

Table S1. Demographics and pathological features of MM samples.

S. No	Parameters	Control (n=24)	MM (n=24)	p-value
1	Age	56.6±18.75	62.75±18.6	NS
2	WBC ($\times 10^9/L$)	8.3±1.6	4.8±1.3	<0.05
3	Hemoglobin (g/L)	13.5±2.5	7.2±1.8	<0.05
4	Platelets ($\times 10^9/L$)	318±40.7	198±62.5	<0.05
5	MM clonal plasma cells (%)	NA	60±25	---
6	Serum creatinine (mg/dL)	0.76±0.13	3.4±1.4	<0.05
7	M protein (g/dL)	NA	4.2±1.2	---

*NA - Not Available

*NS - Not Significant

Table S2: Retention time and matching score information of the metabolites identified using untargeted GC-MS approach as per MSI guidelines.

Sr. No.	Metabolite	Retention Time	Match Score (%)
1	D-Ribo-Hexitol	25.32	82.4
2	Beta-D-Glucopyranosiduronic acid	24.92	88.6
3	Hexadecanoic acid	28.26	96.8
4	1,5-Anhydro-D-sorbitol	24.38	92.0
5	Pseudo uridine	33.88	84.6
6	D-Talofuranose	25.08	94.5
7	Glucofuranoside	23.79	91.3
8	N-Acetyl glucosamine	25.28	97.2
9	Purine	24.05	87.8
10	Beta-D-Galactopyranoside	36.64	93.1
11	Pyrimidine	14.56	85.3
12	2-Piperidinecarboxylic acid	12.96	83.8
13	D-Lactose	28.64	96.5
14	D-Xylofuranose	23.53	81.3
15	L-threonine	14.20	98.6
16	Nonadecanoic acid	33.38	92.4
17	L-Threitol	17.22	89.6
18	D-Glucopyranose	38.78	94.3
19	2-alpha-Mannobiose	42.40	81.8
20	Cystathionine	12.05	83.8
21	Stearate	29.72	96.7
22	Inositol	28.53	95.2
23	L-Asparagine	20.91	97.1
24	Arachidonic acid	33.76	82.6
25	Beta-D-Galactofuranose	41.70	86.4
26	D-Xylopyranose	24.44	84.9
27	Stigmasterol	46.52	96.6
28	Maltitol	42.81	90.8

Table S3. Pathway analysis results showing potential pathways involved in MM.

Sr. No.	Pathway	Total	Hits	Raw <i>p</i>-value	FDR corrected <i>p</i>-value	Impact
1	Pyrimidine metabolism	60	6	0.00032	0.012813	0.18984
2	Alanine, aspartate and glutamate metabolism	24	4	0.000496	0.01322	0.25831
3	Glycine, serine and threonine metabolism	48	4	0.006863	0.13725	0.16843
4	Cysteine and methionine metabolism	56	4	0.011805	0.18888	0.32131
5	Purine metabolism	92	5	0.015056	0.20074	0.02284
6	Nitrogen metabolism	39	3	0.024038	0.27472	0.00763
7	Sulfur metabolism	18	2	0.033241	0.33241	0.07087
8	Citrate cycle (TCA cycle)	20	2	0.040451	0.35407	0.14591
9	Riboflavin metabolism	21	2	0.044259	0.35407	0.14504
10	Pentose and glucuronate interconversions	53	3	0.052779	0.38385	0.05588

Table S4: List of metabolome associated genes identified using Kyoto Encyclopedia of Genes and Genomes (KEGG) and human metabolic data base (HMDB).

ZNRD1	SLC7A7	PUS10	PLA2G4C	PCYOX1	NME4	MTHFR	IDH3B	ENTPD8	CYP2A7	ASL	ADORA2B
ZNF638	SLC7A6	PUS1	PLA2G4B	PCK2	NME3	MTHFD2L	IDH3A	ENTPD3	CYP2A6	ASAH2C	ADORA2A
ZCCHC6	SLC7A1	PUF60	PLA2G4A	PCK1	NME2	MTHFD2	HSD3B7	ENTPD1	CYP2A13	ASAH2	ADORA1
ZCCHC11	SLC52A1	PTGS2	PLA2G3	PC	NME1	MTHFD1	HSD3B2	ENPP3	CYP1B1	ASAH1	ADK
XDH	SLC3A2	PTGS1	PLA2G2F	PARP9	NIT2	MTAP	HSD3B1	ENPP1	CYP1A2	AS3MT	ADH7
UXS1	SLC38A3	PTGR2	PLA2G2E	PARP8	NFS1	MSRB3	HSD17B8	ENOX2	CYP1A1	ART5	ADH6
UROCI	SLC35B3	PTGR1	PLA2G2D	PARP6	NDUFV2	MSRB2	HSD17B7	ENOX1	CYP19A1	ART4	ACOT2
UPRT	SLC35B2	PRODH	PLA2G2A	PARP4	NDUFV1	MSRB1	HSD17B6	EHHADH	CYB5RL	ART3	ACOT1
UPP2	SLC29A3	PPCS	PLA2G1B	PARP3	NDUFS8	MSRA	HSD17B4	EGLN3	CYB5R4	ART1	ACLY
UPP1	SLC29A2	PPAT	PLA2G16	PARP2	NDUFS7	MSMO1	HSD17B2	EGLN2	CYB5R3	ARG2	ACER2
UGP2	SLC27A6	PPARG	PLA2G12B	PARP16	NDUFS6	MOCOS	HSD17B14	EGLN1	CYB5R2	ARG1	ACER1
UGDH	SLC27A4	ppar gamma 2	PLA2G12A	PARP15	NDUFS5	MINA	HSD17B12	DYR	CYB5R1	APRT	ACADS
UCKL1	SLC27A3	POLRMT	PLA2G10	PARP14	NDUFS4	MGMT	HSD17B11	DUOX2	CTPS2	APOBEC3H	AASS
UCK2	SLC27A1	POLR3K	PKM	PARP12	NDUFS3	METAP2	HSD17B10	DUOX1	CTPS1	APOBEC3F	AASDH PPT
UCK1	SLC25A10	POLR3H	PKLR	PARP11	NDUFS2	ME3	HSD17B1	DPYD	CTH	APOBEC3D	AASDH
UAP1L1	SLC25A1	POLR3GL	PIPOX	PARP10	NDUFS1	ME2	HSD11B2	DLD	CTBP1	APOBEC3C	A1CF
UAP1	SLC22A6	POLR3G	PIG59	PARP1	NDUFC2	ME1	HSD11B1	DLAT	CSAD	APOBEC3B	
TYR	SLC1A5	POLR3F	PHYH	PADI6	NDUFB9	MDH2	HPRT1	DKFZp	CS	APOBEC3A	
TYMP	SLC1A4	POLR3E	PHPT1	PADI4	NDUFB7	MDH1	HPGD	DKC1	CRYL1	AOX1	
TWISTNB	SLC19A3	POLR3D	PHGDH	PADI3	NDUFB5	MBD2	HIPK1	DIO3	CPT1B	ANPEP	
TUT1	SLC16A10	POLR3C	PHF8	PADI2	NDUFB4	MBD1	HIF1AN	DIO2	CLC	AMT	
TTR	SLC13A3	POLR3B	PFKP	PADI1	NDUFB3	MAT2B	HIBADH	DIO1	CES5A	ALOX5	
TRPT1	SLC13A2	POLR3A	PFKM	P4HTM	NDUFB2	MAT2A	HADHA	DHPS	CES3	ALOX15B	
TRPM2	SLC13A1	POLR2L	PFKL	P4HA3	NDUFB11	MAT1A	HADH	DHFR L1	CES2	ALOX15	
TPO	SIRT7	POLR2K	PFAS	P4HA2	NDUFB1	MARS2	H6PD	DHFR	CES1	ALOX12B	
TNKS2	SIRT6	POLR2J2	PET112	P4HA1	NDUFA B1	MARS	GSS	DHCR7	CEL F2	ALOX12	
TNKS	SIRT5	POLR2J	PECR	OXER1	NDUFA9	MAOA	GSR	DHCR24	CEL	ALKBH2	
TMLHE	SIRT4	POLR2I	PDHB	OXCT2	NDUFA8	LPL	GRHPR	DDOST	CECR1	ALKBH1	
TIPARP	SIRT3	POLR2H	PDHA2	OXCT1	NDUFA7	LIPG	GPR17	DDO	CDO-1	ALDH9A1	
THNSL1	SIRT2	POLR2G	PDHA1	OTC	NDUFA6	LIPF	GPD1L	DDB2	CDO1	ALDH8A1	
TGM7	SIRT1	POLR2F	ADH5	OLAH	NDUFA5	LIPE	GPD1	DDB1	CDA	ALDH7A1	
TGM6	SERPINA7	POLR2E	ADH4	OGDHL	NDUFA4L2	LIPC	GOT2	DDAH2	CD38	ALDH6A1	

TGM5	SDSL	POLR2 D	ADH1C	OGDH	NDUFA 4	LIAS	GOT1L 1	DDAH 1	CCBL 2	ALDH5 A1	
TGM4	SDS	POLR2 C	ADH1B	NXN	NDUFA 3	LGALS 13	GOT1	DCXR	CCBL 1	ALDH4 A1	
TGM3	SDR16 C5	POLR2 B	ADH1A	NUDT 7	NDUFA 2	LEPRE L2	GENE	DCK	CBS	ALDH3B 2	
TGM2	SDHD	POLR2 A	ADFP	NUDT 2	NDUFA 13	LEPRE L1	GMPS	DAD1	CARS 2	ALDH3B 1	
TGM1	SDHC	POLR1 E	ADCY9	NUDT 12	NDUFA 12	LEPRE 1	GMDS	CYP4Z 1	CARS	ALDH3 A2	
TGDS	SDHB	POLR1 D	ADCY8	NT5M	NDUFA 11	LDHC	GLYAT L1	CYP4X 1	CARN S1	ALDH3 A1	
TET3	SDHA	POLR1 C	ADCY7	NT5E	NDUFA 10	LDHB	GLUL	CYP4F 8	CANT 1	ALDH2	
TET2	SCCPD H	POLR1 B	ADCY6	NT5C3	NDUFA 1	LDHAL 6B	GLUD2	CYP4F 3	CAD	ALDH1B 1	
TET1	SC5DL	POLR1 A	ADCY5	NT5C2	NARS2	LDHAL 6A	GLUD1	CYP4F 22	C5orf4	ALDH1 A3	
TAT	RPN2	PNPLA 8	ADCY4	NT5C1 B	NARS	LDHA	GLS2	CYP4F 2	BST1	ALDH1 A2	
TARSL 2	RPN1	PNPLA 6	ADCY3	NT5C1 A	NAPRT 1	LCMT2	GLS	CYP4F 11	BLVR B	ALDH1 A1	
TARS2	RFK	PNPLA 4	ADCY2	NT5C	NAMPT	LCMT1	GGCT	CYP4B 1	BLVR A	AKR1E2	
TARS	RETSAT	PNPLA 3	ADCY1	NSDHL	NADSY N1	LARS2	GFPT2	CYP4A 22	BHMT 2	AKR1C4	
SULT6 B1	RDH5	PNPLA 2	ADC	NQO2	NADKD 1	LARS	GFPT1	CYP4A 11	BHMT	AKR1C3	
SUCLG 2	RDH16	PNP	ADA	NQO1	NADK	LAP3	GCSH	CYP3A 7	BDH2	AKR1C2	
SUCLG 1	RARS2	PNLIP RP3	ACYP2	NOS3	MTRR	KYNU	GCLM	CYP3A 5	BDH1	AKR1C1	
SUCLA 2	RARS	PNLIP RP2	ACYP1	NOS2	MTR	KMO	GCLC	CYP3A 43	BCHE	AKR1B1 0	
STT3B	QRSL1	PNLIP RP1	ACY3	NOS1	MT- ND6	KDM8	GATM	CYP3A 4	BCAT 2	AKR1B1	
STT3A	QPRT	PNLIP	ACY1	NO66	MT- ND5	KDM2B	GATC	CYP2S 1	BCAT 1	AKR1A1	
STEAP 4	QPCT	PLOD3	ACPT	NNT	MT- ND4L	KDM2A	GAPD HS	CYP2J 2	BBOX 1	AK3	
STEAP 3	QDPR	PLOD2	ACPP	NMRK 2	MT- ND4	ITPA	GAPD H	CYP2F 1	BAAT	AID	
STEAP 2	QARS	PLOD1	ACP6	NMRK 1	MT- ND3	ISYNA1	GALE	CYP2E 1	ASS1	AICDA	
STEAP 1	PYGL	PLB1	ACP5	NMNA T3	MT- ND2	INMT	FOXO4	CYP2D 6	ASRG L1	AHCYL 2	
SORD	PYCRL	PLA2G 6	ACP2	NMNA T2	MT- ND1	IMPDH 2	FDFT1	CYP2C 9	ASPH	AHCYL 1	
SLCO2 A1	PYCR2	PLA2G 5	ACP1	NMNA T1	MTMR7	IMPDH 1	FASN	CYP2C 8	ASPG	AHCY	
SLCO1 C1	PYCR1	PLA2G 4F	ACOT8	NME7	MTMR6	ILVBL	FAAH2	CYP2C 19	ASPD H	AFMID	
SLCO1 B1	PUSL1	PLA2G 4E	ACOT7	NME6	MTMR2	IL4I1	FAAH	CYP2C 18	ASPA	ADPRH	
SLC7A 8	PUS3	PLA2G 4D	ACOT4	NME5	MTMR1	IDH3G	F13A1	CYP2B 6	ASNS	ADORA 3	