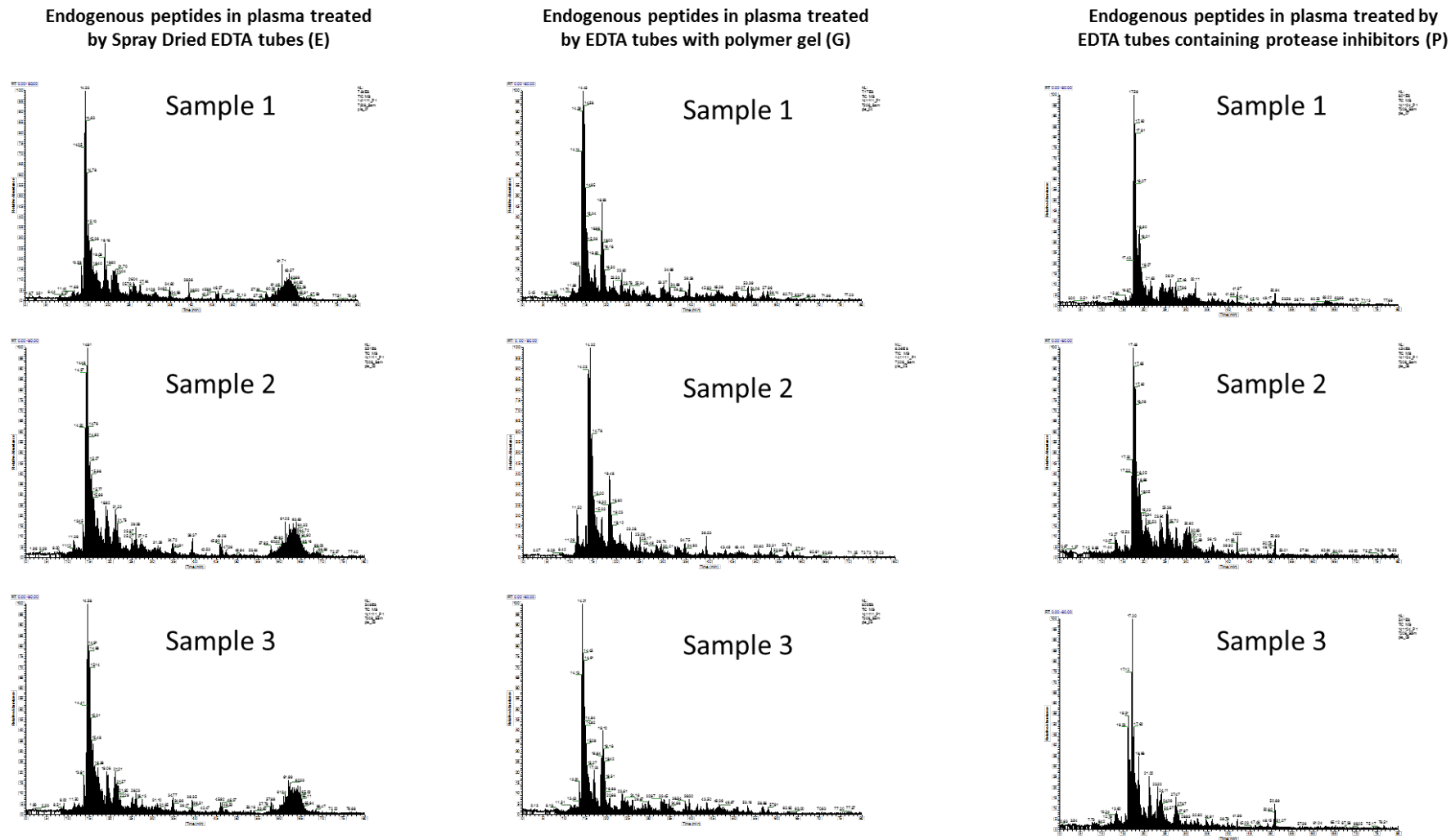


Supplementary Figure 1. MS chromatograms for endogenous peptidomic analysis of plasma samples handled by three different types of EDTA containing blood collection tubes; (i) spray-dried EDTA (E) (ii) EDTA with polymer gel (G) (iii) EDTA tubes containing a proprietary cocktail of protease inhibitors (P)



Supplementary Table 1. Protein concentrations before and after Mars-14 immunodepletion

Sample	Concentration (mg/ ml)	
	Before Depletion	After depletion
1E	60.55	3.518396
1G	60.26	3.566012
1P	60.01	3.631296
2E	59.66	3.538432
2G	59.23	3.684574
2P	59.71	3.857069
3E	59.63	4.2512
3G	59.83	4.283543
3P	60.35	3.792112

Supplementary Table 2. Complete list of peptides identified in all three plasma samples collected in EDTA, gel EDTA and P100 tube

EDTA		Gel EDTA		P100	
Peptide Sequence	Accession	Peptide Sequence	Accession	Peptide Sequence	Accession
SNLDEDIIAEENIVSR	P01024	ADSGEGDFLAEGGGVR	P02671	AAVGTSAAPVPSDNH	P02649
ADDTWEPFASGK	P02766	AAQKENAGEDPGLA	P81605	ADSGEGDFLAEGGGV	P02671
ADSGEGDFLAEGGGVR	P02671	AAQKENAGEDPGLAR	P81605	ADSGEGDFLAEGGGVR	P02671
ADSGEGDFLAEGGGVRGP	P02671	ADSGEGDFLAEGGGVRGP	P02671	ADSGEGDFLAEGGGVRGP	P02671
ADSGEGDFLAEGGGVRGPR	P02671	ADSGEGDFLAEGGGVRGPR	P02671	ALLSPYSYSTTAVVTNPKE	P02766
AINVAVHVF	P02766	ALLSPYSYSTTAVVTNPKE	P02766	DSGEGDFLAEGGGVR	P02671
ALGISPFHEHAEEVFTANDSGPR	P02766	CLKVIVSLTVY		DVSLQLPSR	P01024
APPPISGGGYR	P02675	DSGEGDFLAEGGGVR	P02671	DVVEGEKGAEAAANVTGP	P67809
DSGEGDFLAEGGGVR	P02671	DSGEGDFLAEGGGVRGPR	P02671	EEAGARVQQNVPSGTDGDPQSKPLG	O14791
DSGEGDFLAEGGGVRGPR	P02671	DVSLQLPSR	P01024	EGDFLAEGGGVR	P02671
DVSLQLPSR	P01024	EHFQEVGYAAPPSPPLS	Q16610	GAGSLQPLALEGSLQ	P01308
ENEGFTVTAEKG	P01024	FFPKSRIV	P10909	GEDFLAEGGGVR	P02671

FFPKSRIV	P10909	FFPKSRIV	P10909	GLEELQFSLGSK	P0C0L4
FFPKSRIV	P10909	FFQYDTWKQSTQRL	P01344	GSSGTGGTATWKPGSSGP	P02671
FFQYDTWKQSTQRL	P01344	FKSHALQLNNR	P0C0L4	GSTGNRNPSSGTGGTATWKPGS	P02671
FMGKVVNPQK	P01009	FLSALEEYTKKLNTQ	P02647	GSTGNRNPSSGTGGTATWKPGSSGP	P02671
GDSTFESKSYK	P02671	GAGSLQPLALEGSLQ	P01308	HRIHWESASLL	P01024
GEGDFLAEGGGVR	P02671	GDSTFESKSYK	P02671	HWESASLLR	P01024
GEYGAEALERMF	P69905	GFKSHALQLNN	P0C0L4	IHWESASLL	P01024
GFKSHALQLNN	P0C0L4	GFKSHALQLNNR	P0C0L4	IHWESASLLR	P01024
GFKSHALQLNNR	P0C0L4	GGSTSYGTGSETESPRN	P02671	ITHRIHWESASLL	P01024
GFKSHALQLNNRQI	P0C0L4	GGSTSYGTGSETESPRNPSSAGSWNSGSSGP GSTGNR	P02671	ITHRIHWESASLLR	P01024
GKSSSYSKQFTSSTSYNR	P02671	GKSSSYSKQFTSSTSYNR	P02671	KVEQAVETEPEPELR	P02649
GLEELQFSLGSK	P0C0L4	GLEELQFSLGSK	P0C0L4	LDLIGTIGLSWT	O95528
GLEELQFSLGSKI	P0C0L4	GLEELQFSLGSKI	P0C0L4	LGRQLTSGP	P08697
GLEELQFSLGSKINVK	P0C0L4	GLEELQFSLGSKINVK	P0C0L4	LSALEEYTKKLNTQ	P02647
GLPGPPDVPDHAAYHPFR	Q14624	GLPGPPDVPDHAAYHPFR	Q14624	MEPLGRQLTSGP	P08697
GNTEGLQKSLAELGGHLDQQVEEFR	P06727	GNTEGLQKSLAELGGHLDQQVEEFR	P06727	MSPTGDFLATSHVD	Q8NI36
GSPAINVAVHVFR	P02766	GSESGIFTNTKESSSHHPGIAEFPSR	P02671	NDNEEGFFSAR	P02675
GSSGTGGTATWKPGSSGP	P02671	GSSGTGGTATWKPGSSGP	P02671	NEQEQPLGQWHL	O00391
GSTGNRNPSSGTGGTATWKPGS	P02671	GSTGNRNPSSGTGGTATWKPGS	P02671	NGFKSHALQLNN	P0C0L4
GSTGNRNPSSGTGGTATWKPGSSGP	P02671	GSTGNRNPSSGTGGTATWKPGSSGP	P02671	NGFKSHALQLNNR	P0C0L4
HTFMGVVSLGSPSGEVSHPR	P02765	GWGVMVSHR	P06733	NGFKSHALQLNNRQI	P0C0L4
HWESASLL	P01024	HALQLNNRQI	P0C0L4	NQEQVSPLTLLK	P08697
IHWESASLLR	P01024	HFFPKSRIV	P10909	NQEQVSPLTLLKLGN	P08697
KVEQAVETEPEPELR	P02649	HRIHWESASLL	P01024	NRGDSTFESKSYKMA	P02671
LSALEEYTKKLNTQ	P02647	HTFMGVVSLGSPSGEVSHPR	P02765	NSPLDEENLTQENQDR	P01011
LSRNCVIKELA	Q09FC 8	HTFMGVVSLGSPSGEVSHPRKT	P02765	NSPLDEENLTQENQDRG	P01011
LTDMPQMR	P02671	HWESASLL	P01024	PEVRPTSAVAA	

MELERPGGNEIT	P02671	HWESASLLR	P01024	PGSPRPGSTGTWN	P02671
MEPLGRQLTSGP	P08697	IHWESASLL	P01024	PGSSGTGGTATWKPSSGP	P02671
MGVVSLGSPSGEVSHPRKT	P02765	IHWESASLLR	P01024	PSSAGSWNSGSSGPGSTGNRN	P02671
NDNEEGFFSARGH	P02675	ILRSKLEQ	Q9Y264	RIHWESASLL	P01024
NEPSILEMSR	O14791	ILVGSSRRV		RIHWESASLLR	P01024
NFRPGVLSS	Q14624	IMSASTTTL	P23258	RNPGSSGTGGTATWKPSSGP	P02671
NGFKSHALQLNNR	P0C0L4	ITHRIHWESASLL	P01024	SALEEYTKKLNTQ	P02647
NGFKSHALQLNNRQI	P0C0L4	ITHRIHWESASLLR	P01024	SEETKENEGFTVTAEGK	P01024
NLAFAFSLYR	P01009	KSNEQATSLNTVGGTGGIGGVGGTGGVGNR AP	Q13201	SETSRTAFGGRRVPPNNSNAEDDLPTVEL QGVVPR	P00488
NLQNNAEWVYQGAIR	P04114	KVEQAVETEPEPELR	P02649	SEYQTFFNPR	P00734
NPGSSGTGGTATWKPSSGP	P02671	LEEELQFSLGSK	P0C0L4	SGEGDFLAEGGGVR	P02671
NQEQVSPLTLLK	P08697	LLSPYSYSTTAVVTNPKE	P02766	SKITHRIHWESASLLR	P01024
NQEQVSPLTLLKLGN	P08697	LMIEQNTKSPLFMGKVVNPTQK	P01009	SSKITHRIHWESASLLR	P01024
NRGDSTFESKSY	P02671	LSALEEYTKKLNTQ	P02647	TANNFLLISDDLRS	O75677
NRGDSTFESKSYKM	P02671	MEPLGRQLTSGP	P08697	TDQVLSVLKGEE	P02655
NRGDSTFESKSYKMA	P02671	MEPLGRQLTSGPNQEQVSPLTLLKLGN	P08697	TFAEARL	Q6IE81
NSPLDEENLTQENQDR	P01011	MGVVSLGSPSGEVSHPRKT	P02765	THRIHWESASLL	P01024
PAPPPISGGGYR	P02675	NDNEEGFFSARGH	P02675	THRIHWESASLLR	P01024
PDSPGSGNARPNPDWGTFFEEVSGNV SPGTR	P02671	NEPSILEMSR	O14791	VNDNEEGFFSAR	P02675
PGSSGTGGTATWKPSSGP	P02671	NEQEQLGQWHLS	O00391	VSETESRGSESGIFTN	P02671
PNNPDWGTFFEEVSGNVSPGTR	P02671	NFPWQVFTNIHGR	P00736	WESASLLR	P01024
PYMKLAPGELTIIL	P04114	NFRPGVLSS	Q14624		
QFTSSTSYNR	P02671	NGFKSHALQLNNR	P0C0L4		
QLGLPGPPDVPDHAAYHPFR	Q14624	NGFKSHALQLNNRQ	P0C0L4		
QVNTQAEQLR	P06727	NGFKSHALQLNNRQI	P0C0L4		
QYDTWKQSTQRL	P01344	NGFKSHALQLNNRQIR	P0C0L4		

RIHWESASLL	P01024	NQEQVSPLTLLK	P08697	
RIHWESASLLR	P01024	NQEQVSPLTLLKLG	P08697	
RNPGSSGTGGTATWKPGSSGP	P02671	NRGDSTFESKSY	P02671	
RYTIAALLSPYSYSTTAVVTNPKE	P02766	NRGDSTFESKSYKM	P02671	
SASLHLPKLSITGTDLK	P01009	NRGDSTFESKSYKMA	P02671	
SEAEDASLLSFMQGYMK	P02656	PDWGTFFEEVSGNVSPGTR	P02671	
SEETKENEGFTVTAEGK	P01024	PGFFSPMLGEFVSETESRG	P02671	
SEIPLPPILLGRLG	Q96KP 4	PGPPDVPDHAAYHPFR	Q14624	
SGEGDFLAEGGGVR	P02671	PGSSGTGGTATWKPGSSGP	P02671	
SHALQLNNR	P0C0L4	PNNPDWGTFFEEVSGNVSPGTR	P02671	
SHALQLNNRQI	P0C0L4	PYMKLAPGELTIIL	P04114	
SKTVVLGLALRREGP	Q75VX 8	QFTSSTSINR	P02671	
SLAELGGHLDQQVEEFR	P06727	QKENAGEDPGLA	P81605	
SLAPYAQDTQEKLNHQLEGLTFQMK	P06727	QLGLPGPPDVPDHAAYHPFR	Q14624	
SPLFMGKVVNPTQK	P01009	QVQALLGVAKCWV	Q13702	
SSAGSWNSGSSGPGSTGNR	P02671	REEAPSLRPAPPPISGGGYR	P02675	
SSYSKQFTSSTSINR	P02671	RIHWESAS	P01024	
SSYSKQFTSSTSINR	P02671	RIHWESASLL	P01024	
SYSKQFTSSTSIN	P02671	RIHWESASLLR	P01024	
SYSKQFTSSTSINR	P02671	RLSGALHVYSLGSD	P80108	
TALVELVK	P02768	RPPGFSPFR	P01042	
TEKLVTSGDKELR	P02671	RQLGLPGPPDVPDHAAYHPFR	Q14624	
TFAEARL	Q6IE81	RYTIAALLSPYSYSTTAVVTNPKE	P02766	
TPTLVEVSR	P02768	SALEEYTKKLNTQ	P02647	
TQVNTQAEQLR	P06727	SASLHLPKLSITGTDLK	P01009	
TVGSLAGQPLQER	P02649	SEAEDASLLSFMQGYMK	P02656	
VNDNEEGFFSAR	P02675	SEAEDASLLSFMQGYMKHAT	P02656	

VNDNEEGFFSARGH	P02675	SEAEDASLLSFMQGYMKHATKTA	P02656	
VTEPISAESGEQVER	O14791	SEETKENEGFTVTAEGK	P01024	
WGVMSVSHR	P06733	SGEGDFLAEGGGVR	P02671	
YDTWKQSTQRL	P01344	SGSFRPDSPGSGNARPNPDWGTFF	P02671	
YESDVMGRGHA	P01023	SGSFRPDSPGSGNARPNPDWGTFFEEV	P02671	
YTIAALLSPYSYSTTAVVTNPKE	P02766	SGSSGPGSTGNRNPSSGTGGTATWKPGSS GP	P02671	
		SHALQLNNR	P0C0L4	
		SHALQLNNRQI	P0C0L4	
		SKTVVLGLALRREGP	Q75VX 8	
		SLAELGGHLDQQVEEFR	P06727	
		SNLDEDIIAEENIVSR	P01024	
		SPMYSIITPNILR	P01024	
		SPMYSIITPNILRL	P01024	
		SSKITHRIHWESASLLR	P01024	
		SSSYSKQFTSSTSYNR	P02671	
		SSSYSKQFTSSTSYNRGDST	P02671	
		SSYSKQFTSSTSYNR	P02671	
		STGKTFPGFFS	P02671	
		STGKTFPGFFSPML	P02671	
		STGKTFPGFFSPMLGE	P02671	
		SVFLIKGDKVWVYPPEK	P02790	
		TANNFLISDDLRS	O75677	
		TDQVLSVLKGEE	P02655	
		TGIFTDQVLSVLKGEE	P02655	
		THRIHWESASLL	P01024	
		THRIHWESASLLR	P01024	
		VNDNEEGFFSAR	P02675	

	VNDNEEGFFSARGHRPLD	P02675	
	VPPEWKALTDMPQM	P02671	
	VTEPISAESGEQVERVNEPSILEMSR	O14791	
	VVSLGSPSGEVSHPRKT	P02765	
	WESASLLR	P01024	
	WGVMVSHR	P06733	
	YDTWKQSTQRL	P01344	
	YESDVMGRGHA	P01023	
	YLQGAKIPKPEASFSPR	Q14624	
	YTIAALLSPYSYSTTAVVTNPKE	P02766	

Supplementary Table 3. Endogenous peptides commonly identified in plasma samples (biological triplicate) collected in blood collection tube containing EDTA

Peptide Sequence	Description	Max score	Total score	Query cover	E value	Ident	Accession
ADSGEGDFLAEGGGVR	Fibrinogen alpha chain; Fibrinopeptide A; Fibrinogen alpha chain;	50.3	80.8	100%	5.00E-09	100%	P02671
ADSGEGDFLAEGGGVRGP	Fibrinogen alpha chain; Fibrinopeptide A; Fibrinogen alpha chain;	56.2	86.7	100%	6.00E-11	100%	P02671
ALGISPFHEHAEEVFTANDSGPR	Transthyretin;ATTR;Prealbumin;TBPA;	75.3	87	100%	2.00E-17	100%	P02766
APPPISGGGYR	Fibrinogen beta chain; Fibrinopeptide B; Fibrinogen beta chain;	37.1	47.9	100%	6.00E-05	100%	P02675
DSGEGDFLAEGGGVR	Fibrinogen alpha chain; Fibrinopeptide A; Fibrinogen alpha chain;	47.7	78.3	100%	3.00E-08	100%	P02671
FFQYDTWKQSTQRL	Insulin-like growth factor II	52	52	100%	8.00E-10	100%	P01344
FMGKVVNPTQK	Alpha-1-antitrypsin	39.2	39.2	100%	1.00E-05	100%	P01009
GEGDFLAEGGGVR	Fibrinogen alpha chain	41.8	70.6	100%	2.00E-06	100%	P02671
GFKSHALQLNNR	Complement C4-A	40.9	40.9	100%	4.00E-06	100%	POCOL4
	Complement C4-B	40.9	40.9	100%	4.00E-06	100%	POCOL5
GKSSSYSKQFTSSTSYNR	Fibrinogen alpha chain	57.9	73.4	100%	2.00E-11	100%	P02671

GLEEELQFSLGSK	Complement C4-A	42.6	53	100%	1.00E-06	100%	P0C0L4
	Complement C4-B	42.6	53	100%	1.00E-06	100%	P0C0L5
GLEEELQFSLGSKI	Complement C4-A	46	56.4	100%	1.00E-07	100%	P0C0L4
	Complement C4-B	46	56.4	100%	1.00E-07	100%	P0C0L5
GLPGPPDVPDHAAYHPFR	Inter-alpha-trypsin inhibitor heavy chain H4	62.1	62.1	100%	6.00E-13	100%	Q14624
GNTEGLQKSLAELGGHLDQQVEEFR	Apolipoprotein A-IV	80.8	146	100%	6.00E-19	100%	P06727
GSSGTGGTATWKPGSSGP	Fibrinogen alpha chain	55.4	177	100%	1.00E-10	100%	P02671
GSTGNRNPGSSGTGGTATWKPGS	Fibrinogen alpha chain	71	197	100%	1.00E-15	100%	P02671
GSTGNRNPGSSGTGGTATWKPGSSGP	Fibrinogen alpha chain	79.5	214	100%	2.00E-18	100%	P02671
HWESASLL	Complement C3	29.5	29.5	100%	0.015	100%	P01024
KVEQAVETEPEPELR	Apolipoprotein E	51.1	80	100%	2.00E-09	100%	P02649
LSALEEYTKKLNTQ	Apolipoprotein A-I	46.9	46.9	100%	5.00E-08	100%	P02647
MELERPGGNEIT	Fibrinogen alpha chain	42.6	55.1	100%	1.00E-06	100%	P02671
MEPLGRQLTSGP	Alpha-2-antiplasmin; Alpha-2-AP; Alpha-2-plasmin inhibitor; Alpha-2-PI; Serpin F2;	41.4	41.4	100%	3.00E-06	100%	P08697
MGVVSLGSPSGEVSHPRKT	Alpha-2-HS-glycoprotein	60.9	75.9	100%	2.00E-12	100%	P02765
NDNEEGFFSARGH	Fibrinogen beta chain	45.2	45.2	100%	2.00E-07	100%	P02675
NEPSILEMSR	Apolipoprotein L1	36.3	36.3	100%	1.00E-04	100%	O14791
NGFKSHALQLNNR	Complement C4-A	44.3	44.3	100%	3.00E-07	100%	P0C0L4
	Complement C4-B	44.3	44.3	100%	3.00E-07	100%	P0C0L5
NGFKSHALQLNNRQI	Complement C4-A	51.1	51.1	100%	2.00E-09	100%	P0C0L4
	Complement C4-B	51.1	51.1	100%	2.00E-09	100%	P0C0L5
NLAEFASLYR	Alpha-1-antitrypsin	38.8	38.8	100%	2.00E-05	100%	P01009
NQEQVSPLTLLKLG	Alpha-2-antiplasmin	49.4	59.4	100%	8.00E-09	100%	P08697
NRGDSTFESKSY	Fibrinogen alpha chain	40.9	68.9	100%	4.00E-06	100%	P02671
PAPPPISGGGYR	Fibrinogen beta chain	40.5	51.3	100%	5.00E-06	100%	P02675
PGSSGTGGTATWKPGSSGP	Fibrinogen alpha chain	58.7	214	100%	1.00E-11	100%	P02671

PNNPDWGTFFEEVSGNVSPGTR	Fibrinogen alpha chain	71	116	100%	9.00E-16	100%	P02671
QFTSSTSYNR	Fibrinogen alpha chain	35	50.5	100%	3.00E-04	100%	P02671
QLGLPGPPDVPDHAAYHPFR	Inter-alpha-trypsin inhibitor heavy chain H4	68.5	68.5	100%	6.00E-15	100%	Q14624
QVNTQAEQLR	Apolipoprotein A-IV	35	68.5	100%	3.00E-04	100%	P06727
RIHWESASLL	Complement C3	36.3	45.4	100%	1.00E-04	100%	P01024
RIHWESASLLR	Complement C3	39.7	49.2	100%	1.00E-05	100%	P01024
SEETKENEGFTVTAEGK	Complement C3	55.4	70.8	100%	1.00E-10	100%	P01024
SGEGDFLAEGGGVR	Fibrinogen alpha chain	44.3	73.2	100%	4.00E-07	100%	P02671
SHALQLNNR	Complement C4-A	31.6	31.6	100%	0.003	100%	P0COL4
	Complement C4-B	31.6	31.6	100%	0.003	100%	P0COL5
SKTVVLGLALRREGP	GRB2-associated and regulator of MAPK protein-like	47.7	47.7	100%	3.00E-08	100%	Q75VX8
SLAELGGHLDQQVEEFR	Apolipoprotein A-IV	56.6	124	100%	4.00E-11	100%	P06727
SNLDEDIIAEENIVSR	Complement C3	54.1	70	100%	3.00E-10	100%	P01024
SSAGSWNSGSSGPGSTGNR	Fibrinogen alpha chain	58.3	167	100%	1.00E-11	100%	P02671.2
SSSYSKQTSSTSYNR	Fibrinogen alpha chain	52.4	67.9	100%	1.00E-09	100%	P02671
SSYSKQTSSTSYNR	Fibrinogen alpha chain	49.8	65.3	100%	6.00E-09	100%	P02671
TEKLVTSKGDKELR	Fibrinogen alpha chain	45.6	45.6	100%	1.00E-07	100%	P02671
TPTLVEVSR	Serum albumin	30.8	30.8	100%	0.006	100%	P02768
TQVNTQAEQLR	Apolipoprotein A-IV	38	71.5	100%	3.00E-05	100%	P06727
TVGSLAGQLQER	Apolipoprotein E	42.2	42.2	100%	2.00E-06	100%	P02649
VNDNEEGFFSAR	Fibrinogen beta chain	41.8	41.8	100%	2.00E-06	100%	P02675
VTEPISAESGEQVER	Apolipoprotein L1	49.4	49.4	100%	8.00E-09	100%	O14791
YDTWKQSTQRL	Insulin-like growth factor II	40.9	40.9	100%	3.00E-06	100%	P01344
YESDVMGRGHA	Alpha-2-macroglobulin	39.2	39.2	100%	1.00E-05	100%	P01023

Supplementary Table 4. Endogenous peptides commonly identified in plasma samples (biological triplicate) collected in blood collection tube containing Gel EDTA

Peptide Sequence	Description	Max score	Total score	Query cover	E value	Ident	Accession
PNNPDWGTFFEEVSGNVSPGTR	Fibrinogen alpha chain	71	116	100%	9.00E-16	100%	P02671
ADSGEGDFLAEGGGVR	Fibrinogen alpha chain	50.3	80.8	100%	5.00E-09	100%	P02671
GLEEELQFSLGSK	Complement C4-A	42.6	53	100%	1.00E-06	100%	POCOL4
	Complement C4-B	42.6	53	100%	1.00E-06	100%	POCOL5
DSGEGDFLAEGGGVR	Fibrinogen alpha chain	47.7	78.3	100%	3.00E-08	100%	P02671
LLSPYSYSTTAVVTNPKE	Transthyretin	59.2	59.2	100%	4.00E-12	100%	P02766
ADSGEGDFLAEGGGVRGP	Fibrinogen alpha chain	56.2	86.7	100%	6.00E-11	100%	P02671
NDNEEGFFSARGH	Fibrinogen beta chain	45.2	45.2	100%	2.00E-07	100%	P02675
PGSSGTGGTATWKPGSSGP	Fibrinogen alpha chain	58.7	214	100%	1.00E-11	100%	P02671
NGFKSHALQLNNRQI	Complement C4-A	51.1	51.1	100%	2.00E-09	100%	POCOL4
	Complement C4-B	51.1	51.1	100%	2.00E-09	100%	POCOL5
NGFKSHALQLNNR	Complement C4-A	44.3	44.3	100%	3.00E-07	100%	POCOL4
	Complement C4-B	44.3	44.3	100%	3.00E-07	100%	POCOL5
NQEQVSPLTLLKLG	Alpha-2-antiplasmin	49.4	59.4	100%	8.00E-09	100%	P08697
GSTGNRNPSSGTGGTATWKPGSSGP	Fibrinogen alpha chain	79.5	214	100%	2.00E-18	100%	P02671
GFKSHALQLNNR	Complement C4-A	40.9	40.9	100%	4.00E	100	POCOL4

					-06	%	
	Complement C4-B	40.9	40.9	100%	4.00E-06	100%	P0C0L5
KVEQAVETEPEPELR	Apolipoprotein E	51.1	80	100%	2.00E-09	100%	P02649
SLAELGGHLDQQVEEFR	Apolipoprotein A-IV	56.6	124	100%	4.00E-11	100%	P06727
GLEELQFSLGSKINVK	Complement C4-A	55.4	65.8	100%	1.00E-10	100%	P0C0L4
	Complement C4-B	55.4	65.8	100%	1.00E-10	100%	P0C0L5
ADSGEGDFLAEGGGVRGPR	Fibrinogen alpha chain	59.6	100	100%	5.00E-12	100%	P02671
SKTVVLGLALRREGP	GRB2-associated and regulator of MAPK protein-like	47.7	47.7	100%	3.00E-08	100%	Q75VX8
HALQLNNRQI	Complement C4-A	35.8	35.8	100%	2.00E-04	100%	P0C0L4
	Complement C4-B	35.8	35.8	100%	2.00E-04	100%	P0C0L5
MEPLGRQLTSGP	Alpha-2-antiplasmin	41.4	41.4	100%	3.00E-06	100%	P08697
IHWESASLLR	Complement C3	36.3	45.8	100%	1.00E-04	100%	P01024
QLGLPGPPDVPDHAAYHPFR	Inter-alpha-trypsin inhibitor heavy chain H4	68.5	68.5	100%	6.00E-15	100%	Q14624
PGPPDVPDHAAYHPFR	Inter-alpha-trypsin inhibitor heavy chain H4	56.6	56.6	100%	4.00E-11	100%	Q14624
GLPGPPDVPDHAAYHPFR	Inter-alpha-trypsin inhibitor heavy chain H4	62.1	62.1	100%	6.00E-13	100%	Q14624
MGVSLGSPSGEVSHPRKT	Alpha-2-HS-glycoprotein	60.9	75.9	100%	2.00E-12	100%	P02765.1
SEETKENEGFTVTAEGK	Complement C3	55.4	70.8	100%	1.00E-10	100%	P01024
EHFQEVGYAAPPSPPLS	Extracellular matrix protein 1	57.5	73.4	100%	2.00E-11	100%	Q16610

NRGDSTFESKSYKMA	Fibrinogen alpha chain	51.1	79.1	100%	2.00E-09	100%	P02671
YDTWKQSTQRL	Insulin-like growth factor II	40.9	40.9	100%	3.00E-06	100%	P01344
FFQYDTWKQSTQRL	Insulin-like growth factor II	52	52	100%	8.00E-10	100%	P01344
NQEQVSPLTLK	Alpha-2-antiplasmin	40.5	40.5	100%	5.00E-06	100%	P08697
VVSLGSPSGEVSHPRKT	Alpha-2-HS-glycoprotein	53.7	68.7	100%	4.00E-10	100%	P02765
RIHWESASLL	Complement C3	36.3	45.4	100%	1.00E-04	100%	P01024
DVSLQLPSR	Complement C3	30.8	45.8	100%	0.007	100%	P01024

Supplementary Table 5. Endogenous peptides commonly identified in plasma samples (biological triplicate) collected in blood collection tube containing P100

Peptide Sequence	Description	Max score	Total score	Query cover	E value	Ident	Accession
ADSGEGDFLAEGGGVR	Fibrinogen alpha chain	50.3	80.8	100%	5.00E-09	100%	P02671
GLEEELQFSLGSK	Complement C4-A	42.6	53	100%	1.00E-06	100%	P0C0L4
	Complement C4-B	42.6	53	100%	1.00E-06	100%	P0C0L5
DSGEGDFLAEGGGVR	Fibrinogen alpha chain	47.7	78.3	100%	3.00E-08	100%	P02671
SGEGDFLAEGGGVR	Fibrinogen alpha chain	44.3	73.2	100%	4.00E-07	100%	P02671
ADSGEGDFLAEGGGVRGP	Fibrinogen alpha chain	56.2	86.7	100%	6.00E-11	100%	P02671
SEETKENEGFTVTAEGK	Complement C3	55.4	70.8	100%	1.00E	100	P01024

					-10	%	
NSPLDEENLTQENQDR	Alpha-1-antichymotrypsin	55.4	55.4	100%	9.00E-11	100%	P01011
NGFKSHALQLNNR	Complement C4-A	44.3	44.3	100%	3.00E-07	100%	P0C0L4
	Complement C4-B	44.3	44.3	100%	3.00E-07	100%	P0C0L5
GEGDFLAEGGGVR	Fibrinogen alpha chain	41.8	70.6	100%	2.00E-06	100%	P02671
NQEQVSPLTLLKLG	Alpha-2-antiplasmin	49.4	59.4	100%	8.00E-09	100%	P08697
PSSAGSWNSGSSGPGSTGNRN	Fibrinogen alpha chain	65.1	181	100%	9.00E-14	100%	P02671
KVEQAVETEPEPELR	Apolipoprotein E	51.1	80	100%	2.00E-09	100%	P02649
MEPLGRQLTSGP	Alpha-2-antiplasmin	41.4	41.4	100%	3.00E-06	100%	P08697
LSALEEYTKKLNTQ	Apolipoprotein A-I	46.9	46.9	100%	5.00E-08	100%	P02647
PGSSGTGGTATWKPGSSGP	Fibrinogen alpha chain	58.7	214	100%	1.00E-11	100%	P02671
VNDNEEGFFSAR	Fibrinogen beta chain	41.8	41.8	100%	2.00E-06	100%	P02675
GSTGNRNPSSGTGGTATWKPGSSGP	Fibrinogen alpha chain	79.5	214	100%	2.00E-18	100%	P02671
IHWESASLLR	Complement C3	36.3	45.8	100%	1.00E-04	100%	P01024