

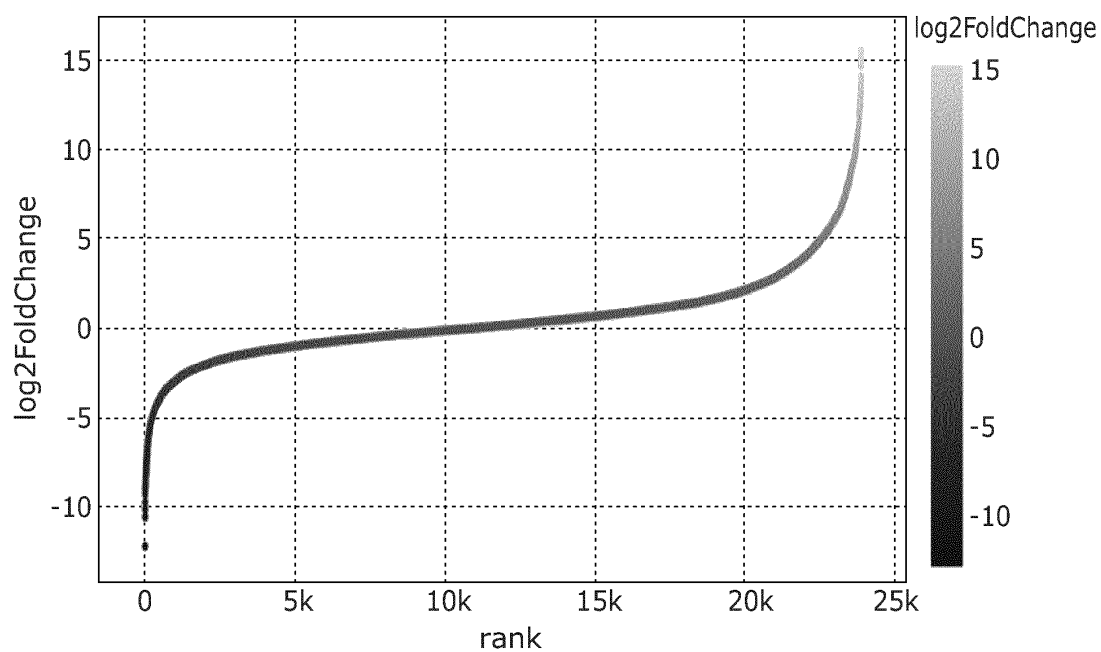


Figure 1

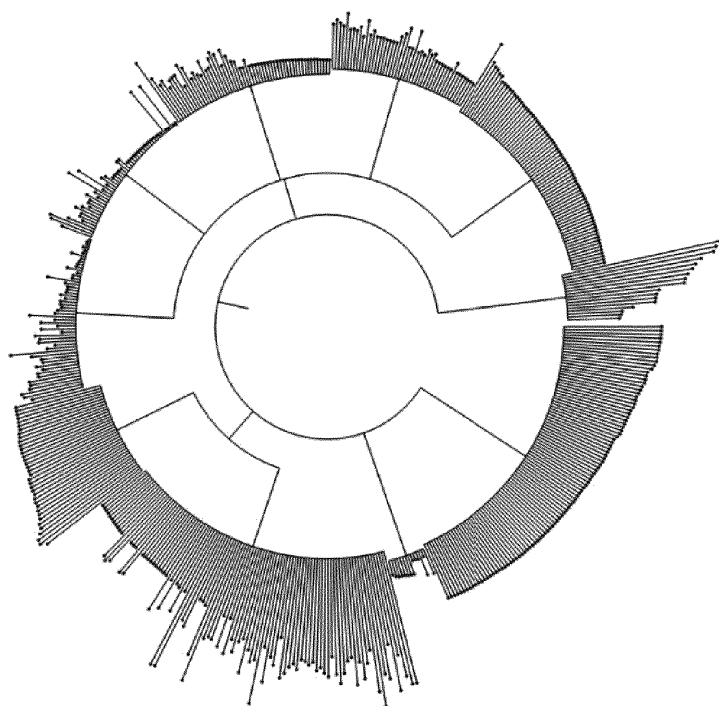


Figure 2

SUBSTITUTE SHEET (RULE 26)

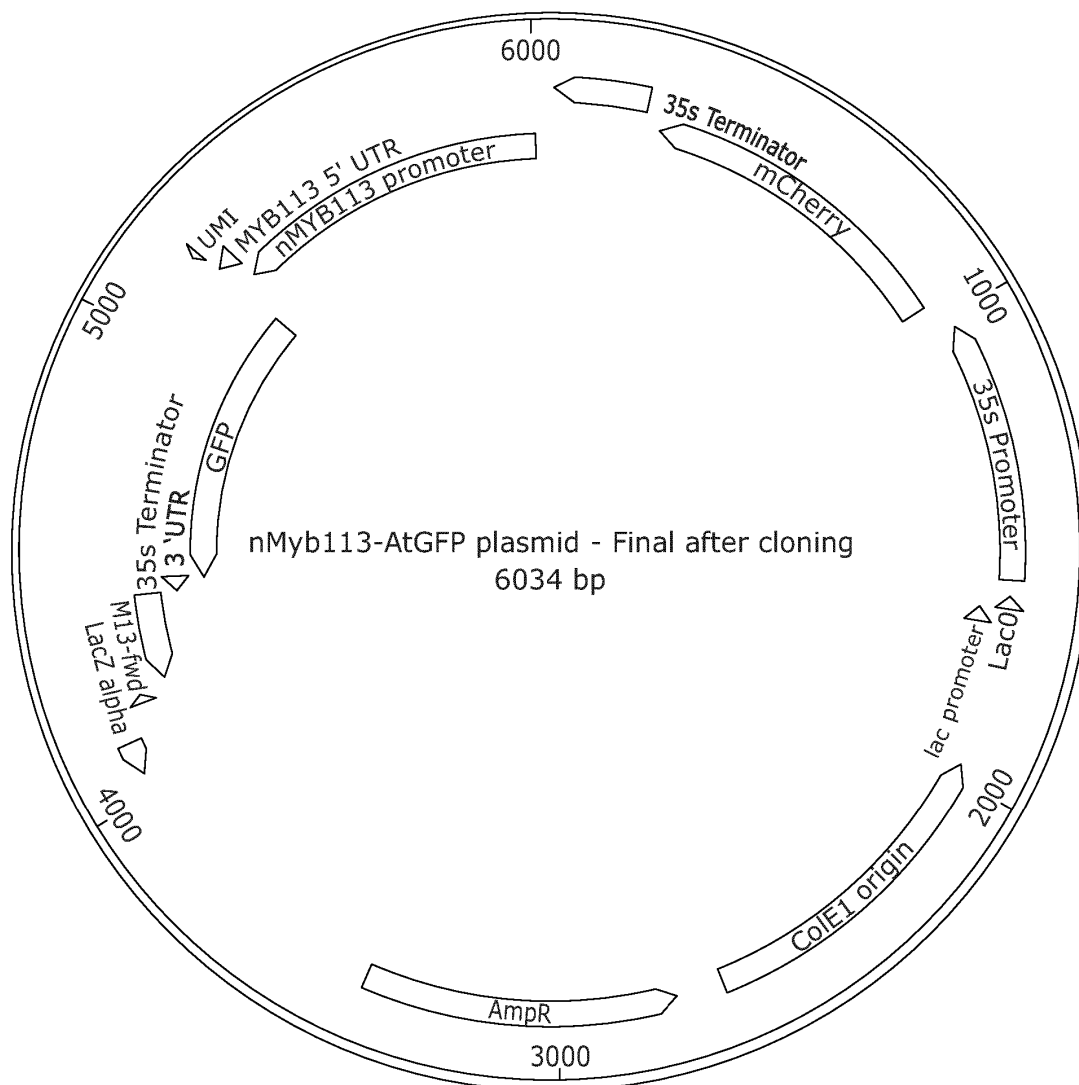


Figure 3

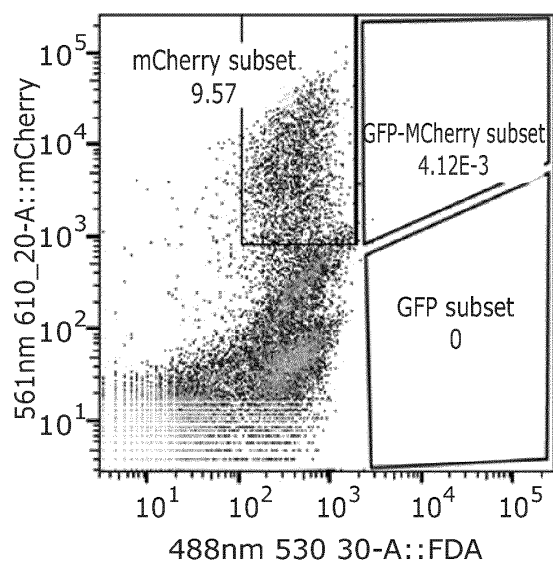


Figure 4(a)

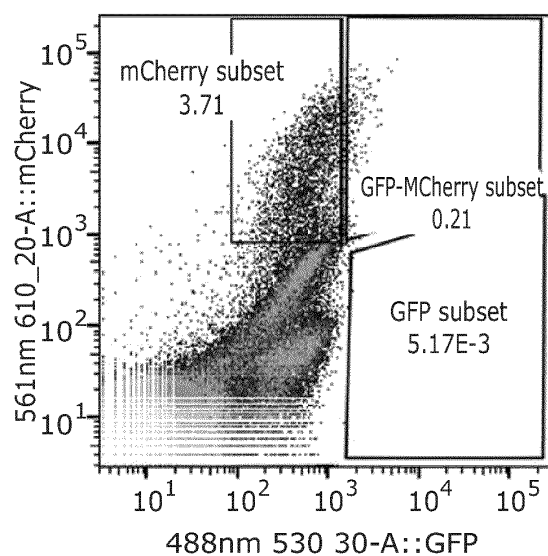


Figure 4(b)

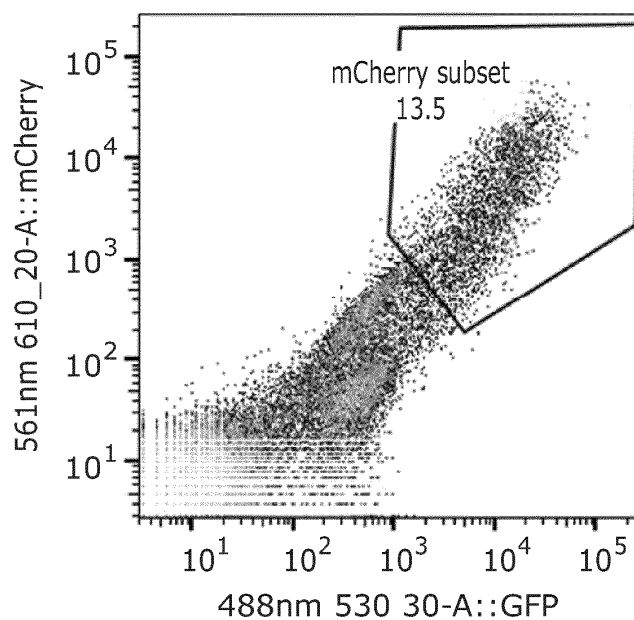


Figure 4(c)

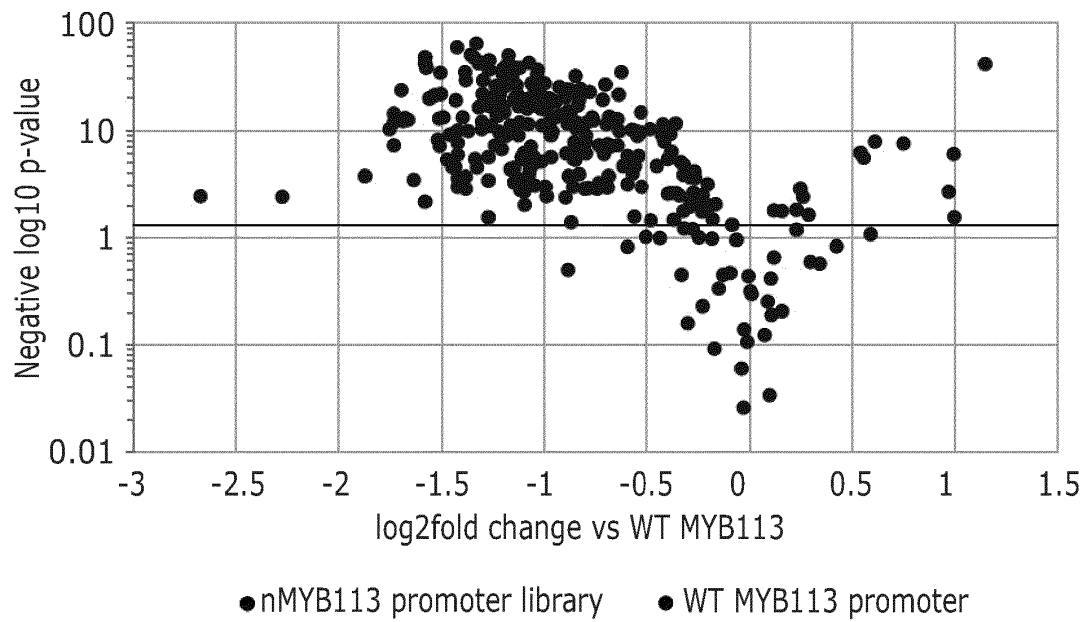


Figure 5

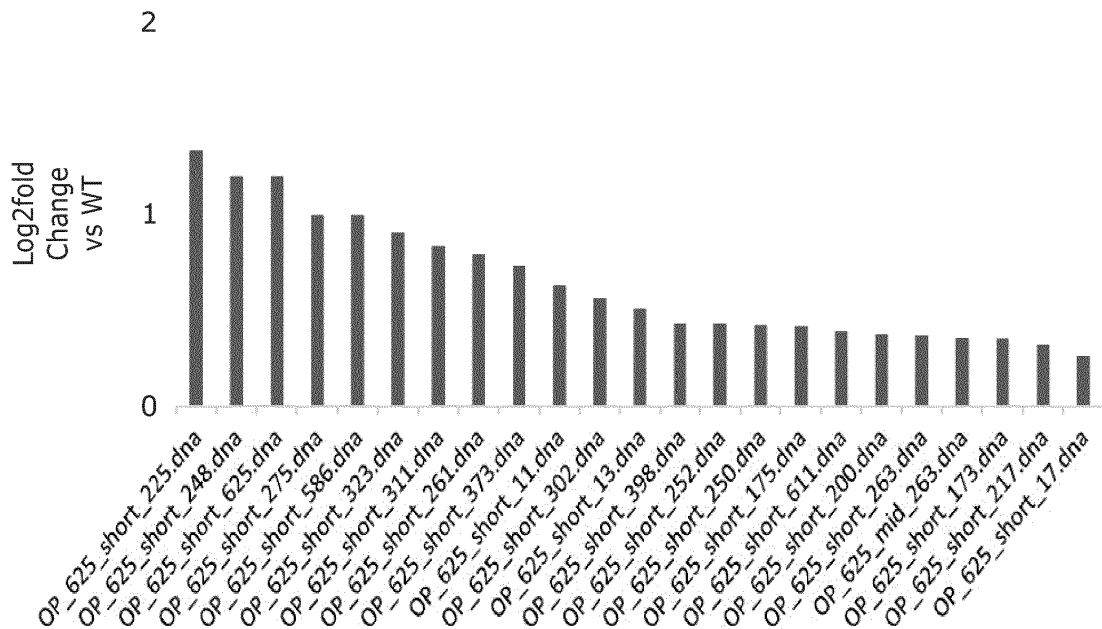


Figure 6

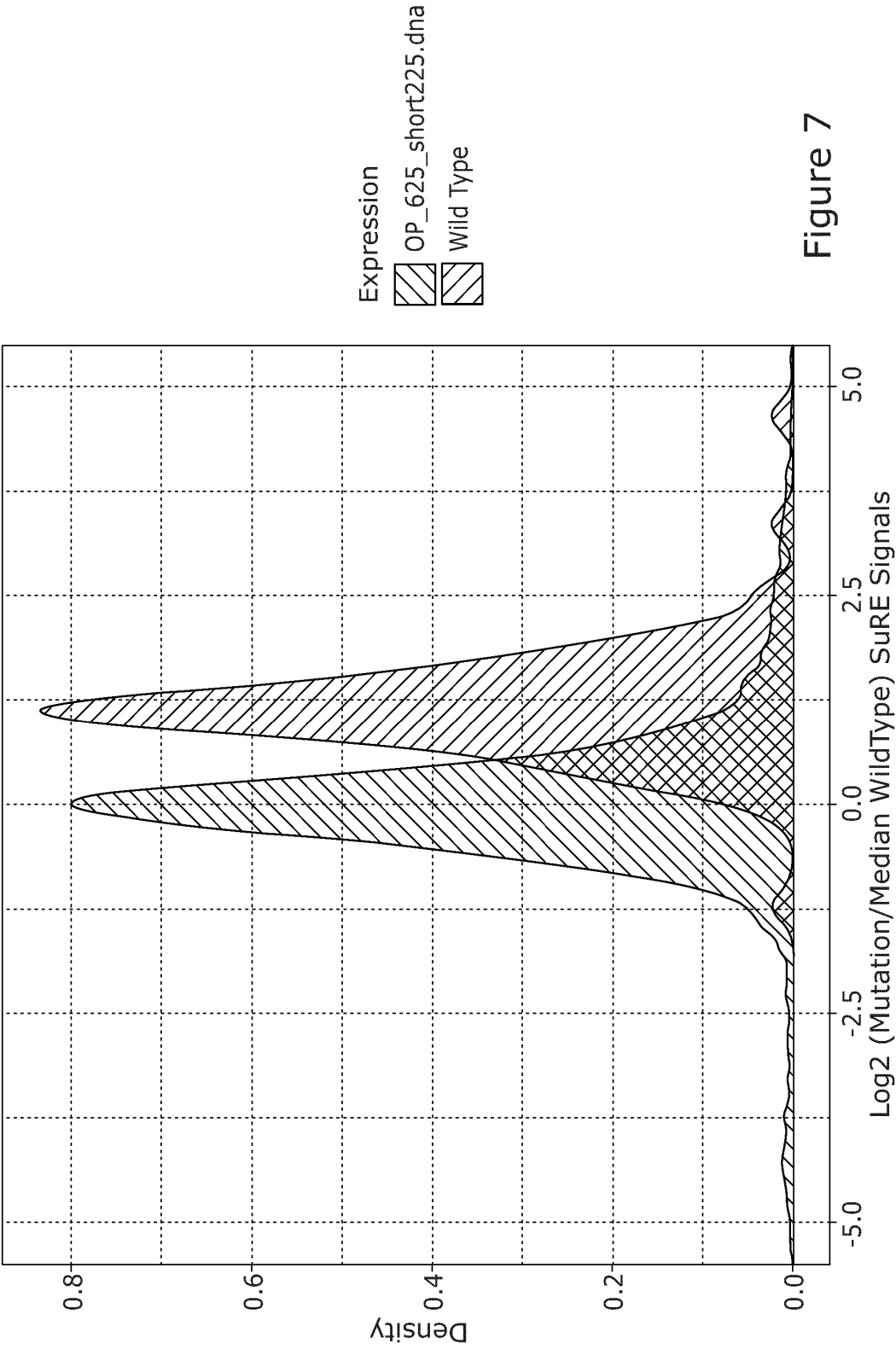
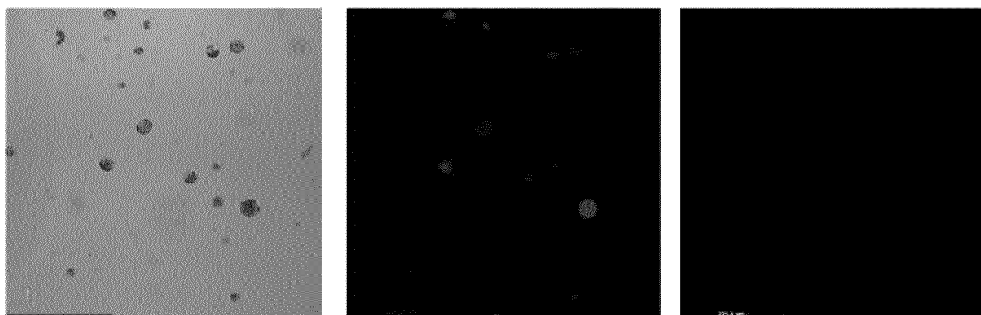


Figure 7

pMYB113 (WT)-GFP//35S-mCherry (transfection control)



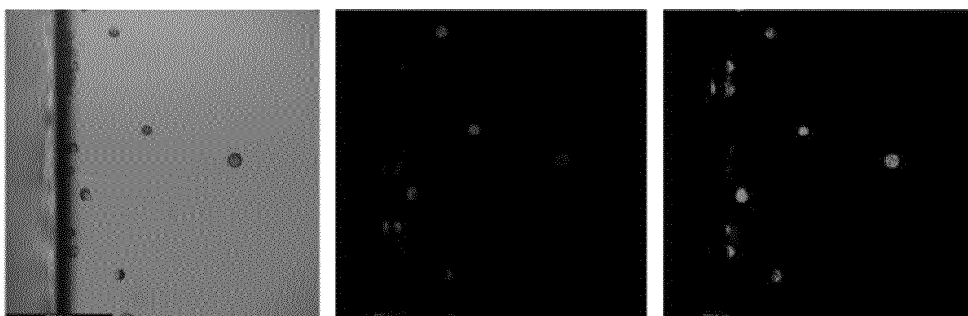
Bright Field

Red filter

Green filter

Figure 8(a)

pMYB113 (variant A2.1DEL)-GFP//35S-mCherry (transfection control)



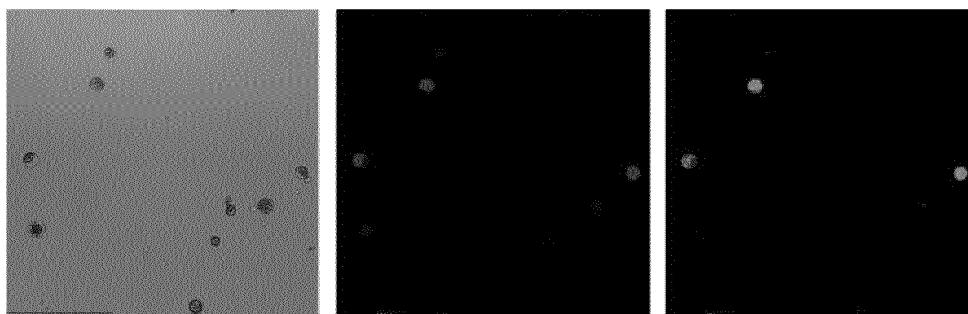
Bright Field

Red filter

Green filter

Figure 8(b)

35S-GFP (expression control) //35S-mCHERRY (transfection control)



Bright Field

Red filter

Green filter

Figure 8(c)

PPO2_-1 pre-aligned sequence	caaccttcagattgtgtttccgattaactaatcggtggatcgggctgaaattgtactg 60
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PPO2_-1 pre-aligned sequence	agtgttcatgacatcttggtgattgatttaaagggtggtgatcggattcggagggttagca 120
variant_50981	agtgttcatgacatcttggtgattgatttaaagggtggtgatcggattcggagggttagca 120

PPO2_-1 pre-aligned sequence	agattctgttttaggtcccgaaacagtagctgggtttgggtggtgtttctttctatttatc 180
variant_50981	agattctgttttaggtcccgaaacagtagctgggtttgggtggtgtttctttctatttatc 180

PPO2_-1 pre-aligned sequence	ttttggtggtgtagctattgtttgttctcttttggcacttattgtgtagccattagagga 240
variant_50981	ttttggtggtgtagctattgtttgttctcttttggcacttattgtgtagccattagagga 240

PPO2_-1 pre-aligned sequence	ataattgtaactctcttattgttatagtgaagcaattcggatcttgtcgatcccggtggt 300
variant_50981	ataattgtaactctcttattgttatagtgaagcaattcggatcttgtcgatcccggtggt 300

PPO2_-1 pre-aligned sequence	gttaccttcgttttgaaggatttttccacgttaaacttggtgttctttatttttagatttt 360
variant_50981	gttaccttcgttttgaaggatttttccacgttaaacttggtgttctttatttttagatttt 360

PPO2_-1 pre-aligned sequence	cgttttcatatttttcgtcataacacaaattggatatgtttattttctgtatatttaaac 420
variant_50981	cgttttcatatttttcgtcataacacaaattggatatgtttattttctgtatatttaaac 420

PPO2_-1 pre-aligned sequence	caaaatagaagagttagtccttttgctacttaacagaaatatttccttggtgataacatat 480
variant_50981	caaaatagaagagttagtccttttgctacttaacagaaatatttccttggtgataacatat 480

PPO2_-1 pre-aligned sequence	taacagttatgttatgggagctaccaacaaaaattaacaaaacttcaaattcttatgcac 540
variant_50981	taacagttatgttatgggagctaccaacaaaaattaacaaaacttcaaattcttatgcac 540

Figure 9
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PPO2_-1 pre-aligned sequence ttaagagtatatattcttgactcacttgatctttactattcttgatgccaatgaaaata 600
variant_50981 ttaagagtatatattcttgactcacttgatctttactattcttgatgccaatgaaaata 600

PPO2_-1 pre-aligned sequence atgttagtcttttgttacttcacaaaatctttcatgtttatcaaaagagaataatgat 660
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PPO2_-1 pre-aligned sequence gatagcatattaatagctattatttgggagctaccaagaaaaatccaataaaaattctc 720
variant_50981 gatagcatattaatagctattatttgggagctaccaagaaaaatccaataaaaattctc 720

PPO2_-1 pre-aligned sequence taacaaattcaaatgtttcagcagatagaggagcaaacctttctagtatattagaga 780
variant_50981 taacaaattcaaatgtttcagcagatagaggagcaaacctttctagtatattagaga 780

PPO2_-1 pre-aligned sequence aacccaaaatgcaccagtttgagcatgaactaacctgcgccagtttcagcctctaagga 840
variant_50981 aacccaaaatgcaccagtttgagcatgaactaacctgcgccagtttcagcctctaagga 840

PPO2_-1 pre-aligned sequence gggagtatactatcttctagatttcttgatgattgtgtctctcgagatgttctttggcga 900
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PPO2_-1 pre-aligned sequence tagctacttgatatttgttctgtttgttgaggacttgacatggattagatgattgtctt 960
variant_50981 tagctacttgatatttgttctgtttgttgaggacttgacatggattagatgattgtctt 960

PPO2_-1 pre-aligned sequence gtctctaaatatacctttgtaactcctattgggtgtacttgggtgcgactttatttca 1020
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PPO2_-1 pre-aligned sequence gaacttcacgaccttgaaaattgaaacatccagatcatgtaccaccctcccactttta 1080
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variant_50981 ccttgtcagttcccttcattttcaccaacatcagattcaaaaaagagaagtataaaaat 1140

Figure 9 (Continued)
SUBSTITUTE SHEET (RULE 26)

PP02_-1 pre-aligned sequence cagaaattaatcaagacaaactaatgtgaaaagtaagtctatggtaaataacacaataa 1200
variant_50981 cagaaattaatcaagacaaactaatgtgaaaagtaagtctatggtaaataacacaataa 1200

PP02_-1 pre-aligned sequence tctctggaccattgacaaacaaagacaaactcatcataaaataaaacgagtttgaccaa 1260
variant_50981 tctctggaccattgacaaacaaagacaaactcatcataaaataaaacgagtttgaccaa 1260

PP02_-1 pre-aligned sequence ctaatgaaattaagtatatgatgtggctttatgttattttctctgtacatatattcaat 1320
variant_50981 ctaatgaaattaagtatatgatgtggctttatgttattttctctgtacatatattcaat 1320

PP02_-1 pre-aligned sequence tcaaatagactatatgttgtattggaataaattaattaaccacacacatgtaagcatg 1380
variant_50981 tcaaatagactatatgttgtattggaataaattaattaaccacacacatgtaagcatg 1380

PP02_-1 pre-aligned sequence gcgtaacttcaaaccacaaacaaaagggttcagctgggaaagtgaatatatacaagttca 1440
variant_50981 gcgtaacttcaaaccacaaacaaaagggttcagctgggaaagtgaatatatacaagttca 1440

PP02_-1 pre-aligned sequence ctccccccagtgagcgaggtattccactcgtgaagatggataaagtcatttcattttcc 1500
variant_50981 ctccccccagtgagcgaggtattccactcgtgaagatggataaagtcatttcattttcc 1500

PP02_-1 pre-aligned sequence atcaataggccggcttcacgcggactcaacaagagaaaaatgaacaagaggagatgtta 1560
variant_50981 atcaataggccggcttcacgcggactcaacaagagaaaaatgaacaagaggagatgtta 1560

PP02_-1 pre-aligned sequence acgttcgataacataaaatatgataaatagagggtatataaggttcgatgtgtttctgaa 1620
variant_50981 acgttcgataacataaaatatgataaatagagggtatataaggttcgatgtgtttctgaa 1620

PP02_-1 pre-aligned sequence cgtggacaataatgtgaacgcgcgatgagcttgataaggcagagttcgcggggagttatac 1680
variant_50981 cgtggacaataatgtgaacgcgcgatgagcttgataaggcagagttcgcggggagttatac 1680

Figure 9 (Continued)

PPO2_-1 pre-aligned sequence tagtttgccacatgttcacggaattggcaagaatgatcaaagcccgctgttactttcca 1740
variant_50981 tagtttgccacatgttcacggaattggcaagaatgatcaaagcccgctgttactttcca 1740

PPO2_-1 pre-aligned sequence gctggcgataacagaactgttggaggacattggtttggaagatgaagagactatttcggt 1800
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PPO2_-1 pre-aligned sequence gactctggtaccaagaaggtggtgaacgtatatattgaaaatgtggagatcaagct 1860
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PPO2_-1 pre-aligned sequence tgaggattgttaaagtttcaattgaatctgttgagattacaactttcatatgtttatggt 1920
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PPO2_-1 pre-aligned sequence tccttgttctgttttttacttttgtttttccatgtaacttttctgttgaaatcagcttc 1980
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PPO2_-1 pre-aligned sequence atgcttgatttccttggagtggttatttaattcactaataaaatcagttactattatgtgg 2040
variant_50981 atgcttgatttccttggagtggttatttaattcactaataaaatcagttactattatgtgg 2040

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PPO2_-1 pre-aligned sequence taaaaataatgatgtttgccgtaaaatcgtttaaataatattattttatacaaatggt 2160
variant_50981 taaaaataatgatgtttgccgtaaaatcgtttaaataatattattttatacaaatggt 2160

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variant_50981 aaaaatattgatattttatttcaaatagacaaaaatattatgacatgtattttaaatgtgat 2220

PPO2_-1 pre-aligned sequence aatattagtagttaattacagacatttacatttaataattaaataaaaatttaggtctttt 2280
variant_50981 aatattagtagttaattacagacatttacatttaataattaaataaaaatttaggtctttt 2280

Figure 9 (Continued)
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PPO2_-1 pre-aligned sequence caaattatTTTTgtcactctagaagaaaaattattggatgcatacataataggagtcttc 2340
variant_50981 caaattatTTTTgtcactctagaagaaaaattattggatgcatacataataggagtcttc 2340

PPO2_-1 pre-aligned sequence gtttatttatttttagtttattgatggagtaatctttatagtaataaatcagaaattata 2400
variant_50981 gtttatttatttttagtttattgatggagtaatctttatagtaataaatcagaaattata 2400

PPO2_-1 pre-aligned sequence aaattaagggaatcgtagctcgaccctttgttccaattagcaaatgaggactgcttata 2460
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PPO2_-1 pre-aligned sequence atataaaa-----taaaaaaaacatgtagaattactcaatctttgtacaaata 2520
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PPO2_-1 pre-aligned sequence ttcaagtcgagggttaaatagacaaaaataatagaatcataagtggaccattattttta 2580
variant_50981 ttcaagtcgagggttaaatagacaaaaataatagaatcataagtggaccattattttta 2580

PPO2_-1 pre-aligned sequence tataaaccgattttttttctttatttattgttgaggagacactatttgtatgagacctaat 2640
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PPO2_-1 pre-aligned sequence ctataattatattgatcaccaatttatatttaatttaaataaacatcaaaattataatttt 2820
variant_50981 ctataattatattgatcaccaatttatatttaatttaaataaacatcaaaattataatttt 2820

Figure 9 (Continued)

PPO2_-1 pre-aligned sequence acgatctattaacttatcatgacttattttttaagttaaaaataaaaaataaatctttaa 2880
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variant_50981 cttctaacttataactaataaaactataagtttatccaaaatgctcccagactattttta 2940

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PPO2_-1 pre-aligned sequence gtctctctctatatatatggatgacctatttgcatttttgcgtgttacttatattttaa 3060
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PPO2_-1 pre-aligned sequence tatctaaccaaaatttttaaaaaataatatatccatttagtgacccaccactcagaccga 3360
variant_50981 tatctaaccaaaatttttaaaaaataatatatccatttagtgacccaccactcagaccga 3360

PPO2_-1 pre-aligned sequence cccgctaaaaatgtaattattaaccttttttatatttaaaagaatactttcttatttctt 3420
variant_50981 cccgctaaaaatgtaattattaaccttttttatatttaaaagaatactttcttatttctt 3420

Figure 9 (Continued)
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PPO2_-1 pre-aligned sequence aaaagttggattagaaataaaaaatcatatcaacagattttaattaaaaaatcaattaa 3480
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PPO2_-1 pre-aligned sequence atcaaaattagagtaaatttttagaataaaaaattacaattaataagtatatgagatat 3600
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PPO2_-1 pre-aligned sequence tatctcaacggttcaattatctttctatgaacattcatttccgacaactgggtactaaaag 3660
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PPO2_-1 pre-aligned sequence agctagaagtctgattacagatttagttaattcaacaatatttacttaataatatatt 3840
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PPO2_-1 pre-aligned sequence tatatagtaatttttttataaaatatatacaaattaagctaagaattcaattactaac 3900
variant_50981 tatatagtaatttttttataaaatatatacaaattaagctaagaattcaattactaac 3900

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variant_50981 cccttaaaattgtattataaattcaatgttaaaattttaatttctcccgtgcttaacatt 3960

Figure 9 (Continued)

PPO2_-1 pre-aligned sequence acttatcaaatttttgtttctatgtagaaaagtactactactcttttgactcgtctagat 4020
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PPO2_-1 pre-aligned sequence gtctctatagatctcctaataagactaaaatttccagttttaagattttcctcacaatt 4080
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Figure 9 (Continued)
SUBSTITUTE SHEET (RULE 26)

PPO2_-1 pre-aligned sequence ttccctctatctctaattatttgcgcgttttgaattgacgaatttaccattttatctcta 4620
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PPO2_-1 pre-aligned sequence ttaattatgaagtggatgaaaat-----ttctacatttttcaaaaataattagtc 4680
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PPO2_-1 pre-aligned sequence caagtaattaggacaaaaggagatttaattatgttcttctgtcaaccgacccaaccg 4800
variant_50981 caagtaattaggacaaaaggagatttaattatgttcttctgtcaaccgacccaaccg 4800

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PPO2_-1 pre-aligned sequence ttatattgttttacatattatataaggcaaggtatagccaaatgaattttcat 5033
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Figure 9 (Continued)

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WT_MYB113 promoter GGAGCAAAGATAATAGAAAATTATCTCACAAATTTTATAAAATTTATATATATGGCATGT 60
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OP625_225      GTGAAGCCTTCACAAATTATTGGAGGTTTATATAGAGAGTGCAGTGACTGCCATATTTT 120
WT_MYB113 promoter GTGAAGCCTTCACAAATTATTGGAGGTTTATATAGAGAGTGCAGTGACTGCCATATTTT 120
*****

OP625_225      ATATCCACGTTTAATTcgtgac-----tagataatgtggTTTTGCTATTGTTTAc 180
WT_MYB113 promoter ATATCCACGTTTAATTcATGCTGAATTTGCTAAAAATTAGTTTGTGTTTCTATTGTTTAG 180
***** ** * * * *****

OP625_225      gt-----atgttgattcttttTAGCAGCCAGACTCTTCGTTCTTTTAAATTACGTAT 240
WT_MYB113 promoter ACAAGAGAAATGGTTCAGTGCAGTTAGCAGCCAGACTCTTCGTTCTTTTAAATTACGTAT 240
***** * * * *****

OP625_225      AATAATAACAATGTCAATAAATCTGTTTGTACTTCTACATGGTTGTCTTTCTATTGCAA 300
WT_MYB113 promoter AATAATAACAATGTCAATAAATCTGTTTGTACTTCTACATGGTTGTCTTTCTATTGCAA 300
*****

OP625_225      CATTTCTTCAAAATATTACAAAAAAGAACTAAAGTTAAAAAGTTATAATAATGTTTT 360
WT_MYB113 promoter CATTTCTTCAAAATATTACAAAAAAGAACTAAAGTTAAAAAGTTATAATAATGTTTT 360
*****

OP625_225      GTTAAAAAGTTATGTATGTTCAACTAAAGTTATATATTTTCATTTTCTGGTTATTTTTGA 420
WT_MYB113 promoter GTTAAAAAGTTATGTATGTTCAACTAAAGTTATATATTTTCATTTTCTGGTTATTTTTGA 420
*****

OP625_225      TTACTAAAATATGTTTAAATAAAAATTGCAACAGATTAATTGAACTGTTATAACATTTGAT 480
WT_MYB113 promoter TTACTAAAATATGTTTAAATAAAAATTGCAACAGATTAATTGAACTGTTATAACATTTGAT 480
*****

OP625_225      CTATATGGACGAATCATGCAACTTTTGATTTTGTTTTATGAGCCGTTGTAATTTTTTTT 540
WT_MYB113 promoter CTATATGGACGAATCATGCAACTTTTGATTTTGTTTTATGAGCCGTTGTAATTTTTTTT 540
*****
```

Figure 10
SUBSTITUTE SHEET (RULE 26)

OP625_225

WT_MYB113 promoter

ATTTAATAAACTTTTAATTATCTACTGTTGCGTATTTTCGGTATAACTTTTTATATAATTT

600

OP625_225

WT_MYB113 promoter

AGAAATATTTATTTATTTAAATAAAGTTGTAATCGTTATTCGACGAATCATTGTAATATT

660

OP625_225

WT_MYB113 promoter

TGATTTTATTTTATAGACCCATGTAATTCCTTAGTTTATTTTGACTGAGCATTGTAACTTT

720

OP625_225

WT_MYB113 promoter

TATAATATTTAATATATACGACCTCATCACTCTGTATAAATTGTTATATAACTAATTTTT

780

OP625_225

WT_MYB113 promoter

AAAACTAAAATATATATTTAAATAAATTATTGCAACCGGTTTATTGAATCAAT

833

Figure 10 (Continued)

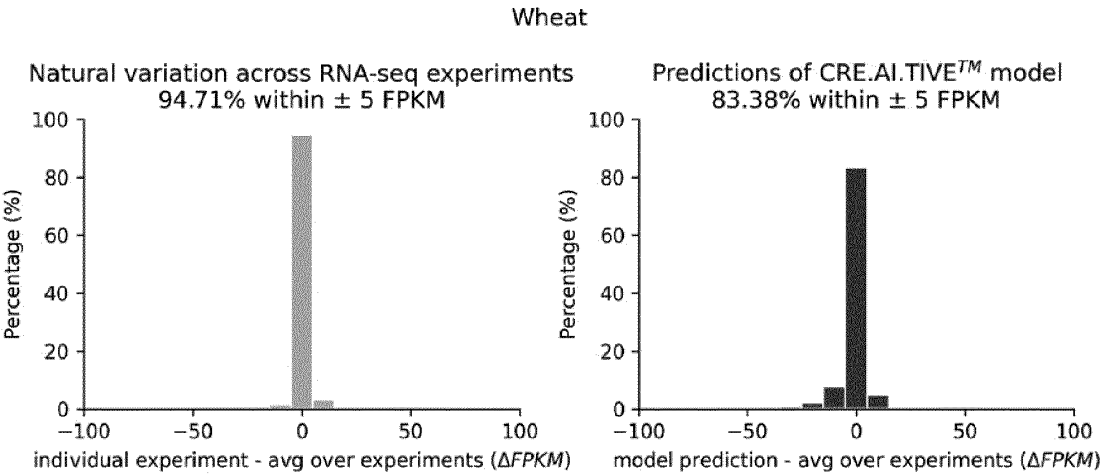


Figure 11(a)

Figure 11(b)

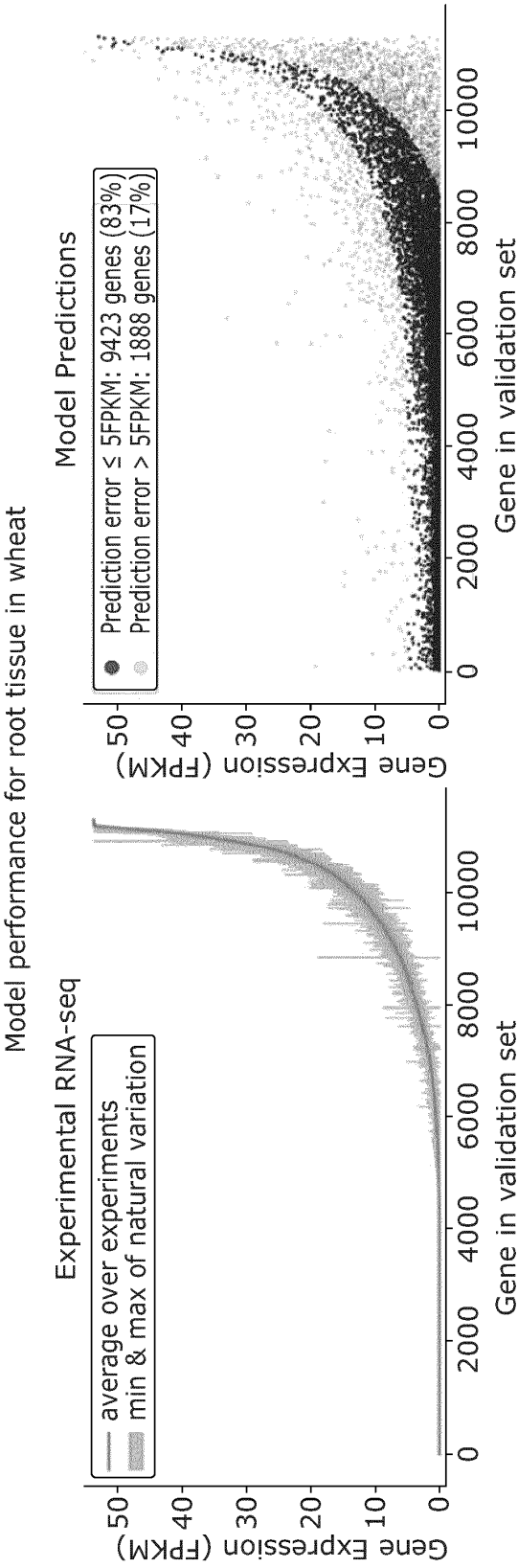


Figure 12(b)

Figure 12(a)

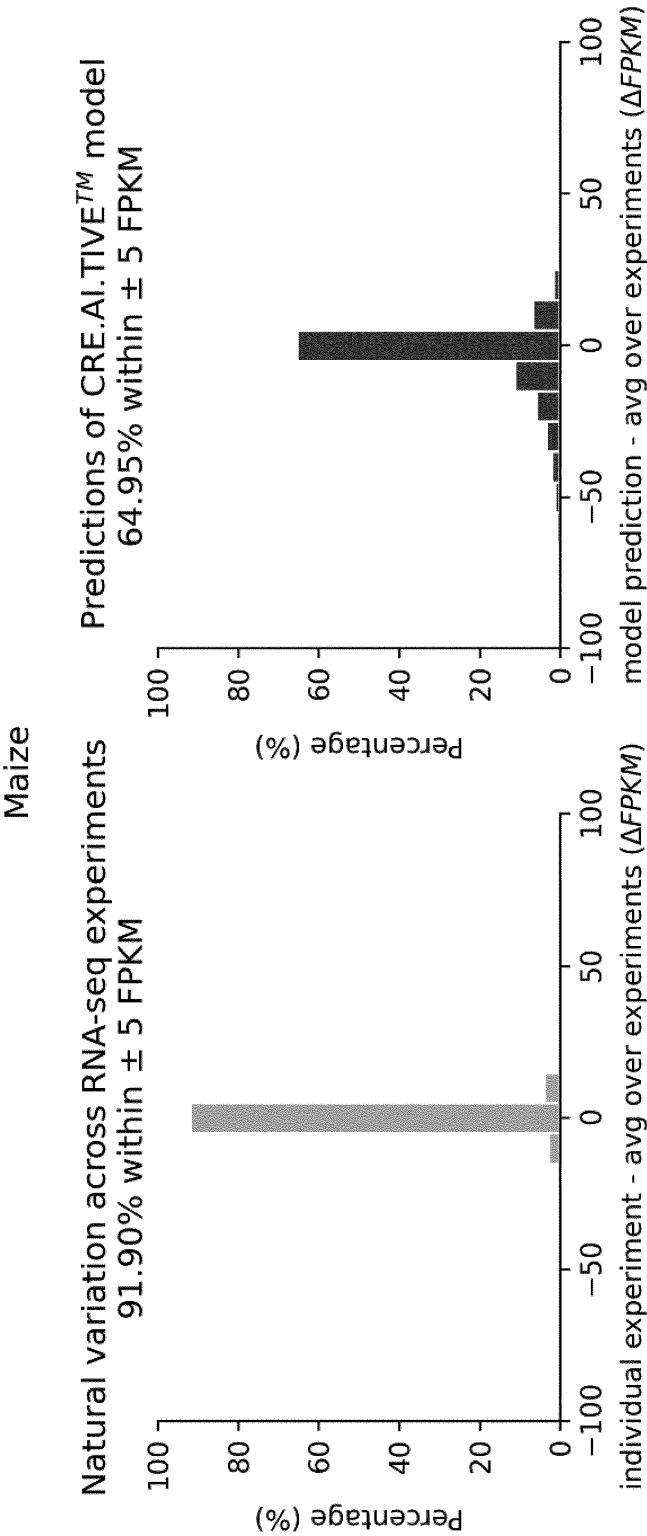


Figure 13(a)

Figure 13(b)

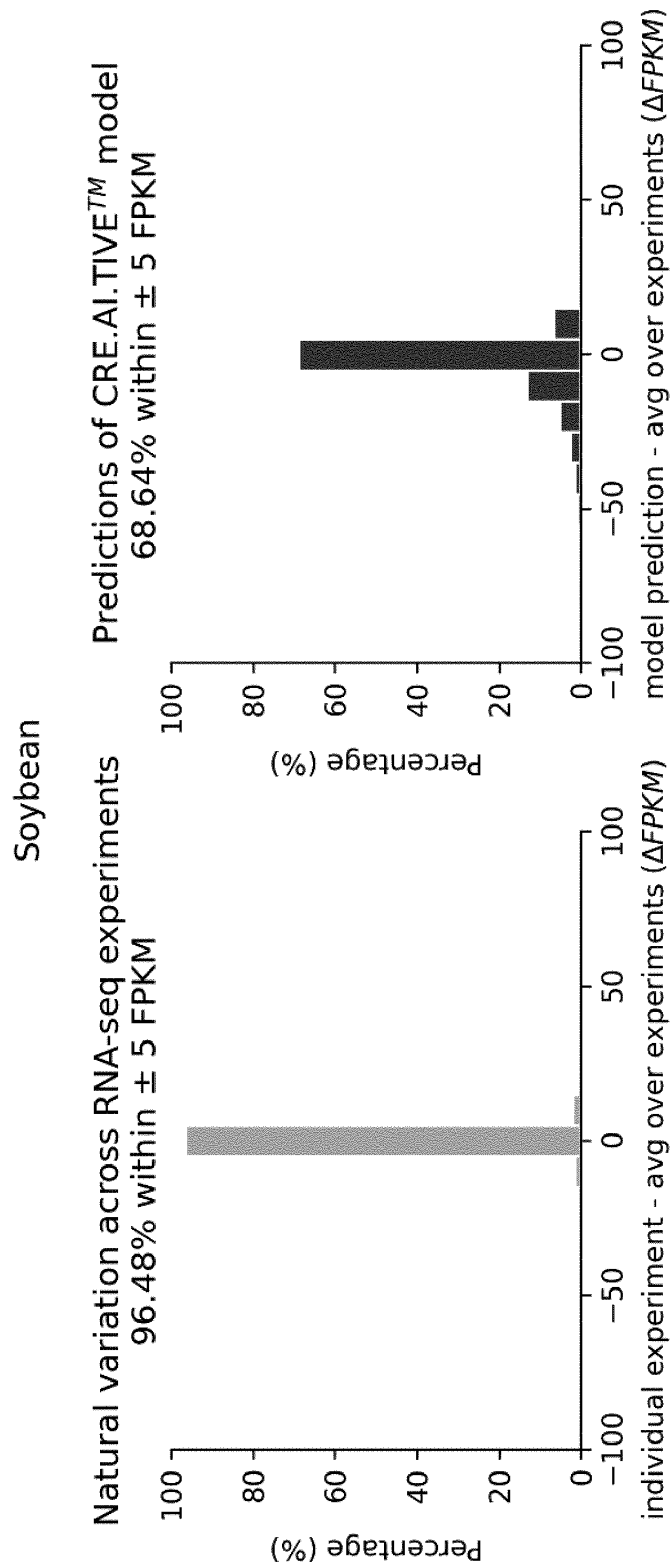


Figure 14(a)

Figure 14(b)