

Actin (ACT)

reference sequence: MF405765.1

forward primer: CGAGCGGGAAATTGTAAGGG

reverse primer: CGATCATGGATGGCTGGAAG

product size: 191 bp

contig number: CTG107765, percentage identity: 95%, E value: 0.00, Gaps (0/615)

Query	454	GGTATCGTTCTCGACTCTGGTGATGGTGTCTAGCCACACCGTGCCCATTTACGAAGGATAC	513
Subject	18164	GGTATTGTTCTTGACTCTGGTGATGGTGTCTAGCCACACTGTGCCATCTATGAAGGATAC	18223
Query	514	GCGCTTCCTCATGCCATTCTTCGTTTGGATCTCGCTGGTCGGGATCTCACGGACTCCCTC	573
Subject	18224	GCGCTTCCTCACGCCATTCTTCGTTTGGATCTTGCTGGCCGTGATCTCACTGATTCTCTC	18283
Query	574	ATGAAGATCCTCACTGAGAGAGGTTACTCCTTCACAACCTCAGCCGAGCGGGAAATTGTA	633
Subject	18284	ATGAAGATTCTCACTGAGAGAGGTTACTCCTTCACAACCTCAGCCGAGCGGGAAATTGTA	18343
Query	634	AGGGACATCAAGGAGAAGCTTGCGTATGTTGCCCTTGATTATGAACAGGAGCTGGAGACT	693
Subject	18344	AGGGACATCAAGGAGAAGCTTGCGTACGTAGCCCTTGATTATGAACAAGAGCTGGAGACT	18403
Query	694	GCCAAGAACAGCTCCTCAGTTGAGAAGAGCTACGAGCTTCCTGATGGTCAGGTATCACG	753
Subject	18404	GCCAAGAACAGCTCCTCAGTTGAGAAGAGCTACGAGCTACCTGACGGTCAGGTATCACG	18463
Query	754	ATTGGCGCAGAGAGGTTCAAGGTGCCCTGAGGTCCTCTTCCAGCCATCCATGATCGGCATG	813
Subject	18464	ATTGGCGCTGAGAGGTTCAAGGTGCCCTGAGGTCCTCTTCCAGCCATCCATGATCGGCATG	18523
Query	814	GAGTCTTCTGGAATCCATGAGACGACCTACAACCTCCATCATGAAGTGTGACGTGGATATC	873
Subject	18524	GAGTCTTCTGGAATCCATGAGACAACCTACAACCTCCATCATGAAGTGTGACGTGGATATC	18583
Query	874	AGGAAGGACCTGTACGGCAACATTGTGCTCAGTGGTGGCACAACCTATGTTCCAGGTATC	933
Subject	18584	AGGAAGGACCTGTATGGCAACATTGTGCTCAGTGGAGGTACAACCATGTTCCAGGTATC	18643
Query	934	GCTGACCGTATGAGCAAGGAGATCACCGCGCTTGCTCCGAGCAGCATGAAGATCAAGGTT	993
Subject	18644	GCTGACCGTATGAGCAAGGAGATCACCGCGCTTGCTCCGAGCAGCATGAAGATCAAGGTT	18703
Query	994	GTCGCCCCACCTGAGAGGAAGTACAGTGTCTGGATCGGAGGGTCCATCCTAGCCTCACTC	1053
Subject	18704	GTTGCTCCTCCTGAGAGGAAGTACAGTGTCTGGATCGGAGGGTCCATTCTAGCCTCGCTC	18763
Query	1054	AGCACTTTCCAACAG	1068
Subject	18764	AGCACTTTCCAACAG	18778

oat sequence:

GGTATTGTTCTTGACTCTGGTGATGGTGTCTAGCCACACTGTGCCATCTATGAAGGATACGCGCTTCCTCACGCCATTCTTCGTTTGGATCTTG
CTGGCCGTGATCTCACTGATTCTCTCATGAAGATTCTCACTGAGAGAGGTTACTCCTTCACAACCTCAGC CGAGCGGGAAATTGTAAGGG ACAT
CAAGGAGAAGCTTGCGTACGTAGCCCTTGATTATGAACAAGAGCTGGAGACTSGCCAAGAACAGCTCCTCAGTTGAGAAGAGCTACGAGTACC
TGACGGTCAGGTGATCAGATTGGCGCTGAGAGGTTCAAGTGCCCTGAGGTCCT TTCCAGCCATCCATGATCG CATGGAGTCTTCTGGAATC
CATGAGACAACCTACAACCTCCATCATGAAGTGTGACGTGGATATCAGGAAGGACCTGTATGGCAACATTGTGCTCAGTGGAGGTACAACCATGT
TCCCAGGTATCGCTGACCGTATGAGCAAGGAGATCACCGCGCTTGCTCCGAGCAGCATGAAGATCAAGGTTGTTGCTCCTCCTGAGAGGAAGTA
CAGTGTCTGGATCGGAGGGTCCATTCTAGCCTCGCTCAGCACTTTCCAACAG

Figure S5. Actin sequence alignment and primer location

reference sequence: U76558.1

reverse primer: CCTCCTCCATGCCCTCAC

contig number: CTG25086, percentage identity: 93%, E value: 0.00, gaps (4/619)

oat sequence:

CAGGTTCATTTCATCGTTGACTGCTTCCTCGAGGTTTGATGGTGCTCTTAACGTTGATGTCAATGAGTTCCAGACCAATCTGGTGCCCTACCCAA
GGATCCATCTCATGCTCTCTCTACGCCCCAGTGAATCTCTGCTGAGAAGGCTTACACGAGCAGCTCTCTGTGTGCTGAGATACCAACAGATGTC
CTTTGAGCCTTCTCCATGATGGCCAAAGTCGACCCCGCCATGGCAAGTACATGGCTCTGCTGTCTGATGTACCGTGGTGATGTGGTGCCCAAG
GATGTGAATGCTGTGGCCACATCAAGACCAAGCGCACTATCCAGTTGTGTGAGCATGGTGCCCACTGGCTTCAAGTGGCGGTATTCAACTACCA
GCCACCCAGCGTTGTCCAGGTGGTGACTTGGCCAAAGGTCCAAGAGGCTGGTGTCATGATCTCCAACATCCACAGTGGTTGTGAAGGTTCTCTCCC
GCATCGACCACAAGTTCGACCTGATGATGCAAAAGCGTGCTTTGTGCCACTGGTACGTGGCTGAGGTCATGAGAGGATATGAGAAAGTTGGTGCTGAG
CCGTGAGGATCTTGCTGCCCTGGAGAAGGATATGAGAAAGTATGGTGCTGAG

Figure S6. α -Tubulin sequence alignment and primer location

Figure S7. α -Tubulin sequence alignment and primer location

reference sequence: KR029492.1

reverse primer: **TGCTGCTGGGAATGATGTTG**

product size: 131 bp

contig number: ctg108160, percentage identity: $\geq 87\%$, E value: $\leq 6.38 \times 10^{-18}$

E value: 6.38*10⁻¹⁸, percentage identity: 95%, gaps 0/61

Query 491 AGGTTATCAATGACAGGTTTGGCATTGTTGAGGGTTTGATGACCACAGTTCATGCCATGAC 551
 |||
 Subject 18579 AGGTTATCAATGACAAGTTTGGCATCGTTGAGGGTTTGATGACCACTGTTTCATGCCATGAC 18639

E value: 2.05*10⁻²⁷, Identity: 89%, gaps 3/104

Query 550 ACTGCAACCCAGAAGACTGTTGATGGTCCTTCCAGCAAGGACTGGAGAGGTGGAAGGGCT 609
 |||||||
 Subject 13442 ACAGCAACCCAGAAGACTGTTGATG-TCCCTCGAGCAAG-ACTGGAGAGGTGGAAGGGCT 13499

```

Query 610      GCCAGCTT-CAACATCATTTCCAAGCAGCACTGGTGCCGCAAAGG 652
               || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Subject 13500  GCTAGCTTTCAACATCATTTCCCAGCAGCACTGGAGTGCTAAGG 13543

```

E value: 3.67*10⁻³⁹, Identity: 87%, gaps 4/145

Query 652 GCTGTTGGCAAGGTGCTCCAGAGCTTAA-CGGAAAGTTGACTGGAATGGCCTTCCGTGT 710
 |||||
 Subject 13670 GCTGTTGGCAAGGTGCTTCCAGCTCTTAACCGGAAAGTTGACCGGAATGGCCTTCCGTGT 13729

Query 711 TCCCACGTGTGATGTTTCTGTTGTTGATCTGACTGTTAGACTTGCGAAGCCAGCAACCTA 770
 |||||
 Subject 13730 CCCAACTGTGCGATGTTTCTGTT-TTGATCTGACCGTTAGACTTGAG-AGGCAGCCACCTA 13787

```

Query 771      TGATCAGATTAAGGCTGCTATCAAG 795
               ||| |||| |||| |||| ||||
Subject 13788  TGAGCAGATCAAGGCT-CGATCAAG 13811

```

oat sequence:

AGGTTATCAATGACAAAGTTTGGCATCGTTGAGGGTTTGATGACCACTGTTTCATGCCATGACACAGCAACCCAGAAGACTGTTGATGTCCCTCGA
GCAAGACTGGAGAGGTGGAAGGGCTGCTAGCTTTCAACATCATTCCCAGCAGCACTGGAGCTGCTAAGGCTGTTGGCAAGGTGCTTCCAGTCCTTAAA
CGAAAGAGTTGACCGGAATGGCCTTCCGTGTCCCAACTGTCGATGTTTCTGTTTGATCTGACCGTTAGACTTGAGAGGCAGCCACCTATGAGCAGATCAAGGCTCGA
TCAAG

Figure S8. GAPDH sequence alignment and primer location

Ubiquitin conjugating enzyme (UBC)

reference sequence: M62720.1

forward primer: CAAGCTGACCCTGCAATTCA

reverse primer: GGGCTCCACTGGTTCTGTA

product size: 135 bp

contig number: CTG29477, percentage identity: $\geq 93\%$, E value: $\leq 1.74 \times 10^{-30}$

E value 2.75×10^{-34} Identities: 96% Gaps: 0/92

```
Query      132  AGGTACGTTCAAGCTGACCCTGCAATTCACAGAAGATTACCCCAACAAGCCACCAACTGT  191
          |||
Subject 65992 AGGTACGTTCAAGCTGACCCTGCAATTCACAGAAGATTATCCCAACAAACCACCAACTGT  65933

Query      192  TCGGTTTGTCTCAAGGATGTTTCACCCAAACANN  223
          |||
Subject 65932 TCGGTTTGTCTCAAGGATGTTTCACCCGAACA  65901
```

E value 1.74×10^{-30} Identities: 95% Gaps: 0/87

```
Query      226  TATGCAGATGGAAGCATCTGCTTGGACATCCTACAGAACCAGTGGAGCCCTATATATGAT  285
          |||
Subject 65783 TATGCAGATGGAAGCATCTGCTTGGATATCTTACAGAACCAGTGGAGCCCATATATGAT  65724

Query      286  GTTGCAGCAATATTGACCTCTATCCAG  312
          |||
Subject 65723 GTTGCAGCAATATTGACCTCTGTCCAG  65697
```

E value 1.52×10^{-37} Identities: 93% Gaps: 0/108

```
Query 310      CAGTCCCTGCTGTGCGACCCGAACCCGAATTCTCCTGCGAACTCTGAAGCAGCCAGAATG  369
          |||
Subject 65027 CAGTCCCTGCTGTGCGACCCGAATCCAAATTCTCCGGCGAACTCTGAAGCAGCCAGGATG  64968

Query      370  TACAGCGAGAACAAGCGCGAGTACAACCGCAAGGTTTCGTGAGGTCGTG  417
          ||
Subject 64967 TATAGCGAGAACAAGCGCGAGTACAACCGCAAAGTTCGTGAGATCGTG  64920
```

oat sequence:

AGGTACGTTCAAGCTGACCCTGCAATTCA CAGAAGATTATCCCAACAAACCACCAACTGTTCGGTTTGTCTCAAGGATGTTTCACCCGAACANN
TATGCAGATGGAAGCATCTGCTTGGATATCTTACAGAACCAGTGGAGCCCATATATGATGTTGCAGCAATATTGACCTCTGTCCAGTCCCTGC
TGTGCGACCCGAATCCAAATTCTCCGGCGAACTCTGAAGCAGCCAGGATGTATAGCGAGAACAAGCGCGAGTACAACCGCAAAGTTCGTGAGAT
CGTG

Figure S9. UBC sequence alignment and primer location

Translation Elongation Factor 1 alpha-subunit

reference sequence: M90077.2

forward primer **AAGGAGGCAGCCAACTTCA**

reverse primer **AGCTCAGCAAACCTTGACAGC**

122 bp

contig number: CTG31755

E value 0.00

Identities:: 92%

Gaps: 2/938

Query	1	AGATGGAGCGCCACCCTCCCAAGTACTCAAAGGCGCGTTATGAAGAAATTGTCAAGGAGG	60
Subject	21225	AGATGGATGCCACCCTCCCAAGTACTCGAAGGCACGTTATGAAGAAATTGTGAAGGAAG	21284
Query	61	TCTCTTCTTACCTGAAGAAGGTTCGGCTACAACCCTGACAAGGTTCCCTTCGTCCTCCATCT	120
Subject	21285	TCTCTTCTTACCTGAAGAAGGTTCGGCTACAACCCTGACAAGGTGCCATTTGTCCTCCATCT	21344
Query	121	CTGGGTTTGAGGGTGACAACATGATTGAGAGGTCCACCAACCTTGACTGGTACAAGGGCC	180
Subject	21345	CTGGGTTTGAGGGTGACAACATGATTGAGAGGTCAACCAACCTTGACTGGTACAAGGGCC	21404
Query	181	CAACCTTCTTGAGGCGCTTGACCAGATCAACGAGCCCAAGAGGCCCTCAGACAAGCCCC	240
Subject	21405	CCACTTGCCTTGAGGCGCTTGACCAGATCAACGAGCCCAAGAGGCCCTCAGACAAGCCCC	21464
Query	241	TCCGTCTTCCCTCCAGGACGTTTACAAGATTGGTGGCATTGGAAGTGTGCCTGTTGGCC	300
Subject	21465	TCCGTCTTCCCTCCAGGATGTTTACAAGATTGGTGGCATTGGAAGTGTGCCTGTTGGCC	21524
Query	301	GTGTTGAGACTGGTGTATCAAGCCTGGTATGGTGTACCTTTGGTCCCCTGGTCTGA	360
Subject	21525	GTGTTGAGACCGGTGTATCAAGCCTGGCATGGTGTACCTTTGGTCCAAGTGGTCTGA	21584
Query	361	CAACTGAGGTCAAGTCCGTTGAGATGCACCATGAGTCTCTCTGGAGGCGCTTCTGGTG	420
Subject	21585	CCACTGAGGTAAAGTCCGTTGAGATGCACCAAGGAGTCTCTCTGGAGGCGCTCCCTGGTG	21644
Query	421	ACAACGTTGGCTTCAATGTCAAGAATGTTGCCGTGAAGGATCTGAAGCGTGGTTTGTGTG	480
Subject	21645	ACAACGTCGGGTCAATGTCAAGAATGTTGCTGTGAAGGATCTGAAGCGTGGGTGTGTGG	21704
Query	481	CATCCAACCTCAAGGATGACCTGCCAAGGAGGAGCCAACTTCACTCCCAGGTATCA	540
Subject	21705	CGTCCAACCTCAAGGATGACCTGCCAAGGAGGAGCCAACTTCACTCCCAGGTATCA	21764
Query	541	TCATGAACCACCCTGGTCAGATTGGCAACGGCTACGCCCCAGTGTGGACTGCCACACCT	600
Subject	21765	TCATGAACCACCCTGGTCAGATAGGCAACGGCTATGCCCCAGTGTGGACTGCCACACTT	21824
Query	601	CGCACATTGCTGTCAAGTTTGTGAGCTGGTGACCAAGATCGACAGGCGATCTGGTAAGG	660
Subject	21825	CGCACATTGCTGTCAAGTTTGTGAGCTGGTGACCAAGATTGACAGACGATCTGGCAAGG	21884
Query	661	AGCTGGAGGCCCTGCCAAGTTCTCTCAAGAATGGTGATGCTGGCATAGTGAAGATGATTC	720
Subject	21885	AGATTGAGAAGGAGCCCAAGTTTCTGAAGAATGGTGATGCTGGGATAGTGAAGATGATTC	21944
Query	721	CCACCAAGCCCATGGTTGTGGAGACCTTTGCTACTTACCCACCTCTTGGTCGTTTGTCTG	780
Subject	21945	CCACCAAGCCCATGGTTGTGGAGACCTTTTCTACTTACCTCCTCTTGGTCGCTTTGTCTG	22004
Query	781	TCCGTGACATGAGGCAAACTGTGGCTGTTGGTGTCATCAAGGGTGTGGAGAAGAAGGACC	840
Subject	22005	TGCGTGACATGAGACAAACGGTTGCTGTTGGTGTCATCAAGGCCGTGGAGAAGAAGGACC	22064
Query	841	CAACCGCGCGCAAGGTGACCAAGGCTGCCATCAAGAAGAAATGAGGGGCTTACCTGAATC	900
Subject	22065	CTACCGTGCCAAGGTGACCAAGGCTGCTGCCAAGAAGAAATGAGGTGTTTACCT-TATC	22123
Query	901	CATCTATGCTCTGCTTTTGTAGAT-CTCTAGTAGTTTAGT	937
Subject	22124	GTTCCATGCTCTGTTTGTAGATACCTAGTAGTTTGT	22161

oat sequence:

AGATGGATGCCACCCTCCCAAGTACTCGAAGGCACGTTATGAAGAAATTGTGAAGGAAGTCTCTTCTTACCTGAAGAAGGTTGGCTACAACCCTGACAAGGTGCCATTTGTCCCCATCTCTGGG
TTTGAGGGTGACAACATGATTGAGAGGTCAACCAACCTTGACTGGTACAAGGGCCCCACCTTGTCTGAGGCGCTTGACCAGATCAACGAGCCCAAGAGGGCCCTCAGACAAGCCCCCTCGTCTTCC
CCTCCAGGATGTTTACAAGATTGGTGGCATTTGGAACCTGTGCCTGTTGGCCGTTTGAGACCGGTGTATCAAGCCTGGCATGGTTGTCACTTTGGTCCAACTGGTCTGACCACTGAGGTTAAGT
CCGTTGAGATGCACCAAGTCTCTCTGGAGGCGCTCCCTGGTGACAACGTCGGGTTCAATGTCAAGAATGTTGCTGTGAAGGATCTCAAGCGTGGGTTTGTGGCGTCCAACTCCAAGGATGAC
CCTGCA**AAGGAGGCAGCCAACTTCA**CTCCCAAGGTCAATCATGTAACCAACCTGGTCAGATAGGCAACGGCTATGCCCCAGTGTGGACTGCCACACTTCGCACATT**AGTGTCAAGTTTGTG**
AGTGGTGACCAAGATTGACAGACGATCTGGCAAGGAGATTGAGAAGGAGCCCAAGTTTCTGAAGAATGGTGATGCTGGGATAGTGAAGATGATCCCAACCAAGCCCATGGTTGTGGAGACCTTTT
CTACTTACCTTCTTGGTGGCTTGGTGGCTGACATGAGACAAACGGTTGCTGTTGGTGTCATCAAGGCCGTGGAGAAGAAGGACCTTACCGTGCCAAGGTGACCAAGGCTGCTGCCAAG
AAGAAATGAGGTGTTTACCT-TATCGTTCCATGTCTGGTTTGTAGATACCTAGTAGTTTGT

Figure S10. EF1 sequence alignment and primer location

Figure S11. TBPII sequence alignment and primer location

ADP-ribosylation factor (ADPR)

reference sequence: AB050957.1

forward primer: CTCATGGTTGGTCTCGATGC

reverse primer: ACATCCCAAACAGTGAAGCT

product size: 143 bp

contig number: CTG25287, percentage identity: $\geq 92\%$, E value: $\leq 1.03 \times 10^{-22}$

E value: 5.56×10^{-64} , Identities: 97%, gaps 0/149

```
Query      1  ATGGGGCTCACGTTACCAAGCTGTTACGCCGCCTCTTCGCCAAGAAGGAGATGAGGATT  60
|||||
Subject 21896 ATGGGGCTCACGTTACCAAGCTGTTACGCCGCCTCTTCGCCAAGAAGGAGATGAGGATT  21955

Query      61  CTCATGGTTGGTCTCGATGCCGCTGGTAAGACCACCATCCTCTACAAGCTCAAGCTCGGA  120
|||||
Subject 21956 CTCATGGTTGGTCTCGATGCCGCTGGTAAGACCACCATCCTCTACAAGCTCAAGCTCGGC  22015

Query      121  GAGATCGTCACCACCATCCCAACCATCGG  149
|||||
Subject 22016 GAGATCGTCACCACCATCCCTACCATCGG  22044
```

E value: 1.03×10^{-22} , Identities: 92%, gaps 0/78

```
Query      148  GGATTCAACGTCGAAACTGTTGAATACAAGAACATCAGCTTCACTGTTTGGGATGTGGGG  207
|||||
Subject 22349 GGATTTAACGTCGAGACTGTCTGAATACAAGAACATCAGCTTCACTGTTTGGGATGTGGGG  22408

Query      208  GGCCAAGACAAGATCAGG  225
||
Subject 22409 GGTCAAGACAAGGTAAGG  22426
```

E value 1.45×10^{-45} Identities: 94% Gaps: 0/123

```
Query      218  AGATCAGGCCCTTGAGGCACTACTTCCAGAATACCAAGGGCTCATTGTTGTTGTTG  277
|||||
Subject 22602 AGATCAGGCCCTTGAGGCACTACTTCCAGAATACAGGGACTCATCTTTGTTGTTG  22661

Query      278  ACAGCAATGATAGGGAACGTGTTGTTGAGGCTAGAGATGAGCTCCACAGAATGCTGAATG  337
|||||
Subject 22662 ACAGCAATGATAGGGAGCGTGTTGTTGAGGCTAGAGATGAGCTCCACAGGATGCTGAATG  22721

Query      338  AGG  340
|||
Subject 22722 AGG  22724
```

E value 1.89×10^{-50} Identities: 96% Gaps: 0/124

```
Query      338  AGGATGAGCTGCGTGATGCTGTGTTGCTTGTATTGCAAACAAACAAGATCTTCCTAATG  397
|||||
Subject 22999 AGGATGAGCTACGTGATGCTGTGTTGCTTGTATTGCAAACAAACAAGATCTTCCCAATG  23058

Query      398  CCATGAATGCTGCTGAAATCACCGACAAGCTTGGTCTGCACTCCCTGCGCCAGCGGCACT  457
|||||
Subject 23059 CCATGAATGCGGCTGAAATCACTGACAAGCTTGGTCTGCACTCCCTGCGCCAGCGGCACT  23118

Query      458  GGTA  461
|||
Subject 23119 GGTA  23122
```

oat sequence:

ATGGGGCTCACGTTACCAAGCTGTTACGCCGCCTCTTCGCCAAGAAGGAGATGAGGATTCTCATGGTTGGTCTCGATGCGCTGGTAAGACCACCATCCTCTACAA
GCTCAAGCTCGGCGAGATCGTCACCACCATCCCTACCATCGGATTTAACGTCGAGACTGTCTGAATACAAGAACATCAGCTTCACTGTTTGGGATGGGGGGTCAAG
ACAAGATCAGGCCCCCTTTGGAGGCACTACTTCCAGAATACACAGGACTCATCTTTGTTGTTGACAGCAATGATAGGGAGCGTGTTGTTGAGGCTAGAGATGAGCTC
CACAGGATGCTGAATGAGGATGAGCTACGTGATGCTGTGTTGCTTGTATTGCAAACAAACAAGATCTTCCCAATGCCATGAATGCGGCTGAAATCACTGACAAGCT
TGGTCTGCACTCCCTGCGCCAGCGGCACTGGTA

Figure S12. ADPR sequence alignment and primer location

Similar to phosphogluconate dehydrogenase (PGD)

reference sequence: Ta30797 (Unigene Cluster)

forward primer: **GCAAAGATGAAACTGGTGGTCA**

reverse primer: **CAACCCACTTTTGTCCGCC**

product size: 90 bp

contig number: CTG22048 percentage identity: $\geq 90\%$, E value: $\leq 1.58 \times 10^{-28}$

E value 1.06×10^{-30} Identities: 90% Gaps: 0/103

```
Query      217  GTTGTTTTTCGACAAGGATGGCGTGCTCGAGCAAATCGGAGAGGGCAAGGGCTACGTGGAT  276
          |||
Subject 40058 GTTGTTTTTCGACAAGGATGGCGTGCTCGAGCAAATCGGGGAAGGGAAGGGCTATGTGGAC  39999

Query      277  ATGTCCACTGTTGATGCTGCAACTTCTTGCAAGATAAGCGAGG  319
          |||
Subject 39998 ATGTCCACCGTTGATGCCGCGACCTCTTGCAAGATAAGTGAGG  39956
```

E value 7.16×10^{-33} Identities: 91% Gaps: 0/105

```
Query      317  AGGCGGTTAAACAAAAGGGCGGAGCTTTTGTGAAGCTCCAGTTTCAGGGAGCAAGAAGC  376
          |||
Subject 39013 AGGCGGTTAAACAAAAGCTGGAGCTTTTGTGAAGCTCCAGTTTCAGGGAGCAAGAAGC  38954

Query      377  CAGCTGAAGATGGCCAATTGGTCATTCTTGCTGCAGGCGACAAGG  421
          |||
Subject 38953 CAGCTGAAGATGGTCAATTGGTTATTCTTGACAGAGGGACAAGG  38909
```

E value 1.48×10^{-41} Identities: 93% Gaps: 0/118

```
Query      419  AGGCACATATATGATGATATGGTCCCTGCATTTGATGTACTTGGAAGAAGTCATTCTTTC  478
          |||
Subject 37645 AGGCACATATATGACGACATGGTCCCTGCCTTTGATGTACTTGGAAGAAAGTCGTTCTTCT  37586

Query      479  TGGGGGAGATGGGAAATGGAGCAAAGATGAAACTGGTGGTCAACATGATCATGGGAAG  536
          |||
Subject 37585 TGGGGGAGATTGGGAAATGGAGCAAAGATGAAACTGGTGGTCAACATGATCATGGGAAG  37528
```

E value 1.58×10^{-28} Identities: 96% Gaps: 0/82

```
Query      535  AGTATGATGAATGCTTTTCTGAGGGACTCTGTTTGGCTGACAAAAGTGGGTTGAGCCCC  594
          |||
Subject 37031 AGTACGATGAATGCCTTTTCTGAGGGACTCTGTTTGGCGGACAAAAGTGGGTTGAGCCCC  36972

Query      595  CAGACGCTTCTTGATGTCCTGG  616
          |||
Subject 36971 CAGACGCTTCTTGATGTCCTGG  36950
```

oat sequence:

AGTGCGACGAGCTCGCCGCGCTGGGCGCTACCGTCGGGGACACGCCCCGGAAGGTCGTCGCCAAGTGCAACTACACCATCGCCATGCTCTCCGA
TCCCAGCGCCGCGCTATCCGTTGTTTTTCGACAAGGATGGCGTGCTCGAGCAAATCGGGGAAGGGAAGGGCTATGTGGACATGTCCACCGTTGAT
GCCGCGACCTCTTGCAAGATAAGTGAGGCAGTTAAACAGAAAGCTGGAGCTTTTGTGAAGCTCCAGTTTCAGGGAGCAAGAAGCCAGCTGAAG
ATGGTCAATTGGTTATTCTTGACGAGGGGACAAGGCACTATATGACGACATGGTCCCTGCCTTTGATGTACTTGGGAAAAAGTCGTTCTTCTT
GGGGGAGATTGGAAATGGA**GCAAAGATGAAACTGGTGGTCA**ACATGATCATGGGAAGTACGATGAATGCCTTTTCTGAGGGACTCTGTTT**GGCG**
GACAAAAGTGGGTTGAGCCCCCAGACGCTTCTTGATGTCCTGG

Figure S13. PGD sequence alignment and primer location

Phenylalanine ammonia lyase (PAL)

reference sequence: MT150275.1

forward primer: GCAACTTCCAGGGCACCC

reverse primer: CTCCGAGAACTGAGCGAACAT

product size: 95 bp

sequence identity: 91%, E-value: 0.00, gaps: 0/1683, contig number: CTG14153

```
Query      1  CAGGTTCCCTTAACGCCGGTGCCTTCGGAACGGACGGACGACAGTCTGCCCCCGCA  60
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142817 CAGGTTCCCTCAACGCCGGTGCCTTCGGAACGGACGGACGACAGTCTGCCCCCGCA 142758

Query      61  GGCAACACGCGCGGCTATGCTCGTCCGCATCAACACCCTCCTCCAGGGTTACTCGGGCAT  120
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142757 GGCAACGCGCGCGGCCATGCTGGTCCGCATCAACACCCTCCTGCAGGGTTACTCGGGGAT 142698

Query     121  CCGCTTCGAGATCCTCGAGGCCATCACCAGCTGCTCAACGCCAATGTCACGCCGTGCTT  180
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142697 CCGCTTCGAGATCCTCGAGGCCATCACCAGCTGCTCAACGCCAAGTCAACCCCGTGCCT 142638

Query     181  GCCGCTCCGGGGACCATCACTGCATCCGGTGACCTTGTGCCGTGTCTTACATTGCCGG  240
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142637 GCCGCTCCGGGGACCATCACCAGCTCGGGCGACCTGCTGCCGTCTCTCTTACATTGCCGG 142578

Query     241  CCTTATCACCGGCCGACAGAATCTGTTGCGGTGGCCCTGATGGCAGCAAGGTGACCGC  300
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142577 CCTTATCACCGGTCGCCAGAACTCCGTGCGCGTGGCCCGATGGCAGCAAGGTGACCGC 142518

Query     301  TGCCGAGGCATTCAAGATCGCCGGGATCGAGCACGGTTCTTTGAGTGCAGCCCAAGGA  360
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142517 TGCCGAGGCGTTCAAGATCGCCGGCATCGAGCACGGTTCTTTGAGTGCAGCCCAAGGA 142458

Query     361  GGGCCTTGCCATGGTGAACGGCACGGCTGTGGGCTCTGGTCTTGTCATCGACCGTGCTCTT  420
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142457 AGGCCTTGCCATGGTGAACGGGACAGCGTGGGGTTCGGGACTTGCGTCGACCGTGCTGTT 142398

Query     421  TGAGGCCAATGTCTCTCGTCCTTGTGAGGTCTTGTCTGCGGTGTTCTGCGAGGTGAT  480
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142397 TGAGGCCAACATCTCGCCATACTCGCTGAGGTCTGTCGCGGTCTTCTGCGAGGTGAT 142338

Query     481  GAACGGCAAGCCGGAGTTCACTGACCACCTGACCCACAAGCTGAAGCACCACCTGGACA  540
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142337 GACCGGCAAGCCGGAGTTACGAGCACCTGACCCACAAGCTGAAGCACCACCTGGGCA 142278

Query     541  GATTGAAGCAGCTGCAATCATGGAGCACATCTTGGAGGGGAAGCTCATACATGAAGCAGGC  600
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142277 GATCGAGGCGGGCGGATCATGGAGCACATCTTGAAGGGAGCTCGTACATGAAGCAGGC 142218

Query     601  AAAGAAGCTTGCGGAGCTCGACCCCTTGATGAAGCCGAAGCAGGACCGGTATGCCCTCCG  660
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142217 CAAGATACAGGGCGAGCTCGACCCCGTGTGAAGCCGAAGCAGGACCGGTACGCGCTCCG 142158

Query     661  CACTTCGCCTCAGTGGCTCGGCCACAAATCGAAGTTATTTCGATTTGCCACCAAGTCGAT  720
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142157 CACGTGCGCGAGTGGCTTGCCCTCAGATCGAGGTTATCCGCTTCGCCACCAAGTCGAT 142098

Query     721  TGAGCGTGAGATCAACTCTGTCAACGACAACCCGCTCATCGAGCTCTCCCGTGGCAAGGC  780
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142097 CGAGCGGAGATCAACTCCGTCAACGACAACCCGCTCATCGATGTCTCCCGTGGCAAGGC 142038

Query     781  CATCCACGGTGGCAACTTCCAAGGCACCCCATTTGGTGTCTCCATGGACAACACCCGCCT  840
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 142037 GATCCATGGGGGCAACTTCCAGGGCACCCCATCGGTGTCTCCATGGACAACACCCGCCT 141978

Query     841  CGCCATTGTGTGCTATTGGCAAGCTGATGTTTCGCGCAGTTCTCGGAGCTCGTGAACGACTT  900
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 141977 TGCCATCGCTGCTATTGGCAAGCTGATGTTTCGCGCAGTTCTCGGAGCTGGTGAACGACTT 141918

Query     901  CTACAACATGGCCTGCCTTCCAACCTGTCCGGTGGGCGCAACCCGAGCTTGGACTATGG  960
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Subject 141917 CTACAACAACGGCCTCCCGTCCAACCTGTCCGGTGGGCGCAACCCGAGCTTGGACTACGG 141858
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oat sequence:

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GGCAAGCTCAGTGTTCGCGCAGTTCTCGGAGCTGGTGAACGACTTCTACAACAACGGCCTCCCGTCCAACCTGTCCGGTGGGCGCAACCCGAGCTTGGACTACGG
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Figure S14. PAL sequence alignment and primer location