Figure S6. Integrative data analysis of simultaneous measurement of metabolite and transcript concentrations in normal lung, lung tumors from untreated EGFR-TL mice, and lung tumors from vehicle, BIBW 2992, rapamycin or BIBW 2992 plus rapamycin-treated EGFR-TL mice.

Heat map shows significant enrichments of KEGG metabolic pathways (composed of genes, metabolites or the combination) across indicated comparisons. The fraction of over- or underexpressed genes, metabolites or both that belong to each tested KEGG metabolic set were assessed, calculating a P value according to the hypergeometric distribution using Genomica software (http://genomica.weizmann.ac.il/). Color scale depicts the logarithm of P value (red, overrepresentation; blue, underrepresentation). The genomic, metabolomic or combined data were log2 transformed and mean-centered. Genes or metabolites whose expression or concentration was 1.5-fold or greater than the mean level were scored. Enrichment of overrepresented or underrepresented genes, metabolites or both that belong to each tested KEGG metabolic pathway (http://www.genome.jp/kegg) was calculated using a hypergeometric test and a false discovery rate (FDR) calculation to account for multiple hypothesis testing.