1. **RNA sequencing analyses**

﻿RNA samples were submitted for sequencing to the Genomics Core Facility at the University of Bergen using Illumina HiSeq 4000 method (Illumina. Inc.. San Diego. CA. USA), and the final cDNA library was sequenced to generate 50 million 75 bp paired-end reads per sample. The resulting data were analyzed as described in Yadetie et al. 2018, using the RNA-Seq analysis workflow adapted from RASflow (Yadetie et al., 2018; Zhang & Jonassen, 2020). The quality of the sequencing reads were checked using FastQCv0.11.8 (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc>). We had altogether 18 high-quality samples, which were aligned to the published genome of Atlantic cod (gadMor1, Ensembl) using HISAT2 v2.1.0 (Kim et al.. 2015). Counts were generated from the alignment using featureCounts from subread v1.6.4 (Liao et al.. 2014). Only the genes with expression levels over one count per million (CPM) in at least one sample in the compared groups were kept and normalized by Trimmed Mean of M values (TMM) (Robinson & Oshlack. 2010) afterwards. Differential expression analysis was performed using edgeR v3.26.0 (McCarthy et al.. 2012). We first invested the effect of oil on the gene expression levels using a generalized linear model (GLM). Genes were considered significantly differentially expressed when FDR < 0.01 and |logFC| ≥ 1. Considering the number of significant genes exposed to different doses of oil, low dose has a smaller effect than high dose, as shown in the Venn diagram. The Venn diagram also indicates that more genes are differentially expressed when the fish are exposed to uv light. We therefore conducted another statistical test to investigate the interaction between the oil and uv light using the factorial model (high-dose oil \* uv light). The genes with FDR < 0.01 are considered significant: the effects of oil on their expression are different due to uv light.

