

30. Knoop, L. L., and Baker, S. J. (2000) The splicing factor U1C represses EWS/FLI-mediated transactivation. *J Biol Chem* **275**, 24865-24871
31. Armknecht, S., Boutros, M., Kiger, A., Nybakken, K., Mathey-Prevot, B., and Perrimon, N. (2005) High-throughput RNA interference screens in Drosophila tissue culture cells. *Methods in enzymology* **392**, 55-73
32. Soeller, W. C., Poole, S. J., and Kornberg, T. (1988) In vitro transcription of the Drosophila engrailed gene. *Genes Dev* **2**, 68-81
33. Wohlschlegel, J. A. (2009) Identification of SUMO-conjugated proteins and their SUMO attachment sites using proteomic mass spectrometry. *Methods Mol Biol* **497**, 33-49
34. Zhou, R., Mohr, S., Hannon, G. J., and Perrimon, N. (2013) Inducing RNAi in Drosophila cells by transfection with dsRNA. *Cold Spring Harbor protocols* **2013**, 461-463
35. Kim, D., Pertea, G., Trapnell, C., Pimentel, H., Kelley, R., and Salzberg, S. L. (2013) TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome biology* **14**, R36
36. Love, M. I., Huber, W., and Anders, S. (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome biology* **15**, 550
37. Herrmann, C., Van de Sande, B., Potier, D., and Aerts, S. (2012) i-cisTarget: an integrative genomics method for the prediction of regulatory features and cis-regulatory modules. *Nucleic Acids Res* **40**, e114
38. Lyne, R., Smith, R., Rutherford, K., Wakeling, M., Varley, A., Guillier, F., Janssens, H., Ji, W., McLaren, P., North, P., Rana, D., Riley, T., Sullivan, J., Watkins, X., Woodbridge, M., Lilley, K., Russell, S., Ashburner, M., Mizuguchi, K., and Micklem, G. (2007) FlyMine: an integrated database for Drosophila and Anopheles genomics. *Genome biology* **8**, R129
39. Brantjes, H., Roose, J., van De Wetering, M., and Clevers, H. (2001) All Tcf HMG box transcription factors interact with Groucho-related co-repressors. *Nucleic Acids Res* **29**, 1410-1419
40. Daniels, D. L., and Weis, W. I. (2005) Beta-catenin directly displaces Groucho/TLE repressors from Tcf/Lef in Wnt-mediated transcription activation. *Nature structural & molecular biology* **12**, 364-371
41. Bouazoune, K., and Brehm, A. (2006) ATP-dependent chromatin remodeling complexes in Drosophila. *Chromosome Res* **14**, 433-449
42. Flores-Saaib, R. D., and Courey, A. J. (2000) Analysis of Groucho-histone interactions suggests mechanistic similarities between Groucho- and Tup1-mediated repression. *Nucleic Acids Res* **28**, 4189-4196
43. Sekiya, T., and Zaret, K. S. (2007) Repression by Groucho/TLE/Grg proteins: genomic site recruitment generates compacted chromatin in vitro and impairs activator binding in vivo. *Mol Cell* **28**, 291-303
44. Edmondson, D. G., Smith, M. M., and Roth, S. Y. (1996) Repression domain of the yeast global repressor Tup1 interacts directly with histones H3 and H4. *Genes Dev* **10**, 1247-1259
45. Patel, S. B., and Bellini, M. (2008) The assembly of a spliceosomal small nuclear ribonucleoprotein particle. *Nucleic Acids Res* **36**, 6482-6493
46. Will, C. L., and Luhrmann, R. (2011) Spliceosome structure and function. *Cold Spring Harb Perspect Biol* **3**
47. Fisher, A. L., Ohsako, S., and Caudy, M. (1996) The WRPW motif of the hairy-related basic helix-loop-helix repressor proteins acts as a 4-amino-acid transcription repression and protein-protein interaction domain. *Mol Cell Biol* **16**, 2670-2677
48. Thorne, N., Inglese, J., and Auld, D. S. (2010) Illuminating insights into firefly luciferase and other bioluminescent reporters used in chemical biology. *Chemistry & biology* **17**, 646-657
49. Kaul, A., Schuster, E., and Jennings, B. H. (2014) The Groucho co-repressor is primarily recruited to local target sites in active chromatin to attenuate transcription. *PLoS genetics* **10**, e1004595