

Score: CV_t (Local, full , Genotype: linear)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

40

50

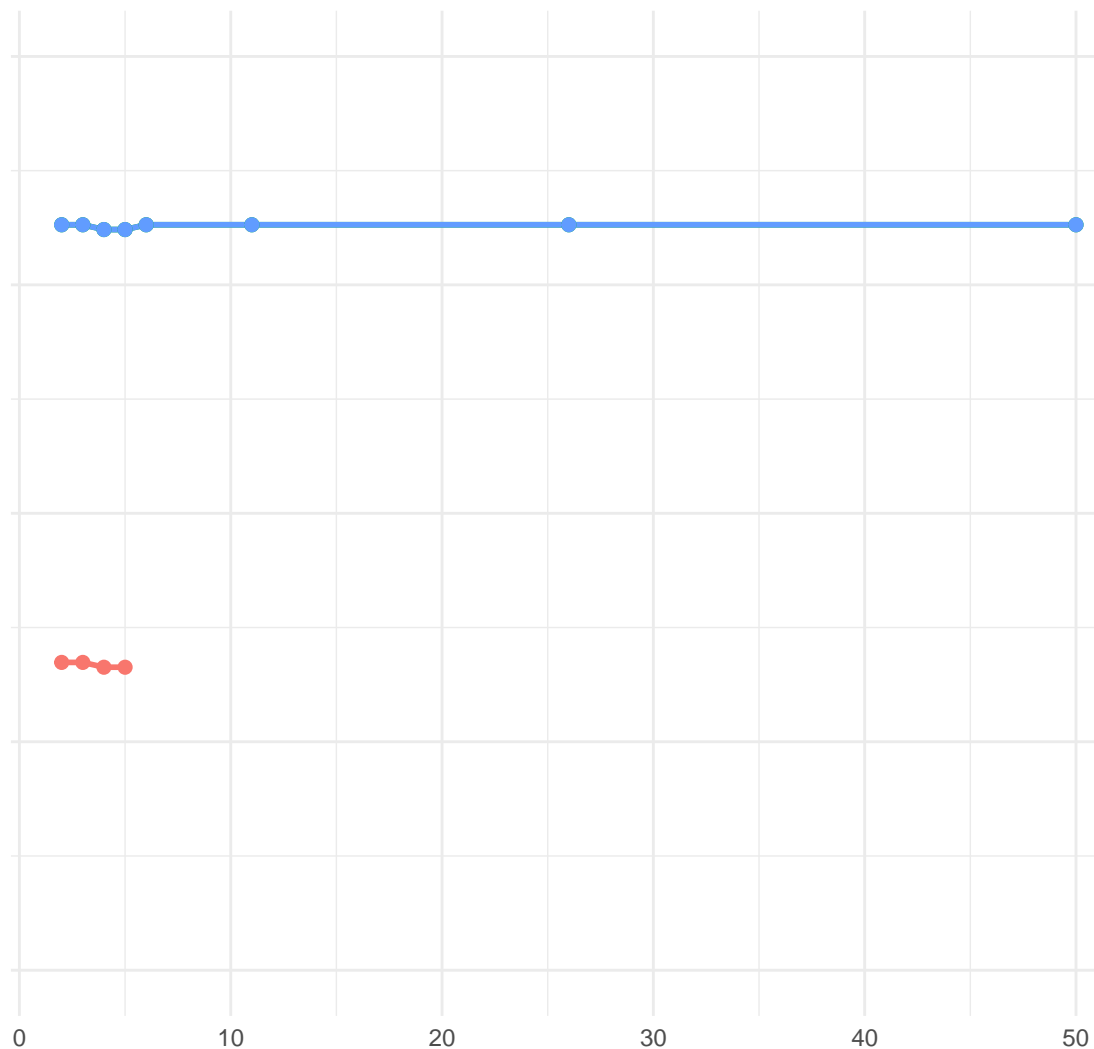
Number of Selected Samples

Summary Statistic

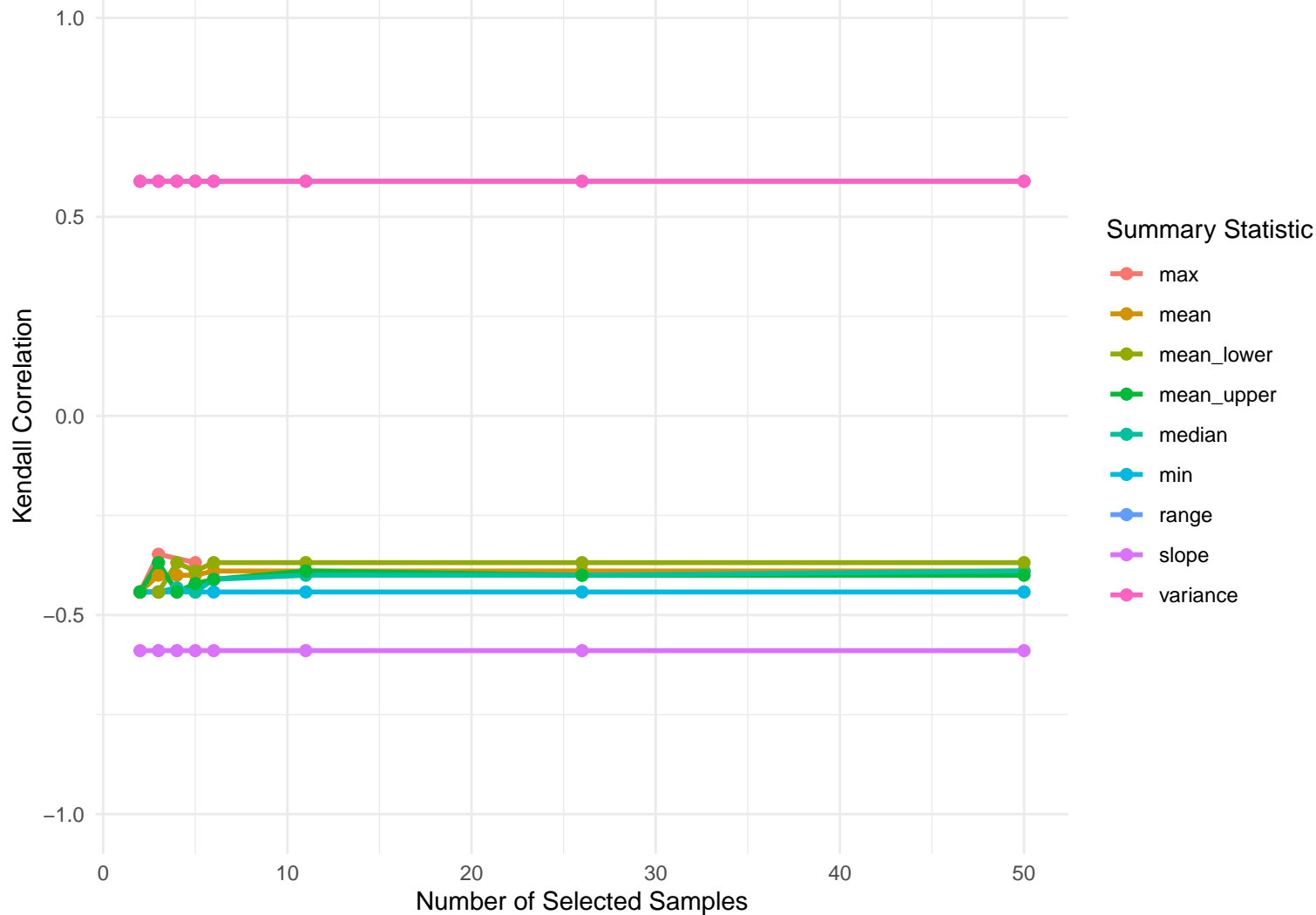
min

range

variance



Score: CV_t (Local, full , Genotype: gaussian)



Score: CV_t (Local, full , Genotype: sinusoidal)

Kendall Correlation

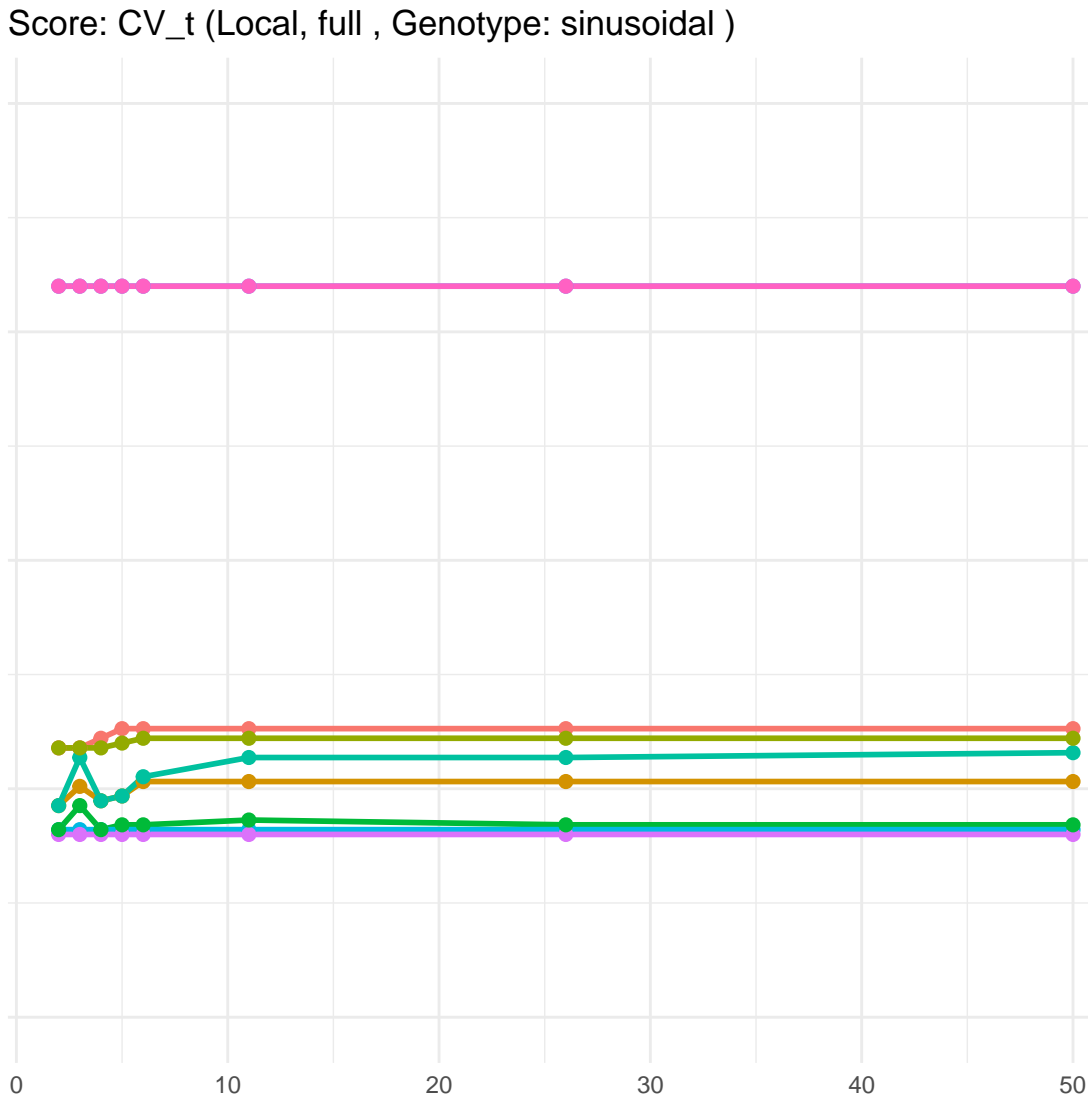
Summary Statistic

- max
- mean
- mean_lower
- mean_upper
- median
- min
- range
- slope
- variance

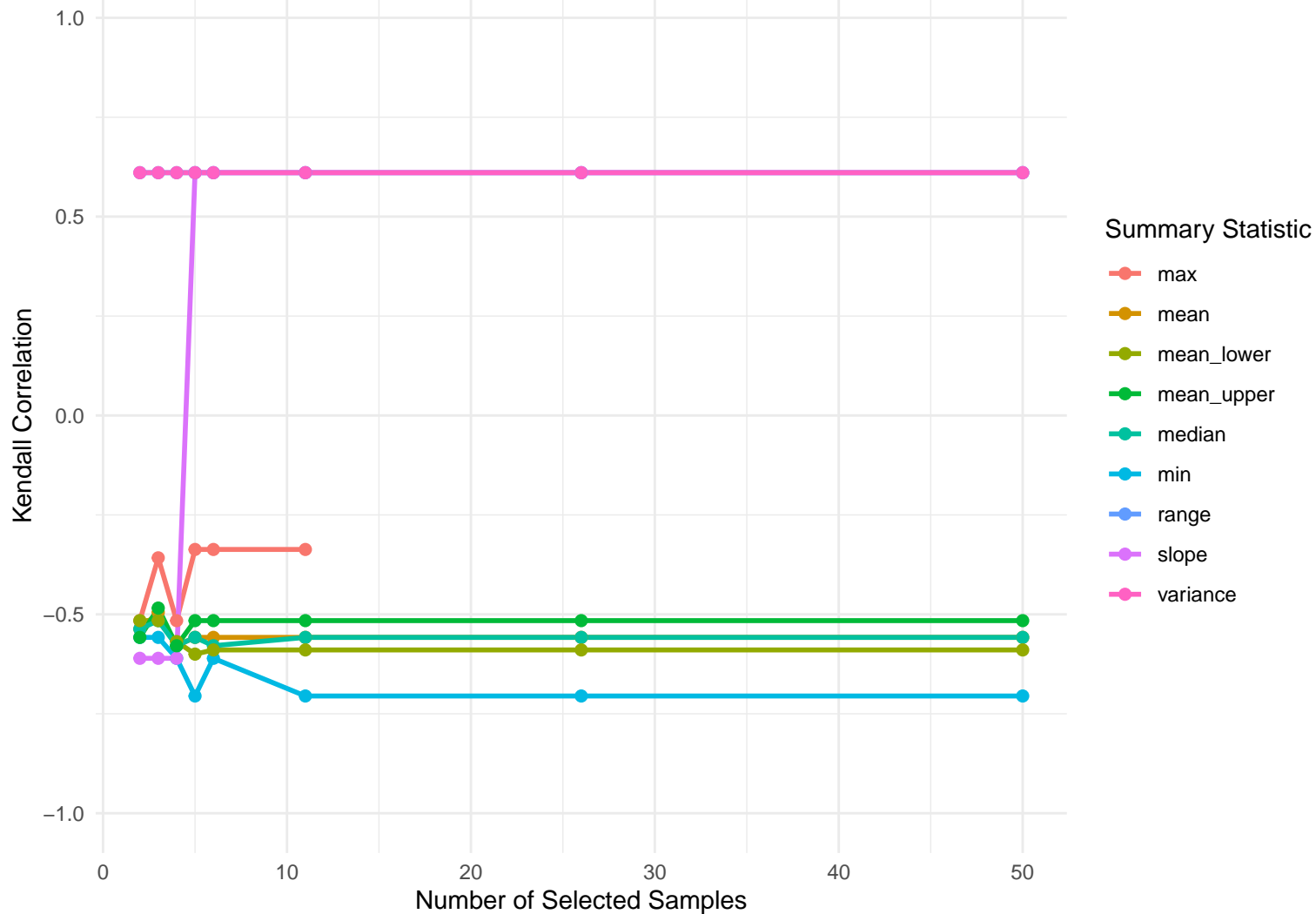
1.0
0.5
0.0
-0.5
-1.0

0 10 20 30 40 50

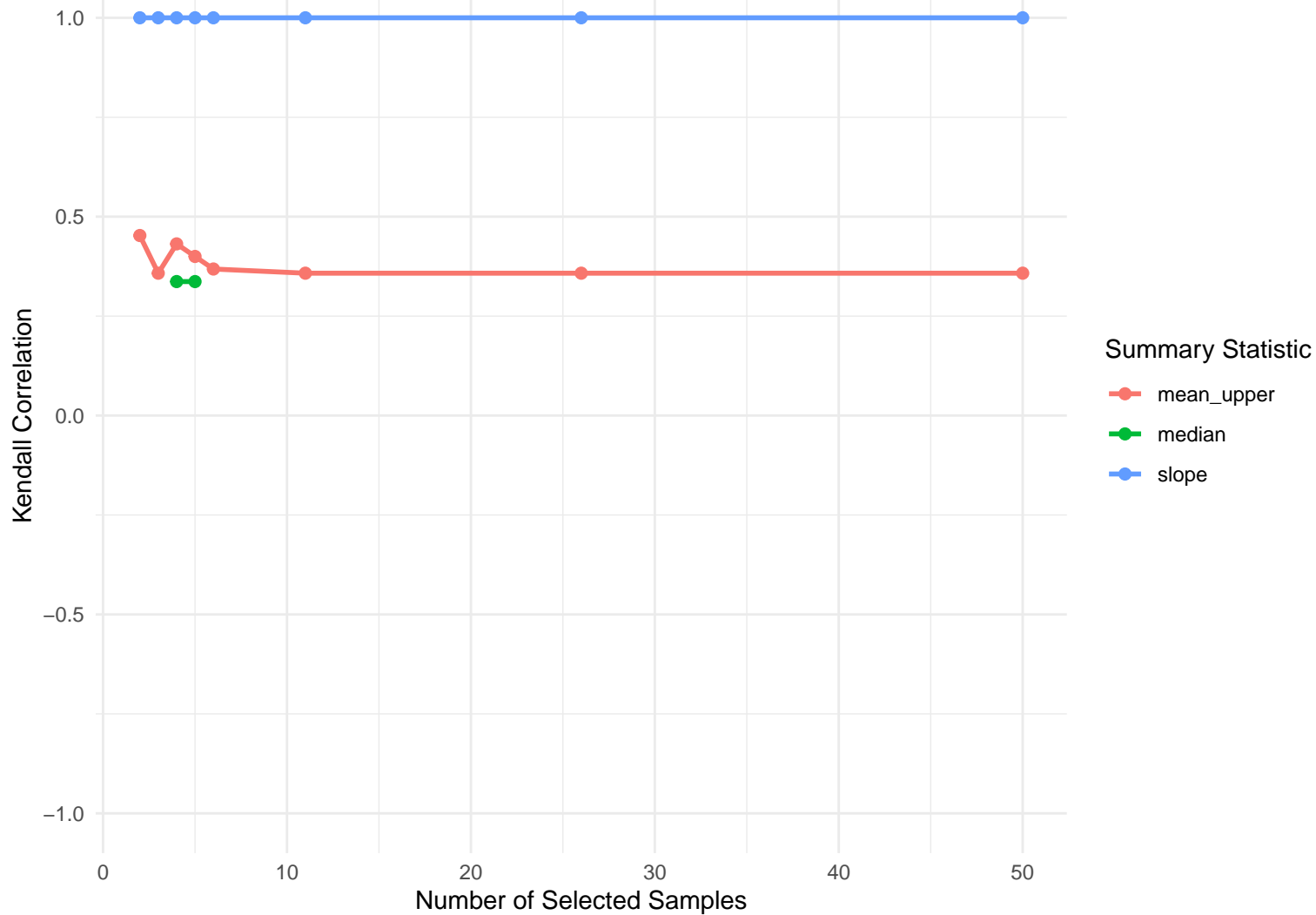
Number of Selected Samples



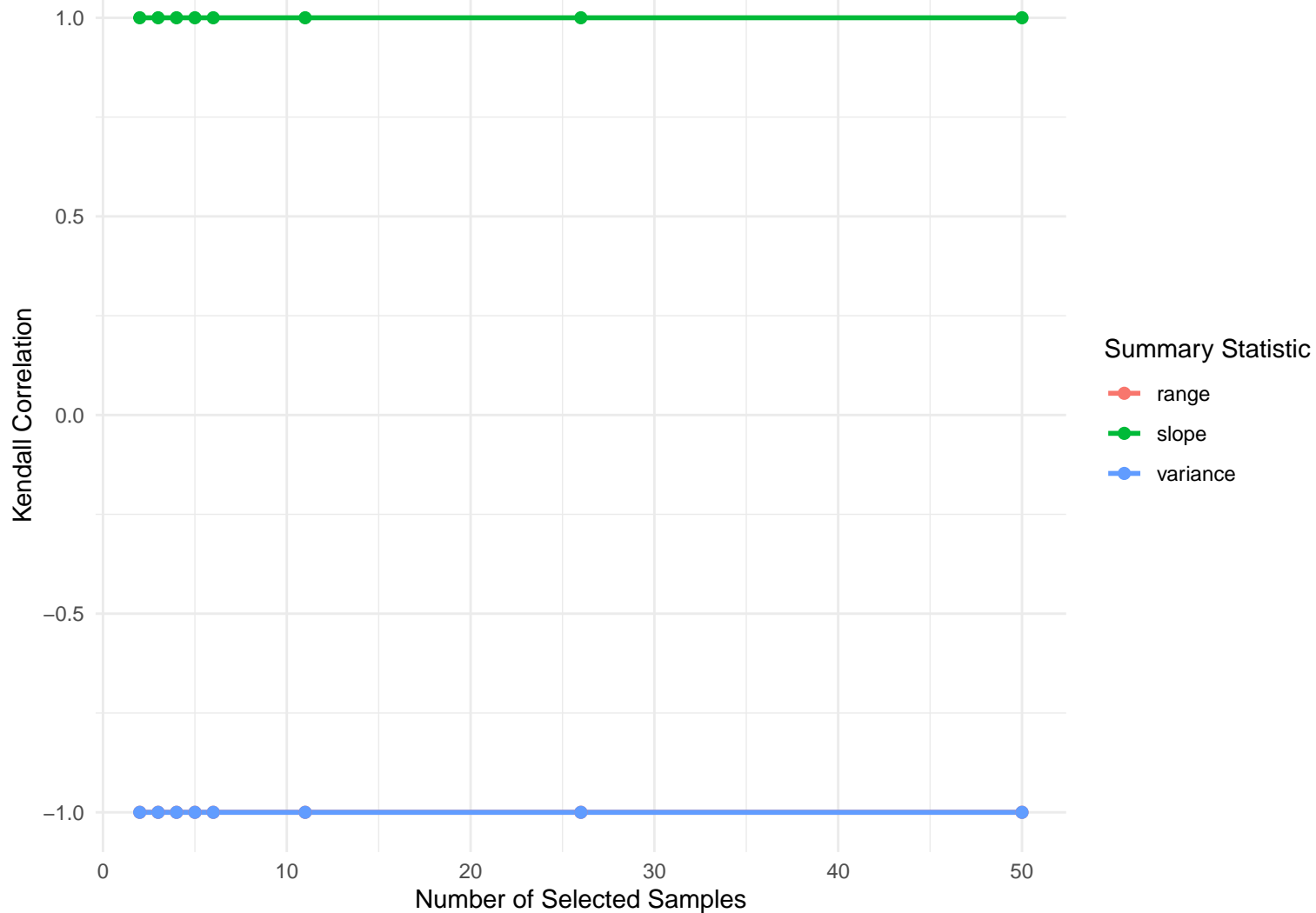
Score: CV_t (Local, full , Genotype: wave)



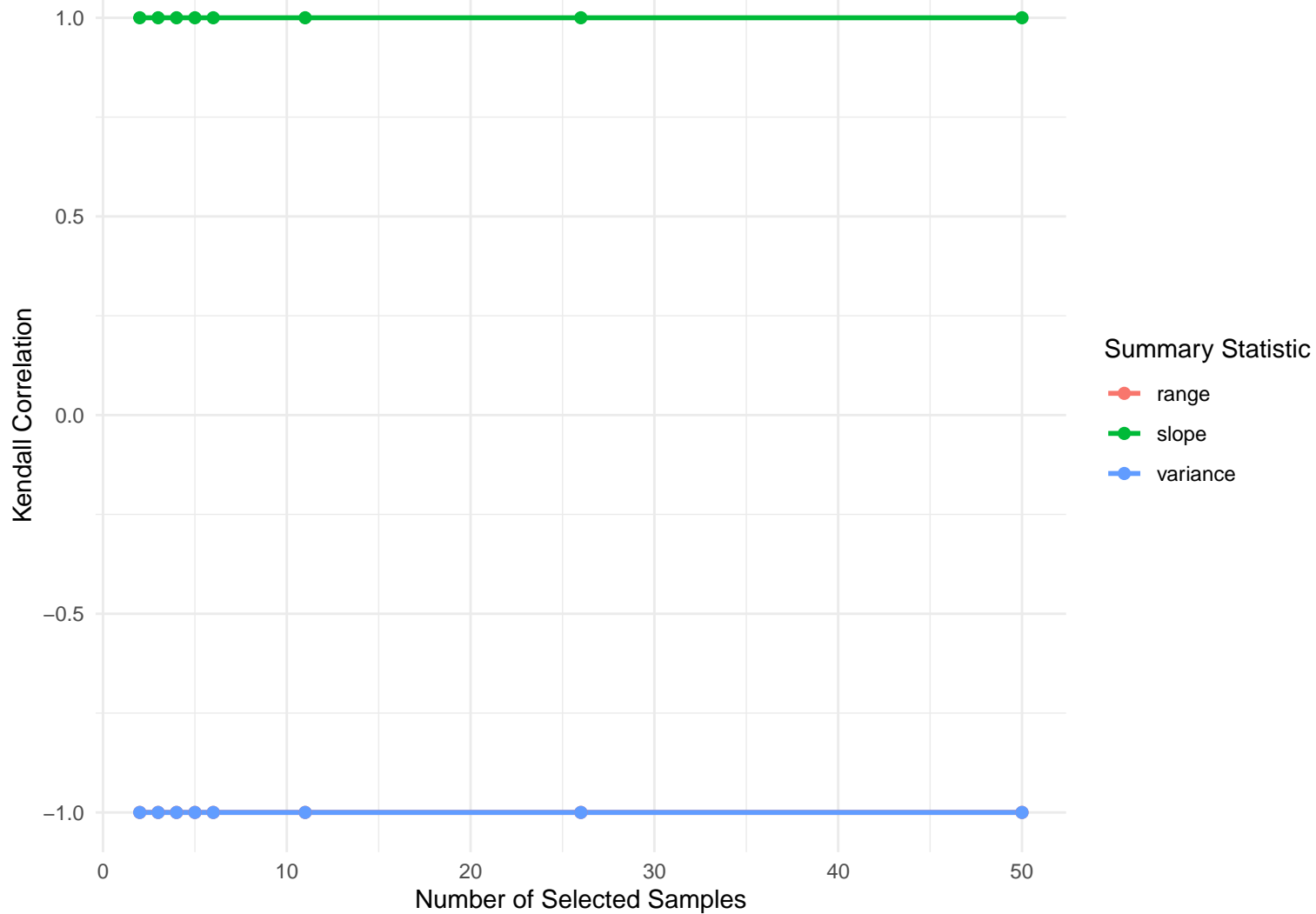
Score: RN (Local, full , Genotype: linear)



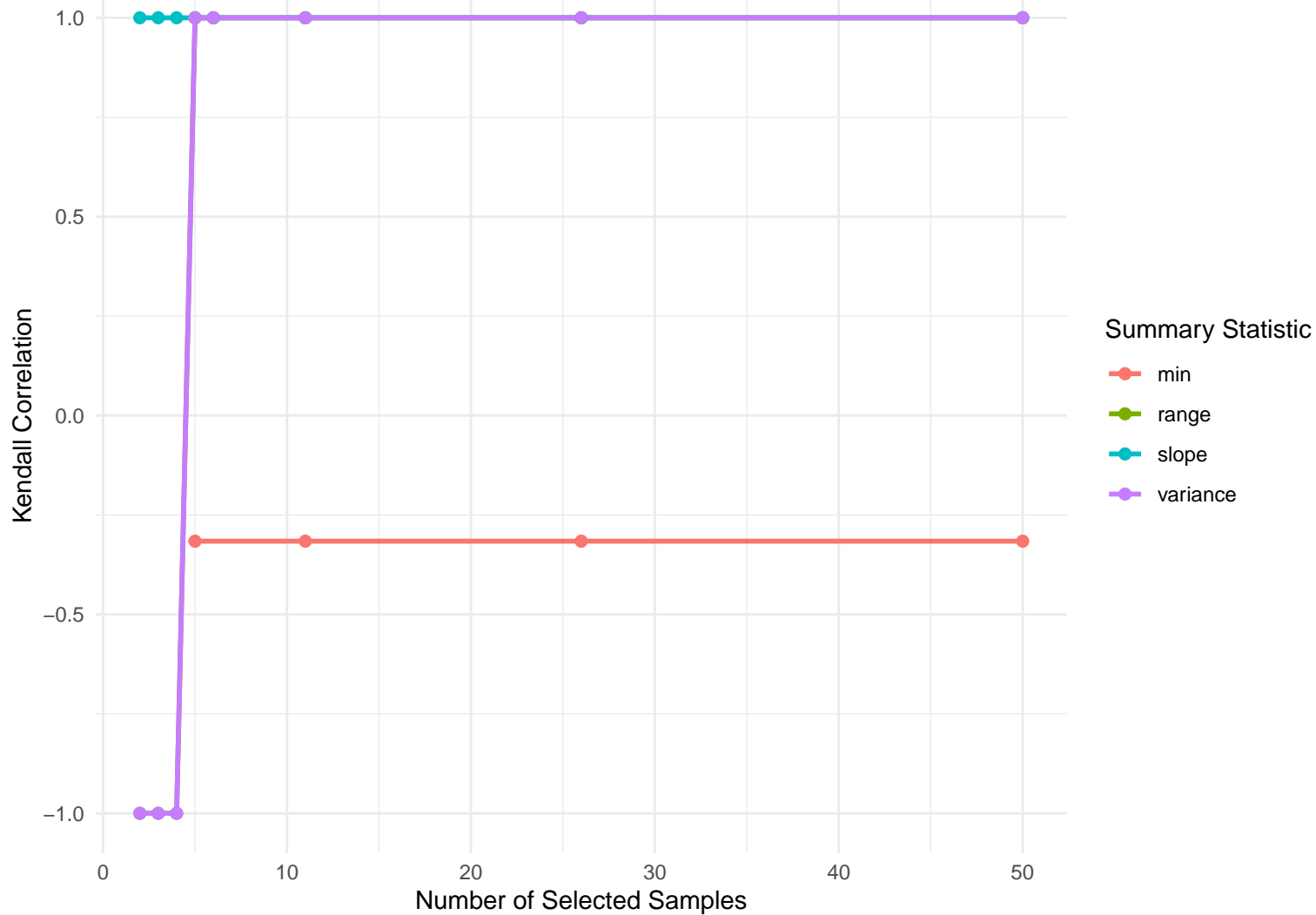
Score: RN (Local, full , Genotype: gaussian)



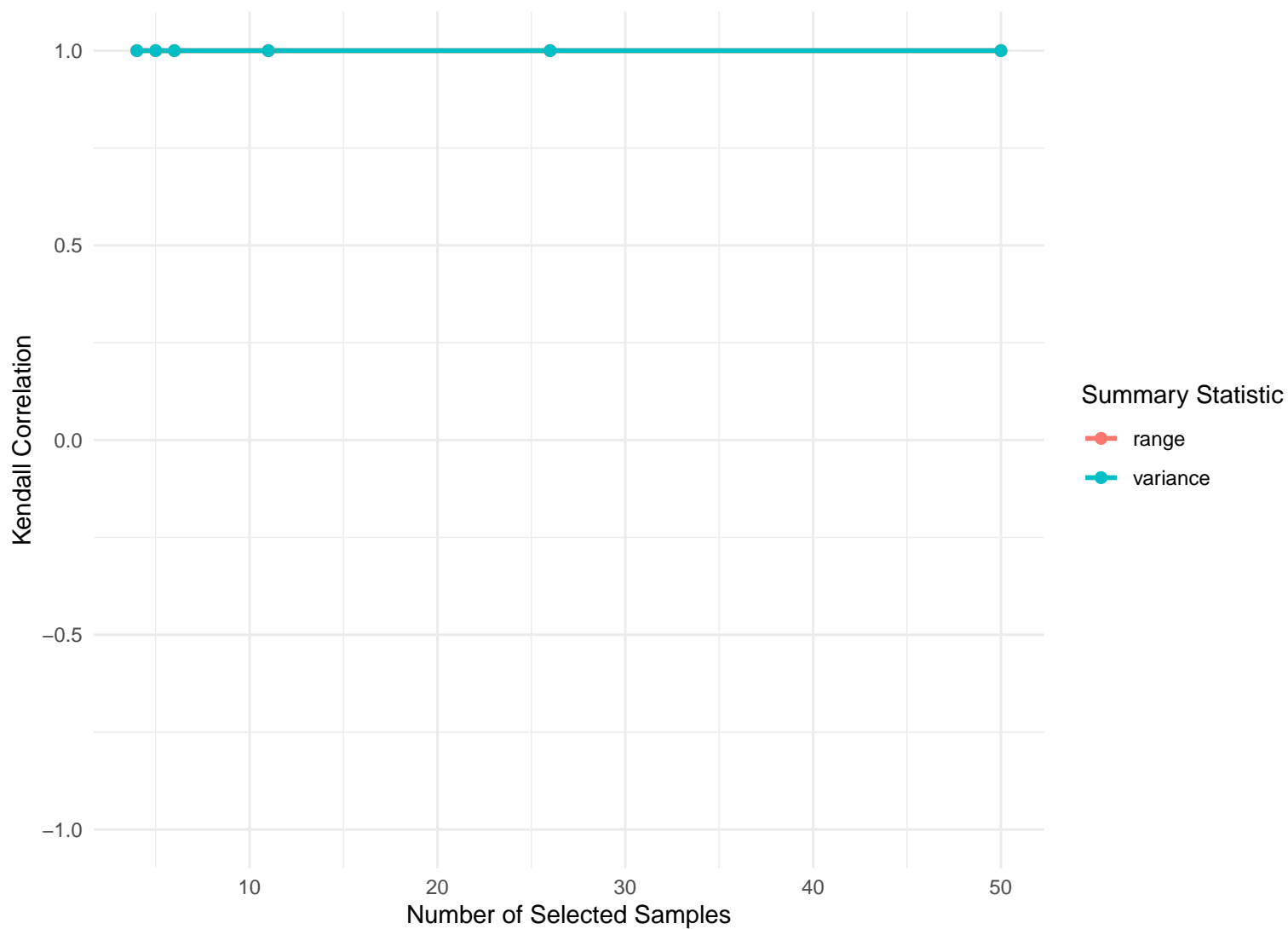
Score: RN (Local, full , Genotype: sinusoidal)



Score: RN (Local, full , Genotype: wave)



Score: RNN (Local, full , Genotype: linear)

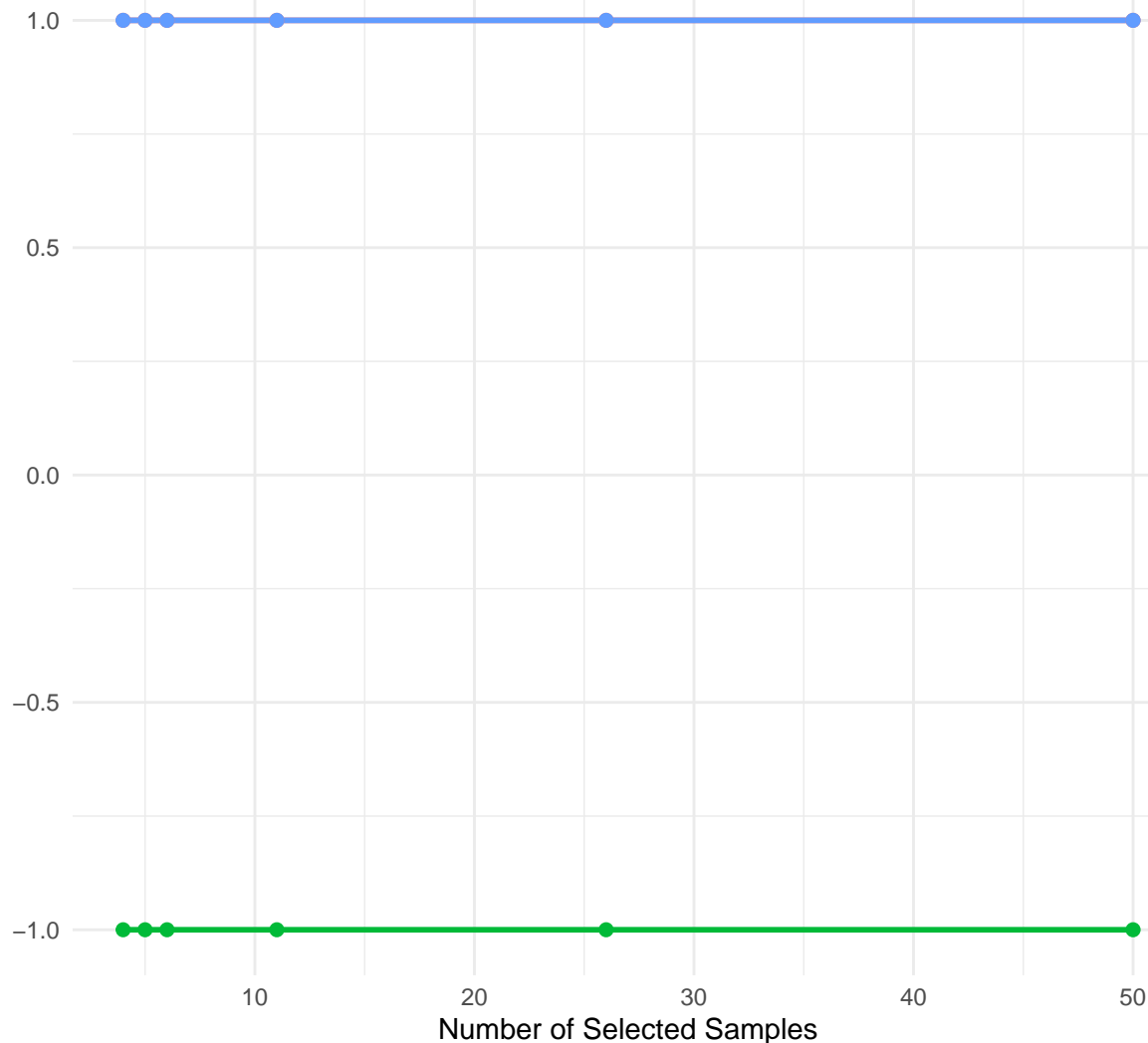


Score: RNN (Local, full , Genotype: gaussian)

Kendall Correlation

Summary Statistic

- range
- slope
- variance

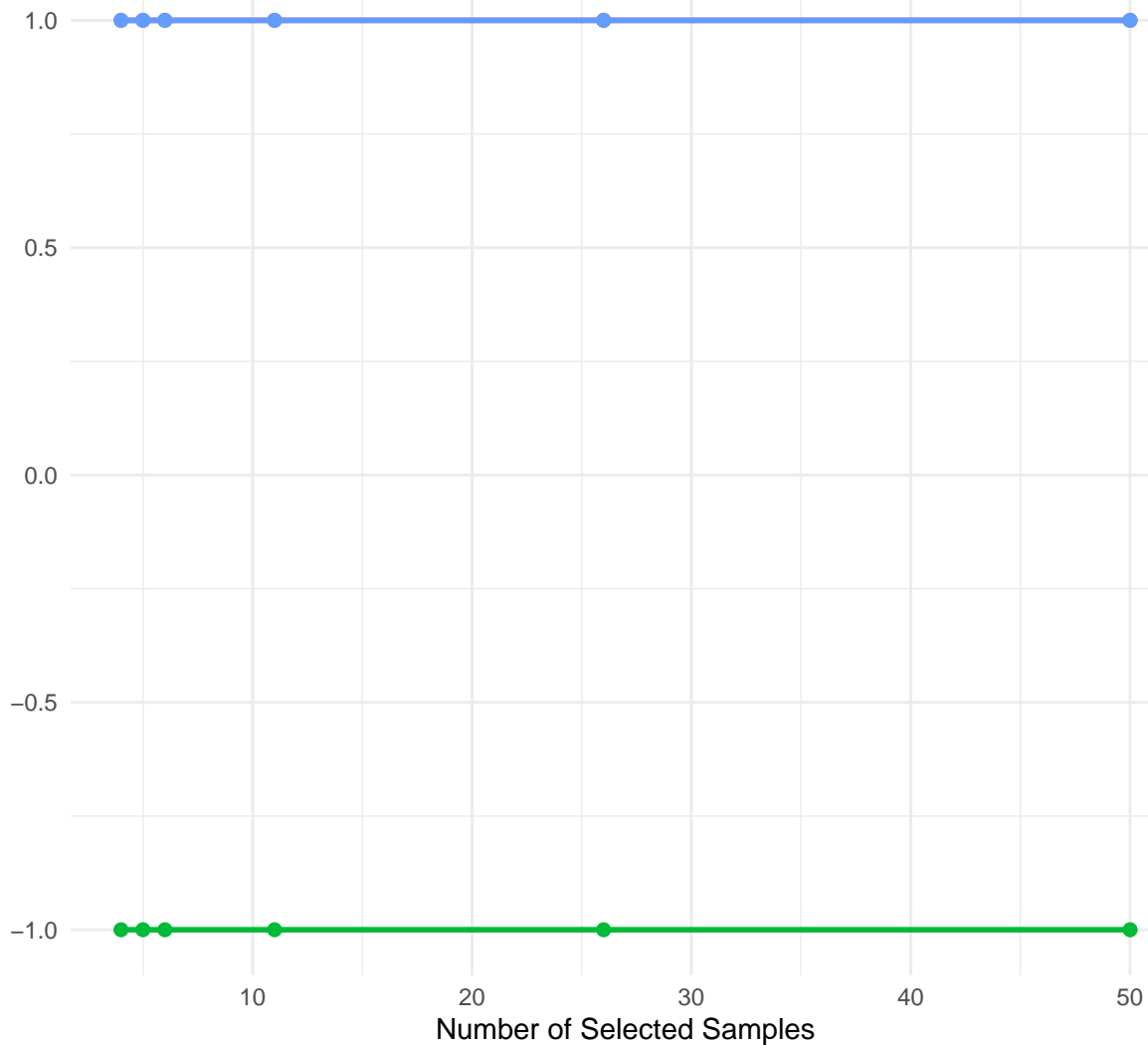


Score: RNN (Local, full , Genotype: sinusoidal)

Kendall Correlation

Summary Statistic

- range
- slope
- variance



Score: RNN (Local, full , Genotype: wave)

Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

10

20

30

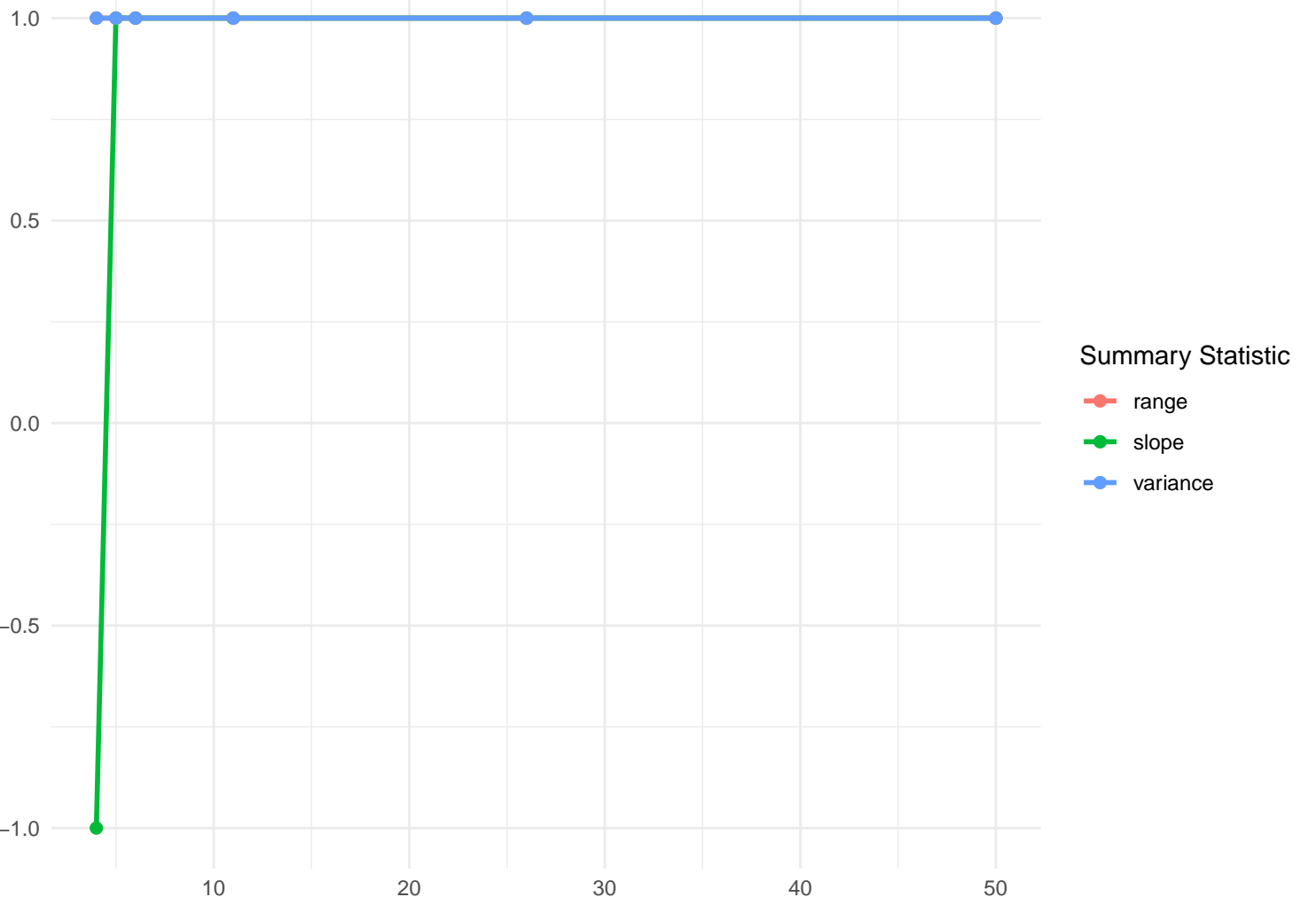
40

50

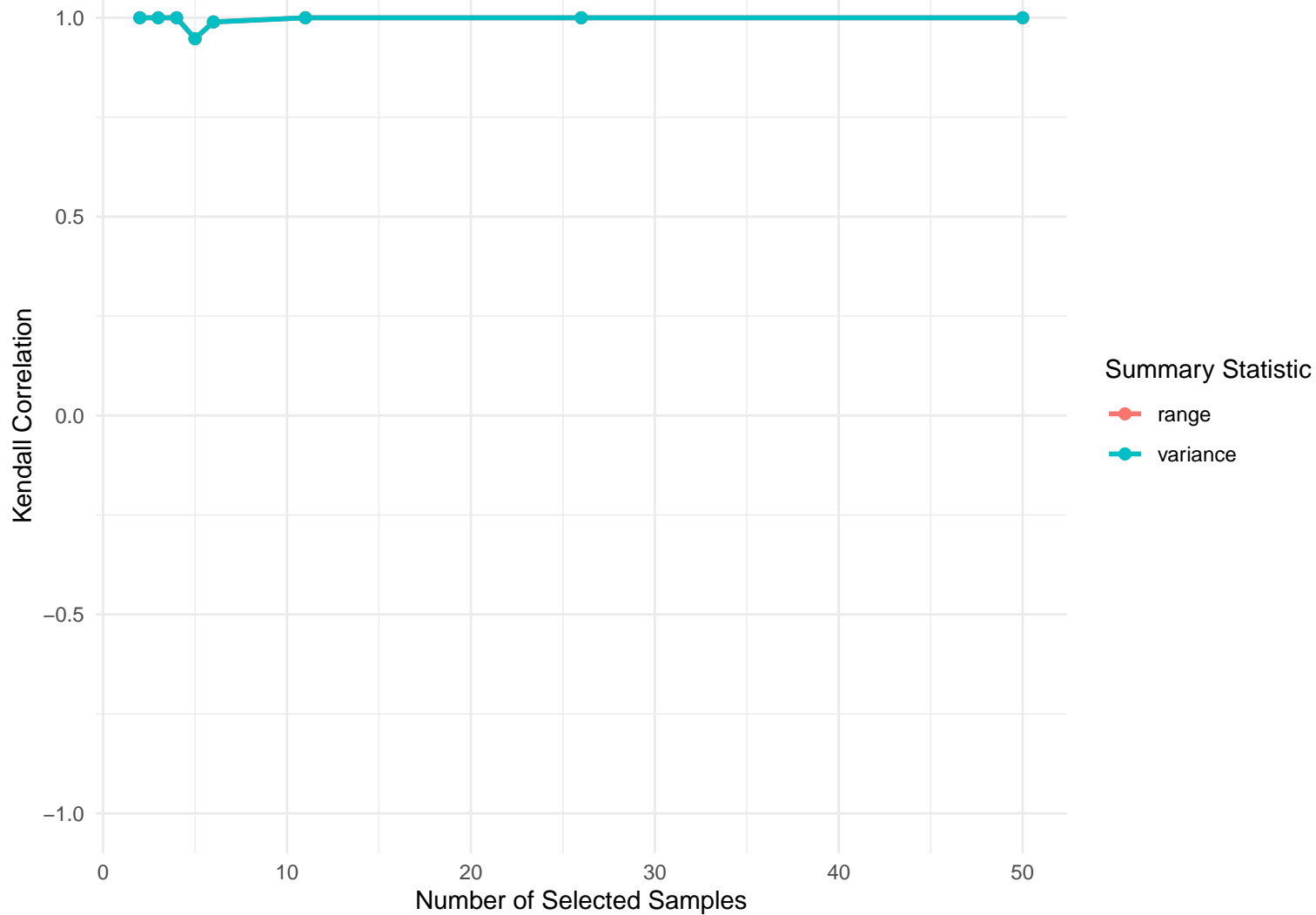
Number of Selected Samples

Summary Statistic

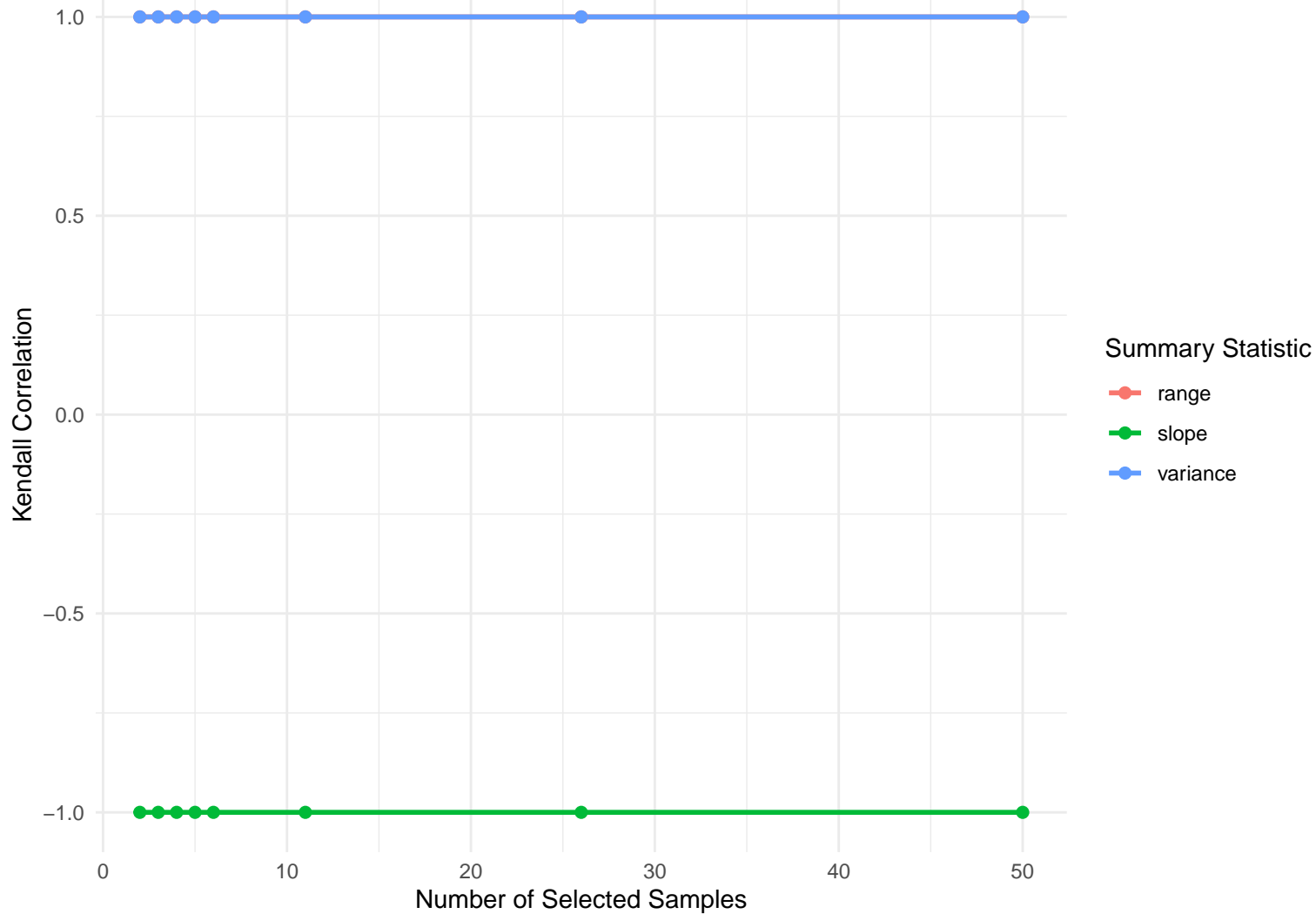
- range
- slope
- variance



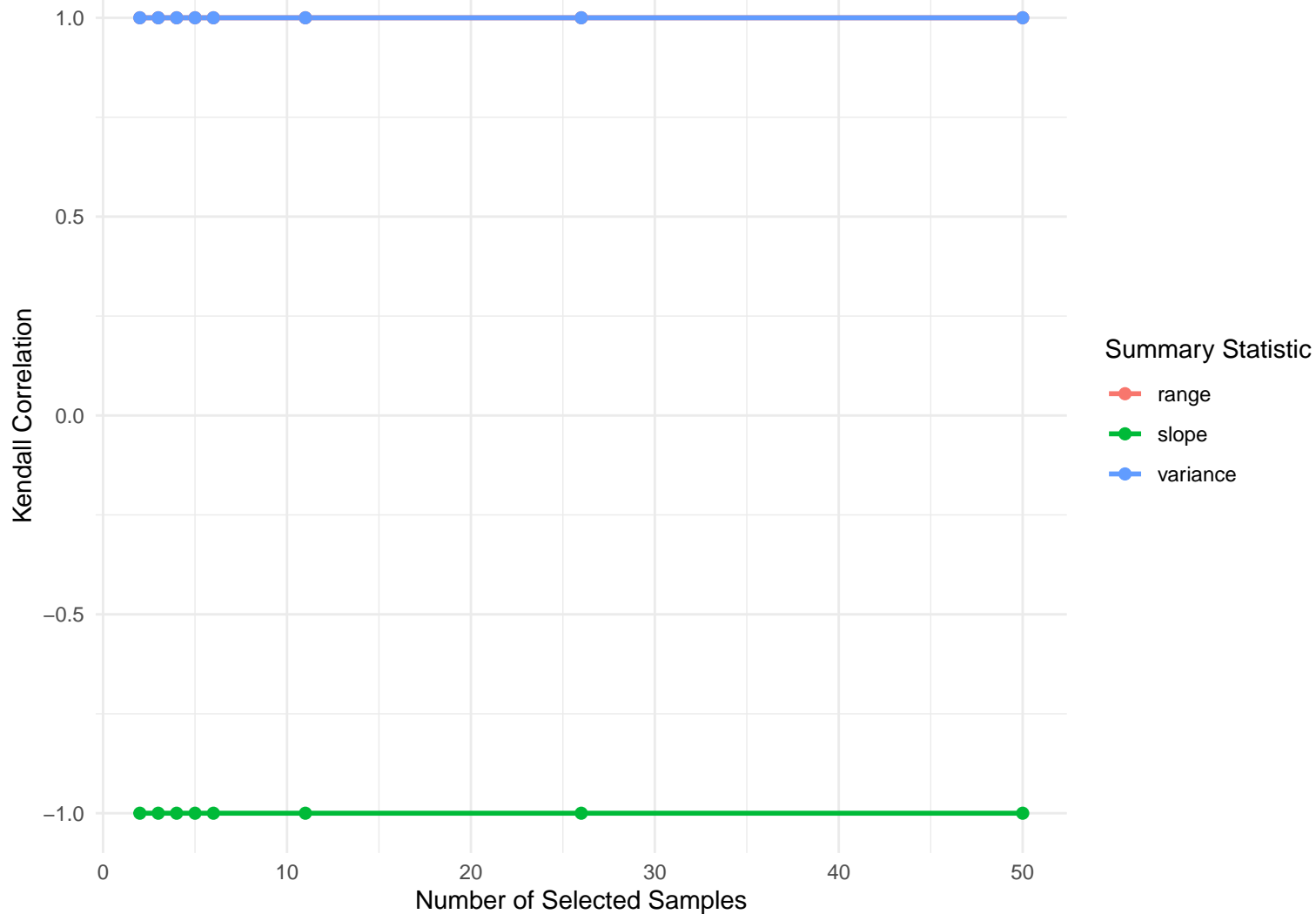
Score: D_slope (Local, full , Genotype: linear)



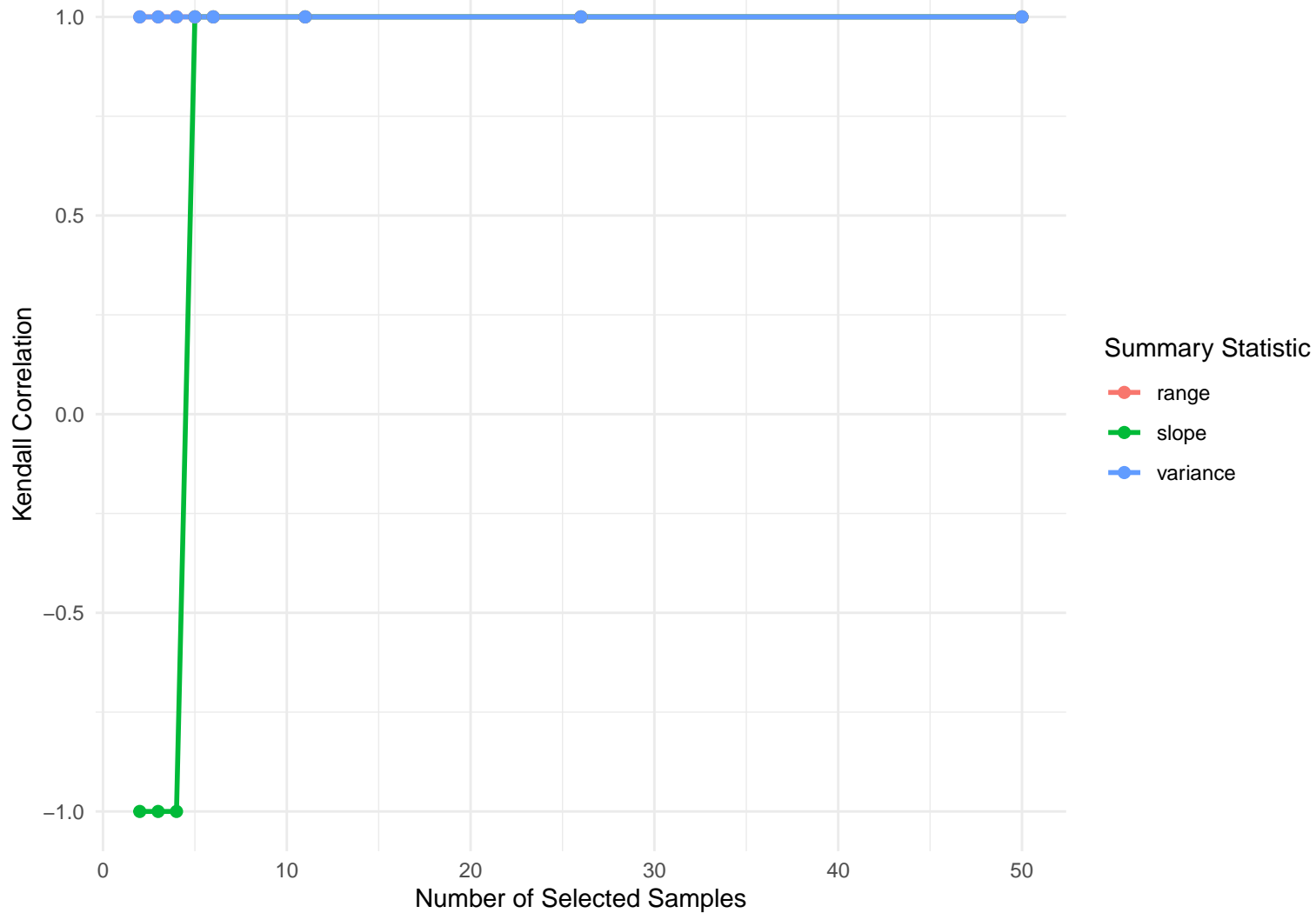
Score: D_slope (Local, full , Genotype: gaussian)



Score: D_slope (Local, full , Genotype: sinusoidal)

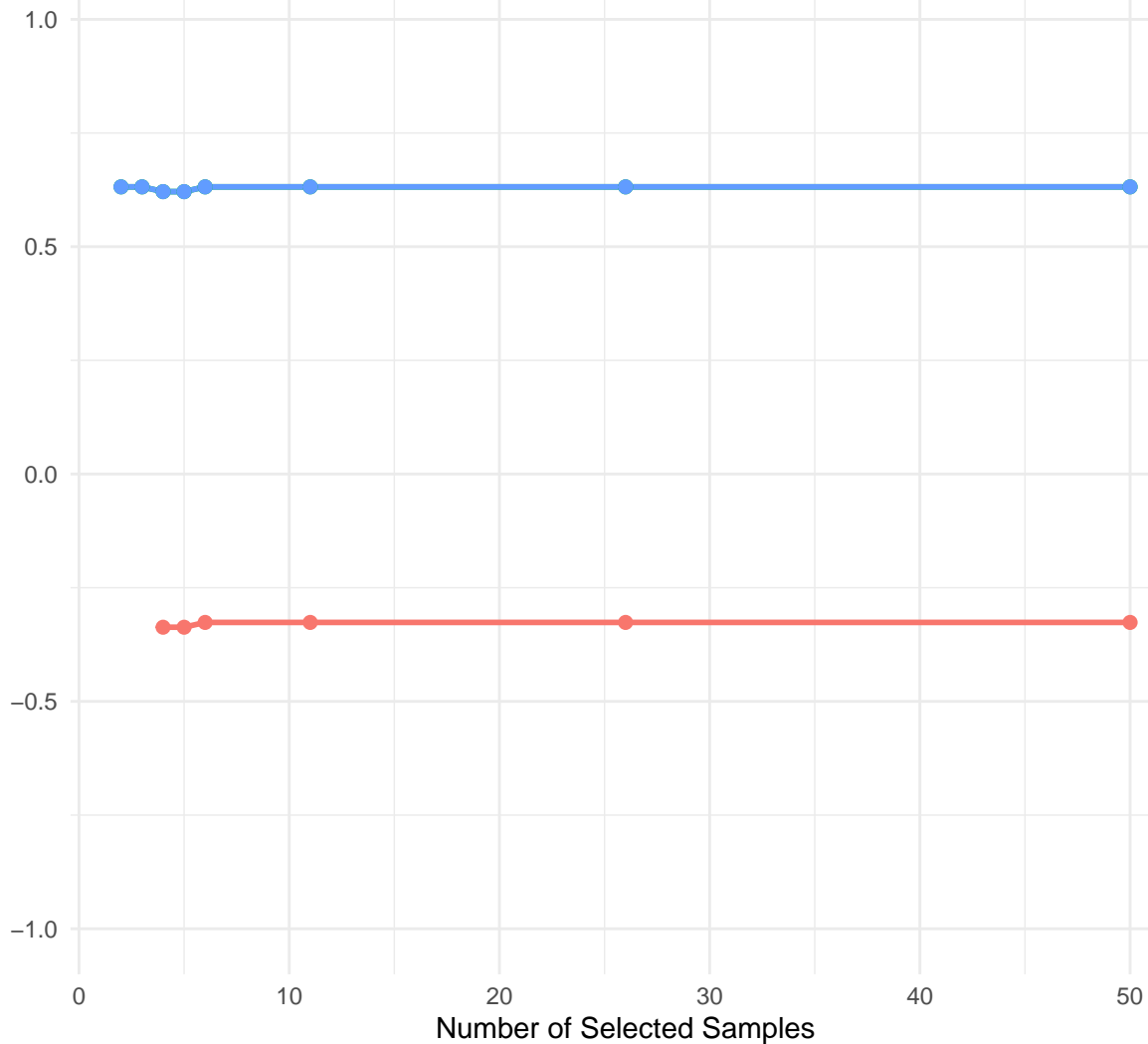


Score: D_slope (Local, full , Genotype: wave)



Score: RC (Local, full , Genotype: linear)

Kendall Correlation



Summary Statistic

- min
- range
- variance

Score: RC (Local, full , Genotype: gaussian)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

40

50

Number of Selected Samples

Summary Statistic

- max
- mean
- mean_lower
- mean_upper
- median
- min
- range
- slope
- variance

0

10

20

30

40

50

Number of Selected Samples

Score: RC (Local, full , Genotype: sinusoidal)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

40

50

Number of Selected Samples

Summary Statistic

- max
- mean
- mean_lower
- mean_upper
- median
- min
- range
- slope
- variance

0

10

20

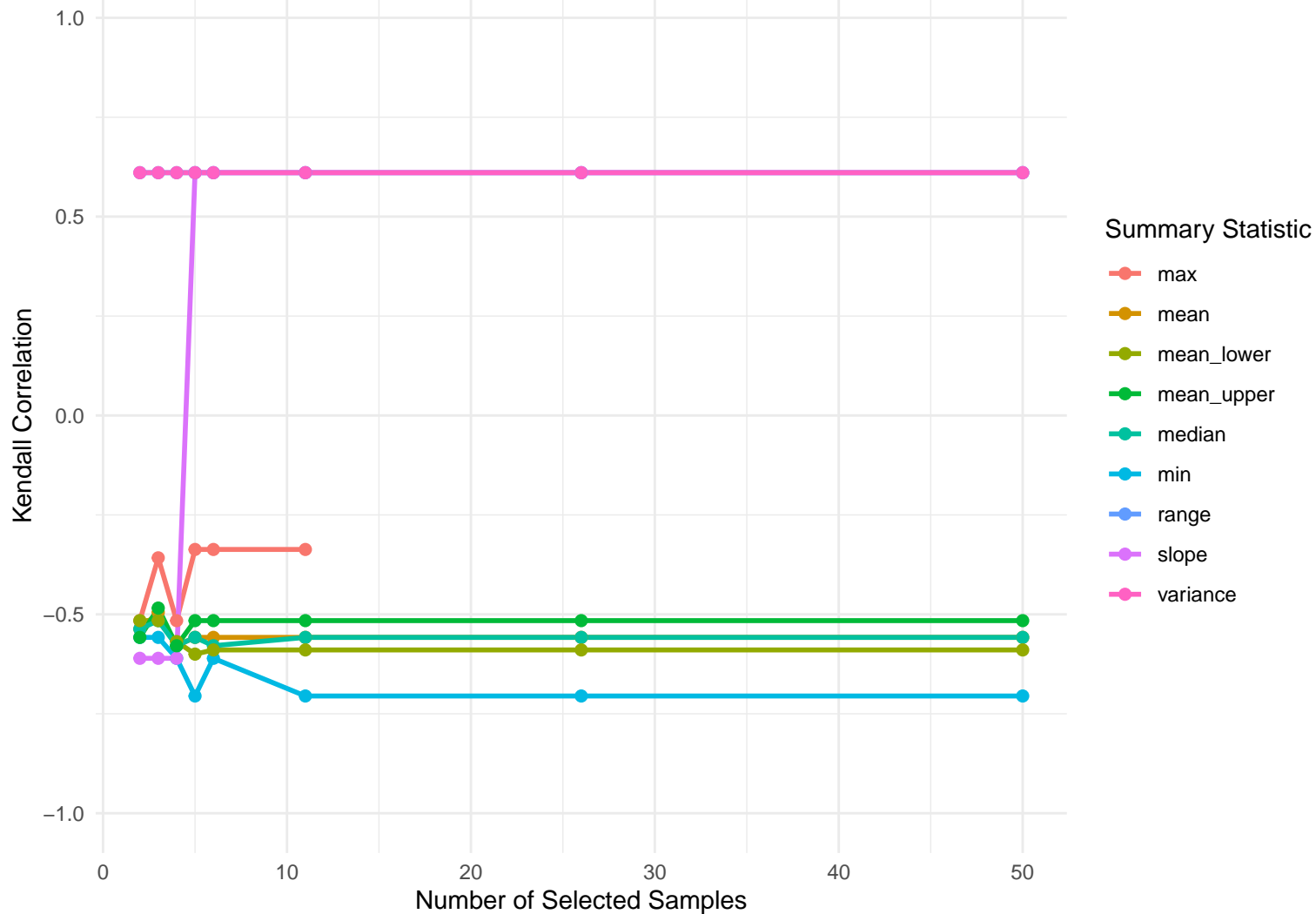
30

40

50

Number of Selected Samples

Score: RC (Local, full , Genotype: wave)



Score: gPi (Local, full , Genotype: linear)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

40

50

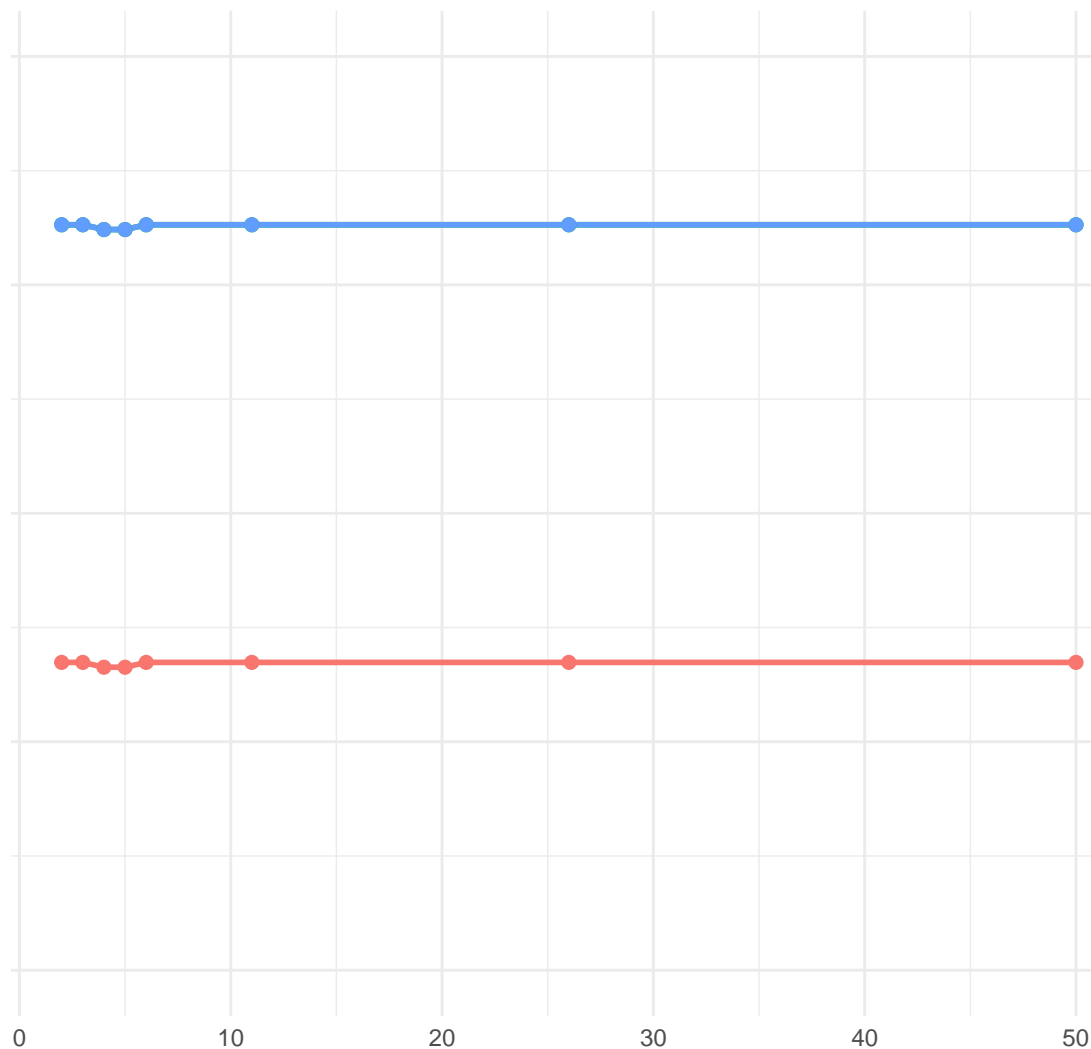
Number of Selected Samples

Summary Statistic

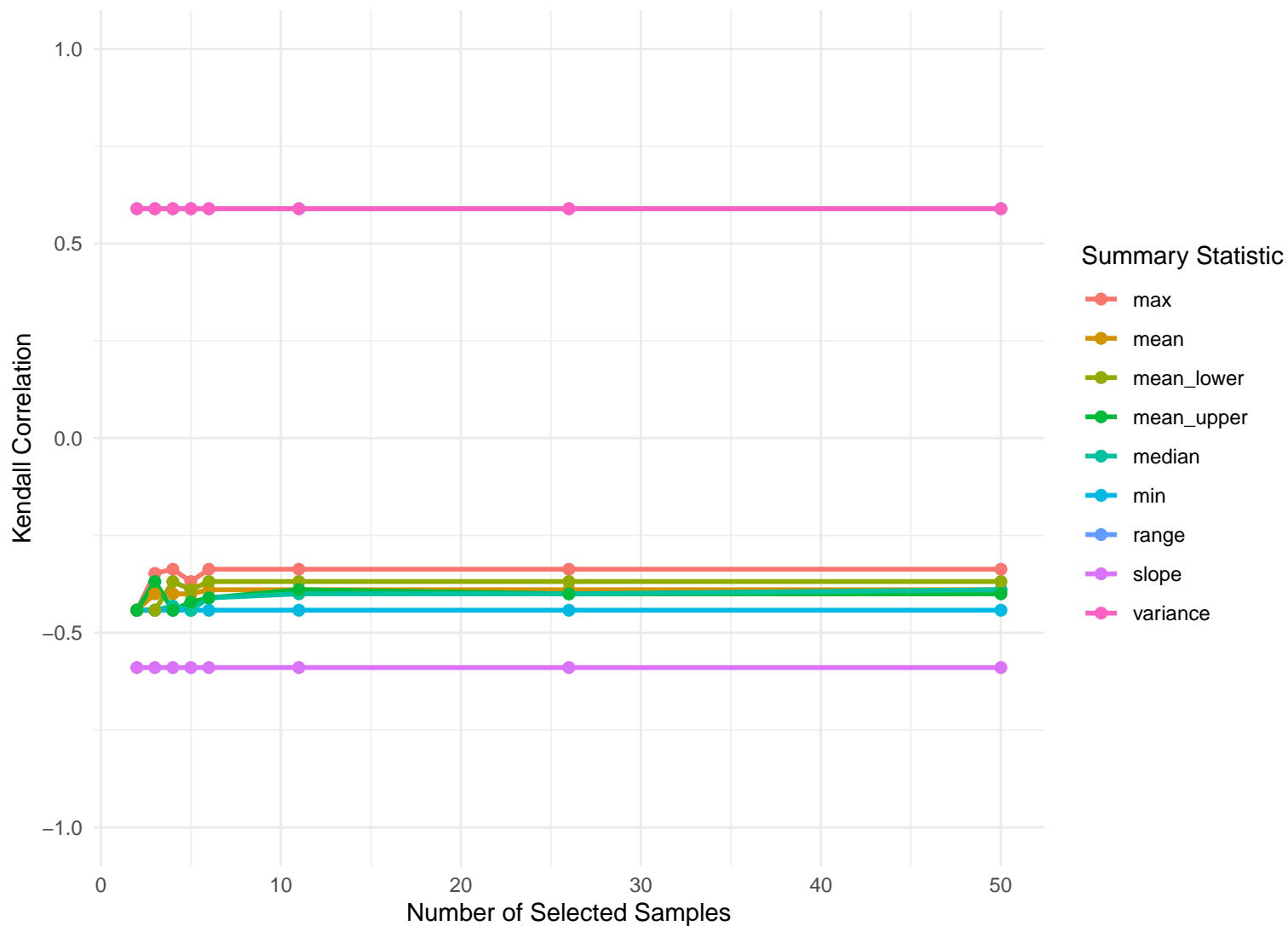
min

range

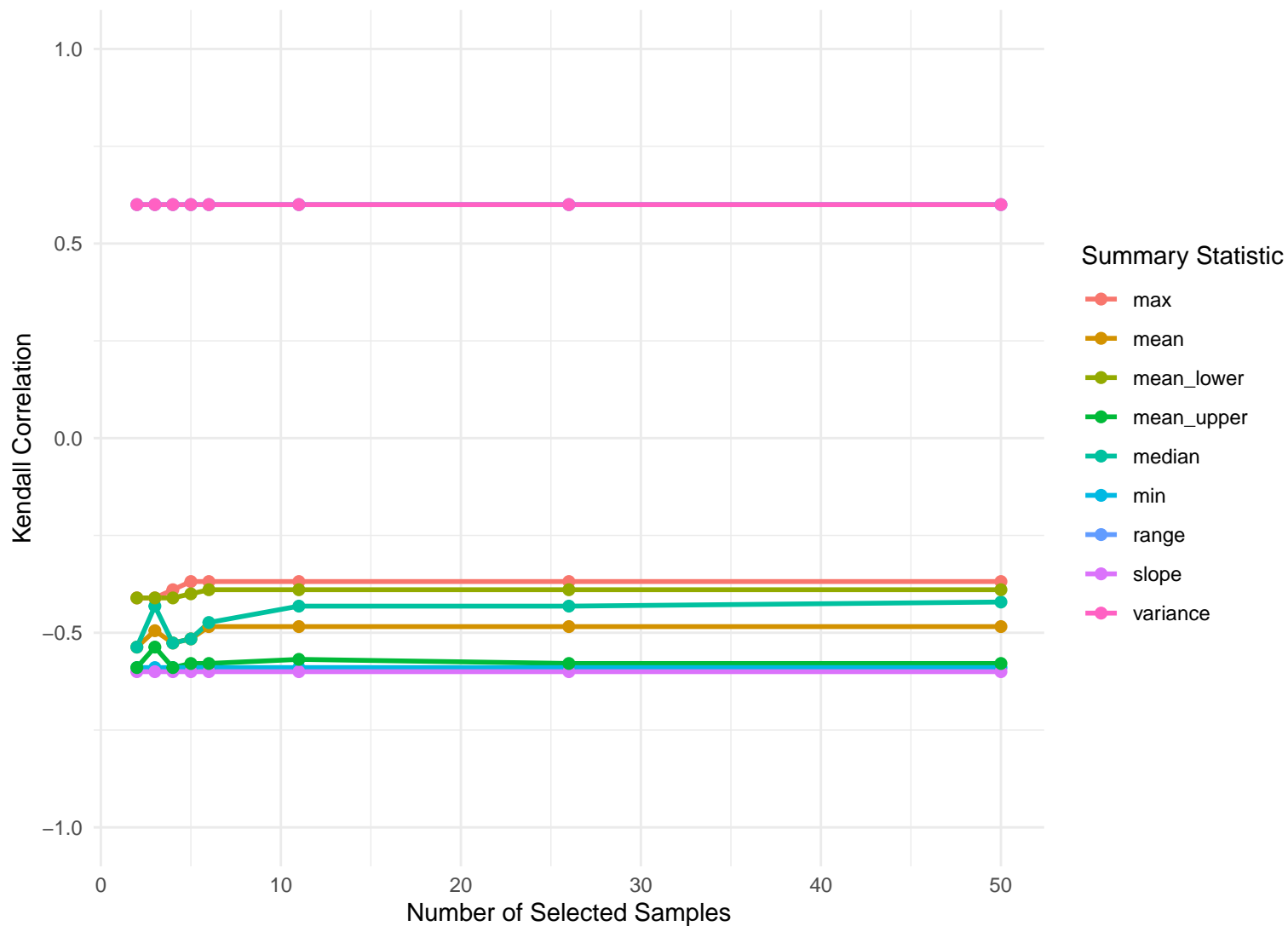
variance



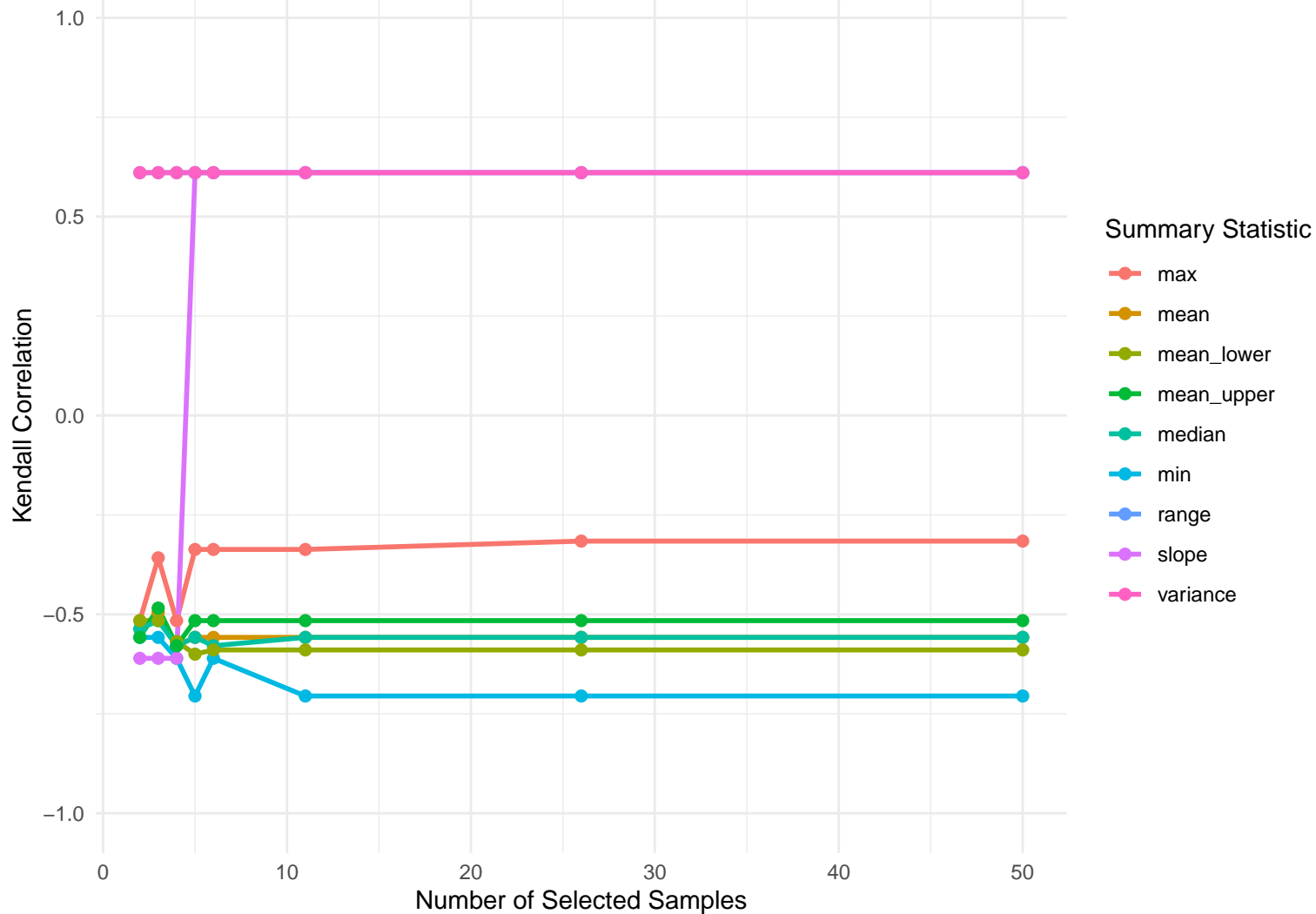
Score: gPi (Local, full , Genotype: gaussian)



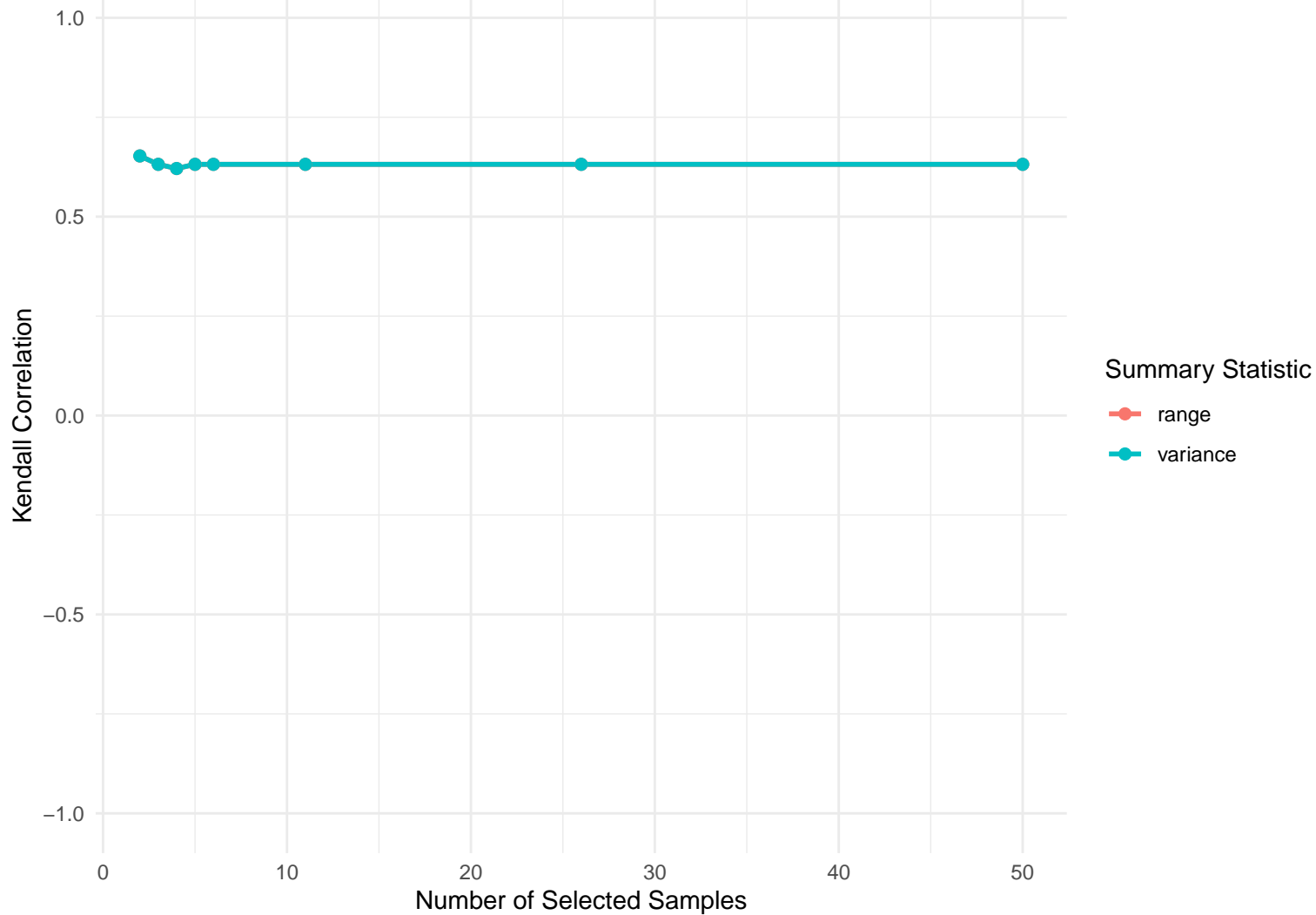
Score: gPi (Local, full , Genotype: sinusoidal)



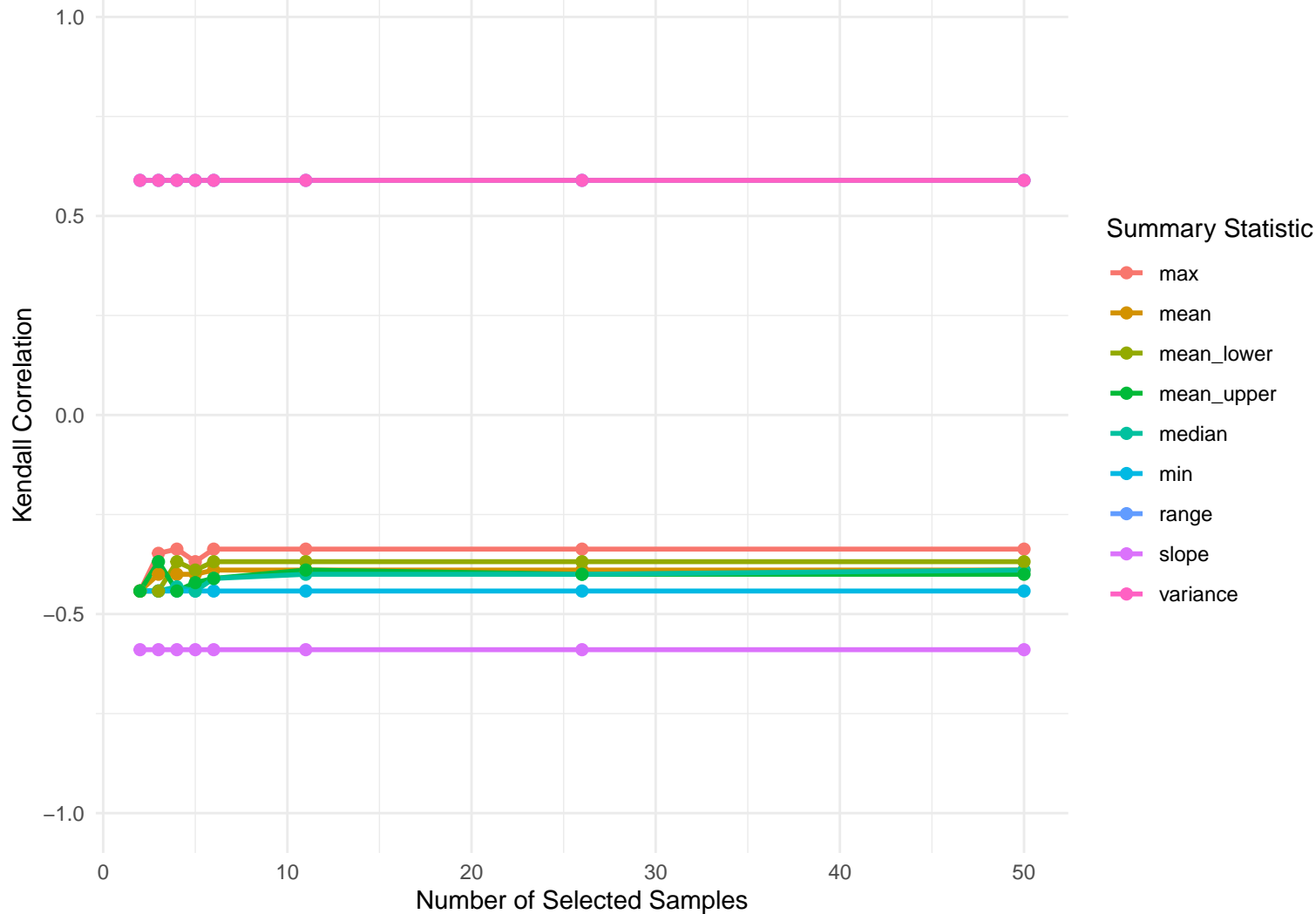
Score: gPi (Local, full , Genotype: wave)



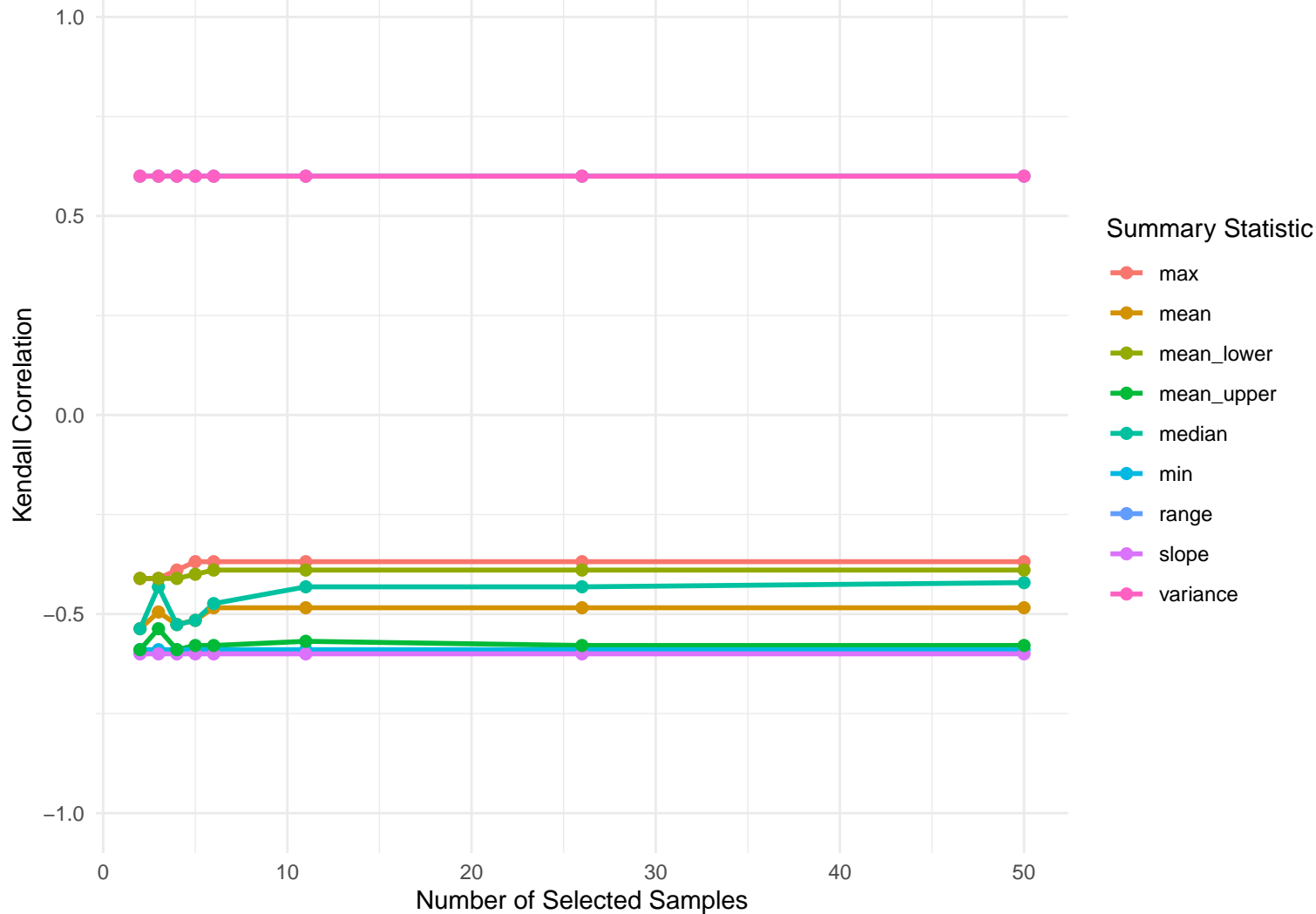
Score: PPF (Local, full , Genotype: linear)



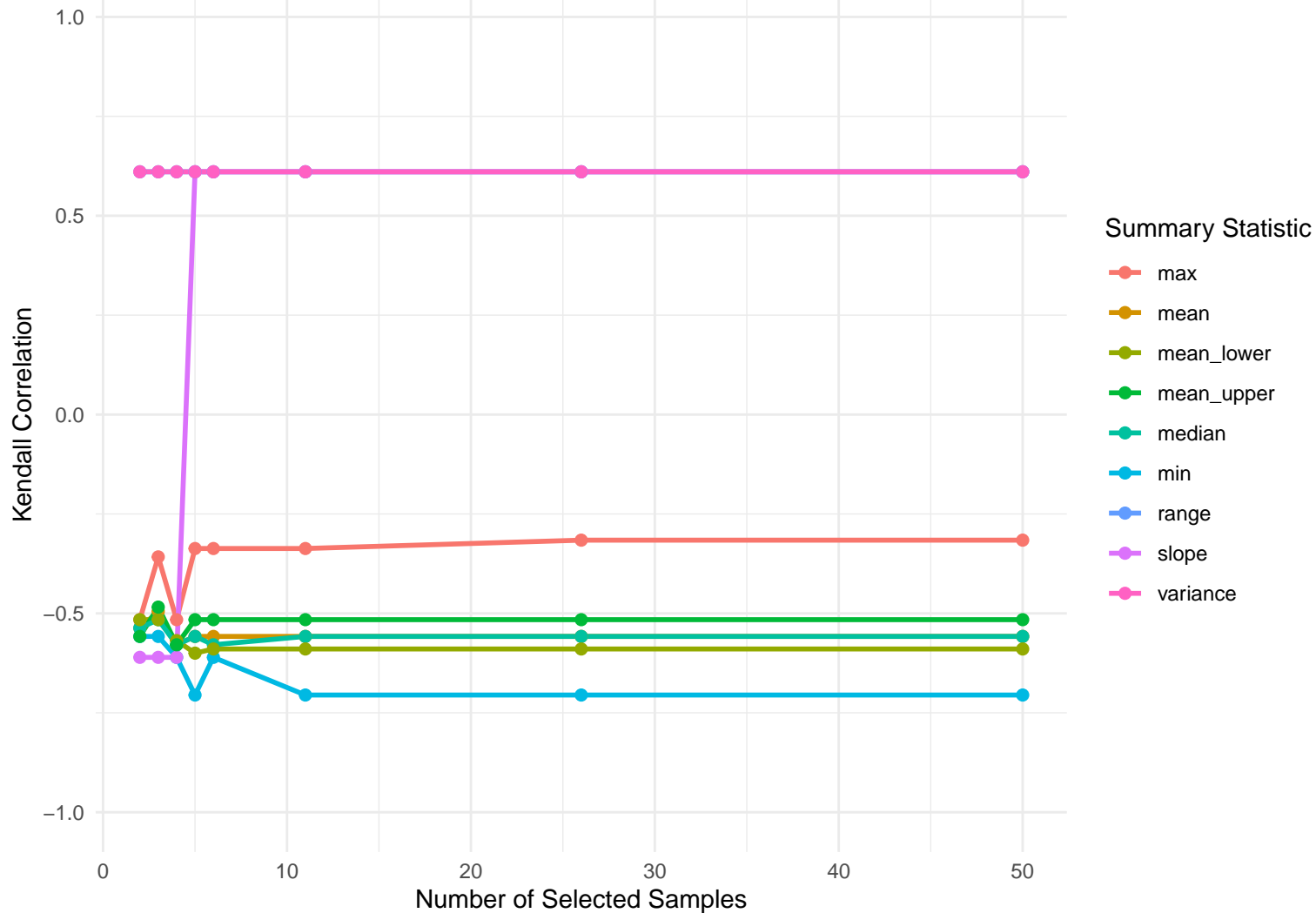
Score: PPF (Local, full , Genotype: gaussian)



Score: PPF (Local, full , Genotype: sinusoidal)



Score: PPF (Local, full , Genotype: wave)



Score: PPI (Local, full , Genotype: linear)

Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

0

10

20

30

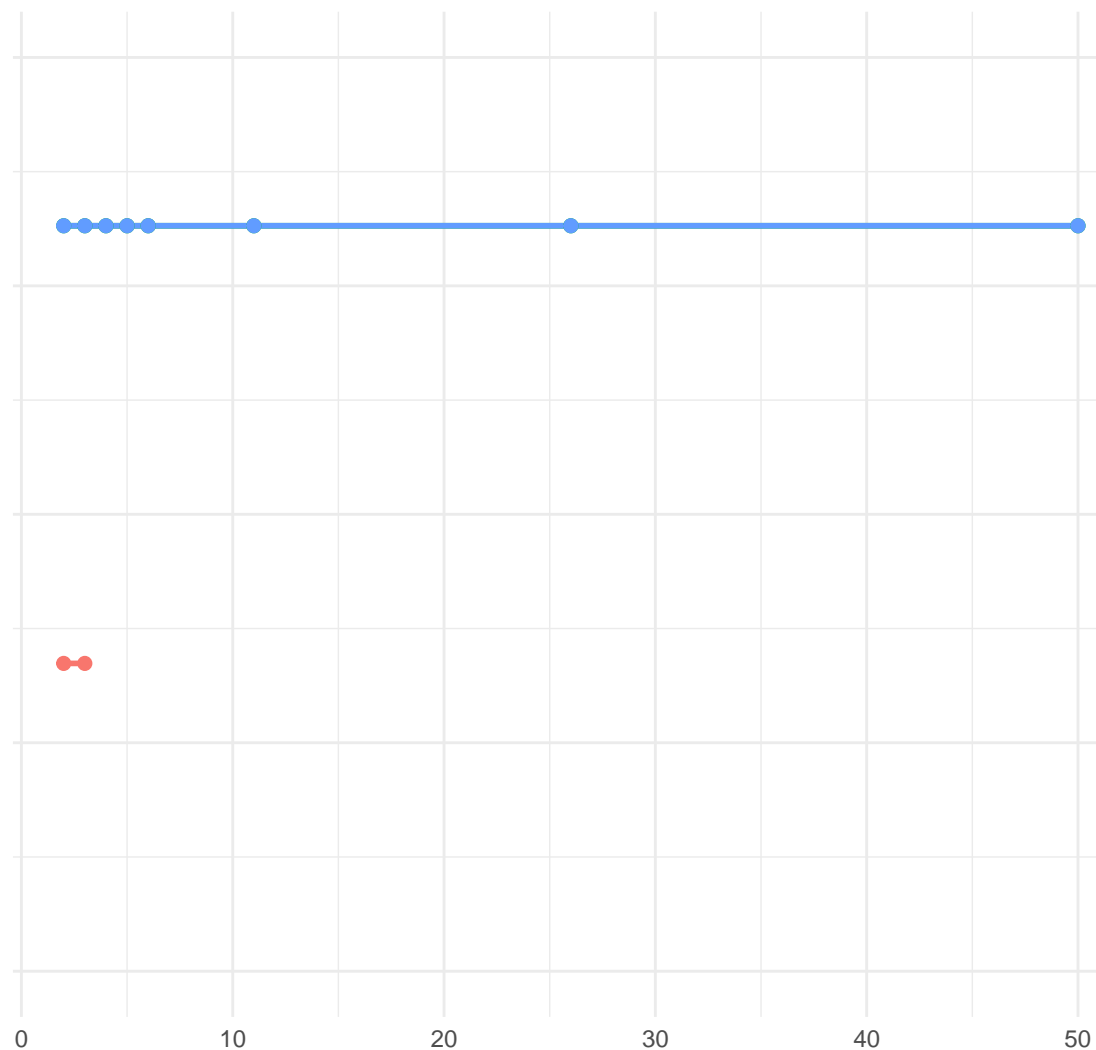
40

50

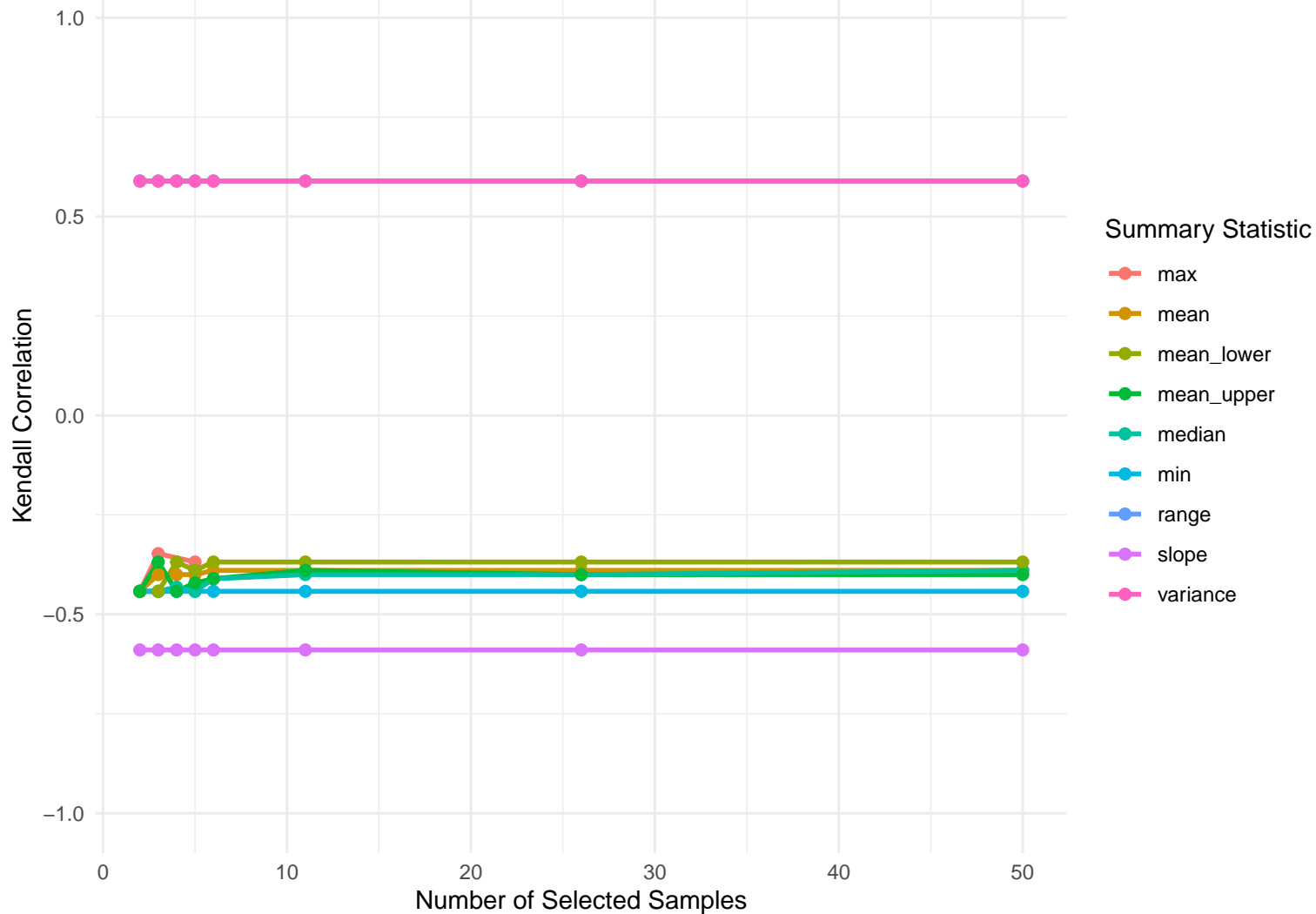
Number of Selected Samples

Summary Statistic

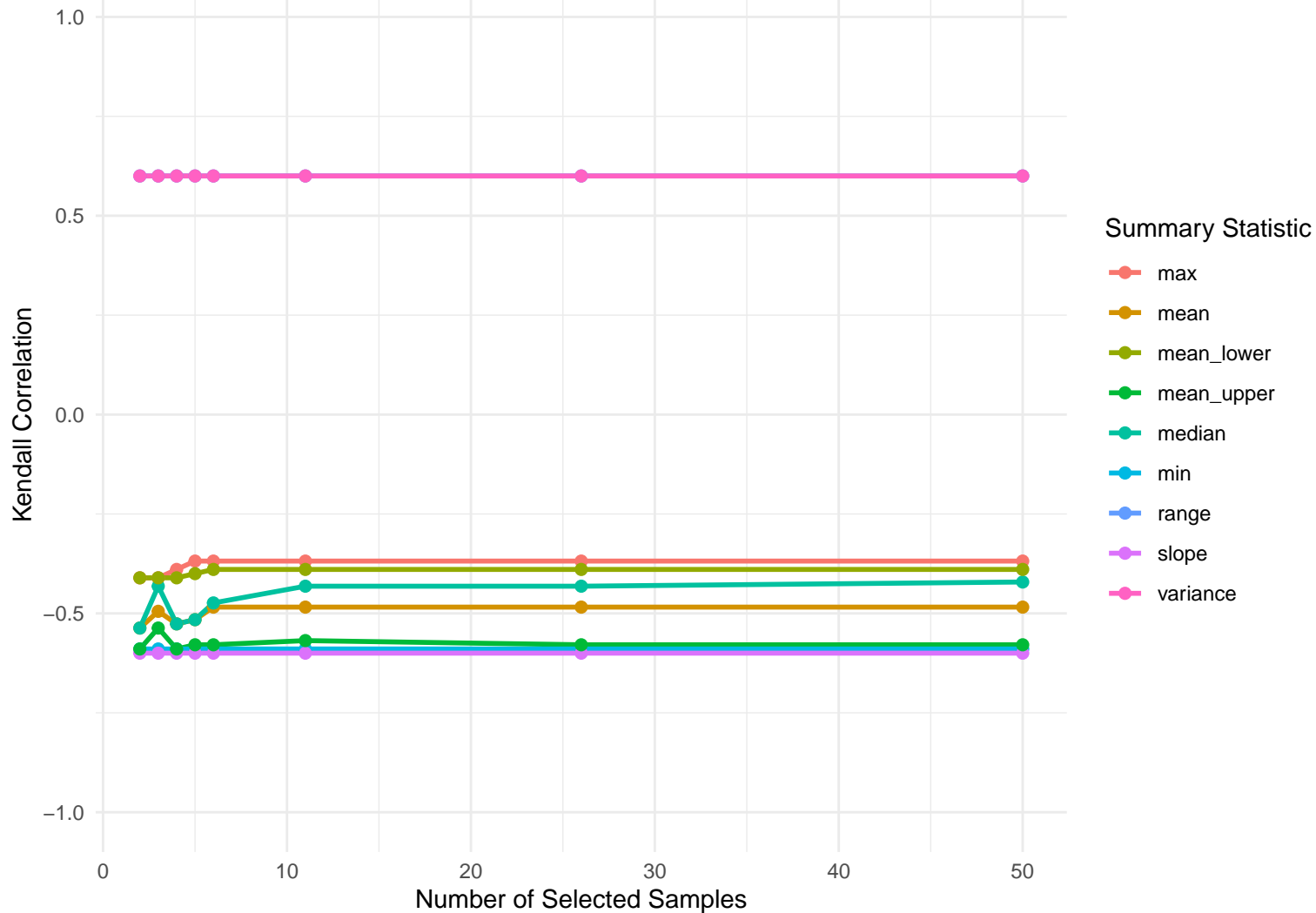
- min
- range
- variance



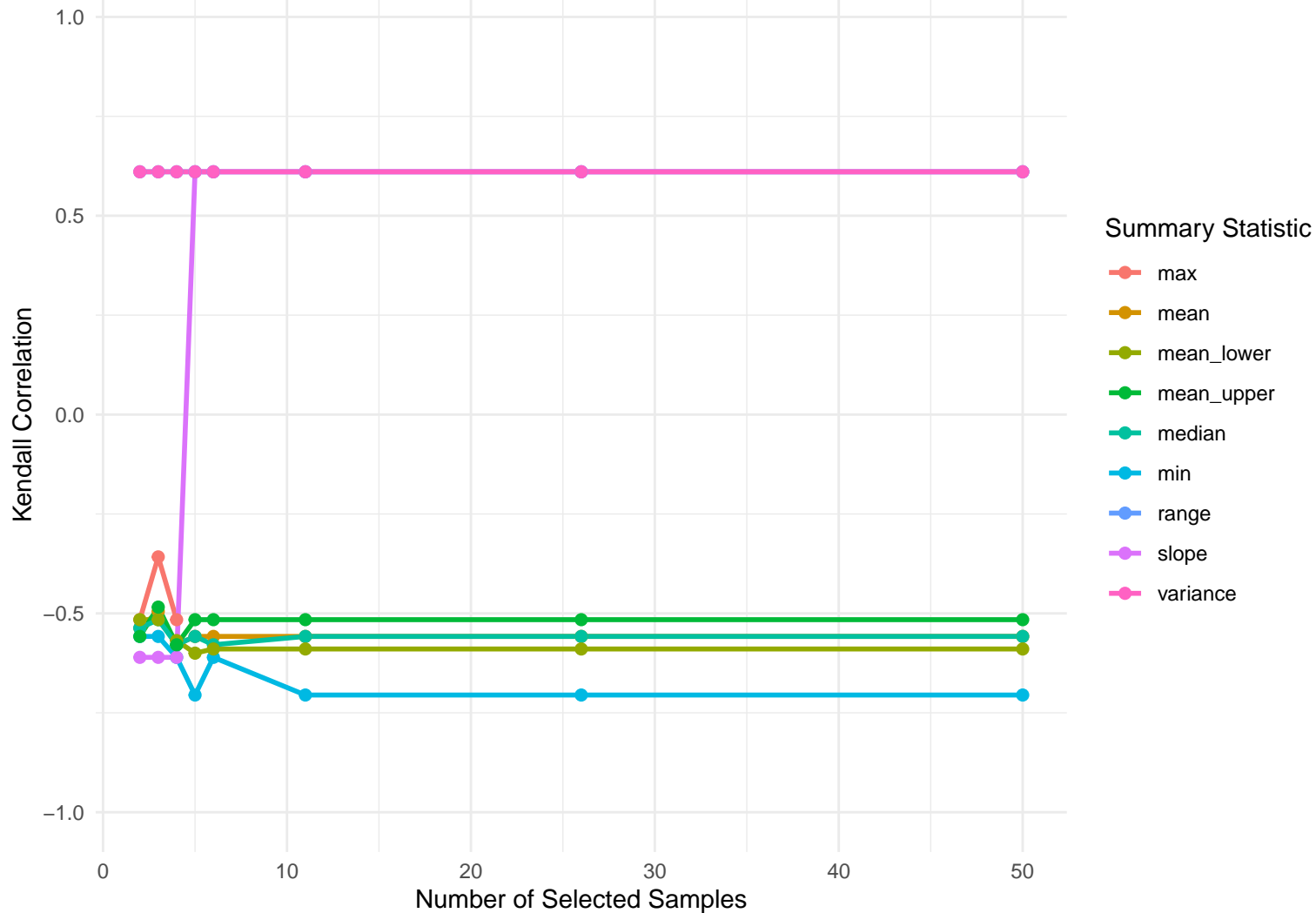
Score: PPI (Local, full , Genotype: gaussian)



Score: PPI (Local, full , Genotype: sinusoidal)



Score: PPI (Local, full , Genotype: wave)



Score: Plmd (Local, full , Genotype: linear)

Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

0

10

20

30

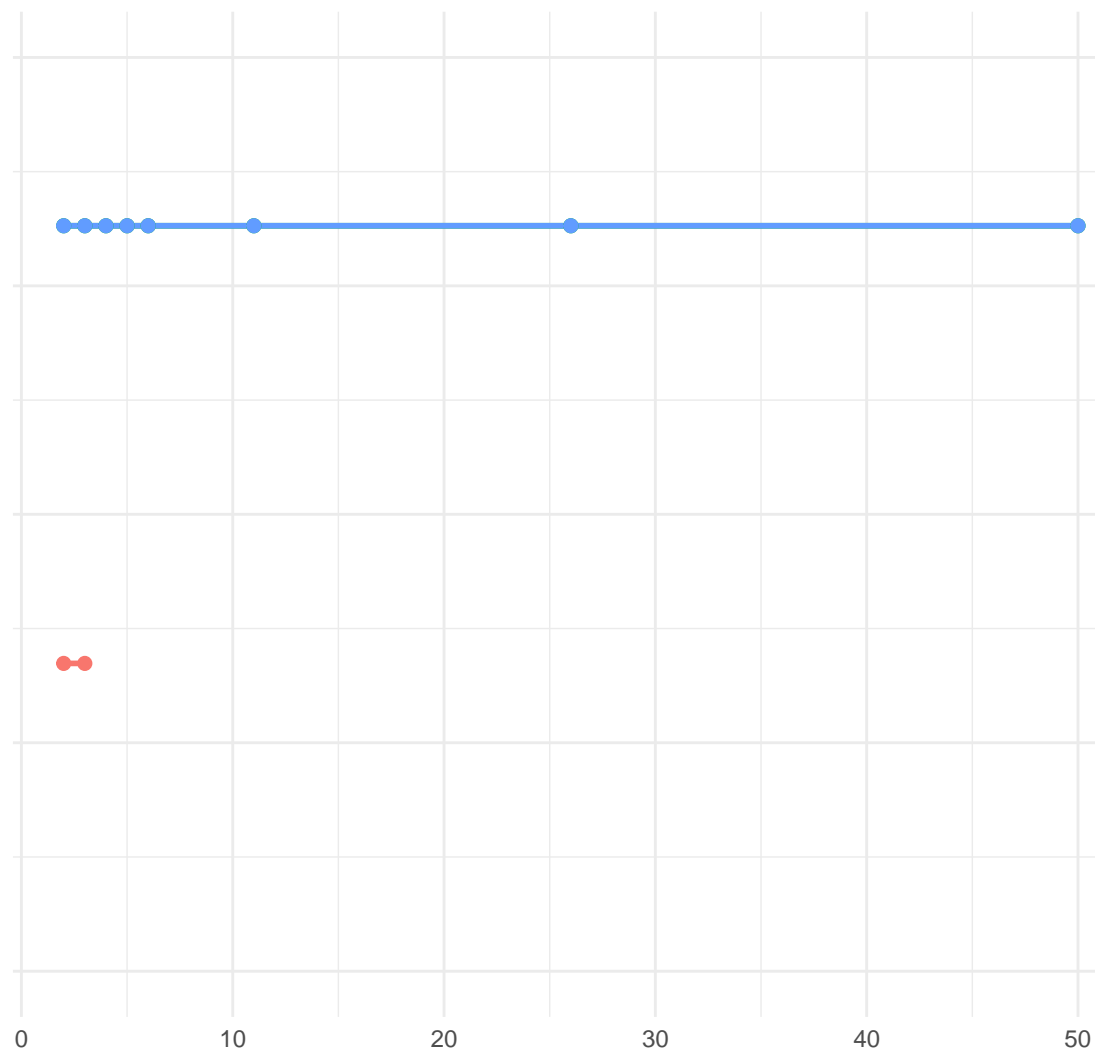
40

50

Number of Selected Samples

Summary Statistic

- min
- range
- variance



Score: Plmd (Local, full , Genotype: gaussian)

Kendall Correlation

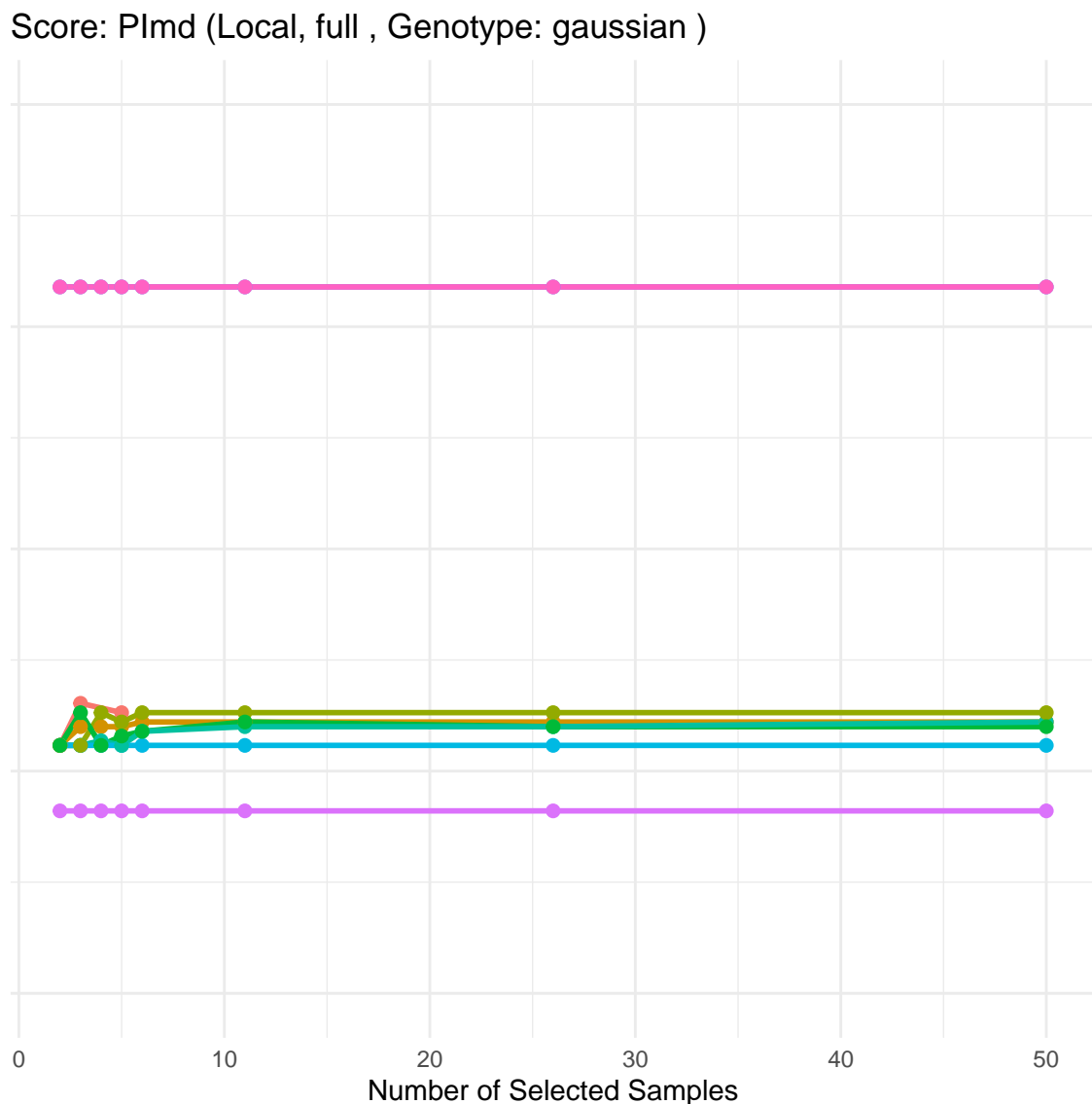
1.0
0.5
0.0
-0.5
-1.0

Number of Selected Samples

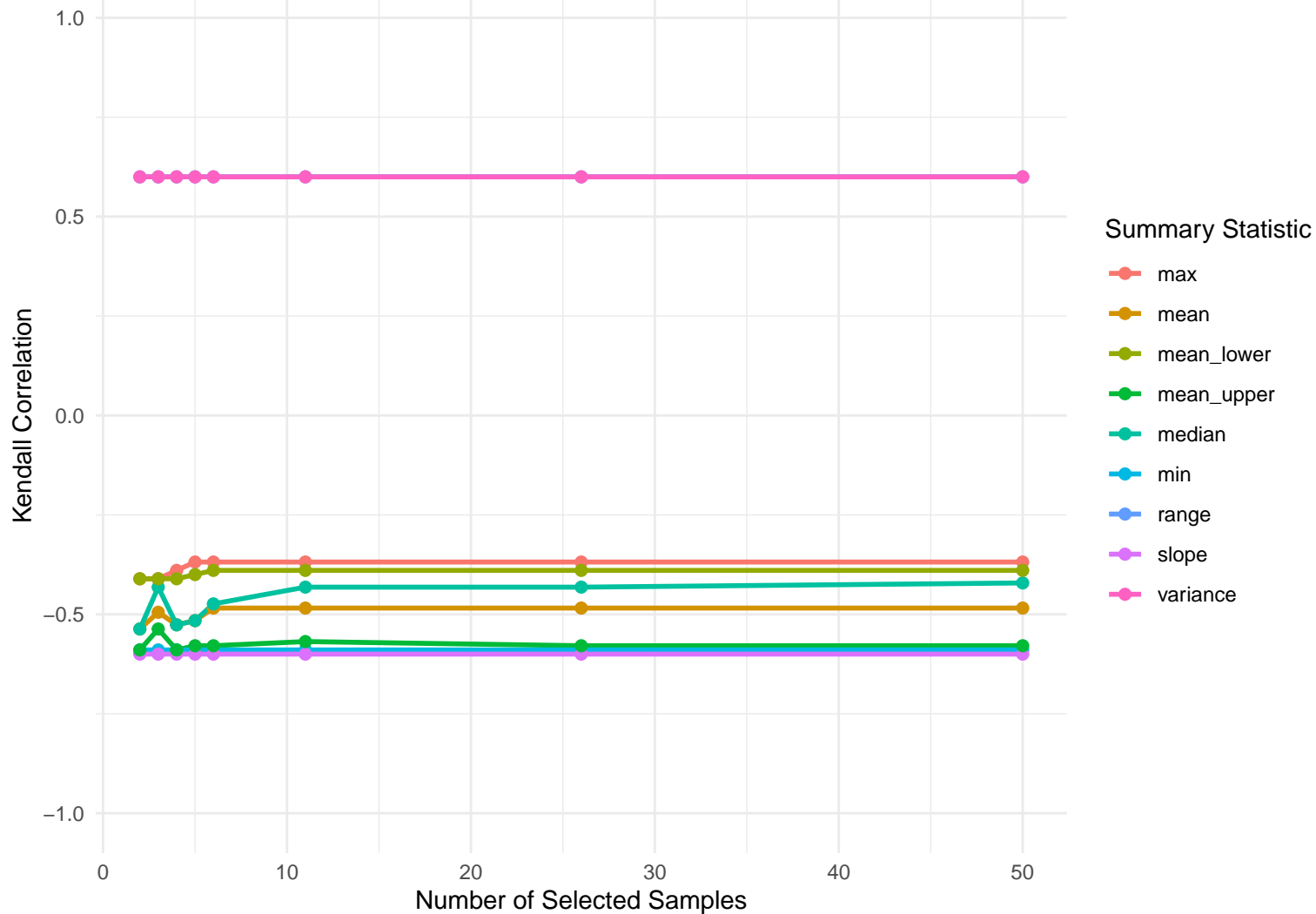
Summary Statistic

- max
- mean
- mean_lower
- mean_upper
- median
- min
- range
- slope
- variance

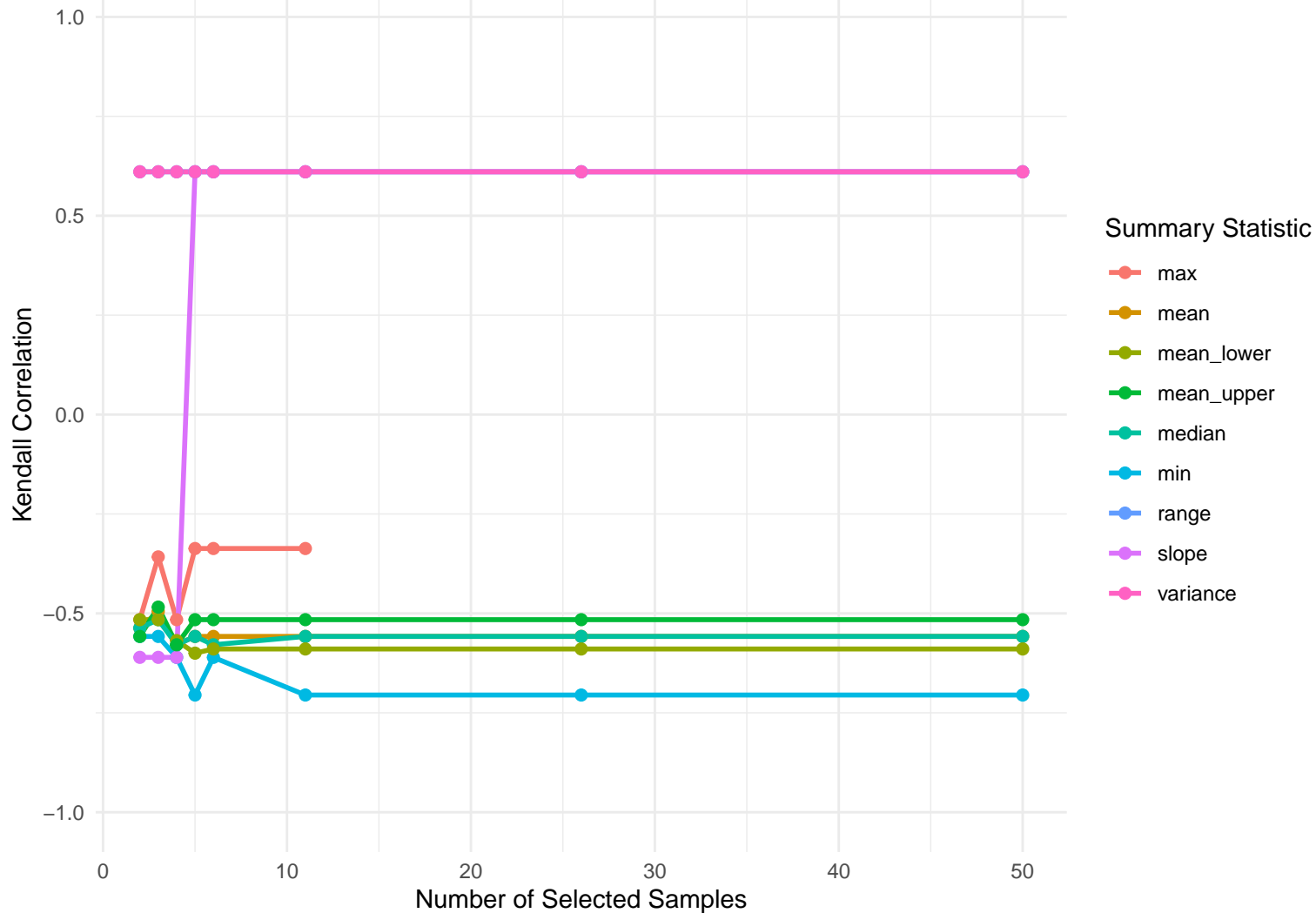
0 10 20 30 40 50



Score: Plmd (Local, full , Genotype: sinusoidal)



Score: Plmd (Local, full , Genotype: wave)



Score: PILSM (Local, full , Genotype: linear)

Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

0

10

20

30

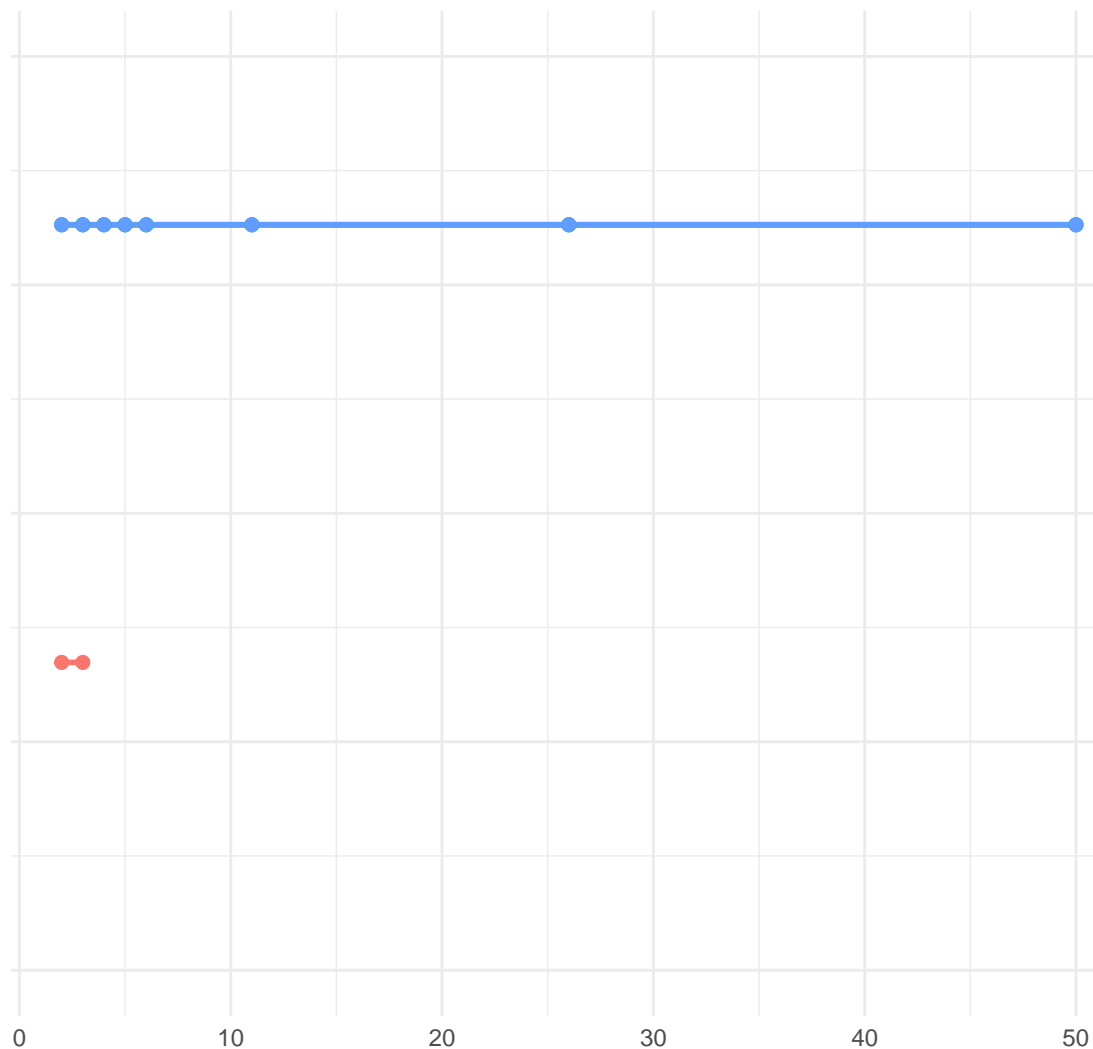
40

50

Number of Selected Samples

Summary Statistic

- min
- range
- variance



Score: PILSM (Local, full , Genotype: gaussian)

Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

0

10

20

30

40

50

Number of Selected Samples

Summary Statistic

- max
- mean
- mean_lower
- mean_upper
- median
- min
- range
- slope
- variance

0

10

20

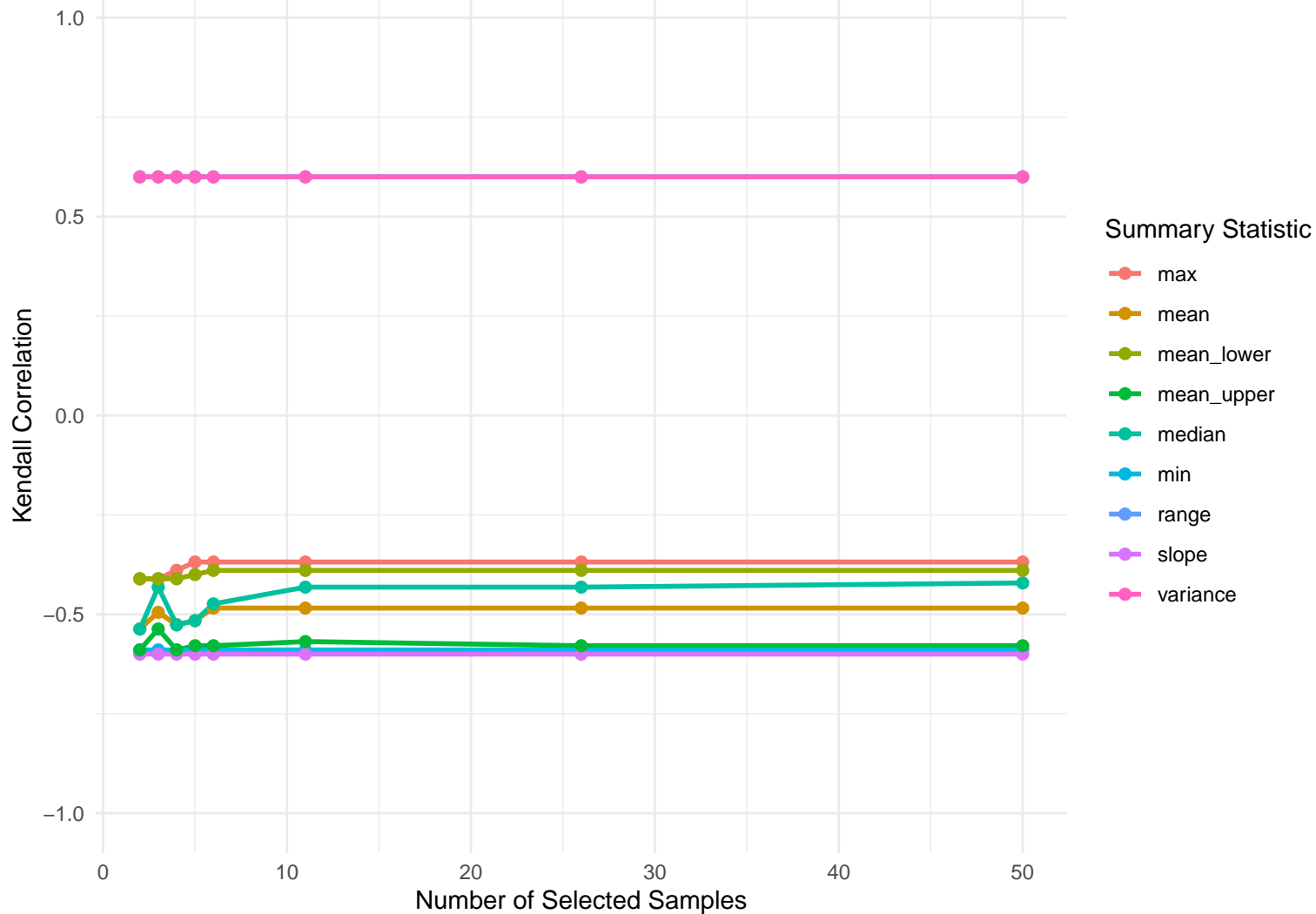
30

40

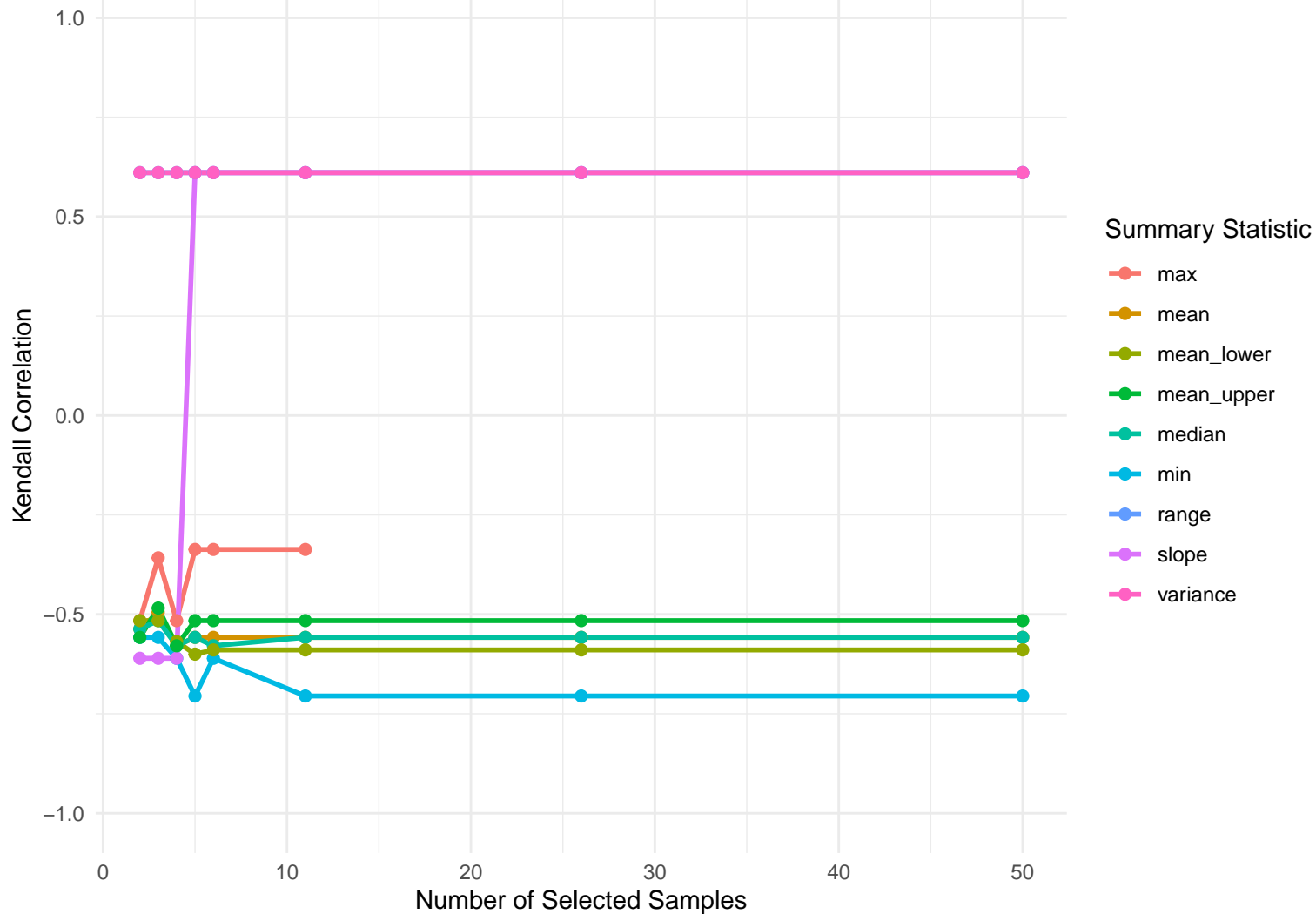
50

Number of Selected Samples

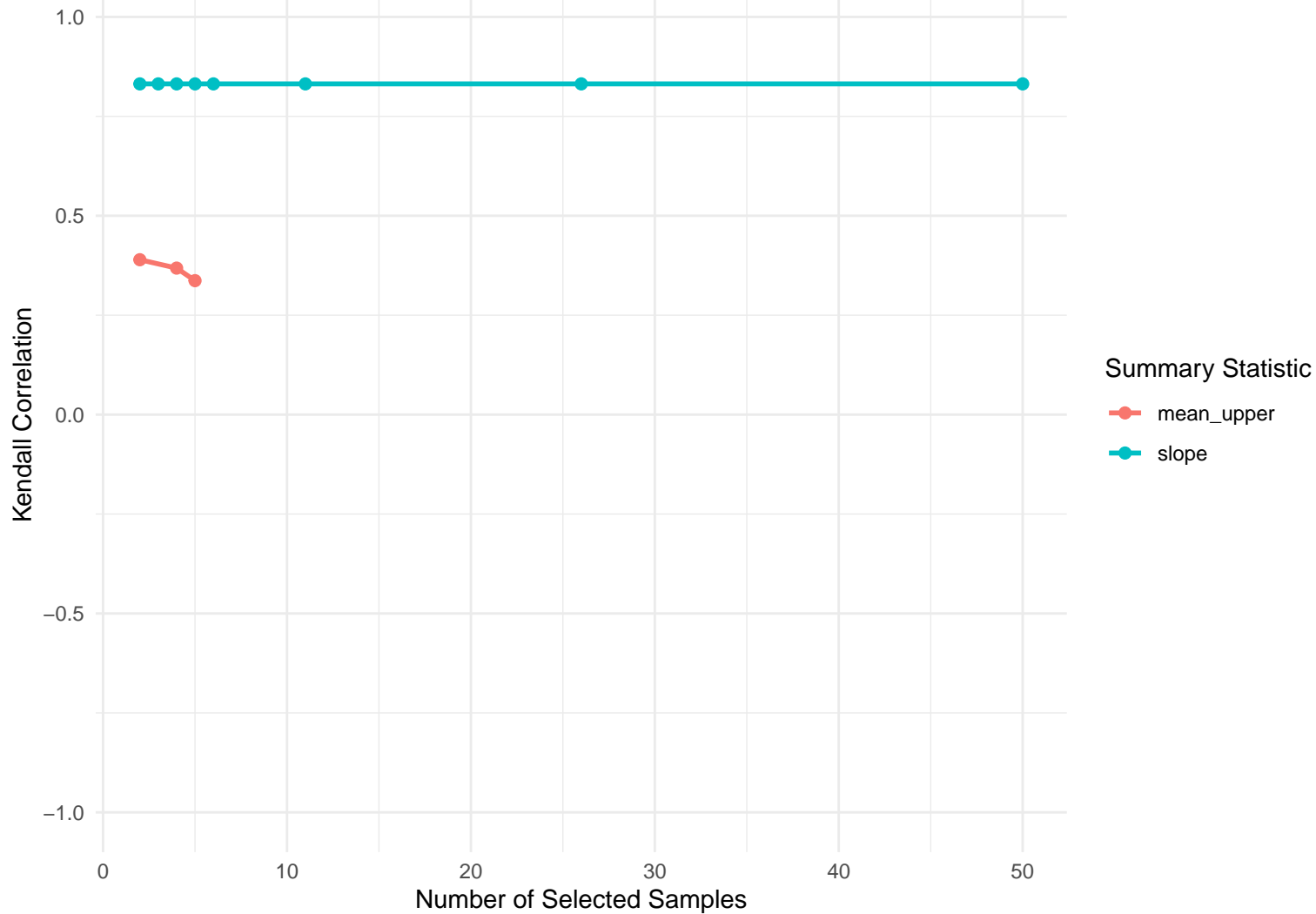
Score: PILSM (Local, full , Genotype: sinusoidal)



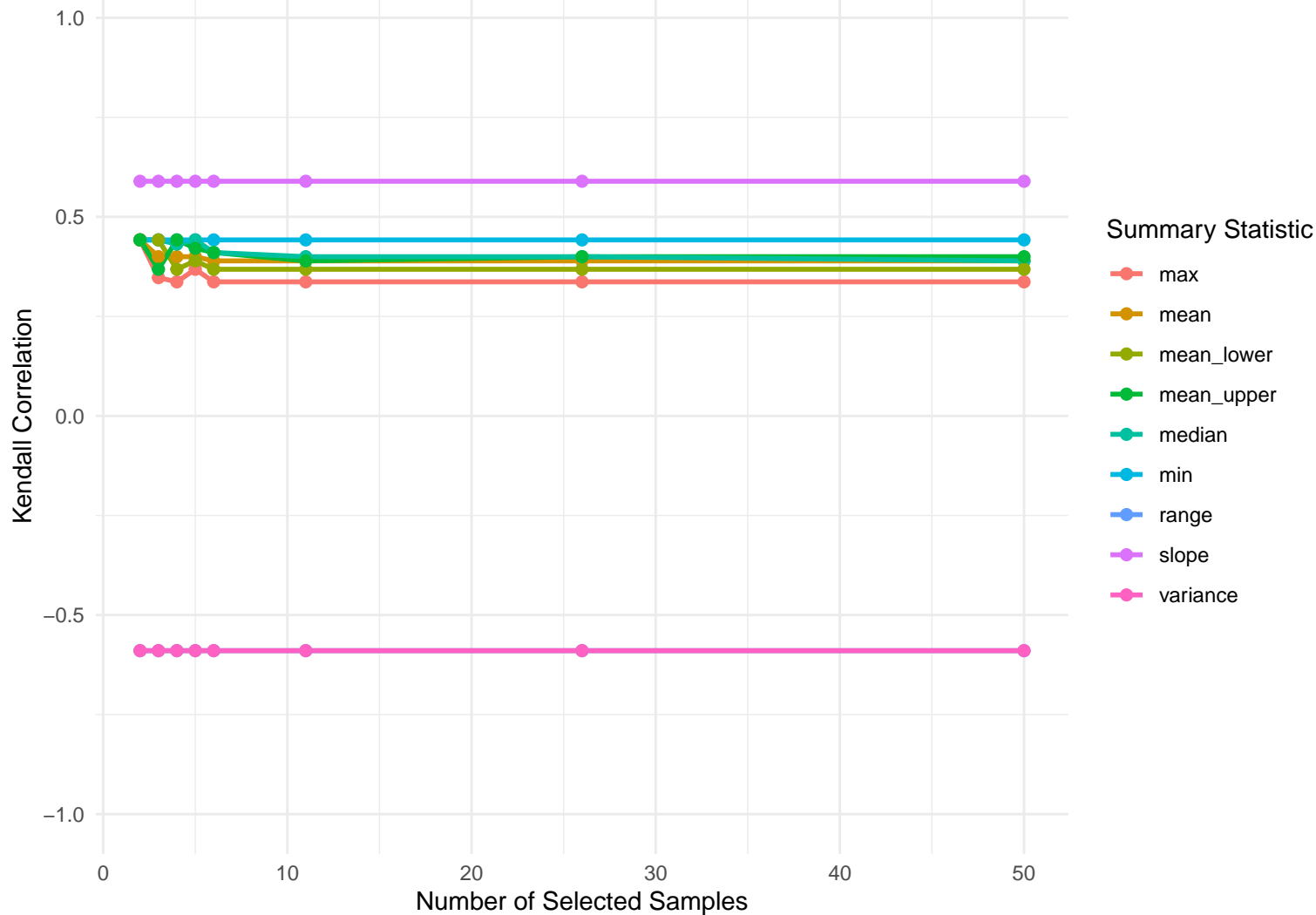
Score: PILSM (Local, full , Genotype: wave)



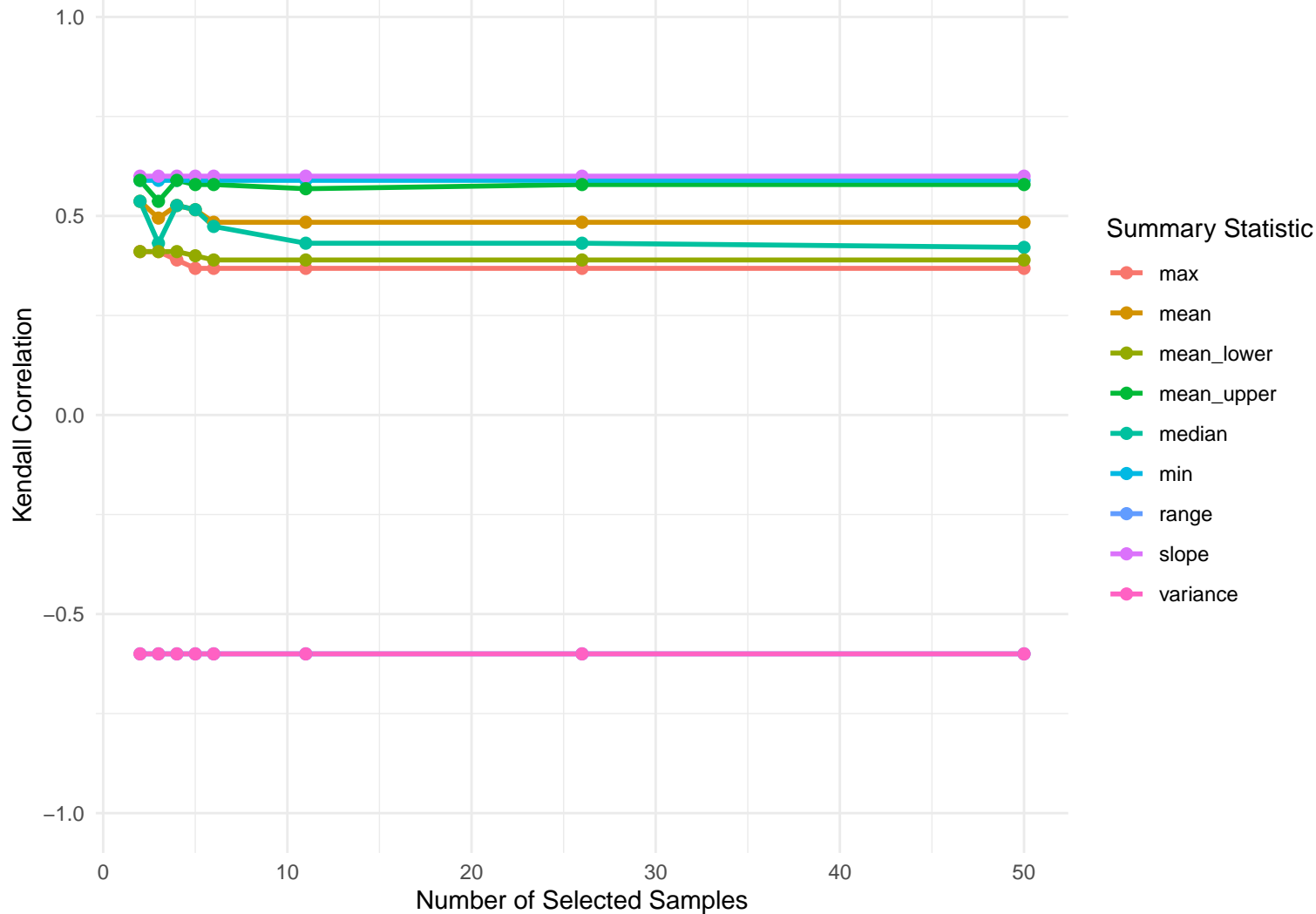
Score: RTR (Local, full , Genotype: linear)



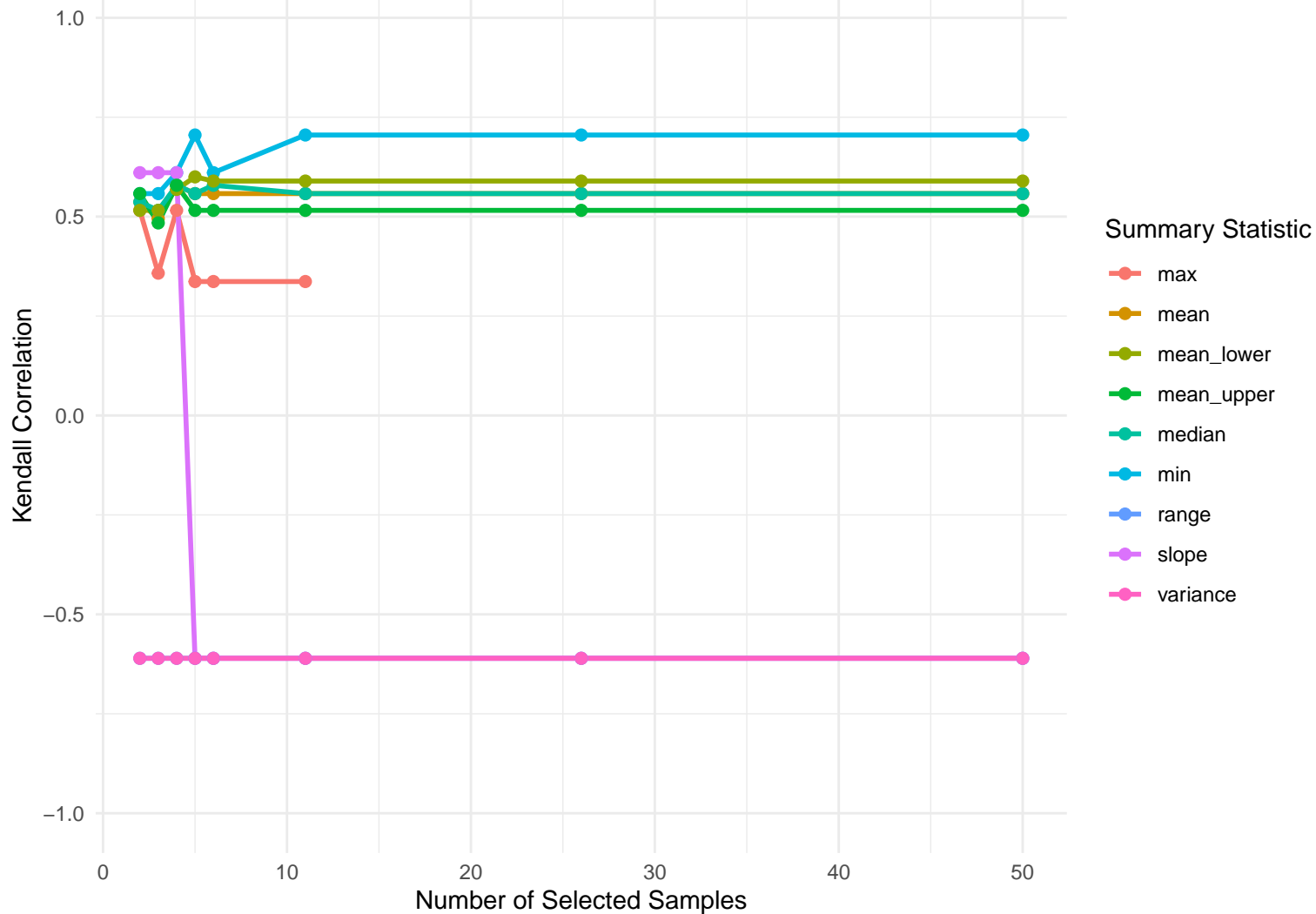
Score: RTR (Local, full , Genotype: gaussian)



Score: RTR (Local, full , Genotype: sinusoidal)

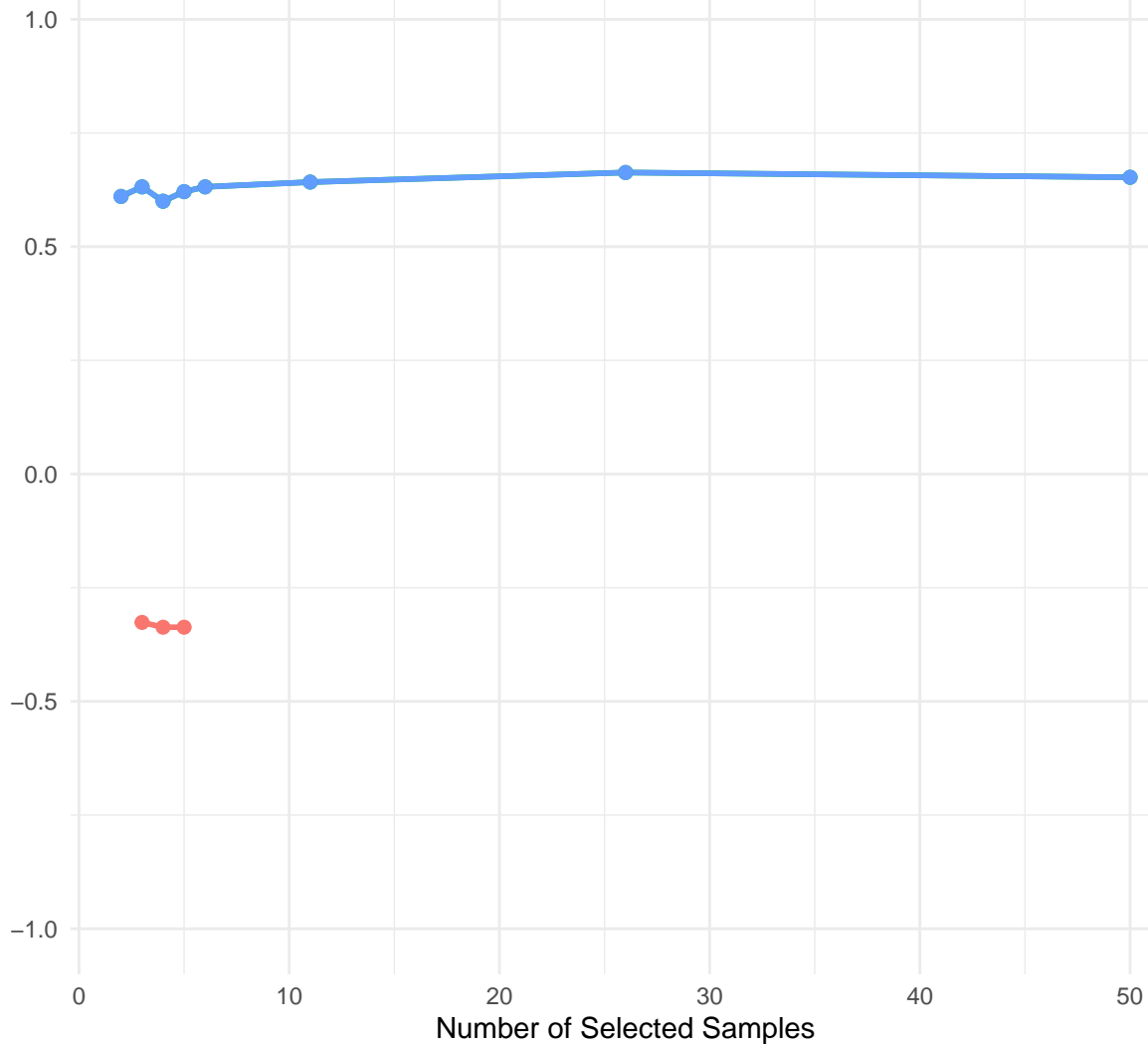


Score: RTR (Local, full , Genotype: wave)



Score: PIR (Local, full , Genotype: linear)

Kendall Correlation



Summary Statistic

- min
- range
- variance

Score: PIR (Local, full , Genotype: gaussian)



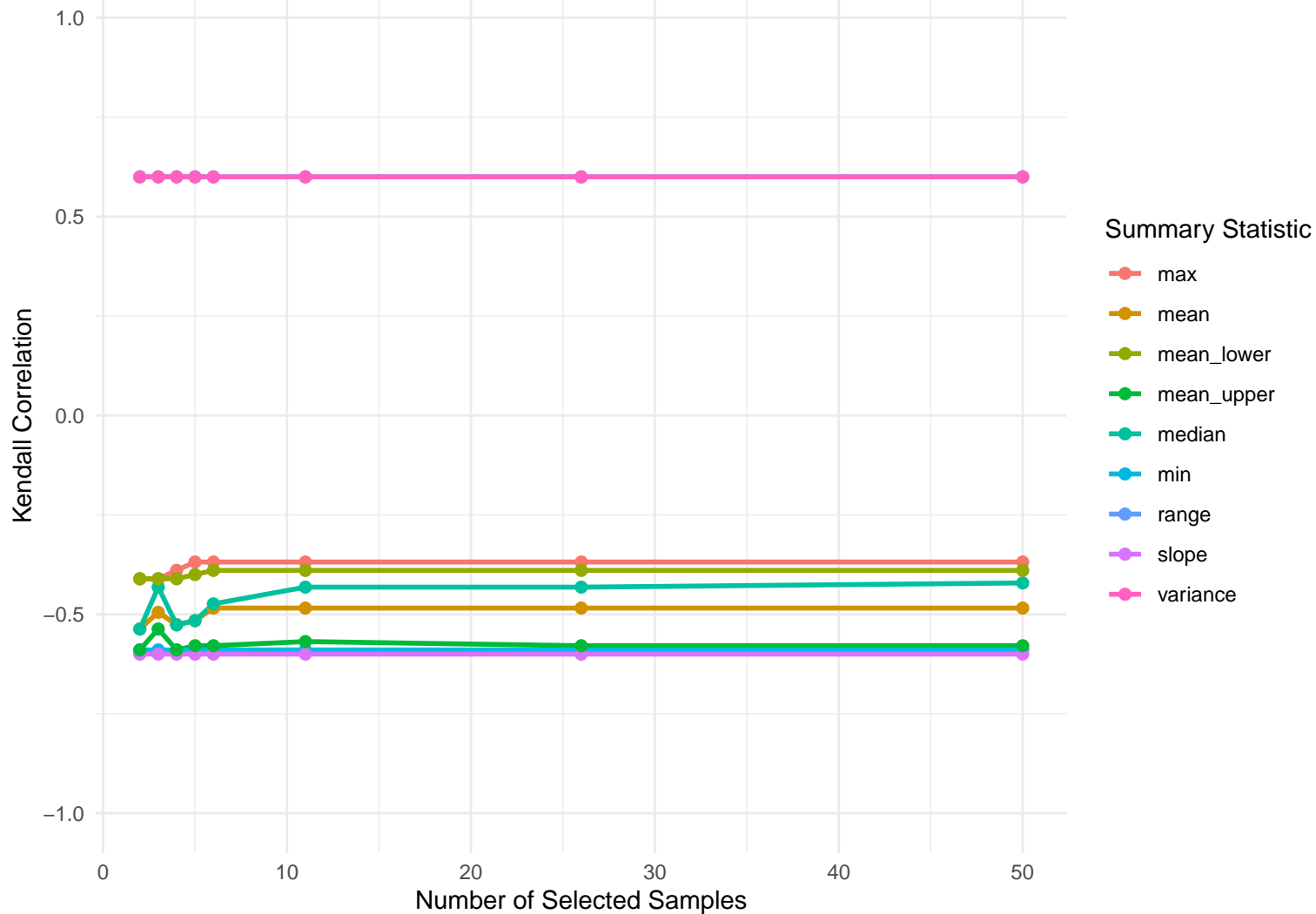
Summary Statistic

- max
- mean
- mean_lower
- mean_upper
- median
- min
- range
- slope
- variance

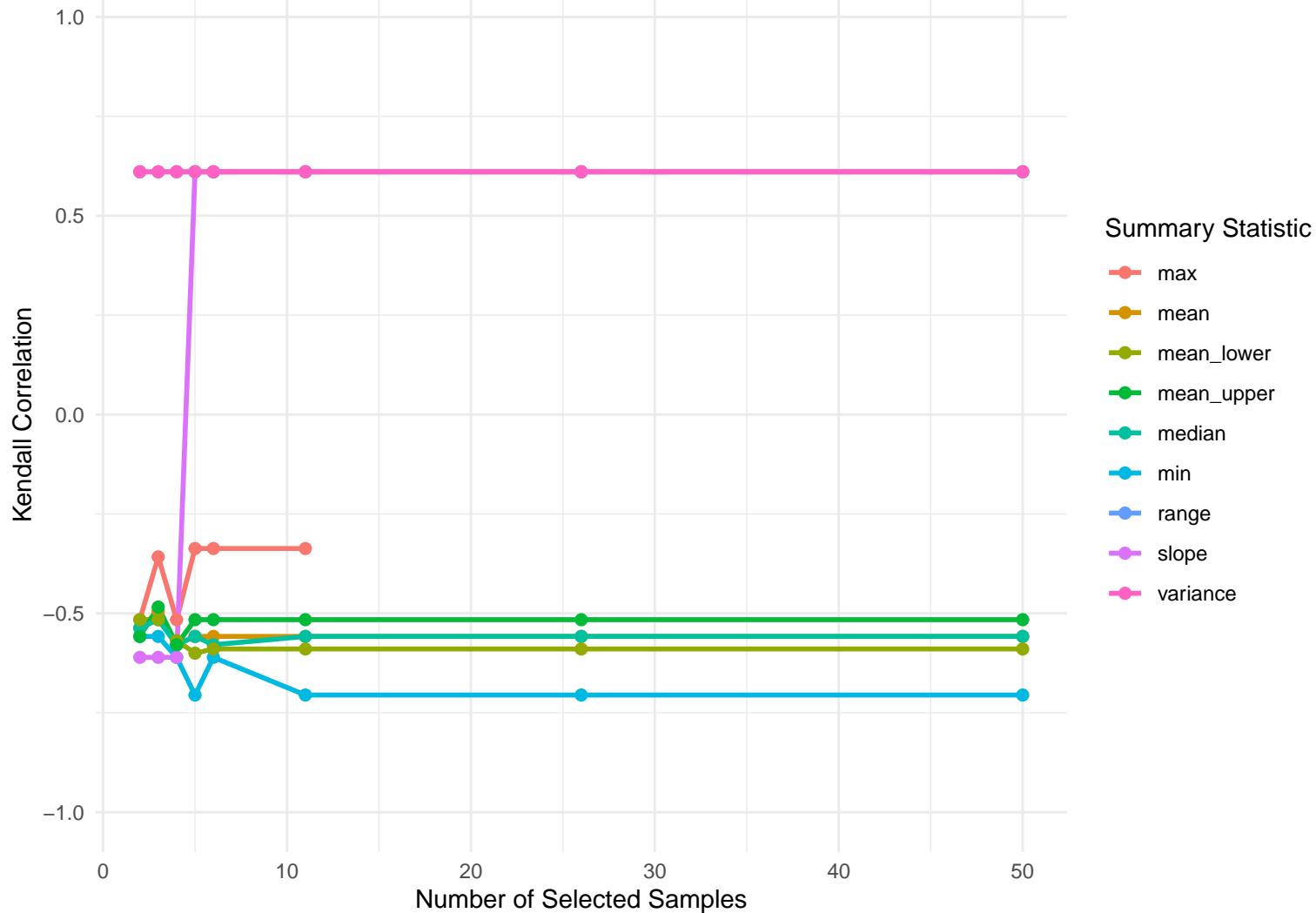
1.0
0.5
0.0
-0.5
-1.0

0 10 20 30
Number of Selected Samples

Score: PIR (Local, full , Genotype: sinusoidal)



Score: PIR (Local, full , Genotype: wave)



Summary Statistic

max

mean

mean lower

mean upper

median

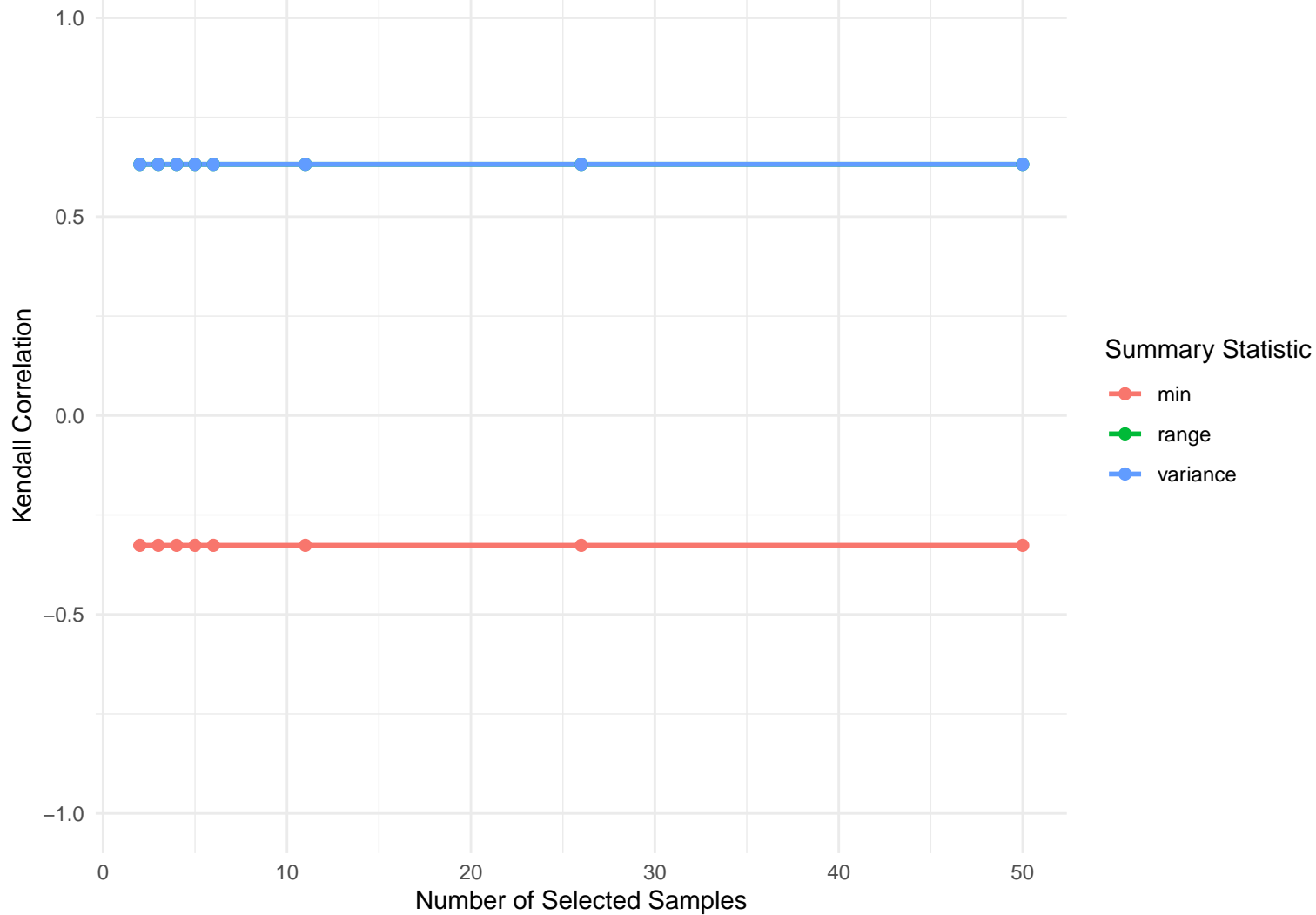
min

range

slope

variance

Score: RDPI (Local, full , Genotype: linear)



Score: RDPI (Local, full , Genotype: gaussian)

Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

0

10

20

30

40

50

Number of Selected Samples

Summary Statistic

- max
- mean
- mean_lower
- mean_upper
- median
- min
- range
- slope
- variance

0

10

20

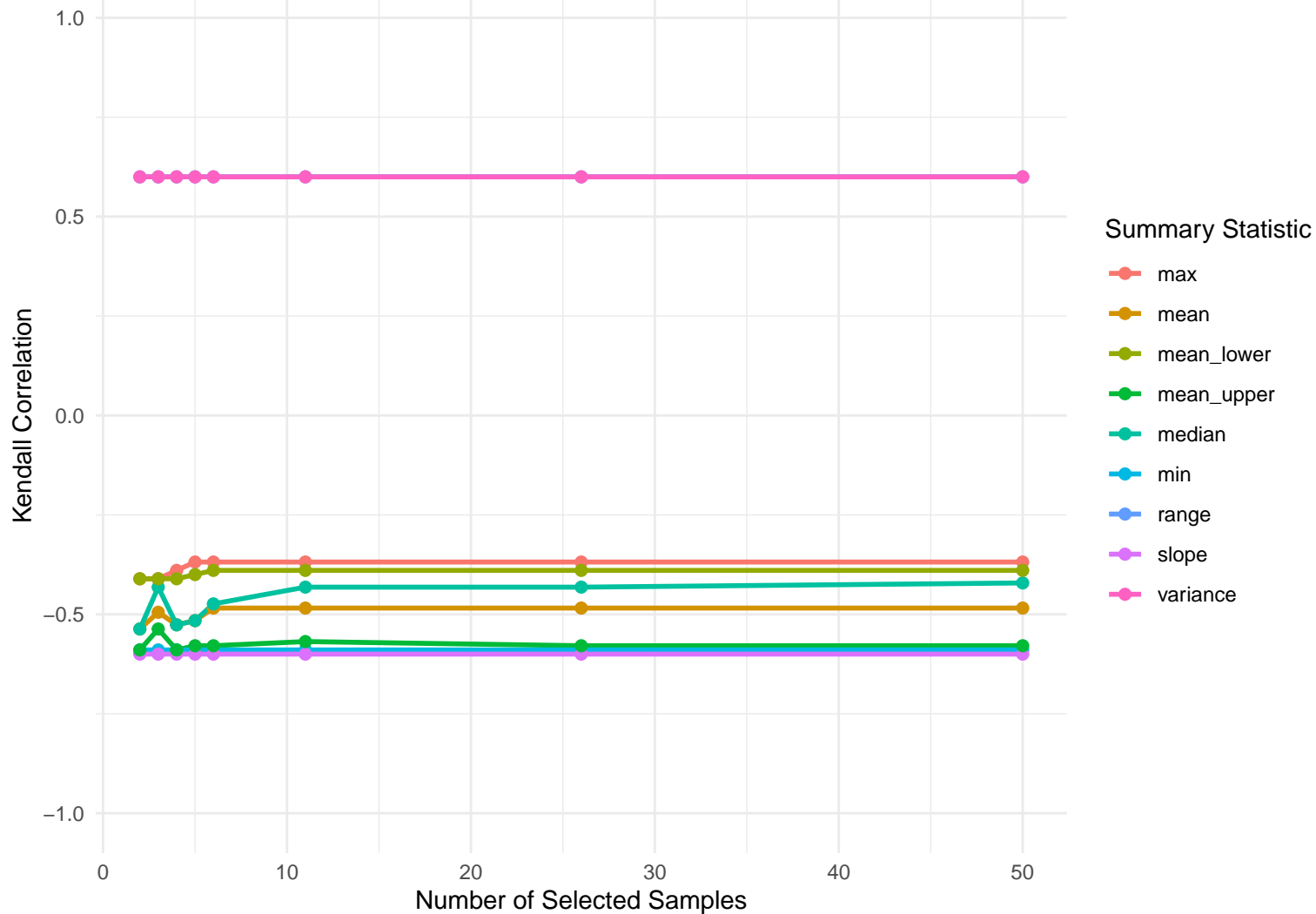
30

40

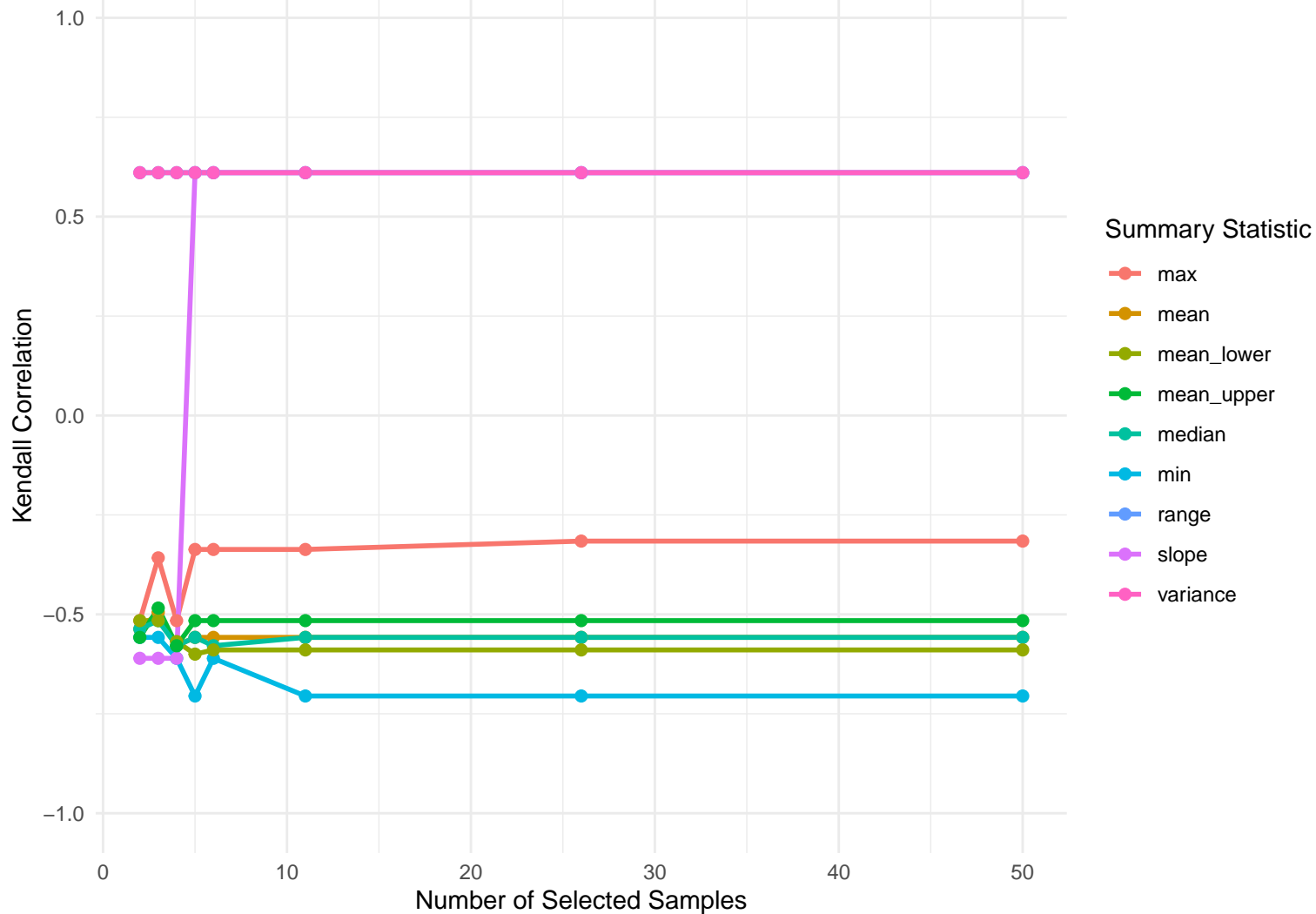
50

Number of Selected Samples

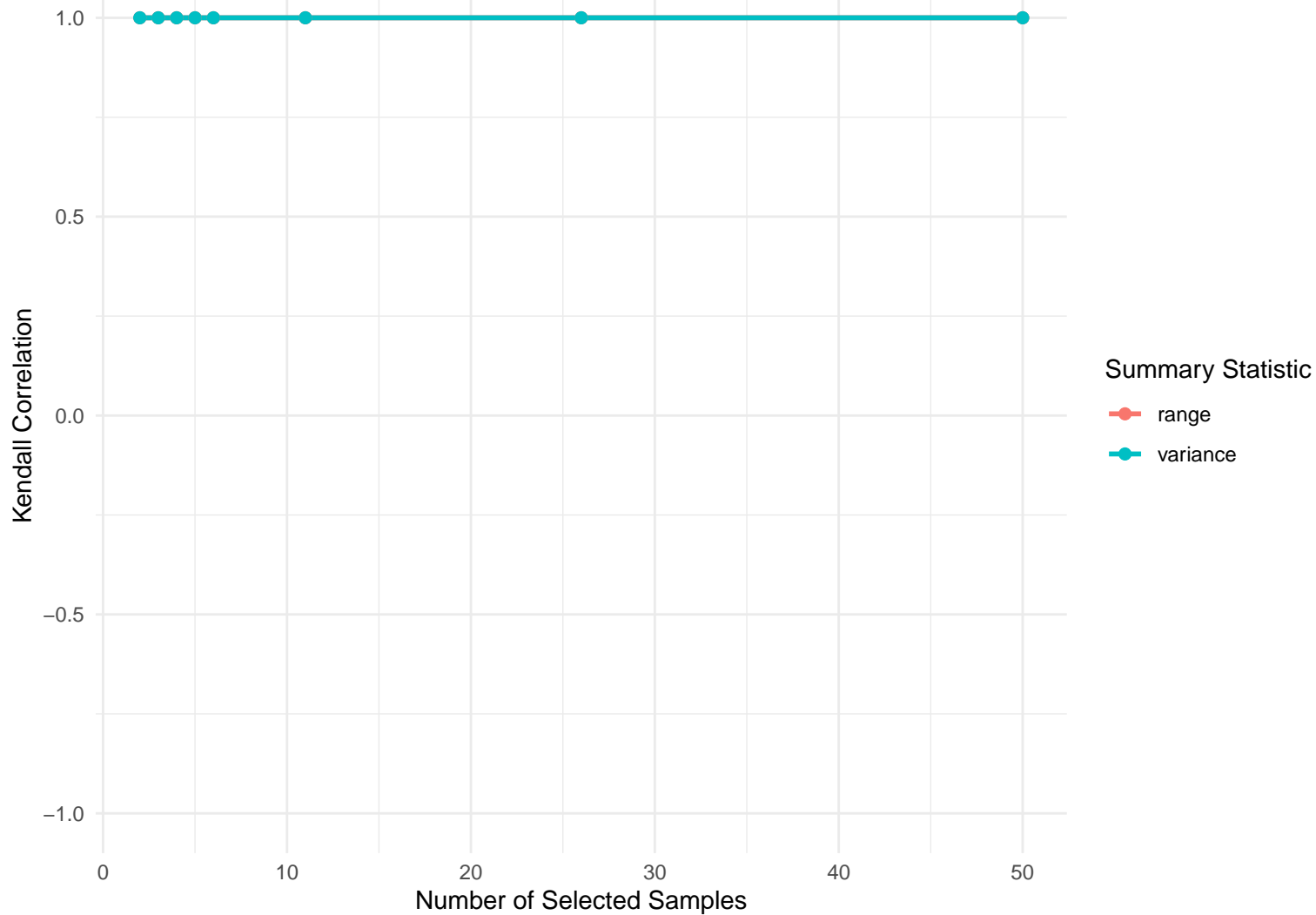
Score: RDPI (Local, full , Genotype: sinusoidal)



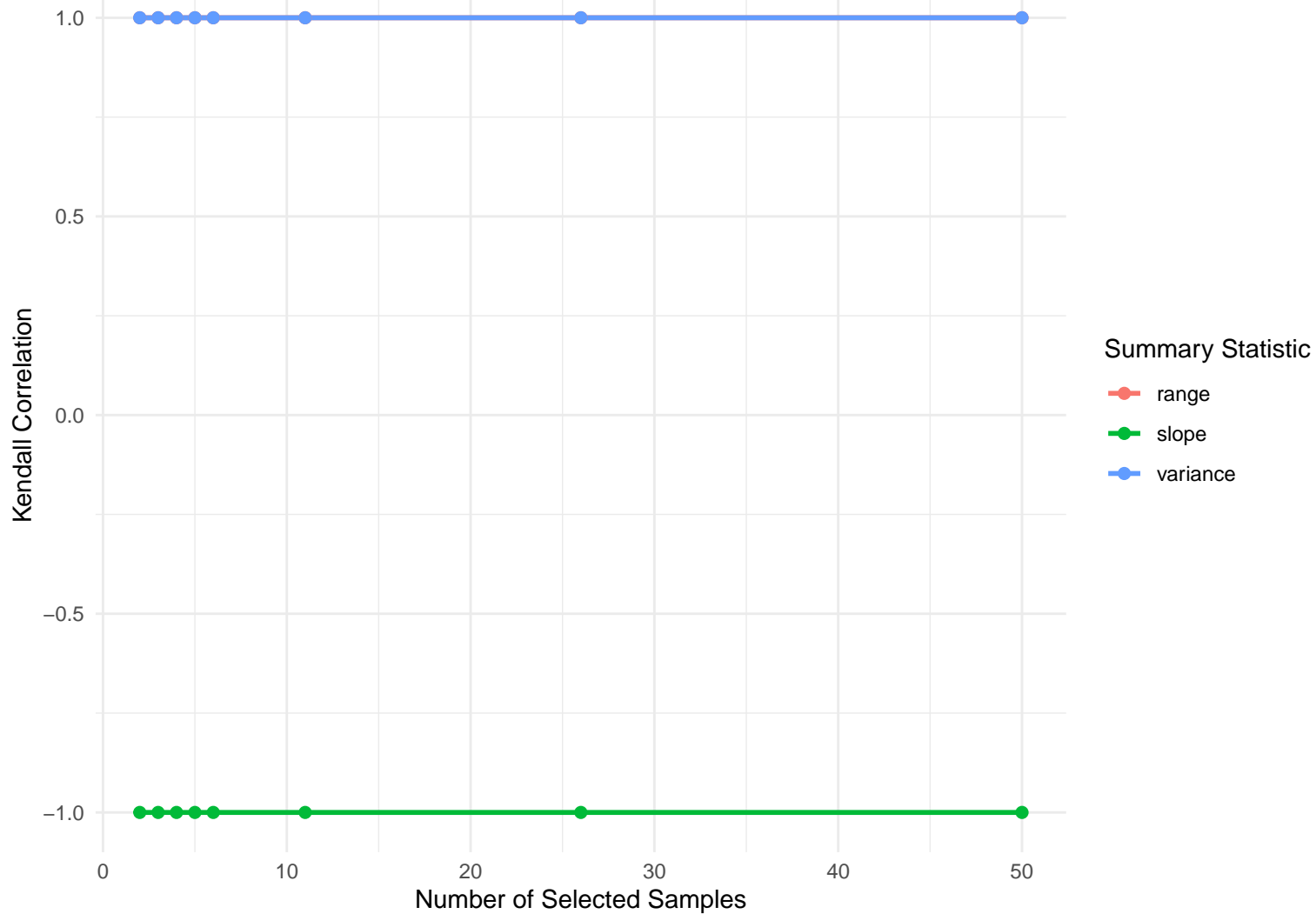
Score: RDPI (Local, full , Genotype: wave)



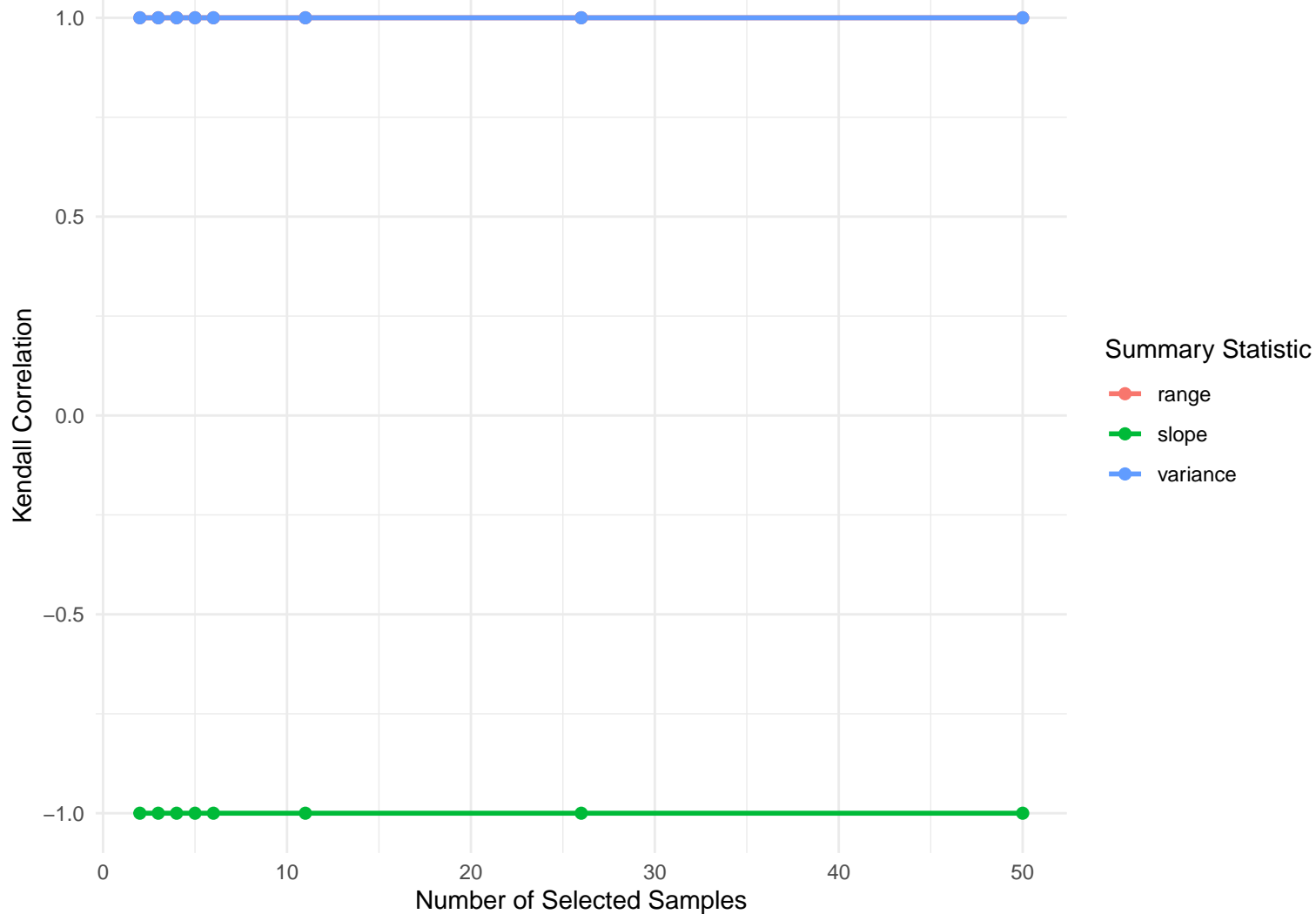
Score: ESPI (Local, full , Genotype: linear)



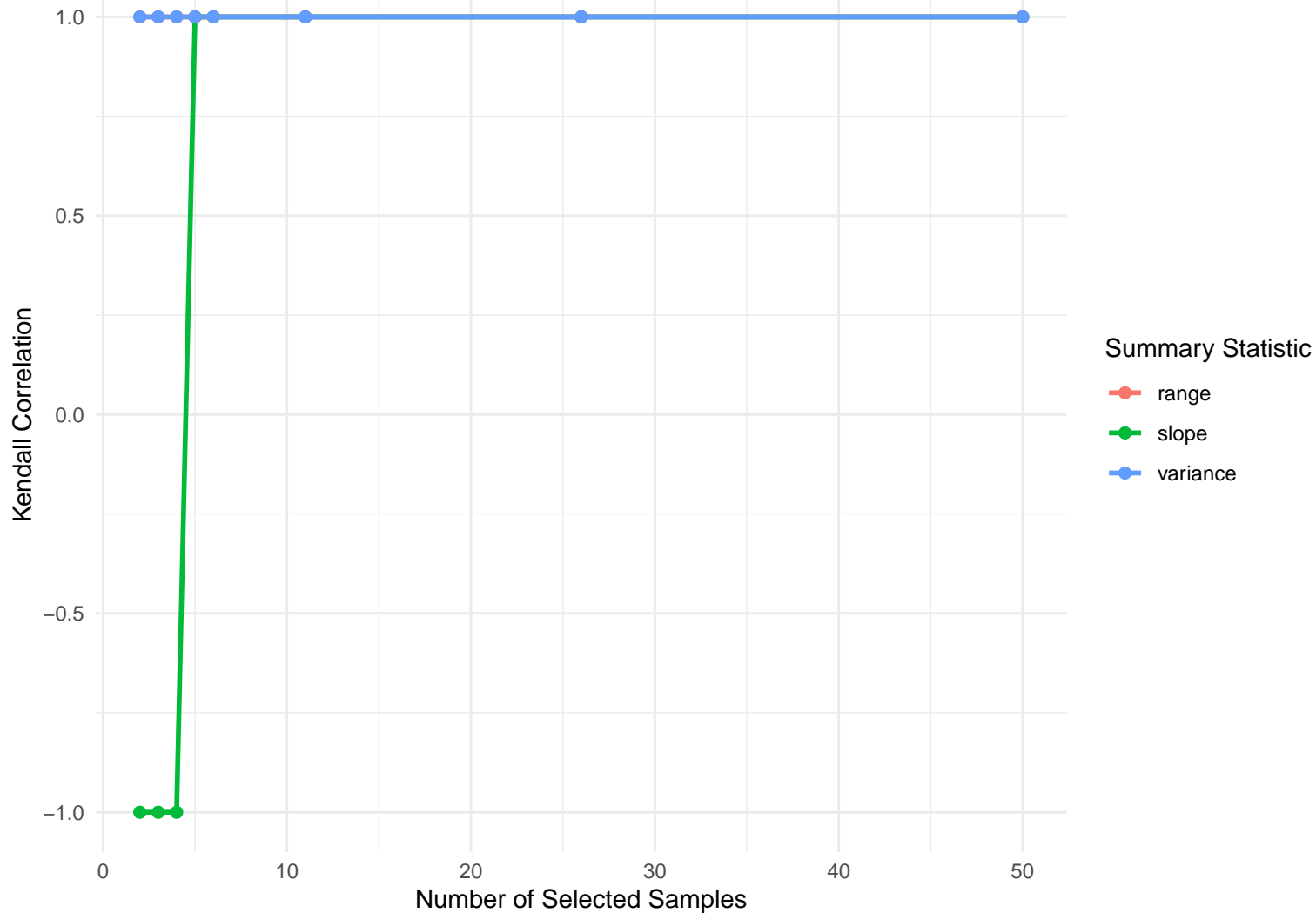
Score: ESPI (Local, full , Genotype: gaussian)



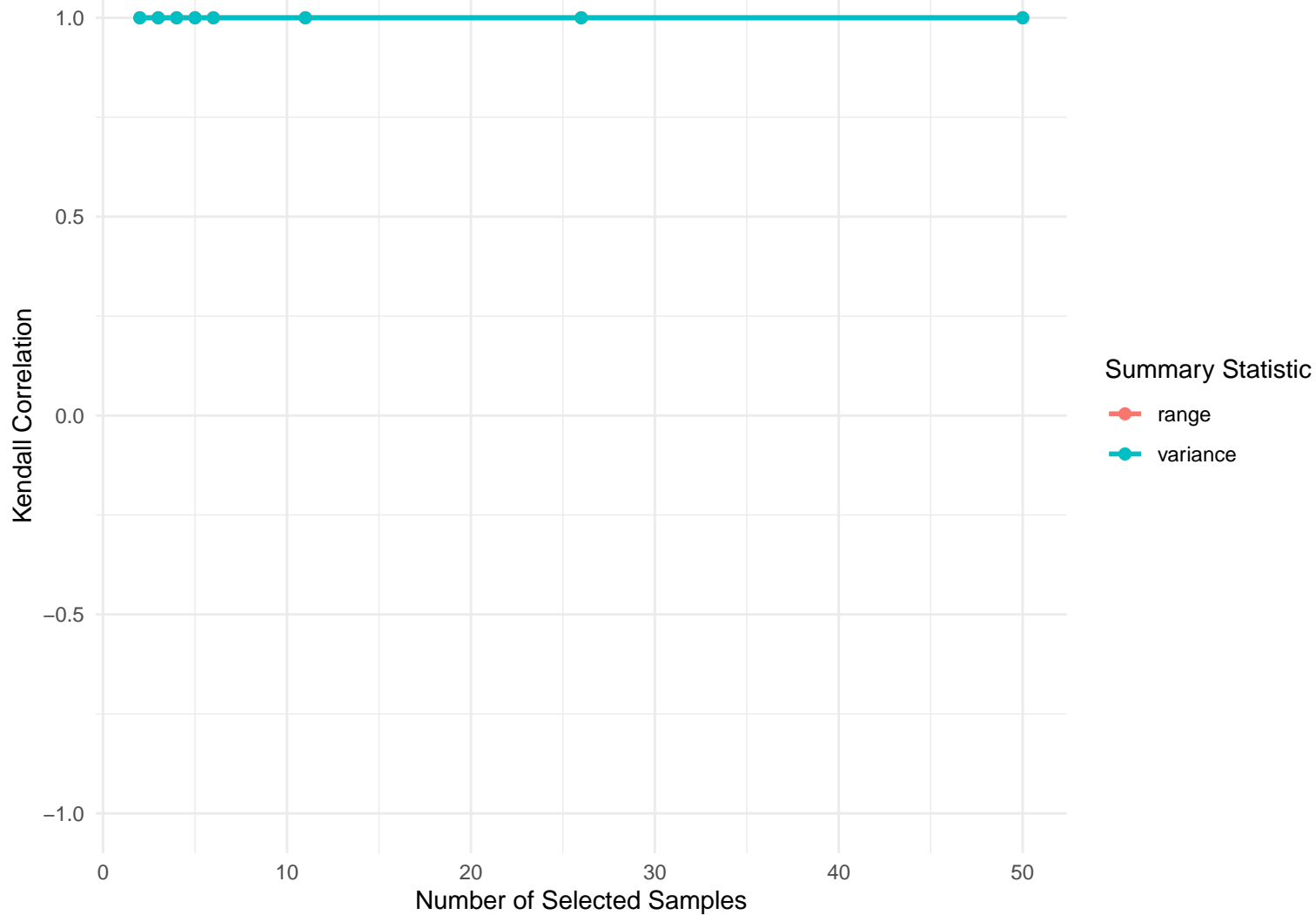
Score: ESPI (Local, full , Genotype: sinusoidal)



Score: ESPI (Local, full , Genotype: wave)



Score: ESPIID (Local, full , Genotype: linear)



Score: ESPIID (Local, full , Genotype: gaussian)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

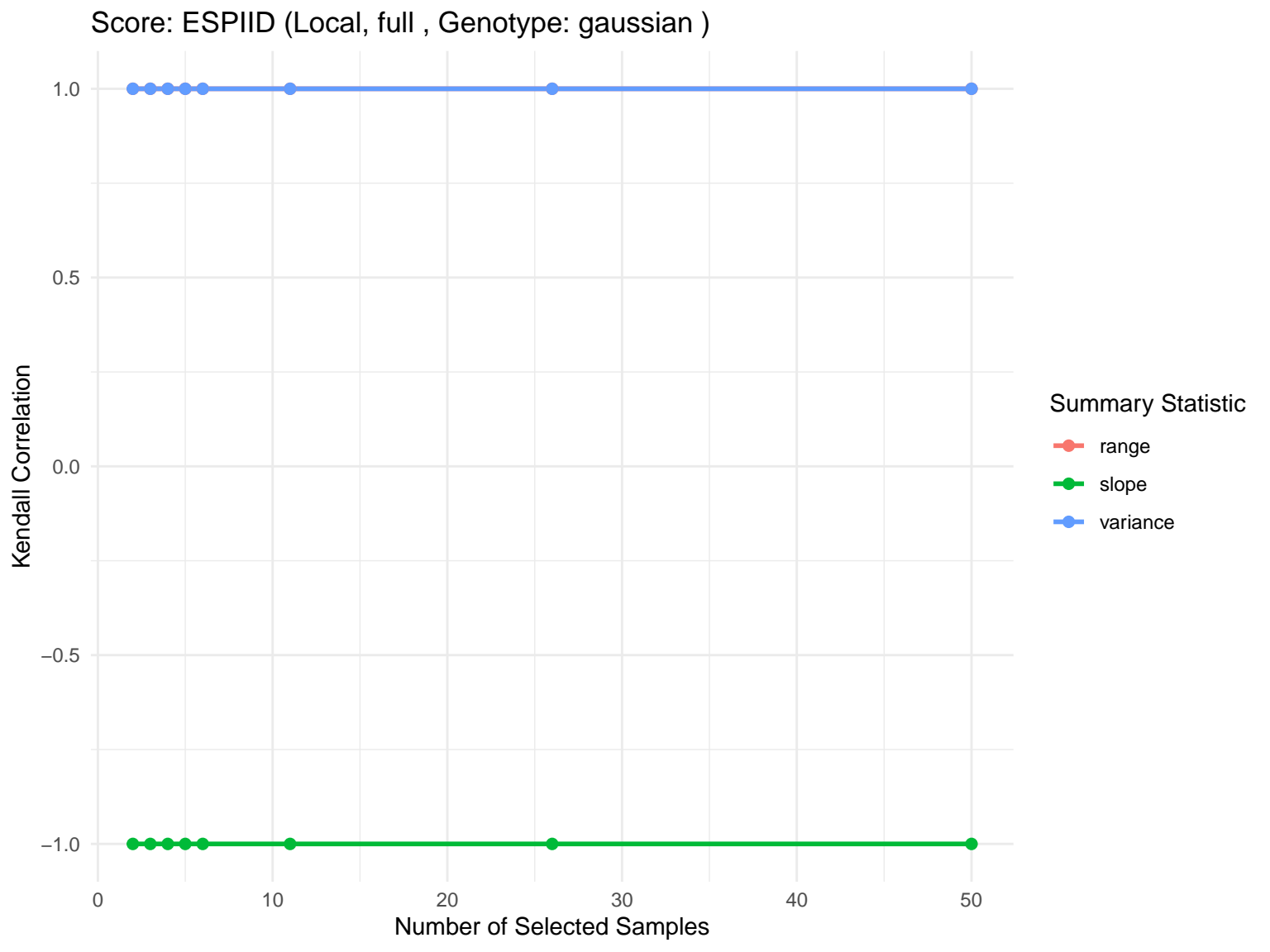
40

50

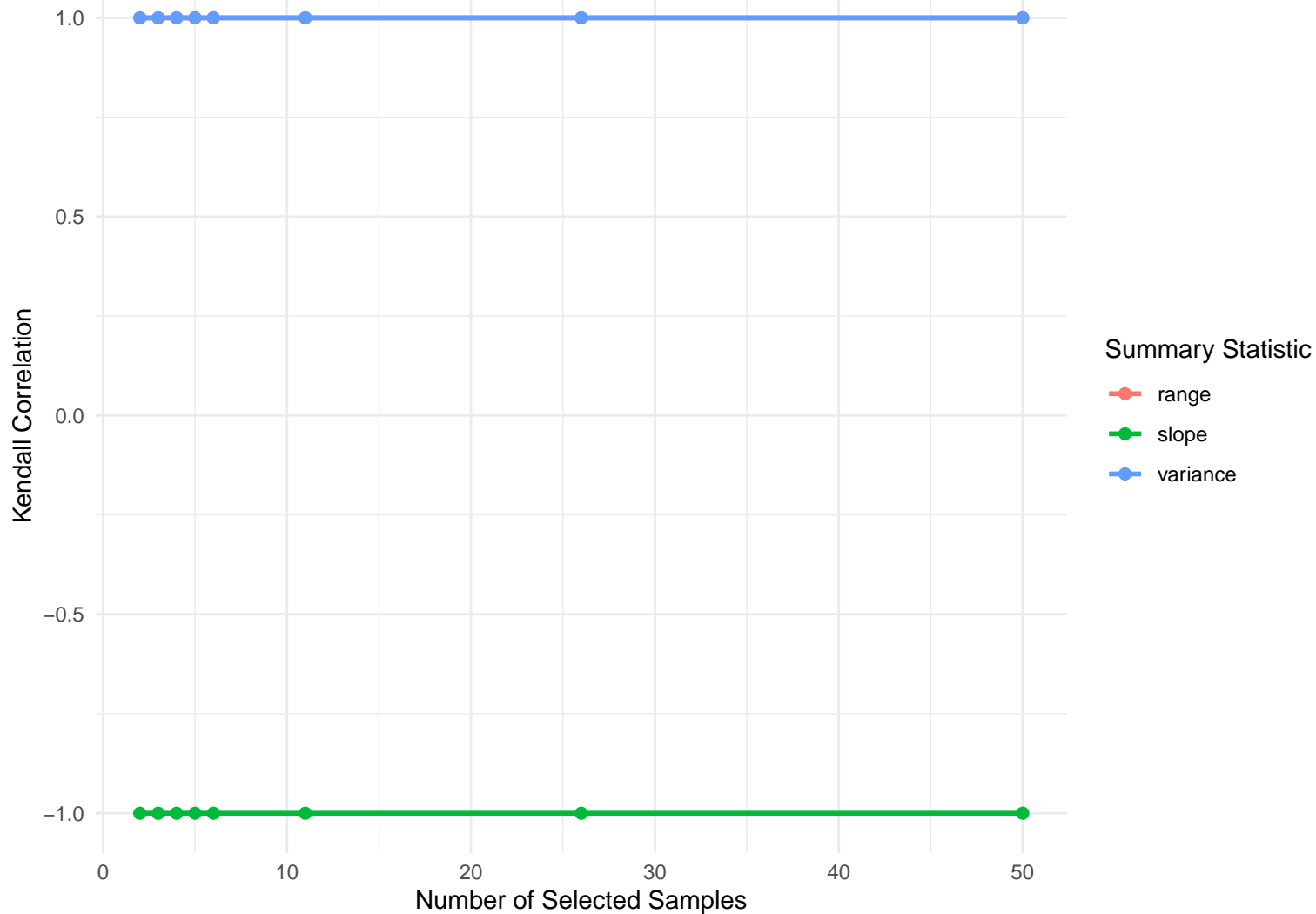
Number of Selected Samples

Summary Statistic

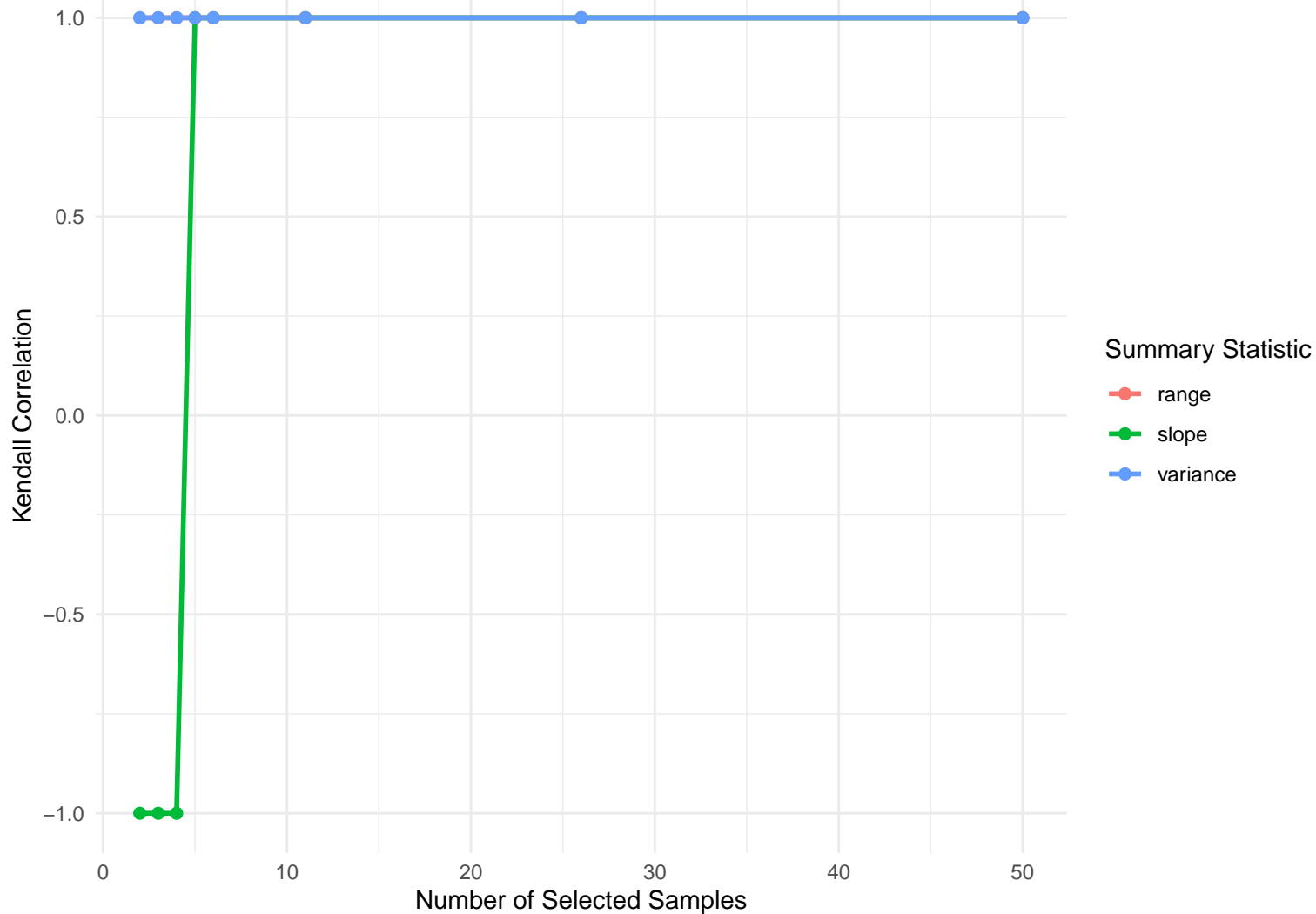
- range
- slope
- variance



Score: ESPIID (Local, full , Genotype: sinusoidal)

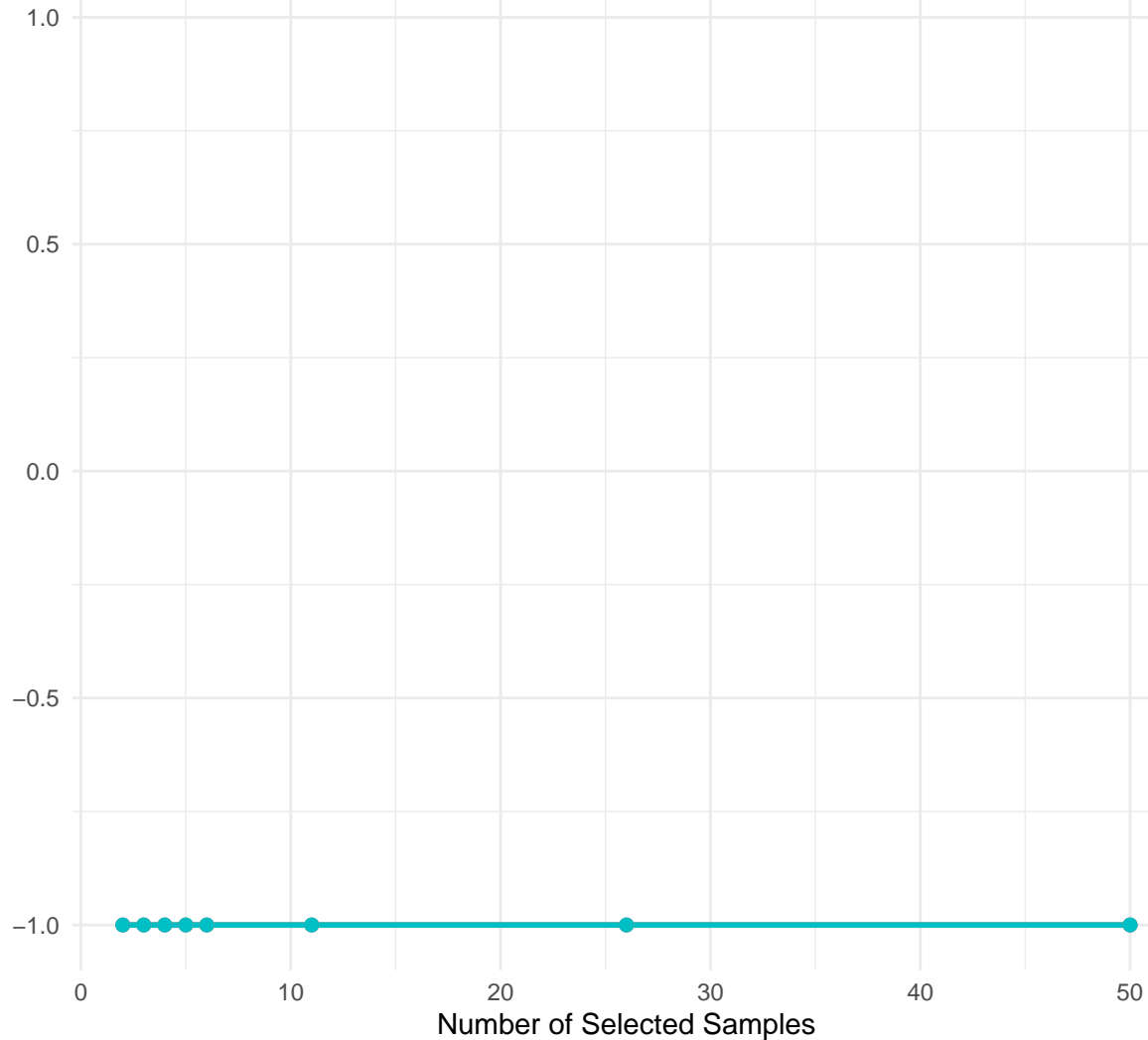


Score: ESPIID (Local, full , Genotype: wave)



Score: PSI (Local, full , Genotype: linear)

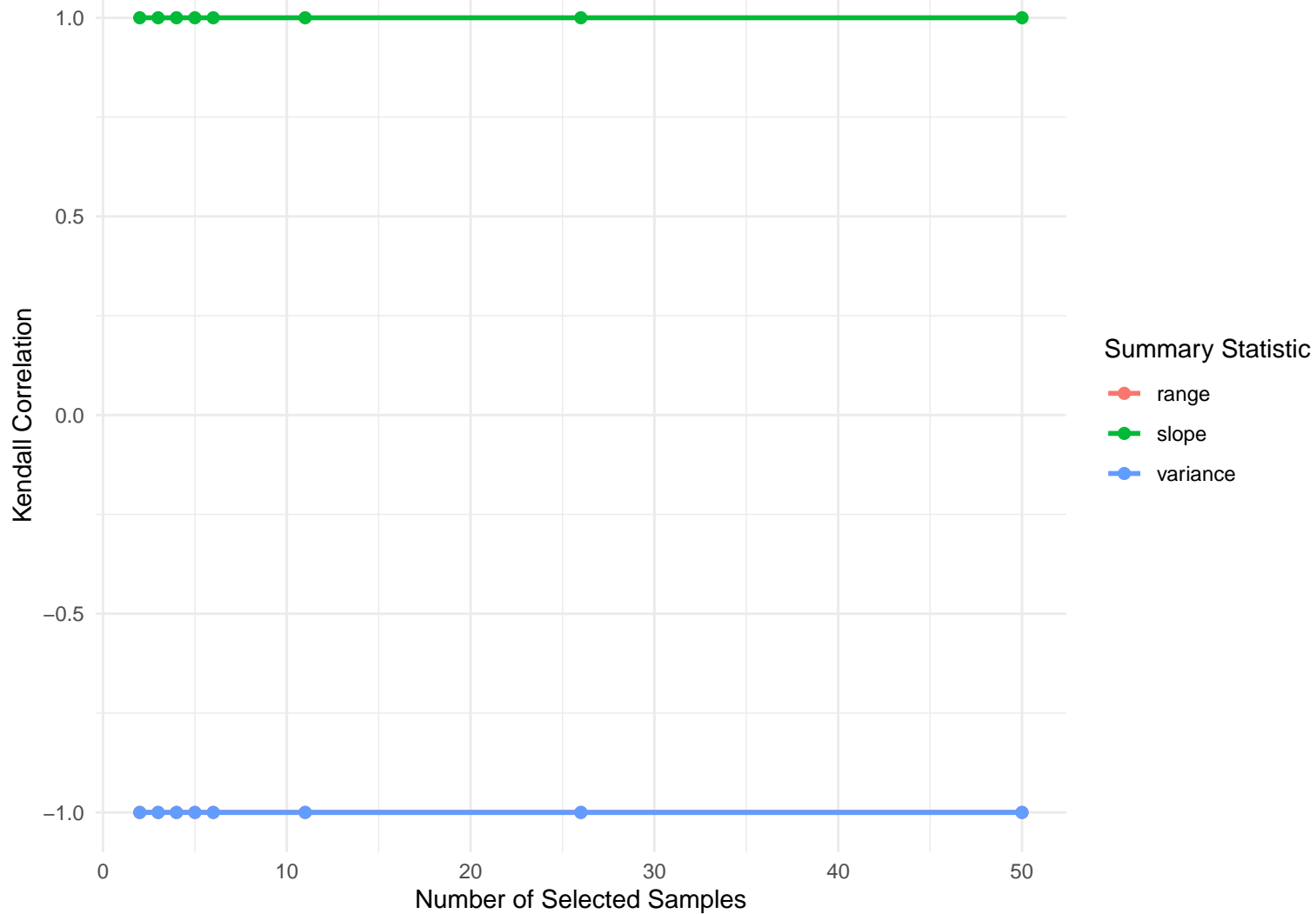
Kendall Correlation



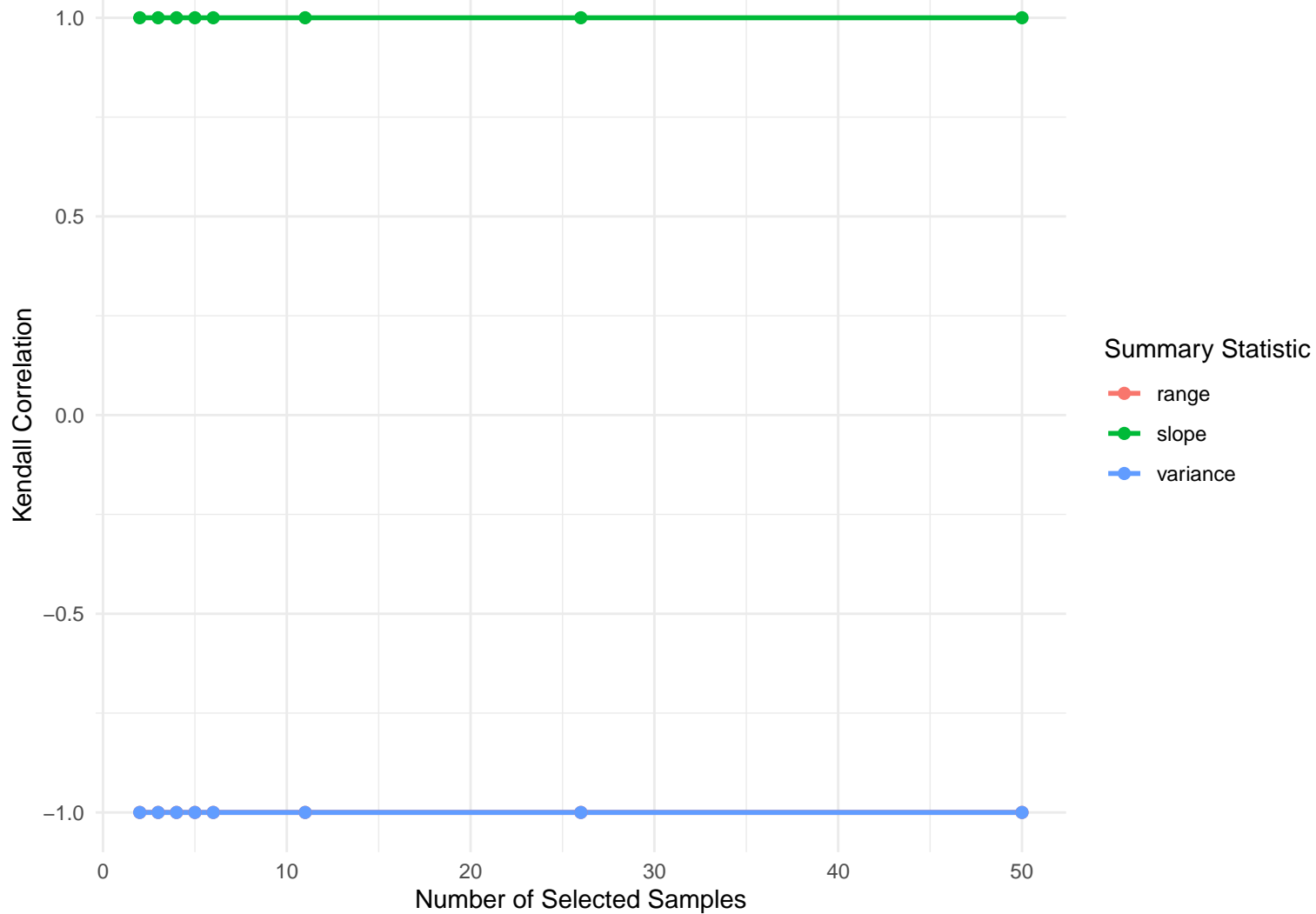
Summary Statistic

- range
- variance

Score: PSI (Local, full , Genotype: gaussian)



Score: PSI (Local, full , Genotype: sinusoidal)



Score: PSI (Local, full , Genotype: wave)

Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

0

10

20

30

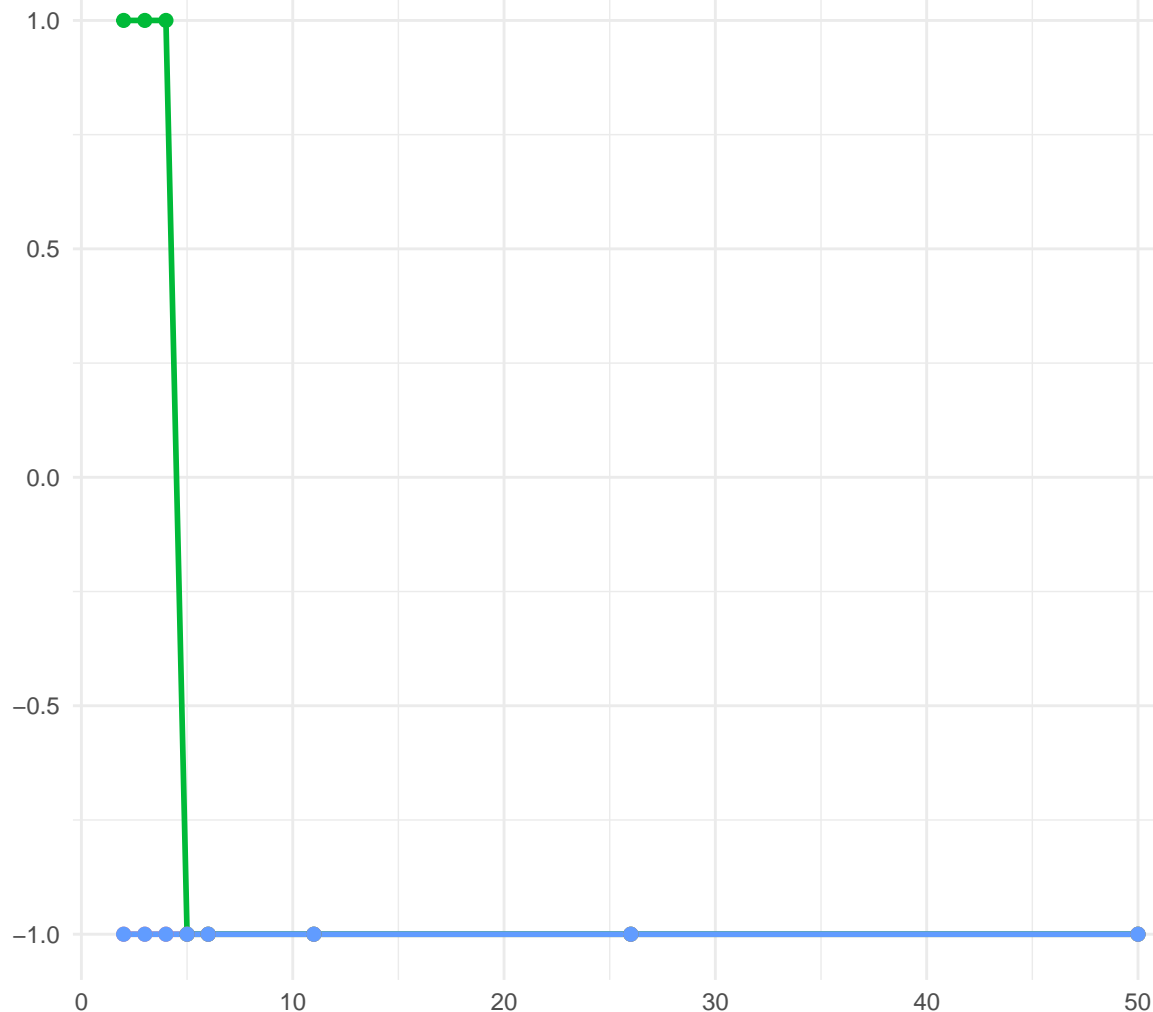
40

50

Number of Selected Samples

Summary Statistic

- range
- slope
- variance



Score: RPI (Local, full , Genotype: linear)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

40

50

Number of Selected Samples

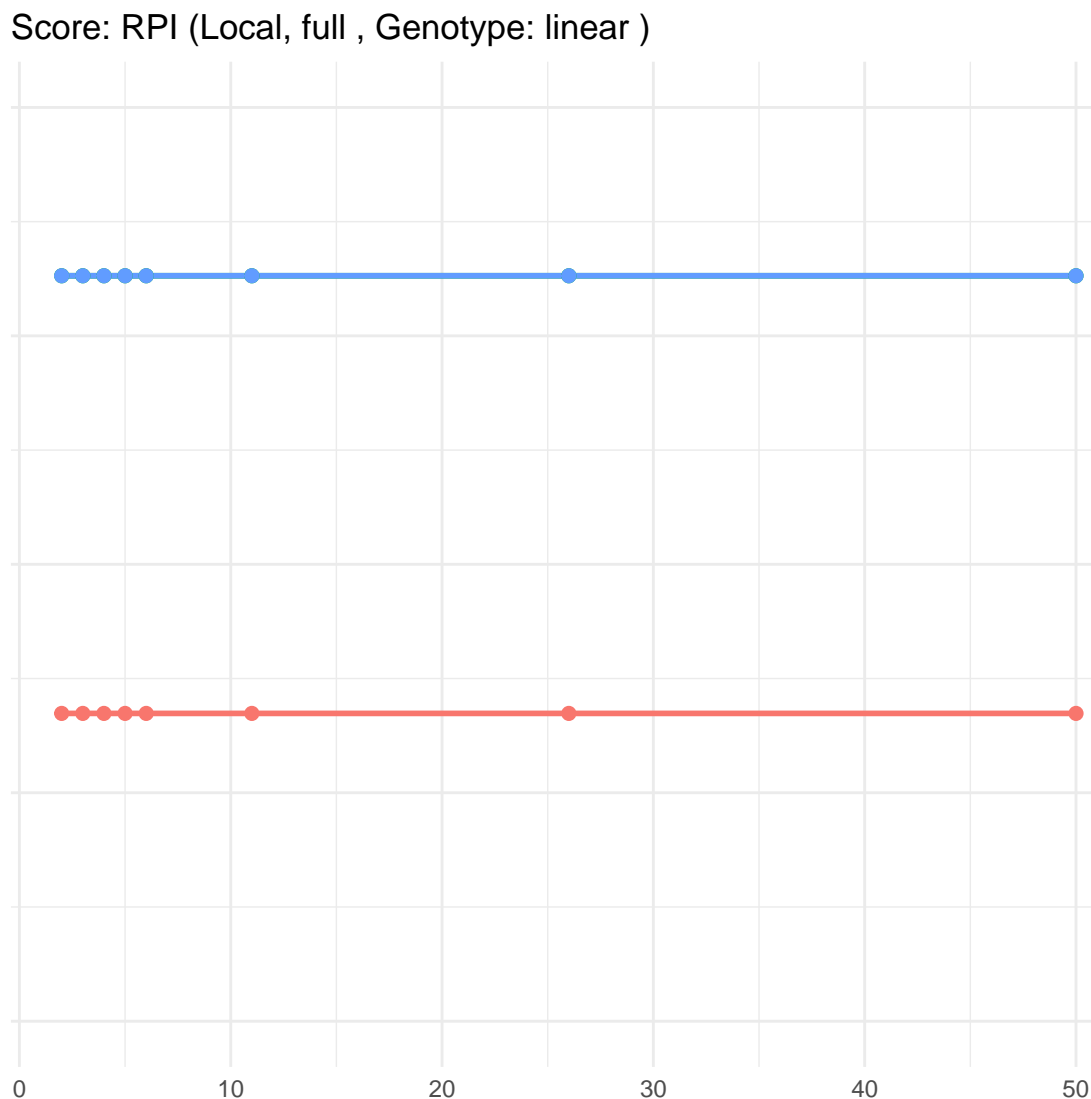
Summary Statistic

min

range

variance

min
range
variance



Score: RPI (Local, full , Genotype: gaussian)



Summary Statistic

max

mean

mean_lower

mean_upper

median

min

range

slope

variance

Number of Selected Samples

Score: RPI (Local, full , Genotype: sinusoidal)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

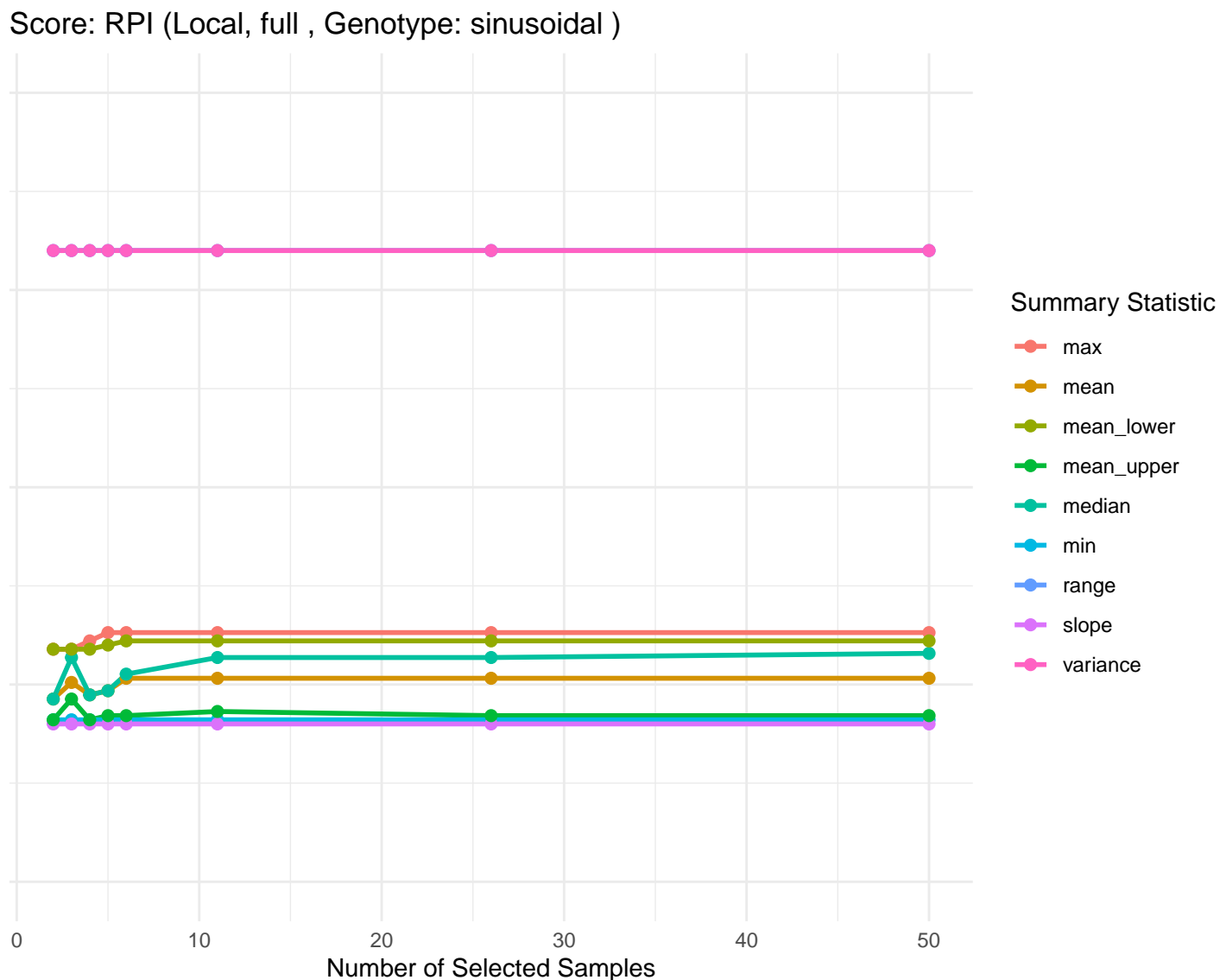
40

50

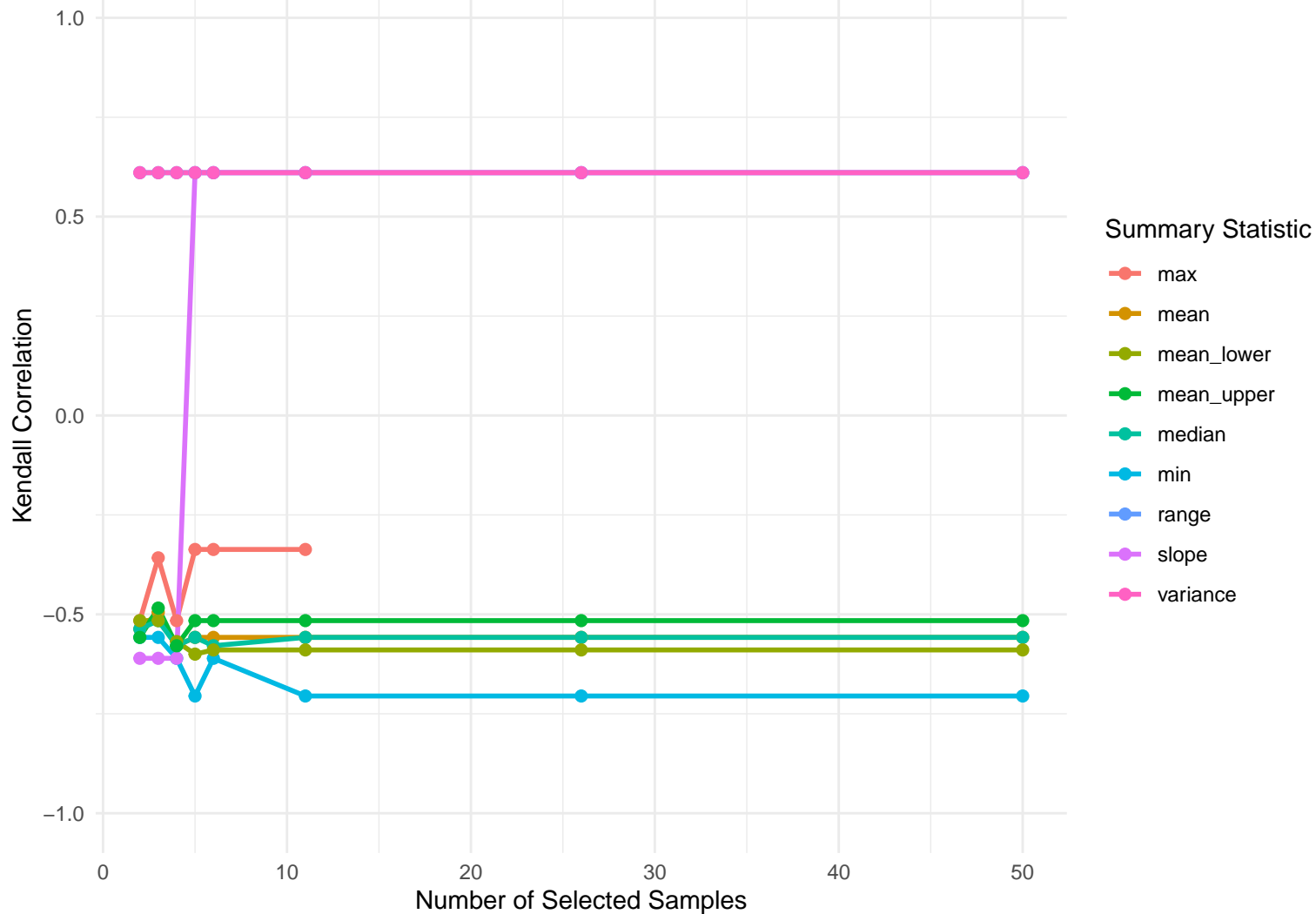
Number of Selected Samples

Summary Statistic

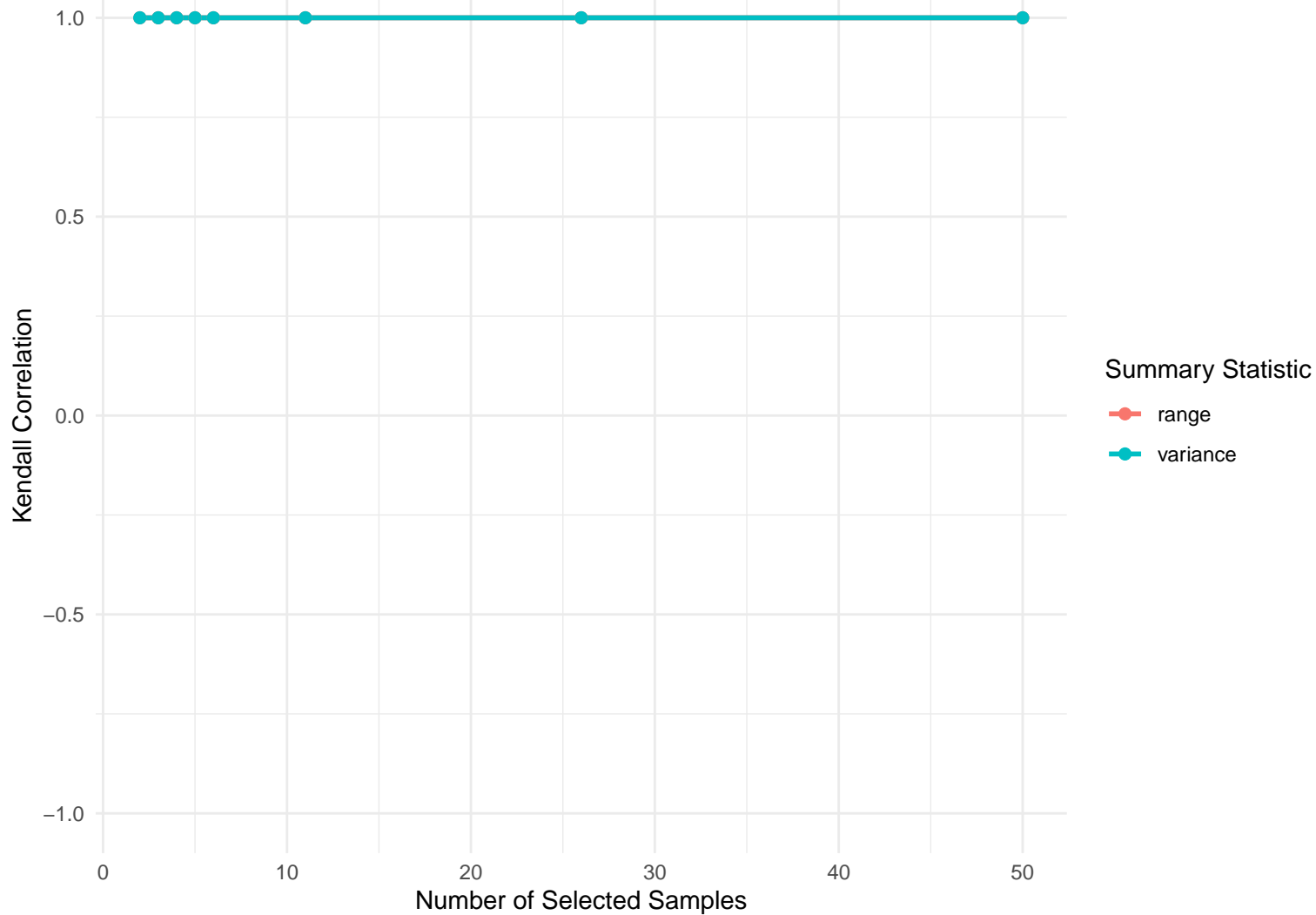
- max
- mean
- mean_lower
- mean_upper
- median
- min
- range
- slope
- variance



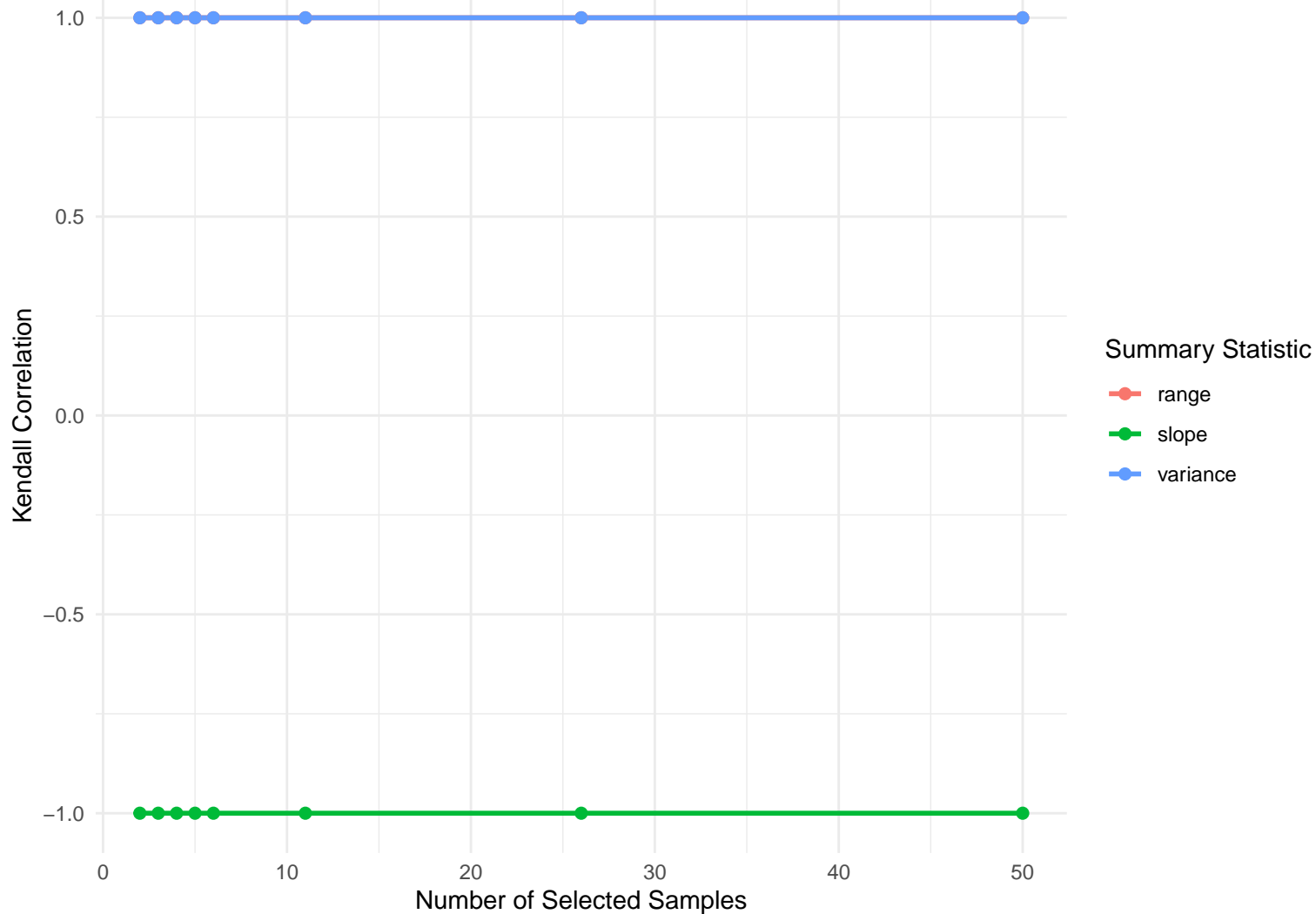
Score: RPI (Local, full , Genotype: wave)



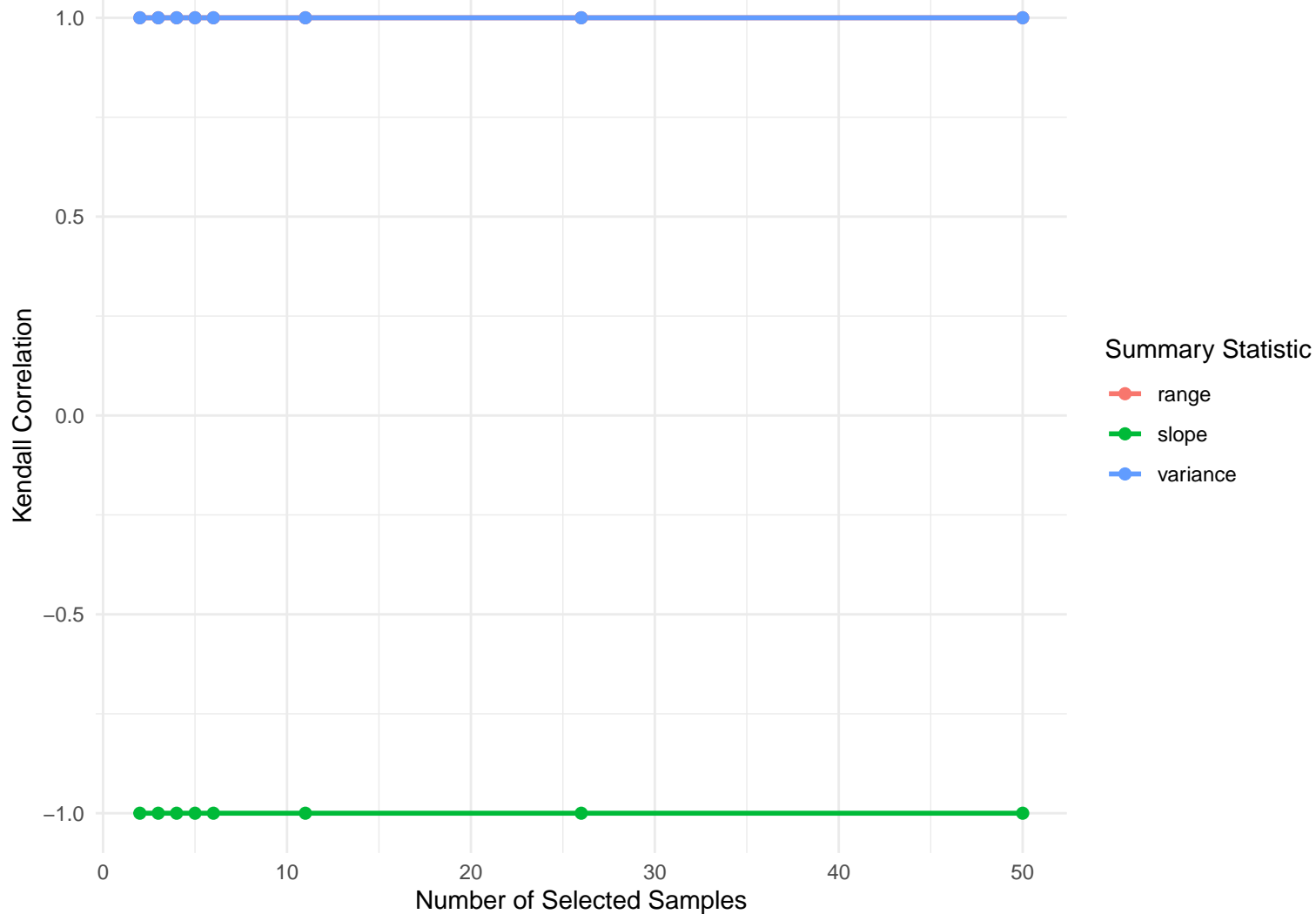
Score: PQ (Local, full , Genotype: linear)



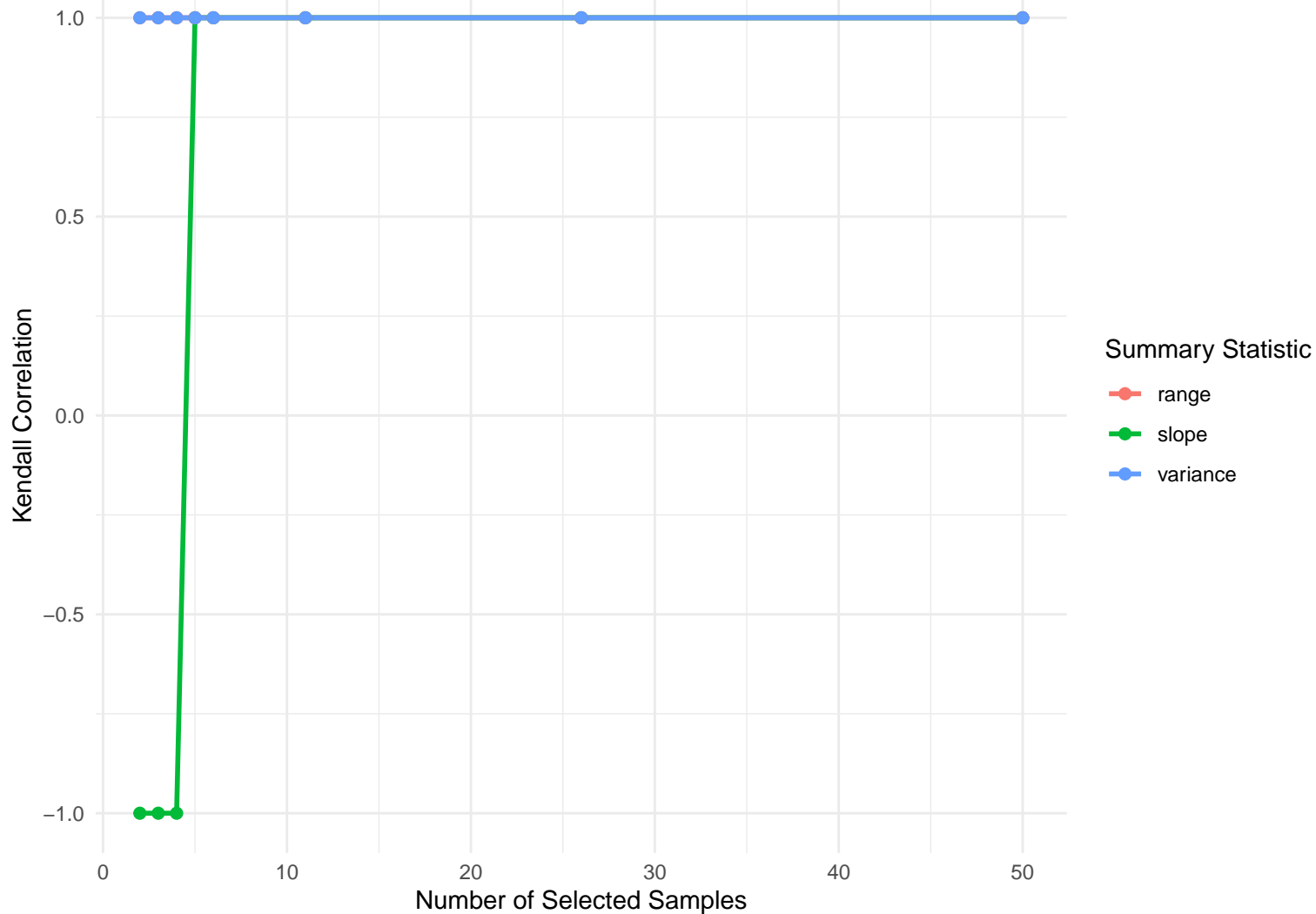
Score: PQ (Local, full , Genotype: gaussian)



Score: PQ (Local, full , Genotype: sinusoidal)



Score: PQ (Local, full , Genotype: wave)



Score: PR (Local, full , Genotype: linear)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

40

50

Number of Selected Samples

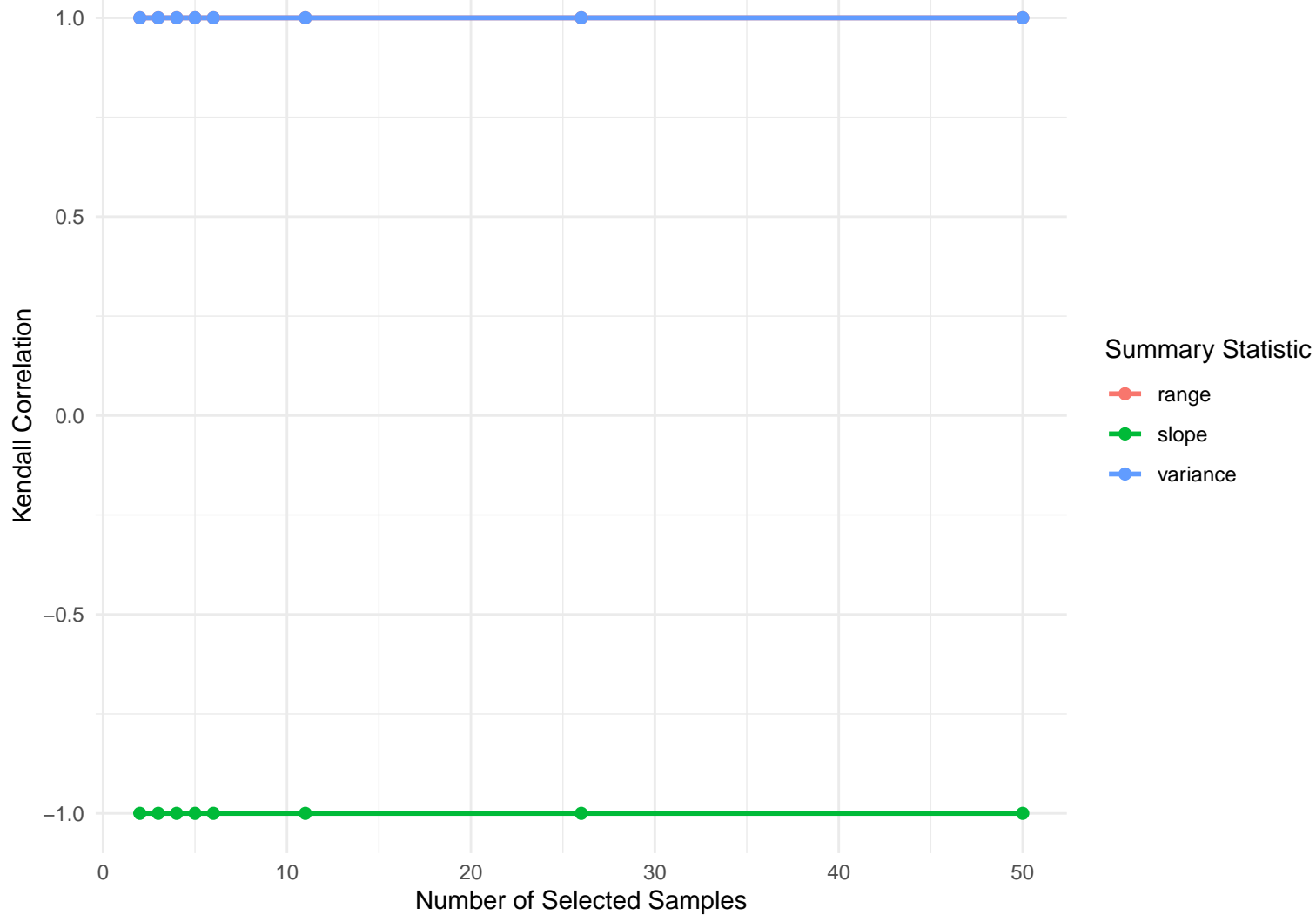
Summary Statistic

range

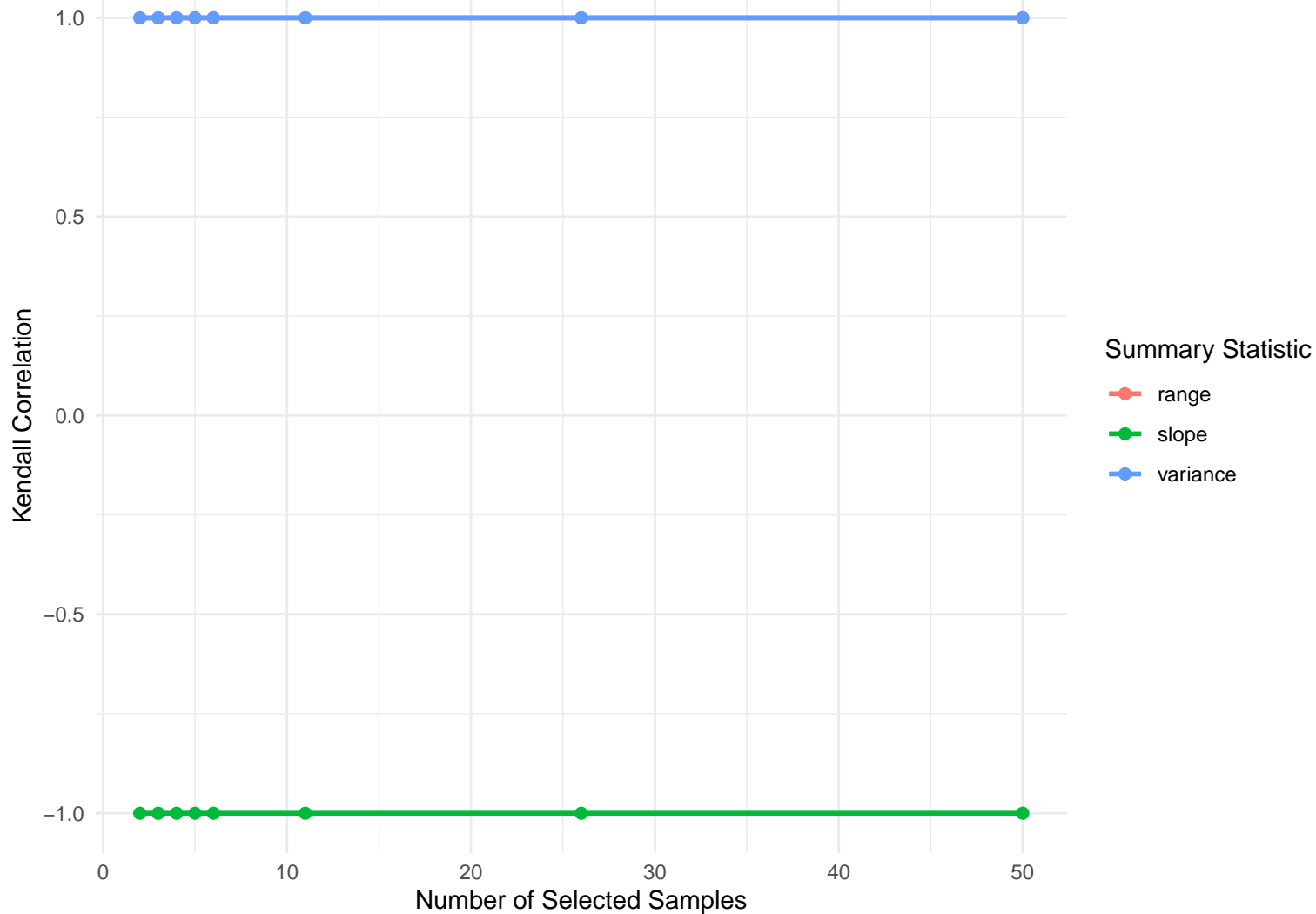
variance



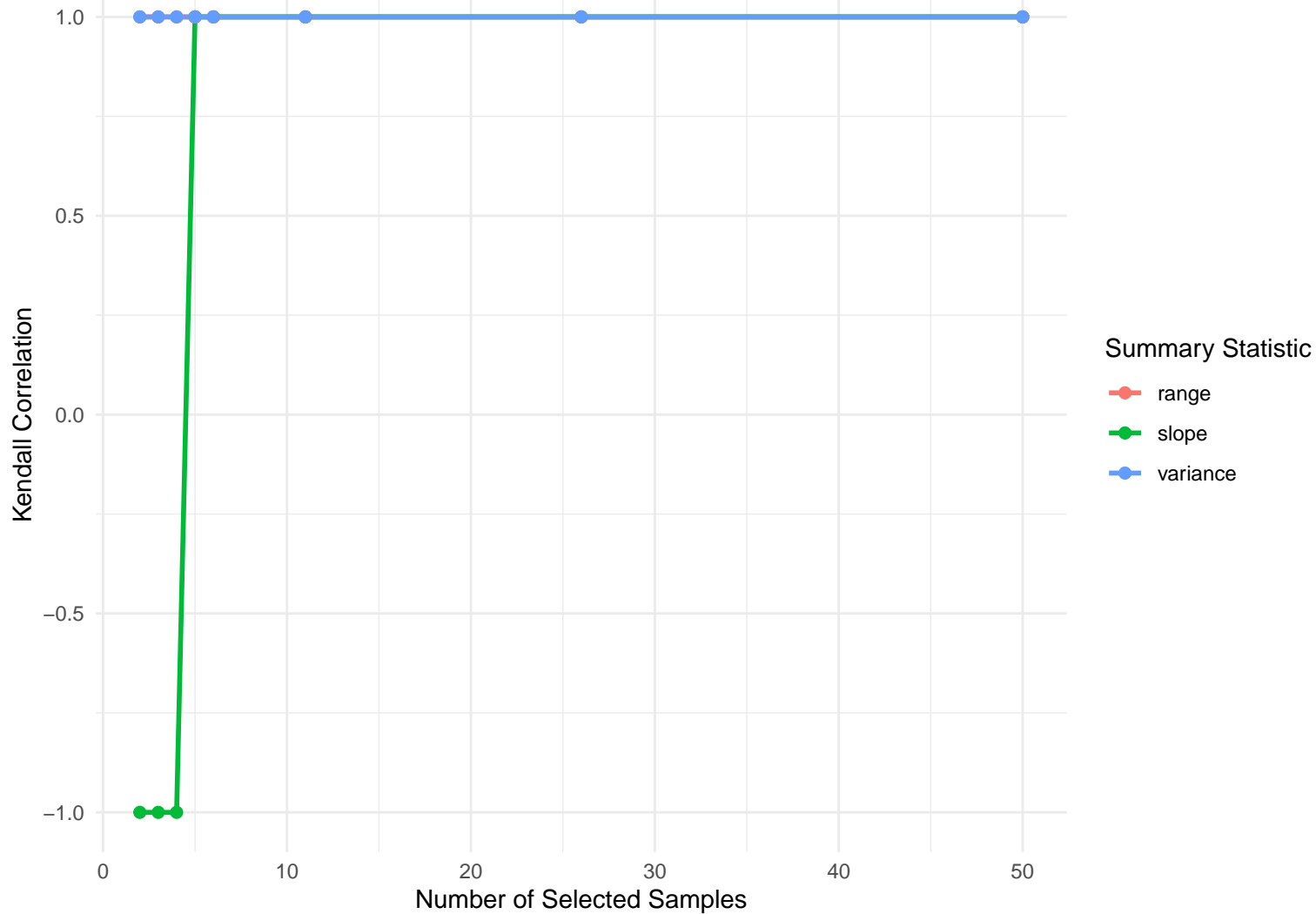
Score: PR (Local, full , Genotype: gaussian)



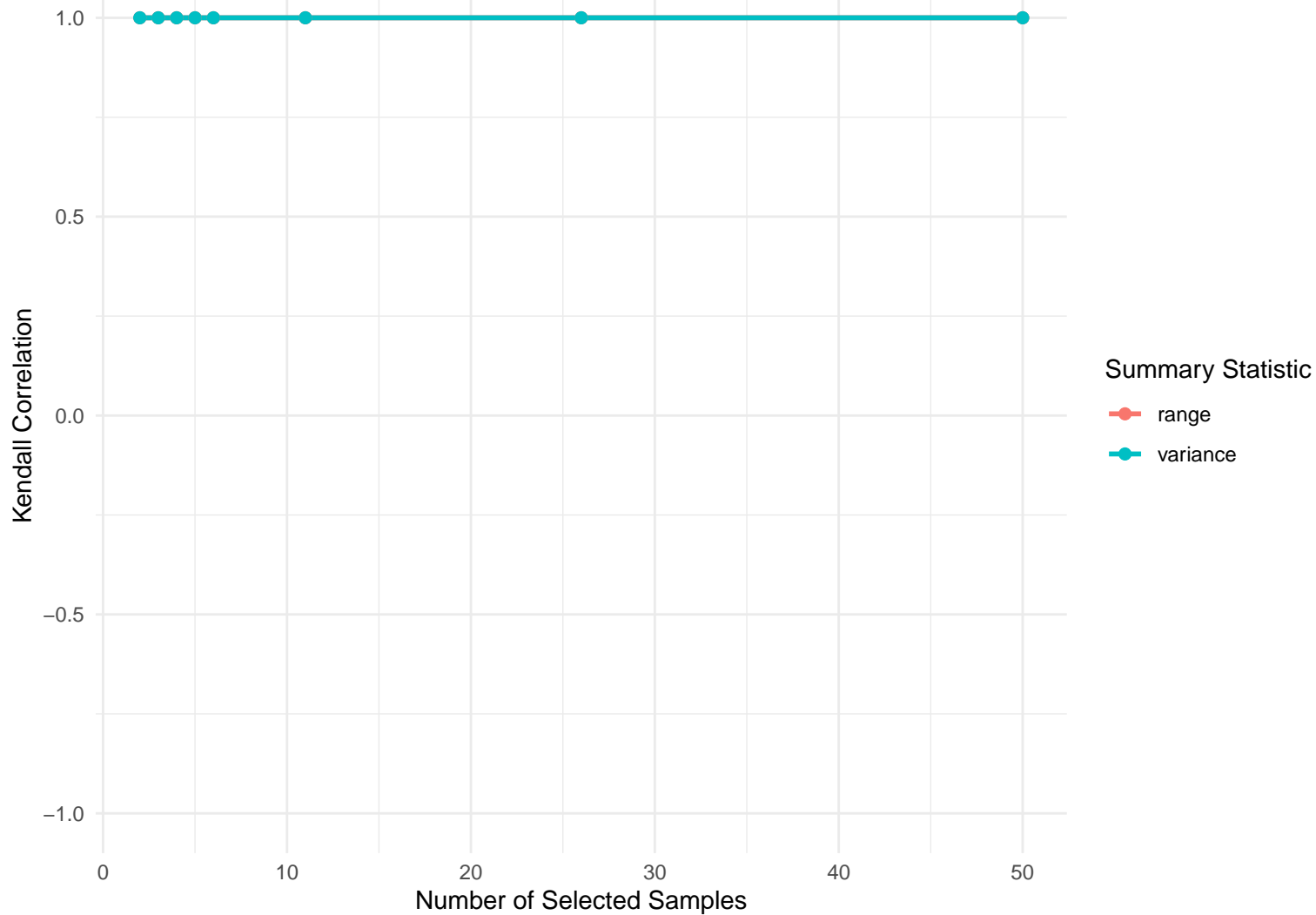
Score: PR (Local, full , Genotype: sinusoidal)



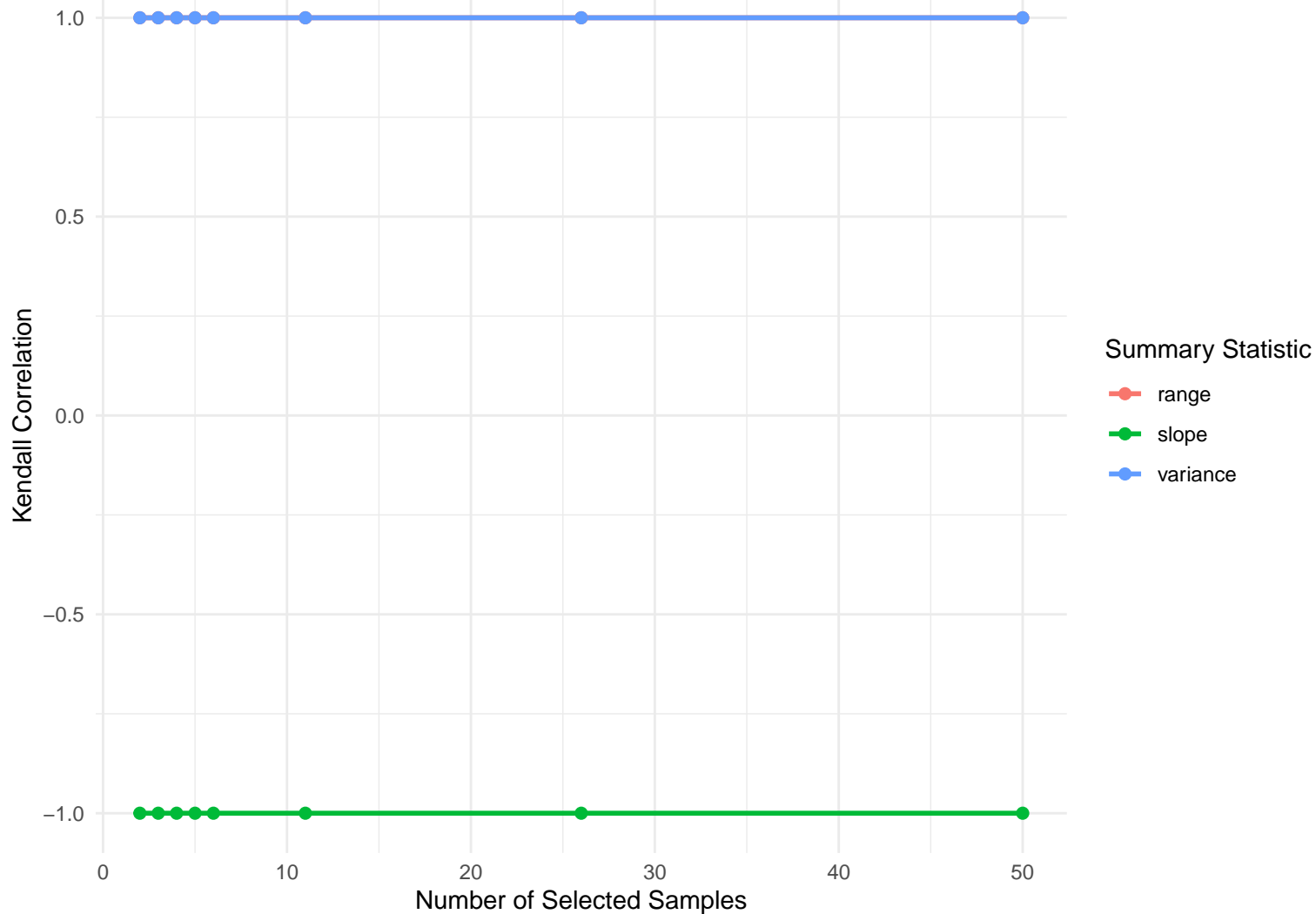
Score: PR (Local, full , Genotype: wave)



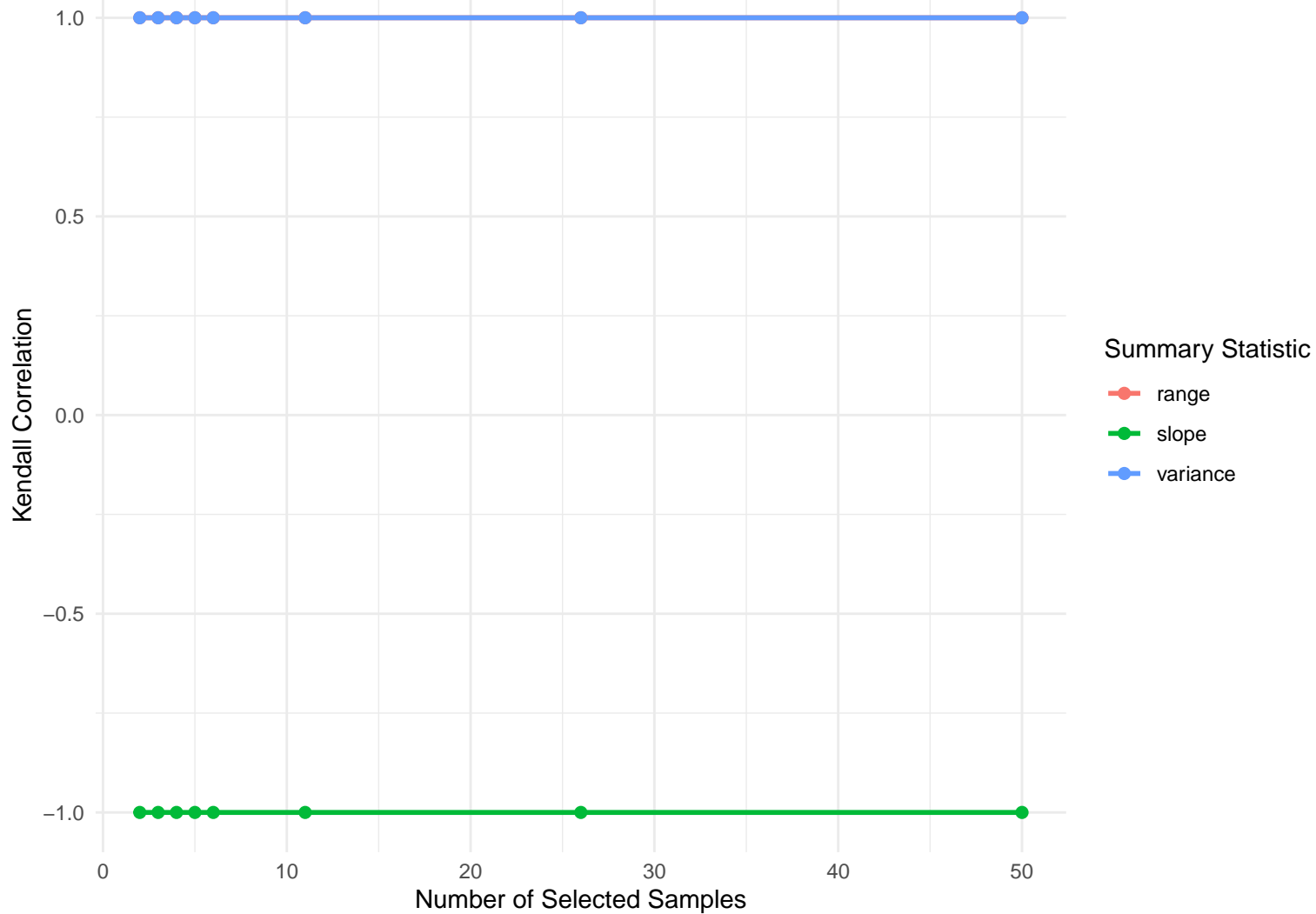
Score: NRW (Local, full , Genotype: linear)



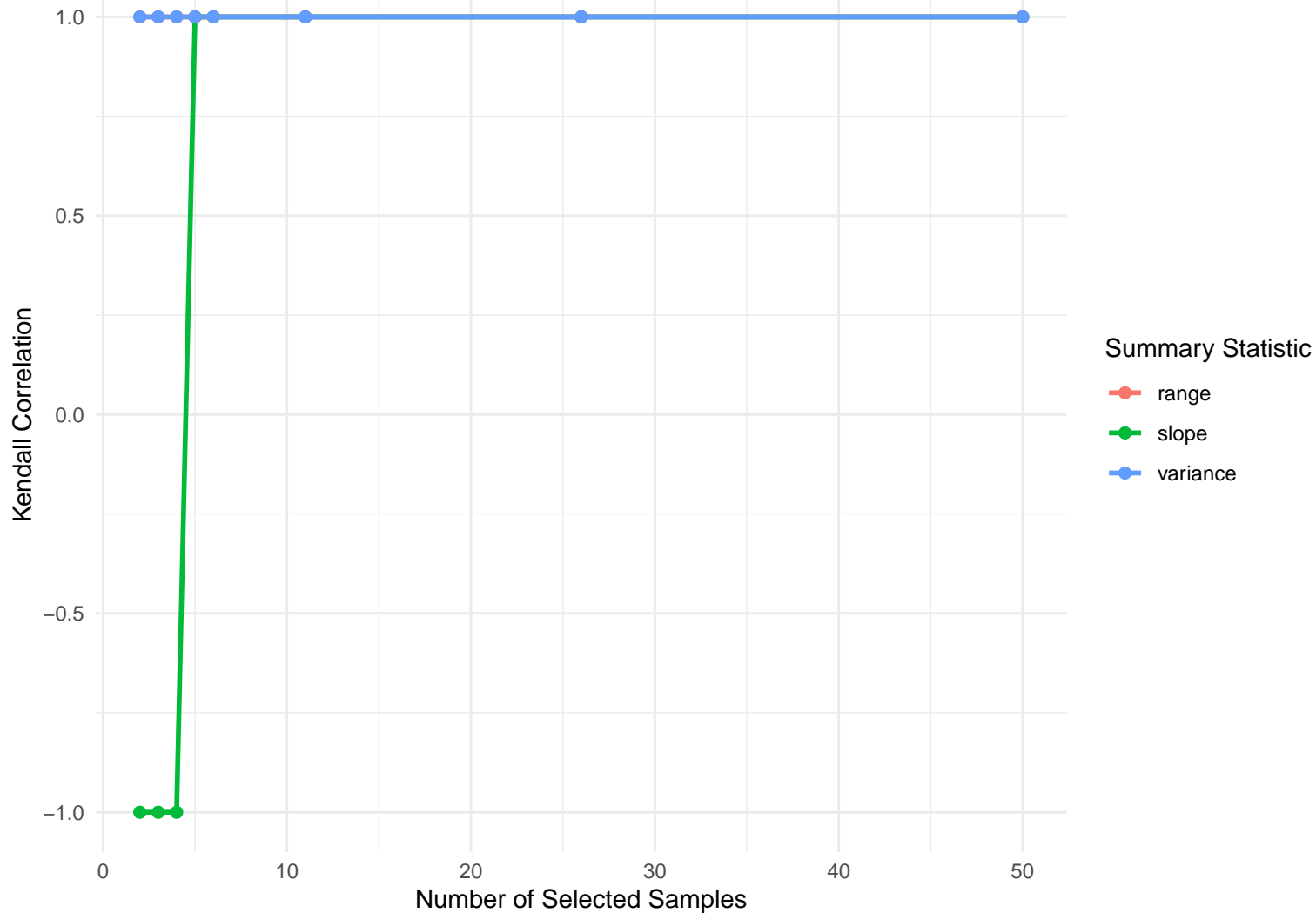
Score: NRW (Local, full , Genotype: gaussian)



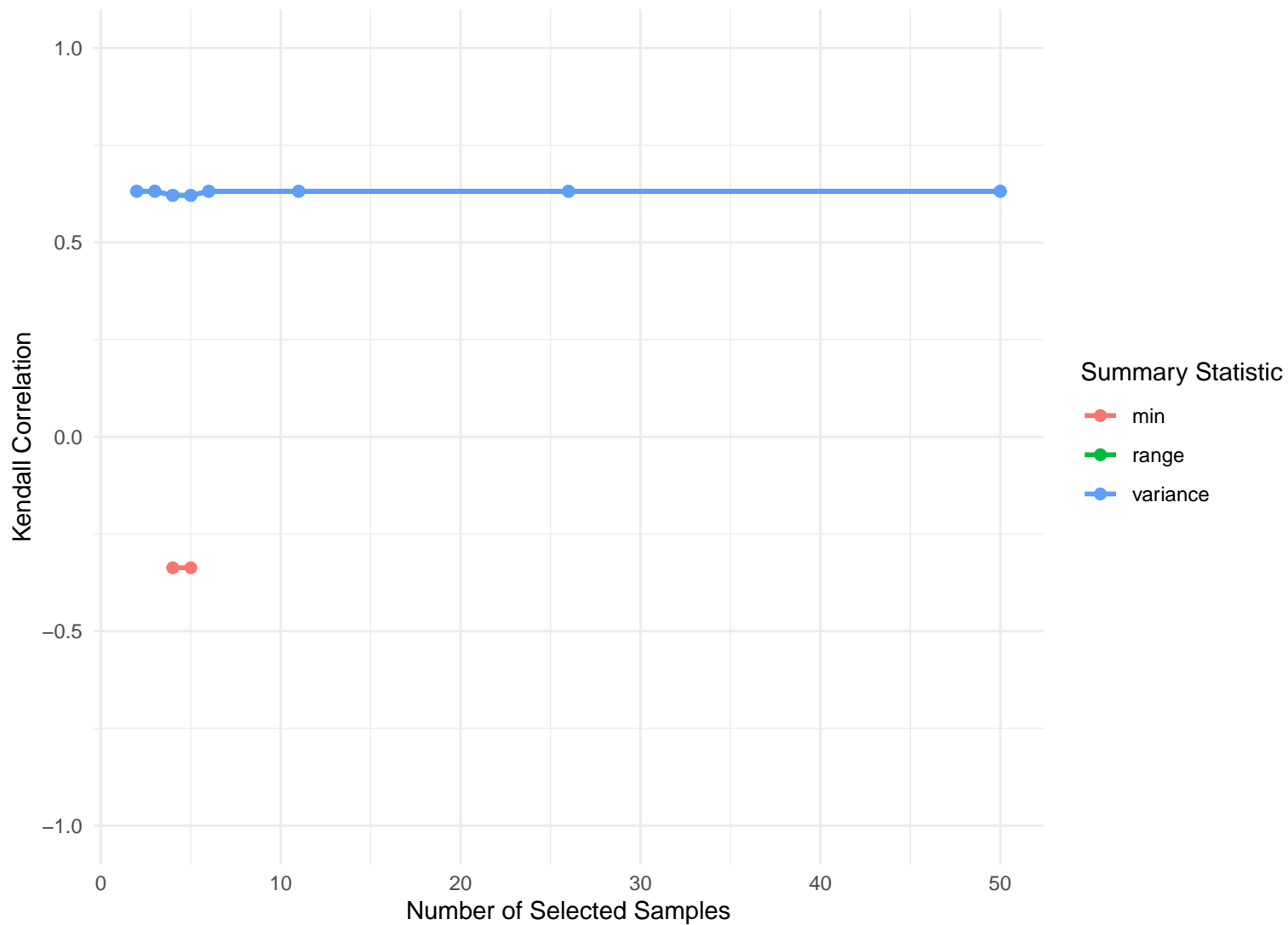
Score: NRW (Local, full , Genotype: sinusoidal)



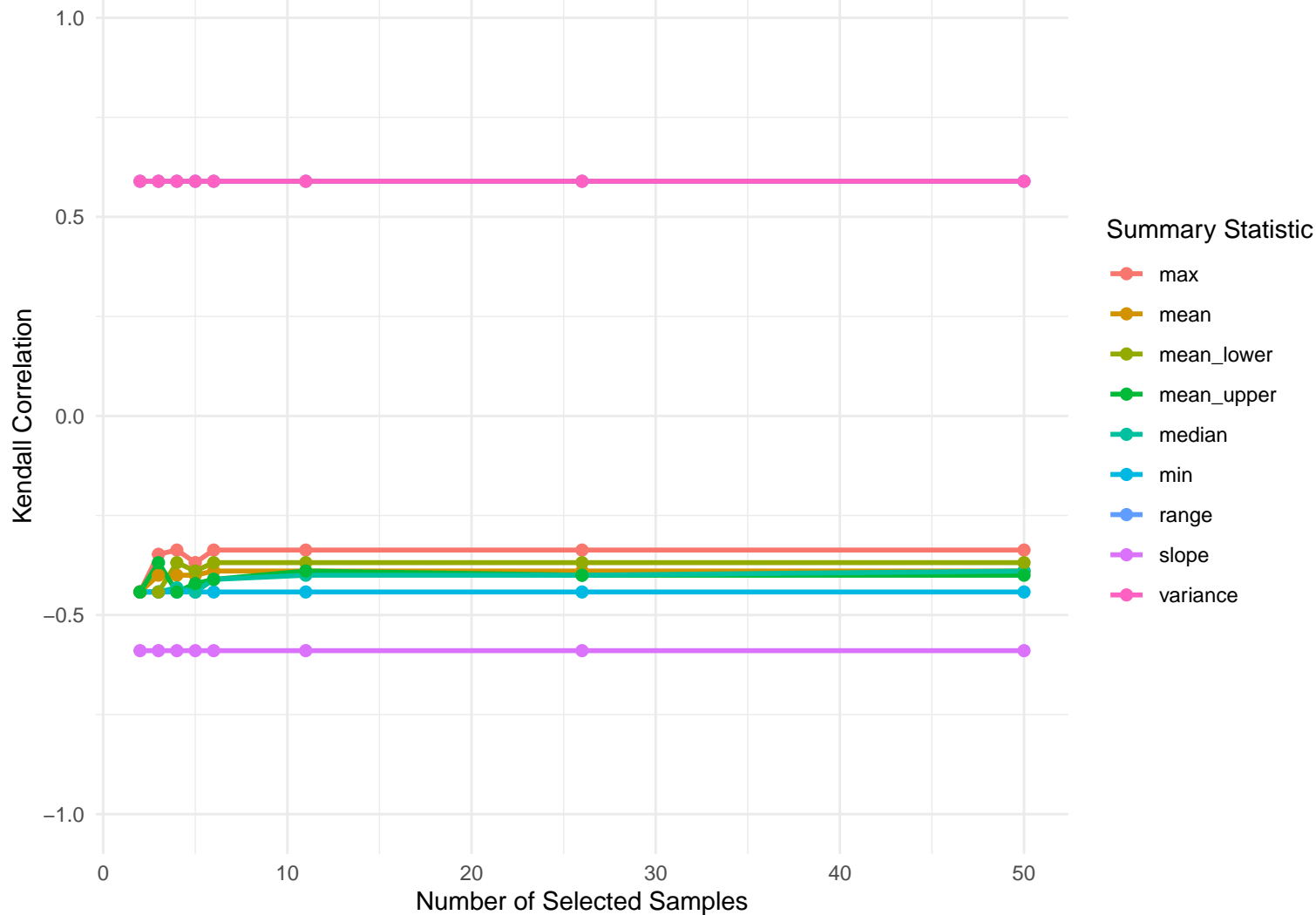
Score: NRW (Local, full , Genotype: wave)



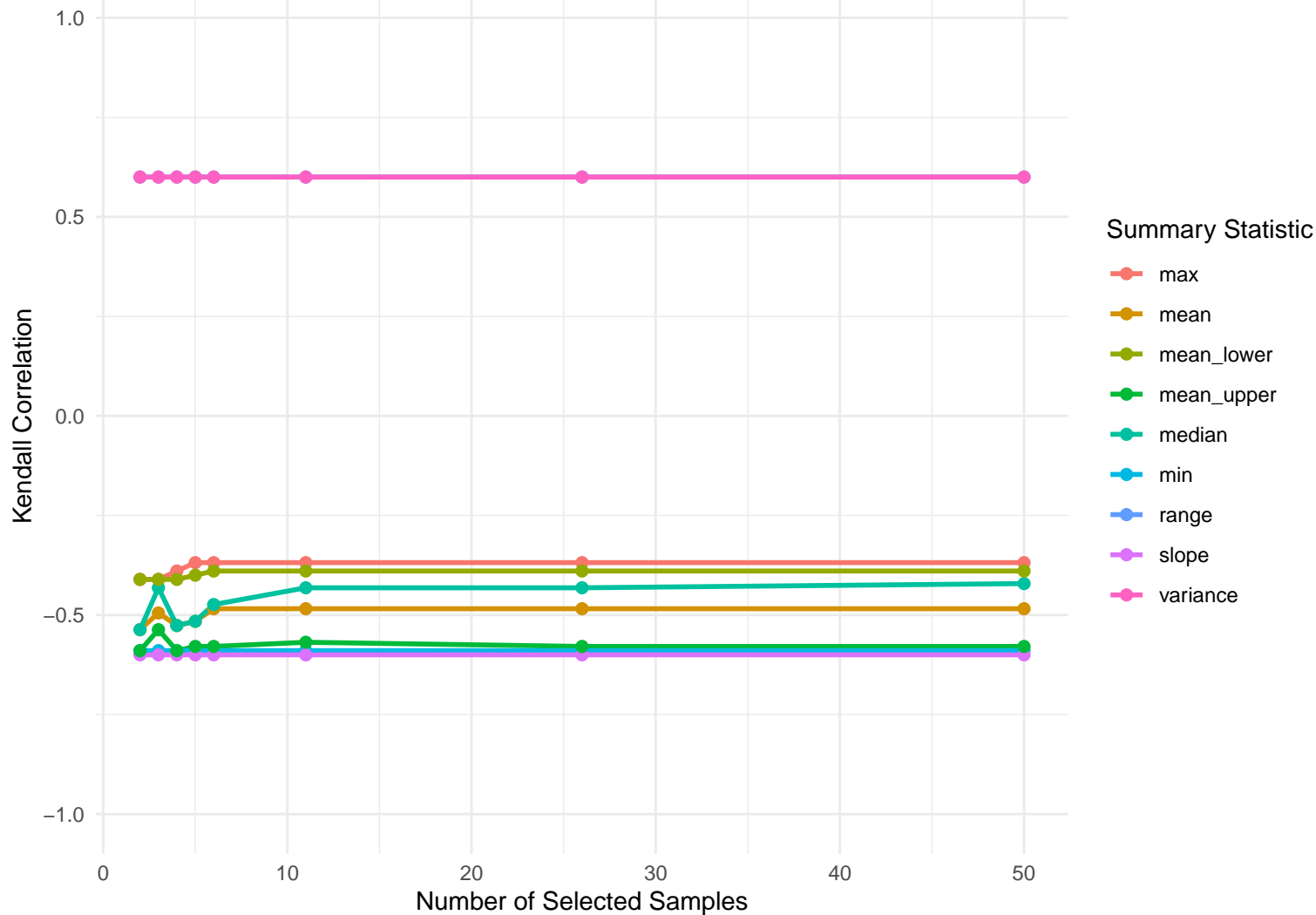
Score: ESP (Local, full , Genotype: linear)



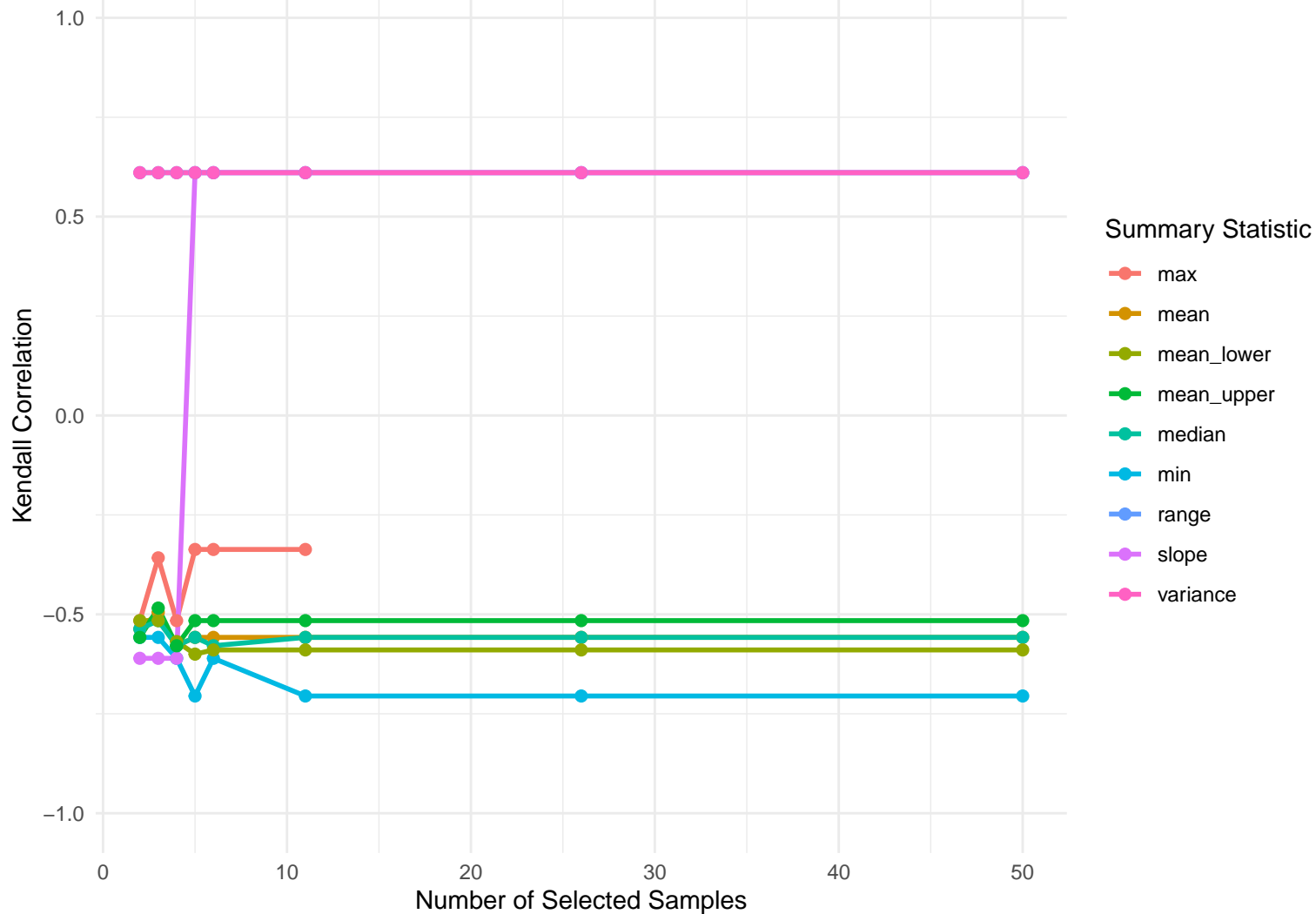
Score: ESP (Local, full , Genotype: gaussian)



Score: ESP (Local, full , Genotype: sinusoidal)



Score: ESP (Local, full , Genotype: wave)



Score: CEV (Local, full , Genotype: linear)

Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

0

10

20

30

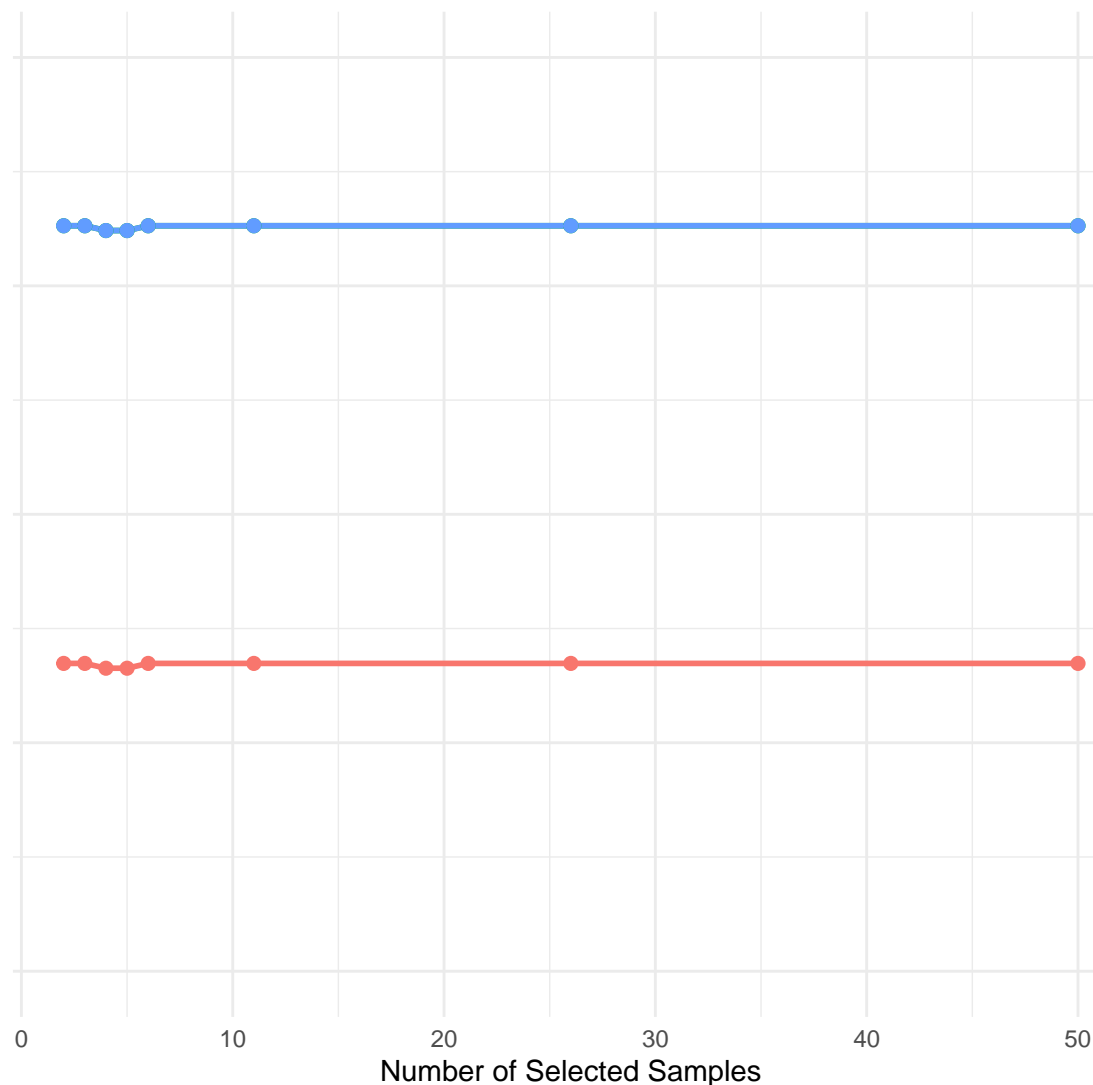
40

50

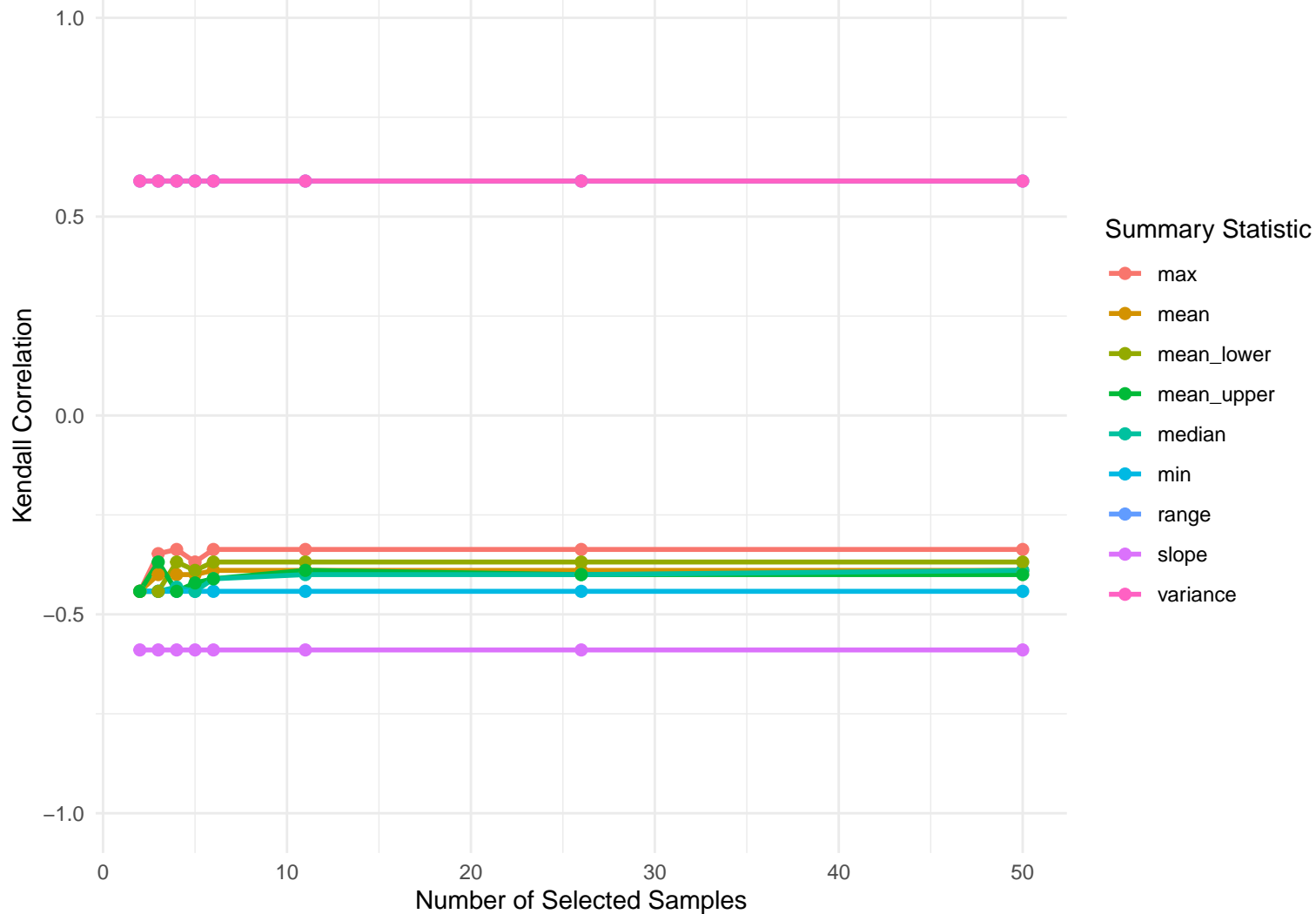
Number of Selected Samples

Summary Statistic

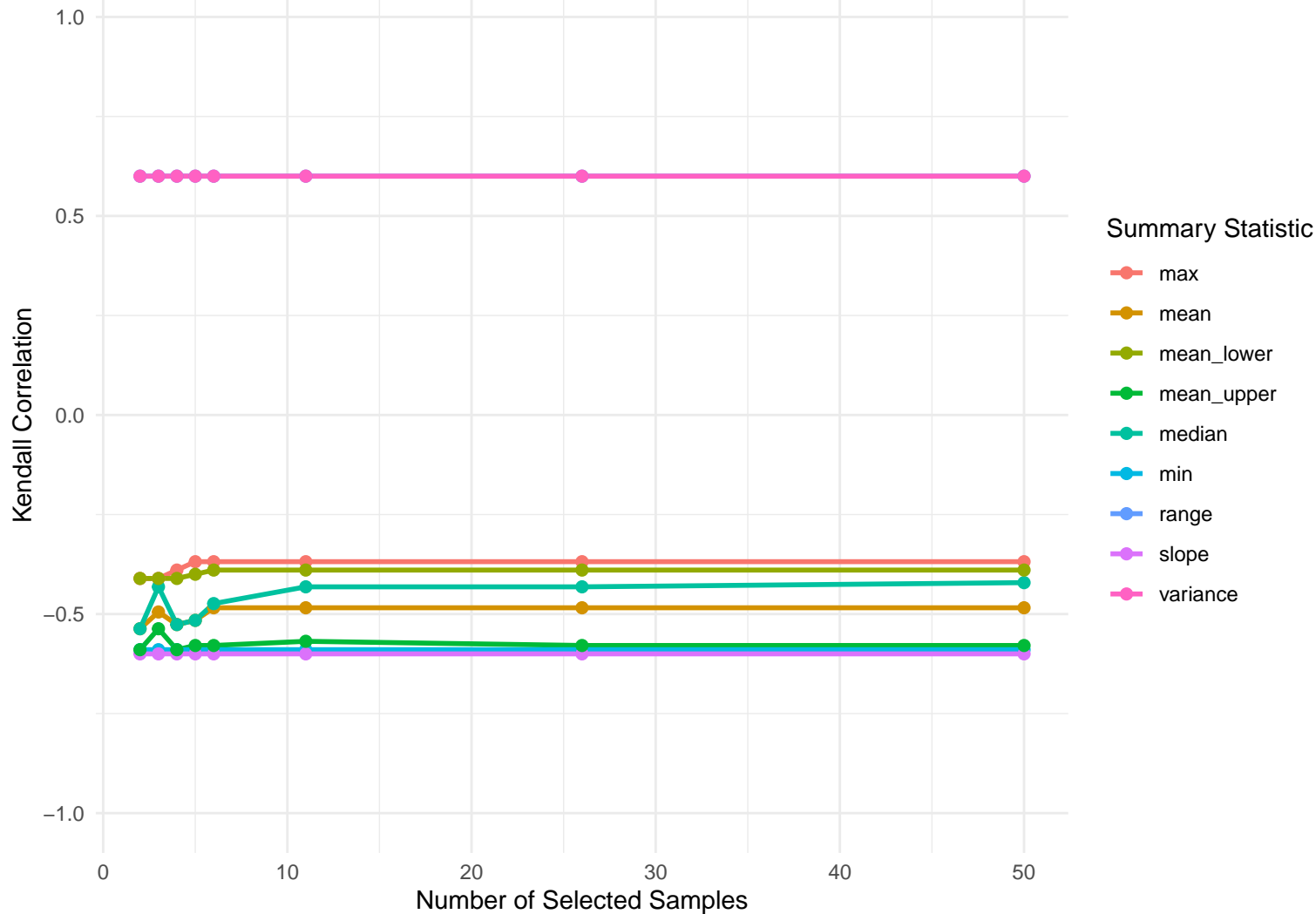
- min
- range
- variance



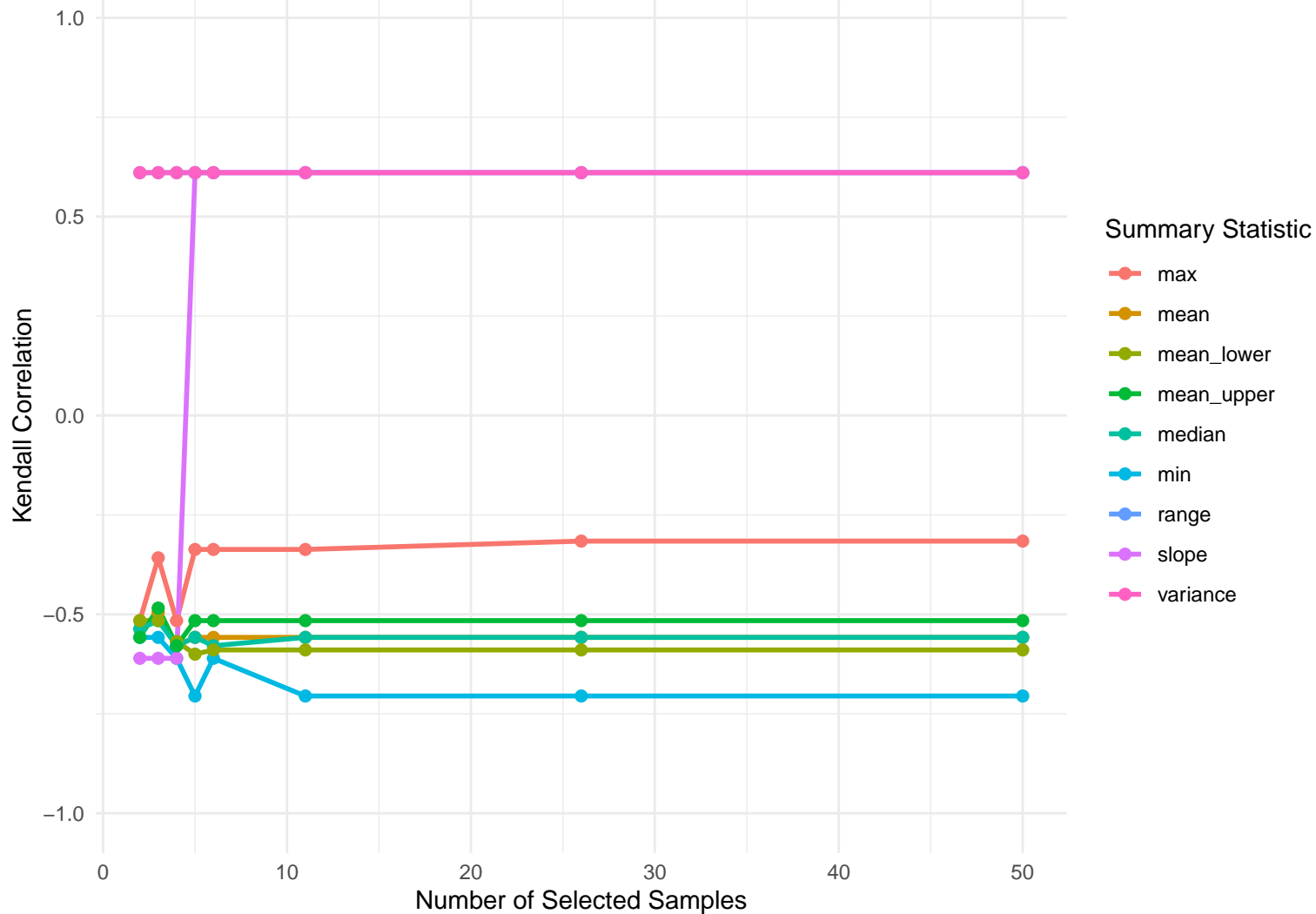
Score: CEV (Local, full , Genotype: gaussian)



Score: CEV (Local, full , Genotype: sinusoidal)



Score: CEV (Local, full , Genotype: wave)



Score: PFI (Local, full , Genotype: linear)

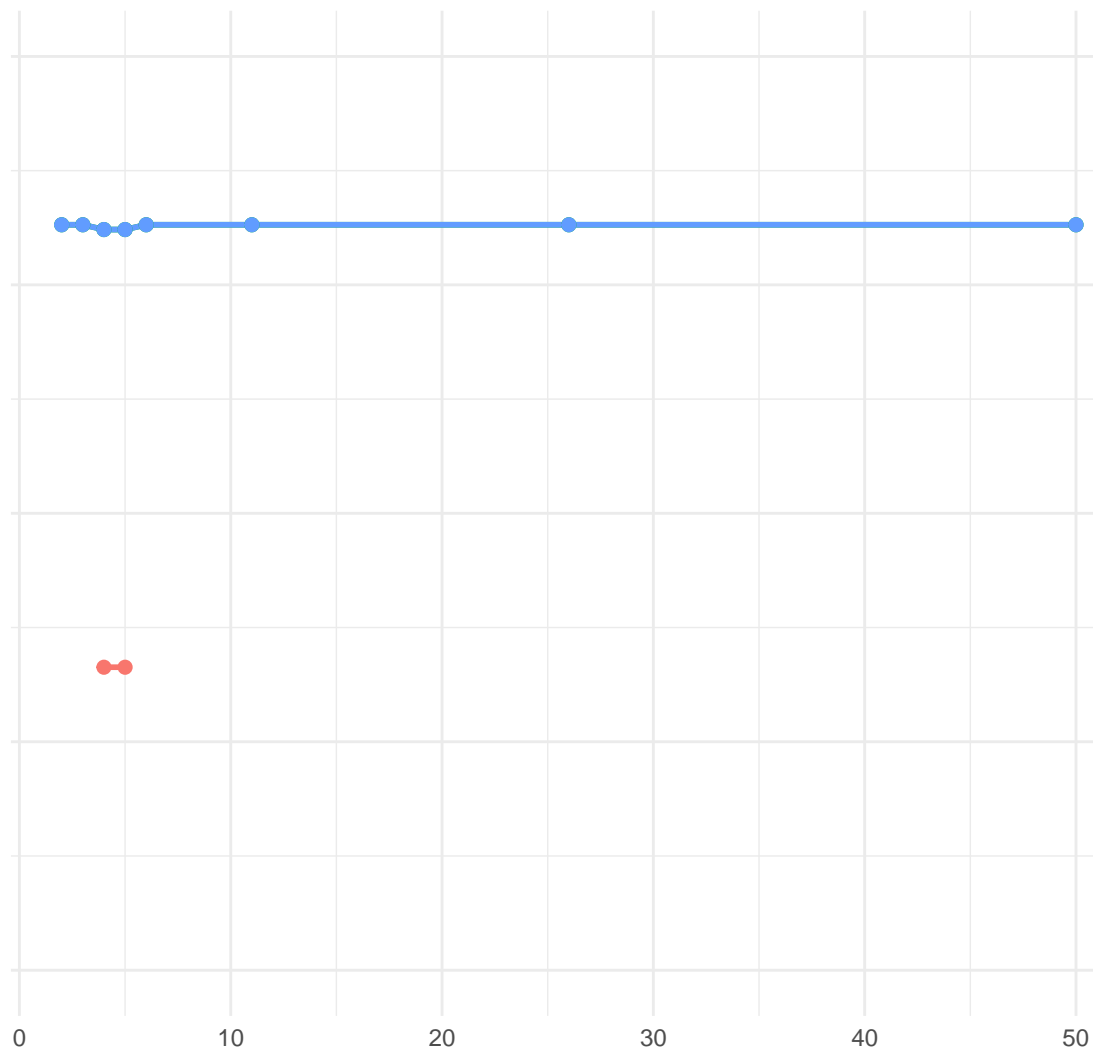
Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

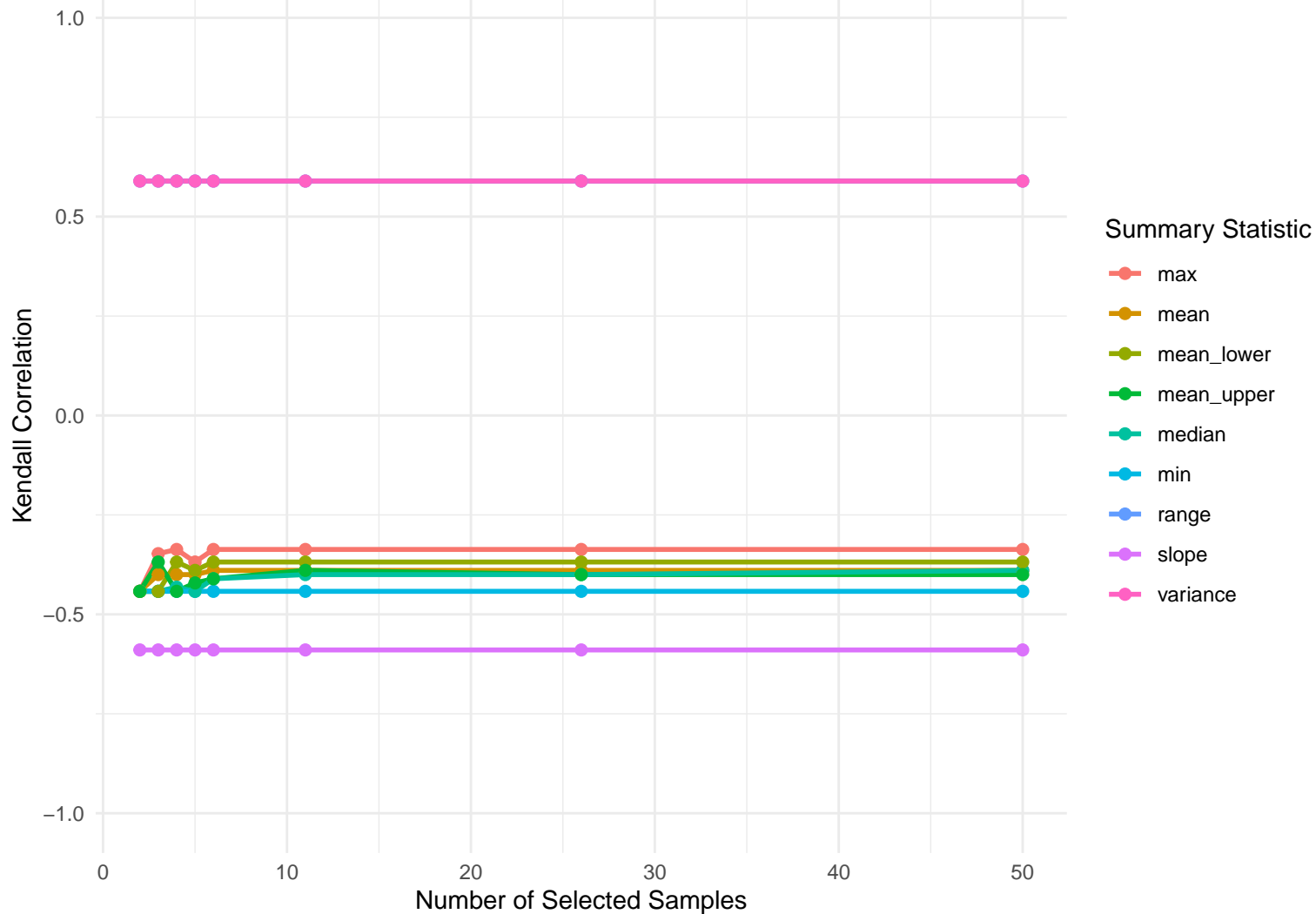
Number of Selected Samples

Summary Statistic

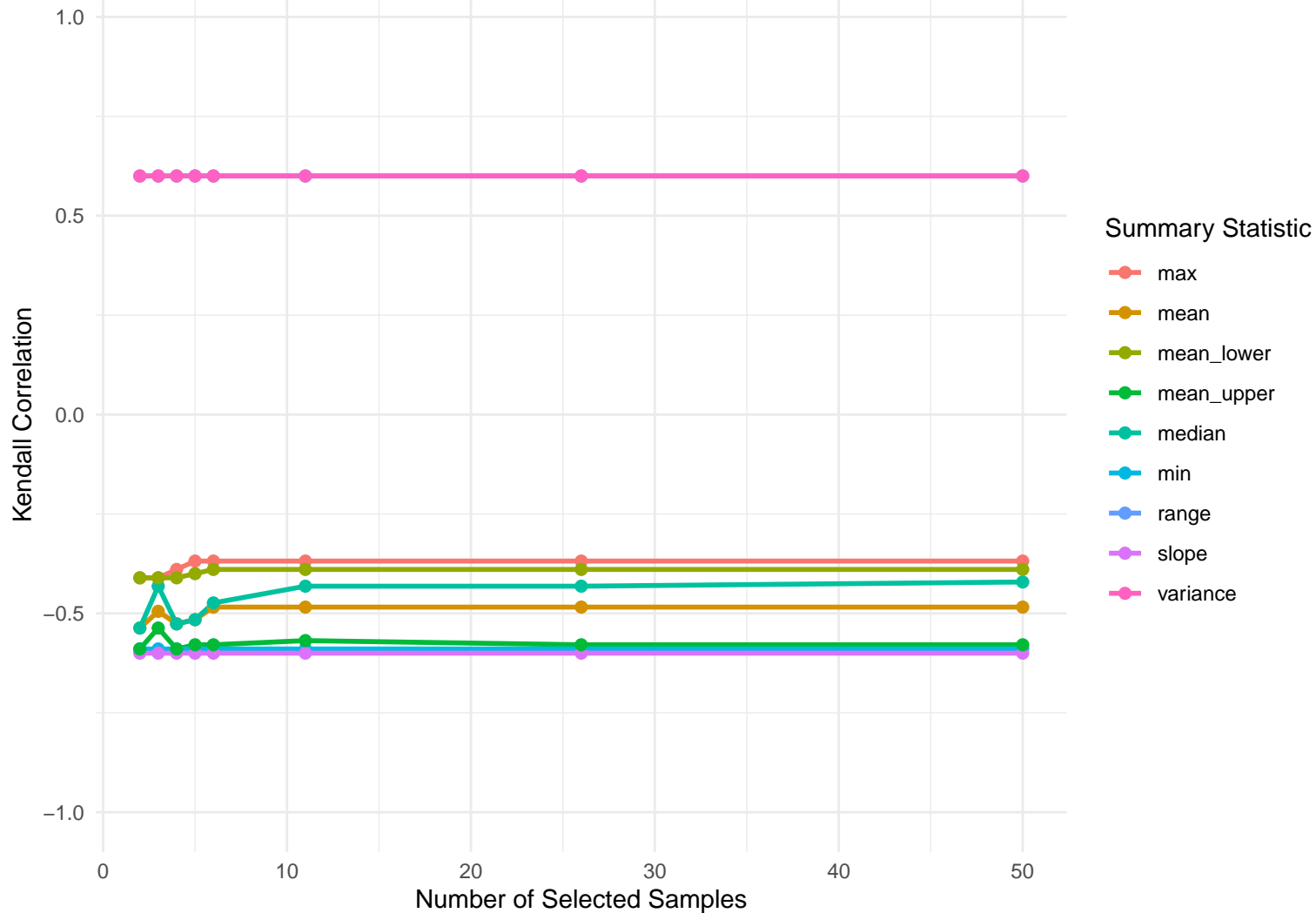
- min
- range
- variance



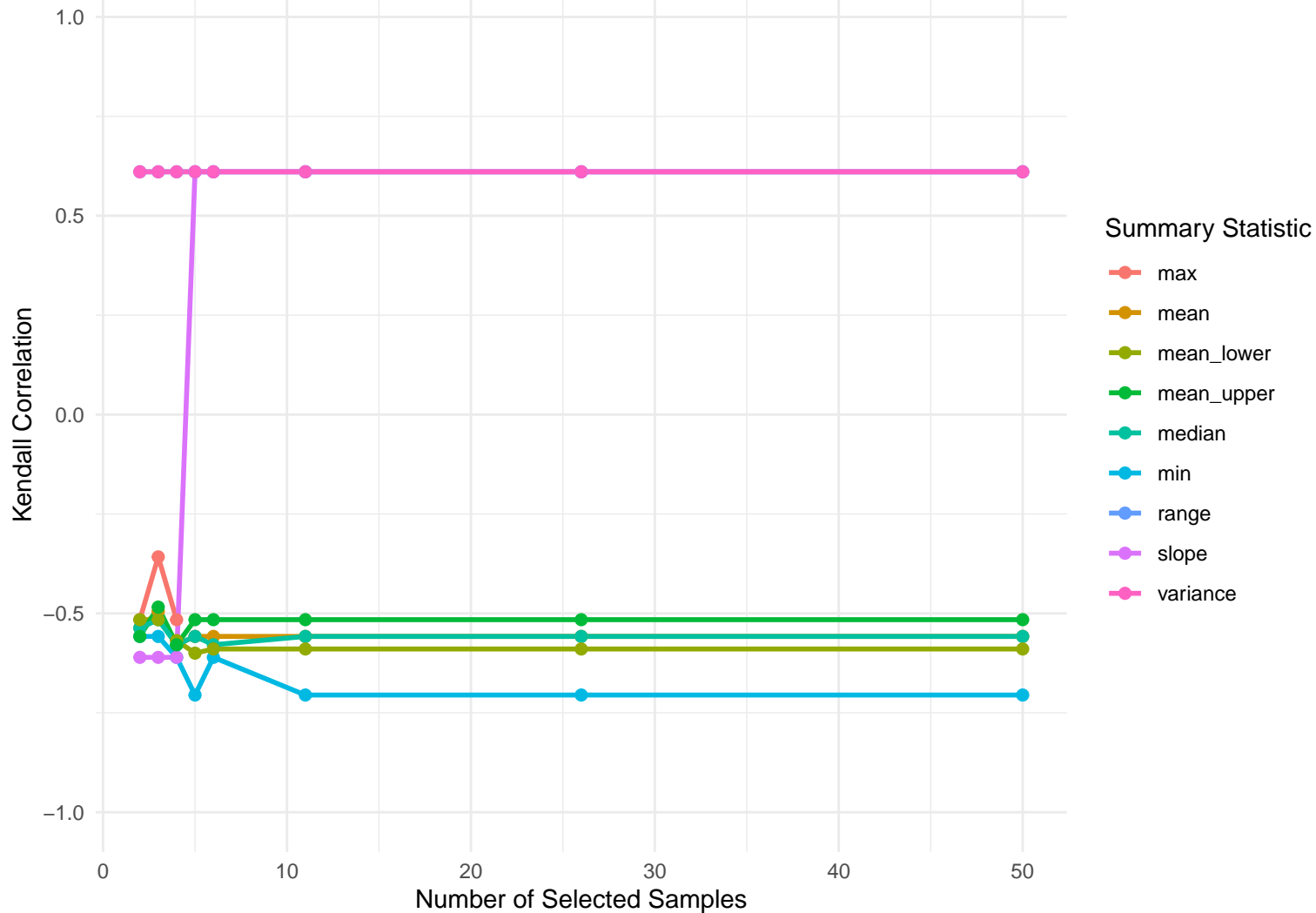
Score: PFI (Local, full , Genotype: gaussian)



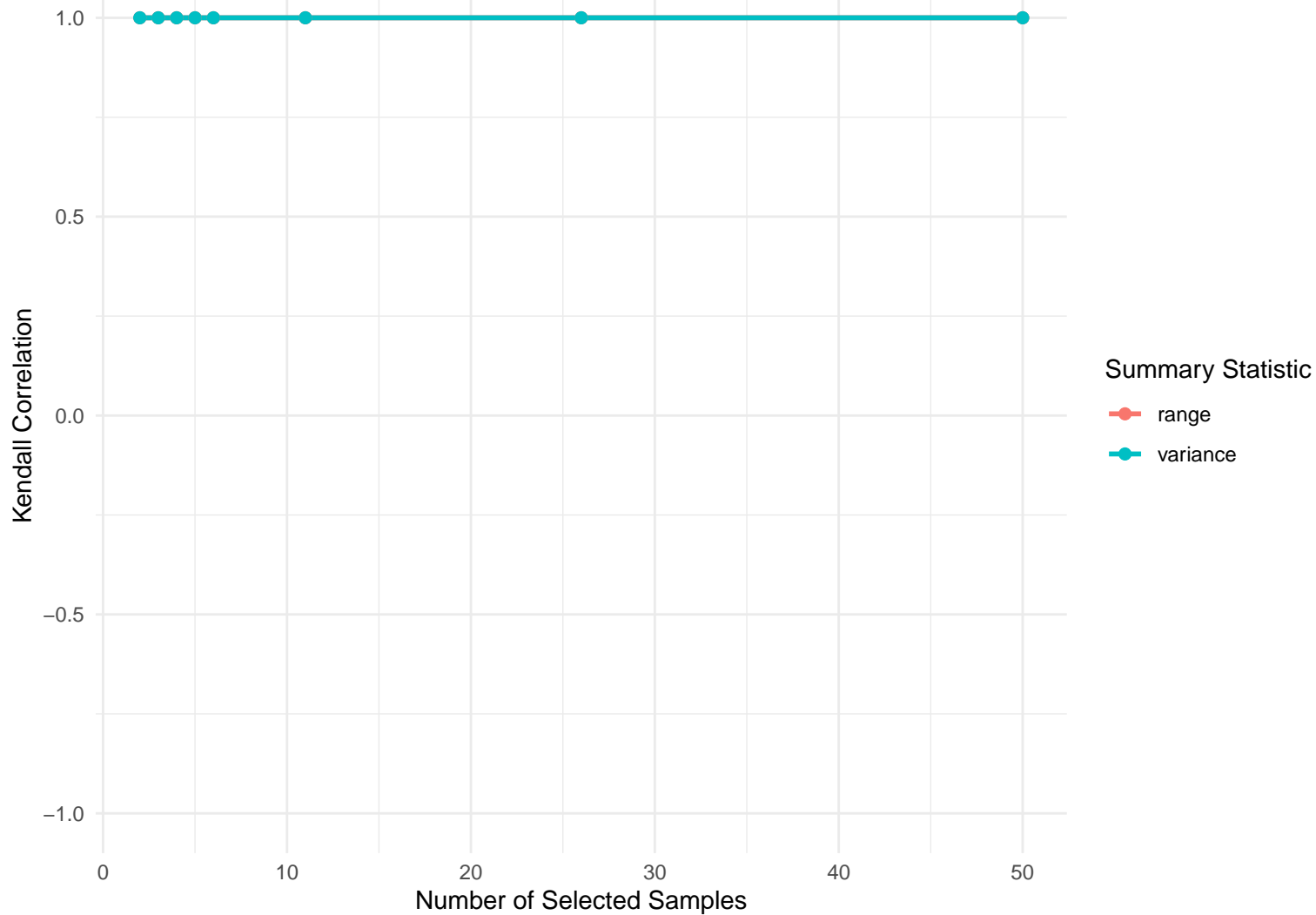
Score: PFI (Local, full , Genotype: sinusoidal)



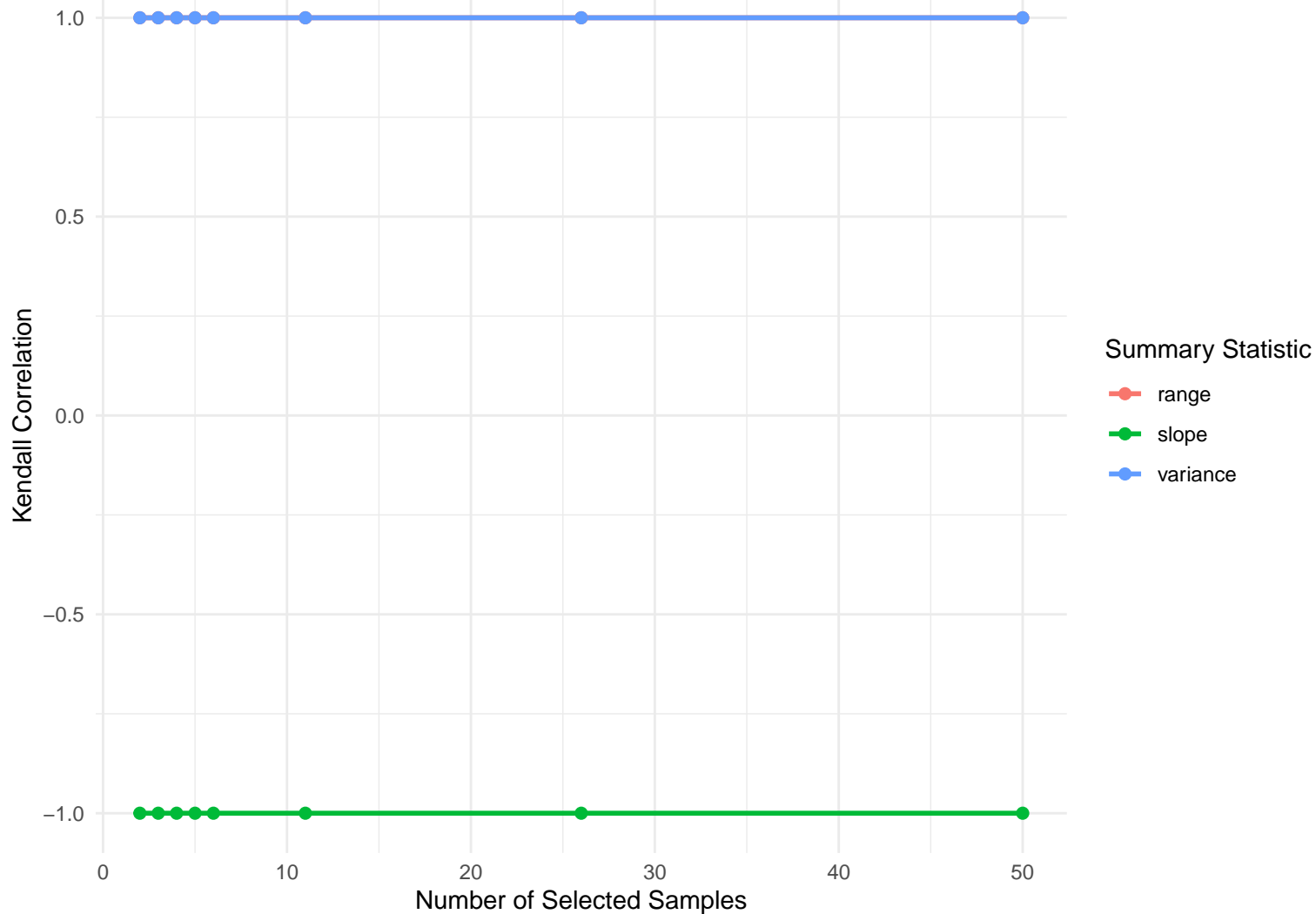
Score: PFI (Local, full , Genotype: wave)



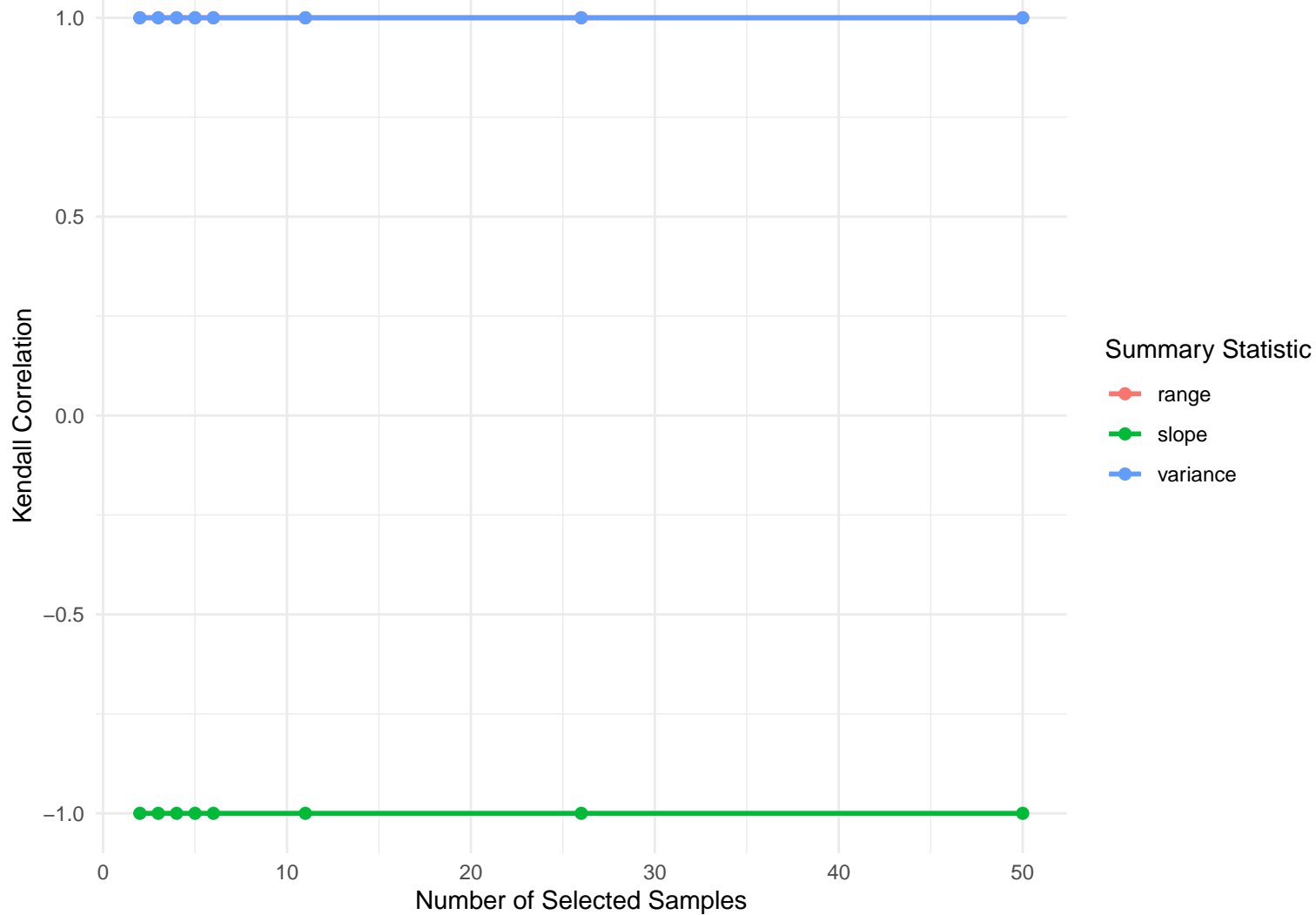
Score: APC (Local, full , Genotype: linear)



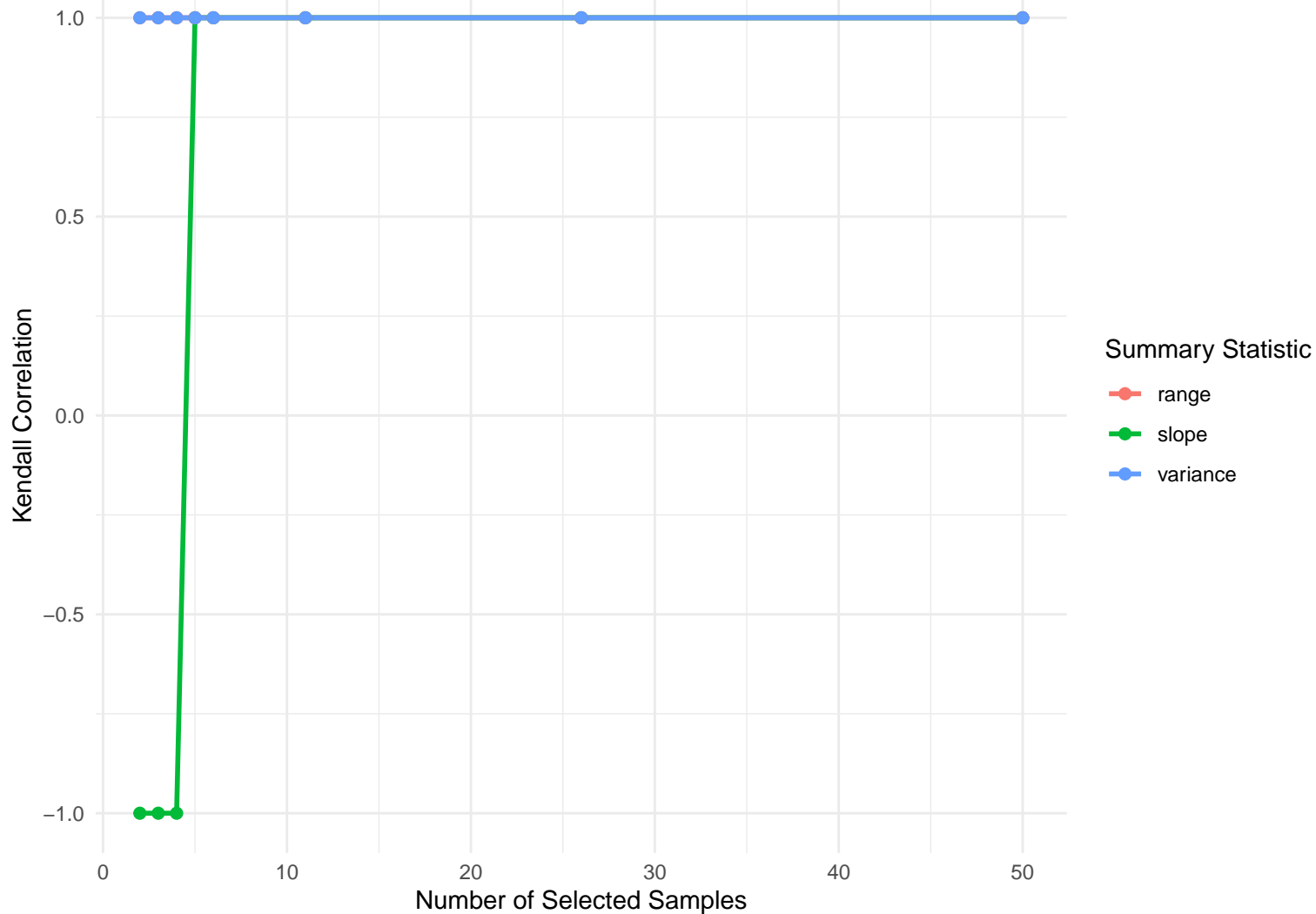
Score: APC (Local, full , Genotype: gaussian)



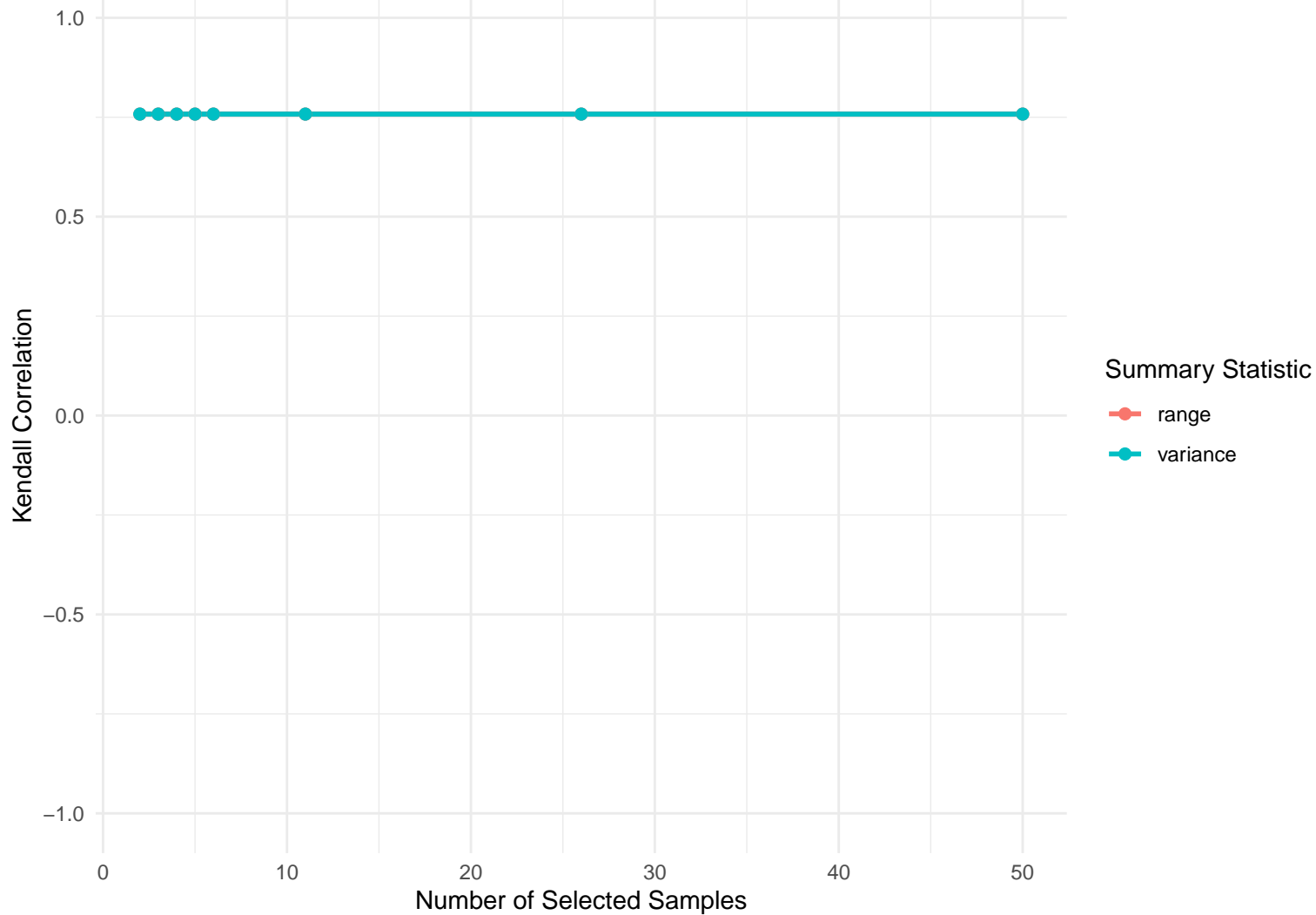
Score: APC (Local, full , Genotype: sinusoidal)



Score: APC (Local, full , Genotype: wave)



Score: SI (Local, full , Genotype: linear)



Score: SI (Local, full , Genotype: gaussian)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

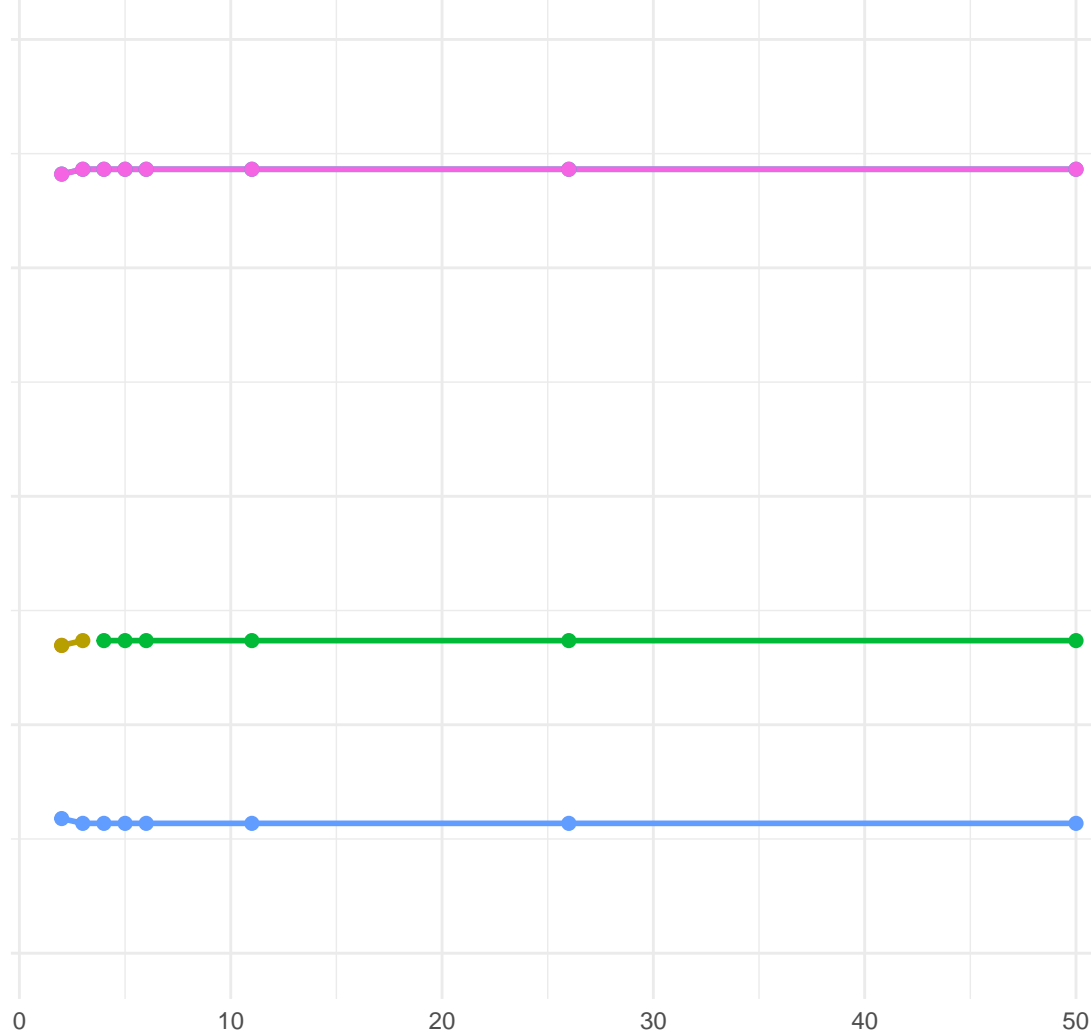
40

50

Number of Selected Samples

Summary Statistic

- mean
- median
- min
- range
- slope
- variance



Score: SI (Local, full , Genotype: sinusoidal)

Kendall Correlation

1.0

0.5

0.0

-0.5

-1.0

0

10

20

30

40

50

Number of Selected Samples

Summary Statistic

mean

mean_upper

median

min

range

slope

variance

0

10

20

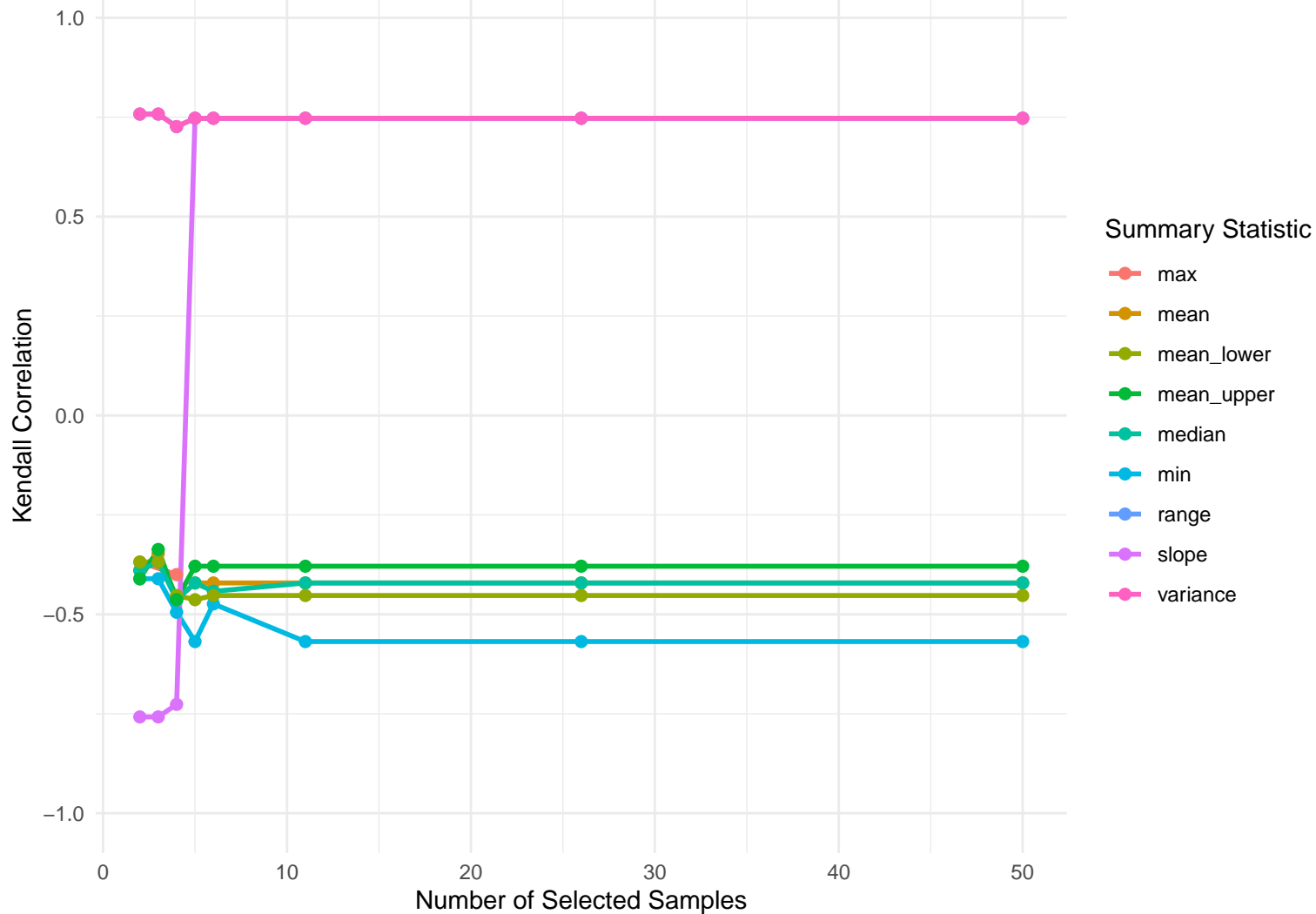
30

40

50

Number of Selected Samples

Score: SI (Local, full , Genotype: wave)



Score: RSI (Local, full , Genotype: linear)

Kendall Correlation

1.0
0.5
0.0
-0.5
-1.0

0

10

20

30

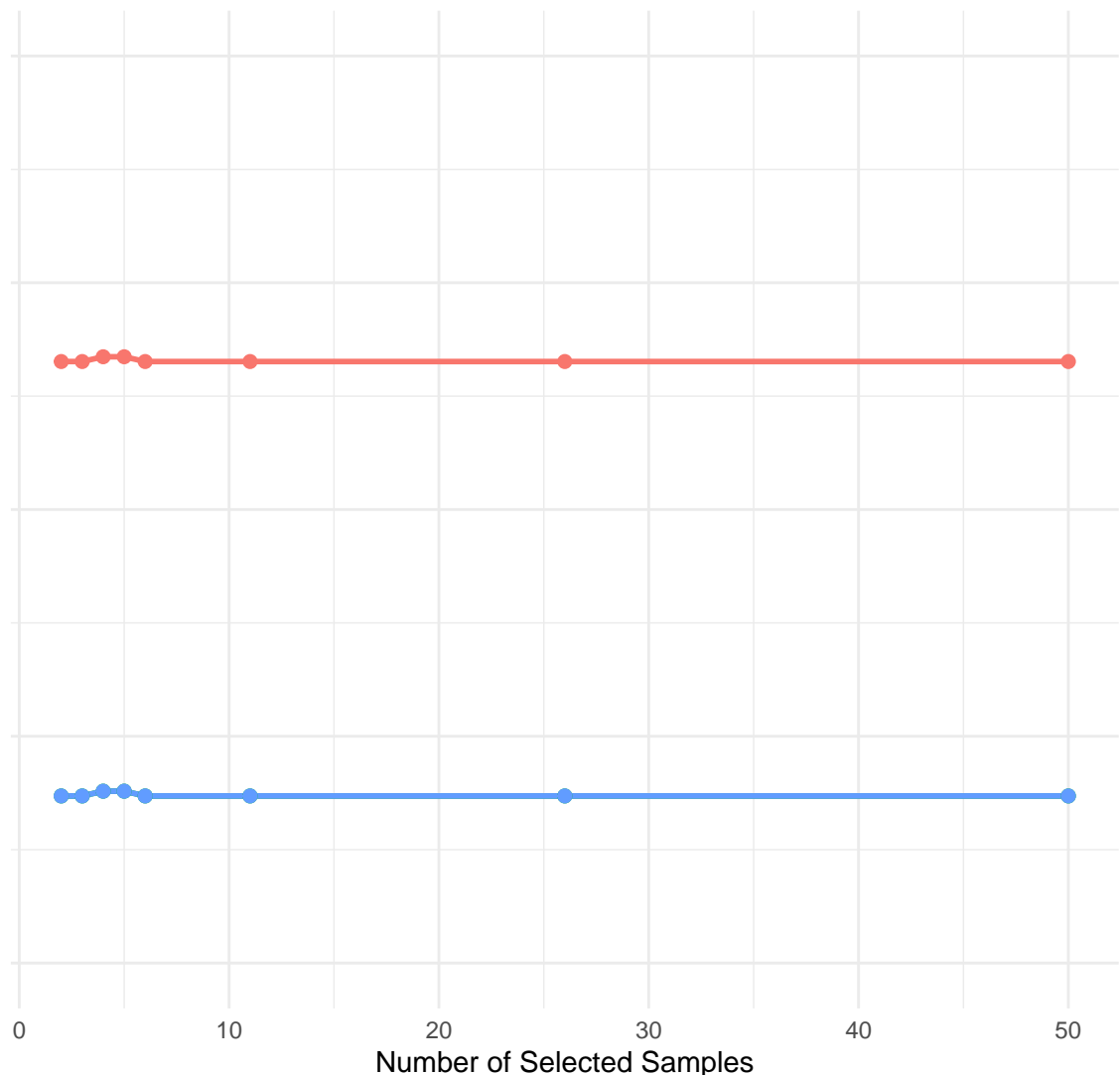
40

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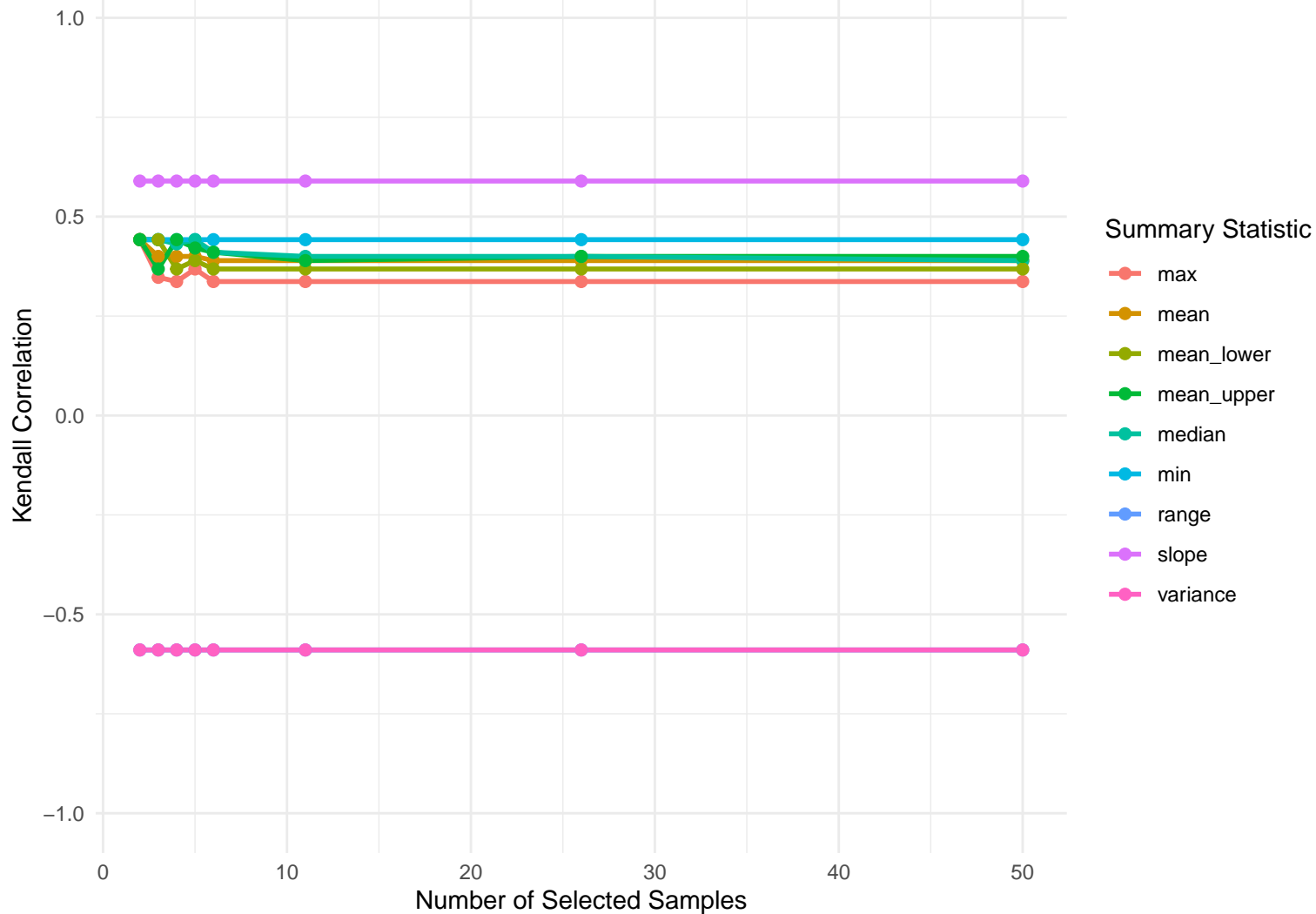
Number of Selected Samples

Summary Statistic

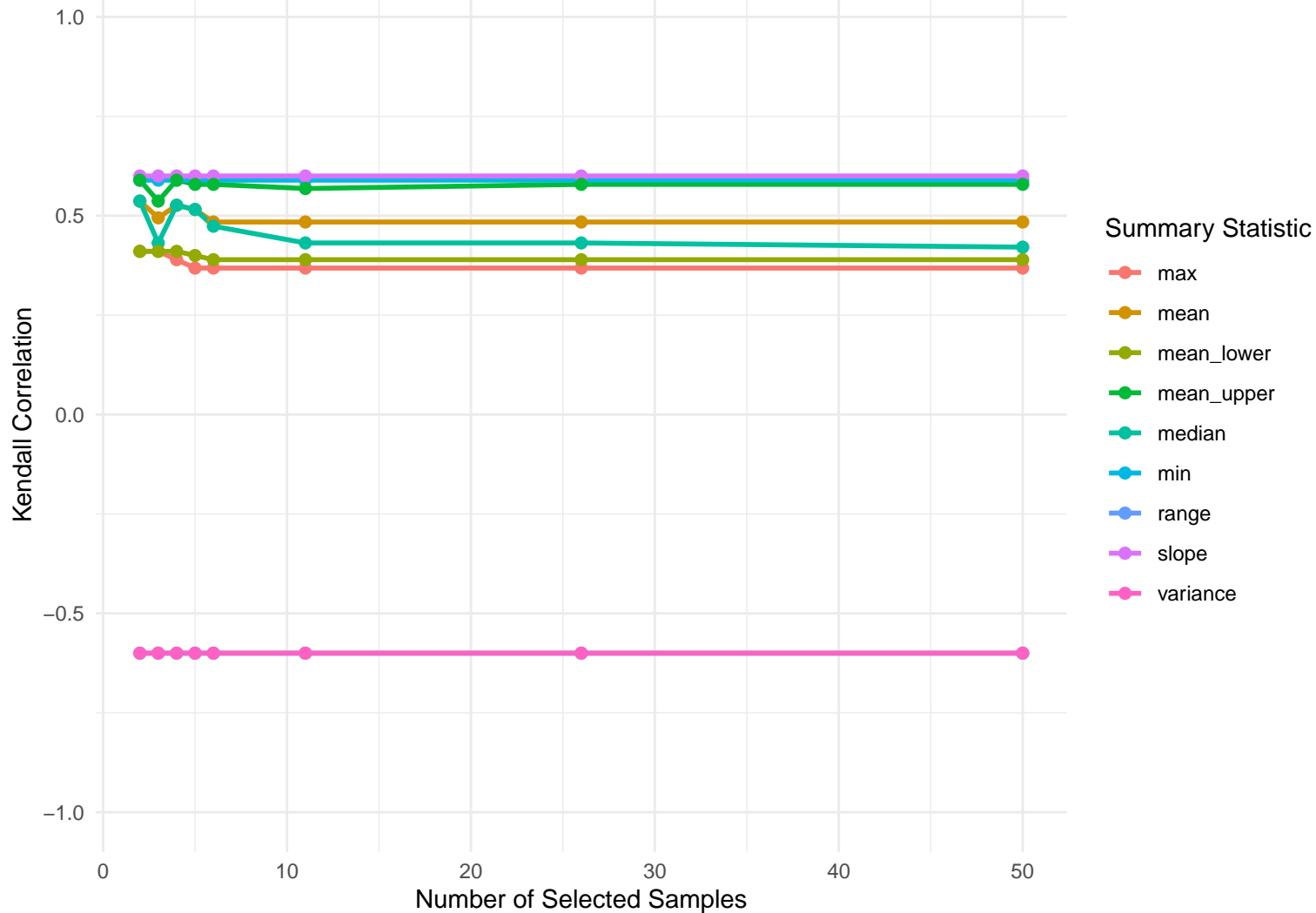
- min
- range
- variance



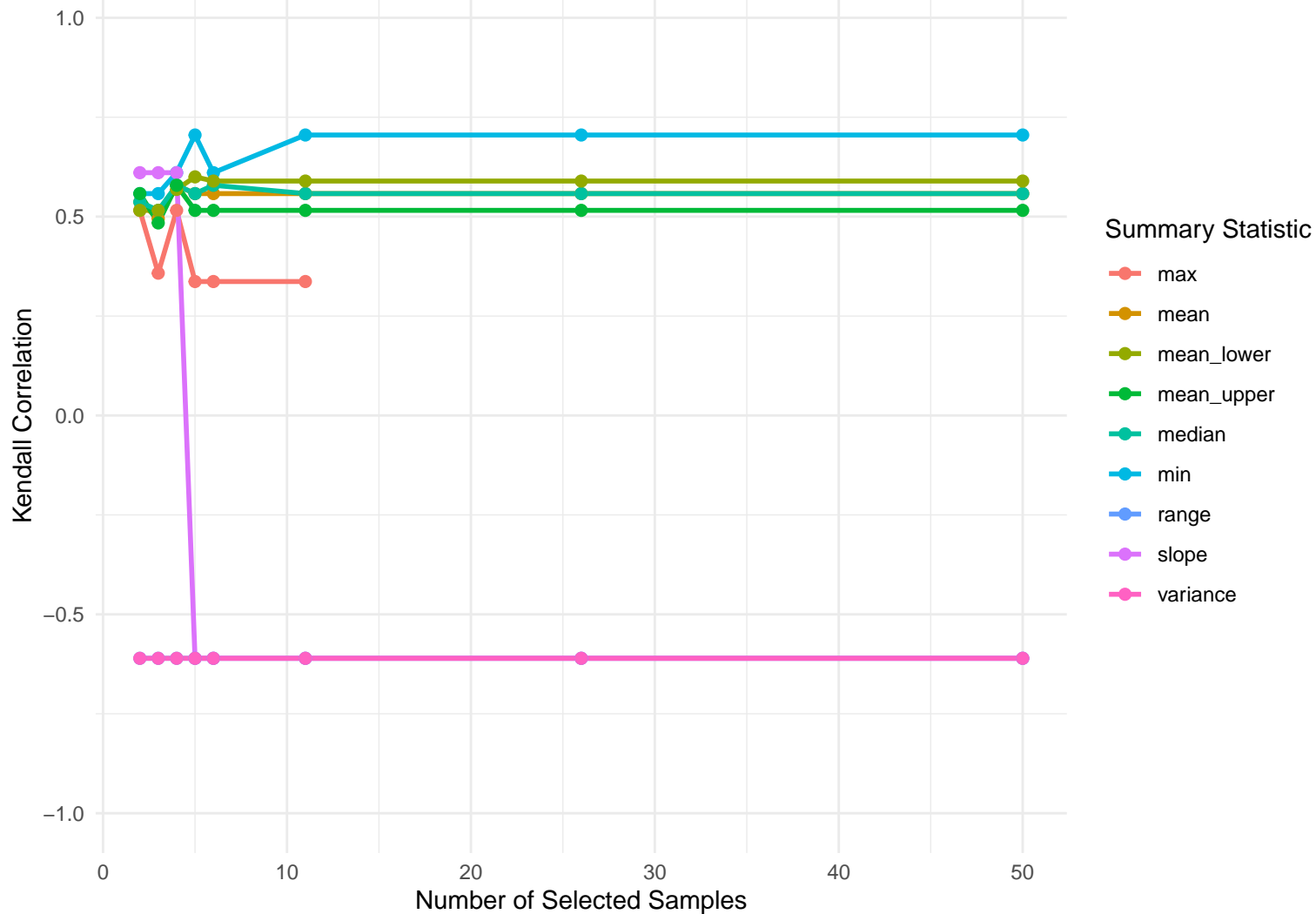
Score: RSI (Local, full , Genotype: gaussian)



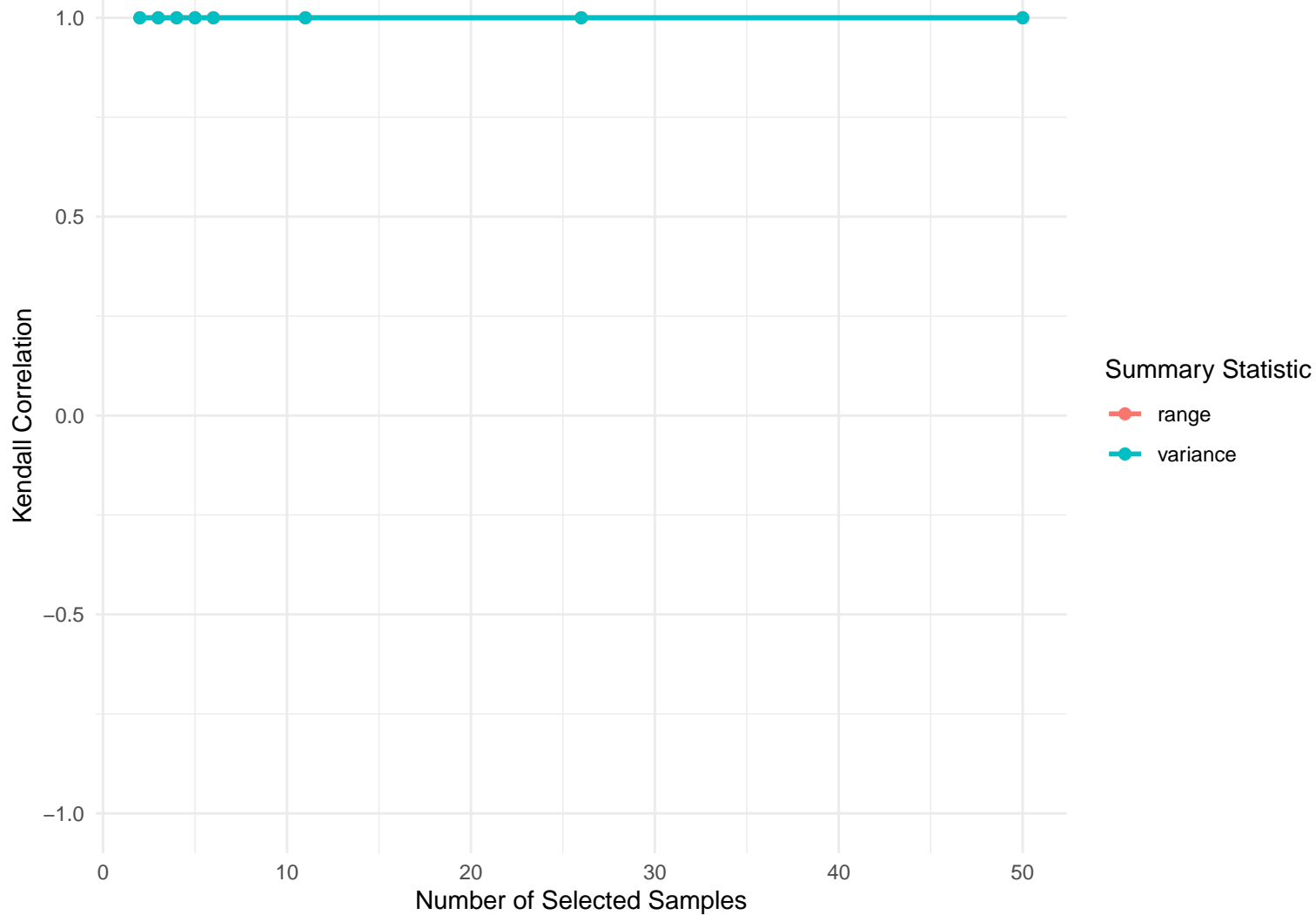
Score: RSI (Local, full , Genotype: sinusoidal)



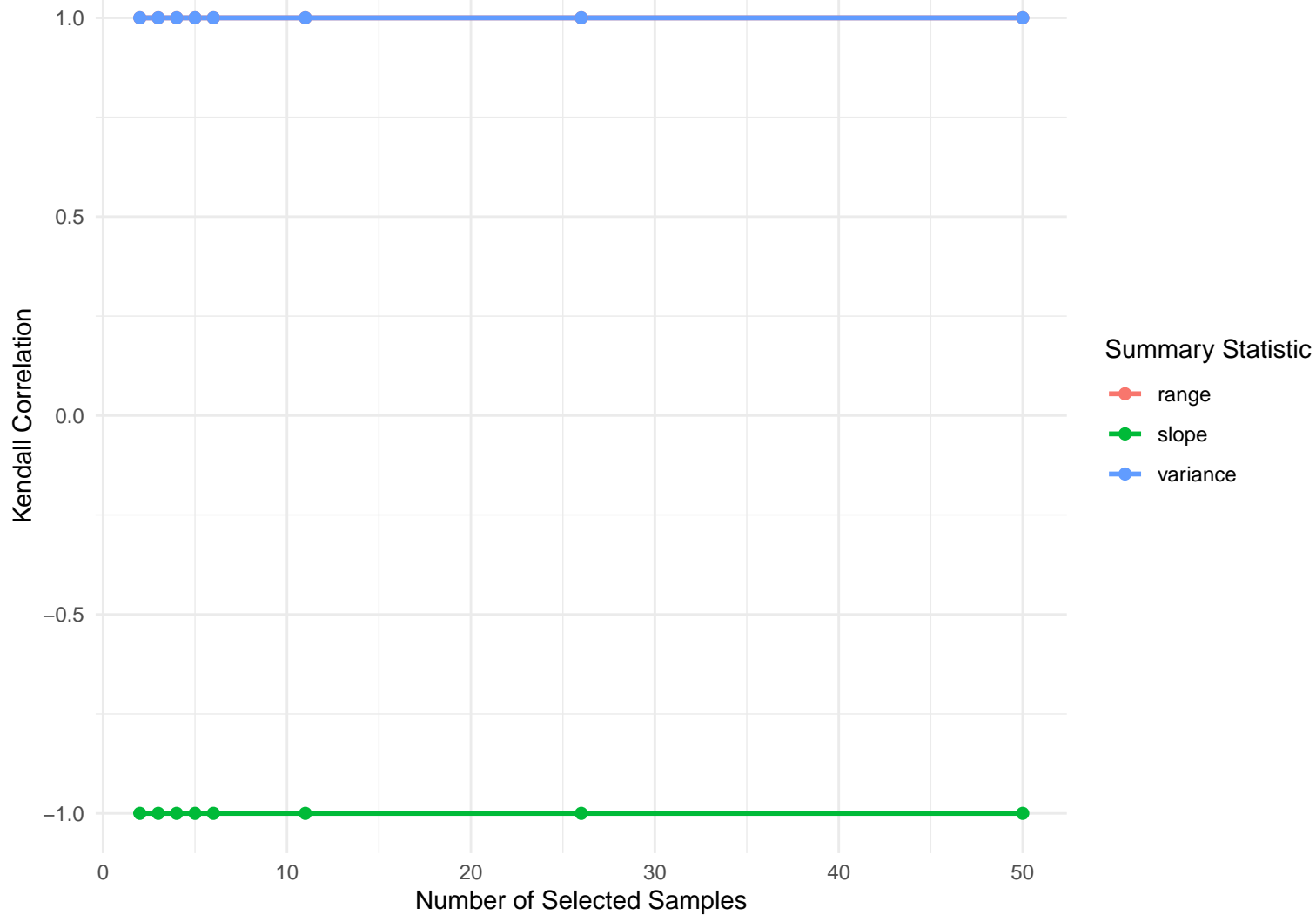
Score: RSI (Local, full , Genotype: wave)



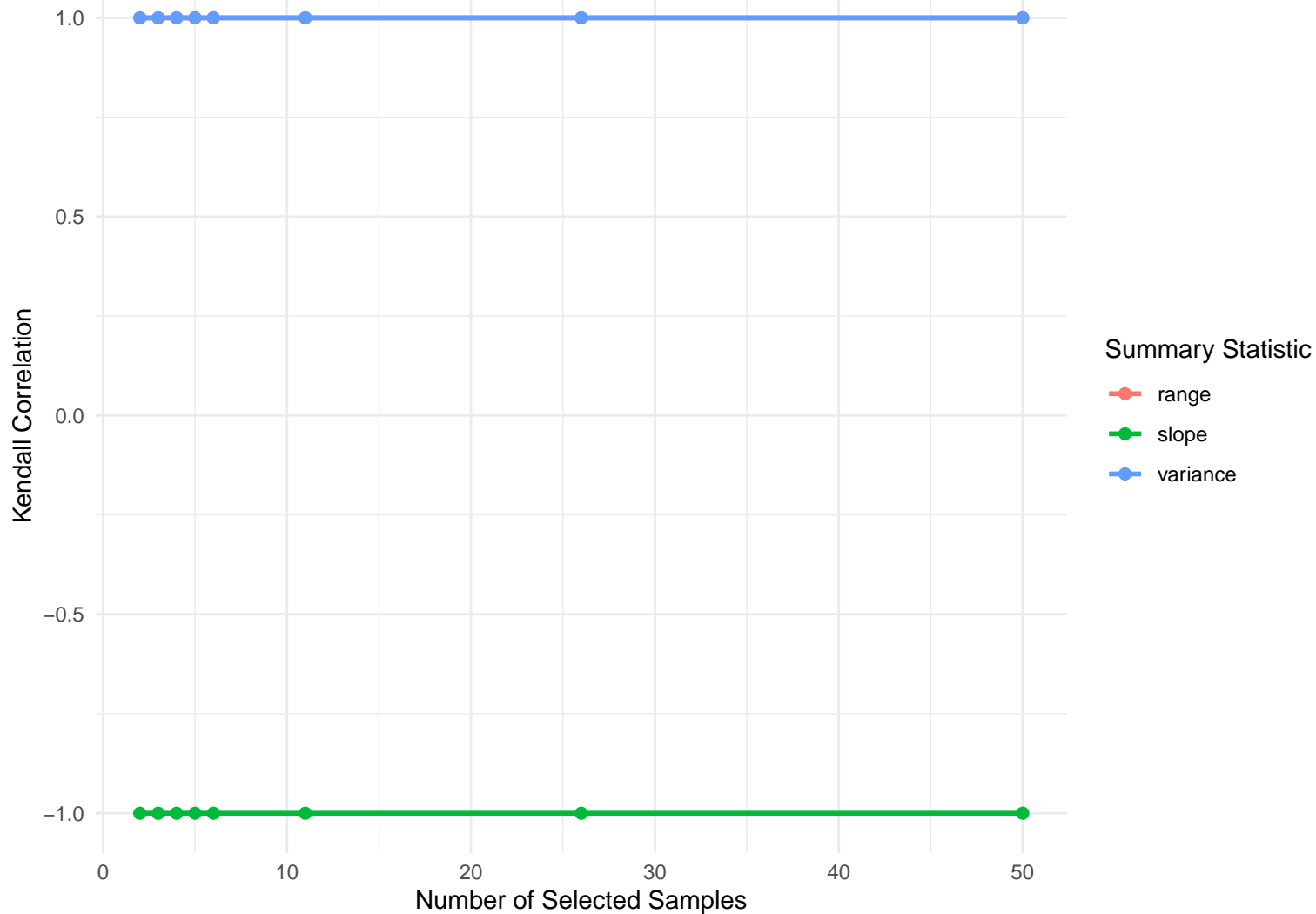
Score: EVS (Local, full , Genotype: linear)



Score: EVS (Local, full , Genotype: gaussian)



Score: EVS (Local, full , Genotype: sinusoidal)



Score: EVS (Local, full , Genotype: wave)

