Cheung et al., Human mediastinal adipose tissue displays certain characteristics of brown fat

Supporting Information

Figure 1

Expression levels of seven selected genes in subcutaneous and mediastinal adipose tissue from microarray analysis

Table 1

Top 20 GO gene sets enriched in mediastinal as compared to subcutaneous adipose tissue identified by gene set enrichment analysis

Figure 2

Volcano plots of the top 20 enriched gene sets in mediastinal as compared to subcutaneous adipose tissue

Figure 1

Expression levels of seven selected genes in subcutaneous and mediastinal adipose tissue from exon array analysis

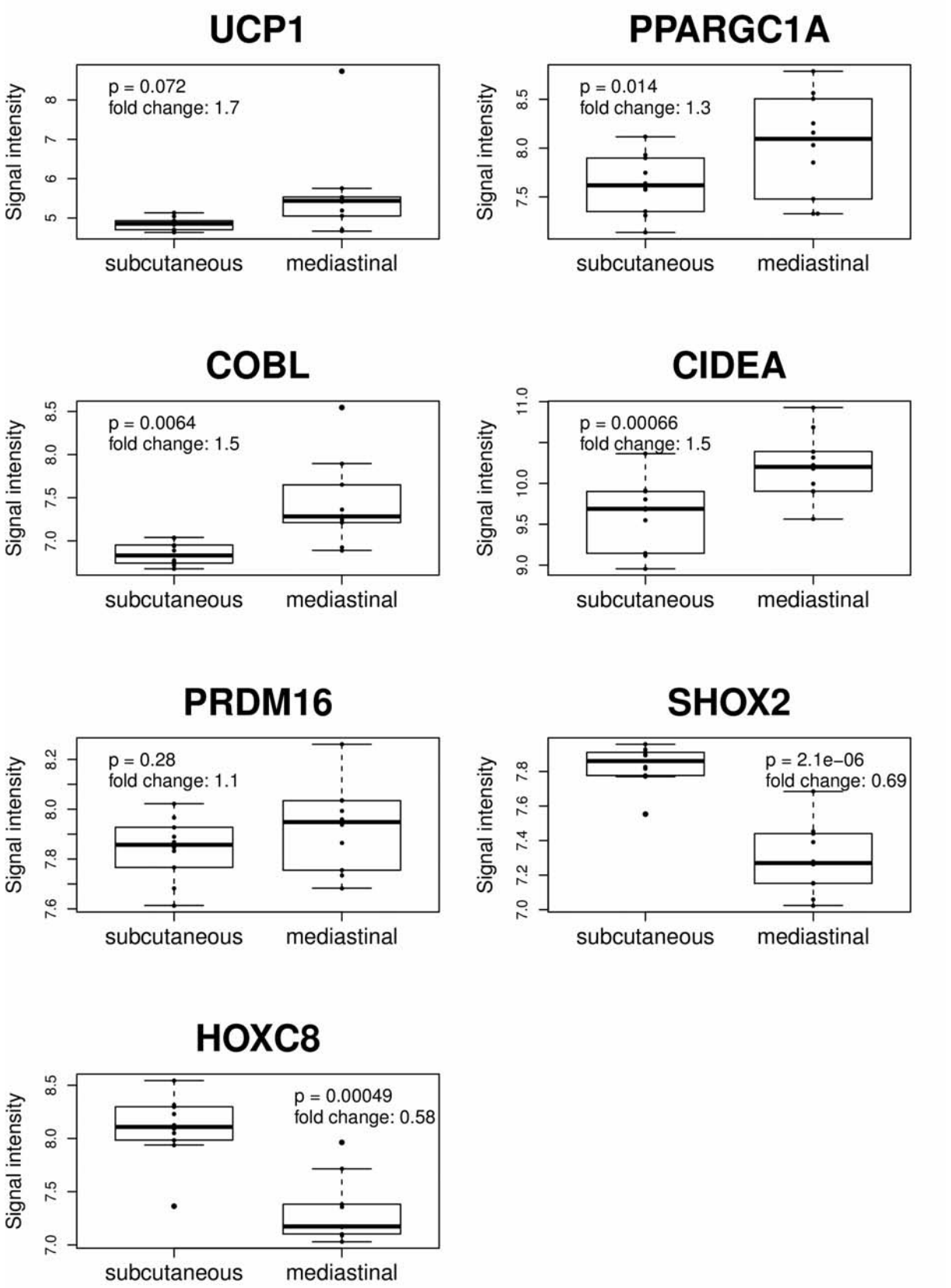


Table 1

Top 20 GO gene sets enriched in mediastinal as compared to subcutaneous adipose tissue identified by gene set enrichment analysis

Gene sets enriched in mediastinal adipose tissue	p	q
GO:0003723 RNA binding	3.68E-06	0.0022
GO:0005759 mitochondrial matrix	4.32E-06	0.0022
GO:0005743 mitochondrial inner membrane	3.29E-05	0.0110
GO:0016568 chromatin modification	0.0002	0.0437
GO:0003735 structural constituent of ribosome	0.0004	0.0714
GO:0006414 translational elongation	0.0006	0.0969
GO:0045449 regulation of transcription	0.0009	0.1254
GO:0008168 methyltransferase activity	0.0010	0.1301
GO:0005747 mitochondrial respiratory chain complex I	0.0017	0.1661
GO:0006412 translation	0.0017	0.1661
GO:0005840 ribosome	0.0019	0.1753
GO:0006635 fatty acid beta-oxidation	0.0024	0.1826
GO:0042645 mitochondrial nucleoid	0.0024	0.1826
GO:0008380 RNA splicing	0.0026	0.1826
GO:0005730 nucleolus	0.0027	0.1826
GO:0005681 spliceosome	0.0030	0.1909
GO:0030529 ribonucleoprotein complex	0.0039	0.2285
GO:0007166 cell surface receptor linked signal transduction	0.0051	0.2721
GO:0008137 NADH dehydrogenase (ubiquinone) activity	0.0052	0.2721
GO:0051539 4 iron, 4 sulfur cluster binding	0.0054	0.2722

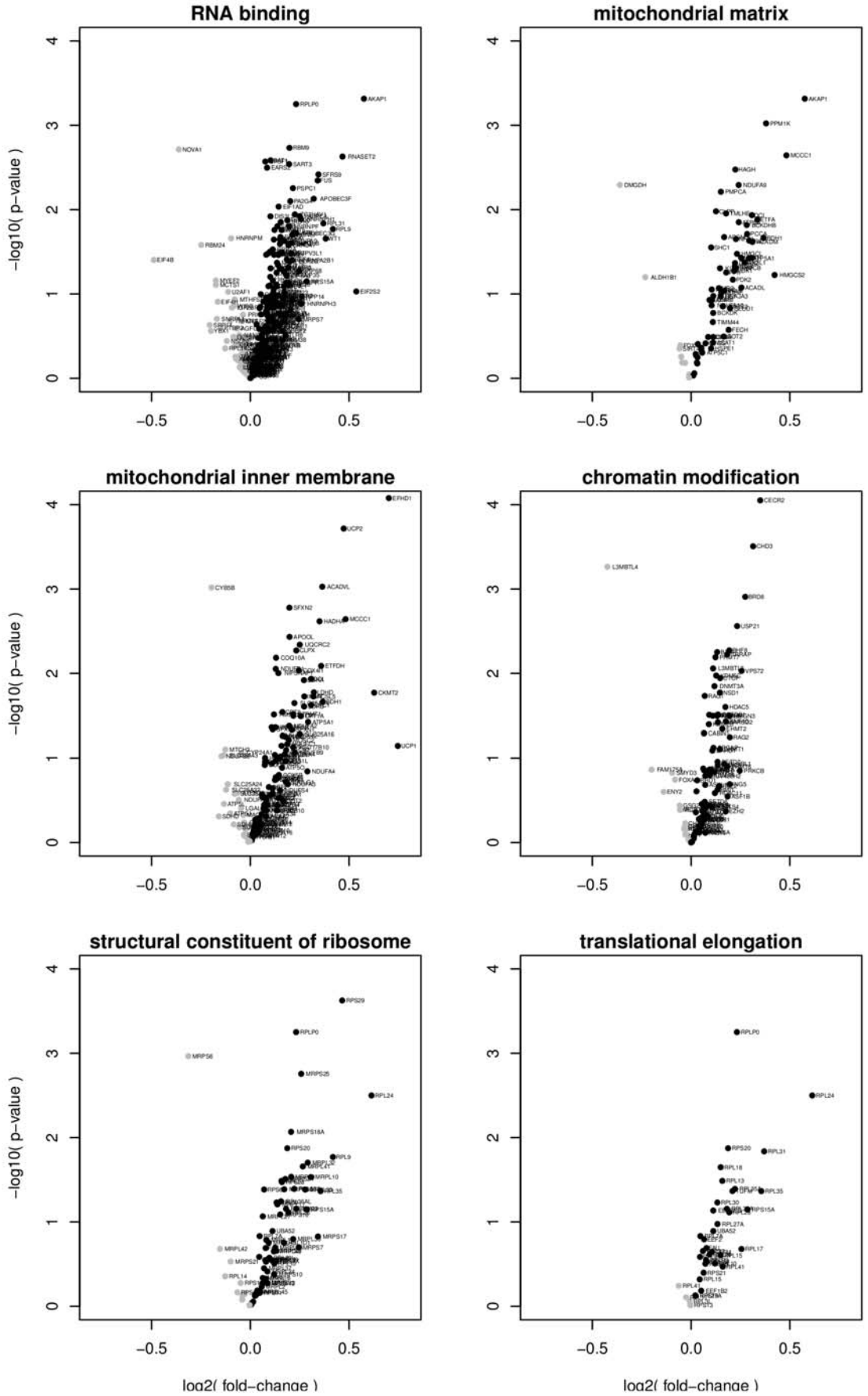
Adjusted p-values (q-values) were calculated using the Benjamini and Hochberg step-up false discovery rate-controlling procedure [1].

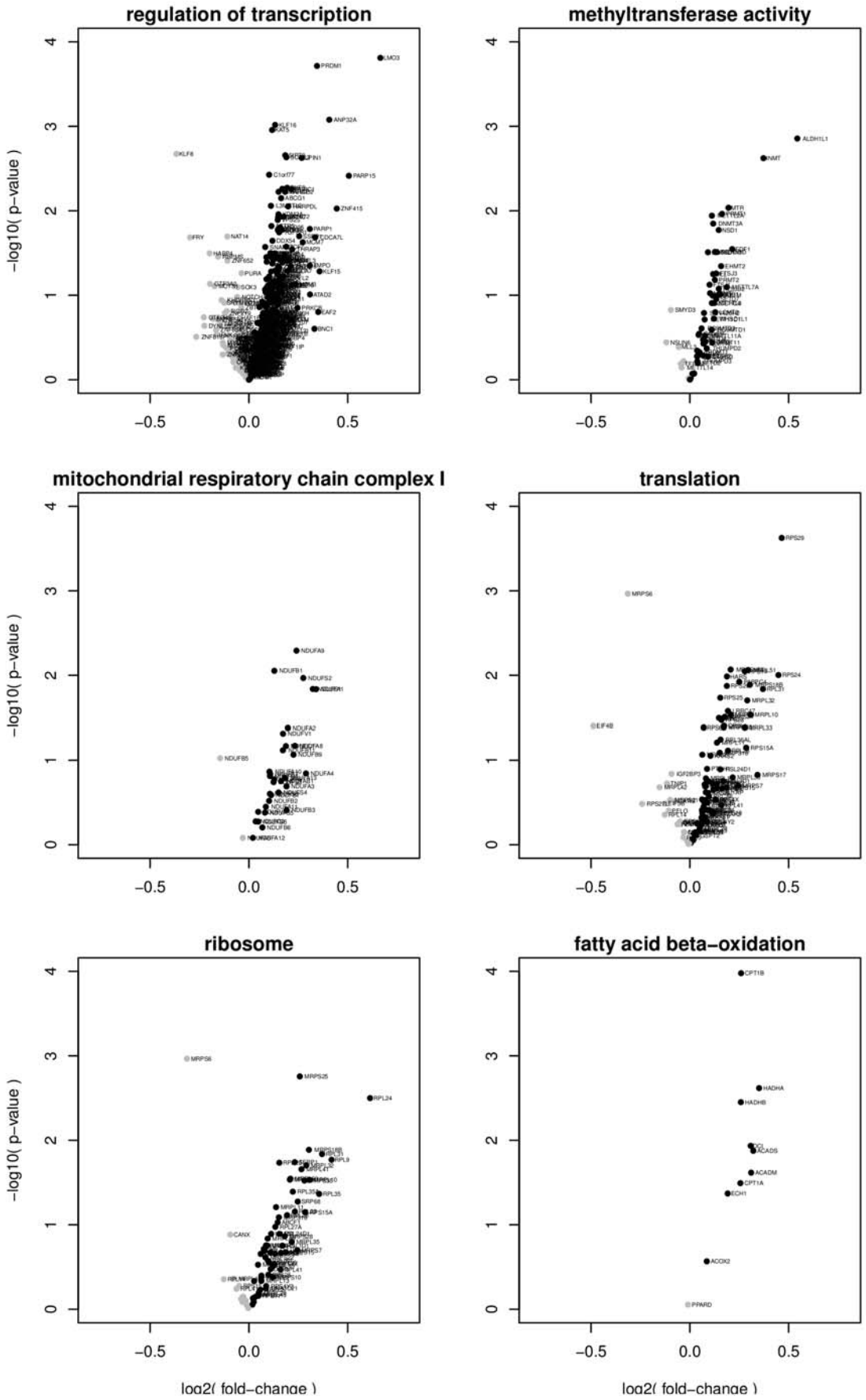
Reference

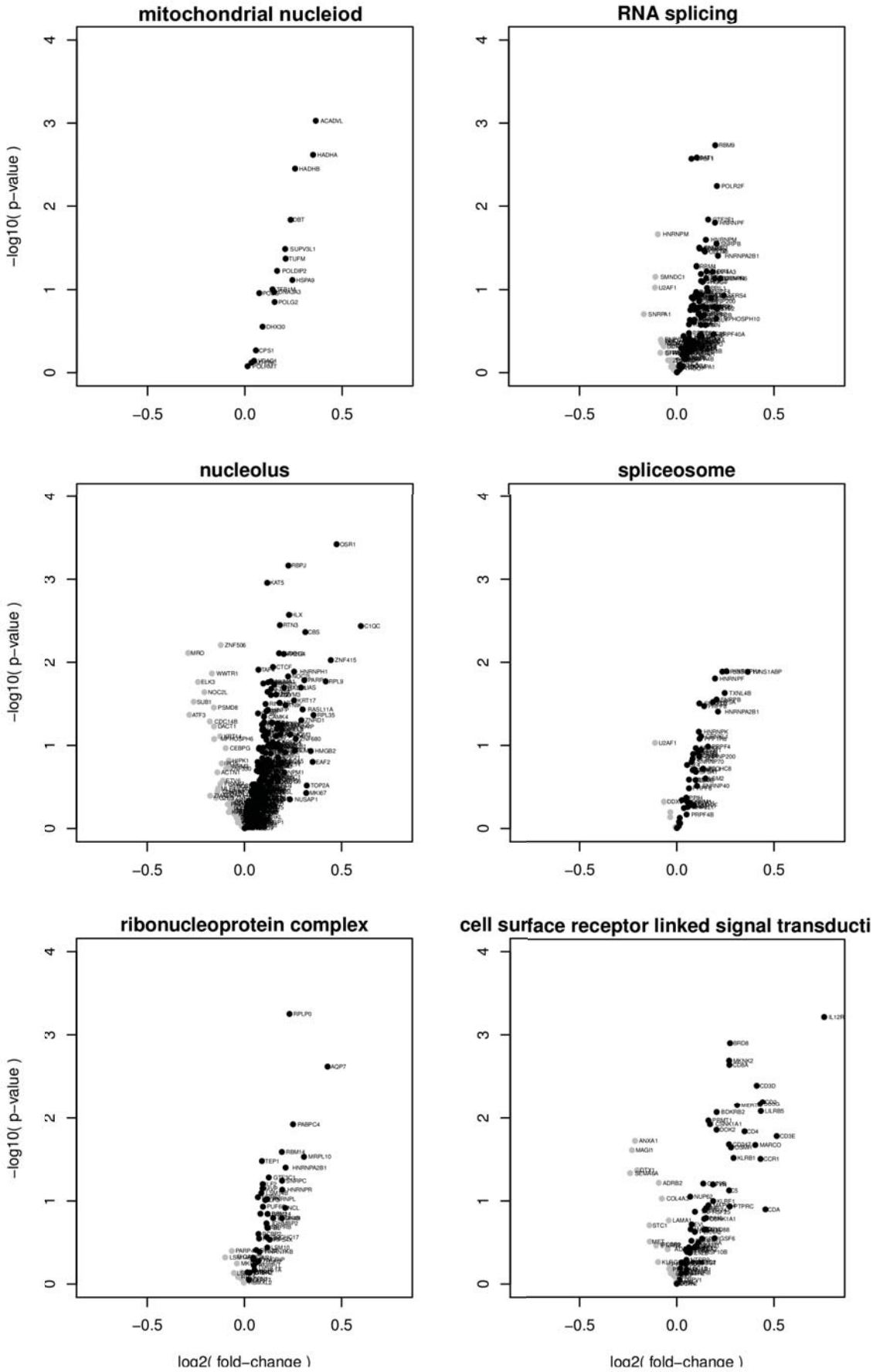
1. Benjamini Y, Hochberg Y (1995) Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing. Journal of the Royal Statistical Society Series B (Methodological) 57: 289–300. doi:10.2307/2346101.

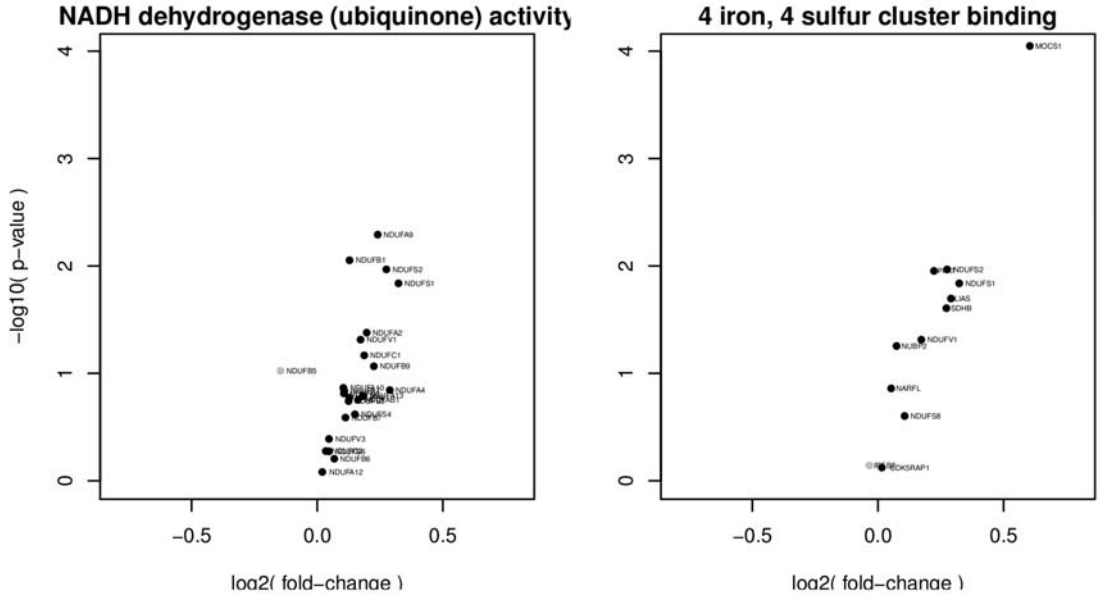
Figure 2

Volcano plots of the top 20 enriched gene sets in mediastinal as compared to subcutaneous adipose tissue




regulation of transcription
methyltransferase activity
mitochondrial respiratory chain complex I
translation
ribosome
fatty acid beta−oxidation
−log10(p−value)
log2(fold−change)
−0.5
0.0
0.5
0
1
2
3
4
PRDM1
LMO3
ANP32A
KLF6
PARP15
ZNF415
NAT14
KLF15
ATAD2
BNC1
ALDH1L1
NMT
DNMT3A
EHMT2
SMYD3
NDUFA9
NDUFB1
NDUFS2
NDUFA2
NDUFV1
NDUFB5
NDUFA4
NDUFB2
NDUFB3
NDUFA12
RPS29
MRPS6
RPS24
RPL31
RPS25
MRPL32
MRPL10
MRPL33
EIF4B
RPS15A
MRPS17
MRPS25
RPL24
RPL35
RPS15A
CANX
CPT1B
HADHA
HADHB
ACAD5
ACADM
CPT1A
ECH1
ACOX2
PPARD


mitochondrial nucleiod
RNA splicing
nucleolus
spliceosome
ribonucleoprotein complex
cell surface receptor linked signal transducti
−log10(p−value)
log2(fold−change)
ACADVL
HADHA
HADHB
C8BT
SUPV3L1
TUFM
POLDIP2
HSPA9
POLG2
DHX30
CPS1
RBM9
POLR2F
HNRNPM
HNRNPA2B1
SMNDC1
U2AF1
SNRPA1
PRPF40A
OSR1
RBPJ
KAT5
C1QC
ZNF506
MRO
ZNF415
CTCF
WWTR1
ELK3
NOC2L
SUB1
PSMD6
ATF3
CEBPG
HMGB2
EAF2
TOP2A
MKI67
NUSAP1
TXNL4B
PRPF4B
RPLP0
AQP7
PABPC4
RBM14
MRPL10
TEP1
HNRNPA2B1
IL12R
BRD8
CD3D
ULBP1
CD4
CD3E
MARCO
KLRB1
CCR1
ANXA1
MAGI1
ADRB2
PTPRC
CD4
STC1


NADH dehydrogenase (ubiquinone) activity
4 iron, 4 sulfur cluster binding
−log10(p−value)
log2(fold−change)
NDUFA9
NDUFB1
NDUFS2
NDUFS1
NDUFA2
NDUFV1
NDUFC1
NDUFB9
NDUFB5
NDUFA4
NDUFV3
NDUFB6
NDUFA12
MOCS1
NDUFS2
NDUFS1
LIAS
SDHB
NDUFV1
NUBPL
NARFL
NDUFS8
CDKSRAP1