

Additional information

Identifying Molecular Phenotypes in Lung Cancer by Integrating Radiomics and Genomics

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Contents

1	File S4: Additional information	3
1.1	Modules showing the relationships of radiomics and biology	4
1.2	Clinical value of modules	4
1.3	Statistical libraries used for the analysis	4

1 File S4: Additional information

1.1 Modules showing the relationships of radiomics and biology

Our analysis revealed 13 modules of coherently expressed radiomic features and molecular pathways. Supplementary file SII contains heatmaps of hierarchical Ward linkage clusterings on the corresponding normalized enrichment scores (NESs) for each of the modules including the complete sets of radiomic feature names and pathway names. All NESs have been transformed to Z-scores before clustering. Here we provide additional information about the module analysis.

1.2 Clinical value of modules

Modules have been associated with clinical information (prognosis, histology, and stage) by combining p-values of random permutation tests on Lung1 and Lung2 in a meta-analysis Z-transformation [1]. The underlying p-values are given in the following tables.

1.3 Statistical libraries used for the analysis

All statistical analyses were carried out using the R software (R Core Team, Vienna, Austria) version 3.1.0 on a Linux environment [2]. The following R and Bioconductor [3] package versions were used:

	1	2	3	4	5	6	7	8	9	10	11	12	13
Z	0.40	0.01	0.43	0.07	0.11	0.23	0.18	0.45	0.01	0.66	0.11	0.00	0.34
Lung1	0.54	0.02	0.43	0.14	0.12	0.30	0.25	0.56	0.02	0.79	0.19	0.01	0.44
Lung2	0.14	0.09	0.50	0.07	0.34	0.24	0.17	0.20	0.13	0.13	0.12	0.04	0.18

Table 1: P-values of random permutation tests of mean CIs of survival times in each module.

	1	2	3	4	5	6	7	8	9	10	11	12	13
Z	0.24	0.12	0.58	0.07	0.01	0.02	0.16	0.64	0.81	0.01	0.02	0.05	0.13
Lung1	0.23	0.21	0.44	0.20	0.01	0.05	0.29	0.70	0.91	0.04	0.03	0.09	0.25
Lung2	0.47	0.09	0.86	0.01	0.13	0.04	0.08	0.33	0.11	0.01	0.19	0.11	0.07

Table 2: P-values of random permutation tests of mean Kruskal-Wallis chi square statistics in each module with respect to histology.

	1	2	3	4	5	6	7	8	9	10	11	12	13
Z	0.62	0.00	0.25	0.01	0.00	0.00	0.00	0.01	0.19	0.01	0.00	0.00	0.00
Lung1	0.73	0.00	0.23	0.01	0.00	0.00	0.00	0.01	0.34	0.04	0.00	0.00	0.00
Lung2	0.21	0.04	0.50	0.22	0.05	0.02	0.10	0.17	0.07	0.02	0.29	0.09	0.02

Table 3: P-values of random permutation tests of mean Kruskal-Wallis chi square statistics in each module with respect to stage.

- R version 3.1.0 (2014-04-10), x86_64-unknown-linux-gnu
- Base packages: base, datasets, graphics, grDevices, grid, methods, parallel, splines, stats, stats4, utils
- Other packages: affy 1.44.0, annotate 1.44.0, AnnotationDbi 1.28.1, Biobase 2.26.0, BiocGenerics 0.12.1, biomaRt 2.22.0, bitops 1.0-6, DBI 0.3.1, eisa 1.18.0, FactoMineR 1.28, genefu 1.15.1, GenomeInfoDb 1.2.3, GGally 0.5.0, ggplot2 1.0.0, GO.db 3.0.0, gplots 2.15.0, graph 1.44.1, GSEABase 1.28.0, gsubfn 0.6-6, GSVA 1.14.1, igraph 0.7.1, inSilicoDb 2.2.0, IRanges 2.0.1, isa2 0.3.3, jetset 1.6.0, lsa 0.73, mclust 4.4, MetaGx 0.0.2, mRMRe 2.0.5, org.Hs.eg.db 3.0.0, plyr 1.8.1, proclim 1.5.1, proto 0.3-10, RadioGx 1.7, RamiGO 1.12.0, RCurl 1.95-4.5, RCytoscape 1.16.0, reshape2 1.4.1, rjson 0.2.15, R.methodsS3 1.6.1, R.oo 1.18.0, RSQLite 1.0.0, R.utils 1.34.0, S4Vectors 0.4.0, SnowballC 0.5.1, survcomp 1.16.0, survival 2.37-7, VennDiagram 1.6.9, WriteXLS 3.5.1, XML 3.98-1.1, XMLRPC 0.3-0, xtable 1.7-4
- Loaded via a namespace (and not attached): affyio 1.34.0, amap 0.8-12, BiocInstaller 1.16.1, bootstrap 2014.4, car 2.0-22, Category 2.32.0, caTools 1.17.1, cluster 1.15.3, colorspace 1.2-4, digest 0.6.6, gdata 2.13.3, genefilter 1.48.1, gtable 0.1.2, gtools 3.4.1, KernSmooth 2.23-13, labeling 0.3, lattice 0.20-29, lava 1.3, leaps 2.9, MASS 7.3-35, Matrix 1.1-4, munsell 0.4.2, nnet 7.3-8, png 0.1-7, preprocessCore 1.28.0, RBGL 1.42.0, RColorBrewer 1.1-2, Rcpp 0.11.3, reshape 0.8.5, rmeta 2.16, scales 0.2.4, scatterplot3d 0.3-35, stringr 0.6.2, SuppDists 1.1-9.1, survivalROC 1.0.3, tcltk 3.1.0, tools 3.1.0, zlibbioc 1.12.0

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