



# CIDC 2.0 BIOINFORMATIC PIPELINES ATAC-SEQ VALIDATION

ESSEX MANAGEMENT

NATIONAL CANCER INSTITUTE (NCI)

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DRAFT

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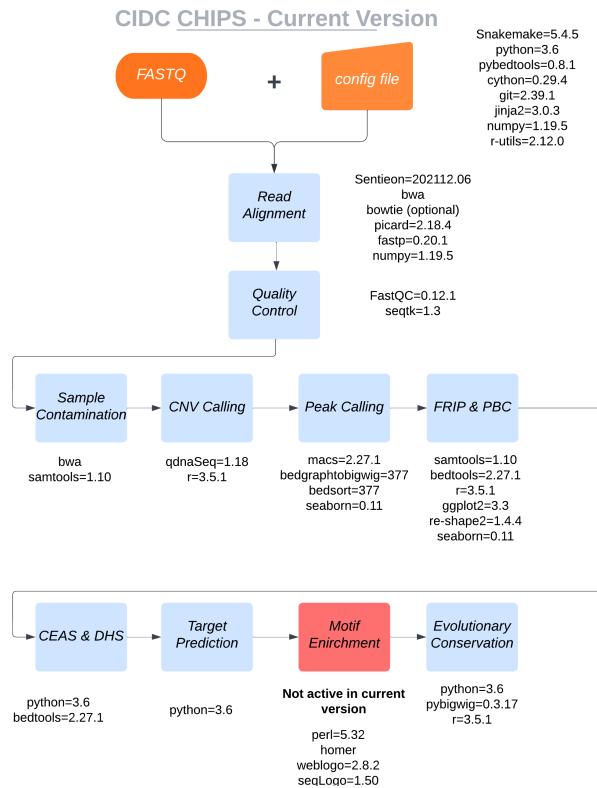
<b>1. <i>Introduction</i> .....</b>	<b>3</b>
<b>2. <i>ChIP-SEQ Pipeline – Validation Dataset</i>.....</b>	<b>8</b>
<b>3. <i>ChIP-SEQ Pipeline – Validation Method</i>.....</b>	<b>8</b>
<b>4. <i>ChIP-Seq Pipeline – Validation Results</i> .....</b>	<b>10</b>
<b>5. <i>ChIP-Seq Pipeline – Appendix I – Tabular Results</i>.....</b>	<b>21</b>

## 1. INTRODUCTION

As part of the planned CIDC enhancements after the migration to the National Cancer Institute (NCI), the bioinformatic pipelines were reviewed by members the National Cancer Institute Computational Genomics and Bioinformatics Branch (NCI-CGBB) and Essex Management (EM). These reviews were carried out to determine which, if any, changes could be made to the pipeline to satisfy the following goals and objectives:

Goals	Objectives
Update and clean up code so that it is easy to read and understand for everyone working in the same code base, thus, making it easier to maintain, debug, and update.	Provide code review to determine areas for clean up and refactoring
Maintain industry standard software to optimize the best combination of biochemistry, mathematics, computer science, data science, and modern data analytics tools.	Review the performance of current packages to determine if current functionality is meeting customer needs (CIMAC Input)
Maintain current software versioning to optimize vendor support and application performance.	Provide gap analysis on current software versions to determine what tools to upgrade
Provide enhancements to pipeline to improve current functionality/performance and better support the stakeholder community the analysis of DNA, while maintaining backward compatibility with previous versions.	Add new functionality and features as desired by

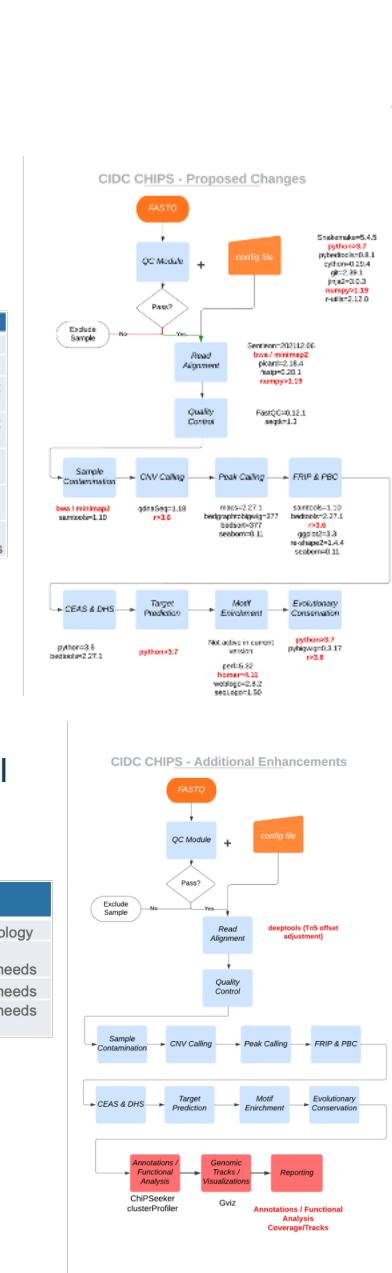
The reviews created schematics of the extant pipelines stood up after the migration from Dana Farber Cancer Institute (DFCI) to NIH STRIDES. The CHIPS (i.e., ATAC-Seq) pipeline was divided into 10 distinct modules:



It was noted that the Motif Enrichment module was inactive in the DFCI and migrated pipelines.  
After thorough review, the following enhancements were planned for the CHIPS Pipeline:

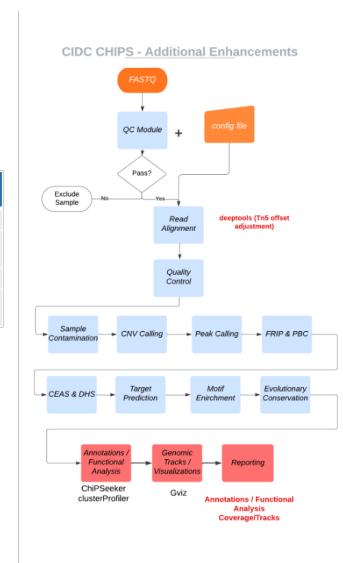
## CIDC CHIPS – Recommended Enhancements

CHIPS Pipeline Recommendations	Reason
Add Homer	For motif enrichment analysis
Upgrade numpy beyond 1.19	CBIIT identified security vulnerability Current version unsupported; update past v3.6
Upgrade r	Current version unsupported; update past v3.6
Upgrade python	Current version unsupported; update past v3.7
Add file validation (QC Module)	To identify corrupt or incorrectly formatted files
Evaluate use of Senteion	Potential cost savings and increased portability
Evaluate bowtie2, bwa-mem and minimap2	Faster processing resulting in cost savings



## CIDC CHIPS – Additional Potential Enhancements

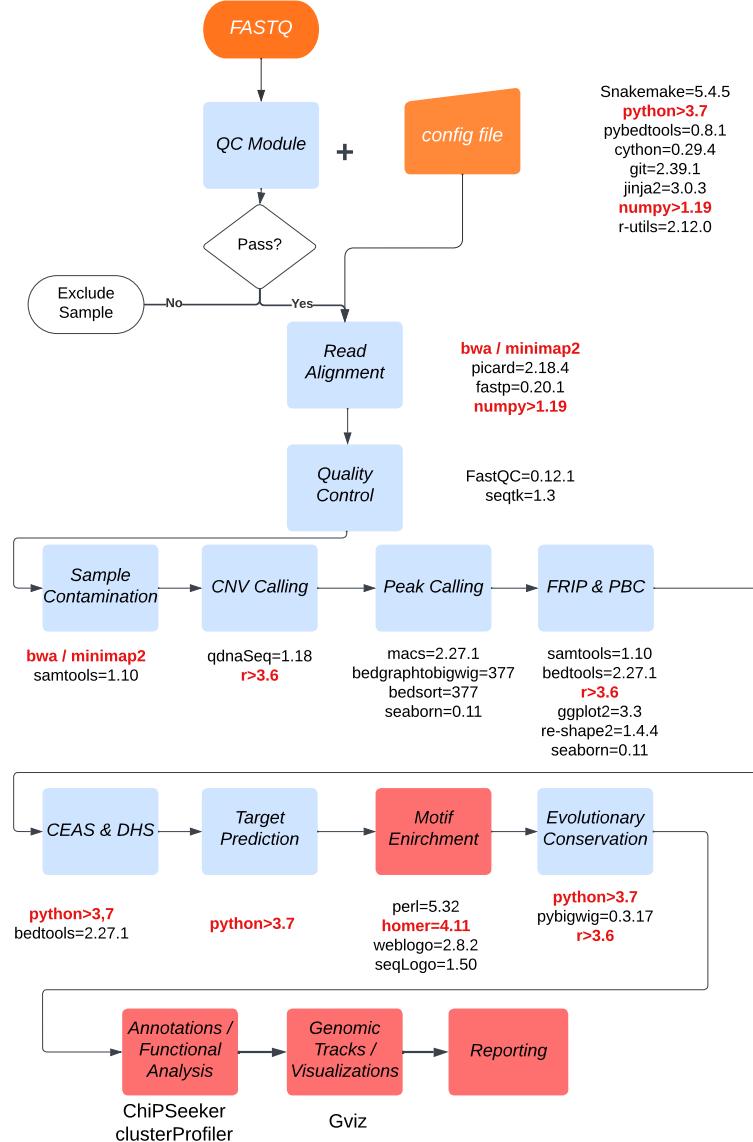
CHIPS Pipeline Potential Enhancements	Reason
Add Tn5 Adjustment tool	Improved reflection of underlying biology
Add Annotations / Functional Analysis Module	Added functionality to meet current needs
Add Genomic Tracks module	Added functionality to meet current needs
Increase information provided in Report	Added functionality to meet current needs



The specific changes associated with the pipeline are enumerated in the figures above. For each module, code refactoring was also performed to increase readability and ease future maintenance and/or upgrade efforts.

**Final Pipeline Design**

## CIDC ATAC-Seq - Enhancements



## 2. CHIP-SEQ PIPELINE – VALIDATION DATASET

### Validation Dataset:

Assay	CIMAC_ID	Trial
ATAC-Seq	CA440YLET.01	14C-0059G
ATAC-Seq	CA440YLEU.01	14C-0059G
ATAC-Seq	CA440YLEV.01	14C-0059G
ATAC-Seq	CA442XD3Q.01	14C-0059G
ATAC-Seq	CA442XD3R.01	14C-0059G
ATAC-Seq	CA442XD3S.01	14C-0059G
ATAC-Seq	CA44M2SRW.01	14C-0059G
ATAC-Seq	CA44O8M8X.01	14C-0059G
ATAC-Seq	CA44O8M8Y.01	14C-0059G
ATAC-Seq	CA44O8MHR.01	14C-0059G

### Additional Validation Data:

Because the Motif Enrichment module was inactive in the extant pipeline, there is no truth set for result validation. The Motif Enrichment module invokes the HOMER *findMotifsGenome.pl* script which includes many parameters that may chance output. There are potentially truth sets available that were created with HOMER. For example:

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21512>

Field Code Changed

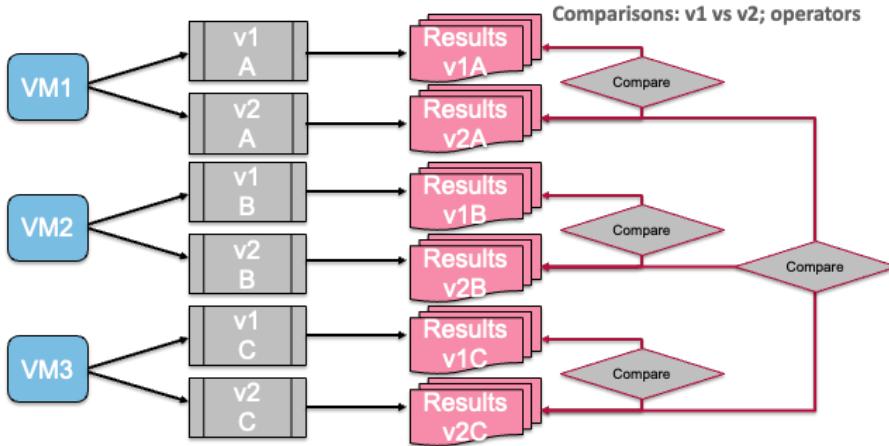
[https://github.com/russell-ryan-lab/ChIPseq\\_ATACseq\\_pipelines/tree/master/data/homer\\_test\\_data](https://github.com/russell-ryan-lab/ChIPseq_ATACseq_pipelines/tree/master/data/homer_test_data)

However, it is unclear from the authors on parameters that were used. Further, the reference genome is not always stated or in some cases is not relevant to the current work (e.g., mouse). Thus, an alternative approach will be used that will evaluate the plausibility and reproducibility of the output.

## 3. CHIP-SEQ PIPELINE – VALIDATION METHOD

**Validation Design:** The validation design is shown below. It will be used to compare the results of the current pipelines (v1) to the enhanced pipeline (v2) as well as assess inter-operator and inter-VM variability.

## Validation Plan for CHIPS



For the full pipeline, three output files will be used for the validation: sorted\_peaks.bed (BED format), sorted\_summits.bed (BED format), and sorted\_peaks.narrowPeak (BED 6+4/narrowPeak format). Note that these are the three result files that are uploaded to the CIDC portal for result reporting. The number of overlapping entries will be first calculated by a specific percentage ( $\geq 90\%$  or 100%) as determined by the start and end coordinates of each entry. The Jaccard index will then be used to determine the similarity of the two datasets. Specific values (i.e., score, signal value, and peak) from the overlapping result will be compared by calculating the Spearman's rank correlation coefficient to measure the strength of association between the corresponding values of the datasets. These comparisons will be carried out as described in the design figure above.

For evaluation of the HOMER module, the “knownResults.txt” output file will be compared between v2 runs from the three separate VMs. This will evaluate the reproducibility of the results and will also be compared against HOMER’s knownTFs/all.motifs file as the source of truth for detecting motifs.

### Acceptance Criteria:

Jaccard Index  $> 0.95$  for all comparisons  
Spearman Correlation  $> 0.95$  for all comparisons

These values were selected based on our validation results when comparing the v1 pipelines to Dana Farber’s previous results as well modifications associated with enhancing the pipeline, namely more stringent post-alignment filtering that reduces low-quality results.

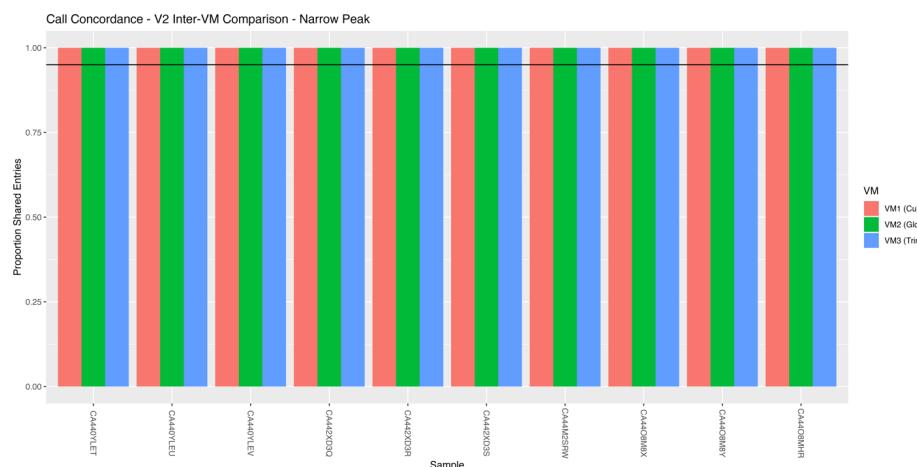
### Investigation of Discrepancies:

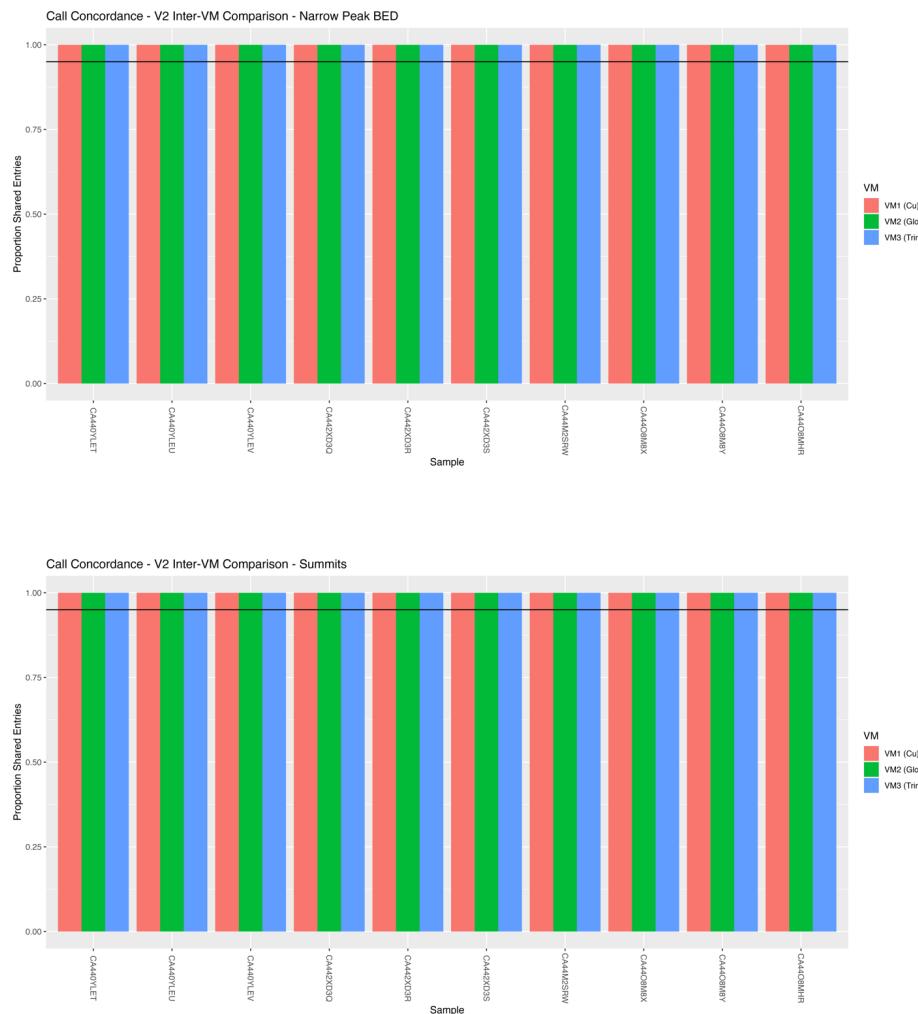
If the comparison metrics do not meet the acceptance criteria, an investigation will be carried out by members of NCI-CGBB and EM. The members to perform the investigation will be designated by Daoud Meerzman, based on expertise and availability. The investigation should last no longer than 10 business days, at which time a report that outlines the problem and suggests solutions will be presented to Daoud Meerzman.

#### 4. CHIP-SEQ PIPELINE – VALIDATION RESULTS

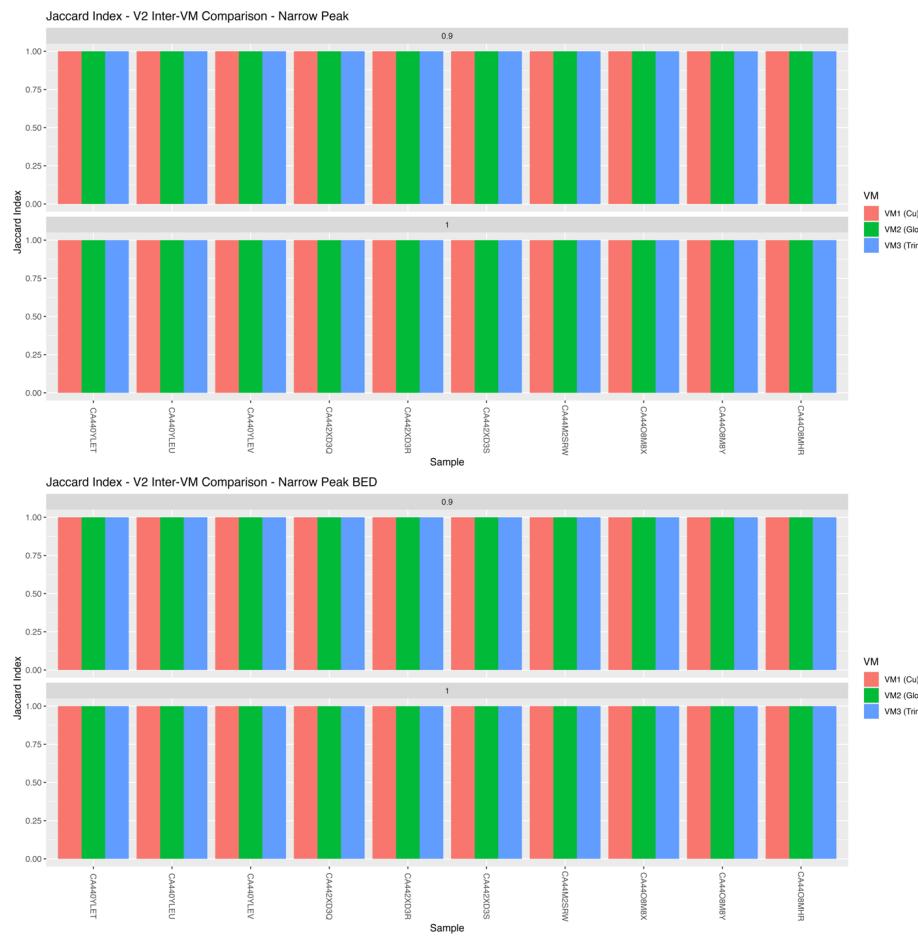
##### Section A: V2 Comparisons

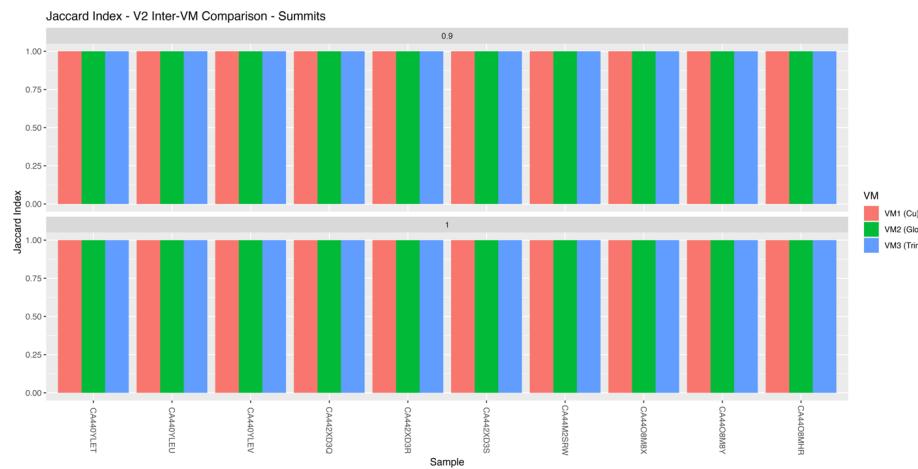
**Shared Entries:** A measure of concordance. Calculated as the proportion of shared peak calls vs the total calls. Calculated for the 3 Portal output files: narrowPeaks, narrowPeaks-bed, summit.



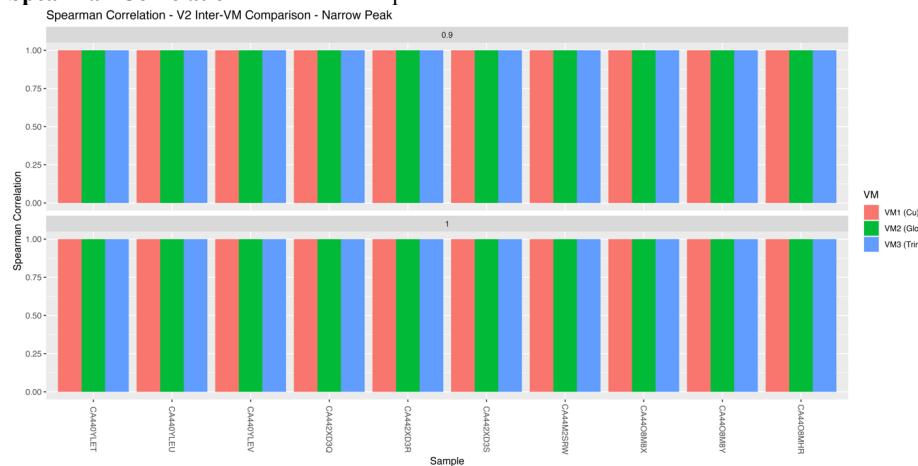


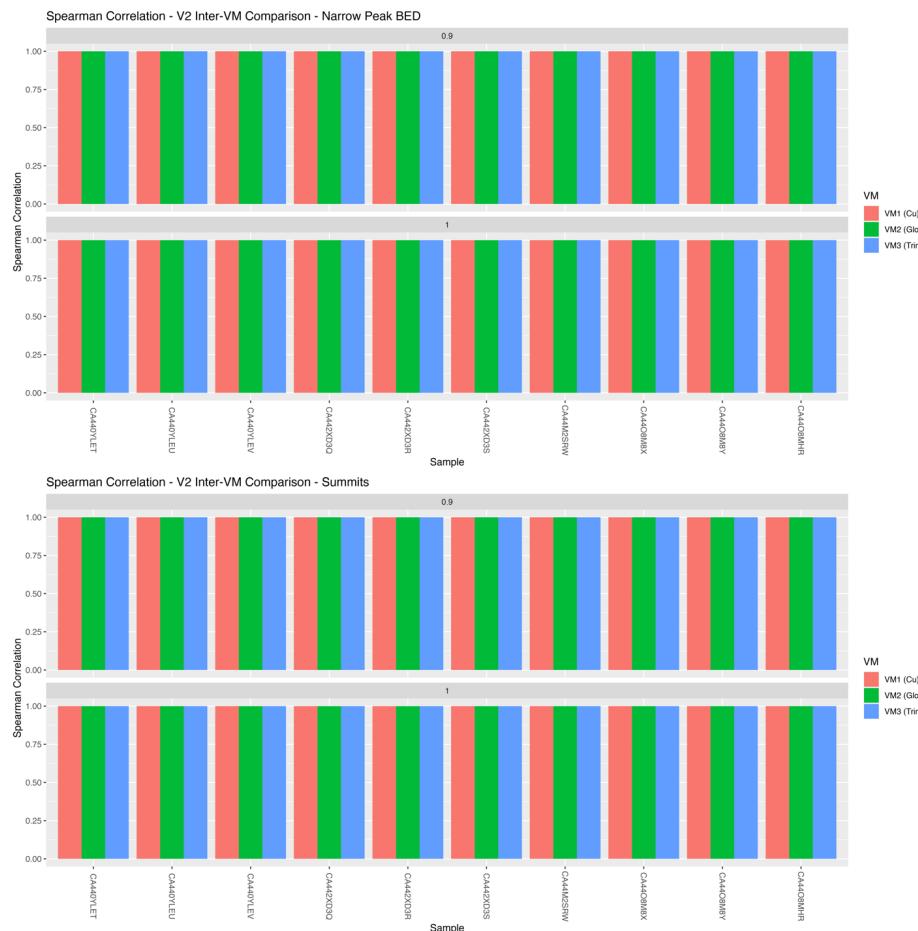
**Jaccard Index:** A measure of concordance and nucleotide overlap. Calculated as the proportion of shared bases for each peak. Calculated for the 3 Portal output files: narrowPeaks, narrowPeaks-bed, summit.





#### Spearman Correlation: Correlation of peak score value.





Homer Comparison: the “knownResults.txt” output file for each VM is compared amongst the VMs to evaluate reproducibility. The output is also compared against Homer’s ‘all.motifs’ file to determine if the results match the expected results of the software.

**VM-to-VM Comparison**

Source VM	Comparison VM	Sample	Concordance
VM1	VM2	CA440YL ET	100%
		CA440YL EV	100%
		CA442XD 3R	100%
		CA44M2 SRW	100%
		CA44O8 M8Y	100%
		CA440YL EU	100%
		CA442XD 3Q	100%
		CA442XD 3S	100%
		CA44O8 M8X	100%
		CA44O8 MHR	100%
VM1	VM3	CA440YL ET	100%
		CA440YL EV	100%
		CA442XD 3R	100%
		CA44M2 SRW	100%
		CA44O8 M8Y	100%
		CA440YL EU	100%
		CA442XD 3Q	100%
		CA442XD 3S	100%
		CA44O8 M8X	100%
		CA44O8 MHR	100%
VM2	VM3	CA440YL ET	100%
		CA440YL EV	100%
		CA442XD 3R	100%
		CA44M2 SRW	100%

**Comparison to Homer Known Results**

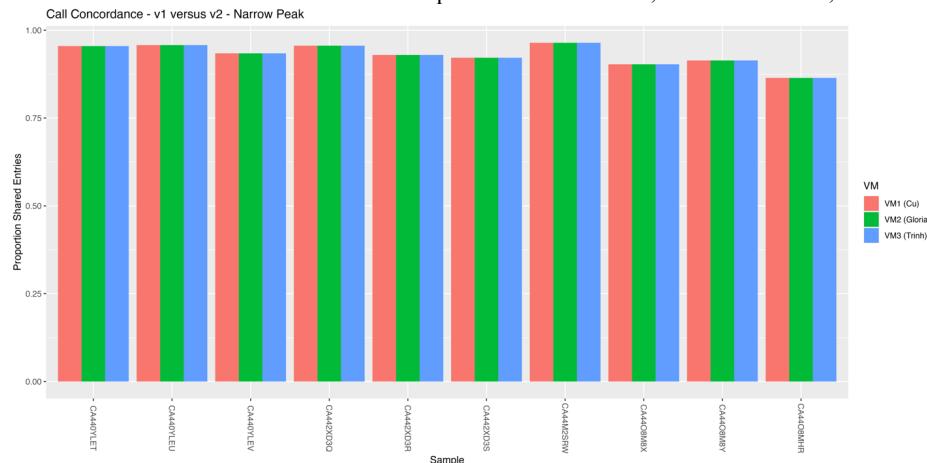
Source VM	Sample	Match Entries	Overlap
VM1	CA440YL ET	1002	100%
	CA440YL EV	1002	100%
	CA442XD 3R	1002	100%
	CA44M2 SRW	1002	100%
	CA44O8 M8Y	1002	100%
	CA440YL EU	1002	100%
	CA442XD 3Q	1002	100%
	CA442XD 3S	1002	100%
	CA44O8 M8X	1002	100%
	CA44O8 MHR	1002	100%
VM1	CA440YL ET	1002	100%
	CA440YL EV	1002	100%
	CA442XD 3R	1002	100%
	CA44M2 SRW	1002	100%
	CA44O8 M8Y	1002	100%
	CA440YL EU	1002	100%
	CA442XD 3Q	1002	100%
	CA442XD 3S	1002	100%
	CA44O8 M8X	1002	100%
	CA44O8 MHR	1002	100%
VM2	CA440YL ET	1002	100%
	CA440YL EV	1002	100%
	CA442XD 3R	1002	100%
	CA44M2 SRW	1002	100%

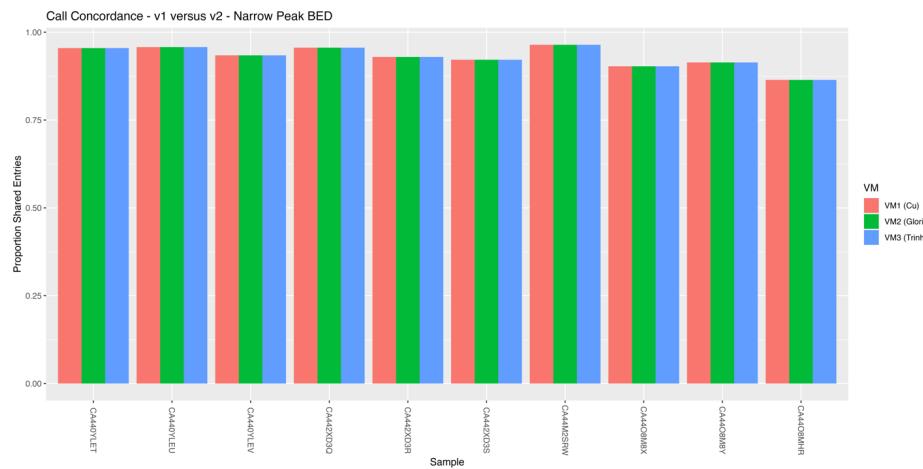
	CA44O8 M8Y	100%		CA44O8 M8Y	1002	100%
	CA440YL EU	100%		CA440YL EU	1002	100%
	CA442XD 3Q	100%		CA442XD 3Q	1002	100%
	CA442XD 3S	100%		CA442XD 3S	1002	100%
	CA44O8 M8X	100%		CA44O8 M8X	1002	100%
	CA44O8 MHR	100%		CA44O8 MHR	1002	100%

### Conclusion: All metrics pass acceptance criteria

#### Section A: V1-to-V2 Comparisons

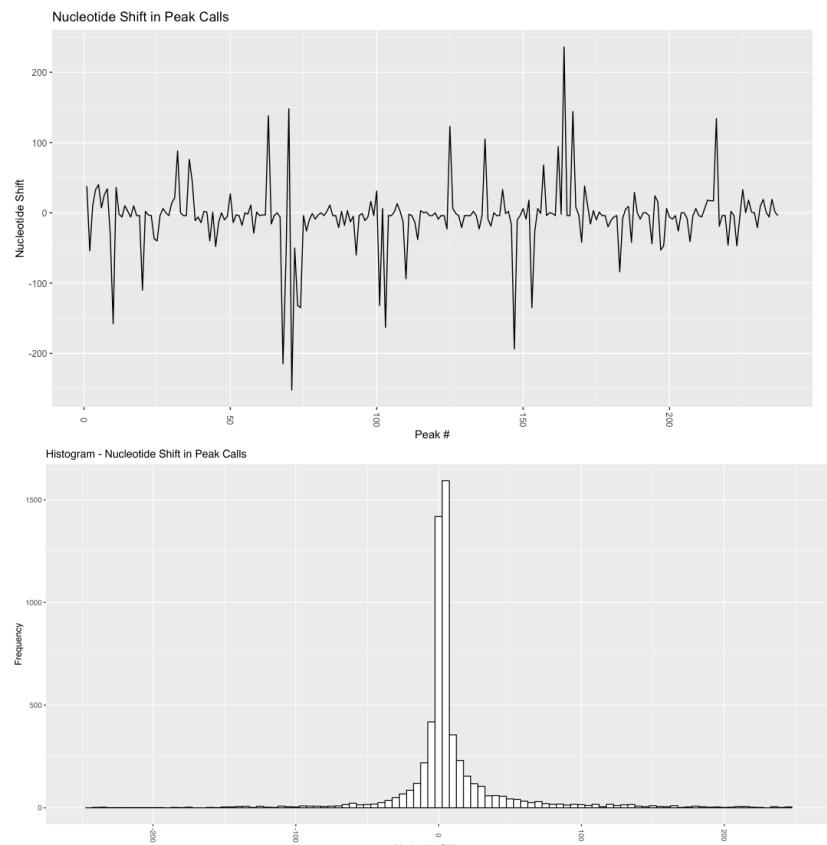
**Shared Entries:** A measure of concordance. Calculated as the proportion of shared peak calls vs the total calls. Calculated for the 3 Portal output files: narrowPeaks, narrowPeaks-bed, summit.



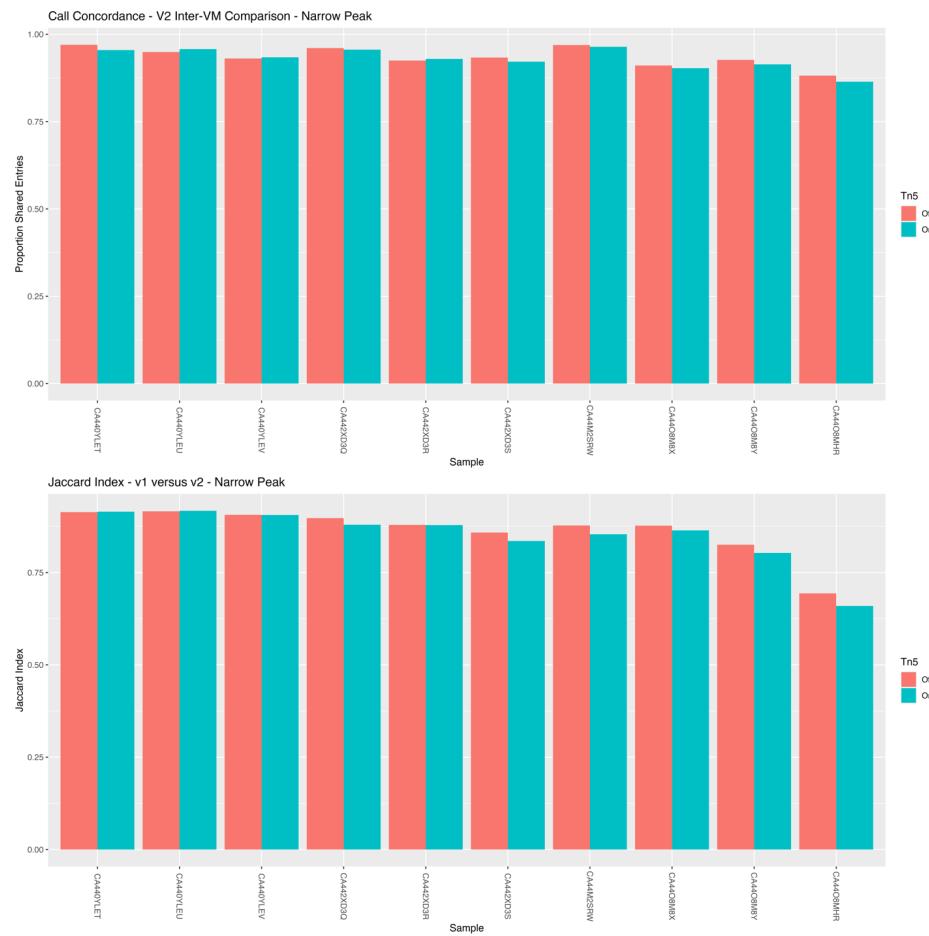


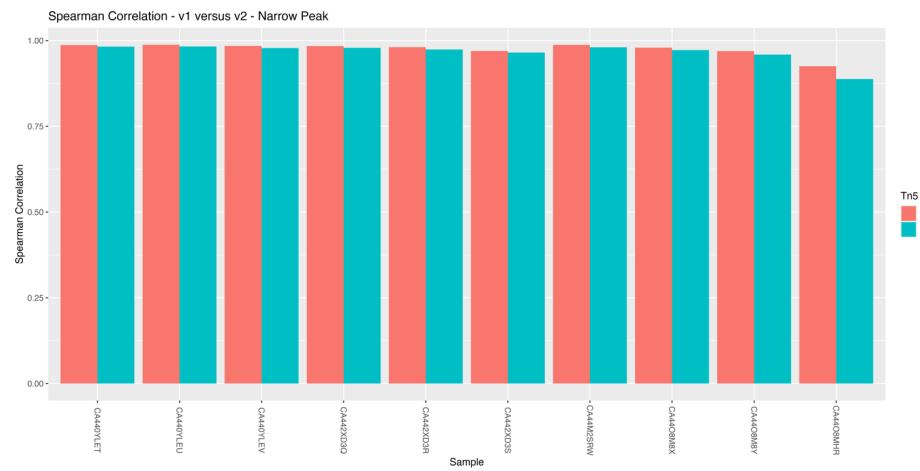
The above results showed that while the concordance between peaks was high between v1 and v2 runs, it was not a perfect match between v1 peak locations and v2 peak locations.

This was investigated further to understand the difference. We first looked at a subsample of peaks between v1 and v2 and calculated the difference in position.



As shown, there is a random distribution of differences, with an average difference in a peak position of ~0 nts. For this reason, we investigated the effect of Tn5 adjustment on peak calling. This causes a marginal increase in concordance between the v1 and v2 outputs.





**Conclusion:**

The enhanced pipeline produces highly reproducible results that can be replicated with high fidelity by different users / different virtual machines. The enhanced pipeline produces similar results to the original (v1) pipeline with generally small (~10s of nucleotides), randomly distributed differences in locations of the peak calls.

## 5. CHIP-SEQ PIPELINE – APPENDIX I – TABULAR RESULTS

V2 Comparisons																
Metric	VM	Overlap	Sample	Value	Metric	VM	Overlap	Sample	Value	Metric	VM	Overlap	Sample	Value		
Jaccard index	VM1 (Cu)	0.9	CA440YLET	1	VM1 (Cu)	0.9	CA440YLET	1	VM1 (Cu)	0.9	CA440YLET	1	VM1 (Cu)	0.9	CA440YLET	1
			CA440YLEV	1	VM1 (Cu)	0.9	CA440YLEV	1	VM1 (Cu)	0.9	CA440YLEV	1	VM1 (Cu)	0.9	CA440YLEV	1
			CA442KD3R	1	VM1 (Cu)	0.9	CA442KD3R	1	VM1 (Cu)	0.9	CA442KD3R	1	VM1 (Cu)	0.9	CA442KD3R	1
			CA44M2SRW	1	VM1 (Cu)	0.9	CA44M2SRW	1	VM1 (Cu)	0.9	CA44M2SRW	1	VM1 (Cu)	0.9	CA44M2SRW	1
			CA4408MBY	1	VM1 (Cu)	0.9	CA4408MBY	1	VM1 (Cu)	0.9	CA4408MBY	1	VM1 (Cu)	0.9	CA4408MBY	1
		1	CA440YLEU	1	VM1 (Cu)	0.9	CA440YLEU	1	VM1 (Cu)	0.9	CA440YLEU	1	VM1 (Cu)	0.9	CA440YLEU	1
			CA442KD3Q	1	VM1 (Cu)	0.9	CA442KD3Q	1	VM1 (Cu)	0.9	CA442KD3Q	1	VM1 (Cu)	0.9	CA442KD3Q	1
			CA442KD3S	1	VM1 (Cu)	0.9	CA442KD3S	1	VM1 (Cu)	0.9	CA442KD3S	1	VM1 (Cu)	0.9	CA442KD3S	1
			CA4408MBX	1	VM1 (Cu)	0.9	CA4408MBX	1	VM1 (Cu)	0.9	CA4408MBX	1	VM1 (Cu)	0.9	CA4408MBX	1
			CA4408MHR	1	VM1 (Cu)	0.9	CA4408MHR	1	VM1 (Cu)	0.9	CA4408MHR	1	VM1 (Cu)	0.9	CA4408MHR	1
VM2 (Gloria)	VM2 (Gloria)	0.9	CA440YLET	1	VM2 (Gloria)	0.9	CA440YLET	1	VM2 (Gloria)	0.9	CA440YLET	1	VM2 (Gloria)	0.9	CA440YLET	1
			CA440YLEV	1	VM2 (Gloria)	0.9	CA440YLEV	1	VM2 (Gloria)	0.9	CA440YLEV	1	VM2 (Gloria)	0.9	CA440YLEV	1
			CA442KD3R	1	VM2 (Gloria)	0.9	CA442KD3R	1	VM2 (Gloria)	0.9	CA442KD3R	1	VM2 (Gloria)	0.9	CA442KD3R	1
			CA44M2SRW	1	VM2 (Gloria)	0.9	CA44M2SRW	1	VM2 (Gloria)	0.9	CA44M2SRW	1	VM2 (Gloria)	0.9	CA44M2SRW	1
			CA4408MBY	1	VM2 (Gloria)	0.9	CA4408MBY	1	VM2 (Gloria)	0.9	CA4408MBY	1	VM2 (Gloria)	0.9	CA4408MBY	1
		1	CA440YLEU	1	VM2 (Gloria)	0.9	CA440YLEU	1	VM2 (Gloria)	0.9	CA440YLEU	1	VM2 (Gloria)	0.9	CA440YLEU	1
			CA442KD3Q	1	VM2 (Gloria)	0.9	CA442KD3Q	1	VM2 (Gloria)	0.9	CA442KD3Q	1	VM2 (Gloria)	0.9	CA442KD3Q	1
			CA442KD3S	1	VM2 (Gloria)	0.9	CA442KD3S	1	VM2 (Gloria)	0.9	CA442KD3S	1	VM2 (Gloria)	0.9	CA442KD3S	1
			CA4408MBX	1	VM2 (Gloria)	0.9	CA4408MBX	1	VM2 (Gloria)	0.9	CA4408MBX	1	VM2 (Gloria)	0.9	CA4408MBX	1
			CA4408MHR	1	VM2 (Gloria)	0.9	CA4408MHR	1	VM2 (Gloria)	0.9	CA4408MHR	1	VM2 (Gloria)	0.9	CA4408MHR	1
VM3 (Trinh)	VM3 (Trinh)	0.9	Spearman's coefficient				Shared Entries				Shared Entries					
			CA440YLET	1	VM2 (Gloria)	1	CA440YLET	1	VM2 (Gloria)	1	CA440YLET	1	VM2 (Gloria)	1	CA440YLET	1
			CA440YLEV	1	VM2 (Gloria)	1	CA440YLEV	1	VM2 (Gloria)	1	CA440YLEV	1	VM2 (Gloria)	1	CA440YLEV	1
			CA442KD3R	1	VM2 (Gloria)	1	CA442KD3R	1	VM2 (Gloria)	1	CA442KD3R	1	VM2 (Gloria)	1	CA442KD3R	1
			CA44M2SRW	1	VM2 (Gloria)	1	CA44M2SRW	1	VM2 (Gloria)	1	CA44M2SRW	1	VM2 (Gloria)	1	CA44M2SRW	1
		1	CA4408MBY	1	VM2 (Gloria)	1	CA4408MBY	1	VM2 (Gloria)	1	CA4408MBY	1	VM2 (Gloria)	1	CA4408MBY	1
			CA440YLEU	1	VM2 (Gloria)	1	CA440YLEU	1	VM2 (Gloria)	1	CA440YLEU	1	VM2 (Gloria)	1	CA440YLEU	1
			CA442KD3Q	1	VM2 (Gloria)	1	CA442KD3Q	1	VM2 (Gloria)	1	CA442KD3Q	1	VM2 (Gloria)	1	CA442KD3Q	1
			CA442KD3S	1	VM2 (Gloria)	1	CA442KD3S	1	VM2 (Gloria)	1	CA442KD3S	1	VM2 (Gloria)	1	CA442KD3S	1
			CA4408MBX	1	VM2 (Gloria)	1	CA4408MBX	1	VM2 (Gloria)	1	CA4408MBX	1	VM2 (Gloria)	1	CA4408MBX	1
VM3 (Trinh)	VM3 (Trinh)	0.9	CA4408MHR	1	VM3 (Trinh)	0.9	CA4408MHR	1	VM3 (Trinh)	0.9	CA4408MHR	1	VM3 (Trinh)	0.9	CA4408MHR	1
			CA440YLET	1	VM3 (Trinh)	1	CA440YLET	1	VM3 (Trinh)	0.9	CA440YLET	1	VM3 (Trinh)	0.9	CA440YLET	1
			CA440YLEV	1	VM3 (Trinh)	1	CA440YLEV	1	VM3 (Trinh)	0.9	CA440YLEV	1	VM3 (Trinh)	0.9	CA440YLEV	1
			CA442KD3R	1	VM3 (Trinh)	1	CA442KD3R	1	VM3 (Trinh)	0.9	CA442KD3R	1	VM3 (Trinh)	0.9	CA442KD3R	1
			CA44M2SRW	1	VM3 (Trinh)	1	CA44M2SRW	1	VM3 (Trinh)	0.9	CA44M2SRW	1	VM3 (Trinh)	0.9	CA44M2SRW	1
		1	CA4408MBY	1	VM3 (Trinh)	0.9	CA4408MBY	1	VM3 (Trinh)	0.9	CA4408MBY	1	VM3 (Trinh)	0.9	CA4408MBY	1
			CA440YLEU	1	VM3 (Trinh)	0.9	CA440YLEU	1	VM3 (Trinh)	0.9	CA440YLEU	1	VM3 (Trinh)	0.9	CA440YLEU	1
			CA442KD3Q	1	VM3 (Trinh)	0.9	CA442KD3Q	1	VM3 (Trinh)	0.9	CA442KD3Q	1	VM3 (Trinh)	0.9	CA442KD3Q	1
			CA442KD3S	1	VM3 (Trinh)	0.9	CA442KD3S	1	VM3 (Trinh)	0.9	CA442KD3S	1	VM3 (Trinh)	0.9	CA442KD3S	1
			CA4408MBX	1	VM3 (Trinh)	0.9	CA4408MBX	1	VM3 (Trinh)	0.9	CA4408MBX	1	VM3 (Trinh)	0.9	CA4408MBX	1
			CA4408MHR	1	VM3 (Trinh)	0.9	CA4408MHR	1	VM3 (Trinh)	0.9	CA4408MHR	1	VM3 (Trinh)	0.9	CA4408MHR	1

V1 vs V2									
Metric	VM	Overlap	Sample	Value	Metric	VM	Overlap	Sample	Value
Overlap	VM1 (Cu)	CA440YLET	0.915		CA440YLET	0.982	VM1 (Cu)	CA440YLET	0.977
		CA440YLEV	0.906		CA440YLEV	0.978		CA440YLEV	0.957
		CA442X3R	0.878		CA442X3R	0.974		CA442X3R	0.958
		CA44M2SRW	0.854		CA44M2SRW	0.980		CA44M2SRW	0.985
		CA4408MBY	0.803		CA4408MBY	0.959		CA4408MBY	0.957
	VM1 (Cu)	CA440YLEU	0.917		CA440YLEU	0.983		CA440YLEU	0.977
		CA442X3Q	0.879		CA442X3Q	0.979		CA442X3Q	0.982
		CA442X3S	0.835		CA442X3S	0.965		CA442X3S	0.960
		CA4408MBX	0.864		CA4408MBX	0.972		CA4408MBX	0.929
		CA4408MHR	0.660		CA4408MHR	0.888		CA4408MHR	0.937
VM1 (Cu)	0.5	CA440YLET	0.877		CA440YLET	0.991	VM1 (Cu)	CA440YLET	0.955
		CA440YLEV	0.865		CA440YLEV	0.990		CA440YLEV	0.934
		CA442X3R	0.831		CA442X3R	0.989		CA442X3R	0.930
		CA44M2SRW	0.821		CA44M2SRW	0.987		CA44M2SRW	0.964
		CA4408MBY	0.740		CA4408MBY	0.983		CA4408MBY	0.914
	0.9	CA440YLEU	0.883		CA440YLEU	0.991		CA440YLEU	0.958
		CA442X3Q	0.837		CA442X3Q	0.990		CA442X3Q	0.956
		CA442X3S	0.776		CA442X3S	0.986		CA442X3S	0.922
		CA4408MBX	0.820		CA4408MBX	0.987		CA4408MBX	0.903
		CA4408MHR	0.578		CA4408MHR	0.916		CA4408MHR	0.864
Overlap	VM2 (Gloria)	CA440YLET	0.594		CA440YLET	0.992	VM2 (Gloria)	CA440YLET	0.762
		CA440YLEV	0.576		CA440YLEV	0.992		CA440YLEV	0.736
		CA442X3R	0.532		CA442X3R	0.991		CA442X3R	0.712
		CA44M2SRW	0.534		CA44M2SRW	0.989		CA44M2SRW	0.744
		CA4408MBY	0.427		CA4408MBY	0.986		CA4408MBY	0.643
	0.9	CA440YLEU	0.615		CA440YLEU	0.993		CA440YLEU	0.777
		CA442X3Q	0.547		CA442X3Q	0.992		CA442X3Q	0.742
		CA442X3S	0.449		CA442X3S	0.989		CA442X3S	0.654
		CA4408MBX	0.528		CA4408MBX	0.988		CA4408MBX	0.692
		CA4408MHR	0.234		CA4408MHR	0.925		CA4408MHR	0.447
Jaccard index	VM2 (Gloria)	CA440YLET	0.915		CA440YLET	0.982	VM2 (Gloria)	CA440YLET	0.977
		CA440YLEV	0.906		CA440YLEV	0.978		CA440YLEV	0.957
		CA442X3R	0.878		CA442X3R	0.974		CA442X3R	0.958
		CA44M2SRW	0.854		CA44M2SRW	0.980		CA44M2SRW	0.985
		CA4408MBY	0.803		CA4408MBY	0.959		CA4408MBY	0.957
	0.9	CA440YLEU	0.917		CA440YLEU	0.983		CA440YLEU	0.977
		CA442X3Q	0.879		CA442X3Q	0.979		CA442X3Q	0.982
		CA442X3S	0.835		CA442X3S	0.965		CA442X3S	0.960
		CA4408MBX	0.864		CA4408MBX	0.972		CA4408MBX	0.929
		CA4408MHR	0.660		CA4408MHR	0.888		CA4408MHR	0.937
Overlap	VM3 (Trinh)	CA440YLET	0.915		CA440YLET	0.982	VM3 (Trinh)	CA440YLET	0.977
		CA440YLEV	0.906		CA440YLEV	0.978		CA440YLEV	0.957
		CA442X3R	0.878		CA442X3R	0.974		CA442X3R	0.958
		CA44M2SRW	0.854		CA44M2SRW	0.980		CA44M2SRW	0.985
		CA4408MBY	0.803		CA4408MBY	0.959		CA4408MBY	0.957
	0.9	CA440YLEU	0.917		CA440YLEU	0.983		CA440YLEU	0.977
		CA442X3Q	0.879		CA442X3Q	0.979		CA442X3Q	0.982
		CA442X3S	0.836		CA442X3S	0.965		CA442X3S	0.960
		CA4408MBX	0.864		CA4408MBX	0.972		CA4408MBX	0.929
		CA4408MHR	0.659		CA4408MHR	0.925		CA4408MHR	0.447
VM3 (Trinh)	0.5	CA440YLET	0.877		CA440YLET	0.991	VM3 (Trinh)	CA440YLET	0.977
		CA440YLEV	0.865		CA440YLEV	0.990		CA440YLEV	0.954
		CA442X3R	0.831		CA442X3R	0.991		CA442X3R	0.958
		CA44M2SRW	0.821		CA44M2SRW	0.987		CA44M2SRW	0.985
		CA4408MBY	0.740		CA4408MBY	0.983		CA4408MBY	0.914
	0.9	CA440YLEU	0.883		CA440YLEU	0.991		CA440YLEU	0.958
		CA442X3Q	0.837		CA442X3Q	0.990		CA442X3Q	0.956
		CA442X3S	0.776		CA442X3S	0.986		CA442X3S	0.922
		CA4408MBX	0.820		CA4408MBX	0.987		CA4408MBX	0.903
		CA4408MHR	0.578		CA4408MHR	0.916		CA4408MHR	0.864