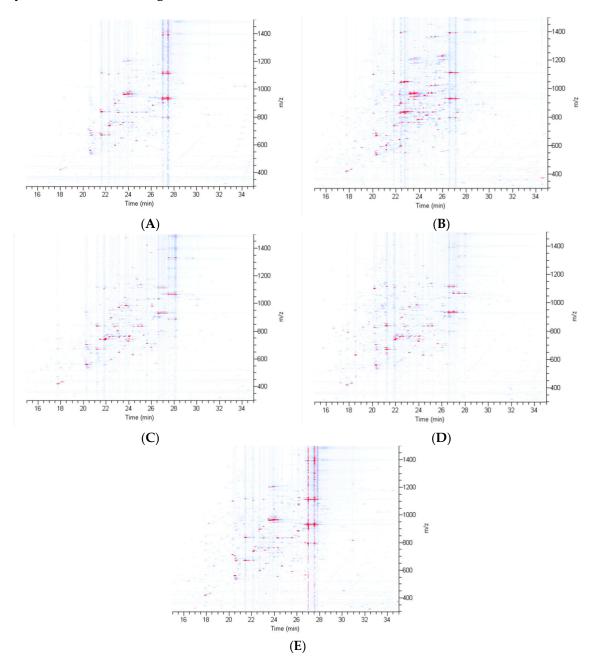
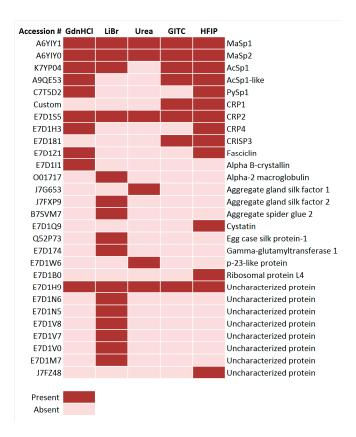
## Supplementary Materials: Comprehensive Proteomic Analysis of Spider Dragline Silk from Black Widows: A Recipe to Build Synthetic Silk Fibers

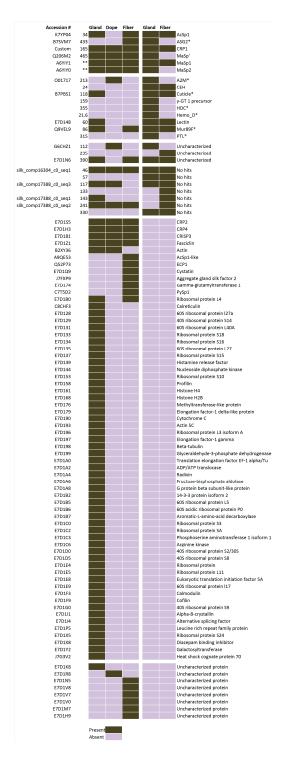
Camille Larracas, Ryan Hekman, Simmone Dyrness, Alisa Arata, Caroline Williams, Taylor Crawford and Craig A. Vierra



**Figure S1.** Density map of in-solution tryptic digestion products obtained from dragline silk treated with different chemical solvents. The *X*-axis reveals the retention time (min) for the precursor ions eluted during nano-LC MS analysis, while the *Y*-axis shows the m/z values (z = +2 to +8); (**A**) GdnHCl; (**B**) GITC; (**C**) urea; (**D**) LiBr; (**E**) HFIP.



**Figure S2.** Chart of presence (dark) or absence (light) of proteins that are predicted within dragline silk using all 5 solvents. Accession numbers are shown on the left and names of the proteins on the right.



**Figure S3.** Chart of presence (black) or absence (light purple) of proteins that are predicted within the MA gland, dope and fiber. Two proteomic data sets are available from *L. hesperus* for comparative purposes. The left panel (gland, dope, and fiber) were conducted with an Orbitrap Fusion™ Tribrid™ mass spectrometer with 5 different solvent treatments and 3 modes of peptide ion dissociation (CID, HCD, and ETD), while the right panel (gland, fiber) was conducted using a LTQ Orbitrap Velos™ mass spectrometer and one mode of ion dissociation (CID) [9]. Accession numbers, scaffolding IDs, and SSTs are listed on the left [9]. Custom indicates the sequence was added into the database manually. No hits indicates the sequences do not match anything in the databases. \* Indicate some peptide sequences that were derived from SSTs that are uncharacterized in *L. hesperus*, but are thought to be homologous to known proteins in different species. \*\* Indicate protein types with more than one predicted protein [9].