Figure S1: OSGEP Protein 3D Model.
**Figure S2:** PCA plot of the two first principal components. Both together explained 84.2% of the selected spot’s variability. Colored dots and numbers are the representation of gels and spots, respectively.
**Figure S3:** Expression profiles, separated into clusters of expression patterns, indicating the number of spots for each cluster. Each line represents the standardized abundance of a spot across all gels and belongs to one of the clusters generated by hierarchical cluster analysis. The spots with increased abundance indicate the 40 proteins up-regulated in GAMOS patient (Figure 7 B). The spots with decreased abundance indicate the 67 proteins down regulated in GAMOS patient (Figure 7 A) (Progenesis Same Spots).
**Figure S4**: Top Canonical Pathways:

| Name                                                                 | p-value     | Overlap |
|---------------------------------------------------------------------|-------------|---------|
| RhoA Signaling                                                      | 6.57E-05    | 4.1 %   |
| Remodeling of Epithelial Adherens Junctions                        | 8.83E-05    | 5.9 %   |
| Death Receptor Signaling                                           | 2.73E-04    | 4.4 %   |
| Regulation of Actin-based Motility by Rho                          | 3.09E-04    | 4.3 %   |
| Nitric Oxide Signaling in the Cardiovascular System                | 3.77E-04    | 4.0 %   |

**Top Networks**

| ID | Associated Network Functions                                                                 | Score |
|----|-----------------------------------------------------------------------------------------------|-------|
| 1  | Cellular Assembly and Organization, Cellular Function and Maintenance, Tissue Development    | 53    |
| 2  | Cancer, Gastrointestinal Disease, Hepatic System Disease                                       | 33    |
| 3  | Cancer, Gastrointestinal Disease, Hepatic System Disease                                       | 26    |
| 4  | Cancer, Neurological Disease, Organismal Injury and Abnormalities                              | 18    |
Figure S5: A comparative depiction (%) of identified proteins categorized into groups according to their biological Function A, Location B generated using PANTHER (protein analysis through evolutionary relationships) classification system (http://www.pantherdb.org/).
**Figure S6:** Top pathways of genes of the downregulated proteins.

**Figure S7:** Top pathways of genes of the upregulated proteins.
**Figure S7:** Protein Sequence Alignment.

**Table S1:** Experimental design: 6 samples run on 3-2D 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 (C: Control samples, G: GAMOS patient G1-G3 triplicates).

| Gel number | Cy3   | Cy5   | Cy2                |
|------------|-------|-------|--------------------|
| G1         | C1    | G1    | Pooled Sample      |
| G2         | G2    | C2    | Pooled Sample      |
| G3         | C3    | G3    | Pooled Sample      |
Table S2: Mass spectrometry list of significant differentially abundant proteins between control and GAMOS patient identified in 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 | Spot No | Accession No | Protein Name | MASCOT ID | PI  | MW  | Cov% | Score |
|-------|---------|--------------|--------------|-----------|-----|-----|------|-------|
| 1     | 1206    | P08779       | Keratin, type I cytoskeletal 16 | K1C16_HUMAN | 4.99 | 51758 | 30   | 64    |
| 2     | 960     | O95411       | TGFBI-induced anti-apoptotic factor 1 | TIAF1_HUMAN | 8.35 | 12691 | 68   | 64    |
| 3     | 1019    | P78332       | RNA-binding protein 6 | RBM6_HUMAN | 5.93 | 129129 | 15   | 58    |
| 4     | 1173    | P49189       | 4-trimethylaminobutyraldehyde dehydrogenase | AL9A1_HUMAN | 5.69 | 54679 | 30   | 57    |
| 5     | 1163    | Q2M1K9       | Zinc finger protein 423 | ZN423_HUMAN | 6.43 | 148877 | 16   | 60    |
| 6     | 1138    | Q96NU7       | Probable imidazolonepropionase | HUTI_HUMAN | 6.15 | 47253 | 24   | 58    |
| 7     | 929     | Q9GZT9       | Egl nine homolog 1 | EGLN1_HUMAN | 8.83 | 46847 | 27   | 68    |
| 8     | 193     | Q15545       | Transcription initiation factor TFID subunit 7 | TAF7_HUMAN | 5.07 | 46348 | 24   | 57    |
| 9     | 1312    | P09382       | Galectin-1 | LEG1_HUMAN | 5.34 | 15048 | 82   | 151   |
| 10    | 1097    | P67936       | Tropomyosin alpha-4 chain | TPM4_HUMAN | 4.67 | 28619 | 55   | 163   |
| 11    | 1200    | Q96P63       | Serpin B12 | SPB12_HUMAN | 5.36 | 46646 | 37   | 88    |
| 12    | 225     | P14625       | Endoplasmic | ENPL_HUMAN | 4.76 | 92696 | 23   | 139   |
| 13    | 1233    | P62937       | Peptidyl-prolyl cis-trans isomerase A | PPIA_HUMAN | 7.68 | 18229 | 85   | 57    |
| 14    | 759     | Q13489       | Baculoviral IAP repeat-containing protein 3 | BIRC3_HUMAN | 5.71 | 69582 | 20   |       |
| 15    | 512     | Q13882       | Protein-tyrosine kinase 6 | PTK6_HUMAN | 6.56 | 52371 | 19   | 66    |
| 16    | 1042    | P08738       | Annexin A5 | ANX5_HUMAN | 4.94 | 35971 | 62   | 191   |
| 17    | 221     | Q14247       | Src substrate cortactin | SRC8_HUMAN | 5.24 | 46348 | 18   | 59    |
| 18    | 1188    | O60812       | Heterogeneous nuclear ribonucleoprotein C-like 1 | HNRC1_HUMAN | 4.93 | 32180 | 36   | 57    |
| 19    | 497     | Q01804       | OTU domain-containing protein 4 | OTUD4_HUMAN | 6.25 | 124823 | 13   | 58    |
| 20    | 972     | P04083       | Annexin A1 | ANXA1_HUMAN | 6.57 | 38918 | 67   | 216   |
| 21    | 1179    | Q5SVZ6       | Zinc finger MYM-type protein 1 | ZMYM1_HUMAN | 7.51 | 131542 | 15   | 60    |
| 22    | 801     | P60709       | Actin, cytoplasmic 1 | ACTB_HUMAN | 5.29 | 42052 | 77   | 162   |
| 23    | 1082    | Q06830       | Peroxiredoxin-1 | PRDX1_HUMAN | 8.27 | 22324 | 87   | 234   |
| 24    | 838     | P07335       | Annexin A2 | ANXA2_HUMAN | 7.57 | 38808 | 69   | 299   |
| 25    | 1110    | A6MYN6       | Putative annexin A2-like protein | AXA2L_HUMAN | 6.49 | 38806 | 73   | 339   |
| 26    | 116     | Q6XZB0       | Lipase member 1 | LIP1_HUMAN | 9.21 | 53926 | 24   | 60    |
| 27    | 812     | P04406       | Glyceraldehyde-3-phosphate dehydrogenase | G3P_HUMAN | 8.57 | 36201 | 69   | 211   |
| 28    | 675     | Q6ZS84       | Uncharacterized protein C1orf122 | CA122_HUMAN | 6.29 | 11521 | 40   | 59    |
| 29    | 1101    | P68104       | Elongation factor 1-alpha 1 | EF1A1_HUMAN | 9.10 | 50451 | 34   | 75    |
| 30    | 559     | Q14980       | Nuclear mitotic apparatus protein 1 | NUMA1_HUMAN | 5.63 | 239199 | 14   | 58    |
| Gene ID | Gene Name                                      | Function                                                                 | Species | Log2FoldChange | FDR   |
|--------|-----------------------------------------------|-------------------------------------------------------------------------|---------|----------------|-------|
| Q9Y6X1 | Stress-associated endoplasmic reticulum protein 1 | SERP1_HUMAN                                                             |         | 8.75           | 4652  |
| Q16587 | Zinc finger protein 74                        | ZNF74_HUMAN                                                             |         | 8.90           | 74115 |
| P23528 | Collin-1                                      | COF1_HUMAN                                                              |         | 8.22           | 18719 |
| Q9BXR6 | Complement factor H-related protein 5         | FHR5_HUMAN                                                              |         | 6.81           | 66430 |
| Q9NWA0 | Mediator of RNA polymerase II transcription subunit 9 | MED9_HUMAN                                                              |         | 6.84           | 16506 |
| Q9HB19 | Pleckstrin homology domain-containing family A member 2 | PKHA2_HUMAN                                                              |         | 8.92           | 47852 |
| P08865 | 40S ribosomal protein SA                      | RSSA_HUMAN                                                              |         | 4.79           | 32947 |
| Q9NYM9 | Integrator complex subunit 13                | INT13_HUMAN                                                             |         | 6.24           | 81144 |
| P0DP23 | Calmodulin-1                                  | CALM1_HUMAN                                                             |         | 4.09           | 16827 |
| P23284 | Peptidyl-prolyl cis-trans isomerase B         | PPIB_HUMAN                                                              |         | 9.42           | 23785 |
| Q9Y4A5 | Transformation/transcription domain-associated protein | TRRAP_HUMAN                                                              |         | 8.49           | 44176 |
| Q8NYA6 | Zinc finger protein 28 homolog               | ZFP28_HUMAN                                                             |         | 9.44           | 10080 |
| P09874 | Poly [ADP-ribose] polymerase I               | PARP1_HUMAN                                                             |         | 8.99           | 11381 |
| P07355 | Annexin A2                                   | ANXA2_HUMAN                                                             |         | 7.57           | 38808 |
| P07737 | Profilin-1                                   | PROF1_HUMAN                                                             |         | 8.44           | 15216 |
| Q9H254 | Spectrin beta chain, non-erythrocytic 4       | SPTN4_HUMAN                                                             |         | 5.72           | 29000 |
| O00186 | Syntaxin-binding protein 3                   | STXB3_HUMAN                                                             |         | 7.98           | 68633 |
| Q8TD57 | Dynein heavy chain 3, axonemal               | DYH3_HUMAN                                                              |         | 6.04           | 47377 |
| Q9UEW3 | Macrophage receptor MARCO                    | MARCO_HUMAN                                                             |         | 8.95           | 52968 |
| Q9Y295 | Developmentally-regulated GTP-binding protein 1 | DRG1_HUMAN                                                              |         | 9.00           | 40802 |
| Q8NCI6 | Beta-galactosidase-1-like protein 3          | GLBL3_HUMAN                                                             |         | 9.05           | 75118 |
| P07355 | Annexin A2                                   | ANXA2_HUMAN                                                             |         | 7.57           | 38808 |
| P47756 | F-actin-capping protein subunit beta         | CAPZB_HUMAN                                                             |         | 5.36           | 31616 |
| Q16587 | Zinc finger protein 74                       | ZNF74_HUMAN                                                             |         | 8.90           | 74115 |
| O15144 | Actin-related protein 2/3 complex subunit 2  | ARPC2_HUMAN                                                             |         | 6.84           | 34426 |
| Q9BYG7 | Protein maestro                              | MSTRO_HUMAN                                                             |         | 9.93           | 29149 |
| Q330K2 | NADH dehydrogenase (ubiquinone) complex I, assembly factor 6 | NDUF6_HUMAN (CHO 38)                                                  |         | 9.44           | 38551 |
| P14618 | Pyruvate kinase PKM                          | KPYM_HUMAN                                                               |         | 7.96           | 58470 |
| P73Z4  | Piwi-like protein 4                          | PIWL4_HUMAN                                                             |         | 9.09           | 97838 |
| Q8WXH0 | Nesprin-2                                    | SYNE2_HUMAN                                                             |         | 5.26           | 80187 |
| Q8TD57 | Dynein heavy chain 3, axonemal               | DYH3_HUMAN                                                              |         | 6.04           | 47377 |
| Q3ZCT8 | Kelch repeat and BTB domain-containing protein 12 | KBTBC_HUMAN                                                             |         | 5.65           | 72077 |
| Q15022 | Polycomb protein SUZ12                      | SUZ12_HUMAN                                                              |         | 8.98           | 83744 |
| P52790 | Hexokinase-3                                 | HKX3_HUMAN                                                              |         | 5.23           | 10061 |
| Q02556 | Interferon regulatory factor 8               | IRF8_HUMAN                                                              |         | 6.38           | 49123 |
| Q9UEW3 | Macrophage receptor MARCO                   | MARCO_HUMAN                                                              |         | 8.95           | 52968 |
| P22392 | Nucleoside diphosphate kinase B             | NDKB_HUMAN                                                              |         | 8.52           | 17401 |
| Q86UR5 | Regulating synaptic membrane exocytosis protein 1 | RIMS1_HUMAN                                                             |         | 9.68           | 19015 |

Note: The table includes various genes and their functions, along with their corresponding species, log2 fold change, and FDR values.
| Theoretical isoelectric point. | Protein accession number for SWISSPROT Database. | Theoretical relative mass. |
|-------------------------------|--------------------------------------------------|---------------------------|
| 70   | Q7Z6M3 | Allergin-1 | MILR1 HUMAN | 7.92 | 39395 | 41 | 59 |
| 71   | Q9NV70 | Exocyst complex component 1 | EXOC1 HUMAN | 6.17 | 102772 | 23 | 58 |
| 72   | Q9UKT9 | Zinc finger protein Aiolos | IKZF3 HUMAN | 6.11 | 59012 | 30 | 59 |
| 73   | P09874 | Poly [ADP-ribose] polymerase 1 | PARP1 HUMAN | 8.99 | 113811 | 22 | 7 |
| 74   | P09651 | Heterogeneous nuclear ribonucleoprotein A1 | ROA1 HUMAN | 9.17 | 38837 | 51 | 142 |
| 75   | P52790 | Hexokinase-3 | HXK3 HUMAN | 5.23 | 100616 | 11 | 57 |
| 76   | Q4G0A6 | Probable ubiquitin carboxyl-terminal hydrolase MINDY-4 | MINY4 HUMAN | 6.47 | 85261 | 18 | 65 |
| 77   | Q9NS84 | Carbohydrate sulfotransferase 7 | CHST7 HUMAN | 9.72 | 54803 | 23 | 57 |
| 78   | P63244 | Receptor of activated protein C kinase 1 | RACK1 HUMAN | 7.60 | 35511 | 63 | 141 |
| 79   | P07437 | Tubulin beta chain | TBB5 HUMAN | 4.78 | 50095 | 52 | 152 |
| 80   | Q01995 | Transgelin | TAGL HUMAN | 8.87 | 22653 | 51 | 66 |
| 81   | P06709 | Actin, cytoplasmic 1 | ACTB HUMAN | 5.29 | 42052 | 55 | 92 |
| 82   | P63261 | Actin, cytoplasmic 2 | ACTG HUMAN | 5.31 | 42108 | 84 | 283 |
| 83   | P1213 | Destrin | DEST HUMAN | 8.06 | 18950 | 53 | 58 |
| 84   | Q8NDG6 | ATP-dependent RNA helicase TDRD9 | TDRD9 HUMAN | 6.62 | 157124 | 17 | 58 |
| 85   | P04406 | Glyceraldehyde-3-phosphate dehydrogenase | G3P HUMAN | 8.57 | 36201 | 63 | 206 |
| 86   | P08238 | Heat shock protein HSP 90- beta | HS90B HUMAN | 4.97 | 83554 | 54 | 170 |
| 87   | Q14980 | Nuclear mitotic apparatus protein 1 | NUMA1 HUMAN | 5.63 | 239199 | 18 | 59 |
| 88   | Q13796 | Protein Shroom2 | SHRM2 HUMAN | 6.64 | 177500 | 18 | 59 |
| 89   | Q43852 | Calumenin | CALU HUMAN | 4.47 | 37198 | 25 | 70 |
| 90   | P49767 | Vascular endothelial growth factor C | VEGFC HUMAN | 7.77 | 49019 | 32 | 58 |
| 91   | P63104 | 14-3-3 protein zeta/delta | 1433Z HUMAN | 4.73 | 27899 | 65 | 184 |
| 92   | Q96NN9 | Apoptosis-inducing factor 3 | AIFM3 HUMAN | 9.20 | 67376 | 23 | 60 |
| 93   | Q9Y2L8 | Zinc finger protein with KRAB and SCAN domains 5 | ZKSC5 HUMAN | 7.43 | 98994 | 19 | 69 |
| 94   | Q8NS86 | Putative E3 ubiquitin-protein ligase UBR7 | UBR7 HUMAN | 4.7 | 49336 | 13 | 58 |
| 95   | P07951 | Tropomyosin beta chain | TPM2 HUMAN | 4.66 | 32945 | 53 | 142 |
| 96   | P50990 | T-complex protein 1 subunit theta | TCPQ HUMAN | 5.42 | 60153 | 41 | 59 |
| 97   | Q6P5S0 | C18orf34 protein | Q6P5S0_HUMAN | 6.34 | 102575 | 18 | 50 |
| 98   | Q15233 | Non-POU domain-containing octamer-binding protein | NONO HUMAN | 9.01 | 54311 | 25 | 58 |
| 99   | Q86UB2 | Basic immunoglobulin-like variable motif-containing protein | BIVM HUMAN | 9.15 | 57479 | 18 | 57 |
| 100  | Q16891 | MICOS complex subunit | MIC60 HUMAN | 6.08 | 84025 | 24 | 58 |
| 101  | Q96LR7 | Uncharacterized protein C2orf50 | CB050 HUMAN | 9.51 | 17941 | 34 | 59 |
| 102  | P03952 | Plasma kallikrein | KLKB1 HUMAN | 8.60 | 73433 | 28 | 61 |
| 103  | Q9BX26 | Synaptosomal protein | SYCP2 HUMAN | 9.01 | 177239 | 13 | 59 |
| 104  | P29692 | Elongation factor 1-delta | EF1D HUMAN | 4.9 | 31217 | 60 | 130 |
| 105  | Q8WVF1 | Protein OSCP1 | OSCP1 HUMAN | 5.75 | 43300 | 34 | 58 |
| 106  | P09493 | Tropomyosin alpha-1 chain | TPM1 HUMAN | 4.69 | 32746 | 42 | 95 |
| 107  | P11142 | Heat shock cognate 71 kDa protein | HSP7C HUMAN | 5.37 | 71082 | 45 | 98 |

a Protein accession number for SWISSPROT Database.
b Theoretical isoelectric point.
c Theoretical relative mass.
c MASCOT coverage
d MASCOT score