Supplemental Table 1 | Characteristics of the participants

Characteristic	**Boys (n=94)**	**Girls (n=91)**
Mean age in months (SD)	51.1 (10.5)	50.1 (11.6)
E. histolytica infected (%)	82 (87)	85 (93)
Mean number of monthly stools *E. histolytica* (+) (range)	2.8 (0-15)	3.15 (0-19)
Baseline blood anti-*E. histolytica* IgG (%)	50 (53)	47 (52)
Malnourished at study entry ages 2-5 years (%)	31(33)	29(32)
Stunted at study entry ages 2-5 years (%)	22 (23)	32(35)
Body mass index at age 10-13 years (SD)	14.1 (1.24)	14.1 (1.13)

Supplemental Table 2: Initial intronic leptin receptor (*LEPR*) SNPs and haplotype associated with *E. histolytica* infection after permutation.

SNP	Location	MAF	X^2 Allelic Permuted P-value EH negative versus infection	X^2 Allelic Permuted P-value EH infection mild versus severe
rs4655537	Intron 6	0.298	NS	0.035
rs6696954	Intron 5	0.295	NS	0.050
rs3828033	Intron 8	0.453	NS	0.035
rs4655555	Intron 14	0.134	0.028	NS
rs12040007	Intron 14	0.132	0.038	NS
rs1892535	Intron 19	0.133	0.038	NS
Haplotype Block 7	Intron2 -intron 6		0.040	0.024

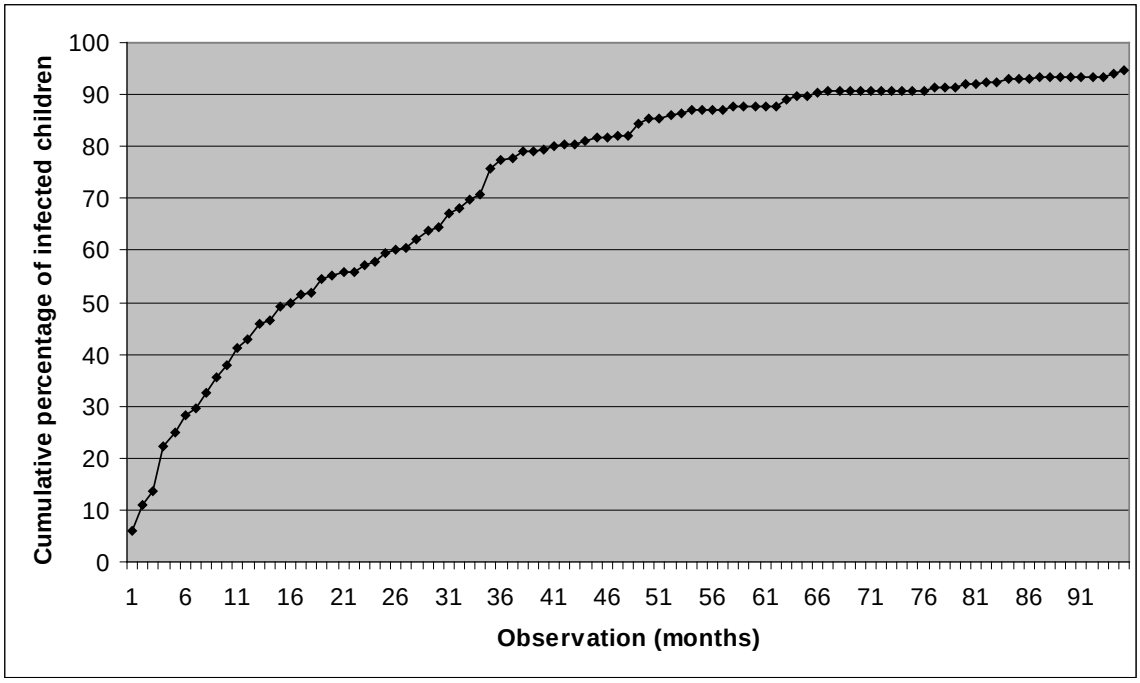
Minor Allele Frequency (MAF); E. histolytica (EH); Single Nucleotide Polymorphism (SNP). Mild (1 or 2 *E. histolytica* infections), Severe (multiple *E. histolytica* infections).

Supplemental Table 3 | Q223R (rs1137101) genotype frequencies by adiposity measurements.

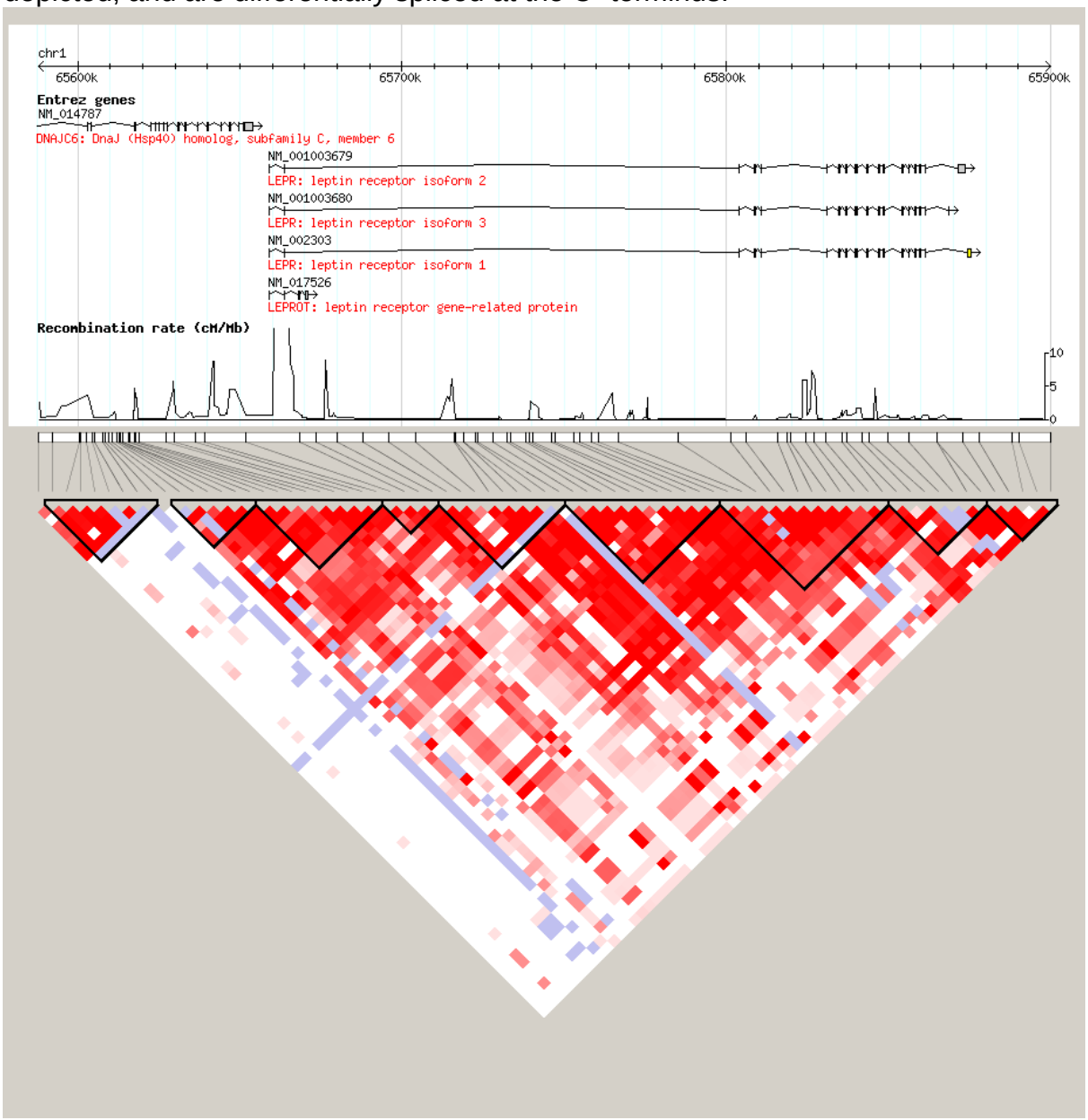
RS1137101	**Not Malnourished**	**Malnourished**	**Not Stunted**	**Stunted**
AA	25% (13)	24% (30)	18% (10)	25% (33)
GA	53% (32)	50% (63)	57% (31)	49% (64)
GG	22% (15)	26% (32)	24% (13)	26% (34)
Chi-Square P-value	chi-square = 0.169, p=0.919		chi-square=1.33, p=0.514	

AA = QQ amino acid, GA= QR amino acid, GG= RR amino acid

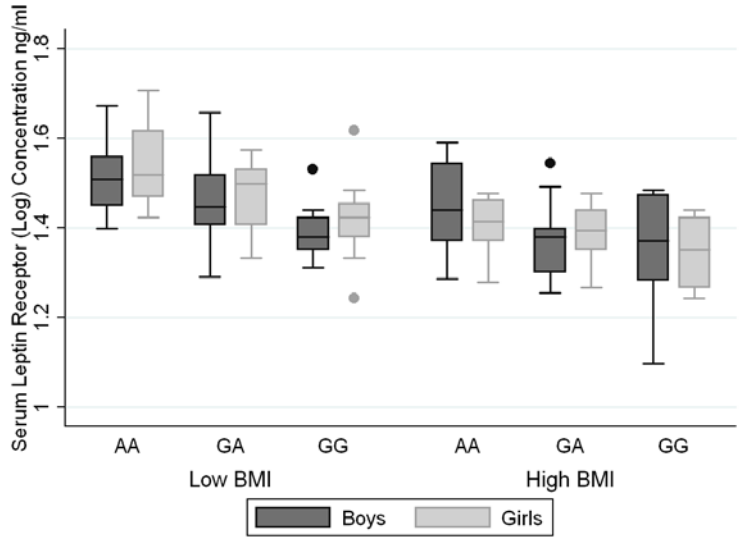
Supplemental Figure 1 | Cumulative percentage of the children (n=185 unrelated children) with *E. histolytica* infection during follow up period of 95 months. Children from the Mirpur community of Dhaka, Bangladesh were enrolled into a prospective observational study of amebiasis in 1999. Children were 2-5 years of age upon enrollment. Children were visited in their homes every other day. Children were tested for amebiasis with each diarrheal illness. In addition, asymptomatic infection with the parasite was detected by testing of monthly surveillance stool samples.

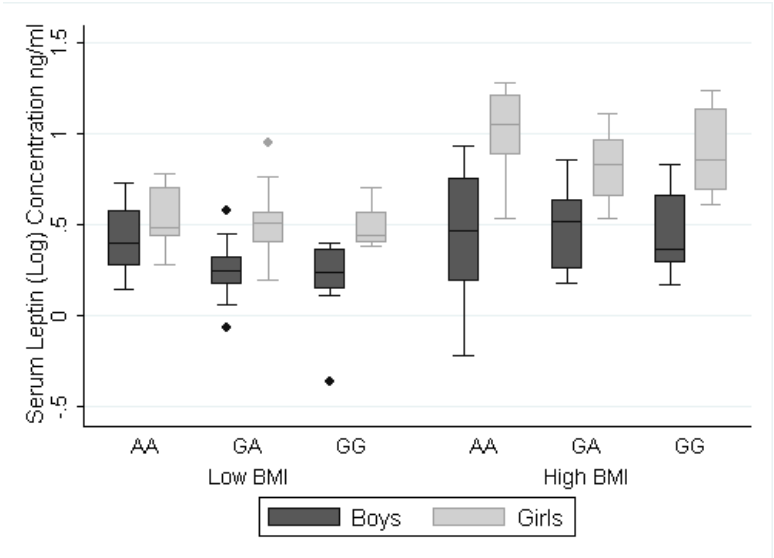


Supplemental Figure 2: Pairwise linkage disequilibrium (LD) plot of the leptin receptor(*29*). Black triangles represent haplotype blocks defined by solid spines of linkage disequilibrium (r^2 >0.8), and the number within each block represents numeric order. Red, white and pink boxes represent statistically significant pairwise LD (LOD >2) using the test statistic D' with ranges of no evidence of LD (white) to strong evidence of LD (red). Blue boxes represent regions of low confidence and statistical significance but a D' = 1(LOD <2). The black vertical lines represent specific SNPs genotyped in this population and their location within the gene. Block 7 represents the region within the leptin receptor with the strongest association signals. The Entrez genes in this region are depicted above the LD plot and boxes denote exons. Three different isoforms of the leptin receptor from *Entrez Genes* are depicted, and are differentially spliced at the C- terminus.



Supplemental Figure 3: Box plots of serum leptin receptor and leptin protein levels stratified by sex, rs1137101 genotypes (AA, AG and GG) and BMI. Line within box is the median, the bottom and top of the box are the 25th and 75th percentile, respectively. The dots represent outliers, and the top and bottom of the whiskers represent the upper and lower adjacent values, respectively. A allele = Glutamine (Q); G allele = Arginine (R).





Supplemental Figure 4: Increased expression of the long isoform of the leptin receptor is associated with the Q223R genotype. Peripheral blood mononuclear cells were isolated from 138 study participants, after RNA extraction and cDNA synthesis the samples were grouped according to LEPR SNP rs1137101 (Q223R) genotype. Transcript levels were measured by qRT-PCR as described in the text. The geographic mean of the PPIA and HPRT housekeeping transcripts were used to normalize mRNA levels between samples and outliers were identified using Grubbs' test. The x-axis indicates the LEPR SNP rs1137101 genotype, the log scale y-axis the qRT-PCR fluorescence relative to the average QR genotype value. A) The Lepr_1 primer set was used to detect the Leptin receptor mRNA variants NM_001003680, and NM_001003679 and NM_002303 B) The NM_002303 mRNA, which encodes the long isoform of the leptin receptor (variant 1), was specifically measured using the Lepr_vb_2 primer set. The long isoform of the leptin receptor transcript was 10x lower in the RR genotypes than in the QQ genotype (Mann-Whitney p=0.0152). It was also decreased relative the expression of this isoform in the heterozygote QR genotype (Mann-Whitney p=0.0267).