WHAT IS CLAIMED IS:

1. A polynucleotide construct comprising a promoter operatively linked to a coding sequence for a selectable marker operatively linked to a transcriptional terminator, wherein the promoter is ~~derived from a fungal species selected from the group of a species of the *Ustilago* genus, a species of the *Aspergillus* genus, a species of the *Rhodosporidium* genus; a species in the Sporobolomyces genus; a species in the Rhodotorula genus~~ selected from the group consisting of a promoter comprising the nucleotide sequence set forth in SEQ ID NO:2, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:3, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:4,a promoter comprising the nucleotide sequence set forth in SEQ ID NO:5; a promoter comprising the nucleotide sequence set forth in SEQ ID NO:51, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:55 and a promoter comprising the nucleotide sequence set forth in SEQ ID NO:56 and wherein the polynucleotide construct provides efficient and dominant selection of a transformed fungal cell of the Pucciniomycotina and Ustilaginomycotina subphyla.

2 The construct of claim 1, wherein the coding sequence encodes a protein that confers resistance to an antibiotic, such as, Hygromycin B, Nourseothricin and Zeocin.

3. The construct of claim 1, wherein the coding sequence encodes a protein that confers resistance to a herbicide.

4. The construct of claim 1 or 3, wherein the coding sequence is selected from the group consisting of a coding sequence comprising the nucleotide sequence set forth in SEQ ID NO:6, a coding sequence comprising the nucleotide sequence set forth in SEQ ID NO:7 and a coding sequence comprising the nucleotide sequence set forth in SEQ ID NO:8.

5. The construct of claim 1, wherein the coding sequence for a selectable marker is at least 60% GC, preferably about 70% GC and most preferably about 75% GC; wherein

at least 70% of the codon triplets end with C or G, preferably more than 80% of the codon triplets end with C or G.

6. The construct of claim 1, wherein the coding sequence for a selectable marker is composed of UCG codons in at least 40% of the serine residues.

7. The construct of any one of claims 1-6, wherein the promoter is derived from a gene encoding glyceraldehyde 3-phosphate dehydrogenase (gpd) or from a gene encoding protein translation elongation factor (tef).

~~8. The construct of any one of claims 1-7, wherein the promoter is selected from the group consisting of a promoter comprising the nucleotide sequence set forth in SEQ ID NO:1, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:2, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:3, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:4,a promoter comprising the nucleotide sequence set forth in SEQ ID NO:5; a promoter comprising the nucleotide sequence set forth in SEQ ID NO:51, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:55 and a promoter comprising the nucleotide sequence set forth in SEQ ID NO:56.~~

~~9~~8. The construct of claim 1, wherein the fungal cell is a species of the *Rhodosporidium* , Sporisorium, Ustilago, Rhodoturula, Pseudozyma or Sporobolomyces (Sporidiobolus) genus.

~~10~~9. An isolated promoter selected from the group consisting of:

(i) a promoter comprising the nucleotide sequence of SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:55 or SEQ ID NO:56;

(ii) a promoter comprising a nucleotide sequence having at least 50% identity with the nucleotide sequence of SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:55 or SEQ ID NO:56;

(iii) a promoter comprising a nucleotide sequence having at least 60% identity with the nucleotide sequence of SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:55 or SEQ ID NO:56;

(iv) a promoter comprising a nucleotide sequence having at least 70% identity with the nucleotide sequence of SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:55 or SEQ ID NO:56;

(v) a promoter comprising a nucleotide sequence having at least 80% identity with the nucleotide sequence of SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:55 or SEQ ID NO:56;

(vi) a promoter comprising a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:55 or SEQ ID NO:56;

(vii) a promoter comprising a nucleotide sequence having at least 95% identity with the nucleotide sequence of SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:55 or SEQ ID NO:56; and

(viii) a promoter comprising a nucleotide sequence having at least 98% identity with the nucleotide sequence of SEQ ID NO:2, SEQ ID NO:51, SEQ ID NO:55 or SEQ ID NO:56,

wherein the promoter drives strong transcription of polynucleotides in a fungal species selected from the group consisting of a species of the *Ustilago* genus, a species of the *Aspergillus* genus, a species of the *Rhodosporidium* genus, a species of Rhodotorula genus, a species of Pseudozyma genus or a species of Sporobolomyces (Sporidiobolus) genus.

~~11~~10. A method for transformation of a fungal cell of a species of the Pucciniomycotina and Ustilaginomycotina subphyla which comprises:

(a) transforming a fungal cell with the construct of any one of claims 1-~~8~~7 and

(b) selecting a transformed fungal colony.

~~12~~11. The method of claim ~~11~~10, wherein the transformation comprises the step of co-culturing said fungal cell with *Agrobacterium tumefaciens* that contains vector

comprising said construct and wherein the co-culturing is performed on a solid co-culturing medium or on a co-culturing membrane that is laid on top of a solid medium.

~~13~~12. The method of claim ~~12~~11, wherein the selection is performed by over-laying a solid selection medium on top of the solid co-culturing medium or by transferring the co-culturing membrane to a solid selection medium.

~~14~~13. The method of claim ~~12~~11 or ~~13~~12, wherein the co-culturing medium and the selection medium contain at least 1.5% agar, preferably between 2% and 3% agar.

~~15~~14. The method of claim any one of claims ~~11~~10-~~14~~13, wherein the fungal cell is a species of the *Rhodosporidium*, Rhodotorula, Pseudozyma, Sporisorium, or Sporobolomyces genera.

~~16. A method of improved gene targeting in a target fungal genome which comprises transforming fungal cells using medium comprising 2-(morpholin-4-yl)-benzo[h]chomen-4-one in an amount sufficient to manipulate the fungal genome, wherein the gene targeting requires a homology region of a targeted fungal genomic sequence of at least 50 nucleotides, preferably more than 500 nucleotides.~~

~~17. The method of claim 16, wherein the amount of 2-(morpholin-4-yl)-benzo[h]chomen-4-one is between about 0.1 μM to about 50 μM.~~

~~18. The method of claim 16 or 17, wherein the transformation is selected from the group consisting of such as *Agrobacterium tumefaciens*-mediated transformation, electroporation and transfection;~~

~~19. A method for reducing false transformants in a targeted genome comprising steps of:~~

(a) designing a coding sequence for a selectable marker, wherein the coding sequence contains codon usage preference that matches to that of the targeted genome;

(b) operatively linking the designed coding sequence to a strong promoter and to a transcriptional terminator to create a construct;

(c) transforming a cell of the targeted genome with the construct; and

(d) selecting transformed cells under maximal concentration of selection agents.

20. The method of claim 19, wherein the selectable marker is a protein that confers antibiotic resistance or herbicide resistance.

21. The method of claim 19 or 20, wherein the coding sequence is selected from the group consisting of a coding sequence comprising the nucleotide sequence set forth in SEQ ID NO:6, a coding sequence comprising the nucleotide sequence set forth in SEQ ID NO:7 and a coding sequence comprising the nucleotide sequence set forth in SEQ ID NO:8.

22. The method of any one of claims 19-21, wherein the strong promoter is derived from a glyceraldehyde 3-phosphate gene (gpd) or translation elongation factor (tef) gene.

23. The method of any one of claims 19-22, wherein the promoter is selected from the group consisting of a promoter comprising the nucleotide sequence set forth in SEQ ID NO:1, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:2, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:3, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:4,a promoter comprising the nucleotide sequence set forth in SEQ ID NO:5, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:51, a promoter comprising the nucleotide sequence set forth in SEQ ID NO:55 and a promoter comprising the nucleotide sequence set forth in SEQ ID NO:56