CLAIMS:

1. A genetically altered plant, plant part thereof or plant cell, wherein the plant, part thereof or plant cell comprises at least one mutation in at least one nucleic acid sequence encoding a nucleotide-binding domain and leucine-rich repeat-containing (NLR) protein, wherein the NLR protein comprises a HD1 domain, and wherein the at least one mutation is a mutation of one or more amino acids in an N-terminal portion of the HD1 domain.

2. A genetically altered plant, plant part thereof or plant cell, wherein the plant, part thereof or plant cell expresses a nucleic acid construct comprising a nucleic acid sequence encoding a mutated NLR protein, wherein the NLR protein comprises a HD1 domain, and wherein the NLR protein comprises a mutation of one or more amino acids in an N-terminal portion of the HD1 domain.

3. The genetically altered plant, plant part thereof or plant cell of any claim 1 or 2, wherein the N-terminal portion of the HD1 domain comprises a sequence as defined in SEQ ID NO: 2, 5, 8, 14, 17, 23, 26 or 29 or a variant or fragment thereof, wherein the variant has at least 60% overall sequence identity to SEQ ID NO: 2, 5, 8, 14, 17, 23, 26 or 29.

4. The genetically altered plant, plant part thereof or plant cell of any one of claims 1 to 3, wherein the at least one mutation is in a RNBS-C motif of the HD1 domain.

5. The genetically altered plant, plant part thereof or plant cell of claim 4, wherein the RNBS-C motif comprises a sequence as defined in SEQ ID NO: 3, 6, 9, 15, 18, 24, 27 or 30 or variant or fragment thereof, wherein the variant has at least 60% overall sequence identity to the sequence defined in SEQ ID NO: 3, 6, 9, 15, 18, 24, 27 or 30.

6. The genetically altered plant, plant part thereof or plant cell of any one of claims 1 to 3, wherein the mutation is a substitution and the substitution is at one or more positions in the NLR amino acid sequence, where the position is selected from 315, 316 or 317 (or a homologous position in a homologous sequence),of any of SEQ ID NO: 32, 34, 36, 41, 43, 47, 49 or 51 or a homolog or functional variant thereof or,

wherein the mutation is a substitution of all or a proportion of the N-terminal portion of the HD1 domain for a corresponding portion in a second NLR protein, wherein the second NLR protein is not inhibited by the pathogen effector, or
wherein the mutation is a substitution of all or a significant proportion of the RNBS-C motif for a corresponding RNBS-C motif in a second NLR protein, wherein the second NLR protein is not inhibited by the pathogen effector.

7. The genetically altered plant, plant part thereof or plant cell of claim 2, wherein the nucleic acid construct expresses a nucleic acid sequence that encodes a NLR protein, wherein the NLR protein is selected from SEQ ID NO: 37, 38, 39, 44, 45, 52, 53, 54, 55, 56, 57, 58 or 59.

8. The genetically altered plant, plant part thereof or plant cell of any one of claims 1 to 7, wherein the plant is a crop plant preferably a solanaceous plant.

9. The genetically altered plant part of any one preceding claim, wherein the plant part is a seed or grain.

10. A method of providing or improving pathogen resistance in a plant, the method comprising introducing at least one mutation into at least one nucleic acid sequence encoding a nucleotide-binding domain and leucine-rich repeat-containing (NLR) protein, wherein the NLR protein comprises a HD1 domain; and wherein the at least one mutation is a mutation of one or more amino acids in an N-terminal portion of the HD1 domain.

11. A method of providing or improving pathogen resistance in a plant, the method comprising introducing and expressing a nucleic acid construct comprising a nucleic acid sequence encoding a mutated NLR protein, wherein the NLR protein comprises a HD1 domain, and wherein the NLR protein comprises a mutation of one or more amino acids in an N-terminal portion of the HD1 domain.

12. The method of claim 10 or 11, wherein the N-terminal portion of the HD1 domain comprises no more than the N-terminal 42 amino acids of the HD1 domain, , wherein the variant has at least 60% overall sequence identity to SEQ ID NO: 2, 5, 8, 14, 17, 23, 26 or 29.

13. The method of any claim 10 or 12, wherein the mutation is a substitution of all or a significant proportion of the RNBS-C motif for a corresponding RNBS-C motif in a second NLR protein, wherein the second NLR protein is not inhibited by the pathogen effector.

14. The method of claim 11, wherein the nucleic acid construct expresses a nucleic acid sequence that encodes a NLR protein, wherein the NLR protein is selected from SEQ ID NO: 37, 38, 39, 44, 45, 52, 53, 54, 55, 56, 57, 58 or 59 or a functional variant or homologue therein .

15. An isolated nucleotide-binding domain and leucine-rich repeat-containing (NLR) protein, wherein the NLR protein comprises a sequence selected from SEQ ID NO: 37, 38, 39, 44, 45, 52, 53, 54, 55, 56, 57, 58, 59, or a functional variant or homologue thereof.