

Comprehensive analysis of trihelix genes and their expression under biotic and abiotic stresses in

Populus trichocarpa

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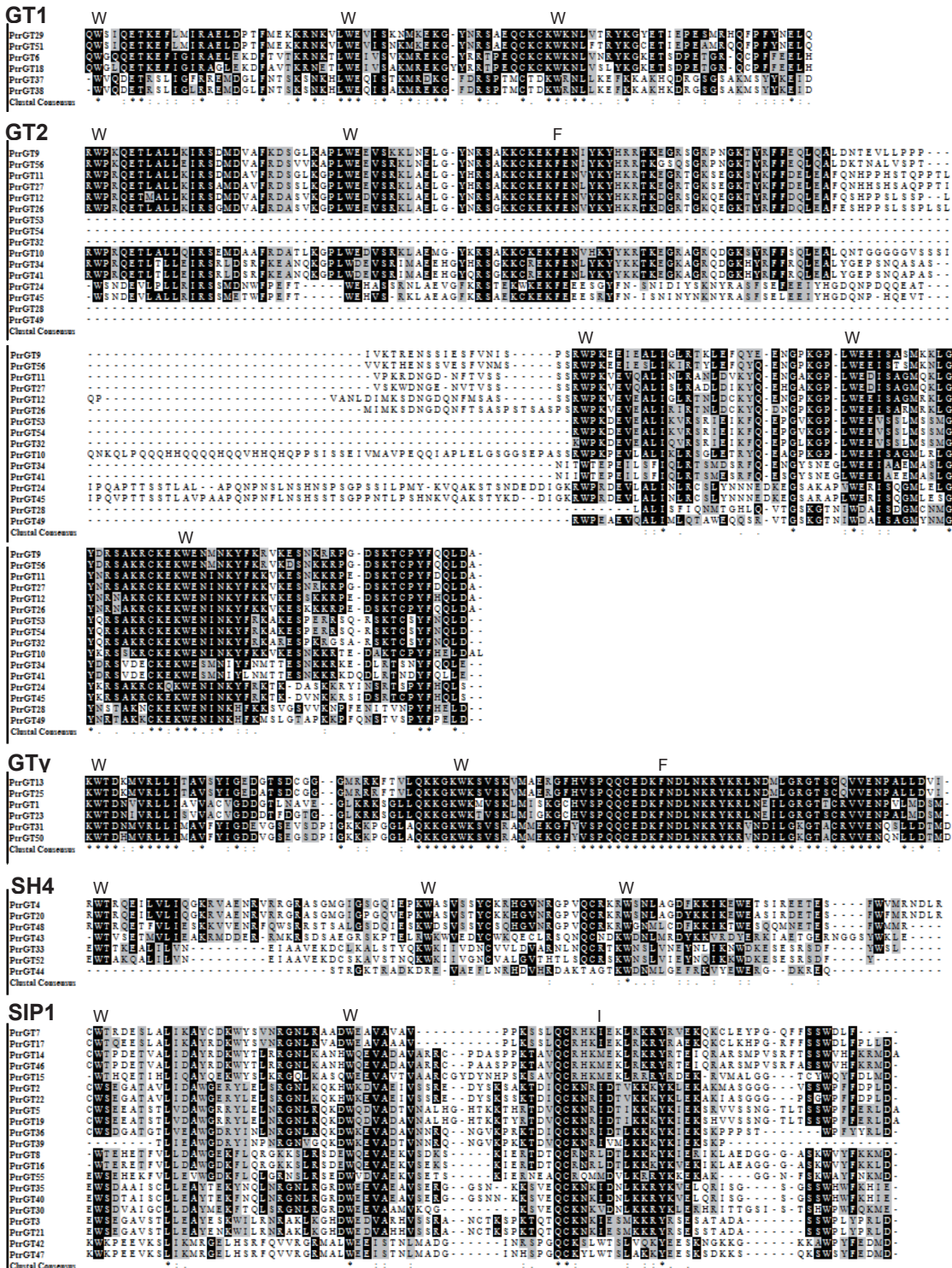
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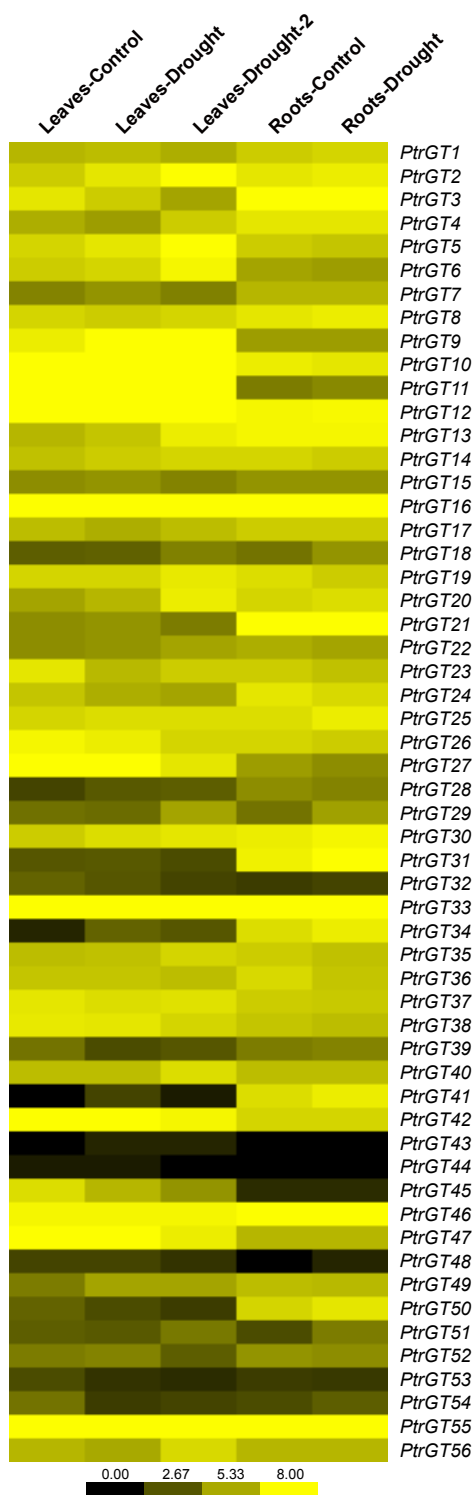
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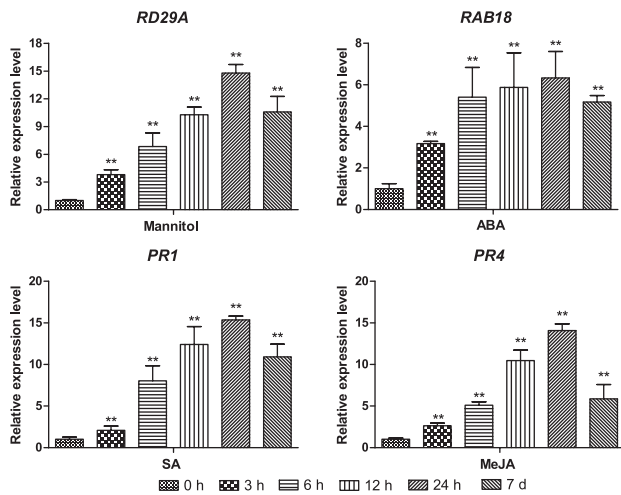
Supplementary Figure S1. Multiple sequence alignment of trihelix genes in *Populus*. Conserved amino acid residues are marked with specific letters.



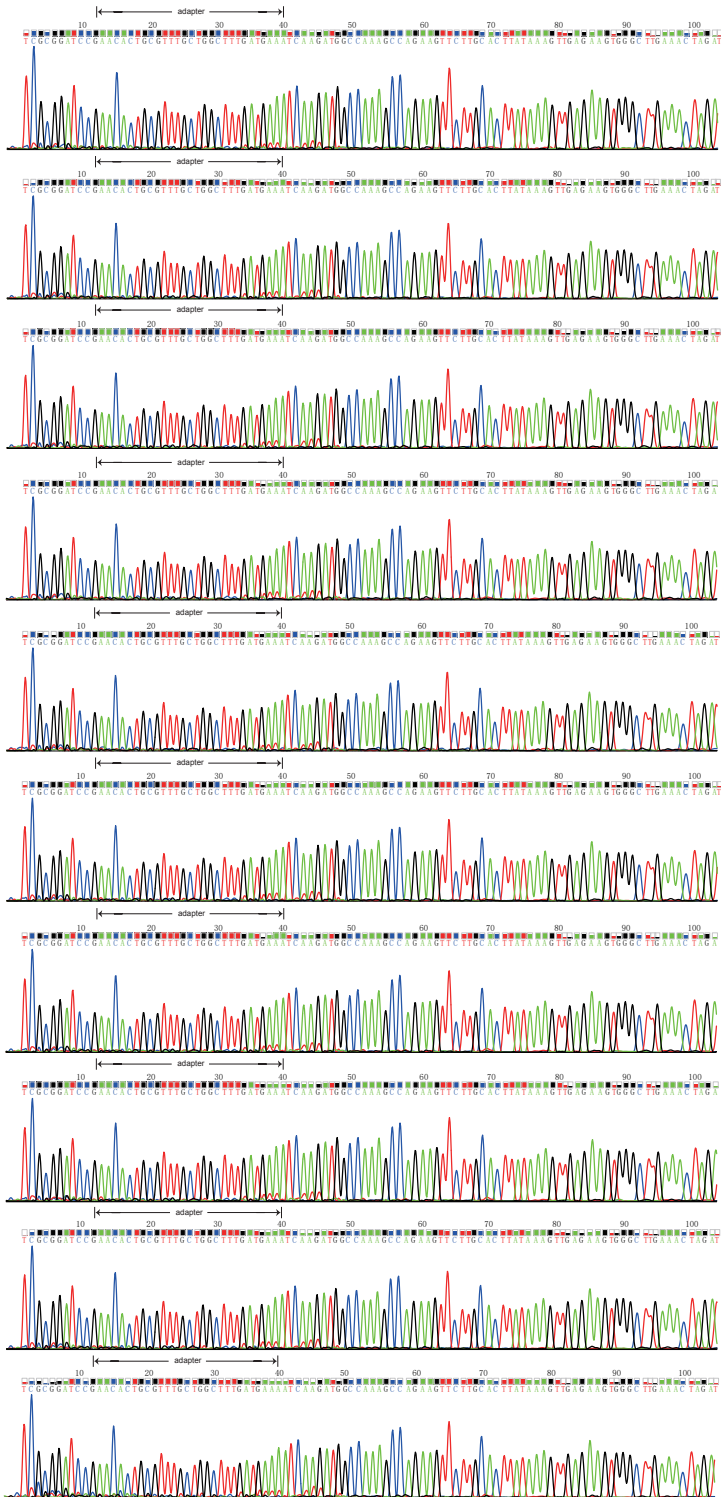
Supplementary Figure S2. Explot analysis of *Populus trihelix* genes in leaves and roots under drought stress. Yellow and black indicate high and low levels of transcript abundances, respectively.



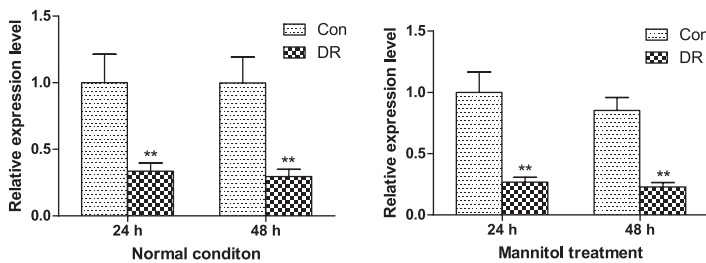
Supplementary Figure S3. The expression levels of marker genes during mannitol, ABA, SA and MeJA treatments.



Supplementary Figure S4. The original sequencing peaks of 5' RLM-RACE.



Supplementary Figure S5. The expression levels of *PtrGT10* in control and DR plants under normal and osmotic conditions.



Supplementary Table S1. Alternative splicing of *Populus trihelix* genes.

| Gene name | Primary transcript | Other transcripts |
|------------------|---------------------------|--|
| PtrGT9 | Potri.001G309100.1 | Potri.001G309100.2 |
| PtrGT10 | Potri.001G454500.1 | Potri.001G454500.2 |
| PtrGT20 | Potri.003G163000.1 | Potri.003G163000.2 |
| PtrGT21 | Potri.003G195300.1 | Potri.003G195300.2 |
| PtrGT24 | Potri.005G051700.1 | Potri.005G051700.2, Potri.005G051700.3 |
| PtrGT25 | Potri.005G191700.1 | Potri.005G191700.2 |
| PtrGT28 | Potri.006G005300.1 | Potri.006G005300.2 |
| PtrGT30 | Potri.006G117300.1 | Potri.006G117300.2 |
| PtrGT32 | Potri.006G221400.1 | Potri.006G221400.2 |
| PtrGT33 | Potri.006G279100.1 | Potri.006G279100.2 |
| PtrGT35 | Potri.008G027000.1 | Potri.008G027000.2 |
| PtrGT36 | Potri.008G071300.1 | Potri.008G071300.2 |
| PtrGT37 | Potri.008G179700.1 | Potri.008G179700.2, Potri.008G179700.3 |
| PtrGT40 | Potri.010G233500.1 | Potri.010G233500.2 |
| PtrGT45 | Potri.013G039100.1 | Potri.013G039100.2 |
| PtrGT47 | Potri.015G093600.1 | Potri.015G093600.2 |
| PtrGT55 | Potri.018G075500.1 | Potri.018G075500.2 |

Supplementary Table S2. List of trihelix genes identified in *Populus* and their sequence characteristics.

| Gene name | Accession number | TF ID | NCBI locus ID | <i>Arabidopsis</i> | Length (a.a.) | M.W. (Da) | pI | Localization |
|-----------|------------------|--------------------|----------------|--------------------|---------------|-----------|-------|--------------|
| | | | | ortholog locus | | | | |
| PtrGT1 | POPTR_0001s05670 | Potri.001G019200.1 | XP_002299233.1 | AT1G21200.1 | 459 | 51475.2 | 5.53 | nucleus |
| PtrGT2 | POPTR_0001s06330 | Potri.001G026000.1 | XP_002297748.1 | AT3G14180.1 | 325 | 36419.90 | 4.94 | nucleus |
| PtrGT3 | POPTR_0001s06580 | Potri.001G028400.1 | XP_002299199.1 | AT3G54390.1 | 352 | 38717.00 | 10.36 | nucleus |
| PtrGT4 | POPTR_0001s13060 | Potri.001G066900.1 | XP_002299351.1 | AT2G33550.1 | 346 | 38046.60 | 6.20 | nucleus |
| PtrGT5 | POPTR_0001s08350 | Potri.001G113600.1 | XP_002299577.1 | AT3G58630.1 | 302 | 34336.30 | 5.25 | nucleus |
| PtrGT6 | POPTR_0001s01210 | Potri.001G129900.1 | XP_002326589.1 | AT2G38250.1 | 296 | 35117.60 | 8.47 | nucleus |
| PtrGT7 | POPTR_0001s15070 | Potri.001G150600.1 | XP_002326679.1 | AT2G44730.1 | 471 | 52310.00 | 8.29 | cytoplasm |
| PtrGT8 | POPTR_0001s18000 | Potri.001G179800.1 | XP_002298141.1 | AT3G24490.1 | 334 | 38374.20 | 4.70 | nucleus |
| PtrGT9 | POPTR_0001s31660 | Potri.001G309100.1 | XP_002298711.1 | AT1G76880.1 | 502 | 57379.40 | 5.34 | nucleus |
| PtrGT10 | POPTR_0001s45870 | Potri.001G454500.1 | XP_002300534.1 | AT1G33240.1 | 794 | 86862.50 | 5.42 | nucleus |
| PtrGT11 | POPTR_0002s06900 | Potri.002G068400.1 | XP_002300920.1 | AT1G76890.2 | 593 | 66528.00 | 5.39 | nucleus |
| PtrGT12 | POPTR_0002s06920 | Potri.002G068600.1 | XP_002302180.1 | AT1G76880.1 | 605 | 67207.10 | 7.94 | nucleus |
| PtrGT13 | POPTR_0002s06930 | Potri.002G068700.1 | XP_002302181.1 | AT1G21200.1 | 420 | 48443.90 | 6.51 | nucleus |
| PtrGT14 | POPTR_0002s14030 | Potri.002G139500.1 | XP_002301240.1 | AT2G44730.1 | 365 | 40637.90 | 9.96 | nucleus |
| PtrGT15 | POPTR_0002s24480 | Potri.002G243300.1 | XP_002301790.1 | AT3G24860.1 | 294 | 33991.10 | 5.93 | nucleus |
| PtrGT16 | POPTR_0003s05470 | Potri.003G056000.1 | XP_002303280.1 | AT3G24490.1 | 413 | 47342.30 | 4.29 | nucleus |
| PtrGT17 | POPTR_0003s08210 | Potri.003G083800.1 | XP_002329555.1 | AT2G44730.1 | 457 | 50734.40 | 8.30 | nucleus |
| PtrGT18 | POPTR_0003s10360 | Potri.003G104500.1 | XP_002304391.1 | AT2G38250.1 | 300 | 35284.80 | 8.06 | nucleus |
| PtrGT19 | POPTR_0003s11850 | Potri.003G118600.1 | XP_002303549.1 | AT3G58630.1 | 290 | 32978.00 | 5.80 | nucleus |
| PtrGT20 | POPTR_0003s16150 | Potri.003G163000.1 | XP_002299351.1 | AT2G33550.1 | 342 | 37593.10 | 7.15 | nucleus |
| PtrGT21 | POPTR_0003s19470 | Potri.003G195300.1 | XP_002303935.1 | AT3G54390.1 | 352 | 38706.90 | 10.23 | nucleus |
| PtrGT22 | POPTR_0003s19840 | Potri.003G198800.1 | XP_002304787.1 | AT3G14180.1 | 365 | 40652.20 | 9.19 | nucleus |
| PtrGT23 | POPTR_0003s20370 | Potri.003G204700.1 | XP_002303892.1 | AT1G21200.1 | 454 | 51187.00 | 6.56 | nucleus |
| PtrGT24 | POPTR_0005s05330 | Potri.005G051700.1 | XP_002319635.1 | AT5G28300.1 | 626 | 71086.90 | 6.64 | nucleus |
| PtrGT25 | POPTR_0005s21390 | Potri.005G191700.1 | XP_002306694.1 | AT1G21200.1 | 438 | 50474.00 | 6.85 | nucleus |
| PtrGT26 | POPTR_0005s21410 | Potri.005G191900.1 | XP_002306695.1 | AT1G76880.1 | 608 | 67986.00 | 6.54 | nucleus |
| PtrGT27 | POPTR_0005s21420 | Potri.005G192000.1 | XP_002307497.1 | AT1G76890.2 | 587 | 65833.60 | 6.35 | nucleus |
| PtrGT28 | POPTR_0006s00710 | Potri.006G005300.1 | XP_002308761.1 | AT1G76890.2 | 295 | 32572.60 | 7.02 | nucleus |
| PtrGT29 | POPTR_0006s10240 | Potri.006G101400.1 | XP_002308224.1 | AT5G01380.1 | 274 | 32831.00 | 8.12 | nucleus |
| PtrGT30 | POPTR_0006s11850 | Potri.006G117300.1 | XP_006381330.1 | AT3G10030.1 | 492 | 53875.50 | 6.63 | cytoplasm |
| PtrGT31 | POPTR_0006s11870 | Potri.006G117500.1 | XP_002326236.1 | AT3G10040.1 | 483 | 55719.30 | 5.40 | nucleus |
| PtrGT32 | POPTR_0006s23800 | Potri.006G221400.1 | XP_002308526.1 | AT1G76890.2 | 618 | 70311.00 | 6.31 | nucleus |
| PtrGT33 | POPTR_0006s29340 | Potri.006G279100.1 | XP_002330777.1 | AT4G31270.1 | 459 | 53622.60 | 4.99 | nucleus |
| PtrGT34 | POPTR_0008s02580 | Potri.008G025600.1 | XP_002311966.1 | AT5G03680.1 | 571 | 66028.00 | 6.60 | nucleus |
| PtrGT35 | POPTR_0008s02730 | Potri.008G027000.1 | XP_002311975.1 | AT3G10030.1 | 499 | 54134.90 | 8.09 | nucleus |
| PtrGT36 | POPTR_0008s07140 | Potri.008G071300.1 | XP_002311242.1 | AT5G05550.2 | 251 | 28839.60 | 9.49 | nucleus |
| PtrGT37 | POPTR_0008s17980 | Potri.008G179700.1 | XP_002312646.1 | AT1G13450.1 | 385 | 44093.40 | 6.66 | nucleus |
| PtrGT38 | POPTR_0010s06510 | Potri.010G055000.1 | XP_002315635.1 | AT1G13450.1 | 384 | 44078.20 | 6.52 | nucleus |
| PtrGT39 | POPTR_0010s19350 | Potri.010G186200.1 | XP_002316198.1 | AT5G05550.2 | 279 | 33004.80 | 10.19 | nucleus |

| | | | | | | | | |
|---------|------------------|--------------------|----------------|-------------|-----|-----------|-------|-------------|
| PtrGT40 | POPTR_0010s23970 | Potri.010G233500.1 | XP_002315355.1 | AT3G10030.1 | 472 | 50892.90 | 8.31 | nucleus |
| PtrGT41 | POPTR_0010s24140 | Potri.010G235000.1 | XP_002316512.1 | AT5G03680.1 | 575 | 66590.50 | 6.19 | nucleus |
| PtrGT42 | POPTR_0012s09780 | Potri.012G095800.1 | XP_002318122.1 | AT5G63420.1 | 916 | 101174.00 | 8.59 | chloroplast |
| PtrGT43 | POPTR_0012s11820 | Potri.012G117500.1 | XP_002332145.1 | AT2G35640.1 | 355 | 39719.70 | 8.36 | nucleus |
| PtrGT44 | POPTR_0012s14050 | Potri.012G132300.1 | XP_002318853.1 | AT2G33550.1 | 994 | 111294.00 | 7.17 | nucleus |
| PtrGT45 | POPTR_0013s03670 | Potri.013G039100.1 | XP_002319635.1 | AT5G28300.1 | 647 | 73253.40 | 6.69 | nucleus |
| PtrGT46 | POPTR_0014s05010 | Potri.014G051200.1 | XP_002327024.1 | AT2G44730.1 | 343 | 38131.60 | 10.63 | chloroplast |
| PtrGT47 | POPTR_0015s10570 | Potri.015G093600.1 | XP_002318122.1 | AT5G63420.1 | 890 | 98789.00 | 8.34 | chloroplast |
| PtrGT48 | POPTR_0015s11710 | Potri.015G105800.1 | XP_002322303.1 | AT2G33550.1 | 299 | 34823.90 | 7.38 | nucleus |
| PtrGT49 | POPTR_0016s00760 | Potri.016G005900.1 | XP_002323120.1 | AT5G47660.1 | 363 | 39937.60 | 5.07 | nucleus |
| PtrGT50 | POPTR_0016s11010 | Potri.016G096300.1 | XP_002326236.1 | AT3G10040.1 | 470 | 53990.00 | 6.39 | nucleus |
| PtrGT51 | POPTR_0016s12470 | Potri.016G117300.1 | XP_002322985.1 | AT5G01380.1 | 279 | 33431.10 | 9.69 | nucleus |
| PtrGT52 | POPTR_0018s04010 | Potri.018G002800.1 | XP_002332103.1 | AT4G31270.1 | 319 | 36550.30 | 5.11 | nucleus |
| PtrGT53 | POPTR_0310s00200 | Potri.018G049500.1 | XP_002324192.1 | AT1G76890.2 | 316 | 36739.80 | 9.89 | peroxisomal |
| PtrGT54 | POPTR_0018s05520 | Potri.018G049700.1 | XP_002324190.1 | AT1G76890.2 | 610 | 70003.40 | 6.45 | nucleus |
| PtrGT55 | POPTR_0018s06120 | Potri.018G075500.1 | XP_002324407.1 | AT3G24490.1 | 354 | 41349.40 | 4.32 | nucleus |
| PtrGT56 | POPTR_0019s02650 | Potri.019G010200.1 | XP_002331882.1 | AT1G76890.2 | 496 | 56887.80 | 5.02 | nucleus |

Supplementary Table S3. Motif sequences of trihelix genes.

| Motif | Width (a.a.) | Best possible match | Domain |
|--------------|-------------------------|---|--|
| 1 | 21 | GYHRS AKQCKCKWENLNKYYK | the third α -helix |
| 2 | 26 | NCWPEQETLALIDIWSEMWIWFNRGN | the first α -helix |
| 3 | 50 | WKDFFERLMKKVMEKQEMMHNKFLETIEKCEHERMCREEAWRMQEMARIN | NA |
| 4 | 41 | KGPLWEEVSRKLAELGYNRS AKKCKEFENVYKYHKRTKEG | the second α -helix in GT2 |
| 5 | 15 | STWPFYFHQLDALYNG | the fourth amphipathic α -helix |
| 6 | 35 | MLADA IKWFG EIVRIESMKMQMVELEKMRMEFQ | NA |
| 7 | 15 | KGPLWEEVSAAMSEK | NA |
| 8 | 29 | REHEIWAHERAWAAARDAAIMAF LQKITG | NA |
| 9 | 29 | SSSRWPKVEILALIQLRTNLECRYQENGP | NA |
| 10 | 50 | HSTTDKGGKKGSPWQRMKWTDNMVRLLITAVFYIGDDGTSDCGGGMRRKFP | the first α -helix in GT γ |
| 11 | 41 | WEQKQWMKKRTLQLEEQQVNIQCQAFELEKQRFKWRFC SK | NA |
| 12 | 28 | RLNDILGRGTSCRVENPALLDTMDYLT | NA |
| 13 | 50 | FFQQQQMEMQWREVF EAREHERQMFEQEWRSMEKLENERLMMEQRWRE | coiled coil |
| 14 | 29 | RTGKQEGKTYRFFDQLEAFQNHPHLSPP | the third α -helix in GT2 |
| 15 | 46 | KEWEKEIRNETEFFWFMRELRRFKLPGFFDREVYYILDGYMWTV | the extended third trihelix |

Supplementary Table S4. Phytohormone- and abiotic stress-related *cis*-elements.

| Element | Core sequence | Function annotation |
|-----------------|----------------------|---|
| ABRE | TACGGTC | Response to abscisic acid |
| CGTCA-motif | CGTCA | Response to MeJA |
| ERE | ATTTCAAA | Response to ethylene |
| G-Box | CACGTT | Response to MeJA |
| TCA-element | GAGAAGAATA | Response to salicylic acid |
| TGACG-motif | TGACG | Response to MeJA |
| W-Box | TTGACC | WRKY binding site involved in abiotic stress responsiveness |
| HSE | AAAAAATTTC | Response to heat stress |
| MBS | TAACTG | MYB binding site involved in drought-inducibility |
| LTR | CCGAAA | Response to low-temperature stress |
| DRE | TACCGACAT | Response to dehydration, low-temp, salt stresses |
| TC-rich repeats | ATTCTCTAAC | Involve in defense and stress responsiveness |
| EIRE | TTCGACC | Response to fungus |
| ELI-box3 | AAACCAATT | Response to fungus |

Supplementary Table S5. Numbers of *cis*-elements in trihelix genes.

| Gene name | <i>Cis</i> -elements related to phytohormone | | | | | | <i>Cis</i> -elements related to abiotic stress responsiveness | | | | | | <i>Cis</i> -elements related to Fungi | |
|----------------|--|--------|-----|------|---------|--------|---|-----|-----|-----|---------|-----|---------------------------------------|----------|
| | AB | CGTCA | ERE | G-Bo | TCA-ele | TGACG | DRE | HSE | LTR | MBS | TC-rich | W | EIRE | ELI-box3 |
| | RE | -motif | | x | ment | -motif | | | | | repeats | box | | |
| <i>PtrGT1</i> | ● | ● | | ● | ● | ● | | ● | ● | ● | ● | | | |
| <i>PtrGT2</i> | ● | ● | | | ● | ● | | ● | ● | | ● | | | |
| <i>PtrGT3</i> | ● | | ● | ● | ● | ● | | ● | | ● | ● | | | |
| <i>PtrGT4</i> | | | | | ● | | | | | | ● | | | |
| <i>PtrGT5</i> | | ● | ● | ● | | ● | | | | ● | | ● | | |
| <i>PtrGT6</i> | | ● | ● | | | ● | | ● | | ● | ● | | | |
| <i>PtrGT7</i> | | ● | | ● | ● | ● | | | | ● | ● | ● | | |
| <i>PtrGT8</i> | | | | | ● | | | ● | | ● | ● | ● | | |
| <i>PtrGT9</i> | | ● | | ● | | ● | | ● | | | | ● | | |
| <i>PtrGT10</i> | ● | | ● | ● | | | | ● | | | ● | | | |
| <i>PtrGT11</i> | ● | | | ● | | | | ● | | ● | ● | ● | | |
| <i>PtrGT12</i> | ● | ● | | ● | ● | ● | | ● | ● | ● | | ● | | |
| <i>PtrGT13</i> | ● | | ● | ● | ● | | | ● | | | ● | ● | ● | |
| <i>PtrGT14</i> | | ● | ● | | ● | ● | ● | ● | ● | ● | ● | ● | | ● |
| <i>PtrGT15</i> | | ● | | | | ● | | ● | ● | | ● | ● | ● | |
| <i>PtrGT16</i> | | ● | | ● | | ● | | ● | | | ● | | | |
| <i>PtrGT17</i> | | ● | ● | ● | ● | ● | | ● | ● | ● | ● | ● | | |
| <i>PtrGT18</i> | ● | | | ● | ● | ● | | ● | ● | | ● | | | |
| <i>PtrGT19</i> | ● | ● | | ● | ● | ● | | | | ● | ● | | | |
| <i>PtrGT20</i> | | | | ● | | | | ● | | ● | ● | ● | | |
| <i>PtrGT21</i> | ● | ● | | ● | | ● | | ● | | ● | ● | ● | | |
| <i>PtrGT22</i> | ● | | | ● | ● | | | ● | ● | ● | ● | | | |
| <i>PtrGT23</i> | ● | ● | | ● | ● | ● | | ● | ● | ● | ● | | | |
| <i>PtrGT24</i> | ● | ● | ● | ● | ● | ● | | ● | ● | ● | | | | |
| <i>PtrGT25</i> | ● | ● | ● | ● | ● | ● | | ● | ● | | ● | | | |
| <i>PtrGT26</i> | ● | ● | ● | ● | ● | ● | | ● | ● | ● | ● | ● | | |
| <i>PtrGT27</i> | ● | ● | ● | ● | ● | ● | | | | | ● | | ● | |
| <i>PtrGT28</i> | | | ● | ● | ● | | | ● | ● | | ● | | | |
| <i>PtrGT29</i> | ● | | ● | ● | ● | ● | | ● | ● | ● | ● | ● | | |
| <i>PtrGT30</i> | ● | | | ● | | | | ● | ● | | | ● | | |
| <i>PtrGT31</i> | ● | | ● | ● | ● | | | ● | | ● | ● | | | |
| <i>PtrGT32</i> | | ● | ● | ● | | ● | | ● | ● | ● | ● | ● | | ● |
| <i>PtrGT33</i> | ● | ● | | | | ● | | ● | ● | ● | ● | | | |
| <i>PtrGT34</i> | ● | | | ● | | | | | ● | ● | ● | ● | | |
| <i>PtrGT35</i> | | ● | ● | | ● | ● | | ● | ● | ● | | ● | | ● |
| <i>PtrGT36</i> | ● | ● | | ● | ● | ● | | ● | ● | ● | ● | ● | | |
| <i>PtrGT37</i> | ● | | | ● | | ● | | ● | | ● | ● | ● | | |
| <i>PtrGT38</i> | | ● | ● | ● | ● | ● | | ● | | ● | ● | ● | | |
| <i>PtrGT39</i> | | ● | | | | ● | | ● | ● | ● | | ● | | |

| | | | | | | | | | | | |
|----------------|---|---|---|---|---|---|---|---|---|---|---|
| <i>PtrGT40</i> | ● | ● | ● | ● | | ● | | | ● | ● | ● |
| <i>PtrGT41</i> | | ● | ● | ● | | ● | ● | | ● | | ● |
| <i>PtrGT42</i> | ● | ● | ● | ● | ● | ● | ● | | ● | ● | ● |
| <i>PtrGT43</i> | | ● | | ● | ● | ● | ● | ● | ● | ● | ● |
| <i>PtrGT44</i> | | ● | ● | | ● | ● | ● | | | ● | ● |
| <i>PtrGT45</i> | ● | | | | | | ● | ● | ● | ● | ● |
| <i>PtrGT46</i> | ● | | ● | ● | | | ● | ● | | ● | |
| <i>PtrGT47</i> | ● | ● | ● | ● | ● | ● | ● | | ● | | ● |
| <i>PtrGT48</i> | ● | ● | ● | ● | ● | ● | | ● | ● | ● | ● |
| <i>PtrGT49</i> | | ● | | | ● | ● | | ● | ● | ● | ● |
| <i>PtrGT50</i> | | | ● | ● | ● | | ● | | ● | ● | ● |
| <i>PtrGT51</i> | ● | | | ● | ● | ● | | | ● | | |
| <i>PtrGT52</i> | ● | ● | | ● | | ● | ● | | ● | ● | ● |
| <i>PtrGT53</i> | | ● | ● | | ● | ● | ● | ● | | | |
| <i>PtrGT54</i> | | ● | | ● | ● | ● | ● | | ● | ● | |
| <i>PtrGT55</i> | | | | ● | ● | | ● | | ● | | ● |
| <i>PtrGT56</i> | | ● | | ● | ● | ● | ● | | ● | | |

Supplementary Table S6. Details of the Gene Ontology annotation.

| Seq. Name | Annotation number | GOs |
|--------------|-------------------|--|
| PtrGT1 | 1 | F:chromatin binding |
| PtrGT2 | 8 | C:nucleus; F:DNA binding; F:sequence-specific DNA binding transcription factor activity; P:transcription, DNA-templated; P:embryo development ending in seed dormancy; P:seed maturation; P:post-translational protein modification; P:positive regulation of transcription, DNA-templated |
| PtrGT3 | 3 | P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding transcription factor activity; F:chromatin binding |
| PtrGT4 | 1 | F:DNA binding |
| PtrGT5 | 2 | P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding transcription factor activity |
| PtrGT6 | 6 | C:nucleus; F:chromatin binding; F:sequence-specific DNA binding transcription factor activity; F:sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated |
| PtrGT7 | 3 | F:chromatin binding; C:vacuole; C:nucleus |
| PtrGT8 | 2 | F:DNA binding; F:chromatin binding |
| PtrGT9 | 2 | F:DNA binding; F:chromatin binding |
| PtrGT10 | 7 | F:DNA binding; F:chromatin binding; P:cellular component organization; P:single-organism cellular process; P:negative regulation of nucleobase-containing compound metabolic process; P:regulation of multicellular organismal development; P:negative regulation of cellular macromolecule biosynthetic process |
| PtrGT11 | 2 | F:DNA binding; F:chromatin binding |
| PtrGT12 | 2 | F:DNA binding; F:chromatin binding |
| PtrGT13 | 1 | F:chromatin binding |
| PtrGT14 | 3 | F:chromatin binding; F:sequence-specific DNA binding transcription factor activity; P:regulation of transcription, DNA-templated |
| PtrGT15 | 2 | F:sequence-specific DNA binding transcription factor activity; P:regulation of transcription, DNA-templated |
| PtrGT16 | 2 | F:DNA binding; F:chromatin binding |
| PtrGT17 | 1 | F:chromatin binding |
| PtrGT18 | 6 | C:nucleus; F:chromatin binding; F:sequence-specific DNA binding transcription factor activity; F:sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated |
| PtrGT19 | 2 | P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding transcription factor activity |
| PtrGT20 | 1 | F:DNA binding |
| PtrGT21 | 2 | F:sequence-specific DNA binding transcription factor activity; P:regulation of transcription, DNA-templated |
| PtrGT22 | 0 | - |
| PtrGT23 | 1 | F:chromatin binding |
| PtrGT24 | 1 | F:chromatin binding |

| | | |
|---------|---|---|
| PtrGT25 | 1 | F:chromatin binding |
| PtrGT26 | 2 | F:DNA binding; F:chromatin binding |
| PtrGT27 | 2 | F:DNA binding; F:chromatin binding |
| PtrGT28 | 4 | F:chromatin binding; F:DNA binding; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding transcription factor activity |
| PtrGT29 | 6 | C:nucleus; F:chromatin binding; F:sequence-specific DNA binding transcription factor activity; F:sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated |
| PtrGT30 | 7 | C:cytoplasm; F:chromatin binding; F:UMP kinase activity; P:nuclear-transcribed mRNA catabolic process; P:pyrimidine nucleotide biosynthetic process; P:nucleotide phosphorylation; P:photoperiodism, flowering |
| PtrGT31 | 4 | P:response to stress; P:pattern specification process; P:regulation of cellular metabolic process; P:meristem development |
| PtrGT32 | 1 | F:chromatin binding |
| PtrGT33 | 6 | F:chromatin binding; P:regulation of transcription, DNA-templated; P:post-translational protein modification; C:plasmodesma; P:positive regulation of transcription, DNA-templated; F:sequence-specific DNA binding transcription factor activity |
| PtrGT34 | 1 | F:chromatin binding |
| PtrGT35 | 5 | C:cytoplasm; F:chromatin binding; F:UMP kinase activity; P:pyrimidine nucleotide biosynthetic process; P:nucleotide phosphorylation |
| PtrGT36 | 0 | - |
| PtrGT37 | 6 | C:nucleus; F:DNA binding; F:chromatin binding; F:sequence-specific DNA binding transcription factor activity; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated |
| PtrGT38 | 6 | C:nucleus; F:DNA binding; F:chromatin binding; F:sequence-specific DNA binding transcription factor activity; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated |
| PtrGT39 | 0 | - |
| PtrGT40 | 7 | C:cytoplasm; F:chromatin binding; F:UMP kinase activity; P:nuclear-transcribed mRNA catabolic process; P:pyrimidine nucleotide biosynthetic process; P:nucleotide phosphorylation; P:photoperiodism, flowering |
| PtrGT41 | 1 | F:chromatin binding |
| PtrGT42 | 7 | C:chloroplast; F:DNA binding; F:chromatin binding; F:RNA binding; F:metal ion binding; P:photosynthesis; P:cellular respiration |
| PtrGT43 | 1 | F:DNA binding |
| PtrGT44 | 3 | F:kinase activity; P:phosphorylation; P:carpel morphogenesis |
| PtrGT45 | 1 | F:chromatin binding |
| PtrGT46 | 1 | F:chromatin binding |
| PtrGT47 | 7 | C:chloroplast; F:DNA binding; F:chromatin binding; F:RNA binding; F:metal ion binding; P:photosynthesis; P:cellular respiration |
| PtrGT48 | 1 | P:regulation of transcription, DNA-templated |
| PtrGT49 | 2 | F:DNA binding; F:chromatin binding |
| PtrGT50 | 4 | P:response to stress; P:pattern specification process; P:regulation of cellular metabolic process; P:meristem development |
| PtrGT51 | 6 | C:nucleus; F:chromatin binding; F:sequence-specific DNA binding transcription factor activity; F:sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated |

| | | |
|---------|---|---|
| PtrGT52 | 6 | F:chromatin binding; P:regulation of transcription, DNA-templated; P:post-translational protein modification; C:plasmodesma; P:positive regulation of transcription, DNA-templated; F:sequence-specific DNA binding transcription factor activity |
| PtrGT53 | 1 | F:chromatin binding |
| PtrGT54 | 1 | F:chromatin binding |
| PtrGT55 | 3 | F:sequence-specific DNA binding transcription factor activity; P:post-translational protein modification; P:positive regulation of transcription, DNA-templated |
| PtrGT56 | 2 | F:DNA binding; F:chromatin binding |

P, F and C represent biosynthetic process, molecular function and cellular component, respectively.

Supplementary Table S7. Primers designed using Primer Premier 5.

| Gene name | Sequences (5'-3') |
|------------------|--|
| <i>PtrGT1</i> | AATGCTGATGAGGACGGGA CAGGGTCTTGAAAAATCGCTG |
| <i>PtrGT2</i> | AGTCACACTCAAACACCAC ACTTCATCGGCAAAACAAG |
| <i>PtrGT3</i> | CACCACAACATCAACAAC TGAGCAATCACAATAACT |
| <i>PtrGT4</i> | GGAGGATGGGTTGTTTTCGGA GCGGGCCTTTTATCATTGGT |
| <i>PtrGT5</i> | TGGCTCTCCCCTGCATCCTTC CCTCCTCGCTATCTGACTCTTG |
| <i>PtrGT6</i> | GGAAGAGGAAGGTTGAAAAA CTCCATTGACTGTCGCCATT |
| <i>PtrGT7</i> | TCGCGTGAAAACGTTAGGAG ACCATGAACATTAAGCCCC |
| <i>PtrGT8</i> | CGGATTGCTTGCAGATTCT TCTCCTCTTCACCGACTT |
| <i>PtrGT9</i> | GGTATTACTGCCACCTCC TCTCGTTCCTTCCTCTTC |
| <i>PtrGT10</i> | CATGTTTCCTCTGATTT CTGATGTTTGTCTCCTA |
| <i>PtrGT11</i> | TTTTCAACAAGCAACCCA AAGCCACCTCCCTCATCC |
| <i>PtrGT12</i> | ATCCATCTTCTTTTCCA AACTTATTCTGCGTCTCC |
| <i>PtrGT13</i> | CCCTTCAGTTAGAAGAACGGAA GCCATCTGCTCATTCTCAAGT |
| <i>PtrGT14</i> | ATGCGAGCCCAGACCCCTACC CCATCTCCAATACCTTACC |
| <i>PtrGT15</i> | CAGAAGCATTAACTATATACTCC AAACGCCTTTATTTGCCCGCCA |
| <i>PtrGT16</i> | CTCTTTTGGTTTGCTTGC TCTTGATGAATTTTGGCT |
| <i>PtrGT17</i> | TGCTCTTCGGGCTAGGAAATATA TCCGTGATCCGGTAATCTAACAA |
| <i>PtrGT18</i> | AGATGTTTGAGCAGGAATG TTTCACTGATGAGTTTGT |
| <i>PtrGT19</i> | TAAGAAACATCTCTCACC TAAAATAATCATCGTCCA |
| <i>PtrGT20</i> | ATGGGTTGTTTTCGGATTTT CCTTGAGCTTGACTTGCTTG |
| <i>PtrGT21</i> | CTTCTGCCAATCCTCCTTT TCTCCCTTTGCCCCCTAT |

| | |
|----------------|--|
| <i>PtrGT22</i> | GAGATGGAGAAGACGAGGA ACGATGGTATTGATGATGG |
| <i>PtrGT23</i> | AGATATGAATGGGTCAGGG GAGAACAAAGGTGGGAATG |
| <i>PtrGT24</i> | GAGTTGGGTTACAAGAGGAGTGC GTTTTTCGGTGCTACAAGCGTTC |
| <i>PtrGT25</i> | ATAGTAGGGGCATACATGGGGTA TTCATATCAACTTGGGCAATCTG |
| <i>PtrGT26</i> | TCTTTTCCAACTTCTCCCC CTTTCATGTTTCGCGTCTCTC |
| <i>PtrGT27</i> | TTCCACAACCCAACTAACGCCAC CTAATAAGAGCTTGAACCTCCACT |
| <i>PtrGT28</i> | CCCTAACGACTTCCCTCT CTAACAAAACCCACAGC |
| <i>PtrGT29</i> | AGAGAAGGATGAAGGAGATG TAGAAGTGCTGTGATAAGGG |
| <i>PtrGT30</i> | GCGCTTCTTCTGCTAGCGTATCT AACGTCATCACCTTGGGTCAAT |
| <i>PtrGT31</i> | GGTTGAAGTGGGTGAGATT TTGTTTGAAGGCAGTTGTT |
| <i>PtrGT32</i> | GCTCTGGTTCTGTTCTCAC CTTCTCTTCCCTCCTTCGG |
| <i>PtrGT33</i> | AGCCTAAAATCCATCGTG TGTTCTTTGAATCAGCAG |
| <i>PtrGT34</i> | GCCACTCAAAGGCACAACAAAAACC AGCCATCTCTGCTGCTATCTCCTCC |
| <i>PtrGT35</i> | CTCTCAAACTAAACCAG CGACCTCCAAGAACAATA |
| <i>PtrGT36</i> | CGAAACAGCAGCAAATGATA CACAACCTGAACTGGAAGCAA |
| <i>PtrGT37</i> | GTGCCAGGCCAACACTCA TATCACCTCCCACCAA |
| <i>PtrGT38</i> | GAGACCCCTGGGAATGGTGCTGAG CATCCTCCAACCAGAATGCTCGCT |
| <i>PtrGT39</i> | TAACACAGACAAGAAACCCACC GCAGCCCCATCAGATAAACCTA |
| <i>PtrGT40</i> | GTCTCAAACTAAACCGG TACGACCTCCAAGAACAA |
| <i>PtrGT41</i> | TATGATAGGAGTGTGGACGA CAAATAAGAATTAGAAGCG |
| <i>PtrGT42</i> | TATTGATTCTTATGCCCC TACCCTAGATTCGTTACC |
| <i>PtrGT43</i> | CAAGCTATGTGGTAGAGAGACC CAATCAATACTAATGTGGGAAA |

| | |
|-----------------|--|
| <i>PtrGT44</i> | ATGGTGTGAAAGTGGATGTGTGGGG GCAAGTGGTGATAACAATCGGCGGC |
| <i>PtrGT45</i> | AGGGATGTTGGAATCGGGT AAGGTGCTTAATTGGTGAA |
| <i>PtrGT46</i> | TTCGGGTAATGCTGGTGGGTTTCG GGCTTCAGGTTCGGGTTTGGGCTC |
| <i>PtrGT47</i> | CGGGTGGACAGGAAGCAA TCTCAGAGTCGGAGGAAT |
| <i>PtrGT48</i> | CTATGTCTTGATGGGAG GATTTTGTTTTTTGGTTG |
| <i>PtrGT49</i> | TCAGATAACTCCATTCCCGC TGTCCTAACCACCCCT |
| <i>PtrGT50</i> | AAGTTGGGTTGCCTTGG TTTATTGCCCTTTTTGCC |
| <i>PtrGT51</i> | ATCTTCTGACGATGAGGA CATTTGAATCTGTTGCTT |
| <i>PtrGT52</i> | GGCTGACTTGCTTGATGTA GTTGCCAATTTGAGGTTTC |
| <i>PtrGT53</i> | TTCATTA ACTATCCTTCG GCACCTTTATGTTCTCAC |
| <i>PtrGT54</i> | CACGGTGAAGAAAGTGATG CTATTTGAAGTTGAAGCCC |
| <i>PtrGT55</i> | TATTTGGATCGTGCCAATATGAAT CATCTGCTCCCTCTTACTGCTCTC |
| <i>PtrGT56</i> | AAGAAAATGGACCAAAGGG AGAGCATCAAGCTGCTGAAA |
| <i>Actin</i> | AGGTTATGCCCTTCCACACG TCGAGGGCAACATACGCAAG |
| <i>RD29A</i> | TTTGAAAATACCAGTAGGAT AGAGTAAAGAATTGGCGTTA |
| <i>RAB18</i> | CTGGACAAGAGAGGTTTAGA TCGTCGTGTTACATCATAACA |
| <i>PRI</i> | TCCCTAATCCTTCCCTCTCG AGGCTTGCACTGTGGTGTCC |
| <i>PR4</i> | CAGACCTGCCCTAATAACCT TTGCTTTGACAGTTCTTGGGA |
| <i>5' GSP</i> | CGGAACAACAAATAGCACCCTG |
| <i>5' Inner</i> | CAACCTTAGCATCCCTGCTGAGA |
| <i>5' Outer</i> | TGGCATCTTCTGTCCGTTTC |
| <i>miR172d</i> | GGAATCTTGATGATGCTGCAT |
| <i>5.8s</i> | GTCTGCCTGGGTGTCACGCAA |

Supplementary Data S1. Information for trihelix genes.

>PtrGT1

MDNSGLGGRFLSGPNSGLLDLESPIHRHQSSQLGHPSLAHQHQVNLVGCDFNDHQPIGLSEVK
GTPSKVYSANFGK GKAVSPFNCASSGNASEDDDDQSFMEDGNGENSTGVKGGKGS PWQRMK
WTDNVVRLLI AVVACVGDGTLNAVEGLKRKSGLLQKKGKWKMVSKLMISKGCHVSPQQCE
DKFNDLNKRYKRLNEILGRGTT CRVVENPVLMDSMPHLSAKAKDDVRKILGSKHLFYKEMCA
YHNGQRIPNCQDLDLQGC SLPLERSSSKDNNGSGEDEAEGNGSDDDGDDDDDES DNEENNA
DEDGERVGLCEGRVND EHAHLWSQSGGRNGFDVEMAAIFQDPAVSPWERKEWIKKQRLQL
LEQRVSIQAQTFELEKQRFKWLRYSK KDKEFERLRLENEWRKLENEQSALQLRQKQLEMDF
RSSEPSFDPACL GIDGVQGRDPIDLSRPQ

>PtrGT2

MDDDDDIQSHSNTTESSSPSPSPDGRITVTVPATATVPPTPPPQQT DNSLALV LPMKSKANGSG
GGGREDCWSEGATAVLIDAWGERYLELSRGNLQKQHWKDV AEIVSSREDYKSAKTDIQCKN
RIDTVKKKYKLEKAKMASGGGVSSWPFDPDLRLIGSTARVP AVASGSKFPYHFRRNQNMKAR
IRKWGKDEDDDDDEDEEEEEEEEEEEEEEDGGWGN SIRMLTQAMLKFG EAYEQAETAQLQ
QV VEMEKTRMKFAKELELQRMQFFMQTQMEISQLKNGRKGGSASGNHHHHHHHHHTGN NIT
ASNNVNNSDS DN

>PtrGT3

MDKETNQECPSLRPNNSTTIKEESPRKIPRGLGAAGVIVTGTGGGGGGGDR LKRDEWSEGA V
STLLEAYESK WILRNRAKLGHDWEDVARHVSSRANCTKSPKTQTQCKNKIESMKKRYRSES
ATADASSWPLYPRLDLLL RGN SATAAVISSPQHQQPAIPASSNP LLLVDPTLGVPQPPPSMTPP
PPPPSPPPQVIVIAQNSHGSNGVDRGQKEDGVDTKLSNHVSDKNAMEVTDSSTPALYSDKKK
TRSKKLKMRKERRKWKREEWEIADSIRWLAEVVVRSEQARM DTMREVEKMRIEAEAKRGE
MDLKRTEIIAKTQLEIAKLFAGGGKGV DSSLRIGRN

>PtrGT4

MALEQQLSLTPTQNPVDGERTNGVDTNIRDGGDDGNKAPRLPRWTRQEILVLIQGKRVAENRV
RRGRASGMGIGSGQIEPKWASVSSYCKRHGVNRGPVQCRKRWSNL AGDFKKIKEWETSIREET
ESFWVMRNDLRRERKLP GFFDREVYDILDGGGGTV PGLALALAPSSTAAEAEVAEEV VFD SG
RSAAAEDGLFSDFEQEEGGGSPEAVVKEVQPIKMAV TAGVANPTPISEKQYQPAPRASQAQVPP
NDKRPATNPEMGSASHEERKRKRFVIDGDEETISLQSHLIDV LERN GKMLTAQLEA QNTNFQLD
REQRKDHADGLVAVLNKLANALGKIADKL

>PtrGT5

MEDLISSSVTPSTAPHSRSLPIREDCWSEEATSTLVDAWGRRYLELNRGNLRQKDWQDVADT
VNALHGHTKKTHRTDVQCKNRIDTIKKKYKIEKSRVSSNGTLTSSWPF FERLDALIGSNFNSSI
KKPPSPSLSPSPVALPLHPSYRRTPPVSSTPPPQPAALAV ALPQKRTL PVDDGGYFRNYSAMA
AAAAAQESDSEEEEEEEEEEF EAGERESVEEDGE GEGIKRLAR AVERFGEVYERVESEK LKQ
MVDLEKQRMKFAKDLEMERMRI FTETQIQLEKIKK GKRAPDNERDY

>PtrGT6

MMFSGGGEGDGLGRINMMPTAAML SPTAEISPRGPPQQPQWGQ QETKEFIGIRAELEKDFTV
TKRNKTLWEIVSVKMREKGYRRTPEQCKCKWKNLVNRYK GKETSDPETGRQC PF FEELHAVF
TERAKNMQRLLLESEAGSTQSRKKMKRTSGDRSSDEFSEEEDEDED DSEEEKPVR SN SRKRKV
EKIIAEKSPRASSTVGGIQEMLKEFLQQQKMEMQWREMMERRSHERQMFEQEWRQSMEK
LERERLMIEQAWREREEQRRIRESRAERRDALLTLLNKLIRENNI

>PtrGT7

METTPCATPKRVPPPCWTRDESLALIKAYCDKWYSVNRGNLRAADWEAVAVAVPPKSSLQCRH
KIEKLRKRYRVEKQKCLEYPGQFFSSWDLFPLLDLSLEIGSLGSKGDQEIDKGNDVGDGFRVKT
GDRYLLTTQKNGKTNGDLDPDEDFGLDPLAFRAAKYSKVHGGFNHGDSESGFGFKSVANK
NLVSVAFGPKDYVGVNGKLTANVGLNCDNGGEGFYKVEKTRGGRKVMPPQGVRLPDYEMIAN
NYGSYVRDFTKGVHSYGGFPLKSLGDGNYNTIDGKPTPDFCDNDDHVEIDYRNDKRDEFGKK
VTNGWSYSPTGFRPKNCGTIDGNSRSNARSRAVNGSVNVGMNGIGDGVKRETDPISSLVSAIE
QATESFVKVEMMKMDMASEIEKMRMEMGLKHNQMILESQQRIVDTLAKAMLEKKKEREKV
EVRPPNSSRNGFSQVAAVEFERIGKSIVKEGEACFT

>PtrGT8

MDDTEDDARYPQNPYGENNQRSYGSNRHKLPGVGNATYSRPVDNQYAVSEDESDDEEEGEHE
GIDDDHEDDDIERHPKRRKLSLVSSYEFAPLGGRNPLTDWTEHETFVLLDAWGEKFLQRGKK
SLRSDEWQEVAEKVSDKSKIERTDTQCRNRLDTLKKKYKIERIKLAEDGGGASKWVYFKKMD
VLMSTSAQQGGLSCGMDSGEYVSMNPRVYSNHSNGFDEMSPGNSELARDEDDSDGLPPK
KRRLGRDCIEQSPFGLLADSIHKFSEIYEKIESSKRQQMLELEKMRMDFQRDLEMQKRQIIRA
QAAIAKIHQVGEEDSISANSA

>PtrGT9

MEASTTFPENSNAATGNRDSDEGDEEMRVKAEEDGQHSTGNRWPKQETLALLKIRSDMDVAF
KDSGLKAPLWEEVSKKLNELGYNRSACKCKEKFENIYKYHRRTKEGRSGRPNKTYRFFEQ
QALDNTEVLLPPPSSDKVHTSMAAALVNPVVFIPNAVPCSIQSPGMNFVDTTSTSTASTSSEEEE
GTRKKKQKLTGFFERLMKEVIEKQENLQNKFLAIEKCEQERIAREEAWKMQELDRIKREREL
LVRERAIAAAKDAAVLAFQKFEQGISVQLPDNPVPMKFPDNQTPVPVSSAPVQLPKNQAVP
VENIVKTRENSIESFVNISPSRWPKEEIEALIGLRTKLEFQYEENGPKGPLWEEISASMKCLGYD
RSAKRCKEKWENMNKYFKRVKESNKRPPGDSKTCYPYFQQLDALYREKNRRVDGSGFELKPEE
LLMHMMGGQDQQQPESATTEDRESENVQDQENYRDKEDGDGDRIVANDPSSMEIME

>PtrGT10

MQQGGGERGSSQSQYAVPQQQQQGDMPPLPSTSAALATHMQQQQVVEEASPISSRPATAA
TTSGGGVMNLDEFMRLSGGGGAEDIAGEDADRTGGIASGNRWPRQETLALLQIRSEMDAA
FRDATLKGPLWEDVSRKLAEMGYKRSACKCKEKFENVHKYKRTKEGRAGRQDGKSYRFFS
QLEALQNTGGGGGVSSSISNVSGVAPQLIGTATTSSLDVAPVSVGIPMPIRTPPPSSQVPQASNIG
SMFPPDLGATVARAAAAGAPVRISFSSNESSSSQSSSEDDDDDEDEGILGGQTSAMGAGTSRKRK
RASLSSSKGETHRMMEFFEGLMKQVMQKQEQAMQHRFLEAIEKREQDRMIRDEAWKRQEMA
RLSREHEIMAQERSISASRDAAIVAFLQKITGQTIHLPTVSIAPLVSQPQPPPTQPQQVQIAPLV
TVSTQPPLQPQMPPLSQVTPQQNKQLPQQQHHQQQHQVHHQHQPSSISSEIVMAVPEQQIA
PLELGGSGSEPASSRWPKEVLAALIKLRSGLETRYQEAGPKGPLWEEISAGMLRLGYKRSSKRC
KEKWENINKYFKKVKESNKKRTEDAKTCYPFHELDALYRKKILGSSSGGAGSTSTSGFDSQIN
RPQKQHQHQESLELDPMPPPMQQTVPQQTQATESQNKNASVDVQASNTVLAGSPFEGGN
GGAEKKPEDIVKELMKQQGTQQQQQLMVDYDKMEEGDSENVNEDEYDEEDDGEDEEED
EALQEERKMAYKIEFQRQNTSNATNGGGSGAPSFLAMVQ

>PtrGT11

MIGDSSVQATSSDVAATATRVATEGEGEGGGGGFGSNSAEEDKTMGVDHEGNRMNYGANRW
PRQETLALLKIRSDMDAVFRDSGLKGPLWEEVSRKLAELGYHRSACKCKEKFENVYKYHKRT
KEGRTGKSEGKSYKFFDELEAFQNHPPHSTQPPTLPPPLPPKAQTASATITTLPWNTNNTAIVS
HATVPSRTNPMDIMSQSIATPTNNRAISMPPISSNPINPSQNAYPSSLQNLTTLLASSSPSSTASD
EELEVSYKRRKRESNWKDFFERLTRDVIKKQEDLQEKFLETIEKYEHERMAREEAWRMQEMA

RINREHETLIQERSTAAAKDAAVVAFLQKISGQQNSVQTQEIPQPTTTTPTAPPSQPLQLRPPPSLA
PVAKLEVPKRDNGDNFTVSSSSRWPKVEVQALINLRANLDVKYQENGAKGPLWEDISAGMQK
LGYNRSARKCKEKWENINKYFKKVKESNKKRPEDSKTCPYFDQLDALYKEKNKMEITVNSDY
AVKPTSTMEPLMVRPEQQWPFQQATQPQTIIEDNERNINIDHNIEDDDDDDDVVVDDDDVDTDE
EDEGGGFVANKSAPLVNGDQ

>PtrGT12

MLGDSSSVLATTTLAASGGGGVGNREAPPLTGGHHEGRNIDVGGEDDKGVIEGHRGIGGNR
WPRQETMALLKIRSDMDVAFRDASVKGPLWEDVSRKLAELGYNRSACKCKEFENVYKYHK
RTKDRSGKQEGKTYRFFDQLEAFQSHPPSLSSPLPPQPTKPHIPPANTIAMPVVNPSNVVGT
RNTVPSTAAATLATNTSQGIVTSAINLAVPPFPSTDPPTICPPSQATNPTNHPRTNIPSSFPNFSSDLN
SNSTSSSTSSDVELQGRKRKRKWKDFFERLMTEVIQKQEETQNKFLEAIKRENERMVREES
WRMQEMARINREREISAQERSIAATKDAAVMAFLQKLSEQQNPGQVQNNPPPTQPPPPALPPIS
QQTPTPTPPPLPVAQVPPPQVANLDMKSDNGDQNFMSASSSRWPKVEVEALIGLRTNLDCK
YQENGPKGPLWEEISAGMRKLGYNRNRKCKEKWENINKYFKKVKESKRRPEDSKTCPYFH
QLDALYKEKNKIDGPSNSTHHMKPQNSVPLMVLPEQQWPPAQEHRPDSMMGDLESDDNQN
QEDGDDKFMDEDEDEASGYEIVANKQTSMTAG

>PtrGT13

MEGNLSQGGMIPGGAPFGGLDLQGSMRVHHQAQHPHTMHHHQHPLHRQGSSTLTSVEEGFPL
TMGFMHNSDQNISMTDYNKGDRGKNSVSEDEPSYTEEGADGHNDAITGKKGTPWQRVKW
TDKMVRLITAVSYIGEDGTSDCGGMRKFTVLQKKGWKSVSKVMAERGFHVSPQQCED
KFNDLNKRYKRLNDMLGRGTSCQVVENPALLDVIDYLTEKEKDDVRKILNSKHLFYEEMCSY
HNGNRLHLPALQRSLLALRSRDDHDNDARRHQHDDLDEDDQEIETDDHDEFEEENHAS
HGDCRGIHGVGGSAKRPRQGGHEDAFSPESKAVWLQKQWMESRTLQLEERKLQIQEML
ELEKQRFKWQRFKRDRELEKLRMENERIKLENEQMALELKRKEMGADFN

>PtrGT14

MSAPIKTGSPSSPQDLTPLQTTAQQLPAPPTHPTNPRRLPPCWTPEDETVALIDAYRDKWYTL
RRGNLKANHWQEVADAVARRCPDASPKTAVQCRHKMEKLRKRYRTEIQRARSMPVSRFTSS
WVHFKRMDAMEKGPQAKADYNSESEGDDNDDNEDDGDIRGSYLENCRNAKNFMNTRSIQ
KLYGNGIGNPGNGDNNGLSGGNSSLGSGNAGGFRIPTGVSVAQPGPKFYAKTEQKHGGSP
NMGVNASDPYPKPKYGGGVGTSSRVMRGSEEMGRKREREPMEELVAVKVLGDGFVRMEQ
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>PtrGT15

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PLPISAQPLARVPCQENYHTRNRNNGVLGEYDDDKGEDEDDDDDEDYGYRSKLRSRINYL
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>PtrGT16

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RIDDDDDDGDIERHPKKQKLKSLVSSYEFAPRVPAPHVAVPAGPKPSVGGRNPLTDWTERETV
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>PtrGT17

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KTLGDRYLLTAQKNGKINGDLDPDEVFDLDPDFALRARKYSKVDGGFSVSKDSGSGFGVSSVA
FRPNDYVGVNGNIKANVGFNCDHGGEVVRLPDHGMMADHYGSYNDFSKGVVDVYEGFPLK
SLGDRNLPMQGLNPKNYKKIDRKPTPDFCDDHVEIDYRIDKRDRFGKKVNDGWSSSFPGFIP
NCCGNIDGKSRSDRSRALKGSVNVGTNGIGDGVRRREADSVALLVSAIEQATESFVKVEMMK
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>PtrGT18

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EVFTERAKNMQRLLLESEAGSTQSRKKVKRINGDRSSDELSEDEDEDESEEEKPARNNSRKRK
GEKNVAEKSPRSPSSSFGGVQEMLKEFFQQQKMEMQWRELMEKRAHERQMFEQEWRSSM
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>PtrGT19

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GKHLSPSPVALPLPPSYRRTPVVSSTPPPQPPALAVALPQKRPLPVDDDDYFRRNYSAMAAAA
AAVESDSEDEDEEFEGGERERAEDVEGEGIKRLALAIERFGEVYERVESEKLLQMV DLEKQ
RMKFAKDLEMERMRIFTETQVQLEKIKKGRAPEDY

>PtrGT20

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ETESFWFMRNDLRRKKLPGFFDREVYDILDGGGGTVQGLALALAPSSAAVEAETIAEGV VFD
SGRSAAAEDGLFSDFEQEEGGRSPEAVVKELQPIKA AVA IPTPISEKQYQPAPQASQAQGLNDK
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RKDHADGLVAVLNKLADALGKIADKL

>PtrGT21

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PPPPPLPPPLPHQTIGTAQNSHGSNGVDRGAKGDGMDTKLSDHVSDKNAMDTDSSTPALYSDK
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>PtrGT22

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CKNRIDTVKKKYKLEKAKIASGGGPGSWPFFDPLDRLIGSTARIPVVGNGNVGSKIPTRVRS
RRGGVNQYHFRNQNVKIRILKHEDDEDDEEGEEEGGAESDDSFPPMKRRRVVVEREVRGK
VGKEKRGGGWGNSIRMLTQAMVKFGEAYEQAESA KLQQV VEMEKTRMEFVKELELQRMQF
FMQTQMGISQLKNARRGGNATS NHYHHQYHRHHTGNNINASNNVNNSDSDN

>PtrGT23

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MKWTDNIVRLLISVVACVGDDDTFDGTGGLKRKSGLLQKKGKWKTVSKLMIGKGCHVSPQQ
CEDKFNDLNKRYKRLNEILGRGTSCRVENPALMDSMPHLSAKAKDDVRKILSSKHLFYKEIC
AYHNGQRIPNCQDFDLQGCSPLERCCKDMNGSGGDEVEGNDDSDDESNEADNNADENG
ESVGQLCERIVNEEHSHLCSQSGRQNSFGVEMTAIFQDTNVPSPWERKEWIKKQRLQLLEQRVN
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>PtrGT24

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ASSRNLAEVGFKRSTKWKKEFEEESGYFN SNIDIYSKNYRASFSFEFEEIYHGDQNPDQOEATA
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FKGICEDIVNKMMAQQEEKHNKLEDIVKRDEEKFAREEAWKKLEMDRINKELELRAHEQAL
AGDRLDTLIKFLKITSGDSYAEILGETSAPDVVKVPKCSNASTSSSLLLAQNPNPASQTSCEQ
LETPTSSTTTLDHQKSTSMPAKSNTSCTENQEPQNPSTLAPNIPQAPTTSSTLALAPQNPNSLN
SHNSPSGPSSILPMYKVVQAKSTSNEDDDIGKRWRPRDEV LALINLRCSLYNNNEDKEGSAKAPV
WERISQGMLELGYKRS AKRCKQK WENINKYFRKTKDASKKRYINSRTSPYFHLSTLYNHGTL
VAPKNRSASPENQSNLSETRHSSSSSQNGTSNSAMHVVEGEKNKVQVPPDFEF

>PtrGT25

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TAVSYIGEDATSDCGGGMRRRFTVLQKKGKWKSVSKVMAERGFHVSPQQCEDKFNDLNKRY
KRLNDMLGRGTSCQVVENPALLDVIDYLTEKDKDDVRKILSSKHLFYEEMCSYHNGNRLHLP
HDPALQRSLLALRSRDDHDNDVRRNQLDDLEDDQEIETDDHDEFGENHASHGDSRGIHG
VLGGS AKRPRPGGHEDVYFGNSSQDPNKGSSYSHPQIAQVDMNQVSPESSRASWLKQWM
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KEMGADFN

>PtrGT26

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IVRASHSTVPSTAAATLATNMSQGIVTSAIYLTVPFPSTNPTILPPSQATNPTNPPHTNIPPSFPN
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VREESWRMQEMTRINREREILAQERSVAASKDAAVMAFLQKLSEEQNPQIQNNPPPSQPPRPP
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CKYQDNGPKGPLWEEISARMRKLGYNRNAKRCKEKWENINKYFKKVESKKKRPEDSKTCP
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>PtrGT27

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KRTKEGRTGKSEGKTYKFFDELEAFQNHSHSAQPPTILAPPLPPPKAQTPTATTATLPWTNSPA
IVSHVTVQSTTNPIDILSQGIATPTTIHSTISPMPLSSNSLNSQDTLPSSLQNLATHLFSSTSSSTA

SDEKLEGSRKRKRKRNRNWKDFLRLTRDVIKKQEDLQKKFLETVEKCEHERMAREDAWRMKE
MARMNRQHEILIQERSTAAAKDAAVFAFLQKISGQQNSTETQAIPQPKLTPPPTQPPQPRPPPTS
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QKLGYNRSARKCKEKWENINKYFKKVKESNRKRPGDSKTCOPYFDQLDALYKEKNKMESRVS
TGYAVKPISTMEPLMVSPEQQCPFEQANQPETIIEDNERDINIDHNIEEDDDDMDDDEEEDEG
VGFEVVANRPASLTNGE

>PtrGT28

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FLESLVMKVMKQEMHKQLVEMIESRERETMIREEAWKQEMERMERDNEARAQETSRL
ALISFIQNMGTGHLQVTGSKGTNIWDAISDGMCMGYNSTAKNCKEKWENINKHFKKSVGSVV
KNPFENITVNPYFHELDVLYNNGFVNLGNGSTNTGKQANCTLGKG

>PtrGT29

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MLWVDAEGAASGSKKAAQLSSDEEEDNEEISEGEKGSRRKRIKKGKAVGGASCSTGNSNSLR
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>PtrGT30

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HRRTAYQIGMMASVMNSLLLQSALEKTGIQTRVQTAFAHQEVSEPYSRQRAIRHLEKGRVVIF
GGIGAGTGNPLFSTDTAAVQASEIHAEAVLKGTVNDGVYDCHSPDSNFIFEHISIRDLVSRGAT
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>PtrGT31

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DTMDLSPKMKDEVKLLNSKHLFFREMCAVHNSCGHAGVASGINNSPEMATDPSHAHQHQAT
QQQQYQRCSTENAVVTNSRTETEGSKMAKMARNEEDDHDESEDEDDYVEDEEEEDD
DDERDDDEEDYEENEDEAVEGNSRHQNGHGHGDEDDHDEKSSRKRPRKEVFSATSSLMQQL
NGEIMNVLRDGAKSSWEKNQWMKLMQLEEQQVNYQCQAFELEKQRLKWVRFSSKKERE
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>PtrGT32

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AQIISYIEKITGQSINLLTRMAPPLQPEISNEPIKEITPTKTDSSHKWPKDEVEALIQVRSRIEIKF

QEPGLKGPLWEEVSSLMSSMGYQRS AKRC KEK WENINKYFRK ARES PKRGS ARSKTCSYFNQ
LDQLYSGTLINYPANTTDM PSSGIEFGIKKQGYTELFEVFSVRRDYLANVRNPLGVSVISSEMGS
SRSEFDGFS DQNT ELEE GSSE QDIEAYKDDKQKDG EQQNGGGGGDEEIEIEN

>PtrGT33

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FGLPENFNDEL FRAIDDYMWCHKEHPD TDPDPDPD TDSEKPDLLHAITNP GTKKQRWR SKS
LRTPMEEKTHKCCREDNSQTIHAE EK PQERCVEENSQIYCTVEKPQRVHAE EEEHQESQVQEST
QIYNAGGKLQTIHAEEDPQESCAEEEPHTIHA EEEPEESPAEEHPQCCSKEKPRAIHLEETQER
YLEENHQTCTNEKPQSILAETQLQESHEEEKPQKCRREN SQNAHGDEKPKIHRGRKKMPS
TEEMKQMMVEKLHENAEMIQAVVNGNFP EMADLEAADSKNIEGFKTDLIRRQGDKLIACLQN
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>PtrGT34

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QETLTLLEIRSRLDSRFKEANQKGPLWDEVSRI MAEEHGYHRSGKKCREKFENLYKYKKTKE
GKAGRQDGKHYRFFRQLEALYGEPSNQASASETHFVNNTLLYQAPMSNTINQESQETFQENKH
SESLSFSNTSEFETSSSENDDLSAIAYNMMNRST EKQKGINESQSLARPKKSWKLKVDFVD
SQMRKLM EKQDAWMEKMLKTIEDREHERMCREEEWTKQELARFDQEHEFWAKERAWIEAR
DAALMEALKKHTEKGLELSSSVEQI AVATQRHNKNPDS AVAKKI QKDKFNITWTEPEILSFIQL
RTSMDSRFQENGYSNEGLWEEIAAEMASLG YDRSVDECKEKWESMNIYFNMTTESNKKRKE
DLRTSNYFQQL ESYNGMNSSPSNSYVGSQVNDNSCFQVQINEGDQHLWNTNKFDLKL NKEKN
QQQLWHNK

>PtrGT35

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TEIESCDYRDYRKDREEWSDAAISCLLEAYTEKY NQLNRGNLRGRDWEEVAEAVSERGGSNK
KSVEQCKNKIDNLKKRYKVELQRISGSGSSWHWFKHIEAIMGNACNGKSGGGGESDGGGGG
GSGGNVNA AVKQVKRYTSGSAAFANTLKT KPVPNLKWRRVVFKISGSALAGNCQNIDPKVAM
QIAREVATASRGGLEIAIVLGGRNFFCGDSWISATGLERPTAYQISM MATVMNSILLQSALEKHG
VQARVQSAFAMPELAEPYSRQRAIRHLEKGRVVIFGGAGAGAGAGAGNPLFTTDTAAALRASE
SIPLLLAFIISCVLLFTGNLDACFFYNVFWLSVNADALLKGTTNVDGVYDNHAGNSNAILDHIS
FREVVSRGVTSM DMMAIT YCEENGIPVVIFNLLEPGNISRALCGDQVGT LIDQAGRIS

>PtrGT36

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VKSKTKPQNDVYPGLASCGESSDDDDMAWFDERVKKKRHRMEDVDLSDGAACRELARAIL
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V

>PtrGT37

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KWRNLLKEFKKAKHQDRGSGSAKMSYYKEIDEILGRNKNSQYKCPTPKVDSYMQFSDKGF
EDTSISFGPVEASARPTLNLERRLDHDGHPLAITAADAVAASGVPPWNWRETPGNGAESQSGF
GRVISVKS GDYTRRIGIDGTTDAIREAIKSAFRLRTRKRAF WLEDEDQIIRALDRDMPLGNYTLHL

DEGLAIKVCLYDQSDHIPMHTEEKIFYTEDDYRDFLSRRGWTCLREFDGYRNIDSMDDL RHDA
IYRGVS

>PtrGT38

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WRNLLKEFKKAKHKDRGSGSAKMSYYKEIDEILRERNKNPQYKSPIPSKVDSYMQFADKGF
DTSISFGPVEASPRPTLNLERLDHHDGHPLAITAADAVAASGVPAWNWRETTPGNGAENQSYGG
RVISVKYGDYTRRIGVDGTADAIKEAIKSAFRLRSKRAFWEDEDQIIRSLDRDMPPGNYTLHL
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IYRGVS

>PtrGT39

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QCKNRIVMLKKKYKIEKSKPPLSWPLCNRLDSLIGTNSNTTNDKKPTSFTVKSKKKPKKRM
FSGLASYSSESSDDDEDDMAWFEERLKKKRHRMEDVGLSDGAACRELARAILKFG EIPERIESS
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FRDLSLQLNYFDK FVVHTDIYDSWIFPYN

>PtrGT40

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GSNNKKSVEQCKNKIDNLKKRYKVELQRISGSGSSWHWFKHIEVIMGNACNGKSSGGGAAAA
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NCQNIDPKVAMQIAQEVATASRVGLEIAIVLGGRNFFCGESWISATGLERPTACQIGMMATVMN
SVLLQSALEKHGVQARVQSAFAMPELAEPYSRQRAIRHLEKGRVVIFGGV GAGAGNPLFTTDT
AAALRASEINADALLKGTIVNGVYD SHAGSSNIILDHISFRDVVSRGATSMDDMAITYCEENGI
PVVVFNLLEPGNISRALCGDQVGT LIDQAGRIS

>PtrGT41

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WPRQETLTLLEIRSRLDSRFKEANQKGPLWDEVSRIMAEHGYQRSKCKREK FENLYKYYKK
TKEGKAGRQDGKHYRFFRQLEALYGEPSNQAPASETHFANNLLYQTPLSNTINQESQETFQEN
KHSELSFSNTSEFETSSSENDDLSAIAYNMMNRSTKQKGVNESQSLAGPKKSWRTKVED
FVDSQMRKLMKQDAWMEKMLKTIEDREYERMCREEEWTKQELARFDREHEFWAKERAWI
ESRDSALMEALKKHA EKGP ELSVVEHIAVATQRHNNNQDSTS AKKI QKDKFNIIWTEPEILSF
IQLRTSMESRFQESGYSNEGLWEEIAEEMASLGYDRSVDECKEKWESMNIYLNMTTESNKKR
KDQDLRTNDYFQLLESYNGMNSSPSNSYLGTVNDNSCFVQVINEGDQQQHLWNTNKFDLK
LNKEKNQQVWHK

>PtrGT42

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YDRYILIDAGVMFPDYDELGVQKIIPDTTFIRRWKHKIEAVIITHGHEDHIGALPWVVPALDHNT
PIYASSFTMELIKKRLKENGIFVPSRLKVFKTKRKFTAGPFEIEPIRVTHSIPDCCGLVLRCADGTI
LHTGDWKIDESPLDGKVFDR ETLEELSKEGVTLMMSDSTNVLSPGRTISESVVADALLRRISAA
KGRITTFASNIHRLG SVKAAADLTGRKLVFVGM SLR TYLDAAWKDGKAPIDPSTLVKVEDID
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>PtrGT43

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>PtrGT44

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TEPSIRLPPWEFQDPTEYYVGC LRVPTTLPSLFELSWYLQEPPEELRFPLRRDVYRDLPGQKE
LFFTISNDPLDCRGITYDILSSIIRTNPSISGATSSSRDSFIGVWDDCINRIVSKFCSVEVVIVRKQPS
SPMVDTLQDEWPVNTGFVRNFC LWRGEETDQLREGQVDPSSSIIEKLLWTYLDLPYILGYAV
GYSVTFCALCRSQDRIIRTDLYSLDLSSPVERLKALVPCYRVAGLLPLLADRCFNNFNNGGTYK
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LVFKPRGLKFKPNNCEQLVEALKYVTQALVALHDLFSMHRDLSWDKVMRRSDSENEWFLSGF
DDAVGAPQLNPVHGIGEARGRHAPEMGRGMHGKVDVWGVGHLVRTCGLGPNGVPKILREL
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>PtrGT45

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SRKLAEAGFKRSAEKCKEKFEESRYFNISNINYNKNYRASFSLEEEIYHGDQNPHEVTAGEK
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MFKRLCEDIVNTMMAQQEEMHNKLEDIVKRDEEKVAKEEARKKLEMDRINKELRAHEQ
ALANDRQATLIRFLKFTSSDSSVEILGEKIAPDPVNPVNSSNASSSSSLVLEQNPNPASQTSNES
QLKTATSSATALDHQKSTSILAKTNTSWTENQEPQNPSTLARNIPQVPTTSSTLAVPAAPQNP
FLNSHSSSTGPPNTPSHNKVQAKSTYKDDIGKRWPRDEV LALINLRCSLYNNNEDKEGSARA
PLWERISQGMLESYKRS AKRCKEKWENINKYFRKTKDVNKKRSIDSRTCPYFHLSTLYNQG
TLVAPDNRSASPENRSSLPETRHSSSSQNGTNSSTLHVGDGKEMVQRVTCEDGGVAAGMYCF
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>PtrGT46

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WVHFKRMDGMEKGPQAKADYNSESEENYRTAGNVMNTRSIQKLYRNGMGNPGTGSNNGL
SGGNSSSGNAGGFRIPTGVSIAQPGPKFYAKPEQKYGGGSPMGVNASPNPNLKPNYGGMGS
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>PtrGT47

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TTFIRWRHKIEAVIITHGHEDHIGALPWVIPALDHHTPIYASSFTMELIKKRLKENGIFVPSRLK
VFKTKRKAAGPFEIEPIRVTHSIPDCCGLVLRCADGTILHTGDWKIDESPLDGKKFDRETLEEL
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RKMVFGMSLRTYLDAWKDGKAPIDPSTLVKVEDIDAYAPKDLLIVTTGSQAEPRAALNLAS
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VLKIVKPQHFLPIHGELLFLKEHELLGKSTGIQHTTVIKNGEMLVSHLRNRRVLSNGFVFLGK
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CLWLDKGKLLDALHKAHAALSSCPVNCPLAHMERTVSEVLRKMVRKYSGRPEVIAVAME
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VDGFEFERELSKEEETSSPSLAEGHSSDSENQDDFRKSFIPSPVNLVKSDEDLVPPWEHVNE
LKEDGTISSDDDSLENQNSRSKGRPVKRNKWKPEEVKSLIKMRGELHSRFQVVRGRMALWE
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>PtrGT48

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WMMRNELRRERKLPSFFDKEVYYVLDGRVITDAIPLSQITFKKQMDCIDRDEAATAEEEEEE
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>PtrGT49

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RKRKSKIEKFLESVMKVMKQEMHKQLVEMIESRERERVIRDEAWKQQEIERMKRDSEAR
AQETSRNALISFIQNMSTSGHVIEVPQPSMTFESHMVNDGGNADAPIQNDFMGDQSNQRWPEAE
VQALIMLQTAWEQSRVTGSKGTNIWDAISAGMYNMGYNRTAKKCKEKWENINKHFKMSLG
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>PtrGT50

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KKKPGGLAQKKGKWKSVSRAMMEKGFYVSPQQCEDKFNDLNKRYKRVNDILGKGTAACRVV
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GDEAIEGNSRHQNGHGQDEDNRDEKSSRKRPRKDVFSATSPLMQQLNGEIMNVLQDVAKSS
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>PtrGT51

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TSRMQRMLRAEAEGAATGLKKKAVKLSDDDEDKNEEIIIEGEGGSRKKIKKGAIGGTSSSGN
SISLKELEDFTKQQIQMEMQWREVFEARENEMMKEMEWRTMKQLENDRIVMERRWRER
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>PtrGT52

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RKEFGLPENFDDELFAIDYMWWSQEQQLDTPDLDLQKADLLDVIANLERYVEENHQTCT
KEKPQTIPAEELHEIQVKEKPQKRLRKEKPQIGNGDEKPKIYSGRKKMPSTEDMEQMMVEKL
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DATS

>PtrGT53

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SRIEIKFQEPGVKGPLWEEVSSLMSSMGYQRS AKRCKEKWENINKYFRKAKESPERRSQRSKT
CSYFNQLDQLYSRLINYPSTTYMPSRGIEFDIEKQGQPEVLEAFVKGKDHDLATITNPPGENIKG
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>PtrGT54

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TLLDGNEHINPPHAILMPRS WHPLEDYTTIKEPFWKQLEKKRWGSEEEEEISGNRTRYFRPLEIEH
VVDESRERCRNLDIKFPINLEAIYSLAKIAEANQTGSGSVLTGDHSPTNAGVSVSSATNRQN
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EMLHRKFLEVIERMDRERTDREETWRHQEAEKHNREAISRAHERASTSNREAQMVS YIERITG
QSINLPIRMAPLLQPEISNEPIKEITSTKSDSHSRWPKDEVEALIKVRSRIEIKFQEPGVKGPLWE
EVSSLMSSMGYQRS AKRCKEKWENINKYFRKAKESPERRSQRSKTCSYFNQLDQLYSSSLINY
PSSTTYMPSRGIEFDIEKQGHSEVLEAFVKGKDHDLATITNPPGENIKGAEMSSSRFEFDGIAEKNE
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>PtrGT55

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HEKFVLLVWGDKFLQLGRNSLRSEDWVDVAEKVSETSKIERNEAQRQMMDVLKRRYKKE
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>PtrGT56

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QALDKTNALVSPTSSDKDHCLMPSASVIPVSFIPNDVPCSVQSPRMNCTDATSTSTASTSSESE
GTRKKKRRLTDFFERLMKEVIEKQENLQNKFLAIEKCEQERIAREEVWKMQELDRIKREQEL
LVHERAIAAAKDAAVLAFQKFSQGPVQLPDNPTVPMKFPDNQTSPALLSKNQAVPVENVV
KTHENS SVESFVNMSSSRWPKEEIESLIKIRTYLEFYQENGPKGPLWEEISTSMKNLGYDRSA

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