Claims:

1. A process for extending the replicative capacity of a metazoan somatic cell population comprising:

decoupling retinoblastoma protein inhibition of cell division cycle advancement during replicative senescence by abrogating cyclin-dependent kinase inhibitor ("CKI") - mediated stabilization of a retinoblastoma protein using genetic amendment;

maintaining telomerase activity by ectopically expressing in the metazoan somatic cell population a nucleic acid sequence encoding a telomere reverse transcriptase ("TERT") protein;

maintaining a bank of cells that is a master cell bank having the genetic amendment and ectopic expression of TERT protein;

cultivating cells from the master cell bank in an *ex vivo* milieu that is a cultivated cell biomass; and

harvesting the cultivated cell biomass for dietary consumption; wherein the genetic amendment comprises

i) genetic amendment of a CDKN2B gene to inactivate a p15 protein in the metazoan somatic cell population to abolish retinoblastoma protein inhibition of the cell cycle during replicative senescence;

ii) genetic amendment of a CDKN2A gene to inactivate a p16 protein in the metazoan somatic cell population to abolish retinoblastoma protein inhibition of the cell cycle during replicative senescence; or

iii) modification of the cell population with a genetic construct that directs ectopic expression of a cyclin-dependent kinase 4 ("CDK4") protein.

2. The process of claim 1, wherein the CDKN2B gene comprises the sequence of NCBI Gene ID: 395076.

3. The process of any one of claims 1-2, wherein the genetic amendment is a mutation of a conserved nucleotide sequence in exon one of the CDKN2B gene.

4. The process of claim 3, wherein the genetic amendment is an insertion mutation made using guide RNAs, said guide RNAs selected from the group consisting of guide RNAs (SEQ ID Nos.

1, 2, 3, 4 and 5) targeting exon one of the CDKN2B gene and is created using clustered regularly-interspaced short palindromic repeats-Cas9 (“CRISPR/Cas9”).

5. The process of claim 3, wherein the genetic amendment is a deletion mutation made using guide RNAs, said guide RNAs selected from the group consisting of guide RNAs (SEQ ID Nos. 1, 2, 3, 4 and 5) targeting exon one of the CDKN2B gene and is created using CRISPR/Cas9.

6. The process of any one of claims 2-5, wherein the metazoan somatic cell population species identity is *Gallus gallus* and the metazoan somatic cell population lineage is skeletal muscle.

7. The process of claim 1, wherein the CDKN2A gene comprises the sequence of NCBI Gene ID: 616369.

8. The process of any one of claims 1 and 7, wherein the genetic amendment is a mutation of a conserved nucleotide sequence in exon two of the CDKN2A gene.

9. The process of claim 8, wherein the genetic amendment is an insertion mutation made using guide RNAs said guide RNAs selected from the group consisting of guide RNAs (SEQ ID Nos. 8, 9 and 10) targeting exon two of the CDKN2A gene and is created using CRISPR/Cas9.

10. The process of claim 8, wherein the genetic amendment is a deletion mutation made using guide RNAs said guide RNAs selected from the group consisting of guide RNAs (SEQ ID Nos. 8, 9 and 10) targeting exon two of the CDKN2A and is created using CRISPR/Cas9.

11. The process of any one of claims 7-10, wherein the metazoan somatic cell population species identity is *Bos taurus* and the metazoan somatic cell population lineage is skeletal muscle.

12. The process of claim 1, wherein the genetic construct directing the expression of the CDK4 protein from a CDK4 gene (NCBI Gene ID:510618) comprises the sequence of SEQ ID NO 12.

13. The process of claim 12, wherein the metazoan somatic cell population species identity is *Gallus gallus* and the metazoan somatic cell population lineage is skeletal muscle.

14. The process of claim 12, wherein modifying the metazoan cell population is with a genetic construct (SEQ ID NO 12) directing expression of a CDK4 protein homolog from a *Bos taurus* CDK4 gene.

15. The process of any one of claims 1-14, wherein cultivating cells from the master cell bank further comprises:

expanding selected cell populations from the master cell bank;

cryopreserving and storing expanded cell populations in a master cell bank stock inventory; seeding and cultivating cells from the master cell bank stock inventory in an ex vivo milieu; and

harvesting cultivated cell biomass for dietary consumption.

16. The process of any one of claims 1-5, 7-10, 12, and 14-15 wherein the metazoan somatic cell population is a skeletal muscle cell population from a species of seafood, poultry, or livestock.

17. The process of claim 16, wherein the metazoan somatic cell population is a skeletal muscle cell population from a species selected from the group consisting of *Gallus gallus, Meleagris gallopavo, Anas platyrhynchos, Bos taurus, Sus scrofa, Ovis aries, Salmo salar, Thunnus thynnus, Gadus morhua, Homarus americanus, Litopenaeus setiferus, Oncorhynchus mykiss, and Oreochromis niloticus.*

18. A clonal cell line of a metazoan somatic cell population derived by a process comprising:

decoupling retinoblastoma protein inhibition of cell division cycle advancement during replicative senescence by abrogating CKI-mediated stabilization of a retinoblastoma protein using genetic amendment;

maintaining telomerase activity by ectopically expressing in the metazoan somatic cell population a nucleic acid sequence encoding a telomere reverse transcriptase (TERT) protein;

maintaining a bank of cells that is a master cell bank having the genetic amendment and ectopic expression of TERT protein;

cultivating cells from the master cell bank in an *ex vivo* milieu that is a cultivated cell biomass; and

harvesting the cultivated cell biomass for dietary consumption; wherein the genetic amendment comprises

i) genetic amendment of a CDKN2B gene to inactivate a p15 protein in the metazoan somatic cell population to abolish retinoblastoma protein inhibition of the cell cycle during replicative senescence; or

ii) genetic amendment of a CDKN2A gene to inactivate a p16 protein in the metazoan somatic cell population to abolish retinoblastoma protein inhibition of the cell cycle during replicative senescence; or

iii) modification of the cell population with a genetic construct that directs ectopic expression of a cyclin-dependent kinase 4 ("CDK4") protein; and

wherein the clonal cell line has indefinite replicative capacity for scalable applications in the industrial production.

19. The clonal cell line of claim 18, wherein CDKN2B gene comprises the sequence of NCBI Gene ID: 395076.

20. The clonal cell line of any one of claims 18-19, wherein the genetic amendment is a mutation of a conserved nucleotide sequence in exon one of the CDKN2B gene.

21. The clonal cell line of claim 20, wherein the genetic amendment is an insertion mutation made using guide RNAs, said guide RNAs selected from the group consisting of (SEQ ID Nos. 1, 2, 3, 4 and 5) targeting exon one of the CDKN2B gene and is created using CRISPR/Cas9.

22. The clonal cell line of claim 20, wherein the genetic amendment is a deletion mutation made using guide RNAs, said guide RNAs selected from the group consisting of (SEQ ID Nos. 1, 2, 3, 4 and 5) targeting exon one of the CDKN2B gene and is created using CRISPR/Cas9.

23. The clonal cell line of any one of claims 19-22, wherein the metazoan somatic cell population species identity is *Gallus gallus* and the metazoan somatic cell population lineage is skeletal muscle.

24. The clonal cell line of claim 18, wherein the CDKN2A gene comprises the sequence of NCBI Gene ID: 616369.

25. The clonal cell line of any one of claims 18 and 24, wherein the genetic amendment is a mutation of a conserved nucleotide sequence in exon two of the CDKN2A.

26. The clonal cell line of claim 25, wherein the genetic amendment is an insertion mutation made using guide RNAs said guide RNAs selected from the group consisting of (SEQ ID NO 8-10) targeting exon two of the CDKN2A and is created using CRISPR/Cas9.

27. The clonal cell line of claim 25, wherein the genetic amendment is a deletion mutation made using guide RNAs said guide RNAs selected from the group consisting of (SEQ ID NO 8-10) targeting exon two of the CDKN2A and is created using CRISPR/Cas9.

28. The clonal cell line of any one of claims 24-27, wherein the metazoan somatic cell population species identity is *Bos taurus* and the metazoan somatic cell population lineage is skeletal muscle.

29. The clonal cell line of claim 18, wherein the genetic construct directing the expression of the CDK4 protein from a CDK4 gene (NCBI Gene ID:510618) comprises the sequence of SEQ ID NO 12.

30. The clonal cell line of any one of claims 18 and 29, wherein the metazoan somatic cell population species identity is *Gallus gallus* and the metazoan somatic cell population lineage is skeletal muscle.

31. The clonal cell line of claim 29, wherein modifying the metazoan cell population is with a genetic construct (SEQ ID NO 12) directing expression of a CDK4 protein homolog from a *Bos taurus* CDK4 gene.

32. The clonal cell line of any one of claims 18-31, wherein cultivating cells from the master cell bank further comprises:

expanding selected cell populations from the master cell bank;

cryopreserving and storing expanded cell populations in a master cell bank stock inventory; seeding and cultivating cells from the master cell bank stock inventory in an ex vivo milieu; and

harvesting cultivated cell biomass for dietary consumption.

33. The clonal cell line of any one of claims 18-22, 24-27, 29, and 31-32 wherein the metazoan somatic cell population is a skeletal muscle cell population from a species of seafood, poultry, or livestock.

34. The clonal cell line of claim 33, wherein the metazoan somatic cell population is a skeletal muscle cell population from a species selected from the group consisting of *Gallus gallus, Meleagris gallopavo, Anas platyrhynchos, Bos taurus, Sus scrofa, Ovis aries, Salmo salar, Thunnus thynnus, Gadus morhua, Homarus americanus, Litopenaeus setiferus, Oncorhynchus mykiss, and Oreochromis niloticus.*

35. The process of any one of claims 1-17 or clonal cell line of any one of claims 18-34, wherein the nucleic acid sequence encoding the TERT protein comprises the sequence of SEQ ID NO: 11.