White-rot basidiomycete *Coriolopsis gallica* HTC is one of the main biodegraders of poplar. In our previous study, we have shown the strong capacity of *C. gallica* HTC to degrade lignocellulose. In this study, equal amounts of total RNA from*C. Gallica* HTC cultures grown in different conditions were pooled together. Illumina paired-end RNA sequencing was performed, and 13.2 million 90-bp paired-end reads were generated. We chose the Merged Assembly of Oases data-set for the following blast searches and gene ontology analyses. The reads were assembled *de novo* into 28,034 transcripts (≥ 100 bp) using combined assembly strategy MAO. The transcripts were annotated using Blast2GO. In all, 18,810 transcripts (≥100 bp) achieved BLASTX hits, of which, 7048 transcripts had GO term and 2074 had ECs. The expression level of 11 lignocellulolytic enzyme genes from the assembled *C. gallica* HTC transcriptome were detected by real-time quantitative polymerase chain reaction. The results showed that expression levels of these genes were affected by carbon source and nitrogen source at the level of transcription. The current abundant transcriptome data allowed the identification of many new transcripts in *C. gallica* HTC. Data provided here represent the most comprehensive and integrated genomic resources for cloning and identifying genes of interest from *C. gallica* HTC. Characterization of *C. gallica* HTC transcriptome provides an effective tool to understand mechanisms underlying cellular and molecular functions of *C. gallica* HTC.