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Data from quantitative serum proteomic analysis after laparoscopic gastric plication

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Data Article

Data from quantitative serum proteomic analysis after laparoscopic gastric plication



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ABSTRACT

Bariatric surgery is an effective treatment for morbid obesity with a sustained weight loss and improvements in metabolic syndrome. We present a label free quantitative shotgun proteomics approach to analyze the serum proteome of obese people who underwent Laparoscopic Gastric Plication (LGP) as a new bariatric surgery. Pre-surgery serum samples of obese individuals were compared with the serum of the same subjects 1–2 months post-surgery (T1) and 4–5 months post-surgery (T2). The data provide a list of 224 quantifiable proteins with at least two unique peptides that were quantifiable in at least 70% of samples. Gene ontology biological processes and molecular functions of differentially regulated proteins between pre- and post-surgery samples were investigated using WebGestalt online tool. In addition, molecular networks of differentially abundant proteins were determined through Ingenuity Pathway Analysis (IPA) software. This report is related to the research article entitled “Serum proteome changes and accelerated reduction of fat mass after Laparoscopic Gastric Plication in morbidly obese patients” (Savedoroudi et al. [1]). Proteomics data have been deposited to the ProteomeXchange

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Consortium (<http://proteomecentral.proteomexchange.org>) via the PRIDE partner repository through the identifier PXD010528.

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Specifications Table

| | |
|----------------------------|--|
| Subject area | Biology |
| More specific subject area | Serum proteomic analysis of obese people undergoing Laparoscopic gastric plication as a relatively new bariatric surgical technique. |
| Type of data | Raw data, Tables and excel file |
| How data was acquired | Data was acquired by LC-MS/MS using a UPLC-nanoESI MS/MS setup with a NanoRSLC system (Dionex, CA, USA) coupled to a Q Exactive HF mass spectrometer (Thermo Scientific, Waltham, USA). The data was analyzed with MaxQuant (version 1.6.0.1). |
| Data format | Raw and analyzed data |
| Experimental factors | Human serum samples were analyzed pre-surgery and post-surgery. Initially, they were depleted of the six most abundant serum proteins. |
| Experimental features | Label-free quantitative proteomics approach was used to analyze the serum samples. Proteins were digested using filter aided sample preparation. LC-MS/MS was used to analyze the purified peptides. The raw-files were analyzed with MaxQuant software (version 1.6.0.1) against the Uniprot human reference FASTA database (August 2017) and processed with Perseus version 1.6.0.2. Biological process and molecular function of differentially regulated proteins were determined using WebGestalt online tool. Meanwhile, their molecular networks were identified by IPA software. |
| Data source location | Laboratory of Medical Mass Spectrometry, Department of Health Science and Technology, Aalborg University, Denmark. |
| Data accessibility | Data are available within this article and from ProteomeXchange Consortium (http://proteomecentral.proteomexchange.org) via the PRIDE partner repository with the dataset identifier PXD010528. |

Value of the data

- These data reveal the effect of laparoscopic gastric plication (LGP) on the proteome profile of obese people for the first time.
- Data in this article provide information about the biological processes, molecular functions and molecular networks of differentially regulated proteins between pre- and post-surgery subjects.
- These findings provide new insight into the underlying molecular mechanism associated with laparoscopic gastric plication that could be useful for further study in development of non-surgical weight loss strategies.

1. Data

This report is associated with the research article aimed at investigating the effect of weight loss due to laparoscopic gastric plication (LGP) as a new bariatric surgical procedure on the human serum proteome [1]. A total of 288 proteins was identified using a shotgun label-free proteomics experiment, of which 224 proteins were quantifiable with at least two unique peptides in 70% of samples or more (Supplementary Table 1). The raw mass data have been deposited to the ProteomeXchange Consortium (<http://proteomecentral.proteomexchange.org>) via the PRIDE partner repository [2] with the dataset identifier PXD010528. The list of submitted proteomics raw-files into the ProteomeXchange and corresponding sample names are shown in Table 1. Significantly regulated proteins between pre- and post-surgery samples were discussed in detail in Savedoroudi et al. [1]. Gene ontology enrichment analysis for biological process and molecular function of differentially regulated proteins at T1 and T2 are represented in Table 2 and Table 3, respectively. In Table 4, molecular networks of differentially regulated proteins are shown.

Table 1

Description of file-names and MaxQuant output in the ProteomeXchange repository PXD010528. MS files were analyzed in MaxQuant. All samples were analyzed in triplicates. Timepoint 1: 1–2 months post-surgery; Timepoint 2: 4–5 months post-surgery.

| Raw file | Sample | MS system |
|----------------------|--------------------------------|---------------|
| 2bef-1 | 2/Before surgery | Q Exactive HF |
| 2bef-2 | 2/Before surgery | Q Exactive HF |
| 2bef-3 | 2/Before surgery | Q Exactive HF |
| 2aft1-1 | 2/After surgery at timepoint 1 | Q Exactive HF |
| 2aft1-2 | 2/After surgery at timepoint 1 | Q Exactive HF |
| 2aft1-3 | 2/After surgery at timepoint 1 | Q Exactive HF |
| 3bef-1 | 3/Before surgery | Q Exactive HF |
| 3bef-2 | 3/Before surgery | Q Exactive HF |
| 3bef-3 | 3/Before surgery | Q Exactive HF |
| 3aft1-1 | 3/After surgery at timepoint 1 | Q Exactive HF |
| 3aft1-2 | 3/After surgery at timepoint 1 | Q Exactive HF |
| 3aft1-3_170725101835 | 3/After surgery at timepoint 1 | Q Exactive HF |
| 3aft2-1 | 3/After surgery at timepoint 2 | Q Exactive HF |
| 3aft2-2 | 3/After surgery at timepoint 2 | Q Exactive HF |
| 3aft2-3 | 3/After surgery at timepoint 2 | Q Exactive HF |
| 4bef-1 | 4/Before surgery | Q Exactive HF |
| 4bef-2 | 4/Before surgery | Q Exactive HF |
| 4bef-3 | 4/Before surgery | Q Exactive HF |
| 4aft1-1 | 4/After surgery at timepoint 1 | Q Exactive HF |
| 4aft1-2 | 4/After surgery at timepoint 1 | Q Exactive HF |
| 4aft1-3 | 4/After surgery at timepoint 1 | Q Exactive HF |
| 5bef-1 | 5/Before surgery | Q Exactive HF |
| 5bef-2 | 5/Before surgery | Q Exactive HF |
| 5bef-3 | 5/Before surgery | Q Exactive HF |
| 5aft1-1 | 5/After surgery at timepoint 1 | Q Exactive HF |
| 5aft1-2 | 5/After surgery at timepoint 1 | Q Exactive HF |
| 5aft1-3 | 5/After surgery at timepoint 1 | Q Exactive HF |
| 5aft2-1 | 5/After surgery at timepoint 2 | Q Exactive HF |
| 5aft2-2 | 5/After surgery at timepoint 2 | Q Exactive HF |
| 5aft2-3 | 5/After surgery at timepoint 2 | Q Exactive HF |
| 6bef-1 | 6/Before surgery | Q Exactive HF |
| 6bef-2 | 6/Before surgery | Q Exactive HF |
| 6bef-3 | 6/Before surgery | Q Exactive HF |
| 6aft1-1 | 6/After surgery at timepoint 1 | Q Exactive HF |
| 6aft1-2 | 6/After surgery at timepoint 1 | Q Exactive HF |
| 6aft1-3 | 6/After surgery at timepoint 1 | Q Exactive HF |
| 6aft2-1 | 6/After surgery at timepoint 2 | Q Exactive HF |
| 6aft2-2 | 6/After surgery at timepoint 2 | Q Exactive HF |
| 6aft2-3 | 6/After surgery at timepoint 2 | Q Exactive HF |
| 7bef-1 | 7/Before surgery | Q Exactive HF |
| 7bef-2 | 7/Before surgery | Q Exactive HF |
| 7bef-3 | 7/Before surgery | Q Exactive HF |
| 7aft1-1 | 7/After surgery at timepoint 1 | Q Exactive HF |
| 7aft1-2 | 7/After surgery at timepoint 1 | Q Exactive HF |
| 7aft1-3 | 7/After surgery at timepoint 1 | Q Exactive HF |
| 7aft2-1 | 7/After surgery at timepoint 2 | Q Exactive HF |
| 7aft2-2 | 7/After surgery at timepoint 2 | Q Exactive HF |
| 7aft2-3 | 7/After surgery at timepoint 2 | Q Exactive HF |
| 8bef-1 | 8/Before surgery | Q Exactive HF |
| 8bef-2 | 8/Before surgery | Q Exactive HF |
| 8bef-3 | 8/Before surgery | Q Exactive HF |
| 8aft1-1 | 8/After surgery at timepoint 1 | Q Exactive HF |
| 8aft1-2 | 8/After surgery at timepoint 1 | Q Exactive HF |
| 8aft1-3_170725085836 | 8/After surgery at timepoint 1 | Q Exactive HF |
| 8aft2-1 | 8/After surgery at timepoint 2 | Q Exactive HF |
| 8aft2-2 | 8/After surgery at timepoint 2 | Q Exactive HF |
| 8aft2-3 | 8/After surgery at timepoint 2 | Q Exactive HF |
| 9bef-1 | 9/Before surgery | Q Exactive HF |

(continued on next page)

Table 1 (continued)

| Raw file | Sample | MS system |
|----------|---------------------------------|---------------|
| 9bef-2 | 9/Before surgery | Q Exactive HF |
| 9bef-3 | 9/Before surgery | Q Exactive HF |
| 9aft1-1 | 9/After surgery at timepoint 1 | Q Exactive HF |
| 9aft1-2 | 9/After surgery at timepoint 1 | Q Exactive HF |
| 9aft1-3 | 9/After surgery at timepoint 1 | Q Exactive HF |
| 10bef-1 | 10/Before surgery | Q Exactive HF |
| 10bef-2 | 10/Before surgery | Q Exactive HF |
| 10bef-3 | 10/Before surgery | Q Exactive HF |
| 10aft1-1 | 10/After surgery at timepoint 1 | Q Exactive HF |
| 10aft1-2 | 10/After surgery at timepoint 1 | Q Exactive HF |
| 10aft1-3 | 10/After surgery at timepoint 1 | Q Exactive HF |
| 10aft2-1 | 10/After surgery at timepoint 2 | Q Exactive HF |
| 10aft2-2 | 10/After surgery at timepoint 2 | Q Exactive HF |
| 10aft2-3 | 10/After surgery at timepoint 2 | Q Exactive HF |
| 11bef-1 | 11/Before surgery | Q Exactive HF |
| 11bef-2 | 11/Before surgery | Q Exactive HF |
| 11bef-3 | 11/Before surgery | Q Exactive HF |
| 11aft1-1 | 11/After surgery at timepoint 1 | Q Exactive HF |
| 11aft1-2 | 11/After surgery at timepoint 1 | Q Exactive HF |
| 11aft1-3 | 11/After surgery at timepoint 1 | Q Exactive HF |
| 11aft2-1 | 11/After surgery at timepoint 2 | Q Exactive HF |
| 11aft2-2 | 11/After surgery at timepoint 2 | Q Exactive HF |
| 11aft2-3 | 11/After surgery at timepoint 2 | Q Exactive HF |
| 12bef-1 | 12/Before surgery | Q Exactive HF |
| 12bef-2 | 12/Before surgery | Q Exactive HF |
| 12bef-3 | 12/Before surgery | Q Exactive HF |
| 12aft1-1 | 12/After surgery at timepoint 1 | Q Exactive HF |
| 12aft1-2 | 12/After surgery at timepoint 1 | Q Exactive HF |
| 12aft1-3 | 12/After surgery at timepoint 1 | Q Exactive HF |
| 14bef-1 | 14/Before surgery | Q Exactive HF |
| 14bef-2 | 14/Before surgery | Q Exactive HF |
| 14bef-3 | 14/Before surgery | Q Exactive HF |
| 14aft1-1 | 14/After surgery at timepoint 1 | Q Exactive HF |
| 14aft1-2 | 14/After surgery at timepoint 1 | Q Exactive HF |
| 14aft1-3 | 14/After surgery at timepoint 1 | Q Exactive HF |
| 14aft2-1 | 14/After surgery at timepoint 2 | Q Exactive HF |
| 14aft2-2 | 14/After surgery at timepoint 2 | Q Exactive HF |
| 14aft2-3 | 14/After surgery at timepoint 2 | Q Exactive HF |
| 15bef-1 | 15/Before surgery | Q Exactive HF |
| 15bef-2 | 15/Before surgery | Q Exactive HF |
| 15bef-3 | 15/Before surgery | Q Exactive HF |
| 15aft1-1 | 15/After surgery at timepoint 1 | Q Exactive HF |
| 15aft1-2 | 15/After surgery at timepoint 1 | Q Exactive HF |
| 15aft1-3 | 15/After surgery at timepoint 1 | Q Exactive HF |
| 17bef-1 | 17/Before surgery | Q Exactive HF |
| 17bef-2 | 17/Before surgery | Q Exactive HF |
| 17bef-3 | 17/Before surgery | Q Exactive HF |
| 17aft1-1 | 17/After surgery at timepoint 1 | Q Exactive HF |
| 17aft1-2 | 17/After surgery at timepoint 1 | Q Exactive HF |
| 17aft1-3 | 17/After surgery at timepoint 1 | Q Exactive HF |
| 17aft2-1 | 17/After surgery at timepoint 2 | Q Exactive HF |
| 17aft2-2 | 17/After surgery at timepoint 2 | Q Exactive HF |
| 17aft2-3 | 17/After surgery at timepoint 2 | Q Exactive HF |
| 18bef-1 | 18/Before surgery | Q Exactive HF |
| 18bef-2 | 18/Before surgery | Q Exactive HF |
| 18bef-3 | 18/Before surgery | Q Exactive HF |
| 18aft1-1 | 18/After surgery at timepoint 1 | Q Exactive HF |
| 18aft1-2 | 18/After surgery at timepoint 1 | Q Exactive HF |
| 18aft1-3 | 18/After surgery at timepoint 1 | Q Exactive HF |
| 21bef-1 | 21/Before surgery | Q Exactive HF |
| 21bef-2 | 21/Before surgery | Q Exactive HF |
| 21bef-3 | 21/Before surgery | Q Exactive HF |

Table 1 (continued)

| Raw file | Sample | MS system |
|--|---|---------------|
| 21aft1-1 | 21/After surgery at timepoint 1 | Q Exactive HF |
| 21aft1-2 | 21/After surgery at timepoint 1 | Q Exactive HF |
| 21aft1-3 | 21/After surgery at timepoint 1 | Q Exactive HF |
| The MaxQuant output in folder "txt" contains a range of files containing important search information. Below file was used for further processing in Perseus post-analysis program and quantitative analysis. | | |
| proteinGroups.txt | File containing all proteins with corresponding label free quantitative information | |

2. Experimental design, materials and methods

2.1. Study cohort and sample treatment

A total of 16 obese subjects undergoing LGP was investigated at three timepoints; pre-surgery (n = 16), at 1–2 months post-surgery (T1, n = 16), at 4–5 months post-surgery (T2, n = 9). The detailed characteristics of patients were mentioned in SAVEDOROU DI ET AL. [1]. The six most abundant serum proteins (albumin, IgG, IgA, antitrypsin, transferrin and haptoglobin) were depleted in the serum samples using the Agilent Multiple Affinity Removal column (4.6 × 50 mm) according to the instructions recommended by the manufacturers (Agilent Technologies, CA, USA). Then, the filter-aided sample preparation (FASP) protocol was utilized to prepare samples as described previously [1,3]. Written consent was obtained from all participants and the institutional review board and the

Table 2

Enrichment analysis of Gene ontology biological process and molecular function for differentially abundant proteins at T1, using WebGestalt online tool.

| Gen set | Description | P-value | Overlap Gen-ID |
|---------------------------|--|----------|--|
| Biological Process | | | |
| GO:0051223 | regulation of protein transport | 4.87E-05 | CRP, GPLD1, APOA1, APOA2, APOD, IL1RAP, LCP1, SRGN, RBP4, SAA1, CD14, ADIPOQ |
| GO:0070201 | regulation of establishment of protein localization | 8.84E-05 | CRP, GPLD1, APOA1, APOA2, APOD, IL1RAP, LCP1, SRGN, RBP4, SAA1, CD14, ADIPOQ |
| GO:0034284 | response to monosaccharide | 0.000109 | GPLD1, APOA2, SERPINF1, APOM, SPARC, THBS1, ADIPOQ |
| GO:0032880 | regulation of protein localization | 0.000256 | CRP, GPLD1, APOA1, APOA2, APOD, IL1RAP, LCP1, SRGN, RBP4, SAA1, CD14, ADIPOQ |
| GO:0009743 | response to carbohydrate | 0.000315 | GPLD1, APOA2, SERPINF1, APOM, SPARC, THBS1, ADIPOQ |
| GO:0009746 | response to hexose | 0.000532 | GPLD1, APOA2, SERPINF1, APOM, THBS1, ADIPOQ |
| GO:0009749 | response to glucose | 0.000532 | GPLD1, APOA2, SERPINF1, APOM, THBS1, ADIPOQ |
| GO:0050707 | regulation of cytokine secretion | 0.000746 | CRP, APOA1, APOA2, IL1RAP, SRGN, SAA1, CD14 |
| GO:0051224 | negative regulation of protein transport | 0.00081 | APOA1, APOA2, APOD, SRGN, ADIPOQ |
| GO:1904950 | negative regulation of establishment of protein localization | 0.00081 | APOA1, APOA2, APOD, SRGN, ADIPOQ |
| Molecular Function | | | |
| GO:0005319 | lipid transporter activity | 0.00279 | APOF, APOA1, APOA2, APOD, APOM, RBP4 |
| GO:0005496 | steroid binding | 0.00279 | GC, APOF, APOA1, APOA2, APOD, SHBG |
| GO:0071813 | lipoprotein particle binding | 0.0101 | CRP, APOA1, APOA2, THBS1 |
| GO:0071814 | protein-lipid complex binding | 0.0101 | CRP, APOA1, APOA2, THBS1 |
| GO:0043178 | alcohol binding | 0.0105 | APOF, APOA1, APOA2, APOD, RBP4 |
| GO:0008289 | lipid binding | 0.0122 | F10, GC, APOF, APOA1, APOA2, APOD, APOM, RBP4, SHBG, THBS1, CD14 |
| GO:0005215 | transporter activity | 0.0128 | GC, HBB, APOF, APOA1, APOA2, APOD, APOM, RBP4 |
| GO:0022892 | substrate-specific transporter activity | 0.0170 | HBB, APOF, APOA1, APOA2, APOD, APOM, RBP4 |
| GO:0015485 | cholesterol binding | 0.0206 | APOF, APOA1, APOA2, APOD |
| GO:0032934 | sterol binding | 0.0206 | APOF, APOA1, APOA2, APOD |

Table 3

Enrichment analysis of Gene ontology biological process and molecular function for differentially abundant proteins at T2, using WebGestalt online tool.

| Gen set | Description | P-value | Overlap Gen-ID |
|---------------------------|---|----------|--------------------|
| Biological Process | | | |
| GO:0010976 | positive regulation of neuron projection development | 0.000151 | FN1, IL1RAP, NRP1 |
| GO:0045666 | positive regulation of neuron differentiation | 0.000151 | FN1, IL1RAP, NRP1 |
| GO:0050769 | positive regulation of neurogenesis | 0.000151 | FN1, IL1RAP, NRP1 |
| GO:0051962 | positive regulation of nervous system development | 0.000151 | FN1, IL1RAP, NRP1 |
| GO:0010975 | regulation of neuron projection development | 0.000262 | FN1, IL1RAP, NRP1 |
| GO:0031346 | positive regulation of cell projection organization | 0.000416 | FN1, IL1RAP, NRP1 |
| GO:0045664 | regulation of neuron differentiation | 0.000416 | FN1, IL1RAP, NRP1 |
| GO:0050767 | regulation of neurogenesis | 0.000618 | FN1, IL1RAP, NRP1 |
| GO:0051960 | regulation of nervous system development | 0.000618 | FN1, IL1RAP, NRP1 |
| GO:0031344 | regulation of cell projection organization | 0.00119 | FN1, IL1RAP, NRP1 |
| Molecular Function | | | |
| GO:0004888 | transmembrane signaling receptor activity | 0.0226 | IL1RAP, NRP1 |
| GO:0099600 | transmembrane receptor activity | 0.0226 | IL1RAP, NRP1 |
| GO:0004872 | receptor activity | 0.0304 | PRG4, IL1RAP, NRP1 |
| GO:0060089 | molecular transducer activity | 0.0304 | PRG4, IL1RAP, NRP1 |
| GO:0038023 | signaling receptor activity | 0.0336 | IL1RAP, NRP1 |
| GO:0004871 | signal transducer activity | 0.0533 | IL1RAP, NRP1 |
| GO:0016301 | kinase activity | 0.135 | NRP1 |
| GO:0016504 | peptidase activator activity | 0.135 | FN1 |
| GO:0016772 | transferase activity, transferring phosphorus-containing groups | 0.135 | NRP1 |
| GO:0016773 | phosphotransferase activity, alcohol group as acceptor | 0.135 | NRP1 |

ethic committee of Shahid Beheshti University approved the study protocol for Human rights (IR.S-BU.ICBS.97/1019).

2.2. LC-MS/MS analysis

Initially, the peptides were resuspended in 2% acetonitrile, 0.1% FA and 0.1% trifluoroacetic acid. LC-MS/MS analysis was carried out on a UPLC-nanoESI MS/MS setup with a Dionex RSLC nanopump (Dionex, CA, USA). The system was coupled online with an emitter for nanospray ionization (New objective picotip 360-20-10) to a Q Exactive HF mass spectrometer (Thermo Scientific, Waltham, USA). The samples were analyzed in a random order, in triplicates. The peptide material was loaded onto a 2cm C18 trapping column (Dionex Acclaim PepMap RSLC C18) and separated using a 75cm C18 reversed-phase column (Dionex Acclaim PepMap RSLC C18). Both columns were kept at 60 °C. The peptides were eluted with a gradient of 98% solvent A (0.1% FA) and 2% solvent B (0.1% FA in acetonitrile), which was increased to 8% solvent B on a 5-min ramp gradient and subsequently to 30% solvent B on a 45-min ramp gradient, at a constant flow rate of 300nL/min. The mass spectrometer was operated in positive mode using a Top15 data-dependent MS/MS scan method. A full MS scan in the 375–1500 m/z range was acquired at a resolution of 120 000 with an AGC target of 3×10^6 and a maximum injection time of 50 ms. Fragmentation of precursor ions was performed by higher-energy C-trap dissociation with a normalized collision energy of 27. MS/MS scans were acquired at a resolution of 15000 with an AGC target of 2×10^5 ; maximum injection time was 100 ms. Dynamic exclusion was set to 5s.

2.3. Data analysis and processing

Mass spectrometry data were analyzed in MaxQuant version 1.6.0.1 and searched against the Uniprot human reference FASTA database (August 2017) [4,5]. Label-free protein quantitation (LFQ) algorithm was performed with a minimum ratio count of 1. Standard settings in MaxQuant were employed, including carbamidomethylation of cysteines as a fixed modification, and acetylation of protein N-terminals, oxidation of methionine, and deamidation of asparagine and glutamine as

Table 4
Networks identified using IPA.

| Top Diseases and Functions | Score | Focus Molecules | Molecules in Network |
|---|-------|-----------------|---|
| T1 Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry | 45 | 19 | Adipokine, ADIPOQ, APCS, APOA1, APOA2, APOA4, APOD, APOF, APOM, C1q, C4BP, C4BPA, Collagen type II, CRP, ERK1/2, F10, Fibrinogen, GC, GPLD1, Growth hormone, HDL, HDL-cholesterol, Histone h4, IL12 (complex), LDL, NADPH oxidase, Pro-inflammatory Cytokine, RARRES2, Rbp, RBP4, SAA1, SERPINF1, SERPINF2, Sod, TTR |
| Cardiovascular System Development and Function, Cellular Movement, Cell-To-Cell Signaling and Interaction | 28 | 13 | Akt, Ap1, collagen, Collagen Alpha1, Collagen type I, Collagen type IV, Collagen type VI, Collagen(s), DBH, DSG2, elastase, Fc gamma receptor, GP1BA, Gp2b3a Receptor, IL1, IL-1R, IL1RAP, Integrin, Iti, ITIH2, ITIH3, Laminin (complex), LCP1, Mek, Mmp, MMP9, p85 (pik3r), Pdgf (complex), PDGF BB, PEPD, SPARC, SRGN, Tgf beta, THBS1, VWF |
| Cellular Assembly and Organization, Nervous System Development and Function, Cell-To-Cell Signaling and Interaction | 18 | 9 | CD14, CFP, Cg, Creb, CRTAC1, ERK, estrogen receptor, F7, FAH, GOT, HBB, HISTONE, Histone h3, Ifn, IFN Beta, Ige, IgG, IgG1, IL12 (family), Immunoglobulin, Insulin, Mapk, NFkB (complex), NRP1, P38 MAPK, PI3K (complex), Pka, PRG4, Rac, RNA polymerase II, SHBG, SRC (family), TCF, Tnf (family), Vegf |
| Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking | 15 | 8 | ACTG2, Actin, APCS, APP, C7, CASP8, caspase, CCL17, CD3, CFI, CLEC10A, CNDP1, CTF1, CYTIP, Ddx3x, DEFA6, Dstn/Dstn1, FETUB, Granzyme, HBG1, IL13, IL10RB, Jnk, LIPA, LRP1, MMRN1, MT1G, PZP, Ras, S100A12, SCAVENGER receptor CLASS A, Sos, SRGN, TCR, ZFP36L1 |
| Inflammatory Response, Infectious Diseases, Inflammatory Disease | 5 | 3 | ADIPOR2, APCS, BBS12, CD163, CD276, CLEC10A, CMKLR1, coagulation factor, CYP19, CYTIP, estrone, FBXO42, Fcgr2, FSH, glycosylphosphatidylinositol, GPER1, GPR119, HFE, IL6, IL17B, IL1RL2, LPAR2, N-cor, NfkB1 RelA, PAX8, Proinsulin, RARRES2, S100A12, SCAVENGER receptor CLASS A, SCN9A, SELENOS, SHBG, SMPDL3A, Timp, TNF |
| T2 Cell-To-Cell Signaling and Interaction, Cell Death and Survival, Inflammatory Response | 21 | 7 | Akt, ANGPTL1, B4GALT5, C4BPB, CHST3, CLEC10A, Collagen type VI, CRP, Enolase, ERK, ERK1/2, EXT1, Fc gamma receptor, Fc receptor, FCER1A, FCN1, FN1, GFRA2, HS6ST1, IL1, IL6, IL1RAP, ITIH3, miR-191-5p (and other miRNAs w/seed AACGGAA), NFkB (complex), NfkB1-RelA, NRP1, PRG4, PRSS38, pyridoxamine, S100A12, SEMA3D, SHBG, Stat3-Stat3, TGFBI |

variable modifications. A maximum of two tryptic missed cleavages was allowed. The false discovery rate (FDR) of identified proteins and peptides was set to a maximum of 1%, using a target-decoy fragment spectra search strategy. Hereby, high confidence identifications were ensured. The “match between runs” feature was enabled to transfer peptide identifications across LC-MS/MS runs, based on accurate retention time and mass-to-charge. The output from MaxQuant, containing the list of proteins identified below 1% FDR, was further filtered and processed in Perseus version 1.6.0.2 [6]. All reverse hits and proteins identified only by site were removed from further analysis, and the data were log 2-transformed. At least two unique peptides were required for a protein quantitation. Additionally, the unique peptides were required to be quantifiable in at least 70% of samples.

2.4. Bioinformatics analysis

Differentially regulated proteins between pre- and post-surgery subjects were functionally categorized based on gene ontology (GO) classification using WEB-based GENE SeT Analysis Toolkit (WebGestalt) [7]. Identification of networks was performed with Ingenuity Pathway Analysis software (IPA; Ingenuity Systems, Redwood City, CA, www.ingenuity.com). Gene symbols and the corresponding protein fold change were imported to IPA software using core analysis. Standard settings in IPA were employed, including: direct and indirect relationships between focused molecules with default settings of 35 molecules/network, based on experimentally observed data (high confidence

predictions and moderate confidence interactions excluded) were considered. All sources of data from human, mouse and rat studies in the Ingenuity Knowledge Base were included.

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Conflict of interest

There is no conflict of interest.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.dib.2019.104077>.

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