

University of Groningen

Method for the identification of single mutations in large genomic regions using massive parallel sequencing

Sturre, Marcel J. G.; Shirzadian-Khorramabad, Reza; Schippers, Jos H. M.; Chin-A-Woeng, Thomas F. C.; Hille, Jacob; Dijkwel, Paul P.

Published in:
Molecular Breeding

DOI:
[10.1007/s11032-008-9213-3](https://doi.org/10.1007/s11032-008-9213-3)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2009

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Sturre, M. J. G., Shirzadian-Khorramabad, R., Schippers, J. H. M., Chin-A-Woeng, T. F. C., Hille, J., & Dijkwel, P. P. (2009). Method for the identification of single mutations in large genomic regions using massive parallel sequencing. *Molecular Breeding*, 23(1), 51-59. DOI: 10.1007/s11032-008-9213-3

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Supplementary Table. Polymorphisms detected between Col-0 and Ler-0

Position	Col-0	Ler-0	Insertion	Left Flank	Right Flank	Database Hit
25557043	G	C		GACAATGACATAACAGAAACACAA	TTAGCAAAAGGCTGATTTGACATTT	ATL8C20161
25557151	A	G		TTCATCAGGTCTTAAATGGGAAGT	TTCTCGGAGAAACCGGGTATTTGGG	MASC01306
25557306	G	A		ATTGTTAGATTAATTGAATTCGTC	AGAAAGAATCTGAAGCAAATGTACT	ATL8C20161
25557345	T	C		GCAAATGTA CTCAATCTGCTGCAG	ATAACAGTCAGTGAAAATGAAGCGT	ATL8C20161
25557360	A	T		CTGCTGCAGTATAACAGTCAGTGA	AATGAAGCGTTCCTTGAAGAAAGGAA	MASC01308
25557480	G	T		TACCTTCAACACTCTCTACAATTC	TTTGTTATTTCACTCAATTTTCTAAT	ATL8C20161
25557491	-4	InDel	TTGC	CTCTCTACAATTCGTTTGTATTTT	ACTCAATTTTCTAATTGATTGGTCG	ATL8C20161
25557513	G	C		TTCACTCAATTTTCTAATTGATTG	TCGTAAATGTGACA ACTGGTTTCTA	PERL1114862
25557514	T	G		TCACTCAATTTTCTAATTGATTGG	CGTAAATGTGACA ACTGGTTTCTAG	ATL8C20161
25557728	-1	InDel	T	CTCATACATTCGGTTACTTTTTTT	CTGCCACAGAATGCAGGATCCTTTT	ATL8C20161
25557812	A	G		AATCAAAGGTTTCAACAAGGGCAC	TTGAATTTGACAAACAGCAAATGGT	MASC01309
25557919	-1	InDel	A	TGTTTCTAACAACATTC CATGAA	TCTTGCAGCTCGGCGTGAAGGAGA	CER455728
25557930	C	A		ACATTC CATGAATCTTGCAGCT	GCGGTGAAGGAGAGCATCTAGAAC	CER437464
25558024	C	T		ACGAAACCTCCCAAGAAACAGCCT	TGACTTGGTATAAGGTAATGTAGTA	CER437465
25558043	T	A		AGCCTCTGACTTGGTATAAGGTAA	GTAGTAGCAACTCTTGGACAAGAAG	CER437467
25558051	C	T		ACTTGGTATAAGGTAATGTAGTAG	AACTCTTGGACAAGAAGCAAGATTG	CER437467
25558081	A	T		TTGGACAAGAAGCAAGATTGTAGA	GATAAAGTTGTGTCTCTAAAATAT	ATL8C20161
25558103	T	A		AAGATAAAGTTGTGTCTCTAAAA	ATCTGATCTTTTGGTAGGTTGTGAT	CER437468
25558103	-1	InDel	A	AAGATAAAGTTGTGTCTCTAAAAT	ATCTGATCTTTTGGTAGGTTGTGAT	CER455729
25558153	G	A		AGAGCCACCTTCTGGGAGTGAGCC	GTTGGGCTTGATATGATCAGTATGG	ATL8C20161
25558201	T	C		GGGAAAGGAATGGCATGGTTAAA	GGTGAAGAGATAGGAAGATATTGGC	ATL8C20161
25558204	T	G		GAAAGGAATGGCATGGTTAAATGG	GAAGAGATAGGAAGATATTGGCCA	ATL8C20161
25558227	C	A		TGAAGAGATAGGAAGATATTGGCC	AGGATTGCTAGAAAGAACAGCCCGA	ATL8C20161
25558398	T	C		CCTTTGTTCAAATTTGTTATTGT	TTTTTTTTGTTTTTGGATGATTAG	CER437469
25558399- 25558401	InDel	-3	TTT	TTGTTCAAATTTGGTTATTGTT	TTTTTGTTTTTGGATGATTAGGTA	CER455730
25558679	G	T		ATGAAACAAAATCCCAATTTTAT	AACTTAACACAGTTTTTCATCATCA	ATL8C20161
25558989- 25559012	InDel	-23	GTTTCCTTGTTCGT CTCAGGGATG	TTGATCTCTTATTAG	TTTTTTTTTATTGAATTTGATTTTGA	ATL8C20161
25559018	-1	InDel	A	TTGTCGTCTCAGGGATGTTTTTT	TTATTGAATTTGATTTTATTGTTCC	ATL8C20161
25559020	T	A		TTGTCGTCTCAGGGATGTTTTTTT	TATTGAATTTGATTTTATTGTTCCA	ATL8C20161

25559047	G	A		TGAATTTGATTTTGATTTTCCAGG	TTTTGATTATGGATTTGACTTTACT	ATL8C20161
25559060	A	G		GATTTTCCAGGGTTTTGATTATGG	TTTGACTTTACTGGCATAGTTACGC	ATL8C20161
25559241	-3	InDel	CAT	CCTAACCTTGATTCCTCTCTTCATA	TATTGCTTGCTTGTGAGGGGACAAA	ATL8C20161
25559459	A	C		CTGGAGGGTCTTGGCCTGCAGACC	ACATGTACGTATGCTTT-TCTTCTT	PERL1114887
25559848	-1	InDel	C	GTCCTTGAATTTCTTCTTCTTCTT	TTTCTTCATGTTTCTTTTCTCTTAC	ATL8C20161
25559850	-14	InDel	TCTTCTTCTTCTTC	GTCCTTGAATTTCTTCTTCTTCTT	TTCTTCATGTTTCTTTTCTCTTACG	ATL8C20161
25559886	G	A		CTTTTCTCTTACGCTTGCTTGCCA	TGTGACTTTAGGAATTGAAGGTTTC	ATL8C20161
25559913- 25559922	InDel	-10	AAGGTTTCCC	TGACTTTAGGAATTG	CACCCTTGGAGATCAACAAGGTAGT	ATL8C20161
25559963	A	G		TGTAGAAACTAAAGAAGATTACAT	ACTGAGGCGCGTGAGAAGCTCCACG	PERL1114891
25560140	G	T		AGTCGAGAACAAGAAGAAGAAGAA	AAGAAGAAGGAGAATAGACAGACAC	ATL8C42488
25560143	G	A		CGAGAACAAGAAGAAGAAGAAGAA	AAGAAGGAGAATAGACAGACACCTC	ATL8C42488
25560146	G	T		GAACAAGAAGAAGAAGAAGAAGAA	AAGGAGAATAGACAGACACCTCTTG	ATL8C42488
25560147- 25560152	InDel	-6	AAGGAG	GAAGAAGAAGAAGAAGAAG	AATAGACAGACACCTCTTGTATGCA	ATL8C42488
25560207	G	T		TGGTCTGTTGCAATCAATTATTAA	CGCTATTCAACTTTTATCTTGTTAT	ATL8C42488
25560209	G	A		GTCTGTTGCAATCAATTATTAAGC	CTATTCAACTTTTATCTTGTTATAT	ATL8C42488
25560222	T	A		AATTATTAAGCGCTATTCAACTTT	TATCTTGTTATATGACTATGCACGA	ATL8C42488
25560226	T	A		ATTAAGCGCTATTCAACTTTTATC	TGTTATATGACTATGCACGATGTGT	ATL8C42488
25560252- 25560275	RA 24/33 bp		AAAGATAATGCTGGGATC TATATG/GTTTGGCTTGTC TTTATGTCTACAACCTTCAG GC	TGTTATATGACTATGCACGATGTGT	CTATAGCGAGTTGGGATCTATATGT	ATL8C42488
25560282	G	A		TAATGCTGGGATCTATATGACTATA	CGAGTTGGGATCTATATGTATTTTAA	PERL1114895
25560291	G	A		GGATCTATATGACTATAGCGAGTTGG	ATCTATATGTATTTAACCTTCGCT	ATL8C42488
25560301	-2	InDel	AC	ATAGCGAGTTGGGATCTATATGT	ATTTTAACCTTCGCTAACTGCTGGA	ATL8C42488
25560319	C	G		TATATGTATTTAACCTTCGCTAA	CTGCTGGATATCTGTTTGCAATGCA	ATL8C42488
25560326	A	C		ATTTTAACCTTCGCTAACTGCTGG	TATCTGTTTGCAATGCATAATAGTA	PERL1114897
25560331	T	A		AACCTTCGCTAACTGCTGGATATC	TGTTTGCAATGCATAATAGTACTTT	ATL8C42488
25560350	-1	InDel	T	ATATCTGTTTGCAATGCATAATAGT[-/T]	ACTTTGTATGATAAGTTGATAACCA	ATL8C42488
25560359- 25560366	InDel	-8	TGATAAGT	CATAATAGTACTTTGTA	TGATAACCAATAACACAAGCTGTAC	ATL8C42488
25560376	C	A		TAAGTTGATAACCAATAACACAAG	TGTACCAAACCGTGGAGGTTATTGA	ATL8C42488
25560377	InDel	-1	T	AAGTTGATAACCAATAACACAAGC	GTACCAAACCGTGGAGGTTATTGAT	ATL8C42488

25560398	G	A		CAATAACACAAGCTGTACCAAACC	TGGAGGTTATTGATATGATCAGTAT	ATL8C42488
25560408	T	C		AGCTGTACCAAACCGTGGAGGTTA	TGATATGATCAGTATGTGGAAAGGC	ATL8C42488
25560435	A	T		ATATGATCAGTATGTGGAAAGGCA	AGGCATAGTTAAATGGTAAAGAGAT	no hit
25560441	A	G		TCAGTATGTGGAAAGGCAAGGCAT	GTTAAATGGTAAAGAGATTGGCCCA	no hit
25560468	InDel	-1	G	TAAATGGTAAAGAGATTGGCCAG	AGTTCTCCAAATGACGAATATGTTA	no hit
25560470	G	A		AATGGTAAAGAGATTGGCCCAGGA	TTCTCCAAATGACGAATATGTTAAA	no hit
25560471	T	C		ATGGTAAAGAGATTGGCCCAGGAG	TCTCCAAATGACGAATATGTTAAAA	no hit
25560474	T	C		GTAAAGAGATTGGCCCAGGAGTTC	CCAAATGACGAATATGTTAAAAAAT	no hit
25560487	T	A		CCCAGGAGTTCTCCAAATGACGAA	ATGTTAAAAAATCCGATTAGAGGCAA	ATL8S1679
25560496	A	G		TCTCCAAATGACGAATATGTTAAA	AATCCGATTAGAGGCAAGCAAATTC	ATL8S1679
25560500	C	T		CAAATGACGAATATGTTAAAAAAT	CGATTAGAGGCAAGCAAATTCGTGC	ATL8S1679
25560501	C	A		AAATGACGAATATGTTAAAAAATC	GATTAGAGGCAAGCAAATTCGTGCC	ATL8S1679
25560505	-2	InDel	AC	ACGAATATGTTAAAAAATCCGATT	AGAGGCAAGCAAATTCGTGCCACTG	ATL8S1679
25560522	G	A		CCGATTAGAGGCAAGCAAATTC	TGCCACTGGTCACTGGATGTGGAGA	ATL8S1679
25560577	-1	InDel	C	TCTGAGATGGTAAACTAGAAAGCC	ATTAGAGTTCTCAGATTTTTTCATTG	ATL8S1679
25560591	G	A		ACTAGAAAGCCATTAGAGTTCTCA	ATTTTTTCATTGTTTTTTTGGCTAAG	ATL8S1679
25560593- 25560606	InDel	-14	TTTTTCATTGTTTT	ATTAGAGTTCTCAGA	TTTGGCTAAGGTATCGTCAAGTTCC	ATL8S1679
25560622	G	A		CATTGTTTTTTTTGGCTAAGGTATC	TCAAGTTCCAGGTACGATCATGAAG	ATL8S1679
25560626	A	T		GTTTTTTTTGGCTAAGGTATCGTCA	GTTCCAGGTACGATCATGAAGATTT	ATL8S1679
25560637	C	G		TAAGGTATCGTCAAGTTCCAGGTA	GATCATGAAGATTTGGGATTCATAT	ATL8S1679
25560657	T	A		GGTACGATCATGAAGATTTGGGAT	CATATGCTACCAAGGGAAACCAAGC	ATL8S1679
25560673	InDel	-1	G	TTTGGGATTCATATGCTACCAAGG	AAACCAAGCAAGATATATATATATA	ATL8S1679
25560676- 25560684	InDel	-9	ACCAAGCAA	ATTCATATGCTACCAAGGGAA	GATATATATATATATATATATCGTTTG	ATL8S1679

25560694	A	T		AGGGAAACCAAGCAAGATATATAT	TATATATATCGTTTGCCTAGTTAAC	ATL8S1679
25560695- 25560702	InDel	-8	TATATATA	CAAGCAAGATATATATA	TCGTTTGCCTAGTTAACACACCTTA	ATL8S1679
25560732	T	A		TGCCTAGTTAACACACCTTACATT	TTTAATTAGGAACACCACAAGATAT	ATL8S1679
25560883	C	T		TTCTTCTTCATTTCTGGAAACCCT	TGTAATCGTTGAGCTCAACCACCGA	no hit
25560959	T	C		TCCAGAGCTTCCCATACTTCAGAA	TCTGCTCATTGACCCAACACATCAT	no hit
25561406	G	C		AGAGAGGAGATGGATTTCGTGGAG	TAAGCTTGCTTAGTGAGATCAAAGG	PERL1114907
25561498	A	G		TTCTTCGTCTTCAACGCATTGAAC	AGTTGTGTACCTCCGAGTCCAAGAT	ATL8C43675
25561958	A	G		TGCTTATTACATACATGGCAGATA	TCCGCGTAGAAGAAGGGTTTAACGG	CER437470
25561965	T	A		TACATACATGGCAGATAATCCGCG	AGAAGAAGGGTTTAACGGAGACGAA	CER437471
25561980	A	G		TAATCCGCGTAGAAGAAGGGTTTA	CGGAGACGAATTTGAACTCTCCGAC	CER437472
25562174	A	G		CTATGGGCCTTCATTTTAATAAAC	GGTCGGATATATCCACCGGACCCGG	CER437473
25562242	G	T		TGTTGTATTTTGGCTTTCCTCATT	CTTCTCAATCTAAGGATTTCCATG	CER437474
25562447	A	T		CTAATTGTGCGCGATGTTTCCATC	CTGATGGAGATCTCGTAGCGAAGCT	ATL8C5828
25562491- 25562493	InDel	-3	TCA	AGCTTCTACCGAAAGCGCCTAA	AGGCGATGGGGATCAGATCAAGCCG	CER455731
25562527	T	A		GGATCAGATCAAGCCGTTGATTCT	TCTCTCTCAGTTTACAAGGATGGGA	ATL8C5828
25563037	C	T		TGGAGTTGAGGAATCTGAACCCTA	AGGCTTTTTAATCTAGATGTGTTTG	CER437475
25563043	T	G		TGAGGAATCTGAACCCTACAGGCT	TTTAATCTAGATGTGTTTGAATACG	CER437476
25563235	C	G		TGGTATTTCTTTGCCTTCTAGTCA	AGTAGGATCGACACATTCTGGATGA	CER437477 / PERL1114918
25563274	T	C		ATTCTGGATGAGCGAGGCAGGGAT	GTGGATACATTCTTTTTCGTTGGGCC	CER437478
25563295	T	C		GATTGTGGATACATTCTTTTTCGT	GGGCCTGAGCCAAAGGATGTTGTAA	CER437479
25563299	G	C		TGTGGATACATTCTTTTTCGTTGG	CCTGAGCCAAAGGATGTTGTAAAGC	CER437480 / PERL1114921
25563382	T	C		TCAGTTGTTTGCCACTGGTTATCA	CAATGTAGGTGGAACACTACAAAGATG	CER437481
25563409	G	A		ATGTAGGTGGAACACTACAAAGATGA	GAGGATGTGGCACAGGTGGACTCGA	CER437482
25563481	T	C		TTATGATGTTCTCTGGCTTGACAT	GAGCATAACAGATGGGAAGAGATACT	CER437483 / PERL1114924
25563634	A	G		GGATGACTCATACTTCTTACACAA	GAGGCTACTCAGATGGGATACTATG	CER437484
25563673	T	A		GGGATACTATGTTAAGGATTCATC	GGAAAAGACTTTGATGGTTGGTGCT	CER437485 / SGCSNP29

25563832	T	C		CTGGAATGACATGAATGAGCCTTC	GTATTCAATGGTCCCGAGGTATAAC	PERL1114927
25563881	T	G		CTTTCTGTCTGAATGGTCTTTTTT	CTTGTTCCGTTATTGTTTTTCTGTA	CER437486
25563956	A	T		CATTTTGGGATTGCAGTTGAATAT	GCAATCCATTGTTTTTCTATTGCAC	CER437487
25563983	A	G		AATCCATTGTTTTTCTATTGCACA	TTATGGATATGTTTGAAGTCTGATA	CER437488
25564034	C	G		ATTATACATCCCTTATCTTGCATA	TATGACACCTTTTATTAATTATTGC	CER437489
25564062	T	C		GACACCTTTTATTAATTATTGCAC	ACTAAAGCAAGTATTTTAAGATCCA	CER437490
25564128- 25564129	InDel	-2	TG	GTTTTACATTGGATATTTGTTTCTG	ACTTCTTTAAGAGTGGAGTGTAAGC	CER455734
25564169	T	A		GAGTGTAAAGCTATGGTTGCATATC	CCACCTCTGATTTGCTTATATCGTA	CER437491
25564201	T	A		TGATTTGCTTATATCGTAGAAAGT	TATCATATATGTAAAGGTCTATTAC	CER437492
25564217	G	A		TAGAAAGTTTATCATATATGTAAA	GTCTATTACTGAGATGAAGACTGGC	CER437493
25564256	T	C		TGAAGACTGGCACTTTTTTCTTTC	TTTTTGTGGAGTAGGTTACTATGC	CER437494
25564349	C	T		TCATAACGCATATGGATATTA	CACATGGCGACTTCCGATGGACTTG	CER437495 / PERL1114933
25564611	A	T		TTTTTCTTTCTCAAATTTAATGGA	GTTTTCTTTTCTTTTGCAGGAGCTG	CER437496
25564613	T	C		TTTCTTTCTCAAATTTAATGGAAG	TTTCTTTTCTTTTGCAGGAGCTGAT	CER437497
25564831	G	C		GTATTATTTTAGTATGCGGTCCAG	TCTAGTCTATGGATATTTGCTTGAT	CER437498 / MASC04435
25564881	A	G		GGATGATCAAGCAGATTGAAATGT	GTGATACTGGTTATTGAGAAAAGAA	CER437499 / MASC04436
25564921	C	A		GAGAAAAGAATACAATTGCGGAAA	TAAACCTGGTGTTGCACTCTAGTC	CER437500 / MASC04437
25566147	G	A		AAGACTGGACCGTAAAGATTCTGT	ATTGAACGGTTTGAACCAGTTTCAC	CER437501 / PERL1114949
25566238	G	A		GGAATATCACACTTTTTAATATAT	TTTGGAGATTTAGACTTAAATAGTT	CER437502
25566424	T	G		TCAGAGGGTCAAATAATCTTACCT	CCATCGTTGCCTAATTATTGTCAA	CER437503
25566431	T	C		GTCAAATAATCTTACCTCCATCG	TGCCTAATTATTGTCAAATCCTTT	CER437504
25566503	A	T		GAAAAATCTTGAATTACACGTTTT	AGAGTCATGAAGAAAAATCAATCTG	CER437505 / PERL1114953
25566527	T	A		AAGAGTCATGAAGAAAAATCAATC	GATTCTGTTGGCTAGATTTGTTTT	CER437506
25566557	-3	InDel	TAT	TGGCTAGATTTGTTTTTTTTAT	ACTGCTTAGTGTTTACTGTTATAGA	CER455735/36/37
25566576	T	C		TTTATACTGCTTAGTGTTTACTG	TATAGAAAGGGTTCTAAGTATGCAA	ATL8C5828
25566644	C	T		AATGTTAGATCCGTGTAGGTGAAA	AAGAAGCCAAAATTCTGTGTA	ATL8C5828
25566652	-1	InDel	A	TCCGTGTAGGTGAAACAAGAAGCC	AAAATTCTGTGTA	ATL8C5828

25566771	T	C		ATATATTCCGTTTCATGAATCTCGT	TCGAATTTAAACTAAAATATTACAC	no hit
25567818	A	T		CACTAAAGAATAGAGAGAAAACAA	ACCATGCAAAAACCTCTCAAAAATT	ATL8C11987
25567882	InDel	-1	C	TAGACAAAGAGCCAAATTTATTCCG	TTTTTGATGTTTACATCAGTATTTG	ATL8C11987
25567927	A	C		ATTTGTTTCTAGCTAGTTTCATATT	TTTAAACTCCATAATCATTGAAAG	ATL8C11987
25567969	T	C		TTTGAAAGACATAAAATACAGATG	TTAAGATCTGTGGATGTTTATATAG	ATL8C11987
25568702	G	A		AACTAGTGAATCCTCATAACTTTG	TTTCTCACTAAAAACAGATGGATGT	CER437507 / PERL1114966
25573445	C	T		AGAAGAAGAAAACCAACAGAAGTA	ATACAATGAAGCCAGTCTTCTTCAG	ATL8C10031
25573483	G	T		AGTCTTCTTCAGTAGGTAATAGTT	TCAGAAAGTTTTCGAAAAACATATT	ATL8C10031
25575680- 25575683	InDel	-4	AGAA	CGGTGATTATTTGAGTCCGTAAT	AAGGAAAAAACAGCGAAGAAGAA	CER455738/39/40
25576646- 25576647	InDel	-2	TT	GATATACGGTCTACTTACAACCTTGA	TTTTTTTTTTTTGTTAAATTACAAC	ATL8C28682
25576695	A	C		ACTTGAAGATTCTACTATCAACAA[A/C]	ACAAAAACAAAAAAAATCTTCTAT	ATL8C28682
25576697	C	A		TTGAAGATTCTACTATCAACAAA[C/A]	AAAAACAAAAAAAATCTTCTATCG	ATL8C28682
25576703	C	A		ATTCTACTATCAACAAAACAAAA[C/A]	AAAAAAAATCTTCTATCGATCGAG	ATL8C28682
25576713	T	A		CAACAAAACAAAAACAAAAAAA[T/A]	CTTCTATCGATCGAGCGAGATATTC	ATL8C28682
25577037	C	T		AACGAATATATCACCTCGCTCGAC[C/T]	TAACATTTATGTGAAACTAAAAGGT	PERL1115077
25577159	T	A		AAATTAATGAATGAAGATATTTT[T/A]	GCATTGCCTGATACATGCATTATAT	ATL8C28682
25577384	G	A		TGGAAAAATGGAAATTATATGAAA[G/A]	CCATTGGAAGTACTATATACAATTT	ATL8C28682
25577471	A	G		AGATAAGACACCTATAATAATTTA[A/G]	GCTTGACATGAAGTGCTAAACAATT	ATL8C28682
25577534- 25577580	InDel	-47	GAAAAACATTGC GGTGAGTACATGT CAATGATTGTCTGA TGAACAAA	CATATATGCACATGAAACTAGGAAA	TTACAAAACAGTAAAAATCAACACC	CER455741
25578129	G	C		ATTTTCATAACCACACAATTTTTT	TTGGATAAGATTCTAGTAATGTGTC	ATL8C28682
25578355	C	T		TACAAGATTTAGGTTTAAATAAGA	GTGTAGGAACCAAGAACTAAGAAC	no hit
25579928	A	G		GGATACAGAGTCAAGATCATCGAT	TGAACGCAGTTACGTTCTTTGTGGA	CER437508
25581953	-1	InDel	T	TATCTTCTTATTTGATCACTGCTTT	GTGTGGCACAGTTTGTCTGAGCTC	ATL8C36413
25581964	G	T		TTGATCACTGCTTTGTGTGGCACA	TTTGTTCTGAGCTCGTCTAGTGTGA	CER437509 / PERL1115109
25582529	C	G		AATACGATTTTATCATTCTTTTAC	AGTTTTTCTTTGGTGCTCTCTGAA	no hit
25582530	A	G		ATACGATTTTATCATTCTTTTACC	GTTTTTCTTTGGTGCTCTCTGAAG	no hit
25584005	A	T		TCCACCAGCTTTGAGTATGTGAGT	ACACCAGCCCTCTTGGCGCAATACA	PERL1115124

25585486	G	A		GGTTTACAAAACCAATTAAGGCC	TAAAGCCCATTTCATCTGCACCGCTA	no hit
25585649	G	T		CAAGAATGGGCCTTTCTGTATAAA	ATTTTTCGAAAACGTTTATGAGCCA	ATL8C35527
25588032	C	T		TCAGCTCATTGATTCTAACATCG	TCTAAACAACCTTATTTATTGGATAC	ATL8C46351
25589108	InDel	-1	G	TGTTTTGTATGCTAATGCCAATG	TCTGATTCAAGAACTCGAAAAAGAT	ATL8C45366
25589134	T	A		CTGATTCAAGAACTCGAAAAAGAT	AAAAAAAAGAAGAAGCTTAGGTTAC	CER437510
25592276	G	T		TCCTCTTTGACAGAGATGT	GCTTGATTTAAGCCGGTGGAAACAG	CER436437
25592276	A	G		GGGGTTTTCTGACTTGCAAGTTTT	TTTAATTCTGGTGTGAGTGAATTA	CER436438
25592646	C	T		TAGATGCTAGACAAGTGAGTTTCT	CTGAAATCCCTCTTCTGTTTATGTG	CER436439
25592932	T	C		TTTACATATCAGAGCCAGTTAATG	AGCTAGATTTGATATTTCTCTGCTT	CER436440 / PERL1115185
25596704	A	T		GTATCATATATTCTGTCTGAACAA	ATTTTCTCTGTTCTCCCTATTGTTA	CER436441
25597781	G	A		GTCCCTCACGGGTTCCAGCATCTC	AAATTCTCGTCTACTGCAACAAAT	CER436442
25598433	A	C		CTAACGCTTGTCTAATCGTAATA	CTCTAACGGTAACTATTTCTAAGTC	ATL8C34962
25598935	C	A		ATTAACAACCTGTTAATAACACAAA	CACAGTCGTTTTGCTCTGTAAGAAA	CER436443
25600108	InDel	-1	T	GCTTGTTATGCTACATGATTTGAG	TTTTTTGGATGGTTTTATGGTATGT	ATL8C34962
25602136	T	C		TTGCAAATAGCATTGAACCTCAGTTA	AACAAGCTTACCGGAGAAATACCAC	CER436444
25602358	C	T		CATCGGTAATGAAGGGCTTTGCGG	CCGCCGCTCAACCAGTGTATCCAAA	CER436445
25604533	-5	InDel	TATTG	TTAGCGATAGGATGATATGTGTATT	CCTAACTCGATCATGAACTTTAATA	ATL8C16826
25604548	G	A		TATGTGTATTCTAACTCGATCAT	AACTTTAATATGTGCTAGAAACATC	ATL8C16826
25604690	A	G		TTAGAATACTTCTTTAACAAAAAA	ACATCCAAATATATACTTTTCACAA	ATL8C16826
25605032	-3	InDel	GAA	AGAATCCAAAGTGAAGAAGAAG	TTGAAAAACAAAAA	ATL8C16826
25605404- 25605405	InDel	-2	AG	ACGAGAGACAGAGAGAGAGAGAG	GGAAATTTGCTACTGAGAGATACAT	ATL8C16826
25605653	T	C		CGTTGCTCTTCATGTTCTCGATTA	TCTCTAGGTTTGTAAACCCTCGA	ATL8C16826
25606222	T	A		ACGGTAATGGTGGTTTGTCTCTG	TAGTTCTTAAGGTAAAGGTTTGGGC	CER436446
25608686	T	C		CGGTTTTAAAAGTTTAAAATGTA	AAGTGTTCCGATTCCGTTTTAAGGTT	ATL8C37237
25609159	T	-1	T	GAACAATTTTTTTTTTTTTTTTTT	GTCAAAAAAGACCGAACAGTATGT	CER455211
25609812- 25609813	InDel	-2	GA	AGTTTTTTTTCAAATCTATGAGA	TTATACAAAACAACACAACATAAAT	CER455212
25613447	T	C		CAATATCATAGGTTGTTAGAAGAA	ACCTTTACCCTACAAAAGTTAAAGA	No hit
25613616	T	C		GATTTACTAGAGGAAGGGGCAACA	TGTCACAAATCAAGTGA AACGTAA	PERL1115367
25615124	C	A		GCAGTATAATAACAGCTATAAAGA	CGAAAATCAAACACCAGACTAGAAA	ATL8C36087
25615827- 25615828	InDel	-2	TC	CGCTCTCTCTCTCTCTCTCTC	ACATTTAACCTACAATACAACAAAA	CER455213

25619417	T	C		TTCCGAGCAGGTGAAACCGAGTAA	TATGCTTAGAATTTTCAGGTTATTTTC	No hit
25620791	T	G		TGTTAAGCAAACCTTTGCAAAGGT	TCCGCATTTAGTTAGATTTTTATTATC CT	CER436447
25623423	T	A		GGTCCCTTGCCTATGTATTATCTG	TTTCATATATGGGATCTGTTTATCA	ATL8C37506
25624328	-1	InDel	A	TTCTTGCATGTCTTTATTTGAAAT	AAAAGTATCGGAGATGTCACAAAA	CER455214
25624831	T	A		ATACAAGTAGTTTCCAACGGTAAA	TTTTTATTGCATTTACTTGAGACTT	CER436448 / PERL1115468
25629542	G	A		GATCTAGTCAAACCTTTATAAAGGG	CGATCACAAATCTACTAGTCGCACA	ATL8C35938
25630081	-2	InDel	AA	AAAATGAAATATCTCTCTCTAAG	AAAATATCTTCTATTGGACCAATT	ATL8C35938
25630362	T	A		TCGCAACGGTAGGGGACTCTATAC	TTGCCTACTTTTTCCACAACGGTAGA	CER436449 / PERL1115489
25632270	C	T		CTCTCAGTGTGCGACTCTTCTCTG	GAAGGTAAACTACTTGAAACCACTC	PERL1115503
25633029	-2	InDel	CA	CTGTTGTCTCTGTGTTTTTACACA	GTCTATTTATTGAAAACCGAAACA	CER455215
25633502	T	G		AAATAAGCCCAATTTGTTTTTTTT	GTTTTTTTTTGGTAAACATTTTTTTT	No hit
25633503	G	T		AATAAGCCCAATTTGTTTTTTTT	TTTTTTTTTGGTAAACATTTTTTTT	No hit
25633524	-1	InDel	G	TTTGTTTTTTTTTTGGTAAACATT	TTTTTTTCTAAGTATGTTAACCAATT	No hit
25634792	C	T		GTGTCATGGCTTGCCCAAATCTTC	TTTGGCTTCTGCGGTTTGC GCGACT	ATL8C2765
25634793	T	C		TGTCATGGCTTGCCCAAATCTTCC	TTGGCTTCTGCGGTTTGC GCGACTG	CER436450
25634821	A	C		GCTTCTGCGGTTTGC GCGACTGAT	ATTCTTCCCAGGAAGATGTTGGCTG	CER436451
25635358	A	C		TAATCACTACAGGTACAGTACATA	AACCTTTTTAAACGCTGAGATCTGT	CER436452
25635809	T	C		ATACATCAGATATGAAAGATATTT	TGCTTAGATAATGAATAATGATACT	CER436453
25636698	A	T		ATACTACTATGAAGAGCTGAAAAA	TTACCTTGTAGGTGCTGCTTGCTCT	CER436454 / PERL1115540
25637093	-1	InDel	C	TTCAAATCAAGTTTTTTTAAAAAAT	CAACGTGAGTAAAACCTCAAGTGCC	CER455216
25637392	T	A		TCTCAAATATGGGTTCTGAATTTTC	CGAAACTCGCCATGTCAAGAAAAAA	CER436455
25637523	A	G		TTTTAACCGTCCCGATATCGTACC	GATTTTCGGTTAAGAAAAAGATTGTT	CER436456 / PERL1115546
25638444	T	C		ATACAAGATCGTTCGTGTTTGTGGT	GGGAACCGATAAGCCCAACCATCAG	PERL1115548
25638450	C	T		GATCGTTCGTGTTTGTGGTTGGGAA	CGATAAGCCCAACCATCAGGACGGA	ATL8C29655
25639036	G	C		TCTGAAGATAACAAGAGTTCAAAA	TTTCGACCATTATAACCAAAAAAAT	No hit
25639337	A	T		AAGTTCAAGATCCTAAGAAAGACC	GTCAGATAGTGTAAACAAAATCTTGT	PERL1115553
25639805	T	A		CATCAAATTCACGTTGATGTTTT	TTTTCTTTTCTTGTGTTTGGCTTCT	ATL8C40740
25639806	InDel	-1	T	ATCAAATTCACGTTGATGTTTT	TTTCTTTTCTTGTGTTTGGCTTCT	ATL8C40740
25639910	-15	InDel	AAAAGAAAGGTCA	TTGTTCCCATAAAA	AAAAGATACTATAACTGATGCGTTA	ATL8C40740

			TT			
25640861	T	C		CAAGACATGTATCATTTTCACCTT	CTTTTGTTGTTAATTTAATTTTGGG	No hit
25640971	T	C		AAACAAAATTTAAGCTAGAGTAAT	ATCAAAACAAAAAAGCAAAGAAAG	No hit
25640980	InDel	-1	A	TTAAGCTAGAGTAATTATCAAAAC	AAAAAAGCAAAGAAAGAGTAAAGTT	CER455217
25641024	A	T		AAAGTTTAAAAAGTGTTATATTTT	TTTTTTTTGCTTTTAGCTAAAATCA	No hit
25641381	C	T		ATCAGAATCAATATTCTCTTGCCA	ATATATCCTTTATATATACACCTT	No hit
25642735	T	C		AACCAGAAACAGAGGACAATGAGT	GGGTGAGGATGGTGAAAACCAAAG	CER436457 / PERL1115569
25643610	G	A		CATGTTTCTTTTATGCATCCACTT	TTTTCTACTCCCTTATTTTGTTAGA	CER436458
25645801	G	T		GTATTCAGTCAGGTTTTTTATCTTA	GCTGAACTTAATGCAAATAATGCA	ATL8S17392
25648602	G	A		GAAGAAATCAGAAAAGCTAGGGATG	CAACAAAGTAACTACAGTCAACAAA	PERL1115588
25649012	C	A		CTCCTATATTCTGGATCACATAACTT	CGAAAGCAATTGGAATAAACAAACA	PERL1115591
25649013- 25649018	InDel	-6	CGAAAG	TATTCTGGATCACATAACTTC	CAATTGGAATAAACAAACATAAGCT	CER455794
25651829	G	A		TGCAAGGAATCAAACGTTAAAAAAA	ACAAGAACGAATCGTCATTACCTGA	ATL8C26272
25652465	G	A		TCACAATAACAAGATCTAGCAGA	ACAAAAAGCTAAGAAGAAGAAGAAA	PERL1115608
25652534	T	A		CCACAACCTTCCCTCTGCTCATATA	CCACAGTCACACCAAAGAAACGATG	ATL8C13476
25653739	-1	InDel	A	TTGGTAAATAGTTTTTCTCCAAC	AATTTGACTATGCTTGTGTTTCA	CER455796
25654447	G	A		CAGGCTTTTGCCTTCTTTCTCCT	CAAGTAGAGCAAGTAAGTAAAGATA	PERL1115620
25656460	C	T		AATATATCTAGCACATGAACAATA	AGTTACTTTATAAGGCCGGAATATC	No hit
25657889	C	A		CGACCACCTTACCCATTCAAGAT	ATTGTTTACGCCAGTCCTTGGGGCT	ATL8C6793
25658217	-1	InDel	A	GATTCTTTAGCACTGACGTAACAA	TATCAGAAAACAAAAAGAACAATGG	No hit
25658498	G	C		TTATTTGAATTTAAATTATGAATA	AAATTCATTTTGATAACAAAAACAT	ATL8C42982
25658888	T	A		GGCTCAATATATTTGAGCTACACA	ATAAAGTAGACCTCCAAATAATAAC	PERL1115642
25659525	A	C		AAACAGTGCAAATGCAACCAGTAT	TGCAATAAGACAGAAACACAAAAGA	PERL1115646
25661672	-6	InDel	AGAGAG	CAGAGAGAGAGAGAGAGAGAG	GGGAAAGTAATTATCGTTTCGCAATA	No hit
25661732	-1	InDel	T	TTTTCATTTTTTTATTAATTTTAA	TTTTTTGGTTTTTAGTAATTCGTAC	No hit
25661921	A	G		ACTTTTGTTGACAGTTGATTTTTC	TTATTTTCTTTCAAAGATTATTAC	ATL8C7222
25661931	-1	InDel	G	CAGTTGATTTTTTATTATTTTCTT	TCAAAGATTATTACTATTGAGATT	ATL8C7222
25662135	C	G		GATGAAGAAATTTTGTACTCGTTT	ATAGAACAAGTTGTAATTGGTACTA	PERL1115656
25662111	G	A		TAAATATGATACTCTTGACAAAAA	TTGGGACTTACTTACTGACAATGAC	ATL8C7222
25662111	-1	InDel	T	TAAATATGATACTCTTGACAAAAAG	TTGGGACTTACTTACTGACAATGAC	ATL8C7222
25662243- 25662350	RA [106/1		TGAGAAAATTTTCATCTACT AAAATGATATCATATGATT	TTACTTACTGACAATGACGATATTA	TTGCAATATTACACCATAATTTTCT	ATL8C7222

	20]	TCCTGTATTTTATTACACA GTTTTTATGAGAAAATTAA AACGAAATTAAGAATTTT GTTGTTAGTCA / ATGTTGTTAACATCAAATC GATAATAGTGGGAATAAA TTTGAGCTATGTGGACCA TGATATTATATTCCAGAAG GACCTATACTTCTTCCCT GAAGAGGGAAAGTTCTGT TTATGGGGAG				
25662693	G	T		TCTAGCTGGTGAAAAAAGATTCAG	TTTTTTTTTACGCACTAGAGAAGAA	ATL8C7222
25662782	C	A		AATAAAGCATTGCATGAGACAAAA	TTAAGAGTAAAATTAATAATCAACC	No hit
25664132	T	G		CATCTTCCTTCTTTCTTTTTTTC	CTCTTCCTTTTCAAGTTTTTACTCA	No hit
25665717	A	G		AACTTATCTCTCCTCTGATCCACC	CTTCGTCTCGTTGTCCTCTCGTTCT	PERL1115673

The short sequence reads of solexa were aligned with SSAKE to assemble *de novo* Ler-0 sequence data. Subsequently the formed contigs were aligned to Col-0 in Seqman and screened for polymorphisms.