SUPPLEMENTARY FIGURE 1

(A)

Haptoglobin peptide sequence:

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  1 MSALGAVIAL LLWGQLFAVD SGNDVTDIAD DGCPKPPEIA HGYVEHSVRY
 51 QCKNYYKLRT EGDGVYTLND KKQWINKAVG DKLPECEADD GCPKPPEIAH
101 GYVEHSVRYQ CKNYYKLRTE GDGVYTLNNE KQWINKAVGD KLPECEAVCG
151 KPKNPANPVQ RILGGHLDAK GSFPWQAKMV SHHNLTTGAT LINEQWLLTT
201 AKNLFLNHSE NATAKDIAPT LTLYVGKKQL VEIEKVVLHP NYSQVDIGLI
251 KLKQKVSVNE RVMPICLPSK DYAEVGRVGY VSGWGRNANF KFTDHLKYVM
301 LPVADQDQCI RHYEGSTVPE KKTPKSPVGV QPILNEHTFC AGMSKYQEDT
351 CYGDAGSAFA VHDLEEDTWY ATGILSFDKS CAVAEYGVYV KVTSIQDWVQ
401 KTIAEN
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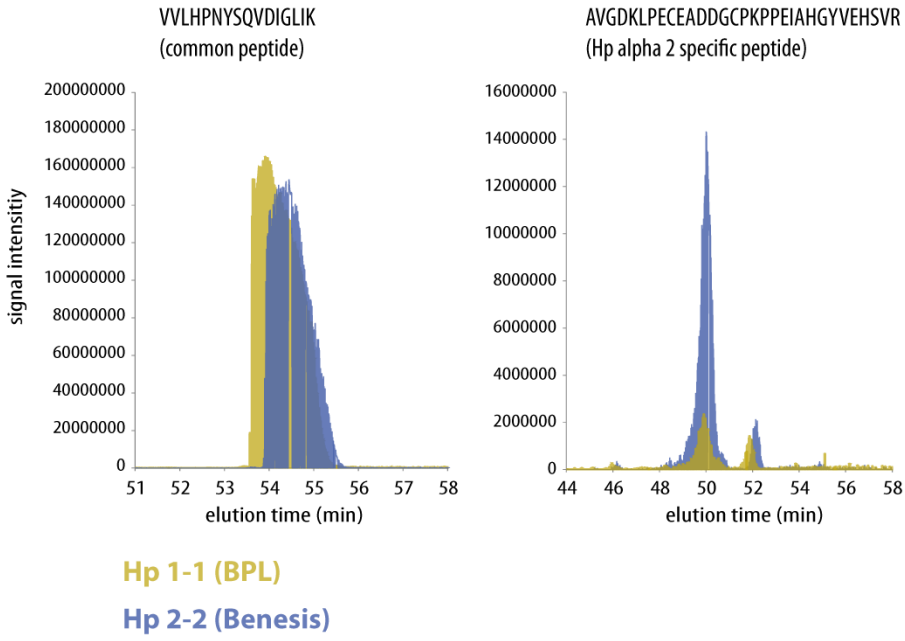
Red or Blue: sequence coverage of LC-MSMS analysis
Blue: Hp 2 specific peptide sequence
Bold: MS detectable Hp 2 specific peptide

(B)



Haptoglobin phenotype determination by mass spectrometry.
The Hp products from BPL (Hp 1-1) and from Benesis Corp. (Hp 2-2) were analyzed by LC-MSMS mass spectrometry with an Orbitrap Velos instrument after digestion with LysC and trypsin. Equal amounts (μg) of both products were digested and analyzed. (A) shows the peptide sequence of Hp 2-2. Highlighted are the sequence coverage obtained by MS analysis, the peptide sequence that is specific for the longer Hp 2 alpha-chain and the Hp 2 specific peptide that is detected by MS. (B) Total ion current chromatograms of a common peptide that is shared by the two Hp phenotypes (left panel) and total ion current chromatogram of the Hp 2 specific peptide. As expected, equal signal intensity was found for the common peptide. The Hp 2 specific peptide appears as a strong signal with the Hp 2-2 sample, while it was only marginally detected as a contaminant in the Hp 1-1 preparation.