The following are the setting used process raw data into the plots shown in the manuscript.

**Figure 2: Genomic instability test**

The file: stabilty\_example.csv

Model: Instability

Targets for normalization ( chromosome (first ‘delta’) ): CHR4

Target order: CHR1,CHR4,CHR8,CHR10,CHR12,CHR17,CHR18,CHR20,CHRX

Sample order: GM25953,GM25975,GM25974,GM25952,Normal

Control sample Second ‘delta’: Normal

**Figure 3: Absolute quantification**

The file: 5 files in the folder ‘Absolute

-- All files can be uploaded at once

-- The reference gene must be included

Model: Absolute

Targets for normalization (endogenous control genes): ACTB,GAPDH

Target order: left blank

*Control cell lines and stages order ------ [used in paper]*

Sample order: NCRM1-IPSC,522-266-2-IPSC,AiW001-2-IPSC,AiW002-2-IPSC,AJC001-5-IPSC,AJG001C4-IPSC,NCRM1-NPC,522-266-2-NPC,AiW001-2-NPC,AiW002-2-NPC,AJC001-5-NPC, AJG001C4-NPC,NCRM1-DA4W,522-266-2-DA4W,AiW001-2-DA4W,AiW002-2-DA4W,AJG001C4-DA4W,AJC001-5-DA4W,NCRM1-DA6W,522-266-2-DA6W,AiW001-2-DA6W,AiW002-2-DA6W,AJG001C4-DA6W,AJC001-5-DA6W

*Control order of stages ----- [another option]*

Sample order : IPSC,NPC,DA4W,DA6W

*Control cell lines order ----- [also works]*

Sample order: NCRM1,522-266-2,AiW001-2,AiW002-2,AJC001-5,AJG001C4

**Statics**

number of groups: 4

One-way Anova

How are groups defined?: Group names are within the sample name.

Groups are defined within the sample name column.

order :IPSC,NPC,DA4W,DA6W

Selection for time series or repeated measures/ linked samples : yes

Selection for parametric or normal distribution: yes

**Figure 4: Relative quantification be two method**

**Relative quantification delta CT model:**

The file: RELATIVE\_example.csv

Model: Relative (delta CT)

Targets for normalization (endogenous control genes): ACTB,GAPDH

Targets order (genes): PAX6,CAMK2A,GRIN1

Sampel order (cell lines, time points): AiW002-2-D0, AiW002-2-D7,KYOU-D0,KYOU-D7

**Relative quantification delta delta CT model**

Control sample (calibrator/reference sample): AiW002-2-D0

Statistic relative:

select: Group names are within the sample name – group names are: D0,D7

select for repeated measures: No --- measures are independent

select for normal distribution: Yes --- Parametric tests

**Figure 5:**

Files : B2M.csv, NRXN3.csv

Genes if file name only: NRXN3,B2M

Name of quencher:TMR

Name of the sample group in the task or content column: sample

Model: Absolute

Targets for normalization (endogenous control genes): B2M

Cut-off : 0.2

Max outilers: 0.5

Sampel order (cell lines, time points) – in this case brain regions and mice original names

Ordered by brain region then saline/cocaine

B4bisNST,B6NST,R6 NST,V3 NST, V4 NST,R5bis NST,R6bisNST,R8bisNST,V2NST,V8NST,B4bisGP,R6 GP,V3 GP,V4 GP,R5bis GP,R6bisGP,R8bisGP,V2GP,V8GP,B4bisSN,R6 SN,V3 SN,V4 SN,R5bis SN,R6bisSN,R8bisSN,V2SN,V8SN

Enter the names of the columns you would like to include for statistical analysis:

Treatement,Region,T\_R

Statistics:

Group names are in the Sample column

Enter column name:

Comparision: