



Upper Panel

- █ Leu3-DBD *in vitro* DIP-chip scaled so most significant on Chr III =1
- █ Leu3-DBD *in vivo* ChIP-chip scaled so most significant on Chr III =1
- ➔ 5' end of ORF and direction of transcription

Lower Panel

- ■ ■ High-resolution nucleosome location (0: phased, 0.5: "fuzzy", 0.75: low-phased, .875: low-fuzzy, 1: nucleosome free)
- ▬ Low-resolution nucleosome occupancy. Scaled so that least occupied on Chr III =1
- Location of Leu3 binding motif, relative affinity (K_a) scale: K_a of best site on Chr III =1 ○ Low-affinity site
- ▬ Predicted Leu3 occupancy of arrayed locus based on DNA sequence alone (GOMER occupancy score)