**Supplementary Table 1.** Annotated label-free proteomics analysis of MM.1S cells that were treated with VLA-4 CRIT and the untreated controls. The samples were analyzed in triplicate, and the ratios of CRIT treated cells and untreated cells were obtained.

| GENE          | FOLD OVER UNTREATED | PUTATIVE FUNCTION                                                                 |
|---------------|---------------------|------------------------------------------------------------------------------------|
| DPP7          | 2.22                | Metabolic serine hydrolase/dipeptidyl peptidase implicated in apoptosis and glucose homeostasis |
| IRF2BPL       | 2.22                | Transcription factor targeted by p53 in response to genotoxic stress               |
| UBA2          | 2.04                | ThiF domain implicated in binding to Ubiquitin E1/2                                |
| RPS15         | 4.08                | Ribosomal protein S15 implicated in p53 function                                    |
| LOC441081     | 1.96                | Sequence of nucleoporin POM121 implicated in regulation of apoptosis                |
| APOA1         | 2.31                | Apolipoprotein A1 implicated in PUFA metabolism                                     |
| KIAA0196, WASHC5 | 2.06              | Strumpellin implicated in actin mediated intracellular vesicle transport            |
| KRT9          | 2.3                 | Type 1 intermediate filament implicated in intracellular vesicle transport          |
| HBA1-2        | 1.5                 | Hemoglobin subunit alpha implicated in intracellular antioxidant mechanisms         |
| PSMD8         | 1.6                 | 26S proteasome component involved in regulated proteolysis                         |
| DCTN2         | 1.5                 | Dynactin subunit 2 involved in microtubule mediated intracellular transport        |
| DDX18         | 1.6                 | ATP-dependent RNA helicase involved in nucleic acid replication                     |
| KRT1          | 1.8                 | Keratin 1, component of intermediate filament system                               |
| WDR43         | 1.5                 | WD40 repeat, component of rigid protein scaffold system implicated in metabolic response to stress |
| SRP72         | 1.6                 | Signal recognition particle subunit involved in protein transport                  |
| F5            | 1.8                 | Multicopper oxidase enzyme involved in electron transport and oxidation of various compounds |
| CASKIN1       | 1.6                 | SH3-like protein binding domain involved in signal transduction and response to stress |
| Gene     | Ratio | Description                                                                 |
|----------|-------|------------------------------------------------------------------------------|
| SEH1L    | 1.5   | Nucleoporin SEH1 involved in mTOR signaling pathway and RNA transport       |
| HLA-DRA  | 1.7   | HLA class II histocompatibility antigen, DR alpha chain, involved in PD-1 signaling |
| DHX30    | 1.9   | DEAD/DEAH box helicase involved in cell organization and biogenesis, including response to stress |
| Sec16A   | 1.6   | Protein transport protein Sec16A                                              |
| AGMAT    | 1.6   | Agmatinase, mitochondria localized enzyme thought to be involved in response to stress |
| SSSCA1   | 1.8   | Sjoegren syndrome/scleroderma autoantigen 1, a Zn ribbon domain 2 protein with unclear function |
| FBL      | 1.9   | rRNA 2'-O-methyltransferase fibrillarin thought to be involved in repair of non-enzymatically damaged proteins |
| C7       | 0.4   | Conserved protein sequence with no known function                            |
| MTDH     | 0.5   | Protein LYRIC, involved in cell organization and biogenesis; regulation of biological process; response to stimulus |
| PDLIM3   | 0.4   | LIM domain consisting of two Zn fingers thought to be involved in mediating protein – protein interactions |
| CCDC86   | 0.5   | Coiled-coil domain-containing protein 86 induced by IL3 and upregulated in multiple cancer types |
| OXSM     | 0.5   | Beta-ketoacyl-ACP synthase involved in fatty acid biosynthesis               |
| GOLPH3   | 0.3   | Golgi phosphoprotein 3 involved in regulation of Golgi trafficking           |
| ATXN2    | 0.3   | Ataxin-2 involved in regulation of mRNA translation                          |