

Supporting Information

S1 - Dimensionality Reduction

As shown in figure Regulation of KIT signalling pathway set, comparison of the pathway set, with and without dimensionality reduction (PCA and Isomap) for LGG and figure Pantothenate and CoA biosynthesis and Retinoate Biosynthesis II pathway set, comparison of the pathway set, with and without dimensionality reduction (PCA and Isomap) for CML, dimensionality reduction worsens the results for the pathways, since the size of the datasets is already small enough and further dimensionality leads to loss of information.

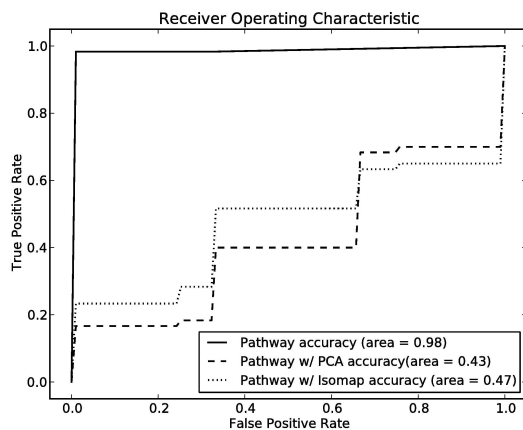


Figure 1: Regulation of KIT signalling pathway set, comparison of the pathway set, with and without dimensionality reduction (PCA and Isomap)

S2 - Partial Pathway Sets

Pathway accuracy depends on which genes are removed from the set. For LGG this is shown in figure 50% of the pathways is removed from the IL2 pathway set, figure 50% of the pathways is removed from the Pantothenate and CoA biosynthesis pathway set, figure 20% of the pathways is removed from the IL2 pathway set and figure 20% of the pathways is removed from the Pantothenate and CoA biosynthesis pathway set. The accuracy depends on which genes are removed. In figure 50% of the pathways is removed from the IL2 pathway set 50% of the genes are removed but the accuracy is not affected as much (compared to figure 50% of the pathways is removed from the IL2 pathway set). For CML it is shown in figure 50% of the pathways is removed from the Regulation of KIT signalling pathway and figure 60% of the pathways is removed from the Regulation of KIT signalling pathway,

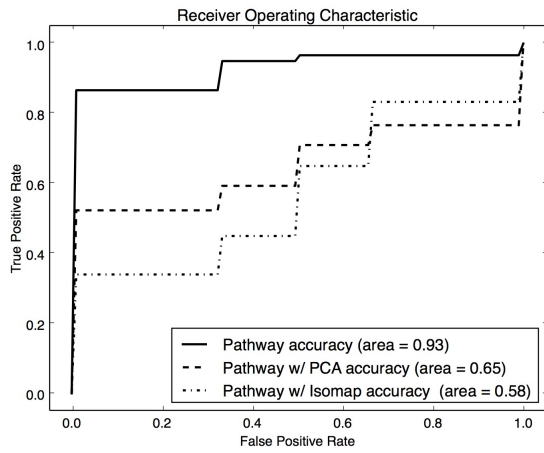


Figure 2: Pantothenate and CoA biosynthesis and Retinoate Biosynthesis II pathway set, comparison of the pathway set, with and without dimensionality reduction (PCA and Isomap)

figure 80% of the pathways is removed from the Regulation of KIT signalling pathway and figure 80% of the pathways is removed from the Regulation of KIT signalling pathway.

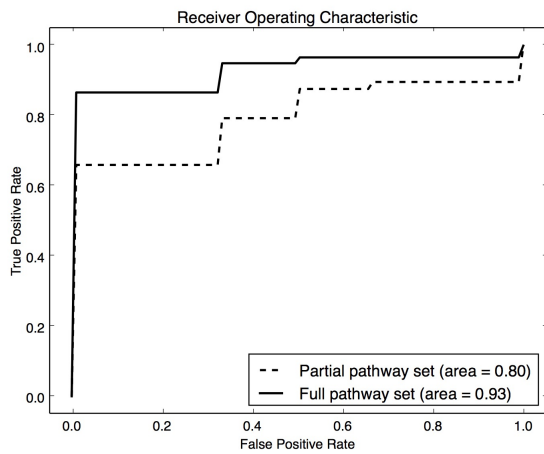


Figure 3: 50% of the pathways is removed from the IL2 pathway set

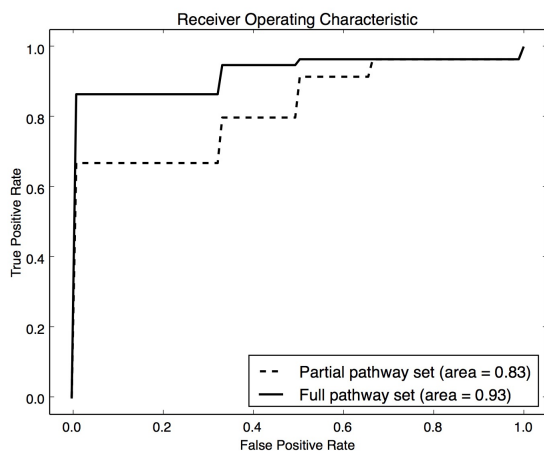


Figure 4: 50% of the pathways is removed from the Pantothenate and CoA biosynthesis pathway set

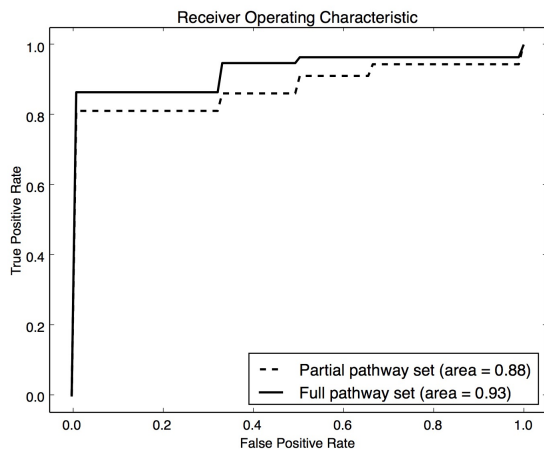


Figure 5: 20% of the pathways is removed from the IL2 pathway set

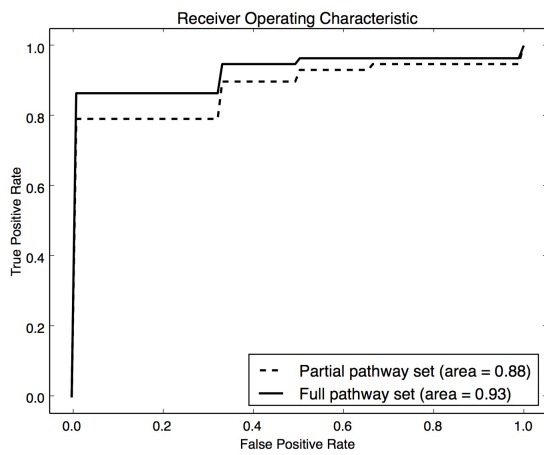


Figure 6: 20% of the pathways is removed from the Pantothenate and CoA biosynthesis pathway set

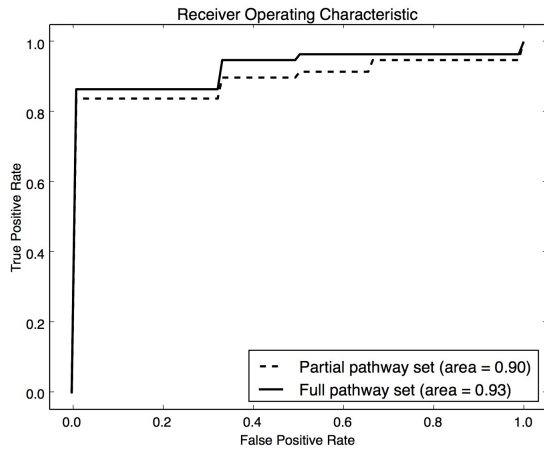


Figure 7: 50% of the pathways is removed from the IL2 pathway set

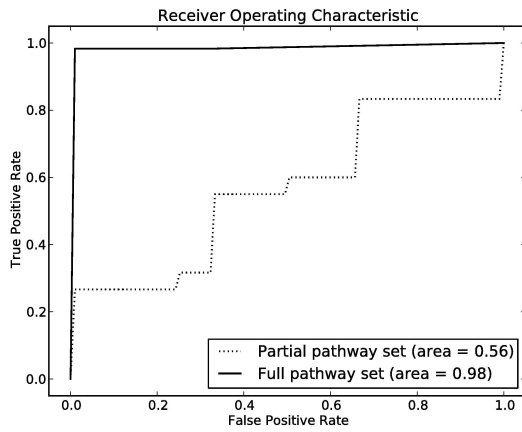


Figure 8: 50% of the pathways is removed from the Regulation of KIT signalling pathway

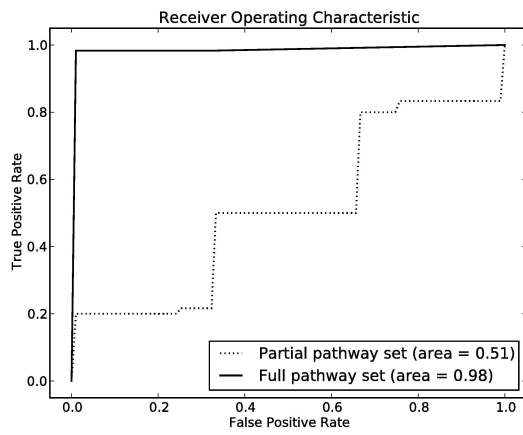


Figure 9: 60% of the pathways is removed from the Regulation of KIT signalling pathway

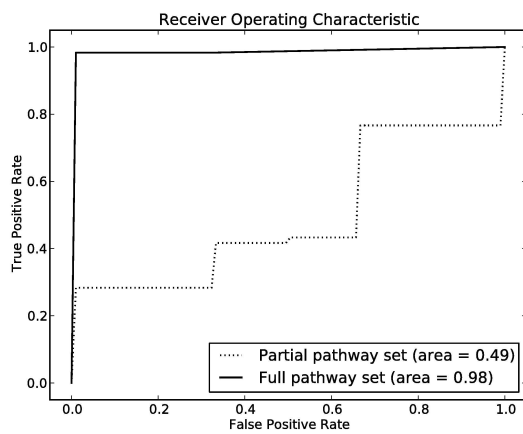


Figure 10: 80% of the pathways is removed from the Regulation of KIT signalling pathway

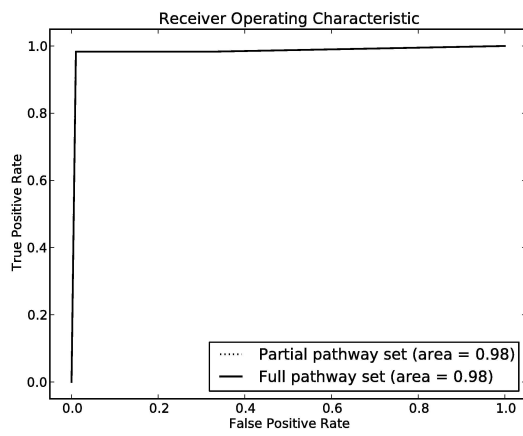


Figure 11: 80% of the pathways is removed from the Regulation of KIT signalling pathway

S3 - Random Sets for LGG

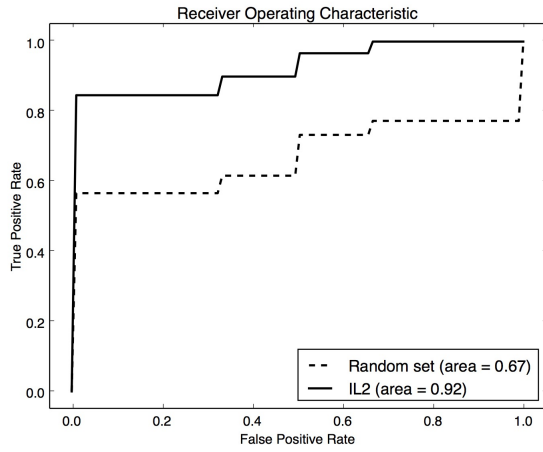


Figure 12: Comparison between IL2 and a random pathway set of 1170 genes

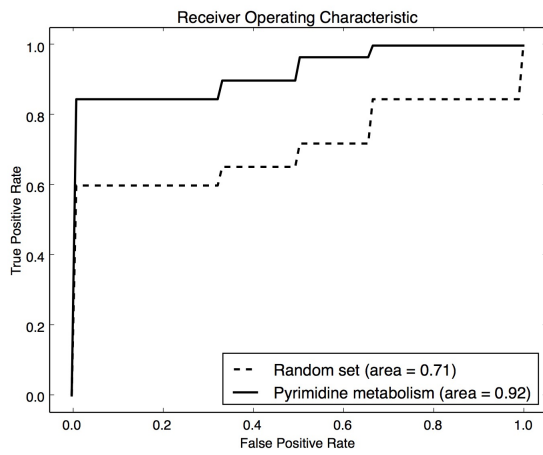


Figure 13: Comparison between Pyrimidine metabolism and a random pathway set of 644 genes

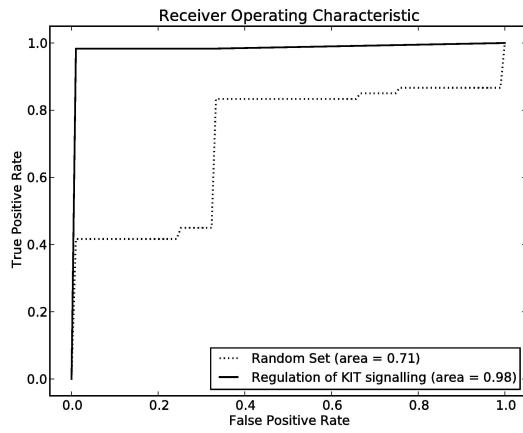


Figure 14: Comparison between Regulation of KIT signalling and a random pathway set of 1170 genes

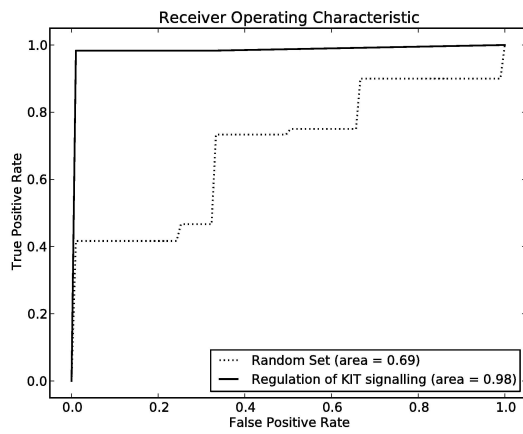


Figure 15: Comparison between Regulation of KIT signalling and a random pathway set of 644 genes

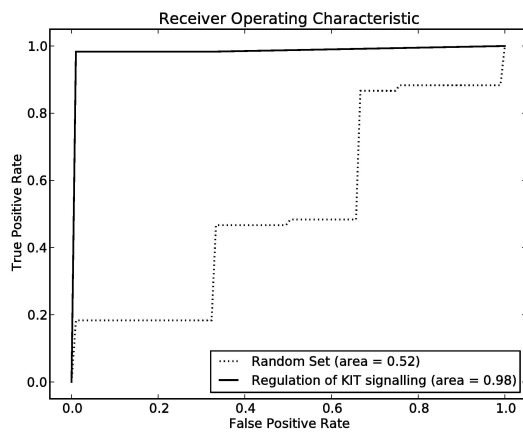


Figure 16: Comparison between Regulation of KIT signalling and a random pathway set of 728 genes