Supplementary Information for

Transcription of functionally related constitutive genes is not coordinated

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Supplementary Figure 1, related to Figure 3: Expression profiles of cell-cycle-stage-regulated genes. (a-c) *SWI5*, *CLB2*, and *NDD1* mRNA distributions for cells in G1 (red), S (blue), and G2 / M (green) phase. Error bars indicate s.e.m.
Supplementary Figure 2, related to Figure 5a: Pair-wise correlation coefficients for mRNAs of genes encoding β-subunits of the proteasome 20S core particle. Error bars indicate s.e.m.
Supplementary Figure 3, related to Figure 5b: Pair-wise correlation coefficients for mRNAs of genes encoding TATA binding protein associated factors involved in transcription initiation. Error bars indicate s.e.m.
Supplementary Figure 4, related to Figure 5c: Pair-wise correlation coefficients for mRNAs of genes encoding subunits of RNA polymerase II. Error bars indicate s.e.m.
Supplementary Figure 5, related to Figure 6: Distribution of nascent mRNAs per cell at the MDN1 transcription sites in the nucleus. (a) The distribution of nascent mRNAs per cell at the wildtype (WT) MDN1 allele. The number of nacent mRNAs were calculated by dividing the intensity of FISH signal at the transcription site in the nucleus by the intensity of individual mRNAs in the cytoplasm. ($\mu$) and ($\sigma^2$) represent the mean and variance, respectively, for a population of N cells. (b) The distribution of nascent mRNAs at the MDN1 allele with 24 PP7 hairpins inserted at the 3’ end. The mean number of nascent mRNAs at the wildtype and PP7 alleles were equal, which demonstrates that both alleles are transcribed identically. Moreover, the nascent mRNAs of the two alleles were only weakly correlated ($r = 0.25 \pm 0.11$). Error bars indicate s.e.m.
Supplementary Figure 6, related to Figure 4 and Figure 5: Distribution of nascent mRNAs per cell at the transcription site in the nucleus.
Supplementary Figure 6, related to Figure 4 and Figure 5: Distribution of nascent mRNAs per cell at the transcription site in the nucleus. (a-l) The number of nacent mRNAs for each gene were calculated by dividing the intensity of FISH signal at the transcription site in the nucleus by the intensity of individual mRNAs in the cytoplasm. $(\mu)$ and $(\sigma^2)$ represent the mean and variance, respectively, for a population of N cells. Error bars indicate s.e.m.
Supplementary Figure 7, related to Figure 4 and Figure 5: Correlation between nascent mRNAs at the transcription site in the nucleus. (a) Pair-wise correlation coefficients between the number of nacent mRNAs at the transcription site for three functionally unrelated genes. (b) Pair-wise correlation coefficients for nascent mRNAs of three genes encoding β-subunits of the proteasome 20S core particle. (c) Correlation coefficients for three genes encoding TATA binding protein associated factors involved in transcription initiation. (d) Correlation between three genes encoding subunits of RNA polymerase II. Error bars indicate s.e.m.
Supplementary Figure 8, related to Figure 7c-f: Mean mRNA abundance of constitutive genes increases over the cell cycle. (a-d) Experimentally measured average mRNA abundance across three different stages of the cell cycle. Differential interference contrast images were used to divide asynchronous cells into three different cell cycle stages based on morphology. Error bars indicate s.e.m.
Supplementary Figure 9, related to Figure 4 and Figure 7: Synchronizing effect of cell division disappears in cells with long cell cycles. (a) Representative FISH images of PRP8 (green) and MDN1 (red) mRNAs in cells grown in glucose-limiting media to achieve a doubling time of 14 hours. The scale bar in DIC image is 2 μm. (b) Heat map of number of MDN1 and PRP8 mRNAs in 397 cells shows that the correlation between these two genes is reduced to 0.05±0.05 from 0.26±0.05 in cells with a doubling time of 90 minutes. Marginal histograms: \( \mu_{MDN1} = 1.0 \pm 0.05, \sigma_{MDN1} = 0.9 \) (top); \( \mu_{PRP8} = 1.0 \pm 0.04, \sigma_{PRP8} = 0.7 \) (right). Error bars indicate s.e.m.
Supplementary Figure 10, related to Figure 2: Coordination in the expression of GAL genes is independent of the galactose concentration used for induction. All cells were induced for 15 minutes with varying concentrations of galactose, as indicated. Nascent or mature mRNAs were present in approximately 90% of cells upon induction with 2% galactose. About 75% of cells were induced with 0.5% galactose and 70% were induced with 0.25% galactose. (a) Heat map shows a high correlation coefficient (r) between the number of GAL10 and GAL1 mRNAs in cells induced with 2% galactose. (b) Correlation between GAL7 and GAL1 mRNAs in cells induced with 2% galactose. (c, d) Pair-wise correlations between GAL genes in cells induced with 0.5% galactose. (e, f) Pair-wise correlations upon induction with 0.25% galactose. Error bars indicate s.e.m.
Supplementary Figure 11, related to Figure 1 and Figure 2: Deletion of histone H2A variant H2A.Z reduces the correlation between GAL1 and GAL10.
Supplementary Figure 11, related to Figure 1 and Figure 2: Deletion of histone H2A variant H2A.Z reduces the correlation between \textit{GAL1} and \textit{GAL10}. (a) Incorporation of H2A.Z makes the +1 and −1 promoter nucleosomes slightly unstable and is thought to promote gene activation by exposing the transcription start site. (b) Deletion of \textit{HTZ1}, the gene encoding H2A.Z, led to a significant decrease in the expression of GAL genes. Only 40% of cells were induced after 30 minutes of induction with 2% galactose. \textit{GAL10} mRNA (red) and \textit{GAL1} mRNA (green) is shown along with DAPI (blue) and DIC image of cells. The scale bar is 2 \mu m. (c) Within the induced population, the percentage of cells actively transcribing both genes in the nucleus fell sharply compared to wild type cells (2% galactose, 15 minutes). (d) Heat map of number of \textit{GAL10} and \textit{GAL1} mRNAs per cell shows a reduced correlation between these two genes compared to wild type cells. The marginal histograms indicate that the mean mRNA abundance was also reduced significantly. $\mu_{\text{GAL10}} = 2.0 \pm 0.4$, $\sigma^2_{\text{GAL10}} = 12.1$ (top); $\mu_{\text{GAL1}} = 3.0 \pm 0.4$, $\sigma^2_{\text{GAL1}} = 30.5$ (right). Error bars indicate s.e.m.
| Gene    | Mean mRNA abundance $^1$ (molecules/cell) | mRNA Half-life$^4$ (min) | Mean protein$^7$ abundance (molecules/cell) |
|---------|-------------------------------------------|--------------------------|-------------------------------------------|
| MDN1    | 1.2                                       | 26                       | 538                                       |
| PRP8    | 1.2                                       | 38                       | 468                                       |
| KAP104  | 0.8                                       | 16                       | 2130                                      |
| PRE3    | 4.5                                       | 16                       | 7250                                      |
| PRE7    | 4                                         | 25                       | —                                         |
| PUP1    | 3.5                                       | 32                       | 11400                                     |
| TAF5    | 1.3                                       | 18                       | 14800 ± 203                               |
| TAF6    | 0.9                                       | 15                       | 6510 ± 1290                               |
| TAF12   | 1.3                                       | 22                       | 930 ± 45                                  |
| RPB1    | 2.9                                       | 24                       | —                                         |
| RPB2    | 3.9                                       | 26                       | 18700                                     |
| RPB3    | 3.3                                       | 18                       | 10000 ± 668                               |
| GAL1    | 0.2                                       | —                        | —                                         |
| GAL7    | 0.1                                       | 18                       | —                                         |
| GAL10   | —                                         | —                        | —                                         |
| NDD1    | 0.4                                       | 30                       | 799                                       |
| SWI5    | 0.8                                       | 17                       | 688                                       |
| CLB2    | 1.1                                       | 13                       | 339                                       |

Supplementary Table 1: Previously published mRNA abundances, mRNA half-lives, and protein abundances for all genes considered in this study.
SUPPLEMENTARY METHODS

Analytical solution for mRNA correlations

Model

The model presented here elaborates on previous work describing fluctuations of protein numbers in a dividing population of cells (Berg, 1978). In between two cell division events, mRNAs of a given gene are assumed to be transcribed randomly, independently of each other, at a rate of $k_i$ messages per minute. Once an mRNA molecule has been generated, it decays with a uniform probability per unit time $k_d$:

\[
\begin{array}{c}
\emptyset \\
\rightarrow \\
k_i \\
\leftarrow \\
k_d \\
\rightarrow \\
RNA
\end{array}
\]

In between cell divisions, transcripts of each gene initiate and decay independently from the other gene. At cell division, the two mRNA populations get partitioned between daughter cells simultaneously, but independently.

In the following sections, we first extract the master equation that describes the time evolution of the number of mRNA of one gene between cell cycles. We then find the solution to this master equation, imposing as a boundary condition that the cells are in a steady state growth, i.e. the number of mRNAs in the cell is the same at each generation. From the master equation, we determine the time-dependent probability distribution for the number of mRNAs of that gene. We show that the probability distribution of the number of mRNAs follow a Poisson distribution at all times. The mean of that Poisson distribution varies over the cell cycle and is equal to the deterministic solution of the continuous differential equation system corresponding to our model.

We use the single gene mRNA probability distribution to compute the predicted values of the observables of the experiments. First, we compute the time-averaged probability distribution of the mRNA number for one gene. This is the formal equivalent of looking at unsynchronized cells that were fixed at a given time: each cell is at a different stage of the cell cycle. Therefore, the time-averaged distributions should reflect the experimentally observed distributions. We can then use the time averaged mRNA probability distribution to compute the mean number of transcripts presents in the cell. Finally, we can compute the correlation between two genes. For the sake of simplicity, we assume here that the two genes have equal appearance and decay rates.
**Master equation**

The probability that an mRNA molecule is transcribed during an infinitesimal time interval $dt$ is equal to $k_i dt$. During the same time interval, an existing mRNA molecule will decay with a probability $k_d dt$. If there are $m$ mRNA molecules in the cell, the probability that one decay event occurs during the interval $dt$ is, therefore, equal to $mk_d dt$. Using these expressions, we can write the master equation that sets the time evolution of the probability $P(m, t)$ to have $m$ transcripts in the cell at time $t$:

$$P(m, t + dt) = P(m, t) + k_d dt [(m + 1)P(m + 1, t) - mP(m, t)]$$
$$+ k_i dt [P(m - 1, t) - P(m, t)]$$  \hspace{1cm} (1)

We introduce the generating function $G(z, t)$ as a mathematical tool to solve the master equation (1):

$$G(z, t) \equiv \sum_{m=0}^{\infty} z^m P(m, t)$$  \hspace{1cm} (2)

We first determine the expression of $G(z, t)$. We can then compute the mRNA probability distributions $P(m, t)$ using the following property of the generating function:

$$P(m, t) = \frac{1}{m!} \lim_{z \to 0} \frac{\partial^m G}{\partial z^m}$$  \hspace{1cm} (3)

We multiply each side of (1) by $z^m$ and sum over $m$ to obtain:

$$\partial_t G = k_d (1 - z) \partial_z G + k_i (z - 1) G$$  \hspace{1cm} (4)

We perform the following variable change:

$$v = k_i (1 - z)$$
$$w = k_i (1 - z) e^{-k_d t}$$

The master equation then appears as a simpler form:

$$\partial_v G = -\frac{G}{k_d}$$  \hspace{1cm} (5)

We integrate the differential equation as follows:

$$G = A(w) e^{-v/k_d}$$  \hspace{1cm} (6)

where $A$ is some function of the variable $w$. Therefore $G$ has the form:

$$G(z, t) = A(k_i (1 - z) e^{-k_d t}) \exp \left[-\frac{k_i}{k_d} (1 - z) \right]$$  \hspace{1cm} (7)

The function $A$ is unknown at this point, but we can determine its expression by imposing conditions corresponding to steady state growth.
Boundary conditions

We impose a steady state growth condition, meaning that the number of mRNAs in the cell is independent of the generation it belongs to. We also assume that mRNAs are equally partitioned between daughter cells at cell division.

Let’s assume a cell has \( j \) mRNAs right before cell division. Then the probability to get \( m \) mRNAs in one of the daughter cells is given by the binomial partitioning probability:

\[
\left( \frac{1}{2} \right)^j \binom{j}{m} \tag{8}
\]

Therefore, the probability of having \( m \) mRNAs in the cell at the beginning of the cell cycle can be expressed in terms of 1) the probabilities of having \( j \) mRNAs in the cell at the end of the cell cycle and 2) binomial partitioning (8):

\[
P(m, t = 0) = \sum_{j=m}^{\infty} P(j, t = T_g) \left( \frac{1}{2} \right)^j \binom{j}{m} \tag{9}
\]

We introduce again the generating function \( G(z, t) \equiv \sum_{m=0}^{\infty} z^m P(m, t) \). The boundary condition can then be written in terms of \( G \):

\[
G(z, t = 0) = G \left( \frac{1+z}{2}, t = T_g \right) \tag{10}
\]

Combining equations (7) and (10), we obtain the following condition on the unknown function \( A \):

\[
\forall x, \quad A(x) = A \left( \frac{x}{2} e^{-k_d T_g} \right) \exp \left( \frac{x}{2k_d} \right) \tag{11}
\]

The condition in (11) is satisfied by the following function:

\[
A(x) = \exp \left( \frac{1}{2k_d} \frac{1}{1 - \frac{1}{2} \exp(-k_d T_g)} x \right) \tag{12}
\]

We write the expression of \( A \) from (12) into (7) and obtain the full expression of \( G(z, t) \):

\[
G(z, t) = \exp \left[ -\frac{k_i}{k_d} (1 - z) \left( 1 - \frac{1}{2} \exp \left( -k_d t \right) \frac{1}{1 - \frac{1}{2} \exp(-k_d T_g)} \right) \right] \tag{13}
\]
Time-dependent probability distribution

Using the property of the generating function (3), we calculate the probability distribution of the mRNA number $P(m, t)$ from the expression of generating function $G(z, t)$ in (13):

$$P(m, t) = \frac{1}{m!} \exp \left[ -\frac{k_i}{k_d} \left( 1 - \frac{1}{2} \exp (-k_d t) \right) \right] \left[ \frac{k_i}{k_d} \left( 1 - \frac{1}{2} \exp (-k_d T_g) \right) \right]^m$$

(14)

We recognize here the expression of a Poisson distribution

$$P(m, t) = \frac{\lambda(t)^m e^{-\lambda(t)}}{m!}$$

(15)

where the mean $\lambda(t)$ is dependent on time:

$$\lambda(t) = \frac{k_i}{k_d} \left( 1 - \frac{1}{2} \exp (-k_d t) \right)$$

(16)

As expected, the time-dependent mean is equal to the deterministic solution of the continuous differential equation system based on our model. The stochastic calculation shows that the mRNAs remain Poisson distributed around this varying mean during the entire cell cycle, even right after cell division.

The expression of $\lambda(t)$ is the product of $k_i/k_d$ by a correction factor. $k_i/k_d$ is the ratio of the generation rate divided by the decay rate of the mRNA molecules, which would be the equilibrium value of the mean number of transcripts in the absence of cell cycle. The absence of a cell cycle is formally equivalent to the limiting case where the cell cycle duration is much longer than the other time scales involved, i.e. $k_d T_g \to \infty$. In this limit, the correction factor is equal to 1 when $t$ reaches infinity. Therefore the mean number of mRNA when the system reaches equilibrium is equal to the expected value: $(t \to \infty) = k_i/k_d$. In the same limiting case ($k_d T_g \to \infty$), we find that the mean number of mRNA at the beginning of the cell cycle is as expected half the number of mRNAs reached as equilibrium: $(t = 0) = k_i/2k_d$.

Time averaged probability distribution

We first compute the probability distribution of the number of mRNA molecules in the cell averaged over the cell cycle $\langle P(m, t) \rangle_t$:

$$\langle P(m, t) \rangle_t \equiv \frac{1}{T_g} \int_{t=0}^{T_g} P(m, t) dt$$

(17)
The development of this expression is not very informative and yields integrals that cannot be solved analytically. However, this integral can be readily estimated numerically. This is the case for all of the following statistical quantities.

### Mean number of transcripts
We can use the expression of the time averaged probability distribution (18) to compute the average number of transcripts $\mu$ present in the cell over the cell cycle. It is an important number: it is the value we have access to in the experiments, as we average together cells from various stages of the cell cycle. By definition,

$$
\mu = \sum_{m=0}^{\infty} m \langle P(m, t) \rangle_t dt \quad (20)
$$

We insert the explicit expression of $\langle P(m, t) \rangle_t$ obtained in (15):

$$
\mu = \sum_{m=0}^{\infty} m \left( \frac{1}{T_g} \int_{t=0}^{T_g} \frac{\lambda(t)^m e^{-\lambda(t)}}{m!} dt \right) \quad (21)
$$

### Variance of the number of transcripts
The variance is defined as follows:

$$
\sigma^2 = \frac{1}{T_g} \int_{t=0}^{T_g} \sum_{m=0}^{\infty} m^2 P(m, t) dt - \left( \frac{1}{T_g} \int_{t=0}^{T_g} \sum_{m=0}^{\infty} m P(m, t) dt \right)^2 \quad (22)
$$

Hence,

$$
\sigma^2 = \sum_{m=0}^{\infty} \frac{m^2}{T_g} \lambda(t)^m e^{-\lambda(t)} dt - \left( \sum_{m=0}^{\infty} \frac{m}{T_g} \lambda(t)^m e^{-\lambda(t)} dt \right)^2 \quad (23)
$$
Joint probability distribution of the number of transcripts
We consider here two genes within the same cell, with mRNAs that are produced and degraded independently. We compute the probability \( Q(m, n, t) \) to observe the \( m \) transcripts of gene 1 and \( n \) transcripts of gene 2 at time \( t \). For simplicity, we assume that the mRNAs expressed by the two genes have the same kinetics (equal values of \( k_i \) and \( k_d \)).

Since the transcripts are independent, \( Q(m, n, t) = P(m, t)P(n, t) \). The correlation in the mRNA abundance of the two genes comes only from the fact that they undergo cell division in synchrony.

Using the expression of \( P(m, t) \) in (18), we can express \( Q(m, n, t) \) as follows:

\[
Q(m, n, t) = \frac{\lambda(t)^{m+n} e^{-2\lambda(t)}}{m! n!} \quad (24)
\]

Hence,

\[
\langle Q(m, n, t) \rangle_t = \frac{1}{T_g} \int_{t=0}^{T_g} \frac{\lambda(t)^{m+n} e^{-2\lambda(t)}}{m! n!} dt \quad (25)
\]

Covariance of transcripts numbers expressed by two genes
The covariance of the number of mRNAs measures how the numbers of transcripts from two different genes change together within the same cell. It is a useful intermediate in the calculation of the correlation coefficient.

By definition, the covariance is equal to:

\[
\text{Cov} \triangleq \sum_{m,n=0}^{\infty} \frac{1}{T_g} \int_{t=0}^{T_g} mn Q(m, n, t) \ dt - \langle n \rangle^2 \quad (26)
\]

\[
\text{Cov} \triangleq \sum_{m,n=0}^{\infty} \frac{mn}{T_g} \int_{t=0}^{T_g} \frac{\lambda(t)^{m+n} e^{-2\lambda(t)}}{m! n!} dt - \left( \sum_{m=0}^{\infty} \frac{m}{T_g} \int_{t=0}^{T_g} \frac{\lambda(t)^m e^{-\lambda(t)}}{m!} dt \right)^2 \quad (27)
\]

Correlation Coefficient
In the case of two identical genes, the correlation coefficient \( r \) is equal to the ratio of the covariance (27) divided by the variance (23):

\[
r = \frac{\text{Cov}}{\sigma^2} \quad (28)
\]
The value of $r$ can be determined by numerical approximations of the sums in the numerator and the denominator.

**Numerical estimates**

In order to compute the numerical values of $r$ for a range of parameters, we wrote a program in Matlab 7.0.1 (TheMathworks). The inputs were the generation time (set invariably to $T_g = 90$ minutes), the mean number of transcripts $\mu$ and the experimental half life $t_{1/2}$. From the values of these macroscopic observables we first computed the microscopic rates as follows:

$$k_d = \frac{\log(2)}{t_{1/2}} - \frac{\log(2)}{T_g}$$

$$k_i = \frac{\mu k_d}{\left(1 - \frac{1}{k_d T_g} \left(1 - \frac{1}{2 - \exp(-k_d T_g)}\right)\right)}$$

Note that the formula linking the molecular $k_d$ to the half life includes a correction term corresponding to mRNA dilution during cell division. Formulas (23) and (27) were then estimated the following way: integrals were evaluated using the adaptive Gauss-Kronrod quadrature algorithm, and the discrete sums over the number of transcripts were truncated at a value arbitrarily set to the largest value between 20 and $5k_i/k_d$. 
FISH Probe Sequences

Ts indicate amino-allyl modified bases.

| Probe | Sequence |
|-------|----------|
| CLB2 182 | TGC GGC TGT TGA TCT TGA TAC GCT TTT TCT AGT AAA TTG AGG AAT CCG AC |
| CLB2 321 | GGA GCT CAG CTC TCC CCT CTT TTA TAG AAG TTA GGC CACCAAATTGCTGA |
| CLB2 427 | TCT ACC GAG TTA TGG ACT ACC TCA GTG CTT GAT CCA ACG CTC TTT AGG GG |
| CLB2 984 | CCC CTT CTT TGA TTT CAT CTT CGC TAC ATG CAC CGT CTG TCT CTG ATG CG |
| CLB2 1242 | ACC CGC CGC TAT AGT GTA TTA GAT TTT CAT CCC ATT TAC CTT TAC CTA AC |
| GAL1 – 1 | TAT GCT CGG CCA CTG GGC CAA TGG TCT TGG TAA TTC TCT TGC GCT AG |
| GAL1 – 2 | ACC AGT CCG ACA CAG AAG GAT CAA TTG TGA CAT AAG AAC CGT CCA ACG GC |
| GAL1 – 3 | GAA GAC AAT CCA CTG CCA GTT GGT ACA TCA CCC TCA CAG AAG ACT TGC AG |
| GAL1 – 4 | TAG CAT CTT TGT TAA CCG TTC GAT GCC GGA TCG AAT TCT GCC GCT CCA GG |
| GAL1 – 5 | TCG TGC TCG ATC CTT GCT CTC CAG AAA GTA AAA CAA CAC CTG ACG TGG CAG C |
| GAL1 – 6 | TGT GCG ACA TCG TCA ACA CTA AAG CCC TGT TTC TTA TGG GCG AGA GAC TC |
| GAL7 80 | TGT AAG CAG CCT CCT GTT GAC CTA ACC AAG GTC TTT TAG CTC TGT GTG GAG |
| GAL7 244 | CCT CAT TGG AAT CAT TCT GTG GTA AAA TAG GTT GAT CGA GCC TAA CGG CAG C |
| GAL7 428 | AGG CTT ATG ATT TTC TCT TGC TCT TCT GGA GAG ATC GTC AGT CAA TCG TGG CC |
| GAL7 541 | CTT GCG AAA CTT CAC TAG GGA TGG ATT CTA AGC ACC AAG CTT GGC CAT GTG G |
| GAL7 765 | GGC GAG GTC CTC CTT CAC CAT TTT GTT AAA TTG GCT AAT TGA GGC AAG CTT C |
| GAL7 878 | ACT CAA TTC ATC ACC AGT CGC ATT CAA AGG AGC CTG ATG GAT ACC CAT TG |
| GAL10 152 | CTC ATA GAA GGG AAT GTG CTT GGT CAA GAC CTC TAA CCT GCC TAC AG |
| GAL10 778 | CGA CAC AAA CCT TCA TTT TCA TTT TAG GCC TCT AGG TAT TGC AGG GCT GC |
| GAL10 925 | GCC CTA TCT GTG TTA GCC GTC AAG TTC AAA ACA TCA CCT GCT CTG CTG CC |
| GAL10 1059 | GCA TAT CTT CAG CGG AAA ATC TGG CCT CGA CAC CCC TTA ACT GTG AAC CA |
| GAL10 1173 | CAA GAA CAA CTG ATT GTG GTC CTT TCA CCT TCA GGT AAA CAA CAA TGC GGG CC |
| GAL10 1448 | ACC TGG AAA AAA TTT GGT GTC CTT CTC ATT ATC TAT CAG CAT GTA CTC GGC GG |
| KAP104 99 | CTA GTT GCA ACA CAT AGT CTT CGG CGG GCT TCC ATG TCG ATG CCA TCT TT |
| KAP104 425 | ATA CCG GGC GTA GTC CTA TTT TGC TTA AGA TCC TGG TAG TGT TG |
| KAP104 1421 | CCT GCC TCT TTT TTC ACA ATA CGG GGT GTA ATG GCC TTG ATG TCC TCC |
| KAP104 2870 | AGT CCT TCT CAG GCA CTA CTA TTT TGCG TGT CCT GAT GTG ATT TGG CTT CC |
| MDN1 794 | TTT GTC GTG GAT AGT GTG GAC CTT AGG GAC GAT AAC GCC ACA GAT TGA CG |
| MDN1 860 | CTC CCG AGT TGA CGA AGA GAG GAA ACC GTC TTA TGA GTA GGG ACA AAG GTT |
| MDN1 1104 | CTA TAA GTA CCC ATC TCC CTT TTT TGA CCC CCG TAG CGA GAA CAC CAG CTC |
| MDN1 1210 | TTT GCA GCC TTT ACA GTC TCT CCT CTG GAT GGA ATG GTT AGT TCG GCC TT |
| MDN1 4350 | CAC CTT TCT GCA AGA AGC ATA TAG CCA CTG GCA GCA AGC TGC TCA TAT CC |
| MDN1 4511 | CTA AGA CCG ATA GTC GGC TGC TTC CTT TTG CTT TAC CAG AGC CAA TG |
NDD1 45  GTA TCT GCA TTA TTG TCC GTA GAG GCC TGT CTT GAG GAA GTT GCA GTT GCC
NDD1 325  CTT TGT GAC AGC AGG AGG TAC AAG TGA ACC TAG AGC TTG CTG TTG TTG TTG
NDD1 430  TGC TCT GGG GAT GCA ACC AAA AAT TCG CTG GGT AAA GAG TTG CCG AAC TG
NDD1 536  TGC TGA GCA CCG TTA GAA TCT GTT ACA AAT CGA AGT GGT GTC TTG GCC GGA G
NDD1 994  TCG TTG TCC TTA GTT AGT GTG CTA GTG CTA TTG ATG GTA TCC TGG GGG GT
NDD1 1251  CTT GGG TAG CTC AGG AAT TTG TAA GGC AGA TGT ACC TGT GGT TGT ACT ATG C
PRE3  39  CAC CAT CCT TAA ATG TCA CGG CCA TAA TTT AGG AGC TTA AAT CTC GCA GTC ACT C
PRE3 104  ATC TGT CAC AGG GTT AGC TAT GTA CGC ACC AGT GGT GGT AGC TGA ATC AG
PRE3 164  TGC GTG TCT GCT GCA AAA CGG CAC ATG ACT ATG TTA TCA TCA CCA CA
PRE3 270  CGT AAC ATA ATT CTT TGA ACA CCG AGG CAG CAG CTC CAG TGT AGG GGG TA
PRE3 556  TCC ACA CCA GCA GCT GTA AAA ACA ACC ATT CTT ATA ACA CCA CCG GAA GAT CC
PRE7  39  GTT CAA TGG GTG TAT TTG AGC CCT CCG AAG ATG ATT CTG ATG CAA TAG TTG CC
PRE7 193  TCG CCG TCT GCT GCA AAT CCA TTC GCC GAC ATG ACT ATG TTA TCA CCA CA
PRE7 385  TCG AAC GAA TAG ACA CGG CCC TTA CCA TCT TCG TCA AGC CCC GCA ATG AT
PRE7 582  GTA GCA GAA GTG AAC GAG TCT TTC ATC ACT TCT ATG TCT TCC ACC GAC
PRP8  520  GTG GTG GTG GTG GAA GTG CTA AGT CGC TGT CCT CTT CAA AAC CAG GAG GTG
PRP8  572  ATG GCA CCA TCG GAT TAT CCA GGT CTG TTG ATC CAG CCG GTC GTG GT
PRP8  655  gccata ctc TTT TCC TTT TCG TGA CAC ATT GCT CTG TTG ATG GGT GAT GGG T
PRP8  904  tG GAG GCC ATG TCA CCT TGA GAA CAA TTA GCT TAT ATC CCT TTG GGG TGG T
PRP8 2617  GAG TAG TGG TAT AGT GCC TCT TAA GAA ATT TAG CCA CAC TCT CCA CGC Gag Tt
PRP8 2879  TTT TGA TTG GGG CGT GCA TAC CAG GAA CAT CCC ATG GAA CAA ATG TTT CTT
PRP8 2968  GTG AGC TCC ACG CTT TAT AGC TTC TCG ATT GTA ATG AGC TGC AGA TAC CC
PRP8 3108  cca TAA CAG AAA ATG TGG TCG TAG CCT CTT CGG GAG TAA TTT CGG GAC CGT Ti
PUP1  51  CTA CAA TGG TTG TAC CGG TGG AAG TTG CTT TAG GTT GTG TGT GCG AGT TT
PUP1 385  TGC GCA TGA ATG GAG AAC AAA TGA GAT CCC GTA GGG TCT ACA CCT GCA AC
PUP1 489  TGG CTT CCT CCT TCG TAA GGT CTT GCT TCC AGT GTG ATT CCA ACA CAG CCA TT
PUP1 683  CTC CTT CAG CAC AGC AGT TGT ACC CCT GGG GAA TTT GTA GCT TTT CTT GCT
RPB1  3  TGG ACC TCT TTT ACT GTA CGG AGT GGA GCA CTA GAA TAC TGT TGT CCT ACC
RPB1 122  CCT AGG GTC GTT TAG ACC ACC AAC AAT TTT CGC TCT CTG GTT ATC CA
RPB1 449  ACC TCC CCT TGA TAC GAG CTG AGT AGG ATC ATC TTA AGA AGG GAC ATC TG
RPB1 569  TTT GAC GCT ACT TAA TAC TGT TAG TTC TTC ATC CCG ATC CCC CCG GTG
RPB1 730  TTC TCA CTT TGT TGA CAC AGT TCT CTT TTG AGG CAA ATG GAT GGG CAC CGC ACC GGT G
RPB1 1195  AAA TCT ATA CGG TCT CCG CTA CTA CGG CTA ATG CAG TG TTT GTG GCA CCG GGG TG
RPB2  758  AAT AGT ACG AGC TGA ACT ACC CTC ACG ACC ATA AAG CTT GAC TTG AAG GG
RPB2  976  TAC CAA GGG CAG TAC CAC GAC GAC CAA TAA AGT CTA ATG CAG TTG CAC GAT C
RPB2 1353  GTT CAC CCC AGT TAC CAG TAG CCA AAG CGT ACT TAA GAC CCG ATG TTA TTG TT
RPB2 1734  TTG CGT GTT TTG GAA CAC CGT GCC AAA CAC CAT TGA CGA AGA CCC TT
RPB2 2134  CGT TTG GCA GGA TCA ACA TCG AGA TCG TT TCC TTA TTT GCC TCT GCA GG
RPB2 2274  TAC CCA TCG CAG ATT GGT AAG TGT TAC GCG GAG ATT GAT TAT GGT CAG GG

RPB3 87    TGG CTA AAG TGG GAA TCT CTG CTA TCA TGA CTC TAC GGA GAG AAC TAA TGG CC
RPB3 273   CGC TTT TCG CGA ACG CTT GCA ATG TTA ACA CCA CTG AAC ACT TAT CAC AG
RPB3 458   TTT CTT TGT GGT AAG TGT TAC CCA TTT GAG A

RPB3 510   TGA CTT TAC CCA TTT GAG A

RPB3 873   TAC CCA TTT GAG ATG CAT TCG TGG GAC CC

SW15 – 1  TGG CTA AAG TGG GAA TCT CTG CTA TAC TCT TTG GAG TGA AGG CCG
SW15 – 2  TGG CTA AAG TGG GAA TCT CTG CTA TAC TCT TTG GAG TGA AGG CCG
SW15 – 3  TGG CTA AAG TGG GAA TCT CTG CTA TAC TCT TTG GAG TGA AGG CCG
SW15 – 4  TGG CTA AAG TGG GAA TCT CTG CTA TAC TCT TTG GAG TGA AGG CCG
SW15 – 5  TGG CTA AAG TGG GAA TCT CTG CTA TAC TCT TTG GAG TGA AGG CCG
SW15 – 6  TGG CTA AAG TGG GAA TCT CTG CTA TAC TCT TTG GAG TGA AGG CCG
SW15 – 7  TGG CTA AAG TGG GAA TCT CTG CTA TAC TCT TTG GAG TGA AGG CCG

TAF5 196   GCT CTC AGC ATG GCC TCT GTA CGG TGG TAT CCC TTT TTA TTA AGG TAC TC
TAF5 381   CTA GTC GCC CGC TAG ATA CTG TAC CAC CTT CTG CAT TCT TCT TGG ATG AC
TAF5 1633  ACT AGG GCG GTG TGA GTA TCC AGG CAT AGC CTG ACG GTT TTA TCT TC
TAF5 1854  TGC AGG CCT TAT CGC TGG ATC CGG TAA ACA CAT AGC AAG CTT TGG CTA
TAF5 2029  CCA TGG CCA CGC ATT TTG TCT TAC ACT TTT TGG GCT TGG TTA TCA TCT
TAF5 2176  TAC CCA TTT GAG ATG CAT TCG TGG TGT TCT GGT TCT GCC TCA GTA TGG GC

TAF6 294   CTT CCT CAT CCA GGT AGT AAA CGG ACT GTC CTC CAC TTA GGT TTA CTC TGG ATC TTT TCA ACC TGG GAG
TAF6 369   TGC TAG CCA ATG TGT AGT AAA AGT TGG TAG ACG AGG CAC TTG CGG TAA TGG C
TAF6 525   TCA CAG AAG CAC TTG CTG TGG TGG AGG TTA CAG GTG TTT GGA GGC TGT TTA
TAF6 747   TGG AAC CAG TTG GTG CAG GCC ACT ATC AGT TCG TAG TGA AGT CAA AAG TGC T

TAF12 62   ACT GTC TCG GTT GCA GTA CCA TAT TTT GCT GAG CTC CTG TGG TCT TGG CAT CAG
TAF12 220   ACT TGC GAC CTT GCC ACG GTT TTA AGG CAT ATC TTT TTA GGG CAT CAT ATA CTC G
TAF12 547   GCA GTT CAA TTC TCT CTT GTA GCT GCT TGG GCC CTG CGG CTC TCT TGG C
TAF12 744   GCT GCT GCT GTT GTT GTT GTT GTT GTA CCC TTT GTT GCT GC
TAF12 800   TGC TGT TTG ACC CTG CGG TTG CTG CTG CTG TTG TTG CTG CGG CGG