Building cellLinesFromPredictors.Rda

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1 Executive Summary

1.1 Introduction

In this report, we produce a matrix of lists containing lists of cell lines comprising the samples in the "Chemo Predictors" quantification table we received for Potti et al. [1]

1.2 Methods

We invoke the analysis script "matchChemoPredictorColumns.Rnw" which describes the matching steps involved in detail.

1.3 Results

We created a "cellLinesFromPredictors" matrix of lists of cell lines. We stored these in RDataObjects as "cellLinesFromPredictors.Rda."

2   Options and Libraries

```
> options(width = 80)
```

3   Invoking matchChemoPredictorColumns.Rnw

All we do here is invoke the earlier analysis script. This file is here to make automation easier using our naming conventions.

```
> Stangle(file.path("RNowebSource", "matchChemoPredictorColumns.Rnw"))

Writing to file matchChemoPredictorColumns.R

> source("matchChemoPredictorColumns.R")

loading  RDataObjects/novartisAll.Rda  from cache
loading  RDataObjects/changAll.Rda  from cache
```

4   Appendix

4.1   File Location

```
> getwd()

[1] "/Users/kabagg/ReproRsch/WebSite"
```

4.2   Saves

4.3   SessionInfo

```
> sessionInfo()

R version 2.8.1 (2008-12-22)
i386-apple-darwin8.11.1

locale:
en_US.UTF-8/en_US.UTF-8/C/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base
```

References

[1] Potti A, Dressman HK, Bild A, et al: Genomic signatures to guide the use of chemotherapeutics. *Nat Med*, **12**:1294-1300, 2006.