

Supplementary table 2: LFH compared to HFH,

log2-fold change &lt; 0 : more abundant in LFH; log2-fold change &gt; 0 : more abundant in HFH

t-test p-value	log2-fold change	Ratio	Uniprot Accession	Gene name	Protein name	Abundance
0.028	-1.40	0.38	Q865V6	CAPG	Macrophage-capping protein	medium
0.034	-1.16	0.45	E1BNY1	CDA	Cytidine deaminase	medium
0.046	-1.10	0.47	E1B8H8	SEC14L3	SEC14 like lipid binding 3	high
0.040	-1.03	0.49	Q9TS74	N/A	Pancreatic elastase inhibitor	high
0.001	-0.96	0.52	Q24K21	DPCD	Protein DPCD	medium
0.003	-0.90	0.53	A2VE99	SEPT11	Septin-11	medium
0.033	-0.88	0.54	Q0P5F2	PSMG1	Proteasome assembly chaperone 1	medium
0.027	-0.81	0.57	P68509	YWHAH	14-3-3 protein eta	high
0.013	-0.81	0.57	P61763	STXBP1	Syntaxin-binding protein 1	medium
0.025	-0.79	0.58	Q3ZC44	HNRNPA B	Heterogeneous nuclear ribonucleoprotein A/B	medium
0.024	-0.78	0.58	P08728	KRT19	Keratin, type I cytoskeletal 19	high
0.024	-0.77	0.58	Q2TBN3	CETN2	Centrin-2	medium
0.004	-0.76	0.59	P68250	YWHAB	14-3-3 protein beta/alpha	high
0.004	-0.74	0.60	A6H7E3	PDLIM1	PDZ and LIM domain 1	high
0.042	-0.73	0.60	P09867	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1	medium
0.015	-0.72	0.61	A5PK51	NAPRT	Nicotinate phosphoribosyltransferase	high
0.000	-0.67	0.63	Q3SZI4	YWHAQ	14-3-3 protein theta	high
0.007	-0.67	0.63	Q3SX14	GSN	Gelsolin	high
0.038	-0.67	0.63	Q3SYR7	RPL9	60S ribosomal protein L9	medium
0.031	-0.64	0.64	Q3ZBL4	LZTFL1	Leucine zipper transcription factor-like protein 1	high
0.009	-0.64	0.64	Q29RI6	CAB39	Calcium-binding protein 39	medium
0.031	-0.64	0.64	F1MYH8	PSMD8	26S proteasome non-ATPase regulatory subunit 8	medium
0.042	-0.62	0.65	A6H768	GALK1	Galactokinase	high
0.045	-0.61	0.66	P52556	BLVRB	Flavin reductase	high
0.008	-0.60	0.66	E1BF20	HNRNPH1	Heterogeneous nuclear ribonucleoprotein H	medium
0.032	0.60	1.52	P07107	DBI	Acyl-CoA-binding protein	high
0.010	0.62	1.54	A7E3S8	ST13	Heat shock 70kD protein binding protein	high
0.044	0.69	1.61	Q3T0F7	MTPN	Myotrophin	medium
0.017	0.69	1.61	F1N2I5	CMBL	Carboxymethylenebutenolidase homolog	medium
0.015	0.72	1.65	F1N3Y1	TCAF2	TRPM8 channel-associated factor 2	medium
0.026	0.74	1.68	A5D9F0	CAMK2D	Calcium/calmodulin-dependent protein kinase II delta	medium
0.020	0.95	1.93	Q5E984	TPT1	Translationally-controlled tumor protein	medium
0.024	0.99	1.98	P62964	CRABP1	Cellular retinoic acid-binding protein 1	medium
0.004	1.06	2.08	F1N549	DPYD	Dihydropyrimidine dehydrogenase [NADP(+)]	medium
0.012	1.10	2.15	F1MMK8	KARS	Lysine--tRNA ligase	medium
0.036	1.38	2.60	Q28042	OVGP1	Oviduct-specific glycoprotein	high
0.043	1.42	2.67	F2FB38	MUC16	Mucin-16	high

Supplementary table 3: LFH compared to MBD

log2-fold change &lt; 0 : more abundant in MBD; log2-fold change &gt; 0 : more abundant in LFH

t-test p-value	log2-fold change	Ratio	Uniprot Accession	Gene name	Protein name	Abundance
0.010	-3.57	0.08	B0JYQ0	ALB	ALB protein	high
0.027	-2.42	0.19	F1MLW7	LOC100297192	Uncharacterized protein; Immunoglobulin light chain, lambda gene cluster, Identity: 97 %	high
0.028	-2.10	0.23	G3N0S9	LOC515150	Uncharacterized protein; Apolipoprotein R, Identity: 100 %	medium
0.049	-2.09	0.24	A5D7Q2	N/A	Putative uncharacterized protein; IgM precursor, Identity: 100 %	high
0.016	-2.09	0.24	G5E604	N/A	Uncharacterized protein; Immunoglobulin light chain variable region, partial, Identity: 100 %	high
0.033	-1.96	0.26	V6F9A3	ApoC3	Apolipoprotein C-III	medium
0.022	-1.96	0.26	G3N0V0	N/A	Uncharacterized protein; Secreted immunoglobulin gamma2 heavy chain constant region, partial, Identity: 99 %	high
0.015	-1.84	0.28	F1MZ96	N/A	Uncharacterized protein; IGK protein, Identity: 98 %	high
0.025	-1.82	0.28	Q29437	N/A	Primary amine oxidase, liver isozyme	high
0.031	-1.77	0.29	Q5GN72	AGP	Alpha-1-acid glycoprotein	high
0.029	-1.59	0.33	A6QPP2	SERPIND1	SERPIND1 protein	high
0.021	-1.49	0.36	P02769	ALB	Serum albumin	high
0.050	-1.30	0.40	C7FE01	N/A	Lactoferrin	high
0.034	-1.26	0.42	Q2KIX7	N/A	Protein HP-25 homolog 1	high
0.037	-1.10	0.47	Q32KP2	LRRC23	Leucine-rich repeat-containing protein 23	medium
0.029	-1.00	0.50	P01045	KNG2	Kininogen-2	medium
0.048	-0.99	0.50	A1L5B6	ANXA5	Annexin	medium
0.010	-0.95	0.52	E1BJ08	LOC785216	Uncharacterized protein; Glutathione S-transferase omega-1 isoform X1, Identity: 100 %	medium
0.035	-0.93	0.53	Q9GLX9	SPON1	Spondin-1	medium
0.016	-0.89	0.54	E1BNY1	CDA	Cytidine deaminase	medium
0.045	-0.86	0.55	A6QP39	MSLN	MSLN protein	high
0.029	-0.74	0.60	Q58CQ2	ARPC1B	Actin-related protein 2/3 complex subunit 1B	medium
0.037	-0.68	0.63	Q9TS74	N/A	Pancreatic elastase inhibitor	high
0.043	0.61	1.52	Q862I1	RPL24	60S ribosomal protein L24	medium
0.048	0.63	1.55	Q32PF2	ACLY	ATP-citrate synthase	high
0.001	0.64	1.55	G5E5C8	TALDO1	Transaldolase	high
0.019	0.64	1.56	P68103	EEF1A1	Elongation factor 1-alpha 1	high
0.019	0.67	1.59	P80177	MIF	Macrophage migration inhibitory factor	high

0.049	0.68	1.60	Q09430	PFN2	Profilin-2	medium
0.006	0.69	1.61	F1N120	LXN	Latexin	medium
0.049	0.70	1.63	A4IF97	MYL12B	Myosin regulatory light chain 12B	high
0.015	0.71	1.64	Q3T057	RPL23	60S ribosomal protein L23	medium
0.001	0.72	1.65	Q3MHM5	TUBB4B	Tubulin beta-4B chain	high
0.037	0.73	1.66	Q5E995	RPS6	40S ribosomal protein S6	high
0.002	0.74	1.67	Q5E9F5	TAGLN2	Transgelin-2	high
0.016	0.75	1.68	Q862B7	N/A	Similar to ribosomal protein S14	medium
0.034	0.77	1.70	P15396	ENPP3	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3	medium
0.029	0.78	1.71	P19858	LDHA	L-lactate dehydrogenase A chain	high
0.012	0.80	1.75	Q3T108	PSMB4	Proteasome subunit beta type-4	medium
0.001	0.81	1.76	Q3T122	EIF3D	Eukaryotic translation initiation factor 3 subunit D	medium
0.038	0.82	1.77	Q3B7M5	LASP1	LIM and SH3 domain protein 1	high
0.039	0.84	1.78	A6H769	RPS7	40S ribosomal protein S7	medium
0.022	0.86	1.81	Q3MHN0	PSMB6	Proteasome subunit beta type-6	medium
0.044	0.90	1.87	Q3ZCC9	SEC13	Protein SEC13 homolog	medium
0.002	0.92	1.89	Q56JX6	RPS28	40S ribosomal protein S28	medium
0.003	0.95	1.93	P84080	ARF1	ADP-ribosylation factor 1	high
0.005	1.04	2.06	Q3T0U2	RPL14	60S ribosomal protein L14	medium
0.009	1.10	2.14	F1N549	DPYD	Dihydropyrimidine dehydrogenase [NADP(+)]	medium
0.037	1.14	2.21	Q0II59	PDXK	Pyridoxal kinase	high
0.001	1.26	2.39	A5PK63	RPS17	40S ribosomal protein S17	medium
0.021	1.36	2.57	Q2KJ93	CDC42	Cell division control protein 42 homolog	medium
0.035	2.01	4.01	F2FB38	MUC16	Mucin-16	high

Supplementary table 4: HFH compared to MBD,

log2-fold change &lt; 0 : more abundant in MBD; log2-fold change &gt; 0 : more abundant in HFH

t-test p-value	log2-fold change	Ratio	Uniprot Accession	Gene name	Protein name	Abundance
0.026	-1.70	0.31	Q2KIX7	N/A	Protein HP-25 homolog 1	high
0.037	-1.65	0.32	Q3ZCH5	AZGP1	Zinc-alpha-2-glycoprotein	high
0.020	-1.62	0.33	A6QPP2	SERPIND1	SERPIND1 protein	high
0.045	-1.56	0.34	P00978	AMBP	Protein AMBP	medium
0.046	-1.15	0.45	P02769	ALB	Serum albumin	high
0.049	-0.95	0.52	P12763	AHSG	Alpha-2-HS-glycoprotein	high
0.016	-0.89	0.54	Q3SZT5	RABL2B	RAB, member of RAS oncogene family-like 2B	low
0.004	-0.87	0.55	Q32PA9	FKBP2	Peptidyl-prolyl cis-trans isomerase FKBP2	medium
0.013	-0.85	0.56	A7E3Q8	PLS3	Plastin-3	medium
0.038	-0.83	0.56	Q32KP2	LRRC23	Leucine-rich repeat-containing protein 23	medium
0.000	-0.79	0.58	F1MIL9	GNE	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	medium
0.031	-0.73	0.60	F1N0V7	RPAP3	RNA polymerase II associated protein 3	medium
0.040	-0.73	0.60	A0A0A0M PA4	N/A	Uncharacterized protein; Ribosomal protein S25-like, Identity: 100 %	medium
0.013	-0.66	0.63	P07107	DBI	Acyl-CoA-binding protein	high
0.007	-0.64	0.64	Q3ZBM5	SNX5	Sorting nexin-5	medium
0.025	-0.64	0.64	P79342	S100A13	Protein S100-A13	medium
0.045	0.62	1.53	Q3SZK8	SLC9A3R1	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	high
0.018	0.64	1.56	Q2HJ60	HNRNPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	medium
0.010	0.66	1.58	P68250	YWHAB	14-3-3 protein beta/alpha	high
0.025	0.67	1.59	Q32KL2	PSMB5	Proteasome subunit beta type-5	high
0.009	0.67	1.60	P62261	YWHAE	14-3-3 protein epsilon	high
0.009	0.69	1.61	P68509	YWHAH	14-3-3 protein eta	high
0.042	0.71	1.63	A2VE99	SEPT11	Septin-11	medium
0.043	0.72	1.65	Q5E9F5	TAGLN2	Transgelin-2	high
0.040	0.74	1.67	Q3ZCF0	DCTN2	Dynactin subunit 2	medium
0.012	0.75	1.69	A6H7G2	DBNL	Drebrin-like protein	medium
0.017	0.76	1.70	Q3T0D0	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	high
0.042	0.77	1.70	Q58DQ3	RPL6	60S ribosomal protein L6	high
0.047	0.81	1.75	E1BND6	LRBA	LPS responsive beige-like anchor protein	high
0.022	0.83	1.78	Q3T0U2	RPL14	60S ribosomal protein L14	medium
0.021	0.87	1.82	Q56JV1	RPS26	40S ribosomal protein S26	medium
0.042	0.92	1.90	Q32PF2	ACLY	ATP-citrate synthase	high
0.036	0.94	1.91	P08728	KRT19	Keratin, type I cytoskeletal 19	high

0.038	0.97	1.96	Q0P5F2	PSMG1	Proteasome assembly chaperone 1	medium
0.046	1.00	2.00	Q862B7	N/A	Similar to ribosomal protein S14	medium
0.021	1.00	2.01	Q2TBN3	CETN2	Centrin-2	medium
0.026	1.02	2.03	Q861U5	N/A	Similar to 40S ribosomal protein S18	high
0.027	1.05	2.08	Q3SYR7	RPL9	60S ribosomal protein L9	medium
0.040	1.10	2.15	Q3B7M5	LASP1	LIM and SH3 domain protein 1	high
0.018	1.14	2.21	Q29S21	KRT7	Keratin, type II cytoskeletal 7	medium
0.043	1.17	2.25	G3N3D4	KCTD12	Potassium channel tetramerization domain containing 12	medium
0.007	1.22	2.33	P61763	STXBP1	Syntaxin-binding protein 1	medium
0.035	1.29	2.45	A6H769	RPS7	40S ribosomal protein S7	medium
0.018	1.39	2.63	Q0II59	PDXK	Pyridoxal kinase	high
0.044	1.42	2.68	Q56K04	CRIP1	Cysteine-rich protein 1	high
0.007	1.60	3.03	Q865V6	CAPG	Macrophage-capping protein	medium
0.011	2.33	5.04	Q2KJ93	CDC42	Cell division control protein 42 homolog	medium

Supplementary table 5: Lact compared to MH,

log2-fold change < 0 : more abundant in MH; log2-fold change > 0 : more abundant in Lact

t-test p-value	log2-fold change	Ratio	Uniprot Accession	Gene name	Protein name	Abundance
0.033	-1.12	0.46	Q58CV8	SULT1C2	Sulfotransferase	high
0.001	-1.01	0.49	F1N2W0	PTGR1	Prostaglandin reductase 1	high
0.018	-0.72	0.61	Q0VCC0	CAPS	Calcyphosin	high
0.010	-0.64	0.64	Q5E983	EEF1B	Elongation factor 1-beta	high
0.004	-0.61	0.65	F6QS88	EPHX2	Epoxide hydrolase 2	high
0.043	0.62	1.54	P21752	TMSB10	Thymosin beta-10	high
0.011	0.63	1.55	F1MYX5	LCP1	Lymphocyte cytosolic protein 1	high
0.048	0.65	1.57	P81644	APOA2	Apolipoprotein A-II	high
0.049	0.67	1.59	A7E307	DDX17	DDX17 protein	high
0.033	0.69	1.62	Q3T046	BDH2	3-hydroxybutyrate dehydrogenase type 2	medium
0.019	0.70	1.62	F1MVK1	N/A	Uncharacterized protein; Complement C4-like isoform X3 , Identity: 93 %	high
0.042	0.73	1.65	Q58CQ2	ARPC1B	Actin-related protein 2/3 complex subunit 1B	high
0.005	0.84	1.79	G3N1U4	SERPINA3-6	Serpin A3-6	high
0.029	0.88	1.83	Q8MJ50	OSTF1	Osteoclast-stimulating factor 1	medium
0.019	0.88	1.84	F1MUP9	VAT1	Vesicle amine transport 1	high
0.004	0.93	1.91	A6QPP2	SERPIND1	SERPIND1 protein	high
0.036	0.99	1.99	F1N3Q7	APOA4	Apolipoprotein A-IV	high
0.041	1.05	2.06	Q5GN72	AGP	Alpha-1-acid glycoprotein	high
0.013	1.08	2.11	P11116	LGALS1	Galectin-1	high

Supplementary table 6: Dry compared to MH,

log2-fold change < 0 : more abundant in MH; log2-fold change > 0 : more abundant in Dry

t-test p-value	log2-fold change	Ratio	Uniprot Accession	Gene name	Protein name	Abundance
0.014	-1.13	0.46	F1N036	DNAJC3	DnaJ homolog subfamily C member 3	high
0.014	-0.75	0.59	F1N2W0	PTGR1	Prostaglandin reductase 1	high
0.014	-0.63	0.65	Q5E983	EEF1B	Elongation factor 1-beta	high
0.034	-0.62	0.65	F6QS88	EPHX2	Epoxide hydrolase 2	high
0.005	-0.61	0.65	O77834	PRDX6	Peroxiredoxin-6	high
0.022	0.60	1.52	Q1RMX2	UBE2D2	Ubiquitin-conjugating enzyme E2 D2	high
0.046	0.63	1.55	E1BN47	CYFIP1	Cytoplasmic FMR1-interacting protein 1	high
0.027	0.65	1.56	F1MX83	S100A11	Protein S100	high
0.029	0.67	1.59	Q3SYU9	MVP	Major vault protein	high
0.007	0.67	1.59	Q3MHR7	ARPC2	Actin-related protein 2/3 complex subunit 2	high
0.044	0.98	1.97	F1MZ96	N/A	Uncharacterized protein; IGK protein, Identity: 98 %	high
0.013	1.20	2.30	F1MYN5	FBLN1	Fibulin-1	high
0.034	1.55	2.92	F1MD73	DMBT1	Uncharacterized protein; Deleted in malignant brain tumors 1 protein isoform X18, Identity: 82 %	high

Supplementary table 7: Lact compared to Dry,

log2-fold change < 0 : more abundant in Dry; log2-fold change > 0 : more abundant in Lact

<b>t-test p-value</b>	<b>log2-fold change</b>	<b>Ratio</b>	<b>Uniprot Accession</b>	<b>Gene name</b>	<b>Protein name</b>	<b>Abundance</b>
0.024	-1.15	0.45	Q58CV8	SULT1C2	Sulfotransferase	high
0.023	-1.11	0.46	Q29RU4	C6	Complement component C6	high
0.030	-1.04	0.48	Q28085	CFH	Complement factor H	high
0.041	-0.81	0.57	Q2KIV8	GSTM3	Glutathione S-transferase mu 3	high
0.048	-0.63	0.65	Q3SZE2	PFDN1	Prefoldin subunit 1	high
0.049	0.61	1.53	Q8MJ50	OSTF1	Osteoclast-stimulating factor 1	medium
0.020	0.68	1.60	A7E307	DDX17	DDX17 protein	high
0.016	0.89	1.86	F1MKS3	N/A	Thioredoxin domain-containing protein 5 precursor	high
0.040	1.02	2.02	Q2KJH6	SERPINH1	Serpin H1	high
0.027	1.28	2.44	Q3T083	SDF2L1	Stromal cell-derived factor 2-like protein 1	high
0.030	1.49	2.81	F1N036	DNAJC3	DnaJ homolog subfamily C member 3	high
0.019	1.62	3.07	A4IF88	RCN1	RCN1 protein	high