

Additional file 4. Detailed protein identifications of serum for the comparison of T12A, T12B and T12C vs T0. Spots with average ratios +/- 1.5 are indicated in bold. Spots are numbered according to Figure 5. Please note that spots that did not provide a valid protein identification by mass spectrometry are not reported.

Spot	T12A vs T0	T12B vs T0	T12C vs T0	P value	Protein Name	Species	Acc. No. ^a	MW ^b	pI ^c	Score ^d	%C ^e	UP ^f	P ^g
1	2.3			0.00016	Alpha 1 antitrypsin	<i>S. aurata</i>	Q4QY84	29.6	5.1	244.6	44.1	9	11
2	1.7			1.1E-06	Alpha 1 antitrypsin	<i>S. aurata</i>	Q4QY84	29.6	5.1	240.5	29.7	6	6
3		1.5		0.000011	Transferrin (fragments)	<i>S. aurata</i>	F2YLA1	74.2	6.3	225.2	11.6	4	4
4		1.9		0.00016	Fibrinogen beta chain	<i>L. crocea</i>	I3K9D6	57.8	7.7	396.1	16.4	2	10
5	1.8	2.0	1.3	0.000055	Fibrinogen beta chain	<i>G. aculeatus</i>	G3Q4A3	55.1	7.0	473.1	18.9	4	11
6	1.4		1.6	0.0081	Fibrinogen beta chain	<i>P. olivaceus</i>	A5JV29	55.7	6.9	95.4	6.7	2	4
7		1.5		0.0016	14 kDa apolipoprotein	<i>S. aurata</i>	Q4QY86	15.9	5.3	40.0	35.7	3	3
8	1.5	1.3	1.3	0.000088	14 kDa apolipoprotein	<i>S. aurata</i>	Q4QY86	15.9	5.3	63.6	11.9	2	2
9	1.5			0.00021	14 kDa apolipoprotein	<i>S. aurata</i>	Q4QY86	15.9	5.3	78.67	11.9	2	2

^aAccession number.

^bCalculated molecular weight of full-length protein in kDa.

^cTheoretical isoelectric point.

^dScore: probability score in Mascot program (the probability that the observed match between the experimental data and mass values calculated from a candidate peptide sequence is a random event).

^ePercent coverage: the minimum coverage of the matched peptide in relation to the full-length sequence.

^fUnique peptides

^gNumber of peptides