1	A common bean truncated CRINKLY4 kinase controls gene-for-gene resistance
2	to the fungus Colletotrichum lindemuthianum
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27	Running title: A truncated CRINKLY4 kinase controls resistance to a fungus
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Highlight

CRINKLY4 receptor-like kinases have been mainly reported to be involved vascular plant development. Here we report an unusual truncated CRINKLY4 kinase, with an unexpected role in resistance against a pathogen.

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36 Abstract

37 Identifying the molecular basis of resistance is critical to promote chemical free cropping system. In plants, NLR constitute the largest family of disease resistance (R) genes 38 39 but they can be rapidly overcome, prompting research of alternative source of resistance. Anthracnose, caused by the fungus Colletotrichum lindemuthianum, is one of the most 40 41 important diseases of common bean. This study aimed to identify the molecular basis of Co-x, an anthracnose *R*-gene conferring total resistance to the extremely virulent *C. lindemuthianum* 42 43 strain 100. To that end, we sequenced the Co-x 58kb target region in the resistant JaloEEP558 44 (Co-x) and identified KTR2/3, an additional gene encoding a truncated and chimeric CRINKLY4 kinase, located within a CRINKLY4 kinase cluster. KTR2/3 presence is strictly 45 correlated with resistance to strain 100 in a diversity panel of common beans. Furthermore, 46 47 KTR2/3 expression is upregulated 24 hours post-inoculation and its transient expression using Agrobacterium-transformation in susceptible genotype increases resistance to strain 100. 48 49 Altogether, our results provide molecular evidence that Co-x encodes a truncated and chimeric CRINKLY4 kinase probably resulting from an unequal recombination event that 50 occurred recently in the Andean domesticated gene pool. This atypical R-gene might act as a 51 52 decoy involved in indirect recognition of a fungal effector.

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54 Keywords: Common bean, *Phaseolus vulgaris*, NLR, disease resistance gene,
 55 CRINKLY4 kinase, anthracnose, unequal crossing-over

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Introduction

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Plants are under constant pathogen challenge. However, successful infection is not an 60 easy accomplishement for the potential pathogens that have to overcome several plant 61 immunity layers. A first layer of immunity resides in the recognition of Microbe/Pathogen-62 Associated Molecular Pattern (MAMP or PAMP) by plant Pattern Recognition Receptor 63 (PRR), the so-called PAMP-Triggered Immunity (PTI) (Bigeard et al., 2015). PRR are 64 surface-localized ligand-binding transmembrane proteins from the Receptor-Like Protein 65 66 (RLP) or Receptor-Like Kinase (RLK) families (Macho and Zipfel, 2014). Although PTI can 67 keep a number of pathogens at bay, some adapted pathogens can counter this first defense 68 layer by releasing effectors in the extracellular matrix or into the plant cell (Toruño et al., 2016). A second layer of plant immunity, called Effector-Triggered Immunity (ETI), is based 69 70 on the recognition of these effector molecules, that were originally referred to as avirulence (Avr) proteins, by the product of plant Resistance genes (R genes) (Jones et al., 2016). 71 72 Strikingly, regardless of the plant, the type of pathogen or the diversity of pathogen Avr proteins, the majority of R genes cloned to date encode intracellular Nucleotide-binding 73 74 Leucine-rich repeat Receptors (NLR) (Baggs et al., 2017; Jones et al., 2016). NLRs can be 75 divided into two major sub-groups by their N-terminal domain: the CNLs, with a Coiled Coil (CC) domain and the TNLs, with a Toll/Interleukin-1 Receptor (TIR) domain (Monteiro and 76 77 Nishimura, 2018). NLR-based immunity often triggers a localized cell death known as the hypersensitive response (HR) (Balint-Kurti, 2019). 78

79 It has initially been proposed that NLRs recognize pathogen Avr proteins via direct interaction (Keen, 1990). However, cases of direct interaction have been demonstrated for 80 only few R-Avr combinations, such as for the TNL N from tobacco that directly recognizes 81 the Tobacco mosaic virus (TMV) protein p50 (Ueda et al., 2006) or for the TNLs L5, L6 and 82 83 M from flax which recognize the Avr proteins AvrL567 and AvrM, respectively, from Melampsora lini, the agent of flax rust (Catanzariti et al., 2010; Dodds et al., 2006). Since no 84 85 physical interaction has been observed for many R-Avr pairs, and because effectors/Avr have a role in promoting infection by manipulating virulence target, another model of indirect 86 87 recognition of the Avr by the R protein emerged. In this model, called the guard model, the R protein recognizes modified-self (the modification of a plant virulence target by the 88 effector/Avr protein), rather than non-self (the effector/Avr itself). The R protein is therefore 89 monitoring or guarding the virulence target specific modification by the effector, resulting in 90 91 immunity activation (van der Hoorn and Kamoun, 2008). One well-studied example

illustrating the guard model is the RIN4 protein of Arabidopsis thaliana, which is the 92 virulence target of at least three different Pseudomonas syringae effectors, AvrB, AvrRpm1, 93 94 and AvrRpt2 (Belkhadir et al., 2004; Kim et al., 2005). AvrB and AvrRpm1 directly interact 95 with the RIN4 protein and induce its phosphorylation, perceived by the CNL RPM1 (Mackey et al., 2002). AvrRpt2 triggers RIN4 cleavage, which is in turn perceived by the CNL RPS2 96 (Axtell et al., 2003; Day et al., 2005; Mackey et al., 2003). Interestingly, an alternative model 97 to the guard model has been proposed: the decoy model. In this model, effector manipulation 98 of plant targets does not always increase pathogen fitness because plant possesses decoys, 99 100 which mimic virulence targets. The manipulation of these decoys by the effectors does not directly affect the pathogen fitness but can be recognized by an NLR (van der Hoorn and 101 102 Kamoun, 2008). For example, the non-functional kinase ZED1 from Arabidopsis is suspected 103 to be a decoy. ZED1 is guarded by the NLR ZAR1 which recognizes ZED1-threonine 104 acetylation by the *P. syringae* effector HopZ1a (Lewis et al., 2013).

105 Common bean (Phaseolus vulgaris L.) is a major pulse crop that is extensively 106 cultivated around the world as a dry grain or fresh vegetable. It is the most important grain 107 legume for human consumption worldwide especially in developing countries in Central and 108 South America and Southeastern Africa (Broughton et al., 2003). In these countries, common 109 bean is a staple food and represents an important source of protein and micronutrients and is 110 consequently a critical component to combat malnutrition for hundreds of millions of smallholder farmers (Messina, 2014) (http://faostat.fao.org/). In addition to its agronomic 111 importance, common bean is an ideal model for crop evolutionary studies thanks to its 112 complex evolution which led to wild forms grouping in three gene pools widely distributed 113 114 from Mexico to South America. Cultivated germplasm arose from two of these ecogeographical gene pools by independent domestication events (Bitocchi et al., 2017). 115 Indeed, recent data suggest that wild *P. vulgaris* originated in Mesoamerica and subsequently 116 117 colonized the Southern hemisphere, giving rise to the Peruvian-Ecuadorian wild populations and the wild Andean gene pool (Bitocchi et al., 2012; Bitocchi et al., 2017; Rendon-Anaya 118 119 et al., 2017). The divergence between the Andean and Mesoamerican wild gene pools was 120 estimated to have occurred ~110,000 to 165,000 years ago (Mamidi et al., 2013; Schmutz et al., 2014). The lower genetic diversity in Andean compared to Mesoamerican wild 121 germplasm is in agreement with the occurrence of a bottleneck prior to domestication in the 122 Andes, that narrowed the subsequent domestication bottleneck (Bitocchi et al., 2017; 123 Rendon-Anaya et al., 2017). Subsequently, common bean was independently domesticated 124

from the Mesoamerican and Andean gene pools ~8000 years ago, while no domestication
event occurred in the Peruvian-Ecuadorian wild population (Bitocchi *et al.*, 2013).

Sequencing of plant genomes has become increasingly routine since the advent of the next-generation sequencing (NGS) technology (Bilsborough, 2013). Common bean is an autogamous diploid (2n = 2x = 22) species with a relatively small genome ~630 Mb (Arumuganathan *et al.*, 1991). In that context, three genome assemblies of cultivated common bean of contrasting origin are available, one for genotype G19833 of Andean origin (Schmutz *et al.*, 2014), and two for genotypes of Mesoamerican origin, BAT93 (Vlasova *et al.*, 2016).

134 Common bean yield stability is affected by a number of pests and diseases. Anthracnose, caused by the hemibiotrophic fungus Colletotrichum lindemuthianum, is one of 135 the major disease of common bean worldwide, especially in temperate regions with cool and 136 137 humid environmental conditions (Pastor-Corrales and Tu, 1989). As use of resistant genotypes is an economic and environmentally friendly way for controlling plant diseases, 138 139 efforts have been made to genetically characterize anthracnose R genes in common bean. The interaction between common bean and C. lindemuthianum fits the gene-for-gene model and 140 nearly 20 specific R genes have been localized in the common bean genome (Meziadi et al., 141 2016). As expected, most of these R genes are organized in clusters of genes co-localized with 142 NLR rich regions (Meziadi et al., 2016). One notable exception is the Co-x R gene, present in 143 144 the Andean genotype JaloEEP558. Indeed, Co-x is located at one end of chromosome 1 in a 145 region devoid of any NLR sequences (Geffroy et al., 2008; Richard et al., 2014) strongly suggesting that Co-x corresponds to a non-canonical R gene. In addition to an academic 146 147 interest, Co-x is also an important R gene at the agronomic level because it confers resistance to C. lindemuthianum strain 100, a highly virulent strain corresponding to race 3993, that 148 overcomes nearly all the known R genes of Mesoamerican origin (Richard et al., 2014). 149 Because of the academic interest and agronomic importance for Co-x, as a long term goal we 150 151 have sought to clone Co-x, and toward this effort we previously delimited the Co-x locus into 152 a 58 kb genomic DNA region that contains eight candidate genes in the sequence of the 153 reference Andean genotype G19833 (Richard et al., 2014).

The objective of the present study was to identify the molecular basis of *Co-x*. To that end, we PCR-amplified long-range fragments in the resistant genotype JaloEEP558 (*Co-x*) to carry out a detailed sequence analysis of the *Co-x* 58kb target region. Analysis of the *Co-x* locus sequence allowed us to identify an additional gene (KTR2/3) present in JaloEEP558 within a small cluster of CRR3 CRINKLY4 kinases. The presence of KTR2/3 is strictly 159 correlated with the resistance to strain 100 of *C. lindemuthianum* in a diversity panel of 160 common bean, and KTR2/3 is upregulated in leaves at 24 hours post-inoculation (hpi). In 161 addition, transient expression experiments confirmed a role for KTR2/3 in the resistance to 162 strain 100. Altogether, our results provide molecular evidence that *Co-x* corresponds to a non-163 canonical *R* gene encoding a truncated and chimeric CRR3 CRINKLY4 kinase which is the 164 result of an unequal recombination event that occurred recently in the Andean domesticated 165 gene pool.

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Materials and methods

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169 Common bean material

To infer whether *Co-x* is a dominant or recessive resistance gene, 149 F2 individuals 170 171 derived from a cross between the Mesoamerican breeding line BAT93 (co-x) and the Andean landrace JaloEEP558 (Co-x) were inoculated with strain 100. In order to study the origin of 172 173 Co-x, a total of 192 cultivated and wild common bean lines of various geographical origins were studied. The evaluated materials include 123 cultivated common bean lines from the 174 175 Bean Coordinated Agriculture Project (BeanCAP) diversity panel. The BeanCAP panel 176 consists of cultivars, germplasm releases, and important breeding lines primarily from North America, and was later augmented with Andean materials from Africa and South America, 177 from the International Center for Tropical Agriculture (CIAT) breeding program, and 178 included some landraces (Cichy et al., 2015). These cultivated beans can be separated into 179 180 subpopulations based on genepool Andean vs Middle American and market type dry bean vs snap bean. The BeanCAP diversity panel was complemented by 27 cultivated lines from our 181 Orsay collection and 41 wild accessions (21 Andean, 17 Mesoamerican and 3 Peruvian-182 Ecuadorian) provided by the CIAT, the United States Department of Agriculture Western 183 Regional Plant Introduction Station (USDA-WRPIS), the National Botanic Garden of 184 Belgium, and Roberto Papa (Università Politecnica delle Marche; one wild accession 185 186 collected from Mexico). The AND277 genotype was a gift from Celeste Gonçalves-Vidigal (Universidade Estadual de Maringa; Brazil). 187

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Inoculation assay with Colletotrichum lindemuthianum strain 100

Infections of common bean with *C. lindemuthianum* were carried out as previously described except for the plants used for the RT-qPCR analysis which were grown in soil instead of vermiculite (Richard *et al.*, 2014). Briefly, 7 days post-sowing in soil, seedlings of

P. vulgaris were inoculated with the C. lindemuthianum strain 100 by spraying an aqueous 193 spore suspension $(2x10^6 \text{ spores/mL})$ on both sides of the two cotyledonary leaves. For the F2 194 individuals and diversity panel lines, symptoms were scored 7 days after infection. For the 195 196 diversity panel, symptoms were scored on two independent replicates (4 plants in each 197 replicate). The kinetics experiments were carried out on JaloEEP558, and water was used as a mock (negative control). A time course gene expression analysis was conducted at 6, 24, 48, 198 199 72, and 96 hpi in JaloEEP558 seedlings infected with the strain 100. For each time, one of the 200 two cotyledonary leaves from three different inoculated plants and control plants were 201 sampled, flash frozen in liquid nitrogen for RNA isolation and RT-qPCR analysis.

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203Amplification of Co-x target region by Long-range PCR, purification and204sequencing

205 Long-range PCR was used to amplify Co-x target region in seven overlapping fragments of ~10 kb using the primers listed in Supplementary Table S1. PCR reactions used 206 207 100 ng of JaloEEP558 DNA added to PCR mix containing milliQ H₂O, LA Taq buffer (TaKaRa), 400 µM of each dNTPs, 0.5 µM of forward and reverse primers, 1.25 units of LA 208 209 Taq (TaKaRa) to a total volume of 25 µL. PCR cycles were performed in a Thermal Cycler (Applied Biosystem). An initial 2-minutes incubation at 94°C was followed by 30 PCR cycles 210 of denaturation (15 seconds at 94°C), annealing (45 seconds) and extension (1 minute per kb 211 at 68°C). After the tenth cycle, 10 seconds of extension were added at each cycle. The 212 213 reaction was completed by a final extension of 15 minutes at 68°C. Amplification products 214 were separated through a 1% agarose gel containing Ethidium Bromide in cold TBE 0.5X 215 buffer (previously cooled down at 4°C). Amplification products were excised from the gel 216 and the DNA was extracted using the NucleoSpin® Gel and PCR Clean-up kit (Macherey-217 Nagel) following supplier's protocole and eluted in 30 µL of milliQ H₂O pre-warmed at 50°C. Purified DNA from LR2.2, LR5, LR6 and LR7 was sequenced at the CNRGV (Toulouse, 218 219 France) using 454 GS-Junior technology (Roche). LR1, LR3 and LR4 were sequenced using 220 Pacific Biosciences PacBio RS II at GATC Biotech (Konstanz, Germany). Annotation was carried out as described in David et al. (2009). Genbank accession numbers are MW328721 221 222 and MW325717.

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224 PCR amplification of *KTR2/3*

The presence of *KTR2/3* was tested using the primers RepetJalo1F and RepetJalo1R (Supplementary Table S1) using Go Taq DNA Polymerase kit (Promega, Charbonnières-les-

Bains, France) in a standard PCR program (start: 94°C for 5 min; amplification: 35 cycles of 94°C for 30 s, 64°C for 30 s, 72°C for 3 min; termination: 72°C for 5 min). PCR products were resolved on 1% agarose gels containing ethidium bromide, run in 0.5X TBE buffer and visualized under UV light. In genotypes carrying *KTR2/3* this PCR reaction generates a 3179 bp fragment (referred to as "3.1 kb band") while in genotypes that do not carry *KTR2/3* it generates a 1639 bp fragment (referred to as "1.7 kb band").

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Cloning and sequencing of KTR2/3

Primers KTR2/3exp-F2 and KTR2/3exp-R were used to amplify a 1563 bp fragment containing *KTR2/3* ORF using standard PCR program and an Advantage HF-2 PCR Taq Polymerase (ClonTech) (Supplementary Table S1). For the 14 genotypes analyzed (Supplementary Table S2), the resulting fragment was cloned into pGEM[®]-T vector (Promega, Charbonnières-les-Bains, France) for sequencing analysis.

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RNA extraction and RT-qPCR analysis

Total RNA was extracted by using the kit for plants NucleoSpin RNA plus 242 243 (Macherey-Nagel, Hœrdt, France). The RNA quantity and purity were determined on a NanoDrop 8000 spectrophotometer (Thermo Fisher Scientific, Waltham, USA) and integrity 244 245 was checked by electrophoresis on a 1% agarose gel. cDNA was synthesized from 1 µg of RNA using the ImProm-IITM Reverse Transcription System according to the manufacturer 246 247 protocol. Quantitative RT-PCR (RT-qPCR) was performed with a LightCycler[®] 96 Instrument in 15 µL volume reaction containing 5 µL of 6 times diluted cDNA, each specific 248 249 primer with a final concentration of 0.1 µM, 7.5 µL SYBR green premix (LightCycler[®] 480 SYBR Green I Master, Roche) and distilled water. Results were analyzed by using the 250 software LightCycler[®] 96 version 1.1. 251

The expression analyses of the genes KTR2/3, KTR2, KTR3 and KFL genes were performed using the gene specific primers listed in Supplementary Table S1. Gene expression was normalized with four reference genes (*PvUkn1*, *PvUkn2*, *PvIDE* and *PvAct11*) (Borges *et al.*, 2012) (Supplementary Table S1). Gene expression in mock condition was used to calibrate gene expression in infected plants for each gene and time point. Relative gene expression in inoculated leaves compared to mock leaves was calculated using the method 2⁻ $\Delta\Delta$ Ct on two biological replicates and three technical replicates (Livak and Schmittgen, 2001).

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Transient transformation of common bean hypocotyles and disease assay with C. 261 lindemuthianum

KTR2/3 open reading frame (ORF) and its putative promoter sequence (corresponding 262 to the 345 bp located between the transcription start codon of KTR2/3 and the stop codon of 263 264 KTR3; Fig. 1) was PCR-amplified using High Fidelity polymerase (Advantage HF2, ClonTech), following the supplier's protocol, with KTR2/3exp-F2 and KTR2/3exp-R primers 265 (Supplementary Table S1) on JaloEPP558 gDNA and was cloned into the expression vector 266 pCambia0390 in BamHI restriction site. The resulting vector (pCambia0390+KTR2/3) or the 267 empty vector (pCambia0390) were transformed into Agrobacterium tumefaciens strain 268 EHA105. Bacteria were grown in YEB liquid culture (5 g/L beef extract, 1 g/L yeast extract, 269 5 g/L peptone, 5 g/L sucrose and 2 mM MgSO₄) supplemented with 200 µM of 270 acetosyringone, overnight at 28°C. After reaching an OD_{600nm} between 0.4 and 1.2, the 271 272 bacterial suspension was pelleted and resuspended in MMAi medium containing 10 mM MES pH 5.8, 10 mM of MgCl₂ and 150 μ M of acetosyringone at an OD_{600nm} of 1 and incubated 1 273 274 hour at room temperature. Meanwhile, the hypocotyls of 8 days-old BAT93 plants, susceptible to strain 100, were cut to have pieces of hypocotyl of 5 to 6 cm. Hypocotyls were 275 276 agroinfiltrated under vacuum for 15 minutes in a beaker containing one of the Agrobacterium 277 suspension, pCambia0390+KTR2/3 or empty pCambia0390. After infiltration, the hypocotyls 278 were dried on towel paper and their extremities were coated with paraffin wax. The 279 hypocotyls were placed on little racks in humid transparent boxes and kept in the dark for one day prior to C. lindemuthianum infection. C. lindemuthianum was prepared as described in 280 Richard *et al.* (2014). The hypocotyls were inoculated with a spore suspension of C. 281 *lindemuthianum* strain 100 at 5×10^6 spores/mL 24 h after agroinfiltration. On each hypocotyl, 282 3 drops of 5 µL each were carefully pipetted. The hypocotyls were then incubated for 7 days 283 in the humid transparent box in a growth chamber at 19°C with 16 h light before disease 284 285 scoring. For each condition (pCambia0390+KTR2/3 or empty pCambia0390), ~60 hypocotyls (~180 droplets) were tested. After 7 days, for each droplet, the symptoms were scored as 286 287 "resistant" (no symptoms) or susceptible (lesions developing). We performed a chi square test 288 (one degree of freedom) to test if the agroinfiltration with pCambia0390+KTR2/3 has a significant effect on the resistance, compared to controlled conditions with the empty vector. 289

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291 **Sequence analysis**

The targeted Co-x region in BAT93 was annotated using an automatic annotation 292 pipeline described in David et al. (2009). The pipeline uses a combination of gene-finding 293

programs and sequence homology with known genes and proteins: the two *ab initio* gene
prediction programs FGENESH (Burset and Guigo, 1996) and GeneMarkhmm (Lukashin and
Borodovsky, 1998), BLAST (Altschul *et al.*, 1997) analyses against the GenBank
nonredundant database and all the *Phaseolus* ESTs available at GenBank (Ramirez *et al.*,
2005). All this information was imported into the annotation platform Artemis (Rutherford *et al.*, 2000) for further manual analysis.

Multiple amino acid sequence alignment of the conserved kinase domain of *CRINKLY* 4 protein sequences was generated using MUSCLE (Edgar, 2004a, b) with default parameters and edited in Seaview for manual adjustments (Gouy *et al.*, 2010). Alignments were subjected to maximum likelihood (ML) analysis using the JTT+I+G model as implemented in PhyML (Guindon and Gascuel, 2003). Relative support for clades was assessed with 100 bootstrap replicates. The resulting phylogenetic tree was displayed using MEGA5 (Tamura *et al.*, 2011).

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Trypan and Aniline blue staining

For the Trypan blue staining, at 8 days post-infection (dpi), leaf discs of JaloEEP558 infected with *C. lindemuthianum* strain 100 were boiled 1 minute in a 3:1 mixture of 96% ethanol and staining solution (100 mL lactic acid, 100 mL phenol, 100 mL glycerol, 100 ml H_2O , and 100 mg Trypan blue (Sigma-AldrichTM, 93590)), rinsed with water and destained overnight in 2.5 g/mL chloral hydrate in water before observation on an optical microscope.

For the aniline blue staining, at 8 dpi, leaves of JaloEEP558 infected with *C*. *lindemuthianum* strain 100 were destained and fixated in 1:3 acetic acid/ethanol until complete discoloration. The saturated destaining/fixation solution was replaced, if necessary. Discs of fixated leaf were incubated in K_2HPO_4 100 mM pH=9.0 solution for 2 h before being transferred in aniline blue staining solution (0.1% aniline blue in K_2HPO_4 100 mM pH=9.0) and observation on an optical microscope.

- 320
- 321 **Results**
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Co-x is a dominant resistance gene

In order to infer the dominant/recessive status of *Co-x*, 149 F2 individuals derived from a cross between BAT93 (susceptible) and JaloEEP558 (resistant) were inoculated with strain 100. The observed segregation data fits the expected 3:1 ratio for one dominant resistance gene (122 resistant and 27 susceptible; χ^2_{1df} =3.76, *P*=0.0525).

Sequencing of the *Co-x* region in JaloEEP558 using Long-Range PCR

We previously fine-mapped Co-x in JaloEEP558 between the marker P05 and K06 330 331 (Richard *et al.*, 2014), defining a 58 kb interval in the genome of the reference genotype 332 G19833 (Schmutz et al., 2014) (Fig. 1). Annotation of the corresponding sequence in BAT93, for which a genome sequence is available (Vlasova et al., 2016), reveals the presence of the 333 same eight genes in G19833 and BAT93: three phosphoinositide-specific phospholipases C 334 (PLC3, PLC2, PLC1), one zinc finger transcription factor (ZnF) and a small cluster of four 335 336 CRINKLY4 kinases (KTR1, KTR2, KTR3, KFL) (Fig. 1). In addition, the intergenic regions are also highly similar between G19833 and BAT93 (>90% nucleic identity) (Fig. 1). 337

In order to recover the target region in JaloEEP558 (Co-x), we PCR-amplified this 338 region in 7 Long-Range (LR) overlapping segments of ~ 9 kb and sequenced these LR 339 340 fragments using a combination of Illumina and PacBio sequencing. The resulting sequences were annotated and compared to the sequence of the susceptible genotype BAT93 (co-x) (Fig. 341 342 1). The sequence of JaloEPP558 contains the 8 genes previously annotated in both G19833 and BAT93 (PLC3, PLC2, PLC1, ZnF, KTR1, KTR2, KTR3, KFL) and highly similar 343 344 intergenic regions (Richard et al., 2014). However, an additional gene referred to as KTR2/3 345 (1185 bp) was identified only in JaloEEP558 (Co-x).

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347The truncated and chimeric CRR3 CRINKLY4 kinase (KTR2/3) is a strong348candidate for the *Co-x* resistance gene

Unlike the kinases KTR1, KTR2, KTR3 (for Kinase TRuncated) and KFL 349 (for Kinase Full Length) present both in the susceptible and resistant genotypes, KTR2/3 is 350 only present in JaloEEP558 (Co-x) (Fig. 1 and Fig. 2A). KTR2/3, like KTR1, KTR2, KTR3 351 and KFL, belongs to the CRINKLY4 kinase family. In A. thaliana, the CRINKLY4 kinase 352 353 family is composed of five genes, ACR4, and four CRINKLY4-RELATED (CRR): AtCRR1, AtCRR2, AtCRR3 and AtCRK1. Phylogenetic analysis revealed that the five kinases present at 354 355 the Co-x locus (KTR1, KTR2, KTR3, KTR2/3 and KFL) belong to the CRINKLY4-RELATED 3 (CRR3) subfamily (Supplementary Fig. S1). However, while KFL corresponds 356 to a classical full length CRINKLY4 kinase, the four other kinases present at Co-x locus, 357 KTR1, KTR2, KTR2/3, and KTR3 are truncated proteins lacking both the extracellular 358 (Crinkly repeats and TNFR domain) and transmembrane domains classically found in 359 CRINKLY4 kinases (Fig. 2B). Instead, these truncated kinases are composed of an unknown 360 361 N-terminal domain of ~100 amino-acid followed by a predicted cytoplasmic serine/threonine

kinase catalytic domain classically found in CRINKLY4 kinase (Fig. 2B; Supplementary Fig. 362 363 S2). BLASTP analysis of KTR2/3 protein sequence revealed that this kind of truncated CRINKLY4 kinases containing this ~100 aa domain, are only found in legumes belonging to 364 the Phaseoleae tribe. Indeed, truncated CRINKLY4 kinase were identified in common bean, 365 at the Co-x locus (this study), in soybean, in the syntenic regions of Co-x locus located on 366 chromosomes Gm11 and Gm18, as well as in Vigna angularis, V. unguiculata, V. radiata and 367 Cajanus cajan. Sequence comparisons of the different truncated kinases present in P. vulgaris 368 at the Co-x locus revealed that KTR2/3 is a chimera between the beginning of the KTR2 (first 369 370 232 bp) and the end of KTR3 (953 bp). Interestingly, the junction region of KTR2/3 contains internal related repeats of either 69 or 78 bp supporting the dynamic nature of the region in 371 372 terms of recombination (Supplementary Fig. S3 and S4). More precisely, in the ~100 aa 373 unknown domain, KTR2/3 contains two 78 bp tandem repeats derived from KTR2 followed 374 by one 69 bp repeat derived from KTR3 (Supplementary Fig. S2, S3 and S4). The exact size 375 of the N terminal unknown domain is variable depending on the number of repeats in each 376 gene: 182 aa in KTR1, 72 aa in KTR2, 110 aa in KTR2/3, 127 aa in KTR3 (Supplementary Fig. S2, S3 and S4). Truncated forms of CRR3 were also found in *Ricinus communis* but with 377 378 a different and also unknown, N-terminal domain (Supplementary Fig. S2). Conversely, the 379 unknown ~100 aa is also present in the genome of Spatholobus suberectus, a traditional chinese medicine also belonging to the Phaseoleae tribe (Qin et al 2019). However, in this 380 381 latter species, the ~100 aa domain is not associated with truncated CCR3 kinase, but present in the N-term of a nuclear inhibitor of protein phosphatase, and in a Mitogen-activated protein 382 383 kinase kinase 1 (MAP3K1). In conclusion, even if truncated CCR3 or the ~100 aa unknown domain are found separately in very few species, truncated CCR3 containing this 384 ~100 aa domain, are only found in legume species from the *Phaseoleae* tribe. 385

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Diversity panel of wild and cultivated common beans

On the basis of these genomic results, KTR2/3 is a strong candidate gene for Co-x R 388 389 gene. In order to confirm that KTR2/3 is Co-x, we used a diversity panel of 192 cultivated and 390 wild common beans from various geographical origins. To infer the presence of KTR2/3, we 391 developed a couple of PCR primers amplifying specifically a 3.1 kb fragment on genotypes containing KTR2/3, while a 1.7 kb fragment is observed for genotypes that do not have 392 KTR2/3 (Fig. 2A, Supplementary Table S2). We identified 37 genotypes presenting the 3.1 kb 393 394 fragment, thus potentially containing KTR2/3. A 1.7 kb fragment was amplified from the 395 other 154 genotypes, implying of the absence of KTR2/3 in those genotypes. The same 192

genotypes were also scored for disease resistance after infection with strain 100 of C. 396 397 *lindemuthianum*. Strikingly, all the genotypes presenting the 3.1 kb band (KTR2/3) were 398 resistant to strain 100 (Supplementary Table S2). Reciprocally, we identified 115 genotypes 399 susceptible to strain 100 and none of them contained KTR2/3. Altogether, these results 400 strongly suggest that KTR2/3 is Co-x. Furthermore, 25 genotypes were resistant to strain 100 401 but did not contain KTR2/3, suggesting that these genotypes possess resistance to strain 100 402 conferred by another R gene. Most of the genotypes containing KTR2/3 are cultivated genotypes of Andean origin (Supplementary Table S2). However, four Meso-American 403 404 genotypes (Raven, Newport, Phantom, Jaguar) were also identified as carrying KTR2/3. Notably, all 41 wild genotypes tested, including 21 Andean wild genotypes, present the 1.7 kb 405 406 fragment, suggesting that KTR2/3 is not present in wild germplasm. We sequenced KTR2/3 407 gene in 14 common bean genotypes of Andean (10 genotypes) and Mesoamerican (4 above-408 mentioned genotypes) origin belonging to various market classes. The KTR2/3 coding sequence (1185 bp) was 100% identical for all 14 genotypes. 409

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Expression pattern of KTR2/3

412 In order to ascertain the involvement of KTR2/3 in anthracnose resistance, we 413 performed an expression analysis of KTR2, KTR2/3, KTR3 and KFL in the leaves of 414 JaloEEP558 after infection with C. lindemuthianum strain 100 (incompatible interaction), using RT-qPCR and gene-specific primers. In particular, to discriminate between KTR2, 415 KTR3 and KTR2/3 we developed primers bordering the junction area of KTR2/3 (Fig. 2; 416 Supplementary Table S1). Temporal gene expression analysis revealed that KTR2/3 is 3 fold 417 up-regulated after infection compared to mock control at 24 hpi (Fig. 3). Conversely, the 418 expression of KTR2, KTR3 and KFL was not modified upon C. lindemuthianum infection 419 (Supplementary Fig. S5; Supplementary Table S3). 420

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The function of *Co-x* confirmed by transient agrobacterium infiltration

In order to confirm the function of KTR2/3 as resistance protein against *C*. *lindemuthianum* strain 100, we developed a transient expression system by vacuuminfiltrating *Agrobacterium* in bean hypocotyls. BAT93 hypocotyls were agroinfiltrated with an expression vector containing or not *KTR2/3* ORF (and its own promotor). Transformed hypocotyls were then inoculated with droplets of strain 100 spore suspension and symptoms were scored at 7 dpi. We scored as "resistant" when no symptoms were observed and as "susceptible" when symptoms were observed at the site of deposition of the droplets 430 (Supplementary Fig. S6). In total 165 and 177 *C. lindemuthianum* droplet-inoculations were 431 scored on hypocotyls agroinfiltrated with the empty pCambia0390 vector and the 432 pCambia0390+*KTR2/3*, respectively. These experiments showed that agroinfiltration with 433 pCambia0390+KTR2/3 (68 droplets scored as "resistant" and 109 as "susceptible") has a 434 significant effect on the resistance compared to controlled conditions with the empty vector 435 (40 droplets scored as "resistant" and 125 as "susceptible") (χ^2_{3df} =19.37; *P* = 1.08E-05), 436 supporting that KTR2/3 is *Co-x*.

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Cytological characterization of the *Co-x* mediated resistance

The interaction between P. vulgaris and C. lindemuthianum has been extensively 439 440 studied at the cytological level in seminal papers (Oconnell and Bailey, 1988; Oconnell et al., 1985). Because the resistance gene KTR2/3 does not encode a classical R protein from the 441 442 NLR family, a characterization of KTR2/3-mediated immunity at the cytological level was conducted. To that end, leaves of JaloEEP558 were inoculated with spores of the strain 100, 443 444 stained with Trypan or aniline blue and observed under the optical microscope at 8 dpi. Fungal structures, such as conidia and appressoria, were observed on the surface of the 445 446 epidermal cells (Figure 4). However, no fungal structure could be observed intracellularly, 447 suggesting that KTR2/3-mediated resistance blocked the fungus at an early step of the infection. In fact, cell death was observed at the site of penetration of the fungus, in the 448 epidermal cells, suggesting the triggering of hypersensitive response (HR), which is a typical 449 early output of NLR-triggered immunity (Figure 4B). Furthermore, callose papillae 450 depositions were observed in some epidermal cells, coinciding with the presence of fungal 451 appressoria (Figure 4A, C and D). Consequently, these observations suggest that, even if 452 KTR2/3 encodes a non-canonical resistance gene, KTR2/3-mediated immunity resembles 453 canonical NLR-mediated immune responses at the cytological level. 454

455

456 **Discussion**

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In common bean, as in other crops, identifying the molecular basis of resistance is critical to promote chemical free cropping systems (Adachi *et al.*, 2020; van Esse *et al.*, 2020). In that context, the *Co-x R* gene is interesting for both applied and academic reasons. At the agronomic level, *Co-x* confers resistance to an extremely virulent strain of *C*. *lindemuthianum*. From a fundamental point of view, we present here molecular evidence that 463 *Co-x* is a non-canonical resistance gene encoding a truncated and chimeric CRINKLY4
464 kinase belonging to the CRR3 subfamily.

Thanks to the recent improvement in sequencing technologies, reference genome 465 sequences are now available for most crop species (Hickey et al., 2019; Michael and 466 VanBuren, 2020). In that context, a major bottleneck for disease R gene cloning is the 467 generation of high-quality sequence information from the genotype of interest carrying the 468 target R gene (Thind et al., 2017). In the present study, the development of a 11X non-gridded 469 BAC library of JaloEEP558 was unsuccessful since after screening with PCR-based markers 470 471 developed from the Co-x locus (Richard et al., 2014), no positive BAC clone was identified 472 (data not shown). In contrast, long-range PCR amplification in combination with long read 473 sequencing enabled sequencing of the Co-x locus in JaloEEP558 (~60 kb). This allowed us to 474 identify an additional gene (KTR2/3) present only in the resistant JaloEEP558 (Co-x). KTR2/3 475 is a chimeric gene consisting of fragments of the two adjacent genes present at the Co-x locus. 476 Consequently, it is worth noting that a re-sequencing strategy based on mapping of short reads 477 would have been inefficient to identify KTR2/3. The democratization of long read sequencing 478 offers new perspectives by enabling not only *de novo* genome but also pan-genome assembly 479 (Michael and VanBuren, 2020). A seminal study in wheat has already exploited pan-genome 480 variation, instead of performing GWAS (Genome-Wide Association Studies) on a reference genome to rapidly clone *R* genes (Arora *et al.*, 2019). 481

The agronomical importance of the *Co-x* cluster is illustrated by the numerous recent 482 papers dealing with this cluster (Chen et al., 2017; Goncalves-Vidigal et al., 2020; Mahiya et 483 484 al., 2019; Murube et al., 2019; Padder et al., 2016; Wu et al., 2020). However, these studies are based on the reference genome of G19833 (Schmutz et al., 2014), where KTR2/3 is not 485 present, blurring the conclusions not only with regard to the gene content but also for the 486 expression analysis by RT-qPCR. Indeed, without knowing the existence of KTR2/3, primer 487 pair supposed to be specific to KTR2 or to KTR3 can also amplify KTR2/3, because these 488 genes present highly similar regions (Supplementary Fig S3 and S4). In the present study, by 489 490 using primer pair specific to KTR2/3 we showed that KTR2/3 is up-regulated in leaves after 491 infection, while KTR2 and KTR3 are not, supporting the involvement of KTR2/3 in resistance (Fig. 2; Fig.3; Supplementary Table S1, Supplementary Fig. S5). Consequently, the Co-x 492 resistance cluster in common bean clearly exemplified the importance of working with the 493 494 genome carrying the target *R* gene (*ie* JaloEEP558) and not only a reference genome.

495 Using a combination of approaches including comparative genomics, diversity panel studies,
496 RT-qPCR experiments and transient expression experiments, we identified *KTR2/3* as the

molecular basis of Co-x. KTR2/3 and the other kinases from the Co-x locus (KTR1, KTR2, 497 KTR3 and KFL), belong to the CRINKLY4 (CR4) family of receptor-like kinases and more 498 precisely to the CRR3 subfamily (Supplementary Fig. S1). CR4 kinases were initially described 499 500 in maize, and have been mainly reported to be involved in plant growth and development in several vascular plants (Becraft et al., 1996; Czyzewicz et al., 2016). More recently, an 501 unexpected role in plant defense was also described for an A. thaliana CR4 homolog (ACR4), 502 against the pathogenic fungus Botrytis cinerea since acr4 mutant displayed an enhanced 503 resistance to the fungus (Czyzewicz et al., 2016; e-Zereen and Ingram, 2012). Furthermore, 504 ACR4 has been shown to localize at the plasma membrane, and more specifically at the 505 plasmodesmata in Arabidopsis or when transiently expressed in Nicotiana benthamiana (Stahl 506 507 and Simon, 2013). Plasmodesmata are plasma membrane-lined tubes that directly connect the cytoplasm of adjacent cells and ACR4 is suspected to have a role in the regulation of the 508 509 trafficking via these plasmodesmata (Stahl and Faulkner, 2016). So how can KTR2/3, a chimeric and truncated CR4 kinase from common bean, act as an R gene against C. 510 511 lindemuthianum? We propose that KTR2/3 could act as a decoy in an indirect recognition system (van der Hoorn and Kamoun, 2008). Indeed, some plant pathogens such as 512 Colletotrichum or Magnaporthe oryzae use plasmodesmata as an effective pathway for 513 intercellular hyphal passage and for effector spread in plant tissues (Kankanala et al., 2007; 514 Liao et al., 2012; Ohtsu et al., 2019). It is also suspected that fungal effectors could manipulate 515 plasmodesmata to promote their opening (Cao et al., 2018; Ohtsu et al., 2019). Consequently, 516 it is tempting to speculate that an effector from C. lindemuthianum strain 100 could manipulate 517 bean plasmodesmata by targeting members of the CR4 family and that bean has evolved a 518 decoy, the truncated CR4 KTR2/3 kinase, guarded by a NLR protein. The resistance against 519 strain 100 segregates as a single dominant gene in the RIL population BAT93 x JaloEEP558. 520 Thus, the putative NLR guarding KTR2/3 could be either monomorphic between BAT93 and 521 JaloEEPP558 or different NLRs in the same genomic region (same NLR cluster) in BAT93 and 522 JaloEEPP558 genomes may guard KTR2/3 leading to an apparent non segregation among 523 524 NLRs. Notably, we showed that KTR2/3 lacks the extracellular and transmembrane domains classically observed for CR4 proteins such as KFL which supports the hypothesis that KTR2/3 525 could be a decoy, that mimics a virulence target (Fig. 2, Supplementary Fig. S2). Indeed, 526 decoys are thought to usually evolve after duplication of an ancestral guardee by diversifying 527 528 selection and are supposed to have no clear biological, cellular, or physiological functions compared to guardees (van der Hoorn and Kamoun, 2008). In agreement with the role of 529 530 KTR2/3 as a decoy/guardee in indirect recognition, we have shown that KTR2/3-mediated

resistance implies HR and callose deposition, which are a hallmark of NLR-mediated 531 532 resistance. Many kinases and pseudokinases are essential for NLR-mediated immunity and are common targets for pathogen effectors, acting as guardees or decoys (Sun et al., 2020). This is 533 the case, for example, of Pto from tomato (Mucyn et al., 2006), and PBS1, ZED1 and CRCK3 534 from Arabidopsis (Ade et al., 2007; Lewis et al., 2013; Zhang et al., 2017). Conversely, the 535 wheat Stb6 R gene encoding a wall-associated receptor kinase (WAK)-like protein has been 536 shown to encode the R gene per se but in that case, it confers pathogen resistance without HR 537 538 (Saintenac et al., 2018). The dominant nature of Co-x fits this model of indirect recognition. Most of the above cited examples of guardees/decoys are involved in indirect recognition of 539 bacteria effectors, thus KTR2/3 constitutes an original example of indirect recognition of an 540 541 effector from a fungal pathogen. Interestingly, KTR2/3 belongs to a small class of kinases termed non- RD kinase that has been proposed to function in plant immunity (Dardick and 542 543 Ronald; 2006). Furthermore, KTR2/3 presents the residues required for catalytic activity in the catalytic loop but not in the ATP-binding pocket and in the P-loop (Dardick and Ronald; 2006) 544 545 (Supplementary Fig. S2). This suggests that KTR2/3 is not functional which is in agreement with our hypothesis that KTR2/3 is a decoy. In order to test whether KTR2/3 is a decoy, the 546 susceptibility to C. lindemuthianum strain 100 should be measured in plants lacking the NLR 547 guarding the decoy (KTR2/3), in presence and absence of KTR2/3. If KTR2/3 is a decoy, rather 548 than a virulence target, the pathogen should not benefit from manipulating KTR2/3 and 549 therefore no differences in susceptibility should be observed between plants with or without 550 KTR2/3. Finally, our results raise the question of what can be considered as an R gene. Indeed, 551 a distinction between PTI and ETI, cannot strictly be maintained (Thomma et al. 2011), and in 552 fact PRRs, NLRs, and any signaling protein could be considered an R gene if the genetics 553 554 follows.

Unequal crossing-over (UCO) has been shown to be one of the main driving forces for 555 genome differences (Thind et al., 2018). Concerning R gene clusters, it has been identified 556 that UCO can increase or decrease the number of paralogs and can in some cases lead to new 557 558 R specificities (Cai and Xu, 2007; Thind et al., 2018). We found that KTR2/3 is a chimeric and additional gene in JaloEEP558 (Co-x) presenting sequence similarities with the 559 560 surrounding genes KTR2 and KTR3. This strongly indicates that KTR2/3 is the result of an intragenic UCO event. The internal related tandem repeats of either 69 bp or 78 bp present in 561 562 both KTR2 and KTR3 are also located at the junction between KTR2 and KTR3 corresponding sequences in KTR2/3 (Supplementary Fig. S2, S3, S4). This suggests that these 563 564 tandem repeats have served as template for this intragenic UCO event. The importance of

UCO in the gain or loss of R genes has been well described for various NLR clusters such as 565 the maize rust Rp1 cluster or the soybean Phytophthora Rps cluster (Ashfield et al., 2012; 566 Richter et al., 1995; Sandhu et al., 2004; Sudupak et al., 1993). Strikingly, using a diversity 567 panel of common bean, we showed that KTR2/3 was present only in cultivated Andean 568 genotypes strongly suggesting that the UCO that gave rise to KTR2/3 occurred recently, after 569 domestication, in the Andean cultivated gene pool. Since domestication is dated 8,000 years 570 ago, the emergence of KTR2/3 is younger than this date. In agreement with the recent origin 571 of KTR2/3, sequencing of KTR2/3 in 14 genotypes belonging to various market classes 572 573 showed that KTR2/3 sequence is 100% identical in all these genotypes. Four genotypes of 574 Mesoamerican origin were also shown to present KTR2/3. However, this does not disprove 575 our hypothesis since these genotypes are known to result from recent breeding programs 576 where Andean resistance genes located at the Co-x cluster were introgressed by back-cross in 577 a Mesoamerican elite background.

The unknown domain located in the N terminal part of the truncated CRR3 578 579 CRINKLY4 kinase remains intriguing. Our research reveals that the sequence coding this domain is only present in the *Phaseolea* tribe suggesting a recent origin. In addition, this 580 581 domain exhibits variable number of repeats in the different KTR genes from P. vulgaris, and 582 is located at the junction between corresponding KTR2 and KTR3 parts of KTR2/3 suggesting a dynamic role in recombination. Most puzzling, this unknown domain was found 583 associated in other genes such as MAP kinase in Spatholobus suberectus which supports its 584 dynamic role in recombination and suggests a functional role in association with kinases. 585 Additional analysis will be required to understand the origin, the mechanism of integration in 586 genes and the potential function of this unknown domain. 587

Notably, several additional anthracnose *R* specifies have been located in the same genomic region as *Co-x*, and described as an allelic serie: *Co-1*, *Co-1*², *Co-1*³ (Melotto and Kelly, 2000), *Co-1*⁴ (Goncalves-Vidigal *et al.*, 2011), *Co-1*⁵ (Goncalves-Vidigal and Kelly, 2006). Except for genotype Widusa carrying *Co-1*⁵, all the genotypes carrying a *Co-1* allele (*Co-1*, *Co-1*², *Co-1*³, and *Co-1*⁴) contain KTR2/3 (Supplementary table S2) which could suggest the involvement of KTR2/3 or an allele of KTR2/3 in these resistance. Further work will be needed to clarify the molecular basis of these *R* genes.

595 Wild populations undoubtedly possess a large reservoir of R genes, but our results 596 show that R gene diversity can be created after domestication. Maintaining evolutionary 597 processes in crops is the core concept behind a dynamic management of genetic resources, 598 and mutation and recombination have been highlighted as efficient mechanisms in

599	experimental populations (Enjalbert et al., 2011; Raquin et al., 2008). Our results reinforce
600	dynamic resistance management in germplasm collections, where the evolution of R genes in
601	cultivated crops constitutes a critical leverage for their adaptation to emerging diseases.
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Figure legends:

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Figure 1: The comparison of *Co-x* target region between JaloEEP558, G19833 and BAT93 reveals the presence of an additional gene (KTR2/3) in JaloEEP558. A schematic representation of the PCR-amplified and sequenced regions of JaloEEP558 genomic DNA are depicted on the top part. The identified genes and their orientation are depicted by black arrows.

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620 Figure 2: Representation of the kinase-containing region at Co-x locus and details of their protein structure. A. Location and orientation of the kinase-encoding genes present at 621 Co-x locus in JaloEEP558 sequence and in the corresponding regions in G19833 and BAT93. 622 The primers used are depicted by arrows. **B.** The kinases present at Co-x locus belong to the 623 624 CRINKLY 4-RELATED 3 kinase type (CCR3). The full length kinase (KFL) present the typical protein structure of CRINKLY 4 kinase with a predicted extracellular part containing 625 626 the Crinkly repeats and the Tumor Necrosis Factor Receptor (TNFR) domain, a transmembrane domain, and an intracellular kinase domain and C-terminal part. The truncated 627 628 kinases present in Co-x locus (KTR2, KTR2/3 and KTR3) lack the extracellular and transmembrane part, which is replaced by an ~100 aa unknown domain boxed in yellow. 629

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Figure 3: Time-course expression analysis of the *P. vulgaris* KTR2/3 gene in JaloEEP558 after inoculation with *C. lindemuthianum* strain 100. The relative abundance of *KTR2/3* transcripts was calculated by comparing KTR2/3 cDNA level in inoculated leaves with mock controls at each respective timepoint at 6, 24, 48, 72 and 96 hours post inoculation (hpi). Data was normalized using the *PvUkn1*, *PvUkn2*, *PvIDE* and *PvAct11* reference genes. Bars represent the mean \pm SD, n=2 independent experiments.

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Figure 4: Micrographs of Trypan blue (A and B) and aniline blue (C and D) stained leaves of JaloEEP558 inoculated with the *C. lindemuthianum* strain 100 under white (A, B and C) and UV (D) light at 8 dpi. Fungal conidia and appressoria are indicated by black arrowheads and black arrows, respectively. Plant epidermal cell responses, such as, cell browning and callose papillae are indicated by white asterisk and white arrows, respectively. Bars = $10 \mu M$

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646	Supplementary data
647	
648	Figure S1: Maximum likelihood (ML) tree based on the protein multiple sequence
649	alignment of CRINKLY 4 kinase domain from various species.
650	
651	Figure S2: Multiple alignment of CRINKLY 4 related 3 (CRR3) protein sequences
652	from Arabidopsis thaliana, Zea mais, Oryza sativa, Glycine max, Medicago truncatula,
653	Ricinus communis and Phaseolus vulgaris.
654	
655	Figure S3: Multiple alignment of nucleic sequences of KTR2 (G19833, JaloEEP558
656	and BAT93) and KTR2/3 (JaloEEP558) showing that the first 232 bp of KTR2/3 are highly
657	similar to the sequence of KTR2.
658	
659	Figure S4: Multiple alignment of nucleic sequences of KTR3 (G19833, JaloEEP558
660	and BAT93) and KTR2/3 (JaloEEP558) showing that the last 953 bp of KTR2/3 are highly
661	similar to the sequence of KTR3.
662	
663	Figure S5: Time-course expression analysis of the P. vulgaris genes KTR2, KTR3
664	and KFL of JaloEEP558 in response to C. lindemuthianum strain 100.
665	
666	Figure S6: Transient expression of $KTR2/3$ in common bean hypocotyls and C.
667	lindemuthianum disease assay scoring at 7 dpi.
668	
669	Table S1: List of primer sequences used in this study (RT-qPCR, cloning).
670	
671	Table S2: Common bean genotypes of various geographical origins tested for
672	resistance to strain 100 of <i>C. lindemuthianum</i> and for the presence of KTR2/3 encoding gene.
673	
674	Table S3: Raw data of the RT-qPCR experiments.
675	
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685	
686	Conflict of interest
687	The authors declare no conflict of interest.
688	
689	Author contribution
690	VG, and MMSR designed the project; MMSR, AG, JCAD, VT, SP, CM, SB, PNM,
691	WM, EB and VG, performed the experiments; MMSR, AG, JCAD, VT, SP, PNM, EB, RP
691 692	WM, EB and VG, performed the experiments; MMSR, AG, JCAD, VT, SP, PNM, EB, RP and VG analyzed and interpreted the data; MMSR, PNM and VG wrote the paper with
691 692 693	WM, EB and VG, performed the experiments; MMSR, AG, JCAD, VT, SP, PNM, EB, RP and VG analyzed and interpreted the data; MMSR, PNM and VG wrote the paper with significant input from all authors.
691 692 693 694	WM, EB and VG, performed the experiments; MMSR, AG, JCAD, VT, SP, PNM, EB, RP and VG analyzed and interpreted the data; MMSR, PNM and VG wrote the paper with significant input from all authors.
 691 692 693 694 695 	WM, EB and VG, performed the experiments; MMSR, AG, JCAD, VT, SP, PNM, EB, RP and VG analyzed and interpreted the data; MMSR, PNM and VG wrote the paper with significant input from all authors. Data Availability Statement
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Figure 1: The comparison of *Co-x* target region between JaloEEP558, G19833 and BAT93 reveals the presence of an additional gene (*KTR2/3*) in JaloEEP558. A schematic representation of the PCR-amplified and sequenced regions of JaloEEP558 genomic DNA are depicted on the top part. The identified genes and their orientation are depicted by black arrows.



Figure 2: Representation of the kinase-containing region at *Co-x* locus and details of their protein structure. **A.** Location and orientation of the kinase-encoding genes present at *Co-x* locus in JaloEEP558 sequence and in the corresponding regions in G19833 and BAT93. The primers used are depicted by arrows. **B.** The kinases present at *Co-x* locus belong to the CRINKLY 4-RELATED 3 kinase type (CCR3). The full length kinase (KFL) present the typical protein structure of CRINKLY 4 kinase with a predicted extracellular part containing the Crinkly repeats and the Tumor Necrosis Factor Receptor (TNFR) domain, a transmembrane domain, and an intracellular kinase domain and C-terminal part. The truncated kinases present in *Co-x* locus (KTR2, KTR2/3 and KTR3) lack the extracellular and transmembrane part, which is replaced by an ~100 aa unknown domain boxed in yellow.

Figure 3

Time-course expression analysis of the *P. vulgaris* KTR2/3 gene in JaloEEP558 after inoculation with *C. lindemuthianum* strain 100. The relative abundance of *KTR2/3* transcripts was calculated by comparing KTR2/3 cDNA level in inoculated leaves with mock controls at each respective timepoint at 6, 24, 48, 72 and 96 hours post inoculation (hpi). Data was normalized using the *PvUkn1*, *PvUkn2*, *PvIDE* and *PvAct11* reference genes. Bars represent the mean ± SD, n=2 independent experiments.



Figure 4

Micrographs of Trypan blue (A and B) and aniline blue (C and D) stained leaves of JaloEEP558 inoculated with the *C*. *lindemuthianum* strain 100 under white (A, B and C) and UV (D) light at 8 dpi. Fungal conidia and appressoria are indicated by black arrowheads and black arrows, respectively. Plant epidermal cell responses, such as, cell browning and callose papillae are indicated by white asterisk and white arrows, respectively. Bars = $10 \mu M$



Fig. S1: KTR2/3 belongs to the CRINKLY 4-RELATED 3 Kinase clade. Maximum likelihood (ML) tree based on the proteic multiple sequence alignment of CRINKLY 4 kinase domain from various species.

CRINKLY 4-RELATED 3



Fig. S2: Multiple alignment of CRINKLY 4 related 3 (CRR3) protein sequences from *Arabidopsis thaliana, Zea mais, Oryza sativa, Glycine max, Medicago truncatula, Ricinus communis* and *Phaseolus vulgaris*. Predicted domains are depicted on the alignment according to Cao *et al.* 2005, as described on the legend below. Truncated kinases (which names are boxed in red) present in *Co-x* region in common bean, *R. communis* and *Glycine max* present only the kinase domains compared to the classical full length *CRINKLY 4* kinases. Note that the truncated CRR3 kinases from *R. communis* lack the 100 aa unknown domain, but possess a different domain instead. Note that the truncated CRR3 kinases from *R. communis* don't present the 100 aa unknown domain, but a different one. The two related repeats of 78 or 69pb are boxed in green or pink arrows, respectively, on the KTR2/3 sequence.



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OS03G43670	MDIVPVVA-	LCCCLVLI	LPSWAYGL	GSMASIAVSY	GEDGPVFCGL	NSDGSHLVTCF	GADASVVY	GAPSRIPFV		-GVTAGDGI	FACGLLLDTNQ	PYCWGSNSYVK	IGVPQPMVE	JAMYSEL
OS05G03620	MI	PLLLLLLL	PLLLLAPASAS	TVAIAAG	PTACAVAEGN	ISTVYCASATNS	SSSAA	VAP-FVSFS		-QVSGGGG	AFVCGLQVGGR	ALFCWPAAAP-	GQLRRVYN	IGPG
Zm2G120839	MT	PRPRLLLLL	AIALPAASAAS	TLAVSASSTS	PTVCGVAEPN	IGTVYCAPLQGF	SSSNSASE	VAPSAIAFA		-ELSAGRG-	-FVCGLQAGGA	ALFCWPSTPAP	QWGQLRRLYN	IGPA
Pv01G243800.1	MKTLTSSSVTLCL-	VVAALLILS	SLPRSSHGLGS	GATLTISDAS	STVCAVVARE	STRRIECYRQG	QIA	SITPNASFS		-TISGGRN-	-YFCGLRSSNS	DLLCWNTSSS-	FERRRLYN	IDSSV
KFLJalo_p	MKTLTSSSVTLCL-	VVAALLILS	SLPRSSHGLGS	GATLTISDAS	STVCAVVARE	STRRIECYRQG	QIA	SITPNASFS		-TISGGRN-	-YFCGLRSSNS	DLLCWNTSSS-	FERRRLYN	IDSSV
Gm11g35390.2	MKTSPSS-VNLCLA	VAVAAVVLILS	SLVPSSHGFGS	GTTLALSDAS	ATVCAVVASE	STRRIECYRQG	QVV	PIAPNVNFS		-SISGGRN-	-YFCGIMSSNS	NLLCWNTNSS-	FEMRRLYN	IKSSV
Gm18g03040.2	MKTPPSSSVNLCLA	VAVAA-VLILS	SLVPSSHGFGS	GATLALSDSS	STVCAVVASE	STRRIECYRQG	QVV	PIAPNVSFS		-SISGGRN-	-YFCGIRSSNS	NLLCWNTSSS-	FERRRLYN	IDSSV
Mt3g0/0800.1	MKNLITHLIFVTA-	1115	LSPSAHTLGS	GTTLSVTDSP	ATVCGIISGE	TTQHIQCYREG	EVE	NILPNVSFS		-SISGGRS-	-YFCGLRSGNY	SLHCWD-SSS-	FQTKRLYS	INDSF
Gm02g42440.2	MKNNKSPFSAATFI	-LFNATLLILS	SSLSPTHALGS.	AATLAATS	SAVCGVVASE	PTRRIACYRHG	EVV	AVAPNVSFS		-AISGGRS-	- IFCGLRSGNI	SLLCWDTLSG-	FQSKRLYN	INGTV
Gm14g06440.1	MKKNKSPFSAATFI	-LFIATLLILS	SSLSPSHALGS.	AATLAVTS	SAVCGVVASE	PTRRIACYRHG	EVV	AVAPNVSFS		-TISGGRS-	-YFCGLRSGNY	SLLCWDTLSA-	FQSKRLYN	INGTV
PV08G223900.1	MKKNNSLFSAVTF1	-LFTVTLLILS	SSLSPSHALGS.	ASTLAVTS	AAVCGVVASE	PTRRIACYSNG	HVV	AVAPNISFS		-AISGGLS-	- IFCGLRSGNY	FLLCWDTLSY-	FQSKRLYN	INDTV
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Bw06G068400 1	MTPPFTLSLS	I.FAVE	SITAVHGLGS.	AATTAVTIGT	ATVCGVVAGE	LHHRIOCSRDG	-RRVF	LTLPNASEE		-TISGGRS-	-FFCGLRSGGW	SLHCWDTAAAD	GAFYPKRVFF	ISDVV
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Bc28833 m0160														
Gm11q35348.1														
Pv01G243600.1														
KTR2Jalo p														
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Gm18g03053.1														
Pv01G243500.1														
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Mt4g035180.1	MAFHHKHLFISI	YFFLSFILLP-	IINTLS	TVSISHTSNS	NQTLICVLQS	QNQQKHS		-NLNCTSFS		-PSIS	-FGTKLELN	SNVS	YS	SQIV <mark>GG-</mark>
AT2G39180	MQP-N	SHIFVIITISS	SLIITVSAYGS	TGTIAAAFGE	NGFFCAIDAS	GKQEVICWDRG	NTNRSLNB	PPGEISGYS	PF	MTSLSGGE	FLCAITSNTS	RAFCWNLEDPS	ENLVPRAE	/QYN
AT3G09780	METRC	SLLFLSLILLY	LPKPGSGFGS	SGPIAASFGG	SAFFCAIDAS	GRQDVICWGKN	YSSPSSPS	SSSSSSSIASSI	SASYNIPS	MAVLSGGD	FLCGILSNTS	QAFCFSSLGSS	SGMDLVPLAY	RTT

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AT3G59420	SAGDYHLCGLRKPIVGRRKNSNII	SSSLVDCWGYNMTRNFVFDKOLF	HSLSAGSEFNCALSSI	KDKSVFCWG	DENSSOVISLIPKEKKFOKIAAG	GYHVCGILDGLES	RVLCWGKSLEFE	EEVTGTSTEEK
OS03G43670	SAGDNHLCALRTSVKGFHSVNG	DTSVIDCWGYNMTATHTVTGAVS	SAISAGSVFNCGLFA	RNRTVFCWG	DESVSGVIGLAPRNVRFQSIGAG	GYHVCGVLENA	QVFCWGRSLEMQ	QMSTPSSTDDG
OS05G03620	QLSQLAVGGGHVAAYDAAARVI	RWWRGGDRFPLWFGG-GFA	-SLVSGDDFTCAVETS	STSAVRCWG	PRGGAVEAGFLNASVS-ALAAG	GSRACGVRRNDGG	VLCSGGGVLA	PRED
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KFLJalo_p	PLENLAVGDTHLCATEVGDGAV	KCWRTGDTFQLPSATDKFA	-SISSGTGFSCGILK1	NSYRVRCWGDT-	SVSDLTERIESVFGNMSML-SLVAG	GSHVCGLNST-GF	LVCGGNNDSGQR	DFP
Gm11g35390.2	PLENLAVGDTHVCATAVGDGTV	RCWRTGDTFRNPSGSDQFA	-SISSGSGFSCGILK1	NGSKVRCWGDT-	NVAQQIENSFGNMSML-SLVAG	GSNICGLNST-GF	LVCSGQL	DFP
Gm18g03040.2	PLENLAVGDTHVCATAVGDGTV	RCWRTGNTFQIVSGSDQFA	-SISSGSGFSCGILK	NGSRVRCWGDT-	NVSEQIENSFRNISML-SLVAG	GSHVCGLNLT-GF	LVCRGSNGSGQF	DIP
Gm02g42440.2	LLEKLALGDSOVCATVVGVGTV	SCWRTNAAFESPSGSDRFD	-SISSGSNFSCGILK	GSDRVRCWGEK-	VGSIARKMESEFGNMSLV-SLVAG	ESHICGLNSI-GP	LVCRGSNSSGQL	DVP
Gm14g06440.1	LFENLALGDSQVCATVVGAGKA	SCWRTNAAFESPSGSDRFD	-SISSGSGFSCGVLKC	GSDRVRCWG	VGSIARKMESEFRNMSMV-SLVAG	ESHVCGLNSS-GY	LVCRGSNNFGQI	DVP
Pv08G223900.1	LFENLALGDFQVCATAVGDGTA	SCWRTDVDFELPSGSDRFS	-SISSGSGFSCGILK(GSNWVRCWG	VEAMARKMENEFGNVSMA-SLVAG	ESHVCGLNSS-GY	LVCRGSNDFGQI	DAP
Rc28162.m0127	VDGAGSV	OCWRGNGSSSNGSPVDSDKFO	-SISSGFGFNCGILKKN	NNSRIMCWG	SNPIGKDIESEFGNMSMM-SIVAG	GSHVCGLNSK-GP	LVCKGSNNFGQ1	DVPL
AT3G55950	LLETLSVGDKQICATVNGTNSI	KCWRGSVSDQSKPPNERFR	-SISSGVGFSCGVSIR	-NNRILCWG	TDPVKSNQIQTGFGNTPMV-TISAG	KSHACGLNTT-GN	LICIGNNDSGQL	NVIA
Gm11g27060.2	QLADVAVGDSQVCAREVQSGVV	RCWRGSGGAQFSSPSESLRFR	-SITCGCGFSCGIVKI	ESGRVVCWGDDNEG	ANRKGSISDEIHREFKNFTMS-SLVAG	VSHVCGLTLH-GA	LVCKGNNDSGQL	GYNNNNNGGVF
Gm18g07000.2 Pv06G068400.1	OLADVSVGDSOVCAREVOSGVV	RCWRGSGGVQFSSPSEGLRFRSF RCWRGNGRMELVSPSESLRFR	-SVTCGRGFSCGUR	ESGRVVCWGDGDEG ESGRVVCWGGGDD-	EGAYTIGOTORKFENISMT-SLVAG	VSHACGLTLH-GA	LICEGNNASGQL	GNSV
Rc29681.m1357								
Rc28833.m0161								
Gm11g35348.1								
Pv01G243600.1								
KTR2Jalo_p								
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Sm18g03053.1								
Pv01G243500.1 TR1Jalo p								
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AT5G47850	ELEELEAGNFRICGVERVSRRL	RCWQPYYLPRPDNYF	RSIALGDNFFCGLSQ1	PPGMISCEG	IAKVP-SGDHYIAIAAG	SRQACAITVDNDV	ECWGQTQS-LPR	EK
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AT3G59420 0803G43670 0805G03620 7	290 300 	AI 310 320	330 340 	VII 350 .11 AETSLKP	360 370 380 	390 III. GTHELSNQ GYYEYANHGEVGS GVCVSDNSSCR GVCVSDNSSCR	400 4 GSKTCKPANSRL CCPLPDSGRP	10 420 clpcsrscpg clpcsrcpg clpcsvgcpD ckvsgbvicRR
AT3G59420 DS03G43670 DS05G03620 Zm2G120839 Pv01G243800.1	290 300 ILDLPPKEPLLAVVGGKFYACGIR DVNIVPMDAVSVGGRFHACGIR LFGYGLAVGDSHACGLRE LFGYGLAVGDSHACALRRE GGGAFEYSG-LALGAERGCATRGI	A 310 320 	330 340 II GFYDLAAGNYFTCCVL' INFELLVAGGNLTCGLV: ISFAFLVAGGNFTCCVA SFEVIVSGNFVCCLT'	350 .111 AETSLKP SANFS SSDFS SNFS	360 370 380 	390 III GYTELSNQ	400 4 ENSPCKFTGSHI GSKTCKPANSRL CGFLPDSGRF CGFMSQSQKF -ECGSYLDSQSL	II 10 420 1I CLPCSYSCPPG CLPCSYGCPD CKVSGDVICRR CGSSGG-ICDA CGSSGG-ICDA
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SYESS	SPCNATADR				VCÇ	FDCSKCASDEC	VSFCLSQKRTK	NRKFMAI	QLRIFVAEIAF	AVILVESVT	IACLYVRYKL	RHCQCSKNE	LRLAKNTT	YSFRKD
FCDTS	SPPPPPPSPR	TPSPPA	1	PSSRRGVS	KGWIAFAVVGA	VGCFAGLCSIV	YCLLFGFCS-H	KKVHNS	-VQPNIASNNN	GGGGGGGAAA	VGSGAP-SPY	GSPNGSLGR	LR	RQLSRV
1 TCKLO	SPPPPPAPAP OTTAPPPPSLSI	PPPPSMSPPPPP	PPPPS	-PSSSRRVS SSSRSKTLT	NGLLAFAIIGS	VGGFAGLCSIV	YCLVFGFCS-N	KKVHNS	VQPNISAAAA	GTGADNNGG(GSNGGGASNI	SGGAAASGSPI	MR	GDFR	RQLSKA TSMI
TCKLQ	OTTAPPPPSLSI	PPPPSMSPPPPP	PPPPS	SSSRSKTLT	NGLLAFAIIGS	VGAFAGICTIV	YCLWSGVCFGK	KKVHSS	-VQPTITRGSS	GSNGGGASNI	ISNSS-ISSMI	MR	Q	TSMI
TCRPQ	OTTAPPPLLPTI	PPPPSQSPPPPP DDDDDDDDDDDDDDDD	STPPPS	SSTRSKTLT	RGLLAFAIIGS	VGAFAGICTIV	HCLWSGVCFGK	KKVHNS	-VQPTITRGSS	GSSGGGASNI	ISNSS-ISSMI	MR	Q'	TSII
ICNTO	OITSPPP	PPPAP	SPPF	RSSRSKILI	TGLLVFAIVGS	VGGFIGICTII	YCLWTGVCFGK	KKVHSS	-VOPTVTRGSS	NSSNS	SASS-IKSVI	MR	0	GSRI
PCWPE	EMLVPAP	PAVVPASP-	PGP-7	AASRSKALT	KGLLAFAIVGC	VGGVAGICTAI	YCLWTGVCFGK	KKKVHNS	VQPTITRGGS	VNGVGGSNN:	SISPPSRSSTI	RR	Q	GSRI
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PCWPQ	QMDVPVP	SQIATPPQ-	PGL-F	CSRSKTLT	KGLLLFAIVGI	IGAVAGLCTVV	YCLWSGVCFGK	KKVHNS	-VQPTITRGGS	LN-CGAFSN-	YSPTSRSSTI	RR	Q	GSRI
7 GLNIS	SMLFPPSPI	PQPPFLPFPPSP	SVLPSE	PSSPSKELT	TGLLVFCIIGS	VGGFAGICTII	YCLWTGVCFGK	KKVHNS	VQPTITRGGS	NGGTTSNI	SGILSRSSTI	MR	Q	SSRA
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1 HTEVP	PLAVPLFPPE	ssqvs	SS	SHEGRKL	KEFVVFMVVGS	VGAFAGLCTIV	YFLWFGAKRVL	VRREVSNS	SVKPTSSESDA	YVDIIPMPNV	GSNGTTFRTF	SS	K	SHGSRR
1 LLSMF	FMSFTILTISIN	MYLVYKAOKG			VTWMKKGW	IPWFYYOHO	NSRPFGTFPD-	JHKKKQK	IIGLLC	AFFOCIFASI	SYALLSROVN	NPIKVSVWP	IIFAFGLL	YSRLSE
0 LLSML	LLSFTILIISI	FDLVYKGQKG			GVTWMKKGW	IPWLYYPYQ	NSKPFGTFPD-		IVGLLC	AIFQSIFASI	SYALLCROVN	NPIKVSVFP	IIFASGLL	YSRLLG
1 NLCE-	SDUUSEN_SU										VENENSAWDK	PT		
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1 DLGA-	-VPVRGFA-SIV	VENMMRSV			GGDLRA	LPVHGFASA	VENAMISIGG-			DLGVSPM	GFASRVENAM	SS-IGG-DL	GTSHSPVH	GFQ
DLGA-	-VPVRGFA-SIV	VENMMRSV			GGDLRA	LPVHGFASA	VENAMISIGG-			DLGVSPM	GFASRVENAM	SS-IGG-DL	GTSHSPVH	GFQ
SLGA-	-LPVYDFA-SAV	VNNAMSST			SGSLGA	LPVYGFASA	VNNAMISTSGS	SLGALPEHGE	SAVNDAMSSTS	GISLGALPVI	GFSSAVDNAI	RSRSRA-DL	GRSSSPVH	GFAMED
1 NLGAS	SSPLHSFA-SLI	LDIAIRSRTSSN	WETSSANS	SYAFGLDNA	IRSRTSSNLET	SSAYSFAFG	VDTAIRSRTSS	SNWETSS	HSFAFEEDRTE	SN-LGSFRVI	SFSSGVDYVI	RSSSGGTDSI	ETSPVH	SFAFAA
NLGAS	SSPLHSFA-SLI -SRLHSFA-SV	LDIAIRSRTSSN VDWAIRS	WETSSANS	SYAFGLDNA	SRTVSNLET	'SSAYSFAFG 'SPVPSFASA	VDTAIRSRTSS EDNNVMRAVPA	ANWETSS	HSFAFEEDRTE	SN-LGSFRVI	PSFSSGVDYVI	RSSSGGTDS	ETSPVH:	SFAFAA
IFGE-	-SRVRSFD-SLV	VDSAIRSS			SATEEDLGS	SPVHVFAMA	EDRAMRSSSGA		DLGTFPFHVFA	TAADMRTIA	RLTKAVSNAK	RHFAEGLFT	RAELIPVT	QAELEP
ILGE-	-SRIHSFC-SV	VDNAIRSR			TASDLGT	SPSPVHSLASA	VANAMSSSSAA	4	PFSQ	LETSPSPVQ	LASAVPSAMS	RSKAA	PFS	QLEVVP
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NDGE SPSFE YFPSS FFLSS	570 570 EPDLPEADR SSCTANSDR 570	580	590 	600	PSQMPENPS VCTPCSLCC ICTPCSLCC 610	KNKTWSRNIA KSGTWSNKNVA NSSCYGICKIR NSSCSDICKLH 620 	FLVVGCVGTS FLVVGCVGTS ATTSKEHEQKE INSNFPDKH	640	FFLYKYCF IGCSVLGFLVN IGSCASALLII III 650	IIGCCVVPR:		680	V	ANHAVL EADPDP DTDQ 700 II K
NDGE SPSFE YFPSS FFLSS NGKIR NMKIQ	570 570 570 570 570 570 570 570 570 570	580 	590 	600 600 551VG-KGS DSQVG-KGS	PSQMPENPS VCTPCSLCQ ICTPCSLCQ 610 	KNKTWSRNIA KSGTWSNKNVA NSSCYGICKIR NSSCSDICKLH 620 CGTVAVKRAI- GTVVAVKRAI	ILVVGCVGTPS PLVVGCVGCTS ATKSKEHEQKE INSNPPDKH II 630	640 MSSDRQKNSI KASDVKKSSI	FFLYKYCF IGCSVLGFLVN IGSCASALLII	IIGCCVVPR:	670	680 .ll. LVYEFMAHG:	FDKNSVI IGKPDLI V 690 SLHNHLHGI SLYQHLHGI	ANHAVL EADPDP DTDQ 700 II K K
RINDSE SPSFE YFPSS FFLSS NGKIR NMKIQ MTRQR	570 570 570 570 570 570 570 570 570 570	580 	590 	[600 11 SSIVG-KGS SQVG-KGS SALIG-EGS	PSQMPENPS VCTPCSLCQ ICTPCSLCQ ICTPCSLCQ 610 	KINKTWSRNIA KSGTWSNKNVA INSSCYGICKIR NSSCSDICKIH 620 11 GTUVAVRAI GTUVAVRAI GTUVAVRAI	ELVVGCVGCTS ELVVGCVGCTS ATKSKEHEQKE NSNFPDKH 630 	640 MSSDKVKSI RASDVKKSI RARKPCKE	FFLYKYCF IGCSVLGFLWA IGSCASALLII III 650	GTACKSSRVI LIGLSFIPRI IIGCCVVPR: 660 LNHAHLLSLI LHHAHLLNLI LHHKHLVGFT	670	680 680 LVYEFMAHG LVYEFMAHG	FDKNSVI IGKPDLI V 690 SLHNHLHGI SLYQHLHGI ALYDHLHPI	ANHAVL EADPDP DTDQ 700 II K K-PNGSS
	570 570 570 570 570 570 570 570	580 ARPUTYEELEG AQEFSYEELEG PAEEFTAQLAA PAEEFTAQLAA RAEEFTAQLAA	590 	600 II SSIVG-KGS EAKIG-EGS EAKIG-EGS EAKIG-EGS	610 - PSQMFQSLCC UCTPCSLCC ICTPCSLCC 610 	KINKTWSRRITA KSGTWSNKNVA INSSCYGICKIR INSSCSDICKIH MSS	ELVVGCVGCTS ELVVGCVGCTS EATKSKEHEQKE NSNFPDKH 630 	640 MSSDQRVRSUU RARKFQEKE SARKFQEKE	FFLYKYCF IGCSVLGFLVN IGSCASALLII 650 	GTACKSSRVI LIGLSFIPRI IIGCCVVPR: 660 LNHAHLLNLI LHIKHLVGF LHIKHLVGF	670 GYCEDECSERL GYCEDECSERL GYCEDESERL GYCEDESERL GYCEDESERL	680 	FDKNSVI IGKPDLI 690 I SLHNHLHGI SLYQHLHGI ALYDHLHDI ALYDHLHDI	ANHAVL EADPDP DTDQ 700 II K KENGSS KNN
 RNDCC SPSFE YFFSS FFLSS NMKLQ MTRQR MTRQR MTRQR MRRQR	570 570 570 570 570 570 570 570 570 570	580 ARRVETYEELEK AQEFSYEELEK PREEFFRQLAR RAEEFTLAELVA RAEEFTLAELVA	590 AADGFKEE ATKDFAAF ATKOFALE ATNNFLLE	600 11 251VG-KGS 520VG-KGS 26XKIG-EGS 26XKIG-EGS 26XKIG-AGS 20XKIG-AGS	610 .I	KINKIWSRNIA KSGTWSNKNVA NISSCYGICKIR NISSCYGICKIR NISSCSDICKLH GCTVAVKRAI- GCTVAVKRAI- GCTVAVKRAI- GCTVAVKRAI- GCTVAVKRAI- GCRVAIKRGE- GCRVAIKRGE-	ELWCCUGCTS FLWWCCUGCTS ATKSKEHEQKE II 630 	640 MSSDRQKNSI RARKFQEKE SKMKKFQEKE SKMKKFQEKE	FFLYKYCF IGCSVLGFLW IGSCASALLII	GTACKSSRVI LIGLSFIPKU LIGCCVVPR: 0660 I. LNNAHLLSLI LHNKHLVGFV LHNKHLVGFV LHNKHLVGFV LHNKHLVGFV	670 GYCESCEGERL GYCESCEGERL GYCESCEGERL GYCESCESERL GYCESCERL GYCESCERLERL GYCESCERLERL	680 .II. LVYEFMAHG: LVYEFMAHG: LVYEYMKNG. LVYEYMKNG.	FPKNSVI IGKPDLI V 690 SLHNHLHGI SLYQHLHPI ALYDHLHPI ALYDHLHPI ALYDHLHPI	ANHAVL EADPDP DTDQ 700 II K KPNGSS KN KNN KNN
 NPGE- SPSFE YFFSS FFLSS FFLSS MTROR MTROR MTROR MRROR MRROR	570 570 1 PDLDELORRR PDLDELORRR 2PDUELCORRR 2PDUELKIRR 8SGFSS-FKD 8SGTSSTKHPD 8SGTSSTKHPD 8SGTSSTKHPD	580 ARRVYTYELEX AREFTRACLAR REEFTLAELVA REEFTLAELVA REEFTLAELVA REEFTLAELVA	590 AADGFKE ATKOFAAE ATKOFAAE ATKNFLLE ATNNFLLE ATNNFLLE	600 11 SSIVG-KGS SSQVG-KGS SAKIG-EGS SAKIG-EGS SAKIG-AGS SNKIG-AGS SNKIG-AGS SNKIG-SGS	PSQMPENPS VCTPCSLCC ICTPCSLCC ICTPCSLCC 610 	620 620 1 GEVALKER GEVALKGE- GREVALKGE- GREVALKGE- GREVALKGE- GREVALKGE- GREVALKGE- GREVALKGE- GREVALKGE- GREVALKGE-	ELWCCUGCTS FLWWCCUGCTS ATKSKEHEQKE II 630 	640 640 MASDROKKIS KASDVKKSI RARKFQEKE SKMKKFQEKE SKMKKFQEKE SKMKKFQEKE	FFLYKYCF IGCSVLGFLVW IGSCASALLII	660 11	670 G70 G70 G70 G70 G70 G70 G70 G	680 .ll. LVYEFMAHG LVYEFMAHG LVYEYMAHG LVYEYMAHG LVYEYMANG LVYEYMANG LVYEYMANG LVYEYMANG LVYEYMANG LVYEYMANG	FPKNSVI IGKPDLI 690 I SLNNHLHGI ALYDHLHDI ALYDHLHDI ALYDHLHDI ALYDHLHDI ALYDHLHDI V VDH1-BI V VDH1-BI	ANHAVL EADPDP DTDQ 700 II K KPNGSS K
IFGE- RNDCC SPSFE YFPSS FFLSS FFLSS NGKIR NMKTQ MTRQR MTRQR MTRQR MTRQR MRRQR MRRQR MRRQR	570 570 570 570 570 570 570 570	580 RRFVFYEELSO PAEETFAQLAA AGEFSYLEELSO RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFSLESLAM	590 AADGFKEF ATGGFSEL ATKGFALF ATKNFLE ATNNFLLE ATNNFSLE ATNNFSLE ATNNFSLE	600 11 251VG-KGS 25VG-KGS 25XIG-EGS 25XIG-EGS 25XIG-AGS 25XIG-AGS 25XIG-AGS 25XIG-AGS 25XIG-AGS	PSQMPENPS VGTPCSLCC ICTPCSLCC -ICTPCSLCC FGUVKCVLRC FSCVFKGLLRP FGVVKGKLAF FGVVKGKLAF FGVVKGKLAF FGVVKGKLAF FGVVKGKLAF	620 620 620 620 620 620 620 620 620 620	FLWCCUGCTS FLWCCUGCTS ATKSKEHEQKE INSNPPDKH 630 	640 640 MARNOR KASDVKKSSI KASDVKKSSI KMKKPOEKE KMKKPOEKE KMKKPOEKE	650 650 650 650 651 652 652 653 654 654 654 654 654 654 654 654	660 	670 GYCEBECGERL GYCEBECGERL GYCEBECGERL GYCEBECGERL GYCEBESDERL GFCEEKDERL GFCEEKDERL GFCEEKDERL GFCEEKDERL	680 680 LVYEYMKIG LVYEFMARG LVYEFMARG LVYEFMARG LVYEFMKIG LVYEYMKIG LVYEYMKIG LVYEYMKIG	FPKNSVI IGKPDLI C 690 I SLHNHLHGI SLYQHLHGI ALYDHLHDI ALYDHLHDI ALYDHLHDI ALYDHLHDI SLSHSHLHDI	ANHAVL EADPDP DTDQ 700 II K KPNGSS KN KNN KNN KNN KNN
IFGE- RNDCC SPSFE YFPSS FFLSS FFLSS INGKIE NMKRQ MTRQP MTRQP MTRQP MTRQP MTRQP MTRQP MTRQP MTRQP MTRQP MRRQR MRRQR	570 570 STONENADR	580 RARVFTYEELEK AQEFSYEELEG PAEEFTFAQLAA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA	590 AADGFKEE ATGGFSEL ATKGFAE ATNRFLLE ATNNFLLE ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE	600 11 SIVG-KGS SQVG-KGS SQVG-KGS SAKIG-EGS SAKIG-EGS SNKIG-AGS SNKIG-AGS SNKIG-AGS SNKIG-AGS	PSQMPENPS VCTPCSLCC ICTPCSLCC ICTPCSLCC 610 	KINKWSRNIX KSGTWSNKNVA NSSCYGICKIR SSCYGICKIR NSSCSDICKLH G20 (SCGC) G20 (SCGC) G20 (SCGC) G20 (SCC) (SCC) (ELWCCUGCTS FLWVCCUGCTS INTKSKEHEQKE INSNPPDKH 630 11. 	640 640 640 640 640 640 640 640 640 640	FFLYKYCF IGCSVLGFLVN IGCSVLGFLVN IGSCASALLII	660 	670 670 670 670 670 670 670 670	680 	FDKNSVI IGKPDLI C 690 SLINHLHG ALYDHLHD ALYDHLHD ALYDHLHD ALYDHLHD ALYDHLHD ALYDHLHD ALYDHLHD	ANHAVL EADPDP DTDQ 700 II K K KNN
NPCC SPSFE YFPSS FFLSS FFLSS MTRQR MTRQR MTRQR MRRQR MRRQR MRRQR MRRQR MRRQR MRRQR	570 570 570 570 570 570 570 570	580 580 AQEFSYELEK AQEFSYELEK REEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELA RAEEFTLAELA RAEEFTLAELVA	590 	600 11 SIVG-KGS SQWG-KGS SQWG-KGS SQKIG-EGS SMKIG-AGS	PSQMPENPS VCTPCSLCC ICTPCSLCC ICTPCSLCC 610 	KINKWSRNIX KSGTWSNKNVA NSSCYGICKIR SSCSDICKLH 620 (1) GTVAVKRI GGTVAIKRGE- GGRVAIKRGE- GGRVAIKRGE- GGRVAIKRGE- GGRVAIKRGE- GGRVAIKRGE- GGRVAIKRGE- GGRVAIKRGE- GGRVAIKRGE- GGRVAIKRGE-	ELWCCUGCTS FLWVCCUGCTS INTKSKEHEQKE II 630 	640 640 640 MASDKKSS RARFORKS RAFFORKS RARFORKS RAFFORK RAFFORKS RA	FLYKYCK IGCSVLGFLVY IGCSVLGFLV IGSCASALLII 650 	660 660 1	670 670 1	680 680 LVYEFMAHG LVYEFMAHG LVYEFMAHG LVYEYMKIG LVYEYKKIG LVYEYKKIG LVYEYKKIG LVYEYKKIG LVYEYKKIG LVYEYKKIG LVYEYKKIG LVYEYKKIG	FDKNSV FDKNSV IGKPDL IGKPDL 690 SLHNHLMP ALYDHLHD ALYDHLHD ALYDHLHD SLHSHLHD ALYDHLHD ALYDHLHD ALYDHLHD IAYDHLHD	ANHAVL EADPDP DTDQ 700 II K K KNN
NDCB SPSFE SPSFE SPFLSS FFLSS FFLSS NGKIR NMKIQ MTRQR MTRQR MTRQR MRRQR MRRQR MRRQR MRRQR MRRQR MRRQR MRRQR MRRQR	570 570 570 570 570 570 570 570	580 AQEFSYEELSQ PAEDETFAQLAR RAEPETLAELVA RAEPETLAELVA RAEPETLAELVA RAEPETLAELVA RAEPETLAELVA RAEPETLAELVA RAEPETLAELVA RAEPETLAELVA	590 I AADGFKEE ATKDFAAE ATKGFAE ATKNFLL ATNNFLL ATNNFLL ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE	600 	PSQMPESPS VCTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC 	KINKWARRITA KISGTWSINKIVA INSSCYGICKIR INSSCSDICKLH COMMUNICATION COMUNICATION COMMUNI	FLWCCVGCTS ATKSKEHEQKE ATKSKEHEQKE II 630 <tr tr=""> </tr>	640 640 640 640 640 640 640 640 640 640	FLXKYCK IGCSVLGFLVV IGCSVLGFLVV 650 	660 	670 670 G70 G70 G70 G70 G70 G70 G70 G	680 	FDKNSVI IGKPDLI	ANHAVL EADPDP DTDQ II KN KEN KNN
NDCC SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE NMK20 MTR07 M	570 570 570 570 570 570 570 570	580 ARRUTYELLE AGETSYEELE PAEETTAQLAA AGETSYEELE PAEETTAQLAA RAEETTLAELVA RAEETTLAELVA RAEETTLAELVA RAEETTLAELVA RAEETTLAELVA RAEETTLAELVA RAEETTLAELVA RAEETTLAELVA	590 	600 53103-KGS 5203-KGS 5204-KGS	PSQMEEDES VGTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC FSCVYKGVLRC FSCVYKGVLRC FSCVYKGVLRC FSCVYKGKLA FGVVYKGKLA YGVVYKGKLA YGVVYKGKLA YGVVYKGKLA	KINKIWSRNITA KSGTWSINKIVA INSSCYGICKIR INSSCSDICKLH G20 II.NI GTVTAVKRAI GREVAIKRGE GREVAIKRGE GREVAIKRGE GREVAIKRGE GREVAIKRGE GREVAIKRGE GREVAIKRGE GREVAIKRGE GREVAIKRGE GREVAIKRGE	FLWQCCVGCTS FLWQCCVGCTS ATKSKEHEQKE INSNPPDKH 630 	640 640 640 640 640 640 640 640	650 650 10520452147 10520452147 10520452147 1052045 105204 1052	660 11	GROUP CONTRACTOR GROUP CONTRACTOR GROUP GROUP CONTACTOR GROUP CONTAC	680 680 	690 	ANHAVL EADPDP DTDQ 700 I K K K NN K
 RNDGE SPSFE YFPSS FFLSS FFLSS MRRCH MRCH M	570 570 570 570 570 570 570 570	580 S80 RARVFTYEELEK AQEFSYBELEC PAEEFTFAQLAA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA RAEEFTLAELVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REEFTLAEVA REFTLAEVA REEFTLAEVA REEFTLAEVA REFTLA	590 AADGFKEF ATGGFSEI ATKDFAAB ATKDFAB ATKNFLLE ATNNFLLE ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE ATNNFSLE	600 1	PSQMPENPS VCTPCSLCC ICTPCSLCC ICTPCSLCC 610 	KINKWSRNIX KSGTWSNKNVA NSSCYGICKIR SSCYGICKIR SCGU COMMENSION GEO CALL GEO CREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE-	FLVWCCVGCTS FLVWCCVGCTS INTSKEHEQKE II 630	640 640 640 640 640 640 640 640 640 640	FFLYKYCF IGCSVLGFLVV IGCSVLGFLVV IGSCASALLII () () () () () () () () () () () () ()	GOACKSERVI LIGLSFIPRI LIGCCVVPR V 660 LNHARLLSL LNHARLLSL LNHARLLSL LNHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL LHHKILVGL	GOOLDER G	680 	690 	ANHAVL EADPDP DTDQ 700 IK K KK KK K K K K K K K K K K NN K K NN K
IFGE- RNDCC SPSFE YFPSS FFLSS FFLSS INGKIE NMRCQ MTRQC MTRQC MRQC M	570 1PTLPPSNP STCNPNADR	580 ACESYTELEQ PAESTFAQLAA RAESTFLAELVA RAESTFLAELVA RAESTLAELVA RAESTLAELVA RAESTLAELVA RAESTLAELVA RAESTLAELVA KAESTSLEALAA RAESTLAELVA RAESTSLEALAA RAESTSLEALAA RAESTSLEALAA RAESTSLEALAA	590 	600 	PSQMPEDES VCTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC 	KINKWSRNIX KSGTWSNKNVA NSSCYGICKIR SSCYGICKIR SSCSDICKLH GTVAVKRI GTVVAVKRI GTVVAVKRI GTVVAVKRI GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE- GREVAIKRGE-	FLWQCCVGCTS FLWQCCVGCTS IATKSKEHEQKE II 630	640 640 640 MSDDKQKNSI KMKKPQEKE KMKKPQEKE KMKKPQEKE KMKKPQEKE KMKKPQEKE KMKKPQEKE KMKKPQEKE KMKKPQEKE KMKKPQEKE	FLXKYCK IGCSVLGFLVK IGCSVLGFLVK IGCSASALLII 550 EFRTELDLISF EFHTELDLISF EFHTELDLISF EFHTELDLISF SELAFLSF AFRSELAFLSF	G60 	670 670 670 670 670 670 670 670	680 	690 690 1GKPDL 690 1GKPDL 690 1.1 SLHNHLHG SLYQHLHG SLYQHLHG ALYDHLHD ALYDHLHD ALYDHLHD ALYDHLHD SLYSHLHD SLYDHLHD SLYDHLHD SLYDHLHD	700 EADPDD DTDQ DTDQ MTDQ TOQ TOQ NTQ KPNGSS KNN KNN KNN KNN KNN KNN KNN KNN KNN KNN KNN KNN KNN KNN
RNDCE SPSFE SPSFE SPSFE SPFLSS FFLSS NGKIR NMRCR MTROR MTROR MTROR MROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MRROR MR MROR MRROR MRROR MRROR MRROR MR MROR MR MROR MR MROR MROR MR MROR	570 II. SCTANSDR SCTANSDR SCTANSDR SCTANSDR POPUEDLOREN RSGTSSTKIPDI RSGSSS-KIVDI RSGSSSS RSGSSS-KIVDI RSGSSS-KIVDI RSGSSSS-KIVDI RSGSSS-KIVDI RSGSSS RSGSSSS RSGSSSS RSGSSS RSGSS	580 	590 	600 551VG-KGS 551VG-KGS 50VG-KGS 50VG-KGS 50VG-KG 50VKIG-AGS 50NKIG-AGS	PSQMESS VCTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC FGVVKCVLRC FGVVKCLLR	620 620 1	FLWQCCVGCTS FLWQCCVGCTS ATKSKEHEQKE II 630 <tr tbold=""> </tr>	640 640 640 640 640 640 640 640 640 640	FFLXKYCK IGCSASALIII 650 650 650 650 650 650 650 650 650 650	660 	670 670 670 670 670 670 670 670	680 	EDKN-SVI IGKP-DLI IGKP-DLI 690 SLENHLHGI SLYQHLHGI ALYDHLHDI ALYDHLHDI ALYDHLHDI ALYDHLHDI SLYDHLDI ALYDHLDI ALYDHLDI SLYDHLHDI SLYDHLHDI SLYDHLHDI	ANHAVL EADPDP DTDQ IIII K
IFGE- RNDGE SPSFE SSSFE S	570 II.S SCTANSDR SSCTANSDR SSCTANSDR SSCTANSDR SSCTANSDR RPDLDELOKRR RPDDELOKRR RSGFSST-FKDI SSGFSSTKHPDI SSGTSSTKHPDI SSGTSSTKHPEI SSGTSTKHPEI	580 	590 	600 500 1 SSIVG-KGS SQVG-KGS SQVG-KGS SQKIG-EGS SNKIG-AG	PSQMEEDES VGTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSCCCC FSCVYKGKLAF FSGVYKGKLAF FGVYKGKLAF YGVYKGKLAF YGVYKGKLAF YGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF FGVYKGKLAF	620 620 1	FLWCCUGCTS FLWCCUGCTS ATKSKEHEQKE (1) 630 	640 640 640 640 640 640 640 640		660 1	GORDEDEREKLE GORDEDEREKLE GORDEDEREKLE GORDEREKLE GORDEREKLE	680 	G90 G90 C G90 C SLENHLEG SLENHLEG SLENHLEG ALYDH	ANHAVL EADPDP DTDQ DTDQ K VI K K K K K K K K K K K K K K K K K NN K
 RNDCC SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE SPSFE MRROR MROR M	570 570 STONPNADR	580 RARVITYELEX AQEFSYBELEX AQEFSYBELEX ADEFTRAQLAS RAESTLAELVA RAESTLAELVA RAESTLAELVA RAESTLAELVA RAESTLAELVA RAESTLAELVA RAESTLAELVA RESTLAELVA RESSLSELAT RTSSSLSELAT RTSSSLSELAT RTSSSLSELAT RTSSSLSELAT RTSSSLSELVA RAVETTLAELAS RAVETTLAELAS	590 AADGFKEE ATGGFKEE ATGGFKEE ATGGFAE ATKOFAA ATKOFAA ATKNFSLE ATNN	600 5100-KGS 5200-KGS 5200-KGS 5200-KGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-AGS 520KIG-VGR 540KIG-VG	PSQMPENPS VCTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC 	KINKIWSRNITA KISGTWSNKIVA NSSCYGICKIR 620 6 GCD 620 6 GGTVAVKRAI GGTVAVKRAI GGTVAVKRAI GGTVAVKRAI GGRVAIKRGE GRRVAIKRGE GGRVAIKRGE GGRVAIKGE GGRVAIKGE GGRVAIKRGE GGRVAI	FLVWCCVGCTS FLVWCCVGCTS INTSKEHEQKE II 630	640 640 640 640 640 640 640 640	FLXKYCK IGCSVLGFLVY IGCSASALLII 550 EFRTELDLSS EFRTELDLSS EFRTELDLSS EFRTELDLSS EFRTELDLSS AFRSELAFLSF A	660 11	670 670 670 670 670 670 670 670	680 680 		ANHAVL ANHAVL EADPDP DTDQ TDQ TDQ TDQ TDQ TDQ TDQ TDQ TOQ
NGKIR NDGK SPSFE SPSFE SPFLSS FFLSS FFLSS NGKIR NMRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRRCR MRC	570 1PTLPPSNP STCNPNADR	580 ARRVFTYEELEK AREFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFTLAELVA RAEFSLEELA RTESTSLEELAN RTESTSLEELAN RTESTSLEELAN RTESTSLEELAN	590 	600 	PSQMPENPS VCTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC ICTPCSLCC 	620 620 1	PLVVGCVGCTS PLVVGCVGCTS ATTKSKEHEQKE II 630 II. SGP SGP SGP SGP 	640 640 640 640 640 640 640 640	FLXKYCK IGCSVLGFLVYCK IGCSVLGFLVYCK IGCSASALLII 650 III 650 IEFRTELDLISF EFHTELDLISF EFHTELDLISF EFHTELDLISF SELAFLSF AFRSELAFLSF AFRSELAFLSF AFRSELAFLSF AFRSELAFLSF AFRSELAFLSF AFRSELAFLSF AFRSELAFLSF AFRSELAFLSF AFRSELAFLSF AFRSELAFLSF AFRSELAFLSF	660 	670 670 670 670 670 670 670 670	680 680 	690 	700 11 2 700 11 700 11 700 700 700 700 700 700 700 700 700 70
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KS03G43670 SSQRRKSSASEADMDGRTTTDGRNVGSSIGDGLRSLEEEISPASPQENLYLQHNF	
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v01G243800.1 SISVVS	E
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m11g35390.2 TISVVS	E
m18g03040.2 TISVVS	E
it3g070800.1 TIS-VS	D
m02g42440.2 TISIVS	D
m14g06440.1 TISIVS	D
v08G223900.1TVSIVS	D
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c28162.m0127TISVVS	E
12G55950ICSIVS	D
m11g27060.2SFSAPL	E
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m11g35348.1	
v01G243600.1	
TR2Jalo p	
v01G243700.1	
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m18g03053.1	
v01g243500.1	E
TIJALO pTIFDVS	E
m11q35376.1	E
m11q35334.1 LMYIPVYA	
m18g03066.1 NS	
m11q35362.1	
T5G47850	
It4q035180.1	
.T2G39180	
xT3G09780	

Figure S3: Multiple alignment of nucleic sequences of KTR2 (G19833, JaloEEP558 and BAT93) and KTR2/3 (JaloEEP558) showing that the first 232bp of KTR2/3 are highly identical to the sequence of KTR2. The unknown domain of \sim 100 amino-acid present in the truncated CRR3 kinases is boxed in yellow. The three related repeats of 78 or 69pb are shown by arrows.

KTR2G19 KTR2JALO	A TG GCT AAT AA CGC AGT TG ATG CAA GG AGT TTC AG TTG GGC AG TGG ACA GT GCC ATA GC G A TG GCT AAT AA CGC AGT TG ATG CAA GG AGT TTC AG TTG GGC AG TGG ACA GT GCC ATA GC G
KTR2BAT	A TG GCT AAT AA CGC AGT TG ATG CAA GG AGT TTC AG TTG GGC AG TGG ACA GT GCC ATA GC G
KIKZ/JUALU	**************************************
KTR2G19	A GT GAG AGT GC GT CAA AT TTG GGA GA ATC TCG TG TCC ACA GT TTT GCT TC GGT AGT GGAC
KTR2JALO KTR2BAT	AGT GAGAGT GC GTC AAAGT GAGAGT GC GTC AA
KTR2/3JALO	A GT GAGAGT GC GTCAA ATTTG GGA GAATC TCG TG TCC ACA GT TTT GCT TC GGT AGT GGAC
KTR2G19	
KTR2JALO	
KTR2/3JALO	GGT GCC ATAAGGAG TAGCA CTG CTT CT GAAGCGG ATT TGG GA GAA TCT CG TGT CCA CAGT
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KTR2G19	T TT GCT TCG GT AGT GGA CG GTG CCA TA AGG AGT AG CAC TGC TT CTG AAG CG G A TTT GG AA T TT GCT TCG GT AGT GGA CG GTG CCA TA AGG AGT AG CAC TGC TT CTG AAG CG G A TTT GG AA
KTR2BAT	T TT GCT TCG GT AGT GGA CG GTG CCA TA AGG AGT AG CAC TGC TT CTG AAG CGG A TTT GG AA
KTR2/3JALO	TTTGCTTCGGTAGTGAACGGTGCCATAAGGAGTAGCACTGCTTCTGAAGCGG ATTTTGGGA
KTR2G19	repeat n°3 (69 bp) 232 pD GCATTCCCAACCCATTATTTGCTTTTGCTTCTGCGTGGGACAAAAGACTGTTGCTGCA
KTR2JALO	G CA TTC CCA AC CCA TTA TT TTG CTT TT GCT TCT GC GTG GGA CA AAA GAA CT GTT GCT GC A G CA TTC CCA AC CCA TTA TT TTG CTT TT GCT TCT GC GTG GGA CA AAA GAA CT GTT GCT GC A
KTR2/3JALO	GTA TCA CCC AT GCA GGG TT TTG CTT CG AGA GTG GA GTA TGC TA TGA GTA GC ATT GGT GGA
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KTR2G19 KTR2JALO	C
KTR2BAT	
KIR2/SUALO	* ****** * *** ****
KTR2G19	A AA GCA GCC AC CAA CAA TT TCT CAA TT CAC AAC AA GAT TTT TT GTG CTG GA AGC ATT AG T
KTR2JALO KTR2BAT	A AA GCA GCC AC CAA CAA TT TCT CAA TT CAC AAC AA GAT TTT TT GTG CTG GA AGC ATT AG T A AA GCA GCC AC CAA CAA TT TCT CAA TT CAC AAC AA GAT TTT TT GTG CTG GA AGC ATT AG T
KTR2/3JALO	<u>GCA GCA GCC AC CAA CAA TT TCT CAG TT GAC AAC AA GAT TC GCG CTG GA AGC TCT AG T</u>
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KTR2G19 KTR2JALO	G TT GTG CAC AG AGG CAA GC TCT TTG AT GGT CGT CA GGT GGC TG TCA AAA GG GCT GAA G TT GTG CAC AG AGG CAA GC TCT TTG AT GGT CGT CA GGT GGC TG TCA AAA GG GCT GAA
KTR2BAT	G TT GTG CAC AG AGG CAA GC TCT TTG AT GGT CGT CA GGT GGC AG TCA AAA GG GCT GAA
	***** ** ** ** ** *** *** *** *** ** **
KTR2G19	– – – ATC AGT TC CAA GAT GA AGG AG– – – TTT CAA GA GAG ATT TG GCT ATT TA TGG ACC CT T
KTR2JALO	– – – ATC AGT TC CAA GAT GA AGG AG– – – TTT CAA GA GAG ATT TG GCT ATT TA TGG ACC CT T – – – ACC AGT TC CAA GAT GA AGG AG– – – TTT CAA GA GGG ATT TG GCT ATT TA TCG ACC CT T
KTR2/3JALO	T GG AGC AGT AG AAC GGT GG AAG AGG CC TTC TGG TG GAG GAG AA CGT CTA GT TTG AAG ATT
KTR2G19 KTR2JALO	T TG CTC CGT CT ACA CCA TA AGC ACT TG GTT GGC CT AGT AGG GT TCT GTA AA GAT AAA GA T T TG CTC CGT CT ACA CCA TA AGC ACT TG GTT GGC CT AGT AGG GT TCT GTA AA GAT AAA GA T
KTR2BAT	T TG CTC CGT TT ACA CCA TA AGC ACT TG GTT GGC CT AGT AGG GT TCT GTA AA GAT AAA GA T
KIK2/SUALO	**** * ** **** * *** *****************
KTR2G19	A AA AGG TTG TT GGT GTA CG AGT ACA CG AAG AAT CG GGC GTT AT ATG ATT AT CTG CAT GA C
KTR2JALO	A AA AGG TTG TT GGT GTA CG AGT ACA CG AAG AAT CG GGC GTT AT ATG ATT AT CTG CAT GA C A AA AGG TTG TT GGT GTA TG AGT ACA CG AAG AAT CG GGC GTT AT ATG ATC AT CTG CAT GA C
KTR2/3JALO	GAA AGG GTG TT GGT GTA TG AGG GCA TG AAG AAT GG GTC ATT GT ATG ATC AT TTA CAT GA G
	**** ********** *** ** ** ****** ** * ****
KTR2G19 KTR2JALO	A AA AAC AAC GT GGA CAG GG AGA GCA GT GCG TTG AA TTC TTG GA GAA TGA GG ATC AAG GT T A AA AAC AAC GT GGA CAG GG AGA GCA GT GCG TTG AA TTC TTG GA GAA TGA GG ATC AAG GT T
KTR2BAT	A AA AAC AAC GT GGA CAG GG AGA GCA GT GCG TTG AA TTC TTG GA GAA TGA GG ATC AAG GT T
KIR2/SUALO	** ***********************************
KTR2G19	G CT TTG GAT GC TTC CCG GG GAA TAG AA TAT CTT CA TAA ACA TG TAG TTC CA TCC ATT AT T
KTR2JALO	G CT TTG GAT GC TTC CCG GG GAA TAG AA TAT CTT CA TAA ACA TG TAG TTC CA TCC ATT AT T G CT TTG GAT GC TTC CCG GG GAA TAG AA TAT CTT CA TAA ACA TG TAG TTC CA TCC ATT AT T
KTR2/3JALO	<u>GCTTTGGATGCTTCCCGAGGAATATATATTTCTGCATAAACATGTAGTTCCATCCA</u>

KTR2G19	C AC AGA GAC AT CAA CTC CT CCA ACA TT CTT CTT GA TGC AAC TT GGA CAG CA AGA GTA TC T C AC AGA GAC AT CAA CTC CT CCA ACA TT CTT CTT GA TGC AAC TT GGA CAG CA AGA GTA TC T
KTR2BAT	CACAGA GAC AT CAA CTC CT CCAACA TT CTT CTT GA TGC AAC TT GGA CAG CAAGA GTA TC T
KTR2/3JALU	** **** ****** * *********************
KTR2G19	G GT TTT GAA TC GTC GTG TT TCA TGA GT CCA GAA GC TGA GCA TG TTT ACT CC GAT ACA CG T
KTR2JALO	G GT TTT GAA TC GTC GTG TT TCA TGA GT CCA GAA GC TGA GCA TG TTT ACT CC GAT ACA CG T G GT TTT GAA TC GTC GTC GTG TT TCA TCA TCA GTA GTA GCA GCA TCA TTT ACT CC GAT ACA CG T
KTR2/3JALO	AACATT GGGAA GGCAG GAACGT TT GGA TACAT TGA TCC TG AGT ACATT GAT CTGAAT
	······································
KTR2G19 KTR2JALO	G TG TTG ACA GC AAA GAG TG ATG TGT AC GGG CTT GG AGT TGT GC TGC TTG AA CTT TTA AC A G TG TTG ACA GC AAA GAG TG ATG TGT AC GGG CTT GG AGT TGT GC TGC TTG AA CTT TTA AC A
KTR2BAT	G TG TTG ACA GC AAA GAG TG ATG TGT AC GGG CTT GG AGT TGT GC TGC TTG AA CTT TTA ACA
KIKZ/JUALU	5 15 1 15 ACAACAAGAG 16 A 16 16 16 17 A 166 A 17 T 66 AGT TGT AC T6C TT6 AA CTTTTAACA ********* *************************
KTR2G19	G GA AAG AAG AC CAC GTT AA AGT TTG GG ATA AAT AG AGA GAC AA GTA TGG TG AAG ATC GC A
KTR2JALO	G GA AAG AAG AC CAC GTT AA AGT TTG GG ATA AAT AG AGA GAC AA GTA TGG TG AAG ATC GC A G GA AAG AAG AC CAC GTT AA AGT TTG GG ATA AAT AG AGA GAC AA GTA TGG TG AAG ATC CC A
KTR2/3JALO	GA AAA AACT GC AGG CAC CA TAT TAC AT GTA CCC TCT GC A
	*** * *** * *** ***
KTR2G19 KTR2JALO	G GG CGT GTT AT TTT GGG TT GGA AAA TG GTG AAA AT TTT GGA TC CAA GGG TT GGA GCA CC C G GG CGT GTT AT TTT GGG TT GGA AAA TG GTG AAA AT TTT GGA TC CAA GGG TT GGA GCA CC C
KTR2BAT	G G C GT GTT AT TTT G G G TT G G A A A TG G TG A A A TT TTT G G A TC CAA G G TT G G A CC C C
KIKZ/JJALO	GAGGTTAGTATTTTGGGTGGAGATTTTGGTGAAAAATTTGGATAAAAGGGTTGGAGAACCC *.* *. ********* ** * ****** ****** ******
KTR2G19	C AT GTT AAT GA AGA AGC AG AGG CAC TG GAA ATA GT GGC CCA TA CAG CGG TT AGT TGT GT A
KTR2JALO	C AT GTT AAT GA AGA AGC AG AGG CAC TG GAA ATA GT GGC CCA TA CAG CGG TT AGT TGT GT A
KTR2/3JALO	CATGTTAATGAAGAAGCAGAGGCACTGGAAATAGTGGCCCATACAGCGGTTAGTTGTATA CGTCTCAATGAAGCCAAGGCACTGAAGTTAGTGGCCCGTACTGCCATCAATTGTGTA
	* * * *** ***** ****** * ******* * *****
KTR2G19	A AT TCG AAA AG GAA AGA TA GGC CAA CT ATG ACT CA GGT AGT GG CCAATT TG GAG ACT GC T
KTR2JALO KTR2BAT	A AT TUG AAA AG GAA AGA TA GGU CAA UT ATG ACT CA GGT AGT GG CCA ATT TG GAG ACT GC T A AT TUG AAA AG GAA AGA TA GGU CAA CT ATG ACT CA GGT AGT GG CCA ATT TG GAG ACT GC T
KTR2/3JALO	<u>A AT GTG GAA GG AAA GGT TA GAC CAA CC AGT GCT CA GGT TGT GT TCA ATT TG GAG AGG GC T</u> * * * * * * * * * * * * * * * * * * *
Kmp 2c1 0	
KTR2JALO	T TAGET ETT TG EGA TAG TAGEE CAT EE TAG T TAGET ETT TG EGA TAG TA GGE CAT EE TAG
KTR2BAT KTR2/3JALO	T TA GCT CTT TG CGA TAG TA GGC CAT CC TAG T TT GCT TAT TT CCG GC GGC GGT AC TAG
	** *** * * * * * * * ***

Figure S4: Multiple alignment of nucleic sequences of KTR3 (G19833, JaloEEP558 and BAT93) and KTR2/3 (JaloEEP558) showing that the last 953bp of KTR2/3 are highly identical to the sequence of KTR3. The unknown domain of ~ 100 amino-acid present in the truncated CRR3 kinases is boxed in yellow. The three related repeats of 78 or 69pb are shown by arrows.

KTR 3G1 9 KTR 3JA LO KTR 3BA T KTR 2/3 JALO	A TG GCG AAT TC AGG AGC AT CCC TTG TC CAT AGT TT TGC TTC GA TAG TGG AA TAT GCT AT T A TG GCG AAT TC AGG AGC AT CCC TTG TC CAT AGT TT TGC TTC GA TAG TGG AA TAT GCT AT T A TG GCG AAT TC AGG AGC AT CCC TTG TC CAT AGT TT TGC TTC GA TAG TGG AA TAT GCT AT T <u>A TG GCT AAT</u>
KTR 3G1 9 KTR 3JALO KTR 3BAT KTR 2/3 JALO	A GA AGT ATT GG AGG AGA TT TGG GGG CA TTT CCT TT GCG TGA TT TTT CTT TC GCA GTG GA G A GA AGT ATT GG AGG AGA TT TGG GGG CA TTT CCT TT GCG TGA TT TTT CTT TC GCA GTG GA G A GA AGT ATT GG AGG AGA TT TGG GGG CA TTT CCT TT GCG TGA TT TTT CTT TC GCA GTG GA G
KTR 3G1 9 KTR 3JALO KTR 3BA T KTR 2/3 JALO	Internal repeat n°1 (69 bp) AAT GCGTG GAG TAG TA TTG GAG GAG AAT GCGTG GAG TAG TA TTG GAG GAG AAT GCGTG GAG TAG TA TTG GAG GAG AAT GCGTG GAG TAG TA TTG GAG GAG ATTT GG GAG CAG TA CCT GGT CG TGG TTT TG CT AGT GCC ATA GC GAG TGA GA GTG CGT CAA ATTT GG GAG AAT CT CCT GGT CG TGG TTT TG CT * *** * *** * ** * * * * * * * * * * *
KTR 3G1 9 KTR 3JA LO KTR 3BA T KTR 2/3 JAL O	T CT ATA GTG GA GAA TAT GA TGA GAA GT GT TGG AG GAG AT TT GAG AGC AT TA T CT ATA GTG GA GAA TAT GA TGA GAA GT GT TGG AG GAG AT TT GAG AGC AT TA T CT ATA GTG GA GAA TAT GA TGA GAA GT GT TGG AG GAG AT TT GAG AGC AT TA T CT ATA GTG GA GAA TAT GA TGA GAA GT GT TGG AG GAG AT TT GAG AGC AT TA T CG GTA GTG GA CGG TGC CA TAA GGA GT AGC ACT GC TTC TGA AG CGG AT TT GGG AGA AT TT GGG AGA AT TT GAG AGC AT TA
KTR 3G1 9 KTR 3JA LO KTR 3BA T KTR 2/3 JAL O	C CC GTG CAT GG TTT TGC TT CGG CAG TG GAG AAT GC AAT GAT AA GTATT GGA C CC GTG CAT GG TTT TGC TT CGG CAG TG GAG AAT GC AAT GAT AA GTATT GGA C CC GTG CAT GC TTT TGC TT CGG CAG TG GAG AAT GC AAT GAT AA GTATT GGA CGT GTC CAC AG TTT TGC TT CGG TAG TGAAC GGT GC CAT AAG GA GTA GCA CT GCT TCT GAA * ** ** ** ************ **** ** ** ** *
KTR 3G1 9 KTR 3JA LO KTR 3BA T KTR 2/3 JALO	GGAG A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT GGAG A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT GGAG A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT GGAG A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT GCGC A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT CCC A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT CCC A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT CCC A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT CCC A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT CCC A TTT GG GAG TAT CA CCC ATG CA GGG TTT TG CTT CGA GA GTG GAG AA TGC TAT GA GT
KTR 3G1 9 KTR 3JA LO KTR 3BA T KTR 2/3 JALO	AGC ATT GGT GG AGA TTT GG GAA CAT CC CAT TCC CC TGT GCA TG GTT TTC AA GTA TTC AC C A GC ATT GGT GG AGA TTT GG GAA CAT CC CAT TCC CC TGT GCA TG GTT TTC AA GTA TTC AC C A GC ATT GGT GG AGA TTT GG GAA TAT CC CAT TCC CC TGT GC TTG GTT TTC AA GTA TTC AC C A GC ATT GGT GG AGA TTT GG GAA TAT CC CAT TCC CC TGT GC TTG GTT TTC AA GTA TTC AC C A CC ATT GGT GG AGA TTT GG GAA CAT CC CAT TCC CC TGT GC ATG GTT TTC AA GTA TTC AC C ******
XTR 3G1 9 XTR 3JA LO XTR 3BA T XTR 2/3 JALO	T TA CTT GAG CT TGC AGC AG CCA CCA AC AAT TTC TC AGT TGA CA ACA AGA TT CGC GCT GG A T TA CTT GAG CT TGC AGC AG CCA CCA AC AAT TTC TC AGT TGA CA ACA AGA TT CGC GCT GG A T TA CTT GAG CT TGC AGC AG CCA CCA AC AAT TTC TC AGT TGA CA ACA AGA TT CGC GCT GG A <u>T TA CTT GAG CT TGC AGC AG CCA CCA AC AAT TTC TC AGT TGA CA ACA AGA TT CGC GCT GG A</u> * * * * * * * * * * * * * * * * * * *
KTR 3G1 9 KTR 3JA LO KTR 3BA T KTR 2/3 JALO	A GC TCT AGT GT TGT GTA CA GGG GAA AA CTC GTT GA TGG TAG TG AGG TTA CA ATA GAA AG A A GC TCT AGT GT TGT GTA CA GGG GAA AA CTC GTT GA TGG TAG TG AGG TTA CA ATA GAA AG A A GC TCT AGT GT TGT GTA CA GGG GAA AA CTC GTT GA TGG TAG TG AGG TTA CA ATA GAA AG A <u>A GC TCT AGT GT TGT GTA CA GGG GAA AA CTC GTT GA TGG TAG TG AGG TTA CA ATA GAA AG A</u> *** *** *** *** *** *** *** *** *** **
TR 3G1 9 TR 3JA LO TR 3BA T TR 2/3 JALO	G TA GAA AGG TG GAG CAG TA GAA CGG TG GAA GAG GC CTT CTG GT GGA GGA GA ACG TCT AG T G TA GAA AGG TG GAG CAG TA GAA CGG TG GAA GAG GC CTT CTG GT GGA GGA GA ACG TCT AG T G TA GAA AGG TG GAG CAG TA GAA CGG TG GAA GAG GC CTT CTG GT GGA GGA GA ACG TCT AG T <u>G TA GAA AGG TG GAG CAG TA GAA CGG TG GAA GAG GC CTT CTG GT GGA GGA GA ACG TCT AG T</u> * * * * * * * * * * * * * * * * * * *
TR 3G1 9 TR 3JALO TR 3BAT TR 2/3 JALO	T TG AAG <mark>A</mark> IT TT GCC CGG TT TAC GTC CC AAG AAC TT GGT TGG GC TGG TTG GG TTG TGT GA G T TG AAG <mark>A</mark> IT TT GCC CGG TT TAC GTC CC AAG AAC TT GGT TGG GC TGG TTG GG TTG TGT GA G T TG AAG <mark>T</mark> IT TT GCC CGG TT TAC GTC CC AAG AAC TT GGT TGG GC TGG TTG GG TTG TGT GA G <u>T TG AAG ATT TT GCC CGG TT TAC GTC CC AAG AAC TT GGT TGG GC TGG TTG GG TTG GG TG GA G</u> ******
TR 3G1 9 TR 3JALO TR 3BAT TR 2/3 JALO	G AG AAA AAT GA AAG GGT GT TGG TGT AT GAG GGC AT GAA GAA TG GGT CAT TG TAT GAT CA T G AG AAA AAT GA AAG GGT GT TGG TGT AT GAG GGC AT GAA GAA TG GGT CAT TG TAT GAT CA T G AG AAA AAT GA AAG GGT GT TGG TGT AT GAG GGC AT GAA GAA TG GGT CAT TG TAT GAT CA T G AG AAA AAT GA AAG GGT GT TGG TGT AT GAG GGC AT GAA GAA TG GGT CAT TG TAT GAT CA T *******
TR 3G1 9 TR 3JALO TR 3BAT TR 2/3 JALO	T TA CAT GAG AA GGG TAG CA GTG TGT TG AAT TCG TG G <mark>A</mark> A AAT GA GGA TAA <mark>A</mark> A ATT GCT TT G T TA CAT GAG AA GGG TAG CA GTG TGT TG AAT TCG TG GAA AAT GA GGA TAA AA ATT GCT TT G T TA CAT GAG AA GGG TAG CA GTG TGT TG AAT TCG TG GAA AAT GA GGA TAA GA ATT GCT TT G T <u>TA CAT GAG AA GGG TAG CA GTG TGT TG AAT TCG TG G</u> A AAT GA GGA TAA AA ATT GCT TT G * * * * * * * * * * * * * * * * * * *
TR 3G1 9 TR 3JALO TR 3BAT TR 2/3 JALO	GAT GCT TCCCG AGG AAT AGAAT ATC TG CAT AAG TT TGG AGT TC CAT CTC CT GTT CAT GG A GAT GCT TCCCG AGG AAT AGAAT ATC TG CAT AAG TT TGG AGT TC CAT CTC CT GTT CAT GG A GAT GCT TCCCG AGG AAT AGCAT ATC TG CAT AAG TA TGG AGT TC CAT CTC CT GTT CAT GG A GAT GCT TCCCG AGG AAT ATTTTTTTTTTTTTTTTT
TR 3G1 9 TR 3JALO TR 3BAT TR 2/3 JALO	G AT ATC AAC CC TTC CAA CA TTC TTC TT GAT GCT AC TTG GAC AG CAA AGG TA TCT AAC AT T G AT ATC AAC CC TTC CAA CA TTC TTC TT GAT GCT AC TTG GAC AG CAA AGG TA TCT AAC AT T G AT ATC AAC CC TTC CAA CA TTC TTC TT GAT GCT AC TTG GAC AG CAA AGG TA TCT AAC AT T <mark>G AT ATC AAC CC TTC CAA CA TTC TTC TT GAT GCT AC TTG GAC AG CAA AGG TA TCT AAC AT T</mark> *** *** *** *** *** *** *** *** *** **
TR 3G1 9 TR 3JALO TR 3BAT TR 2/3 JALO	G GG AAG GCA GC AGG AAC GT TTG GAT AC ATT GAT CC TGA GTA CA TTG ATC TG AAT GTG TT G G GG AAG GCA GC AGG AAC GT TTG GAT AC ATT GAT CC TGA GTA CA TTG ATC TG AAT GTG TT G G GG AAG GCA GC AGG AAC GT TTG GAT AC ATT GAT CC TGA GTA CA TTG ATC TG AAT GTG TT G G GG AAG GCA GC AGG AAC GT TT <u>G GAT AC ATT GAT CC TGA GTA CA TTG ATC TG AAT GTG TT G</u> * * * * * * * * * * * * * * * * * * *
TR 3G1 9 TR 3JA LO TR 3BAT TR 2/3 JALO	A CA ACA AAG AG TGA TGT GT ATG GAT TT GGA GTT GT ACT GCT TG AAC TTT TA ACA GGA AA A A CA ACA AAG AG TGA TGT GT ATG GAT TT GGA GTT GT ACT GCT TG AAC TTT TA ACA GGA AA A A CA ACA AAG AG TGA TGT GT ATG GAT TT GGA GTT GT ACT GCT TG AAC TTT TA ACA GGA AA A <mark>A CA ACA AAG AG TGA TGT GT ATG GAT TT GGA GTT GT ACT GCT TG AAC TTT TA ACA GGA AA A</mark> *** *** *** *** *** *** *** *** *** **
TR 3G1 9 TR 3JALO TR 3BAT TR 2/3 JALO	A AT GGA GGC AC CAT ATT AC ATG TAC CC TCT GCA GA GGT TAG TA TTT TGG GT GGA GAT TT T A AT GGA GGC AC CAT ATT AC ATG TAC CC TCT GCA GA GGT TAG TA TTT TGG GT GGA GAT TT T A AT GGA GGC AC CAT ATT AC ATG TAC CC TCT GCA GA GGT TAG TA TTT TGG GT GGA GAT TT T <u>A AT GGA GGC AC CAT ATT AC ATG TAC CC TCT GCA GA GGT TAG TA TTT TGG GT GGA GAT TT T</u> *******
TR 3G1 9 TR 3JALO TR 3BAT TR 2/3 JALO	G TG AAA AAT TT GGA TAA AA GGG TTG GA GAA CCC CG TCT CAA TG AAG CCA AG GCA CTG AA G G TG AAA AAT TT GGA TAA AA GGG TTG GA GAA CCC CG TCT CAA TG AAG CCA AG GCA CTG AA G G TG AAA AAT TT GGA TAA AA GGG TTG GA GAA CCC CG TCT CAA TG AAG CCA AG GCA CTG AA G G TG AAA AAT TT GGA TAA AA GGG TTG GA GAA CCC CG TCT CAA TG AAG CCA AG GCA CTG AA G *******
TR 3G1 9 TR 3JALO TR 3BAT TR 2/3 JALO	T TA GTG GCC C <mark>G</mark> TAC TGC CA TCA ATT GT GTA AAT GT GGA AGG AA AGG TTA GA CCA ACC AG T T TA GTG GCC CA TAC TGC CA TCA ATT GT GTA AAT GT GGA AGG AA AGG TTA GA CCA ACC AG T T TA GTG GCC CA TAC TGC CA TCA ATT GT GTA AAT GT GGA AGG AA AGG TTA GA CCA ACC AG T <u>T TA GTG GCC CG TAC TGC CA TCA ATT GT GTA AAT GT GGA AGG AA AGG TTA GA CCA ACC AG T</u>
XTR 3G1 9 XTR 3JA LO XTR 3BA T XTR 2/3 JALO	G CT CAG GTT GT GTT CAA TT TGG AGA GG GCT TTT GC TTA TTT CC GG <mark>C GGC GG</mark> TAC TAG G CT CAG GTT GT GCT CAA TT TGG AGA GG GCT TTT GC TTA TTT CC GG <mark>C GG</mark> TAC TAG G CT CAG GTT GT GCT CAA TT TGG AGA GG GCT TTT GC TTA TTT CC GGTAC TAG G CT CAG GTT GT GTT CAA TT TGG AGA GG GCT TTT GC TTA TTT CC GGC GGC GGTAC TAG

Fig. S5: Time-course expression analysis of the *P. vulgaris* genes KTR2, KTR3 and KFL of JaloEEP558 in response to *C. lindemuthianum* strain 100. The relative abundance of *KTR2/3* transcripts was calculated by comparing KTR2/3 cDNA level in inoculated leaves with mock controls at each respective timepoint at 6, 24, 48, 72 and 96 hpi. Data was normalized using the *PvUnk1*, *PvUnk2*, *PvIDE* and *PvAct11* reference genes. Bars represent the mean \pm SD, n=2 independent experiments.









KTR2

Figure S6: Transient expression of KTR2/3 in common bean hypocotyls and *C. lindemuthianum* disease assay scoring at 7 dpi.

A and B. Pictures of JaloEEP558 hypocotyls after agroinfiltration with pCambia0390 (A) or pCambia0390+KTR2/3 (B), and inoculation with *C. lindemuthianum* strain 100. As expected, no symptoms were observed at 7 dpi, since JaloEEP558 is resistant to strain 100.

C and **D**. Pictures of BAT93 hypocotyls after agroinfiltration with pCambia0390 (C) or pCambia0390+KTR2/3 (D), and inoculation with *C*. *lindemuthianum* strain 100. At 7 dpi, typical anthracnose symptoms were massively observed in (C) and only rarely in (D), where droplets of inoculum were deposited.

E. Example of symptoms scoring. When clear browning symptoms were observed, the inoculation spot was scored as susceptible (S), while when no or very limited browning was observed the inoculation spot was scored as resistant (R).



Gene or amplification product name	Primer Name	Primer sequences (5' - 3')	Amplicon size (bp)	Reference
RT-qPCR primers				
Tested genes				
Phvul.001G243600	RepetJalo1F	GTCCCACGCAGAAGCAAAAGC	153	This study
(K1K2)	KTR2q-R	GCCATAGCGAGTGAGAGTGCG		This study
Phvul.001G243700	KTR3q-F	ATGCACAGGGGAATGGGATG	234	This study
(KIK3)	RepetJalo1R	TTGGGAGCAGTACCTGTTCGTG		This study
(KTR2/3)	KTR3q-F	ATGCACAGGGGAATGGGATG	279	This study
	KTR2q-R	GCCATAGCGAGTGAGAGTGCG		This study
Phvul.001G243800	KinaseFL-3F	CGGGATCCGATGCTGCTCGGGGGAATAG	373	This study
(Krl)	KinaseFL-3R	CGGGATCCCATTTCTCCAGCCAAAATACG		This study
Reference genes				
Insulin degrading	IDE-F	GCAACCAACCTTTCATCAGC	156	(Borges et al. 2012)
enzyme (FVIDE)	IDE-R	AGAAATGCCTCAACCCTTTG		(Borges et al. 2012)
Unknown 1	Ukn1-F	ATTCCCATCATGCAGCAAAG	192	(Borges et al. 2012)
(PVUKN1)	Ukn1-R	AGATCCCTCCAGGTCAATCC		(Borges et al. 2012)
Unknown 2 (PyLl(m2)	Ukn2-F	CCAATTCAACCATCCCTCAC	153	(Borges et al. 2012)
(I VOKIZ)	Ukn2-R	AAACTCCTCTGCACCCTCAG		(Borges et al. 2012)
Actin-11 (PrvA et 11)	Act11-F	TGCATACGTTGGTGATGAGG	190	(Borges et al. 2012)
(FVACULI)	Act11-R	AGCCTTGGGGTTAAGAGGAG		(Borges et al. 2012)
KTR2/3 amplification	n			
	RepetJalo1F	GTCCCACGCAGAAGCAAAAGC	3179 in	This study
	RepetJalo1 R	TTGGGAGCAGTACCTGTTCGTG	1639 in BAT93 **	This study
	KTR2/3exp-	CGGGATCCGTCAAATTGGAGATTTTTACAT	1563	This study
	KTR2/3exp-	CGGGATCCCCAATTTGACTAGTACCGCCG		This study
Long Range PCR an	nplification			
LR1	LR1-F	AAGCGAAAAACACGCTCACT	9464	This study
	LR1-R	GTCCTATCTCACTCGCCCTTTAT		
LR2	LR2.2-F	GCAATTAGGGGAATGACACTGCT	7523	This study
	LR2.2-R	ACAAATACCCAAAGCCCTCTCCA		
LR3	LR3-F	TATCTGCGACCAAACAGTGC	10927	This study
	LR3-R	CCGAGGACAATTCACAAGGTA		

Table S1: List of primer sequences used in this study (RT-qPCR, Cloning).

LR4	LR4-F	GACAGTGCCATAGCGAGTGA	9812	This study
	LR4-R	CTCCTTGCCCAGAACTTGAG		
LR5	LR5-F	GAGGAAGGAACCAAAGTCTAACAG	11943	This study
	LR5-R	GCCCTTCTTATTTTTGTCCCAAAC		
LR6	LR6-F	CTCTCCCAACCCAACTCCTGAA	8415	This study
	LR6-R	ACGGTGTCCTTGGTTCATGTCC		
LR7	LR7-F	GGTGGGTGCCTCCAATCAGT	7844	This study
	LR7-R	TTCTCCTCCAATCTCCTTCAACTC		

*: referred to as the 3.1kb band, **: referred to as the 1.7kb band

Supplemental Table S2: Common bean genotypes of various geographical origins tested for resistance to strain 100 of *C. lindemuthianum* and for the presence of *KTR2/3* encoding gene.

^aResistant = R; Susceptible = S; Ambiguous = -.

^b size of the fragment amplified by PCR using RepetJalo1F/R

^c in bold, underlined, genotypes for which KTR2/3 gene was sequenced

^d MA=MesoAmerican

The genotypes presenting a 3.1 Kb band possess KTR2/3, while the genotypes presenting a 1.7 Kb band lack KTR2/3. The blue highlighting shows that all the genotypes presenting the 3.1 Kb band (KTR2/3) are resistant to strain 100 of *C. lindemuthianum* and are cultivated Andean genotypes, with the notable exception of the four Mesoamerican cultivars.

	Gene pool/	BC / ADP ID	Market class / Type	Genotype	Disease	PCR ^{b,c}
	Country of				reaction to	
	origin				strain 100 ^a	
Cultivated	Andean	ADP-1	Red mottle	ROZI KOKO	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-10	Red	CANADA	R	~1.7 Kb
Cultivated	Andean	ADP-102	Purple speckled	Jesca	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-33	Purple speckled	KIJIVU	R	~3.1 Kb
Cultivated	Andean	ADP-427	Light Red Kidney	Badillo	S	~1.7 Kb
Cultivated	Andean	ADP-526	Red mottle	CAL-143	-	~3.1 Kb
Cultivated	Andean	ADP-598	Dark Red Kidney	Charlevoix	R	~3.1 Kb
Cultivated	Andean	ADP-599	Dark Red Kidney	Isles	R	~3.1 Kb
Cultivated	Andean	ADP-602	Light Red Kidney	Sacramento	R	~3.1 Kb
Cultivated	Andean	ADP-608	Cranberry	UI-51	S	~1.7 Kb
Cultivated	Andean	ADP-610	Cranberry	G122	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-611	Red mottle	Pompadour B	R	~1.7 Kb
Cultivated	Andean	ADP-612	Red mottle	ICA Quimbaya	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-617	Cranberry	Red Rider	-	~3.1 Kb
Cultivated	Andean	ADP-621	Yellow	Jalo EEP558	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-623	Light Red Kidney	Drake	R	~3.1 Kb
Cultivated	Andean	ADP-624	Cranberry	Dolly	R	~3.1 Kb
Cultivated	Andean	ADP-626	Dark Red Kidney	Montcalm	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-634	Light Red Kidney	UC Red Kidney	R	~3.1 Kb
Cultivated	Andean	ADP-638	Dark Red Kidney	Red Hawk	R	DNA not available
Cultivated	Andean	ADP-639	Light Red Kidney	Chinook 2000	R	~3.1 Kb
Cultivated	Andean	ADP-640	White Kidney	Beluga	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-641	Cranberry	Capri	S	~1.7 Kb
Cultivated	Andean	ADP-642	Cranberry	Taylor Hort.	S	~1.7 Kb
Cultivated	Andean	ADP-643	Cranberry	Cardinal	S	~1.7 Kb
Cultivated	Andean	ADP-645	White Kidney	Lassen	R	~3.1 Kb
Cultivated	Andean	ADP-646	Yellow	Myasi	S	~1.7 Kb
Cultivated	Andean	ADP-647	Light Red Kidney	Red Kanner	S	~1.7 Kb
Cultivated	Andean	ADP-648	Light Red Kidney	Red Kloud	S	~1.7 Kb
Cultivated	Andean	ADP-650	Light Red Kidney	K-42	R	~3.1 Kb
Cultivated	Andean	ADP-653	Dark Red Kidney	USDK-CBB-15	R	~3.1 Kb
Cultivated	Andean	ADP-655	Dark Red Kidney	Fiero	R	~3.1 Kb
Cultivated	Andean	ADP-656	Dark Red Kidney	Royal Red	R	~3.1 Kb
Cultivated	Andean	ADP-657	Light Red Kidney	Kardinal	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-658	Light Red Kidney	Blush	R	~3.1 Kb
Cultivated	Andean	ADP-660	Cranberry	Krimson	R	~1.7 Kb
Cultivated	Andean	ADP-664	White Kidney	Silver Cloud	R	~3.1 Kb
Cultivated	Andean	ADP-665	White Kidney	USWK-CBB-17	S	~1.7 Kb
Cultivated	Andean	ADP-668	Cranberry	Cran-09	S	~1.7 Kb
Cultivated	Andean	ADP-672	Dark Red Kidney	CDRK	R	~3.1 Kb
Cultivated	Andean	ADP-676	Light Red Kidney	CELRK	R	~3.1 Kb
Cultivated	Andean	ADP-677	Cranberry	Etna	S	~1.7 Kb
Cultivated	Andean	ADP-683	Pink cranberry	Ind. Jamaica Red	S	~1.7 Kb
Cultivated	Andean	ADP-684	Dark Red Kidney	Majesty	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-687	Light Red Kidney	Pink Panther	R	<u>~3.1 Kb</u>
Cultivated	Andean	ADP-7	Yellow	BUKOBA	S	~1.7 Kb
Cultivated	MA ^d	BC007	Great Northern	BelNeb-RR-1	S	~1.7 Kb
Cultivated	MA	BC016	Pinto	Bill Z	S	~1.7 Kb
Cultivated	MA	BC017	Pinto	Ouray	S	~1.7 Kb
Cultivated	MA	BC018	Pinto	Grand Mesa	S	~1.7 Kb
Cultivated	MA	BC020	Pinto	Montrose	S	~1.7 Kb
Cultivated	MA	BC025	Pinto	Arapaho	S	~1.7 Kb

Cultivated	MA	BC026	Small red	DOR 364	S	~1.7 Kb
Cultivated	MA	BC063	Black	Black Magic	S	~1.7 Kb
Cultivated	MA	BC069	Black	Blackhawk	S	~1.7 Kb
Cultivated	MA	BC070	Pinto	Sierra	S	~1.7 Kb
Cultivated	MA	BC073	Pinto	Aztec	S	~1.7 Kb
Cultivated	MA	BC074	Navy	Huron	-	~1.7 Kb
Cultivated	MA	BC075	Black	Raven	R	<u>~3.1 Kb</u>
Cultivated	MA	BC077	Navy	Newport	R	~3.1 Kb
Cultivated	MA	BC079	Pinto	Kodiak	S	~1.7 Kb
Cultivated	MA	BC080	Great Northern	Matterhorn	S	~1.7 Kb
Cultivated	MA	BC084	Black	Phantom	R	~3.1 Kb
Cultivated	MA	BC085	Black	laguar	R	~3.1 Kb
Cultivated	MA	BC086	Navy	Seahawk	S	~1.7 Kb
Cultivated	MA	BC088	Black	Zorro		~1.7 Kb
Cultivated		BC080	Binto	Santa Eo	c	~1.7 Kb
Cultivated	MA	BC005	Pinto	Topaz	5	~1.7 Kb
Cultivated		DC110	Pinto		5	1.7 Kb
Cultivated	IVIA	BC120	Pinto	Ld PdZ	5	1.7 KD
Cultivated	IVIA	BCIZI	Pinto	Baja	5	-1.7 Kb
Cultivated	MA	BC137	Great Northern	Beryl R	S	1.7 Kb
Cultivated	MA	BC139	Great Northern	Sapphire	S	~1.7 Kb
Cultivated	MA	BC141	Small red	Garnet	S	~1.7 Kb
Cultivated	MA	BC142	Pink	ROG 312	S	~1.7 Kb
Cultivated	MA	BC160	Pink	UI-537	S	~1.7 Kb
Cultivated	MA	BC161	Pinto	Common Pinto	S	~1.7 Kb
Cultivated	MA	BC168	Pinto	UI-196	S	~1.7 Kb
Cultivated	MA	BC172	Black	UI-906	S	~1.7 Kb
Cultivated	MA	BC177	Pinto	UI-111	S	~1.7 Kb
Cultivated	MA	BC178	Pinto	UI-114	S	~1.7 Kb
Cultivated	MA	BC180	Great Northern	BelNeb-RR-2	S	~1.7 Kb
Cultivated	MA	BC185	Great Northern	GN#1Sel27	S	~1.7 Kb
Cultivated	MA	BC186	Great Northern	GN Harris	S	~1.7 Kb
Cultivated	MA	BC190	Great Northern	Starlight	S	~1.7 Kb
Cultivated	MA	BC191	Great Northern	Emerson	R	~1.7 Kb
Cultivated	MA	BC193	Great Northern	ABC-Weihing	S	~1.7 Kb
Cultivated	MA	BC195	Great Northern	ABCP-8	S	~1 7 Kb
Cultivated	MA	BC196	Great Northern	Chase	s	~1.7 Kb
Cultivated	MA	BC209	Pinto	AC Pintoba	s	~1.7 Kb
Cultivated	MA	BC215	Black	Δ-55	5	~1.7 Kb
Cultivated		BC215	Great Northorn	N-33	5	~1.7 Kb
Cultivated		BC220	Rinto		5	~1.7 Kb
Cultivated		BC222	Pinto	Quilicy	Э	~1.7 Kb
Cultivated		BC225	Pinto	BUIKE	ĸ	1.7 KD
Cultivated	IVIA NAA	BC225	Pinto	JIVI-120 Dindok	5	1.7 KD
Cultivated	IVIA	BCZZ7	Pinto	Pindak	5	-1.7 Kb
Cultivated	MA	BC228	Pinto	NOCAK	S	1.7 Kb
Cultivated	MA	BC229	Pinto	Holberg	S	~1.7 Kb
Cultivated	MA	BC231	Pinto	Othello	S	~1.7 Kb
Cultivated	MA	BC232	Pinto	NW590	S	~1.7 Kb
Cultivated	MA	BC235	Pinto	USPT-WM-1	S	~1.7 Kb
Cultivated	MA	BC236	Pinto	USPT-CBB-1	S	~1.7 Kb
Cultivated	MA	BC238	Pinto	USPT-ANT-1	S	~1.7 Kb
Cultivated	MA	BC243	Small red	USRM-20	S	~1.7 Kb
Cultivated	MA	BC266	Pink	6R-42	S	~1.7 Kb
Cultivated	MA	BC268	Pink	USWA-61	S	~1.7 Kb
Cultivated	MA	BC271	Small red	Rojo Chiquito	S	~1.7 Kb
Cultivated	MA	BC273	Black mottle	Orca	S	~1.7 Kb
Cultivated	MA	BC278	Pink	Viva	S	~1.7 Kb
Cultivated	MA	BC279	Pink	Roza	S	~1.7 Kb
Cultivated	MA	BC280	Pink	Harold	S	~1.7 Kb
Cultivated	MA	BC297	Great Northern	GN9-4	S	~1.7 Kb
Cultivated	MA	BC306	Navy	Avalanche	S	~1.7 Kb
Cultivated	MA	BC307	Black	Eclipse	R	~1.7 Kb
Cultivated	MA	BC358	Great Northern	Orion	S	~1.7 Kb
Cultivated	MA	BC375	Pink	Yolano	S	~1.7 Kb
Cultivated	MA	BC383	Pinto	Apache	R	~1.7 Kb
Cultivated	MA	BC384	Pinto	Fiesta	S	~1.7 Kb
Cultivated	MA	BC386	Pinto	Buster	S	~1.7 Kb
Cultivated	МА	BC387	Pinto	Medicine Hat	S	~1.7 Kb
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Cultivated	MA	BC393	Navy	Avanti	S	~1.7 Kb
Cultivated	MA	BC-030	Small white	Morales	not tested	~1.7 Kb
Cultivated	MA	BC-258	Small white	NW_395	not tested	~1.7 Kb
Cultivated	MA	BC-260	Small white	USWA 50	not tested	~1.7 Kb
Cultivated	Andean		Cranberry	G19833	R	~1.7 Kb
Cultivated	Andean			MDRK	R	~3.1 Kb
Cultivated	Andean			AFN	S	~1.7 Kb
Cultivated	Andean			Aiguille verte	S	~1.7 Kb
Cultivated	Andean			La victoire	S	~1.7 Kb
Cultivated	Andean/MA			Widusa	S	~1.7 Kb
Cultivated	MA			Mex222	R	~1.7 Kb
Cultivated	MA			AB136	S	~1.7 Kb
Cultivated	MA			BAT93	S	~1.7 Kb
Cultivated	MA			Cornell 49242	S	~1.7 Kb
Cultivated	MA			DOR364	S	~1.7 Kb
Cultivated	MA			Michelite	S	~1.7 Kb
Cultivated	MA			Mz	S	~1.7 Kb
Cultivated	MA			PI 207261	S	~1.7 Kb
Cultivated	MA			То	S	~1.7 Kb
Cultivated	MA			Tu	S	~1.7 Kb
Cultivated				Rosinha	R	~1.7 Kb
Cultivated	Andean			AND277	R	~3.1 Kb
Cultivated	Andean			Kaboon	R	~3.1 Kb
Cultivated	Andean			Perry Marrow	R	~3.1 Kb
Cultivated	Andean			Black Valentine	S	~1.7 Kb
Cultivated				Castelluccisa	S	~1.7 Kb
Cultivated	Andean			Corel	S	~1.7 Kb
Cultivated				Degli Ortolani	S	~1.7 Kb
Cultivated				Fagiolo del	S	~1.7 Kb
				Purgatorio		
Cultivated	MA			G2333	S	~1.7 Kb
Cultivated				Va la vacca	S	~1.7 Kb
Cultivated	MA		Pink	Sutter Pink	S	~1.7 Kb
Wild	Colombian			G24404	R	~1.7 Kb
Wild	Mexico			G11051	R	~1.7 Kb
Wild	Guatemala			G19908	R	~1.7 Kb
Wild	Honduras			G50722	R	~1.7 Kb
Wild	Ecuador			G23582	S	~1.7 Kb
Wild	Peru			G23422	R	~1.7 Kb
Wild	Argentina			G19898	R	~1.7 Kb
Wild	Bolivia			G23442	S	~1.7 Kb
Wild	Argentina			G7469	R	~1.7 Kb
Wild	Peru			G12856	R	~1.7 Kb
Wild	Argentina			G19888	S	~1.7 Kb
Wild	Argentina			G19891	R	~1.7 Kb
Wild	Argentina			G19897	S	~1.7 Kb
Wild	Argentina			G19898	-	~1.7 Kb
Wild	Argentina			G19901	S	~1.7 Kb
Wild	Argentina			G21199	S	~1.7 Kb
Wild	Peru			G23420	S	~1.7 Kb
Wild	Peru			G23421	R	~1.7 Kb
Wild	Bolivia			G23444	R	~1.7 Kb
Wild	Bolivia			G23445	S	~1.7 Kb
Wild	Peru			G23455	S	~1.7 Kb
Wild	Argentina			G19902	R	~1.7 Kb
WIIO	Argentina			ANP 1053	-	~1.7 KD
Wild	Argentina			G19892	-	1.7 KD
Wild	Argentina	<u> </u>		6224104	- c	~1.7 KD
Wild	Movico	<u> </u>		G11056	5 c	1.7 NU
Wild	Costa Pica			623/18	3	1.7 KU ~1 7 Kb
Wild				623410	- c	1.7 KU ~1 7 Kh
Wild	Colombia			623462	s c	1.7 KU ~1 7 Kb
Wild	Mexico			624378	2 2	1.7 KU ~1 7 Kb
Wild	Mexico			624571	-	~1.7 Kb
Wild	Mexico			G24572A	-	~1.7 KU
Wild	Mexico			PI325677	 ۲	~1.7 Kb
Wild	Mexico			G12873	R	~1.7 Kb
				0120/0		1.7 100

Wild	Mexico		PI417770	R	~1.7 Kb
Wild	El Salvador		PI201013	S	~1.7 Kb
Wild	Mexico		G12879	-	~1.7 Kb
Wild	Mexico		86	S	~1.7 Kb
Wild	Ecuador		G23726	R	~1.7 Kb
Wild	El Salvador		G21245	-	~1.7 Kb