Figure S1

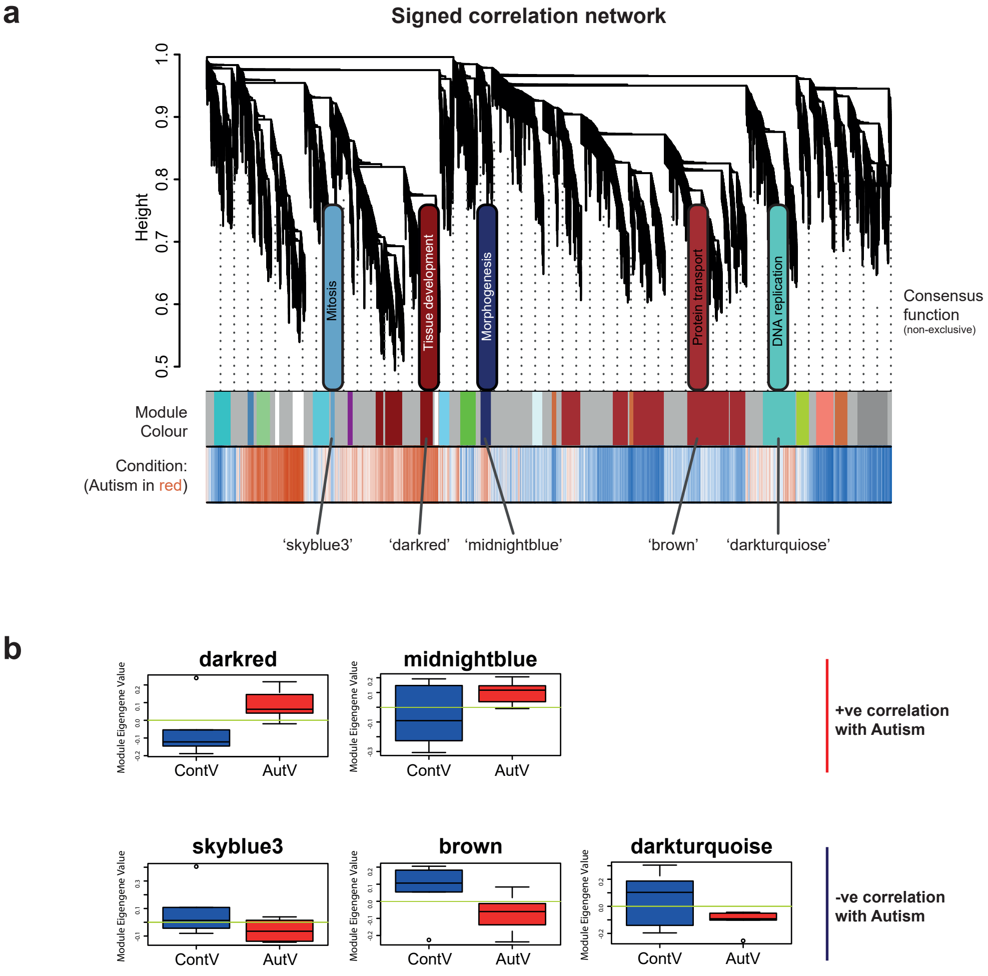

a
Signed correlation network
Height
1.0
0.9
0.8
0.7
0.6
0.5
Mitosis
Tissue development
Morphogenesis
Protein transport
DNA replication
Consensus function
(non-exclusive)
Module Colour
Condition:
(Autism in red)
'skyblue3'
'darkred'
'midnightblue'
'brown'
'darkturquiose'
b
darkred
midnightblue
skyblue3
brown
darkturquoise
Module Eigengene Value
ContV
AutV
+ve correlation with Autism
-ve correlation with Autism

Figure S2

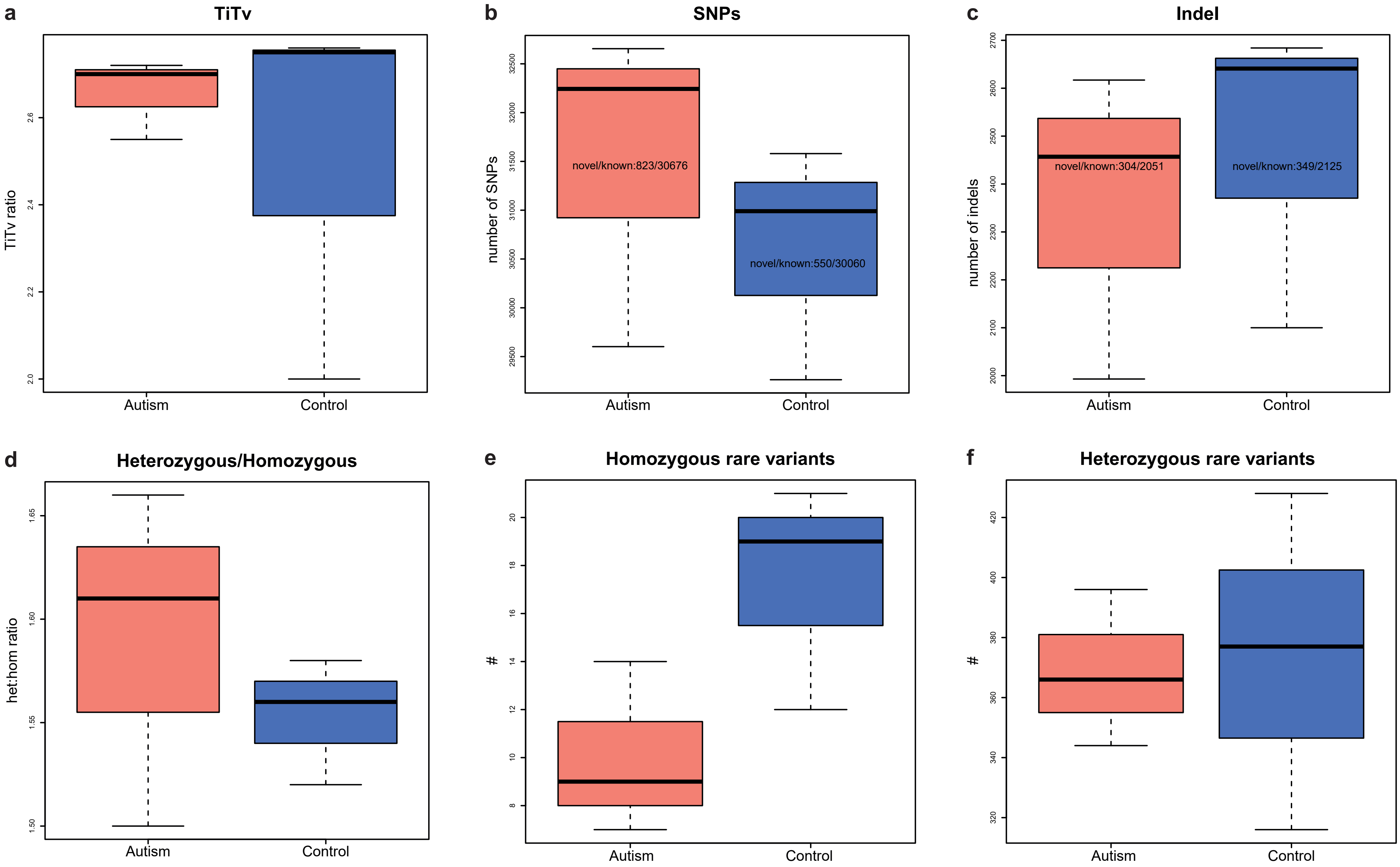

a
TiTv
TiTv ratio
2.0
2.2
2.4
2.6
Autism
Control
b
SNPs
number of SNPs
29500
30000
30500
31000
31500
32000
32500
novel/known:823/30676
novel/known:550/30060
Autism
Control
c
Indel
number of indels
2000
2100
2200
2300
2400
2500
2600
2700
novel/known:304/2051
novel/known:349/2125
Autism
Control
d
Heterozygous/Homozygous
het:hom ratio
1.50
1.55
1.60
1.65
Autism
Control
e
Homozygous rare variants
#
8
10
12
14
16
18
20
Autism
Control
f
Heterozygous rare variants
#
320
340
360
380
400
420
Autism
Control

Figure S3

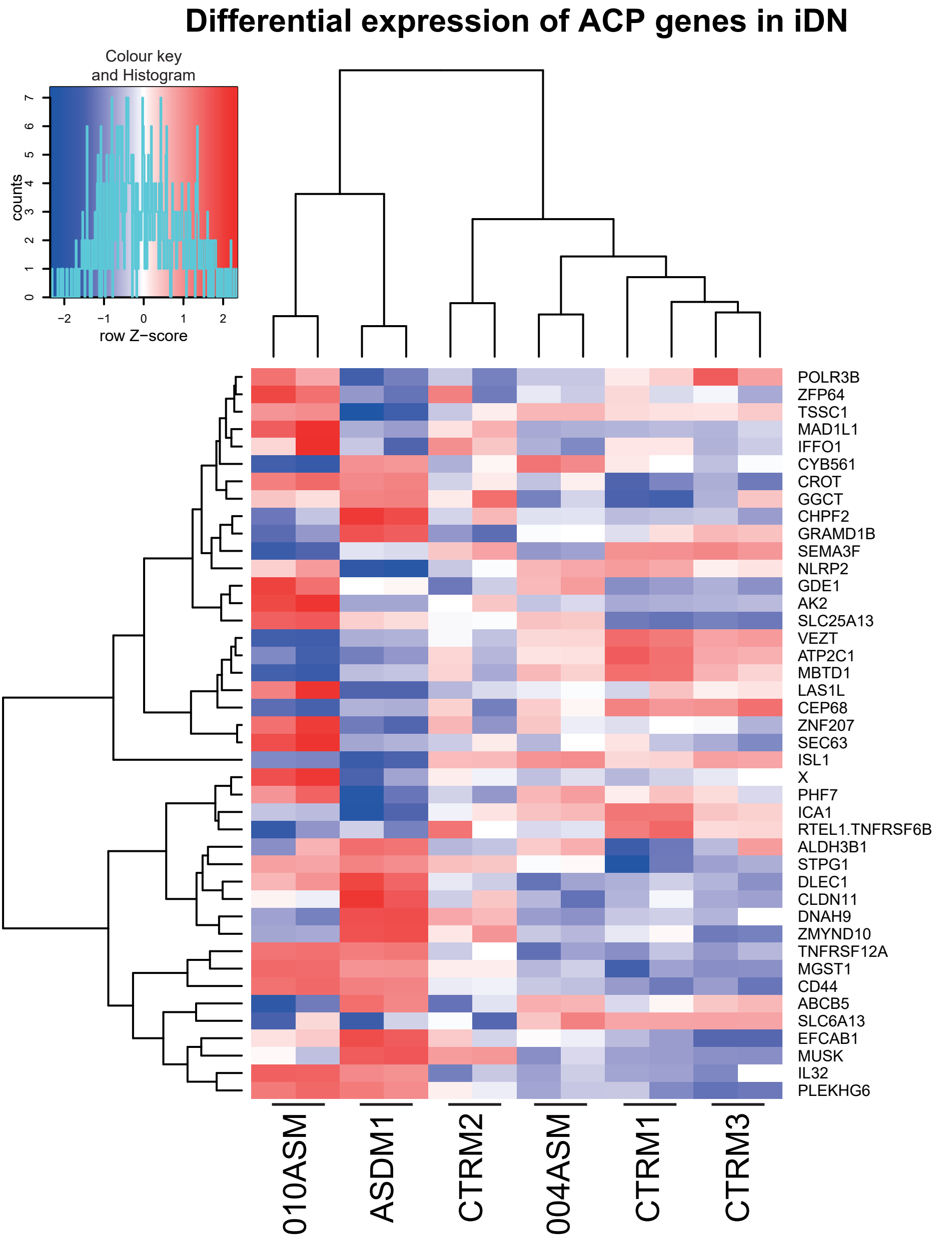

Differential expression of ACP genes in iDN
Colour key
and Histogram
counts
0
1
2
3
4
5
6
7
−2
−1
0
1
2
row Z−score
POLR3B
ZFP64
TSSC1
MAD1L1
IFFO1
CYB561
CROT
GGCT
CHPF2
GRAMD1B
SEMA3F
NLRP2
GDE1
AK2
SLC25A13
VEZT
ATP2C1
MBTD1
LAS1L
CEP68
ZNF207
SEC63
ISL1
X
PHF7
ICA1
RTEL1.TNFRSF6B
ALDH3B1
STPG1
DLEC1
CLDN11
DNAH9
ZMYND10
TNFRSF12A
MGST1
CD44
ABCB5
SLC6A13
EFCAB1
MUSK
IL32
PLEKHG6
010ASM
ASDM1
CTRM2
004ASM
CTRM1
CTRM3

Figure S4

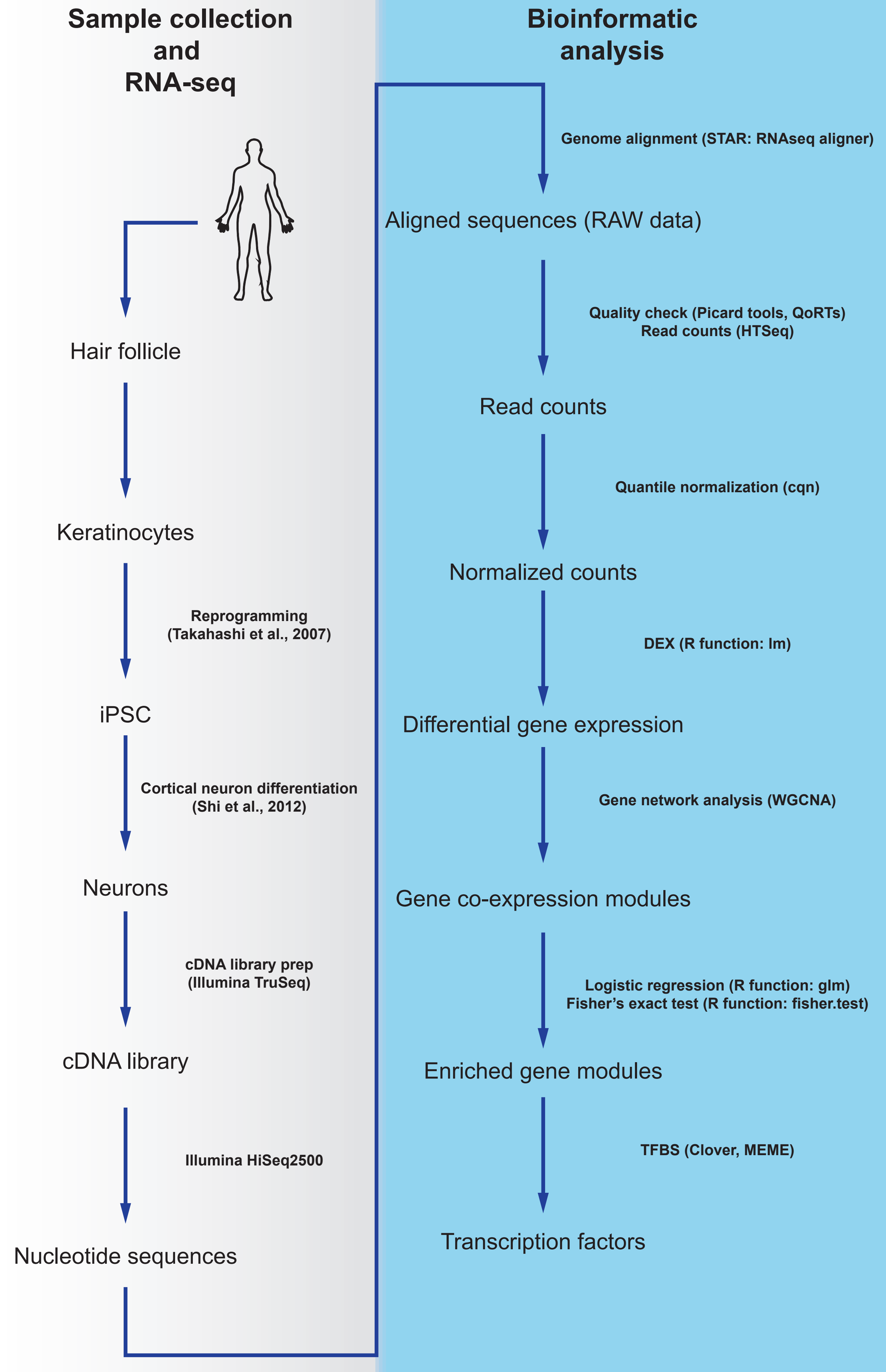

Sample collection and RNA-seq
Hair follicle
Keratinocytes
Reprogramming (Takahashi et al., 2007)
iPSC
Cortical neuron differentiation (Shi et al., 2012)
Neurons
cDNA library prep (Illumina TruSeq)
cDNA library
Illumina HiSeq2500
Nucleotide sequences
Bioinformatic analysis
Genome alignment (STAR: RNAseq aligner)
Aligned sequences (RAW data)
Quality check (Picard tools, QoRTs)
Read counts (HTSeq)
Read counts
Quantile normalization (cqn)
Normalized counts
DEX (R function: lm)
Differential gene expression
Gene network analysis (WGCNA)
Gene co-expression modules
Logistic regression (R function: glm)
Fisher's exact test (R function: fisher.test)
Enriched gene modules
TFBS (Clover, MEME)
Transcription factors

Figure S5

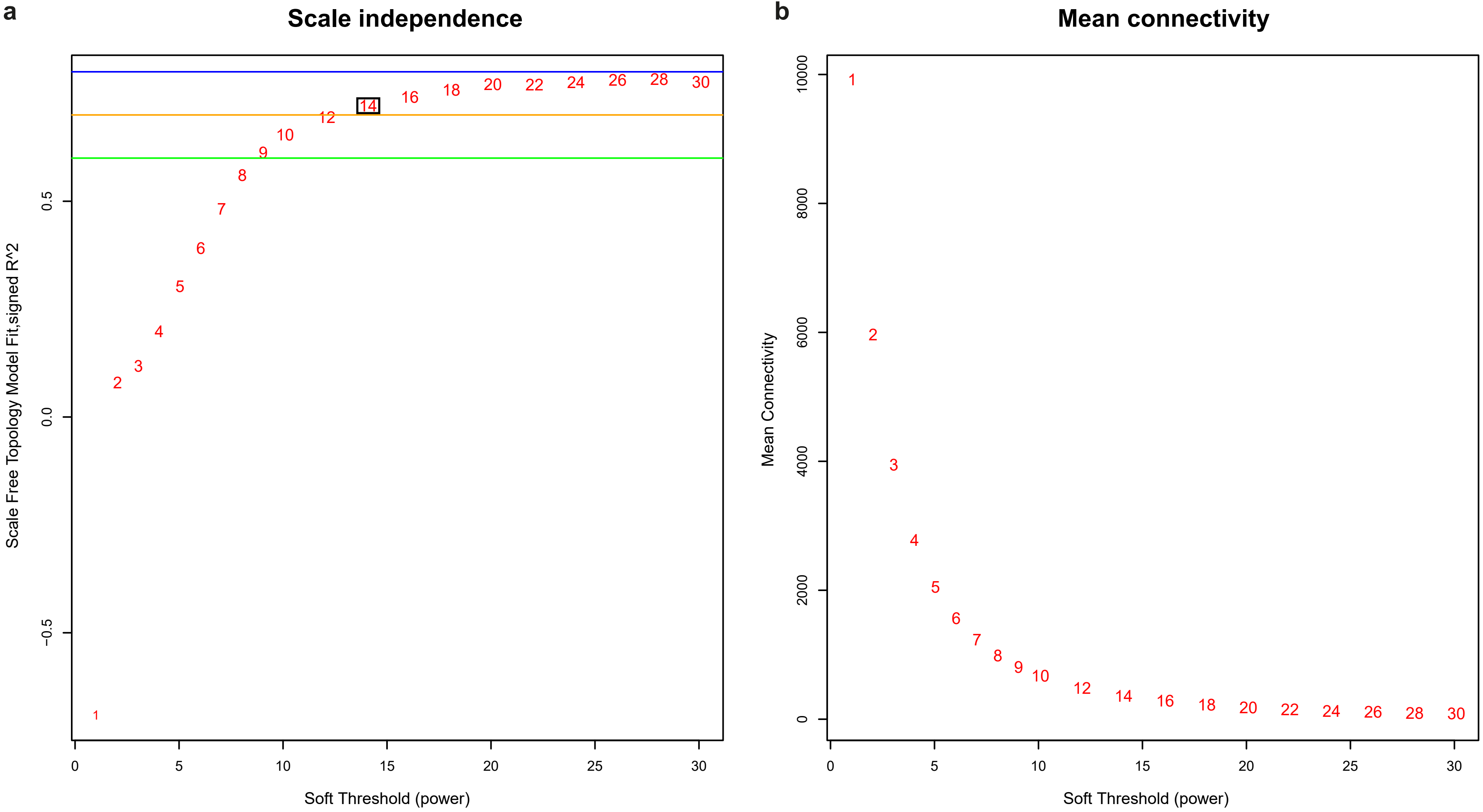

a
Scale independence
Scale Free Topology Model Fit,signed R^2
0.5
0.0
−0.5
1
2
3
4
5
6
7
8
9
10
12
14
16
18
20
22
24
26
28
30
0
5
10
15
20
25
30
Soft Threshold (power)
b
Mean connectivity
Mean Connectivity
10000
8000
6000
4000
2000
0
1
2
3
4
5
6
7
8
9
10
12
14
16
18
20
22
24
26
28
30
0
5
10
15
20
25
30
Soft Threshold (power)

Figure S6

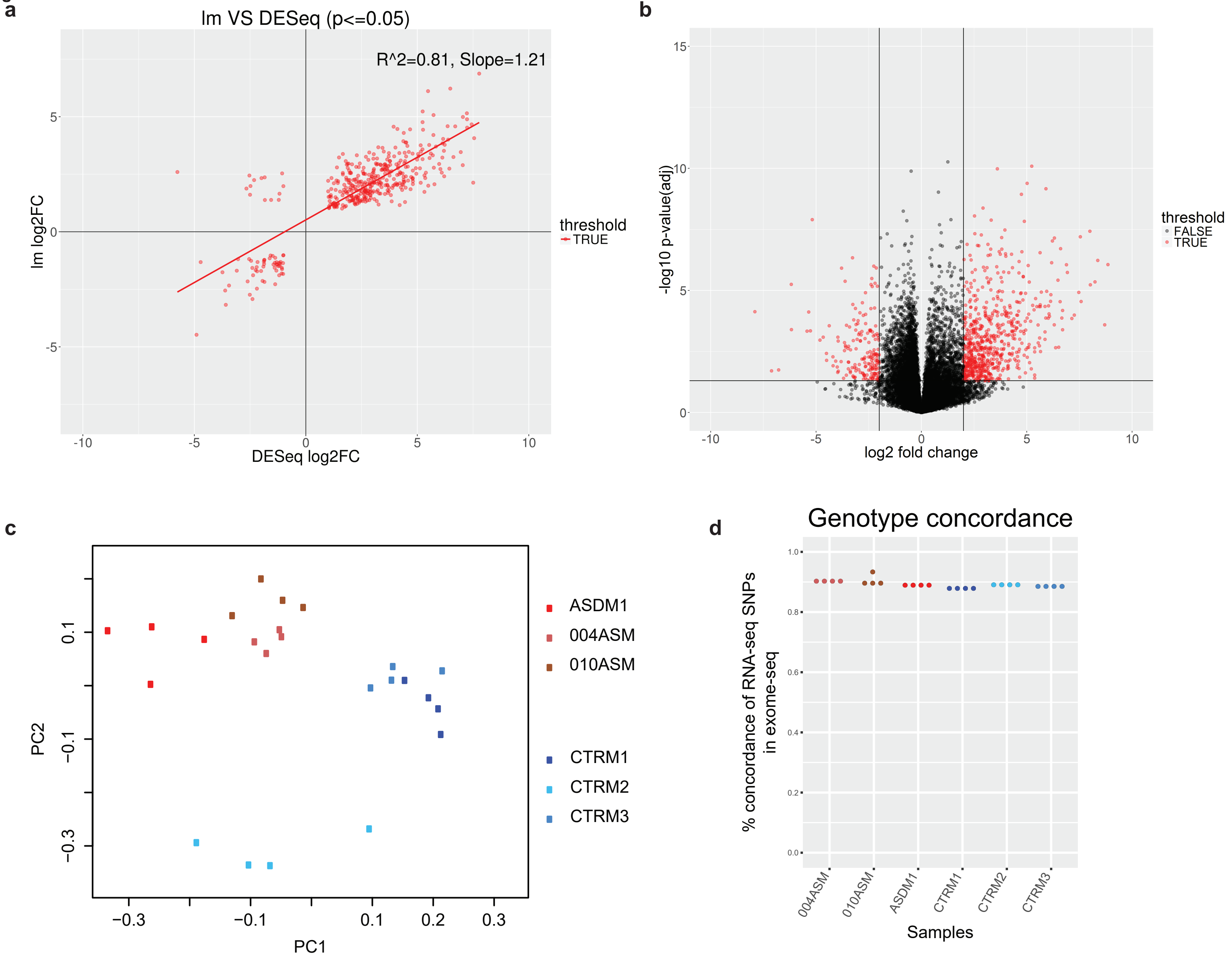

a
lm VS DESeq (p<=0.05)
R^2=0.81, Slope=1.21
lm log2FC
DESeq log2FC
5
0
-5
-10
-5
0
5
10
threshold
TRUE
b
-log10 p-value(adj)
15
10
5
0
-10
-5
0
5
10
log2 fold change
threshold
FALSE
TRUE
c
PC2
PC1
0.1
−0.1
−0.3
−0.3
−0.1
0.1
0.2
0.3
ASDM1
004ASM
010ASM
CTRM1
CTRM2
CTRM3
d
Genotype concordance
% concordance of RNA-seq SNPs in exome-seq
1.0
0.8
0.6
0.4
0.2
0.0
004ASM
010ASM
ASDM1
CTRM1
CTRM2
CTRM3
Samples

Figure S7

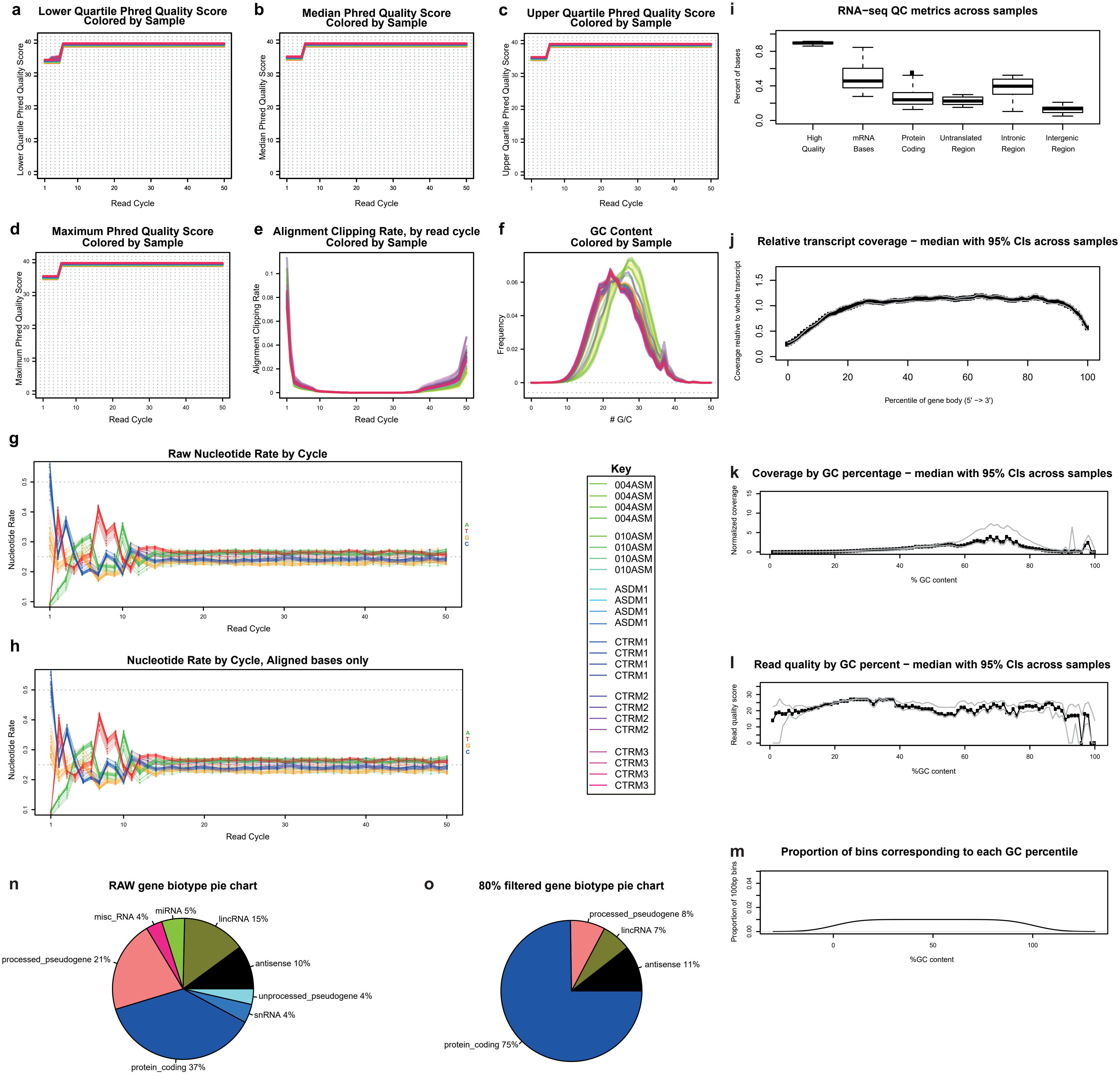
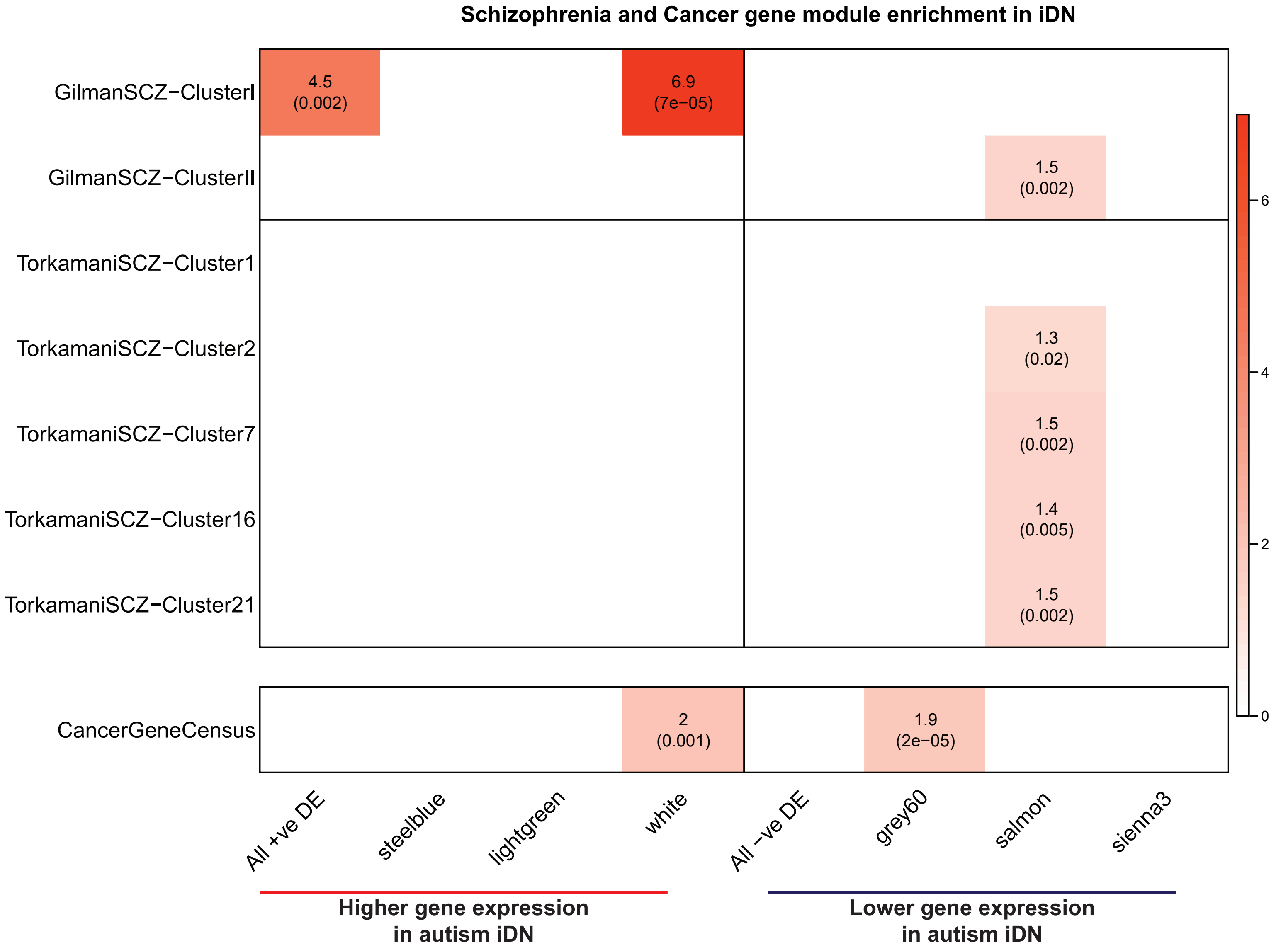

a
Lower Quartile Phred Quality Score
Colored by Sample
Lower Quartile Phred Quality Score
Read Cycle
b
Median Phred Quality Score
Colored by Sample
Median Phred Quality Score
Read Cycle
c
Upper Quartile Phred Quality Score
Colored by Sample
Upper Quartile Phred Quality Score
Read Cycle
i
RNA−seq QC metrics across samples
Percent of bases
High Quality
mRNA Bases
Protein Coding
Untranslated Region
Intronic Region
Intergenic Region
d
Maximum Phred Quality Score
Colored by Sample
Maximum Phred Quality Score
Read Cycle
e
Alignment Clipping Rate, by read cycle
Colored by Sample
Alignment Clipping Rate
Read Cycle
f
GC Content
Colored by Sample
Frequency
G/C
j
Relative transcript coverage − median with 95% CIs across samples
Coverage relative to whole transcript
Percentile of gene body (5' −> 3')
g
Raw Nucleotide Rate by Cycle
Nucleotide Rate
Read Cycle
A
T
G
C
h
Nucleotide Rate by Cycle, Aligned bases only
Nucleotide Rate
Read Cycle
A
T
G
C
Key
004ASM
004ASM
004ASM
004ASM
010ASM
010ASM
010ASM
010ASM
ASDM1
ASDM1
ASDM1
ASDM1
CTRM1
CTRM1
CTRM1
CTRM1
CTRM2
CTRM2
CTRM2
CTRM2
CTRM3
CTRM3
CTRM3
CTRM3
k
Coverage by GC percentage − median with 95% CIs across samples
Normalized coverage
% GC content
l
Read quality by GC percent − median with 95% CIs across samples
Read quality score
%GC content
m
Proportion of bins corresponding to each GC percentile
Proportion of 100bp bins
%GC content
n
RAW gene biotype pie chart
misc_RNA 4%
miRNA 5%
lincRNA 15%
processed_pseudogene 21%
antisense 10%
unprocessed_pseudogene 4%
snRNA 4%
protein_coding 37%
o
80% filtered gene biotype pie chart
processed_pseudogene 8%
lincRNA 7%
antisense 11%
protein_coding 75%

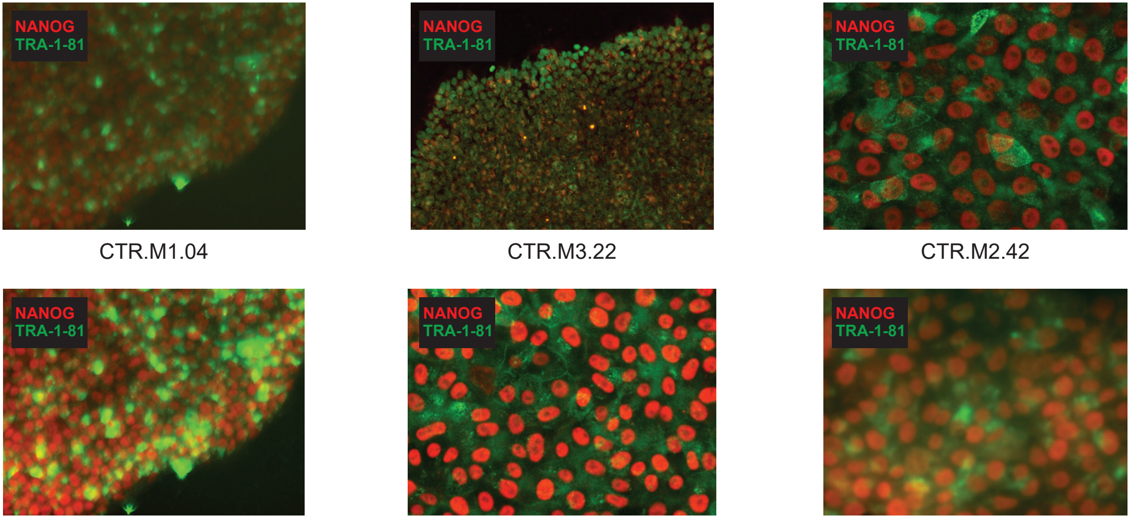
Figure S8



Schizophrenia and Cancer gene module enrichment in iDN

Figure S9

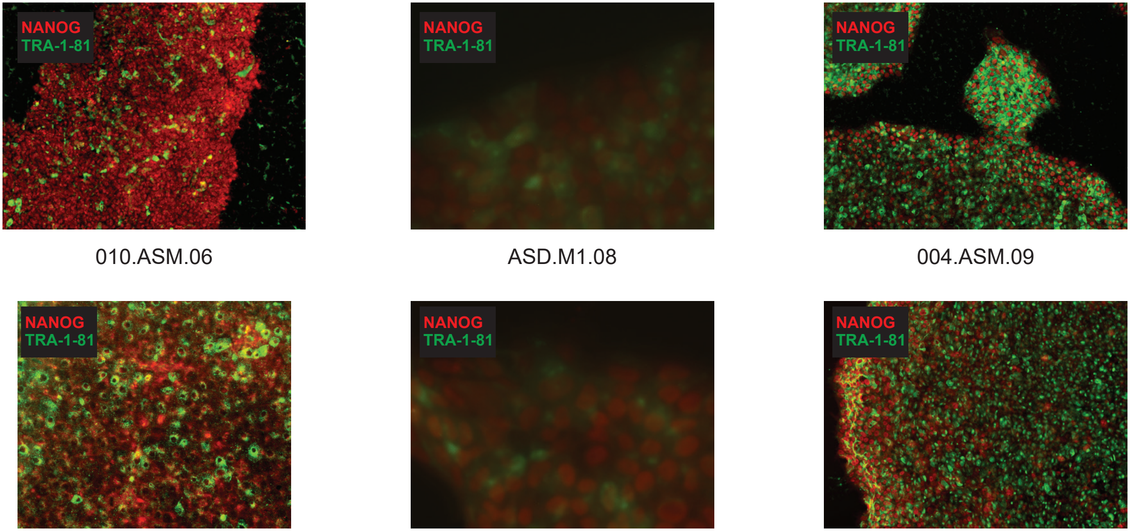
a. Control iPSC lines



CTR.M1.04 CTR.M3.22 CTR.M2.42

CTR.M1.11 CTR.M3.15 CTR.M2.05

b. Autism iPSC lines



010.ASM.06 ASD.M1.08 004.ASM.09

010.ASM.05 ASD.M1.01 004.ASM.01