WHAT IS CLAIMED IS:

1 A Composition which targets 10 to 25-nt contiguous target sequence in a TATA-box region or an enhancer region of a duplicate gene for use in treating a disease caused by overexpression of a duplicated gene in a eukaryotic cell, comprising:

a guide RNA including a guide domain and a backbone or nucleic acid encoding the guide RNA, and

a Cas9 protein originated from *Streptococcus pyogenes* or *Campylobacter jejuni*, or a nucleic acid encoding the Cas9 protein,

wherein the guide domain and the backbone is linked sequentially from 5' to 3' direction,

wherein when the Cas9 protein is originated from *Campylobacter jejuni*, the backbone has a sequence compising 90% or more sequence identity with 5'-GUUUUAGUCCCUGAAAAGGGACUAAAAUAAAGAGUUUGCGGGACUCUGCGGG GUUACAAUCCCCUAAAACCGCUUUU-3' (SEQ ID NO: 328),

wherein when the Cas9 protein is originated from Streptococcus pyogenes, a sequence of the backbone has 90% or more sequence identity with 5'-GUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGC-3' (SEQ ID NO: 329),

wherein the duplicate gene is one or more genes selected from the group consisting of a PMP22 gene, a PLP1 gene, a SOX3 gene, a RAI1 gene, a TBX1 gene, an ELN gene, a JAGGED1 gene, a NSD1 gene, a MMP23 gene, a LMB1 gene, a SNCA gene and an APP gene, .

2. A composition which targets 10 to 25-nt contiguous target sequence in a TATA-box region or an enhancer region of the duplicate gene for use in treating a disease caused by overexpression of a duplicated gene, comprising:

a double-stranded guide RNA including a crRNA, and a tracrRNA,

wherein the crRNA comprises a guide domain and a first complementary domain,

wherein the guide domain and the first complementary domain are linked sequentially from 5' to 3'-end,

wherein the tracrRNA comprises a second complementary domain and a proximal domain, and a tail domain,

wherein the second complementary domain, the proximal domain, and the tail domain are linked sequentially from 5' to 3'-end; and

a Cas9 protein originated from *Streptococcus pyogenes* or *Campylobacter jejuni*, or a nucleic acid encoding the Cas9 protein,

wherein the guide domain and a backbone is linked sequentially from 5' to 3' direction,

wherein the guide domain is capable of targeting 10 to 25-nt contiguous target sequence in the TATA-box region or the enhancer region of the duplicate gene,

wherein when the Cas9 protein is originated from *Campylobacter jejuni*, a first complementary domain is 90% or more identical with 5'-GUUUUAGUCCCUUUUUAAAUUUCUU-3' (SEQ ID NO: 297), the second complementary domain has a sequence compising 90% or more sequence identity with 5'-AAGAAAUUUAAAAAGGGACUAAAAU-3' (SEQ ID NO: 300), the proximal domain is 90% or more identical with 5'-AAAGAGUUUGC-3' (SEQ ID NO: 303), and the tail domain has a sequence compising 90% or more sequence identity with 5'-GGGACUCUGCGGGGUUACAAUCCCCUAAAACCGCUUUU-3' (SEQ ID NO: 305),

wherein when the Cas9 protein is originated from *Streptococcus pyogenes*, the first complementary domain has a sequence compising 90% or more sequence identity with 5'-GUUUUAGAGCUA-3' (SEQ ID NO: 296), the second complementary domain has a sequence compising 90% or more sequency identity with 5'-UAGCAAGUUAAAAU-3' (SEQ ID NO: 299), the proximal domain has a sequence compising 90% or more sequence identity with 5'-

AAGGCUAGUCCG-3’ (SEQ ID NO: 302), and the tail domain has a sequence compising 90% or more sequency identity with 5’-UUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC-3’ (SEQ ID NO: 304),

wherein the duplicate gene is one or more genes selected from the group consisting of a PMP22 gene, a PLP1 gene, a SOX3 gene, an RAI1 gene, a TBX1 gene, an ELN gene, a JAGGED1 gene, an NSD1 gene, an MMP23 gene, an LMB1 gene, a SNCA gene, an APP gene.

3. The composition for use according to claim 1 or 2,

wherein the TATA-box region comprises one or more sequences selected from the group consisting of the 5'-TATA-3' sequence, 5’-TATAWAW-3’ (W=A or T) sequence, 5’-TATAWAWR-3’ (W=A or T, R=A or G), 5'-CATAAAA-3' sequence, 5'-CATAAAA-3' sequence, 5'-TATAA-3' sequence, 5'-TATAAAA-3' sequence, 5'-CATAAATA-3' sequence, 5'-TATATAA-3' sequence, 5'-TATATATATATATAA-3' sequence, 5'-TATATTATA-3' sequence, 5'-TATAAA-3' sequence, 5'-TATAAAATA-3' sequence, 5'-TATATA-3' sequence, 5'-GATTAAAAA-3' sequence, 5'-TATAAAAA-3' sequence, 5'-TTATAA-3' sequence, 5'-TTTTAAAA-3' sequence, 5'-TCTTTAAAA-3' sequence, 5'-GACATTTAA-3' sequence, 5'-TGATATCAA-3' sequence, 5'-TATAAATA-3' sequence, 5'-TATAAGA-3' sequence, 5'-AATAAA-3' sequence, 5'-TTTATA-3' sequence, 5'-CATAAAAA-3' sequence, 5'-TATACA-3' sequence, 5'-TTTAAGA-3' sequence, 5'-GATAAAG-3' sequence, 5'-TATAACA-3' sequence, 5'-TCTTATCTT-3' sequence, 5'-TTGTACTTT-3' sequence, 5'-CATATAA-3' sequence, 5'-TATAAAT-3' sequence, 5'-TATATATAAAAAAAA-3' sequence and 5'-CATAAATAAAAAAAATTA-3' sequence.

4. The composition for use according to claim 1 or 2, wherein the duplicate gene is the PLP1 gene.

5. The composition for use according to claim 1 or 2,

wherein the Cas9 protein is originated from *Streptococcus pyogenes* and the target sequence is selected from SEQ ID NOs: 56 to 93.

6. The composition for use according to claim 1 or 2,

wherein the Cas9 protein is originated from *Campylobacter jejuni* and the target sequence is selected from SEQ ID NOs: 94 to 115.

7. The composition for use according to claim 1 or 2,

wherein the guide RNA and the Cas9 protein in a form of a ribonucleoprotein.

8. The composition for use according to claim 1 or 2,

wherein the composition comprises the nucleic acid encoding the nucleic acid encoding the Cas9 protein.

9. The composition for use according to claim 8,

wherein the composition is in a form of one or more vectors.

10. A guide RNA which target a TATA-box region or an enhancer region of a duplicate gene, for use in treating a disease caused by overexpression of the duplicate gene, comprising:

a guide domain comprising a sequence selected from SEQ ID NOs: 56 to 93; and

a backbone comprising a sequence having 90% or more sequence identity with a sequence 5'-
GUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC
UUGAAAAAGUGGCACCGAGUCGGUGC-3' (SEQ ID NO: 329),

wherein the guide domain and the backbone are linked sequentially from 5' to 3'-end,

wherein the duplicate gene is a human PLP1 gene.

11. A double-stranded guide RNA which targets a TATA-box region or an enhancer region of duplicate gene for use in treating a disease caused by overexpression of a duplicated

gene, comprising:

a crRNA comprising a guide domain represented by a sequence selected from SEQ ID NOs: 56 to 93, and a first complementary domain having 90% or more sequence identity with 5’-GUUUUAGAGCUA-3’ (SEQ ID NO: 296),

wherein the guide domain and the first complementary domain are linked sequentially from 5’ to 3’-end; and

a tracrRNA comprising a second complementary domain having 90% or more sequence identity with 5’-UAGCAAGUUAAAAU-3’ (SEQ ID NO: 299), and a proximal domain having 90% or more sequence identity with 5’-AAGGCUAGUCCG-3’ (SEQ ID NO: 302), and a tail domain having 90% or more sequence identity with 5’-UUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC-3’ (SEQ ID NO: 304),

wherein the second complementary domain, the proximal domain, and the tail domain are linked sequentially from 5’ to 3’-end,

wherein the duplicate gene is a human PLP1 gene.

12. A guide RNA which targets an enhancer region of a duplicate gene for use in treating a disease caused by overexpression of a duplicated gene, comprising:

a guide domain represented by a sequence selected from SEQ ID NOs: 94 to 115; and

a backbone having 90% or more sequence identity with a sequence 5’-GUUUUAGUCCCUGAAAAGGGACUAAAAUAAAGAGUUUGCGGGACUCUGCGGGGUUACAAUCCCCUAAAACCGCUUUU-3’ (SEQ ID NO: 328),

wherein the guide domain and the backbone is linked sequentially from 5’ to 3’-end of the guide RNA,

wherein the duplicate gene is a human PLP1 gene.

13. A double-stranded guide RNA which targets an enhancer region of duplicate gene for use in treating a disease caused by overexpression of a duplicated gene, comprising:

a crRNA comprising a guide domain represented by a sequence selected from SEQ ID NOs: 94 to 115, and a first complementary domain 90% or more identical with 5’-GUUUUAGUCCCUUUUUAAAUUUCUU-3’ (SEQ ID NO: 297),

wherein the guide domain and the first complementary domain are linked sequentially from 5’ to 3’-end; and

a tracrRNA comprising a second complementary domain having 90% or more sequence identity with 5’-AAGAAAUUUAAAAAGGGACUAAAAU-3’ (SEQ ID NO: 300), and a proximal domain having 90% or more sequence identity with 5’-AAAGAGUUUGC-3’ (SEQ ID NO: 303), and a tail domain having 90% or more sequence identity with 5’-GGGACUCUGCGGGGUUACAAUCCCCUAAAACCGCUUUU-3’ (SEQ ID NO: 305),

wherein the second complementary domain, the proximal domain, and the tail domain are linked sequentially from 5’ to 3’-end,

wherein the duplicate gene is a human PLP1 gene.

14. A nucleic acid encoding the guide RNA according to any one of claims 10 to 13.