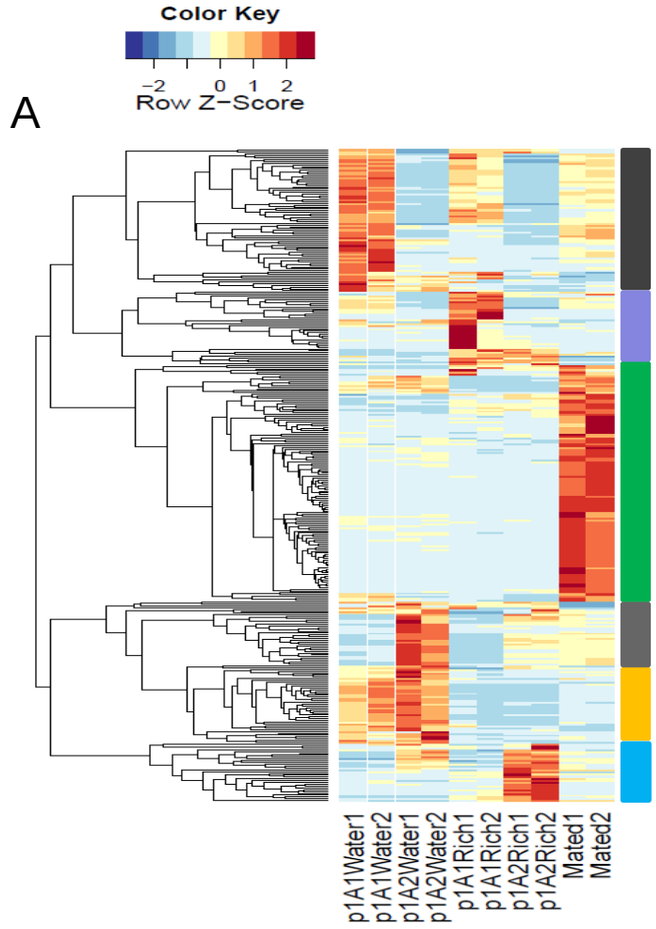

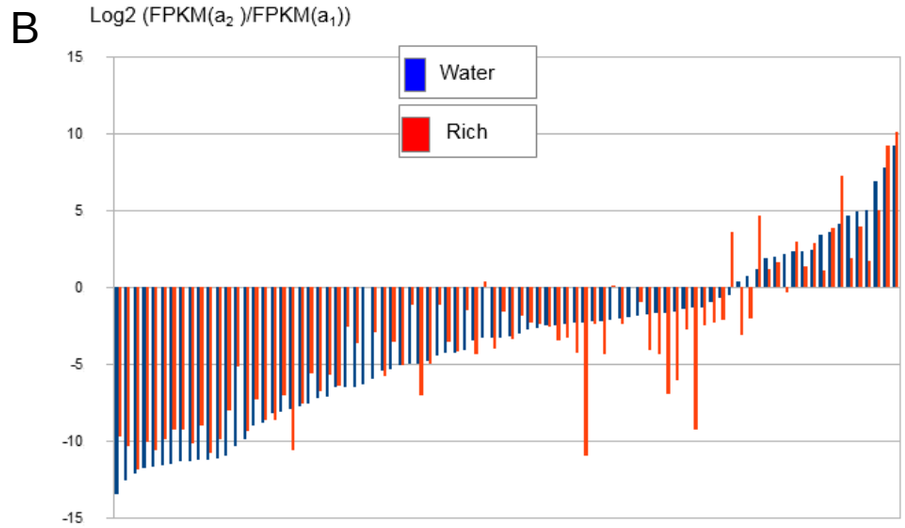

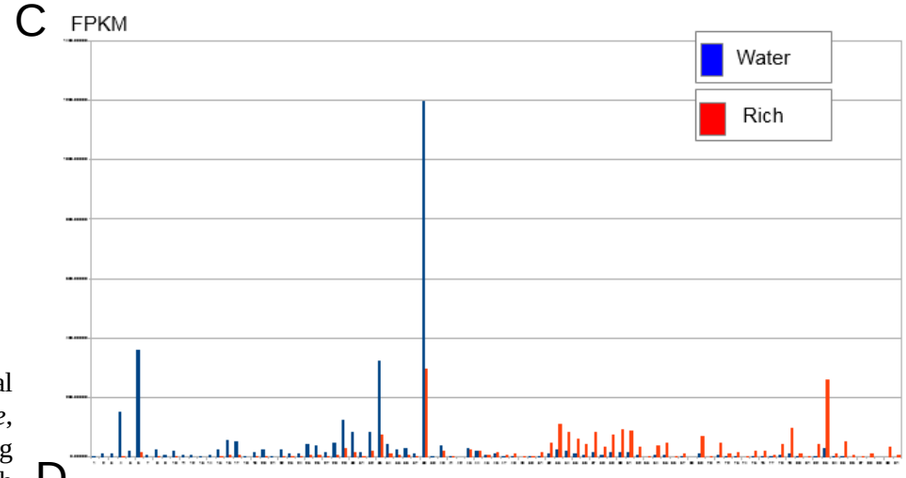

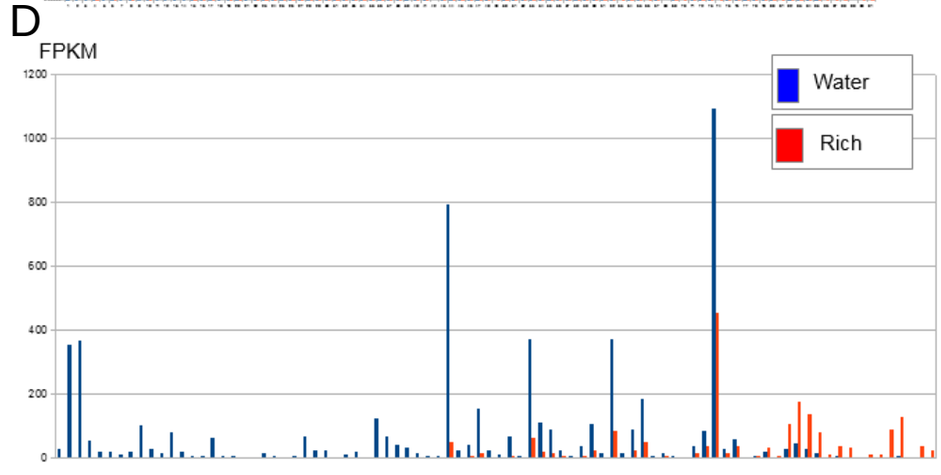

Figure S4. Expression data. A) Heatmap of differential gene expression for two biological replicates each of separated a_1 and a_2 haploid cultures of *Microbotryum lychnidis-dioicae*, assessed with separated a_1 and a_2 sporidia under conducive and non-conducive mating environments (*i.e.*, low nutrient water agar versus nutrient rich medium, respectively) and with mixed a_1 and a_2 sporidia under conducive mating environment. The expression profiles of differentially expressed genes were clustered using Euclidian distance and complete clustering; the resulting tree (left) illustrates the relationships of the five predominant clusters (right, colored bars these correspond to genes up-regulated in A1 vs A2 in water (brown) or in rich media (pink); up-regulated in mated cells (green); genes up-regulated in A2 vs A1 in water (purple) or in rich media (blue); and genes differentially expressed between A1 and A2, either in one media or both (yellow). **B)** Differential expression of the 177 genes identified in the a_1 *Microbotryum lychnidis-dioicae* reference genome as differentially expressed between the two mating types (in a_2 vs a_1) on water agar (in blue) or in a rich medium (in red). The Y axis gives the log2Fold, *i.e.*, the log of the ratio of the FPKM (fragments per kilobase of exon per million fragments mapped, an absolute measure of expression) in a_2 sporidia compared to that in a_1 sporidia. A positive value means that the gene is more expressed in a_2 sporidia and a negative value that the gene is more expressed in a_1 sporidia. The genes are ordered according to increasing values of differential expression on water agar. **C)** Absolute expression (FPKM, fragments per kilobase of exon per million fragments mapped) of the 91 genes identified in the a_1 *Microbotryum lychnidis-dioicae* reference genome as differentially expressed between the two mating types on water agar, in a_1 (in blue) or in a_2 (in red), and located on autosomes. The genes are ordered as in the Figure S3B. D) Absolute expression (FPKM, fragments per kilobase of exon per million fragments mapped) of the 86 genes identified in the a_1 *Microbotryum lychnidis-dioicae* reference genome as differentially expressed between the two mating types on water agar, in a_1 (in blue) or in a_2 (in red), and located on the-mating type chromosome. The genes are ordered as in the Figure S3B.