

CLAIMS

1. A method for assessing whether a patient suffers from a myeloid malignancy or is prone to suffering from a myeloid malignancy, said method comprising
 - determining the presence of one or more mutant alleles of the calreticulin gene in a sample from said patient; and
 - assessing that said patient suffers from a myeloid malignancy or is prone to suffering from a myeloid malignancy when said one or more mutant alleles of the calreticulin gene is present.
2. The method according to claim 1, wherein said one or more mutant alleles comprises a nucleic acid encoding a mutant calreticulin protein.
3. The method according to claim 2, wherein said mutant calreticulin protein is selected from the group consisting of
 - (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2 or 3;
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 4;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 4;
 - (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).

4. The method according to claim 2 or 3, wherein said mutant calreticulin protein is selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2, 3, 5, 6, 7, 9, 10, 11, 13, 14, 15, 17, 18, 19, 21, 22, 23, 25, 26, 27, 29, 30, 31, 33, 34, 35, 37, 38, 39, 41, 42, 43, 45, 46, 47, 49, 50, 51, 53, 54, 55, 57, 58, 59, 61, 62, 63, 65, 66, 67, 69, 70, 71, 73, 74, 75, 77, 78, 79, 81, 82, 83, 85, 86, 87, 89, 90, 91, 93, 94, 95, 97, 98, 99, 101, 102, 103, 105, 106, 107, 109, 110, 111, 113, 114, 115, 117, 118, 119, 121, 122, 123, 125, 126, 127, 129, 130, 131, 133, 134, 135, 137, 138, 139, 141, 142, or 143;
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
 - (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
5. The method according to any one of claims 2 to 4, wherein said mutant calreticulin protein is selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 291, 292, 293, 295, 296, 297, 299, 300, 301, 303, 304, 305, 307, 308, 309, 311, 312, 313, 315, 316, 317, 319, 320, 321, 323, 324, 325, 327, 328, 329, 331, 332, 333, 335, 336, 337, 339, 340, 341, 343, 344, 345,

- 347, 348, 349, 351, 352, 353, 355, 356, 357, 359, 360, 361, 363, 364, 365, 367, 368, 369, 371, 372, 373, 375, 376, 377, 379, 380, 381, 383, 384, 385, 387, 388, 389, 391, 392, 393, 395, 396, 397, 399, 400, 401, 403, 404, 405, 407, 408, 409, 411, 412, 413, 415, 416, 417, 419, 420, 421, 423, 424, 425, 427, 428, 429, 431, 432, or 433;
- (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
- (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
- (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
- (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
- (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
- (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
6. The method according to any one of claims 2 to 5, wherein said mutant calreticulin protein is selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 145, 146, 147, 149, 150, 151, 153, 154, 155, 157, 158, 159, 161, 162, 163, 165, 166, 167, 169, 170, 171, 173, 174, 175, 177, 178, 179, 181, 182, 183, 185, 186, 187, 189, 190, 191, 193, 194, 195, 197, 198, 199, 201, 202, 203, 205, 206, 207, 209, 210, 211, 213, 214, 215, 217, 218, 219, 221, 222, 223, 225, 226, 227, 229, 230, 231, 233, 234, 235, 237, 238, 239, 241, 242, 243, 245, 246, 247, 249, 250, 251, 253, 254, 255, 257, 258, 259, 261, 262, 263, 265, 266, 267, 269, 270, 271, 273, 274, 275, 277, 278, 279, 281, 282, 283, 285,

286, or 287;

- (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
 - (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
7. The method according to any one of claims 1 to 6, wherein said one or more mutant allele of the calreticulin gene is in a region encompassing exon 9 of the calreticulin gene.
8. The method according to any one of claims 1 to 7, wherein said mutant allele has a frameshift mutation compared to the wild-type calreticulin gene.
9. The method according to claim 8, wherein said frameshift mutation is in exon 9 of the calreticulin gene.
10. The method according to claim 8 or 9, wherein said frameshift mutation is the deletion of one nucleotide or the addition of two nucleotides.
11. The method according to any one of claims 8 or 9, wherein $(1 + (3 \times n_0))$ nucleotides

are deleted from the calreticulin gene.

12. The method according to any one of claims 8, 9 and 11, wherein 1, 4, 19, 22, 31, 34, 46, 52 nucleotides are deleted.
13. The method according to any one of claims 8, 9, 11 and 12, wherein 1 nucleotide is deleted and wherein 6 nucleotides are inserted;
wherein 2 nucleotides are deleted and wherein 4 nucleotides are inserted;
wherein 3 nucleotides are deleted and wherein 5 nucleotides are inserted;
wherein 12 nucleotides are deleted and wherein 5 nucleotides are inserted;
wherein 18 nucleotides are deleted and wherein 11 nucleotides are inserted;
wherein 18 nucleotides are deleted and wherein 14 nucleotides are inserted;
wherein 20 nucleotides are deleted and wherein 1 nucleotide is inserted;
wherein 28 nucleotides are deleted and wherein 6 nucleotides are inserted;
wherein 35 nucleotides are deleted and wherein 1 nucleotide is inserted; or
wherein 36 nucleotides are deleted and wherein 2 nucleotides are inserted.
14. The method according to claim 8 or 9, wherein $(2 + (3 \times n_0))$ nucleotides are inserted into the calreticulin gene.
15. The method according to claim 14, wherein 5 nucleotides are inserted.
16. The method according to any one of claims 1 to 15, wherein said calreticulin gene comprises a sequence selected from the group consisting of:
 - a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 290;
 - (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 289;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid comprising a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid comprising a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a)

to (d).

17. The method according to any one of claims 10 to 16, wherein said nucleotide(s) are deleted from and/or inserted into exon 9 of the calreticulin gene.
18. The method according to any one of claims 9 to 17, wherein said exon 9 of the calreticulin gene comprises a sequence selected from the group consisting of:
 - a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO:436;
 - (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO:435;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid comprising a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid comprising a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
19. The method according to any one of claims 1 to 18, wherein said mutant allele comprises a nucleic acid selected from the group consisting of
 - (a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, 144, 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, 288; 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
 - (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, 69, 73, 77, 81, 85, 89, 93, 97, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, 141, 145, 149, 153, 157, 161, 165, 169, 173, 177, 181, 185, 189, 193, 197, 201, 205, 209, 213, 217, 221, 225, 229, 233, 237, 241, 245, 249, 253, 257, 261, 265, 269, 273, 277, 281, 285,

291, 295, 299, 303, 307, 311, 315, 319, 323, 327, 331, 335, 339, 343, 347, 351, 355, 359, 363, 367, 371, 375, 379, 383, 387, 391, 395, 399, 403, 407, 411, 415, 419, 423, 427, or 431;

- (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid comprising a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid comprising a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
20. The method according to any one of claims 1 to 19, wherein said mutant allele is DNA, preferably genomic DNA.
21. The method according to claim 20, wherein the presence of said DNA is determined by sequencing.
22. A method for assessing whether a patient suffers from a myeloid malignancy or is prone to suffering from a myeloid malignancy, said method comprising
- determining the presence of a gene product of one or more mutant alleles of the calreticulin gene in a sample from said patient; and
 - assessing that said patient suffers from a myeloid malignancy or is prone to suffering from a myeloid malignancy when said gene product is present.
23. The method according to claim 22, wherein said one or more mutant alleles comprises a nucleic acid encoding a mutant calreticulin protein.
24. The method according to claim 23, wherein said mutant calreticulin protein is selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2 or 3;
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 4;

- (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 4;
 - (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
25. The method according to claim 23 or 24, wherein said mutant calreticulin protein is selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2, 3, 5, 6, 7, 9, 10, 11, 13, 14, 15, 17, 18, 19, 21, 22, 23, 25, 26, 27, 29, 30, 31, 33, 34, 35, 37, 38, 39, 41, 42, 43, 45, 46, 47, 49, 50, 51, 53, 54, 55, 57, 58, 59, 61, 62, 63, 65, 66, 67, 69, 70, 71, 73, 74, 75, 77, 78, 79, 81, 82, 83, 85, 86, 87, 89, 90, 91, 93, 94, 95, 97, 98, 99, 101, 102, 103, 105, 106, 107, 109, 110, 111, 113, 114, 115, 117, 118, 119, 121, 122, 123, 125, 126, 127, 129, 130, 131, 133, 134, 135, 137, 138, 139, 141, 142, or 143;
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
 - (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);

- (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
26. The method according to any one of claims 23 to 25, wherein said calreticulin protein is selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 291, 292, 293, 295, 296, 297, 299, 300, 301, 303, 304, 305, 307, 308, 309, 311, 312, 313, 315, 316, 317, 319, 320, 321, 323, 324, 325, 327, 328, 329, 331, 332, 333, 335, 336, 337, 339, 340, 341, 343, 344, 345, 347, 348, 349, 351, 352, 353, 355, 356, 357, 359, 360, 361, 363, 364, 365, 367, 368, 369, 371, 372, 373, 375, 376, 377, 379, 380, 381, 383, 384, 385, 387, 388, 389, 391, 392, 393, 395, 396, 397, 399, 400, 401, 403, 404, 405, 407, 408, 409, 411, 412, 413, 415, 416, 417, 419, 420, 421, 423, 424, 425, 427, 428, 429, 431, 432, or 433;
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
 - (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).

27. The method according to any one of claims 23 to 26, wherein said mutant calreticulin protein is selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 145, 146, 147, 149, 150, 151, 153, 154, 155, 157, 158, 159, 161, 162, 163, 165, 166, 167, 169, 170, 171, 173, 174, 175, 177, 178, 179, 181, 182, 183, 185, 186, 187, 189, 190, 191, 193, 194, 195, 197, 198, 199, 201, 202, 203, 205, 206, 207, 209, 210, 211, 213, 214, 215, 217, 218, 219, 221, 222, 223, 225, 226, 227, 229, 230, 231, 233, 234, 235, 237, 238, 239, 241, 242, 243, 245, 246, 247, 249, 250, 251, 253, 254, 255, 257, 258, 259, 261, 262, 263, 265, 266, 267, 269, 270, 271, 273, 274, 275, 277, 278, 279, 281, 282, 283, 285, 286, or 287;
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
 - (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
28. The method according to any one of claims 22 to 27, wherein said allele comprises a nucleic acid selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as

depicted in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, 144, 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, 288; 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;

- (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, 69, 73, 77, 81, 85, 89, 93, 97, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, 141, 145, 149, 153, 157, 161, 165, 169, 173, 177, 181, 185, 189, 193, 197, 201, 205, 209, 213, 217, 221, 225, 229, 233, 237, 241, 245, 249, 253, 257, 261, 265, 269, 273, 277, 281, 285, 291, 295, 299, 303, 307, 311, 315, 319, 323, 327, 331, 335, 339, 343, 347, 351, 355, 359, 363, 367, 371, 375, 379, 383, 387, 391, 395, 399, 403, 407, 411, 415, 419, 423, 427, or 431;
- (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
- (d) a nucleic acid comprising a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
- (e) a nucleic acid comprising a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).

29. The method according to any one of claims 22 to 28, wherein said gene product comprises a nucleic acid selected from the group consisting of

- (a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO:4;
- (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 3;
- (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
- (d) a nucleic acid comprising a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
- (e) a nucleic acid comprising a nucleotide sequence which is degenerate as a result

of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).

30. The method according to any one of claims 22 to 29, wherein said gene product comprises a nucleic acid selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
 - (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 3, 7, 11, 15, 19, 23, 27, 31, 35, 39, 43, 47, 51, 55, 59, 63, 67, 71, 75, 79, 83, 87, 91, 95, 99, 103, 107, 111, 115, 119, 123, 127, 131, 135, 139, or 143;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid comprising a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid comprising a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
31. The method according to any one of claims 22 to 30, wherein said gene product comprises a nucleic acid selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
 - (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 293, 297, 301, 305, 309, 313, 317, 321, 325, 329, 333, 337, 341, 345, 349, 353, 357, 361, 365, 369, 373, 377, 381, 385, 389, 393, 397, 401, 405, 409, 413, 417, 421, 425, 429, or 433;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid comprising a nucleotide sequence with at least 70 % identity to

the nucleotide sequence of the nucleic acids of any one of (a) to (c); and

- (e) a nucleic acid comprising a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).

32. The method according to any one of claims 22 to 31, wherein said gene product comprises a nucleic acid selected from the group consisting of

- (a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
- (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 147, 151, 155, 159, 163, 167, 171, 175, 179, 183, 187, 191, 195, 199, 203, 207, 211, 215, 219, 223, 227, 231, 235, 239, 243, 247, 251, 255, 259, 263, 267, 271, 275, 279, 283, or 287;
- (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
- (d) a nucleic acid comprising a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
- (e) a nucleic acid comprising a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).

33. The method according to any one of claims 22 to 28, wherein said gene product comprises a polypeptide selected from the group consisting of

- a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2 or 3;
- (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 4;
- (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
- (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 4;
- (e) a protein comprising an amino acid sequence encoded by a nucleic acid

hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);

- (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
- (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).

34. The method according to any one of claims 22 to 28 and 33, wherein said gene product comprises a polypeptide selected from the group consisting of

- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2, 3, 5, 6, 7, 9, 10, 11, 13, 14, 15, 17, 18, 19, 21, 22, 23, 25, 26, 27, 29, 30, 31, 33, 34, 35, 37, 38, 39, 41, 42, 43, 45, 46, 47, 49, 50, 51, 53, 54, 55, 57, 58, 59, 61, 62, 63, 65, 66, 67, 69, 70, 71, 73, 74, 75, 77, 78, 79, 81, 82, 83, 85, 86, 87, 89, 90, 91, 93, 94, 95, 97, 98, 99, 101, 102, 103, 105, 106, 107, 109, 110, 111, 113, 114, 115, 117, 118, 119, 121, 122, 123, 125, 126, 127, 129, 130, 131, 133, 134, 135, 137, 138, 139, 141, 142, or 143;
- (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
- (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
- (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
- (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
- (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
- (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).

35. The method according to any one of claims 22 to 28, 33 and 34, wherein said gene product comprises a polypeptide selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 291, 292, 293, 295, 296, 297, 299, 300, 301, 303, 304, 305, 307, 308, 309, 311, 312, 313, 315, 316, 317, 319, 320, 321, 323, 324, 325, 327, 328, 329, 331, 332, 333, 335, 336, 337, 339, 340, 341, 343, 344, 345, 347, 348, 349, 351, 352, 353, 355, 356, 357, 359, 360, 361, 363, 364, 365, 367, 368, 369, 371, 372, 373, 375, 376, 377, 379, 380, 381, 383, 384, 385, 387, 388, 389, 391, 392, 393, 395, 396, 397, 399, 400, 401, 403, 404, 405, 407, 408, 409, 411, 412, 413, 415, 416, 417, 419, 420, 421, 423, 424, 425, 427, 428, 429, 431, 432, or 433;
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
 - (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).

36. The method according to any one of claims 22 to 28, and 33 to 35, wherein said gene product comprises a polypeptide selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 145, 146, 147, 149, 150, 151, 153, 154, 155, 157, 158, 159, 161, 162, 163, 165, 166, 167, 169, 170, 171, 173, 174, 175, 177, 178, 179, 181, 182, 183, 185, 186, 187, 189, 190, 191, 193, 194, 195, 197, 198, 199, 201, 202, 203, 205, 206, 207, 209, 210, 211, 213, 214, 215, 217, 218, 219, 221, 222, 223, 225, 226, 227, 229, 230, 231, 233, 234, 235, 237, 238, 239, 241, 242, 243, 245, 246, 247, 249, 250, 251, 253, 254, 255, 257, 258, 259, 261, 262, 263, 265, 266, 267, 269, 270, 271, 273, 274, 275, 277, 278, 279, 281, 282, 283, 285, 286, or 287;
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
 - (e) a protein comprising an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein comprising an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).

37. The method according to any one of claims 22 to 36, wherein said gene product is mRNA.
38. The method according to claim 37, wherein the presence or amount of said mRNA is determined by RealTime PCR, ReverseTranscriptase PCR, Whole Transcriptome Shotgun Sequencing (RNAseq), in situ hybridization or micro-arrays.
39. The method according to claim 38, wherein the determination by RealTime PCR or ReverseTranscriptase PCR further comprises the steps
 - (i) contacting the nucleic acid in the sample with one or two oligonucleotides;
 - (ii) generating an amplification product containing the target sequence.
40. The method according to any one of claims 22 to 28, and 33 to 36, wherein said gene product is protein.
41. The method according to claim 40, wherein the presence or amount of said protein is determined by immunohistochemistry (IHC), by immunoassay, gel- or blot-based methods, IHC, mass spectrometry, flow cytometry, or FACS.
42. The method according to any one of claims 1 to 41, wherein said patient is a human patient.
43. The method according to any one of claims 1 to 42, wherein said sample is a bone marrow sample.
44. The method according to any one of claims 1 to 42, wherein said sample is a blood sample.
45. The method according to claim 43 or 44, wherein said bone marrow sample is obtained by biopsy.
46. The method according to any one of claims 1 to 45, further comprising administering an inhibitor of a mutant calreticulin to the patient.

47. A nucleic acid selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO:4;
 - (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 2;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
48. The nucleic acid according to claim 47, wherein said nucleic acid is selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
 - (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 2, 6, 10, 14, 18, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 66, 70, 74, 78, 82, 86, 90, 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, 134, 138, or 142;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
49. The nucleic acid according to claim 47 or 48, wherein said nucleic acid is selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as

depicted in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;

- (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 292, 296, 300, 304, 308, 312, 316, 320, 324, 328, 332, 336, 340, 344, 348, 352, 356, 360, 364, 368, 372, 376, 380, 384, 388, 392, 396, 400, 404, 408, 412, 416, 420, 424, 428, or 432;
- (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
- (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
- (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).

50. The nucleic acid according to any one of claims 47 to 49, wherein said nucleic acid is selected from the group consisting of

- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
- (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 146, 150, 154, 158, 162, 166, 170, 174, 178, 182, 186, 190, 194, 198, 202, 206, 210, 214, 218, 222, 226, 230, 234, 238, 242, 246, 250, 254, 258, 262, 266, 270, 274, 278, 282, or 286;
- (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
- (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
- (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).

51. The nucleic acid according to any one of claims 47 to 50, wherein said nucleic acid is cDNA.
52. A nucleic acid selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO:4;
 - (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 3;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
53. The nucleic acid according to claim 52, wherein said nucleic acid is selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
 - (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 3, 7, 11, 15, 19, 23, 27, 31, 35, 39, 43, 47, 51, 55, 59, 63, 67, 71, 75, 79, 83, 87, 91, 95, 99, 103, 107, 111, 115, 119, 123, 127, 131, 135, 139, or 143;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
54. The nucleic acid according to claim 52 or 53, wherein said nucleic acid is selected

from the group consisting of

- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
- (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 293, 297, 301, 305, 309, 313, 317, 321, 325, 329, 333, 337, 341, 345, 349, 353, 357, 361, 365, 369, 373, 377, 381, 385, 389, 393, 397, 401, 405, 409, 413, 417, 421, 425, 429, or 433;
- (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
- (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
- (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).

55. The nucleic acid according to claim 52 or 54, wherein said nucleic acid is selected from the group consisting of

- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
- (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 147, 151, 155, 159, 163, 167, 171, 175, 179, 183, 187, 191, 195, 199, 203, 207, 211, 215, 219, 223, 227, 231, 235, 239, 243, 247, 251, 255, 259, 263, 267, 271, 275, 279, 283, or 287;
- (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
- (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
- (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a)

to (d).

56. The nucleic acid according to any one of claims 52 to 55, wherein said nucleic acid is mRNA.
57. A nucleic acid selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 4;
 - (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 1;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
58. The nucleic acid according to claim 57, wherein said nucleic acid is selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
 - (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, 69, 73, 77, 81, 85, 89, 93, 97, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, or 141;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).

59. The nucleic acid according to claim 57 or 58, wherein said nucleic acid is selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
 - (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 291, 295, 299, 303, 307, 311, 315, 319, 323, 327, 331, 335, 339, 343, 347, 351, 355, 359, 363, 367, 371, 375, 379, 383, 387, 391, 395, 399, 403, 407, 411, 415, 419, 423, 427, or 431;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
60. The nucleic acid according to any one of claims 57 to 59, wherein said nucleic acid is selected from the group consisting of
- (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
 - (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 145, 149, 153, 157, 161, 165, 169, 173, 177, 181, 185, 189, 193, 197, 201, 205, 209, 213, 217, 221, 225, 229, 233, 237, 241, 245, 249, 253, 257, 261, 265, 269, 273, 277, 281, or 285;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid consisting of a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and

- (e) a nucleic acid consisting of a nucleotide sequence which is degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).
61. The nucleic acid according to any one of claims 57 to 60, wherein said nucleic acid is genomic DNA.
62. A protein selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2 or 3;
 - (b) a protein consisting of the amino acid sequence as shown in SEQ ID NO: 4;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
 - (d) a protein encoded by a nucleic acid molecule encoding a protein consisting of the amino acid sequence as shown in SEQ ID NO: 4;
 - (e) a protein consisting of an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70% identity to the protein of any one of (a) to (e); and
 - (g) a protein consisting of an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
63. The protein according to claim 62, wherein said protein is selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2, 3, 5, 6, 7, 9, 10, 11, 13, 14, 15, 17, 18, 19, 21, 22, 23, 25, 26, 27, 29, 30, 31, 33, 34, 35, 37, 38, 39, 41, 42, 43, 45, 46, 47, 49, 50, 51, 53, 54, 55, 57, 58, 59, 61, 62, 63, 65, 66, 67, 69, 70, 71, 73, 74, 75, 77, 78, 79, 81, 82, 83, 85, 86, 87, 89, 90, 91, 93, 94, 95, 97, 98, 99, 101, 102, 103, 105, 106, 107, 109, 110, 111, 113, 114, 115, 117, 118, 119, 121, 122, 123, 125, 126, 127, 129, 130, 131, 133, 134, 135, 137, 138, 139, 141, 142, or 143;
 - (b) a protein consisting of the amino acid sequence as shown in SEQ ID NO: 4, 8,

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12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;

- (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;
- (d) a protein encoded by a nucleic acid molecule encoding a protein consisting of the amino acid sequence as shown in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, or 144;
- (e) a protein consisting of an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
- (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
- (g) a protein consisting of an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).

64. The protein according to claim 62 or 63, wherein said protein is selected from the group consisting of

- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 291, 292, 293, 295, 296, 297, 299, 300, 301, 303, 304, 305, 307, 308, 309, 311, 312, 313, 315, 316, 317, 319, 320, 321, 323, 324, 325, 327, 328, 329, 331, 332, 333, 335, 336, 337, 339, 340, 341, 343, 344, 345, 347, 348, 349, 351, 352, 353, 355, 356, 357, 359, 360, 361, 363, 364, 365, 367, 368, 369, 371, 372, 373, 375, 376, 377, 379, 380, 381, 383, 384, 385, 387, 388, 389, 391, 392, 393, 395, 396, 397, 399, 400, 401, 403, 404, 405, 407, 408, 409, 411, 412, 413, 415, 416, 417, 419, 420, 421, 423, 424, 425, 427, 428, 429, 431, 432, or 433;
- (b) a protein consisting of the amino acid sequence as shown in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
- (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;

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- (d) a protein encoded by a nucleic acid molecule encoding a protein consisting of the amino acid sequence as shown in SEQ ID NO: 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434;
 - (e) a protein consisting of an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein consisting of an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein consisting of an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
65. The protein according to any one of claims 62 to 64, wherein said protein is selected from the group consisting of
- (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 145, 146, 147, 149, 150, 151, 153, 154, 155, 157, 158, 159, 161, 162, 163, 165, 166, 167, 169, 170, 171, 173, 174, 175, 177, 178, 179, 181, 182, 183, 185, 186, 187, 189, 190, 191, 193, 194, 195, 197, 198, 199, 201, 202, 203, 205, 206, 207, 209, 210, 211, 213, 214, 215, 217, 218, 219, 221, 222, 223, 225, 226, 227, 229, 230, 231, 233, 234, 235, 237, 238, 239, 241, 242, 243, 245, 246, 247, 249, 250, 251, 253, 254, 255, 257, 258, 259, 261, 262, 263, 265, 266, 267, 269, 270, 271, 273, 274, 275, 277, 278, 279, 281, 282, 283, 285, 286, or 287;
 - (b) a protein consisting of the amino acid sequence as shown in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
 - (c) a protein as defined in (a) or (b) wherein one or more amino acids are deleted, inserted, added or substituted;

- (d) a protein encoded by a nucleic acid molecule encoding a protein comprising the amino acid sequence as shown in SEQ ID NO: 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, or 288;
 - (e) a protein consisting of an amino acid sequence encoded by a nucleic acid hybridizing under stringent conditions to the complementary strand of nucleic acid molecules as defined in (a) or (c);
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein consisting of an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
 - (f) a protein having at least 70 % identity to the protein of any one of (a) to (e); and
 - (g) a protein consisting of an amino acid sequence encoded by a nucleic acid being degenerate as a result of the genetic code to the nucleotide sequence of a nucleic acid as defined in (a), (d) or (e).
66. A vaccine comprising the protein according to claim 62 or 63.
67. An antibody specifically binding to the protein of any one of claims 62 to 65.
68. An siRNA specifically targeting the nucleic acid of any one of claims 52 to 56.
69. The siRNA according to claim 68, wherein said siRNA consists of a nucleic acid molecule comprising at least ten contiguous bases.
70. The siRNA according to claim 68 or 69, wherein up to 10 % of the contiguous bases are non-complementary.
71. The siRNA according to any one of claims 68 to 70, wherein said siRNA further comprises at least one base at the 5' end and/or at least one base at the 3' end.
72. An inhibitor of a mutant calreticulin for use in the treatment of a myeloid malignancy.

73. Method for treating a myeloid malignancy patient comprising administering an effective amount of an inhibitor of a mutant calreticulin to the patient.
74. The inhibitor according to claim 72, or the method according to claim 46 or 73, wherein said mutant calreticulin is a mutant calreticulin protein as defined in any one of claims 62 to 65.
75. The inhibitor according to claim 72 or 74, or the method according to any one claims 56, 73 or 74, wherein said inhibitor is an antibody.
76. The inhibitor according to claim 72 or 74, or the method according to any one claims 56, 73 or 74, wherein said inhibitor is selected from the group consisting of extracellular binding partners, small binding molecules, aptamers, and intramers.
77. The inhibitor according to claim 72, or the method according to claim 46 or 73, wherein said mutant calreticulin is a nucleic acid as defined in any one of claims 52 to 56.
78. The inhibitor according to claim 72 or 77, or the method according to any one of claims 46, 73 and 77, wherein said inhibitor is selected from the group consisting of siRNA, miRNA, dsRNA, shRNA, stRNA, and antisense molecules.
79. The inhibitor according to any one of claims 72, and 74 to 78; or the method according to any one of claims 1 to 46 and 73 to 78, wherein said myeloid malignancy is a myeloproliferative neoplasm.
80. The inhibitor according to claim 79; or the method according to claim 79, wherein said myeloproliferative neoplasm is primary myelofibrosis (PMF).
81. The inhibitor according to claim 79; or the method according to claim 79, wherein said myeloproliferative neoplasm is essential thrombocythemia (ET).
82. The inhibitor according to any one of claims 72, and 74 to 78; or the method according

to any one of claims 1 to 46 and 73 to 78, wherein said myeloid malignancy is a myelodysplastic syndrome.

83. The inhibitor according to claim 82; or the method according to claim 82, wherein said myelodysplastic syndrome is refractory anemia with ringed sideroblasts and thrombocythemia (RARS-T).
84. The inhibitor according to any one of claims 72, and 74 to 83; or the method according to any one of claims 73 to 83, wherein the patient to be treated is assessed to suffer from a myeloid malignancy or to be prone to suffering from a myeloid malignancy according to any one of claims 1 to 46.
85. The protein according to claim 62 or 63, the antibody according to 67, the siRNA according to any one of claims 68 to 71 or an inhibitor of a mutant calreticulin as defined in any one of claims 72 to 78 for use as a medicament.
86. A vector comprising the nucleic acid according to any one of claims 47 to 51 and 57 to 61.
87. A host cell comprising the nucleic acid according to any one of claims 47 to 51 and 57 to 61 or the vector according to claim 86.
88. A process for the production of the polypeptide according to claim 62 to 65, said process comprising culturing host cells according to claim 87 under conditions allowing the expression of the polypeptide and recovering the produced polypeptide from the culture.

CLAIMS

1. A method for assessing whether a patient suffers from a myeloid malignancy or is prone to suffering from a myeloid malignancy, said method comprising
 - determining the presence of one or more mutant alleles of the calreticulin gene in a sample from said patient; and
 - assessing that said patient suffers from a myeloid malignancy or is prone to suffering from a myeloid malignancy when said one or more mutant alleles of the calreticulin gene is present,wherein said one or more mutant alleles comprises a nucleic acid encoding a mutant calreticulin protein, wherein said mutant calreticulin protein is selected from the group consisting of
 - (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2 or 3; and
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 4.
2. The method according to claim 1, wherein said mutant allele is genomic DNA.
3. The method according to claim 2, wherein the presence of said DNA is determined by sequencing.
4. The method according to any one of claims 1 to 3, wherein said calreticulin gene comprises a sequence selected from the group consisting of:
 - (a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 290;
 - (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 289;
 - (c) a nucleic acid hybridizing under stringent conditions to the complementary strand of the nucleic acid as defined in (a) or (b);
 - (d) a nucleic acid comprising a nucleotide sequence with at least 70 % identity to the nucleotide sequence of the nucleic acids of any one of (a) to (c); and
 - (e) a nucleic acid comprising a nucleotide sequence which is degenerate as a result of

the genetic code to the nucleotide sequence of a nucleic acid of any one of (a) to (d).

5. A method for assessing whether a patient suffers from a myeloid malignancy or is prone to suffering from a myeloid malignancy, said method comprising
 - determining the presence of a gene product of one or more mutant alleles of the calreticulin gene in a sample from said patient; and
 - assessing that said patient suffers from a myeloid malignancy or is prone to suffering from a myeloid malignancy when said gene product is present,
 wherein said one or more mutant alleles comprises a nucleic acid encoding a mutant calreticulin protein, wherein said mutant calreticulin protein is selected from the group consisting of
 - (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 1, 2 or 3; and
 - (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 4.

6. The method according to any one of claims 1 to 5, wherein said mutant calreticulin protein is selected from the group consisting of
 - (a) a protein encoded by a nucleic acid molecule having the nucleic acid sequence as depicted in SEQ ID NO: 5, 6, 7, 9, 10, 11, 13, 14, 15, 17, 18, 19, 21, 22, 23, 25, 26, 27, 29, 30, 31, 33, 34, 35, 37, 38, 39, 41, 42, 43, 45, 46, 47, 49, 50, 51, 53, 54, 55, 57, 58, 59, 61, 62, 63, 65, 66, 67, 69, 70, 71, 73, 74, 75, 77, 78, 79, 81, 82, 83, 85, 86, 87, 89, 90, 91, 93, 94, 95, 97, 98, 99, 101, 102, 103, 105, 106, 107, 109, 110, 111, 113, 114, 115, 117, 118, 119, 121, 122, 123, 125, 126, 127, 129, 130, 131, 133, 134, 135, 137, 138, 139, 141, 142, 143, 145, 146, 147, 149, 150, 151, 153, 154, 155, 157, 158, 159, 161, 162, 163, 165, 166, 167, 169, 170, 171, 173, 174, 175, 177, 178, 179, 181, 182, 183, 185, 186, 187, 189, 190, 191, 193, 194, 195, 197, 198, 199, 201, 202, 203, 205, 206, 207, 209, 210, 211, 213, 214, 215, 217, 218, 219, 221, 222, 223, 225, 226, 227, 229, 230, 231, 233, 234, 235, 237, 238, 239, 241, 242, 243, 245, 246, 247, 249, 250, 251, 253, 254, 255, 257, 258, 259, 261, 262, 263, 265, 266, 267, 269, 270, 271, 273, 274, 275, 277, 278, 279, 281, 282, 283, 285, 286, 287, 291, 292, 293, 295, 296, 297, 299, 300, 301, 303,

304, 305, 307, 308, 309, 311, 312, 313, 315, 316, 317, 319, 320, 321, 323, 324, 325, 327, 328, 329, 331, 332, 333, 335, 336, 337, 339, 340, 341, 343, 344, 345, 347, 348, 349, 351, 352, 353, 355, 356, 357, 359, 360, 361, 363, 364, 365, 367, 368, 369, 371, 372, 373, 375, 376, 377, 379, 380, 381, 383, 384, 385, 387, 388, 389, 391, 392, 393, 395, 396, 397, 399, 400, 401, 403, 404, 405, 407, 408, 409, 411, 412, 413, 415, 416, 417, 419, 420, 421, 423, 424, 425, 427, 428, 429, 431, 432, or 433; and

- (b) a protein comprising the amino acid sequence as shown in SEQ ID NO: 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, 144, 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, 288, 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434.

7. The method according to any one of claims 1 to 6, wherein said mutant allele comprises a nucleic acid selected from the group consisting of

- (a) a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, 144, 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, 288, 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434; and
- (b) a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 1, 5, 9, 13, 17, 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61, 65, 69, 73, 77, 81, 85, 89, 93, 97, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, 141, 145, 149, 153, 157, 161, 165, 169, 173, 177, 181, 185, 189, 193, 197, 201, 205, 209, 213, 217, 221, 225, 229, 233, 237, 241, 245, 249, 253, 257, 261, 265, 269, 273, 277, 281, 285, 291, 295, 299, 303, 307, 311, 315, 319, 323, 327, 331, 335, 339, 343, 347, 351,

355, 359, 363, 367, 371, 375, 379, 383, 387, 391, 395, 399, 403, 407, 411, 415, 419, 423, 427, or 431.

8. The method according to any one of claims 5 to 7, wherein said gene product is mRNA or protein.
9. The method according to claim 8, wherein the presence of said mRNA is determined by RealTime PCR, ReverseTranscriptase PCR, Whole Transcriptome Shotgun Sequencing (RNAseq), in situ hybridization or micro-arrays.
10. The method according to any one of claims 1 to 9, wherein said sample is a bone marrow sample or a blood sample.
11. A nucleic acid selected from the group consisting of
 - (a) a nucleic acid encoding a polypeptide consisting of an amino acid sequence as depicted in SEQ ID NO: 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, 80, 84, 88, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 132, 136, 140, 144, 148, 152, 156, 160, 164, 168, 172, 176, 180, 184, 188, 192, 196, 200, 204, 208, 212, 216, 220, 224, 228, 232, 236, 240, 244, 248, 252, 256, 260, 264, 268, 272, 276, 280, 284, 288, 294, 298, 302, 306, 310, 314, 318, 322, 326, 330, 334, 338, 342, 346, 350, 354, 358, 362, 366, 370, 374, 378, 382, 386, 390, 394, 398, 402, 406, 410, 414, 418, 422, 426, 430, or 434; and
 - (b) a nucleic acid consisting of a nucleotide sequence as depicted in SEQ ID NO: 1, 2, 3, 5, 6, 7, 9, 10, 11, 13, 14, 15, 17, 18, 19, 21, 22, 23, 25, 26, 27, 29, 30, 31, 33, 34, 35, 37, 38, 39, 41, 42, 43, 45, 46, 47, 49, 50, 51, 53, 54, 55, 57, 58, 59, 61, 62, 63, 65, 66, 67, 69, 70, 71, 73, 74, 75, 77, 78, 79, 81, 82, 83, 85, 86, 87, 89, 90, 91, 93, 94, 95, 97, 98, 99, 101, 102, 103, 105, 106, 107, 109, 110, 111, 113, 114, 115, 117, 118, 119, 121, 122, 123, 125, 126, 127, 129, 130, 131, 133, 134, 135, 137, 138, 139, 141, 142, 143, 145, 146, 147, 149, 150, 151, 153, 154, 155, 157, 158, 159, 161, 162, 163, 165, 166, 167, 169, 170, 171, 173, 174, 175, 177, 178, 179, 181, 182, 183, 185, 186, 187, 189, 190, 191, 193, 194, 195, 197, 198, 199, 201, 202, 203, 205, 206, 207, 209, 210, 211, 213, 214, 215, 217, 218, 219, 221, 222,

223, 225, 226, 227, 229, 230, 231, 233, 234, 235, 237, 238, 239, 241, 242, 243, 245, 246, 247, 249, 250, 251, 253, 254, 255, 257, 258, 259, 261, 262, 263, 265, 266, 267, 269, 270, 271, 273, 274, 275, 277, 278, 279, 281, 282, 283, 285, 286, 287, 291, 292, 293, 295, 296, 297, 299, 300, 301, 303, 304, 305, 307, 308, 309, 311, 312, 313, 315, 316, 317, 319, 320, 321, 323, 324, 325, 327, 328, 329, 331, 332, 333, 335, 336, 337, 339, 340, 341, 343, 344, 345, 347, 348, 349, 351, 352, 353, 355, 356, 357, 359, 360, 361, 363, 364, 365, 367, 368, 369, 371, 372, 373, 375, 376, 377, 379, 380, 381, 383, 384, 385, 387, 388, 389, 391, 392, 393, 395, 396, 397, 399, 400, 401, 403, 404, 405, 407, 408, 409, 411, 412, 413, 415, 416, 417, 419, 420, 421, 423, 424, 425, 427, 428, 429, 431, 432, or 433.