

Fig. S1. Illustration shows the position of primers used during primer walking. The primer sequences are shown in the bottom of the Illustration.

A) Reference and cloned sequences:

>Xcc_racel_strain_B100 (1515 bp) (Reference sequence)

**GCGAGCGATTTACACCTTCATCCGCACGCATGAAGGCTGGATGTATTTGGCTGTTGTGATCGATCTGTTTTCCAGGCAGGTTCGT
CGGCTGGGCGATGCGCGATCGGGCCGACACCGAGTTGGTTCGTGCAGGCGGTGTTGTCTGCGGTGTGGCGGCGCAAACCCAACG
CTGGTTGCTTGGTTCAATTCGGACCAAGGGTCTGTCTACACCAGCGATGACTGGCGCAGTTTCCTGGCGTCCCATGGCTTGGTG
TGCAGCATGAGTCGGCGTGGCAACTGCCACGACAACGCACCCGTGGAGAGCTTCTTCGGCCTGCTCAAACGCGAGCGGATCAG
GCGGCTGACCTATCCACCAAGGACGCCGCTCGCGCCGAGGTATTGACTACATCGAGATGTTCTACAACCCCAACCGCCGCC
ACGGTTCAACTGGCGACCTGTACCTGTAGAGTTTGAACGGCGCTACGCGCAACGAGGGTCTTGAGTGTCTACGGAACCCCTGG
GCGTATCAGGTCAATTCATCATTGACTTTCATCAGCCTTGGCGTTCGCCATCCGCAAGGCGCCGAGTGAGCTCGCTTGGTTA
CGGATCGCGGTGTCTCGTCCGATTTCCACGTGCGCCAAAAGCGCGCCCAACTCGGCATCCTCCAGCGATTCTGCTCCTGC
AAGGAACACGAGCTTGCACCCGCGCGCCGCTTGGTCTCTTCGCGCGCTGTGTTTCCTTGGCTTTTGCCGCTTGGCGCT
GCTGCGCTAAAAGCCCAACCGCTGGAGCTGGGCCAATCGTTCTGTGGCTCTCTGGATTCTCTGGTGGTAGCGGGTTGGCTCG
GTCATGCTTTTCTCCTTTGGGTGCTTACGAGTCAACCAAGAAATGGCTCGCGTCAAGTTCGCGCCGGCTTGAATAATTTGGGC
TCCCTCGAAATCAAAAAAATCTGAAAAACAAGACTTAAAAAGAAAGCAAGAGCGCACTTATGCAATGTTTACATTGCGCG
CGCAAAGGGCTCCGCCCTTGTGTGACTCCCCGTAATAATTGATCCATCCATAACTAGAGGTCTCCGGGCACACTAGCCACCA
AGGAGACCAACGATGCGCAAGAGCAAGTTCACCGAGAGCCAGATTGTGCCACGCTGAAGCAGGTGGAGGGCGGCCGCCAGGT
CAAAGATGTGTGCCGTGAGCTGGGCATTTCCGACGCGACGTAACGCTGGAAGTCCAAGTACGGTGGCATGGAGGCAGCTG
ACGTGCAGCGCCTTCGCGACCTGGAGACCGAGCACAGCAAGCTCAAGCGCATGTATGCCGAGCTCGCGATGAAAACTATGCA
CTCAAGGATGTATCGCAAAAAAGCTATAGACCCGGCGCACAAAGCGCCCGCTTCTCGCCTGGCTCGTCGAGCAGCATGGCTGG
AGCGAGCGCCGGGCTGTGCGGTGCTTGGCGTGGCGCGCTCGACAGCACGCTATCGGCGTCTCCGATCGGGATGAGGAGGT
CATTCGCGCTGTTGTCGAATT**

>XccR5_89.2 (2172 bp) (Xcc race 5)

**GCGAGCGATTTACACCTTCATCCGCACGCATGAAGGCTGGATGTATTTGGCTGTTGTGATCGATCTGTTTTCCAGGCAGGTTCGT
CGGCTGGGCGATGCGCGATCGGGCCGACACCGAGTTGGTTCGTGCAGGCGGTGTTGTCTGCGGTGTGGCGGCGCAAACCCAACG
CTGGTTGCTTGGTTCAATTCGGACCAAGGGTCTGTCTACACCAGCGATGACTGGCGCAGTTTCCTGGCGTCCCATGGCTTGGTG
TGCAGCATGAGTCGGCGTGGCAACTGCCACGACAACGCACCCGTGGAGAGCTTCTTCGGCCTGCTCAAACGCGAGCGGATCAG
GCGGCGGACCTATCCACCAAGGACGCCGCTCGCGCCGAGGTATTGACTACATCGAGATGTTCTACAACCCCAACCGCCGCC
ACGGTTCAACTGGCGACCTGTACCTGTAGAGTTTGAACGGCGCTACGCGCAACGAGGGTCTTGAGTGTCTACGGAACCCCTGG
GCGTATCAAGTCGCTCGCCGCTCGGGTCAAACCTGTCTTCAGCGCCTGGCCGTAGCGATGTGATTTAGATCGCGAAATGCA
AGCTCGATCTGCATCCGTCGTGCGTACACATTAACCAACTGCTTTGCGCTGGGCGCCTGCAGCTGCGGGGATGCAACGATGAG
CCAAGGCTCGCGCTCGCGGCTGCGGCCCTCAGACTCGATGACGCACGCGAGACTTTGGCGGGTGGAGCGGCGATTGCACTGTT
TGCGCCCTTGGCGTGCCTTGGCGTAAATCACCAACCTGCAATCGAGTGGATCGCTGCGATTGGCCTGCATCGGCGGTAACCTCG
CATGCACGATTGGACGCCAACACATGCAGTTTCCGGCTGTGATCCACTGATCTGCTTATCCCGCACGTCCTGCGGCTTGAC
TTGCGTGGCGCCGCGCAGTCGCCAACCAACACCAGCCATGGCCGATACAGCGCGGAACACGGTGTCCGGAAGCCGGCGGT
CAGTGACCAGGATCGGGCAACATCGTCCGGAACAGTGCCTCAGTTGTTGCAAGAAGCGTCTTCTGCACCAGGCGATCCC
TGCTGCTTTCCTGGCACTACCATGTCCAGCAAGGTAAGCGTGGCGCCGCCACCGGCACCGCTGCGCGCAGCAGACACCACGA
TTTGTCTGGCTTACAGATCGCTCCAGTCGATGACGATTACCGGCTGCGCGCCGCGCAGCAGCCAGTGCGCCATCTCGTGGTCTGA
TCACTGATCGCTCGACCTGCAAATTGCGATTACTCAACAGGCGATCAACTGCCTTGAGCGGCGCGCGCACCCGCGAGTGCCTC
GGCCACGAAACGTGCGATGTCCATCAGTGTGAGCTGCGTCCGTGCAACAACGCCTCGACCGCATGCAAGCAACGCGCTTCGCG
CAACGCATGCATCCGGGACAGTGGGCGAGCTTCTGCAATACTTCGCTGGCGCGCATGGTTCAGTCAACCTTCTCTGGC
TTAGTCACTTGAAGATTGCGCCATGCGCGCACTTTCTCCAGGCAATTACGTCGCAAGTATTGATTTGCCAGGAAATG
TGGGGAACCTCAGGTTGAGTTCACTTATTAGTTCGATGCGCTCGGCTTGGCTGGCCGGTGGCGGGCCGATGCCCGCAA
GCGGCGGCTTGGTGTGACTCCCCGTAATAATTGATCCATCCATAACTAGAGGTCTCCGGGCACACTAGCCACCAAGGAGAC
CACCAATGCGCAAGAGCAAGTTACCGGAGCCAGATCGTCCACGCTGAAGCAGGTGAGGGCGGTGCGCAGGTCAAGGAT
GTCGTGTCGCGAGCTGGGCATTTCCGATGCGACGTAACGCTGGAAGTCCAAGTACGGCGCATGGAGGCCGCTGACGTGCA
ACGCCTCCGCGACCTGGAGACTGAGCACAACAAGCTCAAACGATGTACCGGATCTCGCGATGAAAAACCATGCATTGAAGG
ATGTCATCGCAAAAAAGCTGTAGACCCGGCGCATAAGCGCCCGCTTCTTGCCTGGCTCATCGAGCAGCATGGCTGGAGCGAGC
GCCGGGCTTGTGCGGTGGTTGGCGTGGCTCGCTCGACAGCACGTTATCGGCGCCGTCGCCGATCGGGATGAGGAGGTTATTGGC
CTGTTGTCGAATT**

>ICMP8 (2172 bp) (race unknown Xcc strain)

**GCGAGCGATTTACACCTTCATCCGCACGCATGAAGGCTGGATGTATTTGGCTGTTGTGATCGATCTGTTTTCCAGGCAGGTTCGT
CGGCTGGGCGATGCGCGATCGGGCCGACACCGAGTTGGTTCGTGCAGGCGGTGTTGTCTGCGGTGTGGCGGCGCAAACCCAACG
CTGGTTGCTTGGTTCAATTCGGACCAAGGGTCTGTCTACACCAGCGATGACTGGCGCAGTTTCCTGGCGTCCCATGGCTTGGTG
TGCAGCATGAGTCGGCGTGGCAACTGCCACGACAACGCACCCGTGGAGAGCTTCTTCGGCCTGCTCAAACGCGAGCGGATCAG
GCGGCGGACCTATCCACCAAGGACGCCGCTCGCGCCGAGGTATTGACTACATCGAGATGTTCTACAACCCCAACCGCCGCC
ACGGTTCAACTGGCGACCTGTACCTGTAGAGTTTGAACGGCGCTACGCGCAACGAGGGTCTTGAGTGTCTACGGAACCCCTGG
GCGTATCAAGTCGCTCGCCGCTCGGGTCAAACCTGTCTTCAGCGCCTGGCCGTAGCGATGTGATTTAGATCGCGAAATGCA**

AGCTCGATCTGCATCCGTGCGTACACATTAACCAACTGCTTTGCGCTGGGCGCCTGCAGCTGCGGGGATGCAACGATGAG
 CCAAGGCTCGCGCTCGCGGCTGCGGCTTCAGACTCGATGACGCACGCGAGACTTTGGCGGGTGGAGCGCGGATTGCACCTGTT
 TGGCCCTTGGCGTGCCTTGGCGTAAATCACCAACCTGCAATCGAGTGGATCGCTGCGATTTGGCCTGCATCGGCGGTAACCTCG
 CATGCACGATTGGACGCCAACACATGCAGTTTCCGGCTGTCGATCCACTGATCTGCTTCATCCCCGCACGTCTCGCGGCTTGAC
 TTGCGTGCGCCCGCGCAGTCGCCAACCCAACACCAGCCATGGCCGATACAGCGCGGAACCACGGTGTCCGGAAGCCGGCGT
 CAGTGACCAGGATCGGGCGAACATCGTCCGGAACAGTGCCTCAGTTGTTGCAAGAAGCGTCTTTCTGCACCAGGCGATCCC
 TGCTGCTTTCTGGCACTACCATGTCCAGCAAGGTAAGCGTGCGGCCGCCACCAGGCACCGCTGCGCGCAGCAGACACCACGA
 TTTGTCTGGCTTACAGATCGCTCCAGTCGATGACGATTAACCGGCTGCGCGCCGCGCAGCAGCCAGTGCGCCATCTCGTGGTCTGA
 TCACTGATCGCTCGACCTGCAAATTGGCATTACTCAACAGGCGATCAACTGCCTTGAGCGGCGCGCGCACCCCGCAGTGCCTC
 GGCCACGAACGTGCGATGTCCATCAGTGTGAGCCTGCGTCCGTGCAACAACGCCTCGACCCGATGCAGCAACCGCGCTTCGCG
 CAACGATGCATCCCGGACAGTGAGTTGGGCAGGCACTTCTGCAATACTTCGCTGGCGCGCATGGTCTGCAACCTTCTCTGGC
 TTAGTCACCTTGAAGATTGCGCCATGCGCGCACTTCTTCCAGGCAATTACGTCGCAAGTGATTGATTGTCAGGAGGAAATG
 TGGGAAACCTCAGGGTCAGGTTCACTTATTAGTCGATGGCGCTCGGCTTGGCTGGCCGGTGCAGCGGGCCCGATGCCCGCAA
 GCGGCGGGTCTTGGTGTGACTCCCGTAAAATTGATCCATCCATAACTAGAGGTCTCCGGGCACACTAGCCACCAAGGAGAC
 CACCAATGCGCAAGAGCAAGTTCACCGAGAGCCAGATCGTCCGACGCTGAAGCAGGTCGAGGGCGGTCCGACAGTCAAGGAT
 GTCTGTGCGAGCTGGGCATTTCCGATGCGACGTAACGTCGGAAGTCCAAGTACGGCGGATGGAGGCCGCTGACGTGCA
 ACGCTCCGCGACCTGGAGACTGAGCACAACAAGCTCAAACGATGTACGCCGATCTCGCGATGGAAAACCATGCATTGAAGG
 ATGTCATCGAAAAAGCTGTAGACCCGGCGCATAAGCGCCCGCTTCTTGCCTGGCTCATCGAGCAGCATGGCTGGAGCGAGC
 GCCGGGCTTGTGCGGTGGTTGGCGTGGCTCGCTCGACAGCAGTTATCGGCGCCGTCGCGATCGGGATGAGGAGGTT**ATTGCG**
CTGTTGTCCGAATT

B) Alignment of Xcc race 5 specific fragment (XccR5_89.2) with reference (Xcc_race1_strain_B100) and race unknown Xcc strain (ICMP8)

Xcc_race1_strain_B100	GCGAGCGATTTCACCTTCAT CCGACGCGATGAAGGCTGGATGATTTGGCTGTTGTGATC	60
XccR5_89.2	GCGAGCGATTTCACCTTCAT CCGACGCGATGAAGGCTGGATGATTTGGCTGTTGTGATC	60
ICMP8	GCGAGCGATTTCACCTTCAT CCGACGCGATGAAGGCTGGATGATTTGGCTGTTGTGATC	60

Xcc_race1_strain_B100	GATCTGTTTTCCAGGCAGGTGTCGGCTGGGCGATGCGCGATCGGGCCGACACCGAGTTG	120
XccR5_89.2	GATCTGTTTTCCAGGCAGGTGTCGGCTGGGCGATGCGCGATCGGGCCGACACCGAGTTG	120
ICMP8	GATCTGTTTTCCAGGCAGGTGTCGGCTGGGCGATGCGCGATCGGGCCGACACCGAGTTG	120

Xcc_race1_strain_B100	GTCGTGCAGGCGGTGTTGTCTGCGGTGTGGCGGCGCAAACCCAACGCTGGTTGCTTGGTT	180
XccR5_89.2	GTCGTGCAGGCGGTGTTGTCTGCGGTGTGGCGGCGCAAACCCAACGCTGGTTGCTTGGTT	180
ICMP8	GTCGTGCAGGCGGTGTTGTCTGCGGTGTGGCGGCGCAAACCCAACGCTGGTTGCTTGGTT	180

Xcc_race1_strain_B100	CATTGGACCAAGGGTCTGTCTACACACGCGATGACTGGCGCAGTTTCTGGCGTCCCAT	240
XccR5_89.2	CATTGGACCAAGGGTCTGTCTACACACGCGATGACTGGCGCAGTTTCTGGCGTCCCAT	240
ICMP8	CATTGGACCAAGGGTCTGTCTACACACGCGATGACTGGCGCAGTTTCTGGCGTCCCAT	240

Xcc_race1_strain_B100	GGCTTGGTGTGAGCATGAGTCGGCGTGGCAACTGCCACGACAACGCACCCGTGGAGAGC	300
XccR5_89.2	GGCTTGGTGTGAGCATGAGTCGGCGTGGCAACTGCCACGACAACGCACCCGTGGAGAGC	300
ICMP8	GGCTTGGTGTGAGCATGAGTCGGCGTGGCAACTGCCACGACAACGCACCCGTGGAGAGC	300

Xcc_race1_strain_B100	TTCTTCGGCCTGCTCAAACGCGAGCGGATCAGGCGGCTGACCTATCCCACCAAGGACGCC	360
XccR5_89.2	TTCTTCGGCCTGCTCAAACGCGAGCGGATCAGGCGGCGGACCTATCCCACCAAGGACGCC	360
ICMP8	TTCTTCGGCCTGCTCAAACGCGAGCGGATCAGGCGGCGGACCTATCCCACCAAGGACGCC	360
	***** *****	
Xcc_race1_strain_B100	GCTCGGCCGAGGTATTGACTACATCGAGATGTTCTACAACCCAACCGCCGACGGT	420
XccR5_89.2	GCTCGGCCGAGGTATTGACTACATCGAGATGTTCTACAACCCAACCGCCGACGGT	420
ICMP8	GCTCGGCCGAGGTATTGACTACATCGAGATGTTCTACAACCCAACCGCCGACGGT	420

Xcc_race1_strain_B100	TCAACTGGCGACCTGTCACCTGTAGAGTTGAACGGCGCTACGCGCAACGAGGCTTGA	480

XccR5_89.2	TCAACTGGCGACCTGTCACCTGTAGAGTTTGAACGGCGCTACGCGCAACGAGGGTCTTGA	480
ICMP8	TCAACTGGCGACCTGTCACCTGTAGAGTTTGAACGGCGCTACGCGCAACGAGGGTCTTGA	480

Xcc_race1_strain_B100	GTGTCTACGGAACCCCTGGGCGTATCAGGTCAATTCATCTTTGACTTTCATCAGCCTTGG	540
XccR5_89.2	GTGTCTACGGAACCCCTGGGCGTATCAAGTCGCTCGCCGCGTCGGGTCAAACCTGTCTTCCA	540
ICMP8	GTGTCTACGGAACCCCTGGGCGTATCAAGTCGCTCGCCGCGTCGGGTCAAACCTGTCTTCCA	540
	***** * * * * *	
Xcc_race1_strain_B100	CG-----TTCGCCATCCGCAAGGCGCCGAGTGAGCTCGC-----	574
XccR5_89.2	GCGCCTGGCCGTAGCGATGTGATTCAGATCGCGAAATGCAAGCTCGATCTGCATCCGTC	600
ICMP8	GCGCCTGGCCGTAGCGATGTGATTCAGATCGCGAAATGCAAGCTCGATCTGCATCCGTC	600
	* * * * * * * * * *	
Xcc_race1_strain_B100	-----	574
XccR5_89.2	GTGCGTACACATTAACCAACTGCTTTGCGCTGGGCGCCTGCAGCTGCGGGGATGCAACGA	660
ICMP8	GTGCGTACACATTAACCAACTGCTTTGCGCTGGGCGCCTGCAGCTGCGGGGATGCAACGA	660
Xcc_race1_strain_B100	TTGGTTACGGATCGCGGTGTCGCT-----CCGATTTCCACGTG-----	613
XccR5_89.2	TGAGCCAAGGCTCGCGCTCGCGCTCGCGCCTTCAGACTCGATGACGCACGCGAGACTT	720
ICMP8	TGAGCCAAGGCTCGCGCTCGCGCTCGCGCCTTCAGACTCGATGACGCACGCGAGACTT	720
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Xcc_race1_strain_B100	-----CGCCAAAAGCGCGC	627
XccR5_89.2	TGGCGGGTGAAGCGGCGATTGCACTGTTTGCGCCCTTGCCGTGCCTTGGCGTAAATCACCA	780
ICMP8	TGGCGGGTGAAGCGGCGATTGCACTGTTTGCGCCCTTGCCGTGCCTTGGCGTAAATCACCA	780
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Xcc_race1_strain_B100	CC-ACCA-----CTCGGCATCCTCCAGCGATT-----	654
XccR5_89.2	ACCTGCAATCGAGTGGATCGTGCATTGGCCTGCATCGCGGTAACCTCGCATGCACGAT	840
ICMP8	ACCTGCAATCGAGTGGATCGTGCATTGGCCTGCATCGCGGTAACCTCGCATGCACGAT	840
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Xcc_race1_strain_B100	-----CTGCTCCTGCAAGGAACACGA	675
XccR5_89.2	TGGACGCCAACACATGCACTTCCGGCTGTCGATCCACTGATCTGCTTCATCCCGCACGT	900
ICMP8	TGGACGCCAACACATGCACTTCCGGCTGTCGATCCACTGATCTGCTTCATCCCGCACGT	900
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Xcc_race1_strain_B100	GC---TCTGCGACCCGCGC-----GCGCCGCTTG---	701
XccR5_89.2	CCTGCGGCTTGACTTGCCTGCGCCCGCGCAGTCGCCAACCCAACACCAGCCATGGCCG	960
ICMP8	CCTGCGGCTTGACTTGCCTGCGCCCGCGCAGTCGCCAACCCAACACCAGCCATGGCCG	960
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Xcc_race1_strain_B100	-----GTCTC-----	706
XccR5_89.2	ATACAGCGCGGAACCACGGTGTCCGGAAGCCGGCGTCAGTGACCAGGATCGGGCGAACAT	1020
ICMP8	ATACAGCGCGGAACCACGGTGTCCGGAAGCCGGCGTCAGTGACCAGGATCGGGCGAACAT	1020
	* * *	
Xcc_race1_strain_B100	-----TTCGCGGCGCTGTGTTTCC-----	725
XccR5_89.2	CGTCCGGAACCAGTGCCCTCAGTTGTTGCAAGAAGCGTCTTTCTGCACCAGGCGATCCCT	1080
ICMP8	CGTCCGGAACCAGTGCCCTCAGTTGTTGCAAGAAGCGTCTTTCTGCACCAGGCGATCCCT	1080
	* * * * * * * * * *	
Xcc_race1_strain_B100	---TTGGCTTTTGGCGCTTGGCGCTGCTGCGCTAAAAGCCAC-----GCG	768
XccR5_89.2	GCTGCTTTCTGGCACTACCATGTCCAGCAAGGTAAGCGTGCGGCCGCCACCGGCACCG	1140
ICMP8	GCTGCTTTCTGGCACTACCATGTCCAGCAAGGTAAGCGTGCGGCCGCCACCGGCACCG	1140
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Xcc_race1_strain_B100	CTTGG---AGCTGGGCAA---TCGTTCTGT-----GGCTCTCTGGATTCTCTGGTGGTAG	818
XccR5_89.2	CTGCGCGCAGCAGACACCACGATTTGTCTGGCTTCCAGATCGCTCCAGTCGATGACGATTA	1200
ICMP8	CTGCGCGCAGCAGACACCACGATTTGTCTGGCTTCCAGATCGCTCCAGTCGATGACGATTA	1200
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Xcc_race1_strain_B100	CGG-----GTTGGCT-----CGGTCATGCTTTCTCCT	846
XccR5_89.2	CCGGCTGCGCGCCGCCAGCAGCCAGTGC GCCATCTCGTGGTCTGATCACTGATCGCTCGA	1260
ICMP8	CCGGCTGCGCGCCGCCAGCAGCCAGTGC GCCATCTCGTGGTCTGATCACTGATCGCTCGA	1260
	* * * * * ** ** ** * * *	
Xcc_race1_strain_B100	TTGGG-----TGCTTAGGAGTCAACCAAAGAAATGGCTCGC-----	882
XccR5_89.2	CCTGCAAATTGCGATTACTCAACAGGCGATCAACTGCCTTGAGCGGCGCGGCACCCGCA	1320
ICMP8	CCTGCAAATTGCGATTACTCAACAGGCGATCAACTGCCTTGAGCGGCGCGGCACCCGCA	1320
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Xcc_race1_strain_B100	-----	882
XccR5_89.2	GTGCGCTCGGCCACGAACGTGCGATGTCCATCAGTGTCAGCCTGCGTCCGTGCAACAACG	1380
ICMP8	GTGCGCTCGGCCACGAACGTGCGATGTCCATCAGTGTCAGCCTGCGTCCGTGCAACAACG	1380
Xcc_race1_strain_B100	-----GTCAAGTTCGCG-----CCGG-----	898
XccR5_89.2	CCTCGACCGCATGCAGCAACGCCGCTTCGCGCAACGCATGCATCCGGACAGTGAGTTGG	1440
ICMP8	CCTCGACCGCATGCAGCAACGCCGCTTCGCGCAACGCATGCATCCGGACAGTGAGTTGG	1440
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Xcc_race1_strain_B100	-----	898
XccR5_89.2	GCAGGCACCTTCTGCAATACTTCGCTGGCGGCATGGTTCGTCAACCTTCTTGCTTGTAGTC	1500
ICMP8	GCAGGCACCTTCTGCAATACTTCGCTGGCGGCATGGTTCGTCAACCTTCTTGCTTGTAGTC	1500
Xcc_race1_strain_B100	---CTTGAAAATTGGGCTCCCTCG-----AAATCAAAAAAATCTGAAAAACAAGA	946
XccR5_89.2	ACCTTGAAGATTGCGCCATGCGCGCAGTCTTCTCCAGGCAATTACGTGCAAGTGATTGA	1560
ICMP8	ACCTTGAAGATTGCGCCATGCGCGCAGTCTTCTCCAGGCAATTACGTGCAAGTGATTGA	1560
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Xcc_race1_strain_B100	CTTAAAGAAAGCAAGA-----GCGCACTTAT-----	976
XccR5_89.2	TTTGCCAGGAGAAATGTGGGGAAACCTCAGGGTCAGGTTCACTTATTAGTCGATGGCGC	1620
ICMP8	TTTGCCAGGAGAAATGTGGGGAAACCTCAGGGTCAGGTTCACTTATTAGTCGATGGCGC	1620
	* * * * * * * * * * * * * * *	
Xcc_race1_strain_B100	-----GCAATGTTTACATTGCGCGCGCAAAGGGCTCCGCCCTTGTGTGCA	1023
XccR5_89.2	TCGGCTTGGCTGGCCTGCGCGGCGCCGATGCCCAGAAAGCGCGGGTCTTGGTGTGCA	1680
ICMP8	TCGGCTTGGCTGGCCTGCGCGGCGCCGATGCCCAGAAAGCGCGGGTCTTGGTGTGCA	1680
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Xcc_race1_strain_B100	CTCCCGTAAAATTGATCCATCCATAACTAGAGGTCTCCGGGCACACTAGCCACCAAGGA	1083
XccR5_89.2	CTCCCGTAAAATTGATCCATCCATAACTAGAGGTCTCCGGGCACACTAGCCACCAAGGA	1740
ICMP8	CTCCCGTAAAATTGATCCATCCATAACTAGAGGTCTCCGGGCACACTAGCCACCAAGGA	1740

Xcc_race1_strain_B100	GACCAACGATGCGCAAGAGCAAGTTCACCGAGAGCCAGATTGTCGCCACGCTGAAGCAGG	1143
XccR5_89.2	GACCACCAATGCGCAAGAGCAAGTTCACCGAGAGCCAGATCGTCGCCACGCTGAAGCAGG	1800
ICMP8	GACCACCAATGCGCAAGAGCAAGTTCACCGAGAGCCAGATCGTCGCCACGCTGAAGCAGG	1800
	***** * *****	
Xcc_race1_strain_B100	TGGAGGCGGCCGCCAGGTCAAAGATGTGTGCCGTGAGCTGGGCATTCCGACGCGACGT	1203
XccR5_89.2	TCGAGGGCGGTGCGCAGGTCAAGGATGTCTGTGCGAGCTGGGCATTTCCGATGCGACGT	1860
ICMP8	TCGAGGGCGGTGCGCAGGTCAAGGATGTCTGTGCGAGCTGGGCATTTCCGATGCGACGT	1860
	* ***** * * * * *	
Xcc_race1_strain_B100	ACTACGTCTGGAAGTCCAAGTACGGTGGCATGGAGGAGCTGACGTGACGCGCTTCCGCG	1263
XccR5_89.2	ACTACGTCTGGAAGTCCAAGTACGGCGGCATGGAGGCGCTGACGTGCAACGCCTCCGCG	1920
ICMP8	ACTACGTCTGGAAGTCCAAGTACGGCGGCATGGAGGCGCTGACGTGCAACGCCTCCGCG	1920
	***** * * * * *	
Xcc_race1_strain_B100	ACCTGGAGACCGAGCACAGCAAGCTCAAGCGCATGTATGCCGAGCTCGGATGGAAAAC	1323
XccR5_89.2	ACCTGGAGACTGAGCACACAACAGCTCAAACGTATGTACGCCGATCTCGGATGGAAAAC	1980

ICMP8	ACCTGGAGACTGAGCACAAACAGCTCAAACGTATGTACGCCGATCTCGCGATGGAAAACC	1980

Xcc_race1_strain_B100	ATGCACTCAAGGATGTCATCGCAAAAAAGCTATAGACCCGGCGCACAAGCGCCGCTTCT	1383
XccR5_89.2	ATGCATTGAAGGATGTCATCGCAAAAAAGCTATAGACCCGGCGCATAAGCGCCGCTTCT	2040
ICMP8	ATGCATTGAAGGATGTCATCGCAAAAAAGCTATAGACCCGGCGCATAAGCGCCGCTTCT	2040

Xcc_race1_strain_B100	CGCCTGGCTCGTCGAGCAGCATGGCTGGAGCGAGCGCCGGCCTGTGCGGTGTTGGCGT	1443
XccR5_89.2	TGCCTGGCTCATCGAGCAGCATGGCTGGAGCGAGCGCCGGCCTGTGCGGTGTTGGCGT	2100
ICMP8	TGCCTGGCTCATCGAGCAGCATGGCTGGAGCGAGCGCCGGCCTGTGCGGTGTTGGCGT	2100

Xcc_race1_strain_B100	GGCGCGCTCGACAGCACGCTATCGGCGTCGTCCCGATCGGGATGAGGAGGTCATTGCGCT	1503
XccR5_89.2	GGCTCGCTCGACAGCACGTTATCGGCGCCGTCCCGATCGGGATGAGGAGGTCATTGCGCT	2160
ICMP8	GGCTCGCTCGACAGCACGTTATCGGCGCCGTCCCGATCGGGATGAGGAGGTCATTGCGCT	2160

Xcc_race1_strain_B100	GTTGTCCGAATT	1515
XccR5_89.2	GTTGTCCGAATT	2172
ICMP8	GTTGTCCGAATT	2172

C) Alignment of Xcc race 5 specific fragment (XccR5_89.2) with race unknown Xcc strain (ICMP8)

XccR5_89.2	GCGAGCGATTTACCTTCATCCGCACGCATGAAGGCTGGATGTATTTGGCTGTTGTGATC	60
ICMP8	GCGAGCGATTTACCTTCATCCGCACGCATGAAGGCTGGATGTATTTGGCTGTTGTGATC	60

XccR5_89.2	GATCTGTTTTCCAGGCAGGTCGTGCGCTGGGCGATGCGCGATCGGGCCGACACCGAGTTG	120
ICMP8	GATCTGTTTTCCAGGCAGGTCGTGCGCTGGGCGATGCGCGATCGGGCCGACACCGAGTTG	120

XccR5_89.2	GTCGTGACGGCGGTGTTGTCTGCGGTGTGGCGGCGCAAACCCAACGCTGGTTGCTTGGTT	180
ICMP8	GTCGTGACGGCGGTGTTGTCTGCGGTGTGGCGGCGCAAACCCAACGCTGGTTGCTTGGTT	180

XccR5_89.2	CATTGCGACCAAGGGTCTGTCTACACCAGCGATGACTGGCGAGTTTCTTGGCGTCCCAT	240
ICMP8	CATTGCGACCAAGGGTCTGTCTACACCAGCGATGACTGGCGAGTTTCTTGGCGTCCCAT	240

XccR5_89.2	GGCTTGGTGTGACGATGAGTCGGCGTGGCAACTGCCACGACAACGCACCCGTGGAGAGC	300
ICMP8	GGCTTGGTGTGACGATGAGTCGGCGTGGCAACTGCCACGACAACGCACCCGTGGAGAGC	300

XccR5_89.2	TTCTTGGCCTGCTCAAACGCGAGCGGATCAGGCGGCGACCTATCCCACCAAGGACGCC	360
ICMP8	TTCTTGGCCTGCTCAAACGCGAGCGGATCAGGCGGCGACCTATCCCACCAAGGACGCC	360

XccR5_89.2	GCTCGCGCCGAGGTATTCGACTACATCGAGATGTTCTACAACCCCAACCGCCGCCACGGT	420
ICMP8	GCTCGCGCCGAGGTATTCGACTACATCGAGATGTTCTACAACCCCAACCGCCGCCACGGT	420

XccR5_89.2	TCAACTGGCGACCTGTACCTGTAGAGTTTGAACGGCGCTACGCGCAACGAGGGTCTTGA	480
ICMP8	TCAACTGGCGACCTGTACCTGTAGAGTTTGAACGGCGCTACGCGCAACGAGGGTCTTGA	480

XccR5_89.2	GTGTCTACGGAACCCCTGGGCGTATCAAGTCGCTCGCCGCGTGGGTCAAACCTGTCTTCCA	540
ICMP8	GTGTCTACGGAACCCCTGGGCGTATCAAGTCGCTCGCCGCGTGGGTCAAACCTGTCTTCCA	540

XccR5_89.2 ICMP8	GCGCCTGGCCGTAGCGATGTGATTTGAGATCGCGAAATGCAAGCTCGATCTGCATCCGTC GCGCCTGGCCGTAGCGATGTGATTTGAGATCGCGAAATGCAAGCTCGATCTGCATCCGTC *****	600 600
XccR5_89.2 ICMP8	GTGCGTACACATTAACCAACTGCTTTGCGCTGGGCGCCTGCAGCTGCGGGGATGCAACGA GTGCGTACACATTAACCAACTGCTTTGCGCTGGGCGCCTGCAGCTGCGGGGATGCAACGA *****	660 660
XccR5_89.2 ICMP8	TGAGCCAAGGCTCGCGCTCGCGCGCTGCGGCCTTCAGACTCGATGACGCACGCGAGACTT TGAGCCAAGGCTCGCGCTCGCGCGCTGCGGCCTTCAGACTCGATGACGCACGCGAGACTT *****	720 720
XccR5_89.2 ICMP8	TGGCGGGTGAGCGGCGATTGCACTGTTTGCGCCCTTGCCGTGCCTTGCGTAAATCACCA TGGCGGGTGAGCGGCGATTGCACTGTTTGCGCCCTTGCCGTGCCTTGCGTAAATCACCA *****	780 780
XccR5_89.2 ICMP8	ACCTGCAATCGAGTGGATCGCTGCGATTGGCCTGCATCGGCGGTAACCTCGATGCACGAT ACCTGCAATCGAGTGGATCGCTGCGATTGGCCTGCATCGGCGGTAACCTCGATGCACGAT *****	840 840
XccR5_89.2 ICMP8	TGGACGCCAACACATGCAGTTTCCGGCTGTCGATCCACTGATCTGCTTATCCCGCACGT TGGACGCCAACACATGCAGTTTCCGGCTGTCGATCCACTGATCTGCTTATCCCGCACGT *****	900 900
XccR5_89.2 ICMP8	CCTGCGGCTTGACTTGCCTGCGCCCGCGCAGTCGCCAACCAACACAGCCCATGGCCG CCTGCGGCTTGACTTGCCTGCGCCCGCGCAGTCGCCAACCAACACAGCCCATGGCCG *****	960 960
XccR5_89.2 ICMP8	ATACAGCGCGGAACCACGGTGTCCGGAAGCCGGCGTCAGTGACCAGGATCGGGCGAACAT ATACAGCGCGGAACCACGGTGTCCGGAAGCCGGCGTCAGTGACCAGGATCGGGCGAACAT *****	1020 1020
XccR5_89.2 ICMP8	CGTCCGGAACCAAGTGCCTCAGTTGTTGCAAGAAGCGTCTTCTGCACCAGGGATCCCT CGTCCGGAACCAAGTGCCTCAGTTGTTGCAAGAAGCGTCTTCTGCACCAGGGATCCCT *****	1080 1080
XccR5_89.2 ICMP8	GCTGCTTCTGCGCACTACCATGTCCAGCAAGTAAGCGTGGCGCCGCCACCGGCACCG GCTGCTTCTGCGCACTACCATGTCCAGCAAGTAAGCGTGGCGCCGCCACCGGCACCG *****	1140 1140
XccR5_89.2 ICMP8	CTGCGCGCAGCAGACACCGATTTGTCTGGCTTCAGATCGCTCCAGTCGATGACGATTA CTGCGCGCAGCAGACACCGATTTGTCTGGCTTCAGATCGCTCCAGTCGATGACGATTA *****	1200 1200
XccR5_89.2 ICMP8	CCGGCTGCGCGCCGCGCAGCAGCCAGTGCGCCATCTCGTGGTCGATCACTGATCGCTCGA CCGGCTGCGCGCCGCGCAGCAGCCAGTGCGCCATCTCGTGGTCGATCACTGATCGCTCGA *****	1260 1260
XccR5_89.2 ICMP8	CCTGCAAATTCGATTACTCAACAGGCGATCAACTGCCTTGAGCGGCGCGCACCCGCA CCTGCAAATTCGATTACTCAACAGGCGATCAACTGCCTTGAGCGGCGCGCACCCGCA *****	1320 1320
XccR5_89.2 ICMP8	GTGCGCTCGGCCACGAACGTGCGATGTCCATCAGTGTGAGCCTGCGTCCGTGCAACAACG GTGCGCTCGGCCACGAACGTGCGATGTCCATCAGTGTGAGCCTGCGTCCGTGCAACAACG *****	1380 1380
XccR5_89.2 ICMP8	CCTCGACCGCATGCAGCAACGCGGTTTCGCGCAACGCATGCCGACAGTGAGTTGG CCTCGACCGCATGCAGCAACGCGGTTTCGCGCAACGCATGCCGACAGTGAGTTGG *****	1440 1440
XccR5_89.2 ICMP8	GCAGGCACCTTCTGCAACTTTCGCTGGCGCGCATGGTCGTCAACCTTCTCTGGCTTAGTC GCAGGCACCTTCTGCAACTTTCGCTGGCGCGCATGGTCGTCAACCTTCTCTGGCTTAGTC	1500 1500

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*****
XccR5_89.2  ACCTTGAAGATTGCGCCATGCGCGCACTTTCTTCCAGGCAATTACGTCGCAAGTGATTGA 1560
ICMP8       ACCTTGAAGATTGCGCCATGCGCGCACTTTCTTCCAGGCAATTACGTCGCAAGTGATTGA 1560
*****

XccR5_89.2  TTTGCCAGGAGAAATGTGGGAAACCTCAGGGTCAGGTTCACTTATTAGTCGATGGCGC 1620
ICMP8       TTTGCCAGGAGAAATGTGGGAAACCTCAGGGTCAGGTTCACTTATTAGTCGATGGCGC 1620
*****

XccR5_89.2  TCGGCTTGCCTGGCCGGTGCGCAGGCGCCGATGCCCGCAAAGCGGCGGTCTTGGTGTGCA 1680
ICMP8       TCGGCTTGCCTGGCCGGTGCGCAGGCGCCGATGCCCGCAAAGCGGCGGTCTTGGTGTGCA 1680
*****

XccR5_89.2  CTCCCGTAAAATTGATCCATCCATAACTAGAGGTCTCCGGGCACACTAGCCACCAAGGA 1740
ICMP8       CTCCCGTAAAATTGATCCATCCATAACTAGAGGTCTCCGGGCACACTAGCCACCAAGGA 1740
*****

XccR5_89.2  GACCACCAATGCGCAAGAGCAAGTTACCGAGAGCCAGATCGTCGCCACGCTGAAGCAGG 1800
ICMP8       GACCACCAATGCGCAAGAGCAAGTTACCGAGAGCCAGATCGTCGCCACGCTGAAGCAGG 1800
*****

XccR5_89.2  TCGAGGGCGGTGCGCCAGGTCAAGGATGTCTGTCGCGAGCTGGGCATTTCCGATGCGACGT 1860
ICMP8       TCGAGGGCGGTGCGCCAGGTCAAGGATGTCTGTCGCGAGCTGGGCATTTCCGATGCGACGT 1860
*****

XccR5_89.2  ACTACGCTGGAAGTCCAAGTACGGCGGCATGGAGGCCGCTGACGTGCAACGCCTCCGCG 1920
ICMP8       ACTACGCTGGAAGTCCAAGTACGGCGGCATGGAGGCCGCTGACGTGCAACGCCTCCGCG 1920
*****

XccR5_89.2  ACCTGGAGACTGAGCACAACAAGCTCAAACGTATGTACGCCGATCTCGCGATGAAAACC 1980
ICMP8       ACCTGGAGACTGAGCACAACAAGCTCAAACGTATGTACGCCGATCTCGCGATGAAAACC 1980
*****

XccR5_89.2  ATGCATTGAAGGATGTCATCGCAAAAAAGCTGTAGACCCGGCGCATAAAGCGCCCGTTCT 2040
ICMP8       ATGCATTGAAGGATGTCATCGCAAAAAAGCTGTAGACCCGGCGCATAAAGCGCCCGTTCT 2040
*****

XccR5_89.2  TGCCTGGCTCATCGAGCAGCATGGCTGGAGCGAGCGCCGGGCTTGTGCGGTGGTTGGCGT 2100
ICMP8       TGCCTGGCTCATCGAGCAGCATGGCTGGAGCGAGCGCCGGGCTTGTGCGGTGGTTGGCGT 2100
*****

XccR5_89.2  GGCTCGCTCGACAGCACGTTATCGGCGCCGTCGCCGATCGGGATGAGGAGGTTATTGCGCT 2160
ICMP8       GGCTCGCTCGACAGCACGTTATCGGCGCCGTCGCCGATCGGGATGAGGAGGTTATTGCGCT 2160
*****

XccR5_89.2  GTTGTCCGAATT 2172
ICMP8       GTTGTCCGAATT 2172
*****

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Fig. S2. Cloned and reference sequences and their alignments. A) The portion of *Xcc* race 1 (B100) genome sequence of where *Xcc*R5-89.2, *Xcc* race 5 specific fragment cloned and sequenced from *Xcc* race 5 and race unknown *Xcc* strain ICMP8; B) Alignment of *Xcc* race 5 specific fragment (*Xcc*R5_89.2) with reference (*Xcc*_race1_strain_B100) and race unknown *Xcc* strain (ICMP8; C) Alignment of *Xcc* race 5 specific fragment (*Xcc*R5_89.2) with race unknown *Xcc* strain (ICMP8). The bold letters indicate the primers positions.

a) Sequence analysis

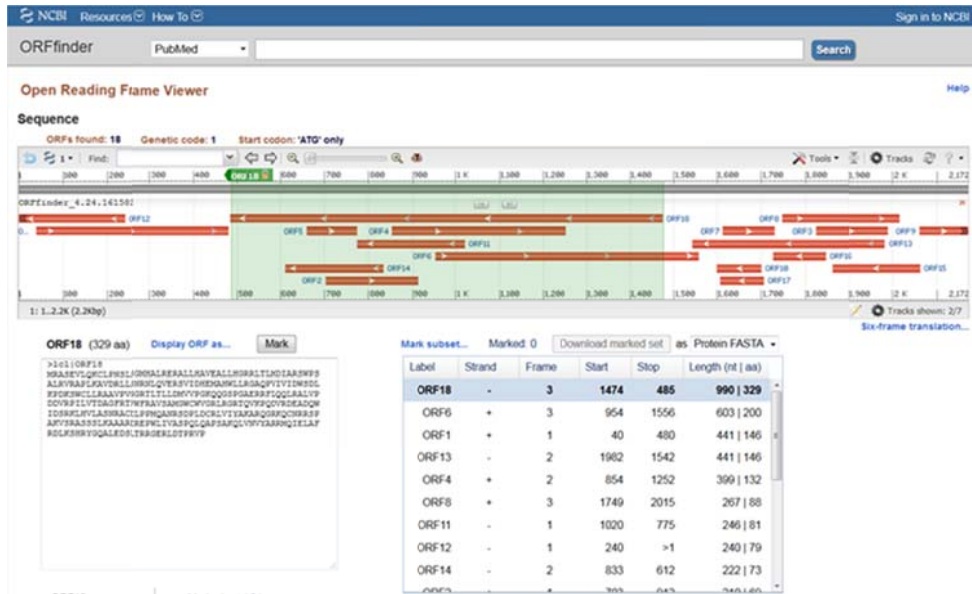
>XccR5_89.2 ORF - strand(1774 to 485)

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CCAAGGTCTGTCTACACCAGCGATGACTGGCGCAGTTTCTGGCGTCCCATGGCTTGGTGTGCAGCATGAGTCGGCGTGGCAACTGCCACGAC
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GTCGCAATT
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>XccR5_89.2 (reverse complement)ORF

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CTTCAGCGTGGCGACGATCTGGCTCTCGTGAACCTTGGCTTGTGCGCATTGGTGGTCTCCTTGGTGGCTAGTGTGCCCGGAGACCTCTAGTTATG
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AGACCCTTGGTCCGAATGAACCAAGCAACAGCGTTGGGTTTGCGCCGCCACCCGACAGACAACCCGCTGACGACCAACTCGGTGTCCGGC
CGATCGCGCATCGCCAGCCGACGACCTGCCTGGAACACAGATCGATCACAACAGCCAAATACATCCAGCCTTTCATGCGTGGGATGAAGGTGA
AATCGCTCCG
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b) ORF prediction



>XccR5_89.2 (329 aa)

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c) Conserved domain search

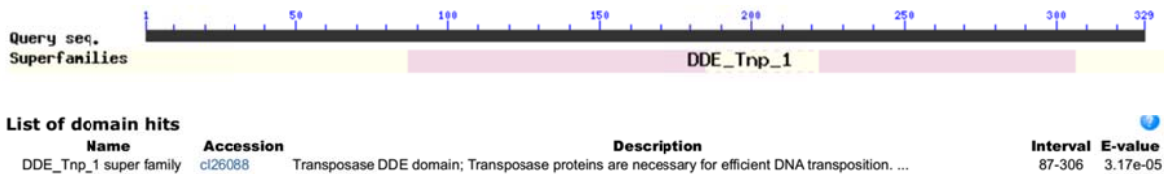


Fig. S3. Sequence analysis of XccR5-89.2 fragment specific to *Xcc* race 5. a) Forward and reverse complements sequences of cloned XccR5-89.2 fragment; b) ORF prediction (ORF Finder, <https://www.ncbi.nlm.nih.gov/orffinder/>); c) conserved domain (CDD, <https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>).