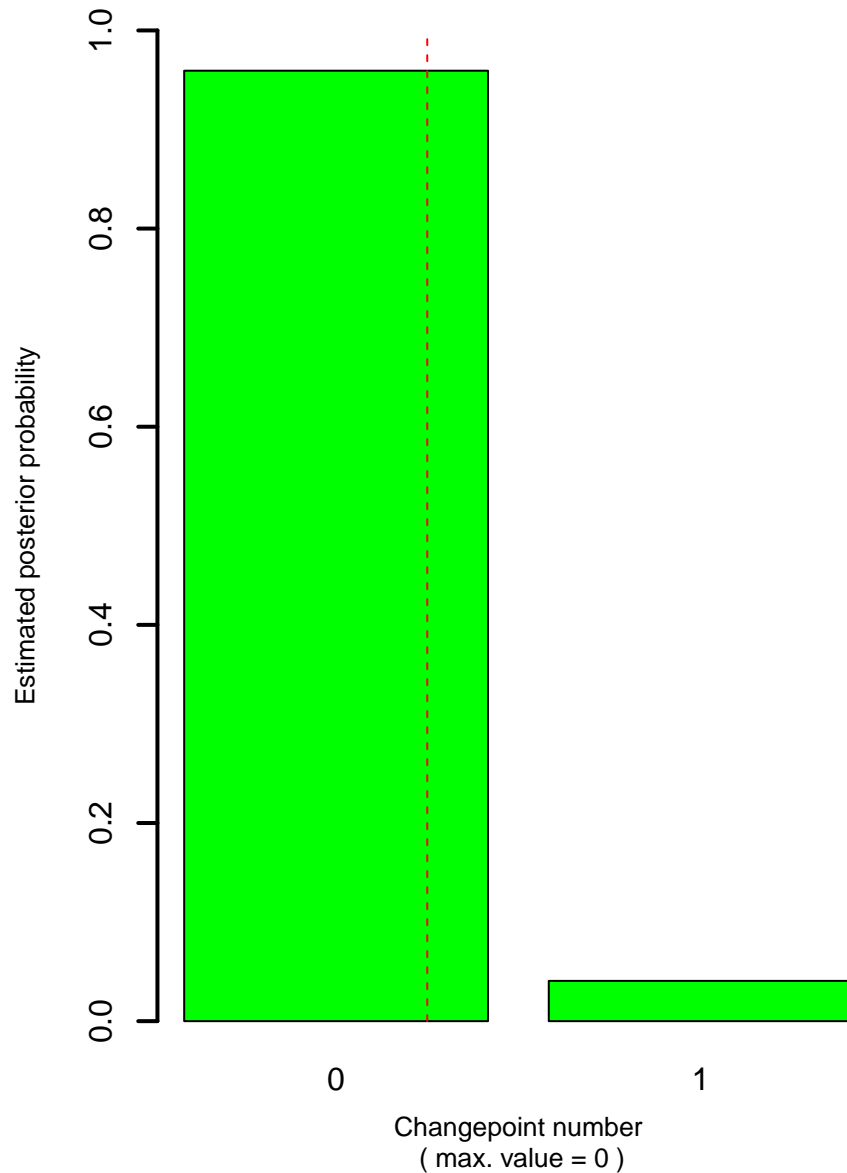


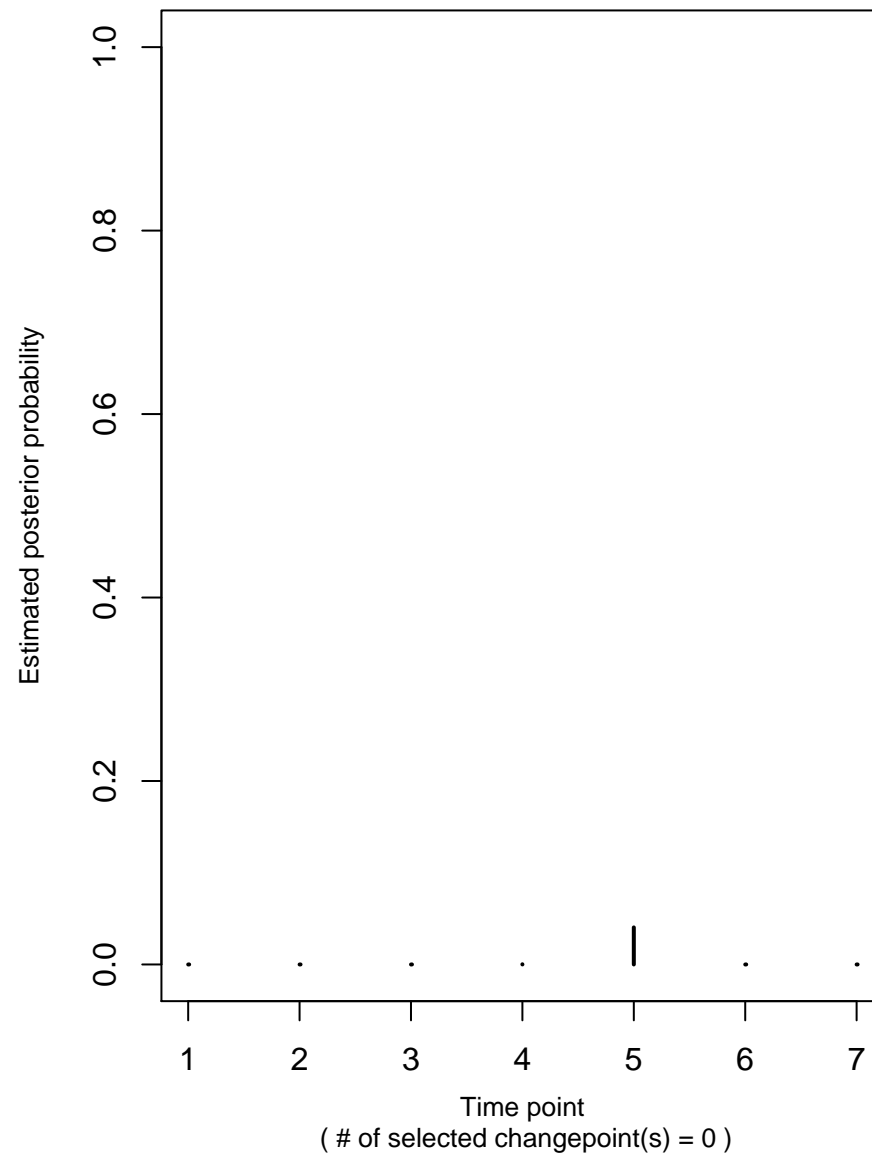
The graph displays the proportion of the population in the 'Infected' compartment over 30 time points. The y-axis represents the proportion, ranging from 1.0 to 1.8. The x-axis represents the time point, ranging from 0 to 30. The proportion starts at 1.0, remains constant until time point 1, then rises sharply to a peak of approximately 1.95 at time point 5. It remains at this peak until time point 10, then falls sharply back to 1.0 at time point 11. It remains at 1.0 until time point 16, then rises sharply to a peak of approximately 1.95 at time point 17. It remains at this peak until time point 19, then falls sharply back to 1.0 at time point 20. It remains at 1.0 until time point 26, then rises sharply to a peak of approximately 1.95 at time point 27, and remains at this peak until time point 30.

Time point	Proportion of population in 'Infected' compartment
0	1.0
1	1.0
2	1.0
3	1.0
4	1.0
5	1.95
6	1.95
7	1.95
8	1.95
9	1.95
10	1.95
11	1.0
12	1.0
13	1.0
14	1.0
15	1.0
16	1.0
17	1.95
18	1.95
19	1.95
20	1.0
21	1.0
22	1.0
23	1.0
24	1.0
25	1.0
26	1.0
27	1.95
28	1.95
29	1.95
30	1.95

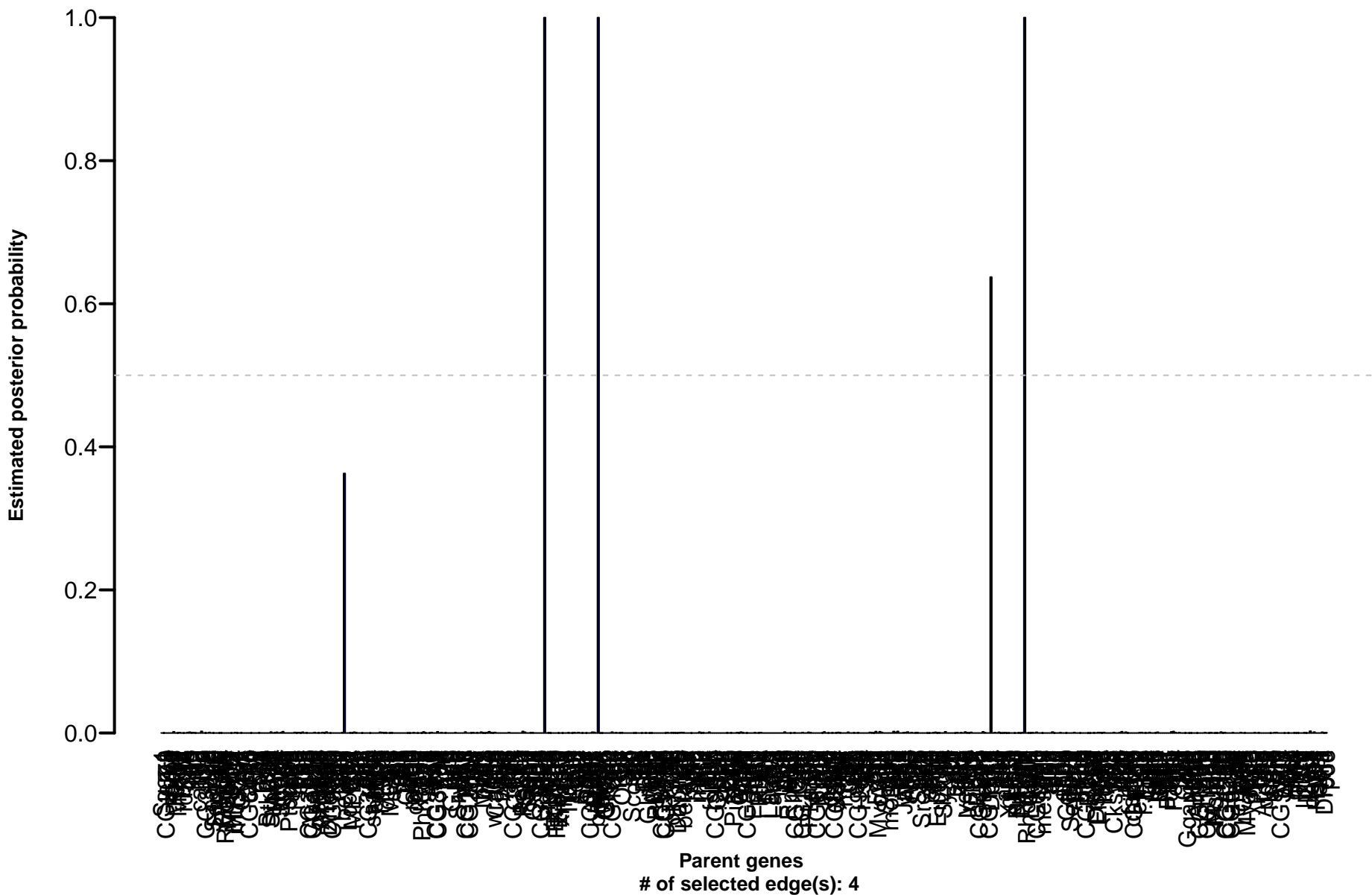
Number of changepoint  
– target gene: rhea –



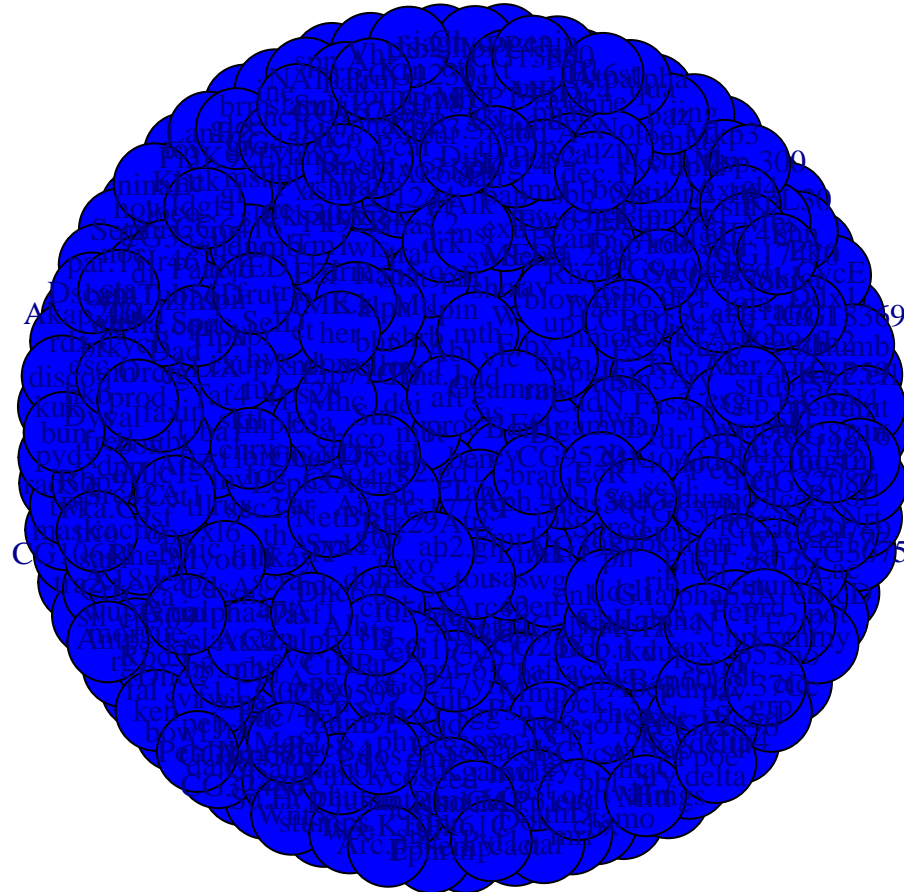
Changepoint position  
– target gene: rhea –



Regulatory model for target gene: rhea  
Temporal segment # 1 : [ 2 , 6 ]



Sub-network # 1  
( time point 2 to 6 )



— Positive interaction  
- - - Negative interaction

**ARTIVA summary page**  
**(interactions are arranged in order of decreasing confidence level)**

<b>parentGene</b>	<b>targetGene</b>	<b>postProb</b>	<b>CPstart</b>	<b>CPend</b>	<b>interactionSign</b>
131	1	1	2	6	+
366	1	1	2	6	-
125	1	1	2	6	+
161	1	0.6373	2	6	+