ChromViz 1.0

a java tool to visualize high throughput (gene expression) data on Chromosomes

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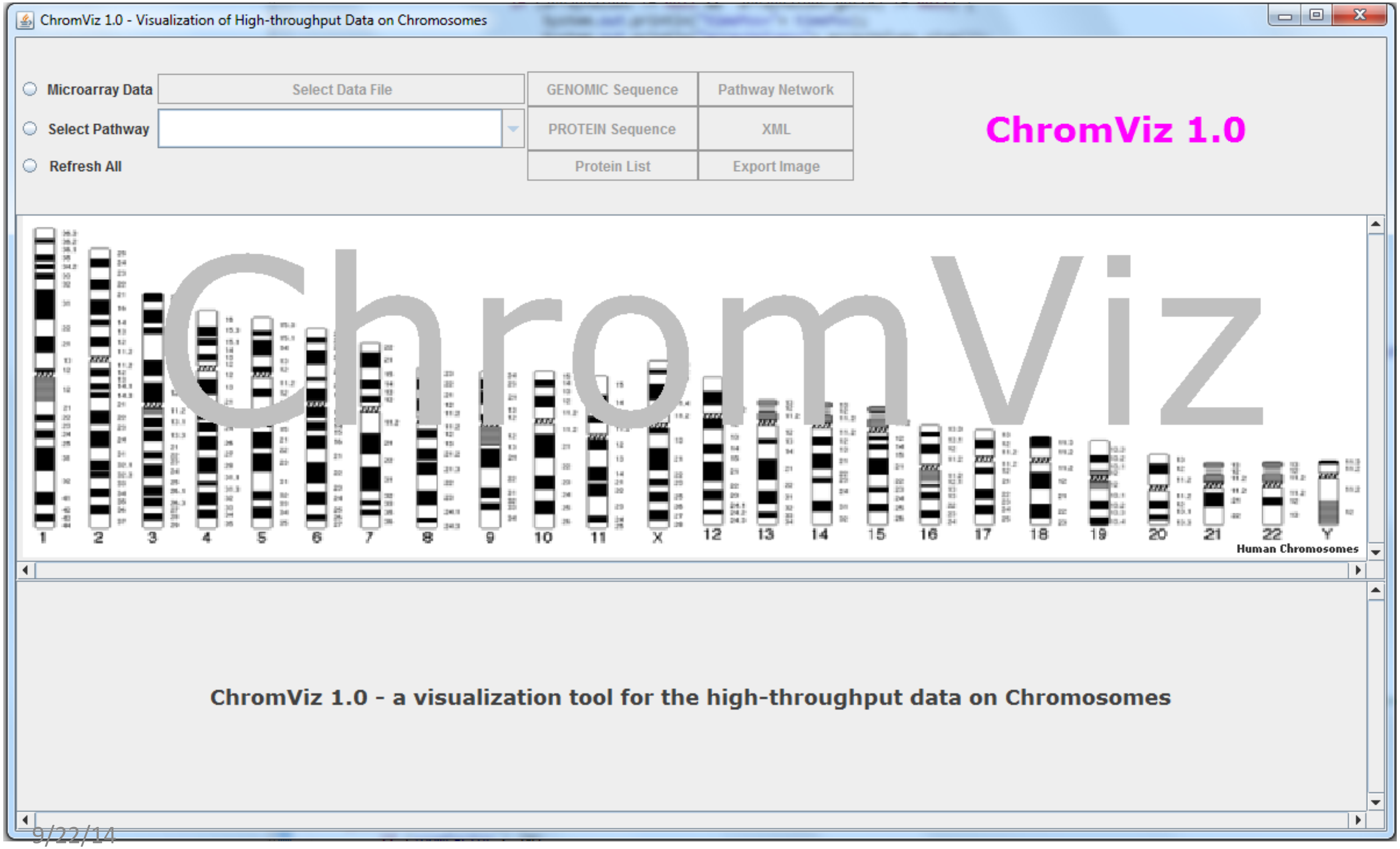
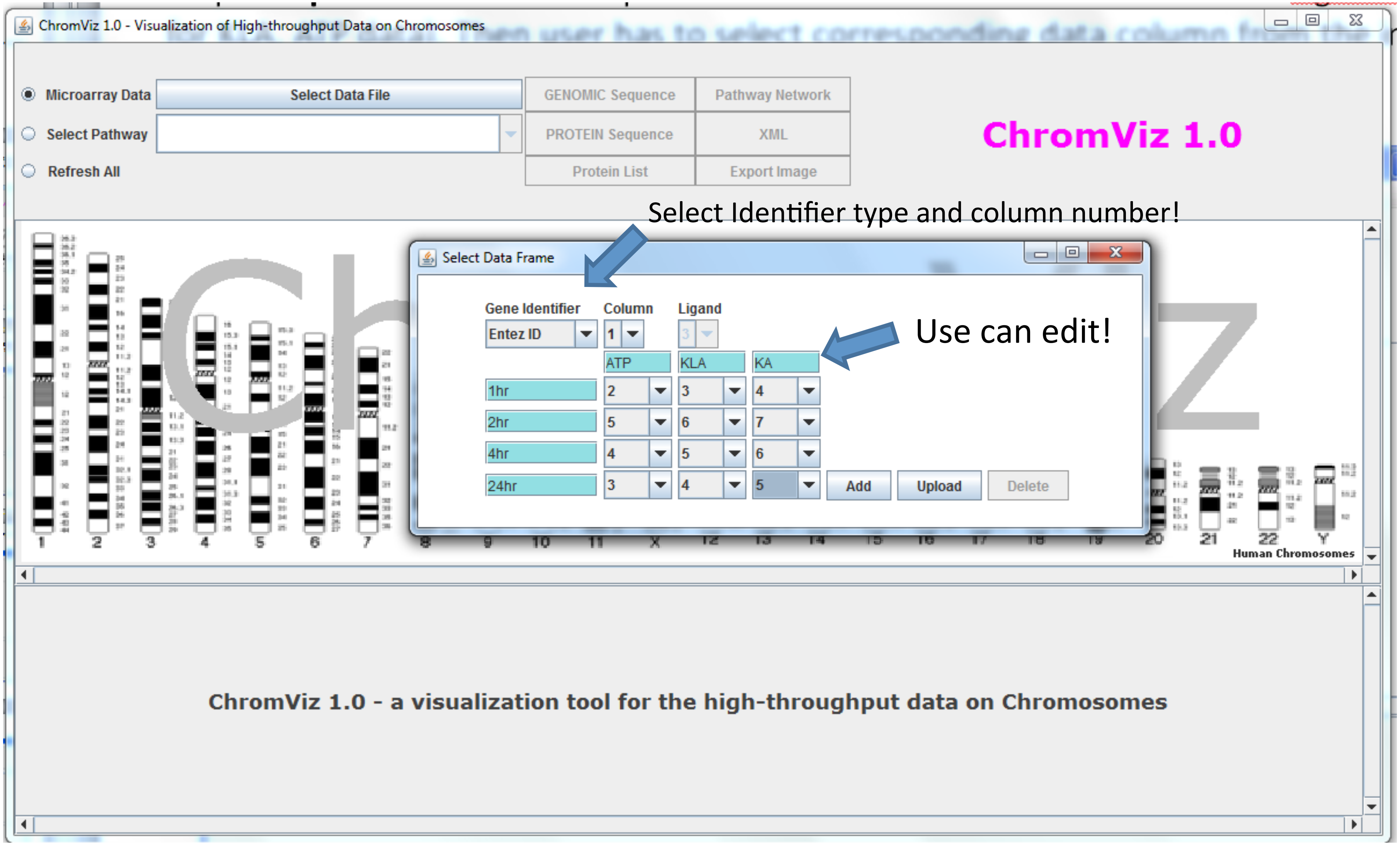
Step 1. The user can upload his/her own data and visualize after pathway selection OR the user can select pathway and can visualize pathway genes on chromosomes along with UCSC genome browser data such as gene co-ordinates etc..


ChromViz 1.0 - Visualization of High-throughput Data on Chromosomes
○ Microarray Data
Select Data File
○ Select Pathway
○ Refresh All
GENOMIC Sequence
Pathway Network
PROTEIN Sequence
XML
Protein List
Export Image
ChromViz 1.0
ChromViz
1
2
3
4
5
6
7
8
9
10
11
X
12
13
14
15
16
17
18
19
20
21
22
Y
Human Chromosomes

ChromViz 1.0 - a visualization tool for the high-throughput data on Chromosomes

Step 2. **Input file Selection**: Expression data selection window. Number of Ligands (Ex: 2 for KLA, ATP data). Then user has to select corresponding data column from the input file.


ChromViz 1.0 - Visualization of High-throughput Data on Chromosomes
● Microarray Data
Select Data File
○ Select Pathway
○ Refresh All
GENOMIC Sequence
Pathway Network
PROTEIN Sequence
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Export Image
ChromViz 1.0
Select Data Frame
Add
Upload
Delete
Human Chromosomes
ChromViz 1.0 - a visualization tool for the high-throughput data on Chromosomes

Select Identifier type and column number!

Use can edit!

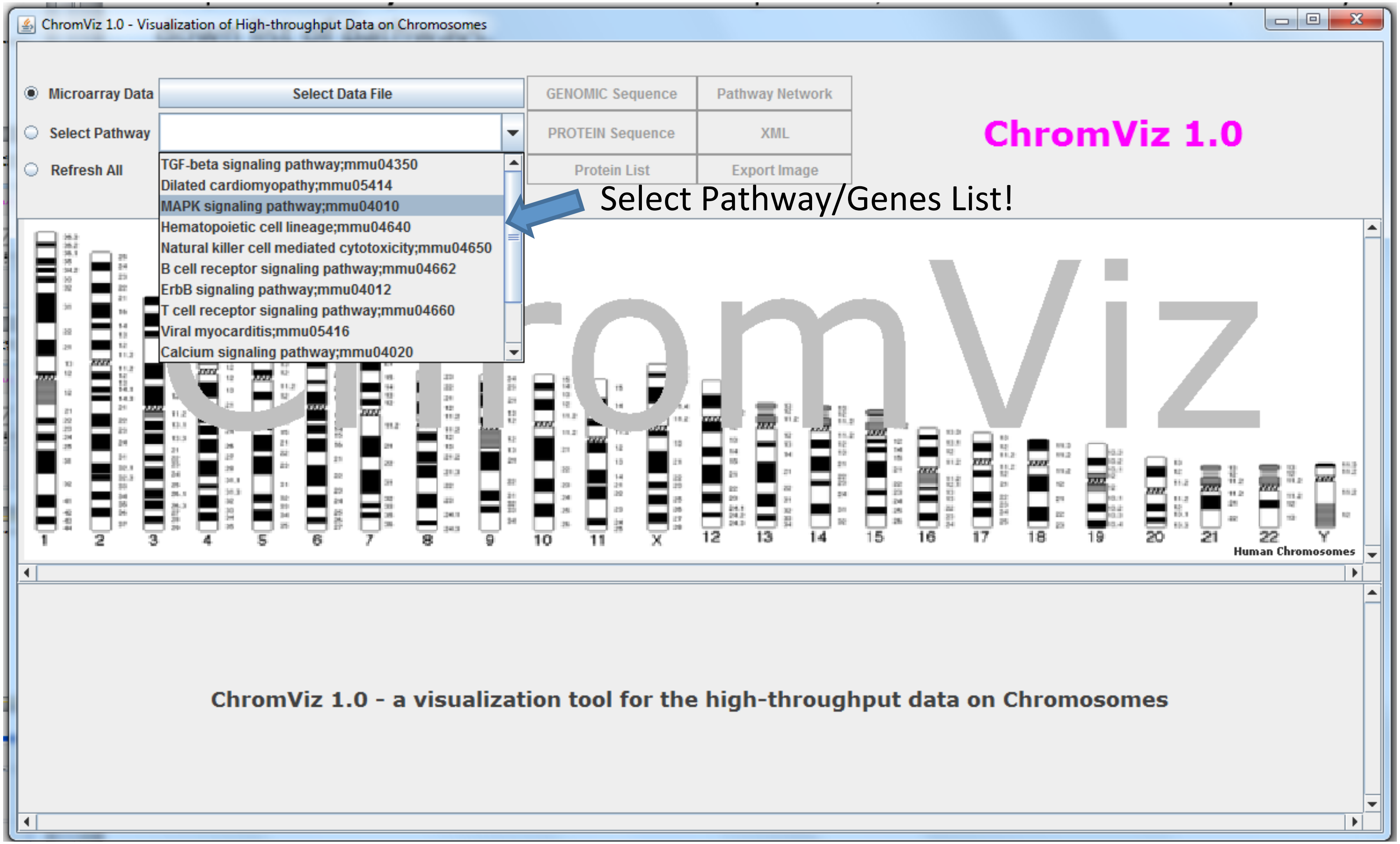
Gene Identifier: Entez ID

Column: 1

Ligand: 3

	ATP	KLA	KA
1hr	2	3	4
2hr	5	6	7
4hr	4	5	6
24hr	3	4	5

Step 3. **Pathway Selection**: Once data uploaded, the user has to select pathway from drop-down list of pathways.


ChromViz 1.0 - Visualization of High-throughput Data on Chromosomes
● Microarray Data
Select Data File
GENOMIC Sequence
Pathway Network
○ Select Pathway
PROTEIN Sequence
XML
○ Refresh All
Protein List
Export Image
TGF-beta signaling pathway;mmu04350
Dilated cardiomyopathy;mmu05414
MAPK signaling pathway;mmu04010
Hematopoietic cell lineage;mmu04640
Natural killer cell mediated cytotoxicity;mmu04650
B cell receptor signaling pathway;mmu04662
ErbB signaling pathway;mmu04012
T cell receptor signaling pathway;mmu04660
Viral myocarditis;mmu05416
Calcium signaling pathway;mmu04020
ChromViz 1.0
ChromViz
1
2
3
4
5
6
7
8
9
10
11
X
12
13
14
15
16
17
18
19
20
21
22
Y
Human Chromosomes

Select Pathway/Genes List!

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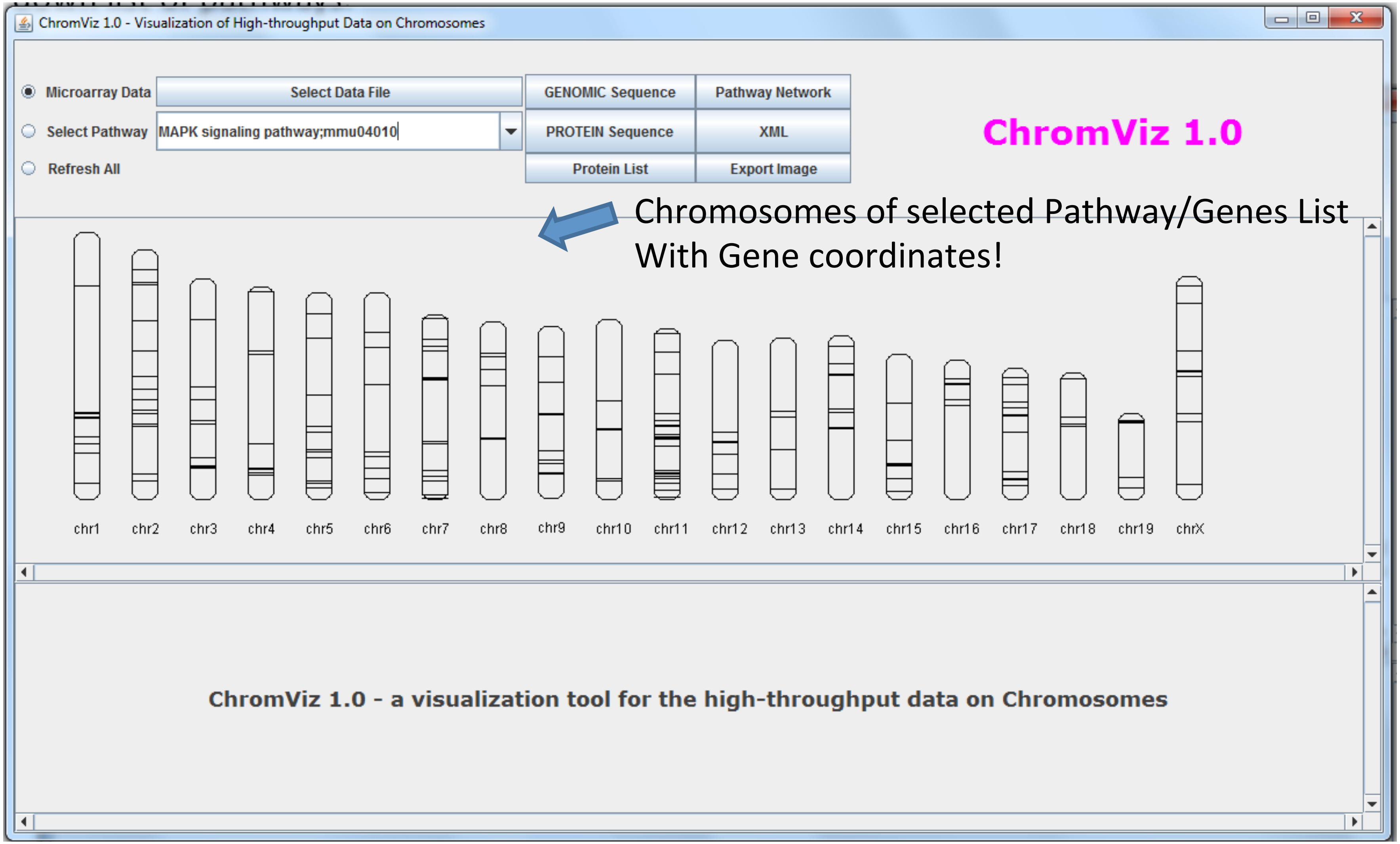
Step 4. Data display on chromosomes.


Select Data File
GENOMIC Sequence
Pathway Network
PROTEIN Sequence
XML
Protein List
Export Image
ChromViz 1.0
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chrX

ChromViz 1.0 - Visualization of High-throughput Data on Chromosomes

● Microarray Data
○ Select Pathway: MAPK signaling pathway;mmu04010
○ Refresh All

Chromosomes of selected Pathway/Genes List
With Gene coordinates!

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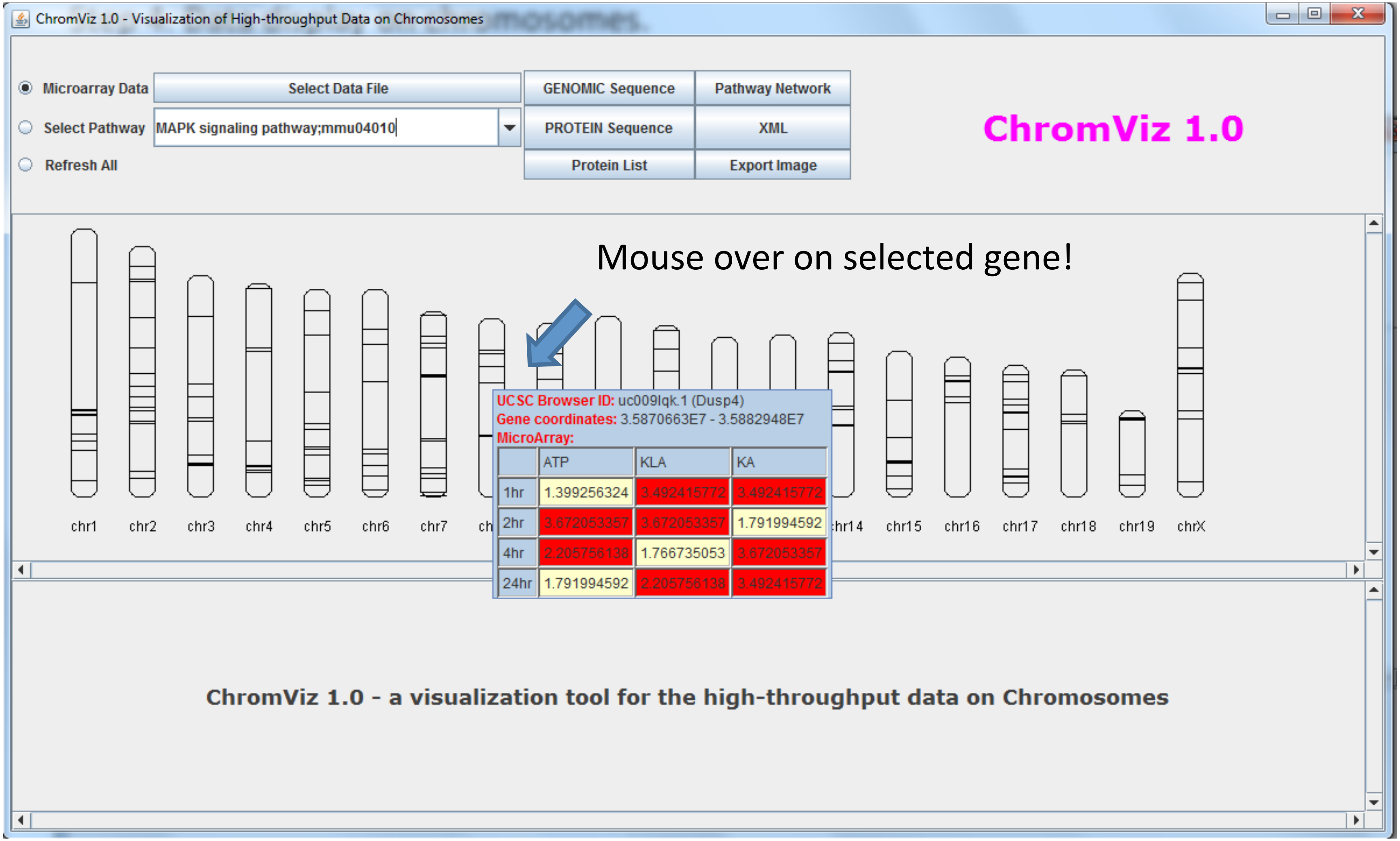
Step 5. **Heat Map** of selected gene on Chromosome. Mouse over on gene mark (red) on chromosome.


ChromViz 1.0 - Visualization of High-throughput Data on Chromosomes
Select Data File
GENOMIC Sequence
Pathway Network
PROTEIN Sequence
XML
Protein List
Export Image
ChromViz 1.0
chr1
chr2
chr3
chr4
chr5
chr6
chr7
ch
chr14
chr15
chr16
chr17
chr18
chr19
chrX

● Microarray Data

○ Select Pathway MAPK signaling pathway;mmu04010

○ Refresh All

Mouse over on selected gene!

UCSC Browser ID: uc009lqk.1 (Dusp4)

Gene coordinates: 3.5870663E7 - 3.5882948E7

MicroArray:

	ATP	KLA	KA
1hr	1.399256324	3.492415772	3.492415772
2hr	3.672053357	3.672053357	1.791994592
4hr	2.205756138	1.766735053	3.672053357
24hr	1.791994592	2.205756138	3.492415772

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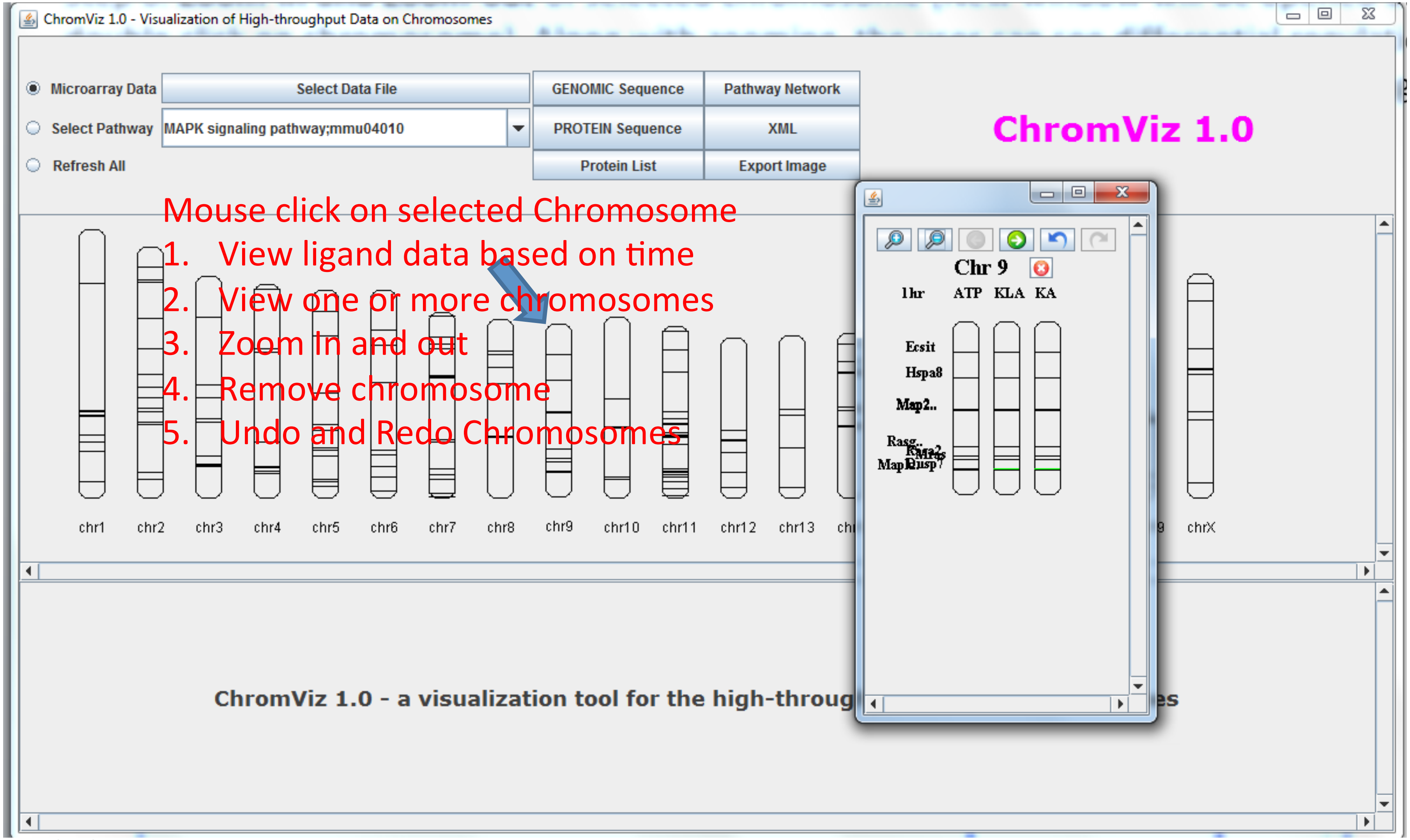
Step 6. **Zoom-in and Zoom-out** of selected chromosome (New window will be opened after double click on chromosome). Along with zooming, the user can see differential regulation of genes (more than one treatment also) on chromosomes at each time point by clicking right OR left buttons.



● Microarray Data

○ Select Pathway: MAPK signaling pathway;mmu04010

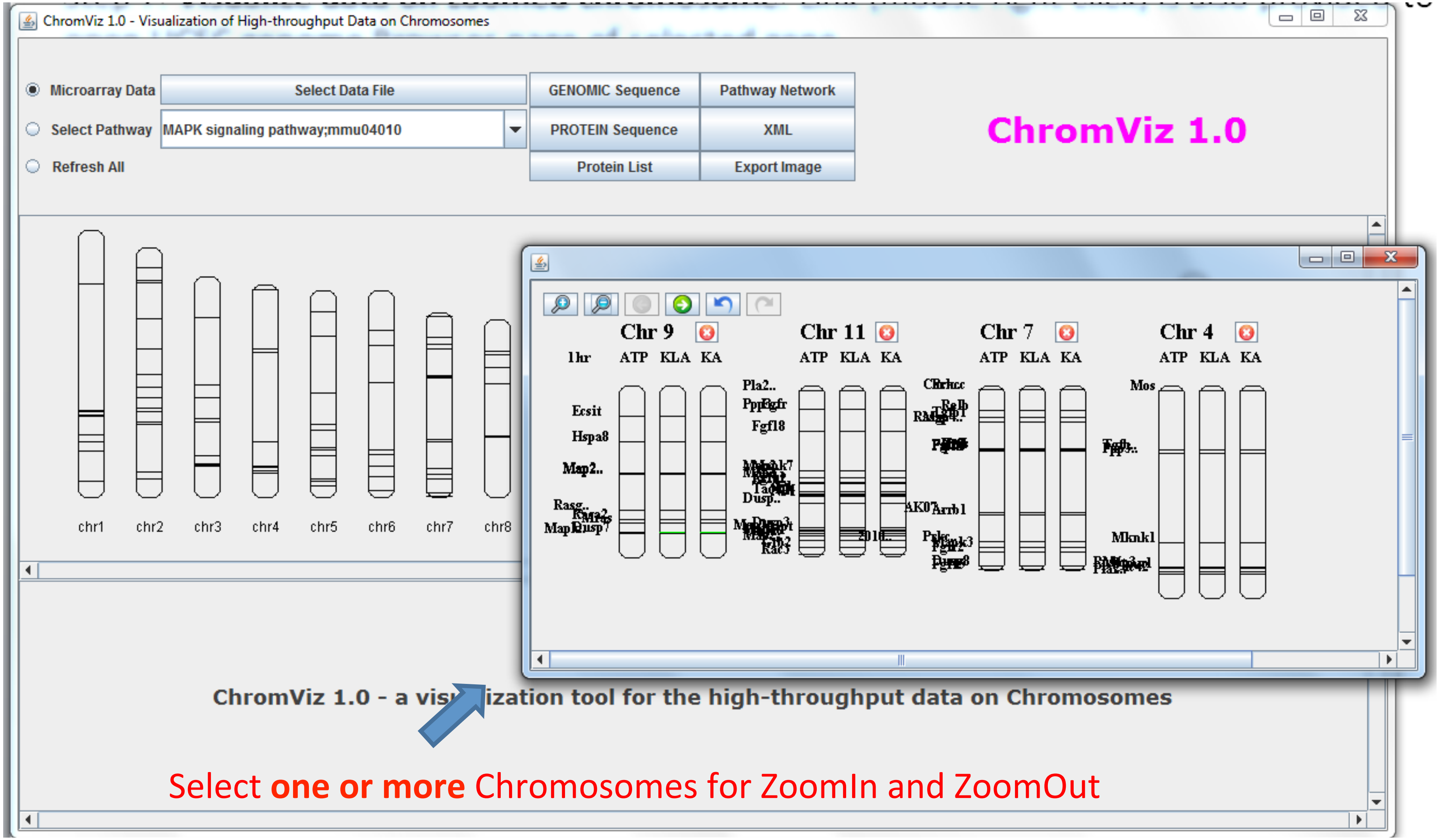
○ Refresh All

Mouse click on selected Chromosome

1. View ligand data based on time
2. View one or more chromosomes
3. Zoom In and out
4. Remove chromosome
5. Undo and Redo Chromosomes

ChromViz 1.0 - Visualization of High-throughput Data on Chromosomes
Select Data File
GENOMIC Sequence
Pathway Network
PROTEIN Sequence
XML
Protein List
Export Image
ChromViz 1.0
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chrX
Chr 9
1hr
ATP
KLA
KA
Ecsit
Hspa8
Map2..
ChromViz 1.0 - a visualization tool for the high-throug
es

Step 7. **Visualize data on zoomed chromosome**. Link (mouse right click) is also provided to open UCSC genome Browser page of selected gene.


ChromViz 1.0 - Visualization of High-throughput Data on Chromosomes
● Microarray Data
Select Data File
○ Select Pathway
MAPK signaling pathway;mmu04010
○ Refresh All
GENOMIC Sequence
Pathway Network
PROTEIN Sequence
XML
Protein List
Export Image
ChromViz 1.0
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
Chr 9
Chr 11
Chr 7
Chr 4
1hr
ATP
KLA
KA
Ecsit
Hspa8
Fgf18
Mos
Mknk1

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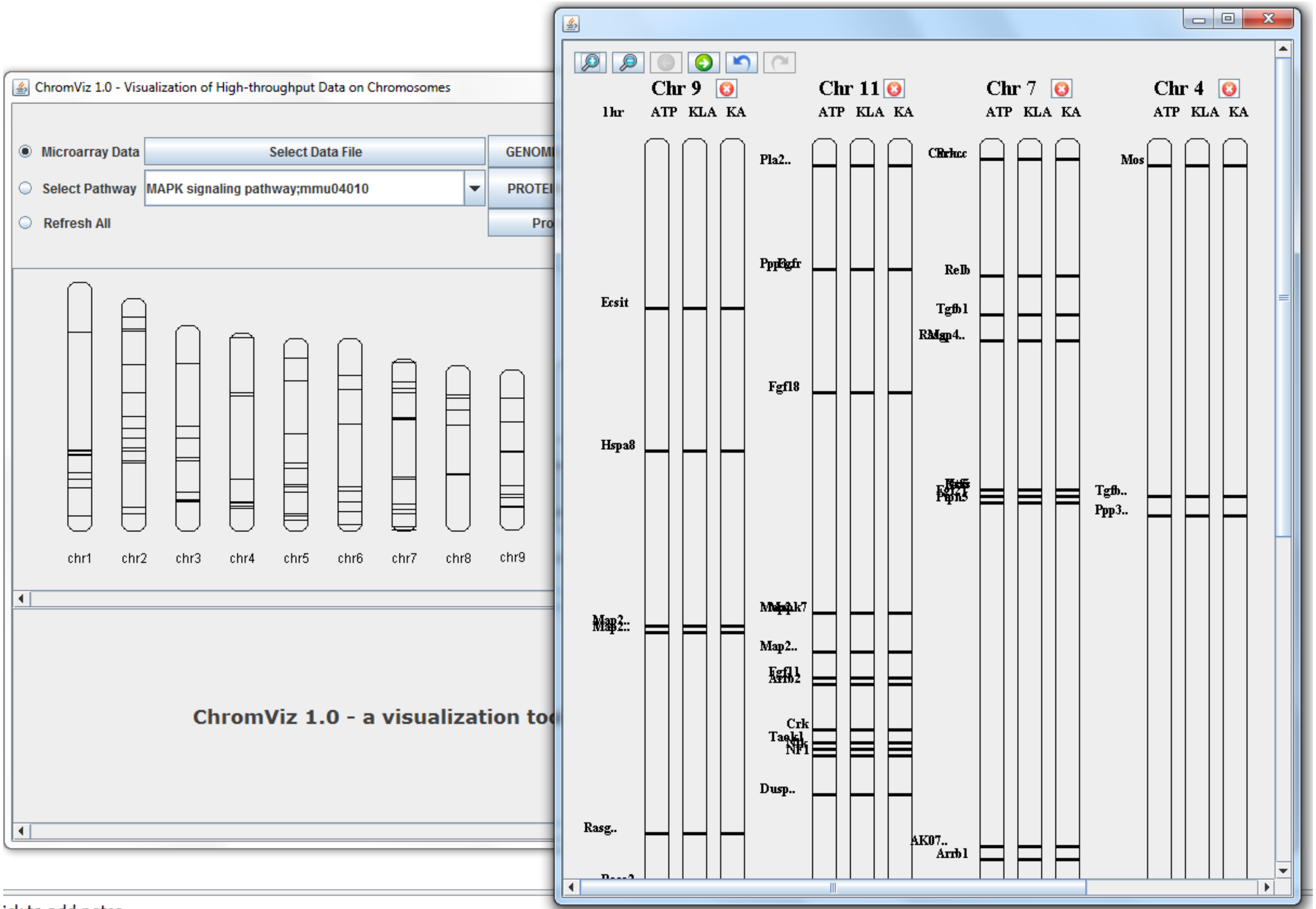
Select **one or more** Chromosomes for ZoomIn and ZoomOut

Step 7. **Visualize data on zoomed chromosome**. Link (mouse right click) is also provided to open UCSC genome Browser page of selected gene.



ChromViz 1.0 - Visualization of High-throughput Data on Chromosomes

● Microarray Data

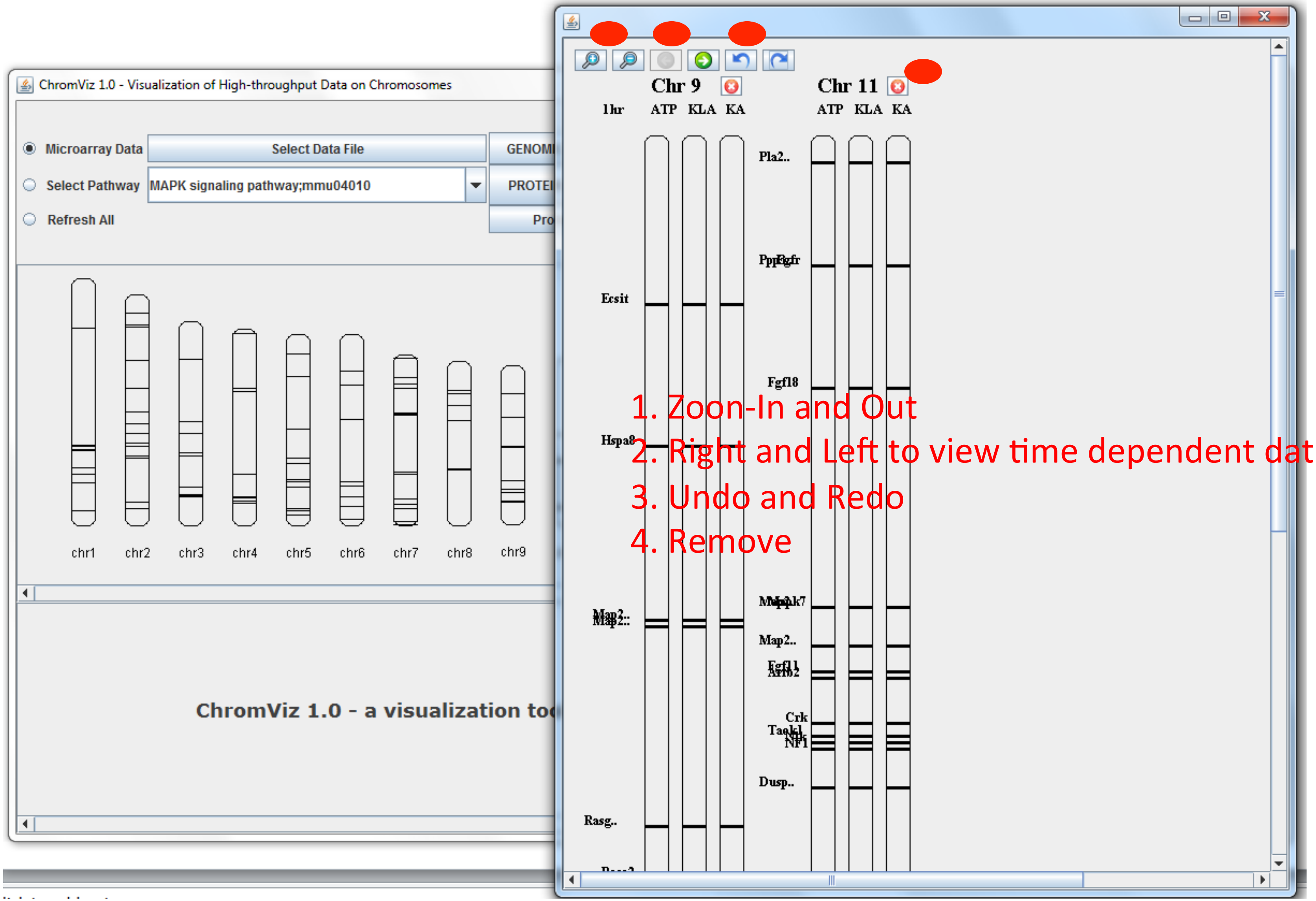
○ Select Pathway: MAPK signaling pathway;mmu04010

○ Refresh All

ChromViz 1.0 - a visualization to

Select Data File
GENOM
PROTE
Pro
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
Chr 9
Chr 11
Chr 7
Chr 4
1hr
ATP
KLA
KA
Ecsit
Hspa8
Map2..
Rasg..
Pla2..
Fgf18
Map2..
Crk
Nf1
Dusp..
Relb
Tgfb1
AK07..
Arrb1
Mos
Tgfb..
Ppp3..

Step 7. **Visualize data on zoomed chromosome**. Link (mouse right click) is also provided to open UCSC genome Browser page of selected gene.



ChromViz 1.0 - Visualization of High-throughput Data on Chromosomes

● Microarray Data

○ Select Pathway: MAPK signaling pathway;mmu04010

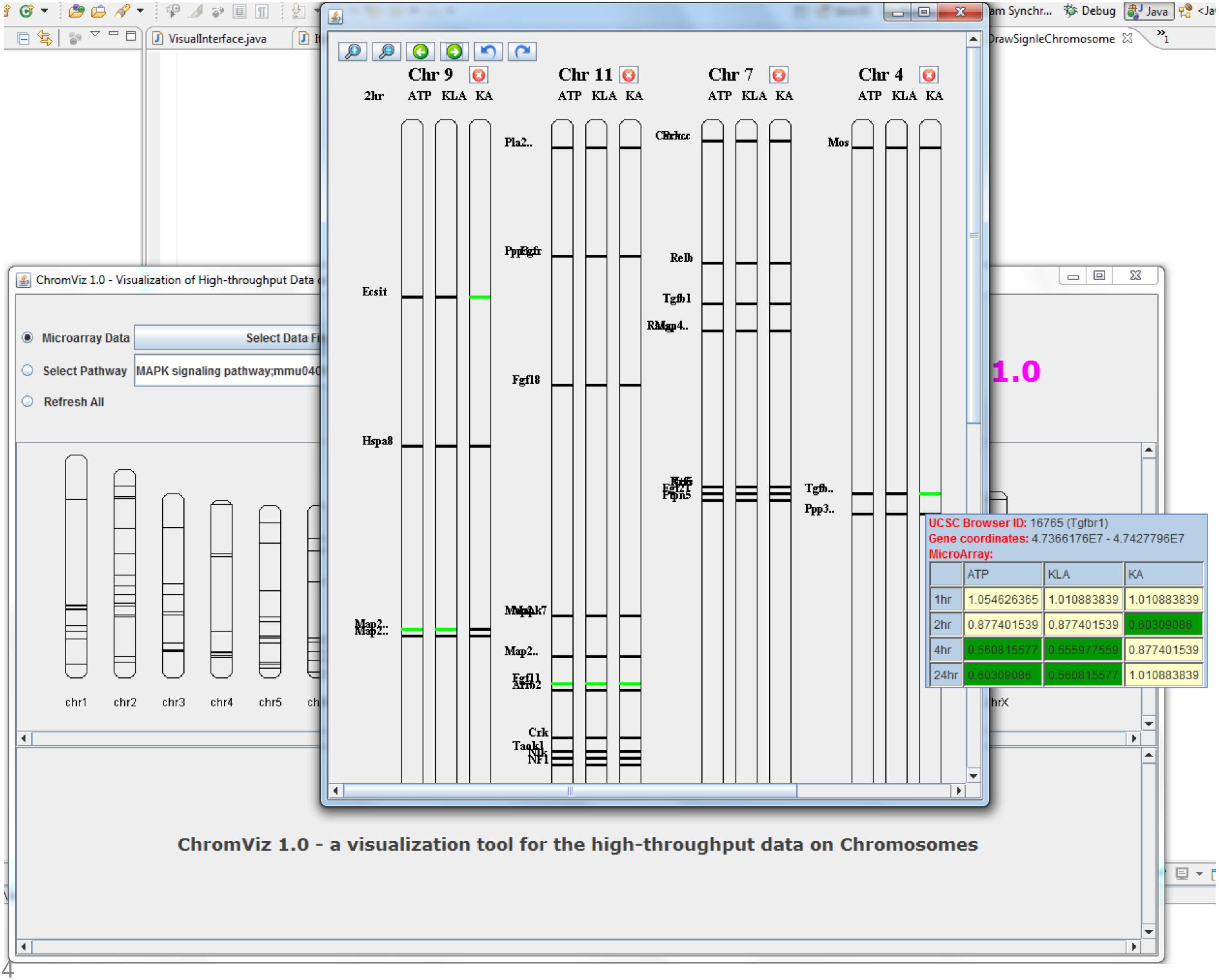
○ Refresh All

ChromViz 1.0 - a visualization to

Select Data File
GENOM
PROTE
Pro
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
Chr 9
Chr 11
1hr
ATP
KLA
KA
ATP
KLA
KA
Pla2..
Ecsit
Fgf18
Hspa8
Map2..
Map2..
Rasg..
Map2..
Crk
Tab1
Nf1
Dusp..

1. Zoon-In and Out
2. Right and Left to view time dependent data
3. Undo and Redo
4. Remove

Step 7. **Visualize data on zoomed chromosome**. Link (mouse right click) is also provided to open UCSC genome Browser page of selected gene.


Chr 9
2hr
ATP
KLA
KA
Chr 11
ATP
KLA
KA
Chr 7
ATP
KLA
KA
Chr 4
ATP
KLA
KA
Ecsit
Hspa8
Map2..
Map2..
Pla2..
PppFgfr
Fgf18
Mapk7
Map2..
Fgf11
Arrb2
Crk
Taok1
Nlk
NF1
Chuk
Relb
Tgfb1
RMap4..
Fgf21
Ppm5
Mos
Tgfb..
Ppp3..
VisualInterface.java
DrawSignleChromosome
Debug
Java
1.0
chr1
chr2
chr3
chr4
chr5
hrX

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● Microarray Data — Select Data Fi

○ Select Pathway — MAPK signaling pathway;mmu040

○ Refresh All

UCSC Browser ID: 16765 (Tgfbr1)
Gene coordinates: 4.7366176E7 - 4.7427796E7
MicroArray:

	ATP	KLA	KA
1hr	1.054626365	1.010883839	1.010883839
2hr	0.877401539	0.877401539	0.60309086
4hr	0.560815577	0.555977559	0.877401539
24hr	0.60309086	0.560815577	1.010883839

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