Supplementary Material Online for

Towards a genome-wide transcriptogram: the *Saccharomyces cerevisiae* case

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1. Ontology

For each GO term presented below we have calculated the fraction of genes in windows of 251 sites that belong to the term, producing smooth profiles that depend on the ordering. For the randomly ordered list, no peaks are seen and no information can be gathered from these plots. For the ordering obtained using Dendogram algorithm, some peaks appear, but the ontology terms are not as concentrated as for the CFM algorithm. Figures **S7-S9** present different GO term profiles, for Random, CFM, and Dendogram orderings. Each panel refers to one GO term and presents the average value of the profile for the random ordering, as well as colored bands associated do deviations from these averages that range from 0 to 2 standard deviation (yellow bands) and from 2 to 4 standard deviations (pale pink bands). The gray region stands for deviations from the random average larger than 4 standard deviations. These standard deviations are calculated from the random ordering profile of each GO term. The peaks are certainly significant in both CFM and Dendogram orderings.

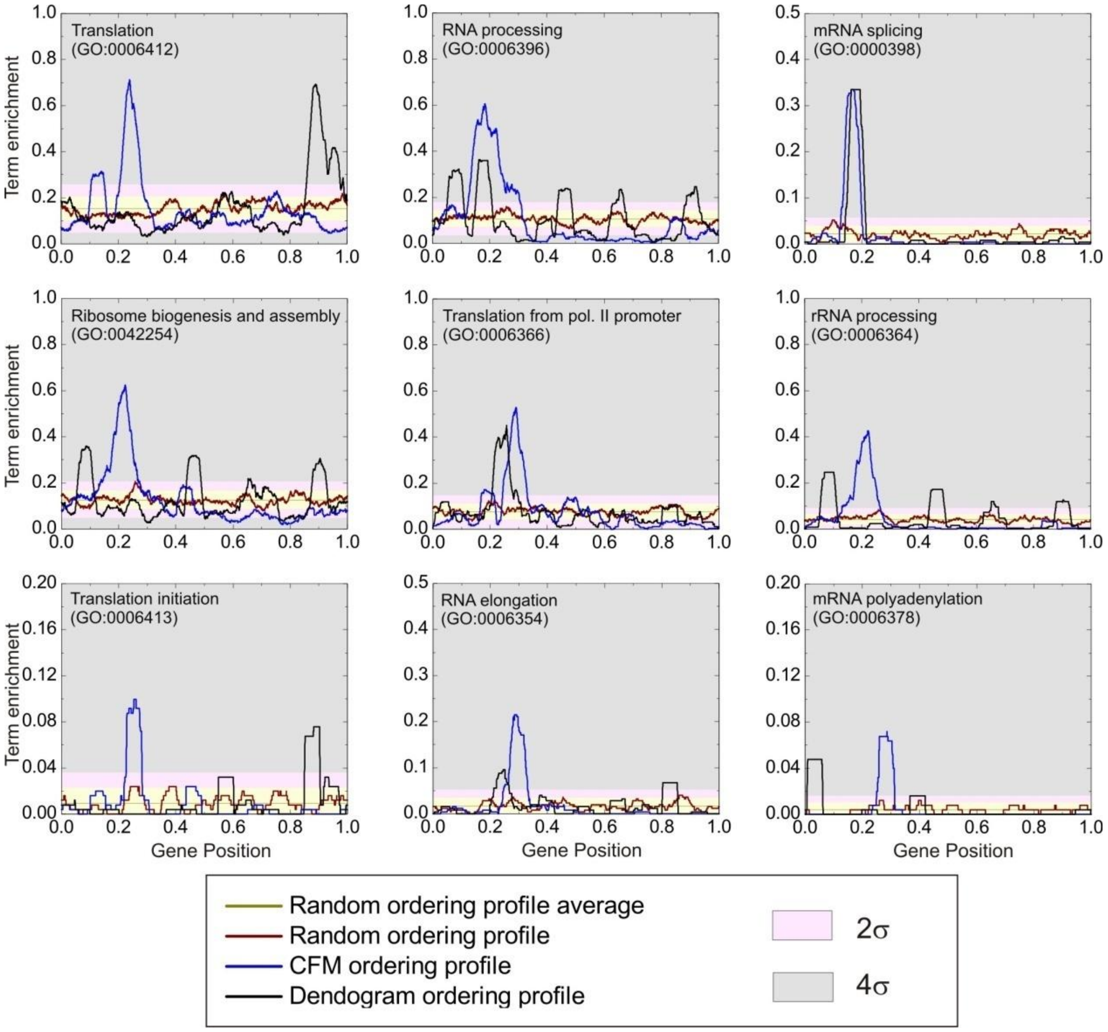

Figure S8. GO term profiles of the ontologies terms indicated (DAVID tools) as the most representative of the genes associated to window modularity peaks 1-3. The colored bands are associated to deviations from the average random ordering profiles larger than 2 and 4 standard deviations.

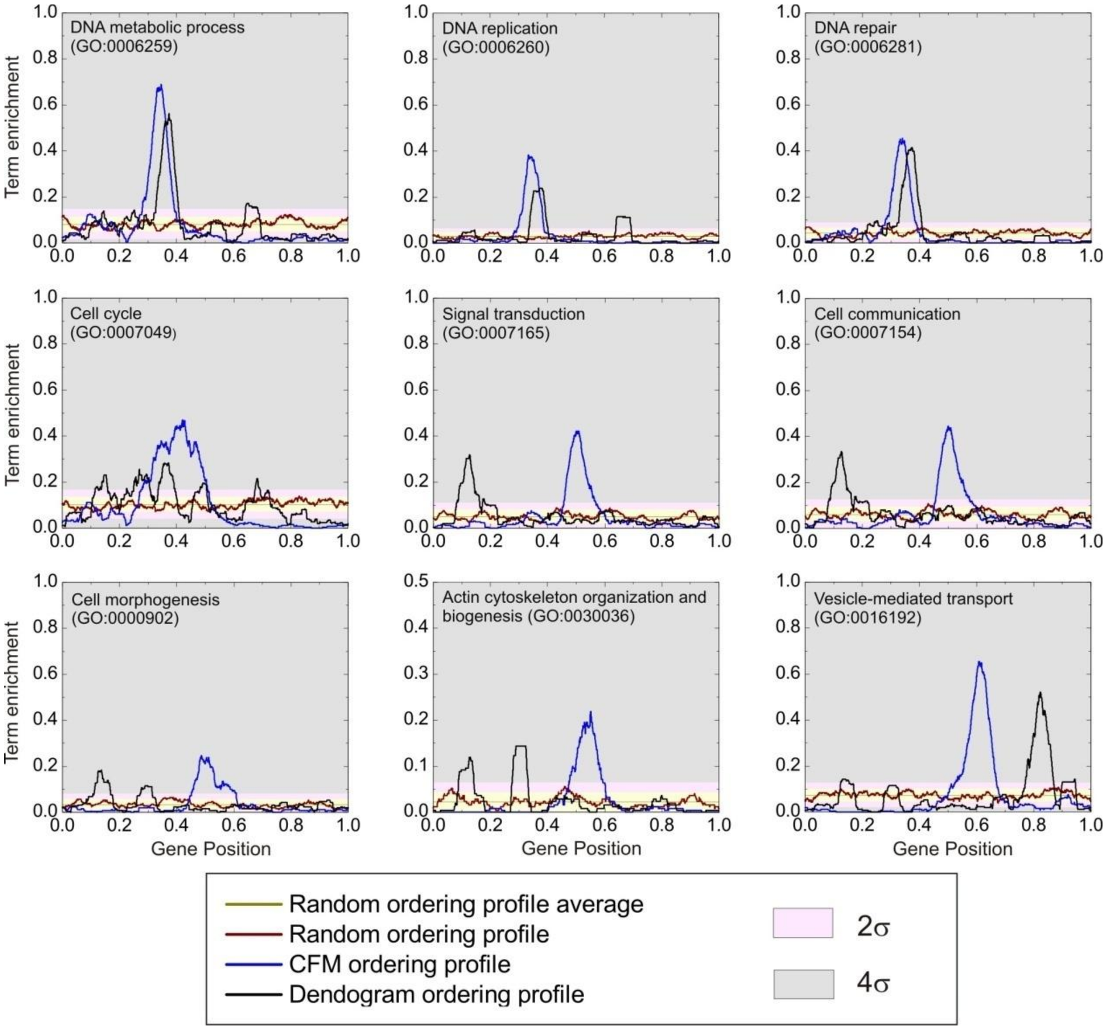

Figure S9. GO term profiles of the ontologies terms indicated (DAVID tools) as the most representative of the genes associated to window modularity peaks 4-6. The colored bands are associated to deviations from the average random ordering profiles larger than 2 and 4 standard deviations.

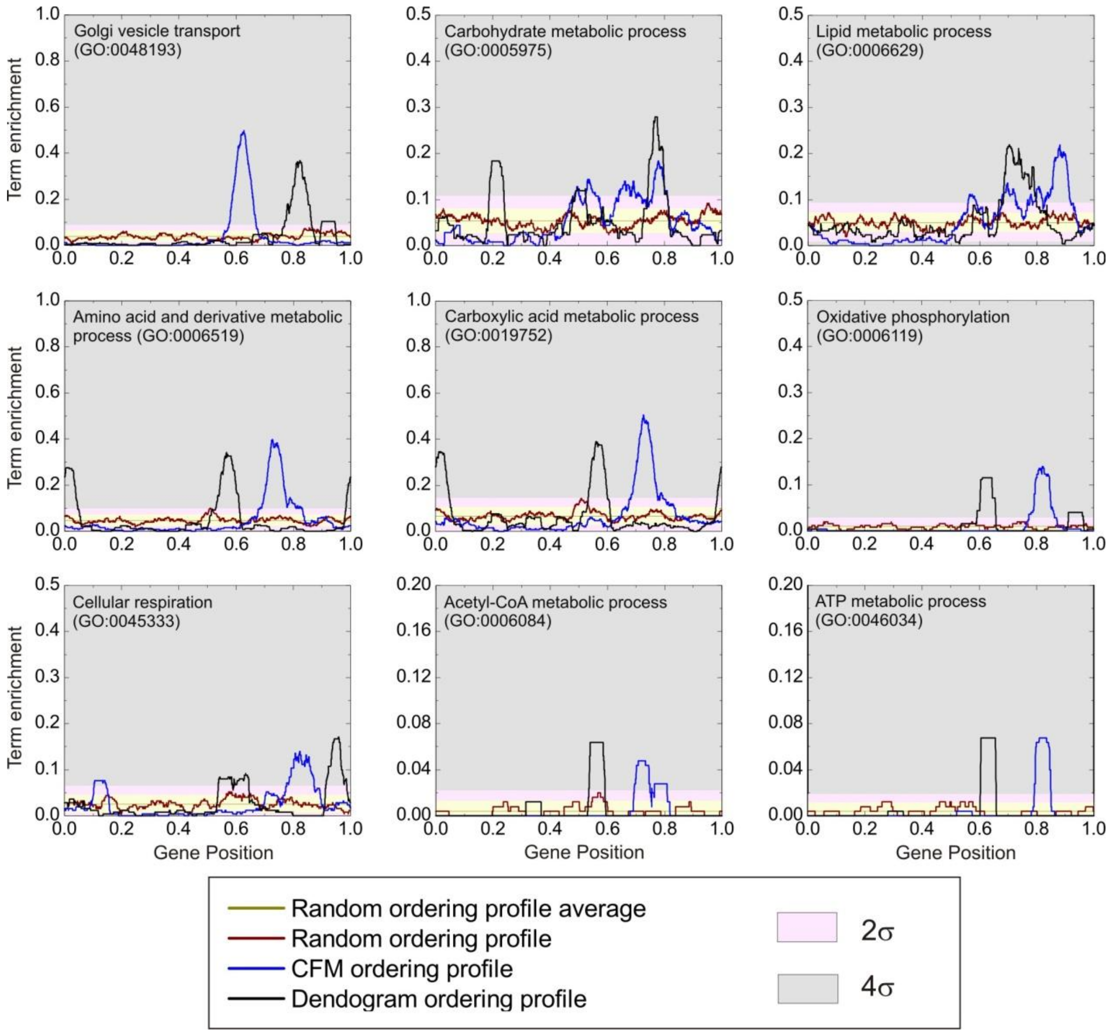

Figure S10. GO term profiles of the ontologies terms indicated (DAVID tools) as the most representative of the genes associated to window modularity peaks 6-7. The colored bands are associated to deviations from the average random ordering profiles larger than 2 and 4 standard deviations.

2. The transcriptogram in the Dendogram ordering for *Saccharomyces cerevisiae*

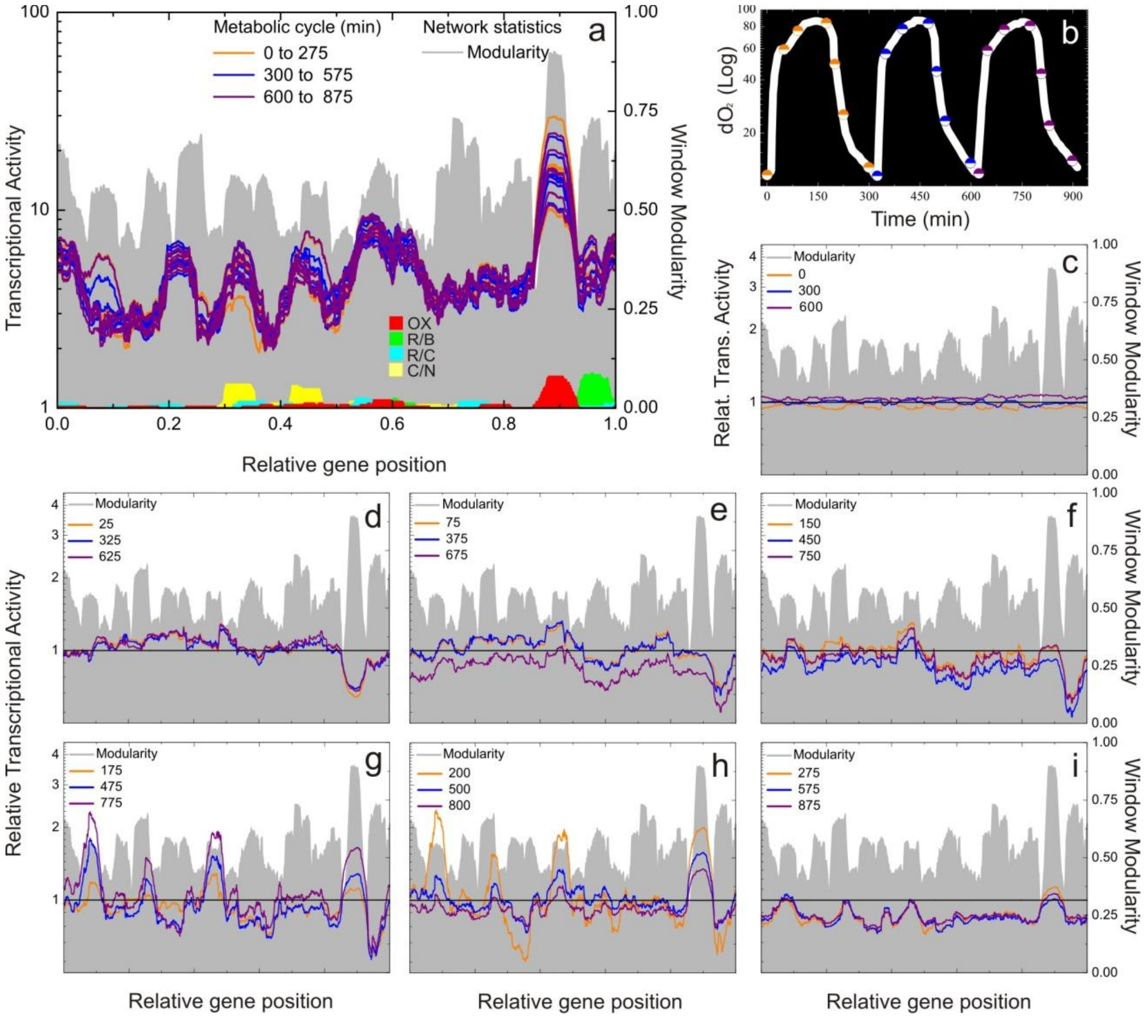

Figure S11. *Saccharomyces cerevisiae* transcriptogram using Dendogram. (**a**) Microarray data available at Gene Expression Omnibus database were projected on Dendogram ordering to obtain the expression profiles, or transcriptograms. Each color is associated to one cycle, as indicated in **b**. Projections on the ordering were performed always considering 251 gene window averages. To guide the eye, the window modularity is depicted as a landscape, together with the distribution of four gene clusters, as described previously based on sentinels genes: Ox (oxidative), R/B (reductive, building), R/C (reductive, charging), and C/N (catabolic,nuclear). (**b**) Plot of dissolved Oxygen versus time in log-linear. Transcriptograms (7 per cycle), were taken at the instants represented by the colored (orange, blue, and purple) dots. (**c – i**)

Relative expression profiles. Transcriptograms were divided by the expression values average of the three transcriptograms at the initial stage of each cycle (t = 0 min, 300 min, 600 min).

3. The transcriptogram in the Random ordering for *Saccharomyces cerevisiae*

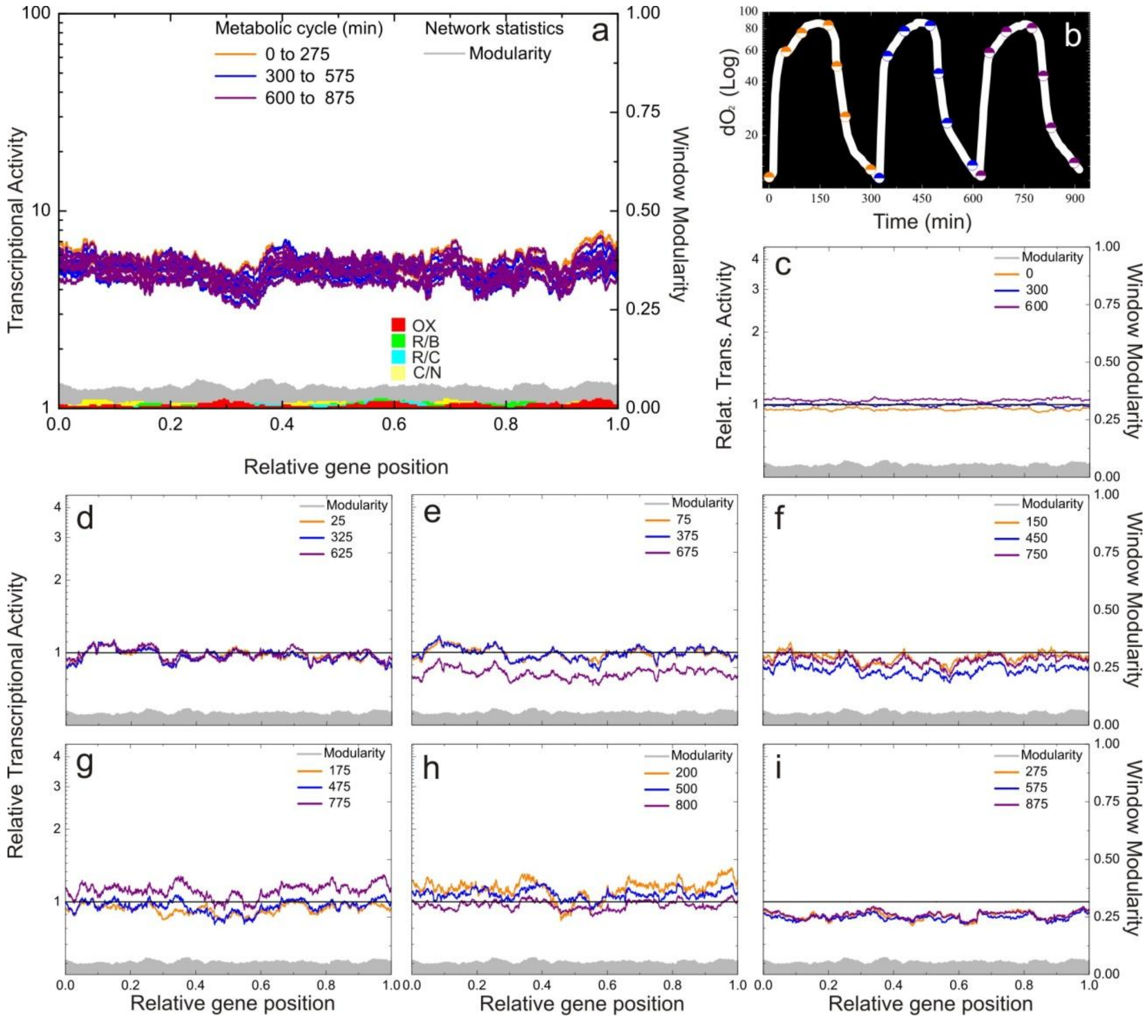

Figure S12. Saccharomyces cerevisiae transcriptogram using Random order. (**a**) Microarray data available at Gene Expression Omnibus database were projected on Dendogram ordering to obtain the expression profiles, or transcriptograms. Each color is associated to one cycle, as explain in **b.** Projections on the ordering were performed always considering 251 gene window averages. To guide the eye, the window modularity is depicted as a landscape, together with the distribution of four gene clusters, as described previously based on sentinels genes: Ox (oxidative), R/B (reductive, building), R/C (reductive, charging), and C/N (catabolic,nuclear). (b) Plot of dissolved Oxygen versus time in log-linear. Transcriptograms (7 per cycle), were taken at the instants represented by the colored (orange, blue, and purple) dots. (**c** – **i**) Relative expression profiles. Transcriptograms were divided by the expression values average of transcriptome (t = 0 min, 300 min, 600 min).

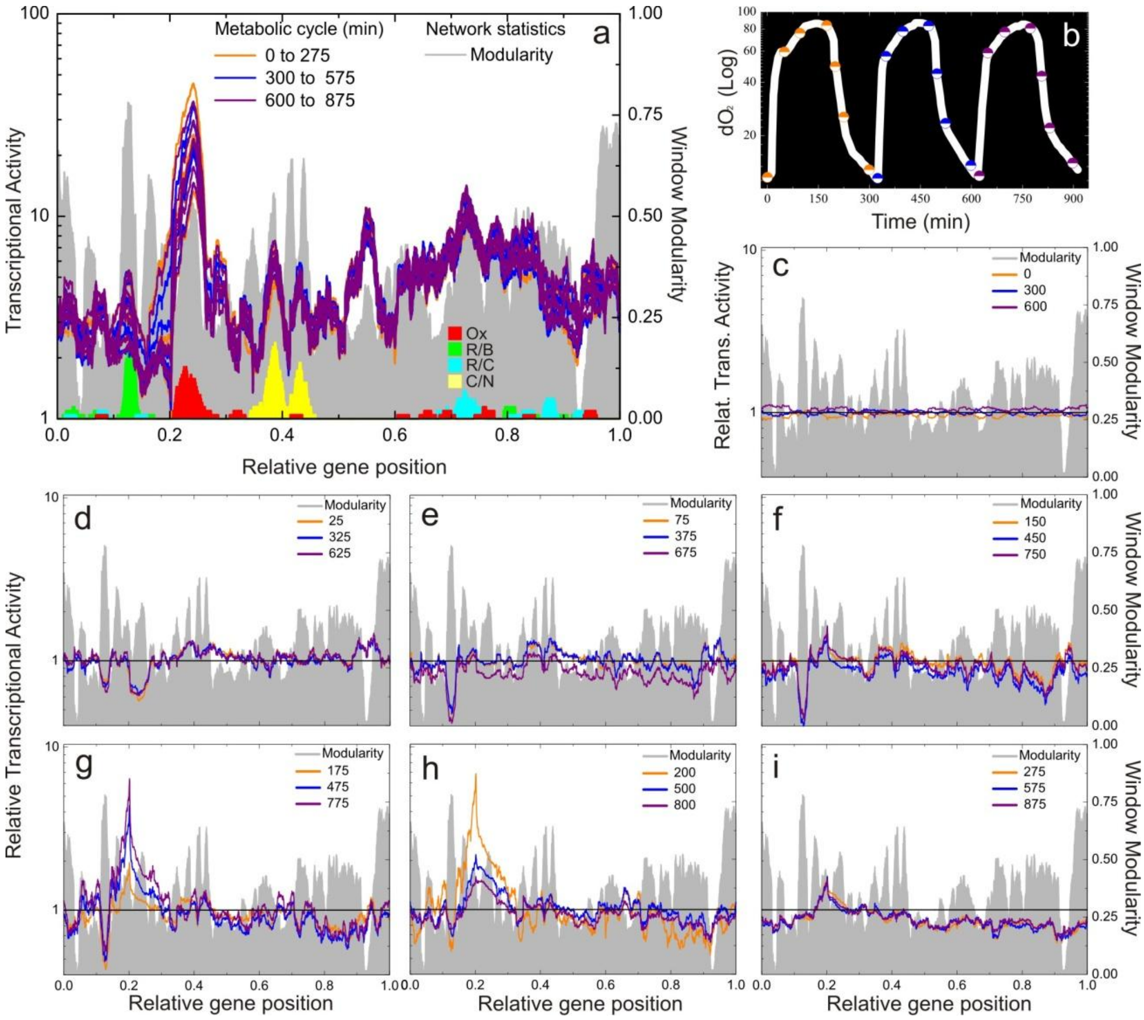

Figure S13. Window modularity for *Saccharomyces cerevisiae* for window size $w = 101$, together with the GO terms Macromolecule catabolic process (GO: 0009057) and Nuclear transport (GO: 0051169). Observe that for this window size these GO peaks are better resolved.

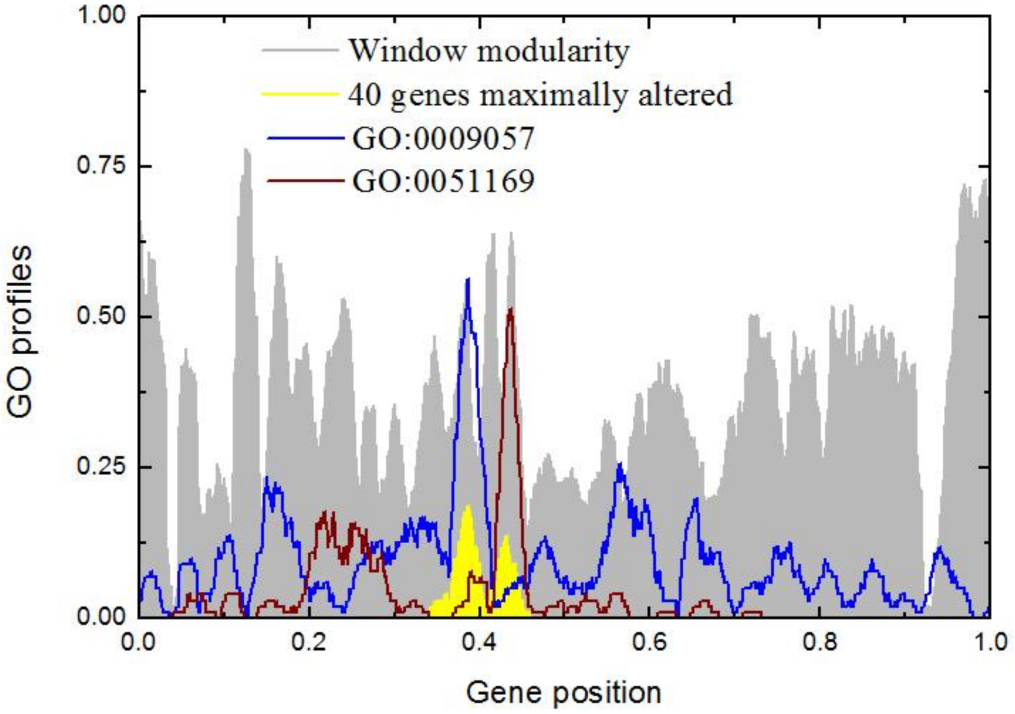

Figure S14. *Saccharomyces cerevisiae* GO profiles for window size $w = 101$ and the localization of the 40 genes that presented their expression levels most altered in the interval 0.35-0.45 (yellow). Macromolecule catabolic process (GO: 0009057) and Nuclear transport (GO: 0051169). Observe that for this window size these GO peaks are better resolved. Gray landscape: window modularity for $w = 101$.

Table S1 (TableS1.xls) The complete list of genes of ***Saccharomyces cerevisiae*** considered in this paper, ordered by CFM method. Columns associated to various GO terms (1 indicates the gene belongs to the term and 0 when it does not).

Table S2 (Table2.xls) The complete list of genes of ***Saccharomyces cerevisiae*** with information on connectivity and clustering of each gene.

Table S3 (TableS3.xls) The 40 genes presenting the most altered expression levels in the interval 0.35-0.45 of the CFM ordering.

Movie S1 (movieS1.mp4) Animation of the transcriptograms as projected on the CFM ordering, on the Dendogram ordering and on a Random ordering. The window size is

251 and all expression levels are taken relative to the average of the three initial states of each cycle

References

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