

**Characterization of the molecular mechanisms underlying  
Glucose Stimulated Insulin Secretion from freshly isolated  
pancreatic beta cells using PTMomics**

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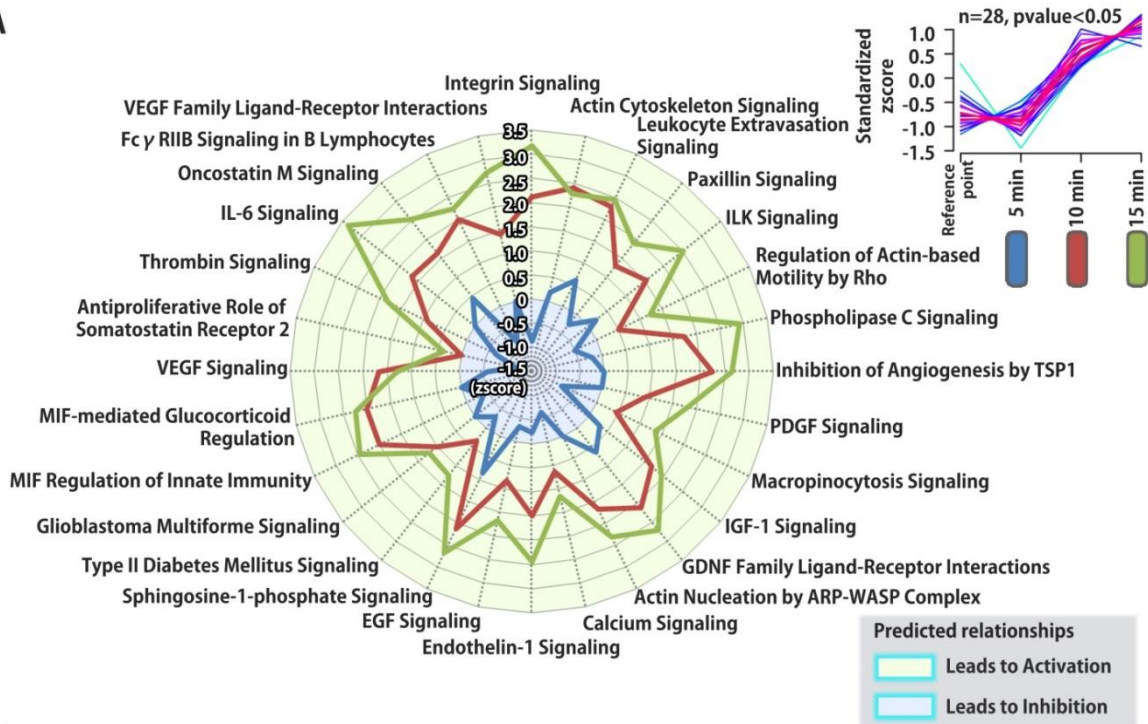
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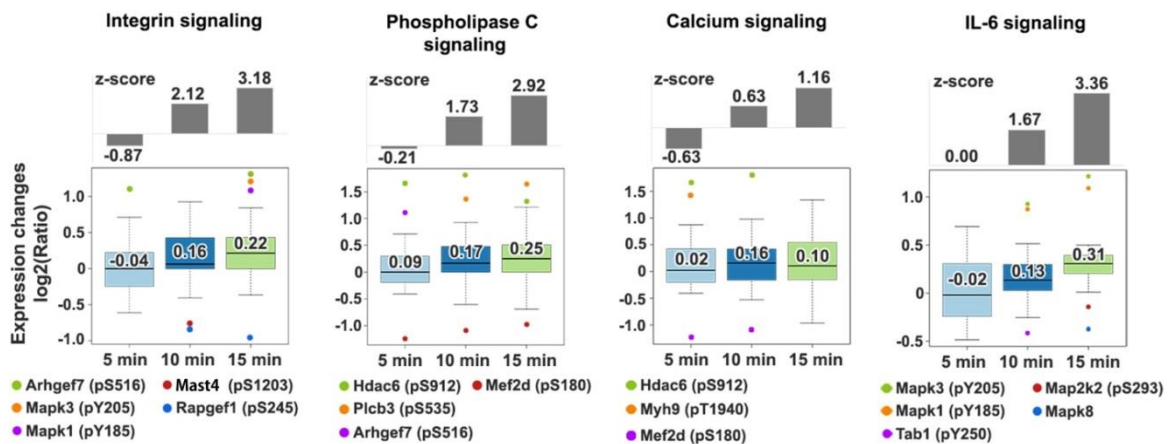
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**Supplemental Figure 1.**

**A**



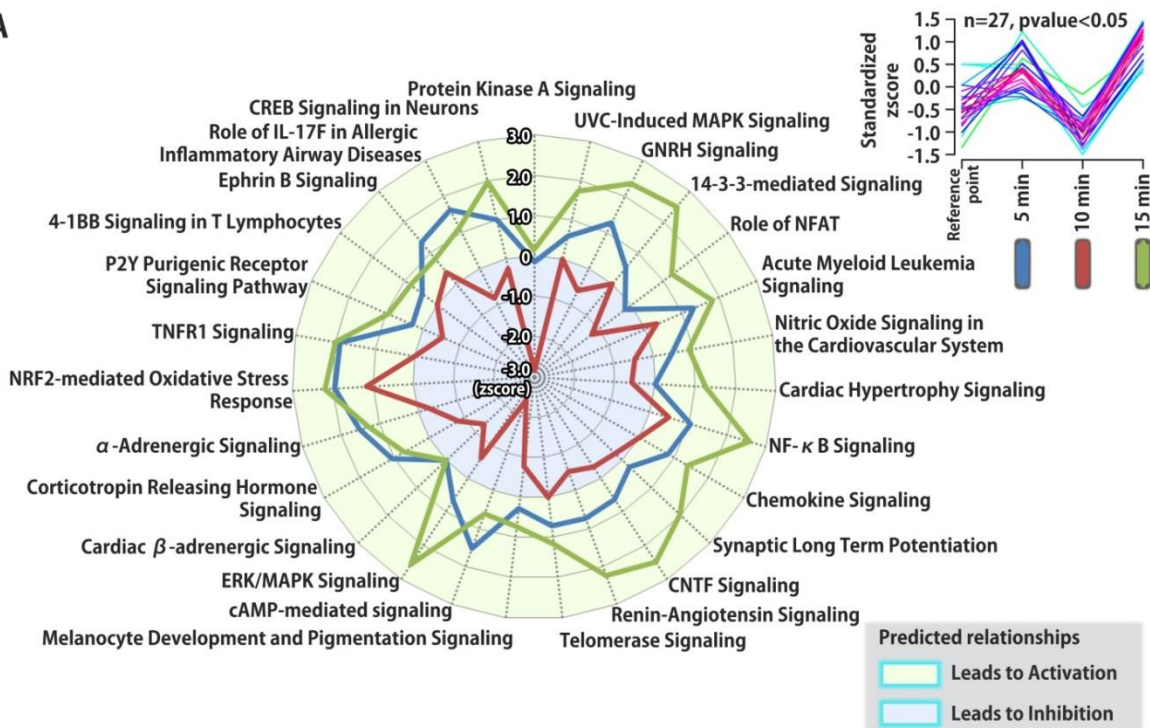
**B**



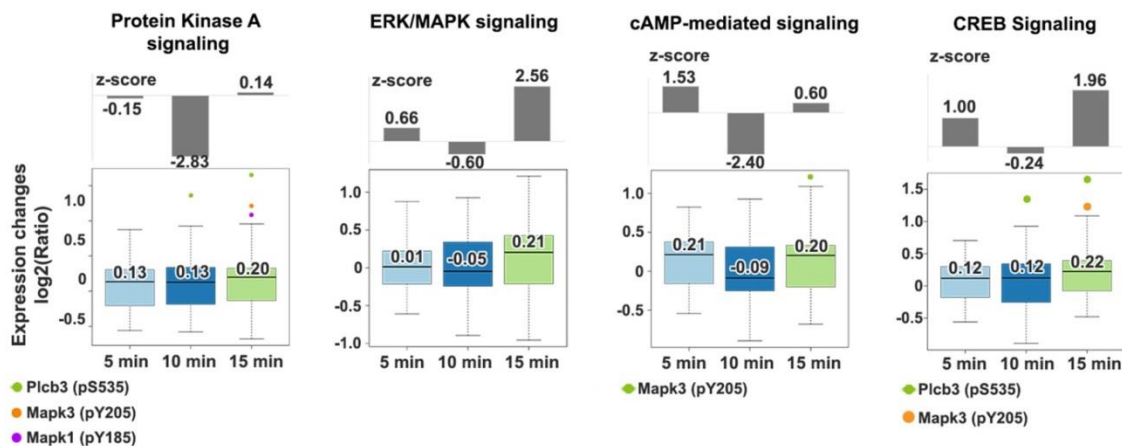
**Supplemental Figure 1. Mapping of affected canonical pathways by glucose stimulated insulin release from beta cells.** (A) Affected canonical signaling pathways in rat pancreatic islets after 5 min, 10 min or 15 min high glucose stimulation on the proteome, phosphoproteome and sialylome using Ingenuity Pathway Analysis (IPA) software are shown as a radar chart. The pathways shown in the radar chart are based on one of three dynamic pathway patterns found from the activation or inhibition z-scores. The pattern is illustrated as a cluster in the right corner. (B) The regulated molecules of four representative signaling pathways were evaluated using interquartile range (IQR) test with significant z-scores (Inhibition < -2 or 2 < Activation).

**Supplemental Figure 2.**

**A**

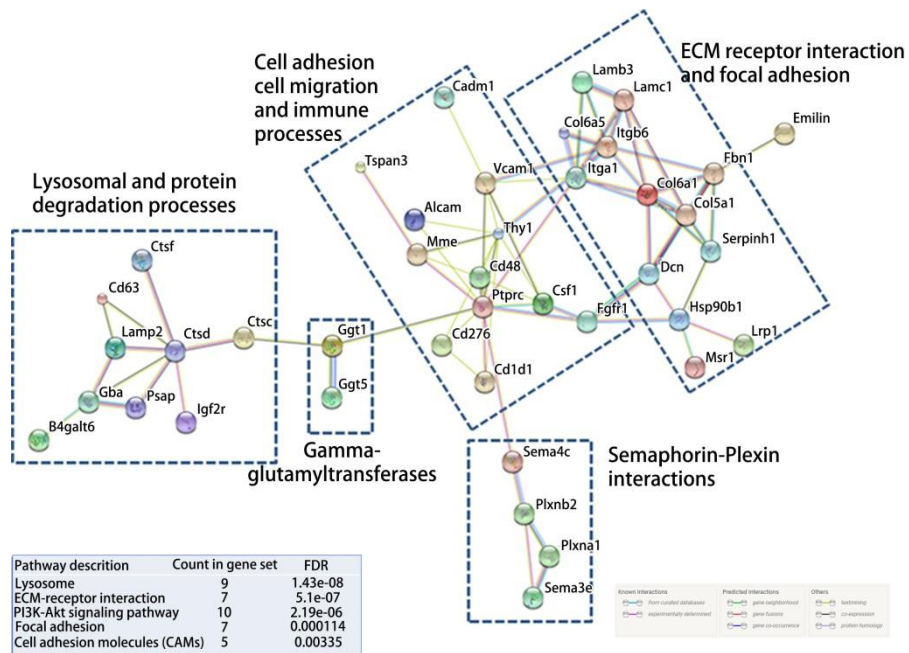


**B**



**Supplemental Figure 2. Mapping of affected canonical pathways by glucose stimulated insulin release from beta cells.** (A) Affected canonical signaling pathways in rat pancreatic islets after 5 min, 10 min or 15 min high glucose stimulation on the proteome, phosphoproteome and sialylome using Ingenuity Pathway Analysis (IPA) software are shown as a radar chart. The pathways shown in the radar chart are based on one of three dynamic pathway patterns found from the activation or inhibition z-scores. The pattern is illustrated as a cluster in the right corner. (B) The regulated molecules of four representative signaling pathways were evaluated using interquartile range (IQR) test with significant z-scores (Inhibition < -2 or 2 < Activation).

**Supplemental Figure 3.**



**Supplemental Figure 3.** Functional interaction network of significantly sialylated proteins after high glucose stimulation according to STRING network analysis. (Small nodes: protein of unknown 3D structure. Large nodes: some 3D structure is known or predicted.)