



Un-infected

Infected  
Isolate 4

**Figure S1. Infection chickpea with isolate 4 (*Fusarium brachygibbosum*).**

**Supplemental Table S1. Information of lines used for this study**

No	Genotypes	Cross/Pedigree	No	Genotypes	Cross/Pedigree
1	17102	X07 TH 92/FLIP 03-123CXGhab5	49	17174	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)
2	17103	X07 TH 83/FLIP 03-84CXGokce (FLIP87-8C)	50	17201	Long term check
3	17104	Long term check	51	17206	X07 TH 73/FLIP 03-110CXILC605
4	17106	X07 TH 94/FLIP 03-80CXMamad-99 (FLIP 93-53C)	52	17212	X07 TH 86/FLIP 03-97CXGhab5
5	17108	X07 TH 78/FLIP 03-123CXILC200	53	17222	Long term check
6	17109	X07 TH 68/FLIP 03-80CXILC191	54	17223	X07 TH 81/FLIP 03-17CXEjere (FLIP97-263C)
7	17110	Long term check	55	17225	Long term check
8	17111	X07 TH 96/FLIP 03-88CXAlmaz (FLIP97-530C)	56	17236	X07 TH 75/FLIP 03-113CXILC3280
9	17112	X07 TH 9/X06TH12XFLIP98-80	57	17244	X07 TH 78/FLIP 03-123CXILC201
10	17114	X07 TH 93/FLIP 03-108CXFLIP97-706C	58	17265	X07 TH 77/FLIP 03-117CXILC196
11	17115	X07 TH 98/FLIP 03-97CX Rafat (FLIP98-121C)	59	17269	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)
12	17116	Long term check	60	17270	Long term check
13	17117	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)	61	M1	X08TH81/S051206XS051424
14	17118	X07 TH 80/FLIP 03-138CXTeji (FLIP97-266C)	62	M2	X08TH66/S051557XS051414
15	17120	X07 TH 73/FLIP 03-110CXILC606	63	M3	X08TH13/S050425XS051424
16	17121	X07 TH 88/FLIP 03-64CXGhab5	64	M4	X08TH66/S051557XS051414
17	17123	X07 TH 77/FLIP 03-117CXILC197	65	M5	X08TH135/X07 TH 124XS051429
18	17124	X07 TH 78/FLIP 03-123CXILC202	66	M6	X08TH14/S050426XS051432
19	17125	Long term check	67	M7	X08TH89/S051574XFLIP 97-220
20	17126	X07 TH 77/FLIP 03-117CXILC194	68	M8	X08TH112/S051524XFLIP 97-173C
21	17127	X07 TH 96/FLIP 03-88CXAlmaz (FLIP97-530C)	69	M9	X08TH66/S051557XS051414
22	17130	X07 TH 86/FLIP 03-97CXGhab4	70	M10	X08TH14/S050426XS051432
23	17132	X07 TH 90/FLIP 03-115CXInci (FLIP93-146C)	71	M11	Susceptible check
24	17135	X07 TH 9/X06TH12XFLIP98-80	72	M12	X08TH13/S050425XS051424
25	17136	X07 TH 96/FLIP 03-88CXAlmaz (FLIP97-530C)	73	M13	X08TH82/S051464XS051432
26	17139	X07 TH 77/FLIP 03-117CXILC192	74	M14	X08TH110/S051432XFLIP 97-111C
27	17141	X07 TH 9/X06TH12XFLIP98-80	75	M15	X08TH94/S001003XFLIP 03-32C
28	17142	X07 TH 77/FLIP 03-117CXILC195	76	M16	X08TH84/S050727XS050028
29	17143	Long term check	77	M17	X08TH110/S051432XFLIP 97-111C
30	17144	X07 TH 84/FLIP 03-88CXGhab3	78	M18	Long term check
31	17145	X07 TH 63/FLIP02-84XILC1929	79	M19	X08TH13/S050425XS051424
32	17147	X07 TH 33/X06TH43XLebanese market	80	M20	X08TH13/S050425XS051424
33	17148	X07 TH 6/X06TH9XTurkish market	81	M21	X08TH14/S050426XS051432
34	17150	X07 TH 94/FLIP 03-80CXMamad-99 (FLIP 93-53C)	82	M22	X08TH81/S051206XS051424
35	17151	X07 TH 44/X06TH60XTurkish market	83	M23	X08TH81/S051206XS051424
36	17153	X07 TH 66/FLIP 03-138CXILC72	84	M24	X08TH59/FLIP02-69CXICC 12004
37	17154	X07 TH 1/X06TH2XLebanese market	85	M25	Malxotra (Local check)
38	17156	X07 TH 91/FLIP 03-117CXFLIP 84-92C	86	M26	X08TH81/S051206XS051424
39	17157	X07 TH 91/FLIP 03-117CXFLIP 84-92C	87	M27	X08TH66/S051557XS051414
40	17158	Long term check	88	M28	X08TH13/S050425XS051424
41	17159	X07 TH 77/FLIP 03-117CXILC193	89	M29	X08TH14/S050426XS051432
42	17161	Long term check	90	M30	X08TH81/S051206XS051424
43	17162	X07 TH 84/FLIP 03-88CXGhab2	91	M31	X08TH60/FLIP03-7CXFLIP 03-32C
44	17163	X07 TH 86/FLIP 03-97CXGhab3	92	M32	X08TH129/FLIP01-41CXFLIP03-36C
45	17165	X07 TH 92/FLIP 03-123CXGhab5	93	M33	X08TH33/S051429XFLIP2005-8C
46	17166	X07 TH 92/FLIP 03-123CXGhab5	94	M34	X85TH143/ILC 629 x FLIP 82-144C
47	17169	X07 TH 63/FLIP02-84XILC1930	95	M35	PI 339223 (Suceptible Check)
48	17172	X07 TH 84/FLIP 03-88CXGhab1	96	M36	X08TH164/X07 TH 75XFLIP01-41C

**Supplemental Table S2. SSR markers used in this study.**

<b>Name</b>	<b>Forward</b>	<b>Reverse</b>
CaSTMS24	AAAGACAGGTTTTAATCCAAAA	CTAATCTTTCTTCTTCTTTTGTCAT
TA42	ATATCGAAATAAATAACAACAGGATGG	TAGTTGATACTTGGATGATAACCAAAA
GA6	ATTTTCTCCGGTGTTCAC	AAACGACAGAGAGTGGCGAT
TA194	TTTTTGGCTTATTAGACTGACTT	TTGCCATAAAATACAAAATCC
TA3a	AATCTCAAAATTCCCCAAAT	ATCGAGGAGAGAAGAACCAT
TR20	ACCTGCTTGTTTAGCACAAAT	CCGCATAGCAATTTATCTTC
TR19	TCAGTATCACGTGTAATTCGT	CATGAACATCAAGTTCTCCA
NCPGR84	GCATGAGAGATGGGTCATTA	GAGGCGCGTGGACTAACA
NCPGR96	CGTGGACTAACCAAACAAAT	CAAGGTCAATTCGTAGAAGG
NCPGR97	CGCGTGGACTAGCAAACA	AAGGAATACGAATCATCCCT
NCPGR101	TCTGCTCTTTGTGCAGAAGAAT	GAAATAATGCGTTCACTGTTG
NCPGR210	AAGGTAGACGTGTGCGTG	CCTGTTATGGAAGATAGGGC
NCPGR215	GTAGCGTGATGTCTTTCTC	GGCGACAACAGATACTCTTC
NCPGR216	GAGCAAGTGTAACACTAGCAAAC	AGCGGATAACAATTCACAC
NCPGR218	TTGCTTCGACACTGTAACAC	GCGTGGACTAACTCTTTTCA
NCPGR219	ATGTGACCAAAGTAAGGGTG	ATAAGTGTAGGGTGTCTCAA
NCPGR221	CATATGCATCATCTCAACCA	TGTCCTTCGTCTTGTCTTC
NCPGR225	TCCGTAACAGTGATGAACAA	TGGGATTACACTGGATAAGG
NCPGR227	CATTTACCCTCACTTCCGTCA	TGGTTCAGACATCACACCAAA
NCPGR232	GGACCGAATGTCCATAAATC	TCTTTTAGGACCCAATGGAG
NCPGR235	GACTAACCGCGATCAACACA	TGGTTTGAGAGGTGATGTGG
NCPGR237	ATTGCTCAGCTTTTGAGGA	CGGGCTGGGAATTAAATAGA
NCPGR240	AAGGGGTGAGTTTTGAGTT	CCCCTTAATTTCTTTCTCCA
NCPGR241	GCGTTTTCCAGAGAAATTCA	GGGAGGAAACATTTTCGTTT
NCPGR242	TCGTCATATCCACCCGATAA	TGGATAATGGTGCGAAAGAA
NCPGR244	TGGACTACTGAATCACTCCCTCT	TGCTAAGTTGTCTGGGTGGA
NCPGR246	GTGGACTAACCCACATAGGA	ACCATTACCAGAAACCATGA
NCPGR248	GGCATTGTATGGAAGGAGGA	CGCGTGGACTACCATATCATT
NCPGR249	CTCTTCGATTTCGATAGGTT	TGTTTTCAGCTAAATTTACG
NCPGR250	CGCGTGGACTAACTTCTGTA	TGGCCTAACAGCTTTCCATT
NCPGR253	ACATTGGTGGCAACTCCATT	GGCGTGGACTAACATCCAATA
NCPGR267	ATTAAGTGTGCTGGAGGAAA	TATAGCCATAAGGGCAACAT
NCPGR269	CGTGGAAGTATCGAAAGGTGT	ATAAGCCAAGGGAGGACGAA
NCPGR272	TGGACTAACAGCTTTCCATT	GTCTTCTGTAGATTGAAGTTGTAAA
NCPGR275	CGAGGAAGCATTCTGCATT	TCCTGGAGCCTCGATTAAA
H3A10	TTTAAGGCTTCAGGTATTGATTTCT	TCACACATGCCAACTTAAATAAAA
NCPGR220	ACTTCTCTACTCAGCCCCCTT	GCCCCTATCTTTCAGACTTT
NCPGR224	TGGAATTAGTTGATGTGACAA	ATTTCCCGTGTCTTTGAGAT
NCPGR228	CAACGGTTAAGAATGTGCAA	GCGTGGACTACTCATGTGTCT
NCPGR229	CAAATTTTTCGCTGTTGTAG	ACACCTCATCTCCCTTTGAA
NCPGR238	GTCCGTGACATTGACACTTT	CATAGTTGGATTGCCTCTCA
NCPGR247	CAATGATTGGTTCTCTCCTC	GGTTTGACTAAAATATGGCG
NCPGR252	TTGCCCTGAGGAATACATTA	GGTTGTTGAAGGCATAACTG
NCPGR254	GCCTTTTTCAATTTCTCTCA	CCCAAAGAAGACAAAACAAC
NCPGR255	TCAGTGGTATTGAGACATCG	CCATCTTCAAAAGTGAACCT
NCPGR268	TCAACTAAGGATTTGCTCG	AGAGCTGAGAGAGTGGACAA

NCPGR274	GTGTGTTGTCGTTTGTCTTG	TTTTGAAGAGCAATCAATCC
NCPGR209	ATTGTTTGTGGAGTGATGG	CACGGTTTCATTGTCTTGTT
NCPGR226	GACTGCATGTTTTCTTCTCG	ACCACTTCAAAGCCTATTCA
NCPGR236	CAACGGTAACATTCTCAACG	TTTTCTTTTGATGTGTTCTTGG
CaSTMS2	ATTTTACTTTACTACTTTTTTCCTTC	AATAAATGGAGTGTAATTTTCATGTA
CaSTMS22	CTCTTCCTCCTCGAGATC	ATAGATAACAATACTCTGTGAGTTGG
CaSTMS28	CCCTTCTAGTGATATTTTG	AAATGTGTTTTATGGAATAAGTCAT
TA180	CATCGTGAATATTGAAGGGT	CGGTAAATAAGTTTCCCTCC
NCPGR76	GAAAGCTGACTCCTCTACCA	GAAAATGCTCTCAGTCAAGG
NCPGR95	AGCCCTTGGATTTCTTTTCT	GTCAATTGAGTTGCAACGAG
NCPGR100	CCATTTTCTACAATCTCATGTCT	GTAGAAAGAGCCAAGAGGCA
NCPGR78	CTCTGTGAGGAGGAAGATGA	AGAAGTTAAAGCAATGCACC
NCPGR79	ATTGGTTTGAGAAGTGATGG	AGAAAAGATGGAGTTCGTGA
NCPGR82	ATTGGTTTGAGAAGTGATGG	GGGAAGTTCAGGACTCTTTT
NCPGR91	ATTGAATCCTTTCTGAACCG	CTGTTCTCTTTTCTCCTCCG
NCPGR93	CAAAGTTTGTTGCTAGGATTC	GAAGATCTCCGACGATGATA
NCPGR98	CATCTTATTTTTCATTTTAGAGGAGG	AGGAAGTGTTATGGAGATGCC
NCPGR99	ATCATGAAGCAAATCCTCAC	TGAACCCAACATAGCATACA
GA102	CAGAGAACCACATGTTTTAGTTGAA	AGTTTTGATGCGTGCCATT
GA16	CACCTCGTACCATGGTTTCTG	TAAATTTTCATCCTCTCCGGC
GAA47	CACTCCTCATGCCAACTCCT	AAAATGGAATAGTCGTATGGGG
TA110	ACACTATAGGTATAGGCATTTAGGCAA	TTCTTTATAAATATCAGACCGGAAAGA
TA140	TTTTGGCATGTTGTAGTAATCATATTT	TGAAATGAAAAAGAAAAGGAAAAAGTA
TA144	TATTTTAATCCGGTGAATATTACCTTT	GTGGAGTCACTATCAACAATCATACAT
TA196	TCTTTTAAATTTTATTATGAAAATACAAATTATA	CCTCGGGAGAGGTAAATGTAATTTT
TA206	GTCCCACTTCCACTTATAAAGGTT	TAACGTATCTTGCAGATTTCAAATAAA
TA21	GTACCTCGAAGATGTAGCCGATA	TTTTCCATTTAGAGTAGGATCTTCTTG
TA27	GATAAAATCATTATTGGGTGTCTTT	TTCAAATAATCTTTCATCAGTCAAATG
TA37	ACTTACATGAATTATCTTTCTTGGTCC	CGTATTCAAATAATCTTTCATCAGTCA
TA89	ATCCTTCACGCTTATTTAGTTTTTACA	CAAGTAAAAGAGTCACTAGACCTCACA
TA96	TGTTTTGGAGAAGAGTGATTC	TGTGCATGCAAATTCTTACT
TAA104	CCCCTAAATTAACAACATAATGG	CGGCTTATGAATTTTTATCATTTACAG
TAA170	TATAGAGTGAGAAGAAGCAAAGAGGAG	TATTTGCATCAATGTTCTGTAGTGTTT
TR2	GGCTTAGAGTTCAAAGAGAGAA	AACCAAGATTGGAAGTTGTG
TR31	CTTAATCGCACATTTACTCTAAAATCA	ATCCATTAAAACACGGTTACCTATAAT
TR43	AGGACGAAACTATTCAAGGTAAGTAGA	AATTGAGATGGTATTAAATGGATAACG
TR58	CTCTATATTTGTTTGTTTTTCGTTTTG	TAAAATGTGTAGGGTGCAGAATAAATA
TS5	GTTGAATAGTACTTTCCCACTTGAGTC	TGAGACTAAAAATCATATATTCCCCC
TS58	GATTTTTATGACCATCAATTCATTTCT	CAATTTTGTCCGATTTTTACTTTTTAT
TS82	CAAAGACATAATCGAGTTAAAGAAAAA	TGGTTAGCTAGAAAATTCAAGGG
H4G07	ATTAGAGGCAAACAAGAACTTGAAAC	TGACACCTAATTTTATTCGGTTTTTAT
SCY17	GACGTGGTGACTATCTAGC	GACGTGGTGAAATAGATACC
TA117	GAAAATCCCAAATTTTTCTTCTTCT	AACCTTATTTAAGAATATGAGAAACACA
TA125	TTGAAATTGAACTGTAACAGAACATAAA	TAGATAGGTGATCACAAGAAGAGAATG
TA130	TCTTTCTTTTGCTTCCAATGT	GTAAATCCCACGAGAAATCAA
TA186	ACAAAATTCTAAAAGTTCCTTCTACCA	GTTGTTAGTCGAATAATTGAGAAAAAGA
TA2	AAATGGAAGAAGAATAAAAAACGAAAC	TTCCATTCTTTATTATCCATATCACTACA
TA30	TCATTAAAAATTCTATTGTCTGTCTT	ATCGTTTTTCTAAACTAAATTGTGCAT
TA59	ATCTAAAGAGAAATCAAAATTGTGCGAA	GCAAATGTGAAGCATGTATAGATAAAG
TAA60	TCATGCTTGTTGGTTAGCTAGAACAAA	GACATAATCGAGTTAAAGAAAA

TR29	GCCCCACTGAAAAATAAAAAAG	ATTTGAACCTCAAGTTCTCG
TS72	CAAACAATCACTAAAAGTATTTGCTCT	AAAAATTGATGGACAAGTGTTATTATG
TA25	AGTTTAATTGGCTGGTTCTAAGATAAC	AGGATGATCTTTAATAAATCAGAATGA
H1B06	GACTCACTCTCCAAATGGAACC	AAGCCCATGAAAACCATATATTC
H1F05	ATAACTCAAATCGTTTCACAAGA	AAACCCCTTTTTATTTTCAATTT
H1F22	GGTTCTGGTCTTCTTGTTACTATTT	ATTGTGTTGTGTTATTTTAACTTTTGG
H1P092	GAACCGGTGTTCCCTTTTT	AAAGGTATAGAATGTGTTTAAATGGA
H3A12	AACCTTAGACTGTGTTTCGCTGA	TCAATCTTTTGTGTTACTATGAATCTG
H6D11	AAAGATGGGAACTTGAGATGTTG	AATAGCTACTCAAGGCTGAAGAAA
TA103x	TGAAATATCTAATGTTGCAATTAGGAC	TATGGATCACATCAAAGAAATAAAAT
TA47	TTTTTATAGGTGTCTTTTTGTGTCTTT	TCTGAATAGGAAATAAGAAAGGTAGGTT
Ts45	TGACACAAAATTGTCTCTTGT	TGTTCTTAACGTAACCTAACCTAA
TA146	CTAAGTTTAATATGTTAGTCCTTAAATTAT	ACGAACGCAACATTAATTTTATATT
TA72	GAAAGATTTAAAAGATTTTCCACGTTA	TTAGAAGCATATTGTTGGGATAAGAGT
TA39	TTAGCGTGGCTAACTTTATTTCG	ATAAATATCCAATTCTGGTAGTTGACG
CaSTMS15	CTTGTGAATTCATATTTACTTATAGAT	ATCCGTAATTTAAGGTAGGTTAAAATA
CaSTMS21	CTACAGTCTTTTGTCTTCTAGCTT	ATATTTTTTAAAGAGGCTTTTGGTAG
TA71	CGATTTAACACAAAACACAAA	CCTATCCATTGTCATCTCGT
TA22	TCTCCAACCCTTTAGATTGA	TCGTGTTTACTGAATGTGGA
TA200	TTTCTCCTCTACTATTATGATCACCAG	TTGAGAGGGTTAGAACTCATTATGTTT
		TTCTTTTGTGTGAAAAAAAATA
		TAGTGA
TA46	TTTATTGCAATAAAACTCATTTCTTATC	GTGGTGTGAGCATAATTCAA
TA135	TGGTTGGAAATTGATGTTTT	ACCTCAAGTTCTCCGAAAGT
TR1	CGTATGATTTTGCCGTCTAT	TGTGATAATTTTCTAAGTGTTTT
TR7	GCATTATTCACCATTTGGAT	GATCCAACGGGAACAAAGAC
TA106	GGGGGAAGATATGTTGGGT	ACTTTCGCGATTACAGCTAAAATA
TS35	GGTCAACATGCATAAGTAATAGCAATA	GCCCTCCTTCTTGCTTACAA
NCPGR40	TGAACGAATCATGGCAAGAG	GAGATTTGAGTTTGACGGTT
NCPGR129	ACGAAGAATTTAATACCGGA	TCAAAAATCCACTTTCCACCA
ICCM0124	CCTCGGGAATTCAACTACCA	GACCATCTTCAAAAGTGAACC
NCPGR278	TGAGACATCGACTATTGGACA	ATGACATTCCAATCGGCTTC
GAA44	AGCAAGCCCATGATTTTCTC	GAATAACTTCACACCGTTTCATAA
H2L102	GAAGAGAAAATGTTTAAATGGGTAAAT	TATTTACTAGGTAAATCCTATTTATTG
CaSTMS12	GTATTTGTTACTGCATATACTTAATTA	CGCGCAGTGATTTAAGCTAT
NCPGR217	GACTACTTGGAATACGTCGC	TCTTTGCTGCCTGATTTTCA
ICCeM036	TTCTTCCGTTCTTTTCCCT	AACTCACTACCCCTAGTAGCAAA
NCPGR149	TTAAAAATTCAGGGGGCTCA	GGTCGAAGCCATTGTTTTGT
NCPGR231	AACCTCCGTCCACACATTTT	CCCCTAGTAGCAAATATTTTGACC
NCPGR234	TTAAAAATTCAGGGGGCTCA	GTATCCTCGGTTTCCCTATC
NCPGR136	GGACTGAGTGAGTTCGTCTT	AACAATATACAATAAATAACCAAGT
CaSTMS10	ATAACAAAAAGATATCTCATCGACTA	ATGCCAGGATTAACAGCACC
GA105	TGAGGAAACACAAAACGACG	GTGGTAGCCCCAAAAGGAACA
ICCeM0018	CACTCGAAAAGCCCCAAAGAG	GAAATTTAGAGAGTCAAGCTTTAC
TS54	TACAAGTTAAAAATGAATAAATATTAATA	CATGCATTTAGGATGAACCA
NCPGR139	TGGGTCTTATTGGGTTTGAT	TTTATGCTTCCTCTTCTTCG
TA176	ATTTGGCTTAAACCCTCTTC	CCAACACCAACACCAACATA
NCPGR199	GGACATAGTAATCTCCGCTG	GGTGAGTTTCTTTTTCCCTT
NCPGR200	TTACACACAACCTTTTCA	AATCAATCCATTTTGCATTC
TA80	CGAATTTTTACATCCGTAATG	GGATTCTATTCAAAGCCCAATC
H4F07	AACGCCTGCATTTTATTTTGT	

NCPGR56	CATGACAATAATGGTGAACG	GATCTTGACTTCTGTTTGTGC
GA9	GAACGGATTGGATGAAGCAT	GTGCAAACAACCCTTTTTGG
H5A04	CTTCTTCCTTTTTGTTGACACCT	ACCGAAAACACTTGTGATTGTTA
NCPGR177	GGGGAAAAATAATGAGGAGG	GGCACCCAATTTTCTCTTAC
GA21	CCCCAGGTGAATTCCTCATA	CTCAACCTTTGTTTCAGCAACAC
TAASH	GGTAGACGCAAAAGAGTGGG	GCCACATTGACCAGGAATG
ICCM0196	GTCGGGTGTGGATAGCAAGT	AACACAATTCCTCAAATAACAAACT
NCPGR171	AAAGACAGCAAAGCAAAGAG	AAAACACCATAAAATTCCACG
NCPGR123	CTCTGCAGACTGAGGGTAAG	TCTGGAGGAGAAGAGACAAA
ICCM0065b	CACGGTGTCTTCCACATGAC	TAAGCCAATACCAAGAGGCG
NCPGR187	CCTTCACTGTCGGTTATGAT	TAACACAAGCCTATGCAATG
NCPGR180	TCCGTAACAGTGATGAACAA	TGGGATTACACTGGATAAGG
ICCeM0028	ATTACCAGGCACTCCACCTG	GGAGAGATCAAGCTCCCAAC
NCPGR43	GAAGTCGAGATGCTGAAAAA	AATTCTAGAAGGGAAGGGTG
CaSTMS4	AATATATGAATTGGTTCAGACATC	AAACAAATAATAGAAAATTATGCTCC
NCPGR145	CCATATGAAGATATTGTGGCA	ATCATGGCAAGAGGTAGGTC
TA34	AAGAGTTGTTCCCTTTCTTTT	CCATTATCATTCTTGTTCCTTCAA
TR26	TCATCGCAGATGATGTAGAA	TTGAACCTCAAGTTCTCTGG
NCPGR33	ACATCTTGAAGTGCCCCAAC	TGCAAGCAGACGGTTACAAG
TA14	TGACTTGCTATTTAGGGAACA	TGGCTAAAGACAATTAAAGTT
H2B19	CTACTTGAAAAATGCTTCCTTCT	AGTTGCGACGAGAGCTAGATATT
ICCM0284a	CGTATCTACACCCGCACTCA	TGGAAAATCCACTTTGATTGG
CESSR433	CTTTTGTCTTGTGATTCCAGCA	CACCACCAACACAATTTTATCC
CESSR53	TACGGGTCTGAATGGAACCTT	TTGTTGCTGCTGTGGTGCTT
TA179	CAGAAGACGCAGTTTGAATAACTT	CGAGAGAGAGAAAGGAAGAAGAG
sp23	CCTCTTGTCTTTGTCTCACGA	GCAACAGGTCGTGGGGAAAA
FocR0-M15	GGAGAGCAGGACAGCAAAGACTA	GGAGAGCAGCTACCCTAGATACACC
FocR1B/C-N5	GAGAGCAGGGTCAGCGTAGATAG	GCAGCAGAAGAGGAAGAAAATGTA
FocR5-L10	GGAAGCTTGGCATGACATAC	AAGCTTGGGCACCCCTCTT
FocR6-O2	GAGCAGTCAATGGCAATGG	AGAGCAGGGTCAGCGTAGATA
FocR6P18	GGAGAGCAGTAGAGTTACAGCAGTATT	GGAGAGCAGCTACCCTAGATACACC
FOCP1	TACGGTACCAGATCATGGCGT	CGCTTTCGATCGTGGCTATG
FOCP2	CATGGTTTCGTTAGGCCAGT	CGCAGTCTTCGTCGTCATTA
HOP78	CTTTTGGCATGAGATTGTAGCCTC	CGTGGGGTTATACCTCTAGGCTA
DST	ATGGTTAAAGACACAAAGCC	GTT TGAAACTCAGTCTCGTTGCG

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**Supplemental Table S3. Number of alleles, gene diversity and polymorphism recorded in 96 chickpea genotypes**

No	Marker	Allele No. (Na)	Gene Diversity (He)	Heterozygosity	PIC	LG	Reference
1	CASTMS12	2	0.4997	0.0030	0.3748	LG1	Lichtenzweig <i>et al.</i> (2005)
2	GA6	3	0.4160	0.0015	0.3295		
3	GA9	2	0.4997	0.0026	0.3748	LG6	Winter <i>et al.</i> (2000)
4	GA16	3	0.4489	0.0016	0.3481		
5	GAA47	2	0.4945	0.0026	0.3722	LG4	Winter <i>et al.</i> (1999)
6	H1P092	5	0.4756	0.0010	0.3625		
7	H2L102	3	0.4347	0.0015	0.3402	LG5	Choudhary <i>et al.</i> (2012)
8	H6D11	4	0.3616	0.0010	0.2962		
9	ICCEM0018	2	0.5000	0.0026	0.3750	LG3	Winter <i>et al.</i> (2000)
10	NCPGR33	2	0.4999	0.0026	0.3749		
11	NCPGR95	2	0.5000	0.0026	0.3749		
12	NCPGR99	4	0.4977	0.0013	0.3738		
13	NCPGR97	4	0.4999	0.0013	0.3749		
14	NCPGR96	3	0.4012	0.0014	0.3207		
15	NCPGR123	3	0.4594	0.0016	0.3539		
16	NCPGR136	2	0.0307	0.0001	0.0302	LG1	Gaur <i>et al.</i> (2011)
17	NCPGR139	5	0.4808	0.0010	0.3652	LG6	Choudhary <i>et al.</i> (2012)
18	NCPGR171	2	0.5000	0.0026	0.3750	LG3	Choudhary <i>et al.</i> (2012)
19	NCPGR200	2	0.3901	0.0030	0.3140	LG6	Choudhary <i>et al.</i> (2012)
20	NCPGR209	3	0.4614	0.0016	0.3549		
21	NCPGR217	2	0.4999	0.0026	0.3749	LG5	Gaur <i>et al.</i> (2011)
22	NCPGR226	2	0.5000	0.0026	0.3750		
23	NCPGR240	2	0.4999	0.0026	0.3749		
24	NCPGR241	2	0.3111	0.0016	0.2627		
25	NCPGR247	3	0.4296	0.0014	0.3373		
26	NCPGR267	2	0.4995	0.0026	0.3747		
27	TA3a	2	0.5000	0.0026	0.3750		
28	SCY17	2	0.4980	0.0026	0.3740		
29	TA25	4	0.3851	0.0010	0.3110		
30	TA125	3	0.4467	0.0016	0.3469		
31	TA47	2	0.5000	0.0026	0.3750		
32	TA80	3	0.4160	0.0014	0.3295	LG6	Winter <i>et al.</i> (2000)
33	TA186	3	0.4945	0.0017	0.3722		
34	TA37	4	0.4687	0.0012	0.3588		
35	TA59	3	0.4704	0.0016	0.3597		
36	TA89	2	0.4934	0.0026	0.3716		
37	TA103x	3	0.4160	0.0014	0.3295		
38	TA117	3	0.4810	0.0017	0.3653		
39	TA144	3	0.4372	0.0015	0.3416		
40	TA176	5	0.4839	0.0010	0.3668	LG6	Winter <i>et al.</i> (1999)

41	TAASH	3	0.3818	0.0013	0.3089	LG5	Winter <i>et al.</i> (2000)
42	TR20	2	0.4997	0.0026	0.3748		
43	TR58	2	0.4986	0.0026	0.3743		
44	TS35	2	0.4991	0.0026	0.3745	LG5	Winter <i>et al.</i> (1999)
45	Ts45	3	0.4042	0.0014	0.3225		
46	TS58	2	0.0103	0.0001	0.0103		
47	TS72	4	0.3750	0.0010	0.3046	LG4	Winter <i>et al.</i> (1999)
48	NCPGR177	2	0.5000	0.0026	0.3750	LG6	Choudhary <i>et al.</i> (2012)
49	CASTMS10	3	0.4322	0.0015	0.3388	LG3	Winter <i>et al.</i> (1999)
50	NCPGR199	3	0.4489	0.0016	0.3481	LG4	Gaur <i>et al.</i> (2011)
51	TA14	3	0.3003	0.0010	0.2552	LG4	Winter <i>et al.</i> (1999)
52	TA72	2	0.4760	0.0025	0.3627		
53	TA2	4	0.4604	0.0012	0.3544	LG4	Winter <i>et al.</i> (1999)
54	TA30	2	0.4760	0.0025	0.3627		
55	TA34	3	0.4970	0.0017	0.3735	LG1	Winter <i>et al.</i> (1999)
56	TR7	2	0.4737	0.0025	0.3615		
57	TR2	5	0.4232	0.0009	0.3337		
58	TA194	2	0.4908	0.0026	0.3703		
59	TS5	3	0.3750	0.0013	0.3046		
60	NCPGR210	2	0.4999	0.0026	0.3749		
61	H5A04	2	0.4660	0.0024	0.3574	LG6	Lichtenzweig <i>et al.</i> (2005)
62	TA42	3	0.4372	0.0015	0.3416		
63	TA146	4	0.4574	0.0012	0.3528		
64	TAA104	2	0.4861	0.0025	0.3679		
65	TA110	2	0.5000	0.0026	0.3750		
66	NCPGR232	3	0.4347	0.0015	0.3402	LG5	Choudhary <i>et al.</i> (2012)
67	TR29	2	0.3750	0.0039	0.3047		
68	TR31	4	0.3047	0.0011	0.2583		
69	TA179	3	0.4479	0.0023	0.3476		
Mean		2.8	0.4422	0.0019	0.3479		