Table S1. **Review of FAANG core/additional assays and relevant work performed in salmonids to date**

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| **FAANG core assays** | **Assay target** | **Example related assays used in salmonids; assay target** |
| **Transcribed loci** |
| RNA-sequencing, stranded protocols [56, 70] | Transcriptome, strand polarity retained | RNA-seq, stranded protocol; transcriptome [71]RNA-seq; double stranded; transcriptome [67-69]RNA-seq; double stranded, miRNA [72]RNA-seq; double stranded; Long non-coding RNA [73]RNA-seq; double stranded; Large intergenic non-coding RNAs [74] |
| **Chromatin accessibility and architecture** |
| Assay for transposase-accessible chromatin sequencing (ATAC-seq) [[60, 75] | Regions of open chromatin, localization of nucleosomes in regulatory sites and positions of DNA-binding proteins | No published examples |
| DNaseI footprinting [59] | Open chromatin, delineate genomic regulatory compartments | No published examples |
| Chromatin immunoprecipitation sequencing (ChIP-seq) | Proteins linking genome architecture to function (FAANG- highly conserved insulator-binding factor, CTCF) [74] | No published examples |
| **Histone modification marks** |
| Chromatin immunoprecipitation sequencing (ChIP-seq) to detect modified histones and characterize associated sequences [61] | Histone H3 lysine 4 trimethylation (H3K4me3), identifies active gene promotors and is enriched at transcription start sitesHistone H3 lysine 27 trimethylation (H3K27me3), marks genes that have been facultatively repressed through regional modificationHistone H3 lysine 27 acetylation (H3K27ac), marks active regulatory elements, may discriminate active from inactive enhancers and promotersH3 lysine 4 monomethylation (H3K4me1), marks enhancers and other distal elements, and is enriched downstream of transcription start sites | Chromosome immune precipitation; relationship between modified histones and gene expression [77] |
| **Additional FAANG Assays** | **Assay target** | **Related assay used in salmonids; assay target** |
| DNA methylation, genome-wide analysis of 5-methylcytosines, nucleotide level resolution [58-59] | Epigenetic mark and regulator of gene expression | Methyl-sensitive AFLP, global methylation changes [78-80]Bisulphite sequencing, nucleotide-level resolution [82] |
| ChIP-seq assays [65] for sequences bound by specific proteins | Transcription factor binding sites | Chromosome Immune Precipitation Assay, regulation of transcription [83-85] |
| Genome conformation; Hi-C [64, 86] for chromosomal conformation capture | Identify distal chromatin elements that are brought together through 3D chromosomal folding | No published examples |

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