	80.17%	77.22%	80.20%
% Exon	36.07%	38.07%	31.87%	36.65%
%r RNA	34.94%	30.28%	33.40%	30.11%

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Supplementary Table 2. Sequences of primers used in PCR and siRNA oligonucleotides used in this study.

Gene ID	**Forward**	**Reverse**
QPCR Primers (Mouse)		
Actb	ACCTTCTACAATGAGCTGCG	CTGGATGGCTACGTACATGG
Arg1	TGCATATCTGCCAAAGACATCG	CGTAGAAGTGTTCCCCAGGGTCTACG
Ccl2	AGGTCCCTGTCATGCTTCTGG	CAGCACTTCTTTGGGACACCTGCTG
Cd36	GATGACGTGGCAAAGAACAG	TCCTCGGGGTCCTGAGTTAT
E33	GGCCTCCACCTCCGAAGA	GAATCCTACCAGCCATCACTC
Il6	ACAAAGCCAGAGTCCTTCAGAG	ACCACAGTGAGGAATGTCCAC
Il10	TGCTTCTATGCAGTTGATGAAGAT	AGCTCCAAGACCAAGGTGTC
Nos2	CCTGGAGACCCACACACTGG	CACAGCCACATTGATCTCCG
Pip2a	TTCTTGCTGTCTTTGGAACTTTGTC	ATGGTCAACCCCACCGTGT
Ptgs2	CGGTTTTGAGTTTGAAGTGGTAACCG	GAGCAACTATTCCAAACCAGCA
Tgfb	GGGGTCTACAACCAACACAACCCG	GCAGGAGCGCACAATCATGT
Tnf	TGTTGCCTCCTCTTTTGCTT	TGGTCACCAAATCAGCGTTA
Taqman Assay Primers (Mouse)		
E330013P06	TGTGACAGTATCCGGCCAATGCTA	ACACTATGGGAAAGCCACTGGGAT
E330013P06-Probe	ATTTCCACCRATCCTCCTATGCTCTGC	
siRNAs (Mouse)		
siE33-Pr-1	GAGACAUCUUCUGAAGACAUU	UGUCUUCAGAAGAUGUCUCUU
siE33-Pr-2	GUUCUGUGACAGUAAUAAAUU	UUUAUUACUGUCACAGAACUU
siE33-Pr-3	GAAGACAUUUCUGAAGAGAUU	UCUCUUCAGAAAUGUCUUCUU
siNTC	ON-TARGET Plus Non-targeting siRNA #1 (Thermo Scientific)	
QPCR primers (Human)		
MIR143HG	AGGGCCAGCAGCAGGC	TCAGGAAATGTCTCTGGCTGTG
PPIA	GACTGAGTGGTTGGATGGCAAG	CGCTTATTCCTGGACCCAAAGCG

Supplementary Table 3. Differentially expressed Refseq lncRNAs identified by RNA-seq in db/dbBMMC relative to db/+BMMC. Table showing differentially expressed known lncRNAs and nearby differentially-expressed genes (DEG) including miRNAs (coverage >=1 in at least one sample and fold change ≥1.5) located within 500kb flanking regions of lncRNAs in db/dbBMMC.

Symbol	Raw Reads		Normalized Coverage		log2 Ratio	DEG(s) * located <500kb		miRNAs located < 500kb	
	db/+	db/db	db/+	db/db		Symbol	log2 Ratio	within lncRNA	Nearby
Gm6578	0	12	0	1.06	3.52				
Olfr856-ps1	5	34	0.29	1.8	2.41				
2010009K17Rik	4	17	0.49	2.58	2.04				
Gm16596	6	30	0.37	1.68	2.02	Eml1, Hhipl1	1.1, 1.27		miR345
2700086A05Rik	2	11	0.23	1.15	1.87	Hoxa10, Hoxa5, Hoxa9	1.92, 1.46, 0.69		miRa, miR196b
Gm6634	7	28	0.37	1.35	1.73				
D030025P21Rik	18	66	0.43	1.45	1.69	Ltbp2	1.34		
Dnm3os	218	769	2.61	8.45	1.69			miR199a-2, miR214	miR199a-2, miR214
0610007N19Rik	25	89	1.6	5.22	1.66	Snord123	0.9		
4933436C20Rik	6	24	0.46	1.6	1.65	Mmp2, Irx5	1.37, 1.1		
Has2as	5	20	0.98	3.37	1.61	Has2	1.17		
3110045C21Rik	6	21	0.5	1.61	1.52	Ddr2, Rgs4, Hsd17b7	1.57, 2.62, 0.63		
2610203C20Rik	179	545	6.6	18.41	1.47			miR125b-1	miR100, miRlet7a-2, miR125b-1
Gm11149	15	47	1.12	3.19	1.46	Ncam1	1.2		
2810408I11Rik	7	23	0.94	2.8	1.46	Ccnyl1	0.89		
E330013P06	28	80	1.95	5.12	1.36	Arhgef37, Ppargc1b, LOC545261	-0.81, -0.65, 0.59	miR145, miR143	miR145, miR143
Rps4y2	31	86	3.13	7.95	1.32				
4930429B21Rik	25	65	1.17	2.9	1.27				
A330069E16Rik	10	28	1.06	2.73	1.27	Pacsin3	1.36		
2810047C21Rik1	27	69	1.56	3.64	1.2				
St5	125	312	2.61	5.98	1.19				

Gm7334	60	150	4.19	9.59	1.18	Btg3	1.18		
2810403D21Rik	8	21	0.75	1.81	1.16				
C130083M11Rik	17	40	0.78	1.67	1.06	Sod3	1.39		
1700007L15Rik	16	38	2.03	4.3	1.04	Heg1	0.89		miR1947
Gm2115	125	275	6.37	12.79	1	9930013L23Rik, Fah, Arnt2	1.6, 0.98, 0.71		
Tubb2a-ps2	16	36	2.16	4.45	1				
E130310I04Rik	25	54	0.63	1.25	0.96	Mylk, Kalrn	1.24, 0.96		
C630043F03Rik	36	74	1.27	2.4	0.89				
A130040M12Rik	85	172	2.5	4.64	0.88	Gm5141	0.6		miR713
Gm10941	7	15	0.94	1.84	0.88				miR1930
4921511C10Rik	24	49	1.56	2.91	0.87				
B430319G15Rik	24	49	0.56	1.05	0.87	Plod2, Plscr2	1.5, 1.46		
D4Ertd617e	26	51	2.95	5.5	0.87	Ptprf, Mpl	0.71, 0.61		
4930447K03Rik	24	47	2.2	3.94	0.82				
9130206I24Rik	33	64	1.09	1.94	0.81				
D430020J02Rik	63	121	2.07	3.64	0.8				
2610019E17Rik	19	36	6.09	10.57	0.76	Dnase1l2, Slc9a3r2	-1.12, 0.79		miR5134
4732491K20Rik	28	52	0.84	1.43	0.74				
E130304I02Rik	4	8	0.54	1	0.73	Zfp507	1.02		
LOC100642166	39	71	2.39	3.98	0.72	Gm15787, Gm10416	-0.66, -0.78		
4933412E12Rik	47	85	2.59	4.29	0.72	Kcnmb4	0.99		
Fcrla	13	24	0.72	1.21	0.71	Olfml2b, Adamts4	1.13, 0.67		
Snhg1	185	329	36.21	58.99	0.7				miR5136
Pvt1	95	168	2.93	4.75	0.69	Myc	0.65		
Ccl25	27	48	2	3.26	0.68	Ctxn1, Cd209d	1.33, 1.05		
4930581F22Rik	76	132	3	4.78	0.66	Cdon	1		
9130024F11Rik	30	52	0.76	1.21	0.65				
Gm15421	575	979	67.44	105.18	0.64				
Gm14005	44	75	0.93	1.45	0.63				

Gm14057	18	31	0.8	1.26	0.63	Gfra4	-1.77		miR103-2
Gm10791	40	68	2.29	3.57	0.63				miR155
1700084J12Rik	5	9	0.66	1.07	0.62	Sdc2	1.56		
Gm13939	23	39	1.62	2.51	0.61	Lgr4	1.33		
A830082N09Rik	113	189	1.37	2.1	0.61	Fam26e, Col10a1, Frk	1.4, 0.86, 0.98		
Npff	43	72	4.07	6.25	0.61	Sp7, Hoxc10, Hoxc9, Hoxc6, Igfbp6	1.49, 1.07, 1.46, 1.2, 0.93		miR688, miR196a-2, miR615
3000002C10Rik	16	27	1.19	1.84	0.6				
LOC545261	24	40	3.67	5.59	0.59	E330013P06, Arhgef37, Ppargc1b	1.36, -0.81, -0.65		miR145, miR143
AI507597	21	35	2.31	3.52	0.59	Epha2, B330016D10Rik, Gm10565, Hspb7	1.6, -0.63, -0.71, 0.77		
Gm5434	46	33	3.01	1.98	-0.59				
Alms1-ps2	20	14	1.61	1.04	-0.6				miR705
Gm11747	27	19	1.56	1	-0.6				
Gm10677	661	474	29.87	19.62	-0.61				
A530088E08Rik	254	181	13.45	8.78	-0.61				
C330013E15Rik	40	28	4.32	2.77	-0.62	AB099516, Mettl7a2	-1.18, -0.97		
B330016D10Rik	154	108	6.8	4.37	-0.63	Epha2, Hspb7, AI507597	1.6, 0.77, 0.59		
4930513N10Rik	132	91	4.44	2.83	-0.65	Ndrg4	1.82		miR1186b
LOC626693	25	17	1.53	0.95	-0.65				miR568
Gm9920	51	35	5.16	3.24	-0.65	Dscc1, Enpp2, Nov	1.82, 0.95, -0.79		
Gm13845	15	10	1.48	0.9	-0.65				miR29a, miR29b-1
4931440J10Rik	28	19	2.96	1.84	-0.66	Fam124a, Serpine3	1.52, 0.87		
Gm11648	67	46	2.33	1.47	-0.66				
Gm15787	119	82	8.09	5.1	-0.66	LOC100642166, Gm10416	0.72, -0.78		

Pldi	18	13	2	1.21	-0.66	Pcbd1, Unc5b, Adamts14	-1.01, 0.93, 0.7		
LOC100859962	21	14	3.81	2.32	-0.67	Blm, Kif7	0.65, 0.81		miR1965
4930441O14Rik	43	29	1.41	0.87	-0.67				
1810012K16Rik	11	7	1.93	1.12	-0.69	Plat, Thsd1	1.16, 0.89		
4931403E22Rik	11	7	1.56	0.91	-0.69	Vldlr	1.46		
Gm10390	129	86	3.08	1.88	-0.7	Sds	-2.57		
2900060B14Rik	59	39	9.38	5.69	-0.71				
Gm10565	74	49	3.99	2.42	-0.71	AI507597	0.59		
1110006O24Rik	31	20	3.84	2.26	-0.73	Msi1	2.14		
5730405O15Rik	54	35	5.78	3.43	-0.73	Gm4984	1.25		
5031425F14Rik	235	153	13.58	8.13	-0.74				
Gm17745	16	10	1.77	1.01	-0.74	Ntn4, Ccdc38	1.65, 0.73		miR1931
Gm15880	44	28	1.45	0.84	-0.76	Blm, Zscan2, Nmb	0.65, -0.91, 0.6		miR1965
2010001M06Rik	10	6	1.88	1.03	-0.76	Vps37d, Stx1a	1.25, 0.65		
Gm10416	18	11	2.66	1.49	-0.78	Gm15787, LOC100642166	-0.66, 0.72		
Gm9199	40	25	2.95	1.69	-0.78				miR687
D930015M05Rik	34	21	2.71	1.53	-0.79	Syt13, Mdk	1.28, 0.6		miR1955
Gm16617	15	9	2	1.09	-0.79	Snord58b, Arhgef40, G630016D24Rik	-1.54, 0.62, -0.88		
Gm16386	28	17	4.45	2.47	-0.81				
A430088P11Rik	124	76	2.62	1.47	-0.82				miR5113
G730013B05Rik	48	29	1.59	0.88	-0.83				
2900005J15Rik	177	108	8.28	4.63	-0.83	Smarcd3	0.76		
1700025N23Rik	27	16	2.84	1.53	-0.84	Klrg2	0.78		
1700012D14Rik	47	28	7.07	3.86	-0.85	Adm	1.57		
4930405A21Rik	11	6	1.05	0.52	-0.88	Myl9	1.36		
Bc1	1	0	1.23	0	-0.96				
Gm9054	28	15	3.75	1.85	-0.97	Ctsk, Ecm1, Bola1	1.19, 0.59, -0.79		
A930007I19Rik	48	26	1.97	0.97	-0.98	Gm9895	-1.94		miR101b

Gpx2-ps1	25	13	2.34	1.11	-1.01	P4ha3, Dnajb13, Plekhb1	1.52, -0.74, -0.73		
Gm13807	35	18	2.56	1.21	-1.04	Syt13, Trp53i11, Prdm11	1.28, -0.95, -0.68		
Slc22a13b	20	11	1.3	0.6	-1.04	Plcd1	0.93		miR26a-1
A730085K08Rik	7	3	1.18	0.46	-1.09				miR138-1
2610035D17Rik	169	87	8.68	4.05	-1.09				
Gm6277	19	9	1.27	0.55	-1.11				miR1901
2610203C22Rik	35	17	2.66	1.18	-1.12	Mybl1, Snord87	0.85, 0.77		
3300005D01Rik	24	11	1.77	0.75	-1.17	Ldhal6b	0.81		
D930028M14Rik	18	7	1.59	0.57	-1.35	Ceacam2, Ceacam10	-0.62, -0.9		
Gm12060	16	6	1.94	0.66	-1.38				
4932441J04Rik	9	3	1.18	0.36	-1.41				
AI463170	9	3	1.58	0.48	-1.41				miR5135
4930520O04Rik	31	12	2.34	0.83	-1.41	Susd5, Cmtm8, Bcl2a1c	2.35, -0.65, 0.73		
4930471G03Rik	9	2	1.28	0.25	-1.81	Hbegf, 2010001M09Rik, Nrg2, Spata24, 0610010O12Rik	1.01, 3.13, -1.08, 1.02, -0.69		
Gm9895	10	2	1.43	0.26	-1.94	Slc1a1, A930007I19Rik	1.87, -0.98		miR101b
Rprl1	3	0	1.17	0	-1.94				
Gm16833	8	1	1.12	0.13	-2.21	Arhgap42	2.23		
A930041C12Rik	21	3	3.52	0.48	-2.47	Tgfbr3, Gfi1	0.84, -0.94		

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Supplementary Table 4. Differentially expressed novel lncRNAs identified by RNA-seq in db/dbBMMC relative to db/+BMMC. Table showing differentially expressed novel lncRNAs and nearby differentially-expressed genes (DEG) including miRNAs (coverage >=1 in at least one sample and fold change ≥1.5) located within 500kb flanking regions of lncRNAs in db/dbBMMC.

Symbol	Chr	Gene Start	Gene End	Strand	Normalized coverage		log2 Ratio	DEG(s) * located <500kb	
					db/+	db/db		Symbol	log2 Ratio
XLOC_009934	chr14	53988397	54080873	+	0.46	1.19	1.26		
XLOC_008488	chr13	52655656	52668673	+	2.73	1.41	-0.93		
XLOC_022091	chr3	1.17E+08	1.17E+08	-	1.65	0.89	-0.8		
XLOC_027444	chr6	52108422	52112151	+	4.4	8.44	0.93	Hoxa10, Hoxa5, 2700086A05Rik, Hoxa9	1.92, 1.46, 1.87, 0.69
XLOC_013863	chr17	26122835	26125865	+	0.68	1.45	1.06	Arhgdig	0.7
XLOC_025108	chr5	64436202	64439498	+	1.04	1.78	0.71		
XLOC_005286	chr11	1.22E+08	1.22E+08	+	1.29	0.68	-0.9		
XLOC_016083	chr18	5141738	5142989	-	0.89	1.88	0.91	Zeb1	0.59
XLOC_018358	chr2	75616068	75620823	+	1.11	0.55	-1	Ttc30a2	0.61
XLOC_003162	chr10	11019155	11028604	-	2.38	3.87	0.7		
XLOC_018419	chr2	90910643	90912849	+	3.34	1.82	-0.87	Pacsin3, A330069E16Rik	1.36, 1.27
XLOC_011486	chr15	96291630	96294025	+	1.45	2.32	0.66		
XLOC_013712	chr17	17232861	17290922	+	0.91	1.51	0.76		
XLOC_006812	chr12	8516892	8528038	+	1.76	2.75	0.64	Wdr35	0.78
XLOC_032799	chr8	64391485	64392225	-	2.96	1.18	-1.25		
XLOC_032233	chr8	94326573	94328652	+	0.18	1.14	2.46	Irx3, Rpgrip1l	1.70, 0.98
XLOC_000064	chr1	23263129	23269201	+	0.91	2.61	1.49		
XLOC_015981	chr18	61799279	61805019	+	3.75	5.76	0.62	E330013P06, Arhgef37, Ppargc1b, LOC545261	1.36, -0.81, -0.65, 0.59
XLOC_023056	chr4	1.17E+08	1.17E+08	+	2.31	3.86	0.74	Tmem53	1.2

XLOC_022689	chr4	16091268	16120188	+	2.13	4.34	1.02	Ripk2	0.88
XLOC_018094	chr2	27951034	27966815	+	2.26	1.39	-0.64	Col5a1	1.53
XLOC_023859	chr4	94863603	94873653	-	1.23	0.66	-0.8		
XLOC_026751	chr5	1.50E+08	1.50E+08	-	0.78	1.39	0.83	6330406I15Rik	2.04
XLOC_000226	chr1	58562003	58568784	+	0.5	1.26	1.24	Aox1	1.01
XLOC_036089	chrX	1.48E+08	1.48E+08	+	5.98	10.15	0.76	Ribc1	0.66
XLOC_034159	chr9	78276728	78277861	+	0.77	1.29	0.67	Cd109, Gsta4	1.28, 1.80
XLOC_013680	chr17	12511770	12518247	+	0.96	2.6	1.4	4732491K20Rik	0.74
XLOC_001697	chr1	1.56E+08	1.56E+08	-	1.99	3.66	0.87	Rgs16	1.06
XLOC_015899	chr18	46774320	46776318	+	1.97	0.48	-1.86	Cdo1	2.15
XLOC_024009	chr4	1.26E+08	1.26E+08	-	2.21	0.82	-1.4		
XLOC_015977	chr18	61607867	61609225	+	1.68	0.59	-1.51	Pdgfrb, E330013P06, Arhgef37, Ppargc1b, LOC545261	1.41, 1.36, -0.81, -0.65, 0.59
XLOC_020121	chr2	1.74E+08	1.74E+08	-	1.57	0.28	-2.36	Pmepa1	0.94
XLOC_030950	chr7	1.21E+08	1.21E+08	-	1.06	2.01	0.92	Rras2, Insc	1.35, 1.42
XLOC_023440	chr4	1.49E+08	1.49E+08	+	4.3	6.56	0.61	Clstn1, Spsb1	0.87, 0.73
XLOC_028216	chr6	54680226	54710351	-	1.6	0.82	-0.95	Fkbp14, Prr15, Ggct	1.36, -1.33, 0.88
XLOC_021413	chr3	1.31E+08	1.31E+08	+	2.08	1.34	-0.63	Sgms2	1.15
XLOC_006144	chr11	1.02E+08	1.02E+08	-	1.86	1.19	-0.64	Itga2b, Fzd2, Cd300lg, Gjc1	0.92, 0.86, -0.73, 0.94

XLOC_025312	chr5	1.06E+08	1.06E+08	+	0.85	1.38	0.69	Gbp6, Gbp10, Gbp11	-1.15, -1.21, -1.00
XLOC_006970	chr12	36023137	36098218	+	1.43	2.52	0.79		
XLOC_027746	chr6	1.18E+08	1.18E+08	+	1.59	2.5	0.64	Ret, Rasgef1a	1.22, -0.60
XLOC_029893	chr7	1.24E+08	1.24E+08	+	0.77	1.89	1.27		
XLOC_034053	chr9	60905344	60906877	+	0.77	2.3	1.43	Uaca	0.65
XLOC_036042	chrX	1.31E+08	1.31E+08	+	0.42	1.01	1.13	.Armcx2, .Armcx1, .Timm8a1, .Armcx6	1.33, 1.50, 0.77, 0.69
XLOC_005445	chr11	31607033	31612704	-	0.97	1.93	0.94	Stc2	1.6
XLOC_026139	chr5	53921133	53932057	-	2.03	1.28	-0.67		
XLOC_014384	chr17	73215869	73216863	+	2.12	0.94	-1.14		
XLOC_023885	chr4	1.06E+08	1.06E+08	-	3.45	2.07	-0.71		
XLOC_017563	chr19	40711748	40713128	-	4.25	2.55	-0.72	Sorbs1, Pdlim1, Aldh18a1	1.37, 1.01, 0.75
XLOC_035826	chrX	47890566	47903555	+	1.68	2.92	0.73		
XLOC_021059	chr3	69411799	69415091	+	0.94	1.48	0.59		
XLOC_007906	chr12	1.14E+08	1.14E+08	-	0.6	1.6	0.96	Crip2, Tmem121	1.14, 0.88
XLOC_004434	chr11	57906304	57916714	+	1.13	0.75	-0.72		