### **Supplementary content – GRFs mutant genes for PCR *in silico* approach**

**Supplementary File 1.** CRISPR-Cas9 amplicon sequences

**grf1-3 Sequence 5’3’**

GGAAAGAAATGGCGGTGCTGCGAGGGACGCTGTTCCCGATCAAAAGTACTGTGAACGACATATTAACAGAGGCCGCCATCGTTCAAGAAAGCCTGTGGAAGGCCAAAATGGCCACAATACTAATGCTGCCG

**grf8-64** **Sequence 5’3’**

CAGCTATGAGCCTCCTGTCGCCACTGCCACAGTTACTGTCATCCACATAGACAACGGCAGATTCTTGTAATCAGCATAAATACTAAACATTCCACTCCTATATGTATCCACTAAGAGGTAACACTGG

**Supplementary File 2.** Oligonucleotides parameters

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Name | Sequence 5’3’ | | | | Expected melting temperature | GC | | | Amplicon size |
| grf1\_3 Forward | | | GGAAAGAAATGGCGGTGCTG | | 63.0 | | 55.0 |
| grf1\_3  Reverse | | | CGGCAGCATTAGTATTGTGGC | | 63.0 | 52.4 | | | 131 bp |
| grf8\_61 Forward | | CAGCTATGAGCCTCCTGTC | | | 62 | 45.5 | | | 127 bp |
| grf8\_61 Reverse | | CCAGTGTTACCTCTTAGTGGAT | | | 63 | 57.9 | | |
| AT1G03400 Forward | | | | GCGGAGCATAGGGTGATAGC |  |  | | | 209 bp |
| AT1G03400 Reverse | | | | TGTAACTTAGGAGCATCGAGCG |  |  | | |

AT1G03400 is the endogenous gene used as sige parameter for amplicons

**Supplementary File 3.** Results from the GRF1 gene ecotype Columbia *(A. thaliana)* sequence searches against the forward reverse and probe sequences in the NCBI (nucleotide database).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Description** | **Accession** | **Blast against the NCBI GenBank** | | **Mismatches (bp) against**  **each accession** | | | **Similarity with the**   **amplicon** |
| **Query Cover** | **Per. ident** | **Forward** | **Reverse** | **Probe** |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1839133136) | [LR782543.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR782543.1?report=genbank&log$=nucltop&blast_rank=1&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1731306554) | [LR699746.2](https://www.ncbi.nlm.nih.gov/nucleotide/LR699746.2?report=genbank&log$=nucltop&blast_rank=2&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1731306447) | [LR699771.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR699771.1?report=genbank&log$=nucltop&blast_rank=3&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1731305693) | [LR699766.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR699766.1?report=genbank&log$=nucltop&blast_rank=4&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1731305467) | [LR699761.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR699761.1?report=genbank&log$=nucltop&blast_rank=5&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1731305462) | [LR699756.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR699756.1?report=genbank&log$=nucltop&blast_rank=6&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1731305318) | [LR699751.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR699751.1?report=genbank&log$=nucltop&blast_rank=7&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1572541210) | [LR215053.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR215053.1?report=genbank&log$=nucltop&blast_rank=8&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana growth-regulating factor 1 (GRF1), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1063701110) | [NM\_127849.4](https://www.ncbi.nlm.nih.gov/nucleotide/NM_127849.4?report=genbank&log$=nucltop&blast_rank=9&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana ecotype 1254 chromosome 2 sequence*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2279796752) | [CP086755.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP086755.1?report=genbank&log$=nucltop&blast_rank=10&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana ecotype 5856 chromosome 2 sequence*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2279796747) | [CP086750.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP086750.1?report=genbank&log$=nucltop&blast_rank=11&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana ecotype 6021 chromosome 2 sequence*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2279796742) | [CP086745.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP086745.1?report=genbank&log$=nucltop&blast_rank=12&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana ecotype 6024 chromosome 2 sequence*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2279792711) | [CP086740.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP086740.1?report=genbank&log$=nucltop&blast_rank=13&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana ecotype 9412 chromosome 2 sequence*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2279792706) | [CP086735.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP086735.1?report=genbank&log$=nucltop&blast_rank=14&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana ecotype 9470 chromosome 2 sequence*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2279790795) | [CP086730.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP086730.1?report=genbank&log$=nucltop&blast_rank=15&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana chromosome 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2265471797) | [CP087127.2](https://www.ncbi.nlm.nih.gov/nucleotide/CP087127.2?report=genbank&log$=nucltop&blast_rank=16&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana isolate t2t\_salk\_col chromosome 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2230635495) | [CP096025.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP096025.1?report=genbank&log$=nucltop&blast_rank=17&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2211310167) | [OW119597.1](https://www.ncbi.nlm.nih.gov/nucleotide/OW119597.1?report=genbank&log$=nucltop&blast_rank=18&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1901035191) | [LR881467.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR881467.1?report=genbank&log$=nucltop&blast_rank=19&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1862939933) | [LR797808.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR797808.1?report=genbank&log$=nucltop&blast_rank=20&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1862939928) | [LR797803.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR797803.1?report=genbank&log$=nucltop&blast_rank=21&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1862939923) | [LR797798.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR797798.1?report=genbank&log$=nucltop&blast_rank=22&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1862939918) | [LR797793.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR797793.1?report=genbank&log$=nucltop&blast_rank=23&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana genome assembly, chromosome: 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1862939913) | [LR797788.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR797788.1?report=genbank&log$=nucltop&blast_rank=24&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana chromosome 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_330250293) | [CP002685.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP002685.1?report=genbank&log$=nucltop&blast_rank=25&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana At2g22840 mRNA for hypothetical protein, partial cds, clone: RAAt2g22840*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_225898131) | [AB493560.1](https://www.ncbi.nlm.nih.gov/nucleotide/AB493560.1?report=genbank&log$=nucltop&blast_rank=26&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana isolate CS906 GRL1 (GRL1) gene, partial cds*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_170678327) | [EU550462.1](https://www.ncbi.nlm.nih.gov/nucleotide/EU550462.1?report=genbank&log$=nucltop&blast_rank=27&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana isolate CS902 GRL1 (GRL1) gene, partial cds*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_170678315) | [EU550456.1](https://www.ncbi.nlm.nih.gov/nucleotide/EU550456.1?report=genbank&log$=nucltop&blast_rank=28&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana isolate CS6799 GRL1 (GRL1) gene, partial cds*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_170678313) | [EU550455.1](https://www.ncbi.nlm.nih.gov/nucleotide/EU550455.1?report=genbank&log$=nucltop&blast_rank=29&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana isolate CS901 GRL1 (GRL1) gene, partial cds*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_170678293) | [EU550445.1](https://www.ncbi.nlm.nih.gov/nucleotide/EU550445.1?report=genbank&log$=nucltop&blast_rank=30&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana transcription activator (GRF1) mRNA, complete cds*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_21539879) | [AY102634.1](https://www.ncbi.nlm.nih.gov/nucleotide/AY102634.1?report=genbank&log$=nucltop&blast_rank=31&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana chromosome 2 clone T20K9 map CIC06C07, complete sequence*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_20197270) | [AC004786.3](https://www.ncbi.nlm.nih.gov/nucleotide/AC004786.3?report=genbank&log$=nucltop&blast_rank=32&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH12ZD08 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress)*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_42467528) | [BX820248.1](https://www.ncbi.nlm.nih.gov/nucleotide/BX820248.1?report=genbank&log$=nucltop&blast_rank=33&RID=F4TBFAGR013) | 100% | 100.00% | 1 | 0 | 0 | 100% |
| [*PREDICTED: Arabidopsis lyrata subsp. lyrata growth-regulating factor 1 (LOC9316532), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1190976351) | [XM\_002878592.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_002878592.2?report=genbank&log$=nucltop&blast_rank=34&RID=F4TBFAGR013) | 100% | 99.23% | 2 | 0 | 0 | 99% |
| [*PREDICTED: Camelina sativa growth-regulating factor 1-like (LOC104713726), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1109159671) | [XM\_010430916.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_010430916.2?report=genbank&log$=nucltop&blast_rank=35&RID=F4TBFAGR013) | 100% | 99.23% | 1 | 0 | 0 | 99% |
| [*PREDICTED: Camelina sativa growth-regulating factor 1 (LOC104751923), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1109080630) | [XM\_010473979.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_010473979.2?report=genbank&log$=nucltop&blast_rank=36&RID=F4TBFAGR013) | 100% | 99.23% | 1 | 0 | 0 | 99% |
| [*PREDICTED: Camelina sativa growth-regulating factor 1-like (LOC104704976), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_727486552) | [XM\_010420970.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_010420970.1?report=genbank&log$=nucltop&blast_rank=37&RID=F4TBFAGR013) | 100% | 99.23% | 1 | 0 | 0 | 99% |
| [*Camelina hispida cultivar hispida voucher DAO 902780 chromosome 2*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2249649981) | [CP094632.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP094632.1?report=genbank&log$=nucltop&blast_rank=38&RID=F4TBFAGR013) | 100% | 98.46% | 1 | 1 | 0 | 98% |
| [*Arabidopsis arenosa genome assembly, chromosome: 4*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1985657903) | [LR999454.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR999454.1?report=genbank&log$=nucltop&blast_rank=39&RID=F4TBFAGR013) | 100% | 98.46% | 2 | 1 | 0 | 98% |
| [*PREDICTED: Brassica rapa growth-regulating factor 1 (LOC103858395), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1827687114) | [XM\_009135745.3](https://www.ncbi.nlm.nih.gov/nucleotide/XM_009135745.3?report=genbank&log$=nucltop&blast_rank=40&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*Brassica oleracea HDEM genome, scaffold: C3*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1516546388) | [LR031872.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR031872.1?report=genbank&log$=nucltop&blast_rank=41&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*Brassica rapa genome, scaffold: A03*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1516519470) | [LR031572.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR031572.1?report=genbank&log$=nucltop&blast_rank=42&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*PREDICTED: Capsella rubella growth-regulating factor 1 (LOC17887921), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1338526739) | [XM\_006293922.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_006293922.2?report=genbank&log$=nucltop&blast_rank=43&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*PREDICTED: Brassica napus growth-regulating factor 1-like (LOC125584397), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2258278264) | [XM\_048752816.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_048752816.1?report=genbank&log$=nucltop&blast_rank=44&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*PREDICTED: Brassica napus growth-regulating factor 1 (LOC106389497), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2258170615) | [XM\_013829762.3](https://www.ncbi.nlm.nih.gov/nucleotide/XM_013829762.3?report=genbank&log$=nucltop&blast_rank=45&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*Brassica rapa genome assembly, chromosome: A03*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2067553137) | [LS974619.2](https://www.ncbi.nlm.nih.gov/nucleotide/LS974619.2?report=genbank&log$=nucltop&blast_rank=46&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*Brassica napus genome assembly, chromosome: C03*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1997692895) | [HG994367.1](https://www.ncbi.nlm.nih.gov/nucleotide/HG994367.1?report=genbank&log$=nucltop&blast_rank=47&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*Brassica napus genome assembly, chromosome: A03*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1997642184) | [HG994357.1](https://www.ncbi.nlm.nih.gov/nucleotide/HG994357.1?report=genbank&log$=nucltop&blast_rank=48&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*Brassica rapa subsp. pekinensis growth-regulating factor 1 mRNA, partial cds*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_401829651) | [JN698986.1](https://www.ncbi.nlm.nih.gov/nucleotide/JN698986.1?report=genbank&log$=nucltop&blast_rank=49&RID=F4TBFAGR013) | 100% | 96.15% | 1 | 1 | 0 | 96% |
| [*PREDICTED: Brassica oleracea var. oleracea growth-regulating factor 1 (LOC106328366), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_922432288) | [XM\_013766798.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_013766798.1?report=genbank&log$=nucltop&blast_rank=50&RID=F4TBFAGR013) | 100% | 95.38% | 1 | 1 | 0 | 95% |
| [*PREDICTED: Eutrema salsugineum growth-regulating factor 1 (LOC18021800), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1350250286) | [XM\_006404687.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_006404687.2?report=genbank&log$=nucltop&blast_rank=51&RID=F4TBFAGR013) | 100% | 94.62% | 1 | 2 | 2 | 95% |
| [*Thlaspi arvense genome assembly, chromosome: 4*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2211108390) | [OU466860.2](https://www.ncbi.nlm.nih.gov/nucleotide/OU466860.2?report=genbank&log$=nucltop&blast_rank=52&RID=F4TBFAGR013) | 100% | 94.62% | 2 | 1 | 1 | 95% |
| [*Raphanus sativus genome assembly, chromosome: 6*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1820521185) | [LR778315.1](https://www.ncbi.nlm.nih.gov/nucleotide/LR778315.1?report=genbank&log$=nucltop&blast_rank=53&RID=F4TBFAGR013) | 98% | 96.88% | 1 | 0 | 0 | 97% |
| [*PREDICTED: Raphanus sativus growth-regulating factor 1 (LOC108836427), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1073028010) | [XM\_018609585.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_018609585.1?report=genbank&log$=nucltop&blast_rank=54&RID=F4TBFAGR013) | 98% | 96.88% | 1 | 0 | 0 | 97% |
| [*Arabis alpina genome assembly, chromosome: 6*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1126731799) | [LT669793.1](https://www.ncbi.nlm.nih.gov/nucleotide/LT669793.1?report=genbank&log$=nucltop&blast_rank=55&RID=F4TBFAGR013) | 93% | 96.69% | 1 | 9 | 2 | 97% |
| [*PREDICTED: Tarenaya hassleriana growth-regulating factor 1 (LOC104807639), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1103909830) | [XM\_010533011.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_010533011.2?report=genbank&log$=nucltop&blast_rank=56&RID=F4TBFAGR013) | 88% | 88.70% | 2 | 15 | 1 | 89% |
| [*PREDICTED: Cucurbita pepo subsp. pepo growth-regulating factor 1-like (LOC111806015), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1333144597) | [XM\_023691334.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_023691334.1?report=genbank&log$=nucltop&blast_rank=57&RID=F4TBFAGR013) | 87% | 92.11% | 2 | 16 | 0 | 92% |
| [*PREDICTED: Cucurbita moschata growth-regulating factor 1-like (LOC111462890), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1279817572) | [XM\_023106693.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_023106693.1?report=genbank&log$=nucltop&blast_rank=58&RID=F4TBFAGR013) | 87% | 92.11% | 2 | 16 | 0 | 92% |
| [*PREDICTED: Cucurbita maxima growth-regulating factor 1-like (LOC111492063), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1281025314) | [XM\_023141237.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_023141237.1?report=genbank&log$=nucltop&blast_rank=59&RID=F4TBFAGR013) | 87% | 91.23% | 2 | 16 | 0 | 91% |
| [*PREDICTED: Syzygium oleosum growth-regulating factor 6-like (LOC115675732), transcript variant X2, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1729946463) | [XM\_030598485.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_030598485.1?report=genbank&log$=nucltop&blast_rank=60&RID=F4TBFAGR013) | 86% | 92.04% | 2 | 17 | 0 | 92% |
| [*PREDICTED: Syzygium oleosum growth-regulating factor 6-like (LOC115675732), transcript variant X1, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1729946461) | [XM\_030598484.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_030598484.1?report=genbank&log$=nucltop&blast_rank=61&RID=F4TBFAGR013) | 86% | 92.04% | 2 | 17 | 0 | 92% |
| [*PREDICTED: Ipomoea triloba growth-regulating factor 2-like (LOC116012194), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1766807651) | [XM\_031251676.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_031251676.1?report=genbank&log$=nucltop&blast_rank=62&RID=F4TBFAGR013) | 86% | 91.15% | 2 | 17 | 0 | 91% |
| [*PREDICTED: Coffea eugenioides growth-regulating factor 1-like (LOC113778176), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1531865994) | [XM\_027323475.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_027323475.1?report=genbank&log$=nucltop&blast_rank=63&RID=F4TBFAGR013) | 86% | 91.15% | 2 | 17 | 0 | 91% |
| [*PREDICTED: Coffea arabica growth-regulating factor 1-like (LOC113700371), transcript variant X2, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1527600702) | [XM\_027220803.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_027220803.1?report=genbank&log$=nucltop&blast_rank=64&RID=F4TBFAGR013) | 86% | 91.15% | 2 | 17 | 0 | 91% |
| [*PREDICTED: Coffea arabica growth-regulating factor 1-like (LOC113700371), transcript variant X1, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1527600700) | [XM\_027220802.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_027220802.1?report=genbank&log$=nucltop&blast_rank=65&RID=F4TBFAGR013) | 86% | 91.15% | 2 | 17 | 0 | 91% |
| [*Ipomoea triloba cultivar NCNSP0323 chromosome 3*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1477772544) | [CP025662.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP025662.1?report=genbank&log$=nucltop&blast_rank=66&RID=F4TBFAGR013) | 86% | 91.15% | 2 | 17 | 0 | 91% |
| [*Ipomoea trifida cultivar NCNSP0306 chromosome 3*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1477771519) | [CP025646.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP025646.1?report=genbank&log$=nucltop&blast_rank=67&RID=F4TBFAGR013) | 86% | 91.15% | 2 | 17 | 0 | 91% |
| [*PREDICTED: Coffea arabica growth-regulating factor 1-like (LOC113697940), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1527594490) | [XM\_027217565.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_027217565.1?report=genbank&log$=nucltop&blast_rank=68&RID=F4TBFAGR013) | 86% | 90.27% | 2 | 17 | 1 | 90% |
| [*PREDICTED: Carica papaya growth-regulating factor 1-like (LOC110809448), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1227893734) | [XM\_022035286.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_022035286.1?report=genbank&log$=nucltop&blast_rank=69&RID=F4TBFAGR013) | 86% | 90.27% | 2 | 17 | 0 | 90% |
| [*PREDICTED: Ipomoea nil growth-regulating factor 1-like (LOC109168875), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1109297175) | [XM\_019317731.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_019317731.1?report=genbank&log$=nucltop&blast_rank=70&RID=F4TBFAGR013) | 86% | 90.27% | 2 | 17 | 0 | 90% |
| [*PREDICTED: Mangifera indica growth-regulating factor 1-like (LOC123214244), transcript variant X2, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2118849368) | [XM\_044634027.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_044634027.1?report=genbank&log$=nucltop&blast_rank=71&RID=F4TBFAGR013) | 86% | 90.27% | 2 | 17 | 1 | 90% |
| [*PREDICTED: Mangifera indica growth-regulating factor 1-like (LOC123214244), transcript variant X1, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2118849366) | [XM\_044634025.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_044634025.1?report=genbank&log$=nucltop&blast_rank=72&RID=F4TBFAGR013) | 86% | 90.27% | 2 | 17 | 1 | 90% |
| [*PREDICTED: Lactuca sativa growth-regulating factor 1 (LOC111910684), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2078427194) | [XM\_023906516.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_023906516.2?report=genbank&log$=nucltop&blast_rank=73&RID=F4TBFAGR013) | 86% | 90.27% | 4 | 17 | 1 | 90% |
| [*PREDICTED: Nymphaea colorata growth-regulating factor 6-like (LOC116249505), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1776108942) | [XM\_031622620.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_031622620.1?report=genbank&log$=nucltop&blast_rank=74&RID=F4TBFAGR013) | 86% | 89.38% | 3 | 17 | 1 | 89% |
| [*PREDICTED: Elaeis guineensis growth-regulating factor 6-like (LOC105060064), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1658053801) | [XM\_010943653.3](https://www.ncbi.nlm.nih.gov/nucleotide/XM_010943653.3?report=genbank&log$=nucltop&blast_rank=75&RID=F4TBFAGR013) | 86% | 89.38% | 3 | 17 | 3 | 89% |
| [*PREDICTED: Camellia sinensis growth-regulating factor 1-like (LOC114276243), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1585656814) | [XM\_028218030.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_028218030.1?report=genbank&log$=nucltop&blast_rank=76&RID=F4TBFAGR013) | 86% | 89.38% | 1 | 17 | 0 | 89% |
| [*PREDICTED: Herrania umbratica growth-regulating factor 1 (LOC110409640), transcript variant X2, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1204886429) | [XM\_021419060.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_021419060.1?report=genbank&log$=nucltop&blast_rank=77&RID=F4TBFAGR013) | 86% | 89.38% | 2 | 17 | 1 | 89% |
| [*PREDICTED: Herrania umbratica growth-regulating factor 1 (LOC110409640), transcript variant X1, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1204886427) | [XM\_021419059.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_021419059.1?report=genbank&log$=nucltop&blast_rank=78&RID=F4TBFAGR013) | 86% | 89.38% | 2 | 17 | 1 | 89% |
| [*PREDICTED: Nicotiana attenuata growth-regulating factor 1-like (LOC109240682), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1111023684) | [XM\_019407347.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_019407347.1?report=genbank&log$=nucltop&blast_rank=79&RID=F4TBFAGR013) | 86% | 89.38% | 2 | 17 | 1 | 89% |
| [*PREDICTED: Rhodamnia argentea growth-regulating factor 6-like (LOC115746381), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2240055116) | [XM\_030682126.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_030682126.2?report=genbank&log$=nucltop&blast_rank=80&RID=F4TBFAGR013) | 86% | 3 | 3 | 17 | 1 | 89% |
| [*Polygonum aviculare genome assembly, chromosome: 10*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2212412588) | [OW204032.1](https://www.ncbi.nlm.nih.gov/nucleotide/OW204032.1?report=genbank&log$=nucltop&blast_rank=81&RID=F4TBFAGR013) | 86% | 89.38% | 2 | 17 | 0 | 89% |
| [*PREDICTED: Erigeron canadensis growth-regulating factor 1-like (LOC122589483), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2097445233) | [XM\_043761777.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_043761777.1?report=genbank&log$=nucltop&blast_rank=82&RID=F4TBFAGR013) | 86% | 89.38% | 4 | 17 | 0 | 89% |
| [*PREDICTED: Carya illinoinensis growth-regulating factor 1-like (LOC122295810), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2082374812) | [XM\_043105073.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_043105073.1?report=genbank&log$=nucltop&blast_rank=83&RID=F4TBFAGR013) | 86% | 89.38% | 1 | 17 | 0 | 89% |
| [*PREDICTED: Juglans microcarpa x Juglans regia growth-regulating factor 1-like (LOC121246929), transcript variant X2, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2031550288) | [XM\_041145253.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_041145253.1?report=genbank&log$=nucltop&blast_rank=84&RID=F4TBFAGR013) | 86% | 89.38% | 1 | 17 | 2 | 89% |
| [*PREDICTED: Juglans microcarpa x Juglans regia growth-regulating factor 1-like (LOC121246929), transcript variant X1, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2031550286) | [XM\_041145252.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_041145252.1?report=genbank&log$=nucltop&blast_rank=85&RID=F4TBFAGR013) | 86% | 89.38% | 1 | 17 | 2 | 89% |
| [*PREDICTED: Eucalyptus grandis growth-regulating factor 6 (LOC104447797), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1973669177) | [XM\_010061513.3](https://www.ncbi.nlm.nih.gov/nucleotide/XM_010061513.3?report=genbank&log$=nucltop&blast_rank=86&RID=F4TBFAGR013) | 86% | 89.38% | 2 | 17 | 0 | 89% |
| [*PREDICTED: Helianthus annuus growth-regulating factor 1 (LOC110889297), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1898409740) | [XM\_022136801.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_022136801.2?report=genbank&log$=nucltop&blast_rank=87&RID=F4TBFAGR013) | 86% | 89.38% | 4 | 17 | 1 | 89% |
| [*PREDICTED: Ipomoea triloba growth-regulating factor 1-like (LOC115998161), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1766778003) | [XM\_031237652.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_031237652.1?report=genbank&log$=nucltop&blast_rank=88&RID=F4TBFAGR013) | 86% | 90.18% | 2 | 18 | 0 | 90% |
| [*Ipomoea triloba cultivar NCNSP0323 chromosome 12*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1477772555) | [CP025671.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP025671.1?report=genbank&log$=nucltop&blast_rank=89&RID=F4TBFAGR013) | 86% | 90.18% | 3 | 18 | 0 | 90% |
| [*Ipomoea trifida cultivar NCNSP0306 chromosome 12*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1477771528) | [CP025655.1](https://www.ncbi.nlm.nih.gov/nucleotide/CP025655.1?report=genbank&log$=nucltop&blast_rank=90&RID=F4TBFAGR013) | 86% | 90.18% | 3 | 18 | 0 | 90% |
| [*PREDICTED: Ipomoea nil growth-regulating factor 2-like (LOC109177869), transcript variant X2, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1109216856) | [XM\_019327346.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_019327346.1?report=genbank&log$=nucltop&blast_rank=91&RID=F4TBFAGR013) | 86% | 90.18% | 3 | 18 | 0 | 90% |
| [*PREDICTED: Ipomoea nil growth-regulating factor 2-like (LOC109177869), transcript variant X1, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1109216854) | [XM\_019327345.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_019327345.1?report=genbank&log$=nucltop&blast_rank=92&RID=F4TBFAGR013) | 86% | 90.18% | 3 | 18 | 0 | 90% |
| [*Cucumis melo genomic scaffold, anchoredscaffold00014*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_733593821) | [LN681823.1](https://www.ncbi.nlm.nih.gov/nucleotide/LN681823.1?report=genbank&log$=nucltop&blast_rank=93&RID=F4TBFAGR013) | 85% | 90.09% | 1 | 16 | 0 | 90% |
| [*Fraxinus pennsylvanica genome assembly, chromosome: 1*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2112917277) | [OU503036.1](https://www.ncbi.nlm.nih.gov/nucleotide/OU503036.1?report=genbank&log$=nucltop&blast_rank=94&RID=F4TBFAGR013) | 84% | 91.82% | 1 | 17 | 0 | 92% |
| [*Polygonum aviculare genome assembly, chromosome: 1*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2212412107) | [OW204023.1](https://www.ncbi.nlm.nih.gov/nucleotide/OW204023.1?report=genbank&log$=nucltop&blast_rank=95&RID=F4TBFAGR013) | 84% | 90.00% | 1 | 17 | 0 | 90% |
| [*PREDICTED: Cucumis melo growth-regulating factor 6-like (LOC103487815), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1035400534) | [XM\_008446301.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_008446301.2?report=genbank&log$=nucltop&blast_rank=96&RID=F4TBFAGR013) | 80% | 91.43% | 2 | >20 | 0 | 91% |
| [*Cucumis melo genomic chromosome, chr\_3*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_733577135) | [LN713257.1](https://www.ncbi.nlm.nih.gov/nucleotide/LN713257.1?report=genbank&log$=nucltop&blast_rank=97&RID=F4TBFAGR013) | 80% | 91.43% | 2 | >20 | 0 | 91% |
| [*PREDICTED: Beta vulgaris subsp. vulgaris growth-regulating factor 2 (LOC104894980), mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_2252580405) | [XM\_010681369.3](https://www.ncbi.nlm.nih.gov/nucleotide/XM_010681369.3?report=genbank&log$=nucltop&blast_rank=98&RID=F4TBFAGR013) | 80% | 94.23% | 1 | >20 | 0 | 94% |
| [*PREDICTED: Morus notabilis growth-regulating factor 1 (LOC21396183), transcript variant X2, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1350295471) | [XM\_024172566.1](https://www.ncbi.nlm.nih.gov/nucleotide/XM_024172566.1?report=genbank&log$=nucltop&blast_rank=99&RID=F4TBFAGR013) | 80% | 91.35% | 2 | >20 | 1 | 91% |
| [*PREDICTED: Morus notabilis growth-regulating factor 1 (LOC21396183), transcript variant X1, mRNA*](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1350295468) | [XM\_010108599.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_010108599.2?report=genbank&log$=nucltop&blast_rank=100&RID=F4TBFAGR013) | 80% | 91.35% | 2 | >20 | 1 | 91% |

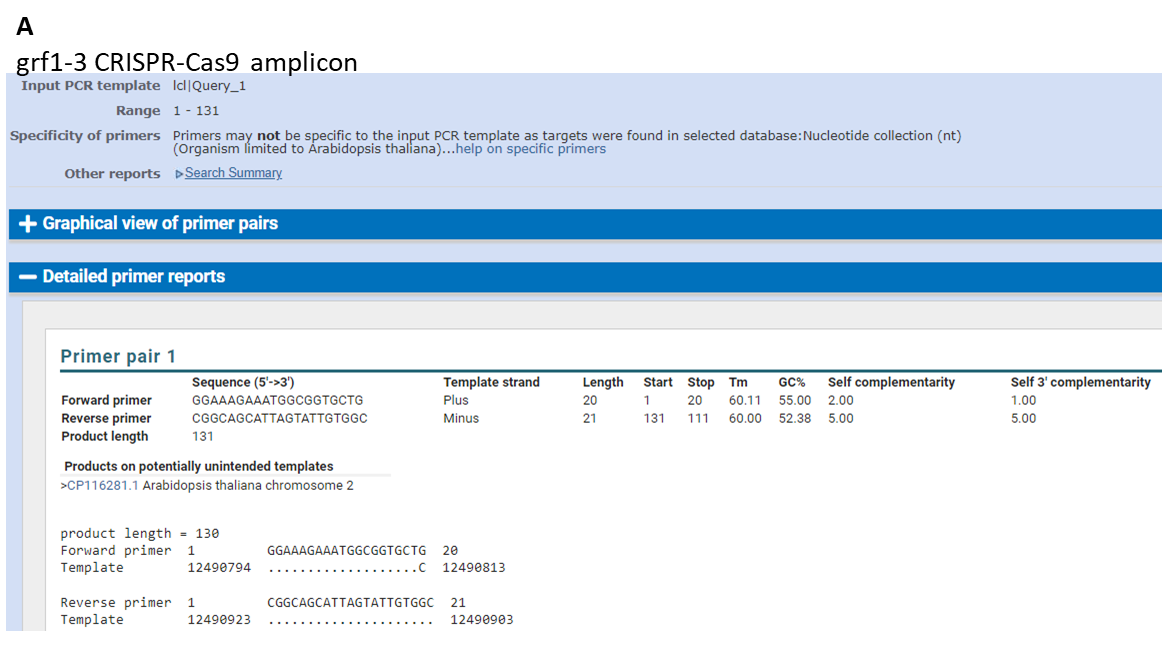
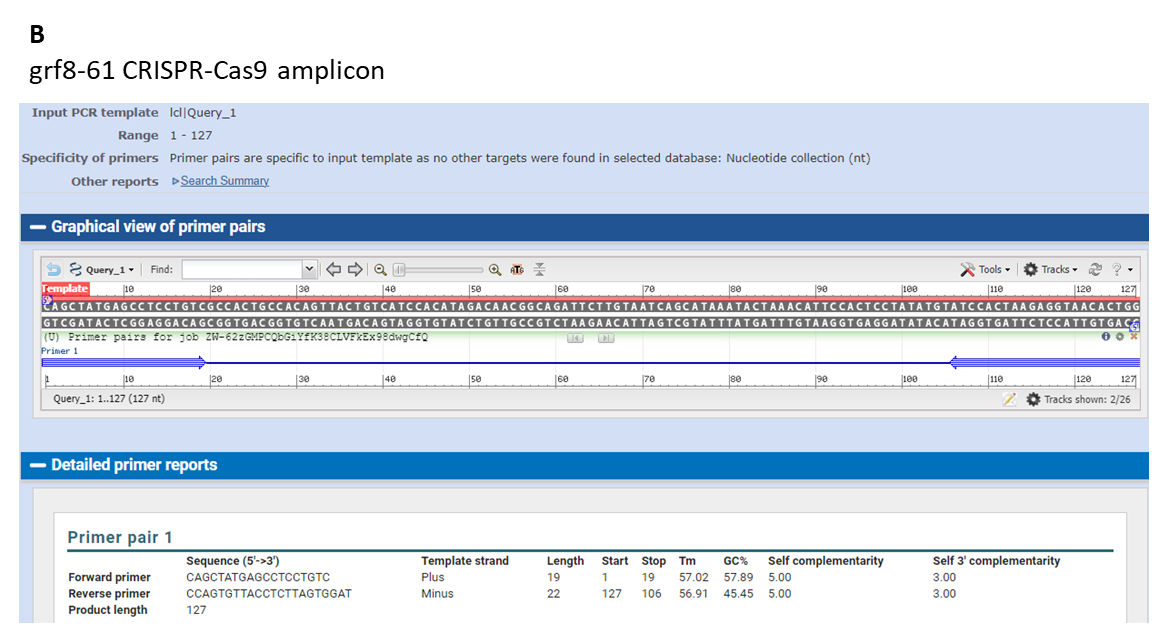
No species or any threshold limitation or selection.

**Supplementary table 4**. Results from the GRF8 gene ecotype Columbia *(A. thaliana)* sequence searches against the forward reverse and probe sequences in the NCBI (nucleotide database).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Description** | **Accession** | **Blast against the NCBI GenBank** | | **Mismatches (bp) against each accession** | | | **Similarity with your amplicon** |
| **Query Cover** | **Per. ident** | **Forward** | **Reverse** | **Probe** |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR782545.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR699748.2 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR699773.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR699768.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR699758.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR699753.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR215055.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana ecotype 1254 chromosome 4 sequence* | CP086757.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana ecotype 5856 chromosome 4 sequence* | CP086752.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana ecotype 6021 chromosome 4 sequence* | CP086747.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana ecotype 6024 chromosome 4 sequence* | CP086742.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana ecotype 9412 chromosome 4 sequence* | CP086737.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana ecotype 9470 chromosome 4 sequence* | CP086732.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana chromosome 4* | CP087129.2 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana isolate t2t\_salk\_col chromosome 4* | CP096027.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | OW119599.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR881469.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR797810.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR797805.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR797800.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR797795.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana chromosome 4* | CP002687.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61* | AL161561.2 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana DNA chromosome 4, BAC clone T19F6, partial sequence (ESSA project)* | AL109619.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence* | AC002343.1 | 100% | 100% | 0 | 3 | 0 | 100% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR699763.1 | 100% | 97,69% | 0 | 3 | 2 | 98% |
| *Arabidopsis thaliana genome assembly, chromosome: 4* | LR797790.1 | 100% | 97,69% | 0 | 3 | 2 | 98% |
| *Arabidopsis thaliana growth-regulating factor 8 (GRF8), partial mRNA* | NM\_118547.2 | 87% | 100% | 0 | 3 | >20 | 100% |
| *Arabidopsis thaliana growth-regulating factor 8 (GRF8), mRNA* | NM\_001341645.1 | 30% | 100% | 0 | 3 | >20 | 100% |
| *Arabidopsis thaliana growth-regulating factor 8 (GRF8), partial mRNA* | NM\_001341644.1 | 30% | 100% | 0 | 3 | >20 | 100% |
| *Arabidopsis thaliana isolate CS902 GRL8 (GRL8) gene, partial cds* | EU550550.1 | 25% | 100% | 0 | 3 | >20 | 100% |
| *Arabidopsis thaliana isolate CS901 GRL8 (GRL8) gene, partial cds* | EU550539.1 | 25% | 100% | 0 | 3 | >20 | 100% |

No species or any threshold limitation or selection.

**Supplementary File 5.** Results from *in silico* PCR. The Panel A shows the summarized result for the grf1-3 amplicon as template. Panel B, shows the grf8-61 amplicon.

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**