Fig. S1. Spectra of the phosphorylated peptides identified in SnRK2.4 TAP experiments. Presented spectra correspond to the peptides as listed in Table 2.
Fig. S2. Spectra of the phosphorylated synthetic peptides identified in \textit{in vitro} kinase activity assays. Presented spectra correspond to the peptides phosphorylated by SnRK2.10 as listed in Table 3.
Fig. S3. Components of SnRK2 subclass I-regulated 5’ mRNA decay pathways contribute to root development and root system architecture responses to salt stress. Root system architecture of quintuple snrk2.1/2.4/2.5/2.7/2.9/2.10, amiRNA lines VCS#2 and VCS#4, xrn4-5 and xrn4-6. Ten days old seedlings transferred to 0 and 75 mM NaCl at the 4-day old stage. Main root length, average lateral root length per main root length, and lateral root density of Col-0, (A) snrk 2.1/2.4/2.5/2.7/2.9/2.10, (B) amiRNA lines VCS#2 and VCS#4, (C) xrn4-5 and xrn4-6 on media supplemented with 0 or 125 mM NaCl. Boxplots denotes span from 25th to the 75th percentile and are centered to the data median. Asterisk denotes p-value of pairwise comparison by least square method: ***<0.001, **<0.01, *<0.05, n>30. (D) Summary of the effects of genotype and genotype-by-salt interaction. Heatmaps presents the p-values from ANOVA analysis of the effect of genotype alone or in the interaction with salt stress level on main root length (MRL), number of lateral roots (noLR), lateral root density (LRD), total root size (TRS) and average lateral root length per main root length (aLRLpMRL); ns-not significant.
Fig. S4. Expression of VCS (VARICOSE) and XRN4 (5' EXORIBONUCLEASE 4) in amiRNA lines VCS #2 and VCS#4 and in T-DNA insertion lines xrn4-5 and xrn4-6. Graphs present data from three biological replicates. Error bars represent SD.
**Fig. S5. Rapid activation of SnRK2.4 and SnRK2.10 in Arabidopsis seedlings.** Ten days-old seedlings grown hydroponically were subjected to a time-course treatment with 150 mM NaCl (left) or 0.5xMS (control, right). In gel kinase assay of crude protein extracts with MBP used as kinase substrate was performed. Band corresponding to the activity of SnRK2.4 and SnRK2.10 present in Col-0 and absent in snrk2.4/2.10 double knock-out mutant, is indicated with an arrow. Coomassie Brilliant Blue staining used as a loading control is presented in the bottom panel. Other MBP-phosphorylating protein kinases detected likely present MAP kinases, not affected by the snrk2.4/2.10 mutation. Arrow indicates the band corresponding to SnRK2.4 and SnRK2.10 protein kinases.
Fig S6. Salt stress induced changes in mRNA abundance of genes encoding SnRK2 protein kinases. Ten days-old seedlings grown in liquid 0.5xMS medium were subjected to control (0.1xMS) and salt treatment (150 mM NaCl in 0.1xMS) for one hour. Values presented are average fragments per kilobase of transcript per million mapped reads (fpkm) from 3 biological replicates. Error bars represent standard error (SEM). Significant changes according to Cuffdiff test statistics are denoted with asterisk (p-value<0.05), n=3.
**Effects of the mutations under control conditions**

- $\text{snrk2.4 vs Col-0 control}$
  - 44 genes

- $\text{snrk2.4/2.10 vs Col-0 control}$
  - 68 genes

- $\text{snrk2.1/2.4/2.5/2.9/2.10 vs Col-0 control}$
  - 485 genes
  
  *(Table S8)*

**Salt specific effects of the mutations**

Col-0 salt vs ctr

- Salt responsive genes (SRG) 1292 genes *(Table S9)*

For each mutant tested:

- SRG
- SRG mutant vs ctr

- Col-0 salt up
- Mutant salt up

- Col-0 salt down
- Mutant salt down

**Fig. S7. Overview of the process of the selection of salt stress regulated genes that are dependent on subclass 1 SnRK2 protein kinases.**

(A) Number of genes differentially expressed between each mutant and Col-0 under control conditions. (B) Summary of the selection of the genes with salt stress regulated expression dependent on subclass 1 SnRK2(s).
**Fig. S8. SnRK2 subclass 1 protein kinases regulate gene expression under non-stressed conditions** (A) Expression profiles of genes misregulated in snrk2.4, snrk2.4/2.10 and snrk2.1/2.4/2.5/2.7/2.9/2.10 under control conditions. Gray color indicates genes which expression was not significantly changed by absolute value of log2(fold change) > 1 (B) GO categories enriched among genes impaired in tested mutants. Heatmap presents corrected p-value (q-value) of the enrichment. Categories that were not enriched in individual genotypes are represented by gray squares (NA). (C) Number genes with expression altered in tested mutants and their overlap between the genotypes.
Fig. S9. Salt-induced expression of **PLASMA MEMBRANE INTRINSIC PROTEINS** (PIP2:5, PIP2:3), **BETA GLUCOSIDASE 6** (BGLU6), **CYTOCHROME P450**, **FAMILY 79, SUBFAMILY B, POLYPEPTIDE 2** (CYP79B2) is dependent on SnRK2 subclass 1 protein kinases signaling. Expression of (A) PIP2:5, (B) PIP2:3, (C) BGLU6, (D) CYP79B2, under control condition (left) and upon salt treatment (right) in Col-0, snrk2.4, snrk2.4/2.10, snrk2.1/2.4/2.5/2.9/2.10 and xrn4-5 lines. Values present are averages of normalized expression levels of 3 replicates and error bars denote standard error. Statistical comparison was done by one-way ANOVA followed by LSD posthoc test (p<0.05). Different letters indicate significant differences. Lack of the letters within one graph indicates lack of the significant differences.