

EXPERIMENTAL WORKFLOW

Previous Data New Data

Microarray Screens

350 genes involved in p53 signaling,
cell cycle regulation, apoptosis,
and DNA damage and repair

**Mouse
NSC
in vitro
model**

Significant changes in 74
genes. 14 selected for
validation by qRT-PCR
(Hicks 2010, 2011).

**Mouse
NSCs**
74
sig chgd

40
shared

**Rat
PBLs**
190
sig chgd

Significant changes in 190
genes. 19 selected for
validation by QuantiGene
Plex in the present study.

**Rat PBL
in vivo
binge
model**

Mouse NSCs

14 validated: Bub1, Card6,
Casp7, Ccna2, Ccnb, Ccnd,
Ccnf, Cdc20, Cdca5, E2f7,
Foxm1, Mcm5, Plk1, Pttg1

QuantiGene Plex

Subset of 19/40 genes
+ 15 others chosen

**Human
LBs
in vitro
model**

Human LBs

7/34 chgd: Pttg1, Tp73,
Hus1, Gadd45a, Atm,
Mutyh, Cd40

Rat PBLs

9/34 chgd: Apaf1, Apex1,
Atm, Ccnb2, Cdc2, Gadd45a,
Myc, Pttg1, Racgap1

Human PBLs

6/34 chgd: Hus1, Tp53,
Mutyh, Myc, Ercc1, Mcm5

**Human
alcoholic
subject
PBLs**

Major Findings

- 1) Multiple genes related to p53 signaling, cell cycle regulation, apoptosis and DNA damage are affected by ethanol
- 2) The specific genes affected can vary in different cell types, but changes in mouse NSCs and rat PBLs are highly correlated
- 3) Levels of Ercc1 and Mcm5 in PBLs of human subjects predict changes in brain volume and neuropsychological deficits

Human Subjects

Medical, Demographic
and Neuroimaging
Correlation analyses