The Baltic Sea is a unique environment that contains unique genetic populations. In order to study these populations on a genetic level basic molecular research is needed. The aim of this thesis was to provide a basic genetic resource for population genomic studies by de novo assembling a transcriptome for the Baltic Sea isopod *Idotea balthica*.

RNA was extracted from a whole single adult male isopod and sequenced using Illumina (125bp PE) RNA-Seq. The reads were preprocessed using FASTQC for quality control, TRIMMOMATIC for trimming, and RCorrector for error correction. The preprocessed reads were then assembled with TRINITY, a de Bruijn graph-based assembler, using different k-mer sizes. The different assemblies were combined and clustered using CD-HIT. The assemblies were evaluated using TRANSRATE for quality and filtering, BUSCO for completeness, and TRANSDECODER for annotation potential. The 25-mer assembly was annotated using PANNZER (protein annotation with z-score) and BLASTX.

The 25-mer assembly represents the best first draft assembly since it contains the most information. However, this assembly shows high levels of polymorphism, which currently cannot be differentiated as paralogs or allelic variants. Furthermore, this assembly is incomplete, which could be improved by sampling additional developmental stages.

Keywords: de novo transcriptome assembly, *Idotea balthica*, isopod, population genomics, RNA-Seq, SNP discovery