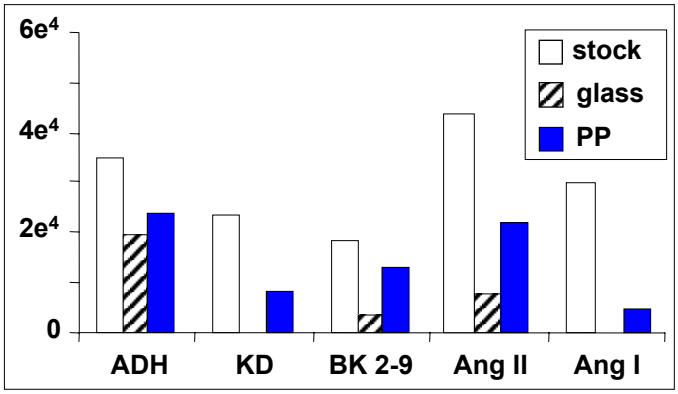
Suppl Table 1

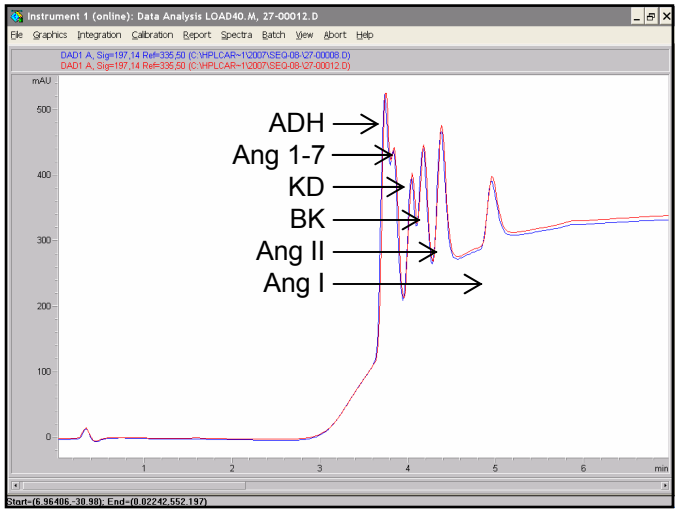
	M+H+ measured	MS^1 m/z	MS^2 m/z
ADH	1085.8	542.9	534.3
Ang I	1297.8	649.4	784.4
Ang II	1048.0	524.2	784.4
Ang 1-7	899.7	450.5	784.4
KD	1189.1	595.3	904.4
BK	1060.6	531.2	522.3
BK 1-8	905.2	453.0	642.3
BK 2-9	905.7	453.0	807.4

Supplementary Table 1 | **MS parameters for the peptides analyzed in this study.** The measured mass value (M+H+) of each peptide was provided by the supplier (AnaSpec; San Jose, CA). The MS^1 values are the predominant parent ion determined by us under the conditions used in these studies. The MS^2 values listed are those used to generate extracted ion chromatograms and signal intensity analyses.

Suppl. Fig 1



Supplementary Figure 1 | Adsorption of peptides to glass & polypropylene. A comparison of peptide recovery from stock standards mix versus equimolar injections from samples prepared in glass or polyethelene vial inserts. A peptide standard mix was prepared in LB vial (500 ml; [10^{-10}M]). The "stock" sample consisted of 200 μl of [10^{-10}M] peptide mix transferred directly to a PP vial insert on the day of analysis. Glass and PP samples consisted of 20 μl of the [10^{-10}M] stock transferred to the vial inserts and diluted 10 fold before lyophylization and reconstitution, thereby exposing analytes to the full surface area of the vial insert with a solution approximating endogenous plasma concentrations of each peptide. Replicate injections of 8.0 μl were analyzed (theoretically 0.8 fmol injected on column).



Supplementary Figure 2 | Offline HPLC fractionation of vasoactive peptides. A chromatogram showing the elution of peptides from a standard mix (10^{-6}M) using diode array UV detection. Establishing the elution times enabled the collection of endogenous low abundance peptides from plasma and standards for LC-MS analysis. Chromatographic resolution of each peptide was forgone to enable collection of peptides of interest in a single low volume fraction.

SUPPLEMENTARY DATA:

{Insert Suppl Table, Suppl fig 1 & 2}

- Agilent XCT Ultra ion trap MS parameters:

Mass Range Mode	Ultra scan
Ion Polarity	Positive
Ion Source Type	Chip ESI
Dry Temp	325°C
Nebulizer	2.0 PSI
Dry Gas	5.0 l/min
Trap Drive	85.0
Octopole RF Amp	108.9 Vpp
Capillary Exit	99.0 V
Skimmer	30.0 V
Oct 1 DC	12.0 V
Oct 2 DC	1.7 V
Scan Begin	400 m/z
Scan End	950 M/z
Averages	1 spectra
Max Accu time	0.5 sec
(smart) ICC Target	0.5×10^6
ICC	on

SUPPLEMENTARY METHODS:

Additional details describing the preparation of standards and samples are listed according to the figures presented for each experiment.

Figure 2; A frozen aliquot of pure peptide [10^{-6}M] was diluted 10x with water. Two vial inserts received either 2 or 20 μl of peptide and were diluted with water to a final volume of 200 μl. Replicate serial injections of 0.01, 0.1, 1.0 μl from each vial were analyzed.

Figure 3; A mix of peptides was prepared in a LB vial by adding 10 μl of each peptide aliquot stock and diluting with water to a final volume of 1.0 ml [10^{-8}M]. 20 μl was transferred to a PP vial insert diluted 10x for replicate injections of 1.0 μl.

Figure 4; An equal volume of methanol and thawed plasma (200 μl vol:vol) was mixed and refrigerated overnight at 4°C in a LB vial. After centrifugation to separate denatured protein, 300 μl of supernatant was subject to 10k MW cutoff spin filtration. Aliquots of the filtrate (100 μl) were transferred to PP sample vial inserts for lyophylization +/- addition of a standards mix (10 μl; 10^{-10}M). Lyophylized samples were reconstituted in 10 μl water, providing a 5x concentrated extract, replicate injections of 1.0 μl were analyzed.

Figure 5; A) A peptide standards mix was prepared as described above (1.0 ml; [10^{-9}M]). Two separate PP vial inserts received either 2 or 20 μl of the mix and were diluted to a final volume of 200 μl with water before lyophylization. Each was reconstituted to 20 μl with water and repeated graded injections of 0.2, 0.4 & 0.8 μl or 2.0, 4.0 & 8.0 μl ensued. **B)** A [10^{-8}M] stock peptide mix was prepared in a LB vial as above. A PP vial insert received 20 μl of the mix and was diluted 10 fold with water. Off-line reverse phase HPLC fractionation was used to process 20 μl of the standards mix. The collected elution fraction (250 μl; directly into PP vial inert) was lyophylized and reconstituted in 20 μl of "eluent A". Replicate, graded injections of 0.2, 0.6 and 0.8 μl were analyzed.

Figure 6; Thawed plasma was spin-filtered (10k MW cutoff) into LB vials and 50 μl was transferred to a PP vial insert. Off-line HPLC fractionation was used to process 45 μl of filtered plasma. After Lyophylization, plasma peptides were reconstituted in 4.5 μl of "eluent A" and replicate 2 μl injections were analyzed.