GREG
GENE REGULATION
GRAPH DATABASE

Studying transcriptional regulation using Graph Databases

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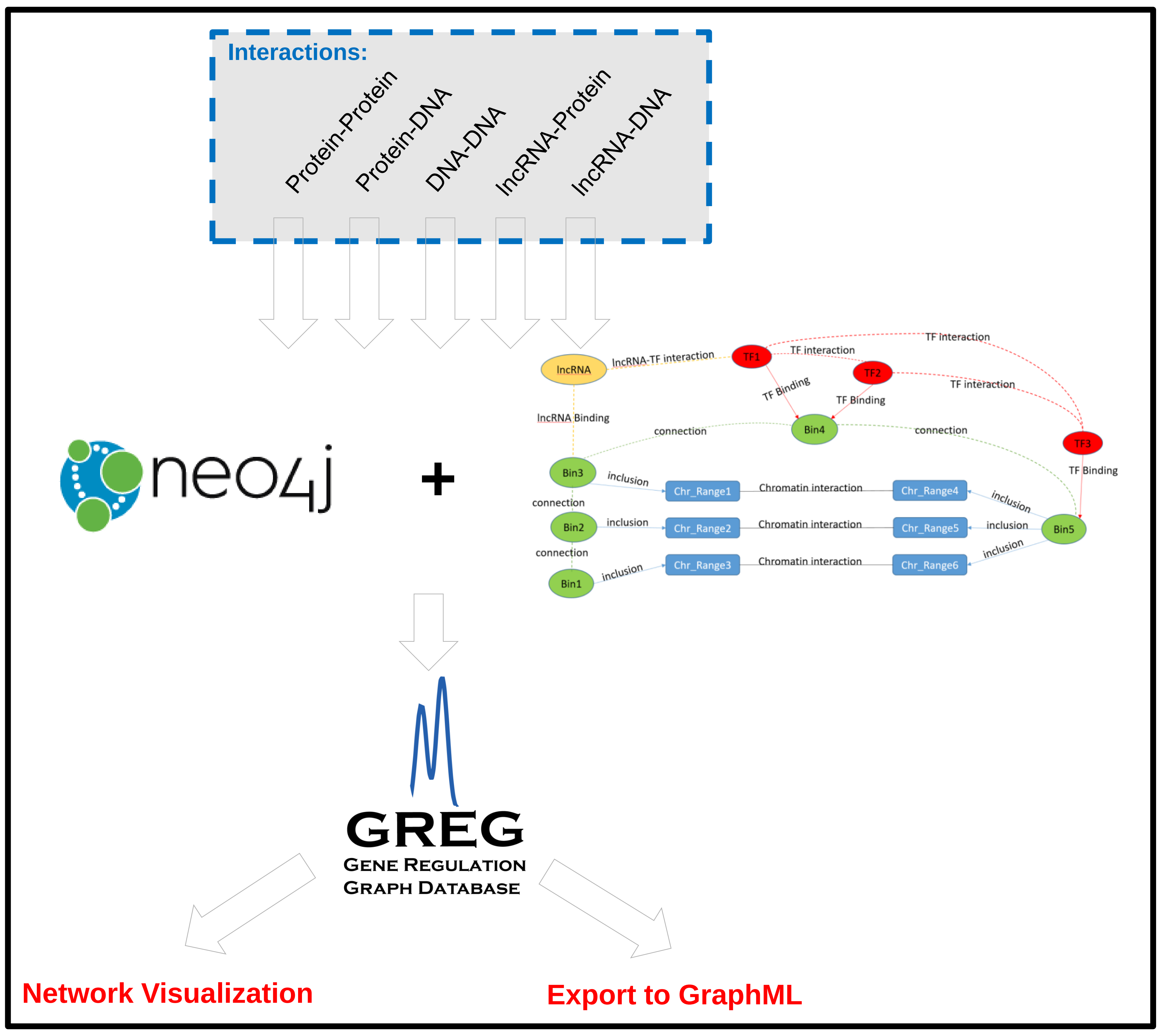
GREG (The Gene Regulation Graph Database) is a graph database written in the Neo4J language.

Its goal is to allow genomic researchers to see in a graphical way all the known **interactions between proteins, lncRNAs, and DNA for a given transcription factor, lncRNA, or a given genomic region** (i.e., its "regulatory landscape").



With GREG...

1. **Find all the interactions for your query TF, lncRNA, or genomic region**! (No need to collect and merge information from different databases).
2. **Get the output as a graph**! (See the complete picture of your query regulation mechanism as a graph. Export the result as GraphML format).
3. **Build advanced graphical queries**! (Ask GREG to **extend** your query to the neighbors of a given node, or ask for the **shortest path** between two given nodes, as well as several other graph-related queries).
4. **Get networks for either one cell type or multiple cell types**! (explore differences between cell types or infer missing data).

EXAMPLES

Step1 Choose Cell lines(Default:All Cell Lines)

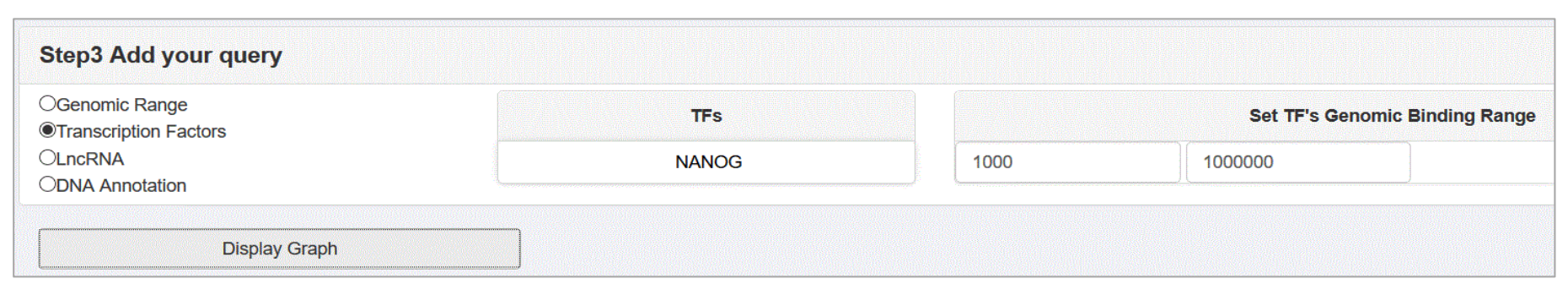
Chosen:H1ESC

Cell Type	Cell Name
All	H1ESC
Stem Cells	IPS6.9
Cancer Cells	IPS19.11
Other	

Step2 Choose chromosome (Default: Chr1 with small bins)

Genome Bin size	Chromosome
Small Bins(2kbp)	chr1

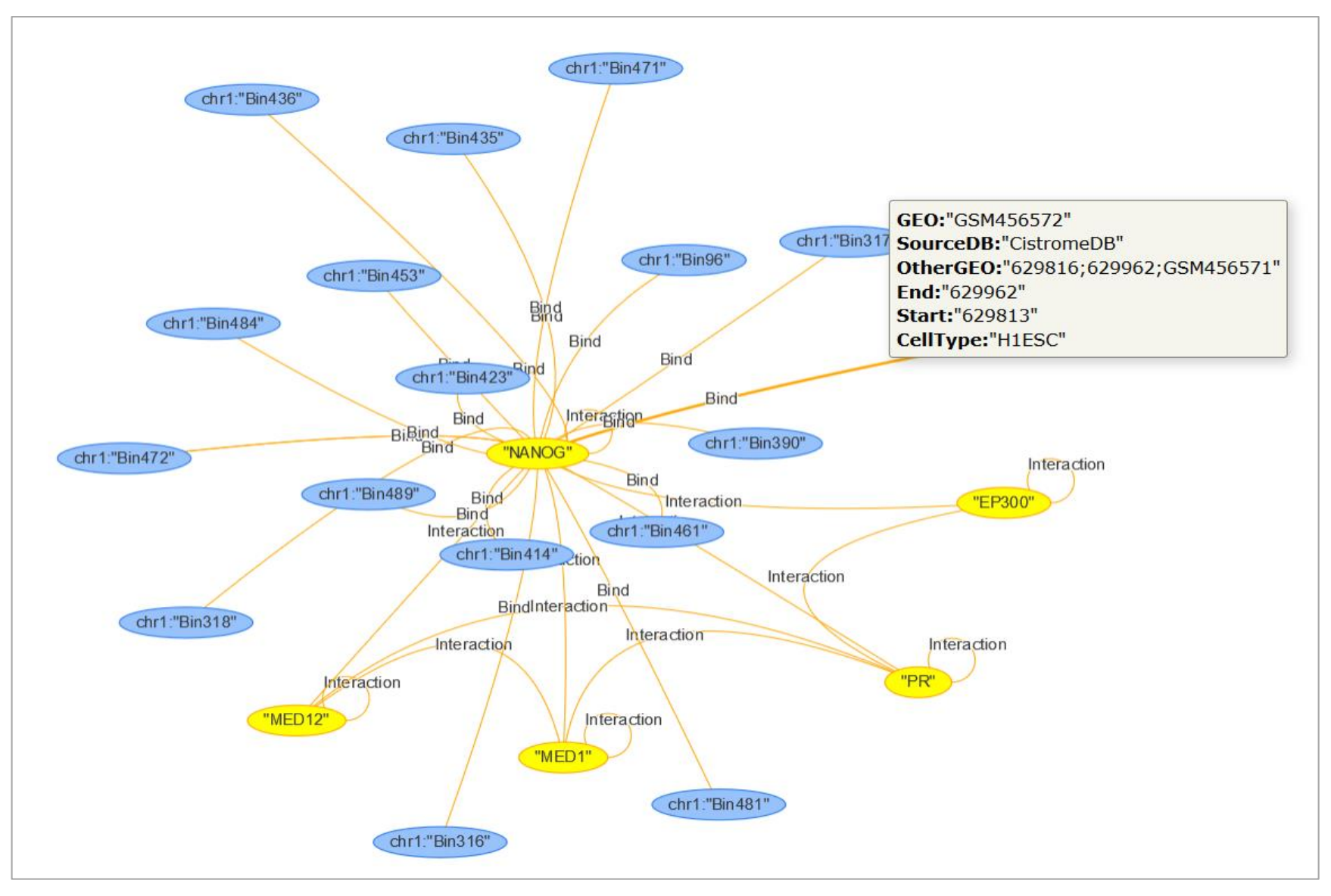
Find interactions for your query TF or lncRNA



Step3 Add your query

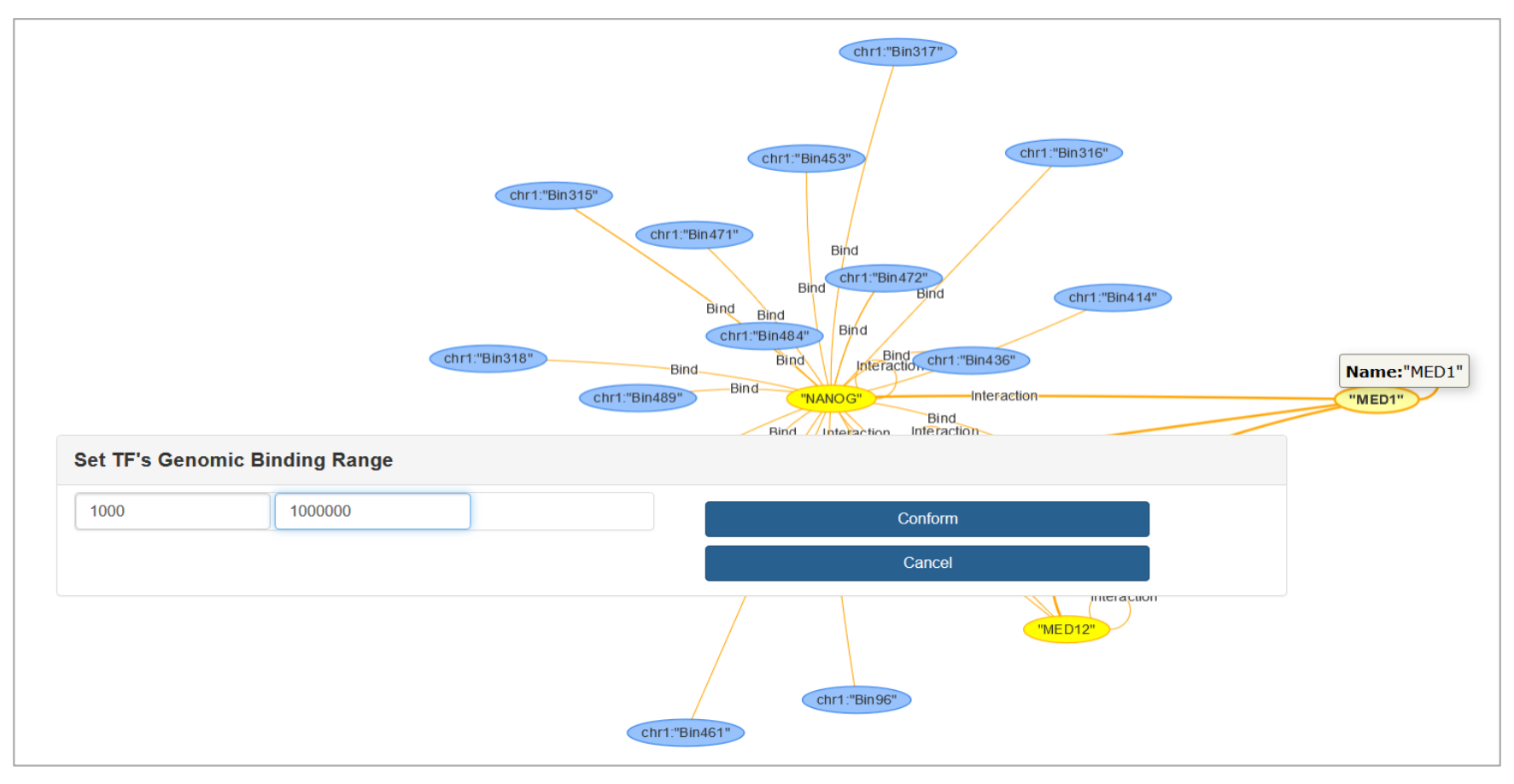
○Genomic Range
●Transcription Factors
○LncRNA
○DNA Annotation

TFs	Set TF's Genomic Binding Range	
NANOG	1000	1000000



GEO:"GSM456572"
SourceDB:"CistromeDB"
OtherGEO:"629816;629962;GSM456571"
End:"629962"
Start:"629813"
CellType:"H1ESC"

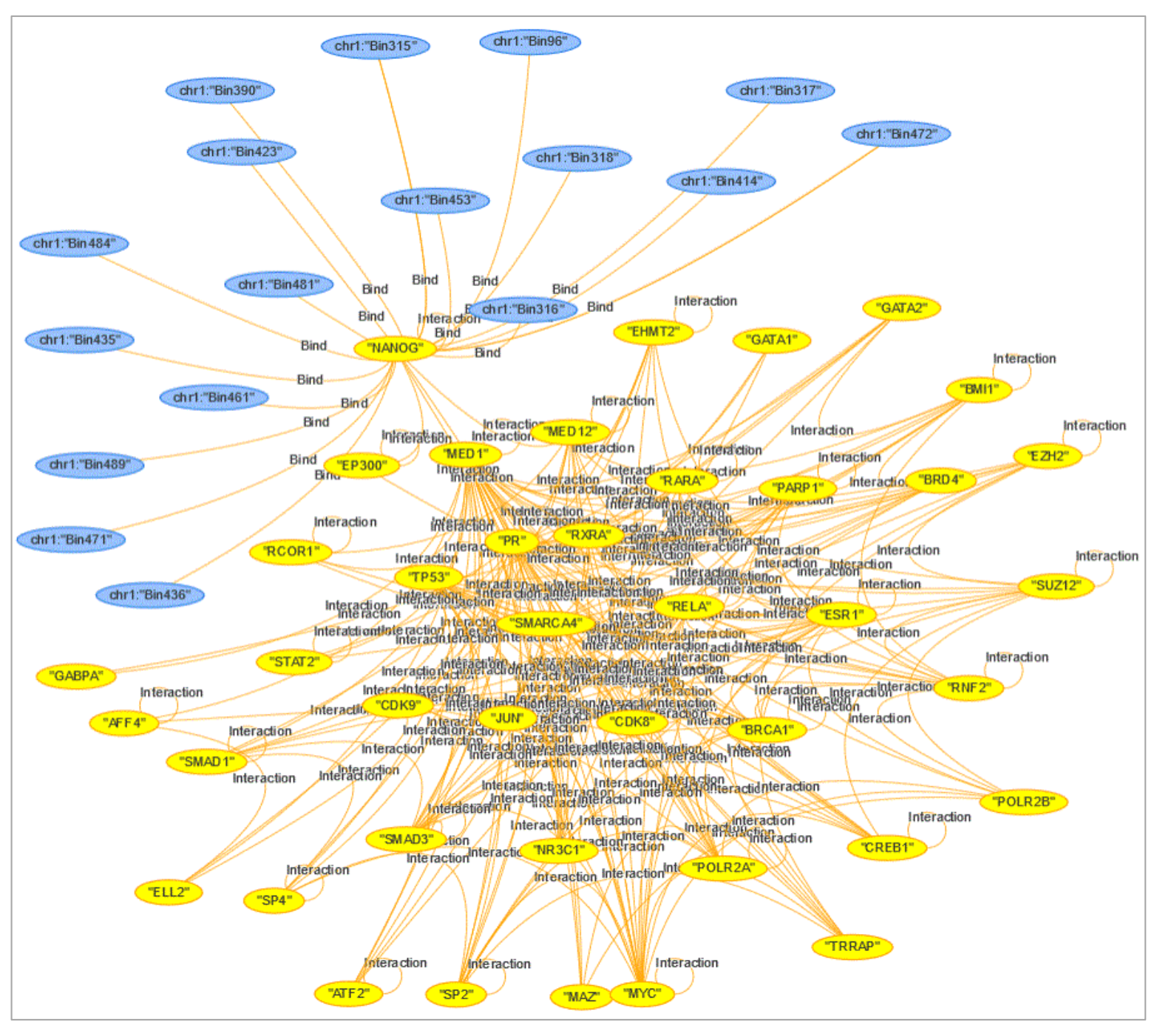
Select a transcription factor and the genomic region of your interest. Get the network with all the interacting TFs, lncRNAs, and DNA ranges for that region.



Name:"MED1"

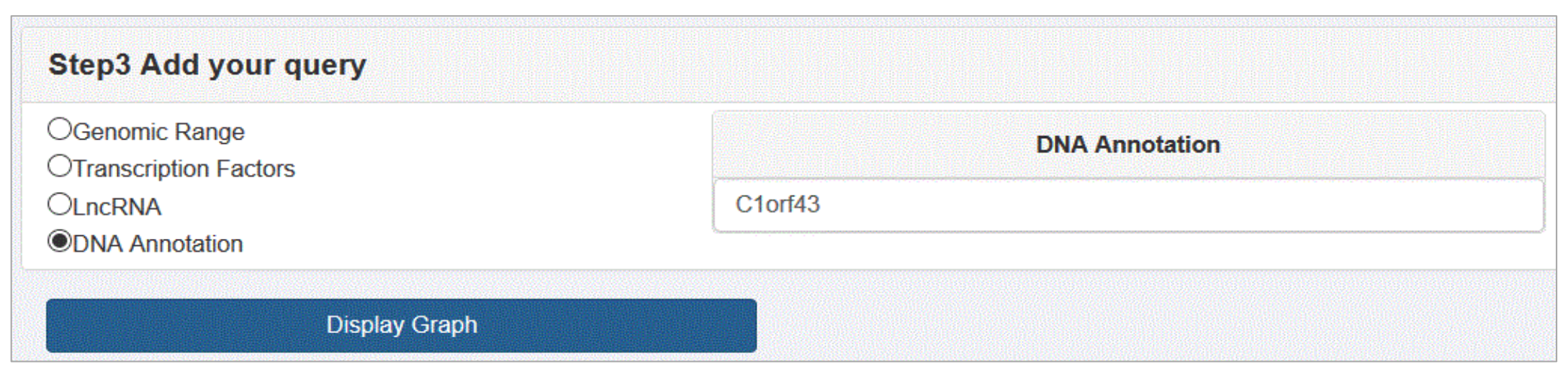
Set TF's Genomic Binding Range

1000 | 1000000



Expand your search: Double-click on any node and find its interactors.

Find interactions for DNA annotations

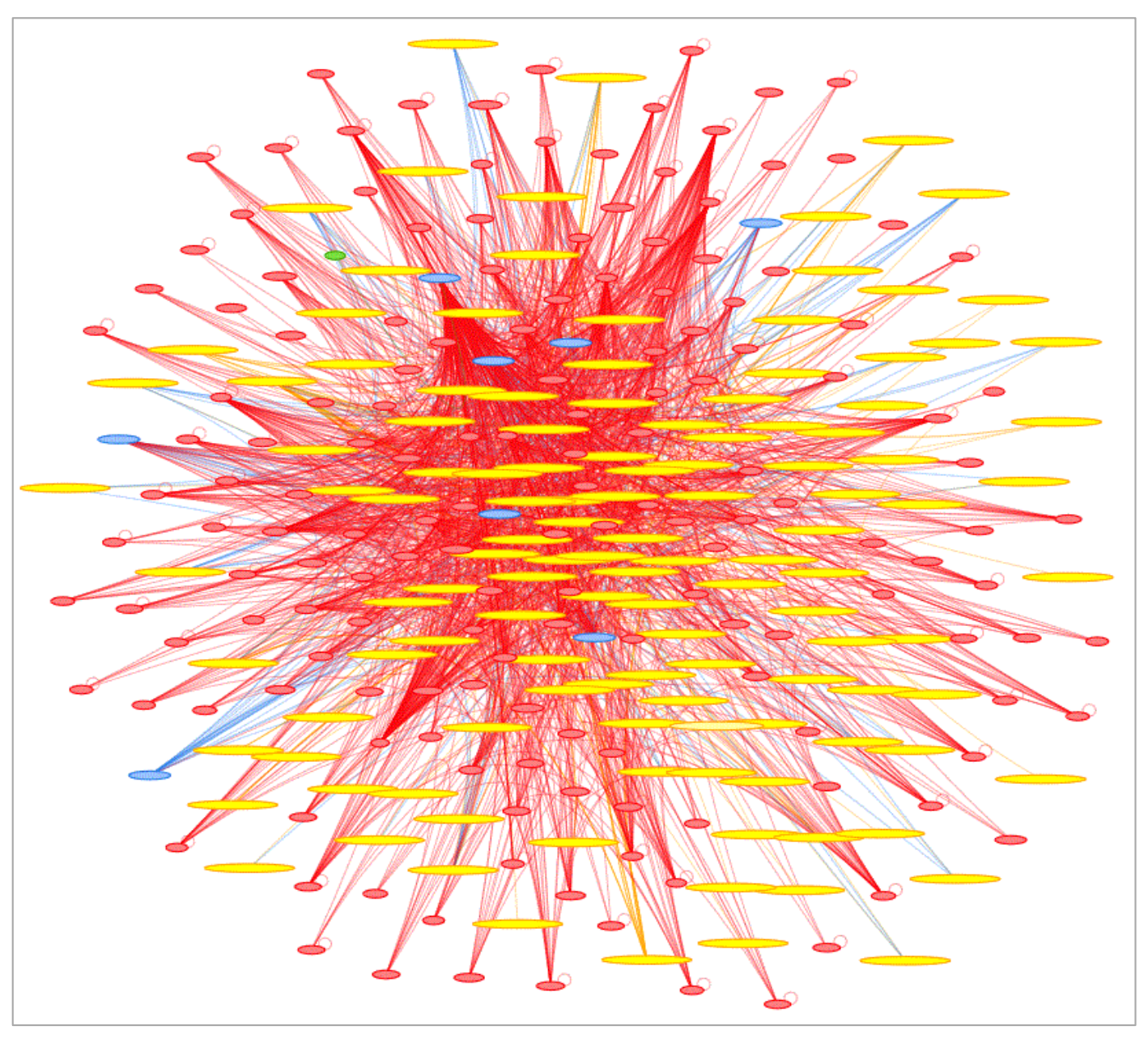


Step3 Add your query

○Genomic Range
○Transcription Factors
○LncRNA
●DNA Annotation

DNA Annotation
C1orf43

Select "DNA annotation" and input the gene name associated to a given DNA region.



Get the network with all the interacting TFs, lncRNAs, and DNA ranges for that region.

Test GREG now:

http://210.38.57.54:8080/index.html

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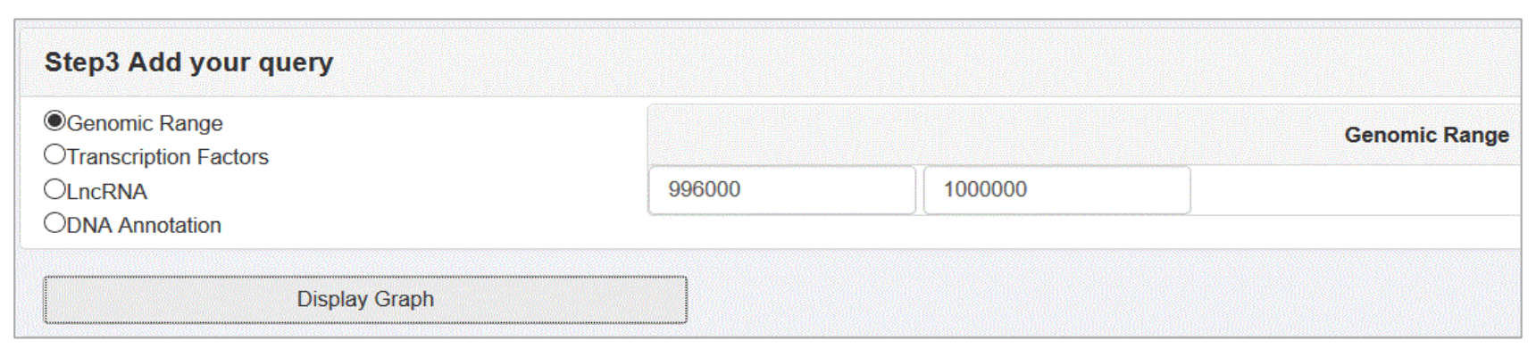
Acknowledgments: Shaurya Jauhari, Rajni Jauhari

Find interactions for a chosen genomic region

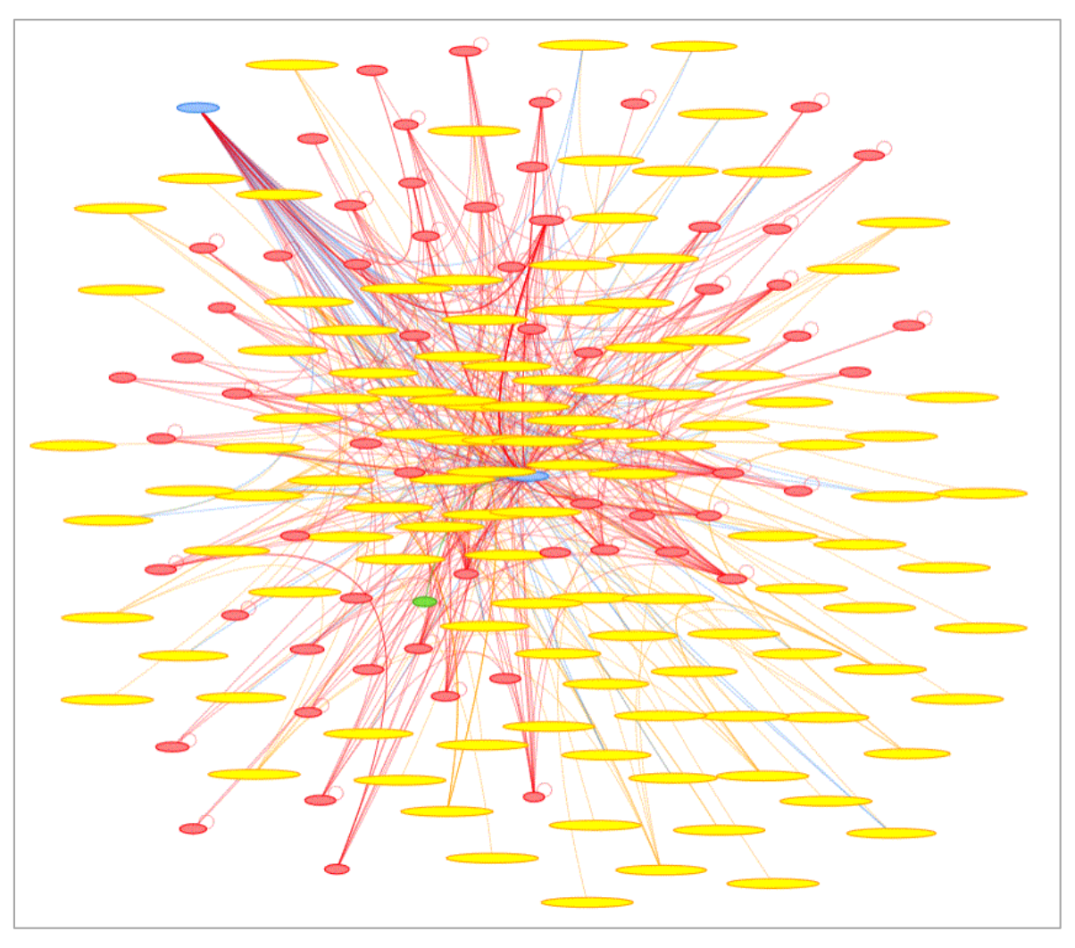


Step3 Add your query

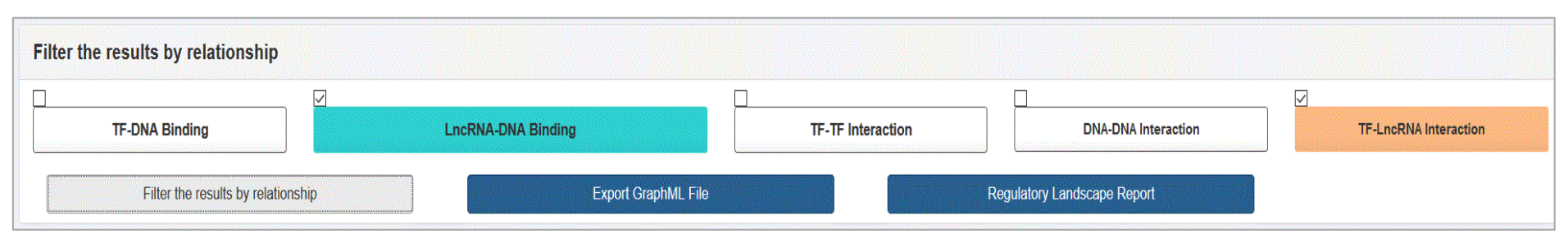
●Genomic Range
○Transcription Factors
○LncRNA
○DNA Annotation

Genomic Range	
996000	1000000

Select "Genomic Range" and input the coordinates of a DNA region for the previously chosen chromosome



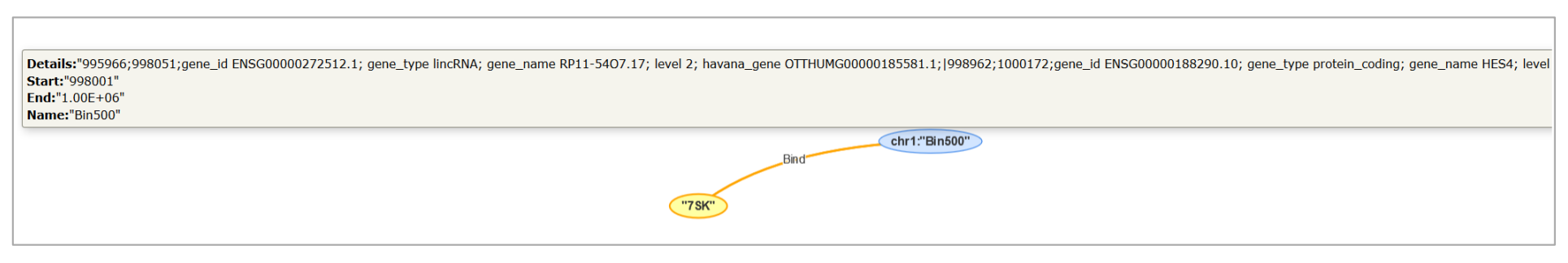
Get the network with all the interacting TFs, lncRNAs, and DNA ranges for that region.



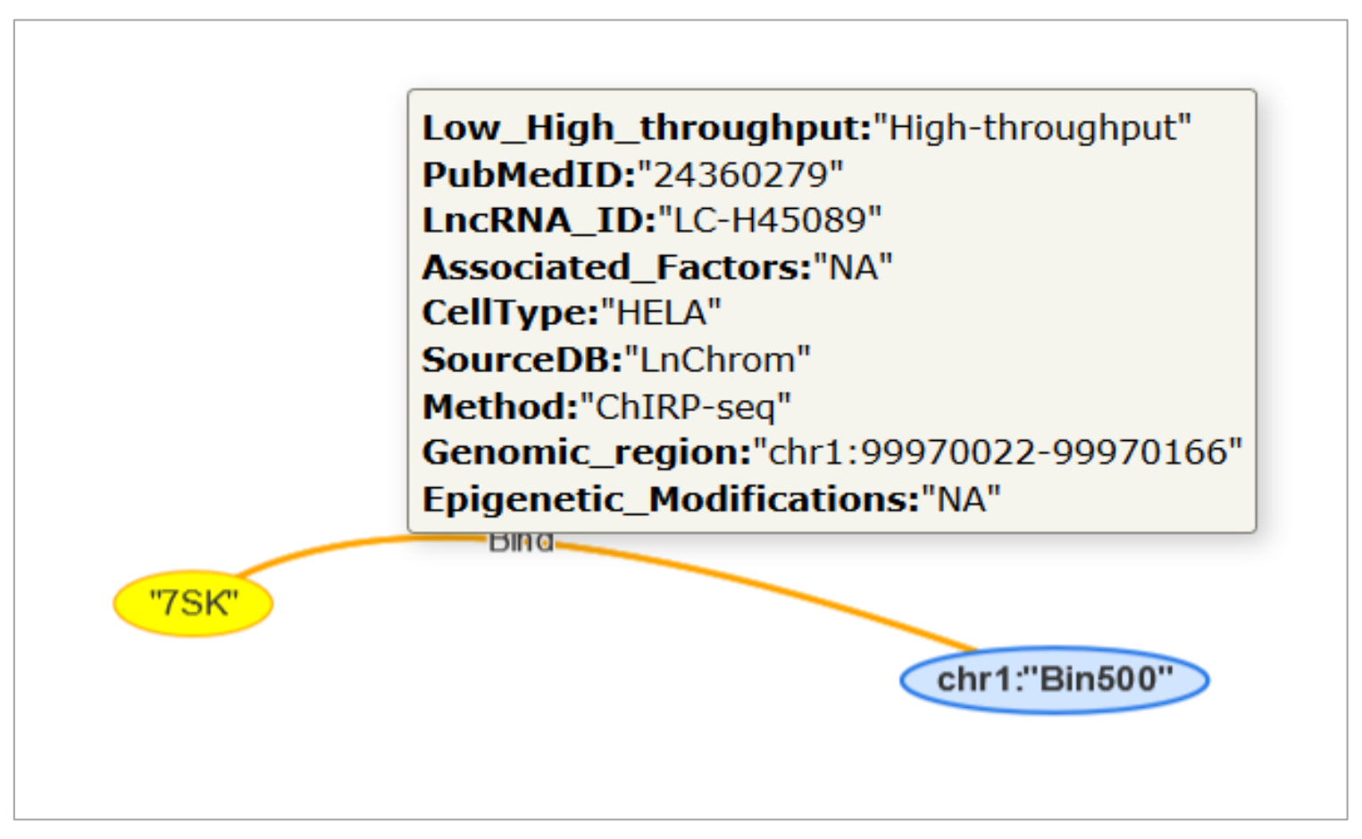
Filter the results by relationship

☐ TF-DNA Binding
☑ LncRNA-DNA Binding
☐ TF-TF Interaction
☐ DNA-DNA Interaction
☑ TF-LncRNA Interaction

Filter your results according to specific relationships (example, lncRNA-TF and lncRNA-DNA).



Details:"995966;998051;gene_id ENSG00000272512.1; gene_type lincRNA; gene_name RP11-54O7.17; level 2; havana_gene OTTHUMG00000185581.1;|998962;1000172;gene_id ENSG00000188290.10; gene_type protein_coding; gene_name HES4; level
Start:"998001"
End:"1.00E+06"
Name:"Bin500"



Low_High_throughput:"High-throughput"
PubMedID:"24360279"
LncRNA_ID:"LC-H45089"
Associated_Factors:"NA"
CellType:"HELA"
SourceDB:"LnChrom"
Method:"ChIRP-seq"
Genomic_region:"chr1:99970022-99970166"
Epigenetic_Modifications:"NA"

Examine the data associated to each node and interaction