

Table 1. Summary of Novel TFIIIC-Occupied Sites

locus*	occupancy							putative A and B boxes [‡]			conserved [§]
	average percentile rank [†]							A	[spacing]	B	
	Tfc1	Tfc6	Rpc82	Rpc40	Brf1	TBP	control				
iSNR52	98	97	98	97	96	98	44	TGGGCTAGCGG [93]	GTTTCGAAACT	yes	
iYML089C	99	94	87	89	93	94	75	TGGCGCTTTGG [32]	GTTTCGAA-CT	yes	
YGR258C	95	91	75	N/A	60	38	12	TTGAAAAACTG [17]	GTTCTACACG	no	
YOR228C	93	94	70	56	35	34	75	TGCCATAAATG [84]	GTTTCGAACCC	yes	
YGR033C	98	95	79	76	87	91	10	TGGT-TGGTAG [29]	GTTTCGAAGCT	no	
YBR154C	98	95	49	83	77	66	27	TCGAATAGAGG [243]	GTTTCGTATCT	no	
YOL141W	97	94	48	66	32	22	48	TCGTATAATTG [36]	GTTCAAGTCG	yes	

* Segment of highest occupancy in the region.

[†] Numbers greater than the established cutoff for each subunit are in bold.

[‡] Putative A and B boxes were determined using the program tRNAscan-SE (1) with *S. cerevisiae* and related yeast sequences (2) and/or visual inspection. Bold bases in the table align with the published consensus for the A box (TRGYBTARYKG) and B box (GTTTCRATYCY) for *S. cerevisiae* tRNAs (3). Numbers in brackets [x] are base pairs between the A and B boxes.

[§] "Yes" indicates that >80% of the consensus bases (bold) are identical in the genomic sequences of *Saccharomyces* species *paradoxus*, *mikatae* and *bayanus* (2).