

## Novel #1

## Novel #2

### Novel #3

## Novel #4

## Novel #5

## Novel #6

## Novel #7

## Novel#8

```
query=chr01:3237626-3237740, target=GG50|c3177_g2_l3, score=2, range=676-696, strand=1
```

---

```
Annot: |tbl_ORD_ID|370403      Q9LSG3.1 RecName: Full=Galacturonosyltransferase B; AltName: Full=Glycosyltransferase QUASIMODO1
```

---

```
target   5' GUGGCUCUGCAUCAUCAGUCGG 3'  
          ::::~::~:~::~:~::~:  
query    3' CAGUGAGAUGAUGAUGCACGU 5'
```

Novel #9

```
query=chr81:7762935-7763839, target=GG41|c2631_g1_i1, score=3.5, range=777-797, strand=1
Annot: gnl|BL_ORD_ID|324572      Q9SE42.1 RecName: Full=Ribulose-phosphate 3-epimerase, cytoplasmic isoform; AltName: Full=Cyt-RPEase; AltName: Full=Penrose-5-phosphate 3-epimerase; Short=PPE; AltName: Full=RPEcyt; AltName: Full=Ribulose-5-phosphate-epimerase

target  5'  GGAUAAUCAAUAUCGUAA 3'
          ::::: ::::: ::::: ::::: :::::
query   3'  CCUUGUGGCGUUGUGCGAU 5'
```

Novel #10

```
query=chr02:15328566-15328749, target=GG52|c3155_g1_i1, score=3, range=630-649, strand=1
Annot: gnl|BL_ORD_ID|5278      B8B9K6.1 RecName: Full=60S ribosomal protein L10a B7F845.1 RecName: Full=60S ribosomal protein L10a

target  5'  GCAAGAU-GAUACGAAAGUGA 3'
          :: :::: ::::: ::::: :::::
query   3'  CGAUCUAGCUGUGCUUUCACU 5'
```

Novel #11

```
query=chr02:22236894-22237044, target=GG40|c2316_g1_i1, score=0, range=691-711, strand=1
Annot: gnl|BL_ORD_ID|5278      K4BV1.1 RecName: Full=Protein SPA, chloroplastic; AltName: Full=Sugar partition-affecting protein; Flags: Precursor

target  5'  UUCCGUAGAAUAACACAUA 3'
          ::::: ::::: ::::: ::::: :::::
query   3'  AAGGCAUCUUUAUUGUGUAGU 5'
```

Novel #12

```
query=chr02:27471405-27471507, target=GG50|c3293_g1_i8, score=4, range=791-810, strand=1
Annot: gnl|BL_ORD_ID|359984      Q94KB2.1 RecName: Full=ML0-like protein 13; Short=AtMlo13; Short=AtMlo20

target  5'  AU-CUCUUUAAACUUAUUUCA 3'
          :. : ::::: ::::: :::::
query   3'  UGUGGGAAAUUUAAAUUAGU 5'
```

Novel #13

```
query=chr04:10607231-10607336, target=GG98|c9128_g1_i1, score=2.5, range=140-159, strand=1
Annot: gnl|BL_ORD_ID|850      A0A140IL90.1 RecName: Full=Noroxonaritidine synthase; AltName: Full=CYP96T1; AltName: Full=Cytochrome P450 96T1

target  5'  GA-CCCGGCCAACGUAAACCA 3'
          :: ::::: ::::: :::::
query   3'  CUAGGGCGUGUGCAGUUGGU 5'
```

Novel #14

```
query=chr04:30762239-30762336, target=GG22|c4367_g1_i1, score=3, range=1930-1950, strand=1
Annot: gnl|BL_ORD_ID|194080      Q2RBN7.1 RecName: Full=Clathrin heavy chain 1

target  5'  CAUGCUIUUUCUCAAACUAAG 3'
          ::::: ::::: ::::: :::::
query   3'  GUAAGGAUAGAAGUUUGAUUU 5'
```

Novel \$15

```
query=chr05:22232500-22232644, target=GG52|c3654_g5_i2, score=4, range=1037-1056, strand=1
Annot: gnl|BL_ORD_ID|210607      Q7XA42.2 RecName: Full=Putative disease resistance protein RGA1; AltName: Full=RGA3-b1b

target  5'  AAGAUUUUGUGACCAUUGA 3'
          :: ::::: ::::: :::::
query   3'  UUGUAAAGUAUGUGGUAAACU 5'
```

Novel #16

```
query=chr05:25199802-25199949, target=GG52|c3471_g1_i1, score=0, range=3077-3097, strand=1
Annot: gnl|BL_ORD_ID|273094      Q8GSA7.1 RecName: Full=Calmodulin-binding transcription activator 3; AltName: Full=Ethylene-induced calmodulin-binding protein 1; Short=EICBP 1; AltName: Full=Ethylene-induced calmodulin-binding protein a; Short=EICBP.a; AltName: Full=Signal-responsive protein 1

target  5'  CAUCCAUUACUCCGUCUUG 3'
          ::::: ::::: ::::: :::::
query   3'  GUAGGUUUUAGGCGGAAAC 5'
```

Novel #17

```
query=chr08:39270564-39270717, target=GG22|c7255_g1_i1, score=0, range=2025-2045, strand=1
Annot: gnl|BL_ORD_ID|371080      O80822.2 RecName: Full=Peroxidase 25; Short=Atperox P25; Flags: Precursor

target  5'  GGCGAGCAAGUCUAUCAGACA 3'
          ::::: ::::: ::::: :::::
query   3'  CCGCUCGUUCAGAUAGUCUGU 5'
```

Novel #18

```
query=chr09:34029225-34029338, target=GG15|c3059_g1_i1, score=3, range=672-692, strand=1
Annot: gnl|BL_ORD_ID|262855      Q6AST1.1 RecName: Full=Homeobox-leucine zipper protein HOX32; AltName: Full=HB-ZIP protein HOX32; AltName: Full=Homeodomain transcription factor HOX32; AltName: Full=Oshox32

target  5'  UUGGGAUCAAGCCUGUCCGG 3'
          ::::: ::::: :::::
query   3'  CCCCUUACUCCGACACAGGU 5'
```

Novel #19

```
query=chr99:40438631-40438862, target=GG15|c2014_g1_i1, score=0.5, range=153-173, strand=1
Annot: gnl|BL_ORD_ID|271714      Q9X1B6.1 RecName: Full=Pollen-specific leucine-rich repeat extensin-like protein 2; Short=AtPEX2; Short=Pollen-specific LRR/EXTENSIN2; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor

target  5' UGGGAUCCUUAUUAUUGAA 3'
      ::::::::::::::::::::
query   3' ACUCUAGGGGAUUAUUAUUAU 5'
```

Novel #20

```
query=chr10:26852029-26852146, target=GG50|c3533_g1_i1, score=3.5, range=1575-1594, strand=1
Annot: gnl|BL_ORD_ID|273933      Q9ZQ96.1 RecName: Full=UDP-glycosyltransferase 73C3

target  5' ACGUUC-UCAUGUGGUCUCUU 3'
      :::: ::::::::::::::
query   3' GGCAGGUAGUACACCAGAGAU 5'
```

Novel #21

```
query=chr11:2322440-2322581, target=GG50|c3177_g2_i1, score=3.5, range=350-371, strand=1
Annot: gnl|BL_ORD_ID|370403      Q9LSG3.1 RecName: Full=Galacturonosyltransferase 8; AltName: Full=Glycosyltransferase QUASIMOD01

target  5' AUAUUGAAAUCCUAUAGUUUAU 3'
      :::::: :: ::::::::::
query   3' UAUUACUCUAGAGAUUCAAUG 5'
```

Novel #22

```
query=chr11:5710224-5710366, target=GG50|c3177_g2_i1, score=0.5, range=1001-1021, strand=1
Annot: gnl|BL_ORD_ID|370403      Q9LSG3.1 RecName: Full=Galacturonosyltransferase 8; AltName: Full=Glycosyltransferase QUASIMOD01

target  5' GAGACAGCAAAACCCUAUCCU 3'
      :::::: ::::::::::::::
query   3' CUCUGUUGUUUGGGAGUAGGA 5'
```

Novel #23

```
Annot: gnl|BL_ORD_ID|11109      F439H1.1 RecName: Full=Probable apyrase 7; Short=AtAPY7; AltName: Full=ATP-diphosphatase; AltName: Full=ATP-diphosphohydrolase; AltName: Full=Adenosine diphosphatase; Short=ADPase; AltName: Full=NTPase; AltName: Full=Nucleoside triphosphate diphosphohydrolase 7

target  5' UUGGUC-AAUAGACCAUUAU 3'
      :: :: ::::::::::::::
query   3' UACAGAUUAUCUGUGGAUA 5'
```

Novel #24

```
query=chr07:1353404-1353488, target=GG22|c5693_g1_i1, score=4, range=228-248, strand=1
Annot: gnl|BL_ORD_ID|278947      Q9SU13.1 RecName: Full=Fasciclin-like arabinogalactan protein 2; Flags: Precursor

target  5' GGGGCGUCGACGACCUCAGCG 3'
      :::: ::::::::::::::
query   3' CCUCGAGGCGUCUGGGGUCCA 5'
```