left\_species\_gff\_file\_path = Brapa\_197\_gene.gff3.sort

right\_species\_gff\_file\_path = Thalophila\_173\_gene.gff3.sort

highlight\_gene\_list = Bra002260,Bra002261

highlight\_link\_list = None

backborn\_color = rgb(135,206,250)

gene\_length = 10

## intergenic\_scale : zoom out intergenic sequence scale into 1/x

intergenic\_scale = 1000

arrow\_size = 5

a\_gene\_color = blue

highlight\_a\_gene\_color = red

b\_gene\_color = blue

highlight\_b\_gene\_color = red

link\_color = pink

link\_opacity = 0.5

highlight\_link\_color = red

highlight\_link\_opacity = 0.8