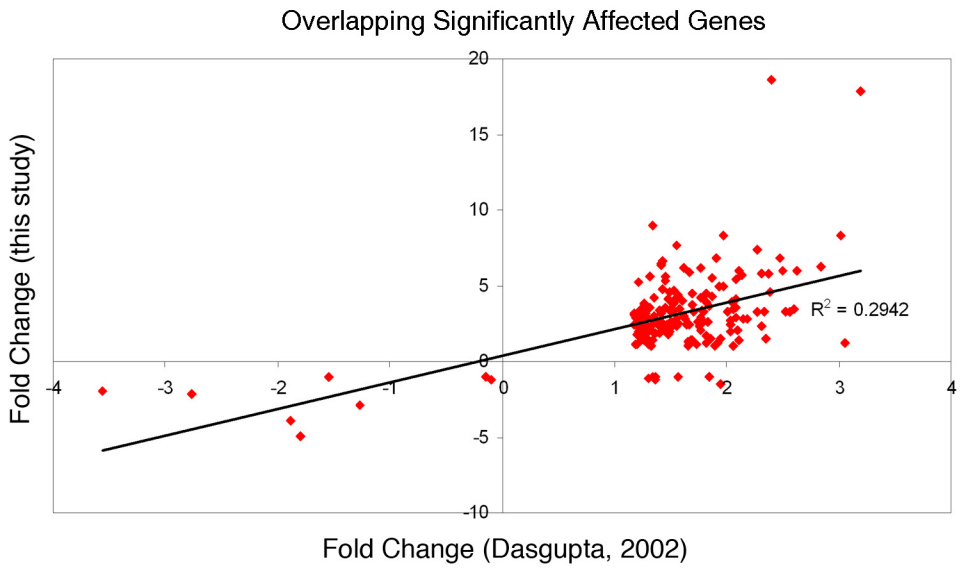
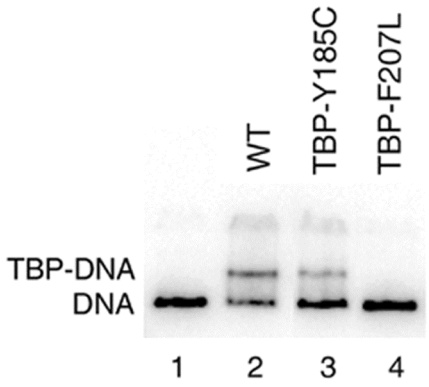
Figure S1



Supplementary Figure 1: Comparison of *mot1-14* microarray datasets from Dasgupta et al. (2002) (1) and the present study. The data sets are well correlated in that the vast majority of the Mot1-regulated genes identified in the two studies are regulated by Mot1 in the same direction. A modest correlation value is in large part attributable to improvements in technology, resulting in quantitative differences in the effects of a *MOT1* mutation.

Figure S2



Supplementary Figure 2: EMSA using radiolabeled *ARG3* promoter DNA (< 1 nM). *ARG3* is a Mot1-repressed promoter whose expression was restored to WT levels by both TBP Y185C and TBP F207L. The experiment was performed as in Figure 3. 10 nM of the WT or mutant TBP proteins was used; the reaction in lane 1 contained DNA alone. The TBP-DNA complex is indicated.

Supplementary Table 1: Comparison with *bur6-2* and *spt20*Δ microarray datasets

Comparison	R^2	% (#) Genes Up-regulated	% Genes Down-regulated	Total in Common
mot1-14 and TBP Y185C	0.4996	**38.33 %** (2389)	**43.35%** (2702)	81.68%
mot1-14 and TBP F207L	0.4229	**36.53%** (2277)	**39.96%** (2491)	76.50%
TBP Y185C and TBP F207L	0.6885	**41.47%** (2585)	**45.21%** (2818)	86.68%
mot1-14 and *spt20*Δ	0.0022	**19.92%** (1178)	**36.93%** (2184)	56.85%
TBP Y185C and *spt20*Δ	0.0016	**19.99%** (1182)	**36.93%** (2184)	56.92%
TBP F207L and *spt20*Δ	0.0027	**20.05%** (1186)	**35.46%** (2097)	55.51%
mot1-14 and *bur6-1*	0.3078	**25.64%** (759)	**46.39%** (1373)	72.03%
TBP Y185C and *bur6-1*	0.2333	**25.44%** (753)	**45.41%** (1344)	70.84%
TBP F207L and *bur6-1*	0.2027	**24.76%** (733)	**43.65%** (1292)	68.41%

To determine the degree of overlap between genes misregulated in the TBP bypass strains and those regulated by SAGA or NC2, published microarray data for *spt20*Δ cells (2) and *bur6* cells (3) were obtained and analyzed using Excel. To eliminate differences between individual data analysis methods, the values for every gene appearing on both of the indicated arrays was determined (using the Microarray Data Parser) and compared without designating cutoffs based on fold change or significance. The total number of genes included in the analysis for each set of comparisons was 6233 (data derived from this study); 5914 (*spt20*Δ); 2960 (*bur6*). Values greater than 1 were designated as up-regulated; values less than -1 were designated as down-regulated. R^2 is the correlation coefficient obtained from the line of best fit after plotting the data in Excel.

Supplementary Table 2: Comparison with TAF1 ΔTAND1 microarray dataset

Comparison	R^2	% (#) Genes Up-regulated	% Genes Down-regulated	Total in common
mot1-14 & TAF1ΔTAND I	0.18004	34.77% (1458)	38.33% (1717)	73.10%
TBP-Y185C & TAF1ΔTAND I	0.17454	35.76% (1486)	39.26% (1750)	75.02%
TBP-F207L & TAF1ΔTAND I	0.1543	35.89% (1518)	38.31% (1692)	74.20%

Comparisons of the indicated microarray datasets were performed as in Supplementary Table 1, using *mot1-14* and bypass data reported here and gene expression in strains harboring a deletion of the TAND1 domain of TAF1 (4). The similarities in the correlations and percent affected genes for all three comparisons indicate that genes affected in TBP-Y185C and TBP-F207L bypass strains are not differentially enriched in TAND1-dependent genes compared to *mot1-14* cells.

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