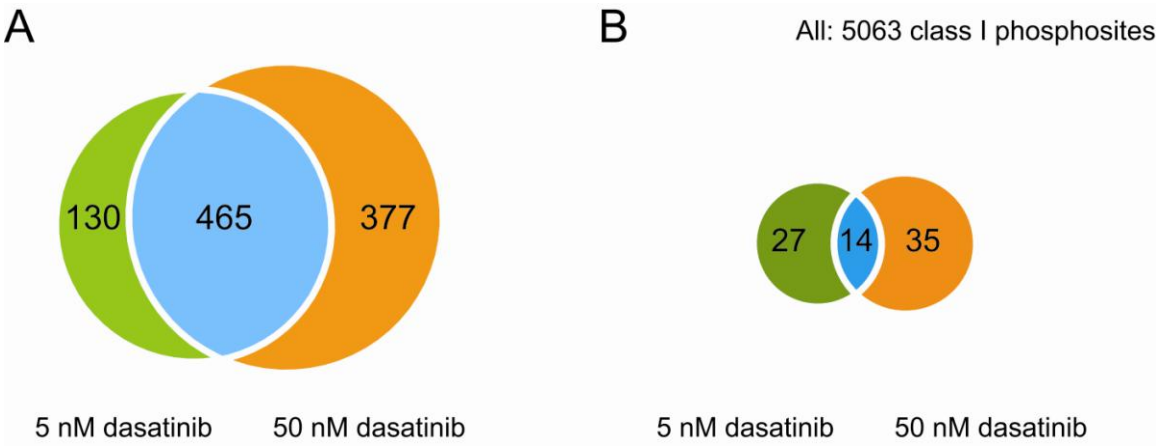
Supplementary figures:



Suppl. figure 1 Overlapped down-regulated **(A)** and up-regulated **(B)** phosphopeptides by different doses of dasatinib. By regulation, a minimal of 2-fold change is requested. Green: data from 5 nM dasatinib; orange: data from 50 nM dasatinib; blue: the overlap.

Supplementary tables

In the following supplementary tables, identification and quantitation results of the class I phosphorylation sites from each experiment are displayed in similar format.

Explanations to table headers:

MaxQuant phospho(STY) ID: *MaxQuant output ID.*

Proteins: *ID of the identified proteins from IPI human database 3.37.*

Protein name: *full name of the proteins being identified.*

Gene name: *the gene name for the proteins being identified.*

Uniprot: *ID of the identified proteins from the Uniprot database.*

Position: *position of the phosphorylated amino acid on the whole sequence protein.*

Modified sequence: *the annotated peptide sequence with depicted phosphorylated Ser, Thr, or Tyr. (ph) is used to represent phosphate group.*

Number of phospho(STY): *the number of phosphorylation sites on that specific peptide.*

Amino acid*: the amino acid being phosphorylated*

Charge: *the charge state of the phosphopeptide*

m/z: *the mass-to-charge ratio of the phosphopeptide*

Mass error (ppm): *the difference of molecular weight in parts per million scale between the measured value and theoretical value.*

Mascot score: *the probability-based score returned by Mascot search engine for peptide identification.*

PTM score: *post translational modification score, used to evaluate the phosphosite localization. Algorithm (REF. 31)*

Localization probability: *calculates the possibility of phosphate group locating on the particular amino acid.*

Score difference: *difference between the best and second best possible assignments of phosphosites. Calculation is based on PTM score.*

PEP: *posterior error probability, used to evaluate how confident the phosphopeptide is being identified. Algorithm (REF. 48)*

Ratio*: the peak-intensity based calculation for fold change according to SILAC labeling states.*

Ratio normalized: *correction of the ratio according to sample 1:1:1 mixing error.*

Ratio significance (B): *statistical parameter to evaluate if the intensity of the peptide is significantly falling outside of a group of intensities of the overall peptides.*

Ratio count: *number of integrated LC peaks for ratio calculation.*

Supplementary table 1:

Nine response patterns for quantified phosphopeptides with class I sites in the U0126 experiment. The pattern numbers are consistent with those in Table 1.

Supplementary table 2:

Nine response patterns for quantified phosphopeptides with class I sites in the SB202190 experiment. The pattern numbers are consistent with those in Table 1.

Supplementary table 3:

Quantified phosphopeptides with class I sites for neuroblast differentiation-associated protein AHNAK

Supplementary table 4:

Quantitation of class I phosphosites which were up-regulated by EGF in both MAPKs inhibitor experiments

Supplementary table 5:

Dasatinib up-regulated proteins at the expression level

Supplementary table 6:

Class I phosphosites which were down-regulated by both 5 nM and 50 nM dasatinib.

Supplementary table 7:

ERK substrate motif in class I phosphopeptides which were down-regulated by 2 concentrations of dasatinib