📄 This report summarizes the quality control and reproducibility assessment of ChIP-seq replicates using the Irreproducible Discovery Rate (IDR) framework. It includes analysis of normalized and cleaned BAM files, detection of spike-in usage (when applicable), correlation heatmaps, PCA plots, FRiP scores, and PCR Bottleneck Coefficient (PBC) metrics. BAM files that failed replicate correlation were identified and excluded from downstream analysis. The goal of this report is to identify high-confidence peaks from biologically consistent replicates and provide transparency on sample quality, filtering decisions, and the reproducibility of ChIP enrichment across conditions.

IDR QC Summary

Generated on: 20250630_231017
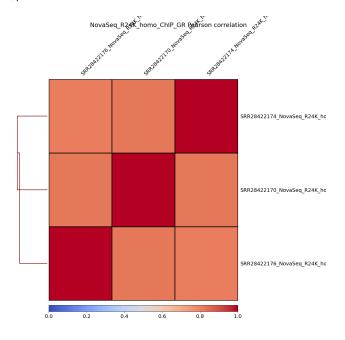
🧬 Spike-In Detection Summary

🖊 Spike detection is performed to determine if exogenous spike was added and information was not available

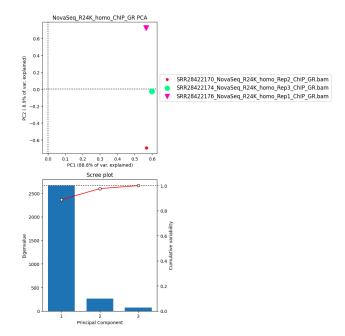| Sample	Spike Type	Spike Reads	Host Reads
SRR28422169	none	0	23545763
SRR28422170	none	0	16184140
SRR28422171	none	0	8684369
SRR28422172	none	0	13152784
SRR28422173	none	0	17153647
SRR28422174	none	0	10579775
SRR28422175	none	0	5550909
SRR28422176	none	0	13999280

📊 Replicate QC Plots

Correlation heatmaps and PCA plots based on replicate BAM files.
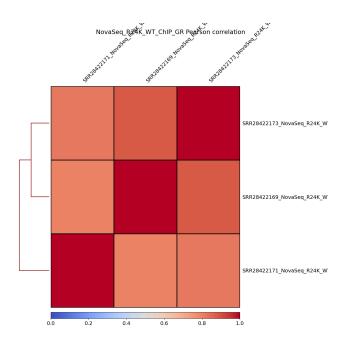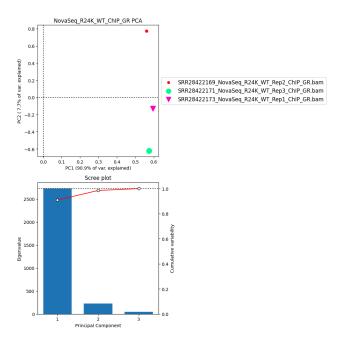
NovaSeq_R24K_homo_ChIP_GR_correlation_heatmap.png

NovaSeq_R24K_homo_ChIP_GR_PCA_plot.png

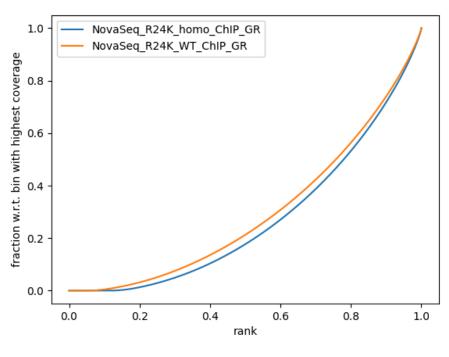NovaSeq_R24K_WT_ChIP_GR_correlation_heatmap.png

NovaSeq_R24K_WT_ChIP_GR_PCA_plot.png
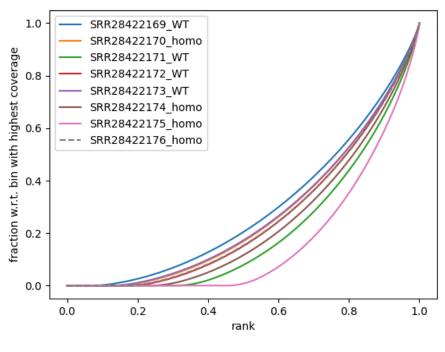
🖋️ Fingerprint Curves (Pre-IDR)

Signal-to-background profiles for all cleaned BAMs and one representative per group.

ChIP-seq fingerprint before IDR

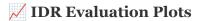Group_preIDR_fingerprint.png

ChIP-seq fingerprint before IDR

preIDR_fingerprint.png

🧬 PCR Bottleneck Coefficient (PBC)

Sample	PBC	N1	Nd	Cutoff	Interpretation
/home/nancy/DATASEt3 /analysis/Renamed_Clea ned/SRR28422169_Nova	**0.9925**	22401641	22570947	≥ 0.9	✅ High complexity

|					
/home/nancy/DATASEt3/analysis/Renamed_Cleaned/...Seq_R24K_WT_Rep2_ChIP_GR.bam					
/home/nancy/DATASEt3/analysis/Renamed_Cleaned/SRR28422170_NovaSeq_R24K_homo_Rep2_ChIP_GR.bam	**0.9902**	15256760	15407461	≥ 0.9	✅ High complexity
/home/nancy/DATASEt3/analysis/Renamed_Cleaned/SRR28422171_NovaSeq_R24K_WT_Rep3_ChIP_GR.bam	**0.9846**	8079319	8205621	≥ 0.9	✅ High complexity
/home/nancy/DATASEt3/analysis/Renamed_Cleaned/SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR.bam	**0.9909**	12502447	12617202	≥ 0.9	✅ High complexity
/home/nancy/DATASEt3/analysis/Renamed_Cleaned/SRR28422173_NovaSeq_R24K_WT_Rep1_ChIP_GR.bam	**0.9899**	16177222	16342942	≥ 0.9	✅ High complexity
/home/nancy/DATASEt3/analysis/Renamed_Cleaned/SRR28422174_NovaSeq_R24K_homo_Rep3_ChIP_GR.bam	**0.9882**	9971489	10090316	≥ 0.9	✅ High complexity
/home/nancy/DATASEt3/analysis/Renamed_Cleaned/SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR.bam	**0.9818**	5106912	5201483	≥ 0.9	✅ High complexity
/home/nancy/DATASEt3/analysis/Renamed_Cleaned/SRR28422176_NovaSeq_R24K_homo_Rep1_ChIP_GR.bam	**0.9887**	13220460	13371272	≥ 0.9	✅ High complexity
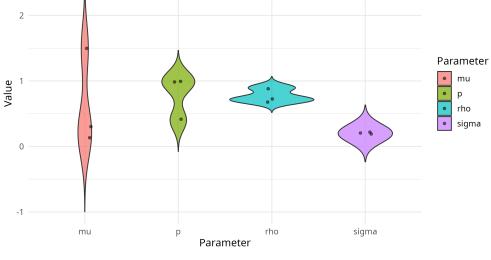
Legend: High (≥ 0.9) Moderate (0.7–0.89) Low (0.5–0.69) Very Low (< 0.5)
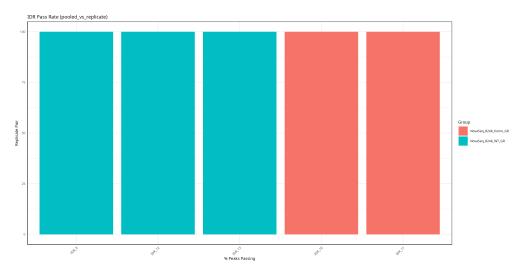
📈 IDR Evaluation Plots

These plots summarize IDR pass rates and parameter distributions for `homer` peaks.
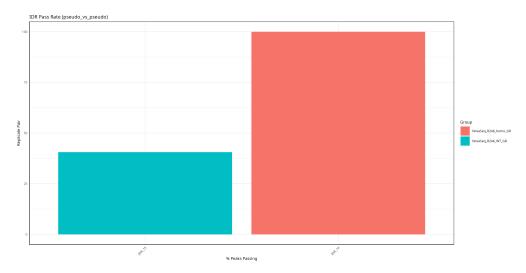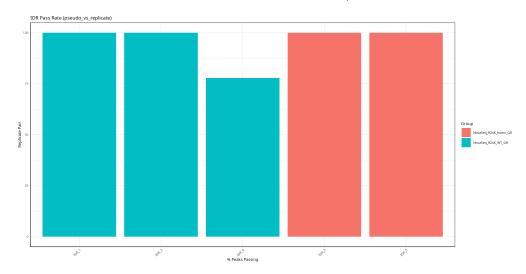
Distribution of Fitted IDR Parameters
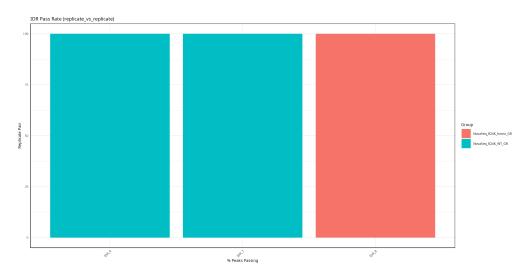

homer_idr_params_violin.png

homer_idr_pass_rate_barplot_bytype_pooled_vs_replicate.png

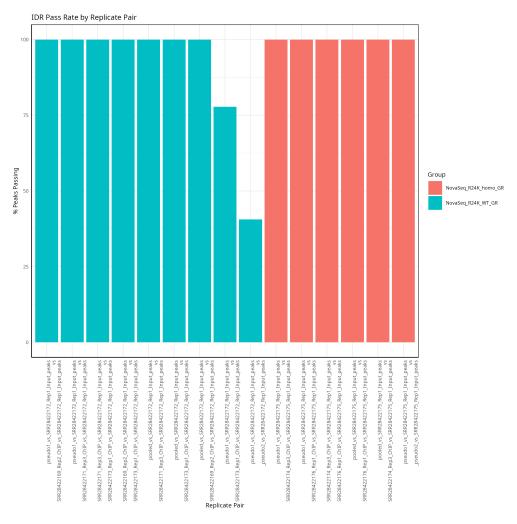homer_idr_pass_rate_barplot_bytype_pseudo_vs_pseudo.png
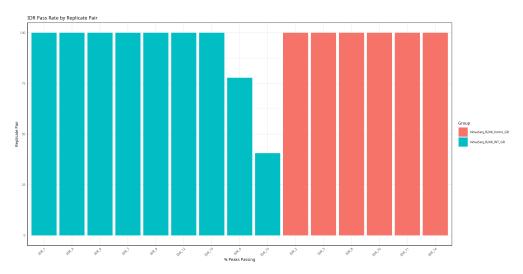
homer_idr_pass_rate_barplot_bytype_pseudo_vs_replicate.png
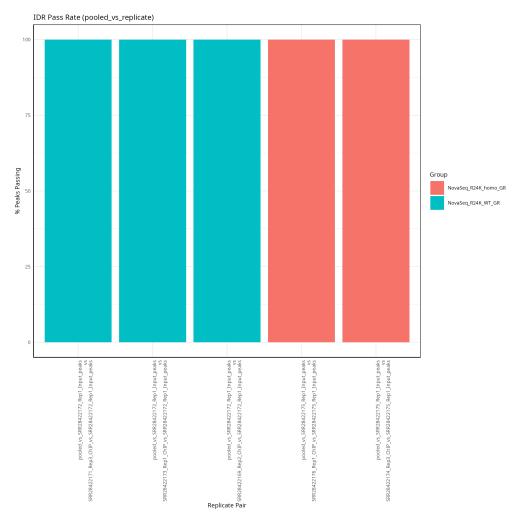
homer_idr_pass_rate_barplot_bytype_replicate_vs_replicate.png
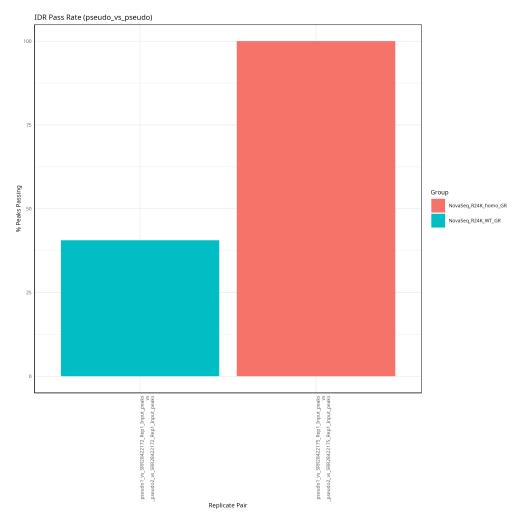
homer_idr_pass_rate_barplot.png

homer_idr_pass_rate_barplot_v2.png

IDR Pass Rate (pooled_vs_replicate)
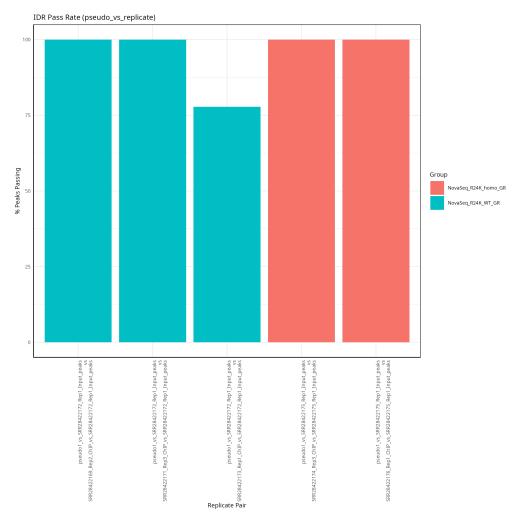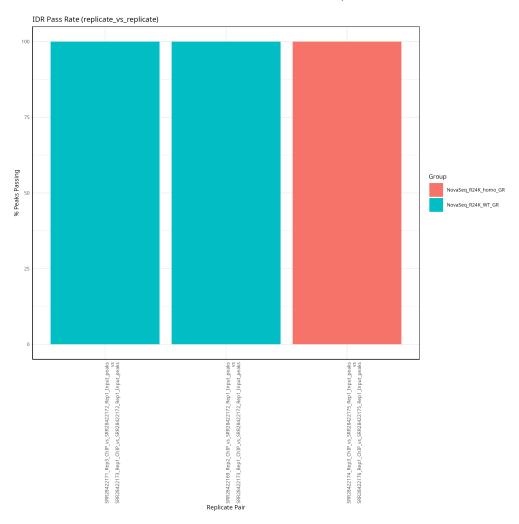
homer_idr_pass_rate_barplot_wrapped_bytype_pooled_vs_replicate.png

homer_idr_pass_rate_barplot_wrapped_bytype_pseudo_vs_pseudo.png
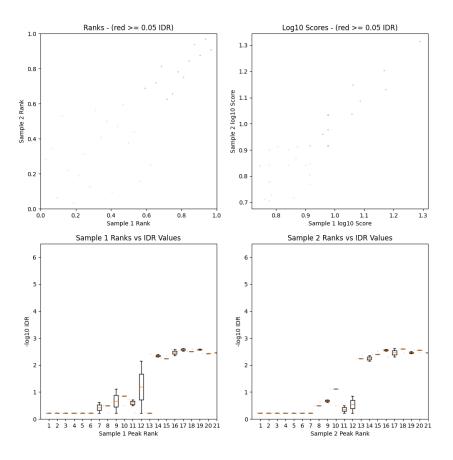
IDR Pass Rate (pseudo_vs_replicate)

homer_idr_pass_rate_barplot_wrapped_bytype_pseudo_vs_replicate.png

IDR Pass Rate (replicate_vs_replicate)
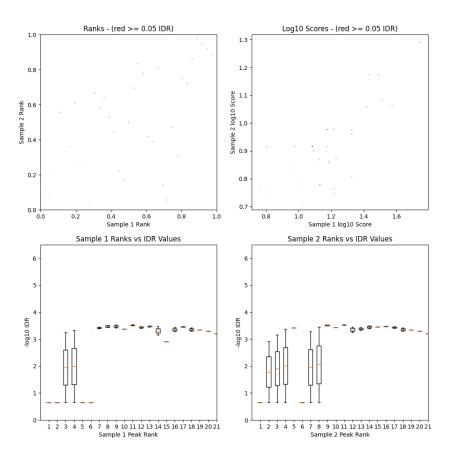
homer_idr_pass_rate_barplot_wrapped_bytype_replicate_vs_replicate.png

pooled_R24K_WT_GR_NovaSeq_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks__vs__
SRR28422173_NovaSeq_R24K_WT_Rep1_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks.idr.txt.png

R24K_WT_GR_NovaSeq_pseudo1_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks__vs__
R24K_WT_GR_NovaSeq_pseudo2_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks.idr.txt.png

R24K_WT_GR_NovaSeq_pseudo1_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks__vs__
SRR28422173_NovaSeq_R24K_WT_Rep1_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks.idr.txt.png

📊 FRiP Scores from Initial Peak Calling

📦 PeakCalling_HOMER

| Sample	Tag Count	Peak Count	FRiP
SRR28422169_NovaSeq_R24K_WT_Rep2_ChIP_GR	0.0001	2819	22743421 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER/narrow_PEAKS/SRR28422169_NovaSeq_R24K_WT_Rep2_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment
SRR28422171_NovaSeq_R24K_WT_Rep3_ChIP_GR	0.0002	1564	8361594 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER/narrow_PEAKS/SRR28422171_NovaSeq_R24K_WT_Rep3_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment
SRR28422173_NovaSeq_R24K_WT_Rep1_ChIP_GR	0.0004	5850	16527626 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER/narrow_PEAKS/SRR28422173_NovaSeq_R24K_WT_Rep1_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment

SRR28422174_NovaSeq_R24K_homo_Rep3_ChIP_GR	0.0001	620	10228681 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER/narrow_PEAKS/SRR28422174_NovaSeq_R24K_homo_Rep3_ChIP_GR_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment
SRR28422176_NovaSeq_R24K_homo_Rep1_ChIP_GR	0.0004	5003	13545283 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER/narrow_PEAKS/SRR28422176_NovaSeq_R24K_homo_Rep1_ChIP_GR_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment

📦 PeakCalling_HOMER_pool_pseudo

Sample	Tag Count	Peak Count	FRiP
pooled_R24K_homo_GR_NovaSeq_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR	Pooled	0.0000	1633 39348047 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER_pool_pseudo/narrow_PEAKS/pooled_R24K_homo_GR_NovaSeq_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment
pooled_R24K_WT_GR_NovaSeq_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR	Pooled	0.0001	5541 47632641 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER_pool_pseudo/narrow_PEAKS/pooled_R24K_WT_GR_NovaSeq_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment
R24K_homo_GR_NovaSeq_pseudo1_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR	Pseudorep1	0.0000	929 19680953 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER_pool_pseudo/narrow_PEAKS/R24K_homo_GR_NovaSeq_pseudo1_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment
R24K_homo_GR_NovaSeq_pseudo2_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR	Pseudorep2	0.0000	827 19668875 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER_pool_pseudo/narrow_PEAKS/R24K_homo_GR_NovaSeq_pseudo2_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment
R24K_WT_GR_NovaSeq_pseudo1_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR	Pseudorep1	0.0002	3729 23804642 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER_pool_pseudo/narrow_PEAKS/R24K_WT_GR_NovaSeq_pseudo1_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment
R24K_WT_GR_NovaSeq_pseudo2_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR	Pseudorep2	0.0001	3537 23813869 /home/nancy/DATASEt3/analysis/PeakCalling_HOMER_pool_pseudo/narrow__PEAKS/R24K_WT_GR_NovaSeq_pseudo2_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR_peaks.narrowPeak FAIL_FRIP: Poor enrichment

◆ High-confidence Peak Metrics

Group	Merged_IDR_Peaks	High_Confidence_Peaks(IDR≤0.01)	Comment
NovaSeq_R24K_homo_GR	8	NA	No replicate IDR file found
NovaSeq_R24K_WT_GR	18	NA	No replicate IDR file found

◆ Replicate Agreement (Rescue & Self-Consistency)

Group	Replicate_vs_Replicate	Pooled_vs_Pseudo	Pseudo_vs_Pseudo	Rescue_Ratio	Self_Consistency_Ratio	Comment
NovaSeq_R24K_homo_GR	NA	NA	Missing data			
NovaSeq_R24K_WT_GR	NA	NA	Missing data			

◆ Jaccard Overlap (Replicate Peak Similarity)

Group	Replicate 1	Replicate 2	Jaccard Index	Intersection	Union	Interpretation
NovaSeq_R24K_homo_GR	SRR28422174_NovaSeq_R24K_homo_Rep3_ChIP_GR_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR	SRR28422176_NovaSeq_R24K_homo_Rep1_ChIP_GR_vs_SRR28422175_NovaSeq_R24K_homo_Rep1_Input_GR	0.08474	35131	2977	❌ Low similarity
NovaSeq_R24K_WT_GR	SRR28422169_NovaSeq_R24K_WT_Rep2_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR	SRR28422171_NovaSeq_R24K_WT_Rep3_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR	0	55072	0	❌ Low similarity
NovaSeq_R24K_WT_GR	SRR28422169_NovaSeq_R24K_WT_Rep2_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR	SRR28422173_NovaSeq_R24K_WT_Rep1_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR	0.000335501	92399	31	❌ Low similarity
NovaSeq_R24K_WT_GR	SRR28422171_NovaSeq_R24K_WT_Rep3_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR	SRR28422173_NovaSeq_R24K_WT_Rep1_ChIP_GR_vs_SRR28422172_NovaSeq_R24K_WT_Rep1_Input_GR	0.0776389	73507	5707	❌ Low similarity

Legend:

- 🔥 High similarity (≥ 0.5)
- ⚠️ Moderate similarity (0.3–0.49)
- ❌ Low similarity (< 0.3)

Value range:

• 0 → No overlap at all

- 1 → Perfect overlap (identical peak sets)