Supplementary Information to:

Template-based assembly of proteomic short reads for de novo antibody sequencing and repertoire profiling

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CDRH3 reconstructions of Herceptin and anti-FLAG-M2
Details of sequence variations in F59 Fab
Description of multiple myeloma light chain sequences.
Supplementary Data.

All reported Stitch analyses are provided with the complete output reports. The supplementary data can be unzipped to browse the interactive HTML reports. The corresponding analysis parameters are provided under the ‘Batch File’ menu in each report.
A) Herceptin

template  ...DTAVYYCAR       YFDYWQGTLTVSS...
de novo     DTAVYYC*SRWGG    SRWGGDFYAMDYWQGTLTVSS
overlap    DTAVYYC*SRWGG     SRWGGDFYAMDYWQGTLTVSS
ref        ...DTAVYYC*SRWGGDFYAMDYWQGTLTVSS...

B) anti-FLAG-M2

template  ...DSA*VYYCAR     YFDYWQGTLTVSS...
de novo     DSA*VYYCAREKFGY   VYYCAREKFGYD*YWQGATLTVSS
overlap    DSA*VYYCAREKFGY   VYYCAREKFGYD*YWQGATLTVSS
ref        ...DSA*VYYCAREKFGYD*YWQGATLTVSS...

Supplementary Figure S1. Detailed view of CDRH3 reconstruction by Stitch of the antibodies shown in main text figure 2. Shown are the selected template sequences, aligned reads, found overlap and known reference sequence.
Supplementary Figure S2. Sequence logos of heavy (A) and light (B) chains of F59 Fab from fractionated serum sample from Refined+Decoy Stitch runs. Sequencing error are highlighted in red boxes.
Supplementary Figure S3. A) Stitch reconstruction of light chains from multiple myeloma patient urine (Chamot-Rooke and colleagues, ref 43). CDRs are annotated, sequence conflicts
highlighted by an asterisk (*) and sequence identity in parentheses, along with the mass error of the predicted Stitch sequence compared to the experimentally determined mass of the intact light chain. B) Sequence logo of P5 light chain from Stitch analysis, with highlighted variants in red boxes.