

Supplementary material

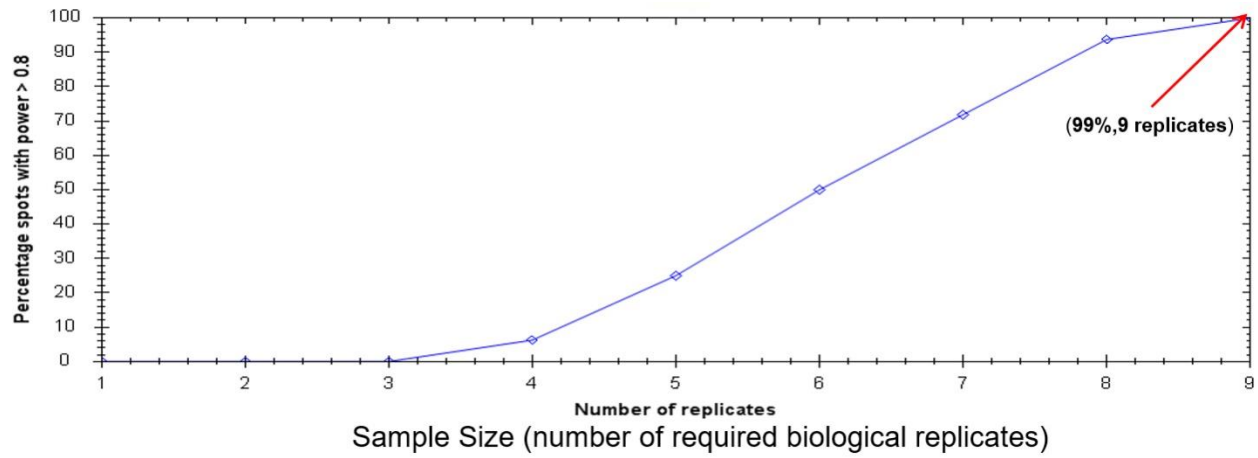


Figure S1: Power calculation for determination of the minimum number of required biological variants for 2-DIGE analysis. The power curve was used to calculate the sample size required to find significant difference with a fold-change of ≥ 1.5 between two paired groups at 98% power and $p\text{-value} \leq 0.05$.

Figure S2: The figure shows the different canonical pathways obtained from IPA functional analysis.

Top Canonical Pathways

Name	p-value	Overlap
Acute Phase Response Signaling	1.34E-06	2.8 % 5/179
LXR/RXR Activation	8.86E-06	3.3 % 4/121
FXR/RXR Activation	1.04E-05	3.2 % 4/126
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	1.12E-03	1.6 % 3/188
Clathrin-mediated Endocytosis Signaling	1.21E-03	1.6 % 3/193

Table S1: Experimental design: 18 samples run on 9 2D-PAGE gels, samples were labeled randomly with Cy3 and Cy5, and a pooled sample was used as an internal standard and was stained with Cy2

Cy2	Cy5	Cy3	Gel
Pooled sample	11 (hyperthyroid)	1 (Euthyroid)	1
Pooled sample	2 (Euthyroid)	12 (hyperthyroid)	2
Pooled sample	13 (hyperthyroid)	5 (Euthyroid)	3
Pooled sample	3 (Euthyroid)	14 (hyperthyroid)	4
Pooled sample	6 (Euthyroid)	16 (hyperthyroid)	5
Pooled sample	17 (hyperthyroid)	7 (Euthyroid)	6
Pooled sample	8 (Euthyroid)	18 (hyperthyroid)	7
Pooled sample	19 (hyperthyroid)	9 (Euthyroid)	8
Pooled sample	10 (Euthyroid)	20 (hyperthyroid)	9

Table S2: Mass spectrometry list of significant differentially abundant proteins between Hyper and Euth identified in urine samples, using 2D-DIGE with. Protein name, accession number, Mascot score, MS % coverage, protein MW and pI values according to Uniprot database are listed.

Sl no	SpotNo	Accession No ^a	Protein Name	MASCOT ID	Pi ^b	MW ^c	Cov%	Score ^d
1.	554	P02787	Serotransferrin	TRFE_HUMAN	6.81	74280	39	104
2.	871	P06702	Protein S100-A9	S10A9_HUMAN	5.71	13291	67	61
3.	933	P04217	Alpha-1B-glycoprotein	A1BG_HUMAN	5.58	54809	36	57
4.	227	P02768	Serum albumin	ALBU_HUMAN	5.92	71317	35	80
5.	210	Q6ZMW3	Echinoderm microtubule-associated protein-like 6	EMAL6_HUMAN	7.71	220270	14	62
6.	983	P02766	Transthyretin	TTHY_HUMAN	5.52	15991	59	60
7.	253	P01833	Polymeric immunoglobulin receptor	PIGR_HUMAN	5.58	84429	36	60
8.	237	P01833	Polymeric immunoglobulin receptor	PIGR_HUMAN	5.58	84429	31	82
9.	162	P03952	Plasma kallikrein	KLKB1_HUMAN	8.6	73433	17	63
10.	258	P04217	Alpha-1B-glycoprotein	A1BG_HUMAN	5.58	54809	36	57
11.	166	P00450	Ceruloplasmin	CERU_HUMAN	5.44	122983	14	58

12.	799	Q6U7Q0	Zinc finger protein 322	ZN322_HUMAN	8.98	48563	43	57
13.	163	Q96PF1	Protein-glutamine gamma-glutamyl transferase Z	TGM7_HUMAN	6.54	80575	16	63
14.	588	Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2_HUMAN	12.05	300179	14	82
15.	593	O00443	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha	P3C2A_HUMAN	8.25	192156	11	58
16.	318	P02768	Serum albumin	ALBU_HUMAN	5.92	71317	48	167
17.	618	Q15257	Serine/threonine-protein phosphatase 2A activator	PTPA_HUMAN	5.63	41098	26	57
18.	526	Q16769	Glutaminyl-peptide cyclotransferase	QPCT_HUMAN	6.12	40965	41	71
19.	215	Q6FIF0	AN1-type zinc finger protein 6	ZFAN6_HUMAN	6.87	23168	27	59
20.	266	Q92878	DNA repair protein RAD50	RAD50_HUMAN	6.48	154823	14	58
21.	584	Q9BUB4	tRNA-specific adenosine deaminase 1	ADAT1_HUMAN	9.20	56156	22	57
22.	882	P29508	SERPINB3	SPB3_HUMAN	6.35	44594	32	85
23.	765	Q9UKF7	Cytoplasmic phosphatidylinositol transfer protein 1	PITC1_HUMAN	5.99	38691	32	57
24.	902	Q16769	Glutaminyl-peptide cyclotransferase	QPCT_HUMAN	6.12	40965	44	80
25.	281	P01833	Polymeric immunoglobulin receptor	PIGR_HUMAN	5.58	84429	32	91
26.	998	Q8N3U1	Putative uncharacterized protein LOC400692	YS014_HUMAN	5.52	12915	46	64

27.	506	Q4V348	Zinc finger protein 658B	Z658B_HUMAN	8.9	97349	24	58
28.	655	O00560	Syntenin-1	SDCB1_HUMAN	7.05	32595	36	60
29.	1032	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	SH3L3_HUMAN	4.82	10488	81	78
30.	959	P13645	Keratin, type I cytoskeletal 10	K1C10_HUMAN	5.13	59020	26	72
31.	770	P01833	Polymeric immunoglobulin receptor	PIGR_HUMAN	5.58	84429	40	138
32.	498	P04746	Pancreatic alpha-amylase	AMYP_HUMAN	6.6	58354	55	99

^a Protein accession number for SWISSPROT Database.

^b Theoretical isoelectric point.

^c Theoretical relative mass.

^d MASCOT score