

This report summarizes the quality control and reproducibility assessment of ChIP-seq replicates using the Irreducible Discovery Rate (IDR) framework. It includes analysis of normalized and cleaned BAM files, detection of spike-in usage (when applicable), correlation heatmaps, PCA plots, FDRiP 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: 20250617_220818



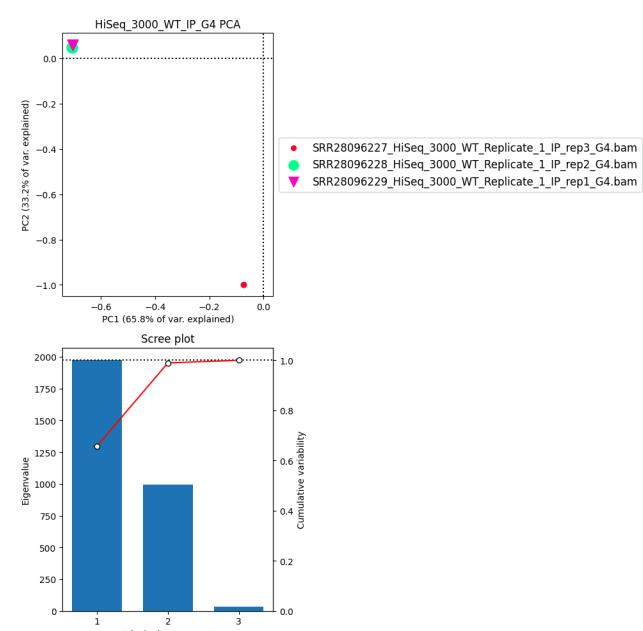
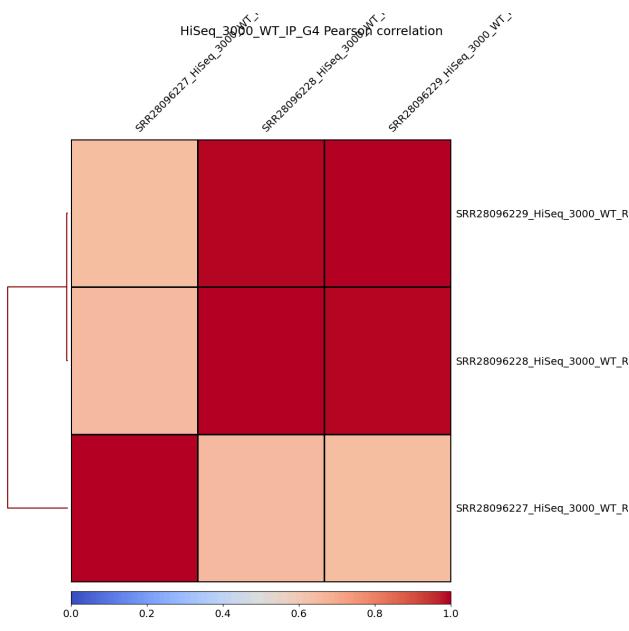
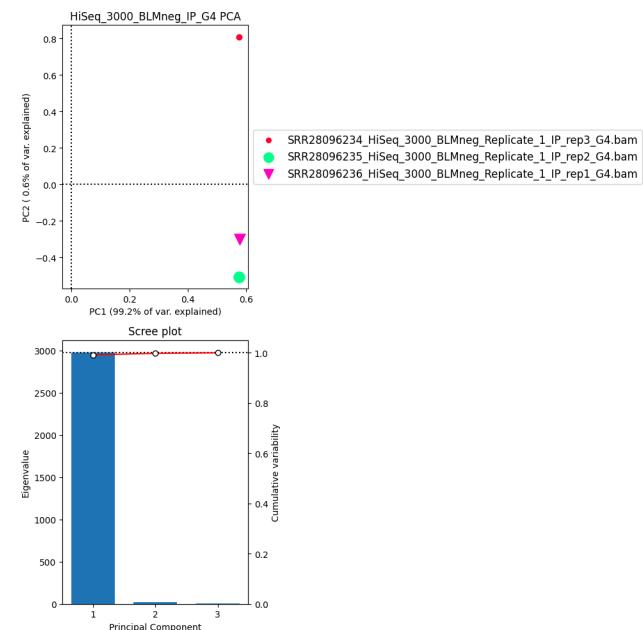
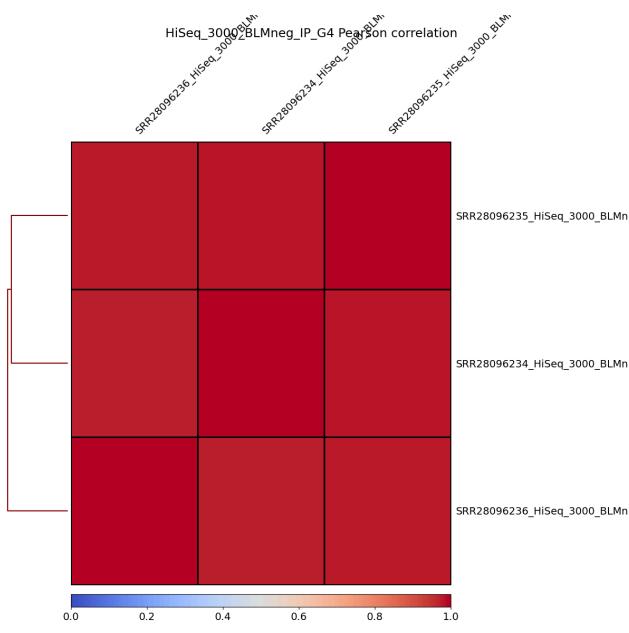
💡 Spike-In Detection Summary

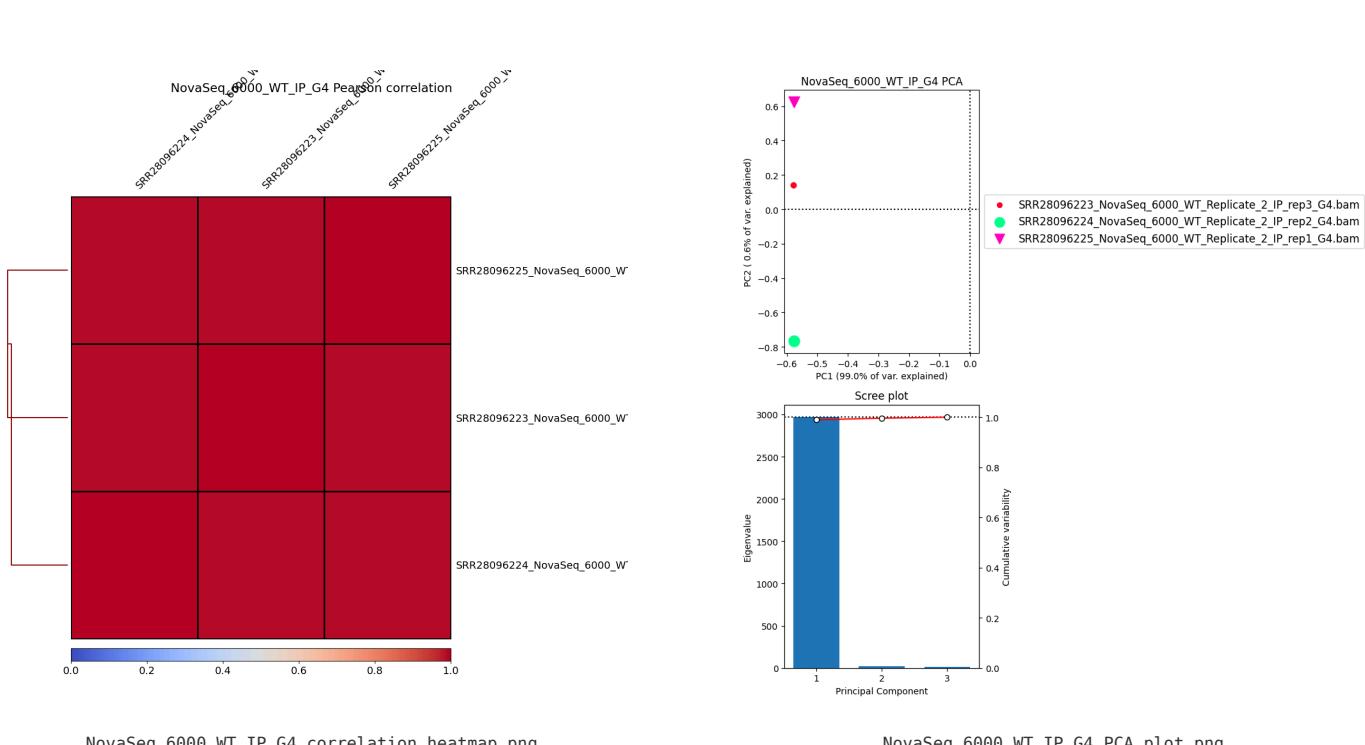
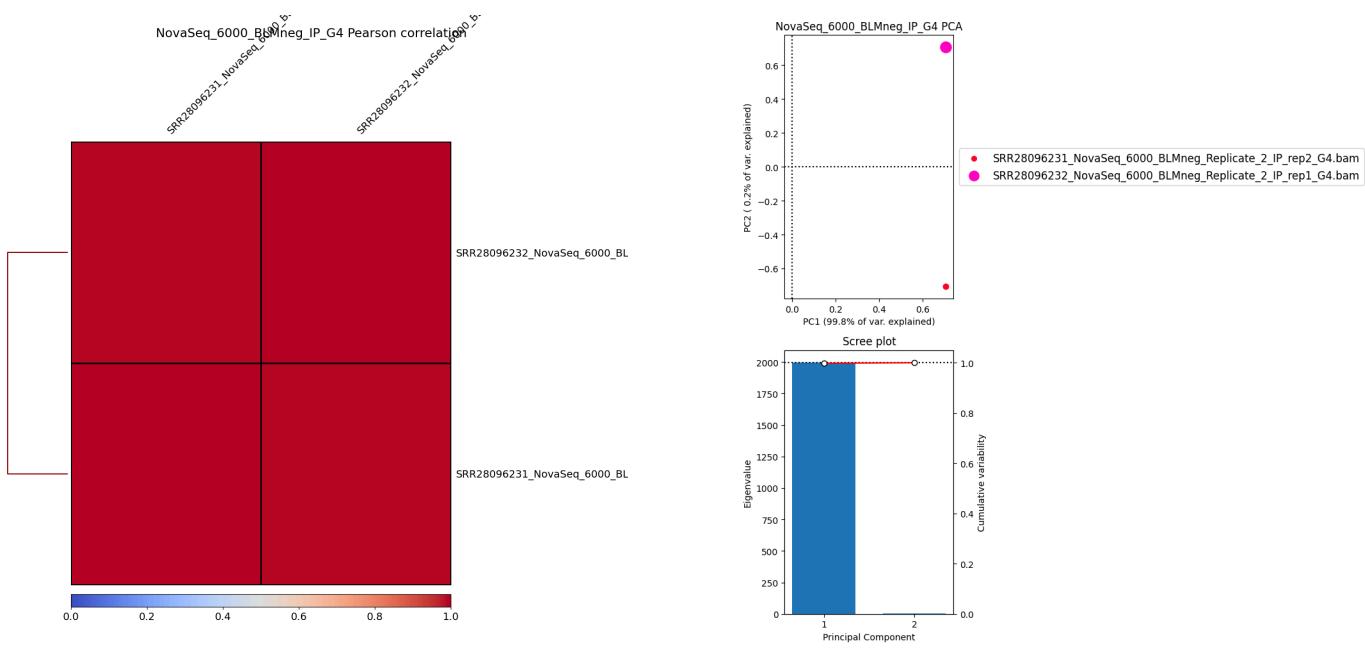
Spike detection is performed to determine if exogenous spike was added and information was not available

Sample	Spike Type	Spike Reads	Host Reads
SRR28096222	mm10	11106	64294511
SRR28096223	mm10	35124	65540595
SRR28096224	mm10	40221	64363044
SRR28096225	mm10	39904	66114164
SRR28096226	mm10	55687	47462781
SRR28096227	mm10	4322	30931302
SRR28096228	mm10	52523	46616127
SRR28096229	mm10	57290	52697766
SRR28096230	mm10	7716	75031161
SRR28096231	mm10	59769	82525475
SRR28096232	mm10	43875	83022183
SRR28096233	mm10	5827	25668788
SRR28096234	mm10	8188	20741749
SRR28096235	mm10	6560	20940268
SRR28096236	mm10	7221	18740451

📊 Replicate QC Plots

Correlation heatmaps and PCA plots based on replicate BAM files.

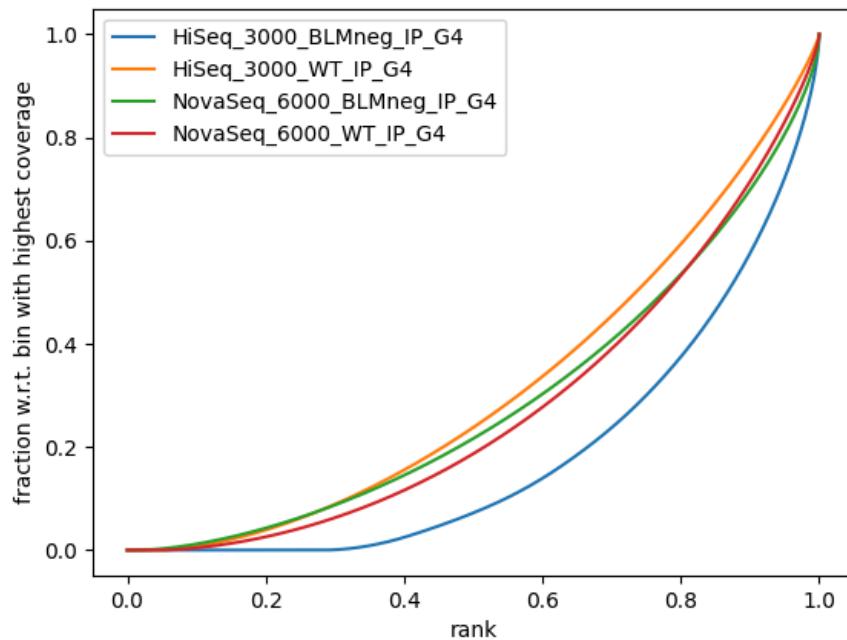




✍ Fingerprint Curves (Pre-IDR)

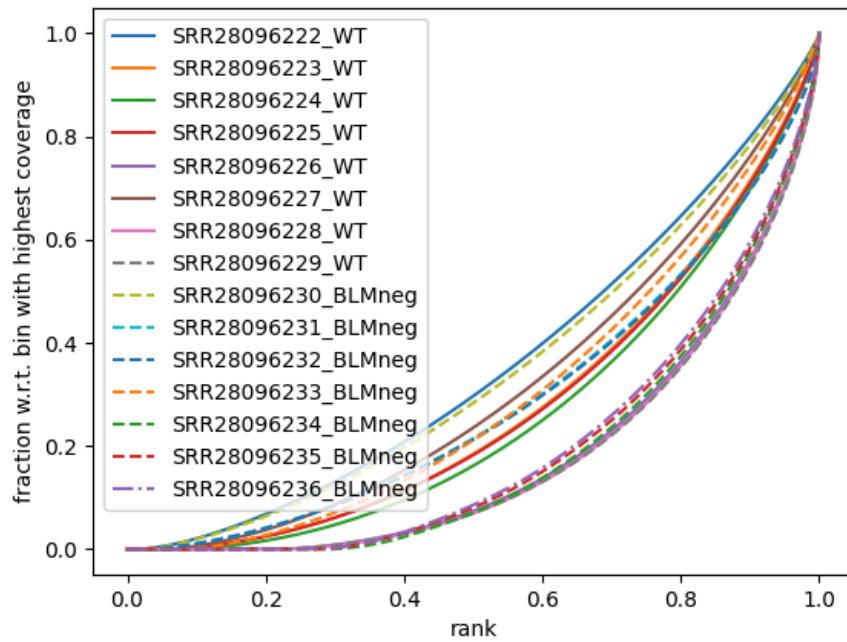
Signal-to-background profiles for all cleaned BAMs and one representative per group.

ChIP-seq fingerprint before IDR



Group_preIDR_fingerprint.png

ChIP-seq fingerprint before IDR



preIDR_fingerprint.png

Rejected Samples

BAM files that failed correlation with other replicates. Moved to analysis/BAM_replicate_fail

Original ID	Renamed BAM(s)
SRR28096227	../../../../BAM_replicate_fail/SRR28096227_HiSeq_3000_WT_Replicate_1_IP_rep3_G4.bam

PCR Bottleneck Coefficient (PBC)

Sample	PBC	N1	Nd	Cutoff	Interpretation
analysis/Renamed_Cleaned/SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4.bam	0.9981	63154240	63271559	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096223_NovaSeq_6000_WT_Replicate_2_IP_rep3_G4.bam	0.9951	64133042	64450921	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096224_NovaSeq_6000_WT_Replicate_2_IP_rep2_G4.bam	0.9966	63184220	63400924	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096225_NovaSeq_6000_WT_Replicate_2_IP_rep1_G4.bam	0.9946	64653334	65005231	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4.bam	0.9971	46779293	46914289	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096227_HiSeq_3000_WT_Replicate_1_IP_rep3_G4.bam	0.9987	30426441	30465083	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096228_HiSeq_3000_WT_Replicate_1_IP_rep2_G4.bam	0.9972	45953671	46083132	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096229_HiSeq_3000_WT_Replicate_1_IP_rep1_G4.bam	0.9968	51901889	52070592	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4.bam	0.9976	73646482	73826011	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096231_NovaSeq_6000_BLMneg_Replicate_2_IP_rep2_G4.bam	0.9982	81273886	81423805	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096232_NovaSeq_6000_BLMneg_Replicate_2_IP_rep1_G4.bam	0.9981	81751727	81905315	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4.bam	0.9958	25037902	25142838	≥ 0.9	✓ High complexity
analysis/Renamed_Cleaned/SRR28096234_HiSeq_3000_BLMneg_Replicate_1_IP_rep3_G4.bam	0.9933	20177467	20312763	≥ 0.9	✓ High complexity

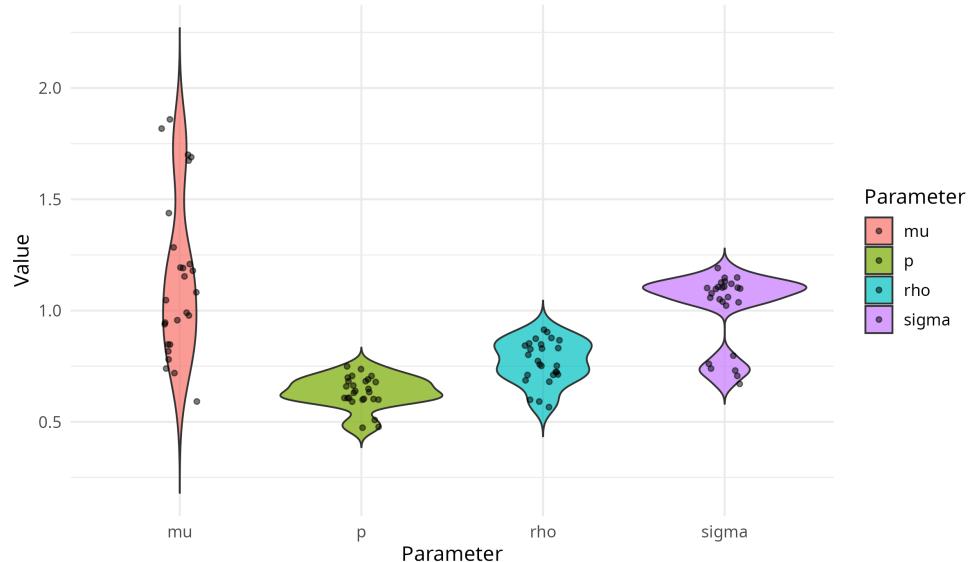
analysis/Renamed_Cleaned/SRR28096235_HiSeq_3000_BLMneg_Replicate_1_IP_rep2_G4.bam	0.9937	20379736	20508694	≥ 0.9	<input checked="" type="checkbox"/> High complexity
analysis/Renamed_Cleaned/SRR28096236_HiSeq_3000_BLMneg_Replicate_1_IP_rep1_G4.bam	0.9947	18270812	18368111	≥ 0.9	<input checked="" type="checkbox"/> High complexity

Legend: High (≥ 0.9) Moderate (0.7–0.89) Low (0.5–0.69) Very Low (< 0.5)

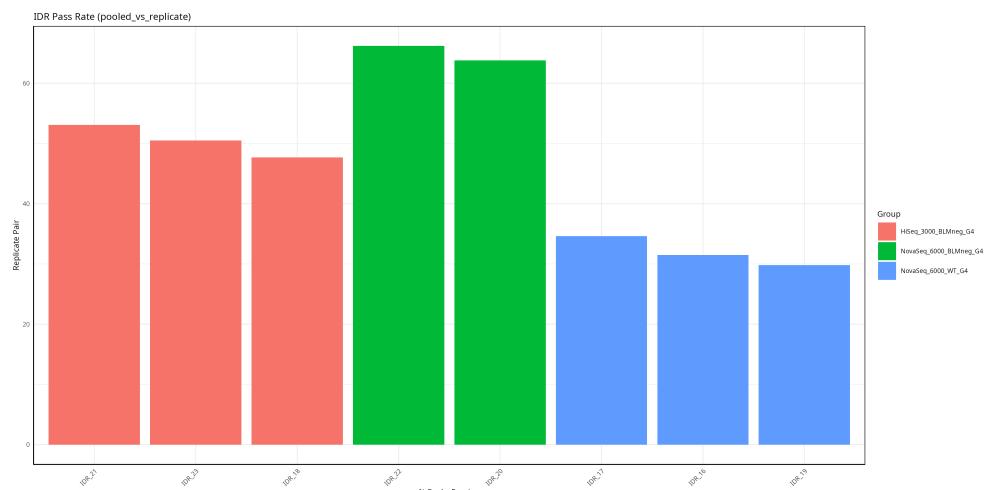
IDR Evaluation Plots

These plots summarize IDR pass rates and parameter distributions for `macs3` peaks.

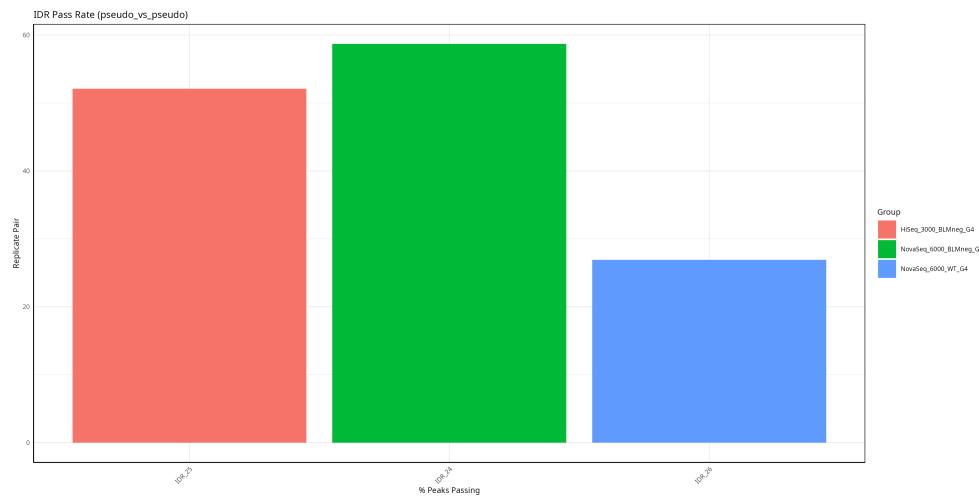
Distribution of Fitted IDR Parameters



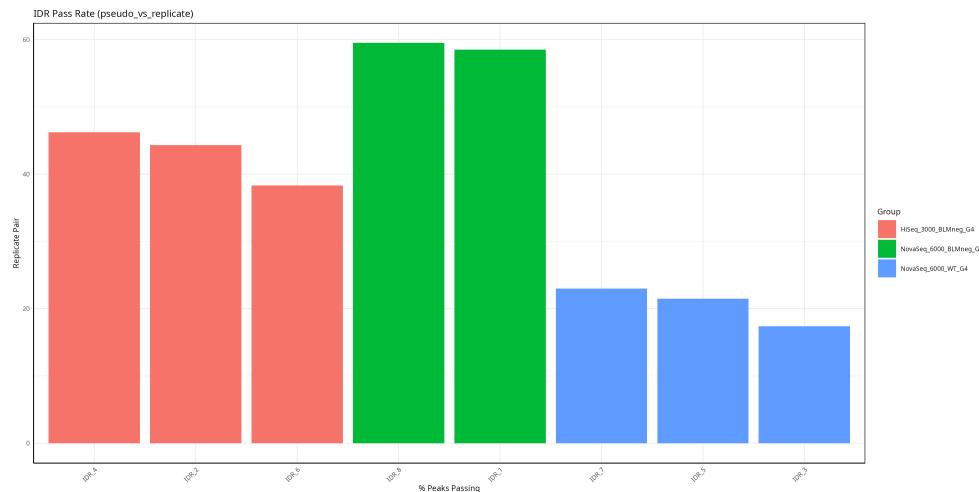
macs3_idr_params_violin.png



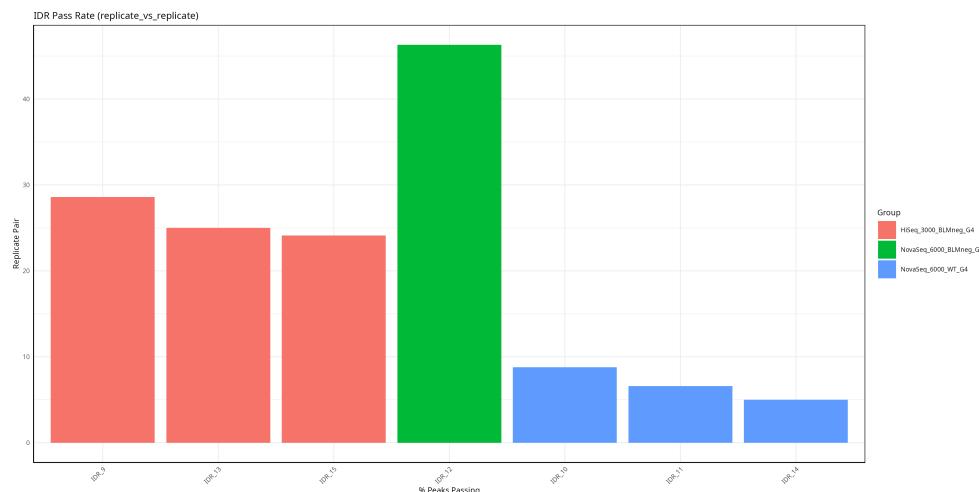
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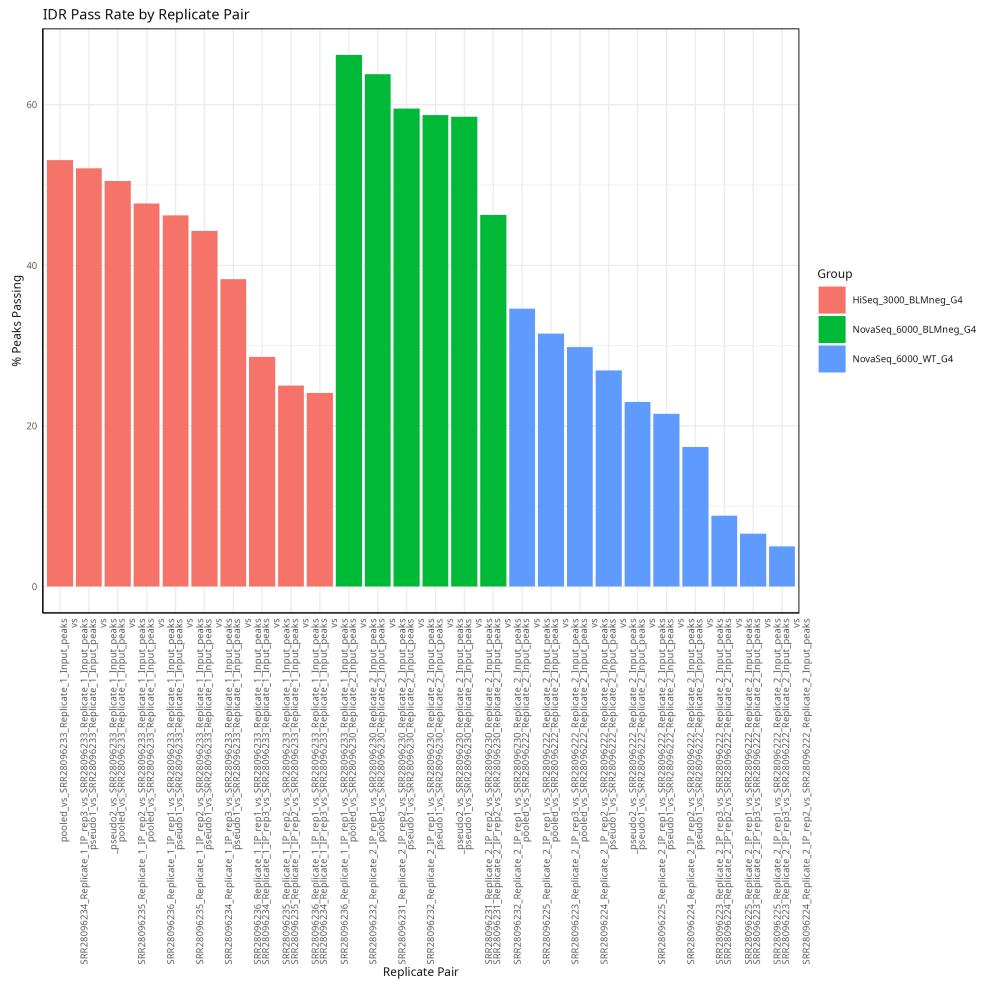
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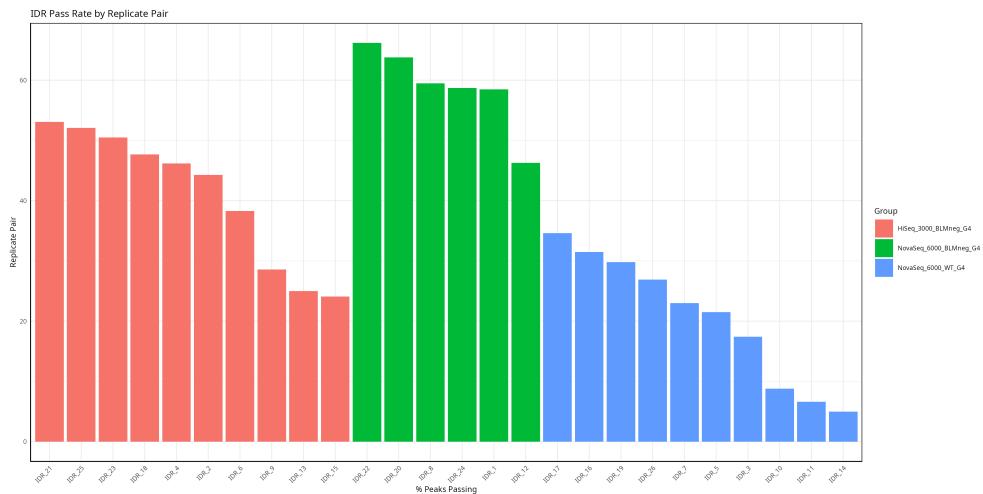
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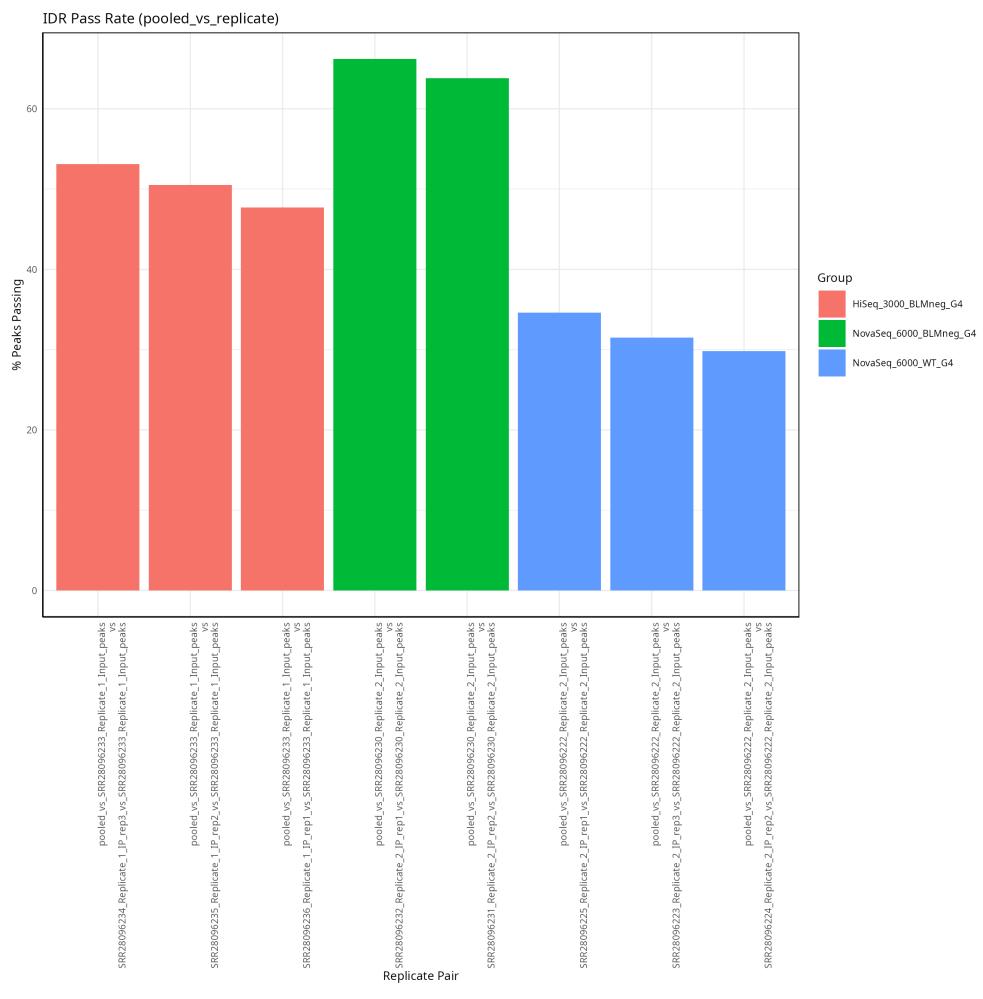
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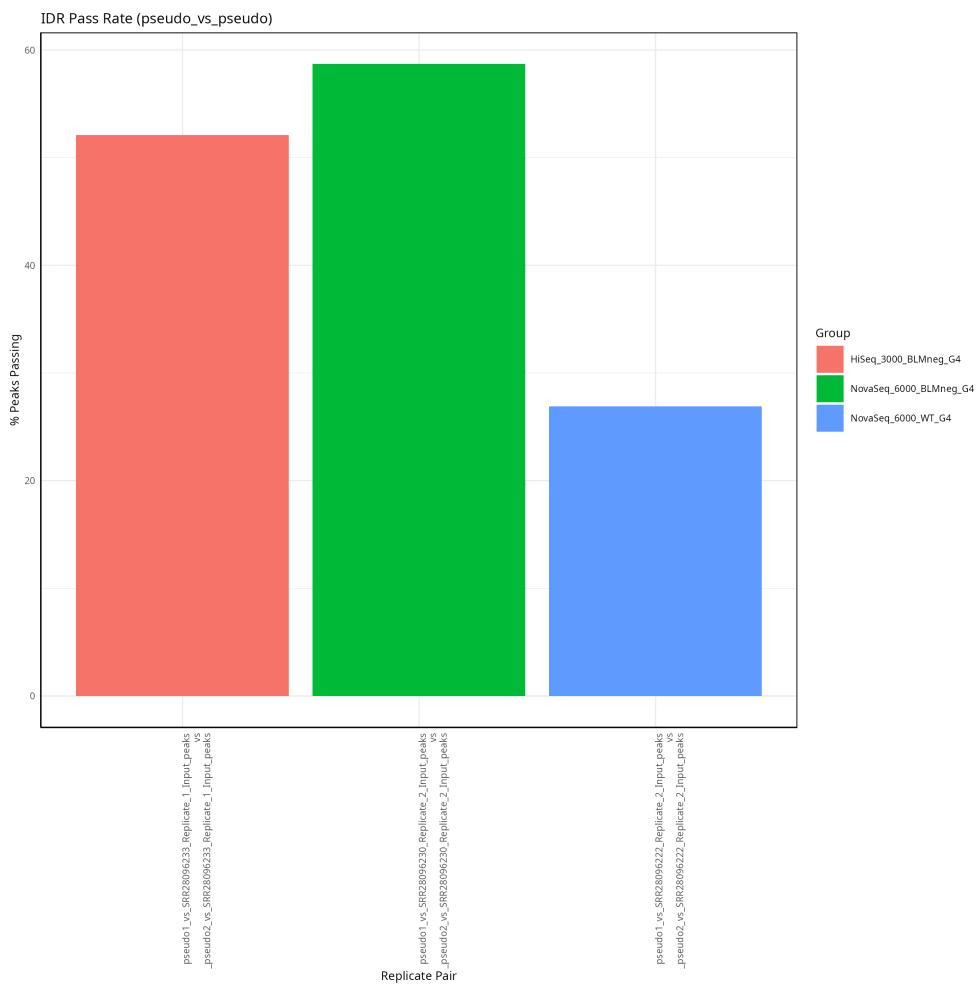
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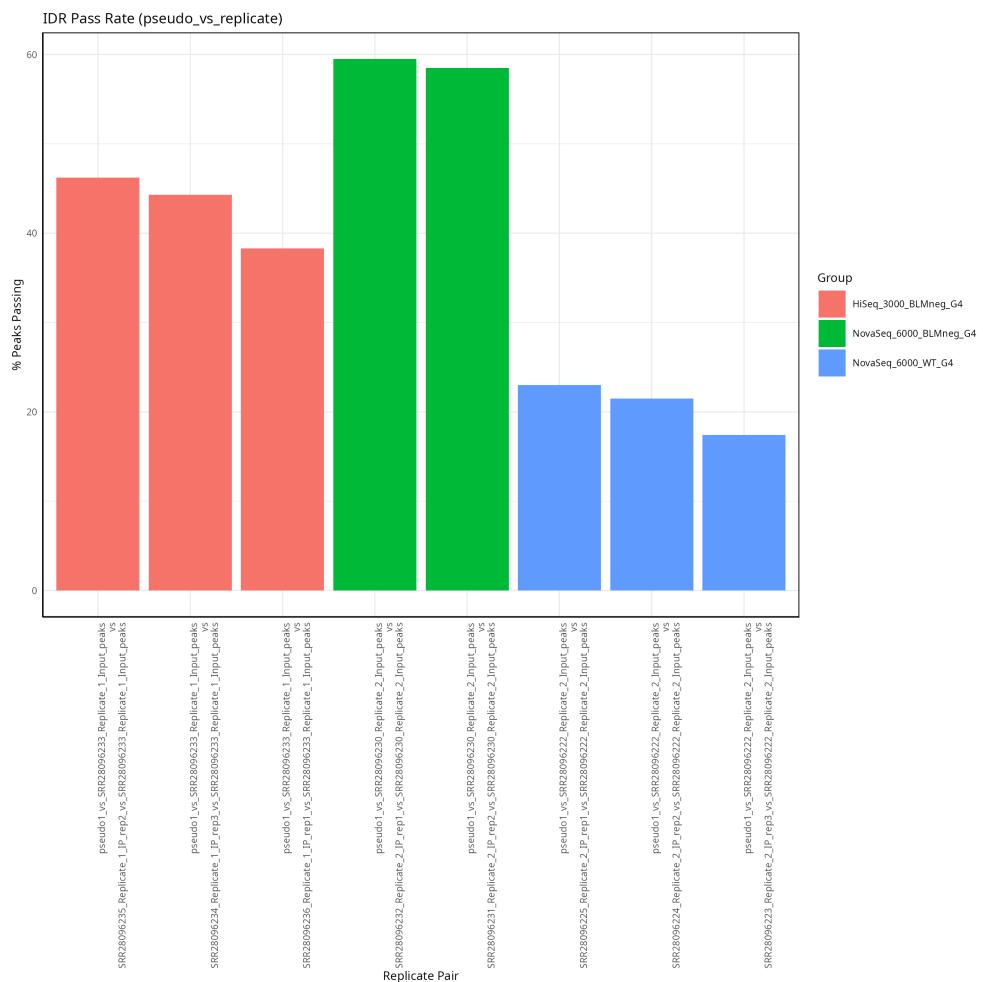
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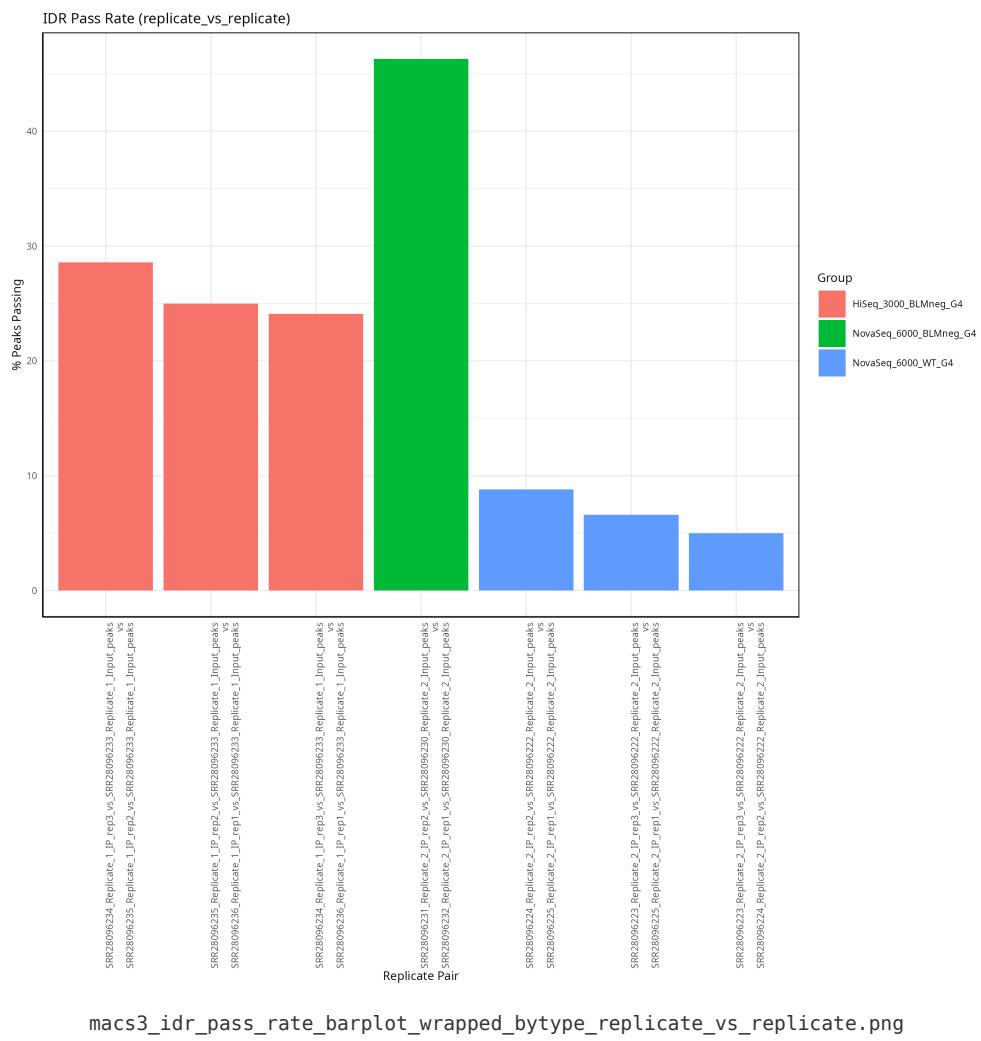
macs3_idr_pass_rate_barplot_wrapped_bytype_pooled_vs_replicate.png

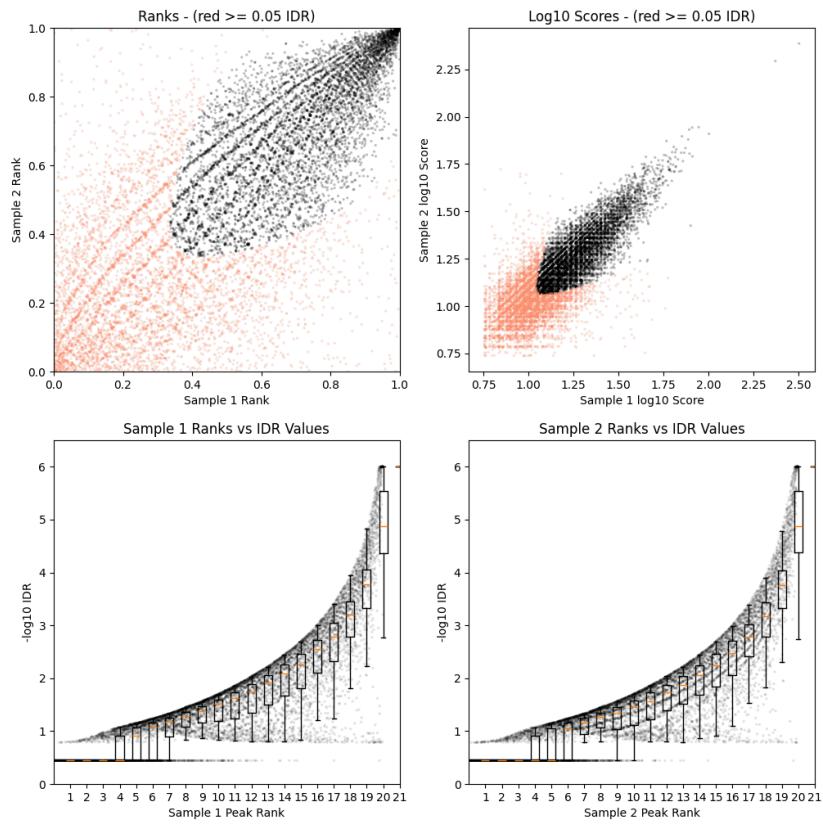


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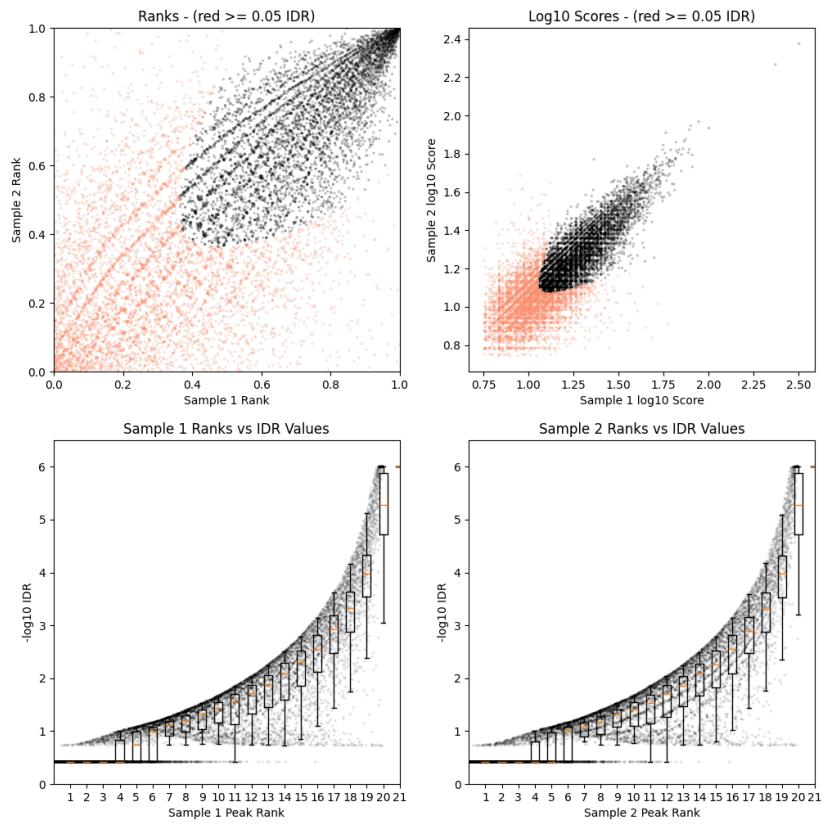


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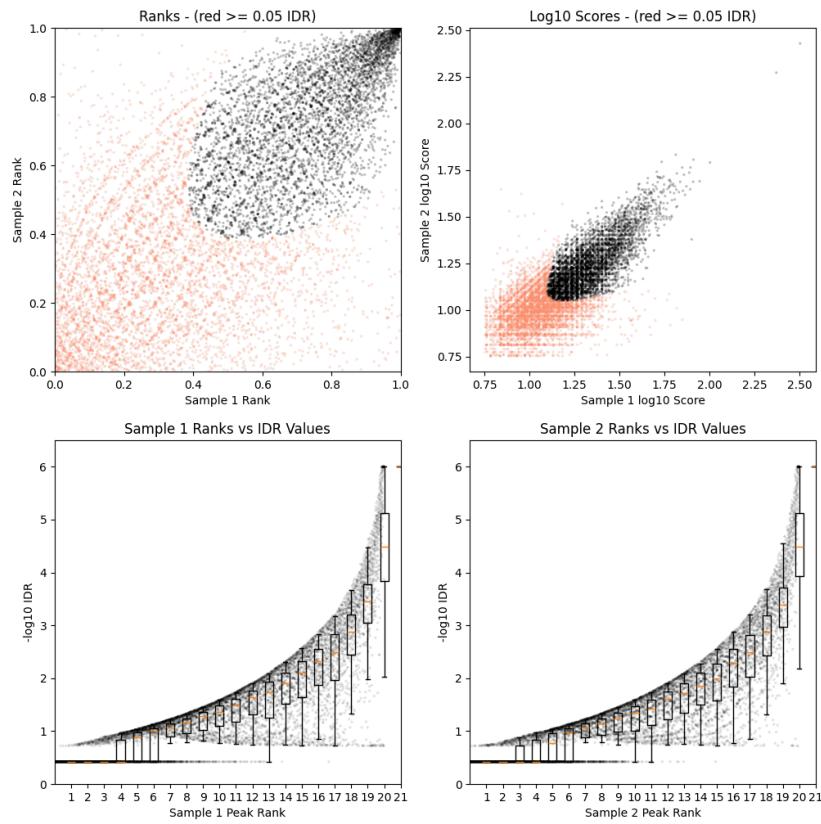




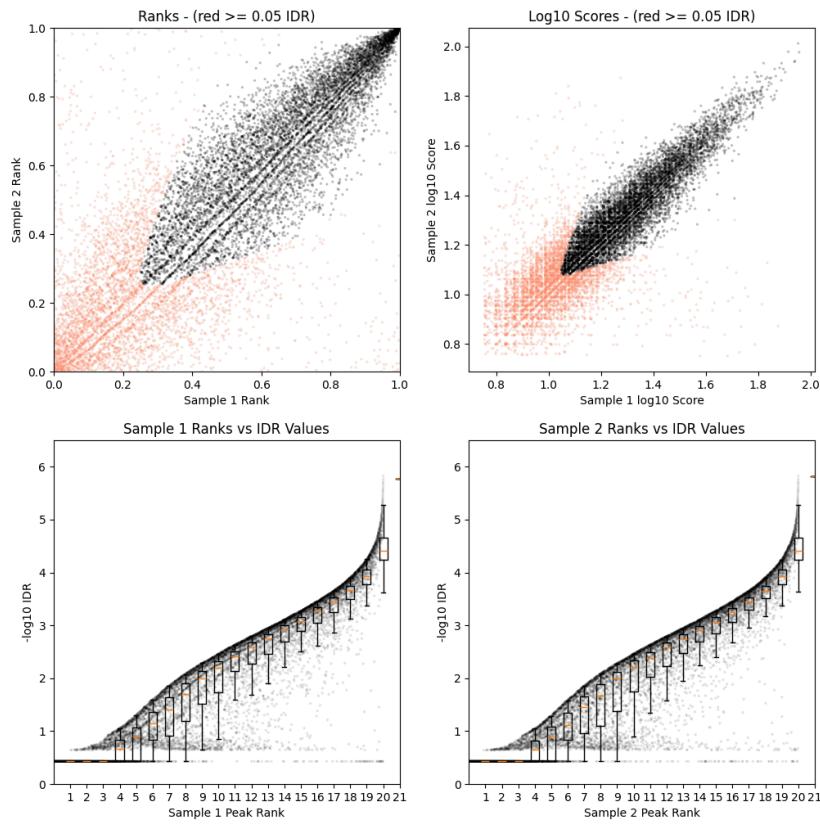
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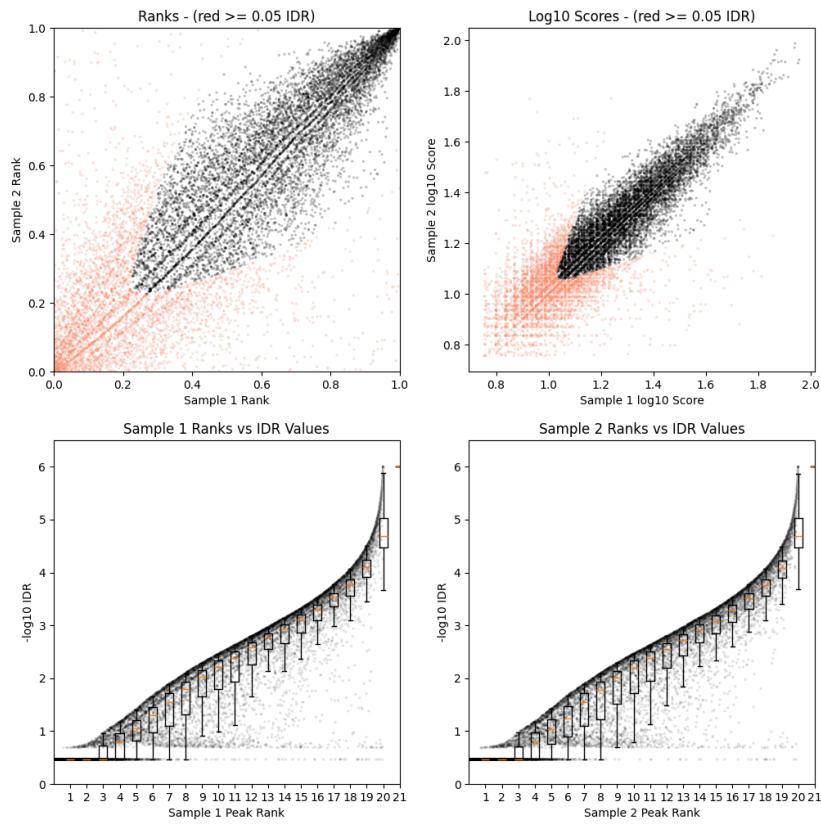
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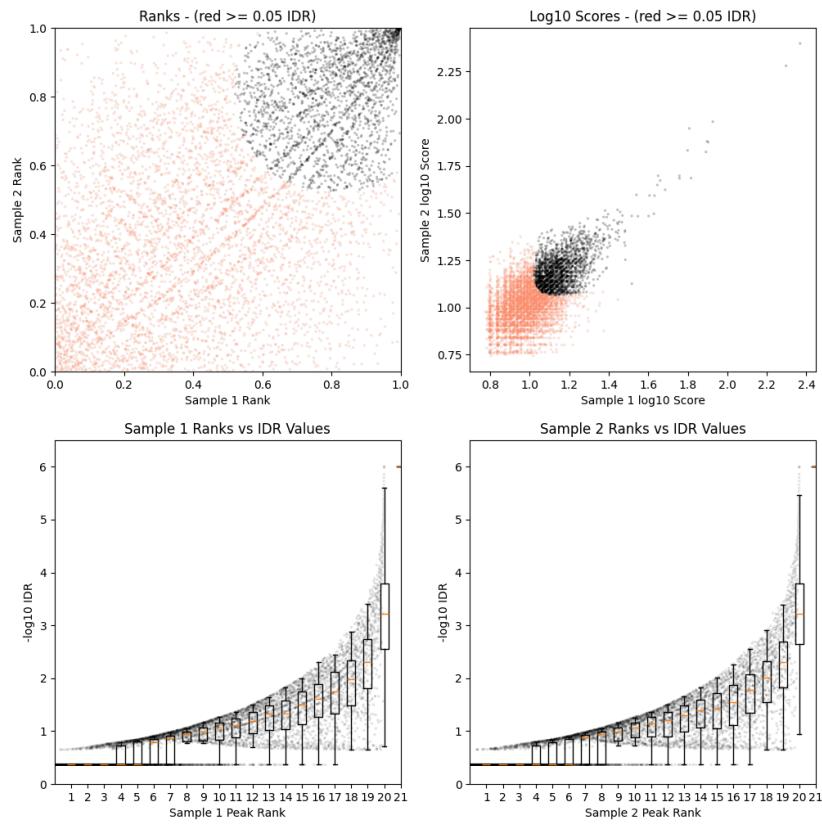
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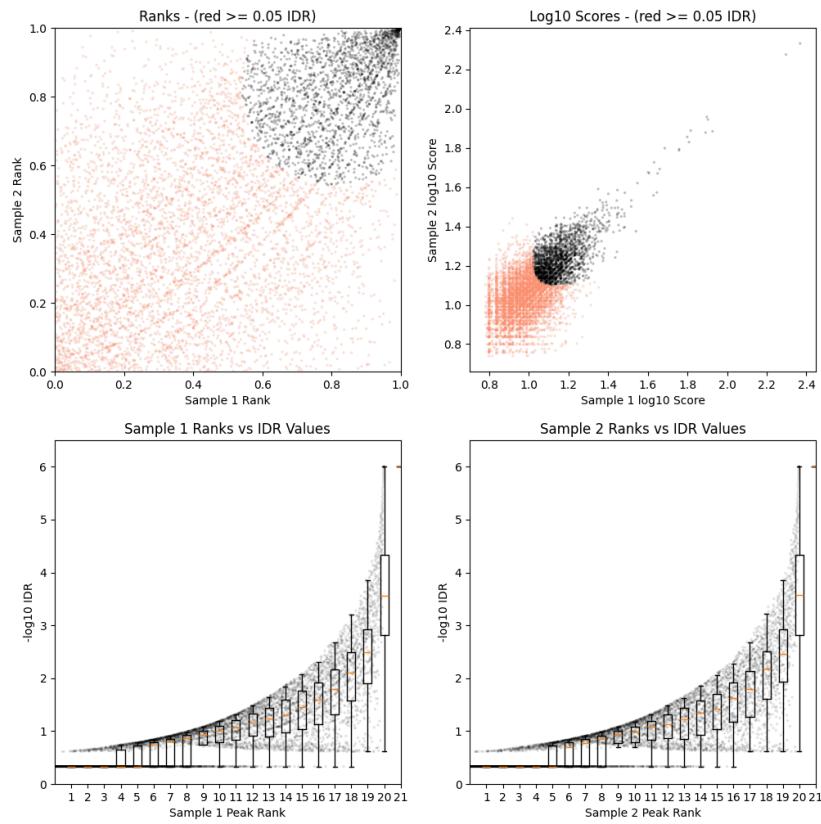
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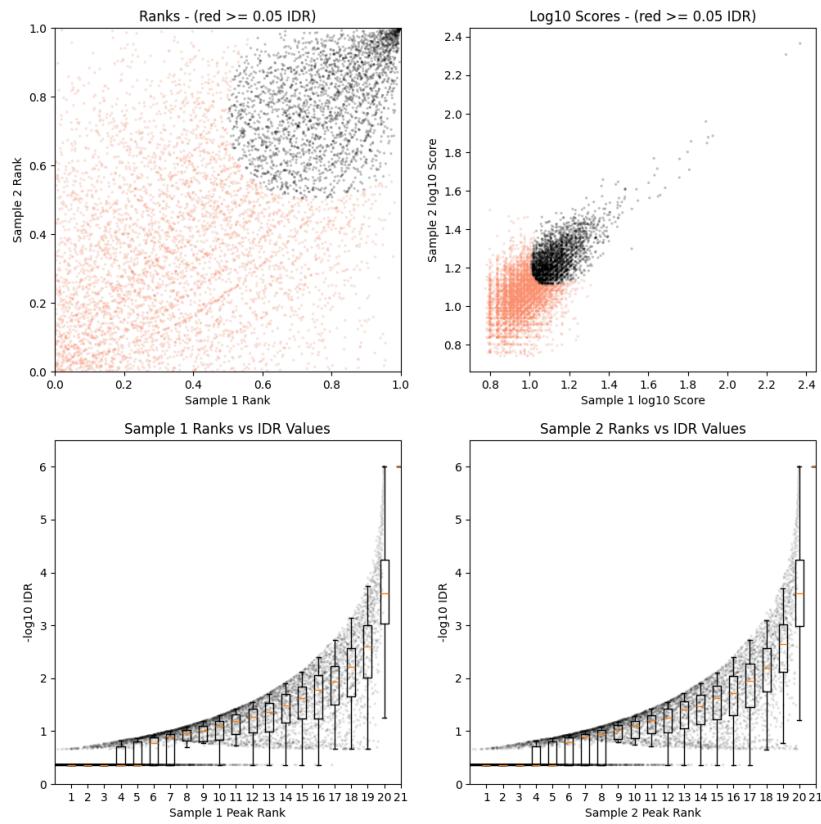
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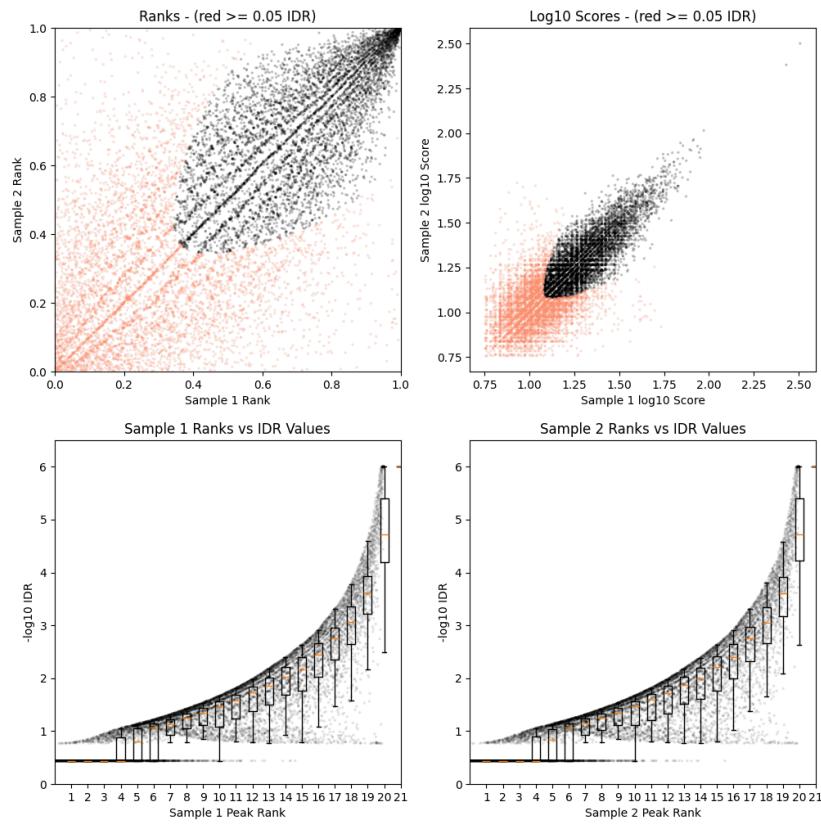
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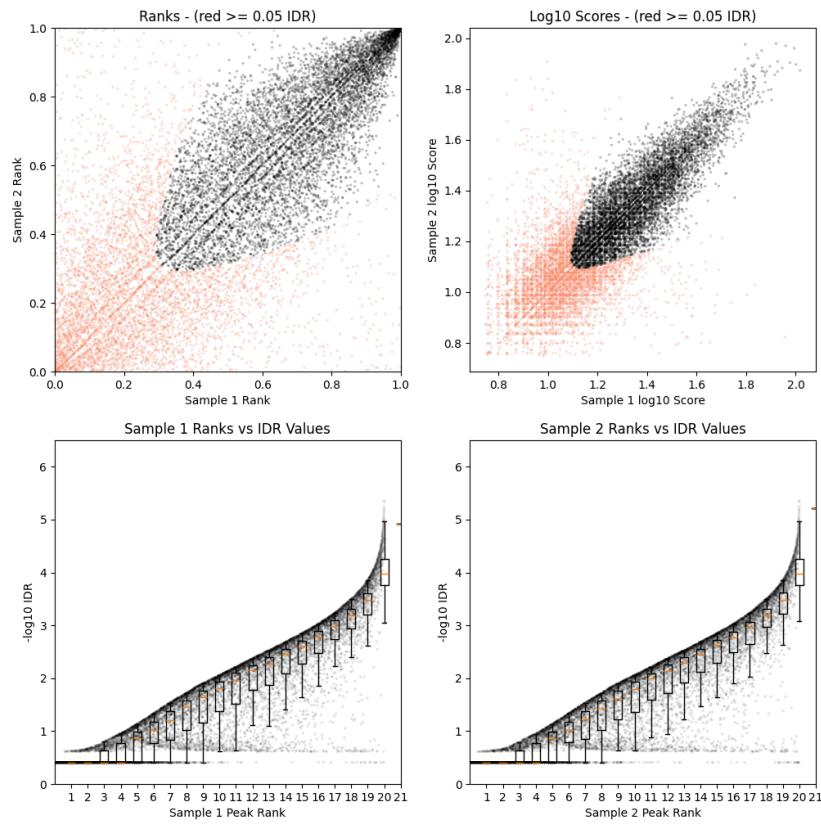
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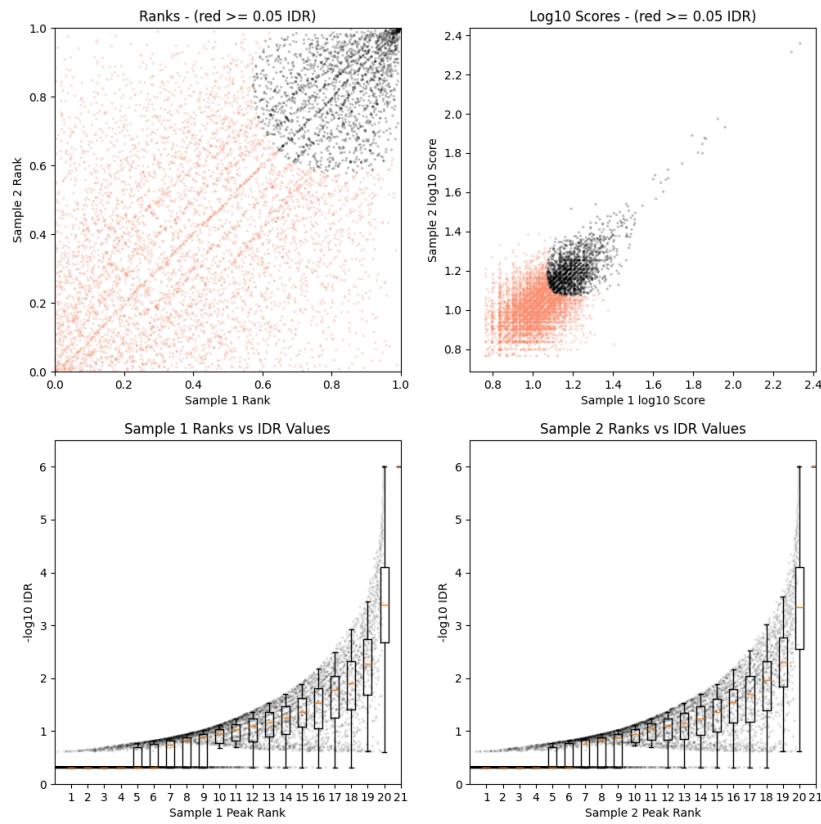
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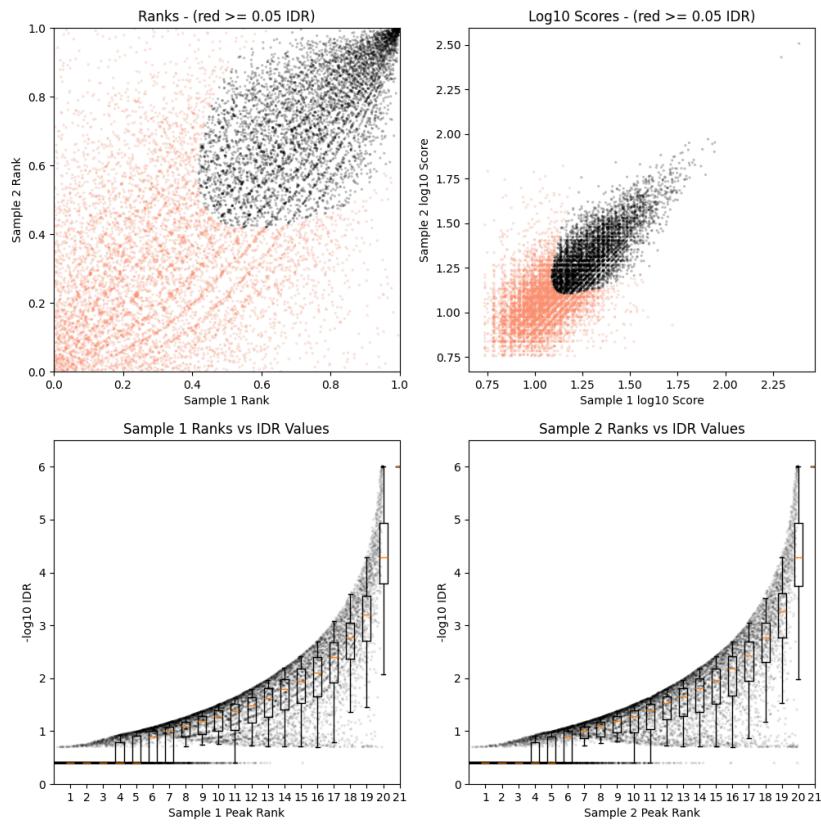
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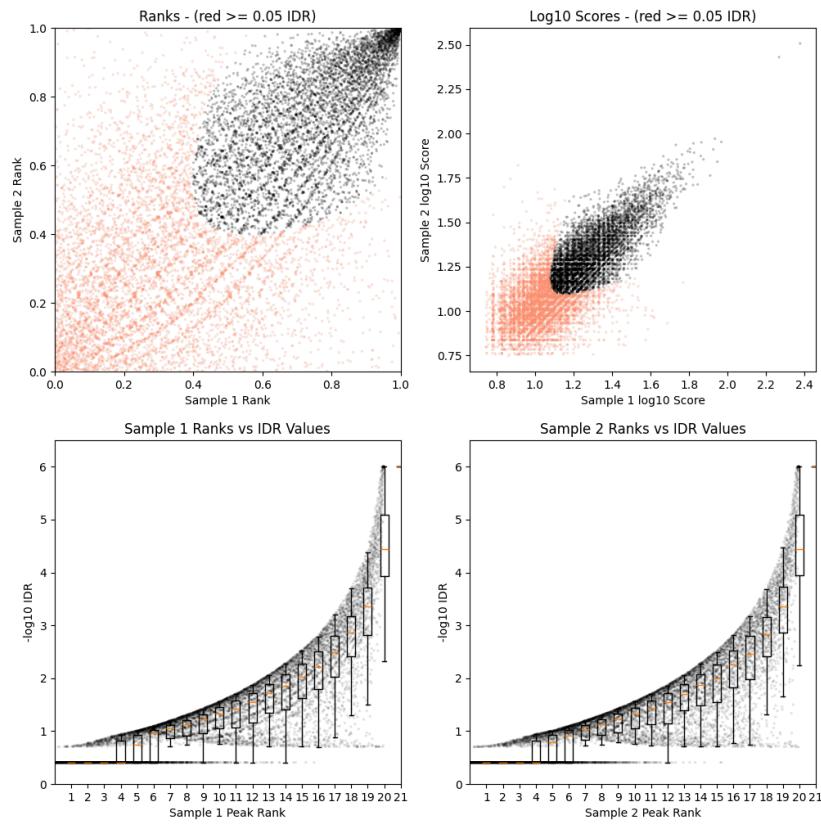
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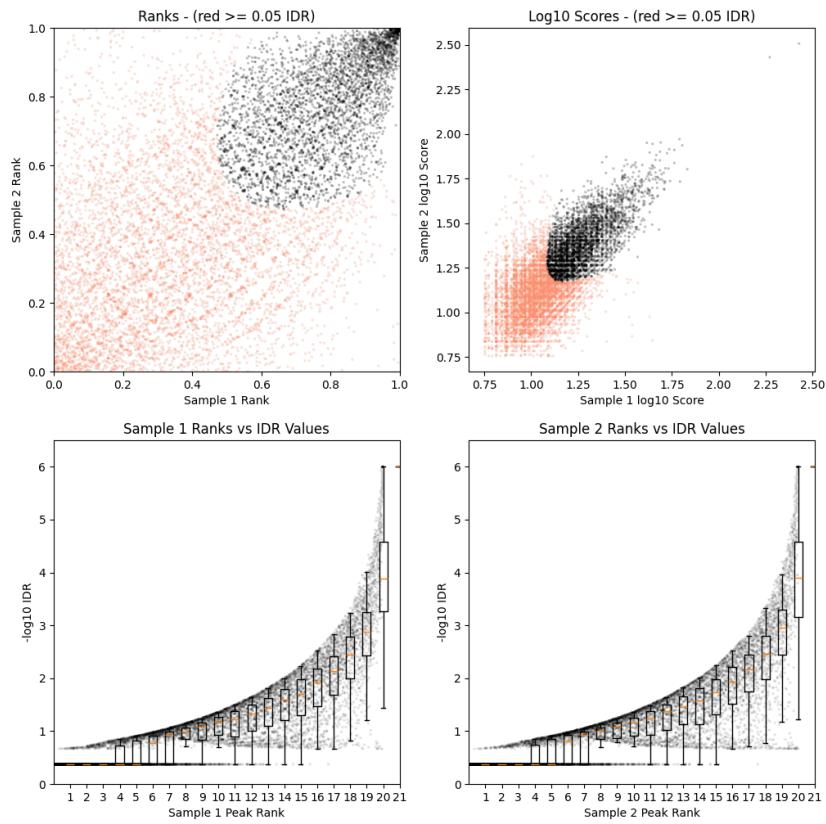
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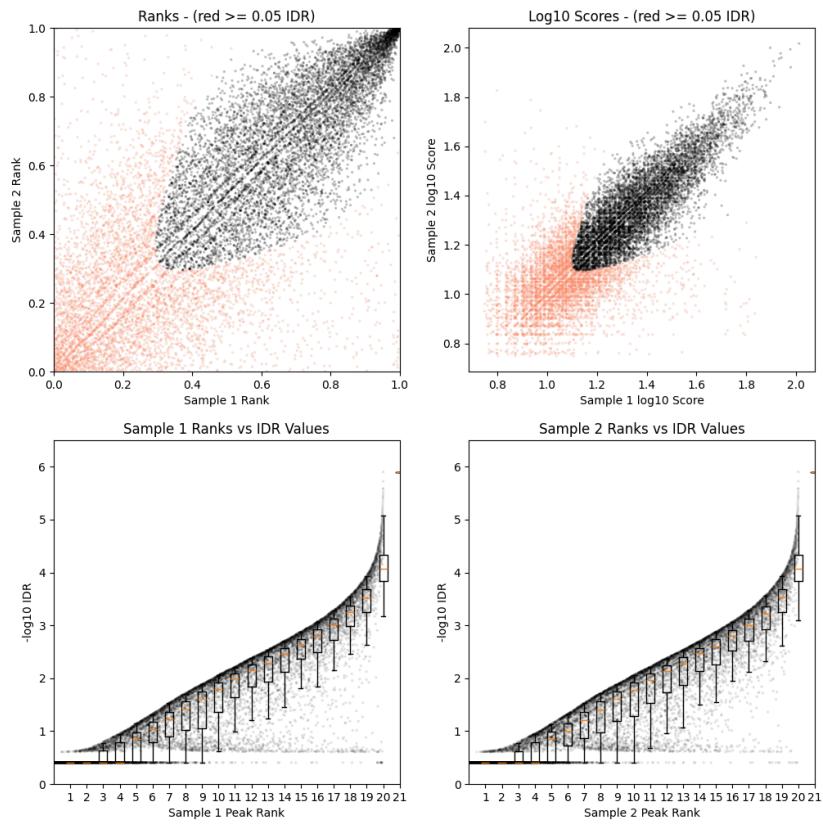
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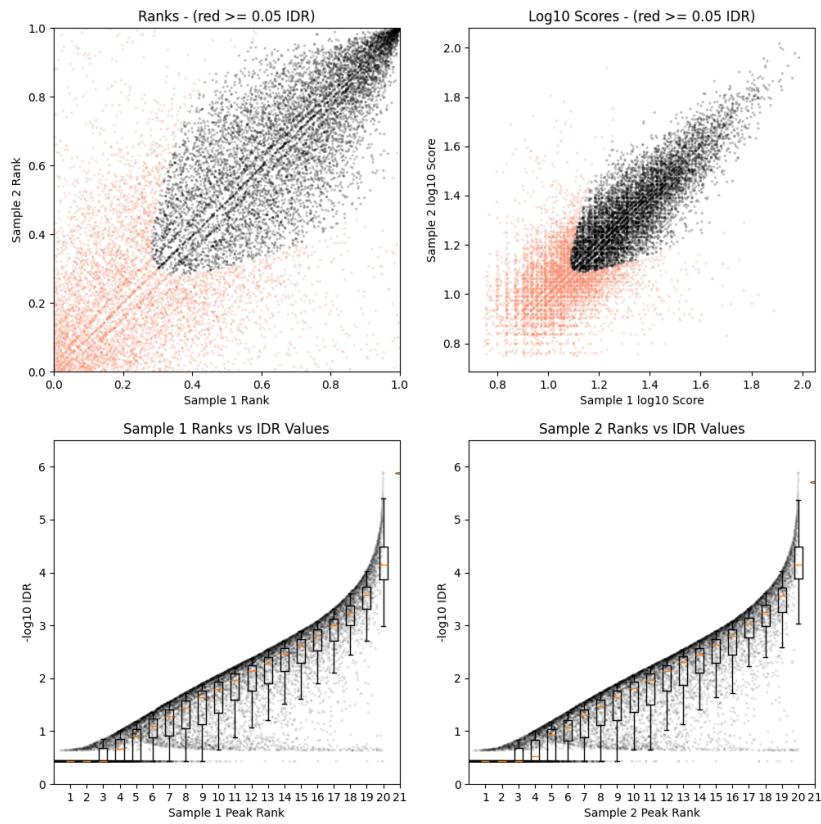
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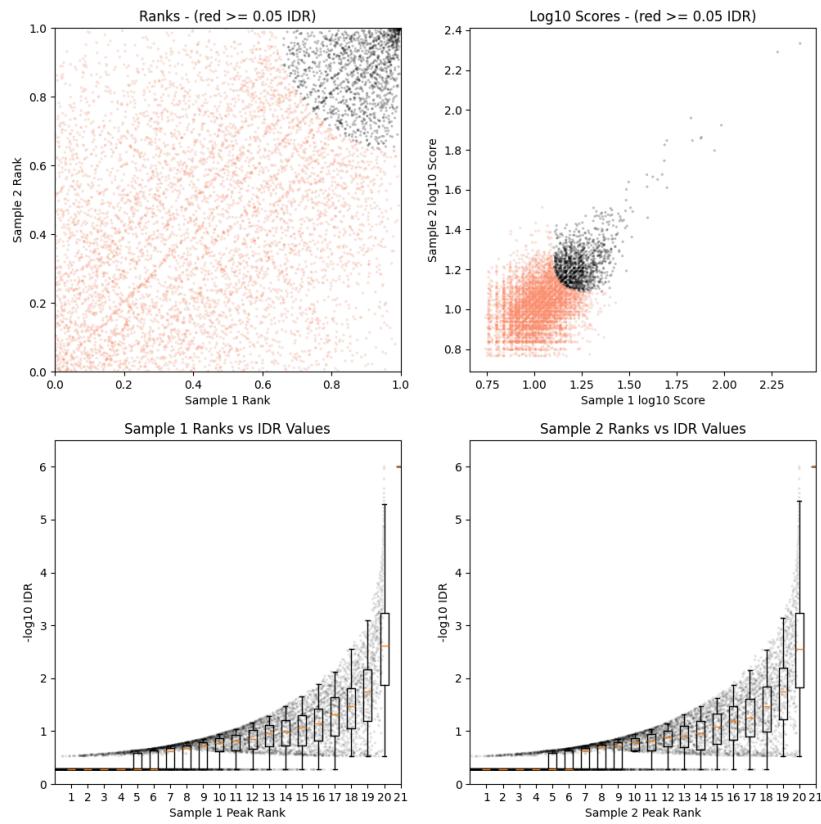
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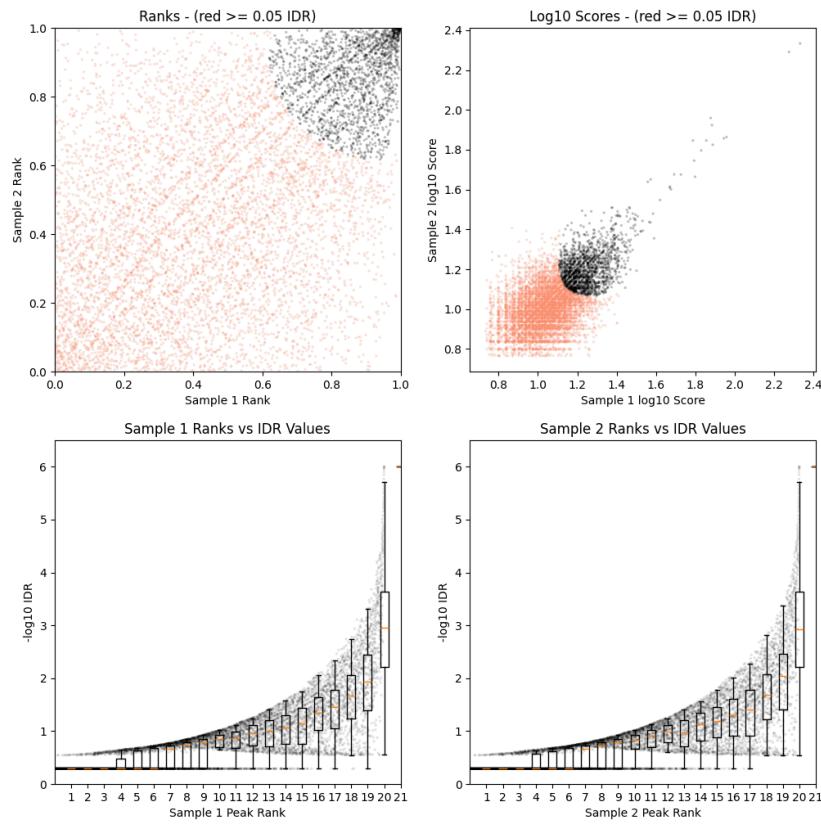
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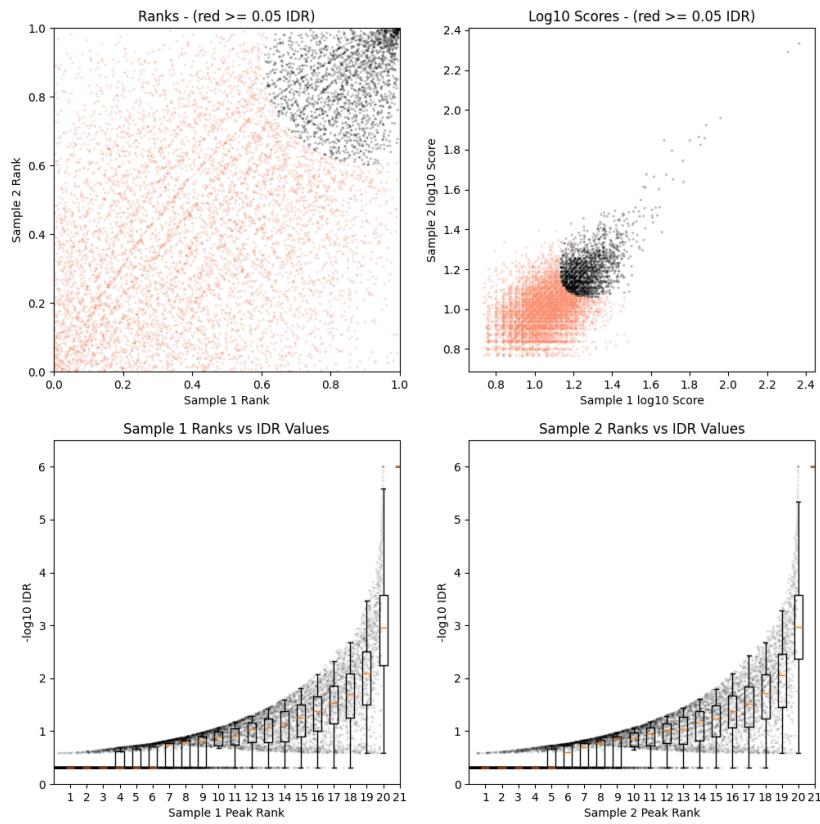
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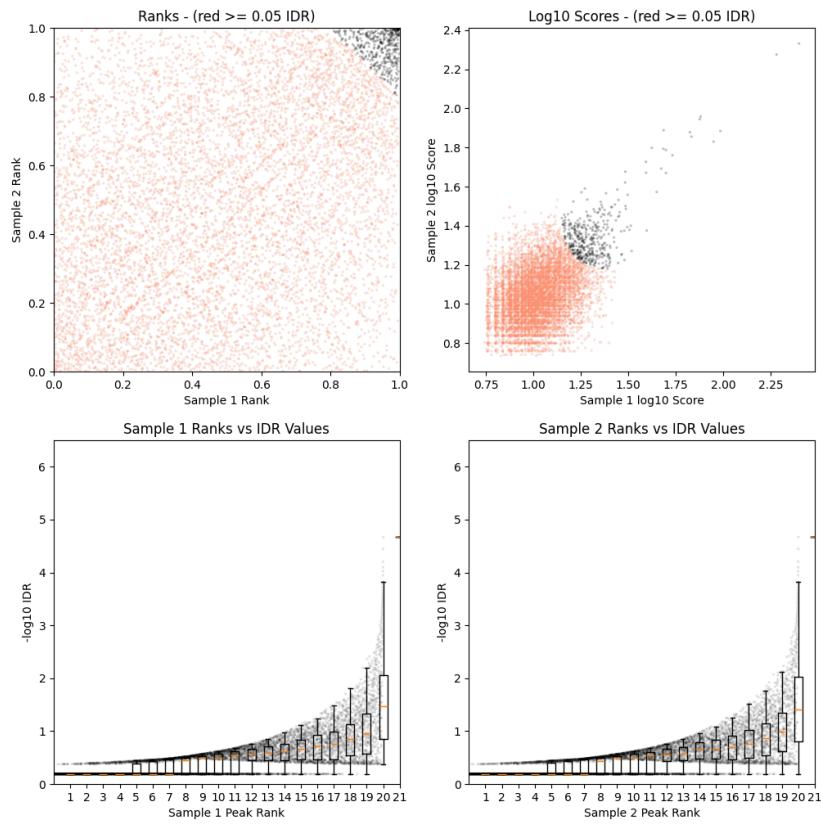
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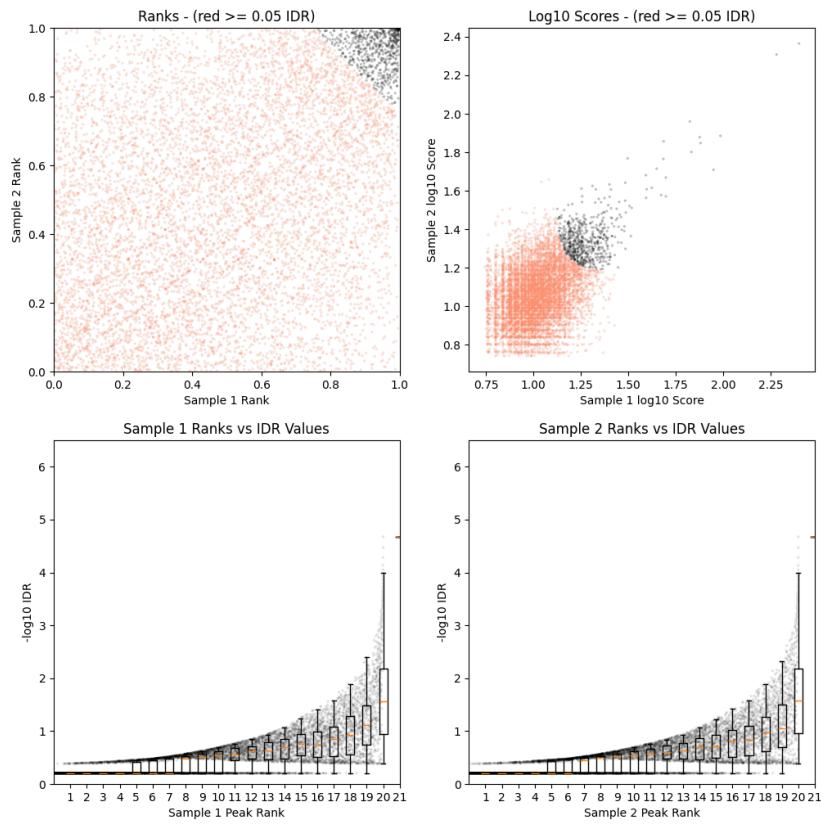
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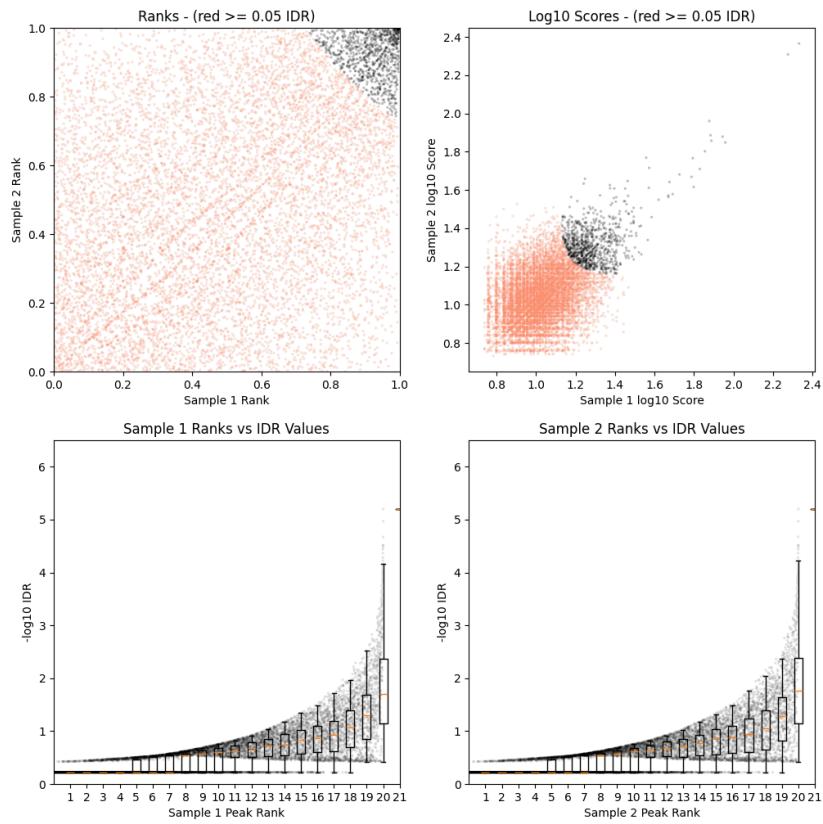
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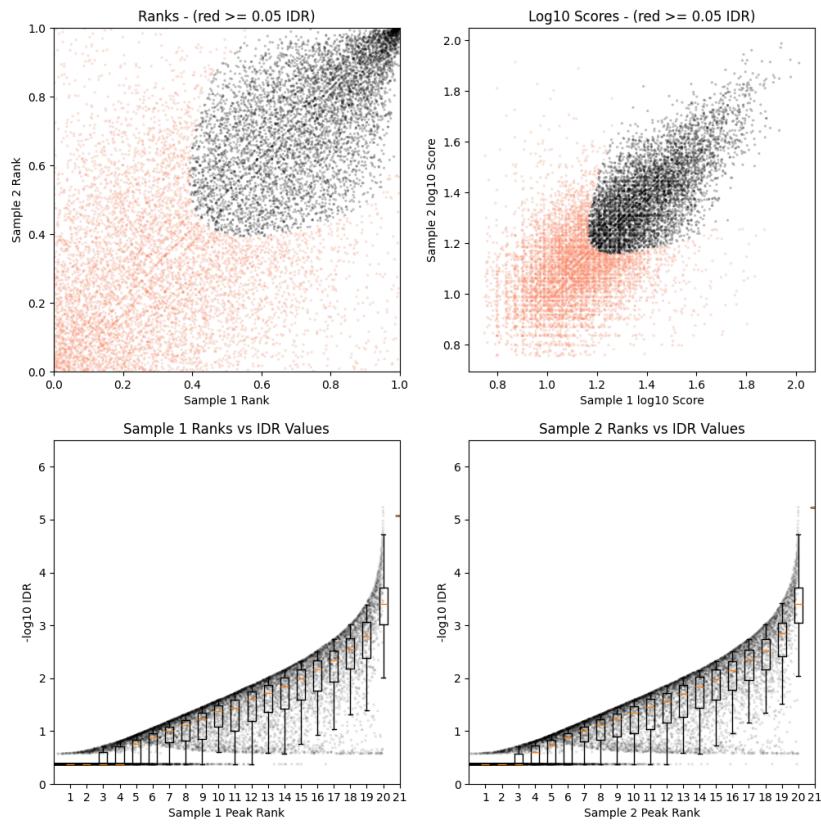
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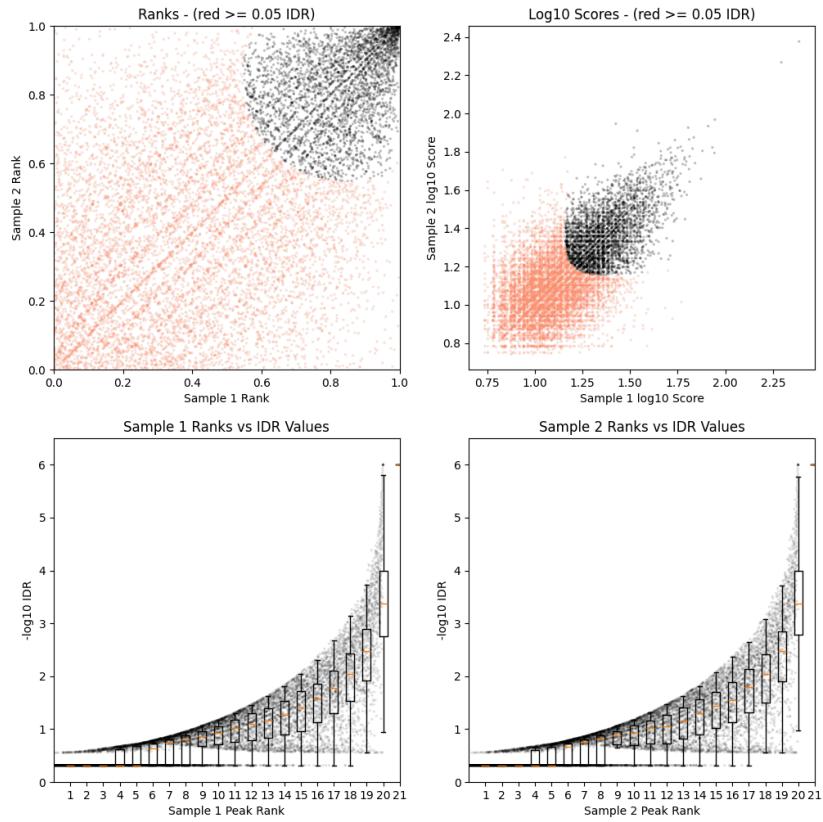
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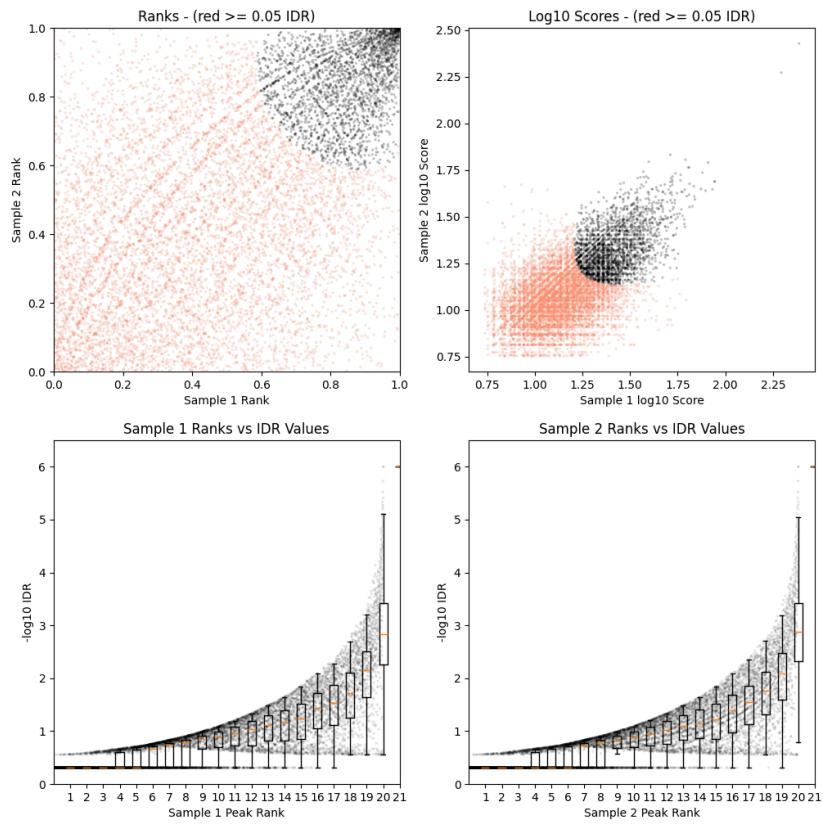
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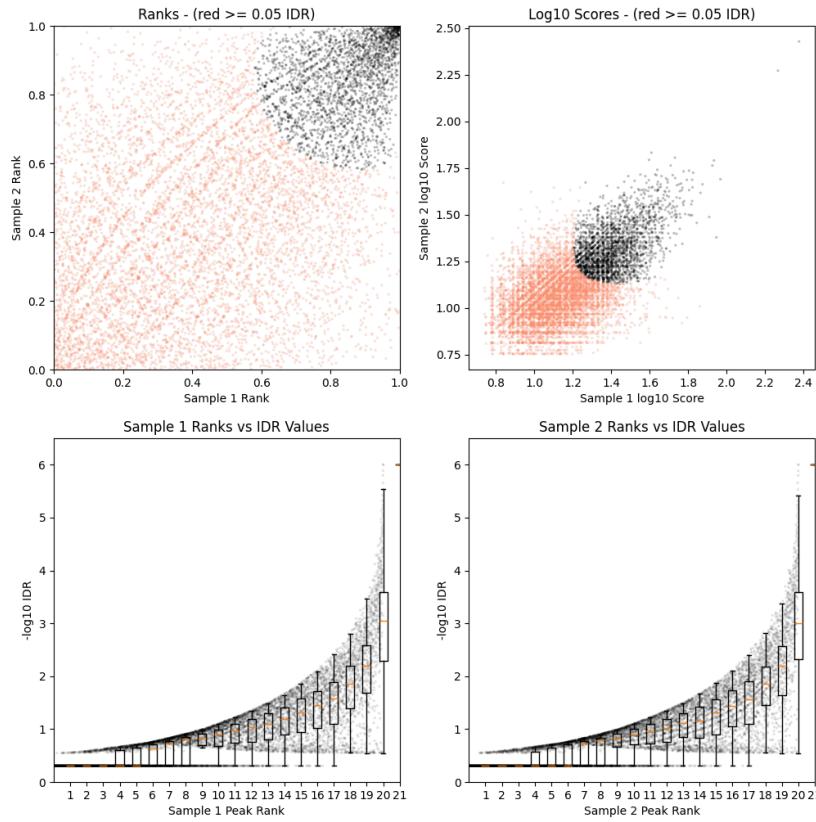
SRR28096231_NovaSeq_6000_BLMneg_Replicate_2_IP_rep2_G4_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4_peaks_vs_RR28096232_NovaSeq_6000_BLMneg_Replicate_2_IP_repl1_G4_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4_peaks.idr.txt.pn



SRR28096234_HiSeq_3000_BLMneg_Replicate_1_IP_rep3_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks_vs_SRR28096235_HiSeq_3000_BLMneg_Replicate_1_IP_rep2_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.idr.txt.png



SRR28096234_HiSeq_3000_BLMneg_Replicate_1_IP_rep3_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks_vs_SRR28096236_HiSeq_3000_BLMneg_Replicate_1_IP_repl_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.idr.txt.png



SRR28096235_HiSeq_3000_BLMneg_Replicate_1_IP_rep2_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks_vs_SRR28096236_HiSeq_3000_BLMneg_Replicate_1_IP_rep1_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.idr.txt.png

FRIP Scores from Initial Peak Calling

PeakCalling_MACS3

Sample	Tag Count	Peak Count	FRIP
SRR28096223_NovaSeq_6000_WT_Replicate_2_IP_rep3_G4	0.0183	1153315	63021842 analysis/PeakCalling_MACS3/narrowPeak/SRR28096223_NovaSeq_6000_WT_Replicate_2_IP_rep3_G4_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
SRR28096224_NovaSeq_6000_WT_Replicate_2_IP_rep2_G4	0.0250	1574125	62952571 analysis/PeakCalling_MACS3/narrowPeak/SRR28096224_NovaSeq_6000_WT_Replicate_2_IP_rep2_G4_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
SRR28096225_NovaSeq_6000_WT_Replicate_2_IP_rep1_G4	0.0267	1689594	63187450 analysis/PeakCalling_MACS3/narrowPeak/SRR28096225_NovaSeq_6000_WT_Replicate_2_IP_rep1_G4_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment

SRR28096228_HiSeq_3000_WT_Replicate_1_IP_rep2_G4	0.0000	218	46024345 analysis/PeakCalling_MACS3/narrowPeak/SRR28096228_HiSeq_3000_WT_Replicate_1_IP_rep2_G4_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4_peaks.narrowPeak FAIL_FRIP: Poor enrichment
SRR28096229_HiSeq_3000_WT_Replicate_1_IP_rep1_G4	0.0000	0	52096083 analysis/PeakCalling_MACS3/narrowPeak/SRR28096229_HiSeq_3000_WT_Replicate_1_IP_rep1_G4_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4_peaks.narrowPeak FAIL_FRIP: Poor enrichment
SRR28096231_NovaSeq_6000_BLMneg_Replicate_2_IP_rep2_G4	0.0273	2226100	81473947 analysis/PeakCalling_MACS3/narrowPeak/SRR28096231_NovaSeq_6000_BLMneg_Replicate_2_IP_rep2_G4_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
SRR28096232_NovaSeq_6000_BLMneg_Replicate_2_IP_rep1_G4	0.0268	2198003	81921154 analysis/PeakCalling_MACS3/narrowPeak/SRR28096232_NovaSeq_6000_BLMneg_Replicate_2_IP_rep1_G4_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
SRR28096234_HiSeq_3000_BLMneg_Replicate_1_IP_rep3_G4	0.0554	1130319	20389087 analysis/PeakCalling_MACS3/narrowPeak/SRR28096234_HiSeq_3000_BLMneg_Replicate_1_IP_rep3_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.narrowPeak OK_FRIP: Moderate signal
SRR28096235_HiSeq_3000_BLMneg_Replicate_1_IP_rep2_G4	0.0525	1079540	20578511 analysis/PeakCalling_MACS3/narrowPeak/SRR28096235_HiSeq_3000_BLMneg_Replicate_1_IP_rep2_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.narrowPeak OK_FRIP: Moderate signal
SRR28096236_HiSeq_3000_BLMneg_Replicate_1_IP_rep1_G4	0.0379	696494	18395801 analysis/PeakCalling_MACS3/narrowPeak/SRR28096236_HiSeq_3000_BLMneg_Replicate_1_IP_rep1_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment

PeakCalling_MACS3_pool_pseudo

Sample	Tag Count	Peak Count	FRIP
BLMneg_G4_HiSeq_3000_pseudo1_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	Pseudorep1	0.0466	1382827 29677608 analysis/PeakCalling_MACS3_pool_pseudo/BLMneg_G4_HiSeq_3000_pseudo1_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4/BLMneg_G4_HiSeq_3000_pseudo1_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment

BLMneg_G4_HiSeq_3000_pseudo2_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	Pseudorep2	0.0466	1383562 29700435 analysis/PeakCalling_MACS3_pool_pseudo/BLMneg_G4_HiSeq_3000_pseudo2_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4/BLMneg_G4_HiSeq_3000_pseudo2_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
BLMneg_G4_NovaSeq_6000_pseudo1_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4	Pseudorep1	0.0267	2184856 81696517 analysis/PeakCalling_MACS3_pool_pseudo/BLMneg_G4_NovaSeq_6000_pseudo1_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4/BLMneg_G4_NovaSeq_6000_pseudo1_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
BLMneg_G4_NovaSeq_6000_pseudo2_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4	Pseudorep2	0.0269	2200492 81707535 analysis/PeakCalling_MACS3_pool_pseudo/BLMneg_G4_NovaSeq_6000_pseudo2_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4/BLMneg_G4_NovaSeq_6000_pseudo2_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
BLMneg_G4_HiSeq_3000_pseudo1_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	Pseudorep1	0.0466	1382827 29677608 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/BLMneg_G4_HiSeq_3000_pseudo1_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
BLMneg_G4_HiSeq_3000_pseudo2_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	Pseudorep2	0.0466	1383562 29700435 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/BLMneg_G4_HiSeq_3000_pseudo2_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
BLMneg_G4_NovaSeq_6000_pseudo1_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4	Pseudorep1	0.0267	2184856 81696517 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/BLMneg_G4_NovaSeq_6000_pseudo1_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
BLMneg_G4_NovaSeq_6000_pseudo2_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4	Pseudorep2	0.0269	2200492 81707535 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/BLMneg_G4_NovaSeq_6000_pseudo2_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
pooled_BLMneg_G4_HiSeq_3000_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	Pooled	0.0419	2484752 59363399 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/pooled_BLMneg_G4_HiSeq_3000_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
pooled_BLMneg_G4_NovaSeq_6000_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4	Pooled	0.0250	4083617 163395101 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/pooled_BLMneg_G4_NovaSeq_6000_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4

			G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
pooled_WT_G4_HiSeq_3000_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4	Pooled	0.0000	0 98120428 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/pooled_WT_G4_HiSeq_3000_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4_peaks.narrowPeak FAIL_FRIP: Poor enrichment
pooled_WT_G4_NovaSeq_6000_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	Pooled	0.0114	2154622 189161863 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/pooled_WT_G4_NovaSeq_6000_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
WT_G4_HiSeq_3000_pseudo1_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4	Pseudorep1	0.0000	115 49060917 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/WT_G4_HiSeq_3000_pseudo1_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4_peaks.narrowPeak FAIL_FRIP: Poor enrichment
WT_G4_HiSeq_3000_pseudo2_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4	Pseudorep2	0.0000	57 49064130 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/WT_G4_HiSeq_3000_pseudo2_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4_peaks.narrowPeak FAIL_FRIP: Poor enrichment
WT_G4_NovaSeq_6000_pseudo1_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	Pseudorep1	0.0139	1314932 94570594 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/WT_G4_NovaSeq_6000_pseudo1_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
WT_G4_NovaSeq_6000_pseudo2_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	Pseudorep2	0.0133	1261544 94569921 analysis/PeakCalling_MACS3_pool_pseudo/narrowPeak/WT_G4_NovaSeq_6000_pseudo2_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
pooled_BLMneg_G4_HiSeq_3000_vs_SR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	Pooled	0.0419	2484752 59363399 analysis/PeakCalling_MACS3_pool_pseudo/pooled_BLMneg_G4_HiSeq_3000_vs_SR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4/pooled_BLMneg_G4_HiSeq_3000_vs_SR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
pooled_BLMneg_G4_NovaSeq_6000_vs_SR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4	Pooled	0.0250	4083617 163395101 analysis/PeakCalling_MACS3_pool_pseudo/pooled_BLMneg_G4_NovaSeq_6000_vs_SR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4/pooled_BLMneg_G4_NovaSeq_6000_vs_SR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment

pooled_WT_G4_HiSeq_3000_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4	Pooled	0.0000	0 98120428 analysis/PeakCalling_MACS3_pool_pseudo/pooled_WT_G4_HiSeq_3000_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4/pooled_WT_G4_HiSeq_3000_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4_peaks.narrowPeak FAIL_FRIP: Poor enrichment
pooled_WT_G4_NovaSeq_6000_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	Pooled	0.0114	2154622 189161863 analysis/PeakCalling_MACS3_pool_pseudo/pooled_WT_G4_NovaSeq_6000_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4/pooled_WT_G4_NovaSeq_6000_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
WT_G4_HiSeq_3000_pseudo1_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4	Pseudorep1	0.0000	115 49060917 analysis/PeakCalling_MACS3_pool_pseudo/WT_G4_HiSeq_3000_pseudo1_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4/WT_G4_HiSeq_3000_pseudo1_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4_peaks.narrowPeak FAIL_FRIP: Poor enrichment
WT_G4_HiSeq_3000_pseudo2_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4	Pseudorep2	0.0000	57 49064130 analysis/PeakCalling_MACS3_pool_pseudo/WT_G4_HiSeq_3000_pseudo2_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4/WT_G4_HiSeq_3000_pseudo2_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4_peaks.narrowPeak FAIL_FRIP: Poor enrichment
WT_G4_NovaSeq_6000_pseudo1_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	Pseudorep1	0.0139	1314932 94570594 analysis/PeakCalling_MACS3_pool_pseudo/WT_G4_NovaSeq_6000_pseudo1_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4/WT_G4_NovaSeq_6000_pseudo1_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment
WT_G4_NovaSeq_6000_pseudo2_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	Pseudorep2	0.0133	1261544 94569921 analysis/PeakCalling_MACS3_pool_pseudo/WT_G4_NovaSeq_6000_pseudo2_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4/WT_G4_NovaSeq_6000_pseudo2_vs_SR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4_peaks.narrowPeak LOW_FRIP: Weak enrichment

♦ High-confidence Peak Metrics

Group	Merged_IDR_Peaks	High_Confidence_Peaks(IDR≤0.01)	Comment
HiSeq_3000_BLMneg_G4	14549	NA	No replicate IDR file found
HiSeq_3000_WT_G4	NA	NA	No merged IDR file
NovaSeq_6000_BLMneg_G4	12270	NA	No replicate IDR file found
NovaSeq_6000_WT_G4	13168	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
HiSeq_3000_BLMneg_G4	NA	NA	Missing data			
HiSeq_3000_WT_G4	NA	NA	Missing data			
NovaSeq_6000_BLMneg_G4	NA	NA	Missing data			
NovaSeq_6000_WT_G4	NA	NA	Missing data			

♦ Jaccard Overlap (Replicate Peak Similarity)

Group	Replicate 1	Replicate 2	Jaccard Index	Intersection	Union	Interpretation
HiSeq_3000_BLMneg_G4	SRR28096234_HiSeq_3000_BLMneg_R replicate_1_IP_rep3_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	SRR28096235_HiSeq_3000_BLMneg_R replicate_1_IP_rep2_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	0.387109	11716136	4535426	⚠️ Moderate similarity
HiSeq_3000_BLMneg_G4	SRR28096234_HiSeq_3000_BLMneg_R replicate_1_IP_rep3_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	SRR28096236_HiSeq_3000_BLMneg_R replicate_1_IP_rep1_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	0.35432	10095056	3576884	⚠️ Moderate similarity
HiSeq_3000_BLMneg_G4	SRR28096235_HiSeq_3000_BLMneg_R replicate_1_IP_rep2_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	SRR28096236_HiSeq_3000_BLMneg_R replicate_1_IP_rep1_G4_vs_SRR28096233_HiSeq_3000_BLMneg_Replicate_1_Input_G4	0.364111	9750592	3550296	⚠️ Moderate similarity
HiSeq_3000_WT_G4	SRR28096228_HiSeq_3000_WT_Replicate_1_IP_rep2_G4_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4	SRR28096229_HiSeq_3000_WT_Replicate_1_IP_rep1_G4_vs_SRR28096226_HiSeq_3000_WT_Replicate_1_Input_G4	0	921	0	✖️ Low similarity
NovaSeq_6000_BLMneg_G4	SRR28096231_NovaSeq_6000_BLMneg_Replicate_2_IP_rep2_G4_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4	SRR28096232_NovaSeq_6000_BLMneg_Replicate_2_IP_rep1_G4_vs_SRR28096230_NovaSeq_6000_BLMneg_Replicate_2_Input_G4	0.549751	8944732	4917371	🔥 High similarity
NovaSeq_6000_WT_G4	SRR28096223_NovaSeq_6000_WT_Replicate_2_IP_rep3_G4_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	SRR28096224_NovaSeq_6000_WT_Replicate_2_IP_rep2_G4_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	0.269929	10660186	2877498	✖️ Low similarity

NovaSeq_6000_WT_G4	SRR28096223_NovaSeq_6000_WT_Replicate_2_IP_rep3_G4_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	SRR28096225_NovaSeq_6000_WT_Replicate_2_IP_rep1_G4_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	0.279313	11083549	3095777	✗ Low similarity
NovaSeq_6000_WT_G4	SRR28096224_NovaSeq_6000_WT_Replicate_2_IP_rep2_G4_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	SRR28096225_NovaSeq_6000_WT_Replicate_2_IP_rep1_G4_vs_SRR28096222_NovaSeq_6000_WT_Replicate_2_Input_G4	0.29364	12617832	3705106	✗ 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)