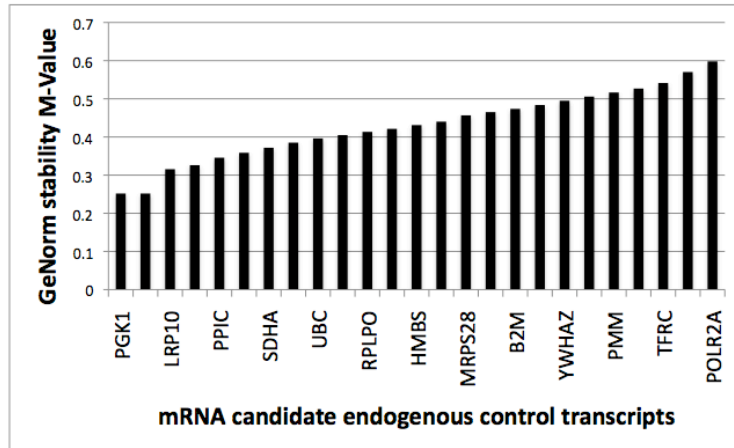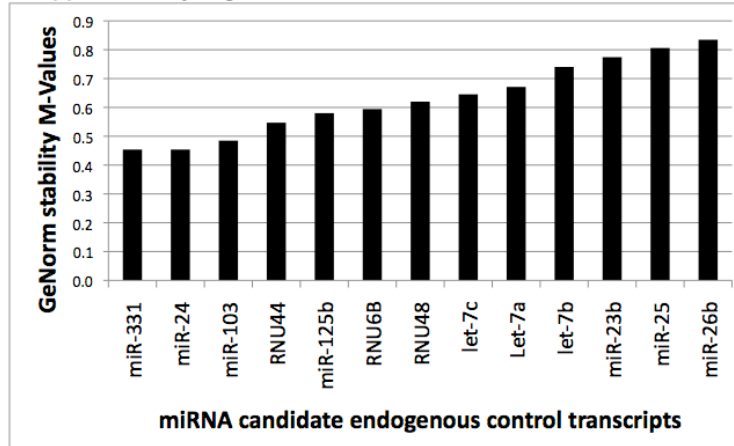**Supplementary Figure 1:** The GeNorm stability M-values for mRNA endogenous control transcript candidates (A) and microRNA endogenous control transcripts (B) for the combined expression data from all adipose tissue panels ("All Adipose Tissue Samples" column in Supplementary Table 3A and 3C).

Supplementary Figure 1A

Supplementary Figure 1B

Supplementary Table 1

Candidate mRNA endogenous control gene details

gene symbol	gene name	ABI assay ID	location	Average CTs	Triplicate CV
18s	Eukaryotic 18S rRNA	Hs99999901_s1	22p12	12.41	0.55%
ACTB	actin, beta	Hs99999903_m1	7p15-p12	23.43	0.35%
B2M	beta-2-microglobulin	Hs99999907_m1	15q21	23.43	0.32%
CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Hs00164002_m1	16p12.1	29.63	0.38%
FABP4	fatty acid binding protein 4, adipocyte	Hs00609791_m1	8q21	21.41	0.49%
G6PD	glucose-6-phosphate dehydrogenase	Hs00166169_m1	Xq28	27.30	0.28%
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	Hs99999905_m1	12p13	23.50	0.29%
GUSB	glucuronidase, beta	Hs99999908_m1	7q21.11	27.96	0.30%
HMBS	hydroxymethylbilane synthase	Hs00609297_m1	11q23.3,	30.20	0.45%
HPRT	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	Hs99999909_m1	Xq26.1	29.80	0.44%
IPO8	importin 8	Hs00183533_m1	12p11.21	30.02	0.31%
LRP10	low density lipoprotein receptor-related protein 10	Hs00204094_m1	14q11.2	27.15	0.24%
MRPS28	mitochondrial ribosomal protein S28	Hs00203983_m1	8q21.1	31.15	0.47%
PGK1	phosphoglycerate kinase 1	Hs99999906_m1	Xq13,	25.72	0.24%
PMM	phosphomannomutase 1	Hs00160195_m1	22q13.2	28.84	0.42%
POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	Hs00172187_m1	17p13.1	29.08	0.33%
PPIA	peptidylprolyl isomerase A (cyclophilin A)	Hs99999904_m1	7p13	24.13	0.29%
PPIC	peptidylprolyl isomerase C (cyclophilin C)	Hs00181460_m1	5q23.2	27.25	0.35%
PSMB6	proteasome (prosome, macropain) subunit, beta type, 6	Hs00382586_m1	17p13	27.65	0.30%
RPLPO	ribosomal protein, large, P0	Hs99999902_m1	12q24.2	24.02	0.29%
SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	Hs00188166_m1	5p15,	26.97	0.36%
TBP	TATA box binding protein	Hs99999910_m1	6q27,	29.82	0.43%
TFRC	transferrin receptor (p90, CD71)	Hs99999911_m1	3q29	27.79	0.37%
TUBB	tubulin, beta polypeptide	Hs00742828_s1	6p21.33	24.86	0.40%
UBC	ubiquitin C	Hs00824723_m1	12q24.3	23.95	0.27%
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Hs00237047_m1	8q23.1	30.81	0.43%

Supplementary Table 2

Candidate microRNA endogenous control gene details

gene symbol	ABI Assay ID	Database Accession ID	location	Average CTs	Average triplicate CV
hsa-let-7a	377	MIMAT0000062	9q22.32, 11q24.1, 22q13.31	27.40	0.47%
hsa-let-7b	378	MIMAT0000063	22q13.31	25.79	0.63%
hsa-let-7c	379	MIMAT0000064	21q21.1	26.26	0.45%
hsa-let-7g	2282	MIMAT0000414	3p21.1	25.15	0.92%
hsa-miR-23b	400	MIMAT0000418	9q22.32	31.52	0.75%
hsa-miR-24	402	MIMAT0000080	9q22.32, 19p13.13	20.64	0.48%
hsa-miR-25	403	MIMAT0000081	7q22.1	29.62	0.31%
hsa-miR-26b	407	MIMAT0000083	2q35	23.37	0.48%
hsa-miR-103	439	MIMAT0000101	5q34, 20p13	29.54	0.60%
hsa-miR-125b	449	MIMAT0000423	11q24.1, 21q21.1	26.71	0.43%
hsa-miR-145	2278	MIMAT0000437	5q32	23.20	0.38%
hsa-miR-331	545	MIMAT0000760	12q22	25.77	0.23%
RNU6B	1093	NR_002752	10p13	29.29	0.42%
RNU44	1094	NR_002750	1q25.1	25.10	0.41%
RNU48	1006	NR_002745	6p21.33	21.96	0.26%

Supplemantary table 3A

MRNA endogenous control candidate Genorm stability values (M-Values). The 3 most stable transcripts are highlighted in dark grey and the following 3 in light grey.

Gene Name	All Adipose Tissues §	Combined SubCut Panels ¶	Oxford Biobank	Rosiglitazone Study	Omental-SubCut Panel	Lipoma-SubCut Panel	Adipocyte Cell Culture
18s	0.570	0.606	0.410	0.548	0.634	0.388	0.184
ACTB	0.484	0.487	0.298	0.398	0.522	0.378	0.317
B2M	0.474	0.445	0.367	0.373	0.493	0.258	0.323
CLN3	0.421	0.334	0.212	0.317	0.328	0.204	0.184
G6PD	0.326	0.309	0.258	0.290	0.381	0.239	0.339
GAPDH	0.465	0.416	0.241	0.410	0.393	0.299	0.282
GUSB	0.440	0.426	0.231	0.433	0.421	0.227	0.347
HMBS	0.431	0.382	0.330	0.341	0.411	0.285	0.288
HPRT	0.385	0.405	0.246	0.227	0.480	0.250	0.269
IPO8	0.359	0.372	0.196	0.249	0.222	0.279	0.248
LRP10	0.316	0.296	0.220	0.305	0.350	0.216	0.312
MRPS28	0.457	0.436	0.339	0.385	0.188	0.398	0.237
PGK1	0.252	0.250	0.149	0.194	0.270	0.273	0.229
PMM	0.517	0.500	0.395	0.473	0.467	0.369	0.243
POLR2A	0.598	0.570	0.288	0.359	0.507	0.323	0.300
PPIA	0.252	0.250	0.149	0.174	0.188	0.167	0.254
PPIC	0.346	0.348	0.266	0.330	0.366	0.315	0.306
PSMB6	0.506	0.512	0.168	0.174	0.538	0.167	0.331
RPLPO	0.413	0.317	0.281	0.261	0.402	0.292	0.260
SDHA	0.372	0.362	0.357	0.276	0.303	0.331	0.366
TBP	0.405	0.455	0.252	0.464	0.239	0.359	0.203
TFRC	0.541	0.537	0.378	0.504	0.590	0.266	0.357
TUBB	0.527	0.524	0.273	0.444	0.457	0.307	0.276
UBC	0.396	0.393	0.319	0.421	0.433	0.185	0.374
YWHAZ	0.495	0.474	0.308	0.489	0.561	0.349	0.293

§Analysis of a single dataset containing the expression values of samples from all the panels found in Table 1 except Adipocytes
¶Analysis of a single dataset containing the expression values of all abdominal subcutaneous samples across the panels

Supplemantary table 3B

MRNA endogenous control candidate Normfinder stability values (SD values). The 3 most stable transcripts are highlighted in dark grey and the following 3 in light grey.

Gene Name	All Adipose Tissues §	Combined SubCut Panels ¶	Oxford Biobank	Rosiglitazone Study	Omental-SubCut Panel	Lipoma-SubCut Panel	Adipocyte Cell Culture
18s	0.866	1.030	0.547	1.131	1.203	0.432	0.126
ACTB	0.478	0.518	0.341	0.405	0.567	0.432	0.334
B2M	0.424	0.412	0.417	0.411	0.487	0.250	0.327
CLN3	0.331	0.263	0.160	0.285	0.294	0.137	0.186
G6PD	0.248	0.239	0.233	0.220	0.355	0.181	0.288
GAPDH	0.422	0.380	0.226	0.436	0.343	0.277	0.245
GUSB	0.391	0.370	0.192	0.452	0.385	0.212	0.382
HMBS	0.379	0.338	0.350	0.343	0.401	0.266	0.231
HPRT	0.362	0.390	0.235	0.222	0.483	0.199	0.267
IPO8	0.274	0.306	0.162	0.212	0.197	0.229	0.210
LRP10	0.218	0.194	0.172	0.262	0.304	0.166	0.330
MRPS28	0.408	0.403	0.342	0.399	0.234	0.461	0.172
PGK1	0.217	0.166	0.120	0.155	0.134	0.198	0.130
PMM	0.514	0.532	0.529	0.468	0.496	0.402	0.227
POLR2A	0.887	0.935	0.259	0.415	0.579	0.309	0.285
PPIA	0.182	0.193	0.108	0.184	0.220	0.190	0.187
PPIC	0.301	0.293	0.261	0.322	0.371	0.327	0.281
PSMB6	0.530	0.561	0.149	0.138	0.627	0.194	0.309
RPLPO	0.290	0.239	0.247	0.214	0.311	0.284	0.232
SDHA	0.322	0.311	0.362	0.188	0.293	0.325	0.374
TBP	0.356	0.432	0.223	0.507	0.227	0.405	0.171
TFRC	0.618	0.592	0.468	0.600	0.889	0.230	0.381
TUBB	0.544	0.568	0.301	0.452	0.501	0.302	0.262
UBC	0.376	0.363	0.347	0.407	0.416	0.129	0.432
YWHAZ	0.504	0.466	0.340	0.598	0.732	0.389	0.263

§Analysis of a single dataset containing the expression values of samples from all the panels found in Table 1 except Adipocytes

¶Analysis of a single dataset containing the expression values of all abdominal subcutaneous samples across the panels

Supplemantary table 3C

MicroRNA endogenous control candidate Genorm stability values (M-Values). The 3 most stable transcripts are highlighted in dark grey and the following 2 in light grey.

Gene Name	All Adipose Tissues§	Combined SubCut Panels¶	Oxford Biobank	Rosiglitazone Study	Omental-SubCut Panel	Lipoma-SubCut Panel	Adipocyte Cell Culture
Let-7a	0.671	0.590	0.413	0.503	0.539	0.772	0.461
let-7b	0.740	0.735	0.454	0.251	0.182	0.875	0.425
let-7c	0.645	0.599	0.441	0.251	0.182	0.504	0.280
let-7g	0.873	0.821	0.587	0.670	0.562	0.919	0.491
miR-103	0.485	0.516	0.387	0.428	0.348	0.325	0.260
miR-125b	0.580	0.577	0.469	0.529	0.386	0.538	0.360
miR-23b	0.774	0.683	0.517	0.517	0.681	0.976	0.614
miR-24	0.454	0.617	0.208	0.376	0.327	0.404	0.317
miR-25	0.806	0.768	0.620	0.589	0.445	0.673	0.348
miR-26b	0.835	0.793	0.501	0.562	0.370	0.325	0.260
miR-331	0.454	0.516	0.208	0.408	0.281	0.456	0.338
RNU6B	0.594	0.710	0.333	0.546	0.492	0.568	0.442
RNU44	0.547	0.556	0.296	0.460	0.515	0.429	0.369
RNU48	0.620	0.642	0.534	0.477	0.466	0.601	0.379

§Analysis of a single dataset containing the expression values of samples from all the panels found in Table 1 except Adipocytes
¶Analysis of a single dataset containing the expression values of all abdominal subcutaneous samples across the panels

Supplemantary table 3D

MicroRNA endogenous control candidate Normfinder stability values (SD values). The 3 most stable transcripts are highlighted in dark grey and the following 2 in light grey.

Gene Name	All Adipose Tissues§	Combined SubCut Panels¶	Oxford Biobank	Rosiglitazone Study	Omental-SubCut Panel	Lipoma-SubCut Panel	Adipocyte Cell Culture
Let-7a	0.471	0.446	0.204	0.346	0.551	0.730	0.455
let-7b	0.875	0.808	0.375	0.355	0.244	1.042	0.345
let-7c	0.576	0.551	0.414	0.340	0.270	0.329	0.200
let-7g	0.973	0.850	0.611	0.996	0.655	1.009	0.665
miR-103	0.261	0.249	0.201	0.291	0.219	0.391	0.201
miR-125b	0.487	0.386	0.480	0.476	0.233	0.531	0.226
miR-23b	0.739	0.595	0.492	0.394	1.189	1.276	1.432
miR-24	0.408	0.449	0.329	0.220	0.353	0.480	0.245
miR-25	0.704	0.702	0.707	0.596	0.479	0.599	0.258
miR-26b	0.757	0.699	0.368	0.456	0.305	0.314	0.290
miR-331	0.419	0.397	0.371	0.331	0.255	0.633	0.315
RNU6B	0.605	0.681	0.370	0.613	0.569	0.667	0.498
RNU44	0.495	0.496	0.334	0.472	0.472	0.272	0.310
RNU48	0.709	0.701	0.592	0.529	0.409	0.804	0.410

§Analysis of a single dataset containing the expression values of samples from all the panels found in Table 1 except Adipocytes
¶Analysis of a single dataset containing the expression values of all abdominal subcutaneous samples across the panels