

Tutorial for ‘Synteny Viewer’

This module provides functions to search and visualize syntenic blocks between any two cucurbit genomes or within a single cucurbit genome. The query interface allows search for synteny between a specific chromosome of the queried genome and the entire compared genome (**Figure 1A**) or search for a specific synteny block (**Figure 1B**). After selecting a specific query genome, the corresponding list of chromosomes are automatically populated. This query returns a circos plot that displays all synteny blocks between the queried chromosome and the compared genome (**Figure 2**) and the list of synteny blocks (**Figure 3**). Clicking each synteny block in the circos plot or the block ID in the list will display the syntenic gene pairs in the block (**Figure 4**). Search for a specific synteny block (**Figure 1B**) will also display the syntenic gene pairs in the block (**Figure 4**). The syntenic gene pair viewer can be zoomed in or out (scrolling the mouse) and moved up or down (holding the mouse and moving up or down).

Search Synteny Blocks

A Search blocks by a given location

Genome:
Watermelon (97103) v2.5

Chromosome/Scaffold:
Cla97Chr01

Choose a genome for comparison:
Watermelon (cordophanus) v2

B OR Search a block by ID

Enter a synteny block ID. Example: cmdcvuB220

Search Reset

Figure 1

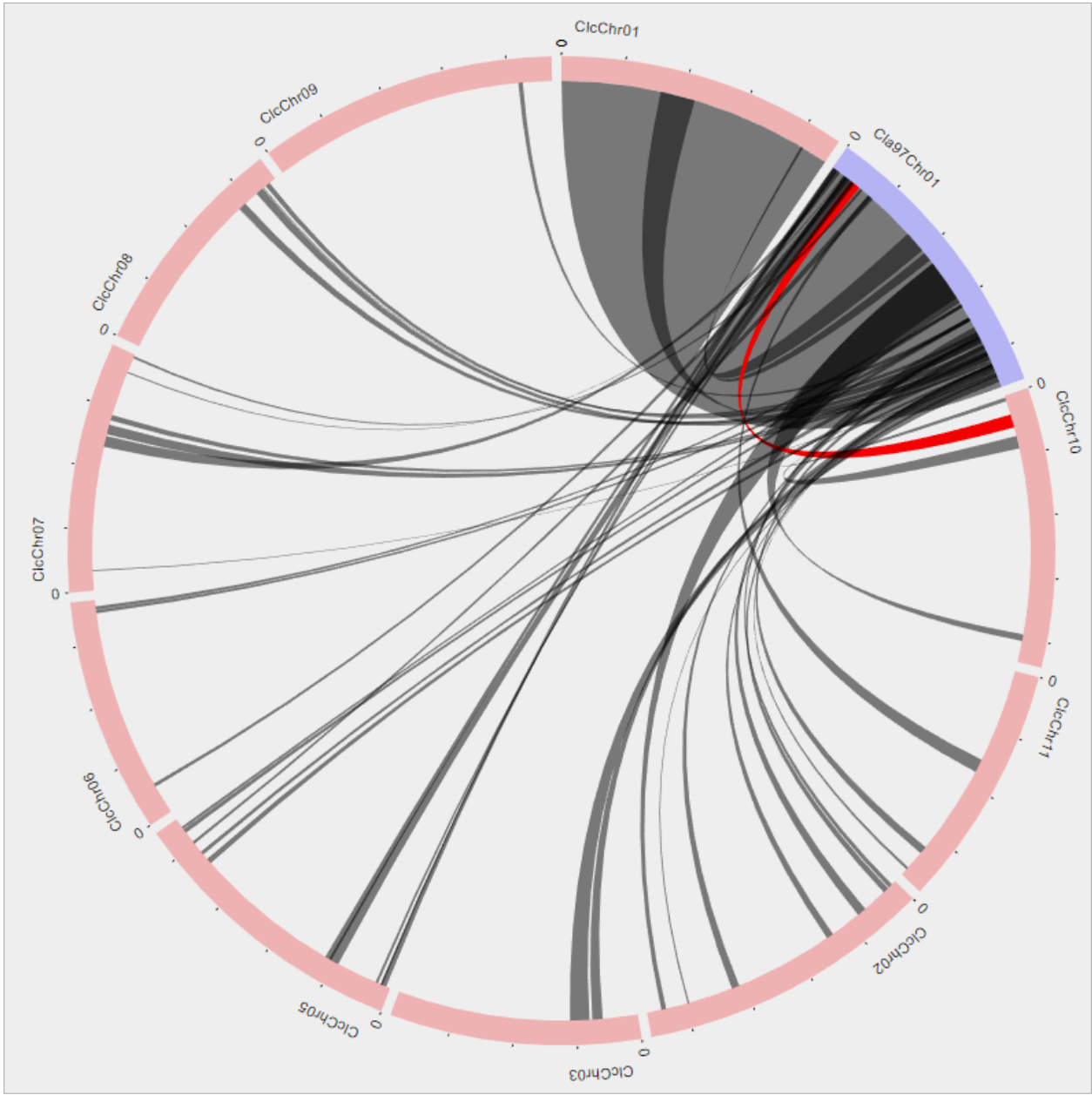


Figure 2

Block	Watermelon (97103) v2.5 (location)	Watermelon (cordophanus) v2 (location)	Score	E value
ccocvuB000	ClcChr01:20751..36803916 (+)	Cla97Chr01:1634..36930550 (+)	105233	0
ccocvuB001	ClcChr01:13174408..17781967 (+)	Cla97Chr01:33216732..33537873 (-)	495	3.9e-29
ccocvuB002	ClcChr01:33160260..33384460 (+)	Cla97Chr01:13202581..16106379 (-)	286	1.8e-11
ccocvuB003	ClcChr01:33063190..33180034 (+)	Cla97Chr01:16546541..17759742 (-)	273	9.4e-11
ccocvuB042	ClcChr10:31770671..32658560 (+)	Cla97Chr01:18261101..23825152 (+)	359	4.4e-17
ccocvuB043	ClcChr10:5487275..7160741 (+)	Cla97Chr01:33610941..34017546 (+)	269	2.1e-11
ccocvuB044	ClcChr10:2567129..4321880 (+)	Cla97Chr01:2983664..4395178 (-)	763	5e-48

Figure 3

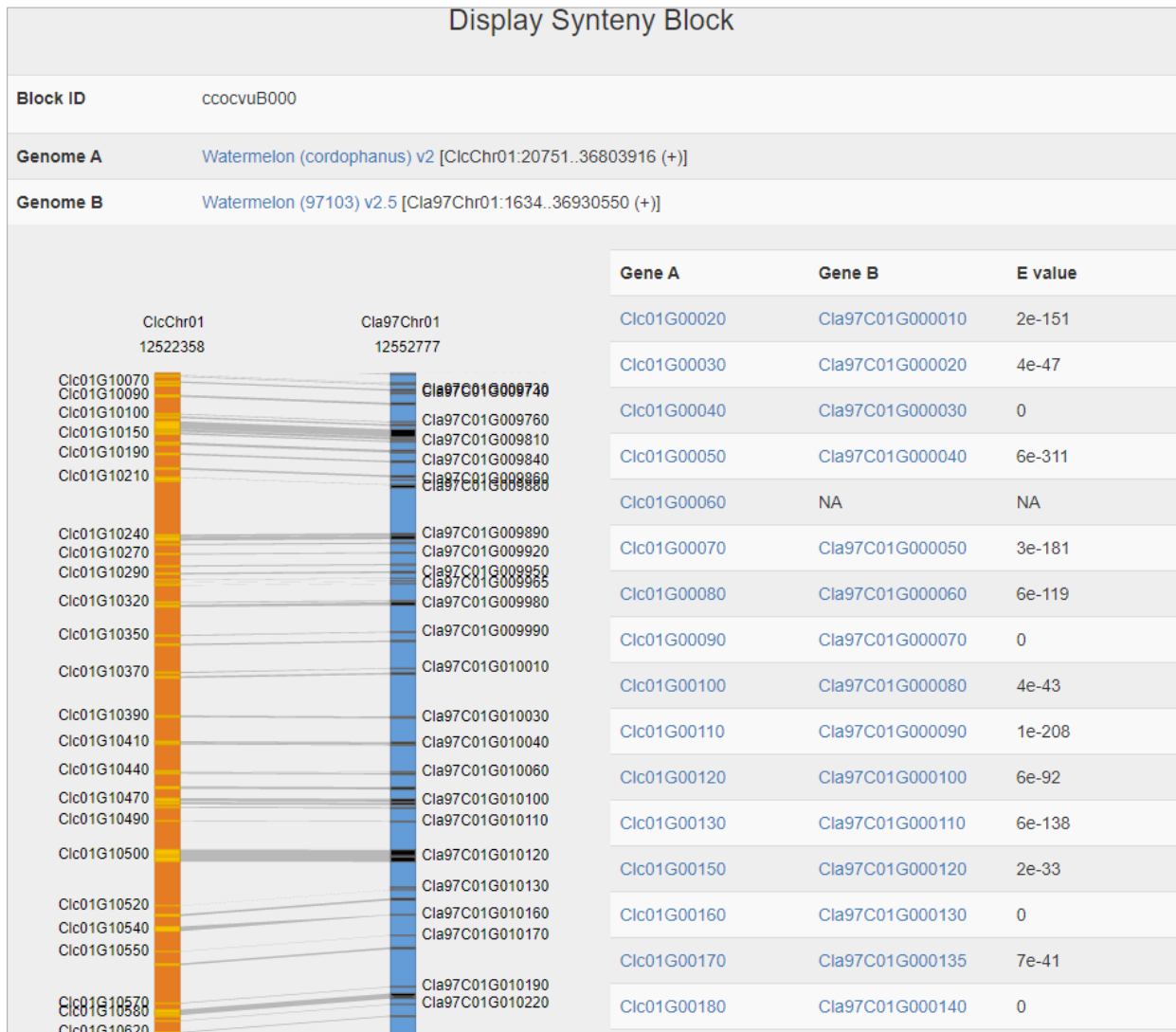


Figure 4