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13. ABSTRACT (Maximum 200 Words) The overall objective of this Idea Award was to develop a novel method for identifying the direct transcriptional targets of oncogenic transcription factors that are important in breast cancer. We have developed STAGE (Sequence Tag Analysis of Genomic Enrichment) as a novel genome-wide method for identifying the chromosomal targets of DNA binding proteins in any sequenced genome. STAGE is based on high-throughput sequencing of concatamerized tags derived from DNA associated with transcription factors that is isolated by chromatin immunoprecipitation. The application of STAGE to oncogenic transcription factors involved in breast cancer can help elucidate their role in gene regulatory networks underlying the disease. We have used STAGE to identify several novel targets of E2F4 in human cells. E2F4 is a transcription factor that is a member of the E2F family of transcription factors that is important in cell proliferation. We have verified many of the novel targets we predicted by STAGE using independent means such as promoter specific PCR and ChIP-chip. We have successfully carried out chromatin immunoprecipitation for c-myc and ER in human cells and are currently analyzing those samples using STAGE.				
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INTRODUCTION

This project is aimed at developing a novel genome-wide method for identifying the direct chromosomal targets of transcription factors that are important in breast cancer. Cancer involves, at least in part, aberrant programs of gene expression often mediated by oncogenic transcription factors activating downstream target genes. Distinguishing between direct and indirect targets of transcription factors is important for reconstructing the transcriptional regulatory networks that underlie complex gene expression programs that are activated in cancer. Indeed, transcription factors have been proposed as targets of anti-cancer therapy [1]. Identification of the target genes of oncogenic transcription factors is therefore of great interest and an area of intensive investigation.

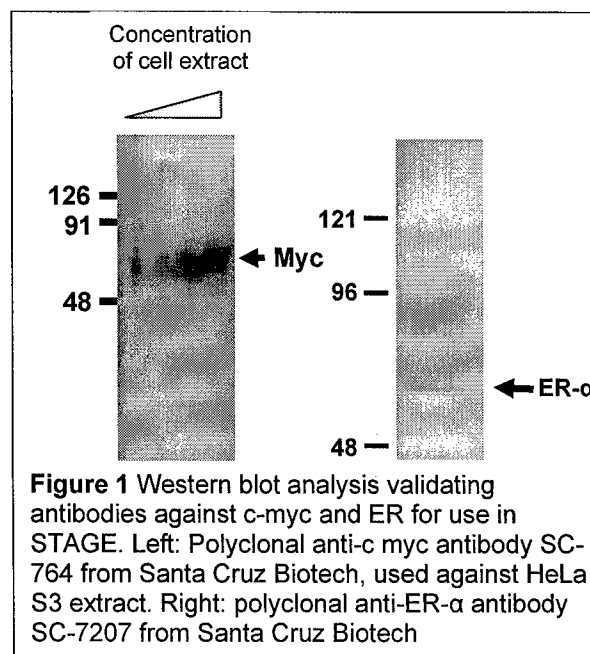
The chromosomal targets of transcription factors can be identified by the technique of ChIP-chip, where DNA occupied by a transcription factor is first isolated after crosslinking and immunoprecipitation, then identified by hybridization to a microarray of regulatory elements. One limitation with the ChIP-chip approach is the lack of availability of truly comprehensive promoter microarrays covering the entire human genome. In the Statement of Work, we proposed to develop a new genomic method named STAGE (Sequence Tag Analysis of Genomic Enrichment) that can potentially overcome some of the limitations of ChIP-chip analysis and can be applied to transcription factors important in breast cancer such as c-myc and ER (estrogen receptor). STAGE is based on high-throughput sequencing of concatamerized tags derived from DNA associated with transcription factors that is isolated by chromatin immunoprecipitation. The application of STAGE to oncogenic transcription factors involved in breast cancer can help elucidate their role in gene regulatory networks underlying the disease.

BODY

The overall objective of this Idea Award was to develop a novel method for identifying the direct transcriptional targets of oncogenic transcription factors that are important in breast cancer. We conceived of STAGE (Sequence Tag Analysis of Genomic Enrichment) as a novel genome-wide method for identifying the chromosomal targets of DNA binding proteins in any sequenced genome. STAGE is conceptually derived from SAGE (Serial Analysis of Gene Expression), but is applied to DNA isolated after chromatin immunoprecipitation (ChIP). The steps of the procedure in brief are as follows (depicted in Figure 1 of attached publication, Kim *et al*): (1) DNA-associated proteins are crosslinked to their target sites in vivo by treating cells with formaldehyde. Crosslinked chromatin is extracted, sheared by sonication, and immunoprecipitated with a specific antibody against a given protein of interest (the standard ChIP procedure). (2) The recovered DNA fragments are amplified by PCR using partially degenerate biotinylated primers and (3) digested with the restriction endonuclease NlaIII, which cuts at 5'-CATG. Biotinylated fragments are isolated using streptavidin beads and split into two pools. (4) Each pool is ligated to a different linker containing a recognition site for MmeI, a type IIS enzyme, as well as a specific primer recognition sequence. (5)

Digestion with MmeI releases 21-basepair tags that are anchored to NlaIII sites derived from the original DNA fragments enriched after ChIP. (6) The two pools are ligated and amplified by nested PCR using the specific primer sequences that were ligated. (7) The ends are trimmed by NlaIII digestion to generate ditags. Ditags at steps 6 and 7 are gel purified to ensure correct-sized fragments are used in subsequent steps. (8) Multiple ditags are concatamerized, cloned and sequenced. Mapping each tag back to the genome sequence can identify the DNA fragments that were present in the ChIP sample and thus identify protein binding loci. STAGE is thus a novel high-throughput experimental approach for identifying protein binding loci that does not rely on any assumptions about the location and distribution of these binding sites on the genome. It is therefore a useful method to identify functional elements in the genome. The coverage or comprehensiveness of this method is limited in principle only by the depth of sequencing, which is a reliable, widely available, automatable, inexpensive and high-throughput procedure. The fact that sequencing is performed on concatamerized (di)tags makes this a truly genomic method that can be quantitative. By analogy to SAGE, the number of times one observes a given tag within a STAGE pool or library should be directly proportional to the enrichment of that sequence in the original ChIP DNA pool. Since it is not dependent on microarray resources (but can complement ChIP-chip analyses), STAGE is applicable to any sequenced genome.

The original proposal was focused on identifying the targets of c-myc and estrogen receptor (ER) in human MCF-7 cells. We initially encountered some technical problems with regard to the use of suitable antibodies that would reliably immunoprecipitate c-myc and ER from cross-linked extracts. Our proposed STAGE method, like ChIP-chip, depends on the immunoprecipitation of proteins of interest crosslinked to their target promoters. We therefore decided to use E2F4 as a candidate protein to develop our method and demonstrate its utility in identifying novel chromosomal targets of any protein of interest in cancer cells. The proof-of-principle of the utility of the approach we proposed to develop during this project has recently been published as an Article in *Nature Methods* [2]. We have thus been successful in accomplishing the core tasks in our original statement of work, with the only difference being that it was applied to E2F4 rather than c-myc and ER. This publication is attached along with this report in the Appendix and we refer to it as "Kim *et al* (2005)" in our accounting of the tasks below. E2F4 is a member of the E2F family of transcription factors that are associated with cell proliferation and cancer, and E2F4 has complex roles in breast cancer. It has been reported to be a tumor suppressor gene [3] as well as an oncogene [4]. It is also reported to mediate the transcription of ER-alpha, (the focus of our Statement of Work) in breast cancer [5].



Below we describe our progress with regard to each of the specific tasks in the Statement of Work, using E2F4 as an example transcription factor. Detailed presentations of data are referenced in the attached publication. We have indicated how they related to each of the specific tasks and sub-tasks in the approved Statement of Work. These details are not duplicated in the body of this report.

At the same time we have obtained and successfully used antibodies that will work for immunoprecipitating c-myc and ER (Figure 1). We also tested the performance of anti-myc antibodies for chromatin immunoprecipitation and successfully validated the binding of c-myc to its target promoters in vivo (Figure 2). We are currently in the process of generating STAGE libraries for large-scale identification of target genes for c-myc and ER using the same strategy we have successfully developed using E2F4 as an example, as described below.

Task 1 *Develop a novel genomic method termed Sequence Tag Analysis of Genomic Enrichment (STAGE) to identify the direct transcriptional targets of c-myc and Estrogen Receptor (ER) in human cells*

We have optimized the experimental methods for successful application of STAGE in mammalian cells (**Task 1.a**). Specifically, we introduced two modifications to the STAGE method in order to achieve success in human cells. First, we implemented a subtraction strategy to improve the enrichment of DNA associated with proteins relative to the overall background. This method is described in Figure 3b of Kim *et al* in the Appendix. Table 1 below summarizes the overall number of STAGE tags we sequenced, both from E2F4 targets in mammalian cells as well as proof-of-principle experiments in yeast. Secondly, we developed an analysis strategy that scored STAGE tags based on their enrichment in the ChIP sample relative to unselected, normal human genomic DNA. We generated a STAGE library from normal human genomic DNA and profiled the background occurrence of tags to control for background in the ChIP sample. This is described in more detail in Kim *et al* in the appendix.

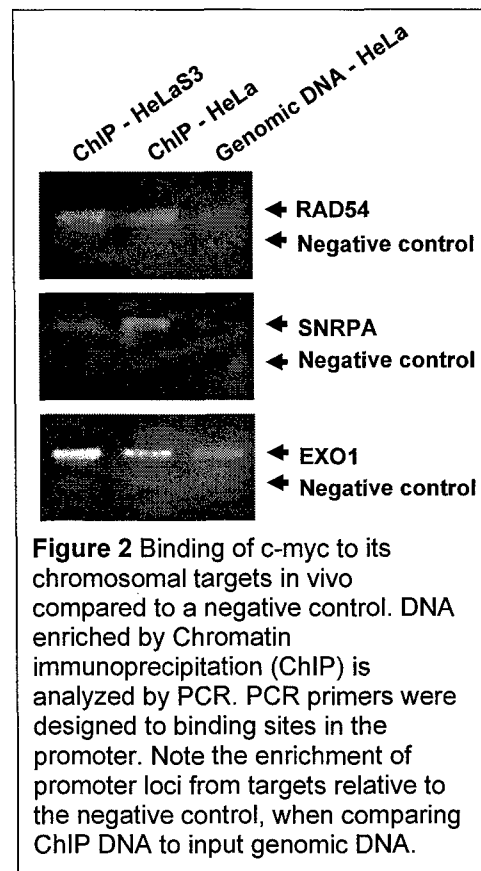


Table 1: Summary of STAGE tags sequenced

Within each set of two rows, the first row shows the total number of tags in each category, followed by the number of distinct tags after duplicates etc. have been removed.

	Total tags	Orphan tags ^a	Positive tags ^b	'One-hit' tags ^c	Multiple-hit (ambiguous) tags
E2F4 STAGE	2830	425 (15%)	2405	1386	1019
	2256		1918	1279	639
E2F4 SubSTAGE	1696	607 (36%)	1089	742	347
	1253		896	646	250
Genomic All tags ^d	7990	1165 (15%)	6825	3277	3548
	5523		4707	3007	1700
Yeast TBP STAGE	1344	294 (22%)	1050	617	433
	763		631	528	103
Yeast HSF STAGE ^e	320	56 (17%)	264	168	96
	259		209	155	54

a – The number of tags that do not match any sequence in the genome. The overall proportion of orphan tags is comparable to that seen in SAGE.

b – The number of tags that show a perfect match to genomic sequence.

c – The number of tags that show only one match to a single position on the genome

d – A subset of the genomic background tags, approximately of the same size as the E2F4 STAGE tags, was used to normalize STAGE scores as described in the paper.

e – Analysis of yeast HSF STAGE tags was not included in the published version of Kim *et al.*

Progress for **Task 1.b**, which was the application of STAGE to c-myc and ER is described above (page 6). **Task 1.b** and **1.c** involved the identification of targets of c-myc and ER in different cells and at different time intervals after stimulation. We have successfully carried out chromatin immunoprecipitation for ER in MCF-7 cells in the presence and absence of estradiol. In parallel we have developed human core promoter microarrays in the lab based on a published primer set [6], which enables the identification of target promoters by ChIP-chip. These chromatin IP samples for ER and the ones currently in progress for c-myc will be analyzed by STAGE.

Task 2 Validation, analysis and interpretation of direct targets of *c-myc* and *ER* identified by STAGE

We have successfully validated target promoters predicted by STAGE (Task 2.a) both by promoter specific PCR as well as by ChIP-chip. This data is shown for E2F4 in Figures 3c and Figure 4 in Kim *et al* in the Appendix. We have carried out a preliminary analysis of DNA motifs present in the promoters of target genes (Task 2.b), and this data is in Table 2 of Kim *et al*. We have also analyzed *c-myc* and *ER* target genes by ChIP-chip using a core promoter microarray. These target genes will serve to cross-validate the predicted targets as identified by STAGE under Task 2.a. We have developed computational algorithms to enable the mapping of mammalian STAGE tags to the genome and score tags as targets (Task 2.b and Task 2.c). We have

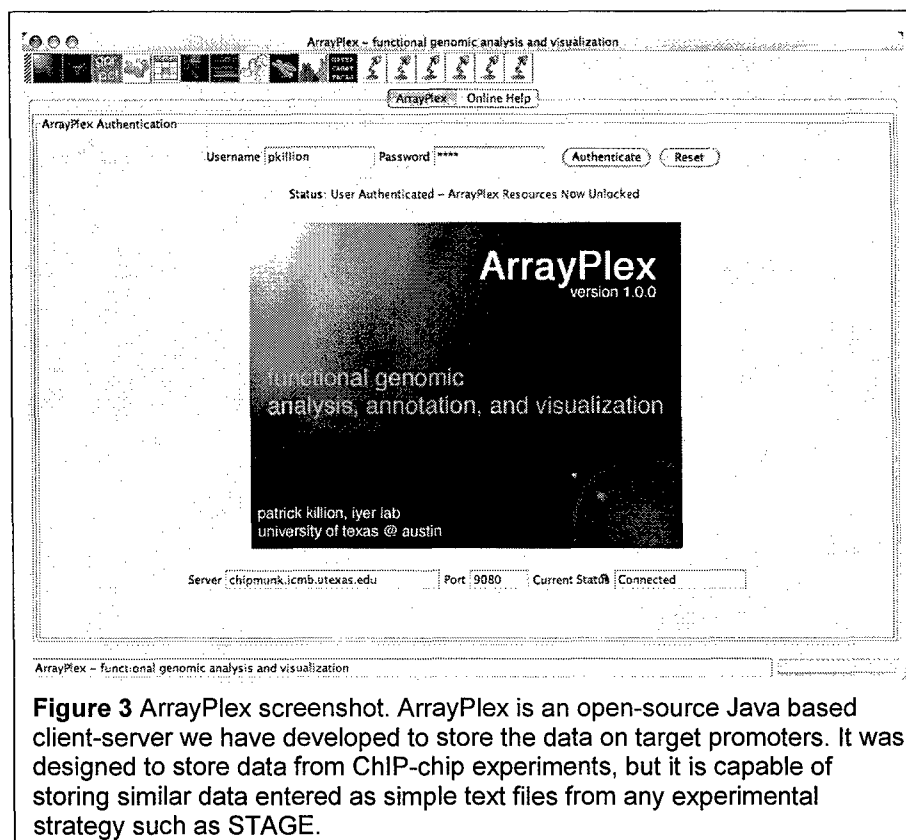


Figure 3 ArrayPlex screenshot. ArrayPlex is an open-source Java based client-server we have developed to store the data on target promoters. It was designed to store data from ChIP-chip experiments, but it is capable of storing similar data entered as simple text files from any experimental strategy such as STAGE.

begun developing a Java based relational database termed ArrayPlex that is capable of storing data on DNA protein interactions and facilitate mining of such data to identify transcriptional regulatory networks (Figure 3). Although ArrayPlex is originally intended to store ChIP-chip data from microarrays, it is flexible enough that it can accept any list of target promoters for a transcription factor such as that generated by STAGE. We are currently developing analysis routines within the extensible ArrayPlex framework that will facilitate data mining of STAGE data and elucidate transcriptional regulatory networks mediated by oncogenic transcription factors.

KEY RESEARCH ACCOMPLISHMENTS

- Developed STAGE (Sequence Tag Analysis of Genomic Enrichment), a novel method to identify the chromosomal targets of transcription factors including oncogenic transcription factors. We have demonstrated proof-of-concept with the transcription factor E2F4.
- Optimized protocols and computational analysis methods for successful application of STAGE in mammalian cells.
- Developed software for matching STAGE derived tags to the human genome sequence and scoring tags as representative of target promoters.
- Verified target promoters predicted by STAGE through independent means such as promoter specific PCR and microarray hybridization (ChIP-chip).
- Began development of ArrayPlex, a Java based relational database and analysis platform for data mining of large-scale target promoter data.

REPORTABLE OUTCOMES

- Published our proof-of-concept of successful development of STAGE, a method to identify targets of oncogenic transcription factors in human cells.
Kim J., Bhinge A.A., Morgan X.C. & Iyer V.R. (2005) Mapping DNA-Protein Interactions in Large Genomes by Sequence Tag Analysis of Genomic Enrichment *Nature Methods* 2: 47-53
- Platform Presentation: "Genome-wide mapping of DNA -protein interactions in large genomes by STAGE — Sequence Tag Analysis of Genomic Enrichment" at the Cold Spring Harbor meeting on "Systems Biology: Genomic Approaches to Transcriptional Regulation", March 2004
- Platform Presentation at the American Society of Microbiology (Texas) meeting, Houston, November 2004
- Grant award R01 HG003532-01 V. Iyer (PI) from NIH/NHGRI "STAGE and FAIRE for Regulatory Element Identification" This is a technology development project funded under the ENCODE Consortium. It is a collaboration between my lab and the lab of Dr. Jason Lieb at University of North Carolina at Chapel Hill. The objective is to develop and combine STAGE with another novel technology for identifying protein binding sites and regulatory elements in the human genome.

CONCLUSIONS

Our proof-of-concept of the development of STAGE (Kim *et al*) illustrates that it is possible to identify the chromosomal targets of a sequence specific transcription factor in human cells. Our results so far suggest that it should be possible to use STAGE to identify the chromosomal targets of any DNA binding protein, including oncogenic transcription factors that are important in breast and other cancers. Identification of direct chromosomal targets of transcription factors will help elucidate the transcriptional regulatory networks mediated by oncogenes during cell proliferation. The significance of STAGE is that it is a genome-wide method that overcomes many of the limitations of ChIP-chip using promoter arrays. Truly comprehensive promoter microarrays that cover all possible regulatory regions from the human genome are not yet widely available. However, we are yet to characterize the true extent of coverage of targets by STAGE. By analogy to STAGE, we expect that the greater the depth of sequencing of STAGE tags, the better the coverage of target genes.

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APPENDICES

Kim J., Bhinge A.A., Morgan X.C. & Iyer V.R. (2005) Mapping DNA-Protein Interactions in Large Genomes by Sequence Tag Analysis of Genomic Enrichment
Nature Methods 2: 47-53

Mapping DNA-protein interactions in large genomes by sequence tag analysis of genomic enrichment

Jonghwan Kim, Akshay A Bhinge, Xochitl C Morgan & Vishwanath R Iyer

Identifying the chromosomal targets of transcription factors is important for reconstructing the transcriptional regulatory networks underlying global gene expression programs. We have developed an unbiased genomic method called sequence tag analysis of genomic enrichment (STAGE) to identify the direct binding targets of transcription factors *in vivo*. STAGE is based on high-throughput sequencing of concatemerized tags derived from target DNA enriched by chromatin immunoprecipitation. We first used STAGE in yeast to confirm that RNA polymerase III genes are the most prominent targets of the TATA-box binding protein. We optimized the STAGE protocol and developed analysis methods to allow the identification of transcription factor targets in human cells. We used STAGE to identify several previously unknown binding targets of human transcription factor E2F4 that we independently validated by promoter-specific PCR and microarray hybridization. STAGE provides a means of identifying the chromosomal targets of DNA-associated proteins in any sequenced genome.

Determining the binding sites of regulatory proteins on the genome is important for reconstructing transcriptional regulatory networks^{1–3}. The binding of a transcription factor to its genomic targets can be assayed by combining chromatin immunoprecipitation (ChIP) and microarray (chip) hybridization. This ChIP-chip method was first developed for yeast⁴, where it has been used to define the targets of more than 100 transcription factors^{2,5,6}.

Although ChIP-chip has also enabled the identification of transcription factor targets in human cells^{7,8}, it is challenging to apply this approach comprehensively to study large and complex genomes. Human promoter microarrays based on core promoters⁷ or CpG islands⁸ cover a subset of all potential regulatory regions and may not adequately represent regions that are distant from genes or within introns. Tiling arrays of polymerase chain reaction (PCR) products⁹ or oligonucleotides¹⁰ have been made for the smallest human chromosomes, but extending such arrays to cover the entire genome is expensive, and the arrays are currently unavailable to most researchers. Although these efforts are underway for the human genome and some model organisms, the development of similar platforms for the mouse, plants, prokaryotes and many other model organisms is lagging.

Here, we address some of these limitations by developing an unbiased genomic method to identify the chromosomal targets of transcription factors. We term this method STAGE, and it is based on high-throughput sequencing of concatemerized tags derived from DNA enriched by ChIP. Cloning and sequencing of ChIP DNA has been carried out previously¹¹, but these efforts did not constitute a high-throughput genomic approach. As a demonstration of its utility, we first used STAGE to map the targets of TATA-box binding protein (TBP) in yeast. We then optimized STAGE and developed analysis algorithms that enabled us to successfully use STAGE to identify several known and new binding targets of transcription factor E2F4 in human cells.

RESULTS

STAGE identifies chromosomal targets in yeast

STAGE is conceptually derived from serial analysis of gene expression (SAGE)^{12,13}, but the template for STAGE consists of genomic loci enriched by ChIP. Briefly, transcription factors are cross-linked to their target sites *in vivo* with formaldehyde. After ChIP with a specific antibody against a given transcription factor, the recovered DNA fragments are amplified by PCR using biotinylated degenerate primers and digested with the four-base cutter (5'-CATG) restriction endonuclease *Nla*III. The biotinylated fragments are isolated using streptavidin beads and ligated to linkers containing a recognition site for *Mme*I, a type IIS restriction enzyme. Digestion with *Mme*I releases 21-base-pair (bp) tags containing *Nla*III sites from DNA fragments enriched after ChIP. Multiple tags are concatemerized, cloned and sequenced. STAGE generates 21-bp tags derived from ChIP DNA (Fig. 1). Mapping these tags to the genome can identify the loci represented in the ChIP sample and thus identify protein-binding locations.

We first used STAGE to identify the targets of yeast TATA-box binding protein (TBP). Out of a total of 1,344 sequenced tags, 294 (22%) did not match any sequence in the yeast genome. The total number of sequenced tags and the number of orphan and ambiguous tags are provided in Supplementary Table 1 online. Out of 1,050 valid STAGE tags, 433 showed multiple hits on the genome and could not be assigned to a single gene; 77 tags had single hits but had no annotated genes within one kilobase (kb). The remainder comprised 437 distinct tags, each of which had

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Formaldehyde cross-linking and IP

Random amplification with biotinylated primer

*Nla*III digestion and binding to streptavidin beads

Division in half and ligation with linkers 1 and 2

Digestion with type IIS enzyme *Mme*I

Ligation and amplification with nested primers 1 and 2

Digestion with *Nla*III and gel purification of ditags

Ligation to make concatemers

Sequencing and analysis

Figure 1 | The STAGE strategy. STAGE is based on high-throughput sequencing of concatemerized tags of defined length that are derived from DNA enriched by ChIP. Proteins were cross-linked to their binding sites *in vivo* with formaldehyde and chromatin was extracted and sheared. The cross-linked protein-DNA complexes were immunoprecipitated, cross-links were reversed and ChIP DNA was amplified by PCR using biotinylated primers. Amplified DNA fragments were digested with *Nla*III, which cuts at 5'-CATG sites. Fragments with ends containing the *Nla*III site were isolated by binding to streptavidin beads. They were separately ligated to one of two linkers containing a *Mme*I site, then incubated with *Mme*I, which cleaves 21 bp away from its recognition site. The 21-bp tags attached to linkers were isolated and ligated to create ditags. Ditags were amplified by PCR using nested primers and trimmed by digesting with *Nla*III. Trimmed ditags were gel purified, concatemerized by ligation, cloned and sequenced.

only one hit on the yeast genome and was located within 1 kb of the start of a gene.

Of the 437 tags, 378 occurred only once in the STAGE pool and 59 occurred multiple times. Seventy-nine putative targets were represented by more than one tag occurrence. The one notable feature of the abundant tags was that a substantial majority mapped within 1 kb of an RNA polymerase III (pol III) promoter. Based on this observation and on the fact that pol III promoters are prominent targets of TBP^{14,15}, we assigned the gene with a pol III promoter as the putative target when a tag mapped near it. In other cases, the nearest gene was assigned as the putative target. Tags that occurred multiple times in the STAGE pool, as well as their putative targets, are listed (Table 1). Sixty-eight of 79 targets represented by multiple tags were genes with an RNA pol III promoter. STAGE thus identified many prominent chromosomal targets of TBP in yeast.

Validation of STAGE targets by microarray hybridization

To compare our STAGE targets to those identified by microarray hybridization, ChIP DNA samples were fluorescently labeled and cohybridized to whole-genome (ORFs + intergenic regions) microarrays with an amplified genomic DNA reference. The occupancy

Table 1 | High-abundance yeast TBP STAGE tags

Tag sequence	nocc	Target gene
CATGATGGAACGAAGACGAC	10	tF(GAA)B
CATGAGAATGTCTTCAGTAT	8	tF(GAA)B
CATGAAGGTGACAAAATGATT	5	tK(CUU)E1
CATGATCAAATCTGTGAAGC	5	tL(CAA)A
CATGCAAATCTAAATAAAAAAC	5	tH(GUG)H
CATGTACTTAACAGATATG	5	RDN 5-1
CATGAGATATGCTGTTCAAG	4	tL(CAA)A
CATGTATATTTGCACTGGCT	4	RDN 5-1
CATGAAACTAGGAAAACGTAC	3	tE(UUC)J
CATGAAGATGATCGATACCG	3	tV(AAC)M1
CATGATGAAGTTTATGATCTGC	3	tW(CCA)K
CATGATGGCAGACTTCCATCG	3	tV(AAC)G2
CATGATGTCGCTATTTCTAAT	3	tY(GUA)J2
CATGCAAGATGTAGACCCAAC	3	YGRW5
CATGCAATCCAGTAGTAGGT	3	SCR1
CATGCAGCTGTTGTATCAAGA	3	tV(AAC)G1
CATGCATGTTTACGTTGTGG	3	tP(AGG)N
CATGGAATGTGCAATTAAGAC	3	tT(AGU)N2
CATGTGGTGAAAAAGATAAC	3	tT(AGU)J
CATGTATCTGAGCATCCAC	3	tG(GCC)O2
CATGTTTACCTCAAAACAAG	3	tV(AAC)K1
CATGTTTCTCTAAAGATGGT	3	tR(UCU)B
CATGAAAACCTCTCAACCTT	2	tH(GUG)E1
CATGAAAAGGTTAATGACTT	2	tT(AGU)O1
CATGAAGACCTATTCGCTTAT	2	tV(AAC)G3
CATGAAGCGCACAAGATTGGA	2	tR(UCU)G3
CATGAATGGCGCAGATTATT	2	tV(AAC)M1
CATGAGGCGCAGCTTTGATT	2	tY(GUA)F2
CATGAGTTGCCATTAGAAACG	2	tW(CCA)G1
CATGATACTGACTTATTGGGC	2	tD(GUC)L1
CATGCAAGACGTAGACCCAAC	2	tI(AAU)I2
CATGCAAGTGTGGCATAAAAG	2	tK(CUU)E2
CATGCAGAAAAGATAAGATGC	2	YPL029W
CATGCTGTGCAACGCCGAG	2	tE(UUC)J
CATGCTGGCAATAGCTTCAA	2	tG(CCC)D
CATGCTTTGTCTTCTGTTAG	2	tP(UGG)O2
CATGGAATAACGAATGGAGAC	2	tA(AGC)K1
CATGGAATCGAACCTTTCAC	2	tN(GUU)N2
CATGGAGTCTAATTTGTGT	2	tN(GUU)O2
CATGGAGTCTTTTATTCCGA	2	tN(GUU)L
CATGGCAAAAACGTAAAGTT	2	tR(UCU)G2
CATGGCGAATTTTACATAT	2	tV(UAC)D
CATGGCGATTATTCATTATG	2	tR(UCU)G3
CATGGCTAGTCAATAAGTGG	2	YGL080W
CATGGGGTAAGTCCGATGGC	2	tV(AAC)E2
CATGGGTTCAAACACTTCCAA	2	tY(GUA)F1
CATGGTGAAAGTTAATCTTT	2	tR(ACG)K
CATGTAAACCATCCCTTTTCA	2	YJL005W
CATGTATAAAACCTACCGCTT	2	tS(CGA)C
CATGTATCAAATGACACGTGA	2	YPRC822
CATGTATGAACTGGGAATTC	2	tS(AGA)B
CATGTCAATGTCCATTCTTT	2	tT(AGU)I2
CATGTCTTTGTGGATTATT	2	tS(CGA)C
CATGTGAGGCTTAGGTGATT	2	tN(GUU)N2
CATGTGTTTGAATTAGCGATC	2	tL(CAA)A
CATGTTACAATTCCTTCCAT	2	tG(UCC)G
CATGTTATGTCAATGGCAG	2	YELC1
CATGTTCAAGGACGGCTTGGT	2	tD(GUC)J1
CATGTTTCTGTTATTCATAA	2	tR(UCU)B

Tags that occurred more than once are listed, including the 4-bp *Nla*III site (5'-CATG). The number of times the tag occurred in the STAGE pool is indicated by nocc. Target genes were designated as described in the text.

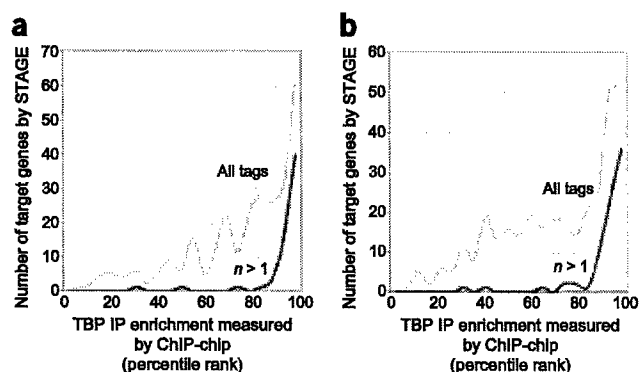


Figure 2 | Correlation between yeast targets predicted by STAGE and ChIP-chip. The enrichment value of yeast TBP targets after ChIP was determined by microarray hybridization. The percentile rank (0–100) of the ratio of ChIP-enriched fragments to genomic DNA was used to determine the ChIP enrichment value for each locus. For each interval of TBP ChIP enrichment values plotted on the x-axis, the number of targets predicted by STAGE is plotted on the y-axis. (a) Comparison between STAGE and ChIP-chip when the same sample was analyzed by both methods. The gray line indicates all predicted STAGE targets, whereas the black line indicates only the subset of 79 target genes predicted by multiple tag occurrences. (b) Comparison between STAGE and ChIP-chip when different ChIP samples were analyzed.

of each promoter by TBP was indicated by the rank of its enrichment in ChIP relative to the reference¹⁶.

STAGE identified increasing numbers of genes as TBP targets with increasing enrichment in ChIP as measured by microarrays (Fig. 2a). This relationship was more pronounced when we considered only genes that were identified as targets by more than one tag occurrence (Fig. 2a). Among the putative TBP targets represented by at least two tag occurrences, 92% had high enrichment values (>90) in ChIP-chip. When the two ChIP samples were independently generated, 91% of the targets predicted by at least two STAGE tag occurrences showed high ChIP-chip enrichment values (Fig. 2b). Thus, identification of chromosomal targets by STAGE correlates well with that by ChIP-chip, especially when the target genes were designated by multiple occurrences of STAGE tags.

STAGE in human cells

We chose transcription factor E2F4 to test STAGE in human cells. E2F4 is a member of the E2F family of transcriptional regulators that functions as a repressor in quiescent and early G₁ cells¹⁷. We first used ChIP and promoter-specific PCR to verify the binding of E2F4 to known target promoters⁷ (Fig. 3a). We then constructed a human E2F4 STAGE pool from these validated ChIP samples.

To reduce and account for background genomic DNA in ChIP, we introduced two enhancements. First, we tested a subtraction step as a potential means of reducing background from nonspecific genomic loci. Briefly, DNA fragments enriched by ChIP were randomly amplified by PCR with degenerate primers, and, in parallel, sheared genomic DNA fragments were amplified using biotinylated degenerate primers. ChIP DNA was hybridized to an excess of biotinylated genomic DNA and biotin-containing heteroduplexes were removed by binding to streptavidin beads. The remaining DNA was used as the input for STAGE. Details of the subtraction procedure are given in **Supplementary Methods** online. In a ChIP sample where the enrichment of an E2F4 target

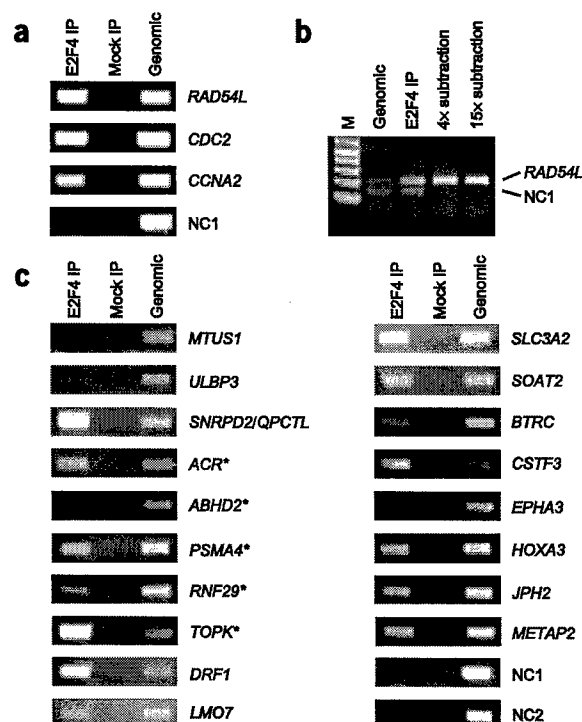


Figure 3 | ChIP of E2F4 targets and validation of STAGE targets by ChIP-PCR. (a) Binding of human E2F4 to known target promoters in fibroblasts. PCR was performed using primers corresponding to the promoters of the indicated genes. The ninth exon of *CCNB1* was used as a negative control for ChIP enrichment (NC1). (b) The subtraction procedure leads to improved enrichment of the *RAD54L* promoter in ChIP. 'M' is a size ladder. (c) Validation of STAGE targets by ChIP-PCR. A subset of 18 promoters out of the 45 predicted by STAGE were randomly chosen. E2F4 binding to the promoters of the indicated genes was assayed by promoter-specific PCR. NC1 is the ninth exon of *CCNB1* and NC2 is the promoter of *ACTB*; both are negative controls. *SNRPD2* and *QPCTL* are divergently transcribed. The putative targets of E2F4 predicted by SubSTAGE are marked by an asterisk.

over background was originally suboptimal, we observed improved enrichment after subtraction (Fig. 3b). Tags from this E2F4 subtraction STAGE (SubSTAGE) pool were combined for analysis with STAGE tags obtained without the subtraction step.

Additionally, we performed STAGE on normal, unselected human genomic DNA to profile tags arising from background genomic DNA that was not enriched by ChIP. This background STAGE pool would thus serve as an analysis control to account for sampling of STAGE tags from highly repetitive regions of the genome. We analyzed approximately 3,500 valid tags to identify targets of E2F4 in human cells.

Targets of human transcription factor E2F4

To overcome the ambiguity inherent in mapping many 21-bp tags to specific locations on the human genome, we developed an algorithm to score tags and genes as putative targets. Each distinct tag was assigned a tag score based on the number of its hits on the genome and the number of its occurrences in the STAGE pool. Details of the scoring method are described (see **Methods** and **Supplementary Methods** online). A higher number of hits on the genome lowered the tag score, and a higher occurrence number in the STAGE pool raised the tag score. For each human gene in

RefSeq^{18,19}, a final STAGE enrichment score was generated that was indicative of the enrichment of its promoter in ChIP. The final STAGE enrichment score for each gene was calculated by dividing its raw score from the ChIP STAGE library by its raw score from the appropriate background genomic STAGE library.

There were 48 putative targets of E2F4 with STAGE enrichment scores greater than a threshold of 900 in either of the two STAGE

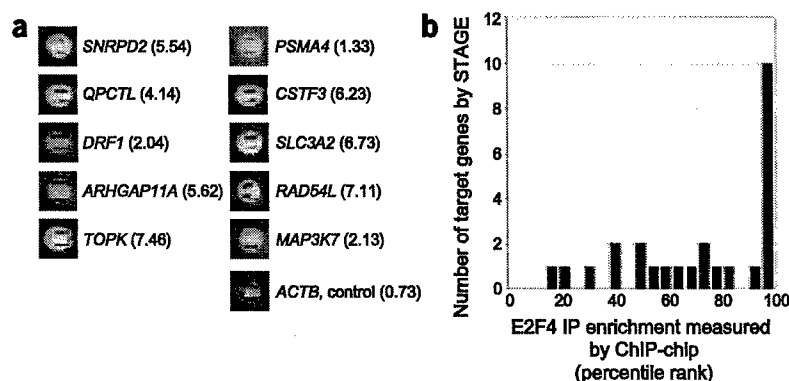
pools (Table 2). Raw scores and final STAGE enrichment scores are available (Supplementary Table 2 online). Most targets were designated by at least one tag with a single hit on the human genome. In addition to previously known targets of E2F4 such as *RAD54L*, *SLC3A2* and *MAP3K7*, which had been identified using a human core promoter microarray⁷, our analysis identified several new targets that had not been identified in previous studies. We also

Table 2 | Human E2F4 targets predicted by STAGE

No.	Gene	Gene Score	E2F4 site	Description
1	<i>MTUS1</i>	1971		Mitochondrial tumor suppressor gene 1
2	<i>ULBP3</i>	1961		UL16 binding protein 3
3	<i>SNRPD2*</i>	1933		Small nuclear ribonucleoprotein D2 polypeptide, 16.5 kDa
	<i>QPCTL*</i>	1923		Hypothetical protein FLJ20084
4	<i>PXK</i>	1015		PX domain-containing serine/threonine kinase
5	<i>FLJ22353</i>	993		Hypothetical protein FLJ22353
6	<i>GAJ</i>	993	Yes	GAJ protein
7	<i>ACR</i>	992		Acrosin
8	<i>RAD54L</i>	992		RAD54-like (<i>S. cerevisiae</i>)
9	<i>AAMP</i>	982		Angio-associated migratory cell protein
10	<i>ABHD2</i>	982		Abhydrolase domain-containing 2
11	<i>BLVRB*</i>	982		Biliverdin reductase B (flavin reductase (NADPH))
	<i>SPTBN4*</i>	982		Spectrin, beta, non-erythrocytic 4
12	<i>DC2</i>	982		DC2 protein
13	<i>FLJ13912</i>	982	Yes	Hypothetical protein FLJ13912
14	<i>FLJ25416</i>	982		Hypothetical protein FLJ25416
15	<i>FLJ32000</i>	982	Yes	Hypothetical protein FLJ32000
16	<i>FLJ90834</i>	982		Hypothetical protein FLJ90834
17	<i>MPV17</i>	982	Yes	MpV17 transgene, murine homolog, glomerulosclerosis
18	<i>PRCP</i>	982		Prolylcarboxypeptidase (angiotensinase C)
19	<i>PSMA4</i>	982		Proteasome (prosome, macropain) subunit, alpha type, 4
20	<i>RNF29</i>	982		Ring finger protein 29
21	<i>TOPK</i>	982	Yes	T-LAK cell-originated protein kinase
22	<i>DRF1</i>	974		Dbf4-related factor 1
23	<i>LMO7</i>	971		LIM domain only 7
24	<i>SLC3A2</i>	971	Yes	Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
25	<i>SOAT2</i>	971		Sterol O-acyltransferase 2
26	<i>ARHGAP11A</i>	965	Yes	KIAA0013 gene product
27	<i>ABC1</i>	961		Amplified in breast cancer 1
28	<i>BTRC</i>	961		Beta-transducin repeat containing
29	<i>GAL3ST1</i>	961		Cerebroside (3'-phosphoadenylylsulfate:galactosylceramide 3') sulfoltransferase
30	<i>CSTF3</i>	961		Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77 kDa
31	<i>CTAG3*</i>	961		Cancer/testis antigen 3
	<i>RIOK1*</i>	961		RIO kinase 1 (yeast)
32	<i>DNALI1</i>	961		Dynein, axonemal, light intermediate polypeptide 1
33	<i>EPHA3</i>	961		EPH receptor A3
34	<i>FIBL-6</i>	961	Yes	Hemicentin
35	<i>FLJ20712</i>	961		Hypothetical protein FLJ20712
36	<i>HIST2H2AC</i>	961		Histone 2, H2ac
37	<i>HOXA3</i>	961		Homeobox A3
38	<i>JPH2</i>	961		Junctophilin 2
39	<i>MAP3K7</i>	961	Yes	Mitogen-activated protein kinase kinase kinase 7
40	<i>METAP2</i>	961	Yes	Methionyl aminopeptidase 2
41	<i>PDGFA</i>	961		Platelet-derived growth factor alpha polypeptide
42	<i>RPL23A</i>	961	Yes	Ribosomal protein L23a
43	<i>SNIP1</i>	961	Yes	Smad nuclear interacting protein
44	<i>CCRL2</i>	926		Chemokine (C-C motif) receptor-like 2
45	<i>C20orf141</i>	913		Chromosome 20 open reading frame 141

An asterisk indicates a bidirectional promoter (a promoter driving the expression of two mRNAs in opposite directions). The presence of consensus E2F4 binding sites in a 3 kb window spanning the start of transcription is also indicated.

Figure 4 | Validation by ChIP-chip of E2F4 targets predicted by STAGE. DNA from an E2F4 ChIP was amplified and labeled with Cy5, and hybridized to a human core-promoter microarray together with a mock IP sample labeled with Cy3. The ratio of Cy5/Cy3 (red/green) signal is an indicator of the binding of E2F4 to the locus at a given spot. (a) New targets identified by STAGE (see Table 2 and Fig. 3c) include *SNRPD2*, *QPCTL*, *DRF1*, *ARHGAP11A*, *TOPK*, *CSTF3* and *PSMA4*. Previously known E2F4 targets that were also identified by STAGE are *SLC3A2*, *RAD54L* and *MAP3K7*. The *ACTB* promoter is a negative control. (b) Correlation between targets predicted by STAGE and ChIP-chip. The average percentile rank (0–100) from two microarray hybridizations, of the ratio of ChIP-enriched fragments to mock IP control DNA was determined for each spot on the microarray. For each interval of E2F4 ChIP enrichment values plotted on the x-axis, the number of targets predicted by STAGE (total 26) is plotted on the y-axis. Ten STAGE predicted targets rank in the top 5% of all spots on the microarray, corresponding to a red/green ratio >2.0.



calculated a significance value for each STAGE enrichment score. All our putative targets (Table 2) had scores with *P* values much lower than 0.01. The score for the *ACTB* (β -actin) gene used as a negative control had a much higher *P* value ($P > 0.5$).

Validation of STAGE in human cells

From the 45 putative target promoters (Table 2), we selected 18 for validation by promoter-specific PCR. Primers were designed to assay a region spanning the ~400 bp upstream of the transcription start site of each gene. We detected E2F4 binding to 15 promoters (Fig. 3c). Including *RAD54L* (Fig. 3a), we could thus independently verify 16 of 19 (84%) binding targets predicted by STAGE.

We used ChIP-chip to further verify the binding of E2F4 to promoters identified by STAGE. DNA from an independent E2F4 ChIP was amplified and labeled with Cy5 and hybridized to a 9,500-element human core promoter microarray²⁰ together with a mock-immunoprecipitated sample labeled with Cy3. Many previously unknown E2F4 targets that we identified by STAGE were indeed enriched in the independent ChIP-chip as indicated by high red/green (Cy5/Cy3) ratios (Fig. 4a). STAGE identified increasing numbers of genes as E2F4 targets with increasing enrichment in ChIP-chip (Fig. 4b). Of the 48 E2F4 target genes identified by STAGE, 26 were represented on the microarray. Ten of these (38%) had ChIP-chip enrichment values in the top 5%, indicating they were bona fide targets. The overlap between the targets identified by STAGE and by ChIP-chip, although modest, was highly significant ($P < 10^{-7}$ based on sampling permutation), showing that STAGE enables the identification of target loci in human cells. This overlap between the targets identified by the two different technologies is comparable to the 43% overlap we observed between our ChIP-chip targets and the set of E2F4 targets previously reported in the literature also using ChIP-chip^{7,8}.

In addition to the identification of E2F4 targets based on the occurrence of tags within a 3-kb window proximal to annotated genes, we separately scored genes as putative targets based on the presence of tags within a region from -10 kb to -6 kb or from -6 kb to -2 kb relative to the start of transcription or within the first intron. These analyses identified 48, 43 and 17 additional putative targets, respectively (Supplementary Tables 3, 4 and 5). Some of these additional putative targets, such as *ACR*, *FLJ22353* and *ULBP3*, had also been identified in our analysis based on the

3-kb proximal region (Table 2). It is possible that E2F4 binds to multiple sites at varying distances upstream of some of its target genes. Approximately 1,400 unique STAGE tags were derived from regions of the genome that were not within 10 kb upstream of, or in, the first intron of any gene. Although we have not validated these as true E2F4 binding sites, binding to sites outside promoters would be consistent with recent reports describing such binding by NF- κ B⁹, c-myc and Sp1 (ref. 10).

DISCUSSION

Our results demonstrate the utility of STAGE as an unbiased genomic method for identifying the chromosomal binding targets of proteins. STAGE identified many new target genes of E2F4 in human fibroblasts that had not been identified in previous studies using targeted core promoter microarrays or CpG island microarrays^{7,8}.

The fraction of orphan STAGE tags that did not match any genomic sequence was generally 15–19%, similar to what has been observed for SAGE^{13,21}. Orphan tags likely arise from a combination of PCR and sequencing errors and cross-contamination from unrelated DNA samples. Half of the 22% orphan tags we observed in one instance in yeast consisted of repeated occurrences of just two distinct tags. We did not observe these two tags in any other STAGE pools. Although it is desirable to minimize the occurrence of such orphan tags, they do not present a problem for STAGE, as they are excluded from analysis.

Although there was significant overlap ($P < 10^{-7}$) between the E2F4 targets that we identified by ChIP-chip and by STAGE, the agreement between the two technologies was not perfect. ChIP-chip involves a complex hybridization step and can be affected by the presence of repetitive DNA, poor PCR product in the microarray spot, differential amplification of ChIP DNA during fluorescent labeling and hence low sensitivity or specificity at certain loci. For example, we identified *PSMA4* as an E2F4 target by STAGE and validated it by ChIP-PCR, but it showed only marginal enrichment in ChIP-chip (Fig. 4a). However, *MAP3K7*, a previously known target of E2F4 that we also identified by STAGE, likewise did not show enrichment in our ChIP-chip, indicating that ChIP-chip is not infallible. For this reason, we believe that the standard low-throughput ChIP-PCR assay is a more reliable measure of whether a locus is a true binding target.

Based on our ChIP-PCR analysis (Fig. 3a,c), we estimate the true positive rate of STAGE in human cells is ~84% in our experiments. This success rate can potentially be improved by enhancements to the analysis algorithms as well as improvements to the ChIP procedure to reduce nonspecific DNA background. Subtraction is one potential means of reducing background. However, it is possible that the subtraction step may be effective only when the initial ChIP enrichment is poor (Fig. 3b). The use of new type III restriction enzymes generating 26-bp tags rather than 21-bp tags may also improve the specificity of STAGE²². However, 70% of all *Nla*III-anchored 21-bp tags in the human genome were unique, whereas 76% of all such 26-bp tags were unique. The improvement in the ability to uniquely localize tags by increasing their lengths from 21 to 26 bp is therefore not likely to be dramatic.

The comprehensiveness of STAGE, by analogy to SAGE, is limited in principle only by the extent of sequencing. We identified dozens of new E2F4 targets after sequencing a few thousand STAGE tags, but we believe our coverage is not saturating for two reasons. First, we observed minimal overlap between the tags generated from the two independent STAGE pools and saw no significant overlap between their predicted targets, even though we verified targets from each pool. Thus, our sampling of tag space, although valid, is relatively sparse. Second, a substantial fraction of the tags in all the combined human STAGE pools was observed only once. These observations suggest that E2F4 STAGE tags generated by further sequencing are likely to be unique and will help predict additional target genes. One way to estimate the false negative rate in future studies would be to compare the predictions from STAGE after saturation sequencing, with predictions made by analyzing ChIP on complete tiling microarrays for a given chromosome⁹.

STAGE has many advantages for the analysis of genome-wide DNA protein interactions, especially in large genomes. First, it does not make assumptions about the location of protein binding sites on the genome. 98% of the human genome is within 1 kb of an *Nla*III site, so binding sites anywhere can potentially be sampled by STAGE. Second, it does not require expensive infrastructure. We estimate that sequencing 30,000 tags, which should allow for extensive coverage of the targets of a single protein, will entail sequencing about 1,200 clones, a cost-efficient option. Third, STAGE is readily applicable to any sequenced organism. Finally, STAGE is not restricted to a specific annotation of a genome; as new transcriptional units are discovered and existing ones become defunct^{23,24}, the same STAGE tag data can be reanalyzed to identify targets based on revised genome annotations.

We envision STAGE as a useful complement to ChIP-chip for analyzing the binding distribution of proteins on the genome. Although STAGE is a high-throughput genomic method, it is less suited than ChIP-chip for repeated quantitative measurements of the binding of a protein under a range of physiological conditions. However, the binding loci predicted by STAGE can be represented on focused microarrays for ChIP-chip. Thus, an initial comprehensive survey of direct binding targets by STAGE, followed by extensive ChIP-chip analysis, can accelerate the discovery of protein-binding regulatory elements in genomes.

METHODS

Cells and antibodies. Yeast cells with a 3×hemagglutinin (HA)-tagged TBP²⁵ were grown at 25 °C in synthetic complete medium minus uracil, collected by centrifugation, resuspended in an

equal volume of prewarmed 39 °C medium and returned to 39 °C. After 10 min, cells were cross-linked by adding formaldehyde (final 1%). Anti-HA antibody (Santa Cruz) at a 1:100 dilution was used for ChIP.

Human foreskin fibroblasts (ATCC CRL 2091) were grown to 60% confluence in 15 cm plates in DMEM containing glucose (1 g/l), antibiotics, and 10% FBS (Hyclone). Cells were washed twice with the same medium lacking FBS and low-serum medium (0.1% FBS) was added. After 72 h, cells were cross-linked with formaldehyde (final 1%). Anti-E2F4 antibody (sc-1082x, Santa Cruz) at a 1:100 dilution was used for ChIP.

STAGE and SubSTAGE. Cross-linking, ChIP, and amplification of ChIP DNA was performed as described previously²⁶, except using a 5'-biotinylated primer during amplification. Further details of ChIP protocols are described in **Supplementary Methods online**. We then followed the LongSAGE protocol (<http://www.sagenet.org/>), except used amplified, biotinylated ChIP DNA as the starting material. Briefly, amplified DNA (1–2 µg) was digested with *Nla*III. The terminal DNA fragments were bound to streptavidin-coated magnetic beads (Dyna) and separated into two tubes. After ligation with linker 1 or 2, which contain recognition sites for *Mme*I, the DNA fragments were released by *Mme*I digestion. The released tags were ligated to generate ditags. Ditags were amplified with nested primers, gel purified and trimmed by *Nla*III digestion. Trimmed ditags were gel purified, concatamerized by ligation and cloned into the pZero 1.0 vector (Invitrogen). Insert sizes were assayed in recombinant clones and clones containing at least ten ditags were sequenced. Details of the subtraction step are provided in **Supplementary Methods online**. For the mock immunoprecipitation control and reference samples (Figs. 3 and 4, respectively), the antibody was omitted. For the genomic control STAGE pool, sheared normal human genomic DNA was used as input into STAGE.

Data analysis and scoring. STAGE yields a list of tags with their number of occurrences in the pool. This number is termed *nocc*. Each valid STAGE tag has anywhere between one and several thousand matches on the human genome. This number is termed *nhit*. Our algorithm for defining target genes was as follows. (1) Map the tags to the human genome. (2) Assign a score to each tag based on *nocc* and *nhit*. (3) For each human gene, identify tags within a user-defined window. (4) Calculate a cumulative score for the gene based on the scores of all tags in the given window. (5) Compare these scores to the experimental and computational control. (6) Genes that show a substantially higher score than the control are putative targets. Further details of the scoring algorithm are provided in **Supplementary Methods online**. For all analyses, we used the July 2003 build of the Human Genome sequence assembly available at <http://genome.ucsc.edu>. Genes used in our analysis were based on the RefSeq Genes annotation at the University of California, Santa Cruz¹⁹.

Controls and P values for STAGE enrichment scores. For an experimental control, we performed STAGE on input genomic DNA without ChIP and calculated background gene scores for all genes in the same manner as described above for STAGE from an actual ChIP. Raw gene scores derived from ChIP STAGE were divided by control scores to obtain the final STAGE enrichment

score. To calculate a *P* value for the STAGE enrichment score, 2,000 tags were computationally selected at random from the redundant pool of all CATG 21-mers in the genome and used to generate scores for each gene as described above. This process was iterated 500 times to obtain a distribution of 500 scores for each gene. For each gene, these scores were fitted to a normal distribution. The experimentally determined STAGE enrichment score for a particular gene was compared to this distribution and a *P* value for the score was obtained. Experimental scores with *P* values less than 0.01 were taken to be significant.

Microarrays. Yeast microarrays including all ORFs and intergenic elements were manufactured as described previously^{5,26}. PCR amplification, fluorescent labeling of ChIP DNA fragments and hybridization were performed as described previously²⁶. The reference hybridization probe was generated from sonicated normal yeast genomic DNA processed identically to the probe for ChIP DNA samples. A GenePix 4000B scanner and GenePix Pro 4.0 software (Axon Instruments) were used for scanning and quantitation. Data were uploaded to a local database for analysis²⁷. The enrichment value of TBP ChIP was calculated by ranking genomic loci according to their red/green fluorescence ratios. We determined the percentile rank (0–100) for each array element and either used it directly as a measure of binding (Fig. 2b) or used the average percentile rank for each element from two replicate hybridizations (Fig. 2a). When multiple microarray elements could potentially represent the promoter of a gene, we averaged their percentile ranks.

PCR primer pairs for human core promoters²⁰ were purchased from the Whitehead Institute (Cambridge, Massachusetts, USA). Promoters were amplified by PCR as recommended by the manufacturer, and microarrays were manufactured as previously described²⁶. PCR products corresponding to 33 additional promoter and control loci, including the genes listed in **Supplementary Table 6** online, were included on the array. E2F4 ChIP DNA fragments and the mock IP reference samples were amplified and labeled by ligation-mediated PCR, using Cy5 and Cy3, respectively⁶. The two fluorescently labeled samples were simultaneously hybridized to the promoter microarray and ChIP enrichment of target loci was calculated by ranking the Cy5/Cy3 (red/green) fluorescence ratios.

PCR and primers. Thirty cycles of PCR were performed for the samples in **Figure 4** in a 25- μ l reaction volume with 1 μ l (4%) of immunoprecipitated material. Primers were designed to assay approximately between –400 bp and +1 of the transcription start site. The ninth exon of *CCNB1* and the core promoter of *ACTB* were negative controls NC1 and NC2, respectively (**Figs. 3a–c** and **4a**). Primer sequences are provided in **Supplementary Table 6** online.

Accession numbers. Microarray data have been deposited in NCBI's Gene Expression Omnibus (GEO, <http://www.ncbi.nlm.nih.gov/geo/>) and are accessible through GEO Series accession number GSE1861.

Note: Supplementary information is available on the Nature Methods website.

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COMPETING INTERESTS STATEMENT

The authors declare that they have no competing financial interests.

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