Time series data: (GSE770)

Summary: The experiment was a time course experiment on LNCaP C4-2 human prostate adenocarcinoma cells following irradiation to a dose of 10 Sv from a Cesium-137 gamma source. Total RNA was extracted from cells at 1, 2, 4, 6, 8, 12, 16, 20 and 24 hours after irradiation. The untreated control sample, labeled 0, was collected concurrently with the cells extracted at 24 hr. After extraction, the samples were processed and hybridized to the Affymetrix (Santa Clara, CA, www.affymetrix.com) HG-U95Av2 chip, and then washed, stained and scanned according to Affymetrix's protocols contained in the GeneChip(R) Expression Analysis Manual. Transcript abundance data from the scans was processed initially with Affymetrix' Microarray Suite 5(R), then by Silicon Genetics' (Redwood City, CA, www.silicongenetics.com) GeneSpring(R).

( I used all the ten samples from the series)

Static data: (GSE41969)

Paper: Genes Associated with Prostate Cancer Are Differentially Expressed in African American and European American Men

Totally 639 tumor samples.



Figure 1. Functional Interaction Network from analysis of genes upregulated in prostate tumors from AAM or EAM. The network derived from Ingenuity Pathways analysis shows a high degree of inherent, functional interrelatedness for a subset of factors from the analyzed gene expression datasets (AAMblue, EAM yellow). Results suggest that AAM and EAM prostate tumors are distinguished at gene level with NFKB and inflammatory cytokine factors primarily upregulated in PCa from AAM; EAM-upregulated genes are centered on TNF. Edges (lines) linking members of both sets to P38MAPK, TNF, and PI3K/AKT genes suggests that the associated pathways are operating to some extent in both EAM and AAM contexts.