Supplement 1: MIAME check list.

ITEM TO CHECK	CHECKLIST	COMMENT
Part 1 Experiment description		
Mouse type	YES	Materials and methods
Experimental variables (runners vs. non-runners, high fat vs. low fat)	YES	Materials and methods
n-count	YES	Materials and methods
Tissues used for slide	YES	Materials and methods
Mouse age, and other variables (wean weight, pooled samples, etc.)	YES	Materials and methods
Part 2 Array design		
Array series	YES	Materials and methods
Deconvoluted spot list with gene names	YES	Materials and methods: Agilent Technologies
Array type (mouse, human, cDNA, oligo, number of genes)	YES	Materials and methods
Array size	YES	Materials and methods
Slide type (and coating)	YES	Materials and methods: Agilent Technologies
Part 3 Samples		
Cy3/Cy5 labels for tissues	YES	Materials and methods
Dye swap? Or reference control?	Not shown	reference control
Labelling protocol used	YES	Materials and methods: Agilent Technologies
Sample extraction protocol used	YES	Materials and methods: Agilent Technologies
Amount of sample labelled	YES	Materials and methods: Agilent Technologies
Part 4 Hybridizations		
Hybridization protocol	YES	Materials and methods: Agilent Technologies
ALL modifications and deviations from the protocol	NO	No modifications
Manual hybridization or automatic chamber?	Not shown	automatic chamber
Number of slides done at the same time	YES	Materials and methods: Agilent Technologies
Hyb time	YES	Materials and methods: Agilent Technologies
Number of washes	YES	Materials and methods: Agilent Technologies
Amount of labelled sample hybridized	YES	Materials and methods: Agilent Technologies
Labelling efficiency	YES	Materials and methods: Agilent Technologies
Part 5 Measurements		
Which version of scanner software used	YES	Materials and methods
Laser power for scan	YES	Materials and methods
Instrument model numbers	YES	Materials and methods
Must save original .tiff format images (composite image is optional)	NO	
Normalization protocol	YES	Materials and methods
Does the scanner software subtract background? How much?	YES	Materials and methods
Spot raw values, background intensity, ch1 and 2 intensity, etc.	NO	
Corresponding gene name	YES	Results
Methods of analysis (MAN, Spotfire, Genespring) be detailed.	YES	Materials and methods
Normalized to controls? Controls removed? All normalization	YES	Materials and methods

parameters		
Lowess or other normalization if used (and parameters)	YES	Materials and methods
Part 6 Normalization controls		
Hypothesis	YES	Materials and methods

Supplement 2: MIQE checklist.

ITEM TO CHECK	IMPORTANCE	CHECKLIST	COMMENT
Experimental design			
Definition of experimental and control groups	E	YES	Materials and methods
Number within each group	E	YES	Materials and methods
Assay carried out by core lab or investigator's lab?	D	Not shown	investigator's lab
Acknowledgement of authors' contributions	D	YES	Materials and methods
Sample			
Description	E	YES	Materials and methods
Volume/mass of sample processed	D	YES	Materials and methods
Microdissection or macrodissection	E	Not shown	Macrodissection
Processing procedure	E	YES	Materials and methods
If frozen - how and how quickly?	E	YES	Materials and methods
If fixed - with what, how quickly?	E	YES	Materials and methods
Sample storage conditions and duration (especially for FFPE samples)	E	YES	Materials and methods
Nucleic acid extraction			
Procedure and/or instrumentation	E	YES	Materials and methods
Name of kit and details of any modifications	E	YES	Materials and methods
Source of additional reagents used	D	YES	Materials and methods
Details of DNase or RNAse treatment	E	YES	Materials and methods
Contamination assessment (DNA or RNA)	E	NO	
Nucleic acid quantification	E	YES	Materials and methods
Instrument and method	E	YES	Materials and methods
Purity (A260/A280)	D	YES	Materials and methods
Yield	D	YES	Materials and methods
RNA integrity method/instrument	E	YES	Materials and methods
RIN/RQI or Cq of 3' and 5' transcripts	E	NO	
Electrophoresis traces	D	YES	Materials and methods
Inhibition testing (Cq dilutions, spike or other)	E	NO	
Reverse transcription			
Complete reaction conditions	E	YES	Materials and methods
Amount of RNA and reaction volume	E	YES	Materials and methods
Priming oligonucleotide (if using GSP) and concentration	E	YES	Materials and methods
Reverse transcriptase and concentration	E	YES	Materials and methods
Temperature and time	E	YES	Materials and methods
Manufacturer of reagents and catalogue numbers	D	YES	Materials and methods
Cqs with and without RT	D	NO	
Storage conditions of cDNA	D	Not Shown	frozen
qPCR target information			
If multiplex, efficiency and LOD of each assay.	E	Not applicable	
Sequence accession number	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Location of amplicon	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Amplicon length	E	YES	Materials and methods: TaqMan gene

			expression assays (Applied biosystems)
In silico specificity screen (BLAST, etc.)	E	Not applicable	
Pseudogenes, retropseudogenes or other homologs?	D	Not applicable	
Sequence alignme	D	Not applicable	
Secondary structure analysis of amplicon	D	Not applicable	
Location of each primer by exon or intron (if applicable)	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
What splice variants are targeted?	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
qPCR Oligonucleotides			
Primer sequences	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
RTPrimerDB Identification Number	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Probe sequences	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Location and identity of any modifications	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Manufacturer of oligonucleotides	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Purification method	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
qPCR protocol			
Complete reaction conditions	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Reaction volume and amount of cDNA/DNA	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Primer, (probe), Mg++ and dNTP concentrations	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Polymerase identity and concentration	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Buffer/kit identity and manufacturer	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Exact chemical constitution of the buffer	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Additives (SYBR Green I, DMSO, etc.)	E	Not applicable	
Manufacturer of plates/tubes and catalog number	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Complete thermocycling parameters	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Reaction setup (manual/robotic)	D	Not shown	manual
Manufacturer of qPCR instrument	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
qPCR validation			
Evidence of optimisation (from gradients)	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Specificity (gel, sequence, melt, or digest)	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
For SYBR Green I, Cq of the NTC	E	Not applicable	
Standard curves with slope and y-intercept	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)

PCR efficiency calculated from slope	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Confidence interval for PCR efficiency or standard error	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
r2 of standard curve	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Linear dynamic range	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Cq variation at lower limit	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Confidence intervals throughout range	D	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
Evidence for limit of detection	E	YES	Materials and methods: TaqMan gene expression assays (Applied biosystems)
If multiplex, efficiency and LOD of each assay.	E	Not applicable	
Data analysis			
qPCR analysis program (source, version)	E	YES	TaqMan gene expression assays (Applied biosystems)
Cq method determination	E	YES	TaqMan gene expression assays (Applied biosystems)
Outlier identification and disposition	E	YES	TaqMan gene expression assays (Applied biosystems)
Results of NTCs	E	YES	Materials and methods
Justification of number and choice of reference genes	E	YES	Materials and methods
Description of normalisation method	E	YES	Materials and methods
Number and concordance of biological replicates	D	YES	Materials and methods
Number and stage (RT or qPCR) of technical replicates	E	YES	Materials and methods
Repeatability (intra-assay variation)	E	YES	TaqMan gene expression assays (Applied biosystems)
Reproducibility (inter-assay variation, %CV)	D	YES	TaqMan gene expression assays (Applied biosystems)
Power analysis	D	NO	
Statistical methods for result significance	E	YES	Materials and methods
Software (source, version)	E	Not applicable	
Cq or raw data submission using RDML	D	NO	

Supplement 3: Gene ontology classifications for upregulated genes.

GO accession	GO term	Count in total	Count in selection	p value
Biological process				
GO:0009987|GO:0008151|GO:0050875	cellular process	11897	870	1.20E-11
GO:0008152	Metabolic process	7797	677	1.03E-25
GO:0065007	Biological regulation	8474	599	0.001872352
GO:0044237	cellular metabolic process	6333	594	4.25E-30
GO:0050789|GO:0050791	regulation of biological process	8148	580	0.001256555
GO:0044238	primary metabolic process	6355	558	5.75E-20
GO:0050794|GO:0051244	regulation of cellular process	7641	549	9.55E-04
GO:0043170|GO:0043283	macromolecule metabolic process	4969	454	5.32E-18
GO:0044260|GO:0034960	Cellular macromolecule metabolic process	4512	440	5.10E-23
GO:0019222	regulation of metabolic process	4149	388	3.19E-16
Molecular function				
GO:0005488	binding	10261	814	1.28E-20
GO:0005515|GO:0045308	protein binding	5433	471	1.71E-14
GO:0003824	catalytic activity	4913	397	3.12E-07
GO:0043167	ion binding	3204	270	9.61E-06
GO:0043169	cation binding	3192	268	1.51E-05
GO:0046872	metal ion binding	3155	265	1.75E-05
GO:0003676	nucleic acid binding	2407	240	1.06E-11
GO:0036094	small molecule binding	2178	191	1.04E-04
GO:0000166	nucleotide binding	2030	183	3.11E-05
GO:0016787	hydrolase activity	2073	155	0.5342791
Cellular component				
GO:0044464	cell part	12437	1004	1.58E-37
GO:0005623	cell	12437	1004	1.58E-37
GO:0005622	intracellular	10601	934	0
GO:0044424	intracellular part	10396	909	0
GO:0043226	organelle	8922	809	0
GO:0043229	intracellular organelle	8897	808	0
GO:0043231	intracellular membrane-bounded organelle	7906	719	9.64E-36
GO:0043227	membrane-bounded organelle	7927	719	2.33E-35
GO:0005737	cytoplasm	7811	660	4.32E-21
GO:0005634	nucleus	4752	477	8.94E-29

Supplement 4: Gene ontology classifications for downregulated genes.

GO accession	GO term	Count in total	Count in selection	p value
Biological process				
GO:0009987|GO:0008151|GO:0050875	cellular process	11897	834	2.22E-18
GO:0008152	metabolic process	7797	686	0
GO:0044237	cellular metabolic process	6333	591	0
GO:0044238	primary metabolic process	6355	577	1.19E-37
GO:0043170|GO:0043283	macromolecule metabolic process	4969	479	1.93E-35
GO:0044260|GO:0034960	cellular macromolecule metabolic process	4512	460	6.46E-40
GO:0006807	nitrogen compound metabolic process	3615	326	1.09E-16
GO:0034641	cellular nitrogen compound metabolic process	3529	322	3.63E-17
GO:0019222	regulation of metabolic process	4149	321	1.55E-07
GO:0009058	biosynthetic process	2962	303	1.18E-23
Molecular function				
GO:0005488	binding	10261	774	2.49E-26
GO:0005515|GO:0045308	protein binding	5433	434	5.68E-14
GO:0003824	catalytic activity	4913	371	7.52E-08
GO:0003676	nucleic acid binding	2407	234	1.34E-14
GO:0036094	small molecule binding	2178	178	7.26E-05
GO:0000166	nucleotide binding	2030	173	7.83E-06
GO:0016787	hydrolase activity	2073	154	0.045249414
GO:0032555	purine ribonucleotide binding	1699	131	0.032515
GO:0032553	ribonucleotide binding	1700	131	0.033185348
GO:0017076	purine nucleotide binding	1707	131	0.038253143
Cellular component				
GO:0005623	cell	12437	1000	0
GO:0044464	cell part	12437	1000	0
GO:0005622	intracellular	10601	963	0
GO:0044424	intracellular part	10396	955	0
GO:0043226	organelle	8922	848	0
GO:0043229	intracellular organelle	8897	846	0
GO:0043227	membrane-bounded organelle	7927	777	0
GO:0043231	intracellular membrane-bounded organelle	7906	776	0
GO:0005737	cytoplasm	7811	763	0
GO:0044444	cytoplasmic part	5378	574	0