

Supplementary Table 1 (2 pages)

			Allele		Brazilian discovery			Indian discovery			Consequence	Gene Symbol	Gene Name
chr	rsID	position	0	1	P value	Beta	SE	P value	Beta	SE			
(A) India-specific													
2	rs2312548	69809264	A	C	0.407	-0.08	0.09	2.24E-06	0.30	0.06	intronic	ANXA4	Annexin IV
(B) Brazil-specific													
2	rs3748934	100376340	A	G	4.88E-06	-19.56	4.32	0.014	2.71	1.10	synonymous	CHST10	Carbohydrate sulfotransferase 10
4	rs1355967	10836785	A	C	1.40E-07	-0.46	0.09	0.169	0.09	0.06	intergenic	CLNK/HS3ST1	Cytokine dependent hematopoietic cell linker/Heparan sulfate-glucosamine 3-sulfotransferase 1
4	rs902174	185892165	A	G	4.60E-06	-0.42	0.09	0.902	0.01	0.06	missense	CENPV	Centromere protein V
7	rs2527214	158447342	A	G	5.98E-06	-0.60	0.13	0.743	-0.03	0.09	intergenic	WDR80/VIPR2	Autophagy related 16 like 2/Vasoactive intestinal peptide receptor 2
10	rs2674355	126052643	A	G	4.01E-06	0.85	0.19	0.060	-0.46	0.24	intergenic	CHST15/OAT	Carbohydrate sulfotransferase 15/Ornithine aminotransferase
11	rs2957710	10334795	A	G	3.18E-06	0.49	0.11	0.918	0.01	0.06	intronic	CAND1.11	Uncharacterized gene
11	rs1484433	15756036	A	C	7.62E-06	-0.41	0.09	0.262	-0.08	0.07	intergenic	INSC/SOX6	INSC spindle orientation adaptor protein/SRY-box transcription factor 6
11	rs11031947	32691220	A	G	3.83E-06	0.41	0.09	0.684	-0.03	0.07	intronic	CCDC73	Coiled-coil domain containing 73
11	rs4078355	124436544	A	G	3.39E-06	0.52	0.11	0.948	0.00	0.07	intergenic	CCDC15/SLC37A2	Coiled-coil domain containing 15/Solute carrier family 37 member 2
15	rs1549520	48256580	A	C	3.06E-06	-0.45	0.10	0.123	0.10	0.06	intronic	ATP8B4	ATPase phospholipid transporting 8B4

Supplementary Table 1 (2 pages)

15	rs8036138	83693160	A	G	8.26E-06	0.41	0.09	-	-	-	intergenic	PDE8A/AKAD13	Phosphodiesterase 8A/A-kinase anchoring protein 13
18	rs8098585	36762038	A	G	6.37E-07	0.46	0.09	0.575	0.04	0.07	intergenic	CELF4/PIK3C3	CUGBP Elav-like family member 4/Phosphatidylinositol 3-kinase catalytic subunit type 3
18	rs12454166	53780638	A	G	3.96E-06	0.60	0.13	0.775	-0.03	0.10	intergenic	NARS1/NEDD4L	Asparaginyl-tRNA synthetase 1/NEDD4 like E3 ubiquitin protein ligase

Table S1. GWAS data for the Indian and Brazilian cohorts used in the VL GWAS (Fakiola et al. 2013) examined separately using a less stringent cut-off of $P < 1 \times 10^{-5}$ to look for potential population-specific associations. None of the regions associated at $P < 1 \times 10^{-5}$ in these separate analyses showed significant association in the combined analysis. Of the hits that were population-specific (1 for India shown in part A; 13 for Brazil shown in part B), 8 were in intergenic regions and the remainder landed in genes with no obvious functional significance. The Betas and allele frequency are shown for Allele 1. Positions are in NCBI human genome Build 36. Where the consequence of the variant is intergenic, the nearest protein-coding genes on either side are shown. Of the genes listed CLNK (also known as MIST) has possible significance for its role in the regulation of immunoreceptor signalling, including PLC-gamma-mediated B cell antigen receptor signalling and FC-epsilon R1-mediated mast cell degranulation (Taken from NCBI: (Cao et al., 1999 [PubMed 10562326]; Goitsuka et al., 2000, 2001 [PubMed 10744659] [PubMed 11463797])). However, the associated variant rs1355967 lies some 540kb downstream of CLNK, where it lies 167kb upstream of HS3ST1.

Fakiola M, Strange A, Cordell HJ, Miller EN, Pirinen M, Su Z, Mishra A, Mehrotra S, Monteiro GR, Band G, Bellenguez C, Dronov S, Edkins S, Freeman C, Giannoulatou E, Gray E, Hunt SE, Lacerda HG, Langford C, Pearson R, Pontes NN, Rai M, Singh SP, Smith L, Sousa O, Vukcevic D, Bramon E, Brown MA, Casas JP, Corvin A, Duncanson A, Jankowski J, Markus HS, Mathew CG, Palmer CN, Plomin R, Rautanen A, Sawcer SJ, Trembath RC, Viswanathan AC, Wood NW, Wilson ME, Deloukas P, Peltonen L, Christiansen F, Witt C, Jeronimo SM, Sundar S, Spencer CC, Blackwell JM, Donnelly P (2013) Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. *Nat Genet* 45: 208-13. doi: ng.2518 [pii] 10.1038/ng.2518