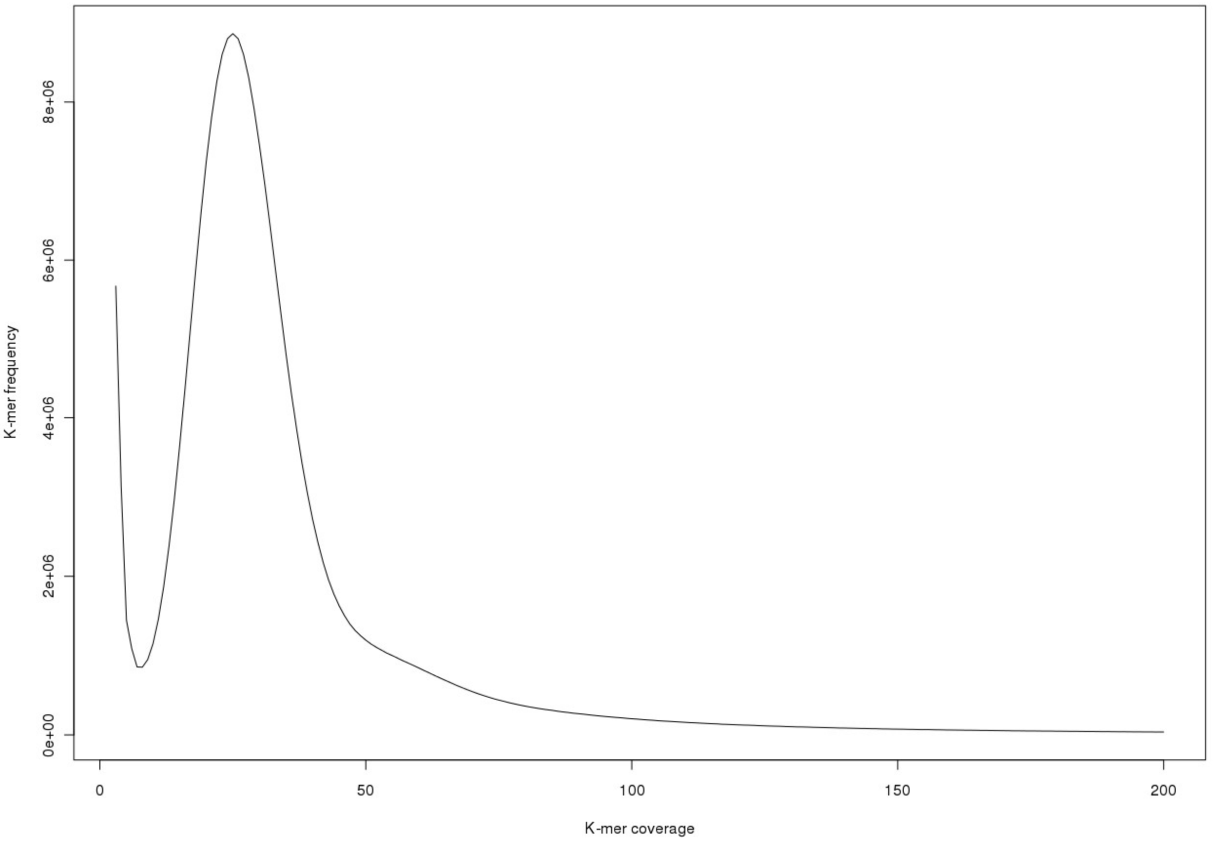
Draft genome sequence of *Cicer reticulatum* L., the wild progenitor of chickpea provides a resource for agronomic trait improvement

SUPPORTING FIGURES



k-mer	k-mer Depth	Total Base used	Avg. Read Len (base)	Estimated Genome Size(bp)
17	29	27,588,914,368	101	802,003,324

N = M* L/(L-K+1); Genome size = T/N
M=29; L=101; K=17; T=27,588,914,368

Figure S1: Estimation of chickpea genome size based on k-mer distribution obtained from Jellyfish.

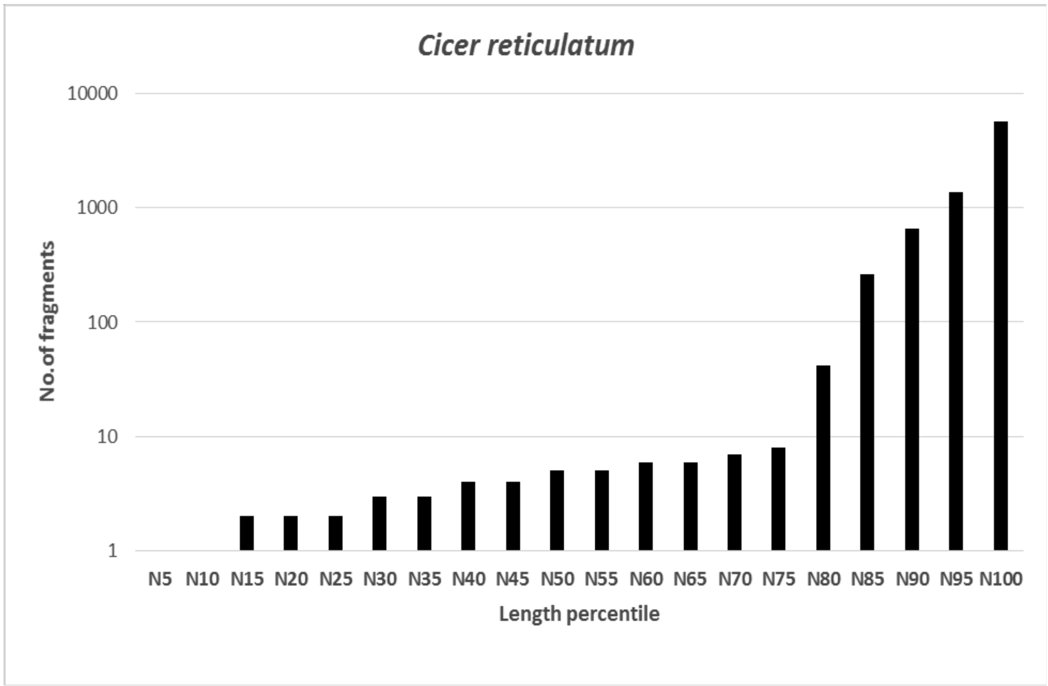


Figure S2. Fragment distribution of *C. reticulatum* genome assembly. Number of fragments covering different percentile of the assembly plotted against different length percentile.

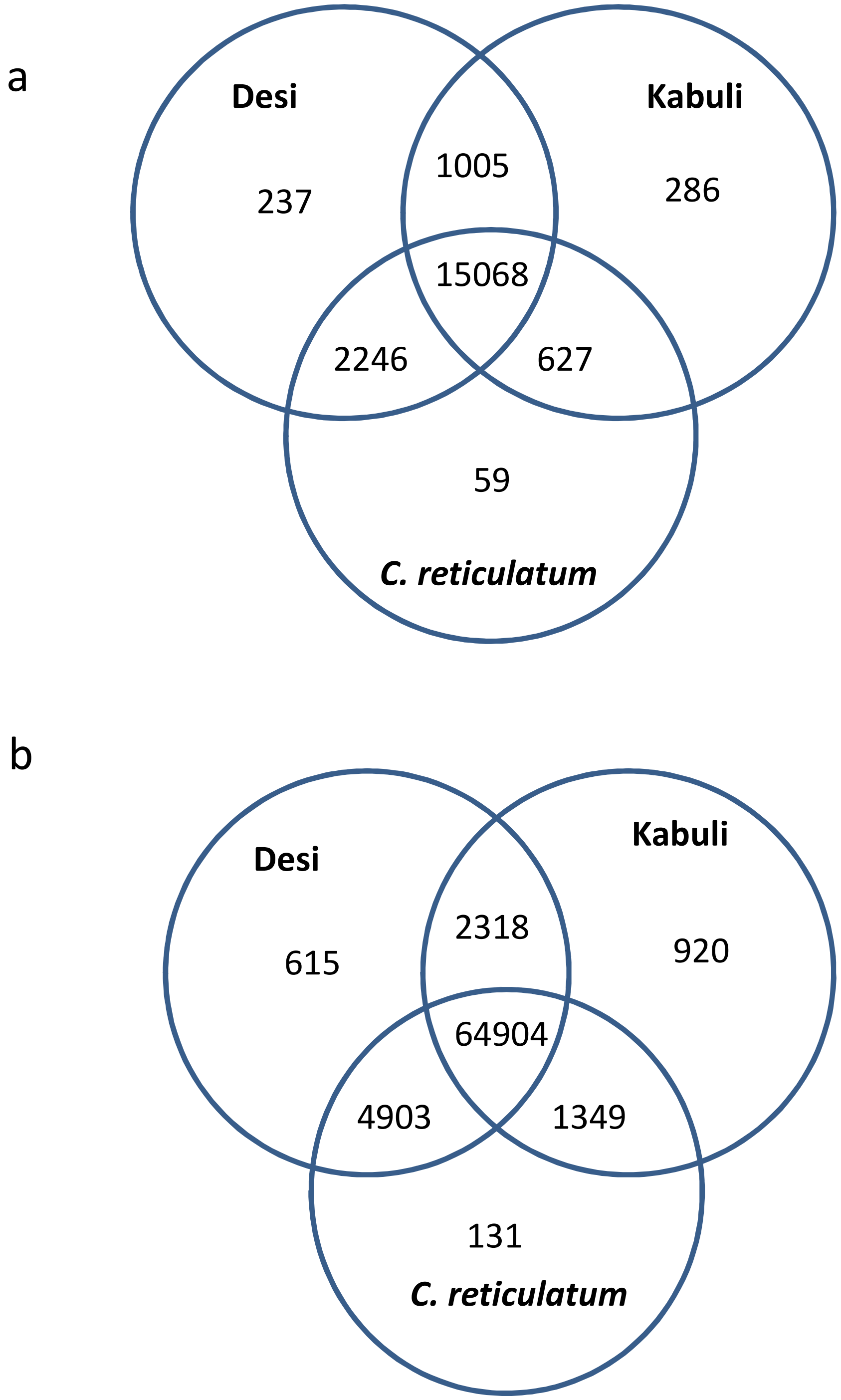
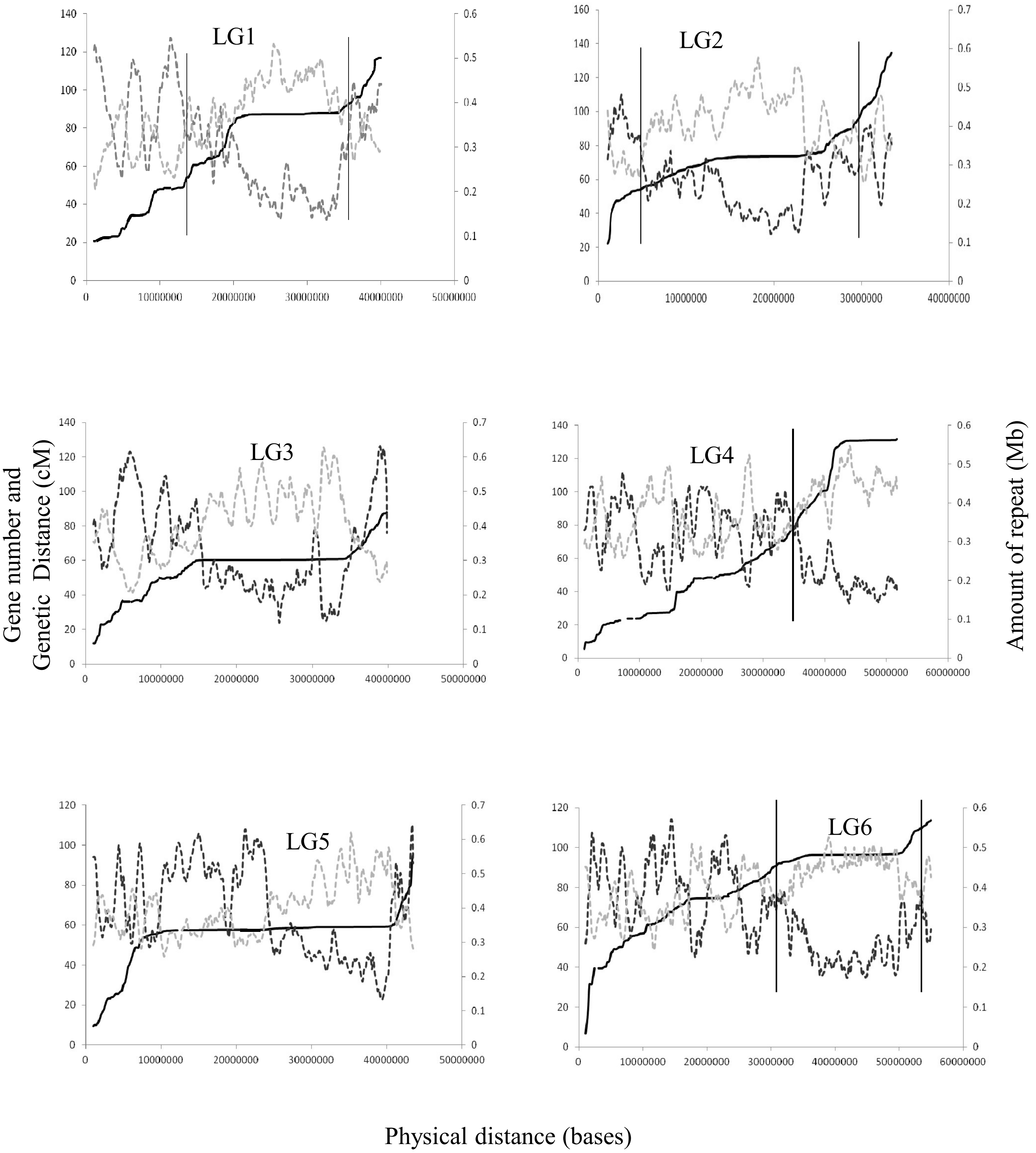


Figure S3. Venn diagram showing clustering of gene families (a) and genes (b) shared among Chickpea cultivars ICC4958 (Desi) and CDC Frontier (Kabuli) and wild chickpea *C. reticulatum*.


LG1
LG2
LG3
LG4
LG5
LG6
Gene number and
Genetic Distance (cM)
Amount of repeat (Mb)
Physical distance (bases)
0
20
40
60
80
100
120
140
160
0.1
0.2
0.3
0.4
0.5
0.6
0.7
10000000
20000000
30000000
40000000
50000000
60000000

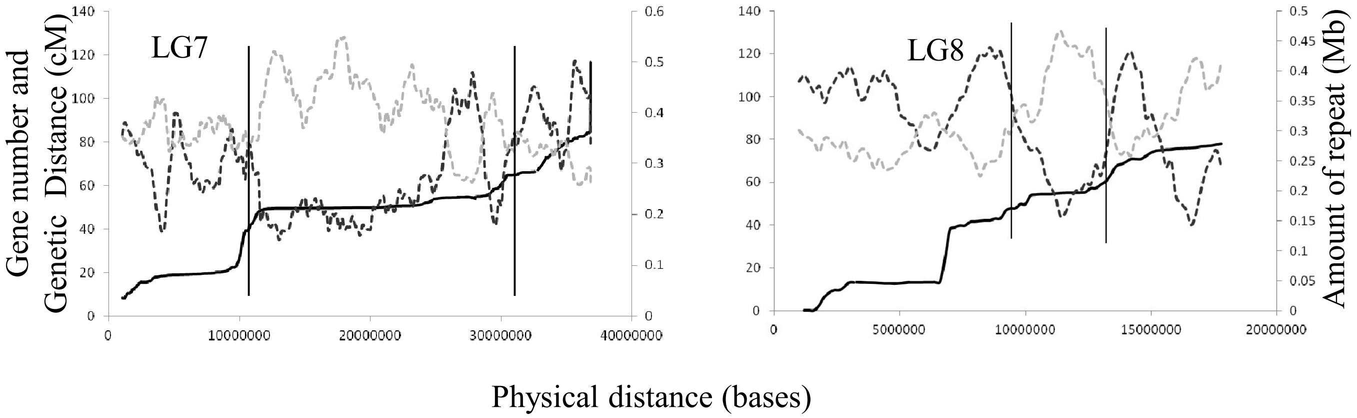


Figure S4. Multidimentional topography of linkage groups of *Cicer reticulatum.* Delineation of pericentromeric regions of LG1-8 was marked based on comparison of physical distance (X-axis) with gene density (left Y-axis, black dotted line), repeat density (right Y-axis, grey dotted line) and average genetic distance (Y-axis, black line). Vertical bars indicate position of transition from euchromatic region to pericentromeric region.

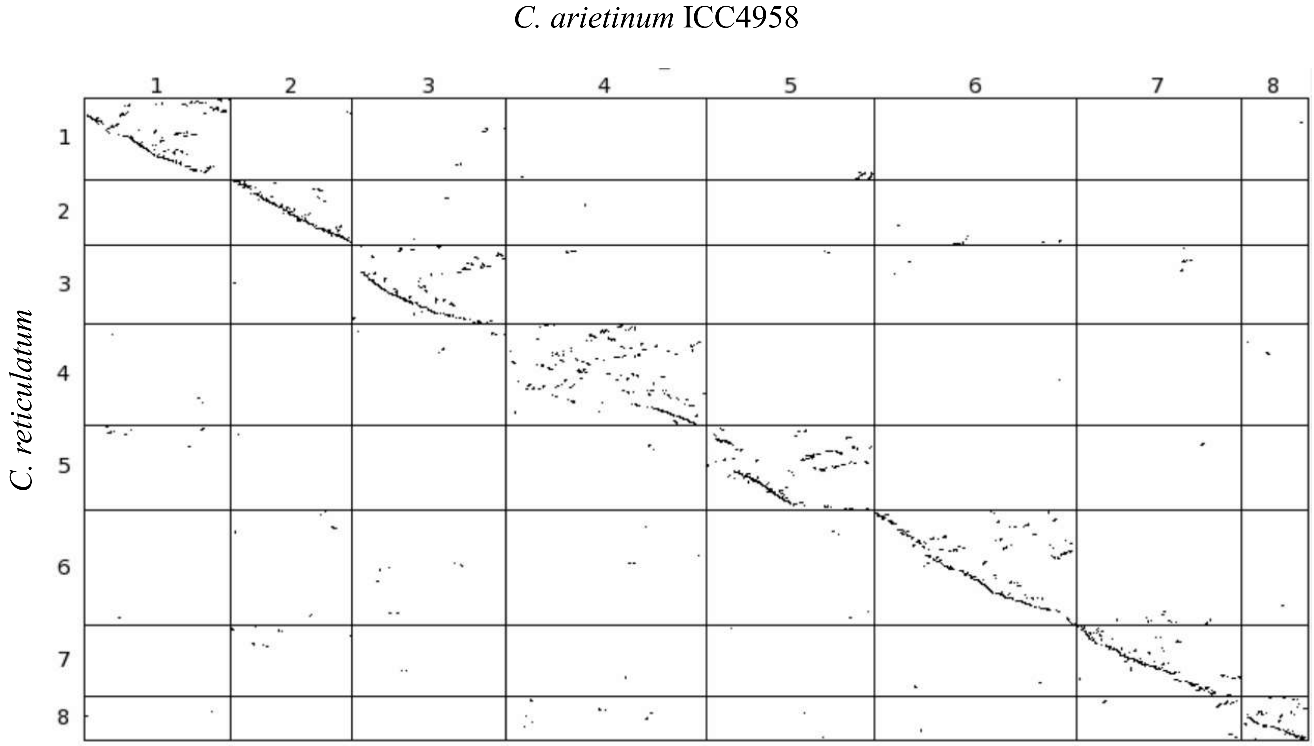


Figure S5. Comparison of *C. reticulatum* and *C. arietinum* ICC4958 chickpea genome assemblies. A dot-plot matrix comparing the chickpea (ICC 4958) and the *C. reticulatum* draft assemblies of eight pseudomolecules corresponding to each linkage groups. Pairwise comparison of all the pseudomolecules two draft genome assemblies were performed using synteny blocks and anchor filtering algorithms of tool SyMap v4.0.

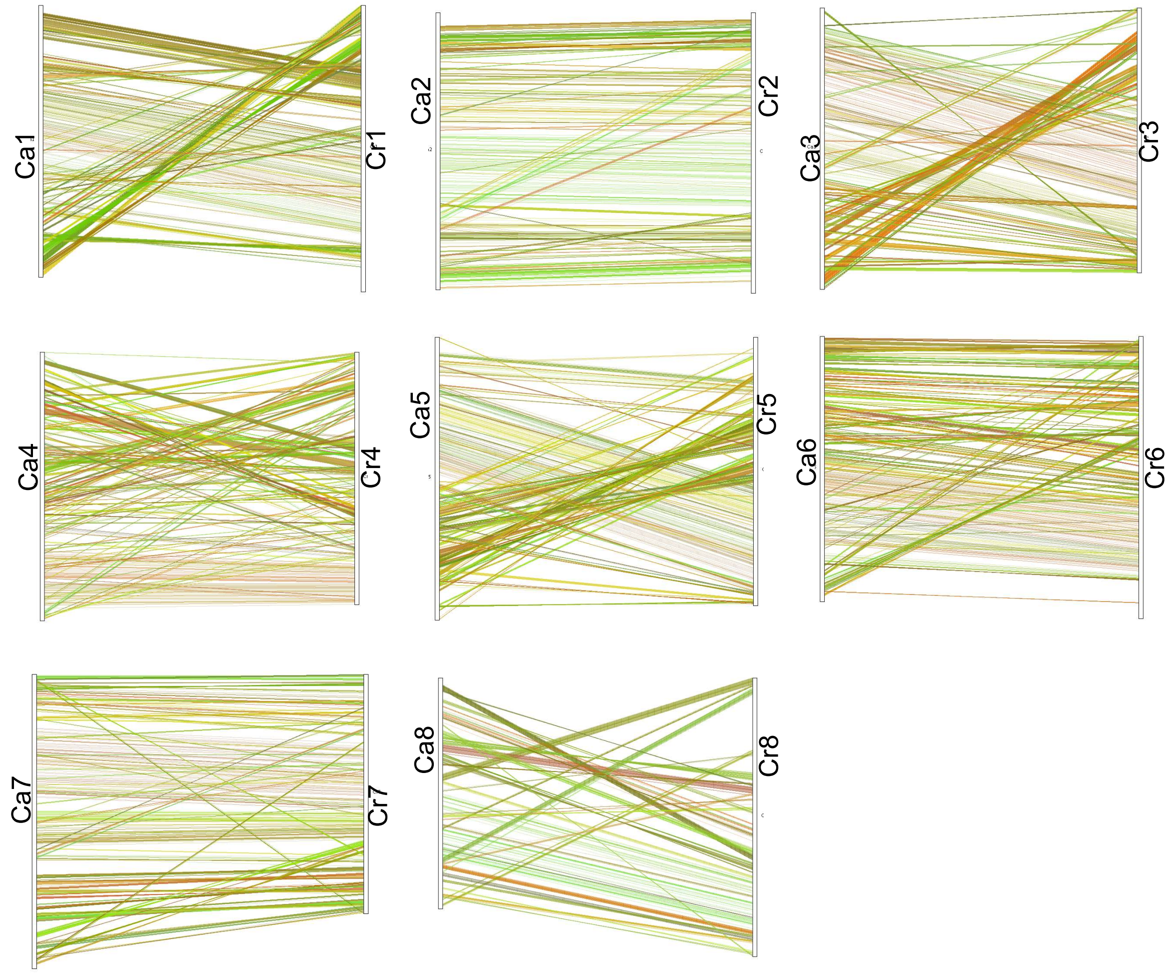


Figure S6. Pairwise collinearity analysis of orthologous genes present in the linkage groups of *desi* (Ca1-8) and *C. reticulatum* (Cr1-8) draft assemblies. Analysis was performed using default parameters of tool MCScanX.

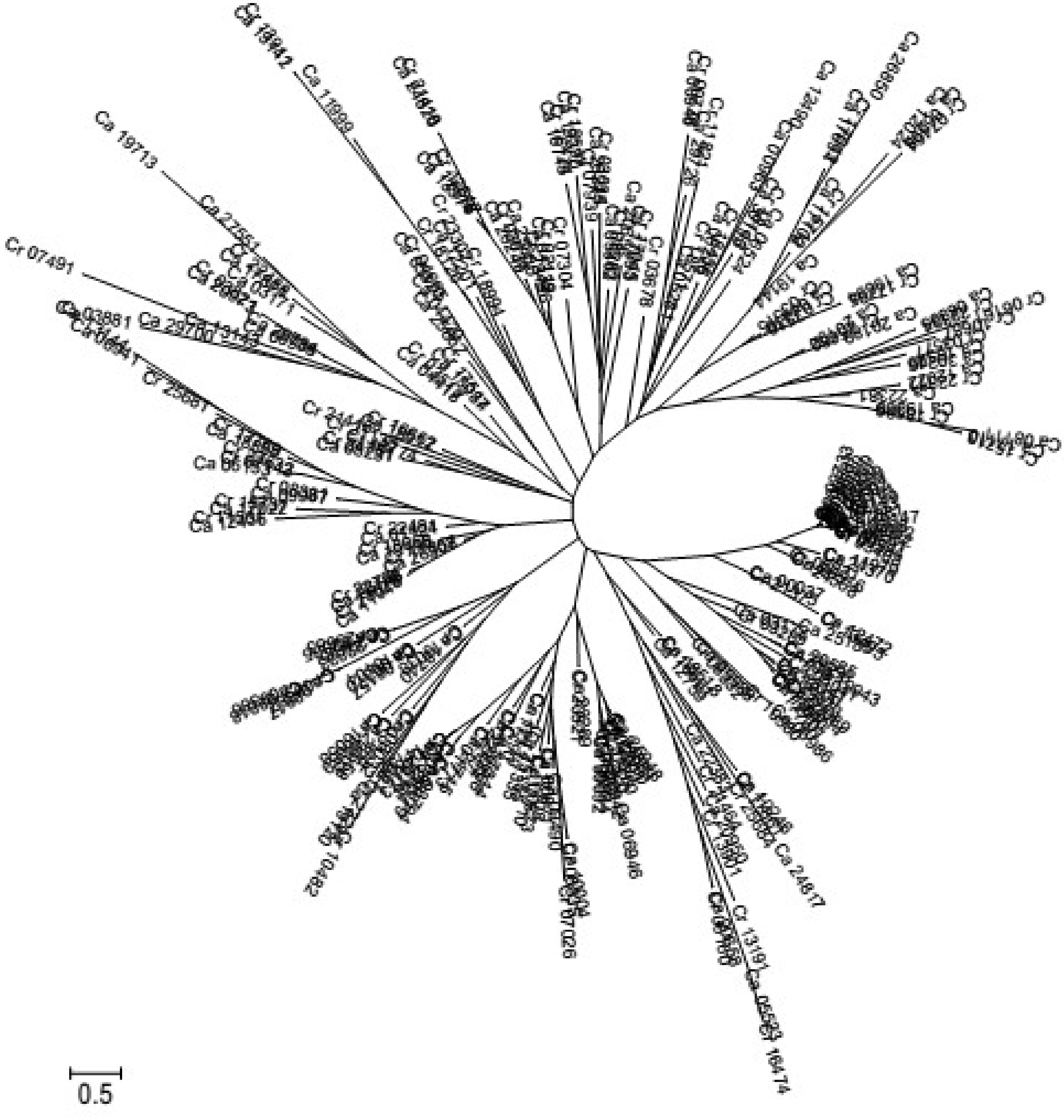


Figure S7: Unrooted phylogenetic relationship between the Rgene homologues of *C. reticulatum* and *C. arietinum*.

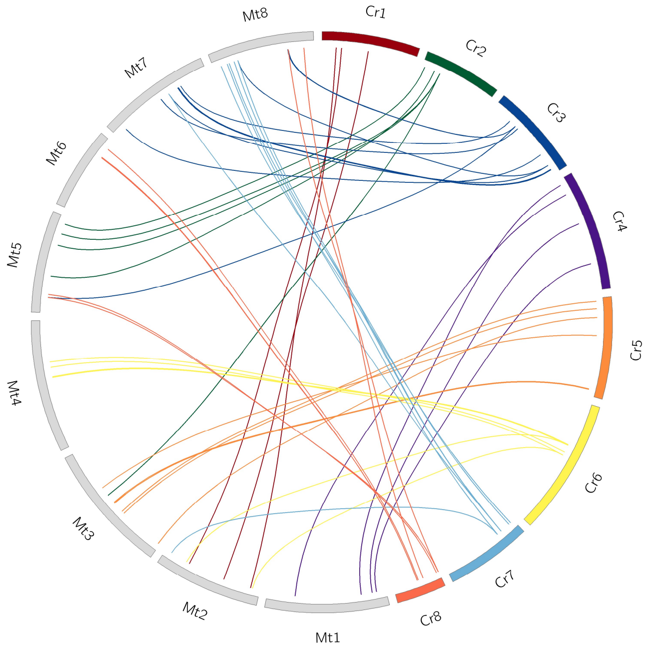


Figure S8. Pairwise collinearity analysis of resistance gene homologues present in the linkage groups of *M. truncatula* (Mt1-8) and *C. reticulatum* (Cr1-8) assemblies. Analysis was performed using default parameters of tool MCScanX and viewed using Circose.

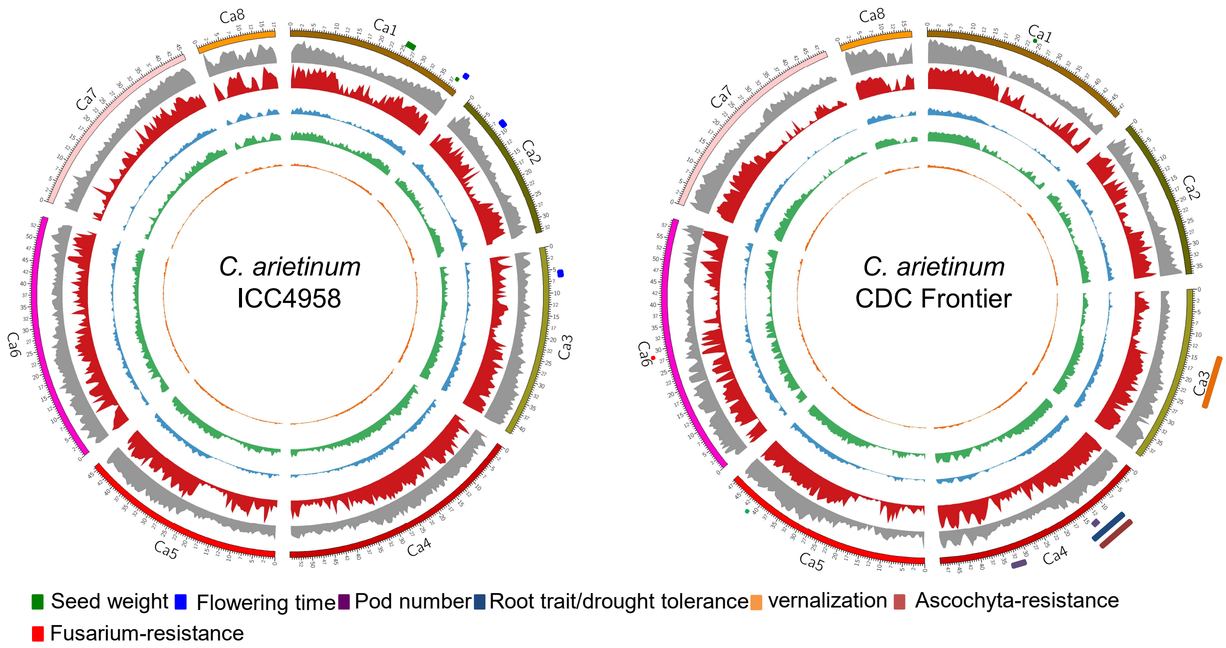


Figure S9 :Genome-wide distribution of sequence diversity (SNP/Indels) between the wild and the domesticated chickpea genotypes. Sequence reads of C. reticulatum were mapped on the pseudomolecules of *desi* (ICC4958) and *kabuli* (CDC Frontier) chickpeas. Circular maps show distribution of densities (in 0.5 Mb) of genes (grey), genomic SNPs (red), SNPs present in genes only (blue), genomic indels (green) and indels present in genes only. SNP and indel scales were kept as 5000 and 2500, respectively. Physical locations of quantitative trait loci (QTL) for different traits, available from literature, are shown as colored bars outside the circles.

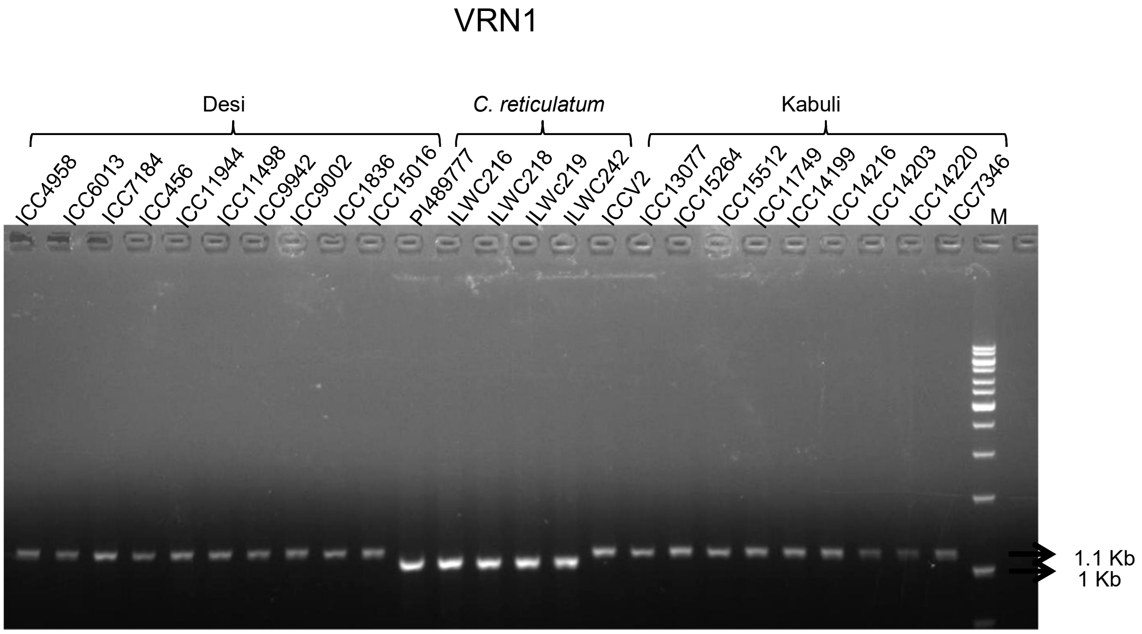


Figure S10. Amplification of the polymorphic sequence present at the 5'UAS of the VRN1 Orthologues in different accessions of the domesticated (*desi* and *kabuli* types) and wild (*C. reticulatum*) chickpeas. Accessions numbers are mentioned above.

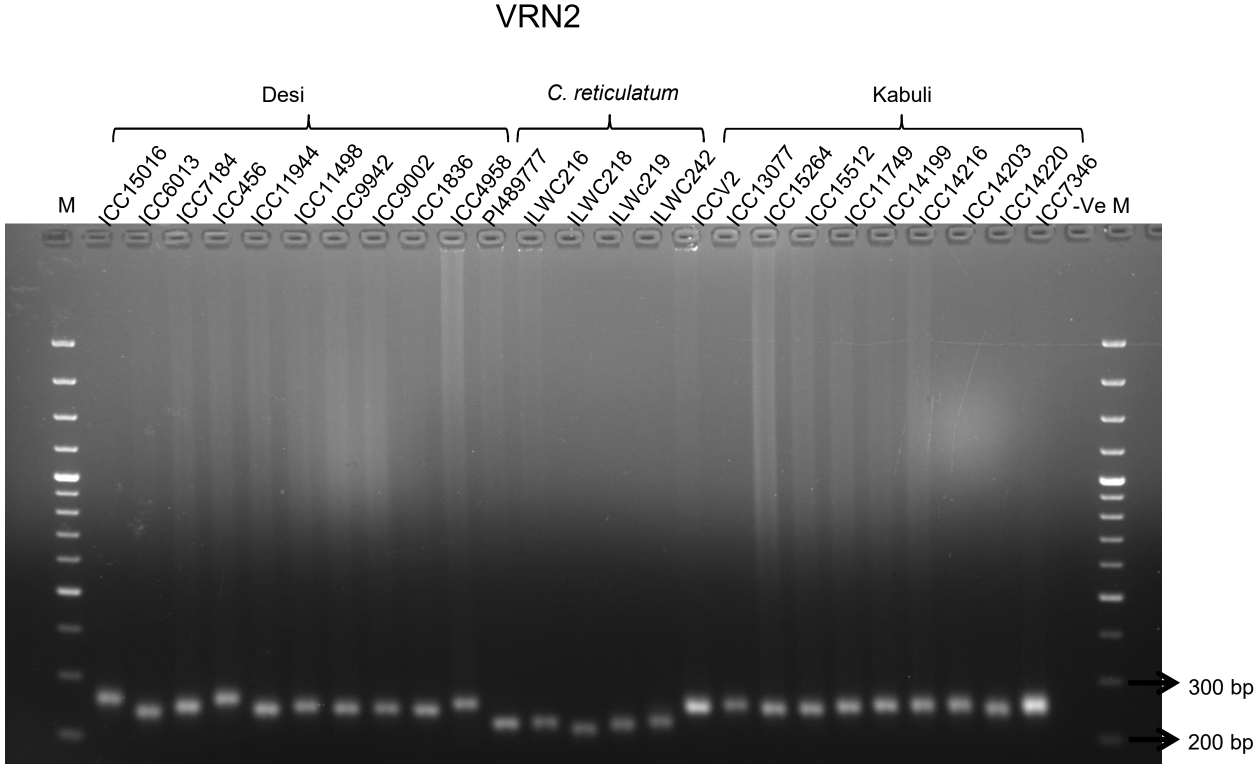


Figure S11. Amplification of the polymorphic sequence present at the 5'UAS of the VRN2 orthologues in different accessions of the domesticated (*desi* and *kabuli* types) and wild (*C. reticulatum*) chickpeas. Accession numbers are mentioned above.

Draft genome sequence of *Cicer reticulatum* L., the wild progenitor of chickpea provides a resource for agronomic trait improvement

SUPPORTING TABLES

Table S1. Sequencing data generated for *Cicer reticulatum* PI489777.
Sequence generated using Illumina HISeq 1000 sequencing platform (WGS, Whole genome shotgun. MP, Mate-pair)

Library type	**Av. Frg. Length (bp)**	**Total bases**	**Filtered**	**Filtered**
			Reads	Bases (Gb)
WGS	180	27,649,198,036	273,754,436	27.375
WGS	500	25,293,107,406	250,426,806	25.043
MP	3000	40,400,605,394	400,005,994	40.000
MP	10000	27,678,782,552	274,047,352	27.404
Total		121,021,693,388	1,198.234,588	119.823

*

Table S2. Comparison of genome assembly using three assembly tools

	ALLPATHS-LG	**SOAPdenovo2**	**MaSuRCA**
No. of scaffolds	7383	39,625	14,315
Min. Scaffold Length (bp)	1000	1000	1000
Max. Scaffold Length (bp)	3,939,974	343,591	2,610,062
Scaffold N50 Length (bp)	216,834	29,639	129,084
Total span (bp)	416,562,993	448,927,573	420,395,857
Valid bases (bp)	379,613,856	205,220,080	379,802,787

Table S3. ALLPATH-LG assembly output

	ALLPATH-LG assembly output
No. Scaffolds	7383
Total span	416,562,993
Min. Scaffold length	1000 bp
Max. Scaffold length	3,939,974 bp
Av. Scaffold length	56421.91 bp
Med. Scaffold length	9973 bp
Scaffold N25 length	530302 bp
Scaffold N50 length	216834 bp
Scaffold N50 index	427
No. of contigs	35,261
Total contig bases	378,554,873 bp
Max. contig length	309,892 bp
Contig N50 length	23,121 bp
Estimated genome size	817,640,084 bp
Estimated repeat content (at K=25 scale)	63%
Coverage	49X

% of WGS reads assembled	91.2
% of MP reads assembled	19.2

Table S4. Anchoring of scaffolds to linkage groups

Linkage groups	Markers mapped	No. of matched scaffolds	Assembled lengths of pseudomolecule
Cr_LG_1	597	174	42,039,305
Cr_LG_2	483	222	33,561,908
Cr_LG_3	520	218	39,846,785
Cr_LG_4	749	249	51,733,763
Cr_LG_5	623	225	43,510,909
Cr_LG_6	694	302	58,232,078
Cr_LG_7	472	187	36,831,687
Cr_LG_8	232	74	21,322,067
Total	4370	1651	327,078,502

Table S5. Statistics of *C. reticulatum* assembly

No. Scaffolds	5723
Total span	416,658,930 bp
Min. Scaffold length	1000 bp
Max. Scaffold length	58,232,078 bp
Av. Scaffold length	72600.57 bp
Med. Scaffold length	4237 bp
N25 length	51,733,763 bp
N50 length	39,846,785 bp
N50 index	5
Total contig bases	378,424,350 bp
Max. Contig length	309,892
N50 contig	23.12 kb
%GC	27.55
%N	8.87

Table S6. Statistics of *C. reticulatum* reads mapped back on assembly

Library	Total reads	Mapped	% Mapped	Uniquely Mapped
180 bp	273,754,436	208,433,504	76.14	161,779,033
500 bp	250,426,806	182,806,783	73.00	133,632,360
3000 bp	400,005,994	185,146,932	46.29	132,288,117
10000 bp	274,047,352	140,649,098	51.32	98,316,040
Total	1,198,234,58	717,036,317	59.84	526,015,550

Table S7. Statistics of reference-based *C. reticulatum* assembly

	***C. reticulatum* on ICC4958**	***C. reticulatum* on CDC Frontier**
LG_1	3,95,15,182	4,78,83,359
LG_2	3,28,63,583	3,62,43,916
LG_3	4,18,37,506	3,95,74,814
LG_4	5,45,07,455	4,87,29,341
LG_5	4,53,83,838	4,76,93,095
LG_6	5,43,37,838	5,88,90,561
LG_7	4,48,58,743	4,84,81,973
LG_8	1,74,87,649	1,63,41,866
LGs	**330,791,794**	**343,838,925**
Unanchored Scaffolds	**109,392,978**	**78,011,200**
Total	**440,184,772**	**421,850,125**

Table S8: Polymorphic simple sequence repeats (SSR) between the wild and two domesticated chickpea draft assemblies and their flanking sequences (submitted as an excel file)

Table S9. Statistics of protein-coding gene annotation in *C. reticulatum* assembly

Number of annotated gene	25,680
Total gene length (kb)	85,786
Average gene length (bp)	3340.89
Average coding sequence length (bp)	1192.195
Number of mRNAs	26,404
Average mRNA length (bp)	3364.35
Total exon length (kb)	34,181
Average number of exons per mRNA	5.31
Average number of exons per gene	5.76
Average exon length (bp)	240
Average intron length (bp)	384

Table S10. Functional annotation of *C. reticulatum* protein-coding genes

Database	Number	Percentage
NCBI ntdb | Trembl | Uniref100	24769	96.45%
Swissprot	17715	68.98%
TAIR	20734	83.74%
KEGG	6888	26.82%
Total Annotated[1]	25075	97.64%

Table S11. Sequence similarity of *C. reticulatum* genes to those of *C. arietinum* ICC4958 (*Desi*) and CDC Frontier (*Kabuli*)

Query coverage=100%, Identity=100%

	ICC4958	CDC Frontier
CDS	4033	3087
Protein	6969	5003

Query coverage=90%, Identity=95%

	ICC4958	CDC Frontier
CDS	20097	17597
Protein	18035	15227

Query coverage=80%, Identity=95%

	ICC4958	CDC Frontier
CDS	21475	19170
Protein	18876	16296

Table S12. ***C. reticulatum*** **statistics of euchromatic and pericentromeric region determination.**

	Chromosome			
	Physical Length	**Genetic Length**	**Kb/cM per chromosome**	**Total No, of Genes**
Chr1	42039305	150.98	278.44	3087
Chr2	33561908	154.53	217.19	2053
Chr3	39846785	91.04	437.68	2685
Chr4	51733763	134.14	385.67	3518
Chr5	43510909	114.46	380.14	2944
Chr6	58232078	125.64	463.48	3837
Chr7	36831687	179.82	204.83	2493
Chr8	21322067	96.21	221.62	1875
Total	327078502			22492
Average			323.6317343	
Percentage				
	Pericentromere region			
	Physical Length	**Genetic Length**	**Kb/cM per chromosome**	**Total No, of Genes**
Chr1	19000000	38.09	498.82	1066
Chr2	24400000	41.2525	591.48	1338
Chr3	18800000	5.084	3697.88	953
Chr4	15500000	45.097	343.70	712
Chr5	16000000	2.209	7243.10	738
Chr6	24400000	23.885	1021.56	1290
Chr7	14800000	8.95	1653.63	754
Chr8	4400000	13.651	322.32	243
Total				7094
Average			1921.560902	
Percentage				31.54010315

	Euchromatin			
	Genetic Length(cM)	**Physical Length**	**Kb/cM euchromatic arms**	**No, of genes**
Chr1	112.89	23.04	204.09	2021
Chr2	113.2775	9.16	80.88	715
Chr3	85.956	21.05	244.86	1732
Chr4	89.043	36.23	406.92	2806
Chr5	112.251	27.51	245.08	2206
Chr6	101.755	33.83	332.49	2547
Chr7	170.87	22.03	128.94	1739
Chr8	82.559	16.92	204.97	1632
Total		163.81		15398

Average			231.0279243	
Percentage				68.45989685

Table S13. Colinear genes (A) and blocks (B) between *C. reticulatum* and *Medicago truncatula* pseudomolecules.

A.

	Lines	**Unique Lines**	**Mt1**	**Mt2**	**Mt3**	**Mt4**	**Mt5**	**Mt6**	**Mt7**	**Mt8**
Cr1	2,615	2,004	137	**1445**	346	346	85	0	161	95
Cr2	1,267	1,058	12	35	72	121	**612**	277	82	56
Cr3	1,986	1,527	280	18	68	41	28	43	**1287**	221
Cr4	2,730	2,183	**2037**	28	148	30	139	14	315	19
Cr5	2,283	1,781	111	192	**1475**	183	156	11	33	122
Cr6	2,613	2,140	33	199	267	**1190**	134	90	62	638
Cr7	1,868	1,506	6	97	61	698	224	0	52	**730**
Cr8	1,792	1,358	198	137	40	434	**643**	172	0	168
	17,154	13,557	2,814	2,151	2,477	3,043	2,021	607	1,992	2,049

B.

	Mt1	**Mt2**	**Mt3**	**Mt4**	**Mt5**	**Mt6**	**Mt7**	**Mt8**	
Cr1	10	41	3	29	8	0	9	9	109
Cr2	1	3	9	7	43	20	7	5	95
Cr3	17	1	7	5	3	4	**44**	15	96
Cr4	**82**	3	14	2	6	2	21	2	132
Cr5	10	4	**52**	8	17	1	4	5	101
Cr6	5	21	16	**61**	12	5	8	22	150
Cr7	1	10	5	14	17	0	7	**46**	100
Cr8	12	8	5	9	10	11	0	11	66
	138	91	111	135	116	43	100	115	849

Table S14. List of resistance gene homologues predicted in *C. reticulatum* genome assemblies (submitted as an excel file).

Table S15. Colinear RGHs between *M. truncatula* and *C. reticulatum* genome assemblies (submitted as an excel file).

Table S16. Sequence diversity between *C. reticulatum* and *C. arietinum* ICC4958 and CDC Frontier

A. *C. reticulatum* reads mapped on *C. arietinum* ICC4958 pseudomolecules

		Raw	**Raw**	**HQ (Q≥30)**	**Raw**	**HQ(Q≥30)**
LGs	**LG Size**	**SNPs + InDels**	**InDels**	**InDels**	**SNPs**	**SNPs**
Ca_LG_1	3,99,01,017	8,52,420	58,833	42,414	7,93,587	2,13,381
Ca_LG_2	3,32,33,457	7,57,453	45,903	31,581	7,11,550	1,70,028
Ca_LG_3	4,22,67,542	9,22,325	59,883	42,568	8,62,442	2,11,478
Ca_LG_4	5,49,92,815	11,48,304	80,246	59,509	10,68,058	2,98,242
Ca_LG_5	4,58,19,701	9,61,555	63,892	45,826	8,97,663	2,24,449
Ca_LG_6	5,48,41,389	11,44,356	74,406	54,184	10,69,950	2,64,837
Ca_LG_7	4,52,79,478	8,67,825	53,492	37,705	8,14,333	1,74,065
Ca_LG_8	1,76,64,089	3,36,952	24,745	16,068	3,12,207	78,637
	33,39,99,488	**69,91,190**	**4,61,400**	**3,29,855**	**65,29,790**	**16,35,117**

B. Number of *C.* arietinum ICC4958 genes carrying SNPs and InDels with respect to *C. reticulatum*

No. of SNPs	**No. of genes**	**No. of InDels**	**No. of genes**
≥ 300	4	≥ 50	2
≥ 200	11	≥ 40	6
≥ 150	36	≥ 30	16
≥ 100	160	≥ 20	90
≥ 50	1142	≥ 10	927
≥ 5	13179	≥ 5	4131
≥ 1	18048	≥ 1	13580
0	5567	0	10035

C. *C. reticulatum* reads mapped on *C. arietinum* CDC Frontier pseudomolecules

		Raw	**Raw**	**HQ (Q≥ 30)**	**Raw**	**HQ(≥ 30)**
LGs	**LG Size**	**SNPs + InDels**	**InDels**	**InDels**	**SNPs**	**SNPs**
Ca_LG	4,83,59,943	7,98,210	80,591	47,977	7,17,619	2,24,468

1						
Ca_LG2	3,66,34,854	6,58,928	63,123	34,728	5,95,805	1,77,782
Ca_LG3	3,99,89,001	7,06,626	73,257	42,858	6,33,369	1,98,082
Ca_LG4	4,91,91,682	8,61,229	95,247	61,404	7,65,982	2,88,742
Ca_LG5	4,81,69,137	7,93,622	81,967	48,510	7,11,655	2,22,091
Ca_LG6	5,94,63,898	9,57,176	98,797	60,719	8,58,379	2,78,679
Ca_LG7	4,89,61,560	7,27,540	68,510	38,478	6,59,030	1,76,207
Ca_LG8	1,64,77,302	2,42,401	28,913	13,810	2,13,488	73,198
	34,72,47,377	**57,45,732**	**5,90,405**	**3,48,484**	**51,55,327**	**16,39,249**

D. Number of *C. arietinum* CDC Frontier genes carrying SNPs and InDels with respect to *C. reticulatum*

No. of SNPs	**No. of genes**	**No. of InDels**	**No. of genes**
≥ 300	8	≥ 50	13
≥ 200	30	≥ 40	26
≥ 150	63	≥ 30	54
≥ 100	176	≥ 20	161
≥ 50	959	≥ 10	1004
≥ 5	13419	≥ 5	3710
≥ 1	19022	≥ 1	12610
0	3961	0	10373

Table S17. Average nucleotide diversities of the wild, and domesticated chickpeas along the linkage groups.

Linkage Groups	**θπ**	
	Wild	**Cultivated**
Cr_LG_1	0.347	0.313
Cr_LG_2	0.319	0.298
Cr_LG_3	0.324	0.265
Cr_LG_4	0.389	0.320
Cr_LG_5	0.313	0.268
Cr_LG_6	0.315	0.304
Cr_LG_7	0.348	0.302
Cr_LG_8	0.293	0.293

Table S18. Flanking sequences of identified SNPs for wild and cultivated mapped on reticulatum for generating markers for large-scale genotyping (submitted as an excel file).

Table S19. Accessions used for diversity and population genetic structure analysis (submitted as an excel file).

Draft genome sequence of *Cicer reticulatum* L., the wild progenitor of chickpea provides a resource for agronomic trait improvement

SUPPORTING TEXT

Text S1. CDS and Protein sequences of 4 RGH obtained by mapping the identified RGF in the advanced draft genome of chickpea ICC4958, onto the *C. reticulatum* genome.

>Cr_26581.1|Cr_LG_2:2743436-2751375|plus|

ATGGAATACCTTTATGGATTTGCGTCTTCTATTTCAAGAGATTTGGTGTGCGGCGTGATAGGT
CAGTTAAGTTATCCCTGCTGCTTCAACAATTTTGTTCAAGACCTTGCAAAAGAAGAAGGTAAT
TTGGCTGCAACAAGAGCTAGTGTCCAAGACCGTGTTACACGAGCCAAGAAGCAAACTAGAAA
CACTGCTGAGGTTGTTGATAAGTGGTTGAAGGATGCTAACATTGTCATGGACAATGTTGATCA
GTTACTACAAATGGCAAAAACAGAAAAGAACTCTTGTCTCGGGAACTGTCCAAATTGGATTT
GGCGATACCGTGTAGGCAGGAAGTTAGCAAAGAAAAAAAGGGACCTTACATTGTGCATTAAA
GAAGGTAGACAATATATACAGATTGAACACCCTGCTGCACTTTCAAGCAATTTTTCTTCTGAT
AAATGTTGGGAGTTTGATAGTAGAAAACCTGCATATGAGGAACTTATGTGTGCTTTGGAAGA
TGATGAGGTTATTATGATTGGATTGTATGGGATGGGGGGTTGTGGTAAAACAATGCTTGCAA
AAGAAGTAGGCAAGAGAGCTGGCCATCTTTTTGATCAAGTGCTTTTTGTTCCTATATCTAGTA
CTGTAGAAGTGGAAAGGATCCAAGAAAAAATTGCAGGCTCTCTTGAATTTGAATTCCAAGAA
AAAGACGAGATGGACAGATCACAACGCTTATGCATGAGGTTATCACAAGAAGAAAGGGTTCT
TGTGATTCTGGATGATGTGTGGCAAATGCTAGATTTTGATGCCATAGGGATTCCTTCTAGTGA
GCATCATAAAGGTTGCAAAGTTCTCATTACCAGTAGATCAGAAGCAGTTTGTACTTTGATGGA
TTGCCAGAAAAAAATTCACCTGTCAACATTAACCAACGATGAAACGTGGGATCTTTTCCAAA
AGCAAGCACTCATATCTGAAGGCACTTGGATTACTGTAAAGAATTTGGCTAAAGAAATTTCA
AATGAATGTAAAGGCTTGCCTGTCGCCATTGTAGCAGTGGCTAGCAGCTTAAAAGGCAAGGC
GGAGGTAGAATGGAAGGTTGCATTGGATAGATTGAGAAGTTCGAAACCTGTTAATATTGAAA
AAGGTTTGCAAAACCCGTACAAGTGCTTGCAGTTAAGCTATGATAATTTGGACACCGAAGAG
GCCAAGTCACTTTTCTTGTTGTGTTCTGTGTTTCCTGAAGATTGTGAAATTCCTGTTGAGCTTT
TAACTAGGTCTGCAATAGGGCTAGGCATTGTTGGAGAAGTTCGCTCATATGAAGGGGCAAGG
GATGAAGTGAGTGCGGCTAAAAATAAGCTCATAAGTTCTTGTTTGTTGCTGGATGTTGATGAA
GGAAAATGTGTCAAAATGCATGACTTAGTTCGCAATGTAGCCCATTGGATTGCGGAGAAGGC
GATTAAGTGTACCTCAGAAAAGGATATGACTTTGGAACATACTTCATTAAGATATCTATGGTG
TGAGAAATTTCCAAATAGTTTGGATTGTTCCAATCTTGACTTTCTACACATTCACACATATACA
CAAGTATCAGATGAAATTTTCAAAGGAATGAGAATGCTCAGAGTTTTGTTTCTTTACAACAAG
GGTCGGGAGAGAAGGCCATTGTTGATTACATCATTAAAATTATTGATGAATCTTCGTTGCATA
GTCCTGAGTAAATGGGATTTAGTTGACATCTTATTTGTGGGAGACATGAAGAAACTTGAAAGT
CTTACATTGTGTGATTGTTCATTCCTTGAATTACCTGATGTGATTACACAACTGACAAACTTGA
GATTGTTGGATTTGTCAGAATGTGACATGAAAATGAATCCGTTTGAAGTAATTGGGAAACAC
ACACAGCTAGAAGAACTGTACTTTGCTGATCGTAGATCGAAATGGGAACTTGAATTCTTAAA
AAAGTTTAGTGTCCCACAAGTGTTACAGAGGTATCAAATACAGTTAGGAAGTATGTTTGCCG
GTTTCCAACAAGAGTTTCTCAATCATCGCAGAACTTTGTTTCTCAGTTATTTGGATACATCTAA

TGCTGCGATTAAGGATTTGGCCAAAAAAGCAGACGTCTTGTGTGTAGCATGTATCGAGGGAG
GTGCTAAAAATATTATCCCTGACATATTTCAAATAGAAGGAGGAAGTATGAATCATTTAACTG
AGCTTTTGATACGCGATTCTAAGGGGATAGAGTGTTTGGTTGACACTTGTCTGATAAACGTAG
GAACTCTCTTCTGCAAGTTGCATTGGCTAAGAATTGAGCACATGGAGCGTTTGGGAGCTTTAT
ACAATGGTCGAAGAATGCCTCTTGGTGGTCATTTTGAGAATTTAGAAGACCTATATATAAGTA
ATTGTCCAAAGCTAACATGTCTCTTCACACTTGCAGTTGCTCAAAATCTGGCACAATTGGAGA
AGTTAGAAGTATTATCTTGTCCTGCACTGAAACATATACTAATNNNNNNNNNNNNNNNNNNN
NNNNNNNNGGAGATAAGTGCATATGATCACAGACTTCTGTTTCCAAAATTAAAAAGCTTCA
TGTTAGAGAGTGTGGTATGCTGGAATACATAATCCCAATCACTTTAGCTCAAGGCCTTGTACA
ATTGGAGAGTATAGAAATCGTATGTAATCATAAGTTGAACTACATATTTGGCCAAAGTACAC
ACAAAGATGGTCAGAATCAAAATGAACTCAAGATCGAGCTTTTGGCCCTGCAAGAGCTTACT
CTTGTTCTCTTGCCAAATATCAATAGCATTTGTCTAGAAGATTGTTATCTAATGTGGCCATCCT
TGTGTCAATTCAATTTGCAAAATTGTGGAGAGTTTTTCATGGTGTCTATCAATACTTGCATGGC
TTTACACAACAATCAGATAATCAACGAAGCTTCACGTCAAATTGTGCAAAATATAAAAGAAG
TTCGAGTCAATAACTGTGAGTTAGAAGGCATCTTTCAGCTAGCAGGACTATCCATTGATGGAG
AAAAAAATCCACTGACATCATGTTTGGAAATGTTGTATTTGGAGAATCTACCTCAGCTCAGAA
GGTTAAAATTTATCTTCTCATCCTGTATGGCAGGAGGGTTACCTCAGTTGAAAGCGCTAAAGA
TAGAAAAGTGCAATCAGCTAGATCAAATCGTTGAGGATATTGGCACTGAAATTCCCTTAGGA
TCATTTGGTTTTCCCAGCCTTATAAGGTTAACACTAATATCATGTCCGATGCTGGGTTCATTGT
TTACAGCATCTACTGCTAAAACCTTGACTTCACTGGAAGAATTGACAATACATGATTGCCATG
GTTTAAAGCAATTACTGACTTATGGAAGAGCTCAGAAAAATACAAGGGGAGAAATAGATCAG
GATGATCAGGACTTTCAGAGTTGTACGACAATGTTCCAAAGTTTGAAAAAGATTAGTATTTTG
AGATGTCATTTGCTGAAGTATATATTACCCGTTTCATTTGCGAGAGGACTGGTGAAATTGGAA
GCTATAGAAATCACAGAGACTCCCGAGCTGAGATATGTATTTGGTCAAAACAGTCATGCTTCC
CATCAATATCTAAACAAGTTCCAAATTGAGCTTCCTGTTTTGGAAAAAGTTGCACTCTATGAT
ATACCAAATATGATTGCCATTTATCCAGAAAACTATCATGCAACATGCTCATCTTGGCAACTT
CTTGTCATGAACGATGTTGGTCTATCAATGAATAATTTGATGGTTGATTTTGGAGCCACAGAC
TCAGATCTTAGTTCTAAAACAGATGAATGGGAAACAAGTATGAGTATTGAGAAGAAGTTAGT
ATCTGTTATTATTGAGAATGGATCCAAAATTGAAGGCGTTTTTCAAATGAATGGATTCCCAAT
CAATGGACAACAAGTGGTGTCCTGGTTAGAAGACCTTAAATTGGTCAATTTGGCAGAGCTAA
TGTACATATGGATGGGTGCTAAACATTTTGCAAGCCTTCAGCATCTTCAGAAAATACACATCT
GCAATTGTCCAAAACTGAAGTCTATCTTCTCCATCTCTGTCTTGAGAGTCCTACCCCTGTTGAA
GATTCTTGTGGTAGAACAGTGTGAGGAATTAGAGCAAATCATTGAAGATGATGAAGAAAATG
AAAATGTCCCGAATTCTAAAGTGTGCTTCTCACAGCTAAAGTTTCTTCTTGTCACACACTGCA
ACAAATTGAAGCATTTGTTTTATATCCCCACATCCCATGAGTTTCCAGAACTGGAGTATCTGT
CTCTCAATCAAAATTCTAGTCTAGTTCAAGTGTTTAAAGTTGGTCCTGGTGTGAGAGAAGGTA
GAATGGAAGCTTTGCTTCCAAAACTCAAACATATAATGCTAATGCAACTGCCAAACCTCAAT
AATATGTGTCAAGGGGTTGAGTTTCACACTCTGACCAATCTTTTGGTGCACAATTGCCCAAAA

ATCTCACTAACTTCAGCGACTACTGTTGAGGACATGCTAAAAATCTATCATCATGACAAGGAA
TTTGGTTTCTATCTCTGTCCACACTTACACGACATAAGTTGTACAACAACAAATGGCCAAGAG
TTCATTACATCAAAGAACAAAAACAAAGGGATACAAGATTTACAATCACAGGAGCAGAAACT
GTCATCCATTCCTTTACCAAACTTGACAGAGAACTGGTTGAAATGCCATTTCCTAGTCATTTTG
CCACACAAGGAAGTTGTGGAGGAGTTGGTTAAAGGACAATCCACGGATGAACCATGTTTGAT
GAGCCAACAAAATCCACTTGAAGAATCTAGAGTTACGATGATTACTGAAGAGGGAACTTCAT
CAAAGAATGTGGAGATGGTAGCTTCGCCAATTCATTCCGATTCTGATAGCTCAAAGTCAGACC
CATTAGTTACATCTCAACGTAGACCACATCCACATTGTGAAATAAGCTTCAGCCAAACTGAGA
CTTACACTAATGAAGAAAACAAAGACCATCCTATAAATACAGTAGACTTGGGGGCCAGTGAT
CTCATCAGTTTATTTCAACCCGTCGAAGAAGATGATGAAGGCCAAATAACCACACCTTGTGTT
TCTGAAGTGACTGAACAACATCATTCAACCAAAGATAACTTAGTTGCGAAGGCACTTTCTGAC
CTGGAAGAGTGTTTGAAAATGCCTCTGAAGGACATAGCTAGCTCTGAGGCTAACAGCCTTCG
CCTTCTAACAGCTCTTAACTTCTTGTCCCACCTTTCTTTAAAAGATGCAGCTGTATCAGATGGA
CTCCAAGCTATAATAGACACTATGCACAGAGAATTCCCAAGCATCCTATGCTCCTTCAAACAA
GGATTTACCCTAGACAAATTTGTTGTGATTGAAGCTCATCATGATGAGGCAGCCATTACTCTT
GCTTCCAAAATTTCCAAAGCAGATAGTTTTTTGGATGAAGCTCAACAGAGGGAAGCAACTTT
GAAGGAACATATCATTCAATTGAAGAAAGAAATAAAAAATCTTGAGGCTGAACTATCTTATC
TTGATGAGAAAAAGGACAAATGCATTCAAGAAACTATAGGGTACAGAATGGAGTTGGAGAA
TGTGAGGAAAGACAAGTATCAAATTGTGGAAGATCAGATGAAAGCTCGGCAAGAAATATTTG
AAGTCGATTATAAATGGTCTGCTTTAAGTAGTCAGTTTCGGTACAACTACATTGTTGAAAGAA
ATCCTTCTTGA

>Cr_25681.1|Cr_LG_2:2743436-2751375|plus|

MEYLYGFASSISRDLVCGVIGQLSYPCCFNNFVQDLAKEEGNLAATRASVQDRVTRAKKQTRNT
AEVVDKWLKDANIVMDNVDQLLQMAKTEKNSCLGNCPNWIWRYRVGRKLAKKKRDLTLCIKE
GRQYIQIEHPAALSSNFSSDKCWEFDSRKPAYEELMCALEDDEVIMIGLYGMGGCGKTMLAKEV
GKRAGHLFDQVLFVPISSTVEVERIQEKIAGSLEFEFQEKDEMDRSQRLCMRLSQEERVLVILDDV
WQMLDFDAIGIPSSEHHKGCKVLITSRSEAVCTLMDCQKKIHLSTLTNDETWDLFQKQALISEGT
WITVKNLAKEISNECKGLPVAIVAVASSLKGKAEVEWKVALDRLRSSKPVNIEKGLQNPYKCLQL
SYDNLDTEEAKSLFLLCSVFPEDCEIPVELLTRSAIGLGIVGEVRSYEGARDEVSAAKNKLISSCLLL
DVDEGKCVKMHDLVRNVAHWIAEKAIKCTSEKDMTLEHTSLRYLWCEKFPNSLDCSNLDFLHIH
TYTQVSDEIFKGMRMLRVLFLYNKGRERRPLLITSLKLLMNLRCIVLSKWDLVDILFVGDMKKLE
SLTLCDCSFLELPDVITQLTNLRLLDLSECDMKMNPFEVIGKHTQLEELYFADRRSKWELEFLKKF
SVPQVLQRYQIQLGSMFAGFQQEFLNHRRTLFLSYLDTSNAAIKDLAKKADVLCVACIEGGAKNII
PDIFQIEGGSMNHLTELLIRDSKGIECLVDTCLINVGTLFCKLHWLRIEHMERLGALYNGRRMPLG
GHFENLEDLYISNCPKLTCLFTLAVAQNLAQLEKLEVLSCPALKHILXXXXXXXXXXEISAYDHR
LLFPKLKKLHVRECGMLEYIIPITLAQGLVQLESIEIVCNHKLNYIFGQSTHKDGQNQNELKIELLA

LQELTLVLLPNINSICLEDCYLMWPSLCQFNLQNCGEFFMVSINTCMALHNNQIINEASRQIVQNIK
EVRVNNCELEGIFQLAGLSIDGEKNPLTSCLEMLYLENLPQLRRLKFIFSSCMAGGLPQLKALKIEK
CNQLDQIVEDIGTEIPLGSFGFPSLIRLTLISCPMLGSLFTASTAKTLTSLEELTIHDCHGLKQLLTYG
RAQKNTRGEIDQDDQDFQSCTTMFQSLKKISILRCHLLKYILPVSFARGLVKLEAIEITETPELRYVF
GQNSHASHQYLNKFQIELPVLEKVALYDIPNMIAIYPENYHATCSSWQLLVMNDVGLSMNNLMV
DFGATDSDLSSKTDEWETSMSIEKKLVSVIIENGSKIEGVFQMNGFPINGQQVVSWLEDLKLVNLA
ELMYIWMGAKHFASLQHLQKIHICNCPKLKSIFSISVLRVLPLLKILVVEQCEELEQIIEDDEENENV
PNSKVCFSQLKFLLVTHCNKLKHLFYIPTSHEFPELEYLSLNQNSSLVQVFKVGPGVREGRMEALL
PKLKHIMLMQLPNLNNMCQGVEFHTLTNLLVHNCPKISLTSATTVEDMLKIYHHDKEFGFYLCPH
LHDISCTTTNGQEFITSKNKNKGIQDLQSQEQKLSSIPLPNLTENWLKCHFLVILPHKEVVEELVKG
QSTDEPCLMSQQNPLEESRVTMITEEGTSSKNVEMVASPIHSDSDSSKSDPLVTSQRRPHPHCEISF
SQTETYTNEENKDHPINTVDLGASDLISLFQPVEEDDEGQITTPCVSEVTEQHHSTKDNLVAKALS
DLEECLKMPLKDIASSEANSLRLLTALNFLSHLSLKDAAVSDGLQAIIDTMHREFPSILCSFKQGFT
LDKFVVIEAHHDEAAITLASKISKADSFLDEAQQREATLKEHIIQLKKEIKNLEAELSYLDEKKDKC
IQETIGYRMELENVRKDKYQIVEDQMKARQEIFEVDYKWSALSSQFRYNYIVERNPS

>Cr_25682.1|Cr_LG_7:17612745-17618450|minus|

ATGAGTGTGCAATCTAGCTTCACCTACGATGTGTATCTGAGCTTCAGAGGTGAAGATACACGA
TTCGGTTTTACTTCAAATCTCTTCGCTGCTCTTAAACAAAGAAGTATCCATACATTTACTGACG
ATGCGCTGCTTCTTAAAGAAGAGAATATATCTCAATCACTTTTTAGGGCAATCGAAGAGTCTA
GGATCTTCATCATTATATTCTCCCCCAACTATGCCTCTTCTAAGTGGTGTTTGGAAGAACTAAC
CACGATCCTAGAGTACTATGAAGAGGGGAAGAAGAAAAATTGGGGAAAAGTTTTACCAATTT
TCTATGACGTTGATCCTTCTGATGTGCGAAACGGGAGAGGAAGTTATGGAGAAGCACTGGAT
AAACATGAAGAGATGTTCAAGGATGACCTTGAGAAGGTCGACAAATGGAGGAGGAGAGATG
GAAACGAATATAAATTTATCGAGAGTATTGTAAAGGAAGTCTTTCGCATGATTTCTCGCGTTT
CTTCTTTACATGTTGCTGGTTACCCTGTTGGATTGGAGTCTCGAGTGGATAAAGTAAACTCAC
TTCTGAATCTTGGGTCTGATGATTTAGTTCAAATGGTAGGGATATGGGGAATTGGTGGAATAG
GGAAGACCACAATTGCTCGAGCCGTATGTAATTCAATCAGTCACTTGTTTGAAGGTTTATGTT
TTCTCAATGATGTGAGACAGAATTCAATGAAGTATGGCTTGGTACATCTCCAAGAGACTGTTC
TTTCTGAGATATGTGGAGATGTAAATAAAATAAAGAGTGTCAACCAAGGAATTCCAATAATA
AAGCAGAAACTCCACCGGAAAAAGGTTCTTTTAGTTCTTGACGACGTTGACAATTTGAAGCA
ACTCCAGGTTATTGCAGGAGCATCTGATTGGTTTGGTCCTGGAAGCAGAATCATCGTTACAAC
TCGGGACAAGCATTTTCTAGTAAGTCATGCGATTGAAAGAATATATGAAGCAGACGCATTAA
GTGAAAAAGAATCTCTTGATTTGCTTAGTTGGAATGCTTTTAAAACCGACAAAGTTGATCCAT
GTTTTGTAGACATTTTAAAACGTGCATTGACTTTTGCTTCTGGGCTTCCATTGGCTTTGCAAGT

AGTAGGCTCCTACTTGTTTGGCAGAAGTATAAATCAGTGGATAAGTGCATTGGATCATTATGA
AAGAGTTCCCGATAAACATATCCAAACAGTACTCAAGATAAGCTACGATTCCTTAGAGGAAG
AAGAGAAGAGTGTTTTTCTTGATATTGCTTGTTTCTTCAATGGACATAAGTTAGAAGACGTCA
AAGATATACTTTTGGCTCGTTATGGTGTATCTGCAAAATATAGTATTGAAGAATTGATTGAAA
AATCTCTCATAAAGATCGATGATGGTCTTGTGACATTACATAACTTGATTCAAGACATGGGTA
GAGAAATTGTCCGACAGGAATCACCATATGAGCCTGGCAAACGCAGTAGGTTATGGCTTCCT
AAAGATGTAGTTTGCGTTTTAGAAAAAAACTCGGGTTCTAGTACAATTGAAAGCTTATTTTTG
GATTTCCCCAAAGATGAAGTGAATTCACATGGACCCAAAGGCCCCACACATCTTCCCAATAG
TTTAAAAGTGTTGAAATGGCGAGGGTATCCTTCAGCGTCATTACCAAATGATTTTCATCCGAA
GAAGCTTGCCATACTCGAGTTACCTGCAAGTTGCGTAGTGACGTTTAGAAGCCTGAAATATAT
GAATTTAAACTACTGTGAACTGATAACTCATATACCTGATGTATCTGGCCTCCCAAATTTAGA
AACATTGTCATTTAGAGATTGTGTGAATTTATCTGAAATTCATGTGTCAGTTGGATTTCTGGAT
AAACTTAAAATCTTGGATGCTGGTCATTGCAAGAAACTTATGGCTTTTCCACCCATCAGATTG
ATCTCTCTTGAACAATTCTATATTTCACATTGCTCAACTCTAGAAAGTTTCCCAGAAATATTGG
GGAAGATGGAAAATTTAACAGAGCTTCGAATCATCGGAAGTCCTATACAAGAATTGCCATTT
TCAATTCAAAACCTAAATCGGCTTCGAAAATTAGAACTACAAATCTGTGGAACGGTTCAGTTG
CCAAGTAGCATTGCCATGTTTTCACAACTTGGTTTGATGTGTGTTTCGAGATGCGAAGGGTTA
TGGTTAACAAAACAGGACATAGGTGAAGAATGGGATACCAAGTCTTCAAAGACAGAACGTCT
TATTCTGTCGTACTGCAATATATCAGATGACTTCCTTCCAATAGGTCTTACTTTGTTTGCCAAT
GTAAAGGATTTGGACCTGTCGGGGAATCATTTCACTATTCTTCACGCGTGCATTAAGGAATGT
CACTTTCTGAGGAACCTTAAGCTGAATGATTGCGTGCTTATACGAGAAATTACAGTGATGCCA
TGTAAATTAGAAACACTTTCTGCAAAACGATGCAAATCCTTGAAATACATGGATCTTACAGG
AGAATGTCACTCTTTGAGAGAACTTACTCTGGATGATTGTATTTATCTTCGAGAAATTAAAGG
GGTTCTGTCAAACTTGGATCATTTCTCTGCAAAAAACTGCACATTATTGACTTCCCAATGTGC
AAGCATGTTAGTGAATCAGGAAATGATCGAAGCTGGAAACAAGATGTTTTCTTTGCCAGGAT
CAAATATTCCGGATTGGTTTGCGCACCGTACAAGTGGAGAGTCAATATCTTTCTGGTTTCGTA
ACAAATTCCCTGCAATTTCTCTGTGTCTTGTTATTGGACAGGAAGATGAGCTACCTATCTCAG
TCAAGTTTAGTCCAAAAGTGCTCATCAATGGCAATGAACTGTCCGGTGGCAATCAGAAAGTC
TACAAGTTCAGGATAGCTACGGATCATATACTTTTGTTTGATGCACGGATGCTAAGTTTTGAA
GATAATGGAGATACAGAATTGTCAGACTATGAGTGGAACCATGTGGTGGTTTCATATGAGGA
TCTTATTACTGACAACGGGGTTCCAATCAGAGTGGTTGCCAAATATAGCGGAATCCATGTATT
TAAACAAACGAGTGGACTGGAGGATATCCAATTCACCAATCCCCGGAAAACATTTATAAATG
CGAATTTGGGTCCCAATTCAATGGCAGAGCCACCTCAAAGAGAAACTTCAGAGAGTCTTTCA
AATAATGAAGTTTATGCTACTTTAAAAGAAAATGACCCTCCTGTCATTCACGGATGTAGTGTC
GACGAGGATGCCGATCTGGATGCAGTATCCTGTGAGGAAGAGTCTTCTTCCAACACTGAAGG
TTCTGATTCAGATGATCCCTTCGACTTGATTAATAGAAAACTCTGTGTTAGTTGGAAGAAAAT
CATATCCTCAGGATCAAGTTCTGGAGATGCAAATCTAAGATCCATTAGCGAGGCTATTAATGC
CTTGGAGTTGTTAATGGTGAAGGACTTATCAGAAGTCTCTTCTGATCCCGCAGCGCATTCCAA

```
ACTTCATCAGCTCTTGGATCTATTGGGTGCAAGTAGCCACCCCAAGGTGACTGTAGAGATGAA
GGAGGCTATTGTGGAGTTCAAGAGAAAGGCCTTTTTATTATTCCAACAATTCCAATCCACTGT
TGAGTCTGTCAAAACACTGAAGGATTTTGAGAAGCATCTGACCAGAATTAAGCAAGAGACTG
TGGAAGGCAAGAGTCGAAGAAAGGACCTAAAAAACTCAATAAAAAGGGTTTCTTTGGGCATC
AAAGCCGAAAATAGTAGTAAAAAGGAGCTAGAGTCAGAAATTGCAGTTTTAAGAAAACAAC
TAGCTACCAAAGAAAGGGACCTTGAACAATTTGTGGTGAATCTCAAGAATCAGGAGGAAACA
CTCTCGACCTATTCAACAAGTTATGCTTCTCTCAACGAGCAAGCTCAATCACTATTAAAACAA
GCTGATGATCTACTTGCTGTAAGCAGTGGGATAAAGGATGAGGGTGAAGCAGCTGAAGTAGA
GCAGAGTAGGCTCAGGTGGACTTGGTCTATTGATCTTACTGGCCAGCTTAATCAGATGAAAA
AAAACATTCTTGGCTTCTAA

>Cr_25682.1|Cr_LG_7:17612745-17618450|minus|

MSVQSSFTYDVYLSFRGEDTRFGFTSNLFAALKQRSIHTFTDDALLLKEENISQSLFRAIEESRIFIIIF
SPNYASSKWCLEELTTILEYYEEGKKKNWGKVLPIFYDVDPSDVRNGRGSYGEALDKHEEMFKD
DLEKVDKWRRRDGNEYKFIESIVKEVFRMISRVSSLHVAGYPVGLESRVDKVNSLLNLGSDDLVQ
MVGIWGIGGIGKTTIARAVCNSISHLFEGLCFLNDVRQNSMKYGLVHLQETVLSEICGDVNKIKSV
NQGIPIIKQKLHRKKVLLVLDDVDNLKQLQVIAGASDWFGPGSRIIVTTRDKHFLVSHAIERIYEAD
ALSEKESLDLLSWNAFKTDKVDPCFVDILKRALTFASGLPLALQVVGSYLFGRSINQWISALDHYE
RVPDKHIQTVLKISYDSLEEEEKSVFLDIACFFNGHKLEDVKDILLARYGVSAKYSIEELIEKSLIKI
DDGLVTLHNLIQDMGREIVRQESPYEPGKRSRLWLPKDVVCVLEKNSGSSTIESLFLDFPKDEVNS
HGPKGPTHLPNSLKVLKWRGYPSASLPNDFHPKKLAILELPASCVVTFRSLKYMNLNYCELITHIP
DVSGLPNLETLSFRDCVNLSEIHVSVGFLDKLKILDAGHCKKLMAFPPIRLISLEQFYISHCSTLESF
PEILGKMENLTELRIIGSPIQELPFSIQNLNRLRKLELQICGTVQLPSSIAMFSQLGLMCVSRCEGLW
LTKQDIGEEWDTKSSKTERLILSYCNISDDFLPIGLTLFANVKDLDLSGNHFTILHACIKECHFLRNL
KLNDCVLIREITVMPCKLETLSAKRCKSLKYMDLTGECHSLRELTLDDCIYLREIKGVLSNLDHFS
AKNCTLLTSQCASMLVNQEMIEAGNKMFSLPGSNIPDWFAHRTSGESISFWFRNKFPAISLCLVIG
QEDELPISVKFSPKVLINGNELSGGNQKVYKFRIATDHILLFDARMLSFEDNGDTELSDYEWNHVV
VSYEDLITDNGVPIRVVAKYSGIHVFKQTSGLEDIQFTNPRKTFINANLGPNSMAEPPQRETSESLS
NNEVYATLKENDPPVIHGCSVDEDADLDAVSCEEESSSNTEGSDSDDPFDLINRKLCVSWKKIISS
GSSSGDANLRSISEAINALELLMVKDLSEVSSDPAAHSKLHQLLDLLGASSHPKVTVEMKEAIVEF
KRKAFLLFQQFQSTVESVKTLKDFEKHLTRIKQETVEGKSRRKDLKNSIKRVSLGIKAENSSKKEL
ESEIAVLRKQLATKERDLEQFVVNLKNQEETLSTYSTSYASLNEQAQSLLKQADDLLAVSSGIKDE
GEAAEVEQSRLRWTWSIDLTGQLNQMKKNILGF
```

>Cr_25683.1|Cr_LG_8:207661-213091|minus|

ATGGATCTATTGAGTGGAGGTGCTGTTGGAGCTGTGATGGGAGAGATTGTAAAACATGATAT
TCAAACAATCAAAAAGGGTCGAGACTTTGGTCCAACACTTGAAATGAACATAGAAACTTTGA
ACACTTTAGCACCTTTAGTAGAAGAAATGAAAAGGTACAGTGATTTATTGGATCGACCCAGA
GATGAAATAGAGAGGTTAGAGAAACACATAAGAGAGGGTCAAGAGCTTGTAACAAAAAGCA
AGAAACTTAATCGATGGAAGTTTCCTTCTTTCCCACGTTACCAATCAAAGCTTCAGAAGAAAG
ATGAGGCTCTTCAGAGACATTTGTCTGTTAATGTTCAAGGTTTGATTGGTGCTCCTGAAGAGC
TTGAATGTTTGGGAATGGTTGAGCCGTTAAATAAGTTGAAGATTGAATTGCTTAAGGATGGTG
TTTCTGTACTTGTTTTGACTAGTTTGGGTGGTTCAGGTAAAAGCACACTTGCTAAGAAGATTT
GTTGGGATCCACAAATCAAAGGAAAGTTTGATGGAAACATCTTCTATGTTACCGTCTCAAAA
ACTCCCAATTTGAACAACATTGTAAAAACACTATTTGAACACTGTGGAAGTCAGGTGCCTGA
GTTTCAAAGCGATGAAGACGCAATTAAGCAACTGAGACATCTTCTGAGGAAGGAGGATCTCA
AAGGGAAAAAATTTGTTGAGGAAGAATCTCAGTCTGAAGAAGATGAACACCTTTGTGAAATT
GACGAGGAGGAAGATCGCAATCAAGTTTGGCCTGAGAAAGATGGGAATCATGGTAAAGTTC
GGCTACATGAAGATGAACTGCTAGCTAAATTTCAGCAGGATGAAAATCAACGTCGTGCGAAA
GATCAACTTGAGGAAGATGAGCAACTTGCAAGGACAATTCAAGAAAGTTTGAACATTGGTTC
TCCTCCTCGACATGGCAATGATTCTTTATTTAAACCTTCTCCCATCAGCTTTCCACTTGGATTC
AGTATATGTGCAGGATGTAATGCTGAGATTGGCCATGGAAGATTTTTAAGCTGCATGGGAGG
TTTATGGCATCCACAATGCTTCTGCTGCCATGCTGATGATTGCCATCTGCCAATCACTGATTAT
GAGTTTTCCATGTCTAGCAACGGTCCTTACCATAAAGCTTGCTACAGGGAGAAGCATCACCCA
AAATGTGGTGTTTGCAAGAATTTTATCCCTGCCAATTCAGCTGGCCTCATTGAGTATAGAGTT
CATCCTTTCTGGCTACAAAAATACTGCCCGACACATGAGCTCGATGGCACTCCTCGTTGTTAC
AGCTGCAGAAGAATGGAGCCAAAGGATTCAAAATATATTTTGCTTGATGATGGTCGAAAGCT
TTGTCTCGATTGTCTAGACTCCGCAATTATGGATAGTCATGAATGCCAACCTCTTTACCTTGAA
ATACTAAAATTTTATGAAGGTTTAAATATGAAAATGGAGCAGCAAGTATCTATGCTTTTGGTC
GAGAGACAAGCACTTAATAAGGCCATGGAAGGAGAAAAGAATGGTCATCACCATTTACCTGA
AAGTAGAGGACTCTGCTTGTCTGAAAAGCAAACTGTCACCACAATTTTAAGAAGACCGTGGA
TTGGGGCAGAAAGACGAGCCACAGACATGATAACCGAGCCTTATAGATTGACTCGTCGTTGT
GAAGTGACAGCCATTCTTGTTTTGTATGGCCTTCCTAGGTTGTTGACAGGATCAATCCTAGCT
CATGAGATAATGCATGCATGGTTAAGGCTTAAAGGTTATCCCAACCTGAGTCCAGAAGTTGA
AGAAGGAATCTGCCAAGTCTTGGCTCATCTGTGGTTAGAATCAGAAATCTTTTCTGGTTCTGC
CAATAATATTGATGCACCATCTTCTTCTTCATCGAAGAAGGGTAAACGGTCTGATTTTGAGAT
GAAACTCGGTGATTTTTTCAAACACCAAATTGAGACAGATACCTCATCAGCCTATGGAGATG
GATTCAGATTAGGCAATCAGGAAGTACTTAAGTATGGACTTAAAAGTACCCTTGATCATATCC
TTTGA

>Cr_25683.1|Cr_LG_8:207661-213091|minus|

MDLLSGGAVGAVMGEIVKHDIQTIKKGRDFGPTLEMNIETLNTLAPLVEEMKRYSDLLDRPRDEI
ERLEKHIREGQELVTKSKKLNRWKFPSFPRYQSKLQKKDEALQRHLSVNVQGLIGAPEELECLGM
VEPLNKLKIELLKDGVSVLVLTSLGGSGKSTLAKKICWDPQIKGKFDGNIFYVTVSKTPNLNNIVK
TLFEHCGSQVPEFQSDEDAIKQLRHLLRKEDLKGKKFVEEESQSEEDEHLCEIDEEEDRNQVWPEK
DGNHGKVRLHEDELLAKFQQDENQRRAKDQLEEDEQLARTIQESLNIGSPPRHGNDSLFKPSPISF
PLGFSICAGCNAEIGHGRFLSCMGGLWHPQCFCCHADDCHLPITDYEFSMSSNGPYHKACYREKH
HPKCGVCKNFIPANSAGLIEYRVHPFWLQKYCPTHELDGTPRCYSCRRMEPKDSKYILLDDGRKL
CLDCLDSAIMDSHECQPLYLEILKFYEGLNMKMEQQVSMLLVERQALNKAMEGEKNGHHHLPES
RGLCLSEKQTVTTILRRPWIGAERRATDMITEPYRLTRRCEVTAILVLYGLPRLLTGSILAHEIMHA
WLRLKGYPNLSPEVEEGICQVLAHLWLESEIFSGSANNIDAPSSSSSKKGKRSDFEMKLGDFFKHQ
IETDTSSAYGDGFRLGNQEVLKYGLKSTLDHIL

>Cr_25684.1|scaffold1496:50823-53723|plus|

ATGGGGAAAGAAATTGTCAGACAAGAATCACCAGAAGAGCCTGGAAATCGCAGTCGGTTAT
GGCTCCCTAAAGATATAGTTCAAGTTCTAGAAGAAAATACGGGAACAAGTAAAATTGAAATC
ATATGTTCAAACTCCCGGATTAAAGTAGAATGGGATGGAGAGGCTTTCAAGAAGATGAGAAA
GCTTAGAACACTAATTATGAGTGGCAGATGCAGTGAAAGTCCCAAACATCTTCCGAATAGCC
TAAGAATACTTCAAATTGAAAATTGGATATGTTCTTCATGGGGTTTACCGTCTGAGTTTTATCC
AAAGGAACTTACCACATGCAATTTTCCCTCTTACTTATCATCATTCGAGTTCAAAGACTTTTTC
AAGAAGGCAAAAGTCGATGACTCTGTTGGGTTGTTGGGTAAACTTAAAACCTTAAATGCTTAT
GGTTGCCTCAGGCTCAGGAAATTACCACCTCTCAAGTTGGTTTCCCTAGAAGAACTCAATCTT
TCAGAGTGTTATCGTCTTGAGAGTTTTCCACCTGTGATAGATGAGTCGTTTGATAAACTTAAA
ACCTTGAGTGTTAGATGTTGCTTCAAGATAAAGAGTATTCCACCTCTTAAGTTGACTTCGCTA
CAAATACTCGATCTTTCACATTGTGATAGTCTCGAGAGTTTTCCAGTTGTGGCGAATGGCTTTC
TTGGAAATCTTAAAACCCTGTTTGTTAAAGGTTGTCGCAATCTCAAGATTATTCCACCTCTCA
AGTTGGATTCCTTAGAAGAACTTGACCTTTCAGGTTGTGTTAGTCTCAATAGTTTTCCATGTGT
GGTGGATGGCTTGTTGGATAAACTTAAAATCTTGAGTATTAAACATTGCATCAAACTTACAAG
TATTCCACCACTCAAGTTGACTTCGTTGAAACAGTTTGATCTTTCATATTGTCCAAGTCTAGAG
AGTTTTCCAGAAATATTAGGAGAGATGAGAAACATACCACAAATTAACTTGTTTAACACTCCC
ATAAAAGAATTGCCGTTTCGATTTCAAAATCTTACTCCGAGTCAAACATTAGATTCCTGTAAT
TGTGGATTTGTTCACTTACCACTTAGTGTTGCTCATGAGATGGTAAAACTGGTTGAACTTACC
ATCCATAGTGAAGAAAAAGTGAGTCCAATGAAATGTTCACTTGTAAAATATCTTTGTCTCAGG
AACATGAAACTTTCAGATGAATCTTTGTCCATATGTCTCATACTGTTTGCTAATGTGAAAGAA
TTACACTTAAATGAAAATCAATTCACAGTTCTTCCTAAATGTATCGAAAAATGCAAATTTTTA
TGGAGGCTTGTCTTGGATAATTGTGAGGAACTTCAAGAGATCAAAGGTATTCCGCCAAGCTTA

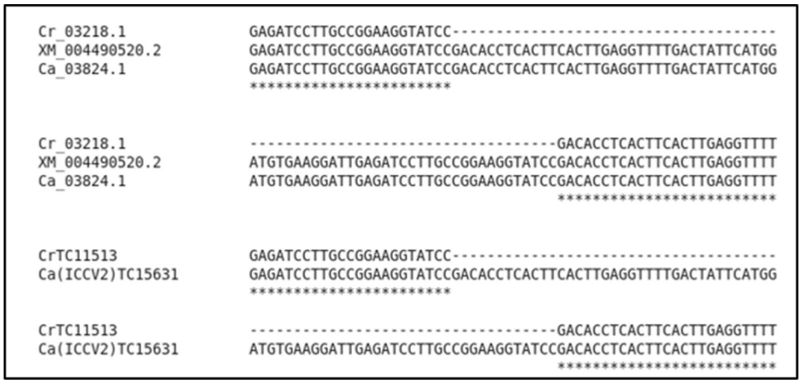
AAAACATTATCAGCATTAAACTGTAAATCATTGACTTCGTCGAGCAAAAGCAAATTACTAAA
TCAGGAATTACATGAGGCTGGAAACACTTGGTTCCGTTTGCCACGAGCAAAGATTCCAGATT
GGTTTGATCACCAATGCTTGGCAGGATTGTCAATTTCTTTCTGGTTTCGTAACAAGTTTCCCGC
CATAGCTCTTTGTGTTGTTTCGCCGTTGACATGGTATGATCATCGACCTCCTATAAAAGTGATC
ATCAATGGCAATACATTTTTTTATAAACACGGTAATATGGACAAAGCACTTTTAGAAAATAAG
TGGAATCATGCAGAGGTTGACTTTGGATTCCCATTCCATTATAGTGGAATTCACGTATTGAAA
GAGAAAAGTGAGATGGAGGTTATTCGATTCACCAACCCAGAAAATGATGATAATATTGAGCT
CACTCTTTAA

>Cr_25684.1|scaffold1496:50823-53723|plus|

MGKEIVRQESPEEPGNRSRLWLPKDIVQVLEENTGTSKIEIICSNSRIKVEWDGEAFKKMRKLRTLI
MSGRCSESPKHLPNSLRILQIENWICSSWGLPSEFYPKELTTCNFPSYLSSFEFKDFFKKAKVDDSV
GLLGKLKTLNAYGCLRLRKLPPLKLVSLEELNLSECYRLESFPPVIDESFDKLKTLSVRCCFKIKSIP
PLKLTSLQILDLSHCDSLESFPVVANGFLGNLKTLFVKGCRNLKIIPPLKLDSLEELDLSGCVSLNSF
PCVVDGLLDKLKILSIKHCIKLTSIPPLKLTSLKQFDLSYCPSLESFPEILGEMRNIPQINLFNTPIKEL
PFRFQNLTPSQTLDSCNCGFVHLPLSVAHEMVKLVELTIHSEEKVSPMKCSLVKYLCLRNMKLSD
ESLSICLILFANVKELHLNENQFTVLPKCIEKCKFLWRLVLDNCEELQEIKGIPPSLKTLSALNCKSL
TSSSKSKLLNQELHEAGNTWFRLPRAKIPDWFDHQCLAGLSISFWFRNKFPAIALCVVSPLTWYD
HRPPIKVIINGNTFFYKHGNMDKALLENKWNHAEVDFGFPFHYSGIHVLKEKSEMEVIRFTNPEND
DNIELTL

Text S2. Sequence alignment of Rgene orthologues in cultivated and wild chickpea. Pepetide and CDS sequences were aligned using ClustalW. Functional annotations are mentioned at the top of the box. Cr represents *C. reticulatum*, Ca represents C. arietinum ICC4958 (*desi*). GenBank accession numbers (XM) are used to denote genes of chickpea CDC Frontier (*kabuli*).

Cr_03218



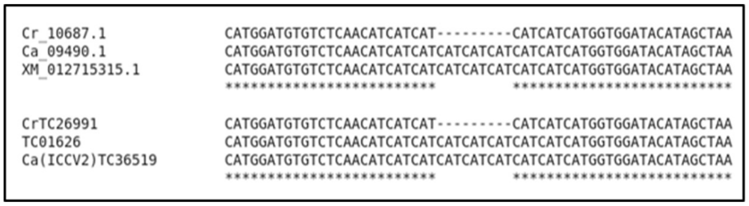
```
Cr_03218.1          GAGATCCTTGCCGGAAGGTATCC-------------------------------------
XM_004490520.2      GAGATCCTTGCCGGAAGGTATCCGACACCTCACTTCACTTGAGGTTTTGACTATTCATGG
Ca_03824.1          GAGATCCTTGCCGGAAGGTATCCGACACCTCACTTCACTTGAGGTTTTGACTATTCATGG
                    ***********************


Cr_03218.1          -----------------------------------GACACCTCACTTCACTTGAGGTTTT
XM_004490520.2      ATGTGAAGGATTGAGATCCTTGCCGGAAGGTATCCGACACCTCACTTCACTTGAGGTTTT
Ca_03824.1          ATGTGAAGGATTGAGATCCTTGCCGGAAGGTATCCGACACCTCACTTCACTTGAGGTTTT
                                                       *************************


CrTC11513           GAGATCCTTGCCGGAAGGTATCC-------------------------------------
Ca(ICCV2)TC15631    GAGATCCTTGCCGGAAGGTATCCGACACCTCACTTCACTTGAGGTTTTGACTATTCATGG
                    ***********************

CrTC11513           -----------------------------------GACACCTCACTTCACTTGAGGTTTT
Ca(ICCV2)TC15631    ATGTGAAGGATTGAGATCCTTGCCGGAAGGTATCCGACACCTCACTTCACTTGAGGTTTT
                                                       *************************
```

Cr_10687

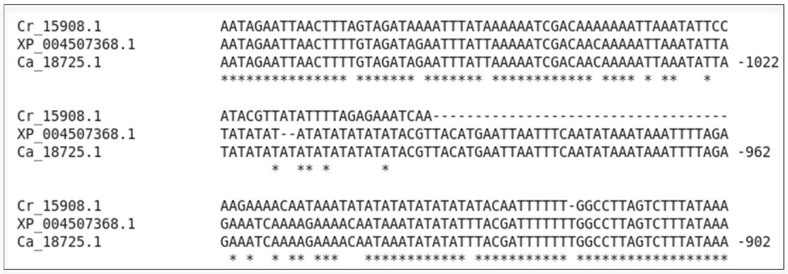


```
Cr_10687.1          CATGGATGTGTCTCAACATCATCAT---------CATCATCATGGTGGATACATAGCTAA
Ca_09490.1          CATGGATGTGTCTCAACATCATCATCATCATCATCATCATCATGGTGGATACATAGCTAA
XM_012715315.1      CATGGATGTGTCTCAACATCATCATCATCATCATCATCATCATGGTGGATACATAGCTAA
                    *************************         **************************

CrTC26991           CATGGATGTGTCTCAACATCATCAT---------CATCATCATGGTGGATACATAGCTAA
TC01626             CATGGATGTGTCTCAACATCATCATCATCATCATCATCATCATGGTGGATACATAGCTAA
Ca(ICCV2)TC36519    CATGGATGTGTCTCAACATCATCATCATCATCATCATCATCATGGTGGATACATAGCTAA
                    *************************         **************************
```

Text S3. Sequence alignment of domestication-associated candidate gene orthologues in cultivated and wild chickpea. Pepetide and CDS sequences were aligned using ClustalW. Functional annotations are mentioned at the top of the box. Cr represents *C. reticulatum*, Ca represents C. arietinum ICC4958 (*desi*). GenBank accession numbers (XP) are used to denote genes/peptides of chickpea CDC Frontier (*kabuli*).

VRN1

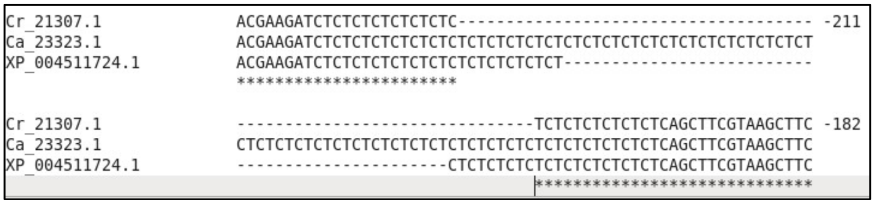


```
Cr_15908.1              AATAGAATTAACTTTAGTAGATAAAATTTATAAAAAATCGACAAAAAAATTAAATATTCC
XP_004507368.1          AATAGAATTAACTTTTGTAGATAGAATTTATTAAAAATCGACAACAAAAATTAAATATTA
Ca_18725.1              AATAGAATTAACTTTTGTAGATAGAATTTATTAAAAATCGACAACAAAAATTAAATATTA -1022
                        *************** ******* ******* ************ **** * **   *  

Cr_15908.1              ATACGTTATATTTTAGAGAAATCAA-----------------------------------
XP_004507368.1          TATATAT--ATATATATATATACGTTACATGAATTAATTTCAATATAAATAAATTTTAGA
Ca_18725.1              TATATATATATATATATATATACGTTACATGAATTAATTTCAATATAAATAAATTTTAGA -962
                              *  ** *      *                                      

Cr_15908.1              AAGAAAACAATAAATATATATATATATATATACAATTTTTT-GGCCTTAGTCTTTATAAA
XP_004507368.1          GAAATCAAAAGAAAACAATAAATATATATTTACGATTTTTTTGGCCTTAGTCTTTATAAA
Ca_18725.1              GAAATCAAAAGAAAACAATAAATATATATTTACGATTTTTTTGGCCTTAGTCTTTATAAA -902
                         * *  * ** ***   ************ *********** ******************
```

VRN2



```
Cr_21307.1              ACGAAGATCTCTCTCTCTCTCTC------------------------------------- -211
Ca_23323.1              ACGAAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
XP_004511724.1          ACGAAGATCTCTCTCTCTCTCTCTCTCTCTCTCT--------------------------
                        ***********************                                     

Cr_21307.1              -------------------------------TCTCTCTCTCTCTCAGCTTCGTAAGCTTC -182
Ca_23323.1              CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAGCTTCGTAAGCTTC
XP_004511724.1          ----------------------CTCTCTCTCTCTCTCTCTCTCTCAGCTTCGTAAGCTTC
                                               *****************************
```