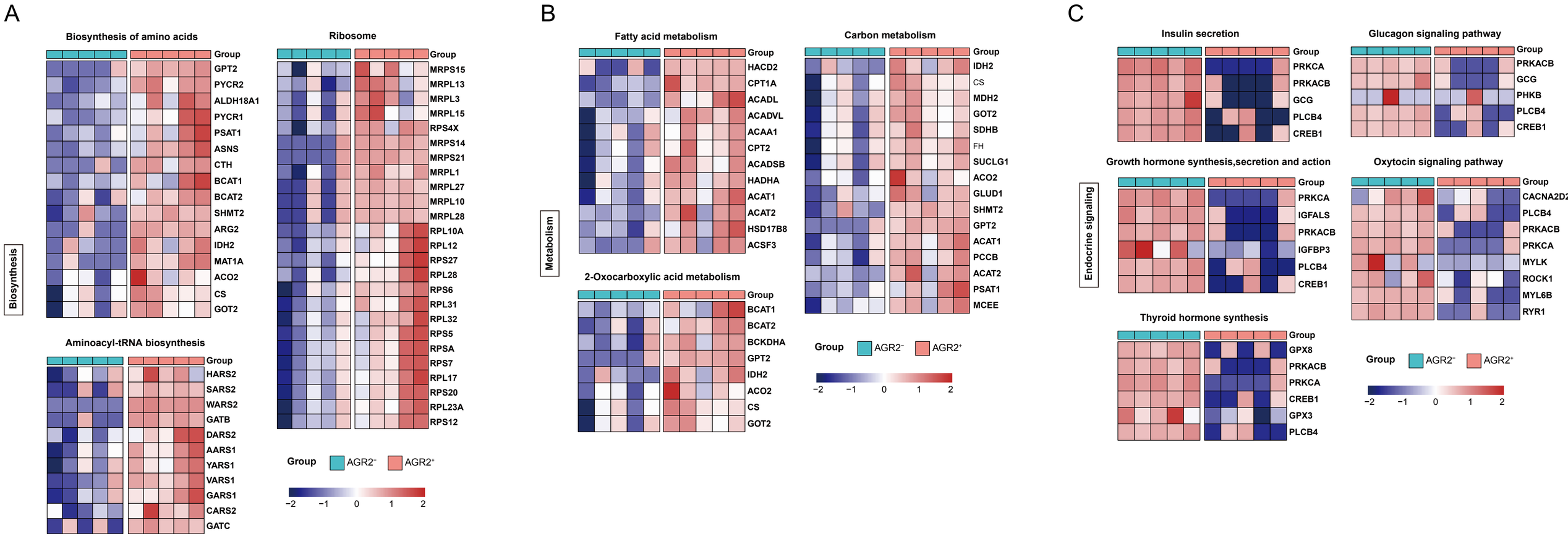


Supplementary Figure S1. Pathway-level heatmaps of representative KEGG pathways in AGR2^{+} and AGR2^{-} tumor subpopulations.
(A) Biosynthesis-related pathways, including biosynthesis of amino acids, aminoacyl-tRNA biosynthesis, and ribosome.
(B) Metabolism-related pathways, including fatty acid metabolism, carbon metabolism, and 2-oxocarboxylic acid metabolism.
(C) Endocrine signaling pathways, including insulin secretion, glucagon signaling pathway, growth hormone synthesis, secretion and action, oxytocin signaling pathway, and thyroid hormone synthesis. Columns represent patient-matched AGR2^{+} and AGR2^{-} samples, and rows represent pathway-associated proteins. Protein abundance is shown as scaled relative expression, with red indicating higher abundance and blue indicating lower abundance.