Supplementary Table S2: Characteristics of 1,269 including 1,108 TFGMS and 161 TFFDMS markers developed from 707 TF genes of chickpea

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16584974	Ca1	11896618	(GAA)6	18	AGGGTAGCATTACAAGTTGGT	TAGAGGAAAATGCCAATGATA	46-855	54-534	Domain of unknown function (DUF1635)	TFGMS1	55.0	140	3	P	0.18
PUID16584975	Ca6	12437191	(CAG)8	24	AATCTCAGCCTCAAACTCAAT	GCTGTTGTGATTTTTGTTGTT	932-3685	1307-1615	B3	TFGMS2	55.6	147	4	P	0.18
PUID16584976	Ca1	11899327	(TAA)5	15	ATTCAGCAGTTAGTTCCAACA	GCATCAGCAAAGTAGACAAAT	23-1294	194-571	No apical meristem (NAM)	TFGMS3	55.1	147	3	P	0.18
PUID16584977	Ca1	11896720	(AGA)8	24	TCAGGATCTAGTGTTGGTGTT	TTATCGAATGCTTTACTCTGC	46-855	54-534	Domain of unknown function (DUF1635)	TFGMS4	55.0	160	3	P	0.19
PUID16584978	Ca1	389097	(TCTCAT)4	24	GGTGCTACTGATTTCAATGTT	AGGAGCATCTTCTTCACTTTC	41-1297	380-691	TCP family transcription factor	TFGMS5	54.4	156	4	P	0.19
PUID16584979	Ca5	10080588	(TTC)9	27	TGCTATTGTGATTCAGTTCCT	AGCATGACAAGTTTAAAAGCA	204-2075	702-836	Myb DNA binding	TFGMS6	55.0	147	4	P	0.19
PUID16584980	Ca6	22249411	(TTCACA)5	30	CCCACTTTCTCACTCACTCTT	ATGGATGATGGAGAGAGAGAG	171-1790	669-1787	GRAS	TFGMS7	56.1	163	4	P	0.20
PUID16584981	Ca8	8841425	(AATAAC)5	30	TCACAGAAGCAGAATCAAAGT	AAAACAAGATGACAACCTCAC	289-2259	1753-1893	HLH	TFGMS8	55.2	148	3	P	0.22
PUID16584982	0	0	(GAA)18	54	AACTTGTCGAAGAAAGACTCC	ATTCAATCACTCATCACCATC	251-1081	614-748	bZIP	TFGMS9	55.3	155	6	P	0.21
PUID16584983	Ca3	10489944	(AACAG)5	25	AGAGAAGAAGTCCAACAATCC	TCAAAGGTACAAAGAAAGTGC	1804-3588	3277-3414	PHD	TFGMS10	55.0	159	3	P	0.22
PUID16584984	Ca6	8368375	(AAAAC)5	25	CGTTGCTTAAGATACCAAAAC	AGAGCTTCCAAGTCTCTTCAT	494-1411	665-826	HomeoBox	TFGMS11	54.4	179	4	P	0.22
PUID16584985	Ca1	11899142	(AATCCA)5	30	ATTCAGCAGTTAGTTCCAACA	GCATCAGCAAAGTAGACAAAT	23-1294	194-571	No apical meristem (NAM)	TFGMS12	55.1	147	4	P	0.22
PUID16584986	Ca1	11905672	(ACA)4	12	AATGCCAAACTCTCATAACAA	ACCATAATTAATCCCACCATT	13-981	352-852	Domain of unknown function (DUF702)	TFGMS13	55.0	163	4	P	0.23
PUID16584987	Ca6	6141841	(ATT)8	24	TCCTTGCCTTGTTCATAGTTA	GGCCCCTGTAGATGATGA	357-2960	852-1157	B3	TFGMS14	55.2	121	3	P	0.23
PUID16584988	Ca3	36810456	(AG)19	38	ACCATTAACAGTCAACCATTG	CAGATATGTTCCTGCATTGAT	218-661	431-580	bZIP	TFGMS15	55.0	153	6	P	0.24
PUID16584989	Ca7	3750508	(TCT)4	12	CAAATTGATGCTTATCAAACC	GGAGAGATGCTTAGACCAAGT	8-592	245-577	AUX-IAA	TFGMS16	54.9	152	5	P	0.24
PUID16584990	Ca1	11899241	(CAA)5	15	TGACAACAGTTCTTGGTCTTT	GCATCAGCAAAGTAGACAAAT	23-1294	194-571	NAM	TFGMS17	54.9	154	3	P	0.25
PUID16584991	Ca1	11896521	(CTA)6	18	CCACCTGTTACTATTCCTTCA	AAGGAGAATCAGAACCTTCAC	46-855	54-534	Domain of unknown function (DUF1635)	TFGMS18	55.0	151	2	P	0.31
PUID16584992	Ca7	8615627	(CTT)9	27	TCGACATGATAACACAAGTCA	GTCTTCTTTTTCTTCCCATGT	657-1982	912-1124	TCP	TFGMS19	55.0	163	4	P	0.26
PUID16584993	Ca7	28547368	(AG)14	28	AGCGGTAGGTACTTAAGAAGG	AAGCTGTCTCCTAAATGGAAG	786-1760	975-1211	SBP	TFGMS20	54.7	155	4	P	0.26
PUID16584994	Ca1	11902768	(CTC)4	12	CCCGAAAAATATAAATCCAGA	TAGGAGGATGAAAAGGAAGAG	159-3215	492-728	SBP	TFGMS21	55.9	175	2	P	0.25
PUID16584995	Ca5	30587245	(CTTCTC)4	24	TTTCATCGTCTACTTGATGGT	CAAGAGCAAGAACAAGAAGAG	333-4583	1497-1719	SWIB	TFGMS22	54.8	157	NA	NA	NA
PUID16584996	0	0	(ATA)7	21	AACCATGCAACTAAACAAATC	GCTAACATGGTAACTCAACTCA	437-1648	1285-1438	F0F1 ATP synthase	TFGMS23	54.4	153	NA	NA	NA
PUID16584997	Ca1	390435	(ATTCTC)5	30	CAACAACAACAAGAATCA	AAGGTGTTGTTGATGAGAATG	41-1297	380-691	TCP	TFGMS24	54.7	153	NA	NA	NA
PUID16584998	0	0	(TC)14	28	GGTAGAGGATGAGGATGAGTT	TTTGTTGGATGTTAAAGGTTG	1553-2188	1563-2095	Ras	TFGMS25	54.8	151	NA	NA	NA
PUID16584999	Ca6	55329451	(TAA)7	21	TCTCATCATCCTTATTTGGAA	GGTTTTGTGCTTGATAAGAAA	522-1952	1269-1388	HomeoBox	TFGMS26	54.8	139	NA	NA	NA
PUID16585000	Ca4	4799223	(GATTCA)6	36	TGCAACTAGAGAAAGCTATGG	GTATAGCAGCAGATCCCATAG	159-3803	2883-3098	Helicase	TFGMS27	55.1	156	NA	NA	NA
PUID16585001	Ca7	889264	(ATT)7	21	TATAAAGTGCTTGTGCAATGA	ATCACTGCAGATCCAAACTT	99-1076	555-731	WRKY	TFGMS28	54.7	149	NA	NA	NA
PUID16585002	Ca5	47007215	(CCATA)4	20	AAAACAACACTCTCCTCTTCC	TATCTTGAGAAGCAACGGATA	540-1652	969-1121	Med26	TFGMS29	55.1	143	NA	NA	NA
PUID16585003	Ca4	36842734	(CAG)8	24	CTAAAGAATGGAATTGGGATT	TAGGAGGATGAAAAGGAAGAG	159-3215	492-728	SBP	TFGMS30	55.0	153	5	P	NA
PUID16585004	Ca3	25672196	(CAA)7	21	TCTTACACCAAAACACAAACA	TGTTGTTGTTGTTGTTGAAGA	199-1638	1063-1200	HLH	TFGMS31	54.3	154	NA	NA	NA
PUID16585005	Ca2	354109	(GA)13	26	ATGGAGGCGAATATATAGGAG	TTTTAAGAAACAACTGCGTTC	114-1025	699-1016	DUF260	TFGMS32	55.1	151	1	M	NSA
PUID16585006	Ca7	41712747	(ACA)4	12	AATGCCAAACTCTCATAACAA	CAGCATCTTGATGACAAGAAC	13-981	352-852	DUF702	TFGMS33	55.0	163	1	M	NSA
PUID16585007	Ca5	166458	(TAA)5	15	ATTCAGCAGTTAGTTCCAACA	AGCTGCCTTATTAGAGTGTCC	23-1294	194-571	NAM	TFGMS34	55.1	147	1	M	NSA
PUID16585008	Ca6	51148047	(ATTT)3	12	CATAAGCATGGGTTTTTACAT	CCTTGTTTCGCCTTCTATTAT	1078-1458	1215-1362	HMG-BOX	TFGMS35	54.4	149	1	M	NSA
PUID16585009	Ca5	30587088	(TCTTGC)3	18	TCTTTATCTTCTGCAAAACCA	TTGATGGTAGAGCAAGAACAT	333-4583	1497-1719	SWIB	TFGMS36	55.3	149	1	M	NSA
PUID16585010	Ca5	30587088	(TCTTGC)3	18	TCTTTATCTTCTGCAAAACCA	TTGATGGTAGAGCAAGAACAT	332-4186	1101-1323	SWIB	TFGMS37	55.3	149	1	M	NSA
PUID16585011	Ca2	2427727	(CCA)4	12	AATCCCTAACTCGTTCTCAAC	GAGAATAGAGCGAGTGTCTTG	1274-6823	4026-4165	PHD	TFGMS38	55.1	147	1	M	NSA
PUID16585012	Ca2	2427727	(CCG)5	15	AATCCCTAACTCGTTCTCAAC	GAGAATAGAGCGAGTGTCTTG	1274-6823	4026-4165	PHD	TFGMS39	55.1	147	1	M	NSA
PUID16585013	0	0	(TGT)5	15	TTAAACCATTCTCAGTCTTCG	GGAGGTGAATATTCTTCCAAT	261-7523	5971-6343	SET	TFGMS40	54.7	149	1	M	NSA
PUID16585014	Ca7	4520174	(CT)7	14	TTTACTCCGCCAGCTTCCTA	TAAACCGCAAAAGCTGAGGT	208-1902	306-1209	Pyrredox	TFGMS41	60.0	265	1	M	NSA
PUID16585015	Ca5	38591946	(ATC)4	12	CTGTACCATCTGAAACCACAT	TCCTATAAGCAAACAAACCAA	653-3472	2851-3211	Jmjc	TFGMS42	55.0	148	1	M	NSA
PUID16585016	Ca7	36417403	(CAA)4	12	AATTAGGCCTGATCTTGTGTT	ACACAGCCTAACAAACTTACG	3506-7105	4535-4777	Helicase_c	TFGMS43	55.5	154	1	M	NSA
PUID16585017	Ca7	36421031	(CAG)4	12	AGTTAGGGTTTGAATCTTTGC	TGAGAAATTGTTACTCCCAAA	3506-7105	4535-4777	Helicase_c	TFGMS44	55.2	170	1	M	NSA
PUID16585018	0	0	(AG)6	12	TGTGAGTGAATGAAAGAAACA	TCAGACATAGTAGCCCAAGAA	431-1837	1454-1639	RPM	TFGMS45	54.3	151	1	M	NSA
PUID16585019	0	0	(CAA)5	15	CAACAACACCTTCTTCAACTC	TTTTGTTGTGAGATGAGTGTG	431-1837	1454-1639	RPM	TFGMS46	54.9	157	1	M	NSA
PUID16585020	Ca5	11382482	(ATT)5	15	TGCATACTTTCAAAAGCAGTT	CCTCATTCATCATAAGAGCAG	208-2628	1597-1782	RPM	TFGMS47	55.4	148	1	M	NSA
PUID16585021	0	0	(CAA)5	15	CAACAACACCTTCTTCAACTC	TTTTGTTGTGAGATGAGTGTG	406-1812	1429-1614	RPM	TFGMS48	54.9	157	1	M	NSA
PUID16585022	Ca4	35416937	(AC)6	12	GAACAAAACCATAGCCATAAA	AAACAACTAACGCCGTAACTA	1046-1738	1478-1642	TCP	TFGMS49	54.6	168	1	M	NSA
PUID16585023	Ca4	35416937	(AT)7	14	GAACAAAACCATAGCCATAAA	ATTACGTTCTGAACAAGACGA	1046-1738	1478-1642	TCP	TFGMS50	54.6	168	1	M	NSA
PUID16585024	Ca6	15321264	(CTT)5	15	TTTGAATGGCACAACCATGT	CTATTGCTCCTCGGTCCAAA	139-1761	264-1359	MFS	TFGMS51	59.8	201	1	M	NSA
PUID16585025	Ca6	1843362	(AAG)5	15	CACCACAACAAGAACACATAA	TTGTGAAGGTGTTTGTTGAAT	129-2029	1379-1636	DUF573	TFGMS52	54.5	149	1	M	NSA
PUID16585026	Ca5	46178268	(CTT)5	15	CCAATCTCTGCTTCCTTTAAT	GATGGACCACAGTCAATAGAA	146-1984	254-634	NAM	TFGMS53	55.3	141	1	M	NSA
PUID16585027	Ca6	22174835	(ACA)4	12	TGAGGAAGTTGAAAGACTGAA	AAAGACATCATCTGTTGCTGA	91-1575	124-402	HSF DNA bind	TFGMS54	55.1	153	1	M	NSA
PUID16585028	Ca1	20825850	(ACA)5	15	ACAACAACCATCACATTTTTC	TCGAACGCTTGGTAGTAGTAG	114-1697	1049-1271	SWIB	TFGMS55	55.0	155	1	M	NSA
PUID16585029	Ca1	20825909	(ACT)4	12	ATCAACATGTTAACCAAGTGC	TTAAAGGCAGATGTTTGGTTA	114-1697	1049-1271	SWIB	TFGMS56	55.2	157	1	M	NSA
PUID16585030	0	0	(CAT)4	12	CAAAAAGCATTGATTTAGGAG	TTCACCACCTTCAGTTGTTAT	437-1648	1285-1438	F0F1 ATP synthase	TFGMS57	54.5	170	1	M	NSA
PUID16585031	0	0	(TCT)6	18	GGCCTTTGTAGTACCTCTCTT	TGGTGATGAGTTTGAGTTTCT	437-1648	1285-1438	F0F1 ATP synthase	TFGMS58	54.4	188	1	M	NSA
PUID16585032	Ca4	23555131	(ATT)5	15	CTCATTTGGCATAAAACTTTG	CTAATTTCATTGCTGGTTTTG	1591-2691	1813-2232	POX	TFGMS59	55.2	152	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585033	0	0	(TTC)7	21	TTTCCATCCACAGAAGAGGC	AATGAGGATGATGCAGAGGG	493-1284	282-411	G-patch	TFGMS60	60.2	126	1	M	NSA
PUID16585034	Ca7	35320563	(CAC)4	12	CGTATTACCATTCAAAAATGC	TAAGGTGAATGCGTTTTACTC	127-1851	967-1197	PWWP	TFGMS61	55.0	151	1	M	NSA
PUID16585035	Ca7	5352133	(TCTCT)3	15	AACACACAAACACAGTTCTCC	AGTGTGATTGAATTGAGGTTG	597-2036	1059-1139	ZfCCCH	TFGMS62	55.1	154	1	M	NSA
PUID16585036	Ca5	36138551	(TGGTGT)3	18	CAAGAGAAGCTAGTCCTGACA	GGCAAATGAGACAAATTCATA	2-1351	592-771	AP2	TFGMS63	54.9	154	1	M	NSA
PUID16585037	Ca3	37789311	(GAA)5	15	TACATGTTCAGCACAGCTAGA	TCTTCTTCTTCGTCCTCTTCT	1350-2753	2155-2292	PHD	TFGMS64	54.7	150	1	M	NSA
PUID16585038	Ca2	15303660	(GAA)6	18	AGAAGAGGACGAAGAAGAAGA	TCTTCTTCTTCGTCCTCTTCT	1350-2753	2155-2292	PHD	TFGMS65	55.1	138	1	M	NSA
PUID16585039	Ca3	37789311	(GAT)5	15	TACATGTTCAGCACAGCTAGA	TCTTCTTCTTCGTCCTCTTCT	1350-2753	2155-2292	PHD	TFGMS66	54.7	150	1	M	NSA
PUID16585040	Ca3	37789311	(GAT)5	15	TACATGTTCAGCACAGCTAGA	GAACCCTTTTTCTTAAATTGC	1804-3588	3277-3414	PHD	TFGMS67	54.7	150	1	M	NSA
PUID16585041	Ca3	10489930	(GT)7	14	ACAATCCATTTTGTGAAACAG	TCTTCTTCTTCGTCCTCTTCT	1804-3588	3277-3414	PHD	TFGMS68	55.2	149	1	M	NSA
PUID16585042	Ca5	27041784	(ATCTC)3	15	GTCTCTCCATATCCTTGAACA	ACGAACAGCGGAAAAATAC	218-1555	1397-1549	Myb	TFGMS69	54.2	166	1	M	NSA
PUID16585043	Ca4	43886809	(ATAC)3	12	CTAAACTACAACCCCCTCAAT	CTTACTCACCCGATCCTAACT	660-1991	725-845	HomeoBox	TFGMS70	55.0	144	1	M	NSA
PUID16585044	Ca7	33643335	(TCA)5	15	AAAGACTTGGTGTTGTTTGAA	GTTTTTGTTGGACGATGATT	324-1505	1044-1139	AP2	TFGMS71	54.9	150	1	M	NSA
PUID16585045	Ca1	10976038	(AAC)4	12	CTTCAAGTCCAGAAACAGAAC	TTACTCTGCTGTTGAACCACT	67-1317	1114-1251	HLH	TFGMS72	54.1	148	1	M	NSA
PUID16585046	Ca1	10976038	(AAG)4	12	CTTCAAGTCCAGAAACAGAAC	TTACTCTGCTGTTGAACCACT	67-1317	1114-1251	HLH	TFGMS73	54.1	148	1	M	NSA
PUID16585047	Ca1	10973305	(ATGT)3	12	GCTGTAGGGTACACTTCTTCA	GCTTACTTACCACATAGACTTTT	67-1317	1114-1251	HLH	TFGMS74	54.6	117	1	M	NSA
PUID16585048	Ca6	57679651	(CAA)5	15	TGAATCAAACACGTGCGAAT	GCGAGCATCATTTTGTGAGA	281-1648	489-1221	TBC	TFGMS75	60.1	275	1	M	NSA
PUID16585049	Ca8	4226976	(GGT)5	15	GAGTTGGTGGGTTTTCTAAAG	ACCAAACAGTTTCAAACAATC	98-835	182-277	HSF DNA bind	TFGMS76	55.6	156	1	M	NSA
PUID16585050	Ca4	4285515	(ATCT)3	12	TGTTGTAGATTTGTCTATGTTGC	AAGGATAAATTCGTGGTCCTA	382-4173	1546-1896	Jmjc	TFGMS77	54.7	148	1	M	NSA
PUID16585051	Ca7	8464653	(GGTGTT)3	18	GAGAAGAAATGGAGGGAGATA	CCACTTTGATTGACACTACCA	171-1229	801-1181	NAM	TFGMS78	55.0	169	1	M	NSA
PUID16585052	Ca4	7384447	(TAG)6	18	ATTTGGATGATAAGTGGGGATT	ATATCATCACTTTCCCAATCA	171-1229	801-1181	NAM	TFGMS79	55.0	148	1	M	NSA
PUID16585053	Ca6	3867135	(AAC)5	15	CTATACACTTCGGTGCTTCTC	TGAGTATTTCAACCATTCAGC	95-1465	233-679	NAM	TFGMS80	54.3	151	1	M	NSA
PUID16585054	Ca6	3867428	(ATGA)3	12	TCATGTGGAAAAAGAGAAAGA	GCAATATTGGAAATTCAGTGT	95-1465	233-679	NAM	TFGMS81	55.1	151	1	M	NSA
PUID16585055	Ca6	3867774	(CAG)6	18	CCAATCCAATCTCAACTATCA	GAGAGTCTTAGGTCGTTCTCC	95-1465	233-679	NAM	TFGMS82	55.2	149	1	M	NSA
PUID16585056	Ca2	14768136	(TGTGG)3	15	GATGATTCATGGTTTTTCTTG	CCACCCTTATCATCAGAGAAT	277-1095	439-546	Cir	TFGMS83	54.7	160	1	M	NSA
PUID16585057	Ca1	48004455	(CAA)4	12	TCAGAGTAACAGCAACAACG	CGATGCAAGTTTTAGAGAGAG	709-3783	1429-1518	PHD	TFGMS84	55.0	150	1	M	NSA
PUID16585058	Ca2	36091161	(CAA)4	12	TCTTGGATTTGTATTCCCTTT	ATACTGATACCAATGGAGTCG	41-652	512-652	WRKY	TFGMS85	55.4	146	1	M	NSA
PUID16585059	Ca8	164263	(AAATTC)3	18	GGATCAACTGCTATTTTTGTG	ATTCCCGTACCTTTATCAGAG	0001-2757	847-1089	Helicase_c	TFGMS86	55.0	176	1	M	NSA
PUID16585060	Ca7	4628092	(AG)8	16	GAAGTTCTGCCACTGAGTTC	TTAGGAACAGCCTTGTCAAT	0002-2005	1221-1371	Myb	TFGMS87	55.0	153	1	M	NSA
PUID16585061	Ca8	1261403	(AG)6	12	CTGAGAAATCTACCGCTCTG	CGTGAGTTTTGGTAATGAGTC	270-2291	1350-1550	RRM	TFGMS88	55.3	147	1	M	NSA
PUID16585062	Ca8	1266265	(CAT)5	15	AGAGAAGAATCAGAGGAAGTCA	ACCATTAGAGGGCTCATTAAG	270-2291	1350-1550	RRM	TFGMS89	54.9	156	1	M	NSA
PUID16585063	Ca8	1261403	(TAAGAG)3	18	CTGAGAAATCTACCGCTCTG	CAACATACCTTACCAGTAGCC	270-2291	1350-1550	RRM	TFGMS90	55.3	147	1	M	NSA
PUID16585064	Ca4	18225184	(CATG)3	12	AAAGTTTAGGAGATTTTACTTGC	TGTCATCGTCACTCATTACAA	36-812	81-230	SET	TFGMS91	53.3	159	1	M	NSA
PUID16585065	Ca6	15843439	(AAC)6	18	TGGAAAGAGAAGTTGAAAAGA	CCATTTGGTAATTCTTTCCTC	152-3118	2654-2935	Jmjc	TFGMS92	54.4	157	1	M	NSA
PUID16585066	Ca7	13320709	(ACC)5	15	CCACAATTGAAAACCAAAAT	CCAACACTACAAAACTCTTCC	1827-4139	3456-3575	HomeoBox	TFGMS93	55.1	163	1	M	NSA
PUID16585067	Ca7	13313482	(ATA)6	18	GCAGAAGGATCAGATACAGAA	GGGAAATTGAACATCTCTGAT	1827-4139	3456-3575	HomeoBox	TFGMS94	54.6	152	1	M	NSA
PUID16585068	Ca7	13320216	(CAC)4	12	TCCTTCAACTTCAAATCTTCA	GTTCTTGTTGAGGAACGAAA	1827-4139	3456-3575	HomeoBox	TFGMS95	55.1	151	1	M	NSA
PUID16585069	Ca7	13320579	(CAGCAA)3	18	AACCGGAATGTTATCAGAGAT	GAGAGTTGAAGAGGAATTGGT	1827-4139	3456-3575	HomeoBox	TFGMS96	55.3	129	1	M	NSA
PUID16585070	Ca7	13319948	(TCT)6	18	GGTGGATTAGGAACGATTAAC	ATTGAAAGCTTCTTCAATTCC	1827-4139	3456-3575	HomeoBox	TFGMS97	55.3	149	1	M	NSA
PUID16585071	Ca7	11287744	(ATG)4	12	CAAAATATGAAGAGAATGGA	GAAGAAGAAGCATTTGACTGA	0008-1972	947-1126	AP2	TFGMS98	50.3	140	1	M	NSA
PUID16585072	0	0	(GGT)5	15	CAATTTCCCTTTTTATCTGGT	TTGATTCTCTTCCATTTTCAC	35-1024	251-409	zf-dof	TFGMS99	55.0	156	1	M	NSA
PUID16585073	Ca7	2334613	(ACA)4	12	CCAAGAAGCAAGTAAATCAGA	CTCCAATCCAATTTCCATAAT	227-1168	251-454	AP2	TFGMS100	54.9	149	1	M	NSA
PUID16585074	Ca4	43493861	(ATTGTA)3	18	TGAACCTTGGTATTCTTCTGA	AACCCAATACAGAAGAGGAAC	573-1883	1401-1847	bHLH MYC	TFGMS101	55.0	148	1	M	NSA
PUID16585075	Ca3	39780715	(AAG)6	18	ATGACAAATCTGAGTCTTTGG	GGCTTCATGTAGTTGTAGGTG	254-2524	2321-2500	Myb	TFGMS102	54.3	156	1	M	NSA
PUID16585076	Ca3	39780715	(AGG)4	12	ATGACAAATCTGAGTCTTTGG	GGCTTCATGTAGTTGTAGGTG	254-2524	2321-2500	Myb	TFGMS103	54.3	156	1	M	NSA
PUID16585077	Ca3	37388954	(CAA)4	12	AGAACTCAATTCTTCCACCAT	TGCATTTAGATATTCACACCA	176-1258	224-400	Myb	TFGMS104	55.3	151	1	M	NSA
PUID16585078	Ca8	13448677	(ACA)4	12	ACTTTAGCAGAATTCCAGACC	AGATAAAGGGGAATTGTTTTG	145-2019	814-1929	GRAS	TFGMS105	55.2	147	1	M	NSA
PUID16585079	Ca8	13448677	(CAA)5	15	ACTTTAGCAGAATTCCAGACC	AGATAAAGGGGAATTGTTTTG	145-2019	814-1929	GRAS	TFGMS106	55.2	147	1	M	NSA
PUID16585080	Ca3	39816016	(AAGG)3	12	TCTCTTTTGAAGGAAGGAAAG	GATAGTTTGGAGGGAGAAGTG	479-1678	764-1003	B3	TFGMS107	55.5	151	1	M	NSA
PUID16585081	Ca3	39817768	(AAT)5	15	CCTCCCGATCAATTCTACTAT	GCCAATTTCTTTCTTTCTTTC	479-1678	764-1003	B3	TFGMS108	55.0	140	1	M	NSA
PUID16585082	Ca3	39817940	(CAA)4	12	CATCATCGTCATCATCTTCA	CCAACTAACAAACTTGGAAAC	479-1678	764-1003	B3	TFGMS109	55.3	143	1	M	NSA
PUID16585083	Ca3	39818014	(GCAG)4	16	GAAACTTCAGTGCTGTTTGAT	AACCGTTTTCCTCCTGTATT	479-1678	764-1003	B3	TFGMS110	54.6	129	1	M	NSA
PUID16585084	0	0	(TGAGAA)3	18	TCAGAACAAGTTTCAATGCTT	GTACTGTGCACACATCACAAC	224-2434	230-1321	GRAS	TFGMS111	55.2	166	1	M	NSA
PUID16585085	Ca6	41935803	(TTG)5	15	TTCACAAAGACAAAAAGGTGT	GCAATCTTTTCCCATTGTACT	335-2389	686-988	B3	TFGMS112	54.9	149	1	M	NSA
PUID16585086	Ca6	1609208	(TTCTCT)3	18	TACCTCCACATCATTTTCATT	CCATAAGGATGATGGAAACTT	257-1750	1106-1735	DUF3633	TFGMS113	54.6	134	1	M	NSA
PUID16585087	Ca3	24503146	(CTC)5	15	CTAACCACACCCTCCTAAAAT	GGCGTAGGATAGTAAAGAAGG	464-1504	581-793	Myb	TFGMS114	55.0	125	1	M	NSA
PUID16585088	Ca4	45517555	(ATT)5	15	GAGGAACCATTTTCTTTCTTC	TAAAGCAGATTCCCTTTTCTC	723-2003	1530-1613	HLH	TFGMS115	54.7	167	1	M	NSA
PUID16585089	Ca4	45517015	(CAT)4	12	TCTGTGTCCAATATGGGTAAG	ATTCATTGTGAGAAACCATTG	723-2003	1530-1613	HLH	TFGMS116	55.1	148	1	M	NSA
PUID16585090	Ca7	6498854	(AGA)4	12	ACGAGATCATTTCGGATTC	CAGGAAAACACAAAGCACTAT	750-1364	761-868	BSD	TFGMS117	55.0	138	1	M	NSA
PUID16585091	Ca7	6501203	(ATAAA)3	15	ACAAGTTGCATTGAAGAAGAA	CGTCAAGGATGACCTATCTCT	750-1364	761-868	BSD	TFGMS118	55.2	148	1	M	NSA
PUID16585092	Ca2	33605379	(CCA)4	12	ACTCCTGAAATGGGTATGTTT	CTCCACCACTACTTGTACCTG	218-1237	569-1039	DUF702	TFGMS119	55.2	150	1	M	NSA
PUID16585093	Ca2	33604031	(TGG)6	18	TTTCTGAGCTTCATTTAGGTG	GTGGATTAAATTCGTTGGACT	218-1237	569-1039	DUF702	TFGMS120	54.9	150	1	M	NSA
PUID16585094	0	0	(AAG)5	15	CATCCAAGACAAAGTTCCTTA	CTCTGGAAATTTAAACAAGCA	101-685	140-499	BTB	TFGMS121	54.6	156	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585095	Ca6	26353426	(GAA)6	18	TGAAGGGTAGAAAGAATCACA	TTCCACATTAAGCAACACTTT	1070-2365	1229-2353	GRAS	TFGMS122	55.0	150	1	M	NSA
PUID16585096	Ca5	223412	(ACTGCC)3	18	TTGACTCATCTACCTCTCCAA	GGAGAAGAGGGTACCATAGAA	265-1221	793-948	ZF HD dimer	TFGMS123	54.9	144	1	M	NSA
PUID16585097	Ca5	223807	(GCA)5	15	CACATGTGGAGGTACAACTCT	GCGTAAACTAGATGGCTGATA	265-1221	793-948	ZF HD dimer	TFGMS124	55.1	169	1	M	NSA
PUID16585098	Ca5	223807	(GTTGAA)3	18	CACATGTGGAGGTACAACTCT	TAACTACCACCATCACCACTC	265-1221	793-948	ZF HD dimer	TFGMS125	55.1	169	1	M	NSA
PUID16585099	Ca8	14720356	(AAC)4	12	AAAACCCTATCGAACAAAATC	GCGGTTAATTCAGTGAAGAAT	97-2433	379-627	SWIRM	TFGMS126	55.0	169	1	M	NSA
PUID16585100	Ca7	3789471	(CAA)5	15	TATGATGGAACCAGAAGAGTG	CAGTGTTGTTTGTTCCTGATT	662-2104	1610-1849	Helicase	TFGMS127	55.2	150	1	M	NSA
PUID16585101	Ca7	3789567	(CATTCT)3	18	TCCTTCTTCTTCTCAACAACA	TTGCAGAATGAGAATGAGAAT	662-2104	1610-1849	Helicase	TFGMS128	55.1	139	1	M	NSA
PUID16585102	Ca7	1376023	(AATT)3	12	AAGCCTTGCTGAATTAATCTT	TTTCACTAAAGCCTAACGAGA	240-1769	1353-1523	WRKY	TFGMS129	55.1	150	1	M	NSA
PUID16585103	Ca4	48385988	(GTTGGA)3	18	ATTTTGTGTTTGGTTGTGATG	AGGCAAAGACACAAGAGGT	131-2884	572-880	B3	TFGMS130	55.9	171	1	M	NSA
PUID16585104	Ca4	7548920	(CAC)5	15	CTCAGATTTCGATTTTTCTCA	GCTTCTTGCTCTTGTTGTTC	234-1424	756-1202	NAD binding	TFGMS131	54.8	144	1	M	NSA
PUID16585105	Ca6	41647287	(CAC)4	12	ACATTGAAAAGTCAGCGATAA	CTCTTTTCTTGCGTTATACCA	233-487	351-475	PRK10365	TFGMS132	55.2	177	1	M	NSA
PUID16585106	Ca6	22249682	(AAC)4	12	TATGTGTGCAGACAGTGGTAA	CCACTGTCTGCACACATATAA	171-1790	669-1787	GRAS	TFGMS133	55.2	143	1	M	NSA
PUID16585107	Ca1	19030570	(TCACAC)3	18	ACATTCACATTCACATTCACA	TTCTGGAGGAGATAGTAGTGGT	171-1790	669-1787	GRAS	TFGMS134	54.7	165	1	M	NSA
PUID16585108	Ca1	34866800	(CCA)4	12	CATACTAGCACTACTTCCACCA	GGAGTGTCAGACAAGAAGAAA	242-2413	1112-1369	Bromodomain	TFGMS135	54.7	144	1	M	NSA
PUID16585109	Ca1	48128422	(AGA)4	12	TCCCTATACCCTTCATTCACT	TTTCAGTATCAAACGGAAGAA	432-1337	483-674	TCP	TFGMS136	55.3	146	1	M	NSA
PUID16585110	Ca1	48128515	(AGA)5	15	TTATCTGGCCAACTGTGTATT	TCTGTTTTTGGTTTCGTGTAT	432-1337	483-674	TCP	TFGMS137	54.9	153	1	M	NSA
PUID16585111	Ca1	48129062	(CAA)4	12	GTGGAAACCTACTCTCCTCAC	GTCCCCTCTGTGAAAGATACT	432-1337	483-674	TCP	TFGMS138	55.4	131	1	M	NSA
PUID16585112	Ca1	48129334	(TAA)6	18	CCGGTGCTACTATTGATACTG	CCAAAGTGGAAAAATGAAAGT	432-1337	483-674	TCP	TFGMS139	55.1	162	1	M	NSA
PUID16585113	Ca5	37947047	(CT)8	16	GTACACAAACAAATCCACGAT	AAGCAACGACAAGATACAAAA	753-1369	752-836	SBP	TFGMS140	55.0	144	1	M	NSA
PUID16585114	Ca5	31241189	(AATTCC)3	18	AAACAACAACATCACAAAACC	TTTGAGAGATCGTTTTTGAAG	53-2030	479-718	Bromodomain	TFGMS141	55.1	157	1	M	NSA
PUID16585115	Ca5	31243405	(GAC)5	15	ACGTGTTCTTGGTATGCTCTA	ATGTGGAGTTGTTATGGAGAA	53-2030	479-718	Bromodomain	TFGMS142	55.1	159	1	M	NSA
PUID16585116	Ca1	389138	(CATCAA)3	18	GTATGTTGGCTGCTCTTAATG	TTCACCTTCACCCATAGTATC	41-1297	380-691	TCP	TFGMS143	55.2	151	1	M	NSA
PUID16585117	Ca1	389097	(TCTCAT)4	24	GGTGCTACTGATTTCAATGTT	GAGGAGGAGGATAATTGGTTA	41-1297	380-691	TCP	TFGMS144	54.4	156	1	M	NSA
PUID16585118	Ca6	29235252	(ATT)6	18	TCCATCAAAACAAGAGAAAGA	TAAATTCCGACCTTATCAATG	735-1496	975-1109	HLH	TFGMS145	55.1	158	1	M	NSA
PUID16585119	0	0	(AGAA)4	16	AAAGGAAAAATTAGGCAGAGA	AAGTGTCCCTGAGGAAAATAC	253-2394	694-999	B3	TFGMS146	55.1	145	1	M	NSA
PUID16585120	Ca6	17370871	(TGGTTC)3	18	CTCAAACACCAGCATAGGTAG	ACTAGTGCATTTTCAGAGAGC	253-2394	694-999	B3	TFGMS147	55.1	144	1	M	NSA
PUID16585121	Ca6	17371099	(TTC)6	18	GAGTATTGGGTCAGGTTCTTT	GAGAATCTTGGTGTTGTTTGA	253-2394	694-999	B3	TFGMS148	54.9	154	1	M	NSA
PUID16585122	Ca4	438817	(ATA)4	12	GAGTGTGGGGAACTAACTTCT	ATCACAACACAGGACATCACT	389-3034	2006-2125	PHD	TFGMS149	55.0	161	1	M	NSA
PUID16585123	Ca4	4747167	(TTA)5	15	GTCGACACAGAATTAGGAAGA	TCATTCATTTATACGGCTCTC	599-1735	1079-1233	Myb DNA binding	TFGMS150	54.5	155	1	M	NSA
PUID16585124	Ca5	33238585	(AAG)6	18	GAGGGATTCCAGATCCAACA	AGCACCACCATCCAAGAAAG	82-804	285-438	LON	TFGMS151	59.9	219	1	M	NSA
PUID16585125	Ca1	12008935	(GTTCAA)3	18	CATTCTTCTTCCAGTCTTTCC	GTTCCCATATTGTGTTCTTCA	109-1142	907-1047	PHD	TFGMS152	55.6	152	1	M	NSA
PUID16585126	Ca3	20827838	(AGAA)3	12	TATTCGTTAGCCTCCATAACA	GGAAACCCTAGGTATTGTTGT	3270-4370	3447-4355	WD40	TFGMS153	55.1	150	1	M	NSA
PUID16585127	Ca3	20843747	(CAT)6	18	CGTTTCCATTAGAGGAGAGAC	ATGAAAGTGATGGTGATAACG	3270-4370	3447-4355	WD40	TFGMS154	55.6	162	1	M	NSA
PUID16585128	Ca1	27450034	(AG)6	12	TCTACAGACACAAAAGGGGTA	TCCTTCGTTATTGTTGTTGTT	589-1512	895-1320	DUF702	TFGMS155	54.9	150	1	M	NSA
PUID16585129	Ca8	5412028	(TAG)5	15	GGGTTAAATTTGATTGGTTGT	CACTTATCTGTCGCACTCTTT	589-1512	895-1320	DUF702	TFGMS156	55.6	150	1	M	NSA
PUID16585130	Ca6	23548564	(AGCAAC)3	18	GTGAGTAGCACAGAGAAATGG	AAAATAGCGAAGAACGTAACC	37-888	262-495	Swi3	TFGMS157	55.0	144	1	M	NSA
PUID16585131	Ca6	23548687	(TCC)5	15	CAAACCCTAACACTAACACCA	TGGTGTTAGTGTTAGGGTTTG	37-888	262-495	Swi3	TFGMS158	55.3	167	1	M	NSA
PUID16585132	Ca1	37691883	(CGC)5	15	CCATGTTTTGTTGTAGGTGAT	GCATTTGTTCTTGAATCTCTC	19-1119	856-1010	Myb DNA binding	TFGMS159	55.0	150	1	M	NSA
PUID16585133	Ca7	1991783	(CCT)4	12	GGAATCGCAATTGATACATAG	ATTTTCTTAGTGGGAAGATGG	492-1448	1107-1448	Zf-B Box	TFGMS160	54.9	168	1	M	NSA
PUID16585134	Ca7	31541402	(AGA)4	12	AGTTACAATTGATGGTGATGG	AAAAGGTATTGGACAAAAGGT	1553-2188	1563-2095	Ras	TFGMS161	54.9	138	1	M	NSA
PUID16585135	Ca7	31541951	(CAA)4	12	GAAATGGGTTTTATGGCTTAT	CACCTTCAAAATCACTCAGTC	1553-2188	1563-2095	Ras	TFGMS162	55.0	142	1	M	NSA
PUID16585136	Ca4	36800034	(ATCGG)3	15	GCCGATCTTAAAGTAGAATGG	ACAAACAAATAGACCTCCACA	602-1432	1016-1186	RPM	TFGMS163	55.7	152	1	M	NSA
PUID16585137	Ca4	36799262	(CCCT)3	12	CAAGAAAACATCACAGCTTCT	AGTCGGAGCAGGAGTAATAGT	602-1432	1016-1186	RPM	TFGMS164	54.8	145	1	M	NSA
PUID16585138	Ca4	36799376	(CCCTAT)3	18	CCCTATCCCTACTATCCCTAA	AGGGATAGGGTTAGGGATAGT	602-1432	1016-1186	RPM	TFGMS165	54.2	148	1	M	NSA
PUID16585139	Ca4	5081434	(TAA)6	18	GTAGTGCAGATAAATGCAAGG	CAAGTTCAGTAACAAACCGATA	135-1787	1365-1622	Myb DNA binding	TFGMS166	55.2	141	1	M	NSA
PUID16585140	Ca4	10419364	(AGC)4	12	TCTATCCTGGCTAACTGTTTTT	CAGGATTGAGTTTTGGTACTG	255-5342	2187-2315	Myb DNA binding	TFGMS167	55.0	152	1	M	NSA
PUID16585141	Ca5	47733924	(ATTT)3	12	ATGTTCATGTACCCAAACAAG	TGGTCAACATTCAATAGTTAGG	61-930	79-456	NAM	TFGMS168	55.0	165	1	M	NSA
PUID16585142	Ca7	12333197	(TCT)5	15	ATCACTTCAAACCCTTTTCTC	GCATGTGAAAGTGAAAGCTAC	315-2303	405-635	FHA	TFGMS169	55.0	150	1	M	NSA
PUID16585143	Ca3	21774741	(CAA)4	12	TGATACCATTGTTCCAAGTTT	CTAAATCAGCAGCAGTAGGTG	110-1948	854-1906	GRAS	TFGMS170	54.7	155	1	M	NSA
PUID16585144	Ca5	42984444	(AACAGA)3	18	TTTTTGAACTCAAACAGAAGC	ATCATCAACAACAAGAACTCG	81-1853	681-833	Myb DNA binding	TFGMS171	54.9	142	1	M	NSA
PUID16585145	Ca1	9653309	(ATG)4	12	ATGCTAATCTCAAACGTCCTT	TTCATGGCATTACTTTTCTGT	127-1245	661-915	Myb DNA binding	TFGMS172	55.7	154	1	M	NSA
PUID16585146	0	0	(CAAG)3	12	CTAAATCTAAACCAACACACGA	TAATGGTTAAGGTTGTTTGGA	54-1457	855-1348	UDPGT	TFGMS173	54.7	155	1	M	NSA
PUID16585147	Ca2	11922227	(ACC)4	12	GAATAGCCCAAATAGGTTCAT	TTATCACAAAATATGGGAAGC	52-1329	874-1144	TCP	TFGMS174	55.0	163	1	M	NSA
PUID16585148	Ca7	30759842	(TCTT)4	16	ACACAAAATTCACAACACCTC	AATGCTTATTACCATCCTTGC	511-3027	988-1620	START	TFGMS175	55.0	150	1	M	NSA
PUID16585149	Ca7	30760228	(TGG)5	15	CAAAATGCGTAGTGAGTCTTC	AAGGAAAGTGATGGAAATAAGA	511-3027	988-1620	START	TFGMS176	55.2	149	1	M	NSA
PUID16585150	0	0	(AG)7	14	GACGAGTTTTGTTGTGAAGAG	CTCGATGAGAACGAGAGATTA	214-1212	853-1128	HSF DNA bind	TFGMS177	55.1	143	1	M	NSA
PUID16585151	0	0	(AGAA)4	16	GACGAGTTTTGTTGTGAAGAG	CGTAACTAACGCAGTACCTTC	214-1212	853-1128	HSF DNA bind	TFGMS178	55.1	143	1	M	NSA
PUID16585152	Ca7	20234897	(AT)6	12	CTGGAACCATTGTATACTTGC	CTCTTCAACTGAACCCTACCT	258-980	490-761	K-Box	TFGMS179	54.9	155	1	M	NSA
PUID16585153	Ca6	55332793	(ACA)6	18	TTCTCTAGTTTCGGAGAATCC	GGTTTTGTGCTTGATAAGAAA	522-1952	1269-1388	HomeoBox	TFGMS180	55.3	156	1	M	NSA
PUID16585154	Ca4	39805445	(TA)8	16	GGCTTCAGCTGTTACAATTAC	TAAATAAGAGGGTGCATTTGA	308-3313	575-715	Myb DNA binding	TFGMS181	54.4	149	1	M	NSA
PUID16585155	Ca4	41865183	(CAA)4	12	AATTAAGGCTAGGGAACAACA	GAGATGAGCCCTATCCCTAC	287-3016	2270-2383	WD40	TFGMS182	55.7	143	1	M	NSA
PUID16585156	Ca4	41865067	(CAG)5	15	TGCAACAGATGTTGTTACAGA	CATGCCTCTGTAACAACATCT	287-3016	2270-2383	WD40	TFGMS183	55.3	170	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585157	0	0	(TTG)5	15	CACCACTGCTATTCATTGTTT	ATCCACTGTGACATCACTGAC	307-1299	925-1056	WRC	TFGMS184	55.3	149	1	M	NSA
PUID16585158	Ca7	5634290	(TTAGGG)3	18	ATACAATCTCTCCCAAAGGAT	CTATCCTGTCCACATCTCAAA	345-1304	909-1172	Myb DNA binding	TFGMS185	54.4	156	1	M	NSA
PUID16585159	Ca3	38759947	(TCAACT)3	18	ATCTAACTCAAAGCCTGGTTC	CATAGCGATCCTCTGAATTAT	102-1280	473-1259	bZIP	TFGMS186	55.2	134	1	M	NSA
PUID16585160	Ca1	12405204	(ATT)4	12	TGTCTCCATTTCCATAAACAC	TTAATGATGTTATTGGCAACC	153-1067	801-965	Zf-Dof	TFGMS187	55.1	147	1	M	NSA
PUID16585161	Ca1	48250303	(TCA)5	15	TCATAACGAGGTTTGTGTATTC	GAACATTGTCAGAAAACATGG	316-1193	925-1059	bZIP	TFGMS188	54.5	157	1	M	NSA
PUID16585162	Ca1	48249785	(TGG)6	18	AGTGACTCTATTGCCTTCCTC	CAACCGCAAATCTTACTTAAA	316-1193	925-1059	bZIP	TFGMS189	55.2	136	1	M	NSA
PUID16585163	Ca2	10253706	(CCG)4	12	ACTTTGTTAAAACTCGCACAC	AAATTGCTCTCCTTCCATTAT	163-1092	448-582	Myb DNA binding	TFGMS190	54.7	161	1	M	NSA
PUID16585164	0	0	(CT)9	18	CGTCACATTTTCTGAGCTAGT	GAGAGAGAGTAGGGTTTTGGA	394-2775	1675-1797	PHD	TFGMS191	54.8	150	1	M	NSA
PUID16585165	0	0	(GCA)5	15	TCATAATTCCGAAAACGATAG	ATTTTCTTCGGTTTTGAGTCT	394-2775	1675-1797	PHD	TFGMS192	54.6	154	1	M	NSA
PUID16585166	Ca5	34512420	(CAG)4	12	GGTTTTCTGGGACATTTTTAT	TTGAACTCTGAGATTGCTGAT	180-2873	2505-2609	WD40	TFGMS193	54.9	149	1	M	NSA
PUID16585167	0	0	(TC)8	16	CTTCACCCCTTGGATTTT	GTTGTTGTTGATGCTGTGAC	180-2873	2505-2609	WD40	TFGMS194	54.9	130	1	M	NSA
PUID16585168	Ca1	1829150	(ATTG)3	12	ACAAAGCAAAAGCTGACAAT	GGCTCCAAAGGTATCTAAGAA	10-717	244-528	Jmjc	TFGMS195	55.2	148	1	M	NSA
PUID16585169	Ca6	28198199	(CAG)4	12	GATAAATCAAGGGTCCTTCC	AATAAGCACAAAGAGAAGTGC	37-1221	127-342	AUX_IAA	TFGMS196	55.1	149	1	M	NSA
PUID16585170	Ca2	30865898	(CAA)4	12	ATCGAGTTCTTCTCGATCTCT	CTACCATCTGCTCTTGCTCTA	240-2327	432-623	ANK	TFGMS197	54.8	149	1	M	NSA
PUID16585171	Ca2	30867621	(CAA)5	15	GCTTGAAGAGTGCTTTGAGT	GGAAAGATGGAGAAGAGATTC	240-2327	432-623	ANK	TFGMS198	54.9	147	1	M	NSA
PUID16585172	Ca3	20509103	(AATA)3	12	AATACTTCTATGTTTCACCAACA	TTTGAATTTAGGACCATCAAG	89-1681	1172-1348	WRKY	TFGMS199	53.3	163	1	M	NSA
PUID16585173	Ca3	20509059	(ATA)6	18	CATTCATTTTCCAACAACAAC	TTTGAATTTAGGACCATCAAG	89-1681	1172-1348	WRKY	TFGMS200	55.6	148	1	M	NSA
PUID16585174	Ca3	20509059	(ATC)4	12	CATTCATTTTCCAACAACAAC	ATTGGTGATAATGAAGGAGGT	89-1681	1172-1348	WRKY	TFGMS201	55.6	148	1	M	NSA
PUID16585175	Ca3	20509103	(CAA)5	15	AATACTTCTATGTTTCACCAACA	ATTGGTGATAATGAAGGAGGT	89-1681	1172-1348	WRKY	TFGMS202	53.3	163	1	M	NSA
PUID16585176	Ca2	30959905	(ATT)5	15	GGTTCTTTCAATTTACAACTTTC	ATGCCACAGAGAAAGAAAAAT	211-588	276-408	Myb DNA binding	TFGMS203	54.1	162	1	M	NSA
PUID16585177	Ca6	53166542	(AG)8	16	TGCAGAGAAAGAGTGAGAAAG	TGCTAACATCTTCAGTTCCTC	2247-3533	2595-3512	TUB	TFGMS204	55.1	152	1	M	NSA
PUID16585178	Ca4	6943933	(TCT)5	15	TCGTGAATATTGCTTCCTTTA	CAAAATAGAAACTGCGAGAAA	203-1390	353-1111	PPZC	TFGMS205	55.3	149	1	M	NSA
PUID16585179	Ca4	6944061	(TTTTTA)3	18	TCTAACGAAAACTGGTTGAAA	TTTCAACCAGTTTTCGTTAGA	203-1390	353-1111	PPZC	TFGMS206	55.2	158	1	M	NSA
PUID16585180	Ca7	19989726	(TGG)6	18	GGTTGTCCTTATGGAGAAAGT	CTACCGCTACCAGTACTACCA	322-1467	1102-1179	ZfCCCH	TFGMS207	54.9	152	1	M	NSA
PUID16585181	Ca1	10712913	(CAG)5	15	TCCAAATTCATCCTCAGAAG	CTCTCATTTTCAAATCACCTG	165-1457	875-995	bZIP	TFGMS208	55.3	162	1	M	NSA
PUID16585182	Ca1	10712913	(GCA)4	12	TCCAAATTCATCCTCAGAAG	CTCTCATTTTCAAATCACCTG	165-1457	875-995	bZIP	TFGMS209	55.3	162	1	M	NSA
PUID16585183	Ca7	6058057	(TCT)5	15	ATTCCCTTAATTCTTCCGTTT	AGAATGGCTTATGAGGAGAAT	586-1209	937-1101	KNOXZ	TFGMS210	56.0	151	1	M	NSA
PUID16585184	Ca7	8420511	(CAG)4	12	CTGTTCGTCGATCACTAATTC	AAAGAAGCAATAATCCAGAGG	1445-2314	1877-2212	Response	TFGMS211	55.0	150	1	M	NSA
PUID16585185	Ca7	8419147	(TCA)5	15	GTCATTGTTTTCTTCCTCCTC	TATGTCAATCGGAAACAACTT	1445-2314	1877-2212	Response	TFGMS212	55.4	150	1	M	NSA
PUID16585186	Ca8	4460537	(ACA)4	12	GTTAGAGTCGGATTTTGGAAT	CTCATTACCCAACTTGTTTGA	120-1178	588-797	SWIB	TFGMS213	55.0	151	1	M	NSA
PUID16585187	Ca8	4460461	(AGA)6	18	AGCGTACAACAACAACAAGAT	CGCATCTTCTTCTACTTGTTC	120-1178	588-797	SWIB	TFGMS214	55.0	167	1	M	NSA
PUID16585188	Ca8	4460304	(GAA)6	18	ATGAAGAGGAAGAGGAGAAAA	TCCTCTTCATTACCATCTTCA	120-1178	588-797	SWIB	TFGMS215	54.8	154	1	M	NSA
PUID16585189	Ca3	9692224	(ATT)5	15	GAATCAATTTCTTCACCGTTA	TCGTCTATGGTGGTTTATCC	286-3552	430-750	SET	TFGMS216	54.5	149	1	M	NSA
PUID16585190	Ca3	9692046	(GGTTTA)3	18	AATTTTCCTCCTCTTCAACAC	CCTCTCGATCATCTCTACTCC	286-3552	430-750	SET	TFGMS217	55.0	150	1	M	NSA
PUID16585191	Ca5	43950855	(TAAT)4	16	CAGAGATAGTGCATGACGAG	TTTGTTCACGGAGAAAGTATC	505-1380	985-1360	NAM	TFGMS218	54.4	164	1	M	NSA
PUID16585192	Ca2	6179700	(ATA)4	12	ATTCCTCAACAACAACAACAA	CATCATGATTCCTCCAAACT	11-988	539-904	SET	TFGMS219	55.6	143	1	M	NSA
PUID16585193	Ca2	6179676	(CAA)6	18	AACCTTCGAGAGTTTCCCTA	AAACTGGTGATGGTGAAATTA	11-988	539-904	SET	TFGMS220	55.6	152	1	M	NSA
PUID16585194	Ca6	10864233	(CT)8	16	CTTTCTCTGATCCTTTTCGAT	GATGCCATGATATTGAATCTG	235-3201	2194-2259	ANK	TFGMS221	55.3	154	1	M	NSA
PUID16585195	Ca3	30320120	(AGA)5	15	GATCTTGAGTGGGATGAGATT	TCCTCTTTTCAACCCTAGACT	130-1335	613-747	BSD	TFGMS222	55.6	151	1	M	NSA
PUID16585196	Ca3	30318959	(TCATT)3	15	ATTAGACCTGTGGAAACCATT	CATCATCTTCAATATCCCAAC	130-1335	613-747	BSD	TFGMS223	55.2	141	1	M	NSA
PUID16585197	Ca5	29821891	(TATGC)3	15	ACGGAAAGTGTGGTTAATTTT	CACCAACACTCACTACCTAGC	425-2239	470-712	Myb DNA binding	TFGMS224	55.4	169	1	M	NSA
PUID16585198	Ca1	10066335	(TCA)5	15	TCCACCAAGTAGTGAAGATTG	GCATTCTGATTTTCTGTTTTG	648-1511	1002-1463	AUX_IAA	TFGMS225	55.3	152	1	M	NSA
PUID16585199	Ca3	28288059	(GCT)5	15	GAAGCATTAGCTGATTCCATA	GACACTTTGAGAATCCCTTTT	835-1743	1282-1434	Myb DNA binding	TFGMS226	54.8	142	1	M	NSA
PUID16585200	Ca3	28289003	(TTTGAT)3	18	GATTAATGGTTGTGATGAGGA	CACTATCCACCTTGTTGTCTC	835-1743	1282-1434	Myb DNA binding	TFGMS227	55.0	144	1	M	NSA
PUID16585201	Ca6	5788961	(ACA)4	12	CAAGTTCTGTTCACAACAACA	TCCTAATGGTTGCATAAAAGA	459-1627	771-1004	SBP	TFGMS228	54.7	146	1	M	NSA
PUID16585202	Ca6	5789033	(ACA)6	18	AAGCTTCTTCCTTAAACCAAA	GTGTCTGTTGTTGTTGTGTTG	459-1627	771-1004	SBP	TFGMS229	55.1	153	1	M	NSA
PUID16585203	0	0	(ATGGAA)3	18	ATCAGGATTTGCTATCCTCTC	AAGAAGAAGAGAGATCCTTGAT	450-4657	1209-1871	START	TFGMS230	55.1	159	1	M	NSA
PUID16585204	Ca3	28536088	(ACA)5	15	ACATCAACGATGCTGCTGAG	CGAGCTTGAGGTCTTTACCG	132-1211	300-555	DSPc	TFGMS231	60.0	249	1	M	NSA
PUID16585205	Ca4	9451512	(ATG)4	12	TCTGAACAGACAACATCAACA	ACTGTCACTTGCCGAGTATTA	138-1349	828-983	Myb DNA binding	TFGMS232	55.1	149	1	M	NSA
PUID16585206	Ca4	9451990	(CT)7	14	ATTTTGATTCTCCTCAGATCC	GAAATCTTTTGCTGCTTATGA	138-1349	828-983	Myb DNA binding	TFGMS233	54.9	145	1	M	NSA
PUID16585207	Ca3	37212970	(ACC)4	12	TCCTATTCCACAACAAATGAG	GTACTTGTGGTGGCATAAAAC	400-948	457-594	HLH	TFGMS234	55.2	153	1	M	NSA
PUID16585208	Ca1	47743300	(AAG)6	18	CGTTCTAGAATTACACCCTCA	ATCTGAGGCTTTTCTCACTTC	50-631	203-328	UBN2	TFGMS235	54.6	147	1	M	NSA
PUID16585209	Ca5	40407133	(CAA)4	12	CTCAAATGCCACTTCAGTAAC	GAGTTGCAGCTTCTAATGATG	153-833	507-710	FHA	TFGMS236	55.1	149	1	M	NSA
PUID16585210	0	0	(CCA)5	15	CGTTACAAATTGGTTATCAGG	CATTACATGTCAAAGGAAATTG	58-624	328-573	K-Box	TFGMS237	54.9	178	1	M	NSA
PUID16585211	Ca2	35411086	(AGAAGC)3	18	AAAGGTATTTCCCATAGGTTG	TTCTATGTTCCAACTCCTTCA	523-1968	616-1353	mTERF	TFGMS238	54.9	145	1	M	NSA
PUID16585212	Ca5	39522908	(CAA)4	12	TAGGTGGTGGTTGTAGAAAGA	TGAAGATCTTTAGGGTTGTGA	12-857	174-341	Zf-Dof	TFGMS239	54.9	154	1	M	NSA
PUID16585213	Ca7	7866499	(ATT)5	15	TATCTCAGACTCTTCCCACAA	CAGTATTAGCCACGTTTCCTA	402-2114	1158-1307	HLH	TFGMS240	54.9	172	1	M	NSA
PUID16585214	Ca7	4598079	(CT)7	14	TTCTCACTCATGCTCTTTCTC	TCTAACACAAACACGATTTCA	216-650	321-425	GATA	TFGMS241	54.8	150	1	M	NSA
PUID16585215	0	0	(TGT)5	15	TGTTGTTGTTGTTGTTGTTGT	TCCACAACAACAACAACAGTA	1-1302	853-1101	Myb DNA binding	TFGMS242	54.9	151	1	M	NSA
PUID16585216	Ca1	3235738	(GCT)5	15	ATAATGGTTACTTTCGGAGGA	TCTTCTTCGTGTTCATGTTCT	178-1098	232-504	Myb DNA binding	TFGMS243	55.4	151	1	M	NSA
PUID16585217	Ca3	21537463	(ATCCA)3	15	GTGCACCAGTCATCAAGTAAT	CATGAATTGAGAACGAAGAAG	90-830	573-782	Acetytransf	TFGMS244	55.2	138	1	M	NSA
PUID16585218	Ca3	21537463	(CAAAC)3	15	GTGCACCAGTCATCAAGTAAT	CATGAATTGAGAACGAAGAAG	90-830	573-782	Acetytransf	TFGMS245	55.2	138	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585219	Ca1	27094555	(CAC)6	18	CCACAACATCATCTTCAATTC	ACGAAAGAGTTTGGTTCAGAT	23-1218	299-1006	mTERF	TFGMS246	55.5	150	1	M	NSA
PUID16585220	Ca1	307793	(AGTTG)3	15	GCTTTCCTTTCTTATGACCAC	CATGAGGACAATGAAGTCAATA	1-1726	956-1189	Bromodomain	TFGMS247	55.6	150	1	M	NSA
PUID16585221	Ca1	311197	(CCTCTC)3	18	CCATTTCAATCTCTTCCTCTT	TGAAGAATTCTGAGTGACCTG	1-1726	956-1189	Bromodomain	TFGMS248	55.1	157	1	M	NSA
PUID16585222	Ca7	24021470	(CAC)4	12	ATTAGTCAAAGCACAAGTCCA	TAATATCACTGCGAAATCCAC	206-1216	356-535	Zf-HD-dimer	TFGMS249	55.1	150	1	M	NSA
PUID16585223	Ca7	34923150	(ATC)7	21	ACCAACCCTACAAGTCTCTTC	GGGAATCCATTAGGATAAAGA	88-903	144-324	Zf-Dof	TFGMS250	55.0	142	1	M	NSA
PUID16585224	Ca5	38383060	(AATT)3	12	GCTCACCTTCCTTTCTAAAAT	GAGTCCCCTAGAATGAGATTG	115-729	217-678	FLO-LFY	TFGMS251	54.5	155	1	M	NSA
PUID16585225	Ca7	8015436	(AAC)4	12	GCACTGTTATGCAGTTTTCAT	ATGATGAAGATGTTGTCTTGC	117-1184	273-473	TCP	TFGMS252	55.5	146	1	M	NSA
PUID16585226	Ca6	26358317	(ACT)7	21	TGGATAACCCTTTTCTTCTTC	AGCATTTGGTTTATGTAACGA	361-1638	1465-1638	GRAS	TFGMS253	55.1	145	1	M	NSA
PUID16585227	Ca6	26358496	(ATTTT)3	15	CCTCTTTTCTTTCTGCTTCTT	TAAGGTAAAACCGTTGGTGTA	361-1638	1465-1638	GRAS	TFGMS254	54.9	151	1	M	NSA
PUID16585228	Ca8	3522565	(AAC)7	21	GATGTGGGTCTCAATCTCATA	TGATAGTTTTGTTTGGAGGAA	142-1602	469-1596	GRAS	TFGMS255	55.0	157	1	M	NSA
PUID16585229	Ca2	14248311	(AATA)3	12	AGAAGGTTAAGAATTGAGGTTG	CCAAAACTTTATGCTTCTCAA	205-1128	271-462	Acetytransf	TFGMS256	54.5	147	1	M	NSA
PUID16585230	Ca2	17282355	(ATC)4	12	AGTGAGGTTGTTTTAGGGTTT	GAGGCATGTAATCAACAATTC	86-1189	701-847	HLH	TFGMS257	54.6	156	1	M	NSA
PUID16585231	Ca7	11430446	(CAA)6	18	CACCAACAACAACGTATCATT	ACATGGTGTTGAGGTTGATAA	6-983	429-974	GRAS	TFGMS258	56.0	160	1	M	NSA
PUID16585232	Ca3	29475806	(CCT)4	12	GAACATTGTTTGAAGCATAGG	AAGAAAGCTCGTAGTCCAGTT	562-984	784-966	Zf-C2H2	TFGMS259	55.0	175	1	M	NSA
PUID16585233	Ca8	4243801	(TGA)6	18	ATAGGGGAAAGCGTAGTTTTA	TTGATAGGCTGTGATGAGATT	61-791	130-348	Myb DNA binding	TFGMS260	55.0	157	1	M	NSA
PUID16585234	Ca7	8615769	(AAGAA)3	15	CGTGAGGTTTGTTTGATCTTA	AGCATACTCAAATGTCCTTCA	657-1982	912-1124	TCP	TFGMS261	55.5	152	1	M	NSA
PUID16585235	Ca7	8614981	(GGA)5	15	TCCAAACGAATAACCTAACAA	ATCTCATCTTCCAAACCCTAA	657-1982	912-1124	TCP	TFGMS262	55.0	153	1	M	NSA
PUID16585236	Ca7	8615383	(TATGAA)3	18	TTATGAATTTTCCACCACCTA	TAAGATCAAACAAACCTCACG	657-1982	912-1124	TCP	TFGMS263	54.8	154	1	M	NSA
PUID16585237	Ca8	4421516	(CTG)6	18	AGTTTCGAACATCAACAACAG	GGTTGAGAGTCACAAATCATC	175-1071	196-498	DUF260	TFGMS264	55.4	156	1	M	NSA
PUID16585238	Ca6	466377	(CTCAAG)3	18	GAACCTCATAATTCATCCACA	GGTTATGTGGTTGTTGTTGTT	779-1438	896-1051	Myb DNA binding	TFGMS265	55.0	160	1	M	NSA
PUID16585239	Ca7	8794579	(TA)8	16	TCATCCATTCATTCAGCTTAT	AAAATGTCACTTCTTGCTGAA	271-909	529-690	HomeoBox	TFGMS266	54.8	135	1	M	NSA
PUID16585240	Ca4	45052617	(CTA)5	15	AAGAAGAAGCCTCTTGTGAAT	TTTGTCTAATTCCACAAGCAT	34-858	505-609	GATA	TFGMS267	54.9	161	1	M	NSA
PUID16585241	Ca1	35115366	(CAA)4	12	TTAGGCTTCAACACCACTTTA	CTCTTCAAGAAAAGCAGATTG	355-1137	652-816	Homebox	TFGMS268	55.2	148	1	M	NSA
PUID16585242	Ca1	35114925	(GTG)5	15	TCTTTTCAGATGGATCTGTGT	GTGGAGGAAGAAGATCAAGTT	355-1137	652-816	Homebox	TFGMS269	54.7	153	1	M	NSA
PUID16585243	Ca1	35112262	(TTGAA)3	15	TGATGATTCAACCTCAAAATC	ACCACCACAGTTATCATCATC	355-1137	652-816	Homebox	TFGMS270	55.1	158	1	M	NSA
PUID16585244	Ca4	32780320	(ATGGT)3	15	TCCCATCAAGATGCTAAAATA	AATCAATCTTTGAGTTGTTGC	486-902	489-872	AUX_IAA	TFGMS271	55.0	149	1	M	NSA
PUID16585245	Ca5	45592771	(TAA)7	21	ACCACCACAAGAAGATTACAA	CCATAGCTGACAAATGAGAAG	97-1074	196-375	Zf-Dof	TFGMS272	54.7	143	1	M	NSA
PUID16585246	Ca5	45592771	(TAC)5	15	ACCACCACAAGAAGATTACAA	CCATAGCTGACAAATGAGAAG	97-1074	196-375	Zf-Dof	TFGMS273	54.7	143	1	M	NSA
PUID16585247	Ca5	45592893	(TGC)5	15	CTTCTCATTTGTCAGCTATGG	TTAGCAAACCCTGTTGAATTA	97-1074	196-375	Zf-Dof	TFGMS274	55.2	157	1	M	NSA
PUID16585248	Ca7	21805504	(AGC)4	12	CTGGTGTATTTTTCGTCAGTC	CAAGATTCAAAATAGGGGTCT	464-667	529-661	FAR1	TFGMS275	54.9	156	1	M	NSA
PUID16585249	Ca3	3414005	(TCA)5	15	CTCATTTGAAAAAGAAGCTGA	GCCATTTGAATATCTGTTTGA	384-1046	123-266	Myb DNA binding	TFGMS276	55.0	145	1	M	NSA
PUID16585250	Ca3	31975587	(GGAAG)3	15	TTCGAGTAGTAGTGGAGAAGC	CATCGAGGTATCAGTTCTTGA	169-1638	994-1122	HLH	TFGMS277	54.0	151	1	M	NSA
PUID16585251	Ca4	14812670	(GAA)6	18	AGTAATGATGCAATGAAGACG	GCATCAATTAAGTTTTGTTCG	255-3230	2772-2894	HomeoBox	TFGMS278	55.4	149	1	M	NSA
PUID16585252	Ca5	47007624	(CACG)3	12	TTGAACCAATTTCGTAACTGTA	ACAGGTAGTGGGTATATTCCAG	540-1652	969-1121	Med26	TFGMS279	55.1	145	1	M	NSA
PUID16585253	Ca1	42161413	(GTT)6	18	TGTTGATGTTGTTGTTGTTGT	CAAACGTCAACAATTACAGGT	105-2279	918-1322	POX	TFGMS280	54.9	149	1	M	NSA
PUID16585254	Ca8	4627990	(TGT)5	15	AGAAGGGTTCATGAGAAAAAG	ACTTTTCGTTCTTCGTCTTCT	105-2279	918-1322	POX	TFGMS281	55.2	168	1	M	NSA
PUID16585255	Ca3	39742820	(GAGAGT)3	18	AGGTTGGTTGTCTTAAGTTGA	TTTCTGCTTCACTTGATCTTC	163-2043	1608-1944	Response	TFGMS282	54.0	149	1	M	NSA
PUID16585256	Ca4	11554290	(AAG)4	12	GACCTCCAACAACAATAACAA	CCACTGGTGAAAGTTTATTTG	63-1673	1216-1475	Myb DNA binding	TFGMS283	55.2	149	1	M	NSA
PUID16585257	Ca4	11554351	(ATG)4	12	TAATGAAGTTGAAGCAAAAGG	CCACTGGTGAAAGTTTATTTG	63-1673	1216-1475	Myb DNA binding	TFGMS284	54.9	147	1	M	NSA
PUID16585258	Ca4	11553680	(CCA)4	12	GTCCAAGAAAGATCAACAACA	TCTTCTTCTTCTTCCATGCTA	63-1673	1216-1475	Myb DNA binding	TFGMS285	55.3	154	1	M	NSA
PUID16585259	Ca4	11554351	(GAA)5	15	TAATGAAGTTGAAGCAAAAGG	TAGGAGTTTGAGCTGACTCTG	63-1673	1216-1475	Myb DNA binding	TFGMS286	54.9	147	1	M	NSA
PUID16585260	0	0	(AGA)4	12	GGAGAAGGTAAAGGTAAAGGA	AAGAGTTCTTCTTCCACTGCT	229-1293	679-774	AP2	TFGMS287	54.4	149	1	M	NSA
PUID16585261	Ca7	43305901	(ATC)4	12	CTGTTACCAAGGAGGAATTTT	CCATTTAGTAATTGCATGGAC	10-567	256-387	Myb DNA binding	TFGMS288	55.1	150	1	M	NSA
PUID16585262	Ca8	4022386	(CAG)5	15	CACACTTTTCCACATCTTCAT	GAAACGAAGAACTACCACCA	415-1980	1162-1314	AP2	TFGMS289	55.1	151	1	M	NSA
PUID16585263	Ca7	12121206	(TTTC)4	16	CTCGTCTATGCTGTATTAGGC	CGGTGGACACTCACTACTACT	415-1980	1162-1314	AP2	TFGMS290	54.5	150	1	M	NSA
PUID16585264	Ca4	45415318	(ATAA)4	16	AGTGTATGCCTCCATTGACTA	GGTCACTTGTGTTGTCTTGTT	270-1436	395-509	HomeoBox	TFGMS291	54.8	145	1	M	NSA
PUID16585265	Ca4	45415195	(ATAAA)3	15	GGAAGAAATCAATGAAAAACC	AGGCCAAATTTCTTGTACTCT	270-1436	395-509	HomeoBox	TFGMS292	55.4	159	1	M	NSA
PUID16585266	Ca4	45415513	(ATG)4	12	TTGAAAACATTGACTTGATCC	GGTCACTTGTGTTGTCTTGTT	270-1436	395-509	HomeoBox	TFGMS293	55.2	147	1	M	NSA
PUID16585267	Ca4	45415513	(ATG)5	15	TTGAAAACATTGACTTGATCC	ATATGGATGCTCACTACATGC	270-1436	395-509	HomeoBox	TFGMS294	55.2	147	1	M	NSA
PUID16585268	Ca7	27235019	(AAAC)3	12	ACACAATACAAGGGCTACAAA	CCCATAAAGAAAATCTGGAGT	411-1628	1311-1511	TCP	TFGMS295	55.0	171	1	M	NSA
PUID16585269	Ca7	27236676	(TGG)5	15	GTTGTTTCTCCCATTTTTCTT	CATTCTCATCATTCTCTTCCA	411-1628	1311-1511	TCP	TFGMS296	55.0	157	1	M	NSA
PUID16585270	Ca7	27236080	(TTA)5	15	TAGTATCCGCAATGTCAGTGT	CGAAGAATACCACAACAATTT	411-1628	1311-1511	TCP	TFGMS297	55.8	151	1	M	NSA
PUID16585271	Ca5	47218992	(CGGAGC)3	18	CATAGTCAATCCCCCAATAAT	CAACCCTCATCCTTTTTCTAT	646-3210	1475-1575	Zf-CCCH	TFGMS298	55.5	148	1	M	NSA
PUID16585272	Ca6	28099917	(AGT)4	12	CCAACAATTTTCTTCTTCCTT	ACCTCACATATTTCCCAGAAT	385-2919	874-1506	START	TFGMS299	55.2	142	1	M	NSA
PUID16585273	Ca3	17180326	(ACA)4	12	CAAGTTCAGAAGCCTAATTCA	GAAGACCAGAAAGTCTACGTG	242-2649	1847-1951	WD40	TFGMS300	54.9	145	1	M	NSA
PUID16585274	Ca2	28016351	(AAT)4	12	TGGCATAAAAGTTTGTCCTAA	CACGACGGCAACTACTACTAT	242-2743	2052-2362	B3	TFGMS301	55.2	182	1	M	NSA
PUID16585275	Ca1	24070590	(CAA)4	12	AATTTCACAGCAAAACATCTC	CATAAGCTGAGACTGCAAAAG	777-4139	1152-1460	B3	TFGMS302	54.5	142	1	M	NSA
PUID16585276	Ca1	24070990	(CAA)5	15	CCCAACAGACTCAACAGAAT	GTTGCTGTTCTGAGATGTTTT	777-4139	1152-1460	B3	TFGMS303	55.1	146	1	M	NSA
PUID16585277	Ca1	24070590	(CAG)4	12	AATTTCACAGCAAAACATCTC	CGTTTGTAACAACGACTGC	777-4139	1152-1460	B3	TFGMS304	54.5	142	1	M	NSA
PUID16585278	0	0	(CAG)5	15	TTACAAACGCCGCTAAAC	TACTGGTTGCTGTACACACTG	777-4139	1152-1460	B3	TFGMS305	55.1	168	1	M	NSA
PUID16585279	Ca1	24071234	(CAGCAA)3	18	GATGATCCATCGAAGATATTG	CTGTTGTTGTTGTTGTTGATG	777-4139	1152-1460	B3	TFGMS306	54.6	153	1	M	NSA
PUID16585280	Ca1	6750581	(TC)8	16	ACGAAATCCAACGTATACAAA	TCCTTGAAGAATCCACAAATA	1463-3502	1850-2154	B3	TFGMS307	54.9	153	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585281	Ca1	6750581	(TCT)6	18	ACGAAATCCAACGTATACAAA	TCCTTGAAGAATCCACAAATA	1463-3502	1850-2154	B3	TFGMS308	54.9	153	1	M	NSA
PUID16585282	Ca1	13994160	(AAC)6	18	TGAATGTGGTTCTAAATGGAG	GAAATGCAACAGTCAAAAGAG	603-2816	1371-2030	START	TFGMS309	55.2	150	1	M	NSA
PUID16585283	Ca3	23905366	(AATTT)3	15	TCTTTGTTCTCATTTGTGGAG	AGATGAAAACGAGAGAGAGGT	1067-1870	1448-1528	Zf-CCCH	TFGMS310	55.4	150	1	M	NSA
PUID16585284	Ca3	23905324	(ATTAC)3	15	ACCTCTCTCTCGTTTTCATCT	CAACGAGAAAAACAACGACTA	1067-1870	1448-1528	Zf-CCCH	TFGMS311	54.8	184	1	M	NSA
PUID16585285	Ca3	29567332	(TTCT)4	16	AGAGAGTGACGTGTCCTTAGA	CTGAGAGTTCTTCTCCTCGAT	589-2772	2371-2637	Ank	TFGMS312	54.1	151	1	M	NSA
PUID16585286	Ca1	3999638	(ACA)6	18	TAAAGGTTCTGAGAGAGCAAA	GAAACTTACATGCTTGTGCTT	226-1611	445-651	TCP	TFGMS313	54.6	149	1	M	NSA
PUID16585287	Ca1	3998897	(ATC)4	12	AAAAGCCTTAAACATTGGTTC	TTCCACCAGTCAGTAACTCAG	226-1611	445-651	TCP	TFGMS314	55.2	166	1	M	NSA
PUID16585288	Ca1	3999015	(TC)7	14	TCACCCTCATTTATCATCATC	ATCTTTCTCCTTTGCTCTCTC	226-1611	445-651	TCP	TFGMS315	54.9	142	1	M	NSA
PUID16585289	Ca1	1049812	(CT)7	14	GGAAAAAGGAAAAACGAATAC	AGCTTCAAATTGTAATTGCTG	131-3114	2161-2259	Ank	TFGMS316	54.8	153	1	M	NSA
PUID16585290	Ca2	30034444	(AAGA)3	12	TTTTTGAGCTGAGAAGAAGAA	AAGATTCTGATGCAGTCTTTG	62-1438	149-634	Hat	TFGMS317	54.7	159	1	M	NSA
PUID16585291	Ca2	30034459	(AGA)5	15	ACCCTAACCACTTTCTTTTTG	AAGATTCTGATGCAGTCTTTG	62-1438	149-634	Hat	TFGMS318	55.2	174	1	M	NSA
PUID16585292	Ca6	12437191	(ATC)4	12	AATCTCAGCCTCAAACTCAAT	CTACAACTTGTTGCTGCTGTT	932-3685	1307-1615	B3	TFGMS319	55.6	147	1	M	NSA
PUID16585293	Ca1	47290885	(ATTTT)4	20	AGGAATTAAGGTGATGAAAGC	GTTTAACAAGACGGACCAAAT	470-1447	473-883	DUF822	TFGMS320	55.2	164	1	M	NSA
PUID16585294	Ca6	5509384	(TGT)5	15	AATCTTTCTTTCTTTCCCAAG	GTTGTTCCTTCATGTTTTCAG	323-1897	1592-1735	HLH	TFGMS321	54.5	151	1	M	NSA
PUID16585295	Ca6	21433878	(ATA)4	12	TTTCTTCAGACTTGTTGGAAA	GTCATAAACGAAACTCAATGC	420-3143	2127-2381	Bromodomain	TFGMS322	55.2	154	1	M	NSA
PUID16585296	Ca8	5508378	(AAC)4	12	TTGTTGACGACCTACTTGACT	TTTGAGAGAGAAACTGGTTGA	35-1177	920-1027	GATA	TFGMS323	55.0	149	1	M	NSA
PUID16585297	Ca8	5569895	(GAGTT)3	15	AATCCAATCGAAGAGAGAGAG	ACTCTAGGGTTTTCACTTTCC	149-3886	1601-1738	GYF	TFGMS324	55.3	154	1	M	NSA
PUID16585298	Ca6	21718856	(GGA)6	18	TAAAGGAATGATCCATTGAAG	TGAGAGAAATGATGAGTCCAT	52-1188	727-879	Myb DNA binding	TFGMS325	54.4	156	1	M	NSA
PUID16585299	Ca6	21718856	(GGT)6	18	TAAAGGAATGATCCATTGAAG	TGAGAGAAATGATGAGTCCAT	52-1188	727-879	Myb DNA binding	TFGMS326	54.4	156	1	M	NSA
PUID16585300	0	0	(AT)6	12	CGAGATCAGACCATCATTACT	AGTGACATTGTTTGTAAAGCAG	191-1627	947-1183	DOG	TFGMS327	54.3	157	1	M	NSA
PUID16585301	Ca3	25672140	(AAC)4	12	CAACTACGTTCATGTTCCATT	ATCGAAAAAGAAGCGTTAAA	199-1638	1063-1200	HLH	TFGMS328	55.2	149	1	M	NSA
PUID16585302	Ca3	25672329	(CAC)6	18	TATGGGAAACAACAACACTTC	GAAGTGTTGTTGTTTCCCATA	199-1638	1063-1200	HLH	TFGMS329	55.2	153	1	M	NSA
PUID16585303	Ca7	10115566	(TCTGAA)3	18	TGAACTATCCCCTTTAGGAAC	GAAGTTGATGAGTTTGATTCG	235-1188	742-897	AP2	TFGMS330	55.0	153	1	M	NSA
PUID16585304	Ca6	12569883	(AC)12	24	TTCTTTTTGTTTCTCACCAAC	CCTTTGGTGTAAAAGGGTACT	840-2244	1029-1292	TCP	TFGMS331	54.6	138	1	M	NSA
PUID16585305	Ca6	12571338	(ATT)6	18	CAAGCACAAACATTTTCTCTC	GAATCTCATCCTCCTCCATAC	840-2244	1029-1292	TCP	TFGMS332	55.2	153	1	M	NSA
PUID16585306	Ca6	12572068	(CAA)5	15	GTCAAGGTGTGATATTCGTGT	TGAATGTCCTAATTGGATTTG	840-2244	1029-1292	TCP	TFGMS333	55.0	151	1	M	NSA
PUID16585307	Ca6	12581322	(CATTTT)3	18	TTGATATGCTAGCTGTTGTCA	AGTGAATGAAGCTGTTTGAGA	840-2244	1029-1292	TCP	TFGMS334	54.6	144	1	M	NSA
PUID16585308	Ca6	12572633	(GGA)5	15	TCTCATCTTCAGAGGTTTTCA	GAGACAGAGAATTGGACTGAA	840-2244	1029-1292	TCP	TFGMS335	55.1	149	1	M	NSA
PUID16585309	Ca6	12572722	(TCA)6	18	TGCTTCTTCTGCTACTACTGC	AGTGAATGAAGCTGTTTGAGA	840-2244	1029-1292	TCP	TFGMS336	55.3	148	1	M	NSA
PUID16585310	Ca1	14717136	(CAA)5	15	CAAGAGATCATTCAAAATGGA	TTTCACTTCATCACTACACCA	132-1361	232-434	Myb DNA binding	TFGMS337	55.3	153	1	M	NSA
PUID16585311	0	0	(TGC)7	21	CTTCAAACCAAAACAAGACAC	ACAAATTGTGTCTTGTTTTGG	286-1980	1273-1485	Sigma70	TFGMS338	54.9	169	1	M	NSA
PUID16585312	Ca1	16679439	(ATT)4	12	AGAAGGGACATAGAGATCGTT	CATTTCATTTCTCATTGAAG	368-1387	971-1348	NAM	TFGMS339	54.6	160	1	M	NSA
PUID16585313	Ca1	16680825	(TATTT)3	15	GTGAAAGAGGGTCTTTATCTTG	ACATCGTCAAGAAGAAGACAA	368-1387	971-1348	NAM	TFGMS340	54.8	150	1	M	NSA
PUID16585314	Ca4	8052238	(GATGAA)3	18	AAGAGAAACGCATGAATGAT	AAAAGAAACCCATTGGATAAG	257-1462	278-1124	Tub	TFGMS341	54.9	164	1	M	NSA
PUID16585315	Ca3	2709400	(ACC)5	15	ACAAATGTTGGAGCAAGAAC	ACATAAGTAAGCCAAGTCTGC	396-1229	300-440	Zf Bbox	TFGMS342	55.3	154	1	M	NSA
PUID16585316	Ca3	2708823	(GTG)5	15	TTGTTTAATGGTGAAGTTGATG	GCTTCATCTTCATCTTCCATA	396-1229	300-440	Zf Bbox	TFGMS343	55.3	147	1	M	NSA
PUID16585317	Ca4	48122127	(ATG)4	12	AAAGACGCAAAACATTAACAC	CACACTGTGGATTCTTGTCTC	495-2333	1050-1157	HomeoBox	TFGMS344	54.7	159	1	M	NSA
PUID16585318	Ca4	48124978	(GAA)7	21	TGACATCTCCAACAACAAGAT	GGGTGATTGGTTGTATGTATG	495-2333	1050-1157	HomeoBox	TFGMS345	55.6	147	1	M	NSA
PUID16585319	Ca2	34272501	(ACA)4	12	CTTTCTCAATTCCTTCCAACT	CAGGGAATGTTGATGGTAGTA	37-972	529-709	WRKY	TFGMS346	55.2	151	1	M	NSA
PUID16585320	Ca2	34273826	(ATG)4	12	TTTCCATGGCTAATGAGAATA	CATTGAAACTTGTATGAGAAGG	37-972	529-709	WRKY	TFGMS347	55.0	147	1	M	NSA
PUID16585321	Ca1	21506671	(ATC)6	18	CATATATCCAAGGTGTGGTTG	GTGGTCCAGTGATAATGTTGT	168-824	186-713	YABBY	TFGMS348	55.4	150	1	M	NSA
PUID16585322	Ca1	21506671	(ATCA)3	12	CATATATCCAAGGTGTGGTTG	GTGGTCCAGTGATAATGTTGT	168-824	186-713	YABBY	TFGMS349	55.4	150	1	M	NSA
PUID16585323	Ca2	2409718	(CAA)4	12	GACTACAAGTTTCTTCCGTCA	CTTTGTGTGCTAATTTTTCTCA	423-1283	627-788	HomeoBox	TFGMS350	54.6	152	1	M	NSA
PUID16585324	Ca1	16011527	(CAG)4	12	GTCAATCAAGACCAATTTTCA	AGACTGGTGCTTCCTCTAAGT	217-624	349-552	Histone	TFGMS351	55.2	134	1	M	NSA
PUID16585325	Ca1	46719766	(TCATAA)3	18	GCCAACTTCTTCTTTTTCTTC	CGAGAGTGTGAATTTGGAAT	149-1957	212-1261	mTERF	TFGMS352	55.1	175	1	M	NSA
PUID16585326	Ca7	9867672	(AAC)4	12	CTGCAACTTCATTCTCATCAT	CCACGAACTCTCTTAACCTTT	51-924	774-845	ZfC2H2	TFGMS353	55.4	154	1	M	NSA
PUID16585327	Ca7	9867339	(AAGAAC)3	18	ATACTTCCCCTGAAGAAGATG	TGAACAACAATCAAAGACTCA	51-924	774-845	ZfC2H2	TFGMS354	55.0	142	1	M	NSA
PUID16585328	0	0	(GTT)5	15	GTTTCCTCTGAAGATGTTGAA	AACAAGGGAGAGAAAGAGAGA	239-2206	521-773	Myb DNA binding	TFGMS355	54.5	154	1	M	NSA
PUID16585329	0	0	(TC)7	14	TTTCATCATCTCCTGAATTTG	GAAGAACAAGGGAGATAGTCC	239-2206	521-773	Myb DNA binding	TFGMS356	55.3	190	1	M	NSA
PUID16585330	Ca1	5765349	(AAC)5	15	AACAACAACACTCCTGGTTTA	TGATGTAAGCTTCCAAGAGAC	55-924	709-813	HomeoBox	TFGMS357	54.8	145	1	M	NSA
PUID16585331	Ca1	5765412	(ACA)5	15	TTCACCAACTGTAATAACACTAC	TGATCTTGGCTTTAACAGAAG	55-924	709-813	HomeoBox	TFGMS358	51.5	166	1	M	NSA
PUID16585332	Ca2	26835722	(AAC)4	12	TCATGGCTTCATCCTCTAGTA	TCTCCAATTGTAACCATCATC	21-1746	1251-1427	WRKY	TFGMS359	55.1	152	1	M	NSA
PUID16585333	Ca2	26832522	(CAA)6	18	CCTTTTAACCCTGAGATGATT	ACTTTCACCCCTTAATTTGTT	21-1746	1251-1427	WRKY	TFGMS360	55.0	155	1	M	NSA
PUID16585334	Ca1	15319914	(TCTTTC)5	30	ATTTAATTTTGGGAGCAACA	CTGCTTTAGTGAATTTGGTTG	1135-3129	1207-1332	PHD	TFGMS361	54.9	144	1	M	NSA
PUID16585335	Ca8	8841187	(AAC)6	18	GCAGTTAGGGTTAGGTTCTTC	CTTGGAATTGAAATTGAAGTG	289-2259	1753-1893	HLH	TFGMS362	54.8	156	1	M	NSA
PUID16585336	Ca7	19466439	(TCTCT)3	15	GCCCTTGAGTTGAGTTAAGAC	AAACTATGGAAATGGAAGGTT	239-1300	437-1273	AUX-IAA	TFGMS363	55.7	145	1	M	NSA
PUID16585337	Ca4	21852453	(AAC)6	18	ACTGACAACAACACACATCAA	AATTGGATGAAGAAAAAGGAG	132-1655	504-764	Myb DNA binding	TFGMS364	54.8	144	1	M	NSA
PUID16585338	Ca4	21853060	(ACA)4	12	GTCATGGTAGTGTTGTTGCTT	CTGATGAATGAAAACATTGCT	132-1655	504-764	Myb DNA binding	TFGMS365	55.2	144	1	M	NSA
PUID16585339	Ca4	21852247	(ACA)6	18	TCTAAAGTTTCTTCCTTTTTCG	GTGAGGATTTTGTTGAATTTG	132-1655	504-764	Myb DNA binding	TFGMS366	54.9	158	1	M	NSA
PUID16585340	Ca4	21852384	(CAA)4	12	CAAATTCAACAAAATCCTCAC	TGGCTCATCTTCATCACTAAG	132-1655	504-764	Myb DNA binding	TFGMS367	54.8	148	1	M	NSA
PUID16585341	0	0	(TA)7	14	TAAATCCAAAGTTTTGTCTGC	GGCTGAATATGGCTTTACTCT	363-2039	523-803	NAM	TFGMS368	54.7	166	1	M	NSA
PUID16585342	Ca6	789811	(AGA)6	18	AGCACTGAGGTCATATTCAGA	AAATCTCATCGATCCTTCTTC	258-2126	279-1385	GRAS	TFGMS369	55.0	145	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585343	Ca3	14027023	(AAC)5	15	ATACCATGAAACTTGCCTAGC	CCAAGACCTGATAGAATTTCA	326-2341	1697-1996	B3	TFGMS370	56.1	143	1	M	NSA
PUID16585344	Ca3	14025567	(AGG)4	12	GTAAGCAGAGTCACCTAGTGC	CACAAAGAAAAGAGAAAGAGAGA	326-2341	1697-1996	B3	TFGMS371	54.4	156	1	M	NSA
PUID16585345	Ca3	14022308	(TCTCTT)3	18	AAGCTTTATGAAGGAGAGACAA	AAGCTCAGACACAACTGAGAC	326-2341	1697-1996	B3	TFGMS372	55.1	133	1	M	NSA
PUID16585346	Ca2	7604019	(GAA)5	15	CATGTTCTTAAGGTTTGGATG	TAAGTAAGCTTCCTCACACCA	145-924	328-495	Zf-HD	TFGMS373	54.8	148	1	M	NSA
PUID16585347	0	0	(AAC)6	18	ATATTTCCACCATTCACCTTT	GACAAGCTGAAAATGTTTGAC	247-1272	607-795	WRKY	TFGMS374	55.1	158	1	M	NSA
PUID16585348	0	0	(CAT)11	33	GGAAGAGAACATGAAGTGTGA	TACATGTGATGATGTTGATGG	247-1272	607-795	WRKY	TFGMS375	55.3	158	1	M	NSA
PUID16585349	Ca2	11702592	(ACT)5	15	CAGTGCTCAAGCAGCTATAAT	TACAAACCAAACCCTACACAG	126-410	174-407	PLN03217	TFGMS376	55.1	152	1	M	NSA
PUID16585350	Ca6	58334550	(CAA)4	12	TTGTTTGCTCCGTAATTTTAG	GACAGTGTTGGAAAGACAAAG	34-1125	475-621	HLH	TFGMS377	55.0	153	1	M	NSA
PUID16585351	Ca6	58334307	(TGTTCA)4	24	GAATCACAGCCATTAACCAT	CTCTCGATGAGGTGGTAGTTA	34-1125	475-621	HLH	TFGMS378	55.0	147	1	M	NSA
PUID16585352	Ca1	11286316	(GAA)5	15	GTGTCTTCAAAAGAATGATCG	TCCTAATTCAATCACTGATCC	337-2598	349-1467	GRAS	TFGMS379	54.9	159	1	M	NSA
PUID16585353	Ca8	1872182	(CAC)4	12	TTATGTTCCCTTTCCTCTCTC	CGAGGAATGTTTTATCTGTTG	508-1521	1177-1452	HSF	TFGMS380	55.1	151	1	M	NSA
PUID16585354	Ca3	9307016	(AAT)5	15	AAGATTCATGAAACCTCAATTC	GTGGGTCCTTTCATTATTTTT	234-1247	861-1118	Myb DNA binding	TFGMS381	55.0	157	1	M	NSA
PUID16585355	Ca6	15272295	(GGT)6	18	TCCTGTTGAGATTGAGAAAGA	GCTTCTCCCCTAAAATTCATA	237-1841	468-1132	Bromodomain	TFGMS382	55.1	149	1	M	NSA
PUID16585356	Ca5	31758233	(TGT)5	15	GGAAACTCCTTGAGACTCTTC	TCAACAACAACACCAGAAAAT	286-2301	1174-2010	DnaJ	TFGMS383	54.7	147	1	M	NSA
PUID16585357	Ca3	30969715	(ATT)4	12	AACAGTAGTATGCATGGGTTG	TATCAGTTAGGGTTGAGCTTG	670-1548	979-1071	HLH	TFGMS384	55.2	153	1	M	NSA
PUID16585358	Ca7	13582408	(CAA)5	15	GATGAGAGTTCCTCCTGTTTC	CCTCTTCCACTTCTTCTTGTT	198-1793	699-1787	GRAS	TFGMS385	55.4	200	1	M	NSA
PUID16585359	Ca6	12728676	(AAAT)3	12	TCAAAATCACTGGTGCTAGTT	TGGAATTGGAATCTCTTGTAA	488-2101	521-1591	GRAS	TFGMS386	55.1	156	1	M	NSA
PUID16585360	Ca1	12948538	(AT)6	12	TGTATCAAGTAGAGCAGCACA	GCATGAAAATTCAGAGAGAAA	267-1541	762-914	Myb DNA binding	TFGMS387	54.7	150	1	M	NSA
PUID16585361	Ca3	19075803	(AG)6	12	TTTGGATATATGAGGATGGTG	AAGTTTCACTTTTGTGCCTTA	391-1329	754-888	Myb DNA binding	TFGMS388	55.0	177	1	M	NSA
PUID16585362	Ca3	17936119	(ATAA)3	12	GAGCAAGTAGGGTGTAGATCA	GCAATTTAAAACCATGACAAG	108-1175	129-278	Myb DNA binding	TFGMS389	54.5	141	1	M	NSA
PUID16585363	Ca3	29972354	(TAGGGT)3	18	TTTTCTTCTTTCTCCAAAACC	ACCTTAGAGGAAAAGGTCTCA	261-1139	765-953	KH1	TFGMS390	55.3	148	1	M	NSA
PUID16585364	Ca8	8417199	(ATG)5	15	TGGAAGAAGTGTTGTTGAAAT	CATCATCACTTCCAAAACATT	363-1553	747-902	Myb DNA binding	TFGMS391	54.9	153	1	M	NSA
PUID16585365	Ca1	10019673	(TTC)5	15	GAAAATCTTCGGTGTTAGGTT	CAAGGTGAACCAGGATTAAG	126-1172	444-578	Myb DNA binding	TFGMS392	55.1	144	1	M	NSA
PUID16585366	Ca5	32220400	(AATAA)3	15	CCATACGACGGAATAATAACA	CCACTACTTTGTCCATTACCA	295-890	502-681	bZIP	TFGMS393	55.3	133	1	M	NSA
PUID16585367	Ca5	21801455	(GAG)5	15	CGGATTGAACTTTCTTCAAC	AAGAGAGAAGCAAAGACCTTC	210-1232	258-500	FHA	TFGMS394	54.9	134	1	M	NSA
PUID16585368	Ca7	34321017	(AAG)4	12	ATCAGAATTTGACAAGGAGGT	CTTCTTCTTTTGATGGTGTTG	712-1293	832-1122	B3	TFGMS395	55.3	153	1	M	NSA
PUID16585369	Ca7	34321017	(GAA)6	18	ATCAGAATTTGACAAGGAGGT	CTTCTTCTTTTGATGGTGTTG	712-1293	832-1122	B3	TFGMS396	55.3	153	1	M	NSA
PUID16585370	Ca4	1220689	(AACAAT)3	18	AACACTTCCTTTTCAAACTCC	CCAATCCATACTCTAACACCA	78-839	402-500	AP2	TFGMS397	55.1	150	1	M	NSA
PUID16585371	Ca2	14623906	(AGC)5	15	AGCAACTTCCATGAGCTTT	TCCCTTTCTCTTTCTCTTTTC	225-998	540-950	DUF3594	TFGMS398	55.1	129	1	M	NSA
PUID16585372	0	0	(ATGC)3	12	AGACTAGATGGGTTATGCAGTT	TGGCAACCTATACTCAAACAT	408-1298	771-905	Myb DNA binding	TFGMS399	54.7	166	1	M	NSA
PUID16585373	Ca1	4325015	(AATC)3	12	AGAGTTGCAATGTTGTTGAGT	ACGAAGAGAGTGTTAGGGTTT	117-1241	345-1100	mTERF	TFGMS400	54.9	145	1	M	NSA
PUID16585374	Ca5	38579922	(ATG)5	15	TTTTGAAGTTAGGGATGAACA	CATCAACCTTCTCACTCACAT	541-1443	1105-1185	ZfCCCH	TFGMS401	55.0	149	1	M	NSA
PUID16585375	Ca1	2744133	(AAT)5	15	TTCTCTGCTTCTACATCCATC	AACTGAATCTTTTAGTTTACCC	287-5644	5360-5506	HomeoBox	TFGMS402	54.6	163	1	M	NSA
PUID16585376	Ca5	46510392	(AAG)6	18	TATTATTGGGAGGAGACAACC	AATGAACCTCCGATTGAGAT	130-1089	481-660	bZIP	TFGMS403	55.7	166	1	M	NSA
PUID16585377	Ca5	30816603	(GAA)5	15	GCTACAATTGGCATATGAAAG	TAGCAGCTGATAGTTGCTCTT	100-1257	556-699	HLH	TFGMS404	55.1	151	1	M	NSA
PUID16585378	0	0	(GGC)5	15	ATACGTGGGAGAGAAAAAGAT	AAGCCCATTTCATTTACACTT	236-1222	572-652	ZfCCCH	TFGMS405	54.6	162	1	M	NSA
PUID16585379	Ca1	2632048	(GAA)5	15	AGAAGAAGAAGAAGAGGTGGT	TTCTTCTCCCTTCTCCTCA	357-2489	1146-1205	ZfCCCH	TFGMS406	53.9	149	1	M	NSA
PUID16585380	Ca1	2631745	(GAG)6	18	GGAAGCAGAAACAGTAGAGGT	CTCCCTTCTCCTCATCAAC	357-2489	1146-1205	ZfCCCH	TFGMS407	55.3	165	1	M	NSA
PUID16585381	Ca4	5495431	(TGT)5	15	GTTGGTGTTGGTTGTAACATT	TCAACCAACTTTGTCTATGAAG	386-1366	815-970	HLH	TFGMS408	54.9	143	1	M	NSA
PUID16585382	Ca1	23712291	(TAA)5	15	CTTAACCATGAGTATTAAACAAG	ATCTGTTTTTGCCAGAACTTT	201-968	558-659	tify	TFGMS409	50.7	116	1	M	NSA
PUID16585383	Ca4	46457630	(CTT)6	18	CCCTCTTTTCATTTCTCTCAT	TCTCTTTGAGGAAGAACGTG	1-744	274-402	HLH	TFGMS410	55.1	156	1	M	NSA
PUID16585384	Ca5	40078153	(ATCACA)3	18	CATGTCCAATAACCATCACAT	TTCTTCGTCGCTATAATCATC	62-1936	209-1360	EIN3	TFGMS411	55.7	151	1	M	NSA
PUID16585385	Ca5	40076484	(ATG)4	12	TGAGGATTATTTTTCATTGG	AAAGGATGTCAAATCACAATG	62-1936	209-1360	EIN3	TFGMS412	52.8	158	1	M	NSA
PUID16585386	Ca5	18185574	(AAATT)3	15	ATTCGGATAAATGGCTTACTT	TCTCCAAGACAACTTATGAAAA	1323-2081	1353-1502	Sigma70	TFGMS413	54.8	152	1	M	NSA
PUID16585387	Ca6	20762847	(AGAGA)3	15	AGGAGGGGTTTTCTCTTTATT	GAAACTGTTTTGTCGTTGAAG	162-875	492-641	HLH	TFGMS414	55.2	166	1	M	NSA
PUID16585388	0	0	(TGA)6	18	TTTTGTTTTCTGGGAAATTG	AATCCTATTCTCCCCTTCTCT	162-875	492-641	HLH	TFGMS415	55.4	149	1	M	NSA
PUID16585389	Ca6	20762848	(TTA)5	15	AAGGAGGGGTTTTCTCTTTAT	AATCCTATTCTCCCCTTCTCT	162-875	492-641	HLH	TFGMS416	55.2	134	1	M	NSA
PUID16585390	Ca4	4988607	(AAT)6	18	TCATTTCTTGTCCCTAATGAA	AGGTCGAGGCTAGTATAGGAA	312-1070	339-1025	AUX-IAA	TFGMS417	54.9	152	1	M	NSA
PUID16585391	Ca7	26882637	(AGTG)3	12	TCACCTTCTGCTTTCTTACAG	GATAAAGGCAAACAGAAACAA	29-592	239-472	SBP	TFGMS418	54.9	152	1	M	NSA
PUID16585392	0	0	(AT)9	18	ACCAACTAAAAGAATCAGAGC	TCGAAAATGGTGGTAGATAAA	231-998	468-731	FAR1	TFGMS419	53.0	158	1	M	NSA
PUID16585393	Ca2	26158080	(TGC)5	15	AGATCGGTGATAAGGAGTTTT	ACAGGCAGATGTCCATAACTA	107-1144	259-427	FHA	TFGMS420	54.6	157	1	M	NSA
PUID16585394	Ca6	29745989	(TG)8	16	TGATGATTCTTCACTTTCTCC	ACTCATCAATCAAGAGGATCA	439-885	445-813	YABBY	TFGMS421	54.4	147	1	M	NSA
PUID16585395	Ca4	4368581	(ATC)5	15	AAAGAACCATTTCCAAGAGAC	AAATTTATCATCCCAAGGACT	502-1671	1336-1413	ZfCCCH	TFGMS422	55.0	152	1	M	NSA
PUID16585396	Ca8	14983014	(CATTT)3	15	TAACACCATCATCTCTCTCCA	TTTGGGTTTTGATTTGTGTAG	105-542	368-524	HTH	TFGMS423	55.7	173	1	M	NSA
PUID16585397	Ca4	3715855	(CCCTTC)3	18	AAATAACATCAGAAGGCACTG	ATTGTGACTCAAGGCCTAAAT	198-1661	330-473	PHD	TFGMS424	54.6	135	1	M	NSA
PUID16585398	Ca4	42774790	(CAA)4	12	CTTTCAAACTTTGTTCCAATG	GTAAAGGGTGGTTTGAATTTT	416-1084	500-955	DUF702	TFGMS425	55.1	145	1	M	NSA
PUID16585399	Ca8	3154271	(CAA)5	15	AGCAAGTGTTCTACACCAAGA	AACAGGGGAAAGATCTTGTAA	54-1037	516-653	HLH	TFGMS426	55.1	139	1	M	NSA
PUID16585400	0	0	(AAAATG)3	18	CTGATGAAACGATGTGATGTA	CTTTTCCTAACGCCTCTGTAT	405-1076	477-572	AP2	TFGMS427	54.5	150	1	M	NSA
PUID16585401	Ca7	1270756	(AG)6	12	TGAGAATGATTTTGAAGAGGA	TTCCATTCTACATTCCACAGT	368-1570	800-892	HLH	TFGMS428	55.0	153	1	M	NSA
PUID16585402	Ca1	9679421	(ACGTTA)3	18	ACATCCTAAGACACCATCCTT	TGTTTTCTGTTTCTTCATCGT	66-953	639-821	ovate	TFGMS429	55.2	164	1	M	NSA
PUID16585403	Ca2	6182801	(TGAT)4	16	GACCTCACAATGGAGACAGTA	TTTAAGATTTGCTGAATCCTG	186-854	294-545	DUF260	TFGMS430	55.1	128	1	M	NSA
PUID16585404	Ca7	28548004	(AATT)6	24	GCTCCTCCATTAACTCATTTC	AGGGTGAAAGTGAGATCTTTT	786-1760	975-1211	SBP	TFGMS431	55.5	168	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585405	Ca7	7474741	(ATC)5	15	GCAAGTCATGCACAAAAGTAT	CTTATCTGAACTTGTGGTGGT	112-1014	136-288	Myb DNA binding	TFGMS432	55.5	148	1	M	NSA
PUID16585406	Ca2	3204755	(AAAGAT)3	18	CCATGGATAAAGAAGAAATGA	CCAAACTCCTCTGATCCATA	357-1247	789-950	HomeoBox	TFGMS433	54.4	145	1	M	NSA
PUID16585407	Ca2	3204755	(AGATAT)3	18	CCATGGATAAAGAAGAAATGA	CCAAACTCCTCTGATCCATA	357-1247	789-950	HomeoBox	TFGMS434	54.4	145	1	M	NSA
PUID16585408	Ca2	3204627	(ATG)5	15	GAAATGATGATGAGTTGGAAA	CCAAACTCCTCTGATCCATA	357-1247	789-950	HomeoBox	TFGMS435	55.1	145	1	M	NSA
PUID16585409	Ca2	3204755	(TATAG)4	20	CCATGGATAAAGAAGAAATGA	TTCTTCTTTATCCATGGCTTT	357-1247	789-950	HomeoBox	TFGMS436	54.4	145	1	M	NSA
PUID16585410	Ca8	14961209	(ATC)4	12	ATTTCAGCTTGTAGGCAATC	AATTCGCACCTTACAATATCA	221-1375	713-976	Myb DNA binding	TFGMS437	54.6	149	1	M	NSA
PUID16585411	Ca8	14955395	(CCT)5	15	CATCATCTGTTGCCTCTTAGT	TTTCGAAGATGCAAGAAGTAG	221-1375	713-976	Myb DNA binding	TFGMS438	54.5	167	1	M	NSA
PUID16585412	Ca5	43831503	(TATTA)3	15	CCAATAACAACACACTCTTCC	ATCTTGATGCAAGACTAAGCA	454-1473	613-699	bZIP	TFGMS439	54.7	165	1	M	NSA
PUID16585413	0	0	(CGGTT)3	15	CTGTTCTCTCGGTGACATCT	ATTGTTTTCACAGAGCTTCAA	497-1072	788-979	Histone	TFGMS440	55.3	149	1	M	NSA
PUID16585414	Ca4	45445882	(TAT)5	15	GGCAAATATGGTTGTTGAGTA	CAACAACAAGCACGTAATAGA	1-583	344-475	Myb DNA binding	TFGMS441	55.3	149	1	M	NSA
PUID16585415	Ca1	2948290	(AAT)4	12	GCTGCTTTTAAAATGAGAGGT	GAAATTGAGCCAGAGCTAGTA	17-340	191-301	AP2	TFGMS442	55.5	159	1	M	NSA
PUID16585416	0	0	(CATT)4	16	TATCTAGCTAGGGTGCAGTGA	AAATTTTGATTCAGAGGAACC	95-710	194-439	FHA	TFGMS443	55.3	141	1	M	NSA
PUID16585417	Ca5	36711446	(AAC)4	12	TCTTTCCATTTTCCAACACTA	GTGTTGTAGTTGGTTGTTGTG	18-611	93-374	HSF	TFGMS444	55.0	151	1	M	NSA
PUID16585418	Ca5	36711369	(CAC)4	12	AACACAACCTCAACAAACATC	AATTGTTGGTTTGTTCATCAG	18-611	93-374	HSF	TFGMS445	55.0	149	1	M	NSA
PUID16585419	Ca3	31248824	(CCAAAA)3	18	AAATGGATTTTGATTCTCCTC	ACTCCTCTAAACACCCTTTTG	100-669	403-504	AP2	TFGMS446	54.9	148	1	M	NSA
PUID16585420	Ca3	31248872	(TATCAT)3	18	TCTACTTCCCTGAAAATTCCT	TCATTCGTAAGGGTATTGTTG	100-669	403-504	AP2	TFGMS447	54.7	150	1	M	NSA
PUID16585421	Ca6	5689236	(TGC)5	15	ACCTGTCTCTGTGTCTGATGT	AGCCTCACTTTTCTCAGTTGT	135-788	591-761	LIM	TFGMS448	54.5	152	1	M	NSA
PUID16585422	Ca7	20120728	(CTT)5	15	CATCAAAAGGCTTCTCCTAAT	TTTTGAAAGTAGTGGCTTTGA	128-840	677-832	Myb DNA binding	TFGMS449	55.3	157	1	M	NSA
PUID16585423	Ca7	20120215	(TTG)6	18	AGAAAACAAAGAGAAGGAAACA	TGAAGAAGAAGCACTTAATGG	128-840	677-832	Myb DNA binding	TFGMS450	55.0	149	1	M	NSA
PUID16585424	Ca6	35239470	(CAA)5	15	CTATCCTTAATTTTCCCGAAG	TTTCTATTGAAGGAGAGGGTAG	69-443	141-293	AP2	TFGMS451	54.9	141	1	M	NSA
PUID16585425	Ca4	44394673	(ATGCA)4	20	GAAAAAGACAGAGGAAAAAGAA	GCCTTAGCCAAAGACATTTAC	253-1314	376-510	ZfB-Box	TFGMS452	54.7	163	1	M	NSA
PUID16585426	Ca2	7604031	(ACA)4	12	GTTTGGATGCATAACAACAAG	CTCAGCATTCATATCAGCTTT	368-1354	575-736	Zf-HD	TFGMS453	55.8	153	1	M	NSA
PUID16585427	Ca3	3617903	(CAA)5	15	TAGATGTTAGAGCCATGGACA	GATTTTTGGTGTTGTTTGTGT	368-1354	575-736	Zf-HD	TFGMS454	55.9	152	1	M	NSA
PUID16585428	Ca3	23992706	(ACAT)3	12	GAAAGGAAAAGCAAAAGAAAG	TTTATGTCATGAGAACCACAA	144-1238	195-572	NAM	TFGMS455	55.3	149	1	M	NSA
PUID16585429	Ca6	16432035	(ATCAAC)3	18	CAACACTAAACTTCCATCTTCA	GAGAGCAAGATGATGAATCTG	144-1238	195-572	NAM	TFGMS456	54.7	150	1	M	NSA
PUID16585430	Ca5	47316816	(AAAAG)3	15	AAATACATAACCAGCTCAACG	GGGGTGTAGTTTAAGGTTGTT	267-1331	930-1310	NAM	TFGMS457	54.6	154	1	M	NSA
PUID16585431	Ca5	30726721	(AGAA)3	12	TGAAGCTTCTTTTCGTTTTT	CCCACTTTCTTTCTCTCTCTA	272-739	473-652	bZIP	TFGMS458	54.6	161	1	M	NSA
PUID16585432	Ca5	30725711	(CT)8	16	TCATTTATAGAAGCAGCACCT	ATCTATTGGGTTTGGTTGAAT	272-739	473-652	bZIP	TFGMS459	54.4	148	1	M	NSA
PUID16585433	Ca7	4490042	(AGA)4	12	ACTGGATCGGATTATTCTTCT	AATCAGATGATTCTGACGATG	215-1000	485-601	ZfCCCH	TFGMS460	54.5	145	1	M	NSA
PUID16585434	Ca2	3582806	(AAT)6	18	CCTTCTATGGTTTCATCATCA	GTTGGTGGAACATTCTCATTA	191-1456	230-373	Myb DNA binding	TFGMS461	55.2	155	1	M	NSA
PUID16585435	Ca5	34474930	(GTT)5	15	GAGTACTGGATTGAGCAAGTG	CTCTCTCTTCATCCCAGCTAT	64-1329	355-505	tify	TFGMS462	55.0	144	1	M	NSA
PUID16585436	Ca4	10152488	(ATC)4	12	CTAAAGACCCTACCCTTTTTG	GTTCATTGGATTTTGTACAGG	400-1437	583-687	GATA	TFGMS463	54.9	151	1	M	NSA
PUID16585437	Ca3	25757444	(TTC)5	15	TTCCTTAACCAGACTTTCCTC	GAAGGATACGATTAGGGTGTT	223-2466	1180-1662	YDG-SRA	TFGMS464	55.2	161	1	M	NSA
PUID16585438	Ca6	3941697	(GGGTTC)3	18	AATCTGGAAGGGACATAAGAG	AAGAAAGGGCTCACTAGCTC	38-1195	410-484	ZfCCCH	TFGMS465	55.0	151	1	M	NSA
PUID16585439	Ca4	1493962	(CAA)4	12	GCATCGAATCACTATCACTTC	GTCGAAATTCAGGTTTATTCC	63-1118	905-1091	WRKY	TFGMS466	54.9	141	1	M	NSA
PUID16585440	Ca3	38615698	(ACCA)3	12	TCACGAGTTTTTGTTTATGGT	GAGAAATACGAGCCTAGGAAG	144-1427	864-1085	Myb DNA binding	TFGMS467	54.9	151	1	M	NSA
PUID16585441	Ca3	38614643	(ATT)4	12	CCAGATACGTTTTTCTCACTG	CGCTAATGCTAATTTTAATGC	144-1427	864-1085	Myb DNA binding	TFGMS468	55.1	147	1	M	NSA
PUID16585442	Ca4	9472194	(AGTT)3	12	CGTGTGTCTCTAACCATCTTC	CTACCTCCTTCCATTTTCTGT	184-984	441-954	B3	TFGMS469	54.9	150	1	M	NSA
PUID16585443	Ca1	12131386	(CATGG)3	15	TTGAAGAGGTTGAGAATGGTA	CCATGCATGTGATTTCAGTAT	189-1130	891-995	GATA	TFGMS470	55.0	150	1	M	NSA
PUID16585444	Ca4	10978720	(ATC)4	12	ATGACCAGTGAATATGTGCTC	ACAATGATGTTTTCCTTGATG	214-1401	991-1092	WD40	TFGMS471	55.1	143	1	M	NSA
PUID16585445	Ca5	166287	(GGA)6	18	TGACAACAGTTCTTGGTCTTT	GGGAGAGGGAGTAACAAAGTA	23-1294	194-571	NAM	TFGMS472	54.9	154	1	M	NSA
PUID16585446	Ca8	8740817	(AC)6	12	ACAAATAACCATTCACTCCAA	CTTGCATTGAACAAAGAAACT	98-814	365-580	PLATZ	TFGMS473	54.7	137	1	M	NSA
PUID16585447	Ca8	8740776	(TGA)5	15	ATTGAAAACCAAGAGACCACT	CCACCTGTTATCATCATCATC	98-814	365-580	PLATZ	TFGMS474	55.4	147	1	M	NSA
PUID16585448	Ca6	7956690	(AAGA)5	20	TTCTTCATTGAATGGGTCTAA	GAATTTTGGATTGAAACAGGT	350-1219	752-847	AP2	TFGMS475	54.9	140	1	M	NSA
PUID16585449	Ca5	44475116	(GATGC)3	15	GAAAGACACCTCATGGTGATA	CGAAAGATAACCAACACAATC	350-1004	468-722	BTB	TFGMS476	55.1	136	1	M	NSA
PUID16585450	Ca5	44475116	(TCG)5	15	GAAAGACACCTCATGGTGATA	CGAAAGATAACCAACACAATC	350-1004	468-722	BTB	TFGMS477	55.1	136	1	M	NSA
PUID16585451	Ca5	44128202	(GAAACA)3	18	TAGTAGAATGCGTTCACGTTT	GAAAGACCAACAAAGCTTAGAC	175-1149	616-933	BTB	TFGMS478	55.3	151	1	M	NSA
PUID16585452	Ca5	12081922	(CAA)4	12	TACTCAATCACTCCGAAACAT	AATTTCTTCGTGTTGCATATC	163-1050	181-375	CBFD-NFYB	TFGMS479	54.8	142	1	M	NSA
PUID16585453	Ca1	7441737	(ACA)4	12	AGAACACACAGAGACAGTGCT	AATTGATGTGTTGTTGTGGTT	258-878	588-758	CBFD-NFYB	TFGMS480	55.0	148	1	M	NSA
PUID16585454	Ca1	7441625	(CTCTT)4	20	CAACACTTTCCCTTCACTTC	AGAACAAGCTCTTGAGGAAGT	258-878	588-758	CBFD-NFYB	TFGMS481	54.8	153	1	M	NSA
PUID16585455	0	0	(AGT)5	15	TACAATTCACCCTATGCAACT	TTGGAGCTTTGTAACATTAGG	667-1458	769-867	B3	TFGMS482	54.9	157	1	M	NSA
PUID16585456	0	0	(ATT)4	12	CCTAATGTTACAAAGCTCCAA	ATATTTTGAAACTCCCTGGAT	667-1458	769-867	B3	TFGMS483	54.8	150	1	M	NSA
PUID16585457	Ca7	32382865	(ACA)4	12	AACACAACAAGGAATCAACTG	TTGTTCTGGATTTTCGTTCTA	299-1066	632-1039	DUF3594	TFGMS484	55.2	155	1	M	NSA
PUID16585458	Ca7	32386407	(TC)7	14	ATAAAATGAAAACGGAGTCGT	AAACACAAGTCTTGATTTCTCA	299-1066	632-1039	DUF3594	TFGMS485	55.5	139	1	M	NSA
PUID16585459	Ca5	24717508	(AAT)6	18	AATCAAGAGATCCACTTCACC	TGTTCATGTGCATGATTATTG	567-1598	720-851	Myb DNA binding	TFGMS486	55.7	150	1	M	NSA
PUID16585460	Ca1	43957682	(AAT)4	12	ACCAACCCAATCTTCAATAAT	CAGAACTTCCTTCTCCTAAGC	76-1020	106-480	NAM	TFGMS487	55.1	153	1	M	NSA
PUID16585461	Ca1	43957788	(TAA)5	15	GCTTAGACCCTTTATCATGTG	CAAAACAGCTTTCAACACTTT	76-1020	106-480	NAM	TFGMS488	54.1	150	1	M	NSA
PUID16585462	Ca5	45765485	(GCTCG)3	15	GCAACAGTTCTCAATGGTTAG	CATCATTTTGAGTTTGGACAT	150-866	291-440	HomeoBox	TFGMS489	55.1	152	1	M	NSA
PUID16585463	Ca3	29764445	(AGC)4	12	AAGGATCGTTGTGACCTTTAT	GCTCAAATTTCAAACAACCTA	184-1095	256-393	HLH	TFGMS490	55.3	138	1	M	NSA
PUID16585464	Ca5	10157517	(AATGAA)3	18	ATTTGTGAATGCAAGAGAGTG	GTCATTGTATTCAGCAGTTGG	62-1003	776-979	HMG-Box	TFGMS491	55.5	151	1	M	NSA
PUID16585465	Ca4	45595098	(AGT)4	12	AAAGGTAAGAGTGTTGGAAGC	GTTTCAAACTTGCAAAAACTC	126-2153	1350-1484	WRC	TFGMS492	55.3	150	1	M	NSA
PUID16585466	Ca4	45593163	(ATC)5	15	CTAAGCATTTGTTGTTGGTGT	ACCACCAATCCGACTACTACT	126-2153	1350-1484	WRC	TFGMS493	55.4	154	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585467	Ca4	12176311	(AAC)4	12	CAGATCCATCACACTTCAATC	CCTGTTGGAAATTTCTAGGTT	107-2095	992-2092	GRAS	TFGMS494	55.5	154	1	M	NSA
PUID16585468	Ca6	13246141	(TTGGG)3	15	AGATTTGGATCCATCTTTCAT	TGCTGAGTCTGAATCTGAAGT	178-2199	358-429	ZfCCCH	TFGMS495	55.2	149	1	M	NSA
PUID16585469	Ca6	38815940	(CAA)4	12	GTTGTCATCAACATCATCTCC	GGAACAAAGAAAGAAGGATTC	243-2444	1365-2438	GRAS	TFGMS496	55.3	153	1	M	NSA
PUID16585470	Ca8	2979232	(AAAAT)3	15	AGTTGGGACCATTTATTTTTC	CGTGTGTCCAGTTCTCAGC	209-1852	266-589	Response-reg	TFGMS497	54.9	154	1	M	NSA
PUID16585471	Ca4	48319757	(AAC)4	12	TTCCCATTCAGTCATTTAATC	CTTTCGTCAATTATTTGCAGT	189-1841	504-692	bZIP	TFGMS498	54.2	146	1	M	NSA
PUID16585472	Ca4	48319757	(AATC)3	12	TTCCCATTCAGTCATTTAATC	CAAGTCTTTGTCATCTTTGCT	189-1841	504-692	bZIP	TFGMS499	54.2	146	1	M	NSA
PUID16585473	Ca4	48319757	(ACT)4	12	TTCCCATTCAGTCATTTAATC	CTTTCGTCAATTATTTGCAGT	189-1841	504-692	bZIP	TFGMS500	54.2	146	1	M	NSA
PUID16585474	Ca4	48319615	(TAAA)5	20	AAAGCATGCACTAATCACAGT	CTTTCGTCAATTATTTGCAGT	189-1841	504-692	bZIP	TFGMS501	55.1	139	1	M	NSA
PUID16585475	Ca5	16679503	(ATTTCA)3	18	CCTAAATTCCTCTTCATTTCA	CGAGATCTGGTTGAGAAGAG	280-2460	652-747	ANK	TFGMS502	53.8	147	1	M	NSA
PUID16585476	Ca5	16679458	(TC)9	18	TTTCAATTTCGAAGACGTTAC	CTGATCAATCTGAATGGAAAA	280-2460	652-747	ANK	TFGMS503	54.7	146	1	M	NSA
PUID16585477	Ca3	37101948	(AATTGT)4	24	GGAACAACTCAAGCTCAGTAA	AAAGTGTACACCGAAGCAAT	407-3094	818-1051	SBP	TFGMS504	54.8	164	1	M	NSA
PUID16585478	Ca3	37102110	(CTT)5	15	TTACTCGCACACTTCATAAGC	ATCCTTAGATCAGAGGAACCA	407-3094	818-1051	SBP	TFGMS505	55.8	150	1	M	NSA
PUID16585479	Ca1	4385831	(CAG)4	12	TGATTGCAGGAACTTCATTAT	AAGAAGATGAAGAGGAGTTGG	410-3625	1793-2035	Helicase	TFGMS506	54.9	159	1	M	NSA
PUID16585480	Ca6	17262215	(AAT)4	12	CAGATTTTCCGTCTATCAATG	CCAACAAGAGCTGAACTTTTA	380-5683	515-685	HomeoBox	TFGMS507	54.9	151	1	M	NSA
PUID16585481	Ca7	39769444	(ATTTCA)3	18	TTCTTCCCAATTTCATTTAC	CTTTGGTTGAAATCAGAATGA	324-2393	609-704	ANK	TFGMS508	52.0	172	1	M	NSA
PUID16585482	Ca7	39769443	(TCT)6	18	TCTTCCCAATTTCATTTACA	AACAATGAGATCTGGAACATC	324-2393	609-704	ANK	TFGMS509	53.3	140	1	M	NSA
PUID16585483	Ca5	44152835	(ATCC)3	12	ACATCCATCACACATCACAC	AGAGAGAGAAATTGAGGGAAA	238-2583	1420-1548	Myb DNA binding	TFGMS510	54.7	151	1	M	NSA
PUID16585484	0	0	(AG)10	20	CAGAAAGAAAAATACGAGCTG	CAGAACCCAGTTCTCATGTAA	333-1382	624-701	ZfCCCH	TFGMS511	54.7	136	1	M	NSA
PUID16585485	Ca4	7970786	(TGG)8	24	ATCCGGTAAATCAACATGAAT	CTTGTGAGTATTCGTGTGTTG	333-1382	624-701	ZfCCCH	TFGMS512	55.9	157	1	M	NSA
PUID16585486	Ca5	29397576	(AAG)4	12	TATTTTTCCCCCTTCTGTAAC	CCAAGAACAGAACAAGAAGAA	481-1458	892-987	AP2	TFGMS513	55.0	143	1	M	NSA
PUID16585487	Ca5	29398059	(CTT)5	15	AGTTCTTCCACAAATTCAACC	CCAAGAACAGAACAAGAAGAA	481-1458	892-987	AP2	TFGMS514	55.8	152	1	M	NSA
PUID16585488	Ca5	29399148	(TAT)5	15	TTAGTTTCACAGCTGGTTTTT	GCTCTCTTAATCTTAATTTTAGC	481-1458	892-987	AP2	TFGMS515	54.4	166	1	M	NSA
PUID16585489	Ca5	29397838	(TTTTA)3	15	GGATCGAAAGGATTGTCTATT	TTGTGTGTTGTTGTAAAAATCC	481-1458	892-987	AP2	TFGMS516	54.9	164	1	M	NSA
PUID16585490	Ca6	18445177	(AAATA)3	15	TGAAGTTGCAAAACTTAAGGA	TAATCTACCACGGACCTGTAA	288-1445	1218-1340	bZIP	TFGMS517	55.4	146	1	M	NSA
PUID16585491	Ca2	32544871	(TTC)6	18	TCCTTTTCTTCTTCTTCAACC	CCGTATTGAATGTACCAACAG	216-1943	780-821	ZfCCCH	TFGMS518	55.3	136	1	M	NSA
PUID16585492	Ca4	11573408	(ACC)5	15	ACTATTATGCACCCACTGAAG	TCAGAGAGAATGCAGGAGTT	290-2170	578-832	Myb DNA binding	TFGMS519	54.5	138	1	M	NSA
PUID16585493	Ca4	11573184	(CCA)4	12	TTTCCCTCTTCAAAATTAACC	GCAGAGACGAAGAAGATGATA	290-2170	578-832	Myb DNA binding	TFGMS520	55.2	146	1	M	NSA
PUID16585494	Ca8	3456989	(TCT)5	15	GTAAATCCCTAATGGCTCACT	AGTGAGCCATTAGGGATTTAC	189-2045	1670-1904	Acetytransf	TFGMS521	55.0	149	1	M	NSA
PUID16585495	Ca1	10893797	(AATAA)4	20	CCTTTTTGGGTTCTTATGATT	ATTACACGAAGGATGAATTTG	196-1995	307-1269	EIN3	TFGMS522	55.0	151	1	M	NSA
PUID16585496	Ca3	33153988	(ATTTA)3	15	CTCACGCACATGCTAATATCT	GGAGAAAACATAGTGCTTCAA	177-1844	1131-1325	Sigma70	TFGMS523	55.6	162	1	M	NSA
PUID16585497	Ca6	7098590	(TTTGA)3	15	TGTATAACGACTCAGGTTGCT	TGCAGAAAGTACTTCACCAAT	452-1480	473-873	NAM	TFGMS524	55.1	151	1	M	NSA
PUID16585498	Ca3	38103222	(GTTGTG)3	18	TTCAAGTATCTAGCGATACGG	GAATCGTTTTACTCCCTTTTC	156-596	297-518	Histone	TFGMS525	54.9	168	1	M	NSA
PUID16585499	0	0	(CAGAAT)3	18	AGATTGGTCAAACTAGGGTTC	CCAGAAGACAAAGAACAAGAA	117-1022	260-474	TCP	TFGMS526	54.9	149	1	M	NSA
PUID16585500	0	0	(TAA)6	18	CAATCATCATCTGCTCATTCT	TTCTTCCTCTTCCTTCAACTT	117-1022	260-474	TCP	TFGMS527	55.3	149	1	M	NSA
PUID16585501	Ca3	31369872	(ATTGTT)3	18	ATAGACACTAGGCATGGTTTG	ACGCGATAAGATTTGAGGT	111-677	573-668	NAM	TFGMS528	54.5	141	1	M	NSA
PUID16585502	Ca1	2602547	(TCT)5	15	CAACATGGTAACACTGATCCT	GGGTGAGGAAAAGAAAATCTA	283-720	310-546	SBP	TFGMS529	55.0	165	1	M	NSA
PUID16585503	Ca6	54244146	(CTCACT)3	18	CCTTCTGCTGCTTCTTCTTAT	GAGAAGAGAAAATCCCTTTTG	230-682	236-298	Myb	TFGMS530	55.7	149	1	M	NSA
PUID16585504	Ca3	27639237	(CAG)4	12	TGAGGATAATGCTATTTCAGG	GCCAGTCATAAAACCAGTAAA	192-1121	906-998	bZIP	TFGMS531	54.6	154	1	M	NSA
PUID16585505	Ca4	16650296	(ACTTGC)4	24	TGAACTCGTATCTTCTGCTTC	ATCATGCTTCACAACTTCATC	1-309	95-844	ovate	TFGMS532	54.8	172	1	M	NSA
PUID16585506	Ca1	3651073	(ATG)6	18	GACAAGACCAAATGTCACTTC	CAGAAAGCGTTTCATAATTGA	239-787	413-607	K-Box	TFGMS533	54.6	163	1	M	NSA
PUID16585507	Ca1	3650780	(CAG)4	12	TAACAACCAACTTCTGAGAGC	GGGAATACTTACAAACCCTTC	239-787	413-607	K-Box	TFGMS534	54.8	151	1	M	NSA
PUID16585508	Ca1	15966248	(AAAAGA)3	18	ATCTCTTTCTTCCCCACTAAA	CATCAAAGCGTAATCAAAAAG	170-856	377-526	HLH	TFGMS535	54.7	195	1	M	NSA
PUID16585509	Ca2	23025109	(AGAA)3	12	GCCACACCATTCTAATCACTA	ATCACACAACACTGAAAGCTC	73-732	301-576	K-Box	TFGMS536	55.3	158	1	M	NSA
PUID16585510	Ca7	33300264	(TTTCT)3	15	GTTCCCCTCCTGAACTACTAC	CCCTAGAGAAAACCAAGTCAT	233-934	536-640	Tify	TFGMS537	54.5	155	1	M	NSA
PUID16585511	Ca1	41981704	(ATG)4	12	AAGTACCCATTTTGATAAACG	ATATTTACAAAGCGTGCTCGT	98-703	161-259	AP2	TFGMS538	53.7	139	1	M	NSA
PUID16585512	Ca6	4566075	(TTC)5	15	ACAACTTACTGTCGTTGGAAA	ATTTCAAATCCTTCGTGAAAC	397-912	421-636	PC4	TFGMS539	55.0	147	1	M	NSA
PUID16585513	Ca6	24448166	(ACT)4	12	CTTTTGAACAGAGGAATTGAC	TGTTGTTGATGAAGGAATTGT	183-1043	381-518	Myb DNA binding	TFGMS540	54.1	150	1	M	NSA
PUID16585514	Ca6	24448036	(ATC)6	18	CAATTCCTTCATCAACAACAC	TGATCTTCCCATCTTATTTCA	183-1043	381-518	Myb DNA binding	TFGMS541	55.6	154	1	M	NSA
PUID16585515	Ca6	24448166	(ATTCTC)3	18	CTTTTGAACAGAGGAATTGAC	TGGTAATCTTCCAGCTATCAA	183-1043	381-518	Myb DNA binding	TFGMS542	54.1	150	1	M	NSA
PUID16585516	Ca5	42499312	(AG)6	12	ATGGTTTTGCTCACATTCTTA	AACTCACACAGAACACTGCTT	220-951	496-747	K-Box	TFGMS543	55.0	151	1	M	NSA
PUID16585517	Ca5	42504567	(ATGTA)3	15	GGTATGAAGCATGCATAAAGA	TCTCAATTCTCTTCAATTCCA	220-951	496-747	K-Box	TFGMS544	55.5	160	1	M	NSA
PUID16585518	Ca2	14595057	(CTTG)4	16	CCAACAAACAACACTTCAAAC	TGAACTCAGAATTTGGATGAT	260-958	482-652	CBFD-NFYB	TFGMS545	55.7	162	1	M	NSA
PUID16585519	Ca8	4876424	(CAT)4	12	ATGCCATTGAAGTAATGTGTC	AGTCGACCCAAGTAATAGCTC	155-808	482-631	HomeoBox	TFGMS546	55.1	150	1	M	NSA
PUID16585520	Ca6	27827123	(TCA)5	15	CATGACAGTGGTGAGAAAAGT	GATTTTTCGATGTCTCTTTCC	31-612	313-522	Histone	TFGMS547	55.2	147	1	M	NSA
PUID16585521	Ca8	2014051	(CCTCAA)3	18	CTACCGTGCTTTTCTTCATAA	GCCTTCACTTGTCTGTTATTG	205-1065	886-1005	HomeoBox	TFGMS548	54.9	176	1	M	NSA
PUID16585522	Ca1	15606739	(CAC)4	12	GCGACTCAACGATTCTTCT	GATTCATCTTCCTCCCTCAT	203-1003	425-598	WRKY	TFGMS549	55.5	142	1	M	NSA
PUID16585523	Ca3	81453	(AATG)3	12	CATCCCTCTTTTTTATTCAACA	CCAGCAAAGTAAAGAACTCAA	203-922	506-886	NAM	TFGMS550	54.5	151	1	M	NSA
PUID16585524	Ca3	81453	(ACTC)3	12	CATCCCTCTTTTTTATTCAACA	CTAAAAATGGAGGAGGAAGAG	203-922	506-886	NAM	TFGMS551	54.5	151	1	M	NSA
PUID16585525	Ca2	31677179	(GAA)6	18	AAGAGTGAAGTGTGGTTTCCT	CCAAATGTGTCGTTTTATTCT	203-922	506-886	NAM	TFGMS552	55.5	148	1	M	NSA
PUID16585526	Ca3	80260	(TTCATT)4	24	AATGAGCTACTGCTGTCTTCA	AAGGAAACCACACTTCACTCT	203-922	506-886	NAM	TFGMS553	55.4	157	1	M	NSA
PUID16585527	Ca3	80320	(TTTGAG)4	24	ATTCCACTTGTTGCTGATAAA	TAAAAGCGAAGGGTTGAGTAT	203-922	506-886	NAM	TFGMS554	55.0	151	1	M	NSA
PUID16585528	0	0	(TGT)5	15	TCTTCATCGCTATCTTCAAAC	AAGAGCCACAGAGAGTAAACC	453-803	129-320	bZIP	TFGMS555	54.8	162	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585529	Ca4	41989223	(AG)6	12	TTTTTCTTCTCACTTCGATCA	TAGAAACGAAAGCTGAAAAGC	343-747	439-651	Histone	TFGMS556	55.2	127	1	M	NSA
PUID16585530	Ca3	9395043	(TTG)5	15	CTAGCTTGGTGGATGATGA	CAACAAAGTGGTTGTGTTTCT	4-606	370-468	AP2	TFGMS557	54.5	156	1	M	NSA
PUID16585531	Ca5	28183450	(ATA)11	33	TTGAGCACAAAGTTTCCTCT	TCCCTTCAATAGGTAAATTCC	304-786	502-609	ACT	TFGMS558	55.2	151	1	M	NSA
PUID16585532	Ca5	19048743	(CAC)4	12	CTTATGACATGAGGAAGCAAC	ATTTCTCTCACAATCAAATGG	149-715	290-535	Acetytransf	TFGMS559	55.0	150	1	M	NSA
PUID16585533	0	0	(ATC)4	12	TCATCATGATCTTCAATTTCC	AAAGTTCCAAAGGTCAATCTC	158-1443	203-589	NAM	TFGMS560	55.0	148	1	M	NSA
PUID16585534	0	0	(CAT)4	12	TAATGGGTACCATGCAATTAT	GAAGCAACAAGTCTATCCAAA	158-1443	203-589	NAM	TFGMS561	54.6	150	1	M	NSA
PUID16585535	Ca4	7121052	(AGT)5	15	GTGGTGCAACGATAGTAACTC	CAAAAAGCTGTGAAAAATAGC	231-683	534-644	WRKY	TFGMS562	54.9	156	1	M	NSA
PUID16585536	Ca6	53652536	(CAA)7	21	TCAACTGTTCAACAACATCCT	GAGGAGGAGCACAAGAACTAT	60-1295	1095-1232	HLH	TFGMS563	55.6	163	1	M	NSA
PUID16585537	0	0	(TGG)5	15	ATAGCACTGCACTGTCTCTTC	ACTCCTTCAACTTCAAACACA	735-1502	843-1256	whirly	TFGMS564	54.8	148	1	M	NSA
PUID16585538	Ca5	10990120	(TGA)6	18	CTTTATCATGTTCACCAGAGG	TAATCTCTTCTTCCACCCTTT	1234-2835	2269-2577	FAR1	TFGMS565	54.8	156	1	M	NSA
PUID16585539	Ca8	502255	(CAAG)3	12	AAATTCCTAAAACAGCAGGAT	ACTAGCTGAACTGCCTTCTTC	77-1834	692-919	FHA	TFGMS566	54.8	149	1	M	NSA
PUID16585540	Ca1	13755937	(AGAA)3	12	AAATTGAACCTGAACAACGTA	ATCCTTACATTCCTCTGCTGT	2791-6567	5737-6108	SET	TFGMS567	54.9	148	1	M	NSA
PUID16585541	Ca1	13754931	(TCT)5	15	TACGCTTTTATCTCCGATCTA	TCGAGATTAGAAAACCCTAGC	2791-6567	5737-6108	SET	TFGMS568	54.6	149	1	M	NSA
PUID16585542	Ca4	36799412	(AGGG)3	12	AGGGATAGGGTTAGGGATAGT	CCCTATCCCTACTATCCCTAA	118-948	154-234	ZfCCCH	TFGMS569	54.9	145	1	M	NSA
PUID16585543	Ca4	36800180	(ATCCG)3	15	ACAAACAAATAGACCTCCACA	GCCGATCTTAAAGTAGAATGG	118-948	154-234	ZfCCCH	TFGMS570	54.7	152	1	M	NSA
PUID16585544	Ca4	36799529	(GATAGG)3	18	AGTCGGAGCAGGAGTAATAGT	CAAGAAAACATCACAGCTTCT	118-948	154-234	ZfCCCH	TFGMS571	54.9	148	1	M	NSA
PUID16585545	Ca7	37049869	(CAG)5	15	CTGAACCAATTGAAGTTGAAG	AAGAAAAACCTAGCTCCAAAA	148-780	457-627	LIM	TFGMS572	55.0	155	1	M	NSA
PUID16585546	Ca5	7675124	(ATTA)3	12	CTCGTAATTTCTTCAATCCAA	GGGCTAATGAGCATTAATAGA	64-759	283-576	K-Box	TFGMS573	54.7	158	1	M	NSA
PUID16585547	0	0	(AG)8	16	GAAGTTTGTGAAGGAGTTGAA	TCTCTCTCTCTCTCTCTCTCTCA	484-1650	1392-1536	Myb DNA binding	TFGMS574	54.6	146	1	M	NSA
PUID16585548	Ca6	17342710	(AAC)4	12	TTCCACTCTCAACTAAAATGG	ATCTTTGATGGGAAGAGTGTT	38-454	134-337	FHA	TFGMS575	54.6	161	1	M	NSA
PUID16585549	Ca7	32855092	(TGT)5	15	TGAAGTGGTTTCTGAGTTGTT	TACTGTGAAAGACACATGCAC	125-1216	854-1030	WRC	TFGMS576	54.9	151	1	M	NSA
PUID16585550	Ca8	3998720	(AAAT)3	12	AATGCCAAAATTTCTTCTGT	TTGATGCTCTTCAAGCTACTC	308-811	605-754	AP2	TFGMS577	54.1	151	1	M	NSA
PUID16585551	Ca8	3998446	(ATG)4	12	CAGGAATCTTGTTCAAGTCAA	ACATAACAACAAACCCTTTCA	308-811	605-754	AP2	TFGMS578	55.4	165	1	M	NSA
PUID16585552	Ca8	3998448	(TGGTTA)3	18	TTCAGGAATCTTGTTCAAGTC	TGACAAACTTAATGGGAGAGA	308-811	605-754	AP2	TFGMS579	54.5	143	1	M	NSA
PUID16585553	Ca7	31541951	(CAA)4	12	GAAATGGGTTTTATGGCTTAT	CACCTTCAAAATCACTCAGTC	159-794	582-752	Zf-Dof	TFGMS580	55.0	142	1	M	NSA
PUID16585554	Ca4	4747167	(TTA)5	15	GTCGACACAGAATTAGGAAGA	GATGATGATTCTCTTCAACCA	567-1703	1047-1202	Myb DNA binding	TFGMS581	54.5	155	1	M	NSA
PUID16585555	Ca6	42716986	(ATT)4	12	ACCTCTTGTTTTCTTTCTTGC	TTTGTAAAAGGGTAGCTAGGG	185-459	404-459	Zf-Dof	TFGMS582	55.4	149	1	M	NSA
PUID16585556	Ca6	42716798	(CAC)4	12	CCATACCAACTGCTTATCTTG	ACTTCCTCCATTAGGTTGAGA	185-459	404-459	Zf-Dof	TFGMS583	55.0	146	1	M	NSA
PUID16585557	Ca2	4036194	(TGA)7	21	GGCTCTTGATACCCTTACAAT	CATCATCATGTTAATGCAATG	22-1077	742-951	TCP	TFGMS584	55.0	160	1	M	NSA
PUID16585558	Ca6	1609146	(TCATTT)3	18	CCTTCCTTTTCAACCTCTATT	CCATAAGGATGATGGAAACTT	257-1725	1106-1725	DUF3633	TFGMS585	54.4	153	1	M	NSA
PUID16585559	Ca6	1609208	(TTCTCT)3	18	TACCTCCACATCATTTTCATT	TATATGCAAGGGTGAGAAAGA	257-1725	1106-1725	DUF3633	TFGMS586	54.6	134	1	M	NSA
PUID16585560	Ca6	21497375	(AAT)5	15	ATTGCTCAAGTTGTCAATGAT	TGTATTGCAGCTTCCTAACTC	294-1139	468-578	bZIP	TFGMS587	54.8	148	1	M	NSA
PUID16585561	0	0	(ACAT)3	12	CAAGCTTCGTTAGTGAAGAGA	CTCCACTGAGTCCAATAACTG	231-1772	1050-1262	Sigma70	TFGMS588	55.1	157	1	M	NSA
PUID16585562	Ca5	30587088	(CTT)6	18	TCTTTATCTTCTGCAAAACCA	CAAGAGCAAGAACAAGAAGAG	332-4186	2864-3088	SWIB	TFGMS589	55.3	149	1	M	NSA
PUID16585563	Ca5	30587245	(CTTCTC)4	24	TTTCATCGTCTACTTGATGGT	CAAGAGCAAGAACAAGAAGAG	332-4186	2864-3088	SWIB	TFGMS590	54.8	157	1	M	NSA
PUID16585564	Ca5	30587245	(TTCTCC)3	18	TTTCATCGTCTACTTGATGGT	TTGATGGTAGAGCAAGAACAT	332-4186	2864-3088	SWIB	TFGMS591	54.8	157	1	M	NSA
PUID16585565	Ca5	30597169	(AAGA)3	12	GCTGATCAGTTGTGGTAGAAG	CGACTTGAATCTCTCCTGTAA	84-709	282-635	PTZ00368	TFGMS592	55.0	161	1	M	NSA
PUID16585566	Ca1	6750597	(TC)8	16	TACCCAGATGAGATCTACGAA	GGATGGTATCACTGTTTGTGT	220-1209	904-1059	Myb DNA binding	TFGMS593	54.9	152	1	M	NSA
PUID16585567	Ca1	6750597	(TCT)6	18	TACCCAGATGAGATCTACGAA	GGATGGTATCACTGTTTGTGT	220-1209	904-1059	Myb DNA binding	TFGMS594	54.9	152	1	M	NSA
PUID16585568	Ca1	6738406	(TGGTGT)3	18	TAGTTTATTGGGTTTTCACCA	GATCAGCAGTCAAAACAAGAC	58-966	187-342	Myb DNA binding	TFGMS595	54.9	163	1	M	NSA
PUID16585569	Ca7	8420056	(AAC)4	12	AGGTCCAAAGAAAAGTGAACTA	CATTGTTTTCTTCCTCCTCTT	140-952	242-577	Response-reg	TFGMS596	54.9	152	1	M	NSA
PUID16585570	Ca5	21386462	(ATG)5	15	TATGTCAATCGGAAACAACTT	CTGTTCGTCGATCACTAATTC	140-952	242-577	Response-reg	TFGMS597	54.8	148	1	M	NSA
PUID16585571	0	0	(CAC)5	15	CCCGTCTCCTCCGCCATA	CATCATTAGTGTCCGTAGGTT	223-801	223-304	tify	TFGMS598	64.5	169	1	M	NSA
PUID16585572	Ca3	23622409	(AAC)6	18	CCAAATTAGCTCAAACACAAG	TGAAGAGAGATTTTCAACTGG	9-683	297-470	WRKY	TFGMS599	55.2	152	1	M	NSA
PUID16585573	Ca2	4036035	(TCA)7	21	CAACCAAAAAGACAAGAATGA	GGCTCTTGATACCCTTACAAT	51-836	177-380	TCP	TFGMS600	55.5	160	1	M	NSA
PUID16585574	Ca8	3997874	(AAG)4	12	ACATAACAACAAACCCTTTCA	CAGGAATCTTGTTCAAGTCAA	181-684	238-387	AP2	TFGMS601	54.8	154	1	M	NSA
PUID16585575	Ca8	3997837	(AG)9	18	TGACAAACTTAATGGGAGAGA	CACCTTCCATCTTCTTCTTCT	181-684	238-387	AP2	TFGMS602	55.0	154	1	M	NSA
PUID16585576	Ca8	3998306	(CATAAC)3	18	TTGATGCTCTTCAAGCTACTC	CACCTTCCATCTTCTTCTTCT	181-684	238-387	AP2	TFGMS603	55.0	143	1	M	NSA
PUID16585577	Ca5	11382482	(ATT)5	15	TGCATACTTTCAAAAGCAGTT	CCTCATTCATCATAAGAGCAG	159-1967	936-1121	RRM	TFGMS604	55.4	149	1	M	NSA
PUID16585578	Ca8	8639326	(AGA)4	12	TGAGATTGGTGTAAAGAAAGG	AATTTGTCCACCTTAGCCTAC	57-220	57-167	Myb DNA binding	TFGMS605	54.6	155	1	M	NSA
PUID16585579	Ca5	29821891	(TATGC)3	15	ACGGAAAGTGTGGTTAATTTT	CACCAACACTCACTACCTAGC	1-02522	9-218	Myb DNA binding	TFGMS606	55.4	169	1	M	NSA
PUID16585580	Ca4	38422591	(AGA)4	12	TTGAGAAGCACTCAAAGAAAG	CAACACGGAATATACGTTCTC	198-974	501-761	YTH1	TFGMS607	55.1	132	1	M	NSA
PUID16585581	Ca4	4988759	(TAT)6	18	AGGTCGAGGCTAGTATAGGAA	TCATTTCTTGTCCCTAATGAA	19-261	19-258	AUX-IAA	TFGMS608	55.0	153	1	M	NSA
PUID16585582	Ca3	31212701	(ATC)4	12	TGATATGAGAGGTTCTTCAGC	ACTTGTTGTTTACCAAGCTCA	13-351	58-159	AP2	TFGMS609	54.6	150	1	M	NSA
PUID16585583	Ca5	166458	(AATCCA)5	30	ATTCAGCAGTTAGTTCCAACA	TTCTTCTTCAGTTGGATGAAA	23-1294	194-571	NAM	TFGMS610	55.1	147	3	P	NSA
PUID16585584	Ca1	390511	(CAA)5	15	GAAGTAAGCAAGTAGGCTTCC	AAGGTGTTGTTGATGAGAATG	41-1297	380-691	TCP family transcription factor	TFGMS611	55.1	157	3	P	NSA
PUID16585585	Ca4	43891008	(AATTAA)4	24	AATGAATTGGTTTGTTCTGTG	CGCAATTAAGAACTTCCATTA	660-1991	725-845	HomeoBox	TFGMS612	55.2	148	3	P	NSA
PUID16585586	Ca1	389670	(GGC)4	12	AATAACAACAACGAAAGTGGT	GTTTGAAGAAGGTTGTTGGAT	41-1297	380-691	TCP	TFGMS613	54.0	148	4	P	NSA
PUID16585587	Ca1	389726	(TTC)4	12	ATCCAAACGAGAATTACATGA	TTCACCTTCACCCATAGTATC	41-1297	380-691	TCP family transcription factor	TFGMS614	54.7	152	3	P	NSA
PUID16585588	Ca3	21366252	(TCC)6	18	CCTTAGCTTTGACAATTCCTT	CAGAGAGGTAATCATTGTTGG	148-660	175-324	WRKY	TFGMS615	55.4	155	3	P	NSA
PUID16585589	Ca5	166695	(TCAC)3	12	CAAACCCCTCCTTCAAGTAA	GCATCAGCAAAGTAGACAAAT	23-1294	194-571	NAM	TFGMS616	56.8	152	4	P	NSA
PUID16585590	Ca5	166052	(TCCC)3	12	CGAGTATACAAGAGAGCAGGA	AGCTGCCTTATTAGAGTGTCC	23-1294	194-571	No apical meristem (NAM)	TFGMS617	55.4	147	3	P	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585591	Ca8	5196786	(GAA)4	12	GTTATGGTGTGAATTTTGAGG	TAGATCTCACACACACAATGG	32-766	332-493	Zf-HD	TFGMS618	54.7	143	3	P	NSA
PUID16585592	Ca2	30868340	(CAG)7	21	TTGGTTAAGGATGTTCCTTCT	ACCGTAGTCTGAGGAAGAAAG	240-2327	432-623	ANK	TFGMS619	55.5	154	3	P	NSA
PUID16585593	0	0	(ATTCT)4	20	GGGTCATCATCAAAACCA	AGTTCTGAAGTCATGGTAGGG	137-733	275-421	TCP	TFGMS620	54.9	147	2	P	NSA
PUID16585594	Ca4	22196748	(TTG)9	27	CAGGAGTTGAAACTGAAACAC	CCATTGTCCTTAGCTTAAAAA	1-1302	853-1101	Myb DNA binding	TFGMS621	54.9	155	3	P	NSA
PUID16585595	Ca7	19831349	(CT)18	36	ACCGCCTCAATTTCTTCTTA	TAATTTCACGGACAGTGTCTT	191-838	345-610	PLAT2	TFGMS622	56.6	148	4	P	NSA
PUID16585596	Ca6	466443	(CAA)7	21	CAAGCTCACACTGAACTCTCT	GTTGTTGAGTTGTGGTGATTT	779-1438	896-1051	Myb DNA binding	TFGMS623	54.8	146	3	P	NSA
PUID16585597	Ca5	47725906	(TGT)7	21	ATATTTTTGTTGTTGGTGTCG	GCACAGGTGAAGCATAGTAGT	105-2279	918-1322	POX	TFGMS624	55.2	155	4	P	NSA
PUID16585598	Ca3	16813885	(ATTCAT)6	36	CCTTTCATTCATCACTTCAAC	AGGATAAAGGTGAAGCAAATC	300-967	1392-1535	HLH	TFGMS625	54.8	165	5	P	NSA
PUID16585599	0	0	(AT)16	32	TTGTCACCATTATCTCCACTC	CCAATATCTATTCATCTTCACCT	295-1413	637-909	Thioredoxine	TFGMS626	55.1	144	4	P	NSA
PUID16585600	Ca7	20120406	(GAA)8	24	AACATCATCATCAAGTTGGAG	GGTTGTGCTGGAAATAACTC	128-840	677-832	Myb DNA binding	TFGMS627	55.1	154	3	P	NSA
PUID16585601	Ca1	7416772	(CAT)4	12	ATCAAACAAAAGACCAGTTGA	GTTTTGCATATCTACCAGCAG	30-2006	1-564	START	TFGMS628	54.9	147	5	P	NSA
PUID16585602	Ca7	17774538	(AAAAAC)3	18	GGTGTTGAAAACAAAGAAAAC	TCCTTATGTTGCAATGTATCC	428-1636	1043-1531	MFMR	TFGMS629	54.0	141	4	P	NSA
PUID16585603	Ca1	26033416	(AT)6	12	GGCTTACTATCTTGCCAATG	GGAAGAGTGAAAGTCTTGGTT	253-3357	2689-3213	SBP	TFGMS630	55.1	150	4	P	NSA
PUID16585604	Ca3	38689024	(TCA)6	18	AACACTTGAACATTTCAAACC	CAAGTTCCTTCTTCTTCTTCC	58-1188	258-976	Myb	TFGMS631	54.3	153	3	P	NSA
PUID16585605	Ca4	1123733	(ACA)8	24	TAAGGGCAGCTTTTGAGGAA	TGGTGATGAAGATGAAGAGGAA	29-736	171-510	DUF640	TFGMS632	60.0	250	4	P	NSA
PUID16585606	Ca4	7122162	(GT)6	12	GAAGAATCAACAACATCCTCA	CAAAAAGCTGTGAAAAATAGC	724-1293	732-810	WRKY	TFGMS633	55.2	161	6	P	NSA
PUID16585607	0	0	(ATTTT)3	15	CGAAGACAACATTTTTATTAGG	AATGATCAACTACCCATTGTG	573-1883	1401-1847	bHLH MYC	TFGMS634	53.6	151	3	P	NSA
PUID16585608	0	0	(TTC)4	12	CATAGCCTTCATCTCATTCAT	ATGAATGAGATGAAGGCTATG	224-2434	230-1321	GRAS	TFGMS635	54.4	146	3	P	NSA
PUID16585609	0	0	(TCAC)4	16	CAAACCCAAACGCAAACA	CACGAAAACCAGTATCTTCAG	186-1187	604-713	tify	TFGMS636	59.1	151	3	P	NSA
PUID16585610	Ca1	27450034	(ATT)4	12	TCTACAGACACAAAAGGGGTA	TTATGATGAGTGTGTTGGTGA	589-1512	895-1320	DUF702	TFGMS637	54.9	150	3	P	NSA
PUID16585611	Ca6	5237688	(CAA)5	15	TGTTCCTTCTTCATCTTCAAA	TGATCTATTTTCTTGCCACAT	49-1863	1177-1296	HOX	TFGMS638	55.1	151	2	P	NSA
PUID16585612	Ca4	5082391	(TCA)4	12	TTCATAACTCCAAGAACCTCA	CTTTGTCACCAATAAATCGTC	135-1787	1365-1622	Myb DNA binding	TFGMS639	55.0	149	3	P	NSA
PUID16585613	Ca4	5018179	(ATA)4	12	TGTATCTCACCCAAAAGAAGA	TAATCTTGAACGCTCATTTGT	307-1599	336-716	bZIP	TFGMS640	55.0	143	3	P	NSA
PUID16585614	Ca7	11430566	(CAT)6	18	TGTTTAGGCTAGTCAATTTTCA	TCTTGTTGTTGTTGTTGTTGA	6-983	429-974	GRAS	TFGMS641	54.5	166	4	P	NSA
PUID16585615	Ca5	32787926	(ATA)4	12	GAAACAAATCCAAGTCAAGAA	GTTGAAACTTTGAGGAACTTG	502-1095	609-735	HLH	TFGMS642	54.5	147	3	P	NSA
PUID16585616	Ca6	24448740	(TC)6	12	ACCAACTCACATCTAGAAGCA	TGTTGTTGATGAAGGAATTGT	183-1043	381-518	Myb DNA binding	TFGMS643	55.0	157	4	P	NSA
PUID16585617	Ca4	16278898	(ACTACC)3	18	GTCTTGGTGTTCTTGCTTTC	ATGAAACAAGTGAAGAGGTGA	1-1145	333-467	CCT	TFGMS644	55.0	152	3	P	NSA
PUID16585618	Ca1	389670	(GGC)4	12	AATAACAACAACGAAAGTGGT	AAGATGAAGAAGAAGCTCCAC	41-1297	380-691	TCP family transcription factor	TFGMS645	54.0	148	3	P	NSA
PUID16585619	Ca1	390303	(TCT)5	15	ATCCAACAACCTTCTTCAAAC	AAGATGAAGAAGAAGCTCCAC	41-1297	380-691	TCP	TFGMS646	55.8	140	3	P	NSA
PUID16585620	Ca5	166287	(CAA)5	15	TGACAACAGTTCTTGGTCTTT	GGGAGAGGGAGTAACAAAGTA	23-1294	194-571	No apical meristem (NAM)	TFGMS647	55.1	154	2	P	NSA
PUID16585621	Ca5	166695	(TCAC)3	12	CAAACCCCTCCTTCAAGTAA	GGAATAATGAGAGTGACAAGC	23-1294	194-571	No apical meristem (NAM)	TFGMS648	56.8	152	4	P	NSA
PUID16585622	0	0	(AAAT)3	12	CCTTGTTTCGCCTTCTATTAT	CATAAGCATGGGTTTTTACAT	238-618	312-459	HMG- BOX	TFGMS649	55.4	149	2	P	NSA
PUID16585623	Ca4	7706345	(AGG)4	12	CAAGAACAGAGATAGCCTTGA	TAAATCAAGCTCTTCCCACCT	1070-3409	1435-1669	SBP	TFGMS650	54.9	144	3	P	NSA
PUID16585624	Ca5	30587088	(CTT)6	18	TCTTTATCTTCTGCAAAACCA	CAAGAGCAAGAACAAGAAGAG	333-4583	1497-1719	SWIB	TFGMS651	55.3	149	3	P	NSA
PUID16585625	Ca5	30587245	(TTCTCC)3	18	TTTCATCGTCTACTTGATGGT	TTGATGGTAGAGCAAGAACAT	333-4583	1497-1719	SWIB	TFGMS652	54.8	157	2	P	NSA
PUID16585626	Ca5	30587088	(CTT)6	18	TCTTTATCTTCTGCAAAACCA	CAAGAGCAAGAACAAGAAGAG	332-4186	1101-1323	SWIB	TFGMS653	55.3	149	3	P	NSA
PUID16585627	Ca5	30587245	(CTTCTC)4	24	TTTCATCGTCTACTTGATGGT	CAAGAGCAAGAACAAGAAGAG	332-4186	1101-1323	SWIB	TFGMS654	54.8	157	6	P	NSA
PUID16585628	Ca5	30587245	(TTCTCC)3	18	TTTCATCGTCTACTTGATGGT	TTGATGGTAGAGCAAGAACAT	332-4186	1101-1323	SWIB	TFGMS655	54.8	157	2	P	NSA
PUID16585629	0	0	(AG)6	12	TGTGAGTGAATGAAAGAAACA	TCAGACATAGTAGCCCAAGAA	406-1812	1429-1614	RPM	TFGMS656	54.3	151	4	P	NSA
PUID16585630	Ca4	30317401	(CTT)4	12	CACTTTCTCCATTCTCAACTG	TCCTGCCTTTTCTTCTTTAGT	900-2052	1779-2048	SNF2	TFGMS657	55.0	143	2	P	NSA
PUID16585631	Ca4	35417258	(CCATT)4	20	TTCATTTAGCTTGAAGCACTC	CCTTCCTGGACATCTTAATTT	1046-1738	1478-1642	TCP	TFGMS658	55.0	150	4	P	NSA
PUID16585632	0	0	(CT)10	20	AAGACCGTTGCTCATTACC	TTTCAACTTTTTCACCATCAG	3100-6000	229-1128	Amino oxidase	TFGMS659	55.2	151	6	P	NSA
PUID16585633	Ca7	32855952	(TTTGAT)6	36	CAAGAAGGTGAAGTTAAAGCA	ATTCAACCTCACAGTTTCAGA	145-1233	874-1008	WRC	TFGMS660	55.0	155	4	P	NSA
PUID16585634	0	0	(TAT)4	12	GCCAGACGAATTTAAAGTACC	TATAACTGTGAGGTTCCCATT	13-2676	2274-2591	SET	TFGMS661	55.7	156	3	P	NSA
PUID16585635	Ca4	40578103	(TGG)4	12	ATAGTTCACAAACTGGTGGAG	CACCAAAACCAAAATTAACAC	4225-4545	4957-5257	Jmjc	TFGMS662	54.3	147	3	P	NSA
PUID16585636	Ca6	27673714	(GTT)4	12	CAGAATAGGTGTTGATGGAAA	AAGTTGAAGGGGACAAACTAC	65-1474	956-1204	Auxin_resp	TFGMS663	55.2	138	4	P	NSA
PUID16585637	0	0	(CT)7	14	GTTTCAGGGAACATCGTTT	GTTCTGCGCAGTAAAAGAGTA	325-1467	505-753	SWIRM	TFGMS664	55.0	121	4	P	NSA
PUID16585638	Ca5	23874393	(AG)13	26	TACAAAAGAATCAAACCCAAG	TTTCTTCCACAATTCTCGTTA	357-1349	819-1136	BTB	TFGMS665	54.6	165	6	P	NSA
PUID16585639	Ca5	23874598	(TC)13	26	ACCTTCCAACAAATACTCTCC	CAAGTAAGGAACAAGAAAAGAAA	229-753	442-750	BTB	TFGMS666	54.9	157	4	P	NSA
PUID16585640	Ca7	5352233	(CT)8	16	AACGTGTGAATGAAGGAACTA	GGGAGAGAAGAGAAGAGAGAA	597-2036	1059-1139	ZfCCCH	TFGMS667	54.9	154	3	P	NSA
PUID16585641	Ca3	37789311	(GAA)5	15	TACATGTTCAGCACAGCTAGA	TCTTCTTCTTCGTCCTCTTCT	1804-3588	3277-3414	PHD	TFGMS668	54.7	150	2	P	NSA
PUID16585642	Ca2	15303660	(GAA)6	18	AGAAGAGGACGAAGAAGAAGA	CCAAATTCTAAATTCCAAACC	1804-3588	3277-3414	PHD	TFGMS669	55.1	138	3	P	NSA
PUID16585643	Ca3	37789311	(GAC)4	12	TACATGTTCAGCACAGCTAGA	AGGTACAAAGAAAGTGCAACA	1804-3588	3277-3414	PHD	TFGMS670	54.7	150	2	P	NSA
PUID16585644	Ca4	43891170	(AGA)8	24	GTTTATGGTGTTGAAGGTTGA	TACTCTACGCTTCTTCCCTCT	660-1991	725-845	HomeoBox	TFGMS671	55.2	149	2	P	NSA
PUID16585645	Ca5	45306950	(ATG)4	12	TATAAACCACGCAAGTATTCG	GTACCCATCAAATCAACTTCA	213-1883	942-1172	PWWP	TFGMS672	55.6	146	2	P	NSA
PUID16585646	Ca8	8364902	(CTA)7	21	CACAAGGGTTTATGATAGTGC	CCATGATAAGAAGACAACCTG	125-2557	989-1666	START	TFGMS673	54.9	150	4	P	NSA
PUID16585647	Ca6	37387965	(GAA)6	18	TGTTCTGAATTCTGTTTCAGG	ACCCAACAATAAAGAACACAA	1-1215	1098-1215	DNA bind	TFGMS674	55.4	150	4	P	NSA
PUID16585648	Ca6	3867508	(AAAGAG)5	30	GATGCACATCATCTTCTTCTG	TCCACTTCCACCTATTTTATG	95-1465	233-679	NAM	TFGMS675	55.8	147	3	P	NSA
PUID16585649	Ca4	42357099	(TGA)4	12	AAATTGAGCATGAATGGTATG	CCTCTCACTATAACCCAACAA	14-1012	395-631	DOG1	TFGMS676	55.2	173	4	P	NSA
PUID16585650	Ca5	30989819	(TTC)4	12	GATACGAGCAACTAACCACAC	CTCTTTGAAGAGGAAAAGTGG	380-1585	686-943	ARID	TFGMS677	54.9	166	2	P	NSA
PUID16585651	Ca7	4875496	(CGTAA)4	20	GAATGTTGTTGATAGGTTGGA	TGATTGATGGAATAAGGAGAG	74-2470	1994-2305	BTB	TFGMS678	55.1	142	3	P	NSA
PUID16585652	Ca5	38288717	(AAC)7	21	TGAACAACGTTTCTTCTCTTC	GTTTTGGAACTGAAATCAACA	763-1605	1048-1176	HLH	TFGMS679	54.7	148	3	P	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585653	Ca2	3451762	(CACAAA)4	24	GGAGGTTATAACAACACCAAC	AAATAGTCATGCAACTCAAGC	1700-2668	1931-2113	Zf-HD	TFGMS680	53.7	150	2	P	NSA
PUID16585654	Ca5	27757413	(CCT)4	12	AAGTAAACCACACGAGTTCCT	TATGAAGCTTTCAACATCAGG	332-2893	2198-2506	B3	TFGMS681	55.5	144	3	P	NSA
PUID16585655	0	0	(AG)8	16	ACTTACTGCAAAAGAGCAACA	AGAAAGACCTTGTCCTTCAAC	1827-4139	3456-3575	HomeoBox	TFGMS682	55.5	147	2	P	NSA
PUID16585656	Ca6	13476735	(ACA)4	12	GTTTGAACATAGGGAACTCCT	GTTGTTCATGTAGTTGGTGGT	351-3140	750-890	HLH	TFGMS683	54.9	150	2	P	NSA
PUID16585657	Ca7	11287223	(CAA)4	12	ATCACAGAAACAATGCCTTTA	TTTGACCCTTCTAACAACAAA	0008-1972	947-1126	AP2	TFGMS684	55.0	149	3	P	NSA
PUID16585658	Ca6	42715963	(GGA)7	21	TTTTGGAGGAGGAGATATAGG	TTCCAAACCACTTGAAGATAA	35-828	251-433	zf-dof	TFGMS685	55.1	136	3	P	NSA
PUID16585659	Ca7	2334917	(TTC)7	21	AATGGAAGTGGAAGTAGTGGT	TGGACCAGTAATCTGAAGAAG	227-1168	251-454	AP2	TFGMS686	55.3	139	3	P	NSA
PUID16585660	Ca6	27650321	(CCA)4	12	CCATTGGTATTAGGGTATTCA	GGTCGTAGATTGAAAGAGGTT	580-3216	2719-2872	PHD	TFGMS687	54.2	149	3	P	NSA
PUID16585661	Ca3	39818017	(AAGA)6	24	ACTTCAGTGCTGTTTGATTTG	CCATCATATCTACCTCCTCCT	479-1678	764-1003	B3	TFGMS688	55.6	155	2	P	NSA
PUID16585662	Ca3	39817380	(ACTCAC)3	18	TAAGGAGAAGAAATTGGAAGC	CAAGTCTGTTCAGTTTCCCTA	479-1678	764-1003	B3	TFGMS689	55.4	158	3	P	NSA
PUID16585663	Ca3	39817471	(TATCAA)4	24	CCAAGGTCTAACTCACACTCA	TTCTTCTTCTTCTTCCTCCTC	479-1678	764-1003	B3	TFGMS690	55.4	134	2	P	NSA
PUID16585664	0	0	(TGAATT)4	24	AAACTGTTCTTGTTGTTGTGG	GGCATTACAATTGTTTCTTCA	224-2434	230-1321	GRAS	TFGMS691	55.3	144	2	P	NSA
PUID16585665	Ca6	1609146	(TCATTT)3	18	CCTTCCTTTTCAACCTCTATT	TCTGGTTCATGAAAAATTCAC	257-1750	1106-1735	DUF3633	TFGMS692	54.4	153	3	P	NSA
PUID16585666	Ca5	224208	(AT)6	12	TCAACAACAACACTCCTTTTT	GTGGTGCTCACAATATGATTC	265-1221	793-948	ZF HD dimer	TFGMS693	54.9	148	4	P	NSA
PUID16585667	Ca5	222915	(CTTTG)5	25	AATGGAGAAAAAGCAGAAGAC	GGTTTGGATGCATAACAATAA	265-1221	793-948	ZF HD dimer	TFGMS694	55.3	144	4	P	NSA
PUID16585668	Ca1	3737225	(GAT)4	12	ACTTCAGTTTGAGAACCCATT	AATCAATACTGGCAGAACAAA	246-1163	492-749	Bromodomain	TFGMS695	55.4	145	2	P	NSA
PUID16585669	Ca4	7561185	(GAGAAA)4	24	TGAAACTTCAGAGGTTGGTAA	TTCCTCTGTAGAGGTTTTTCC	234-1424	756-1202	NAD binding	TFGMS696	55.0	144	3	P	NSA
PUID16585670	Ca3	30149012	(TTTTGT)3	18	TAGGCTTCTCTTTATTGCTGA	TTGATATGGTTGGAGGTAGAA	119-1228	188-364	Zf-Dof	TFGMS697	54.7	147	2	P	NSA
PUID16585671	0	0	(CCT)4	12	GGTCAAATGGTTAATTCTTCC	AGACACTGTCATTGCTGAACT	753-1369	752-836	SBP	TFGMS698	55.2	156	3	P	NSA
PUID16585672	Ca1	12343313	(ATC)4	12	CATATGGATCGATAATTCCAG	TCCAATGAGTAATGCAGAAGT	793-3417	2914-3075	PHD	TFGMS699	54.7	152	3	P	NSA
PUID16585673	Ca5	31241318	(CCAATT)3	18	AATTCCCTTCTCCATAACAAC	TCAAATTCAAACCGAGTAAGA	53-2030	479-718	Bromodomain	TFGMS700	54.8	145	3	P	NSA
PUID16585674	Ca3	36426872	(TCATCT)5	30	TTCGCAACCGCTTCTACTCT	TGCGAATCACGTTTCTCAAA	115-1524	471-1191	Glycotransf	TFGMS701	60.2	211	3	P	NSA
PUID16585675	Ca4	4748367	(GAA)6	18	AGGCTTCCTAGTGAATCAATC	GATGATGATTCTCTTCAACCA	599-1735	1079-1233	Myb DNA binding	TFGMS702	55.1	160	2	P	NSA
PUID16585676	Ca5	34050111	(CGG)5	15	CTGAGGATTTTGAAATTGAAC	TCATCTACACTCCGATCTCAC	293-1000	296-397	WRKY	TFGMS703	54.0	145	3	P	NSA
PUID16585677	Ca6	6029323	(AG)8	16	ATCTCTGGCTGAAAGAAAAAT	GACAAAGAAAGCTGAGTGAAA	193-1119	196-1116	GAGA bind	TFGMS704	54.9	136	4	P	NSA
PUID16585678	0	0	(GA)12	24	GAAAACCCAAGAGAGAGAGAG	GCTGTTGTTGTGAGTTTCTTC	193-1119	196-1116	GAGA bind	TFGMS705	54.9	138	4	P	NSA
PUID16585679	Ca3	20843382	(AGT)4	12	GCCATAAACGATGATAACGAT	CTAGAGCAACTGCTACCTCTG	3270-4370	3447-4355	WD40	TFGMS706	56.7	143	4	P	NSA
PUID16585680	Ca3	20843695	(CAT)4	12	ACCATCATAACCATCATCATC	TCATTAAACAAAACCGTCTGT	3270-4370	3447-4355	WD40	TFGMS707	54.6	143	2	P	NSA
PUID16585681	Ca3	20843695	(CATCAC)3	18	ACCATCATAACCATCATCATC	GGAAACCCTAGGTATTGTTGT	3270-4370	3447-4355	WD40	TFGMS708	54.6	143	2	P	NSA
PUID16585682	Ca3	28704381	(AAT)7	21	CCCAAACATCTCTCTCTCTTT	TGAAGGCTTGTCCATTTATTA	90-1529	159-428	BTB	TFGMS709	55.2	143	3	P	NSA
PUID16585683	Ca4	42629317	(AAC)4	12	CCACAGGACACAGATAGTAGC	CTGACCTTACAACAACCTCTG	68-1096	176-427	Myb DNA binding	TFGMS710	54.9	166	2	P	NSA
PUID16585684	Ca1	37689960	(TC)7	14	TGAGAACAAGACCAGAGTCAC	GTGTTATTGTTGGACCTCAAG	19-1119	856-1010	Myb DNA binding	TFGMS711	55.3	144	4	P	NSA
PUID16585685	Ca4	5081434	(AAT)7	21	GTAGTGCAGATAAATGCAAGG	CAAGTTCAGTAACAAACCGATA	135-1787	1365-1622	Myb DNA binding	TFGMS712	55.2	141	3	P	NSA
PUID16585686	Ca4	5081312	(ATA)10	30	CGGTTTGTTACTGAACTTGAA	GGTTGAACTTGGAGTGGTATT	135-1787	1365-1622	Myb DNA binding	TFGMS713	55.6	150	3	P	NSA
PUID16585687	Ca3	21774818	(AAC)8	24	ACACACTTCAAGAAACTTCCA	GATCTTGTTGTGTTGATGGTT	110-1948	854-1906	GRAS	TFGMS714	54.9	150	2	P	NSA
PUID16585688	Ca4	5571877	(CAA)4	12	GACTATTCAATCCACTGGTCA	TTGAAATCAGTTACCTTCTCG	54-1457	855-1348	UDPGT	TFGMS715	55.1	159	2	P	NSA
PUID16585689	Ca7	20231155	(TAT)6	18	GGTTTGTTCCCTTTTACTTGT	ACGTCTTCAAAATAGGGAAAT	258-980	490-761	K-Box	TFGMS716	55.0	141	3	P	NSA
PUID16585690	Ca6	55332933	(AAT)12	36	AACAAGTAGGTGTTGGAATGA	GGTTTTGTGCTTGATAAGAAA	522-1952	1269-1388	HomeoBox	TFGMS717	54.7	168	6	P	NSA
PUID16585691	Ca6	20514111	(TTGATA)3	18	GTGGAAGTGAATTCAAGTGAG	GTCCAACACCATAACAATCAT	775-1506	835-1002	SET	TFGMS718	54.8	148	3	P	NSA
PUID16585692	Ca4	41865183	(CAG)4	12	AATTAAGGCTAGGGAACAACA	GAGATGAGCCCTATCCCTAC	287-3016	2270-2383	WD40	TFGMS719	55.7	143	2	P	NSA
PUID16585693	Ca3	38759963	(AAT)11	33	GGTTCTTCATCATCAACTTCA	ATCTAGCTTGGCTTTGAGAAG	102-1280	473-1259	bZIP	TFGMS720	55.2	141	2	P	NSA
PUID16585694	Ca4	4799331	(TTG)4	12	GCACTAAATGCGTTAAGAAAA	TGCGTTTTCTTTTAGTGCTTA	159-3803	2883-3098	Helicase	TFGMS721	55.1	144	2	P	NSA
PUID16585695	Ca2	10253324	(AAC)7	21	CAGTATCATGATTTTCGGTGT	GTGGTTGTTCGTATTGAGAGA	163-1092	448-582	Myb DNA binding	TFGMS722	55.1	119	2	P	NSA
PUID16585696	Ca4	26511560	(CAGCAA)4	24	ACAGCAACAGCAACAACAG	TTGAATGTGTGGTATGTTGTG	180-2873	2505-2609	WD40	TFGMS723	55.8	153	4	P	NSA
PUID16585697	Ca2	18879056	(AT)6	12	TAATGGATGCTCCTTTCTTTT	CTATGGAATTTCTCATGGTTG	217-1842	1267-1410	HLH	TFGMS724	55.7	173	3	P	NSA
PUID16585698	0	0	(GTG)6	18	TTCCGTAATCATCAGTATCGT	ATTTCTCAATCCTCCGTGA	329-1825	1220-1480	Myb DNA binding	TFGMS725	54.8	147	2	P	NSA
PUID16585699	0	0	(GAG)4	12	AGGCTTCCTTGAGGATATTTA	AAATTGCACAAACAGTATCGT	83-1732	149-529	DNMT1-RFD	TFGMS726	54.9	149	2	P	NSA
PUID16585700	Ca3	20508952	(CTTT)3	12	CCTAAATTCAAATCAGCTCAA	CTCAGTAGTTGGAGAAGCAAA	89-1681	1172-1348	WRKY	TFGMS727	54.8	150	2	P	NSA
PUID16585701	Ca1	203312	(TTA)8	24	TGATGATTATTTCGTTTCCTC	GCAACTAGAAGACGCTGATAA	238-2373	1387-1563	RRM	TFGMS728	54.4	152	4	P	NSA
PUID16585702	Ca1	10712885	(AGC)4	12	CTTTTAGCTGCACAACAGTTT	CTCTCATTTTCAAATCACCTG	165-1457	875-995	bZIP	TFGMS729	55.1	190	4	P	NSA
PUID16585703	Ca7	6057942	(CT)10	20	ATTCTCCTCATAAGCCATTCT	TTCTCGATCTATACGTCAACC	586-1209	937-1101	KNOXZ	TFGMS730	54.7	150	4	P	NSA
PUID16585704	Ca3	28289003	(AG)10	20	GATTAATGGTTGTGATGAGGA	GTAAATTACCGTGTTTGTTCG	835-1743	1282-1434	Myb DNA binding	TFGMS731	55.0	144	6	P	NSA
PUID16585705	Ca3	28287606	(TA)6	12	AACATAGTTGTTTGGCAACAT	CACTATCCACCTTGTTGTCTC	835-1743	1282-1434	Myb DNA binding	TFGMS732	54.8	144	3	P	NSA
PUID16585706	Ca4	19324	(AAG)7	21	TCCATGTGATTGTTGAGTGTA	GTTTCAGATTAACGGTTGTTG	216-1859	441-683	bZIP	TFGMS733	54.9	151	2	P	NSA
PUID16585707	0	0	(AG)7	14	TTAAGTGAAAACTGAGGCAAC	GTGAGTGAGAATCGAAGATGA	450-4657	1209-1871	START	TFGMS734	54.8	145	4	P	NSA
PUID16585708	Ca7	6116635	(TAA)4	12	TAGTTTCAGCTCAGGAATTTG	CTGCATCATTTTCTCAAACAT	252-1391	378-1127	PP2C	TFGMS735	54.9	151	3	P	NSA
PUID16585709	Ca4	9449960	(TTG)5	15	TACTACTTCACCTGGCTTTTG	AGGGTAGAAAACATGGAAAAG	138-1349	828-983	Myb DNA binding	TFGMS736	54.8	178	2	P	NSA
PUID16585710	0	0	(TTTG)3	12	CATTTGTTGGATTGTGAAGTT	TCATACAAAACCCTTCTCAAA	315-1658	666-929	Myb DNA binding	TFGMS737	55.2	159	2	P	NSA
PUID16585711	Ca3	26594514	(ACA)7	21	TTTCAGTGTTTGTGGAAGACT	CCTTCTTGTTGGAATTGAACT	99-923	702-809	GATA	TFGMS738	54.9	146	4	P	NSA
PUID16585712	Ca4	22197042	(AG)8	16	CATGATTGTTATGGTGGTCTT	GTCAACAACTTCAATTTCCAA	1-1302	853-1101	Myb DNA binding	TFGMS739	54.9	150	3	P	NSA
PUID16585713	Ca1	3235738	(GGAAGT)3	18	ATAATGGTTACTTTCGGAGGA	TCTTCTTCGTGTTCATGTTCT	178-1098	232-504	Myb DNA binding	TFGMS740	55.4	151	2	P	NSA
PUID16585714	Ca5	31194921	(ATG)6	18	CATGAAGGCCTATAACAAGAA	GAGCTTCTACTCGTCATCATC	243-563	375-455	HMG Box	TFGMS741	54.7	145	2	P	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585715	Ca7	24022020	(CT)6	12	TCAACCCTACAACACTTCATC	ATTTCCAAGTGCTAAAAGCAT	206-1216	356-535	Zf-HD-dimer	TFGMS742	55.1	132	3	P	NSA
PUID16585716	Ca7	24021097	(TTGGAA)3	18	ATGATGTTGGTGTTTCAAGAG	TTTAGCATCTGCATCTATGGT	206-1216	356-535	Zf-HD-dimer	TFGMS743	55.1	159	2	P	NSA
PUID16585717	Ca6	15107755	(TTCCCA)3	18	ATTTCCATTCTATGCCTTTTC	AACCATTAACTCGTTTTCACA	222-1244	750-863	GATA	TFGMS744	55.1	150	2	P	NSA
PUID16585718	Ca7	34922983	(TAA)14	42	CAAACTCACTTTCAGCTCTTG	GTTATGCATCTCATGGTGAAC	88-903	144-324	Zf-Dof	TFGMS745	55.4	154	4	P	NSA
PUID16585719	Ca6	26358709	(AGAA)5	20	GTGATCTGTCATCGTTTCAAT	AGGAAGCTTTGAGAAAGAGAA	361-1638	1465-1638	GRAS	TFGMS746	55.0	141	2	P	NSA
PUID16585720	Ca6	26357925	(TAG)7	21	AAGCCTTCTATATTGCAAACC	CAAAATCCATCCCTAGAACTT	361-1638	1465-1638	GRAS	TFGMS747	55.4	146	3	P	NSA
PUID16585721	0	0	(AGAA)3	12	GATGAGAAAATCCAAGAGGTC	GAGTCTCTCAATTCTCTTTTGG	106-549	214-321	GATA	TFGMS748	55.3	150	2	P	NSA
PUID16585722	Ca4	46398833	(AGATGA)3	18	CGATGAATTCGAAGAAGCAATA	TGAACCTAACCAAATTCTTGA	148-540	158-303	AP2	TFGMS749	55.7	159	2	P	NSA
PUID16585723	Ca5	29786484	(AC)7	14	GAAGAGGTGGAGAAAGATCC	AGCCAAAAGAACAAGAAGAAG	362-4102	764-1159	AAA	TFGMS750	55.3	132	3	P	NSA
PUID16585724	Ca5	29786557	(TGT)4	12	AGAAGAAGGAGGTTTGTCATC	CTTTCTGTGTGTGTGTGTGTC	362-4102	764-1159	AAA	TFGMS751	55.0	159	2	P	NSA
PUID16585725	Ca5	29786541	(TTC)5	15	TCATCGGAAGAAGAAGAAGAT	TTCTTTCCTTTCTTTCCTTTC	362-4102	764-1159	AAA	TFGMS752	55.7	169	2	P	NSA
PUID16585726	Ca2	17282543	(CAA)7	21	ATGCCTTCAAGTTTCAACAC	TTCGTATTGTTGTTGTTGTTG	86-1189	701-847	HLH	TFGMS753	55.3	148	3	P	NSA
PUID16585727	Ca6	23263526	(ATTG)3	12	GTGGTTCCTTATGATTTGTTG	GGGTTTAATTACAAACCATCC	141-1481	384-1448	GRAS	TFGMS754	54.7	149	2	P	NSA
PUID16585728	Ca7	8795456	(TAA)8	24	AAATGGATTGAAGGAATCAGT	TCGAACCATTTGTAAAAACAC	271-909	529-690	HomeoBox	TFGMS755	55.2	153	3	P	NSA
PUID16585729	Ca1	20106435	(TAA)7	21	TGAGATAATGGAGCTTGAATC	AGCTTGTTGAAGTGACACAGT	108-692	276-401	HLH	TFGMS756	54.5	152	4	P	NSA
PUID16585730	Ca4	32780320	(ATGGT)3	15	TCCCATCAAGATGCTAAAATA	AATCAATCTTTGAGTTGTTGC	710-1126	684-1096	AUX_IAA	TFGMS757	55.0	149	2	P	NSA
PUID16585731	Ca3	31978552	(GCT)4	12	GATGAGTATGGAAATGGGAAT	AGATGATGATGATCCACAGAT	169-1638	994-1122	HLH	TFGMS758	55.4	151	3	P	NSA
PUID16585732	Ca1	4865629	(CTGATT)4	24	CGCAGATTATATCTCACGGTA	ATTCTCCAAATCTTCAGGTTC	22-1449	604-771	BSD	TFGMS759	55.6	148	2	P	NSA
PUID16585733	Ca8	4628420	(GAA)8	24	TCTTGGGACATAGAATTTGAA	GAAGCCAATGGTAGAAGAAAT	105-2279	918-1322	POX	TFGMS760	54.9	149	3	P	NSA
PUID16585734	Ca3	39742820	(GA)16	32	AGGTTGGTTGTCTTAAGTTGA	TTTCTGCTTCACTTGATCTTC	163-2043	1608-1944	Response	TFGMS761	54.0	149	6	P	NSA
PUID16585735	Ca3	1482592	(TA)10	20	TTTCTTGTCCATGCAATTACT	ATGTTTCAAATTAAGGCAGA	10-567	256-387	Myb DNA binding	TFGMS762	55.0	146	3	P	NSA
PUID16585736	Ca3	30954905	(ACTTTC)3	18	GAGAAGGGGACTGTGAACTAC	GTTGAAGGTTGAAGAAAGAAA	225-1850	288-542	Bromodomain	TFGMS763	55.4	162	3	P	NSA
PUID16585737	Ca1	1953808	(CT)8	16	GCCATTCTTCACTCTTTCTTT	GTTCAAATCCGAAACGTAAAT	163-2832	1186-1491	B3	TFGMS764	55.3	148	4	P	NSA
PUID16585738	Ca1	1953808	(TC)8	16	GCCATTCTTCACTCTTTCTTT	GTTCAAATCCGAAACGTAAAT	163-2832	1186-1491	B3	TFGMS765	55.3	148	4	P	NSA
PUID16585739	Ca2	34852663	(AGA)8	24	TGAAGAAGAGGAAGAAGAAGG	GAATCAACTTTTGTGCCATTA	257-2983	854-1102	Bromodomain	TFGMS766	55.5	153	4	P	NSA
PUID16585740	Ca4	24593381	(AAG)5	15	CATCCAAGACAAAATTCCTTA	CTCTGGAAATTTAAACAAGCA	150-1937	1392-1751	BTB	TFGMS767	54.5	158	2	P	NSA
PUID16585741	Ca1	5668632	(AG)6	12	GTAGAAAAGGGAGAGATGGAA	TAACGTCTCCAAAAATCTCAA	2164-5712	3577-3960	APG6	TFGMS768	55.1	159	4	P	NSA
PUID16585742	Ca1	5668632	(AG)8	16	GTAGAAAAGGGAGAGATGGAA	TAACGTCTCCAAAAATCTCAA	2164-5712	3577-3960	APG6	TFGMS769	55.1	159	2	P	NSA
PUID16585743	Ca6	12437200	(CAA)5	15	CTCAAACTCAATCACATTTCC	GCTGTTGTGATTTTTGTTGTT	932-3685	1307-1615	B3	TFGMS770	54.8	153	2	P	NSA
PUID16585744	Ca6	19840998	(CTA)6	18	GAAATTCAATCTGAACATCCA	TTGTCAACATTCACAGAAGAA	219-1424	1095-1271	WRKY	TFGMS771	55.1	146	3	P	NSA
PUID16585745	Ca8	5569895	(TTGAG)4	20	AATCCAATCGAAGAGAGAGAG	AGTTACCATCTCAATCCACAG	149-3886	1601-1738	GYF	TFGMS772	55.3	154	2	P	NSA
PUID16585746	Ca6	2782209	(TATTTT)4	24	AGATGAGGAAGAGGAAAATGA	ATCGTTGTCCTTCATTTGATA	163-1038	163-888	mTERF	TFGMS773	55.5	150	2	P	NSA
PUID16585747	Ca7	10115566	(TGAATT)4	24	TGAACTATCCCCTTTAGGAAC	GAAGTTGATGAGTTTGATTCG	235-1188	742-897	AP2	TFGMS774	55.0	153	3	P	NSA
PUID16585748	Ca6	12572480	(GCA)7	21	GGTGAAAATCAGAATCATCAG	CCAACTTGGTTTTCCTCTTTA	840-2244	1029-1292	TCP	TFGMS775	54.7	157	3	P	NSA
PUID16585749	Ca4	8051984	(ACCCT)5	25	TTCCTAAACGACATCTTCAAC	CTTCTCTCTGCTTCATCTTCA	257-1462	278-1124	Tub	TFGMS776	54.5	153	5	P	NSA
PUID16585750	Ca4	8052130	(ATG)7	21	GAAACTGAGCACTAGGAGTTG	CAGTTTCTTCCACAAAAGCTA	257-1462	278-1124	Tub	TFGMS777	54.3	169	3	P	NSA
PUID16585751	Ca2	34273833	(AAT)7	21	TTCTCTCTTTCCATGGCTAAT	CATTGAAACTTGTATGAGAAGG	37-972	529-709	WRKY	TFGMS778	55.7	154	2	P	NSA
PUID16585752	0	0	(TC)12	24	GTAACCCCAGTTGAGAAGTTT	TGCTTTGTAGTGAGTGTGTGT	554-1651	1073-1219	HLH	TFGMS779	55.0	147	4	P	NSA
PUID16585753	Ca7	10016192	(TTG)4	12	GTGCAGTTTGACAATCTACCTA	TGACCAAAGTAAAACACCACT	227-1240	521-655	Myb DNA binding	TFGMS780	54.7	166	3	P	NSA
PUID16585754	Ca2	2409848	(AG)11	22	TGAGAAAAATTAGCACACAAAG	ACATATTCATGCTGTTGTTCC	423-1283	627-788	HomeoBox	TFGMS781	55.0	143	6	P	NSA
PUID16585755	Ca4	13721224	(AT)6	12	TAGTCAATGGTCCTTGAAAAG	AAACTGCTTTCCTGTTGTATG	517-4470	2197-2277	PHD	TFGMS782	54.6	163	3	P	NSA
PUID16585756	Ca2	26834137	(CAA)4	12	AAAACAACAACTCTTCAATGC	ACCTTCAACTCTCCATCTTTT	21-1746	1251-1427	WRKY	TFGMS783	54.6	155	2	P	NSA
PUID16585757	Ca8	15607448	(TCC)4	12	TAAATCGCCTAGAGATGTTCA	CATAACTTGTTCCGAGTCTTG	209-886	377-472	AP2	TFGMS784	55.2	155	2	P	NSA
PUID16585758	Ca7	19466375	(TCTCTT)3	18	TTGTGTTTGTGTTTAAGAGCA	GGTGTGTAGCAGAAGAGAAGA	239-1300	437-1273	AUX-IAA	TFGMS785	54.6	142	2	P	NSA
PUID16585759	Ca4	21853025	(CAC)4	12	CTTTAGGGAAATGTGTGCTTA	TTGTTGTAATTGTTGCTGTTG	132-1655	504-764	Myb DNA binding	TFGMS786	54.8	151	2	P	NSA
PUID16585760	Ca2	7604070	(TC)6	12	CCCTAGAAACATGATGAAGAA	CCTTCAAGAGAGAGAGAGACC	145-924	328-495	Zf-HD	TFGMS787	54.5	165	2	P	NSA
PUID16585761	Ca5	9961692	(TGC)5	15	ATTGATGATGAACCATTATGC	ACAACAACAACATCAACAACA	88-1548	1231-1487	WRKY	TFGMS788	54.9	144	3	P	NSA
PUID16585762	Ca8	7165244	(CT)6	12	AGAGAACCCAATACCAAAAAC	CTGACGCAGTAGCCTTCTT	99-491	249-479	SWIB	TFGMS789	54.9	174	3	P	NSA
PUID16585763	Ca1	11285919	(TAT)8	24	AGAAGAATCCAAATCCAAAAC	GAAGCCTCTTTCTCCTGATAC	337-2598	349-1467	GRAS	TFGMS790	55.0	148	3	P	NSA
PUID16585764	Ca7	19621697	(AG)11	22	GGAGAGTTTGTTTGTTGAAAA	CACTCGAAATAAATCACCAAC	33-2006	426-566	HLH	TFGMS791	54.6	144	4	P	NSA
PUID16585765	0	0	(TGT)5	15	AGATTCTTCATTGTTGGCATA	TGGATTCAACAAGTATTGGAC	91-1293	175-312	HLH	TFGMS792	54.9	140	3	P	NSA
PUID16585766	Ca6	15271372	(TA)8	16	TCTAAAGAGTCTCCCTCAGAAA	AATCACTTCCTGAAGAACTCC	237-1841	468-1132	Bromodomain	TFGMS793	55.1	141	4	P	NSA
PUID16585767	Ca1	12928971	(CTT)9	27	TAAGTTGTGGCTGTGAGAGAT	TATTGAGATTCCTCGTCACAC	267-1541	762-914	Myb DNA binding	TFGMS794	55.0	157	3	P	NSA
PUID16585768	Ca8	8417363	(TTA)6	18	GCTTAAGCTTTGTTGTTGTTG	CAACAACAACATCATCAAACA	363-1553	747-902	Myb DNA binding	TFGMS795	55.5	150	2	P	NSA
PUID16585769	Ca7	34320789	(ATG)4	12	CTTCTCCATCAACAACAAATC	CTTGTTTCCAAGTGACAATTC	712-1293	832-1122	B3	TFGMS796	54.8	161	3	P	NSA
PUID16585770	Ca2	34653566	(GAA)7	21	AGCAAAGAAGAAGAAGAGGAA	CTTCTTCTTTTGATGGTGTTG	712-1293	832-1122	B3	TFGMS797	55.2	143	2	P	NSA
PUID16585771	Ca2	34095011	(CAT)5	15	CAACCATCTTTTGAGTTCATC	TGGTTGAGGAAGTTATGTTGT	269-2008	461-685	BTB	TFGMS798	54.8	150	2	P	NSA
PUID16585772	Ca6	14811478	(GA)16	32	AGTCAATCCGTAAGAAGAAGC	CAAAGAAAGATTTCAAAGTCG	279-3524	1269-1346	Ank	TFGMS799	55.4	145	4	P	NSA
PUID16585773	Ca6	20762882	(TTTA)3	12	GGTAAGGTTGCTTGGTTAAAG	ATCATCACCATCACCACTTAC	162-875	492-641	HLH	TFGMS800	55.7	151	2	P	NSA
PUID16585774	Ca2	10330535	(AG)9	18	GGAAGAATGGCATAAAAATG	CTCTCGAGGTAGGTGTGTTTA	252-1031	465-843	HLH	TFGMS801	54.8	154	4	P	NSA
PUID16585775	Ca2	32867739	(GAA)11	33	CAAGTGAATGAATTCTCAAGC	CTCTCTTTCCTCTCATCTTCC	344-1408	907-1416	EIN3	TFGMS802	55.1	152	2	P	NSA
PUID16585776	Ca4	13652216	(TGG)6	18	GTCGTCGGAGAAATAGTCTTC	CTCAAATATCTCTCCCAACCT	210-875	318-503	ovate	TFGMS803	55.6	153	2	P	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585777	Ca1	15378933	(AAT)7	21	ACCTTATCAATGATTGCTTCA	CAAGACAAAGAGGAAATTGTG	3-953	387-533	HLH	TFGMS804	54.9	154	2	P	NSA
PUID16585778	Ca7	19942079	(TTC)7	21	AGTGATTCTCTGTGTCTCTGC	AGAATAGAAAACGGCAATGTT	220-1137	682-837	HLH	TFGMS805	54.5	155	3	P	NSA
PUID16585779	Ca4	48201455	(TTC)4	12	GATGGTGAAAAGAGGAGTGTT	CTCTCTAAGTAGCGGAAGAGG	1-251	78-227	DUF702	TFGMS806	55.8	152	2	P	NSA
PUID16585780	Ca2	2580068	(AG)6	12	TCAAAATAGTTCTTCCTTTGG	CAATCTCAGACCTTAGTGTGC	527-5338	647-961	BAH	TFGMS807	53.9	155	4	P	NSA
PUID16585781	Ca7	28550286	(TC)7	14	GCGCTTAAAAGATCTCACTTT	TCGTTTTGTCTGGTACTTGAT	786-1760	975-1211	SBP	TFGMS808	55.7	148	3	P	NSA
PUID16585782	Ca7	28550154	(TC)9	18	TTCAGAAACGAGAGCAGACTA	ACTCACACTTGCACTCTCACT	786-1760	975-1211	SBP	TFGMS809	55.5	161	3	P	NSA
PUID16585783	Ca4	30264977	(CT)11	22	TCTCTCATCCTCTTTCTTTCC	GATCCAAAGAATGGAATAACC	234-1139	756-944	KH1	TFGMS810	55.2	147	4	P	NSA
PUID16585784	Ca8	14954627	(TGT)5	15	TTCAATACCGTCTTCATCTTC	ATGAAGATGATGATTTCGATG	221-1375	713-976	Myb DNA binding	TFGMS811	54.5	151	4	P	NSA
PUID16585785	Ca2	10253324	(AAC)7	21	CAGTATCATGATTTTCGGTGT	GTGGTTGTTCGTATTGAGAGA	210-664	495-629	Myb DNA binding	TFGMS812	55.1	119	2	P	NSA
PUID16585786	Ca7	8015993	(TCA)4	12	TGGTTTAAGCCAACCTAGTAA	AGGTACCTGGTGGTGGTAAT	17-447	191-388	TCP	TFGMS813	54.4	140	3	P	NSA
PUID16585787	Ca2	3410251	(TA)8	16	AATGTTCTTCCCCTCACTCTA	ACTCCCAAACTCTCAAGTAGC	52-321	103-264	Zf-HD	TFGMS814	55.5	136	3	P	NSA
PUID16585788	Ca5	34474846	(TGT)4	12	TCTTAGTAACGCCATGGTAAA	GAGACATACATACGCCCATTA	64-1329	355-505	tify	TFGMS815	55.2	153	3	P	NSA
PUID16585789	Ca6	10053750	(TGAT)4	16	TGATTGTGGATTCTTCGATAC	TGGCGATTTAGATAGTGGTAA	706-1158	814-990	bZIP	TFGMS816	55.2	150	2	P	NSA
PUID16585790	Ca2	11263883	(TC)13	26	CCACCACACAGAAGAAAGAA	GGTGGTGTGTGTAGTTGTGA	470-1462	734-895	HomeoBox	TFGMS817	56.3	148	6	P	NSA
PUID16585791	Ca5	35861292	(CTTC)7	28	TCTAGAAGCTTCCTACTTCACC	CGAAAGTGAGTGTTGAGAAAG	221-1324	359-637	HSF	TFGMS818	54.7	163	4	P	NSA
PUID16585792	0	0	(TC)15	30	CCACCACCTACGTAAAATAAA	GTTTGAACCTCCTTGAAAGAT	144-1262	462-1238	Tub	TFGMS819	54.5	171	4	P	NSA
PUID16585793	Ca7	12021104	(ACACAA)4	24	CCTCTCTTATTTTGTTTGTCAAC	TTCCTTCGAAATTGAGTAAAG	129-1130	906-1088	WRKY	TFGMS820	54.9	165	3	P	NSA
PUID16585794	0	0	(GA)18	36	GACATGGTTCGATTTGGAT	CACACTCACTCTCTTCTTCTTCT	292-2019	664-840	WRKY	TFGMS821	55.7	153	6	P	NSA
PUID16585795	Ca4	12176090	(AAC)7	21	CCCAAAACATCAACAATCTTA	AGGGTCTAGAAAAATTGTTGG	107-2095	992-2092	GRAS	TFGMS822	55.3	132	2	P	NSA
PUID16585796	Ca6	38814576	(AG)12	24	TACCACTTTTATACGCTGCAC	ATGAATGAACGAATGTGACTC	243-2444	1365-2438	GRAS	TFGMS823	55.7	145	4	P	NSA
PUID16585797	Ca5	46073597	(ATT)7	21	GTTTCACGAACAAAGATTCTG	ACCTCTACTCTCAGCTCCACT	92-2116	230-565	Response-reg	TFGMS824	55.0	151	3	P	NSA
PUID16585798	Ca5	29398059	(CCTTCT)3	18	AGTTCTTCCACAAATTCAACC	TTTCGAGGAAAGCTTCTAAGT	481-1458	892-987	AP2	TFGMS825	55.8	152	2	P	NSA
PUID16585799	Ca6	9118284	(AG)10	20	AGGTAGTTGAAGAAACGAACC	AGAAGCAGGATCAATACCTTT	198-1349	942-1085	bZIP	TFGMS826	55.1	153	5	P	NSA
PUID16585800	Ca3	31064037	(GA)10	20	CCTCTGAAATGGGACTGTT	AACACTTCCCCACACAAAC	177-608	423-524	AP2	TFGMS827	55.0	141	5	P	NSA
PUID16585801	Ca6	54244269	(GTCATA)3	18	GTTCCTATTCCAATGCCTTAT	ATGAGACCGATAAGAAGAAGC	230-682	236-298	Myb	TFGMS828	55.0	153	3	P	NSA
PUID16585802	Ca1	3651235	(AT)6	12	TGATGATGATGATGATAGCAG	GACTTGAAAGTAACCACGAGA	239-787	413-607	K-Box	TFGMS829	54.5	153	2	P	NSA
PUID16585803	Ca2	11661488	(ATC)4	12	AGCAAATTTCATGCTACAAAC	TCCTAGTTCAATTCCTGATGA	167-1003	386-547	HomeoBox	TFGMS830	54.8	151	2	P	NSA
PUID16585804	Ca4	45736093	(TTC)6	18	GCAGCTATTCATTCATCTTCT	ATGTACCAAGCCATACTCTTG	141-692	543-608	AP2	TFGMS831	53.9	158	3	P	NSA
PUID16585805	Ca4	12023919	(CTCATC)4	24	CCACTAATACAAGGAAGCAAA	AGTCGCTCTTATTGGACTTGT	2-511	152-253	S1FA	TFGMS832	54.8	156	3	P	NSA
PUID16585806	Ca7	32855952	(TTTGAT)6	36	CAAGAAGGTGAAGTTAAAGCA	ATTCAACCTCACAGTTTCAGA	125-1216	854-1030	WRC	TFGMS833	55.0	155	5	P	NSA
PUID16585807	Ca8	1742958	(ACT)6	18	CTAGGTTTACCCTTTCCCATA	TTGACTCTTCTTCTTCAAACG	2-1246	2-1246	Jmjc	TFGMS834	55.1	161	2	P	NSA
PUID16585808	Ca8	3997990	(AG)6	12	CACCTTCCATCTTCTTCTTCT	AAGCTACTGAAGTTGGTGCTA	308-811	605-754	AP2	TFGMS835	55.2	155	3	P	NSA
PUID16585809	Ca8	3997990	(TC)9	18	CACCTTCCATCTTCTTCTTCT	TGACAAACTTAATGGGAGAGA	308-811	605-754	AP2	TFGMS836	55.2	155	2	P	NSA
PUID16585810	0	0	(TC)14	28	GGTAGAGGATGAGGATGAGTT	TTTGTTGGATGTTAAAGGTTG	159-794	582-752	Zf-Dof	TFGMS837	54.8	151	3	P	NSA
PUID16585811	Ca8	15220963	(ATCAAA)4	24	AAGTACTGTGAATGCTTCCAA	CTTGCTGAATATACGTGTGGT	492-863	711-824	CXC	TFGMS838	55.1	156	4	P	NSA
PUID16585812	Ca6	21496611	(TA)10	20	TCATCAGAGGTTGCTTCTAAA	TCAGGAAATTAAGGTAGAATGAG	294-1139	468-578	bZIP	TFGMS839	55.3	147	4	P	NSA
PUID16585813	Ca5	30587088	(TCTTGC)3	18	TCTTTATCTTCTGCAAAACCA	TTGATGGTAGAGCAAGAACAT	332-4186	2864-3088	SWIB	TFGMS840	55.3	149	3	P	NSA
PUID16585814	Ca8	5196644	(TTC)4	12	TAGATCTCACACACACAATGG	GTTATGGTGTGAATTTTGAGG	43-881	316-477	Zf-HD	TFGMS841	54.4	143	4	P	NSA
PUID16585815	Ca8	3997837	(CT)6	12	TGACAAACTTAATGGGAGAGA	TCAACGACACTTCTCTTTCTC	181-684	238-387	AP2	TFGMS842	55.0	154	3	P	NSA
PUID16585816	Ca7	2713430	(TAAA)3	12	CAAAGTCTAACCAATTTCACG	AGAGTCATGTGCGTTGATAAG	316-1242	358-534	WRKY	TFGMS843	55.1	148	2	P	NSA
PUID16585817	Ca4	44660343	(AG)10	20	GGACACACAACAGAGAGAAAA	ACGAGGATTGTAAGGAGTACC	145-918	172-582	DUF3594	TFGMS844	55.3	167	6	P	NSA
PUID16585818	Ca1	389726	(TTC)4	12	ATCCAAACGAGAATTACATGA	CAAATTTGAATCAGAAACTGC	41-1297	380-691	TCP	TFGMS845	54.7	152	NV	NV	NV
PUID16585819	0	0	(CTC)4	12	CCCGAAAAATATAAATCCAGA	CTCGTTTGTTTGCTCTATTGT	159-3215	492-728	SBP	TFGMS846	55.9	175	NV	NV	NV
PUID16585820	Ca5	166052	(TCCC)3	12	CGAGTATACAAGAGAGCAGGA	GGAATAATGAGAGTGACAAGC	23-1294	194-571	NAM	TFGMS847	54.9	147	NV	NV	NV
PUID16585821	0	0	(TGC)4	12	TTAAACCATTCTCAGTCTTCG	GGAGGTGAATATTCTTCCAAT	261-7523	5971-6343	SET	TFGMS848	54.7	149	NV	NV	NV
PUID16585822	Ca5	38592092	(GCTT)3	12	TTTCTACGATGATATGGAGGA	GAAAACATGTCGTTTTGGATA	653-3472	2851-3211	Jmjc	TFGMS849	54.8	145	NV	NV	NV
PUID16585823	Ca7	36416882	(GCT)4	12	GTAAGATAACAGCTGCCAAAA	CTCCAGAAAACGATTCCTAAT	3506-7105	4535-4777	Helicase_c	TFGMS850	54.9	155	NV	NV	NV
PUID16585824	Ca5	11385849	(GCA)4	12	GTTCAACAACAAAGACTTGCT	TTAACCTGTGGTTCAGCTTAC	208-2628	1597-1782	RPM	TFGMS851	54.7	148	NV	NV	NV
PUID16585825	Ca2	24235872	(GA)6	12	GCAAAATAAGCACAAGTGAAA	TTTTCAATCCATTCAGGTAAG	26-1420	509-1378	SNF2	TFGMS852	55.8	149	NV	NV	NV
PUID16585826	Ca4	30311837	(GAT)4	12	AACCTAAGGGAGCTAATGTTG	GTGCAAGCAAAGCTATAGTCA	900-2052	1779-2048	SNF2	TFGMS853	55.3	149	NV	NV	NV
PUID16585827	Ca4	35416702	(GCG)4	12	GTTGATGATGAAACAACGAAT	GGTTGAGGAGAAAATTAAAGC	1046-1738	1478-1642	TCP	TFGMS854	55.1	176	NV	NV	NV
PUID16585828	Ca4	35393450	(CGC)4	12	GGTTACGTTCTGAACAAGATG	GTTGATGATGAAACAACGAAT	180-860	255-419	TCP	TFGMS855	54.9	192	NV	NV	NV
PUID16585829	Ca7	5511848	(TCA)4	12	AAGTGGAAACTGATGATCAAA	TTACCGAAGGTGATAAGCTCT	104-7564	4097-4236	Helicase_c	TFGMS856	54.8	156	NV	NV	NV
PUID16585830	Ca6	1843362	(GAA)4	12	CACCACAACAAGAACACATAA	TTGTGAAGGTGTTTGTTGAAT	129-2029	1379-1636	DUF573	TFGMS857	54.5	149	NV	NV	NV
PUID16585831	Ca6	9328054	(TCT)4	12	GCTGTTTGTTTGATGAATCTC	GGATAGTGAAGGCTCTCTTGT	30-2006	1-564	START	TFGMS858	54.9	159	NV	NV	NV
PUID16585832	Ca5	30597009	(TTTC)3	12	CGACTTGAATCTCTCCTGTAA	GCTGATCAGTTGTGGTAGAAG	349-852	368-822	UMSBP	TFGMS859	54.7	161	NV	NV	NV
PUID16585833	Ca6	27235614	(GT)6	12	TTACTCTCCATGTTAATTGTGG	TTAACTTCTGCAAACAAAACC	1318-2892	1585-1917	Response_reg	TFGMS860	54.5	151	NV	NV	NV
PUID16585834	Ca3	37789311	(GAC)4	12	TACATGTTCAGCACAGCTAGA	TCATCGTCATATTTGAAATCC	1350-2753	2155-2292	PHD	TFGMS861	54.7	150	NV	NV	NV
PUID16585835	0	0	(TG)6	12	TCAGAGTGTGTGTGTGTTT	TCTTCTTCTTCGTCCTCTTCT	1804-3588	3277-3414	PHD	TFGMS862	54.9	150	NV	NV	NV
PUID16585836	Ca6	37388188	(TGT)4	12	TTTGGTGAATGAAGAGAGAAA	TCAATGCAATCCTAGAAAATC	1-1215	1098-1215	DNA bind	TFGMS863	55.1	159	NV	NV	NV
PUID16585837	Ca3	38688349	(GGT)4	12	AAGGAATTGTGGATGGTAGAT	ACCTTCAAACAAACCTCTTTC	58-1188	258-976	Myb	TFGMS864	55.1	142	NV	NV	NV
PUID16585838	Ca6	22709964	(CTC)4	12	TCGGATAATACACAACTTCAAA	GAGAAACAGGGTGGATGAC	268-2064	1408-1716	B3	TFGMS865	55.0	167	NV	NV	NV

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585839	Ca5	38289000	(TGG)4	12	TGGAACACAACCTACTCTGTT	CCATCAAAACTCAAATCTTCA	763-1605	1048-1176	HLH	TFGMS866	54.8	165	NV	NV	NV
PUID16585840	Ca1	48002802	(TCTT)3	12	CAACACGCTTCTGACTAAACT	AAAGTTGTGAAGTGAAACTGC	709-3783	1429-1518	PHD	TFGMS867	54.9	146	NV	NV	NV
PUID16585841	Ca6	11668373	(GCT)4	12	CTTCACTCCTAGCTTTTCACA	TACTTTTTCAGCAGCTTCAGT	745-3502	2824-3072	SWIRM	TFGMS868	54.9	152	NV	NV	NV
PUID16585842	Ca6	10028556	(TAC)4	12	AAATATCCGGAAGTATCTCCA	GGCTTTGTTATGTTTGAGGTT	1700-2668	1931-2113	Zf-HD	TFGMS869	55.4	134	NV	NV	NV
PUID16585843	Ca8	1262041	(TGG)4	12	ATAACATTCAAGGTGTTGGTG	CAACATACCTTACCAGTAGCC	270-2291	1350-1550	RRM	TFGMS870	55.0	155	NV	NV	NV
PUID16585844	Ca6	26810868	(TAAA)3	12	AATAACACTTTTTCCGTTCCT	TTGTCTTGGACCTTCACTCTA	135-647	564-638	Myb	TFGMS871	54.7	148	NV	NV	NV
PUID16585845	Ca7	33481019	(CCTT)3	12	TGTTCATAAGCTTCACCAAAT	ATCAGAAAAGGAAGCGTTATC	260-1330	872-1141	SANT	TFGMS872	55.0	165	NV	NV	NV
PUID16585846	Ca7	33480716	(TAT)4	12	CACATACAAGGCTAATTTGAA	AGCAAAAATCATAGCAACAAC	260-1330	872-1141	SANT	TFGMS873	53.2	152	NV	NV	NV
PUID16585847	Ca7	13905747	(GAA)4	12	TGAATTCACGGACTATGTTTT	ATCCGTTTGCTATTGATCTCT	258-1493	279-1145	Tub	TFGMS874	54.8	150	NV	NV	NV
PUID16585848	Ca7	13320410	(TCA)4	12	TGGTATGGTAACAGACAAACA	TTGGATCTCTTTGATGTTGTT	1827-4139	3456-3575	HomeoBox	TFGMS875	54.0	177	NV	NV	NV
PUID16585849	Ca4	43512749	(TCT)4	12	TGACATGGAATCTGATCTACC	CCATCCATCAGATAGTTTGAG	573-1883	1401-1847	bHLH MYC	TFGMS876	55.0	149	NV	NV	NV
PUID16585850	Ca3	37389044	(GTA)4	12	TGGAATTAACAACATGGAACT	CATCAACATGTTTTGTGTTTG	176-1258	224-400	Myb	TFGMS877	54.7	155	NV	NV	NV
PUID16585851	Ca4	5747457	(TTC)4	12	CCATGAGAGCTAACCTTAAAA	CGGGAGTATAACGAAACTGAT	155-2932	2374-2635	Jmjc	TFGMS878	54.1	144	NV	NV	NV
PUID16585852	0	0	(CTT)4	12	TCACCTTCACCAGTTTCTTTA	GTTAAAGTTGCTGAAGCGATA	335-2386	515-805	Jmjc	TFGMS879	55.0	152	NV	NV	NV
PUID16585853	Ca7	16571186	(GTT)4	12	GTTTTGTTTGAAGGCTTTTTC	CCAAATCTCATCAATTCTTCA	461-1090	581-1081	mTERF	TFGMS880	55.8	149	NV	NV	NV
PUID16585854	Ca3	39816982	(GAG)4	12	CAGTTAGAGAAGTTGCAGCAG	GCCAATTTCTTTCTTTCTTTC	479-1678	764-1003	B3	TFGMS881	55.6	156	NV	NV	NV
PUID16585855	Ca3	39818014	(GGCA)3	12	GAAACTTCAGTGCTGTTTGAT	TAGAAAGGAACTGTGATGAGC	479-1678	764-1003	B3	TFGMS882	54.6	129	NV	NV	NV
PUID16585856	Ca4	47905073	(TGT)4	12	AACTGAAGCACAAGCTACAAG	TCATCACCATTGTCACTATCA	56-1318	77-947	Tub	TFGMS883	55.0	159	NV	NV	NV
PUID16585857	Ca4	45517811	(TAA)4	12	TCTTCTGAGTGTTTTTCATTCA	AAAAACCCTTCTCATTGTGTT	723-2003	1530-1613	HLH	TFGMS884	55.2	152	NV	NV	NV
PUID16585858	Ca4	1103152	(TTGG)3	12	TTATGAAAATGATGGGTTGTC	AGACAACAGTGCCAAACTAAG	517-969	589-942	NAM	TFGMS885	55.0	156	NV	NV	NV
PUID16585859	Ca2	3920987	(GAT)4	12	TCGAAAAACTGGACCTATACC	ACATCGATCAGTATTGTCTGG	Dec-25	287-425	PHD	TFGMS886	55.9	143	NV	NV	NV
PUID16585860	Ca6	33679310	(GCC)4	12	TCTACGAATGCTTTTCTCAAC	CACATCACCACTAACAGGAAC	80-2647	890-1057	PHD	TFGMS887	54.9	141	NV	NV	NV
PUID16585861	0	0	(TGA)4	12	CCCAAATTGATTTTGTTGTAG	TAGTTTTGAGGGTTTTAAGCA	14-1066	350-505	Myb	TFGMS888	54.9	142	NV	NV	NV
PUID16585862	Ca4	48385876	(GGA)4	12	TAAAAGTGTTGGTGTTGGAGT	ATTTCATTTCAGCAACAAGTC	131-2884	572-880	B3	TFGMS889	54.8	151	NV	NV	NV
PUID16585863	0	0	(TGT)4	12	AGAAGGTTGAGGTAGTCAAGG	AACCCAAACTGTTCAATAGAGT	1-1359	940-1203	BTB	TFGMS890	55.1	148	NV	NV	NV
PUID16585864	Ca7	32809256	(GAAT)3	12	ACATGGTTACTTCAACCTTCA	GTGTCTCAAACATTCCCTTC	351-1823	1140-1295	AP2	TFGMS891	54.7	155	NV	NV	NV
PUID16585865	Ca6	17049312	(CTT)4	12	ATCATCCACAACACACTCTTC	CTCTCTCACCTTTACCTTTCC	119-1228	188-364	Zf-Dof	TFGMS892	54.9	156	NV	NV	NV
PUID16585866	Ca1	48129602	(GAG)4	12	ATTTGTTTCTGACAGCTTTTC	AAGCAATTGAAGGATAAGGAT	432-1337	483-674	TCP	TFGMS893	53.9	159	NV	NV	NV
PUID16585867	Ca1	389670	(GGT)4	12	AATAACAACAACGAAAGTGGT	TGAGAATGAGATTGTGAATCC	41-1297	380-691	TCP	TFGMS894	54.0	148	NV	NV	NV
PUID16585868	Ca4	439269	(TGG)4	12	CAAAAAGCTGTTATCAACTGG	CACTGAGCACTCTGGAGTAAC	389-3034	2006-2125	PHD	TFGMS895	55.2	146	NV	NV	NV
PUID16585869	Ca3	20831311	(CTCG)3	12	ATTGAACAAGTGGTAGCAAAA	GTGGAAAATAGCACACAAAAC	3270-4370	3447-4355	WD40	TFGMS896	55.1	151	NV	NV	NV
PUID16585870	Ca3	20832380	(TGA)4	12	CGGATTTGATTCATGTAGAAG	GAGGACTAACTGGAGGAGTTC	3270-4370	3447-4355	WD40	TFGMS897	54.9	149	NV	NV	NV
PUID16585871	Ca5	39847615	(CTT)4	12	CAACCTTTAACATCCAACAAA	GTGACACACTTGATGAACCTT	1553-2188	1563-2095	Ras	TFGMS898	55.3	148	NV	NV	NV
PUID16585872	Ca7	3355529	(TGC)4	12	TTGAGTATGATGTTGGGATGT	TGCACATGCAGTTTCTACATA	560-3937	3254-3562	B3	TFGMS899	55.4	152	NV	NV	NV
PUID16585873	Ca7	3356094	(TGT)4	12	AGCAGTGTCAGATTTTGTGAT	CAACAACAACAGTTACAGCAG	560-3937	3254-3562	B3	TFGMS900	54.9	152	NV	NV	NV
PUID16585874	Ca5	32189146	(TTA)4	12	TGTTCTGTAGTGCAAGAGGTT	CTAAAAGAGATTGCGTTCAAG	114-1877	669-788	HomeoBox	TFGMS901	55.1	151	NV	NV	NV
PUID16585875	0	0	(TTG)4	12	ACCGTCCGATTGGTTATTAT	CGTAACTAACGCAGTACCTTC	214-1212	853-1128	HSF DNA bind	TFGMS902	56.0	144	NV	NV	NV
PUID16585876	Ca1	2837375	(TCT)4	12	TCAAAGATTCCTTAACATTGC	GAAGCAGAAGTGCTTATACCA	250-2382	703-1011	B3	TFGMS903	54.7	144	NV	NV	NV
PUID16585877	Ca6	55329451	(TAA)4	12	TCTCATCATCCTTATTTGGAA	TTAATGGAAATGGTTCAGCTA	522-1952	1269-1388	HomeoBox	TFGMS904	54.8	139	NV	NV	NV
PUID16585878	Ca6	55329451	(TAG)4	12	TCTCATCATCCTTATTTGGAA	CCAACACCTACTTGTTGAAGA	522-1952	1269-1388	HomeoBox	TFGMS905	54.8	139	NV	NV	NV
PUID16585879	Ca4	39795924	(TTC)4	12	TTTCAAACAACACACCACAC	GATAAATCCACAATTCGCATA	308-3313	575-715	Myb DNA binding	TFGMS906	55.3	150	NV	NV	NV
PUID16585880	Ca6	41281599	(GCT)4	12	TAGGGAATGGTATCAAGATGA	AAATGGTTCCGACAAGTTC	307-1299	925-1056	WRC	TFGMS907	54.7	156	NV	NV	NV
PUID16585881	Ca7	5635095	(TGG)4	12	GAGAAGAGGTGGAGGAATTTA	TAAATTCCTCCACCTCTTCTC	345-1304	909-1172	Myb DNA binding	TFGMS908	55.1	131	NV	NV	NV
PUID16585882	Ca5	15825973	(GATT)3	12	TTGTCATTCCAAGTGGTATTT	GCCTCACTGTATGCTTGTAGA	44-1435	620-808	RING	TFGMS909	54.7	162	NV	NV	NV
PUID16585883	Ca6	18027925	(TAT)4	12	AATTCAATAGCCTCTCTTCGT	TCTACCATGAATTTTGCAGAT	290-1525	560-715	Myb DNA binding	TFGMS910	54.9	141	NV	NV	NV
PUID16585884	Ca6	18026293	(TGT)4	12	GCTACAGTCACAGATTGCTCT	TGCAGAGATAAGATGAATTGG	290-1525	560-715	Myb DNA binding	TFGMS911	54.8	149	NV	NV	NV
PUID16585885	Ca6	18027925	(TTA)4	12	AATTCAATAGCCTCTCTTCGT	TCTACCATGAATTTTGCAGAT	290-1525	560-715	Myb DNA binding	TFGMS912	54.9	141	NV	NV	NV
PUID16585886	0	0	(TGG)4	12	GATCCAAGGCTGTTGAAGT	GCTACCACCATAACCTCCTC	53-670	68-265	CSD	TFGMS913	55.2	155	NV	NV	NV
PUID16585887	0	0	(CTTT)3	12	TAAGAAATTGCCGTCTGTCTA	AACCAAAATTGACTGATTGAG	80-682	110-406	YTH1	TFGMS914	55.3	144	NV	NV	NV
PUID16585888	Ca7	889496	(TTG)4	12	CACGCTTGTTATTTTGTGAA	CACCATTTCCTACTGTCACAC	99-1076	555-731	WRKY	TFGMS915	55.0	149	NV	NV	NV
PUID16585889	Ca2	10254490	(TCG)4	12	GTTTCTTCTTCCATTCAACCT	ACTATACTTCCCCGAAGACAT	163-1092	448-582	Myb DNA binding	TFGMS916	55.0	150	NV	NV	NV
PUID16585890	Ca5	34509970	(GCA)4	12	TTCCTCGTGGAGATACAGATA	CCATTTGCACTACCATTTAAG	180-2873	2505-2609	WD40	TFGMS917	54.9	144	NV	NV	NV
PUID16585891	0	0	(TCG)4	12	TCCGTAATCATCAGTATCGTC	GTTACCCTTATGGCATCTTG	329-1825	1220-1480	Myb DNA binding	TFGMS918	55.2	180	NV	NV	NV
PUID16585892	Ca2	30868473	(TTTA)3	12	TAGAGCAAGAGCAGATGGTAG	CATGAATTTTGTTCTTTGGAC	240-2327	432-623	ANK	TFGMS919	55.1	165	NV	NV	NV
PUID16585893	Ca5	3947535	(TGA)4	12	GAATCATCATAGCCAAATTGA	CATCATCATGTTAATGCAATG	157-1230	877-1086	TCP	TFGMS920	55.2	148	NV	NV	NV
PUID16585894	Ca1	203312	(TTC)4	12	TGATGATTATTTCGTTTCCTC	GCAACTAGAAGACGCTGATAA	238-2373	1387-1563	RRM	TFGMS921	54.4	152	NV	NV	NV
PUID16585895	Ca7	8419862	(GTT)4	12	CCATCATTGTGTCTTTTAAGG	CATCAGCCTTTTTCACTTATG	1445-2314	1877-2212	Response	TFGMS922	54.8	160	NV	NV	NV
PUID16585896	Ca8	4460360	(GAT)4	12	TGGTTCAAAGGAAGATACAGA	TGTGGAGACAGGCTACATAAT	120-1178	588-797	SWIB	TFGMS923	55.0	154	NV	NV	NV
PUID16585897	Ca3	30319786	(GAT)4	12	AGAAGAGTTGAGTTGGGATGT	CGTGTGTATGCACATGTATCT	130-1335	613-747	BSD	TFGMS924	55.4	149	NV	NV	NV
PUID16585898	Ca1	10065563	(GT)6	12	AATAAAAGGTGTTTGGGGTAG	CCTTCATAGGTTGATTTGATG	648-1511	1002-1463	AUX_IAA	TFGMS925	55.0	143	NV	NV	NV
PUID16585899	0	0	(CT)6	12	CTTTCTCTCTATCCTCCTTCAA	ACAGTAGCAACAGATCCAAGA	450-4657	1209-1871	START	TFGMS926	54.6	143	NV	NV	NV
PUID16585900	Ca4	9451990	(TTCT)3	12	ATTTTGATTCTCCTCAGATCC	AGGGTAGAAAACATGGAAAAG	138-1349	828-983	Myb DNA binding	TFGMS927	54.9	145	NV	NV	NV

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585901	Ca3	37212123	(TGA)4	12	CCTCAAATGATCCAAACTTTA	CCAATGATAGGAAGAAAAGGT	400-948	457-594	HLH	TFGMS928	54.5	153	NV	NV	NV
PUID16585902	Ca5	35389451	(CGA)4	12	GATATATCCGATACAGCGTTT	AACTTCGAGCCTTTTTCTTAC	363-1097	954-1088	ZfB Box	TFGMS929	53.7	149	NV	NV	NV
PUID16585903	Ca6	29256025	(GTG)4	12	GAGGAAGTTACCAAAAGCAAC	GGTTACATGTTTTGCATTCAT	31-816	271-351	ZfC2H2	TFGMS930	55.7	162	NV	NV	NV
PUID16585904	Ca4	6180269	(TGCT)3	12	CAGGAGGAGGACATCTCTAAT	GGATCCATTATCCATATCACA	115-903	706-825	HomeoBox	TFGMS931	55.0	158	NV	NV	NV
PUID16585905	Ca4	22195121	(TCA)4	12	CTTCCTCCTCTTATCATTGCT	GAATCTAACAGCTTTGGTCAC	1-1302	853-1101	Myb DNA binding	TFGMS932	55.3	180	NV	NV	NV
PUID16585906	Ca4	22196962	(TTG)4	12	TGTTCCGTTCACTAGTTGTCT	CGCTTCTTCTCTCTCTCTCTC	1-1302	853-1101	Myb DNA binding	TFGMS933	55.0	169	NV	NV	NV
PUID16585907	Ca1	3235738	(GAA)4	12	ATAATGGTTACTTTCGGAGGA	TCTTCTTCGTGTTCATGTTCT	178-1098	232-504	Myb DNA binding	TFGMS934	55.4	151	NV	NV	NV
PUID16585908	Ca5	41254342	(TG)6	12	AGGAAGAGAAAGAGGACAAGA	GCTCAAAATATCTAAGCAGAGG	549-1787	1647-1778	B-box	TFGMS935	54.9	134	NV	NV	NV
PUID16585909	Ca4	5155600	(TTG)4	12	TTTGGTAAGGCTAATATGACG	TATATCGAAGACGAATTGGAA	221-1420	854-1144	DUF573	TFGMS936	54.8	152	NV	NV	NV
PUID16585910	Ca7	8015348	(TCT)4	12	CAACAACAACTCTCTGGAAAC	TGATTGGAAGATGAAGAGTTG	117-1184	273-473	TCP	TFGMS937	54.9	155	NV	NV	NV
PUID16585911	Ca6	13184584	(TGA)4	12	GAACTAATTGTTGGGGAACTT	ACTTCACCTTCTAGCCCTTTA	32-1249	608-826	SET	TFGMS938	54.9	145	NV	NV	NV
PUID16585912	Ca5	29786557	(GAA)4	12	AGAAGAAGGAGGTTTGTCATC	AGCCAAAAGAACAAGAAGAAG	362-4102	764-1159	AAA	TFGMS939	55.0	159	NV	NV	NV
PUID16585913	Ca5	37147069	(GAA)4	12	AGGTGGAAAACAATATGGAAT	GCCTGAGTTTCCTAAAGAGTC	229-1044	412-588	Zf-HD-dimer	TFGMS940	55.1	119	NV	NV	NV
PUID16585914	Ca5	37146985	(GAG)4	12	AACCCAAACTCCAAATAAAAC	GAATCCCATTTCTTCTTCTTC	229-1044	412-588	Zf-HD-dimer	TFGMS941	54.9	157	NV	NV	NV
PUID16585915	Ca7	2713430	(TAAA)3	12	CAAAGTCTAACCAATTTCACG	AGAGTCATGTGCGTTGATAAG	735-1505	807-938	Plant Zn clusf	TFGMS942	55.1	148	NV	NV	NV
PUID16585916	0	0	(GAT)4	12	TTGTTTGTGCAAAGTTTAAGAG	ATCCCAATTTTCAAACACAG	193-1002	330-743	Whisly	TFGMS943	55.1	153	NV	NV	NV
PUID16585917	Ca6	58554755	(GTTT)3	12	TGCTTTTCTCTACTGGCTTTA	AGACACAAGATCATCCAAGTG	499-972	586-765	bZIP	TFGMS944	54.8	163	NV	NV	NV
PUID16585918	Ca5	27301868	(GA)6	12	TGTTTAGCTGCATGAAGTTGT	CTTCACTCTTCACTCTCCTCA	276-1082	576-698	AP2	TFGMS945	56.2	148	NV	NV	NV
PUID16585919	Ca5	45592893	(TCA)4	12	CTTCTCATTTGTCAGCTATGG	TTAGCAAACCCTGTTGAATTA	97-1074	196-375	Zf-Dof	TFGMS946	55.2	157	NV	NV	NV
PUID16585920	0	0	(TA)6	12	CATAGTCGGAGGTGATAACTG	CGATGTAGCCAAATGTAAAAG	137-1651	992-1117	PSP	TFGMS947	54.9	143	NV	NV	NV
PUID16585921	Ca1	4865701	(GTA)4	12	CAAGCAATAACGGTAAAAAGA	CTATACCGTTTCAAATCCAAA	22-1449	604-771	BSD	TFGMS948	55.0	152	NV	NV	NV
PUID16585922	Ca8	4628307	(CGA)4	12	CAAGTTCTTGTTGTTGAAACC	GATGATTTCAACATGGGAATA	105-2279	918-1322	POX	TFGMS949	54.9	152	NV	NV	NV
PUID16585923	Ca2	22141288	(GCA)4	12	GTTGGAGGAGAAGATGAAGAT	CCAGATTAGCTTCAATTGTTC	105-2279	918-1322	POX	TFGMS950	54.9	151	NV	NV	NV
PUID16585924	Ca2	32955094	(TCTA)3	12	TGCTCAATTTTTAGCTTCAAC	ATCTGAAACAAGAGACCCACT	581-1390	1175-1312	bZIP	TFGMS951	55.0	166	NV	NV	NV
PUID16585925	Ca8	4023096	(CTA)4	12	GTCCTCCACCACATTTGTTA	GTGGTTGTGAAATGAGAGAAG	415-1980	1162-1314	AP2	TFGMS952	55.9	149	NV	NV	NV
PUID16585926	Ca8	4020082	(GAA)4	12	AAGGAAAAAGAGTTGGATCTG	TTGACAAAATTTCACACCAA	415-1980	1162-1314	AP2	TFGMS953	55.2	158	NV	NV	NV
PUID16585927	Ca8	4020199	(GGT)4	12	TTGGGTTTTCAATGGATAGTA	ATTTGATCAAGAGGGTCTCAT	415-1980	1162-1314	AP2	TFGMS954	54.8	164	NV	NV	NV
PUID16585928	Ca8	4020168	(TAG)4	12	GGAACGTTGAAGAAAAGAACT	CAGTTGCTAACAAATGTGGTG	415-1980	1162-1314	AP2	TFGMS955	55.3	160	NV	NV	NV
PUID16585929	Ca4	45420293	(GAT)4	12	GTGCTGAATGTTATGCACTTT	GGGTTTTTCATTGATTTCTTC	270-1436	395-509	HomeoBox	TFGMS956	55.5	135	NV	NV	NV
PUID16585930	Ca4	45415195	(TA)6	12	GGAAGAAATCAATGAAAAACC	AGGCCAAATTTCTTGTACTCT	270-1436	395-509	HomeoBox	TFGMS957	55.4	159	NV	NV	NV
PUID16585931	Ca7	27236578	(TGT)4	12	CAATGTGACCTCCTTGTACTT	ATATAGAACCAGAGGCAGAGC	411-1628	1311-1511	TCP	TFGMS958	54.3	150	NV	NV	NV
PUID16585932	Ca7	33739638	(GAA)4	12	ATGCCTCTTTCGAACTTTACT	ACTTTCATCATCGTCATCATC	236-2587	2033-2326	ARID	TFGMS959	55.0	167	NV	NV	NV
PUID16585933	Ca7	10684263	(CTTT)3	12	TTCATTAGTCACAAGCAAACA	GAAAATGGTTGATCAGTTGAA	248-1897	1175-1327	Myb DNA binding	TFGMS960	54.5	151	NV	NV	NV
PUID16585934	Ca8	12526570	(GAT)4	12	ATCAAGCTGTTTGGTAGAACA	GATATCCCTTCTTGACCAACT	204-1583	307-515	Myb DNA binding	TFGMS961	55.1	149	NV	NV	NV
PUID16585935	Ca3	17180152	(GCA)4	12	CAGTCTAACAGGAATGATGGA	TGCTTTCGTTTTCTGTTACTC	242-2649	1847-1951	WD40	TFGMS962	55.2	140	NV	NV	NV
PUID16585936	Ca6	22661507	(TGC)4	12	GCACAGATTCATCTATGGTGT	TATTTGCGTGATCTTAAGGAG	566-4963	3938-4087	PHD	TFGMS963	55.1	151	NV	NV	NV
PUID16585937	Ca1	17402954	(TTTA)3	12	TGGGATGAATTCAACTTTAGA	TGACCCATTCAAGGTATTAAA	202-2907	1747-1842	Ank	TFGMS964	54.9	157	NV	NV	NV
PUID16585938	Ca1	24070712	(GCA)4	12	CAACAAGCTAGCCTCTTACAG	CATAAGCTGAGACTGCAAAAG	777-4139	1152-1460	B3	TFGMS965	54.8	154	NV	NV	NV
PUID16585939	0	0	(GGTT)3	12	AAAAAGACGAACACAGCACTA	CACGTTTCGTTAACTCACTCT	1067-1870	1448-1528	Zf-CCCH	TFGMS966	55.3	153	NV	NV	NV
PUID16585940	Ca2	10060265	(TCA)4	12	GGGAGTTCTGAGTCTTTAGGA	GACCAGATTCTTCTGGAAATAA	115-2715	2533-2661	Myb DNA binding	TFGMS967	55.2	145	NV	NV	NV
PUID16585941	Ca3	29569841	(CTG)4	12	CTGCAATAAATGATGCTCAAC	ATGGGAAATGGAGAAGGA	589-2772	2371-2637	Ank	TFGMS968	56.0	149	NV	NV	NV
PUID16585942	Ca1	3999887	(TCA)4	12	ACATCATCAACAATGGTCTTC	ATGTTGTTGTCCTAGTTGGAA	226-1611	445-651	TCP	TFGMS969	54.9	151	NV	NV	NV
PUID16585943	Ca1	5666044	(TTG)4	12	AAAAACAAGGAACCAAAGAAG	ATCTCCTCTATCATTGGTGGT	2164-5712	3577-3960	APG6	TFGMS970	55.3	126	NV	NV	NV
PUID16585944	Ca5	37494945	(TGCC)3	12	AGCTATTCTTCGTGAAAGGTT	CTCTGTCACACATCAGAAGGT	634-1692	997-1110	GATA	TFGMS971	55.0	154	NV	NV	NV
PUID16585945	Ca6	5509444	(TCTT)3	12	ATACACCCTCAACTTTGGTTT	CAACAACAACAACACAAGCTA	323-1897	1592-1735	HLH	TFGMS972	55.3	153	NV	NV	NV
PUID16585946	Ca3	27665600	(GAA)4	12	GAGACCCATTGTGGTTTACTT	AGGTAGGGTTTGTGTTACCTT	288-1684	1406-1657	K tetra	TFGMS973	55.7	161	NV	NV	NV
PUID16585947	Ca8	5564500	(TGA)4	12	CCCATTGATTACTTGAAACAC	ACTCTAGGGTTTTCACTTTCC	149-3886	1601-1738	GYF	TFGMS974	54.7	150	NV	NV	NV
PUID16585948	Ca1	15487460	(GTT)4	12	GTTCCCAGTCTTGAGAAAGAG	CCACACTTCATCTTCATCTTC	255-683	267-425	HTH	TFGMS975	55.7	154	NV	NV	NV
PUID16585949	Ca5	30616947	(TTC)4	12	AGCTAACAAAGAAAAACACGA	GAAAAACAAACTCCCTCCTTA	100-1014	757-861	GATA	TFGMS976	54.6	148	NV	NV	NV
PUID16585950	Ca3	23643849	(TAA)4	12	GGATGGACCTAAGAAGACATT	TAACCCTTTTCTCCTCTTTGT	192-527	393-431	WRKY	TFGMS977	54.8	149	NV	NV	NV
PUID16585951	Ca6	12572288	(CTT)4	12	GATCTTTTCAACAAAGCAAGA	AAAACACAATGAACTTTGCAC	840-2244	1029-1292	TCP	TFGMS978	54.8	147	NV	NV	NV
PUID16585952	Ca6	12571282	(TC)6	12	CAGTGTCTGAATTTTCGTCAT	TTCTCCATTGTAGGAGTAGCA	840-2244	1029-1292	TCP	TFGMS979	55.3	158	NV	NV	NV
PUID16585953	Ca6	12572068	(TCA)4	12	GTCAAGGTGTGATATTCGTGT	TTTCCCTTTGTGATCTGAATA	840-2244	1029-1292	TCP	TFGMS980	55.0	151	NV	NV	NV
PUID16585954	Ca5	30179966	(GCT)4	12	CACACTTTAAAGCAACCTCAT	AACTAATAGAGCTGCGTCCTT	286-1980	1273-1485	Sigma70	TFGMS981	54.7	134	NV	NV	NV
PUID16585955	Ca5	30179302	(TTC)4	12	TATTTAATCAATCAGCCTTGG	ATGAGGTTGCTTTAAAGTGTG	286-1980	1273-1485	Sigma70	TFGMS982	54.6	149	NV	NV	NV
PUID16585956	0	0	(TGG)4	12	GTCCCTATTCTTCCGATCTC	AAAATTCTGTACTTGCTGCTG	396-1229	300-440	Zf Bbox	TFGMS983	55.3	149	NV	NV	NV
PUID16585957	Ca4	48122188	(TACA)3	12	TCTCACAAAGATTCCTTCCTT	AGCATGAACCGTACAAAAATA	495-2333	1050-1157	HomeoBox	TFGMS984	55.6	161	NV	NV	NV
PUID16585958	0	0	(GGT)4	12	TCTAAAAGGCCTTATGGTTCT	CTATCACCACTCACAACAACTC	304-1134	742-846	WD40	TFGMS985	54.9	164	NV	NV	NV
PUID16585959	Ca1	46719697	(TTC)4	12	GATAACTTGAAACCGCCATAC	ACGAATTCATTTGTTGGTGT	149-1957	212-1261	mTERF	TFGMS986	56.3	142	NV	NV	NV
PUID16585960	0	0	(TGT)4	12	GACATCCGTCCCAGTTACTA	CATCAATTAACCTCACAAACC	239-2206	521-773	Myb DNA binding	TFGMS987	55.1	133	NV	NV	NV
PUID16585961	0	0	(TTG)4	12	GGAATAGTAGAAGGGGGTGTA	CAACACCTTCAAAATTACCAC	239-2206	521-773	Myb DNA binding	TFGMS988	54.9	151	NV	NV	NV
PUID16585962	Ca4	13727564	(TCC)4	12	AGTTTCAAATTCCCTGTCAAT	AGATGGATGTGTTTGATTTTG	517-4470	2197-2277	PHD	TFGMS989	55.3	158	NV	NV	NV

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16585963	0	0	(TAA)4	12	GGTGAGAAAAGGCAAATAGAT	CCATAACATCAGTATCCCAAA	295-1413	637-909	Thioredoxine	TFGMS990	55.2	148	NV	NV	NV
PUID16585964	Ca1	5765349	(TCT)4	12	AACAACAACACTCCTGGTTTA	TGATGTAAGCTTCCAAGAGAC	55-924	709-813	HomeoBox	TFGMS991	54.8	145	NV	NV	NV
PUID16585965	Ca2	26833724	(GGT)4	12	GGACAATTGGATTCTGGTACT	TCATCTTTAGGTTCATCCTTG	21-1746	1251-1427	WRKY	TFGMS992	55.6	156	NV	NV	NV
PUID16585966	Ca8	15607448	(TCT)4	12	TAAATCGCCTAGAGATGTTCA	CATAACTTGTTCCGAGTCTTG	209-886	377-472	AP2	TFGMS993	55.2	155	NV	NV	NV
PUID16585967	Ca8	8840253	(CT)6	12	TCTCAAATTCAACCTAAATGC	CTGCTATCCACCTCTTTCAC	289-2259	1753-1893	HLH	TFGMS994	54.7	146	NV	NV	NV
PUID16585968	Ca8	8841717	(GGT)4	12	ACGGAATGCTTTCTTTTACTT	CAAAACTCAGAATCTCACCAG	289-2259	1753-1893	HLH	TFGMS995	55.0	139	NV	NV	NV
PUID16585969	0	0	(CT)6	12	ACTCCTAAACCTTTTTGTTGC	GGCAGAGAGAAAGAGAGAGAG	239-1300	437-1273	AUX-IAA	TFGMS996	55.3	167	NV	NV	NV
PUID16585970	Ca3	27041765	(TGT)4	12	TGAGTATCCCTTAATCACGAA	TGCACAGTAACAACAACTCAG	872-2200	1685-2017	MATH	TFGMS997	54.9	146	NV	NV	NV
PUID16585971	Ca4	11053035	(GAT)4	12	AGGTTTTCAAGAAAAGTGGAC	GAGGATCAATAACAGCATTTG	363-2039	523-803	NAM	TFGMS998	55.1	147	NV	NV	NV
PUID16585972	Ca4	11052375	(TCAA)3	12	AAGTATGATCCTGGGTCAGTT	CTCAGGTGATTCAGAAAAATG	363-2039	523-803	NAM	TFGMS999	55.2	151	NV	NV	NV
PUID16585973	Ca6	789811	(TTA)4	12	AGCACTGAGGTCATATTCAGA	AAATCTCATCGATCCTTCTTC	258-2126	279-1385	GRAS	TFGMS1000	55.0	145	NV	NV	NV
PUID16585974	Ca7	5426491	(CTT)4	12	AGTTGGTAATCCCTCATTTTC	ATCTCAGAAGACAAAGGGAAG	1540-3402	1606-1848	Helicase	TFGMS1001	54.8	156	NV	NV	NV
PUID16585975	Ca7	5427952	(TCG)4	12	ATCTCGGGATCAACATTACTT	GTCAATGAACAGATCGAAGAC	1540-3402	1606-1848	Helicase	TFGMS1002	55.3	158	NV	NV	NV
PUID16585976	Ca1	22350311	(TGT)4	12	TTGTTGATGTTGATGTTGCT	CCTATCAACCTATCGAACCTT	88-1548	1231-1487	WRKY	TFGMS1003	55.0	144	NV	NV	NV
PUID16585977	Ca5	40620289	(TA)6	12	TGGATATATGGAAAGCAAAGA	TGAAACCACCAACAAAACTAT	39-728	399-560	HomeoBox	TFGMS1004	55.0	159	NV	NV	NV
PUID16585978	Ca5	31758233	(TTG)4	12	GGAAACTCCTTGAGACTCTTC	TCAACAACAACACCAGAAAAT	286-2301	1174-2010	DnaJ	TFGMS1005	54.7	147	NV	NV	NV
PUID16585979	Ca4	48077178	(TTAT)3	12	CCAACTTTTTAGTCTTTGATTTG	TCCTCAGAACCATAACTTTGA	121-585	208-384	bZIP	TFGMS1006	55.1	143	NV	NV	NV
PUID16585980	Ca3	39292008	(TTTG)3	12	TTCTTTTCTCTCTTGCATTTG	CCAAAATCATCATCATAAACG	100-1755	502-789	BTB	TFGMS1007	55.0	164	NV	NV	NV
PUID16585981	Ca3	4829696	(TTA)4	12	CATCATTTCATTTCCATTCTC	GTGGTGGACATGTTTTATTTT	198-1748	1401-1577	WRKY	TFGMS1008	54.6	152	NV	NV	NV
PUID16585982	Ca1	45076076	(CTTT)3	12	CCTTTGGTTGTAGATGGTGT	GGAACCAAACGTGAGTATAAA	253-5448	3460-4341	KAT11	TFGMS1009	55.0	141	NV	NV	NV
PUID16585983	Ca8	8417363	(TGT)4	12	GCTTAAGCTTTGTTGTTGTTG	CAAGAAGTGAAGATGAAATGG	363-1553	747-902	Myb DNA binding	TFGMS1010	55.5	150	NV	NV	NV
PUID16585984	Ca8	8417501	(TTG)4	12	AGAAATTGAAGAAGGGTTTGT	CATCATCACTTCCAAAACATT	363-1553	747-902	Myb DNA binding	TFGMS1011	54.7	186	NV	NV	NV
PUID16585985	Ca7	34321017	(GAA)4	12	ATCAGAATTTGACAAGGAGGT	GAGGGATAGTGTTGTTGTTGA	712-1293	832-1122	B3	TFGMS1012	55.3	153	NV	NV	NV
PUID16585986	0	0	(TTC)4	12	GTGGAATTTCATATGGGTTTA	TCCACTCAGAGATACTCTCCA	408-1298	771-905	Myb DNA binding	TFGMS1013	54.2	153	NV	NV	NV
PUID16585987	Ca6	3654970	(TAA)4	12	GCCTTATTCTCACAGTTGGTA	CTCAAAACCACAAAGAATCAC	30-764	168-320	AP2	TFGMS1014	54.6	133	NV	NV	NV
PUID16585988	Ca1	2741494	(CTTC)3	12	ATCTTTCCTCTTCTCGTTGTC	GGAAGTTGAAGCCTATGAAAT	287-5644	5360-5506	HomeoBox	TFGMS1015	55.2	167	NV	NV	NV
PUID16585989	Ca5	30816603	(TGT)4	12	GCTACAATTGGCATATGAAAG	TAGCAGCTGATAGTTGCTCTT	100-1257	556-699	HLH	TFGMS1016	55.1	151	NV	NV	NV
PUID16585990	Ca3	36687785	(GTTG)3	12	AAAACCCTCCAATTATCAAAG	AAGCATCATGCAAAGAATAAG	236-1222	572-652	ZfCCCH	TFGMS1017	55.0	154	NV	NV	NV
PUID16585991	0	0	(GAG)4	12	AGAAGAAGAAGAGGTGGTAGG	ACCTCTACTGTTTCTGCTTCC	357-2489	1146-1205	ZfCCCH	TFGMS1018	54.4	151	NV	NV	NV
PUID16585992	Ca6	20762848	(TTA)4	12	AAGGAGGGGTTTTCTCTTTAT	CTCTTCTCTTCTCTCCCACAC	162-875	492-641	HLH	TFGMS1019	55.2	134	NV	NV	NV
PUID16585993	Ca1	12710098	(GAG)4	12	AACTTGTGGAAGCATCTGTTA	CACCTGGAATAACAGTACGAA	521-901	686-814	ACT	TFGMS1020	55.1	151	NV	NV	NV
PUID16585994	Ca2	26158349	(TGG)4	12	AATAATAGGAGGGAAGGGTTT	AATTGCTGAAGCTGAAGATTA	107-1144	259-427	FHA	TFGMS1021	55.1	152	NV	NV	NV
PUID16585995	Ca1	21136404	(TATT)3	12	AGACAGTGCAGCAAGATCTAC	TGACAGCTGAAATTAACCACT	234-845	336-593	K-Box	TFGMS1022	54.8	150	NV	NV	NV
PUID16585996	Ca8	892496	(GATT)3	12	GGAGTTAAGTCGAGTTGATAGAA	ACAACCACTTCCATTTACACA	264-1031	462-740	Acetytransf	TFGMS1023	54.6	156	NV	NV	NV
PUID16585997	Ca2	35557054	(CTT)4	12	CTAGGGTTCGAGGAGTATGTT	GAAGCACCGTAGTCGTAAAC	199-783	280-471	Histone	TFGMS1024	55.1	149	NV	NV	NV
PUID16585998	Ca4	42774790	(TCA)4	12	CTTTCAAACTTTGTTCCAATG	GTAAAGGGTGGTTTGAATTTT	416-1084	500-955	DUF702	TFGMS1025	55.1	145	NV	NV	NV
PUID16585999	Ca4	8751680	(GTG)4	12	TGCAGTAGAAGAAGCAGAGAG	AGACCTATCTTTTCCGTTTTG	100-1488	1015-1389	NAM	TFGMS1026	55.3	153	NV	NV	NV
PUID16586000	Ca6	4214592	(CT)6	12	AGGGAAGAGGAATAAAGTTTG	GATCTGCAAGAATGTGAAAAG	509-3874	3146-3454	B3	TFGMS1027	54.4	135	NV	NV	NV
PUID16586001	Ca4	48201292	(TGT)4	12	ATCACCGTTAATCCAAATCTC	ACATCACCAAAACCTTAACAA	1-251	78-227	DUF702	TFGMS1028	55.7	150	NV	NV	NV
PUID16586002	Ca7	28547530	(GCT)4	12	CTTGGGATTCCAATATAAATG	GAAGAAATGAGTTAATGGAGGA	786-1760	975-1211	SBP	TFGMS1029	53.9	152	NV	NV	NV
PUID16586003	Ca7	28548004	(GCTA)3	12	GCTCCTCCATTAACTCATTTC	CAACTTCAAGCTCAATGTTTT	786-1760	975-1211	SBP	TFGMS1030	55.5	168	NV	NV	NV
PUID16586004	Ca7	28549569	(GGT)4	12	GTGTGTTTACATGAGGGAGTG	CAACTTCAAGCTCAATGTTTT	786-1760	975-1211	SBP	TFGMS1031	55.5	154	NV	NV	NV
PUID16586005	Ca7	28547876	(TAT)4	12	AACAACGTACGCCATATTATT	CACTTTAACCCACAACAACAG	786-1760	975-1211	SBP	TFGMS1032	54.1	152	NV	NV	NV
PUID16586006	Ca7	28550154	(TTTG)3	12	TTCAGAAACGAGAGCAGACTA	AGGGTGAAAGTGAGATCTTTT	786-1760	975-1211	SBP	TFGMS1033	55.5	161	NV	NV	NV
PUID16586007	Ca7	7893649	(TCT)4	12	TCTAGCTTTGTTCCACAATTC	TTAATTCATGTTCCAACTTCC	232-978	511-660	BSD	TFGMS1034	54.7	133	NV	NV	NV
PUID16586008	0	0	(GTT)4	12	TCTCTCTTTCTCTCTCTCTCTCA	GGTAAGTCTTCATAACGAACG	121-900	154-929	HSF	TFGMS1035	54.5	172	NV	NV	NV
PUID16586009	Ca7	7474564	(CTC)4	12	TTAGGACAATCAATGAAGCAT	ATGAGGAAGCATAACAGGAGT	112-1014	136-288	Myb DNA binding	TFGMS1036	54.9	153	NV	NV	NV
PUID16586010	Ca7	7475343	(TTC)4	12	TGGAAGAAGTGAAACAACATT	TATGTTGGCCTGTTATTGGTA	112-1014	136-288	Myb DNA binding	TFGMS1037	54.9	155	NV	NV	NV
PUID16586011	Ca5	43835460	(TGCT)3	12	TGTCTCGAATACTTACGATCC	CCATCTTCAGAGAGAAACTCA	454-1473	613-699	bZIP	TFGMS1038	54.5	133	NV	NV	NV
PUID16586012	0	0	(TTC)4	12	CCATTCTAGCCCTATTTGTTT	TTGTTAAGATGTGGAAAAAGC	1-488	363-431	Myb DNA binding	TFGMS1039	55.2	144	NV	NV	NV
PUID16586013	Ca4	2002236	(TTC)4	12	ATTTCACATCCATCAATTCAG	ATACACCAACACAGATTGCAT	2-220	2-187	ovate	TFGMS1040	55.0	179	NV	NV	NV
PUID16586014	Ca5	36711442	(TCAT)3	12	AGTTTCTTTCCATTTTCCAAC	GTAGTTGGTTGTTGTGGTTGT	18-611	93-374	HSF	TFGMS1041	55.0	150	NV	NV	NV
PUID16586015	Ca2	6862359	(TTTG)3	12	GAATGCCTCATTTATTTCTGA	ACAAACTAATACTGGCAGCAG	73-423	151-306	Myb DNA binding	TFGMS1042	54.6	114	NV	NV	NV
PUID16586016	Ca7	20120510	(TCA)4	12	CAAACACGTTTGATCTTTCTC	CTCTCATGCTACGTTTTGAAG	128-840	677-832	Myb DNA binding	TFGMS1043	55.0	145	NV	NV	NV
PUID16586017	Ca3	26542714	(TTGA)3	12	ATCTCTTCATCAGTTGGATGG	TGTTATTTCTTCTTTCATCACTG	333-1499	1068-1451	NAM	TFGMS1044	56.6	150	NV	NV	NV
PUID16586018	Ca2	25291741	(TTCT)3	12	TCTCTTCTATCACTTCGCTTG	TGGGATAATGACAAATATGATG	157-1347	1024-1236	RRM	TFGMS1045	55.0	158	NV	NV	NV
PUID16586019	Ca3	3616994	(TCT)4	12	AAGCTGATATGAATGCTGAGA	CGTTAACAGCACAGTACTCAA	368-1354	575-736	Zf-HD	TFGMS1046	55.2	158	NV	NV	NV
PUID16586020	Ca3	25756988	(TTC)4	12	ACCAGTTTTCTTCTTCTCAGC	CTGGTTAAGGAAGAGGATGTT	223-2466	1180-1662	YDG-SRA	TFGMS1047	55.4	151	NV	NV	NV
PUID16586021	Ca3	38615300	(GGA)4	12	CATAGACGCTGAAAGAGCTTA	AGTCAGAGCTCCAATTTCAA	144-1427	864-1085	Myb DNA binding	TFGMS1048	55.2	147	NV	NV	NV
PUID16586022	Ca3	38615518	(TCT)4	12	GTTTTCTTCGTCAAAAACCA	ACTCCCTTTTCATCCTCTATG	144-1427	864-1085	Myb DNA binding	TFGMS1049	55.4	144	NV	NV	NV
PUID16586023	Ca4	9472194	(GTTA)3	12	CGTGTGTCTCTAACCATCTTC	CTACCTCCTTCCATTTTCTGT	184-984	441-954	B3	TFGMS1050	54.9	150	NV	NV	NV
PUID16586024	Ca6	10054407	(TCTA)3	12	TCTGTTGTTTTCCTCTATTGG	CAACTAACACCAAGAAGCAAC	706-1158	814-990	bZIP	TFGMS1051	54.6	150	NV	NV	NV

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16586025	Ca3	22060177	(GCA)4	12	TTATAAGCAGCACCTTCAAAT	ATTCCCTGATTCAAATATGGT	191-2011	1241-1996	SMC prok	TFGMS1052	54.5	150	NV	NV	NV
PUID16586026	Ca8	3683250	(TAAA)3	12	GCGCTAAAAGAGACACATAAA	CAATATGTTAACGACGGAGAC	296-1000	689-997	DUF260	TFGMS1053	55.1	149	NV	NV	NV
PUID16586027	0	0	(TC)6	12	AAACTGCGTCGTGTGTTT	TTATGGGTTTCGTCAAAGTTA	209-961	224-616	DUF3594	TFGMS1054	55.1	155	NV	NV	NV
PUID16586028	Ca5	12078869	(CTT)4	12	GGATCTCACATCACACCATAC	TATCGAGCTTCTTCTTCATTG	163-1050	181-375	CBFD-NFYB	TFGMS1055	55.2	140	NV	NV	NV
PUID16586029	Ca7	11192806	(GTG)4	12	AAGAGGTTCAAGAATTGAAGG	AGCCATAGAGAAAGTGGTTTT	108-974	531-695	HomeoBox	TFGMS1056	55.2	149	NV	NV	NV
PUID16586030	Ca7	32386290	(TTC)4	12	CTGAAAACCTCTTCAACAGTG	ATCTCTTTCAACCCTAAAACG	299-1066	632-1039	DUF3594	TFGMS1057	55.1	156	NV	NV	NV
PUID16586031	Ca7	12022627	(TTAA)3	12	TCTGCACCTGATGCTACTAAT	TGAAACTGTCGGTTCTGTAAC	129-1130	906-1088	WRKY	TFGMS1058	55.2	147	NV	NV	NV
PUID16586032	Ca4	45596042	(TTG)4	12	AACCGTCAGTCATGAGATTC	GTTGTCGATCAAAAGTATTGC	126-2153	1350-1484	WRC	TFGMS1059	55.0	150	NV	NV	NV
PUID16586033	Ca5	21386676	(TCA)4	12	CAAGATTATCATTTGGACGAC	AAATGGTGCTAATTTGGATCT	725-2170	1739-2074	Response-reg	TFGMS1060	54.7	150	NV	NV	NV
PUID16586034	Ca6	38815534	(TTC)4	12	TATCTGAAAACCCTCTTCCTC	CCATGATTAACCTCAAAAGTG	243-2444	1365-2438	GRAS	TFGMS1061	55.1	141	NV	NV	NV
PUID16586035	Ca6	17265368	(GAAG)3	12	AAAGAGCTCGAGAGACAAGAT	ACGTTTTTCCTCTCGTTTAGT	380-5683	515-685	HomeoBox	TFGMS1062	55.1	156	NV	NV	NV
PUID16586036	Ca3	29120707	(GAA)4	12	GGAGGAAGAGGAAGAGAGAAT	GAGAGGACCTCAATTTCTTGT	238-2583	1420-1548	Myb DNA binding	TFGMS1063	55.7	172	NV	NV	NV
PUID16586037	Ca5	44152835	(GATC)3	12	ACATCCATCACACATCACAC	AGAGAGAGAAATTGAGGGAAA	238-2583	1420-1548	Myb DNA binding	TFGMS1064	54.7	151	NV	NV	NV
PUID16586038	Ca5	24343863	(GTTT)3	12	AGATGCATGTTTGATTCTCTT	TGGTCAGAAGACACTATGGAG	491-1504	821-991	CBFD-NFYB	TFGMS1065	54.0	159	NV	NV	NV
PUID16586039	Ca5	36756738	(GTT)4	12	GGGATTCAGATTTGTGATTTA	CAGAGAATATACCGACGTTTG	147-1436	1197-1268	bZIP	TFGMS1066	54.2	195	NV	NV	NV
PUID16586040	Ca5	26429761	(TGA)4	12	AAGAGAGAAGTGGGAGAGAGA	TCCTTCTCTGATATCCTTAATTC	155-1210	837-1075	WRKY	TFGMS1067	54.9	164	NV	NV	NV
PUID16586041	Ca2	32544903	(TTC)4	12	CTTTCTCTGGAGCTTTGATTT	CCGTATTGAATGTACCAACAG	216-1943	780-821	ZfCCCH	TFGMS1068	55.5	168	NV	NV	NV
PUID16586042	Ca8	3456870	(GCG)4	12	TATATATGGCCATGAAGTTCG	AGATAAGGGTTTTGAGGAATG	189-2045	1670-1904	Acetytransf	TFGMS1069	55.3	140	NV	NV	NV
PUID16586043	Ca4	8299437	(GAG)4	12	GAAGTCAGCACATGGAAAAT	TCATCCTCTGCAGTACTAAGG	37-1437	475-609	BSD	TFGMS1070	55.2	157	NV	NV	NV
PUID16586044	Ca3	38103222	(CTTT)3	12	TTCAAGTATCTAGCGATACGG	GAATCGTTTTACTCCCTTTTC	156-596	297-518	Histone	TFGMS1071	54.9	168	NV	NV	NV
PUID16586045	0	0	(CTA)4	12	GATTTCAATCATCATCTGCTC	TCCTTTGCACACAATCTATTT	117-1022	260-474	TCP	TFGMS1072	54.8	152	NV	NV	NV
PUID16586046	Ca3	31369487	(TAT)4	12	TTTGCCCATAAATACACTCAC	ATTCTTCCATGATGAATCTCC	111-677	573-668	NAM	TFGMS1073	55.3	153	NV	NV	NV
PUID16586047	Ca1	27139182	(TGAT)3	12	AAGTAGAGAAGGGATTTGTGG	ATTGGATGGAGGTAACAAAAT	2-625	8-268	mTERF	TFGMS1074	55.1	162	NV	NV	NV
PUID16586048	Ca1	5452940	(TTTA)3	12	AAGAGCTCATATAGCAATCCA	TGAAACTTCTTATTTTCTGTCG	220-447	253-370	Myb DNA binding	TFGMS1075	54.4	171	NV	NV	NV
PUID16586049	Ca1	21485683	(TGA)4	12	TGTCAAGAACTCTCCAATCTG	TACTCAATCACAACCCTCAAC	1-984	466-852	NAM	TFGMS1076	55.4	155	NV	NV	NV
PUID16586050	0	0	(TTTC)3	12	TTTATGAGGATATGGGTGCTA	AAACCCAAATTCTTTCTCCTA	126-827	528-752	Acetytransf	TFGMS1077	54.9	138	NV	NV	NV
PUID16586051	Ca5	37896821	(TGT)4	12	GGTATGACCAGAACATTTGAA	AACATCAATTCAATCATGGAG	299-940	581-790	Histone	TFGMS1078	55.1	142	NV	NV	NV
PUID16586052	0	0	(TGA)4	12	TCAACAATACCCTTTAGTGGA	CAAGTCTAGAACTCTGGCAAA	84-902	123-266	Myb DNA binding	TFGMS1079	54.8	153	NV	NV	NV
PUID16586053	Ca4	41986308	(TCAA)3	12	CCATAACACAAAAGTGAGCAT	GAAGAAAAGACCGATTTTAATG	343-747	439-651	Histone	TFGMS1080	55.3	169	NV	NV	NV
PUID16586054	Ca7	34655351	(GAT)4	12	TCAAATGTGAGACTGATGTGA	AAAATTCAAAAGACCAGGTTC	41-772	149-301	HomeoBox	TFGMS1081	55.0	143	NV	NV	NV
PUID16586055	Ca3	9394912	(TTG)4	12	CATTAGAAACACAACCACTTTG	AGTTCAATGCAACAACAATTC	4-606	370-468	AP2	TFGMS1082	55.0	149	NV	NV	NV
PUID16586056	Ca5	28184701	(TCA)4	12	CTCTTAAATCAGCTGTCTCCA	AAAGTGGTGAAGAGAAAATGA	304-786	502-609	ACT	TFGMS1083	54.9	149	NV	NV	NV
PUID16586057	Ca3	39347450	(TTC)4	12	GAGAACTCAAAAGGAACCCTA	CAAAACCTACGTATTGTCGTC	171-695	318-518	Acetytransf	TFGMS1084	55.2	140	NV	NV	NV
PUID16586058	Ca5	44394479	(TCT)4	12	AAACTTGAGCATCACAAAGAA	CACAAGAACACACAAAGAAAA	173-718	212-508	K-Box	TFGMS1085	55.2	177	NV	NV	NV
PUID16586059	Ca2	31928132	(TTC)4	12	AGGGTTCCTTCTTCTTCTACA	AACTGATGAAGTGAGGACAAA	164-796	230-328	AP2	TFGMS1086	54.8	141	NV	NV	NV
PUID16586060	Ca8	9320772	(GAA)4	12	AAATTAAGACCACCAAGCTCT	ACAACCAAGATACTTCTGCAA	71-949	803-946	Zf-Dof	TFGMS1087	54.8	186	NV	NV	NV
PUID16586061	Ca4	1103152	(TTGG)3	12	TTATGAAAATGATGGGTTGTC	AGACAACAGTGCCAAACTAAG	505-957	577-930	NAM	TFGMS1088	55.0	156	NV	NV	NV
PUID16586062	Ca6	21278800	(GCA)4	12	TTATCACTCTCCTTTCCCTTC	CTTGCGAATAGGGACGAC	616-1152	793-1071	Myb DNA binding	TFGMS1089	55.1	152	NV	NV	NV
PUID16586063	Ca2	3236367	(TTAA)3	12	CGATACATTTTGGCCATCTAT	GATGGAGTGAAGTTTGAGATG	247-525	250-483	PLN03217	TFGMS1090	56.7	142	NV	NV	NV
PUID16586064	Ca1	20214017	(TAG)4	12	CACTCATGTCCTCAGAAGAAG	GAATTGTAACGGTTCAACAAA	83-592	326-589	DUF260	TFGMS1091	55.0	156	NV	NV	NV
PUID16586065	Ca4	16278173	(TTA)4	12	TGCAATGATTACTGCATCATA	ATGAAACAAGTGAAGAGGTGA	189-1520	1344-1472	Zf B-Box	TFGMS1092	55.3	134	NV	NV	NV
PUID16586066	Ca8	3998027	(TCT)4	12	TCAACGACACTTCTCTTTCTC	GCAAAAAGTGATGTTGTTGAT	308-811	605-754	AP2	TFGMS1093	54.7	155	NV	NV	NV
PUID16586067	Ca5	39847615	(CTT)4	12	CAACCTTTAACATCCAACAAA	GTGACACACTTGATGAACCTT	159-794	582-752	Zf-Dof	TFGMS1094	55.3	148	NV	NV	NV
PUID16586068	Ca8	12526570	(GAT)4	12	ATCAAGCTGTTTGGTAGAACA	GATATCCCTTCTTGACCAACT	204-1583	384-515	Myb DNA binding	TFGMS1095	55.1	149	NV	NV	NV
PUID16586069	Ca5	3947535	(TGA)4	12	GAATCATCATAGCCAAATTGA	CAACCAAAAAGACAAGAATGA	22-1077	742-951	TCP	TFGMS1096	55.2	148	NV	NV	NV
PUID16586070	Ca5	30597009	(TTTC)3	12	CGACTTGAATCTCTCCTGTAA	GCTGATCAGTTGTGGTAGAAG	349-852	388-822	PTZ00368	TFGMS1097	54.7	161	NV	NV	NV
PUID16586071	Ca5	5343555	(TGT)4	12	CTCCAACTTTTTCAGCATCTA	CCACCTCTAACCCTAAGTCAT	231-1772	1050-1262	Sigma70	TFGMS1098	54.9	156	NV	NV	NV
PUID16586072	0	0	(TGG)4	12	GATCCAAGGCTGTTGAAGT	GCTACCACCATAACCTCCTC	53-670	68-265	CSD	TFGMS1099	55.2	155	NV	NV	NV
PUID16586073	Ca7	13905777	(GAA)4	12	TGTTTCCACACCTTACAAACT	AGTAACCGATGGCTACAAACT	228-1463	249-1115	Tub	TFGMS1100	54.8	149	NV	NV	NV
PUID16586074	Ca4	43512703	(TCT)4	12	TCCTATATTTTCCATCCTCCT	GCAGTATGTGTTTGTGAATCC	85-789	541-672	HLH	TFGMS1101	54.5	146	NV	NV	NV
PUID16586075	Ca7	8421284	(CTG)4	12	AAAGAAGCAATAATCCAGAGG	TGCTTGATTGATATCTTCCAT	140-952	242-577	Response-reg	TFGMS1102	55.3	150	NV	NV	NV
PUID16586076	Ca4	35393450	(CGC)4	12	GGTTACGTTCTGAACAAGATG	GTTGATGATGAAACAACGAAT	61-705	157-321	TCP	TFGMS1103	54.9	192	NV	NV	NV
PUID16586077	Ca8	3998282	(TCA)4	12	AAGCTACTGAAGTTGGTGCTA	TTCAGGAATCTTGTTCAAGTC	181-684	238-387	AP2	TFGMS1104	54.6	165	NV	NV	NV
PUID16586078	Ca5	11385849	(GCA)4	12	GTTCAACAACAAAGACTTGCT	TTAACCTGTGGTTCAGCTTAC	159-1967	936-1121	RRM	TFGMS1105	54.7	148	NV	NV	NV
PUID16586079	Ca4	45186457	(TGAA)3	12	ATGGAGGAAATTCTGAAACAT	AAGGAACTGTCTGTTGAAA	2-298	49-156	HomeoBox	TFGMS1106	55.2	150	NV	NV	NV
PUID16586080	Ca5	41254342	(TG)6	12	AGGAAGAGAAAGAGGACAAGA	GCTCAAAATATCTAAGCAGAGG	546-1784	588-722	CCT	TFGMS1107	54.9	134	NV	NV	NV
PUID16586081	0	0	(CTA)4	12	TGGAAACTTAGGAAGAACAAA	TGATGATCAAATCCAGAAAAC	36-686	168-374	TCP	TFGMS1108	54.3	147	NV	NV	NV
PUID16586082	Ca7	2833252	(AGC)5	15	AGTGCGGATACAAAGATGATA	CAGAACAAACCCTAACAGTTG	375-875	462-557	GATA	TFFDMS1-TYPE-II	54.9	139	4	P	0.35
PUID16586083	Ca1	40494061	(GGT)4	12	CATGAACAACATCATCAACAA	TACCATAAGCTGAACCATGAC	218-1237	569-1039	DUF702	TFFDMS2-TYPE-II	55.3	148	2	P	0.36
PUID16586084	Ca3	28081736	(TTG)4	12	CTTCAATACCATCAAAACCAG	TTGTGATCTGAAAAGGAAGAA	277-3637	1624-1802	bZIP	TFFDMS3-TYPE-II	54.8	149	NA	NA	NA
PUID16586085	0	0	(CAA)5	15	TTGGGTCAACAAATATGAGTC	TTGTTCTTGAACCCTTAACAA	437-1648	1285-1438	F0F1 ATP synthase	TFFDMS4-TYPE-II	55.1	149	1	M	NSA
PUID16586086	Ca4	2153465	(GAA)5	15	AAGATGACATGGACGAAGAC	ACTCGAATATCTTCTGGCATT	9-1310	771-875	HLH	TFFDMS5-TYPE-II	55.0	172	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16586087	0	0	(GTG)5	15	GCTGCTTCCAGATCTGTTCC	TCACCTGAAAATCACCACCA	3-563	21-252	SelP	TFFDMS6-TYPE-II	60.0	244	1	M	NSA
PUID16586088	Ca7	21322216	(GAC)6	18	GCAAACCTTCCAAACGTGAT	TGTTTTCTCCAGAACATGAGGA	331-978	468-610	Peptidase	TFFDMS7-TYPE-II	60.0	230	1	M	NSA
PUID16586089	Ca3	39816713	(GCA)6	18	TGATGGAGTTGATGCAAGGA	CTCTTCCTCTTGCTGCTGCT	479-1678	288-552	B3	TFFDMS8-TYPE-II	60.2	176	1	M	NSA
PUID16586090	Ca3	39817055	(GGA)5	15	AGGAGGAGGTAGATATGATGG	TGCCAGTTAGTTTCTTTGGT	479-1678	764-1003	B3	TFFDMS9-TYPE-II	54.8	156	1	M	NSA
PUID16586091	Ca5	31241164	(ACG)4	12	GGATCTTCAAAAACGATCTCT	AACCATGTTTACTGTCAGTCG	53-2030	479-718	Bromodomain	TFFDMS10-TYPE-II	55.1	143	1	M	NSA
PUID16586092	Ca1	17343358	(AGA)5	15	TCTGGTCACAGTGGCACTTC	GCCACAAGTCGTGCTTTACA	15-482	366-435	RVT2	TFFDMS11-TYPE-II	59.9	236	1	M	NSA
PUID16586093	Ca1	6738568	(ACACCA)3	18	GATCAGCAGTCAAAACAAGAC	TAGTTTATTGGGTTTTCACCA	110-1060	776-931	Myb DNA binding	TFFDMS12-TYPE-II	55.0	162	1	M	NSA
PUID16586094	Ca7	5634910	(AGTGGG)3	18	TAAGAATCGATTAATGCAAGG	CTGAGTTCAAGTTTGGTTCTG	345-1304	909-1172	Myb DNA binding	TFFDMS13-TYPE-II	54.8	206	1	M	NSA
PUID16586095	Ca1	13302369	(TC)6	12	ATTTTGCGGTAAATTCGGTG	TCCCAACCCTGAAAACAAAG	130-1236	195-1089	DUF789	TFFDMS14-TYPE-II	59.8	183	1	M	NSA
PUID16586096	Ca1	6631474	(GAA)6	18	TCAAAAACAAAATGGGTCCAA	TGCGATCAAACCTCTGAGTCT	71-682	123-531	DUF2431	TFFDMS15-TYPE-II	60.2	273	1	M	NSA
PUID16586097	Ca7	8015985	(TCA)4	12	GCCAACCTAGTAAAGTTGTTG	AAATCCTCCAAGAGAAAAAGA	117-1184	273-473	TCP	TFFDMS16-TYPE-II	54.3	152	1	M	NSA
PUID16586098	Ca5	37147435	(ACC)4	12	ACGGTGAACTAACCTCTCAAT	GTGATAGCAGTGGAGTTACCA	229-1044	412-588	Zf-HD-dimer	TFFDMS17-TYPE-II	55.4	159	1	M	NSA
PUID16586099	Ca8	4243300	(TCC)5	15	TCCACAAAAAGGAACAAACACA	CCCCGTTTGAGAGAGTACCA	61-791	99-348	MADF	TFFDMS18-TYPE-II	60.4	199	1	M	NSA
PUID16586100	Ca4	45053532	(AAC)4	12	TGAAAATAGGTACAGCCAAAC	CCTTCAAAATCTGAATTTTCC	34-858	505-609	GATA	TFFDMS19-TYPE-II	54.6	149	1	M	NSA
PUID16586101	Ca7	17597964	(AGC)5	15	TAGCCACATCCCAGGAAAAC	AATCGAAACACGAAAGTCGAG	73-672	366-513	DUF1639	TFFDMS20-TYPE-II	59.9	227	1	M	NSA
PUID16586102	Ca6	58555002	(AGAGGA)3	18	AACATCTTCAGGGTCAACTTT	CACTAGCAGGACCCAAATAG	499-972	586-765	bZIP	TFFDMS21-TYPE-II	55.4	157	1	M	NSA
PUID16586103	Ca3	31977211	(ATC)4	12	AGGATGTTGATTTTGAATCTG	TGAATCAGGTGTAGGAACTTG	169-1638	994-1122	HLH	TFFDMS22-TYPE-II	54.3	163	1	M	NSA
PUID16586104	Ca5	28253414	(CTG)4	12	AACTTCAACATGATTTGGCTA	GAAGGTGAAAAGTCAGGAAAT	19-588	58-360	DUF260	TFFDMS23-TYPE-II	55.0	151	1	M	NSA
PUID16586105	Ca4	1220485	(ATC)4	12	CAAGAAGTTTCTTCCACTTCA	TGATTCTTTGATTTGTGAGGT	78-839	402-500	AP2	TFFDMS24-TYPE-II	54.7	155	1	M	NSA
PUID16586106	Ca2	14624000	(GCA)4	12	CTTTAATCATGCCAGCTCTAC	TTTCGTTTTCTTCTTCCTTCT	225-998	540-950	DUF3594	TFFDMS25-TYPE-II	54.4	165	1	M	NSA
PUID16586107	Ca5	43355916	(GAA)4	12	CTCTCATCACAATCTGTCCAT	CTTCTCAGAGTGATGTTCCTG	387-1316	561-722	HomeoBox	TFFDMS26-TYPE-II	55.0	143	1	M	NSA
PUID16586108	0	0	(GCG)4	12	GATTTGATTTTCTGGGTTCTC	CATAACCGATCATCAATCATAA	405-1076	477-572	AP2	TFFDMS27-TYPE-II	55.4	150	1	M	NSA
PUID16586109	Ca4	45445882	(TTG)4	12	GGCAAATATGGTTGTTGAGTA	AAAAAGAAGCTTTTGGGTAAG	1-583	344-475	Myb DNA binding	TFFDMS28-TYPE-II	55.3	185	1	M	NSA
PUID16586110	Ca8	5768514	(AAT)7	21	CAGTACGGTAAGATTGAAGGA	CAACAGCAACATTGTTTGTAA	64-480	82-237	HomeoBox	TFFDMS29-TYPE-II	54.6	162	1	M	NSA
PUID16586111	Ca3	31248988	(AAC)4	12	TTATCATCCAATGATGAATCC	ATCCTGAAGAGTTGGATTCAT	100-669	403-504	AP2	TFFDMS30-TYPE-II	54.8	155	1	M	NSA
PUID16586112	Ca3	3617519	(CCA)4	12	AACCAGAAGAACCACCACTT	TAAGATGAAGAGATCGGAGGT	368-1354	575-736	Zf-HD	TFFDMS31-TYPE-II	56.2	142	1	M	NSA
PUID16586113	Ca7	11324531	(TGGGT)3	15	GTTTGAGTCCGGTTTTTGT	ACAACTCATTCTCCGTCTTCT	17-544	188-325	bZIP	TFFDMS32-TYPE-II	55.1	158	1	M	NSA
PUID16586114	0	0	(TCT)4	12	CAAATCAGATGGTGAAACAAT	GATGTAAAACTCATTCCACCA	117-1022	260-474	TCP	TFFDMS33-TYPE-II	55.1	156	1	M	NSA
PUID16586115	Ca3	6887527	(AAGA)3	12	TTCATCTTCTCCTTCTTCCTC	AGGAATTTTCTGTGCTCTTCT	1-741	142-276	Myb DNA binding	TFFDMS34-TYPE-II	55.2	150	1	M	NSA
PUID16586116	Ca1	8828268	(AGA)5	15	AAATTAAGATCCGTGGTCAAT	TGGATCCAACCATTAATCATA	113-805	320-704	WRKY	TFFDMS35-TYPE-II	55.3	154	1	M	NSA
PUID16586117	Ca5	37896821	(TTG)4	12	GGTATGACCAGAACATTTGAA	AACATCAATTCAATCATGGAG	299-940	581-790	Histone	TFFDMS36-TYPE-II	55.1	142	1	M	NSA
PUID16586118	Ca3	81357	(TTC)4	12	ACGCTTCAAGTATTGAACAAC	CCAAATGTGTCGTTTTATTCT	203-922	506-886	NAM	TFFDMS37-TYPE-II	54.7	150	1	M	NSA
PUID16586119	Ca5	36652764	(CAA)4	12	CATGGAACAAGAAAGAGATTG	TCTCTTATTTCTGCTACCCACT	297-779	390-536	AP2	TFFDMS38-TYPE-II	55.0	147	1	M	NSA
PUID16586120	Ca8	9320749	(GAT)4	12	TGAAGAAGAAGAAGCAGAGTC	ACAACCAAGATACTTCTGCAA	71-949	803-946	Zf-Dof	TFFDMS39-TYPE-II	54.1	163	1	M	NSA
PUID16586121	Ca7	32856022	(GAA)4	12	GAAGTGTGTTTGTTTGATTTTG	TCTTCAACAACAACAACAACA	125-1216	854-1030	WRC	TFFDMS40-TYPE-II	55.0	151	1	M	NSA
PUID16586122	Ca7	31541402	(AGA)4	12	AGTTACAATTGATGGTGATGG	AAAAGGTATTGGACAAAAGGT	159-794	582-752	Zf-Dof	TFFDMS41-TYPE-II	54.9	138	1	M	NSA
PUID16586123	Ca3	35530256	(AAG)4	12	GACAAAGGAGAAGAAATGGAT	GCTTTTGTGTTGGTATTTGAG	1-398	90-269	ovate	TFFDMS42-TYPE-II	55.0	153	1	M	NSA
PUID16586124	0	0	(TCT)4	12	CAAATCAGATGGTGAAACAAT	CCAGAAGACAAAGAACAAGAA	36-686	168-374	TCP	TFFDMS43-TYPE-II	55.1	156	1	M	NSA
PUID16586125	Ca1	10682877	(TCATGA)4	24	ATCATCATGAAGCATCCATAG	TATCGGATATAGCTTTTGCAC	18-362	219-359	GRAS	TFFDMS44-TYPE-II	55.1	156	1	M	NSA
PUID16586126	Ca5	164592	(GAT)6	18	ATGAGTCAAAGCCATAGTCAC	GGGAGAGGGAGTAACAAAGTA	23-1294	194-571	NAM	TFFDMS45-TYPE-II	54.4	153	5	P	NSA
PUID16586127	Ca7	32855979	(TTG)7	21	TTATTGTTGTTCAAGGAAAGG	GTGGAACCTGTTTCTTCTTCT	145-1233	874-1008	WRC	TFFDMS46-TYPE-II	54.6	146	4	P	NSA
PUID16586128	Ca7	2833134	(GGC)4	12	CAACTGTTAGGGTTTGTTCTG	ATCAACTGTCATCACACCATT	375-875	462-557	GATA	TFFDMS47-TYPE-II	55.0	170	2	P	NSA
PUID16586129	Ca4	35416327	(TGT)5	15	TTGGCATACGTATTCTTCTTC	CCTTCCTGGACATCTTAATTT	1046-1738	1478-1642	TCP	TFFDMS48-TYPE-II	54.7	153	3	P	NSA
PUID16586130	Ca7	20545387	(ACA)5	15	ACTGTTGACCCAAAAGTGGC	TCCATGTGAAACTGGTTGGA	291-2417	546-1806	Xan	TFFDMS49-TYPE-II	60.0	216	2	P	NSA
PUID16586131	Ca2	27760734	(GAA)4	12	GTGATGCACTTGTTTTTGAAT	TAGATTCTTTTGTTGCTTTGG	353-862	352-526	B3	TFFDMS50-TYPE-II	55.3	147	2	P	NSA
PUID16586132	Ca3	39817055	(GAA)5	15	AGGAGGAGGTAGATATGATGG	TTGAGCATAGAGCTCCAATTA	479-1678	764-1003	B3	TFFDMS51-TYPE-II	54.8	156	2	P	NSA
PUID16586133	Ca6	21497375	(AAT)5	15	ATTGCTCAAGTTGTCAATGAT	TGTATTGCAGCTTCCTAACTC	294-1247	846-1007	Bzip	TFFDMS52-TYPE-II	54.8	148	2	P	NSA
PUID16586134	Ca5	223659	(ACC)5	15	GAGTGGTGATGGTGGTAGTTA	TAACTACCACCATCACCACTC	265-1221	793-948	ZF HD dimer	TFFDMS53-TYPE-II	55.0	137	2	P	NSA
PUID16586135	Ca3	7104895	(CAA)4	12	CAAACACTTCTTCCTCTCTCA	TGAGATCTCTCAGAACCTGAA	33-1031	189-338	HLH	TFFDMS54-TYPE-II	54.7	159	2	P	NSA
PUID16586136	Ca2	11922573	(CGC)4	12	CTCCAACATGTTTGTGCTATT	ACTACTTCAACCCTAGCTCGT	52-1329	874-1144	TCP	TFFDMS55-TYPE-II	55.3	158	3	P	NSA
PUID16586137	0	0	(ATT)7	21	GAGGTGGAAAAATGGGGAAT	CCAAGTGCTGATGGTGTCAT	99-1076	354-522	WRKY	TFFDMS56-TYPE-II	60.0	186	3	P	NSA
PUID16586138	Ca2	10253308	(AAC)7	21	GCAACGACGGAGAAAACAGT	TCAGCAACGTTGGAGTCTTG	163-1092	288-420	Myb DNA binding,	TFFDMS57-TYPE-II	60.3	160	3	P	NSA
PUID16586139	Ca3	26827414	(ACC)5	15	GCAAAGGTTGCAAACAAACA	AAGGGACAATTTGGTGGTGA	73-1467	204-1365	Transferase	TFFDMS58-TYPE-II	59.8	205	2	P	NSA
PUID16586140	Ca7	19989656	(CTG)4	12	TTAGTTTAGGTCCTGGTGGTT	GTTTTCCAATTTGAAGGTTTC	322-1467	1102-1179	ZfCCCH	TFFDMS59-TYPE-II	55.4	151	2	P	NSA
PUID16586141	Ca2	3174683	(TCT)7	21	GCGCCACAATTCTTGTTCTT	TCGAAAATTGCAGCTACCCT	36-1232	147-1194	DHQS	TFFDMS60-TYPE-II	60.3	279	2	P	NSA
PUID16586142	Ca7	5272678	(TCGGAA)3	18	TCGTATTGTTGCATAGGAGAT	ACACTTTCTCAAACCCTAACC	267-1244	1092-1196	WD40	TFFDMS61-TYPE-II	54.9	173	2	P	NSA
PUID16586143	Ca3	37212719	(ATATGA)4	24	ACGATGCAATCGAATATCTTA	AATTCTTGAAGCTTCTTTTGC	400-948	457-594	HLH	TFFDMS62-TYPE-II	55.0	150	3	P	NSA
PUID16586144	Ca3	26594189	(AATGAA)4	24	AATAGTTCCAAAGGGTGAGAA	TGACTCATTTTGGTTTTGTCT	99-923	702-809	GATA	TFFDMS63-TYPE-II	55.5	142	4	P	NSA
PUID16586145	Ca3	30974188	(AATT)3	12	GTACCCTTCCCTTTCTGAATA	AAGAACTATGCAGCAACAATAA	483-920	513-899	AUX_IAA	TFFDMS64-TYPE-II	55.0	146	2	P	NSA
PUID16586146	Ca7	38472298	(CAAGCC)3	18	ATGTCCATGCAAGTAAACAAG	CGACGACCTCTACCTTCTACT	8-1024	218-538	TCP	TFFDMS65-TYPE-II	55.3	137	2	P	NSA
PUID16586147	0	0	(GAT)5	15	AAATCGCACAACACAAGCTG	CAGTTTCGTCCTCGACATGA	137-688	6-393	IPP-2	TFFDMS66-TYPE-II	59.9	254	3	P	NSA
PUID16586148	Ca8	4243323	(TCC)5	15	AACCTAGCTTCTCCAACATTC	ATAATTCTCTCCGCAAAATCT	61-791	130-348	Myb DNA binding	TFFDMS67-TYPE-II	55.2	150	3	P	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16586149	Ca8	4421282	(CAA)4	12	GCAACTTATATTGGTCCTCAA	CAAAGTCAAAGAAGGAGACAA	175-1071	196-498	DUF260	TFFDMS68-TYPE-II	54.5	152	2	P	NSA
PUID16586150	Ca1	35114861	(TGA)4	12	GTGGGAACAAGAGAGAGTTTT	GCCTCTCAGAAAATTCCCTAT	355-1137	652-816	Homebox	TFFDMS69-TYPE-II	55.1	146	2	P	NSA
PUID16586151	Ca8	4626215	(CCT)6	18	TTGATTAAAAGCTCTCTGCTG	ATACCAACAACCAACAACAAC	105-2279	918-1322	POX	TFFDMS70-TYPE-II	55.2	150	3	P	NSA
PUID16586152	Ca1	3999529	(AAC)5	15	CTCTCAACATCAACACTTTCC	GAGAGATGCTATGTGTTTTGC	226-1611	445-651	TCP	TFFDMS71-TYPE-II	54.8	140	5	P	NSA
PUID16586153	Ca3	25672716	(GAA)4	12	GACTGTTGTTACTGGTGGAGA	TGTCCATCTTGCTAATCTTTG	199-1638	1063-1200	HLH	TFFDMS72-TYPE-II	55.2	149	2	P	NSA
PUID16586154	0	0	(AAAGAG)3	18	ACCACAAACATGTCTCAAATC	CTAAGATGGTCATTCATTTGG	554-1651	1073-1219	HLH	TFFDMS73-TYPE-II	55.0	153	4	P	NSA
PUID16586155	Ca6	29746111	(GAT)4	12	AGGACAGTGTCACAGAAGTTG	TTCAGAAAAGGAGAAAGTGAA	439-885	445-813	YABBY	TFFDMS74-TYPE-II	55.3	149	2	P	NSA
PUID16586156	0	0	(GAT)4	12	AAAATTCTTCTGGGTTGACTC	GTTTCCGTATCCTTGATCTCT	26-888	809-864	bZIP	TFFDMS75-TYPE-II	55.0	153	2	P	NSA
PUID16586157	Ca1	2346126	(AAC)6	18	TGGGTTTGAGTTCTAAACAAG	CATTTCACAGCTTCTGATTGT	342-636	480-635	Zf-Dof	TFFDMS76-TYPE-II	54.6	151	5	P	NSA
PUID16586158	Ca2	23951109	(TGA)4	12	TGTCTCATCTGAAAAAGATTGA	TTGGTTTCTTCATCAACAACT	132-1220	159-1004	AUX-IAA	TFFDMS77-TYPE-II	55.1	150	2	P	NSA
PUID16586159	Ca4	45595013	(GTA)5	15	GGCGGAATAATTGAAGTAGTAG	CAATTACATGGGAAAGTTCAA	126-2153	1350-1484	WRC	TFFDMS78-TYPE-II	55.0	158	3	P	NSA
PUID16586160	0	0	(AAC)4	12	GAGAGAACAAACCCTCTGATT	TGTAAAACTCATTCCACCAAC	117-1022	260-474	TCP	TFFDMS79-TYPE-II	55.0	150	2	P	NSA
PUID16586161	Ca4	470897	(AAG)4	12	AAAAGAAGATCTCGAAGGAAG	ACTGTTCATAATCCCCATAGC	78-497	225-425	Histone	TFFDMS80-TYPE-II	54.6	152	2	P	NSA
PUID16586162	Ca6	4566075	(TTTTTC)4	24	ACAACTTACTGTCGTTGGAAA	ATTTCAAATCCTTCGTGAAAC	397-912	421-636	PC4	TFFDMS81-TYPE-II	55.0	147	3	P	NSA
PUID16586163	0	0	(AGA)4	12	TCATCAGAAGCAAGAAGAAGA	AAAAACTCTATTTGCTGACCA	141-692	543-608	AP2	TFFDMS82-TYPE-II	55.4	148	2	P	NSA
PUID16586164	Ca7	32855979	(TTG)7	21	TTATTGTTGTTCAAGGAAAGG	GTGGAACCTGTTTCTTCTTCT	125-1216	854-1030	WRC	TFFDMS83-TYPE-II	54.6	146	2	P	NSA
PUID16586165	Ca1	9791512	(AAT)4	12	AGGTAATGATGATGATGATGG	TGTTTTTCTATCAGGATGTGG	40-444	343-429	HomeoBox	TFFDMS84-TYPE-II	54.8	148	2	P	NSA
PUID16586166	Ca1	9791574	(ATG)5	15	AATTCAGGTCCTACAAAATCC	GAGCAGTGTGCCTATGATATT	40-444	343-429	HomeoBox	TFFDMS85-TYPE-II	54.8	151	2	P	NSA
PUID16586167	Ca4	35416175	(CAA)5	15	AAACAACTAACGCCGTAACTA	TTGGCATACGTATTCTTCTTC	61-705	157-321	TCP	TFFDMS86-TYPE-II	54.5	153	3	P	NSA
PUID16586168	0	0	(AAC)4	12	GAGAGAACAAACCCTCTGATT	TCTTCCTCTTCCTTCAACTTT	36-686	168-374	TCP	TFFDMS87-TYPE-II	55.0	150	2	P	NSA
PUID16586169	Ca4	1124457	(CAC)5	15	TGTAGCCTCACCAACAGCAC	AGGGCGGTGATTCTTAAGGT	29-736	171-510	DUF640	TFFDMS1-TYPE-I	59.9	186	3	P	0.35
PUID16586170	Ca8	5412472	(ACA)5	15	AAGAAGGATTGTCCTCATGTT	CACTTATCTGTCGCACTCTTT	589-1512	895-1320	DUF702	TFFDMS2-TYPE-I	55.3	146	2	P	0.35
PUID16586171	Ca7	11430204	(ACA)4	12	CCCCAAGACTACTTCAACTTT	CGTTTAACATCCACATGAGTT	6-983	429-974	GRAS	TFFDMS3-TYPE-I	55.2	133	3	P	0.36
PUID16586172	Ca4	7121052	(AGT)5	15	GTGGTGCAACGATAGTAACTC	TCAAAACAAGTTCTCTCTCTCTC	724-1293	732-810	WRKY	TFFDMS4-TYPE-I	54.9	156	3	P	0.37
PUID16586173	Ca4	43513782	(GAA)5	15	GAAAGAAGATCACAAGCCTTT	CAAAGGTATCTTGAGTGGTTG	573-1883	1401-1847	bHLH MYC	TFFDMS5-TYPE-I	55.3	155	5	P	0.37
PUID16586174	Ca4	5018413	(CTG)4	12	GTTTCTGAAGATGCTCCAAG	ATGATATGGGAGTCAACAATG	307-1599	336-716	bZIP	TFFDMS6-TYPE-I	55.1	153	2	P	0.37
PUID16586175	Ca5	40667569	(ACC)10	30	GTCACTTTCAGCCTCCTTCG	ATCACGAGAGTCGTCGGAAG	558-1781	384-714	EamA	TFFDMS7-TYPE-I	60.0	192	6	P	0.33
PUID16586176	Ca4	5080649	(AAT)4	12	GAGAAAGAGGATATTGGGAGA	CTAACTCCAACATTCCTTGTG	135-1787	1365-1622	Myb DNA binding	TFFDMS8-TYPE-I	55.0	151	3	P	0.34
PUID16586177	Ca4	16278173	(TTA)4	12	TGCAATGATTACTGCATCATA	ATTCATTAGCTCGAAGACCAT	1-1145	333-467	CCT	TFFDMS9-TYPE-I	55.3	134	4	P	0.33
PUID16586178	0	0	(TGT)4	12	CTGGTGAGATTTCTGAGAATG	TTGGAAATGGTAATGGTAGTG	224-2434	230-1321	GRAS	TFFDMS10-TYPE-I	54.9	128	3	P	0.31
PUID16586179	0	0	(CAA)6	18	TGCTTCACCTTGTCATCTCG	CGCTTGGTTTCCACAATCTT	218-1237	354-822	DUF702	TFFDMS11-TYPE-I	60.0	259	3	P	0.32
PUID16586180	Ca6	24448426	(AGA)4	12	GGATTAATTATCTCCGACCAG	GGACATCTTTCTGAAACTGAA	183-1043	381-518	Myb DNA binding	TFFDMS12-TYPE-I	55.4	122	2	P	0.32
PUID16586181	Ca3	38689529	(TAC)5	15	ACAAGGGTACTTGTGGAATTT	CTTGAATCATCAACAACACCT	58-1188	258-976	Myb	TFFDMS13-TYPE-I	55.3	167	3	P	0.34
PUID16586182	Ca6	1614988	(CTT)4	12	TTCTTTCTTACTTGTGGCTTG	TATATGCAAGGGTGAGAAAGA	257-1750	1106-1735	DUF3633	TFFDMS14-TYPE-I	55.0	153	2	P	0.31
PUID16586183	Ca1	390303	(TCT)5	15	ATCCAACAACCTTCTTCAAAC	GAGGAGGAGGATAATTGGTTA	41-1297	380-691	TCP domain	TFFDMS15-TYPE-I	54.9	140	2	P	0.31
PUID16586184	Ca1	11897074	(CAA)6	18	AAGAGAAAGAGATGAAGCACA	TCAATTCCTCTTCTTTGTTGA	46-855	54-534	Domain of unknown function (DUF1635)	TFFDMS16-TYPE-I	55.1	150	3	P	0.23
PUID16586185	Ca5	32788349	(AGA)4	12	GAAAGAAAGAATCCATCCAAG	TGTTCTGTCCATCTTGCTTAT	502-1095	609-735	HLH	TFFDMS17-TYPE-I	55.5	141	2	P	0.32
PUID16586186	Ca1	11899747	(GAT)6	18	ATGAGTCAAAGCCATAGTCAC	TTCTTCTTCAGTTGGATGAAA	23-1294	194-571	No apical meristem (NAM)	TFFDMS18-TYPE-I	55.1	153	3	P	0.33
PUID16586187	Ca2	354109	(GA)13	26	ATGGAGGCGAATATATAGGAG	TTTTAAGAAACAACTGCGTTC	114-1025	12-327	LOB domain-containing protein 41 (LBD41)/DU	TFFDMS19-TYPE-I	55.1	151	5	P	0.34
PUID16586188	Ca1	11906203	(ATA)5	15	TGGTGGTTCTAATGGAAGTAA	ACCATAATTAATCCCACCATT	13-981	352-852	DUF702	TFFDMS20-TYPE-I	54.8	155	2	P	0.35
PUID16586189	Ca1	11903308	(CAC)8	24	CTAAAGAATGGAATTGGGATT	CTCGTTTGTTTGCTCTATTGT	159-3215	492-728	SBP	TFFDMS21-TYPE-I	55.0	153	3	P	0.38
PUID16586190	Ca7	41713061	(ATA)5	15	ATATGGTGGTGGCTGATGGT	GAAACCAGCATCTTGATGACAA	13-981	342-840	DUF702	TFFDMS22-TYPE-I	60.1	206	1	M	NSA
PUID16586191	Ca4	821062	(GAA)6	18	TTTTGCTGTCACACCAGCTC	GGCTAAGCTAAAAAGTCCAGCA	483-4514	432-1224	ABC membrane	TFFDMS23-TYPE-I	60.0	178	1	M	NSA
PUID16586192	Ca3	38689331	(AGA)4	12	TAATTAGGGTTTTGTGAGTGC	ATGGTGATGTTGTTACCAAAG	58-1188	258-976	Myb	TFFDMS24-TYPE-I	54.6	144	1	M	NSA
PUID16586193	Ca3	38689529	(GAA)4	12	ACAAGGGTACTTGTGGAATTT	AGAACAAGCTATTGCAAATGA	58-1188	258-976	Myb	TFFDMS25-TYPE-I	55.3	167	1	M	NSA
PUID16586194	Ca4	23476815	(AAC)5	15	TGTGCCCCATTTCACTACAA	GTGCACCATGCTTGAATGAG	64-696	21-252	U-box	TFFDMS26-TYPE-I	60.0	223	1	M	NSA
PUID16586195	Ca6	16572788	(TCA)5	15	CTATGTCCGCACCCGATACT	ATGCCAAACAACTGAAAGGC	163-1292	144-1989	DAO	TFFDMS27-TYPE-I	60.0	150	1	M	NSA
PUID16586196	0	0	(GGA)6	18	GATTTTCCCTGGTTGTCGAA	CAAACCCTAAACCTGCTCCA	1-918	465-696	RRM	TFFDMS28-TYPE-I	59.9	245	1	M	NSA
PUID16586197	Ca4	46151798	(TTC)7	21	AATGGGGTCATTGGATGAAA	ACCCGAAGCTGCAATGTACT	1751623	555-1281	DUF620	TFFDMS29-TYPE-I	60.0	257	1	M	NSA
PUID16586198	Ca6	29195786	(CAA)6	18	TGGGCTTACTACTGCCAAGG	GCTTGAAATTCCAGACAGAGG	46-855	54-534	DUF1635	TFFDMS30-TYPE-I	60.3	267	1	M	NSA
PUID16586199	0	0	(TGG)5	15	TCAAAAACAGCAGCAACAGC	GACGGCGCTAACTTCAAAAC	189-992	366-642	DUF668	TFFDMS31-TYPE-I	60.2	137	1	M	NSA
PUID16586200	Ca4	19436034	(TAT)6	18	TGAAAGAAGAGAGCCCCAAA	GCAACCAAGAGGCTGTTAGC	78-752	3-582	PP2C	TFFDMS32-TYPE-I	59.9	245	1	M	NSA
PUID16586201	Ca1	31367623	(TCT)8	24	CAATGAAAGCGCTGGTGATA	GGTGCAGACTAAAACAGCCC	251-1480	153-720	Peptidase	TFFDMS33-TYPE-I	59.8	140	1	M	NSA
PUID16586202	Ca7	35180540	(ATC)4	12	TCTTGAATCCAGCAGATTTAG	TGTATTTCTCTTTTCCTCGTG	92-1738	1214-1727	bHLH MYC	TFFDMS34-TYPE-I	54.8	150	1	M	NSA
PUID16586203	Ca2	27922104	(GGC)5	15	TGGAACAACATATTTTGCATTACA	ATTGCCAAAAACTTCAACGG	65-1777	123-1422	AMP-binding	TFFDMS35-TYPE-I	59.3	154	1	M	NSA
PUID16586204	0	0	(CAA)5	15	ATCCAAACAACAACGCTTCC	CGGAGTTCAGGGAAGAATGA	167-2392	123-2175	DUF740	TFFDMS36-TYPE-I	60.0	163	1	M	NSA
PUID16586205	Ca6	17415710	(GAA)5	15	CTGTTGCGCCTTTTAACACA	CGTCCCAAAAATTATCCCCT	37-684	285-585		TFFDMS37-TYPE-I	59.9	262	1	M	NSA
PUID16586206	Ca6	14690745	(CAA)6	18	CCATCACCACCAACCCTAAC	AGAAGAGAGGGCGGAGTAGG	1421371	318-786	Hyccin	TFFDMS38-TYPE-I	60.1	215	1	M	NSA
PUID16586207	0	0	(GAA)5	15	CAATTGCAGCGTCTCTCTCA	GGAGGAATGGAACGGAGAAT	42-1124	45-342	RWD	TFFDMS39-TYPE-I	60.3	120	1	M	NSA
PUID16586208	Ca2	18151922	(GTT)5	15	TGCAAAGAGATGAGAAGGGTG	GCTCCCATTGTATTTGTGGC	64-1059	51-951	NAD binding	TFFDMS40-TYPE-I	60.4	214	1	M	NSA
PUID16586209	Ca5	3220268	(TCA)6	18	ACCGTCTTCGTCATCCCTTA	GATTTATGGCCAAATCCCCT	238-1005	78-648	NAP	TFFDMS41-TYPE-I	59.6	240	1	M	NSA
PUID16586210	Ca6	36101249	(GAT)5	15	GTGTCGAAGAAAGGCGAAAG	AACAACAACAAAACCTCCCG	208-1614	303-657	SPR	TFFDMS42-TYPE-I	60.0	121	1	M	NSA

NCBI Probe IDs	Chromosomes	Physical positions (bp)	Microsatellite repeat-motifs	Microsatellite repeat length (bp)	Forward Primer sequences (5'-3')	Reverse Primer sequences (5'-3')	ORF position (bp)	Functional domain position (bp)	Functional domain	Types of genic microsatellite markers	Actual annealing temperature (0C)	Size (bp) of alleles amplified	Total number of alleles amplified among chickpea varieties	Polymorphic potential monomorphic (M)/polymorphic (P)	R2 value of marker loci showing significant association (P ≤ 0.05) with three major seed and pod traits
PUID16586211	Ca8	2557055	(TGAT)3	12	GCTCTAAGACCCAATTGTTTT	GAATCAGTGATGAAGAAGACG	296-1183	626-788	HomeoBox	TFFDMS43-TYPE-I	55.2	151	1	M	NSA
PUID16586212	Ca4	11600566	(TGG)5	15	GTGGACTGATAAGATGGTGAG	CAGCCATAACCTTTGATACAG	102-1448	450-719	Myb DNA binding	TFFDMS44-TYPE-I	54.6	155	1	M	NSA
PUID16586213	0	0	(GGT)4	12	GTAGTGTAACTGCCTCCAAAA	GAAGGTTTTTGTTATGGCAAC	677	201-677	Med7	TFFDMS45-TYPE-I	54.7	150	1	M	NSA
PUID16586214	Ca4	3369236	(GGT)4	12	AACTTGAAGGAGACAGAGCTT	TCATTCAGATCTTCCTTGTTG	182-904	212-877	AUX-IAA	TFFDMS46-TYPE-I	55.0	152	1	M	NSA
PUID16586215	Ca3	18495957	(TCT)4	12	TACAACTCTTTCTGCACCTGT	TGAAATTGGTAGTGGTTGTAGA	1-271	122-254	Myb DNA binding	TFFDMS47-TYPE-I	55.1	161	1	M	NSA
PUID16586216	Ca1	47285537	(AGA)4	12	GAGACTACCGACATGGAAAG	ACCATACATTCTCAAACCAGA	5-153	5-150	DUF822	TFFDMS48-TYPE-I	54.8	100	1	M	NSA
PUID16586217	Ca6	56151673	(GAA)4	12	CAGACTTCGATGGTTGAATTA	TATCTCATGGTCTGTTCTTCC	139-351	166-303	Myb DNA binding	TFFDMS49-TYPE-I	55.4	154	1	M	NSA
PUID16586218	Ca2	29204228	(TTGT)3	12	GTTGTTGTGGTATCGATGATT	TACTCAAGCAAGTGAGTAGGC	657-1757	1503-1640	PHD	TFFDMS50-TYPE-I	54.9	160	2	P	NSA
PUID16586219	Ca2	1682568	(AAT)5	15	TTAATGTTGCTTGTGGGGGT	AAAGCCATTGGAACAAAACG	162-1277	27-597	Peptidase	TFFDMS51-TYPE-I	60.2	259	2	P	NSA
PUID16586220	Ca6	3418800	(GAGAAA)5	30	TCAGACGGTTTTGGTTTTCC	TTGGGAAAACTTGTTCGAGG	197-1165	228-783	Lipase GDSL	TFFDMS52-TYPE-I	59.9	264	3	P	NSA
PUID16586221	Ca6	5765009	(CCA)8	24	ACATTGTTGGTCGTGTTTGC	GGGTGATGTTGGAAGGATGA	375-1433	252-933	Branch	TFFDMS53-TYPE-I	59.5	259	3	P	NSA
PUID16586222	Ca2	36340571	(TGG)5	15	GACGGAGACGAAGGAGTGTC	CAGCACGATAAGCATCAGGA	140-1336	279-1194	Coprogen	TFFDMS54-TYPE-I	59.8	247	3	P	NSA
PUID16586223	Ca7	32855067	(TGT)5	15	TGGTGTCCACTCACCAAAGA	TTTCCAGAAACTTCAGGGTCA	145-1233	228-360	WRC	TFFDMS55-TYPE-I	60.1	252	5	P	NSA
PUID16586224	Ca1	7419551	(ACC)4	12	AAGACTTCCATCTTCCAAACT	CTGCCGATGTATTGATGTATT	30-2006	1-564	START	TFFDMS56-TYPE-I	54.6	154	3	P	NSA
PUID16586225	Ca7	17777145	(ATGG)3	12	AGGTTTACCATCAGCTTCACT	CATTCCTGTAAGGAGACAACA	428-1636	1043-1531	MFMR	TFFDMS57-TYPE-I	55.6	157	3	P	NSA
PUID16586226	Ca1	26026300	(TCC)4	12	TAGCTACTTCCCCTTTCTTCA	TGTAGCAGGTTTCATGTTCTT	253-3357	2689-3213	SBP	TFFDMS58-TYPE-I	55.9	152	3	P	NSA
PUID16586227	Ca4	13333701	(CAC)5	15	CATCCTCGACAAACCCCTTA	TTCAAATTCCCTTGTGGAGG	186-1187	320-525	tify	TFFDMS59-TYPE-I	59.9	243	3	P	NSA
PUID16586228	Ca2	28230844	(TTC)10	30	TCTTTCGCTTTCACTCCCTC	GGTGGAAGCGGTTATTGAGA	231-2345	135-738	Lectin	TFFDMS60-TYPE-I	59.6	227	2	P	NSA
PUID16586229	Ca6	16493630	(CAA)8	24	GAGCTACCAAAACCTCATCACA	AATGGCGAGGTTGAGATTTG	105-959	150-318	zf-Dof	TFFDMS61-TYPE-I	59.2	157	4	P	NSA
PUID16586230	Ca6	5237510	(CAA)5	15	TGTGTTTTCCCTTGTGAAGGT	GAAGTTCTTGTGCAGGAGCC	49-1863	525-927	POX	TFFDMS62-TYPE-I	59.5	223	2	P	NSA
PUID16586231	Ca5	26146967	(CAC)5	15	ACACAATCCATCAGAACCCC	TTTTCCCAAACTGATCGAGG	255-956	147-486	DUF640	TFFDMS63-TYPE-I	59.6	254	2	P	NSA
PUID16586232	Ca1	16385748	(TTG)6	18	CTGTGGCTGTGCTGTCTGTT	ATTGTTGTGGGCTGAGGAAT	145-1464	48-447	Cyclin	TFFDMS64-TYPE-I	60.1	217	5	P	NSA
PUID16586233	Ca5	7861188	(CAT)6	18	CCTCACCAAATCAAACACCA	GCATTGACTAATGATGGTGGG	59-949	294-843	DUF579	TFFDMS65-TYPE-I	59.4	129	3	P	NSA
PUID16586234	Ca5	2855431	(TGA)6	18	ACACCCCAAGTCTGTTCAGG	GCAAGAAGTTAACGAGATGCG	1-794	558-690	zf-C3HC4	TFFDMS66-TYPE-I	60.0	228	4	P	NSA
PUID16586235	Ca7	41713107	(ATA)5	15	TGGTGGTTCTAATGGAAGTAA	CAGCATCTTGATGACAAGAAC	13-981	352-852	Domain of unknown function (DUF702)	TFFDMS67-TYPE-I	55.9	155	3	P	NSA
PUID16586236	Ca7	29125055	(TCT)6	18	TAGAGTTTGGGCGAGGATTG	ATTCCAAAGCGACGAGTTGT	91-1065	339-939	Methyltransf	TFFDMS68-TYPE-I	60.2	275	5	P	NSA
PUID16586237	Ca5	27118508	(GAAA)3	12	AGCTATGCCTCCTGATAAACT	GAGTAGTGGCTTCTGTTTGAA	75-1238	641-773	bZIP	TFFDMS69-TYPE-I	55.0	167	2	P	NSA
PUID16586238	Ca3	39398787	(ATC)8	24	ACCGTTCTCTAGGACGACCA	TGAGTGAAGATGATGACGGC	358-1953	252-1266	PORR	TFFDMS70-TYPE-I	59.7	216	3	P	NSA
PUID16586239	Ca7	2833265	(AGC)5	15	TGAATCAGTTGAGAGTGCGG	AAAGTGTCTTGGGGCCTTTT	75-875	390-483	GATA	TFFDMS71-TYPE-I	60.0	212	2	P	NSA
PUID16586240	Ca5	47841226	(AGA)5	15	GGTTGGCTTGCTGTTCAAGT	GAAGTTTGAGAGGACCGTCG	56-379	3-243	Auxin	TFFDMS72-TYPE-I	60.3	166	2	P	NSA
PUID16586241	Ca6	36101249	(GAT)5	15	GTGTCGAAGAAAGGCGAAAG	AACAACAACAAAACCTCCCG	208-1614	303-657	SPRY	TFFDMS73-TYPE-I	60.0	121	2	P	NSA
PUID16586242	0	0	(CTT)4	12	ATTTATCCTTGAGGTCGATGT	GAATCAGAAGCTCAAATGGA	302-1060	893-1048	Myb DNA binding	TFFDMS74-TYPE-I	55.3	152	2	P	NSA

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