Supporting Information

to

GeLC-MRM quantitation of mutant KRAS oncoprotein in complex biological samples

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Table S1

Figures S1-S4

Table S1. List of peptides monitored with corresponding precursor and fragment ion m/z values.

Peptide	Sequence	Light/ Heavy	Precursor (m/z) (2+)	Fragment ions (m/z) (+)
WT RAS	LVVVGAGGVGK	light	478.3	743.4, 644.3, 213.2, 312.2
WT RAS	LVVVGAGGVGK	heavy	482.3	751.5, 652.4, 213.2, 312.2
KRAS G12V	LVVVGAVGVGK	light	499.3	785.5,686.4, 587.3, 213.2
KRAS G12V	LVVVGAVGVGK	heavy	503.3	793.5, 694.4, 595.4, 213.2
KRAS G13D	LVVVGAGDVGK	light	507.3	801.4, 702.4, 603.3, 213.2
KRAS G13D	LVVVGAGDVGK	heavy	511.3	809.5, 710.4, 611.3, 213.2
HRAS/NRAS	QGVEDAFYTLVR	light	699.4	984.5, 869.5, 798.5, 651.4
HRAS/NRAS	QGVEDAFYTLVR	heavy	704.4	994.5, 879.5, 808.5, 661.4

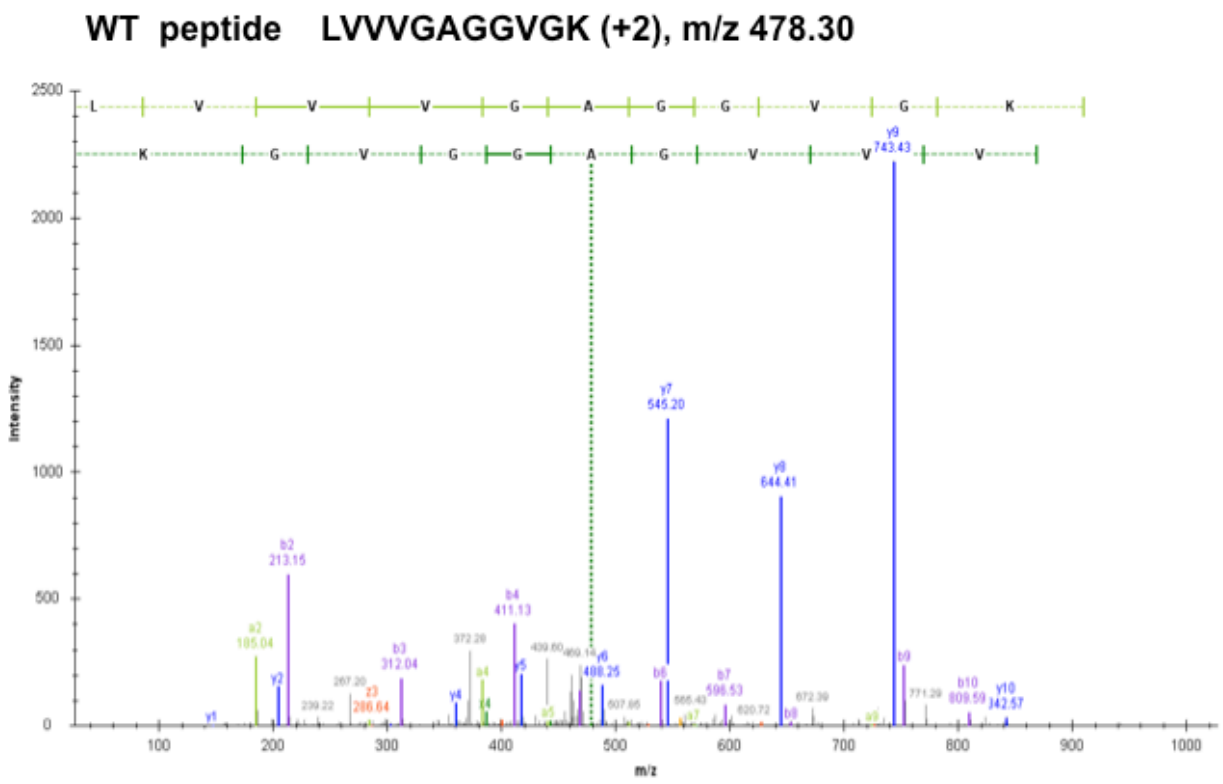

Figure S1. MS/MS spectrum for wild-type RAS peptide LVVVGAGGVGK.

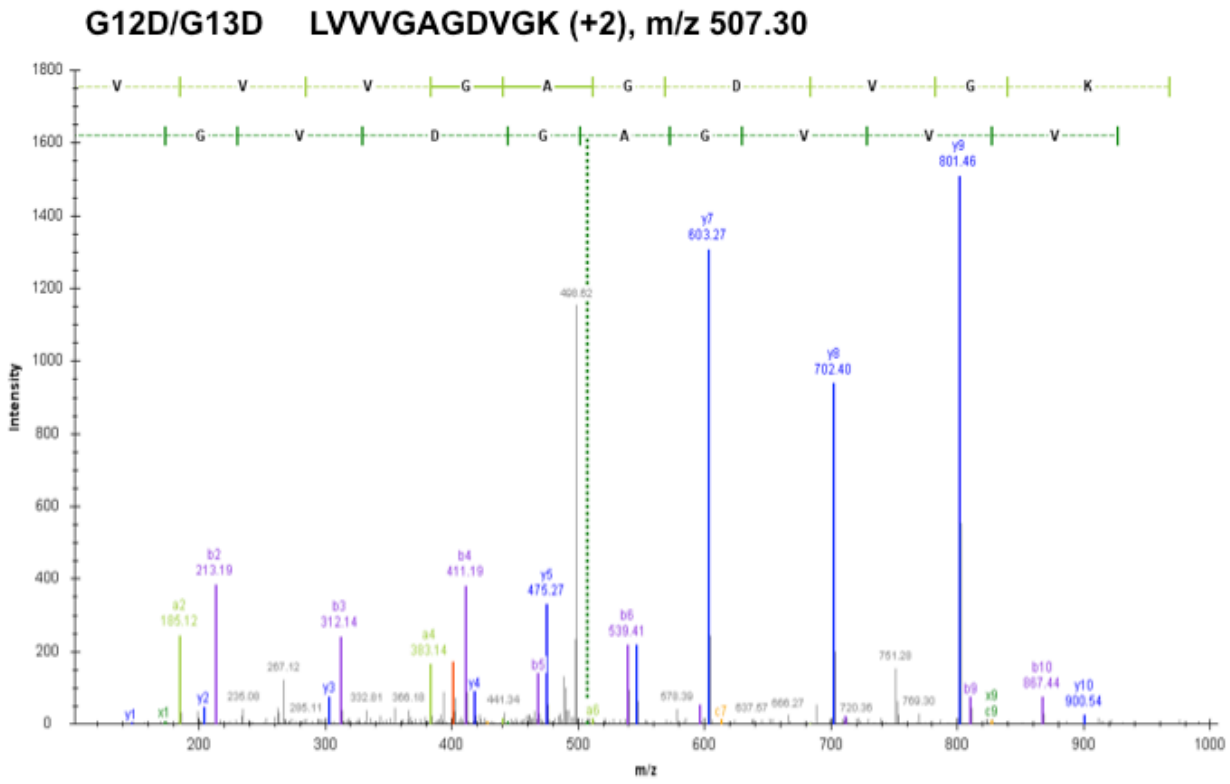

Figure S2. MS/MS spectrum for G13D mutant RAS peptide LVVVGAGDVGK.

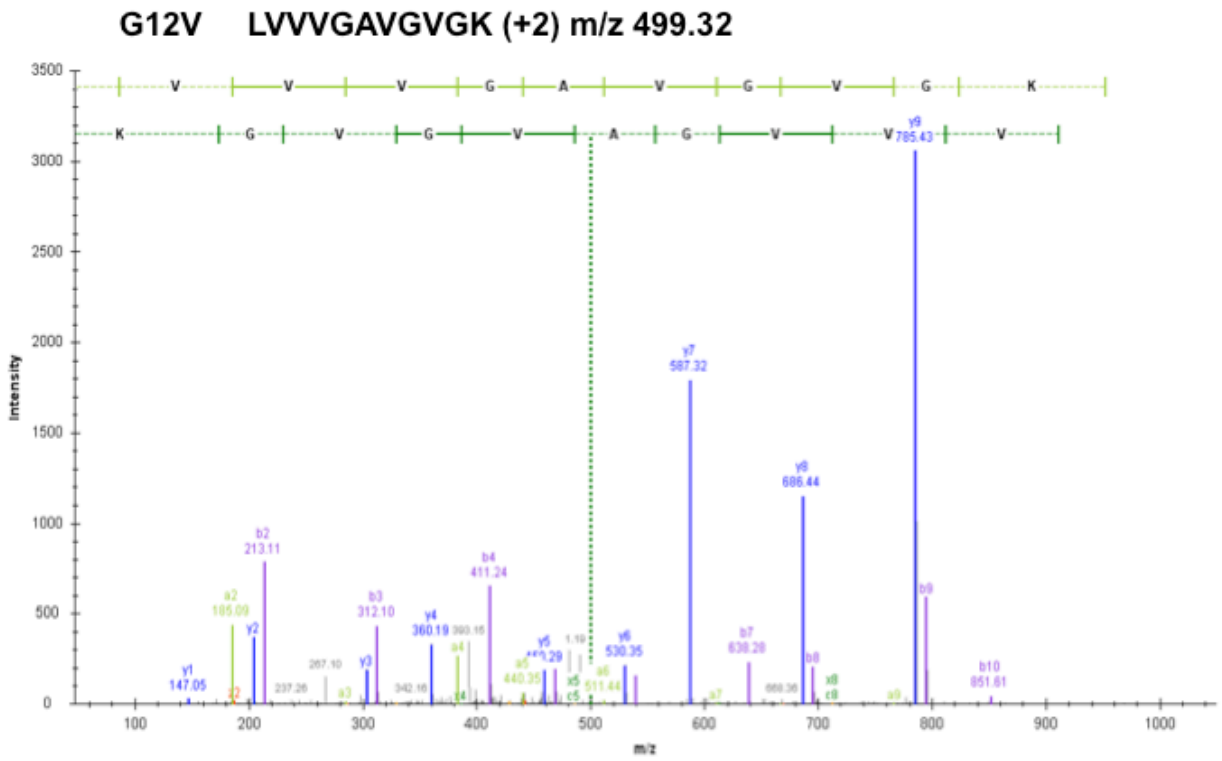

Figure S3. MS/MS spectrum for G12V mutant RAS peptide LVVVGAVGVGK.

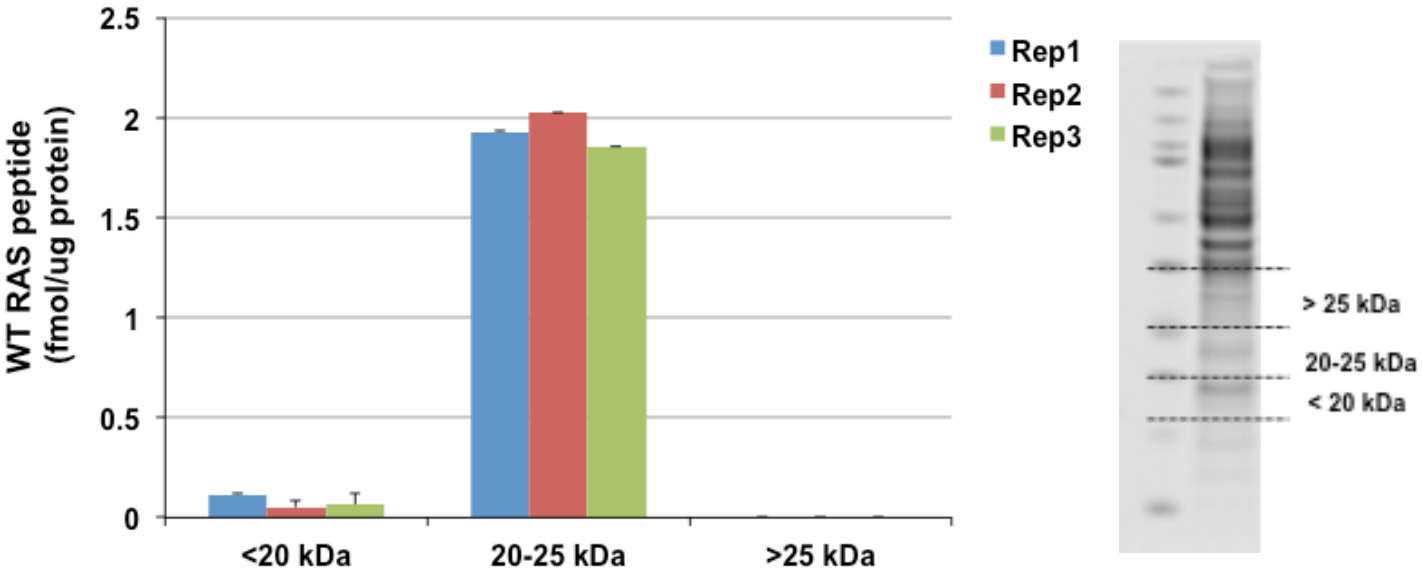

Figure S4. Characterization of GeLC-MRM method. Three GeLC-MRM process replicates were performed (50 µg cell lysate per lane, three MS technical replicates per process replicate). Gel bands were excised in three groupings (>25kDa, 20-25 kDa and <20 kDa) as indicated in the photo at right.