

Supplementary Information for: Notch and MAML-1 complexation do not detectably alter the DNA binding specificity of the transcription factor CSL

Cristina Del Bianco^{1,2}, Anastasia Vedenko³, Sung Hee Choi¹, Michael F. Berger^{3,5,6}, Leila Shokri³, Martha L. Bulyk^{3-5,7}, and Stephen C. Blacklow^{1,4,5,7,8}

¹Department of Biological Chemistry and Molecular Pharmacology and Department of Pathology, Harvard Medical School, Boston, MA 02115

²Current Address: Cibio Centro Interdipartimentale Biologia Integrata, University of Trento, Trento, IT

³Departments of Medicine and ⁴Pathology, Harvard Medical School and Brigham and Women's Hospital, Boston, MA 02115

⁵Committee on Higher Degrees in Biophysics, Harvard University, Cambridge, MA 02138

⁶Current Address: The Broad Institute of MIT and Harvard, Cambridge, MA, 02142

⁷Division of Health Sciences & Technology, Harvard Medical School, Boston, MA 02115

⁸Dana Farber Cancer Institute, Department of Cancer Biology, Boston, MA 02115

Address correspondence to S.C.B.: sblacklow@partners.org and M.L.B. at mlbulyk@receptor.med.harvard.edu

Figure S2. Heatmap of ungapped 8-mers bound in PBMs. Shown are all ungapped 8-mers bound at a PBM enrichment score of at least 0.30 in at least 1 PBM experiment in our data set. PBM experiments are clustered along the x-axis according to similarity in ungapped 8-mer binding profiles; ungapped 8-mers are clustered along the y-axis according to similarity across PBM experiments. Color bar indicates enrichment scores.

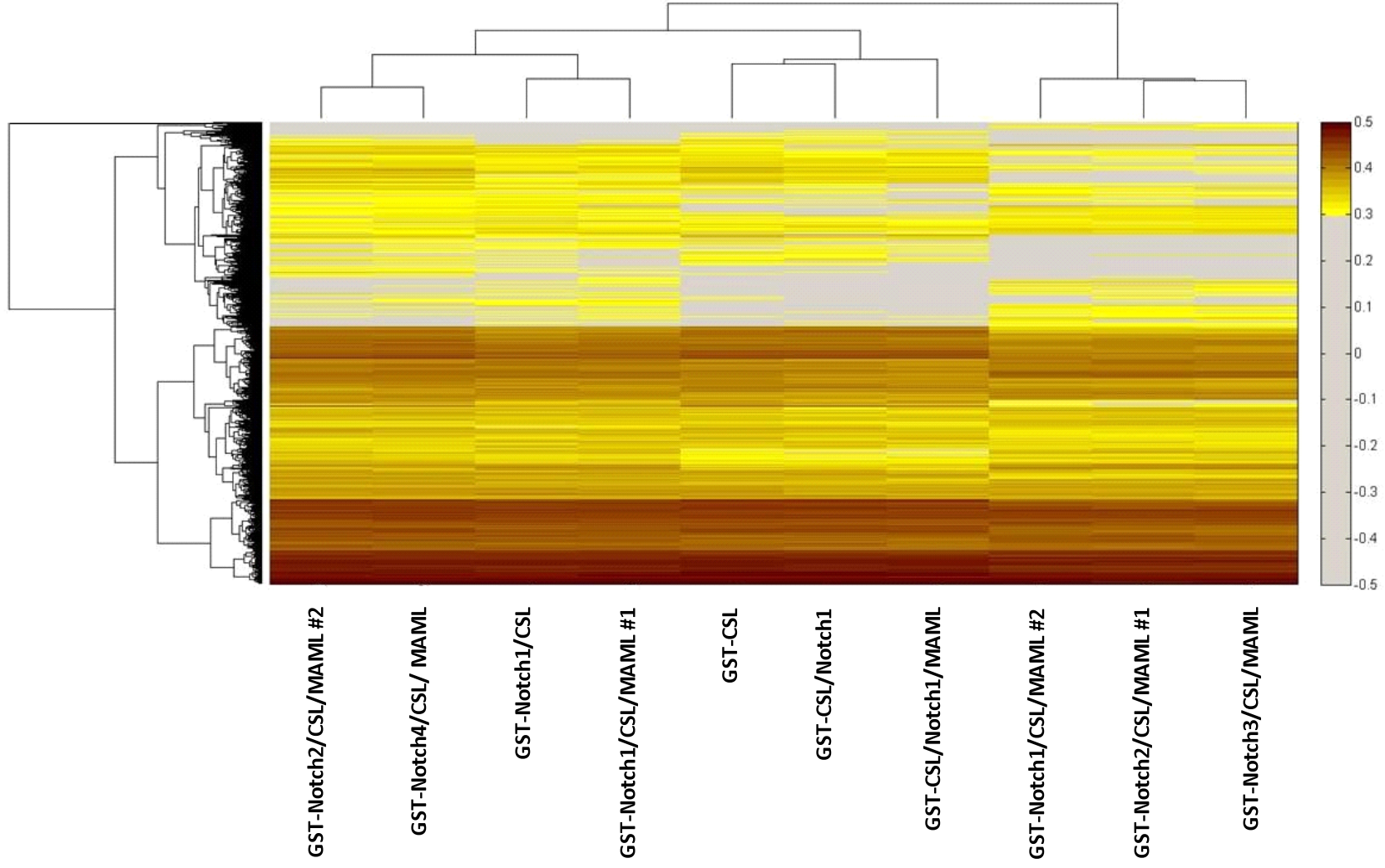


Figure S2