Table S1. GO-terms identified with enrichment analysis comparing cDNA clones with a population effect against the reference set (8588 analysed cDNA clones) with BLAST2GO [1,2]. The following information is given: GO-ID, term, p-value after correcting for the False Discovery rate (FDR) [3], number of cDNA clones representing that GO-term with a population effect (Test), and among the 8588 cDNA clones (Reference).

GO-ID	Term	FDR corrected p-value	Test	Reference
GO:0015671	oxygen transport	4E-17	21	37
GO:0015669	gas transport	4E-17	21	37
GO:0019882	antigen processing and presentation	1E-09	15	42
GO:0006955	immune response	2E-07	15	66
GO:0006810	transport	4E-06	46	784
GO:0051234	establishment of localization	4E-06	46	786
GO:0002376	immune system process	5E-06	15	88
GO:0051179	localization	2E-05	46	826
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	2E-03	6	16
GO:0048002	antigen processing and presentation of peptide antigen	2E-03	6	16
GO:0016998	cell wall macromolecule catabolic process	4E-03	5	11

References

1. Conesa A, Gotz S, Garcia-Gomez JM, Terol J, Talon M, et al. (2005) Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. Bioinformatics 21: 3674-3676.
2. Gotz S, Garcia-Gomez JM, Terol J, Williams TD, Nagaraj SH, et al. (2008) High-throughput functional annotation and data mining with the Blast2GO suite. Nucleic Acids Research 36: 3420-3435.
3. Benjamini Y, Yekutieli D (2001) The control of the false discovery rate in multiple testing under dependency. Annals of Statistics 29: 1165-1188.