A   LC-MS/MS protein identification list (crude membrane fraction)

↓

1020 proteins identified with FDR < 1 % and present in any samples

↓

686 proteins identified having at least 2 peptides and present in at least 2 samples

↓

86 significantly changed proteins identified following non-parametric statistical test (36 down- and 50 up-regulated proteins)

↓

Principal Component Analysis (PCA), Hierarchical Clustering and Ingenuity Pathway Analysis (IPA)

B   LC-MS/MS protein identification list (cytosolic fraction)

↓

633 proteins identified with FDR < 1 % and present in any samples

↓

364 proteins identified having at least 2 peptides and present in at least 2 samples

↓

31 significantly changed proteins identified following non-parametric statistical test (14 down- and 17 up-regulated proteins)

↓

Principal Component Analysis (PCA) Hierarchical Clustering Ingenuity Pathway Analysis (IPA)

S3 Fig. LC-MS/MS data analysis of insoluble and soluble fractions. LC-MS/MS data analysis of insoluble (A) and soluble (B) fractions identified 1020 crude membrane proteins and 633 cytosolic proteins with FDR < 1 % respectively. 686 crude membrane proteins and 364 cytosolic proteins were identified which had at least two unique peptides in one experimental condition and were present in at least two experimental conditions. Following ranking and log transformation 86 (36 down- and 50 up-regulated) and 31 (14 down- and 17 up-regulated) significantly changed proteins respectively for crude membrane and cytosolic fractions were identified in sunitinib treated versus vehicle control.