Table 3 Examples of rules induced for *transcription*

A total of 5402 rules was generated for *transcription*. Using Michalski's rule quality measure (Torgo, 1993), we selected rules that cover the highest number of genes encoding proteins involved in *transcription* (cf. coverage) and that exhibit the highest ability to discern these genes from genes involved in all other processes (cf. accuracy).

30MIN - 4H(Constant) AND 1H - 8H(Decreasing) AND 16H - 24H(Increasing) => Process(transcription)

0MIN - 1H(Constant) AND 30MIN - 4H(Increasing) AND 8H - 16H(Decreasing) AND 16H - 24H(Decreasing) => Process(transcription)

15MIN - 1H(Decreasing) AND 30MIN - 4H(Constant) AND 6H - 24H(Increasing) => Process(transcription)

The three rules shown in the Table had a Michalski's-value of 0,75 (μ x accuracy + (1 - μ) x coverage; where $\mu = 0.5 + 0.25$ x accuracy). There was a total of 50 rules for *transcription* with Michalski's-value 0,75. Intervals where gene expression profiles fit the template for "increasing" are colored red, while intervals which fit the template for "decreasing" are colored green (description of "increasing/decreasing" templates see Methods).