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(54) Titre : TOLERANCE A LA SECHERESSE ET A LA CHALEUR CHEZ LES PLANTES
(54) Title: DROUGHT AND HEAT TOLERANCE IN PLANTS

(57) Abrégé/Abstract:

Methods and materials for modulating heat and/or drought tolerance in plants are disclosed. For example, nucleic acids encoding heat and/or drought-tolerance polypeptides are disclosed as well as methods for using such nucleic acids to transform plant cells. Also disclosed are plants having increased heat and/or drought tolerance and plant products produced from plants having increased heat and/or drought tolerance.

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(54) Title: DROUGHT AND HEAT TOLERANCE IN PLANTS

(57) Abstract: Methods and materials for modulating heat and/or drought tolerance in plants are disclosed. For example, nucleic acids encoding heat and/or drought-tolerance polypeptides are disclosed as well as methods for using such nucleic acids to transform plant cells. Also disclosed are plants having increased heat and/or drought tolerance and plant products produced from plants having increased heat and/or drought tolerance.



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DROUGHT AND HEAT TOLERANCE IN PLANTS

SEQUENCE LISTING

This description contains a sequence listing in electronic form in ASCII text format. A copy of
5 the sequence is available from the Canadian Intellectual Property Office.

TECHNICAL FIELD

This document relates to methods and materials involved in modulating drought and/or
heat tolerance in plants. For example, this document provides plants having increased drought
10 and/or heat tolerance as well as materials and methods for making plants having increased
drought and/or heat tolerance.

BACKGROUND

Due to their sessile nature, plants are constantly under the threat of temperature stress
15 when they are subjected to a wide range of temperature variation in different habitats and
climates during growing seasons and even diurnally. Most economically valuable plants,
including those used in agriculture, horticulture, forestry, biomass for bioconversion, and other
industries (e.g., the paper industry or pharmaceutical/chemical industries where plants are used
as production factories for proteins or other compounds) are exposed to higher than optimal
20 temperatures, or heat stress, during some stages of their life cycle from seed germination to seed
maturation (Maestri et al. *Plant Mol. Biol.* 48:667-681 (2002)). Heat stress is one of the most
common stresses in crop production. Under heat stress, plants can succumb to a variety of
physiological and developmental damages, including dehydration due to increased transpiration,
impairment of photosynthetic carbon assimilation, inhibition of translocation of assimilates,
25 increased respiration, reduced organ size due to a decrease in the duration of developmental
phases, disruption of seed development, and a reduction in fertility (Berry and Bjorkman, *Ann.*
Rev. Plant Physiol. 31:491-543 (1980); Cheikh and Jones, *Plant Physiol.* 106:45-51 (1994)).
Thus, exposure to heat stress often results in reduced yield and overall decreased crop quality
(Maestri et al. *Plant Mol. Biol.* 48:667-681 (2002)).

In the field, heat stress is often associated with other stresses, such as drought and high light, which presents even greater challenge to plants. Plants exposed to low water or drought conditions typically have low yields of plant material, seeds, fruit and other edible products. Some areas of the world consistently have very low rainfall and therefore have problems growing sufficient food crops for their population.

Thus, there is a need for methods of increasing drought and/or heat tolerance in plants.

SUMMARY

This document provides methods and materials related to plants having increased heat and/or drought tolerance. For example, this document provides transgenic plants and plant cells having increased heat and/or drought tolerance, nucleic acids used to generate transgenic plants and plant cells having increased heat and/or drought tolerance, and methods for making plants and plant cells having increased heat and/or drought tolerance. Such plants having increased heat and/or drought tolerance may be useful to produce biomass which may be converted to a liquid fuel or other chemicals and/or to produce crops with increased yield and/or quality.

Methods of producing a plant are provided herein. In one aspect, a method comprises growing a plant cell comprising an exogenous nucleic acid. The exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide. The Hidden Markov Model (HMM) bit score of the amino acid sequence of the polypeptide is greater than about 20, using an HMM generated from the amino acid sequences depicted in one of Figures 1-16. The plant has a difference in drought tolerance or heat tolerance as compared to a control plant that does not comprise the exogenous nucleic acid.

In another aspect, a method comprises growing a plant cell comprising an exogenous nucleic acid. The exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence set forth in SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 60, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 73, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120,

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188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 209, 212, 214, 216, 218, 220,
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5 252, 253, 254, 256, 258, 260, 262, 264, 266, 268, 269, 271, 273, 275, 277, 279, 280,
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 1286, 1287, 1288, 1290, 1292, 1293, 1294, 1296, 1298, 1300, 1302, 1304, 1306,
 1311, 1313, 1315, 1317, 1319, 1321, 1323, 1324, 1325, 1326, 1327, 1329, 1331,
 15 1333, 1334, 1336, 1338, 1340, 1342, 1343, 1345, 1347, 1349, 1350, 1351, 1353,
 1354, 1356, 1358, 1360, or 1361. A plant produced from the plant cell has a
 difference in drought tolerance or heat tolerance compared to a control plant that does
 not comprise the exogenous nucleic acid.

In another aspect, the polypeptide can comprise a sulfotransferase 1 domain
 20 having 70 percent or greater sequence identity to the sulfotransferase 1 domain of
 SEQ ID NO:590 or orthologs thereof such as those identified in the sequence listing;
 an AN1-like zinc finger domain having 70 percent or greater sequence identity to the
 AN1-like zinc finger domain of SEQ ID NO:742 or SEQ ID NO:749 or orthologs
 thereof such as those identified in the sequence listing and an A20-like zinc finger
 25 domain having 70 percent or greater sequence identity to the A20-like zinc finger
 domain of SEQ ID NO:742 or SEQ ID NO:749 or orthologs thereof such as those
 identified in the sequence listing; a short chain dehydrogenase domain having 70
 percent or greater sequence identity to the short chain dehydrogenase domain of SEQ
 ID NO:1012 or orthologs thereof such as those identified in the sequence listing; a
 30 trehalose-phosphatase domain having 70 percent or greater sequence identity to the
 trehalose-phosphatase domain of or SEQ ID NO:1129 or orthologs thereof such as
 those identified in the sequence listing; a synaptobrevin-related polypeptide having 70
 percent or greater sequence identity to the synaptobrevin-related polypeptide of SEQ
 ID NO:160 or orthologs thereof such as those identified in the sequence listing; an

HSF-type DNA-binding domain having 70 percent or greater sequence identity to the HSF-type DNA-binding domain of SEQ ID NO:311 or SEQ ID NO:364 or orthologs thereof such as those identified in the sequence listing; a DnaJ domain having 70 percent or greater sequence identity to the DnaJ domain of SEQ ID NO:60 or

5 orthologs thereof such as those identified in the sequence listing; or a KH_2 domain having 70 percent or greater sequence identity to the KH_2 domain of SEQ ID NO:1311 or orthologs thereof such as those identified in the sequence listing.

In another aspect, a method comprises growing a plant cell comprising an exogenous nucleic acid. The exogenous nucleic acid comprises a regulatory region

10 operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence, or a fragment thereof, set forth in SEQ ID NO: 1, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 59, 61, 72, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 128, 129, 131, 133, 135, 137, 140, 141,

15 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 210, 211, 213, 215, 217, 219, 221, 223, 226, 227, 230, 232, 236, 238, 241, 243, 245, 247, 249, 251, 255, 257, 259, 261, 263, 265, 267, 270, 272, 274, 276, 278, 281, 283, 285, 287, 306, 308, 310, 313, 318, 324, 328, 331, 333, 342, 345, 347, 352, 354, 357, 359, 361,

20 363, 365, 367, 372, 374, 376, 378, 380, 382, 384, 386, 388, 391, 393, 395, 397, 399, 403, 406, 409, 411, 415, 417, 425, 427, 429, 437, 439, 441, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 471, 473, 475, 477, 479, 482, 484, 486, 488, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 517, 521, 523, 525, 527, 529, 532, 534, 537, 539, 542, 544, 546, 549, 551, 554, 556, 560, 563, 565, 567, 571, 573,

25 575, 577, 579, 581, 583, 585, 587, 589, 601, 606, 609, 611, 613, 622, 624, 626, 628, 630, 633, 637, 639, 641, 643, 645, 649, 652, 657, 659, 670, 672, 677, 679, 681, 683, 686, 689, 693, 695, 697, 699, 701, 703, 704, 710, 713, 716, 718, 720, 722, 724, 728, 730, 732, 736, 739, 750, 758, 762, 764, 766, 770, 772, 776, 778, 780, 782, 784, 786, 788, 790, 792, 794, 800, 802, 804, 806, 814, 818, 820, 822, 824, 826, 828, 830, 831,

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 1322, 1328, 1330, 1332, 1335, 1337, 1339, 1341, 1344, 1346, 1348, 1352, 1355,
 10 1357, 1359 or 1362, or a fragment thereof. A plant produced from the plant cell has a
 difference in drought tolerance or heat tolerance as compared to a control plant that
 does not comprise the exogenous nucleic acid.

Methods of modulating drought in a plant are provided herein. In one aspect,
 a method comprises introducing into a plant cell an exogenous nucleic acid, that
 15 comprises a regulatory region operably linked to a nucleotide sequence encoding a
 polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is
 greater than about 20, using an HMM generated from the amino acid sequences
 depicted in one of Figures 1-16. A plant produced from the plant cell has a difference
 in drought tolerance as compared to a control plant that does not comprise the
 20 exogenous nucleic acid.

In another aspect, a method of modulating drought tolerance comprises
 introducing into a plant cell an exogenous nucleic acid that comprises a regulatory
 region operably linked to a nucleotide sequence encoding a polypeptide having 80
 percent or greater sequence identity to an amino acid sequence set forth in SEQ ID
 25 NO: 442, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 469, 470, 472,
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 20 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1140, 1142, 1144, 1146, 1148, 1150,
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 1168, 1170, 1172, 1174, 1175, 1177, 1179, 1181, 1182, 1184, 1186, 1294, 1311,
 1313, 1315, 1317, 1319, 1321, 1323, 1324, 1325, 1326, 1327, 1329, 1331, 1333,
 1334, 1336, 1338, 1340, 1342, 1343, 1345, 1347, 1349, 1350, 1351, 1353, 1354,
 25 1356, 1358, 1360, or 1361. A plant produced from the plant cell has a difference in
 drought tolerance as compared to a control plant that does not comprise the
 exogenous nucleic acid.

In another aspect, a method of modulating drought tolerance comprises
 introducing into a plant cell an exogenous nucleic acid, that comprises a regulatory
 30 region operably linked to a nucleotide sequence having 80 percent or greater sequence
 identity to a nucleotide sequence set forth in SEQ ID NO: 923, 994, 905, 921, 804,
 837, 828, 930, 996, 928, 868, 645, 641, 695, 505, 1067, 501, 466, 718, 860, 503, 624,
 628, 630, 639, 686, 806, 479, 764, 1060, 1052, 1120, 1105, 546, 780, 460, 814, 800,
 499, 643, 670, 679, 1253, 927, 716, 1081, 128, 585, 581, 864, 1049, 1107, 523, 1076,

652, 1095, 1099, 1101, 497, 830, 507, 622, 140, 772, 532, 542, 549, 226, 1149, 210, 587, 583, 866, 527, 1097, 1103, 1141, 1019, 486, 1229, 1249, 739, 697, 701, 1011, 563, 1122, 1243, 1208, 1247, 1009, 1124, 699, 1206, 72, 565, 1245, 1021, 1008, 942, 948, 818, 794, 967, 986, 786, 936, 940, 984, 855, 946, 982, 1291, 919, 822, 824, 907, 5 750, 909, 934, 903, 826, 95, 965, 950, 611, 575, 1190, 484, 454, 1036, 722, 444, 456, 1192, 1034, 720, 831, 911, 838, 917, 468, 1257, 659, 1173, 1139, 1176, 938, 1063, 1032, 862, 758, 450, 509, 554, 1259, 458, 1217, 972, 477, 462, 954, 1163, 956, 525, 556, 1145, 1165, 1065, 677, 609, 762, 537, 1169, 884, 1198, 1085, 1109, 1211, 1029, 689, 1070, 1233, 770, 1047, 1194, 551, 446, 633, 1167, 1078, 1213, 730, 448, 766, 10 895, 511, 925, 495, 1239, 1235, 1057, 1074, 1202, 544, 1083, 1024, 1220, 1224, 1200, 613, 683, 672, 976, 517, 1227, 471, 1255, 1237, 473, 728, 521, 464, 1241, 1155, 681, 736, 539, 1017, 513, 835, 657, 534, 1044, 649, 1026, 560, 1171, 579, 1038, 529, 1091, 1147, 637, 452, 1072, 1180, 833, 1040, 1089, 482, 493, 732, 1115, 626, 899, 606, 1178, 1087, 1042, 1111, 577, 1251, 475, 858, 724, 1183, 693, 1143, 15 1185, 1054, 1187, 571, 713, 847, 1196, 573, 1204, 601, 441, 488, 567, 589, 703, 704, 710, 1260, 1126, 1127, 1128, 1295, 802, 1303, 1297, 1301, 1299, 820, 1312, 1314, 1316, 1318, 1320, 1322, 1328, 1330, 1332, 1335, 1337, 1339, 1341, 1344, 1346, 1348, 1352, 1355, 1357, 1359 or 1362, or a fragment thereof. A plant produced from the plant cell has a difference in drought tolerance as compared to a control plant that 20 does not comprise the exogenous nucleic acid.

Methods of modulating heat in a plant are provided herein. In one aspect, a method comprises introducing into a plant cell an exogenous nucleic acid, that comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is 25 greater than about 20, using an HMM generated from the amino acid sequences depicted in one of Figures 10-14. A plant produced from the plant cell has a difference in heat tolerance as compared to a control plant that does not comprise the exogenous nucleic acid.

In another aspect, a method of modulating heat tolerance comprises 30 introducing into a plant cell an exogenous nucleic acid that comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence set forth in SEQ ID NO: 60, 62, 64, 65, 66, 67, 68, 69, 70, 71, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 130, 132,

134, 136, 138, 142, 144, 146, 148, 150, 152, 154, 156, 158, 915, 364, 366, 368, 369, 370, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 390, 392, 394, 396, 398, 400, 401, 402, 404, 405, 407, 408, 410, 412, 413, 414, 416, 418, 419, 420, 421, 422, 423, 424, 426, 428, 430, 431, 432, 433, 434, 435, 436, 438, 440, 753, 754, 755, 756, 760, 768, 769, 774, 775, 777, 779, 783, 785, 789, 791, 793, 945, 1293, 311, 312, 314, 315, 316, 317, 319, 320, 321, 322, 323, 325, 326, 327, 329, 330, 332, 334, 335, 336, 337, 338, 339, 340, 341, 343, 344, 346, 348, 349, 350, 351, 353, 355, 356, 358, 360, 362, 876, 878, 880, 882, 886, 887, 888, 889, 890, 891, 893, 894, 897, 898, 901, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 212, 214, 216, 218, 220, 222, 224, 225, 228, 229, 231, 233, 234, 235, 237, 239, 240, 242, 244, 246, 248, 250, 252, 253, 254, 256, 258, 260, 262, 264, 266, 268, 269, 271, 273, 275, 277, 279, 280, 282, 284, 286, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 307, 309, 998, 1001, 1003, 1005, 1007, 1188, 1262, 1264, 1265, 1267, 1269, 1271, 1273, 1274, 1276, 1277, 1279, 1281, 1283, 1285, 1286, 1287, 1288, 1290, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 902, 904, 906, 908, 910, 913, 914, or 920. A plant produced from the plant cell has a difference in heat tolerance as compared to a control plant that does not comprise the exogenous nucleic acid.

20 In another aspect, a method of modulating heat tolerance comprises introducing into a plant cell an exogenous nucleic acid, that comprises a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence set forth in SEQ ID NO: 877, 1263, 790, 1261, 875, 792, 201, 354, 85, 77, 75, 415, 46, 207, 333, 203, 382, 83, 411, 81, 425, 406, 189, 93, 223, 44, 345, 79, 199, 417, 42, 219, 352, 185, 193, 89, 205, 386, 365, 91, 211, 195, 217, 429, 213, 187, 221, 359, 40, 197, 357, 331, 215, 183, 191, 367, 318, 87, 378, 48, 157, 155, 306, 361, 439, 52, 50, 437, 308, 54, 153, 1002, 782, 1266, 1268, 1275, 881, 784, 1278, 1280, 1004, 778, 879, 1282, 1006, 1289, 1284, 1270, 788, 883, 1272, 776, 135, 259, 109, 245, 121, 28, 115, 261, 151, 145, 328, 313, 24, 20, 391, 99, 409, 272, 1, 342, 347, 374, 131, 372, 111, 103, 107, 388, 125, 117, 18, 380, 123, 129, 26, 399, 143, 283, 30, 167, 403, 287, 137, 281, 169, 161, 14, 165, 181, 12, 38, 163, 173, 324, 177, 34, 97, 175, 171, 101, 285, 36, 276, 274, 232, 56, 270, 376, 278, 58, 59, 16, 230, 141, 32, 267, 227, 159, 241, 133, 249, 397, 247, 263, 149, 393, 395, 257, 243, 251, 113, 265, 119, 384, 427, 147, 255, 61, 22, 238, 236, 105, 310, or 363, or a fragment

thereof. A plant produced from the plant cell has a difference in heat tolerance as compared to a control plant that does not comprise the exogenous nucleic acid.

Plant cells comprising an exogenous nucleic acid are provided herein. In one aspect, the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is greater than about 20, using an HMM based on the amino acid sequences depicted in one of Figures 1-16. A plant produced from the cells has a difference in drought tolerance or heat tolerance as compared to a control plant that does not comprise the exogenous nucleic acid. In another aspect, the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 60, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 73, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 127, 130, 132, 134, 136, 138, 139, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 179, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 209, 212, 214, 216, 218, 220, 222, 224, 225, 228, 229, 231, 233, 234, 235, 237, 239, 240, 242, 244, 246, 248, 250, 252, 253, 254, 256, 258, 260, 262, 264, 266, 268, 269, 271, 273, 275, 277, 279, 280, 282, 284, 286, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 307, 309, 311, 312, 314, 315, 316, 317, 319, 320, 321, 322, 323, 325, 326, 327, 329, 330, 332, 334, 335, 336, 337, 338, 339, 340, 341, 343, 344, 346, 348, 349, 350, 351, 353, 355, 356, 358, 360, 362, 364, 366, 368, 369, 370, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 390, 392, 394, 396, 398, 400, 401, 402, 404, 405, 407, 408, 410, 412, 413, 414, 416, 418, 419, 420, 421, 422, 423, 424, 426, 428, 430, 431, 432, 433, 434, 435, 436, 438, 440, 442, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 470, 472, 474, 476, 478, 480, 481, 483, 485, 487, 489, 490, 491, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 515, 516, 518, 519, 520, 522, 524, 526, 528, 530, 531, 533, 535, 536, 538, 540, 541, 543, 545, 547, 548, 550, 552, 553, 555, 557, 558, 559, 561, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 602, 603, 604, 605, 607, 608, 610, 612, 614, 615, 616, 617, 618, 619, 620, 621, 623, 625, 627, 629, 631, 632, 634, 635, 636, 638, 640, 642, 644, 646, 647, 648, 650,

651, 653, 654, 655, 656, 658, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 671,
673, 674, 675, 676, 678, 680, 682, 684, 685, 687, 688, 690, 691, 692, 694, 696, 698,
700, 702, 705, 706, 707, 708, 709, 711, 712, 714, 715, 717, 719, 721, 723, 725, 726,
727, 729, 731, 733, 734, 735, 737, 738, 740, 741, 742, 743, 744, 745, 746, 747, 748,
5 749, 751, 752, 753, 754, 755, 756, 757, 759, 760, 761, 763, 765, 767, 768, 769, 771,
773, 774, 775, 777, 779, 781, 783, 785, 787, 789, 791, 793, 795, 796, 797, 798, 799,
801, 803, 805, 807, 808, 809, 810, 811, 812, 813, 815, 816, 817, 819, 821, 823, 825,
827, 829, 832, 834, 836, 839, 840, 841, 842, 843, 844, 845, 846, 848, 849, 850, 851,
852, 853, 854, 856, 857, 859, 861, 863, 865, 867, 869, 870, 871, 872, 873, 874, 876,
10 878, 880, 882, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 896, 897, 898, 900,
901, 902, 904, 906, 908, 910, 912, 913, 914, 915, 916, 918, 920, 922, 924, 926, 929,
931, 932, 933, 935, 937, 939, 941, 943, 944, 945, 947, 949, 951, 952, 953, 955, 957,
958, 959, 960, 961, 962, 963, 964, 966, 968, 969, 970, 971, 973, 974, 975, 977, 978,
979, 980, 981, 983, 985, 987, 988, 989, 990, 991, 992, 993, 995, 997, 998, 999, 1000,
15 1001, 1003, 1005, 1007, 1010, 1012, 1013, 1014, 1015, 1016, 1018, 1020, 1022,
1023, 1025, 1027, 1028, 1030, 1031, 1033, 1035, 1037, 1039, 1041, 1043, 1045,
1046, 1048, 1050, 1051, 1053, 1055, 1056, 1058, 1059, 1061, 1062, 1064, 1066,
1068, 1069, 1071, 1073, 1075, 1077, 1079, 1080, 1082, 1084, 1086, 1088, 1090,
1092, 1093, 1094, 1096, 1098, 1100, 1102, 1104, 1106, 1108, 1110, 1112, 1113,
20 1114, 1116, 1117, 1118, 1119, 1121, 1123, 1125, 1129, 1130, 1131, 1132, 1133,
1134, 1135, 1136, 1137, 1138, 1140, 1142, 1144, 1146, 1148, 1150, 1151, 1152,
1153, 1154, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1164, 1166, 1168, 1170,
1172, 1174, 1175, 1177, 1179, 1181, 1182, 1184, 1186, 1188, 1189, 1191, 1193,
1195, 1197, 1199, 1201, 1203, 1205, 1207, 1209, 1210, 1212, 1214, 1215, 1216,
25 1218, 1219, 1221, 1222, 1223, 1225, 1226, 1228, 1230, 1231, 1232, 1234, 1236,
1238, 1240, 1242, 1244, 1246, 1248, 1250, 1252, 1254, 1256, 1258, 1262, 1264,
1265, 1267, 1269, 1271, 1273, 1274, 1276, 1277, 1279, 1281, 1283, 1285, 1286,
1287, 1288, 1290, 1292, 1293, 1294, 1296, 1298, 1300, 1302, 1304, or 1311, 1313,
1315, 1317, 1319, 1321, 1323, 1324, 1325, 1326, 1327, 1329, 1331, 1333, 1334,
30 1336, 1338, 1340, 1342, 1343, 1345, 1347, 1349, 1350, 1351, 1353, 1354, 1356,
1358, 1360, or 1361. A plant produced from the plant cell has a difference in drought
tolerance or heat tolerance as compared to a control plant that does not comprise the
exogenous nucleic acid.

In another aspect, the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NO:

1, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,
5 56, 58, 59, 61, 72, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105,
107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 128, 129, 131, 133, 135, 137, 140,
141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173,
175, 177, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 210,
211, 213, 215, 217, 219, 221, 223, 226, 227, 230, 232, 236, 238, 241, 243, 245, 247,
10 249, 251, 255, 257, 259, 261, 263, 265, 267, 270, 272, 274, 276, 278, 281, 283, 285,
287, 306, 308, 310, 313, 318, 324, 328, 331, 333, 342, 345, 347, 352, 354, 357, 359,
361, 363, 365, 367, 372, 374, 376, 378, 380, 382, 384, 386, 388, 391, 393, 395, 397,
399, 403, 406, 409, 411, 415, 417, 425, 427, 429, 437, 439, 441, 444, 446, 448, 450,
452, 454, 456, 458, 460, 462, 464, 466, 468, 471, 473, 475, 477, 479, 482, 484, 486,
15 488, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 517, 521, 523, 525, 527,
529, 532, 534, 537, 539, 542, 544, 546, 549, 551, 554, 556, 560, 563, 565, 567, 571,
573, 575, 577, 579, 581, 583, 585, 587, 589, 601, 606, 609, 611, 613, 622, 624, 626,
628, 630, 633, 637, 639, 641, 643, 645, 649, 652, 657, 659, 670, 672, 677, 679, 681,
683, 686, 689, 693, 695, 697, 699, 701, 703, 704, 710, 713, 716, 718, 720, 722, 724,
20 728, 730, 732, 736, 739, 750, 758, 762, 764, 766, 770, 772, 776, 778, 780, 782, 784,
786, 788, 790, 792, 794, 800, 802, 804, 806, 814, 818, 820, 822, 824, 826, 828, 830,
831, 833, 835, 837, 838, 847, 855, 858, 860, 862, 864, 866, 868, 875, 877, 879, 881,
883, 884, 895, 899, 903, 905, 907, 909, 911, 917, 919, 921, 923, 925, 927, 928, 930,
934, 936, 938, 940, 942, 946, 948, 950, 954, 956, 965, 967, 972, 976, 982, 984, 986,
25 994, 996, 1002, 1004, 1006, 1008, 1009, 1011, 1017, 1019, 1021, 1024, 1026, 1029,
1032, 1034, 1036, 1038, 1040, 1042, 1044, 1047, 1049, 1052, 1054, 1057, 1060,
1063, 1065, 1067, 1070, 1072, 1074, 1076, 1078, 1081, 1083, 1085, 1087, 1089,
1091, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1115, 1120, 1122,
1124, 1126, 1127, 1128, 1139, 1141, 1143, 1145, 1147, 1149, 1155, 1163, 1165,
30 1167, 1169, 1171, 1173, 1176, 1178, 1180, 1183, 1185, 1187, 1190, 1192, 1194,
1196, 1198, 1200, 1202, 1204, 1206, 1208, 1211, 1213, 1217, 1220, 1224, 1227,
1229, 1233, 1235, 1237, 1239, 1241, 1243, 1245, 1247, 1249, 1251, 1253, 1255,
1257, 1259, 1260, 1261, 1263, 1266, 1268, 1270, 1272, 1275, 1278, 1280, 1282,
1284, 1289, 1291, 1295, 1297, 1299, 1301, 1303, 1312, 1314, 1316, 1318, 1320,

1322, 1328, 1330, 1332, 1335, 1337, 1339, 1341, 1344, 1346, 1348, 1352, 1355,
1357, 1359 or 1362, or a fragment thereof. A plant produced from the plant cell has a
difference in drought or heat tolerance as compared to a control plant that does not
comprise the exogenous nucleic acid. A transgenic plant comprising such a plant cell
5 is also provided.

Transgenic plants of any aspect provided herein can be a member of a species
selected from the group consisting of *Panicum virgatum* (switchgrass), *Sorghum*
bicolor (sorghum, sudangrass), *Miscanthus giganteus* (miscanthus), *Saccharum* sp.
(energycane), *Populus balsamifera* (poplar), *Zea mays* (corn), *Glycine max* (soybean),
10 *Brassica napus* (canola), *Triticum aestivum* (wheat), *Gossypium hirsutum* (cotton),
Oryza sativa (rice), *Helianthus annuus* (sunflower), *Medicago sativa* (alfalfa), *Beta*
vulgaris (sugarbeet), or *Pennisetum glaucum* (pearl millet).

Isolated nucleic acids are also provided. In one aspect, an isolated nucleic
acid comprises a nucleotide sequence having 80% or greater sequence identity to the
15 nucleotide sequence set forth in SEQ ID NO: 1, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30,
32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 59, 61, 72, 75, 77, 79, 81, 83, 85,
87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123,
125, 128, 129, 131, 133, 135, 137, 140, 141, 143, 145, 147, 149, 151, 153, 155, 157,
159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 181, 183, 185, 187, 189, 191, 193,
20 195, 197, 199, 201, 203, 205, 207, 210, 211, 213, 215, 217, 219, 221, 223, 226, 227,
230, 232, 236, 238, 241, 243, 245, 247, 249, 251, 255, 257, 259, 261, 263, 265, 267,
270, 272, 274, 276, 278, 281, 283, 285, 287, 306, 308, 310, 313, 318, 324, 328, 331,
333, 342, 345, 347, 352, 354, 357, 359, 361, 363, 365, 367, 372, 374, 376, 378, 380,
382, 384, 386, 388, 391, 393, 395, 397, 399, 403, 406, 409, 411, 415, 417, 425, 427,
25 429, 437, 439, 441, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468,
471, 473, 475, 477, 479, 482, 484, 486, 488, 493, 495, 497, 499, 501, 503, 505, 507,
509, 511, 513, 517, 521, 523, 525, 527, 529, 532, 534, 537, 539, 542, 544, 546, 549,
551, 554, 556, 560, 563, 565, 567, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589,
601, 606, 609, 611, 613, 622, 624, 626, 628, 630, 633, 637, 639, 641, 643, 645, 649,
30 652, 657, 659, 670, 672, 677, 679, 681, 683, 686, 689, 693, 695, 697, 699, 701, 703,
704, 710, 713, 716, 718, 720, 722, 724, 728, 730, 732, 736, 739, 750, 758, 762, 764,
766, 770, 772, 776, 778, 780, 782, 784, 786, 788, 790, 792, 794, 800, 802, 804, 806,
814, 818, 820, 822, 824, 826, 828, 830, 831, 833, 835, 837, 838, 847, 855, 858, 860,
862, 864, 866, 868, 875, 877, 879, 881, 883, 884, 895, 899, 903, 905, 907, 909, 911,

917, 919, 921, 923, 925, 927, 928, 930, 934, 936, 938, 940, 942, 946, 948, 950, 954,
 956, 965, 967, 972, 976, 982, 984, 986, 994, 996, 1002, 1004, 1006, 1008, 1009,
 1011, 1017, 1019, 1021, 1024, 1026, 1029, 1032, 1034, 1036, 1038, 1040, 1042,
 1044, 1047, 1049, 1052, 1054, 1057, 1060, 1063, 1065, 1067, 1070, 1072, 1074,
 5 1076, 1078, 1081, 1083, 1085, 1087, 1089, 1091, 1095, 1097, 1099, 1101, 1103,
 1105, 1107, 1109, 1111, 1115, 1120, 1122, 1124, 1126, 1127, 1128, 1139, 1141,
 1143, 1145, 1147, 1149, 1155, 1163, 1165, 1167, 1169, 1171, 1173, 1176, 1178,
 1180, 1183, 1185, 1187, 1190, 1192, 1194, 1196, 1198, 1200, 1202, 1204, 1206,
 1208, 1211, 1213, 1217, 1220, 1224, 1227, 1229, 1233, 1235, 1237, 1239, 1241,
 10 1243, 1245, 1247, 1249, 1251, 1253, 1255, 1257, 1259, 1260, 1261, 1263, 1266,
 1268, 1270, 1272, 1275, 1278, 1280, 1282, 1284, 1289, 1291, 1295, 1297, 1299,
 1301, 1303, 1312, 1314, 1316, 1318, 1320, 1322, 1328, 1330, 1332, 1335, 1337,
 1339, 1341, 1344, 1346, 1348, 1352, 1355, 1357, 1359 or 1362, or a fragment thereof.

In another aspect, an isolated nucleic acid comprises a nucleotide sequence
 15 encoding a polypeptide having 80% or greater sequence identity to the amino acid
 sequence set forth in SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 17, 19, 21, 23,
 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 60, 62, 63, 64, 65, 66,
 67, 68, 69, 70, 71, 73, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104,
 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 127, 130, 132, 134, 136, 138,
 20 139, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172,
 174, 176, 178, 179, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204,
 206, 208, 209, 212, 214, 216, 218, 220, 222, 224, 225, 228, 229, 231, 233, 234, 235,
 237, 239, 240, 242, 244, 246, 248, 250, 252, 253, 254, 256, 258, 260, 262, 264, 266,
 268, 269, 271, 273, 275, 277, 279, 280, 282, 284, 286, 288, 289, 290, 291, 292, 293,
 25 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 307, 309, 311, 312, 314,
 315, 316, 317, 319, 320, 321, 322, 323, 325, 326, 327, 329, 330, 332, 334, 335, 336,
 337, 338, 339, 340, 341, 343, 344, 346, 348, 349, 350, 351, 353, 355, 356, 358, 360,
 362, 364, 366, 368, 369, 370, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 390,
 392, 394, 396, 398, 400, 401, 402, 404, 405, 407, 408, 410, 412, 413, 414, 416, 418,
 30 419, 420, 421, 422, 423, 424, 426, 428, 430, 431, 432, 433, 434, 435, 436, 438, 440,
 442, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 470, 472,
 474, 476, 478, 480, 481, 483, 485, 487, 489, 490, 491, 492, 494, 496, 498, 500, 502,
 504, 506, 508, 510, 512, 514, 515, 516, 518, 519, 520, 522, 524, 526, 528, 530, 531,
 533, 535, 536, 538, 540, 541, 543, 545, 547, 548, 550, 552, 553, 555, 557, 558, 559,

561, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,
591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 602, 603, 604, 605, 607, 608, 610,
612, 614, 615, 616, 617, 618, 619, 620, 621, 623, 625, 627, 629, 631, 632, 634, 635,
636, 638, 640, 642, 644, 646, 647, 648, 650, 651, 653, 654, 655, 656, 658, 660, 661,
5 662, 663, 664, 665, 666, 667, 668, 669, 671, 673, 674, 675, 676, 678, 680, 682, 684,
685, 687, 688, 690, 691, 692, 694, 696, 698, 700, 702, 705, 706, 707, 708, 709, 711,
712, 714, 715, 717, 719, 721, 723, 725, 726, 727, 729, 731, 733, 734, 735, 737, 738,
740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 751, 752, 753, 754, 755, 756, 757,
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10 787, 789, 791, 793, 795, 796, 797, 798, 799, 801, 803, 805, 807, 808, 809, 810, 811,
812, 813, 815, 816, 817, 819, 821, 823, 825, 827, 829, 832, 834, 836, 839, 840, 841,
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865, 867, 869, 870, 871, 872, 873, 874, 876, 878, 880, 882, 885, 886, 887, 888, 889,
890, 891, 892, 893, 894, 896, 897, 898, 900, 901, 902, 904, 906, 908, 910, 912, 913,
15 914, 915, 916, 918, 920, 922, 924, 926, 929, 931, 932, 933, 935, 937, 939, 941, 943,
944, 945, 947, 949, 951, 952, 953, 955, 957, 958, 959, 960, 961, 962, 963, 964, 966,
968, 969, 970, 971, 973, 974, 975, 977, 978, 979, 980, 981, 983, 985, 987, 988, 989,
990, 991, 992, 993, 995, 997, 998, 999, 1000, 1001, 1003, 1005, 1007, 1010, 1012,
1013, 1014, 1015, 1016, 1018, 1020, 1022, 1023, 1025, 1027, 1028, 1030, 1031,
20 1033, 1035, 1037, 1039, 1041, 1043, 1045, 1046, 1048, 1050, 1051, 1053, 1055,
1056, 1058, 1059, 1061, 1062, 1064, 1066, 1068, 1069, 1071, 1073, 1075, 1077,
1079, 1080, 1082, 1084, 1086, 1088, 1090, 1092, 1093, 1094, 1096, 1098, 1100,
1102, 1104, 1106, 1108, 1110, 1112, 1113, 1114, 1116, 1117, 1118, 1119, 1121,
1123, 1125, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1140,
25 1142, 1144, 1146, 1148, 1150, 1151, 1152, 1153, 1154, 1156, 1157, 1158, 1159,
1160, 1161, 1162, 1164, 1166, 1168, 1170, 1172, 1174, 1175, 1177, 1179, 1181,
1182, 1184, 1186, 1188, 1189, 1191, 1193, 1195, 1197, 1199, 1201, 1203, 1205,
1207, 1209, 1210, 1212, 1214, 1215, 1216, 1218, 1219, 1221, 1222, 1223, 1225,
1226, 1228, 1230, 1231, 1232, 1234, 1236, 1238, 1240, 1242, 1244, 1246, 1248,
30 1250, 1252, 1254, 1256, 1258, 1262, 1264, 1265, 1267, 1269, 1271, 1273, 1274,
1276, 1277, 1279, 1281, 1283, 1285, 1286, 1287, 1288, 1290, 1292, 1293, 1294,
1296, 1298, 1300, 1302, 1304, or 1311, 1313, 1315, 1317, 1319, 1321, 1323, 1324,
1325, 1326, 1327, 1329, 1331, 1333, 1334, 1336, 1338, 1340, 1342, 1343, 1345,
1347, 1349, 1350, 1351, 1353, 1354, 1356, 1358, 1360, or 1361.

In another aspect, methods of identifying a genetic polymorphism associated with variation in drought tolerance or heat tolerance are provided. The methods include providing a population of plants, and determining whether one or more genetic polymorphisms in the population are genetically linked to the locus for a polypeptide selected from the group consisting of the polypeptides depicted in Figures 1-16 and functional homologs thereof. The correlation between variation in drought tolerance or heat tolerance in plants of the population and the presence of the one or more genetic polymorphisms in plants of the population is measured, thereby permitting identification of whether or not the one or more genetic polymorphisms are associated with such variation. The population can be a population of switchgrass, sorghum, sugar cane, or miscanthus plants.

In another aspect, methods of making a plant line are provided. The methods include determining whether one or more genetic polymorphisms in a population of plants is associated with the locus for a polypeptide selected from the group consisting of the polypeptides depicted in Figures 1-16 and functional homologs thereof; identifying one or more plants in said population in which the presence of at least one allele at the one or more genetic polymorphisms is associated with variation in drought tolerance or heat tolerance; crossing each of the one or more identified plants with itself or a different plant to produce seed; crossing at least one progeny plant grown from the seed with itself or a different plant; and repeating the crossing steps for an additional 0-5 generations to make the plant line, where at least one allele is present in the plant line. The population can be a population of switchgrass, sorghum, sugar cane, or miscanthus plants.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although methods and materials similar or equivalent to those described herein can be used to practice the invention, suitable methods and materials are described below. In case of conflict with any publication, patent application, patent, or other reference mentioned herein, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims. The word “comprising” in the claims may be replaced by “consisting essentially of” or by “consisting of,” according to standard practice in patent law.

The claimed invention relates to a method of producing a plant, said method comprising growing a plant cell comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory

region operably linked to a nucleotide sequence encoding a polypeptide, wherein the polypeptide has at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 749, and wherein said plant has increased drought tolerance or heat tolerance as compared to a control plant that does not comprise said nucleic acid.

The claimed invention also relates to a method of modulating drought tolerance in a plant, said method comprising introducing into a plant cell an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the polypeptide has at least 80% sequence identity to the amino acid sequence of SEQ ID NO:749, and wherein a plant produced from said plant cell has increased drought tolerance as compared to a control plant that does not comprise said exogenous nucleic acid.

The claimed invention also relates to a plant cell comprising an exogenous nucleic acid for use in producing a plant having increased drought tolerance or heat tolerance as compared to a control plant that does not comprise said exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the polypeptide has at least 80% sequence identity to the amino acid sequence of SEQ ID NO:749.

The claimed invention also relates to a plant cell comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the polypeptide has at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 749, and wherein the plant cell is from a plant that is selected for having increased drought tolerance or heat tolerance as compared to a control plant that does not comprise said nucleic acid, and wherein said plant is a member of a species selected from the group consisting of *Panicum virgatum* (switchgrass), *Sorghum bicolor* (sorghum, sudangrass), *Miscanthus giganteus* (miscanthus), *Saccharum* sp. (energycane), *Populus balsamifera* (poplar), *Zea mays* (corn), *Glycine max* (soybean), *Brassica napus* (canola), *Triticum aestivum* (wheat), *Gossypium hirsutum* (cotton), *Oryza sativa* (rice), *Helianthus annuus* (sunflower), *Medicago sativa* (alfalfa), *Beta vulgaris* (sugarbeet), and *Pennisetum glaucum* (pearl millet)..

The claimed invention also relates to a nucleic acid for producing a plant having a difference in drought tolerance or heat tolerance as compared to a control plant that does not comprise said nucleic acid, said nucleic acid comprising: a first nucleotide sequence encoding a polypeptide having 80% or greater sequence identity to the amino acid sequence set forth in SEQ ID NO:749; and a second nucleotide sequence comprising a regulatory region operably linked to the first nucleotide sequence, wherein the first nucleotide sequence is heterologous to the second nucleotide sequence.

The claimed invention also relates to a method of identifying whether a polymorphism is associated with variation in drought tolerance or heat tolerance, said method comprising: a) determining

whether one or more genetic polymorphisms in a population of plants is associated with the locus for a polypeptide of SEQ ID NO:749 and functional homologs thereof; and b) measuring the correlation between variation in said drought tolerance in plants of said population and the presence of said one or more genetic polymorphisms in plants of said population, thereby identifying whether or not said one or more genetic polymorphisms are associated with variation in drought tolerance or heat tolerance.

The claimed invention also relates to a method of making a plant line, said method comprising: a) determining whether one or more genetic polymorphisms in a population of plants is associated with a locus for a gene encoding the polypeptide of SEQ ID NO:749 and functional homologs thereof; b) identifying one or more plants in said population in which the presence of at least one allele at said one or more genetic polymorphisms is associated with variation in drought tolerance or heat tolerance; c) crossing each said one or more identified plants with itself or a different plant to produce seed; d) crossing at least one progeny plant grown from said seed with itself or a different plant; and e) repeating steps c) and d) for an additional 0-5 generations to make said plant line, wherein said at least one allele is present in said plant line.

SEQ ID NO:749 is as follows.

```

Met Ala Gln Arg Thr Glu Lys Glu Glu Thr Glu Phe Lys Val Leu Glu
1      5      10     15
Thr Leu Thr Thr Thr Thr Thr Thr Leu Cys Thr Asn Asn Cys Gly Val
      20     25     30
Thr Ala Asn Pro Ala Thr Asn Asn Met Cys Gln Lys Cys Phe Asn Ala
      35     40     45
Ser Leu Val Ser Ala Ala Ala Gly Val Val Glu Ser Gly Ser Ile Leu
      50     55     60
Lys Arg Ser Ala Arg Ser Val Asn Leu Arg Ser Ser Pro Ala Lys Val
      65     70     75     80
Val Ile Arg Pro Arg Glu Ile Asp Ala Val Lys Lys Arg Asp Gln Gln
      85     90     95
Ile Val Asn Arg Cys Ser Gly Cys Arg Lys Lys Val Gly Leu Thr Gly
      100    105    110
Phe Arg Cys Arg Cys Gly Glu Leu Phe Cys Ser Glu His Arg Tyr Ser
      115    120    125
Asp Arg His Asp Cys Ser Tyr Asp Tyr Lys Thr Ala Gly Arg Glu Ala
      130    135    140
Ile Ala Arg Glu Asn Pro Val Val Lys Ala Ala Lys Met Val Lys Val
      145    150    155    160

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DESCRIPTION OF THE DRAWINGS

Figure 1 is an alignment of Ceres SEEDLINE ID no.ME00029 (SEQ ID NO:442) with homologous and/or orthologous sequences, including, Public GI ID no.72384401 (SEQ ID NO:443), Ceres CLONE ID no.1079382 (SEQ ID NO:445), Ceres CLONE ID no.1853461 (SEQ ID NO:447), Ceres CLONE ID no.1626485 (SEQ ID NO:451), Ceres CLONE ID no.1713920 (SEQ ID NO:459), Ceres CLONE ID no.1772747 (SEQ ID NO:463), Ceres CLONE ID no.225960 (SEQ ID NO:465), Public GI ID no.115443807 (SEQ ID NO:470), and Ceres CLONE ID no.569388 (SEQ ID NO:483). In all the alignment figures shown herein, a dash in an aligned sequence represents a gap, *i.e.*, a lack of an amino acid at that position. Identical amino acids or conserved amino acid substitutions among aligned sequences are identified by boxes. Figure 1 and the other alignment figures provided herein were generated using the program MUSCLE version 3.52.

Figure 2 is an alignment of Ceres SEEDLINE ID no.ME00045 (SEQ ID NO:489) with homologous and/or orthologous sequences, including, Ceres CLONE ID no.571200 (SEQ ID NO:494), Ceres CLONE ID no.1928532 (SEQ ID NO:496), Ceres ANNOT ID no.1490637 (SEQ ID NO:498), Ceres CLONE ID no.295496 (SEQ ID NO:514), Public GI ID no.115463637 (SEQ ID NO:515), and Ceres CLONE ID no.1999444 (SEQ ID NO:518).

Figure 3 is an alignment of Ceres SEEDLINE ID no.ME02190 (SEQ ID NO:568) with homologous and/or orthologous sequences, including, Ceres CLONE ID no.695006 (SEQ ID NO:578) and Ceres ANNOT ID no.1527488 (SEQ ID NO:584).

Figure 4 is an alignment of Ceres SEEDLINE ID no.ME02549 (SEQ ID NO:590) with homologous and/or orthologous sequences, including, Ceres ANNOT ID no.1501305 (SEQ ID NO:623), Ceres CLONE ID no.607280 (SEQ ID NO:627), Public GI ID no.92887174 (SEQ ID NO:632), Ceres CLONE ID no.1857162 (SEQ ID NO:634), Public GI ID no.115477272 (SEQ ID NO:674), and Ceres CLONE ID no.264002 (SEQ ID NO:682).

Figure 5 is an alignment of Ceres SEEDLINE ID no.ME02865 (SEQ ID NO:705) with homologous and/or orthologous sequences, including, Public GI ID no.79320952 (SEQ ID NO:706) and Public GI ID no.79320957 (SEQ ID NO:707).

Figure 6 is an alignment of Ceres SEEDLINE ID no.ME03227 (SEQ ID NO:711) with homologous and/or orthologous sequences, including, Ceres CLONE ID no.964616 (SEQ ID NO:714), Ceres CLONE ID no.100009667 (SEQ ID NO:715), Ceres ANNOT ID no.1444568 (SEQ ID NO:719), Ceres CLONE ID no.719489 (SEQ ID NO:725), Ceres CLONE ID no.587748 (SEQ ID NO:733), Public GI ID no.125528114 (SEQ ID NO:734), and Ceres CLONE ID no.274172 (SEQ ID NO:737).

Figure 7 is an alignment of Ceres SEEDLINE ID no.ME04477 (SEQ ID NO:742) with homologous and/or orthologous sequences, including, Ceres CLONE ID no.1620215 (SEQ ID NO: 759); Public GI ID no. 38016527 (SEQ ID NO: 796); Ceres CLONE ID no.1798756 (SEQ ID NO: 763); Public GI ID no. 75133829 (SEQ ID NO: 799); Ceres ANNOT ID no.1460527 (SEQ ID NO: 801); Public GI ID no.119720772 (SEQ ID NO: 857); Ceres CLONE ID no.708446 (SEQ ID NO: 859); Public GI ID no.92896423 (SEQ ID NO: 892); Ceres CLONE ID no.1387149 (SEQ ID NO: 912); Public GI ID no.5031281 (SEQ ID NO: 953); Ceres CLONE ID no.1775820 (SEQ ID NO: 955); Public GI ID no.35187687 (SEQ ID NO: 988); Public GI ID no.115468934 (SEQ ID NO: 991); Public GI ID no.118424243 (SEQ ID NO: 1000); Ceres ANNOT ID no.6063957 (SEQ ID NO: 1010); CeresClone:1030374 (SEQ ID NO: 1306); Public GI ID no. 113196593 (SEQ ID NO: 798); Public GI ID no.112819496 (SEQ ID NO: 999), and Public GI ID no.169363 (SEQ ID NO: 1215).

Figure 8 is an alignment of Ceres SEEDLINE ID no.ME18396 (SEQ ID NO:1012) with homologous and/or orthologous sequences, including, Ceres CLONE ID no.287430 (SEQ ID NO:1018), Ceres ANNOT ID no.451889 (SEQ ID NO:1020), Ceres CLONE ID no.936084 (SEQ ID NO:1055), Ceres CLONE ID no.1792501 (SEQ ID NO:1066), Ceres ANNOT ID no.1437875 (SEQ ID NO:1068), Public GI ID no.1853968 (SEQ ID NO:1093), Public GI ID no.27530032 (SEQ ID NO:1094), Ceres CLONE ID no.1834483 (SEQ ID NO:1110), Public GI ID no.84579418 (SEQ ID NO:1113), Public GI ID no.15077030 (SEQ ID NO:1117), and Public GI ID no.13752458 (SEQ ID NO:1118).

Figure 9 is an alignment of Ceres SEEDLINE ID no.ME20095 (SEQ ID NO:1129) with homologous and/or orthologous sequences, including, Public GI ID no.72255610 (SEQ ID NO:933), Ceres CLONE ID no.1927040 (SEQ ID NO:926), Ceres CLONE ID no.1562633 (SEQ ID NO:1140), Ceres ANNOT ID no.1692728 (SEQ ID NO:1142), Ceres CLONE ID no.921110 (SEQ ID NO:1144), Ceres CLONE ID no.1791180 (SEQ ID NO:1146), Ceres CLONE ID no.527891 (SEQ ID NO:1148), Ceres ANNOT ID no.1522414 (SEQ ID NO:1150), and Public GI ID no.51458330 (SEQ ID NO:1182).

Figure 10 is an alignment of Ceres CLONE ID no.31309 (SEQ ID NO:60) with homologous and/or orthologous sequences, including, Ceres CLONE ID no.872030 (SEQ ID NO:62), Ceres CLONE ID no.100029223 (SEQ ID NO:74), Ceres CLONE ID no.1939845 (SEQ ID NO:98), Ceres CLONE ID no.2015383 (SEQ ID NO:102), Ceres CLONE ID no.1607893 (SEQ ID NO:104), Ceres CLONE ID no.1075133 (SEQ ID NO:152), and Ceres CLONE ID no.1218065 (SEQ ID NO:915).

Figure 11 is an alignment of Ceres LOCUS ID no.At2g26150 (SEQ ID NO:364) with homologous and/or orthologous sequences, including, Ceres ANNOT ID no.1455221 (SEQ ID NO:407), Public GI ID no.729774 (SEQ ID NO:408), Ceres CLONE ID no.1414288 (SEQ ID NO:410), Public GI ID no.115482048 (SEQ ID NO:413), and Public GI ID no.56117815 (SEQ ID NO:421).

Figure 12 is an alignment of Ceres LOCUS ID no.At1g32330 (SEQ ID NO:311) with homologous and/or orthologous sequences, including, Ceres ANNOT ID no.1538958 (SEQ ID NO:319), Public GI ID no.115521213 (SEQ ID NO:320), Public GI ID no.42415865 (SEQ ID NO:321), Public GI ID no.729775 (SEQ ID NO:322), Public GI ID no.11386827 (SEQ ID NO:323), Public GI ID no.115456675 (SEQ ID NO:326), and Public GI ID no.89274218 (SEQ ID NO:335).

Figure 13 is an alignment of Ceres CLONE ID no.41543 (SEQ ID NO:160) with homologous and/or orthologous sequences, including, Ceres CLONE ID no.1837065 (SEQ ID NO:162), Ceres ANNOT ID no.1531178 (SEQ ID NO:184), Ceres CLONE ID no.470694 (SEQ ID NO:242), Public GI ID no.92867368 (SEQ ID NO:253), Ceres CLONE ID no.859707 (SEQ ID NO:256), Ceres CLONE ID no.392275 (SEQ ID NO:268), Ceres CLONE ID no.1828394 (SEQ ID NO:282), and Public GI ID no.115466694 (SEQ ID NO:294).

Figure 14 is an alignment of Ceres CLONE ID no.14572 (SEQ ID NO:2) with homologous and/or orthologous sequences, including, Public GI ID no.115470807 (SEQ ID NO:5), Ceres CLONE ID no.1842931 (SEQ ID NO:15), Ceres CLONE ID no.321308 (SEQ ID NO:17), Ceres CLONE ID no.1725811 (SEQ ID NO:19), Ceres CLONE ID no.1357455 (SEQ ID NO:21), Ceres CLONE ID no.943370 (SEQ ID NO:23), Ceres CLONE ID no.1327712 (SEQ ID NO:25), Ceres CLONE ID no.1764692 (SEQ ID NO:27), and Ceres ANNOT ID no.1512656 (SEQ ID NO:41).

Figure 15 is an alignment of Ceres SEEDLINE ID no. ME02401 (SEQ ID NO:749) with homologous and/or orthologous sequences, including, Ceres CLONE ID no.1847516 (SEQ ID NO:1195), Ceres CLONE ID no.1961986 (SEQ ID NO:1201), and Ceres ANNOT ID no.6091930 (SEQ ID NO:1207).

Figure 16 is an alignment of Ceres SEEDLINE ID no. ME004246 (SEQ ID NO:1311) with homologous and/or orthologous sequences, including, CeresClone:971761 (SEQ ID NO: 1313), CeresClone:1946574 (SEQ ID NO: 1331), CeresClone:2055551 (SEQ ID NO: 1340), CeresClone:100045499 (SEQ ID NO: 1347), CeresClone:1465853 (SEQ ID NO: 1353), and CeresClone:753982 (SEQ ID NO: 1360).

DETAILED DESCRIPTION

The invention features methods and materials related to increasing heat and/or drought tolerance in plants. In some embodiments, the plants may have increased heat and drought tolerance. The methods can include transforming a plant cell with a nucleic acid encoding a heat and/or drought-tolerance polypeptide, wherein expression of the polypeptide results in increased heat and/or drought tolerance. Plant cells produced using such methods can be grown to produce plants having an increased heat and/or drought tolerance. Such plants, and the seeds of such plants, may be used to produce, for example, may be used to produce biomass and/or to produce crops with increased yield and/or quality.

I. Definitions:

“Amino acid” refers to one of the twenty biologically occurring amino acids and to synthetic amino acids, including D/L optical isomers.

“Cell type-preferential promoter” or “tissue-preferential promoter” refers to a promoter that drives expression preferentially in a target cell type or tissue, respectively, but may also lead to some transcription in other cell types or tissues as well.

5 “Control plant” refers to a plant that does not contain the exogenous nucleic acid present in a transgenic plant of interest, but otherwise has the same or similar genetic background as such a transgenic plant. A suitable control plant can be a non-transgenic wild type plant, a non-transgenic segregant from a transformation experiment, or a transgenic plant that contains an exogenous nucleic acid other than
10 the exogenous nucleic acid of interest.

“Domains” are groups of substantially contiguous amino acids in a polypeptide that can be used to characterize protein families and/or parts of proteins. Such domains have a “fingerprint” or “signature” that can comprise conserved primary sequence, secondary structure, and/or three-dimensional conformation.
15 Generally, domains are correlated with specific in vitro and/or in vivo activities. A domain can have a length of from 10 amino acids to 400 amino acids, e.g., 10 to 50 amino acids, or 25 to 100 amino acids, or 35 to 65 amino acids, or 35 to 55 amino acids, or 45 to 60 amino acids, or 200 to 300 amino acids, or 300 to 400 amino acids.

“Exogenous” with respect to a nucleic acid indicates that the nucleic acid is
20 part of a recombinant nucleic acid construct, or is not in its natural environment. For example, an exogenous nucleic acid can be a sequence from one species introduced into another species, i.e., a heterologous nucleic acid. Typically, such an exogenous nucleic acid is introduced into the other species via a recombinant nucleic acid construct. An exogenous nucleic acid can also be a sequence that is native to an
25 organism and that has been reintroduced into cells of that organism. An exogenous nucleic acid that includes a native sequence can often be distinguished from the naturally occurring sequence by the presence of non-natural sequences linked to the exogenous nucleic acid, e.g., non-native regulatory sequences flanking a native sequence in a recombinant nucleic acid construct. In addition, stably transformed
30 exogenous nucleic acids typically are integrated at positions other than the position where the native sequence is found. It will be appreciated that an exogenous nucleic acid may have been introduced into a progenitor and not into the cell under

consideration. For example, a transgenic plant containing an exogenous nucleic acid can be the progeny of a cross between a stably transformed plant and a non-transgenic plant. Such progeny are considered to contain the exogenous nucleic acid.

“Expression” refers to the process of converting genetic information of a polynucleotide into RNA through transcription, which is catalyzed by an enzyme, RNA polymerase, and into protein, through translation of mRNA on ribosomes.

“Heterologous polypeptide” as used herein refers to a polypeptide that is not a naturally occurring polypeptide in a plant cell, e.g., a transgenic *Panicum virgatum* plant transformed with and expressing the coding sequence for a nitrogen transporter polypeptide from a *Zea mays* plant.

“Isolated nucleic acid” as used herein includes a naturally-occurring nucleic acid, provided one or both of the sequences immediately flanking that nucleic acid in its naturally-occurring genome is removed or absent. Thus, an isolated nucleic acid includes, without limitation, a nucleic acid that exists as a purified molecule or a nucleic acid molecule that is incorporated into a vector or a virus. A nucleic acid existing among hundreds to millions of other nucleic acids within, for example, cDNA libraries, genomic libraries, or gel slices containing a genomic DNA restriction digest, is not to be considered an isolated nucleic acid.

“Modulation” of the level of tolerance to a stimulus (e.g., drought conditions or heat shock conditions) refers to the change in the level of tolerance of the indicated stimulus that is observed as a result of expression of, or transcription from, an exogenous nucleic acid in a plant cell. The change in level is measured relative to the corresponding level in control plants.

“Nucleic acid” and “polynucleotide” are used interchangeably herein, and refer to both RNA and DNA, including cDNA, genomic DNA, synthetic DNA, and DNA or RNA containing nucleic acid analogs. Polynucleotides can have any three-dimensional structure. A nucleic acid can be double-stranded or single-stranded (i.e., a sense strand or an antisense strand). Non-limiting examples of polynucleotides include genes, gene fragments, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, siRNA, micro-RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, nucleic acid probes and nucleic acid primers. A polynucleotide may contain unconventional or modified nucleotides.

“Operably linked” refers to the positioning of a regulatory region and a sequence to be transcribed in a nucleic acid so that the regulatory region is effective for regulating transcription or translation of the sequence. For example, to operably link a coding sequence and a regulatory region, the translation initiation site of the translational reading frame of the coding sequence is typically positioned between one and about fifty nucleotides downstream of the regulatory region. A regulatory region can, however, be positioned as much as about 5,000 nucleotides upstream of the translation initiation site, or about 2,000 nucleotides upstream of the transcription start site.

“Polypeptide” as used herein refers to a compound of two or more subunit amino acids, amino acid analogs, or other peptidomimetics, regardless of post-translational modification, e.g., phosphorylation or glycosylation. The subunits may be linked by peptide bonds or other bonds such as, for example, ester or ether bonds. Full-length polypeptides, truncated polypeptides, point mutants, insertion mutants, splice variants, chimeric proteins, and fragments thereof are encompassed by this definition.

“Progeny” includes descendants of a particular plant or plant line. Progeny of an instant plant include seeds formed on F₁, F₂, F₃, F₄, F₅, F₆ and subsequent generation plants, or seeds formed on BC₁, BC₂, BC₃, and subsequent generation plants, or seeds formed on F₁BC₁, F₁BC₂, F₁BC₃, and subsequent generation plants. The designation F₁ refers to the progeny of a cross between two parents that are genetically distinct. The designations F₂, F₃, F₄, F₅ and F₆ refer to subsequent generations of self- or sib-pollinated progeny of an F₁ plant.

“Regulatory region” refers to a nucleic acid having nucleotide sequences that influence transcription or translation initiation and rate, and stability and/or mobility of a transcription or translation product. Regulatory regions include, without limitation, promoter sequences, enhancer sequences, response elements, protein recognition sites, inducible elements, protein binding sequences, 5' and 3' untranslated regions (UTRs), transcriptional start sites, termination sequences, polyadenylation sequences, introns, and combinations thereof. A regulatory region typically comprises at least a core (basal) promoter. A regulatory region also may include at least one control element, such as an enhancer sequence, an upstream element or an upstream activation region (UAR). For example, a suitable enhancer is a cis-regulatory element (-212 to -154) from the upstream region of the octopine

synthase (ocs) gene. Fromm et al., *The Plant Cell*, 1:977-984 (1989).

“Up-regulation” refers to regulation that increases the level of an expression product (mRNA, polypeptide, or both) relative to basal or native states.

“Vector” refers to a replicon, such as a plasmid, phage, or cosmid, into which another DNA segment may be inserted so as to bring about the replication of the inserted segment. Generally, a vector is capable of replication when associated with the proper control elements. The term “vector” includes cloning and expression vectors, as well as viral vectors and integrating vectors. An “expression vector” is a vector that includes a regulatory region.

II. Polypeptides

Polypeptides described herein include heat and/or drought-tolerance polypeptides. Heat and/or drought-tolerance polypeptides can be effective to increase heat and/or drought-tolerance when expressed in a plant or plant cell. Such polypeptides typically contain at least one domain indicative of heat and/or drought-tolerance polypeptides, as described in more detail herein. Heat and/or drought-tolerance polypeptides typically have an HMM bit score that is greater than 20 for an HMM model based on one of the alignments set forth in Figures 1-16, as described in more detail herein. In some embodiments, heat and/or drought-tolerance polypeptides have greater than 80% identity to SEQ ID NO:442, SEQ ID NO:489, SEQ ID NO:568, SEQ ID NO:590, SEQ ID NO:705, SEQ ID NO:711, SEQ ID NO:742, SEQ ID NO:1012, SEQ ID NO:1129, SEQ ID NO:60, SEQ ID NO:364, SEQ ID NO:311, SEQ ID NO:160, SEQ ID NO:2, SEQ ID NO:749, SEQ ID NO:1311, or SEQ ID NO:57, as described in more detail herein.

A. Domains Indicative of Heat and/or Drought-Tolerance Polypeptides

A drought-tolerance polypeptide can be a RNA polymerase Rpb4 family member. The eukaryotic RNA polymerase subunit RPB4 forms a heterodimer with subunit RPB7 that reversibly associates with the RNA polymerase II core. SEQ ID NO:442 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres SEEDLINE ID No. ME00029 (SEQ ID NO:441), that is predicted to encode a RNA polymerase Rpb4 polypeptide.

A drought-tolerance polypeptide can contain a sulfotransferase 1 domain characteristic of polypeptides belonging to the sulfotransferase family. Members of the sulfotransferase family catalyze the transfer of sulfate groups to specific compounds. SEQ ID NO:590, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres SEEDLINE ID No. ME02549 (SEQ ID NO:589), is predicted to encode a polypeptide containing a sulfotransferase 1 domain.

A drought-tolerance polypeptide can contain an AN1-like zinc finger (zf-AN1) and an A20-like zinc finger (zf-A20) domain. The AN1-like zinc finger domain was first identified as a zinc finger at the C-terminus of An1, a ubiquitin-like protein in *Xenopus laevis*. The AN1-like zinc finger domain is characterized by the pattern, C-X2-C-X(9-12)-C-X(1-2)-C-X4-C-X2-H-X5-H-X-C Where X can be any amino acid, and numbers in brackets indicate the number of residues. In A20, the A20-like zinc finger domain mediates self-association and IL-1-induced NF-kappa B activation. SEQ ID NO:742, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres Clone ID No. 24255 (SEQ ID NO:1241), is predicted to encode a polypeptide containing an AN1-like zinc finger domain and a A20-like zinc finger domain. SEQ ID NO:749, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres SEEDLINE ID No. ME02401, is also predicted to encode a polypeptide containing an AN1-like zinc finger domain and a A20-like zinc finger domain.

A drought-tolerance polypeptide can contain a short chain dehydrogenase (adh_short) domain. Most polypeptides containing a short chain dehydrogenase domain are polypeptides of about 250 to 300 amino acid residues, and are NAD- or NADP-dependent oxidoreductases. SEQ ID NO:1012, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres SEEDLINE ID No. 18396 (SEQ ID NO:1260), is predicted to encode a polypeptide containing a short chain dehydrogenase domain.

A drought-tolerance polypeptide can contain a trehalose-phosphatase (Trehalose_PPase) domain characteristic of trehalose phosphatase polypeptides. Trehalose phosphatases catalyze the de-phosphorylation of trehalose-6-phosphate to trehalose and orthophosphate. Trehalose is a common disaccharide in bacteria, fungi, and invertebrates that appears to play a role in desiccation tolerance. SEQ ID NO:1129, which sets forth the amino acid sequence of an *Arabidopsis* clone,

identified herein as Ceres SEEDLINE ID No. ME20095 (SEQ ID NO:1126), is predicted to encode a polypeptide containing a trehalose-phosphatase domain.

A heat-tolerance polypeptide can be a synaptobrevin-related polypeptide. SEQ ID NO:160, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres CLONE ID no.41543 (SEQ ID NO:159), is predicted to encode a synaptobrevin-related polypeptide.

A heat-tolerance polypeptide can contain an HSF-type DNA-binding domain, which is predicted to be characteristic of heat shock factor transcription activator.

Heat shock factor transcription activators are often found associated with heat shock

protein promoters during heat shock. SEQ ID NO:311, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres LOCUS ID

no.At1g32330 (SEQ ID NO:310), is predicted to encode a polypeptide containing an

HSF-type DNA-binding domain. SEQ ID NO:364, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres LOCUS ID

no.At2g26150 (SEQ ID NO:363), is also predicted to encode a polypeptide containing an HSF-type DNA-binding domain.

A heat-tolerance polypeptide can contain a DnaJ domain. The prokaryotic heat shock protein DnaJ interacts with the chaperone hsp70-like DnaK protein.

Structurally, the DnaJ protein consists of an N-terminal conserved domain (called 'J'

domain) of about 70 amino acids, a glycine-rich region ('G' domain') of about 30

residues, a central domain containing four repeats of a CXXCXGXG motif ('CRR'

domain) and a C-terminal region of 120 to 170 residues. SEQ ID NO:60, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres

CLONE ID no.31309 (SEQ ID NO:58), is predicted to encode an polypeptide

containing a DnaJ domain.

A drought-tolerance polypeptide can contain a KH₂ domain. Most polypeptides containing a KH₂ domain are typically around 70 amino acids and are

present in a wide variety of quite diverse nucleic acid-binding proteins. It has been shown to bind RNA. Like many other RNA-binding motifs, KH motifs are found in

one or multiple copies, each motif is necessary for in vitro RNA binding activity,

suggesting that they may function cooperatively or, in the case of single KH motif proteins (for example, Mer1p), independently. According to structural analysis the

KH domain can be separated in two groups. The first group or type-1 contain a beta-alpha-alpha-beta-beta-alpha structure, whereas in the type-2 the two last beta-sheet

are located in the N terminal part of the domain (alpha-beta-beta-alpha-alpha-beta). Sequence similarity between these two folds are limited to a short region (VIGXXGXXI) in the RNA binding motif. This motif is located between helices 1 and 2 in type-1 and between helices 2 and 3 in type-2. SEQ ID NO:1311, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as Ceres SEEDLINE ID No. ME04246 (SEQ ID NO:1362), is predicted to encode a polypeptide containing a KH_2 domain.

B. Functional Homologs Identified by Reciprocal BLAST

In some embodiments, one or more functional homologs of a reference heat and/or drought-tolerance polypeptide defined by one or more of the Pfam descriptions indicated above are suitable for use as heat and/or drought-tolerance polypeptides. A functional homolog is a polypeptide that has sequence similarity to a reference polypeptide, and that carries out one or more of the biochemical or physiological function(s) of the reference polypeptide. A functional homolog and the reference polypeptide may be natural occurring polypeptides, and the sequence similarity may be due to convergent or divergent evolutionary events. As such, functional homologs are sometimes designated in the literature as homologs, or orthologs, or paralogs. Variants of a naturally occurring functional homolog, such as polypeptides encoded by mutants of a wild type coding sequence, may themselves be functional homologs. Functional homologs can also be created via site-directed mutagenesis of the coding sequence for a heat and/or drought-tolerance polypeptide, or by combining domains from the coding sequences for different naturally-occurring heat and/or drought-tolerance polypeptides ("domain swapping"). The term "functional homolog" is sometimes applied to the nucleic acid that encodes a functionally homologous polypeptide.

Functional homologs can be identified by analysis of nucleotide and polypeptide sequence alignments. For example, performing a query on a database of nucleotide or polypeptide sequences can identify homologs of heat and/or drought-tolerance polypeptides. Sequence analysis can involve BLAST, Reciprocal BLAST, or PSI-BLAST analysis of nonredundant databases using a heat and/or drought-tolerance polypeptide amino acid sequence as the reference sequence. Amino acid sequence is, in some instances, deduced from the nucleotide sequence. Those polypeptides in the database that have greater than 40% sequence identity are candidates for further evaluation for suitability as a heat and/or drought-tolerance

polypeptide. Amino acid sequence similarity allows for conservative amino acid substitutions, such as substitution of one hydrophobic residue for another or substitution of one polar residue for another. If desired, manual inspection of such candidates can be carried out in order to narrow the number of candidates to be
 5 further evaluated. Manual inspection can be performed by selecting those candidates that appear to have domains present in heat and/or drought-tolerance polypeptides, *e.g.*, conserved functional domains.

Conserved regions can be identified by locating a region within the primary amino acid sequence of a heat and/or drought-tolerance polypeptide that is a repeated
 10 sequence, forms some secondary structure (*e.g.*, helices and beta sheets), establishes positively or negatively charged domains, or represents a protein motif or domain.

See, e.g., the Pfam web site describing consensus sequences for a variety of protein motifs and domains on the World Wide Web at sanger.ac.uk/Software/Pfam/ and pfam.janelia.org/. A description of the information included at the Pfam database is
 15 described in Sonnhammer *et al.*, *Nucl. Acids Res.*, 26:320-322 (1998); Sonnhammer *et al.*, *Proteins*, 28:405-420 (1997); and Bateman *et al.*, *Nucl. Acids Res.*, 27:260-262 (1999). Conserved regions also can be determined by aligning sequences of the same or related polypeptides from closely related species. Closely related species preferably are from the same family. In some embodiments, alignment of sequences
 20 from two different species is adequate.

Typically, polypeptides that exhibit at least about 20% amino acid sequence identity are useful to identify conserved regions. Conserved regions of related polypeptides exhibit at least 45% amino acid sequence identity (*e.g.*, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% amino acid sequence identity).
 25 In some embodiments, a conserved region exhibits at least 92%, 94%, 96%, 98%, or 99% amino acid sequence identity.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:442 are provided in Figure 1 and in the sequence listing. Such functional homologs include Public GI ID no.72384401 (SEQ ID NO:443),
 30 Ceres CLONE ID no.1079382 (SEQ ID NO:445), Ceres CLONE ID no.1853461 (SEQ ID NO:447), Ceres CLONE ID no.1626485 (SEQ ID NO:451), Ceres CLONE ID no.1713920 (SEQ ID NO:459), Ceres CLONE ID no.1772747 (SEQ ID NO:463), Ceres CLONE ID no.225960 (SEQ ID NO:465), Public GI ID no.115443807 (SEQ ID NO:470), and Ceres CLONE ID no.569388 (SEQ ID NO:483). Other functional

homologs of SEQ ID NO:442 include Ceres CLONE ID no.1915549 (SEQ ID NO:449), Ceres CLONE ID no.529871 (SEQ ID NO:453), Ceres CLONE ID no.1067079 (SEQ ID NO:455), Ceres CLONE ID no.1079572 (SEQ ID NO:457), Ceres ANNOT ID no.1456550 (SEQ ID NO:461), Ceres CLONE ID no.1437889 (SEQ ID NO:469), Ceres CLONE ID no.2014249 (SEQ ID NO:472), Ceres CLONE ID no.2033133 (SEQ ID NO:474), Ceres CLONE ID no.707404 (SEQ ID NO:476), Ceres CLONE ID no.1770680 (SEQ ID NO:478), Ceres ANNOT ID no.1450989 (SEQ ID NO:480), Public GI ID no.72384445 (SEQ ID NO:481), Ceres CLONE ID no.1059299 (SEQ ID NO:485), and Ceres ANNOT ID no.6008086 (SEQ ID NO:487). In some cases, a functional homolog of SEQ ID NO:442 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:442.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:489 are provided in Figure 2 and in the sequence listing. Such functional homologs include Ceres CLONE ID no.571200 (SEQ ID NO:494), Ceres CLONE ID no.1928532 (SEQ ID NO:496), Ceres ANNOT ID no.1490637 (SEQ ID NO:498), Ceres CLONE ID no.295496 (SEQ ID NO:514), Public GI ID no.115463637 (SEQ ID NO:515), and Ceres CLONE ID no.1999444 (SEQ ID NO:518). Other functional homologs of SEQ ID NO:489 include Public GI ID no.147844794 (SEQ ID NO:490), Public GI ID no.147842279 (SEQ ID NO:491), Public GI ID no.145355441 (SEQ ID NO:492), Ceres ANNOT ID no.1461381 (SEQ ID NO:500), Ceres ANNOT ID no.1440313 (SEQ ID NO:502), Ceres ANNOT ID no.1448275 (SEQ ID NO:504), Ceres ANNOT ID no.1437838 (SEQ ID NO:506), Ceres ANNOT ID no.1501275 (SEQ ID NO:508), Ceres CLONE ID no.1644562 (SEQ ID NO:510), Ceres CLONE ID no.1925967 (SEQ ID NO:512), Public GI ID no.115435904 (SEQ ID NO:516), Public GI ID no.125552168 (SEQ ID NO:519), Public GI ID no.125594093 (SEQ ID NO:520), Ceres CLONE ID no.221188 (SEQ ID NO:522), Ceres ANNOT ID no.1477714 (SEQ ID NO:524), Ceres CLONE ID no.1787953 (SEQ ID NO:526), Ceres ANNOT ID no.1531210 (SEQ ID NO:528), Ceres CLONE ID no.521176 (SEQ ID NO:530), Public GI ID no.22327055 (SEQ ID NO:531), Ceres ANNOT ID no.1508824 (SEQ ID NO:533), Ceres CLONE ID no.38879 (SEQ ID NO:535), Public GI ID no.42569309 (SEQ ID NO:536), Ceres CLONE ID no.1817784 (SEQ ID NO:538), Ceres CLONE ID no.284637 (SEQ ID

NO:540), Public GI ID no.125596251 (SEQ ID NO:541), Public GI ID no.125554300 (SEQ ID NO:543), Ceres CLONE ID no.1935437 (SEQ ID NO:545), Ceres ANNOT ID no.1455622 (SEQ ID NO:547), Public GI ID no.55771354 (SEQ ID NO:548), Ceres ANNOT ID no.1514655 (SEQ ID NO:550), Ceres CLONE ID no.1848736 (SEQ ID NO:552), Public GI ID no.125569872 (SEQ ID NO:553), Ceres CLONE ID no.1645078 (SEQ ID NO:555), Ceres CLONE ID no.1790573 (SEQ ID NO:557), Public GI ID no.4567251 (SEQ ID NO:558), Ceres CLONE ID no.444113 (SEQ ID NO:561), Public GI ID no.125525355 (SEQ ID NO:562), Ceres ANNOT ID no.6028854 (SEQ ID NO:564), and Ceres ANNOT ID no.6115356 (SEQ ID NO:566). In some cases, a functional homolog of SEQ ID NO:489 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:489.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:568 are provided in Figure 3 and in the sequence listing. Such functional homologs include Ceres CLONE ID no.695006 (SEQ ID NO:578) and Ceres ANNOT ID no.1527488 (SEQ ID NO:584). Other functional homologs of SEQ ID NO:568 include Public GI ID no.79318519 (SEQ ID NO:569), Public GI ID no.79318537 (SEQ ID NO:570), Ceres CLONE ID no.956998 (SEQ ID NO:572), Ceres CLONE ID no.978154 (SEQ ID NO:574), Ceres CLONE ID no.1035628 (SEQ ID NO:576), Ceres CLONE ID no.464169 (SEQ ID NO:580), Ceres ANNOT ID no.1474075 (SEQ ID NO:582), Ceres ANNOT ID no.1474073 (SEQ ID NO:586), and Ceres ANNOT ID no.1527486 (SEQ ID NO:588). In some cases, a functional homolog of SEQ ID NO:568 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:568.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:590 are provided in Figure 4 and in the sequence listing. Such functional homologs include Ceres ANNOT ID no.1501305 (SEQ ID NO:623), Ceres CLONE ID no.607280 (SEQ ID NO:627), Public GI ID no.92887174 (SEQ ID NO:632), Ceres CLONE ID no.1857162 (SEQ ID NO:634), Public GI ID no.115477272 (SEQ ID NO:674), and Ceres CLONE ID no.264002 (SEQ ID NO:682). Other functional homologs of SEQ ID NO:590 include Public GI ID

no.147822456 (SEQ ID NO:591), Public GI ID no.144923935 (SEQ ID NO:592),
Public GI ID no.140038730 (SEQ ID NO:593), Public GI ID no.78708014 (SEQ ID
NO:594), Public GI ID no.115481362 (SEQ ID NO:595), Public GI ID no.125531350
(SEQ ID NO:596), Public GI ID no.125525598 (SEQ ID NO:597), Public GI ID
5 no.77548630 (SEQ ID NO:598), Public GI ID no.46798895 (SEQ ID NO:599),
Public GI ID no.125564653 (SEQ ID NO:600), Ceres CLONE ID no.998865 (SEQ
ID NO:602), Public GI ID no.125556140 (SEQ ID NO:603), Public GI ID
no.125534482 (SEQ ID NO:604), Public GI ID no.125550135 (SEQ ID NO:605),
Ceres CLONE ID no.639816 (SEQ ID NO:607), Public GI ID no.125562170 (SEQ
10 ID NO:608), Ceres CLONE ID no.1797059 (SEQ ID NO:610), Ceres CLONE ID
no.1031510 (SEQ ID NO:612), Ceres CLONE ID no.1973081 (SEQ ID NO:614),
Public GI ID no.125561002 (SEQ ID NO:615), Public GI ID no.125541732 (SEQ ID
NO:616), Public GI ID no.125560677 (SEQ ID NO:617), Public GI ID no.125559115
(SEQ ID NO:618), Public GI ID no.15809903 (SEQ ID NO:619), Public GI ID
15 no.30681703 (SEQ ID NO:620), Public GI ID no.9759556 (SEQ ID NO:621), Ceres
ANNOT ID no.1448303 (SEQ ID NO:625), Ceres ANNOT ID no.1448305 (SEQ ID
NO:629), Ceres ANNOT ID no.1448307 (SEQ ID NO:631), Public GI ID
no.92888243 (SEQ ID NO:635), Public GI ID no.92879395 (SEQ ID NO:636), Ceres
CLONE ID no.528876 (SEQ ID NO:638), Ceres ANNOT ID no.1448352 (SEQ ID
20 NO:640), Ceres ANNOT ID no.1437745 (SEQ ID NO:642), Ceres ANNOT ID
no.1464146 (SEQ ID NO:644), Ceres ANNOT ID no.1437744 (SEQ ID NO:646),
Public GI ID no.92894684 (SEQ ID NO:647), Ceres CLONE ID no.3964 (SEQ ID
NO:650), Public GI ID no.13272389 (SEQ ID NO:651), Ceres ANNOT ID
no.1481203 (SEQ ID NO:653), Public GI ID no.15227699 (SEQ ID NO:654), Public
25 GI ID no.92886084 (SEQ ID NO:655), Public GI ID no.15239947 (SEQ ID NO:656),
Ceres CLONE ID no.34878 (SEQ ID NO:658), Ceres CLONE ID no.150484 (SEQ
ID NO:660), Public GI ID no.21553545 (SEQ ID NO:661), Public GI ID
no.15222843 (SEQ ID NO:662), Public GI ID no.38230552 (SEQ ID NO:663),
Public GI ID no.3420008 (SEQ ID NO:664), Public GI ID no.15230602 (SEQ ID
30 NO:665), Public GI ID no.3420004 (SEQ ID NO:666), Public GI ID no.2129586
(SEQ ID NO:667), Public GI ID no.15217849 (SEQ ID NO:668), Public GI ID
no.15227704 (SEQ ID NO:669), Ceres ANNOT ID no.1465750 (SEQ ID NO:671),
Ceres CLONE ID no.1983975 (SEQ ID NO:673), Public GI ID no.15226028 (SEQ
ID NO:675), Public GI ID no.115459524 (SEQ ID NO:676), Ceres CLONE ID

no.1793353 (SEQ ID NO:678), Ceres ANNOT ID no.1467399 (SEQ ID NO:680), Ceres CLONE ID no.1982930 (SEQ ID NO:684), Public GI ID no.125540700 (SEQ ID NO:685), Ceres ANNOT ID no.1448743 (SEQ ID NO:687), Public GI ID no.50251910 (SEQ ID NO:688), Ceres CLONE ID no.1836748 (SEQ ID NO:690),

5 Public GI ID no.3420006 (SEQ ID NO:691), Public GI ID no.92879376 (SEQ ID NO:692), Ceres CLONE ID no.838941 (SEQ ID NO:694), Ceres ANNOT ID no.1437746 (SEQ ID NO:696), Ceres ANNOT ID no.6017241 (SEQ ID NO:698), Ceres ANNOT ID no.6085947 (SEQ ID NO:700), and Ceres ANNOT ID no.6017242 (SEQ ID NO:702). In some cases, a functional homolog of SEQ ID NO:590 has an

10 amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:590.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:705 are provided in Figure 5 and in the sequence listing.

15 Such functional homologs include Public GI ID no.79320952 (SEQ ID NO:706) and Public GI ID no.79320957 (SEQ ID NO:707). Other functional homologs of SEQ ID NO:705 include Public GI ID no.6692094 (SEQ ID NO:708) and Public GI ID no.145323049 (SEQ ID NO:709). In some cases, a functional homolog of SEQ ID NO:705 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%,

20 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:705.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:711 are provided in Figure 6 and in the sequence listing. Such functional homologs include Ceres CLONE ID no.964616 (SEQ ID NO:714),

25 Ceres CLONE ID no.100009667 (SEQ ID NO:715), Ceres ANNOT ID no.1444568 (SEQ ID NO:719), Ceres CLONE ID no.719489 (SEQ ID NO:725), Ceres CLONE ID no.587748 (SEQ ID NO:733), Public GI ID no.125528114 (SEQ ID NO:734), and Ceres CLONE ID no.274172 (SEQ ID NO:737). Other functional homologs of SEQ ID NO:711 include Public GI ID no.144923134 (SEQ ID NO:712), Ceres ANNOT ID

30 no.1471437 (SEQ ID NO:717), Ceres CLONE ID no.1270484 (SEQ ID NO:721), Ceres CLONE ID no.1075098 (SEQ ID NO:723), Public GI ID no.18412211 (SEQ ID NO:727), Ceres CLONE ID no.20358 (SEQ ID NO:729), Ceres CLONE ID no.1915503 (SEQ ID NO:731), Public GI ID no.115440619 (SEQ ID NO:735), Public GI ID no.125572387 (SEQ ID NO:738), and Ceres ANNOT ID no.6015812

(SEQ ID NO:740). In some cases, a functional homolog of SEQ ID NO:711 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:711.

5 Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:742 are provided in Figure 7 and in the sequence listing. Such functional homologs include Public GI ID no.147783026 (SEQ ID NO: 743), Public GI ID no.119367488 (SEQ ID NO: 744), Public GI ID no.147860340 (SEQ ID NO: 745), Public GI ID no.115477170 (SEQ ID NO: 757), Ceres CLONE ID
10 no.1620215 (SEQ ID NO: 759), Ceres CLONE ID no.1931889 (SEQ ID NO: 761), Ceres CLONE ID no.1798756 (SEQ ID NO: 763), Ceres CLONE ID no.1918424 (SEQ ID NO: 767), Ceres CLONE ID no.1845154 (SEQ ID NO: 771), Public GI ID no. 38016527 (SEQ ID NO: 796), Ceres Clone ID no. 1084216 (SEQ ID NO: 797), Public GI ID no. 113196593 (SEQ ID NO: 798), Public GI ID no. 75133829 (SEQ ID
15 NO: 799), Ceres ANNOT ID no.1460527 (SEQ ID NO: 801), Ceres Annot ID no. 8644540 (SEQ ID NO: 805), Ceres ANNOT ID no.1450673 (SEQ ID NO: 807), Public GI ID no. 116778802 (SEQ ID NO: 808), Public GI ID no. 116778893 (SEQ ID NO: 809), Public GI ID no. 116778998 (SEQ ID NO: 810), Public GI ID no. 157849766 (SEQ ID NO: 811), Public GI ID no. 159474166 (SEQ ID NO: 812),
20 Public GI ID no. 168036656 (SEQ ID NO: 813), Ceres ANNOT ID no.1456578 (SEQ ID NO: 815), Public GI ID no. 168053490 (SEQ ID NO: 816), Public GI ID no. 193237563 (SEQ ID NO: 817), Ceres Clone ID no. 100879386 (SEQ ID NO: 819), Ceres Clone ID no. 2055733 (SEQ ID NO: 823), Ceres Clone ID no. 2056478 (SEQ ID NO: 825), Ceres CLONE ID no.13007 (SEQ ID NO: 832), Ceres CLONE ID
25 no.5522 (SEQ ID NO: 834), Ceres CLONE ID no.30543 (SEQ ID NO: 836), Ceres CLONE ID no.14203 (SEQ ID NO: 839), Ceres CLONE ID no.975913 (SEQ ID NO: 846), Ceres CLONE ID no.967417 (SEQ ID NO: 848), Public GI ID no.119720772 (SEQ ID NO: 857), Ceres CLONE ID no.708446 (SEQ ID NO: 859), Ceres CLONE ID no.1614593 (SEQ ID NO: 863), Ceres CLONE ID no.2025938
30 (SEQ ID NO: 885), Public GI ID no.92896423 (SEQ ID NO: 892), Ceres CLONE ID no.634261 (SEQ ID NO: 900), Ceres CLONE ID no.1387149 (SEQ ID NO: 912), Ceres CLONE ID no.1423851 (SEQ ID NO: 918), Ceres CLONE ID no.1589047 (SEQ ID NO: 939), Ceres CLONE ID no.1748922 (SEQ ID NO: 944), Public GI ID no.5031281 (SEQ ID NO: 953), Ceres CLONE ID no.1775820 (SEQ ID NO: 955),

Ceres CLONE ID no.1787151 (SEQ ID NO: 957), Ceres CLONE ID no.1765871 (SEQ ID NO: 973), Ceres CLONE ID no.1990071 (SEQ ID NO: 977), Public GI ID no.35187687 (SEQ ID NO: 988), Public GI ID no.125556051 (SEQ ID NO: 989), Public GI ID no.125561658 (SEQ ID NO: 990), Public GI ID no.115468934 (SEQ ID NO: 991), Public GI ID no.115470773 (SEQ ID NO: 992), Public GI ID no.115444813 (SEQ ID NO: 993), Public GI ID no.112819496 (SEQ ID NO: 999), Public GI ID no.118424243 (SEQ ID NO: 1000), Ceres ANNOT ID no.6063957 (SEQ ID NO: 1010), Public GI ID no.169363 (SEQ ID NO:1215), Ceres CLONE ID no.24255 (SEQ ID NO: 1242), Ceres Clone ID no. 1030374 (SEQ ID NO: 1306), Ceres Clone ID no. 1738028 (SEQ ID NO: 1308), Public GI ID no. 115455855 (SEQ ID NO: 1309), and Public GI ID no. 193237563 (SEQ ID NO: 1310). In some cases, a functional homolog of SEQ ID NO:742 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:742.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1012 are provided in Figure 8 and in the sequence listing. Such functional homologs include Ceres CLONE ID no.287430 (SEQ ID NO:1018), Ceres ANNOT ID no.451889 (SEQ ID NO:1020), Ceres CLONE ID no.936084 (SEQ ID NO:1055), Ceres CLONE ID no.1792501 (SEQ ID NO:1066), Ceres ANNOT ID no.1437875 (SEQ ID NO:1068), Public GI ID no.1853968 (SEQ ID NO:1093), Public GI ID no.27530032 (SEQ ID NO:1094), Ceres CLONE ID no.1834483 (SEQ ID NO:1110), Public GI ID no.84579418 (SEQ ID NO:1113), Public GI ID no.15077030 (SEQ ID NO:1117), and Public GI ID no.13752458 (SEQ ID NO:1118). Other functional homologs of SEQ ID NO:1012 include Public GI ID no.147865685 (SEQ ID NO:1013), Public GI ID no.119503368 (SEQ ID NO:1014), Public GI ID no.72161874 (SEQ ID NO:1015), Public GI ID no.91780661 (SEQ ID NO:1016), Ceres ANNOT ID no.835908 (SEQ ID NO:1022), Public GI ID no.38326750 (SEQ ID NO:1023), Ceres CLONE ID no.1939396 (SEQ ID NO:1025), Ceres CLONE ID no.403637 (SEQ ID NO:1027), Public GI ID no.42539907 (SEQ ID NO:1028), Ceres CLONE ID no.1836494 (SEQ ID NO:1030), Public GI ID no.15192945 (SEQ ID NO:1031), Ceres CLONE ID no.1607947 (SEQ ID NO:1033), Ceres CLONE ID no.115880 (SEQ ID NO:1035), Ceres CLONE ID no.1074009 (SEQ ID NO:1037), Ceres CLONE ID no.476073 (SEQ ID NO:1039), Ceres CLONE ID no.554053 (SEQ

ID NO:1041), Ceres CLONE ID no.391449 (SEQ ID NO:1045), Ceres CLONE ID no.1846400 (SEQ ID NO:1048), Ceres ANNOT ID no.1475185 (SEQ ID NO:1050), Public GI ID no.115457148 (SEQ ID NO:1051), Ceres ANNOT ID no.1454960 (SEQ ID NO:1053), Public GI ID no.50346893 (SEQ ID NO:1056), Ceres CLONE ID

5 no.1931526 (SEQ ID NO:1058), Ceres ANNOT ID no.1454260 (SEQ ID NO:1061), Public GI ID no.115456131 (SEQ ID NO:1062), Ceres CLONE ID no.159151 (SEQ ID NO:1064), Ceres CLONE ID no.1842801 (SEQ ID NO:1071), Ceres CLONE ID no.533030 (SEQ ID NO:1073), Ceres CLONE ID no.1931881 (SEQ ID NO:1075), Ceres ANNOT ID no.1480006 (SEQ ID NO:1077), Ceres CLONE ID no.1895007

10 (SEQ ID NO:1079), Public GI ID no.3598863 (SEQ ID NO:1080), Ceres ANNOT ID no.1471735 (SEQ ID NO:1082), Ceres CLONE ID no.1937530 (SEQ ID NO:1084), Ceres CLONE ID no.1833050 (SEQ ID NO:1086), Ceres CLONE ID no.644213 (SEQ ID NO:1088), Ceres CLONE ID no.568154 (SEQ ID NO:1090), Ceres CLONE ID no.527598 (SEQ ID NO:1092), Ceres ANNOT ID no.1487614 (SEQ ID

15 NO:1096), Ceres ANNOT ID no.1541881 (SEQ ID NO:1098), Ceres ANNOT ID no.1488465 (SEQ ID NO:1100), Ceres ANNOT ID no.1488468 (SEQ ID NO:1102), Ceres ANNOT ID no.1541884 (SEQ ID NO:1104), Ceres ANNOT ID no.1454972 (SEQ ID NO:1106), Ceres ANNOT ID no.1475186 (SEQ ID NO:1108), Ceres CLONE ID no.686198 (SEQ ID NO:1112), Public GI ID no.84579420 (SEQ ID

20 NO:1114), Ceres CLONE ID no.605144 (SEQ ID NO:1116), Public GI ID no.15077028 (SEQ ID NO:1119), Ceres ANNOT ID no.1454963 (SEQ ID NO:1121), Ceres ANNOT ID no.6030208 (SEQ ID NO:1123), and Ceres ANNOT ID no.6076767 (SEQ ID NO:1125). In some cases, a functional homolog of SEQ ID

NO:1012 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%,

25 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1012.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1129 are provided in Figure 9 and in the sequence listing. Such functional homologs include Public GI ID no.72255610 (SEQ ID NO:933),

30 Ceres SEEDLINE ID no.ME20095 (SEQ ID NO:1129), Ceres CLONE ID no.1562633 (SEQ ID NO:1140), Ceres ANNOT ID no.1692728 (SEQ ID NO:1142), Ceres CLONE ID no.921110 (SEQ ID NO:1144), Ceres CLONE ID no.1791180 (SEQ ID NO:1146), Ceres CLONE ID no.527891 (SEQ ID NO:1148), Ceres ANNOT ID no.1522414 (SEQ ID NO:1150), and Public GI ID no.51458330 (SEQ ID

NO:1182). Other functional homologs of SEQ ID NO:1129 include Public GI ID no.18399940 (SEQ ID NO:63), Ceres ANNOT ID no.6107929 (SEQ ID NO:73), Ceres ANNOT ID no.1473094 (SEQ ID NO:96), Ceres ANNOT ID no.1503955 (SEQ ID NO:127), Ceres ANNOT ID no.1526501 (SEQ ID NO:139), Public GI ID

5 no.15235713 (SEQ ID NO:179), Public GI ID no.15234552 (SEQ ID NO:180), Ceres ANNOT ID no.1520801 (SEQ ID NO:209), Ceres ANNOT ID no.1443434 (SEQ ID NO:467), Public GI ID no.30696058 (SEQ ID NO:559), Ceres ANNOT ID no.1509601 (SEQ ID NO:648), Ceres ANNOT ID no.1451912 (SEQ ID NO:726), Ceres ANNOT ID no.6017545 (SEQ ID NO:741), Ceres ANNOT ID no.1504999

10 (SEQ ID NO:765), Ceres ANNOT ID no.1456402 (SEQ ID NO:773), Ceres ANNOT ID no.1496359 (SEQ ID NO:781), Ceres ANNOT ID no.1447260 (SEQ ID NO:842), Ceres ANNOT ID no.1469023 (SEQ ID NO:861), Ceres ANNOT ID no.1474186 (SEQ ID NO:865), Ceres ANNOT ID no.1527596 (SEQ ID NO:867), Ceres CLONE ID no.1919624 (SEQ ID NO:896), Ceres CLONE ID no.677797 (SEQ ID NO:916),

15 Public GI ID no.7960729 (SEQ ID NO:932), Ceres CLONE ID no.941845 (SEQ ID NO:1043), Public GI ID no.30683008 (SEQ ID NO:1046), Public GI ID no.42568786 (SEQ ID NO:1059), Ceres CLONE ID no.255364 (SEQ ID NO:1069), Public GI ID no.147771549 (SEQ ID NO:1130), Public GI ID no.144924741 (SEQ ID NO:1131), Public GI ID no.121594508 (SEQ ID NO:1132), Public GI ID no.91202290 (SEQ ID

20 NO:1133), Public GI ID no.89900939 (SEQ ID NO:1134), Public GI ID no.77917672 (SEQ ID NO:1135), Public GI ID no.77165252 (SEQ ID NO:1136), Public GI ID no.115375374 (SEQ ID NO:1137), Public GI ID no.110602449 (SEQ ID NO:1138), Public GI ID no.125540573 (SEQ ID NO:1151), Public GI ID no.125561519 (SEQ ID NO:1152), Public GI ID no.125528345 (SEQ ID NO:1153), Public GI ID

25 no.116310408 (SEQ ID NO:1154), Public GI ID no.115483332 (SEQ ID NO:1156), Public GI ID no.125575640 (SEQ ID NO:1157), Public GI ID no.115476368 (SEQ ID NO:1158), Public GI ID no.115478841 (SEQ ID NO:1159), Public GI ID no.115467158 (SEQ ID NO:1160), Public GI ID no.72384477 (SEQ ID NO:1161), Public GI ID no.116054703 (SEQ ID NO:1162), Ceres CLONE ID no.1786317 (SEQ

30 ID NO:1164), Ceres CLONE ID no.1791336 (SEQ ID NO:1166), Ceres CLONE ID no.1877752 (SEQ ID NO:1168), Ceres CLONE ID no.1821191 (SEQ ID NO:1170), Ceres CLONE ID no.446838 (SEQ ID NO:1172), Ceres CLONE ID no.1556915 (SEQ ID NO:1174), Public GI ID no.90200725 (SEQ ID NO:1175), Ceres CLONE ID no.1580247 (SEQ ID NO:1177), Ceres CLONE ID no.644201 (SEQ ID

NO:1179), Ceres CLONE ID no.538689 (SEQ ID NO:1181), Ceres CLONE ID no.817225 (SEQ ID NO:1184), and Ceres CLONE ID no.923842 (SEQ ID NO:1186).

In some cases, a functional homolog of SEQ ID NO:1129 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%,

5 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1129.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:60 are provided in Figure 10 and in the sequence listing.

Such functional homologs include Ceres CLONE ID no.872030 (SEQ ID NO:62),
 10 Ceres CLONE ID no.100029223 (SEQ ID NO:74), Ceres CLONE ID no.1939845 (SEQ ID NO:98), Ceres CLONE ID no.2015383 (SEQ ID NO:102), Ceres CLONE ID no.1607893 (SEQ ID NO:104), Ceres CLONE ID no.1075133 (SEQ ID NO:152), and Ceres CLONE ID no.1218065 (SEQ ID NO:915). Other functional homologs of SEQ ID NO:60 include Public GI ID no.15227919 (SEQ ID NO:64), Public GI ID
 15 no.9843641 (SEQ ID NO:65), Public GI ID no.124294789 (SEQ ID NO:66), Public GI ID no.15233446 (SEQ ID NO:67), Public GI ID no.115477679 (SEQ ID NO:68), Public GI ID no.42407552 (SEQ ID NO:69), Public GI ID no.125562450 (SEQ ID NO:70), Public GI ID no.115469980 (SEQ ID NO:71), Ceres ANNOT ID no.1442539 (SEQ ID NO:76), Ceres ANNOT ID no.1442538 (SEQ ID NO:78), Ceres
 20 ANNOT ID no.1460661 (SEQ ID NO:80), Ceres ANNOT ID no.1452884 (SEQ ID NO:82), Ceres ANNOT ID no.1450523 (SEQ ID NO:84), Ceres ANNOT ID no.1442257 (SEQ ID NO:86), Ceres ANNOT ID no.1541121 (SEQ ID NO:88), Ceres ANNOT ID no.1480481 (SEQ ID NO:90), Ceres ANNOT ID no.1487713 (SEQ ID NO:92), Ceres ANNOT ID no.1456204 (SEQ ID NO:94), Ceres CLONE ID
 25 no.1387402 (SEQ ID NO:100), Ceres CLONE ID no.972919 (SEQ ID NO:106), Ceres CLONE ID no.1645860 (SEQ ID NO:108), Ceres CLONE ID no.1042804 (SEQ ID NO:110), Ceres CLONE ID no.1606678 (SEQ ID NO:112), Ceres CLONE ID no.684496 (SEQ ID NO:114), Ceres CLONE ID no.1062366 (SEQ ID NO:116), Ceres CLONE ID no.1722931 (SEQ ID NO:118), Ceres CLONE ID no.746169 (SEQ
 30 ID NO:120), Ceres CLONE ID no.1050475 (SEQ ID NO:122), Ceres CLONE ID no.1728904 (SEQ ID NO:124), Ceres CLONE ID no.1698538 (SEQ ID NO:126), Ceres CLONE ID no.1762328 (SEQ ID NO:130), Ceres CLONE ID no.1590072 (SEQ ID NO:132), Ceres CLONE ID no.471593 (SEQ ID NO:134), Ceres CLONE ID no.1031667 (SEQ ID NO:136), Ceres CLONE ID no.1826085 (SEQ ID NO:138),

Ceres CLONE ID no.373932 (SEQ ID NO:142), Ceres CLONE ID no.1797836 (SEQ ID NO:144), Ceres CLONE ID no.1102774 (SEQ ID NO:146), Ceres CLONE ID no.842287 (SEQ ID NO:148), Ceres CLONE ID no.568205 (SEQ ID NO:150), Ceres ANNOT ID no.6108997 (SEQ ID NO:154), Ceres ANNOT ID no.6023609 (SEQ ID NO:156), and Ceres ANNOT ID no.6017906 (SEQ ID NO:158). In some cases, a functional homolog of SEQ ID NO:60 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:60.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:364 are provided in Figure 11 and in the sequence listing. Such functional homologs include Ceres ANNOT ID no.1455221 (SEQ ID NO:407), Public GI ID no.729774 (SEQ ID NO:408), Ceres CLONE ID no.1414288 (SEQ ID NO:410), Public GI ID no.115482048 (SEQ ID NO:413), and Public GI ID no.56117815 (SEQ ID NO:421). Other functional homologs of SEQ ID NO:364 include Ceres ANNOT ID no.1485538 (SEQ ID NO:366), Ceres ANNOT ID no.1538505 (SEQ ID NO:368), Public GI ID no.8347238 (SEQ ID NO:369), Public GI ID no.125542955 (SEQ ID NO:370), Public GI ID no.115446219 (SEQ ID NO:371), Ceres CLONE ID no.1597127 (SEQ ID NO:373), Ceres CLONE ID no.1584568 (SEQ ID NO:375), Ceres CLONE ID no.286056 (SEQ ID NO:377), Ceres ANNOT ID no.1543432 (SEQ ID NO:379), Ceres CLONE ID no.1728062 (SEQ ID NO:381), Ceres ANNOT ID no.1448950 (SEQ ID NO:383), Ceres CLONE ID no.771500 (SEQ ID NO:385), Ceres ANNOT ID no.1485096 (SEQ ID NO:387), Ceres CLONE ID no.1646104 (SEQ ID NO:389), Public GI ID no.111184724 (SEQ ID NO:390), Ceres CLONE ID no.1362475 (SEQ ID NO:392), Ceres CLONE ID no.597906 (SEQ ID NO:394), Ceres CLONE ID no.615781 (SEQ ID NO:396), Ceres CLONE ID no.538713 (SEQ ID NO:398), Ceres CLONE ID no.1794141 (SEQ ID NO:400), Public GI ID no.5821138 (SEQ ID NO:401), Public GI ID no.886742 (SEQ ID NO:402), Ceres CLONE ID no.1814498 (SEQ ID NO:404), Public GI ID no.7158882 (SEQ ID NO:405), Ceres ANNOT ID no.1452564 (SEQ ID NO:412), Public GI ID no.125557431 (SEQ ID NO:414), Ceres ANNOT ID no.1442880 (SEQ ID NO:416), Ceres ANNOT ID no.1463437 (SEQ ID NO:418), Public GI ID no.42415865 (SEQ ID NO:419), Public GI ID no.33087081 (SEQ ID NO:420), Public GI ID no.115521217 (SEQ ID NO:422), Public GI ID no.115521211 (SEQ ID

NO:423), Public GI ID no.115521215 (SEQ ID NO:424), Ceres ANNOT ID no.1454376 (SEQ ID NO:426), Ceres CLONE ID no.835571 (SEQ ID NO:428), Ceres ANNOT ID no.1500046 (SEQ ID NO:430), Public GI ID no.110738569 (SEQ ID NO:431), Public GI ID no.125542510 (SEQ ID NO:432), Public GI ID
5 no.30686034 (SEQ ID NO:433), Public GI ID no.125570883 (SEQ ID NO:434), Public GI ID no.42562463 (SEQ ID NO:435), Ceres CLONE ID no.100043265 (SEQ ID NO:436), Ceres ANNOT ID no.6089790 (SEQ ID NO:438), and Ceres ANNOT ID no.6043635 (SEQ ID NO:440). In some cases, a functional homolog of SEQ ID NO:364 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%,
10 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:364.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:311 are provided in Figure 12 and in the sequence listing. Such functional homologs include Ceres ANNOT ID no.1538958 (SEQ ID NO:319),
15 Public GI ID no.115521213 (SEQ ID NO:320), Public GI ID no.42415865 (SEQ ID NO:321), Public GI ID no.729775 (SEQ ID NO:322), Public GI ID no.11386827 (SEQ ID NO:323), Public GI ID no.115456675 (SEQ ID NO:326), and Public GI ID no.89274218 (SEQ ID NO:335). Other functional homologs of SEQ ID NO:311 include Public GI ID no.125546035 (SEQ ID NO:312), Ceres CLONE ID no.125228
20 (SEQ ID NO:314), Public GI ID no.115465055 (SEQ ID NO:315), Public GI ID no.125553080 (SEQ ID NO:316), Public GI ID no.8920606 (SEQ ID NO:317), Ceres CLONE ID no.1919643 (SEQ ID NO:325), Public GI ID no.429155 (SEQ ID NO:327), Ceres CLONE ID no.1194199 (SEQ ID NO:329), Public GI ID no.15236631 (SEQ ID NO:330), Ceres ANNOT ID no.1523420 (SEQ ID NO:332),
25 Ceres ANNOT ID no.1447046 (SEQ ID NO:334), Public GI ID no.25296101 (SEQ ID NO:336), Public GI ID no.15228440 (SEQ ID NO:337), Public GI ID no.6624612 (SEQ ID NO:338), Public GI ID no.125588688 (SEQ ID NO:339), Public GI ID no.115470859 (SEQ ID NO:340), Public GI ID no.15228865 (SEQ ID NO:341), Ceres CLONE ID no.1571069 (SEQ ID NO:343), Public GI ID no.115455903 (SEQ
30 ID NO:344), Ceres ANNOT ID no.1459422 (SEQ ID NO:346), Ceres CLONE ID no.1577511 (SEQ ID NO:348), Public GI ID no.115451657 (SEQ ID NO:349), Public GI ID no.15225255 (SEQ ID NO:350), Public GI ID no.125545695 (SEQ ID NO:351), Ceres ANNOT ID no.1471817 (SEQ ID NO:353), Ceres ANNOT ID no.1440896 (SEQ ID NO:355), Public GI ID no.119393868 (SEQ ID NO:356), Ceres

ANNOT ID no.1517025 (SEQ ID NO:358), Ceres ANNOT ID no.1512410 (SEQ ID NO:360), and Ceres ANNOT ID no.6035498 (SEQ ID NO:362). In some cases, a functional homolog of SEQ ID NO:311 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%,
 5 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:311.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:160 are provided in Figure 13 and in the sequence listing. Such functional homologs include Ceres CLONE ID no.1837065 (SEQ ID NO:162),
 10 Ceres ANNOT ID no.1531178 (SEQ ID NO:184), Ceres CLONE ID no.470694 (SEQ ID NO:242), Public GI ID no.92867368 (SEQ ID NO:253), Ceres CLONE ID no.859707 (SEQ ID NO:256), Ceres CLONE ID no.392275 (SEQ ID NO:268), Ceres CLONE ID no.1828394 (SEQ ID NO:282), and Public GI ID no.115466694 (SEQ ID NO:294). Other functional homologs of SEQ ID NO:160 include Ceres CLONE ID
 15 no.1895763 (SEQ ID NO:164), Ceres CLONE ID no.1850460 (SEQ ID NO:166), Ceres CLONE ID no.1808074 (SEQ ID NO:168), Ceres CLONE ID no.1832882 (SEQ ID NO:170), Ceres CLONE ID no.1978977 (SEQ ID NO:172), Ceres CLONE ID no.1918742 (SEQ ID NO:174), Ceres CLONE ID no.1940023 (SEQ ID NO:176), Ceres CLONE ID no.1923495 (SEQ ID NO:178), Ceres CLONE ID no.1851388
 20 (SEQ ID NO:182), Ceres ANNOT ID no.1477681 (SEQ ID NO:186), Ceres ANNOT ID no.1508800 (SEQ ID NO:188), Ceres ANNOT ID no.1455597 (SEQ ID NO:190), Ceres ANNOT ID no.1532016 (SEQ ID NO:192), Ceres ANNOT ID no.1478526 (SEQ ID NO:194), Ceres ANNOT ID no.1492567 (SEQ ID NO:196), Ceres ANNOT ID no.1515273 (SEQ ID NO:198), Ceres ANNOT ID no.1461979 (SEQ ID NO:200),
 25 Ceres ANNOT ID no.1439702 (SEQ ID NO:202), Ceres ANNOT ID no.1448044 (SEQ ID NO:204), Ceres ANNOT ID no.1483370 (SEQ ID NO:206), Ceres ANNOT ID no.1445651 (SEQ ID NO:208), Ceres ANNOT ID no.1490863 (SEQ ID NO:212), Ceres ANNOT ID no.1501043 (SEQ ID NO:214), Ceres ANNOT ID no.1527507 (SEQ ID NO:216), Ceres ANNOT ID no.1498633 (SEQ ID NO:218), Ceres ANNOT
 30 ID no.1465403 (SEQ ID NO:220), Ceres ANNOT ID no.1510956 (SEQ ID NO:222), Ceres ANNOT ID no.1457735 (SEQ ID NO:224), Public GI ID no.15224711 (SEQ ID NO:225), Ceres CLONE ID no.40062 (SEQ ID NO:228), Public GI ID no.15220315 (SEQ ID NO:229), Ceres CLONE ID no.36480 (SEQ ID NO:231), Ceres CLONE ID no.2443 (SEQ ID NO:233), Public GI ID no.30685375 (SEQ ID

NO:234), Public GI ID no.126009434 (SEQ ID NO:235), Ceres CLONE ID no.965753 (SEQ ID NO:237), Ceres CLONE ID no.948834 (SEQ ID NO:239), Public GI ID no.33347409 (SEQ ID NO:240), Ceres CLONE ID no.643614 (SEQ ID NO:244), Ceres CLONE ID no.1049362 (SEQ ID NO:246), Ceres CLONE ID no.546675 (SEQ ID NO:248), Ceres CLONE ID no.522046 (SEQ ID NO:250), Ceres CLONE ID no.651076 (SEQ ID NO:252), Public GI ID no.92897590 (SEQ ID NO:254), Ceres CLONE ID no.634176 (SEQ ID NO:258), Ceres CLONE ID no.1041432 (SEQ ID NO:260), Ceres CLONE ID no.1065203 (SEQ ID NO:262), Ceres CLONE ID no.555361 (SEQ ID NO:264), Ceres CLONE ID no.704227 (SEQ ID NO:266), Ceres CLONE ID no.100819945 (SEQ ID NO:269), Ceres CLONE ID no.282584 (SEQ ID NO:271), Ceres CLONE ID no.1448469 (SEQ ID NO:273), Ceres CLONE ID no.241246 (SEQ ID NO:275), Ceres CLONE ID no.234443 (SEQ ID NO:277), Ceres CLONE ID no.293549 (SEQ ID NO:279), Public GI ID no.109450926 (SEQ ID NO:280), Ceres CLONE ID no.1803923 (SEQ ID NO:284), Ceres CLONE ID no.2024557 (SEQ ID NO:286), Ceres CLONE ID no.1820364 (SEQ ID NO:288), Public GI ID no.125554274 (SEQ ID NO:289), Public GI ID no.125531165 (SEQ ID NO:290), Public GI ID no.125541514 (SEQ ID NO:291), Public GI ID no.125557559 (SEQ ID NO:292), Public GI ID no.125557844 (SEQ ID NO:293), Public GI ID no.115449295 (SEQ ID NO:295), Public GI ID no.115481182 (SEQ ID NO:296), Public GI ID no.20177639 (SEQ ID NO:297), Public GI ID no.115471021 (SEQ ID NO:298), Public GI ID no.115456011 (SEQ ID NO:299), Public GI ID no.125588290 (SEQ ID NO:300), Public GI ID no.115477799 (SEQ ID NO:301), Public GI ID no.115471385 (SEQ ID NO:302), Public GI ID no.125599705 (SEQ ID NO:303), Public GI ID no.115489810 (SEQ ID NO:304), Public GI ID no.55276718 (SEQ ID NO:305), Ceres ANNOT ID no.6025568 (SEQ ID NO:307), and Ceres ANNOT ID no.6091128 (SEQ ID NO:309). In some cases, a functional homolog of SEQ ID NO:160 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:160.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:2 are provided in Figure 14 and in the sequence listing. Such functional homologs include Public GI ID no.115470807 (SEQ ID NO:5), Ceres CLONE ID no.1842931 (SEQ ID NO:15), Ceres CLONE ID no.321308 (SEQ ID

NO:17), Ceres CLONE ID no.1725811 (SEQ ID NO:19), Ceres CLONE ID no.1357455 (SEQ ID NO:21), Ceres CLONE ID no.943370 (SEQ ID NO:23), Ceres CLONE ID no.1327712 (SEQ ID NO:25), Ceres CLONE ID no.1764692 (SEQ ID NO:27), and Ceres ANNOT ID no.1512656 (SEQ ID NO:41). Other functional

5 homologs of SEQ ID NO:2 include Public GI ID no.18403425 (SEQ ID NO:3), Public GI ID no.11994285 (SEQ ID NO:4), Public GI ID no.108706298 (SEQ ID NO:6), Public GI ID no.15233585 (SEQ ID NO:7), Public GI ID no.125599279 (SEQ ID NO:8), Public GI ID no.115450865 (SEQ ID NO:9), Public GI ID no.22773244 (SEQ ID NO:10), Public GI ID no.92874749 (SEQ ID NO:11), Ceres CLONE ID

10 no.1857034 (SEQ ID NO:13), Ceres CLONE ID no.1059300 (SEQ ID NO:29), Ceres CLONE ID no.1804869 (SEQ ID NO:31), Ceres CLONE ID no.378863 (SEQ ID NO:33), Ceres CLONE ID no.1930271 (SEQ ID NO:35), Ceres CLONE ID no.2034728 (SEQ ID NO:37), Ceres CLONE ID no.1866421 (SEQ ID NO:39), Ceres ANNOT ID no.1463492 (SEQ ID NO:43), Ceres ANNOT ID no.1459391 (SEQ ID NO:45), Ceres ANNOT ID no.1442920 (SEQ ID NO:47), Ceres ANNOT ID

15 no.6011447 (SEQ ID NO:49), Ceres ANNOT ID no.6068218 (SEQ ID NO:51), Ceres ANNOT ID no.6044121 (SEQ ID NO:53), and Ceres ANNOT ID no.6100755 (SEQ ID NO:55). In some cases, a functional homolog of SEQ ID NO:2 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%,

20 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:2.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:749 are provided in Figure 15 and in the sequence listing. Such functional homologs include Ceres CLONE ID no.1847516 (SEQ ID NO:1195),

25 Ceres CLONE ID no.1961986 (SEQ ID NO:1201), and Ceres ANNOT ID no.6091930 (SEQ ID NO:1207). Other functional homologs of SEQ ID NO:749 include Ceres CLONE ID no.2025938 (SEQ ID NO:885), Ceres CLONE ID no.1821214 (SEQ ID NO:1189), Ceres CLONE ID no.1040399 (SEQ ID NO:1191), Ceres CLONE ID no.1093691 (SEQ ID NO:1193), Ceres CLONE ID no.974539

30 (SEQ ID NO:1197), Ceres CLONE ID no.1832340 (SEQ ID NO:1199), Ceres CLONE ID no.1933211 (SEQ ID NO:1203), Ceres CLONE ID no.997558 (SEQ ID NO:1205), Ceres ANNOT ID no.6041596 (SEQ ID NO:1209), Public GI ID no.125564176 (SEQ ID NO:1210), Ceres CLONE ID no.1836064 (SEQ ID NO:1212), Ceres CLONE ID no.1909693 (SEQ ID NO:1214), Public GI ID

no.40287480 (SEQ ID NO:1216), Ceres CLONE ID no.1765346 (SEQ ID NO:1218), Public GI ID no.125546008 (SEQ ID NO:1219), Ceres CLONE ID no.1950900 (SEQ ID NO:1221), Public GI ID no.41350259 (SEQ ID NO:1222), Public GI ID no.125588210 (SEQ ID NO:1223), Ceres CLONE ID no.1954395 (SEQ ID NO:1225), Public GI ID no.18403408 (SEQ ID NO:1226), Ceres CLONE ID no.2010121 (SEQ ID NO:1228), Ceres ANNOT ID no.6011486 (SEQ ID NO:1230), Public GI ID no.25082726 (SEQ ID NO:1231), Public GI ID no.113196593 (SEQ ID NO:1232), Ceres CLONE ID no.1843021 (SEQ ID NO:1234), Ceres CLONE ID no.1931194 (SEQ ID NO:1236), Ceres CLONE ID no.1652996 (SEQ ID NO:1238), Ceres CLONE ID no.1930044 (SEQ ID NO:1240), Ceres CLONE ID no.24255 (SEQ ID NO:1242), Ceres ANNOT ID no.6034955 (SEQ ID NO:1244), Ceres ANNOT ID no.6119444 (SEQ ID NO:1246), Ceres ANNOT ID no.6063956 (SEQ ID NO:1248), Ceres ANNOT ID no.6015461 (SEQ ID NO:1250), Ceres CLONE ID no.696244 (SEQ ID NO:1252), Ceres ANNOT ID no.1468973 (SEQ ID NO:1254), Ceres CLONE ID no.2019529 (SEQ ID NO:1256), and Ceres CLONE ID no.1492169 (SEQ ID NO:1258). In some cases, a functional homolog of SEQ ID NO:749 has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:749.

Examples of amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1311 are provided in Figure 16 and in the sequence listing. Such functional homologs include CeresClone:971761 (SEQ ID NO: 1313), CeresClone:1946574 (SEQ ID NO: 1331), CeresClone:2055551 (SEQ ID NO: 1340), CeresClone:100045499 (SEQ ID NO: 1347), CeresClone:1465853 (SEQ ID NO: 1353), CeresClone:753982 (SEQ ID NO: 1360), CeresClone:1076093 (SEQ ID NO: 1315), CeresClone:1627875 (SEQ ID NO: 1317), CeresAnnot:1508362 (SEQ ID NO: 1319), CeresAnnot:1526950 (SEQ ID NO: 1321), CeresClone:1832333 (SEQ ID NO: 1323), GI:74272607 (SEQ ID NO: 1324), GI:192910782 (SEQ ID NO: 1325), GI:157342563 (SEQ ID NO: 1326), GI:159483497 (SEQ ID NO: 1327), CeresClone:1839999 (SEQ ID NO: 1329), CeresClone:467335 (SEQ ID NO: 1333), GI:168010087 (SEQ ID NO: 1334), CeresClone:1728202 (SEQ ID NO: 1336), CeresClone:1994239 (SEQ ID NO: 1338), CeresAnnot:8704704 (SEQ ID NO: 1342), GI:115453877 (SEQ ID NO: 1343), CeresClone:1646411 (SEQ ID NO: 1345), CeresClone:100920260 (SEQ ID NO: 1349), GI:116786147 (SEQ ID NO: 1350),

GI:116783944 (SEQ ID NO: 1351), GI:82623397 (SEQ ID NO: 1354),
 CeresAnnot:8656662 (SEQ ID NO: 1356), CeresClone:1417803 (SEQ ID NO: 1358),
 and GI:145345927 (SEQ ID NO: 1361). In some cases, a functional homolog of SEQ
 ID NO:1311 has an amino acid sequence with at least 40% sequence identity, *e.g.*,
 5 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or
 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1311.

The identification of conserved regions in a heat and/or drought-tolerance
 polypeptide facilitates production of variants of heat and/or drought-tolerance
 polypeptides. Variants of heat and/or drought-tolerance polypeptides typically have
 10 10 or fewer conservative amino acid substitutions within the primary amino acid
 sequence, *e.g.*, 7 or fewer conservative amino acid substitutions, 5 or fewer
 conservative amino acid substitutions, or between 1 and 5 conservative substitutions.
 A useful variant polypeptide can be constructed based on one of the alignments set
 forth in Figures 1-16. Such a polypeptide includes the conserved regions, arranged in
 15 the order depicted in the Figure from amino-terminal end to carboxy-terminal end.
 Such a polypeptide may also include zero, one, or more than one amino acid in
 positions marked by dashes. When no amino acids are present at positions marked by
 dashes, the length of such a polypeptide is the sum of the amino acid residues in all
 conserved regions. When amino acids are present at all positions marked by dashes,
 20 such a polypeptide has a length that is the sum of the amino acid residues in all
 conserved regions and all dashes.

C. Functional Homologs Identified by HMMER

In some embodiments, useful heat and/or drought-tolerance polypeptides
 include those that fit a Hidden Markov Model based on the polypeptides set forth in
 25 any one of Figures 1-16. A Hidden Markov Model (HMM) is a statistical model of a
 consensus sequence for a group of functional homologs. See, Durbin et al.,
Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids,
 Cambridge University Press, Cambridge, UK (1998). An HMM is generated by the
 program HMMER 2.3.2 with default program parameters, using the sequences of the
 group of functional homologs as input. The multiple sequence alignment is generated
 30 by ProbCons (Do et al., *Genome Res.*, 15(2):330-40 (2005)) version 1.11 using a set
 of default parameters: -c, --consistency REPS of 2; -ir, --iterative-refinement REPS
 of 100; -pre, --pre-training REPS of 0. ProbCons is a public domain software
 program provided by Stanford University.

The default parameters for building an HMM (hmmbuild) are as follows: the default “architecture prior” (archpri) used by MAP architecture construction is 0.85, and the default cutoff threshold (idlevel) used to determine the effective sequence number is 0.62. HMMER 2.3.2 was released October 3, 2003 under a GNU general
 5 public license, and is available from various sources on the World Wide Web such as hmmer.janelia.org; hmmer.wustl.edu; and fr.com/hmmer232/. Hmmbuild outputs the model as a text file.

The HMM for a group of functional homologs can be used to determine the likelihood that a candidate heat and/or drought-tolerance polypeptide sequence is a
 10 better fit to that particular HMM than to a null HMM generated using a group of sequences that are not structurally or functionally related. The likelihood that a candidate polypeptide sequence is a better fit to an HMM than to a null HMM is indicated by the HMM bit score, a number generated when the candidate sequence is fitted to the HMM profile using the HMMER hmmsearch program. The following
 15 default parameters are used when running hmmsearch: the default E-value cutoff (E) is 10., the default bit score cutoff (T) is negative infinity, the default number of sequences in a database (Z) is the real number of sequences in the database, the default E-value cutoff for the per-domain ranked hit list (domE) is infinity, and the default bit score cutoff for the per-domain ranked hit list (domT) is negative infinity.
 20 A high HMM bit score indicates a greater likelihood that the candidate sequence carries out one or more of the biochemical or physiological function(s) of the polypeptides used to generate the HMM. A high HMM bit score is at least 20, and often is higher. Slight variations in the HMM bit score of a particular sequence can occur due to factors such as the order in which sequences are processed for alignment
 25 by multiple sequence alignment algorithms such as the ProbCons program. Nevertheless, such HMM bit score variation is minor.

The heat and/or drought-tolerance polypeptides discussed below fit the indicated HMM with an HMM bit score greater than 20 (e.g., greater than 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, or 500). In some embodiments, the HMM bit
 30 score of a heat and/or drought-tolerance polypeptide discussed below is about 50%, 60%, 70%, 80%, 90%, or 95% of the HMM bit score of a functional homolog provided in Sequence Listing. In some embodiments, a heat and/or drought-tolerance polypeptide discussed below fits the indicated HMM with an HMM bit score greater than 20, and has a domain indicative of a heat and/or drought-tolerance polypeptide.

In some embodiments, a heat and/or drought-tolerance polypeptide discussed below fits the indicated HMM with an HMM bit score greater than 20, and has 70% or greater sequence identity (e.g., 75%, 80%, 85%, 90%, 95%, or 100% sequence identity) to an amino acid sequence shown in any one of Figures 1-16.

5 Polypeptides are shown in the sequence listing that have HMM bit scores greater than 270 when fitted to an HMM generated from the amino acid sequences set forth in Figure 1. Such polypeptides include Ceres SEEDLINE ID no.ME00029 (SEQ ID NO:442), Public GI ID no.72384401 (SEQ ID NO:443), Ceres CLONE ID no.1079382 (SEQ ID NO:445), Ceres CLONE ID no.1853461 (SEQ ID NO:447),
 10 Ceres CLONE ID no.1626485 (SEQ ID NO:451), Ceres CLONE ID no.1713920 (SEQ ID NO:459), Ceres CLONE ID no.1772747 (SEQ ID NO:463), Ceres CLONE ID no.225960 (SEQ ID NO:465), Public GI ID no.115443807 (SEQ ID NO:470), Ceres CLONE ID no.569388 (SEQ ID NO:483), Ceres CLONE ID no.1915549 (SEQ ID NO:449), Ceres CLONE ID no.529871 (SEQ ID NO:453), Ceres CLONE ID
 15 no.1067079 (SEQ ID NO:455), Ceres CLONE ID no.1079572 (SEQ ID NO:457), Ceres ANNOT ID no.1456550 (SEQ ID NO:461), Ceres CLONE ID no.1437889 (SEQ ID NO:469), Ceres CLONE ID no.2014249 (SEQ ID NO:472), Ceres CLONE ID no.2033133 (SEQ ID NO:474), Ceres CLONE ID no.707404 (SEQ ID NO:476), Ceres CLONE ID no.1770680 (SEQ ID NO:478), Ceres ANNOT ID no.1450989
 20 (SEQ ID NO:480), Public GI ID no.72384445 (SEQ ID NO:481), Ceres CLONE ID no.1059299 (SEQ ID NO:485), and Ceres ANNOT ID no.6008086 (SEQ ID NO:487).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 100 when fitted to an HMM generated from the amino acid sequences set forth in Figure 2. Such polypeptides include Ceres SEEDLINE ID no.ME00045
 25 (SEQ ID NO:489), Ceres CLONE ID no.571200 (SEQ ID NO:494), Ceres CLONE ID no.1928532 (SEQ ID NO:496), Ceres ANNOT ID no.1490637 (SEQ ID NO:498), Ceres CLONE ID no.295496 (SEQ ID NO:514), Public GI ID no.115463637 (SEQ ID NO:515), Ceres CLONE ID no.1999444 (SEQ ID NO:518), Public GI ID no.147844794 (SEQ ID NO:490), Public GI ID no.147842279 (SEQ ID NO:491),
 30 Public GI ID no.145355441 (SEQ ID NO:492), Ceres ANNOT ID no.1461381 (SEQ ID NO:500), Ceres ANNOT ID no.1440313 (SEQ ID NO:502), Ceres ANNOT ID no.1448275 (SEQ ID NO:504), Ceres ANNOT ID no.1437838 (SEQ ID NO:506), Ceres ANNOT ID no.1501275 (SEQ ID NO:508), Ceres CLONE ID no.1644562 (SEQ ID NO:510), Ceres CLONE ID no.1925967 (SEQ ID NO:512), Public GI ID

no.115435904 (SEQ ID NO:516), Public GI ID no.125552168 (SEQ ID NO:519),
 Public GI ID no.125594093 (SEQ ID NO:520), Ceres CLONE ID no.221188 (SEQ
 ID NO:522), Ceres ANNOT ID no.1477714 (SEQ ID NO:524), Ceres CLONE ID
 no.1787953 (SEQ ID NO:526), Ceres ANNOT ID no.1531210 (SEQ ID NO:528),
 5 Ceres CLONE ID no.521176 (SEQ ID NO:530), Public GI ID no.22327055 (SEQ ID
 NO:531), Ceres ANNOT ID no.1508824 (SEQ ID NO:533), Ceres CLONE ID
 no.38879 (SEQ ID NO:535), Public GI ID no.42569309 (SEQ ID NO:536), Ceres
 CLONE ID no.1817784 (SEQ ID NO:538), Ceres CLONE ID no.284637 (SEQ ID
 NO:540), Public GI ID no.125596251 (SEQ ID NO:541), Public GI ID no.125554300
 10 (SEQ ID NO:543), Ceres CLONE ID no.1935437 (SEQ ID NO:545), Ceres ANNOT
 ID no.1455622 (SEQ ID NO:547), Public GI ID no.55771354 (SEQ ID NO:548),
 Ceres ANNOT ID no.1514655 (SEQ ID NO:550), Ceres CLONE ID no.1848736
 (SEQ ID NO:552), Public GI ID no.125569872 (SEQ ID NO:553), Ceres CLONE ID
 no.1645078 (SEQ ID NO:555), Ceres CLONE ID no.1790573 (SEQ ID NO:557),
 15 Public GI ID no.4567251 (SEQ ID NO:558), Ceres CLONE ID no.444113 (SEQ ID
 NO:561), Public GI ID no.125525355 (SEQ ID NO:562), Ceres ANNOT ID
 no.6028854 (SEQ ID NO:564), and Ceres ANNOT ID no.6115356 (SEQ ID
 NO:566).

Polypeptides are shown in the sequence listing that have HMM bit scores
 20 greater than 150 when fitted to an HMM generated from the amino acid sequences set
 forth in Figure 3. Such polypeptides include Ceres SEEDLINE ID no.ME02190
 (SEQ ID NO:568), Ceres CLONE ID no.695006 (SEQ ID NO:578), Ceres ANNOT
 ID no.1527488 (SEQ ID NO:584), Public GI ID no.79318519 (SEQ ID NO:569),
 Public GI ID no.79318537 (SEQ ID NO:570), Ceres CLONE ID no.956998 (SEQ ID
 25 NO:572), Ceres CLONE ID no.978154 (SEQ ID NO:574), Ceres CLONE ID
 no.1035628 (SEQ ID NO:576), Ceres CLONE ID no.464169 (SEQ ID NO:580),
 Ceres ANNOT ID no.1474075 (SEQ ID NO:582), Ceres ANNOT ID no.1474073
 (SEQ ID NO:586), and Ceres ANNOT ID no.1527486 (SEQ ID NO:588).

Polypeptides are shown in the sequence listing that have HMM bit scores
 30 greater than 120 when fitted to an HMM generated from the amino acid sequences set
 forth in Figure 4. Such polypeptides include Ceres SEEDLINE ID no.ME02549
 (SEQ ID NO:590), Ceres ANNOT ID no.1501305 (SEQ ID NO:623), Ceres CLONE
 ID no.607280 (SEQ ID NO:627), Public GI ID no.92887174 (SEQ ID NO:632),
 Ceres CLONE ID no.1857162 (SEQ ID NO:634), Public GI ID no.115477272 (SEQ

ID NO:674), Ceres CLONE ID no.264002 (SEQ ID NO:682), Public GI ID no.147822456 (SEQ ID NO:591), Public GI ID no.144923935 (SEQ ID NO:592), Public GI ID no.140038730 (SEQ ID NO:593), Public GI ID no.78708014 (SEQ ID NO:594), Public GI ID no.115481362 (SEQ ID NO:595), Public GI ID no.125531350 (SEQ ID NO:596), Public GI ID no.125525598 (SEQ ID NO:597), Public GI ID no.77548630 (SEQ ID NO:598), Public GI ID no.46798895 (SEQ ID NO:599), Public GI ID no.125564653 (SEQ ID NO:600), Ceres CLONE ID no.998865 (SEQ ID NO:602), Public GI ID no.125556140 (SEQ ID NO:603), Public GI ID no.125534482 (SEQ ID NO:604), Public GI ID no.125550135 (SEQ ID NO:605), Ceres CLONE ID no.639816 (SEQ ID NO:607), Public GI ID no.125562170 (SEQ ID NO:608), Ceres CLONE ID no.1797059 (SEQ ID NO:610), Ceres CLONE ID no.1031510 (SEQ ID NO:612), Ceres CLONE ID no.1973081 (SEQ ID NO:614), Public GI ID no.125561002 (SEQ ID NO:615), Public GI ID no.125541732 (SEQ ID NO:616), Public GI ID no.125560677 (SEQ ID NO:617), Public GI ID no.125559115 (SEQ ID NO:618), Public GI ID no.15809903 (SEQ ID NO:619), Public GI ID no.30681703 (SEQ ID NO:620), Public GI ID no.9759556 (SEQ ID NO:621), Ceres ANNOT ID no.1448303 (SEQ ID NO:625), Ceres ANNOT ID no.1448305 (SEQ ID NO:629), Ceres ANNOT ID no.1448307 (SEQ ID NO:631), Public GI ID no.92888243 (SEQ ID NO:635), Public GI ID no.92879395 (SEQ ID NO:636), Ceres CLONE ID no.528876 (SEQ ID NO:638), Ceres ANNOT ID no.1448352 (SEQ ID NO:640), Ceres ANNOT ID no.1437745 (SEQ ID NO:642), Ceres ANNOT ID no.1464146 (SEQ ID NO:644), Ceres ANNOT ID no.1437744 (SEQ ID NO:646), Public GI ID no.92894684 (SEQ ID NO:647), Ceres CLONE ID no.3964 (SEQ ID NO:650), Public GI ID no.13272389 (SEQ ID NO:651), Ceres ANNOT ID no.1481203 (SEQ ID NO:653), Public GI ID no.15227699 (SEQ ID NO:654), Public GI ID no.92886084 (SEQ ID NO:655), Public GI ID no.15239947 (SEQ ID NO:656), Ceres CLONE ID no.34878 (SEQ ID NO:658), Ceres CLONE ID no.150484 (SEQ ID NO:660), Public GI ID no.21553545 (SEQ ID NO:661), Public GI ID no.15222843 (SEQ ID NO:662), Public GI ID no.38230552 (SEQ ID NO:663), Public GI ID no.3420008 (SEQ ID NO:664), Public GI ID no.15230602 (SEQ ID NO:665), Public GI ID no.3420004 (SEQ ID NO:666), Public GI ID no.2129586 (SEQ ID NO:667), Public GI ID no.15217849 (SEQ ID NO:668), Public GI ID no.15227704 (SEQ ID NO:669), Ceres ANNOT ID no.1465750 (SEQ ID NO:671), Ceres CLONE ID no.1983975 (SEQ ID NO:673), Public GI ID no.15226028 (SEQ

ID NO:675), Public GI ID no.115459524 (SEQ ID NO:676), Ceres CLONE ID no.1793353 (SEQ ID NO:678), Ceres ANNOT ID no.1467399 (SEQ ID NO:680), Ceres CLONE ID no.1982930 (SEQ ID NO:684), Public GI ID no.125540700 (SEQ ID NO:685), Ceres ANNOT ID no.1448743 (SEQ ID NO:687), Public GI ID
 5 no.50251910 (SEQ ID NO:688), Ceres CLONE ID no.1836748 (SEQ ID NO:690), Public GI ID no.3420006 (SEQ ID NO:691), Public GI ID no.92879376 (SEQ ID NO:692), Ceres CLONE ID no.838941 (SEQ ID NO:694), Ceres ANNOT ID no.1437746 (SEQ ID NO:696), Ceres ANNOT ID no.6017241 (SEQ ID NO:698), Ceres ANNOT ID no.6085947 (SEQ ID NO:700), and Ceres ANNOT ID no.6017242
 10 (SEQ ID NO:702).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 55 when fitted to an HMM generated from the amino acid sequences set forth in Figure 5. Such polypeptides include Ceres SEEDLINE ID no.ME02865 (SEQ ID NO:705), Public GI ID no.79320952 (SEQ ID NO:706), Public GI ID
 15 no.79320957 (SEQ ID NO:707), Public GI ID no.6692094 (SEQ ID NO:708), and Public GI ID no.145323049 (SEQ ID NO:709).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 185 when fitted to an HMM generated from the amino acid sequences set forth in Figure 6. Such polypeptides include Ceres SEEDLINE ID no.ME03227
 20 (SEQ ID NO:711), Ceres CLONE ID no.964616 (SEQ ID NO:714), Ceres CLONE ID no.100009667 (SEQ ID NO:715), Ceres ANNOT ID no.1444568 (SEQ ID NO:719), Ceres CLONE ID no.719489 (SEQ ID NO:725), Ceres CLONE ID no.587748 (SEQ ID NO:733), Public GI ID no.125528114 (SEQ ID NO:734), Ceres CLONE ID no.274172 (SEQ ID NO:737), Public GI ID no.144923134 (SEQ ID
 25 NO:712), Ceres ANNOT ID no.1471437 (SEQ ID NO:717), Ceres CLONE ID no.1270484 (SEQ ID NO:721), Ceres CLONE ID no.1075098 (SEQ ID NO:723), Public GI ID no.18412211 (SEQ ID NO:727), Ceres CLONE ID no.20358 (SEQ ID NO:729), Ceres CLONE ID no.1915503 (SEQ ID NO:731), Public GI ID no.115440619 (SEQ ID NO:735), Public GI ID no.125572387 (SEQ ID NO:738), and
 30 Ceres ANNOT ID no.6015812 (SEQ ID NO:740).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 110 when fitted to an HMM generated from the amino acid sequences set forth in Figure 7. Such polypeptides include Ceres SEEDLINE ID no.ME04477 (SEQ ID NO:742), Ceres CLONE ID no.1620215 (SEQ ID NO: 759); Ceres CLONE

ID no.1798756 (SEQ ID NO: 763); Public GI ID no. 38016527 (SEQ ID NO: 796);
Public GI ID no. 75133829 (SEQ ID NO: 799); Ceres ANNOT ID no.1460527 (SEQ
ID NO: 801); Public GI ID no.119720772 (SEQ ID NO: 857); Ceres CLONE ID
no.708446 (SEQ ID NO: 859); Public GI ID no.92896423 (SEQ ID NO: 892); Ceres
5 CLONE ID no.1387149 (SEQ ID NO: 912); Public GI ID no.5031281 (SEQ ID NO:
953); Ceres CLONE ID no.1775820 (SEQ ID NO: 955); Public GI ID no.35187687
(SEQ ID NO: 988); Public GI ID no.115468934 (SEQ ID NO: 991); Public GI ID
no.118424243 (SEQ ID NO: 1000); Ceres ANNOT ID no.6063957 (SEQ ID NO:
1010); Public GI ID no. 113196593 (SEQ ID NO: 798); Public GI ID no.112819496
10 (SEQ ID NO: 999); Public GI ID no.147783026 (SEQ ID NO: 743); Public GI ID
no.119367488 (SEQ ID NO: 744); Public GI ID no.147860340 (SEQ ID NO: 745);
Public GI ID no.115477170 (SEQ ID NO: 757); Ceres CLONE ID no.1931889 (SEQ
ID NO: 761); Ceres CLONE ID no.1918424 (SEQ ID NO: 767); Ceres CLONE ID
no.1845154 (SEQ ID NO: 771); Ceres Clone ID no. 1084216 (SEQ ID NO:
15 797); Ceres Annot ID no. 8644540 (SEQ ID NO: 805); Ceres ANNOT ID
no.1450673 (SEQ ID NO: 807); Public GI ID no. 116778802 (SEQ ID NO: 808);
Public GI ID no. 116778893 (SEQ ID NO: 809); and Public GI ID no. 116778998
(SEQ ID NO: 810); Public GI ID no. 157849766 (SEQ ID NO: 811); Public GI ID no.
159474166 (SEQ ID NO: 812); Public GI ID no. 168036656 (SEQ ID NO: 813);
20 Ceres ANNOT ID no.1456578 (SEQ ID NO: 815); Public GI ID no. 168053490 (SEQ
ID NO: 816); Public GI ID no. 193237563 (SEQ ID NO: 817); Ceres Clone ID no.
100879386 (SEQ ID NO: 819); Ceres Clone ID no. 2055733 (SEQ ID NO: 823);
Ceres Clone ID no. 2056478 (SEQ ID NO: 825); Ceres CLONE ID no.13007 (SEQ
ID NO: 832); Ceres CLONE ID no.5522 (SEQ ID NO: 834); Ceres CLONE ID
25 no.30543 (SEQ ID NO: 836); Ceres CLONE ID no.14203 (SEQ ID NO: 839); Ceres
CLONE ID no.975913 (SEQ ID NO: 846); Ceres CLONE ID no.967417 (SEQ ID
NO: 848); Ceres CLONE ID no.1614593 (SEQ ID NO: 863); Ceres CLONE ID
no.2025938 (SEQ ID NO: 885); Ceres CLONE ID no.634261 (SEQ ID NO: 900);
Ceres CLONE ID no.1423851 (SEQ ID NO: 918); Ceres CLONE ID no.1589047
30 (SEQ ID NO: 939); Ceres CLONE ID no.1748922 (SEQ ID NO: 944); Ceres CLONE
ID no.1787151 (SEQ ID NO: 957); Ceres CLONE ID no.1765871 (SEQ ID NO:
973); Ceres CLONE ID no.1990071 (SEQ ID NO: 977); Public GI ID no.125556051
(SEQ ID NO: 989); Public GI ID no.125561658 (SEQ ID NO: 990); Public GI ID
no.115470773 (SEQ ID NO: 992); Public GI ID no.115444813 (SEQ ID NO: 993);

GI ID no. 169363 (SEQ ID NO: 1215) and Ceres CLONE ID no.24255 (SEQ ID NO: 1242).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 215 when fitted to an HMM generated from the amino acid sequences set forth in Figure 8. Such polypeptides include Ceres SEEDLINE ID no.ME18396 (SEQ ID NO:1012), Ceres CLONE ID no.287430 (SEQ ID NO:1018), Ceres ANNOT ID no.451889 (SEQ ID NO:1020), Ceres CLONE ID no.936084 (SEQ ID NO:1055), Ceres CLONE ID no.1792501 (SEQ ID NO:1066), Ceres ANNOT ID no.1437875 (SEQ ID NO:1068), Public GI ID no.1853968 (SEQ ID NO:1093), Public GI ID no.27530032 (SEQ ID NO:1094), Ceres CLONE ID no.1834483 (SEQ ID NO:1110), Public GI ID no.84579418 (SEQ ID NO:1113), Public GI ID no.15077030 (SEQ ID NO:1117), Public GI ID no.13752458 (SEQ ID NO:1118), Public GI ID no.147865685 (SEQ ID NO:1013), Public GI ID no.119503368 (SEQ ID NO:1014), Public GI ID no.72161874 (SEQ ID NO:1015), Public GI ID no.91780661 (SEQ ID NO:1016), Ceres ANNOT ID no.835908 (SEQ ID NO:1022), Public GI ID no.38326750 (SEQ ID NO:1023), Ceres CLONE ID no.1939396 (SEQ ID NO:1025), Ceres CLONE ID no.403637 (SEQ ID NO:1027), Public GI ID no.42539907 (SEQ ID NO:1028), Ceres CLONE ID no.1836494 (SEQ ID NO:1030), Public GI ID no.15192945 (SEQ ID NO:1031), Ceres CLONE ID no.1607947 (SEQ ID NO:1033), Ceres CLONE ID no.115880 (SEQ ID NO:1035), Ceres CLONE ID no.1074009 (SEQ ID NO:1037), Ceres CLONE ID no.476073 (SEQ ID NO:1039), Ceres CLONE ID no.554053 (SEQ ID NO:1041), Ceres CLONE ID no.391449 (SEQ ID NO:1045), Ceres CLONE ID no.1846400 (SEQ ID NO:1048), Ceres ANNOT ID no.1475185 (SEQ ID NO:1050), Public GI ID no.115457148 (SEQ ID NO:1051), Ceres ANNOT ID no.1454960 (SEQ ID NO:1053), Public GI ID no.50346893 (SEQ ID NO:1056), Ceres CLONE ID no.1931526 (SEQ ID NO:1058), Ceres ANNOT ID no.1454260 (SEQ ID NO:1061), Public GI ID no.115456131 (SEQ ID NO:1062), Ceres CLONE ID no.159151 (SEQ ID NO:1064), Ceres CLONE ID no.1842801 (SEQ ID NO:1071), Ceres CLONE ID no.533030 (SEQ ID NO:1073), Ceres CLONE ID no.1931881 (SEQ ID NO:1075), Ceres ANNOT ID no.1480006 (SEQ ID NO:1077), Ceres CLONE ID no.1895007 (SEQ ID NO:1079), Public GI ID no.3598863 (SEQ ID NO:1080), Ceres ANNOT ID no.1471735 (SEQ ID NO:1082), Ceres CLONE ID no.1937530 (SEQ ID NO:1084), Ceres CLONE ID no.1833050 (SEQ ID NO:1086), Ceres CLONE ID no.644213 (SEQ ID NO:1088), Ceres CLONE ID no.568154 (SEQ

ID NO:1090), Ceres CLONE ID no.527598 (SEQ ID NO:1092), Ceres ANNOT ID no.1487614 (SEQ ID NO:1096), Ceres ANNOT ID no.1541881 (SEQ ID NO:1098), Ceres ANNOT ID no.1488465 (SEQ ID NO:1100), Ceres ANNOT ID no.1488468 (SEQ ID NO:1102), Ceres ANNOT ID no.1541884 (SEQ ID NO:1104), Ceres ANNOT ID no.1454972 (SEQ ID NO:1106), Ceres ANNOT ID no.1475186 (SEQ ID NO:1108), Ceres CLONE ID no.686198 (SEQ ID NO:1112), Public GI ID no.84579420 (SEQ ID NO:1114), Ceres CLONE ID no.605144 (SEQ ID NO:1116), Public GI ID no.15077028 (SEQ ID NO:1119), Ceres ANNOT ID no.1454963 (SEQ ID NO:1121), Ceres ANNOT ID no.6030208 (SEQ ID NO:1123), and Ceres ANNOT ID no.6076767 (SEQ ID NO:1125).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 105 when fitted to an HMM generated from the amino acid sequences set forth in Figure 9. Such polypeptides include Ceres SEEDLINE ID no.ME20095 (SEQ ID NO:1129), Public GI ID no.72255610 (SEQ ID NO:933), Ceres SEEDLINE ID no.ME20095 (SEQ ID NO:1129), Ceres CLONE ID no.1562633 (SEQ ID NO:1140), Ceres ANNOT ID no.1692728 (SEQ ID NO:1142), Ceres CLONE ID no.921110 (SEQ ID NO:1144), Ceres CLONE ID no.1791180 (SEQ ID NO:1146), Ceres CLONE ID no.527891 (SEQ ID NO:1148), Ceres ANNOT ID no.1522414 (SEQ ID NO:1150), Public GI ID no.51458330 (SEQ ID NO:1182), Public GI ID no.18399940 (SEQ ID NO:63), Ceres ANNOT ID no.6107929 (SEQ ID NO:73), Ceres ANNOT ID no.1473094 (SEQ ID NO:96), Ceres ANNOT ID no.1503955 (SEQ ID NO:127), Ceres ANNOT ID no.1526501 (SEQ ID NO:139), Public GI ID no.15235713 (SEQ ID NO:179), Public GI ID no.15234552 (SEQ ID NO:180), Ceres ANNOT ID no.1520801 (SEQ ID NO:209), Ceres ANNOT ID no.1443434 (SEQ ID NO:467), Public GI ID no.30696058 (SEQ ID NO:559), Ceres ANNOT ID no.1509601 (SEQ ID NO:648), Ceres ANNOT ID no.1451912 (SEQ ID NO:726), Ceres ANNOT ID no.6017545 (SEQ ID NO:741), Ceres ANNOT ID no.1504999 (SEQ ID NO:765), Ceres ANNOT ID no.1456402 (SEQ ID NO:773), Ceres ANNOT ID no.1496359 (SEQ ID NO:781), Ceres ANNOT ID no.1447260 (SEQ ID NO:842), Ceres ANNOT ID no.1469023 (SEQ ID NO:861), Ceres ANNOT ID no.1474186 (SEQ ID NO:865), Ceres ANNOT ID no.1527596 (SEQ ID NO:867), Ceres CLONE ID no.1919624 (SEQ ID NO:896), Ceres CLONE ID no.677797 (SEQ ID NO:916), Public GI ID no.7960729 (SEQ ID NO:932), Ceres CLONE ID no.941845 (SEQ ID NO:1043), Public GI ID no.30683008 (SEQ ID NO:1046), Public GI ID no.42568786

(SEQ ID NO:1059), Ceres CLONE ID no.255364 (SEQ ID NO:1069), Public GI ID no.147771549 (SEQ ID NO:1130), Public GI ID no.144924741 (SEQ ID NO:1131), Public GI ID no.121594508 (SEQ ID NO:1132), Public GI ID no.91202290 (SEQ ID NO:1133), Public GI ID no.89900939 (SEQ ID NO:1134), Public GI ID no.77917672
 5 (SEQ ID NO:1135), Public GI ID no.77165252 (SEQ ID NO:1136), Public GI ID no.115375374 (SEQ ID NO:1137), Public GI ID no.110602449 (SEQ ID NO:1138), Public GI ID no.125540573 (SEQ ID NO:1151), Public GI ID no.125561519 (SEQ ID NO:1152), Public GI ID no.125528345 (SEQ ID NO:1153), Public GI ID no.116310408 (SEQ ID NO:1154), Public GI ID no.115483332 (SEQ ID NO:1156),
 10 Public GI ID no.125575640 (SEQ ID NO:1157), Public GI ID no.115476368 (SEQ ID NO:1158), Public GI ID no.115478841 (SEQ ID NO:1159), Public GI ID no.115467158 (SEQ ID NO:1160), Public GI ID no.72384477 (SEQ ID NO:1161), Public GI ID no.116054703 (SEQ ID NO:1162), Ceres CLONE ID no.1786317 (SEQ ID NO:1164), Ceres CLONE ID no.1791336 (SEQ ID NO:1166), Ceres CLONE ID
 15 no.1877752 (SEQ ID NO:1168), Ceres CLONE ID no.1821191 (SEQ ID NO:1170), Ceres CLONE ID no.446838 (SEQ ID NO:1172), Ceres CLONE ID no.1556915 (SEQ ID NO:1174), Public GI ID no.90200725 (SEQ ID NO:1175), Ceres CLONE ID no.1580247 (SEQ ID NO:1177), Ceres CLONE ID no.644201 (SEQ ID NO:1179), Ceres CLONE ID no.538689 (SEQ ID NO:1181), Ceres CLONE ID
 20 no.817225 (SEQ ID NO:1184), and Ceres CLONE ID no.923842 (SEQ ID NO:1186).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 55 when fitted to an HMM generated from the amino acid sequences set forth in Figure 10. Such polypeptides include Ceres CLONE ID no.31309 (SEQ ID NO:60), Ceres CLONE ID no.872030 (SEQ ID NO:62), Ceres CLONE ID
 25 no.100029223 (SEQ ID NO:74), Ceres CLONE ID no.1939845 (SEQ ID NO:98), Ceres CLONE ID no.2015383 (SEQ ID NO:102), Ceres CLONE ID no.1607893 (SEQ ID NO:104), Ceres CLONE ID no.1075133 (SEQ ID NO:152), Ceres CLONE ID no.1218065 (SEQ ID NO:915), Public GI ID no.15227919 (SEQ ID NO:64), Public GI ID no.9843641 (SEQ ID NO:65), Public GI ID no.124294789 (SEQ ID
 30 NO:66), Public GI ID no.15233446 (SEQ ID NO:67), Public GI ID no.115477679 (SEQ ID NO:68), Public GI ID no.42407552 (SEQ ID NO:69), Public GI ID no.125562450 (SEQ ID NO:70), Public GI ID no.115469980 (SEQ ID NO:71), Ceres ANNOT ID no.1442539 (SEQ ID NO:76), Ceres ANNOT ID no.1442538 (SEQ ID NO:78), Ceres ANNOT ID no.1460661 (SEQ ID NO:80), Ceres ANNOT ID

no.1452884 (SEQ ID NO:82), Ceres ANNOT ID no.1450523 (SEQ ID NO:84), Ceres ANNOT ID no.1442257 (SEQ ID NO:86), Ceres ANNOT ID no.1541121 (SEQ ID NO:88), Ceres ANNOT ID no.1480481 (SEQ ID NO:90), Ceres ANNOT ID no.1487713 (SEQ ID NO:92), Ceres ANNOT ID no.1456204 (SEQ ID NO:94), Ceres CLONE ID no.1387402 (SEQ ID NO:100), Ceres CLONE ID no.972919 (SEQ ID NO:106), Ceres CLONE ID no.1645860 (SEQ ID NO:108), Ceres CLONE ID no.1042804 (SEQ ID NO:110), Ceres CLONE ID no.1606678 (SEQ ID NO:112), Ceres CLONE ID no.684496 (SEQ ID NO:114), Ceres CLONE ID no.1062366 (SEQ ID NO:116), Ceres CLONE ID no.1722931 (SEQ ID NO:118), Ceres CLONE ID no.746169 (SEQ ID NO:120), Ceres CLONE ID no.1050475 (SEQ ID NO:122), Ceres CLONE ID no.1728904 (SEQ ID NO:124), Ceres CLONE ID no.1698538 (SEQ ID NO:126), Ceres CLONE ID no.1762328 (SEQ ID NO:130), Ceres CLONE ID no.1590072 (SEQ ID NO:132), Ceres CLONE ID no.471593 (SEQ ID NO:134), Ceres CLONE ID no.1031667 (SEQ ID NO:136), Ceres CLONE ID no.1826085 (SEQ ID NO:138), Ceres CLONE ID no.373932 (SEQ ID NO:142), Ceres CLONE ID no.1797836 (SEQ ID NO:144), Ceres CLONE ID no.1102774 (SEQ ID NO:146), Ceres CLONE ID no.842287 (SEQ ID NO:148), Ceres CLONE ID no.568205 (SEQ ID NO:150), Ceres ANNOT ID no.6108997 (SEQ ID NO:154), Ceres ANNOT ID no.6023609 (SEQ ID NO:156), and Ceres ANNOT ID no.6017906 (SEQ ID NO:158).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 55 when fitted to an HMM generated from the amino acid sequences set forth in Figure 11. Such polypeptides include Ceres LOCUS ID no.At2g26150 (SEQ ID NO:364), Ceres ANNOT ID no.1455221 (SEQ ID NO:407), Public GI ID no.729774 (SEQ ID NO:408), Ceres CLONE ID no.1414288 (SEQ ID NO:410), Public GI ID no.115482048 (SEQ ID NO:413), Public GI ID no.56117815 (SEQ ID NO:421), Ceres ANNOT ID no.1485538 (SEQ ID NO:366), Ceres ANNOT ID no.1538505 (SEQ ID NO:368), Public GI ID no.8347238 (SEQ ID NO:369), Public GI ID no.125542955 (SEQ ID NO:370), Public GI ID no.115446219 (SEQ ID NO:371), Ceres CLONE ID no.1597127 (SEQ ID NO:373), Ceres CLONE ID no.1584568 (SEQ ID NO:375), Ceres CLONE ID no.286056 (SEQ ID NO:377), Ceres ANNOT ID no.1543432 (SEQ ID NO:379), Ceres CLONE ID no.1728062 (SEQ ID NO:381), Ceres ANNOT ID no.1448950 (SEQ ID NO:383), Ceres CLONE ID no.771500 (SEQ ID NO:385), Ceres ANNOT ID no.1485096 (SEQ ID NO:387),

Ceres CLONE ID no.1646104 (SEQ ID NO:389), Public GI ID no.111184724 (SEQ ID NO:390), Ceres CLONE ID no.1362475 (SEQ ID NO:392), Ceres CLONE ID no.597906 (SEQ ID NO:394), Ceres CLONE ID no.615781 (SEQ ID NO:396), Ceres CLONE ID no.538713 (SEQ ID NO:398), Ceres CLONE ID no.1794141 (SEQ ID NO:400), Public GI ID no.5821138 (SEQ ID NO:401), Public GI ID no.886742 (SEQ ID NO:402), Ceres CLONE ID no.1814498 (SEQ ID NO:404), Public GI ID no.7158882 (SEQ ID NO:405), Ceres ANNOT ID no.1452564 (SEQ ID NO:412), Public GI ID no.125557431 (SEQ ID NO:414), Ceres ANNOT ID no.1442880 (SEQ ID NO:416), Ceres ANNOT ID no.1463437 (SEQ ID NO:418), Public GI ID no.42415865 (SEQ ID NO:419), Public GI ID no.33087081 (SEQ ID NO:420), Public GI ID no.115521217 (SEQ ID NO:422), Public GI ID no.115521211 (SEQ ID NO:423), Public GI ID no.115521215 (SEQ ID NO:424), Ceres ANNOT ID no.1454376 (SEQ ID NO:426), Ceres CLONE ID no.835571 (SEQ ID NO:428), Ceres ANNOT ID no.1500046 (SEQ ID NO:430), Public GI ID no.110738569 (SEQ ID NO:431), Public GI ID no.125542510 (SEQ ID NO:432), Public GI ID no.30686034 (SEQ ID NO:433), Public GI ID no.125570883 (SEQ ID NO:434), Public GI ID no.42562463 (SEQ ID NO:435), Ceres CLONE ID no.100043265 (SEQ ID NO:436), Ceres ANNOT ID no.6089790 (SEQ ID NO:438), and Ceres ANNOT ID no.6043635 (SEQ ID NO:440).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 50 when fitted to an HMM generated from the amino acid sequences set forth in Figure 12. Such polypeptides include Ceres LOCUS ID no.At1g32330 (SEQ ID NO:311), Ceres ANNOT ID no.1538958 (SEQ ID NO:319), Public GI ID no.115521213 (SEQ ID NO:320), Public GI ID no.42415865 (SEQ ID NO:321), Public GI ID no.729775 (SEQ ID NO:322), Public GI ID no.11386827 (SEQ ID NO:323), Public GI ID no.115456675 (SEQ ID NO:326), Public GI ID no.89274218 (SEQ ID NO:335), Public GI ID no.125546035 (SEQ ID NO:312), Ceres CLONE ID no.125228 (SEQ ID NO:314), Public GI ID no.115465055 (SEQ ID NO:315), Public GI ID no.125553080 (SEQ ID NO:316), Public GI ID no.8920606 (SEQ ID NO:317), Ceres CLONE ID no.1919643 (SEQ ID NO:325), Public GI ID no.429155 (SEQ ID NO:327), Ceres CLONE ID no.1194199 (SEQ ID NO:329), Public GI ID no.15236631 (SEQ ID NO:330), Ceres ANNOT ID no.1523420 (SEQ ID NO:332), Ceres ANNOT ID no.1447046 (SEQ ID NO:334), Public GI ID no.25296101 (SEQ ID NO:336), Public GI ID no.15228440 (SEQ ID NO:337), Public GI ID no.6624612

(SEQ ID NO:338), Public GI ID no.125588688 (SEQ ID NO:339), Public GI ID no.115470859 (SEQ ID NO:340), Public GI ID no.15228865 (SEQ ID NO:341), Ceres CLONE ID no.1571069 (SEQ ID NO:343), Public GI ID no.115455903 (SEQ ID NO:344), Ceres ANNOT ID no.1459422 (SEQ ID NO:346), Ceres CLONE ID no.1577511 (SEQ ID NO:348), Public GI ID no.115451657 (SEQ ID NO:349), Public GI ID no.15225255 (SEQ ID NO:350), Public GI ID no.125545695 (SEQ ID NO:351), Ceres ANNOT ID no.1471817 (SEQ ID NO:353), Ceres ANNOT ID no.1440896 (SEQ ID NO:355), Public GI ID no.119393868 (SEQ ID NO:356), Ceres ANNOT ID no.1517025 (SEQ ID NO:358), Ceres ANNOT ID no.1512410 (SEQ ID NO:360), and Ceres ANNOT ID no.6035498 (SEQ ID NO:362).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 25 when fitted to an HMM generated from the amino acid sequences set forth in Figure 13. Such polypeptides include Ceres CLONE ID no.41543 (SEQ ID NO:160) Ceres CLONE ID no.1837065 (SEQ ID NO:162), Ceres ANNOT ID no.1531178 (SEQ ID NO:184), Ceres CLONE ID no.470694 (SEQ ID NO:242), Public GI ID no.92867368 (SEQ ID NO:253), Ceres CLONE ID no.859707 (SEQ ID NO:256), Ceres CLONE ID no.392275 (SEQ ID NO:268), Ceres CLONE ID no.1828394 (SEQ ID NO:282), Public GI ID no.115466694 (SEQ ID NO:294), Ceres CLONE ID no.1895763 (SEQ ID NO:164), Ceres CLONE ID no.1850460 (SEQ ID NO:166), Ceres CLONE ID no.1808074 (SEQ ID NO:168), Ceres CLONE ID no.1832882 (SEQ ID NO:170), Ceres CLONE ID no.1978977 (SEQ ID NO:172), Ceres CLONE ID no.1918742 (SEQ ID NO:174), Ceres CLONE ID no.1940023 (SEQ ID NO:176), Ceres CLONE ID no.1923495 (SEQ ID NO:178), Ceres CLONE ID no.1851388 (SEQ ID NO:182), Ceres ANNOT ID no.1477681 (SEQ ID NO:186), Ceres ANNOT ID no.1508800 (SEQ ID NO:188), Ceres ANNOT ID no.1455597 (SEQ ID NO:190), Ceres ANNOT ID no.1532016 (SEQ ID NO:192), Ceres ANNOT ID no.1478526 (SEQ ID NO:194), Ceres ANNOT ID no.1492567 (SEQ ID NO:196), Ceres ANNOT ID no.1515273 (SEQ ID NO:198), Ceres ANNOT ID no.1461979 (SEQ ID NO:200), Ceres ANNOT ID no.1439702 (SEQ ID NO:202), Ceres ANNOT ID no.1448044 (SEQ ID NO:204), Ceres ANNOT ID no.1483370 (SEQ ID NO:206), Ceres ANNOT ID no.1445651 (SEQ ID NO:208), Ceres ANNOT ID no.1490863 (SEQ ID NO:212), Ceres ANNOT ID no.1501043 (SEQ ID NO:214), Ceres ANNOT ID no.1527507 (SEQ ID NO:216), Ceres ANNOT ID no.1498633 (SEQ ID NO:218), Ceres ANNOT ID no.1465403 (SEQ ID NO:220), Ceres ANNOT ID no.1510956

(SEQ ID NO:222), Ceres ANNOT ID no.1457735 (SEQ ID NO:224), Public GI ID no.15224711 (SEQ ID NO:225), Ceres CLONE ID no.40062 (SEQ ID NO:228), Public GI ID no.15220315 (SEQ ID NO:229), Ceres CLONE ID no.36480 (SEQ ID NO:231), Ceres CLONE ID no.2443 (SEQ ID NO:233), Public GI ID no.30685375

5 (SEQ ID NO:234), Public GI ID no.126009434 (SEQ ID NO:235), Ceres CLONE ID no.965753 (SEQ ID NO:237), Ceres CLONE ID no.948834 (SEQ ID NO:239), Public GI ID no.33347409 (SEQ ID NO:240), Ceres CLONE ID no.643614 (SEQ ID NO:244), Ceres CLONE ID no.1049362 (SEQ ID NO:246), Ceres CLONE ID no.546675 (SEQ ID NO:248), Ceres CLONE ID no.522046 (SEQ ID NO:250), Ceres

10 CLONE ID no.651076 (SEQ ID NO:252), Public GI ID no.92897590 (SEQ ID NO:254), Ceres CLONE ID no.634176 (SEQ ID NO:258), Ceres CLONE ID no.1041432 (SEQ ID NO:260), Ceres CLONE ID no.1065203 (SEQ ID NO:262), Ceres CLONE ID no.555361 (SEQ ID NO:264), Ceres CLONE ID no.704227 (SEQ ID NO:266), Ceres CLONE ID no.100819945 (SEQ ID NO:269), Ceres CLONE ID

15 no.282584 (SEQ ID NO:271), Ceres CLONE ID no.1448469 (SEQ ID NO:273), Ceres CLONE ID no.241246 (SEQ ID NO:275), Ceres CLONE ID no.234443 (SEQ ID NO:277), Ceres CLONE ID no.293549 (SEQ ID NO:279), Public GI ID no.109450926 (SEQ ID NO:280), Ceres CLONE ID no.1803923 (SEQ ID NO:284), Ceres CLONE ID no.2024557 (SEQ ID NO:286), Ceres CLONE ID no.1820364

20 (SEQ ID NO:288), Public GI ID no.125554274 (SEQ ID NO:289), Public GI ID no.125531165 (SEQ ID NO:290), Public GI ID no.125541514 (SEQ ID NO:291), Public GI ID no.125557559 (SEQ ID NO:292), Public GI ID no.125557844 (SEQ ID NO:293), Public GI ID no.115449295 (SEQ ID NO:295), Public GI ID no.115481182 (SEQ ID NO:296), Public GI ID no.20177639 (SEQ ID NO:297), Public GI ID

25 no.115471021 (SEQ ID NO:298), Public GI ID no.115456011 (SEQ ID NO:299), Public GI ID no.125588290 (SEQ ID NO:300), Public GI ID no.115477799 (SEQ ID NO:301), Public GI ID no.115471385 (SEQ ID NO:302), Public GI ID no.125599705 (SEQ ID NO:303), Public GI ID no.115489810 (SEQ ID NO:304), Public GI ID no.55276718 (SEQ ID NO:305), Ceres ANNOT ID no.6025568 (SEQ ID NO:307),

30 and Ceres ANNOT ID no.6091128 (SEQ ID NO:309).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 85 when fitted to an HMM generated from the amino acid sequences set forth in Figure 14. Such polypeptides include Ceres CLONE ID no.14572 (SEQ ID NO:2), Public GI ID no.115470807 (SEQ ID NO:5), Ceres CLONE ID no.1842931

(SEQ ID NO:15), Ceres CLONE ID no.321308 (SEQ ID NO:17), Ceres CLONE ID no.1725811 (SEQ ID NO:19), Ceres CLONE ID no.1357455 (SEQ ID NO:21), Ceres CLONE ID no.943370 (SEQ ID NO:23), Ceres CLONE ID no.1327712 (SEQ ID NO:25), Ceres CLONE ID no.1764692 (SEQ ID NO:27), Ceres ANNOT ID

5 no.1512656 (SEQ ID NO:41), Public GI ID no.18403425 (SEQ ID NO:3), Public GI ID no.11994285 (SEQ ID NO:4), Public GI ID no.108706298 (SEQ ID NO:6), Public GI ID no.15233585 (SEQ ID NO:7), Public GI ID no.125599279 (SEQ ID NO:8), Public GI ID no.115450865 (SEQ ID NO:9), Public GI ID no.22773244 (SEQ ID NO:10), Public GI ID no.92874749 (SEQ ID NO:11), Ceres CLONE ID no.1857034

10 (SEQ ID NO:13), Ceres CLONE ID no.1059300 (SEQ ID NO:29), Ceres CLONE ID no.1804869 (SEQ ID NO:31), Ceres CLONE ID no.378863 (SEQ ID NO:33), Ceres CLONE ID no.1930271 (SEQ ID NO:35), Ceres CLONE ID no.2034728 (SEQ ID NO:37), Ceres CLONE ID no.1866421 (SEQ ID NO:39), Ceres ANNOT ID no.1463492 (SEQ ID NO:43), Ceres ANNOT ID no.1459391 (SEQ ID NO:45), Ceres

15 ANNOT ID no.1442920 (SEQ ID NO:47), Ceres ANNOT ID no.6011447 (SEQ ID NO:49), Ceres ANNOT ID no.6068218 (SEQ ID NO:51), Ceres ANNOT ID no.6044121 (SEQ ID NO:53), and Ceres ANNOT ID no.6100755 (SEQ ID NO:55).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 70 when fitted to an HMM generated from the amino acid sequences set

20 forth in Figure 15. Such polypeptides include Ceres SEEDLINE ID no.ME02401 (SEQ ID NO:749), Ceres CLONE ID no.1847516 (SEQ ID NO:1195), Ceres CLONE ID no.1961986 (SEQ ID NO:1201), Ceres ANNOT ID no.6091930 (SEQ ID NO:1207), Ceres CLONE ID no.2025938 (SEQ ID NO:885), Ceres CLONE ID no.1821214 (SEQ ID NO:1189), Ceres CLONE ID no.1040399 (SEQ ID NO:1191),

25 Ceres CLONE ID no.1093691 (SEQ ID NO:1193), Ceres CLONE ID no.974539 (SEQ ID NO:1197), Ceres CLONE ID no.1832340 (SEQ ID NO:1199), Ceres CLONE ID no.1933211 (SEQ ID NO:1203), Ceres CLONE ID no.997558 (SEQ ID NO:1205), Ceres ANNOT ID no.6041596 (SEQ ID NO:1209), Public GI ID no.125564176 (SEQ ID NO:1210), Ceres CLONE ID no.1836064 (SEQ ID

30 NO:1212), Ceres CLONE ID no.1909693 (SEQ ID NO:1214), Public GI ID no.169363 (SEQ ID NO:1215), Public GI ID no.40287480 (SEQ ID NO:1216), Ceres CLONE ID no.1765346 (SEQ ID NO:1218), Public GI ID no.125546008 (SEQ ID NO:1219), Ceres CLONE ID no.1950900 (SEQ ID NO:1221), Public GI ID no.41350259 (SEQ ID NO:1222), Public GI ID no.125588210 (SEQ ID NO:1223),

Ceres CLONE ID no.1954395 (SEQ ID NO:1225), Public GI ID no.18403408 (SEQ ID NO:1226), Ceres CLONE ID no.2010121 (SEQ ID NO:1228), Ceres ANNOT ID no.6011486 (SEQ ID NO:1230), Public GI ID no.25082726 (SEQ ID NO:1231), Public GI ID no.113196593 (SEQ ID NO:1232), Ceres CLONE ID no.1843021 (SEQ ID NO:1234), Ceres CLONE ID no.1931194 (SEQ ID NO:1236), Ceres CLONE ID no.1652996 (SEQ ID NO:1238), Ceres CLONE ID no.1930044 (SEQ ID NO:1240), Ceres CLONE ID no.24255 (SEQ ID NO:1242), Ceres ANNOT ID no.6034955 (SEQ ID NO:1244), Ceres ANNOT ID no.6119444 (SEQ ID NO:1246), Ceres ANNOT ID no.6063956 (SEQ ID NO:1248), Ceres ANNOT ID no.6015461 (SEQ ID NO:1250), Ceres CLONE ID no.696244 (SEQ ID NO:1252), Ceres ANNOT ID no.1468973 (SEQ ID NO:1254), Ceres CLONE ID no.2019529 (SEQ ID NO:1256), and Ceres CLONE ID no.1492169 (SEQ ID NO:1258).

Polypeptides are shown in the sequence listing that have HMM bit scores greater than about 300 when fitted to an HMM generated from the amino acid sequences set forth in Figure 16. Such polypeptides include Ceres SEEDLINE ID no. ME004246 (SEQ ID NO: 1311), CeresClone:971761 (SEQ ID NO: 1313), CeresClone:1946574 (SEQ ID NO: 1331), CeresClone:2055551 (SEQ ID NO: 1340), CeresClone:100045499 (SEQ ID NO: 1347), CeresClone:1465853 (SEQ ID NO: 1353), CeresClone:753982 (SEQ ID NO: 1360), CeresClone:1076093 (SEQ ID NO: 1315), CeresClone:1627875 (SEQ ID NO: 1317), CeresAnnot:1508362 (SEQ ID NO: 1319), CeresAnnot:1526950 (SEQ ID NO: 1321), CeresClone:1832333 (SEQ ID NO: 1323), GI:74272607 (SEQ ID NO: 1324), GI:192910782 (SEQ ID NO: 1325), GI:157342563 (SEQ ID NO: 1326), GI:159483497 (SEQ ID NO: 1327), CeresClone:1839999 (SEQ ID NO: 1329), CeresClone:467335 (SEQ ID NO: 1333), GI:168010087 (SEQ ID NO: 1334), CeresClone:1728202 (SEQ ID NO: 1336), CeresClone:1994239 (SEQ ID NO: 1338), CeresAnnot:8704704 (SEQ ID NO: 1342), GI:115453877 (SEQ ID NO: 1343), CeresClone:1646411 (SEQ ID NO: 1345), CeresClone:100920260 (SEQ ID NO: 1349), GI:116786147 (SEQ ID NO: 1350), GI:116783944 (SEQ ID NO: 1351), GI:82623397 (SEQ ID NO: 1354), CeresAnnot:8656662 (SEQ ID NO: 1356), CeresClone:1417803 (SEQ ID NO: 1358), and GI:145345927 (SEQ ID NO: 1361).

D. Percent Identity

In some embodiments, a heat and/or drought-tolerance polypeptide has an amino acid sequence with at least 20% sequence identity, *e.g.*, 21%, 22%, 24%, 27%, 30%, 33%, 38%, 45%, 46%, 49%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to one of the amino acid sequences set forth in SEQ ID NO:442, SEQ ID NO:489, SEQ ID NO:568, SEQ ID NO:590, SEQ ID NO:705, SEQ ID NO:711, SEQ ID NO:742, SEQ ID NO:1012, SEQ ID NO:1129, SEQ ID NO:60, SEQ ID NO:364, SEQ ID NO:311, SEQ ID NO:160, SEQ ID NO:2, SEQ ID NO:749, SEQ ID NO: 1131, and SEQ ID NO:57.

Polypeptides having such a percent sequence identity often have a domain indicative of a heat and/or drought-tolerance polypeptide and/or have an HMM bit score that is greater than 20, as discussed above. Amino acid sequences of heat and/or drought-tolerance polypeptides having at least 20% sequence identity to one of the amino acid sequences set forth in SEQ ID NO:442, SEQ ID NO:489, SEQ ID NO:568, SEQ ID NO:590, SEQ ID NO:705, SEQ ID NO:711, SEQ ID NO:742, SEQ ID NO:1012, SEQ ID NO:1129, SEQ ID NO:60, SEQ ID NO:364, SEQ ID NO:311, SEQ ID NO:160, SEQ ID NO:2, SEQ ID NO: 1131, and SEQ ID NO:749 are provided in Figures 1-16.

“Percent sequence identity” refers to the degree of sequence identity between any given reference sequence, *e.g.*, SEQ ID NO:2, and a candidate heat and/or drought-tolerance sequence. A candidate sequence typically has a length that is from 80 percent to 200 percent of the length of the reference sequence, *e.g.*, 82, 85, 87, 89, 90, 93, 95, 97, 99, 100, 105, 110, 115, 120, 130, 140, 150, 160, 170, 180, 190, or 200 percent of the length of the reference sequence. A percent identity for any candidate nucleic acid or polypeptide relative to a reference nucleic acid or polypeptide can be determined as follows. A reference sequence (*e.g.*, a nucleic acid sequence or an amino acid sequence) is aligned to one or more candidate sequences using the computer program ClustalW (version 1.83, default parameters), which allows alignments of nucleic acid or polypeptide sequences to be carried out across their entire length (global alignment). Chenna et al., *Nucleic Acids Res.*, 31(13):3497-500 (2003).

ClustalW calculates the best match between a reference and one or more candidate sequences, and aligns them so that identities, similarities and differences can be determined. Gaps of one or more residues can be inserted into a reference

sequence, a candidate sequence, or both, to maximize sequence alignments. For fast pairwise alignment of nucleic acid sequences, the following default parameters are used: word size: 2; window size: 4; scoring method: percentage; number of top diagonals: 4; and gap penalty: 5. For multiple alignment of nucleic acid sequences, the following parameters are used: gap opening penalty: 10.; gap extension penalty: 5.0; and weight transitions: yes. For fast pairwise alignment of protein sequences, the following parameters are used: word size: 1; window size: 5; scoring method: percentage; number of top diagonals: 5; gap penalty: 3. For multiple alignment of protein sequences, the following parameters are used: weight matrix: blosum; gap opening penalty: 10.; gap extension penalty: 0.5; hydrophilic gaps: on; hydrophilic residues: Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg, and Lys; residue-specific gap penalties: on. The ClustalW output is a sequence alignment that reflects the relationship between sequences. ClustalW can be run, for example, at the Baylor College of Medicine Search Launcher site (searchlauncher.bcm.tmc.edu/multi-align/multi-align.html) and at the European Bioinformatics Institute site on the World Wide Web (ebi.ac.uk/clustalw).

To determine percent identity of a candidate nucleic acid or amino acid sequence to a reference sequence, the sequences are aligned using ClustalW, the number of identical matches in the alignment is divided by the length of the reference sequence, and the result is multiplied by 100. It is noted that the percent identity value can be rounded to the nearest tenth. For example, 78.11, 78.12, 78.13, and 78.14 are rounded down to 78.1, while 78.15, 78.16, 78.17, 78.18, and 78.19 are rounded up to 78.2.

In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:442. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:442 are provided in Figure 1. Such polypeptides include Public GI ID no.72384401 (SEQ ID NO:443), Ceres CLONE ID no.1079382 (SEQ ID NO:445), Ceres CLONE ID no.1853461 (SEQ ID NO:447), Ceres CLONE ID no.1626485 (SEQ ID NO:451), Ceres CLONE ID no.1713920 (SEQ ID NO:459), Ceres CLONE ID no.1772747

(SEQ ID NO:463), Ceres CLONE ID no.225960 (SEQ ID NO:465), Public GI ID no.115443807 (SEQ ID NO:470), and Ceres CLONE ID no.569388 (SEQ ID NO:483).

In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 30% sequence identity, *e.g.*, 30%, 35%, 40%, 48%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:489. Amino acid sequences of polypeptides having greater than 30% sequence identity to the polypeptide set forth in SEQ ID NO:489 are provided in Figure 2. Such polypeptides include Ceres CLONE ID no.571200 (SEQ ID NO:494), Ceres CLONE ID no.1928532 (SEQ ID NO:496), Ceres ANNOT ID no.1490637 (SEQ ID NO:498), Ceres CLONE ID no.295496 (SEQ ID NO:514), Public GI ID no.115463637 (SEQ ID NO:515), and Ceres CLONE ID no.1999444 (SEQ ID NO:518).

In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 35% sequence identity, *e.g.*, 37%, 40%, 45%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:568. Amino acid sequences of polypeptides having greater than 35% sequence identity to the polypeptide set forth in SEQ ID NO:568 are provided in Figure 3. Such polypeptides include Ceres CLONE ID no.695006 (SEQ ID NO:578) and Ceres ANNOT ID no.1527488 (SEQ ID NO:584).

In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 25% sequence identity, *e.g.*, 28%, 32%, 40%, 44%, 48%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:590. Amino acid sequences of polypeptides having greater than 25% sequence identity to the polypeptide set forth in SEQ ID NO:590 are provided in Figure 4. Such polypeptides include Ceres ANNOT ID no.1501305 (SEQ ID NO:623), Ceres CLONE ID no.607280 (SEQ ID NO:627), Public GI ID no.92887174 (SEQ ID NO:632), Ceres CLONE ID no.1857162 (SEQ ID NO:634), Public GI ID no.115477272 (SEQ ID NO:674), and Ceres CLONE ID no.264002 (SEQ ID NO:682).

In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, *e.g.*, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid

sequence set forth in SEQ ID NO:705. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:705 are provided in Figure 5. Such polypeptides include Public GI ID no.79320952 (SEQ ID NO:706) and Public GI ID no.79320957 (SEQ ID NO:707).

5 In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 30% sequence identity, *e.g.*, 33%, 41%, 45%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:711. Amino acid sequences of polypeptides having greater than 30% sequence identity to the polypeptide set forth in
10 SEQ ID NO:711 are provided in Figure 6. Such polypeptides include Ceres CLONE ID no.964616 (SEQ ID NO:714), Ceres CLONE ID no.100009667 (SEQ ID NO:715), Ceres ANNOT ID no.1444568 (SEQ ID NO:719), Ceres CLONE ID no.719489 (SEQ ID NO:725), Ceres CLONE ID no.587748 (SEQ ID NO:733), Public GI ID no.125528114 (SEQ ID NO:734), and Ceres CLONE ID no.274172
15 (SEQ ID NO:737).

In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 30% sequence identity, *e.g.*, 35%, 38%, 43%, 47%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:742. Amino acid
20 sequences of polypeptides having greater than 30% sequence identity to the polypeptide set forth in SEQ ID NO:742 are provided in Figure 7. Such polypeptides include Public GI ID no.115477170 (SEQ ID NO:757), Ceres CLONE ID no.1620215 (SEQ ID NO:759), Ceres CLONE ID no.1931889 (SEQ ID NO:761), Ceres ANNOT ID no.1460527 (SEQ ID NO:801), Ceres CLONE ID no.975913 (SEQ ID NO:846),
25 Ceres CLONE ID no.708446 (SEQ ID NO:859), Ceres CLONE ID no.1748922 (SEQ ID NO:944), Ceres CLONE ID no.1775820 (SEQ ID NO:955), Public GI ID no.115468934 (SEQ ID NO:991), and Public GI ID no.118424243 (SEQ ID NO:1000).

In some cases, a drought-tolerance polypeptide has an amino acid sequence
30 with at least 35% sequence identity, *e.g.*, 36%, 40%, 47%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1012. Amino acid sequences of polypeptides having greater than 35% sequence identity to the polypeptide set forth in SEQ ID NO:1012 are provided in Figure 8. Such polypeptides include Ceres CLONE

ID no.287430 (SEQ ID NO:1018), Ceres ANNOT ID no.451889 (SEQ ID NO:1020), Ceres CLONE ID no.936084 (SEQ ID NO:1055), Ceres CLONE ID no.1792501 (SEQ ID NO:1066), Ceres ANNOT ID no.1437875 (SEQ ID NO:1068), Public GI ID no.1853968 (SEQ ID NO:1093), Public GI ID no.27530032 (SEQ ID NO:1094),

5 Ceres CLONE ID no.1834483 (SEQ ID NO:1110), Public GI ID no.84579418 (SEQ ID NO:1113), Public GI ID no.15077030 (SEQ ID NO:1117), and Public GI ID no.13752458 (SEQ ID NO:1118).

In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 30% sequence identity, *e.g.*, 31%, 35%, 40%, 41%, 49%, 50%, 52%,

10 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1129. Amino acid sequences of polypeptides having greater than 30% sequence identity to the polypeptide set forth in SEQ ID NO:1129 are provided in Figure 9. Such polypeptides include Public GI ID no.72255610 (SEQ ID NO:933), Ceres SEEDLINE

15 ID no.ME20095 (SEQ ID NO:1129), Ceres CLONE ID no.1562633 (SEQ ID NO:1140), Ceres ANNOT ID no.1692728 (SEQ ID NO:1142), Ceres CLONE ID no.921110 (SEQ ID NO:1144), Ceres CLONE ID no.1791180 (SEQ ID NO:1146), Ceres CLONE ID no.527891 (SEQ ID NO:1148), Ceres ANNOT ID no.1522414 (SEQ ID NO:1150), and Public GI ID no.51458330 (SEQ ID NO:1182).

20 In some cases, a heat-tolerance polypeptide has an amino acid sequence with at least 25% sequence identity, *e.g.*, 26%, 27%, 30%, 32%, 40%, 42%, 47%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:60. Amino acid sequences of polypeptides having greater than 25% sequence identity to the

25 polypeptide set forth in SEQ ID NO:60 are provided in Figure 10. Such polypeptides include Ceres CLONE ID no.872030 (SEQ ID NO:62), Ceres CLONE ID no.100029223 (SEQ ID NO:74), Ceres CLONE ID no.1939845 (SEQ ID NO:98), Ceres CLONE ID no.2015383 (SEQ ID NO:102), Ceres CLONE ID no.1607893 (SEQ ID NO:104), Ceres CLONE ID no.1075133 (SEQ ID NO:152), and Ceres

30 CLONE ID no.1218065 (SEQ ID NO:915).

In some cases, a heat-tolerance polypeptide has an amino acid sequence with at least 25% sequence identity, *e.g.*, 27%, 28%, 31%, 36%, 44%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:364. Amino acid

sequences of polypeptides having greater than 25% sequence identity to the polypeptide set forth in SEQ ID NO:364 are provided in Figure 11. Such polypeptides include Ceres ANNOT ID no.1455221 (SEQ ID NO:407), Public GI ID no.729774 (SEQ ID NO:408), Ceres CLONE ID no.1414288 (SEQ ID NO:410),
 5 Public GI ID no.115482048 (SEQ ID NO:413), and Public GI ID no.56117815 (SEQ ID NO:421).

In some cases, a heat-tolerance polypeptide has an amino acid sequence with at least 25% sequence identity, *e.g.*, 29%, 35%, 40%, 47%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity,
 10 to the amino acid sequence set forth in SEQ ID NO:311. Amino acid sequences of polypeptides having greater than 25% sequence identity to the polypeptide set forth in SEQ ID NO:311 are provided in Figure 12. Such polypeptides include Ceres ANNOT ID no.1538958 (SEQ ID NO:319), Public GI ID no.115521213 (SEQ ID NO:320), Public GI ID no.42415865 (SEQ ID NO:321), Public GI ID no.729775
 15 (SEQ ID NO:322), Public GI ID no.11386827 (SEQ ID NO:323), Public GI ID no.115456675 (SEQ ID NO:326), and Public GI ID no.89274218 (SEQ ID NO:335).

In some cases, a heat-tolerance polypeptide has an amino acid sequence with at least 25% sequence identity, *e.g.*, 30%, 33%, 40%, 45%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity,
 20 to the amino acid sequence set forth in SEQ ID NO:160. Amino acid sequences of polypeptides having greater than 25% sequence identity to the polypeptide set forth in SEQ ID NO:160 are provided in Figure 13. Such polypeptides include Ceres CLONE ID no.1837065 (SEQ ID NO:162), Ceres ANNOT ID no.1531178 (SEQ ID NO:184), Ceres CLONE ID no.470694 (SEQ ID NO:242), Public GI ID no.92867368 (SEQ ID NO:253), Ceres CLONE ID no.859707 (SEQ ID NO:256), Ceres CLONE ID
 25 no.392275 (SEQ ID NO:268), Ceres CLONE ID no.1828394 (SEQ ID NO:282), and Public GI ID no.115466694 (SEQ ID NO:294).

In some cases, a heat-tolerance polypeptide has an amino acid sequence with at least 20% sequence identity, *e.g.*, 21%, 22%, 30%, 35%, 40%, 45%, 50%, 52%,
 30 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:2. Amino acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:2 are provided in Figure 14. Such polypeptides include Public GI ID no.115470807 (SEQ ID NO:5), Ceres CLONE ID no.1842931

(SEQ ID NO:15), Ceres CLONE ID no.321308 (SEQ ID NO:17), Ceres CLONE ID no.1725811 (SEQ ID NO:19), Ceres CLONE ID no.1357455 (SEQ ID NO:21), Ceres CLONE ID no.943370 (SEQ ID NO:23), Ceres CLONE ID no.1327712 (SEQ ID NO:25), Ceres CLONE ID no.1764692 (SEQ ID NO:27), and Ceres ANNOT ID
 5 no.1512656 (SEQ ID NO:41).

In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 20% sequence identity, *e.g.*, 22%, 23%, 30%, 35%, 40%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:749. Amino
 10 acid sequences of polypeptides having greater than 20% sequence identity to the polypeptide set forth in SEQ ID NO:749 are provided in Figure 15. Such polypeptides include Ceres CLONE ID no.1847516 (SEQ ID NO:1195), Ceres CLONE ID no.1961986 (SEQ ID NO:1201), and Ceres ANNOT ID no.6091930 (SEQ ID NO:1207).

In some cases, a drought-tolerance polypeptide has an amino acid sequence with at least 30% sequence identity, *e.g.*, 31%, 35%, 40%, 41%, 49%, 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1311. Amino
 15 acid sequences of polypeptides having greater than 30% sequence identity to the polypeptide set forth in SEQ ID NO:1311 are provided in Figure 16. Such polypeptides include CeresClone:971761 (SEQ ID NO: 1313), CeresClone:1946574 (SEQ ID NO: 1331), CeresClone:2055551 (SEQ ID NO: 1340), CeresClone:100045499 (SEQ ID NO: 1347), CeresClone:1465853 (SEQ ID NO: 1353), CeresClone:753982 (SEQ ID NO: 1360), CeresClone:1076093 (SEQ ID NO: 1315), CeresClone:1627875 (SEQ ID NO: 1317), CeresAnnot:1508362 (SEQ ID NO: 1319), CeresAnnot:1526950 (SEQ ID NO: 1321), CeresClone:1832333 (SEQ ID NO: 1323), GI:74272607 (SEQ ID NO: 1324), GI:192910782 (SEQ ID NO: 1325), GI:157342563 (SEQ ID NO: 1326), GI:159483497 (SEQ ID NO: 1327), CeresClone:1839999 (SEQ ID NO: 1329), CeresClone:467335 (SEQ ID NO: 1333),
 20 GI:168010087 (SEQ ID NO: 1334), CeresClone:1728202 (SEQ ID NO: 1336), CeresClone:1994239 (SEQ ID NO: 1338), CeresAnnot:8704704 (SEQ ID NO: 1342), GI:115453877 (SEQ ID NO: 1343), CeresClone:1646411 (SEQ ID NO: 1345), CeresClone:100920260 (SEQ ID NO: 1349), GI:116786147 (SEQ ID NO: 1350), GI:116783944 (SEQ ID NO: 1351), GI:82623397 (SEQ ID NO: 1354),
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CeresAnnot:8656662 (SEQ ID NO: 1356), CeresClone:1417803 (SEQ ID NO: 1358), and GI:145345927 (SEQ ID NO: 1361).

E. Other Sequences

It should be appreciated that a heat and/or drought-tolerance polypeptide can include additional amino acids that are not involved in heat and/or drought-tolerance, and thus such a polypeptide can be longer than would otherwise be the case. For example, a heat and/or drought-tolerance polypeptide can include a purification tag, a chloroplast transit peptide, a mitochondrial transit peptide, an amyloplast peptide, or a leader sequence added to the amino or carboxy terminus. In some embodiments, a heat and/or drought-tolerance polypeptide includes an amino acid sequence that functions as a reporter, e.g., a green fluorescent protein or yellow fluorescent protein.

III. Nucleic Acids

Nucleic acids described herein include nucleic acids that are effective to increase heat and/or drought tolerance when transcribed in a plant or plant cell. Such nucleic acids include those that encode a heat and/or drought-tolerance polypeptide.

A. Nucleic acids encoding heat and/or drought-tolerance polypeptides

Nucleic acids encoding heat and/or drought-tolerance polypeptides are described herein. Such nucleic acids include SEQ ID NO:441, SEQ ID NO:488, SEQ ID NO:567, SEQ ID NO:589, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:710, SEQ ID NO:1241, SEQ ID NO:1260, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:363, SEQ ID NO:310, SEQ ID NO:159, SEQ ID NO:1, SEQ ID NO:1188, SEQ ID NO:1311, and SEQ ID NO:56, as described in more detail below. A nucleic acid also can be a fragment that is at least 40% (e.g., at least 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 99%) of the length of the full-length nucleic acid set forth in SEQ ID NO:441, SEQ ID NO:488, SEQ ID NO:567, SEQ ID NO:589, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:710, SEQ ID NO:1241, SEQ ID NO:1260, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:363, SEQ ID NO:310, SEQ ID NO:159, SEQ ID NO:1, SEQ ID NO:1008, and SEQ ID NO:56.

A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:441. Alternatively, a drought-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:441. For example, a drought-tolerance nucleic acid can have a nucleotide

sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:441 or a functional homolog thereof such as those identified in the sequence listing.

5 A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:488. Alternatively, a drought-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:488. For example, a drought-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:488 or a
10 functional homolog thereof such as those identified in the sequence listing.

A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:567. Alternatively, a drought-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:567. For example, a drought-tolerance nucleic acid can have a nucleotide
15 sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:567 or a functional homolog thereof such as those identified in the sequence listing.

A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:589. Alternatively, a drought-tolerance nucleic acid can be a
20 variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:589. For example, a drought-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:589 or a functional homolog thereof such as those identified in the sequence listing.

25 A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:703. Alternatively, a drought-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:703. For example, a drought-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%,
30 or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:703 or a functional homolog thereof such as those identified in the sequence listing.

A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:710. Alternatively, a drought-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID

NO:710. For example, a drought-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:710 or a functional homolog thereof such as those identified in the sequence listing.

5 A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1241. Alternatively, a drought-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1241. For example, a drought-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%,
10 or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1241 or a functional homolog thereof such as those identified in the sequence listing.

 A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1260. Alternatively, a drought-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID
15 NO:1260. For example, a drought-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1260 or a functional homolog thereof such as those identified in the sequence listing.

 A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1126. Alternatively, a drought-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID
20 NO:1126. For example, a drought-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1126 or
25 a functional homolog thereof such as those identified in the sequence listing.

 A heat-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:58. Alternatively, a heat-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:58. For example,
30 a heat-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:58 or a functional homolog thereof such as those identified in the sequence listing.

A heat-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:363. Alternatively, a heat-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:363. For example, a heat-tolerance nucleic acid can have a nucleotide sequence with at least
5 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:363 or a functional homolog thereof such as those identified in the sequence listing.

A heat-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:310. Alternatively, a heat-tolerance nucleic acid can be a variant of
10 the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:310. For example, a heat-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:310 or a functional homolog thereof such as those identified in the sequence listing.

A heat-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:159. Alternatively, a heat-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:159. For example, a heat-tolerance nucleic acid can have a nucleotide sequence with at least
15 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:159 or a functional homolog thereof such as those identified in the sequence listing.

A heat-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1. Alternatively, a heat-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1. For example,
25 a heat-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1 or a functional homolog thereof such as those identified in the sequence listing.

A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1008. Alternatively, a drought-tolerance nucleic acid can be a
30 variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1008. For example, a drought-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%,

or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1008 or a functional homolog thereof such as those identified in the sequence listing.

A heat-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:56. Alternatively, a heat-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:56. For example, a heat-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, *e.g.*, 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:56.

A drought-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1362. Alternatively, a drought-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1362. For example, a drought-tolerance nucleic acid can have a nucleotide sequence with at least 30% sequence identity, *e.g.*, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1362 or a functional homolog thereof such as those identified in the sequence listing.

Isolated nucleic acid molecules can be produced by standard techniques. For example, polymerase chain reaction (PCR) techniques can be used to obtain an isolated nucleic acid containing a nucleotide sequence described herein. PCR can be used to amplify specific sequences from DNA as well as RNA, including sequences from total genomic DNA or total cellular RNA. Various PCR methods are described, for example, in PCR Primer: A Laboratory Manual, Dieffenbach and Dveksler, eds., Cold Spring Harbor Laboratory Press, 1995. Generally, sequence information from the ends of the region of interest or beyond is employed to design oligonucleotide primers that are identical or similar in sequence to opposite strands of the template to be amplified. Various PCR strategies also are available by which site-specific nucleotide sequence modifications can be introduced into a template nucleic acid. Isolated nucleic acids also can be chemically synthesized, either as a single nucleic acid molecule (*e.g.*, using automated DNA synthesis in the 3' to 5' direction using phosphoramidite technology) or as a series of oligonucleotides. For example, one or more pairs of long oligonucleotides (*e.g.*, >100 nucleotides) can be synthesized that contain the desired sequence, with each pair containing a short segment of complementarity (*e.g.*, about 15 nucleotides) such that a duplex is formed when the oligonucleotide pair is annealed. DNA polymerase is used to extend the oligonucleotides, resulting in a single, double-stranded nucleic acid molecule per

oligonucleotide pair, which then can be ligated into a vector. Isolated nucleic acids of the invention also can be obtained by mutagenesis of, e.g., a naturally occurring DNA.

B. Use of Nucleic Acids to Modulate Expression of Polypeptides

Expression of a Heat and/or Drought-tolerance Polypeptide

5 A nucleic acid encoding one of the heat and/or drought-tolerance polypeptides described herein can be used to express the polypeptide in a plant species of interest, typically by transforming a plant cell with a nucleic acid having the coding sequence for the polypeptide operably linked in sense orientation to one or more regulatory regions. Suitable polynucleotides include full-length nucleic acids encoding heat
10 and/or drought-tolerance polypeptides or fragments of such full-length nucleic acids. In some embodiments, a complement of the full-length nucleic acid or a fragment thereof can be used. Typically, a fragment is at least 50 nucleotides, e.g., at least 50, 55, 60, 75, 100, 200, 300, 500, 600, 700, 1000, 2000 nucleotides or more.

 It will be appreciated that because of the degeneracy of the genetic code, a
15 number of nucleic acids can encode a particular heat and/or drought-tolerance polypeptide; *i.e.*, for many amino acids, there is more than one nucleotide triplet that serves as the codon for the amino acid. Thus, codons in the coding sequence for a given heat and/or drought-tolerance polypeptide can be modified such that optimal expression in a particular plant species is obtained, using appropriate codon bias
20 tables for that species.

 In some cases, expression of a heat and/or drought-tolerance polypeptide inhibits one or more functions of an endogenous polypeptide. For example, a nucleic acid that encodes a dominant negative polypeptide can be used to inhibit protein function. A dominant negative polypeptide typically is mutated or truncated relative
25 to an endogenous wild type polypeptide, and its presence in a cell inhibits one or more functions of the wild type polypeptide in that cell, *i.e.*, the dominant negative polypeptide is genetically dominant and confers a loss of function. The mechanism by which a dominant negative polypeptide confers such a phenotype can vary but often involves a protein-protein interaction or a protein-DNA interaction. For
30 example, a dominant negative polypeptide can be an enzyme that is truncated relative to a native wild type enzyme, such that the truncated polypeptide retains domains involved in binding a first protein but lacks domains involved in binding a second protein. The truncated polypeptide is thus unable to properly modulate the activity of the second protein. See, e.g., US 2007/0056058. As another example, a point

mutation that results in a non-conservative amino acid substitution in a catalytic domain can result in a dominant negative polypeptide. See, e.g., US 2005/032221. As another example, a dominant negative polypeptide can be a transcription factor that is truncated relative to a native wild type transcription factor, such that the

5 truncated polypeptide retains the DNA binding domain(s) but lacks the activation domain(s). Such a truncated polypeptide can inhibit the wild type transcription factor from binding DNA, thereby inhibiting transcription activation.

C. Constructs/Vectors

Recombinant constructs provided herein can be used to transform plants or

10 plant cells in order to increase drought and/or heat tolerance. A recombinant nucleic acid construct can comprise a nucleic acid encoding a heat and/or drought-tolerance polypeptide as described herein, operably linked to a regulatory region suitable for expressing the heat and/or drought-tolerance polypeptide in the plant or cell. Thus, a nucleic acid can comprise a coding sequence that encodes any of the heat and/or

15 drought-tolerance polypeptides as set forth in SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 60, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 73, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 127, 130, 132, 134, 136, 138, 139, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162,

20 164, 166, 168, 170, 172, 174, 176, 178, 179, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 209, 212, 214, 216, 218, 220, 222, 224, 225, 228, 229, 231, 233, 234, 235, 237, 239, 240, 242, 244, 246, 248, 250, 252, 253, 254, 256, 258, 260, 262, 264, 266, 268, 269, 271, 273, 275, 277, 279, 280, 282, 284, 286, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305,

25 307, 309, 311, 312, 314, 315, 316, 317, 319, 320, 321, 322, 323, 325, 326, 327, 329, 330, 332, 334, 335, 336, 337, 338, 339, 340, 341, 343, 344, 346, 348, 349, 350, 351, 353, 355, 356, 358, 360, 362, 364, 366, 368, 369, 370, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 390, 392, 394, 396, 398, 400, 401, 402, 404, 405, 407, 408, 410, 412, 413, 414, 416, 418, 419, 420, 421, 422, 423, 424, 426, 428, 430, 431, 432, 433,

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5 676, 678, 680, 682, 684, 685, 687, 688, 690, 691, 692, 694, 696, 698, 700, 702, 705,
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856, 857, 859, 861, 863, 865, 867, 869, 870, 871, 872, 873, 874, 876, 878, 880, 882,
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983, 985, 987, 988, 989, 990, 991, 992, 993, 995, 997, 998, 999, 1000, 1001, 1003,
1005, 1007, 1010, 1012, 1013, 1014, 1015, 1016, 1018, 1020, 1022, 1023, 1025,
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20 1050, 1051, 1053, 1055, 1056, 1058, 1059, 1061, 1062, 1064, 1066, 1068, 1069,
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1094, 1096, 1098, 1100, 1102, 1104, 1106, 1108, 1110, 1112, 1113, 1114, 1116,
1117, 1118, 1119, 1121, 1123, 1125, 1129, 1130, 1131, 1132, 1133, 1134, 1135,
1136, 1137, 1138, 1140, 1142, 1144, 1146, 1148, 1150, 1151, 1152, 1153, 1154,
25 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1164, 1166, 1168, 1170, 1172, 1174,
1175, 1177, 1179, 1181, 1182, 1184, 1186, 1188, 1189, 1191, 1193, 1195, 1197,
1199, 1201, 1203, 1205, 1207, 1209, 1210, 1212, 1214, 1215, 1216, 1218, 1219,
1221, 1222, 1223, 1225, 1226, 1228, 1230, 1231, 1232, 1234, 1236, 1238, 1240,
1242, 1244, 1246, 1248, 1250, 1252, 1254, 1256, 1258, 1262, 1264, 1265, 1267,
30 1269, 1271, 1273, 1274, 1276, 1277, 1279, 1281, 1283, 1285, 1286, 1287, 1288,
1290, 1292, 1293, 1294, 1296, 1298, 1300, 1302, 1304, 1305, 1311, 1313, 1315,
1317, 1319, 1321, 1323, 1324, 1325, 1326, 1327, 1329, 1331, 1333, 1334, 1336,
1338, 1340, 1342, 1343, 1345, 1347, 1349, 1350, 1351, 1353, 1354, 1356, 1358,
1360, or 1361. The heat and/or drought-tolerance polypeptide encoded by a

recombinant nucleic acid can be a native heat and/or drought-tolerance polypeptide, or can be heterologous to the cell. Examples of suitable regulatory regions are described in the section entitled "Regulatory Regions."

Vectors containing recombinant nucleic acid constructs such as those
5 described herein also are provided. Suitable vector backbones include, for example, those routinely used in the art such as plasmids, viruses, artificial chromosomes, BACs, YACs, or PACs. Suitable expression vectors include, without limitation, plasmids and viral vectors derived from, for example, bacteriophage, baculoviruses, and retroviruses. Numerous vectors and expression systems are commercially
10 available from such corporations as Novagen (Madison, WI), Clontech (Palo Alto, CA), Stratagene (La Jolla, CA), and Invitrogen/Life Technologies (Carlsbad, CA).

The vectors provided herein also can include, for example, origins of replication, scaffold attachment regions (SARs), and/or markers. A marker gene can confer a selectable phenotype on a plant cell. For example, a marker can confer
15 biocide resistance, such as resistance to an antibiotic (*e.g.*, kanamycin, G418, bleomycin, or hygromycin), or an herbicide (*e.g.*, glyphosate, chlorsulfuron or phosphinothricin). In addition, an expression vector can include a tag sequence designed to facilitate manipulation or detection (*e.g.*, purification or localization) of the expressed polypeptide. Tag sequences, such as luciferase, β -glucuronidase
20 (GUS), green fluorescent protein (GFP), glutathione S-transferase (GST), polyhistidine, c-myc, hemagglutinin, or Flag™ tag (Kodak, New Haven, CT) sequences typically are expressed as a fusion with the encoded polypeptide. Such tags can be inserted anywhere within the polypeptide, including at either the carboxyl or amino terminus.

25 D. Regulatory regions

The choice of regulatory regions to be included in a recombinant construct depends upon several factors, including, but not limited to, efficiency, selectability, inducibility, desired expression level, and cell- or tissue-preferential expression. It is a routine matter for one of skill in the art to modulate the expression of a coding
30 sequence by appropriately selecting and positioning regulatory regions relative to the coding sequence. Transcription of a nucleic acid can be modulated in a similar manner.

Some suitable regulatory regions initiate transcription only, or predominantly, in certain cell types. Methods for identifying and characterizing regulatory regions in

plant genomic DNA are known, including, for example, those described in the following references: Jordano *et al.*, *Plant Cell*, 1:855-866 (1989); Bustos *et al.*, *Plant Cell*, 1:839-854 (1989); Green *et al.*, *EMBO J.*, 7:4035-4044 (1988); Meier *et al.*, *Plant Cell*, 3:309-316 (1991); and Zhang *et al.*, *Plant Physiology*, 110:1069-1079 (1996).

Examples of various classes of regulatory regions are described below. Some of the regulatory regions indicated below as well as additional regulatory regions are described in more detail in U.S. Patent Application Ser. Nos. 60/505,689; 60/518,075; 60/544,771; 60/558,869; 60/583,691; 60/619,181; 60/637,140; 60/757,544; 60/776,307; 10/957,569; 11/058,689; 11/172,703; 11/208,308; 11/274,890; 60/583,609; 60/612,891; 11/097,589; 11/233,726; 11/408,791; 11/414,142; 10/950,321; 11/360,017; PCT/US05/011105; PCT/US05/23639; PCT/US05/034308; PCT/US05/034343; and PCT/US06/038236; PCT/US06/040572; and PCT/US07/62762.

For example, the sequences of regulatory regions p326, YP0144, YP0190, p13879, YP0050, p32449, 21876, YP0158, YP0214, YP0380, PT0848, PT0633, YP0128, YP0275, PT0660, PT0683, PT0758, PT0613, PT0672, PT0688, PT0837, YP0092, PT0676, PT0708, YP0396, YP0007, YP0111, YP0103, YP0028, YP0121, YP0008, YP0039, YP0115, YP0119, YP0120, YP0374, YP0101, YP0102, YP0110, YP0117, YP0137, YP0285, YP0212, YP0097, YP0107, YP0088, YP0143, YP0156, PT0650, PT0695, PT0723, PT0838, PT0879, PT0740, PT0535, PT0668, PT0886, PT0585, YP0381, YP0337, PT0710, YP0356, YP0385, YP0384, YP0286, YP0377, PD1367, PT0863, PT0829, PT0665, PT0678, YP0086, YP0188, YP0263, PT0743 and YP0096 are set forth in the sequence listing of PCT/US06/040572; the sequence of regulatory region PT0625 is set forth in the sequence listing of PCT/US05/034343; the sequences of regulatory regions PT0623, YP0388, YP0087, YP0093, YP0108, YP0022 and YP0080 are set forth in the sequence listing of U.S. Patent Application Ser. No. 11/172,703; the sequence of regulatory region PR0924 is set forth in the sequence listing of PCT/US07/62762; and the sequences of regulatory regions p530c10, pOsFIE2-2, pOsMEA, pOsYp102, and pOsYp285 are set forth in the sequence listing of PCT/US06/038236.

It will be appreciated that a regulatory region may meet criteria for one classification based on its activity in one plant species, and yet meet criteria for a different classification based on its activity in another plant species.

i. Broadly Expressing Promoters

A promoter can be said to be “broadly expressing” when it promotes transcription in many, but not necessarily all, plant tissues. For example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the shoot, shoot tip (apex), and leaves, but weakly or not at all in tissues such as roots or stems. As another example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the stem, shoot, shoot tip (apex), and leaves, but can promote transcription weakly or not at all in tissues such as reproductive tissues of flowers and developing seeds. Non-limiting examples of broadly expressing promoters that can be included in the nucleic acid constructs provided herein include the p326, YP0144, YP0190, p13879, YP0050, p32449, 21876, YP0158, YP0214, YP0380, PT0848, and PT0633 promoters. Additional examples include the cauliflower mosaic virus (CaMV) 35S promoter, the mannopine synthase (MAS) promoter, the 1’ or 2’ promoters derived from T-DNA of *Agrobacterium tumefaciens*, the figwort mosaic virus 34S promoter, actin promoters such as the rice actin promoter, and ubiquitin promoters such as the maize ubiquitin-1 promoter. In some cases, the CaMV 35S promoter is excluded from the category of broadly expressing promoters.

ii. Root Promoters

Root-active promoters confer transcription in root tissue, *e.g.*, root endodermis, root epidermis, or root vascular tissues. In some embodiments, root-active promoters are root-preferential promoters, *i.e.*, confer transcription only or predominantly in root tissue. Root-preferential promoters include the YP0128, YP0275, PT0625, PT0660, PT0683, and PT0758 promoters. Other root-preferential promoters include the PT0613, PT0672, PT0688, and PT0837 promoters, which drive transcription primarily in root tissue and to a lesser extent in ovules and/or seeds. Other examples of root-preferential promoters include the root-specific subdomains of the CaMV 35S promoter (Lam *et al.*, *Proc. Natl. Acad. Sci. USA*, 86:7890-7894 (1989)), root cell specific promoters reported by Conkling *et al.*, *Plant Physiol.*, 93:1203-1211 (1990), and the tobacco RD2 promoter.

iii. Maturing Endosperm Promoters

In some embodiments, promoters that drive transcription in maturing endosperm can be useful. Transcription from a maturing endosperm promoter typically begins after fertilization and occurs primarily in endosperm tissue during

seed development and is typically highest during the cellularization phase. Most suitable are promoters that are active predominantly in maturing endosperm, although promoters that are also active in other tissues can sometimes be used. Non-limiting examples of maturing endosperm promoters that can be included in the nucleic acid constructs provided herein include the napin promoter, the Arcelin-5 promoter, the phaseolin promoter (Bustos *et al.*, *Plant Cell*, 1(9):839-853 (1989)), the soybean trypsin inhibitor promoter (Riggs *et al.*, *Plant Cell*, 1(6):609-621 (1989)), the ACP promoter (Baerson *et al.*, *Plant Mol. Biol.*, 22(2):255-267 (1993)), the stearyl-ACP desaturase promoter (Slocombe *et al.*, *Plant Physiol.*, 104(4):167-176 (1994)), the soybean α' subunit of β -conglycinin promoter (Chen *et al.*, *Proc. Natl. Acad. Sci. USA*, 83:8560-8564 (1986)), the oleosin promoter (Hong *et al.*, *Plant Mol. Biol.*, 34(3):549-555 (1997)), and zein promoters, such as the 15 kD zein promoter, the 16 kD zein promoter, 19 kD zein promoter, 22 kD zein promoter and 27 kD zein promoter. Also suitable are the Osgt-1 promoter from the rice glutelin-1 gene (Zheng *et al.*, *Mol. Cell Biol.*, 13:5829-5842 (1993)), the beta-amylase promoter, and the barley hordein promoter. Other maturing endosperm promoters include the YP0092, PT0676, and PT0708 promoters.

iv. Ovary Tissue Promoters

Promoters that are active in ovary tissues such as the ovule wall and mesocarp can also be useful, *e.g.*, a polygalacturonidase promoter, the banana TRX promoter, the melon actin promoter, YP0396, and PT0623. Examples of promoters that are active primarily in ovules include YP0007, YP0111, YP0092, YP0103, YP0028, YP0121, YP0008, YP0039, YP0115, YP0119, YP0120, and YP0374.

v. Embryo Sac/Early Endosperm Promoters

To achieve expression in embryo sac/early endosperm, regulatory regions can be used that are active in polar nuclei and/or the central cell, or in precursors to polar nuclei, but not in egg cells or precursors to egg cells. Most suitable are promoters that drive expression only or predominantly in polar nuclei or precursors thereto and/or the central cell. A pattern of transcription that extends from polar nuclei into early endosperm development can also be found with embryo sac/early endosperm-preferential promoters, although transcription typically decreases significantly in later endosperm development during and after the cellularization phase. Expression in the zygote or developing embryo typically is not present with embryo sac/early endosperm promoters.

Promoters that may be suitable include those derived from the following genes: *Arabidopsis* viviparous-1 (see, GenBank No. U93215); *Arabidopsis* atmycl (see, Urao (1996) *Plant Mol. Biol.*, 32:571-57; Conceicao (1994) *Plant*, 5:493-505); *Arabidopsis* FIE (GenBank No. AF129516); *Arabidopsis* MEA; *Arabidopsis* FIS2 (GenBank No. AF096096); and FIE 1.1 (U.S. Patent 6,906,244). Other promoters that may be suitable include those derived from the following genes: maize MAC1 (see, Sheridan (1996) *Genetics*, 142:1009-1020); maize Cat3 (see, GenBank No. L05934; Abler (1993) *Plant Mol. Biol.*, 22:10131-1038). Other promoters include the following *Arabidopsis* promoters: YP0039, YP0101, YP0102, YP0110, YP0117, YP0119, YP0137, DME, YP0285, and YP0212. Other promoters that may be useful include the following rice promoters: p530c10, pOsFIE2-2, pOsMEA, pOsYp102, and pOsYp285.

vi. Embryo Promoters

Regulatory regions that preferentially drive transcription in zygotic cells following fertilization can provide embryo-preferential expression. Most suitable are promoters that preferentially drive transcription in early stage embryos prior to the heart stage, but expression in late stage and maturing embryos is also suitable. Embryo-preferential promoters include the barley lipid transfer protein (Ltp1) promoter (*Plant Cell Rep* (2001) 20:647-654), YP0097, YP0107, YP0088, YP0143, YP0156, PT0650, PT0695, PT0723, PT0838, PT0879, and PT0740.

vii. Photosynthetic Tissue Promoters

Promoters active in photosynthetic tissue confer transcription in green tissues such as leaves and stems. Most suitable are promoters that drive expression only or predominantly in such tissues. Examples of such promoters include the ribulose-1,5-bisphosphate carboxylase (RbcS) promoters such as the RbcS promoter from eastern larch (*Larix laricina*), the pine cab6 promoter (Yamamoto *et al.*, *Plant Cell Physiol.*, 35:773-778 (1994)), the Cab-1 promoter from wheat (Fejes *et al.*, *Plant Mol. Biol.*, 15:921-932 (1990)), the CAB-1 promoter from spinach (Lubberstedt *et al.*, *Plant Physiol.*, 104:997-1006 (1994)), the cab1R promoter from rice (Luan *et al.*, *Plant Cell*, 4:971-981 (1992)), the pyruvate orthophosphate dikinase (PPDK) promoter from corn (Matsuoka *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:9586-9590 (1993)), the tobacco Lhcb1*2 promoter (Cerdan *et al.*, *Plant Mol. Biol.*, 33:245-255 (1997)), the *Arabidopsis thaliana* SUC2 sucrose-H⁺ symporter promoter (Truernit *et al.*, *Planta*, 196:564-570 (1995)), and thylakoid membrane protein promoters from spinach (psaD,

psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other photosynthetic tissue promoters include PT0535, PT0668, PT0886, YP0144, YP0380 and PT0585.

viii. Vascular Tissue Promoters

Examples of promoters that have high or preferential activity in vascular bundles include YP0087, YP0093, YP0108, YP0022, and YP0080. Other vascular tissue-preferential promoters include the glycine-rich cell wall protein GRP 1.8 promoter (Keller and Baumgartner, *Plant Cell*, 3(10):1051-1061 (1991)), the Commelina yellow mottle virus (CoYMV) promoter (Medberry *et al.*, *Plant Cell*, 4(2):185-192 (1992)), and the rice tungro bacilliform virus (RTBV) promoter (Dai *et al.*, *Proc. Natl. Acad. Sci. USA*, 101(2):687-692 (2004)).

ix. Inducible Promoters

Inducible promoters confer transcription in response to external stimuli such as chemical agents or environmental stimuli. For example, inducible promoters can confer transcription in response to hormones such as gibberellic acid or ethylene, or in response to light or drought. Examples of drought-inducible promoters include YP0380, PT0848, YP0381, YP0337, PT0633, YP0374, PT0710, YP0356, YP0385, YP0396, YP0388, YP0384, PT0688, YP0286, YP0377, PD1367, and PD0901. Examples of nitrogen-inducible promoters include PT0863, PT0829, PT0665, and PT0886. Examples of shade-inducible promoters include PR0924 and PT0678. An example of a promoter induced by salt is rd29A (Kasuga *et al.*, *Nature Biotech* 17: 287-291 (1999)).

x. Basal Promoters

A basal promoter is the minimal sequence necessary for assembly of a transcription complex required for transcription initiation. Basal promoters frequently include a "TATA box" element that may be located between about 15 and about 35 nucleotides upstream from the site of transcription initiation. Basal promoters also may include a "CCAAT box" element (typically the sequence CCAAT) and/or a GGGCG sequence, which can be located between about 40 and about 200 nucleotides, typically about 60 to about 120 nucleotides, upstream from the transcription start site.

xi. Stem Promoters

A stem promoter may be specific to one or more stem tissues or specific to stem and other plant parts. Stem promoters may have high or preferential activity in, for example, epidermis and cortex, vascular cambium, procambium, or xylem.

Examples of stem promoters include YP0018 which is disclosed in US20060015970 and CryIA(b) and CryIA(c) (Braga et al., *Journal of New Seeds* 5:209-221 (2003)).

xii. Other Promoters

Other classes of promoters include, but are not limited to, shoot-preferential, callus-preferential, trichome cell-preferential, guard cell-preferential such as PT0678, tuber-preferential, parenchyma cell-preferential, and senescence-preferential promoters. Promoters designated YP0086, YP0188, YP0263, PT0758, PT0743, PT0829, YP0119, and YP0096, as described in the above-referenced patent applications, may also be useful.

10 xiii. Other Regulatory Regions

A 5' untranslated region (UTR) can be included in nucleic acid constructs described herein. A 5' UTR is transcribed, but is not translated, and lies between the start site of the transcript and the translation initiation codon and may include the +1 nucleotide. A 3' UTR can be positioned between the translation termination codon and the end of the transcript. UTRs can have particular functions such as increasing mRNA stability or attenuating translation. Examples of 3' UTRs include, but are not limited to, polyadenylation signals and transcription termination sequences, *e.g.*, a nopaline synthase termination sequence.

It will be understood that more than one regulatory region may be present in a recombinant polynucleotide, *e.g.*, introns, enhancers, upstream activation regions, transcription terminators, and inducible elements. Thus, for example, more than one regulatory region can be operably linked to the sequence of a polynucleotide encoding a heat and/or drought-tolerance polypeptide.

Regulatory regions, such as promoters for endogenous genes, can be obtained by chemical synthesis or by subcloning from a genomic DNA that includes such a regulatory region. A nucleic acid comprising such a regulatory region can also include flanking sequences that contain restriction enzyme sites that facilitate subsequent manipulation.

30 IV. Transgenic Plants and Plant Cells

A. Transformation

The invention also features transgenic plant cells and plants comprising at least one recombinant nucleic acid construct described herein. A plant or plant cell can be transformed by having a construct integrated into its genome, *i.e.*, can be stably

transformed. Stably transformed cells typically retain the introduced nucleic acid with each cell division. A plant or plant cell can also be transiently transformed such that the construct is not integrated into its genome. Transiently transformed cells typically lose all or some portion of the introduced nucleic acid construct with each
5 cell division such that the introduced nucleic acid cannot be detected in daughter cells after a sufficient number of cell divisions. Both transiently transformed and stably transformed transgenic plants and plant cells can be useful in the methods described herein.

Transgenic plant cells used in methods described herein can constitute part or
10 all of a whole plant. Such plants can be grown in a manner suitable for the species under consideration, either in a growth chamber, a greenhouse, or in a field. Transgenic plants can be bred as desired for a particular purpose, *e.g.*, to introduce a recombinant nucleic acid into other lines, to transfer a recombinant nucleic acid to other species, or for further selection of other desirable traits. Alternatively,
15 transgenic plants can be propagated vegetatively for those species amenable to such techniques. As used herein, a transgenic plant also refers to progeny of an initial transgenic plant provided the progeny inherits the transgene. Seeds produced by a transgenic plant can be grown and then selfed (or outcrossed and selfed) to obtain seeds homozygous for the nucleic acid construct.

20 Transgenic plants can be grown in suspension culture, or tissue or organ culture. For the purposes of this invention, solid and/or liquid tissue culture techniques can be used. When using solid medium, transgenic plant cells can be placed directly onto the medium or can be placed onto a filter that is then placed in contact with the medium. When using liquid medium, transgenic plant cells can be placed onto a flotation device, *e.g.*, a porous
25 membrane that contacts the liquid medium. A solid medium can be, for example, Murashige and Skoog (MS) medium containing agar and a suitable concentration of an auxin, *e.g.*, 2,4-dichlorophenoxyacetic acid (2,4-D), and a suitable concentration of a cytokinin, *e.g.*, kinetin.

When transiently transformed plant cells are used, a reporter sequence
30 encoding a reporter polypeptide having a reporter activity can be included in the transformation procedure and an assay for reporter activity or expression can be performed at a suitable time after transformation. A suitable time for conducting the assay typically is about 1-21 days after transformation, *e.g.*, about 1-14 days, about 1-7 days, or about 1-3 days. The use of transient assays is particularly convenient for

rapid analysis in different species, or to confirm expression of a heterologous heat and/or drought-tolerance polypeptide whose expression has not previously been confirmed in particular recipient cells.

Techniques for introducing nucleic acids into monocotyledonous and
5 dicotyledonous plants are known in the art, and include, without limitation, *Agrobacterium*-mediated transformation, viral vector-mediated transformation, electroporation and particle gun transformation, *e.g.*, U.S. Patents 5,538,880; 5,204,253; 6,329,571 and 6,013,863. If a cell or cultured tissue is used as the recipient tissue for transformation, plants can be regenerated from transformed cultures if desired, by techniques known to those skilled in
10 the art.

B. Screening/selection

A population of transgenic plants can be screened and/or selected for those members of the population that have a trait or phenotype conferred by expression of the transgene. For example, a population of progeny of a single transformation event
15 can be screened for those plants having a desired level of expression of a heat and/or drought-tolerance polypeptide or nucleic acid. Physical and biochemical methods can be used to identify expression levels. These include Southern analysis or PCR amplification for detection of a polynucleotide; Northern blots, S1 RNase protection, primer-extension, or RT-PCR amplification for detecting RNA transcripts; enzymatic
20 assays for detecting enzyme or ribozyme activity of polypeptides and polynucleotides; and protein gel electrophoresis, Western blots, immunoprecipitation, and enzyme-linked immunoassays to detect polypeptides. Other techniques such as *in situ* hybridization, enzyme staining, and immunostaining also can be used to detect the presence or expression of polypeptides and/or polynucleotides. Methods for
25 performing all of the referenced techniques are known. As an alternative, a population of plants comprising independent transformation events can be screened for those plants having a desired trait, such as increased drought tolerance or increased heat tolerance. Selection and/or screening can be carried out over one or more generations, and/or in more than one geographic location. In some cases,
30 transgenic plants can be grown and selected under conditions which induce a desired phenotype or are otherwise necessary to produce a desired phenotype in a transgenic plant. In addition, selection and/or screening can be applied during a particular developmental stage in which the phenotype is expected to be exhibited by the plant. Selection and/or screening can be carried out to choose those transgenic plants having

a statistically significant difference in heat and/or drought tolerance relative to a control plant that lacks the transgene. Selected or screened transgenic plants have an altered phenotype as compared to a corresponding control plant, as described in the “Transgenic Plant Phenotypes” section herein.

5 C. Plant Species

The polynucleotides and vectors described herein can be used to transform a number of monocotyledonous and dicotyledonous plants and plant cell systems, including species from one of the following families: *Acanthaceae*, *Alliaceae*, *Alstroemeriaceae*, *Amaryllidaceae*, *Apocynaceae*, *Arecaceae*, *Asteraceae*,
 10 *Berberidaceae*, *Bixaceae*, *Brassicaceae*, *Bromeliaceae*, *Cannabaceae*, *Caryophyllaceae*, *Cephalotaxaceae*, *Chenopodiaceae*, *Colchicaceae*, *Cucurbitaceae*, *Dioscoreaceae*, *Ephedraceae*, *Erythroxylaceae*, *Euphorbiaceae*, *Fabaceae*, *Lamiaceae*, *Linaceae*, *Lycopodiaceae*, *Malvaceae*, *Melanthiaceae*, *Musaceae*, *Myrtaceae*, *Nyssaceae*, *Papaveraceae*, *Pinaceae*, *Plantaginaceae*, *Poaceae*,
 15 *Rosaceae*, *Rubiaceae*, *Salicaceae*, *Sapindaceae*, *Solanaceae*, *Taxaceae*, *Theaceae*, or *Vitaceae*.

Suitable species may include members of the genus *Abelmoschus*, *Abies*, *Acer*, *Agrostis*, *Allium*, *Alstroemeria*, *Ananas*, *Andrographis*, *Andropogon*, *Artemisia*, *Arundo*, *Atropa*, *Berberis*, *Beta*, *Bixa*, *Brassica*, *Calendula*, *Camellia*, *Camptotheca*,
 20 *Cannabis*, *Capsicum*, *Carthamus*, *Catharanthus*, *Cephalotaxus*, *Chrysanthemum*, *Cinchona*, *Citrullus*, *Coffea*, *Colchicum*, *Coleus*, *Cucumis*, *Cucurbita*, *Cynodon*, *Datura*, *Dianthus*, *Digitalis*, *Dioscorea*, *Elaeis*, *Ephedra*, *Erianthus*, *Erythroxylum*, *Eucalyptus*, *Festuca*, *Fragaria*, *Galanthus*, *Glycine*, *Gossypium*, *Helianthus*, *Hevea*, *Hordeum*, *Hyoscyamus*, *Jatropha*, *Lactuca*, *Linum*, *Lolium*, *Lupinus*, *Lycopersicon*,
 25 *Lycopodium*, *Manihot*, *Medicago*, *Mentha*, *Miscanthus*, *Musa*, *Nicotiana*, *Oryza*, *Panicum*, *Papaver*, *Parthenium*, *Pennisetum*, *Petunia*, *Phalaris*, *Phleum*, *Pinus*, *Poa*, *Poinsettia*, *Populus*, *Rauwolfia*, *Ricinus*, *Rosa*, *Saccharum*, *Salix*, *Sanguinaria*, *Scopolia*, *Secale*, *Solanum*, *Sorghum*, *Spartina*, *Spinacea*, *Tanacetum*, *Taxus*, *Theobroma*, *Triticosecale*, *Triticum*, *Uniola*, *Veratrum*, *Vinca*, *Vitis*, and *Zea*.

30 Suitable species include *Panicum* spp. or hybrids thereof, *Sorghum* spp. or hybrids thereof, sudangrass, *Miscanthus* spp. or hybrids thereof, *Saccharum* spp. or hybrids thereof, *Erianthus* spp., *Populus* spp., *Andropogon gerardii* (big bluestem), *Pennisetum purpureum* (elephant grass) or hybrids thereof (e.g., *Pennisetum purpureum* x *Pennisetum typhoidum*), *Phalaris arundinacea* (reed canarygrass),

Cynodon dactylon (bermudagrass), *Festuca arundinacea* (tall fescue), *Spartina pectinata* (prairie cord-grass), *Medicago sativa* (alfalfa), *Arundo donax* (giant reed) or hybrids thereof, *Secale cereale* (rye), *Salix* spp. (willow), *Eucalyptus* spp. (eucalyptus), *Triticosecale* (*Triticum* - wheat X rye), *Tripsicum dactyloides* (Eastern gammagrass), *Leymus cinereus* (basin wildrye), *Leymus condensatus* (giant wildrye),
 5 and bamboo.

In some embodiments, a suitable species can be a wild, weedy, or cultivated sorghum species such as, but not limited to, *Sorghum alnum*, *Sorghum amylum*, *Sorghum angustum*, *Sorghum arundinaceum*, *Sorghum bicolor* (such as bicolor, guinea, caudatum, kafir, and durra), *Sorghum brachypodium*, *Sorghum bulbosum*,
 10 *Sorghum burmahicum*, *Sorghum controversum*, *Sorghum drummondii*, *Sorghum ecarinatum*, *Sorghum exstans*, *Sorghum grande*, *Sorghum halepense*, *Sorghum interjectum*, *Sorghum intrans*, *Sorghum laxiflorum*, *Sorghum leiocladum*, *Sorghum macrospermum*, *Sorghum matarankense*, *Sorghum miliaceum*, *Sorghum nigrum*,
 15 *Sorghum nitidum*, *Sorghum plumosum*, *Sorghum propinquum*, *Sorghum purpureosericeum*, *Sorghum stipoides*, *Sorghum sudanense*, *Sorghum timorense*, *Sorghum trichocladum*, *Sorghum versicolor*, *Sorghum virgatum*, *Sorghum vulgare*, or hybrids such as *Sorghum* × *alnum*, *Sorghum* × *sudangrass* or *Sorghum* × *drummondii*.

20 Suitable species also include *Helianthus annuus* (sunflower), *Carthamus tinctorius* (safflower), *Jatropha curcas* (jatropha), *Ricinus communis* (castor), *Elaeis guineensis* (palm), *Linum usitatissimum* (flax), and *Brassica juncea*.

Suitable species also include *Beta vulgaris* (sugarbeet), and *Manihot esculenta* (cassava).

25 Suitable species also include *Lycopersicon esculentum* (tomato), *Lactuca sativa* (lettuce), *Musa paradisiaca* (banana), *Solanum tuberosum* (potato), *Brassica oleracea* (broccoli, cauliflower, brusselsprouts), *Camellia sinensis* (tea), *Fragaria ananassa* (strawberry), *Theobroma cacao* (cocoa), *Coffea arabica* (coffee), *Vitis vinifera* (grape), *Ananas comosus* (pineapple), *Capsicum annum* (hot & sweet pepper), *Allium cepa* (onion),
 30 *Cucumis melo* (melon), *Cucumis sativus* (cucumber), *Cucurbita maxima* (squash), *Cucurbita moschata* (squash), *Spinacea oleracea* (spinach), *Citrullus lanatus* (watermelon), *Abelmoschus esculentus* (okra), and *Solanum melongena* (eggplant).

Suitable species also include *Papaver somniferum* (opium poppy), *Papaver orientale*, *Taxus baccata*, *Taxus brevifolia*, *Artemisia annua*, *Cannabis sativa*, *Camptotheca acuminata*, *Catharanthus roseus*, *Vinca rosea*, *Cinchona officinalis*, *Colchicum autumnale*, *Veratrum californica*, *Digitalis lanata*, *Digitalis purpurea*,
 5 *Dioscorea* spp., *Andrographis paniculata*, *Atropa belladonna*, *Datura stomonium*, *Berberis* spp., *Cephalotaxus* spp., *Ephedra sinica*, *Ephedra* spp., *Erythroxylum coca*, *Galanthus wornorii*, *Scopolia* spp., *Lycopodium serratum* (= *Huperzia serrata*), *Lycopodium* spp., *Rauwolfia serpentina*, *Rauwolfia* spp., *Sanguinaria canadensis*, *Hyoscyamus* spp., *Calendula officinalis*, *Chrysanthemum parthenium*, *Coleus*
 10 *forskohlii*, and *Tanacetum parthenium*.

Suitable species also include *Parthenium argentatum* (guayule), *Hevea* spp. (rubber), *Mentha spicata* (mint), *Mentha piperita* (mint), *Bixa orellana*, and *Alstroemeria* spp.

Suitable species also include *Rosa* spp. (rose), *Dianthus caryophyllus*
 15 (carnation), *Petunia* spp. (petunia) and *Poinsettia pulcherrima* (poinsettia).

Suitable species also include *Nicotiana tabacum* (tobacco), *Lupinus albus* (lupin), *Uniola paniculata* (oats), bentgrass (*Agrostis* spp.), *Populus tremuloides* (aspen), *Pinus* spp. (pine), *Abies* spp. (fir), *Acer* spp. (maple), *Hordeum vulgare* (barley), *Poa pratensis* (bluegrass), *Lolium* spp. (ryegrass) and *Phleum pratense*
 20 (timothy).

Thus, the methods and compositions can be used over a broad range of plant species, including species from the dicot genera *Brassica*, *Carthamus*, *Glycine*, *Gossypium*, *Helianthus*, *Jatropha*, *Parthenium*, *Populus*, and *Ricinus*; and the monocot genera *Elaeis*, *Festuca*, *Hordeum*, *Lolium*, *Oryza*, *Panicum*, *Pennisetum*,
 25 *Phleum*, *Poa*, *Saccharum*, *Secale*, *Sorghum*, *Triticosecale*, *Triticum*, and *Zea*. In some embodiments, a plant is a member of the species *Panicum virgatum* (switchgrass), *Sorghum bicolor* (sorghum, sudangrass), *Miscanthus giganteus* (miscanthus), *Saccharum* sp. (energycane), *Populus balsamifera* (poplar), *Zea mays* (corn), *Glycine max* (soybean), *Brassica napus* (canola), *Triticum aestivum* (wheat),
 30 *Gossypium hirsutum* (cotton), *Oryza sativa* (rice), *Helianthus annuus* (sunflower), *Medicago sativa* (alfalfa), *Beta vulgaris* (sugarbeet), or *Pennisetum glaucum* (pearl millet).

In certain embodiments, the polynucleotides and vectors described herein can be used to transform a number of monocotyledonous and dicotyledonous plants and plant cell systems, wherein such plants are hybrids of different species or varieties of a specific species (*e.g.*, *Saccharum* sp. X *Miscanthus* sp., *Saccharum* sp. X *Sorghum* sp., *Panicum virgatum* x *Panicum amarum*, *Panicum virgatum* x *Panicum amarulum*,
 5 *Pennisetum purpureum* x *Pennisetum typhoidum*).

D. Transgenic Plant Phenotypes

In some embodiments, a plant in which expression of a heat and/or drought-tolerance polypeptide is modulated can have increased heat tolerance or drought
 10 tolerance. In some cases, a plant in which expression of a heat and/or drought-tolerance polypeptide is modulated can exhibit both heat tolerance and drought tolerance. The phenotype of a transgenic plant in which expression of a heat and/or drought-tolerance polypeptide is modulated and a corresponding control plant that either lacks the transgene or does not express the transgene can be evaluated under
 15 particular environmental conditions that are useful for simulating drought conditions. The phenotype of a transgenic plant in which expression of a heat and/or drought-tolerance polypeptide is modulated and a corresponding control plant can also be evaluated under heat shock conditions.

For example, a heat and/or drought-tolerance polypeptide described herein can
 20 be expressed in a transgenic plant, resulting in increased growth as compared to a plant that does not express the polypeptide when grown under drought conditions or heat shock conditions, or following such conditions. Growth can be assessed with physiological parameters such as, for example, plant height, number of new shoots, number of new leaves, leaf length, seedling area, or seed number.

In some cases, a transgenic plant expressing a heat and/or drought tolerance polypeptide described herein can exhibit a height that is from about 5% to about 100% greater (*e.g.*, about 5% to about 12%; about 5% to about 40%; about 5% to about 80%; about 7% to about 20%; about 10% to about 15%; about 10% to about 50%; about 10% to about 90%; about 20% to about 25%; about 20% to about 45%;
 25 about 20% to about 75%; about 25% to about 60%; about 25% to about 100%; about 30% to about 50%; about 30% to about 70%; about 40% to about 50%; about 45% to about 60%; about 50% to about 80%; about 55% to about 75%; about 60% to about 80%; about 60% to about 95%; about 75% to about 100%; about 80% to about 100%; about 90% to about 95%; or about 95% to about 100% greater) than a plant not
 30

expressing the polypeptide when grown under drought conditions or heat shock conditions, or following such conditions.

In some instances, a transgenic plant expressing a heat and/or drought-tolerance polypeptide can exhibit greater leaf area or greater leaf length than a
5 corresponding control plant that does not express the polypeptide when grown under heat shock conditions or drought conditions, or following such conditions. For example, a transgenic plant expressing a heat and/or drought-tolerance polypeptide can have a leaf area that is 5% to about 100% greater (*e.g.*, about 5% to about 7%; about 5% to about 20%; about 8% to about 80%; about 10% to about 20%; about 10%
10 to about 25%; about 10% to about 50%; about 10% to about 90%; about 15% to about 25%; about 20% to about 45%; about 20% to about 70%; about 25% to about 40%; about 25% to about 100%; about 30% to about 50%; about 30% to about 70%; about 40% to about 50%; about 45% to about 60%; about 50% to about 80%; about 55% to about 75%; about 60% to about 80%; about 60% to about 95%; about 75% to about
15 100%; about 80% to about 100%; about 90% to about 95%; or about 95% to about 100% greater) than a corresponding control plant that does not express the polypeptide when grown under heat shock conditions or drought conditions, or following such conditions. In another example, a transgenic plant expressing a heat and/or drought-tolerance polypeptide can have a leaf length that is from about 5% to
20 about 100% greater (*e.g.*, about 5% to about 12%; about 5% to about 40%; about 5% to about 80%; about 7% to about 20%; about 10% to about 15%; about 10% to about 50%; about 10% to about 90%; about 20% to about 25%; about 20% to about 45%; about 20% to about 75%; about 25% to about 60%; about 25% to about 100%; about 30% to about 50%; about 30% to about 70%; about 40% to about 50%; about 45% to
25 about 60%; about 50% to about 80%; about 55% to about 75%; about 60% to about 80%; about 60% to about 95%; about 75% to about 100%; about 80% to about 100%; about 90% to about 95%; or about 95% to about 100% greater) than a corresponding control plant that does not express the polypeptide when grown under heat shock conditions or drought conditions, or following such conditions.

30 In other cases, when a polypeptide described herein is expressed in a transgenic plant, the transgenic plant can exhibit a seed number (number of seeds per plant) from about 10% to about 95% greater (*e.g.*, from about 10% to about 20%; from about 10% to about 50%; from about 10% to about 70%; from about 20% to about 60%; from about 20% to about 75%; from about 25% to about 85%; from about

30% to about 70%; from about 35% to about 90%; from about 40% to about 60%; from about 40% to about 85%; from about 50% to about 80%; from about 50% to about 90%; or from about 70% to about 90% greater) than a control plant not expressing the polypeptide when grown under heat shock conditions or drought conditions. In certain cases, when a polypeptide described herein is expressed in a transgenic plant, the transgenic plant can exhibit an increase in seed weight per plant from about 5% to about 100% greater (*e.g.*, about 5% to about 12%; about 5% to about 40%; about 5% to about 80%; about 7% to about 20%; about 10% to about 15%; about 10% to about 50%; about 10% to about 90%; about 20% to about 25%; about 20% to about 45%; about 20% to about 75%; about 25% to about 60%; about 25% to about 100%; about 30% to about 50%; about 30% to about 70%; about 40% to about 50%; about 45% to about 60%; about 50% to about 80%; about 55% to about 75%; about 60% to about 80%; about 60% to about 95%; about 75% to about 100%; about 80% to about 100%; about 90% to about 95%; or about 95% to about 100% greater) than the seed weight in a plant not expressing the polypeptide when grown under heat shock conditions or drought conditions.

Transgenic plants expressing a heat and/or drought-tolerance polypeptide also can exhibit a lower transpiration rate compared to control plants of the same genetic background. Transpiration rate is another physiological parameter that is indicative of how well a plant can tolerate drought conditions. For example, plants with a low transpiration rate are expected to lose water more slowly than plants with higher transpiration rates and therefore would be expected to better withstand drought conditions (*i.e.*, have better drought tolerance). When a polypeptide described herein is expressed in a transgenic plant, the transgenic plant can exhibit a transpiration rate that is reduced by about 0.25% to 100% (*e.g.*, 0.27%, 0.3%, 0.43%, 0.55%, 0.7%, 0.99%, 1%, 2%, 4%, 6%, 8%, 10%, 12%, 15%, 18%, 22%, 28%, 35%, 37%, 42%, 45%, 47%, 50%, 55%, 64%, 68%, 71%, 75%, 77%, 80%, 83%, 86%, 89%, 90%, 92%, 95%, 98%, or 99%) as compared to the transpiration rate in a corresponding control plant when grown under drought conditions.

In some cases, a transgenic plant expressing a heat and/or drought-tolerance polypeptide described herein can exhibit a decreased change in photosynthetic activity ($\Delta Fv/Fm$) after exposure to heat shock conditions as compared to a corresponding control plant that does not express the polypeptide when grown under the same

conditions. In some cases, a transgenic plant expressing a heat and/or drought-tolerance polypeptide described herein can exhibit an increased change in photosynthetic activity ($\Delta Fv/Fm-D_2$) two days post heat-shock treatment as compared to a corresponding control plant that does not express the polypeptide when grown

5 under the same conditions. For example, a transgenic plant expressing a heat and/or drought-tolerance polypeptide can exhibit a $\Delta Fv/Fm$ of from about 0.1 to about 0.8 (e.g., about 0.2 to about 0.28; about 0.2 to about 0.32; about 0.22 to about 0.35; about 0.29 to about 0.4; about 0.3 to about 0.45; about 0.33 to about 0.41; about 0.35 to about 0.5; about 0.4 to about 0.8; about 0.46 to about 0.52; about 0.5 to about 0.65; about 0.5 to about 0.8; about 0.6 to about 0.7; about 0.6 to about 0.9; about 0.65 to about 0.75; about 0.7 to about 0.9; or about 0.75 to about 0.8) or a $\Delta Fv/Fm-D_2$ range of from about 0.03 to about 0.8 (e.g., about 0.03 to about 0.08; about 0.03 to about 0.032; about 0.04 to about 0.05; about 0.09 to about 0.4; about 0.05 to about 0.5; about 0.075 to about 0.1; about 0.08 to about 0.2; about 0.3 to about 0.45; about 0.33 to about 0.41; about 0.35 to about 0.5; about 0.4 to about 0.8; about 0.46 to about 0.52; about 0.5 to about 0.65; about 0.5 to about 0.8; about 0.6 to about 0.7; about 0.6 to about 0.9; about 0.65 to about 0.75; about 0.7 to about 0.9; about 0.75 to about 0.85; or about 0.8 to about 0.9). In some embodiments, photosynthetic activity can be reduced by about 0.25% to about 100% (e.g., about 0.25% to about 0.4%, about 0.25% to about 1%, about 0.25% to about 5%, about 0.5% to about 10%, about 1% to about 5%, about 1% to about 10%, about 2% to about 8%, about 3% to about 20%, about 5% to about 7%; about 5% to about 20%; about 5% to about 45%, about 8% to about 80%; about 10% to about 20%; about 10% to about 25%; about 10% to about 50%; about 10% to about 90%; about 15% to about 25%; about 20% to about 45%; about 20% to about 70%; about 25% to about 40%; about 25% to about 99%; about 30% to about 50%; about 30% to about 70%; about 40% to about 50%; about 45% to about 60%; about 50% to about 80%; about 55% to about 75%; about 60% to about 80%; about 60% to about 95%; about 75% to about 99%; about 80% to about 99%; about 90% to about 95%; or about 95% to about 100%) as compared to the

30 photosynthetic activity in a corresponding control plant following heat shock conditions.

Typically, a difference in the heat and/or drought tolerance in a transgenic plant relative to a control plant is considered statistically significant at $p \leq 0.05$ with an appropriate parametric or non-parametric statistic, *e.g.*, Chi-square test, Student's t-test, Mann-Whitney test, or F-test. In some embodiments, a difference in the heat and/or drought tolerance is statistically significant at $p < 0.1$, $p < 0.05$, or $p < 0.01$.

The phenotype of a transgenic plant is evaluated relative to a control plant. A plant is said "not to express" a polypeptide when the plant exhibits less than 10%, *e.g.*, less than 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.1%, or 0.01%, of the amount of polypeptide or mRNA encoding the polypeptide exhibited by the plant of interest. Expression can be evaluated using methods including, for example, RT-PCR, Northern blots, S1 RNase protection, primer extensions, Western blots, protein gel electrophoresis, immunoprecipitation, enzyme-linked immunoassays, chip assays, and mass spectrometry. It should be noted that if a polypeptide is expressed under the control of a tissue-preferential or broadly expressing promoter, expression can be evaluated in the entire plant or in a selected tissue. Similarly, if a polypeptide is expressed at a particular time, *e.g.*, at a particular time in development or upon induction, expression can be evaluated selectively at a desired time period.

V. Plant Breeding

Genetic polymorphisms are discrete allelic sequence differences in a population. Typically, an allele that is present at 1% or greater is considered to be a genetic polymorphism. The discovery that polypeptides disclosed herein can increase heat and/or drought tolerance is useful in plant breeding, because genetic polymorphisms exhibiting a degree of linkage with loci for such polypeptides are more likely to be correlated with variation in heat and/or drought tolerance. For example, genetic polymorphisms linked to the loci for such polypeptides are more likely to be useful in marker-assisted breeding programs to create lines having increased heat and/or drought tolerance.

Thus, one aspect of the invention includes methods of identifying whether one or more genetic polymorphisms are associated with heat and/or drought tolerance. Such methods involve determining whether genetic polymorphisms in a given population exhibit linkage with the locus for one of the polypeptides depicted in Figures 1-16 and/or a functional homolog thereof. The correlation is measured between variation in heat and/or drought tolerance in plants of the population and the

presence of the genetic polymorphism(s) in plants of the population, thereby identifying whether or not the genetic polymorphism(s) are associated with variation for the trait. If the presence of a particular allele is statistically significantly correlated with a modulation in heat and/or drought tolerance, the allele is associated with variation for the trait and is useful as a marker for the trait. If, on the other hand, the presence of a particular allele is not significantly correlated with the desired modulation, the allele is not associated with variation for the trait and is not useful as a marker.

Such methods are applicable to populations containing the naturally occurring endogenous polypeptide rather than an exogenous nucleic acid encoding the polypeptide, *i.e.*, populations that are not transgenic for the exogenous nucleic acid. It will be appreciated, however, that populations suitable for use in the methods may contain a transgene for another, different trait, *e.g.*, herbicide resistance.

Genetic polymorphisms that are useful in such methods include simple sequence repeats (SSRs, or microsatellites), rapid amplification of polymorphic DNA (RAPDs), single nucleotide polymorphisms (SNPs), amplified fragment length polymorphisms (AFLPs) and restriction fragment length polymorphisms (RFLPs). SSR polymorphisms can be identified, for example, by making sequence specific probes and amplifying template DNA from individuals in the population of interest by PCR. For example, PCR techniques can be used to enzymatically amplify a genetic marker associated with a nucleotide sequence conferring a specific trait (*e.g.*, nucleotide sequences described herein). PCR can be used to amplify specific sequences from DNA as well as RNA, including sequences from total genomic DNA or total cellular RNA. When using RNA as a source of template, reverse transcriptase can be used to synthesize complementary DNA (cDNA) strands. Various PCR methods are described, for example, in PCR Primer: A Laboratory Manual, Dieffenbach and Dveksler, eds., Cold Spring Harbor Laboratory Press, 1995.

Generally, sequence information from polynucleotides flanking the region of interest or beyond is employed to design oligonucleotide primers that are identical or similar in sequence to opposite strands of the template to be amplified. Primers are typically 14 to 40 nucleotides in length, but can range from 10 nucleotides to hundreds of nucleotides in length. Template and amplified DNA is repeatedly denatured at a high temperature to separate the double strand, then cooled to allow annealing of primers and the extension of nucleotide sequences through the

microsatellite, resulting in sufficient DNA for detection of PCR products. If the probes flank an SSR in the population, PCR products of different sizes will be produced. See, *e.g.*, U.S. Patent 5,766,847.

5 PCR products can be qualitative or quantitatively analyzed using several techniques. For example, PCR products can be stained with a fluorescent molecule (*e.g.*, PicoGreen[®] or OliGreen[®]) and detected in solution using spectrophotometry or capillary electrophoresis. In some cases, PCR products can be separated in a gel matrix (*e.g.*, agarose or polyacrylamide) by electrophoresis, and size-fractionated bands comprising PCR products can be visualized using nucleic acid stains. Suitable
10 stains can fluoresce under UV light (*e.g.*, Ethidium bromide, GR Safe, SYBR[®] Green, or SYBR[®] Gold). The results can be visualized via transillumination or epi-illumination, and an image of the fluorescent pattern can be acquired using a camera or scanner, for example. The image can be processed and analyzed using specialized software (*e.g.*, ImageJ) to measure and compare the intensity of a band of interest
15 against a standard loaded on the same gel.

Alternatively, SSR polymorphisms can be identified by using PCR product(s) as a probe against Southern blots from different individuals in the population. See, U.H. Refseth et al., (1997) *Electrophoresis* 18: 1519. Briefly, PCR products are separated by length through gel electrophoresis and transferred to a membrane. SSR-
20 specific DNA probes, such as oligonucleotides labeled with radioactive, fluorescent, or chromogenic molecules, are applied to the membrane and hybridize to bound PCR products with a complementary nucleotide sequence. The pattern of hybridization can be visualized by autoradiography or by development of color on the membrane, for example.

25 In some cases, PCR products can be quantified using a real-time thermocycler detection system. For example, Quantitative real-time PCR can use a fluorescent dye that forms a DNA-dye-complex (*e.g.*, SYBR[®] Green), or a fluorophore-containing DNA probe, such as single-stranded oligonucleotides covalently bound to a fluorescent reporter or fluorophore (*e.g.* 6-carboxyfluorescein or
30 tetrachlorofluorescein) and quencher (*e.g.*, tetramethylrhodamine or dihydrocyclopyrroloindole tripeptide minor groove binder). The fluorescent signal allows detection of the amplified product in real time, thereby indicating the presence

of a sequence of interest, and allowing quantification of the copy number of a sequence of interest in cellular DNA or expression level of a sequence of interest from cellular mRNA.

The identification of RFLPs is discussed, for example, in Alonso-Blanco et al. (5) (*Methods in Molecular Biology*, vol.82, "Arabidopsis Protocols", pp. 137-146, J.M. Martinez-Zapater and J. Salinas, eds., c. 1998 by Humana Press, Totowa, NJ); Burr ("Mapping Genes with Recombinant Inbreds", pp. 249-254, in Freeling, M. and V. Walbot (Ed.), *The Maize Handbook*, c. 1994 by Springer-Verlag New York, Inc.: New York, NY, USA; Berlin Germany; Burr et al. *Genetics* (1998) 118: 519; and 10 Gardiner, J. et al., (1993) *Genetics* 134: 917). For example, to produce a RFLP library enriched with single- or low-copy expressed sequences, total DNA can be digested with a methylation-sensitive enzyme (*e.g.*, *PstI*). The digested DNA can be separated by size on a preparative gel. Polynucleotide fragments (500 to 2000 bp) can be excised, eluted and cloned into a plasmid vector (*e.g.*, pUC18). Southern blots of 15 plasmid digests can be probed with total sheared DNA to select clones that hybridize to single- and low-copy sequences. Additional restriction endonucleases can be tested to increase the number of polymorphisms detected.

The identification of AFLPs is discussed, for example, in EP 0 534 858 and US Pat. 5,878,215. In general, total cellular DNA is digested with one or more 20 restriction enzymes. Restriction halfsite-specific adapters are ligated to all restriction fragments and the fragments are selectively amplified with two PCR primers that have corresponding adaptor and restriction site specific sequences. The PCR products can be visualized after size-fractionation, as described above.

In some embodiments, the methods are directed to breeding a plant line. Such 25 methods use genetic polymorphisms identified as described above in a marker assisted breeding program to facilitate the development of lines that have increased heat and/or drought tolerance. Once a suitable genetic polymorphism is identified as being associated with variation for the trait, one or more individual plants are identified that possess the polymorphic allele correlated with the desired variation. 30 Those plants are then used in a breeding program to combine the polymorphic allele with a plurality of other alleles at other loci that are correlated with the desired variation. Techniques suitable for use in a plant breeding program are known in the art and include, without limitation, backcrossing, mass selection, pedigree breeding, bulk selection, crossing to another population and recurrent selection. These

techniques can be used alone or in combination with one or more other techniques in a breeding program. Thus, each identified plants is selfed or crossed a different plant to produce seed which is then germinated to form progeny plants. At least one such progeny plant is then selfed or crossed with a different plant to form a subsequent
5 progeny generation. The breeding program can repeat the steps of selfing or outcrossing for an additional 0 to 5 generations as appropriate in order to achieve the desired uniformity and stability in the resulting plant line, which retains the polymorphic allele. In most breeding programs, analysis for the particular polymorphic allele will be carried out in each generation, although analysis can be
10 carried out in alternate generations if desired.

In some cases, selection for other useful traits is also carried out, e.g., selection for fungal resistance or bacterial resistance. Selection for such other traits can be carried out before, during or after identification of individual plants that possess the desired polymorphic allele.

15 **VI. Articles of Manufacture**

Transgenic plants provided herein have various uses in the agricultural and energy production industries. For example, transgenic plants described herein can be used to make animal feed and food products. Such plants, however, are often particularly useful as a feedstock for energy production.

20 Transgenic plants described herein often produce higher yields of grain and/or biomass per hectare, relative to control plants that lack the exogenous nucleic acid. In some embodiments, such transgenic plants provide equivalent or even increased yields of grain and/or biomass per hectare relative to control plants when grown under conditions of reduced inputs such as fertilizer and/or water. Thus, such transgenic
25 plants can be used to provide yield stability at a lower input cost and/or under environmentally stressful conditions such as drought. In some embodiments, plants described herein have a composition that permits more efficient processing into free sugars, and subsequently ethanol, for energy production. In some embodiments, such plants provide higher yields of ethanol, other biofuel molecules, and/or sugar-derived
30 co-products per kilogram of plant material, relative to control plants. By providing higher yields higher yields under environmentally stressful conditions such as drought conditions and/or heat shock conditions, the transgenic plants described herein

improve profitability for farmers and processors as well as decrease costs to consumers.

Seeds from transgenic plants described herein can be conditioned and bagged in packaging material by means known in the art to form an article of manufacture.

5 Packaging material such as paper and cloth are well known in the art. A package of seed can have a label, *e.g.*, a tag or label secured to the packaging material, a label printed on the packaging material, or a label inserted within the package, that describes the nature of the seeds therein.

The invention will be further described in the following examples, which do
10 not limit the scope of the invention described in the claims.

VII. Examples

Example 1 – Transgenic *Arabidopsis* plants

The following symbols are used in the Examples with respect to *Arabidopsis*
15 transformation: T₁: first generation transformant; T₂: second generation, progeny of self-pollinated T₁ plants; T₃: third generation, progeny of self-pollinated T₂ plants; T₄: fourth generation, progeny of self-pollinated T₃ plants. Independent transformations are referred to as events.

Nucleic acids that were isolated from *Arabidopsis thaliana* plants, and cloned
20 into a Ti plasmid vector, CRS338, under the control of a 35S promoter, p32449 promoter, or p326 promoter, as indicated. Each construct contained a phosphinothricin acetyltransferase gene which confers FinaleTM resistance to transformed plants. Wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) plants were transformed separately with each construct. The transformations were
25 performed essentially as described in Bechtold *et al.*, *C.R. Acad. Sci. Paris*, 316:1194-1199 (1993). introduced into *Arabidopsis* plants.

Transgenic *Arabidopsis* lines containing SEQ ID NO:441, SEQ ID NO:488, SEQ ID NO:567, SEQ ID NO:589, SEQ ID NO:704, SEQ ID NO:710, SEQ ID NO:1241, SEQ ID NO:1260, SEQ ID NO:1128, SEQ ID NO:59, SEQ ID NO:363,
30 SEQ ID NO:310, SEQ ID NO:159, SEQ ID NO:1, SEQ ID NO:1008, or SEQ ID NO:56 were designated ME00029, ME00045, ME02190, ME02549, ME02865, ME03227, ME04477, ME18396, ME20095, ME02932, ME18240, ME20867, ME03268, ME06551, ME02401, or ME06919, respectively. The presence of each vector containing a nucleic acid described above in the respective transgenic

Arabidopsis line transformed with the vector was confirmed by Finale™ resistance, PCR amplification from green leaf tissue extract, and/or sequencing of PCR products.

Example 2 – Screening for drought tolerance in transgenic *Arabidopsis* seedlings

- 5 Soil was made from 60% Sunshine Mix #5 (Sun Gro; Bellevue, Washington, USA) and 40% vermiculite. For each superpool, 3 flats were seeded with about 3000 seeds. Prior to seeding, each flat was watered with 2 L of filtered water and the surface was misted. The flats were covered with a humidity dome and kept in the dark at 4° C for 3 days.
- 10 After 3 days of cold treatment, the flats covered with humidity domes were transferred to a greenhouse and covered with a shade cloth (day 1). The humidity domes were removed on day 4, or when cotyledons are fully expanded. Each flat was watered with 2 L water within 1 day of removing the humidity domes by adding filtered water to the bottom of the flat and allowing 30-45 minutes for absorption of
- 15 the water. On days 6 and 8, the flats were assessed for Finale™ resistance. On day 10, the no-hole flats were removed from the bottom of each flat to speed soil drying. The flats were watered in no-hole flats as above after 2.5 weeks and 4 weeks. Candidates with increased height, increased branching, normal siliques, larger rosettes, and persistent flowering, as compared to the wild-type Ws seedlings that
- 20 were grown and treated in the same conditions were selected for analysis in a chronic soil drought assay.

Chronic Soil Drought Assay

- Soil was made from 60% Sunshine Mix #5 (Sun Gro; Bellevue, Washington, USA) and 40% vermiculite. For each candidate event, 24 pots were prepared in a 24-
- 25 pot no-hole flat with 28 grams of dry soil in each pot, and 4 L of filtered water was added to the tray. The water was allowed to soak into the soil and the soil surface was misted before seeding. For each candidate event, 18 pots were seeded with 3-5 seeds each of candidate seeds and 6 pots were seeded with 3-5 seeds each of wild-type control seeds. The seeded pots were covered with a humidity dome and kept in the
- 30 dark at 4° C for 3 days.

 After 3 days of cold treatment, the pots covered with humidity domes were transferred to a Conviron® growth chamber set at 22° C, 16:8 hour light:dark cycle, 70% humidity, and 120 µE light intensity. The humidity domes were removed on day

5, or when cotyledons are fully expanded. After removal of the domes, each pot was irrigated to saturation with 0.5X Hoagland's solution, allowing the excess solution to drain. Seedlings were then thinned to 1 per pot. On day 8 or 9, the pots were irrigated to saturation with filtered water, allowing the excess water to drain after about 30 minutes of soaking, and the weight of each 24-pot flat was recorded. Each pot contained about 107 g water at saturation. Each pot was allowed to dry to about 15% of saturation between waterings. 30 g of water was added at each watering. Rosette area was measured at day 19. On day 24, plants were staked and measurements were taken of the longest leaf and the plant height. Terminal plant height was measured at the cease of flowering. The plants were allowed to dry and seed weight was measured. Final resistance of a cauline leaf was determined at day 24. Significance of drought tolerance measurements was assessed using a one-tailed Student's t-test, assuming unequal variance, at $p \leq 0.5$.

15 Example 3 – Screening for heat tolerance in transgenic Arabidopsis seedlings

Agar plates were made from the media composed of 2.15 g/L MS salt (PhytoTechnology Laboratories®), 5 g/L sucrose (Sigma), 0.7% agar (PhytoTechnology Laboratories®), pH 5.7. For each superpool, 3000 seeds were sterilized using 30% Clorox containing 0.1% Triton X-100 and plated onto two agar plates at a density of 1500 seeds per plate. The plates were wrapped with vent tape and kept in the dark at 4° C for 3 days.

After 3 days of stratification, the plates were transferred to a Conviron® growth chamber set at 22° C, 16:8 hour light:dark cycle, 70% humidity, and 60 μ E light intensity. The seedlings were grown in the chamber for 3.5-4 days. For heat shock, the plates were placed in an incubator set at 47° C for 2 hours. After heat shock, the plates were transferred back to the Conviron® growth chamber and the seedlings were allowed to recover and grow for several days (about 7 days). Candidates with enhanced root growth and greenness of leaves, faster emergence of photosynthetically active true leaves and increased size of rosettes, as compared to the wild-type Ws seedlings that were grown and treated in the same conditions were selected for analysis in a heat shock assay.

Heat Shock I Assay

Seeds were plated on heat germination agar plates containing 45 mL of half-strength MS medium (2.15g MS salt (*PhytoTechnology Laboratories*®), 5g sucrose (Sigma), and 0.7% agar (*PhytoTechnology Laboratories*®) per liter, pH 5.7) per Petri
5 dish (square, 100 mm X 15 mm). One transgenic event (40 seeds) and 9 wild-type Ws control seeds were plated on each plate. Plates were wrapped with vent tape and placed in the dark at 4° C for 3 days. Plates were then transferred into a Conviron® growth chamber set at 22° C, 16:8 hour light:dark cycle, and 70% humidity with fluorescent lamps emitting a light intensity of about 60 µE.

10 After the plants were grown in the Conviron® growth chamber for 3-4 days, the plates were treated at 47° C in a Yamato IC800 incubator for 1 hour 50 minutes. Following the heat treatment, the plates were placed immediately back into the Conviron® growth chamber. On the 7th, 9th, and 11th day at 22° C after the heat treatment, the plates were scanned using Epson Perfection 4870 scanner. The area of
15 each seedling (green area) was quantified using the WinRhizo software (Regent Instruments). The transgenic status of each plant was assessed by Finale™ resistance.

The seedling area (a measure of growth after heat treatment) of transgenic plants was compared to that of the pooled controls comprising non-transgenic segregants and wild-type Ws controls grown on the same plate. Significance of heat
20 tolerance was assessed using a one-tailed Student's t-test, assuming unequal variance, at $p \leq 0.5$.

Heat Shock II Assay

Seeds were plated on heat germination agar plates containing 45 mL of half-strength MS medium (2.15g MS salt (*PhytoTechnology Laboratories*®), 5g sucrose
25 (Sigma-Aldrich®), and 0.7% agar (*PhytoTechnology Laboratories*®) per liter, pH 5.7) per Petri dish (square, 100 mm X 15 mm). One transgenic event (30 seeds), 4 wild-type Ws control seeds, and 2 seeds of a transgenic positive control were plated on each plate. Plates were wrapped with vent tape and placed in the dark at 4° C for 3 days. Plates were then transferred into a Conviron® growth chamber set at 22° C,
30 16:8 hour light:dark cycle, and 70% humidity with fluorescent lamps emitting a light intensity of about 60 µE.

After the plants were grown in the Conviron® growth chamber for 11 days, the plates were scanned using a CF imager (Technologica) to record the PSII operating

efficiency ($\Delta\Phi_{PSII}$) and seedling area. The plates were then transferred to a Conviron® reach-in heat chamber set at 42°C for 5 hours. Following the heat treatment, the plants were immediately scanned using the CF imager, and then transferred back into the Conviron® growth chamber. After 2 and 4 days of recovery in the growth chamber, the plates were scanned using the CF imager again. The transgenic status of each plant was assessed by Finale™ resistance.

The differences in the PSII operating efficiency and seedling size prior to heat shock, immediately after heat shock, and after recovery following heat shock were calculated. The differences in the PSII operating efficiency and seedling size of transgenic plants were compared to the pooled controls comprising non-transgenic segregants and wild-type Ws controls grown on the same plate. Significance of heat tolerance was assessed using a one-tailed Student's t-test, assuming unequal variance, at $p \leq 0.5$.

Example 4 – Results for ME00029 events

T₂ and T₃ seed from two events of ME00029 containing SEQ ID NO:441 under control of a p32449 promoter was analyzed for rosette area, terminal plant height, and seed yield as described in Example 2. The results are provided in Table 1.

Table 1: Chronic drought response of seedlings from ME00029

Plants	Measurement	Control Population	
		Internal	Pooled
T ₂ seedlings from event -01 of ME00029	Rosette Area	N.S.	Sig.
T ₂ seedlings from event -04 of ME00029	Rosette Area	N.A.	Sig.
T ₂ seedlings from event -01 of ME00029	Longest Leaf	N.S.	Sig.
T ₂ seedlings from event -01 of ME00029	Terminal Plant Height	Sig.	Sig.
T ₃ seedlings from event -01 of ME00029	Terminal Plant Height	Sig.	Sig.
T ₂ seedlings from event -04 of ME00029	Terminal Plant Height	N.A.	Sig.
T ₃ seedlings from event -04 of ME00029	Terminal Plant Height	N.A.	Sig.
T ₃ seedlings from event -01 of ME00029	Seed Yield	N.S.	Sig.

N.A.- results not available due to insufficient sample size ($n < 5$); N.S.- not significant; Sig.- significant ($p \leq 0.5$).

Example 5 – Results for ME00045 events

T₂ and T₃ seed from three events of ME00045 containing SEQ ID NO:488 under control of a p32449 promoter was analyzed for rosette area, terminal plant height, longest leaf length, and seed yield as described in Example 2. The results are provided in Table 2.

Table 2: Chronic drought response of seedlings from ME00045

Plants	Measurement	Control Population		
		Internal	Pooled	Ws
T ₃ seedlings from event -02 of ME00045	Rosette Area	N.S.	N.S.	Sig.
T₃ seedlings from event -02 of ME00045	Rosette Area	N.S.	N.S.	N.S.
T ₂ seedlings from event -07 of ME00045	Rosette Area	N.A.	N.S.	Sig.
T₂ seedlings from event -07 of ME00045	Rosette Area	N.S.	N.S.	Sig.
T ₂ seedlings from event -08 of ME00045	Rosette Area	N.A.	N.S.	Sig.
T₂ seedlings from event -08 of ME00045	Rosette Area	N.S.	N.S.	N.S.
T ₃ seedlings from event -02 of ME00045	Longest Leaf	Sig.	Sig.	Sig.
T₃ seedlings from event -02 of ME00045	Longest Leaf	N.S.	N.S.	N.S.
T ₂ seedlings from event -07 of ME00045	Longest Leaf	N.A.	N.S.	Sig.
T₂ seedlings from event -07 of ME00045	Longest Leaf	N.S.	N.S.	N.S.
T ₂ seedlings from event -08 of ME00045	Longest Leaf	N.A.	N.S.	Sig.
T₂ seedlings from event -08 of ME00045	Longest Leaf	N.S.	N.S.	N.S.
T ₃ seedlings from event -02 of ME00045	Terminal Plant Height	N.S.	N.S.	N.S.
T₃ seedlings from event -02 of ME00045	Terminal Plant Height	N.S.	N.S.	N.S.*
T ₂ seedlings from event -07 of ME00045	Terminal Plant Height	N.A.	Sig.	Sig.
T₂ seedlings from event -07 of ME00045	Terminal Plant Height	N.S.	Sig.	Sig.
T ₂ seedlings from event -08 of ME00045	Terminal Plant Height	N.A.	N.S.*	N.S.

T₂ seedlings from event -08 of ME00045	Terminal Plant Height	N.S.	N.S.	Sig.
T ₃ seedlings from event -02 of ME00045	Seed Yield	Sig.	N.S.*	Sig.
T₃ seedlings from event -02 of ME00045	Seed Yield	N.S.	N.S.	N.S.
T ₂ seedlings from event -07 of ME00045	Seed Yield	N.A.	N.S.	N.S.
T₂ seedlings from event -07 of ME00045	Seed Yield	N.S.	N.S.	N.S.
T ₂ seedlings from event -08 of ME00045	Seed Yield	N.A.	N.S.*	Sig.
T₂ seedlings from event -08 of ME00045	Seed Yield	N.S.	N.S.	Sig.

N.A.- results not available due to insufficient sample size; N.S.- not significant ($p>0.10$); N.S.*- not significant ($0.5<p<0.10$); Sig.- significant ($p<0.5$). Data in bold represents a second independent replicate.

5

Example 6 – Results for ME02190 events

T₂ and T₄ seed from two events of ME02190 containing SEQ ID NO:567 under control of a 35S promoter was analyzed for rosette area, terminal plant height, and longest leaf length as described in Example 2. The results are provided in Table 3.

10

Table 3: Chronic drought response of seedlings from ME02190

Plants	Measurement	Control Population	
		Internal	Pooled
T ₂ seedlings from event -10 of ME02190	Rosette Area	N.S.	Sig.
T ₄ seedlings from event -02 of ME02190	Longest Leaf	N.A.	Sig.
T ₂ seedlings from event -10 of ME02190	Longest Leaf	N.S.	Sig.
T ₄ seedlings from event -02 of ME02190	Terminal Plant Height	N.A.	Sig.
T ₂ seedlings from event -10 of ME02190	Terminal Plant Height	N.S.	Sig.

N.A.- results not available due to insufficient sample size ($n<5$); N.S.- not significant; Sig.- significant ($p\leq 0.5$).

Example 7 – Results for ME02549 events

T₂ and T₃ seed from three events of ME02549 containing SEQ ID NO:589 under control of a 35S promoter was analyzed for rosette area, terminal plant height, and longest leaf length as described in Example 2. The results are provided in Table

5 4.

Table 4: Chronic drought response of seedlings from ME02549

Plants	Measurement	Control Population		
		Internal	Pooled	Ws
T ₂ seedlings from event -01 of ME02549	Rosette Area	Sig.	N.S.	Sig.
T ₃ seedlings from event -01 of ME02549	Rosette Area	Sig.	N.S.	N.S.
T ₂ seedlings from event -02 of ME02549	Rosette Area	N.S.*	N.S.*	Sig.
T ₃ seedlings from event -02 of ME02549	Rosette Area	N.S.	N.S.	Sig.
T ₂ seedlings from event -05 of ME02549	Rosette Area	N.A.	N.S.	Sig.
T ₃ seedlings from event -05 of ME02549	Rosette Area	N.S.	N.S.*	Sig.
T ₃ seedlings from event -01 of ME02549	Longest Leaf	N.S.	N.S.	Sig.
T ₃ seedlings from event -02 of ME02549	Longest Leaf	N.S.	N.S.	Sig.
T ₃ seedlings from event -05 of ME02549	Longest Leaf	N.S.	N.S.	Sig.
T ₂ seedlings from event -01 of ME02549	Terminal Plant Height	N.A.	N.S.	N.S.
T ₃ seedlings from event -01 of ME02549	Terminal Plant Height	N.S.	N.S.	Sig.
T ₃ seedlings from event -02 of ME02549	Terminal Plant Height	N.S.	Sig.	Sig.
T ₂ seedlings from event -05 of ME02549	Terminal Plant Height	N.A.	N.S.	N.S.
T ₃ seedlings from event -05 of ME02549	Terminal Plant Height	Sig.	N.S.	Sig.

N.A.- results not available due to insufficient sample size (n<5); N.S.- not significant; N.S.*- not significant (0.5<p<0.10); Sig.- significant (p<0.5).

10

Example 8 – Results for ME02865 events

T₂ and T₃ seed from two events of ME02865 containing SEQ ID NO:704 under control of a 35S promoter was analyzed for rosette area, terminal plant height, longest leaf length, and seed weight as described in Example 2. The results are provided in Table 5.

Table 5: Chronic drought response of seedlings from ME02865

Plants	Measurement	Control Population	
		Internal	Pooled
T ₂ seedlings from event -02 of ME02865	Rosette Area	N.S.	N.S.
T ₃ seedlings from event -02-01 of ME02865	Rosette Area	-	N.S.
T ₃ seedlings from event -02-02 of ME02865	Rosette Area	N.S.	N.S.
T ₂ seedlings from event -05 of ME02865	Rosette Area	-	Sig.
T ₃ seedlings from event -05-01 of ME02865	Rosette Area	-	Sig.
T ₃ seedlings from event -05-02 of ME02865	Rosette Area	N.S.	N.S.
T ₂ seedlings from event -02 of ME02865	Longest Leaf	N.S.	N.S.
T ₃ seedlings from event -02-01 of ME02865	Longest Leaf	-	N.S.
T ₃ seedlings from event -02-02 of ME02865	Longest Leaf	N.S.*	Sig.
T ₂ seedlings from event -05 of ME02865	Longest Leaf	-	Sig.
T ₃ seedlings from event -05-01 of ME02865	Longest Leaf	-	N.S.
T ₃ seedlings from event -05-02 of ME02865	Longest Leaf	N.S.	Sig.
T ₂ seedlings from event -02 of ME02865	Terminal Plant Height	Sig.	Sig.
T ₃ seedlings from event -02-01 of ME02865	Terminal Plant Height	-	N.S.*
T ₃ seedlings from event -02-02 of ME02865	Terminal Plant Height	N.S.	Sig.
T ₂ seedlings from event -05 of ME02865	Terminal Plant Height	-	Sig.
T ₃ seedlings from event -05-01 of ME02865	Terminal Plant Height	-	N.S.*
T ₃ seedlings from event -05-02 of ME02865	Terminal Plant Height	N.S.*	Sig.
T ₂ seedlings from event -02 of ME02865	Seed Weight	N.S.	N.S.

T ₃ seedlings from event -02-01 of ME02865	Seed Weight	-	N.S.
T ₃ seedlings from event -02-02 of ME02865	Seed Weight	Sig.	N.S.
T ₂ seedlings from event -05 of ME02865	Seed Weight	-	Sig.
T ₃ seedlings from event -05-01 of ME02865	Seed Weight	-	N.S.
T ₃ seedlings from event -05-02 of ME02865	Seed Weight	N.S.	N.S.*

N.A.- results not available due to insufficient sample size (n<5); N.S.- not significant; N.S.*- not significant (0.5<p<0.10); Sig.- significant (p<0.5).

The physical appearances of T₁ ME02865 plants were similar to those of corresponding control plants grown under standard conditions. There were no observable or statistically significant differences between T₂ plants from events -02 and -05 of ME02865 and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture when grown under standard conditions.

Example 9 – Results for ME03227 events

T₂ and T₃ seed from two events of ME03227 containing SEQ ID NO:710 under control of a 35S promoter was analyzed for rosette area, terminal plant height, and longest leaf length as described in Example 2. The results are provided in Table 6.

Table 6: Chronic drought response of seedlings from ME03227

Plants	Measurement	Control Population	
		Internal	Pooled
T ₂ seedlings from event -01 of ME03227	Rosette Area	N.A.	Sig.
T ₃ seedlings from event -01 of ME03227	Rosette Area	N.A.	Sig.
T ₂ seedlings from event -05 of ME03227	Rosette Area	N.A.	Sig.
T ₃ seedlings from event -05 of ME03227	Rosette Area	N.A.	Sig.
T ₃ seedlings from event -05 of ME03227	Longest Leaf	N.A.	Sig.
T ₃ seedlings from event -01 of ME03227	Terminal Plant Height	N.A.	N.S.*
T ₃ seedlings from event -05 of ME03227	Terminal Plant Height	N.A.	N.S.*

N.A.- results not available due to insufficient sample size (n<5); N.S.- not significant; N.S.*- not significant (0.5<p<0.10); Sig.- significant (p≤0.5).

Example 10 – Results for ME04477 events

T₂ seed from five events of ME04477 containing SEQ ID NO:1241 under control of a 35S promoter was analyzed for rosette area, terminal plant height, and longest leaf length as described in Example 2. The results are provided in Table 7.

Table 7: Chronic drought response of seedlings from ME04477

Plants	Measurement	Control Population	
		Internal	Pooled
T ₂ seedlings from event -03 of ME04477	Rosette Area	N.A.	Sig.
T ₂ seedlings from event -01 of ME04477	Longest Leaf	N.A.	Sig.
T ₂ seedlings from event -02 of ME04477	Longest Leaf	N.A.	Sig.
T ₂ seedlings from event -03 of ME04477	Longest Leaf	N.A.	Sig.
T ₂ seedlings from event -04 of ME04477	Longest Leaf	Sig.	Sig.
T ₂ seedlings from event -05 of ME04477	Longest Leaf	N.A.	Sig.
T ₂ seedlings from event -01 of ME04477	Terminal Plant Height	N.A.	Sig.
T ₂ seedlings from event -02 of ME04477	Terminal Plant Height	N.A.	Sig.
T ₂ seedlings from event -03 of ME04477	Terminal Plant Height	N.A.	Sig.
T ₂ seedlings from event -04 of ME04477	Terminal Plant Height	Sig.	Sig.
T ₂ seedlings from event -05 of ME04477	Terminal Plant Height	N.A.	Sig.

N.A.- results not available due to insufficient sample size (n<5); N.S.- not significant; Sig.- significant (p<0.5).

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Example 11 – Results for ME18396 events

T₂ seed from one event of ME18396 containing SEQ ID NO:1260 under control of a p326 promoter was analyzed for rosette area and terminal plant height as described in Example 2. The results are provided in Table 8.

Table 8: Chronic drought response of seedlings from ME18396

Plants	Measurement	Control Population	
		Internal	Pooled
T ₂ seedlings from event -02 of ME18396	Rosette Area	N.S.	Sig.
T ₂ seedlings from event -02 of ME18396	Terminal Plant Height	Sig.	Sig.

N.S.- not significant; Sig.- significant (p<0.5).

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Example 12 – Results for ME20095 events

T₂ and T₃ seed from two events of ME20095 containing SEQ ID NO:1128 under control of a 35S promoter was analyzed for rosette area, longest leaf length, terminal plant height, and seed yield as described in Example 2. The results are provided in Table 9.

10

Table 9: Chronic drought response of seedlings from ME20095

Plants	Measurement	Control Population	
		Internal	Pooled
T ₂ seedlings from event -01 of ME20095	Rosette Area	Sig.	Sig.
T ₃ seedlings from event -01-01 of ME20095	Rosette Area	N.S.	N.S.
T ₃ seedlings from event -01-02 of ME20095	Rosette Area	N.S.	N.S.
T ₂ seedlings from event -04 of ME20095	Rosette Area	Sig.	Sig.
T ₃ seedlings from event -04-01 of ME20095	Rosette Area	N.S.	N.S.
T ₃ seedlings from event -04-02 of ME20095	Rosette Area	N.S.	N.S.*
T ₂ seedlings from event -01 of ME20095	Longest Leaf	N.S.	Sig.
T ₃ seedlings from event -01-01 of ME20095	Longest Leaf	Sig.	Sig.
T ₃ seedlings from event -01-02 of ME20095	Longest Leaf	N.S.	N.S.
T ₂ seedlings from event -04 of ME20095	Longest Leaf	Sig.	Sig.
T ₃ seedlings from event -04-01 of ME20095	Longest Leaf	Sig.	Sig.
T ₃ seedlings from event -04-02 of ME20095	Longest Leaf	N.S.*	Sig.

T ₂ seedlings from event -01 of ME20095	Terminal Plant Height	N.S.	Sig.
T ₃ seedlings from event -01-01 of ME20095	Terminal Plant Height	N.S.*	Sig.
T ₃ seedlings from event -01-02 of ME20095	Terminal Plant Height	N.S.	N.S.*
T ₂ seedlings from event -04 of ME20095	Terminal Plant Height	Sig.	Sig.
T ₃ seedlings from event -04-01 of ME20095	Terminal Plant Height	Sig.	Sig.
T ₃ seedlings from event -04-02 of ME20095	Terminal Plant Height	N.S.	Sig.
T ₂ seedlings from event -01 of ME20095	Seed Weight	Sig.	Sig.
T ₃ seedlings from event -01-01 of ME20095	Seed Weight	Sig.	N.S.*
T ₃ seedlings from event -01-02 of ME20095	Seed Weight	Sig.	Sig.
T ₂ seedlings from event -04 of ME20095	Seed Weight	N.S.	N.S.
T ₃ seedlings from event -04-01 of ME20095	Seed Weight	N.S.	N.S.
T ₃ seedlings from event -04-02 of ME20095	Seed Weight	N.S.	N.S.

N.S.- not significant; N.S.*- not significant ($0.5 < p < 0.10$); Sig.- significant ($p < 0.5$).

T₁ ME20095 plants showed delayed flowering and prolonged vegetative growth compared to corresponding control plants grown under standard conditions. There were no observable or statistically significant differences between T₂ plants from events -02 and -04 of ME20095 and control plants in germination, onset of flowering, fertility, and general morphology/architecture when grown under standard conditions. Rosette area in T₂ plants from events -02 and -04 was significantly larger and seed yield was increased as compared to corresponding control plants grown under standard conditions.

Example 13 – Results for ME02401 events

T₂ and T₃ seed from two events of ME02401 containing SEQ ID NO:749 under control of a 35S promoter was analyzed for rosette area, terminal plant height, and longest leaf length as described in Example 2. The results are provided in Table 10.

Table 10: Chronic drought response of seedlings from ME02401

Plants	Measurement	Control Population	
		Internal	Pooled
T ₂ seedlings from event -05 of ME02401	Rosette Area	N.A.	N.S.*
T ₃ seedlings from event -01 of ME02401	Longest Leaf	N.S.*	Sig.
T ₂ seedlings from event -05 of ME02401	Longest Leaf	N.A.	Sig.
T ₃ seedlings from event -01 of ME02401	Terminal Plant Height	Sig.	Sig.
T ₂ seedlings from event -05 of ME02401	Terminal Plant Height	N.A.	Sig.

N.A.- results not available due to insufficient sample size (n<5); N.S.- not significant; N.S.*- not significant (0.5<p<0.10); Sig.- significant (p<0.5).

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Example 14 – Results for ME02932 events

T₂ and T₃ seed from two events of ME02932 containing SEQ ID NO:59 under control of a 35S promoter was analyzed for seedling area following a Heat Shock I assay as described in Example 3. The results are provided in Table 11.

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Table 11: ME02932 seedling area following Heat Shock I assay

Plants	Average seedling area	SE	N	p-value
T ₂ seedlings from event -01 of ME02932	0.07	0.008	33	8.77E-04
T ₂ non-transgenic segregants of event -01 of ME02932	0.04	0.006	15	
T ₃ seedlings from event -01 of ME02932	0.10	0.003	40	2.21E-04
T ₃ non-transgenic segregants of event -01 of ME02932	0.07	0.007	9	
T ₂ seedlings from event -03 of ME02932	0.08	0.012	21	1.29E-02
T ₂ non-transgenic segregants of event -03 of ME02932	0.04	0.009	23	
T ₃ seedlings from event -03 of ME02932	0.09	0.004	36	1.54E-03
T ₃ non-transgenic segregants of event -03 of ME02932	0.07	0.005	13	

The physical appearances of T₁ ME02932 plants were similar to those of corresponding control plants grown under standard conditions. There were no observable or statistically significant differences between T₂ plants from events -01 and -03 of ME02932 and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture when grown under standard conditions.

Example 15 – Results for ME18240 events

T₂ and T₃ seed from three events of ME18240 containing SEQ ID NO:363 under control of a 35S promoter was analyzed for seedling area following a Heat Shock I assay and change in photosynthetic activity during a Heat Shock II assay as described in Example 3. The results are provided in Tables 12 and 13.

Table 12: ME18240 seedling area following Heat Shock I assay

Plants	Average seedling area	SE	N	p-value
T ₂ seedlings from event -02 of ME18240	0.08	0.007	27	4.22E-08
T ₂ non-transgenic segregants of event -02 of ME18240	0.03	0.004	16	
T ₃ seedlings from event -02 of ME18240	0.14	0.007	31	5.83E-11
T ₃ non-transgenic segregants of event -02 of ME18240	0.06	0.007	14	
T ₂ seedlings from event -03 of ME18240	0.13	0.007	35	3.31E-05
T ₂ non-transgenic segregants of event -03 of ME18240	0.08	0.01	14	
T ₃ seedlings from event -03 of ME18240	0.14	0.008	28	5.13E-06
T ₃ non-transgenic segregants of event -03 of ME18240	0.09	0.008	19	
T ₂ seedlings from event -04 of ME18240	0.13	0.008	33	2.39E-07
T ₂ non-transgenic segregants of event -04 of ME18240	0.06	0.009	16	
T ₃ seedlings from event -04 of ME18240	0.13	0.008	29	4.68E-05
T ₃ non-transgenic segregants of event -04 of ME18240	0.08	0.008	18	

Table 13: ME18240 $\Delta F_v/F_m$ in response to Heat Shock II assay

Plants	Average $\Delta F_v/F_m$	SE	N	p-value
T ₂ seedlings from event -02 of ME18240	0.24	0.013	47	3.64E-05
T ₂ non-transgenic segregants of event -02 of ME18240	0.32	0.016	25	
T ₃ seedlings from event -02 of ME18240	0.36	0.012	43	1.92E-04
T ₃ non-transgenic segregants of event -02 of ME18240	0.43	0.016	22	
T ₂ seedlings from event -03 of ME18240	0.24	0.010	41	9.27E-11
T ₂ non-transgenic segregants of event -03 of ME18240	0.37	0.011	28	
T ₃ seedlings from event -03 of ME18240	0.33	0.011	24	1.91E-02
T ₃ non-transgenic segregants of event -03 of ME18240	0.39	0.022	10	
T ₂ seedlings from event -04 of ME18240	0.21	0.009	43	5.55E-17
T ₂ non-transgenic segregants of event -04 of ME18240	0.40	0.007	29	
T ₃ seedlings from event -04 of ME18240	0.28	0.011	46	9.38E-11
T ₃ non-transgenic segregants of event -04 of ME18240	0.41	0.008	21	

Where $\Delta F_v/F_m = F_v/F_m$ prior to heat shock – F_v/F_m after heat shock.

The physical appearances of T₁ ME18240 plants were similar to those of
 5 corresponding control plants grown under standard conditions. There were no
 observable or statistically significant differences between T₂ plants from events -02, -
 03, and -04 of ME18240 and control plants in germination, onset of flowering, rosette
 area, fertility, and general morphology/architecture when grown under standard
 conditions.

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Example 16 – Results for ME20867 events

T₂ and T₃ seed from four events of ME20867 containing SEQ ID NO:310
 under control of a 35S promoter was analyzed for seedling area following a Heat
 Shock I assay and change in photosynthetic activity during a Heat Shock II assay as
 15 described in Example 3. The results are provided in Tables 14 and 15.

Table 14: ME20867 seedling area in response to Heat Shock I assay

Plants	Average seedling area	SE	N	p-value
T ₂ seedlings from event -01 of ME20867	0.14	0.008	28	4.86E-07
T ₂ non-transgenic segregants of event -01 of ME20867	0.07	0.011	12	
T ₃ seedlings from event -01 of ME20867	0.07	0.007	31	9.84E-10
T ₃ non-transgenic segregants of event -01 of ME20867	0.01	0.010	16	
T ₂ seedlings from event -02 of ME20867	0.13	0.006	37	1.03E-02
T ₂ non-transgenic segregants of event -02 of ME20867	0.08	0.024	3	
T ₃ seedlings from event -02 of ME20867	0.09	0.006	32	6.01E-07
T ₃ non-transgenic segregants of event -02 of ME20867	0.02	0.011	9	
T ₂ seedlings from event -04 of ME20867	0.12	0.006	31	1.47E-02
T ₂ non-transgenic segregants of event -04 of ME20867	0.10	0.010	9	
T ₃ seedlings from event -04 of ME20867	0.03	0.005	20	2.14E-04
T ₃ non-transgenic segregants of event -04 of ME20867	0.01	0.007	12	
T ₂ seedlings from event -05 of ME20867	0.11	0.009	30	1.51E-02
T ₂ non-transgenic segregants of event -05 of ME20867	0.08	0.012	10	
T ₃ seedlings from event -05 of ME20867	0.03	0.004	23	1.98E-04
T ₃ non-transgenic segregants of event -05 of ME20867	0.01	0.005	20	

Table 15: ME20867 $\Delta F_v/F_m - D_2$ in response to Heat Shock II assay

Plants	Average $\Delta F_v/F_m - D_2$	SE	N	p-value
T ₂ seedlings from event -01 of ME20867	0.03	0.012	33	2.17E-08
T ₂ non-transgenic segregants of event -01 of ME20867	-0.07	0.008	12	
T ₃ seedlings from event -01 of ME20867	0.21	0.010	44	3.71E-12
T ₃ non-transgenic segregants of event -01 of ME20867	0.06	0.015	22	

T ₂ seedlings from event -02 of ME20867	0.06	0.011	25	9.39E-11
T ₂ non-transgenic segregants of event -02 of ME20867	-0.10	0.006	12	
T ₃ seedlings from event -02 of ME20867	0.25	0.012	50	4.79E-08
T ₃ non-transgenic segregants of event -02 of ME20867	0.06	0.029	16	
T ₂ seedlings from event -04 of ME20867	0.17	0.010	43	8.71E-11
T ₂ non-transgenic segregants of event -04 of ME20867	0.03	0.014	22	
T ₃ seedlings from event -04 of ME20867	0.16	0.011	24	1.39E-03
T ₃ non-transgenic segregants of event -04 of ME20867	0.06	0.027	9	
T ₂ seedlings from event -05 of ME20867	0.21	0.016	28	1.35E-09
T ₂ non-transgenic segregants of event -05 of ME20867	0.07	0.012	31	
T ₃ seedlings from event -05 of ME20867	0.24	0.015	19	3.72E-03
T ₃ non-transgenic segregants of event -05 of ME20867	0.18	0.015	14	

$\Delta Fv/Fm - D_2 = Fv/Fm$ immediately after heat shock $- Fv/Fm$ after 2 days recovery.

The physical appearances of T₁ ME20867 plants were similar to those of corresponding control plants grown under standard conditions. There were no observable or statistically significant differences between T₂ plants from events -01, -02, -04 and -05 of ME20867 and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture when grown under standard conditions.

10 Example 17 – Results for ME03268 events

T₂ and T₃ seed from one event of ME03268, and T₃ and T₄ seed from one event of ME03268, each containing SEQ ID NO:159 under control of a 35S promoter, was analyzed for seedling area following a Heat Shock I assay as described in Example 3. The results are provided in Table 16.

15

Table 16: ME03268 seedling area in response to Heat Shock I assay

Plants	Average seedling area	SE	N	p-value
T ₂ seedlings from event -02 of ME03268	0.165	0.015	26	1.09E-03
T ₂ non-transgenic segregants of event -02 of ME03268	0.070	0.024	3	
T ₃ seedlings from event -02 of ME03268	0.137	0.009	40	1.97E-07
T ₃ non-transgenic segregants of event -02 of ME03268	0.048	0.012	9	
T ₃ seedlings from event -03 of ME03268	0.062	0.007	26	3.65E-02
T ₃ non-transgenic segregants of event -03 of ME03268	0.037	0.011	4	
T ₄ seedlings from event -03 of ME03268	0.094	0.008	30	3.96E-03
T ₄ non-transgenic segregants of event -03 of ME03268	0.054	0.012	10	

The physical appearances of T₁ ME03268 plants were similar to those of corresponding control plants grown under standard conditions. There were no observable or statistically significant differences between T₂ plants from events -02 and -03 of ME03268 and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture when grown under standard conditions.

10 *Example 18 – Results for ME06551 events*

T₃ and T₄ seed from two events of ME06551 containing SEQ ID NO:1 under control of a 35S promoter was analyzed for change in photosynthetic activity during a Heat Shock II assay as described in Example 3. The results are provided in Table 17.

15 **Table 17: ME06551 $\Delta F_v/F_m$ in response to Heat Shock II assay**

Plants	Average $\Delta F_v/F_m$	SE	N	p-value
T ₃ seedlings from event -04 of ME06551	0.42	0.016	11	1.32E-02
T ₃ non-transgenic segregants of event -04 of ME06551	0.47	0.012	15	
T ₄ seedlings from event -04 of ME06551	0.39	0.006	49	4.73E-03

T ₄ non-transgenic segregants of event -04 of ME06551	0.43	0.014	11	
T ₃ seedlings from event -05 of ME06551	0.39	0.013	11	4.21E-04
T ₃ non-transgenic segregants of event -05 of ME06551	0.46	0.010	13	
T ₄ seedlings from event -05 of ME06551	0.39	0.007	50	4.79E-02
T ₄ non-transgenic segregants of event -05 of ME06551	0.41	0.010	17	

Where $\Delta F_v/F_m = F_v/F_m$ prior to heat shock – F_v/F_m after heat shock.

The physical appearances of T₁ ME06551 plants were similar to those of corresponding control plants grown under standard conditions. There were no observable or statistically significant differences between T₂ plants from events -04 and -05 of ME06551 and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture when grown under standard conditions.

Example 19 – Results for ME06919 events

T₂ and T₃ seed from two events of ME06919 containing SEQ ID NO:56 under control of a 35S promoter was analyzed for change in photosynthetic activity during a Heat Shock II assay as described in Example 3. The results are provided in Table 18.

Table 18: ME06919 $\Delta F_v/F_m$ in response to Heat Shock II assay

Plants	Average $\Delta F_v/F_m$	SE	N	p-value
T ₂ seedlings from event -03 of ME06919	0.433	0.007	65	2.55E-09
T ₂ non-transgenic segregants of event -03 of ME06919	0.497	0.008	37	
T ₃ seedlings from event -03 of ME06919	0.281	0.013	46	1.87E-03
T ₃ non-transgenic segregants of event -03 of ME06919	0.341	0.015	18	
T ₂ seedlings from event -04 of ME06919	0.490	0.007	21	3.06E-04
T ₂ non-transgenic segregants of event -04 of ME06919	0.531	0.009	26	
T ₃ seedlings from event -04 of ME06919	0.296	0.006	44	6.15E-08
T ₃ non-transgenic segregants of event -04 of ME06919	0.412	0.018	18	

Where $\Delta F_v/F_m = F_v/F_m$ prior to heat shock – F_v/F_m after heat shock.

The physical appearances of T₁ ME06919 plants were similar to those of corresponding control plants grown under standard conditions. There were no observable or statistically significant differences between T₂ plants from events -03 and -04 of ME06919 and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture when grown under standard conditions.

Example 20 – Results for ME04246 events

T₂ and T₃ seed from two events of ME04246 containing SEQ ID NO:1362 under control of a 35S promoter was analyzed for rosette area, terminal plant height, and longest leaf length as described in Example 2. The results are provided in Table 19.

Table 19: Chronic drought response of seedlings from ME04246

Plants	Measurement	Control Population		
		Internal	Pooled	Ws
T ₂ seedlings from event -01 of ME04246	Longest Leaf	Sig.	Sig.	N.S.
T ₂ seedlings from event -03 of ME04246	Longest Leaf	N.S.	N.S.	N.S.
T ₂ seedlings from event -04 of ME04246	Longest Leaf	N.S.	N.S.	N.S.
T ₂ seedlings from event -01 of ME04246	Dry Biomass	N.A.	N.S.*	Sig.
T ₂ seedlings from event -02 of ME04246	Dry Biomass	N.A.	N.A.	N.S.
T ₂ seedlings from event -04 of ME04246	Dry Biomass	N.A.	N.S.*	Sig.

N.A.- results not available due to insufficient sample size (n<5); N.S.- not significant; N.S.*- not significant (0.5<p<0.10); Sig.- significant (p<0.5).

T₂ ME04246 plants showed increased vegetative biomass compared to corresponding control plants under water-limiting conditions as measured directly and to a lesser degree by longest leaf length. There were no observable or statistically significant differences between T₁ plants from events -01,-03 and -04 of ME04246 and control plants in germination, onset of flowering, fertility, and general morphology/architecture when grown under standard conditions.

Example 21 – Determination of Functional Homologs by Reciprocal BLAST

A candidate sequence was considered a functional homolog of a reference sequence if the candidate and reference sequences encoded proteins having a similar function and/or activity. A process known as Reciprocal BLAST (Rivera *et al.*, *Proc.*

Natl. Acad. Sci. USA, 95:6239-6244 (1998)) was used to identify potential functional homolog sequences from databases consisting of all available public and proprietary peptide sequences, including NR from NCBI and peptide translations from Ceres clones.

5 Before starting a Reciprocal BLAST process, a specific reference polypeptide was searched against all peptides from its source species using BLAST in order to identify polypeptides having BLAST sequence identity of 80% or greater to the reference polypeptide and an alignment length of 85% or greater along the shorter sequence in the alignment. The reference polypeptide and any of the aforementioned
10 identified polypeptides were designated as a cluster.

 The BLASTP version 2.0 program from Washington University at Saint Louis, Missouri, USA was used to determine BLAST sequence identity and E-value. The BLASTP version 2.0 program includes the following parameters: 1) an E-value cutoff of 1.0e-5; 2) a word size of 5; and 3) the -postsw option. The BLAST sequence
15 identity was calculated based on the alignment of the first BLAST HSP (High-scoring Segment Pairs) of the identified potential functional homolog sequence with a specific reference polypeptide. The number of identically matched residues in the BLAST HSP alignment was divided by the HSP length, and then multiplied by 100 to get the BLAST sequence identity. The HSP length typically included gaps in the alignment,
20 but in some cases gaps were excluded.

 The main Reciprocal BLAST process consists of two rounds of BLAST searches; forward search and reverse search. In the forward search step, a reference polypeptide sequence, "polypeptide A," from source species SA was BLASTed against all protein sequences from a species of interest. Top hits were determined
25 using an E-value cutoff of 10^{-5} and a sequence identity cutoff of 35%. Among the top hits, the sequence having the lowest E-value was designated as the best hit, and considered a potential functional homolog or ortholog. Any other top hit that had a sequence identity of 80% or greater to the best hit or to the original reference polypeptide was considered a potential functional homolog or ortholog as well. This
30 process was repeated for all species of interest.

 In the reverse search round, the top hits identified in the forward search from all species were BLASTed against all protein sequences from the source species SA.

A top hit from the forward search that returned a polypeptide from the aforementioned cluster as its best hit was also considered as a potential functional homolog.

Functional homologs were identified by manual inspection of potential functional homolog sequences. Representative functional homologs for SEQ ID NO:442, SEQ ID NO:489, SEQ ID NO:568, SEQ ID NO:590, SEQ ID NO:705, SEQ ID NO:711, SEQ ID NO:742, SEQ ID NO:1012, SEQ ID NO:1129, SEQ ID NO:60, SEQ ID NO:364, SEQ ID NO:311, SEQ ID NO:160, SEQ ID NO:2, and SEQ ID NO:749 are shown in Figures 1-15, respectively.

Example 22 – Determination of Functional Homologs by Hidden Markov Models

Hidden Markov Models (HMMs) were generated by the program HMMER 2.3.2. To generate each HMM, the default HMMER 2.3.2 program parameters, configured for global alignments, were used.

An HMM was generated using the sequences shown in Figure 1 as input. These sequences were fitted to the model and a representative HMM bit score for each sequence is shown in the Sequence Listing. Additional sequences were fitted to the model, and representative HMM bit scores for any such additional sequences are shown in the Sequence Listing. The results indicate that these additional sequences are functional homologs of SEQ ID NO:442.

The procedure above was repeated and an HMM was generated for each group of sequences shown in Figures 2-15 using the sequences shown in each Figure as input for that HMM. A representative bit score for each sequence is shown in the Sequence Listing. Additional sequences were fitted to certain HMMs, and representative HMM bit scores for such additional sequences are shown in the Sequence Listing. The results indicate that these additional sequences are functional homologs of the sequences used to generate that HMM.

Other Embodiments

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims.

CLAIMS**WHAT IS CLAIMED IS:**

1. A method of producing a plant, said method comprising growing a plant cell comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the polypeptide has at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 749, and wherein said plant has increased drought tolerance or heat tolerance as compared to a control plant that does not comprise said nucleic acid.
2. The method of claim 1, wherein the polypeptide has at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 749.
3. The method of claim 1 or 2, wherein said polypeptide comprises the sequence of SEQ ID NO: 749.
4. A method of modulating drought tolerance in a plant, said method comprising introducing into a plant cell an exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the polypeptide has at least 80% sequence identity to the amino acid sequence of SEQ ID NO:749, and wherein a plant produced from said plant cell has increased drought tolerance as compared to a control plant that does not comprise said exogenous nucleic acid.
5. The method of claim 4, wherein the polypeptide has at least 90% sequence identity to the amino acid sequence of SEQ ID NO:749.
6. The method of claim 4 or 5, wherein said polypeptide comprises SEQ ID NO: 749.
7. A plant cell comprising an exogenous nucleic acid for use in producing a plant having increased drought tolerance or heat tolerance as compared to a control plant that does not comprise said exogenous nucleic acid, said exogenous nucleic acid comprising a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the polypeptide has at least 80% sequence identity to the amino acid sequence of SEQ ID NO:749.
8. The plant cell of claim 7, wherein the polypeptide has at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 749.

9. The plant cell of claim 7 or 8, wherein said polypeptide comprises SEQ ID NO: 749.
10. The plant cell of claim 7, 8 or 9, wherein said plant is a member of a species selected from the group consisting of *Panicum virgatum*, *Sorghum bicolor*, *Miscanthus giganteus*, *Saccharum* sp., *Populus balsamifera*, *Zea mays*, *Glycine max*, *Brassica napus*, *Triticum aestivum*, *Gossypium hirsutum*, *Oryza sativa*, *Helianthus annuus*, *Medicago sativa*, *Beta vulgaris*, and *Pennisetum glaucum*.
11. Use of a plant cell comprising an exogenous nucleic acid for producing a plant having increased drought tolerance or heat tolerance as compared to a control plant that does not comprise said exogenous nucleic acid, wherein said exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide, wherein the polypeptide has at least 80% sequence identity to the amino acid sequence of SEQ ID NO:749.
12. The use of claim 11, wherein the polypeptide has at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 749.
13. The use of claim 11 or 12, wherein said polypeptide comprises SEQ ID NO: 749.
14. The use of claim 11, 12, or 13, wherein said plant is a member of a species selected from the group consisting of *Panicum virgatum*, *Sorghum bicolor*, *Miscanthus giganteus*, *Saccharum* sp., *Populus balsamifera*, *Zea mays*, *Glycine max*, *Brassica napus*, *Triticum aestivum*, *Gossypium hirsutum*, *Oryza sativa*, *Helianthus annuus*, *Medicago sativa*, *Beta vulgaris*, and *Pennisetum glaucum*.
15. A nucleic acid for use in producing a plant having a difference in drought tolerance or heat tolerance as compared to a control plant that does not comprise said nucleic acid, said nucleic acid comprising:
 - a first nucleotide sequence encoding a polypeptide having 80% or greater sequence identity to the amino acid sequence set forth in SEQ ID NO:749; and
 - a second nucleotide sequence comprising a regulatory region operably linked to the first nucleotide sequence,wherein the first nucleotide sequence is heterologous to the second nucleotide sequence.

16. A method of identifying whether a polymorphism is associated with variation in drought tolerance or heat tolerance, said method comprising:

a) determining whether one or more genetic polymorphisms in a population of plants is associated with the locus of the gene encoding the polypeptide of SEQ ID NO:749 or a polypeptide that has at least 80% sequence identity to the amino acid sequence of SEQ ID NO:749; and

b) measuring the correlation between variation in said drought tolerance in plants of said population and the presence of said one or more genetic polymorphisms in plants of said population, thereby identifying whether or not said one or more genetic polymorphisms are associated with variation in drought tolerance or heat tolerance.

17. A method of making a plant line, said method comprising:

a) determining whether one or more genetic polymorphisms in a population of plants is associated with the locus of the gene encoding the polypeptide of SEQ ID NO:749 or a polypeptide that has at least 80% sequence identity to the amino acid sequence of SEQ ID NO:749;

b) identifying one or more plants in said population in which the presence of at least one allele at said one or more genetic polymorphisms is associated with variation in drought tolerance or heat tolerance;

c) crossing each said one or more identified plants with itself or a different plant to produce seed;

d) crossing at least one progeny plant grown from said seed with itself or a different plant; and

e) repeating steps c) and d) for an additional 0-5 generations to make said plant line, wherein said at least one allele is present in said plant line.

18. The method of claim 16 or 17, wherein said population is a population of switchgrass, sorghum, sugar cane, or miscanthus plants.

SEQ-ID:NO:459	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	ARILDHKYDQ	LQQTSD	46
SEQ-ID:NO:451	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	SLILEHKEYEQ	LQQTSD	46
SEQ-ID:NO:447	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	ALILEHKEYEQ	LQQTSD	46
SEQ-ID:NO:442	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	SLILEHKEYEQ	LQQTSD	46
SEQ-ID:NO:443	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	SLILEHKEYEQ	LQQTSD	46
SEQ-ID:NO:445	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	SLILEHKEYEQ	LQQTSD	47
SEQ-ID:NO:483	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	SLILEHKEYEQ	LQQTSD	47
SEQ-ID:NO:470	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	AIILEHKEYEQ	LQQTSD	47
SEQ-ID:NO:463	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	AIILEHKEYEQ	LQQTSD	48
SEQ-ID:NO:465	MSGEEEE-NA	AELKI GEEFL	KAKCLMNCEV	AIILEHKEYEQ	LQQTSD	49
SEQ-ID:NO:459	PTNQISQVFE	KSMQYVKRFS	RYKNPDVAVRQ	VREVLSRYKL	AEFELCVLGN	96
SEQ-ID:NO:451	PMNQVSQVFE	KSLQYVKRFS	RYKNPDVAVRQ	VREILARYQL	AEFELCVLGN	96
SEQ-ID:NO:447	PMNQVSQVFE	KSLQYVKRFS	RYKNPDVAVRQ	VREILSRHQL	AEFELCVLGN	96
SEQ-ID:NO:442	PMNQVSQVFE	KSLQYVKRFS	RYKNPDVAVRQ	VREILSRHQL	AEFELCVLGN	96
SEQ-ID:NO:443	PMNQVSQVFE	KSLQYVKRFS	RYKNPDVAVRQ	VREILSRHQL	AEFELCVLGN	96
SEQ-ID:NO:445	PMNQVSQVFE	KSLQYVKRFS	RYKNPDVAVRQ	VREILSRHQL	AEFELCVLGN	97
SEQ-ID:NO:483	GADQVSQVFE	KSLQYVKRFS	RYKNPDVAVRQ	VREILSRHQL	AEFELCVLGN	97
SEQ-ID:NO:470	PSSQVSQVFE	KSLQYVKRFS	RYKNPDVAVRQ	VREILSRHQL	AEFELCVLGN	97
SEQ-ID:NO:463	PSSQVSQVFE	KSLQYVKRFS	RYKNPDVAVRQ	VREILSRHQL	AEFELCVLGN	98
SEQ-ID:NO:465	PSSQVSQVFE	KSLQYVKRFS	RYKNPDVAVRQ	VREILSRHQL	AEFELCVLGN	99
SEQ-ID:NO:459	LCPETVEEAT	ALVPSIKSKG	RM---LEDDA	EKMLHDL SL	IKKFE	138
SEQ-ID:NO:451	LCPETVEEAT	AMVPSIKSRG	RA---QDDA	EKMLNDL SL	IKKFE	138
SEQ-ID:NO:447	LCPETVEEAT	AMVPSIKTG	RA---HDDA	ERMLNDL SL	IKKFE	138
SEQ-ID:NO:442	LCPETVEEAT	AMVPSIKTG	RA---HDDA	EKMLNDL SL	IKKFE	138
SEQ-ID:NO:443	LCPETVEEAT	AMVPSIKTG	RA---HDDA	EKMLNDL SL	IKKFE	138
SEQ-ID:NO:445	LCPETVEEAT	AMVPSIKTG	RA---HDDA	EKMLNDL SL	IKKFE	139
SEQ-ID:NO:483	LCPDTADEAK	ALVPSLVPGG	RF---DSDR	VDKMLNDL SL	IKKFE	139
SEQ-ID:NO:470	LCPDTSDEAS	ALVPSLRSKG	RFVGDGSEK	DKMLNDL SL	IKKFE	142
SEQ-ID:NO:463	LCPDTSGEAT	ALVPSLRSKG	RFVGDGSEK	EKMLNDL SL	IKKFE	143
SEQ-ID:NO:465	LCPDTSGEAT	ALVPSLRSKG	RFVGDGSEK	EKMLNDL SL	IKKFE	144

Figure 1

SEQ-ID:NO:514	MDAAVRKAAG	AGIARA	PALV	LALVA	AGAF	L	ISYN	FFIT	MLF	HGGG	---	G	46									
SEQ-ID:NO:515	-----MSGR	KNAGKA	SPFL	LLLI	SVG	CF	ATYN	FLTM	VG	HGR	SRDA	GPR	44									
SEQ-ID:NO:518	-----MSGR	KNAGRT	SPWL	LLLI	SAG	CF	ATYN	FLTM	---	HGR	GRD	GPR	41									
SEQ-ID:NO:489	-----	-----MGKA	SGLL	FL	G	FFV	VTYN	LLTL	V	HNR	S	---	G	34								
SEQ-ID:NO:498	-----	-----MGRAS	LLV	LI	LLT	TG	ATYN	LVAM	IM	HYRS	IGK	WAH	38									
SEQ-ID:NO:494	-----	-----MGRAS	SLL	II	FLV	G	ATYN	NVTM	IR	HYGS	SE	---	G	36								
SEQ-ID:NO:496	-----MI	SR	KNMGS	ASPL	LL	---	ATYN	LV	VM	HNR	SI	SKLT	44									
SEQ-ID:NO:514	GAAATAGTR	DI	PVVAMP	AWMR	AAAD	TEAR	RR	PFH	VAL	TATD	APYS	RWQ	CRV	96								
SEQ-ID:NO:515	KILGGVGG	VG	G	-----	GGSD	P	---	SK	RFH	VAL	TATD	ALYS	QWQ	SRV	82							
SEQ-ID:NO:518	KLLDGGG	SYG	S	-----R	SGSD	P	---	AK	RFH	VAL	TATD	ALYS	QWQ	SR	80							
SEQ-ID:NO:489	SNSDGSPL	LD	PVQMPL	NIR	KAK	SS	---	PA	PFH	VAL	TATD	APYN	KWQ	CR	81							
SEQ-ID:NO:498	DDSDGQI	F	LD	PVTE	MPED	VK	KAKNA	---	KM	PFH	VAL	TATD	APYS	KWQ	CR	85						
SEQ-ID:NO:494	AVNDGAL	F	FD	PI	TE	MPD	HVK	NRK	TS	---	KV	PFH	VAL	TATD	APYN	KWQ	CRV	83				
SEQ-ID:NO:496	YNSDGGI	F	VD	PI	I	EMPES	VR	KLK	RA	---	KM	PFH	VAL	TATD	APYS	KWQ	CR	91				
SEQ-ID:NO:514	MYFWYKRM	QA	RP	GGEA	MGGF	TRVL	HSG	KPD	GLM	DEI	PT	FN	VDPL	PAG	KD	H	146					
SEQ-ID:NO:515	MYWYREMR	DI	RP	GSD	---	MGGF	TRI	LHSG	KPD	GLM	DEI	PT	LV	VDPL	PE	GAD	R	131				
SEQ-ID:NO:518	MHYWYKEM	RD	RP	GSD	---	MGGF	TRI	LHSG	KPD	GLM	DEI	PT	MV	VDPL	PE	GKD	K	129				
SEQ-ID:NO:489	MYWYKQKKA	---	LP	GSD	---	MGGF	TRI	LHSG	NSD	NLM	DEI	PT	FN	VDPL	PP	G	LDR	130				
SEQ-ID:NO:498	MYWYKQKKD	---	LP	GSE	---	MGGF	TRI	LHSG	KPD	NLM	DEI	PT	FN	VDPL	PAG	L	DQ	134				
SEQ-ID:NO:494	MYWYKQKQK	K	LP	GSE	---	MGGF	TRI	LHSG	NP	NLM	DEI	PT	V	VDPL	PAG	L	DR	132				
SEQ-ID:NO:496	MYWYKQKQD	---	LP	GSE	---	MGGF	TRI	LHSG	NP	NLM	NEI	PT	V	VDPL	PAG	L	DR	140				
SEQ-ID:NO:514	GYVVLNRP	WA	FV	QWL	Q	KAKI	EEEYI	LMA	EP	DHI	FV	K	PL	PN	LAH	DD	P	AAF	196			
SEQ-ID:NO:515	GYI	VLNRP	WA	FV	QWL	KKSNI	KEDYV	LMA	EP	DHI	FV	R	PL	PN	LAH	G	D	E	P	181		
SEQ-ID:NO:518	GYI	VLNRP	WA	FV	QWL	QRA	K	DEDYI	LMA	EP	DHV	F	V	K	PL	PN	LAH	G	D	E	179	
SEQ-ID:NO:489	GYVVLNRP	WA	FV	QWL	NR	ATI	KEDYV	LMA	EP	DHV	F	V	N	PL	PN	LAH	G	G	F	P	180	
SEQ-ID:NO:498	GYVVLNRP	WA	FV	QWL	E	KASI	EEEYI	LMA	EP	DHV	F	I	N	PL	PN	LAH	G	G	L	P	184	
SEQ-ID:NO:494	GYI	VLNRP	WA	FV	QWL	E	K	EEEYV	LMA	EP	DHI	F	V	R	PL	PN	LAH	G	G	H	P	182
SEQ-ID:NO:496	GYI	VLNRP	WA	FV	QWL	E	K	EEEYV	LMA	EP	DHI	F	V	T	PL	PN	LAH	G	G	Y	P	190

Figure 2

SEQ-ID:NO:514	PFFYI	T	P	S	E	H	E	K	I	I	R	K	Y	Y	A	K	E	R	G	P	V	T	D	I	D	P	I	G	N	S	P	V	I	I	K	K	T	I	L	E	K	I	A	P	T	W	246							
SEQ-ID:NO:515	PFFYI	K	P	T	E	N	E	I	I	L	R	K	F	F	P	E	E	I	G	N	S	P	V	I	I	D	P	I	I	G	N	S	P	V	I	I	K	K	A	Q	L	E	K	I	A	P	T	W	231					
SEQ-ID:NO:518	PFFYI	N	P	T	V	N	E	K	I	L	R	K	F	F	P	E	E	E	K	G	P	V	S	K	I	D	P	I	I	G	N	S	P	V	I	I	K	K	A	Q	L	E	K	I	A	P	T	W	229					
SEQ-ID:NO:489	PFFYI	T	P	E	K	Y	E	N	I	V	R	K	Y	Y	P	A	E	E	M	G	P	V	T	N	I	D	P	I	I	G	N	S	P	V	I	I	S	K	E	S	L	E	K	I	A	P	T	W	230					
SEQ-ID:NO:498	PFFYI	K	P	A	D	H	E	S	I	I	R	K	Y	Y	P	E	E	E	K	G	P	V	T	N	V	D	P	I	I	G	N	S	P	V	I	I	K	K	E	L	L	E	K	I	A	P	T	W	234					
SEQ-ID:NO:494	PFFYI	R	P	D	E	N	E	K	I	I	R	K	F	Y	P	E	E	E	L	G	P	V	T	N	V	D	P	I	I	G	N	S	P	V	I	I	R	K	D	L	I	A	K	I	A	P	T	W	232					
SEQ-ID:NO:496	PFFYI	K	P	D	Q	N	E	K	L	L	R	K	F	F	P	E	E	E	M	G	P	V	T	N	I	D	P	I	I	G	N	S	P	V	I	I	K	K	E	L	L	E	K	I	A	P	T	W	240					
SEQ-ID:NO:514	MN	V	S	I	Q	M	K	E	D	E	T	D	K	V	F	G	W	V	L	E	M	Y	A	Y	A	V	A	S	A	L	H	G	V	H	I	L	R	I	K	D	F	M	I	Q	P	P	F	D	296					
SEQ-ID:NO:515	MN	I	S	L	K	M	K	E	D	V	E	T	D	K	A	F	G	W	V	L	E	M	Y	A	Y	A	V	A	S	A	L	H	G	V	H	I	S	L	R	I	K	D	F	M	I	Q	P	P	W	281				
SEQ-ID:NO:518	MN	V	S	L	K	M	K	E	D	Q	D	T	D	K	A	F	G	W	V	L	E	M	Y	A	Y	A	V	A	S	A	L	H	G	V	H	I	S	L	R	I	K	D	F	M	I	Q	P	P	W	279				
SEQ-ID:NO:489	MN	V	S	L	T	M	K	N	D	P	E	T	D	K	A	F	G	W	V	L	E	M	Y	G	I	A	S	A	S	A	I	H	G	V	R	H	I	L	R	I	K	D	F	M	L	Q	P	P	W	280				
SEQ-ID:NO:498	MN	I	S	L	K	M	K	R	D	Q	E	T	D	K	A	F	G	W	V	L	E	M	Y	A	Y	A	V	A	S	A	A	L	H	D	V	Q	H	I	L	R	I	K	D	F	M	V	Q	P	P	W	284			
SEQ-ID:NO:494	MN	I	S	L	K	M	K	E	D	P	E	T	D	K	A	F	G	W	V	L	E	M	Y	A	Y	A	V	A	S	A	A	L	H	G	V	R	H	I	L	R	I	K	D	F	M	L	Q	P	P	W	282			
SEQ-ID:NO:496	MN	V	S	L	K	M	K	D	D	P	E	T	D	K	T	F	G	W	V	L	E	M	Y	A	Y	A	V	A	S	A	A	L	H	G	V	Q	H	V	L	Q	I	K	D	F	M	L	Q	P	P	W	290			
SEQ-ID:NO:514	T	K	L	Q	N	T	F	I	I	H	F	T	Y	G	C	D	Y	S	L	K	I	G	E	L	T	Y	G	K	V	G	E	W	R	F	D	K	R	S	F	P	D	I	R	P	P	P	R	N	L	T	L	P	346	
SEQ-ID:NO:515	A	K	S	D	N	T	F	I	I	H	T	Y	T	G	C	D	Y	T	L	K	I	G	E	L	T	Y	G	K	I	G	E	W	R	F	D	K	R	S	Y	L	R	I	S	P	P	P	R	N	L	T	L	P	331	
SEQ-ID:NO:518	L	K	T	D	N	T	F	I	I	H	T	Y	T	G	C	D	Y	T	N	E	I	G	E	L	T	Y	G	K	I	G	E	W	R	F	D	K	R	S	Y	L	E	I	S	P	P	P	R	N	L	S	L	P	329	
SEQ-ID:NO:489	L	S	T	K	G	K	F	I	I	H	L	Y	T	Y	G	C	D	Y	N	M	K	I	G	E	L	T	Y	G	K	I	G	E	W	R	F	D	K	R	S	H	L	R	I	G	P	P	P	R	N	M	S	L	P	330
SEQ-ID:NO:498	L	A	T	G	K	N	F	I	I	H	L	Y	T	Y	G	C	D	Y	N	L	K	I	G	E	L	T	Y	G	K	I	G	E	W	R	F	D	K	R	S	Y	L	G	I	G	P	M	P	R	N	L	A	L	P	334
SEQ-ID:NO:494	L	E	T	N	K	K	Y	I	I	H	L	Y	T	Y	G	C	D	Y	N	M	K	I	G	E	L	T	Y	G	K	V	G	E	W	R	F	D	K	R	S	H	L	R	I	G	P	P	P	K	N	L	P	L	P	332
SEQ-ID:NO:496	L	E	V	G	K	K	Y	I	I	H	L	Y	T	Y	G	C	D	Y	N	M	K	I	G	E	L	T	Y	G	K	I	G	E	W	R	F	D	K	R	S	F	L	R	I	G	P	P	P	R	N	L	P	L	P	340
SEQ-ID:NO:514	P	P	G	V	P	E	S	V	T	I	L	V	K	M	V	N	E	A	S	A	I	G	E	L	T	Y	G	K	V	G	E	W	R	F	D	K	R	S	F	P	D	I	R	P	P	P	R	N	L	P	L	P	375	
SEQ-ID:NO:515	P	P	G	V	P	E	S	V	A	T	I	L	V	K	M	V	N	E	A	T	A	I	G	E	L	T	Y	G	K	V	G	E	W	R	F	D	K	R	S	F	L	R	I	G	P	P	P	R	N	L	P	L	P	360
SEQ-ID:NO:518	P	P	G	V	P	E	S	V	T	I	L	V	K	M	V	N	E	A	T	A	I	G	E	L	T	Y	G	K	V	G	E	W	R	F	D	K	R	S	F	L	R	I	G	P	P	P	R	N	L	P	L	P	358	
SEQ-ID:NO:489	P	P	G	V	P	E	S	V	T	I	L	V	K	M	V	N	E	A	T	A	I	G	E	L	T	Y	G	K	V	G	E	W	R	F	D	K	R	S	F	L	R	I	G	P	P	P	R	N	L	P	L	P	358	
SEQ-ID:NO:498	P	P	R	G	V	P	E	S	V	T	I	L	V	K	M	V	N	E	A	T	A	I	G	E	L	T	Y	G	K	V	G	E	W	R	F	D	K	R	S	F	L	R	I	G	P	P	P	R	N	L	P	L	P	362
SEQ-ID:NO:494	P	P	G	V	P	E	S	V	T	I	L	V	K	M	V	N	E	A	S	A	I	G	E	L	T	Y	G	K	V	G	E	W	R	F	D	K	R	S	F	L	R	I	G	P	P	P	R	N	L	P	L	P	360	
SEQ-ID:NO:496	P	P	G	V	P	E	S	V	T	I	L	V	K	M	V	N	E	A	T	A	I	G	E	L	T	Y	G	K	V	G	E	W	R	F	D	K	R	S	F	L	R	I	G	P	P	P	R	N	L	P	L	P	368	

Figure 2 (continued)

SEQ-ID-NO:584	MRK	VLV	AVLI VSMVAS	HFENVA	---	---	22
SEQ-ID-NO:568	MMK	KQVTI VA	ALLI MMALCS	SLNMVAEQL	GPDCYDGCS	TACVQRDPRK	50
SEQ-ID-NO:578	MKK	MVVA	MMLI FLI ST	QMESVE	---	---	23
SEQ-ID-NO:584	---	---	---	---	---	---	26
SEQ-ID-NO:568	TSRCDRKCSI	---	SDAS	SGVSEQI DN	XMMKKQVTI V	AALLI LVAL S	100
SEQ-ID-NO:578	---	---	PDAA	---	---	---	27
SEQ-ID-NO:584	---	---	---	---	---	---	62
SEQ-ID-NO:568	SNLDMVAEQ	---	DCMDAC	TTGCVQSNTR	LT SRCDI KCG	IRCGPDSSEVE	150
SEQ-ID-NO:578	---	---	LGPGDCYDGC	STACVQRDSR	KT SRCDRKCS	IRCGPDAKKA	63
	---	---	DCLDGC	TTACVQSDSR	LQARCDRKCS	IRCGPDSITK	
SEQ-ID-NO:584	DHITG	66					
SEQ-ID-NO:568	GETGA	155					
SEQ-ID-NO:578	EDMG	67					

Figure 3

SEQ-ID-NO:682	MSSSSVQ---	-----	-QTAFPEQEA	DAE--GETNP	ELYQHFAFLV	34
SEQ-ID-NO:674	-----	-----	-MAEGRQLEA	QSMV-----VVPT	ATGDKGDDI L	26
SEQ-ID-NO:634	-----	-----	-----MVS KS	HDV-----YS	SWDDEFKKLV	20
SEQ-ID-NO:590	MATSSMKSP	MAI PSFSMCH	KLELLKEGKIT	RDVPKAEDEE	GLSCFEQEML	50
SEQ-ID-NO:623	MPASTITSMV	-----	-LNHFTKNQA	NDN--GEDLE	RLTNECKELL	37
SEQ-ID-NO:632	MASTDLTN--	-----	-MKEDQSRDG	QET--TSKVN	KVSHDYNNLI	35
SEQ-ID-NO:627	MAPTNVT CF-	-----	-REENESEKKG	EET--TIEED	KLSEQECKELI	36
SEQ-ID-NO:682	SSLPSSKGLS	NNKFYRHDQG	WHCSVVGVVG	AMVADACFSA	RPSDVI VATL	84
SEQ-ID-NO:674	SSLPTREGWW	TFVYLY-DG	CMMDRQAAMS	VSLVRAQFVP	RDDVLLATY	74
SEQ-ID-NO:634	QSEPKKGWA	GSNL YFY-QG	FWCPSLV LKA	FJ SFQKHQA	FNSDII VATE	69
SEQ-ID-NO:590	DSLPERGWR	TRYLYLF-QG	FWCQAKEI QA	TMSFQKHQS	LENDVVLAT I	99
SEQ-ID-NO:623	LSLPERKGWR	TACL YKY-KG	FWCQPKEL QA	I SFQKHFE P	RDTDVI LASI	86
SEQ-ID-NO:632	LSLPRENGCE	TQYMYFF-HG	FWCPSTLI QS	VNSFQNNFHA	KDSDI VVASI	84
SEQ-ID-NO:627	LSLPRERGWR	TRYLYLF-QG	FWCQPLEI QA	I TFQKHQA	KDSDI VATI	85
SEQ-ID-NO:682	PKSGTTWMKS	LLYATVHRRE	RPVVGAAADQ	HPLNSWGPHE	LTKFFEYQLY	134
SEQ-ID-NO:674	PKCGTTWL KA	LSFAIANRHR	HPV--VSAGH	HPLLTQSPHD	LVPFLEPFR	122
SEQ-ID-NO:634	PKCGTTWL KA	LTFSITLYRNQ	FPW--DE	NPLTFGPHQ	LVRF FEYDLY	114
SEQ-ID-NO:590	PKSGTTWL KA	LTFTLNRHR	FDPV-ASSTN	HPLFTSNPHD	LVPF FEYKLY	148
SEQ-ID-NO:623	PKSGTTWL KA	LSFAI LNRKK	FA---ISSND	HPLLVSNPHD	LAPFFEYKLY	133
SEQ-ID-NO:632	PKSGTTWL KG	LAYAI VNRQH	ET---SLENN	HPLLFNPHD	LVPFQFEVNL Y	131
SEQ-ID-NO:627	PKSGTTWL KA	LTFAI VNRHT	HSI T-TSMSS	HPLLTSNPHE	LVPF EYTVY	134
SEQ-ID-NO:682	TRDR--VP--	--DLDRP--	DPRLFATHVP	FVSLPSSMVA	TPGCKI VYVC	176
SEQ-ID-NO:674	HI HP--LA--	--AALDAIP--	SPRLGT HMP	HHLPPR-I	--GCRI VYLC	161
SEQ-ID-NO:634	LNNP--FP--	--DLRNV CAY	QPRLFSTHAP	YATLPIT S-I K	DSGCKI VYI C	157
SEQ-ID-NO:590	ANGD--VP--	--DL SGLA--	SPRLFATHLP	FGSLKET-I E	KPGVKV VYLC	189
SEQ-ID-NO:623	ADKQ--VP--	--DL SKLP--	DPRLFATHI P	FASLQDS-I K	KSNCR I IYI C	174
SEQ-ID-NO:632	GDKD--GPLP	QI DVSNMT--	EPRLFATHMP	FPSLPKS-VK	ESNCKI IYI C	176
SEQ-ID-NO:627	GNAPSHVP--	--NLSNMT--	EPRLFATHI P	FHALAKS-I K	ESNSRI IYI C	177

Figure 4

SEQ-ID-NO:682	RDPKDHVLSL	WDFVNKYFRV	KDGLEPLSVE	AAAELEFCAGL	TPFGPYWDHV	226
SEQ-ID-NO:674	REPDKDVJST	WHFMNK-VI-	--EGFSIDFD	KAFELFVDGC	SPFGPIWNHY	207
SEQ-ID-NO:634	RNPMDFISL	WLFSAK-LR-	DNQESLSLD	EAFDKFYHGI	SAHGPFFDHV	205
SEQ-ID-NO:590	RNPFDTFIS	WHYTNN-IK-	SESVSPVLLD	QAFDLYCRGV	IGFGPFWEHM	237
SEQ-ID-NO:623	RNPFDTFIS	WTFSNK-LR-	SETVPPLLE	ETFKMYCEGV	VGF GPFWDHM	222
SEQ-ID-NO:632	RNPFDTFVS	WIFI NK-IRL	RKSLTELITL	ESFERYCKGI	CLFGPFWDNM	225
SEQ-ID-NO:627	RNPLDTFVST	WIFLNK-IK-	PEHLPEFELG	EAFEKYCKGI	IGFGPTWDQM	225
SEQ-ID-NO:682	LGWRAHRAD	PDKVLFFRYE	EMQRDPAAHV	RRLAEFVGLP	FSSEEEEDGGV	276
SEQ-ID-NO:674	LGYNKHHVEE	PDRVLFLLKYD	DMADPAGHV	KKLAEFLLRVP	FTDDEVDAGV	257
SEQ-ID-NO:634	LGWKASQEN	PNKILFLNFE	DLKEDMDSHL	KLAMFLGVP	FTDDEEKQGV	255
SEQ-ID-NO:590	LGWRESLKR	PEKVFFLRYE	DLKDDIETNL	KRLATFLLELP	FTEEEEERKGV	287
SEQ-ID-NO:623	LGWKESELER	QDKVLFLLKYE	DMKADVT FYL	KKI AKFLGCP	FSMEEEEKEGV	272
SEQ-ID-NO:632	LGYLKESIER	PDRVLFLLKYE	DLKEDVNFHIT	KRIAEFVGIP	FTQEEENNGV	275
SEQ-ID-NO:627	LGWKESIAR	PSKVLFLKYE	DLKEDVNFHV	KRIAEFLGCP	FTSEEEEGDGT	275
SEQ-ID-NO:682	VDAVVGLCSE	ERMRGMAPTK	G-----GRT	EFPIGVVPNS	SFFRQGMVGD	320
SEQ-ID-NO:674	VEEVRLCSF	EKL SRLPVNS	SMVACRGVD	---ERPKNNS	VFFRKCKVRD	304
SEQ-ID-NO:634	VEKIAKICSE	ENLKELEVNIM	K-----DVH	---TSGVPHT	HFFRKGEVGD	296
SEQ-ID-NO:590	VKAI AELCSF	ENLKKLEVNK	S-----NKS	---IKNFENR	FLFRKGEVSD	328
SEQ-ID-NO:623	VEKIASLCSF	EKMKNLEVNK	S-----GRS	---ITNFENK	HLFRKAEVGD	313
SEQ-ID-NO:632	IENIKLCSF	ESMKEIEGNQ	S-----GTI	---SGDIEKE	FYFRKGEI GD	316
SEQ-ID-NO:627	LESIKLCSF	EKMKELEANK	S-----GTF	---ARNFERK	YLF RKAE MGD	316
SEQ-ID-NO:682	WVNHLSPFMA	RRI DAITADK	FRGSSIVV--	-----	-----	348
SEQ-ID-NO:674	WKNYLT EEMA	KKL DAAJEEK	LKGSGLTL--	-----	-----	332
SEQ-ID-NO:634	WSNYLT PFM	ECLEKLI QEK	LNGSGLTFKL	LSETANNI AS	P-----	337
SEQ-ID-NO:590	WVNYSPLSQV	ERLSALVDDK	LNGSGLTFRL	S-----	-----	359
SEQ-ID-NO:623	WVNYSPLSMV	KQLSQLIEEK	LGGSGIEFKV	FPYTSTTPST	SPRLFAAHI P	363
SEQ-ID-NO:632	WVNYSPLSMV	EKL SKVMEEK	LNGSGLSFKV	CA-----	-----	348
SEQ-ID-NO:627	WVNYSPLSMG	EKLSQIMEEK	LNGSGLSF--	-----	-----	344

Figure 4 (continued)

YSSLPESI KK	SNCREVYI YR	NPFNVVASWF	HFSNVEGEPE	KLDEEYF
-------------	-------------	------------	------------	---------

Figure 4 (continued)

SEQ-ID-NO:682
SEQ-ID-NO:674
SEQ-ID-NO:634
SEQ-ID-NO:590
SEQ-ID-NO:623
SEQ-ID-NO:632
SEQ-ID-NO:627

SEQ-ID-NO:707	MASNKVSFFL	VLCLCI LLAG	ECIESPI FTG	NKCSDPITGMD	KDGKCLDYCH	50
SEQ-ID-NO:705	MASNKVSFFL	VLCLCVLSTA	EFGEAQILTG	IKCPDPNGHD	KEDKCNLYCL	50
SEQ-ID-NO:706	MASNKVSF F	LF LCVLSTA	EFGEAQNPRG	RKCEDPNGVD	QAKKCY YCN	50
SEQ-ID-NO:707	AQGYPGGSCQ	GF DQGYMCV	CKVG			74
SEQ-ID-NO:705	NQNYMGSSCQ	GYKNH-YMCE	CYVG			73
SEQ-ID-NO:706	EQGFLGGSCQ	GYTNH-YMCE	CYVG			73

Figure 5

SEQ-ID-NO:734	MPPSYTP	AR	LRLLVLF	LAAS	LSLL	LFAQTLA	SSS	---	AAAS	AEAEVSD	---	44
SEQ-ID-NO:737	---	MPPARF	VHLILLATLS		LLL	---AQTLA	SSSPAPASAA	TAGE	PGD	---	---	41
SEQ-ID-NO:711	---	MSTISPSLA	VIAFLFL	LL	NLS	---SVFAD	PST	---	EGGE	IRLPSE	KIN	44
SEQ-ID-NO:714	---	MSTFSPSLA	VLSCI	LLSLS	LVS	---	SEI	---	NKGG	IRLPSE	---	37
SEQ-ID-NO:719	---	MSKFSAT--F	TCVTL	FLSS	LCF	---PIALS	ETG	---	AGIL	LQEVITRE	---	40
SEQ-ID-NO:715	---	MPCFTATPF	YLLTL	FLFF	YFS	---PQIAQ	SSP	---	DNSR	SIRLPSPD	GFT	44
SEQ-ID-NO:725	---	MPKSSR	FLVVAIAVAA		LCVI	LPVAAA	ADL	---	EDPG	VLRLPSD	---	40
SEQ-ID-NO:733	---	MAGITKTSH	FSVVLI	AVVA	LCV	---FPAAT	SDN	---	VASA	VLGLPSH	---	41
SEQ-ID-NO:734	---	PCAAPVSD	GGSEAQL	CPV	RCFRP	DPVCG	ADGVTYWCGC	PEAACAGARV				92
SEQ-ID-NO:737	---	PCAATAAD	GDGDVPL	CPV	RCFRP	DPVCG	ADGVTYWCGC	PEAACAGARV				89
SEQ-ID-NO:711	GEKNRGEF	CE	GIAKPASCPV		QCFRP	DPVCG	EDSVTYWCGC	ADALCHGV	RV			94
SEQ-ID-NO:714	---	KTNGEFCG	KTSKPASCPV		KCFRA	DPVCG	EDGVTYWCGC	ADALCHGV	RV			85
SEQ-ID-NO:719	---	DGKGDA	CA	GLKAPASCPV	NCFRA	DPVCG	VDGVTYWCGC	ADALCSGT	RV			88
SEQ-ID-NO:715	I	ADNEGVC	A	RFTKPASCPV	TCFRT	EPVCG	VDGVTYWCGC	ADALYCA	GT	RV		94
SEQ-ID-NO:725	---	SLCG	K-TTPSSCPA		KCFRA	DPVCG	ADGVTYWCGC	AEAAACAG	VEV			83
SEQ-ID-NO:733	VAGEGKNL	CS	A-AA	PSSCPV	KCFRT	DPVCS	VDGVTYWCGC	SEAA	YASA	QI		90
SEQ-ID-NO:734	ARRGYCEV	GA	G-SAPV	SGQA	LLL	VHI VWLF	VLGA	AVL	LG	F	L	132
SEQ-ID-NO:737	ARRGYCEV	GA	G-SAPV	SGQA	LLL	VHI VWLF	VLGA	AVL	LG	F	L	129
SEQ-ID-NO:711	VKQGA	CDVGN	GVGLSV	PGQA	LLL	I HI VWM	LLGFSI	L	FG	L	F	135
SEQ-ID-NO:714	SKPGA	CDVGN	GVGLSV	PGQA	LLL	I HI VWM	ALGFSI	L	FG	X		126
SEQ-ID-NO:719	DKLGA	CEVGS	GGSS	SLPGQA	LLL	I HI VWLI	LLGFS	LL	FG	F		129
SEQ-ID-NO:715	AKSGF	CEVGN	GGSA	SVPGQA	LLL	VHI VWLI	LLGF	F	VL	CGL	F	135
SEQ-ID-NO:725	AKLGF	CEVGN	GGSA	PJPGQA	LLL	VHI VWLI	VLGFS	V	L	FG	F	124
SEQ-ID-NO:733	AKLGF	CEVGN	GGSV	TLSGQA	LLL	VHI VWLI	VLGFS	V	F	FG	L	131

Figure 6

SEQ_ID_NO:999	MAQREQERTQ	EARKLRAPE	NHVRQQLAD	FPGNPATQKP	LP ~~E~~ LLLG	47
SEQ_ID_NO:759	MAQRDKEET	E---MKVSE	SLSLCINNCG	FSGNPATKNN	CSKCYK	41
SEQ_ID_NO:1215	MAQKAQKNDIT	D---FKVPE	PLTPCATA	AAATST---	---	31
SEQ_ID_NO:799	MEEQQAAG	G---GGGG	GASMCANGCG	FFGSEATKKL	CSKCYRDQLK	46
SEQ_ID_NO:1010	MAERQEVSG	-----GM	AA ~~E~~ MCANACG	FFGSAATKNL	CSKCYKE	38
SEQ_ID_NO:857	MS ~~E~~ QNSITS	F---PPT	EPKLC ~~D~~ NGCG	FFGSPNNNL	CSKCYRS	41
SEQ_ID_NO:796	MAEEHRCQA	-----P	--QLCANNCG	FFGSPITQNL	CSECYRG	35
SEQ_ID_NO:801	MAEEQHRCQE	-----P	--RLCVNCCG	FFGSPATQNL	CSKCYGD	36
SEQ_ID_NO:892	MAEEHRCQA	-----	AQRLCANNCG	FFGSPAMQDL	CSKCYRD	36
SEQ_ID_NO:859	MAEEHRCQA	-----PE	GHRLC ~~S~~ NCCG	FFGSPATMNL	CSKCYRD	38
SEQ_ID_NO:763	MAEEHRCQA	-----PE	GHRLCVNCCG	FFGSSATMNL	CSKCYRD	38
SEQ_ID_NO:742	MAEEHRCET	-----PE	GHRLCVNCCG	FFGSSATMNL	CSNCCYGD	38
SEQ_ID_NO:912	MAEEHP ~~C~~ QQT	-----PE	GHRLCVNCCG	FFGSSATMNL	CSNCCYGD	38
SEQ_ID_NO:955	MAQESWKQES	EETRVHA-PE	APILCINCCG	FFGSSMTNNM	CSKCYRD	46
SEQ_ID_NO:1000	MAQESWKQES	H---APE	APILCINCCG	FFGSSMTNNM	CSKCYRD	41
SEQ_ID_NO:1306	MDHDKTGCS	P---PE	GPKLCINCCG	FFGSAATMNM	CSKCHKT	40
SEQ_ID_NO:798	MEQNETGCQV	P---PD	APMLCVNCCG	FFGSAATMNP	CSKCHKD	40
SEQ_ID_NO:953	MEHEETGCQP	H---PE	GPILCVNCCG	FFGSAATMNM	CSKCHKD	40
SEQ_ID_NO:988	MEHKETGCQQ	-----PK	GPILCVNCCG	FFGSAATMNM	CSKCHKE	39
SEQ_ID_NO:991	MEHKETGCQQ	-----PE	GPILCVNCCG	FFGSAATMNM	CSKCHKE	39
SEQ_ID_NO:999	---	GHGRTIT	SSAGLSLPS	VL ~~D~~ KRSRQA	---	72
SEQ_ID_NO:759	---	I ~~S~~ TGIM	TQ ~~P~~ ALTFSK	EKA ~~R~~ SSFLRL	---	67
SEQ_ID_NO:1215	---	I ~~S~~ EP ~~S~~ R	FFDAF---	---	---	42
SEQ_ID_NO:799	DLVANEEEE	---	STAAAAADE	Q ~~A~~ CSGGCG	FFGSKETNNM	96
SEQ_ID_NO:1010	HLIKTAKQE	---	ASAAVVVGGA	VKCAADGCG	FFGSSATNNM	77
SEQ_ID_NO:857	LR ~~A~~ EEDQT	---	AVAKAAVEKS	LKLPSCSLIT	APAPK	74
SEQ_ID_NO:796	LQ ~~L~~ KEQQS	---	SSAKQAFNHT	LVPSSSL	---	61
SEQ_ID_NO:801	LR ~~Q~~ SQPLN	---	QLLAPSSAS	V---SSFSS	---	60
SEQ_ID_NO:892	LQ ~~M~~ KEQRS	---	SSAKLVLNQT	LIPQSSNSS	LDTGIH	71
SEQ_ID_NO:859	LR ~~L~~ KEEQ	---	AKTKSTIETA	LSGSSSATV	---	65
SEQ_ID_NO:763	LC ~~L~~ KEQEA	---	SSLKSALSSS	P---SSSIT	---	62
SEQ_ID_NO:742	LC ~~L~~ KQQQQ	---	ASMKSTVESS	L---SPVIA	---	62
SEQ_ID_NO:912	LC ~~L~~ K ~~N~~ QQQ	---	ASMKSTVESS	LSAASP ~~S~~	---	64
SEQ_ID_NO:955	FI---K	---	LMEAPVVEKK	VITSAASS	---	67
SEQ_ID_NO:1000	FV---KLM	---	EMDAPVVDKK	LITASS	---	64
SEQ_ID_NO:1306	ILFQEQG	---	AKLASAVSGS	PSN ~~L~~ KETFT	---	68
SEQ_ID_NO:798	LMKQQQT	---	ELAAASSGSI	ANGGSGSPGK	E	69
SEQ_ID_NO:953	MM ~~L~~ KEEQ	---	KLAASSFGNI	VNGTSNSNGN	E	69
SEQ_ID_NO:988	MI ~~M~~ KQEQ	---	KLAASSIDSI	VNGGDSGKE	---	66
SEQ_ID_NO:991	MI ~~M~~ KQEQ	---	KLAASSIDSI	VNGGDSGKE	---	66

Figure 7

SEQ_ID_NO:999	---	---	VRRRW	L---	SLRLS	HLWRRWPPR	SRRRRR	103
SEQ_ID_NO:759	---	---	PERSD	YQ--	RRDLIT	QDDKGI	QAKNDSTTI	99
SEQ_ID_NO:1215	---	---	---	---	TPATSS	RSRKSLPLE	DAANADRTV	67
SEQ_ID_NO:799	CSKCYRDHLK	ATS--	PLESS	S--	SSPATA	STTDITVPIA	PATTAPTSL	141
SEQ_ID_NO:1010	CSGCMDFLK	DAHASP	PAVAD	K--	VMLAA	EKQPAQAQS	AATSSSTAPA	123
SEQ_ID_NO:857	---	---	QPLET	K--	PASVET	VVIAETSSVP	PVATGQDEG	105
SEQ_ID_NO:796	---	---	PSSSS	A--	RSSFSA	SLPAKEEPSA	GTKETKVE	92
SEQ_ID_NO:801	---	---	PTVDM	I--	KNQIAP	VLVVEGDEKG	EFKAE--PT	89
SEQ_ID_NO:892	---	---	PSSIS	P--	SVMI VS	SSTPTVELVA	AAAGP--SE	100
SEQ_ID_NO:859	---	---	TATAT	V--	ASSVES	PSAPVESLPQ	PVLI--SP	94
SEQ_ID_NO:763	---	---	VVESI	S--	QVPLLA	LHEVNRESAV	PEIAS--AA	91
SEQ_ID_NO:742	---	---	PVLEN	Y--	AAELE	PTTKKTEEK	PIQIP--TE	91
SEQ_ID_NO:912	---	---	---	---	SPEIQS	ISTSTAPVV	QIYAAEQI	89
SEQ_ID_NO:955	---	---	---	---	TAPLET	KRDDAPAAAA	TEAVAEKQA	92
SEQ_ID_NO:1000	---	---	---	---	TVPFET	AKQDDTVPDA	AAMDDKQPA	89
SEQ_ID_NO:1306	---	---	ADLVD	A--	GTKSE	PVAVSVQAVA	EVVAPEEAA	99
SEQ_ID_NO:798	---	---	PDSAI	T--	TVHVDA	GSSDSMI VSM	QASHESLLN	100
SEQ_ID_NO:953	---	---	PVAA	GV	DVQAHLVE	PKTSLQPSF	SFGSGSGGS	103
SEQ_ID_NO:988	---	---	PIIAG	HA	EVAVAQVE	VKTLVAQPAE	IAGPSEGT	100
SEQ_ID_NO:991	---	---	PIIAG	HA	EVAVAQVE	VKTLVAQPAE	IAGPSEGT	100
SEQ_ID_NO:999	---	---	KTSA	---	VNRCSRCRK	VGLTGFRRCRC	GHLFCGEHRY	137
SEQ_ID_NO:759	---	---	KI VEEKQE	---	VNRCSGCRRK	VGLTGFRRCRC	GD MF CSEHRY	137
SEQ_ID_NO:1215	---	---	ASEP--KRA	---	VNRCSGCRRR	VGLTGFRRCRC	GD L FCAEHRY	104
SEQ_ID_NO:799	KGKEEEATAA	ASSSAA	AAK	---	PNRCVACRKK	VGLLGFECCRC	GGTFCSTHRH	191
SEQ_ID_NO:1010	---	---	AVKA--AAA	---	PNRCASCRRK	VGLLGFPCCRC	GGTFCALHRY	160
SEQ_ID_NO:857	---	---	EPSK--PAR	---	PNRCFSCNKK	VGVMGFKCKC	GSTFCGSHRY	142
SEQ_ID_NO:796	---	---	EEEV--QVIT	---	PNRCLSCKKR	VGLTGFKCRC	GMVFCG HRY	129
SEQ_ID_NO:801	---	---	VVVP--QQK	---	PNRCLTCRRR	VGLTGFCNCR	GMVFCGTHRY	126
SEQ_ID_NO:892	---	---	AEP--KVQ	---	PNRCGTCCRR	VGLTGFKCRC	GLT CGGTHRY	137
SEQ_ID_NO:859	---	---	DI AA--PVQ	---	ANRCGACRR	VGLTGFKCRC	GTTCGSHRY	131
SEQ_ID_NO:763	---	---	EQRS--QQQ	---	PNRCMVCRKR	VGLTGFRCKC	GVTCGSHRY	128
SEQ_ID_NO:742	---	---	QSP--PQR	---	PNRCTVCRKR	VGLTGFCMCRC	GTTCGSHRY	128
SEQ_ID_NO:912	---	---	EKIQQQR	---	PNRCTVCRKR	VGLTGFCMCRC	GTTCGTHRY	127
SEQ_ID_NO:955	---	---	EQEPKPP	---	SNRCLTCRKK	VGLTGFCQCR	GDTFCSTHRY	130
SEQ_ID_NO:1000	---	---	QEPP--KPP	---	SNRCLTCRKK	VGLTGFCQCR	GGTFCSLHRY	126
SEQ_ID_NO:1306	---	---	AKP--KEG	---	PSRCTTCNKR	VGLTGFKCRC	GDLFCGTHRY	135
SEQ_ID_NO:798	---	---	ENNVVKEVP	---	PNRCSACRR	VGLTGFCNCR	GDLFCGTHRY	140
SEQ_ID_NO:953	---	---	GEAK--PEG	---	PNRCSACRR	VGLTGFCNCR	GDLFCGTHRY	140
SEQ_ID_NO:988	---	---	VNPKGREG	---	PNRCSACRR	VGLTGFCNCR	GDLFCGTHRY	138
SEQ_ID_NO:991	---	---	VNPKGREG	---	PNRCSACRR	VGLTGFCNCR	GDLFCGTHRY	138

Figure 7 (Continued)

SEQ_ID_NO:999	SDRHGCSYDY	KSAARDAIAR	DNPVVRAAKI	VRF	170
SEQ_ID_NO:759	SDRHDCSFDY	KAAGRESIAR	QNPVVKAALKI	I RL	170
SEQ_ID_NO:1215	TD RHDCSYDY	KTVGREAIAR	ENPVVKAALKI	VKV	137
SEQ_ID_NO:799	ADKHACTFDF	KKSDREKIAR	ENPLI VAPKI	TKF	224
SEQ_ID_NO:1010	AEKHACDFDF	KAAGREKIAR	NNPLVVAAKI	NKI	193
SEQ_ID_NO:857	PEKHECSFDF	KEVGRGAIAR	ANPVVKADKV	QRI	175
SEQ_ID_NO:796	PGTTGLGF--	-----	-----	---	137
SEQ_ID_NO:801	PEQHDCEFDY	KSLGKEQIAR	ANPVVKGEKL	QRI	159
SEQ_ID_NO:892	PEQHGCDFDF	KGMGREEIAR	ANPVVKGEKL	NKI	170
SEQ_ID_NO:859	PEKHACGDFDF	KAVGREEIAR	ANPVI KGEKL	RRI	164
SEQ_ID_NO:763	PENHGCTFDF	KKVGREEIAR	ANPLVKAEL	EKI	161
SEQ_ID_NO:742	PEVHGCTFDF	KSAGREEIAR	ANPLVIAAKL	QKI	161
SEQ_ID_NO:912	PEVHGCTFDF	KSAGREEIAR	ANPLVIAAKL	QKI	160
SEQ_ID_NO:955	TDSHCCTFDY	KKVAREQIAR	QNPVVMAEKI	NKI	163
SEQ_ID_NO:1000	TDSHECTFDY	KKVAREQIAR	QNPVVI AEKI	NKI	159
SEQ_ID_NO:1306	ADVHNCSFDY	HVA AQEAIAR	ANPVVKADKL	DKI	168
SEQ_ID_NO:798	SDKHDCPFYDY	RSAAQDAIAR	ANPVVKAEKL	DKL	173
SEQ_ID_NO:953	SDKHDCPYDY	HTAARDVIAR	ANPVVKADKL	EKI	173
SEQ_ID_NO:988	SDKHDCQFDY	RTAARDAIAR	ANPVVKAEKL	DKI	171
SEQ_ID_NO:991	SDKHDCQFDY	RTAARDAIAR	ANPVVKAEKL	DKI	171

Figure 7 (Continued)

SEQ-ID-NO:1068	--MATASSTID	SSLSPLRLG	KVALVTGGAT	GI GESI	ARLF	CRHGAKVCI	A	48
SEQ-ID-NO:1018	MAAGSSPS	FSSSKRLEG	KVALVTGGAT	GI GEAI	VRLF	MEHGAKVCI	A	49
SEQ-ID-NO:1066	MSAAGSSPS	ASSSTKRLEG	KVALVTGGAT	GI GEAI	VRLF	REHGAKVCI	A	49
SEQ-ID-NO:1055	MSAAGSSSS	SSTSAKRLEG	KVALVTGGAS	GI GEAI	VRLF	RQHGAHVCI	A	50
SEQ-ID-NO:1020	MSAAA	ASSPAPRLES	KVALVTGGAS	GI GEAI	VRLF	REHGAKVCI	A	45
SEQ-ID-NO:1110	MAAASSF	ISLTKRLEV	KVALVTGGAS	GI GKCT	AKVF	AQHGAKVVI	A	47
SEQ-ID-NO:1113	MAATSQV	MTSTKRLEG	KVALITGGAS	GI GECT	AKLF	AEHGAKVVI	A	40
SEQ-ID-NO:1118	MASTQL	LTAARRLEG	KVALITGGAS	GI GECT	AKLF	AEHGAKVVI	A	47
SEQ-ID-NO:1117	MASTQL	LPAARRLEG	KVAIVTGGAR	GI GECT	AKLF	AEHGAKVVI	A	45
SEQ-ID-NO:1093	MAANGSV	LSPVVKRLEG	KVAIVTGGAS	GI GECT	AKLF	AEHGAKVVI	A	46
SEQ-ID-NO:1012	MAVSA	VSAPIRRLEG	KVAIVTGGAS	GI GECT	AKLF	AEHGAKVVI	A	46
SEQ-ID-NO:1094	MAHVS	VSAVVKRLEG	KVAIVTGGAS	GI GECT	AKLF	AEHGAKVVI	A	46
SEQ-ID-NO:1068	DLQDNLGQNV	CESLGGEPK	TQYIHCDDVT	EDDV	RQAVDF	TVDKFGIT	LDI	97
SEQ-ID-NO:1018	DIQDEAGQQL	RDALGGDAQ	AMFVHCDVT	EEDV	SRAVDA	AAERFGAL	DV	99
SEQ-ID-NO:1066	DVQDEAGQRL	RDALGD--QD	VMFVHCDVT	EEDV	SRAVDA	AAERFGAL	DI	97
SEQ-ID-NO:1055	DVQDEAGQQL	RDSLGGD--PD	VLFFVHCDVT	EEDI	SRAVDA	TAEKFGIT	DI	99
SEQ-ID-NO:1020	DIQDEAGQKL	RDSLGGD--QD	VLFFVHCDVS	EEDV	SRAVDA	TAEKFGIT	DI	94
SEQ-ID-NO:1110	DIQDDLGHV	CEAI GP--SN	CSYVHCNDVT	EDDI	KNVADK	AVATHGKLDI		95
SEQ-ID-NO:1110	DIQDDLGHV	CEAI GT--SN	SLYVHCNDVT	EEDI	KNVADT	AVTTHGKLDI		88
SEQ-ID-NO:1118	DIQDDLGHV	VEAI GT--SN	SLYVHCNDVT	EDDI	KNVADN	AVTTHGKLDI		95
SEQ-ID-NO:1117	DIQDDLGHV	CKDLGQ--SS	SVFVHCDVT	EEDI	KNVADT	AVSKYGKLDI		93
SEQ-ID-NO:1093	DIQDDLGLSL	CNEL--KS	ALYVHCNDVT	EEDI	KNVADT	AVSKYGKLDI		92
SEQ-ID-NO:1012	DIQDDLGLSL	CKHL--ES	ASVYVHCNDVT	EEDV	KNVADT	AVSKYGKLDI		92
SEQ-ID-NO:1094	DIQDDLGLSV	CNEL--KS	AVYVHCNDVT	EEDV	KNVADT	AVSKYGKLDI		92
SEQ-ID-NO:1068	MVNNAGLGGP	PCP--DIRKVA	LSDFEKFVFDV	NVKG	GVFLG	GMK		146
SEQ-ID-NO:1018	MVNNAGVTGT	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		148
SEQ-ID-NO:1066	MVNNAGITGN	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		146
SEQ-ID-NO:1055	MVNNAGITGD	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		148
SEQ-ID-NO:1020	MVNNAGITGD	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		143
SEQ-ID-NO:1110	MVNNAGITGD	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		144
SEQ-ID-NO:1113	MVNNAGITGD	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		137
SEQ-ID-NO:1118	MVNNAGITGD	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		144
SEQ-ID-NO:1117	MVNNAGITGD	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		143
SEQ-ID-NO:1093	MVNNAGITGD	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		141
SEQ-ID-NO:1012	MVNNAGITGD	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		141
SEQ-ID-NO:1094	MVNNAGITGD	KVT--DIRTV	FAEARVRLDV	NVKG	GVFLG	GMK		141

Figure 8

SEQ-ID-NO:1068	KGSI VSLCSV	ASAI GGI GPH	AYT GSKHAVL	GLTRSAEEL	GKHGI RVNCV	196
SEQ-ID-NO:1018	RGSI VSLASV	ASAI GGI GPH	VYT ASKHAVV	GLTKSVAEEL	GRHGV RVNCV	198
SEQ-ID-NO:1066	RGSI VSLASV	ASVI GGMGPH	AYT GSKHAVV	GLTKSVAEEL	GRHGV RVNCV	196
SEQ-ID-NO:1055	KGSI VSLASV	ASVI GGMGPH	AYT ASKHAVV	GLTKSVAEEL	GRHGI RVNCV	198
SEQ-ID-NO:1020	KGSI I SLGSV	SSVI GGLGPH	SYT ATKHAVV	GLTKNAEEL	GKHGI RVNCV	193
SEQ-ID-NO:1110	SGSI I STSSV	SSLI GATATH	AYC ASKHAVL	GLTRNAEEL	GQFGI RVNCL	194
SEQ-ID-NO:1113	SGTI I SSSSL	SSHL GGTASH	AYC CSKHAI A	GLTKNAEEL	GQFGI RVNCL	187
SEQ-ID-NO:1118	SGNI I STASL	SST MGGSSH	AYC GSKHAVL	GLTRNAEEL	GQFGI RVNCL	194
SEQ-ID-NO:1117	RGSI VTTASI	CSVI GGI GTH	AYT SSKHGLV	GLM RNAAVDL	GRYGI RVNCV	193
SEQ-ID-NO:1093	RGCI INTASV	AGCI GGGATH	AYT SSKHALV	GLTKNTAEEL	GQFGI RVNCV	191
SEQ-ID-NO:1012	RGSI INTASV	AGLI GGVATH	AYT SSKHALI	GLMKSTAEEL	GQFGI RVNCV	191
SEQ-ID-NO:1094	RGCI INTSSI	AGCRGT GSPH	AYV VSKHGLE	GLTKNTAEEL	GQFGI RVNCV	191
SEQ-ID-NO:1068	SPYGVATSLA	VAHL PEDEET	EDALI GFRSF	IGRANALQ	VELT VDDVAN	245
SEQ-ID-NO:1018	SPYAVPTALS	MPHL PQGARA	DDALKDFLAF	VGGEANLK	VDA MPEDVAQ	247
SEQ-ID-NO:1066	SPYAVPTALS	MPHL PQGARA	DDSLKDFLAF	VGGEANLK	VDVMP R DVAE	245
SEQ-ID-NO:1055	SPYAVPTALS	MPHL PQGEOK	GDAVRDFLAF	VGSEANLK	VDLLPKDVAE	247
SEQ-ID-NO:1020	SPYAVPTALS	MPYL PQGERK	DDALKDFEAF	VGSEANLK	VDLLPKDVAQ	242
SEQ-ID-NO:1110	SPYALATPLA	TGFL GGNDDE	-----LEKA	MSKSANLK	VYL KAEDIAN	237
SEQ-ID-NO:1113	SAVGIATPLT	KKI TGLEKEA	-----FESA	MNLTANLK	VT LKTDDAAY	230
SEQ-ID-NO:1118	SPFGLPTALG	KKFSGI KNEE	E-----FENV	LNFAGNLK	PKFNVEDVAN	238
SEQ-ID-NO:1117	SPNVVPTEMG	RKLFKV KDGG	E-----F	PSFYWSLKN	DI LREEDVGE	235
SEQ-ID-NO:1093	SPFAI VTPLL	NKYFNL DEEG	-----V	RKTYMNLK	WYPVPNDVAE	231
SEQ-ID-NO:1012	SPYVPTPLT	KKHANI DEEG	-----V	REI YSNLK	VHL VPNDVAE	231
SEQ-ID-NO:1094	SPYL VATPML	KKYFNL DEEG	-----V	REAYSNLK	SYL VPNDVAE	231
SEQ-ID-NO:1068	AVLFLASDEA	RYI SGDNLML	DGGFTCTNHS	LRV---FR--	---	280
SEQ-ID-NO:1018	AVLYLASDEA	RYVSAVNL MV	DGGFTAVNNN	LRA---FED-	---	283
SEQ-ID-NO:1066	AVLYLASDEA	RYVSALNL MV	DGGFTAVNNH	LKA---FED-	---	281
SEQ-ID-NO:1055	AVLYLASDEA	RYI SALNL VV	DGGFTSVNGN	LKA---FED-	---	283
SEQ-ID-NO:1020	AVLYLASDEA	RYI SALNL MV	DGGFTSVNNH	LRA---FED-	---	278
SEQ-ID-NO:1110	AALYPA SEEC	RYVSGHNL F	DGGFTVNNPS	LQM---FQYP	DGS	277
SEQ-ID-NO:1113	AALFLV SDEA	KYI SGQNL LI	DGC SYANTIS	FNF---FKYG	EEL	270
SEQ-ID-NO:1118	AALYLASDEA	KYVSGHNL F	DGGFSVCNSV	IKV---FQYP	DS-	277
SEQ-ID-NO:1117	AVVYLGSDES	KCVSGLNLI V	DGGFTVNNQA	LCS---FRS-	---	271
SEQ-ID-NO:1093	AALYLASDES	KFVSSHNLVI	DGGLNSNVG	FPM---FEM-	---	267
SEQ-ID-NO:1012	AALYLAGDES	KYVSGHNLVL	DGGFTNVI G	FSV---FGQS	E--	269
SEQ-ID-NO:1094	AALFLAGDES	NYVSGHSLLL	DGGYTTNAG	FSPNAGFSPG	QSE	274

Figure 8 (continued)

SEQ-ID-NO:933	DRAFMSKMR	RTVKLAKCF	PTAI VTGRCL	DKVYNFVKLA	ELYYAGSHGM	175
SEQ-ID-NO:1142	DKAVMSPVMR	AAVRNVAKYF	PTAI VSGRSR	NKVF EFVKLK	ELYYAGSHGM	183
SEQ-ID-NO:1146	DKAFMSPA MR	AAVRNVAKYF	PTAI VSGRSR	KKVCE FVKLK	ELYYAGSHGM	182
SEQ-ID-NO:1140	DKAFMSPVMR	AAVRNVAKYF	PTAI VSGRSR	KKVFE FVKLT	ELYYAGSHGM	183
SEQ-ID-NO:1144	ANAVMSDEMR	AAVRHVASLF	PTAI I SGRSR	DKVDFDVKLT	ELYYAGSHGM	183
SEQ-ID-NO:926	DRAFMSDAMR	SAVRNVAKYF	PTAI I SGRSR	DKVYELVGLT	ELFYAGSHGM	187
SEQ-ID-NO:1129	DCAYMSSAMR	SAVRNVAKYF	PTAI I SGRSR	DKVYEFVNL S	ELYYAGSHGM	188
SEQ-ID-NO:1148	DSAFMSDNMR	AAVKVAEYF	PTAI I SGRSR	DKVYEFVGV S	DLYYAGSHGM	184
SEQ-ID-NO:1150	DNAFMSADMR	STVKEVAKYF	PTAI I SGRSR	DKVYEFVGLT	ELYYAGSHGM	189
SEQ-ID-NO:1182	DRAFMSGAMR	ATVRNVAKYF	PTAI I SGRSR	DKVYDFVGLA	ELYYAGSHGM	186
SEQ-ID-NO:933	DI KGPAKGFS	RHK	---RVKQSL	LYQPASDYLP	MI DEVYRQLL	214
SEQ-ID-NO:1142	DI MAPSANHE	HSA	---EKSKQAN	LFQPAHDFLP	MI DEVTKSLL	223
SEQ-ID-NO:1146	DI VT SAPEHN	TEK	---GKEAN	LFQPALEFLP	MI DEVSKSLL	220
SEQ-ID-NO:1140	DI VT SAAHA	TEK	---GKEAN	LFQPACEFLP	MI NEVSKQLV	221
SEQ-ID-NO:1144	DI MGPI RKSE	SNCHHVECV R	STDSECKEVN	LFQPASEFLP	MI AEVFNLS	233
SEQ-ID-NO:926	DI MGPKHTE	SDDGHPNRVR	SIDQEGKEVN	LFQPAREFLP	MI DEVFRTL V	237
SEQ-ID-NO:1129	DI MSPAGESL	NHEHSRTV	SVYEQKGDVN	LFQPASEFLP	MI DKVLC SLI	236
SEQ-ID-NO:1148	DI I GPSRQSI	SDNHPDCI S	SADKQGVQVN	LFQPAAEFLP	MI NEVLGLLK	233
SEQ-ID-NO:1150	DI MGPIRQSV	SDDHRNCI K	STDKQGN EVN	LFQPAREFLP	MI DEVYSLV	238
SEQ-ID-NO:1182	DI MGPIRQSVS	DDY---SCL R	STNKQGKEVN	LFQPAGEFLP	MI DEVFRSLI	233
SEQ-ID-NO:933	EKTKST PGVI	VENNKFCASV	HFRCVDEKKW	SELVLQVRSV	LNEYPRCLKN	264
SEQ-ID-NO:1142	QVVSGL EGAT	VENNKFCVSV	HYRNVAEKDW	KLVARLVNEV	LEAFPRCLKVT	273
SEQ-ID-NO:1146	EATSGI KGAN	VENNKFCVSV	HYRNVAEKDW	KVVARLVNEV	LEAFPRCLKVT	270
SEQ-ID-NO:1140	EVTSSI EGAR	VENNKFCVSV	HYRNVAEKDW	KVAGLVKQV	LEAFPRCLKVT	271
SEQ-ID-NO:1144	ESI KGI EGAR	MEDNKFCVSV	HYRNVAPHDY	ETVHQRTAV	LKDYPPQLRLT	283
SEQ-ID-NO:926	ENTKDI KGAK	VENHKFCISV	HYRNVEEKNW	PII AQCVHDI	LKDYPPRLRLT	287
SEQ-ID-NO:1129	ESTKDI KGVK	VEDNKFCISV	HYRNVEEKNW	TLVAQCVD DV	IRTPYPKRLRLT	286
SEQ-ID-NO:1148	ECTEDI EGAT	VENNKFCVSV	HYRNVDEESW	QI VQQRVYDV	LKEYPRRLRLT	283
SEQ-ID-NO:1150	RI TEDI KGAT	VENNKFCVSV	HYRNVDDQDNW	KSMGERVQDV	IKKYPRRLRLT	288
SEQ-ID-NO:1182	ELTKDI TGAK	VENNKFCVSV	HYRNVDEKSNW	SALGESVDEL	LKHYPRLRLT	283

Figure 9 (continued)

SEQ-ID-NO:933	QGRKVFEI RP	MI EWDKGKAL	EFLLES LGFG	NSNNVFPVYI	GDDRTDEDAF	314
SEQ-ID-NO:1142	NCRMVLEVRP	VI DWDKGKAV	EFLQSLGLN	DSENVIPYI	GDDRTDEDAF	323
SEQ-ID-NO:1146	NCRMVLEVRP	VI DWDKGKAV	EFLQSLGLN	DSENVIPYI	GDDRTDEDAF	320
SEQ-ID-NO:1140	NCRMVLEVRP	VI DWDKGKAV	EFLRSLGLS	DSEDDVPI YI	GDDRTDEDAF	321
SEQ-ID-NO:1144	HGRKVLEVRP	VI DWNKGGKAV	EFLLES LGLN	ESDDVLPYI	GDDKTDEDAF	333
SEQ-ID-NO:926	HGRKVLEVRP	VI DWNKGGKAV	EFLLES LGLN	DRDDVLPYI	GDDKTDEDAF	337
SEQ-ID-NO:1129	HGRKVEI RP	VI DWDKGKAV	TFLES LGLN	NCDDVLPYI	GDDRTDEDAF	336
SEQ-ID-NO:1148	HGRKVLEVRP	VI DWDKGKAV	TFLES LGLN	NCDDVLPYI	GDDRTDEDAF	332
SEQ-ID-NO:1150	HGRKVEI RP	VI DWDKGKAL	EFLLES LGLN	NCDDVLPYI	GDDRTDEDAF	338
SEQ-ID-NO:1182	HGRKVLEVRP	VI DWDKGKAV	EFLLES LGLN	NCDDVLPYI	GDDRTDEDAF	333
SEQ-ID-NO:933	KLLRDR -GEG	CGVLVSKF PK	DT DAS YL QD	PSEASDEF LA	TI GGVEI NAA	363
SEQ-ID-NO:1142	KVLRQR -NCG	YGI LVSVQPK	ET EAFYSLRD	PSEV -MEFLN	FL VVRWKKHSV	371
SEQ-ID-NO:1146	KVLRKR -NCG	YGI LVSVQPK	DT EAFYSLRD	PSEV -MAFLN	SL VVRWKKHSL	368
SEQ-ID-NO:1140	KVLRER -SCG	YGI LVSVQPK	DT EAFYSLRD	PSEV -MGFLN	SL VVRWKKHPL	369
SEQ-ID-NO:1144	KVLKAN -NHG	YGI LVSVQPK	DSDAFYSLRD	PSEV -MEFLR	TL AAWKEGSS	381
SEQ-ID-NO:926	KVLKEG -NMG	YGI LVSVQPK	ESNA FSVRD	PSEV -KKFLK	AL VVRWKRLEE	385
SEQ-ID-NO:1129	KVLRDGNHG	YGI LVSAV PK	DSNAFYSLRD	PSEV -MEFLK	SL VTWKRSMG	385
SEQ-ID-NO:1148	KVLKEA -NKG	YGI LVSAV PK	ESNA FYSLRD	PSEV -MEFLT	SL AEWKSS LQ	380
SEQ-ID-NO:1150	KVLRER -NCG	YGI FVSKSPK	ESNA FYSLRD	PAEV -MEFLK	SL VTWKKSSA	386
SEQ-ID-NO:1182	KVLRER -NKG	YGI LVSAV PK	ESSAFYSLRD	PSEV -MEFLK	CL VSWKKSSG	381
SEQ-ID-NO:933	KSVKRMVY					
SEQ-ID-NO:1142	-----					
SEQ-ID-NO:1146	-----					
SEQ-ID-NO:1140	-----					
SEQ-ID-NO:1144	-----					
SEQ-ID-NO:926	A-----					
SEQ-ID-NO:1129	-----					
SEQ-ID-NO:1148	AR-----					
SEQ-ID-NO:1150	L-----					
SEQ-ID-NO:1182	FSY-----					

Figure 9 (continued)

SEQ-ID-NO:74	MYATLPSPFL	PKSLHAFSPN	KTSSSLRTSA	RAAEFKSATIA	TEGNS	45
SEQ-ID-NO:60	---MAGTL---	VNSAGRFSPG	NCILPQQRITA	RFYSGTARFP	TGAPSFKAS	44
SEQ-ID-NO:915	---MAGTL---	VNSAGRFSPG	NCILPQQRITA	RFYSGTARFP	TGAPSFKAS	44
SEQ-ID-NO:62	---MSGTLIYS	AVNSLRSSPG	NS-LRQPKPT	RLHNGNARFP	TGATSFASA	47
SEQ-ID-NO:152	---MSGTLIYL	GVNSLRSSPG	NS-LRQPKPT	RLHNGNARLS	TGATSFASA	47
SEQ-ID-NO:98	---MLSSLPI'S	NSISLS---	---SISPPSA	SLRFRPPPLA	AASTAYFTSK	41
SEQ-ID-NO:102	---MLSPRPAM	SPSFLAFRPG	SP-AA SPPPS	PRLNGPPPLS	ASFSA	42
SEQ-ID-NO:104	---MA---FS	SSSSPCFFP	---SHNLTNL	RYNKHNSPM	SASF	35
SEQ-ID-NO:74	---AQTILNAEPAV	---AVALLAGS	LYEILRVERIT	ASLNEIKTAY	RSLAKVYHPD	83
SEQ-ID-NO:60	AQTILNAEPAV	TESVRRRVSS	LYELLKVNET	ASLTEIKTAY	RSLAKVYHPD	94
SEQ-ID-NO:915	AQTILNAEPAV	TESVRRRVSS	LYELLKVNET	ASLTEIKTAY	RSLAKVYHPD	94
SEQ-ID-NO:62	AQTILNAEPAV	TESVRRRVSS	LYELLKVNET	ASLTEIKTAY	RSLAKVYHPD	97
SEQ-ID-NO:152	AQTILNAEPAV	TESVRRRVSS	LYELLKVNET	ASLTEIKTAY	RSLAKVYHPD	97
SEQ-ID-NO:98	QQKASPSGYL	SRPGMAACTS	LYEVLGI SVG	ASNQEI KAY	RRLARVCHPD	91
SEQ-ID-NO:102	---STAVTA	PDHAAASSS	FYDVLGLRPG	ASPREIKTAY	RRLA L VHPD	88
SEQ-ID-NO:104	---T SERPGT	ARSTRAIT PSS	LYEVLGL QI G	ADTMEIKSAY	RRLARV VHPD	82
SEQ-ID-NO:74	A---NRSSSD	GRDFIEIRNA	YATLSDP TAR	AVYDMSLGV R	---ARRIR---	125
SEQ-ID-NO:60	A---SESD	GRDFMEI HKA	YATLADPTTR	AI YDSTLRVP	---RRRVHAGA	137
SEQ-ID-NO:915	A---SESD	GRDFMEI HKA	YATLADPTTR	AI YDSTLRVP	---RRRVHAGA	137
SEQ-ID-NO:62	A---SSED	GRDFMEI HKA	YATLADPTTR	AI YDSTLGAR	---GRRMHAGA	141
SEQ-ID-NO:152	A---SSED	GRDFMEI HKA	YATLADPTTR	AI YDSTLGAR	---GRRMHAGA	141
SEQ-ID-NO:98	VVTI DRKDS	ADEFMKI HAA	YSTLSDPDKR	AVYDSKL W-	---RCOR	134
SEQ-ID-NO:102	AAP-HPAS	AEDFI RVHAA	YSTLSDPDKR	ADYDRRLLS	AGRRAHPAA	137
SEQ-ID-NO:104	V---GNLNSS	ADEFMKVHSA	YATLSDPGKR	ADYDRSLFV-	-----RPEM	122
SEQ-ID-NO:74	---TRVYP-	---LRRWETDQ	CW			140
SEQ-ID-NO:60	MGRSGRVYA-	---LRRWETDQ	CW			157
SEQ-ID-NO:915	MGRSGRVYA-	---LRRWETDQ	CW			157
SEQ-ID-NO:62	TGRTSRVYP-	---LRRWETDQ	CW			161
SEQ-ID-NO:152	MGRTSRVYP-	---LRRWETDQ	CW			161
SEQ-ID-NO:98	PLTSAISMFSG	YTGSRWETDQ	CW			156
SEQ-ID-NO:102	LGRSPSPFAR	RSRRTWETDQ	CW			159
SEQ-ID-NO:104	VGRSCS-PVG	YSGRRWETDQ	CW			143

Figure 10

SEQ-ID:NO:408	ME	DV	MK	V	K	V	E	---	ED	---	---	---	GL	PT	AV	LP	ME	GL	HD	VG	PP	FL	SK	TK	36		
SEQ-ID:NO:364	ME	-	EL	K	V	E	ME	---	EET	VT	FT	IG	SV	---	SP	RP	ME	GL	NE	TG	PP	FL	TK	TK	49		
SEQ-ID:NO:407	ME	-	GV	V	K	-	E	---	EET	VT	CT	IG	GG	---	SP	RP	ME	GL	NE	VG	PP	FL	TK	TK	48		
SEQ-ID:NO:421	MD	-	GA	SG	-	-	-	---	---	---	---	---	---	SG	GG	EG	ST	T	Q	NA	PP	FL	SK	TK	37		
SEQ-ID:NO:410	MD	KP	VA	PG	T	I	-	---	KEE	L	E	Q	PP	---	AP	RP	ME	GL	HE	VG	PP	FL	TK	TK	50		
SEQ-ID:NO:413	MD	-	PA	AG	L	I	V	---	KEE	M	L	E	S	Q	Q	Q	Q	Q	Q	R	Q	ED	G	G	A	-	47
SEQ-ID:NO:408	YEM	VED	S	S	T	D	-	---	QVI	S	W	S	T	T	R	N	-	---	---	---	---	---	---	---	---	86	
SEQ-ID:NO:364	YEM	VED	P	A	T	D	-	---	TVV	S	W	S	N	G	R	N	-	---	---	---	---	---	---	---	---	99	
SEQ-ID:NO:407	YEM	VED	P	S	T	D	-	---	TVV	S	W	S	G	G	R	N	-	---	---	---	---	---	---	---	---	98	
SEQ-ID:NO:421	YDM	VDD	P	S	T	D	-	---	AI	V	S	W	S	A	T	N	N	-	---	---	---	---	---	---	---	87	
SEQ-ID:NO:410	FDL	VED	P	A	T	D	-	---	AVL	S	W	S	R	A	G	N	-	---	---	---	---	---	---	---	---	100	
SEQ-ID:NO:413	YDL	VED	P	A	T	D	-	---	GVV	S	W	S	R	A	G	N	-	---	---	---	---	---	---	---	---	97	
SEQ-ID:NO:408	LNT	Y	G	F	R	K	V	D	-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	127	
SEQ-ID:NO:364	LNT	Y	G	F	R	K	I	D	-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	142	
SEQ-ID:NO:407	LNT	Y	G	F	R	K	V	D	-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	139	
SEQ-ID:NO:421	LNT	Y	G	F	R	K	V	D	-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	137	
SEQ-ID:NO:410	LNT	Y	G	F	R	K	V	D	-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	144	
SEQ-ID:NO:413	LNT	Y	G	F	R	K	V	D	-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	140	
SEQ-ID:NO:408	MN	Q	G	S	G	A	C	I	-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	177	
SEQ-ID:NO:364	NQ	Q	SG	M	SC	V	-	---	EV	G	Y	G	F	D	GE	-	---	---	---	---	---	---	---	---	---	192	
SEQ-ID:NO:407	TQ	Q	GG	G	A	C	I	-	EL	G	Q	F	E	FE	GE	-	---	---	---	---	---	---	---	---	---	189	
SEQ-ID:NO:421	GQ	SS	SV	G	AC	V	-	---	EV	G	K	F	G	L	EE	E	-	---	---	---	---	---	---	---	---	187	
SEQ-ID:NO:410	RQ	RA	PA	S	CL	-	---	---	EV	G	E	F	G	FE	EE	E	-	---	---	---	---	---	---	---	---	194	
SEQ-ID:NO:413	SO	Q	SL	T	S	CL	-	---	EV	G	E	F	G	FE	EE	E	-	---	---	---	---	---	---	---	---	190	
SEQ-ID:NO:408	AM	GE	K	I	E	T	Q	E	-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	226	
SEQ-ID:NO:364	AME	Q	R	L	V	T	E	-	KR	Q	Q	M	M	T	FL	-	---	---	---	---	---	---	---	---	---	241	
SEQ-ID:NO:407	AME	D	R	L	R	S	T	E	-	RK	Q	Q	R	V	M	T	FL	-	---	---	---	---	---	---	---	238	
SEQ-ID:NO:421	TM	V	Q	R	L	Q	G	M	E	-	Q	R	Q	Q	M	M	S	FL	-	---	---	---	---	---	---	237	
SEQ-ID:NO:410	AME	E	R	L	R	V	A	E	-	Q	Q	V	Q	M	M	G	FL	-	---	---	---	---	---	---	---	244	
SEQ-ID:NO:413	AME	D	R	L	R	A	E	-	Q	Q	V	Q	M	M	G	FL	-	---	---	---	---	---	---	---	---	240	

Figure 11

SEQ-ID:NO:408	QKRRLLTMT P	---	---	---	---
SEQ-ID:NO:364	RKRRLLTST P	---	---	---	---
SEQ-ID:NO:407	RKRRLLTASP	---	---	---	---
SEQ-ID:NO:421	RRLLKQDGI AE	TTEQATPPDG	QI VKYQPMMN	ETAKAMLRKI	MKWDT PRVES
SEQ-ID:NO:410	RRRPI DNT P	---	---	---	---
SEQ-ID:NO:413	RRRPL DNV P	---	---	---	---
SEQ-ID:NO:408	---	SVTG	SDQPM-NYSS	SLE	---
SEQ-ID:NO:364	---	SLGT	MEENL	LHD	---
SEQ-ID:NO:407	---	SVEN	LQEVA SVALG	SSQFVDYMN-	---
SEQ-ID:NO:421	FNKNPDNYLI	GdGT SPSSAM	DSSSST SWNS	GVTL QEVPPPS	SVQST QI PMS
SEQ-ID:NO:410	---FY	SDC---	ESEQLDSQ LKMFES	GV-LNGLNE	---
SEQ-ID:NO:413	---FY	DPGETSQTEQ	LDSPY-LFDS	GV-LNELSEP	GI ---
SEQ-ID:NO:408	---	---	---	---	---
SEQ-ID:NO:364	---	---	---	---	---
SEQ-ID:NO:407	---	---	---	---	---
SEQ-ID:NO:421	TGTQCHI PSA	EKPEI LVPQ	AAASANVMKD	GTHAASTI PT	SQADVI MPDI
SEQ-ID:NO:410	---	---	---	---	---
SEQ-ID:NO:413	---	---	---	---	---
SEQ-ID:NO:408	---	---	---	---	---
SEQ-ID:NO:364	---	---	---	---	---
SEQ-ID:NO:407	---	---	---	---	---
SEQ-ID:NO:421	PSVPEI VPKS	I LDI PEDNYM	APEITDDGFMD	PSSL GSP I D	LDC---
SEQ-ID:NO:410	---	---	PELENLAVN	TQELGKGS I D	DGN---
SEQ-ID:NO:413	---	---	PELENLAVN	I QDLGKGKVD	EER---
SEQ-ID:NO:408	---	---	---	---	---
SEQ-ID:NO:364	---	---	---	---	---
SEQ-ID:NO:407	---	---	---	---	---
SEQ-ID:NO:421	---	---	---	---	---
SEQ-ID:NO:410	---	---	---	---	---
SEQ-ID:NO:413	---	---	---	---	---
SEQ-ID:NO:408	SV----	V TAN	GDMEIPVADD	I WEELL SEDL	I SGDRAAEEV
SEQ-ID:NO:364	---	PT KE	EQCLEAMNVM	MRDGNL	---
SEQ-ID:NO:407	I ASSMDTASG	GSTLD AVNET	I WEELL TDDL	VSGE--PNEV	VVSDEPEVD-
SEQ-ID:NO:421	---	LSPG	ADI DDLLSNS	I WDDLLQTPI	---
SEQ-ID:NO:410	---	LTQV	SDQSE-LNDD	FMAELLVEDF	GDKA-----
SEQ-ID:NO:413	---	QNQT	NGQAE-LGDD	FMAELLVEDF	TGKE-----

Figure 11 (continued)

SEQ-ID-NO:408	---	VEVEDLV	VKTPEW	---	LQDLVDQLGF	---	---	---	351
SEQ-ID-NO:364	---	VKVEDLV	GSPLDWD	---	LHDMVDQMGI	---	---	---	345
SEQ-ID-NO:407	---	VEVEDLV	AKPVDW	---	FQDLVDQMGI	---	---	---	392
SEQ-ID-NO:421	---	I SRGNEVQPT	ENGWDNNT	---	LQDLTEQMGL	---	---	---	502
SEQ-ID-NO:410	---	GR	---	---	VNDLAQQLGY	---	---	---	357
SEQ-ID-NO:413	---	GK	---	---	I DELAQQLGY	---	---	---	358
SEQ-ID-NO:408	---	---	---	---	---	---	---	---	351
SEQ-ID-NO:364	---	---	---	---	---	---	---	---	345
SEQ-ID-NO:407	SFLN	---	---	---	---	---	---	---	396
SEQ-ID-NO:421	---	---	---	---	---	---	---	---	502
SEQ-ID-NO:410	---	---	---	---	---	---	---	---	357
SEQ-ID-NO:413	---	---	---	---	---	---	---	---	358

Figure 11 (continued)

SEQ-ID-NO:326	MEAAVAAA	-----AAGAV	TTTAVAPPPGA	AVSNGVATAP	PPFLMKTYEM	45
SEQ-ID-NO:335	MDGVTGGDSK	-----SGEAT	TAPPLRNPHIP	ATLLGTNALP	PPFLSKTYDM	45
SEQ-ID-NO:311	MDVSKVTSD	G-----GGDSM	ETKPSPPQP	AALLS-SNAP	PPFLSKTYDM	45
SEQ-ID-NO:322	MEPNSSGSGK	AAVGDGGGG	APMLQAPAP	APMPS-ANAP	PPFLVKTYDM	49
SEQ-ID-NO:323	MEPNSSGSGK	AAV--GDGVG	APMLQATAP	APIPS-ANAP	PPFLVKTYDM	47
SEQ-ID-NO:319	MDGNTTAS	-----GGDAS	TSGGVALAAP	VPMASQSNSP	PPFLSKTYDM	44
SEQ-ID-NO:321	MDGRASSV	-----GGEAS	-----PAPAP	VPIITN-ANAP	PPFLSKTYEM	38
SEQ-ID-NO:320	MDGASGGSG	-----GGEGS	TTT-----QIPAP	TPMILN-ANAP	PPFLSKTYDM	40
SEQ-ID-NO:326	VDDPATDAVV	SWGPGNNSFV	VWNITPEFARD	LLPKYFKHNS	FSSFVRQLNT	95
SEQ-ID-NO:335	VEDPASDAIV	SWSPANNSFV	VWDPPEFSRS	LLPRYFKHNN	FSSFVRQLNT	95
SEQ-ID-NO:311	VDDHNTDSIV	SWSANNSFI	VWKPPPEFARD	LLPKNFKHNN	FSSFVRQLNT	95
SEQ-ID-NO:322	VDDPSTDKI	SWSPTNNSFV	VWDPPEFAKD	LLPKYFKHNN	FSSFVRQLNT	99
SEQ-ID-NO:323	VDDPSTDKI	SWSPTNNSFV	VWDPPEFAKD	LLPKYFKHNN	FSSFVRQLNT	97
SEQ-ID-NO:319	VDDPETDAVV	SWSPTNNSFV	VWNPPEFARD	LLPKYFKHNN	FSSFVRQLNT	94
SEQ-ID-NO:321	VEDPSTDIV	SWSPTNNSFV	VWNPPEFARD	LLPKHFKHNN	FSSFVRQLNT	88
SEQ-ID-NO:320	VDDPSTDIV	SWSATNNSFV	VWDPPEFARD	LLPKFFKHNN	FSSFVRQLNT	90
SEQ-ID-NO:326	YGFRKVDPR	WEFANEGLR	GQKHLKLTIN	RRKPTHGNNQ	VQ-----	137
SEQ-ID-NO:335	YGFRKVDPR	WEFANEGLR	GQKHLKLTIS	RRKSTQGHGS	SSSSNPQ---	142
SEQ-ID-NO:311	YGFRKVDPR	WEFANEGLR	GQKHLQSI	RRKPAHGQ	GHQRSQ----	141
SEQ-ID-NO:322	YGFRKVDPR	WEFANEGLR	GQKHLKSI	RRKPAHGHAQ	QQQPHGHAQ	149
SEQ-ID-NO:323	YGFRKVDPR	WEFANEGLR	GQKHLKSI	RRKPAHGHAQ	QQQPHGHAQ	147
SEQ-ID-NO:319	YGFRKVDPR	WEFANEGLR	GQKHLRTIS	RRKPAHGHTN	QQPQ-----	138
SEQ-ID-NO:321	YGFRKVDPR	WEFANEGLR	GQKHLKLTIT	RRKPAHGHNQ	QAQ-----	131
SEQ-ID-NO:320	YGFRKVDPR	WEFANEGLR	GQQLKLSIS	RRKPAHGHTQ	QAQ-----	134
SEQ-ID-NO:326	---QPLPAA	PVPACVEVGK	FGMEEEIEM	KRDKNVLMQE	LVRLRQQQQT	184
SEQ-ID-NO:335	---SHQGHMA	SLSSCCEVGK	FGLEEEVEQL	KRDKNVLMQE	LVKL RQQQSS	189
SEQ-ID-NO:311	---HSNGQNS	SVSACCEVGK	FGLEEEVERL	KRDKNVLMQE	LVRLRQQQSS	188
SEQ-ID-NO:322	QQMQPPGHSA	SVGACCEVGK	FGLEEEVERL	KRDKNVLMQE	LVRLRQQQSS	199
SEQ-ID-NO:323	QQMQPPGHSA	SVGACCEVGK	FGLEEEVERL	KRDKNVLMQE	LVRLRQQQQA	197
SEQ-ID-NO:319	---QARGQNS	TVGACCEVGK	FGLEEEVERL	KRDKNVLMQE	LVRLRQQQSS	185
SEQ-ID-NO:321	---QAHGQSS	SVGACCEVGK	FGLEEEVERL	KRDKNVLMQE	LVRLRQQQQA	178
SEQ-ID-NO:320	---QPHGQSS	SVGACCEVGK	FGLEEEVERL	KRDKNVLMQE	LVRLRQQQQT	181

Figure 12

SEQ-ID-NO:326	TDHQLQT ^L GK	RLQGM ^E QRQ ^Q	QMSFLAKAM	HSPGFLAQFV	Q---QNE ^{NS} R	231
SEQ-ID-NO:335	TDSKLQSMVK	SLQ ^T MEQRQ ^Q	QIMSF ^L AKAV	QNP ^T FLSQFI	QK---Q ^T D ^{SG} N	237
SEQ-ID-NO:311	TDNQLQTMVQ	RLQGM ^E NRQ ^Q	QLMSFLAKAV	QSP ^H FLSQFL	QQNQ ^Q NE ^{SN}	238
SEQ-ID-NO:322	TDNQLQGMVQ	RLQGM ^E L ^R Q ^Q	QMSFLAKAV	NSPGFLAQFV	Q---QQNE ^{SN}	246
SEQ-ID-NO:323	TDNQLQGMVQ	RLQGM ^E L ^R Q ^Q	QMSFLAKAV	NRPGFLAQFV	Q---QQNE ^{SN}	244
SEQ-ID-NO:319	TDNQLQTMVQ	RLQGM ^E QRQ ^Q	QMSFLAKAM	QSPGFLAQFV	Q---QQNE ^{SS}	232
SEQ-ID-NO:321	TDNQLQSMVQ	RLQGM ^E QRQ ^Q	QMSFLAKAV	QSPGFLAQFV	Q---QQNE ^{SS}	225
SEQ-ID-NO:320	T ^D GQLQTMVQ	RLQGM ^E QRQ ^Q	QMSFLAKAV	QSPG ^F FAQFV	Q---QQN ^{DS} N	228
SEQ-ID-NO:326	RRI ^V AS ^N KKR	RLP ^K QDGS ^L -	DSESAS ^L DGQ	VKYQPMINE	AAKAMLRKIL	280
SEQ-ID-NO:335	MHVTEASKKR	RLT-----	EDAAAA ^S DGQ	VKYQPI ^R SD	STM ^S MM ^W MM	280
SEQ-ID-NO:311	RRI ^S DT ^S KKR	RF ^K R ^D G ^I VR-	NDSAT ^P DGQ	VKYQPP ^M HE	QAKAM ^F KQLM	287
SEQ-ID-NO:322	KRI ^A EGSKKR	RIKQDI ^E SQ-	DPSVT ^P ADGQ	VKYQPGINE	AAKAMLR ^E LS	295
SEQ-ID-NO:323	KRI ^A EGSKKR	RIKQDI ^E SQ-	DPSVT ^P ADGQ	VKYQPGINE	AAKAMLR ^E LS	293
SEQ-ID-NO:319	RRI ^T EANKKR	RLK ^P EDV ^{SE} -	NEGSSA ^P DGQ	VKYQPQ ^M NE	AAKAMLRQVM	281
SEQ-ID-NO:321	RRI ^T EANKKR	RLKQEG ^I GE-	MEHTAA ^S DGQ	VKYQPLINE	AAKAMLRQMM	274
SEQ-ID-NO:320	RRI ^T EV ^N KKR	RLKQDGI ^A ET	TEQA ^T PPDGQ	VKYQPM ^M NE	TAKAMLRKIM	278
SEQ-ID-NO:326	KLDSS ^H R ^F ES	MGNS ^I -DN ^F LL	ENYMP ^N GQGL	DSS-SS ^T R ^{NS}	GVT ^L AEV ^P AN	328
SEQ-ID-NO:335	-----KMEP	--N ^T DEK ^F PF	-----	-----SPN ^R DS	GVT ^F QEV---	301
SEQ-ID-NO:311	-----KMEP	YKTGDDG ^F LL	GNGT ^S IT ^T EGT	EMET ^S SNQ ^{VS}	GIT ^L KEM---	328
SEQ-ID-NO:322	KLDSS ^P RL ^{EN}	FSN ^S PE ^S FLI	GDGSP ^Q SN-	-----SSG ^R VS	GVT ^L QEV ^P PT	340
SEQ-ID-NO:323	KLDSS ^P RLDN	FSN ^S PE ^S FLI	GDGSP ^Q SN-	-----SSG ^R VS	GVT ^L QEV ^P PT	338
SEQ-ID-NO:319	KMDAPSRL ^{ES}	YDTN ^L DG ^F LI	NGSP ^S SSAK	DSGSS ^S SRMS	GVT ^L QEV---	328
SEQ-ID-NO:321	KLDT ^S -R ^{LES}	FSN ^N ADNYLI	GDHSS ^S SGAT	DRGNS ^L SR ^T IS	GVT ^L QV ^P PL ^T	323
SEQ-ID-NO:320	KWD ^T P-R ^{VES}	FNK ^N PDNYLI	GDGT ^S PS ^S AM	DSS ^S SS ^T SW ^{NS}	GVT ^L QEV ^P PS	327
SEQ-ID-NO:326	S-GLPYVA ^{ITS}	SGLSAI ^C -ST	ST ^P QI ^Q ---	---CPV ^V LDN	GI ^P KE ^V PN ^{MS}	369
SEQ-ID-NO:335	-----LPT ^T	SGQS ^Q AY---	-----	-----	-----	313
SEQ-ID-NO:311	-----PTA	SEI ^Q SS ^S PI ^E	T ^T PE ^I ---	VSAASEA ^T EN	-----	356
SEQ-ID-NO:322	S-GKPL ^N TA	SAI ^A Q ^S SL ^P	ATSEM ^Q SS ^{-H}	LGT ^C CEI ^T NN	QLSNI ^I PLV ^G	388
SEQ-ID-NO:323	S-GKPL ^N TA	SAI ^A Q ^S SL ^P	ATSEM ^Q SS ^{-H}	LGT ^C CEI ^T NN	QLSNI ^I PLV ^G	386
SEQ-ID-NO:319	-----PAA	SGI ^S G ^H GP ^{MA}	AJ ^I SEI ^Q SS ^{PH}	IASSEKAT ^{AS}	QFPE ^S L-LV ^G	370
SEQ-ID-NO:321	T ^I QSSH ^I PSA	TGI ^I -GD ^D PS ^T	GKSEI ^I ST ^P Q	VMA ^C DEV ^T KA	QYSNV ^N SV ^G	372
SEQ-ID-NO:320	SVQSTQ ^I PV ^S	TGT ^Q CHI ^I PSA	EKPE ^L SV ^P Q	AAASAN ^V M ^K D	-----G	368

Figure 12 (continued)

SEQ-ID-NO:282	MAI VYALVAR	GTVVLAEF	VSGNAGAVAR	RI LEKLP-PD	ADSR	49
SEQ-ID-NO:256	MP L YAVVAR	GATVLAEF	AATNAGAVAR	QVLERLPGG	ADSHVSYTQD	50
SEQ-ID-NO:268	MAI L YALVAR	GTVVLAEF	AATNAGAVAR	QVLERLPGG	ADSHVSYTQD	50
SEQ-ID-NO:294	MAI L YAVVAR	GTVVLAEF	AATNAGAVAR	QVLERLPGG	ADSHVSYTQD	50
SEQ-ID-NO:160	MAI L YALVAR	GTVVLAEF	TSTNASTI AK	QI LEKVP-GD	NDSNVSYSQD	49
SEQ-ID-NO:242	MG L YALVGR	GSVLAEFSG	TITNASAI AR	QI LEKI P-GN	NDTHVSYSQD	49
SEQ-ID-NO:253	MG L YALVAR	GSVLAEFSG	TITNAAAI AR	QI LEKI P-GN	NDTHVSYSQD	49
SEQ-ID-NO:162	MAI L YALVAR	GSVLAEF	ASTNASAI AR	QI LDKI P-GD	NDNVSYSQD	49
SEQ-ID-NO:184	MAI L YALVAR	GSVLAEF	TATNASAI AR	QI LDKI P-GN	DDSNVSYSQD	49
SEQ-ID-NO:282	RYI FHVLRAD	AGITFLCMAN	DTFGRRIPFL	YLEDIQMRFM	KNYGRVAHSA	99
SEQ-ID-NO:256	RYVFHAKRTD	-GITALCMAD	DAAGRRI PFA	FLEDIHGKFV	KTYGRAALT A	99
SEQ-ID-NO:268	RYVFHAKRTD	-GITALCMAD	DAAGRRI PFA	FLEDIHGKFV	KTYGRAALT A	99
SEQ-ID-NO:294	RYVFHAKRTD	-GITALCMAD	EAGRRIPFA	FLEDIHGKFV	KTYGRAALT S	99
SEQ-ID-NO:160	RYVFHVKRTD	-GLTVLCMAE	ETAGRRIPFA	FLEDIHQRFV	RTYGRAVHT A	98
SEQ-ID-NO:242	RYI FHVKRTD	-GLTVLCMAD	DTAGRRIPFA	FLEDIHQKFV	RTYGRAVHSA	98
SEQ-ID-NO:253	RYI FHVKRTD	-GLTVLCMAD	DSVGRRI PFA	FLEEIHQRFV	RSYGRAVLT A	98
SEQ-ID-NO:162	RYI FHVKRTD	-GLTVLCMAD	ESAGRRIPFA	FLEDIHQRFV	RTYGRAI FSA	98
SEQ-ID-NO:184	RYI FHVKRTD	-GLTVLCMAD	ETAGRRIPFA	FLEDIHQRFV	RTYGRAVIT A	98
SEQ-ID-NO:282	LAYAMNDEFS	RVLHHQMEFF	SSNPSADITLN	RLRGEVSEIH	TVMVDNI EKI	149
SEQ-ID-NO:256	LAYAMNDEFS	RVLSQQMDYY	SNQPSADQIN	LMRGEI SQVR	SVMIDNI DKV	149
SEQ-ID-NO:268	LAYAMNDEFS	RVLSQQMDYY	SNQPSADRI N	RMARGEI SQVR	SVMIDNI DKV	149
SEQ-ID-NO:294	LAYGMNDEFS	RVLSQQMDYY	SNQPSADRI N	RMARGEI SQVR	SVMIDNI DKV	149
SEQ-ID-NO:160	LAYAMNEEFS	RVLSQQIDYY	SNQPSADRI N	RI KGEINQVR	GVMENI DKV	148
SEQ-ID-NO:242	QPYGMNEEFS	RVLSQQMEYY	SSDPNADRI N	RLKGEMSQR	NVMENI DKV	148
SEQ-ID-NO:253	EAYAMNDEFS	RVLNQQMEYF	SSDPNADRI N	RLKGEMSQR	NVMENI DKV	148
SEQ-ID-NO:162	LPYGMNDEFS	RVLSQQMEYY	SSDPNADRI N	RLKGEMSQR	NVMENI DKV	148
SEQ-ID-NO:184	QAYAMNDEFS	RVLSQQMEYY	TNDPNADRI N	RLKGEMSQR	NVMENI DKV	148
SEQ-ID-NO:282	LDRGDRISLL	VDKTSITMQDS	AFHFRKQSKR	LRRALWMKNA	KLLAVLTVAJ	199
SEQ-ID-NO:256	LERGDRILDLL	VDKTTIMQGN	TVRFKQARR	YRSTTWWRNV	KLTAALITLL	199
SEQ-ID-NO:268	LERGDRLELL	VDKTANMQGN	TVRFKQARR	FRNTVWRNV	KLTAALITLL	199
SEQ-ID-NO:294	LERGDRLDML	VDKTANMQGN	TVRFKQARR	FRNTVWRNV	KLTAALITLL	199
SEQ-ID-NO:160	LDGERLELL	VDKTANMQGN	TVRFKQARR	FRNTVWRNV	KLTAALITLL	198
SEQ-ID-NO:242	LDRGDRLELL	VDKTANMQGN	TVRFKQARR	FRNTVWRNV	KLTAALITLL	198
SEQ-ID-NO:253	LDRGDRLELL	VDKAANMQGN	TVRFKQARR	FRNTVWRNV	KLTAALITLL	198
SEQ-ID-NO:162	LDRGDRLELL	VDKTANMQGN	TVRFKQARR	FRNTVWRNV	KLTAALITLL	198
SEQ-ID-NO:184	LDRGDRLELL	VDKTANMQGN	TVRFKQARR	FRNTVWRNV	KLTAALITLL	198

Figure 13

SEQ-ID-NO:282	VVLLYLLI SA	FCGGLSLPSC	RS	221
SEQ-ID-NO:256	LVI VYI AL FF	VCHGFTLPTC	IR	221
SEQ-ID-NO:268	LVI I YVVL VF	VCHGFTLPTC	IR	221
SEQ-ID-NO:294	TVI I YVVL VF	MCHGFTLPTC	IR	221
SEQ-ID-NO:160	LVI I YI AVAF	LCHGPTLPSC	F -	219
SEQ-ID-NO:242	LVI VYVVLAF	VCHGPAALPSC	F -	219
SEQ-ID-NO:253	IVI AVVVLAF	VCHGPAALPSC	F -	219
SEQ-ID-NO:162	LVI I YVVLAF	VCHGFTLPTC	IK	220
SEQ-ID-NO:184	LVI I YVVLAF	VCHGFTLPTC	IK	220

Figure 13 (continued)

SEQ-ID-NO:17	M	---	---	---	---	RIHPASPT	---	---	9
SEQ-ID-NO:27	M	---	---	---	---	RIHPAAA	---	---	10
SEQ-ID-NO:2	M	LI PVKI QS	LFSYLLLLNL	---	---	AMRVHPI PRN	I-NNTLHHH	---	49
SEQ-ID-NO:23	M	---	---	---	---	RVHPI PRN	LNNITLHHH	---	19
SEQ-ID-NO:15	M	---	---	---	---	RVHPLPKK	---	RNI TI QYE	17
SEQ-ID-NO:41	M	---	---	---	---	RVHPLPKK	---	RNI TI QFY	17
SEQ-ID-NO:21	M	---	---	---	---	KVHPVPRK	---	RNI SI QFG	17
SEQ-ID-NO:19	M	---	---	---	---	RVHPVPRK	---	RNI TERC	17
SEQ-ID-NO:25	M	---	---	---	---	RVHPAPRK	---	RTI AVQRC	17
SEQ-ID-NO:5	M	---	---	---	---	RVHPAPRK	---	RTI AVQRR	17
SEQ-ID-NO:17	---	---	---	---	---	AGGKK	DLRRLPHVYS	---	44
SEQ-ID-NO:27	---	---	---	---	---	AGGKK	DLRRLPHVYS	---	45
SEQ-ID-NO:2	HH-NPT	---	---	---	---	REPCK	NLRRLPHI FN	---	89
SEQ-ID-NO:23	HRRNPT	---	---	---	---	REPCK	NLRRLPHI FS	---	61
SEQ-ID-NO:15	MNPT TRSQA	---	ETLL GCSNK	---	---	KLRLPHI FS	RVLELPLRSE	---	67
SEQ-ID-NO:41	PLTSSAG	---	---	---	---	KLRLPHI FS	RVLELPLRSD	---	59
SEQ-ID-NO:21	GDGGMSEA	---	QALL-GIAGK	---	---	KLRLPHVFS	RVLELPLRSD	---	66
SEQ-ID-NO:19	VNPAAATAV	---	---	---	---	KLRLPHI FS	RVLELPLRSD	---	62
SEQ-ID-NO:25	AAALSA	---	---	---	---	KLRLPHI FA	RVLELPLRSD	---	59
SEQ-ID-NO:5	CGVAAAAG	---	---	---	---	KLRLPHI FA	RVLELPLRSD	---	61
SEQ-ID-NO:17	AFHFVAAAPAA	GARAAAT-VR	---	---	---	VRTVRI HPGV	---	---	93
SEQ-ID-NO:27	AFHFVAAAGAR	---	GAGV-VQ	---	---	VRTVRI HPGV	---	---	89
SEQ-ID-NO:2	CFRFVAETVG	LCNGDGE-MR	---	---	---	AYMVEI HPGI	---	---	135
SEQ-ID-NO:23	CFRFVAETEG	LC-DGGE-MR	---	---	---	AYVVDI HPGI	---	---	105
SEQ-ID-NO:15	CFKFVAETDG	---	RI GDVVR	---	---	AHTVEI HPGV	---	---	110
SEQ-ID-NO:41	CFRFVAETDD	---	NI GD-MR	---	---	AHTVEI HPGV	---	---	101
SEQ-ID-NO:21	CFRFVAETDG	---	---	---	---	AHTVEI HPGV	---	---	106
SEQ-ID-NO:19	GRFVAATDV	---	LWGD-VQ	---	---	AQT VQI HPGV	---	---	99
SEQ-ID-NO:25	ELRFVAATEG	F--SPGG-AC	---	---	---	AHALEI HPGV	---	---	100
SEQ-ID-NO:5	ALRFVAAADG	FT-PSGG-AS	---	---	---	AHALEI HPGV	---	---	103

Figure 14

SEQ-ID:NO:17	DS----	MELD	RWRSRLPEPT	CPAMAVAGYV	DGQLVVTVPK	GPAAEEGADA	139
SEQ-ID:NO:27	DD----	MELD	RWRSRLPEAS	RPAMAVAGYV	DGQLVVTVPK	GREGSEGADA	135
SEQ-ID:NO:2	DE----	LELD	VWRFRLPEST	RPELVTVASV	DGDLIVTVPK	NAEEED-DDG	180
SEQ-ID:NO:23	DE----	LELD	MWRFRLPETT	RPELVTVVCV	DGVLIVTVPK	MVPEEE--DG	149
SEQ-ID:NO:15	DD----	LELD	MWRFRLPETT	RPELASAVYE	DGELIVTVPK	GGEEVENLEDG	156
SEQ-ID:NO:41	DD----	LELD	MWRFRLPETT	RPELASAVLA	DGELIVTVPK	GEEGG--DG	145
SEQ-ID:NO:21	DQ----	LELD	MWRFRLPEST	RPELASAVFY	DGELIVTVPK	GHEEEN--DG	150
SEQ-ID:NO:19	DDLDTLELN	RWRFRLPFST	RPALATAAYT	RPALATAAYT	SGELVVTIPK	GAGPEE--EDG	148
SEQ-ID:NO:25	DDRTATFELD	RWRFRLPPCT	RPTMATATYA	RPTMATATYA	EGELIVTVPK	GAVPDE--G	147
SEQ-ID:NO:5	DD-GAVFELD	RWRFRLPPCT	LPAMATATYA	LPAMATATYA	DGELVVTVPK	GAA PDD--DG	150
SEQ-ID:NO:17	G-----	QGEV	TWRCGGGK	-----I TGR	LVVVQ	162	
SEQ-ID:NO:27	G-----	QGEV	TWRYCSGK	-----I SGR	LVVVQ	158	
SEQ-ID:NO:2	G-----	GGD	---FQGI G	-----SGR	LVLVQ	198	
SEQ-ID:NO:23	G-----	GGD	---FQGM A	-----SGR	LVLVQ	164	
SEQ-ID:NO:15	G-----	GGD	---ELRGGMGN	GNNNNNNNR	LVLVQ	183	
SEQ-ID:NO:41	N-----	GNNN	NGEFRGGMG	---NNNNNR	LVLVQ	171	
SEQ-ID:NO:21	D-----	GDR	---GMG	---GGR	LVLVQ	165	
SEQ-ID:NO:19	EVQEFFGGG	SNGLGGRD	SNGLGGRD	---SH-	LVLVQ	175	
SEQ-ID:NO:25	D-----	GNAD	GAAI LGSG	---AERV	LVFVQ	170	
SEQ-ID:NO:5	D-----	GA	AAAVLGSG	---VVES	VLLLV	171	

Figure 14 (continued)

SEQ-ID-NO.1201	MAQRDKK--EE	PTELRAPE--I	T-----LCAN	NCGFPGNPAT	QNLCSQSCFSA	43
SEQ-ID-NO.1207	MAQRDKKV--EE	PTELRAPE--L	T-----LCAN	SCGFPGNPAT	NNLCQAQCFQA	44
SEQ-ID-NO.1195	MAQRTEK--E	ETEFKVPETL	T-----LCVN	NCGVTGNPAT	NNMCQKCFSA	43
SEQ-ID-NO.749	MAQRTEK--E	ETEFKVLEIL	T T T T T L C T N	NCGVTANPAT	NNMCQKCFNA	48
SEQ-ID-NO.1201	ATASMSSSPT	S--SSSSSTA	PAPAA-----	PPQPRPAIAE	LASPADAAVA	86
SEQ-ID-NO.1207	ATASSASASV	SPPSPSSSSLS	PSPAVFKFDE	QQHARPSATA	-VFADRPAAEQ	93
SEQ-ID-NO.1195	TTAATSSSSS	S--SSTNNTA	TSATD-----	DKSSRSSTPTR	-SQDNRSDSA	85
SEQ-ID-NO.749	SLVSAAAGVV	E---SGSL	-----	KRSARSVNLR	-SSPAKVVR	83
SEQ-ID-NO.1201	APAPEAAKAP	ART-----	-----	-SANRCSSCR	KRVGLTGFR	118
SEQ-ID-NO.1207	PPAPASARPI	RITTS-----	-----TSSS	SSVNRCQSCR	KRVGLTGFR	131
SEQ-ID-NO.1195	PPTTAATTAT	ATTNSPMTAS	NRSGYDTAEK	KSVNRCGSCR	KRVGLTGFR	135
SEQ-ID-NO.749	PREIDAVKKR	DQ-----	-----	-TVNRCGSCR	KRVGLTGFR	115
SEQ-ID-NO.1201	RCGELFCGAH	RYSDRHGCSY	DYKGAARDAI	ARENPVVRAA	KI VRF	163
SEQ-ID-NO.1207	RCGELFCGAH	RYSDRHDCCF	DYKAVVGRDAI	ARENPVVRAA	KI VRF	176
SEQ-ID-NO.1195	RCGELFCSDH	RYSDRHDCSY	DYKAAAGREAI	ARENPVVKAA	KI I RV	180
SEQ-ID-NO.749	RCGELFCSEH	RYSDRHDCSY	DYKTAGREAI	ARENPVVKAA	KMVKV	160

Figure 15

SEQ_ID_NO:1360	MA	QI	SKKR	KFVADGVFLA	ELNEMLTREL	GEDGFAGVEI	RVTPMRTEII	49
SEQ_ID_NO:1340	MAT	QI	SKKK	KFVSDGVFYA	ELNEMLTREL	AEDGYSGVEV	RVTPMRTEII	49
SEQ_ID_NO:1347	MAT	QI	SKKK	KFVSDGVFYA	ELNEMLTREL	AEDGYSGVEV	RVTPMRTEII	49
SEQ_ID_NO:1311	MAT	QI	SKKR	KFVADGVFYA	ELNEVL TREL	AEDGYSGVEV	RVTPMRTEII	49
SEQ_ID_NO:1313	MAT	QI	SKKR	KFVADGVFYA	ELNEVL TREL	AEDGYSGVEV	RVTPMRTEII	49
SEQ_ID_NO:1353	MAT	QMSKKR		KFVADGVFFA	ELNEVL TREL	AEDGYSGVEV	RVTPMRTEII	49
SEQ_ID_NO:1331	MAT	QI	SKKR	KFVADGVFFA	ELNEVL TREL	AEDGYSGVEV	RVTPMRTEII	50
SEQ_ID_NO:1360	I	RAT	RTQNVL	GEKGRRI REL	TSVVQKRNF	PDGGVELYAE	KVLNRGLCAV	99
SEQ_ID_NO:1340	I	RAT	RTQNVL	GEKGRRI REL	TSVVQKRNF	PENGVELYAE	KVVNRGLCAI	99
SEQ_ID_NO:1347	I	RAT	RTQNVL	GEKGRRI REL	TSVVQKRNF	PENGVELYAE	KVVNRGLCAI	99
SEQ_ID_NO:1311	I	RAT	RTQNVL	GEKGRRI REL	TSLVQKRKF	PQDSVELYAE	KVANRGLCAI	99
SEQ_ID_NO:1313	I	RAT	RTQNVL	GEKGRRI REL	TSLVQKRFF	PQDSVELYAE	KVANRGLCAI	99
SEQ_ID_NO:1353	I	RAT	RTQAVL	GEKGRRI REL	TSVVQKRKF	PENSVELYAE	KVNHRGLCAI	99
SEQ_ID_NO:1331	I	RAT	RTQNVL	GEKGRRI REL	TSVVQKRKF	PENSVELYAE	KVNNRGLCAI	100
SEQ_ID_NO:1360	AQAE	SLRYKL		L GGLAVRRAC	YGVLR FVMES	GAKGCEVVS	GKLRAQRAKS	149
SEQ_ID_NO:1340	AQAE	SLRYKL		L GGLAVRRAC	YGVLR FVMES	GAKGCEVI VS	GKLRAQRAKS	149
SEQ_ID_NO:1347	AQAE	SLRYKL		L GGLAVRRAC	YGVLR FVMES	GAKGCEVI VS	GKLRAQRAKS	149
SEQ_ID_NO:1311	AQAE	SLRYKL		L GGLAVRRAC	YGVLR FVMES	GAKGCEVI VS	GKLRAA RAKL	148
SEQ_ID_NO:1313	AQAE	SLRYKL		L GGLAVRRAC	YGVLR FVMES	GAKGCEVI VS	GKLRAA RAKS	149
SEQ_ID_NO:1353	AQAE	SLRYKL		L GGLAVRMAC	YGVLR FVMES	GAKGCEVI VS	GKLRAQRAKS	149
SEQ_ID_NO:1331	AQAE	SLRYKL		L GGLAVRRAC	YGVLR FIMES	GAKGCEVI VS	GKLRAQRAKS	150
SEQ_ID_NO:1360	-----	-----	-----	-----	-----	-----	-----	149
SEQ_ID_NO:1340	MKFK	DGYMI S		SGQPVNEYI D	AAVRHVLLRQ	GV L GI KVKI M	LDWDPK	195
SEQ_ID_NO:1347	MKFK	DGYMI S		SGQPVNEYI D	-----	-----	-----	169
SEQ_ID_NO:1311	-----	-----	-----	-----	-----	-----	-----	148
SEQ_ID_NO:1313	-----	-----	-----	-----	-----	-----	-----	150
SEQ_ID_NO:1353	M	-----	-----	SGQPVKDYI D	SAVRHVLLRQ	GV	-----	181
SEQ_ID_NO:1331	MKFK	DGYMI S		SGHPVNEYI D	SAVRHVLLR	-----	-----	179

Figure 16