

SUPPLEMENTARY DATA

Supplementary Table 1. Polyphenolic composition of the red grape extract used during the study.

Powder humidity (%)	4.2
Total Polyphenols as catechin equivalent (eq) (%)	108.2
Total Polyphenols as gallic acid equivalent (%) (Folin–Ciocalteu method)	64.4
Procyanidins as catechin equivalent (%) (Vanillin method)	17.9
Procyanidins profile by High Performance Liquid Chromatography (HPLC) (%):	
Catechin as catechin eq	2.07
Epicatechin as epicatechin eq	0.53
Procyanidin dimer B1 as dimer B1 eq	1.97
Procyanidin dimer B1 as dimer B2 eq	1.11
Anthocyanins (Ribereau Gayon method) (%)	4.3
Anthocyanins profile by (HPLC) (%):	
Delphinidin as delphinidin eq	0.08
Cyanidin as cyanidin eq	0.014
Petunidin as petunidin eq	0.1
Peonidin as peonidin eq	0.11
Malvidin as malvidin eq	0.1
Resveratrol by HPLC as trans resveratrol eq (ppm)	533
Pesticides (ppm) (Liste Pharmacopée Européenne 5 ^{ème} Ed)	In compliance with European regulations

SUPPLEMENTARY DATA

Supplementary Table 2. RT-PCR primer sequences.

CKMT2 forward : CTCATCGATGACCACTTTCTG CKMT2 reverse : ATTCCACATGAACTCCCAGC
CPT1b forward :TACAACAGGTGGTTTGACA CPT1b reverse: CAGAGGTGCCCAATGATG
UCP3 forward: ATGGACGCCTACAGAACCAT UCP3 reverse: CTGGGCCACCATCTTTATCA
PGC1a forward: TCCTCTGACCCCAGAGTCAC PGC1a reverse: CTTGGTTGGCTTTATGAGGAGG
NRF1 forward: GCTGCTGCTGTGGCAACAGG NRF1 reverse: TTGGGTTTGGAGGGTGAGAT
NRF2 forward: CCAAGTCCTGCATTGGGTGG NRF2 reverse: GCAAAAACCTGCCATAGTTGG
PPARa forward: GCTATCATTACGGAGTCCACG PPARa reverse: AGCTGCGGTCGCACTTGTC
PPARb forward: ACTGCCGCTTCCAGAAGTGC PPARb reverse: GCCACCAGCTTCCTCTTCTC

SUPPLEMENTARY DATA

Supplementary Table 3. Systemic and muscle antioxidant defenses: vitamin E, plasma SOD, GSH/GSSG (18PCB/20PP); muscle Gpx, Mn-SOD, SOD, catalase activities (9PCB/10PP). There were no significant differences among groups. Values are given as means \pm SEM (18PCB/20PP).

	Baseline		Post 8wk supplementation		Post 6d Fructose after 8wk supplementation	
	PCB	PP	PCB	PP	PCB	PP
Plasma vitamin E ($\mu\text{mol/L}$)	26.3 \pm 1.4	25.3 \pm 1.9	25.0 \pm 1.8	24.3 \pm 1.1	25.0 \pm 1.8	25.5 \pm 1.8
SOD activity (U/mg Hb)	1.60 \pm 0.11	1.64 \pm 0.06	1.61 \pm 0.05	1.50 \pm 0.09	1.67 \pm 0.09	1.62 \pm 0.07
GSH/GSSG	20.85 \pm 2.78	18.59 \pm 2.31	20.92 \pm 3.41	16.73 \pm 1.62	18.60 \pm 2.62	18.59 \pm 2.02
GPx (mU/g wet weight)	6518 \pm 500	6390 \pm 890	6598 \pm 533	6220 \pm 482	5916 \pm 521	6904 \pm 635
Mn-SOD (U/g wet weight)	58 \pm 4	63 \pm 7	66 \pm 5	64 \pm 6	73 \pm 9	66 \pm 6
SOD (U/g wet weight)	264 \pm 14	272 \pm 18	265 \pm 15	269 \pm 13	283 \pm 14	298 \pm 12
Catalase (U/g wet weight)	9553 \pm 1626	8851 \pm 1745	8570 \pm 1352	8191 \pm 1661	7246 \pm 1439	8009 \pm 1189

SUPPLEMENTARY DATA

Supplementary Table 4. Inflammatory cytokines and adipokines throughout study exploration visits; plasma inflammatory cytokines and adipokines of recruited subjects. There were no significant differences among groups. Values are given as means \pm SEM (18PCB/20PP).

	Baseline		Post 8wk supplementation		Post 6d Fructose after 8wk supplementation	
	PCB	PP	PCB	PP	PCB	PP
IL-1 α (pg/ml)	1.10 \pm 0.25	1.08 \pm 0.12	1.10 \pm 0.22	0.93 \pm 0.06	1.06 \pm 0.18	1.01 \pm 0.08
IL-1 β (pg/ml)	1.40 \pm 0.06	1.48 \pm 0.07	1.44 \pm 0.06	1.64 \pm 0.17	1.45 \pm 0.08	1.49 \pm 0.06
IL-6 (pg/ml)	1.73 \pm 0.26	1.84 \pm 0.28	1.56 \pm 0.18	1.57 \pm 0.25	1.46 \pm 0.14	1.64 \pm 0.19
IL-4 (pg/ml)	2.05 \pm 0.20	2.51 \pm 0.20	2.35 \pm 0.22	2.40 \pm 0.20	2.41 \pm 0.22	2.27 \pm 0.33
TNF- α (pg/ml)	2.51 \pm 0.19	2.86 \pm 0.21	2.50 \pm 0.17	2.70 \pm 0.22	2.84 \pm 0.27	2.79 \pm 0.19
Interferon- γ (pg/ml)	2.28 \pm 0.19	2.68 \pm 0.30	2.26 \pm 0.23	2.32 \pm 0.16	2.04 \pm 0.05	2.29 \pm 0.20
Adiponectin (μ g/ml)	9.6 \pm 1.1	7.3 \pm 0.7	9.9 \pm 1.1	7.8 \pm 1.1	9.3 \pm 1.0	7.5 \pm 1.0
Leptin (ng/ml)	25.7 \pm 4.8	22.6 \pm 4.1	27.5 \pm 4.8	24.9 \pm 5.0	28.6 \pm 5.5	25.3 \pm 4.6
Ghrelin (pg/ml)	439 \pm 66	307 \pm 46	387 \pm 52	349 \pm 43	441 \pm 49	354 \pm 46
Resistin (ng/ml)	3.6 \pm 0.4	3.9 \pm 0.3	3.7 \pm 0.5	3.6 \pm 0.4	3.8 \pm 0.6	3.5 \pm 0.3

SUPPLEMENTARY DATA

Supplementary Table 5. List of the differentially regulated genes in response to Polyphenols/Placebo between the 2 groups.

Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
ARHGEF26	Rho guanine nucleotide exchange factor (GEF) 26	26084	1.28 ± 0.07	0.93 ± 0.05	1.38	0.0007
SEL1L3	sel-1 suppressor of lin-12-like 3 (<i>C. elegans</i>)	23231	1.16 ± 0.03	0.92 ± 0.04	1.26	0.0007
NELL1	NEL-like 1 (chicken)	4745	0.63 ± 0.11	1.30 ± 0.14	0.48	0.002
ZNF44	zinc finger protein 44	51710	1.08 ± 0.06	0.77 ± 0.06	1.41	0.002
ENO1	enolase 1, (alpha)	2023	0.79 ± 0.07	1.33 ± 0.14	0.60	0.002
ABLIM3	actin binding LIM protein family, member 3	22885	1.16 ± 0.03	0.95 ± 0.04	1.22	0.002
FAM217A	family with sequence similarity 217, member A	222826	0.66 ± 0.11	1.35 ± 0.15	0.49	0.002
DLEU2L	deleted in lymphocytic leukemia 2-like	79469	0.80 ± 0.12	1.67 ± 0.21	0.48	0.002
BC067907	clone IMAGE	30330955	0.78 ± 0.07	1.08 ± 0.06	0.73	0.002
IGFN1	immunoglobulin-like and fibronectin type III domain containing 1	91156	1.29 ± 0.28	0.47 ± 0.09	2.75	0.003
SMG6	Smg-6 homolog, nonsense mediated mRNA decay factor (<i>C. elegans</i>)	23293	1.19 ± 0.07	0.93 ± 0.03	1.29	0.003
TUSC3	tumor suppressor candidate 3	7991	1.21 ± 0.07	0.90 ± 0.07	1.35	0.003
HNRNPA1L2	heterogeneous nuclear ribonucleoprotein A1-like 2	144983	1.07 ± 0.04	0.87 ± 0.03	1.23	0.003
LRRK2	leucine-rich repeat kinase 2	120892	0.88 ± 0.05	1.18 ± 0.07	0.74	0.003
AGAP2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	116986	1.01 ± 0.04	1.27 ± 0.06	0.80	0.003
DAZAP2	DAZ associated protein 2	9802	1.10 ± 0.05	0.87 ± 0.04	1.26	0.003
ART3	ADP-ribosyltransferase 3	419	1.01 ± 0.07	1.56 ± 0.17	0.65	0.004
TMEM214	transmembrane protein 214	54867	1.08 ± 0.04	0.89 ± 0.03	1.22	0.004
SCIMP	SLP adaptor and CSK interacting membrane protein	388325	0.64 ± 0.12	1.21 ± 0.20	0.53	0.004
HPYR1	<i>Helicobacter pylori</i> responsive 1	93668	0.78 ± 0.09	1.77 ± 0.37	0.44	0.004
HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	9146	1.10 ± 0.05	0.89 ± 0.03	1.24	0.004
GZF1	GDNF-inducible zinc finger protein 1	64412	1.08 ± 0.05	0.88 ± 0.03	1.23	0.005
SUB1	SUB1 homolog (<i>S. cerevisiae</i>)	10923	1.10 ± 0.04	0.92 ± 0.02	1.20	0.005

SUPPLEMENTARY DATA

Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
TGIF1	TGFB-induced factor homeobox 1	7050	0.88 ± 0.11	1.39 ± 0.14	0.64	0.005
TRB@	T cell receptor beta locus	6957	0.80 ± 0.06	1.20 ± 0.11	0.66	0.005
MTMR1	myotubularin related protein 1	8776	1.40 ± 0.16	0.84 ± 0.09	1.66	0.005
ECHDC1	enoyl CoA hydratase domain containing 1	55862	1.08 ± 0.04	0.88 ± 0.04	1.23	0.005
SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	9120	0.71 ± 0.10	1.19 ± 0.14	0.60	0.005
CHN2	chimerin (chimaerin) 2	1124	0.78 ± 0.09	1.40 ± 0.22	0.56	0.005
DRAM1	DNA-damage regulated autophagy modulator 1	55332	1.10 ± 0.04	0.90 ± 0.04	1.22	0.006
HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	3290	1.25 ± 0.13	0.86 ± 0.05	1.46	0.006
PGM3	phosphoglucomutase 3	5238	1.14 ± 0.04	0.94 ± 0.03	1.21	0.006
RNGTT	RNA guanylyltransferase and 5'-phosphatase	8732	0.70 ± 0.07	1.03 ± 0.08	0.68	0.006
AATF	apoptosis antagonizing transcription factor	26574	1.05 ± 0.03	0.89 ± 0.03	1.19	0.006
ABLIM3	actin binding LIM protein family, member 3	22885	1.17 ± 0.06	0.92 ± 0.05	1.27	0.006
AIM2	absent in melanoma 2	9447	0.57 ± 0.11	1.57 ± 0.36	0.36	0.007
LBX1	ladybird homeobox 1	10660	0.92 ± 0.04	1.17 ± 0.06	0.79	0.007
KPNB1	karyopherin (importin) beta 1	3837	1.16 ± 0.04	0.94 ± 0.04	1.23	0.007
LIMD1	LIM domains containing 1	8994	0.84 ± 0.07	1.51 ± 0.24	0.56	0.007
TTC37	tetratricopeptide repeat domain 37	9652	0.92 ± 0.04	1.14 ± 0.05	0.81	0.007
GRM7	glutamate receptor, metabotropic 7	2917	0.65 ± 0.06	1.42 ± 0.39	0.46	0.007
COL19A1	collagen, type XIX, alpha 1	1310	1.35 ± 0.50	7.49 ± 3.88	0.18	0.007
CRB1	crumbs homolog 1 (Drosophila)	23418	1.28 ± 0.15	0.72 ± 0.14	1.79	0.007
ERO1L	ERO1-like (S. cerevisiae)	30001	1.09 ± 0.06	0.86 ± 0.04	1.27	0.007
SCARNA1	small Cajal body-specific RNA 1	677774	0.68 ± 0.12	1.06 ± 0.08	0.64	0.008
ANKH	ankylosis, progressive homolog (mouse)	56172	1.71 ± 0.31	0.95 ± 0.10	1.80	0.008
LRRC3C	leucine rich repeat containing 3C	100505591	0.86 ± 0.12	1.32 ± 0.17	0.65	0.008

SUPPLEMENTARY DATA

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DHDDS	dehydrodolichyl diphosphate synthase	79947	1.36 ± 0.14	0.84 ± 0.10	1.63	0.008
LOC100270679	clone IMAGE:3879206	100270679	0.93 ± 0.17	1.59 ± 0.19	0.58	0.008
IGSF9	immunoglobulin superfamily, member 9	57549	0.89 ± 0.12	1.64 ± 0.35	0.54	0.008
SPINK4	serine peptidase inhibitor, Kazal type 4	27290	1.36 ± 0.14	0.86 ± 0.16	1.58	0.008
HBG1	hemoglobin, gamma A	3047	0.67 ± 0.17	1.80 ± 0.42	0.37	0.008
ACOX3	acyl-CoA oxidase 3, pristanoyl	8310	1.18 ± 0.06	0.96 ± 0.04	1.23	0.008
STARD8	StAR-related lipid transfer (START) domain containing 8	9754	1.14 ± 0.04	0.95 ± 0.03	1.19	0.009
SCGB2B2	secretoglobin, family 2B, member 2	284402	0.79 ± 0.08	1.10 ± 0.09	0.71	0.009
GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa	9328	0.82 ± 0.09	1.71 ± 0.35	0.48	0.009
CARD11	caspase recruitment domain family, member 11	84433	1.09 ± 0.15	0.57 ± 0.10	1.92	0.009
GAS6	growth arrest-specific 6	2621	0.85 ± 0.15	1.52 ± 0.21	0.56	0.009
CD300LG	CD300 molecule-like family member g	146894	2.19 ± 0.70	0.94 ± 0.07	2.33	0.009
SYS1	SYS1 Golgi-localized integral membrane protein homolog (<i>S. cerevisiae</i>)	90196	1.13 ± 0.07	0.88 ± 0.04	1.28	0.01
ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2	27	1.11 ± 0.08	0.86 ± 0.04	1.30	0.01
RPA2	replication protein A2, 32kDa	6118	1.07 ± 0.05	0.89 ± 0.03	1.21	0.01
MAP7D3	MAP7 domain containing 3	79649	1.04 ± 0.05	0.85 ± 0.04	1.23	0.01
GNAI3	guanine nucleotide binding protein , alpha inhibiting activity polypeptide 3	2773	1.10 ± 0.03	0.94 ± 0.04	1.18	0.01

SUPPLEMENTARY DATA

Supplementary Table 6. List of the differentially regulated genes in response to fructose load between PP and PCB group.

Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
LZTS1	leucine zipper, putative tumor suppressor 1	11178	0.55 ± 0.11	3.03 ± 1.49	0.18	0.002
LOC100131551	uncharacterized LOC100131551	100131551	0.63 ± 0.14	1.72 ± 0.38	0.37	0.008
UBE2DNL	ubiquitin-conjugating enzyme E2D N-terminal like (pseudogene)	100131816	0.82 ± 0.13	1.77 ± 0.28	0.46	0.008
GUCY2GP	guanylate cyclase 2G homolog (mouse), pseudogene	390003	0.71 ± 0.09	1.38 ± 0.2	0.52	0.003
RASGEF1A	RasGEF domain family, member 1A	221002	0.69 ± 0.1	1.27 ± 0.17	0.54	0.003
ZNF157	zinc finger protein 157	7712	0.67 ± 0.05	1.19 ± 0.18	0.56	0.003
KIAA1530	KIAA1530	57654	0.75 ± 0.1	1.32 ± 0.24	0.57	0.007
LOC729454	destrin-like	729454	0.78 ± 0.14	1.37 ± 0.11	0.57	0.002
SYN2	synapsin II	6854	0.74 ± 0.07	1.27 ± 0.12	0.58	0.0003
CIDEB	cell death-inducing DFFA-like effector b	27141	0.79 ± 0.1	1.33 ± 0.17	0.59	0.006
CNOT4	CCR4-NOT transcription complex, subunit 4	4850	0.76 ± 0.09	1.28 ± 0.14	0.6	0.004
KRTAP3-3	keratin associated protein 3-3	85293	0.75 ± 0.08	1.26 ± 0.14	0.6	0.001
LENG8	leukocyte receptor cluster (LRC) member 8	114823	0.71 ± 0.07	1.17 ± 0.11	0.61	0.001
ANK2	ankyrin 2, neuronal	287	0.79 ± 0.05	1.3 ± 0.13	0.61	0.001
PRM2	protamine 2	5620	0.72 ± 0.1	1.17 ± 0.12	0.61	0.007
KRTAP19-8	keratin associated protein 19-8	728299	0.79 ± 0.04	1.27 ± 0.17	0.62	0.007
CR626360	Homo sapiens cDNA, FLJ18587.		0.73 ± 0.13	1.17 ± 0.09	0.62	0.008
ITGA9	integrin, alpha 9	3680	0.89 ± 0.09	1.42 ± 0.16	0.63	0.005
MOP-1	mop-1 (RNA)	643616	0.77 ± 0.06	1.21 ± 0.15	0.63	0.007
OTUD6A	OTU domain containing 6A	139562	0.76 ± 0.04	1.19 ± 0.15	0.63	0.004
FCRL6	Fc receptor-like 6	343413	0.75 ± 0.1	1.19 ± 0.1	0.64	0.006
LOC100128304	uncharacterized LOC100128304	100128304	0.94 ± 0.11	1.47 ± 0.16	0.64	0.009
LINC00264	long intergenic non-protein coding RNA 264	645528	0.83 ± 0.08	1.29 ± 0.13	0.64	0.004
PAQR4	progesterin and adipoQ receptor family member IV	124222	0.74 ± 0.05	1.15 ± 0.16	0.64	0.005
COMTD1	catechol-O-methyltransferase domain containing 1	118881	0.81 ± 0.05	1.25 ± 0.2	0.65	0.009
RTN4RL1	reticulon 4 receptor-like 1	146760	0.78 ± 0.04	1.21 ± 0.15	0.65	0.003
PCIF1	PDX1 C-terminal inhibiting factor 1	63935	0.86 ± 0.06	1.31 ± 0.16	0.66	0.006

SUPPLEMENTARY DATA

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CYS1	cystin 1	192668	0.77 ± 0.06	1.17 ± 0.08	0.66	0.001
KCNH5	potassium voltage-gated channel, subfamily H (eag-related), member 5	27133	0.74 ± 0.08	1.12 ± 0.08	0.66	0.004
LOC145757	uncharacterized LOC145757	145757	0.72 ± 0.04	1.09 ± 0.12	0.66	0.003
LOC100130152	uncharacterized LOC100130152	100130152	0.75 ± 0.08	1.13 ± 0.09	0.66	0.004
PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	26051	0.82 ± 0.07	1.24 ± 0.13	0.66	0.005
SMPDL3B	acid sphingomyelinase-like phosphodiesterase	27293	0.82 ± 0.09	1.23 ± 0.1	0.66	0.007
ATP8	ATP synthase protein 8 (F-ATPase subunit 8)	4509	0.77 ± 0.06	1.16 ± 0.09	0.67	0.002
RNASE13	ribonuclease, RNase A family, 13 (non-active)	440163	0.81 ± 0.04	1.22 ± 0.12	0.67	0.003
PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	94274	0.8 ± 0.08	1.19 ± 0.09	0.67	0.005
PTAFR	platelet-activating factor receptor	5724	0.81 ± 0.06	1.2 ± 0.11	0.67	0.01
ZNF568	zinc finger protein 568	374900	0.9 ± 0.06	1.33 ± 0.15	0.68	0.006
PCDH19	protocadherin 19	57526	0.82 ± 0.12	1.21 ± 0.07	0.68	0.008
WISP3	WNT1 inducible signaling pathway protein 3	8838	0.73 ± 0.07	1.07 ± 0.08	0.68	0.006
TAS1R3	taste receptor, type 1, member 3	83756	0.8 ± 0.09	1.18 ± 0.05	0.68	0.003
ROPN1L	ropporin 1-like	83853	0.82 ± 0.08	1.19 ± 0.08	0.69	0.006
ZNF333	zinc finger protein 333	84449	0.76 ± 0.09	1.11 ± 0.06	0.69	0.009
LOC283854	uncharacterized LOC283854	283854	0.76 ± 0.05	1.1 ± 0.09	0.69	0.005
LOC100128508	PP12100	100128508	0.73 ± 0.09	1.05 ± 0.03	0.69	0.001
SLCO4A1	solute carrier organic anion transporter family, member 4A1	28231	0.98 ± 0.05	1.4 ± 0.12	0.7	0.003
AC007952.5	Uncharacterized protein ENSP00000382042		0.73 ± 0.06	1.05 ± 0.07	0.7	0.004
PSD	pleckstrin and Sec7 domain containing	5662	0.79 ± 0.06	1.12 ± 0.1	0.7	0.008
POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	5437	0.8 ± 0.07	1.14 ± 0.09	0.7	0.008
LOC113230	uncharacterized LOC113230	113230	0.82 ± 0.06	1.17 ± 0.11	0.71	0.01
LOC100507637	uncharacterized LOC100507637	100507637	0.81 ± 0.06	1.13 ± 0.06	0.71	0.002
FBXL6	F-box and leucine-rich repeat protein 6	26233	0.79 ± 0.04	1.11 ± 0.08	0.71	0.002
GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	2805	0.8 ± 0.02	1.12 ± 0.11	0.71	0.003
AQP1	aquaporin 1 (Colton blood group)	358	0.74 ± 0.04	1.03 ± 0.03	0.72	0.0001

SUPPLEMENTARY DATA

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IQGAP2	IQ motif containing GTPase activating protein 2	10788	0.79 ± 0.02	1.1 ± 0.11	0.72	0.005
TTYH1	tweety homolog 1 (Drosophila)	57348	0.79 ± 0.09	1.1 ± 0.05	0.72	0.009
PPP3R1	protein phosphatase 3, regulatory subunit B, alpha	5534	0.88 ± 0.08	1.22 ± 0.08	0.72	0.01
TRBV25-1	T cell receptor beta variable 25-1	28562	0.85 ± 0.07	1.18 ± 0.08	0.72	0.006
CHST11	carbohydrate sulfotransferase 11	50515	0.86 ± 0.03	1.19 ± 0.12	0.72	0.006
ENDOV	endonuclease V	284131	0.79 ± 0.08	1.09 ± 0.05	0.72	0.005
SYNGR4	synaptogyrin 4	23546	0.77 ± 0.05	1.06 ± 0.07	0.73	0.006
GEN1	Gen homolog 1, endonuclease	348654	0.71 ± 0.07	0.98 ± 0.06	0.73	0.008
MLYCD	malonyl-CoA decarboxylase	23417	0.71 ± 0.07	0.98 ± 0.13	0.73	0.005
HLA-A	major histocompatibility complex, class I, A	3105	0.86 ± 0.03	1.18 ± 0.07	0.73	0.001
SIAE	sialic acid acetyltransferase	54414	0.83 ± 0.05	1.13 ± 0.05	0.73	0.0003
AGFG2	ArfGAP with FG repeats 2	3268	0.86 ± 0.04	1.17 ± 0.09	0.73	0.003
TOMM40L	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	84134	0.89 ± 0.04	1.2 ± 0.12	0.74	0.006
TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	92609	0.83 ± 0.02	1.12 ± 0.06	0.74	0.0002
C19orf54	chromosome 19 open reading frame 54	284325	0.83 ± 0.03	1.12 ± 0.09	0.74	0.007
CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	1160	0.81 ± 0.04	1.09 ± 0.08	0.74	0.003
OXNAD1	oxidoreductase NAD-binding domain containing 1	92106	0.83 ± 0.04	1.12 ± 0.09	0.74	0.004
TIMP4	TIMP metalloproteinase inhibitor 4	7079	0.76 ± 0.08	1.03 ± 0.03	0.74	0.003
TRMU	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	55687	0.85 ± 0.06	1.14 ± 0.07	0.75	0.006
LOC100132217	uncharacterized LOC100132217	100132217	0.83 ± 0.05	1.12 ± 0.07	0.75	0.009
DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	25822	0.78 ± 0.06	1.05 ± 0.04	0.75	0.003
ANO8	anoctamin 8	57719	0.83 ± 0.04	1.11 ± 0.06	0.75	0.002
FAM65A	family with sequence similarity 65, member A	79567	0.84 ± 0.05	1.12 ± 0.06	0.75	0.002
LY6G6D	lymphocyte antigen 6 complex, locus G6D	58530	0.78 ± 0.06	1.04 ± 0.05	0.75	0.007
CYGB	cytoglobin	114757	0.81 ± 0.05	1.07 ± 0.06	0.75	0.006
HSPBP1	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	23640	0.86 ± 0.04	1.14 ± 0.09	0.75	0.009
SPHK1	sphingosine kinase 1	8877	0.81 ± 0.04	1.07 ± 0.07	0.75	0.005

SUPPLEMENTARY DATA

Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
ATXN7L1	ataxin 7-like 1	222255	0.91 ± 0.07	1.2 ± 0.07	0.76	0.008
OR6C74	olfactory receptor, family 6, subfamily C, member 74	254783	0.82 ± 0.05	1.08 ± 0.07	0.76	0.004
HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	11100	0.79 ± 0.04	1.04 ± 0.09	0.76	0.01
LETM1	leucine zipper-EF-hand containing transmembrane protein 1	3954	0.8 ± 0.05	1.05 ± 0.07	0.76	0.006
CSNK1D	casein kinase 1, delta	1453	0.86 ± 0.05	1.13 ± 0.07	0.76	0.004
MRPS18B	mitochondrial ribosomal protein S18B	28973	0.8 ± 0.02	1.05 ± 0.05	0.76	0.0004
PRELID1	PRELI domain containing 1	27166	0.84 ± 0.06	1.1 ± 0.06	0.76	0.01
MTRF1L	mitochondrial translational release factor 1-like	54516	0.79 ± 0.08	1.03 ± 0.03	0.76	0.008
TEX264	testis expressed 264	51368	0.84 ± 0.06	1.1 ± 0.07	0.76	0.01
H1FNT	H1 histone family, member N, testis-specific	341567	0.79 ± 0.05	1.03 ± 0.06	0.77	0.006
GLTPD1	glycolipid transfer protein domain containing 1	80772	0.86 ± 0.06	1.13 ± 0.06	0.77	0.004
KRT7	keratin 7	3855	0.77 ± 0.04	1 ± 0.07	0.77	0.007
NUDCD3	NudC domain containing 3	23386	0.87 ± 0.04	1.14 ± 0.06	0.77	0.005
LOC400558	uncharacterized LOC400558	400558	0.83 ± 0.03	1.08 ± 0.05	0.77	0.0004
SUSD4	sushi domain containing 4	55061	0.82 ± 0.05	1.07 ± 0.06	0.77	0.005
MRPL12	mitochondrial ribosomal protein L12	6182	0.84 ± 0.06	1.09 ± 0.07	0.77	0.01
CCDC103	coiled-coil domain containing 103	388389	0.76 ± 0.04	0.99 ± 0.05	0.77	0.001
FBRSL1	fibrosin-like 1	57666	0.77 ± 0.04	1 ± 0.06	0.77	0.005
LOC100128107	uncharacterized LOC10012810	100128107	0.83 ± 0.03	1.07 ± 0.08	0.78	0.008
UCP3	uncoupling protein 3 (mitochondrial, proton carrier)	7352	1.05 ± 0.06	0.82 ± 0.09	0.78	0.04
CDH22	cadherin 22, type 2	64405	0.83 ± 0.02	1.07 ± 0.07	0.78	0.004
ND4	mitochondrially encoded NADH dehydrogenase 4	4538	0.86 ± 0.04	1.1 ± 0.07	0.78	0.007
RPP30	ribonuclease P/MRP 30kDa subunit	10556	0.93 ± 0.05	1.2 ± 0.06	0.78	0.004
MT-CO2	mitochondrially encoded cytochrome c oxidase II	4513	0.84 ± 0.03	1.08 ± 0.07	0.78	0.006
TOP3A	topoisomerase (DNA) III alpha	7156	0.89 ± 0.03	1.14 ± 0.07	0.78	0.006
P2RX3	purinergic receptor P2X, ligand-gated ion channel, 3	5024	0.85 ± 0.03	1.09 ± 0.06	0.78	0.003
HOXA10	homeobox A10	3206	0.82 ± 0.04	1.06 ± 0.06	0.78	0.007

SUPPLEMENTARY DATA

Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
POLR1A	polymerase (RNA) I polypeptide A, 194kDa	25885	0.9 ± 0.07	1.16 ± 0.07	0.78	0.01
TYMP	thymidine phosphorylase	1890	0.85 ± 0.05	1.08 ± 0.04	0.79	0.002
ESRRA	estrogen-related receptor alpha	2101	0.85 ± 0.03	1.08 ± 0.05	0.79	0.002
CECR5	cat eye syndrome chromosome region, candidate 5	27440	0.79 ± 0.05	1 ± 0.04	0.79	0.004
TMEM201	transmembrane protein 201	199953	0.85 ± 0.02	1.07 ± 0.04	0.79	0.0003
POLRMT	polymerase (RNA) mitochondrial (DNA directed)	5442	0.85 ± 0.04	1.08 ± 0.05	0.79	0.006
ENDOG	endonuclease G	2021	0.83 ± 0.03	1.05 ± 0.06	0.79	0.007
CCND3	cyclin D3	896	0.9 ± 0.07	1.14 ± 0.04	0.79	0.009
NR2F6	nuclear receptor subfamily 2, group F, member 6	2063	0.81 ± 0.05	1.03 ± 0.04	0.79	0.004
PPP2R2D	protein phosphatase 2, regulatory subunit B, delta	55844	0.82 ± 0.04	1.04 ± 0.05	0.79	0.008
C17orf101	chromosome 17 open reading frame 101	79701	0.81 ± 0.04	1.03 ± 0.06	0.79	0.007
TMEM164	transmembrane protein 164	84187	0.89 ± 0.04	1.12 ± 0.06	0.79	0.005
SLC15A4	solute carrier family 15, member 4	121260	0.79 ± 0.04	1 ± 0.04	0.8	0.003
ADRBK1	adrenergic, beta, receptor kinase 1	156	0.88 ± 0.04	1.1 ± 0.03	0.8	0.001
PWWP2B	PWWP domain containing 2B	170394	0.86 ± 0.03	1.08 ± 0.05	0.8	0.004
ZNF672	zinc finger protein 672	79894	0.85 ± 0.03	1.06 ± 0.07	0.8	0.009
KRT81	keratin 81	3887	0.84 ± 0.03	1.05 ± 0.05	0.8	0.005
KCNH3	potassium voltage-gated channel, subfamily H (eag-related), member 3	23416	0.81 ± 0.05	1.01 ± 0.04	0.8	0.007
ATAD3A	ATPase family, AAA domain containing 3A	55210	0.87 ± 0.03	1.08 ± 0.05	0.8	0.004
AACS	acetoacetyl-CoA synthetase	65985	0.9 ± 0.05	1.12 ± 0.05	0.81	0.008
PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B	26472	0.86 ± 0.04	1.06 ± 0.03	0.81	0.003
UQCR10	ubiquinol-cytochrome c reductase, complex III subunit X	29796	0.9 ± 0.06	1.11 ± 0.05	0.81	0.01
NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, (NADH-coenzyme Q reductase)	374291	0.86 ± 0.03	1.06 ± 0.05	0.81	0.005
IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)	3500	0.82 ± 0.03	1.01 ± 0.03	0.82	0.002
NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, (NADH-coenzyme Q reductase)	4728	0.84 ± 0.03	1.03 ± 0.05	0.82	0.007
PSKH1	protein serine kinase H1	5681	0.84 ± 0.04	1.03 ± 0.04	0.82	0.007
NEK6	NIMA (never in mitosis gene a)-related kinase 6	10783	0.95 ± 0.04	1.16 ± 0.06	0.82	0.009

SUPPLEMENTARY DATA

Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
SMCR7	Smith-Magenis syndrome chromosome region, candidate 7	125170	0.89 ± 0.02	1.08 ± 0.05	0.82	0.007
KIAA1274	KIAA1274	27143	0.92 ± 0.05	1.12 ± 0.04	0.82	0.008
DHODH	dihydroorotate dehydrogenase	1723	0.84 ± 0.04	1.02 ± 0.04	0.82	0.006
NCLN	nicalin	56926	0.87 ± 0.03	1.05 ± 0.05	0.82	0.01
PET112L	PET112-like (yeast)	5188	0.88 ± 0.03	1.07 ± 0.05	0.82	0.009
TBC1D10B	TBC1 domain family, member 10B	26000	0.82 ± 0.03	0.99 ± 0.04	0.82	0.01
FAM195A	family with sequence similarity 195, member A	84331	0.85 ± 0.02	1.03 ± 0.04	0.82	0.003
C19orf12	chromosome 19 open reading frame 12	83636	0.84 ± 0.03	1.02 ± 0.04	0.83	0.007
ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	3707	0.95 ± 0.04	1.14 ± 0.04	0.83	0.007
NECAB3	N-terminal EF-hand calcium binding protein 3	63941	0.86 ± 0.03	1.03 ± 0.04	0.83	0.005
PTMS	parathyrosin	5763	0.87 ± 0.03	1.05 ± 0.03	0.83	0.003
ZBTB17	zinc finger and BTB domain containing 17	7709	0.88 ± 0.04	1.06 ± 0.04	0.83	0.008
SNX12	sorting nexin 12	29934	0.91 ± 0.04	1.09 ± 0.04	0.84	0.009
LOC100129324	uncharacterized LOC100129324	100129324	0.9 ± 0.04	1.07 ± 0.04	0.84	0.009
LYPLA2	lysophospholipase II	11313	0.92 ± 0.03	1.09 ± 0.03	0.84	0.005
MCART1	mitochondrial carrier triple repeat 1	92014	0.88 ± 0.03	1.04 ± 0.04	0.85	0.009
C16orf5	chromosome 16 open reading frame 5	29965	0.96 ± 0.03	1.13 ± 0.04	0.85	0.005
TUFM	Tu translation elongation factor, mitochondrial	7284	0.83 ± 0.03	0.98 ± 0.03	0.85	0.006
RNASEK	ribonuclease, RNase K	440400	0.86 ± 0.03	1 ± 0.03	0.86	0.008
NBPF14	neuroblastoma breakpoint family, member 14	25832	1.19 ± 0.04	1.02 ± 0.03	1.16	0.01
EFNB2	ephrin-B2	1948	1.15 ± 0.04	0.97 ± 0.03	1.18	0.009
THSD1	thrombospondin, type I, domain containing 1	55901	1.15 ± 0.03	0.97 ± 0.03	1.19	0.004
BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	9184	1.17 ± 0.05	0.98 ± 0.03	1.19	0.009
MBIP	MAP3K12 binding inhibitory protein 1	51562	1.17 ± 0.06	0.98 ± 0.03	1.19	0.009
SRSF11	serine/arginine-rich splicing factor 11	9295	1.14 ± 0.04	0.95 ± 0.04	1.2	0.01
ALG10B	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog B (yeast)	144245	1.18 ± 0.06	0.98 ± 0.03	1.21	0.008
GAS5	growth arrest-specific 5 (non-protein coding)	60674	1.24 ± 0.06	1.02 ± 0.04	1.22	0.008

SUPPLEMENTARY DATA

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BOD1L	biorientation of chromosomes in cell division 1-like	259282	1.13 ± 0.06	0.93 ± 0.03	1.22	0.008
TMEM64	transmembrane protein 64	169200	1.19 ± 0.05	0.98 ± 0.04	1.22	0.009
LTBP1	latent transforming growth factor beta binding protein 1	4052	1.15 ± 0.06	0.94 ± 0.03	1.22	0.009
RNF145	ring finger protein 145	153830	1.21 ± 0.06	0.99 ± 0.04	1.22	0.008
C9orf130	chromosome 9 open reading frame 130	286354	1.17 ± 0.05	0.95 ± 0.02	1.23	0.002
LUC7L3	LUC7-like 3 (<i>S. cerevisiae</i>)	51747	1.14 ± 0.05	0.93 ± 0.04	1.23	0.007
SREK1	splicing regulatory glutamine/lysine-rich protein 1	140890	1.18 ± 0.05	0.96 ± 0.04	1.23	0.006
AKAP11	A kinase (PRKA) anchor protein 11	11215	1.19 ± 0.06	0.96 ± 0.05	1.24	0.009
FAM82A1	family with sequence similarity 82, member A1	151393	1.15 ± 0.05	0.93 ± 0.04	1.24	0.003
ZNF845	zinc finger protein 845	91664	1.18 ± 0.05	0.95 ± 0.04	1.24	0.003
MTSS1	metastasis suppressor 1	9788	1.18 ± 0.04	0.95 ± 0.06	1.24	0.008
CCPG1	cell cycle progression 1	9236	1.13 ± 0.04	0.91 ± 0.03	1.24	0.001
ZNF566	zinc finger protein 566	84924	1.12 ± 0.05	0.9 ± 0.04	1.24	0.003
C4orf43	chromosome 4 open reading frame 43	55319	1.27 ± 0.05	1.02 ± 0.06	1.25	0.006
BPTF	bromodomain PHD finger transcription factor	2186	1.24 ± 0.06	1 ± 0.05	1.25	0.008
OSBPL9	oxysterol binding protein-like 9	114883	1.14 ± 0.05	0.92 ± 0.06	1.25	0.008
TARDBP	TAR DNA binding protein	23435	1.22 ± 0.04	0.97 ± 0.06	1.25	0.008
ANKRD13C	ankyrin repeat domain 13C	81573	1.16 ± 0.04	0.93 ± 0.04	1.25	0.002
EXD3	exonuclease 3'-5' domain containing 3	54932	1.07 ± 0.03	0.86 ± 0.03	1.25	0.0003
TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	6872	1.19 ± 0.04	0.95 ± 0.05	1.25	0.006
PAN2	PAN2 poly(A) specific ribonuclease subunit homolog (<i>S. cerevisiae</i>)	9924	1.23 ± 0.06	0.99 ± 0.05	1.25	0.008
SIRPA	signal-regulatory protein alpha	140885	1.15 ± 0.06	0.92 ± 0.04	1.25	0.009
PRMT10	protein arginine methyltransferase 10 (putative)	90826	1.1 ± 0.07	0.88 ± 0.03	1.25	0.006
GOLGA8A	golgin A8 family, member A	23015	1.21 ± 0.04	0.97 ± 0.06	1.25	0.007
PQLC3	PQ loop repeat containing 3	130814	1.23 ± 0.06	0.98 ± 0.04	1.25	0.003
ORMDL1	ORM1-like 1 (<i>S. cerevisiae</i>)	94101	1.17 ± 0.08	0.93 ± 0.03	1.26	0.008
LOC100190939	uncharacterized LOC100190939	100190939	1.21 ± 0.04	0.96 ± 0.05	1.26	0.003

SUPPLEMENTARY DATA

Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
LOC100507547	uncharacterized LOC100507547	100507547	1.09 ± 0.06	0.86 ± 0.05	1.26	0.007
LOC100129387	uncharacterized LOC100129387	100129387	1.23 ± 0.08	0.97 ± 0.04	1.27	0.009
CREBZF	CREB/ATF bZIP transcription factor	58487	1.19 ± 0.07	0.94 ± 0.05	1.27	0.01
ZNF223	zinc finger protein 223	7766	1.2 ± 0.08	0.94 ± 0.05	1.28	0.008
TTC14	tetratricopeptide repeat domain 14	151613	1.15 ± 0.05	0.9 ± 0.05	1.28	0.003
FILIP1	filamin A interacting protein 1	27145	1.07 ± 0.05	0.84 ± 0.05	1.28	0.004
SRSF5	serine/arginine-rich splicing factor 5	6430	1.24 ± 0.07	0.97 ± 0.03	1.29	0.003
FAM161A	family with sequence similarity 161, member A	84140	1.18 ± 0.06	0.92 ± 0.05	1.29	0.008
PM20D2	peptidase M20 domain containing 2	135293	1.17 ± 0.05	0.91 ± 0.06	1.29	0.005
ABCA10	ATP-binding cassette, sub-family A (ABC1), member 10	10349	1.27 ± 0.06	0.99 ± 0.05	1.29	0.003
NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	83594	1.21 ± 0.09	0.94 ± 0.04	1.29	0.01
L3MBTL3	l(3)mbt-like 3 (Drosophila)	84456	1.26 ± 0.06	0.98 ± 0.05	1.29	0.003
PLGLB1	plasminogen-like B1	5343	1.39 ± 0.07	1.08 ± 0.08	1.29	0.007
GABPA	GA binding protein transcription factor, alpha subunit 60kDa	2551	1.23 ± 0.09	0.95 ± 0.05	1.3	0.007
METTL20	methyltransferase like 20	254013	1.25 ± 0.06	0.97 ± 0.04	1.3	0.001
C1orf109	chromosome 1 open reading frame 109	54955	1.17 ± 0.05	0.9 ± 0.04	1.3	0.001
CASP8AP2	caspase 8 associated protein 2	9994	1.22 ± 0.11	0.94 ± 0.02	1.3	0.006
PDE5A	phosphodiesterase 5A, cGMP-specific	8654	1.21 ± 0.07	0.93 ± 0.06	1.3	0.007
ICK	intestinal cell (MAK-like) kinase	22858	1.2 ± 0.07	0.92 ± 0.04	1.3	0.003
EYA4	eyes absent homolog 4 (Drosophila)	2070	1.24 ± 0.06	0.95 ± 0.05	1.3	0.003
MYF5	myogenic factor 5	4617	1.18 ± 0.07	0.9 ± 0.03	1.31	0.002
POC5	POC5 centriolar protein homolog (Chlamydomonas)	134359	1.22 ± 0.08	0.93 ± 0.05	1.31	0.004
ZNF559	zinc finger protein 559	84527	1.28 ± 0.11	0.98 ± 0.03	1.31	0.006
LOC100131829	uncharacterized LOC100131829	100131829	1.29 ± 0.09	0.98 ± 0.06	1.32	0.006
HIST1H1D	histone cluster 1, H1d	3007	1.08 ± 0.09	0.82 ± 0.03	1.32	0.006
LRRK2	leucine-rich repeat kinase 2	120892	1.21 ± 0.08	0.92 ± 0.07	1.32	0.01
ZNF227	zinc finger protein 227	7770	1.19 ± 0.08	0.9 ± 0.05	1.33	0.007

SUPPLEMENTARY DATA

Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
C15orf5	chromosome 15 open reading frame 5	81698	1.48 ± 0.04	1.12 ± 0.11	1.33	0.004
DZIP1	DAZ interacting protein 1	22873	1.2 ± 0.07	0.9 ± 0.07	1.33	0.004
GGH	gamma-glutamyl hydrolase (conjugase, foyllypolygammaglutamyl hydrolase)	8836	1.17 ± 0.1	0.88 ± 0.02	1.33	0.009
RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	51735	1.29 ± 0.08	0.97 ± 0.03	1.33	0.001
FLJ13197	hypothetical FLJ13197	79667	1.34 ± 0.07	1 ± 0.07	1.34	0.003
TOPORS	topoisomerase I binding, arginine/serine-rich, E3 ubiquitin protein ligase	10210	1.23 ± 0.1	0.92 ± 0.05	1.34	0.006
ZNF92	zinc finger protein 92	168374	1.25 ± 0.07	0.93 ± 0.05	1.34	0.001
HMCN2	hemicentin 2	256158	1.2 ± 0.07	0.89 ± 0.06	1.35	0.002
KNTC1	kinetochore associated 1	9735	1.23 ± 0.09	0.91 ± 0.05	1.35	0.006
MEGF10	multiple EGF-like-domains 10	84466	1.35 ± 0.04	0.99 ± 0.1	1.36	0.009
KLHL26	kelch-like 26 (Drosophila)	55295	1.23 ± 0.13	0.9 ± 0.03	1.36	0.009
GGTA1	glycoprotein, alpha-galactosyltransferase 1 pseudogene	2681	1.27 ± 0.12	0.93 ± 0.04	1.36	0.009
VSIG8	V-set and immunoglobulin domain containing 8	391123	1.18 ± 0.08	0.87 ± 0.07	1.37	0.006
ARHGAP24	Rho GTPase activating protein 24	83478	1.41 ± 0.11	1.03 ± 0.07	1.37	0.006
DKFZp686M1136	uncharacterized LOC399832	399832	1.56 ± 0.15	1.13 ± 0.1	1.39	0.01
IFI44	interferon-induced protein 44	10561	1.35 ± 0.1	0.96 ± 0.04	1.4	0.001
KLF5	Kruppel-like factor 5 (intestinal)	688	1.21 ± 0.08	0.86 ± 0.06	1.4	0.005
NR2C1	nuclear receptor subfamily 2, group C, member 1	7181	1.23 ± 0.15	0.88 ± 0.02	1.4	0.01
MTBP	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein	27085	1.44 ± 0.1	1.02 ± 0.11	1.41	0.008
DMRT2	doublesex and mab-3 related transcription factor 2	10655	1.34 ± 0.12	0.95 ± 0.05	1.41	0.005
COLEC12	collectin sub-family member 12	81035	1.43 ± 0.13	1.01 ± 0.09	1.43	0.008
ZNF441	zinc finger protein 441	126068	1.35 ± 0.11	0.94 ± 0.07	1.43	0.006
DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	203522	1.35 ± 0.11	0.94 ± 0.09	1.44	0.01
CECR7	cat eye syndrome chromosome region, candidate 7 (non-protein coding)	100130418	1.27 ± 0.11	0.88 ± 0.07	1.44	0.007
USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene)	9098	1.39 ± 0.11	0.95 ± 0.09	1.46	0.006
DUX4L4	double homeobox 4 like 4	441056	1.14 ± 0.12	0.78 ± 0.07	1.46	0.008
APOC1	apolipoprotein C-1	341	1.56 ± 0.16	1.07 ± 0.09	1.46	0.009

SUPPLEMENTARY DATA

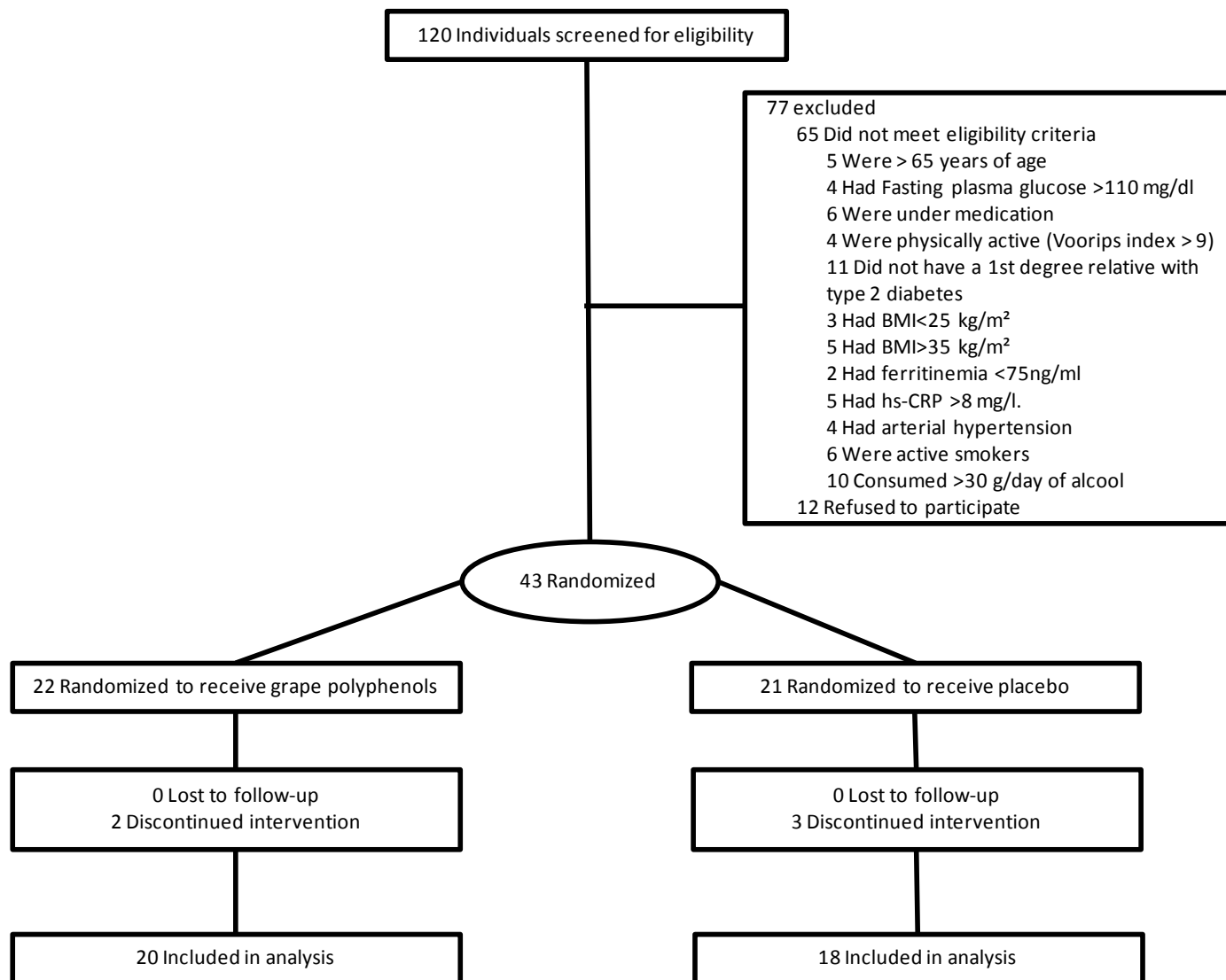
Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
SPDYE5	speedy homolog E5 (<i>Xenopus laevis</i>)	442590	1.27 ± 0.1	0.86 ± 0.07	1.47	0.002
LOC100422391	polymerase (RNA) III (DNA directed) polypeptide G (32kD) pseudogene	100422391	1.33 ± 0.12	0.9 ± 0.07	1.48	0.003
TTC28	tetratricopeptide repeat domain 28	23331	1.28 ± 0.09	0.87 ± 0.05	1.48	0.0004
PRH2	proline-rich protein HaeIII subfamily 2	5555	1.44 ± 0.21	0.97 ± 0.05	1.49	0.01
GAS1	growth arrest-specific 1	2619	1.34 ± 0.11	0.87 ± 0.05	1.53	0.001
H2AFB2	H2A histone family, member B2	474381	1.29 ± 0.13	0.84 ± 0.12	1.54	0.007
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	12	1.46 ± 0.18	0.95 ± 0.09	1.54	0.01
IRAK4	interleukin-1 receptor-associated kinase 4	51135	1.36 ± 0.17	0.88 ± 0.07	1.56	0.005
LOC100505585	uncharacterized LOC100505585	100505585	1.27 ± 0.13	0.82 ± 0.08	1.56	0.006
SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	9120	1.69 ± 0.13	1.07 ± 0.1	1.58	0.001
C10orf68	chromosome 10 open reading frame 68	79741	1.48 ± 0.14	0.93 ± 0.17	1.6	0.004
ABI3BP	ABI family, member 3 (NESH) binding protein	25890	1.58 ± 0.18	0.97 ± 0.1	1.62	0.007
GOLGA7B	golgin A7 family, member B	401647	1.27 ± 0.18	0.78 ± 0.08	1.63	0.007
LOC154822	uncharacterized LOC154822	154822	1.35 ± 0.14	0.83 ± 0.09	1.64	0.002
EFCAB7	EF-hand calcium binding domain 7	84455	1.44 ± 0.12	0.86 ± 0.1	1.67	0.002
GXYLT2	glucoside xylosyltransferase 2	727936	1.76 ± 0.27	1.05 ± 0.14	1.68	0.008
ARPP21	cAMP-regulated phosphoprotein, 21kDa	10777	1.34 ± 0.15	0.8 ± 0.12	1.68	0.006
EME1	essential meiotic endonuclease 1 homolog 1 (<i>S. pombe</i>)	146956	1.56 ± 0.16	0.93 ± 0.14	1.69	0.007
COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	1285	1.44 ± 0.18	0.85 ± 0.09	1.69	0.006
CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	4166	1.46 ± 0.16	0.86 ± 0.13	1.7	0.008
MAPK4	mitogen-activated protein kinase 4	5596	1.3 ± 0.13	0.76 ± 0.1	1.7	0.002
GRAPL	GRB2-related adaptor protein-like	400581	1.04 ± 0.1	0.61 ± 0.11	1.71	0.005
MSTN	myostatin	2660	1.59 ± 0.21	0.91 ± 0.1	1.75	0.006
DCLK1	doublecortin-like kinase 1	9201	1.44 ± 0.16	0.82 ± 0.14	1.75	0.003
CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	1134	1.32 ± 0.2	0.7 ± 0.07	1.9	0.002
CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	1134	1.4 ± 0.16	0.73 ± 0.07	1.91	0.001
ATP8B5P	ATPase, class I, type 8B, member 5, pseudogene	158381	1.29 ± 0.2	0.65 ± 0.08	1.99	0.006

SUPPLEMENTARY DATA

Symbol	Gene Name	Gene ID	FC PCB	FC PP	ratio PCB/PP	p-value
CHD5	chromodomain helicase DNA binding protein 5	26038	1.18 ± 0.18	0.58 ± 0.08	2.01	0.002
BLK	B lymphoid tyrosine kinase	640	1.65 ± 0.31	0.81 ± 0.13	2.03	0.006
DLEU2L	deleted in lymphocytic leukemia 2-like	79469	2.21 ± 0.49	1.05 ± 0.17	2.09	0.006
APC2	adenomatosis polyposis coli 2	10297	1.58 ± 0.29	0.74 ± 0.13	2.15	0.004
CLEC4M	C-type lectin domain family 4, member M	10332	1.46 ± 0.23	0.62 ± 0.2	2.36	0.002
S100A7L2	S100 calcium binding protein A7-like 2	645922	2.35 ± 0.59	0.97 ± 0.32	2.41	0.007
ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	6484	1.93 ± 0.63	0.69 ± 0.17	2.82	0.005
FAM197Y2P	family with sequence similarity 197, Y-linked, member 2, pseudogene	252946	2.66 ± 0.98	0.81 ± 0.11	3.28	0.01
LINC00112	long intergenic non-protein coding RNA 112	54089	3.6 ± 1.6	0.82 ± 0.15	4.38	0.007

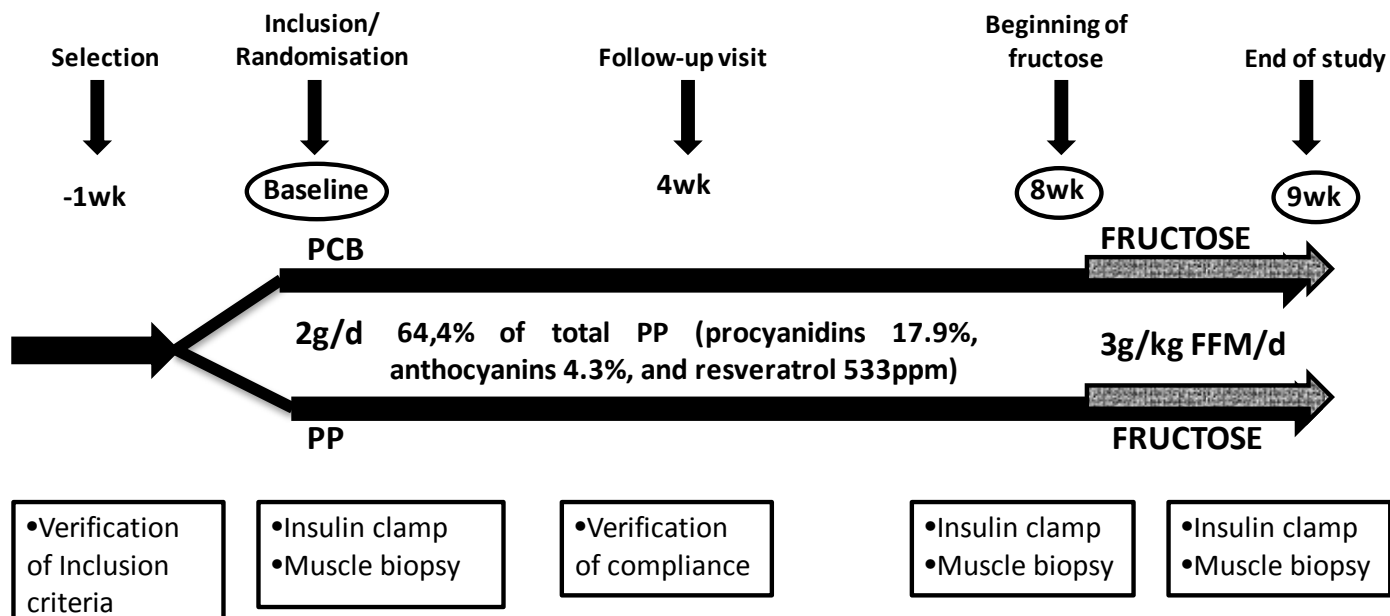
SUPPLEMENTARY DATA

Supplementary Figure 1. Flow of participants through study phases.



SUPPLEMENTARY DATA

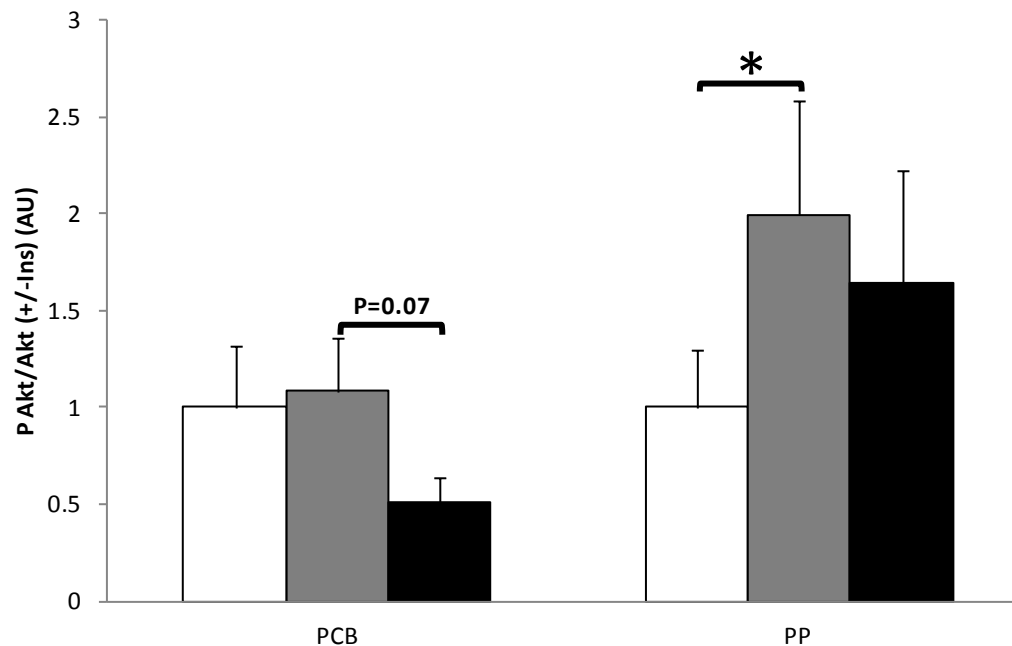
Supplementary Figure 2. Research protocol procedure.



SUPPLEMENTARY DATA

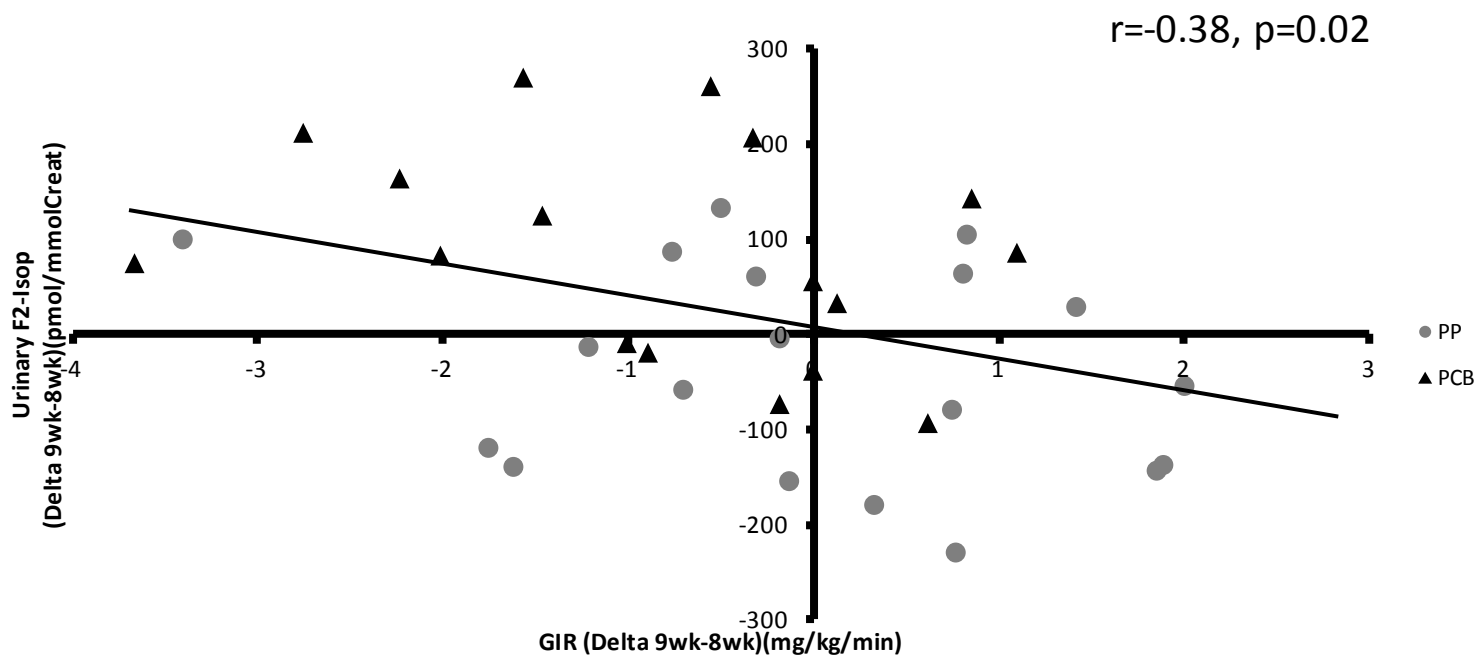
Supplementary Figure 3. Protective effects of polyphenol (PP) supplementation on fructose-induced insulin resistance.

Fold increase in PAkt/Akt ratio (AU) from basal to insulin-stimulated conditions (5PCB/7PP) at baseline (white bars), after 8 weeks of PCB or PP supplementation (grey bars) and after 6 days of high fructose diet (HFrD) with PCB/PP supplementations (black bars); * $p < 0.05$ for statistical pre- and post- intervention comparisons within each group via the Wilcoxon signed rank-sum test, data are means \pm SEM; Mann-Whitney U test was used for inter group comparisons; data are means \pm SEM.



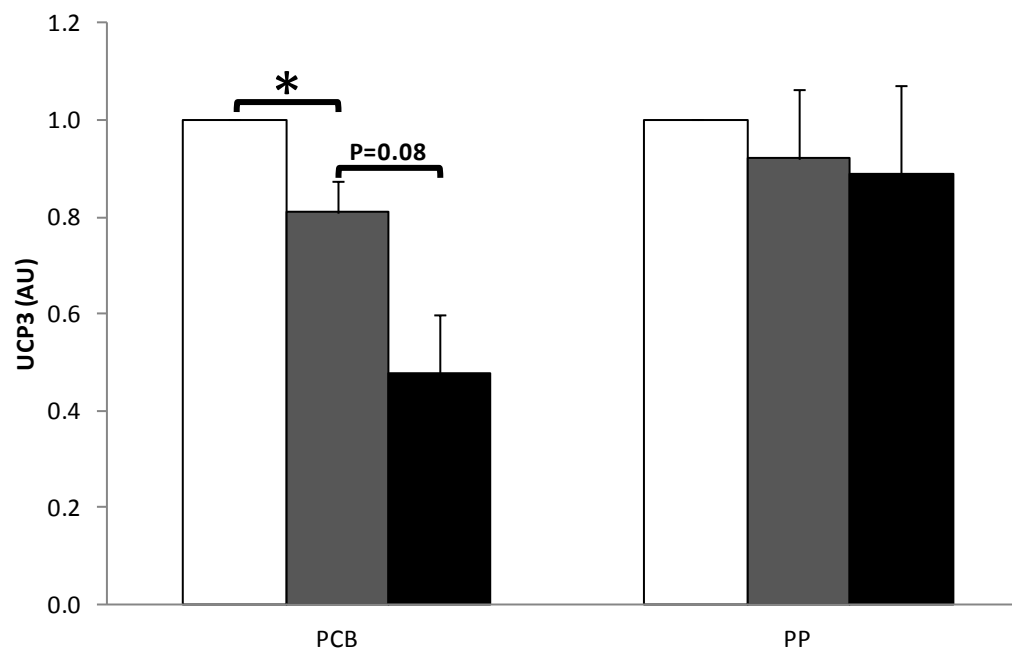
SUPPLEMENTARY DATA

Supplementary Figure 4. Relationship between fructose induced oxidative stress and altered insulin sensitivity. Correlations with Spearman rank correlations tests between Urinary F2-Isoprostanes (pmol/mmol Creat) and Glucose Infusion Rate (GIR) (mg/kg/min) after fructose overload (Delta 9wk-8wk) (N=36); black triangles=PCB(N=17) group, grey circles=PP group (N=19).



SUPPLEMENTARY DATA

Supplementary Figure 5. Variations of mitochondrial uncoupling in skeletal muscle after polyphenolic intake and fructose overload
On muscle extracts obtained at baseline (white bars), after 8 weeks of PCB or PP (grey bars) supplementation and after 6 days of HFrD with PCB/PP supplementations (black bars); uncoupling protein 3 (UCP3) level was measured by western blot, normalized to α -tubulin, and expressed as fold induction relative to baseline (5PCB/7PP); * $p < 0.05$ for statistical pre- and post- intervention comparisons within each group via the Wilcoxon signed rank-sum test; Mann-Whitney U test was used for inter group comparisons; data are means \pm SEM.



SUPPLEMENTARY DATA

Supplementary Figure 6. Association between mitochondrial function variation and insulin response. Correlations between Vmax palmitoyl carnitine ($\mu\text{molO}_2/\text{min}/\text{g}$ fibers) and glucose infusion rate (GIR) ($\text{mg}/\text{kg}/\text{min}$) after fructose load (Delta 9wk-8wk) in (A) the PCB group (N=7) and (B) in the PP group (N=9); correlations were established with Spearman rank correlations tests.

