CLAIMS

What is claimed is

1. A transposon comprising a heterologous polynucleotide between left and right transposon ends, wherein the left end comprises SEQ ID NO: 7 and the right end comprises SEQ ID NO: 8, wherein the transposon is transposable by a transposase having the sequence of SEQ ID NO:782.
2. The transposon of claim 1, further comprising a sequence at least 90% identical to SEQ ID NO: 12 immediately adjacent to the left transposon end and between the left transposon end and the heterologous polynucleotide and a sequence at least 90% identical to SEQ ID NO: 15 immediately adjacent to the right transposon end and between the right transposon end and the heterologous polynucleotide.
3. The transposon of claim 1, wherein the heterologous polynucleotide comprises a heterologous promoter that is active in eukaryotic cells.

4. The transposon of claim 3, wherein the promoter is operably linked to at least one or more of: i) an open reading frame; ii) a nucleic acid encoding a selectable marker; iii) a nucleic acid encoding a counter-selectable marker;

iii) a nucleic acid encoding a regulatory protein; iv) a nucleic acid encoding an inhibitory RNA.

5. The transposon of claim 3, wherein the heterologous promoter comprises a sequence selected from SEQ ID NOS: 325-409.
6. The transposon of claim 3, wherein the heterologous polynucleotide comprises in operable linkage with the heterologous promoter, one or more of: i) a nucleic acid encoding a selectable marker; ii) a nucleic acid encoding a counter-selectable marker; iii) a nucleic acid encoding a regulatory protein; and iv) a nucleic acid encoding an inhibitory RNA.
7. The transposon of claim 1, wherein the heterologous polynucleotide comprises a heterologous enhancer that is active in eukaryotic cells.
8. The transposon of claim 7, wherein the heterologous enhancer is selected from SEQ ID NOS: 304-324.
9. The transposon of claim 1, wherein the heterologous polynucleotide comprises a heterologous intron that is spliceable in eukaryotic cells.
10. The transposon of claim 9, wherein the nucleotide sequence of the heterologous intron is selected from SEQ ID NOS: 412-472.

11. The transposon of claim 1, wherein the heterologous polynucleotide comprises an insulator sequence.
12. The transposon of claim 11, wherein the nucleic acid sequence of the insulator is selected from SEQ ID NOS: 286-292.
13. The transposon of claim 1, wherein the heterologous polynucleotide comprises or encodes a selectable marker.
14. The transposon of claim 13, wherein the selectable marker is selected from a glutamine synthetase enzyme, a dihydrofolate reductase enzyme, a puromycin acetyltransferase enzyme, a blasticidin acetyltransferase enzyme, a hygromycin B phosphotransferase enzyme, an aminoglycoside 3′-phosphotransferase enzyme and a fluorescent protein.
15. The transposon of claim 1, wherein the target sequence 5′-TTAA-3′ is immediately adjacent to each of SEQ ID NOS:7 and 8 distal from the heterologous polynucleotide.
16. A eukaryotic cell whose genome comprises a transposon comprising a heterologous polynucleotide between left and right transposon

ends, wherein the left end comprises SEQ ID NO:7 and the right end comprises SEQ ID NO:8, wherein the transposon is transposable by a transposase having the sequence of SEQ ID NO:782.

17. The eukaryotic cell of claim 16, wherein the cell is an animal cell.
18. The animal cell of claim 17, wherein the cell is a mammalian cell.
19. The mammalian cell of claim 18, wherein the cell is a rodent cell.
20. The mammalian cell of claim 18, wherein the cell is a human cell.

21. The transposon of claim 1, wherein the heterologous polynucleotide comprises two open reading frames, each operably linked to a separate promoter.
22. The transposon of claim 21, wherein the heterologous polynucleotide further comprises a sequence selected from SEQ ID NOS: 596-779.
23. The eukaryotic cell of claim 16, wherein the target sequence 5′-TTAA-3′ is immediately adjacent to each of SEQ ID NOS:7 and 8 distal from the heterologous polynucleotide.