Figure S1. Representative bone marrow aspirate images of ITP and MM. (A) Bone marrow aspirate showing presence of immature forms of megakaryocytes in loose clusters in patient with ITP, using Leishman-Giemsa stain, at x20 magnification. (B) Bone marrow aspirate showing syncytial sheets of neoplastic plasma cells in patients with MM, including immature forms (black arrows), using Leishman Giemsa stain, at x40 magnification. ITP, Idiopathic thrombocytopenic purpura; MM, multiple myeloma.

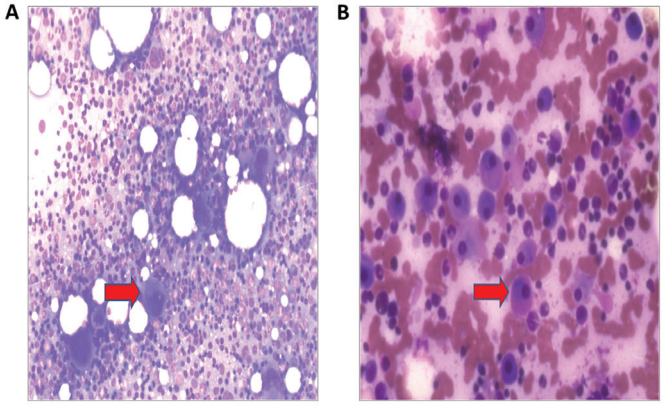

Figure S2. Analyses of the upregulated proteins using DAVID bioinformatics tool. The top 10 (A) biological processes, (B) molecular functions and (C) biochemical pathways identified using DAVID. DAVID, Database for Annotation, Visualization and Integrated Discovery.

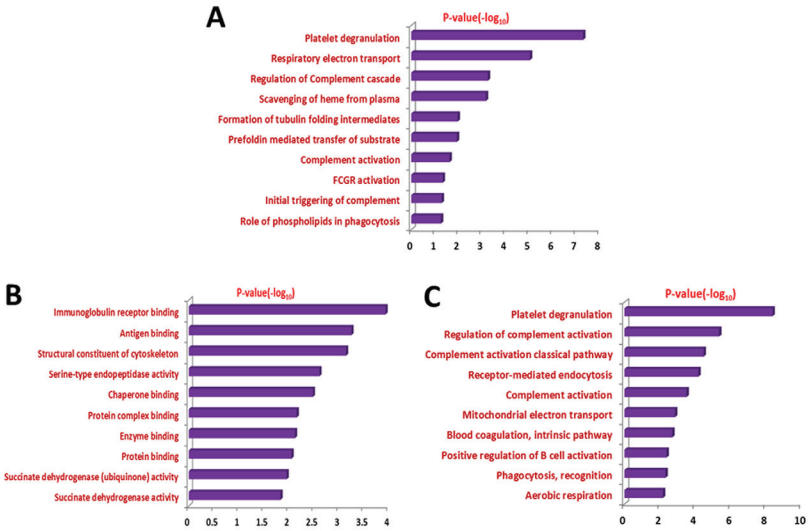

Figure S3. Analyss of the downregulated protein using DAVID bioinformatics tool. The top 10 (A) biological processes, (B) molecular functions and (C) biochemical pathways identified using DAVID. DAVID, Database for Annotation, Visualization and Integrated Discovery.

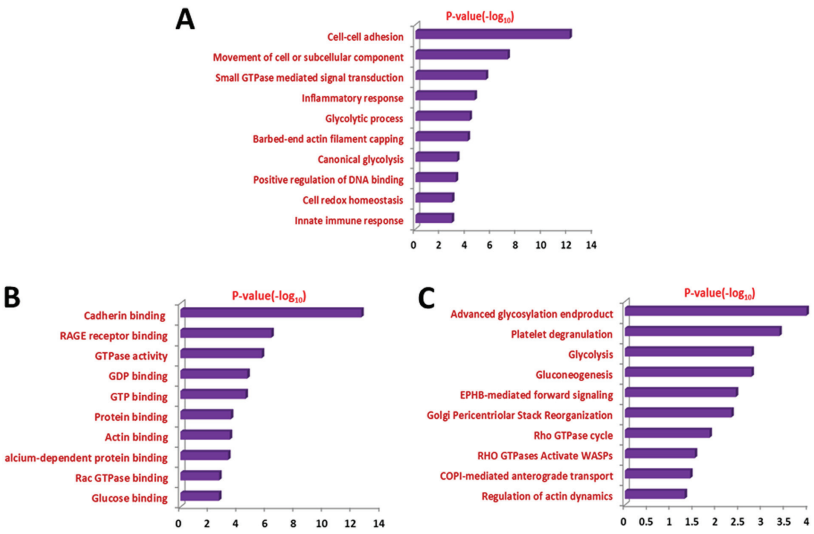

Figure S4. Bioinformatics analysis of the upregulated protein dataset using Protein Analysis THrough Evolutionary Relationships. The (A) molecular function (B) biological processes (C) protein classes and (D) the pathways involved are shown.

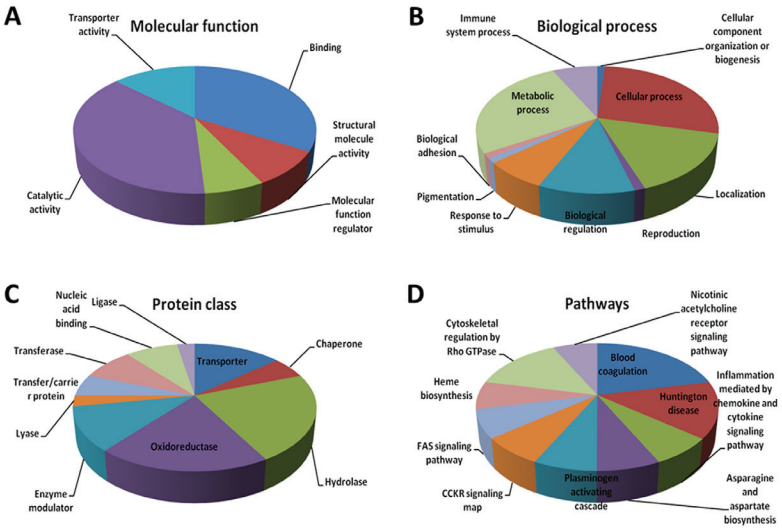

Figure S5. Bioinformatics analysis of the downregulated protein dataset using Protein Analysis THrough Evolutionary Relationships. The (A) molecular function (B) biological processes (C) protein classes and (D) pathways involved are shown.

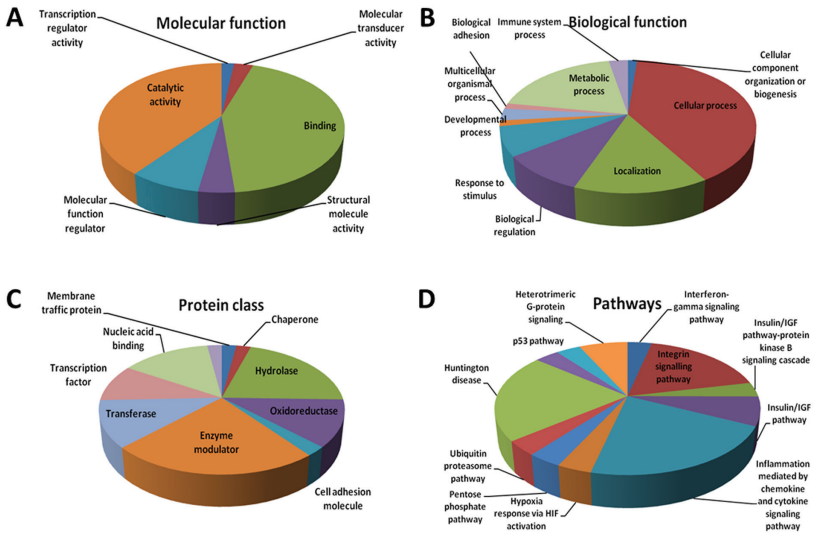

Figure S6. Protein-protein interaction network of the upregulated proteins identified in mononuclear cells from patients with multiple myeloma using the Search Tool for the Retrieval of Interacting Genes/Proteins. Marginal zone B and B1 cell specific protein and its associated protein is highlighted as a red circle indicating a high confidence level of interaction. The different types of interaction are shown by the different coloured lines.

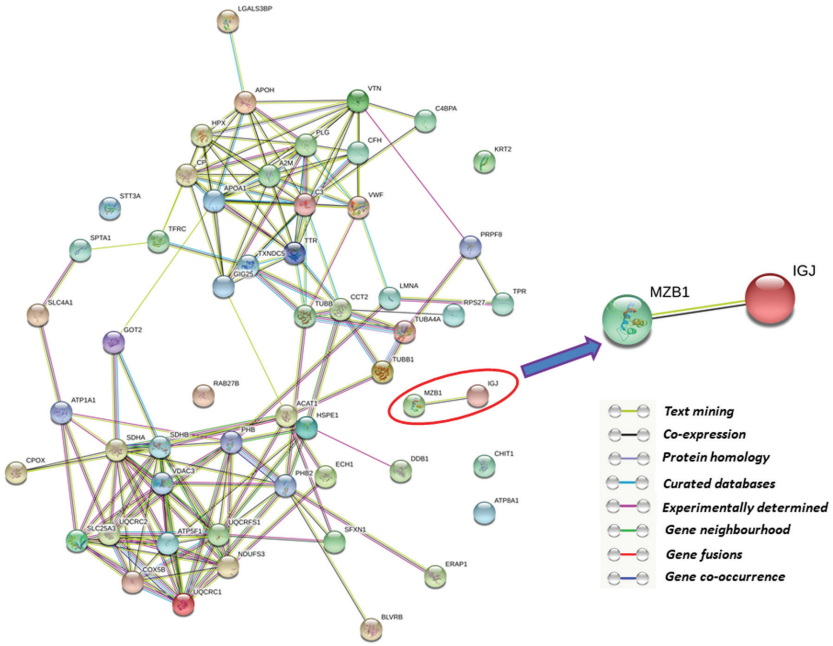

Figure S7. Protein-protein interaction network of marginal zone B and B1 cell specific protein created using Ingenuity Pathway Analysis for the upregulated proteins identified in mononuclear cells from patients with multiple myeloma. The red color indicates proteins that were identified in the present study and the proteins without color were not identified. The color intensity represents the fold-change of proteins i.e. Higher intensity represents higher fold-change. Dashed lines indicate indirect functional relationships between the molecules, whereas continuous lines indicate direct physical relationships between the molecules. The different shapes of the molecules represent the protein classes of the molecules as indicated in the figure.

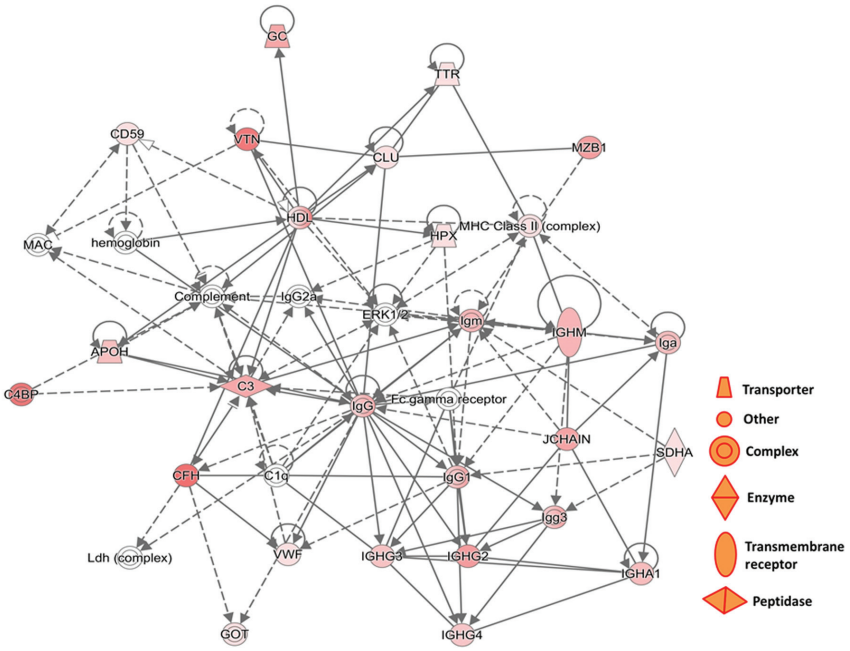

Figure S8. Western blot analysis of MZB1 protein in the supernatant of RPMI-8226 control cells and RPMI-8226 with knockdown of MZB1. Lane 1, supernatant of RPMI-8226, lane 2, supernatant of RPMI 8226-shMZB1 _3. MZB1 marginal zone B and B1 cell specific protein.

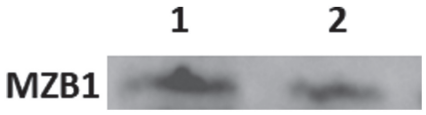

Figure S9. Representative flow cytometry plots showing an increased level of sub-G_1 population in RPMI-8226 cells with knockdown of MZB1 using shRNA and in control cells with scramble shRNA. The red circles represent the G_0/G_1 population. Sh, short hairpin; MZB1 marginal zone B and B1 cell specific protein.