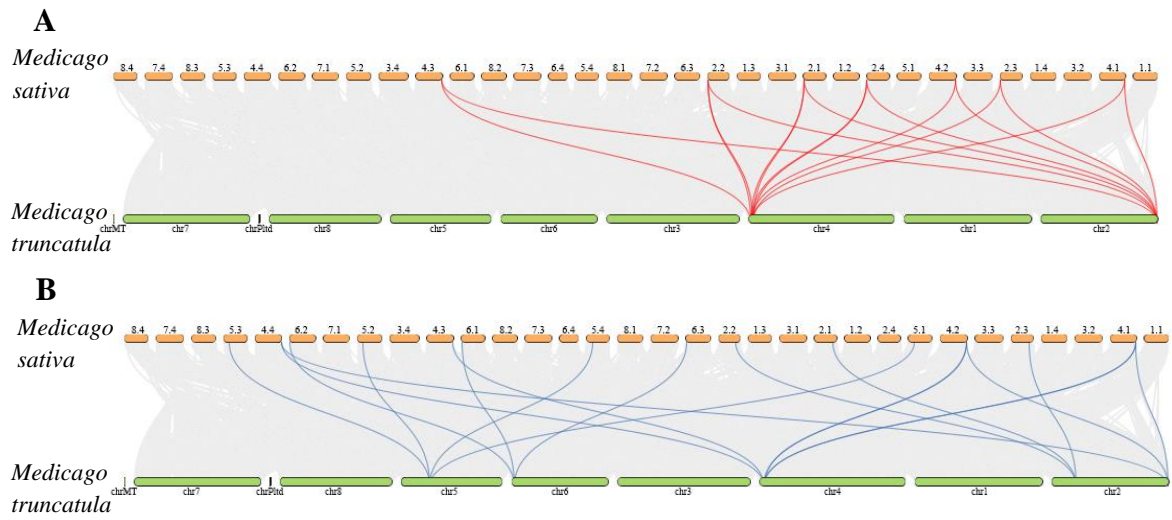
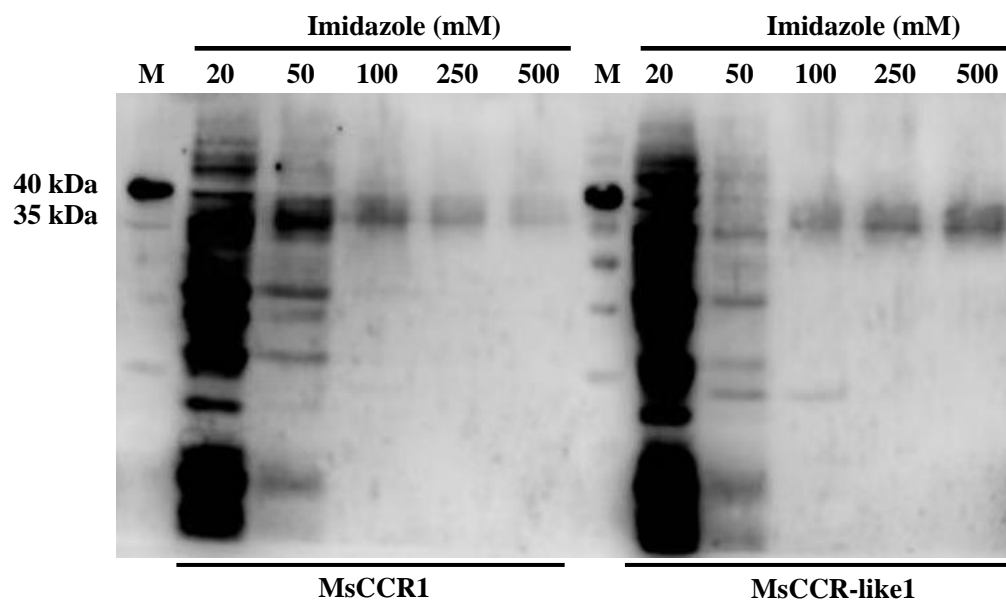


## Figure S1



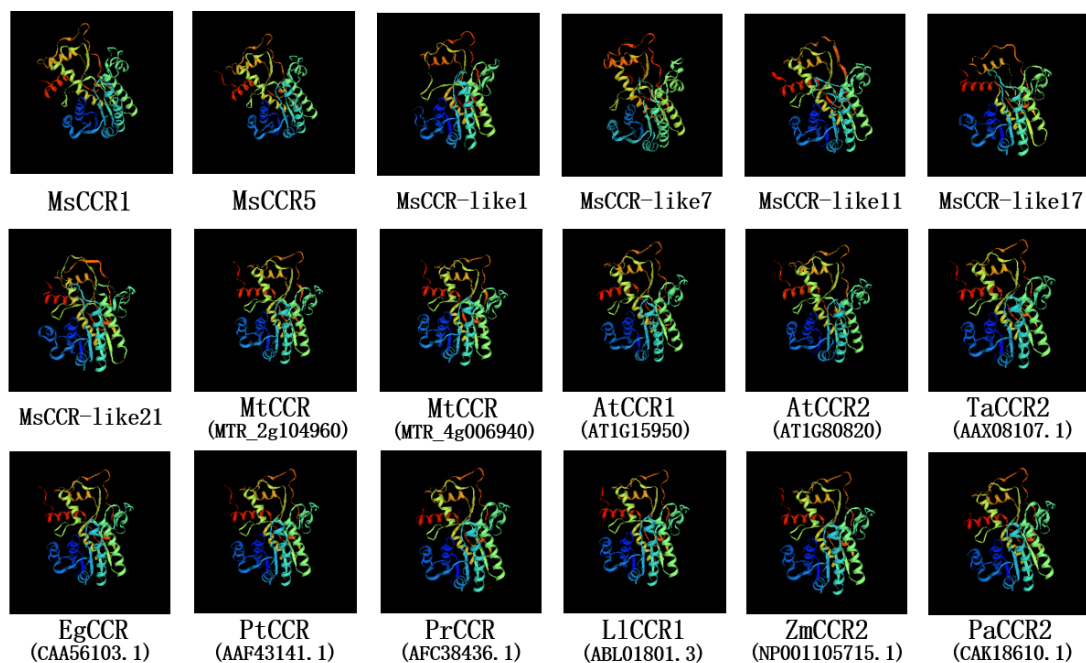
**Figure S1.** The chromosome location and synteny analysis of *CCR/CCR-like* genes in *M. sativa* and *M. truncatula*. Gray lines in the background indicate the collinear blocks within *M. sativa* and *M. truncatula*. The red (**A**, *MsCCRs*) or blue (**B**, *MsCCR-like*s) curves highlight the syntenic *CCR/CCR-like* gene pairs.

**Figure S2**



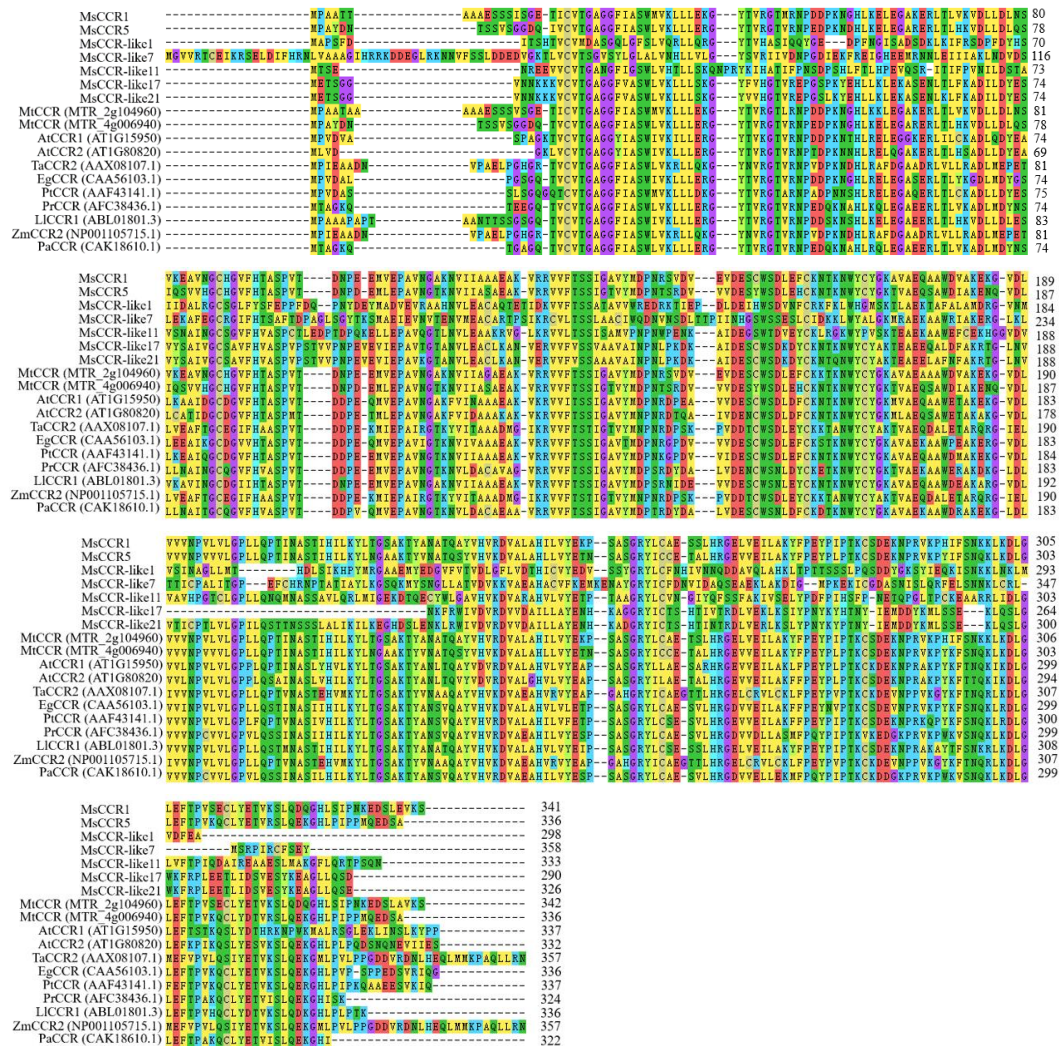
**Figure S2.** Western blot profile of recombinant MsCCR1 and MsCCR-like1. M: protein marker.

**Figure S3**



**Figure S3.** Predicted three-dimensional structures of MsCCR/MsCCR-likes and other bona fide CCRs.

**Figure S4**



**Figure S4.** Alignments of the MsCCR/MsCCR-like proteins and other bona fide CCRs.

**Table S1.** Properties of *CCR* genes and the predicted *CCR* proteins in *M. sativa*

Gene Name	Chromosome Location	Homologous Gene in <i>M. truncatula</i>	Locus Tag of Homologous Gene	pI	Theoretical MW (Da)	Protein Length
<i>MsCCR1</i>	chr2.1: 1039704 - 1044022	<i>MtCCR1</i>	MTR_2g104960	5.90	37205.54	341
<i>MsCCR2</i>	chr2.2: 1307658 - 1311376	<i>MtCCR1</i>	MTR_2g104960	5.90	37187.51	341
<i>MsCCR3</i>	chr2.3: 140748 - 144403	<i>MtCCR1</i>	MTR_2g104960	5.90	37187.51	341
<i>MsCCR4</i>	chr2.4: 712408 - 716186	<i>MtCCR1</i>	MTR_2g104960	5.90	37187.51	341
<i>MsCCR5</i>	chr4.1: 88441560 - 88444191	<i>MtCCR1-2</i>	MTR_4g006940	5.89	37271.43	336
<i>MsCCR6</i>	chr4.2: 92674173 - 92676815	<i>MtCCR1-2</i>	MTR_4g006940	5.89	37271.43	336
<i>MsCCR7</i>	chr4.3: 88471169 - 88473810	<i>MtCCR1-2</i>	MTR_4g006940	5.89	37271.43	336
<i>MsCCR-like1</i>	chr5.4: 20239570 - 20242878	<i>MtCCR-like SNL6</i>	MTR_5g029990	5.00	33606.88	298
<i>MsCCR-like2</i>	chr5.3: 18940776 - 18944245	<i>MtCCR-like SNL6</i>	MTR_5g029990	5.00	33609.87	298
<i>MsCCR-like3</i>	chr5.2: 18815018 - 18818013	<i>MtCCR-like SNL6</i>	MTR_5g029990	5.00	33575.85	298
<i>MsCCR-like4</i>	chr5.1: 20561135 - 20564090	<i>MtCCR-like SNL6</i>	MTR_5g029990	5.00	33589.88	298
<i>MsCCR-like5</i>	chr6.1: 1696762 - 1702383	<i>MtCCR-like SNL6-2</i>	MTR_6g406250	7.48	39783.82	358
<i>MsCCR-like6</i>	chr6.2: 1718684 - 1724261	<i>MtCCR-like SNL6-2</i>	MTR_6g406250	7.48	39849.89	358
<i>MsCCR-like7</i>	chr6.3: 1881162 - 1886448	<i>MtCCR-like SNL6-2</i>	MTR_6g406250	7.48	39852.90	358
<i>MsCCR-like8</i>	15006: 7272 - 10850	<i>MtCCR1-3</i>	MTR_2g028620	5.89	36599.74	333
<i>MsCCR-like9</i>	chr2.3: 60709715 - 60713293	<i>MtCCR1-3</i>	MTR_2g028620	5.89	36599.74	333
<i>MsCCR-like10</i>	chr2.1: 62319777 - 62323333	<i>MtCCR1-3</i>	MTR_2g028620	5.89	36623.79	333
<i>MsCCR-like11</i>	chr2.2: 59055829 - 59059406	<i>MtCCR1-3</i>	MTR_2g028620	5.94	36642.83	333
<i>MsCCR-like12</i>	chr4.4: 89890905 - 89894155	<i>MtCCR1-4</i>	MTR_4g009040	5.54	35926.18	325
<i>MsCCR-like13</i>	chr4.3: 86683346 - 86686357	<i>MtCCR1-4</i>	MTR_4g009040	5.41	36184.27	326
<i>MsCCR-like14</i>	chr4.2: 91110498 - 91113703	<i>MtCCR1-4</i>	MTR_4g009040	5.43	36043.25	326
<i>MsCCR-like15</i>	chr8.3: 39385671 - 39389109	<i>MtCCR1-4</i>	MTR_4g009040	5.78	36175.44	325
<i>MsCCR-like16</i>	chr8.2: 38259260 - 38262698	<i>MtCCR1-4</i>	MTR_4g009040	5.78	36175.44	325
<i>MsCCR-like17</i>	chr4.2: 90649870 - 90653251	<i>MtCCR1-4</i>	MTR_4g009040	5.93	32349.96	290
<i>MsCCR-like18</i>	chr4.1: 85995762 - 85999167	<i>MtCCR1-4</i>	MTR_4g009040	6.26	36075.51	325
<i>MsCCR-like19</i>	chr2.4: 48916854 - 48920360	<i>MtCCR1-4</i>	MTR_4g009040	5.52	35988.13	326
<i>MsCCR-like20</i>	chr2.2: 46570633 - 46574128	<i>MtCCR1-4</i>	MTR_4g009040	5.94	35874.04	325
<i>MsCCR-like21</i>	chr4.1: 86755522 - 86759200	<i>MtCCR1-4</i>	MTR_4g009040	5.95	36177.50	326
<i>MsCCR-like22</i>	chr2.3: 48445104 - 48452492	<i>MtCCR1-4</i>	MTR_4g009040	5.94	35861.04	325
<i>MsCCR-like23</i>	15007: 40384 - 43962	<i>MtCCR1-3</i>	MTR_2g028620	5.89	36599.74	333

**Table S2.** Motif compositions of CCR proteins from *M. sativa*.

Motif No.	Width	Sequences
Motif 1	41	
Motif 2	42	
Motif 3	41	
Motif 4	21	
Motif 5	21	
Motif 6	21	
Motif 7	25	
Motif 8	35	
Motif 9	29	
Motif 10	15	
Motif 11	21	
Motif 12	29	
Motif 13	15	
Motif 14	6	
Motif 15	29	
Motif 16	6	
Motif 17	6	
Motif 18	8	
Motif 19	11	
Motif 20	8	



**Table S3.** Sequences of the CCR proteins in important bona fide CCRs.

Protein names	IDs	Sequences
AtCCR1	At1G15950	mpvdvaspagktvcvtgaggyiaswivkillergytkgtvrnpddpknthrlgleggerlilckadldyealkaai dgcgvfhtaspvtddeqmvpeavngakfvinaaaekvrvvtssigavymdnrdpeavdescwsldfck kntknwycygmvaeqaawetakekgvdlvlnpvlvlgpplqptinaslyhvkyltgsaktyanltqayvdvrdv alahvlveyeapsasgryllaesarhrgevveilaklfpeyplptkckdeknprakpykftnqkikldgleftstkqsylda sqesvengikigs
AtCCR2	At1G80820	mlvdgklvcvtgaggyiaswivklilergytrgtvrnpdpknhlrelqgakerlthlsadlldyealcaticdgcgvf htaspmtdpetmlepavngakfvinaaaekvrvvtssigavymdnrdtqavndencwsldfckntknwyc ygkmlaeqsawetakakgvdlvlnpvlvlgpplqsainaslilhikyltgsaktyanltqayvdvrdvalghvlveya psasgrylaetalhrgevveilakffpeyplptkcsdeknprakpykfttqkikldgleftkpkqslsyesvkslqekghlp lpqdsnqneviies
PtCCR	AAF43141.1	mpvdasslsggqtcvtgaggyiaswivklldkgytrgtarnpadpnnshlrelegaerltlckadlldyeslkeai qgcgvfhtaspvtddeemvepavngtknviaaaekvrvvtssigavymdpnkdpvdescwsldfck ntknwycygvkavaeqaawmakekgvdlvvnnpvlvlgplfqptvnasivhikyltgsaktyansvqayvhvrdv alahilvfetpsasgrylcsesvlhrgevveilakffpeyptkcsdeknprkqpykfsnqklrdlgleftpvkqclyetv kslqerghlpipkqaaeesvkiq
PtrCCR2	ACC63879.1	mpvdasslsggqtcvtgaggyiaswivklldkgytrgtarnpadpknshlrglegaeerltlckadlldyeslkeai qgcgvfhtaspvtddeemvepavngtknviaaaekvrvvtssigavymdpnkdpvdescwsldfck ntknwycygvkavaeqaawmakekgvdlvvnnpvlvlgplfqptvnasithikyltgsaktyansvqayvhvrdv alahilvfetpsasgrylcsesvlhrgevveilakffpeyptkcsdeknprkqpykfsnqklrdlgleftpvkqclyetv kslqekghlpipkqaaeeslkiq
EgCCR	CAA56103.1	mpvdalpgsgqtcvtgaggyiaswivklilergytrgtvrnpddpknghlrelegaserltlykgdlmdygsleeaik gcdgvvhtaspvtddeqmvpeavigtknvinaaaekvrvvtssigavtmdpnrgdpvdescwsldfckst knwycygvkavaekaawpeakergvdlvvinpvlvlgpllqstinasihikyltgsaktyansvqayvhvkdvallah vlvletpsasgrylcaesvlhrgdvveilakffpeynvptkcsdevnprvkpykfsnqklrdlgleftpvkqclyetvksl qekghlpvpsppedsvriqg
PhCCR1	AHX56186.1	mrsvsgqvvcvtgaggyiaswlvkillekgytrgtvrnpddpknghlrelegakerltlckadlldyqslreaingcdg vfhtaspvtddeqmvpeavigtknvinaaaeanvrvvtssigavymdnrdpetvvdetcsdpdfckntknw ycygmvaeqaaweakekgvdlvvinpvlvlgpplqstinasihikyltgsaktyansvqayvdvdalahill yetpeasgrylcaesvlhrgdvveilskffpeyptkcsdvtkprvkpykfsnqklrdlgleftpvkqclyetvkslqek ghlpipkqdepiiriqp
LICCR1	ABL01801.3	mpaaapaptaantssgsgqtcvtgaggyiaswivklilergytrgtvrnpddsknshlkelegaeerltlhkvdlldle svkavingcdgihtaspvtdnpeemvepavngaknviaaaekvrvvtssigavymdpnsrndeivdescwsn leyckntknwycygvkavaeqaawdeakargvdlvvnnpvlvlgpllqstmnastihikyltgsaktyanatqayvhv kdvalahvlveyepsasgrylcsesslhrgeveilakyfpeyptkcsdeknprakaytsnkrldlgleftpvhqcl dtvkslqdkghlpptk
PrCCR	AFC38436.1	mtagkqtteegqtcvtgaggyiaswlvklilergytrgtvrnpedqknahlkqlegaeerltlvkadlmdynslinain gcqgvfhvaspvtddeemvepavngtknvlacavagvrvvtssigavymdpnsrdyaldvencwsnldfck etknwycygvktaekaawerakdkgldlvvnnpvlgpvlqssinasihikyltgsaktyansvqayvhvrdvae ahilvyespsasgrylcaesvlhrgdvdlasmfpqypiptkvkedgkprvkpwksnqklrdlgleftpakqclyet vislqekghisk
PaCCR	CAK18610.1	mtagkqtgagqtcvtgaggyiaswlvklilergytrgtvrnpedqknahlrqlegaeerltlvkadlmdynslinaitg cqgvfhvaspvtddpvqmvpeavngtknvlacaeaavrvvtssigavymdpntrdyaldvdescwsnldfckdt knwycygvkavaekaawdrakekgldlvvnnpvlgpvlqssinasihikyltgsaktyansvqayvhvrdvaea hilvyespsasgrylcaesvlhrgdvvellemfqpypiptkckddgkprvkpwksnqklrdlgleftpakqclyet vislqekghi
ZmCCR1	NP001105488 .1	mtvvdavvsstdagapaaatavpagngqtcvtgaaggyiaswlvklillekgytkgtvrnpddpknahlkaldgaa erlilckadlldydaicravqgcgvfhtaspvtddeqmvpeavrgteyvinaaaegavrvvtssigavtmdpkrg pdvvdvdescwsldfcketrnwycygvkavaehaawetarrgvdlvvnnpvlvlgpplqatvnasiahikylgdsar tfanavqayvdvrdadahrvfesprasgrhlcaervlhredvvrilaklfpeypvparcsdevnprkqpykfsnqklr dlglqfrpvsqsyldtvknlqekghlpvgertteaadkdaptaemqgggiara
TaCCR1	ABE01883.1	mtvvaaaaaaaqelpghgqtcvtgaaggyiaswlvklilergytkgtvrnpddpknahlkaldgaerlvlckadll dydaicaavegchgvfhtaspvtddeqmvpeavrgteyvinaaadagtrrvgtssigavtmdpnrgdpvvd scwsldfckktknwycygvkavaeqaawekaaargvdlvvnnpvlvlgpplqptvnasaahikylgdsakkyana vqayvnvrdvaaahrvfeapgasgrhlcaervlhredvvhilgklfpeypvptrcsdevnprkqpykmsnqklqdl

		glqftpvnslslyetvkslqekghlpaprkdilpaeldgata
TaCCR2	AAX08107.1	mpieaadnvpaelpghgrtvcvtgaggfiaswlvkrllqkgynvrgtvmnpvdpkndhlrafdgaadrllradlme petlveaftgcegifhaasptddpekniepairgkyvitaadmgikrvvftstigtvymnpnrpskpvdtdcwsd leyckktanwycyaktvaeqdaletarqrgielivnpvvlvgpllqptvnastehvmkyltgsaktyvnaaqayvhvk dvaeahrvryeapgahgryicaegtllhrgeclrvlcklfpeypvptckckdevnppvkgykftnqrklldgmefvpvl qsiyetvkslqekgmlpvlppgddvrdnlheqlmmkpaqlrm
ZmCCR2	NP001105715 .1	mptaeattvppeelssgggrtvcvtgaggfiaswlvkrllqkgytvrgtvmnpvdpkndhlraldgavdrllradlldp qslaeafsgcdgvfhaasptddpemmiepairgtryvmaadagvkrvvtssigtvymnpyrpskpvdtdcw sdleyckntqnwycyaktvaeqgawevarkrgldlvvnpvvlvgpllqptvnastdhvmkyltgsattyvnaaqay vhvrdvaeahrvryeaphahgryicaestlhrgdclrvlaklfpeypvptckckdqvnpvpygkftnqrklldgmdfv pvlqclyetvtslqekgmlpvlptkqdhqdlgks
StCCR	NP001274901 .1	mpsesgkvvcvtgaggfiaswlvkllelqkgytvrgtvmnpddpknghlkelegakerlillradlldyqslreaiygcdg vfhtasptddpeqmvepavigtknvitaaeakvgrvvtssigtvymdnrapdkvvdetewsdlgfckntknw ycygmtvaektawdearekgvdlvvinpvlvgpllqptvnasvlhilkyltgsaktyansiqayvhvkdvahalillye apsasgryicaesvlhrgdvveilakffpeypiptkcsdetrprakpykftnqklldlgftpvkqclyetvkslqekghl piptqndepikihs
OsCCR	CAD21520.1	mssnfeannnngkqlvcvtgaggfigswvkvellirgyhvrgtardpadsknahllelegadqrlsclradvldaaslr aafsgchgfvfhaspvsndpdlvpvavegtrnvinaadmgvrrvvtssygavhmnpsrspdavldetewsdylef crqtdnlyccakmmaemtateeaakrglelavvpsmtmgpmlqqlnfssnhvarylmgtkksynpavaayvdv rdvarahlvryerpdargrylcigtvlhraellrmlrdlfpqypatakceddgkpmakpykfsnqrklldgleftplrksl heavlcmmqkshlpiypvpkraly
TpCCR	PNY09320.1	mstydnislvsqtdqtcvtgaggfiaswlvkllelqkgytvkgtrmpdpknshlkelegarerlthkvdlldlksiqsv ihgchgfvfhtasptdnpeemlepavgygtnviiisaaekvrrvvtssigtvymnpntrsrdvvdesywsdleyckn tknwycygmtvaeqsawdiakenqvdlvvinpvlvgpllqptvnastmhilkylngsaktyvnatqsyvsvkdv ahvlvyetnsasgryicsdaslhrgevveilakyfpeyplptk
PdCCR	AGS10092.1	mtvvdaassaaavaqpagnqtcvtgaggyiaswlvkllelqkgytvkgtrmpdpknahlralegaerlilckadl ldydaicravqgcqgvfhtasptddpeqmvepavrgteyvisaaaeagtrrrvvtssigavtmdpnrgpdvvdes cwsdlefccktrnwycygvkaeaaqawdaarhrgvdlvvinpvlvgpllqptvnasighvlyldgsartfanavq ayvdvrdvadahrvfespraagrhlcaervlhrdvdldaklfpeypvptcrsdevnprkqpykfsnqklrdlglefts vsqsyldtvklqekghlpvpvpdeqtateakktvapaelqqggiara
HvCCR	AAN71760.1	mtvvdaaaavaqelpghgqtcvtgaaggyiaswlvkllelqkgytvkgtrmpdpknahlkaldgaerlvlckadlld ydaicaavegchgfvfhtasptddpeqmvepavrgteyvidaadagtrrrvvtssigavtmdpnrgpdvvdesc wsdlefccktknwycygvkaeaaqawekarargvdlvvinpvlvgpllqptvnasaahilkylldgsarkyanavq ayvdvrdvagahlrveapqasgrylcaervlhrqdvvhilaklfpeypvptcrsdevnprkqpykmsnqklqldglk ftpvnslslyetvkslqekghlpvprkdilapqldgata
MtCCR1	XP003604238 .1	mpaydntssvsggdqtcvtgaggfiaswlvkllelqkgytvrgtvmnpdpknghlkelegarerlthkvdlldlqsiqs vvhgchgfvfhtasptdnpeemlepavngtknviiisaaekvrrvvtssigtvymdntrsrdvvdesywsdlehc kntknwycygmtvaeqsawdiakenqvdlvvinpvlvgpllqptvnastihilkylngaaktyvnatqsyvhkdv alahllvyetnsasgryicetalhrgevveilakyfpeyplptkcsdeknprvkpykfsnqklldgleftpvkqcltydt vrsdqekghlppmqedsa
MtCCR-li ke SNL6	MTR_5g0299 90	mapsfditshtvcvmdasqqlgflvqrlrqgytvhasiqqygenpfnisadsdklifrdsdpdyhsiidalrgcsglf ysfepldqpnpydeymadvevraahnleacaqtetidkvvtssatavvwredrtiepdldeihwsdvnfcrkfl whgmsktlaektafalamdrgvnmvsinagllmthdlsikhpylrgaaemyedgvftvdlglvldthicvyedvss ygrylcfnihtqddavqlahkltpatasslpqsddygksyieqkisknklmlmvdfa
MtCCR-li ke SNL6 2	MTR_6g4062 50	mgvvrtcaikrseldifhrnlvaaagihrrkdddeglrknklfsslddedvgktlvcvtsgvsylglalvnhllvlgysvrii v dnpgdreklreirheemrnnleiiiaklndvdslvkafegrgifhtsaftdpaglsygtksmaeievnvtenvmeacart psikrcvftsslaaciwdnvnsdlttppinhgswsseslcidkklwyalgkmraekaawrianergkltticpalitgpe fchrnptataylkaqkmysngllatvdvkkvaeahacvfkemnenaygryicfdnvidaqaeklakdigmpke kicgdasnislqryelsnnklrmlsrpircsen
AtCCR-li ke	AT4g30470	mdhdkstscvvldastvvgfwilkkllsrgysvhaairngeseieemiremetteerlvvydvldvdyqsilvslkte nvvfclldspegydekevdlervgainvveacgrtesiekivfsslstasiwrndnigtqkdvdekcsddqfcrskklw halakmlsekaawalamdrlnmvsinpvlvgpsvaqharnptmsylkgaaqmyengvlayvdvklfladvhira fedvsacgryfcfnqivnteeeklveslsplimppryenemhgsevyeerlrnnksklveagsac



**Table S4.** Primer sequences for RT-qPCR.

Primer name	sequences	T <sub>m</sub> (°C)	Product length
<i>Group Ia</i>	F: TTATGTGCTGAAAGTTCAC	57.94	159 bp
	R: CTCCAATCCCAAATCCTTCAGT	58.03	
<i>Group Ib</i>	F: GAGGCTAACTTTGCATAAGGTTGA	59.30	161 bp
	R: ACGCTATAATCACATTCTTTGT	53.92	
<i>Group II</i>	F: ACAGCGTTTGCCTTAGCAATGGAC	64.40	158 bp
	R: AAAAATCCTAAATCAACGGTCA	54.28	
<i>Group III</i>	F: TTGTATTTGGCAAGACAATGTGAA	57.85	213 bp
	R: TGACAAAATTCAGGACCTGTGATA	58.12	
<i>Group IV</i>	F: AGAAGCAGCAAAACGCGTGGGT	66.01	142 bp
	R: CCCCTCAACTTACAGTACTCAAC	60.56	
<i>MsCCR-like17</i>	F: CTGGACTTAACGTGAATAAG	51.38	165 bp
	R: GAAATTGAAGAGTATATATCCCA	51.24	
<i>Actin2</i>	F: AAAAGGATGCCTATGTTGGTG	56.48	186 bp
	R: TAAGTGGAGCCTCAGTTAGAAGTA	58.42	