SUPPLEMENTARY INFORMATION

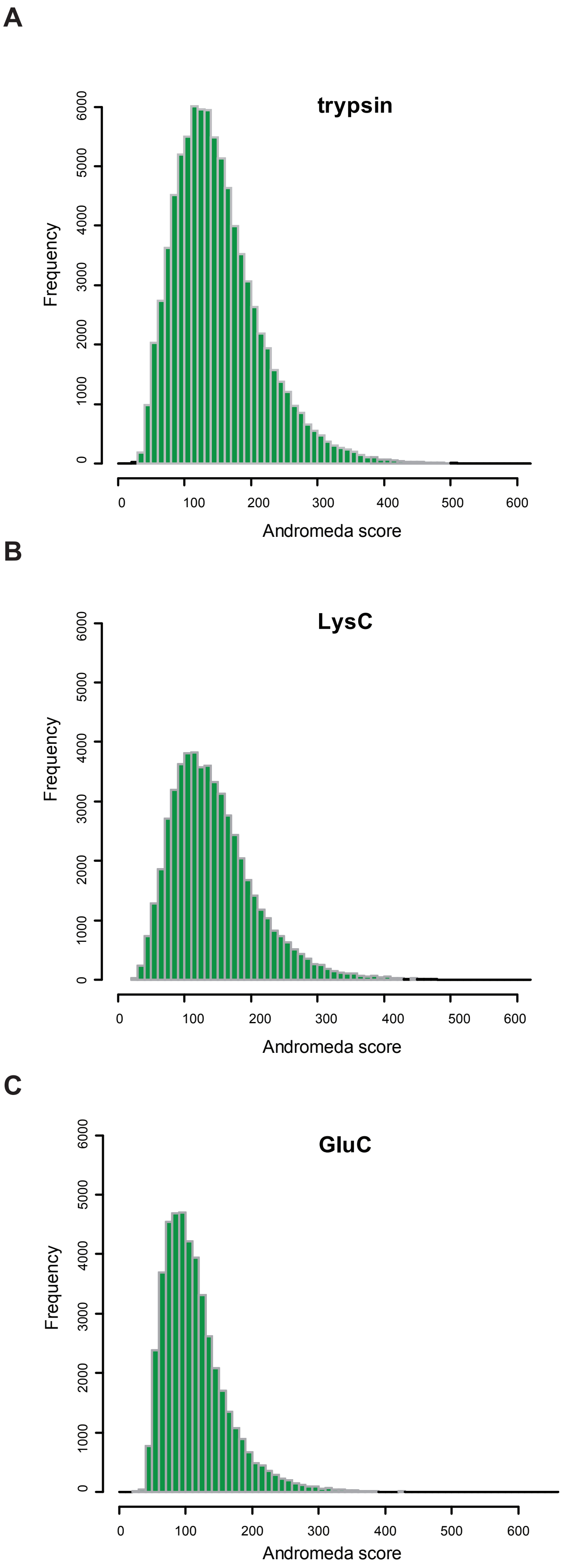
Figure S1: Peptide score distribution from three enzyme digestion.

Figure S2: Distribution of identified genes from the proteome and transcriptome data across the different chromosomes. Proteins and transcripts identified on the Y chromosome are nearly sequence identical to genes on other chromosomes.

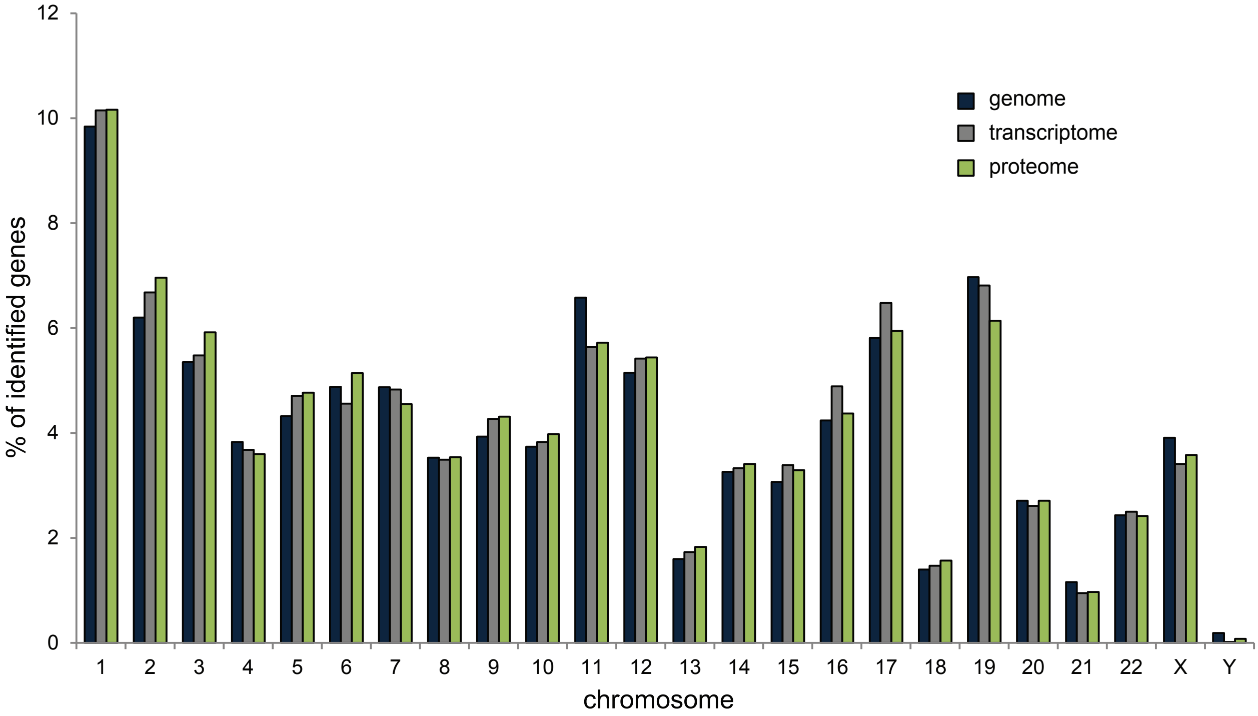
Figure S3: Enrichment analysis of the two populations of transcripts from the bimodal distribution of the transcript abundance. We separated the two parts of the distribution by cutting it with the green and red lines around the local minimum to achieve almost pure populations of the left part ($\log_2$FPKM<-3) and the right part ($\log_2$FPKM>0). Enrichment analysis was performed on these populations using Fisher exact test. P-values are given in brackets.

Figure S4: Comparison of genome coverage from proteomic and transcriptomic approaches. **A.** Proteomic and transcriptomic coverage of molecular complexes annotated by the CORUM database. **B.** Density plot of KEGG pathways showing the relative coverage of KEGG pathways on the proteomic level vs. the transcriptomic level. Identical coverage of a pathway by both methods would have a ratio of 1 between coverage of proteomics and transcriptomics, and would fall on the red line in the figure. The mean ratio (0.9) is indicated in green.

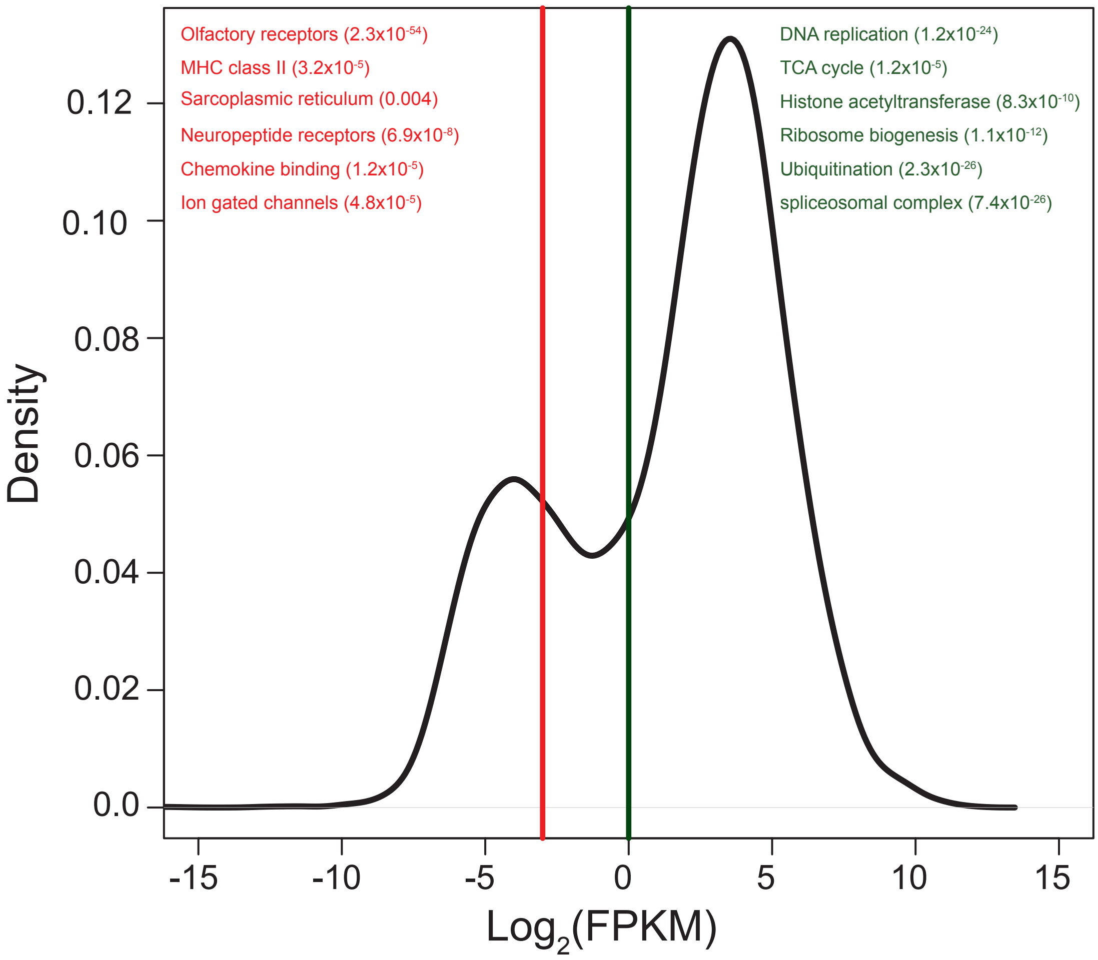
Supplementary figure 1



Supplementary figure 2

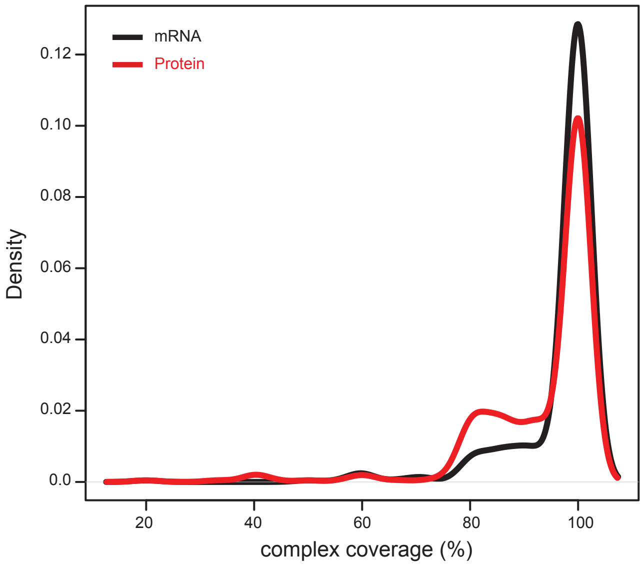


Supplementary figure 3

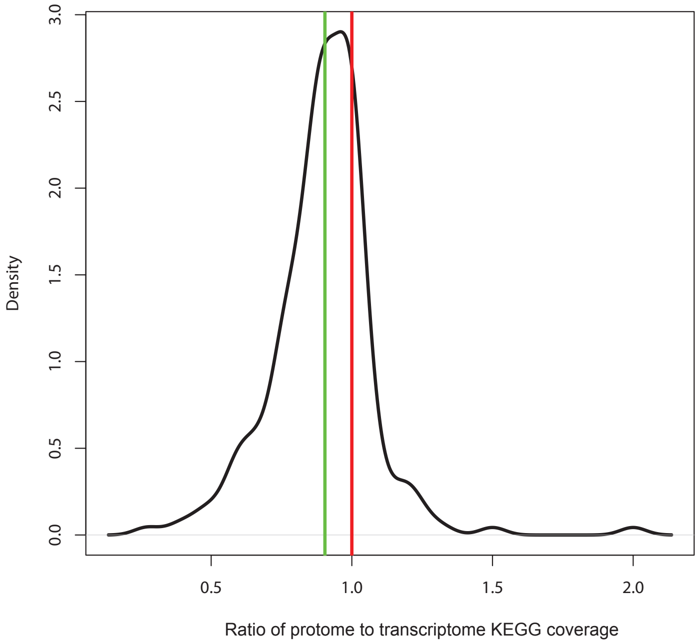


Supplementary figure 4

A



B



Supplementary tables

Table S1: List of peptide and protein identification from different runs.

Table S2: Distribution of protein and mRNA identification in the various chromosomes. Proteins and transcripts identified on the Y chromosome are nearly sequence identical to genes on other chromosomes.

Table S3: List of peptides that mapped to potentially novel exons based on GENSCAN prediction

Table S4: List of genes identified by RNA-seq.

Table S5: Estimated copy number versus absolute copy number. Protein Expressed Sequence Tag (PrEST) copy number data are from Zeiler et al. Molecular and Cellular Proteomics *in revision*.

Table S6: The most abundant proteins that contribute to the 50% proteome mass calculated according to the iBAQ values from trypsin digestion data.

Table S7: Estimated protein absolute amounts based on iBAQ intensities. Quantification is given as fmol protein and as copy number per cell. Copy numbers below 500 (highlighted in blue) are considered unreliable.