

## SUPPLEMENTARY TABLES

**Supplementary Table 1. The differentially expressed mRNAs in MT group compared with DM group.**

<b>ProbeName</b>	<b>p-value</b>	<b>Fold Change</b>	<b>Regulation</b>	<b>Symbol</b>	<b>Gene.ID</b>
A_55_P2293013	0.0493	14.3262	up	<i>Ces2a</i>	102022
A_51_P327751	0.0070	5.6606	up	<i>Ifit1</i>	15957
A_66_P128537	0.0042	5.5516	up	<i>Isg15</i>	100038880
A_52_P595871	0.0076	5.3079	up	<i>Cyp1a2</i>	13077
A_52_P402786	0.0365	4.9779	down	<i>Prom1</i>	19126
A_51_P269404	0.0118	4.5178	up	<i>Fmo3</i>	14262
A_55_P2083649	0.0088	4.2690	up	<i>Alas1</i>	11655
A_51_P359570	0.0164	4.0861	up	<i>Ifit3</i>	15959
A_51_P491667	0.0013	3.9660	down	<i>Derl3</i>	70377
A_55_P2107775	0.0096	3.9027	up	<i>Apol9a</i>	223672
A_51_P377856	0.0005	3.5075	up	<i>Gstt3</i>	103140
A_55_P2102060	0.0139	2.9184	up	<i>Gstm3</i>	14864
A_55_P1966438	0.0045	2.6146	up	<i>Gstm2</i>	14863
A_51_P503625	0.0068	2.5512	up	<i>Gsta3</i>	14859
A_65_P02177	0.0024	2.5473	up	<i>Gstm4</i>	14865
A_55_P1966432	0.0068	2.4931	up	<i>Gstm1</i>	14862
A_55_P2065231	0.0036	2.4913	up	<i>Gstm3</i>	14864
A_51_P367866	0.0311	2.3314	down	<i>Egr1</i>	13653
A_55_P2077628	0.0048	2.1923	up	<i>Dcxr</i>	67880
A_55_P1961423	0.0126	2.1791	up	<i>Gsta3</i>	14859
A_51_P284486	0.0022	2.0296	up	<i>Gstm2</i>	14863
A_55_P2147136	0.0080	1.8937	up	<i>Akr1d1</i>	208665
A_51_P138044	0.0199	1.8759	up	<i>Foxo1</i>	56458
A_51_P132978	0.0223	1.7969	up	<i>Idh1</i>	15926
A_55_P2002893	0.0346	1.7207	up	<i>Pfkfb1</i>	18639
A_55_P2012974	0.0232	1.5369	up	<i>Sdha</i>	66945
A_52_P200359	0.0064	1.5185	up	<i>Aco2</i>	11429
A_51_P393897	0.0319	1.5009	up	<i>Mpi</i>	110119
A_51_P335419	0.0050	1.4977	up	<i>Csl</i>	71832
A_55_P1953980	0.0411	1.4949	up	<i>Sdhb</i>	67680
A_51_P337269	0.0449	1.4874	up	<i>Aldob</i>	230163
A_51_P290139	0.0099	1.4839	up	<i>Dlst</i>	78920
A_55_P2146780	0.0161	1.4751	up	<i>Sdhc</i>	66052
A_51_P130110	0.0360	1.4560	up	<i>Idh3b</i>	170718
A_51_P184284	0.0106	1.4417	up	<i>Dld</i>	13382
A_51_P445662	0.0120	1.4218	up	<i>Hsd17b4</i>	15488
A_52_P43150	0.0152	1.3433	up	<i>Baat</i>	12012
A_55_P1988424	0.0202	1.3282	up	<i>Tpi1</i>	21991
A_51_P172573	0.0293	1.3242	up	<i>Sod2</i>	20656
A_52_P600822	0.2236	1.3220	up	<i>Prkecz</i>	18762
A_51_P409893	0.0221	1.3214	up	<i>Prkar2a</i>	19087
A_55_P1970670	0.0309	1.2969	up	<i>Scp2</i>	20280
A_51_P276063	0.0318	1.2544	up	<i>Phyh</i>	16922
A_55_P2148873	0.0336	1.2515	up	<i>Cat</i>	12359
A_51_P117995	0.0340	1.2481	up	<i>Pfkm</i>	18642
A_51_P110888	0.0490	1.2452	down	<i>Pck2</i>	74551

The differentially expressed mRNAs discussed in this study are listed in the table. The full list of 2801 differentially expressed mRNAs can be obtained from the contact author.

**Supplementary Table 2. Metabolites detected and identified by GC/MS in MT group compared with DM group. Metabolites which VIP > 1 and p-value < 0.05 have been shown in Supplementary Table 2. If the value of log2 fold change is positive, the content of that metabolite in MT group is greater than DM group, If the value of log2 fold change is negative, the content of that metabolite in MT group is less than DM group.**

Metabolites	RetentionTime	m/z	VIP	p-value	Fold change	log2 fold change
(-)-Dihydrocarveol	10.7197	180	2.781200	0.015461	0.195113	-2.357615
1-Kestose	29.3104	204	1.557960	0.020102	3.066278	1.616489
21-hydroxypregnenolone 1	28.0997	243	3.370050	0.000286	0.215912	-2.211485
2-amino-2-methylpropane-1,3-diol 1	10.7711	155	2.572560	0.027227	0.183154	-2.448871
2'-deoxyadenosine 5'-monophosphate	27.3751	169	2.798090	0.005003	0.378206	-1.402758
3-hydroxybenzyl alcohol	12.9109	135	3.799540	0.001584	0.236527	-2.079921
4-Androsten-11beta-ol-3,17-dione 4	26.6908	259	1.687070	0.013457	0.280722	-1.832788
4-hydroxyphenylacetic acid	15.0040	177	2.454940	0.034226	0.173412	-2.527727
4-Methylbenzyl alcohol	10.1250	130	2.721800	0.002808	0.000003	-18.448369
Acetol 4	15.6426	97	1.614060	0.006122	0.382779	-1.385416
alpha-Santonin 1	21.1897	105	3.031090	0.004159	1.65E+06	20.655095
Aminomalonic acid	12.9258	232	1.015300	0.004899	0.624170	-0.679990
Anandamide 2	25.9614	91	1.117360	0.006817	0.495450	-1.013190
androsterone 1	23.7097	91	3.305390	0.004738	0.234040	-2.095171
asparagine 3	14.7457	244	1.961870	0.003549	0.462710	-1.111818
beta-hydroxypyruvate	10.9797	260	2.313570	0.015057	0.320784	-1.640327
D-(glycerol 1-phosphate)	16.3312	266	1.592740	0.037797	0.613434	-0.705020
D-galacturonic acid 2	18.2821	299	1.537300	0.044932	0.621460	-0.686267
Digitoxose 2	14.5501	244	2.439590	0.031031	0.258178	-1.953560
dihydrocoumarin 1	15.5767	217	2.377920	0.008405	22.517975	4.493005
D-Talose 2	17.9603	211	2.120540	0.007450	4.407770	2.140049
flavin adenine degrad product	16.0677	191	3.786310	0.001679	0.202274	-2.305614
Gluconic lactone 1	17.5683	204	3.352460	0.016084	4.226876	2.079592
glutamic acid	14.7319	257	1.025780	0.025270	0.403922	-1.307851
glutaraldehyde 3	10.4367	85	2.147390	0.033205	3.115126	1.639291
glycolic acid	7.4198	103	1.078320	0.048699	0.571583	-0.806966
histidine 2	18.0133	154	2.437710	0.024060	0.436661	-1.195415
hydrocinnamic acid	12.3431	104	2.377290	0.001093	3.291242	1.718632
mannitol	18.0940	304	1.196990	0.017301	2.132601	1.092614
mannose 2	17.8777	367	3.113380	0.005807	2.70E+06	21.363729
methyl trans-cinnamate	12.1706	103	1.533310	0.001448	2.113743	1.079800
N-Acetyl-L-leucine 2	12.6438	156	1.906730	0.041585	0.535818	-0.900186
N-Methyl-L-glutamic acid 3	12.8749	98	1.102860	0.001963	0.559949	-0.836631
Octadecanol	20.2316	328	1.522260	0.014993	2.314538	1.210724
oxalic acid	8.1371	190	3.197850	0.025987	0.387441	-1.367950
oxamic acid	10.2087	171	3.429640	0.009827	2.65E+08	27.981225
phosphate	10.3103	158	5.607730	0.000002	0.109505	-3.190938
ribose-5-phosphate 1	19.5842	299	2.334980	0.028852	5.696613	2.510104
Threitol	13.3109	217	1.179820	0.020816	4.131765	2.046758
tryptophan 1	20.7595	202	1.295940	0.039507	0.475206	-1.073376
xanthine	18.9413	243	1.717660	0.001189	1.915535	0.937747

**Supplementary Table 3. Primers used in qRT-PCR.**

<b>Name</b>	<b>Sequence 5'-3'</b>	<b>Application</b>
Alas1 F	GGCTGTCATGGAGACTGTGAA	for <i>Alas1</i> gene
Alas1 R	GCATTGGTGGCAAGGAGGT	for <i>Alas1</i> gene
ces2a F	ACACAGCAGCACGGATGAT	for <i>ces2a</i> gene
ces2a R	GGCAGAGTCTTGGTCCAGAA	for <i>ces2a</i> gene
Cyp1a2 F	GCACTACCAAGACTTCAACAAGAA	for <i>Cyp1a2</i> gene
Cyp1a2 R	GCAGGATGGCTAAGAAGAGGAA	for <i>Cyp1a2</i> gene
Derl3 F	TTCTCTTCGGTGGTGTTCCTTATGA	for <i>Derl3</i> gene
Derl3 R	ATGGAGGCATAGGCAATGTGAA	for <i>Derl3</i> gene
Fmo3 F	TCTGACTGGTGGTACACAAGG	for <i>Fmo3</i> gene
Fmo3 R	TGTCTGGATGGTGGTGCTATT	for <i>Fmo3</i> gene
prom1F	TAGCATCAGACCAAGCCTAAGC	for <i>prom1</i> gene
prom1R	TCATAAGGTTTCGCAGAGCAACT	for <i>prom1</i> gene
GAPDH F	ACCACAGTCCATGCCATCAC	for control <i>GAPDH</i> gene
GAPDH R	TCCACCACCTGTTGCTGTA	for control <i>GAPDH</i> gene