Supplementary material

Table S1. Summary of iCORN corrections.

Table S2. Illumina mapping statistics and SNP predictions.

Table S3. Orthologue list of genes that vary between *L. mexicana* U1103, *L. major* Friedlin, *L. infantum* JPCM5 and *L. braziliensis* M2904.

Table S4. List of multicopy genes in *L. mexicana* U1103, *L. major* Friedlin, *L. infantum* JPCM5, *L. braziliensis* M2904.

Table S5. The orthologue groups organised by their presence in the different *Leishmania* species as multicopy arrays.

Table S6. Species-specific genes that are in multicopy arrays,

Table S7. Chromosome "somy" calls in *Leishmania* species by scaled mean read depth coverage across the whole chromosome.

Table S8. Pfam domains that are over-represented in genes encoded on the supernumerary chromosomes and those that are over-represented in genes that are multicopy arrays on disomic chromosomes. The chi^2 p-value shown is uncorrected so a Bonferroni corrected p-value threshold of $p<10^{-5}$ was used.

Figure S1. Distribution of read depth along *L. major* Friedlin disomic and tetrasomic chromosomes

Figure S2. Distribution of read depth along chromosomes of *L. mexicana* U1103.

Figure S3. Distribution of normalised allele frequencies according to inferred ploidy for *L. mexicana* and *L. braziliensis* chromosomes (individual chromosomes)**.**

Figure S4. Validation of chromosome copy number.

Figure S5. Number of arrays on each chromosome of *L. mexicana* U1103 and M379.