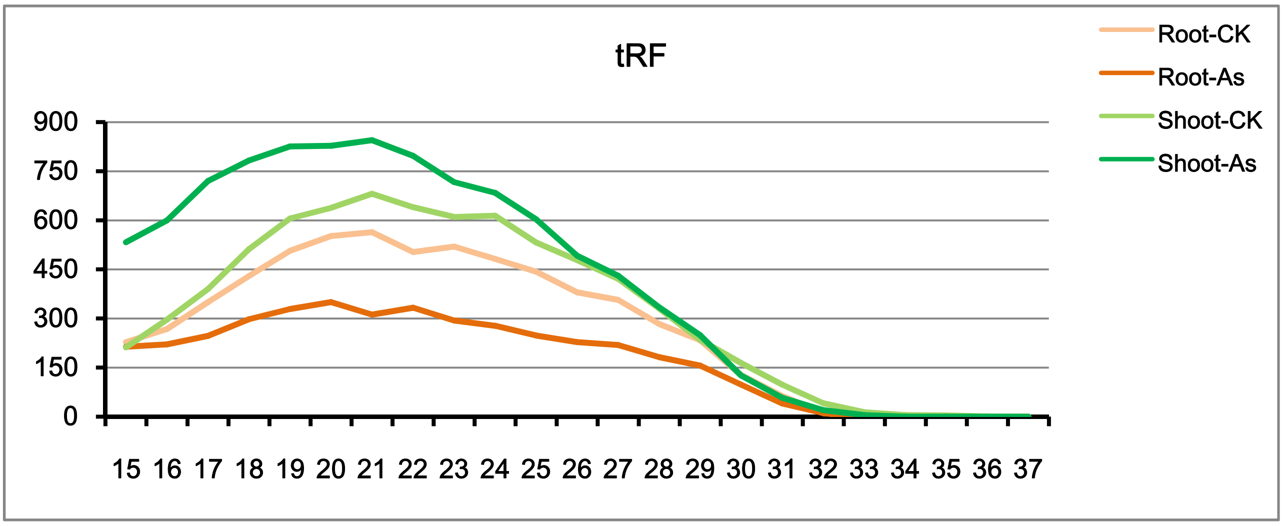
Figure S1 Sequence diversities of small RNAs mapped onto (**A**) tRNAs and (**B**) rRNAs in rice roots and shoots under arsenic stress. X axes indicate small RNAs (sRNAs) of different sequence length. Y axes measure the sRNA diversities, i.e. the numbers of different sRNA sequences. Root-CK: sRNAs in rice roots under normal growth condition. Root-As: sRNAs in rice roots under arsenic stress. Shoot-CK: sRNAs in rice shoots under normal growth condition. Shoot-As: sRNAs in rice shoots under arsenic stress. tRF: sRNAs mapped onto tRNAs. rRF: sRNAs mapped onto rRNAs.

A


tRF
Root-CK
Root-As
Shoot-CK
Shoot-As
900
750
600
450
300
150
0
15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37

B

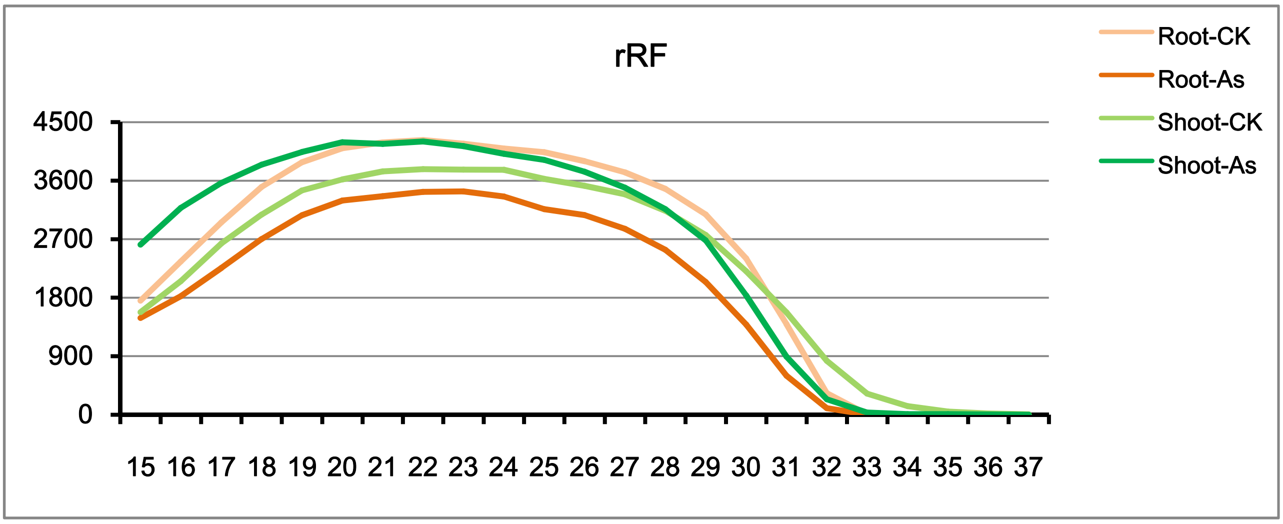
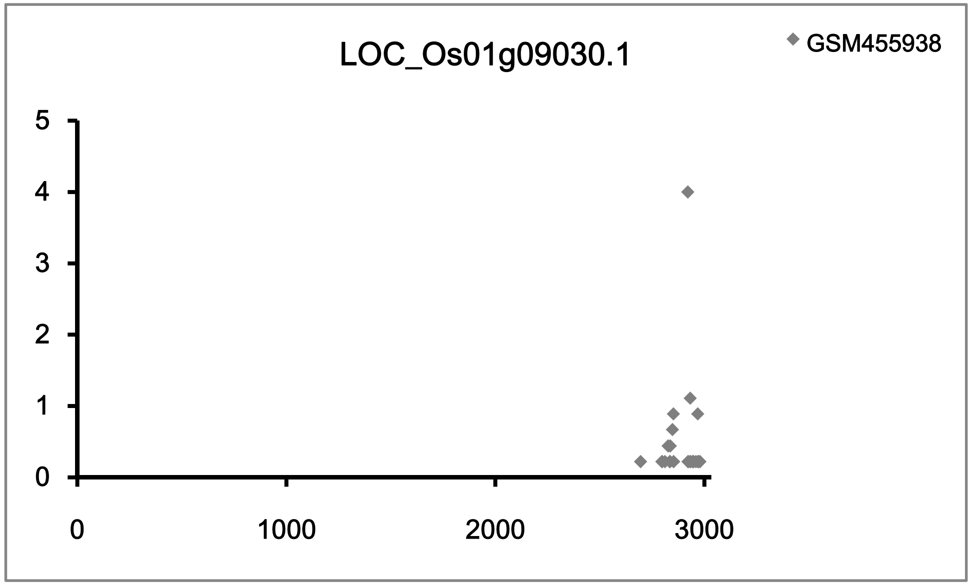
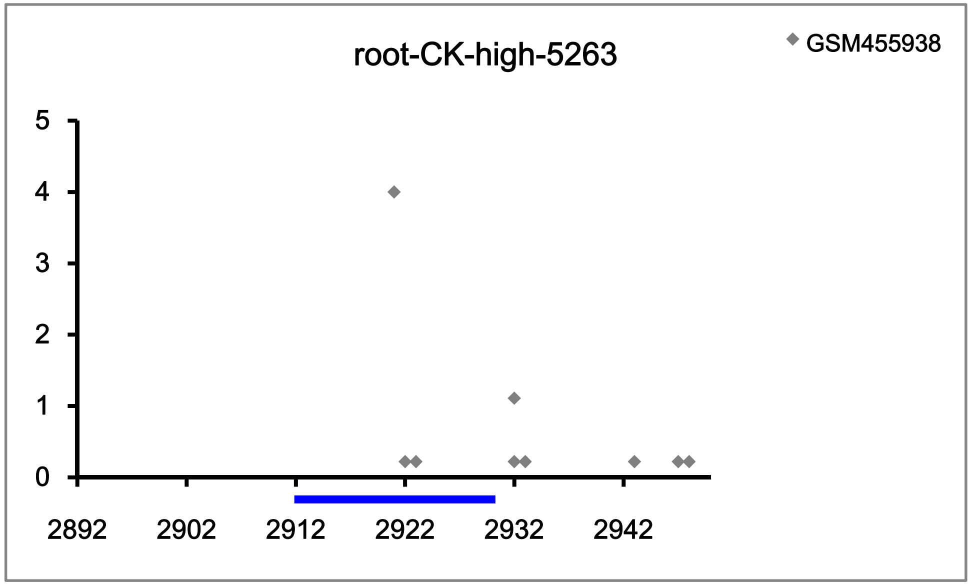
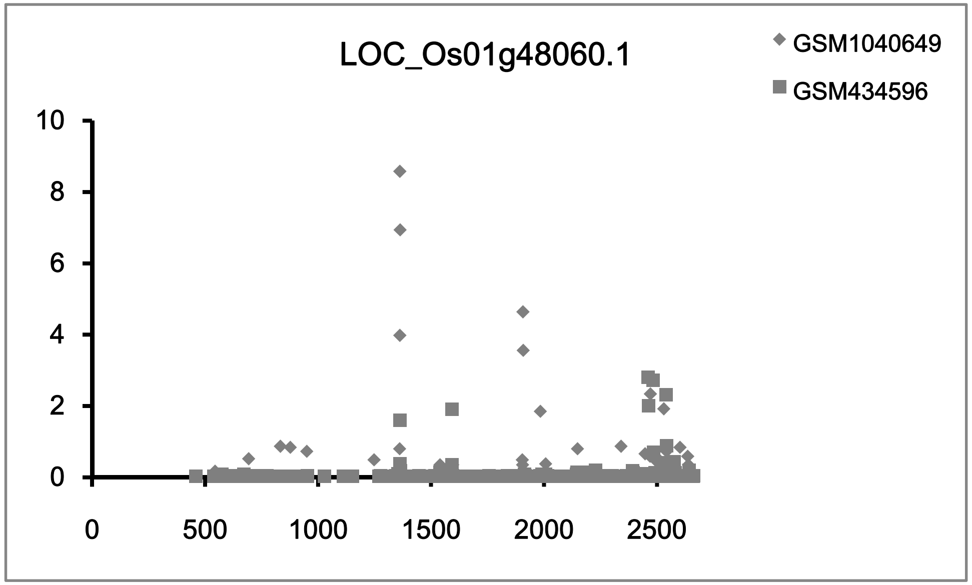
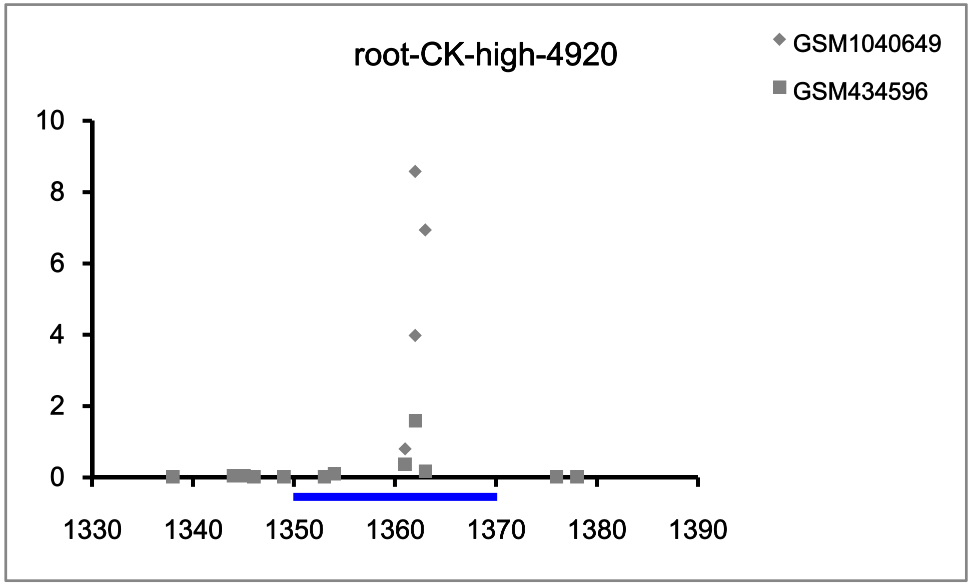

rRF
Root-CK
Root-As
Shoot-CK
Shoot-As
4500
3600
2700
1800
900
0
15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37

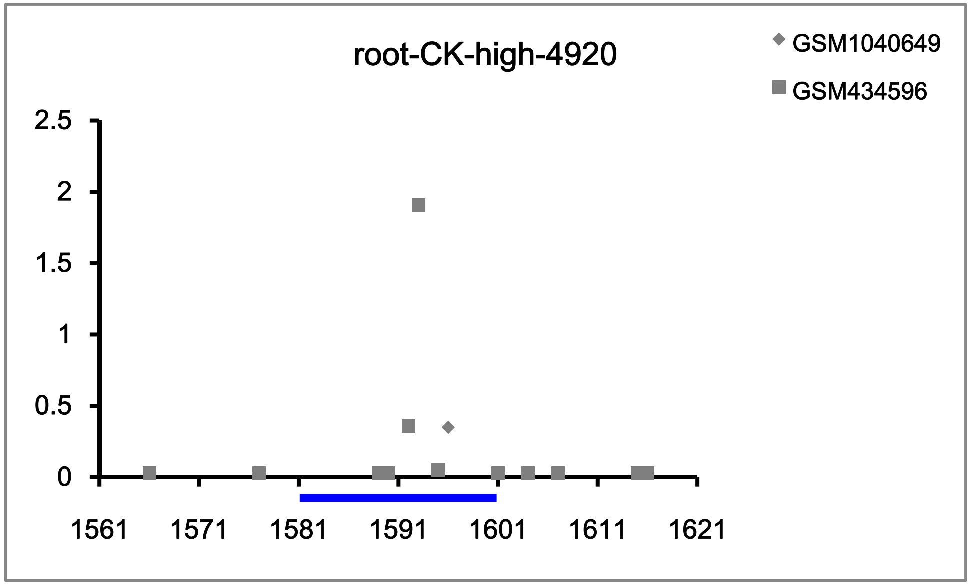
Figure S2 Degradome sequencing data-based evidence showing the protein-coding targets regulated by the arsenic stress-responsive small RNAs. On each page, the degradome sequencing evidence is displayed as target plots (t-plots) for each small RNA (sRNA)--target pairs. The first t-plot presents the global distribution of degradome signals along the full-length target transcript, with transcript ID and degradome-seq data set IDs shown on the top. The other panel(s) provide(s) a detailed view of degradome signals surrounding the predicted binding site (blue line) of the arsenic-responsive sRNA (ID shown on the top) on the target transcript, which clearly shows the degradome-seq evidence (marked by red arrowheads) supporting the regulatory relationship. For each t-plot, the Y axis measures the degradome signal intensity in RPM (reads per million), and the X axis indicate the position on the target transcript.

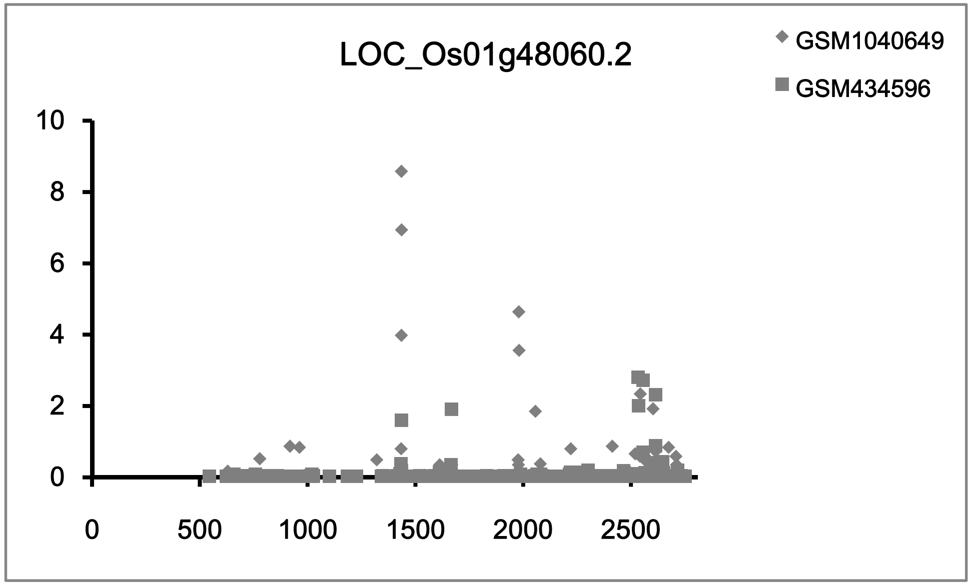

LOC_Os01g09030.1
◆ GSM455938
5
4
3
2
1
0
0
1000
2000
3000

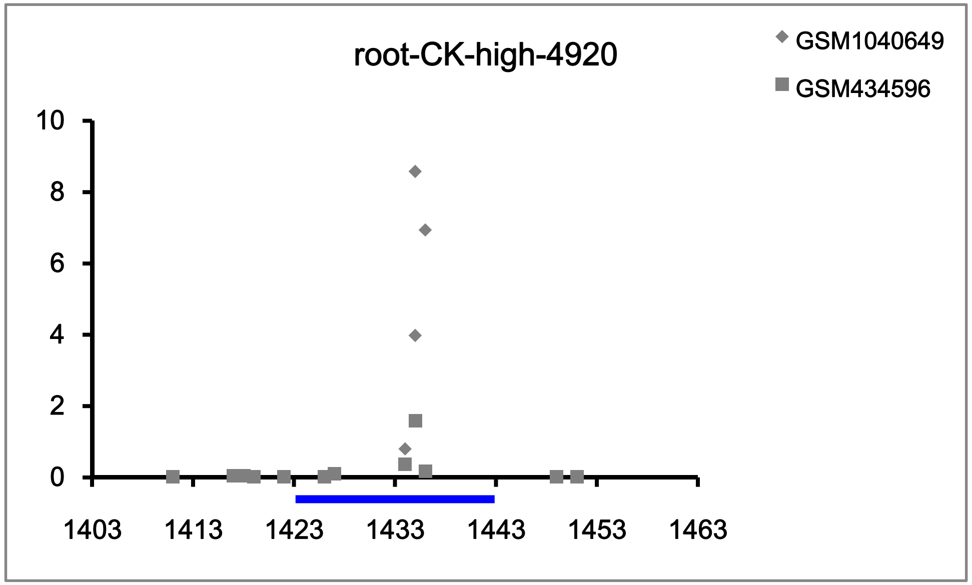

root-CK-high-5263
◆ GSM455938
5
4
3
2
1
0
2892
2902
2912
2922
2932
2942

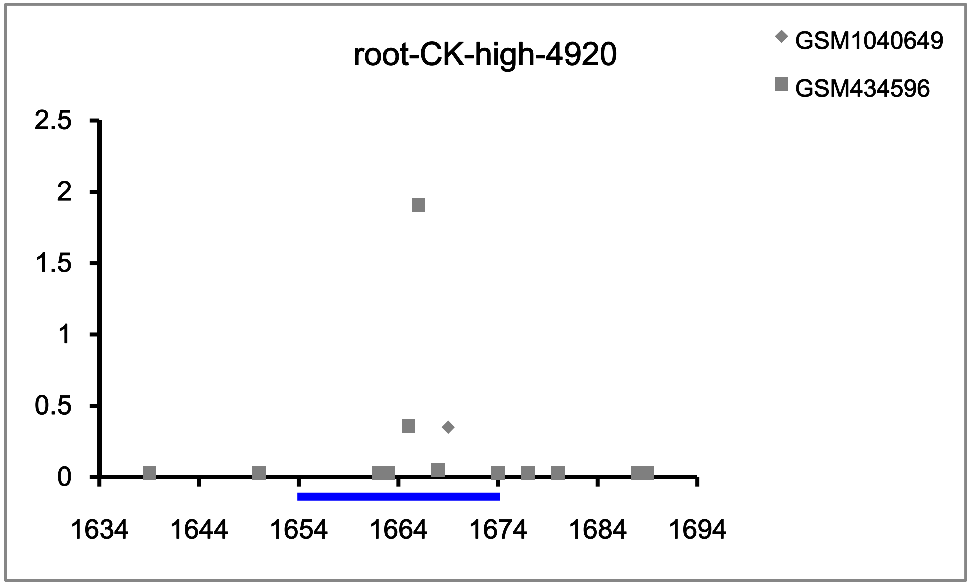

LOC_Os01g48060.1
GSM1040649
GSM434596
10
8
6
4
2
0
0
500
1000
1500
2000
2500

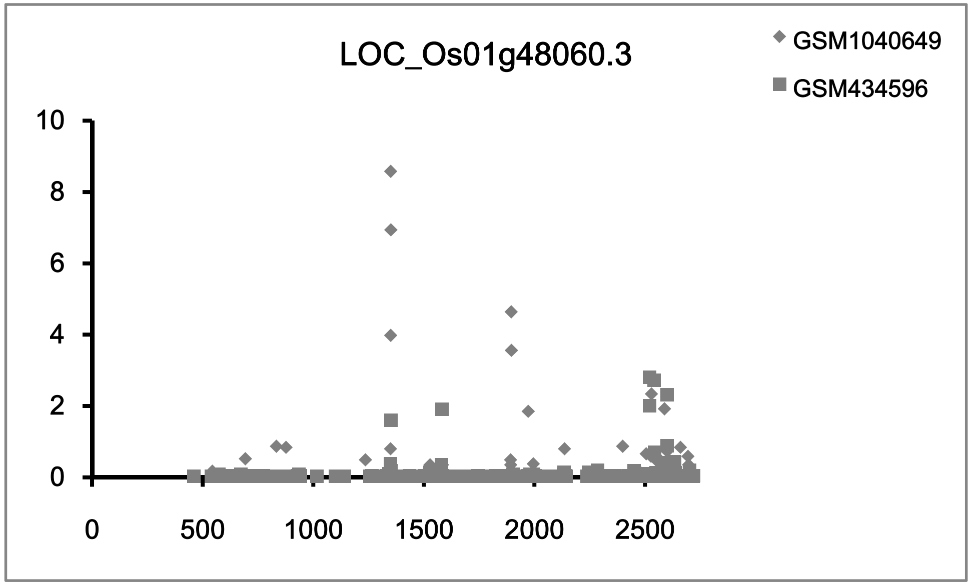

root-CK-high-4920
GSM1040649
GSM434596
10
8
6
4
2
0
1330
1340
1350
1360
1370
1380
1390

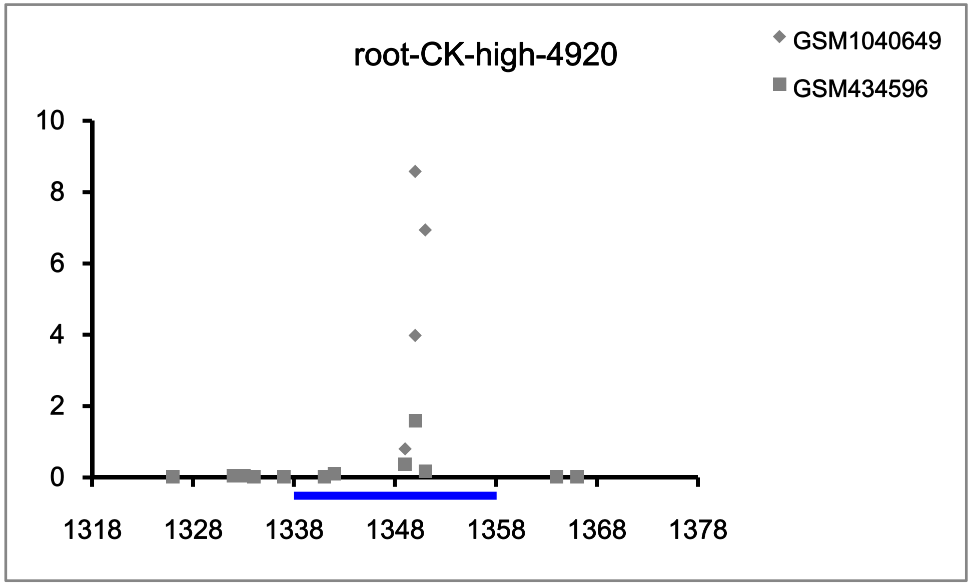

root-CK-high-4920
GSM1040649
GSM434596
2.5
2
1.5
1
0.5
0
1561
1571
1581
1591
1601
1611
1621

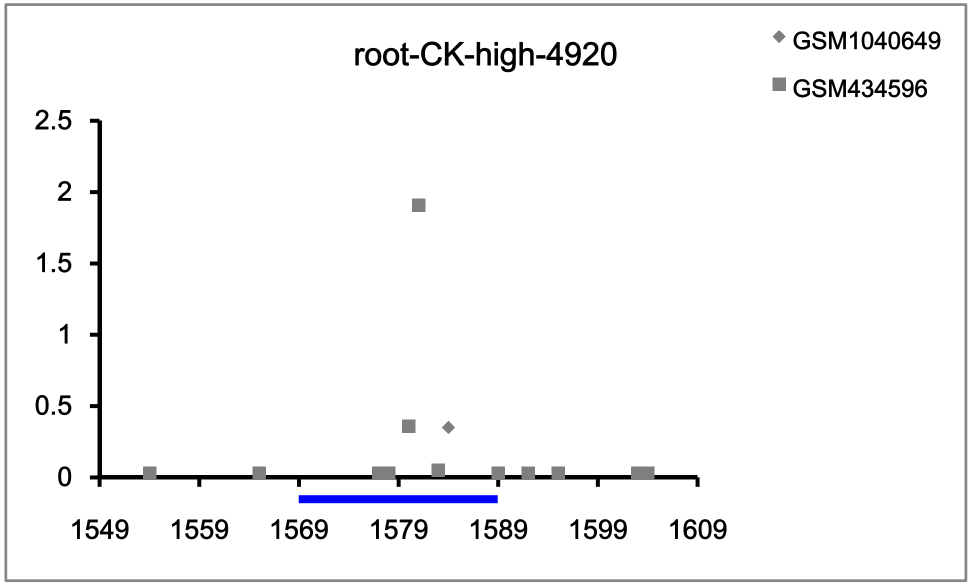

LOC_Os01g48060.2
◆ GSM1040649
■ GSM434596
10
8
6
4
2
0
0
500
1000
1500
2000
2500

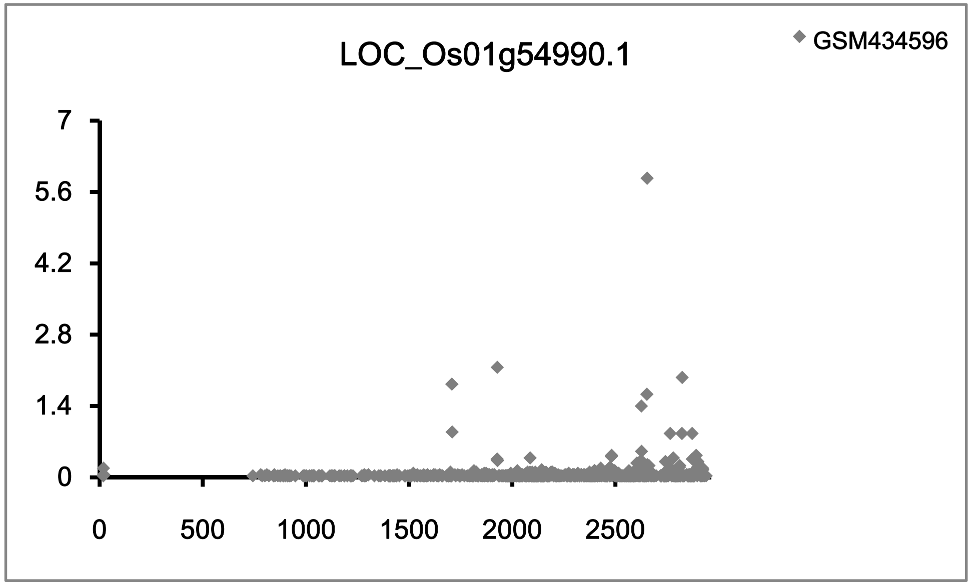

root-CK-high-4920
◆ GSM1040649
■ GSM434596
10
8
6
4
2
0
1403
1413
1423
1433
1443
1453
1463

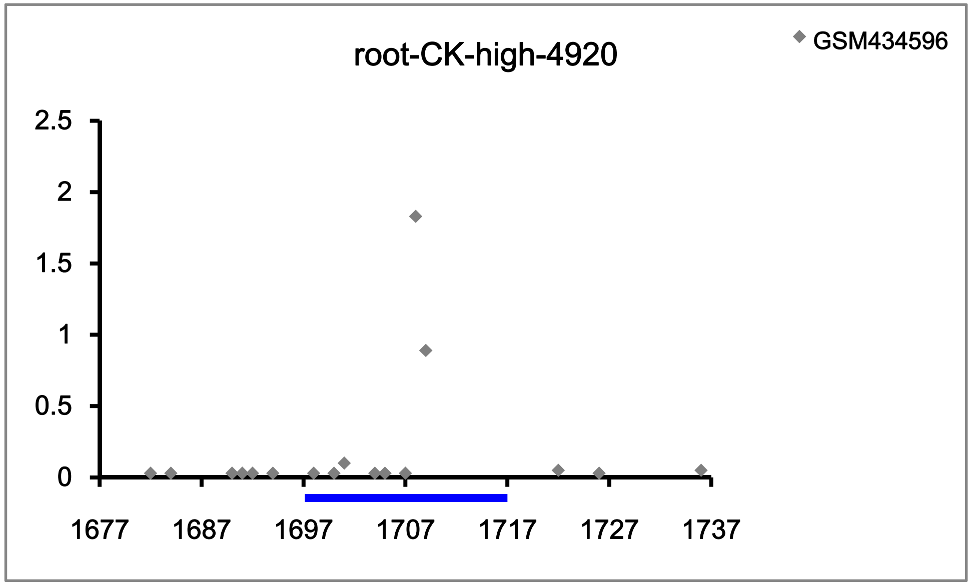

root-CK-high-4920
◆ GSM1040649
■ GSM434596
2.5
2
1.5
1
0.5
0
1634
1644
1654
1664
1674
1684
1694

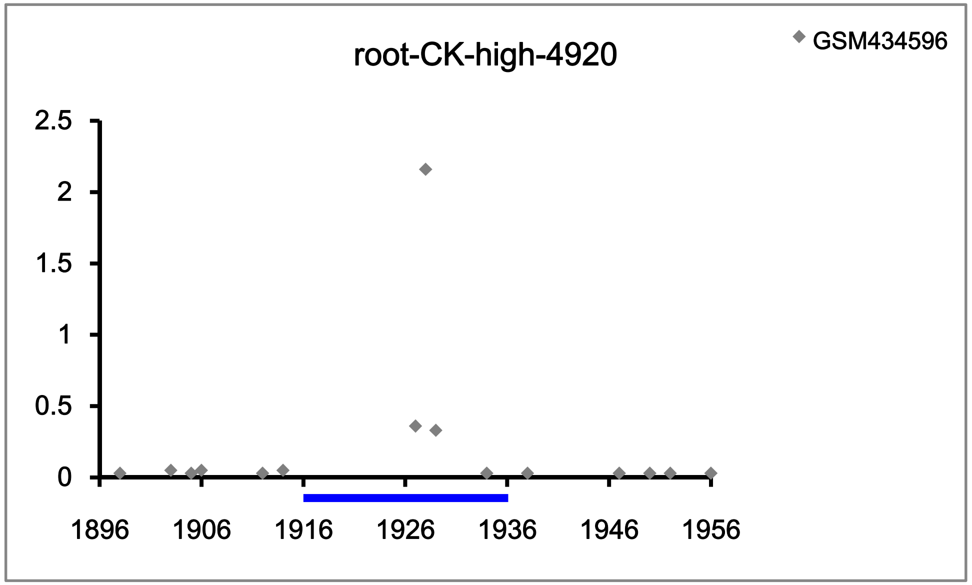

LOC_Os01g48060.3
GSM1040649
GSM434596
10
8
6
4
2
0
0
500
1000
1500
2000
2500

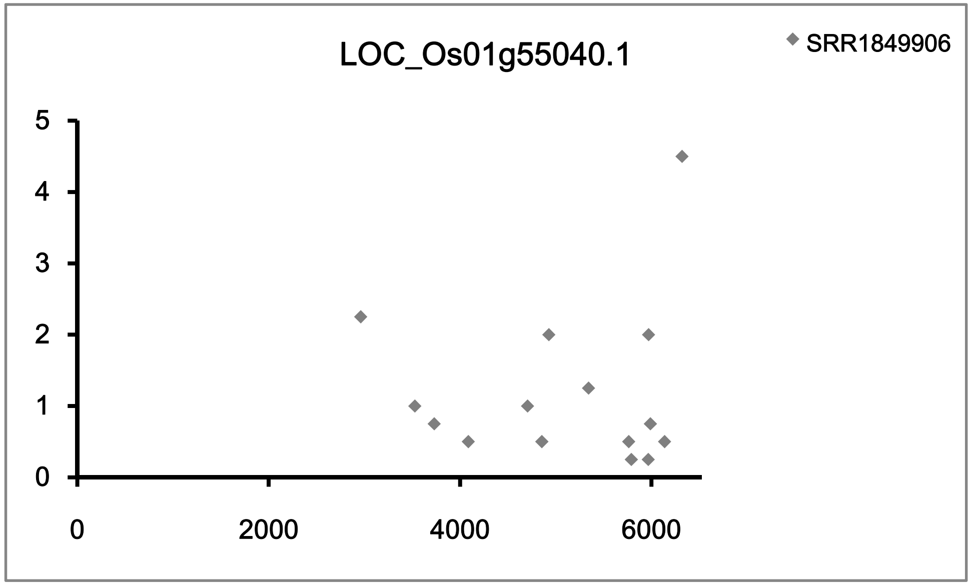

root-CK-high-4920
GSM1040649
GSM434596
10
8
6
4
2
0
1318
1328
1338
1348
1358
1368
1378

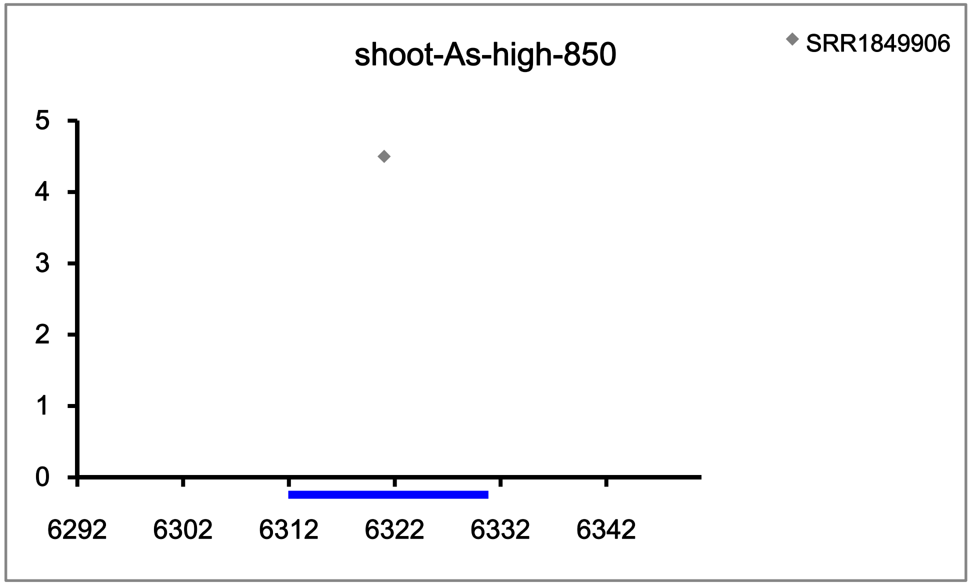

root-CK-high-4920
GSM1040649
GSM434596
2.5
2
1.5
1
0.5
0
1549
1559
1569
1579
1589
1599
1609

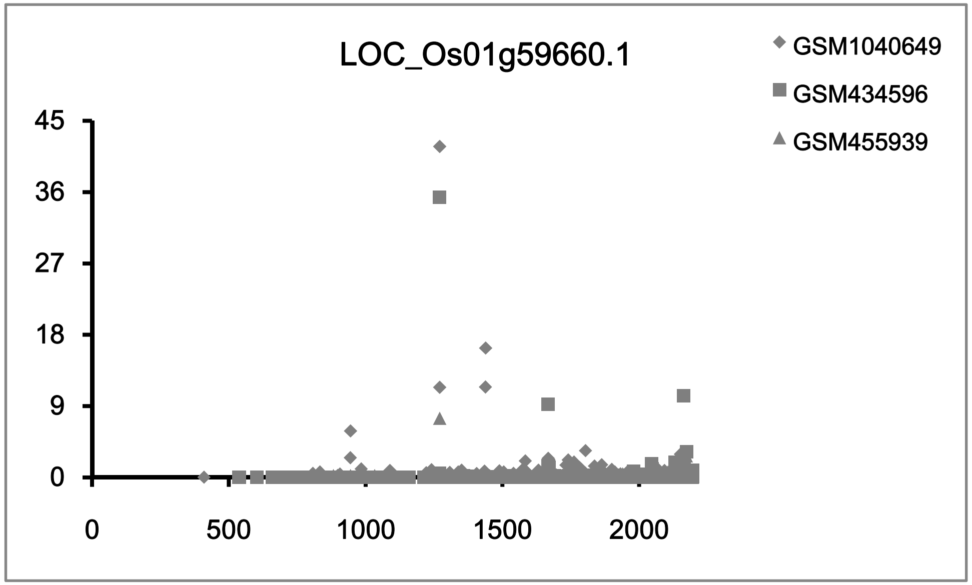

LOC_Os01g54990.1
GSM434596
7
5.6
4.2
2.8
1.4
0
0
500
1000
1500
2000
2500

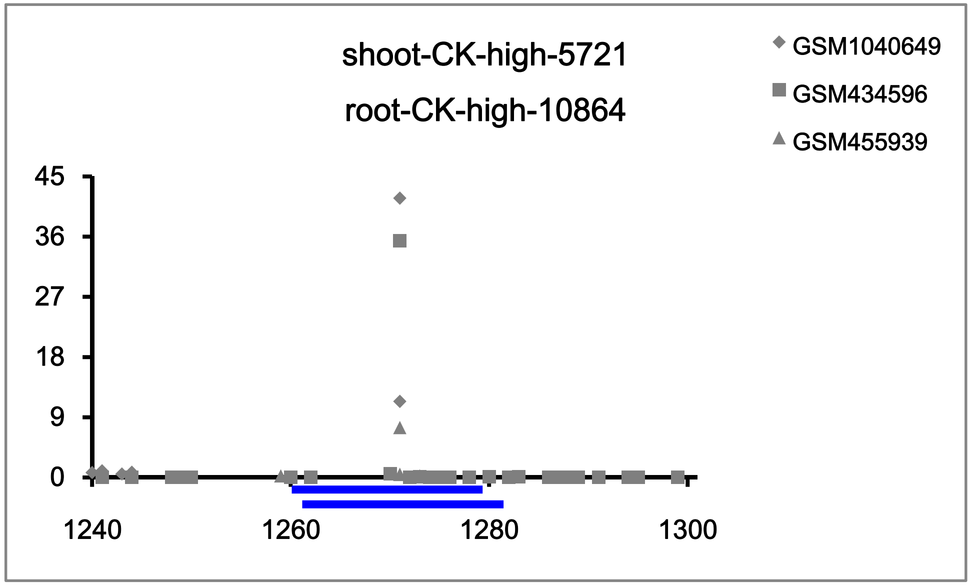

root-CK-high-4920
GSM434596
2.5
2
1.5
1
0.5
0
1677
1687
1697
1707
1717
1727
1737

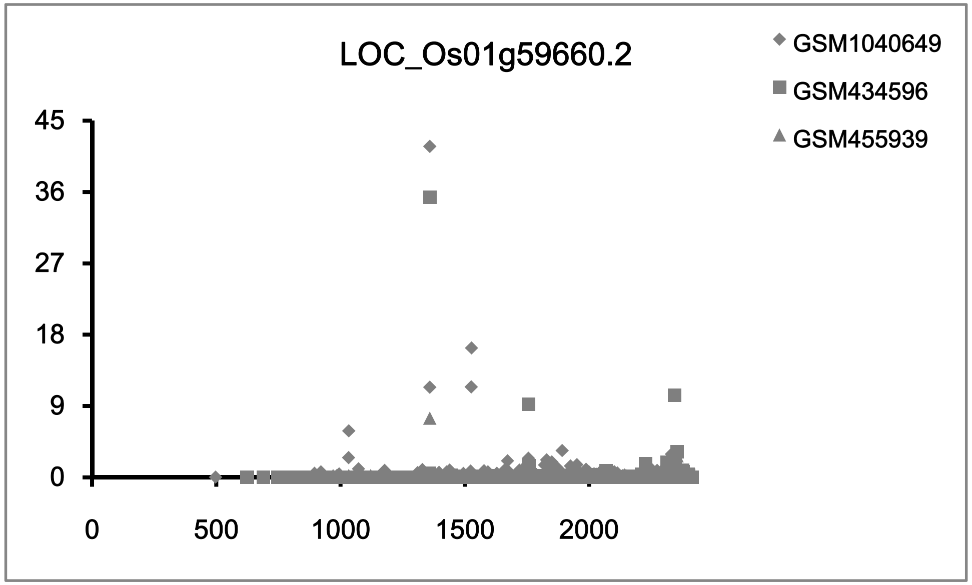

root-CK-high-4920
GSM434596
2.5
2
1.5
1
0.5
0
1896
1906
1916
1926
1936
1946
1956

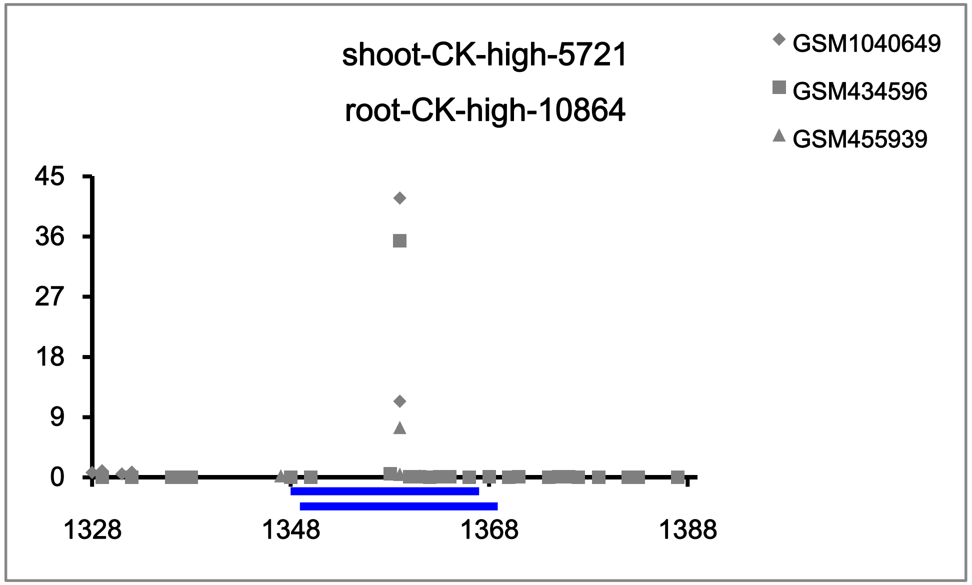

LOC_Os01g55040.1
SRR1849906
5
4
3
2
1
0
0
2000
4000
6000

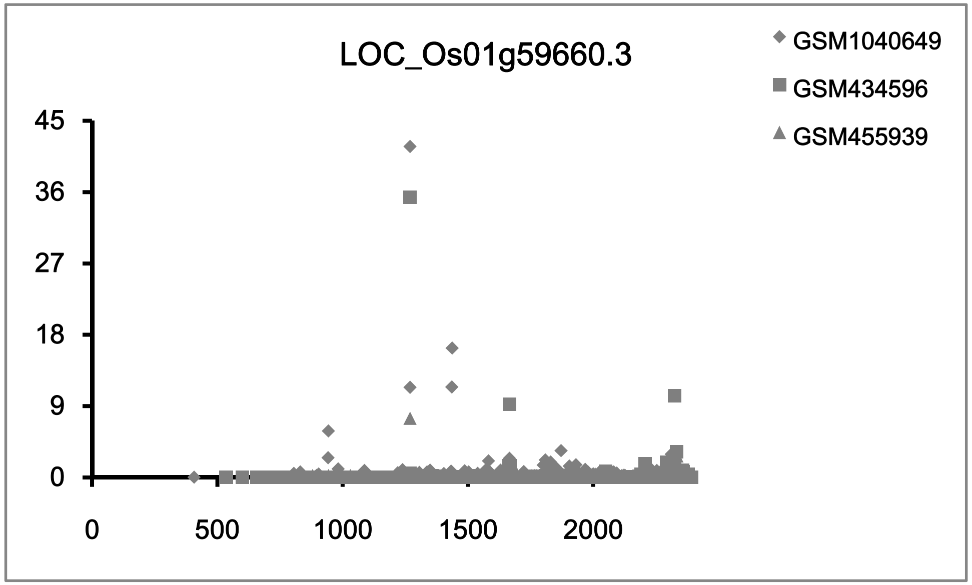

shoot-As-high-850
SRR1849906
5
4
3
2
1
0
6292
6302
6312
6322
6332
6342

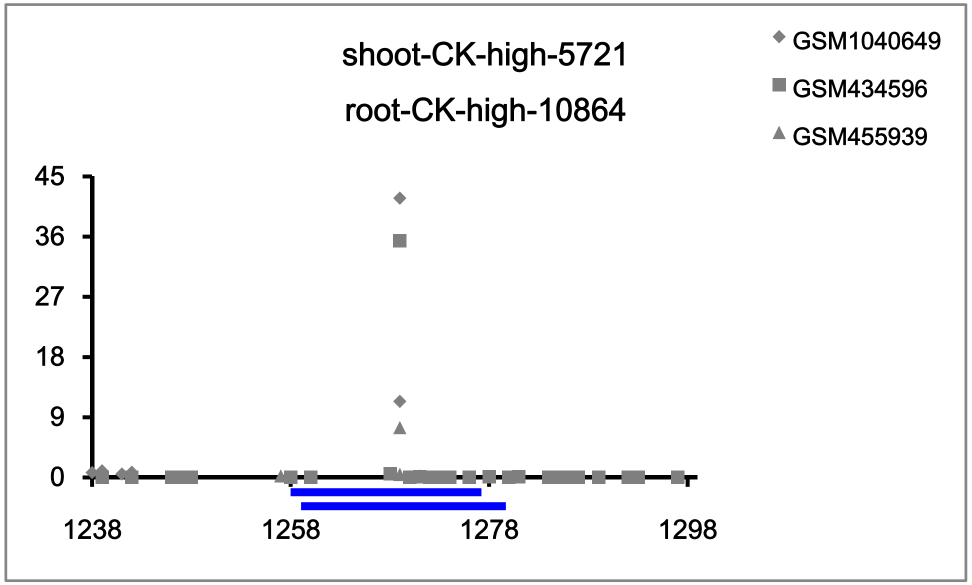

LOC_Os01g59660.1
GSM1040649
GSM434596
GSM455939
45
36
27
18
9
0
0
500
1000
1500
2000

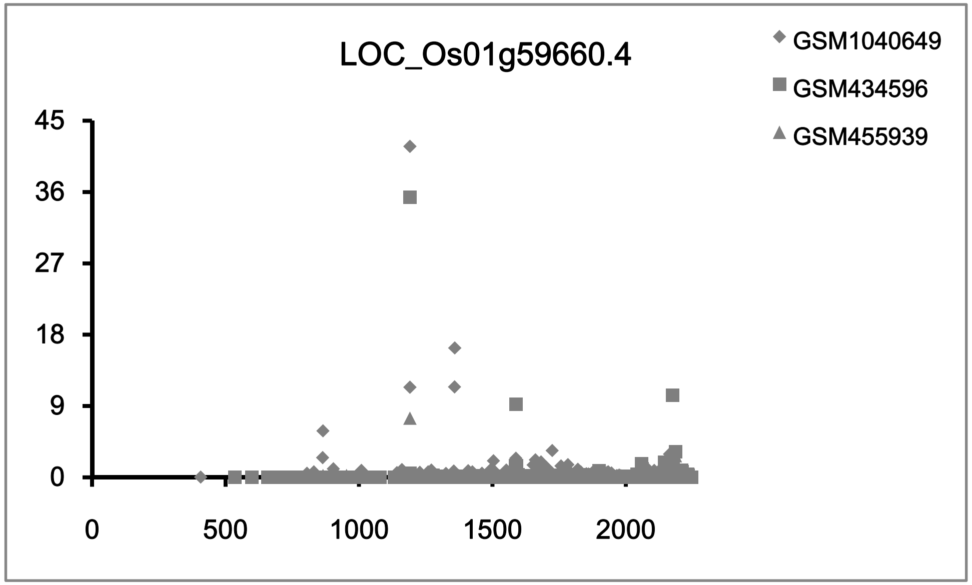

shoot-CK-high-5721
root-CK-high-10864
GSM1040649
GSM434596
GSM455939
45
36
27
18
9
0
1240
1260
1280
1300

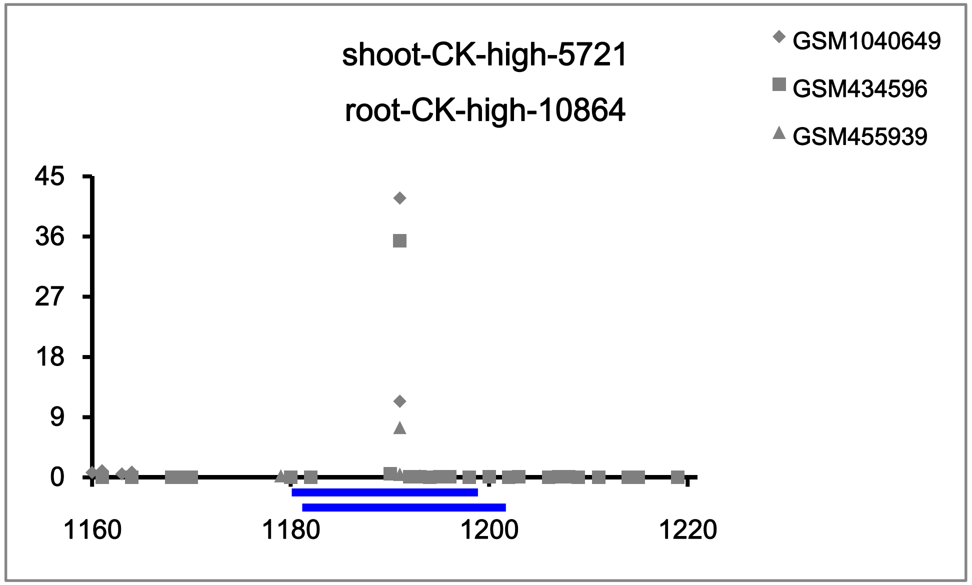

LOC_Os01g59660.2
◆ GSM1040649
■ GSM434596
▲ GSM455939
45
36
27
18
9
0
0
500
1000
1500
2000

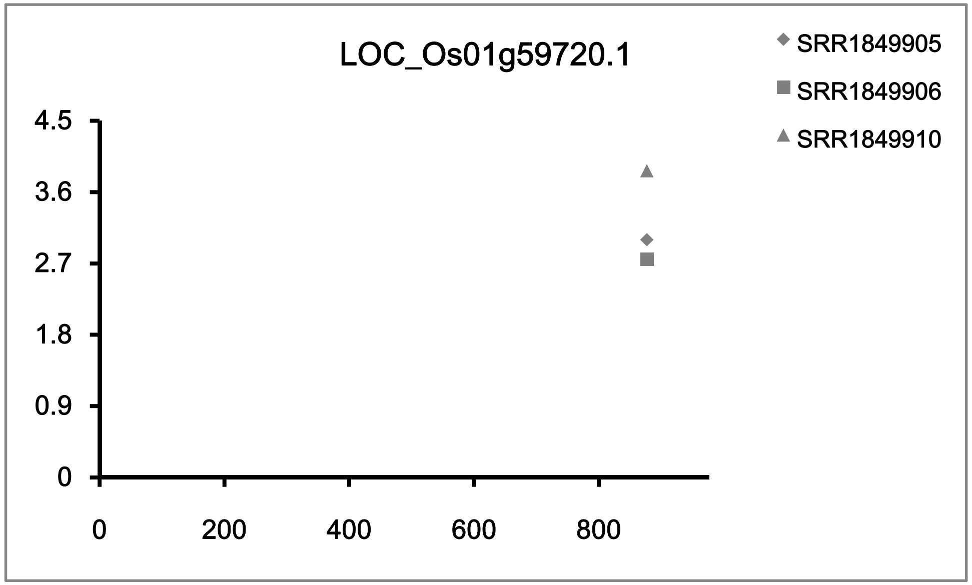

shoot-CK-high-5721
root-CK-high-10864
◆ GSM1040649
■ GSM434596
▲ GSM455939
45
36
27
18
9
0
1328
1348
1368
1388

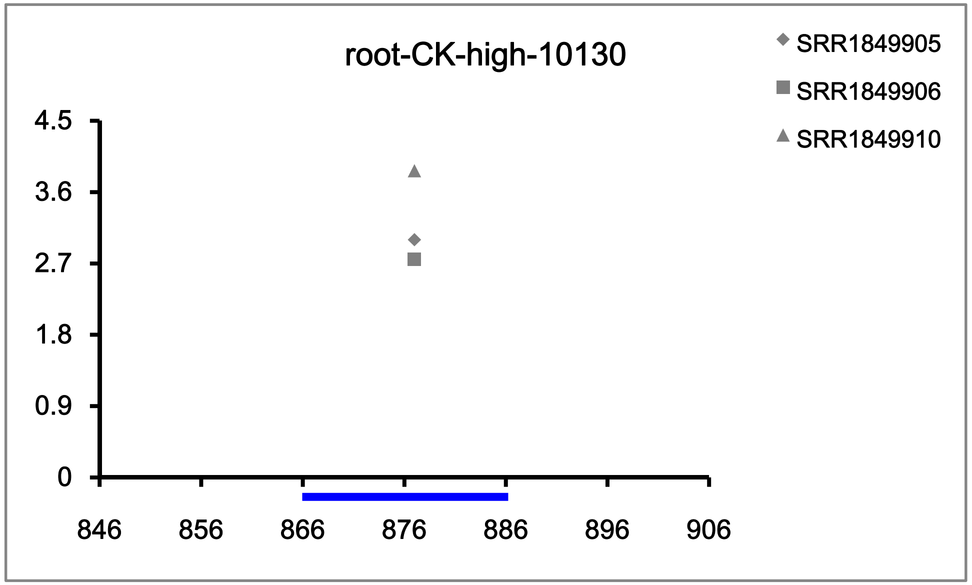

LOC_Os01g59660.3
◆ GSM1040649
■ GSM434596
▲ GSM455939
45
36
27
18
9
0
0
500
1000
1500
2000

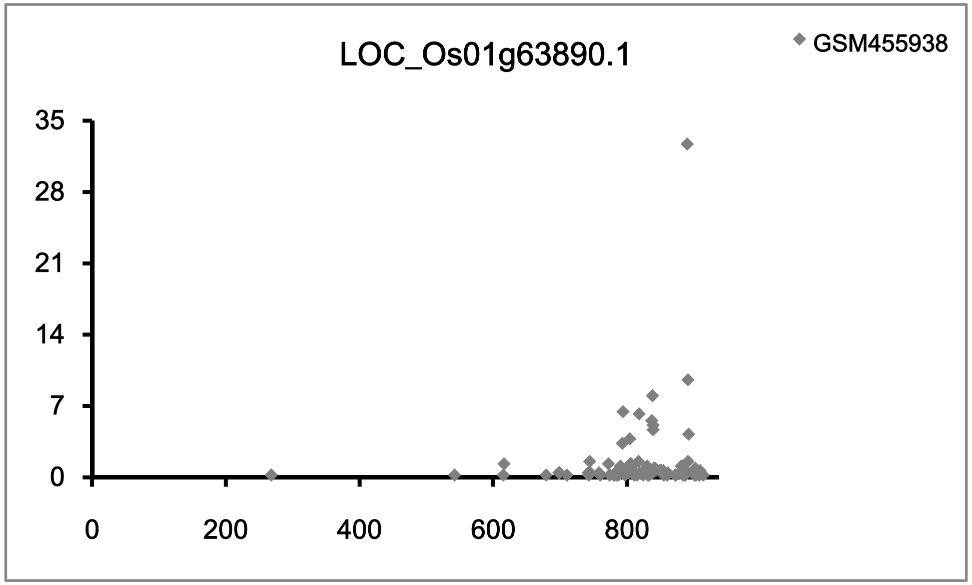

shoot-CK-high-5721
root-CK-high-10864
◆ GSM1040649
■ GSM434596
▲ GSM455939
45
36
27
18
9
0
1238
1258
1278
1298

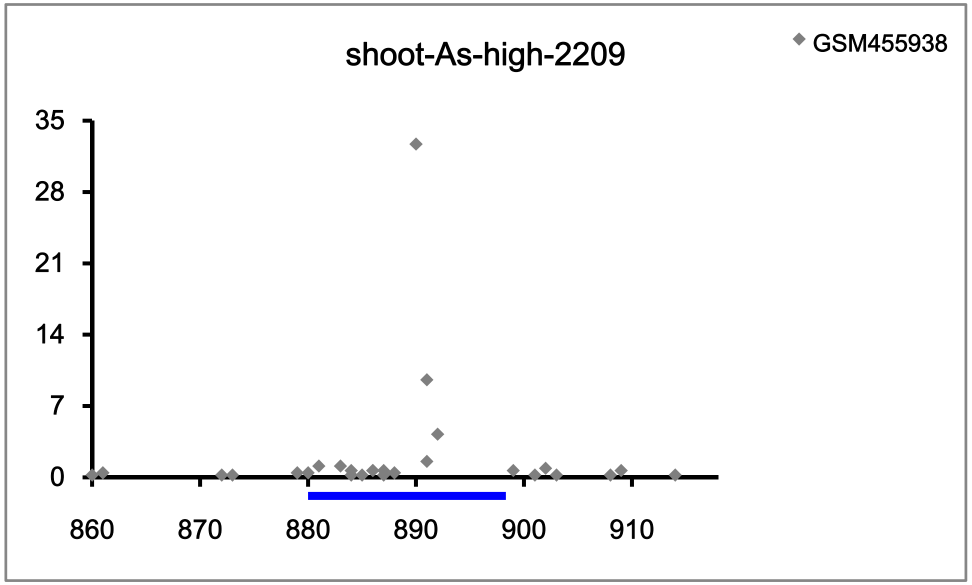

LOC_Os01g59660.4
◆ GSM1040649
■ GSM434596
▲ GSM455939
45
36
27
18
9
0
0
500
1000
1500
2000

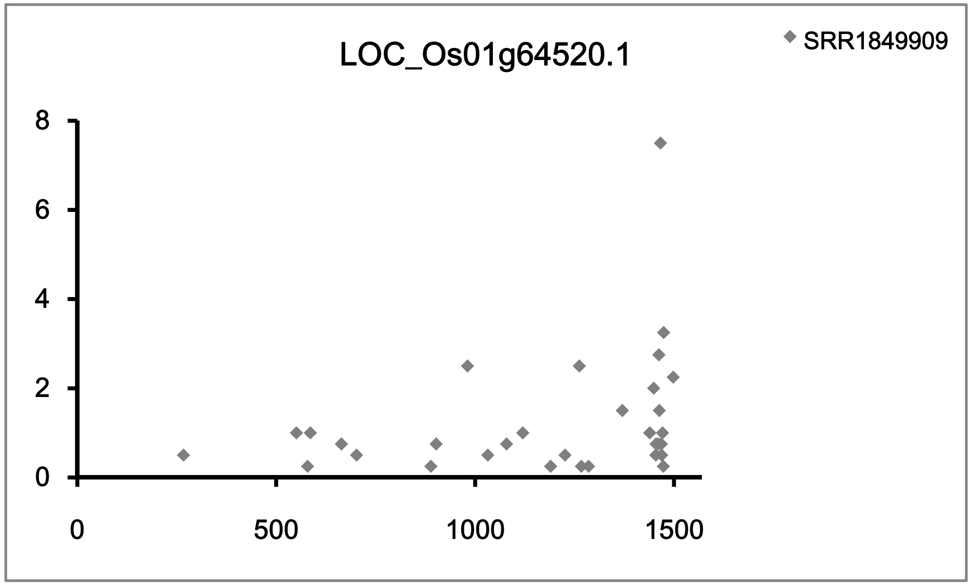

shoot-CK-high-5721
root-CK-high-10864
◆ GSM1040649
■ GSM434596
▲ GSM455939
45
36
27
18
9
0
1160
1180
1200
1220

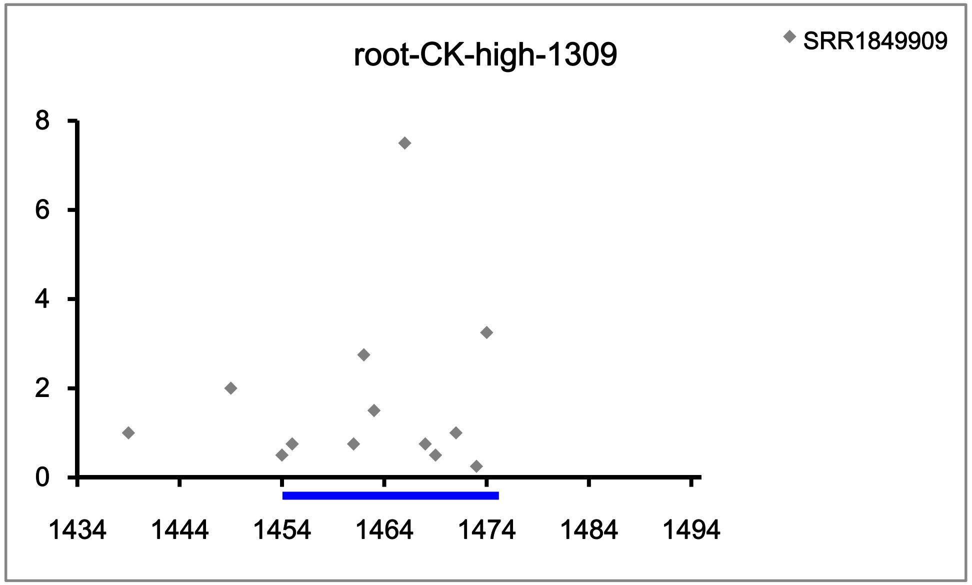

LOC_Os01g59720.1
◆ SRR1849905
■ SRR1849906
▲ SRR1849910
4.5
3.6
2.7
1.8
0.9
0
0
200
400
600
800

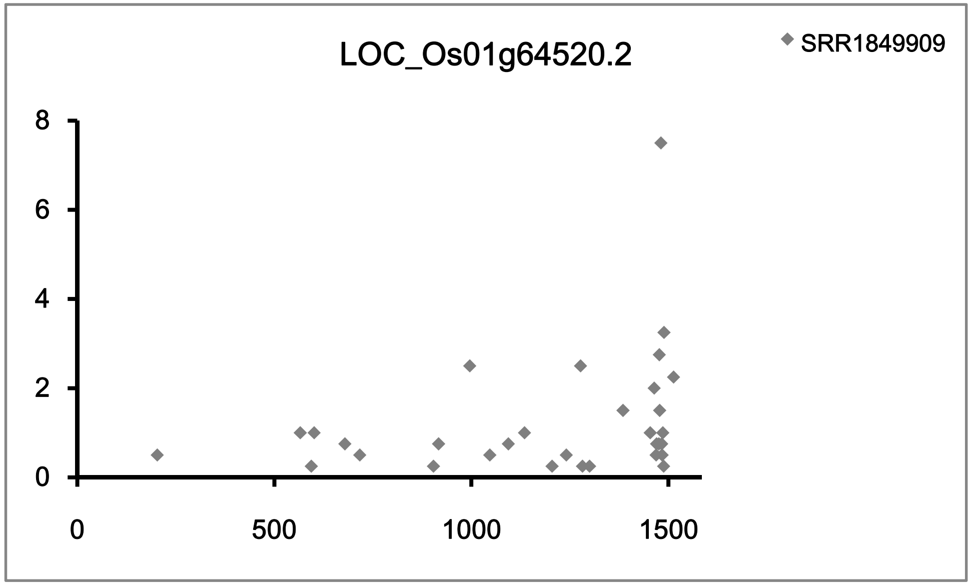

root-CK-high-10130
◆ SRR1849905
■ SRR1849906
▲ SRR1849910
4.5
3.6
2.7
1.8
0.9
0
846
856
866
876
886
896
906

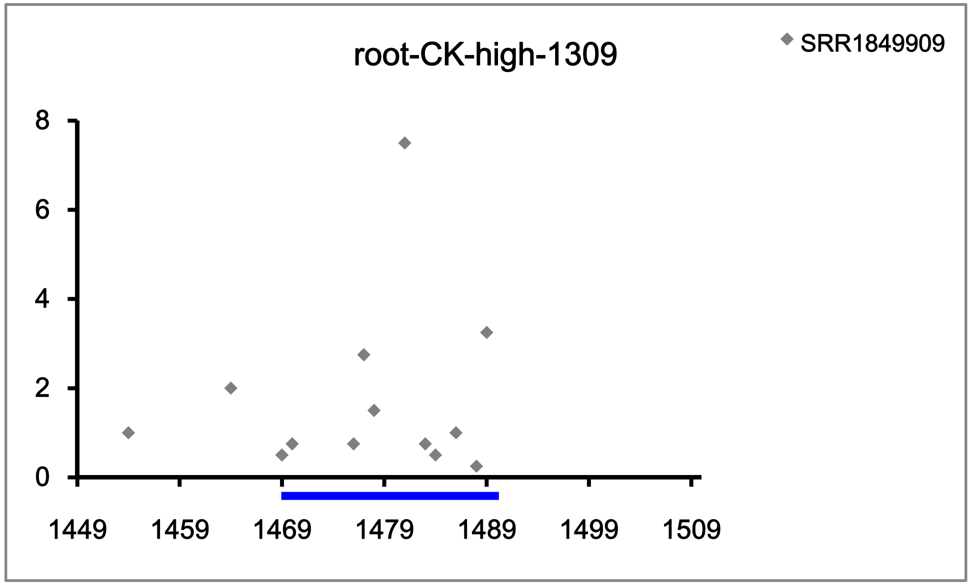

LOC_Os01g63890.1

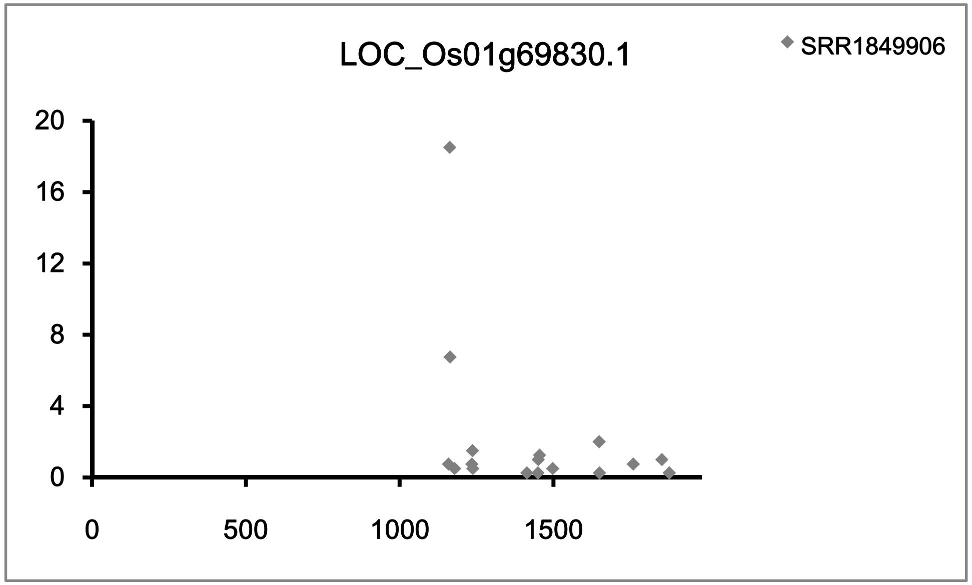

shoot-As-high-2209

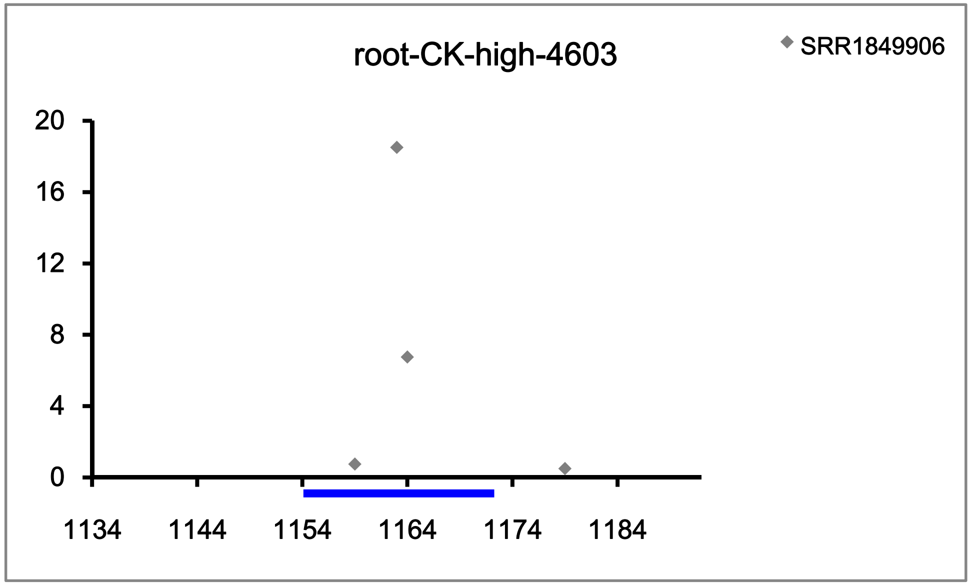

LOC_Os01g64520.1

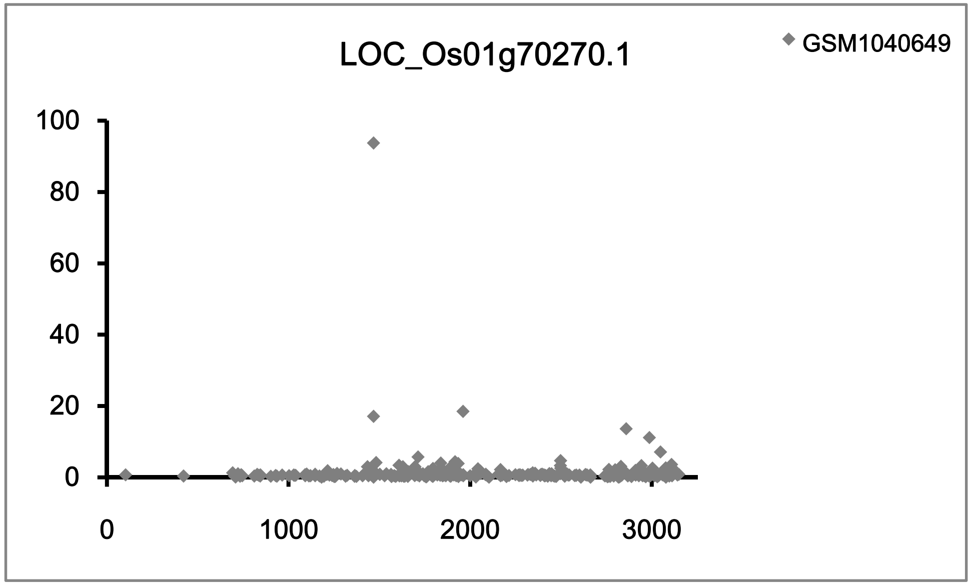

root-CK-high-1309

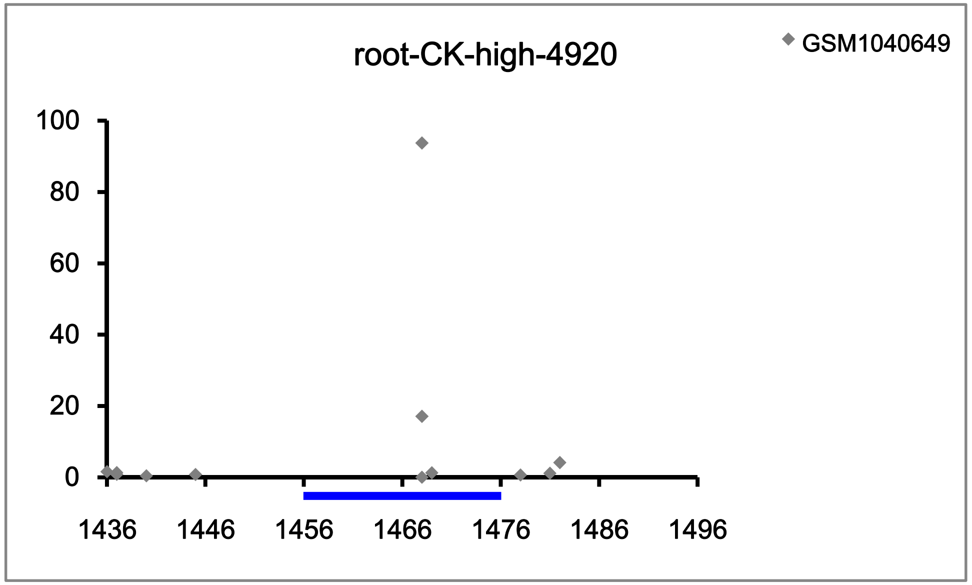

LOC_Os01g64520.2
SRR1849909
8
6
4
2
0
0
500
1000
1500

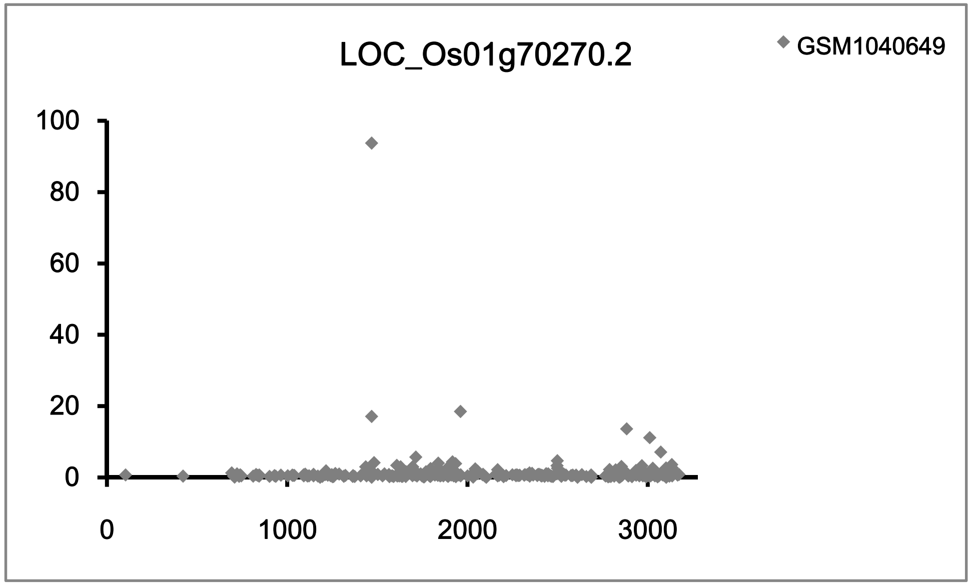

root-CK-high-1309
SRR1849909
8
6
4
2
0
1449
1459
1469
1479
1489
1499
1509

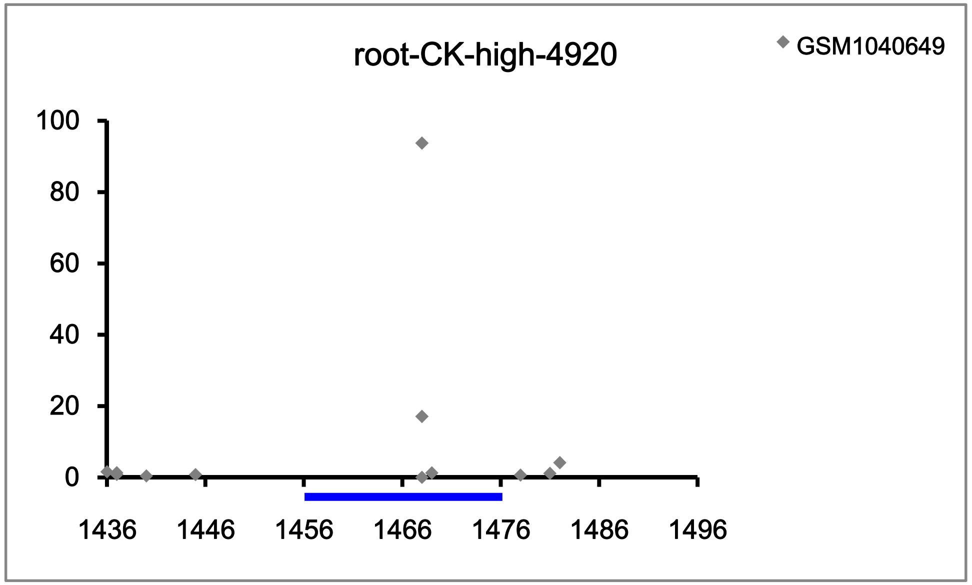

LOC_Os01g69830.1
SRR1849906
20
16
12
8
4
0
0
500
1000
1500

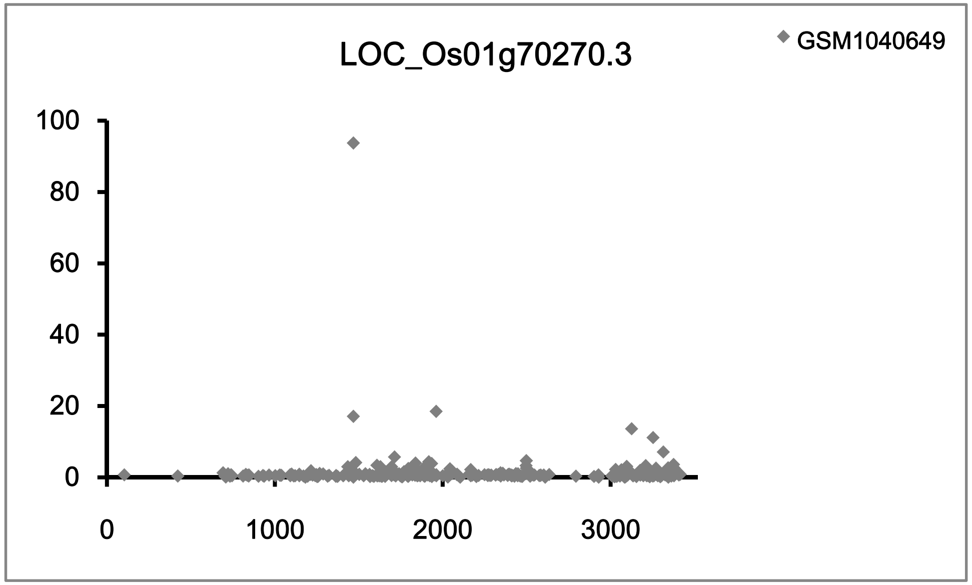

root-CK-high-4603
SRR1849906
20
16
12
8
4
0
1134
1144
1154
1164
1174
1184

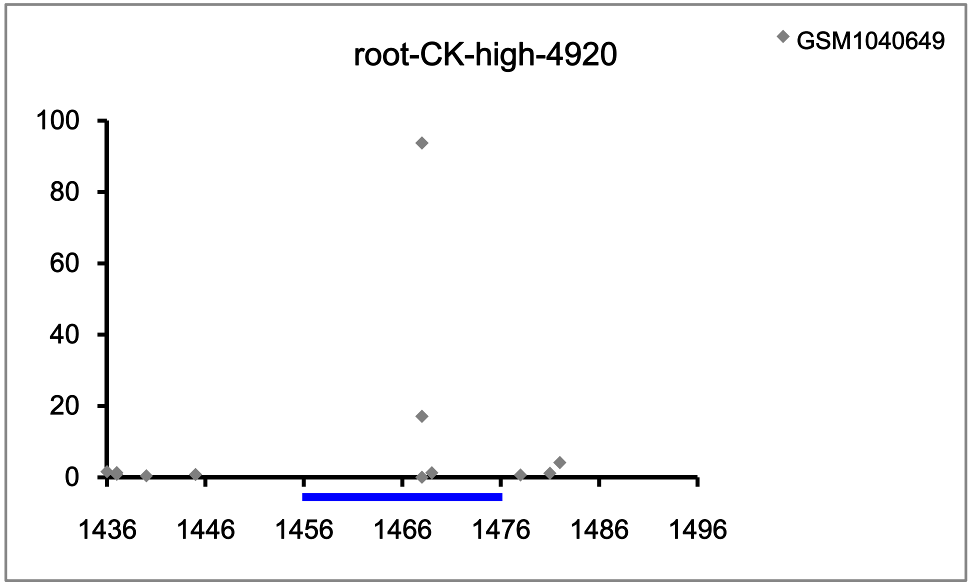

LOC_Os01g70270.1
GSM1040649
100
80
60
40
20
0
0
1000
2000
3000

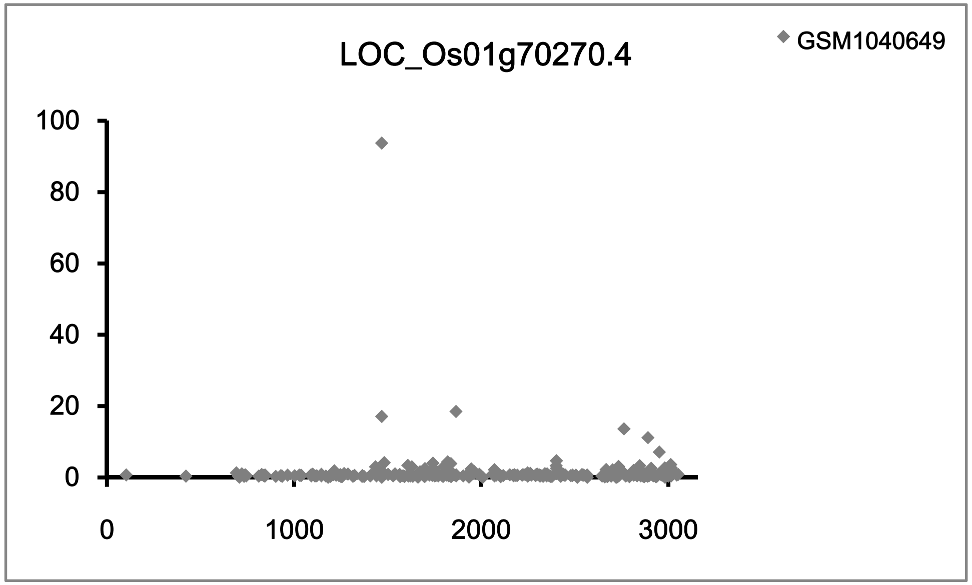

root-CK-high-4920
GSM1040649
100
80
60
40
20
0
1436
1446
1456
1466
1476
1486
1496

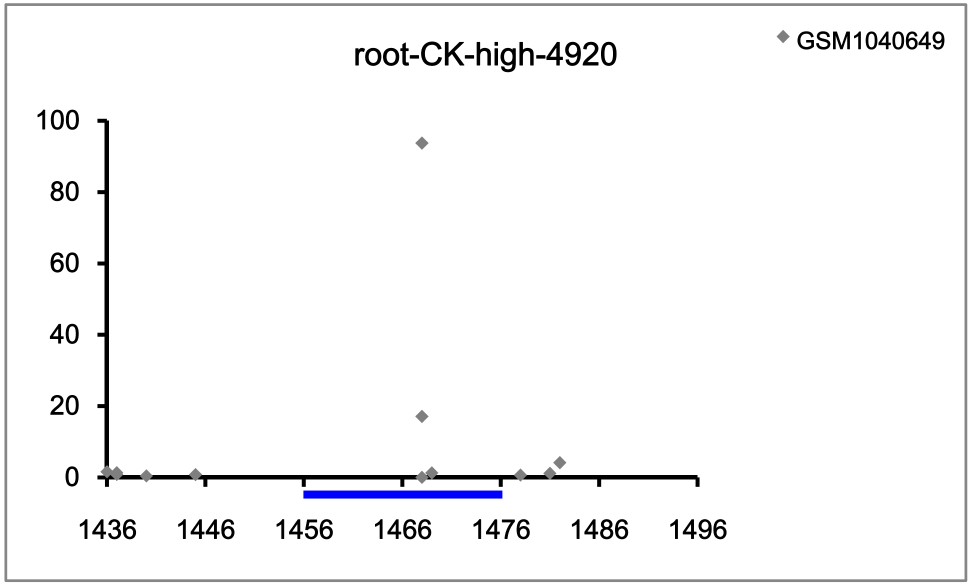

LOC_Os01g70270.2
GSM1040649
100
80
60
40
20
0
0
1000
2000
3000

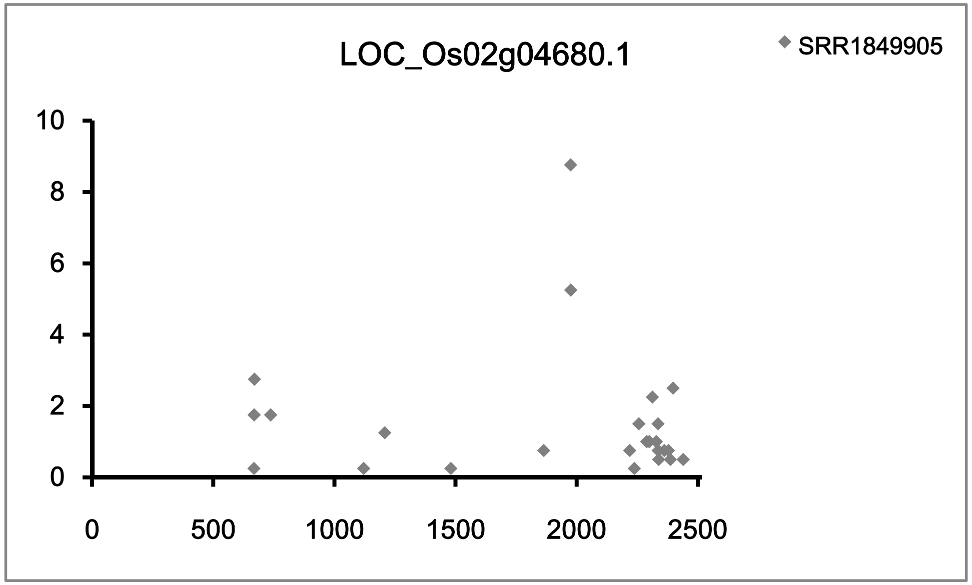

root-CK-high-4920
GSM1040649
100
80
60
40
20
0
1436
1446
1456
1466
1476
1486
1496

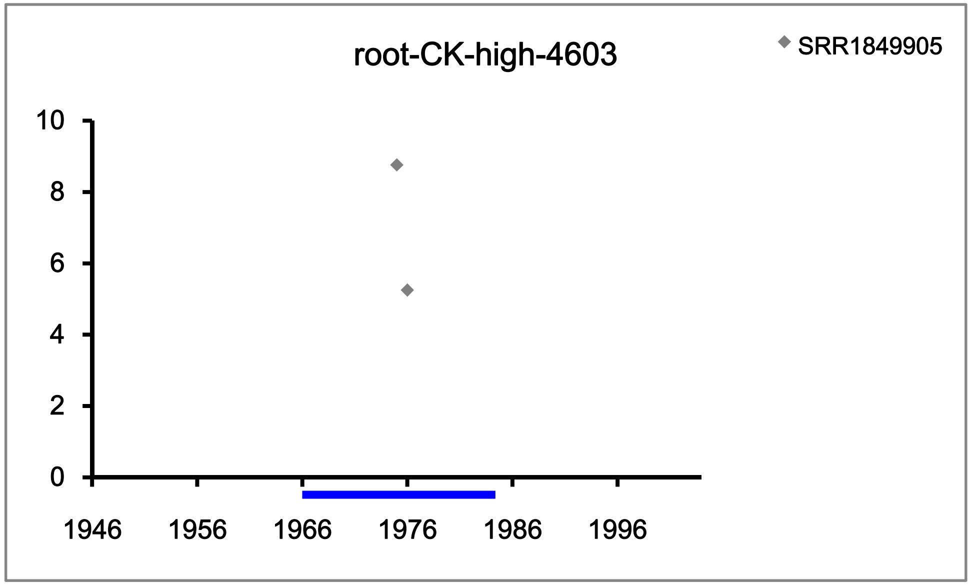

LOC_Os01g70270.3
GSM1040649
100
80
60
40
20
0
0
1000
2000
3000

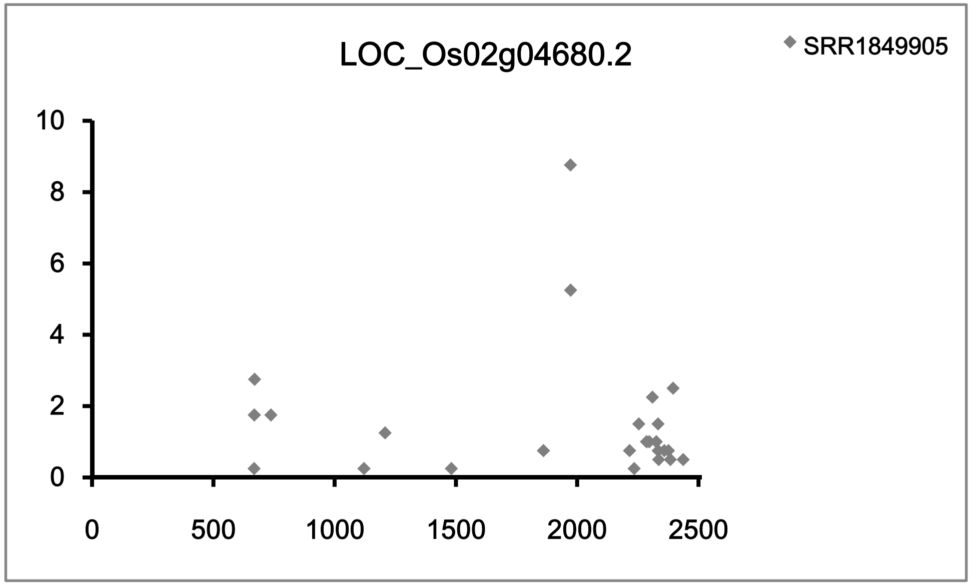

root-CK-high-4920
GSM1040649
100
80
60
40
20
0
1436
1446
1456
1466
1476
1486
1496

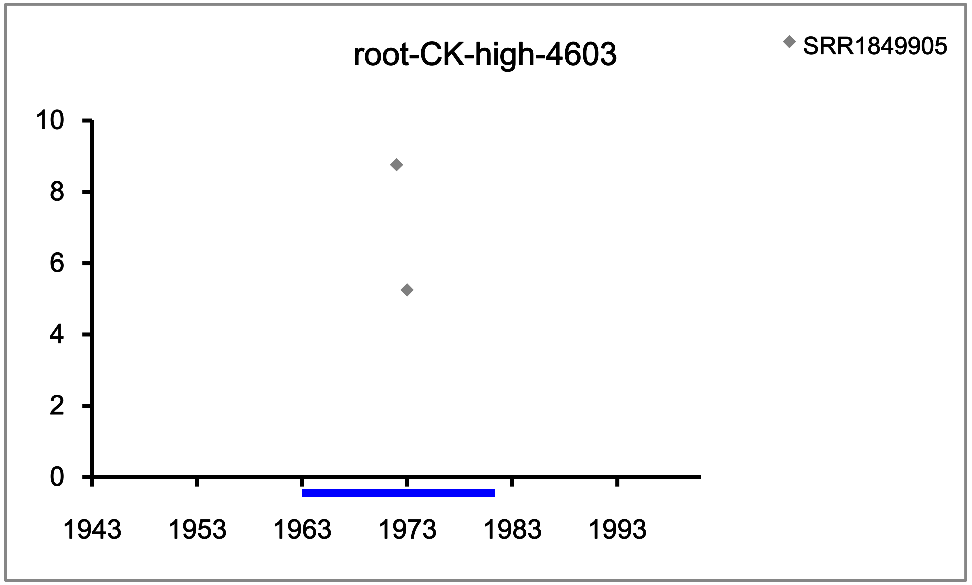

LOC_Os01g70270.4
GSM1040649
100
80
60
40
20
0
0
1000
2000
3000

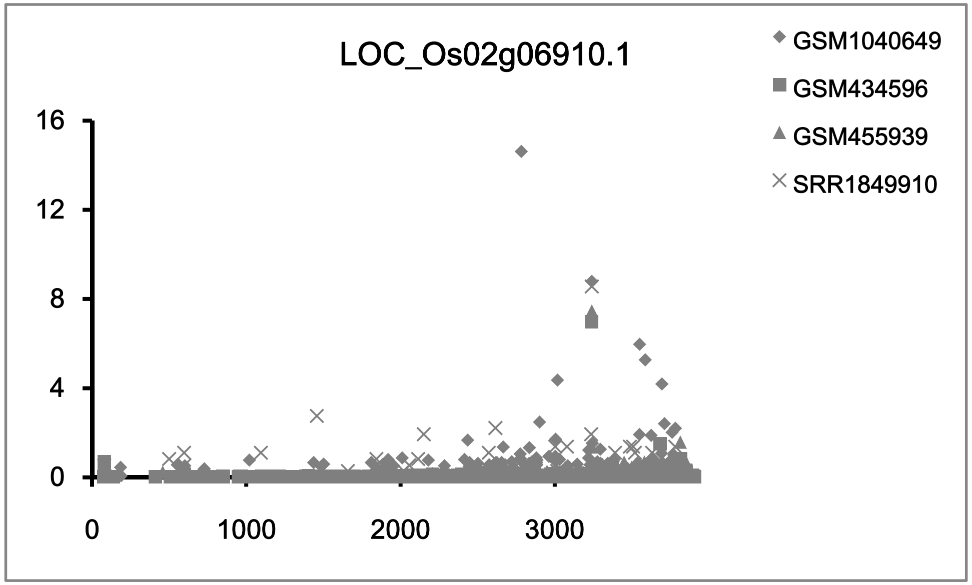

root-CK-high-4920
GSM1040649
100
80
60
40
20
0
1436
1446
1456
1466
1476
1486
1496

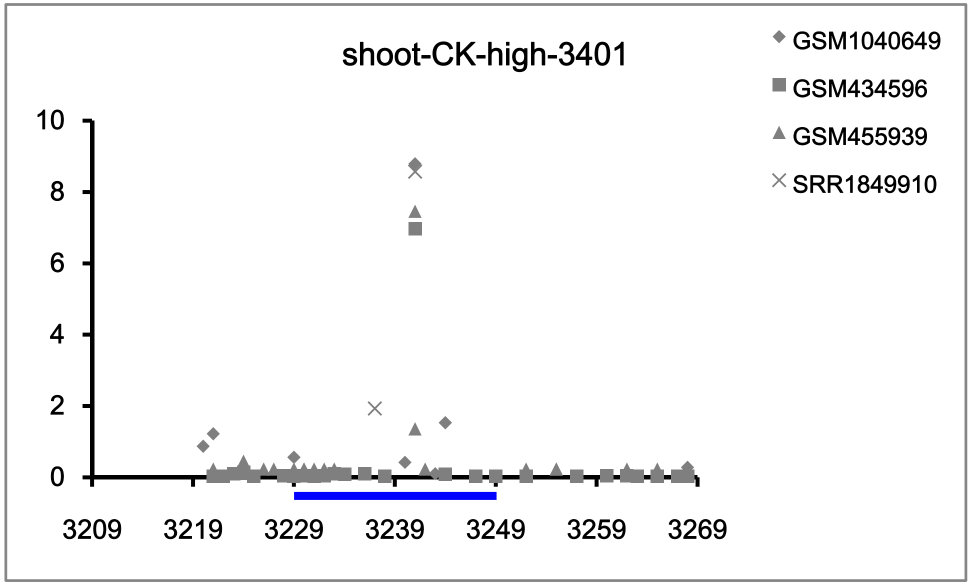

LOC_Os02g04680.1
SRR1849905
10
8
6
4
2
0
0
500
1000
1500
2000
2500

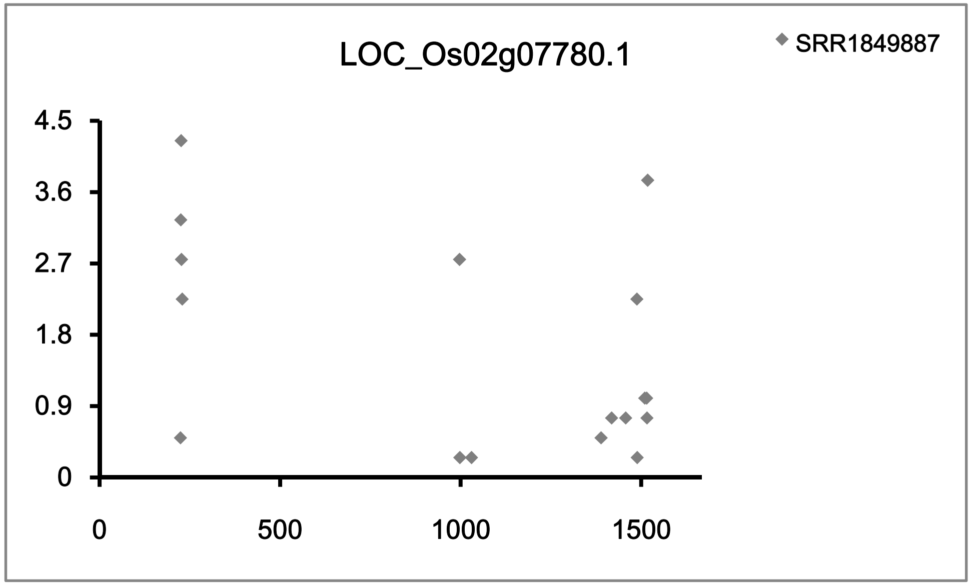

root-CK-high-4603
SRR1849905
10
8
6
4
2
0
1946
1956
1966
1976
1986
1996

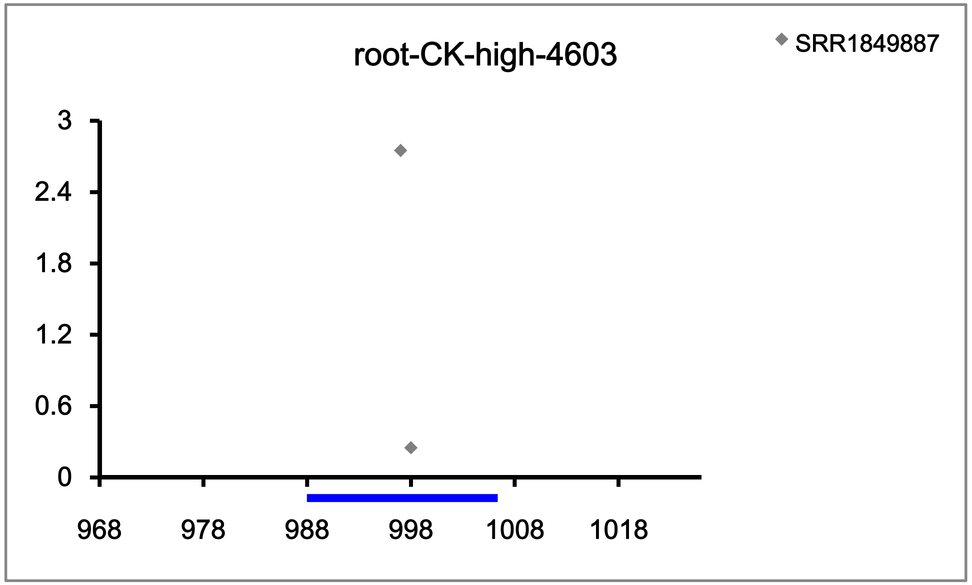

LOC_Os02g04680.2
SRR1849905
10
8
6
4
2
0
0
500
1000
1500
2000
2500

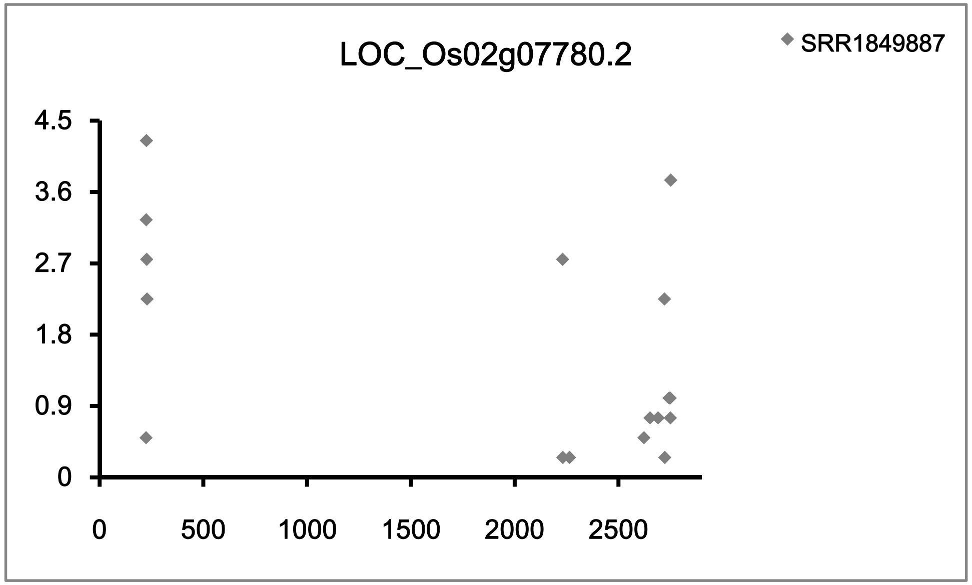

root-CK-high-4603
SRR1849905
10
8
6
4
2
0
1943
1953
1963
1973
1983
1993

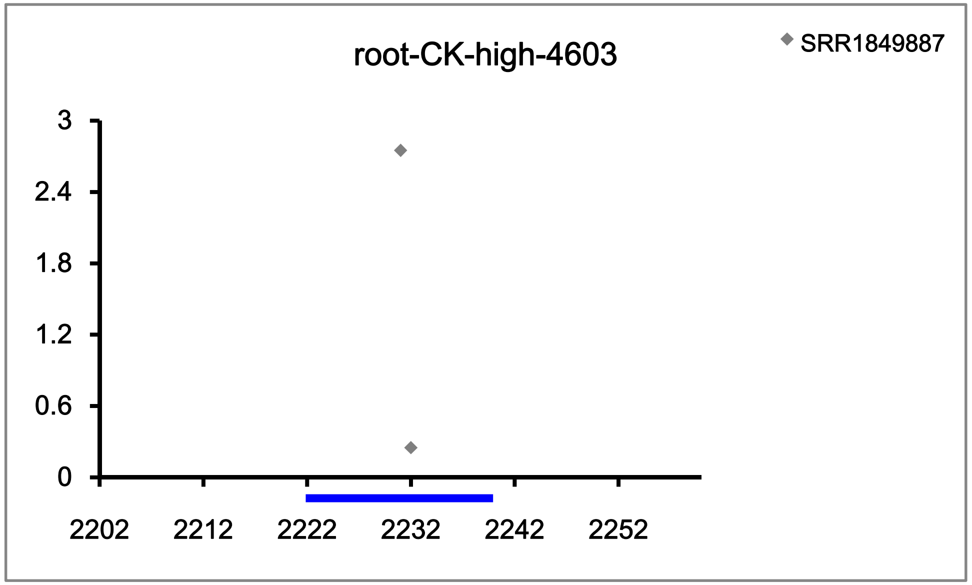

LOC_Os02g06910.1
GSM1040649
GSM434596
GSM455939
SRR1849910
16
12
8
4
0
0
1000
2000
3000

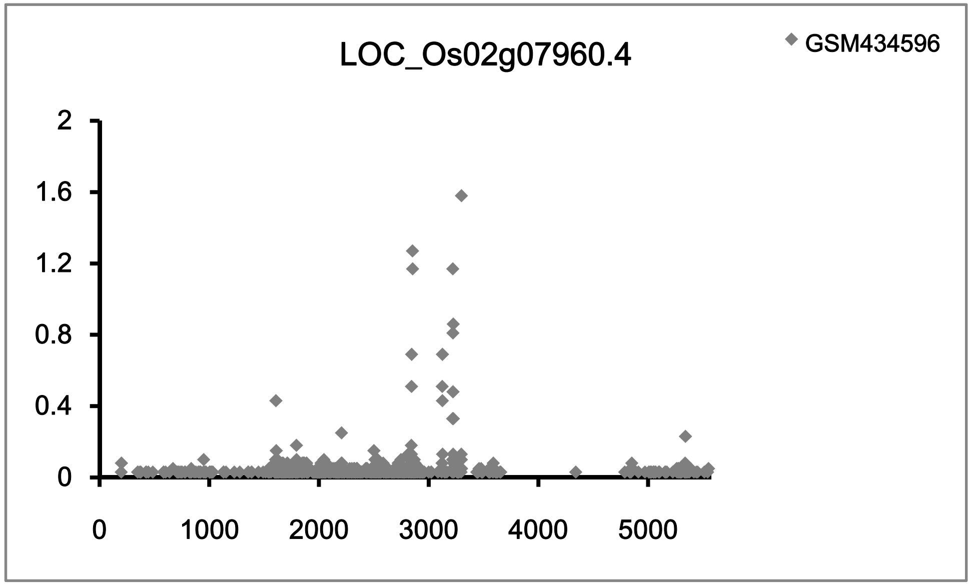

shoot-CK-high-3401
GSM1040649
GSM434596
GSM455939
SRR1849910
10
8
6
4
2
0
3209
3219
3229
3239
3249
3259
3269

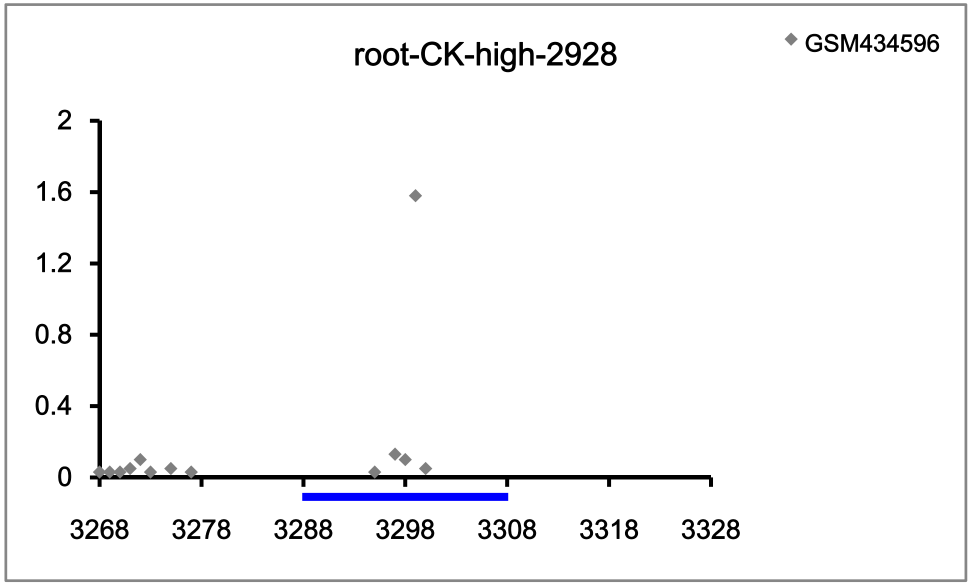

LOC_Os02g07780.1
SRR1849887
4.5
3.6
2.7
1.8
0.9
0
0
500
1000
1500

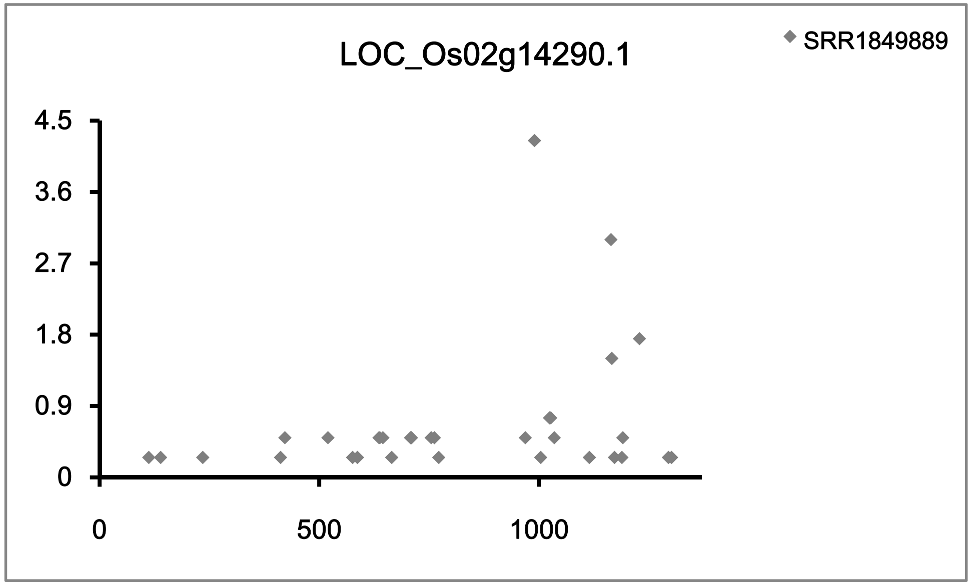

root-CK-high-4603
SRR1849887
3
2.4
1.8
1.2
0.6
0
968
978
988
998
1008
1018

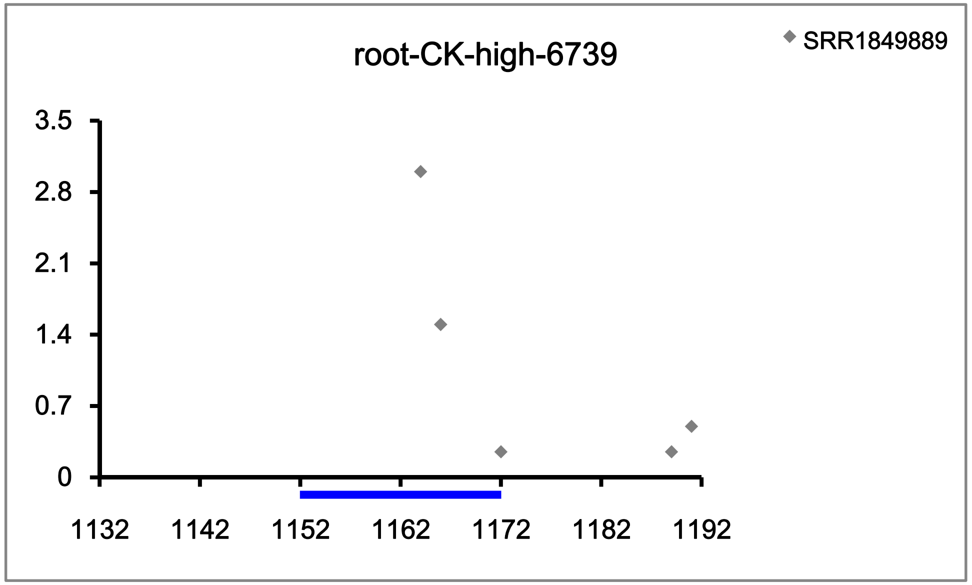

LOC_Os02g07780.2
SRR1849887
4.5
3.6
2.7
1.8
0.9
0
0
500
1000
1500
2000
2500

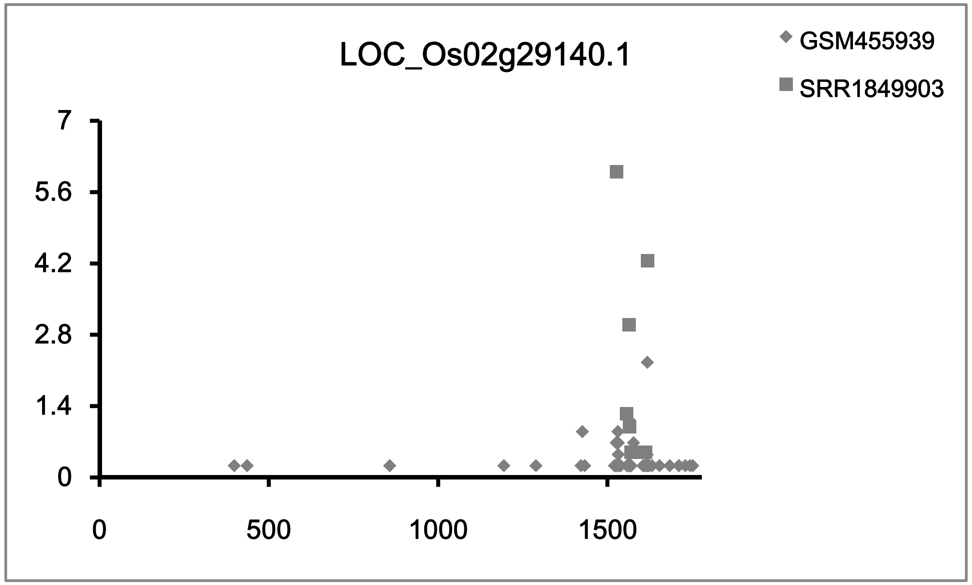

root-CK-high-4603
SRR1849887
3
2.4
1.8
1.2
0.6
0
2202
2212
2222
2232
2242
2252

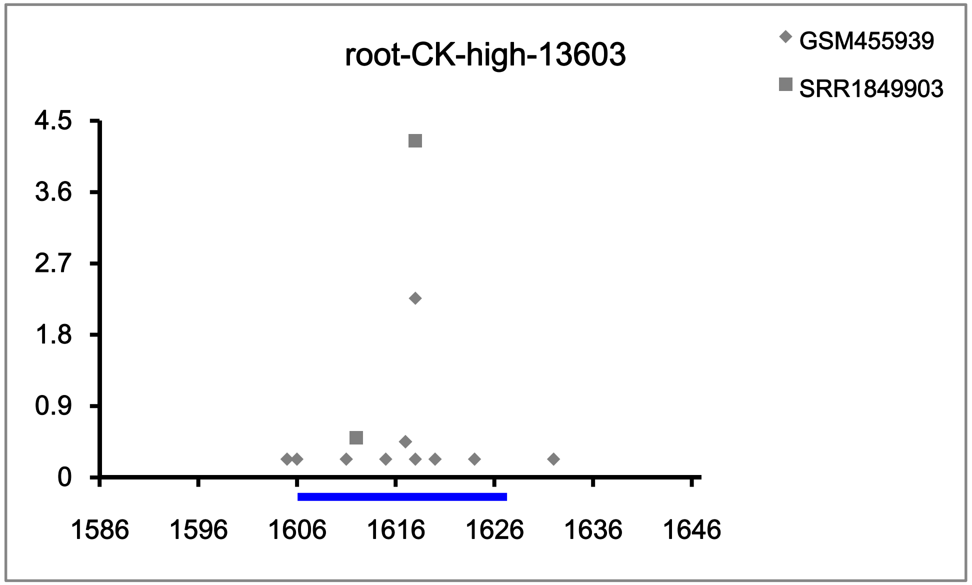

LOC_Os02g07960.4
GSM434596
2
1.6
1.2
0.8
0.4
0
0
1000
2000
3000
4000
5000

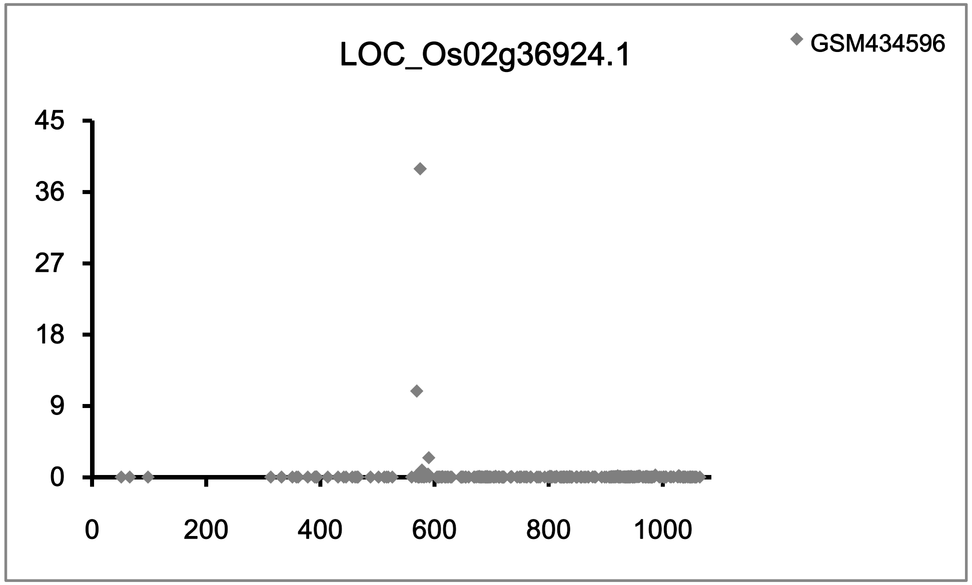

root-CK-high-2928
GSM434596
2
1.6
1.2
0.8
0.4
0
3268
3278
3288
3298
3308
3318
3328

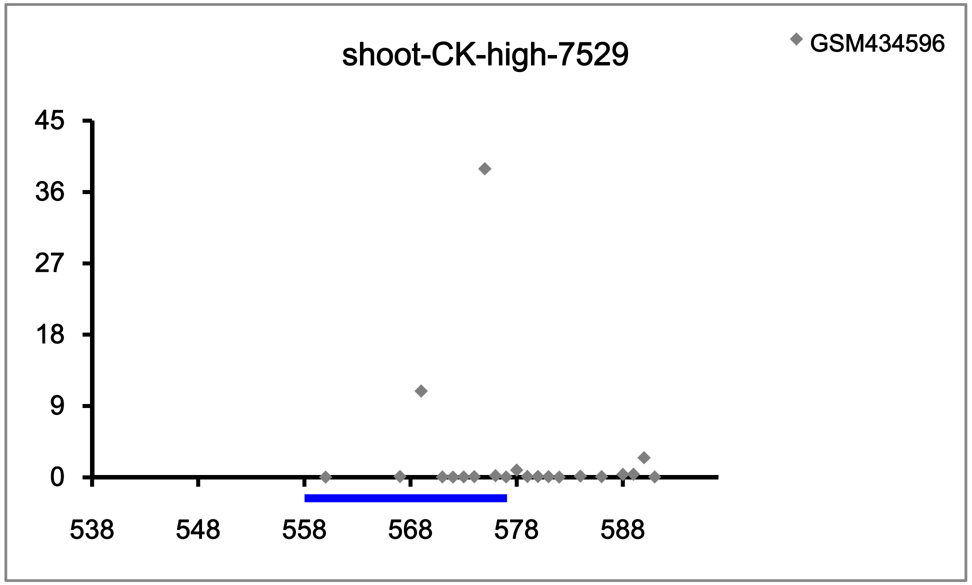

LOC_Os02g14290.1
SRR1849889
4.5
3.6
2.7
1.8
0.9
0
0
500
1000

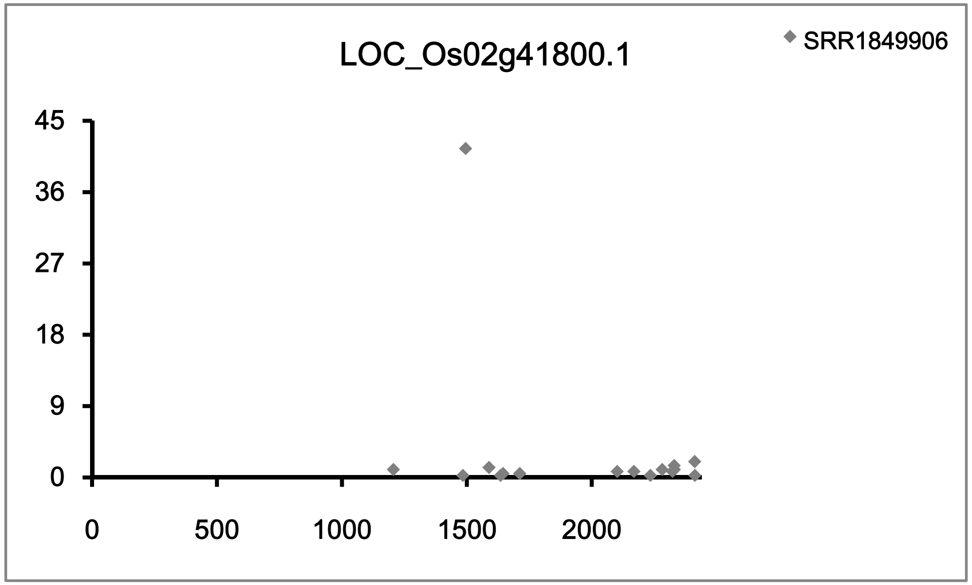

root-CK-high-6739
SRR1849889
3.5
2.8
2.1
1.4
0.7
0
1132
1142
1152
1162
1172
1182
1192

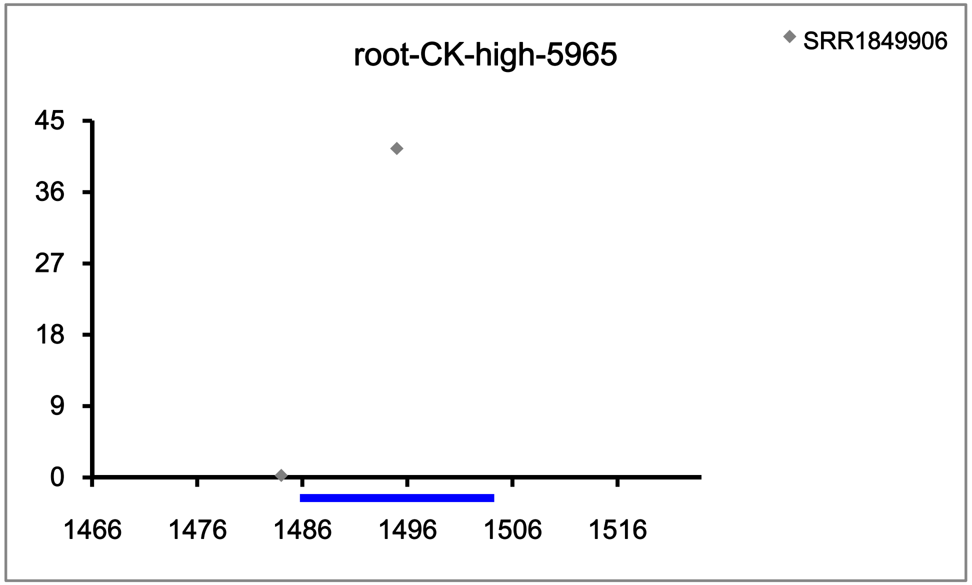

LOC_Os02g29140.1
GSM455939
SRR1849903
7
5.6
4.2
2.8
1.4
0
0
500
1000
1500

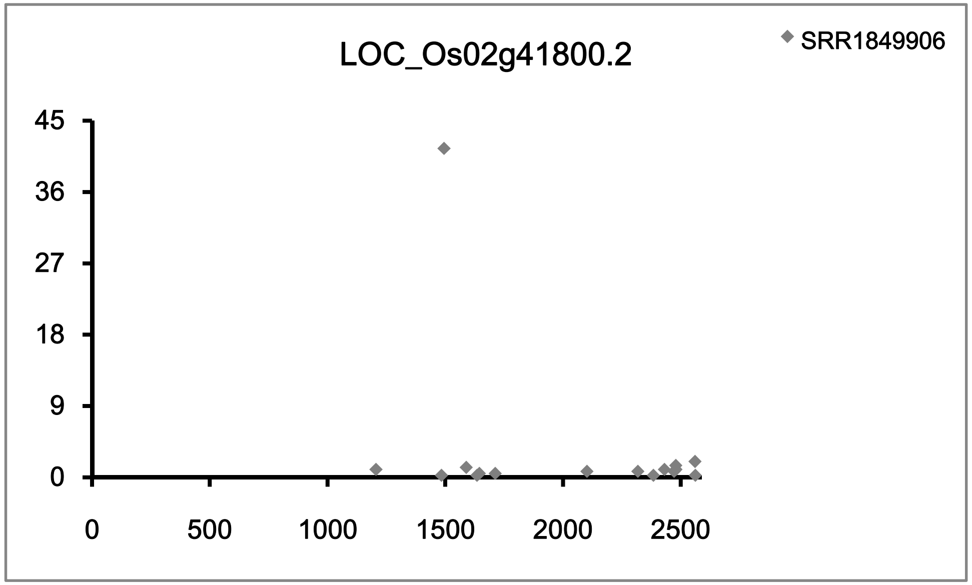

root-CK-high-13603
GSM455939
SRR1849903
4.5
3.6
2.7
1.8
0.9
0
1586
1596
1606
1616
1626
1636
1646

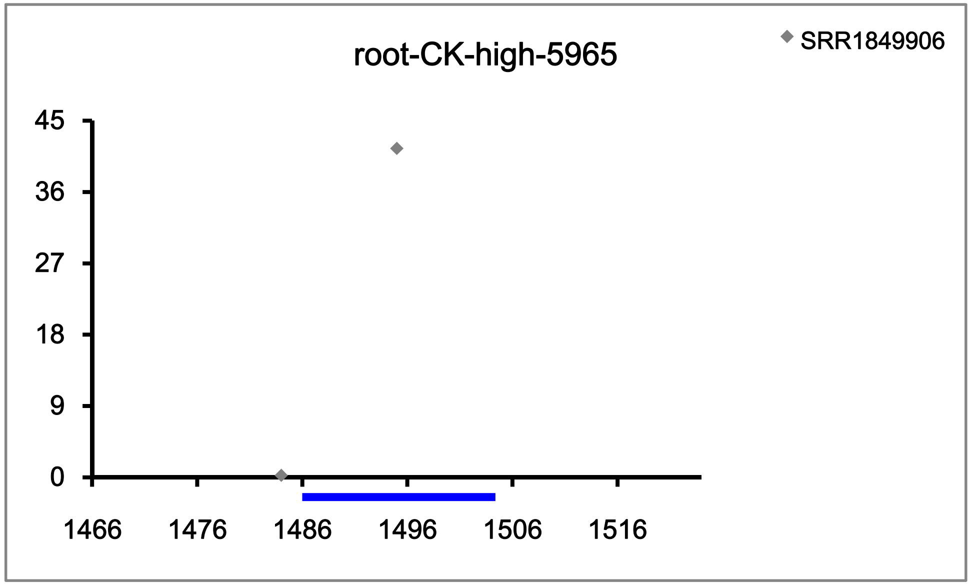

LOC_Os02g36924.1
GSM434596
45
36
27
18
9
0
0
200
400
600
800
1000

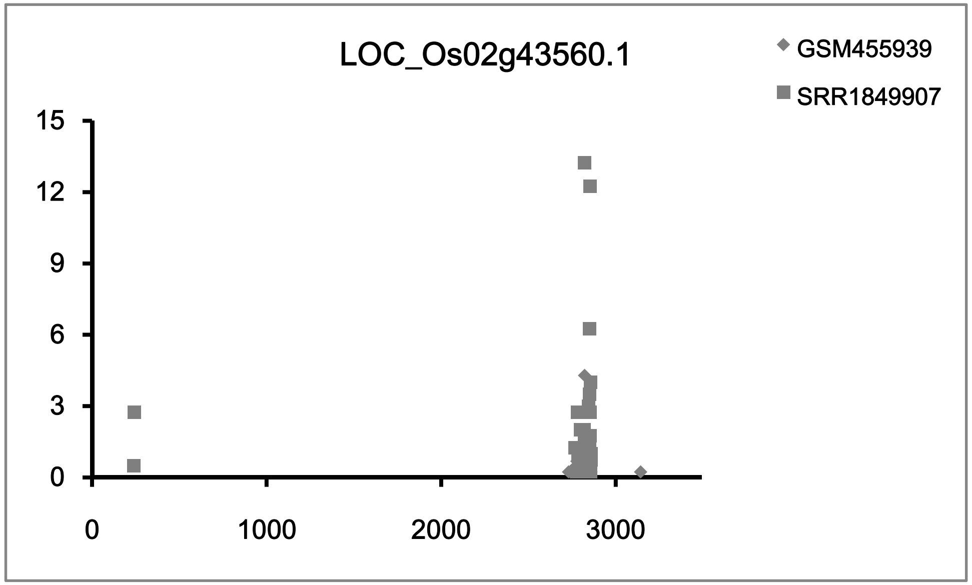

shoot-CK-high-7529
GSM434596
45
36
27
18
9
0
538
548
558
568
578
588

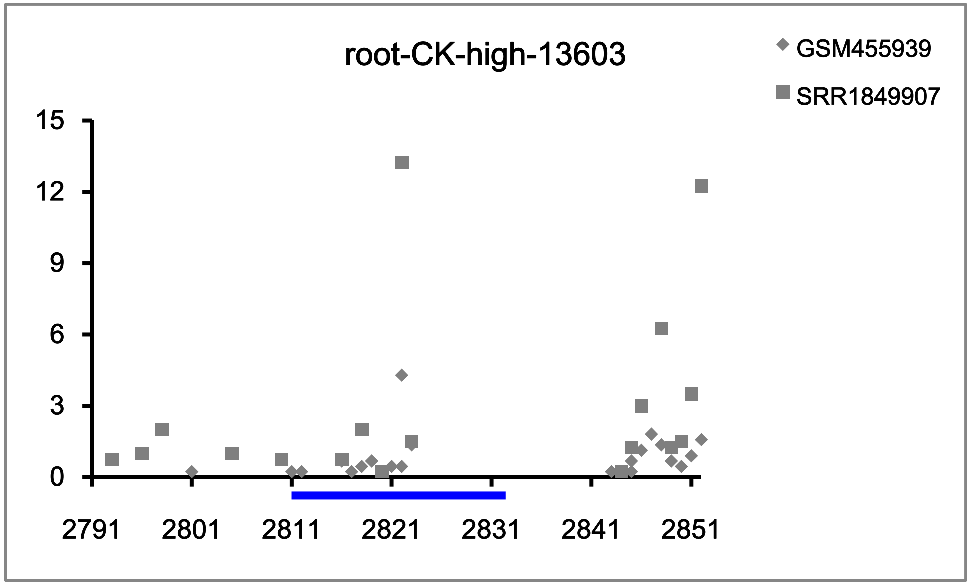

LOC_Os02g41800.1
SRR1849906
45
36
27
18
9
0
0
500
1000
1500
2000

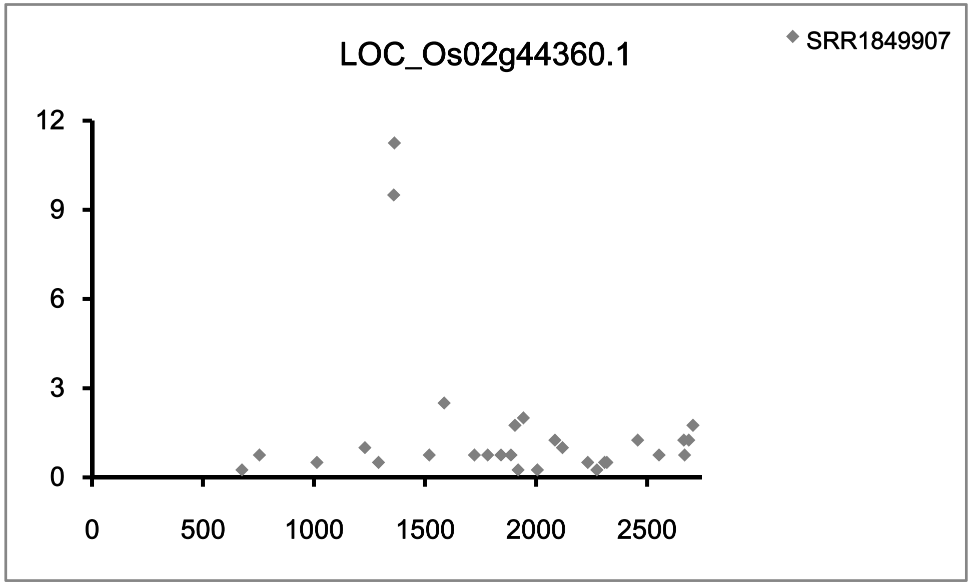

root-CK-high-5965
SRR1849906
45
36
27
18
9
0
1466
1476
1486
1496
1506
1516

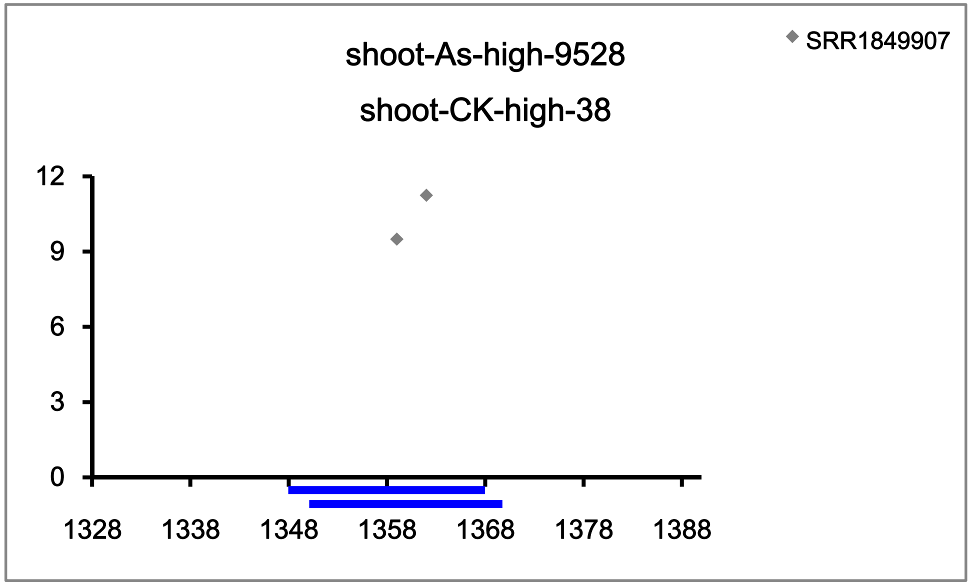

LOC_Os02g41800.2
SRR1849906
45
36
27
18
9
0
0
500
1000
1500
2000
2500

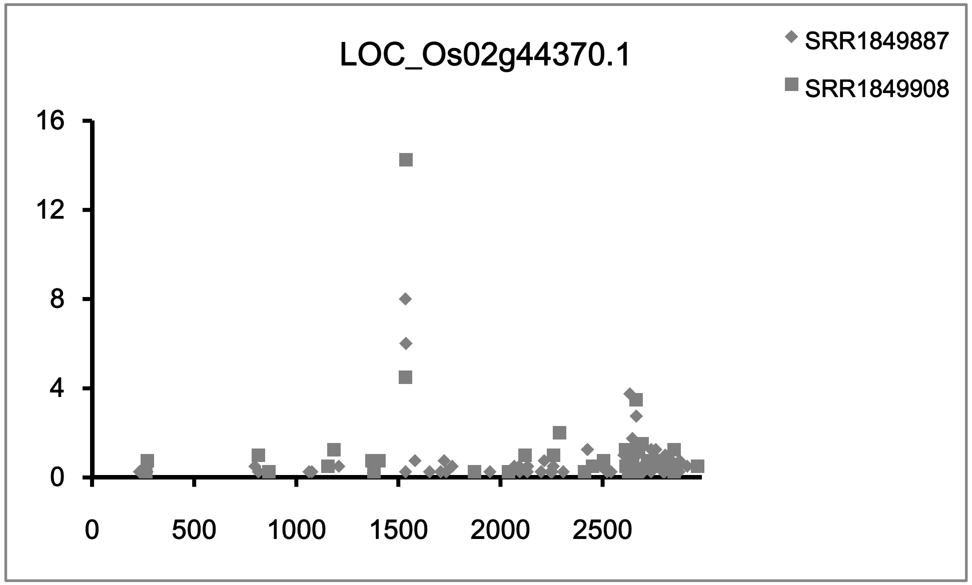

root-CK-high-5965
SRR1849906
45
36
27
18
9
0
1466
1476
1486
1496
1506
1516

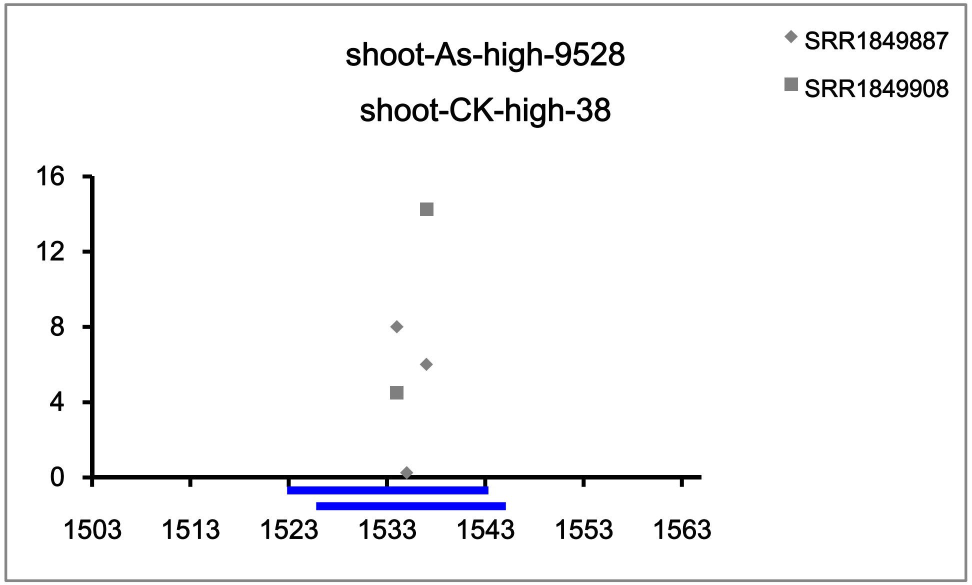

LOC_Os02g43560.1
GSM455939
SRR1849907
15
12
9
6
3
0
0
1000
2000
3000

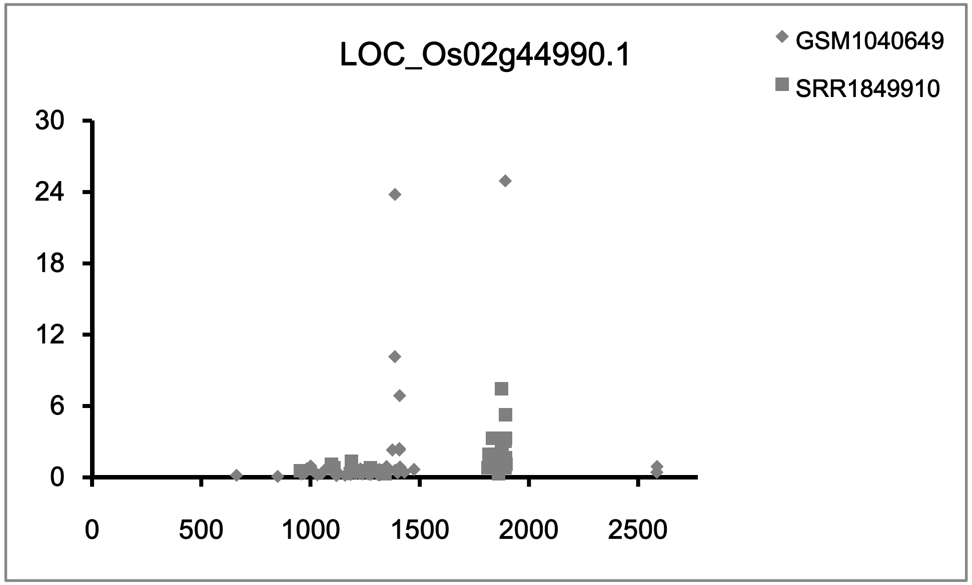

root-CK-high-13603
GSM455939
SRR1849907
15
12
9
6
3
0
2791
2801
2811
2821
2831
2841
2851

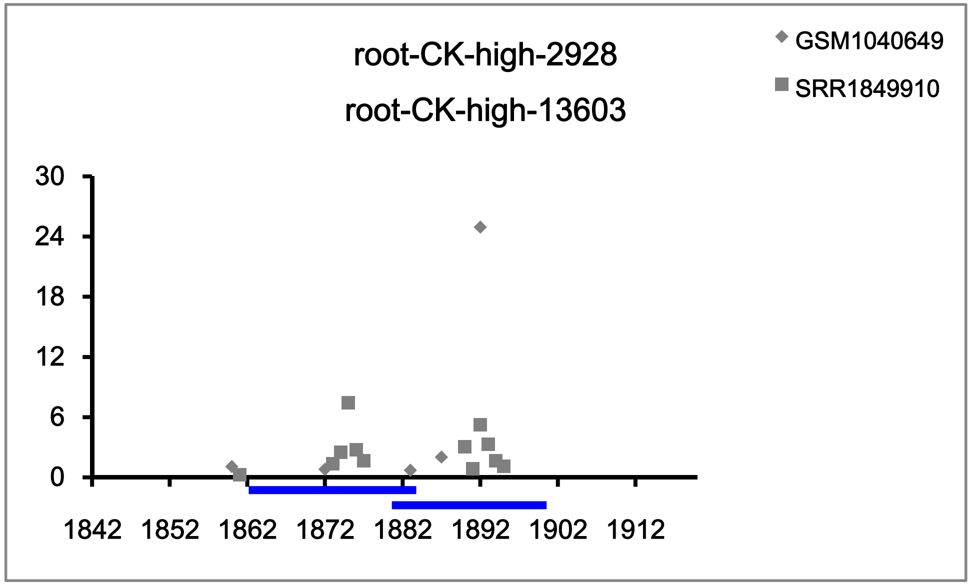

LOC_Os02g44360.1
SRR1849907
12
9
6
3
0
0
500
1000
1500
2000
2500

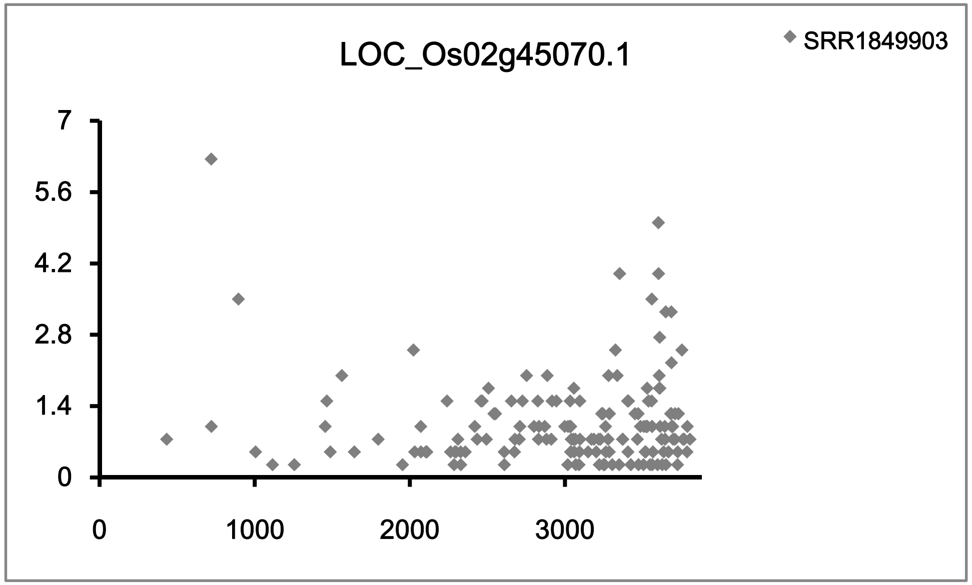

shoot-As-high-9528
shoot-CK-high-38
SRR1849907
12
9
6
3
0
1328
1338
1348
1358
1368
1378
1388

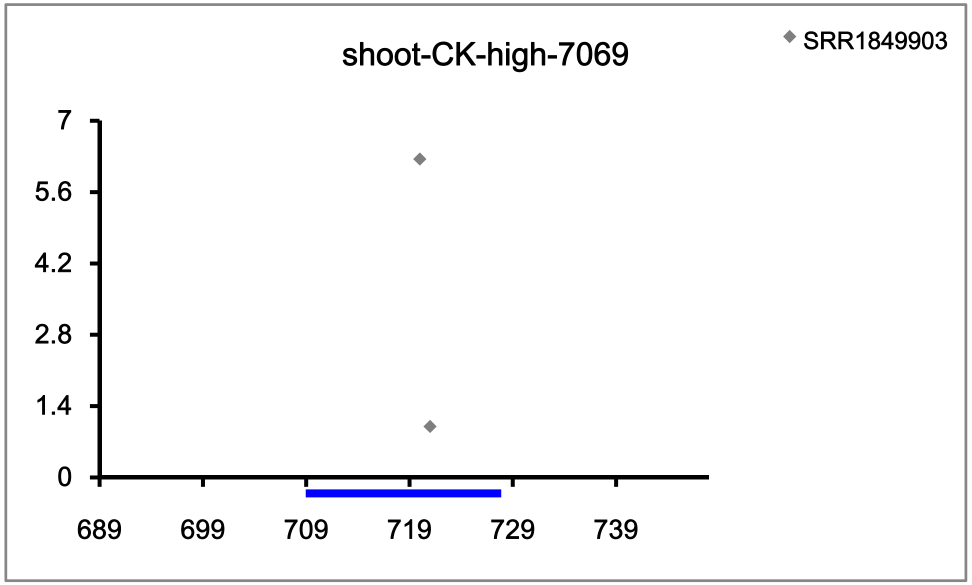

LOC_Os02g44370.1
SRR1849887
SRR1849908
16
12
8
4
0
0
500
1000
1500
2000
2500

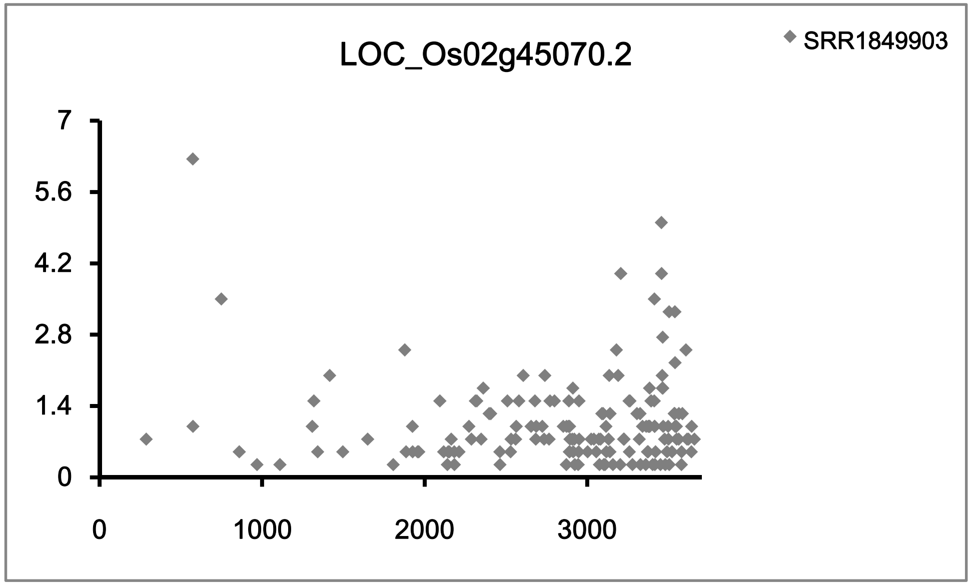

shoot-As-high-9528
shoot-CK-high-38
SRR1849887
SRR1849908
16
12
8
4
0
1503
1513
1523
1533
1543
1553
1563

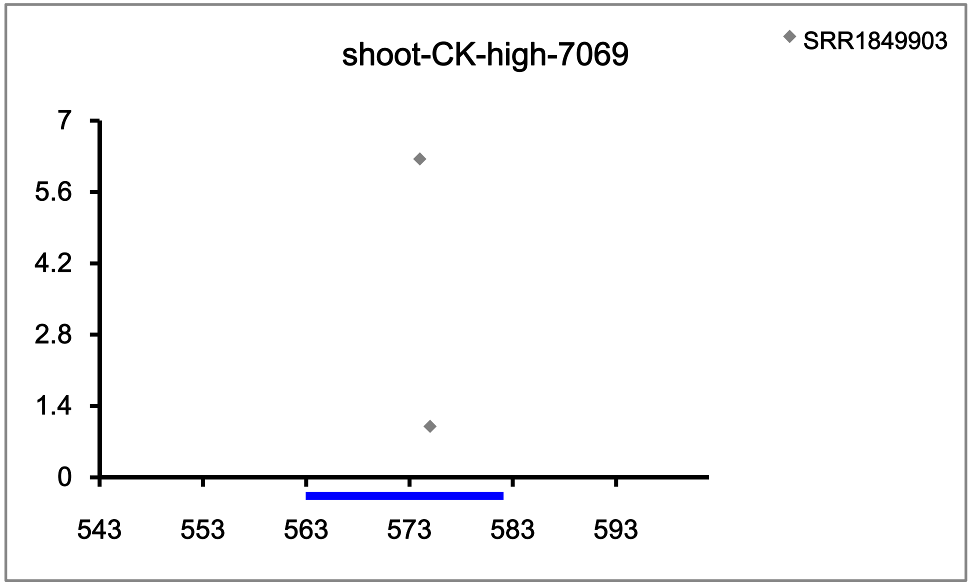

LOC_Os02g44990.1
GSM1040649
SRR1849910
30
24
18
12
6
0
0
500
1000
1500
2000
2500

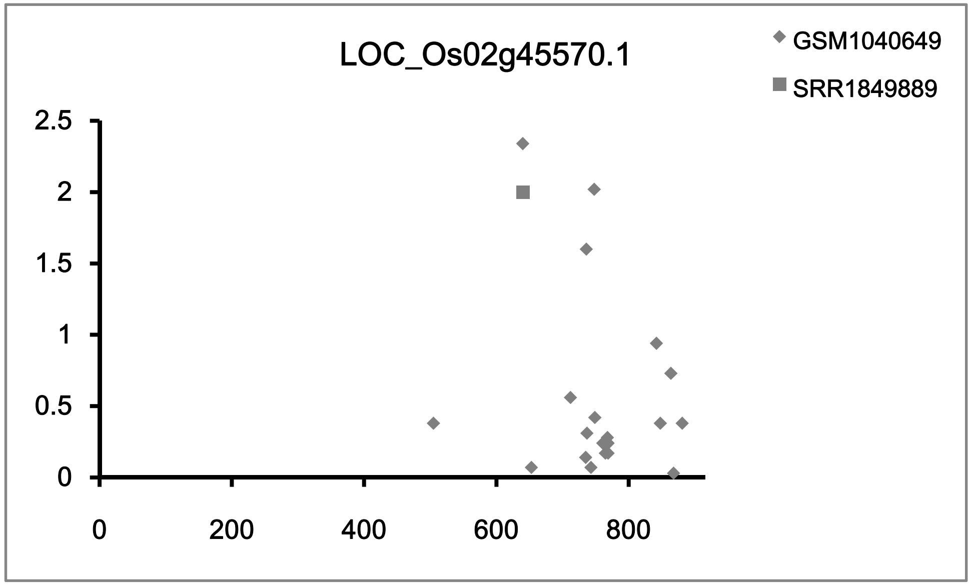

root-CK-high-2928
root-CK-high-13603
GSM1040649
SRR1849910
30
24
18
12
6
0
1842
1852
1862
1872
1882
1892
1902
1912

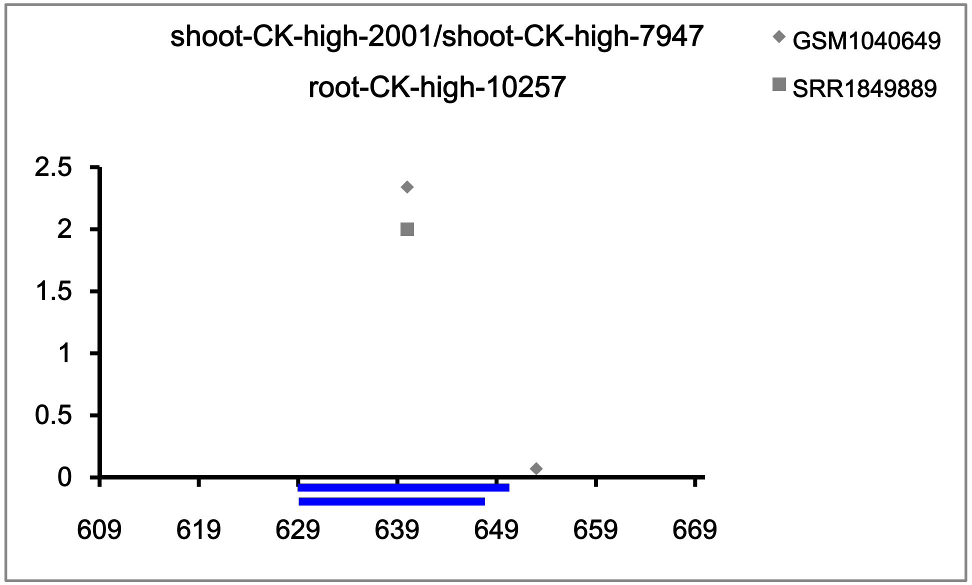

LOC_Os02g45070.1
SRR1849903
7
5.6
4.2
2.8
1.4
0
0
1000
2000
3000

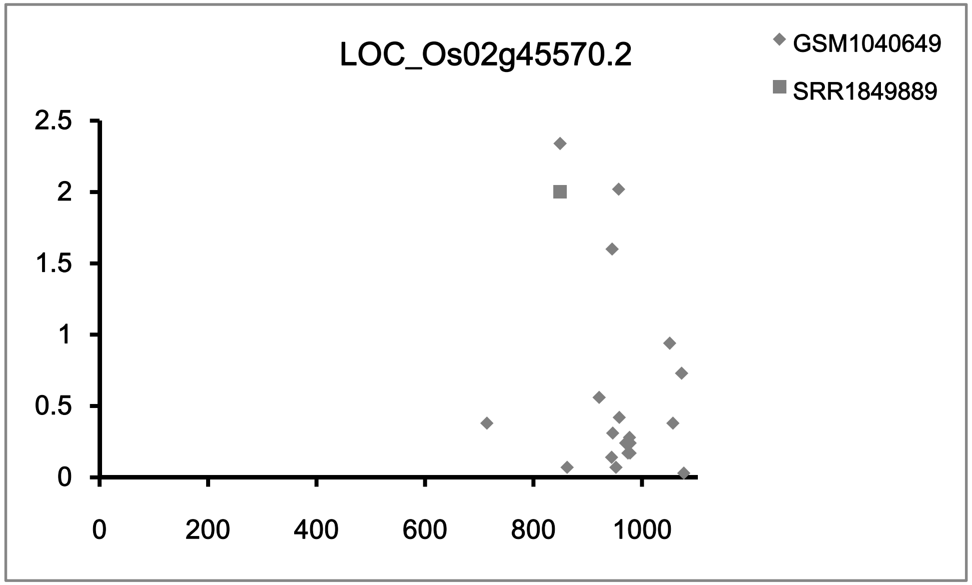

shoot-CK-high-7069
SRR1849903
7
5.6
4.2
2.8
1.4
0
689
699
709
719
729
739

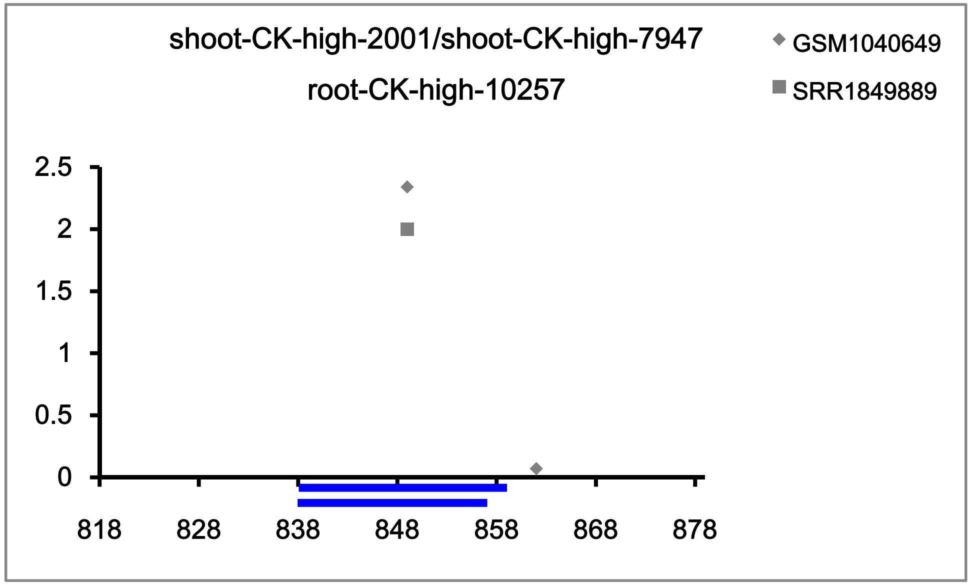

LOC_Os02g45070.2
◆ SRR1849903
7
5.6
4.2
2.8
1.4
0
0
1000
2000
3000

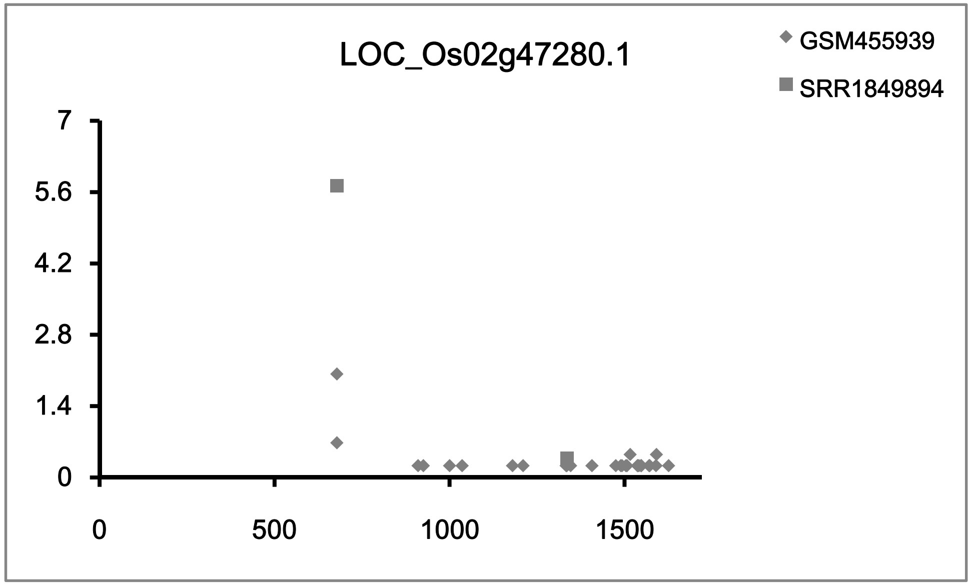

shoot-CK-high-7069
◆ SRR1849903
7
5.6
4.2
2.8
1.4
0
543
553
563
573
583
593

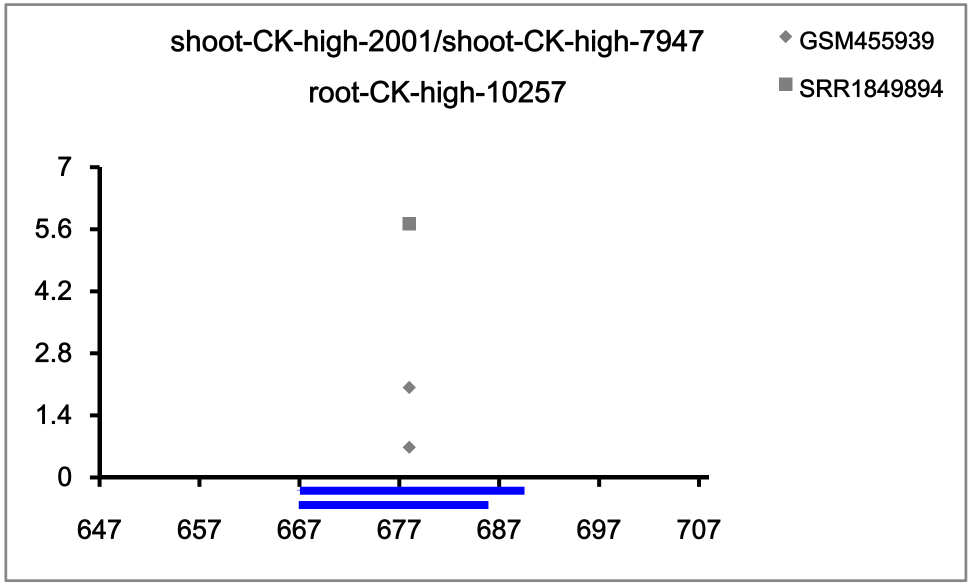

LOC_Os02g45570.1
◆ GSM1040649
■ SRR1849889
2.5
2
1.5
1
0.5
0
0
200
400
600
800

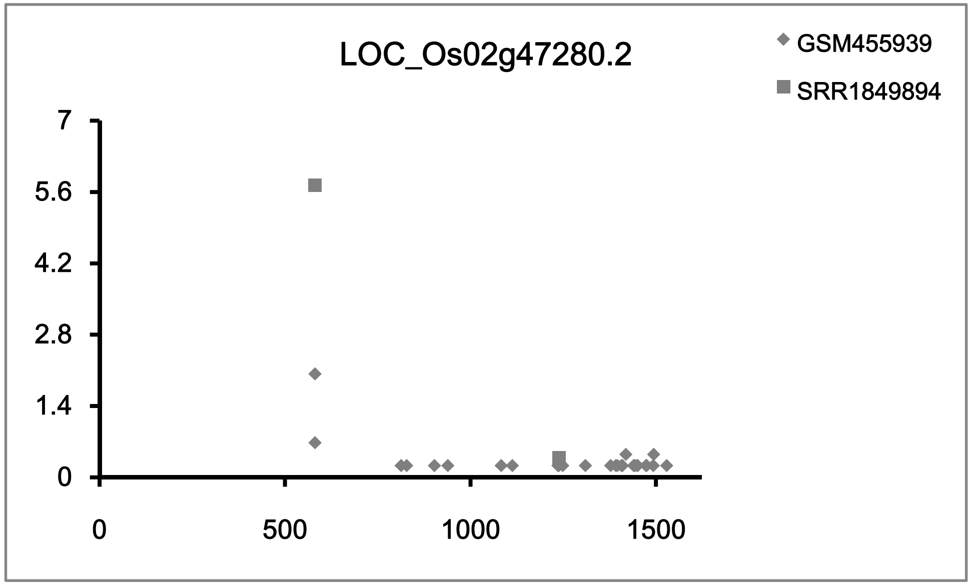

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
◆ GSM1040649
■ SRR1849889
2.5
2
1.5
1
0.5
0
609
619
629
639
649
659
669

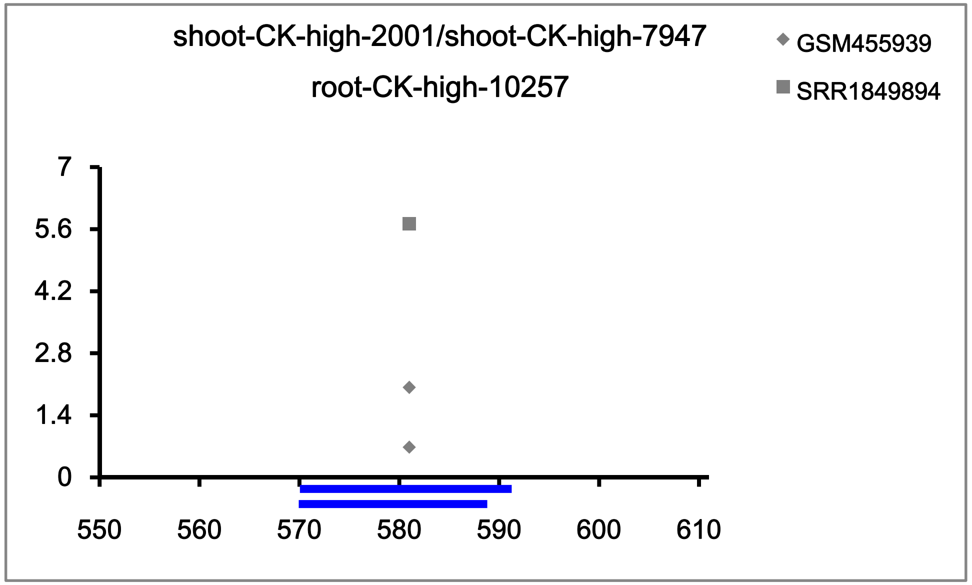

LOC_Os02g45570.2
◆ GSM1040649
■ SRR1849889
2.5
2
1.5
1
0.5
0
0
200
400
600
800
1000

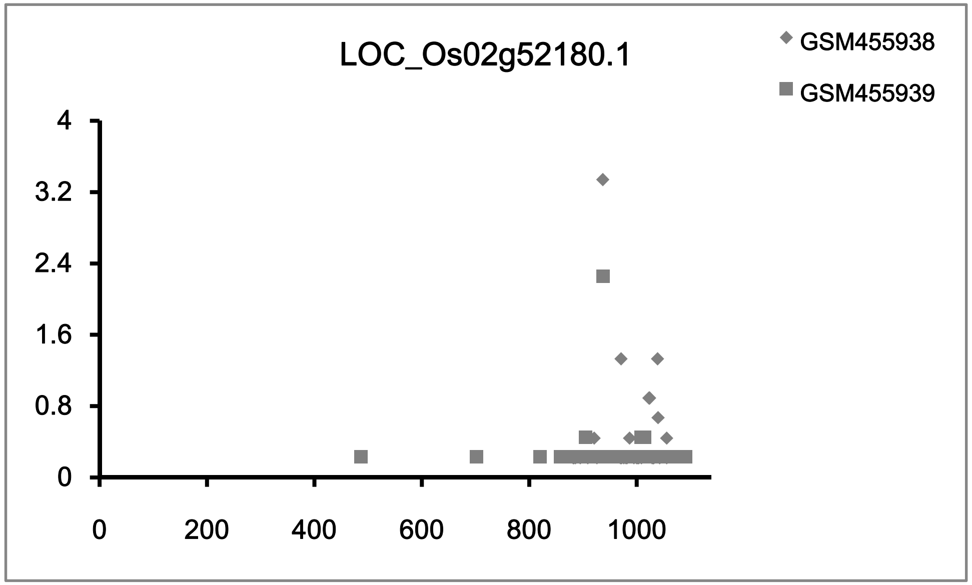

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
◆ GSM1040649
■ SRR1849889
2.5
2
1.5
1
0.5
0
818
828
838
848
858
868
878

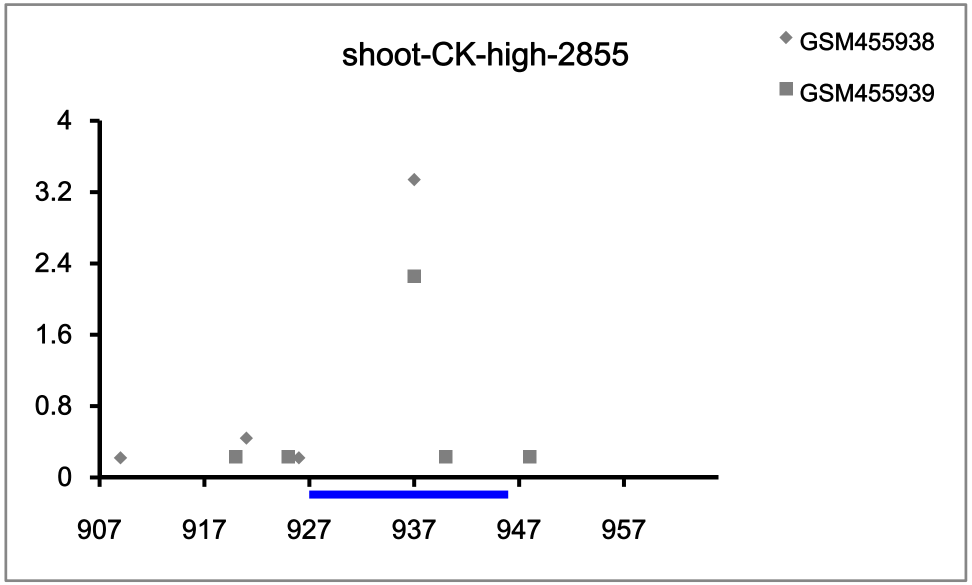

LOC_Os02g47280.1
◆ GSM455939
■ SRR1849894
7
5.6
4.2
2.8
1.4
0
0
500
1000
1500

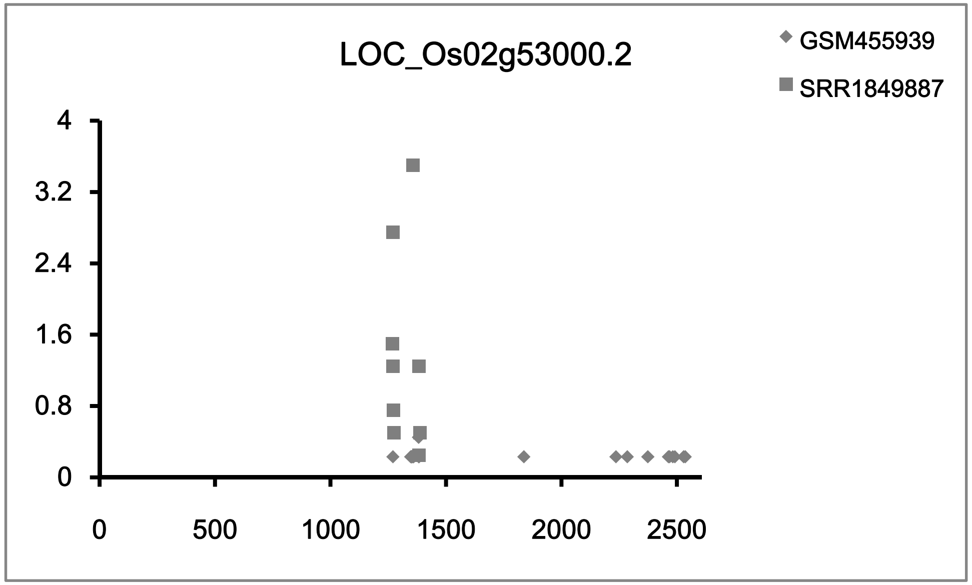

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
◆ GSM455939
■ SRR1849894
7
5.6
4.2
2.8
1.4
0
647
657
667
677
687
697
707

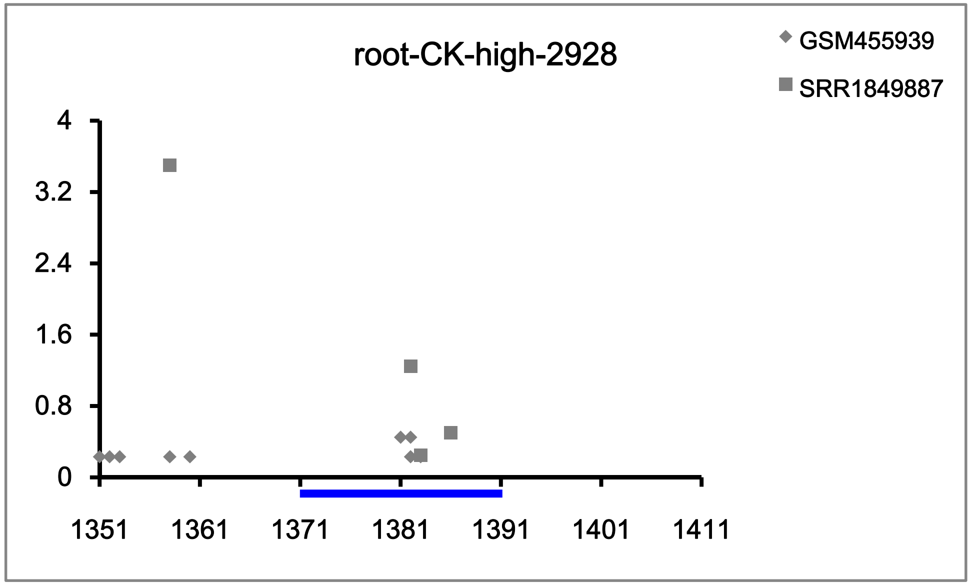

LOC_Os02g47280.2
GSM455939
SRR1849894
7
5.6
4.2
2.8
1.4
0
0
500
1000
1500

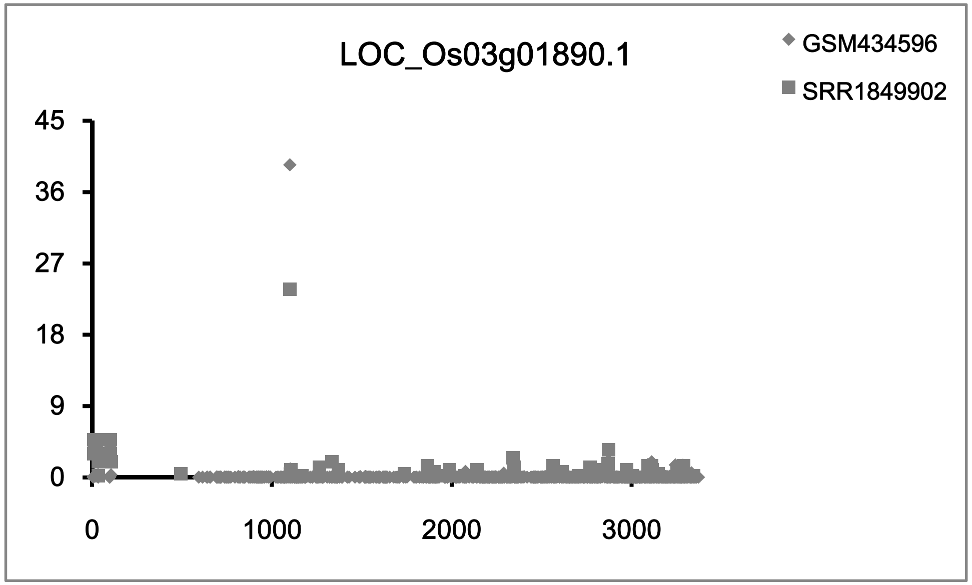

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
GSM455939
SRR1849894
7
5.6
4.2
2.8
1.4
0
550
560
570
580
590
600
610

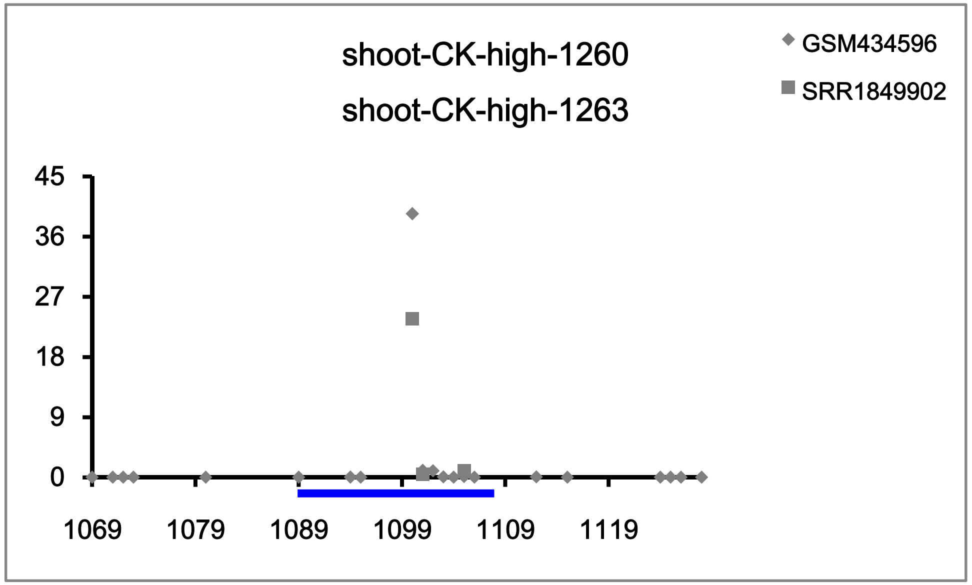

LOC_Os02g52180.1
GSM455938
GSM455939
4
3.2
2.4
1.6
0.8
0
0
200
400
600
800
1000

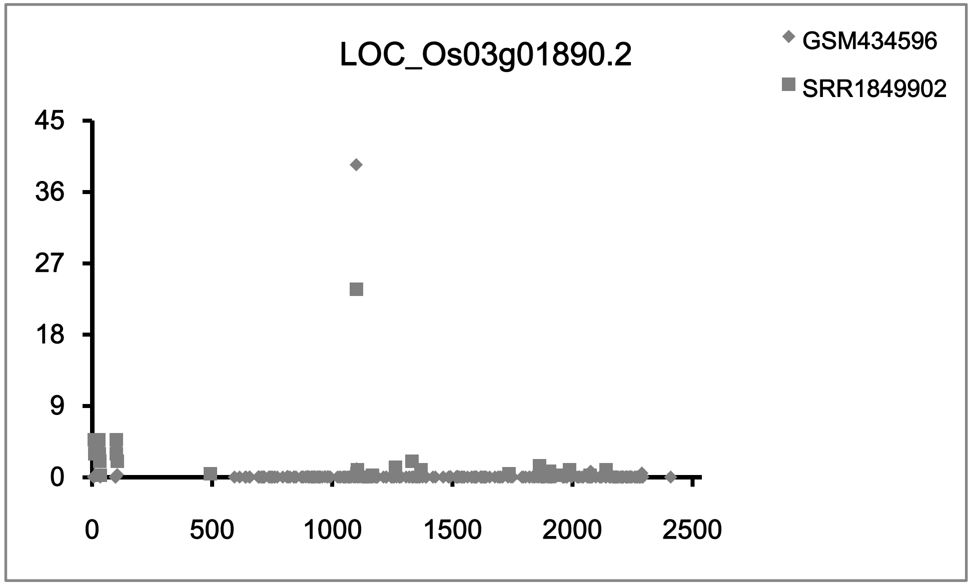

shoot-CK-high-2855
GSM455938
GSM455939
4
3.2
2.4
1.6
0.8
0
907
917
927
937
947
957

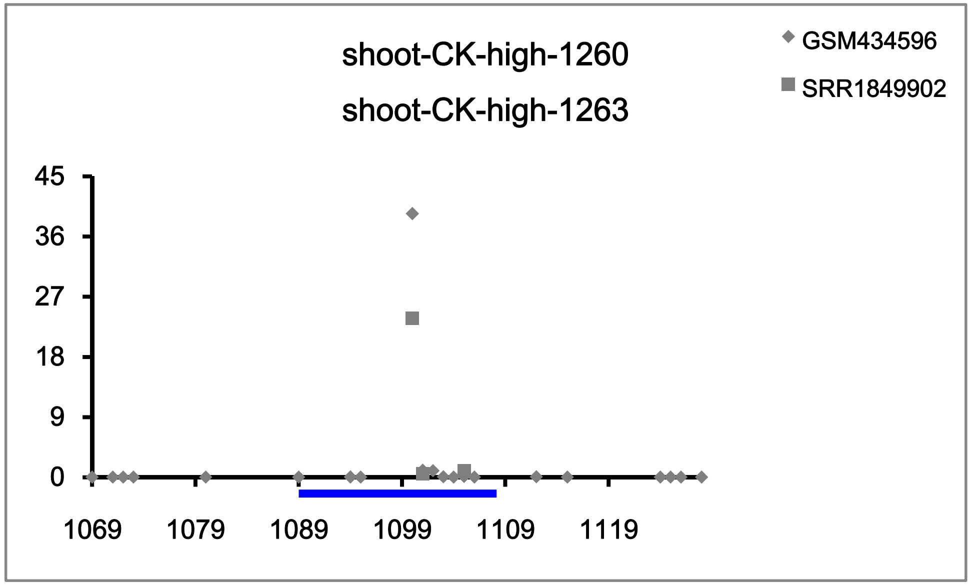

LOC_Os02g53000.2
GSM455939
SRR1849887
4
3.2
2.4
1.6
0.8
0
0
500
1000
1500
2000
2500

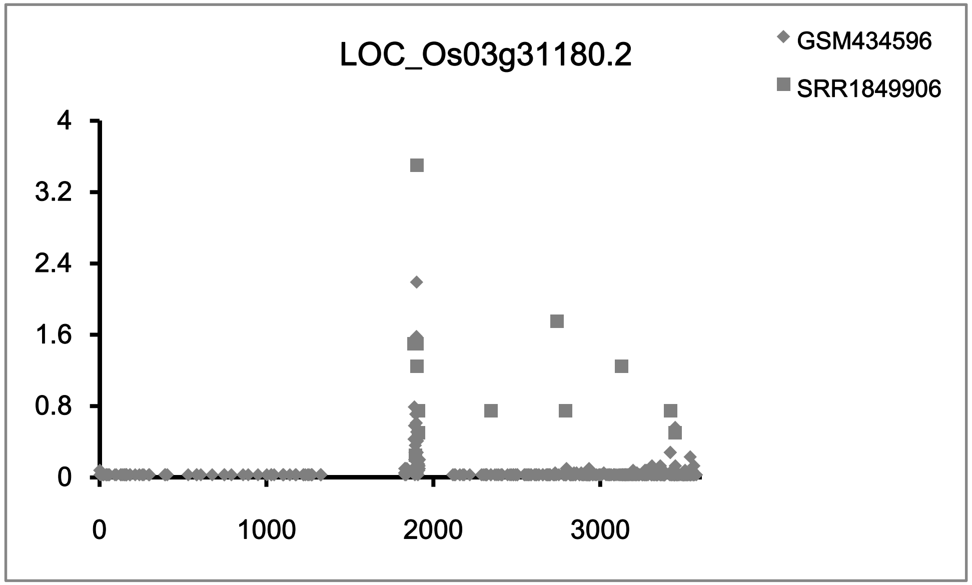

root-CK-high-2928
GSM455939
SRR1849887
4
3.2
2.4
1.6
0.8
0
1351
1361
1371
1381
1391
1401
1411

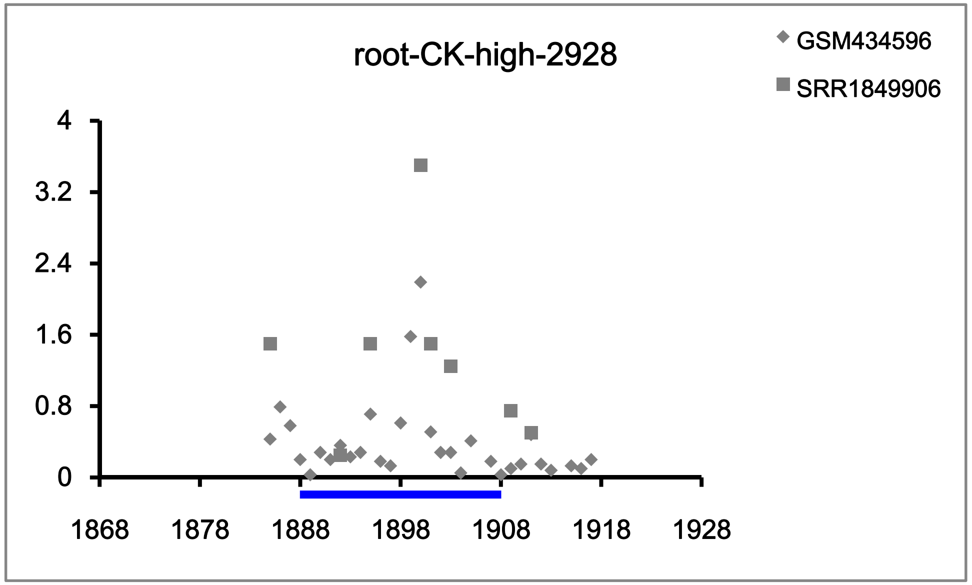

LOC_Os03g01890.1
GSM434596
SRR1849902
45
36
27
18
9
0
0
1000
2000
3000

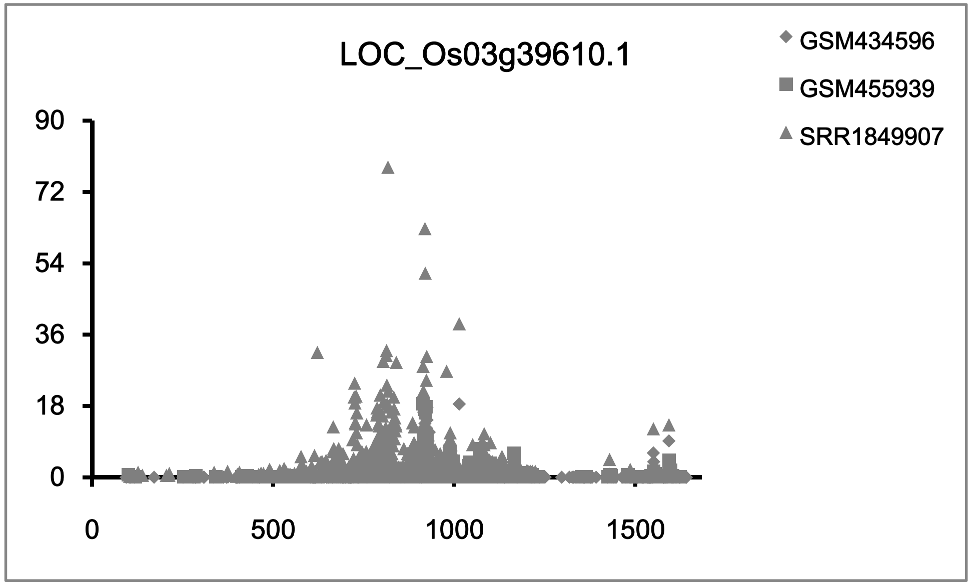

shoot-CK-high-1260
shoot-CK-high-1263
GSM434596
SRR1849902
45
36
27
18
9
0
1069
1079
1089
1099
1109
1119

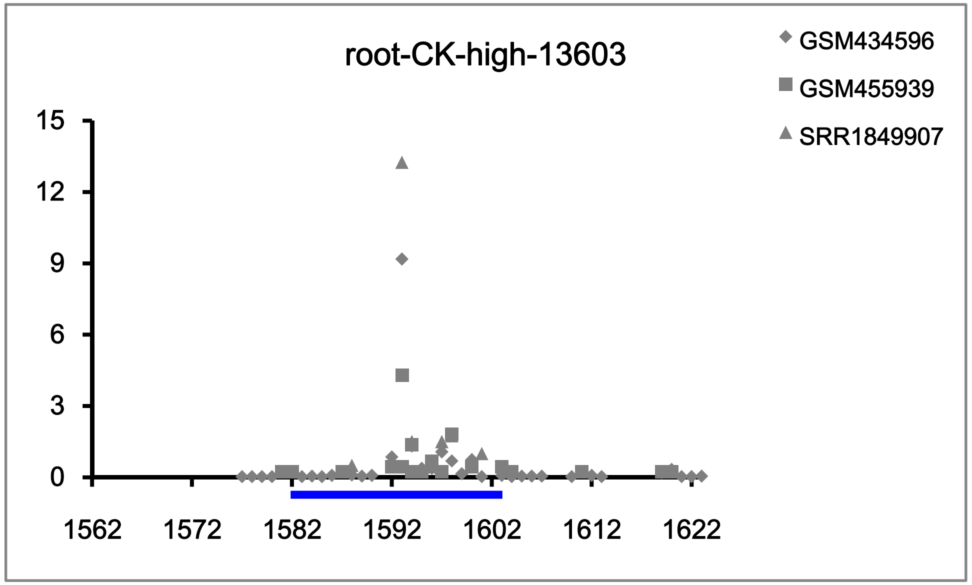

LOC_Os03g01890.2
◆ GSM434596
■ SRR1849902
45
36
27
18
9
0
0
500
1000
1500
2000
2500

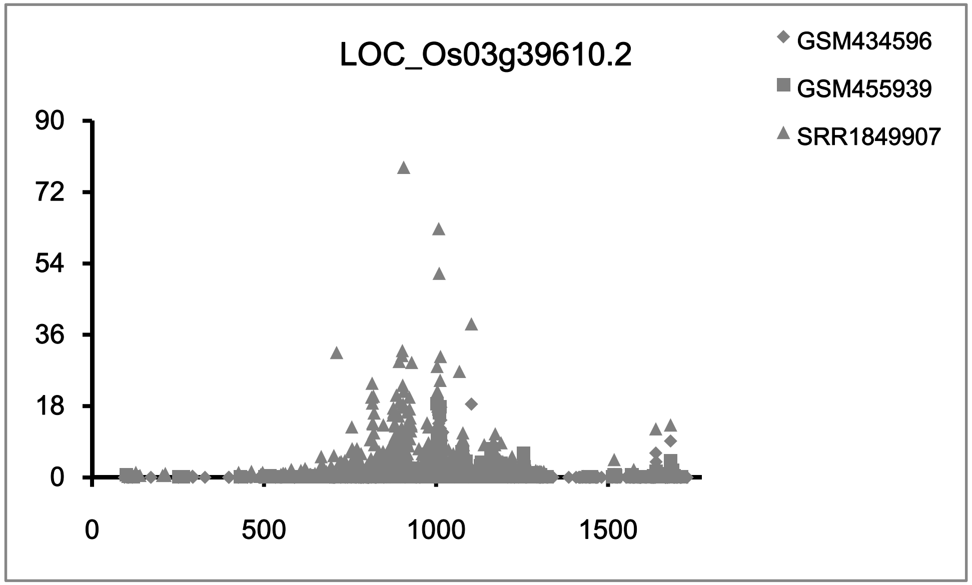

shoot-CK-high-1260
shoot-CK-high-1263
◆ GSM434596
■ SRR1849902
45
36
27
18
9
0
1069
1079
1089
1099
1109
1119

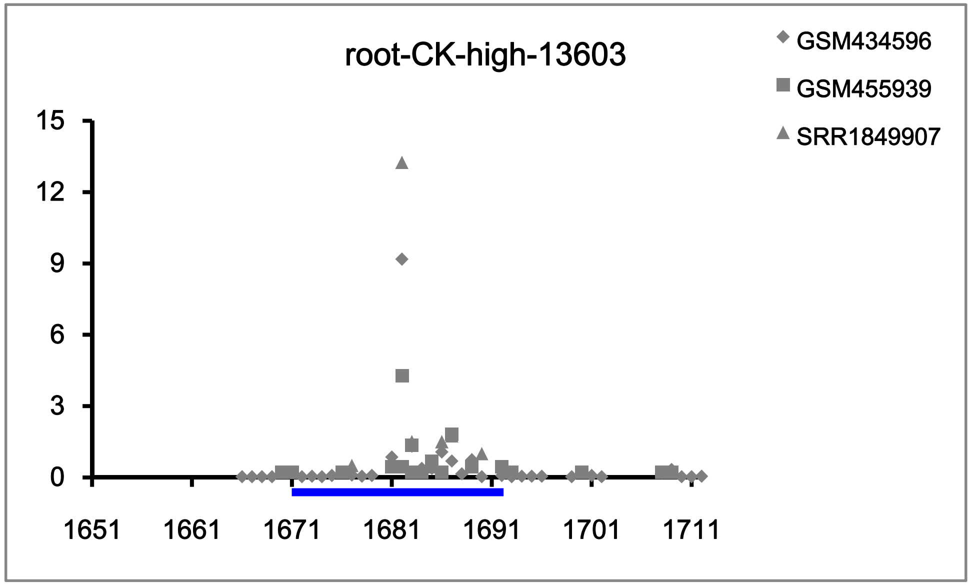

LOC_Os03g31180.2
◆ GSM434596
■ SRR1849906
4
3.2
2.4
1.6
0.8
0
0
1000
2000
3000

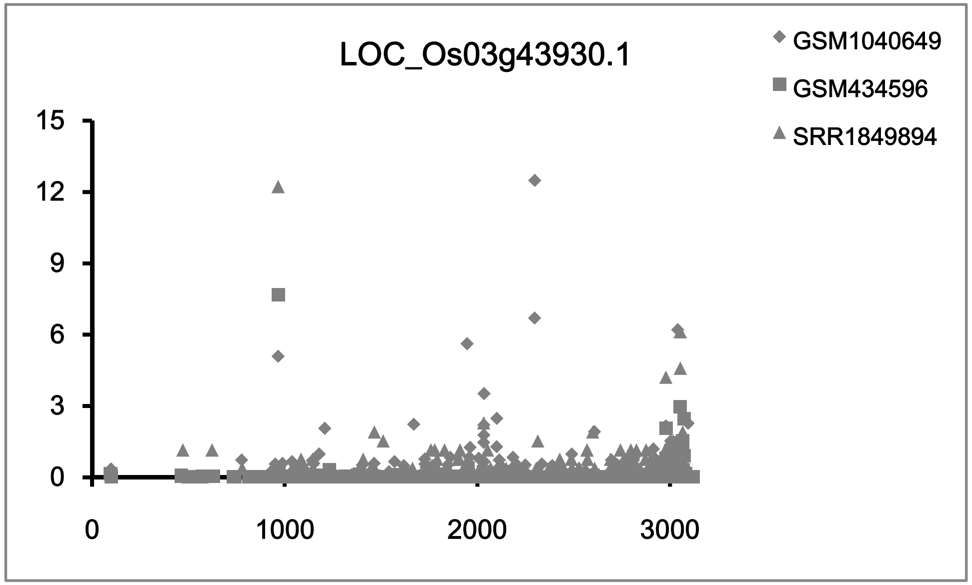

root-CK-high-2928
◆ GSM434596
■ SRR1849906
4
3.2
2.4
1.6
0.8
0
1868
1878
1888
1898
1908
1918
1928

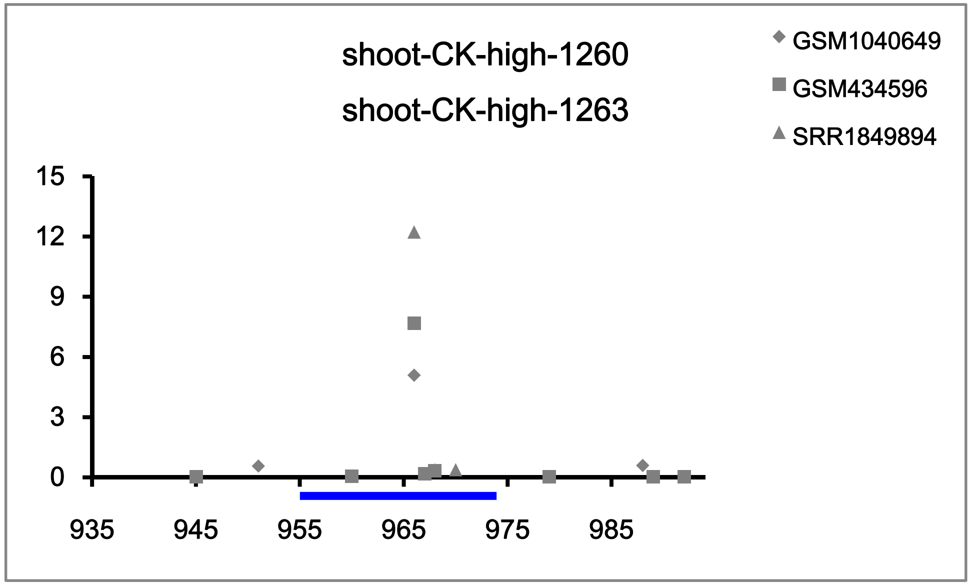

LOC_Os03g39610.1
GSM434596
GSM455939
SRR1849907
90
72
54
36
18
0
0
500
1000
1500

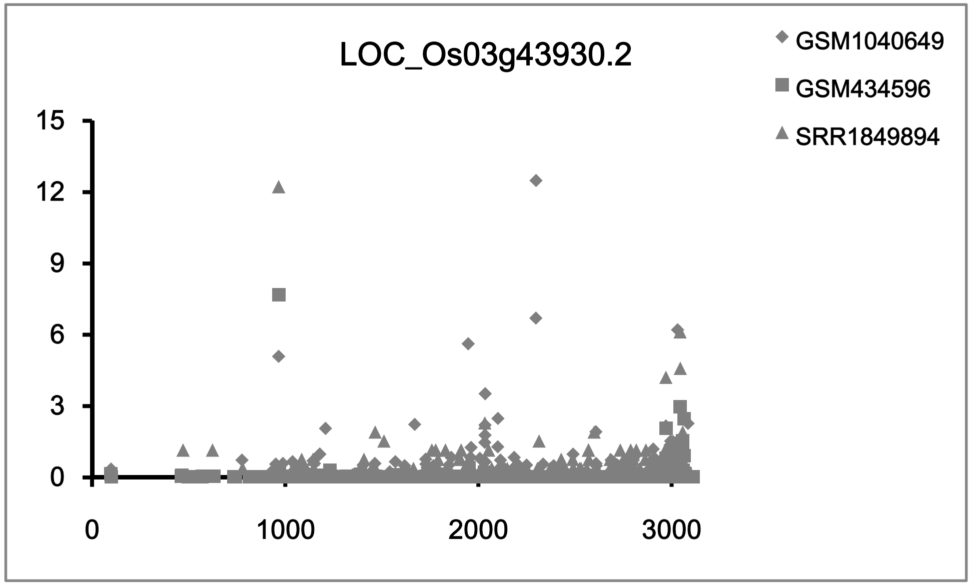

root-CK-high-13603
GSM434596
GSM455939
SRR1849907
15
12
9
6
3
0
1562
1572
1582
1592
1602
1612
1622

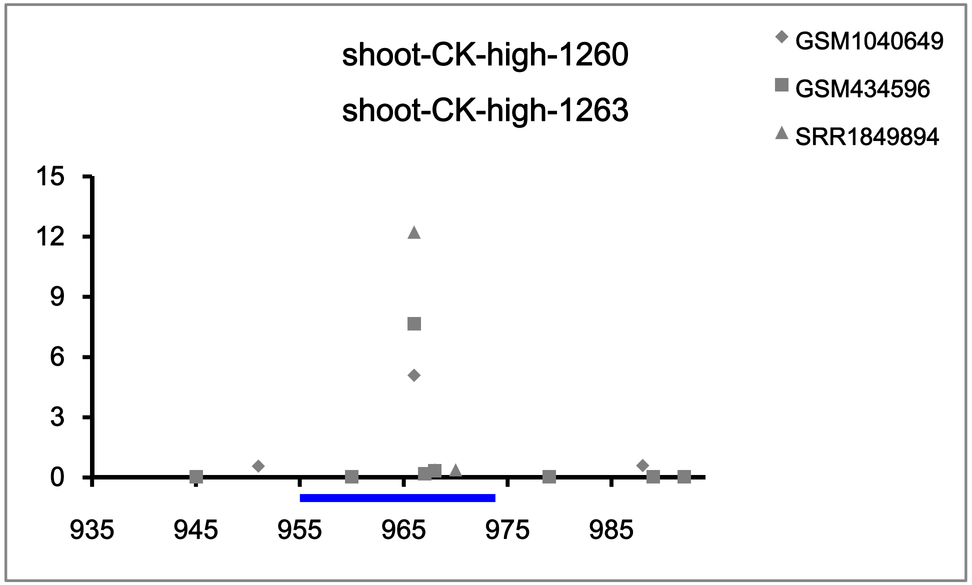

LOC_Os03g39610.2
GSM434596
GSM455939
SRR1849907
90
72
54
36
18
0
0
500
1000
1500

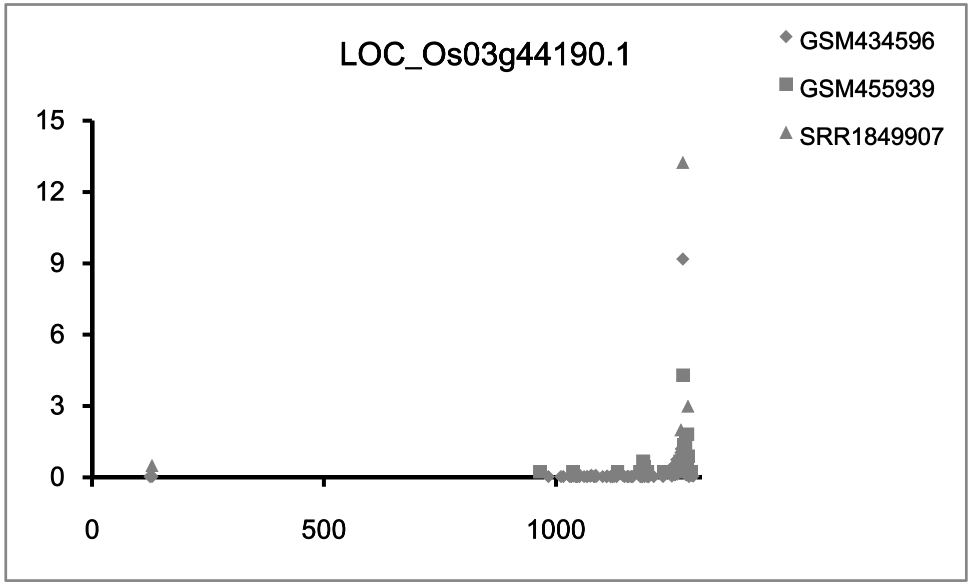

root-CK-high-13603
GSM434596
GSM455939
SRR1849907
15
12
9
6
3
0
1651
1661
1671
1681
1691
1701
1711

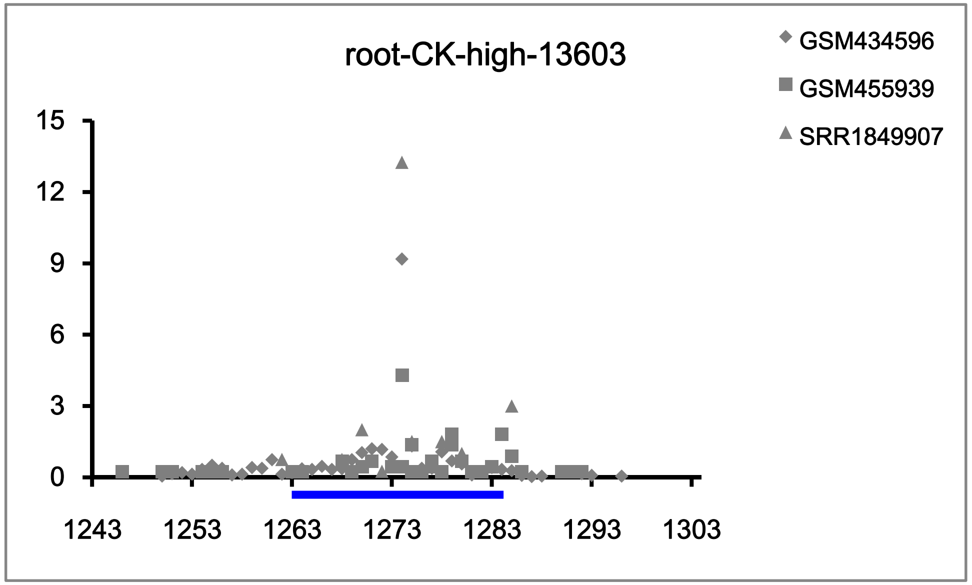

LOC_Os03g43930.1
GSM1040649
GSM434596
SRR1849894
15
12
9
6
3
0
0
1000
2000
3000

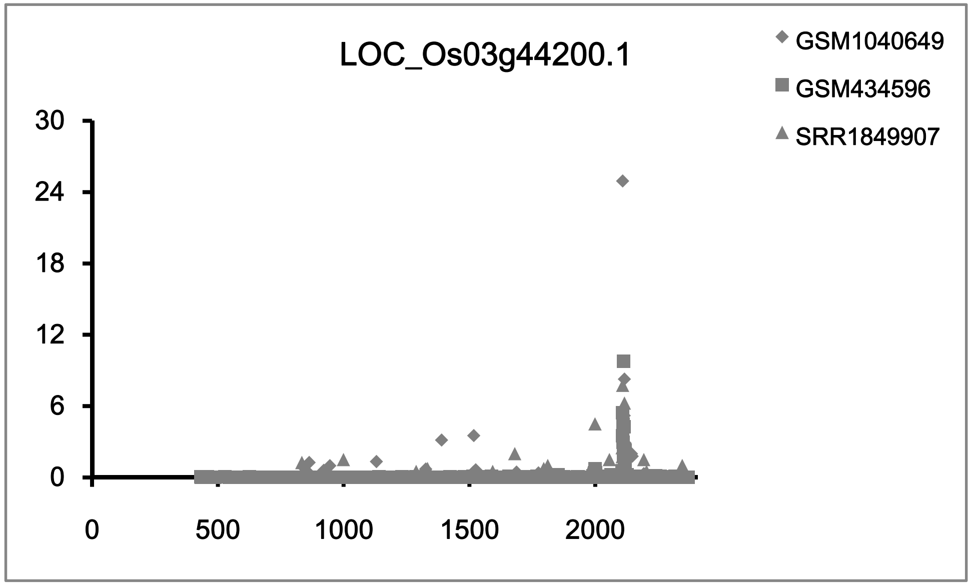

shoot-CK-high-1260
shoot-CK-high-1263
GSM1040649
GSM434596
SRR1849894
15
12
9
6
3
0
935
945
955
965
975
985

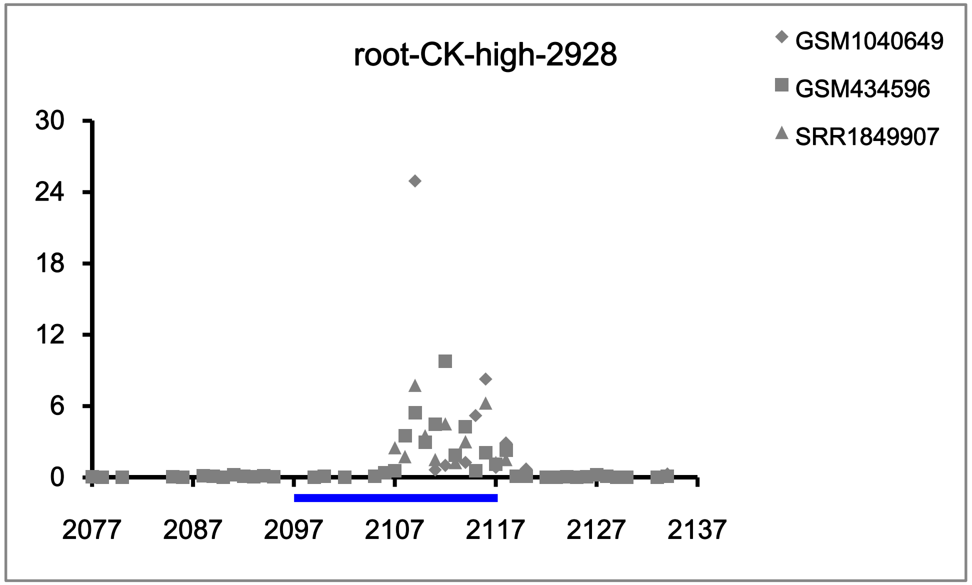

LOC_Os03g43930.2
GSM1040649
GSM434596
SRR1849894
15
12
9
6
3
0
0
1000
2000
3000

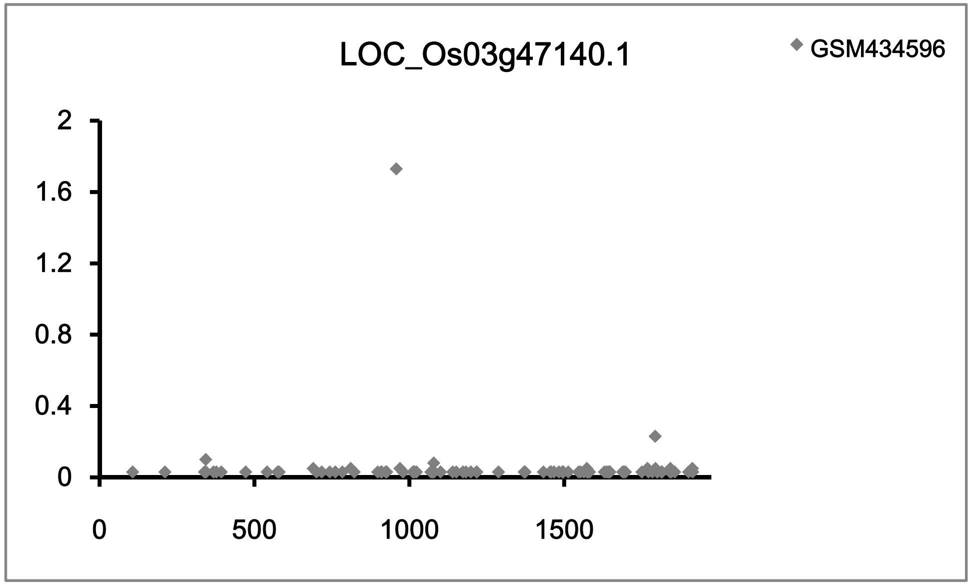

shoot-CK-high-1260
shoot-CK-high-1263
GSM1040649
GSM434596
SRR1849894
15
12
9
6
3
0
935
945
955
965
975
985

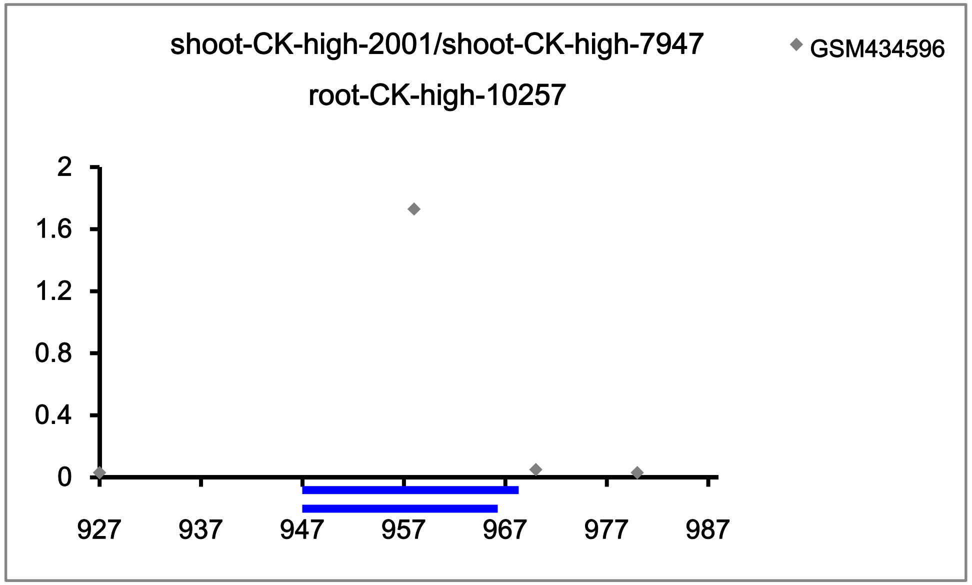

LOC_Os03g44190.1
GSM434596
GSM455939
SRR1849907
15
12
9
6
3
0
0
500
1000

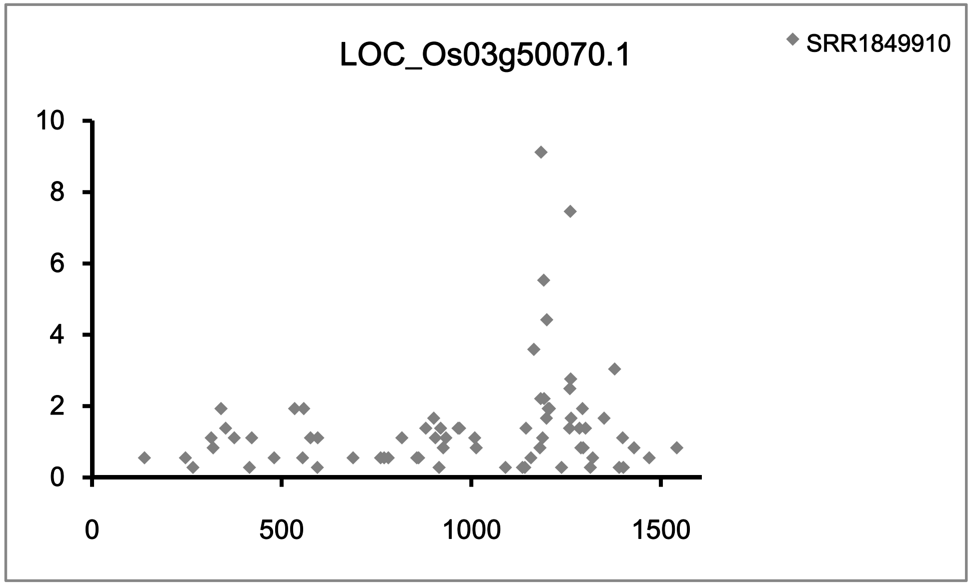

root-CK-high-13603
GSM434596
GSM455939
SRR1849907
15
12
9
6
3
0
1243
1253
1263
1273
1283
1293
1303

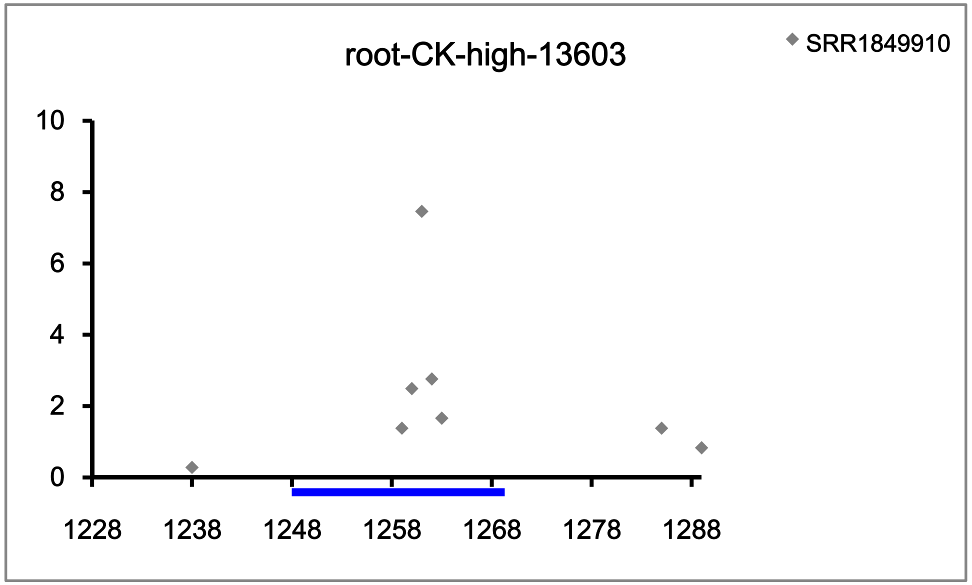

LOC_Os03g44200.1
GSM1040649
GSM434596
SRR1849907
30
24
18
12
6
0
0
500
1000
1500
2000

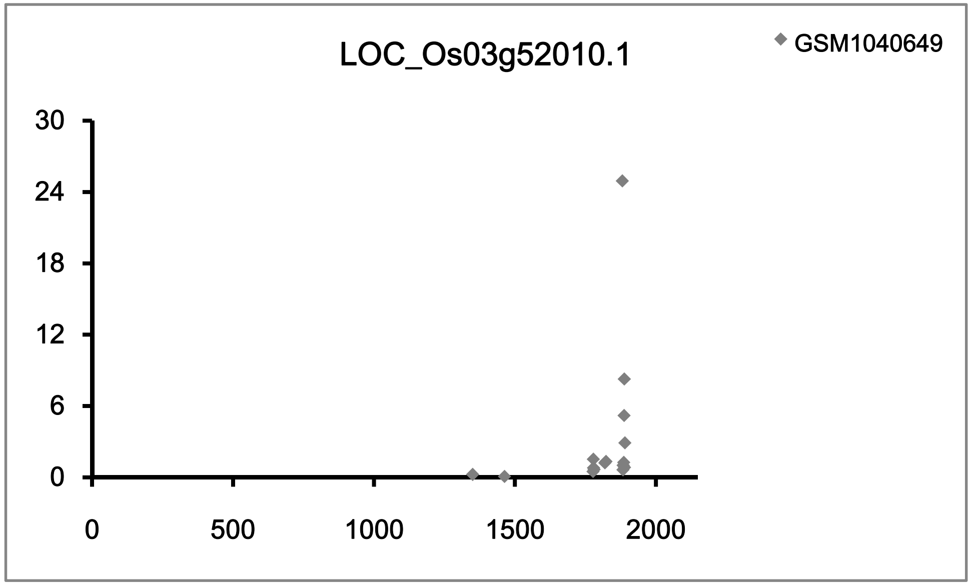

root-CK-high-2928
GSM1040649
GSM434596
SRR1849907
30
24
18
12
6
0
2077
2087
2097
2107
2117
2127
2137

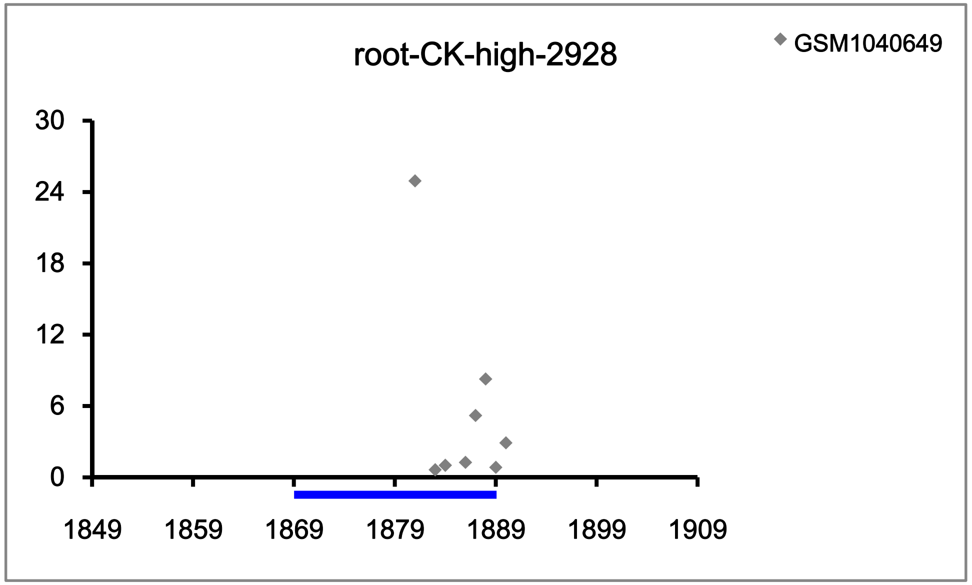

LOC_Os03g47140.1
GSM434596
2
1.6
1.2
0.8
0.4
0
0
500
1000
1500

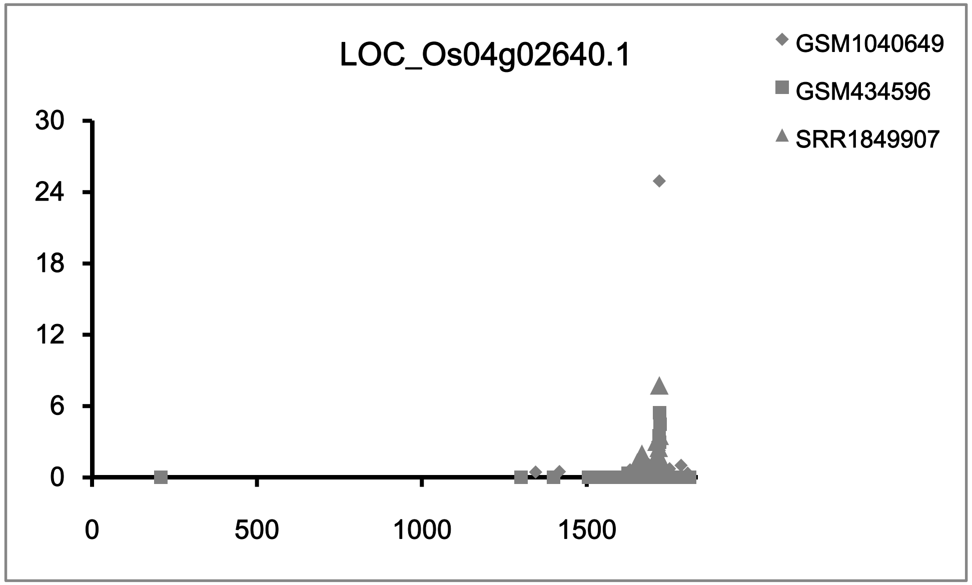

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
GSM434596
2
1.6
1.2
0.8
0.4
0
927
937
947
957
967
977
987

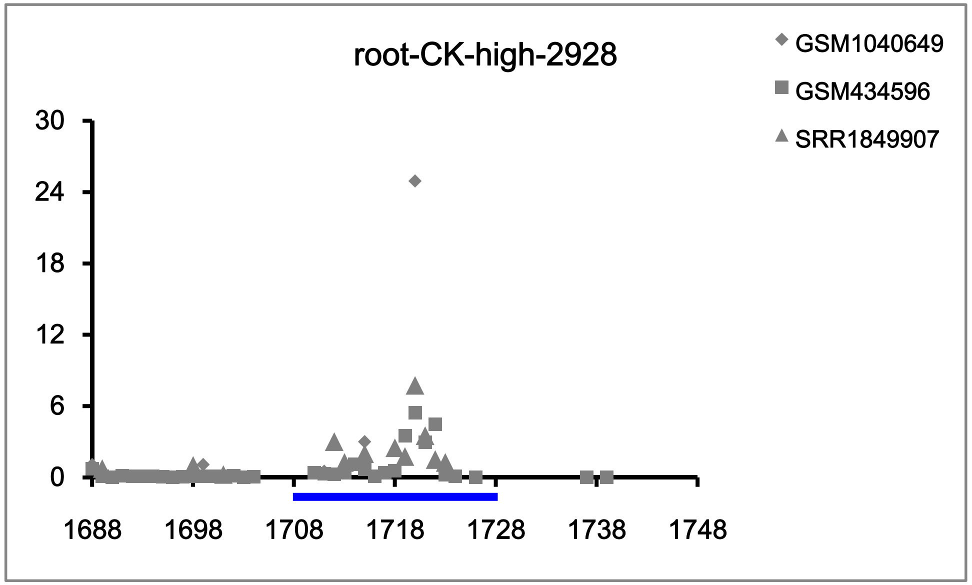

LOC_Os03g50070.1
SRR1849910
10
8
6
4
2
0
0
500
1000
1500

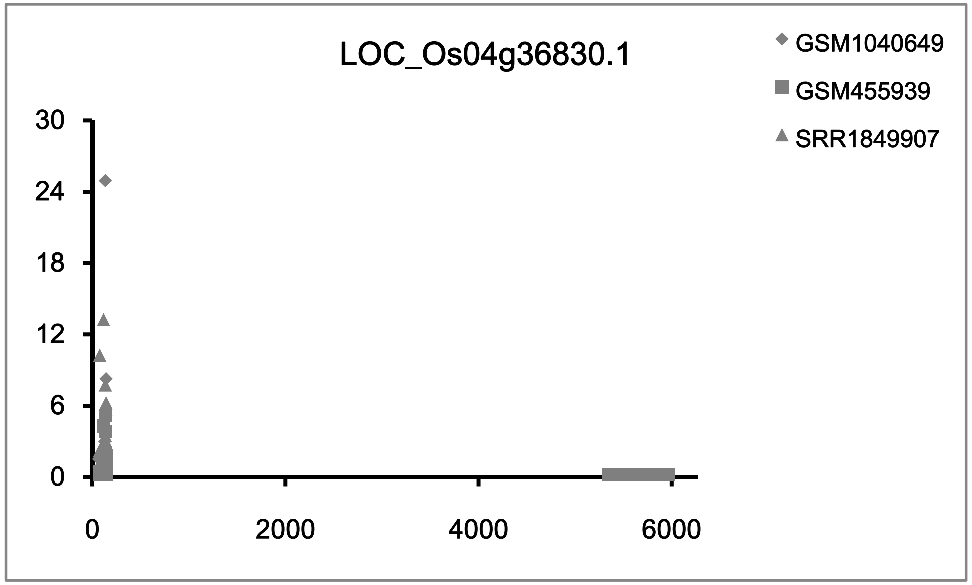

root-CK-high-13603
SRR1849910
10
8
6
4
2
0
1228
1238
1248
1258
1268
1278
1288

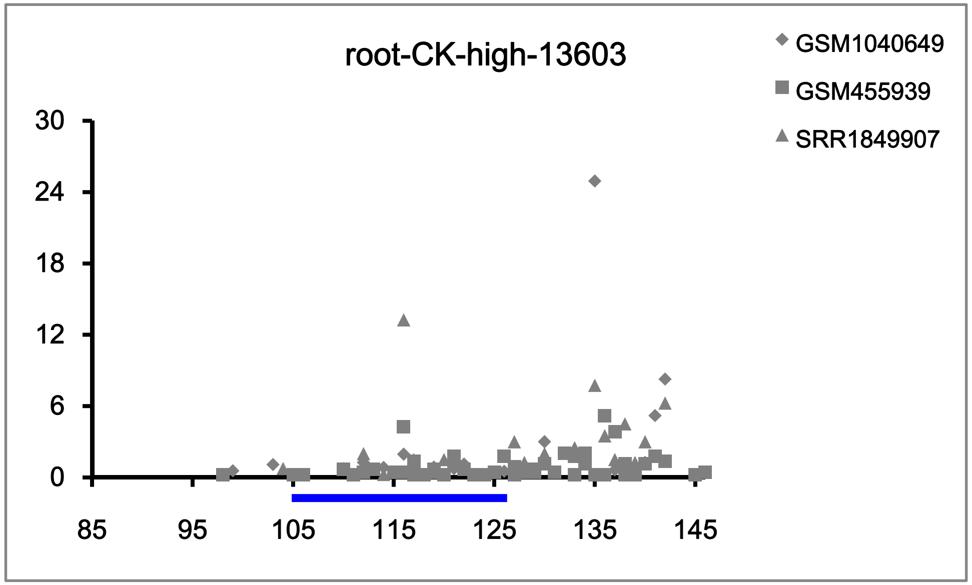

LOC_Os03g52010.1
◆ GSM1040649
30
24
18
12
6
0
0
500
1000
1500
2000

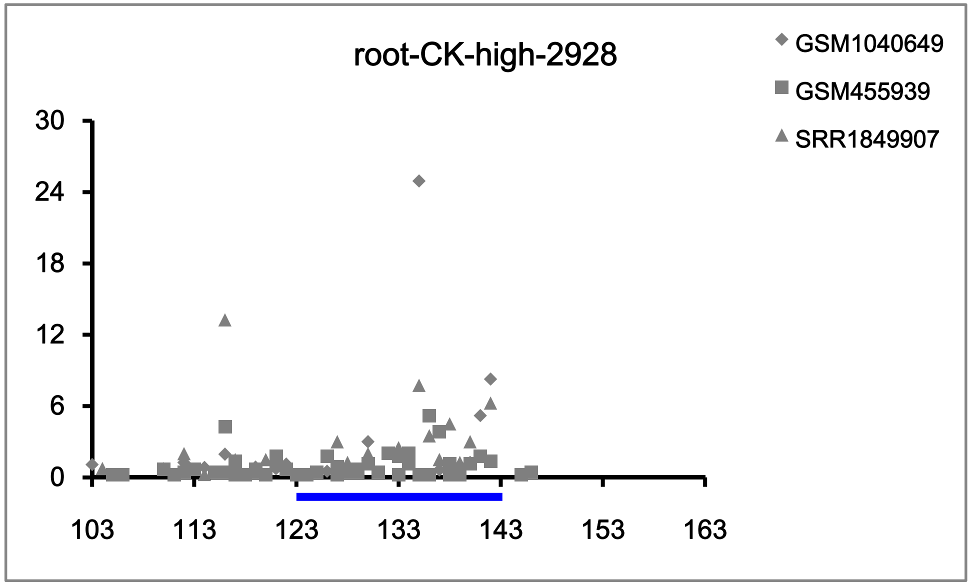

root-CK-high-2928
◆ GSM1040649
30
24
18
12
6
0
1849
1859
1869
1879
1889
1899
1909

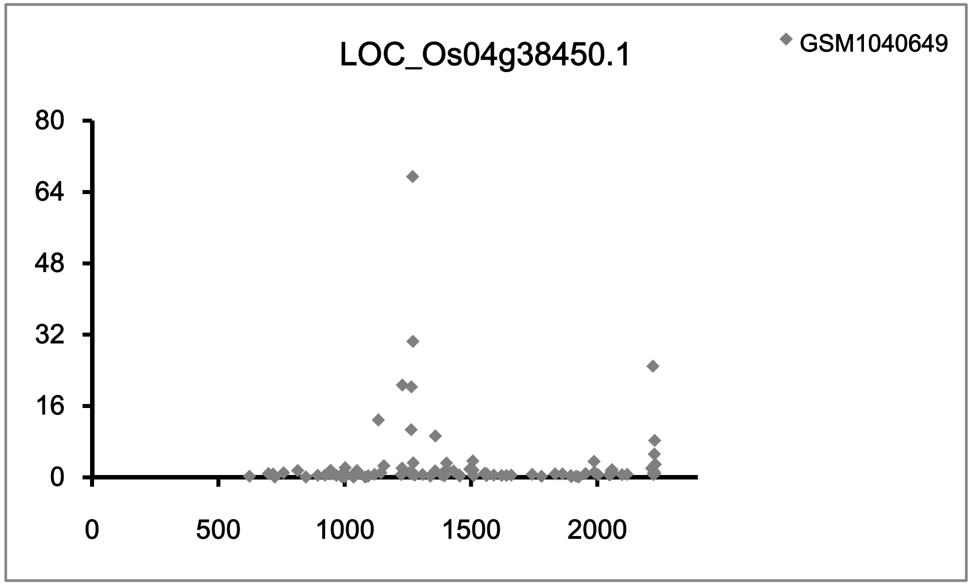

LOC_Os04g02640.1
◆ GSM1040649
■ GSM434596
▲ SRR1849907
30
24
18
12
6
0
0
500
1000
1500

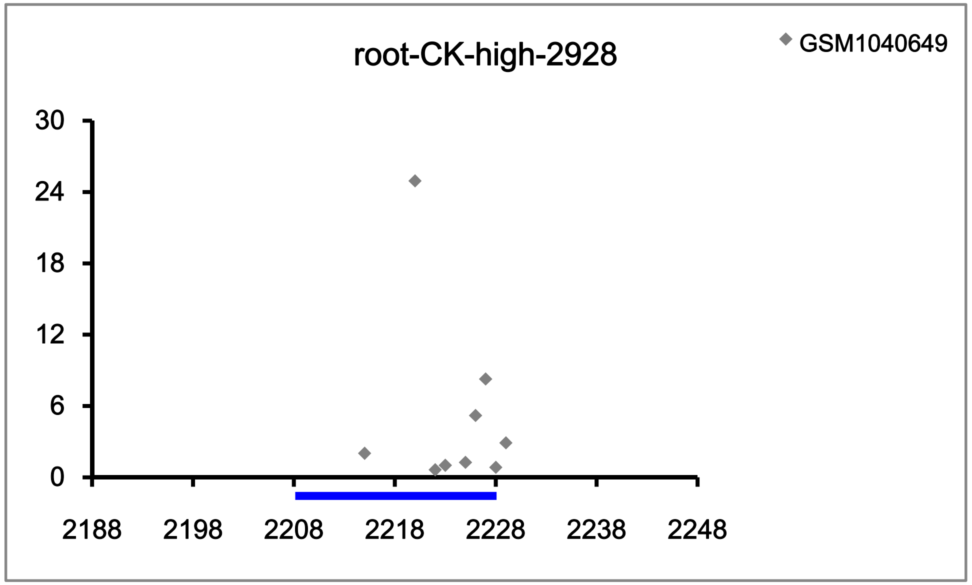

root-CK-high-2928
◆ GSM1040649
■ GSM434596
▲ SRR1849907
30
24
18
12
6
0
1688
1698
1708
1718
1728
1738
1748

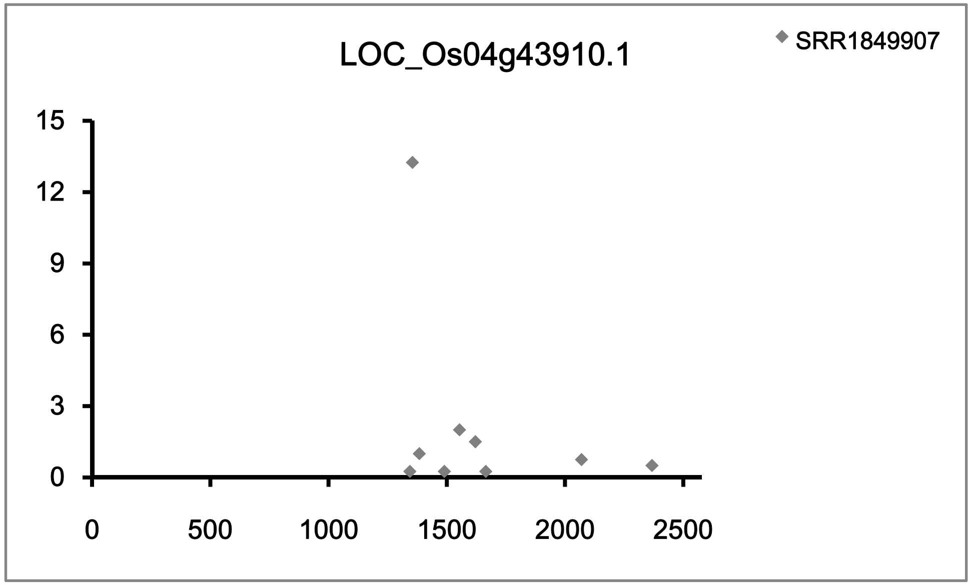

LOC_Os04g36830.1
◆ GSM1040649
■ GSM455939
▲ SRR1849907
30
24
18
12
6
0
0
2000
4000
6000

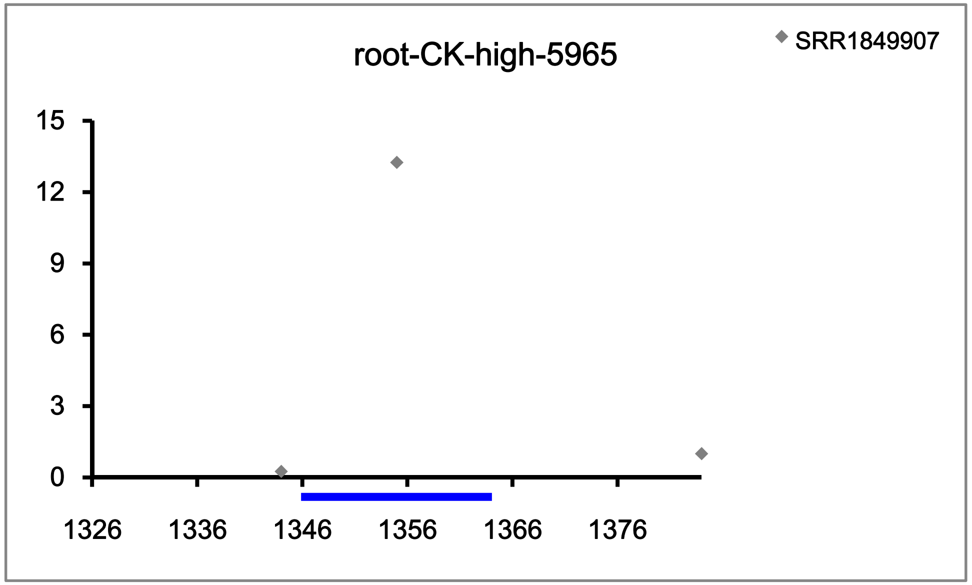

root-CK-high-13603
◆ GSM1040649
■ GSM455939
▲ SRR1849907
30
24
18
12
6
0
85
95
105
115
125
135
145

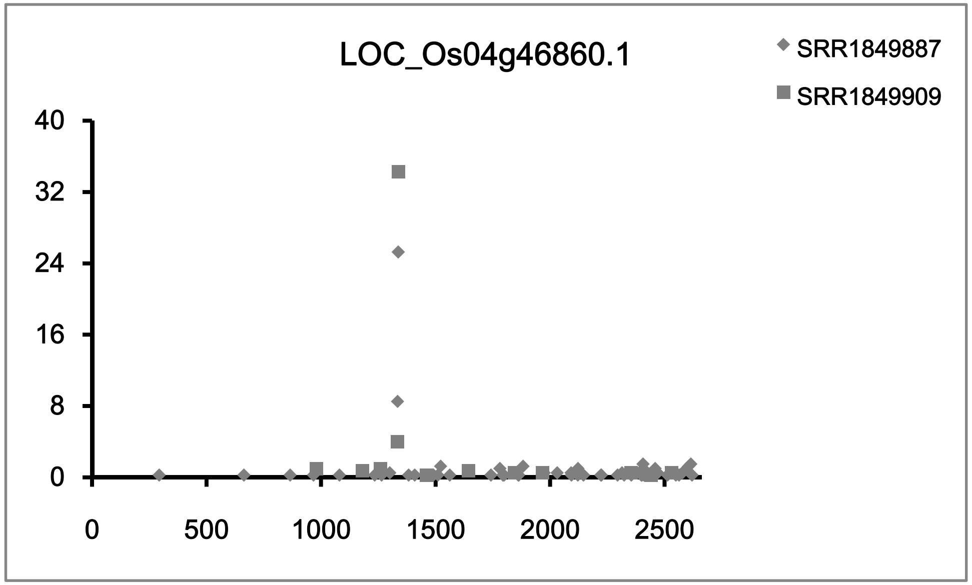

root-CK-high-2928
◆ GSM1040649
■ GSM455939
▲ SRR1849907
30
24
18
12
6
0
103
113
123
133
143
153
163

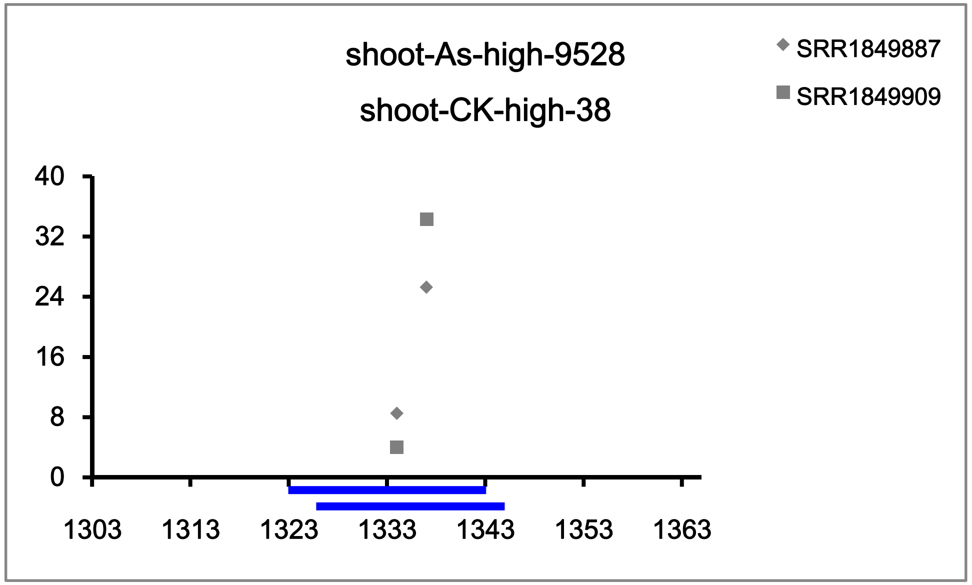

LOC_Os04g38450.1
GSM1040649
80
64
48
32
16
0
0
500
1000
1500
2000

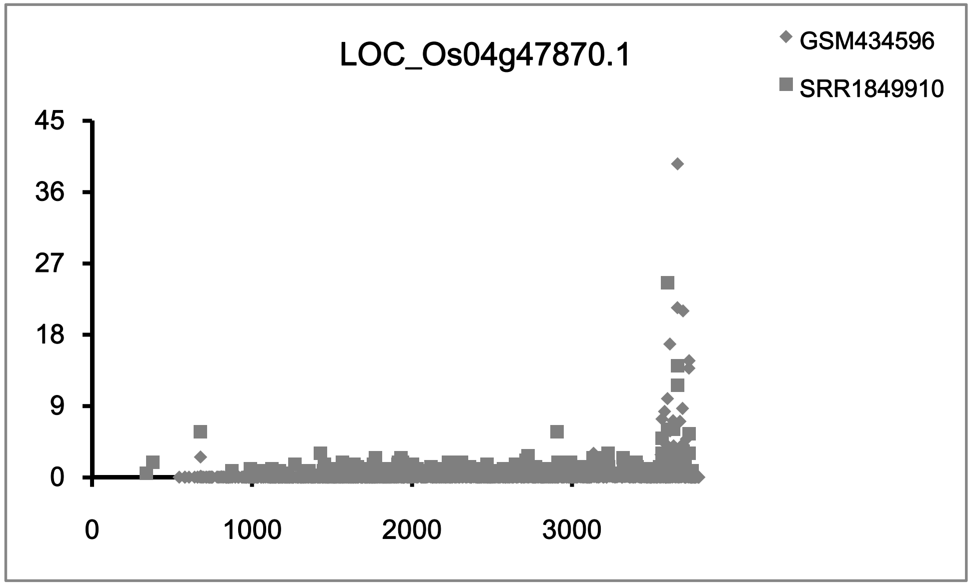

root-CK-high-2928
GSM1040649
30
24
18
12
6
0
2188
2198
2208
2218
2228
2238
2248

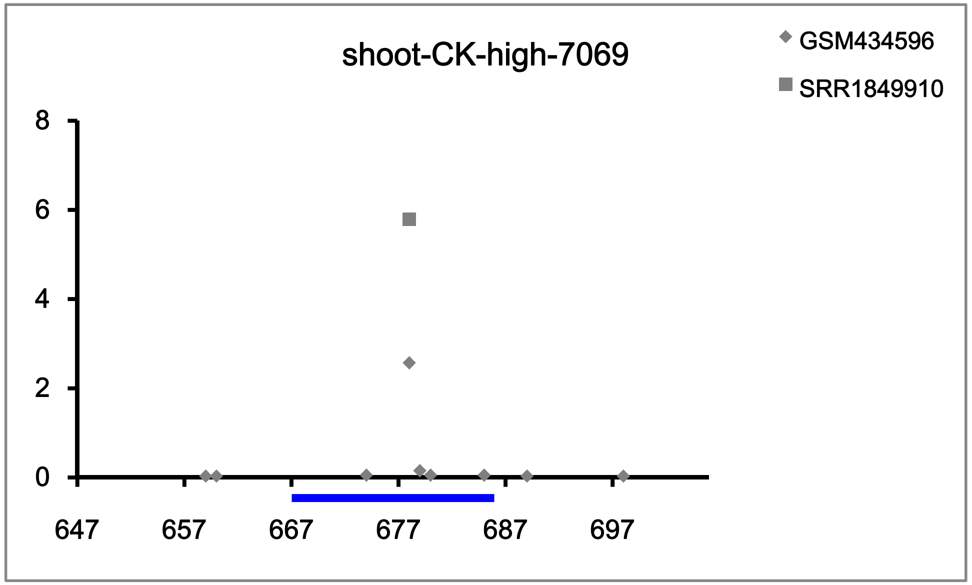

LOC_Os04g43910.1
SRR1849907
15
12
9
6
3
0
0
500
1000
1500
2000
2500

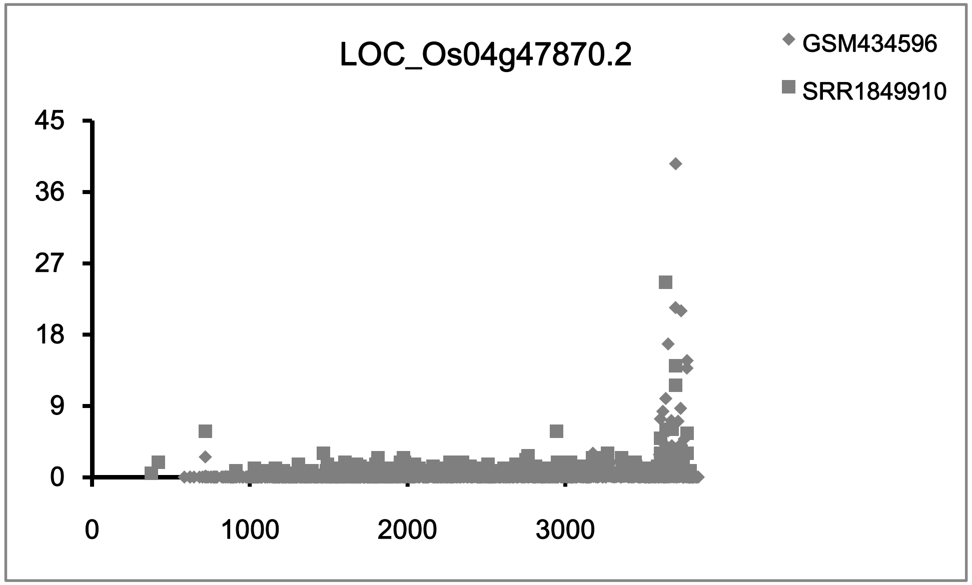

root-CK-high-5965
SRR1849907
15
12
9
6
3
0
1326
1336
1346
1356
1366
1376

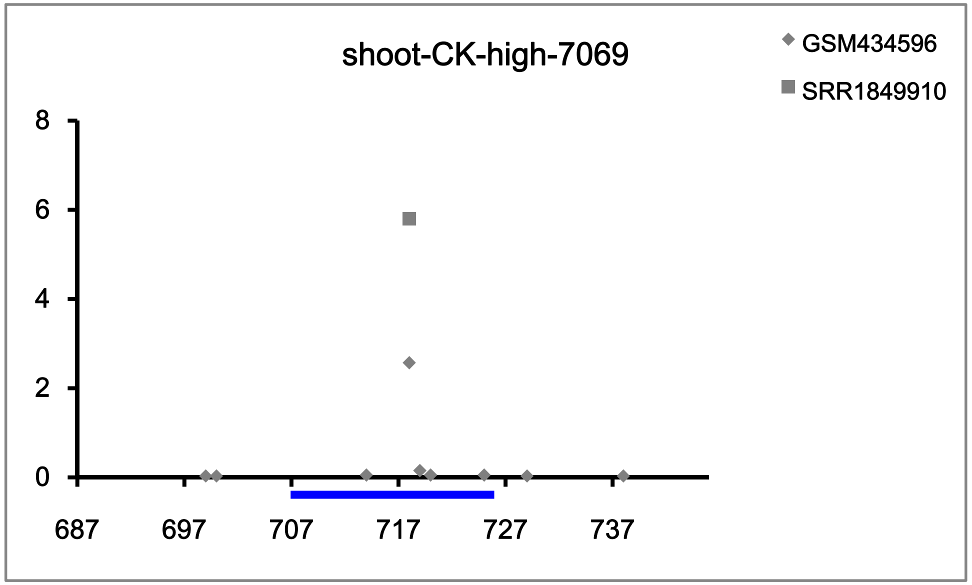

LOC_Os04g46860.1
◆ SRR1849887
■ SRR1849909
40
32
24
16
8
0
0
500
1000
1500
2000
2500

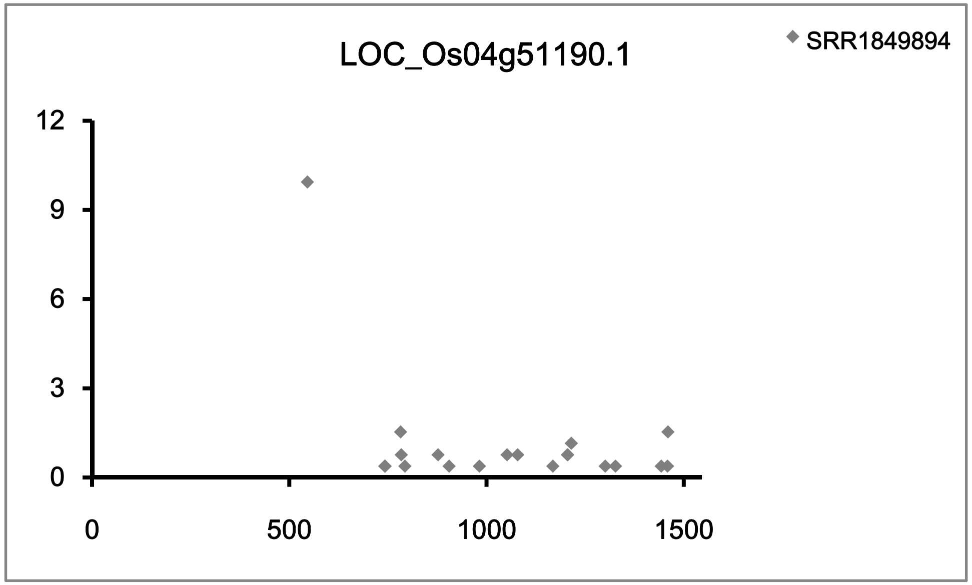

shoot-As-high-9528
shoot-CK-high-38
◆ SRR1849887
■ SRR1849909
40
32
24
16
8
0
1303
1313
1323
1333
1343
1353
1363

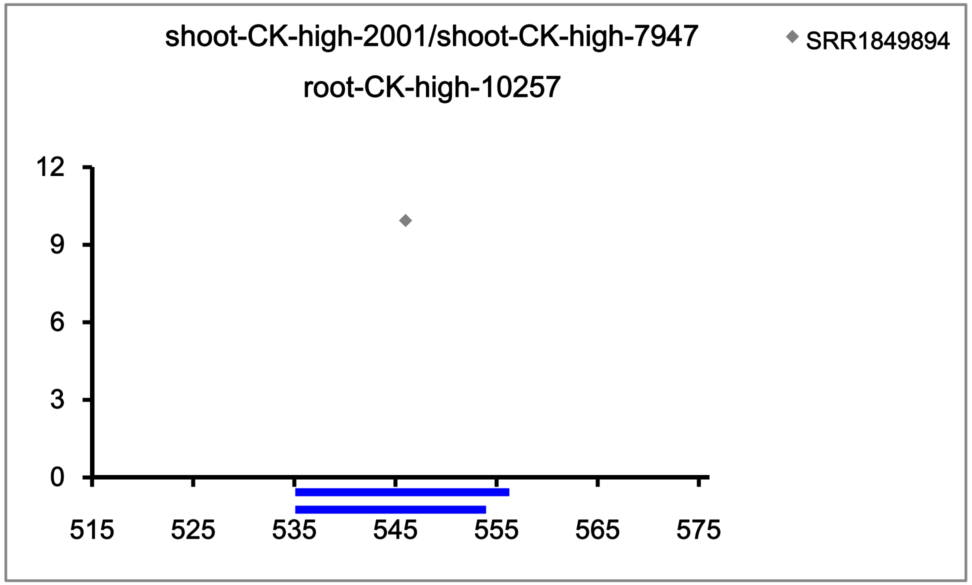

LOC_Os04g47870.1
◆ GSM434596
■ SRR1849910
45
36
27
18
9
0
0
1000
2000
3000

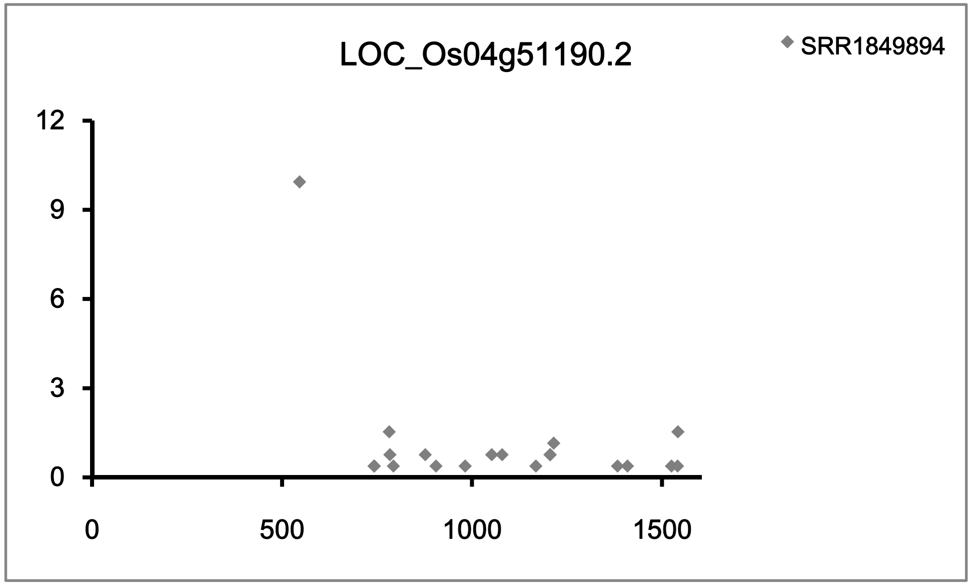

shoot-CK-high-7069
◆ GSM434596
■ SRR1849910
8
6
4
2
0
647
657
667
677
687
697

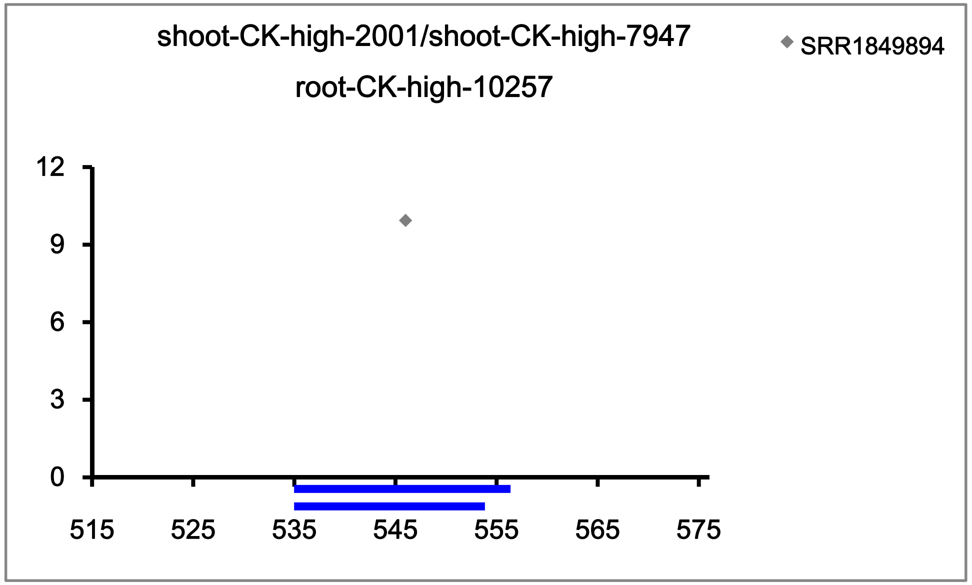

LOC_Os04g47870.2
◆ GSM434596
■ SRR1849910
45
36
27
18
9
0
0
1000
2000
3000

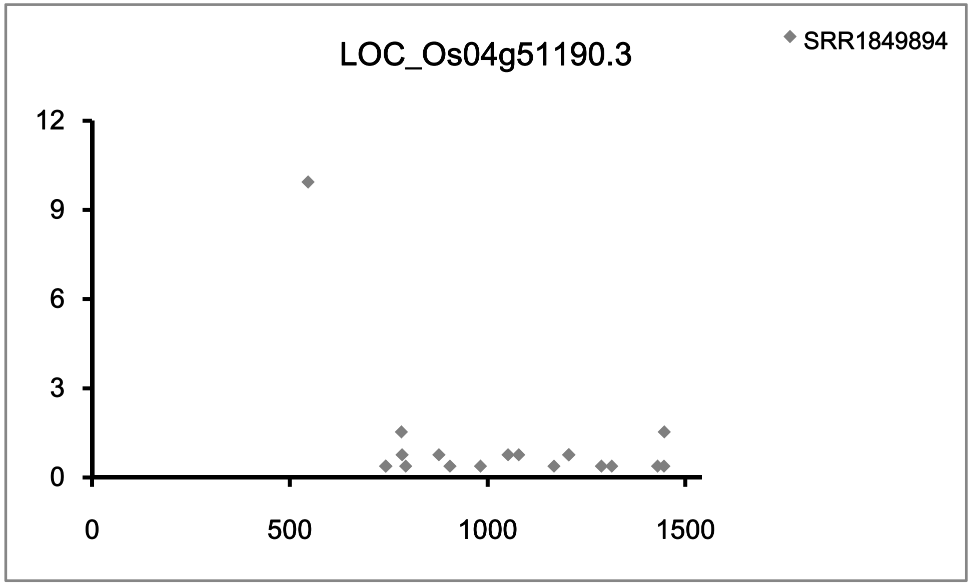

shoot-CK-high-7069
◆ GSM434596
■ SRR1849910
8
6
4
2
0
687
697
707
717
727
737

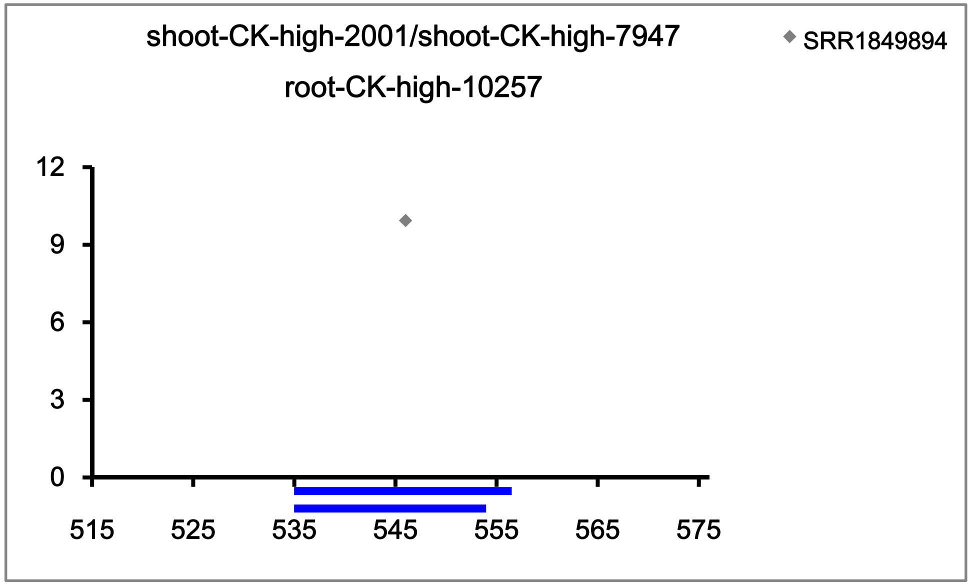

LOC_Os04g51190.1
◆ SRR1849894
12
9
6
3
0
0
500
1000
1500

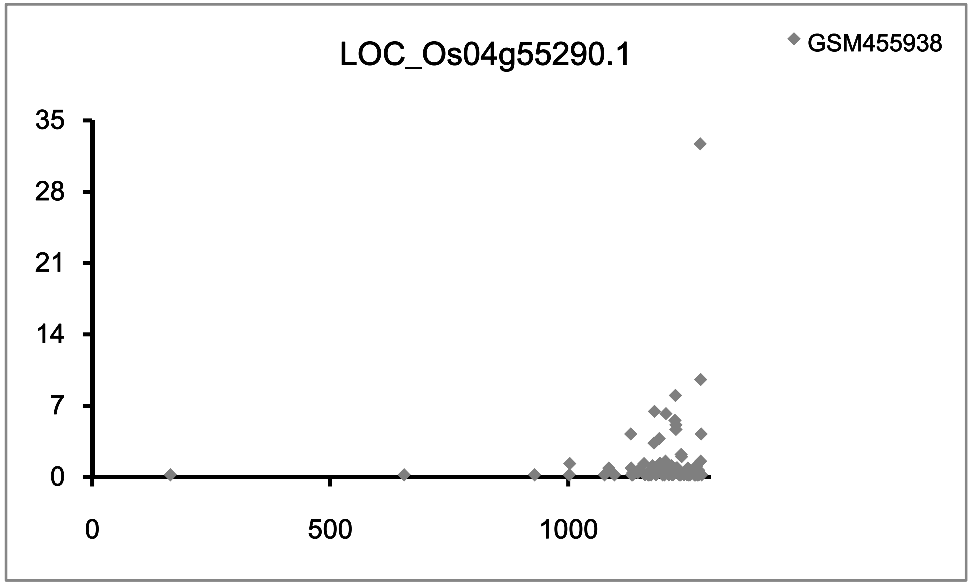

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
◆ SRR1849894
12
9
6
3
0
515
525
535
545
555
565
575

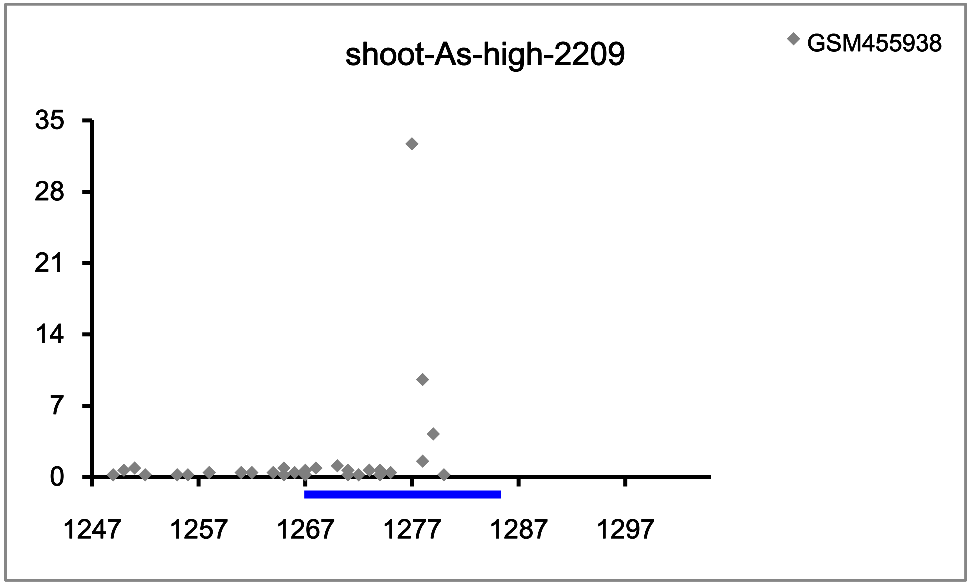

LOC_Os04g51190.2
SRR1849894
12
9
6
3
0
0
500
1000
1500

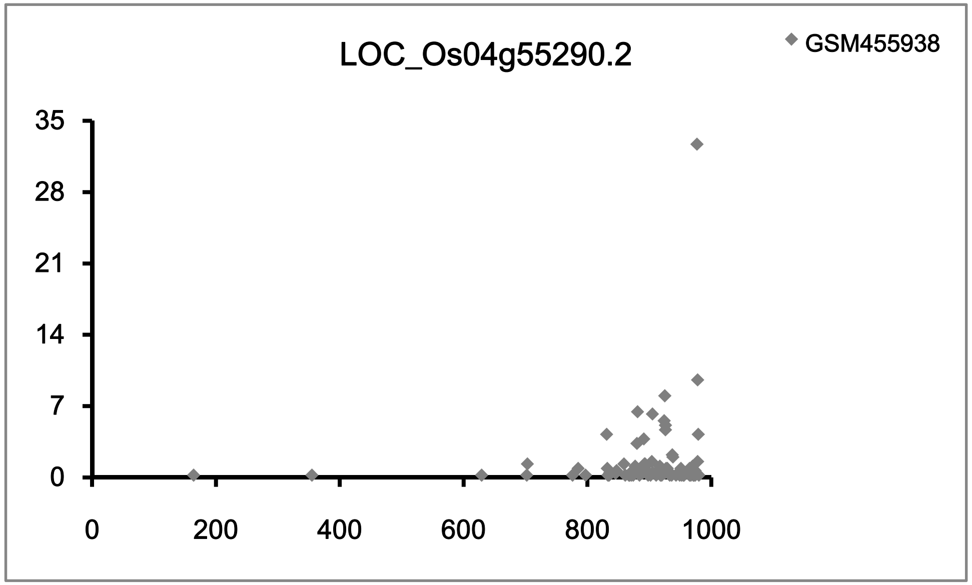

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
SRR1849894
12
9
6
3
0
515
525
535
545
555
565
575

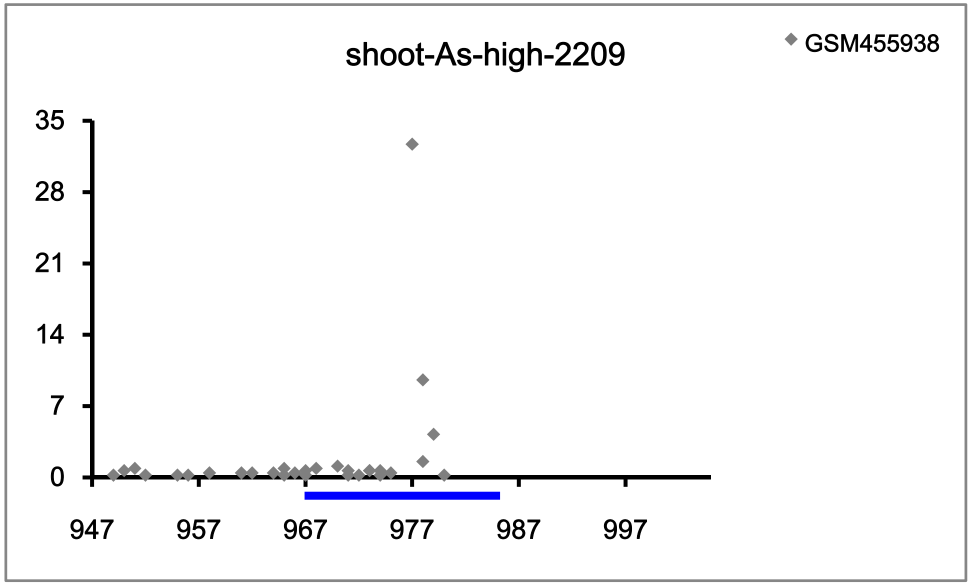

LOC_Os04g51190.3
SRR1849894
12
9
6
3
0
0
500
1000
1500

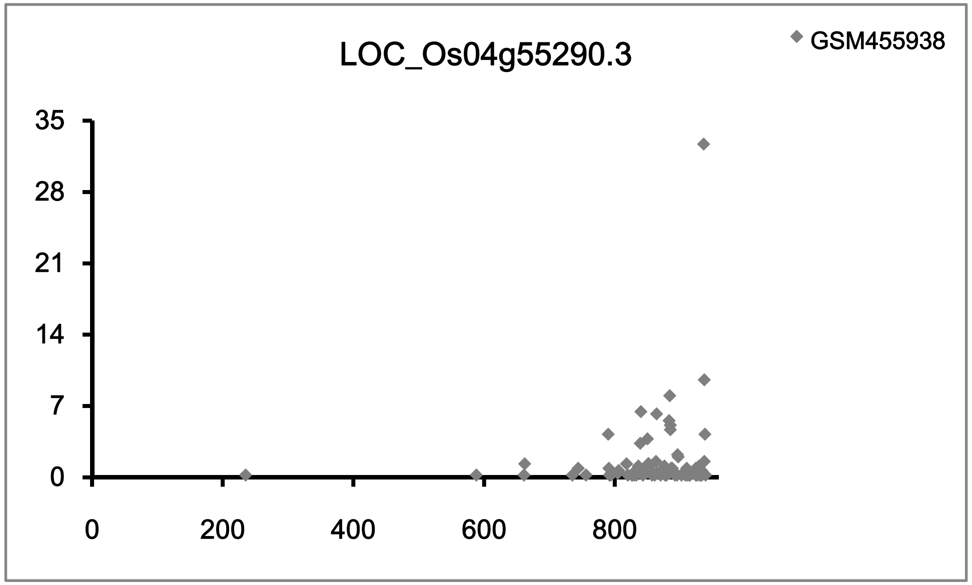

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
SRR1849894
12
9
6
3
0
515
525
535
545
555
565
575

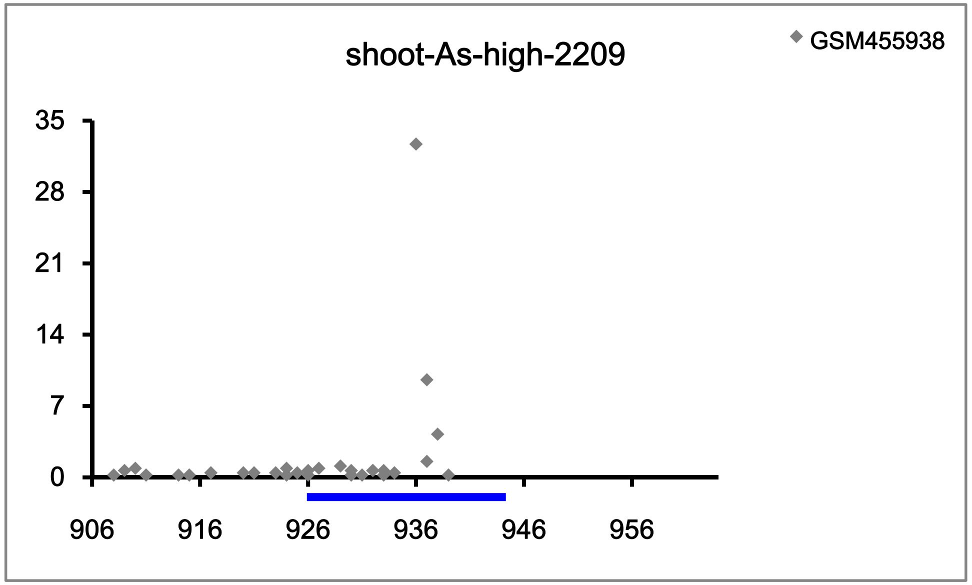

LOC_Os04g55290.1
GSM455938
35
28
21
14
7
0
0
500
1000

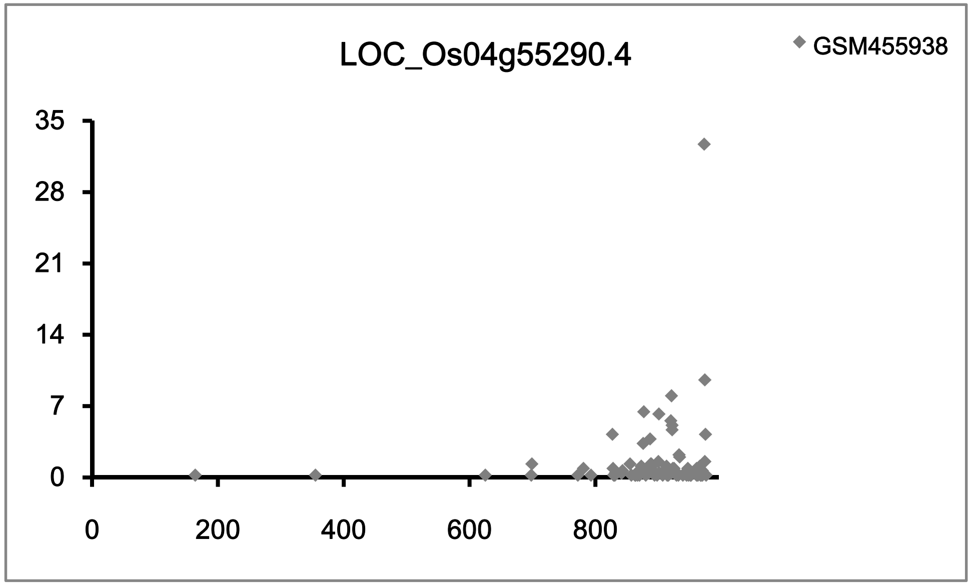

shoot-As-high-2209
GSM455938
35
28
21
14
7
0
1247
1257
1267
1277
1287
1297

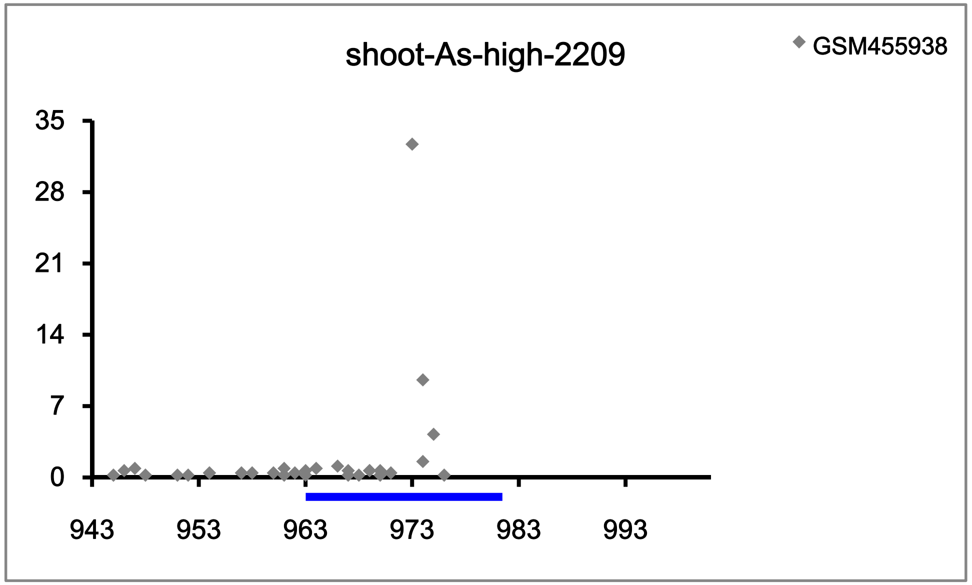

LOC_Os04g55290.2
GSM455938
35
28
21
14
7
0
0
200
400
600
800
1000

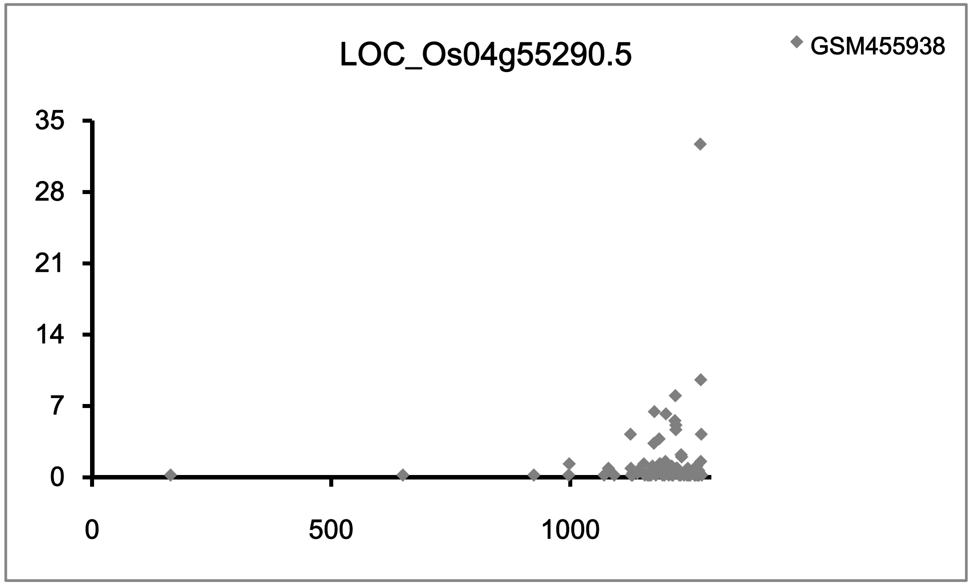

shoot-As-high-2209
GSM455938
35
28
21
14
7
0
947
957
967
977
987
997

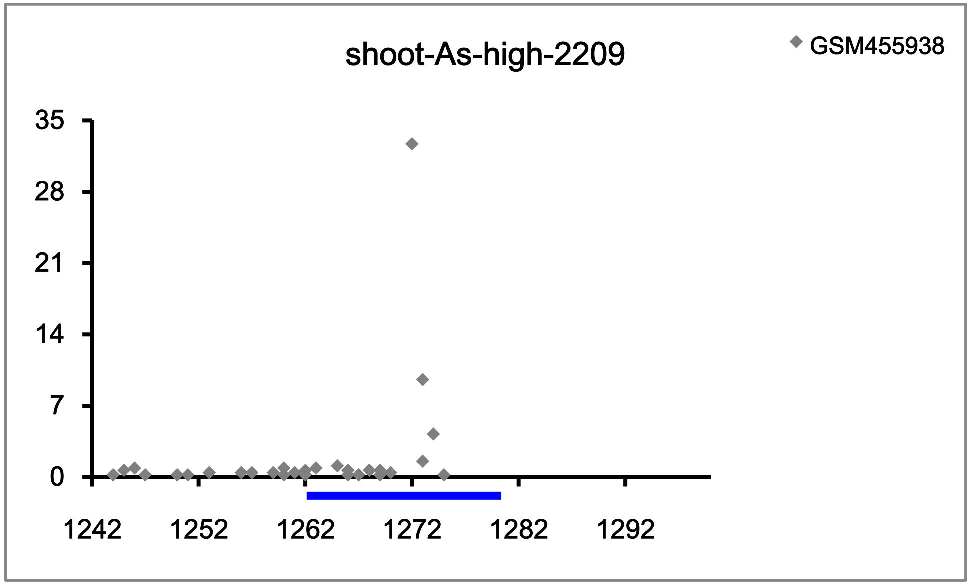

LOC_Os04g55290.3
GSM455938
35
28
21
14
7
0
0
200
400
600
800

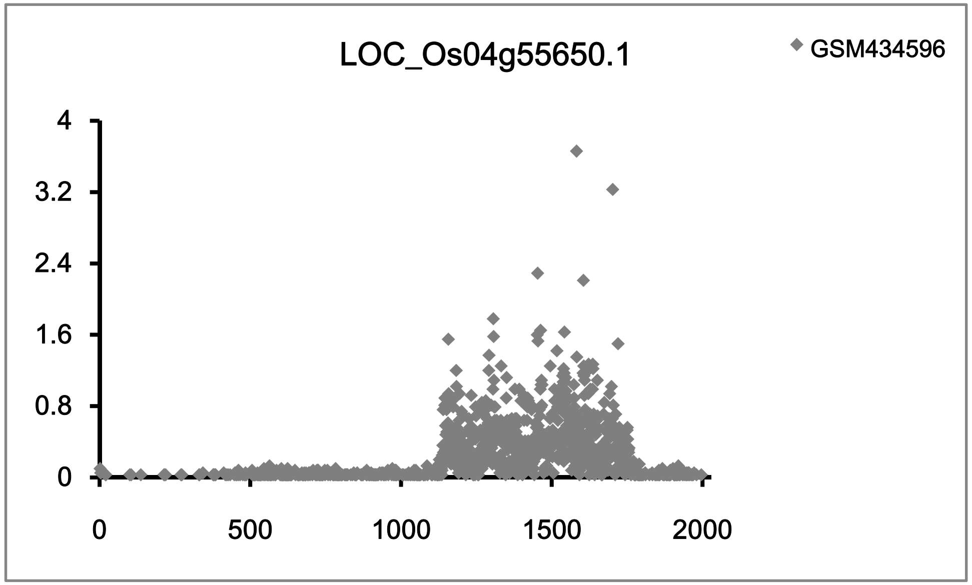

shoot-As-high-2209
GSM455938
35
28
21
14
7
0
906
916
926
936
946
956

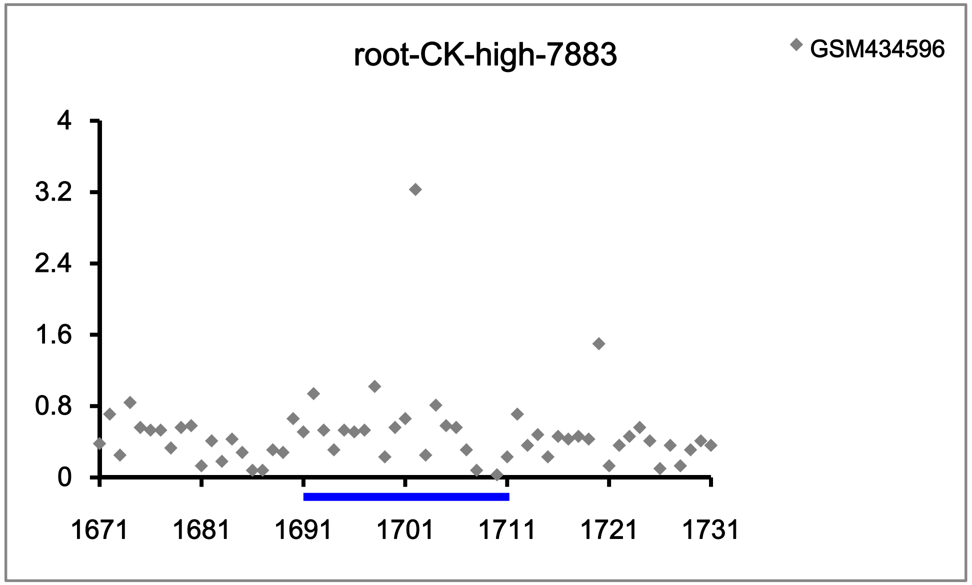

LOC_Os04g55290.4
GSM455938
35
28
21
14
7
0
0
200
400
600
800

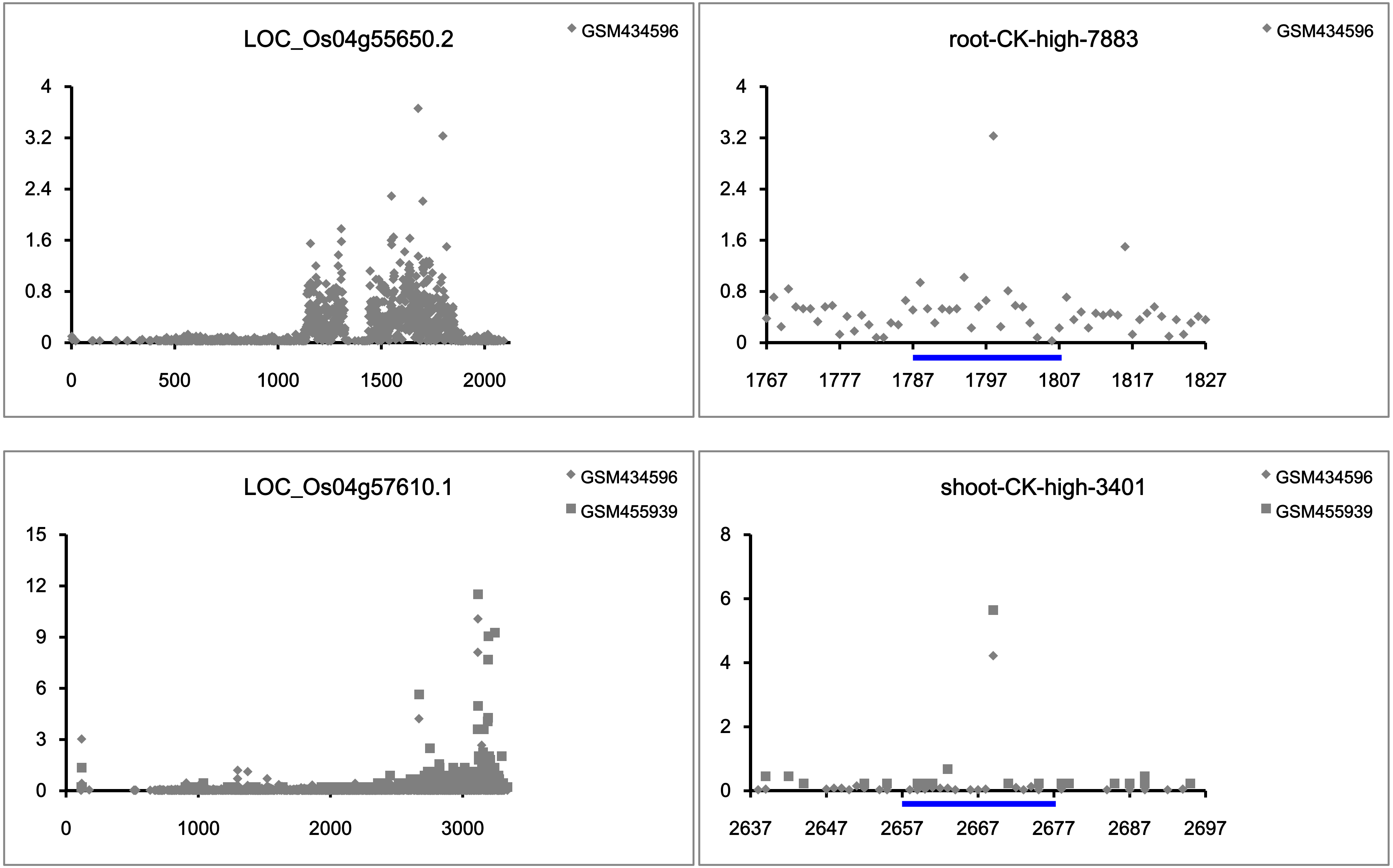

shoot-As-high-2209
GSM455938
35
28
21
14
7
0
943
953
963
973
983
993

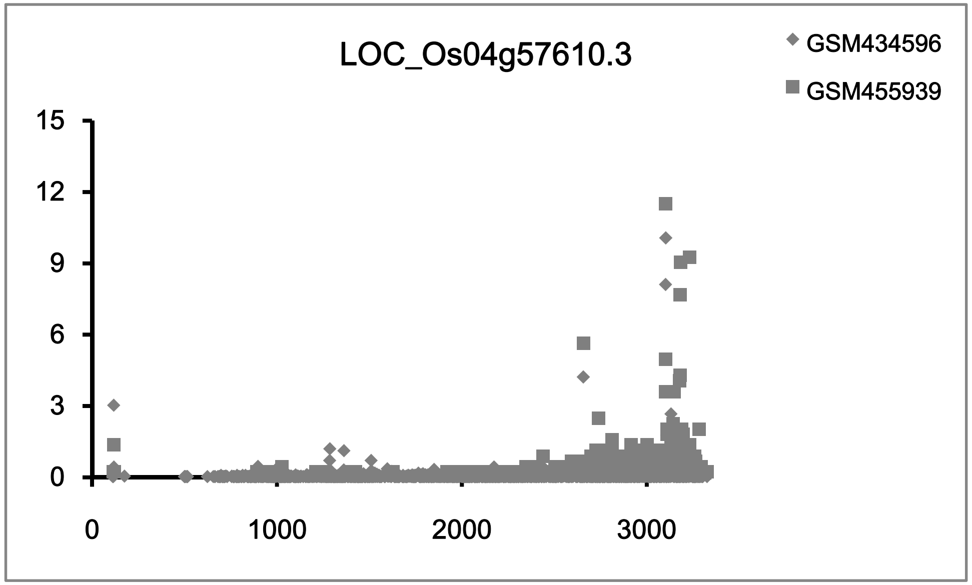

LOC_Os04g55290.5
GSM455938
35
28
21
14
7
0
0
500
1000

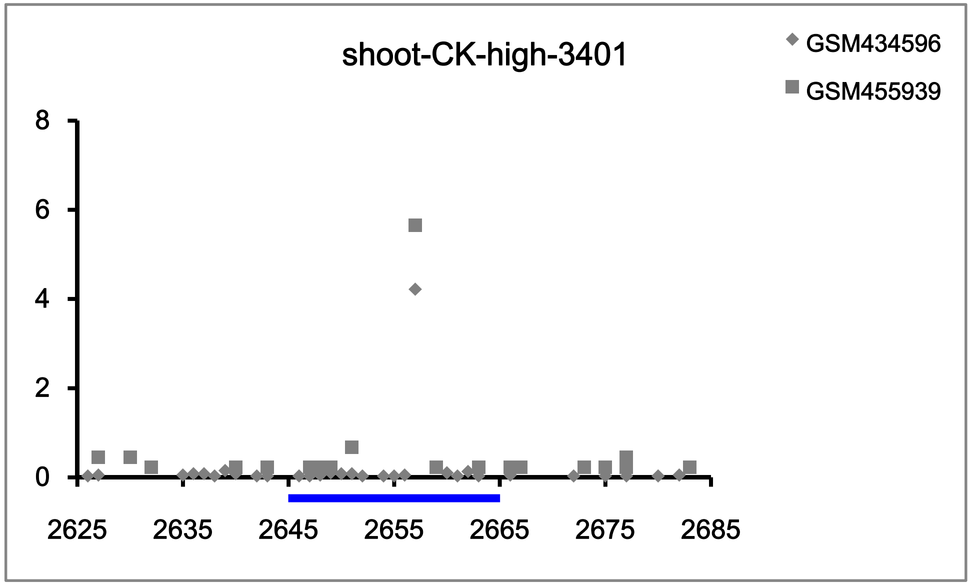

shoot-As-high-2209
GSM455938
35
28
21
14
7
0
1242
1252
1262
1272
1282
1292

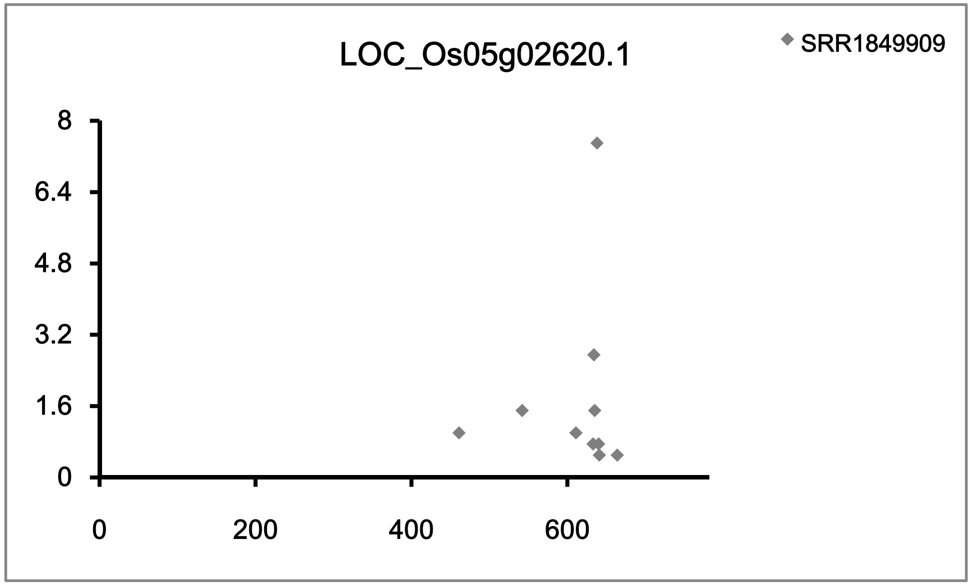

LOC_Os04g55650.1
GSM434596
4
3.2
2.4
1.6
0.8
0
0
500
1000
1500
2000

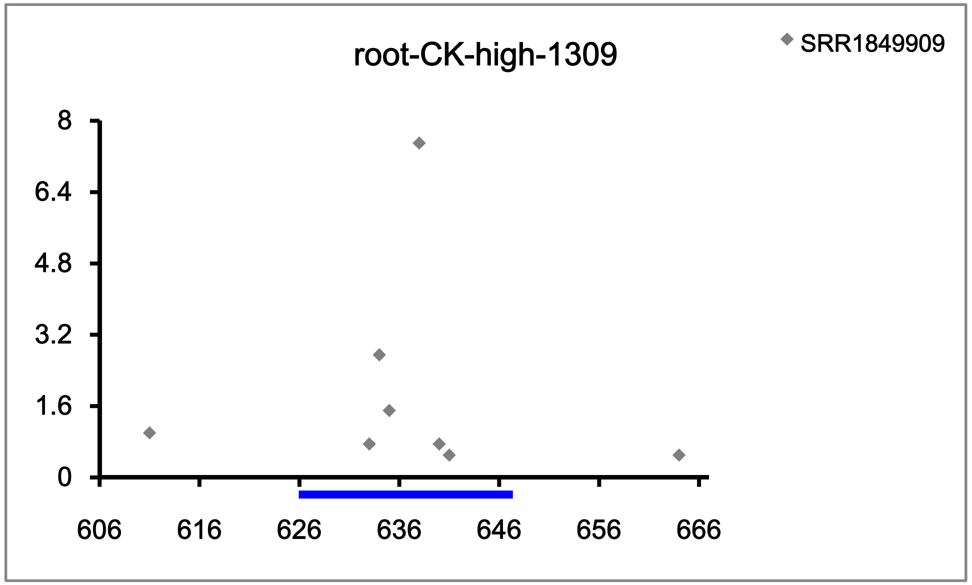

root-CK-high-7883
GSM434596
4
3.2
2.4
1.6
0.8
0
1671
1681
1691
1701
1711
1721
1731

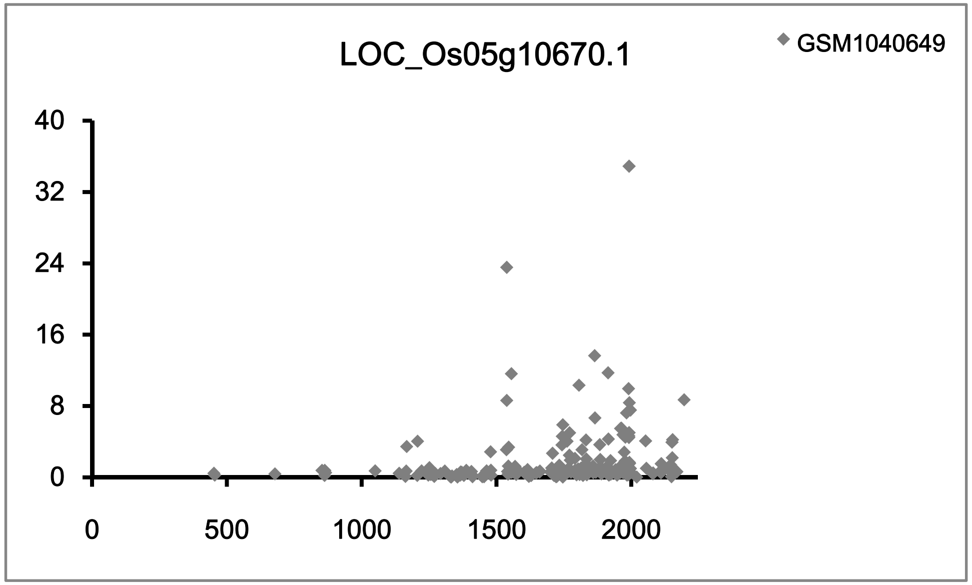

LOC_Os04g55650.2
GSM434596
4
3.2
2.4
1.6
0.8
0
0
500
1000
1500
2000
root-CK-high-7883
GSM434596
4
3.2
2.4
1.6
0.8
0
1767
1777
1787
1797
1807
1817
1827
LOC_Os04g57610.1
GSM434596
GSM455939
15
12
9
6
3
0
0
1000
2000
3000
shoot-CK-high-3401
GSM434596
GSM455939
8
6
4
2
0
2637
2647
2657
2667
2677
2687
2697

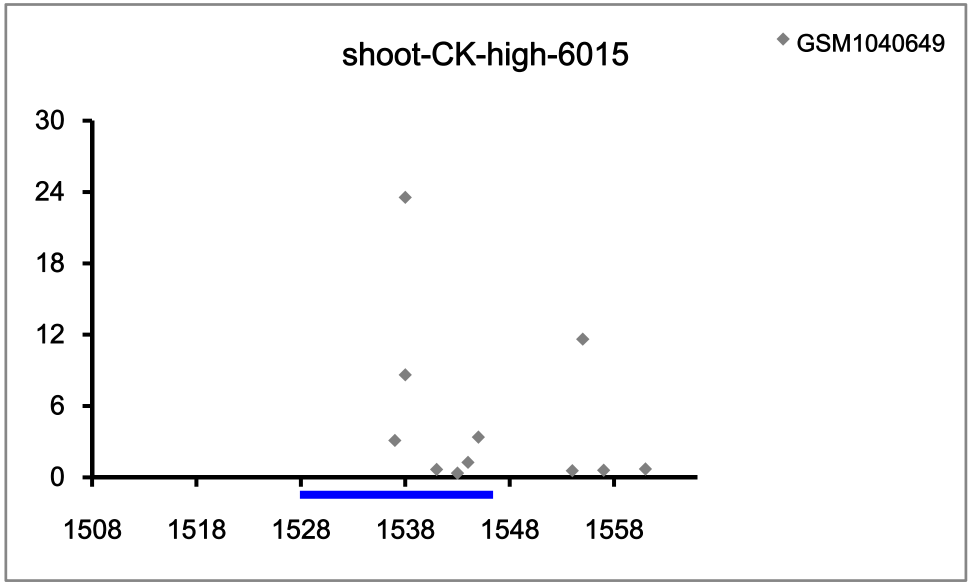

LOC_Os04g57610.3
◆ GSM434596
■ GSM455939
15
12
9
6
3
0
0
1000
2000
3000

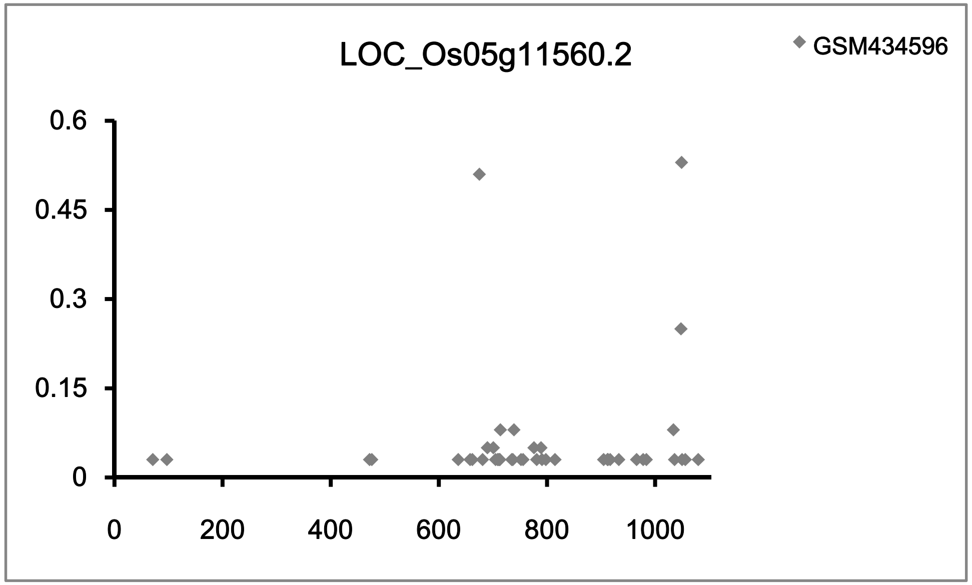

shoot-CK-high-3401
◆ GSM434596
■ GSM455939
8
6
4
2
0
2625
2635
2645
2655
2665
2675
2685

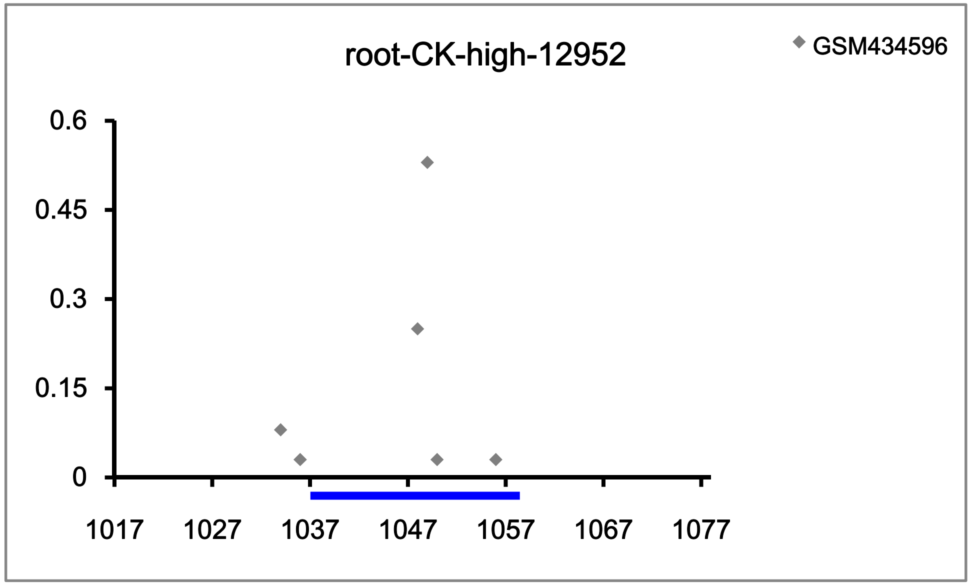

LOC_Os05g02620.1
◆ SRR1849909
8
6.4
4.8
3.2
1.6
0
0
200
400
600

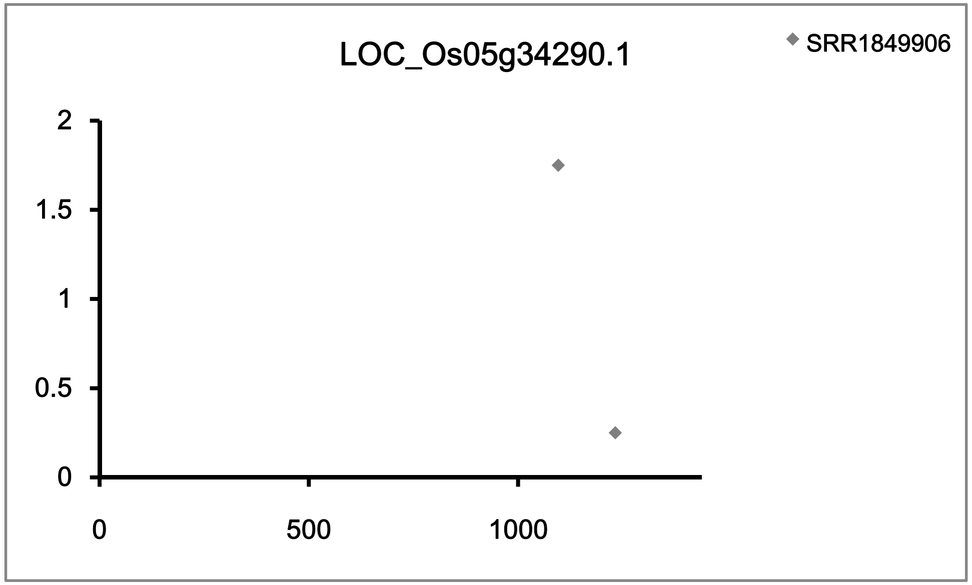

root-CK-high-1309
◆ SRR1849909
8
6.4
4.8
3.2
1.6
0
606
616
626
636
646
656
666

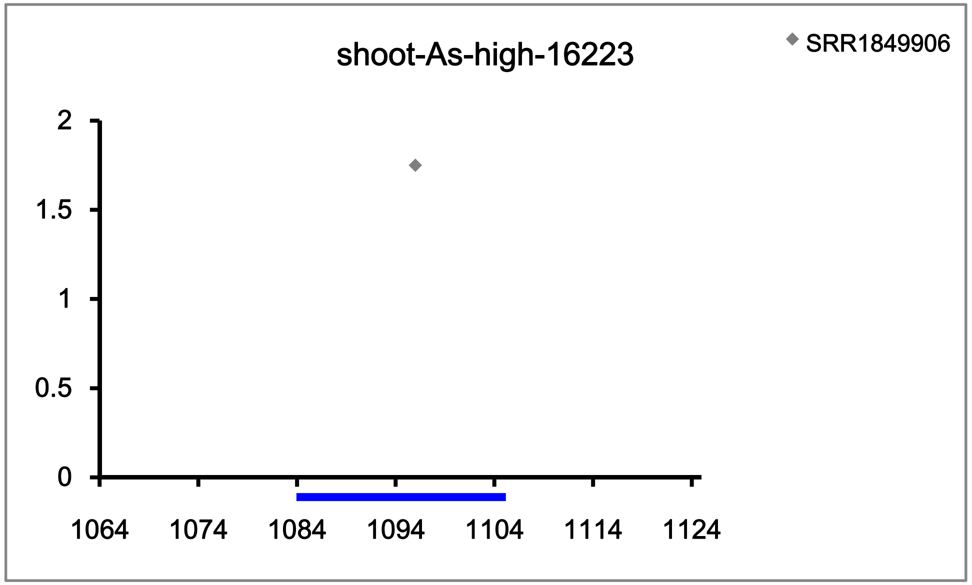

LOC_Os05g10670.1
GSM1040649
40
32
24
16
8
0
0
500
1000
1500
2000

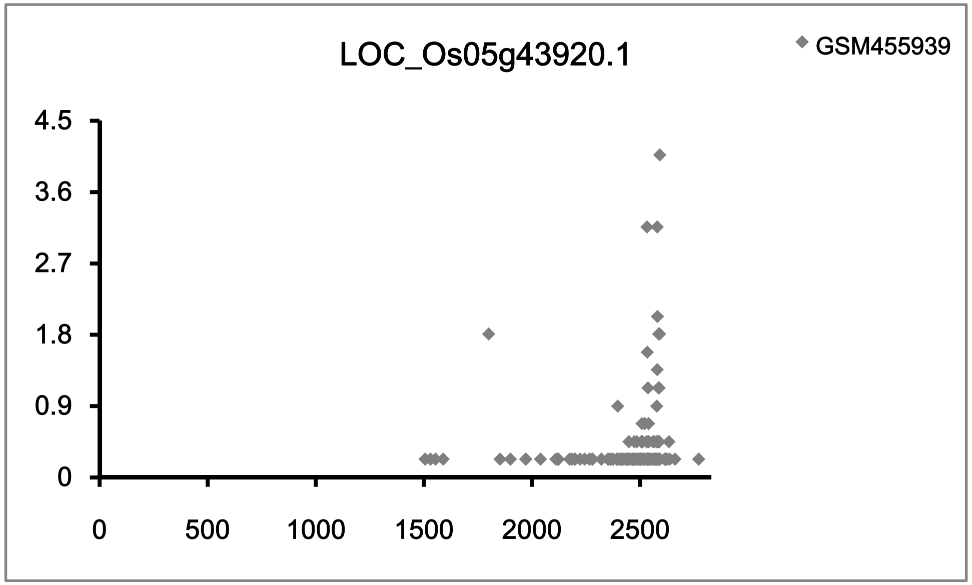

shoot-CK-high-6015
GSM1040649
30
24
18
12
6
0
1508
1518
1528
1538
1548
1558

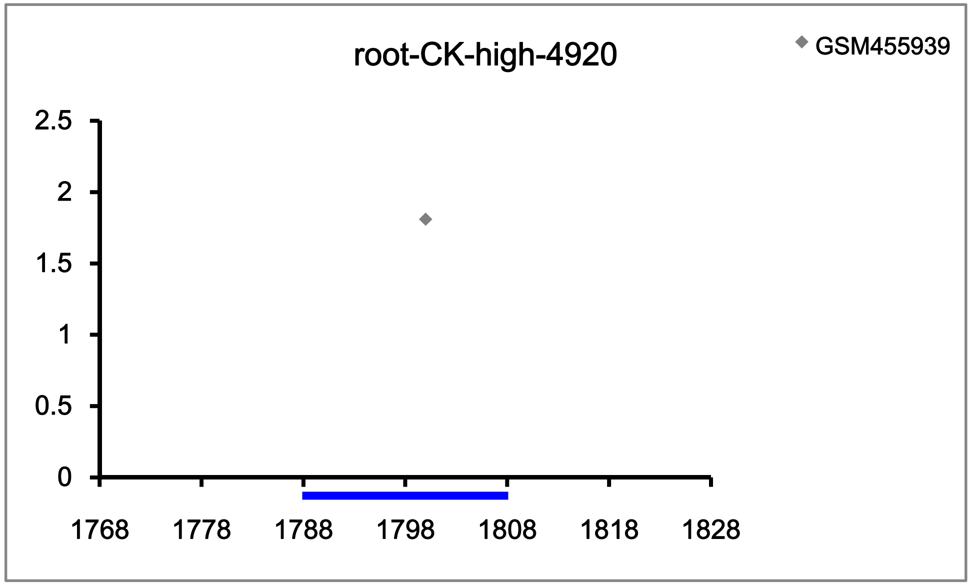

LOC_Os05g11560.2
GSM434596
0.6
0.45
0.3
0.15
0
0
200
400
600
800
1000

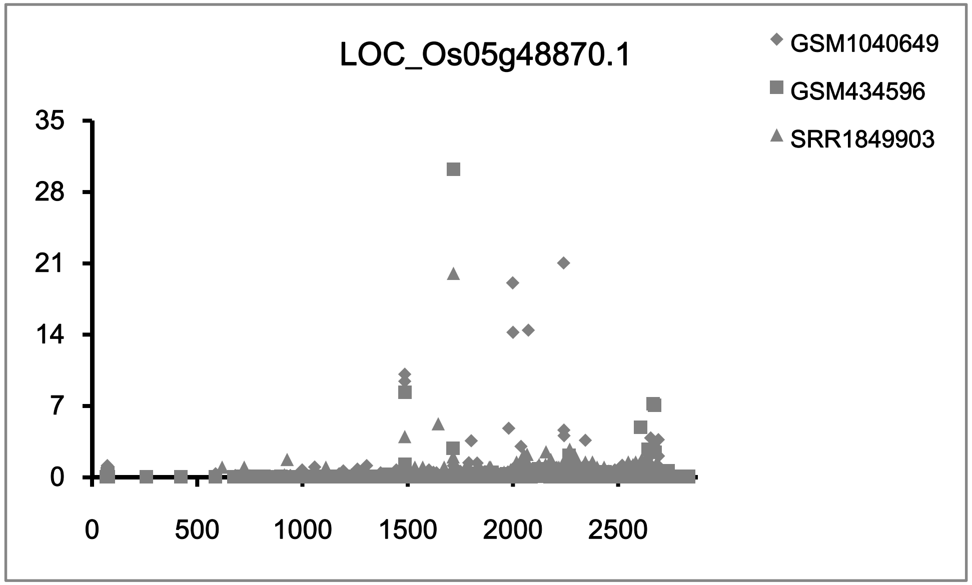

root-CK-high-12952
GSM434596
0.6
0.45
0.3
0.15
0
1017
1027
1037
1047
1057
1067
1077

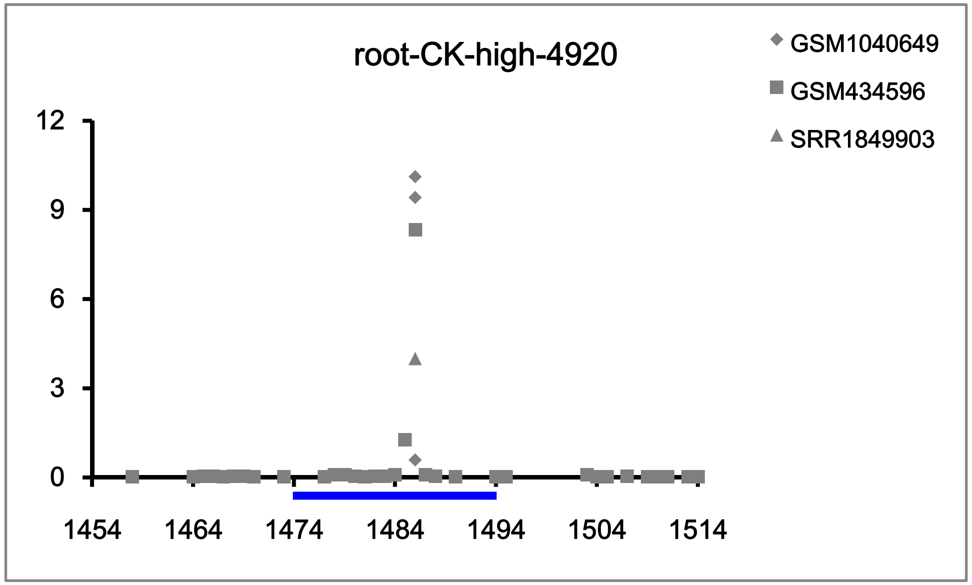

LOC_Os05g34290.1
◆ SRR1849906
2
1.5
1
0.5
0
0
500
1000

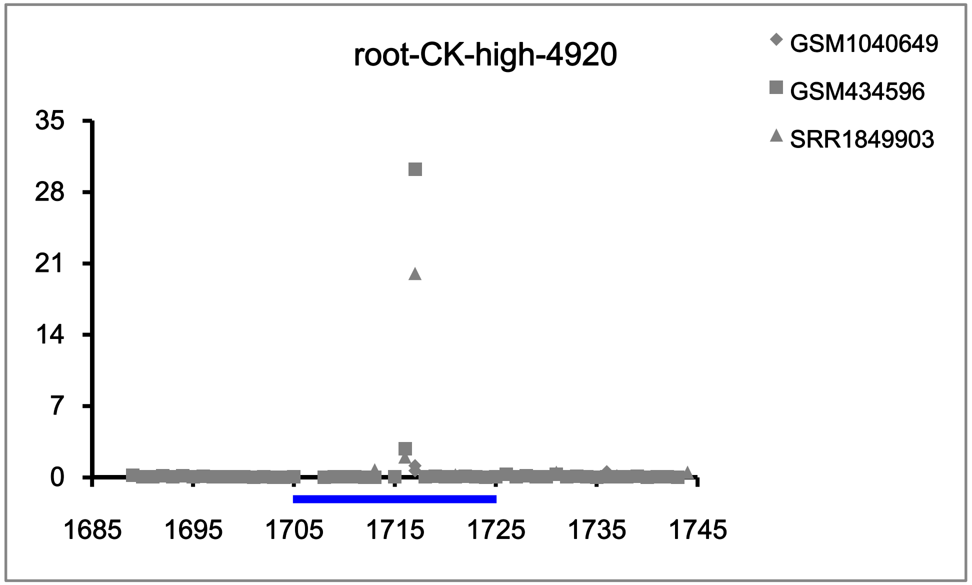

shoot-As-high-16223
◆ SRR1849906
2
1.5
1
0.5
0
1064
1074
1084
1094
1104
1114
1124

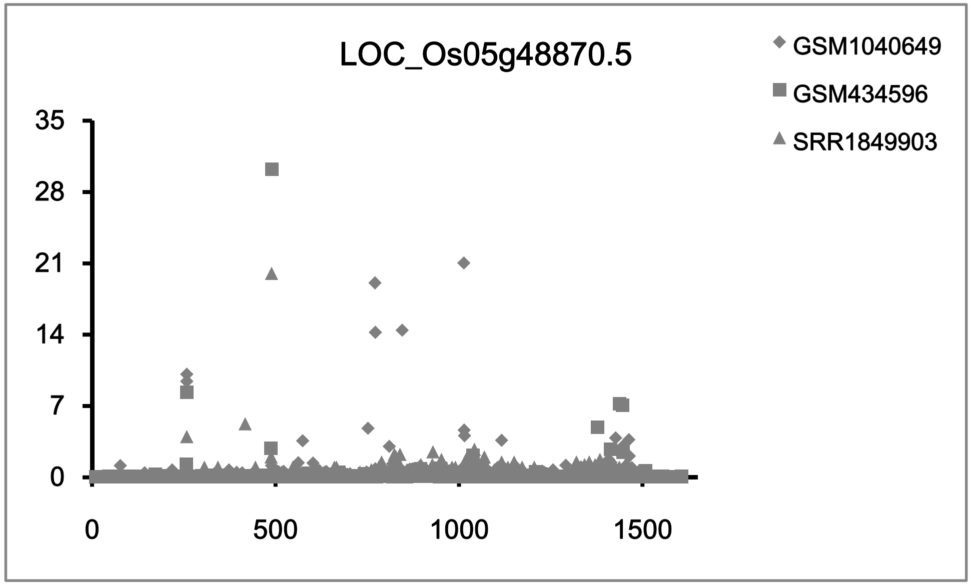

LOC_Os05g43920.1
◆ GSM455939
4.5
3.6
2.7
1.8
0.9
0
0
500
1000
1500
2000
2500

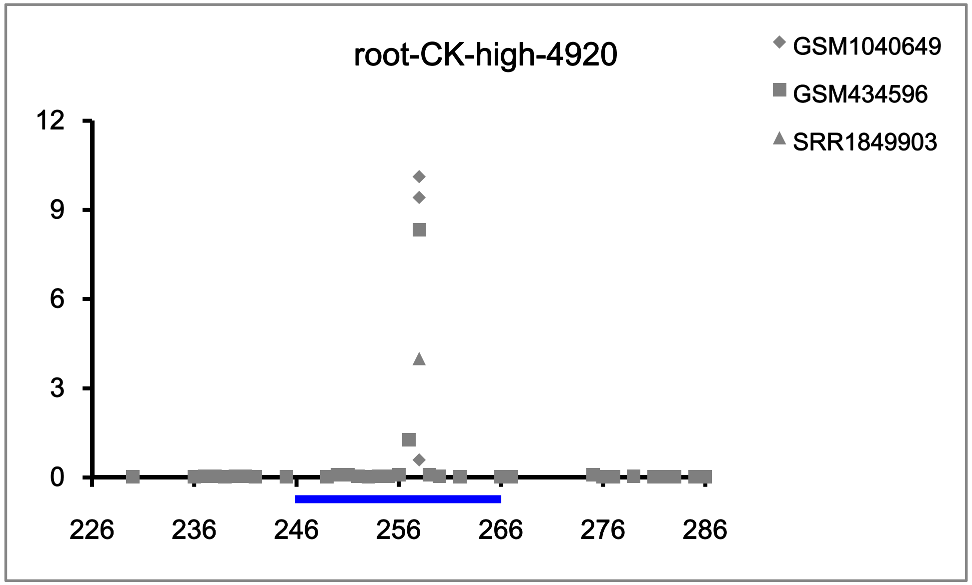

root-CK-high-4920
◆ GSM455939
2.5
2
1.5
1
0.5
0
1768
1778
1788
1798
1808
1818
1828

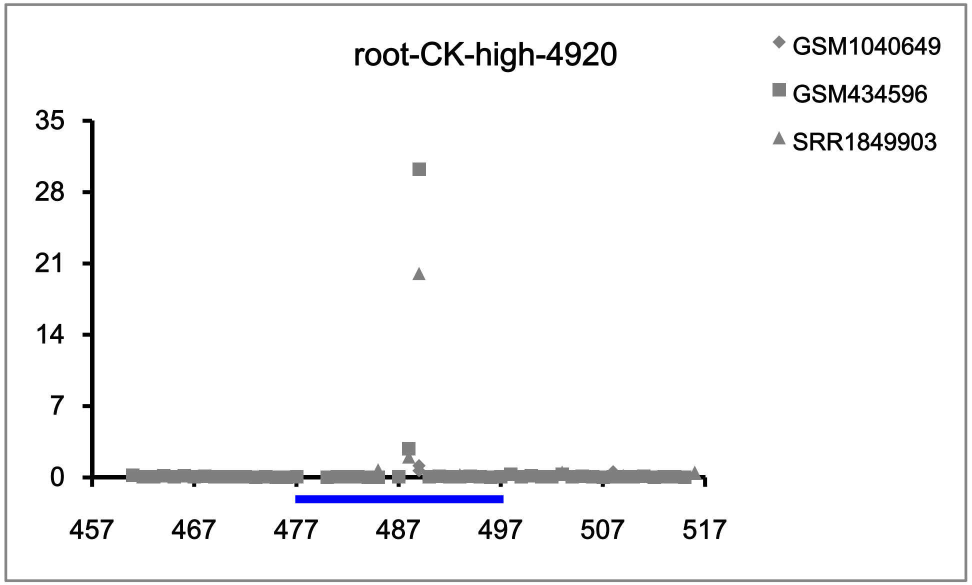

LOC_Os05g48870.1
◆ GSM1040649
■ GSM434596
▲ SRR1849903
35
28
21
14
7
0
0
500
1000
1500
2000
2500

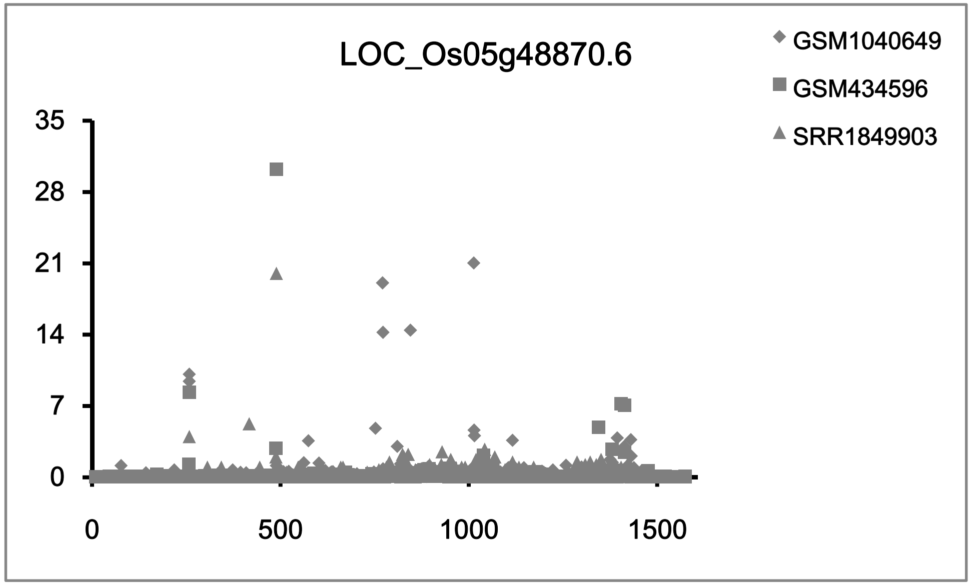

root-CK-high-4920
◆ GSM1040649
■ GSM434596
▲ SRR1849903
12
9
6
3
0
1454
1464
1474
1484
1494
1504
1514

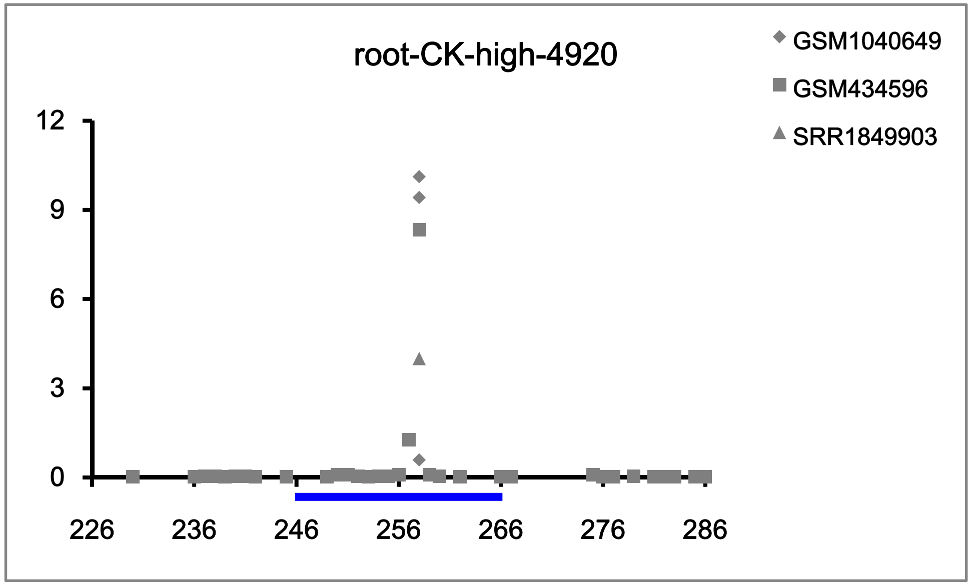

root-CK-high-4920
◆ GSM1040649
■ GSM434596
▲ SRR1849903
35
28
21
14
7
0
1685
1695
1705
1715
1725
1735
1745

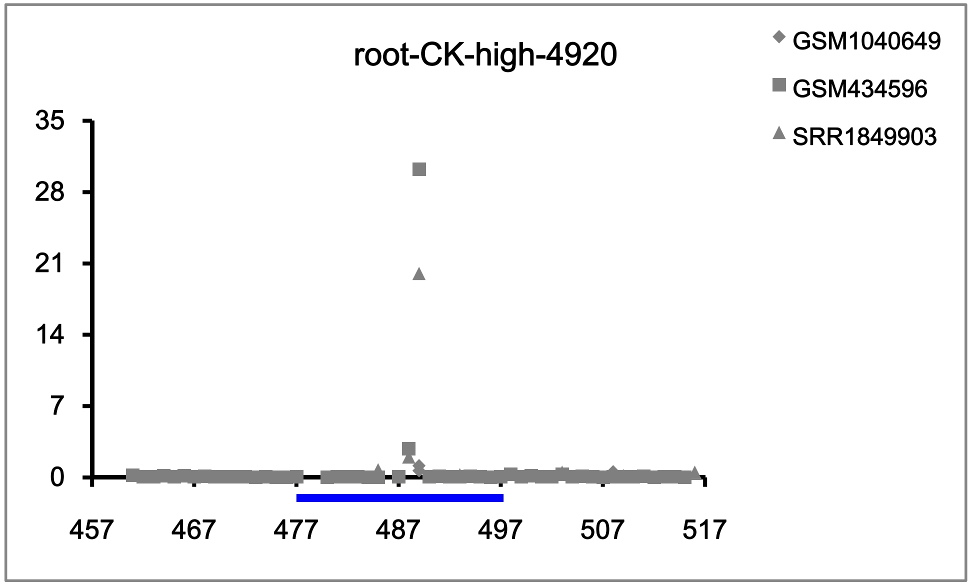

LOC_Os05g48870.5
◆ GSM1040649
■ GSM434596
▲ SRR1849903
35
28
21
14
7
0
0
500
1000
1500

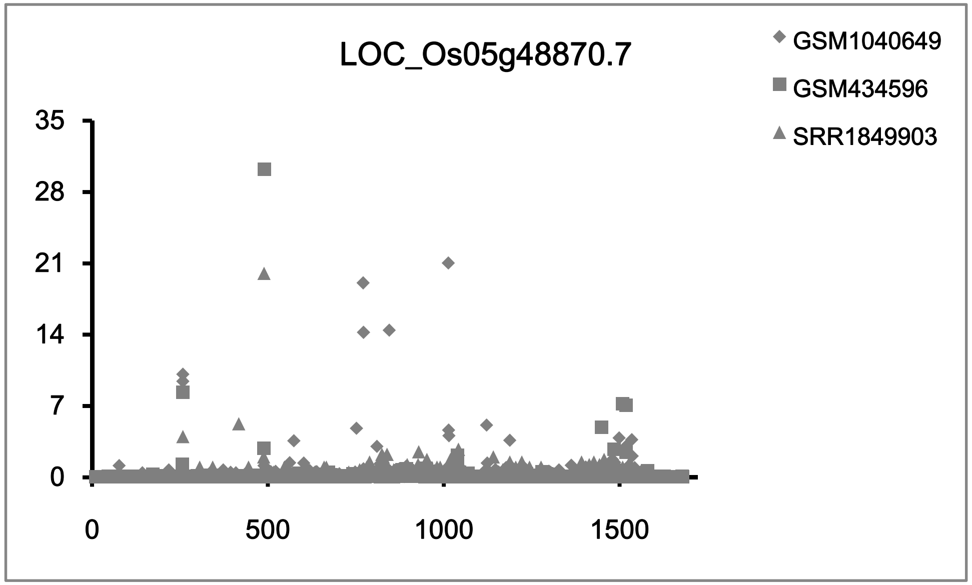

root-CK-high-4920
◆ GSM1040649
■ GSM434596
▲ SRR1849903
12
9
6
3
0
226
236
246
256
266
276
286

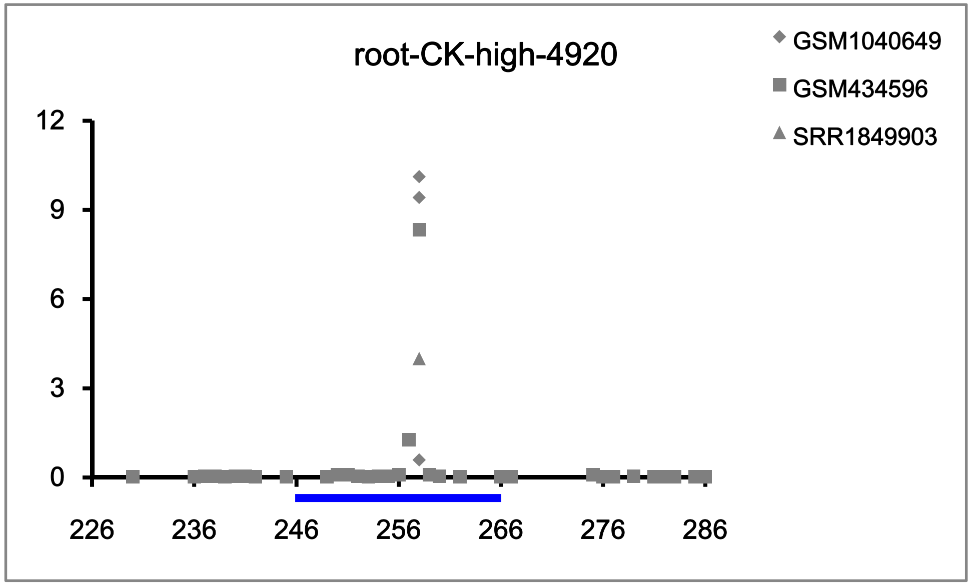

root-CK-high-4920
◆ GSM1040649
■ GSM434596
▲ SRR1849903
35
28
21
14
7
0
457
467
477
487
497
507
517

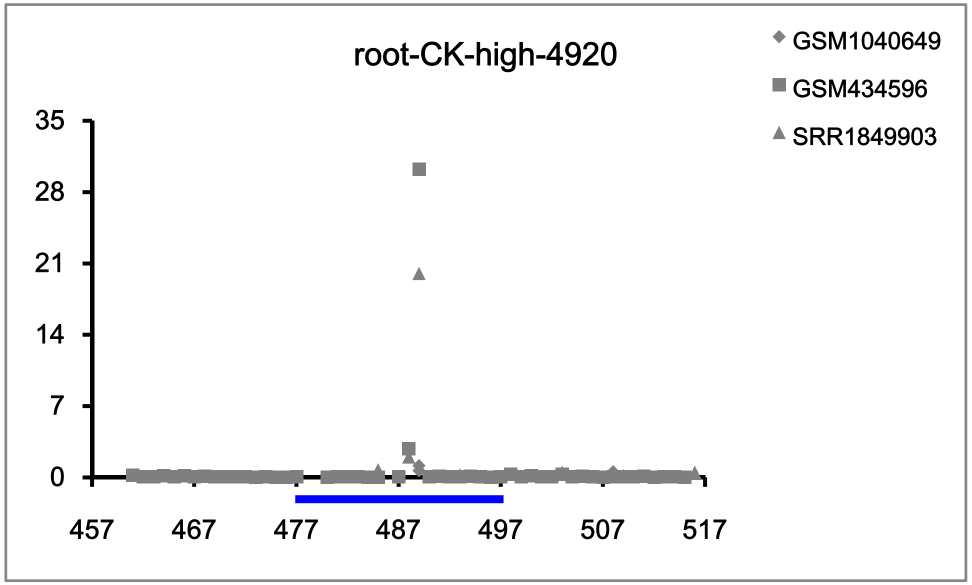

LOC_Os05g48870.6
GSM1040649
GSM434596
SRR1849903
35
28
21
14
7
0
0
500
1000
1500

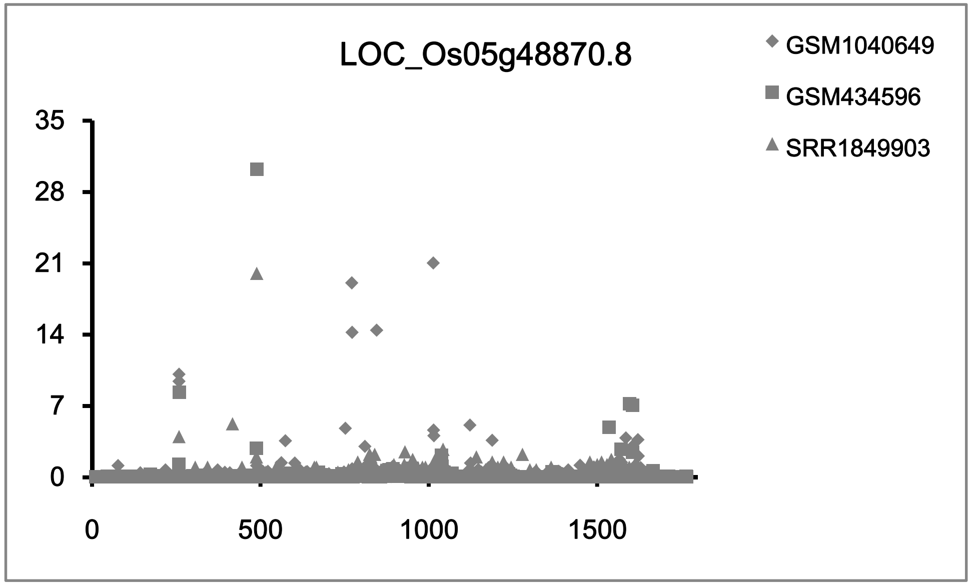

root-CK-high-4920
GSM1040649
GSM434596
SRR1849903
12
9
6
3
0
226
236
246
256
266
276
286

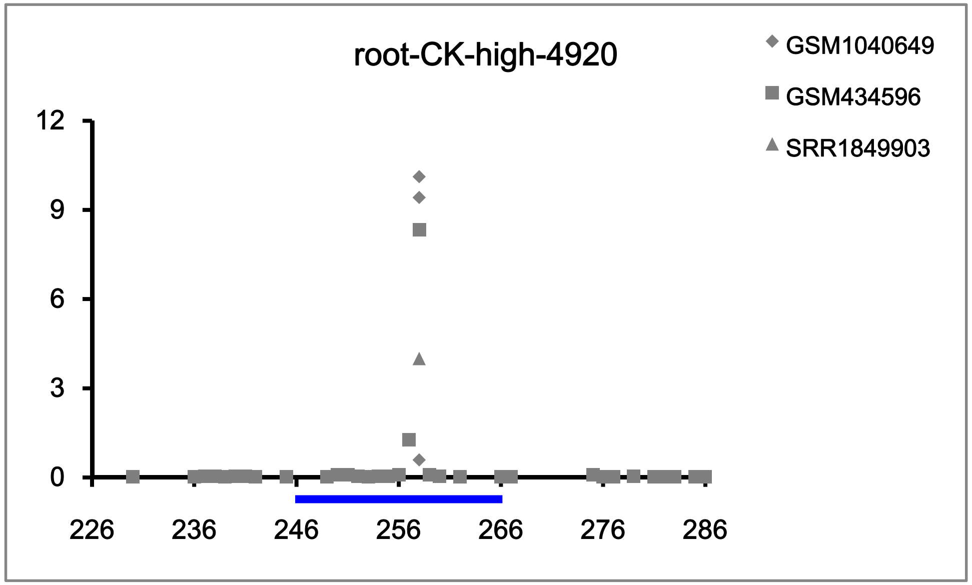

root-CK-high-4920
GSM1040649
GSM434596
SRR1849903
35
28
21
14
7
0
457
467
477
487
497
507
517

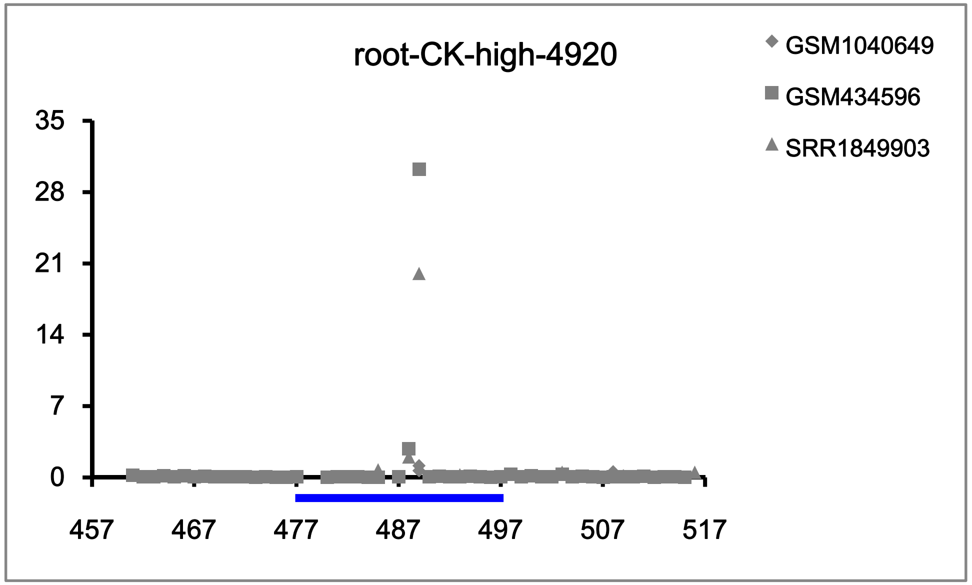

LOC_Os05g48870.7
GSM1040649
GSM434596
SRR1849903
35
28
21
14
7
0
0
500
1000
1500

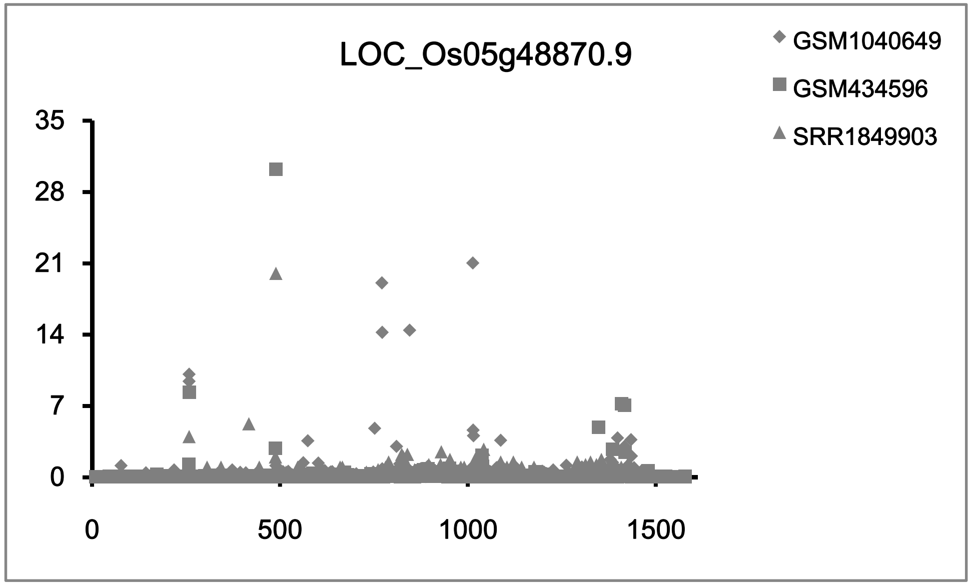

root-CK-high-4920
GSM1040649
GSM434596
SRR1849903
12
9
6
3
0
226
236
246
256
266
276
286

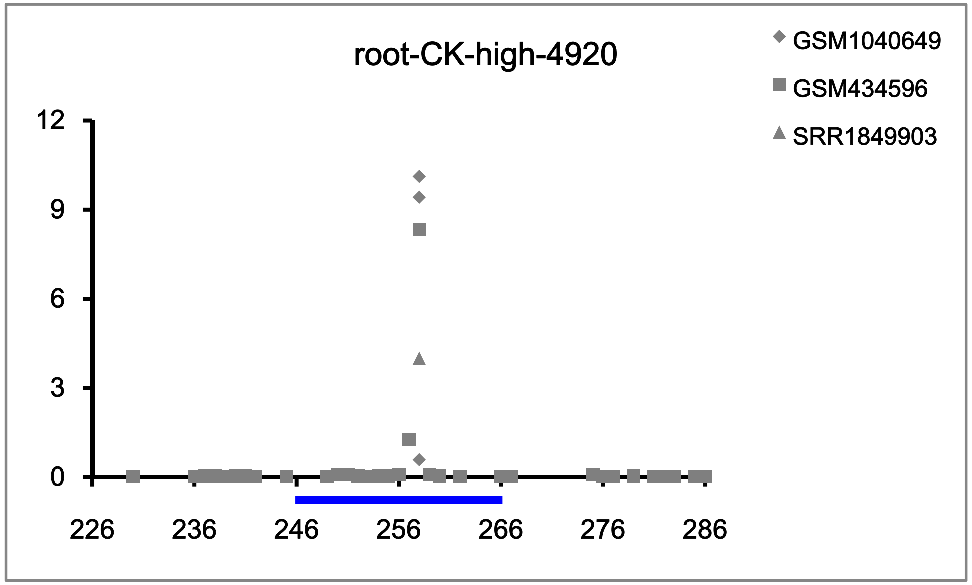

root-CK-high-4920
GSM1040649
GSM434596
SRR1849903
35
28
21
14
7
0
457
467
477
487
497
507
517

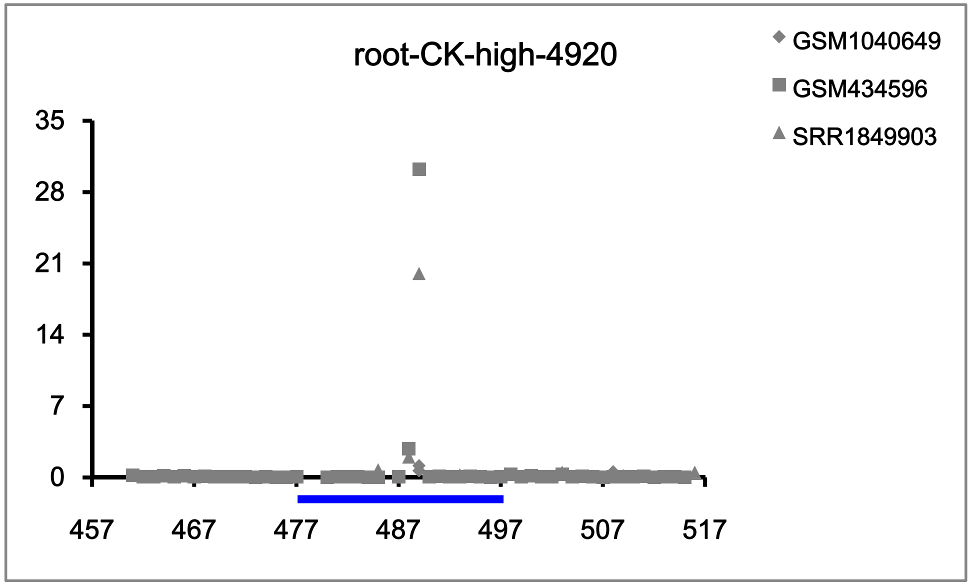

LOC_Os05g48870.8
◆ GSM1040649
■ GSM434596
▲ SRR1849903
35
28
21
14
7
0
0
500
1000
1500

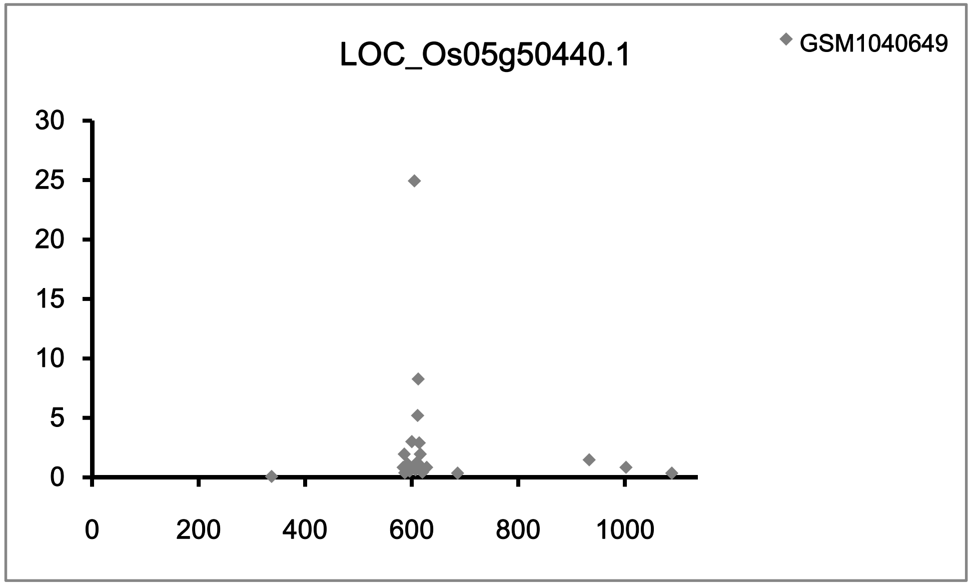

root-CK-high-4920
◆ GSM1040649
■ GSM434596
▲ SRR1849903
12
9
6
3
0
226
236
246
256
266
276
286

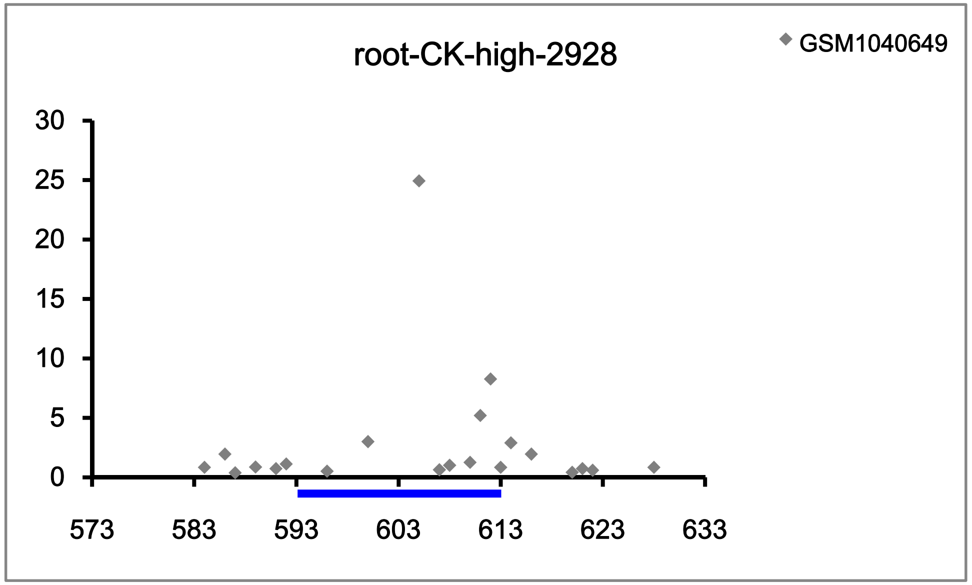

root-CK-high-4920
◆ GSM1040649
■ GSM434596
▲ SRR1849903
35
28
21
14
7
0
457
467
477
487
497
507
517

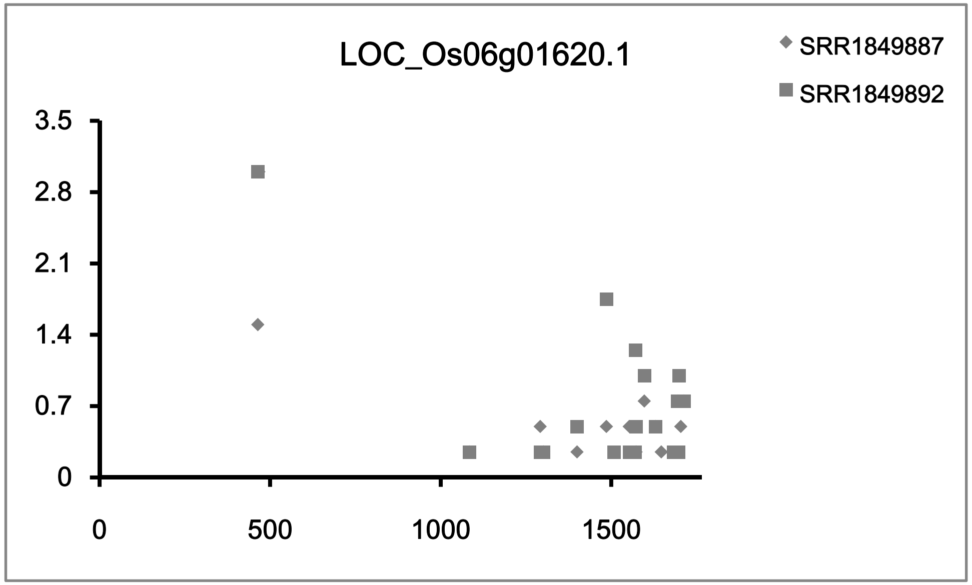

LOC_Os05g48870.9
◆ GSM1040649
■ GSM434596
▲ SRR1849903
35
28
21
14
7
0
0
500
1000
1500

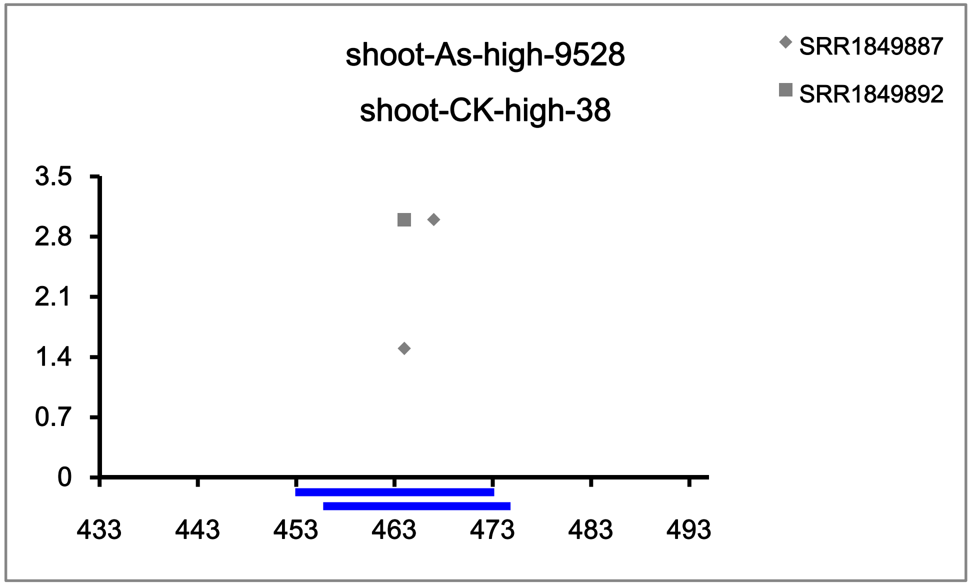

root-CK-high-4920
◆ GSM1040649
■ GSM434596
▲ SRR1849903
12
9
6
3
0
226
236
246
256
266
276
286

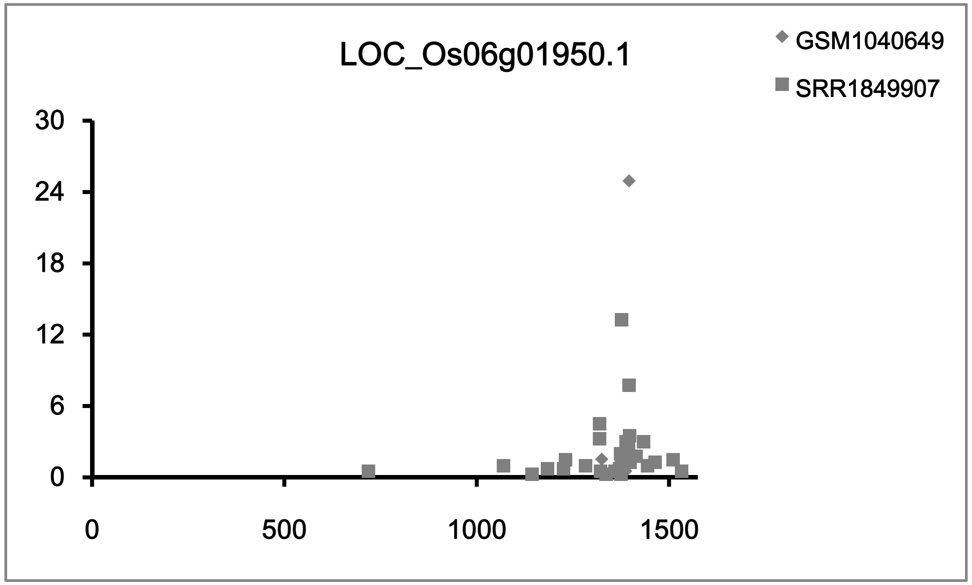

root-CK-high-4920
◆ GSM1040649
■ GSM434596
▲ SRR1849903
35
28
21
14
7
0
457
467
477
487
497
507
517

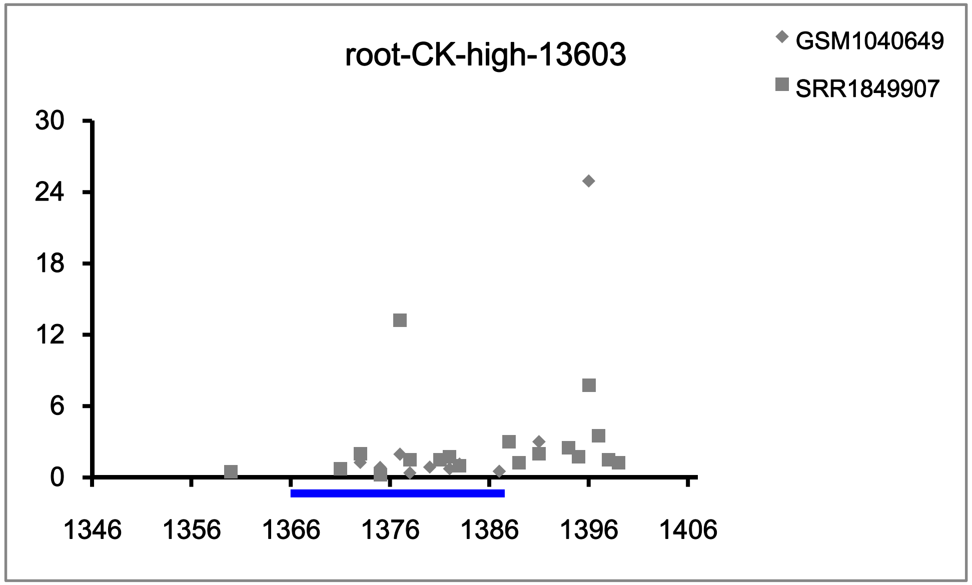

LOC_Os05g50440.1
GSM1040649
30
25
20
15
10
5
0
0
200
400
600
800
1000

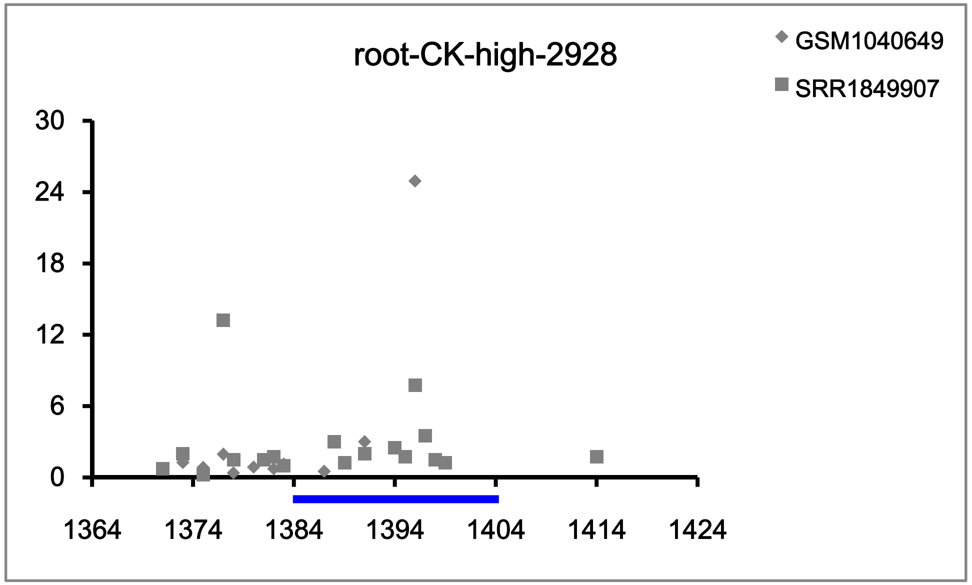

root-CK-high-2928
GSM1040649
30
25
20
15
10
5
0
573
583
593
603
613
623
633

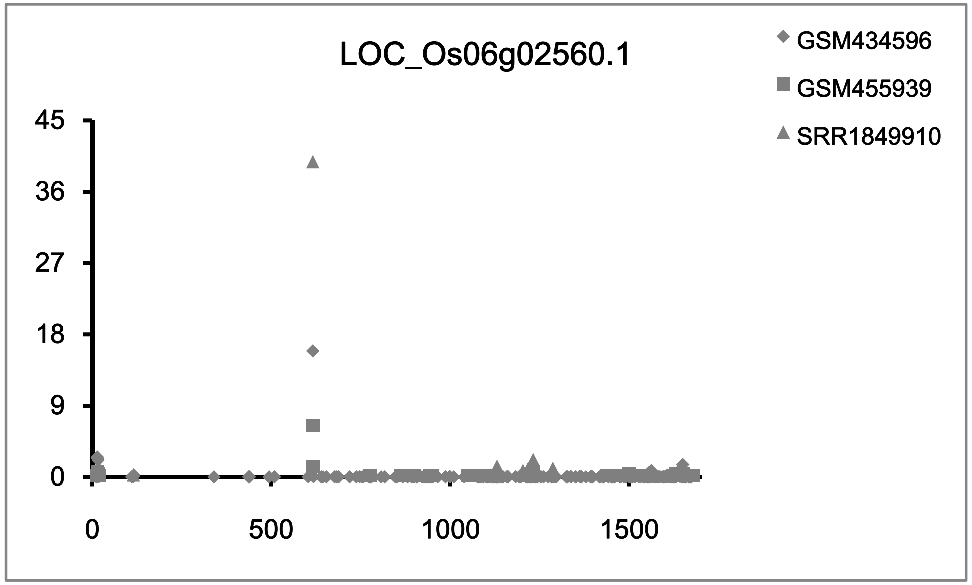

LOC_Os06g01620.1
SRR1849887
SRR1849892
3.5
2.8
2.1
1.4
0.7
0
0
500
1000
1500

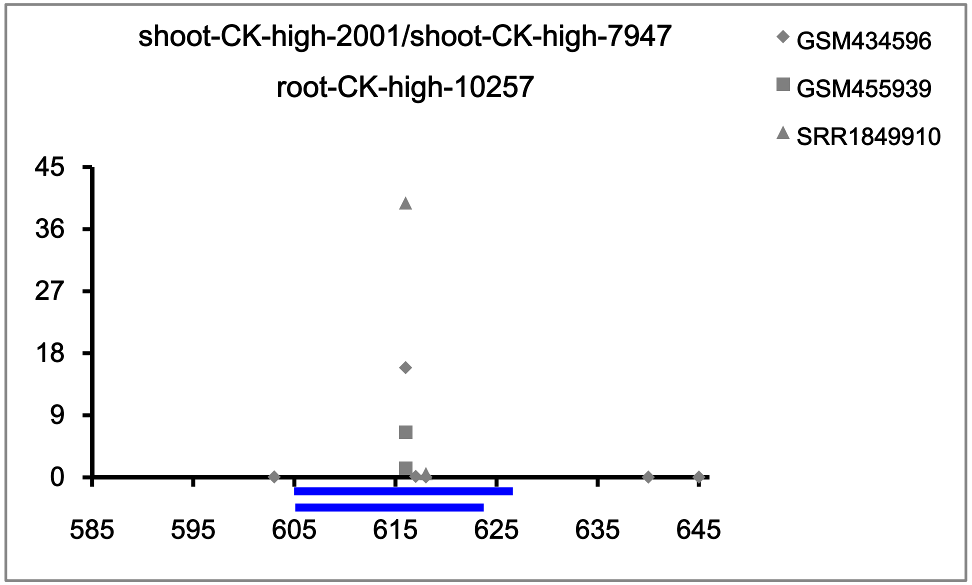

shoot-As-high-9528
shoot-CK-high-38
SRR1849887
SRR1849892
3.5
2.8
2.1
1.4
0.7
0
433
443
453
463
473
483
493

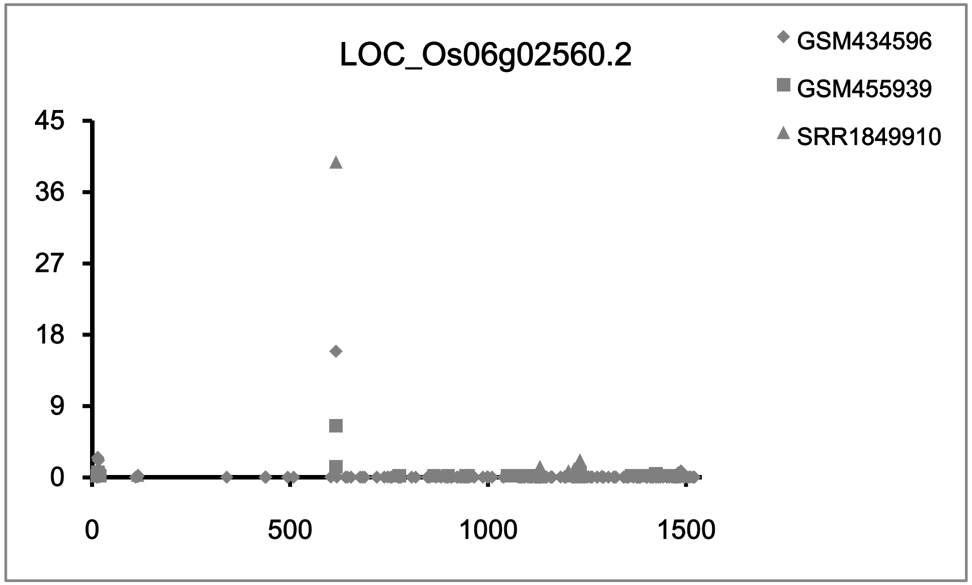

LOC_Os06g01950.1
GSM1040649
SRR1849907
30
24
18
12
6
0
0
500
1000
1500

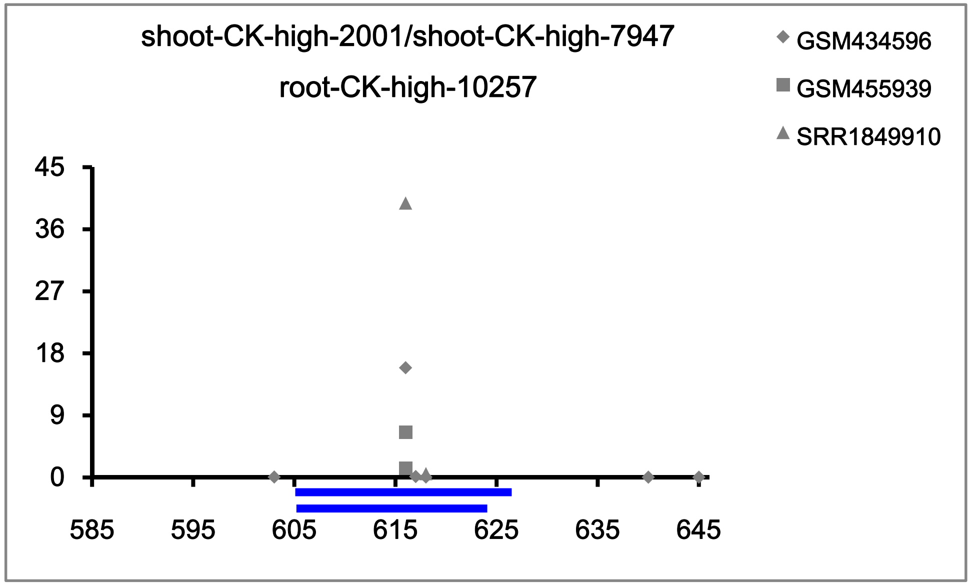

root-CK-high-13603
GSM1040649
SRR1849907
30
24
18
12
6
0
1346
1356
1366
1376
1386
1396
1406

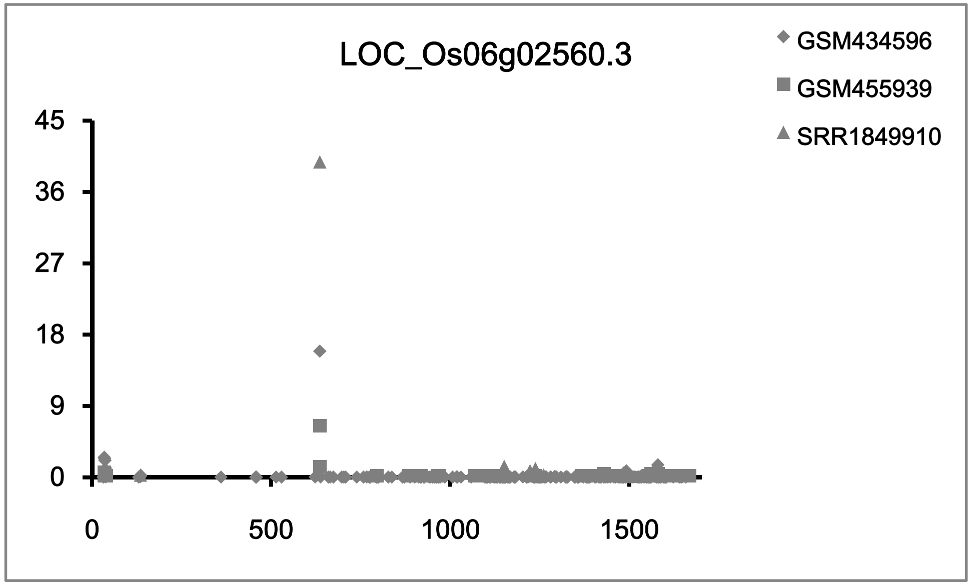

root-CK-high-2928
GSM1040649
SRR1849907
30
24
18
12
6
0
1364
1374
1384
1394
1404
1414
1424

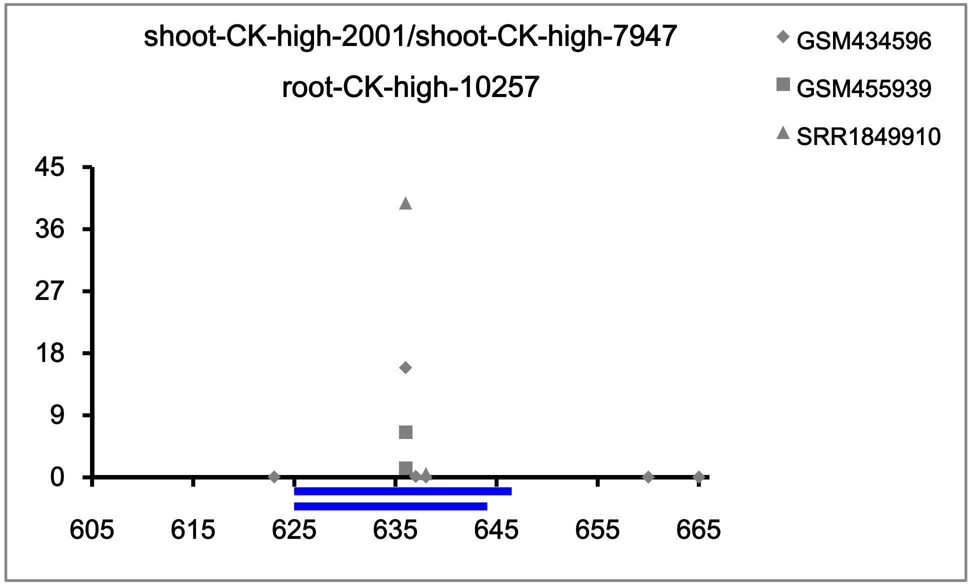

LOC_Os06g02560.1
GSM434596
GSM455939
SRR1849910
45
36
27
18
9
0
0
500
1000
1500

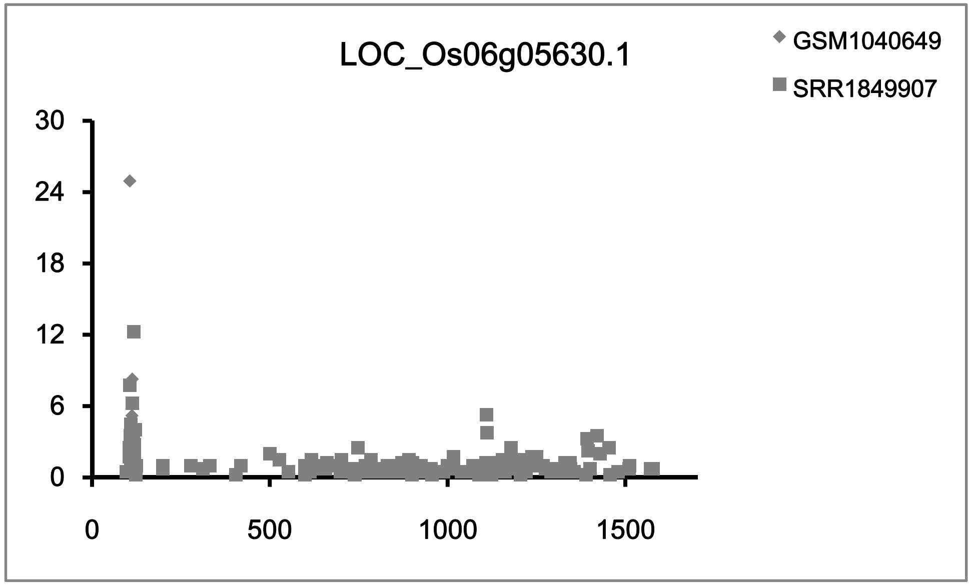

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
GSM434596
GSM455939
SRR1849910
45
36
27
18
9
0
585
595
605
615
625
635
645

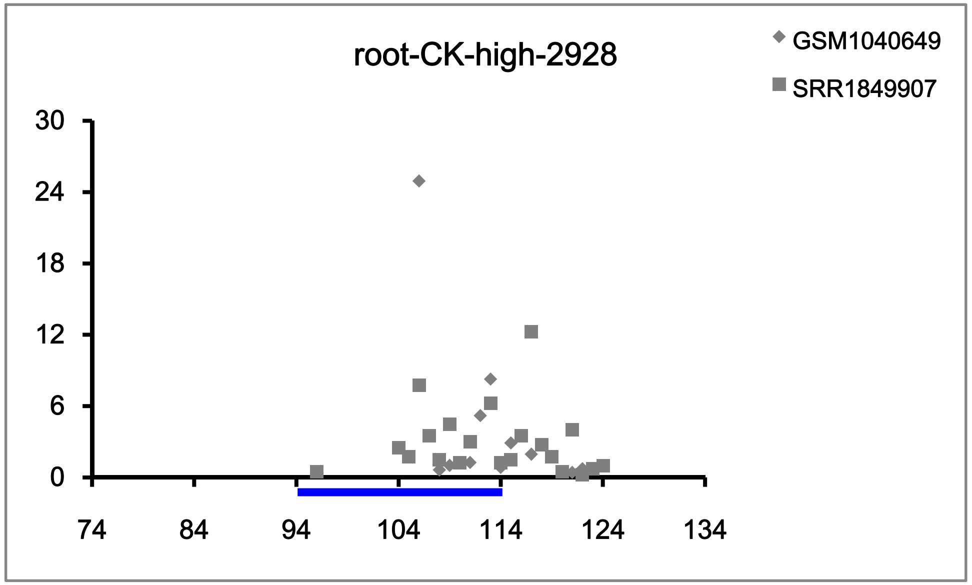

LOC_Os06g02560.2
GSM434596
GSM455939
SRR1849910
45
36
27
18
9
0
0
500
1000
1500

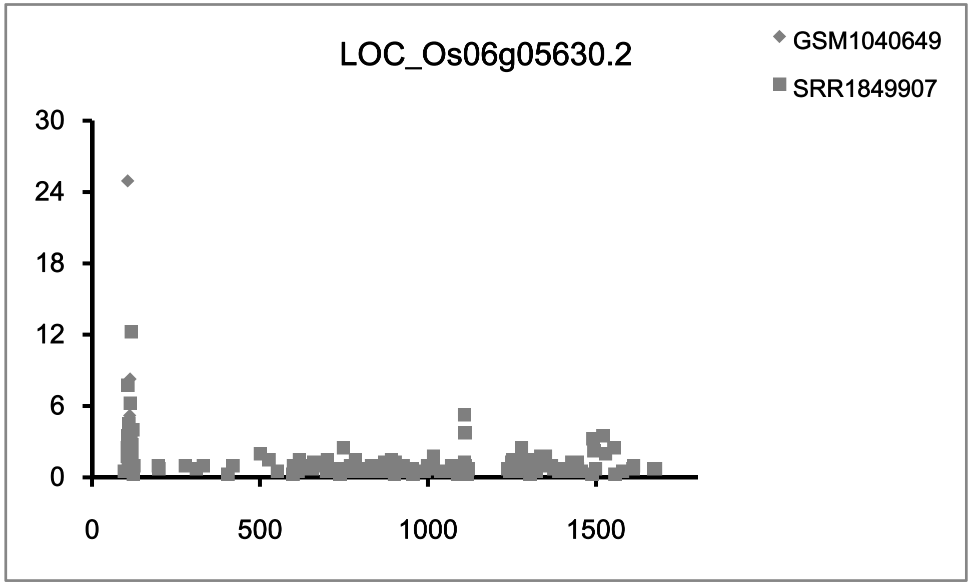

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
GSM434596
GSM455939
SRR1849910
45
36
27
18
9
0
585
595
605
615
625
635
645

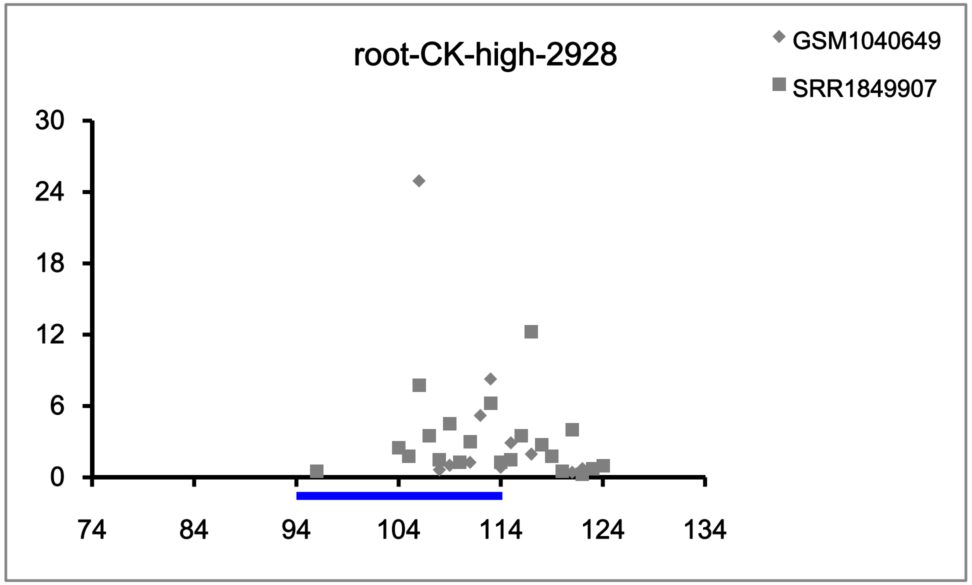

LOC_Os06g02560.3
GSM434596
GSM455939
SRR1849910
45
36
27
18
9
0
0
500
1000
1500

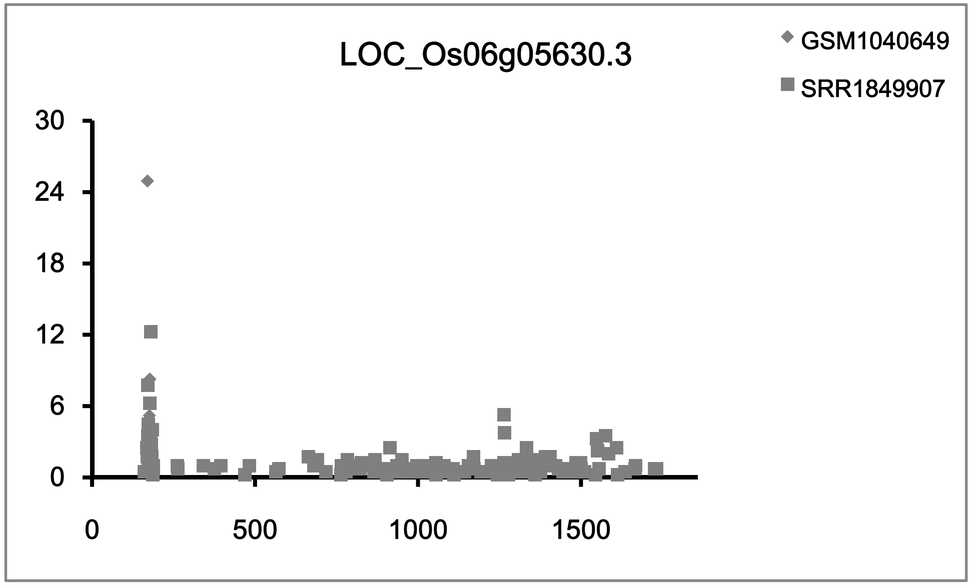

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
GSM434596
GSM455939
SRR1849910
45
36
27
18
9
0
605
615
625
635
645
655
665

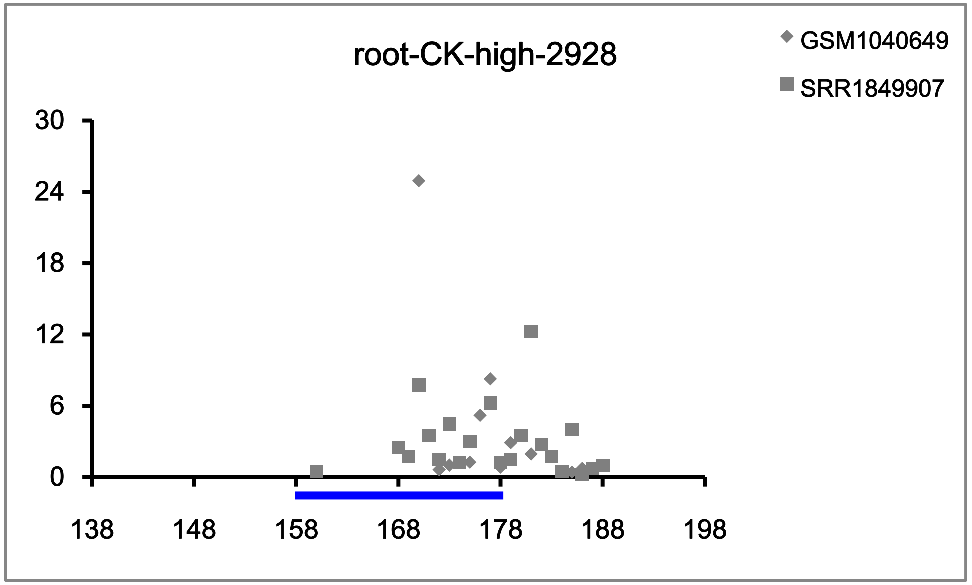

LOC_Os06g05630.1
GSM1040649
SRR1849907
30
24
18
12
6
0
0
500
1000
1500

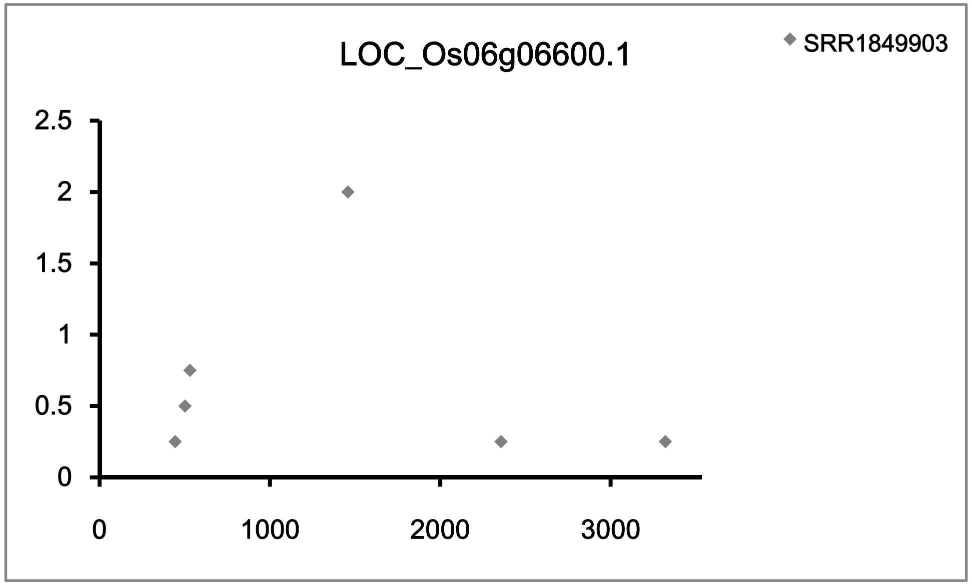

root-CK-high-2928
GSM1040649
SRR1849907
30
24
18
12
6
0
74
84
94
104
114
124
134

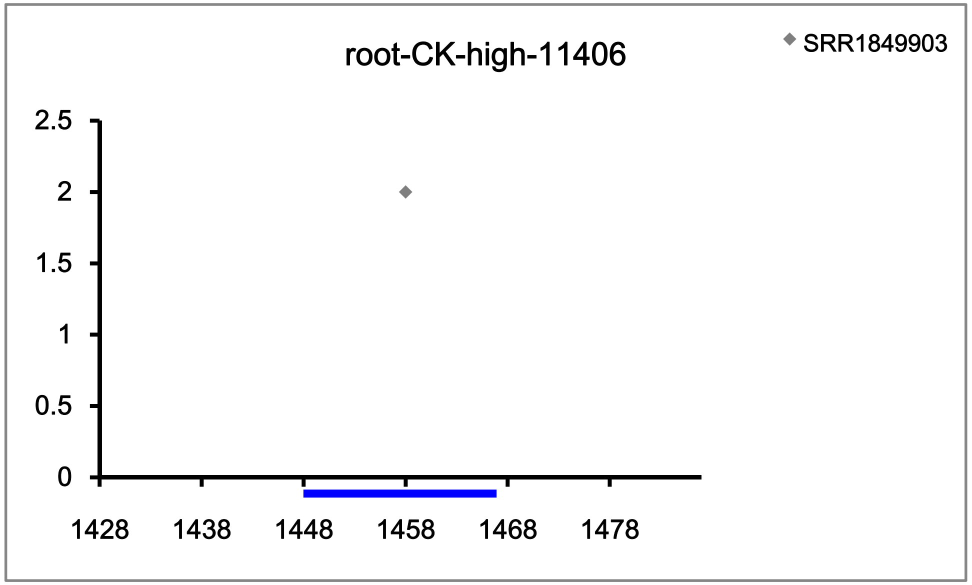

LOC_Os06g05630.2
GSM1040649
SRR1849907
30
24
18
12
6
0
0
500
1000
1500

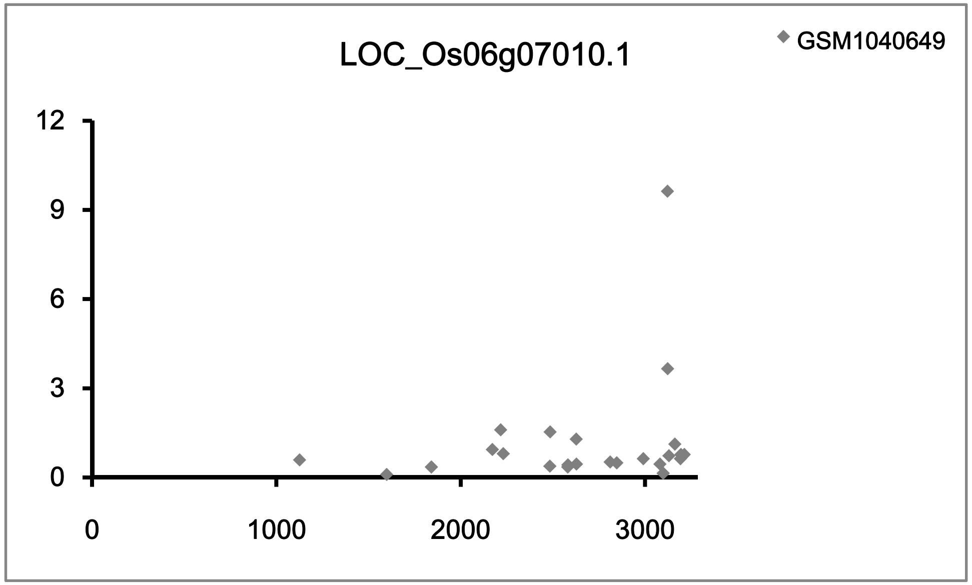

root-CK-high-2928
GSM1040649
SRR1849907
30
24
18
12
6
0
74
84
94
104
114
124
134

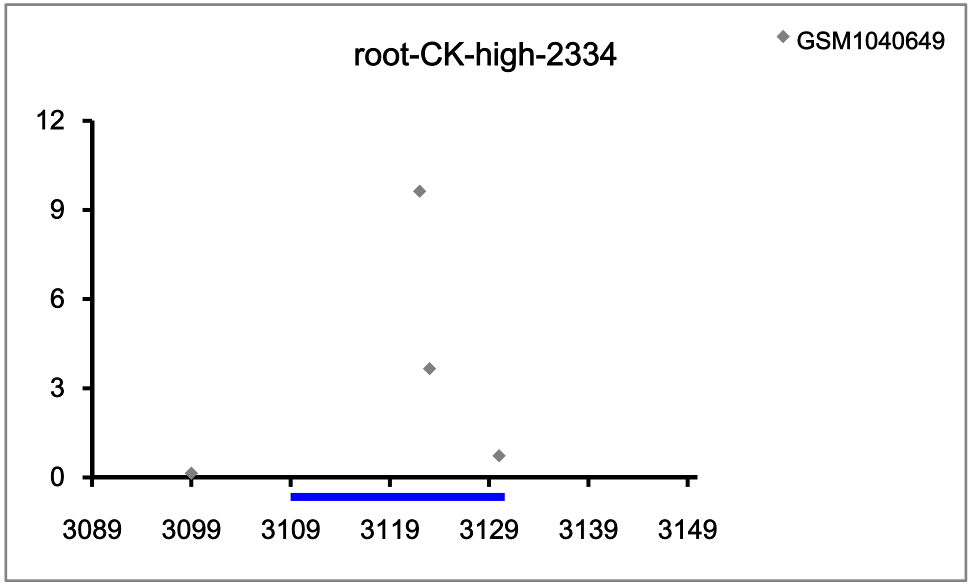

LOC_Os06g05630.3
GSM1040649
SRR1849907
30
24
18
12
6
0
0
500
1000
1500

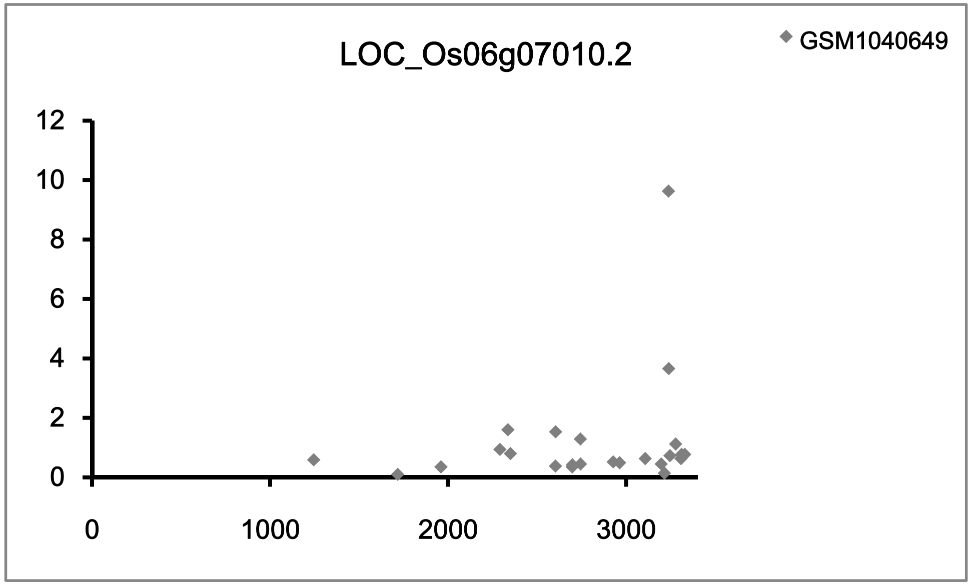

root-CK-high-2928
GSM1040649
SRR1849907
30
24
18
12
6
0
138
148
158
168
178
188
198

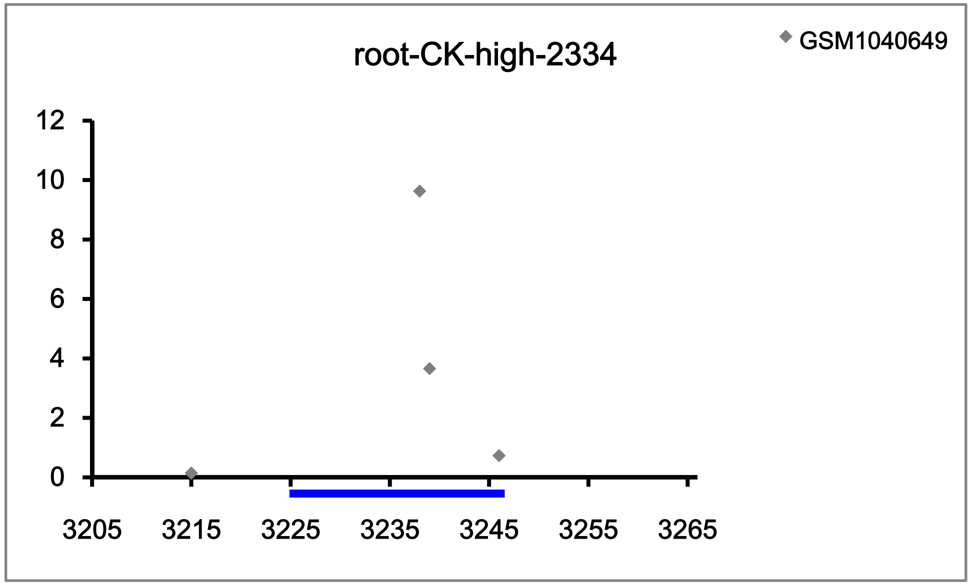

LOC_Os06g06600.1
SRR1849903
2.5
2
1.5
1
0.5
0
0
1000
2000
3000

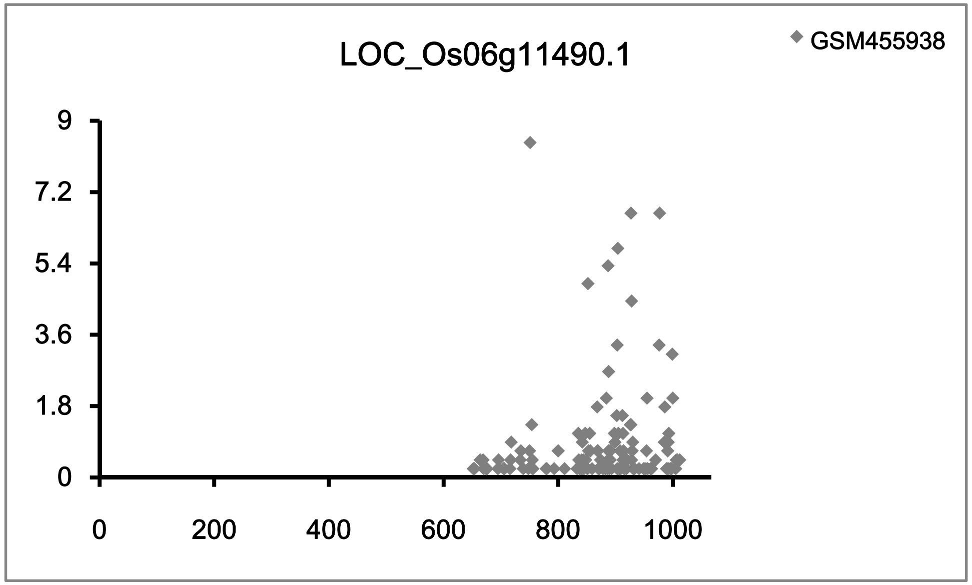

root-CK-high-11406
SRR1849903
2.5
2
1.5
1
0.5
0
1428
1438
1448
1458
1468
1478

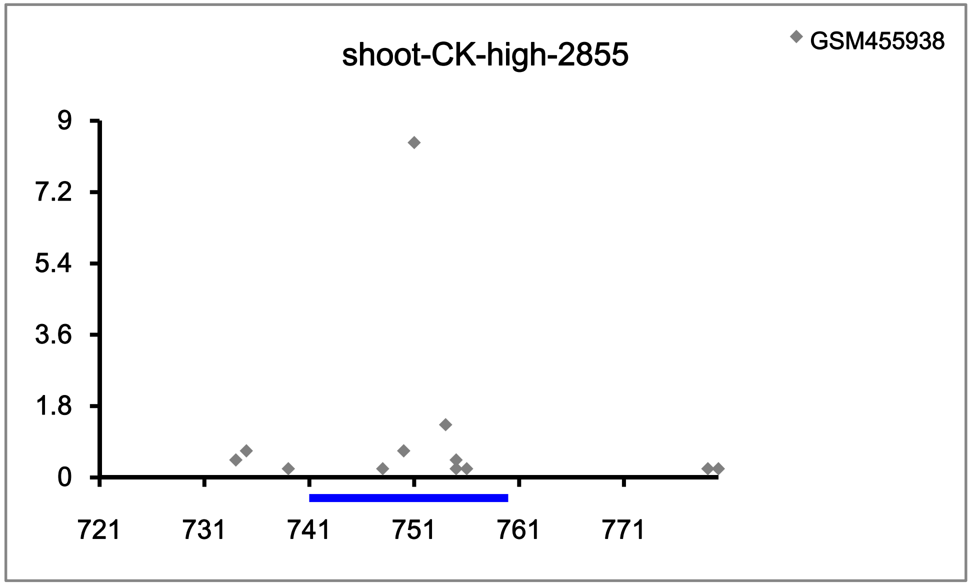

LOC_Os06g07010.1
GSM1040649
12
9
6
3
0
0
1000
2000
3000

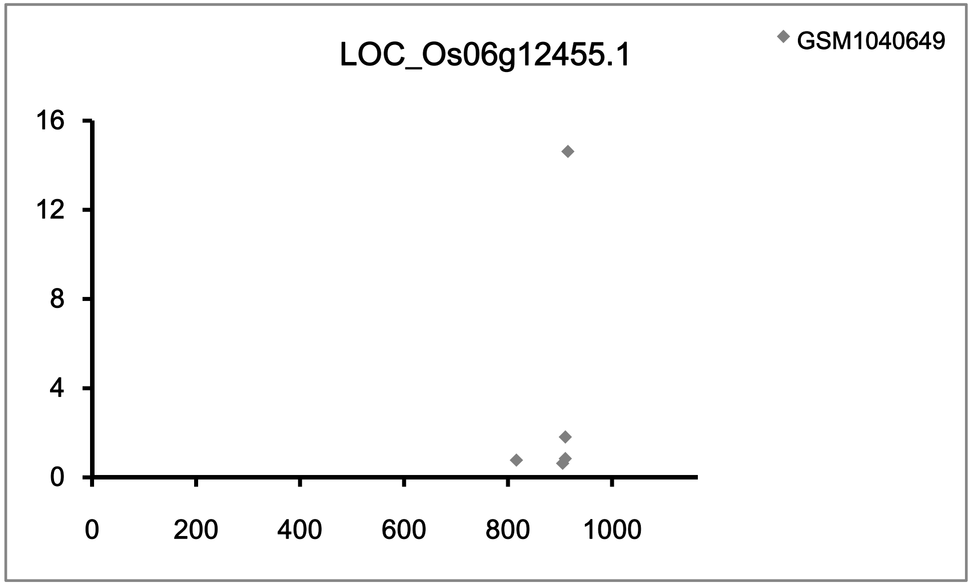

root-CK-high-2334
GSM1040649
12
9
6
3
0
3089
3099
3109
3119
3129
3139
3149

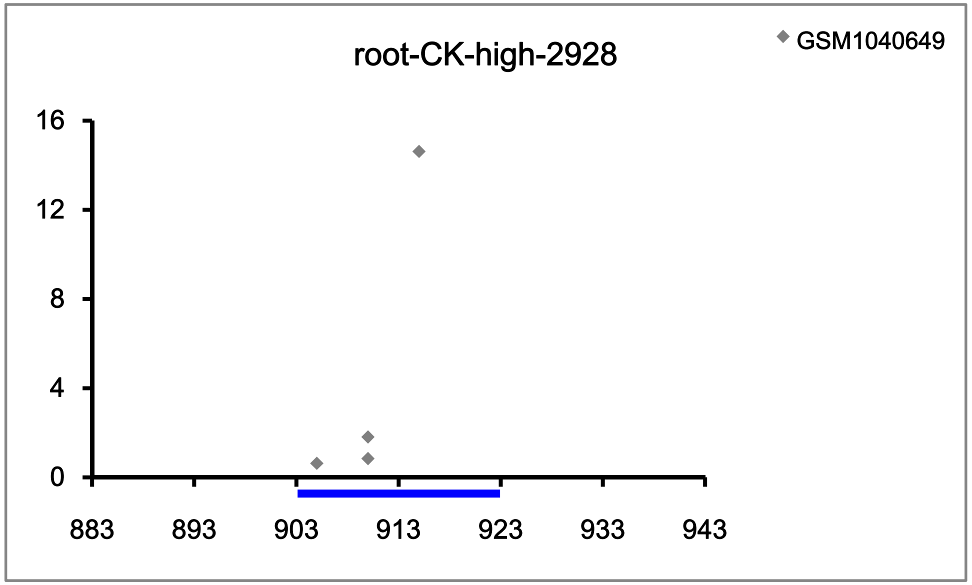

LOC_Os06g07010.2
◆ GSM1040649
12
10
8
6
4
2
0
0
1000
2000
3000

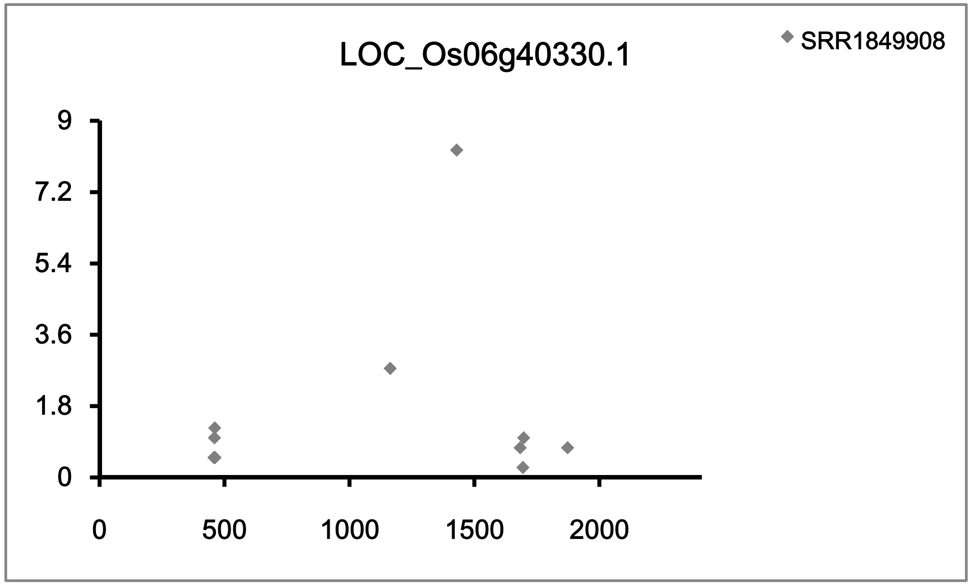

root-CK-high-2334
◆ GSM1040649
12
10
8
6
4
2
0
3205
3215
3225
3235
3245
3255
3265

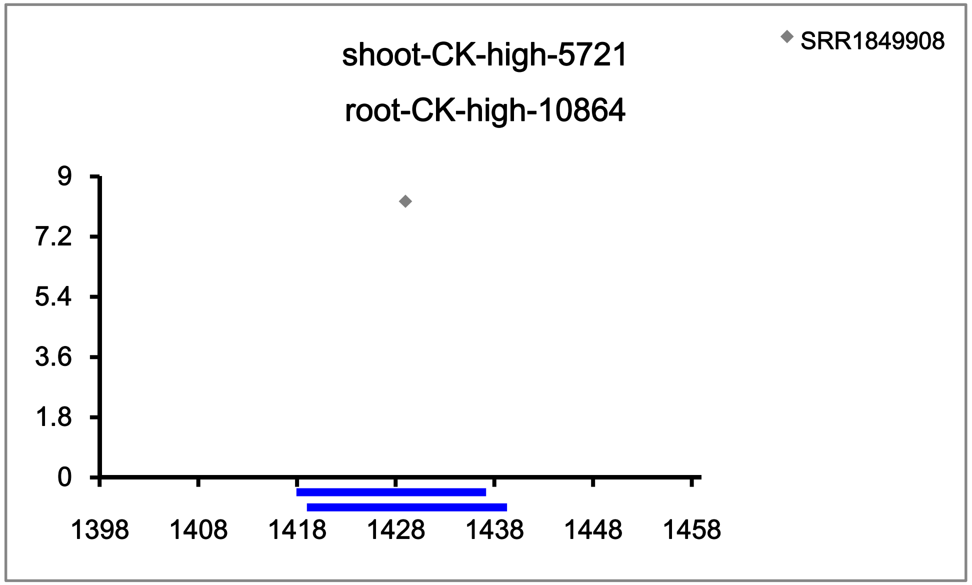

LOC_Os06g11490.1
◆ GSM455938
9
7.2
5.4
3.6
1.8
0
0
200
400
600
800
1000

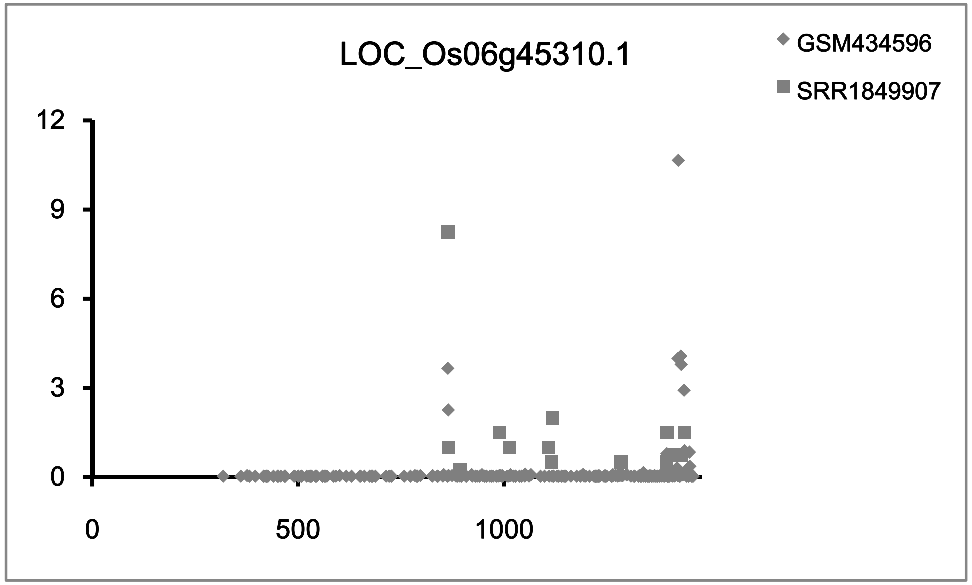

shoot-CK-high-2855
◆ GSM455938
9
7.2
5.4
3.6
1.8
0
721
731
741
751
761
771

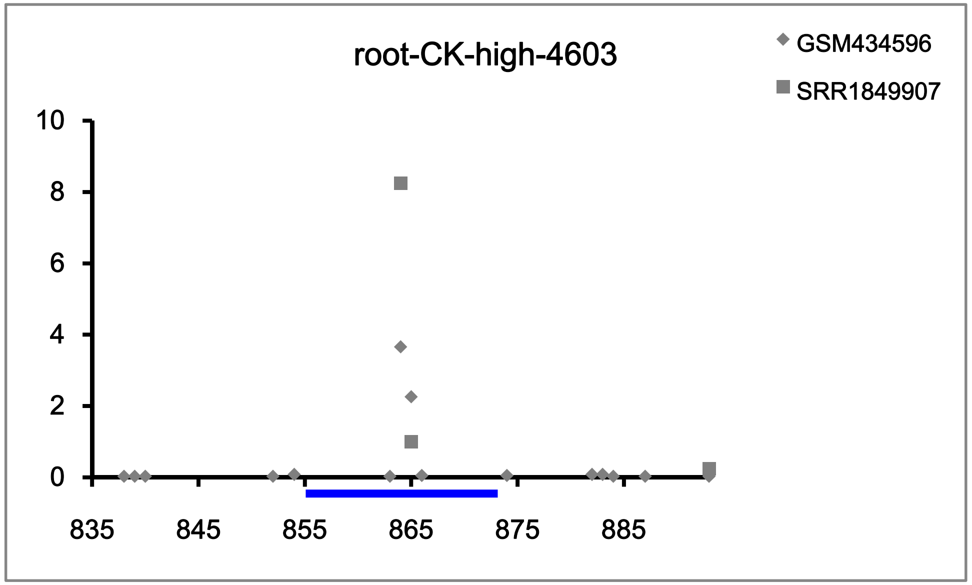

LOC_Os06g12455.1
GSM1040649
16
12
8
4
0
0
200
400
600
800
1000

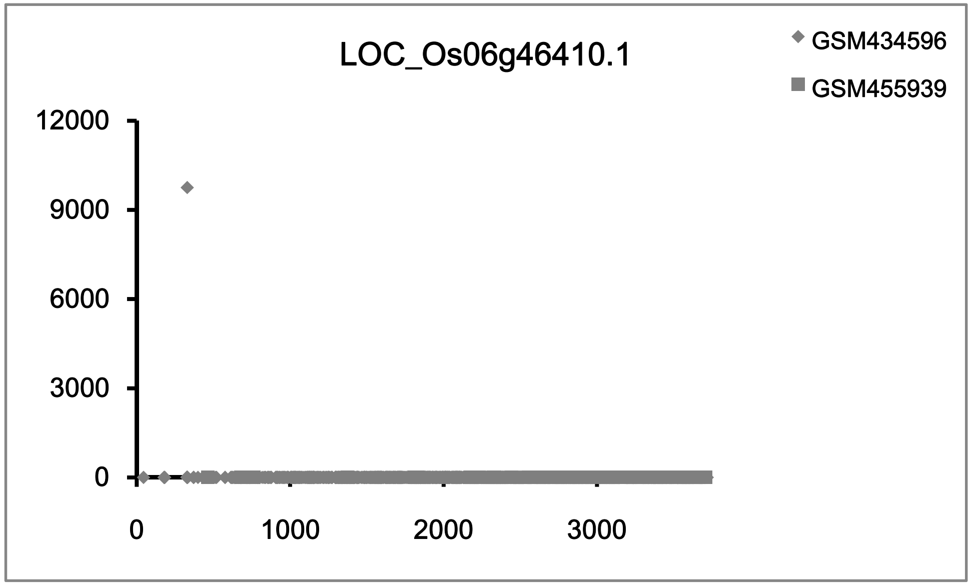

root-CK-high-2928
GSM1040649
16
12
8
4
0
883
893
903
913
923
933
943

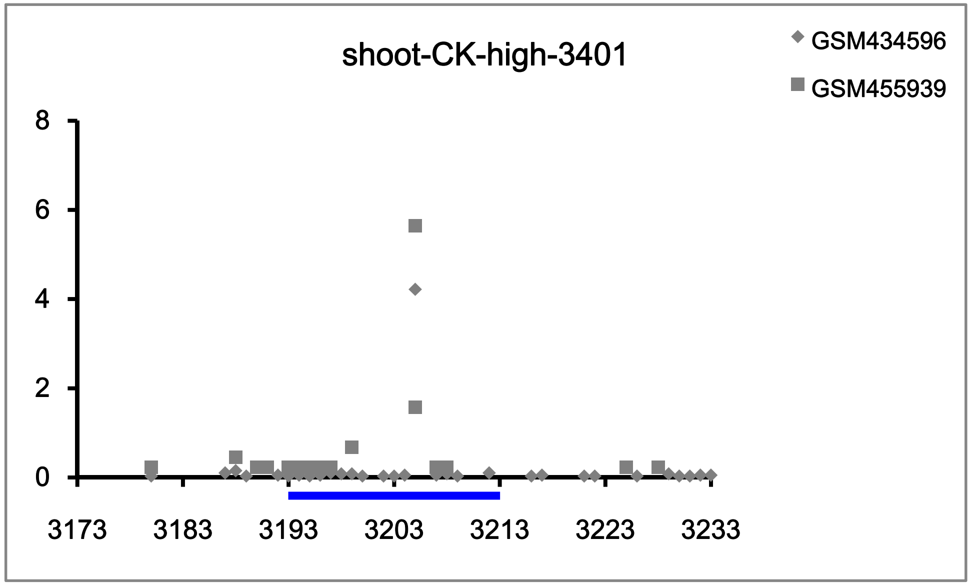

LOC_Os06g40330.1
SRR1849908
9
7.2
5.4
3.6
1.8
0
0
500
1000
1500
2000

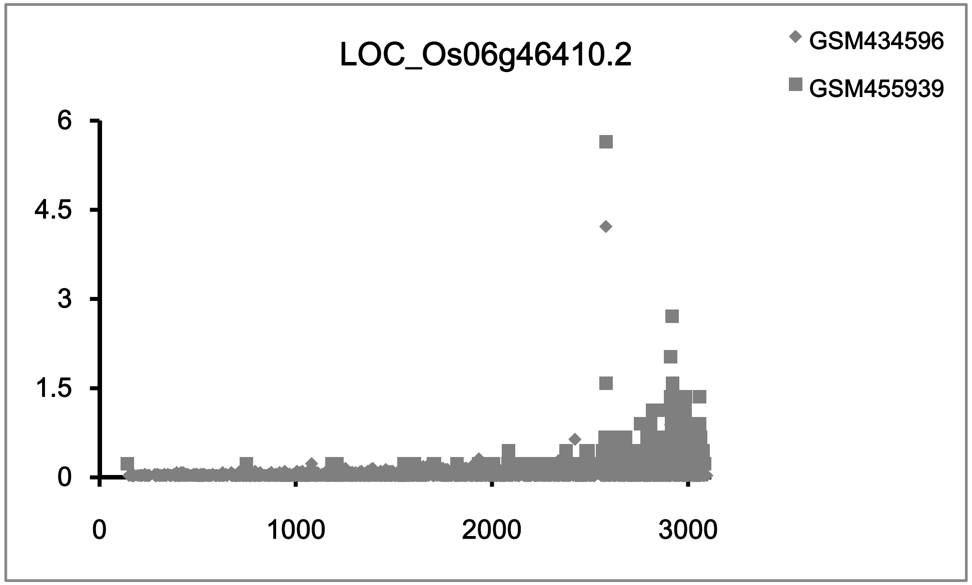

shoot-CK-high-5721
root-CK-high-10864
SRR1849908
9
7.2
5.4
3.6
1.8
0
1398
1408
1418
1428
1438
1448
1458

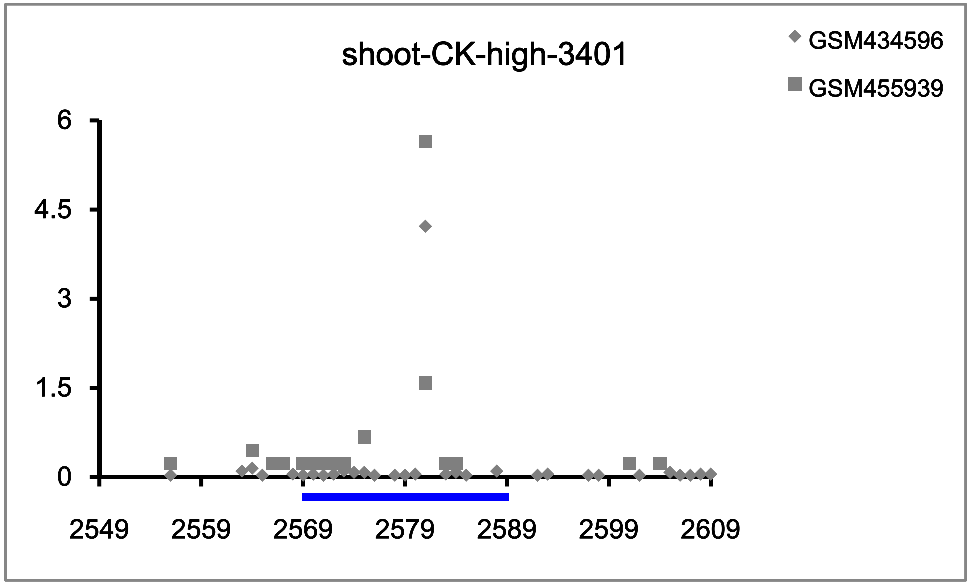

LOC_Os06g45310.1
GSM434596
SRR1849907
12
9
6
3
0
0
500
1000

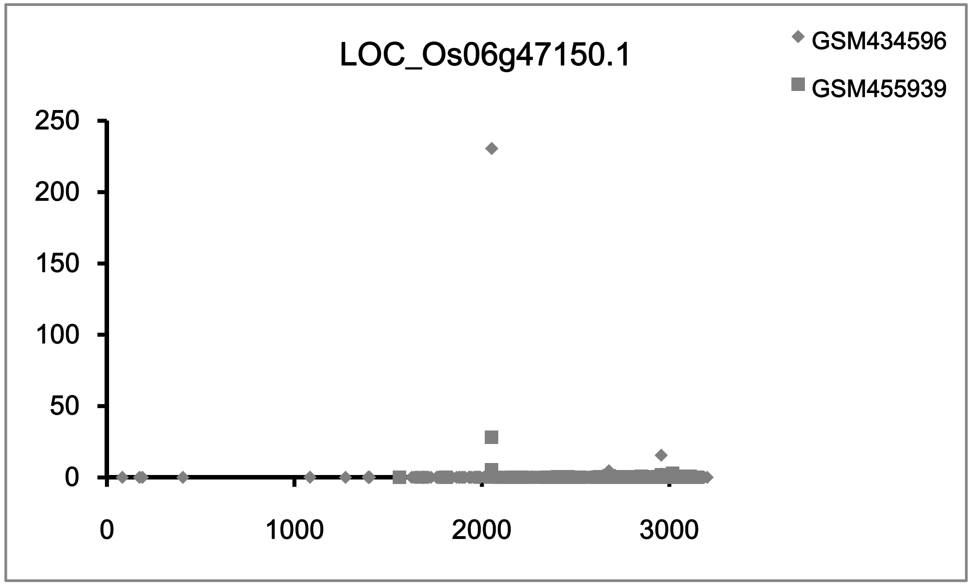

root-CK-high-4603
GSM434596
SRR1849907
10
8
6
4
2
0
835
845
855
865
875
885

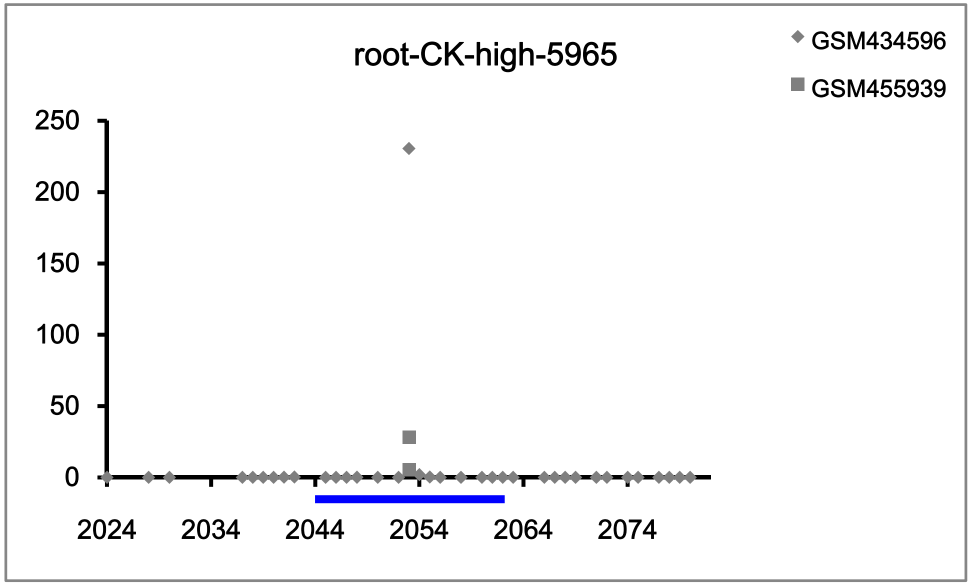

LOC_Os06g46410.1
GSM434596
GSM455939
12000
9000
6000
3000
0
0
1000
2000
3000

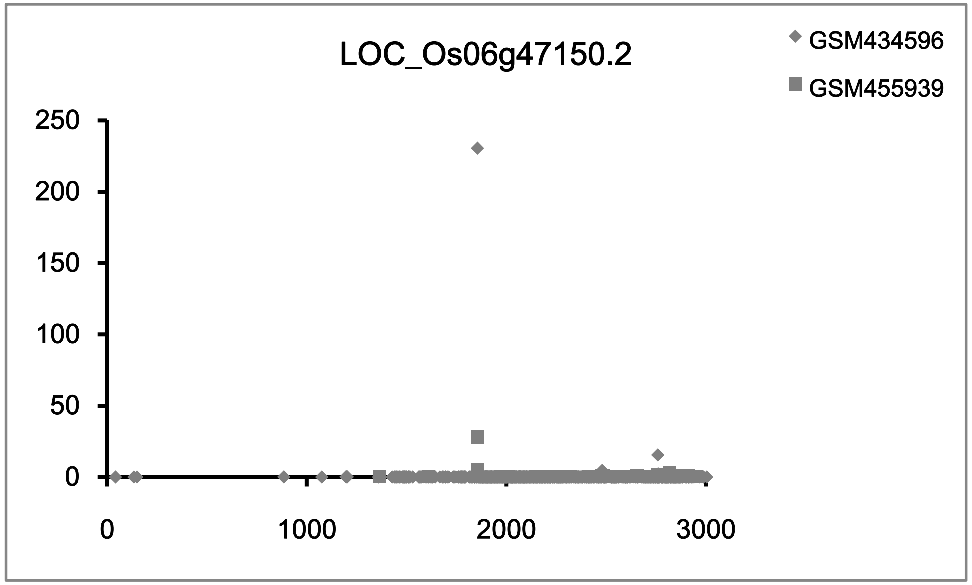

shoot-CK-high-3401
GSM434596
GSM455939
8
6
4
2
0
3173
3183
3193
3203
3213
3223
3233

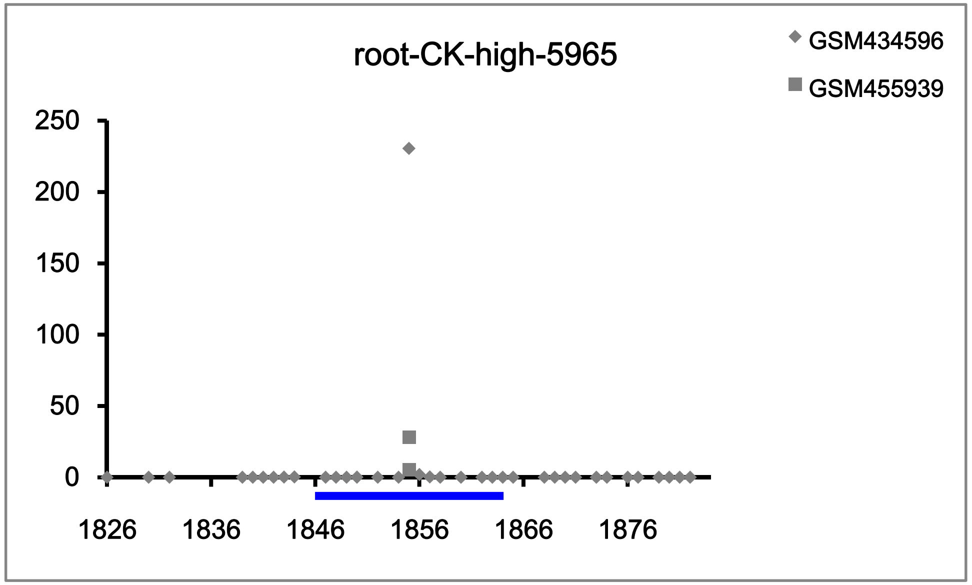

LOC_Os06g46410.2
GSM434596
GSM455939
6
4.5
3
1.5
0
0
1000
2000
3000

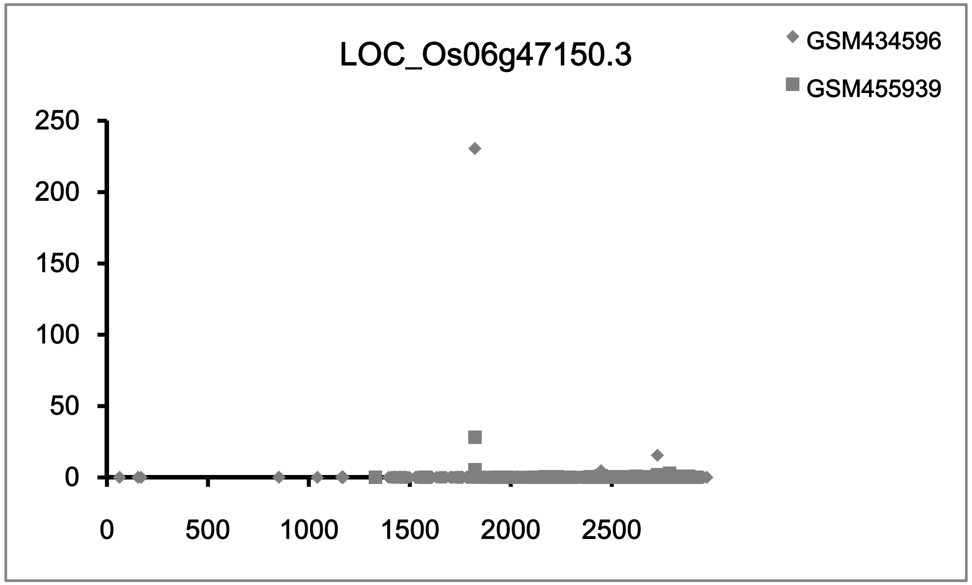

shoot-CK-high-3401
GSM434596
GSM455939
6
4.5
3
1.5
0
2549
2559
2569
2579
2589
2599
2609

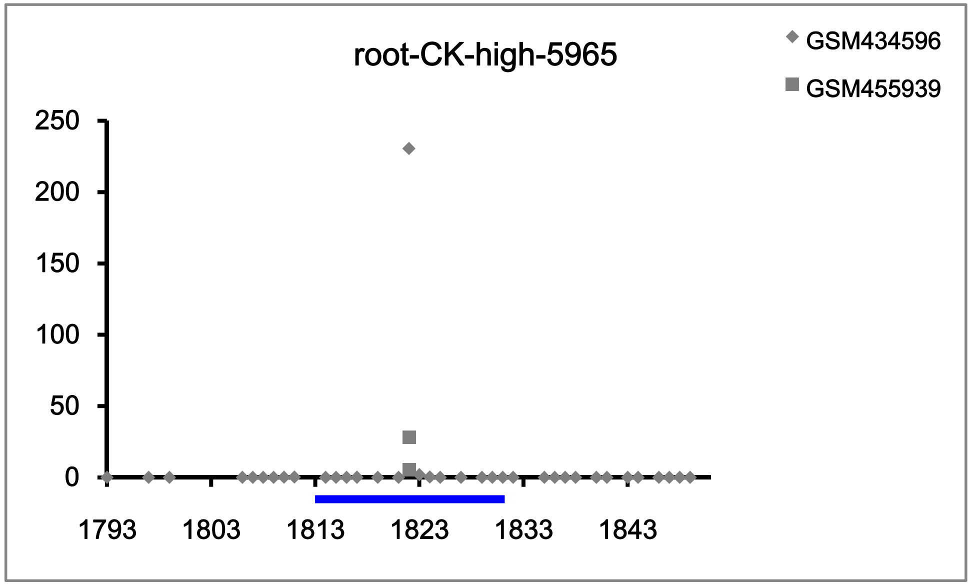

LOC_Os06g47150.1
GSM434596
GSM455939
250
200
150
100
50
0
0
1000
2000
3000

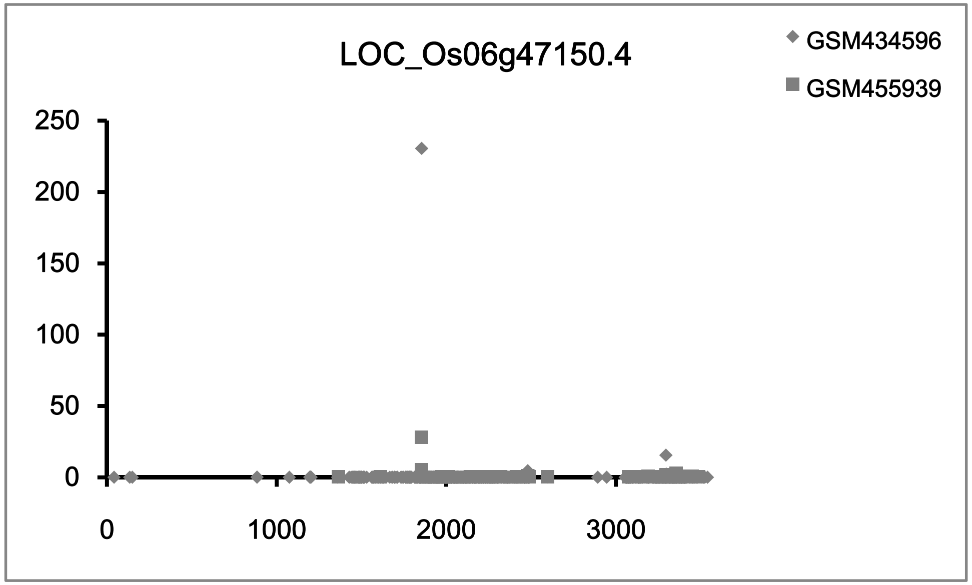

root-CK-high-5965
GSM434596
GSM455939
250
200
150
100
50
0
2024
2034
2044
2054
2064
2074

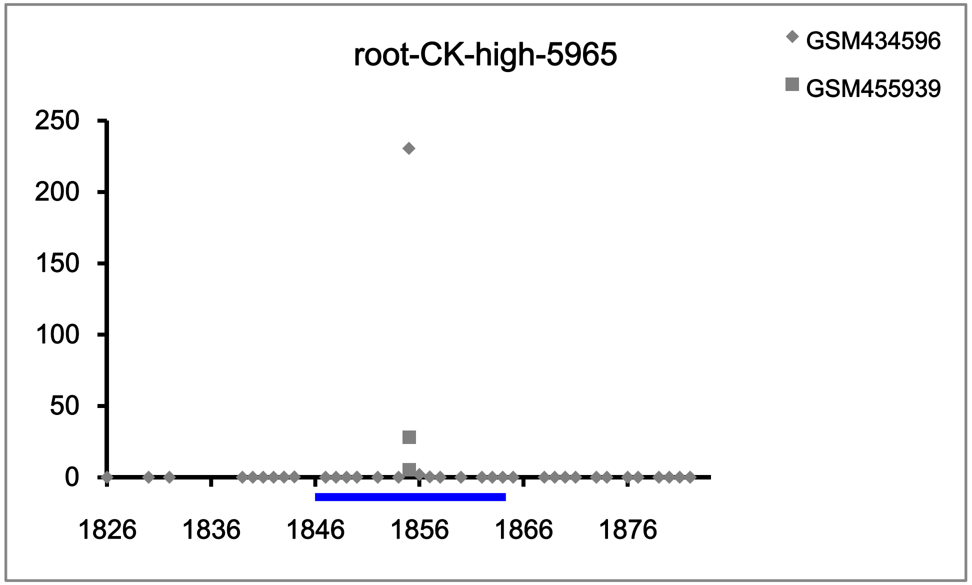

LOC_Os06g47150.2
GSM434596
GSM455939
250
200
150
100
50
0
0
1000
2000
3000

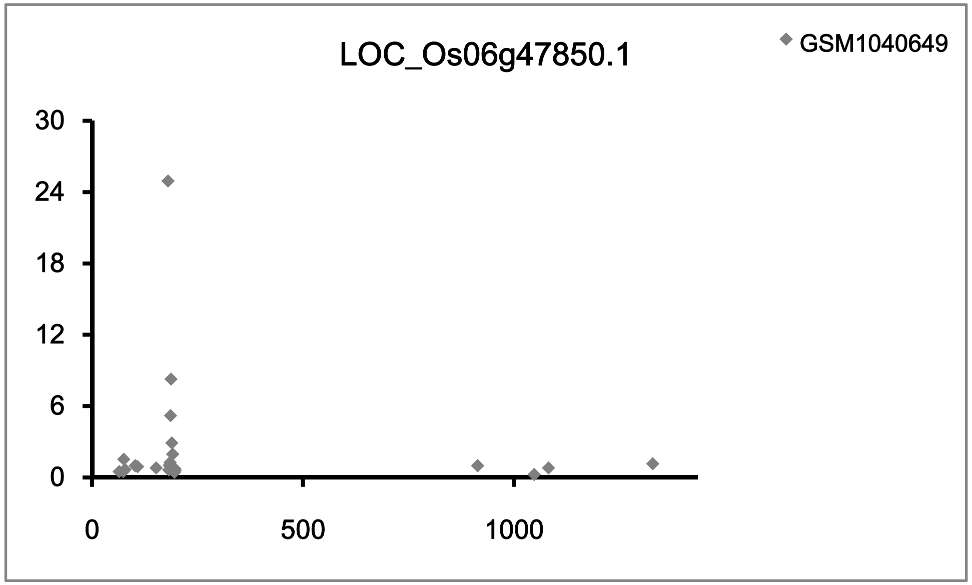

root-CK-high-5965
GSM434596
GSM455939
250
200
150
100
50
0
1826
1836
1846
1856
1866
1876

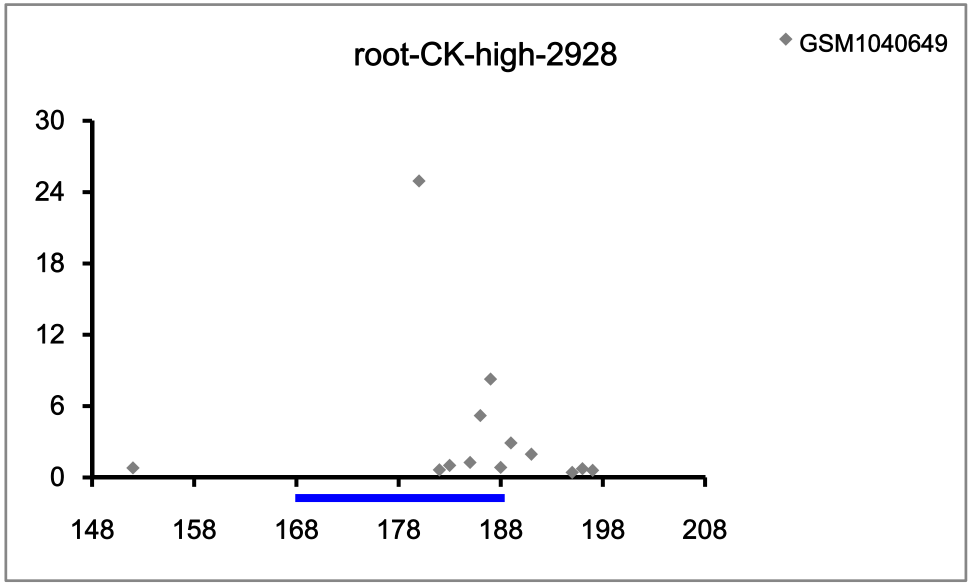

LOC_Os06g47150.3
GSM434596
GSM455939
250
200
150
100
50
0
0
500
1000
1500
2000
2500

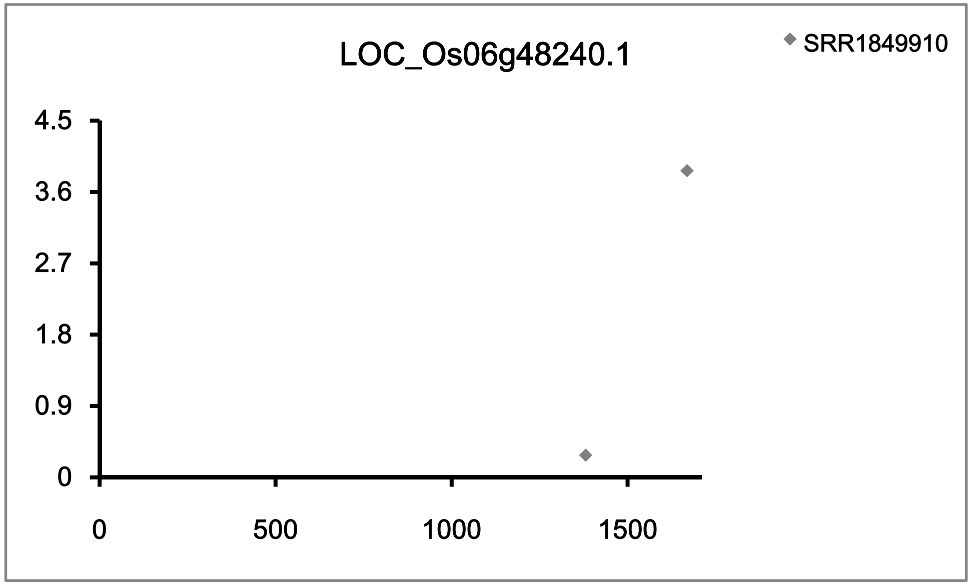

root-CK-high-5965
GSM434596
GSM455939
250
200
150
100
50
0
1793
1803
1813
1823
1833
1843

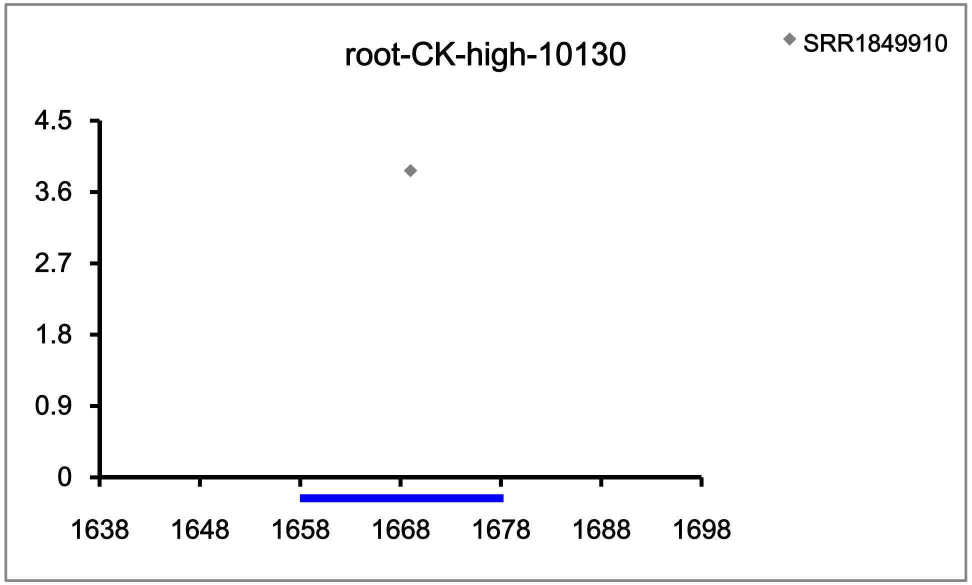

LOC_Os06g47150.4
GSM434596
GSM455939
250
200
150
100
50
0
0
1000
2000
3000

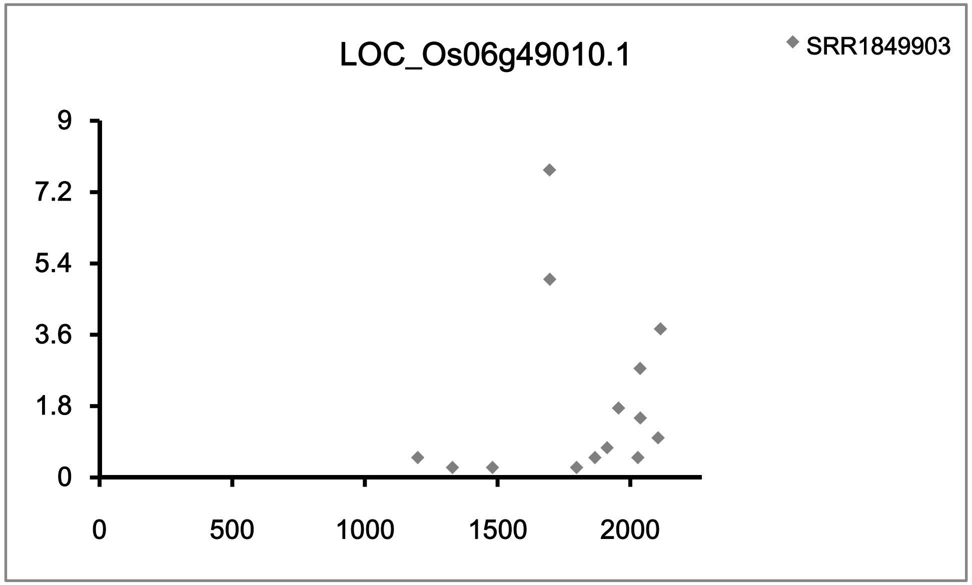

root-CK-high-5965
GSM434596
GSM455939
250
200
150
100
50
0
1826
1836
1846
1856
1866
1876

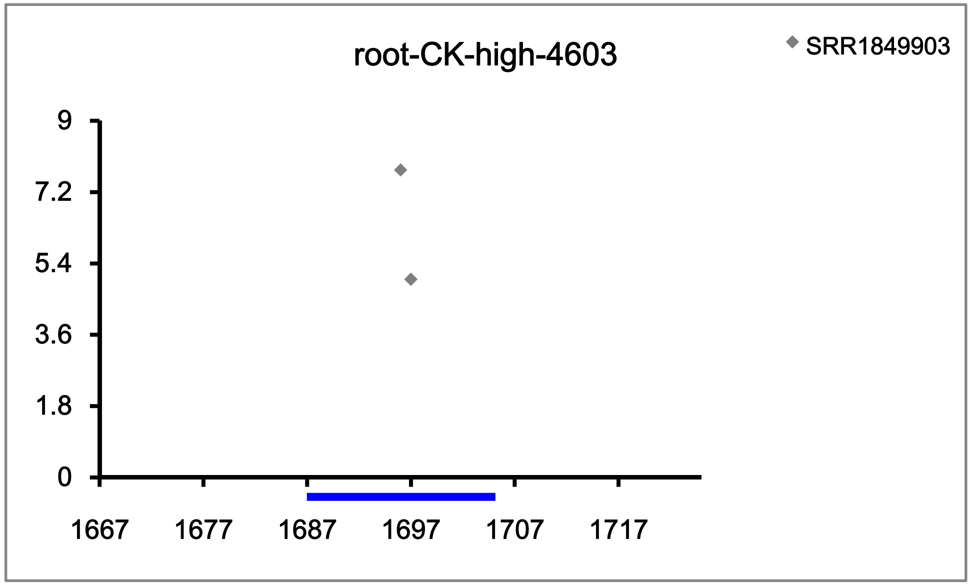

LOC_Os06g47850.1
GSM1040649
30
24
18
12
6
0
0
500
1000

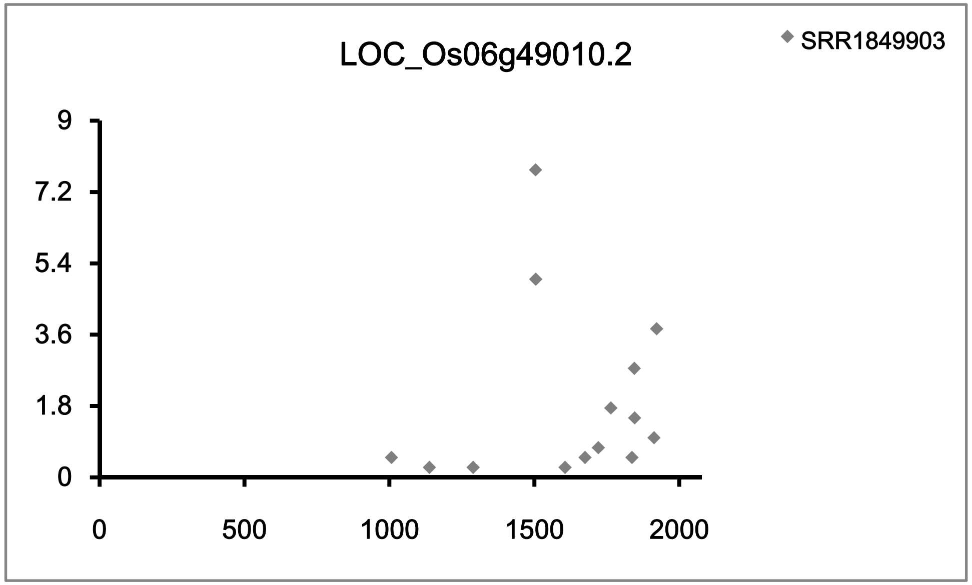

root-CK-high-2928
GSM1040649
30
24
18
12
6
0
148
158
168
178
188
198
208

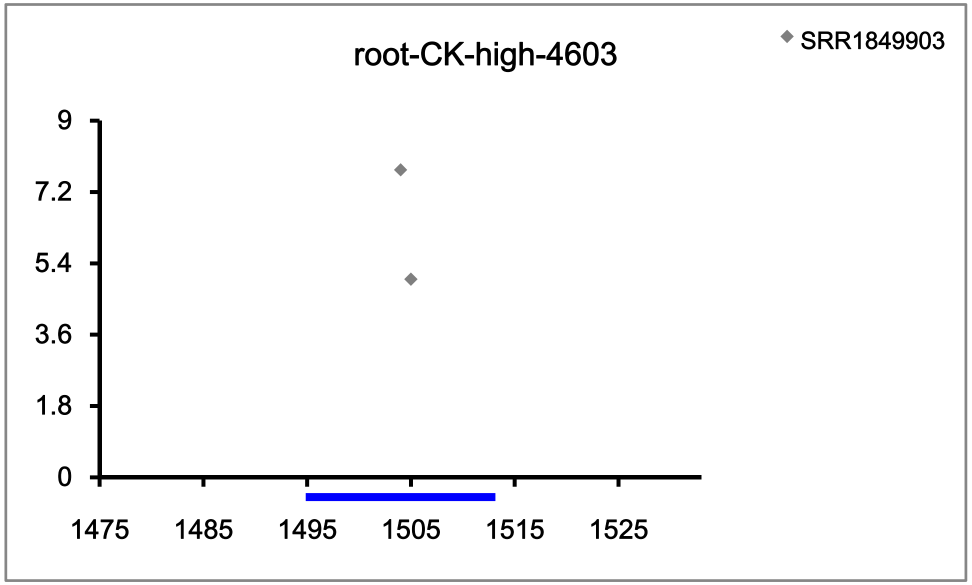

LOC_Os06g48240.1
◆ SRR1849910
4.5
3.6
2.7
1.8
0.9
0
0
500
1000
1500

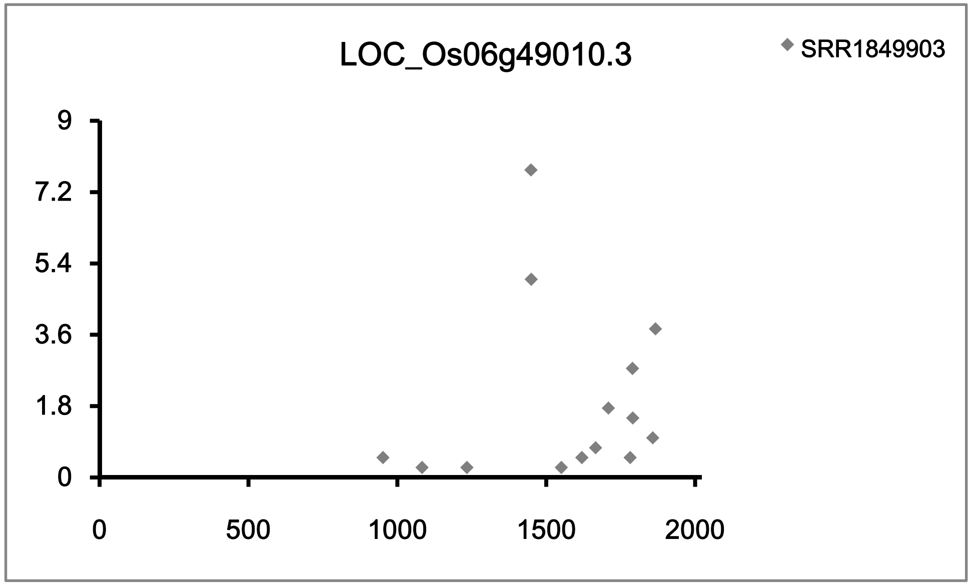

root-CK-high-10130
◆ SRR1849910
4.5
3.6
2.7
1.8
0.9
0
1638
1648
1658
1668
1678
1688
1698

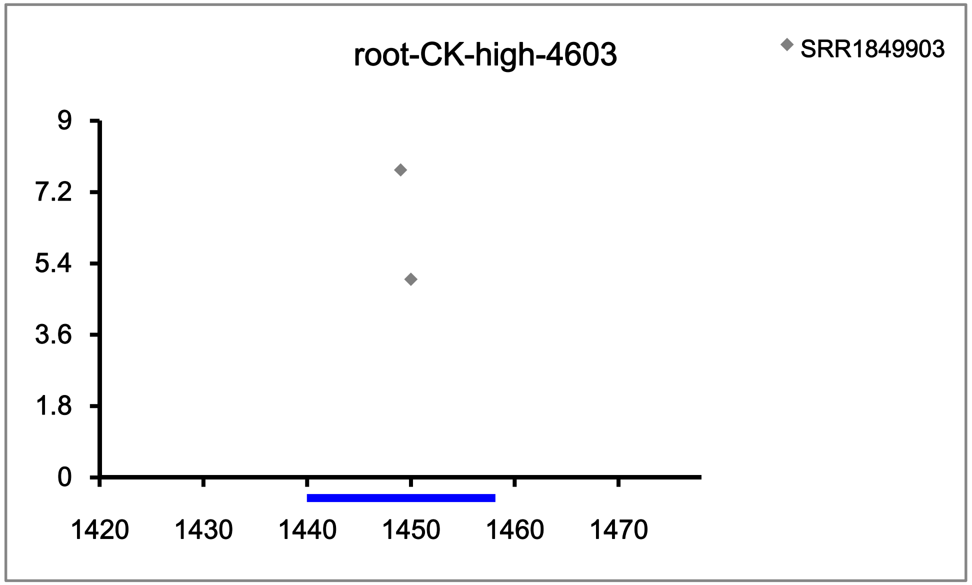

LOC_Os06g49010.1
◆ SRR1849903
9
7.2
5.4
3.6
1.8
0
0
500
1000
1500
2000

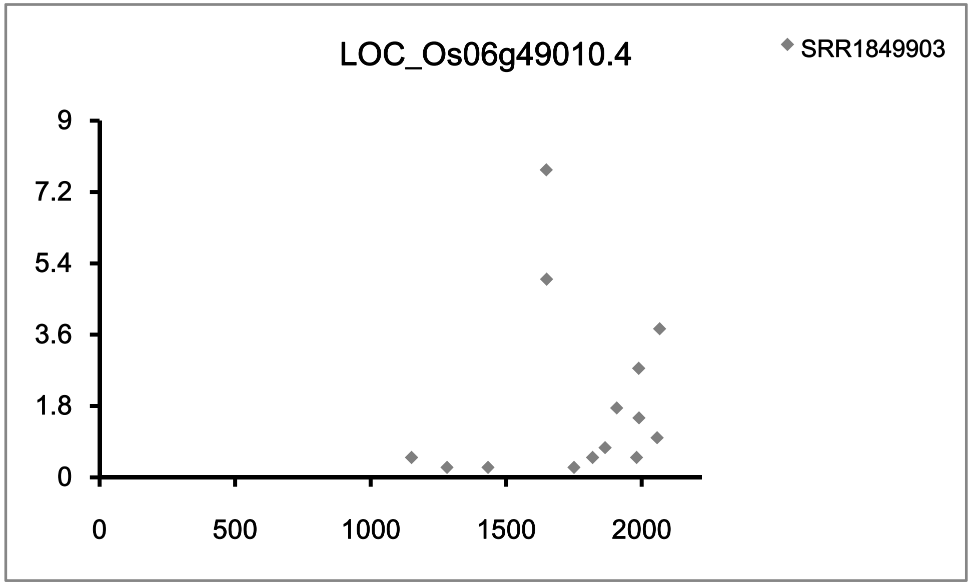

root-CK-high-4603
◆ SRR1849903
9
7.2
5.4
3.6
1.8
0
1667
1677
1687
1697
1707
1717

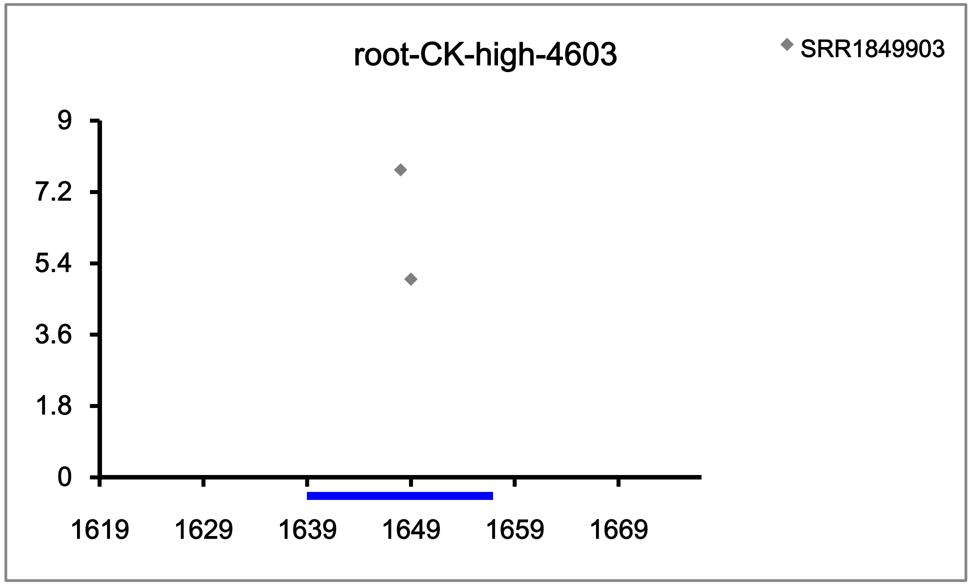

LOC_Os06g49010.2
SRR1849903
9
7.2
5.4
3.6
1.8
0
0
500
1000
1500
2000

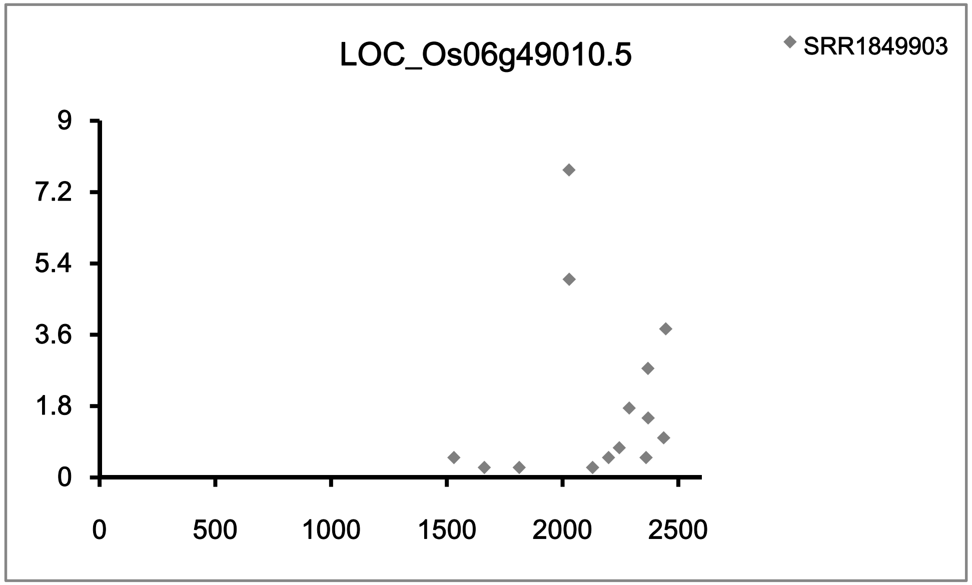

root-CK-high-4603
SRR1849903
9
7.2
5.4
3.6
1.8
0
1475
1485
1495
1505
1515
1525

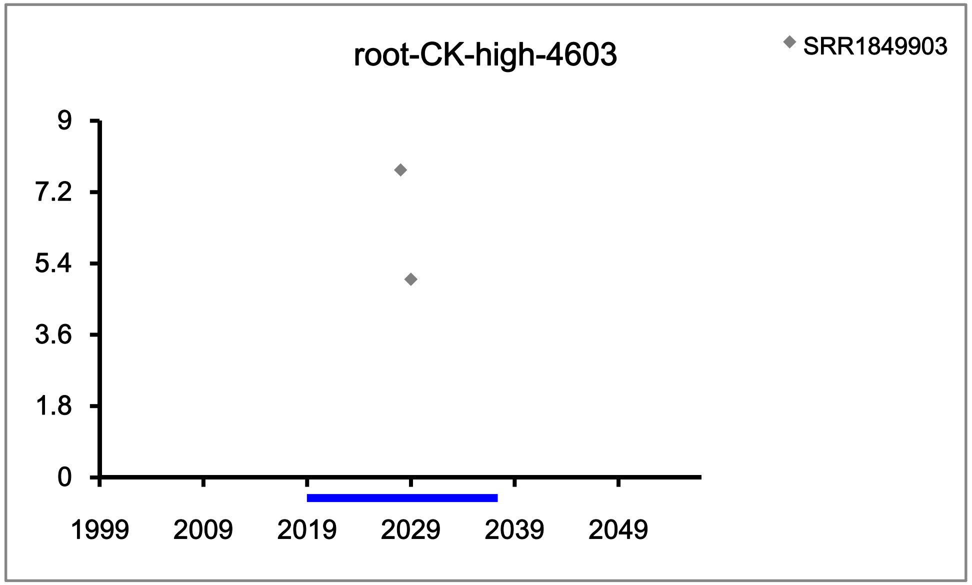

LOC_Os06g49010.3
SRR1849903
9
7.2
5.4
3.6
1.8
0
0
500
1000
1500
2000

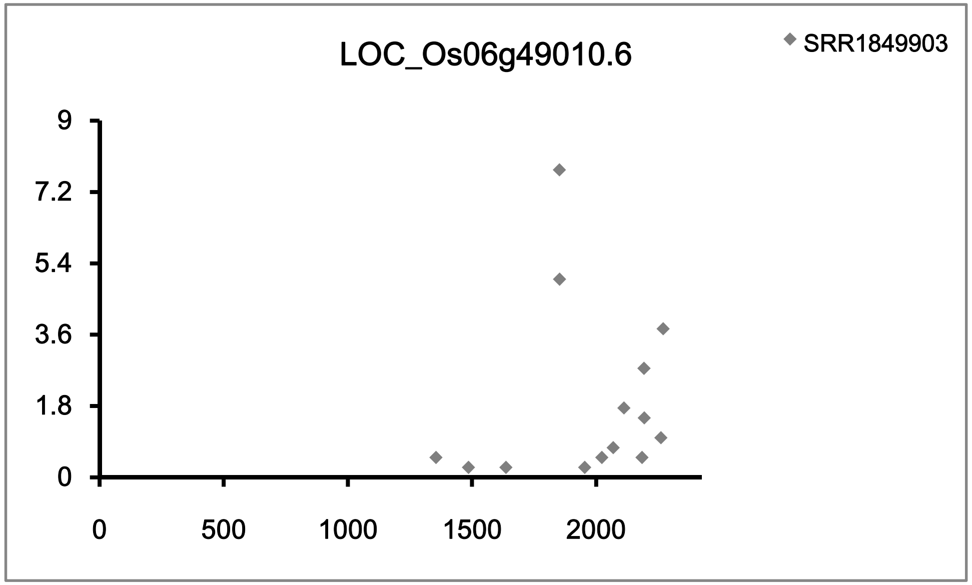

root-CK-high-4603
SRR1849903
9
7.2
5.4
3.6
1.8
0
1420
1430
1440
1450
1460
1470

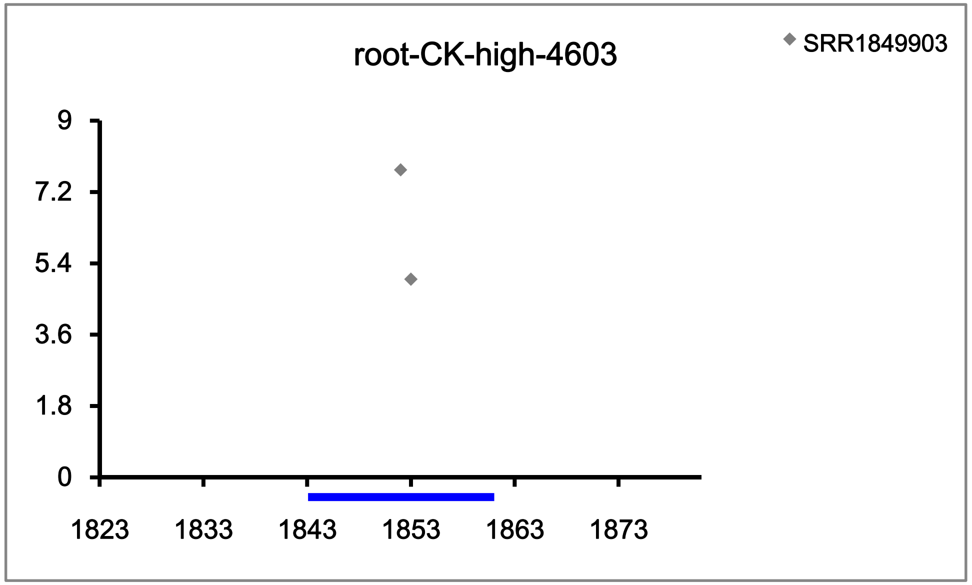

LOC_Os06g49010.4
SRR1849903
9
7.2
5.4
3.6
1.8
0
0
500
1000
1500
2000

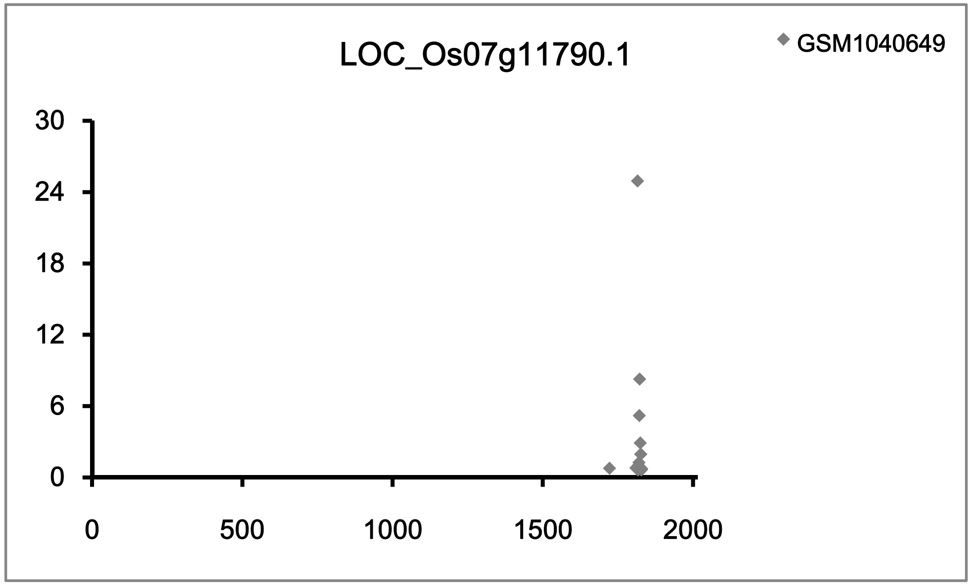

root-CK-high-4603
SRR1849903
9
7.2
5.4
3.6
1.8
0
1619
1629
1639
1649
1659
1669

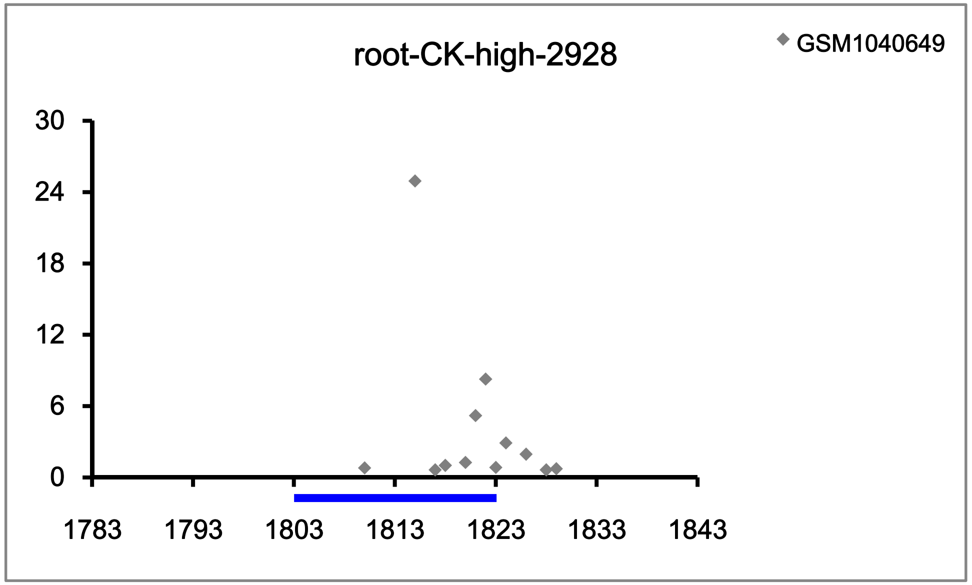

LOC_Os06g49010.5
SRR1849903
9
7.2
5.4
3.6
1.8
0
0
500
1000
1500
2000
2500

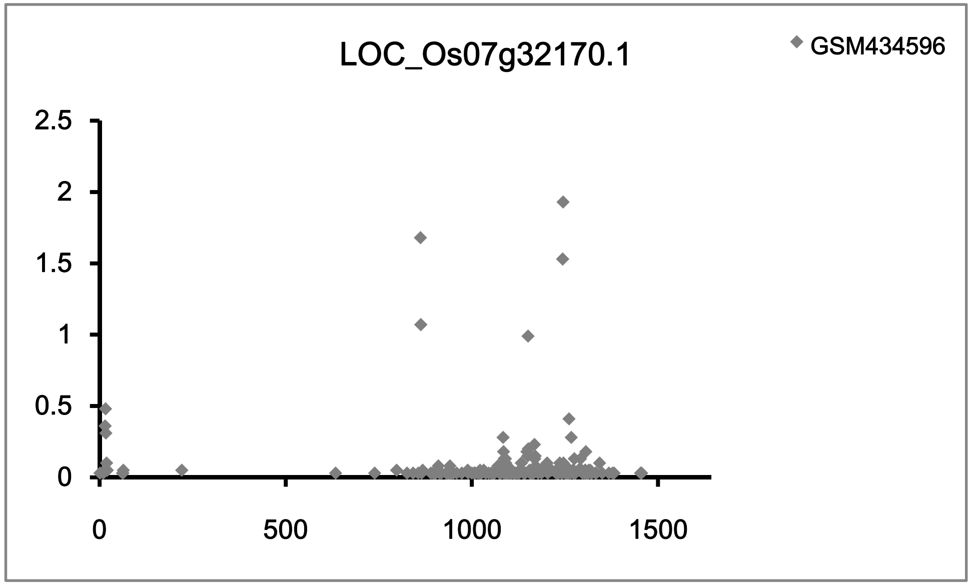

root-CK-high-4603
SRR1849903
9
7.2
5.4
3.6
1.8
0
1999
2009
2019
2029
2039
2049

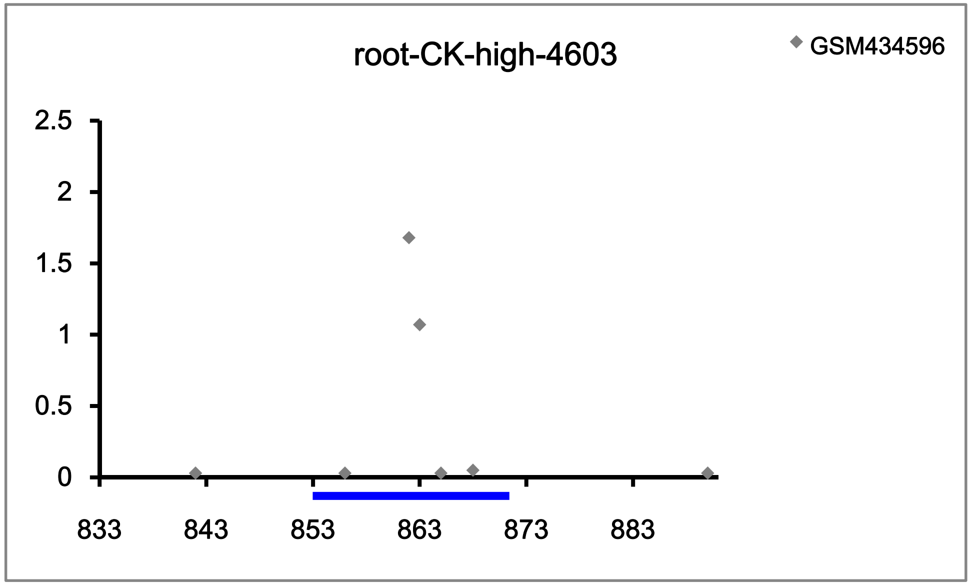

LOC_Os06g49010.6
SRR1849903
9
7.2
5.4
3.6
1.8
0
0
500
1000
1500
2000

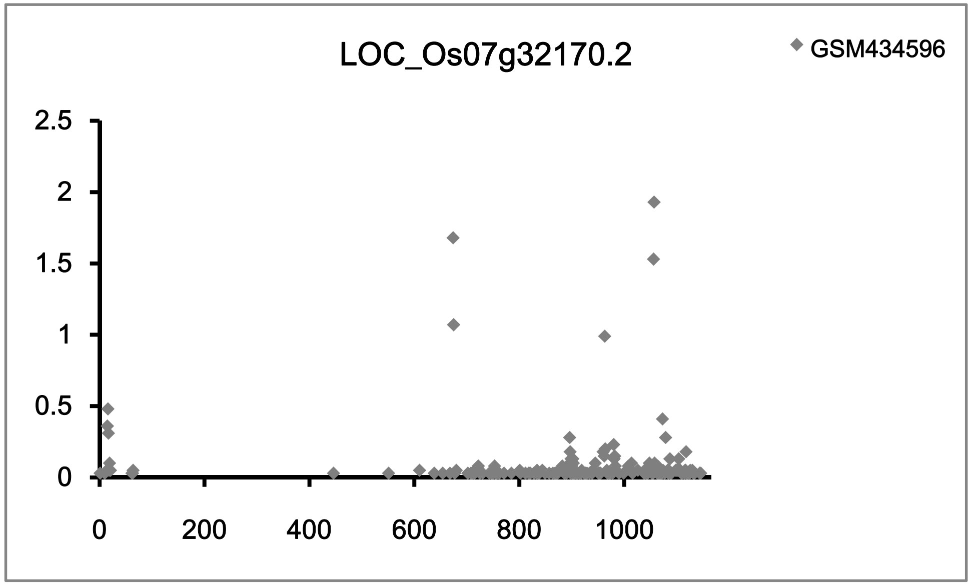

root-CK-high-4603
SRR1849903
9
7.2
5.4
3.6
1.8
0
1823
1833
1843
1853
1863
1873

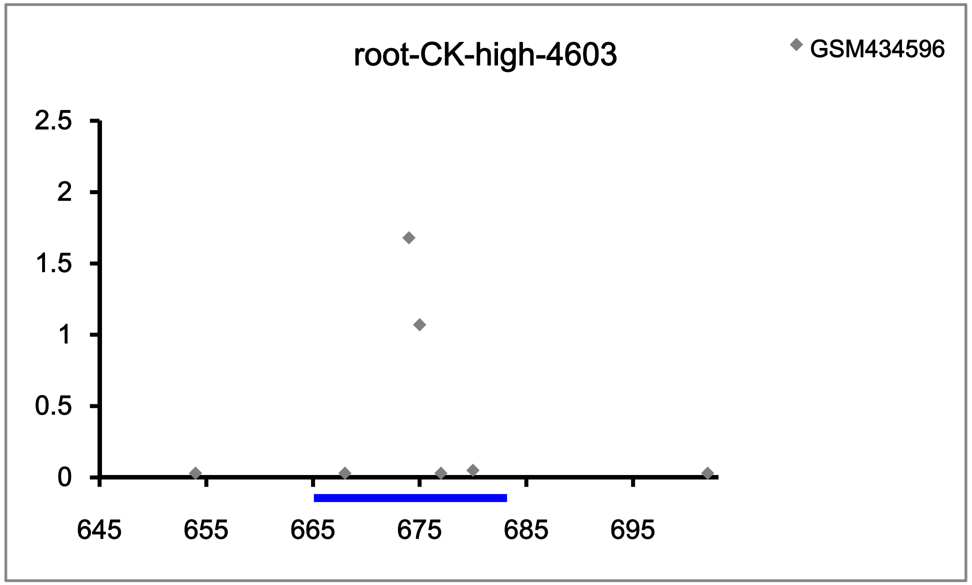

LOC_Os07g11790.1
GSM1040649
30
24
18
12
6
0
0
500
1000
1500
2000

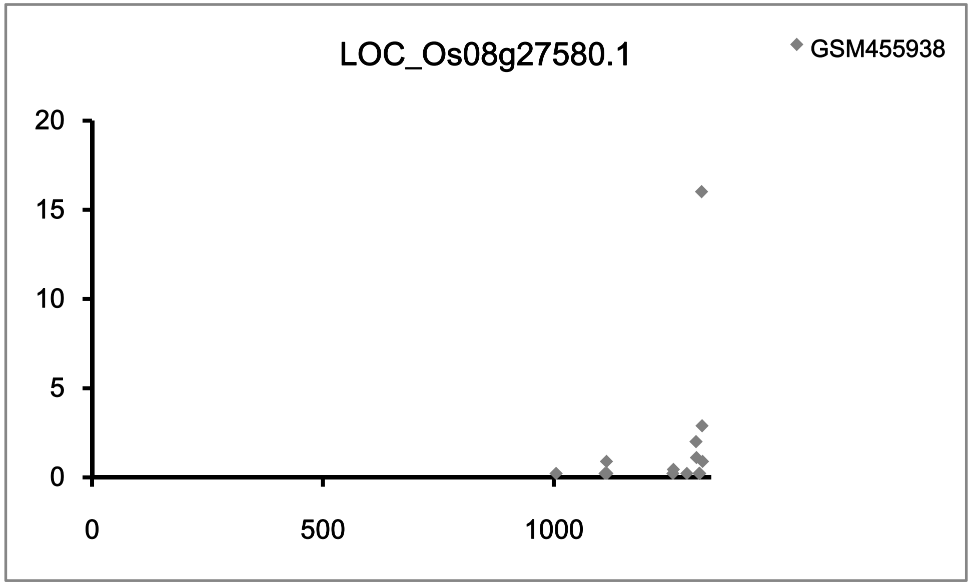

root-CK-high-2928
GSM1040649
30
24
18
12
6
0
1783
1793
1803
1813
1823
1833
1843

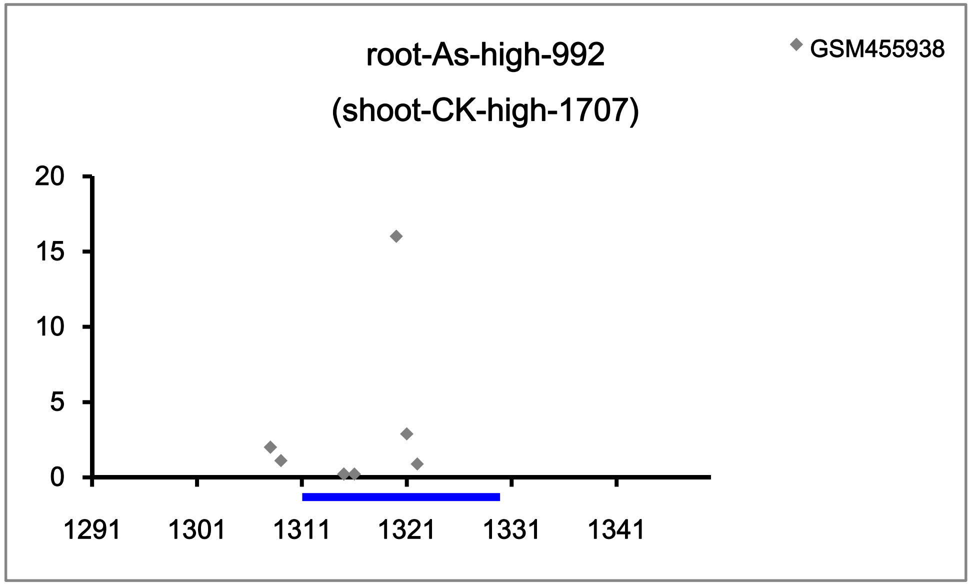

LOC_Os07g32170.1
GSM434596
2.5
2
1.5
1
0.5
0
0
500
1000
1500

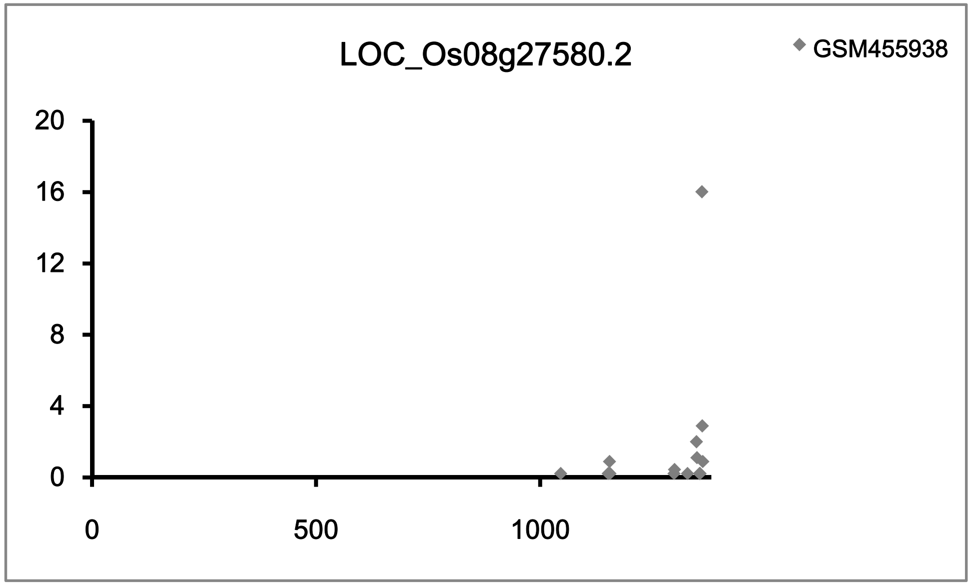

root-CK-high-4603
GSM434596
2.5
2
1.5
1
0.5
0
833
843
853
863
873
883

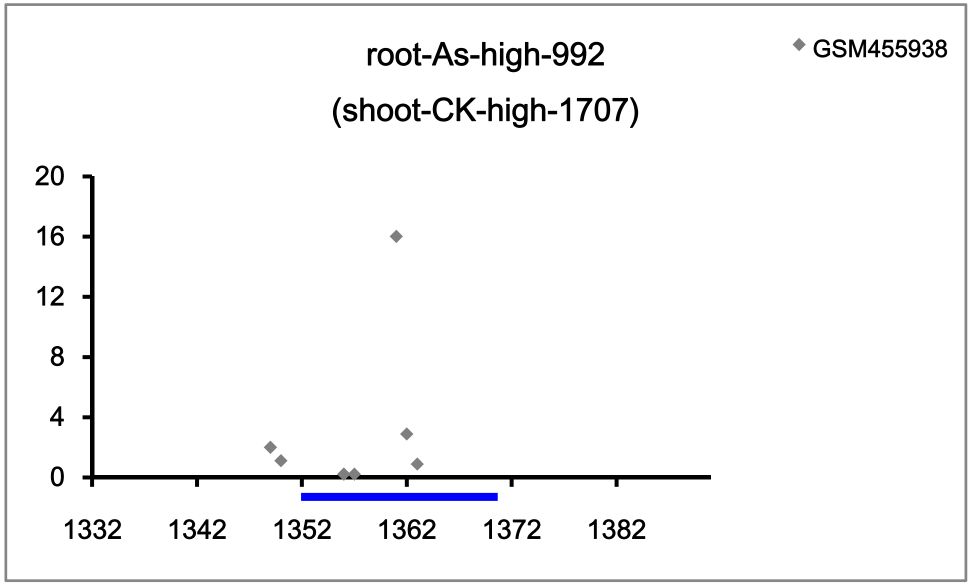

LOC_Os07g32170.2
GSM434596
2.5
2
1.5
1
0.5
0
0
200
400
600
800
1000

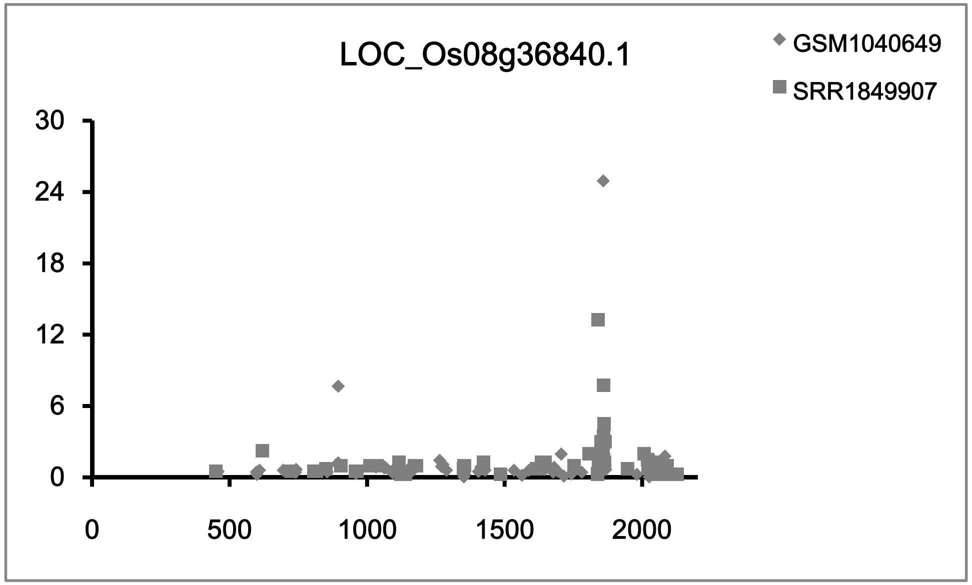

root-CK-high-4603
GSM434596
2.5
2
1.5
1
0.5
0
645
655
665
675
685
695

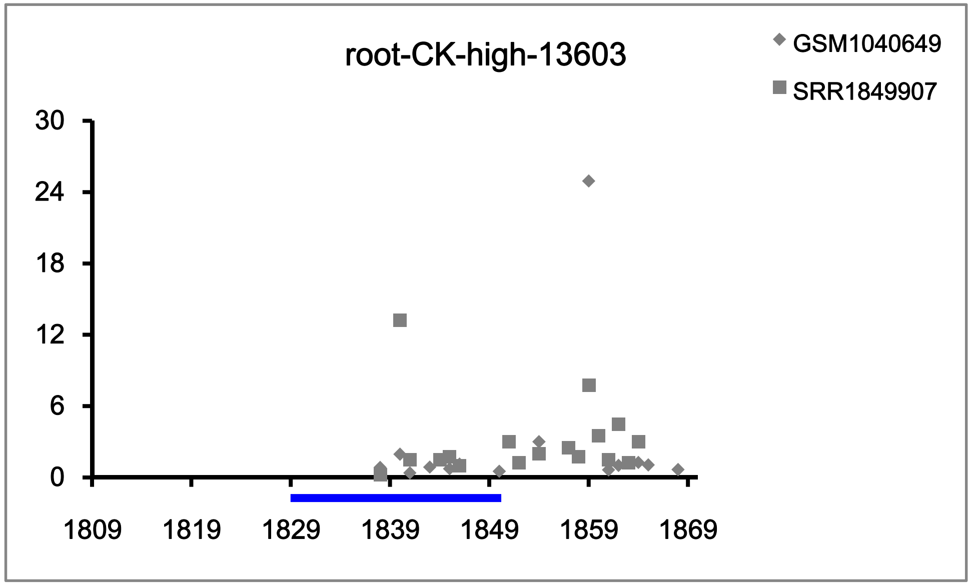

LOC_Os08g27580.1
◆ GSM455938
20
15
10
5
0
0
500
1000

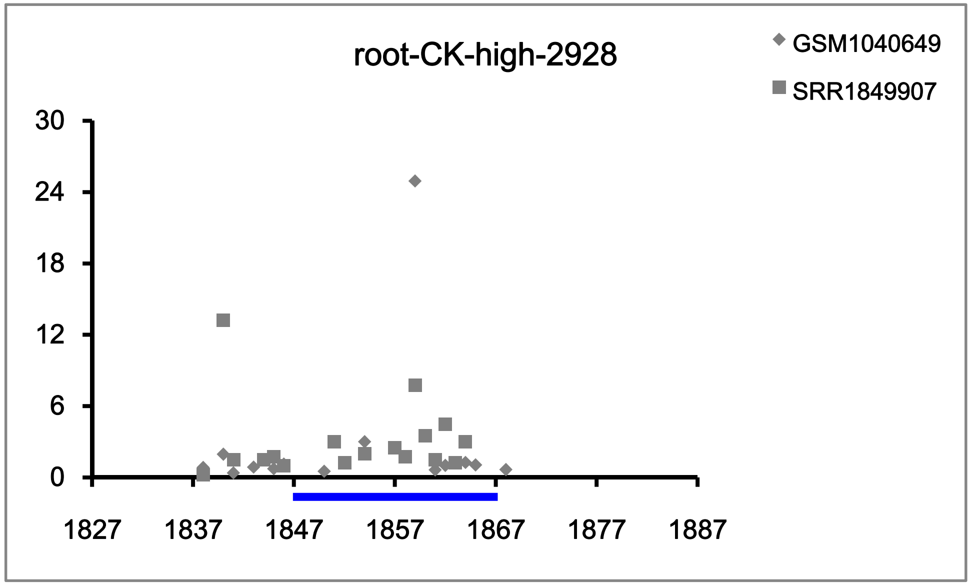

root-As-high-992
(shoot-CK-high-1707)
◆ GSM455938
20
15
10
5
0
1291
1301
1311
1321
1331
1341

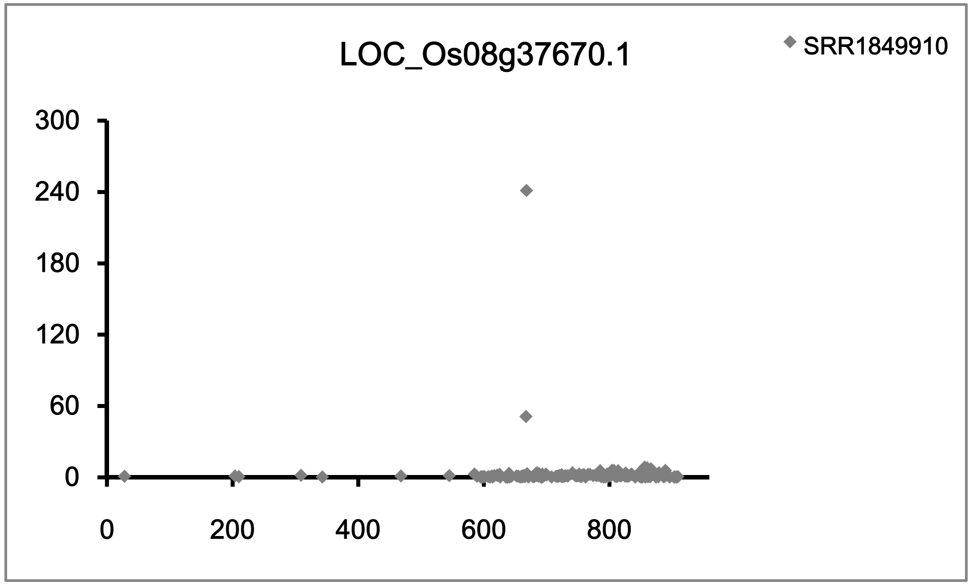

LOC_Os08g27580.2
◆ GSM455938
20
16
12
8
4
0
0
500
1000

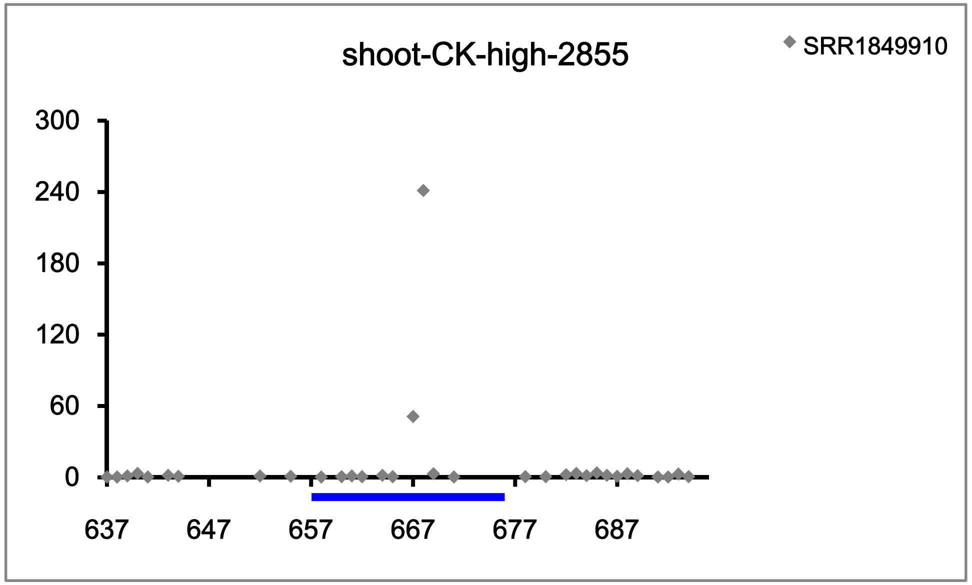

root-As-high-992
(shoot-CK-high-1707)
◆ GSM455938
20
16
12
8
4
0
1332
1342
1352
1362
1372
1382

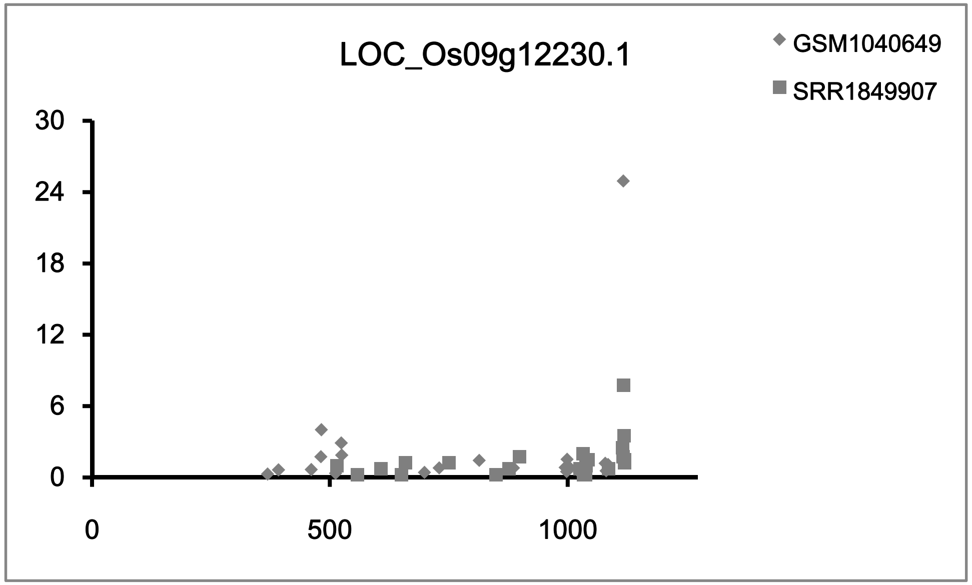

LOC_Os08g36840.1
GSM1040649
SRR1849907
30
24
18
12
6
0
0
500
1000
1500
2000

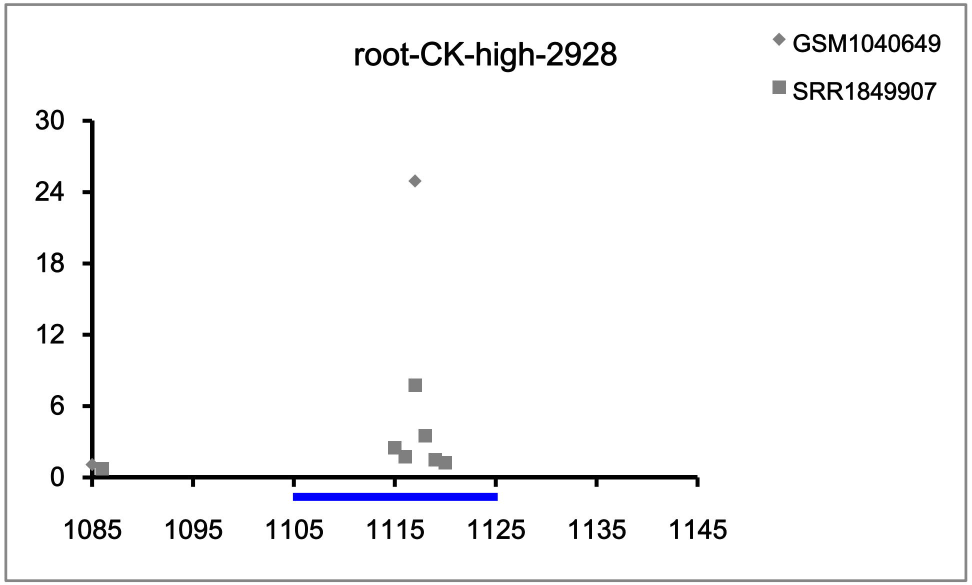

root-CK-high-13603
GSM1040649
SRR1849907
30
24
18
12
6
0
1809
1819
1829
1839
1849
1859
1869

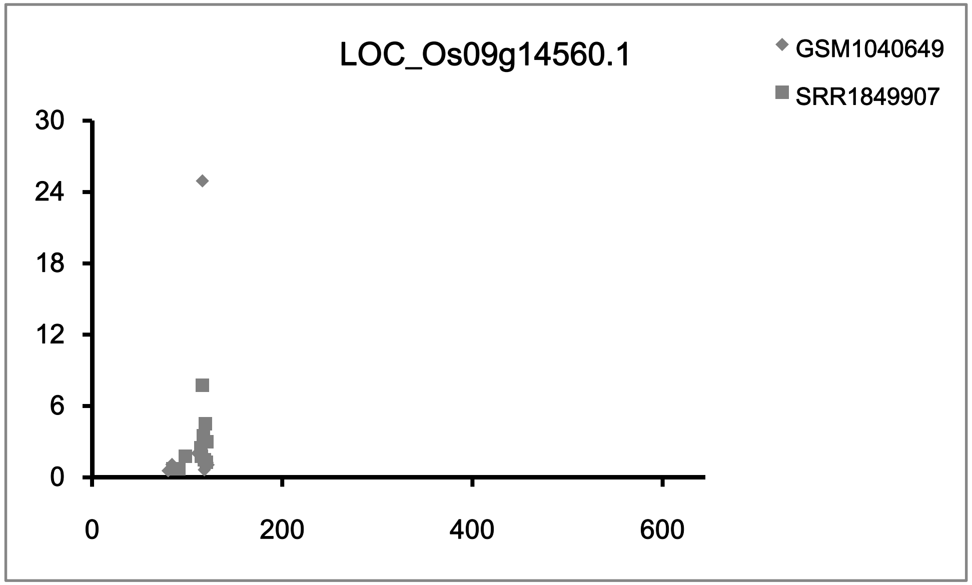

root-CK-high-2928
GSM1040649
SRR1849907
30
24
18
12
6
0
1827
1837
1847
1857
1867
1877
1887

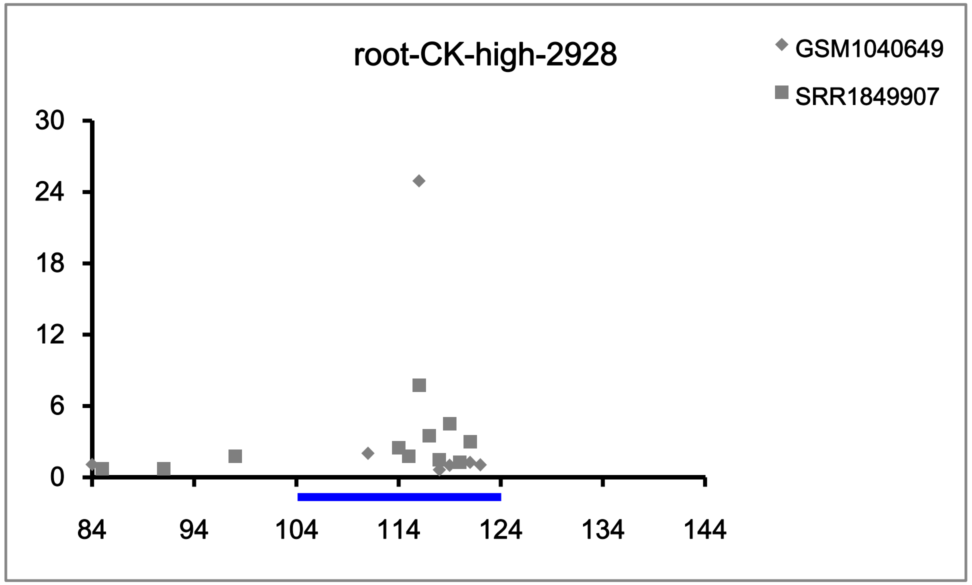

LOC_Os08g37670.1
◆ SRR1849910
300
240
180
120
60
0
0
200
400
600
800

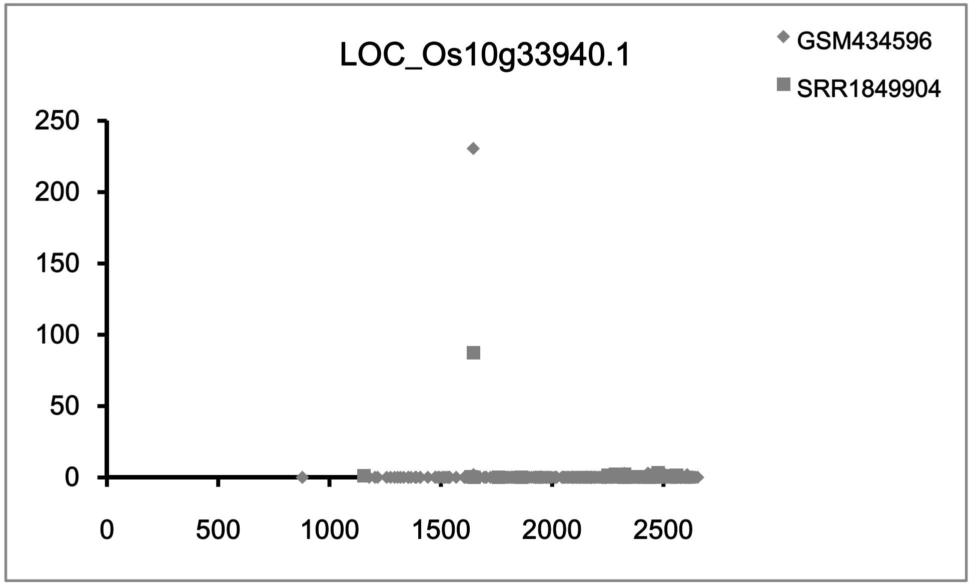

shoot-CK-high-2855
◆ SRR1849910
300
240
180
120
60
0
637
647
657
667
677
687

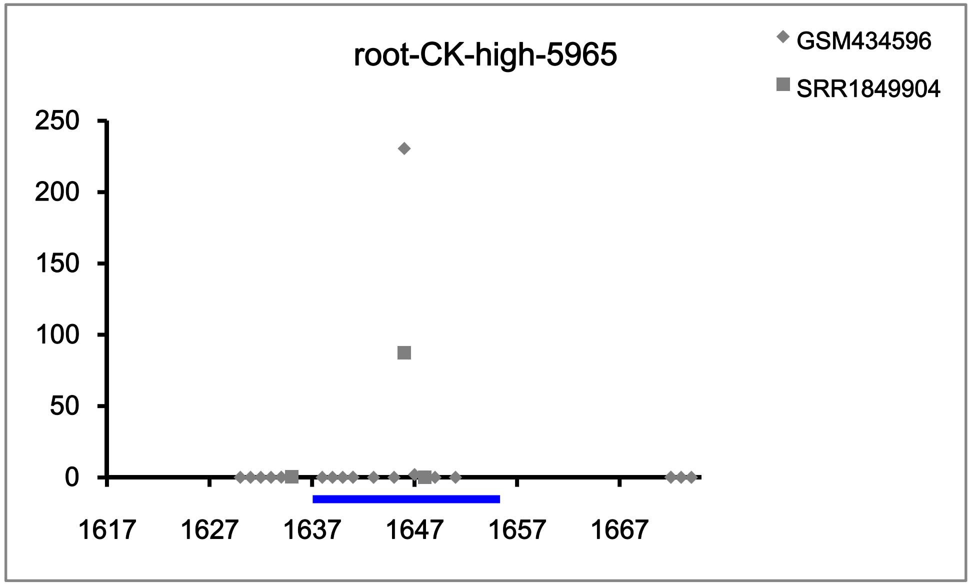

LOC_Os09g12230.1
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
0
500
1000

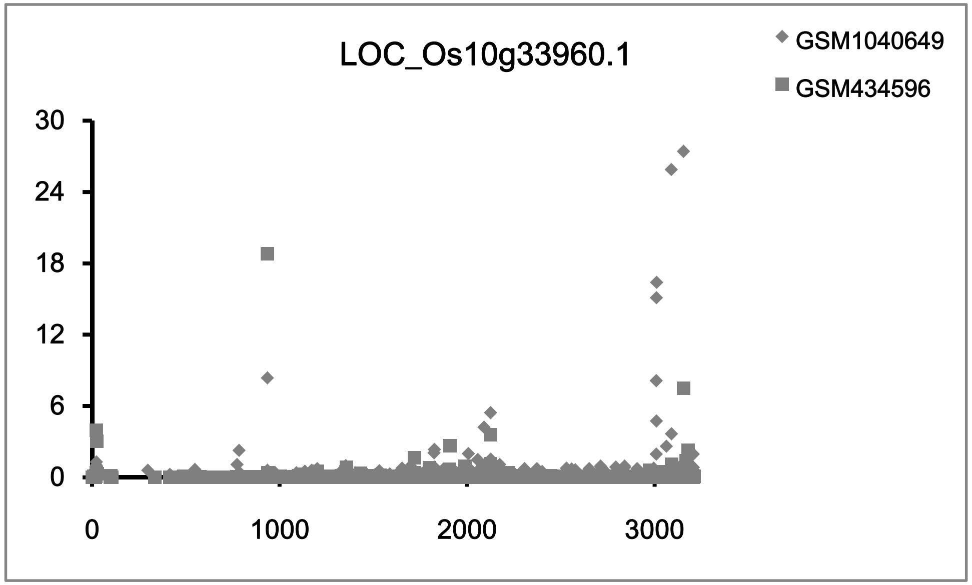

root-CK-high-2928
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
1085
1095
1105
1115
1125
1135
1145

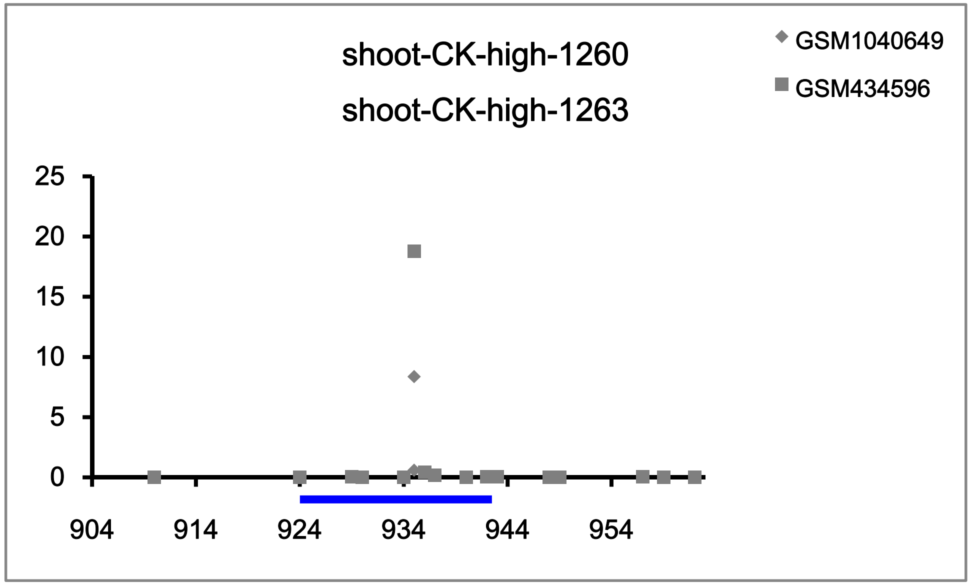

LOC_Os09g14560.1
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
0
200
400
600

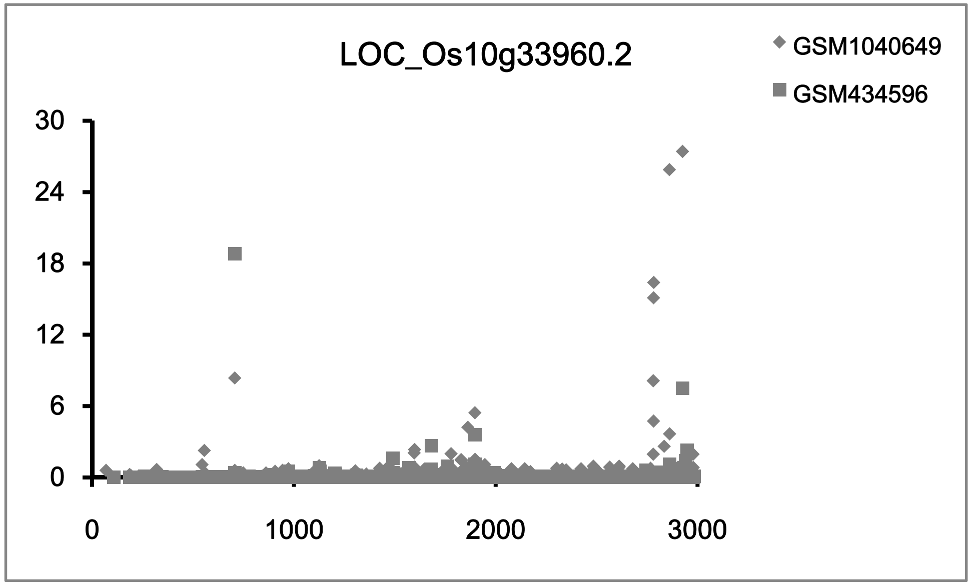

root-CK-high-2928
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
84
94
104
114
124
134
144

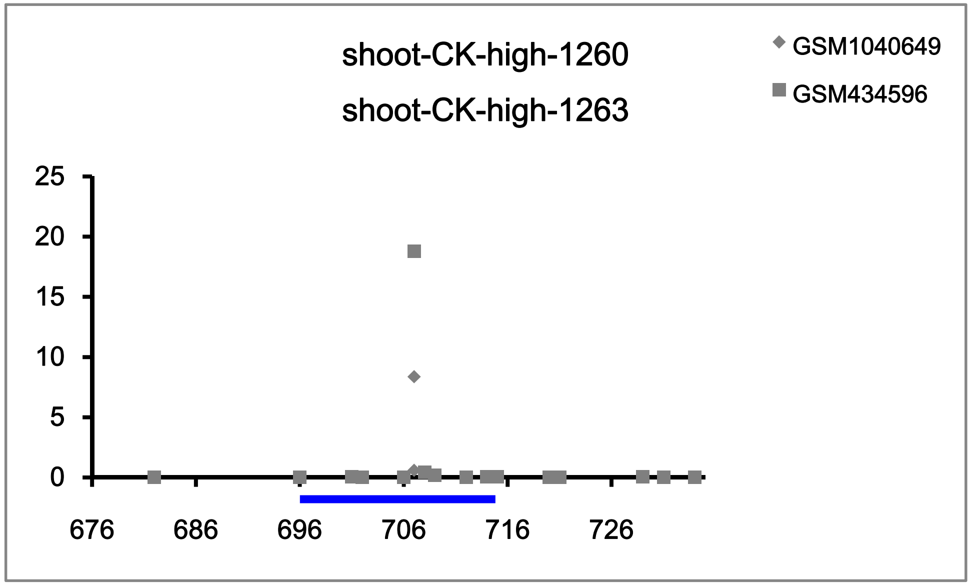

LOC_Os10g33940.1
◆ GSM434596
■ SRR1849904
250
200
150
100
50
0
0
500
1000
1500
2000
2500

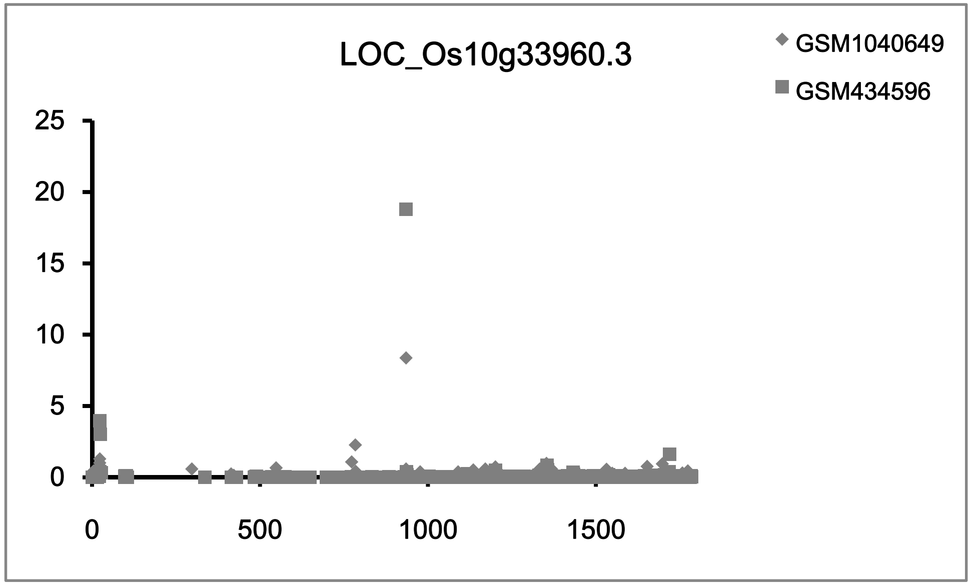

root-CK-high-5965
◆ GSM434596
■ SRR1849904
250
200
150
100
50
0
1617
1627
1637
1647
1657
1667

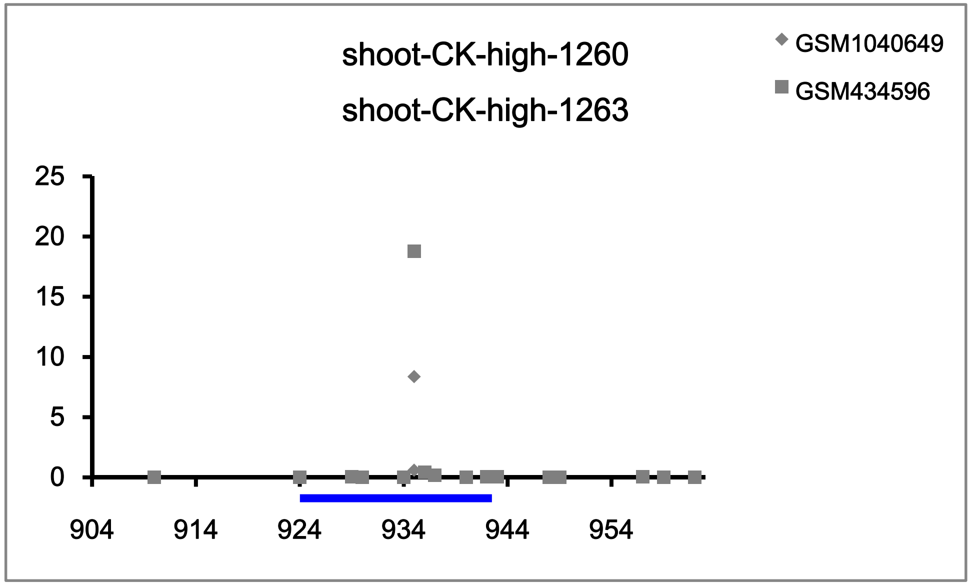

LOC_Os10g33960.1
◆ GSM1040649
■ GSM434596
30
24
18
12
6
0
0
1000
2000
3000

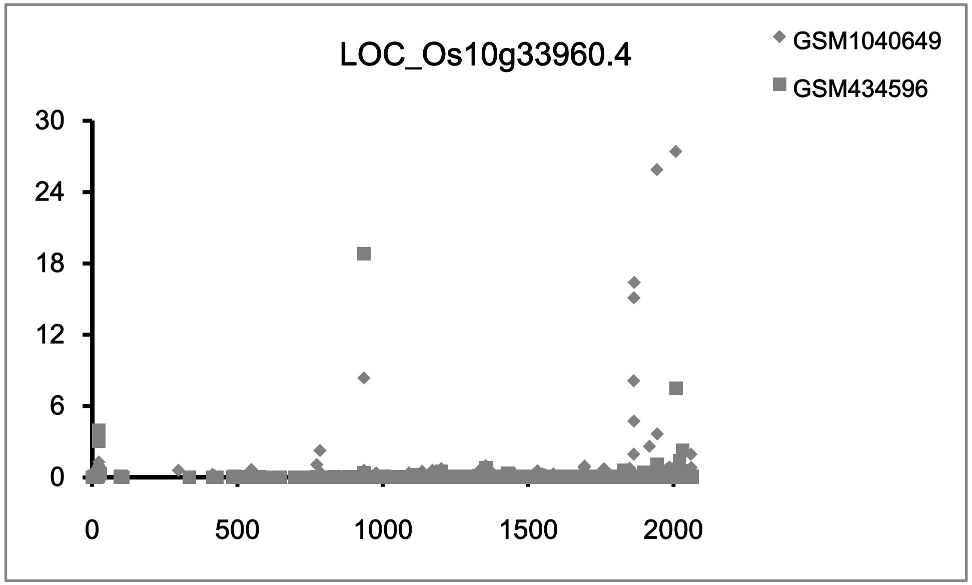

shoot-CK-high-1260
shoot-CK-high-1263
◆ GSM1040649
■ GSM434596
25
20
15
10
5
0
904
914
924
934
944
954

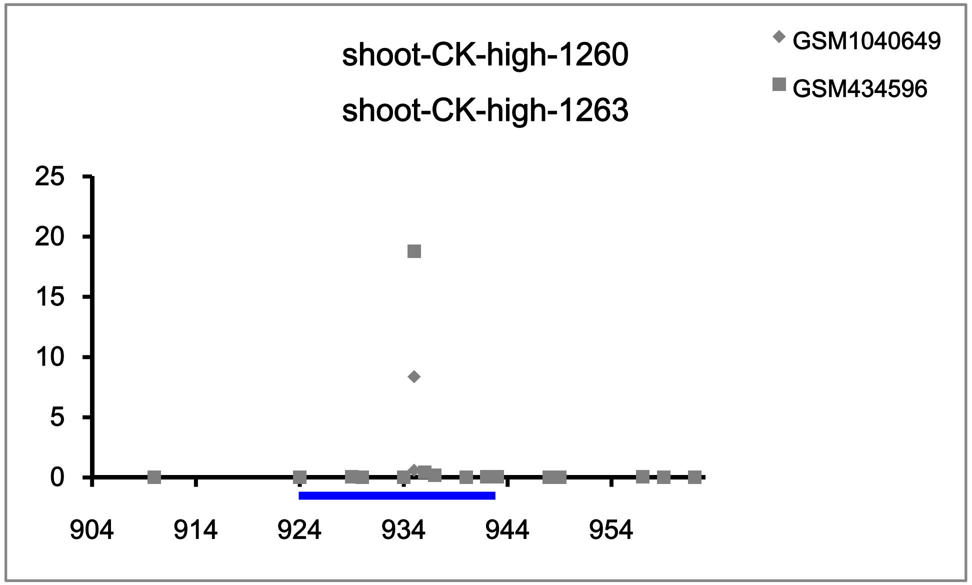

LOC_Os10g33960.2
◆ GSM1040649
■ GSM434596
30
24
18
12
6
0
0
1000
2000
3000

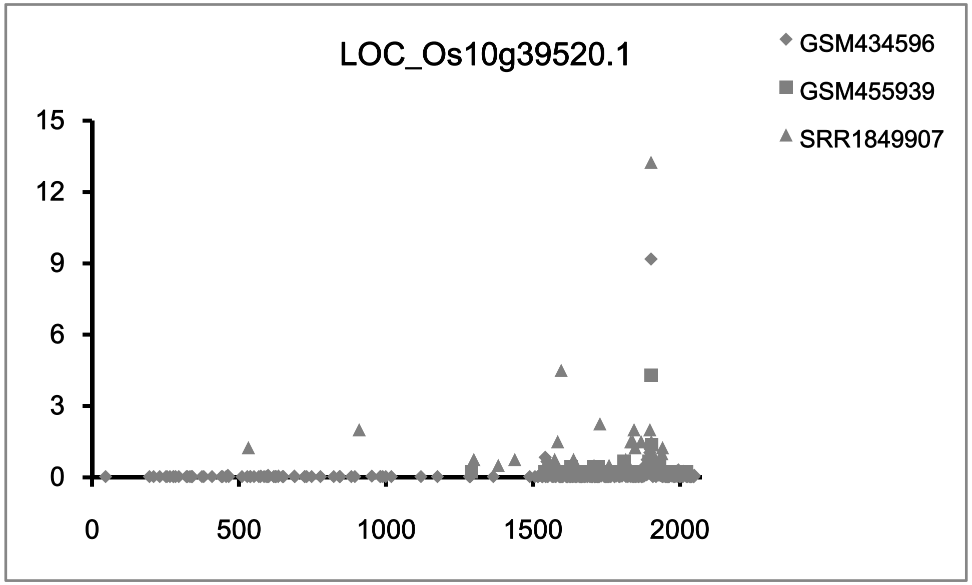

shoot-CK-high-1260
shoot-CK-high-1263
◆ GSM1040649
■ GSM434596
25
20
15
10
5
0
676
686
696
706
716
726

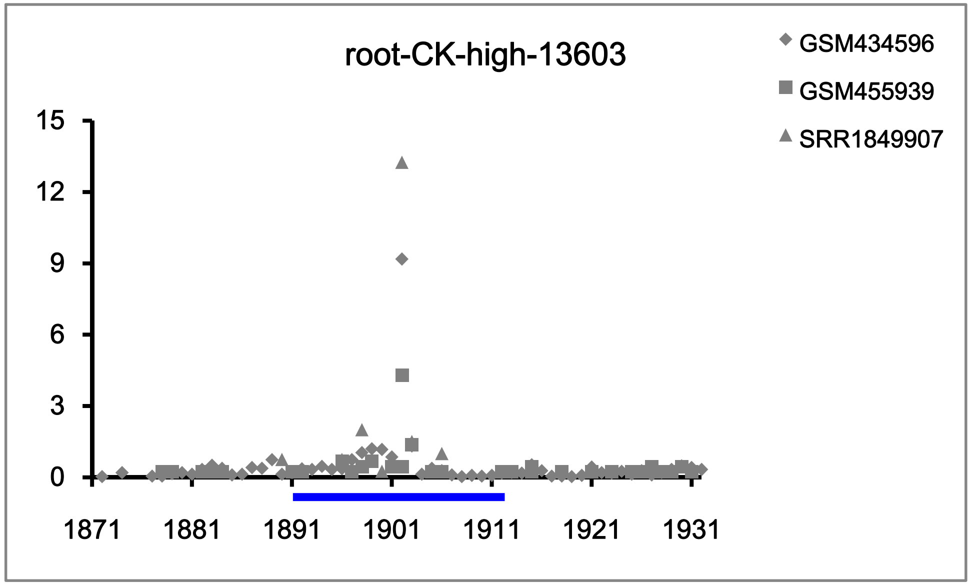

LOC_Os10g33960.3
GSM1040649
GSM434596
25
20
15
10
5
0
0
500
1000
1500

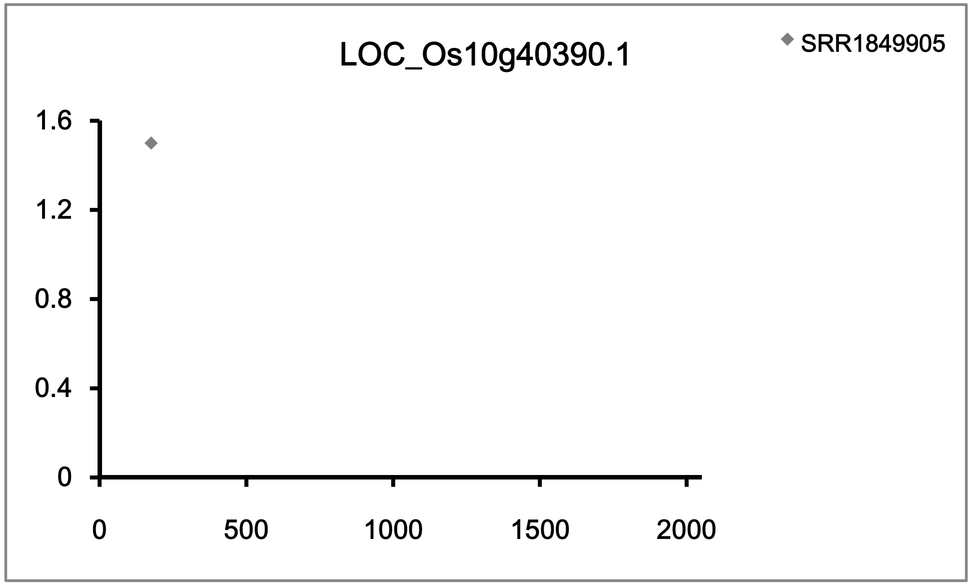

shoot-CK-high-1260
shoot-CK-high-1263
GSM1040649
GSM434596
25
20
15
10
5
0
904
914
924
934
944
954

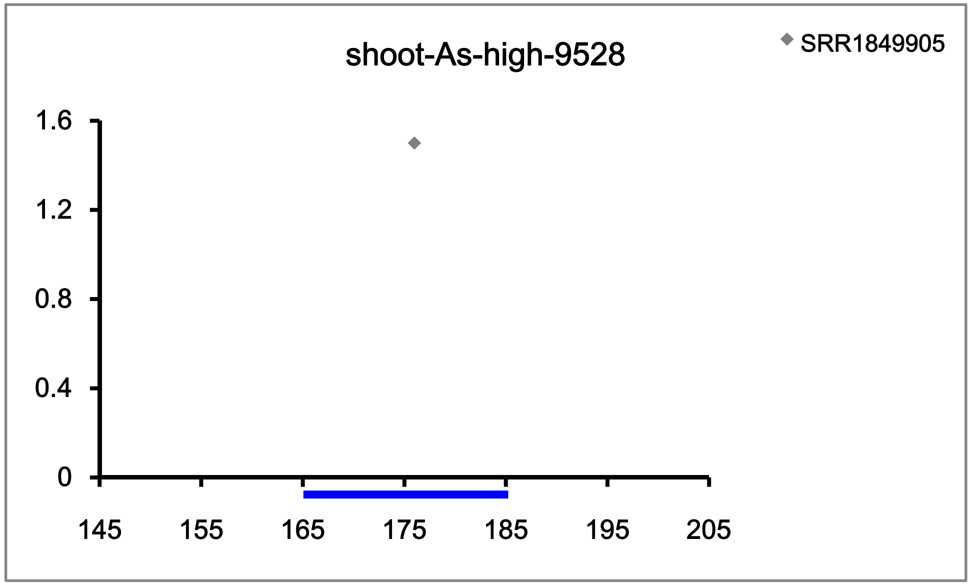

LOC_Os10g33960.4
GSM1040649
GSM434596
30
24
18
12
6
0
0
500
1000
1500
2000

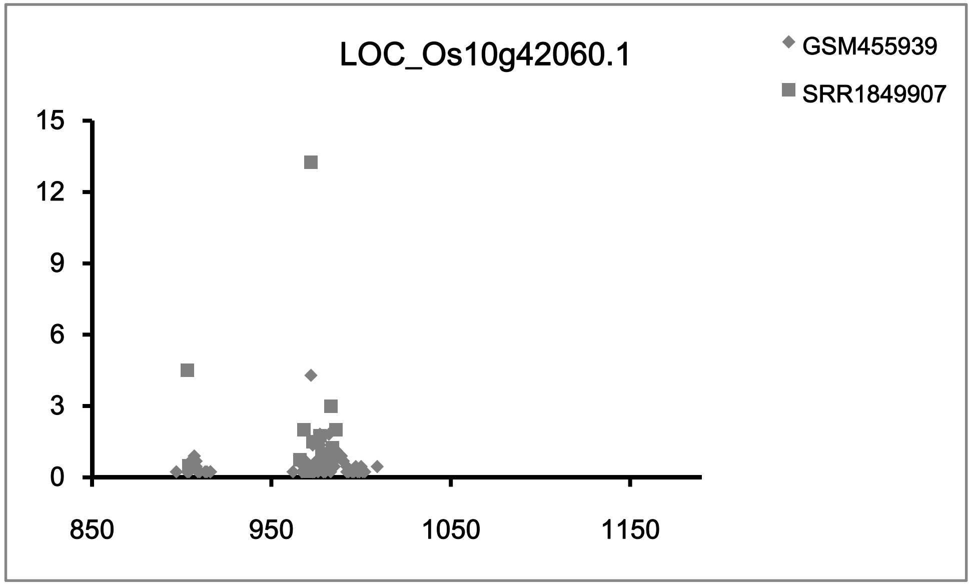

shoot-CK-high-1260
shoot-CK-high-1263
GSM1040649
GSM434596
25
20
15
10
5
0
904
914
924
934
944
954

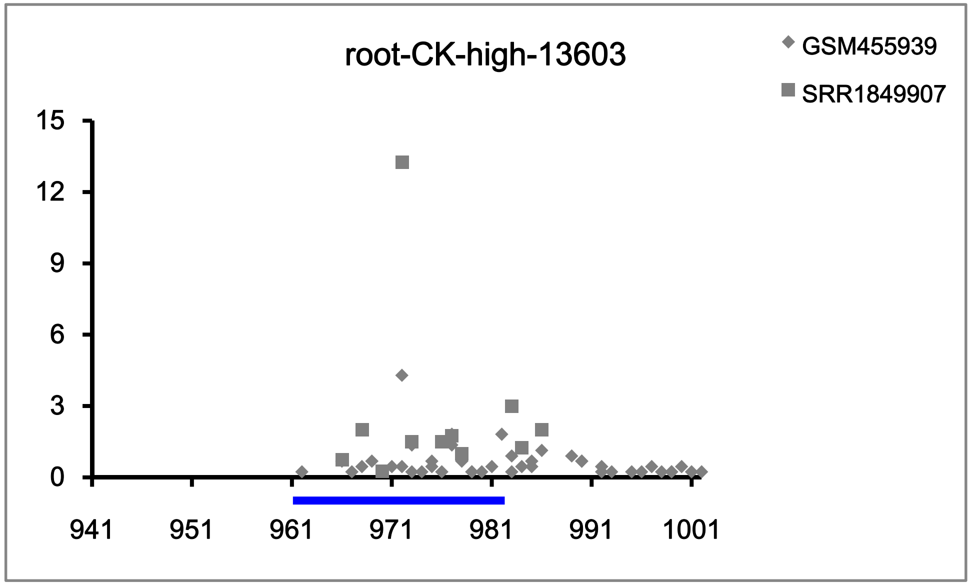

LOC_Os10g39520.1
GSM434596
GSM455939
SRR1849907
15
12
9
6
3
0
0
500
1000
1500
2000

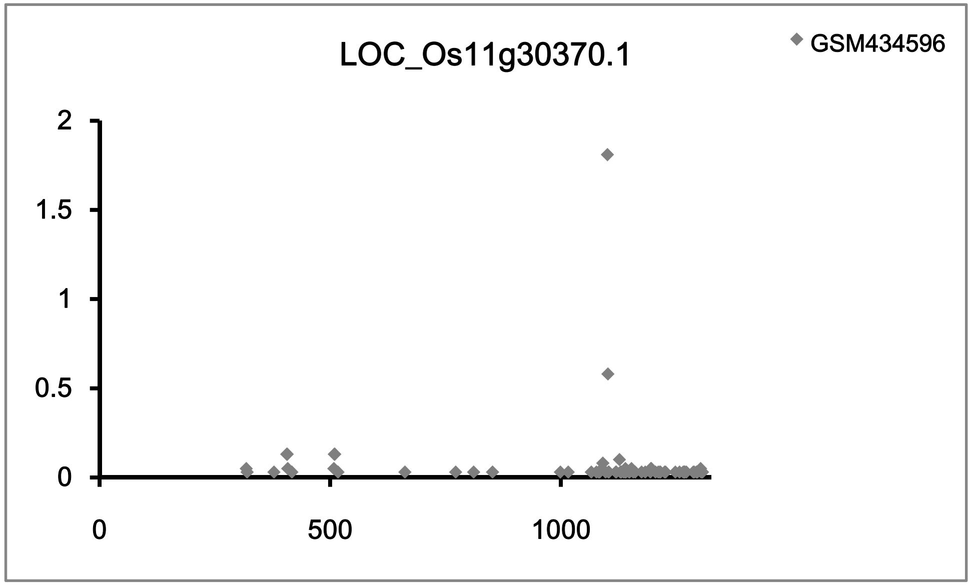

root-CK-high-13603
GSM434596
GSM455939
SRR1849907
15
12
9
6
3
0
1871
1881
1891
1901
1911
1921
1931

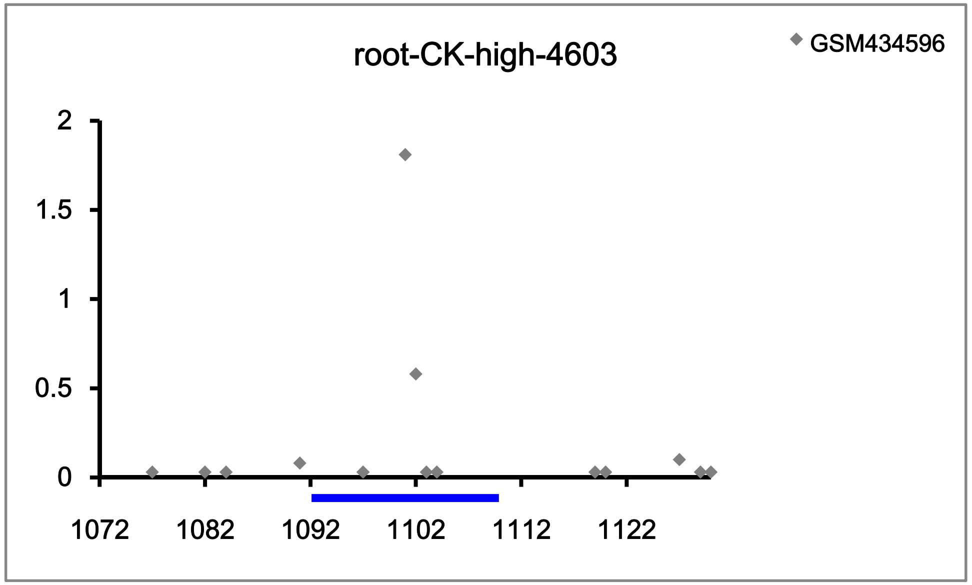

LOC_Os10g40390.1
SRR1849905
1.6
1.2
0.8
0.4
0
0
500
1000
1500
2000

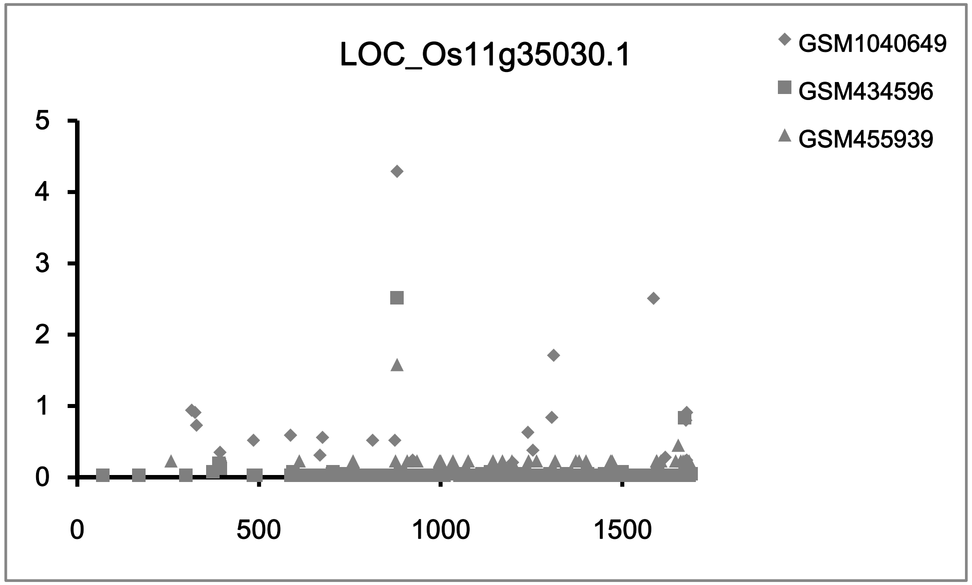

shoot-As-high-9528
SRR1849905
1.6
1.2
0.8
0.4
0
145
155
165
175
185
195
205

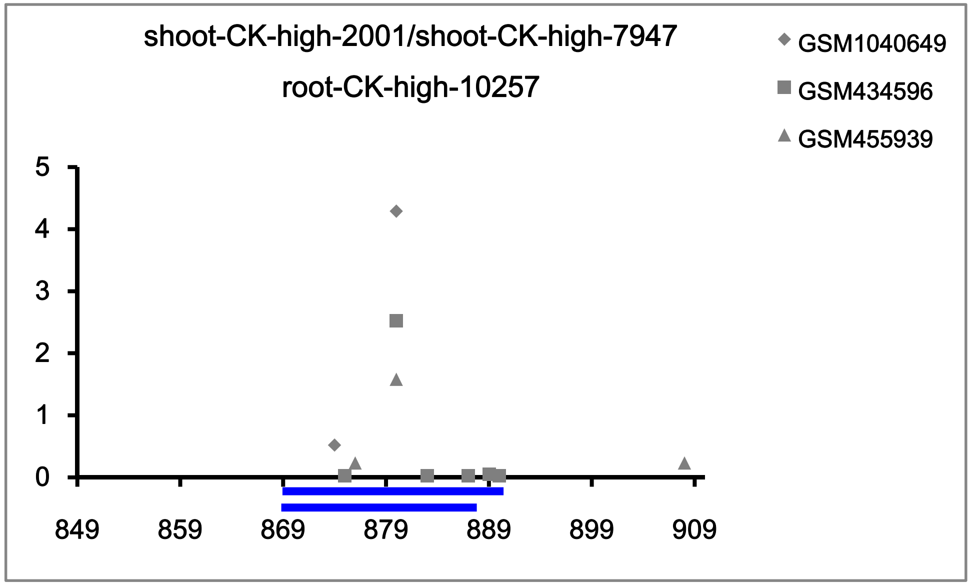

LOC_Os10g42060.1
GSM455939
SRR1849907
15
12
9
6
3
0
850
950
1050
1150

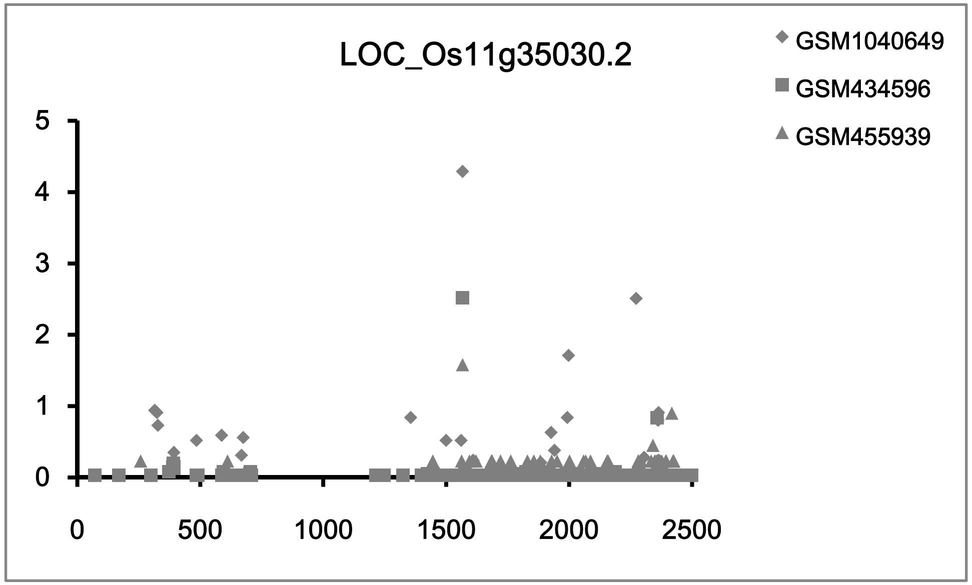

root-CK-high-13603
GSM455939
SRR1849907
15
12
9
6
3
0
941
951
961
971
981
991
1001

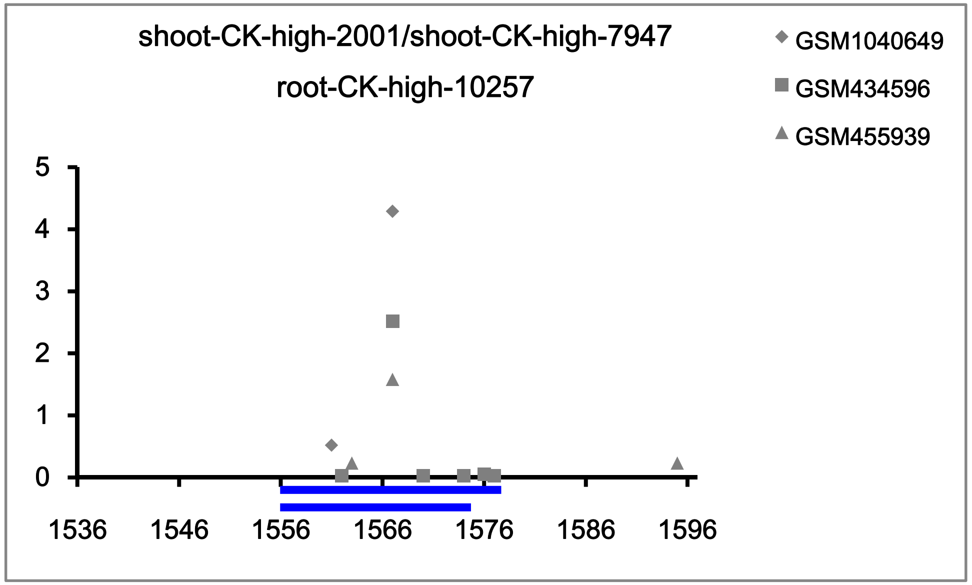

LOC_Os11g30370.1
GSM434596
2
1.5
1
0.5
0
0
500
1000

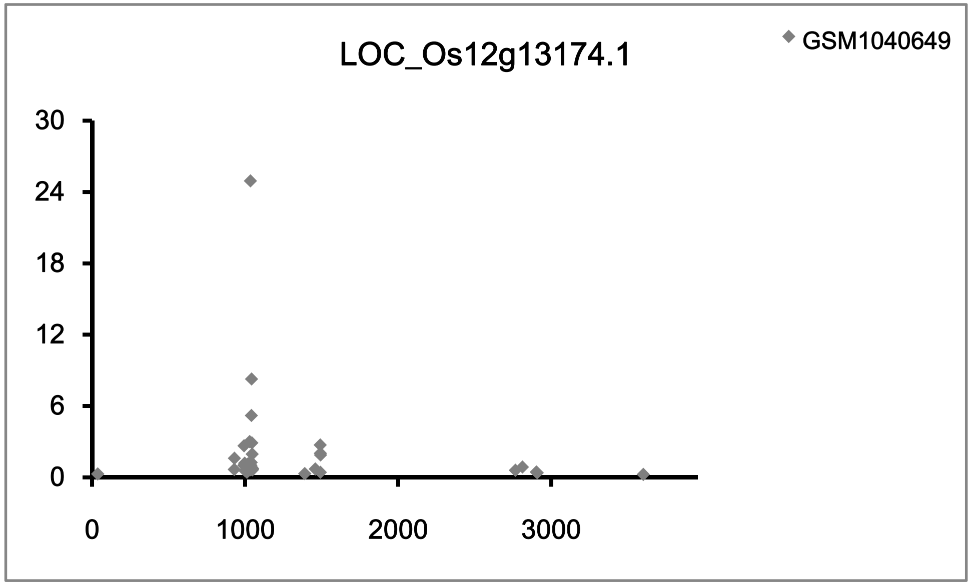

root-CK-high-4603
GSM434596
2
1.5
1
0.5
0
1072
1082
1092
1102
1112
1122

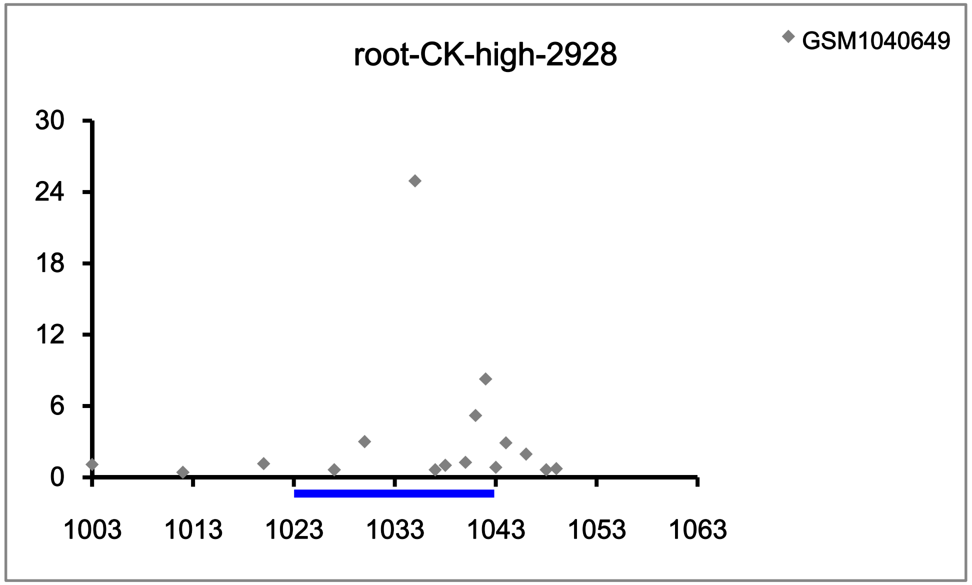

LOC_Os11g35030.1
GSM1040649
GSM434596
GSM455939
5
4
3
2
1
0
0
500
1000
1500

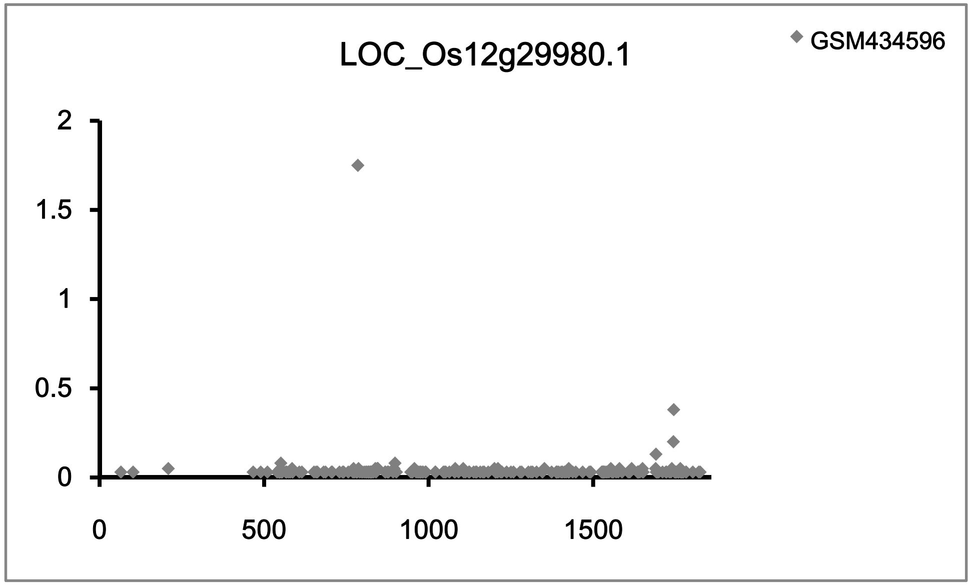

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
GSM1040649
GSM434596
GSM455939
5
4
3
2
1
0
849
859
869
879
889
899
909

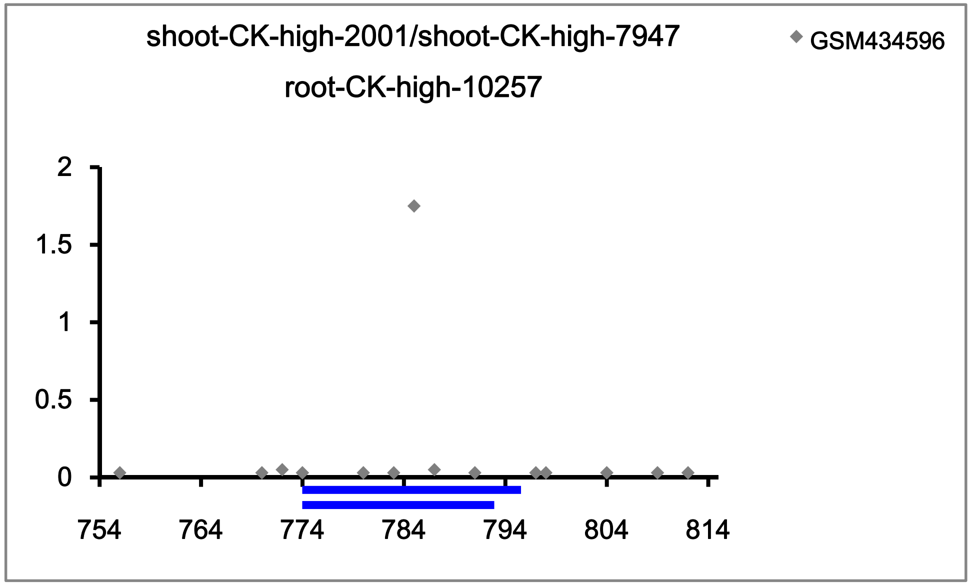

LOC_Os11g35030.2
GSM1040649
GSM434596
GSM455939
5
4
3
2
1
0
0
500
1000
1500
2000
2500

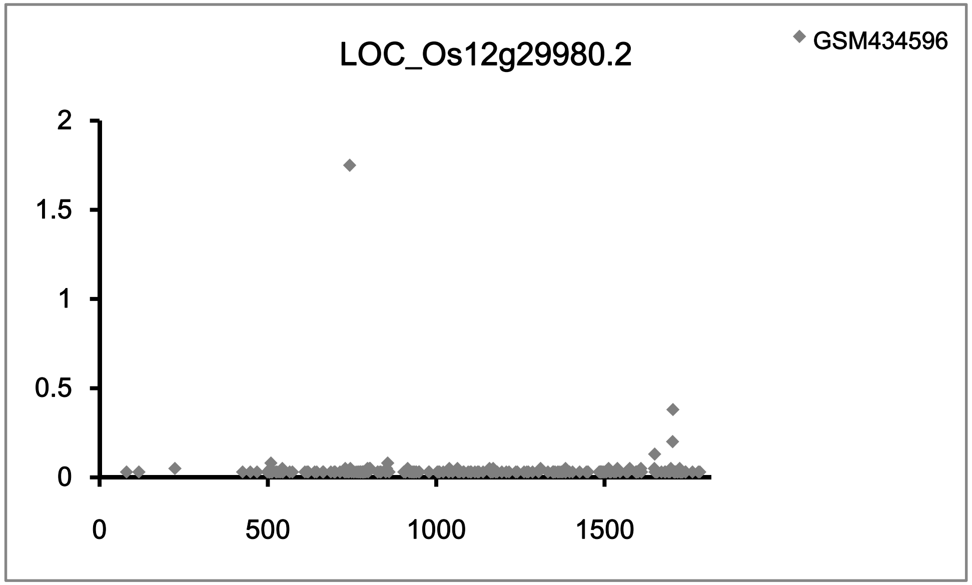

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
GSM1040649
GSM434596
GSM455939
5
4
3
2
1
0
1536
1546
1556
1566
1576
1586
1596

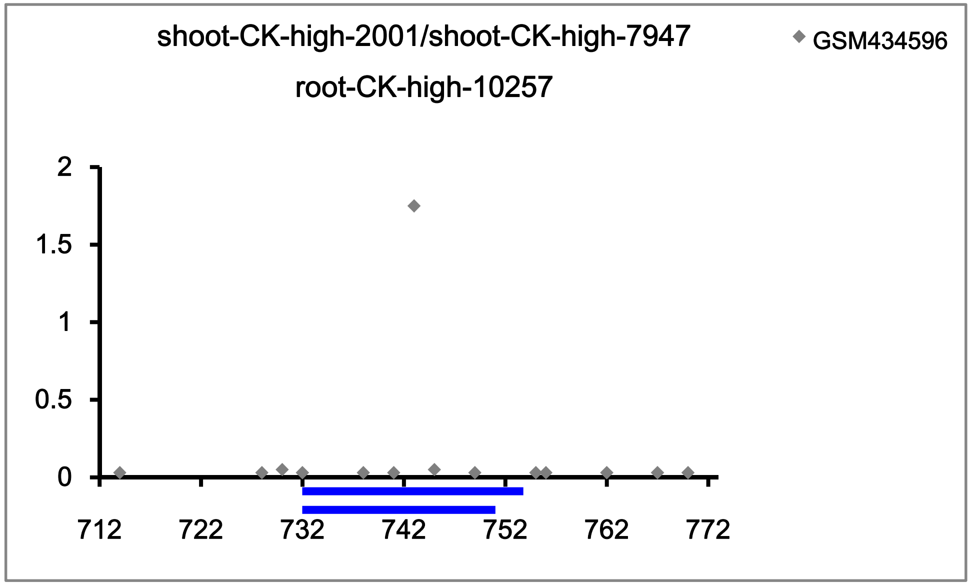

LOC_Os12g13174.1
GSM1040649
30
24
18
12
6
0
0
1000
2000
3000

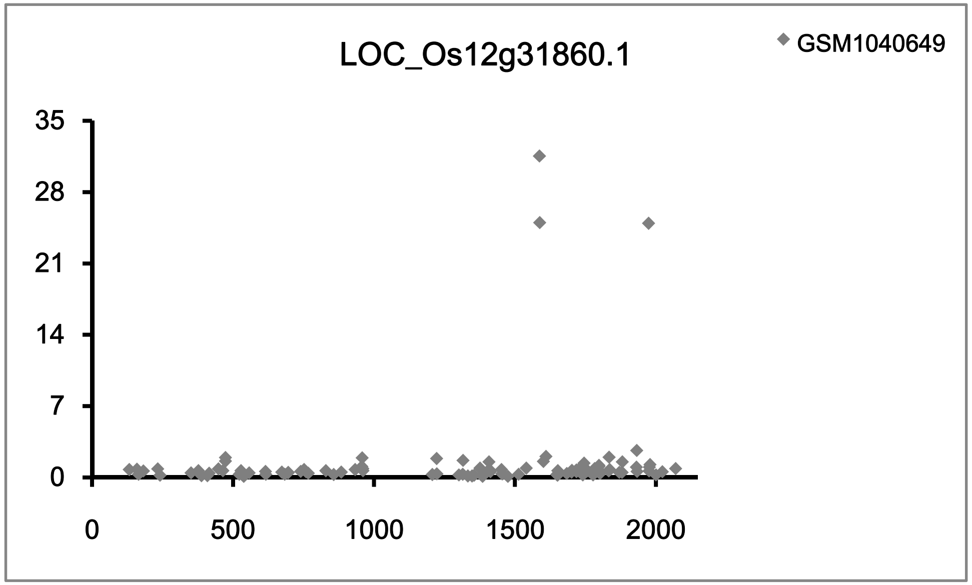

root-CK-high-2928
GSM1040649
30
24
18
12
6
0
1003
1013
1023
1033
1043
1053
1063

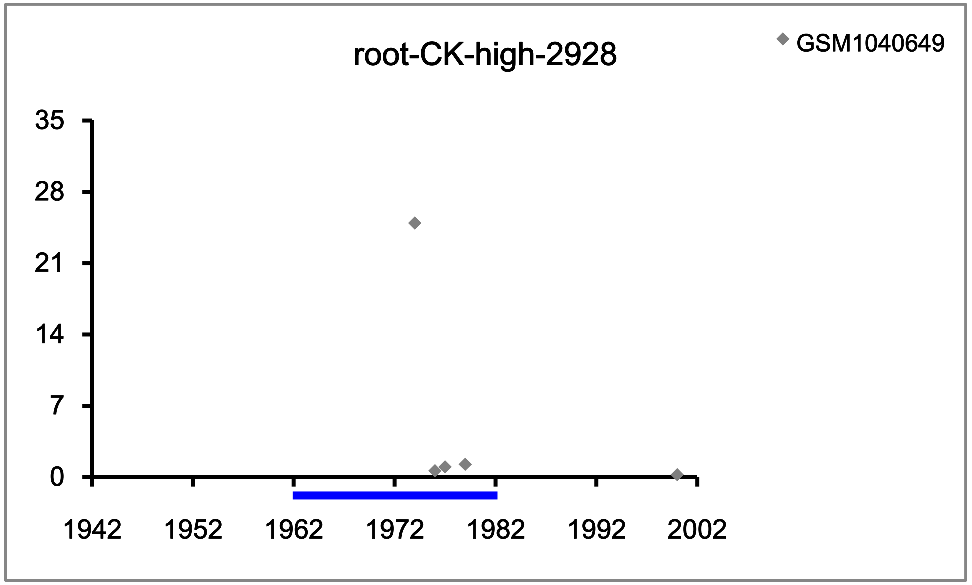

LOC_Os12g29980.1
GSM434596
2
1.5
1
0.5
0
0
500
1000
1500

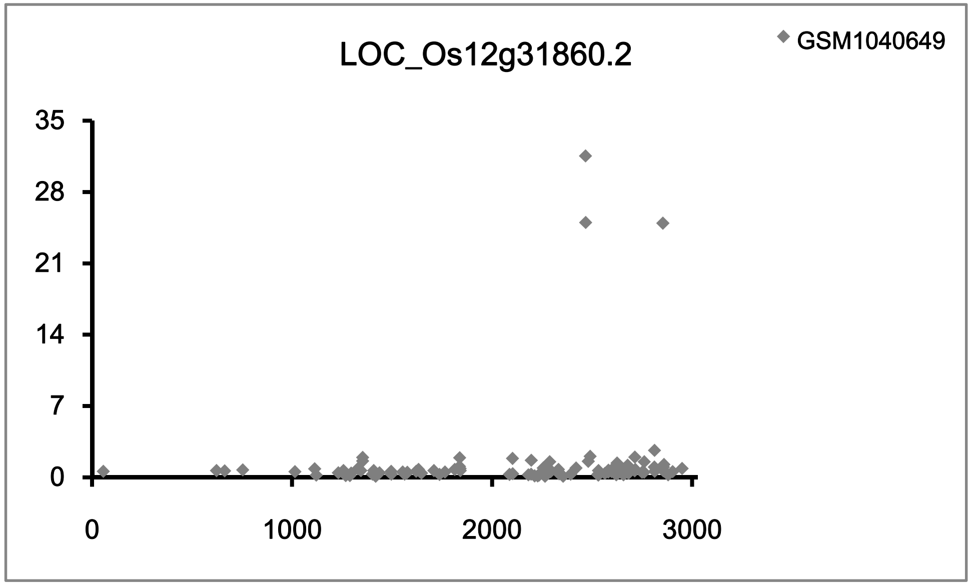

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
GSM434596
2
1.5
1
0.5
0
754
764
774
784
794
804
814

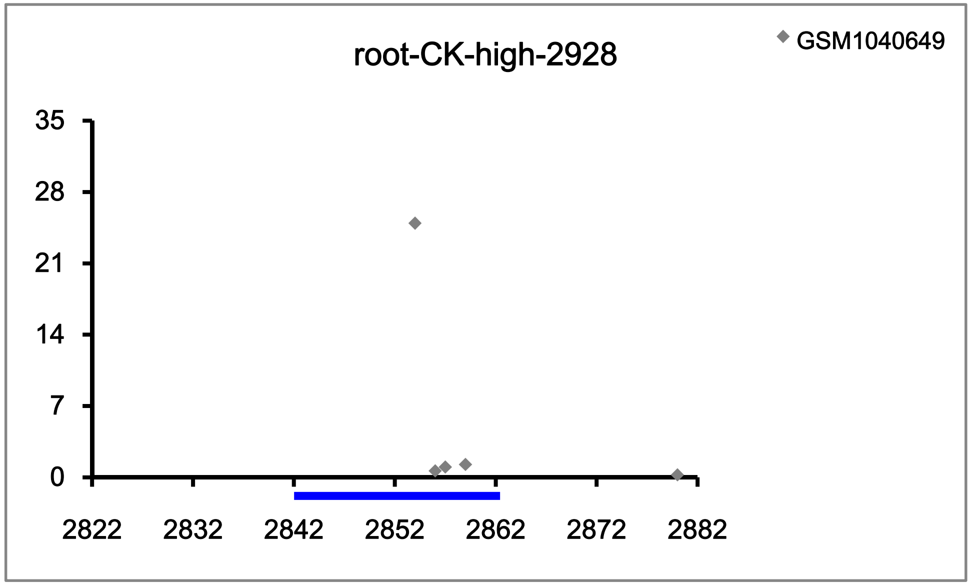

LOC_Os12g29980.2
GSM434596
2
1.5
1
0.5
0
0
500
1000
1500

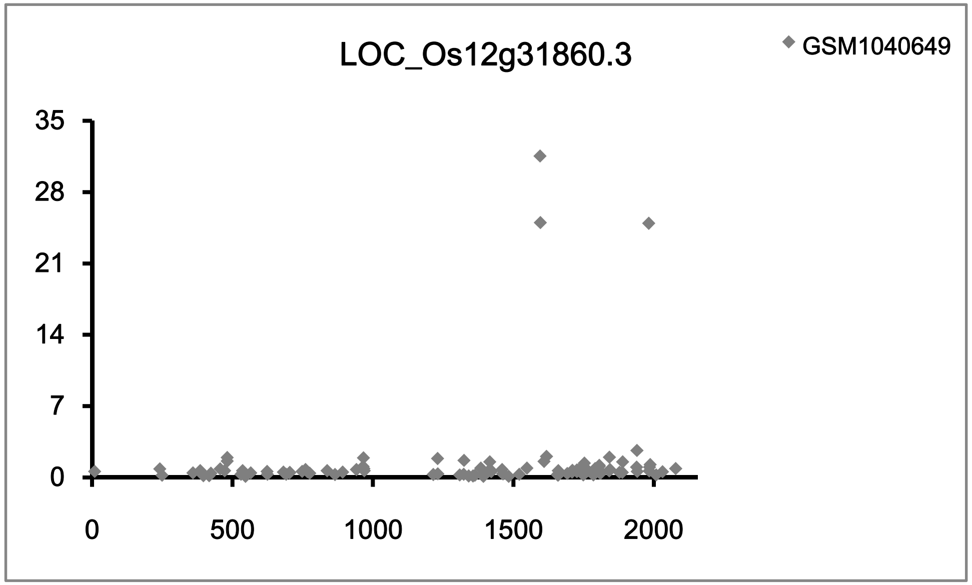

shoot-CK-high-2001/shoot-CK-high-7947
root-CK-high-10257
GSM434596
2
1.5
1
0.5
0
712
722
732
742
752
762
772

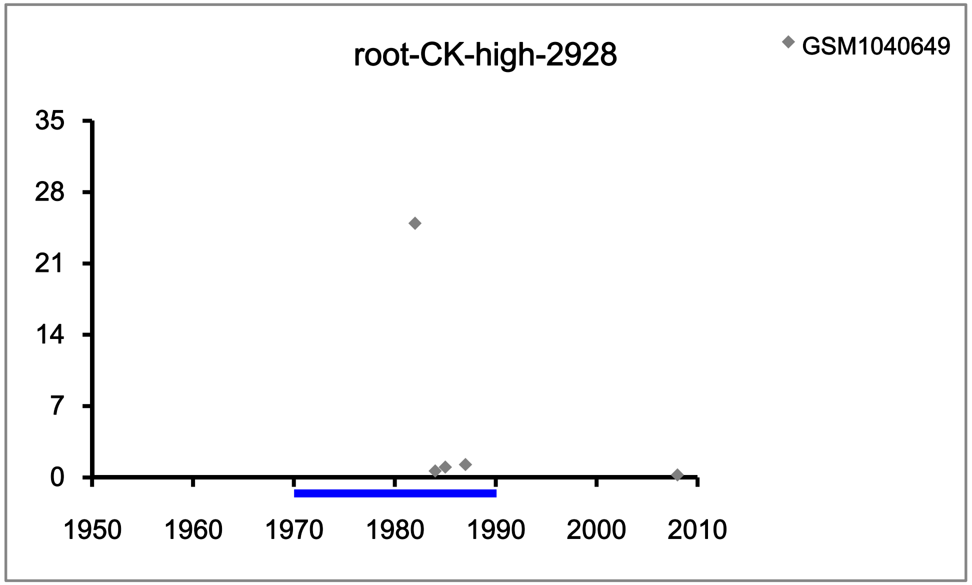

LOC_Os12g31860.1
GSM1040649
35
28
21
14
7
0
0
500
1000
1500
2000

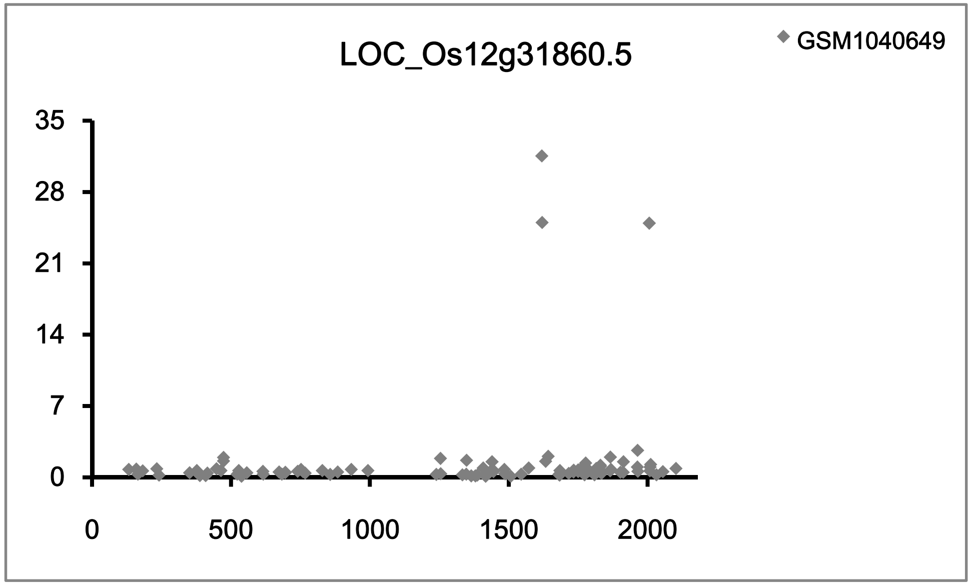

root-CK-high-2928
GSM1040649
35
28
21
14
7
0
1942
1952
1962
1972
1982
1992
2002

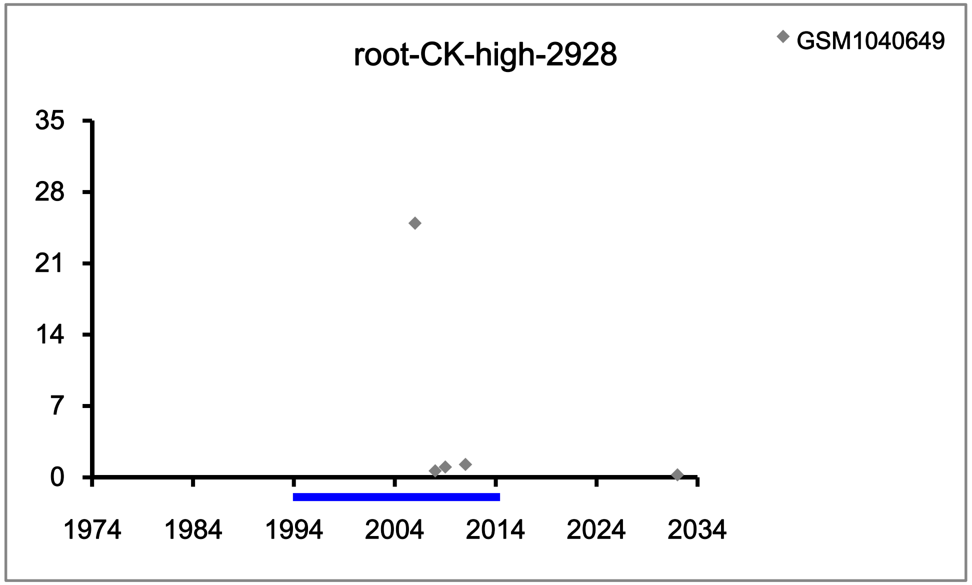

LOC_Os12g31860.2
GSM1040649
35
28
21
14
7
0
0
1000
2000
3000

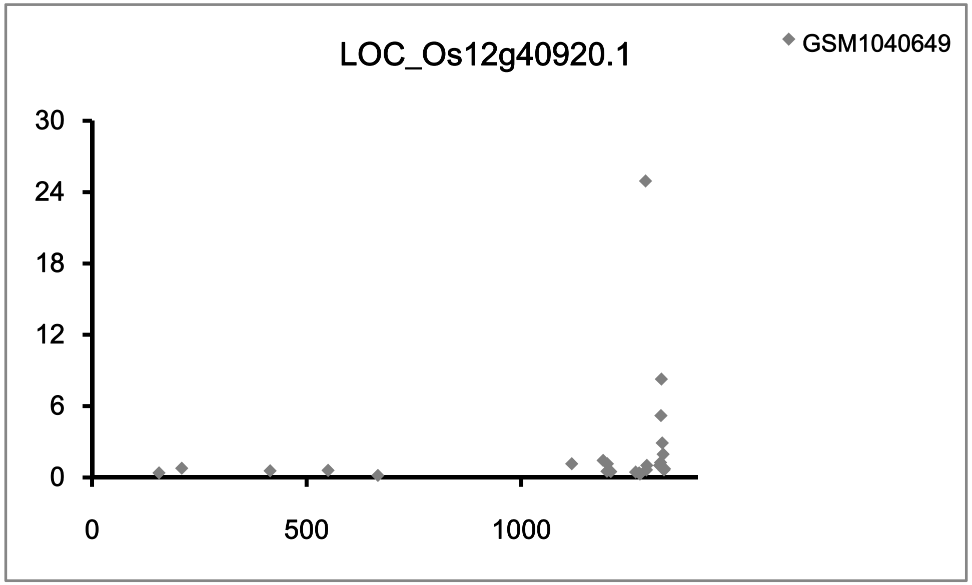

root-CK-high-2928
GSM1040649
35
28
21
14
7
0
2822
2832
2842
2852
2862
2872
2882

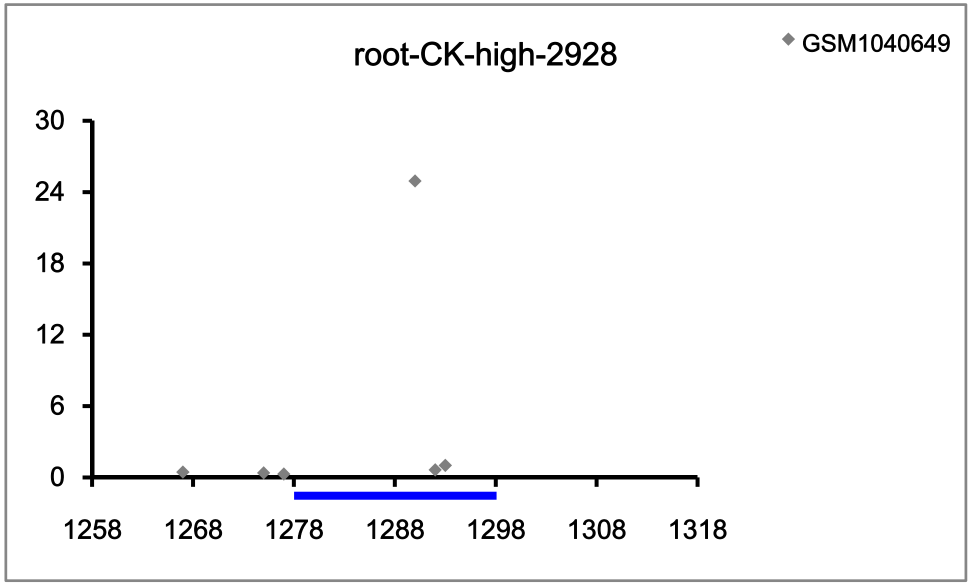

LOC_Os12g31860.3
GSM1040649
35
28
21
14
7
0
0
500
1000
1500
2000

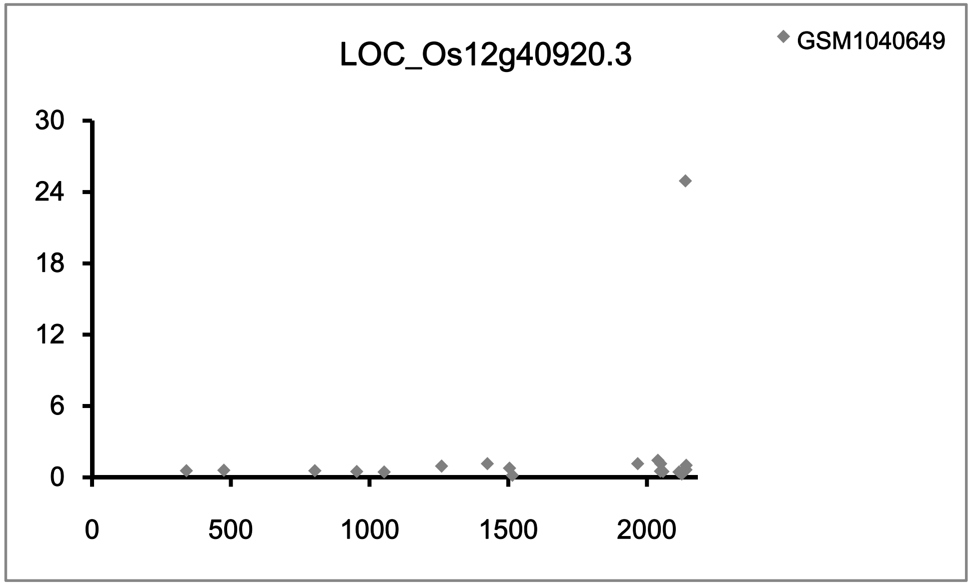

root-CK-high-2928
GSM1040649
35
28
21
14
7
0
1950
1960
1970
1980
1990
2000
2010

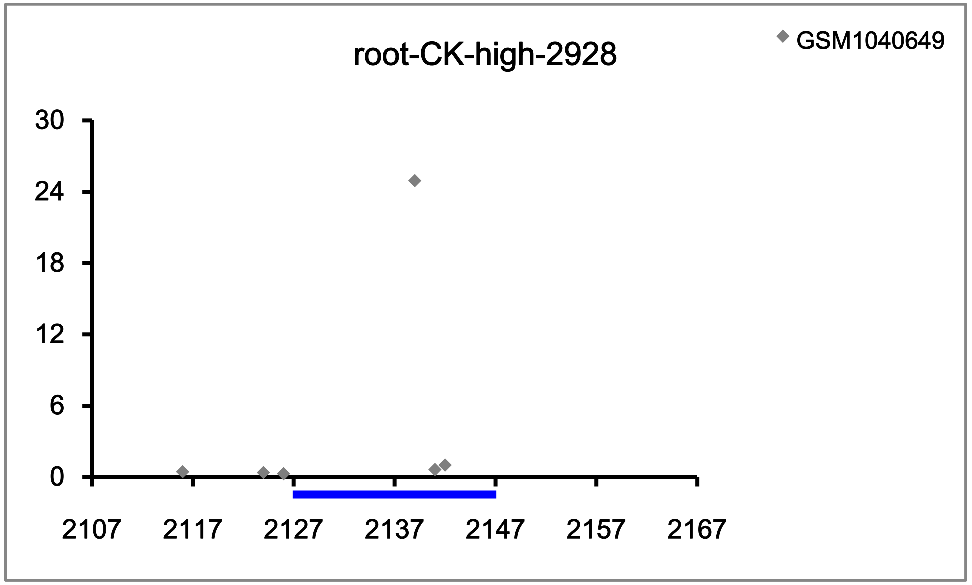

LOC_Os12g31860.5
GSM1040649
35
28
21
14
7
0
0
500
1000
1500
2000

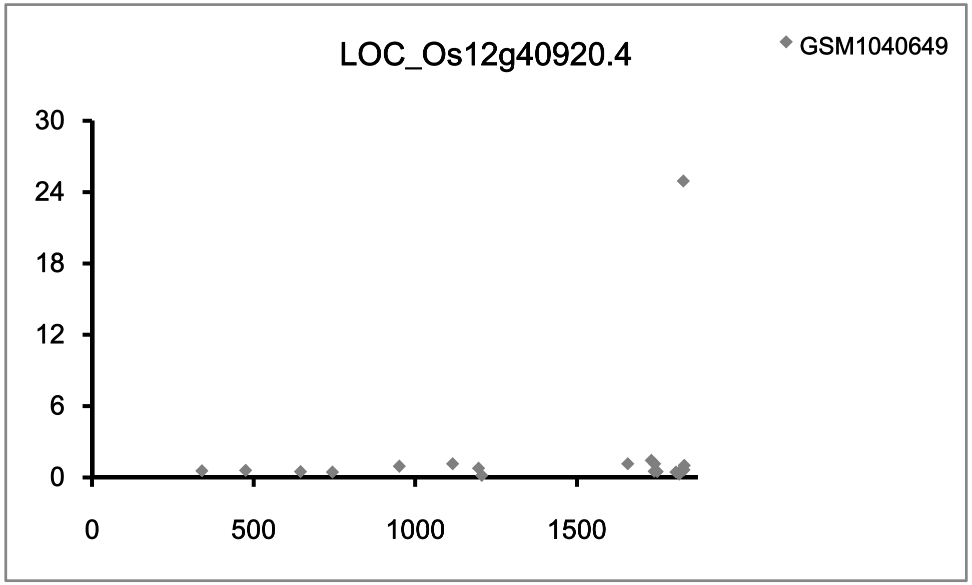

root-CK-high-2928
GSM1040649
35
28
21
14
7
0
1974
1984
1994
2004
2014
2024
2034

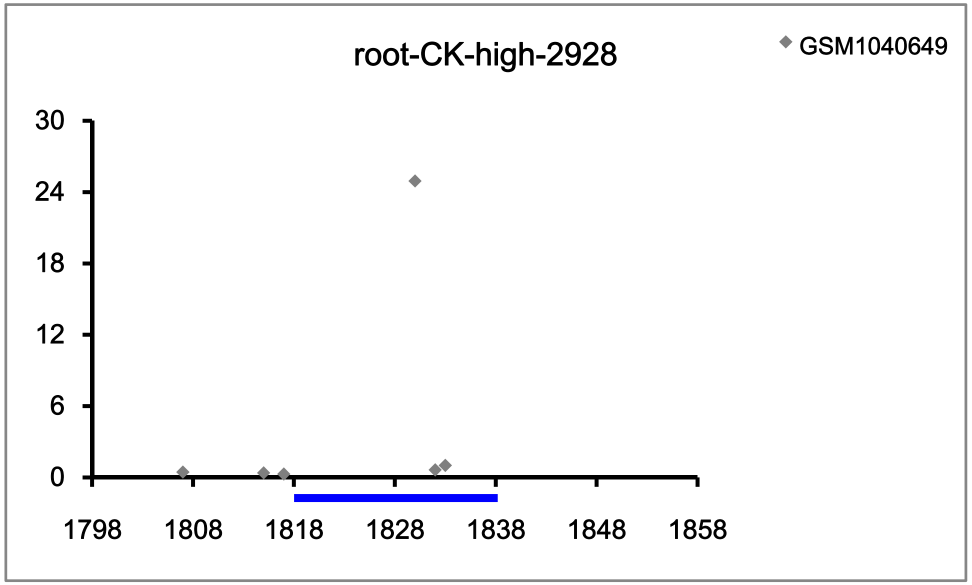

LOC_Os12g40920.1
GSM1040649
30
24
18
12
6
0
0
500
1000

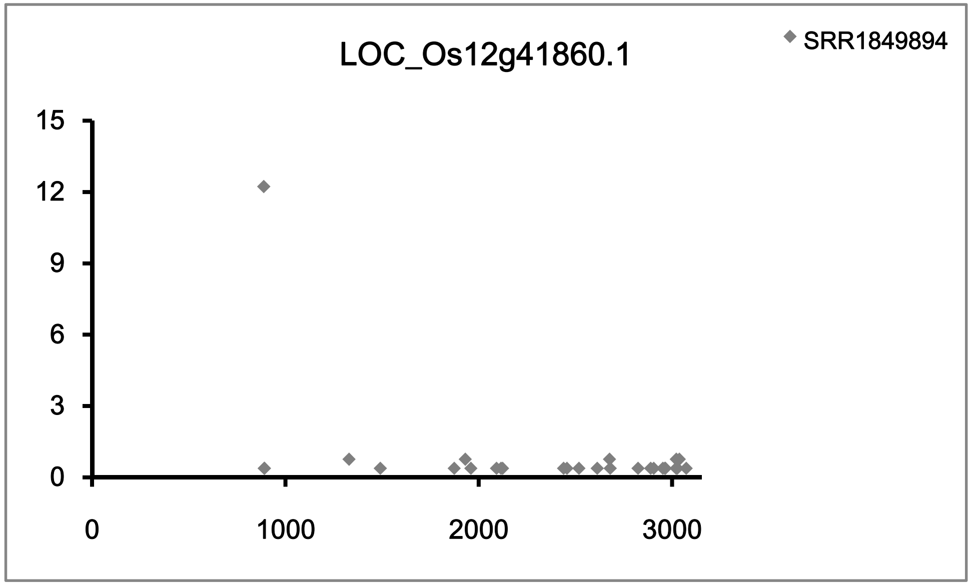

root-CK-high-2928
GSM1040649
30
24
18
12
6
0
1258
1268
1278
1288
1298
1308
1318

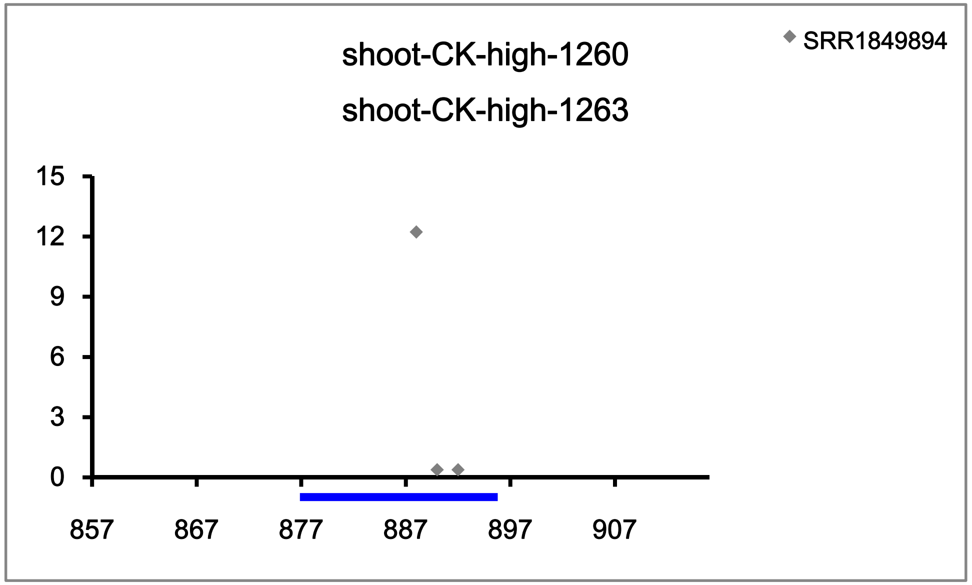

LOC_Os12g40920.3
GSM1040649
30
24
18
12
6
0
0
500
1000
1500
2000

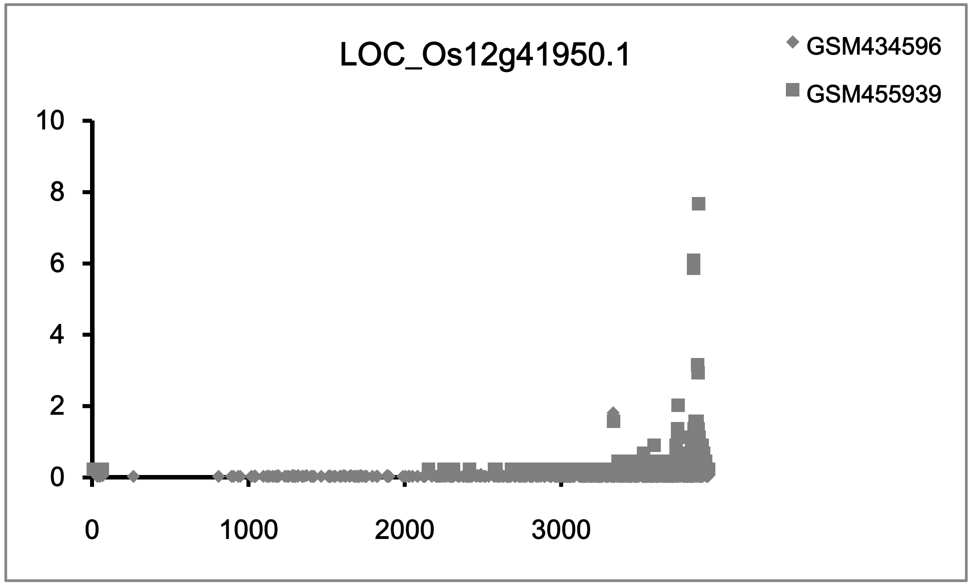

root-CK-high-2928
GSM1040649
30
24
18
12
6
0
2107
2117
2127
2137
2147
2157
2167


LOC_Os12g40920.4
GSM1040649
30
24
18
12
6
0
0
500
1000
1500


root-CK-high-2928
GSM1040649
30
24
18
12
6
0
1798
1808
1818
1828
1838
1848
1858


LOC_Os12g41860.1
◆ SRR1849894
15
12
9
6
3
0
0
1000
2000
3000


shoot-CK-high-1260
shoot-CK-high-1263
◆ SRR1849894
15
12
9
6
3
0
857
867
877
887
897
907


LOC_Os12g41950.1
◆ GSM434596
■ GSM455939
10
8
6
4
2
0
0
1000
2000
3000

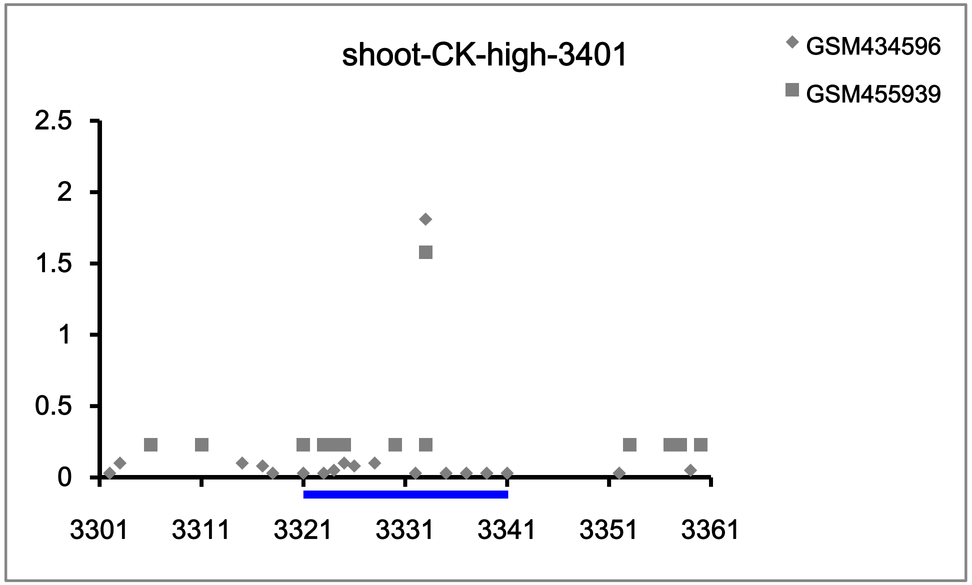

shoot-CK-high-3401
◆ GSM434596
■ GSM455939
2.5
2
1.5
1
0.5
0
3301
3311
3321
3331
3341
3351
3361

Figure S3 GO term enrichment in "MF" (Molecular Function) of protein-coding target transcripts.

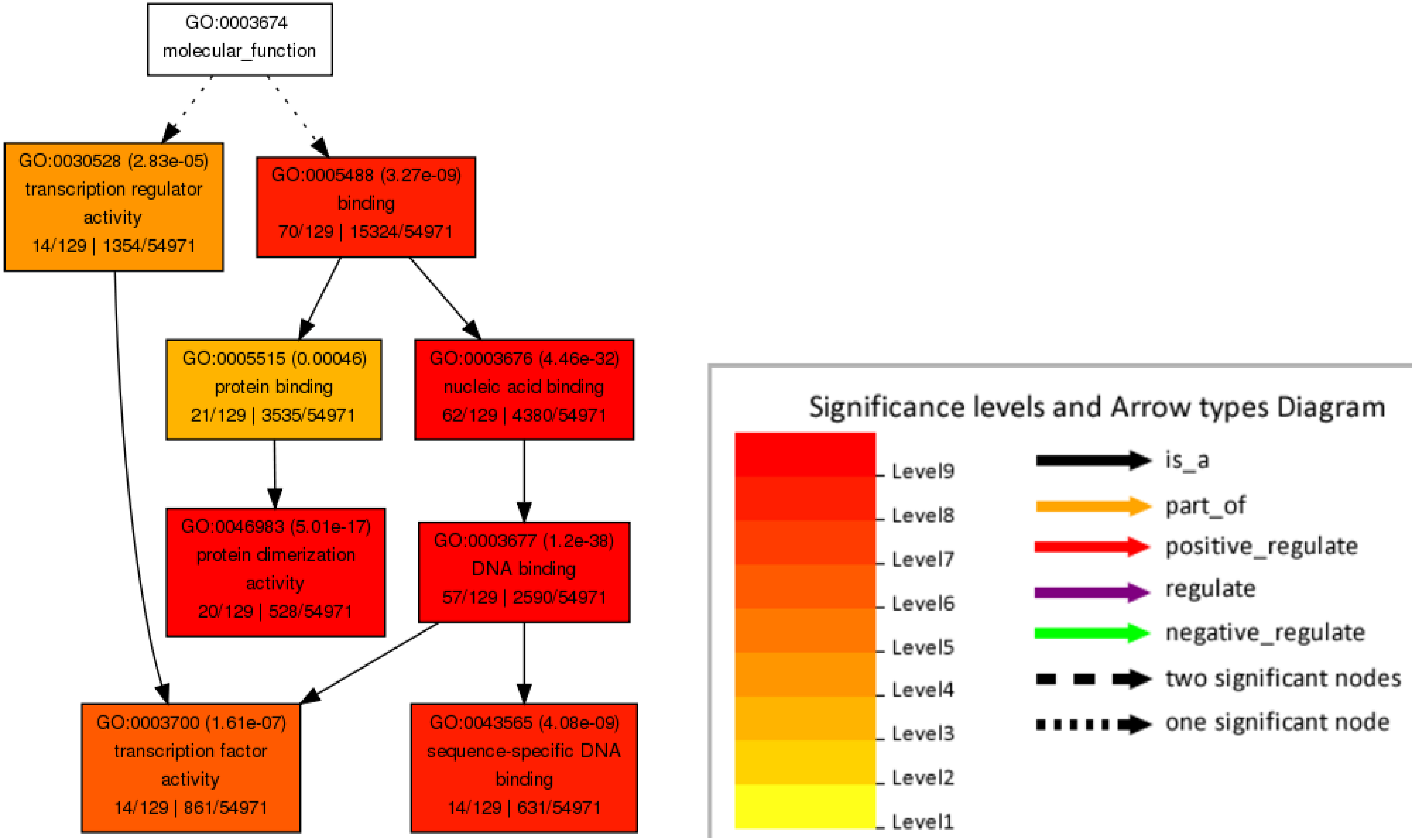

GO:0003674
molecular_function
GO:0030528 (2.83e-05)
transcription regulator activity
14/129 | 1354/54971
GO:0005488 (3.27e-09)
binding
70/129 | 15324/54971
GO:0005515 (0.00046)
protein binding
21/129 | 3535/54971
GO:0003676 (4.46e-32)
nucleic acid binding
62/129 | 4380/54971
GO:0046983 (5.01e-17)
protein dimerization activity
20/129 | 528/54971
GO:0003677 (1.2e-38)
DNA binding
57/129 | 2590/54971
GO:0003700 (1.61e-07)
transcription factor activity
14/129 | 861/54971
GO:0043565 (4.08e-09)
sequence-specific DNA binding
14/129 | 631/54971
Significance levels and Arrow types Diagram
Level9
Level8
Level7
Level6
Level5
Level4
Level3
Level2
Level1
is_a
part_of
positive_regulate
regulate
negative_regulate
two significant nodes
one significant node

Figure S4 GO term enrichment in "CC" (Cellular Component) of protein-coding target transcripts.

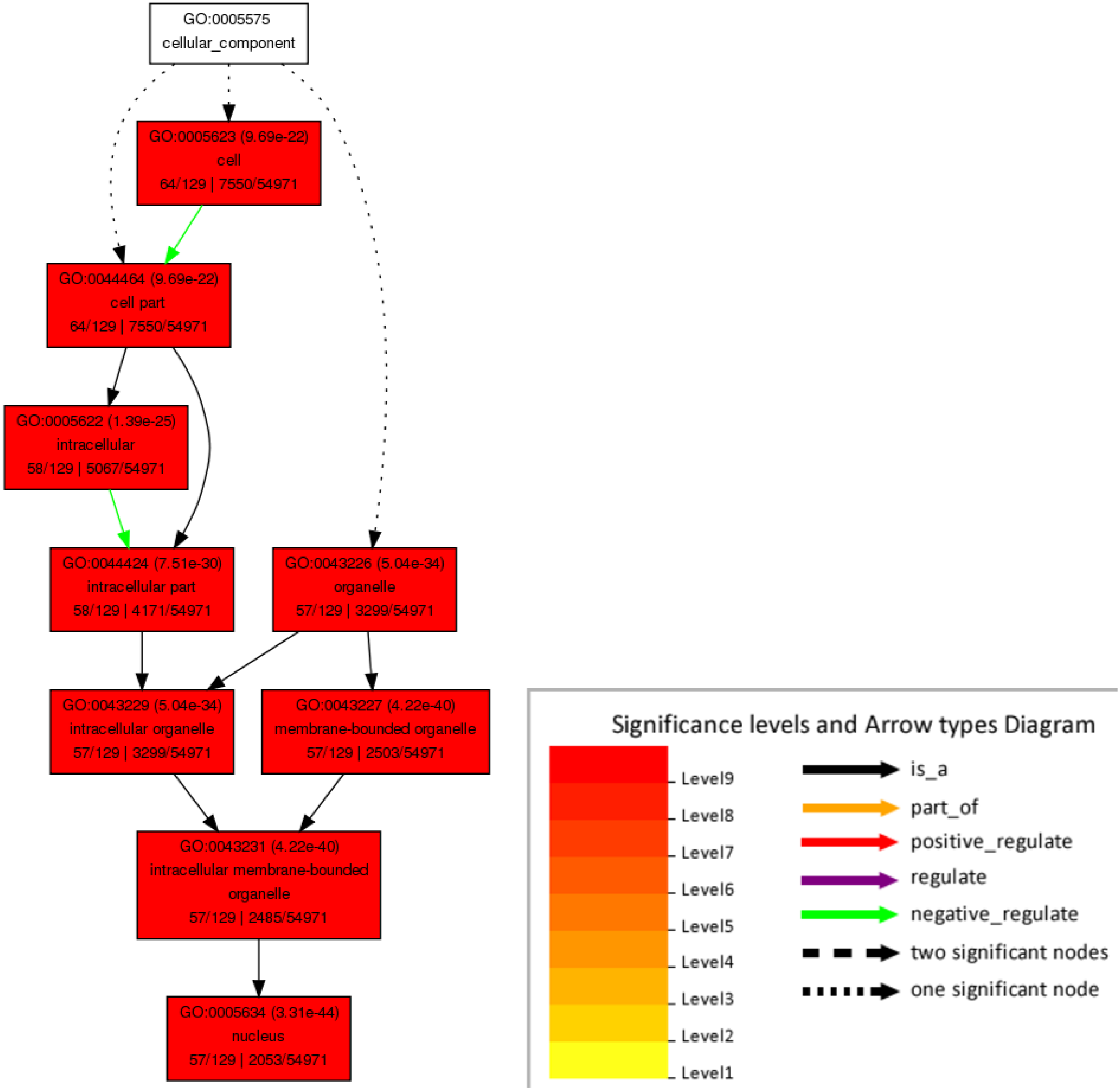
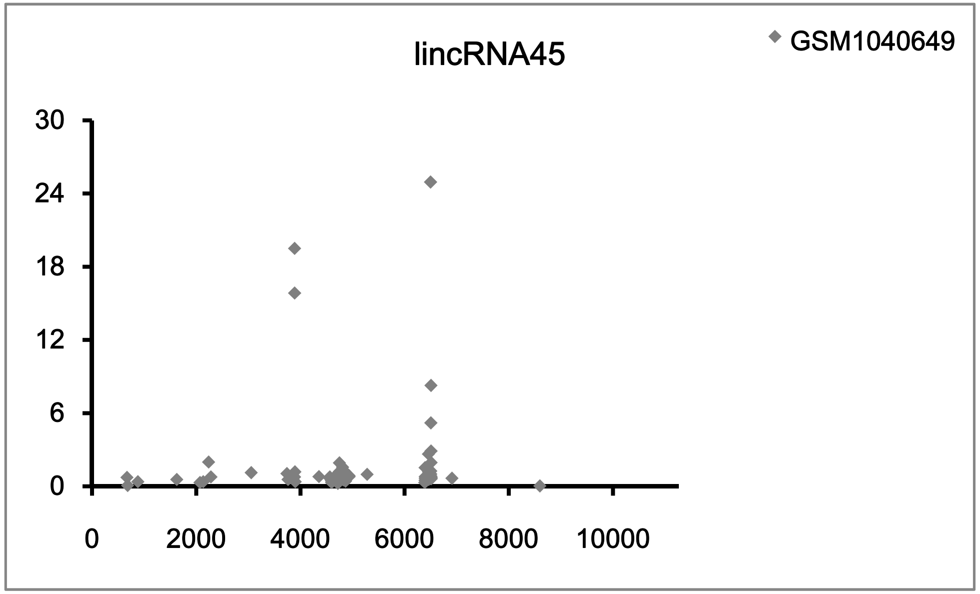
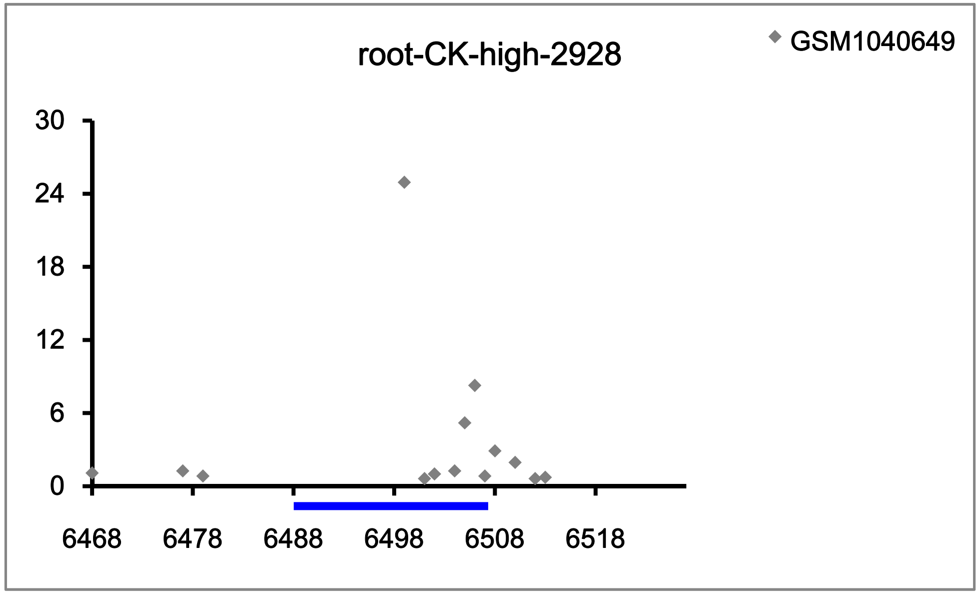

GO:0005575
cellular_component
GO:0005623 (9.69e-22)
cell
64/129 | 7550/54971
GO:0044464 (9.69e-22)
cell part
64/129 | 7550/54971
GO:0005622 (1.39e-25)
intracellular
58/129 | 5067/54971
GO:0044424 (7.51e-30)
intracellular part
58/129 | 4171/54971
GO:0043226 (5.04e-34)
organelle
57/129 | 3299/54971
GO:0043229 (5.04e-34)
intracellular organelle
57/129 | 3299/54971
GO:0043227 (4.22e-40)
membrane-bounded organelle
57/129 | 2503/54971
GO:0043231 (4.22e-40)
intracellular membrane-bounded organelle
57/129 | 2485/54971
GO:0005634 (3.31e-44)
nucleus
57/129 | 2053/54971
Significance levels and Arrow types Diagram
Level9
Level8
Level7
Level6
Level5
Level4
Level3
Level2
Level1
is_a
part_of
positive_regulate
regulate
negative_regulate
two significant nodes
one significant node

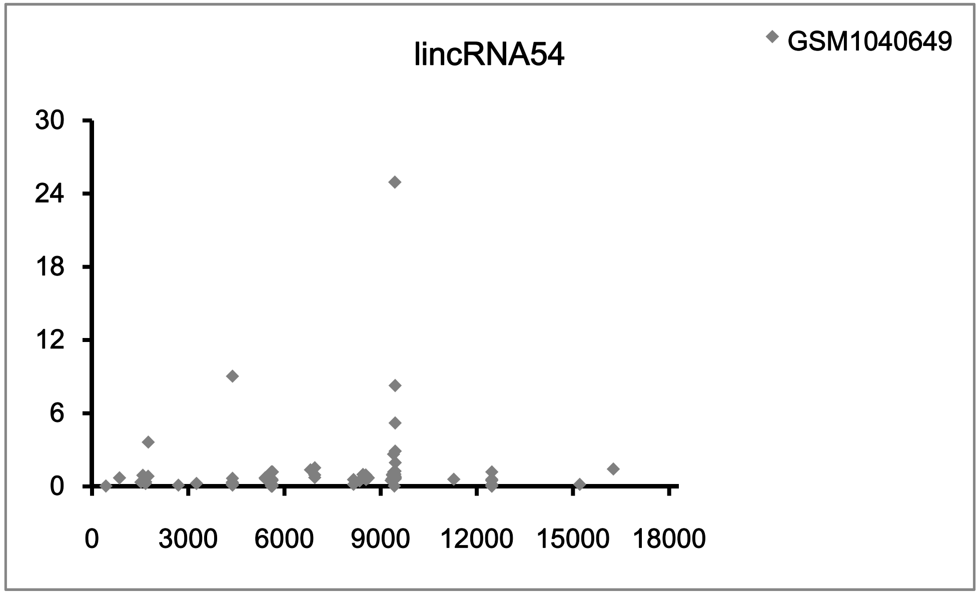
Figure S5 Regulatory network between arsenic stress-responsive small RNAs and protein-coding targets.

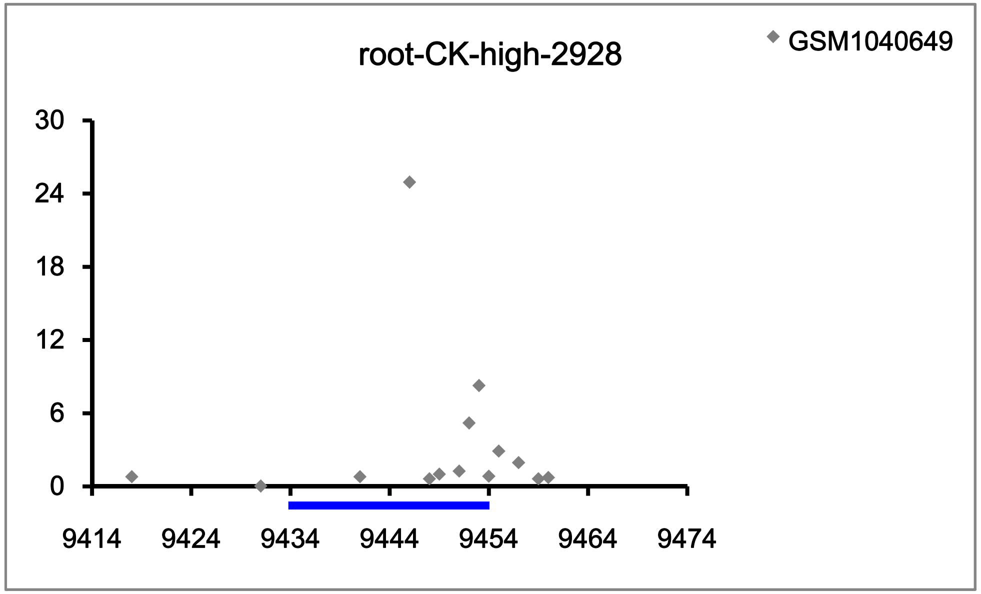

Protein-coding targets
sRNAs repressed by As in roots
sRNAs induced by As in roots
sRNAs repressed by As in shoots
sRNAs induced by As in shoots
root-CK-high-13603
LOC_Os03g50070.1
LOC_Os02g43560.1
LOC_Os03g44190.1
LOC_Os03g39610.2
LOC_Os10g42060.1
LOC_Os10g39520.1
LOC_Os03g39610.1
LOC_Os02g29140.1
LOC_Os02g44990.1
LOC_Os08g36840.1
LOC_Os06g01950.1
LOC_Os04g36830.1
root-CK-high-2928
LOC_Os06g47850.1
LOC_Os03g52010.1
LOC_Os02g07960.4
LOC_Os12g40920.4
LOC_Os02g53000.2
LOC_Os06g05630.2
LOC_Os04g02640.1
LOC_Os03g31180.2
LOC_Os12g31860.3
LOC_Os12g13174.1
LOC_Os07g11790.1
LOC_Os04g38450.1
LOC_Os12g40920.1
LOC_Os06g05630.1
LOC_Os06g12455.1
LOC_Os09g12230.1
LOC_Os12g40920.3
LOC_Os05g50440.1
LOC_Os12g31860.1
LOC_Os12g31860.2
LOC_Os03g44200.1
LOC_Os09g14560.1
LOC_Os12g31860.5
LOC_Os06g05630.3
LOC_Os03g47140.1
LOC_Os02g47280.2
LOC_Os04g51190.1
LOC_Os02g47280.1
LOC_Os04g51190.2
LOC_Os02g45570.2
shoot-CK-high-2001
LOC_Os04g51190.3
LOC_Os06g02560.1
LOC_Os02g45570.1
LOC_Os06g02560.2
LOC_Os12g29980.2
LOC_Os06g02560.3
osa-miR396a-5p/osa-miR396b-5p
LOC_Os11g35030.1
LOC_Os12g29980.1
LOC_Os11g35030.2
shoot-CK-high-7947
root-CK-high-4920
LOC_Os01g70270.3
LOC_Os05g48870.7
LOC_Os05g48870.1
LOC_Os01g48060.3
LOC_Os05g48870.6
LOC_Os01g70270.4
LOC_Os01g48060.1
LOC_Os05g48870.9
LOC_Os01g54990.1
LOC_Os05g48870.8
LOC_Os05g43920.1
LOC_Os01g70270.2
LOC_Os05g48870.5
LOC_Os01g70270.1
LOC_Os01g48060.2
root-CK-high-4603
LOC_Os06g45310.1
LOC_Os06g49010.6
LOC_Os06g49010.3
LOC_Os02g04680.2
LOC_Os06g49010.5
LOC_Os06g49010.1
LOC_Os01g69830.1
LOC_Os07g32170.2
LOC_Os11g30370.1
LOC_Os07g32170.1
LOC_Os06g49010.2
LOC_Os02g07780.2
LOC_Os02g07780.1
LOC_Os06g49010.4
LOC_Os02g04680.1
LOC_Os03g43930.1
LOC_Os03g01890.2
LOC_Os03g43930.2
shoot-CK-high-1260
LOC_Os10g33960.1
LOC_Os03g01890.1
LOC_Os10g33960.2
LOC_Os12g41860.1
LOC_Os10g33960.3
LOC_Os10g33960.4
shoot-CK-high-1263
root-CK-high-5965
LOC_Os06g47150.3
LOC_Os02g41800.2
LOC_Os06g47150.2
LOC_Os06g47150.4
LOC_Os10g33940.1
LOC_Os06g47150.1
LOC_Os02g41800.1
LOC_Os04g43910.1
LOC_Os01g59660.3
shoot-CK-high-5721
LOC_Os01g59660.4
LOC_Os01g59660.2
LOC_Os06g40330.1
LOC_Os01g59660.1
root-CK-high-10864
LOC_Os02g06910.1
LOC_Os04g57610.1
LOC_Os12g41950.1
shoot-CK-high-3401
LOC_Os06g46410.1
LOC_Os06g46410.2
LOC_Os04g57610.3
LOC_Os10g40390.1
LOC_Os04g46860.1
shoot-As-high-9528
LOC_Os06g01620.1
LOC_Os02g44370.1
shoot-CK-high-38
LOC_Os02g44360.1
LOC_Os01g63890.1
LOC_Os04g55290.1
LOC_Os04g55290.5
shoot-As-high-2209
LOC_Os04g55290.3
LOC_Os04g55290.4
LOC_Os04g55290.2
LOC_Os04g47870.2
LOC_Os04g47870.1
shoot-CK-high-7069
LOC_Os02g45070.2
LOC_Os02g45070.1
LOC_Os06g11490.1
shoot-CK-high-2855
LOC_Os08g37670.1
LOC_Os02g52180.1
LOC_Os08g27580.2
root-As-high-992
shoot-CK-high-1707
LOC_Os08g27580.1
LOC_Os01g64520.2
root-CK-high-1309
LOC_Os05g02620.1
LOC_Os01g64520.1
LOC_Os01g59720.1
root-CK-high-10130
LOC_Os06g48240.1
LOC_Os06g07010.1
root-CK-high-2334
LOC_Os06g07010.2
LOC_Os04g55650.1
root-CK-high-7883
LOC_Os04g55650.2
shoot-As-high-850
LOC_Os01g55040.1
root-CK-high-11406
LOC_Os06g06600.1
shoot-As-high-16223
LOC_Os05g34290.1
root-CK-high-12952
LOC_Os05g11560.2
shoot-CK-high-6015
LOC_Os05g10670.1
shoot-CK-high-7529
LOC_Os02g36924.1
root-CK-high-6739
LOC_Os02g14290.1

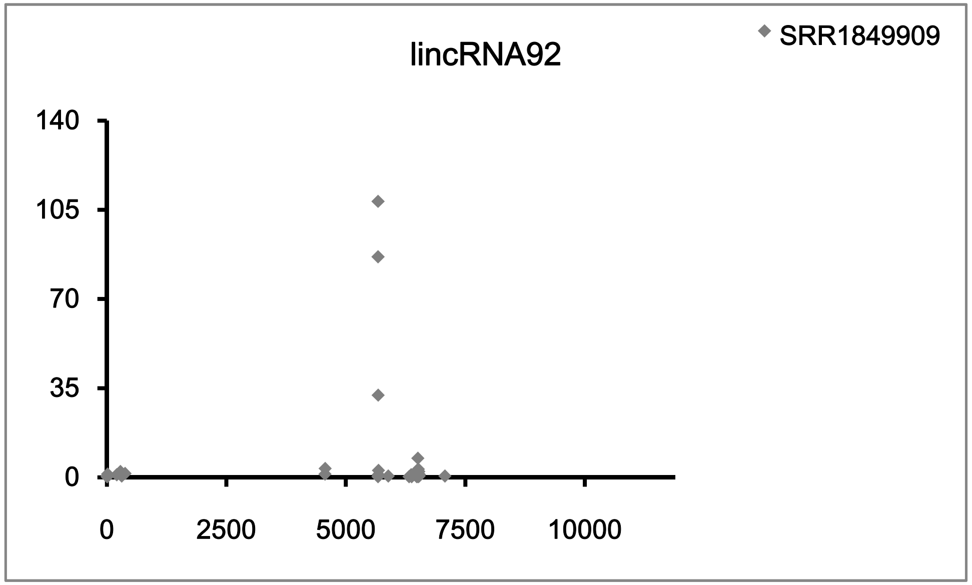
Figure S6 Degradome sequencing data-based evidence showing the long non-coding RNAs (lncRNAs) regulated by the arsenic stress-responsive small RNAs. On each page, the degradome sequencing evidence is displayed as target plots (t-plots) for each small RNA (sRNA)--target pairs. The first t-plot presents the global distribution of degradome signals along the full-length target transcript, with lncRNA ID and degradome-seq data set IDs shown on the top. The other panel(s) provide(s) a detailed view of degradome signals surrounding the predicted binding site (blue line) of the arsenic-responsive sRNA (ID shown on the top) on the target transcript, which clearly shows the degradome-seq evidence (marked by red arrowheads) supporting the regulatory relationship. For each t-plot, the Y axis measures the degradome signal intensity in RPM (reads per million), and the X axis indicate the position on the target transcript.

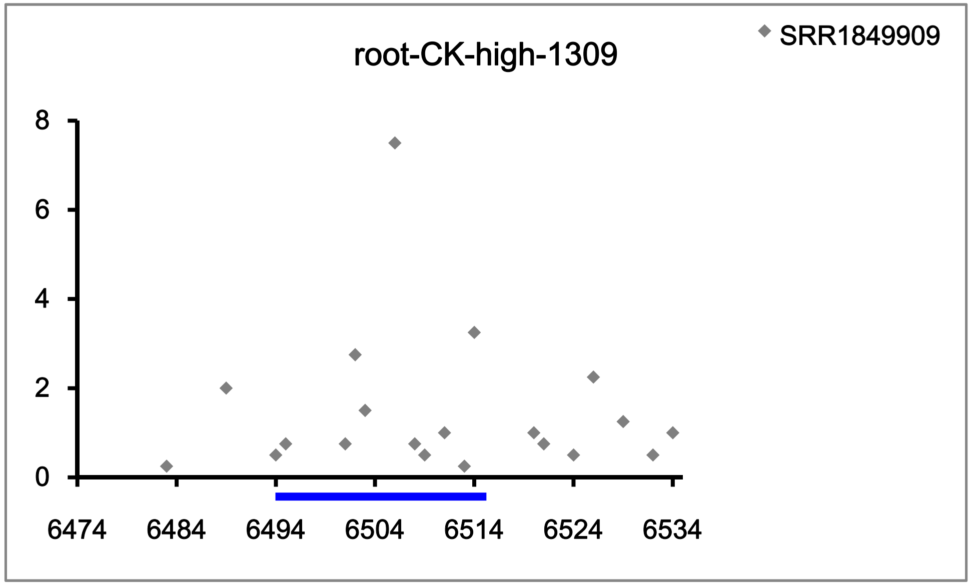

lincRNA45
GSM1040649
30
24
18
12
6
0
0
2000
4000
6000
8000
10000

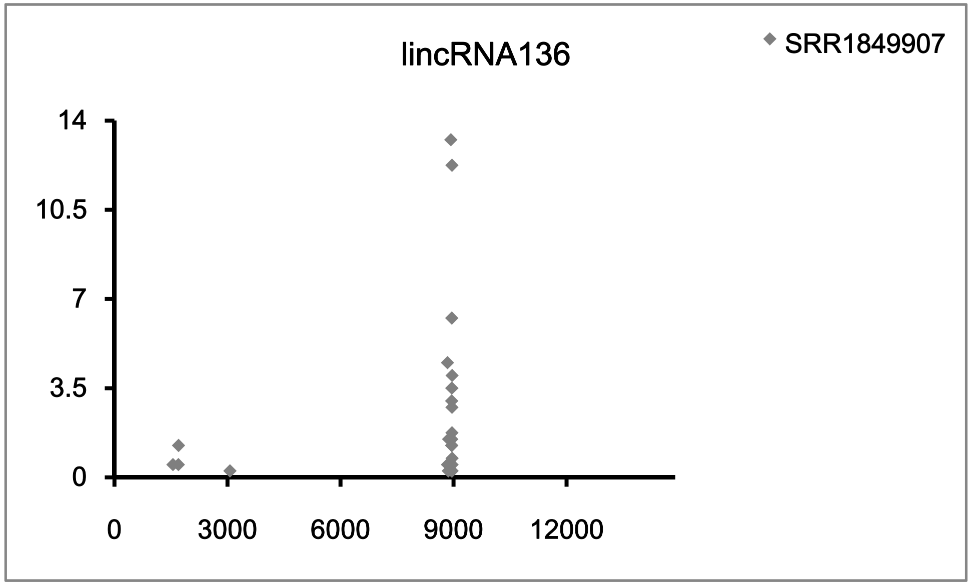

root-CK-high-2928
GSM1040649
30
24
18
12
6
0
6468
6478
6488
6498
6508
6518

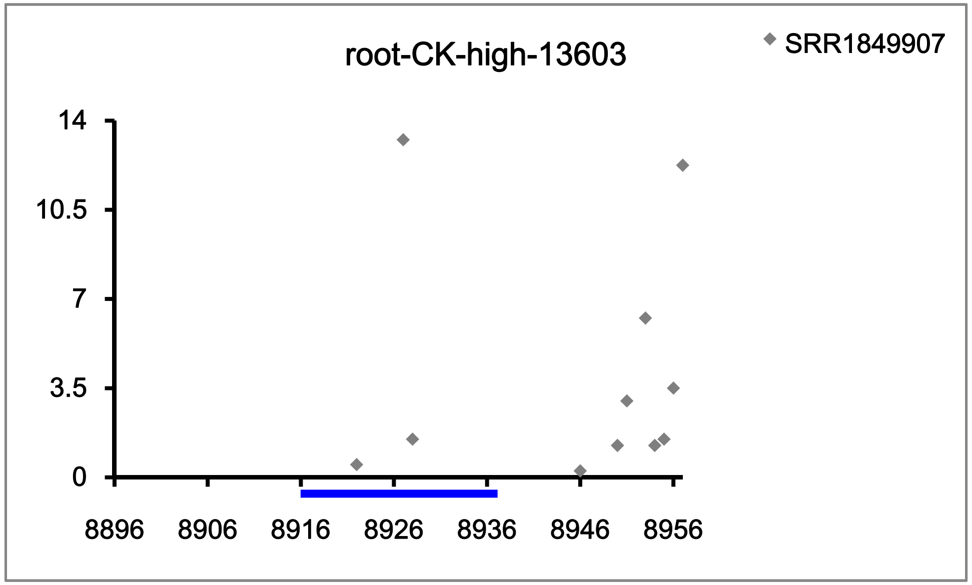

lincRNA54
GSM1040649
30
24
18
12
6
0
0
3000
6000
9000
12000
15000
18000

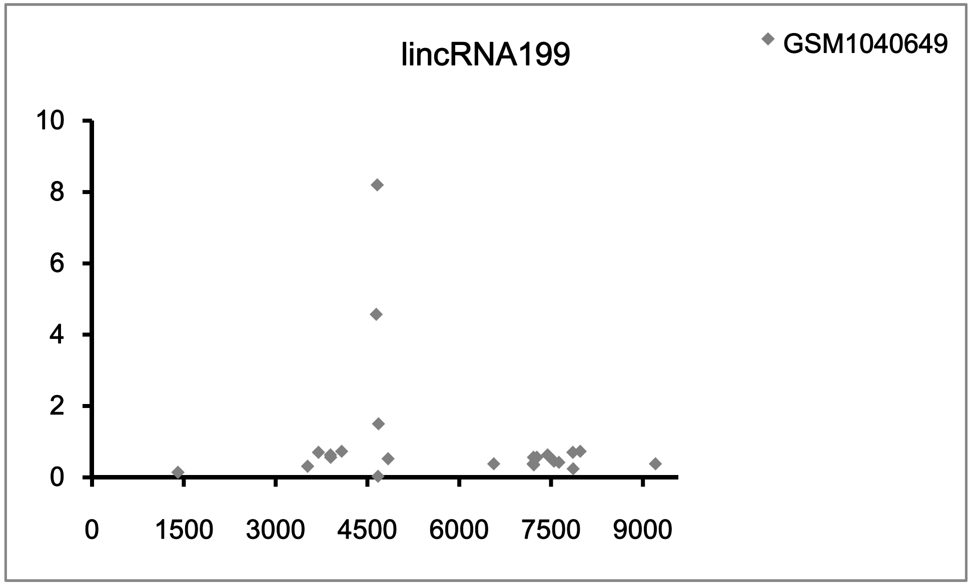

root-CK-high-2928
GSM1040649
30
24
18
12
6
0
9414
9424
9434
9444
9454
9464
9474

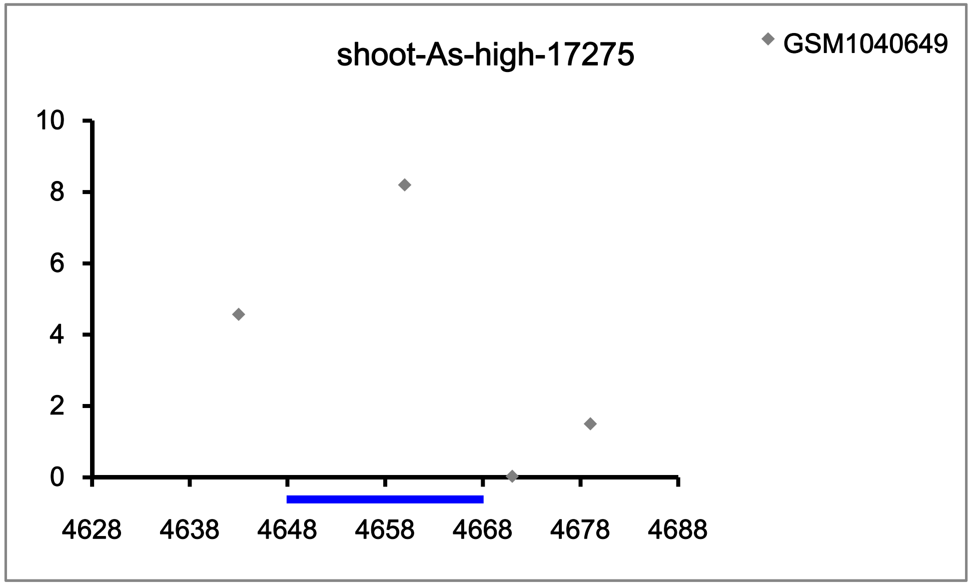

lincRNA92
SRR1849909
140
105
70
35
0
0
2500
5000
7500
10000

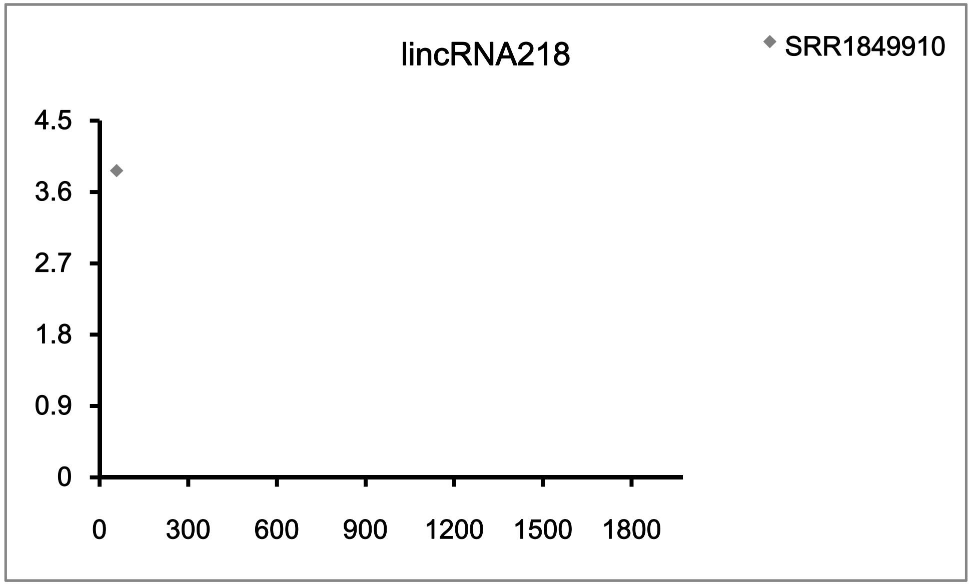

root-CK-high-1309
SRR1849909
8
6
4
2
0
6474
6484
6494
6504
6514
6524
6534

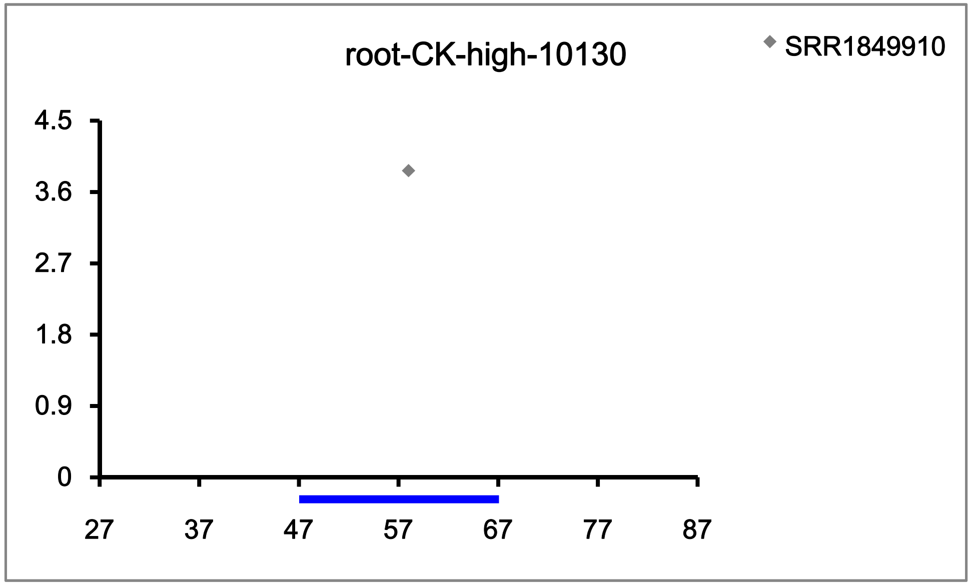

lincRNA136
SRR1849907
14
10.5
7
3.5
0
0
3000
6000
9000
12000

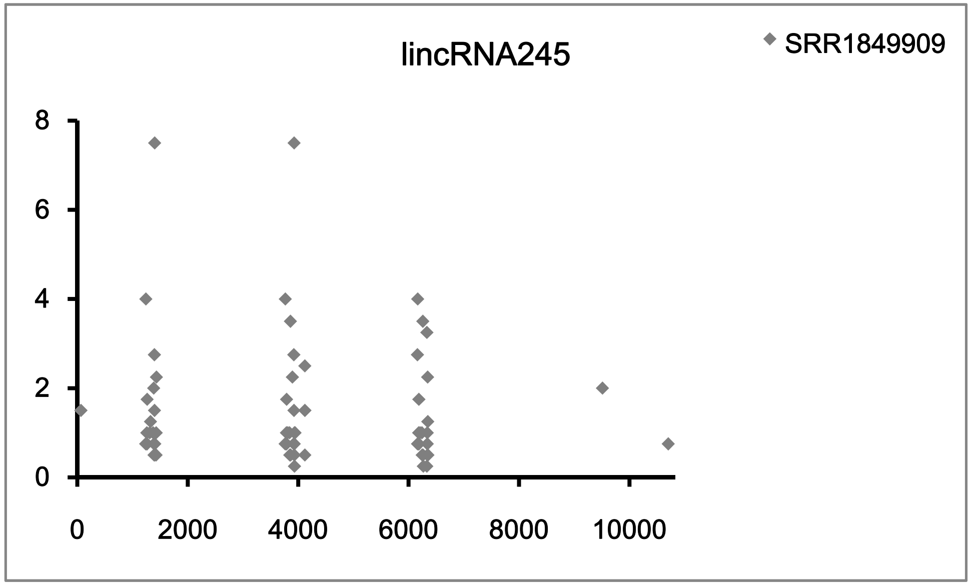

root-CK-high-13603
SRR1849907
14
10.5
7
3.5
0
8896
8906
8916
8926
8936
8946
8956

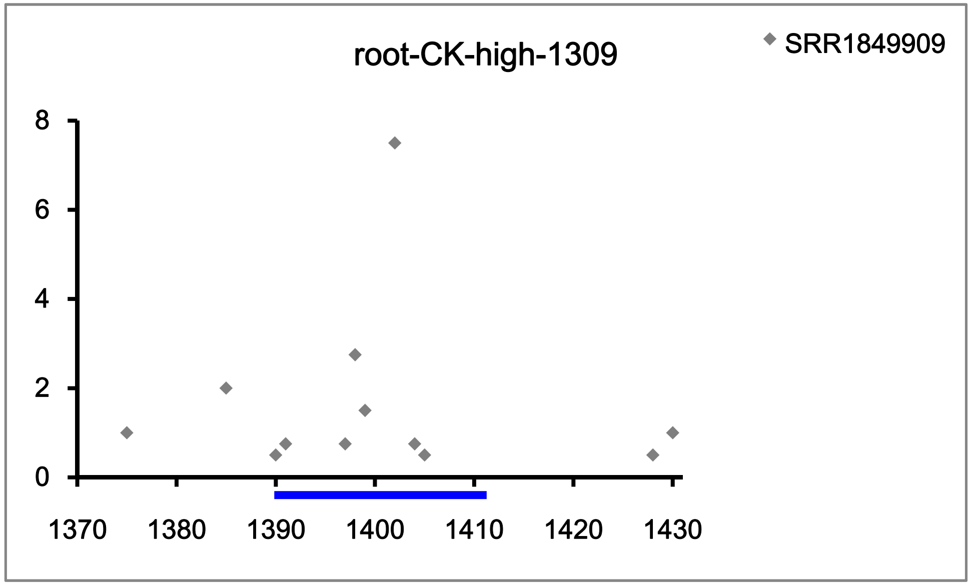

lincRNA199
GSM1040649
10
8
6
4
2
0
0
1500
3000
4500
6000
7500
9000

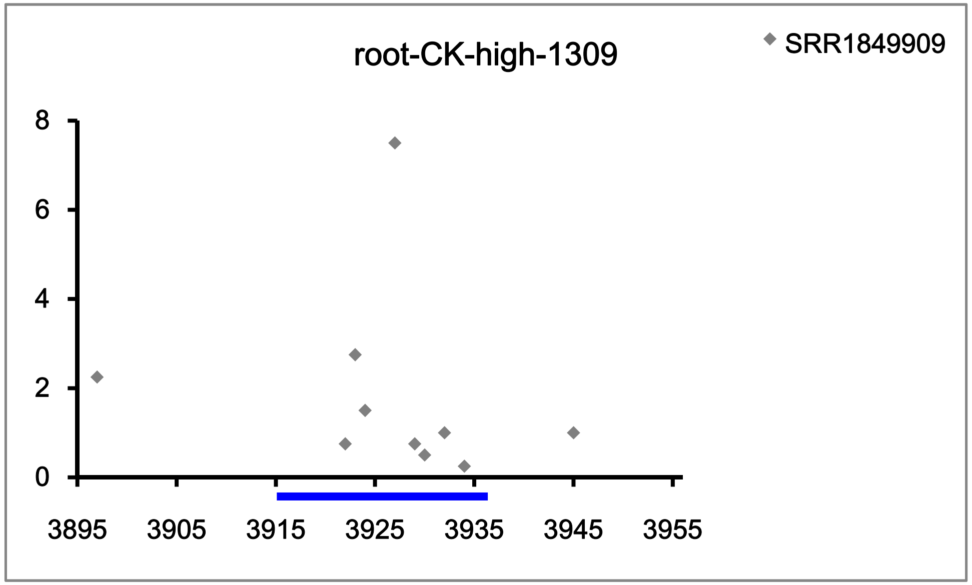

shoot-As-high-17275
GSM1040649
10
8
6
4
2
0
4628
4638
4648
4658
4668
4678
4688

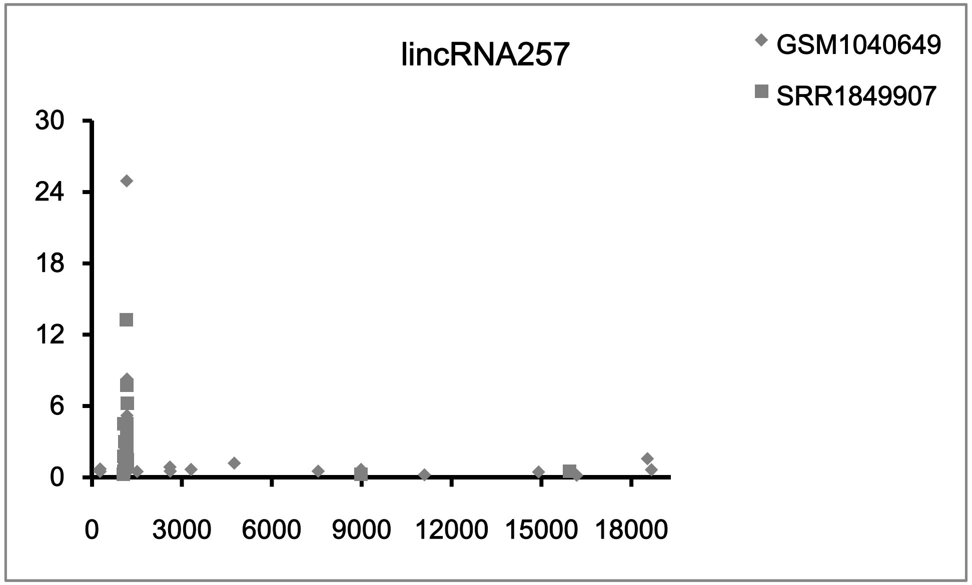

lincRNA218
SRR1849910
4.5
3.6
2.7
1.8
0.9
0
0
300
600
900
1200
1500
1800

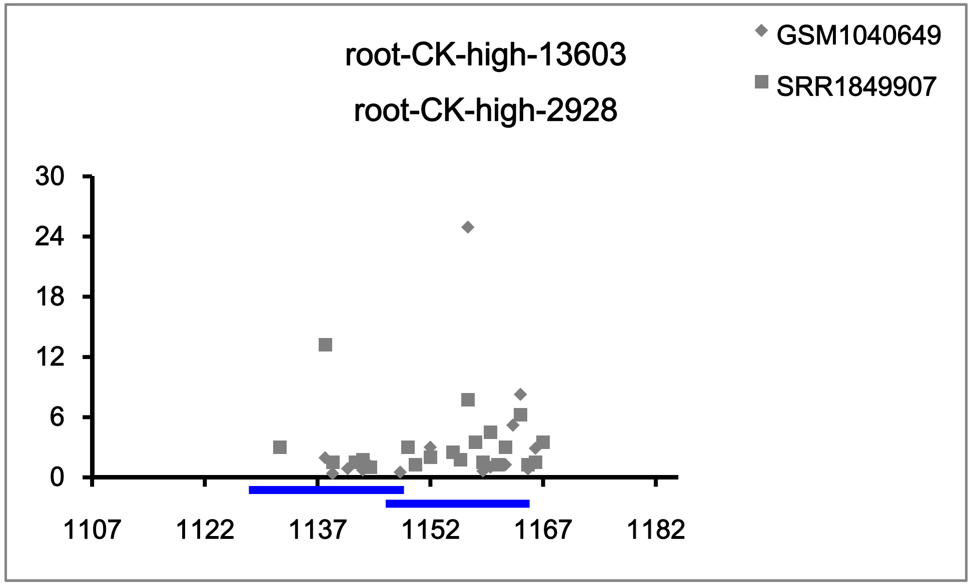

root-CK-high-10130
SRR1849910
4.5
3.6
2.7
1.8
0.9
0
27
37
47
57
67
77
87

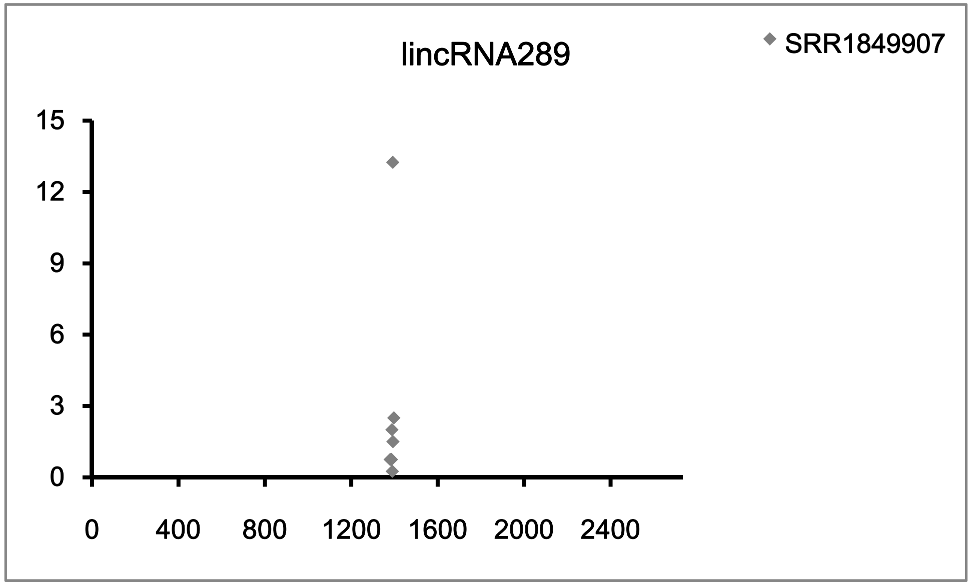

lincRNA245
◆ SRR1849909
8
6
4
2
0
0
2000
4000
6000
8000
10000

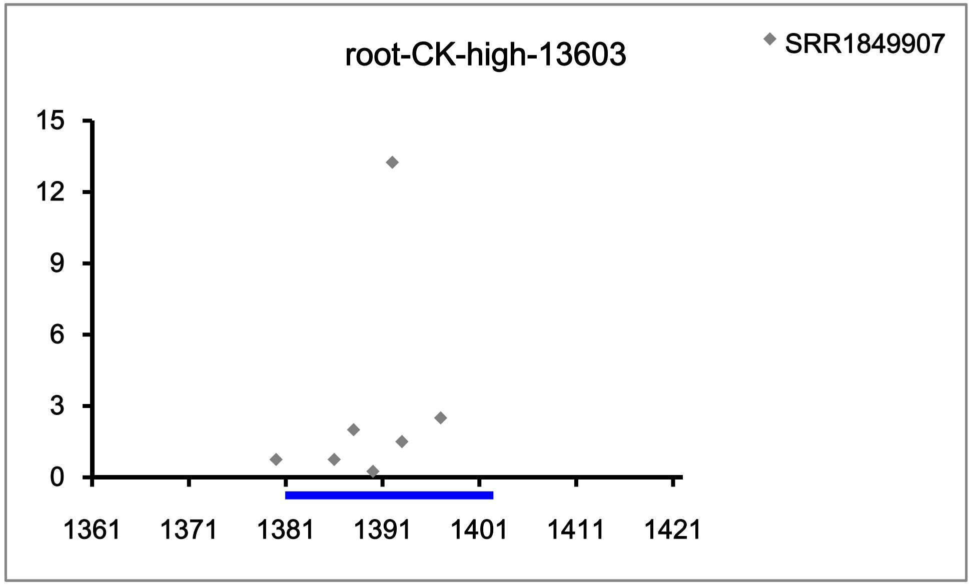

root-CK-high-1309
◆ SRR1849909
8
6
4
2
0
1370
1380
1390
1400
1410
1420
1430

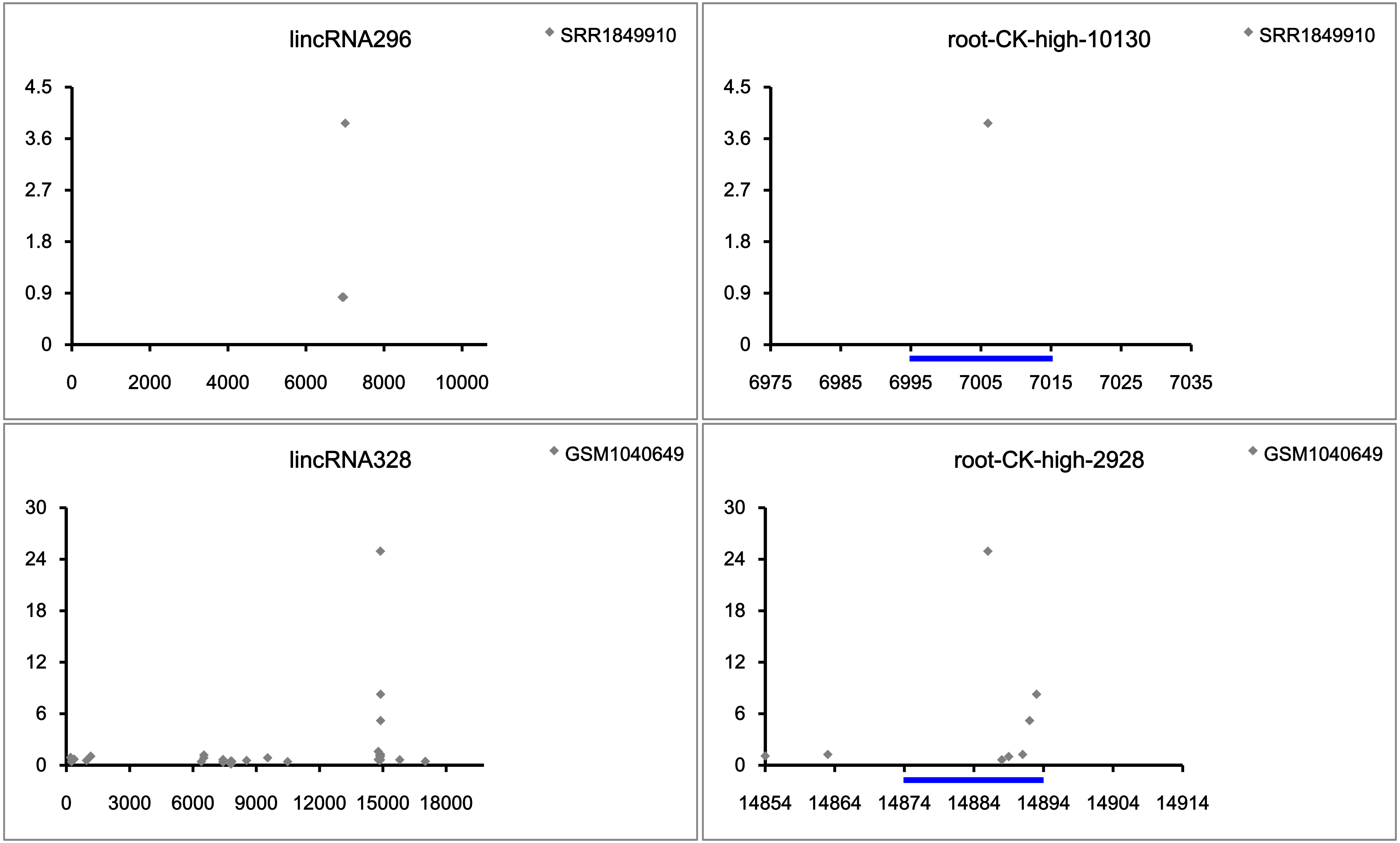

root-CK-high-1309
◆ SRR1849909
8
6
4
2
0
3895
3905
3915
3925
3935
3945
3955

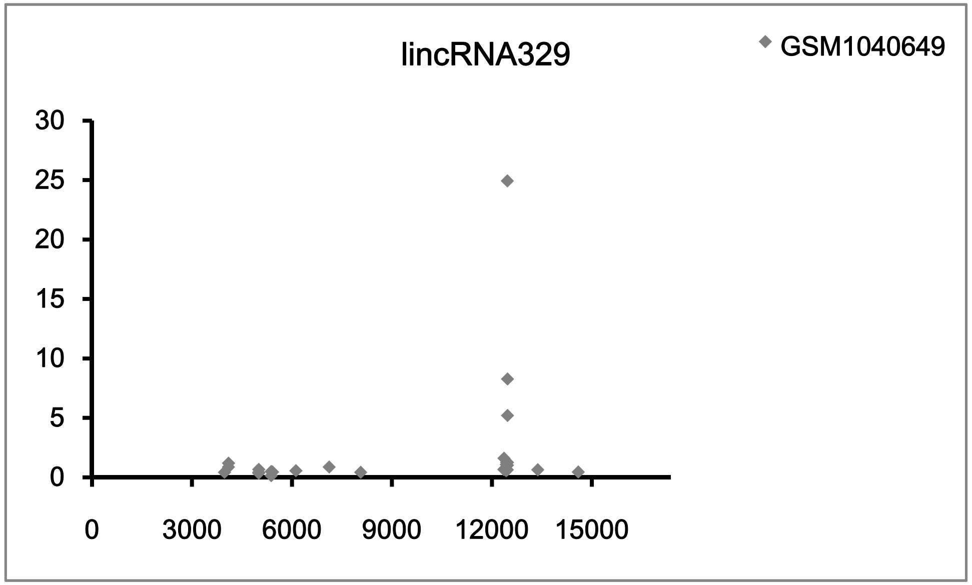

lincRNA257
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
0
3000
6000
9000
12000
15000
18000

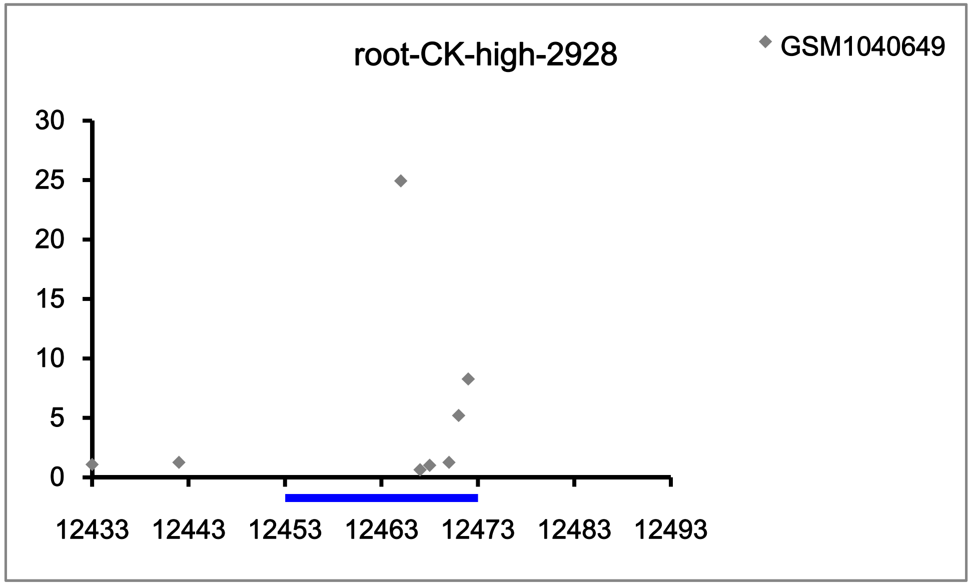

root-CK-high-13603
root-CK-high-2928
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
1107
1122
1137
1152
1167
1182

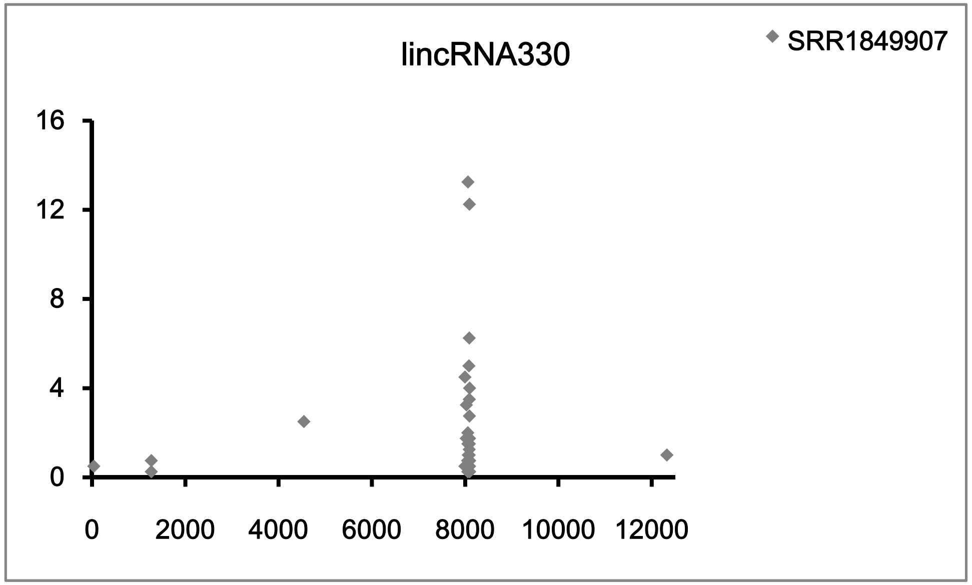

lincRNA289
◆ SRR1849907
15
12
9
6
3
0
0
400
800
1200
1600
2000
2400

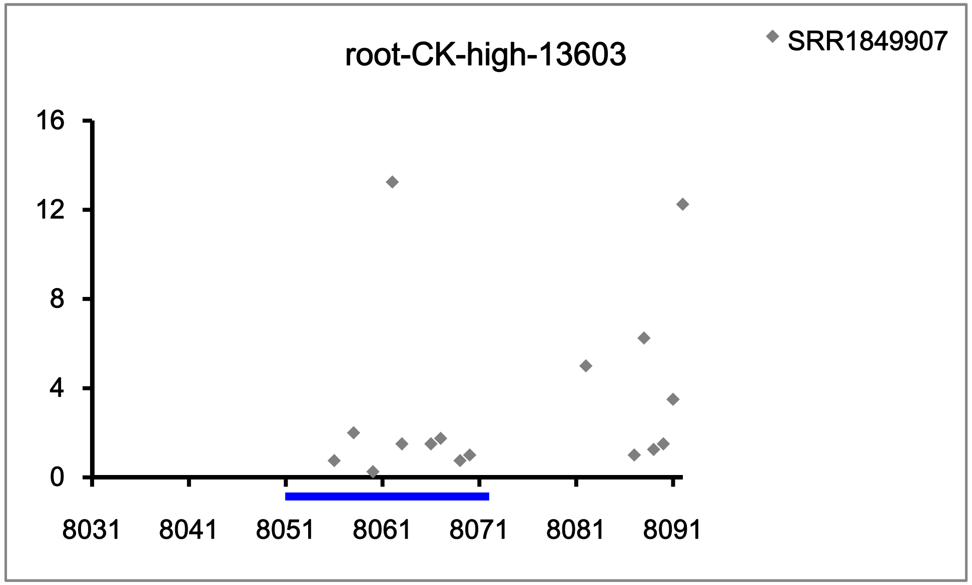

root-CK-high-13603
◆ SRR1849907
15
12
9
6
3
0
1361
1371
1381
1391
1401
1411
1421

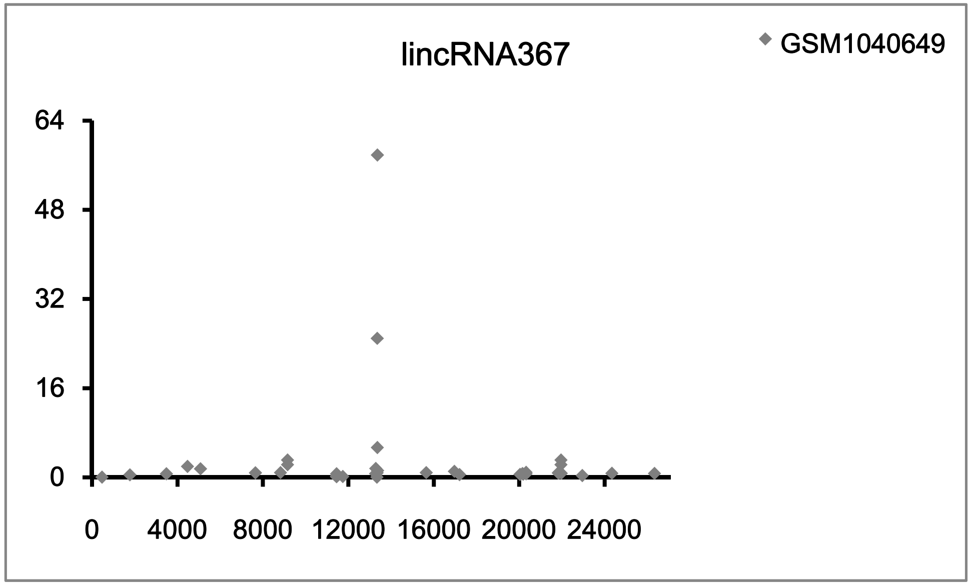

lincRNA296
SRR1849910
4.5
3.6
2.7
1.8
0.9
0
0
2000
4000
6000
8000
10000
root-CK-high-10130
SRR1849910
4.5
3.6
2.7
1.8
0.9
0
6975
6985
6995
7005
7015
7025
7035
lincRNA328
GSM1040649
30
24
18
12
6
0
0
3000
6000
9000
12000
15000
18000
root-CK-high-2928
GSM1040649
30
24
18
12
6
0
14854
14864
14874
14884
14894
14904
14914

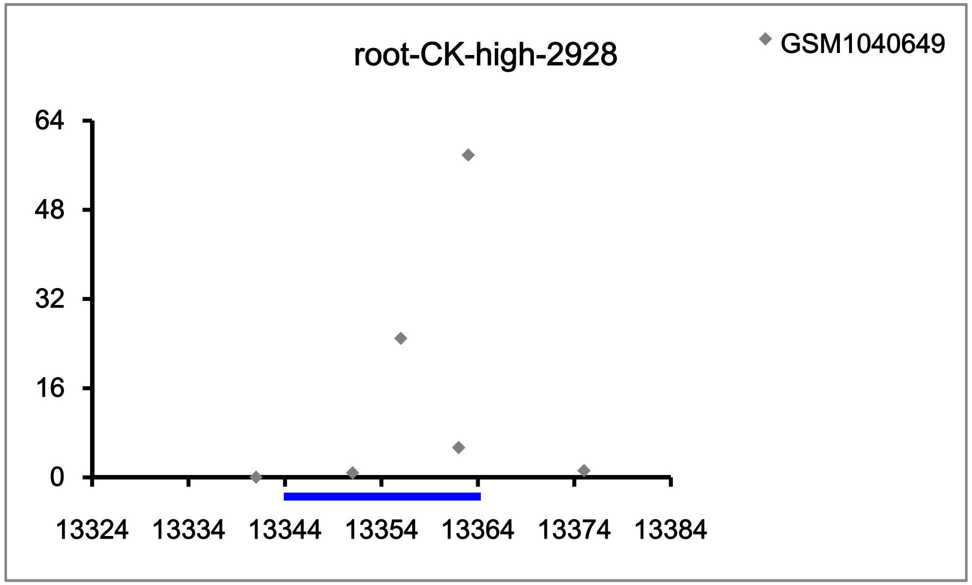

lincRNA329

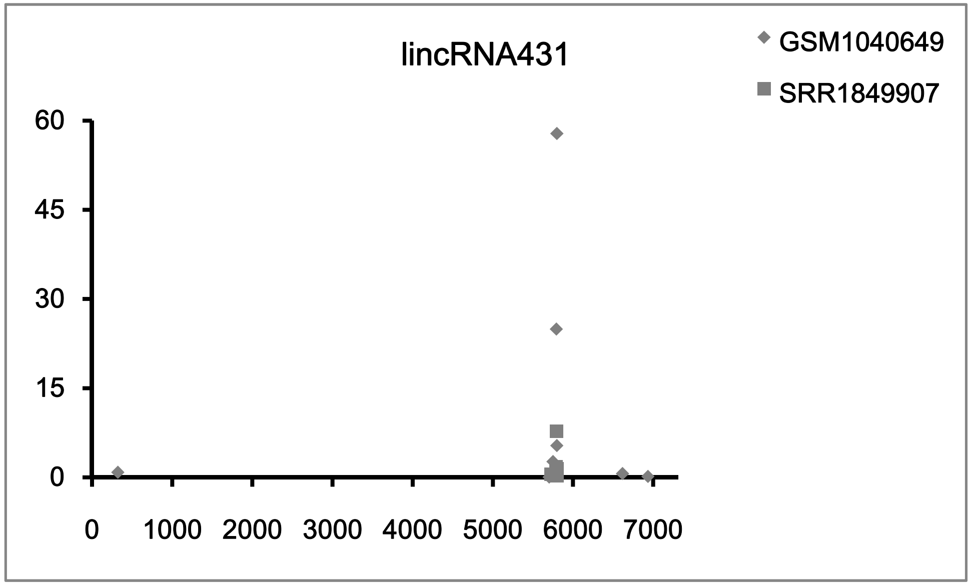

root-CK-high-2928

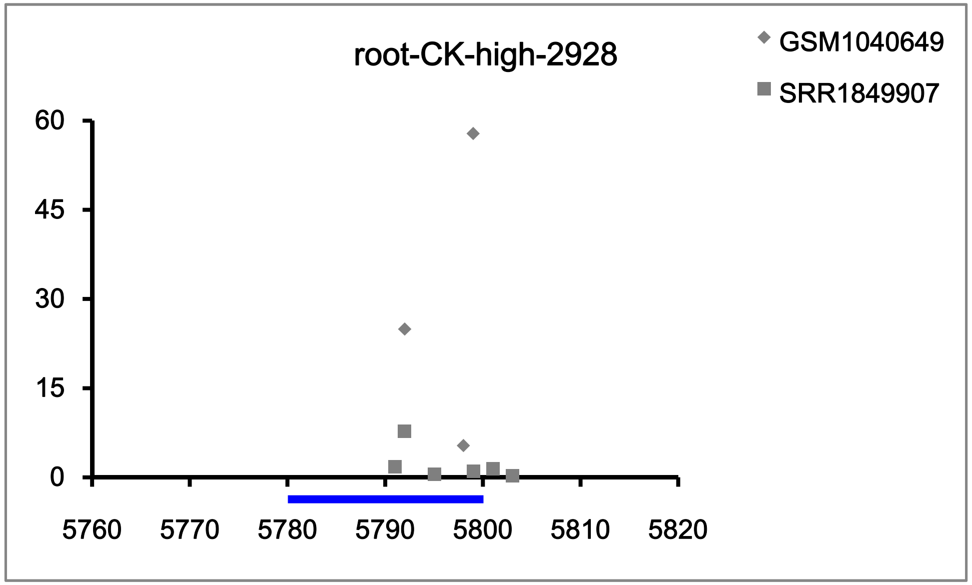

lincRNA330

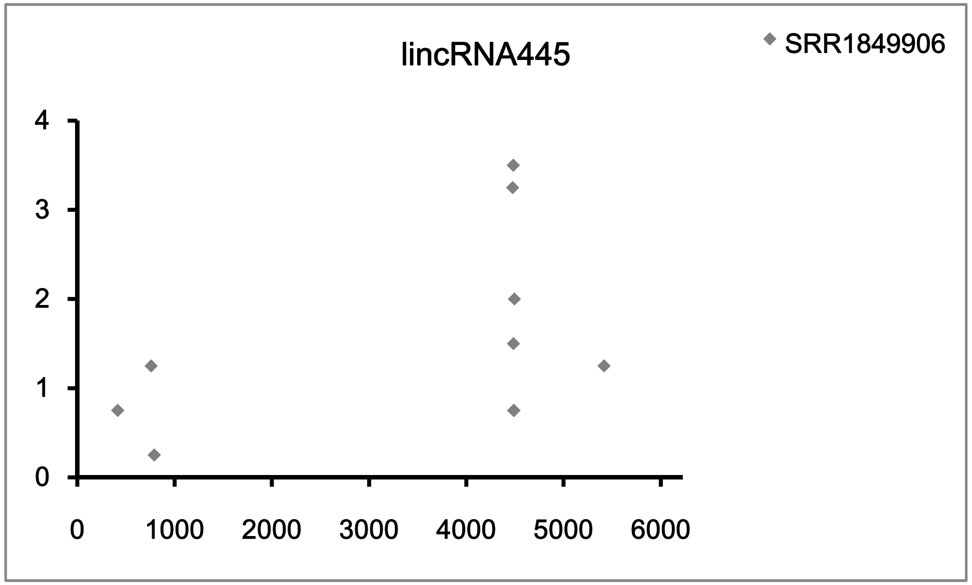

root-CK-high-13603

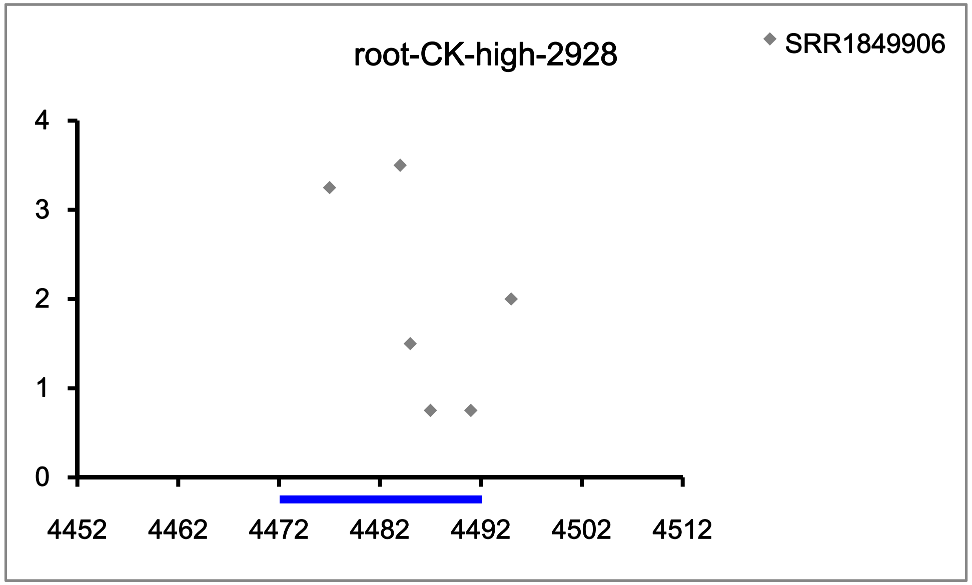

lincRNA367
GSM1040649
64
48
32
16
0
0
4000
8000
12000
16000
20000
24000

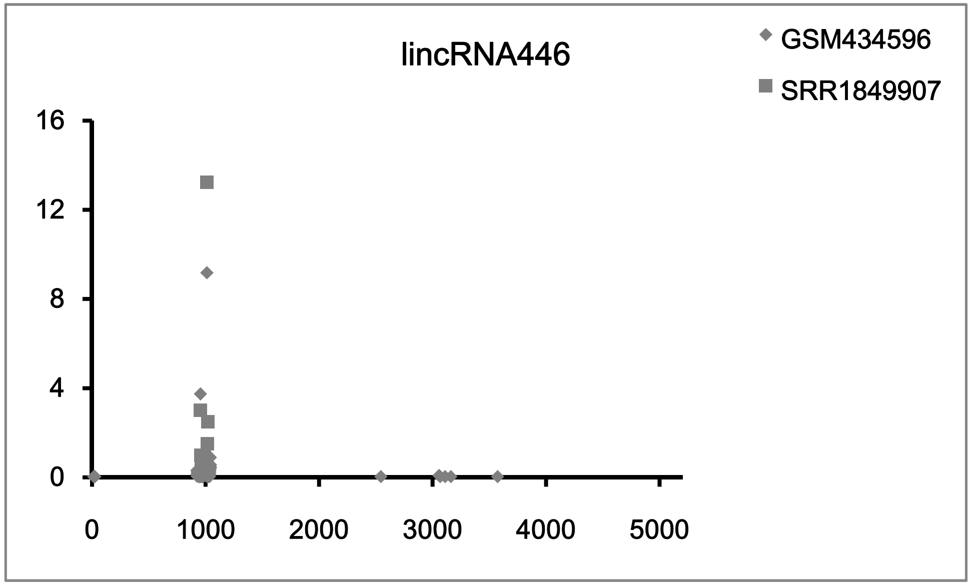

root-CK-high-2928
GSM1040649
64
48
32
16
0
13324
13334
13344
13354
13364
13374
13384

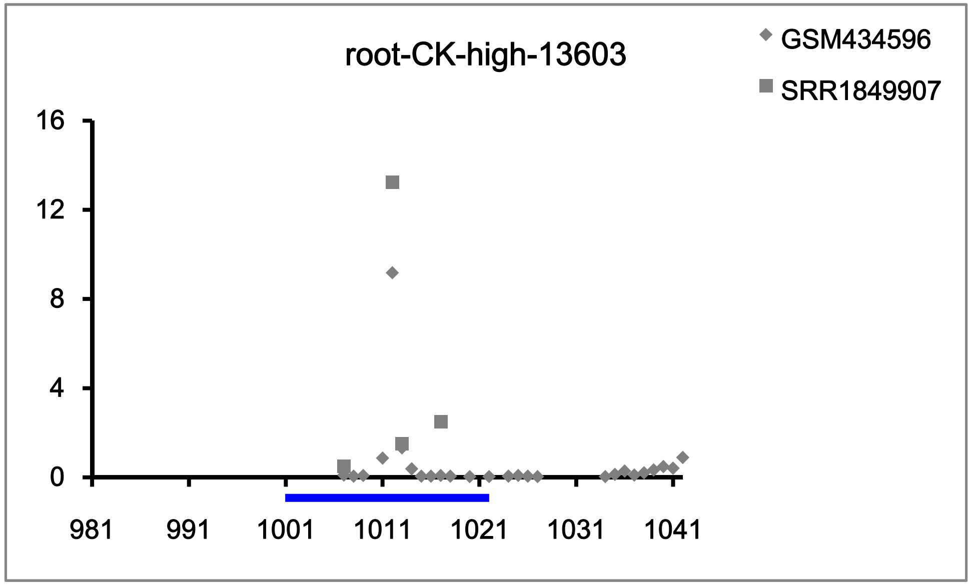

lincRNA431
GSM1040649
SRR1849907
60
45
30
15
0
0
1000
2000
3000
4000
5000
6000
7000

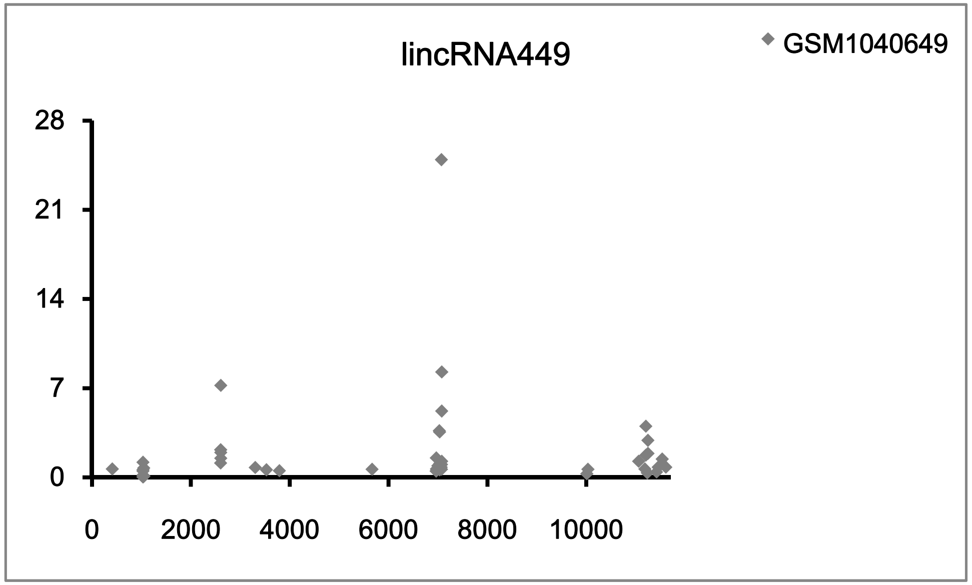

root-CK-high-2928
GSM1040649
SRR1849907
60
45
30
15
0
5760
5770
5780
5790
5800
5810
5820

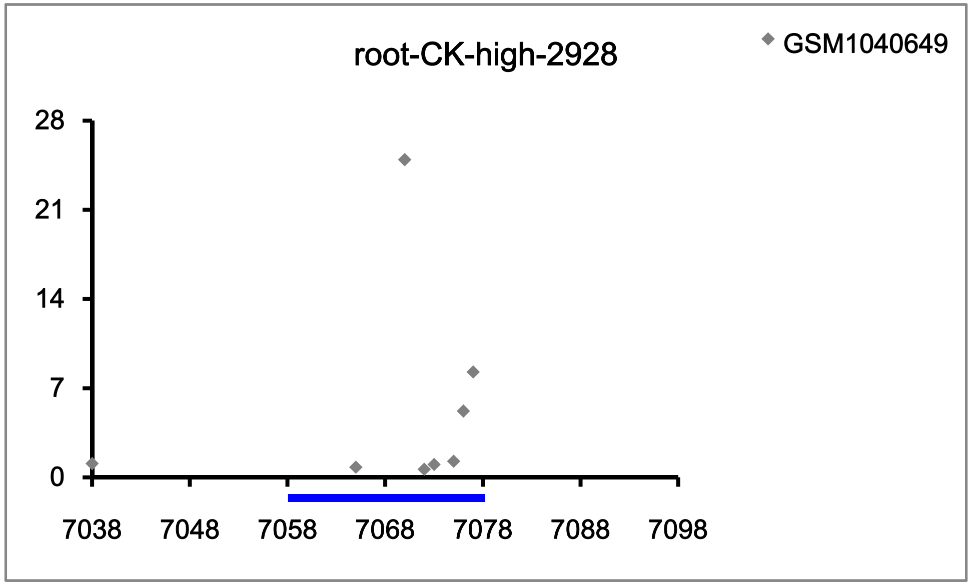

lincRNA445
SRR1849906
0
1
2
3
4
0
1000
2000
3000
4000
5000
6000

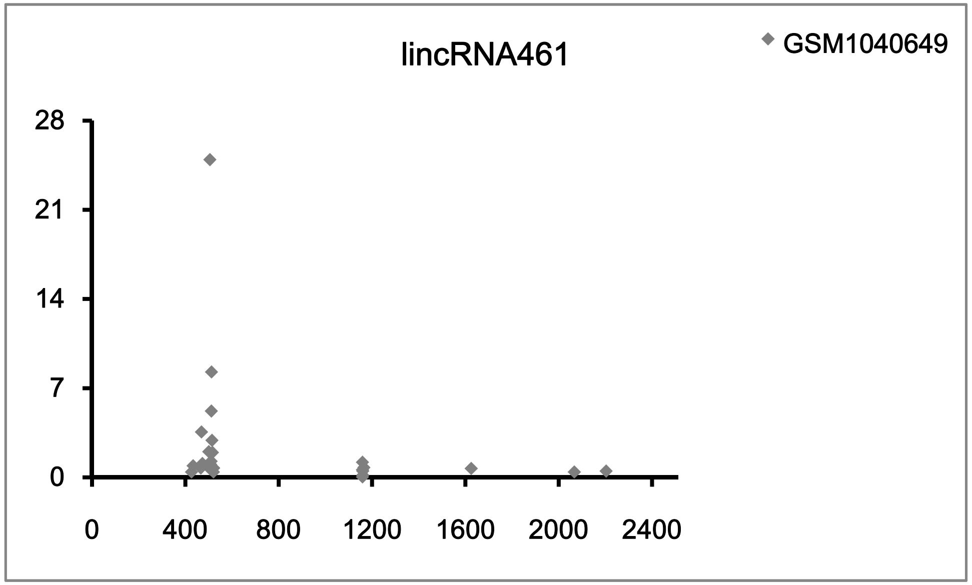

root-CK-high-2928
SRR1849906
0
1
2
3
4
4452
4462
4472
4482
4492
4502
4512

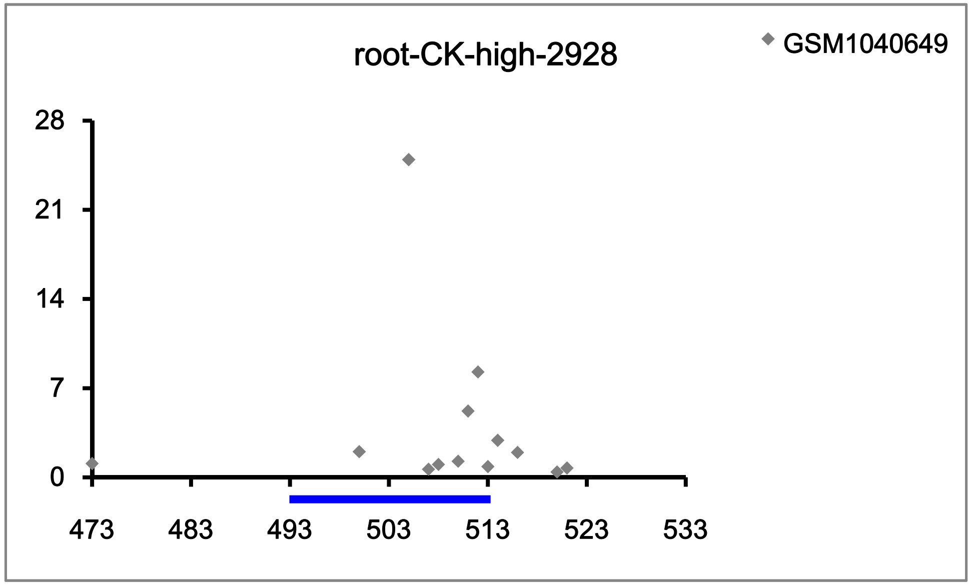

lincRNA446
GSM434596
SRR1849907
0
4
8
12
16
0
1000
2000
3000
4000
5000

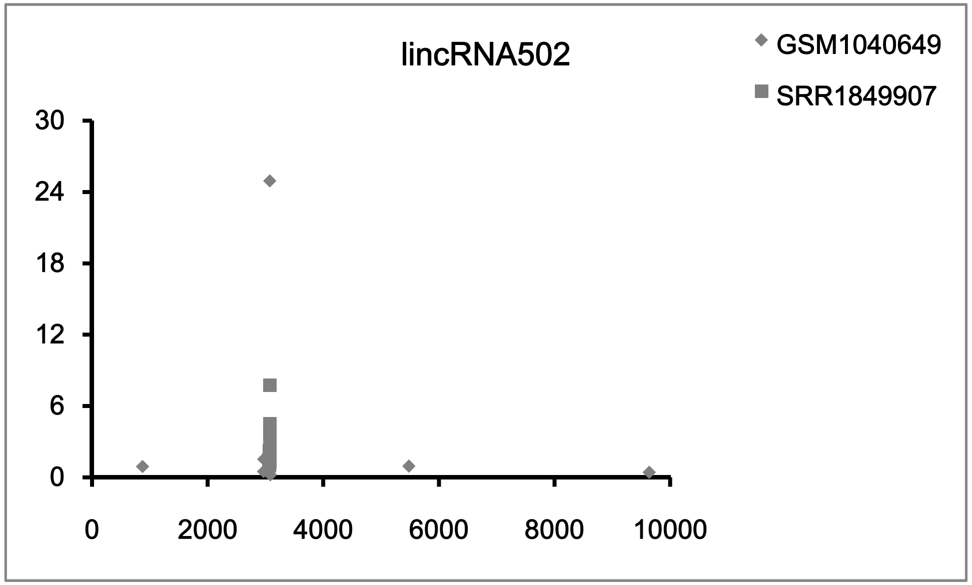

root-CK-high-13603
GSM434596
SRR1849907
0
4
8
12
16
981
991
1001
1011
1021
1031
1041

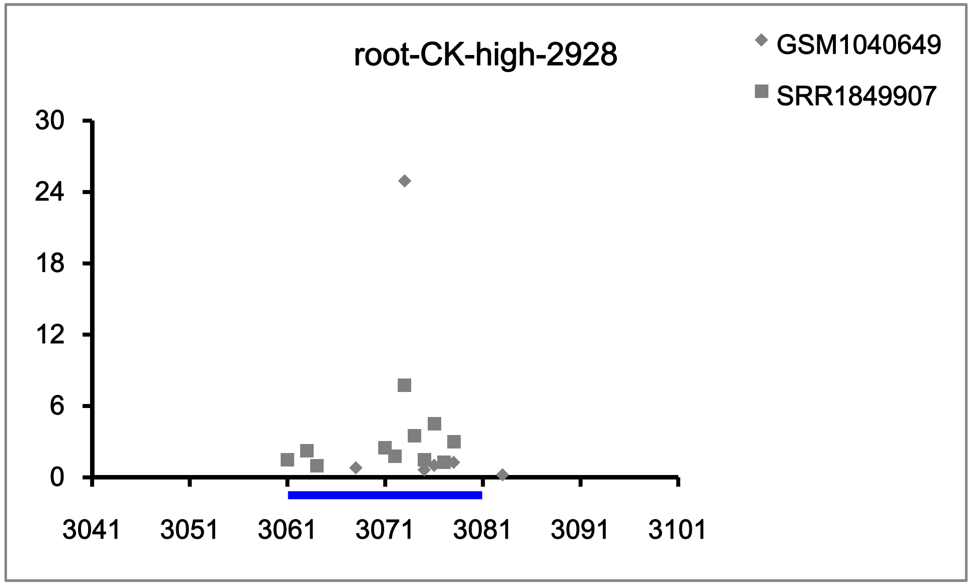

lincRNA449
GSM1040649
28
21
14
7
0
0
2000
4000
6000
8000
10000

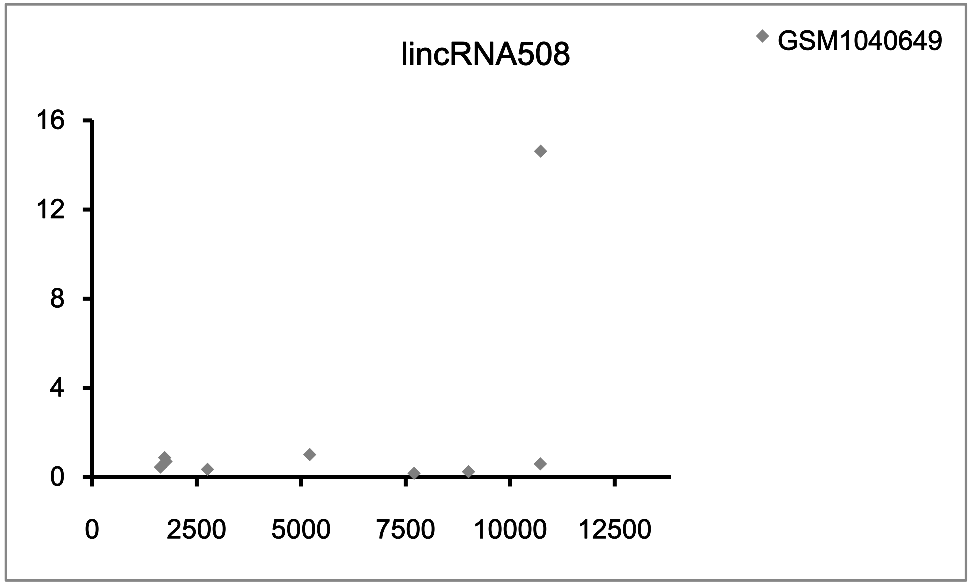

root-CK-high-2928
GSM1040649
28
21
14
7
0
7038
7048
7058
7068
7078
7088
7098

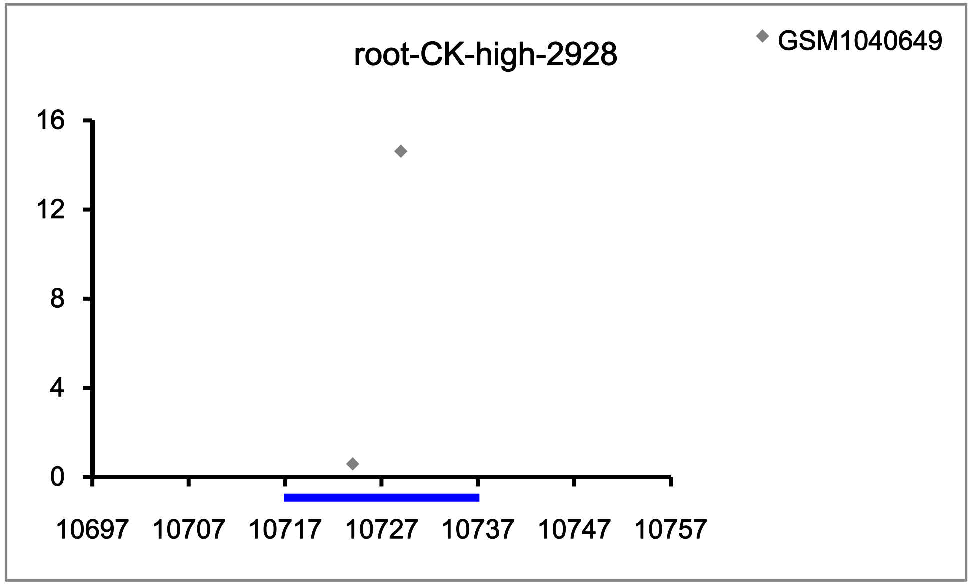

lincRNA461
GSM1040649
28
21
14
7
0
0
400
800
1200
1600
2000
2400

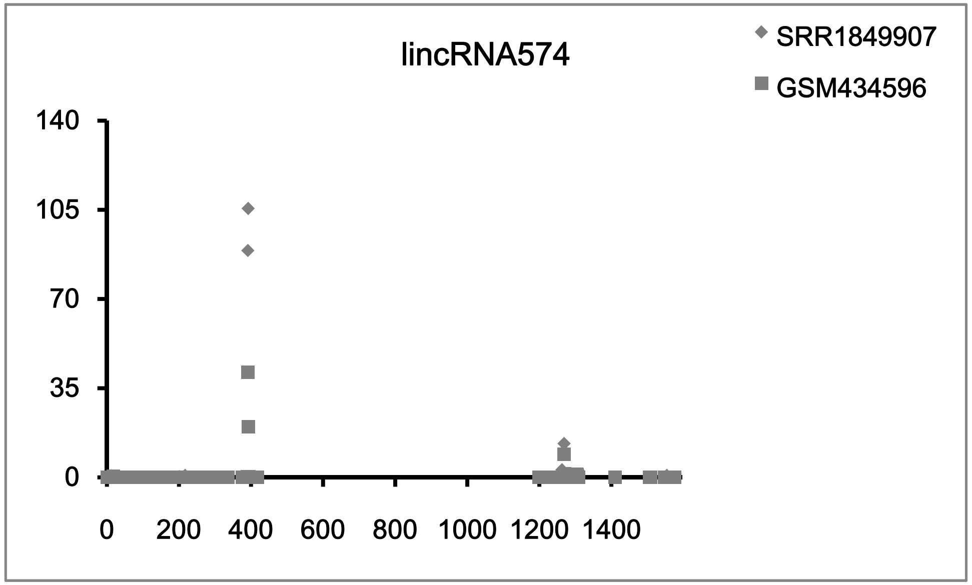

root-CK-high-2928
GSM1040649
28
21
14
7
0
473
483
493
503
513
523
533

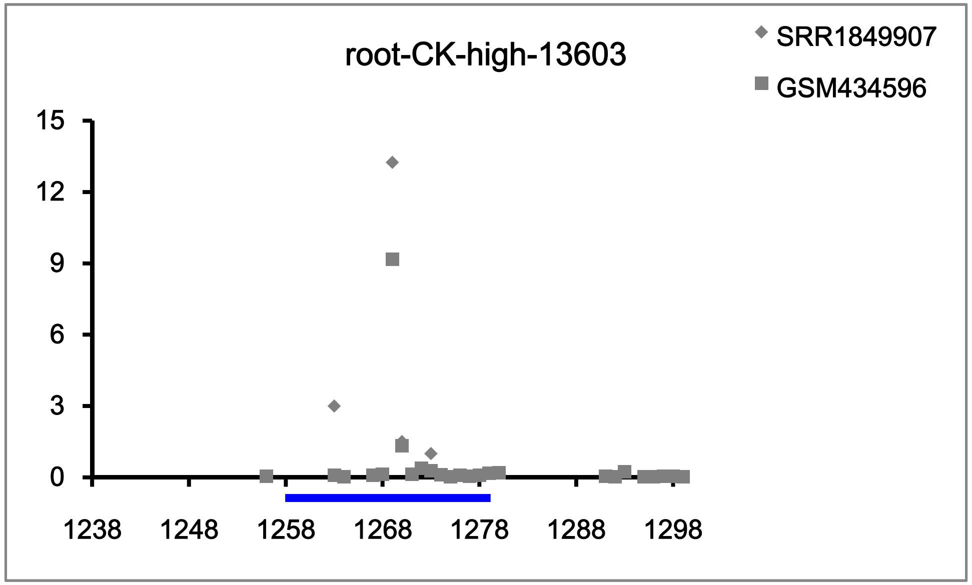

lincRNA502
GSM1040649
SRR1849907
30
24
18
12
6
0
0
2000
4000
6000
8000
10000

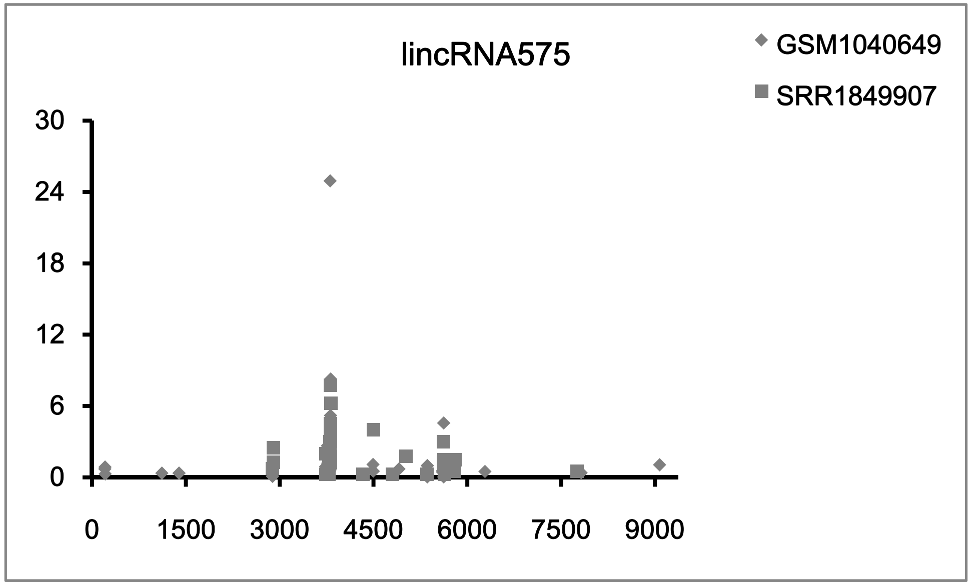

root-CK-high-2928
GSM1040649
SRR1849907
30
24
18
12
6
0
3041
3051
3061
3071
3081
3091
3101

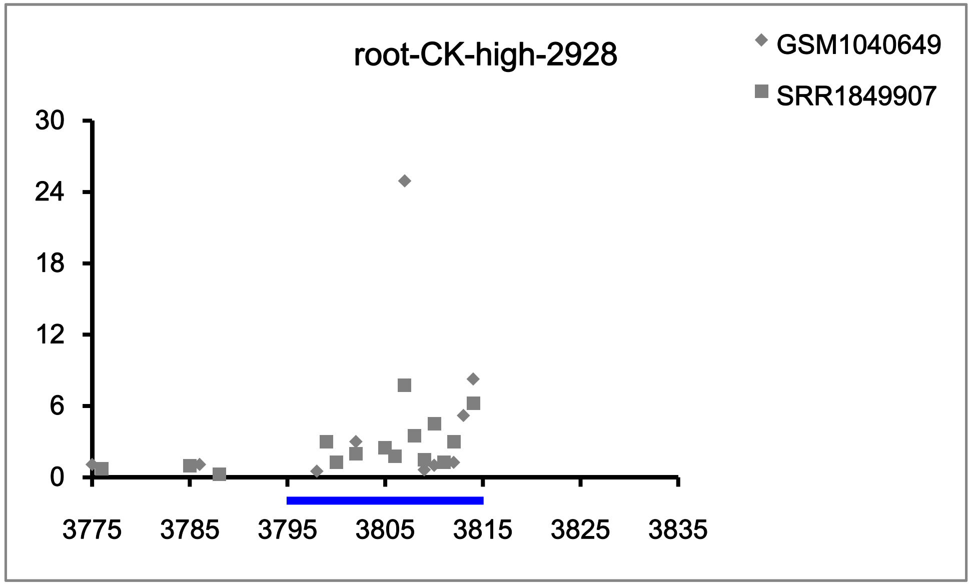

lincRNA508
GSM1040649
16
12
8
4
0
0
2500
5000
7500
10000
12500

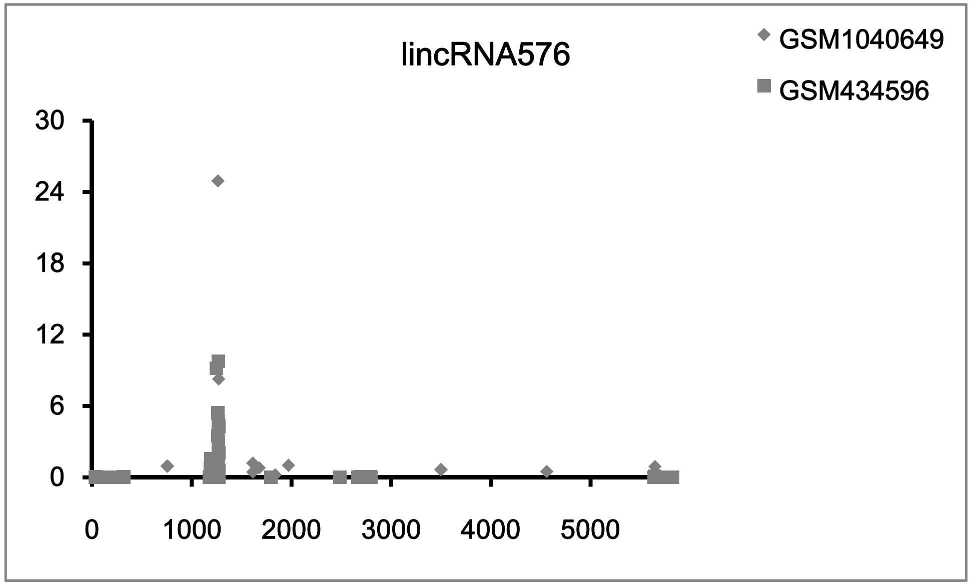

root-CK-high-2928
GSM1040649
16
12
8
4
0
10697
10707
10717
10727
10737
10747
10757

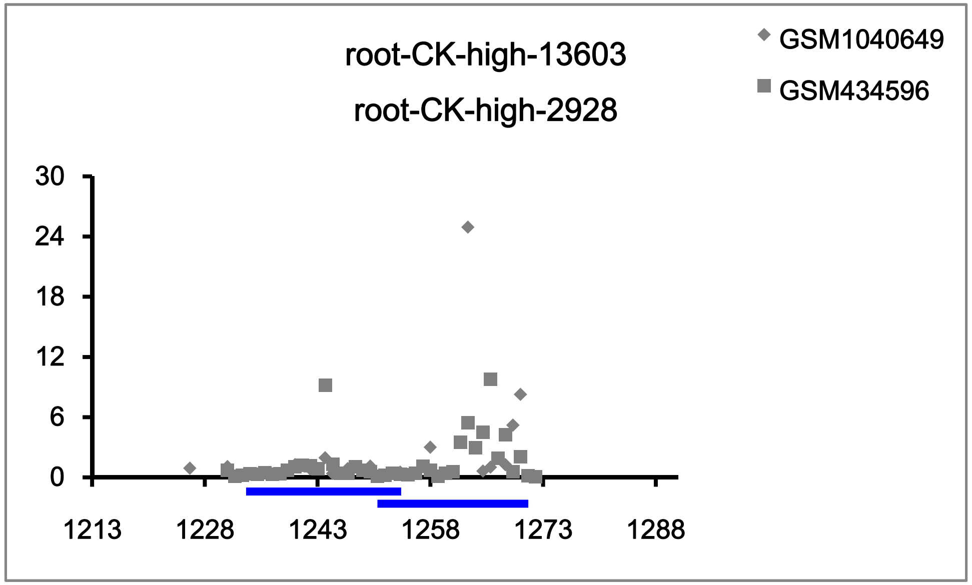

lincRNA574
◆ SRR1849907
■ GSM434596
140
105
70
35
0
0
200
400
600
800
1000
1200
1400

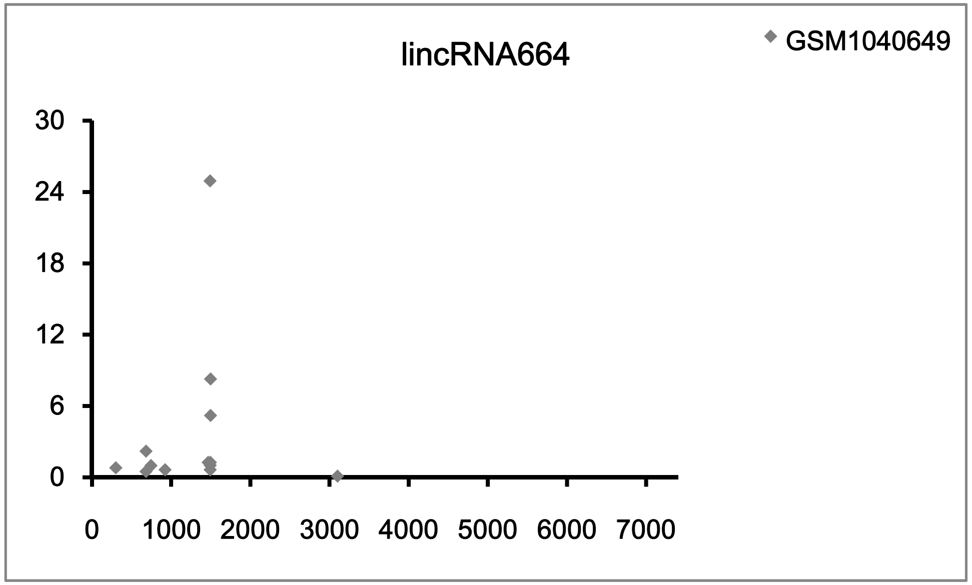

root-CK-high-13603
◆ SRR1849907
■ GSM434596
15
12
9
6
3
0
1238
1248
1258
1268
1278
1288
1298

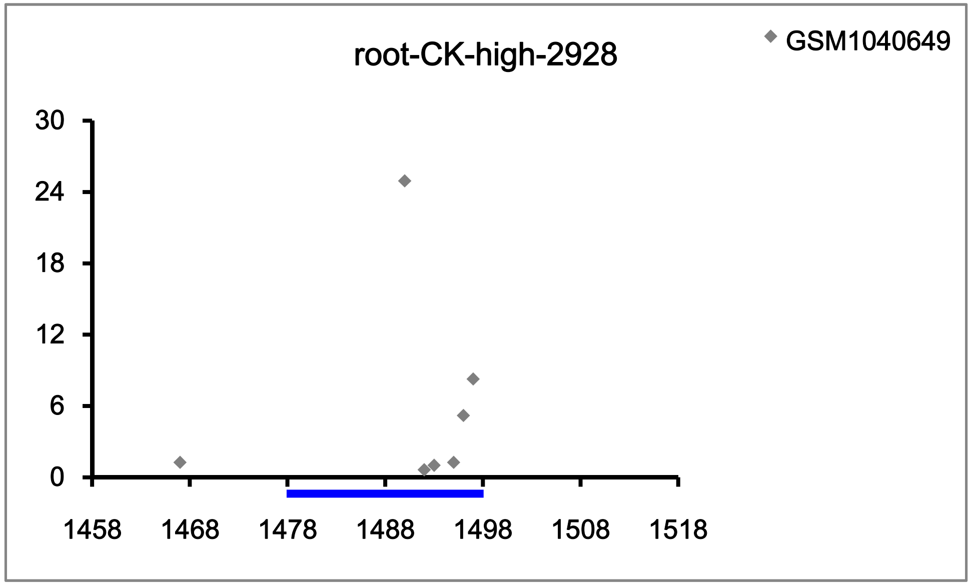

lincRNA575
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
0
1500
3000
4500
6000
7500
9000

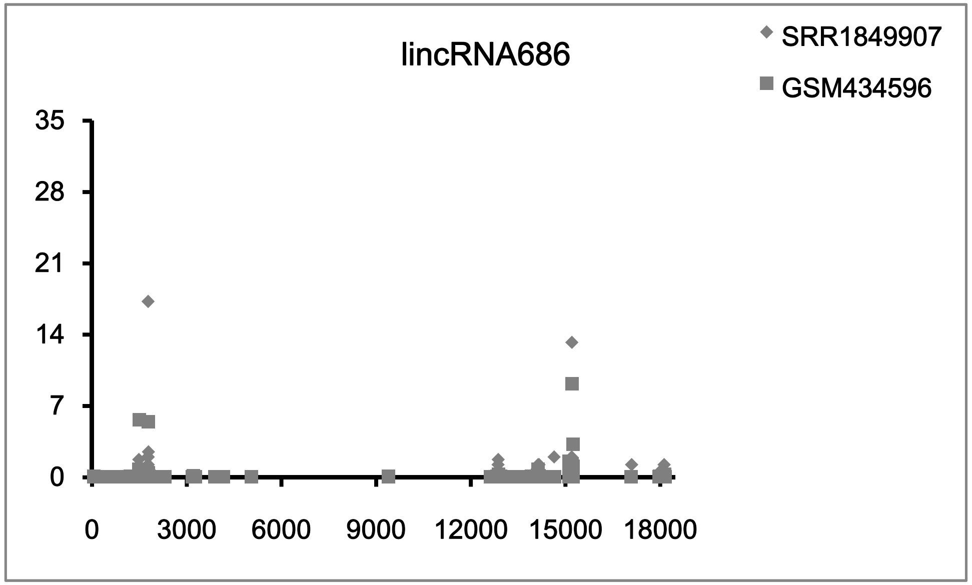

root-CK-high-2928
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
3775
3785
3795
3805
3815
3825
3835

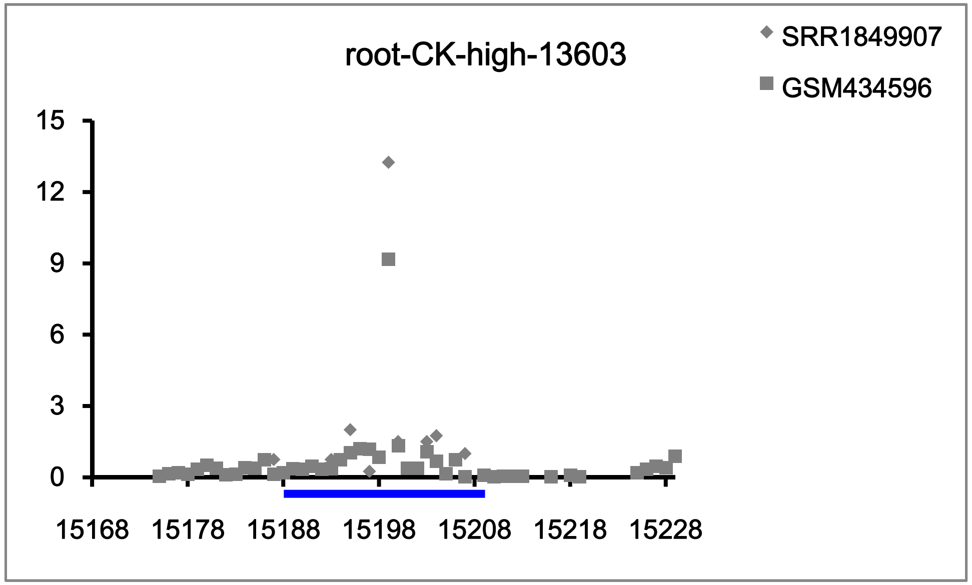

lincRNA576
GSM1040649
GSM434596
30
24
18
12
6
0
0
1000
2000
3000
4000
5000

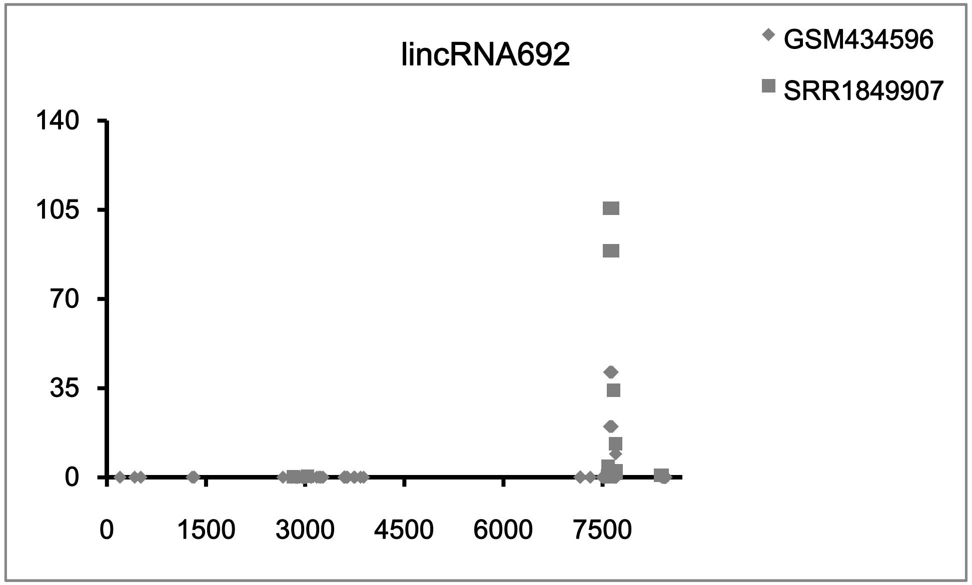

root-CK-high-13603
root-CK-high-2928
GSM1040649
GSM434596
30
24
18
12
6
0
1213
1228
1243
1258
1273
1288

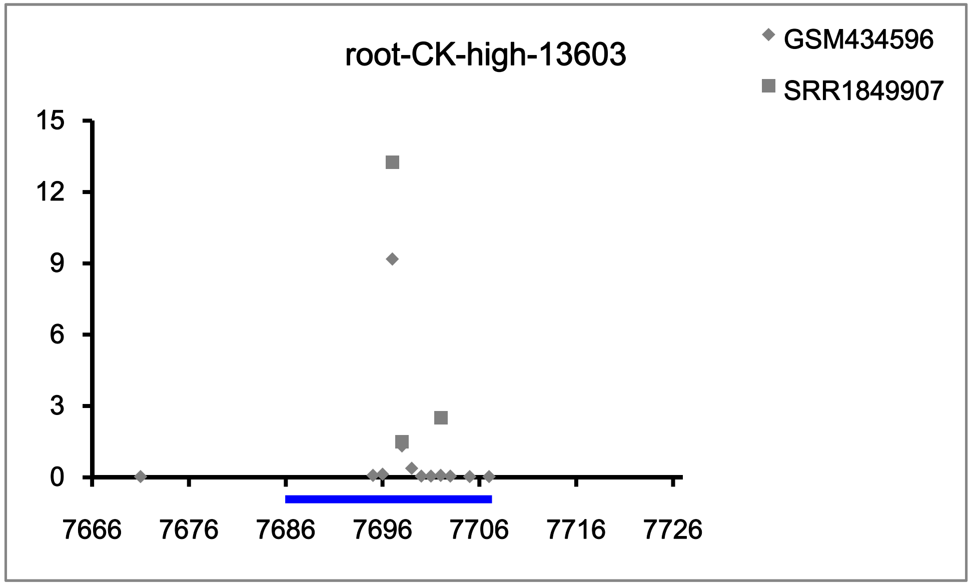

lincRNA664
GSM1040649
30
24
18
12
6
0
0
1000
2000
3000
4000
5000
6000
7000

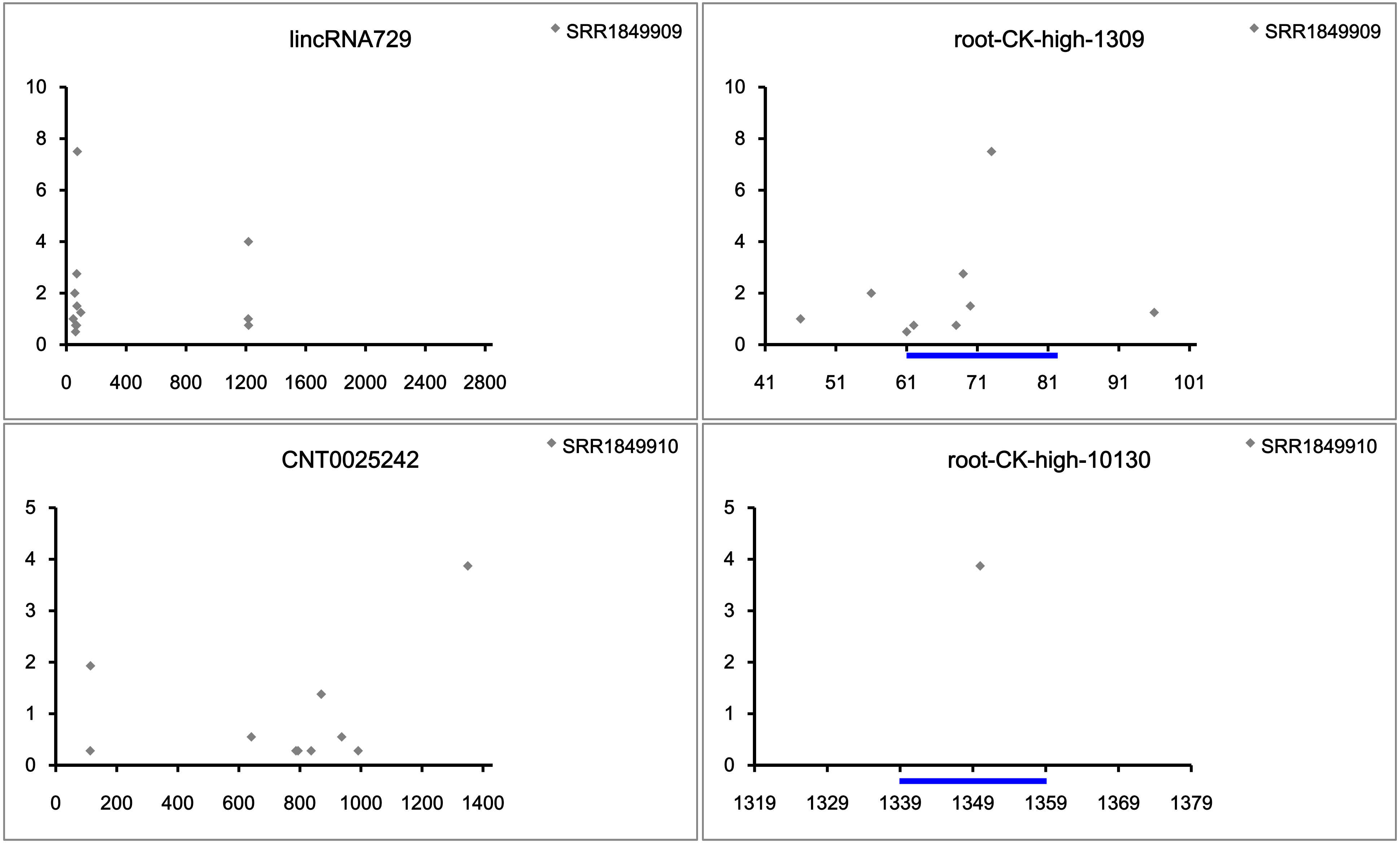

root-CK-high-2928
GSM1040649
30
24
18
12
6
0
1458
1468
1478
1488
1498
1508
1518

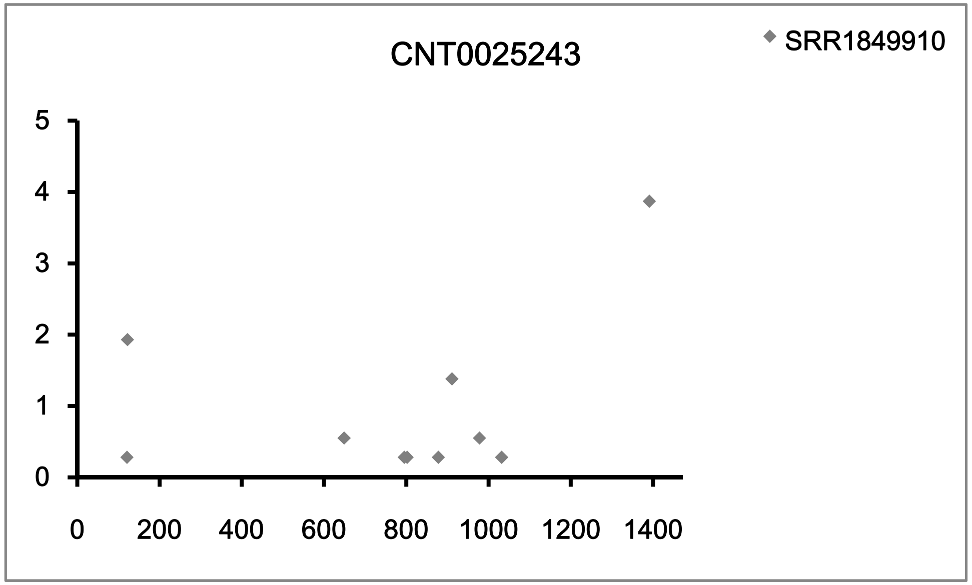

lincRNA686
◆ SRR1849907
■ GSM434596
35
28
21
14
7
0
0
3000
6000
9000
12000
15000
18000

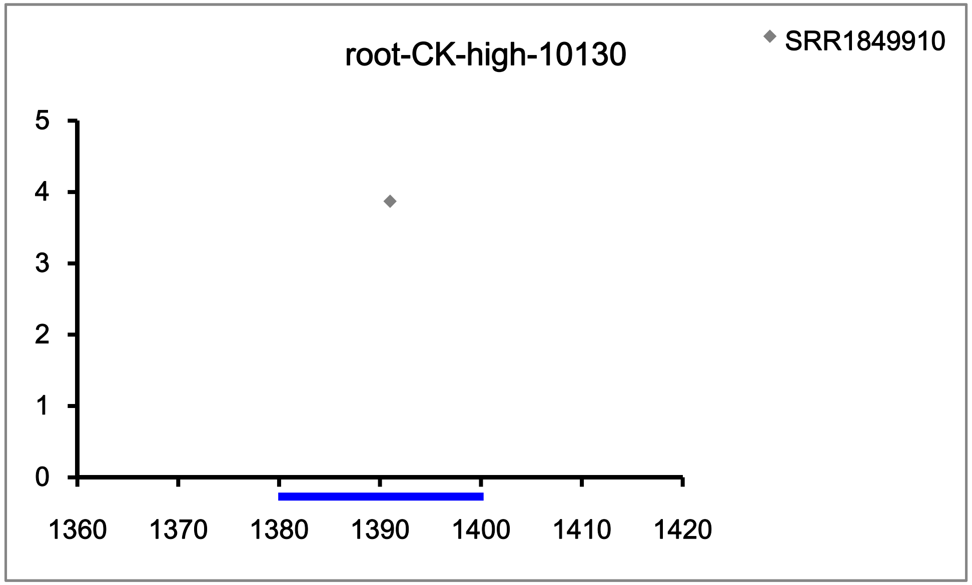

root-CK-high-13603
◆ SRR1849907
■ GSM434596
15
12
9
6
3
0
15168
15178
15188
15198
15208
15218
15228

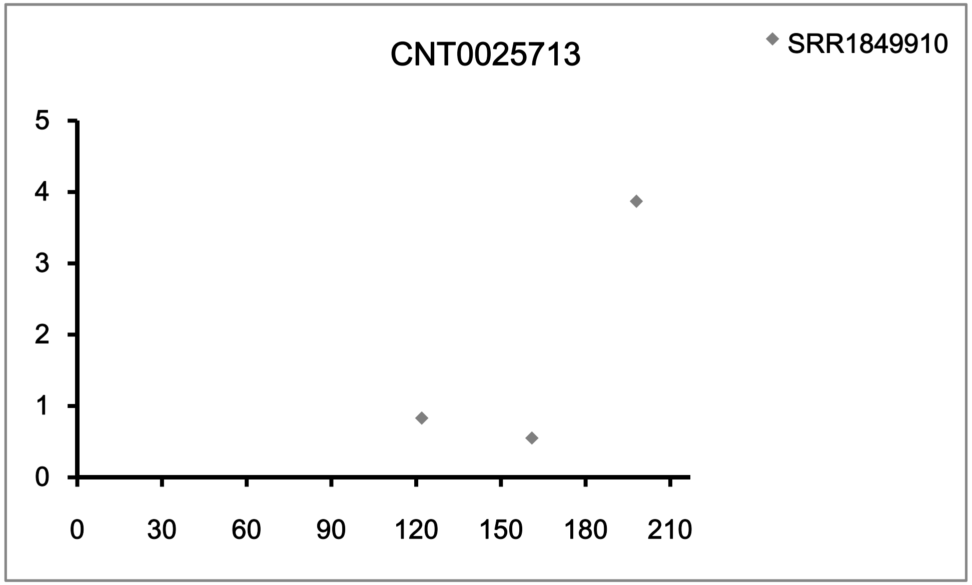

lincRNA692
◆ GSM434596
■ SRR1849907
140
105
70
35
0
0
1500
3000
4500
6000
7500

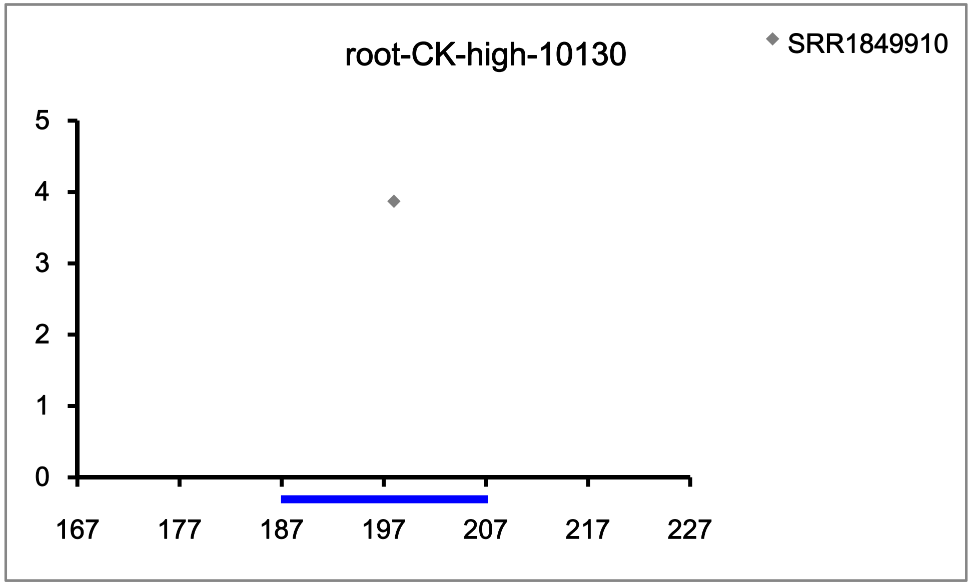

root-CK-high-13603
◆ GSM434596
■ SRR1849907
15
12
9
6
3
0
7666
7676
7686
7696
7706
7716
7726

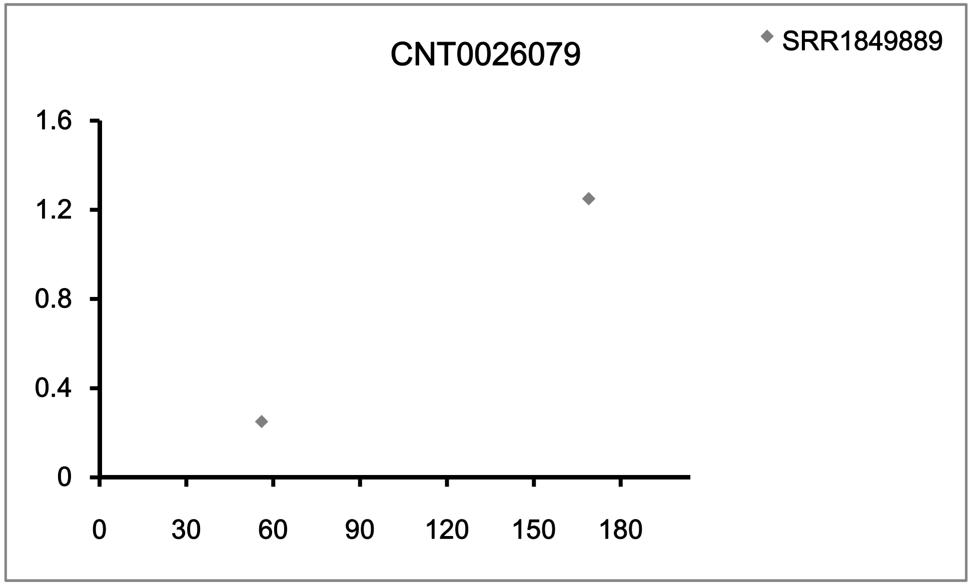

lincRNA729
SRR1849909
10
8
6
4
2
0
0
400
800
1200
1600
2000
2400
2800
root-CK-high-1309
SRR1849909
10
8
6
4
2
0
41
51
61
71
81
91
101
CNT0025242
SRR1849910
5
4
3
2
1
0
0
200
400
600
800
1000
1200
1400
root-CK-high-10130
SRR1849910
5
4
3
2
1
0
1319
1329
1339
1349
1359
1369
1379

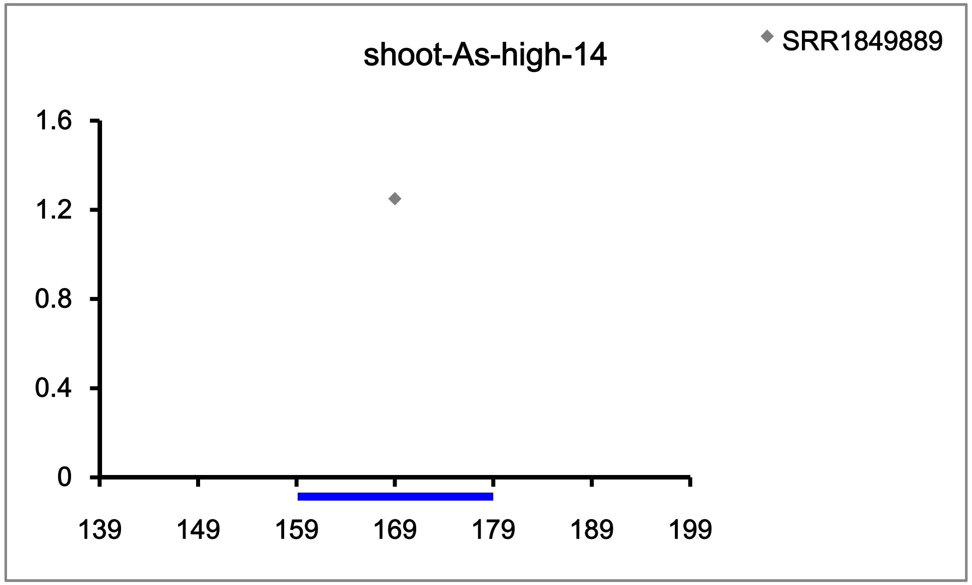

CNT0025243

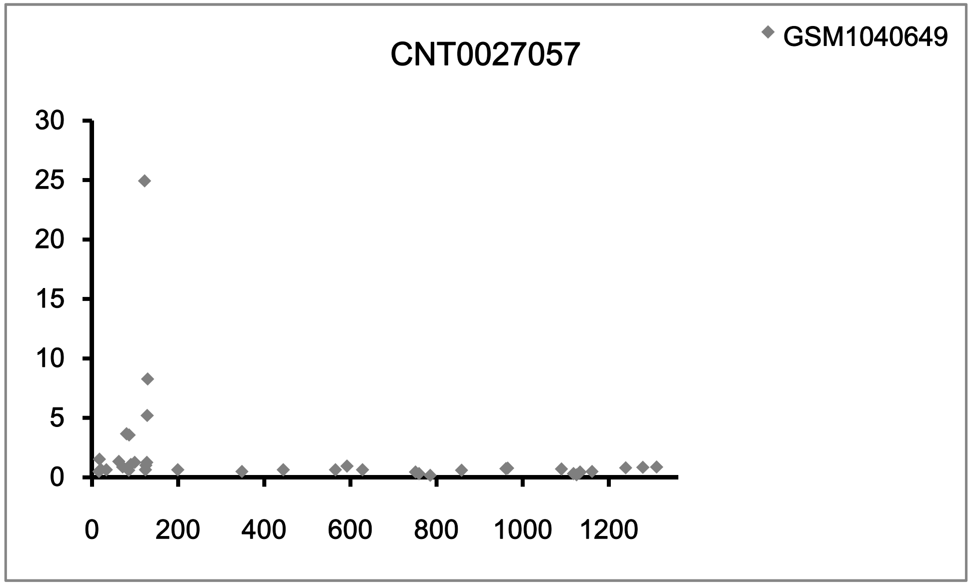

root-CK-high-10130

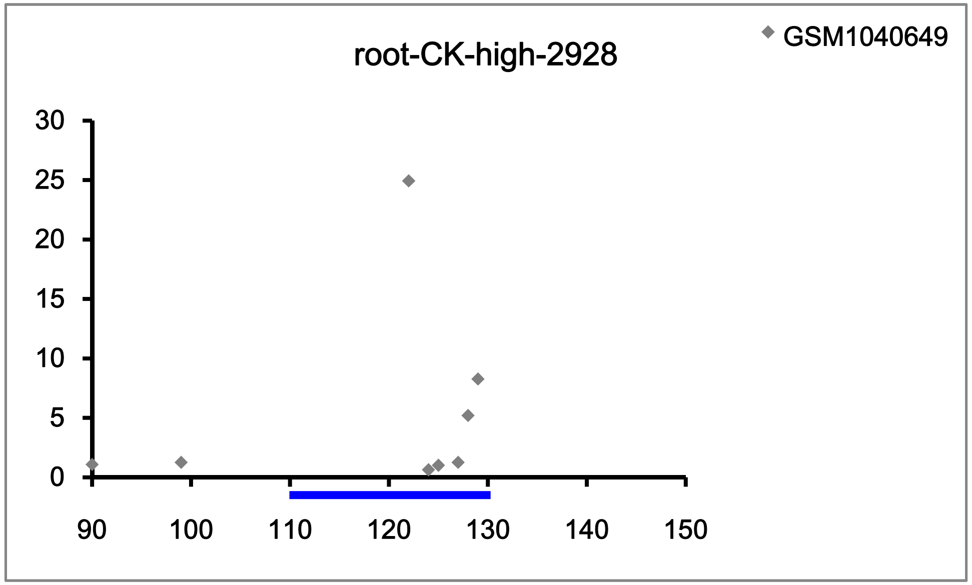

CNT0025713

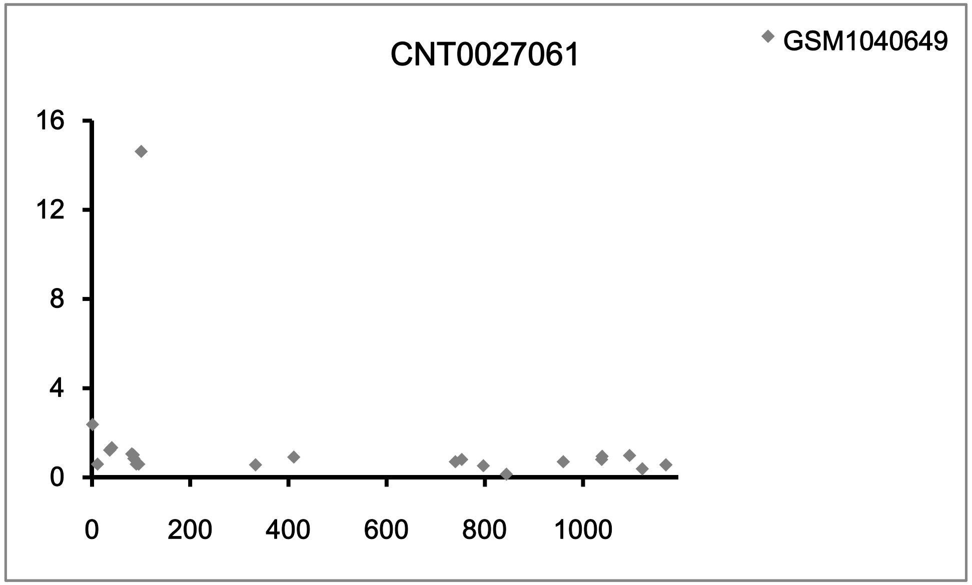

root-CK-high-10130

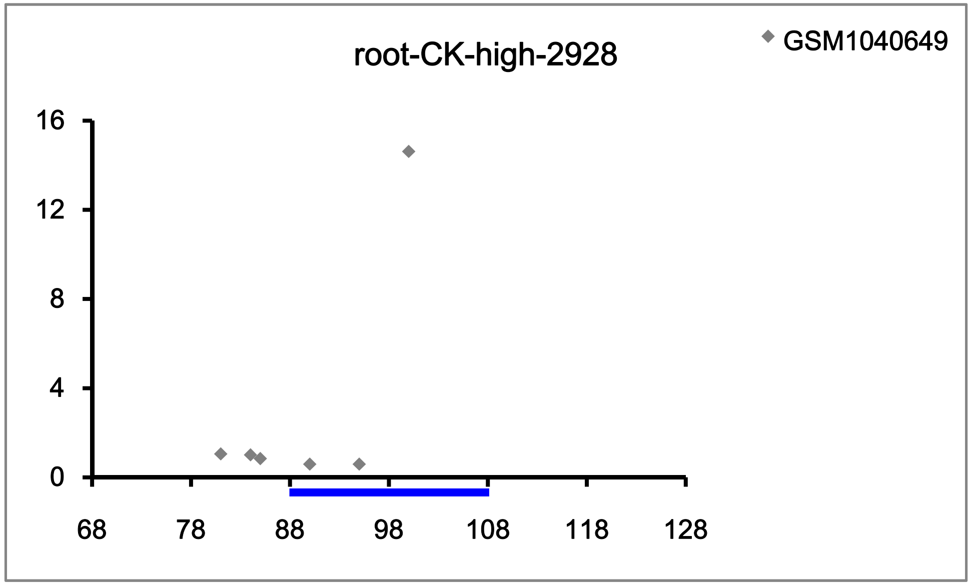

CNT0026079
SRR1849889
1.6
1.2
0.8
0.4
0
0
30
60
90
120
150
180

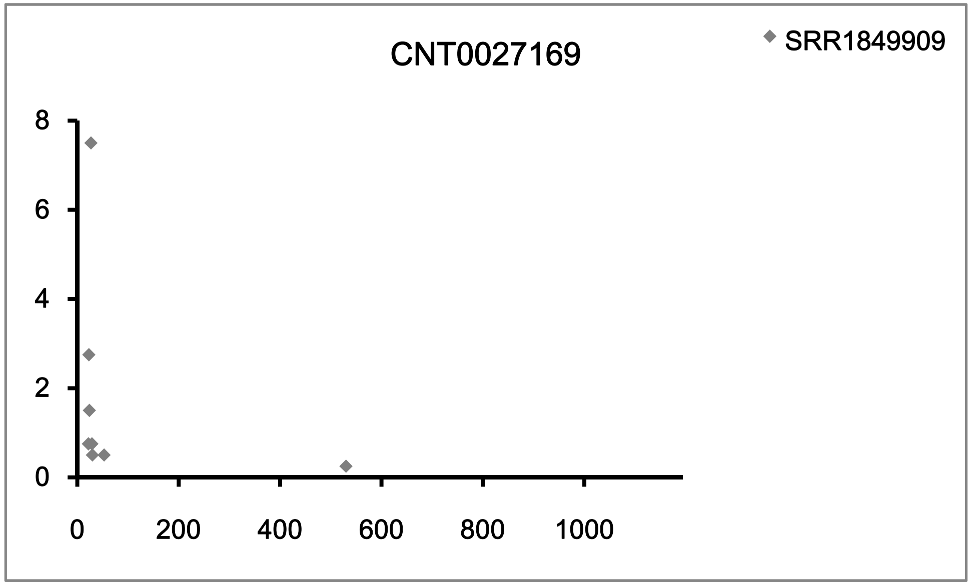

shoot-As-high-14
SRR1849889
1.6
1.2
0.8
0.4
0
139
149
159
169
179
189
199

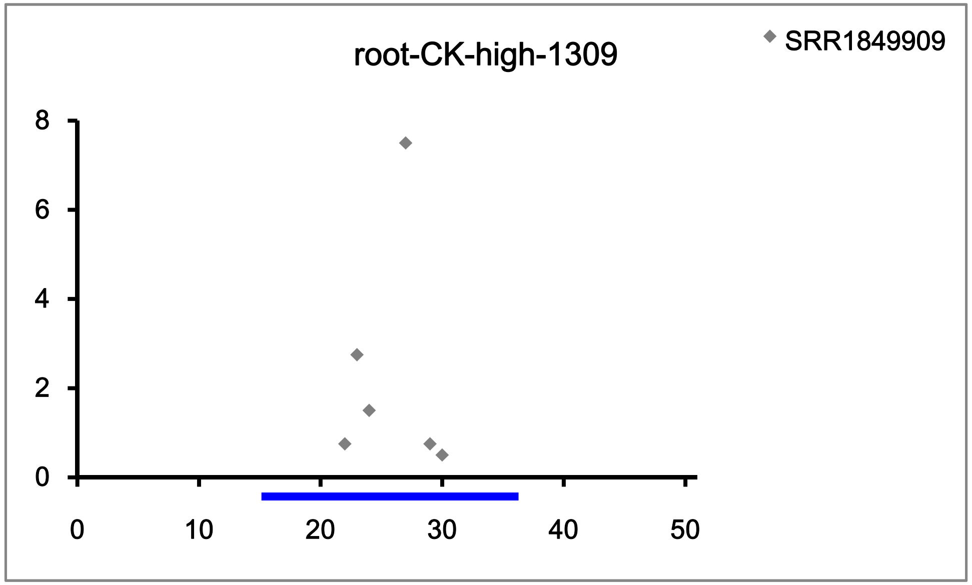

CNT0027057
GSM1040649
30
25
20
15
10
5
0
0
200
400
600
800
1000
1200

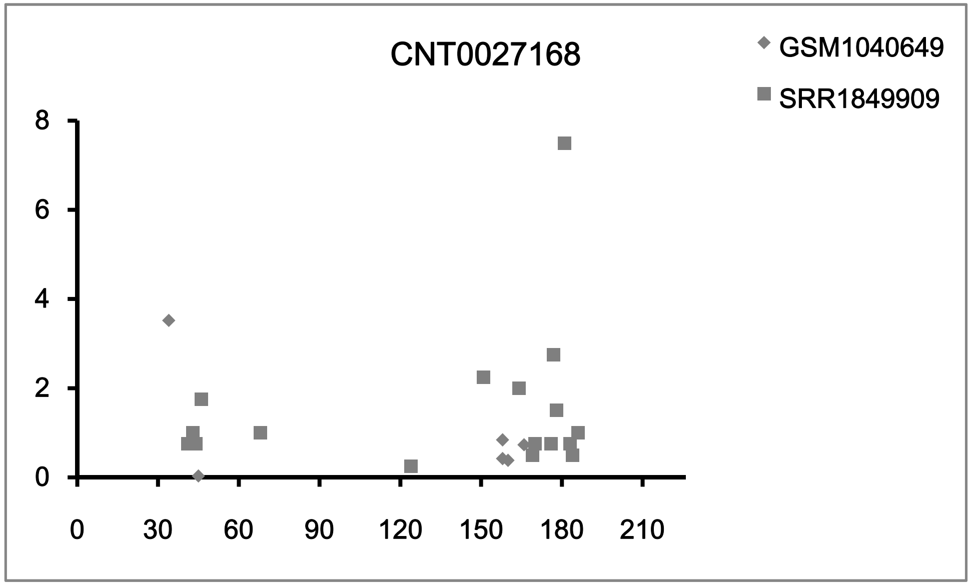

root-CK-high-2928
GSM1040649
30
25
20
15
10
5
0
90
100
110
120
130
140
150

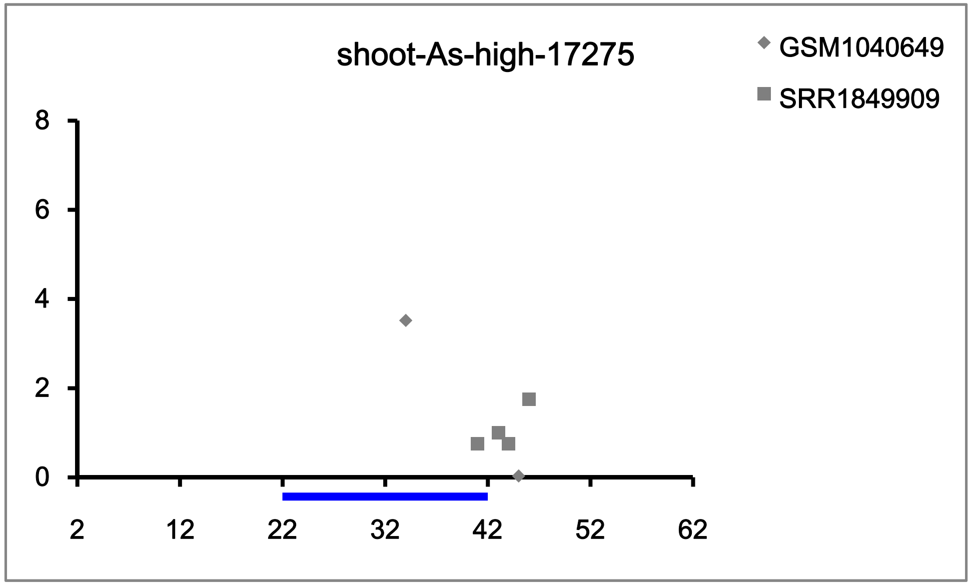

CNT0027061
GSM1040649
16
12
8
4
0
0
200
400
600
800
1000

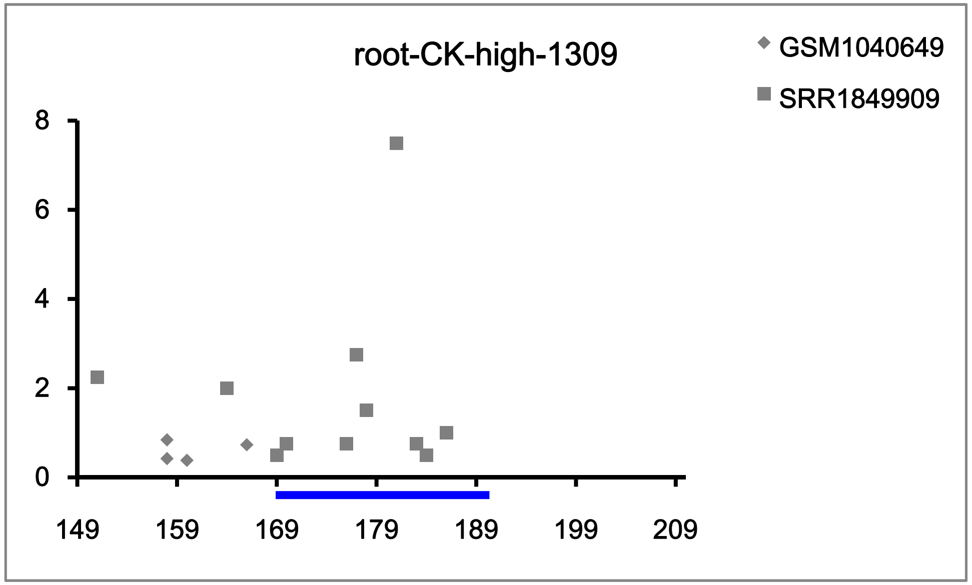

root-CK-high-2928
GSM1040649
16
12
8
4
0
68
78
88
98
108
118
128

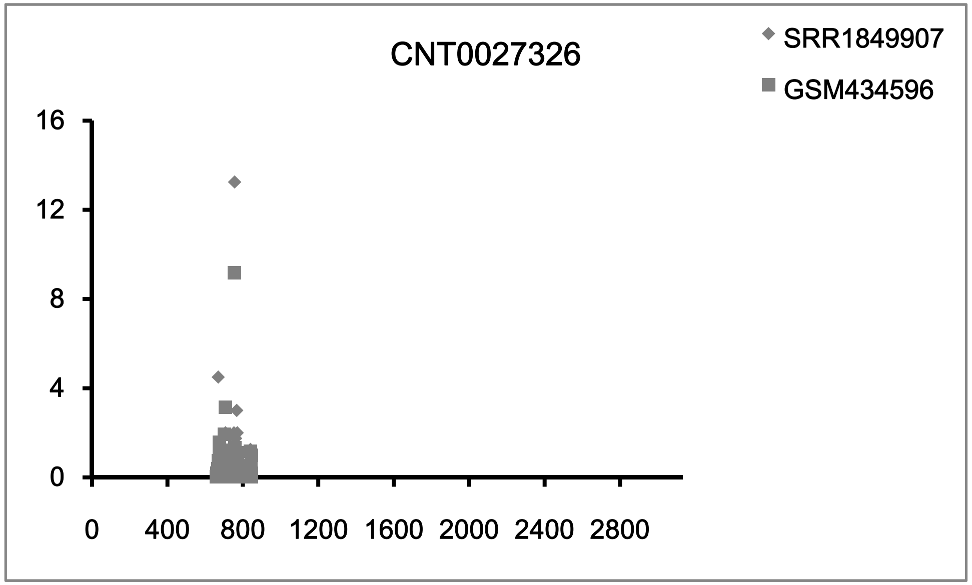

CNT0027169
SRR1849909
8
6
4
2
0
0
200
400
600
800
1000

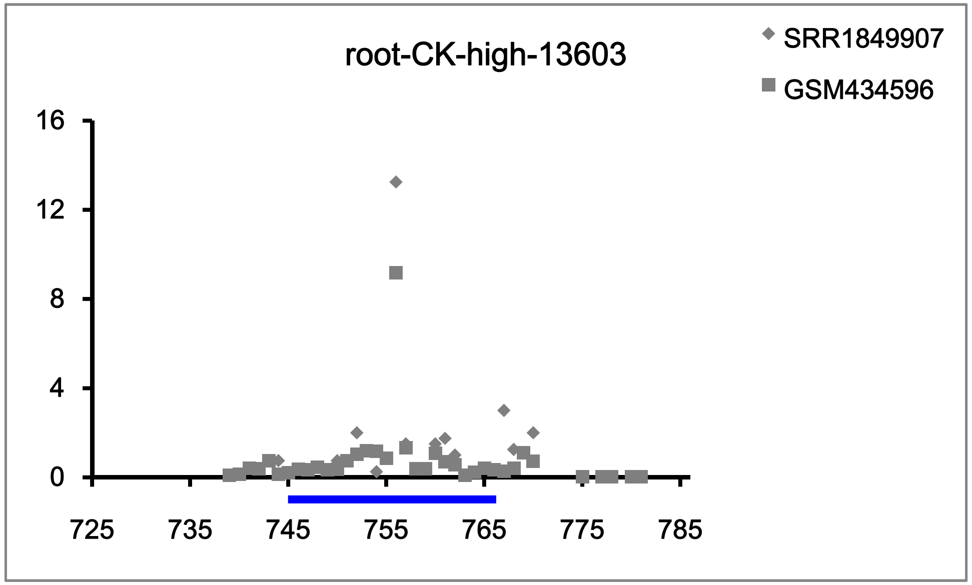

root-CK-high-1309
SRR1849909
8
6
4
2
0
0
10
20
30
40
50

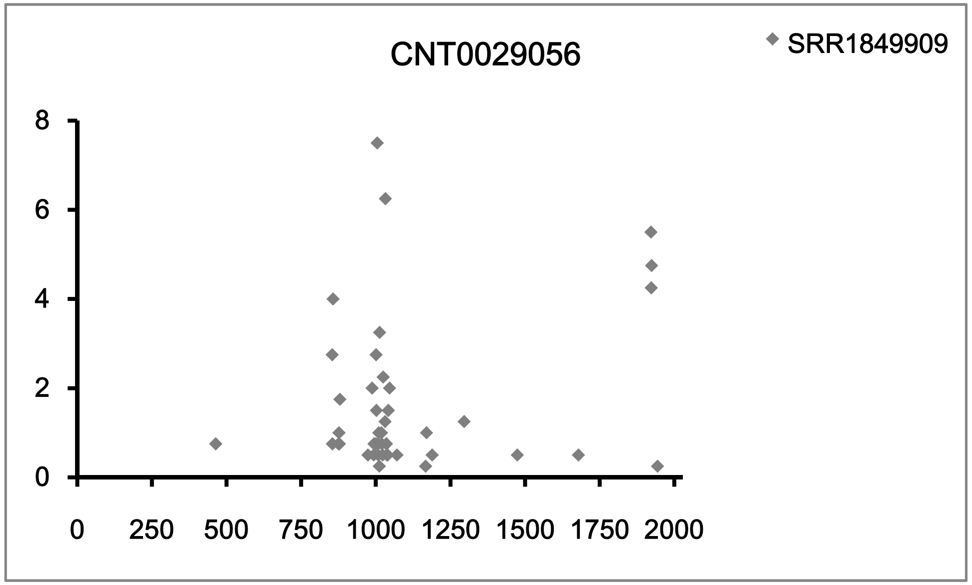

CNT0027168
◆ GSM1040649
■ SRR1849909
8
6
4
2
0
0
30
60
90
120
150
180
210

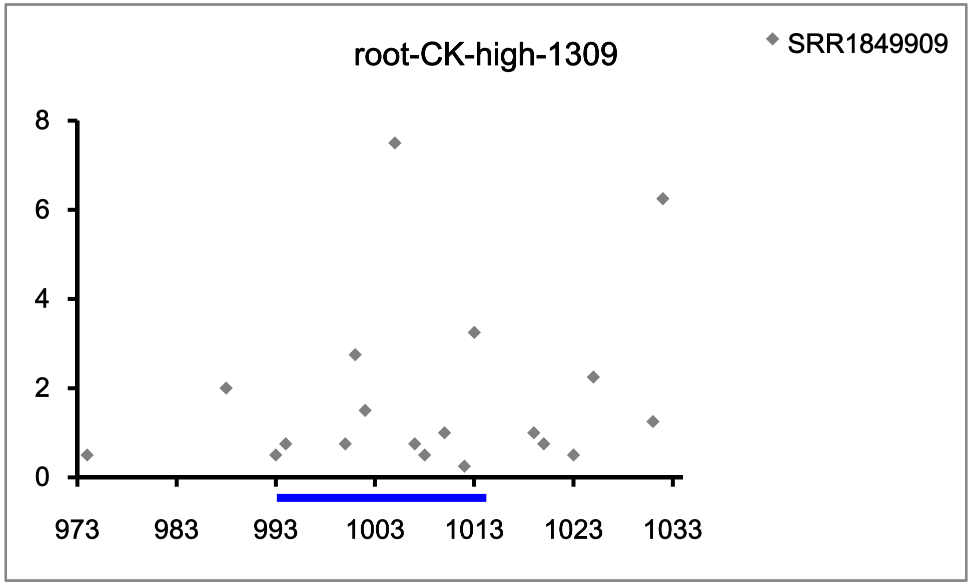

shoot-As-high-17275
◆ GSM1040649
■ SRR1849909
8
6
4
2
0
2
12
22
32
42
52
62

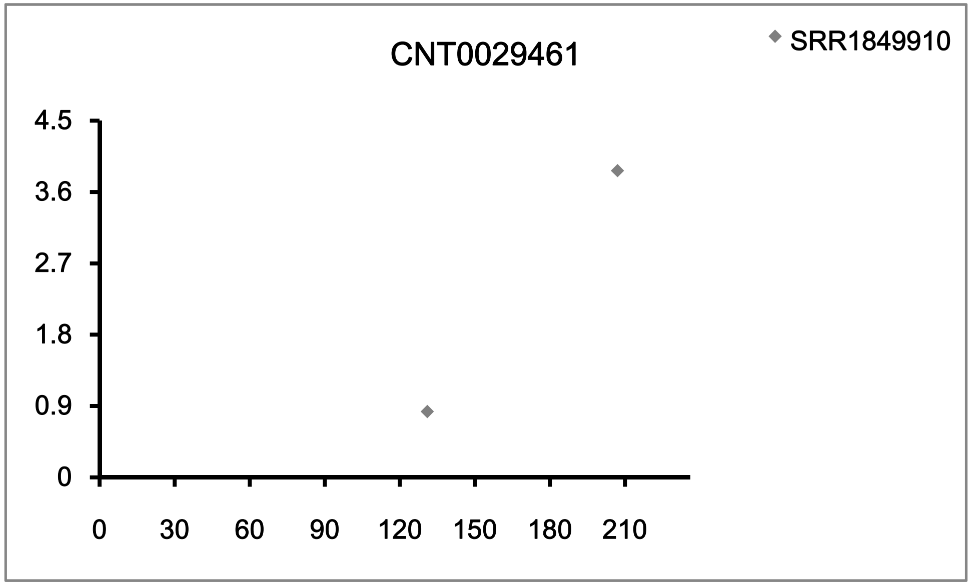

root-CK-high-1309
◆ GSM1040649
■ SRR1849909
8
6
4
2
0
149
159
169
179
189
199
209

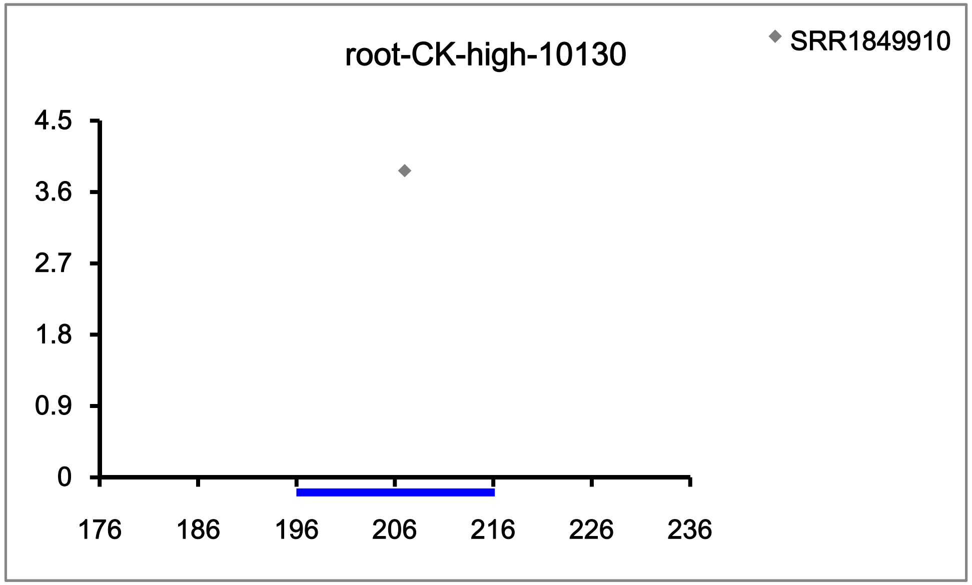

CNT0027326
SRR1849907
GSM434596
0
4
8
12
16
0
400
800
1200
1600
2000
2400
2800

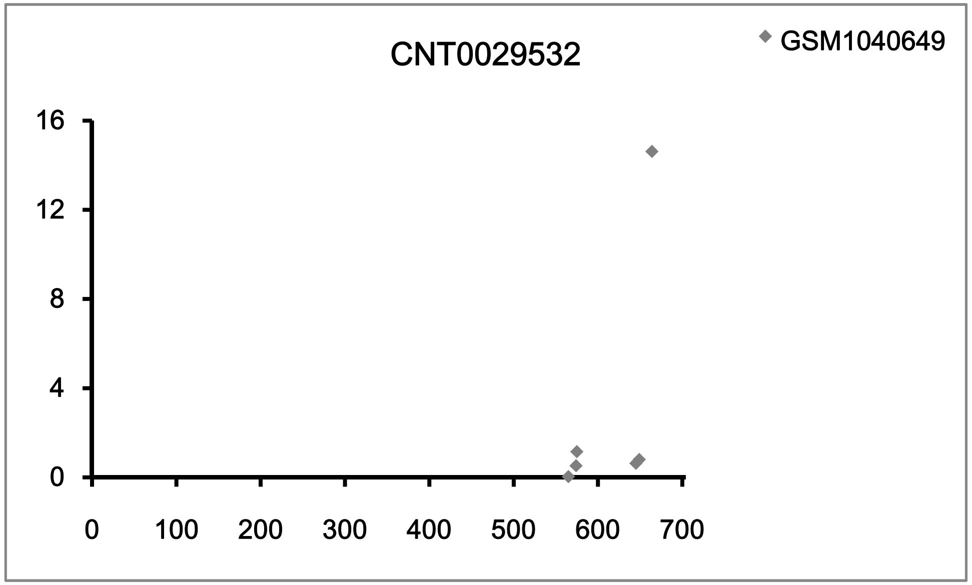

root-CK-high-13603
SRR1849907
GSM434596
0
4
8
12
16
725
735
745
755
765
775
785

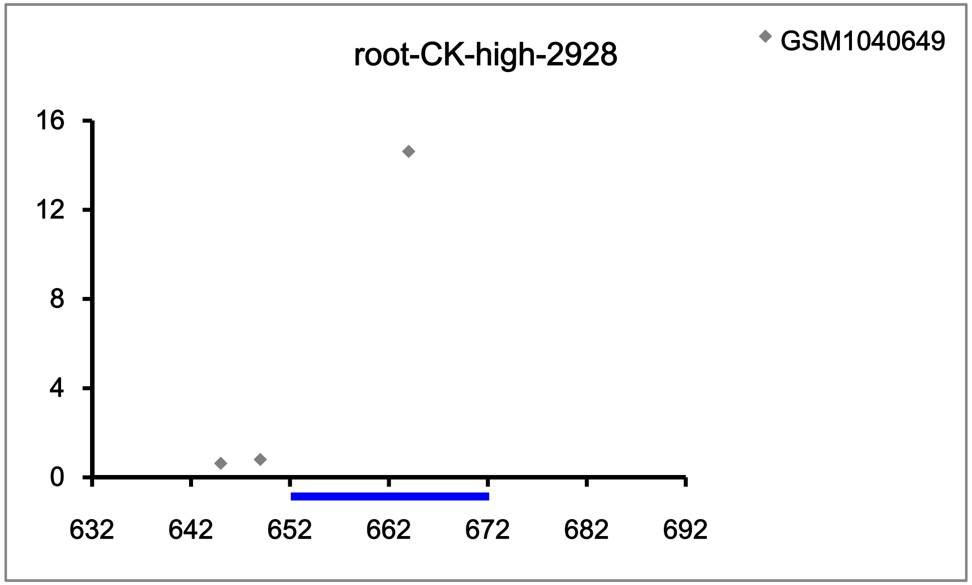

CNT0029056
SRR1849909
0
2
4
6
8
0
250
500
750
1000
1250
1500
1750
2000

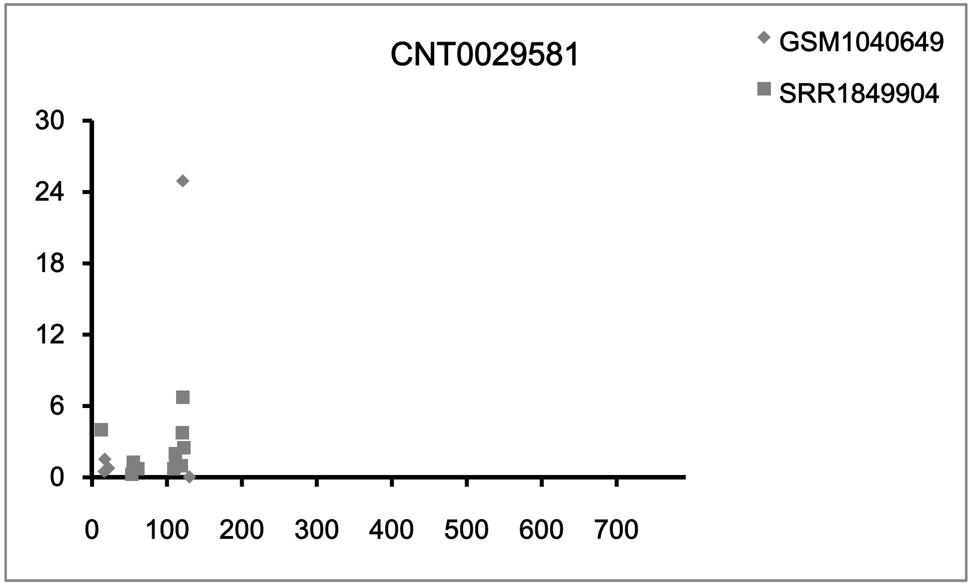

root-CK-high-1309
SRR1849909
0
2
4
6
8
973
983
993
1003
1013
1023
1033

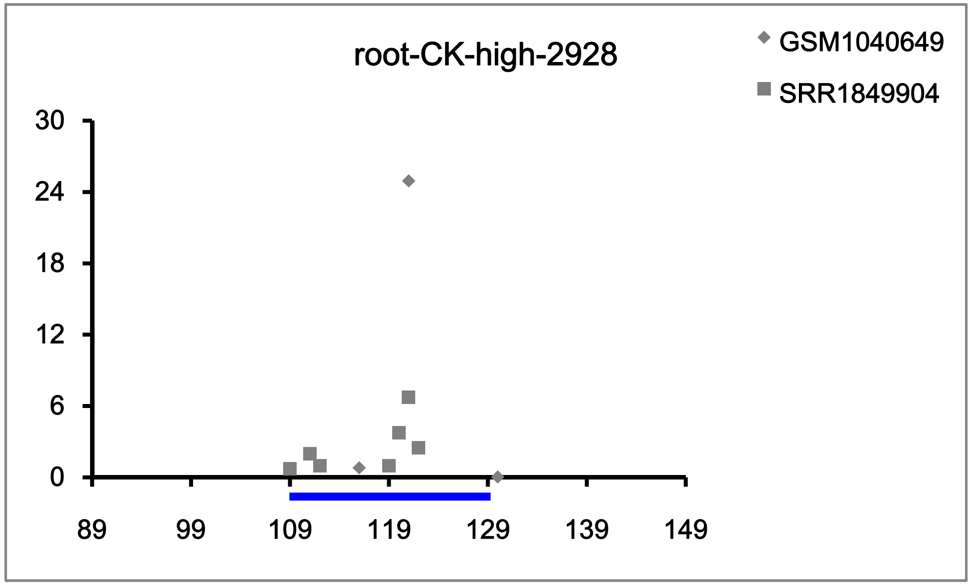

CNT0029461
SRR1849910
4.5
3.6
2.7
1.8
0.9
0
0
30
60
90
120
150
180
210

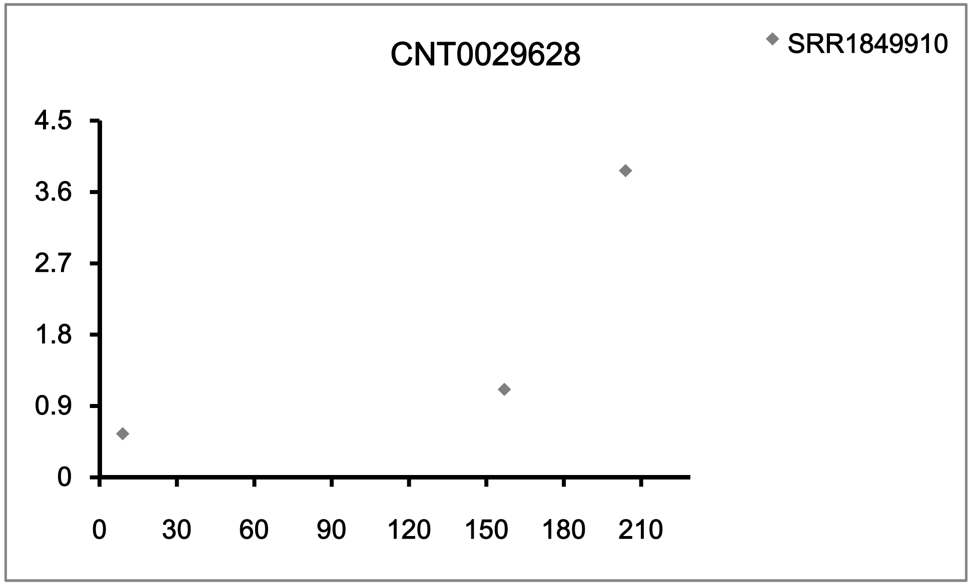

root-CK-high-10130
SRR1849910
4.5
3.6
2.7
1.8
0.9
0
176
186
196
206
216
226
236

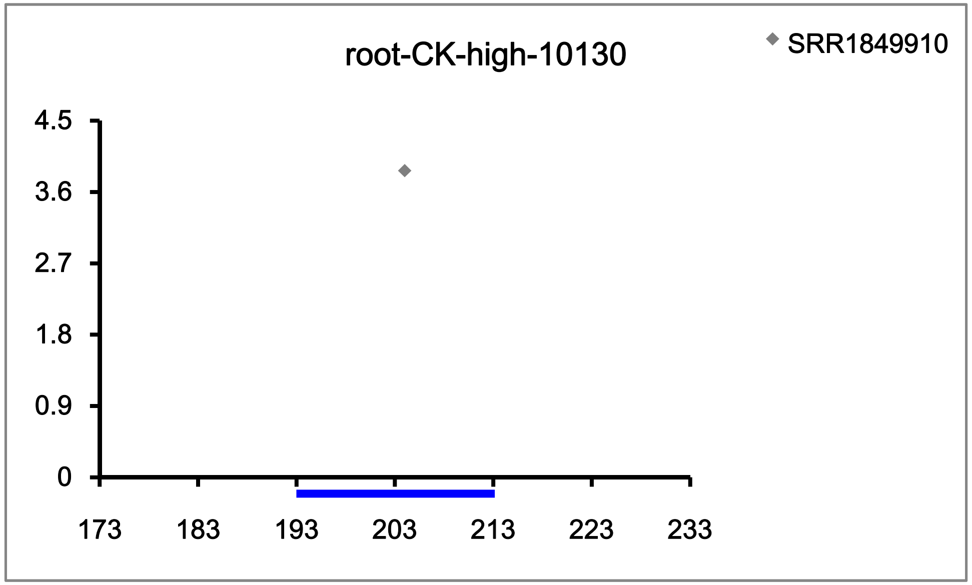

CNT0029532
GSM1040649
16
12
8
4
0
0
100
200
300
400
500
600
700

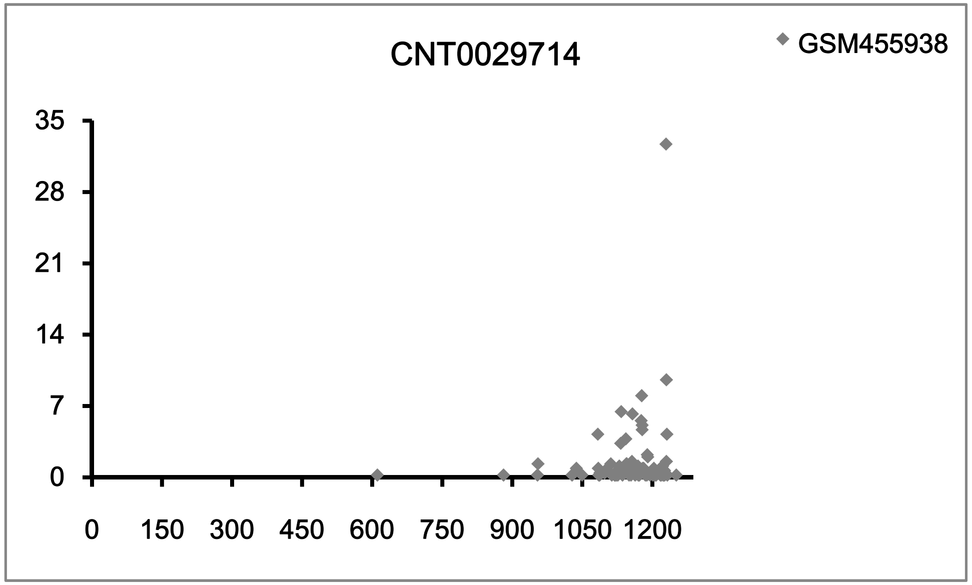

root-CK-high-2928
GSM1040649
16
12
8
4
0
632
642
652
662
672
682
692

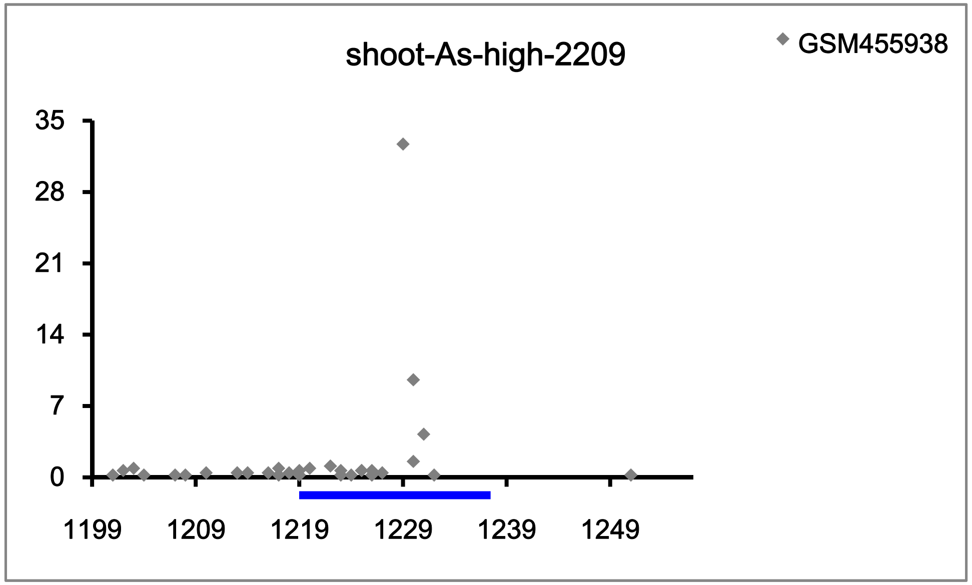

CNT0029581
GSM1040649
SRR1849904
30
24
18
12
6
0
0
100
200
300
400
500
600
700

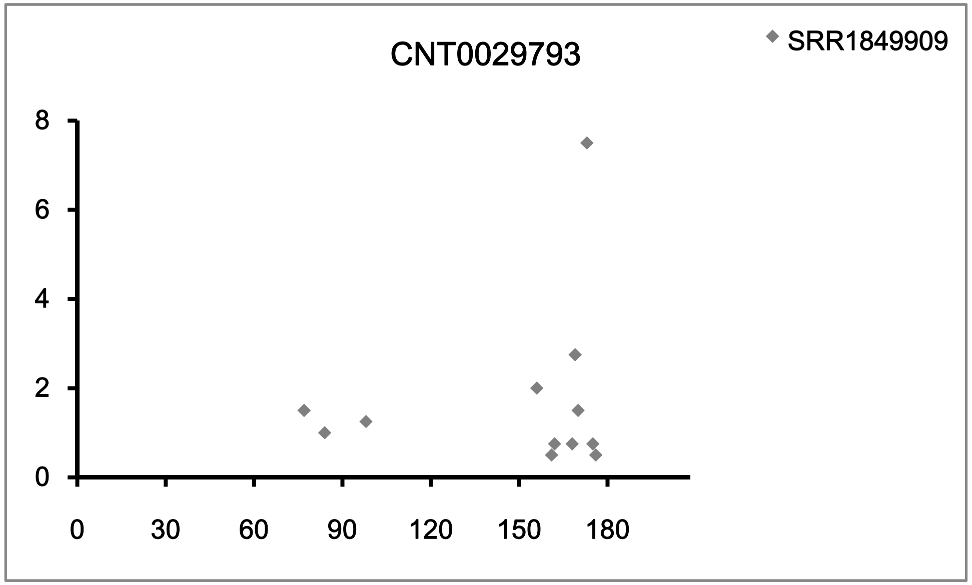

root-CK-high-2928
GSM1040649
SRR1849904
30
24
18
12
6
0
89
99
109
119
129
139
149

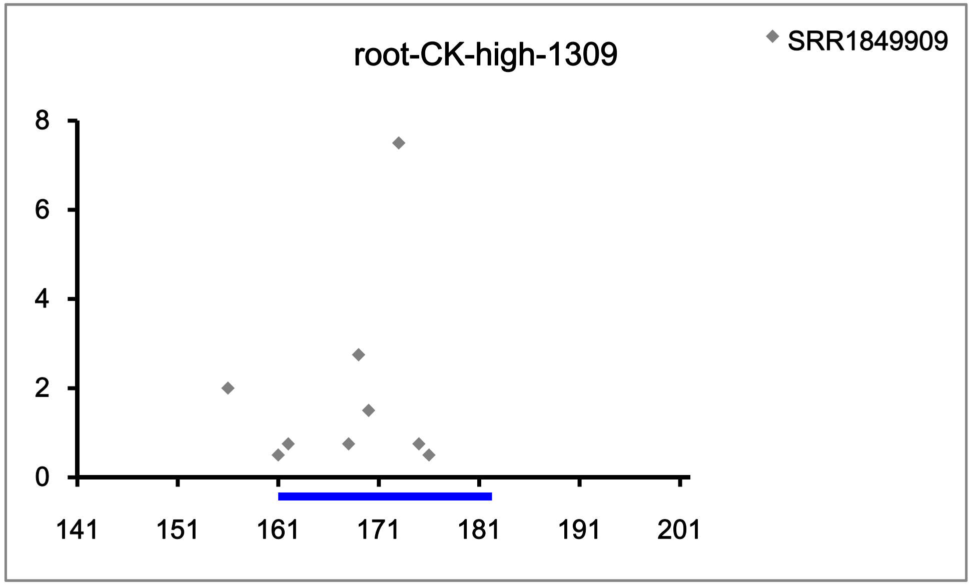

CNT0029628
SRR1849910
4.5
3.6
2.7
1.8
0.9
0
0
30
60
90
120
150
180
210

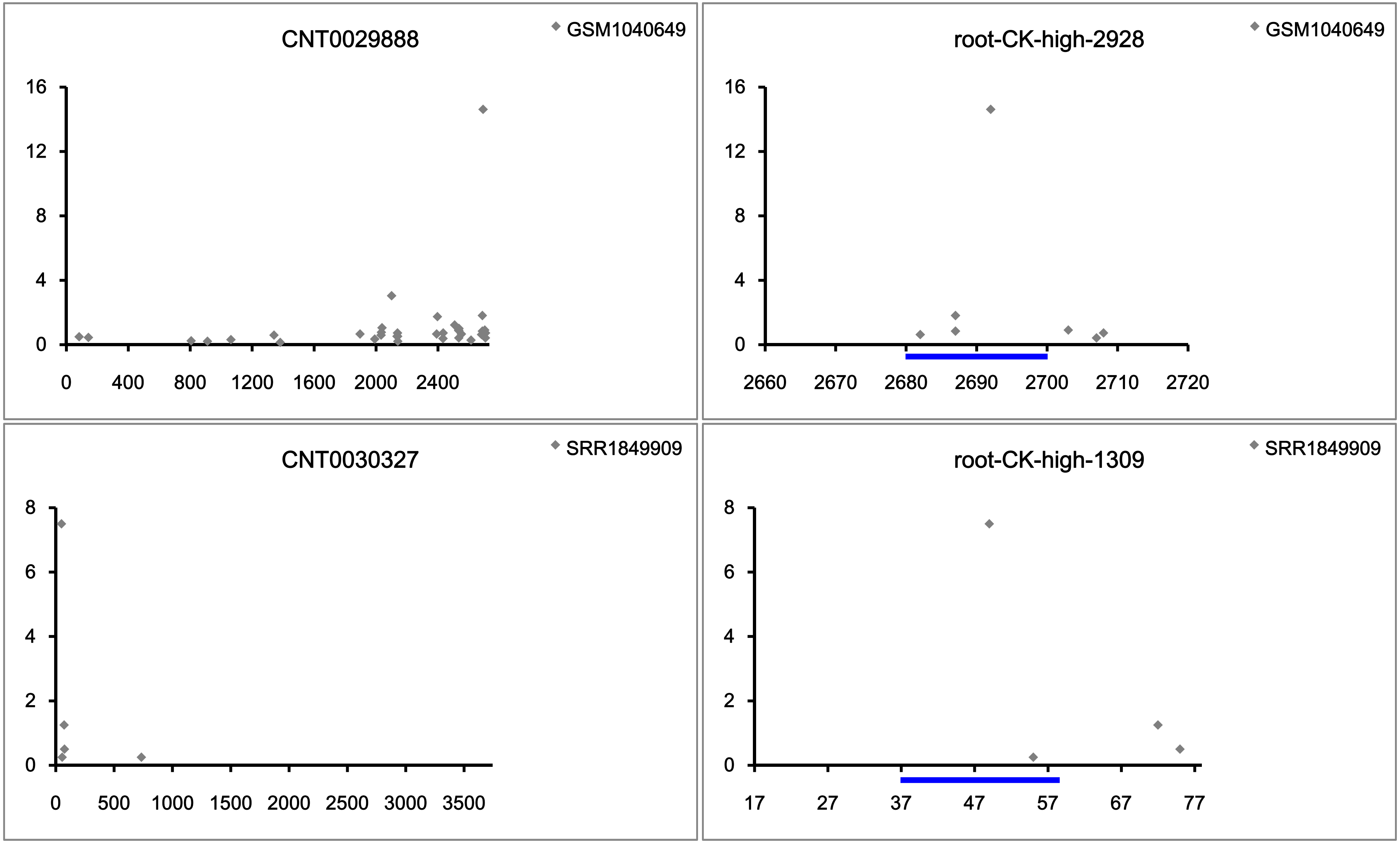

root-CK-high-10130
SRR1849910
4.5
3.6
2.7
1.8
0.9
0
173
183
193
203
213
223
233

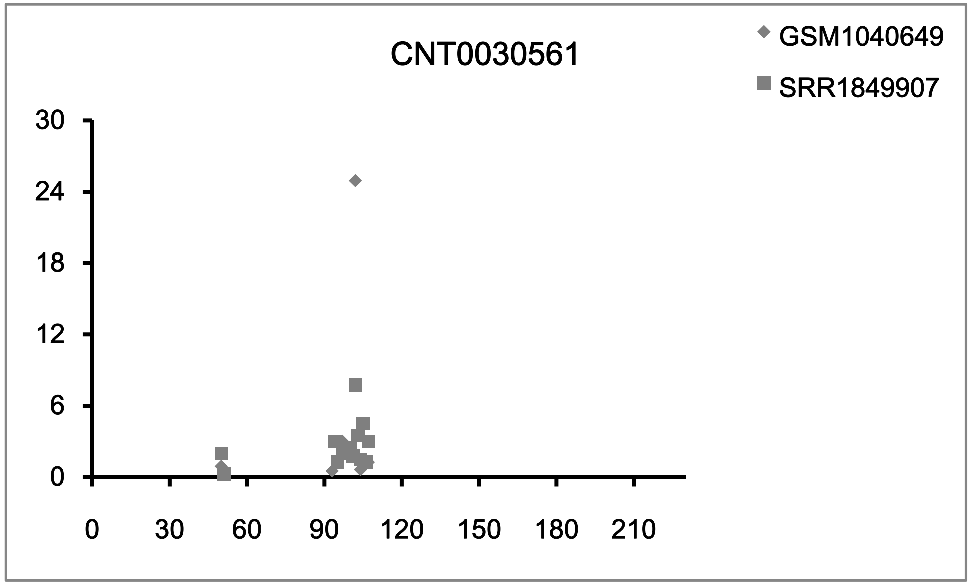

CNT0029714
GSM455938
35
28
21
14
7
0
0
150
300
450
600
750
900
1050
1200

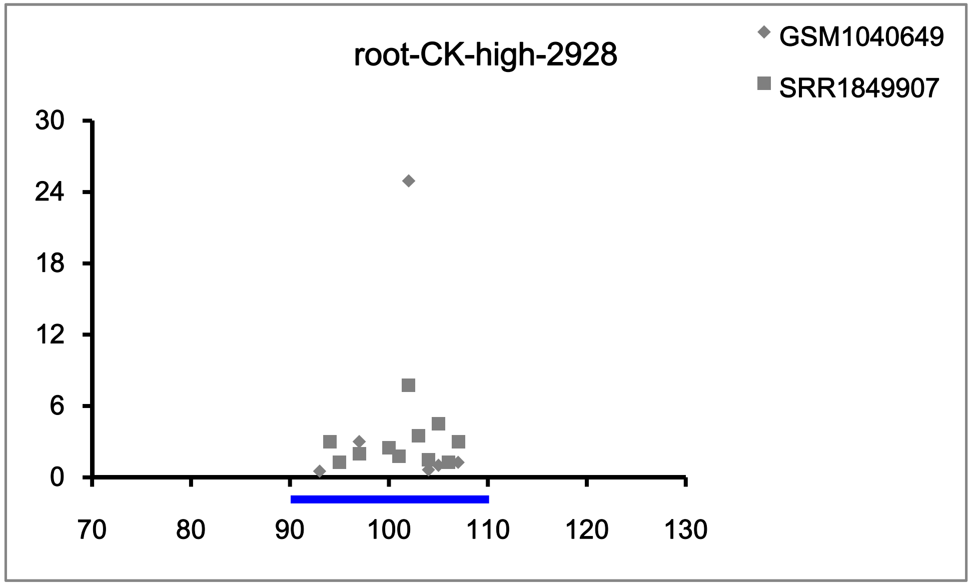

shoot-As-high-2209
GSM455938
35
28
21
14
7
0
1199
1209
1219
1229
1239
1249

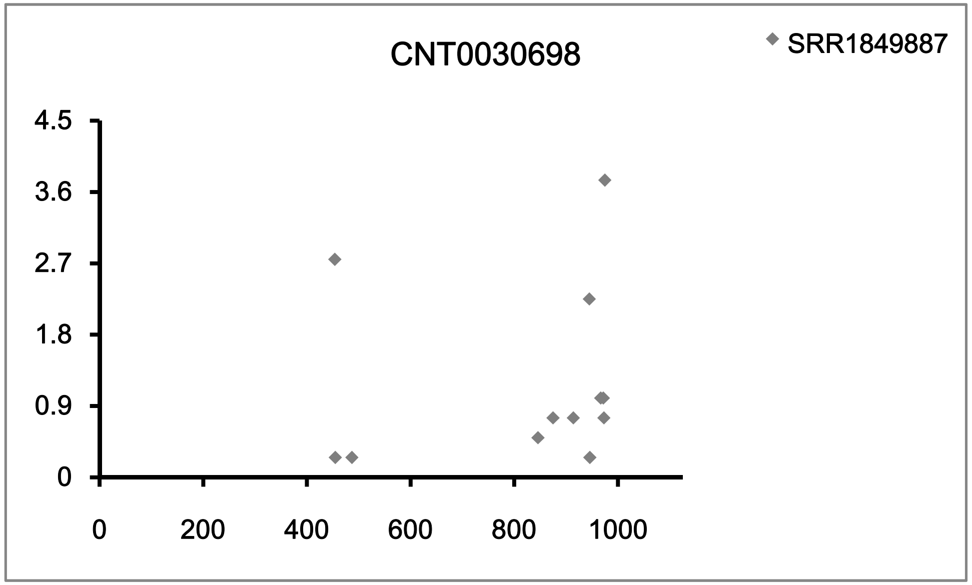

CNT0029793
SRR1849909
8
6
4
2
0
0
30
60
90
120
150
180

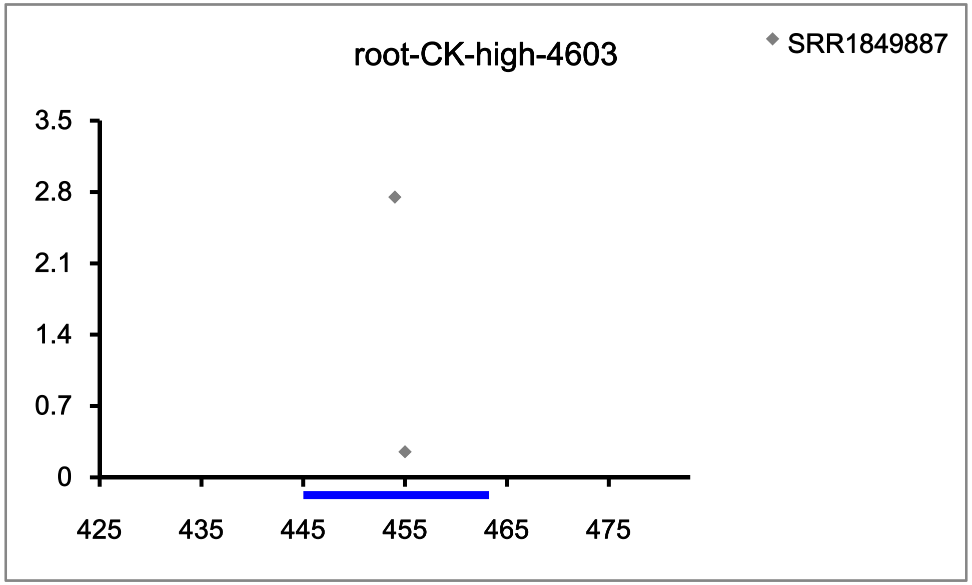

root-CK-high-1309
SRR1849909
8
6
4
2
0
141
151
161
171
181
191
201

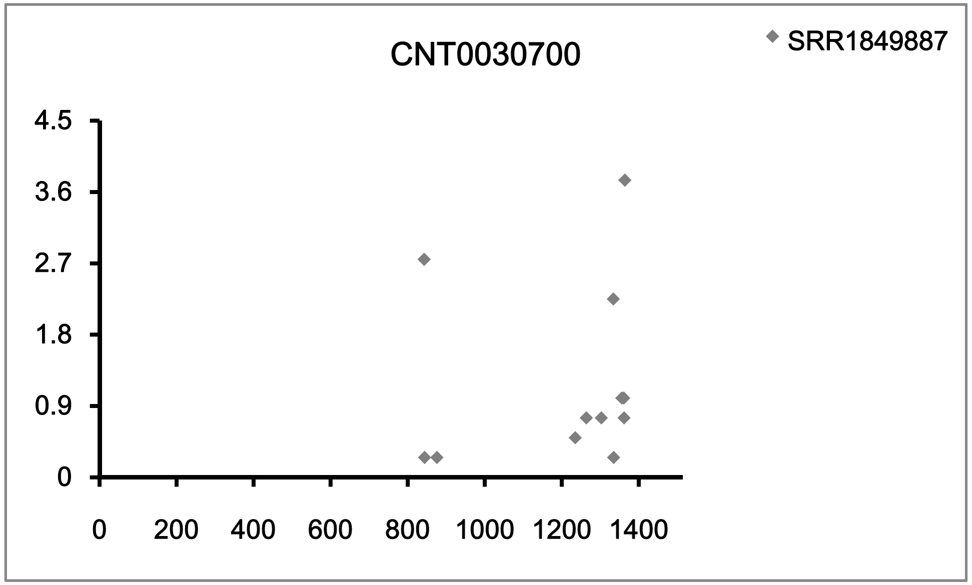

CNT0029888
GSM1040649
16
12
8
4
0
0
400
800
1200
1600
2000
2400
root-CK-high-2928
GSM1040649
16
12
8
4
0
2660
2670
2680
2690
2700
2710
2720
CNT0030327
SRR1849909
8
6
4
2
0
0
500
1000
1500
2000
2500
3000
3500
root-CK-high-1309
SRR1849909
8
6
4
2
0
17
27
37
47
57
67
77

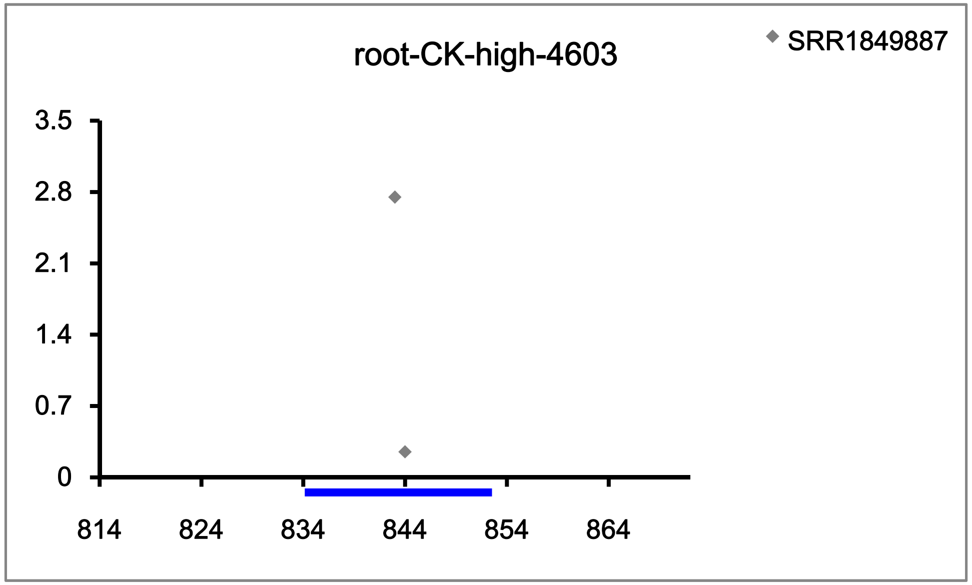

CNT0030561
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
0
30
60
90
120
150
180
210

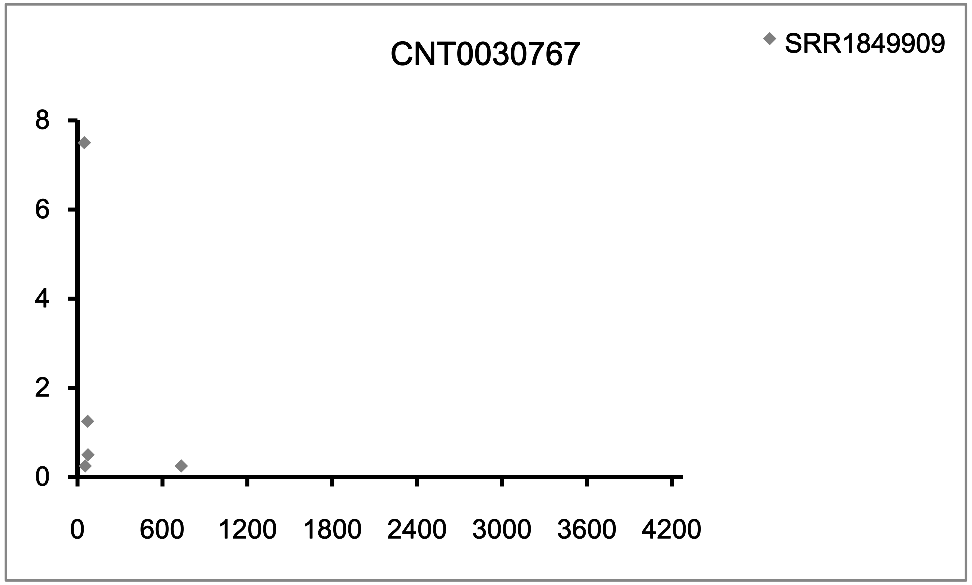

root-CK-high-2928
◆ GSM1040649
■ SRR1849907
30
24
18
12
6
0
70
80
90
100
110
120
130

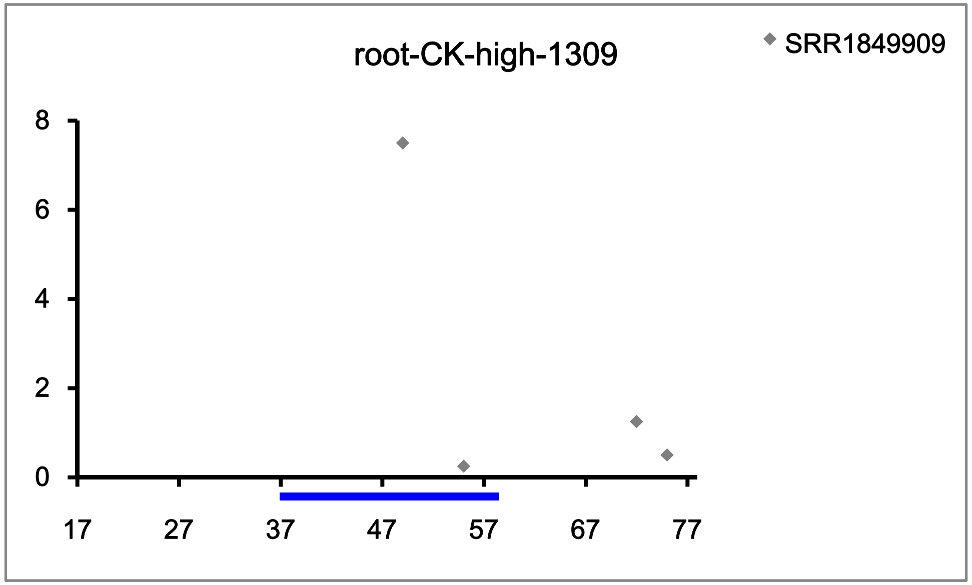

CNT0030698
◆ SRR1849887
4.5
3.6
2.7
1.8
0.9
0
0
200
400
600
800
1000

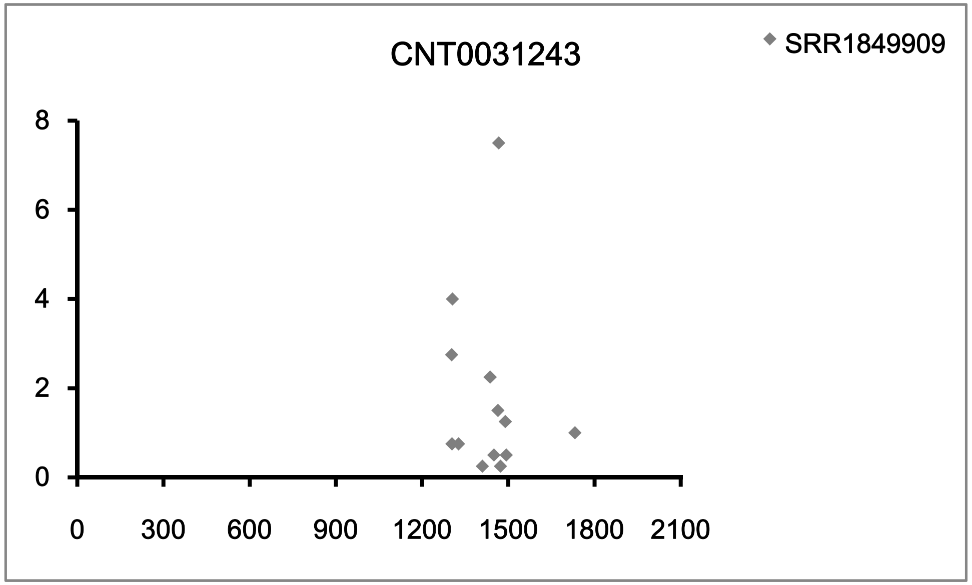

root-CK-high-4603
◆ SRR1849887
3.5
2.8
2.1
1.4
0.7
0
425
435
445
455
465
475

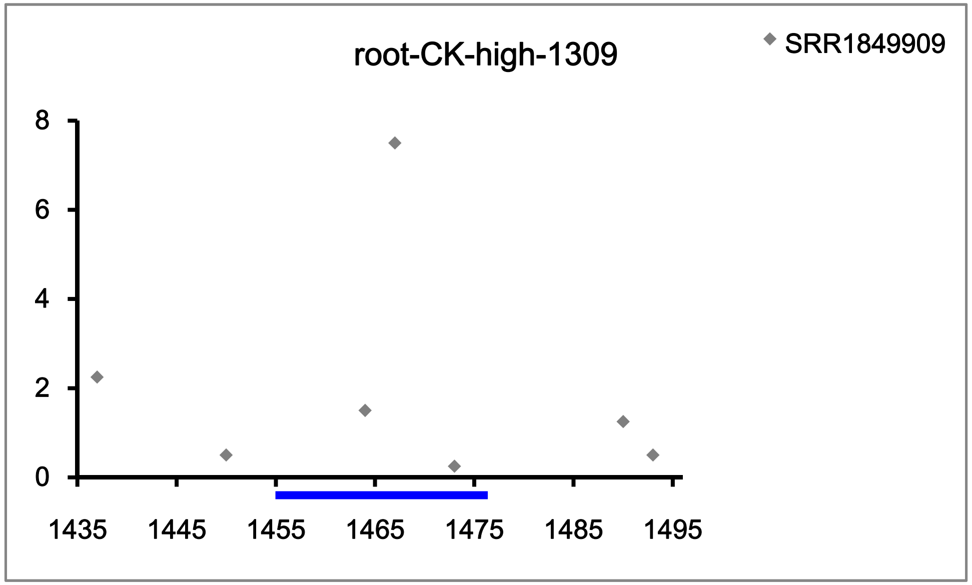

CNT0030700
SRR1849887
4.5
3.6
2.7
1.8
0.9
0
0
200
400
600
800
1000
1200
1400

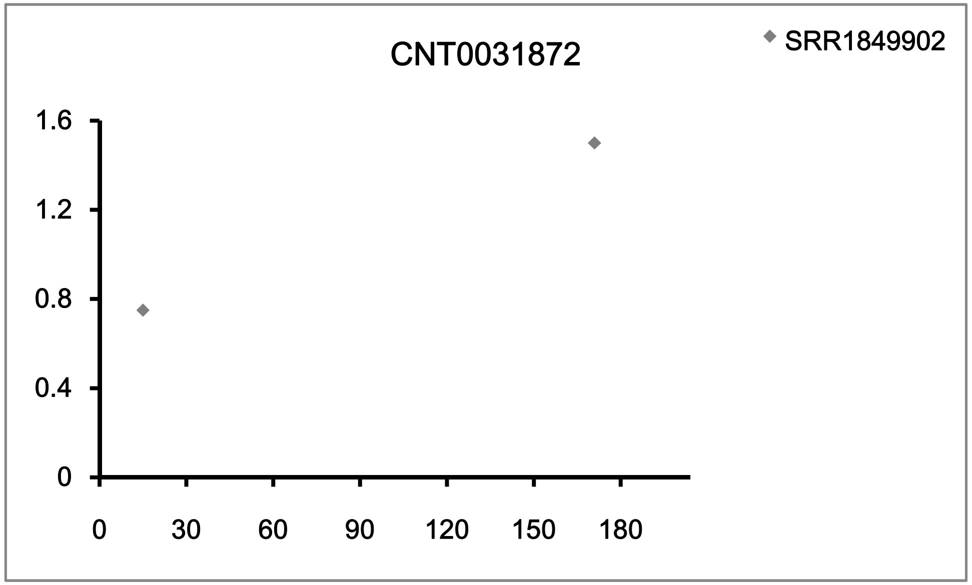

root-CK-high-4603
SRR1849887
3.5
2.8
2.1
1.4
0.7
0
814
824
834
844
854
864

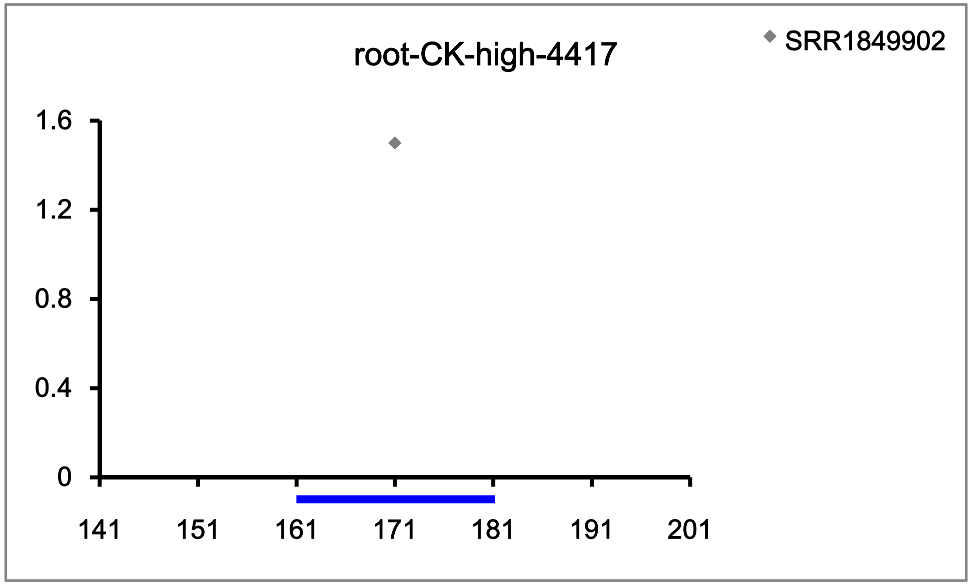

CNT0030767
SRR1849909
8
6
4
2
0
0
600
1200
1800
2400
3000
3600
4200

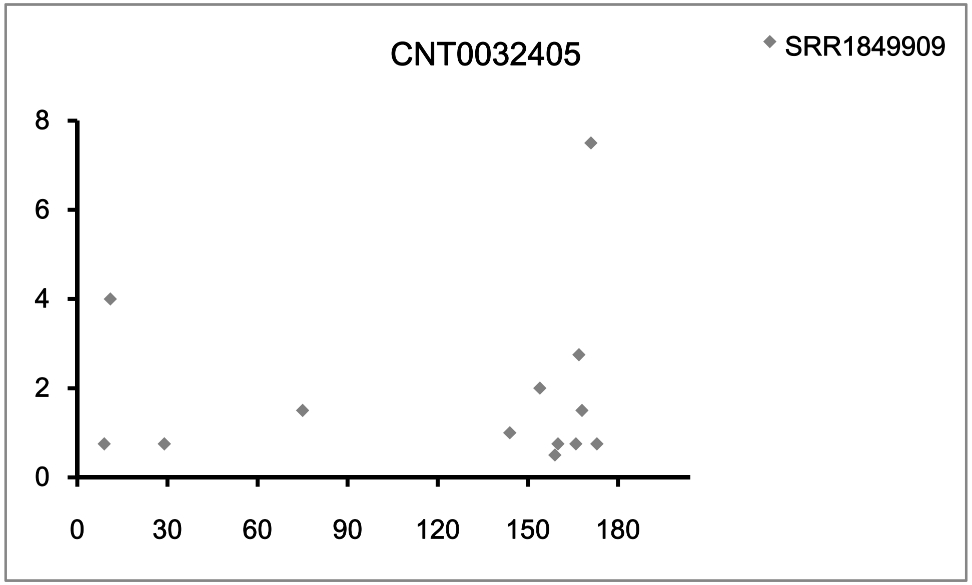

root-CK-high-1309
SRR1849909
8
6
4
2
0
17
27
37
47
57
67
77

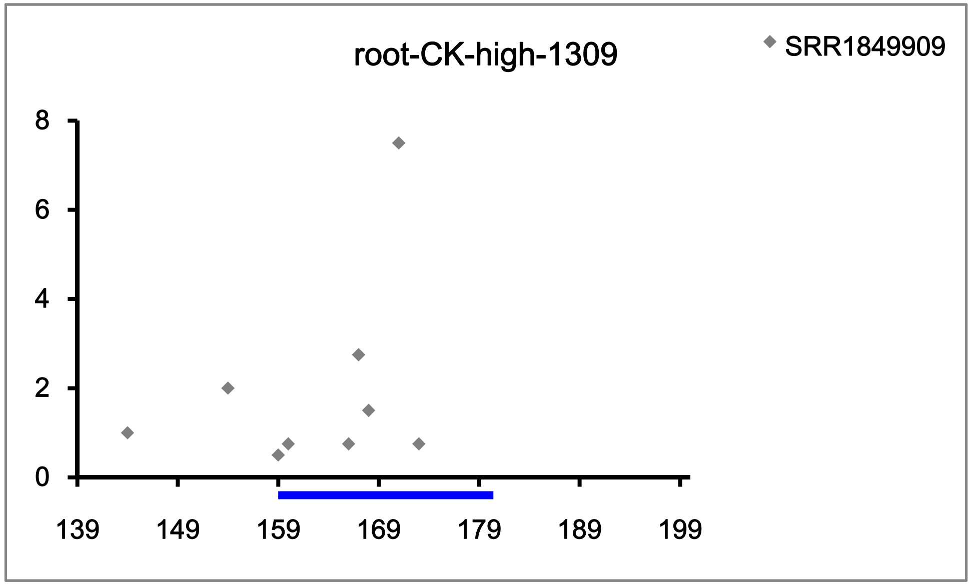

CNT0031243
SRR1849909
8
6
4
2
0
0
300
600
900
1200
1500
1800
2100

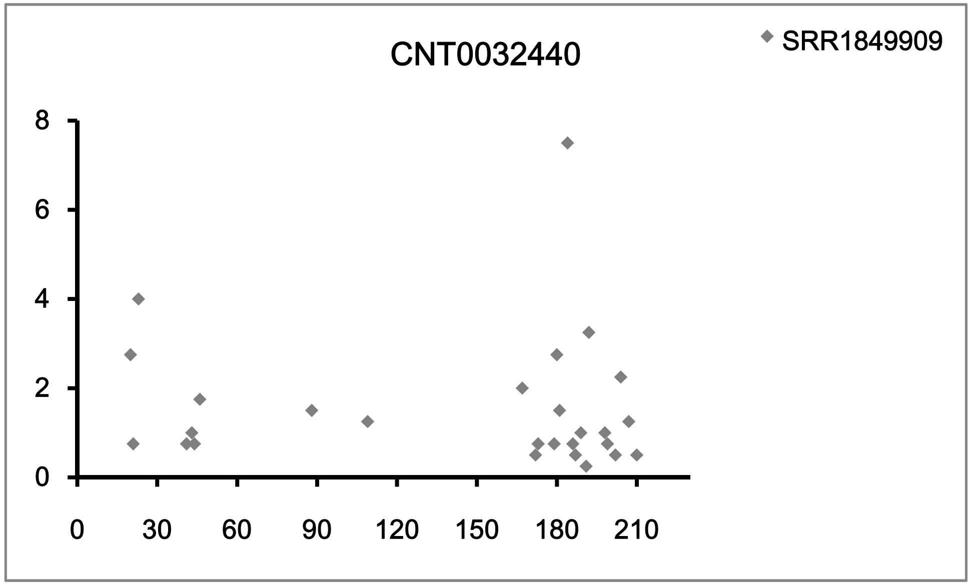

root-CK-high-1309
SRR1849909
8
6
4
2
0
1435
1445
1455
1465
1475
1485
1495

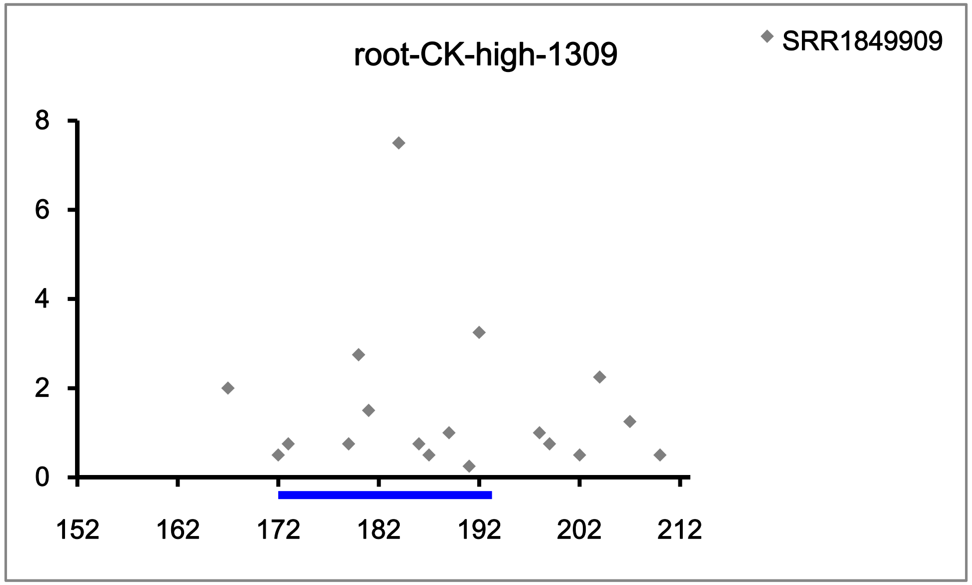

CNT0031872
SRR1849902
1.6
1.2
0.8
0.4
0
0
30
60
90
120
150
180

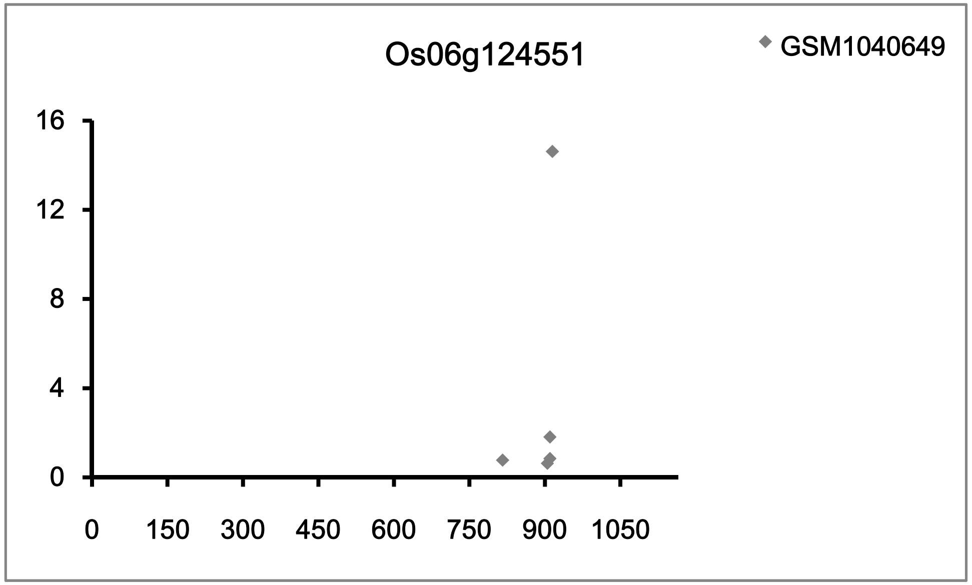

root-CK-high-4417
SRR1849902
1.6
1.2
0.8
0.4
0
141
151
161
171
181
191
201

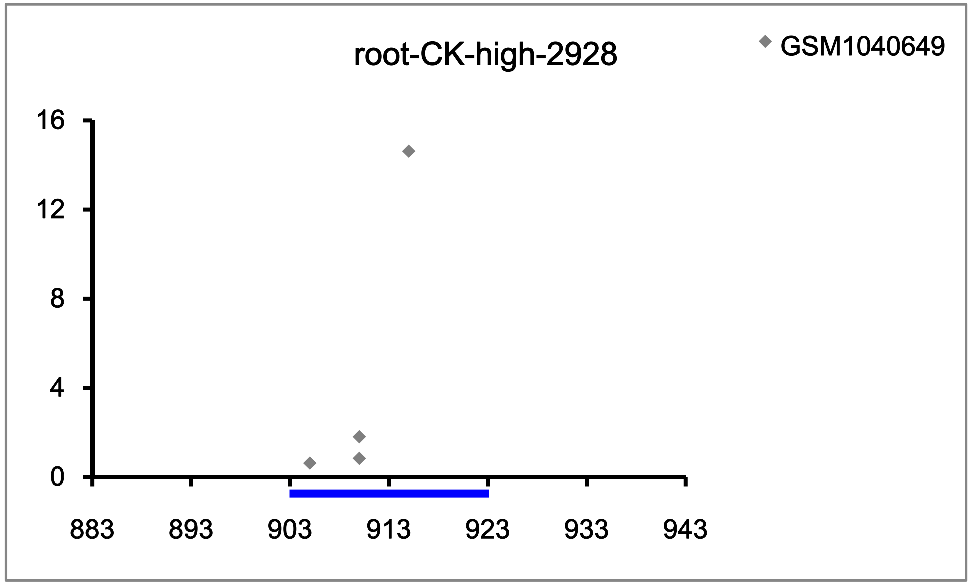

CNT0032405
◆ SRR1849909
0
2
4
6
8
0
30
60
90
120
150
180

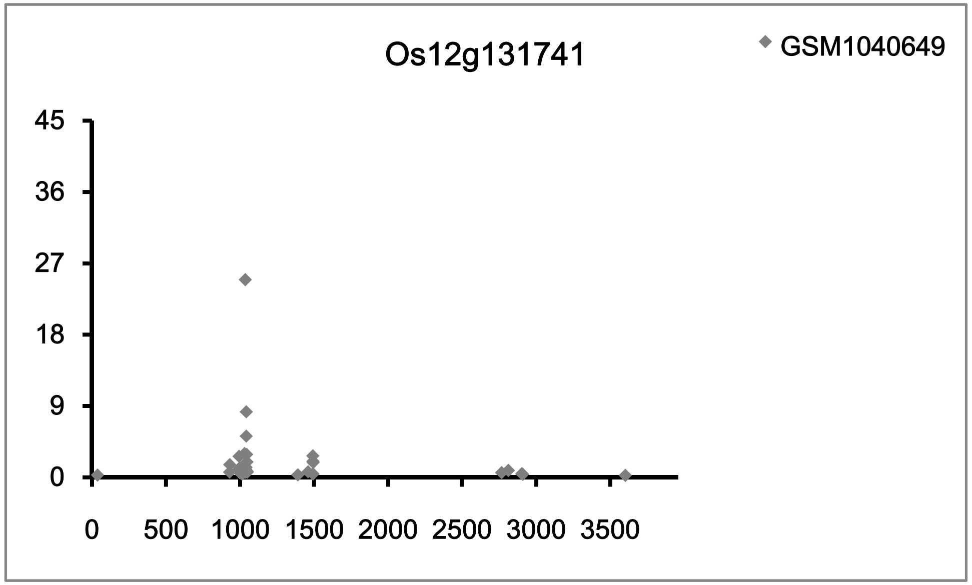

root-CK-high-1309
◆ SRR1849909
0
2
4
6
8
139
149
159
169
179
189
199


CNT0032440
◆ SRR1849909
0
2
4
6
8
0
30
60
90
120
150
180
210


root-CK-high-1309
◆ SRR1849909
0
2
4
6
8
152
162
172
182
192
202
212


Os06g124551
GSM1040649
16
12
8
4
0
0
150
300
450
600
750
900
1050


root-CK-high-2928
GSM1040649
16
12
8
4
0
883
893
903
913
923
933
943


Os12g131741
GSM1040649
45
36
27
18
9
0
0
500
1000
1500
2000
2500
3000
3500

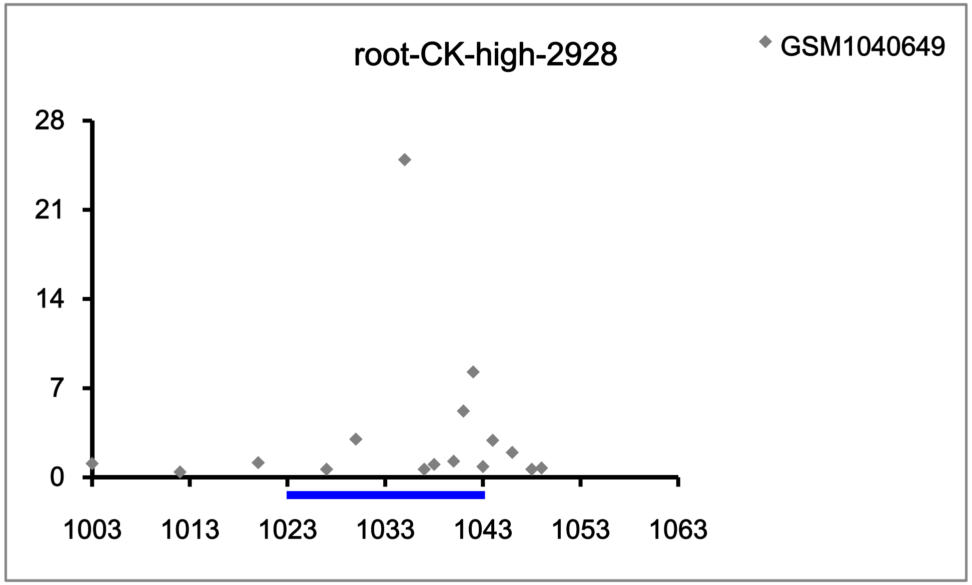

root-CK-high-2928
GSM1040649
28
21
14
7
0
1003
1013
1023
1033
1043
1053
1063

Table S1 List of rice As-responsive miRNAs identified in this study

Category	miRNA	Sequence	sRNA ID
MiRNAs repressed by As in rice roots	osa-miR1428e-3p	UAAGAUAAUGCCAUGAAUUUG	root-CK-high-77
MiRNAs repressed by As in rice roots	osa-miR171c-5p	GGAUAUUGGUGCGGUUCAAUC	root-CK-high-561
MiRNAs repressed by As in rice roots	osa-miR1862d	ACUAGGUUUGUUUAUUUUGGGACG	root-CK-high-756
MiRNAs repressed by As in rice roots	osa-miR2871a-3p	UAUUUUAGUUUCUAUGGUCAC	root-CK-high-823
MiRNAs repressed by As in rice roots	osa-miR156c-3p	GCUCACUUCUCUCUCUGUCAGC	root-CK-high-831
MiRNAs repressed by As in rice roots	osa-miR159a.2	UUGCAUGCCCCAGGAGCUGCA	root-CK-high-842
MiRNAs repressed by As in rice roots	osa-miR3979-3p	CUUCGGGGGAGGAGAGAAGC	root-CK-high-1561
MiRNAs repressed by As in rice roots	osa-miR3979-5p	UCUCUCUCUCCCUUGAAGGC	root-CK-high-1916
MiRNAs repressed by As in rice roots	osa-miR156h-5p	UGACAGAAGAGAGUGAGCAC	root-CK-high-2472
MiRNAs repressed by As in rice roots	osa-miR1871	AUGGCUCUGAUAUCAUGUUGGUUU	root-CK-high-2970
MiRNAs repressed by As in rice roots	osa-miR156l-3p	GCUCACUUCUCUUUCUGUCAGC	root-CK-high-4558
MiRNAs repressed by As in rice roots	osa-miR1423-5p	AGGCAACUACACGUUGGGCGCUCG	root-CK-high-4770
MiRNAs repressed by As in rice roots	osa-miR5144-5p	UUCUUGUGCUGCUGAAGAGAC	root-CK-high-5089
MiRNAs repressed by As in rice roots	osa-miR5540	UUGUGCGAGAUCGACGGUAUA	root-CK-high-5714
MiRNAs repressed by As in rice roots	osa-miR171f-5p	UGUUGGCAUGGUUCAAUCAAA	root-CK-high-6140
MiRNAs repressed by As in rice roots	osa-miR156b-3p	GCUCACUCUCUAUCUGUCAGC	root-CK-high-8453
MiRNAs repressed by As in rice roots	osa-miR156j-3p	GCUCGCUCCUCUUUCUGUCAGC	root-CK-high-9201
MiRNAs repressed by As in rice roots	osa-miR396b-5p	UUCCACAGCUUUCUUGAACUG	root-CK-high-10257
MiRNAs repressed by As in rice roots	osa-miR169r-3p	UGGCAAGUCUCCUCGGCUACC	root-CK-high-11189
MiRNAs repressed by As in rice roots	osa-miR166a-5p	GGAAUGUUGUCUGGUUCAAGG	root-CK-high-11266
MiRNAs repressed by As in rice roots	osa-miR1850.1	UGGAAAGUUGGGAGAUUGGGG	root-CK-high-11392
MiRNAs repressed by As in rice roots	osa-miR535-3p	GUGCUUUCUCCCGUUGUCACU	root-CK-high-11802
MiRNAs repressed by As in rice roots	osa-miR5814	AAUCAAGUUAGGAACCAUGCAAGU	root-CK-high-11843
MiRNAs repressed by As in rice roots	osa-miR166b-5p	GGAAUGUUGUCUGGCUCGGGG	root-CK-high-11997
MiRNAs repressed by As in rice roots	osa-miR397a	UCAUUGAGUGCAGCGUUGAUG	root-CK-high-12836
MiRNAs repressed by As in rice roots	osa-miR5794	UGAGGAAUCACUAGUAGUCGU	root-CK-high-13321
MiRNAs induced by As in rice shoots	osa-miR1428e-3p	UAAGAUAAUGCCAUGAAUUUG	shoot-As-high-94

MiRNAs induced by As in rice shoots	osa-miR1427	UGCGGAACCGUGCGGUGGCGC	shoot-As-high-1758
MiRNAs induced by As in rice shoots	osa-miR5542	UUUGAGAAGGUAUCAUGAGAU	shoot-As-high-3351
MiRNAs induced by As in rice shoots	osa-miR6251	UGUGUAGCCACAUUGUAAGGG	shoot-As-high-8166
MiRNAs induced by As in rice shoots	osa-miR169h	UAGCCAAGGAUGACUUGCCUG	shoot-As-high-8573
MiRNAs induced by As in rice shoots	osa-miR1863a	AGCUCUGAUACCAUGUUAGAUUAG	shoot-As-high-8704
MiRNAs induced by As in rice shoots	osa-miR812h	AAGACGGAUGAUUAAAGUUGGACA	shoot-As-high-14795
MiRNAs repressed by As in rice shoots	osa-miR169i-5p.2	UGGUGAUAAGGGUGUAGCUCUG	shoot-CK-high-6605
MiRNAs repressed by As in rice shoots	osa-miR5788	UGGAUGUGACAUACUCUAGUA	shoot-CK-high-7436
MiRNAs repressed by As in rice shoots	osa-miR160f-3p	GCAUUGAGGGAGUCAUGCAGG	shoot-CK-high-7605
MiRNAs repressed by As in rice shoots	osa-miR166i-5p	AAUGCAGUUUGAUCCAAGAUC	shoot-CK-high-7700
AS-responsive miRNAs enriched in AGO1	osa-miR5794	UGAGGAAUCACUAGUAGUCGU	root-CK-high-13321
AS-responsive miRNAs enriched in AGO1	osa-miR169r-3p	UGGCAAGUCUCCUCGGCUACC	root-CK-high-11189
AS-responsive miRNAs enriched in AGO1	osa-miR396b-5p	UUCCACAGCUUUCUUGAACUG	root-CK-high-10257
AS-responsive miRNAs enriched in AGO1	osa-miR5144-5p	UUCUUGUGCUGCUGAAGAGAC	root-CK-high-5089

Table S2 Annotations of the protein-coding transcripts targeted by As-responsive sRNAs

Transcript ID	Annotation	GO ID	GO term	GO category
LOC_Os01g09030.1	2-aminoethanethiol dioxygenase, putative, expressed	GO:0003824	catalytic activity	F
LOC_Os01g09030.1	2-aminoethanethiol dioxygenase, putative, expressed	GO:0008152	metabolic process	P
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0008152	metabolic process	P
LOC_Os01g48060.1	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0008152	metabolic process	P
LOC_Os01g48060.2	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0008152	metabolic process	P
LOC_Os01g48060.3	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0008152	metabolic process	P
LOC_Os01g54990.1	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0000003	reproduction	P
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0009607	response to biotic stimulus	P
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0006950	response to stress	P
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0007165	signal transduction	P
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0005975	carbohydrate metabolic process	P

LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0009987	cellular process	P
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0005886	plasma membrane	C
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0005575	cellular_component	C
LOC_Os01g55040.1	1,3-beta-glucan synthase component, putative, expressed	GO:0016740	transferase activity	F
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0007165	signal transduction	P
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0040007	growth	P
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0008219	cell death	P
LOC_Os01g59660.1	MYB family transcription factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0007165	signal transduction	P
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0040007	growth	P
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0008219	cell death	P
LOC_Os01g59660.2	MYB family transcription factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0040007	growth	P
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0008150	biological_process	P
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0008219	cell death	P
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g59660.3	MYB family transcription factor, putative, expressed	GO:0007165	signal transduction	P
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0007165	signal transduction	P
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0040007	growth	P
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0008219	cell death	P

LOC_Os01g59660.4	MYB family transcription factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g59720.1	expressed protein	GO:0016020	membrane	C
LOC_Os01g59720.1	expressed protein	GO:0005575	cellular_component	C
LOC_Os01g59720.1	expressed protein	GO:0005515	protein binding	F
LOC_Os01g59720.1	expressed protein	GO:0005488	binding	F
LOC_Os01g59720.1	expressed protein	GO:0005773	vacuole	C
LOC_Os01g59720.1	expressed protein	GO:0006810	transport	P
LOC_Os01g59720.1	expressed protein	GO:0009987	cellular process	P
LOC_Os01g59720.1	expressed protein	GO:0005886	plasma membrane	C
LOC_Os01g63890.1	G10 protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g63890.1	G10 protein, putative, expressed	GO:0005829	cytosol	C
LOC_Os01g63890.1	G10 protein, putative, expressed	GO:0008150	biological_process	P
LOC_Os01g64520.1	uricase, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g64520.1	uricase, putative, expressed	GO:0005777	peroxisome	C
LOC_Os01g64520.1	uricase, putative, expressed	GO:0008152	metabolic process	P
LOC_Os01g64520.1	uricase, putative, expressed	GO:0003824	catalytic activity	F
LOC_Os01g64520.2	uricase, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g64520.2	uricase, putative, expressed	GO:0005777	peroxisome	C
LOC_Os01g64520.2	uricase, putative, expressed	GO:0008152	metabolic process	P
LOC_Os01g64520.2	uricase, putative, expressed	GO:0003824	catalytic activity	F
LOC_Os01g69830.1	OsSPL2 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os01g69830.1	OsSPL2 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os01g69830.1	OsSPL2 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os01g69830.1	OsSPL2 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g69830.1	OsSPL2 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g69830.1	OsSPL2 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0009838	abscission	P
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0005515	protein binding	F
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0009536	plastid	C
LOC_Os01g70270.1	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0009838	abscission	P
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0005515	protein binding	F
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0009536	plastid	C
LOC_Os01g70270.2	auxin response factor, putative, expressed	GO:0009987	cellular process	P

LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0009838	abscission	P
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0005515	protein binding	F
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0009536	plastid	C
LOC_Os01g70270.3	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0009838	abscission	P
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0005515	protein binding	F
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0009536	plastid	C
LOC_Os01g70270.4	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os02g04680.1	OsSPL3 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os02g04680.1	OsSPL3 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os02g04680.1	OsSPL3 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os02g04680.1	OsSPL3 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g04680.1	OsSPL3 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g04680.1	OsSPL3 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g04680.1	OsSPL3 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g04680.2	OsSPL3 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os02g04680.2	OsSPL3 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os02g04680.2	OsSPL3 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os02g04680.2	OsSPL3 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g04680.2	OsSPL3 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g04680.2	OsSPL3 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g04680.2	OsSPL3 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g06910.1	auxin response factor 6, putative, expressed	GO:0009908	flower development	P
LOC_Os02g06910.1	auxin response factor 6, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os02g06910.1	auxin response factor 6, putative, expressed	GO:0005634	nucleus	C
LOC_Os02g06910.1	auxin response factor 6, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g06910.1	auxin response factor 6, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g06910.1	auxin response factor 6, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g07780.1	OsSPL4 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os02g07780.1	OsSPL4 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os02g07780.1	OsSPL4 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os02g07780.1	OsSPL4 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g07780.1	OsSPL4 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g07780.1	OsSPL4 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P

LOC_Os02g07780.1	OsSPL4 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g07780.2	OsSPL4 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os02g07780.2	OsSPL4 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os02g07780.2	OsSPL4 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os02g07780.2	OsSPL4 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g07780.2	OsSPL4 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g07780.2	OsSPL4 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g07780.2	OsSPL4 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g07960.4	STRUBBELIG-RECEPTOR FAMILY 3 precursor, putative, expressed	GO:0008150	biological_process	P
LOC_Os02g07960.4	STRUBBELIG-RECEPTOR FAMILY 3 precursor, putative, expressed	GO:0007165	signal transduction	P
LOC_Os02g07960.4	STRUBBELIG-RECEPTOR FAMILY 3 precursor, putative, expressed	GO:0016301	kinase activity	F
LOC_Os02g07960.4	STRUBBELIG-RECEPTOR FAMILY 3 precursor, putative, expressed	GO:0000166	nucleotide binding	F
LOC_Os02g07960.4	STRUBBELIG-RECEPTOR FAMILY 3 precursor, putative, expressed	GO:0006464	protein modification process	P
LOC_Os02g07960.4	STRUBBELIG-RECEPTOR FAMILY 3 precursor, putative, expressed	GO:0005886	plasma membrane	C
LOC_Os02g14290.1	scramblase, putative, expressed	GO:0003674	molecular_function	F
LOC_Os02g14290.1	scramblase, putative, expressed	GO:0009536	plastid	C
LOC_Os02g14290.1	scramblase, putative, expressed	GO:0005739	mitochondrion	C
LOC_Os02g14290.1	scramblase, putative, expressed	GO:0008150	biological_process	P
LOC_Os02g29140.1	ankyrin, putative, expressed	GO:0005575	cellular_component	C
LOC_Os02g29140.1	ankyrin, putative, expressed	GO:0008150	biological_process	P
LOC_Os02g29140.1	ankyrin, putative, expressed	GO:0005488	binding	F
LOC_Os02g36924.1	OsMADS27 - MADS-box family gene with MIKCc type-box, expressed	GO:0009791	post-embryonic development	P
LOC_Os02g36924.1	OsMADS27 - MADS-box family gene with MIKCc type-box, expressed	GO:0009987	cellular process	P
LOC_Os02g36924.1	OsMADS27 - MADS-box family gene with MIKCc type-box, expressed	GO:0005515	protein binding	F
LOC_Os02g36924.1	OsMADS27 - MADS-box family gene with MIKCc type-box, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g36924.1	OsMADS27 - MADS-box family gene with MIKCc type-box, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g36924.1	OsMADS27 - MADS-box family gene with MIKCc type-box, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g41800.1	auxin response factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g41800.1	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os02g41800.1	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os02g41800.1	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os02g41800.1	auxin response factor, putative, expressed	GO:0003723	RNA binding	F
LOC_Os02g41800.1	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g41800.1	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g41800.1	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g41800.2	auxin response factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g41800.2	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os02g41800.2	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os02g41800.2	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os02g41800.2	auxin response factor, putative, expressed	GO:0003723	RNA binding	F
LOC_Os02g41800.2	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g41800.2	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g41800.2	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g43560.1	WRKY34, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g43560.1	WRKY34, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g43560.1	WRKY34, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0008150	biological_process	P
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0016043	cellular component organization	P
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0009653	anatomical structure morphogenesis	P

LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0016049	cell growth	P
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0005515	protein binding	F
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0009987	cellular process	P
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g44360.1	scarecrow transcription factor family protein, putative, expressed	GO:0009536	plastid	C
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0008150	biological_process	P
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0016043	cellular component organization	P
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0016049	cell growth	P
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0005515	protein binding	F
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0009987	cellular process	P
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os02g44370.1	scarecrow, putative, expressed	GO:0009536	plastid	C
LOC_Os02g44990.1	OsFBDUF13 - F-box and DUF domain containing protein, expressed	GO:0003674	molecular_function	F
LOC_Os02g44990.1	OsFBDUF13 - F-box and DUF domain containing protein, expressed	GO:0005575	cellular_component	C
LOC_Os02g44990.1	OsFBDUF13 - F-box and DUF domain containing protein, expressed	GO:0008150	biological_process	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0006950	response to stress	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0009607	response to biotic stimulus	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0005737	cytoplasm	C
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0004518	nuclease activity	F
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0040029	regulation of gene expression, epigenetic	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0009987	cellular process	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0005515	protein binding	F
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0009628	response to abiotic stimulus	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0005829	cytosol	C
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0003723	RNA binding	F
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0005634	nucleus	C
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0008152	metabolic process	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0000003	reproduction	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os02g45070.1	PINHEAD, putative, expressed	GO:0009790	embryo development	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0006950	response to stress	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0009607	response to biotic stimulus	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0005737	cytoplasm	C
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0004518	nuclease activity	F
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0040029	regulation of gene expression, epigenetic	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0009987	cellular process	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0005515	protein binding	F
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0009628	response to abiotic stimulus	P

LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0005829	cytosol	C
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0003723	RNA binding	F
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0005634	nucleus	C
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0008152	metabolic process	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0000003	reproduction	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os02g45070.2	PINHEAD, putative, expressed	GO:0009790	embryo development	P
LOC_Os02g45570.1	growth regulating factor protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os02g45570.1	growth regulating factor protein, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g45570.2	growth regulating factor protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os02g45570.2	growth regulating factor protein, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g47280.1	growth-regulating factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os02g47280.1	growth-regulating factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g47280.2	growth-regulating factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os02g47280.2	growth-regulating factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os02g52180.1	plastocyanin-like domain containing protein, putative, expressed	GO:0003674	molecular_function	F
LOC_Os02g52180.1	plastocyanin-like domain containing protein, putative, expressed	GO:0005488	binding	F
LOC_Os02g52180.1	plastocyanin-like domain containing protein, putative, expressed	GO:0016020	membrane	C
LOC_Os02g53000.2	lysM domain-containing GPI-anchored protein precursor, putative, expressed	GO:0003674	molecular_function	F
LOC_Os02g53000.2	lysM domain-containing GPI-anchored protein precursor, putative, expressed	GO:0009056	catabolic process	P
LOC_Os02g53000.2	lysM domain-containing GPI-anchored protein precursor, putative, expressed	GO:0005886	plasma membrane	C
LOC_Os02g53000.2	lysM domain-containing GPI-anchored protein precursor, putative, expressed	GO:0016020	membrane	C
LOC_Os03g01890.1	START domain containing protein, expressed	GO:0007275	multicellular organismal development	P
LOC_Os03g01890.1	START domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os03g01890.1	START domain containing protein, expressed	GO:0005634	nucleus	C
LOC_Os03g01890.1	START domain containing protein, expressed	GO:0030154	cell differentiation	P
LOC_Os03g01890.1	START domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os03g01890.1	START domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os03g01890.1	START domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os03g01890.1	START domain containing protein, expressed	GO:0008289	lipid binding	F
LOC_Os03g01890.1	START domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os03g01890.2	START domain containing protein, expressed	GO:0007275	multicellular organismal development	P
LOC_Os03g01890.2	START domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os03g01890.2	START domain containing protein, expressed	GO:0005634	nucleus	C
LOC_Os03g01890.2	START domain containing protein, expressed	GO:0030154	cell differentiation	P
LOC_Os03g01890.2	START domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os03g01890.2	START domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os03g01890.2	START domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os03g01890.2	START domain containing protein, expressed	GO:0008289	lipid binding	F
LOC_Os03g01890.2	START domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os03g31180.2	diacylglycerol kinase 1, putative, expressed	GO:0016301	kinase activity	F
LOC_Os03g31180.2	diacylglycerol kinase 1, putative, expressed	GO:0005575	cellular_component	C
LOC_Os03g31180.2	diacylglycerol kinase 1, putative, expressed	GO:0007165	signal transduction	P
LOC_Os03g31180.2	diacylglycerol kinase 1, putative, expressed	GO:0006464	protein modification process	P
LOC_Os03g31180.2	diacylglycerol kinase 1, putative, expressed	GO:0005488	binding	F
LOC_Os03g39610.1	chlorophyll A-B binding protein, putative, expressed	GO:0016020	membrane	C
LOC_Os03g39610.1	chlorophyll A-B binding protein, putative, expressed	GO:0009536	plastid	C
LOC_Os03g39610.1	chlorophyll A-B binding protein, putative, expressed	GO:0009579	thylakoid	C
LOC_Os03g39610.1	chlorophyll A-B binding protein, putative, expressed	GO:0009628	response to abiotic stimulus	P
LOC_Os03g39610.1	chlorophyll A-B binding protein, putative, expressed	GO:0005622	intracellular	C
LOC_Os03g39610.1	chlorophyll A-B binding protein, putative, expressed	GO:0005488	binding	F
LOC_Os03g39610.1	chlorophyll A-B binding protein, putative, expressed	GO:0015979	photosynthesis	P

LOC_Os03g39610.2	chlorophyll A-B binding protein, putative, expressed	GO:0009536	plastid	C
LOC_Os03g39610.2	chlorophyll A-B binding protein, putative, expressed	GO:0016020	membrane	C
LOC_Os03g39610.2	chlorophyll A-B binding protein, putative, expressed	GO:0009579	thylakoid	C
LOC_Os03g39610.2	chlorophyll A-B binding protein, putative, expressed	GO:0005773	vacuole	C
LOC_Os03g39610.2	chlorophyll A-B binding protein, putative, expressed	GO:0006091	generation of precursor metabolites and energy	P
LOC_Os03g39610.2	chlorophyll A-B binding protein, putative, expressed	GO:0015979	photosynthesis	P
LOC_Os03g39610.2	chlorophyll A-B binding protein, putative, expressed	GO:0005622	intracellular	C
LOC_Os03g39610.2	chlorophyll A-B binding protein, putative, expressed	GO:0005488	binding	F
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0005634	nucleus	C
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0007275	multicellular organismal development	P
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0000003	reproduction	P
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0009791	post-embryonic development	P
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0009790	embryo development	P
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0009908	flower development	P
LOC_Os03g43930.1	START domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0005634	nucleus	C
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0007275	multicellular organismal development	P
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0000003	reproduction	P
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0009791	post-embryonic development	P
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0009790	embryo development	P
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0009908	flower development	P
LOC_Os03g43930.2	START domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0006950	response to stress	P
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0009607	response to biotic stimulus	P
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0009856	pollination	P
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0003674	molecular_function	F
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0006810	transport	P
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0009987	cellular process	P
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0009056	catabolic process	P
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0005737	cytoplasm	C
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0009991	response to extracellular stimulus	P
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0016043	cellular component organization	P
LOC_Os03g44200.1	beclin-1, putative, expressed	GO:0007154	cell communication	P
LOC_Os03g47140.1	growth regulating factor protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os03g47140.1	growth regulating factor protein, putative, expressed	GO:0005515	protein binding	F
LOC_Os03g47140.1	growth regulating factor protein, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os03g50070.1	DUF1295 domain containing protein, putative, expressed	GO:0003824	catalytic activity	F
LOC_Os03g50070.1	DUF1295 domain containing protein, putative, expressed	GO:0016020	membrane	C
LOC_Os03g50070.1	DUF1295 domain containing protein, putative, expressed	GO:0005773	vacuole	C
LOC_Os03g50070.1	DUF1295 domain containing protein, putative, expressed	GO:0005575	cellular_component	C
LOC_Os03g50070.1	DUF1295 domain containing protein, putative, expressed	GO:0008152	metabolic process	P
LOC_Os03g50070.1	DUF1295 domain containing protein, putative, expressed	GO:0005886	plasma membrane	C
LOC_Os03g50070.1	DUF1295 domain containing protein, putative, expressed	GO:0006629	lipid metabolic process	P

LOC_Os03g52010.1	lecithin cholesterol acyltransferase, putative, expressed	GO:0016020	membrane	C
LOC_Os03g52010.1	lecithin cholesterol acyltransferase, putative, expressed	GO:0005773	vacuole	C
LOC_Os03g52010.1	lecithin cholesterol acyltransferase, putative, expressed	GO:0016740	transferase activity	F
LOC_Os03g52010.1	lecithin cholesterol acyltransferase, putative, expressed	GO:0006629	lipid metabolic process	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0016043	cellular component organization	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0016049	cell growth	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0009987	cellular process	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0006629	lipid metabolic process	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0005783	endoplasmic reticulum	C
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0008152	metabolic process	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0006950	response to stress	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0009628	response to abiotic stimulus	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0003824	catalytic activity	F
LOC_Os04g02640.1	3-ketoacyl-CoA synthase 6, putative, expressed	GO:0016740	transferase activity	F
LOC_Os04g36830.1	DUF567 domain containing protein, putative, expressed	GO:0003674	molecular_function	F
LOC_Os04g36830.1	DUF567 domain containing protein, putative, expressed	GO:0005575	cellular_component	C
LOC_Os04g36830.1	DUF567 domain containing protein, putative, expressed	GO:0008150	biological_process	P
LOC_Os04g38450.1	gamma-glutamyltranspeptidase 1 precursor, putative, expressed	GO:0005576	extracellular region	C
LOC_Os04g38450.1	gamma-glutamyltranspeptidase 1 precursor, putative, expressed	GO:0008152	metabolic process	P
LOC_Os04g38450.1	gamma-glutamyltranspeptidase 1 precursor, putative, expressed	GO:0005575	cellular_component	C
LOC_Os04g38450.1	gamma-glutamyltranspeptidase 1 precursor, putative, expressed	GO:0006950	response to stress	P
LOC_Os04g38450.1	gamma-glutamyltranspeptidase 1 precursor, putative, expressed	GO:0005618	cell wall	C
LOC_Os04g38450.1	gamma-glutamyltranspeptidase 1 precursor, putative, expressed	GO:0016740	transferase activity	F
LOC_Os04g38450.1	gamma-glutamyltranspeptidase 1 precursor, putative, expressed	GO:0009056	catabolic process	P
LOC_Os04g38450.1	gamma-glutamyltranspeptidase 1 precursor, putative, expressed	GO:0009987	cellular process	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0007165	signal transduction	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0008150	biological_process	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0003723	RNA binding	F
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0009987	cellular process	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0040007	growth	P
LOC_Os04g43910.1	auxin response factor, putative, expressed	GO:0019748	secondary metabolic process	P
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0008150	biological_process	P
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0016043	cellular component organization	P
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0016049	cell growth	P
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0005515	protein binding	F
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0009987	cellular process	P

LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os04g46860.1	scarecrow, putative, expressed	GO:0009536	plastid	C
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0006950	response to stress	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0009607	response to biotic stimulus	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0005737	cytoplasm	C
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0004518	nuclease activity	F
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0040029	regulation of gene expression, epigenetic	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0009987	cellular process	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0005515	protein binding	F
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0009628	response to abiotic stimulus	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0005829	cytosol	C
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0003723	RNA binding	F
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0008152	metabolic process	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0000003	reproduction	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os04g47870.1	PINHEAD, putative, expressed	GO:0009790	embryo development	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0006950	response to stress	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0009607	response to biotic stimulus	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0005737	cytoplasm	C
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0004518	nuclease activity	F
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0040029	regulation of gene expression, epigenetic	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0009987	cellular process	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0005515	protein binding	F
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0009628	response to abiotic stimulus	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0005829	cytosol	C
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0003723	RNA binding	F
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0008152	metabolic process	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0000003	reproduction	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os04g47870.2	PINHEAD, putative, expressed	GO:0009790	embryo development	P
LOC_Os04g51190.1	growth-regulating factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g51190.1	growth-regulating factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os04g51190.2	growth-regulating factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g51190.2	growth-regulating factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os04g51190.3	growth-regulating factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g51190.3	growth-regulating factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os04g55290.1	G10 protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g55290.1	G10 protein, putative, expressed	GO:0005829	cytosol	C
LOC_Os04g55290.1	G10 protein, putative, expressed	GO:0008150	biological_process	P
LOC_Os04g55290.2	G10 protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g55290.2	G10 protein, putative, expressed	GO:0005829	cytosol	C
LOC_Os04g55290.2	G10 protein, putative, expressed	GO:0008150	biological_process	P

LOC_Os04g55290.3	G10 protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g55290.3	G10 protein, putative, expressed	GO:0005829	cytosol	C
LOC_Os04g55290.3	G10 protein, putative, expressed	GO:0008150	biological_process	P
LOC_Os04g55290.4	G10 protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g55290.4	G10 protein, putative, expressed	GO:0005829	cytosol	C
LOC_Os04g55290.4	G10 protein, putative, expressed	GO:0008150	biological_process	P
LOC_Os04g55290.5	G10 protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g55290.5	G10 protein, putative, expressed	GO:0005829	cytosol	C
LOC_Os04g55290.5	G10 protein, putative, expressed	GO:0008150	biological_process	P
LOC_Os04g55650.1	oryzain alpha chain precursor, putative, expressed	GO:0005576	extracellular region	C
LOC_Os04g55650.1	oryzain alpha chain precursor, putative, expressed	GO:0008152	metabolic process	P
LOC_Os04g55650.1	oryzain alpha chain precursor, putative, expressed	GO:0006950	response to stress	P
LOC_Os04g55650.1	oryzain alpha chain precursor, putative, expressed	GO:0009628	response to abiotic stimulus	P
LOC_Os04g55650.1	oryzain alpha chain precursor, putative, expressed	GO:0005575	cellular_component	C
LOC_Os04g55650.1	oryzain alpha chain precursor, putative, expressed	GO:0005773	vacuole	C
LOC_Os04g55650.1	oryzain alpha chain precursor, putative, expressed	GO:0016787	hydrolase activity	F
LOC_Os04g55650.1	oryzain alpha chain precursor, putative, expressed	GO:0005515	protein binding	F
LOC_Os04g55650.1	oryzain alpha chain precursor, putative, expressed	GO:0009536	plastid	C
LOC_Os04g55650.2	oryzain alpha chain precursor, putative, expressed	GO:0005576	extracellular region	C
LOC_Os04g55650.2	oryzain alpha chain precursor, putative, expressed	GO:0008152	metabolic process	P
LOC_Os04g55650.2	oryzain alpha chain precursor, putative, expressed	GO:0006950	response to stress	P
LOC_Os04g55650.2	oryzain alpha chain precursor, putative, expressed	GO:0009628	response to abiotic stimulus	P
LOC_Os04g55650.2	oryzain alpha chain precursor, putative, expressed	GO:0005575	cellular_component	C
LOC_Os04g55650.2	oryzain alpha chain precursor, putative, expressed	GO:0005773	vacuole	C
LOC_Os04g55650.2	oryzain alpha chain precursor, putative, expressed	GO:0016787	hydrolase activity	F
LOC_Os04g55650.2	oryzain alpha chain precursor, putative, expressed	GO:0005515	protein binding	F
LOC_Os04g55650.2	oryzain alpha chain precursor, putative, expressed	GO:0009536	plastid	C
LOC_Os04g57610.1	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os04g57610.1	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os04g57610.1	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g57610.1	auxin response factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os04g57610.1	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os04g57610.1	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os04g57610.1	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os04g57610.3	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os04g57610.3	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os04g57610.3	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os04g57610.3	auxin response factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os04g57610.3	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os04g57610.3	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os04g57610.3	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os05g10670.1	zinc finger CCCH type family protein, putative, expressed	GO:0006950	response to stress	P
LOC_Os05g10670.1	zinc finger CCCH type family protein, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os05g10670.1	zinc finger CCCH type family protein, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os05g10670.1	zinc finger CCCH type family protein, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os05g10670.1	zinc finger CCCH type family protein, putative, expressed	GO:0005886	plasma membrane	C
LOC_Os05g10670.1	zinc finger CCCH type family protein, putative, expressed	GO:0003676	nucleic acid binding	F
LOC_Os05g11560.2	aquaporin protein, putative, expressed	GO:0006810	transport	P
LOC_Os05g11560.2	aquaporin protein, putative, expressed	GO:0005215	transporter activity	F
LOC_Os05g11560.2	aquaporin protein, putative, expressed	GO:0016020	membrane	C
LOC_Os05g11560.2	aquaporin protein, putative, expressed	GO:0009987	cellular process	P
LOC_Os05g11560.2	aquaporin protein, putative, expressed	GO:0008150	biological_process	P

LOC_Os05g11560.2	aquaporin protein, putative, expressed	GO:0005886	plasma membrane	C
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0006810	transport	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0009987	cellular process	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0005488	binding	F
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0008152	metabolic process	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0005215	transporter activity	F
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0006950	response to stress	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0009607	response to biotic stimulus	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0005975	carbohydrate metabolic process	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0009056	catabolic process	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0019748	secondary metabolic process	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0008150	biological_process	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0005829	cytosol	C
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0016787	hydrolase activity	F
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os05g34290.1	glutathione gamma-glutamylcysteinyltransferase 1, putative, expressed	GO:0016740	transferase activity	F
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0003677	DNA binding	F
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0005634	nucleus	C
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0008152	metabolic process	P
LOC_Os05g43920.1	auxin response factor 14, putative, expressed	GO:0009987	cellular process	P
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0003677	DNA binding	F
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0005634	nucleus	C
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0009791	post-embryonic development	P
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0008152	metabolic process	P
LOC_Os05g48870.1	auxin response factor 15, putative, expressed	GO:0009987	cellular process	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0008150	biological_process	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0016043	cellular component organization	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0016049	cell growth	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0005515	protein binding	F
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0009987	cellular process	P
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g01620.1	scarecrow, putative, expressed	GO:0009536	plastid	C
LOC_Os06g01950.1	phosphoglycerate mutase, putative, expressed	GO:0005575	cellular_component	C
LOC_Os06g01950.1	phosphoglycerate mutase, putative, expressed	GO:0008152	metabolic process	P
LOC_Os06g01950.1	phosphoglycerate mutase, putative, expressed	GO:0003824	catalytic activity	F

LOC_Os06g02560.1	growth-regulating factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g02560.1	growth-regulating factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g02560.2	growth-regulating factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g02560.2	growth-regulating factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g02560.3	growth-regulating factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g02560.3	growth-regulating factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g05630.1	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0005576	extracellular region	C
LOC_Os06g05630.1	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0008152	metabolic process	P
LOC_Os06g05630.1	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0005515	protein binding	F
LOC_Os06g05630.1	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0016787	hydrolase activity	F
LOC_Os06g05630.1	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0006629	lipid metabolic process	P
LOC_Os06g05630.2	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0005576	extracellular region	C
LOC_Os06g05630.2	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0008152	metabolic process	P
LOC_Os06g05630.2	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0005515	protein binding	F
LOC_Os06g05630.2	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0016787	hydrolase activity	F
LOC_Os06g05630.2	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0006629	lipid metabolic process	P
LOC_Os06g05630.3	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0005576	extracellular region	C
LOC_Os06g05630.3	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0008152	metabolic process	P
LOC_Os06g05630.3	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0005515	protein binding	F
LOC_Os06g05630.3	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0016787	hydrolase activity	F
LOC_Os06g05630.3	GDSL-like lipase/acylhydrolase, putative, expressed	GO:0006629	lipid metabolic process	P
LOC_Os06g06600.1	OsFBX187 - F-box domain containing protein, expressed	GO:0003674	molecular_function	F
LOC_Os06g06600.1	OsFBX187 - F-box domain containing protein, expressed	GO:0008150	biological_process	P
LOC_Os06g11490.1	plastocyanin-like domain containing protein, putative, expressed	GO:0003674	molecular_function	F
LOC_Os06g11490.1	plastocyanin-like domain containing protein, putative, expressed	GO:0005488	binding	F
LOC_Os06g11490.1	plastocyanin-like domain containing protein, putative, expressed	GO:0016020	membrane	C
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0040007	growth	P
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0003677	DNA binding	F
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0000003	reproduction	P
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0008150	biological_process	P
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0008219	cell death	P
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g40330.1	MYB family transcription factor, putative, expressed	GO:0007165	signal transduction	P
LOC_Os06g45310.1	OsSPL11 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os06g45310.1	OsSPL11 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os06g45310.1	OsSPL11 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g45310.1	OsSPL11 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g45310.1	OsSPL11 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g45310.1	OsSPL11 - SBP-box gene family member, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os06g45310.1	OsSPL11 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g46410.1	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os06g46410.1	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os06g46410.1	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g46410.1	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g46410.1	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g46410.1	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F

LOC_Os06g46410.2	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os06g46410.2	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os06g46410.2	auxin response factor, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g46410.2	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g46410.2	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g46410.2	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0000003	reproduction	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0007165	signal transduction	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0009908	flower development	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0008150	biological_process	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0003723	RNA binding	F
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0009987	cellular process	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0040007	growth	P
LOC_Os06g47150.1	auxin response factor 18, putative, expressed	GO:0019748	secondary metabolic process	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0000003	reproduction	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0007165	signal transduction	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0009908	flower development	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0008150	biological_process	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0003723	RNA binding	F
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0009987	cellular process	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0040007	growth	P
LOC_Os06g47150.2	auxin response factor 18, putative, expressed	GO:0019748	secondary metabolic process	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0000003	reproduction	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0007165	signal transduction	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0009908	flower development	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0008150	biological_process	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0003723	RNA binding	F
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0009987	cellular process	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0040007	growth	P
LOC_Os06g47150.3	auxin response factor 18, putative, expressed	GO:0019748	secondary metabolic process	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0000003	reproduction	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0007165	signal transduction	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0009058	biosynthetic process	P

LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0009908	flower development	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0005634	nucleus	C
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0008150	biological_process	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0003723	RNA binding	F
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0009987	cellular process	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0040007	growth	P
LOC_Os06g47150.4	auxin response factor 18, putative, expressed	GO:0019748	secondary metabolic process	P
LOC_Os06g47850.1	zinc finger family protein, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g47850.1	zinc finger family protein, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g47850.1	zinc finger family protein, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g48240.1	AAA ATPase, putative, expressed	GO:0005623	cell	C
LOC_Os06g48240.1	AAA ATPase, putative, expressed	GO:0008152	metabolic process	P
LOC_Os06g48240.1	AAA ATPase, putative, expressed	GO:0000166	nucleotide binding	F
LOC_Os06g48240.1	AAA ATPase, putative, expressed	GO:0016787	hydrolase activity	F
LOC_Os06g48240.1	AAA ATPase, putative, expressed	GO:0009056	catabolic process	P
LOC_Os06g48240.1	AAA ATPase, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g49010.1	OsSPL12 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os06g49010.1	OsSPL12 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os06g49010.1	OsSPL12 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os06g49010.1	OsSPL12 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g49010.1	OsSPL12 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g49010.1	OsSPL12 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g49010.1	OsSPL12 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g49010.2	OsSPL12 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os06g49010.2	OsSPL12 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os06g49010.2	OsSPL12 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os06g49010.2	OsSPL12 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g49010.2	OsSPL12 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g49010.2	OsSPL12 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g49010.2	OsSPL12 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g49010.3	OsSPL12 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os06g49010.3	OsSPL12 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os06g49010.3	OsSPL12 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os06g49010.3	OsSPL12 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g49010.3	OsSPL12 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g49010.3	OsSPL12 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g49010.3	OsSPL12 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g49010.4	OsSPL12 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os06g49010.4	OsSPL12 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os06g49010.4	OsSPL12 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os06g49010.4	OsSPL12 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g49010.4	OsSPL12 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g49010.4	OsSPL12 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g49010.4	OsSPL12 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g49010.5	OsSPL12 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os06g49010.5	OsSPL12 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os06g49010.5	OsSPL12 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os06g49010.5	OsSPL12 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g49010.5	OsSPL12 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P

LOC_Os06g49010.5	OsSPL12 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g49010.5	OsSPL12 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os06g49010.6	OsSPL12 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os06g49010.6	OsSPL12 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os06g49010.6	OsSPL12 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os06g49010.6	OsSPL12 - SBP-box gene family member, expressed	GO:0007275	multicellular organismal development	P
LOC_Os06g49010.6	OsSPL12 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os06g49010.6	OsSPL12 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os06g49010.6	OsSPL12 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os07g11790.1	terpene synthase, putative, expressed	GO:0005575	cellular_component	C
LOC_Os07g11790.1	terpene synthase, putative, expressed	GO:0009607	response to biotic stimulus	P
LOC_Os07g11790.1	terpene synthase, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os07g11790.1	terpene synthase, putative, expressed	GO:0009987	cellular process	P
LOC_Os07g11790.1	terpene synthase, putative, expressed	GO:0006629	lipid metabolic process	P
LOC_Os07g11790.1	terpene synthase, putative, expressed	GO:0003824	catalytic activity	F
LOC_Os07g32170.1	OsSPL13 - SBP-box gene family member, expressed	GO:0009791	post-embryonic development	P
LOC_Os07g32170.1	OsSPL13 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os07g32170.1	OsSPL13 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os07g32170.1	OsSPL13 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os07g32170.1	OsSPL13 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os07g32170.1	OsSPL13 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os08g36840.1	glycoprotein 3-alpha-L-fucosyltransferase A, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os08g36840.1	glycoprotein 3-alpha-L-fucosyltransferase A, putative, expressed	GO:0006464	protein modification process	P
LOC_Os08g36840.1	glycoprotein 3-alpha-L-fucosyltransferase A, putative, expressed	GO:0005975	carbohydrate metabolic process	P
LOC_Os08g36840.1	glycoprotein 3-alpha-L-fucosyltransferase A, putative, expressed	GO:0016740	transferase activity	F
LOC_Os08g36840.1	glycoprotein 3-alpha-L-fucosyltransferase A, putative, expressed	GO:0008152	metabolic process	P
LOC_Os08g36840.1	glycoprotein 3-alpha-L-fucosyltransferase A, putative, expressed	GO:0005794	Golgi apparatus	C
LOC_Os08g37670.1	plastocyanin-like domain containing protein, putative, expressed	GO:0003674	molecular_function	F
LOC_Os08g37670.1	plastocyanin-like domain containing protein, putative, expressed	GO:0005488	binding	F
LOC_Os08g37670.1	plastocyanin-like domain containing protein, putative, expressed	GO:0016020	membrane	C
LOC_Os09g12230.1	ubiquitin-conjugating enzyme, putative, expressed	GO:0019538	protein metabolic process	P
LOC_Os09g12230.1	ubiquitin-conjugating enzyme, putative, expressed	GO:0009056	catabolic process	P
LOC_Os09g12230.1	ubiquitin-conjugating enzyme, putative, expressed	GO:0009987	cellular process	P
LOC_Os09g12230.1	ubiquitin-conjugating enzyme, putative, expressed	GO:0006464	protein modification process	P
LOC_Os09g12230.1	ubiquitin-conjugating enzyme, putative, expressed	GO:0005886	plasma membrane	C
LOC_Os09g12230.1	ubiquitin-conjugating enzyme, putative, expressed	GO:0003824	catalytic activity	F
LOC_Os10g33940.1	auxin response factor 18, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os10g33940.1	auxin response factor 18, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os10g33940.1	auxin response factor 18, putative, expressed	GO:0005634	nucleus	C
LOC_Os10g33940.1	auxin response factor 18, putative, expressed	GO:0009987	cellular process	P
LOC_Os10g33940.1	auxin response factor 18, putative, expressed	GO:0003723	RNA binding	F
LOC_Os10g33940.1	auxin response factor 18, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os10g33940.1	auxin response factor 18, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os10g33940.1	auxin response factor 18, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os10g33960.1	START domain containing protein, expressed	GO:0007275	multicellular organismal development	P
LOC_Os10g33960.1	START domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os10g33960.1	START domain containing protein, expressed	GO:0005634	nucleus	C
LOC_Os10g33960.1	START domain containing protein, expressed	GO:0030154	cell differentiation	P
LOC_Os10g33960.1	START domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os10g33960.1	START domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os10g33960.1	START domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os10g33960.1	START domain containing protein, expressed	GO:0008289	lipid binding	F

LOC_Os10g33960.1	START domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os10g33960.2	START domain containing protein, expressed	GO:0007275	multicellular organismal development	P
LOC_Os10g33960.2	START domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os10g33960.2	START domain containing protein, expressed	GO:0005634	nucleus	C
LOC_Os10g33960.2	START domain containing protein, expressed	GO:0030154	cell differentiation	P
LOC_Os10g33960.2	START domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os10g33960.2	START domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os10g33960.2	START domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os10g33960.2	START domain containing protein, expressed	GO:0008289	lipid binding	F
LOC_Os10g33960.2	START domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os10g33960.3	START domain containing protein, expressed	GO:0007275	multicellular organismal development	P
LOC_Os10g33960.3	START domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os10g33960.3	START domain containing protein, expressed	GO:0005634	nucleus	C
LOC_Os10g33960.3	START domain containing protein, expressed	GO:0030154	cell differentiation	P
LOC_Os10g33960.3	START domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os10g33960.3	START domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os10g33960.3	START domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os10g33960.3	START domain containing protein, expressed	GO:0008289	lipid binding	F
LOC_Os10g33960.3	START domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os10g33960.4	START domain containing protein, expressed	GO:0007275	multicellular organismal development	P
LOC_Os10g33960.4	START domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os10g33960.4	START domain containing protein, expressed	GO:0005634	nucleus	C
LOC_Os10g33960.4	START domain containing protein, expressed	GO:0030154	cell differentiation	P
LOC_Os10g33960.4	START domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os10g33960.4	START domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os10g33960.4	START domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os10g33960.4	START domain containing protein, expressed	GO:0008289	lipid binding	F
LOC_Os10g33960.4	START domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os10g39520.1	MLO domain containing protein, putative, expressed	GO:0006950	response to stress	P
LOC_Os10g39520.1	MLO domain containing protein, putative, expressed	GO:0016020	membrane	C
LOC_Os10g39520.1	MLO domain containing protein, putative, expressed	GO:0008219	cell death	P
LOC_Os10g39520.1	MLO domain containing protein, putative, expressed	GO:0005515	protein binding	F
LOC_Os10g39520.1	MLO domain containing protein, putative, expressed	GO:0005886	plasma membrane	C
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0008150	biological_process	P
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0030154	cell differentiation	P
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0016043	cellular component organization	P
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0016049	cell growth	P
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0005515	protein binding	F
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0009987	cellular process	P
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os10g40390.1	scarecrow, putative, expressed	GO:0009536	plastid	C
LOC_Os11g30370.1	OsSPL19 - SBP-box gene family member, expressed	GO:0009908	flower development	P
LOC_Os11g30370.1	OsSPL19 - SBP-box gene family member, expressed	GO:0003677	DNA binding	F
LOC_Os11g30370.1	OsSPL19 - SBP-box gene family member, expressed	GO:0005634	nucleus	C
LOC_Os11g30370.1	OsSPL19 - SBP-box gene family member, expressed	GO:0009058	biosynthetic process	P
LOC_Os11g30370.1	OsSPL19 - SBP-box gene family member, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os11g30370.1	OsSPL19 - SBP-box gene family member, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os11g35030.1	growth regulating factor protein, putative, expressed	GO:0005634	nucleus	C

LOC_Os11g35030.1	growth regulating factor protein, putative, expressed	GO:0005515	protein binding	F
LOC_Os11g35030.1	growth regulating factor protein, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os11g35030.2	growth regulating factor protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os11g35030.2	growth regulating factor protein, putative, expressed	GO:0005515	protein binding	F
LOC_Os11g35030.2	growth regulating factor protein, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os12g29980.1	growth regulating factor protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os12g29980.1	growth regulating factor protein, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os12g29980.2	growth regulating factor protein, putative, expressed	GO:0005634	nucleus	C
LOC_Os12g29980.2	growth regulating factor protein, putative, expressed	GO:0007275	multicellular organismal development	P
LOC_Os12g31860.1	ureide permease, putative, expressed	GO:0005623	cell	C
LOC_Os12g31860.1	ureide permease, putative, expressed	GO:0005215	transporter activity	F
LOC_Os12g31860.1	ureide permease, putative, expressed	GO:0006810	transport	P
LOC_Os12g31860.1	ureide permease, putative, expressed	GO:0009987	cellular process	P
LOC_Os12g31860.2	ureide permease, putative, expressed	GO:0005623	cell	C
LOC_Os12g31860.2	ureide permease, putative, expressed	GO:0005215	transporter activity	F
LOC_Os12g31860.2	ureide permease, putative, expressed	GO:0006810	transport	P
LOC_Os12g31860.2	ureide permease, putative, expressed	GO:0009987	cellular process	P
LOC_Os12g31860.3	ureide permease, putative, expressed	GO:0005623	cell	C
LOC_Os12g31860.3	ureide permease, putative, expressed	GO:0005215	transporter activity	F
LOC_Os12g31860.3	ureide permease, putative, expressed	GO:0006810	transport	P
LOC_Os12g31860.3	ureide permease, putative, expressed	GO:0009987	cellular process	P
LOC_Os12g31860.5	ureide permease, putative, expressed	GO:0005623	cell	C
LOC_Os12g31860.5	ureide permease, putative, expressed	GO:0008150	biological_process	P
LOC_Os12g40920.1	bZIP transcription factor domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os12g40920.1	bZIP transcription factor domain containing protein, expressed	GO:0005515	protein binding	F
LOC_Os12g40920.1	bZIP transcription factor domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os12g40920.1	bZIP transcription factor domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os12g40920.1	bZIP transcription factor domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os12g40920.3	bZIP transcription factor domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os12g40920.3	bZIP transcription factor domain containing protein, expressed	GO:0005515	protein binding	F
LOC_Os12g40920.3	bZIP transcription factor domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os12g40920.3	bZIP transcription factor domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os12g40920.3	bZIP transcription factor domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os12g40920.4	bZIP transcription factor domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os12g40920.4	bZIP transcription factor domain containing protein, expressed	GO:0005515	protein binding	F
LOC_Os12g40920.4	bZIP transcription factor domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os12g40920.4	bZIP transcription factor domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os12g40920.4	bZIP transcription factor domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0003677	DNA binding	F
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0005634	nucleus	C
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0007275	multicellular organismal development	P
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0009058	biosynthetic process	P
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0000003	reproduction	P
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0009791	post-embryonic development	P
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0009790	embryo development	P
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0009908	flower development	P
LOC_Os12g41860.1	START domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
LOC_Os12g41950.1	auxin response factor, putative, expressed	GO:0009908	flower development	P
LOC_Os12g41950.1	auxin response factor, putative, expressed	GO:0009719	response to endogenous stimulus	P
LOC_Os12g41950.1	auxin response factor, putative, expressed	GO:0005634	nucleus	C

LOC_Os12g41950.1	auxin response factor, putative, expressed	GO:0009058	biosynthetic process	P
LOC_Os12g41950.1	auxin response factor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
LOC_Os12g41950.1	auxin response factor, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F