# Bioinformatic Analyses at the IMI

- **DNA-seq** (targeted, WES, WGS; matched- and non-matched; color space): variant calling, mutational patterns, clonal evolution, ethnicity, relation
- **RNA-seq** (bulk): expression analysis, fusion genes
- **Single cell omics** (RNA-seq, ATAC-seq): expression analysis, clustering, velocity
- **Microarrays** (SNP, aCGH, gene expression, 850K, 450K): CNV calling, expression analysis, methylation analysis
- **Bisulfite sequencing** (RRBS, WGBS): methylation
- **ChIP-seq**: transcription factor binding sites, histones
- **4C-seq, Hi-C-seq**: 3D chromatin structure
- **ATAC-seq**: chromatin structure
- **STARR-seq**: enhancer structure
- **Additionally**: pathway analyses, geneset enrichment, data integration and annotation

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- **DNA-seq** (targeted, WES, WGS; matched- und non-matched; color space): Varianten Calling, Mutational Patterns, Klonale Evolution, Ethnizität, Verwandschaft
- **RNA-seq** (bulk): Expressions-Analyse, Fusionsgene
- **Single cell omics** (RNA-seq, ATAC-seq): Expressions-Analyse, Cluster-Analyse, Velocity
- **Microarrays** (SNP, aCGH, gene expression, 850K, 450K): CNV Calling, Expressions-Analyse, Methylatierungs-Analyse
- **Bisulfite sequencing** (RRBS, WGBS): Methylatierung
- **ChIP-seq**: TranscriptionsfaKtor Bindungsstellen, Histone
- **4C-seq, Hi-C-seq**: 3D Chromatin Structur
- **ATAC-seq**: Chromatin Structur
- **STARR-seq**: Enhancer Structur
- **Zusätzlich**: Pathway-Analysen, Geneset Enrichment, Datenintegration und -annotation