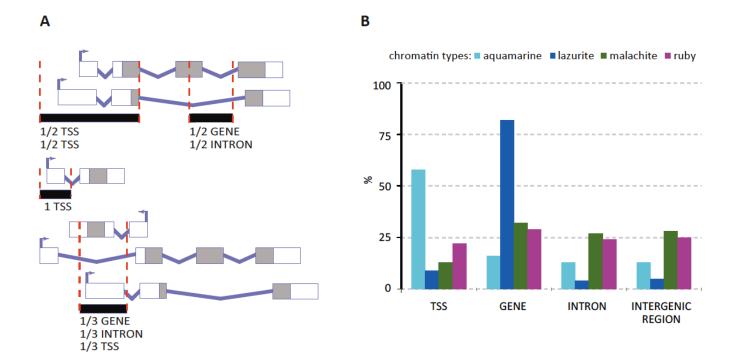
## **Supplementary Material**

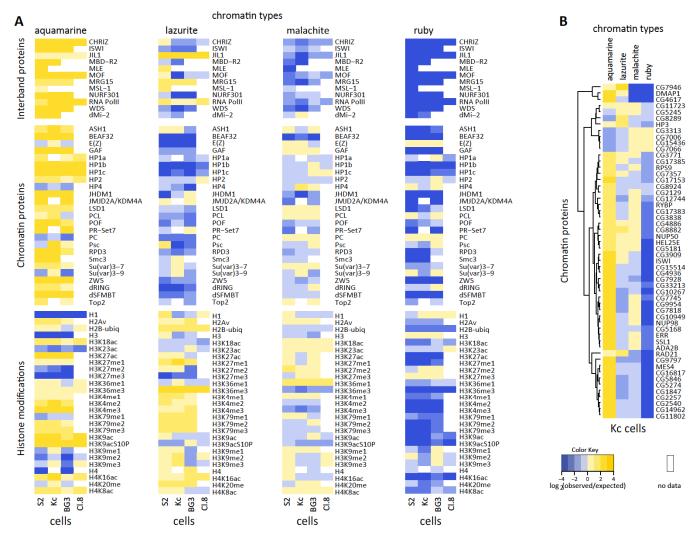
## Protein and Genetic Composition of Four Chromatin Types in *Drosophila* melanogaster Cell Lines

Lidiya V. Boldyreva<sup>1</sup>, Fyodor P. Goncharov<sup>1</sup>, Olga V. Demakova<sup>1</sup>, Tatyana Yu. Zykova<sup>1</sup>, Victor G. Levitsky<sup>2,3</sup>, Nikolay N. Kolesnikov<sup>1</sup>, Alexey V. Pindyurin<sup>1,2,3</sup>, Valeriy F. Semeshin<sup>1</sup> and Igor F. Zhimulev<sup>1,3,\*</sup>



**Supplementary Fig. (1).** Overlap between the four chromatin types and gene structure. **A.** Assignment of weighted classes to chromatin domains when they overlap with two or more different transcripts or genes. Bent arrows indicate the positions of TSSs. Grey boxes represent coding parts of exons and white boxes correspond to 5' and 3' UTRs. Introns are shown as broken lines. Black horizontal bars depict different scenarios of possible overlaps between chromatin domains and genes for all localization classes: TSS, GENE, INTRON and INTERGENIC REGION. Red vertical dashed lines show the positions of chromatin domains relative to the gene structure. **B.** Enrichment of the four chromatin types within different portions of genes. Y axis shows the fraction of each of the four chromatin types (aquamarine, lazurite, malachite, ruby) belonging to the TSS, GENE, INTRON and INTERGENIC REGION localization classes (X axis). Note that chromatin types span different portions of the euchromatic part of the genome: 12.68% (aquamarine), 16.82% (lazurite), 22.45% (malachite) and 48.05% (ruby) (see also Table 1).

<sup>&</sup>lt;sup>1</sup>Institute of Molecular and Cellular Biology of the Siberian Branch of the Russian Academy of Sciences, Novosibirsk 630090, Russia; <sup>2</sup>Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences, Novosibirsk 630090, Russia; <sup>3</sup>Novosibirsk State University, Novosibirsk 630090, Russia



**Supplementary Fig. (2).** Protein composition of the four chromatin types in S2, Kc, BG3 and Cl.8 cells. Data are presented as a log<sub>2</sub>-transformed ratio of the observed and expected overlap between the protein-bound regions and each of the four chromatin types. **A.** Heat maps of the enrichment (yellow) and depletion (blue) for proteins and histone modifications mapped by ChIP-chip in S2, Kc, BG3 and Cl.8 cell lines [13]. **B.** Heat map of the enrichment (yellow) and depletion (blue) for putative chromatin proteins mapped by DamID in Kc cells [16].

**Supplementary Table 1.** Numbers of aquamarine chromatin domains in the *Drosophila* genome that display features found in the reference interbands: CHRIZ and GAF binding and TSSs in the all four cell types analyzed (S2, Kc, BG3 and Cl.8 cells).

CHRIZ	TSS	GAF	Number of Aquamarine Domains	
+	+		2259	3991
+	+	+	1732	
	+	+	435	
		+	410	1757
+			315	
+		+	203	
	+		103	
			291	
Total			5748	