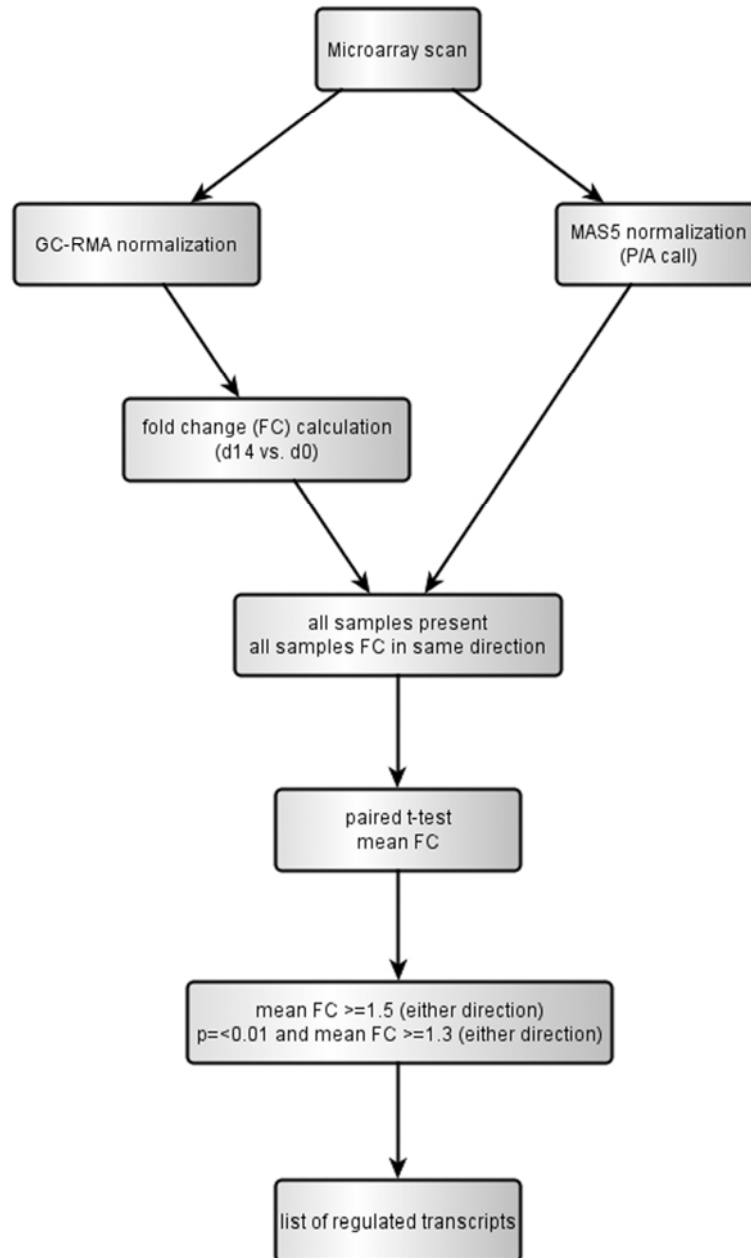


Quercetin and monocyte gene expression



1

2 Fig. S1. Diagram of microarray analysis workflow. MAS5 normalization and calculation of
3 present (P) and absent (A) calls was conducted with Affymetrix Expression Console software,
4 GC-RMA normalization with R statistical package and Bioconductor as supplied by the
5 MADMAX platform, paired Student's *t*-test was calculated with Microsoft Excel. The list of
6 differentially regulated transcripts was generated as Affymetrix Probeset IDs and
7 corresponding Entrez gene IDs.

8 Table S2

9 Genes selected for verification and endogenous controls with corresponding assay ID's

Gene Symbol	Gene Name	TaqMan Assay ID
<i>C1GALT1</i> ^{b)}	core 1 synthase, glycoprotein-N-acetylgalacto-samine 3-beta-galactosyltransferase, 1	Hs00863328_g1
<i>CPT1B</i>	carnitine palmitoyltransferase 1B (muscle)	Hs00189258_m1
<i>EGR1</i>	early growth response 1	Hs00152928_m1
<i>GAPDH</i> ^{a)}	glyceraldehyde-3-phosphate dehydrogenase	Hs99999905_m1
<i>GM2A</i>	GM2 ganglioside activator	Hs00166197_m1
<i>GPX3</i>	glutathione peroxidase 3 (plasma)	Hs00173566_m1
<i>GZMA</i>	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	Hs00196206_m1
<i>HBA1</i>	hemoglobin, alpha 1	Hs00361191_g1
<i>HDGF</i>	hepatoma-derived growth factor (high-mobility group protein 1-like)	Hs00610314_m1
<i>IL7R</i>	interleukin 7 receptor	Hs00233682_m1
<i>IQGAP1</i>	IQ motif containing GTPase activating protein 1	Hs00182622_m1
<i>MALAT1</i>	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	Hs00273907_s1
<i>MGA</i>	MAX gene associated	Hs00861170_m1
<i>MGLL</i>	monoglyceride lipase	Hs00200752_m1
<i>NFKB2</i>	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	Hs00174517_m1
<i>OPRS1</i>	opioid receptor, sigma 1	Hs00195337_m1
<i>PLEC1</i>	plectin 1, intermediate filament binding protein 500kDa	Hs00356977_m1
<i>PLEKHA2</i>	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	Hs00329763_s1
<i>SAMHD1</i>	SAM domain and HD domain 1	Hs00210019_m1
<i>SERPINB9</i>	serpin peptidase inhibitor, clade B (ovalbumin), member 9	Hs00244603_m1
<i>SMC3</i> ^{c)}	structural maintenance of chromosomes 3	Hs00271322_m1
<i>SOD2</i>	superoxide dismutase 2, mitochondrial	Hs00167309_m1
<i>ST3GAL1</i> ^{b)}	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	Hs00161688_m1
<i>TBP</i> ^{a)}	TATA box binding protein	Hs99999910_m1
<i>TLE4</i>	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	Hs00419101_m1
<i>TNF</i>	tumour necrosis factor (TNF superfamily, member 2)	Hs00174128_m1

^{a)} endogenous control, ^{b)} qRT-PCR 96-well format, ^{c)} qRT-PCR LDA and 96-well

Quercetin and monocyte gene expression

11 Table S3

12 Differentially expressed genes representing hemopoiesis and immune-system

Entrez Gene ID	Gene Symbol	Gene name	mean fold change	P
3428	<i>IFI16</i>	interferon, gamma-inducible protein 16	4.31	0.231
567	<i>B2M</i>	beta-2-microglobulin	3.85	0.052
5788	<i>PTPRC</i>	protein tyrosine phosphatase, receptor type, C	2.65	0.094
51752	<i>ERAP1</i>	endoplasmic reticulum aminopeptidase 1	2.60	0.081
604	<i>BCL6</i>	B-cell CLL/lymphoma 6	2.44	0.121
3140	<i>MRI</i>	major histocompatibility complex, class I-related	2.28	0.271
1316	<i>KLF6</i>	Kruppel-like factor 6	2.17	0.085
3717	<i>JAK2</i>	Janus kinase 2	2.09	0.254
6891	<i>TAP2</i>	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	2.08	0.345
6693	<i>SPN</i>	Sialophorin	1.93	0.194
1499	<i>CTNNB1</i>	catenin (cadherin-associated protein), beta 1, 88kDa	1.86	0.136
3134	<i>HLA-F</i>	major histocompatibility complex, class I, F	1.78	0.121
669	<i>BPGM</i>	2,3-bisphosphoglycerate mutase	1.65	0.361
90338	<i>ZNF160</i>	zinc finger protein 160	1.64	0.089
64167	<i>ERAP2</i>	endoplasmic reticulum aminopeptidase 2	1.59	0.400
8763	<i>CD164</i>	CD164 molecule, sialomucin	1.58	0.147
3077	<i>HFE</i>	Hemochromatosis	1.55	0.122
9935	<i>MAFB</i>	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	1.55	0.238
4791	<i>NFKB2</i>	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	1.54	0.001
91	<i>ACVR1B</i>	activin A receptor, type IB	-1.31	0.007
9759	<i>HDAC4</i>	histone deacetylase 4	-1.51	0.149

Quercetin and monocyte gene expression

1021	<i>CDK6</i>	cyclin-dependent kinase 6	-1.52	0.261
6223	<i>RPS19</i>	ribosomal protein S19	-1.55	0.120
2309	<i>FOXO3</i>	forkhead box O3	-1.57	0.184
1050	<i>CEBPA</i>	CCAAT/enhancer binding protein (C/EBP), alpha	-1.63	0.041
4090	<i>SMAD5</i>	SMAD family member 5	-1.64	0.248
4297	<i>MLL</i>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>)	-1.66	0.176
914	<i>CD2</i>	CD2 molecule	-1.72	0.161
6261	<i>RYR1</i>	ryanodine receptor 1 (skeletal)	-1.76	0.285
11184	<i>MAP4K1</i>	mitogen-activated protein kinase kinase kinase 1	-1.77	0.036
3111	<i>HLA-DOA</i>	major histocompatibility complex, class II, DO alpha	-1.81	0.103
3707	<i>ITPKB</i>	inositol 1,4,5-trisphosphate 3-kinase B	-1.87	0.110
92	<i>ACVR2A</i>	activin A receptor, type IIA	-1.90	0.177
1958	<i>EGR1</i>	early growth response 1	-2.14	0.292
3575	<i>IL7R</i>	interleukin 7 receptor	-2.26	0.101

Genes in this list represent the significantly enriched GO terms: hemopoietic lymphoid organ development, immune system development, hemopoiesis, myeloid cell differentiation, and antigen processing and presentation of peptide antigen via MHC class I; genes in bold have been additionally measured by qRT-PCR; mean fold change from three microarray experiments; modified Fisher Exact *P*-value.

Quercetin and monocyte gene expression

14 Table S4

15 Differentially expressed genes representing nucleic acid metabolism

Entrez Gene ID	Gene symbol	Gene name	Mean fold change	P
80205	<i>CHD9</i>	chromodomain helicase DNA binding protein 9	7.81	0.063
9126	<i>SMC3</i>	structural maintenance of chromosomes 3	6.45	0.085
3006	<i>HIST1H1C</i>	histone cluster 1, H1c	5.07	0.087
546	<i>ATRX</i>	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, <i>S. cerevisiae</i>)	4.93	0.189
9643	<i>MORF4L2</i>	mortality factor 4 like 2	3.92	0.136
6648	<i>SOD2</i>	superoxide dismutase 2, mitochondrial	3.49	0.103
6430	<i>SFRS5</i>	splicing factor, arginine/serine-rich 5	3.13	0.224
472	<i>ATM</i>	ataxia telangiectasia mutated	3.04	0.033
7150	<i>TOP1</i>	topoisomerase (DNA) I	2.88	0.204
55704	<i>CCDC88A</i>	coiled-coil domain containing 88A	2.71	0.138
3181	<i>HNRNPA2B1</i>	heterogeneous nuclear ribonucleoprotein A2/B1	2.61	0.092
1890	<i>TYMP</i>	thymidine phosphorylase	2.58	0.309
604	<i>BCL6</i>	B-cell CLL/lymphoma 6	2.44	0.121
23049	<i>SMG-1</i>	PI-3-kinase-related kinase SMG-1	2.26	0.121
3017	<i>HIST1H2BD</i>	histone cluster 1, H2bd	2.16	0.143
9169	<i>SFRS2IP</i>	splicing factor, arginine/serine-rich 2, interacting protein	2.16	0.287
58517	<i>RBM25</i>	RNA binding motif protein 25	2.10	0.047
7307	<i>U2AF1</i>	U2 small nuclear RNA auxiliary factor 1	2.04	0.042
5937	<i>RBMS1</i>	RNA binding motif, single stranded interacting protein 1	2.02	0.220
8363	<i>HIST1H4J</i>	histone cluster 1, H4j	2.00	0.150
11335	<i>CBX3</i>	chromobox homolog 3 (HP1 gamma homolog, <i>Drosophila</i>)	1.98	0.215

Quercetin and monocyte gene expression

7290	<i>HIRA</i>	HIR histone cell cycle regulation defective homolog A (<i>S. cerevisiae</i>)	1.97	0.072
4670	<i>HNRNPM</i>	heterogeneous nuclear ribonucleoprotein M	1.95	0.134
6421	<i>SFPQ</i>	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	1.92	0.065
8349	<i>HIST2H2BE</i>	histone cluster 2, H2be	1.89	0.070
23451	<i>SF3B1</i>	splicing factor 3b, subunit 1, 155kDa	1.89	0.132
4683	<i>NBN</i>	Nibrin	1.84	0.117
7019	<i>TFAM</i>	transcription factor A, mitochondrial	1.79	0.233
3020	<i>H3F3A</i>	H3 histone, family 3A	1.76	0.088
55729	<i>ATF7IP</i>	activating transcription factor 7 interacting protein	1.73	0.040
8337	<i>HIST2H2AA3</i>	histone cluster 2, H2aa3	1.69	0.003
8450	<i>CUL4B</i>	cullin 4B	1.68	0.253
2967	<i>GTF2H3</i>	general transcription factor IIH, polypeptide 3, 34kDa	1.65	0.093
473	<i>RERE</i>	arginine-glutamic acid dipeptide (RE) repeats	1.63	0.154
5980	<i>REV3L</i>	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	1.63	0.039
3189	<i>HNRNPH3</i>	heterogeneous nuclear ribonucleoprotein H3 (2H9)	1.61	0.007
4287	<i>ATXN3</i>	ataxin 3	1.61	0.007
54205	<i>CYCS</i>	cytochrome c, somatic	1.60	0.162
84897	<i>TBRG1</i>	transforming growth factor beta regulator 1	1.54	0.131
29896	<i>TRA2A</i>	transformer-2 alpha	1.51	0.190
8971	<i>H1FX</i>	H1 histone family, member X	1.41	0.009
2966	<i>GTF2H2</i>	general transcription factor IIH, polypeptide 2, 44kDa	1.38	0.006
7508	<i>XPC</i>	xeroderma pigmentosum, complementation group C	-1.37	0.006
2067	<i>ERCC1</i>	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	-1.38	0.00034
4221	<i>MEN1</i>	multiple endocrine neoplasia I	-1.43	0.008
9759	<i>HDAC4</i>	histone deacetylase 4	-1.51	0.149
55870	<i>ASH1L</i>	ash1 (absent, small, or homeotic)-like (<i>Drosophila</i>)	-1.51	0.108

Quercetin and monocyte gene expression

3014	<i>H2AFX</i>	H2A histone family, member X	-1.52	0.062
7468	<i>WHSC1</i>	Wolf-Hirschhorn syndrome candidate 1	-1.54	0.071
25929	<i>GEMIN5</i>	gem (nuclear organelle) associated protein 5	-1.55	0.102
10075	<i>HUWE1</i>	HECT, UBA and WWE domain containing 1	-1.56	0.066
23030	<i>JMJD2B</i>	jumonji domain containing 2B	-1.59	0.228
64858	<i>DCLRE1B</i>	DNA cross-link repair 1B (PSO2 homolog, <i>S. cerevisiae</i>)	-1.59	0.216
116138	<i>KLHDC3</i>	kelch domain containing 3	-1.61	0.010
10919	<i>EHMT2</i>	euchromatic histone-lysine N-methyltransferase 2	-1.63	0.224
399687	<i>MYO18A</i>	myosin XVIII A	-1.63	0.198
9521	<i>EEF1E1</i>	eukaryotic translation elongation factor 1 epsilon 1	-1.64	0.188
4297	<i>MLL</i>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>)	-1.66	0.176
4782	<i>NFIC</i>	nuclear factor I/C (CCAAT-binding transcription factor)	-1.67	0.148
3575	<i>IL7R</i>	interleukin 7 receptor	-2.26	0.101
54904	<i>WHSC1L1</i>	Wolf-Hirschhorn syndrome candidate 1-like 1	-3.59	0.126

Genes in this list represent the significantly enriched GO terms: DNA metabolic process, RNA splicing via transesterification reactions, and nuclear mRNA splicing via spliceosome; the GO term RNA metabolic process was omitted due to the large number of genes ($n = 151$); genes in bold have been additionally measured by qRT-PCR; mean fold change from three microarray experiments; modified Fisher Exact P -value.

Quercetin and monocyte gene expression

17 Table S5

18 Differentially expressed genes representing apoptosis-related biological processes

19

Entrez gene ID	Gene Symbol	Gene name	mean fold change	<i>P</i>
3428	IFI16	interferon, gamma-inducible protein 16	4.31	0.231
4194	MDM4	Mdm4 p53 binding protein homolog (mouse)	4.27	0.091
64135	IFIH1	interferon induced with helicase C domain 1	3.66	0.371
6648	SOD2	superoxide dismutase 2, mitochondrial	3.49	0.103
6772	STAT1	signal transducer and activator of transcription 1, 91kDa	2.94	0.393
7150	TOP1	topoisomerase (DNA) I	2.88	0.204
837	CASP4	caspase 4	2.74	0.276
5788	PTPRC	protein tyrosine phosphatase, receptor type, C	2.65	0.094
301	ANXA1	annexin A1	2.57	0.018
6789	STK4	serine/threonine kinase 4	2.54	0.132
355	FAS	Fas (TNF receptor superfamily, member 6)	2.47	0.354
5272	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	2.45	0.086
604	BCL6	B-cell CLL/lymphoma 6	2.44	0.121
9774	BCLAF1	BCL2-associated transcription factor 1	2.41	0.084
114548	NLRP3	NLR family, pyrin domain containing 3	2.32	0.225
8743	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	2.24	0.312
9021	SOCS3	suppressor of cytokine signaling 3	2.18	0.213
331	XIAP	X-linked inhibitor of apoptosis	2.13	0.154
8837	CFLAR	CASP8 and FADD-like apoptosis regulator	2.13	0.006
3717	JAK2	Janus kinase 2	2.09	0.254

Quercetin and monocyte gene expression

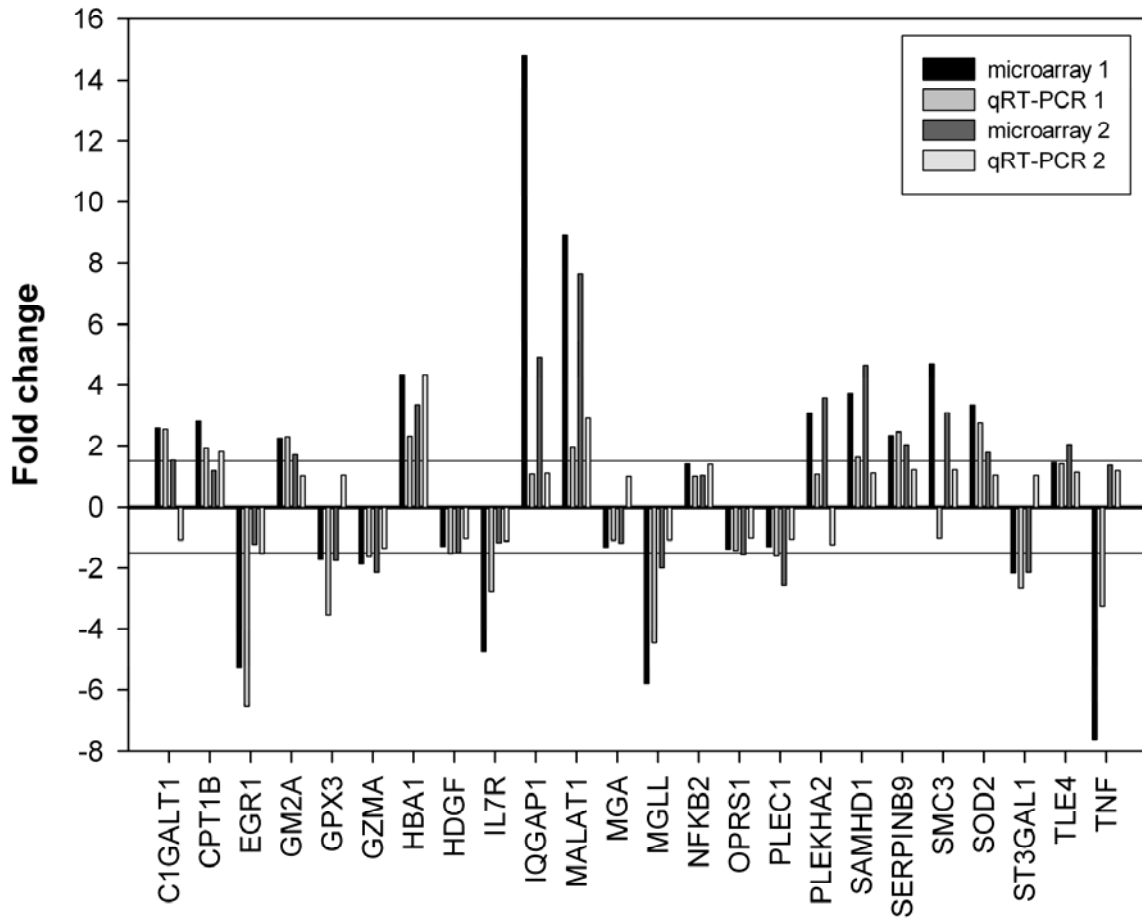
285237	C3orf38	chromosome 3 open reading frame 38	2.08	0.316
9262	STK17B	serine/threonine kinase 17b	1.97	0.050
6693	SPN	Sialophorin	1.93	0.194
5894	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	1.79	0.133
4671	NAIP	NLR family, apoptosis inhibitory protein	1.78	0.014
7072	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	1.75	0.128
8797	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	1.74	0.208
2730	GCLM	glutamate-cysteine ligase, modifier subunit	1.69	0.331
6788	STK3	serine/threonine kinase 3 (STE20 homolog, yeast)	1.66	0.220
3635	INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	1.60	0.095
54205	CYCS	cytochrome c, somatic	1.60	0.162
8539	API5	apoptosis inhibitor 5	1.56	0.051
91	ACVR1B	activin A receptor, type IB	-1.31	0.007
3002	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	-1.32	0.004
5134	PDCD2	programmed cell death 2	-1.43	<0.001
9647	PPM1F	protein phosphatase 1F (PP2C domain containing)	-1.52	0.155
26999	CYFIP2	cytoplasmic FMR1 interacting protein 2	-1.54	0.141
10783	NEK6	NIMA (never in mitosis gene a)-related kinase 6	-1.55	0.154
943	TNFRSF8	tumour necrosis factor receptor superfamily, member 8	-1.57	0.170
2309	FOXO3	forkhead box O3	-1.57	0.184
23429	RYBP	RING1 and YY1 binding protein	-1.60	0.135
399687	MYO18A	myosin XVIII A	-1.63	0.198
9521	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	-1.64	0.188
79960	PHF17	PHD finger protein 17	-1.66	0.150
203068	TUBB	tubulin, beta	-1.66	0.153
5326	PLAGL2	pleiomorphic adenoma gene-like 2	-1.71	0.011
914	CD2	CD2 molecule	-1.72	0.161

Quercetin and monocyte gene expression

6261	RYR1	ryanodine receptor 1 (skeletal)	-1.76	0.285
2308	FOXO1	forkhead box O1	-1.85	0.014
3001	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	-1.89	0.037
3315	HSPB1	heat shock 27kDa protein 1	-1.93	0.097
55201	MAP1S	microtubule-associated protein 1S	-1.94	0.143

Genes in this list represent the significantly enriched GO terms: programmed cell death and positive regulation of programmed cell death; genes in bold have been additionally measured by qRT-PCR; mean fold change from three microarray experiments; modified Fisher Exact *P*-value.

Quercetin and monocyte gene expression



21
 22 Fig. S6. Comparison of gene expression fold change measured by microarray, LDA qRT-PCR
 23 and 96-well TaqMan qRT-PCR (*C1GALT1* and *ST3GAL1*) from two subjects. LDA results
 24 are given as mean of duplicate measurements and 96-well TaqMan results as mean of
 25 triplicate measurements. qRT-PCR fold change was calculated with the comparative C_t
 26 method using GAPDH as endogenous control. A reference line is given at a fold change value
 27 of ± 1.5 .

Quercetin and monocyte gene expression

28 Table S7

29 Mean fold changes of selected genes measured by LDA and 96-well qRT-PCR in different

30 quercetin supplementation groups

31

Gene Symbol	Fold change		
	50mg <i>mean of n = 3</i>	100mg <i>subject 1/2</i>	150mg <i>mean of n = 3</i>
<i>C1GALT1</i>	-1.19	-1.61 / -1.40	1.41
<i>CPT1B</i>	1.01	1.42 / 1.37	1.69
<i>EGR1</i>	-1.13	-3.17 / -1.73	-2.62
<i>GM2A</i>	-1.04	-1.25 / 1.20	1.40
<i>GPX3</i>	1.04	1.11 / - 1.20	-1.30
<i>GZMA</i>	-1.44	-1.34 / 1.14	-1.21
<i>HBA1/2</i>	2.20	-3.83 / 3.56	3.26
<i>HDGF</i>	-1.02	1.02 / -1.17	-1.09
<i>IL7R</i>	-1.33	-1.06 / 1.48	-1.12
<i>IQGAP1</i>	-1.07	1.12 / -1.07	1.15
<i>MALAT1</i>	1.21	2.35 / 1.41	2.49
<i>MGA</i>	-1.25	1.05 / 1.00	-1.06
<i>MGLL</i>	-1.04	-1.30 / 1.00	-1.38
<i>NFKB2</i>	-1.02	1.05 / 1.25	1.16
<i>OPRS1</i>	-1.05	1.15 / 1.12	-1.20
<i>PLEC1</i>	-1.10	1.46 / -1.07	-1.05
<i>PLEKHA2</i>	-1.02	-1.21 / -1.58	-1.12
<i>SAMHD1</i>	-1.01	-1.07 / -1.03	1.28
<i>SERPINB9</i>	1.04	-1.17 / 1.21	1.50
<i>SMC3</i>	-1.11	-1.03 / -1.26	1.09
<i>SOD2</i>	-1.06	1.05 / -1.04	1.53
<i>ST3GAL1</i>	-1.18	-1.10 / 1.13	-1.09
<i>TLE4</i>	1.07	1.02 / -1.06	1.22
<i>TNF</i>	1.27	1.07 / -1.29	-1.64

32