Glycoproteomic Approach Identifies KRAS as a Positive Regulator of CREG1 in Non-small Cell Lung Cancer Cells

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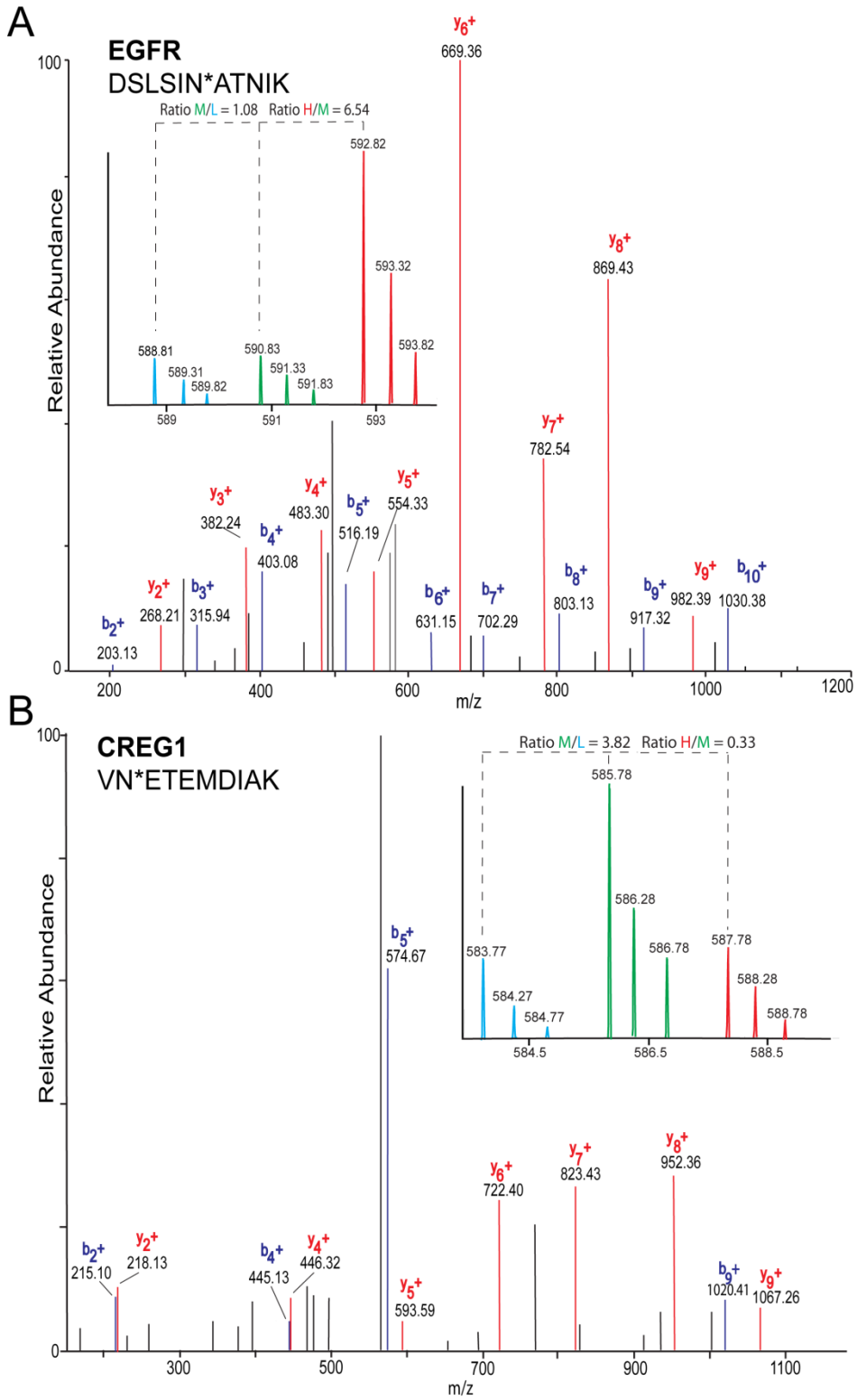

Figure S1. MS/MS mass spectrum of the identified glycopeptide. b- (blue) and y- (red) fragments allow for the mapping of the site of glycosylation as indicated by *. Inset is representative MS1 spectrum of the quantified glycopeptide derived from each cell line: HBE4-L (light blue), A549-M (green), and HCC827-H (red). (A) DSLSINATNIK derived from EGFR, and (B) VNETEMDIAK derived from CREG1.

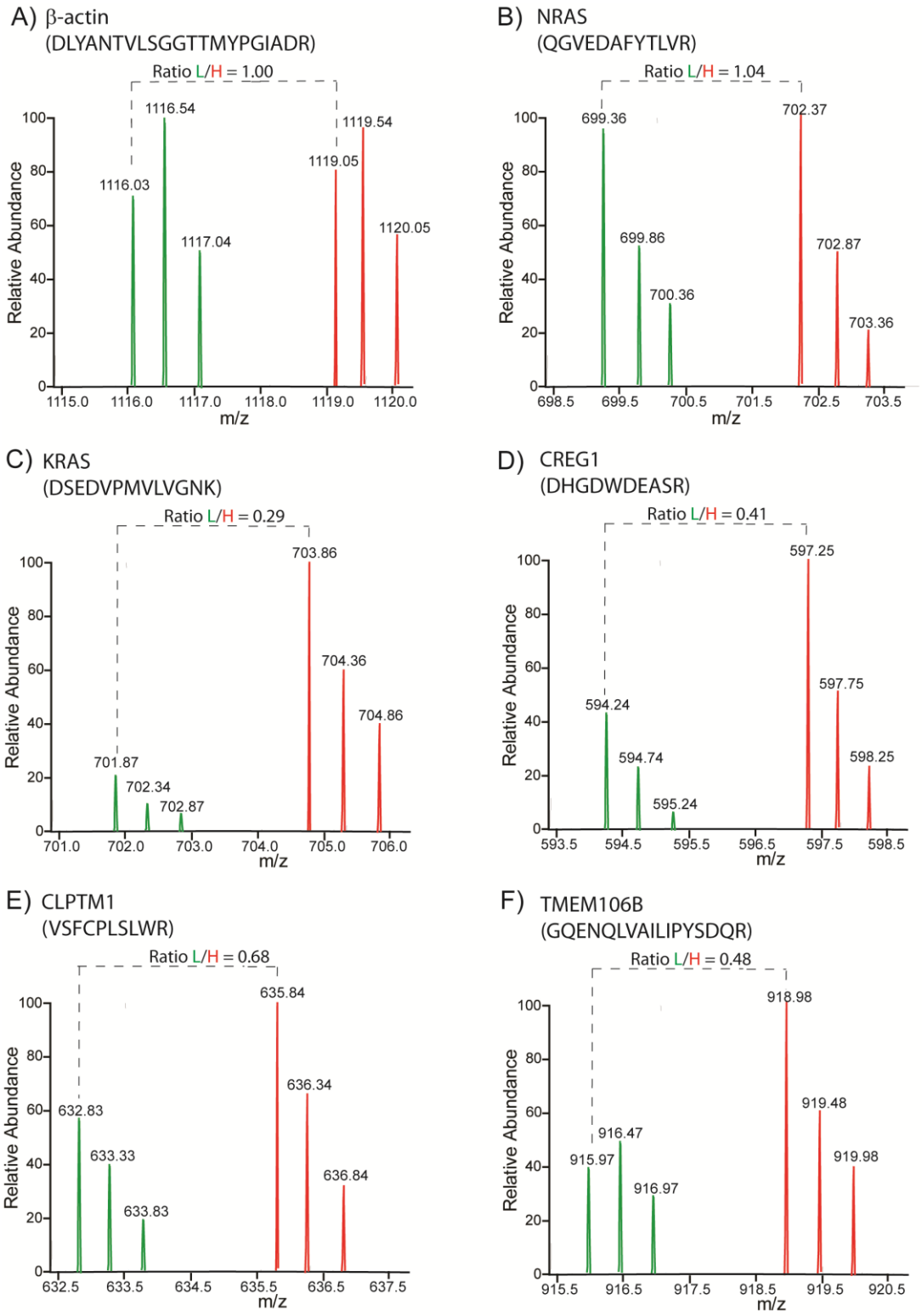

Figure S2. Representative MS1 spectra from Double SILAC analysis of isotopically labeled light (L) $^{siRNA\text{-}KRAS}$A549 -K0R0 (green) cells compared to labeled heavy (H) A549-K4R6 (red) cells. β-actin and NRAS peptide levels remain in 1:1 ratio (A&B), whereas reduced peptide levels were observed in KRAS, CREG1, CLPTM1, and TMEM106B as a result of siRNA targeting KRAS (C-F).