

CLAIMS

1. A pharmaceutical composition comprising:
 - a) a virus comprising a vector, wherein the vector comprises one or more transgenes encoding a polypeptide selected from the group consisting of a Collagen alpha-1 (VII) chain polypeptide, a Lysyl hydroxylase 3 polypeptide, and a chimeric polypeptide thereof; and
 - b) a pharmaceutically acceptable carrier.
2. The pharmaceutical composition of claim 1, wherein the virus is an adenovirus, adeno-associated virus, retrovirus, lentivirus, sendai virus, herpes simplex virus, vaccinia virus, or any hybrid virus thereof.
3. The pharmaceutical composition of claim 1, wherein the virus is a herpes simplex virus (HSV).
4. The pharmaceutical composition of any of claims 1 to 3, wherein the virus is replication-defective.
5. The pharmaceutical composition of claim 3, wherein the herpes simplex virus is a herpes simplex type 1 virus, a herpes simplex type 2 virus, or any derivatives thereof.
6. The pharmaceutical composition of claim 3, wherein the herpes simplex virus comprises a modified envelope.
7. The pharmaceutical composition of claim 6, wherein the modified envelope alters the herpes simplex virus tissue tropism relative to a wild-type herpes simplex virus.
8. The pharmaceutical composition of claim 6, wherein the modified envelope comprises a mutant herpes simplex virus glycoprotein.
9. The pharmaceutical composition of claim 1, wherein the vector is an HSV-1 amplicon or an HSV-1 hybrid amplicon.

10. The pharmaceutical composition of claim 9, wherein the HSV-1 hybrid amplicon is an HSV/AAV hybrid amplicon, an HSV/EBV hybrid amplicon, and HSV/EBV/RV hybrid amplicon, or an HSV/*Sleeping Beauty* hybrid amplicon.
11. The pharmaceutical composition of claim 1, wherein the vector is a recombinant herpes simplex virus genome.
12. The pharmaceutical composition of claim 11, wherein the recombinant herpes simplex virus genome is a recombinant HSV-1 genome, a recombinant HSV-2 genome, or any derivatives thereof.
13. The pharmaceutical composition of claim 11 or 12, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in an immediate early herpes simplex virus gene.
14. The pharmaceutical composition of claim 13, wherein the herpes simplex virus gene is selected from the group consisting of ICP0, ICP4, ICP22, ICP27, ICP47, tk, UL41, and UL55.
15. The pharmaceutical composition of any of claims 11 to 14, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP4 and ICP22 genes.
16. The pharmaceutical composition of any of claims 11 to 14, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0 and ICP4 genes.
17. The pharmaceutical composition of claim 15 or claim 16, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, and ICP22 genes.
18. The pharmaceutical composition of any of claims 15 to 17, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, and ICP27 genes.

19. The pharmaceutical composition of any of claims 15 to 18, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, ICP27, and UL55 genes.
20. The pharmaceutical composition of any of claims 15 to 18, wherein the inactivating mutation is a deletion of the coding sequence of the genes.
21. The pharmaceutical composition of any of claims 15 to 20, further comprising an inactivating mutation in the ICP47 gene.
22. The pharmaceutical composition of any of claims 11 to 21, further comprising an inactivating mutation in the UL41 gene.
23. The pharmaceutical composition of any of claims 11 to 22, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within one or more viral gene loci.
24. The pharmaceutical composition of any of claims 11 to 23, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within one or more of the ICP4 viral gene loci.
25. The pharmaceutical composition of any of claims 11 to 24, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within the UL41 viral gene locus.
26. The pharmaceutical composition of claim 1, wherein the vector is capable of replicating within a target cell when delivered into said target cell.
27. The pharmaceutical composition of claim 1, wherein the pharmaceutically acceptable carrier is suitable for topical or transdermal administration.
28. The pharmaceutical composition of claim 1, wherein the one or more transgenes comprises an miRNA binding site.
29. The pharmaceutical composition of claim 1, wherein the one or more transgenes are operably linked to one or more heterologous promoters.

30. The pharmaceutical composition of claim 29, wherein the one or more heterologous promoters are selected from the group consisting of the human cytomegalovirus (HCMV) immediate early promoter, the elongation factor-1 (EF1) promoter, and any combinations thereof.
31. The pharmaceutical composition of claim 1, wherein the vector comprises a transgene encoding a Collagen alpha-1 (VII) chain polypeptide.
32. The pharmaceutical composition of claim 1, wherein the vector comprises two transgenes, wherein each transgene encodes a Collagen alpha-1 (VII) chain polypeptide.
33. The pharmaceutical composition of claim 1, wherein the Collagen alpha-1 (VII) chain polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 2.
34. The pharmaceutical composition of claim 1, wherein the collagen alpha-1 (VII) chain polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 2.
35. The pharmaceutical composition of claim 1, wherein the Collagen alpha-1 (VII) chain polypeptide enhances, increases, augments, and/or supplements anchoring fibril formation of a subject when the polypeptide is expressed in one or more target cells of the subject.
36. The pharmaceutical composition of claim 1, wherein the Collagen alpha-1 (VII) chain polypeptide enhances, increases, augments, and/or supplements epithelial basement membrane organization and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.
37. The pharmaceutical composition of claim 1, wherein the Lysyl hydroxylase 3 polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 4.
38. The pharmaceutical composition of claim 1, wherein the Lysyl hydroxylase 3 polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 4.

39. The pharmaceutical composition of claim 1, wherein the Lysyl hydroxylase 3 polypeptide enhances, increases, augments, and/or supplements the formation of hydroxylysine residues on one or more collagen polypeptides of a subject when the Lysyl hydroxylase 3 polypeptide is expressed in one or more target cells of the subject.
40. The pharmaceutical composition of claim 1, wherein the Lysyl hydroxylase 3 polypeptide enhances, increases, augments, and/or supplements anchoring fibril formation, epithelial basement membrane organization, and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.
41. The pharmaceutical composition of claim 1, wherein the vector comprises at least a first transgene and a second transgene.
42. The pharmaceutical composition of claim 41, wherein the first transgene encodes a Collagen alpha-1 (VII) chain polypeptide and the second transgene encodes a Lysyl hydroxylase 3 polypeptide.
43. The pharmaceutical composition of claim 1, wherein the vector comprises a transgene that is polycistronic.
44. The pharmaceutical composition of claim 43, wherein the polycistronic transgene encodes a Collagen alpha-1 (VII) chain polypeptide on a first open reading frame (ORF) and a Lysyl hydroxylase 3 polypeptide on a second open reading frame (ORF).
45. The pharmaceutical composition of claim 44, wherein the first and second ORFs are separated by an internal ribosomal entry site (IRES).
46. The pharmaceutical composition of any of claims 42 to 45, wherein the Collagen alpha-1 (VII) chain polypeptide and the Lysyl hydroxylase 3 polypeptide are at about an equimolar ratio when the polypeptides are expressed in one or more target cells of a subject.

47. The pharmaceutical composition of any of claims 42 to 45, wherein the Collagen alpha-1 (VII) chain polypeptide and the Lysyl hydroxylase 3 polypeptide enhance, increase, augment, and/or supplement anchoring fibril formation, epithelial basement membrane organization, and/or epithelial basement adherence of a subject when the polypeptides are expressed in one or more target cells of the subject.
48. The pharmaceutical composition of claim 1, wherein the chimeric polypeptide comprises a linker polypeptide between the Collagen alpha-1 (VII) chain polypeptide and the Lysyl hydroxylase 3 polypeptide.
49. The pharmaceutical composition of claim 48, wherein the linker polypeptide is a T2A, P2A, E2A, or F2A linker polypeptide.
50. The pharmaceutical composition of claim 48 or 49, wherein the linker polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10 or SEQ ID NO: 12.
51. The pharmaceutical composition of any of claims 48 to 50, wherein the chimeric polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26 or SEQ ID NO: 28.
52. The pharmaceutical composition of any of claims 48 to 51, wherein the chimeric polypeptide enhances, increases, augments, and/or supplements anchoring fibril formation, epithelial basement membrane organization, and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.
53. A method of providing prophylactic, palliative, or therapeutic relief of a wound, disorder, or disease of the skin in a subject, the method comprising topically or transdermally administering a pharmaceutical composition capable of enhancing, increasing, augmenting, and/or supplementing the levels of a Collagen alpha-1 (VII) chain polypeptide and/or a Lysyl hydroxylase 3 polypeptide in one or more cells of the subject.

54. The method of claim 53, wherein the pharmaceutical composition comprises:
- a) a virus comprising a vector, wherein the vector comprises one or more transgenes encoding a polypeptide selected from the group consisting of a Collagen alpha-1 (VII) chain polypeptide, a Lysyl hydroxylase 3 polypeptide, and a chimeric polypeptide thereof; and
 - b) a pharmaceutically acceptable carrier.
55. The method of claim 54, wherein the virus is an adenovirus, adeno-associated virus, retrovirus, lentivirus, sendai virus, herpes simplex virus, vaccinia virus, or any hybrid virus thereof.
56. The method of claim 54, wherein the virus is a herpes simplex virus (HSV).
57. The method of any of claims 54 to 56, wherein the virus is replication-defective.
58. The method of claim 56, wherein the herpes simplex virus is a herpes simplex type 1 virus, a herpes simplex type 2 virus, or any derivatives thereof.
59. The method of claims 56, wherein the herpes simplex virus comprises a modified envelope.
60. The method of claim 59, wherein the modified envelope alters the herpes simplex virus tissue tropism relative to a wild-type herpes simplex virus.
61. The method of claim 59, wherein the modified envelope comprises a mutant herpes simplex virus glycoprotein.
62. The method of claim 54, wherein the vector is an HSV-1 amplicon or an HSV-1 hybrid amplicon.
63. The method of claim 62, wherein the HSV-1 hybrid amplicon is an HSV/AAV hybrid amplicon, an HSV/EBV hybrid amplicon, and HSV/EBV/RV hybrid amplicon, or an HSV/*Sleeping Beauty* hybrid amplicon.
64. The method of claim 54, wherein the vector is a recombinant herpes simplex virus genome.

65. The method of claim 64, wherein the recombinant herpes simplex virus genome is a recombinant HSV-1 genome, a recombinant HSV-2 genome, or any derivatives thereof.
66. The method of claim 64 or 65, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in an immediate early herpes simplex virus gene.
67. The method of claim 66, wherein the herpes simplex virus gene is selected from the group consisting of ICP0, ICP4, ICP22, ICP27, ICP47, tk, UL41, and UL55.
68. The method of any of claims 64 to 67, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP4 and ICP22 genes.
69. The method of any of claims 64 to 67, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0 and ICP4 genes.
70. The method of claim 68 or claim 69, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, and ICP22 genes.
71. The method of any of claims 68 to 70, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, and ICP27 genes.
72. The method of any of claims 68 to 71, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, ICP27, and UL55 genes.
73. The method of any of claims 68 to 72, wherein the inactivating mutation is a deletion of the coding sequence of the genes.
74. The method of any of claims 68 to 73, further comprising an inactivating mutation in the ICP47 gene.
75. The method of any of claims 64 to 74, further comprising an inactivating mutation in the UL41 gene.

76. The method of any of claims 64 to 75, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within one or more viral gene loci.
77. The method of any of claims 64 to 76, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within one or more of the ICP4 viral gene loci.
78. The method of any of claims 64 to 77, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within the UL41 viral gene locus.
79. The method of claim 54, wherein the vector is capable of replicating within a target cell when delivered into said target cell.
80. The method of claim 54, wherein the pharmaceutically acceptable carrier is suitable for topical or transdermal administration.
81. The method of claim 54, wherein the one or more transgenes comprises an miRNA binding site.
82. The method of claim 54, wherein the one or more transgenes are operably linked to one or more heterologous promoters.
83. The method of claim 82, wherein the one or more heterologous promoters are selected from the group consisting of the human cytomegalovirus (HCMV) immediate early promoter, the elongation factor-1 (EF1) promoter, and any combinations thereof.
84. The method of claim 54, wherein the vector comprises a transgene encoding a Collagen alpha-1 (VII) chain polypeptide.
85. The method of claim 54, wherein the vector comprises two transgenes, wherein each transgene encodes a Collagen alpha-1 (VII) chain polypeptide.
86. The method of claim 54, wherein the Collagen alpha-1 (VII) chain polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 2.

87. The method of claim 54, wherein the Collagen alpha-1 (VII) chain polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 2.
88. The method of claim 54, wherein the Collagen alpha-1 (VII) chain polypeptide enhances, increases, augments, and/or supplements anchoring fibril formation of a subject when the polypeptide is expressed in one or more target cells of the subject.
89. The method of claim 54, wherein the Collagen alpha-1 (VII) chain polypeptide enhances, increases, augments, and/or supplements epithelial basement membrane organization and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.
90. The method of claim 54, wherein the Lysyl hydroxylase 3 polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 4.
91. The method of claim 54, wherein the Lysyl hydroxylase 3 polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 4.
92. The method of claim 54, wherein the Lysyl hydroxylase 3 polypeptide enhances, increases, augments, and/or supplements the formation of hydroxylysine residues on one or more collagen polypeptides of a subject when the Lysyl hydroxylase 3 polypeptide is expressed in one or more target cells of the subject.
93. The method of claim 54, wherein the Lysyl hydroxylase 3 polypeptide enhances, increases, augments, and/or supplements anchoring fibril formation, epithelial basement membrane organization, and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.
94. The method of claim 54, wherein the vector comprises at least a first transgene and a second transgene.
95. The method of claim 94, wherein the first transgene encodes a Collagen alpha-1 (VII) chain polypeptide and the second transgene encodes a Lysyl hydroxylase 3 polypeptide.

96. The method of claim 54, wherein the vector comprises a transgene that is polycistronic.
97. The method of claim 96, wherein the polycistronic transgene encodes a Collagen alpha-1 (VII) chain polypeptide on a first open reading frame (ORF) and a Lysyl hydroxylase 3 polypeptide on a second open reading frame (ORF).
98. The method of claim 97, wherein the first and second ORFs are separated by an internal ribosomal entry site (IRES).
99. The method of any of claims 95 to 98, wherein the Collagen alpha-1 (VII) chain polypeptide and the Lysyl hydroxylase 3 polypeptide are at about an equimolar ratio when the polypeptides are expressed in one or more target cells of a subject.
100. The method of any of claims 95 to 98, wherein the Collagen alpha-1 (VII) chain polypeptide and the Lysyl hydroxylase 3 polypeptide enhance, increase, augment, and/or supplement anchoring fibril formation, epithelial basement membrane organization, and/or epithelial basement adherence of a subject when the polypeptides are expressed in one or more target cells of the subject.
101. The method of claim 54, wherein the chimeric polypeptide comprises a linker polypeptide between the Collagen alpha-1 (VII) chain polypeptide and the Lysyl hydroxylase 3 polypeptide.
102. The method of claim 101, wherein the linker polypeptide is a T2A, P2A, E2A, or F2A linker polypeptide.
103. The method of claim 101 or 102, wherein the linker polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10 or SEQ ID NO: 12.
104. The method of any of claims 101 to 103, wherein the chimeric polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26 or SEQ ID NO: 28.

105. The method of any of claims 101 to 104, wherein the chimeric polypeptide enhances, increases, augments, and/or supplements anchoring fibril formation, epithelial basement membrane organization, and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.
106. The method of claim 53, wherein the pharmaceutical composition is administered one, two three, four, five or more times per day.
107. The method of claim 53, wherein the pharmaceutical composition is administered to one or more affected and/or unaffected areas of the subject.
108. The method of claim 53, wherein the disease or disorder of the skin is one or more of epidermolysis bullosa, skin cancer, psoriasis, lichen planus, lupus, rosacea, eczema, cutaneous candidiasis, cellulitis, impetigo, decubitus ulcers, erysipelas, ichthyosis vulgaris, dermatomyositis, acrodermatitis, stasis dermatitis, nethertons syndrome, epidermolysis bullosa simplex (LAMB3 gene), autosomal recessive congenital ichthyosis, xeroderma pigmentosa, and pemphigoid.
109. An isolated chimeric polypeptide, wherein the isolated chimeric polypeptide comprises;
- a) a Collagen alpha-1 (VII) chain polypeptide;
 - b) a Lysyl hydroxylase 3 polypeptide; and
 - c) a linker polypeptide;
- wherein the Collagen alpha-1 (VII) chain polypeptide and the Lysyl hydroxylase 3 polypeptide are separated by the linker polypeptide.
110. The isolated chimeric polypeptide of claim 109, wherein the Collagen alpha-1 (VII) chain polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 2.
111. The isolated chimeric polypeptide of claim 109, wherein the Lysyl hydroxylase 3 polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 4.

112. The isolated chimeric polypeptide of claim 109, wherein the linker polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10 or SEQ ID NO: 12.
113. The isolated chimeric polypeptide of any of claims 109 to 112, wherein the isolated chimeric polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26 or SEQ ID NO: 28.
114. A polynucleotide encoding the chimeric polypeptide of any of claims 109 to 113.
115. A vector comprising the polynucleotide of claim 114.
116. The vector of claim 115, wherein the vector is an HSV-1 amplicon or an HSV-1 hybrid amplicon.
117. The vector of claim 116 wherein the HSV-1 hybrid amplicon is an HSV/AAV hybrid amplicon, an HSV/EBV hybrid amplicon, and HSV/EBV/RV hybrid amplicon, or an HSV/*Sleeping Beauty* hybrid amplicon.
118. The vector of claim 115, wherein the vector is a recombinant herpes simplex virus genome.
119. The vector of claim 118, wherein the recombinant herpes simplex virus genome is a recombinant HSV-1 genome, a recombinant HSV-2 genome, or any derivatives thereof.
120. The vector of claim 118 or 119, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in an immediate early herpes simplex virus gene.
121. The vector of claim 120, wherein the herpes simplex virus gene is selected from the group consisting of ICP0, ICP4, ICP22, ICP27, ICP47, tk, UL41, and UL55.
122. The vector of any of claims 118 to 121, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP4 and ICP22 genes.

123. The vector of any of claims 118 to 121, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0 and ICP4 genes.
124. The vector of claim 122 or claim 123, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, and ICP22 genes.
125. The vector of any of claims 122 to 124, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, and ICP27 genes.
126. The vector of any of claims 122 to 125, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, ICP27, and UL55 genes.
127. The vector of any of claims 122 to 126, wherein the inactivating mutation is a deletion of the coding sequence of the genes.
128. The vector of any of claims 122 to 127, further comprising an inactivating mutation in the ICP47 gene.
129. The vector of any of claims 118 to 128, further comprising an inactivating mutation in the UL41 gene.
130. The vector of any of claims 118 to 129, wherein the recombinant herpes simplex virus genome comprises the polynucleotide within one or more viral gene loci.
131. The vector of any of claims 118 to 130, wherein the recombinant herpes simplex virus genome comprises the polynucleotide within one or more of the ICP4 viral gene loci.
132. The vector of any of claims 118 to 131, wherein the recombinant herpes simplex virus genome comprises the polynucleotide within the UL41 viral gene locus.
133. A vector comprising one or more polynucleotides encoding a Collagen alpha-1 (VII) chain polypeptide, a Lysyl hydroxylase 3 polypeptide, a Keratin type I cytoskeletal

- 17 polypeptide, or any combinations thereof, wherein the vector is a recombinant herpes simplex virus genome.
134. The vector of claim 133, wherein the recombinant herpes simplex virus genome is a recombinant HSV-1 genome, a recombinant HSV-2 genome, or any derivatives thereof.
135. The vector of claim 133 or claim 134, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in an immediate early herpes simplex virus gene.
136. The vector of claim 135, wherein the herpes simplex virus gene is selected from the group consisting of ICP0, ICP4, ICP22, ICP27, ICP47, tk, UL41, and UL55.
137. The vector of any of claims 133 to 136, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP4 and ICP22 genes.
138. The vector of any of claims 133 to 136, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0 and ICP4 genes.
139. The vector of claim 137 or claim 138, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, and ICP22 genes.
140. The vector of any of claims 137 to 139, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, and ICP27 genes.
141. The vector of any of claims 137 to 140, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, ICP27, and UL55 genes.
142. The vector of any of claims 137 to 141, wherein the inactivating mutation is a deletion of the coding sequence of the genes.
143. The vector of any of claims 137 to 142, further comprising an inactivating mutation in the ICP47 gene.

144. The vector of any of claims 133 to 143, further comprising an inactivating mutation in the UL41 gene.
145. The vector of any of claims 133 to 144, wherein the recombinant herpes simplex virus genome comprises the one or more polynucleotides within one or more viral gene loci.
146. The vector of any of claims 133 to 145, wherein the recombinant herpes simplex virus genome comprises the one or more polynucleotides within one or more of the ICP4 viral gene loci.
147. The vector of any of claims 133 to 146, wherein the recombinant herpes simplex virus genome comprises the one or more polynucleotides within the UL41 viral gene locus.
148. The vector of any of claims 133 to 147, wherein the vector comprises one polynucleotide encoding a Collagen alpha-1 (VII) chain polypeptide.
149. The vector of any of claims 133 to 147, wherein the vector comprises two polynucleotides encoding a Collagen alpha-1 (VII) chain polypeptide.
150. A host cell comprising the vector of any of claims 115 to 149.
151. A method of collecting a herpes simplex virus, wherein a vector of interest is packaged within said herpes simplex virus, the method comprising:
 - a) contacting a host cell with a vector encoding a helper virus;
 - b) contacting said host cell with a vector of any of claims 115 to 117; and
 - c) collecting the Herpes simplex virus generated by said host cell.
152. A method of collecting a herpes simplex virus, wherein a vector of interest is packaged within said herpes simplex virus, the method comprising:
 - a) contacting a complementing host cell with a vector of any of claims 118 to 149; and
 - b) collecting the herpes simplex virus generated by said complementing host cell.

153. The method of claim 151 or 152, wherein the herpes simplex virus is a herpes simplex type 1 virus, a herpes simplex type 2 virus, or any derivatives thereof.
154. A kit comprising:
- a) the pharmaceutical composition of any of claims 1 to 52; and
 - b) instructions for administering the pharmaceutical composition.
155. A pharmaceutical composition comprising:
- a) a virus comprising a vector, wherein the vector comprises one or more transgenes encoding a polypeptide selected from the group consisting of a Collagen alpha-1 (VII) chain polypeptide, a Lysyl hydroxylase 3 polypeptide, a Keratin type I cytoskeletal 17 polypeptide, and a chimeric polypeptide thereof; and
 - b) a pharmaceutically acceptable carrier.
156. The pharmaceutical composition of claim 155, wherein the virus is an adenovirus, adeno-associated virus, retrovirus, lentivirus, sendai virus, herpes simplex virus, vaccinia virus, or any hybrid virus thereof.
157. The pharmaceutical composition of claim 155, wherein the virus is a herpes simplex virus (HSV).
158. The pharmaceutical composition of any of claims 155 to 157, wherein the virus is replication-defective.
159. The pharmaceutical composition of any of claims 155 to 158, wherein the herpes simplex virus is a herpes simplex type 1 virus, a herpes simplex type 2 virus, or any derivatives thereof.
160. The pharmaceutical composition of any of claims 155 to 159, wherein the vector is an HSV-1 amplicon or an HSV-1 hybrid amplicon.
161. The pharmaceutical composition of claim 160, wherein the HSV-1 hybrid amplicon is an HSV/AAV hybrid amplicon, an HSV/EBV hybrid amplicon, and HSV/EBV/RV hybrid amplicon, or an HSV/*Sleeping Beauty* hybrid amplicon.

162. The pharmaceutical composition of any of claims 155 to 159, wherein the vector is a recombinant herpes simplex virus genome.
163. The pharmaceutical composition of claim 162, wherein the recombinant herpes simplex virus genome is a recombinant HSV-1 genome, a recombinant HSV-2 genome, or any derivatives thereof.
164. The pharmaceutical composition of claim 162 or 163, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in an immediate early herpes simplex virus gene.
165. The pharmaceutical composition of claim 164, wherein the herpes simplex virus gene is selected from the group consisting of ICP0, ICP4, ICP22, ICP27, ICP47, tk, UL41, and UL55.
166. The pharmaceutical composition of any of claims 162 to 165, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP4 and ICP22 genes.
167. The pharmaceutical composition of any of claims 162 to 165, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0 and ICP4 genes.
168. The pharmaceutical composition of claim 166 or claim 167, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, and ICP22 genes.
169. The pharmaceutical composition of any of claims 166 to 168, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, and ICP27 genes.
170. The pharmaceutical composition of any of claims 166 to 169, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, ICP27, and UL55 genes.

171. The pharmaceutical composition of any of claims 166 to 170, wherein the inactivating mutation is a deletion of the coding sequence of the genes.
172. The pharmaceutical composition of any of claims 166 to 171, further comprising an inactivating mutation in the ICP47 gene.
173. The pharmaceutical composition of any of claims 162 to 172, further comprising an inactivating mutation in the UL41 gene.
174. The pharmaceutical composition of any of claims 162 to 173, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within one or more viral gene loci.
175. The pharmaceutical composition of any of claims 162 to 174, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within one or more of the ICP4 viral gene loci.
176. The pharmaceutical composition of any of claims 162 to 175, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within the UL41 viral gene locus.
177. The pharmaceutical composition of claim 155, wherein the vector is capable of replicating within a target cell when delivered into said target cell.
178. The pharmaceutical composition of claim 155, wherein the pharmaceutically acceptable carrier is suitable for topical or transdermal administration.
179. The pharmaceutical composition of claim 155, wherein the pharmaceutically acceptable carrier is suitable for subcutaneous or intradermal administration.
180. The pharmaceutical composition of claim 155, wherein the one or more transgenes comprises an miRNA binding site.
181. The pharmaceutical composition of any of claims 155 to 180, wherein the vector comprises a transgene encoding a Collagen alpha-1 (VII) chain polypeptide.

182. The pharmaceutical composition of any of claims 155 to 180, wherein the vector comprises a transgene encoding a Lysyl hydroxylase 3 polypeptide.
183. The pharmaceutical composition of any of claims 155 to 180, wherein the vector comprises a transgene encoding a Keratin type I cytoskeletal 17 polypeptide.
184. The pharmaceutical composition of any of claims 155 to 180, wherein the Collagen alpha-1 (VII) chain polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 2.
185. The pharmaceutical composition of any of claims 155 to 180, wherein the Collagen alpha-1 (VII) chain polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 2.
186. The pharmaceutical composition of any of claims 155 to 180, wherein the Collagen alpha-1 (VII) chain polypeptide enhances, increases, augments, and/or supplements anchoring fibril formation of a subject when the polypeptide is expressed in one or more target cells of the subject.
187. The pharmaceutical composition of any of claims 155 to 180, wherein the Collagen alpha-1 (VII) chain polypeptide enhances, increases, augments, and/or supplements epithelial basement membrane organization and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.
188. The pharmaceutical composition of any of claims 155 to 180, wherein the Lysyl hydroxylase 3 polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 4.
189. The pharmaceutical composition of any of claims 155 to 180, wherein the Lysyl hydroxylase 3 polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 4.
190. The pharmaceutical composition of any of claims 155 to 180, wherein the Lysyl hydroxylase 3 polypeptide enhances, increases, augments, and/or supplements the

formation of hydroxylysine residues on one or more collagen polypeptides of a subject when the Lysyl hydroxylase 3 polypeptide is expressed in one or more target cells of the subject.

191. The pharmaceutical composition of any of claims 155 to 180, wherein the Lysyl hydroxylase 3 polypeptide enhances, increases, augments, and/or supplements anchoring fibril formation, epithelial basement membrane organization, and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.
192. The pharmaceutical composition of any of claims 155 to 180, wherein the Keratin type I cytoskeletal 17 polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 30.
193. The pharmaceutical composition of any of claims 155 to 180, wherein the Keratin type I cytoskeletal 17 polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 30.
194. The pharmaceutical composition of any of claims 155 to 180, wherein the Keratin type I cytoskeletal 17 polypeptide enhances, increases, augments, and/or supplements wound healing in a subject.
195. The pharmaceutical composition of claim any of claims 155 to 194, wherein the vector comprises at least a first transgene and a second transgene.
196. The pharmaceutical composition of claim 195, wherein the first transgene and the second transgene each encode a Collagen alpha-1 (VII) chain polypeptide.
197. The pharmaceutical composition of claim 195, wherein the first transgene encodes a Collagen alpha-1 (VII) chain polypeptide and the second transgene encodes a Lysyl hydroxylase 3 polypeptide.
198. The pharmaceutical composition of claim 195, wherein the first transgene encodes a Collagen alpha-1 (VII) chain polypeptide and the second transgene encodes a Keratin type I cytoskeletal 17 polypeptide.

199. The pharmaceutical composition of claim 195, wherein the first transgene encodes a Lysyl hydroxylase 3 polypeptide and the second transgene encodes a Keratin type I cytoskeletal 17 polypeptide.
200. The pharmaceutical composition of claim 155, wherein the vector comprises at least a first transgene, a second transgene, and a third transgene.
201. The pharmaceutical composition of claim 200, wherein the first transgene encodes a Collagen alpha-1 (VII) chain polypeptide, the second transgene encodes a Lysyl hydroxylase 3 polypeptide, and the third transgene encodes a Keratin type I cytoskeletal 17 polypeptide.
202. A method of providing prophylactic, palliative, or therapeutic relief of a wound, disorder, or disease of the skin in a subject, the method comprising administering to the subject a pharmaceutical composition comprising a vector, wherein the vector is a recombinant herpes simplex virus genome, and wherein the pharmaceutical composition is capable of enhancing, increasing, augmenting, and/or supplementing the levels of a Collagen alpha-1 (VII) chain polypeptide and/or a Lysyl hydroxylase 3 polypeptide and/or a Keratin type I cytoskeletal 17 polypeptide in one or more cells of the subject.
203. The method of claim 202, wherein the pharmaceutical composition comprises:
- a) a virus comprising the vector, wherein the vector comprises one or more transgenes encoding a polypeptide selected from the group consisting of a Collagen alpha-1 (VII) chain polypeptide, a Lysyl hydroxylase 3 polypeptide, a Keratin type I cytoskeletal 17 polypeptide, and a chimeric polypeptide thereof; and
 - b) a pharmaceutically acceptable carrier.
204. The method of claim 203, wherein the virus is an adenovirus, adeno-associated virus, retrovirus, lentivirus, sendai virus, herpes simplex virus, vaccinia virus, or any hybrid virus thereof.
205. The method of claim 203, wherein the virus is a herpes simplex virus (HSV).

206. The method of any of claims 203 to 205, wherein the virus is replication-defective.
207. The method of any of claim 203 to 206, wherein the herpes simplex virus is a herpes simplex type 1 virus, a herpes simplex type 2 virus, or any derivatives thereof.
208. The method of any of claims 202 to 207, wherein the recombinant herpes simplex virus genome is a recombinant HSV-1 genome, a recombinant HSV-2 genome, or any derivatives thereof.
209. The method of claim 202 to 208, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in an immediate early herpes simplex virus gene.
210. The method of claim 209, wherein the herpes simplex virus gene is selected from the group consisting of ICP0, ICP4, ICP22, ICP27, ICP47, tk, UL41, and UL55.
211. The method of any of claims 202 to 210, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP4 and ICP22 genes.
212. The method of any of claims 202 to 210, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0 and ICP4 genes.
213. The method of claim 211 or claim 212, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, and ICP22 genes.
214. The method of any of claims 211 to 213, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, and ICP27 genes.
215. The method of any of claims 211 to 214, wherein the recombinant herpes simplex virus genome comprises an inactivating mutation in the ICP0, ICP4, ICP22, ICP27, and UL55 genes.
216. The method of any of claims 211 to 215, wherein the inactivating mutation is a deletion of the coding sequence of the genes.

217. The method of any of claims 211 to 216, further comprising an inactivating mutation in the ICP47 gene.
218. The method of any of claims 202 to 217, further comprising an inactivating mutation in the UL41 gene.
219. The method of any of claims 202 to 218, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within one or more viral gene loci.
220. The method of any of claims 202 to 219, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within one or more of the ICP4 viral gene loci.
221. The method of any of claims 202 to 220, wherein the recombinant herpes simplex virus genome comprises the one or more transgenes within the UL41 viral gene locus.
222. The method of claim 202, wherein the vector is capable of replicating within a target cell when delivered into said target cell.
223. The method of claim 203, wherein the pharmaceutically acceptable carrier is suitable for topical or transdermal administration.
224. The method of claim 203, wherein the pharmaceutically acceptable carrier is suitable for subcutaneous or intradermal administration.
225. The method of claim 203, wherein the one or more transgenes comprises an miRNA binding site.
226. The method of any of claims 202 to 225, wherein the vector comprises a transgene encoding a Collagen alpha-1 (VII) chain polypeptide.
227. The method of any of claims 202 to 225, wherein the vector comprises a transgene encoding a Lysyl hydroxylase 3 polypeptide.

228. The method of any of claims 202 to 225, wherein the vector comprises a transgene encoding a Keratin type I cytoskeletal 17 polypeptide.
229. The method of any of claims 202 to 225, wherein the Collagen alpha-1 (VII) chain polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 2.
230. The method of any of claims 202 to 225, wherein the Collagen alpha-1 (VII) chain polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 2.
231. The method of any of claims 202 to 225, wherein the Collagen alpha-1 (VII) chain polypeptide enhances, increases, augments, and/or supplements anchoring fibril formation of a subject when the polypeptide is expressed in one or more target cells of the subject.
232. The method of any of claims 202 to 225, wherein the Collagen alpha-1 (VII) chain polypeptide enhances, increases, augments, and/or supplements epithelial basement membrane organization and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.
233. The method of any of claims 202 to 225, wherein the Lysyl hydroxylase 3 polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 4.
234. The method of any of claims 202 to 225, wherein the Lysyl hydroxylase 3 polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 4.
235. The method of any of claims 202 to 225, wherein the Lysyl hydroxylase 3 polypeptide enhances, increases, augments, and/or supplements the formation of hydroxylysine residues on one or more collagen polypeptides of a subject when the Lysyl hydroxylase 3 polypeptide is expressed in one or more target cells of the subject.
236. The method of any of claims 202 to 225, wherein the Lysyl hydroxylase 3 polypeptide enhances, increases, augments, and/or supplements anchoring fibril

formation, epithelial basement membrane organization, and/or epithelial basement adherence of a subject when the polypeptide is expressed in one or more target cells of the subject.

237. The method of any of claims 202 to 225, wherein the Keratin type I cytoskeletal 17 polypeptide has at least 80% sequence identity to the sequence of SEQ ID NO: 30.
238. The method of any of claims 202 to 225, wherein the Keratin type I cytoskeletal 17 polypeptide is a fragment, wherein the fragment has at least 100 consecutive amino acids of SEQ ID NO: 30.
239. The method of any of claims 202 to 225, wherein the Keratin type I cytoskeletal 17 polypeptide enhances, increases, augments, and/or supplements wound healing in a subject.
240. The method of any of claims 202 to 239, wherein the vector comprises at least a first transgene and a second transgene.
241. The method of claim 240, wherein the first transgene and the second transgene each encode a Collagen alpha-1 (VII) chain polypeptide.
242. The method of claim 240, wherein the first transgene encodes a Collagen alpha-1 (VII) chain polypeptide and the second transgene encodes a Lysyl hydroxylase 3 polypeptide.
243. The method of claim 240, wherein the first transgene encodes a Collagen alpha-1 (VII) chain polypeptide and the second transgene encodes a Keratin type I cytoskeletal 17 polypeptide.
244. The method of claim 240, wherein the first transgene encodes a Lysyl hydroxylase 3 polypeptide and the second transgene encodes a Keratin type I cytoskeletal 17 polypeptide.
245. The method of any of claims 202 to 239, wherein the vector comprises at least a first transgene, a second transgene, and a third transgene.

246. The method of claim 245, wherein the first transgene encodes a Collagen alpha-1 (VII) chain polypeptide, the second transgene encodes a Lysyl hydroxylase 3 polypeptide, and the third transgene encodes a Keratin type I cytoskeletal 17 polypeptide.
247. The method of any of claims 202 to 246, wherein the pharmaceutical composition is administered topically or transdermally to the subject.
248. The method of any of claims 202 to 246, wherein the pharmaceutical composition is administered subcutaneously or intradermally to the subject.
249. The method of any of claims 202 to 248, wherein the pharmaceutical composition is administered one, two three, four, five or more times per day.
250. The method of any of claims 202 to 249, wherein the pharmaceutical composition is administered to one or more affected and/or unaffected areas of the subject.
251. The method of any of claims 202 to 250, wherein the disease or disorder of the skin is one or more of epidermolysis bullosa, skin cancer, psoriasis, lichen planus, lupus, rosacea, eczema, cutaneous candidiasis, cellulitis, impetigo, decubitus ulcers, erysipelas, ichthyosis vulgaris, dermatomyositis, acrodermatitis, stasis dermatitis, nethertons syndrome, epidermolysis bullosa simplex (LAMB3 gene), autosomal recessive congenital ichthyosis, xeroderma pigmentosa, and pemphigoid.