

Supplementary material 1

Primers designed and used for Amplifluor-like SNP analysis

Forward primer for Frontier/ ICC4958-type allele:

KATU-C22-SNP-F7: GAAGGTGACCAAGTTCATGC **TCCCTATAAAATGTCCAAACTTTCT**

Forward primer for Yubileiniy/ICC7255-type allele:

KATU-C22-SNP-F8: GAAGGTCGGAGTCAACGGAT **TCCCTATAAACGTACAAACTTTCTG**

Common Reverse primer

KATU-C22-SNP-R2: **AGGTGTCACTATAGTTAAAAAGC**

Reverse complement **GCTTTTAACTATAGTGACACCT**

Size of amplicon: 119 bp

Sequence of two Universal probes

Universal probe 1:

5' -FAM-AGCGATGCGTTCGAGCATCGC (T*-BHQ1) GAAGGTGACCAAGTTCATGCT-3'

Universal probe 2:

5' -VIC-AGGACGCTGAGATGCGTCC (T*-BHQ1) GAAGGTCGGAGTCAACGGATT-3'

Primers designed and used for sequencing

KATU-C22-F5: **CTCAACAAATCAAGACTGTATCAAG**

KATU-C22-R4: **CACCATGAGCAACAGCTACTAG**

KATU-C22-R4 (Rev-Com): **CTAGTAGCTGTTGCTCATGGTGA**

Size of amplicon: 1,235 bp

Sequence of Reference genes used for qPCR

CaCAC-F: **CATGGACTAGACCACCAATTCA**

CaCAC-R: **AACAGTGTTGTACCCGCTCTTT**

Size of amplicon: 110 bp (Reddy et al., 2016)

CaGAPDH-F: **CCAAGGTCAAGATCGGAATCA**

CaGAPDH-R: **CAAAGCCACTCTAGCAACCAAA**

Size of amplicon: 65 bp (Garg et al., 2010)

Supplementary material 2

Selected annotated SNP in chickpea database.

2103. rs853191221 [*Cicer arietinum*]

GAATTTGTACCTTCACTACAAGTTC[G/T]TCAAAACACTGCTCAACATTTACTC

Chromosome: Ca4:38617150 Gene:LOC101496214 (GeneView) Functional
Consequence: missense Validated: no info

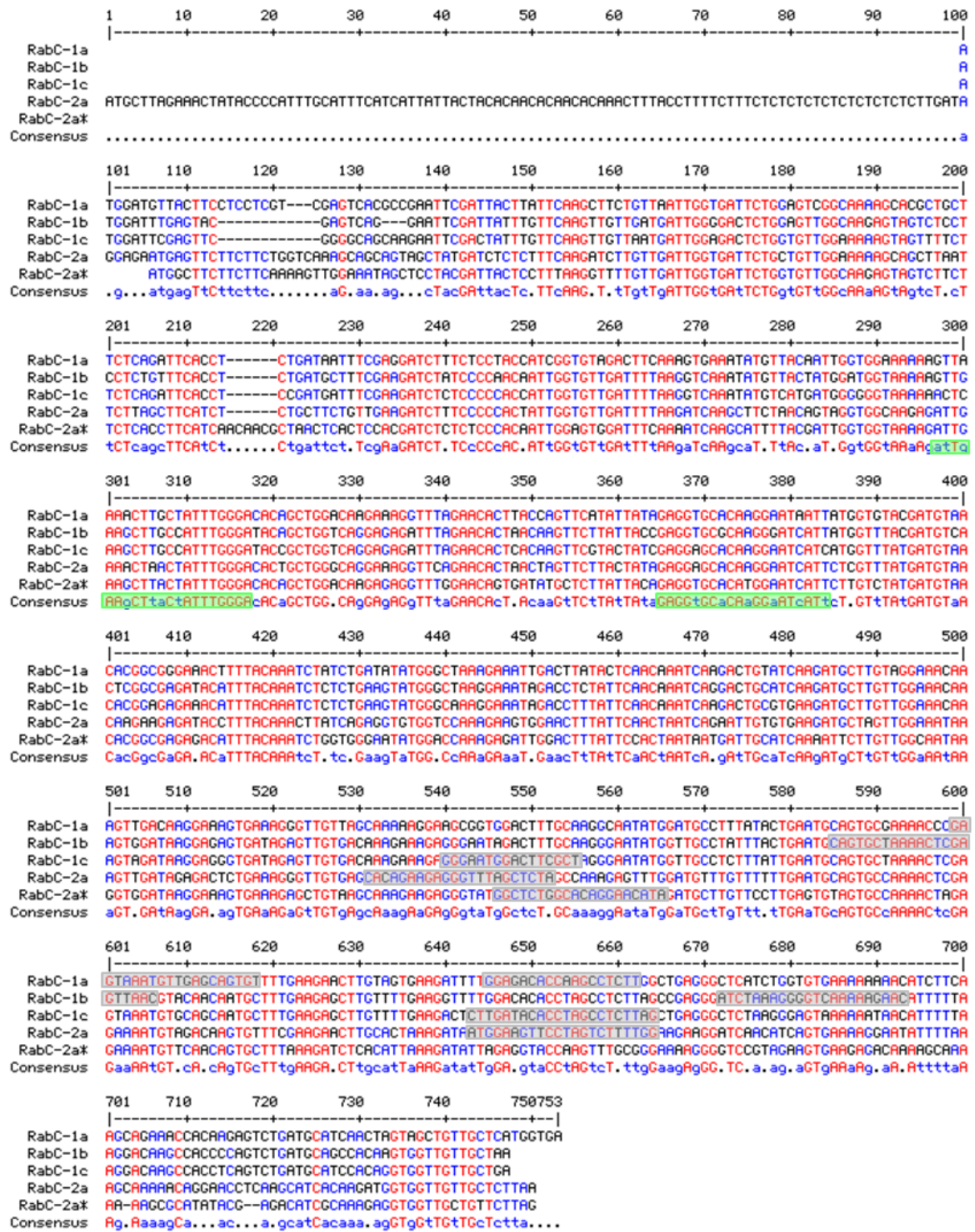
Annotated mRNA sequence from NCBI database, closest to the above fragment with SNP (with reverse-complement orientation). Start- and Stop-codons are indicated in green and red, respectively. The position of annotated SNP is indicated in yellow.

>XM_012715175.1 PREDICTED: *Cicer arietinum* ras-related protein RABC1-like (LOC101496214), transcript variant X2, mRNA

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Supplementary material 3

Alignment of five isoforms of the *CaRabC* gene identified in chickpea. Green boxes in the consensus sequence indicate the binding sites of qPCR primers for expression analysis of *CaRabC* gene for all five isoforms combined. The positions of qPCR primer pairs for expression analysis of *CaRabC* gene targeting each isoform specifically are shown in grey boxes.



Supplementary material 4

The fragment of genomic DNA, chromosome 4, retrieved from chickpea database matching the sequence LOC101496214 from the Supplementary 2 above. Start- and Stop-codons are indicated in green and in red, respectively. Exons are shown in Capital letters and introns are by letters in normal case. Primers used for sequencing are highlighted in pink. Primers used for Amplifluor-like SNP analysis (as shown in the Supplementary material 1) are highlighted in blue. Annotated and used SNPs are shown in yellow, in Capital and in normal case letters, respectively. The identified 11 SNP are shown in Bold in squired brackets.

>Ca4: 38,622,857 – 38,615,990 (reverse-complement)

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