**Supplementary Tables**

Supplementary Table 1: Clinical symptoms, hematological as well as biochemical parameters of healthy subject and VL patients before and after anti-leishmanial therapy. n: number of sample, SGOT: Serum glutamic oxaloacetic transaminase, SGPT: Serum glutamic pyruvic transaminase.

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| Study groups | Healthy (n=13) |  Visceral Leishmaniasis (VL) Patients (n=13) |
|  Before treatment |  After treatment |
|  | Male(n= 8) | Female (n=5) | Male(n= 9) | Female (n=4) | Male(n= 9) | Female (n=4) |
| Age | 25-45 | 25-45 | 25-45 | 25-45 | 25-45 | 25-45 |
| Weight (Kg) | 55-75 | 45-65 | 52-69 | 42.5-62 | 53.1-72.6 | 42.6-63 |
| Body MassIndex (Kg/m2) | 23.12± 2.91 | 18.8± 1.75 | 14.46±2.27 | 12.89±2.02 | 19.90±1.96 | 15.51±1.77 |
| BodyTemperature (in ⁰F) | 97.5±0.5 | 97.5±0.45 | 100.56±1.892 | 100.76±1.831 | 97.22±0.375 | 97.4±0.35 |
| Hepatomegaly(in cm) | 0 | 0 | 3.3±2.26 | 2.8±1.76 | 0.7±0.948 | 0.59±0.827 |
| Splenomegaly(in cm) | 0 | 0 | 7.8±3.39 | 6.9±2.99 | 0.8±1.135 | 0.71±1.035 |
| Haemoglobins(g/dl) | 12.76±0.955 | 10.98±0.865 | 7±1.44 | 5.8±1.84 | 9.31±0.896 | 8.1±0.692 |
| WBC (white blood cells) (per mm2) | 6760±1581.37 | 6978±1248.56 | 2650±949.10 | 2715±1045.10 | 5309±486.85 | 5509±687.15 |
| Lymphocytes (%) | 32.46±5.73 | 33.81± 6.9 | 43.5±8.195 | 45.8± 6.5 | 27.6±2.547 | 29.5±2.74 |
| SGOT (U/L) | 8±4.358 | 7.743±3.745 | 36±16.013 | 31±13.935 | 28.4±8.60 | 21.4±7.122 |
| SGPT (U/L) | 8±1.581 | 7.4±1.437 | 31±13.730 | 29.96±14.533 | 23±9.281 | 21.7±7.836 |
| Blood Urea (mg/dl) | 20.5±4.725 | 20±5.581 | 24.1±6.849 | 23.6±7.581 | 20.31±11.834 | 21±10.721 |
| Serum Creatinine (mg/dl) | 0.7±0.158 | 0.56±0.132 | 0.468±0.153 | 0.442±0.144 | 0.49±0.154 | 0.50±0.143 |
| Sodium (mEq/L) | 137±7.582 | 142±5.342 | 139.8±3.049 | 140.3±4.836 | 136.6±5.253 | 139±3.789 |
| Potassium (mEq/L) | 4.44±0.650 | 4.23±0.526 | 4.26±0.337 | 3.9±0.454 | 4.77±0.934 | 5±1.432 |

Supplementary table 2: HLA A0201 restricted 9 mer epitopes. Antigen specific cytotoxic T cell epitopes was predicted by SYFPEITHY using matrix-based algorithm. Peptide binders to MHC-I molecules from protein sequences or sequences alignment was predicted using RANKPEP which is a Position Specific Scoring Matrices (PSSMs) based bioinformatics tool. Immune Epitope Database (IEDB, a database which includes the tool that predicts the MHC class I and class II binding epitopes) was used to experimentally measure immune epitopes.

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| **Peptide** | **Start Position** | **SYFPEITHY** | **RANKPEP** | **IEDB** | **Query Coverage** | **Identity** |
| S L A K L K D A V  | 446 | 26 | 78.0 | 2.7 | 100 | 88 |
| L L I V V M D G L | 17 | 25 | 66.0 | 2.6 | 77 | 86 |
| A T I A G V E A V  | 435 | 25 | 64.0 | 2.6 | 88 | 75 |
| K L K D A V D S I  | 449 | 25 | 89.0 | 4.0 | 100 | 67 |
| A L K S G M Y D V  | 408 | 24 | 88.0 | 2.3 | 100 | 67 |
| T L S P V P V F I  | 497 | 22 | 80.0 | 1.7 | 77 | 86 |

Supplementary table 3: HLA DRB1 0401 restricted 15 mer epitopes. Immune Epitope Database (IEDB, a database which includes the tool that predicts the MHC class I and class II binding epitopes) was used to experimentally measure immune epitopes. Antigen specific cytotoxic T cell epitopes was predicted by SYFPEITHY using matrix-based algorithm. NETMHC II is a server, which predicts binding of peptides to HLA-DR using artificial neuron networks.

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| Peptide | **Start****Position** | **IEDB** | **SYFPEITHI** | **NETMHC II** | **Query****Coverage** | **Identity** |
| LGAFTKEGSTLHLIG | 114 | 1.46 |  22 |  SB (27.9) |  60 |  78 |
| SRRFRSVRAHGTAVG |  51 | 2.93 |  22 |  WB(62) |  46 |  100 |
| CVNFRGDRVIEMTRA | 278 | 3.34 |  22 |  WB(98.6) |  86 |  77 |
| YDAVHMASTPFMDAQ |  33 | 3.82 |  26 |  WB(148.9) |  53 |  75 |
| TLHLIGLLSDGGVHS | 123 | 3.90 |  20 |  WB(57.6)  |  46 |  100 |