Supplementary Tables

for ”Genomic encoding of transcriptional burst kinetics” by Larsson A. *et al.*

Supplementary Table 1 - Transcriptional burst kinetics inferred in Fibroblasts for C57Bl6 and CAST alleles. Transcriptome-wide inference of transcriptional burst kinetics using the maximum likelihood and profile likelihood. Burst kinetics was inferred from allele-resolved single-cell RNA-seq data from 224 primary adult fibroblasts. Inference was made using maximum likelihood and profile likelihood (code available on github: https://github.com/sandberg-lab/txburst). For profile likelihood the point estimates are followed by lower and upper confidence intervals. Mean expression corresponds to the mean number of unique UMIs detected per gene and cell.

Supplementary Table 2 - Linear regression results from core promoter element effect on burst size, frequency and mean expression. Result from the estimation of the effect of the presence of either of a TATA element or Initiator element (INR) on burst size (sheet 1), burst frequency (sheet 2) and mean expression (sheet 3) as well as their interaction with each other (TATA:INR) and the length of the gene (gl:TATA and gl:INR respectively). Ordinary linear squares (OLS) was used to estimate the parameters. Abbreviations: Dep. Variable: Dependent Variable, gl: gene length (log10 scale), Df: Degrees of freedom, AIC: Akaike information criterion, BIC: Bayesian information criterion, coef: regression coefficient, std err: standard error of the regression coefficient, t: t-statistic, P>|t|: p-value of the t-statistic, 0.025: Lower bound of the 95% confidence interval of the parameters, 0.975: Upper bound of the 95% confidence interval, Cond. No.: Condition Number, bs: burst size (log10 scale), bf: burst frequency (log10 scale), me: mean expression (log10 scale).

Supplementary Table 3 - Transcriptional burst kinetics inferred in Embryonic stem cells for C57Bl6 and CAST alleles. Transcriptome-wide inference of transcriptional burst kinetics using the maximum likelihood and profile likelihood. Burst kinetics was inferred from allele-resolved single-cell RNA-seq data from 188 embryonic stem cells. Inference was made using maximum likelihood and profile likelihood (code available on github: https://github.com/sandberg-lab/txburst). For profile likelihood the point estimates are followed by lower and upper confidence intervals. Mean expression corresponds to the mean number of unique UMIs detected per gene and cell.

Supplementary Table 4 - Significant differences in transcriptional burst kinetics between fibroblasts and embryonic stem cells. Comparison of transcriptional burst kinetics between fibroblasts (n = 224 cells) and embryonic stem cells (n = 188 cells). Burst kinetic parameters per cell type is listed together with p-values from the profile likelihood significance test for a difference in burst frequency or size between cell types.

Supplementary Table 5 - Significant differences in transcriptional burst kinetics between CAST and C57 alleles in fibroblasts. Comparison of transcriptional burst kinetics between genotypes for the fibroblast cells (n = 224 cells). Burst kinetic parameters per cell type is listed together with p-values from the profile likelihood significance test for a difference in burst frequency or size between cell types.

Supplementary Table 6 - Transcriptional burst kinetics in mouse and human fibroblasts. Comparison of transcriptional burst kinetics between mouse and human (n = 163 cells) fibroblasts (n = 1609 one-to-one orthologs). The C57 allele is used in mouse and haplotype designated in 'A' in human (we have no information regarding whether this is the paternal or maternal allele). Burst kinetic parameters per species is listed with their respective gene name and corresponding mean expression.