CLAIMS

1. An engineered *Saccharomyces* strain comprising:

    a. a surface displayed binding agent, wherein the binding agent has a binding affinity to a target microorganism;

    b. any one of:

        i. an anchor moiety comprising a cell wall anchor region selected from Cwp2p, Sed1p, Ccw12p or Flo1p protein operably linked to the binding agent; or

        ii. a stem comprising a transmembrane protein operably linked to a transactivator via a conditionally cleavable peptide; wherein the surface displayed binding agent is operably linked to the stem.

2. An engineered *Saccharomyces* strain comprising a display cassette comprising:

    a. a sequence encoding a surface displayed binding agent, wherein the binding agent has a binding affinity to a target microorganism;

    b. a sequence encoding any one of:

        i. an anchor moiety comprising a cell wall anchor region selected from Cwp2p, Sed1p, Ccw12p or Flo1p protein, wherein the sequence encoding the anchor moiety and the binding agent are encoded in a single cistron; or

        ii. a stem comprising a transmembrane protein, operably linked to a transactivator via a conditionally cleavable peptide; wherein the surface displayed binding agent is operably linked to the stem.

3. The engineered *Saccharomyces* strain of claim 1 or 2, wherein the strain is *Saccharomyces cerevisiae var. boulardii (S. boulardii)*.

4. The engineered *Saccharomyces* strain of claim 1 or 2, wherein the stem comprises a cell wall protein domain operably linked to the transmembrane protein.

5. The engineered *Saccharomyces* strain of claim 4, wherein the cell wall protein domain is Mid2 protein (Mid2p) and the transmembrane protein is Wsc1p(C8A).

6. The engineered *Saccharomyces* strain of claim 1 or 2, wherein the target microorganism is a pathobiont, a commensal microorganism, or a pathogen.

7. The engineered *Saccharomyces* strain of claim 6, wherein the target microorganism is selected from a group consisting of *Norovirus, Listeria monocytogenes, Clostridium pathobionts, Clostridium difficile, Clostridium perfringens, Campylobacter coli,*

Staphylococcus aureus, methicillin-resistant Staphylococcus aureus (MRSA), Streptococcus pyogenes, Salmonella, P. aeruginosa, E. coli.

8. The engineered *Saccharomyces* strain of claim 1 or 2, wherein the binding agent comprises one or more of a group consisting of: peptides, proteins, antibodies, nanobodies, single chain fragments thereof, and combinations thereof.

9. The engineered *Saccharomyces* strain of claim 1 or 2, wherein the binding agent is selected from CLM-1 (norovirus), cell binding domain of any one of ϕCP26F (PlyCP26F from *C. difficile/perfringens*), endolysin Ply500 (*Listeria monocytogenes)*, PlyP35 (*Listeria monocytogenes)*, LysGH15B (*Staphylococcus aureus)*, endolysin LysGH15 (*Staphylococcus aureus)*, LysSA97(*Staphylococcus aureus)*, ZW88 (*Staphylococcus aureus)*, phiCcolBB35 (*Campylobacter coli*), PlyC (*Streptococcus pyogenes*).

10. The engineered *Saccharomyces* strain of claim 1 or 2, wherein the conditionally cleavable peptide is cleavable in presence of ubiquitinase.

11. The engineered *Saccharomyces* strain of claim 1 or 2, wherein the transactivator comprises an RNA-guided DNA endonuclease enzyme Cas9, or a scRNA-binding motif and a transcription activator domain, or a RNA stem loop recognition domain recognition domain selected from MCP, PCP, or Com.

12. The engineered *Saccharomyces* strain of claim 1, wherein

    i. the transactivator is operably linked to the transmembrane protein via a first split ubiquitin fragment; and

    ii. further comprising a second split ubiquitin fragment operably linked to a transmembrane protein on a second stem;

    wherein physical interaction between the first split ubiquitin fragment and the second split ubiquitin fragment releases the transactivator.

13. The engineered *Saccharomyces* strain of claim 1 or 2, wherein the transactivator can initiate the expression of one or more of, a reporter, a biomolecule, a transcriptional activation domain or an RNA stem loop recognition domain.

14. The engineered *Saccharomyces* strain of claim 13, wherein the reporter is selected from a fluorescent protein or a luminescence protein, the biomolecule is selected from a group consisting of an antibody, a single-chain variable fragment (scFv), a nanobody, an enzyme, or an antimicrobial peptide, the transcriptional activator is VP64.

15. The engineered *Saccharomyces* strain of claim 2, wherein the display cassette further comprises a promoter and a terminator sequence.

16. The engineered yeast strain of claim 15, wherein the promoter is selected from TDH3, CCW12, WSC1, FAU1 and the terminator is selected from ADH1 or CYC1.

17. The engineered *Saccharomyces* strain of any one of claims 1-16, for use in treating gut disease.

18. The engineered *Saccharaomyces* strain of any one of claims 1-17, further comprising a second binding agent, wherein the second binding agent is capable of binding to a second target microorganism and the first binding agent is different from the second binding agent.

19. A method of constructing an engineered *Saccharomyces* cell, the method comprising:

    i. providing a *Saccharomyces* cell;

    ii. providing a display cassette of any one of claims 2-18; and

    integrating the display cassette into an intergenic site of the *Saccharomyces* cell genome.

20. The method of constructing an engineered *Saccharomyces* cell of claim 19, wherein the strain is *S. boulardii* and the intergenic site is selected from Chr VII, XII, XV, XVI, or combinations thereof.

21. Use of the engineered *Saccharomyces* strain of any one of claims 1-18 in the manufacture of a medicament for treating a norovirus infection.

22. The engineered *Saccharomyces* strain of any one of claims 1-18, for use in the treatment of a norovirus infection.

23. Use of the engineered *Saccharomyces* strain of any one of claims 1-16 in the manufacture of a medicament for treating gut disease.