Annotation tracks available a MuG VRE's genome browser

Data	Source
Saccharomyces cerevisiae	
Gene and Gene predictions	Saccharomyces Genome Database [1]
Gene structure / UTRs / transcribed regions	Yassour et al, 2009 [2]
Gene Models / introns / 5' 3' UTR's / unannotated transcripts	Nagalakshimi et al. 2008 [3]
Transcription Start sites	Zhang, Z and Dietrich FS. 200 [4]
Chromatin modifications	Kirmizis A. et al. 2007 [5]
Nucleosome positions	Mavrich et al. 2008 [6]
Digital genomic footprinting	Hesselberth et al. 2009 [7]
H2A.Z nucleosome positions	Albert et al. 2007 [8]
H2A/H2B, H2A.Z/H2A.Z, H2A.Z/H2B log2 ChIp chip ratio	Guillemette et al. 2005 [9]
H3K4ac_set1D_on_WT, set1D_H3K4ac_on_H3, WT_H3K4ac_on_H3, WT_H3K4me3_on_H3	Guillemette et al. 2011 [10]
anti-Ac, H2AK7aci, H2BK16ac, H3K14ac, H3K18ac, H3K4me1, H3K4me2, H3K4me3, H3K9ac, H4K12ac, H4K16ac, H4K5ac, H4K8ac, mock, RNA PolII ChIP_chip	Liu et al. 2005 [11]
predicted average nucleosome occupancy, predicted nucleosome potential score, nucleosome sequence read count	Field et al. 2008 [12]
nucleosome positions, nucleoatac signal, nucleosome calling occurrences	Schep et al. 2015 [13]
ORC, Mcm2p binding, ARS sequences	Xu et al. 2006 [14]
ORC, ARS, Nucleosome positioning	Eaton et al. 2010 [15]
TATA_elements	Rhee and Ough 2012 [16]
Bur1, Cet1 (Capping enzyme), Ctk1 Elf1, Kin28 (TFIIH), Paf1, Pcf11, Ser2P (RNA Pol II), Ser5P (RNA Pol II), Ser7P (RNA Pol II), Rpb3 (RNA Pol II), Spn1 (Iws1), Spt16, Spt4, Spt5, Spt6, Spt6deltaC, Tfg1 (TFIIF), TFIIB	Mayer et al. 2010 [17]
Gal4, Phd1, Rap1, Reb1	Rhee and Pugh 2011 [18]
Nucleosome architecture through cell cycle	Deniz et al. 2016 [19]
Drosophila melanogaster	
Genes, Transcripts	
Chromatin types through protein binding sites	Filion et al. 2010 [20]
Nucleosome organization	Mavrich et al 2008 [21]
Homo sapiens	
Refseq Genes	
Gencode Genes	

1. Saccharomyces Genome Database. Available: http://www.yeastgenome.org

2. Yassour M1, Kaplan T, Fraser HB, Levin JZ, Pfiffner J, Adiconis X, Schroth G, Luo S, Khrebtukova I, Gnirke A, Nusbaum C, Thompson DA, Friedman N, Regev A. Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. Proc Natl Acad Sci U S A. 2009. 106(9):3264-9.

3. Nagalakshmi U1, Wang Z, Waern K, Shou C, Raha D, Gerstein M, Snyder M. The transcriptional landscape of the yeast genome defined by RNA sequencing. Science. 2008 6;320(5881):1344-1349.

4. Zhang Z, Dietrich FS. Mapping of transcription start sites in Saccharomyces cerevisiae using 5' SAGE. Nucleic Acids Res. 2005. 33(9):2838-51

5. Kirmizis A, Santos-Rosa H, Penkett CJ, Singer MA, Vermeulen M, Mann M, Bähler J, Green RD, Kouzarides T. Arginine methylation at histone H3R2 controls deposition of H3K4 trimethylation. Nature. 2007; 449(7164):928-932.

6. Mavrich TN, Ioshikhes IP, Venters BJ, Jiang C, Tomsho LP, Qi J, Schuster SC, Albert I, Pugh BF A barrier nucleosome model for statistical positioning of nucleosomes throughout the yeast genome. Genome Res. 2008 18(7):1073-1083.

7. Hesselberth JR, Chen X, Zhang Z, Sabo PJ, Sandstrom R, Reynolds AP, Thurman RE, Neph S, Kuehn MS, Noble WS, Fields S, Stamatoyannopoulos JA. Global mapping of protein-DNA interactions in vivo by digital genomic footprinting. Nat Methods. 2009. 6(4):283-289.

8. Albert I, Mavrich TN, Tomsho LP, Qi J, Zanton SJ, Schuster SC, Pugh BF. Translational and rotational settings of H2A.Z nucleosomes across the Saccharomyces cerevisiae genome. Nature. 2007;446(7135):572-576.

9. Guillemette B, Bataille AR, Gévry N, Adam M, Blanchette M, Robert F, Gaudreau L. Variant histone H2A.Z is globally localized to the promoters of inactive yeast genes and regulates nucleosome positioning. PLoS Biol. 2005; 3(12):e384.

10. Guillemette B, Drogaris P, Lin HH, Armstrong H, Hiragami-Hamada K, Imhof A, Bonneil E, Thibault P, Verreault A, Festenstein RJ. H3 lysine 4 is acetylated at active gene promoters and is regulated by H3 lysine 4 methylation. PLoS Genet. 2011;7(3):e1001354.

11. Liu CL, Kaplan T, Kim M, Buratowski S, Schreiber SL, Friedman N, Rando OJ. Single-nucleosome mapping of histone modifications in S. cerevisiae. PLoS Biol. 2005; 3(10):e328.

12. Field Y, Kaplan N, Fondufe-Mittendorf Y, Moore IK, Sharon E, Lubling Y, Widom J, Segal E. Distinct modes of regulation by chromatin encoded through nucleosome positioning signals. PLoS Comput Biol. 2008; 4(11):e1000216.

13. Schep AN, Buenrostro JD, Denny SK, Schwartz K, Sherlock G, Greenleaf WJ. Structured nucleosome fingerprints enable high-resolution mapping of chromatin architecture within regulatory regions. Genome Res. 2015; 25(11):1757-1770.

14. Xu W, Aparicio JG, Aparicio OM, Tavaré S. Genome-wide mapping of ORC and Mcm2p binding sites on tiling arrays and identification of essential ARS consensus sequences in S. cerevisiae. BMC Genomics. 2006 26;7:276.

15. Eaton ML, Galani K, Kang S, Bell SP, MacAlpine DM. Conserved nucleosome positioning defines replication origins. Genes Dev. 2010;24(8):748-753

16. Rhee HS, Pugh BF. Genome-wide structure and organization of eukaryotic pre-initiation complexes. Nature. 2012 18;483(7389):295-301.

17. Mayer A, Lidschreiber M, Siebert M, Leike K, Söding J, Cramer P. Uniform transitions of the general RNA polymerase II transcription complex. Nat Struct Mol Biol. 2010; 17(10):1272-1278.

18. Rhee HS, Pugh BF Comprehensive genome-wide protein-DNA interactions detected at single-nucleotide resolution. Cell. 2011 9;147(6):1408-1419.

19. Deniz Ö, Flores O, Aldea M, Soler-López M, Orozco M. Nucleosome architecture throughout the cell cycle. Sci Rep. 2016 28;6:19729.

20. Filion GJ, van Bemmel JG, Braunschweig U, Talhout W, Kind J, Ward LD, Brugman W, de

Castro IJ, Kerkhoven RM, Bussemaker HJ, van Steensel B. Systematic protein location mapping reveals five principal chromatin types in Drosophila cells. Cell. 2010 15;143(2):212-24.

21. Mavrich TN, Jiang C, Ioshikhes IP, Li X, Venters BJ, Zanton SJ, Tomsho LP, Qi J, Glaser RL, Schuster SC, Gilmour DS, Albert I, Pugh BF. Nucleosome organization in the Drosophila genome Nature. 2008 15;453(7193):358-62.