Title

Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen Phytophthora capsici

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Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen *Physophthora Capsici*

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DISCLAIMER

Title: Genome sequencing and mapping reveal loss of heterozygosity as a mechanism for rapid adaptation in the vegetable pathogen *Phytophthora capsici*.

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Running title: Adaptation in *Phytophthora capsici*.

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ABSTRACT: The oomycete vegetable pathogen *Phytophthora capsici* has shown remarkable adaptation to fungicides and new hosts. Like other members of this destructive genus, *P. capsici* has an explosive epidemiology, rapidly producing massive numbers of asexual spores on infected hosts. In addition, *P. capsici* can remain dormant for years as sexually-recombined oospores, making it difficult to produce crops at infested sites, and allowing outcrossing populations to maintain significant genetic variation. Genome sequencing, development of a high-density genetic map, and integrative genomic/genetic characterization of *P. capsici* field isolates and intercross progeny revealed significant mitotic loss of heterozygosity (LOH) and higher levels of SNVs than those reported for humans, plants, and *P. infestans*. LOH was detected in clonally propagated field isolates and sexual progeny, cumulatively affecting >30% of the genome. LOH altered genotypes for more than 11,000 single nucleotide variant (SNV) sites and showed a strong association with changes in mating type and pathogenicity. Overall, it appears that LOH may provide a rapid mechanism for fixing alleles and may be an important component of adaptability for *P. capsici*.

INTRODUCTION

Phytophthora capsici is a virulent, hemibiotrophic pathogen of vegetable crops, inflicting significant losses worldwide (Leonian 1922; Erwin and Ribeiro 1996; Gevens et al. 2008; Lamour and Kamoun 2009; Meitz et al. 2010; Lamour et al. 2011). It's main hosts are peppers and cucurbits and during the last ninety years *P. capsici* has spread geographically as agricultural cultivation of these hosts has intensified; dynamically adapting to fungicides and new hosts (Leonian 1922; Erwin and Ribeiro 1996; Lamour and Hausbeck 2001; Hausbeck and Lamour 2004; Gevens et al. 2008; Hurtado-Gonzales et al. 2008; Lamour and Kamoun 2009; Meitz et al. 2010; Lamour et al. 2011; Gobena et al. 2012). Like other members of this destructive genus (e.g. the late blight pathogen *P. infestans* and the sudden oak death pathogen *P. ramorum*), *P. capsici* has an explosive epidemiology, rapidly producing massive numbers of asexual spores on infected hosts (Lamour and Hausbeck 2001; Hausbeck and Lamour 2004; Lamour and Kamoun 2009) (Fig. 1B-G). In addition, *P. capsici* often features meiosis between two mating types, producing thick-walled oospores that remain dormant for years, making it very difficult to produce crops at infested sites, and allowing outcrossing populations to maintain significant genetic variation (Fig. 1A). Members of this genus are notoriously plastic in field and laboratory scenarios and we examined the molecular basis for rapid adaptation in *P. capsici* through genome sequencing, development of a high-density genetic map, and integrative genomic/genetic characterization of *P. capsici* field isolates and intercross progeny. Development of these tools and subsequent analyses revealed significant mitotic loss of heterozygosity (LOH) in clonally propagated field isolates as well as multiple sexual progeny. Follow-up tests revealed a strong association of LOH with changes in mating type and loss of pathogenicity.

RESULTS

Genome sequencing, assembly and annotation

Assembling the nuclear genome of a diploid organism with frequent nucleotide variants can be difficult and a partially inbred line of *P. capsici* (LT1534) was developed for sequencing (Supplementary Fig. 1) (Hurtado-Gonzales and Lamour 2009; Gobena et al. 2012). The 64 Mbp reference genome was assembled using Arachne from 30X paired and singleton 454 FLX and Titanium genomic DNA reads, 5X Sanger paired reads, 56,448 Sanger ESTs, and 1,260 full-length cDNA sequences. This resulted in 917 scaffolds and an N50 of 706 kbp (Supplementary Table 1). The size of the *P. capsici* genome is intermediate among the sequenced oomycetes, larger than *Albugo* and *Pythium ultimum* (up to 45 Mbp) (Levesque et al. 2010; Kemen et al. 2011), but more compact than *P. ramorum*, *P. sojae*, *Hyaloperonospora arabidopsis* and *P. infestans* at 65, 95, 100, and 240 Mbp, respectively (Tyler et al. 2006; Haas et al. 2009; Baxter et al. 2010). The *P. capsici* draft genome had fewer scaffolds and/or larger scaffold N50, which may reflect hybrid assembly or fewer repeat sequences in *P. capsici* (19%) than *P. infestans*, *P. sojae* or *P. ramorum* (74%, 39%, and 28%, respectively) (Tyler et al. 2006; Haas et al. 2009). Like other Phytophthora species, the majority of *P. capsici* repeats were retrotransposons (84%) with long terminal repeats, of which 57% were Gypsy elements. The mitochondrial genome (80,148 bp) was assembled in 4 scaffolds.

Gene model prediction using a training set of 16.4 million sequencing-by-synthesis mRNA-sequences from nine life stages predicted 19,805 genes supported by cDNA sequences (50%) or previously identified proteins (75%) (Supplementary Tables 2 and 3). After excluding 2,682 genes with homology to transposable elements, *P. capsici* had a similar gene content to *P. infestans*, *P. sojae* and *P. ramorum* (17,797, 16,988 and 14,451, respectively) (Tyler et al. 2006; Haas et al. 2009) and had slightly more core eukaryotic genes identified compared to these other species (Supplementary Fig. 2). The non-repetitive gene density in *P. capsici* (268/Mbp) was higher than other Phytophthora species (74/Mbp in *P. infestans*, 179/Mb in *P. sojae* and 222/Mb in *P. ramorum*) (Tyler et al. 2006; Haas et al. 2009).

Comparison to other Phytophthora species

Genome comparisons revealed almost perfect scaffold-level synteny between the gene models of *P. capsici, P. ramorum* and *P. sojae*, with very little duplication (Fig. 2A, B). There was also extensive synteny with *P. infestans* genes (Supplementary Fig. 3). The genome organization of *P. capsici* was similar to other Phytophthora species, with ⅔ of the genes located in gene-rich blocks that have a conserved order and few repeats (median intergenic distance 351 bp), separated by relatively gene-poor regions without order conservation and more repetitive sequences (median intergenic distance ~3kb; Fig. 2C) (Haas et al. 2009). Like *P. infestans*, the 365 predicted *P. capsici* genes without a homolog resided predominantly in gene-poor genomic regions (Fig. 2C) (Haas et al. 2009; Raffaele et al. 2010).

Seventy eight percent of the predicted *P. capsici* genes clustered into 2,483 candidate multigene families. Among these families, there are cytoplasmic effector genes of the RxLR type including homologs of known avirulence genes in *P. infestans* (Whisson et al. 2007; Dou et al. 2008; Boutemy et al. 2011). *P. capsici* had 357 RxLR effector genes, which is a similar to the numbers reported for *P. sojae* and *P. ramorum*, whereas *P. infestans* had > 500 (Tyler et al. 2006; Haas et al. 2009). *Phytophthora capsici* also had 29 putative full length and 70 pseudogenes for Crinkling and Necrosis (CRN) effectors, an ancient class of intracellular effector proteins that share a highly conserved N-terminal domain, required for translocation, and diverse C-terminal effector domains (Haas et al. 2009). While markedly fewer than in *P. infestans*, the majority of predicted CRN effector domains were conserved between species.

Single nucleotide variation (SNV) and genetic mapping

Nucleotide diversity was assessed in seven *P. capsici* field isolates (including parental isolates TN1 and TN2) and an isolate of the sister species *P. tropicalis* by restriction-site associated DNA (RAD) sequencing (Supplementary Table 4) (Baird et al. 2008). Between 5 and 9 million sequencing-by-synthesis reads, flanked by a *Sgr*AI restriction site, were generated per isolate (Table S5). The reads were aligned to the *P. capsici* reference genome and covered ~2.3 Mbp at a depth of ≥30-fold (Kim et al. 2009; Baranzini et al. 2010; Bell et al. 2011). The SNV density among *P. capsici* isolates was 23.4/kb (range 16.9 - 25.9/kb) and between *P. capsici* and the closely related species *P. tropicalis* was 51.7/kb (Supplementary Tables 6 and 7; Supplementary Figs. 4 and 5). This is much higher than the SNV diversity observed among *P. infestans* strains (0.65/Kb average) and between *P. infestans* T30-4 and species in its clade (7.67/Kb average) (Raffaele et al. 2010). The nucleotide diversity (π) was 0.012 (range 0.009 - 0.016), ~16-fold higher than *H. sapiens* and ~4-fold higher than obtained by RAD in natural stickleback populations and most outbred plant species. The threespined stickleback (*Gasterosteus aculeatus* L.) is an outcrossing species of fish studied to better understand adaptive evolution (Hohenlohe et al. 2010).

In addition, the inheritance of SNV's was examined in 65 putative F_1 intercross progeny by *Pst*I-based RAD (Supplementary Figs. 1 and 6; Supplementary Table 8). Of these 65 isolates, two were found to be clonally derived from the TN2 parent and three additional isolates were clonal to progeny isolates. The remaining 60 true F1 progeny were genotyped at bi-allelic sites exhibiting either a di- or tri-modal distribution where the peaks corresponded to homozygous reference alleles, heterozygotes, and homozygous alternate alleles (Supplementary Fig. 7) (Kim et al. 2009). Genotypes were imputed at 500,352 nucleotides with ≥10 uniquely aligned reads in ≥55 progeny. Homozygosity was inferred when >90% reads displayed one allele, and heterozygosity when 20-80% of reads displayed one allele. We have previously shown such genotype imputation to be >99% accurate (Kim et al. 2009; Baranzini et al. 2010; Bell et al. 2011). Forty-five percent (9,254) of SNVs showing Mendelian inheritance were in coding regions, and 3,382 (37%) of these were non-synonymous (Supplementary Fig. 8a, Supplementary Table 10). The distribution of mutations in *Phytophthora* clade 1c species is in a similar range with 35% of SNV's in coding regions, 41% of which are non-synonymous (Raffaele et al. 2010). This was surprising since there is typically extensive purifying selection on genes. A parsimonious explanation of these findings is that rates of mutation relative to generation times are much greater in *P. capsici* than higher eukaryotes.

A total of 20,568 SNVs were either polymorphic in the parents and had Mendelian segregation ($\chi^2 \geq 0.05$), or were homozygous for opposite alleles in the parents and heterozygous in progeny that did not exhibit loss of heterozygosity (LOH) (marker spacing 3,111 bp; Supplementary Table 9). A genetic map was developed using markers on the 108 scaffolds that had sufficient SNVs for independent genetic linkage analysis in the F_1 progeny. Of these, 92 scaffolds had SNV's that were inherited as a single co-segregating block, while markers on 15 scaffolds broke into 2 blocks and markers on the largest scaffold (Scaffold 1) broke into three blocks (Supplementary Table 11; Supplementary Fig. 9). Scaffold-level linkage groups were inherited with LOD scores of ≥7. Following scaffold-level linkage analysis, a genetic map of *P. capsici* was constructed with 1,136 SNVs that had segregation patterns <95% similar.

The genetic map was 1,654 centiMorgans (cM) in length and comprised eighteen linkage groups accounting for 84% (54Mbp) of the reference genome and containing ~90% of the predicted genes (Fig. 3; Supplementary Table 12). The order for the majority of markers was the same on the genetic and physical maps. Genetic linkage analysis localized the mating type locus to a ~300kb critical region on scaffold block 4.1 in LG10.

Loss of heterozygosity

Integrated genomic and genetic analysis allowed assessment of chromosomal variation among the 65 putative F_1 intercross progeny. Twenty-three F_1 isolates and two clonal isolates contained regions with LOH. LOH was identified by homozygosity at all markers in ≥ 2 adjacent (linked) RAD sequences that were incompatible with parental genotypes (Supplementary Fig. 10; Supplementary Table 13). The minimum length of LOH tracts varied from 299 bp to >1 Mbp. LOH occurred in 14 of the 18 LGs and in 59 scaffolds or scaffold blocks. Fifty-four percent (11,048) of SNVs exhibited LOH in at least one isolate and the LOH was bidirectional. The frequency and distribution of LOH tracts varied among isolates and 36.5% (19.7 Mbp) of the genome was affected by LOH in at least one isolate. Two isolates (TN37 and TN47) had LOH exceeding 10% of the genome (Supplementary Table 14). Interestingly, LOH showed bias toward gene-rich regions (Supplementary Fig. 8B, C). Given the requirements of informative parental genotypes, at least two adjacent RAD tags to be affected, and that LOH was sought only in the mapped genome, the true extent of LOH is likely to be considerably higher.

Sub-chromosomal mitotic LOH has several molecular mechanisms including deletions (resulting in hemizygosity) and translocations (resulting in homozygosity) associated with homologous and non-homologous recombination or gene conversion (Chamnanpunt et al. 2001; Cvitanich et al. 2006). Of note, mutagenesis-induced LOH in *P. capsici* was not associated with sub-chromosomal deletions (Hulvey et al. 2010). In only one of 12 isolates was LOH due to hemizygosity as assessed by batched, normalized sequence coverage plots (Bell et al. 2011) (Fig. 4A-C). Forty-five percent (4,967) of the marker nucleotides exhibiting LOH were exonic, 17% (1,911) were in coding regions and 3.5% (391) were predicted to be non-synonymous, affecting 264 genes. Phenotypic consequences of genome diversity were sought among F_1 progeny. Five F_1 isolates switched mating type from A2 to A1 between assessments in 2005 and RAD sequencing in 2010, while one switched from A1 to A2 (Fig. 5A). Isolates were in storage for most of this interval and were sub-cultured < 10 times. Four of the isolates that switched from A2 to A1 had >800 Kbp tracts of LOH encompassing a region that appears to contain the mating type locus (or loci) on LG10 (Fig. 5A). TN25, which changed from A1 to A2, did not exhibit LOH at the mating type locus but did have >1.6 Mbp LOH in LG16. However, A1 mating type isolates TN37 and TN70 had similar LOH on LG16, but did not change mating type. Thus, LOH at the mating type locus was associated with mating type switch in four of six isolates.

LOH was also associated with a loss of pathogenicity to pepper and cucumber fruit. Between tests in 2005 and 2011, progeny isolates TN37 and TN47 became unable to infect wounded or un-wounded fruit (Fig. 5B). In 2011, host cells consistently elicited a strong hypersensitive response (cell necrosis) at point of inoculation, suggesting loss of a factor necessary for infection, such as an Avh protein. This is characteristic of Phytophthora Avh proteins, which evolve rapidly in a presumed host-pathogen arms race (Tyler et al. 2006; Whisson et al. 2007; Jiang et al. 2008; Haas et al. 2009). These isolates had similar growth rates *in vitro* in 2005 and 2011 even after substantial LOH (Supplementary Table 14). Indeed, the TN37 and TN47 genomes each had > 10% LOH and share an LOH tract on LG1 (17_31,860 - 17_870,195 and 105_51,382 - 105_63734; Supplementary Tables 13-14). A plausible explanation is that LOH changed the expression or expressed sequence of one or more *P. capsici* effectors in the avirulent isolates.

DISCUSSION

In summary, the genome sequence of *P. capsici* was typical for the genus in organization and gene content. A prototypical, dense genetic map indicated the recombination rate of *P. capsici* to be 38.7 kbp/cM, an order of magnitude less than yeast, but 30-fold higher than *H. sapiens* (Li and Freudenberg

2009). SNV density and diversity among *P. capsici* genomes was much higher than in other eukaryotes and coding and non-synonymous variants were remarkably common. This suggests that germline mutation rates may be much higher in *P. capsici* than in *H. sapiens*, *Saccharomyces cerevisiae*, *Drosophila melanogaster* and *P. infestans*, or that purifying selection was less (Baranzini et al. 2010). The overall SNV diversity for the seven *P. capsici* field isolates was similar, but markedly different from the *P. tropicalis* isolate. The isolates from Peru and Argentina appear to be part of long-lived, widely dispersed clonal lineages where, unlike the situation for the North America isolates, sexual recombination may be rare (Hurtado-Gonzales et al. 2008; Gobena et al. 2012). Interestingly, the isolates from Peru and Argentina share the most polymorphic loci and may be derived from a common, invasive population or widely dispersed clonal lineage. The high level of SNV diversity in *P. capsici* has practical implications for research. The SNV's can be used to finely map segregating phenotypes in larger populations of progeny, conduct sensitive analyses of population structure and overall dynamics, and to track the fate of numerous heterozygous loci during asexual growth (e.g. tracking LOH).

Phytophthora capsici populations are often characterized by high levels of diversity and rapid adaptation (Leonian 1922; Erwin and Ribeiro 1996; Lamour and Hausbeck 2001; Hausbeck and Lamour 2004; Gevens et al. 2008; Hurtado-Gonzales et al. 2008; Lamour and Kamoun 2009; Meitz et al. 2010; Lamour et al. 2011; Gobena et al. 2012). In addition to elevated genetic diversity, *P. capsici* genomes also had a remarkably high frequency of mitotic LOH occurring more commonly in gene rich areas. Mitotic genomic instability was also recently described in *P. ramorum* (Vercauteren et al. 2011), suggesting LOH may be a general characteristic of oomycetes. Here we show loss of pathogenicity and mating type switches are likely phenotypic consequences of mitotic LOH. For the latter, the evidence for causality of LOH was strong: four of five progeny that switched from the A2 to the A1 mating type had tracts of LOH spanning the region where mating type maps in this cross. This was reminiscent of the mating type locus in the fungus *Candida albicans*, where a repressor suppresses switching to the mating-competent form (Morschhauser 2010). Loss of mating type heterozygosity relieves this repression, ensuring that only mating type homozygous cells are mating-competent. An ability to switch mating type has important consequences, particularly in northern latitudes where survival of the winter or fallow months requires thick-walled, sexually-produced oospores (Lamour et al. 2011). It also provides a mechanism to introgress mutations efficiently into a population (Supplementary Figure 10). The fungicide mefenoxam, for example, is strongly inhibitory to *P. capsici* and has been widely used in some areas. Mefenoxam resistance is inherited in *P. capsici* as a single incompletely dominant trait (Lamour and Hausbeck 2000; Lamour and Hausbeck 2001). Mating type switches in a rare, partially resistant field isolate will double the chances for outcrossing. In addition to aiding introgression of a novel resistance allele by sexual reproduction, LOH could directly catalyze the conversion to full resistance. Using the SNV markers presented here, it should be possible to detect instances of LOH within naturally occurring isolates.

The dramatic expansion of repeated sequences observed in several pathogen lineages of oomycetes (*P. infestans*, *H. arabidopsidis*) and fungi (*Puccinia graminis* f. sp. tritici, *Melampsora larci-populina*, *Blumeria graminis*) was proposed to contribute to fast adaptation (Haas et al. 2009; Spanu et al. 2010). A clear correlation was indeed observed between the rate of gene evolution and the amount of flanking repeats (Raffaele et al. 2010). By contrast, the *P. capsici* genome is rather compact, with a relatively low repeat content, and yet shows remarkable plasticity. This plasticity may be due in part to LOH which represents an alternative mechanism for rapidly generating diversity, preferentially affecting gene dense regions. Previous studies suggest a role for LOH in adaptive evolution (Rosenberg 2011). It has, for example, been associated with oncogenesis and embryonic stem cell adaptation in *H. sapiens* (Narva et al. 2010), and fluconazole resistance in *C. albicans* (Forche et al. 2011). Here we extend these observations, suggesting that the co-occurrence of frequent mitotic LOH and high nucleotide diversity in genes may provide a general mechanism for rapid adaptation in *P. capsici*. In addition, LOH may contribute to the difficulties encountered when studying oomycetes in the laboratory (e.g. loss of pathogenicity and virulence) and the overall success of oomycetes as plant pathogens.

METHODS

Isolates. Three *in vitro* crosses were completed to produce a moderately inbred isolate for sequencing the reference genome (Hurtado-Gonzales and Lamour 2009). Crosses include an F1, and two recurrent backcrosses (BC1 and BC2). An isolate from the BC2 progeny was chosen for genome sequencing based on growth rate and asexual and sexual spore production (Hurtado-Gonzales and Lamour 2009). The initial cross was between an A1 isolate recovered from cucumber in Michigan in 1997 (TN1) and an A2 isolate recovered from pumpkin in Tennessee in 2004 (TN2). The backcrosses were to the TN2 parent. Crosses were made by co-culturing the parental isolates on V8-juice agar plates, incubating the plates for 8 to 12 weeks in darkness, and then separating the sexual oospores from the subtending asexual mycelium and other asexual spores (sporangia and zoospores) through mechanical shearing and an enzyme treatment to destroy the asexual material (Lamour and Hausbeck 2000). The enzymes not only destroy the asexual material; they stimulate oospore germination. Germinating oospores were harvested using a 5µl pipette while looking at the spores under a light microscope. Once harvested, the germinated spores are placed onto V8 media, sub-cultured to produce mycelium for DNA and to conduct mating type analysis, and then stored long term (3 to 5 years) in water with sterile hemp seeds.

The progeny from all of the crosses were genotyped using AFLP markers, tested for mating type, assessed for growth rate on agar media, and assayed for pathogenicity and virulence on detached pepper (variety Early Jalapeno) and cucumber fruit (various varieties) (Hurtado-Gonzales and Lamour 2009). All fruit inoculations were conducted on two fruit and the experiments repeated twice. Pathogenicity was assessed by placing a 7mm plug of mycelium at both a wounded and non-wounded site. Wounded sites are distal and non-wounded sites proximal to the stem end of the fruit. Pathogenicity to pepper fruit was assessed in 2005 and 2011. Sixty-nine progeny from the F1 were further analyzed using a focused re-sequencing strategy (outlined below). In addition, the mating type was tested at three different time intervals: within 6 months of the cross, at the time of the focused re-sequencing, and one year following the re-sequencing.

Genome sequencing and assembly. High quality genomic DNA was prepared from the isolate selected for genome sequencing using a phenol/chloroform protocol. Aliquots from the same batch of DNA were submitted to 454 Inc. (Branford, CT) and to the Joint Genome Institute (JGI, Walnut Creek, CA) for 454- and Sanger-based sequencing, respectively. A total of 2,451,737 random shotgun genomic reads, 2,022,402 paired-end reads (2.3 Kb), and 833,606 paired-end reads (18.0 Kb) were produced using the 454 Titanium chemistry. In addition, 197,306 random genomic paired-end reads from a 6.3Kb plasmid library, 146,588 paired-end reads from a 34.7Kb fosmid library and 65,000 ESTs were produced at the JGI using Sanger sequencing. Additionally, 1,260 full-length cDNA sequences were generated by Sanger sequencing and cDNA sequence assembly.

The sequence reads were assembled using a modified version of Arachne v.20071016 (Jaffe et al. 2003) with parameters maxcliq1=100, n_haplotypes=2 and BINGE_AND_PURGE=True. The output of this assembly was passed through Rebuilder and SquashOverlaps with parameters to merge adjacent assembled alternative haplotypes, and subsequently run through another complete Arachne assembly process to finalize the assembly. Prior to assembly, redundant 454 pairs (defined as at least 98% identical across their length) were removed and a single pair retained. An error correction step was applied to all 454 data that attempted to set bps to equal the Sanger sequence. This was accomplished by shredding the Sanger sequence to a similar size as the 454 reads and then aligning these shredded reads and the 454 simultaneously. Where the 454 read sequence had no support we changed the 454 read sequence to match the Sanger read sequence. This removed many of the 454 sequence errors (primarily indels and occasional bp substitutions) and coalesced the haplotyopes if the Sanger data was all from one haplotype. Error correction was also applied during the Arachne assembly process by screening each scaffold against bacterial proteins, organelle sequences and GenBank using Megablast against Genbank NR and blastp against a set of known microbial proteins. Twenty-eight scaffolds identified as prokaryotic contamination were removed. We classified additional scaffolds as mitochondrion (4), small repetitive (6), alternative haplotyope (17), and less than 1kb (1050). The final assembly consists of 971 scaffold sequences, with half of the genome contained in 29 scaffolds of at least 705.7 kb in length and contigs greater than 34.6kb. Scaffolds ranged in size from 1 kb to 2.1 Mb with an N50 of 705.7 kb (Supplementary Table 1). The genome size was tested using the approach outlined by Baxter with nt by nt coverage calculated by aligning back to the reference (Baxter et al. 2010). This resulted in an estimated genome size of approximately 55 Mbp. We also estimated the genome size by measuring the percentage of all reads that were captured by the assembly using a high quality 10,000 read subset (average quality >= 35, length >= 100 and no missing bases) and extrapolating genome size if the assembly had captured all the reads. We extrapolated up from the genome size that doesn't include gaps (56.1 Mb) and 97.44% of the reads were captured leading to an estimated genome size of approximately 57 Mbp. Both estimates likely underestimate the genome size due to over alignment of repeat copies, possibly explaining the discrepancy between our gapped genome size (64.1 Mb) and these lower estimates of total genome size. Nevertheless, both estimates are similar to the non-gapped genome size (56.1 Mb) suggesting that the assembly is missing very little of the non-repetitive genome.

In addition, total RNA was isolated from different growth conditions (rich media, starvation, and sporulating), pooled, and submitted to both 454 and the JGI for Sanger cDNA and EST sequencing. At the JGI, ESTs were produced as previously described with the following modification: 2 cDNA libraries were constructed and sequenced and the size ranges of the cDNA library inserts were 0.6k-2kb and >2kb (Jeffries et al. 2007).

Genome sequence analysis and annotation of gene families. The genome assembly of *Phytophthora capsici* LT1534 was annotated using the JGI Annotation Pipeline, which combines several gene predictors: A) cDNA-based gene models were derived from 1260 full-length cDNAs and 11,090 consensus sequences clustered from 56,448 ESTs, and then mapped to genomic sequence, B) protein-based gene models were predicted using FGENESH+ (Salamov and Solovyev 2000) and GeneWise (Birney et al. 2004) seeded by BLASTx alignments of genomic sequence against sequences from the NCBI non-redundant protein set nr, and C) *ab initio* gene models were predicted using FGENESH trained on the set of putative full-length genes and reliable protein-based models. GeneWise models were completed using scaffold data to find start and stop codons. ESTs, EST clusters, EST contigs, and full length cDNAs were used to verify, complete, and extend the gene models. Because multiple gene models per locus were often generated, a single representative gene model for each locus was chosen based on homology and EST support, and used for further analysis. This led to a filtered set of 19,805 gene models (including 2,682 genes with homology to transposable elements) with their properties and support by different lines of evidence summarized in Supplementary Tables 2 and 3. All gene-based analyses were done on the full 19,805 gene set. A total of 56,448 ESTs are available in Genbank under the title "DOE Joint Genome Institute *Phytophthora capsici* EST project". An additional 1260 full length cDNAs are available in Genbank under the title "DOE Joint Genome Institute *Phytophthora capsici* cDNA project". The genome sequence is available at http://genome.jgi-psf.org/Phyca11/Phyca11.home.html.

All predicted gene models were functionally annotated by the JGI Annotation Pipeline using InterProScan (Zdobnov and Apweiler 2001) and hardware-accelerated double-affine Smith-Waterman alignments (http://www.timelogic.com/) against highly curated databases such as SwissProt (Bairoch et al. 2005), KEGG (Ogata et al. 1999), and Pfam (Bateman et al. 2004). KEGG hits were used to map EC numbers (Bairoch 2000), and InterPro, KEGG, and SwissProt hits were used to map GO terms (Ashburner et al. 2000). In addition, predicted proteins were annotated according to KOG classification (Koonin et al. 2004). Protein targeting predictions were made with signalP (Nielsen et al. 1999) and TMHMM (Krogh et al. 2001). Finally, all proteins were aligned by BLASTp to proteins in nr and to each other; after the latter analysis the alignment scores were used as a distance metric for clustering by MCL (http://www.micans.org/mcl/) into a first draft of 2,483 candidate multigene families. The same method was used to group genes with those of other *Phytophthora* species. We used BLASTP to identify Crinkler (CRN) coding genes from the *P. capsici* gene model set (Supplementary Table 16). For this purpose, 16 well characterized CRN proteins from *P. infestans* were searched against the *P. capsici* protein data set. Sequences with significant hits (E= <10-5) were retrieved and a non-redundant CRN-like protein set was created (Win et al. 2006). CRN-like protein sequences were manually examined for the presence of LFLAK motifs and C-terminal effector domains. To determine whether candidates are full length or pseudogenes, we aligned our CRN candidates with previously characterized CRNs. CRN proteins of at least 250 amino acid residues or more and that aligned with both the N and C-terminal domains of PiCRNs were considered full length (Haas et al. 2009). Finally, we used SignalP3.0 to identify predicted secretion signals for all CRN candidates (Supplementary Table 16). Candidate RxLR effectors were mined via the protocol outlined previously (Haas et al. 2009). In brief, all open reading frames greater than 210 nucleotides (70 AA) from the genome were generated and translated to amino acid coding sequences. Those containing an RXLR (Arg - Anything - Leu - Arg) between 30 - 60 amino acids from the start, a signal peptide score greater than .9, and a cleavage site prior to the RXLR are considered effectors (Supplementary Table 17).

The CEGMA pipeline was used to compare the completeness and continuity of six Oomycete genomes (Parra et al. 2007). CEGMA checks the completeness and continuity of genome assemblies on the basis of 248 core eukaryotic genes. Here, we compared the CEGMA analyses (without KOG 69) for the genomes of *P. sojae, P. ramorum, P. infestans, Pythium ultimum,* and *Hyaloperonospora arabidopsis* to the draft genome of *P. capsici* reported here (Supplementary Table 15).

Transposon-like coding sequences were identified by searching the annotated protein-coding sequences of *P. capsici* against databases of transposon sequences with TransposonPSI (http://transposonpsi.sf.net). Nucleotide sequences corresponding to the coding regions of the annotated protein coding genes were searched against the TransposonPSI collection of transposon protein sequences using BLASTX. This included ORFs derived from mobile elements discovered in other sequenced Phytophthora genomes. In addition, the *P. capsici* protein sequences were searched against a collection of PSI-BLAST profiles corresponding to common families of transposable elements, including Gypsy-retrotransposons and Piggybac-transposons. Any *P. capsici* annotated coding sequence identified by having a BLAST E-value of at most 1e-10 was identified and reported, yielding 2,682 candidate gene annotations with transposon homology (see: Pcap.annot_transposon_mining.maxE_1e-10.txt.gz). Transposon family (PSI-BLAST) and top transposon protein BLASTX match are provided.

Scaffolds, gene models clusters, and annotations thereof, may be accessed at the JGI *P. capsici* portal (http://www.jgi.doe.gov/capsici/) (Grigoriev et al. 2012).

Focused re-sequencing. Restriction site Associated DNA (RAD) sequencing was employed to identify and genotype single base substitutions in 7 field isolates (including the parents TN1 and TN2) and 69 progeny (TN3 – TN71) of the F1 cross (Baird et al. 2008). Briefly, genomic DNA was digested with the 6bp recognition restriction endonuclease *Pst*I or the 8bp recognition *Sgr*AI (Floragenex, Inc.). The digested DNA was sheared to between 200 and 500 bp and adaptors ligated which contained sequencing priming sites and an isolate-specific 5bp tag (Baird et al. 2008). Between 5 and 9 million sequencing-by-synthesis reads of length 72 nt were generated per isolate using an Illumina GAII sequencer (Supplementary Fig. 6, Supplementary Tables 5 and 8). The short reads abutting the restriction site are referred to as RAD tags. The RAD approach reduces complexity by focusing the sequencing to the regions directly adjacent (left and right) to a restriction site and the isolate-specific 5bp tags allow multiplexed sequencing. Reads were aligned to the *P. capsici* reference, covering ~2 million nucleotides at a depth of ≥30-fold (Supplementary Tables 5 and 8) (Kim et al. 2009; Baranzini et al. 2010; Bell et al. 2011).

SNV discovery and genotyping. Alignments of the RAD sequence and subsequent variant detection were carried out using the Genomic Short-read Nucleotide Alignment Program (GSNAP (Wu and Nacu 2010)) and the Alpheus pipeline (Miller et al. 2008), as described (Kim et al. 2009; Baranzini et al. 2010; Bell et al. 2011). Reads were aligned to the *P. capsici* genome assembly (version 11) and alignments retained that matched the genome with 95% identity or higher and that had ≤5 equally high scoring alignments. Reads with equally good hits to more than one genomic region, reflecting repeat content or redundancy in the assembly, were not considered uniquely aligned. Four isolates were excluded from analysis due to insufficient aligned reads (Supplementary Fig. 6). Read count–based allele frequencies of bi-allelic nucleotide variants had a tri-modal distribution, with peaks corresponding to homozygous reference alleles, heterozygotes, and homozygous alternate alleles (Supplementary Fig. 7) (Kim et al. 2009).

Potential segregating SNV sites were identified in the parents and progeny using the following criteria: ≥10X unique sequence coverage, an average quality score ≥20 and an alternate allele frequency ≥20% within unique reads. This pool of potential segregating sites was then analyzed across all lines and SNV genotyping criteria were developed based on a visual assessment of the distribution of alternate alleles at different levels of unique sequence coverage (Supplementary Fig. 7). SNVs were genotyped at the identified segregating SNV sites for all lines with at least 10X unique coverage where alternate allele frequency within unique reads was <10% (homozygous for the reference allele), >20% and <80% (heterozygous), or >90% (homozygous for the alternate allele). Our final pool of markers was limited to loci with 5 or fewer missing genotypes in the progeny. This approach does not enrich or bias for gene rich areas of the genome.

Nucleotide density and diversity was calculated for SNV sites in the *Sgr*AI RAD tags from the *P. capsici* parents and five additional unrelated isolates (two of which represent very large clonal populations in Peru and Argentina) and a *P. tropicalis* isolate. Heterozygosity and homozygosity were distinguished by allele frequency cutoffs of 15% and 85% and there was no requirement for number of missing genotypes in the isolates. SNV diversity was calculated as previously described (Begun et al. 2007).

Loss of heterozygosity and clonal isolates. Loss of Heterozygosity (LOH) was assessed using graphical genotypes constructed by ordering the SNV loci according to (i) the genetic linkage of markers in the individual scaffolds and (ii) the genetic linkage of markers from all scaffolds together (see below). The minimum tracts of LOH were calculated for regions with continuous, uninterrupted switching of loci to either the reference or alternate allele (homozygosity) in a way that is impossible by normal meiosis or clonal reproduction (Judd and Petes 1988). To avoid minor genotyping errors, LOH was only assigned for tracts where the switched loci spanned at least two different sequencing sites. In addition, the junction of LOH versus non-LOH in an isolate with good sequence coverage was analyzed to compare the coverage on either side of the junction.

Genetic similarity of the parents and progeny was assessed in JMP Genomics by analyzing a relationship matrix for our final pool of markers using a Fast Ward Hierarchical clustering at the default settings. Alleles were assumed to be identical by descent. Putative clones were confirmed using the graphical genotypes. Genetic similarity analyses revealed three clonal lineages. One clonal lineage contained the parent isolate TN2 and the (mistaken) F1 progeny TN3 and TN50. Two other clonal lineages were derived from true F1 progeny and included isolates TN56, TN57, and TN63 in one clonal lineage and isolates TN8 and TN11 in another clonal lineage (Supplementary Fig. 11). This was not surprising since occasional sporangia survive the enzymatic treatment used to destroy asexual propagules, and premature oospore germination can produce sporangia that appear to be discrete oospore progeny. A single isolate of each lineage was retained for genetic linkage analysis**.** Apomixis, which occurred in other crosses stemming from these parents, is another possible explanation for the clones of the TN2 parent (Hurtado-Gonzales and Lamour 2009).

Genetic linkage analysis. Putative segregating markers were analyzed using a Chi-square test for simple Mendelian inheritance (5% significance). A total of 20,568 SNVs were either polymorphic in the parents and had Mendelian segregation ($\chi2 \geq 0.05$), or were homozygous for opposite alleles in the parents and heterozygous in progeny that did not exhibit LOH. These were used for genetic linkage analysis (average marker spacing 3,111 bp; Supplementary Table 9).

A total of 3,141 SNVs exhibited segregation ratios <5% by $\chi 2$-test. Some of these clustered in blocks and may reflect gene conversion, as described in other Phytophthora species (Chamnanpunt et al. 2001; Cvitanich et al. 2006). An additional ~100 loci were heterozygous in both parents and all progeny and may reflect assembly artifacts, copy number variants or obligate heterozygosity.

Mendelian markers were further analyzed using JoinMap 4.1 at the default settings for a CP type cross (heterogeneously heterozygous with phase unknown) (van Ooijen 2011). Initially, markers from individual scaffolds were analyzed to determine if they are inherited as a linked unit (expected if the scaffold is assembled correctly). If a scaffold broke into more than one piece, the pieces are referred to as scaffold blocks. Following this, markers from all the scaffolds, or scaffold blocks, were analyzed together to produce a linkage map. The LGs were further refined to include only markers with segregation patterns <95% similar and to exclude isolates showing any LOH within the LG. Markers are named with the scaffold number followed by the nucleotide position on the scaffold. Additional information was included for the markers used in JoinMap 4.1 to designate the three possible segregation scenarios: *hk* = heterozygous in both parents, *nn* = Parent 1 is homozygous and Parent 2 is heterozygous, and *lm* = Parent 1 is heterozygous and Parent 2 is homozygous.

The SNV genotyping error rates were assessed for both parents (TN1 and TN2) at 95 polymorphic sites in portions of 30 genes across 14 linkage groups by Sanger sequencing of PCR products. Of these 190 genotypes, all but 5 were confirmed. The 5 genotypes that differed occurred on a single gene that switched to homozygosity at all 5 sites.

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AUTHOR CONTRIBUTIONS

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Figure 1: Life cycle. Thick walled dormant sexual oospores (**A**) are produced when plants are infected with both the A1 and A2 mating types. Asexual reproduction following infection rapidly creates very large populations of sporangia on the surface of the infected plants (**B-D, G**). Sporangia can detach and cause infection directly or, in the presence of free water, release 20-40 bi-flagellate swimming zoospores (**E**) that swim to plants and cause infection indirectly (**F**).

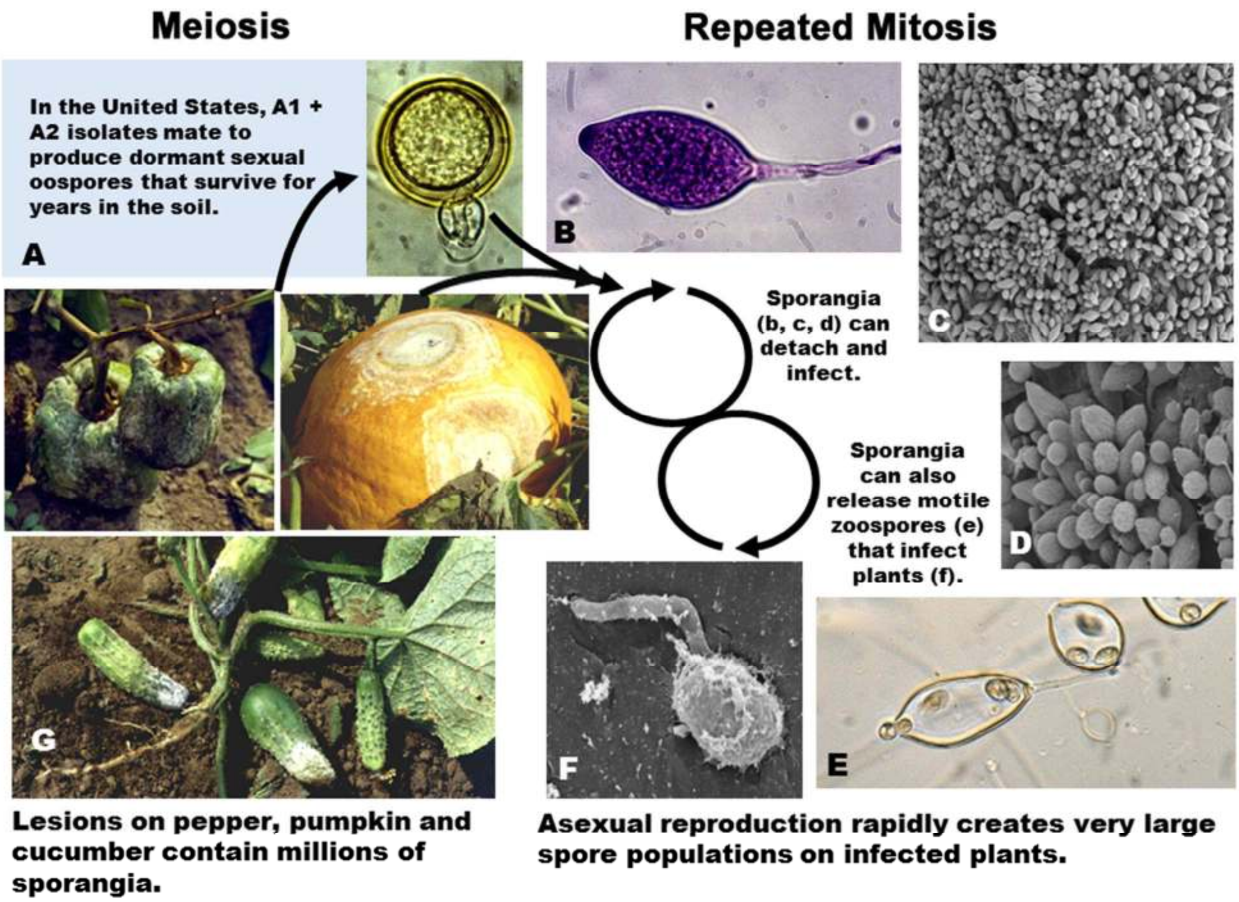
Figure 2: Synteny and genome architecture of *P. capsici*. Pairwise comparison of gene models from *P. capsici* to *P. ramorum* (**A**) and *P. sojae* (**B**). Sequences other than gene models were replaced with Ns. Maximal unique matches in all 6 frames were used as anchors for amino-acid-based alignment with the PROmer package of MUMmer. Scaffolds >450 kbp are shown (*P. capsici*: 46 Mb, *P. ramorum*: 36 Mb, *P. sojae*: 58 Mb). Scaffolds were ordered to maximize the center diagonal. There were some translocations, which possibly were assembly errors. A small region of *P. sojae* (top) had no syntenic genes in *P. capsici.* (**C**) *P. capsici* whole genome architecture illustrated by the distribution of all predicted genes according to the length of their 5' (X-axis) and 3' (Y-axis) intergenic regions, counted by two-dimensional binning. The color scale shows number of genes in bins. In addition, the 365 predicted proteins for which no homolog was found (10e-5 e-value cutoff) are indicated as dots.

Figure 3: The 1654cM *P. capsici* genetic map. The map contains 1,136 SNV markers and 18 linkage groups (LG's). Linkage groups are colored by genome scaffold.

Figure 4: Ploidy for LOH regions. (A) Normalized sequence coverage of RAD tags across 50,649 nt of a 850,537 nt LOH tract on scaffold 4 (LG10) at nt 86,143 - 936,679 encompassing the mating type locus. The 6 isolates with LOH are denoted by red dots. Normalized coverage was obtained by dividing the average coverage across the tract by the total unique coverage for each sample. Parents are in light blue and non-LOH progeny are dark blue. **(B)** Normalized coverage of tags across 14,143 nt of a

415,652 nt LOH tract on scaffold 35 (LG16) at nt 141,346 - 556,998. Five isolates with LOH are in red. TN58 had ½ of the expected coverage, indicating LOH to reflect a sub-chromosomal deletion. **(C)** Normalized coverage of tags across 22,124 nt f a 655,528 nt LOH tract on scaffold 1 (LG9) at nt 87,441 - 742,969. TN50 had LOH of this region.

Figure 5: LOH in *P. capsici.* (A) Graphical genotypes for LG10 in the region of scaffold 4 encompassing the mating type locus in parents (TN1 and TN2, black) and 59 F_1 progeny. R = reference allele and A = alternate allele. Red asterisks to the left of the marker names denote unambiguous LOH loci. Dots represent missing genotypes. Six progeny had LOH in this region (in red), including four that switched mating type from A2 to A1 and two that remained A1 following LOH. Group 1: progeny 10, 13, 15, 16, 26, 29, 31, 35, 37-41, 46, 51, 54, 59-61, 64-66, 70, 71, and 9. Group 2: progeny 14, 17, 19-24, 27, 30, 33, 36, 42-45, 49, 5, 55, 58, 62, 67, and 68. **(B)** Association of LOH with loss of pathogenicity of *P. capsici* isolates in wound inoculated jalapeno fruits between 2005 and 2011. TN1 and TN2 are the parents. TN31 was representative for all progeny except TN37 and TN47. In 2011, the TN37 and TN47 genomes had 10.4% and 11.1% LOH, respectively, and these isolates no longer infected wounded fruit.



In the United States, A1 + A2 isolates mate to produce dormant sexual oospores that survive for years in the soil.

Sporangia (b, c, d) can detach and infect.

Sporangia can also release motile zoospores (e) that infect plants (f).

Lesions on pepper, pumpkin and cucumber contain millions of sporangia.

Asexual reproduction rapidly creates very large spore populations on infected plants.

Figure 1

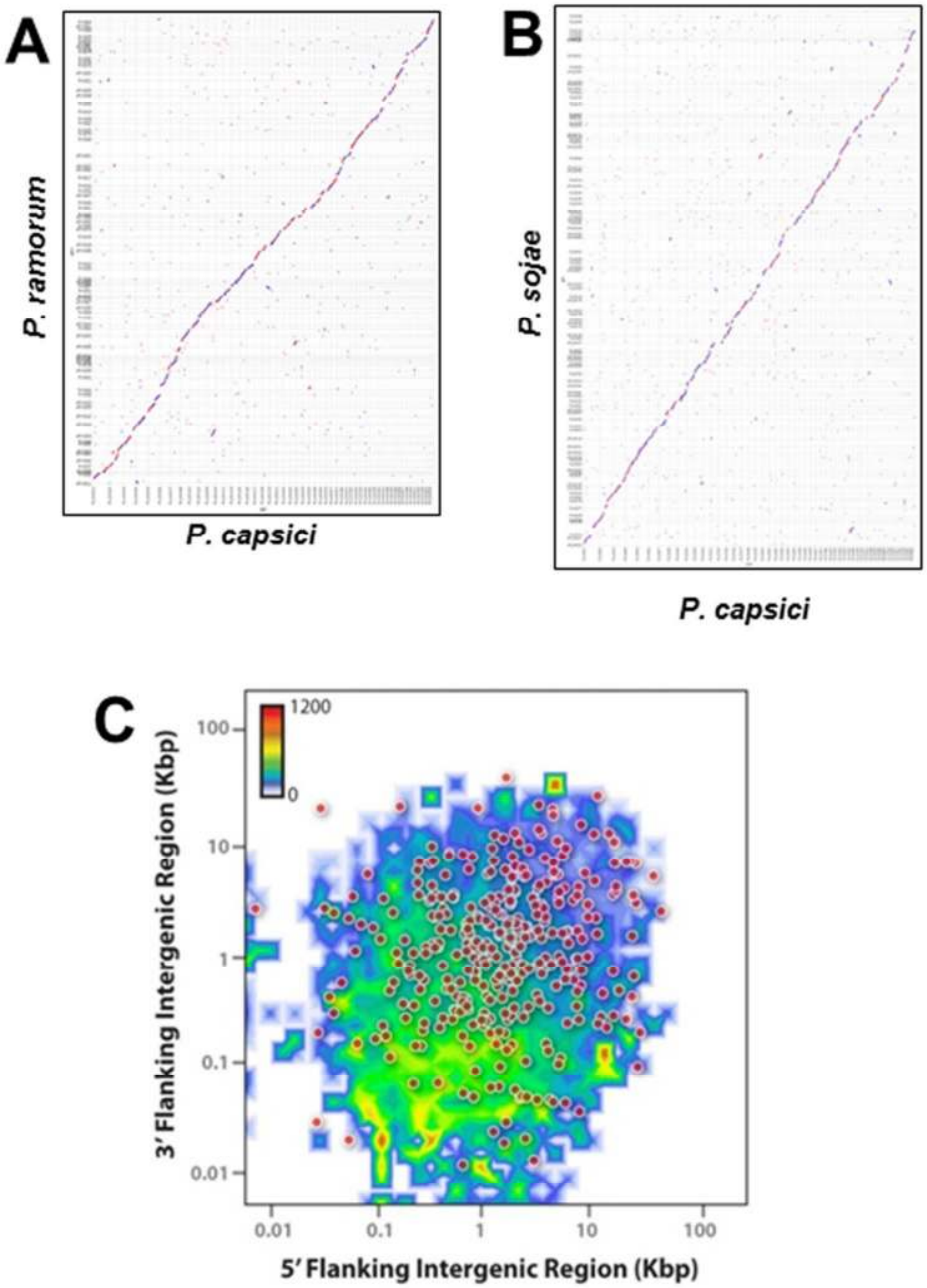

A
P. ramorum
P. capsici
B
P. sojae
P. capsici
C
1200
0
100
10
1
0.1
0.01
3′ Flanking Intergenic Region (Kbp)
0.01
0.1
1
10
100
5′ Flanking Intergenic Region (Kbp)

Figure 2

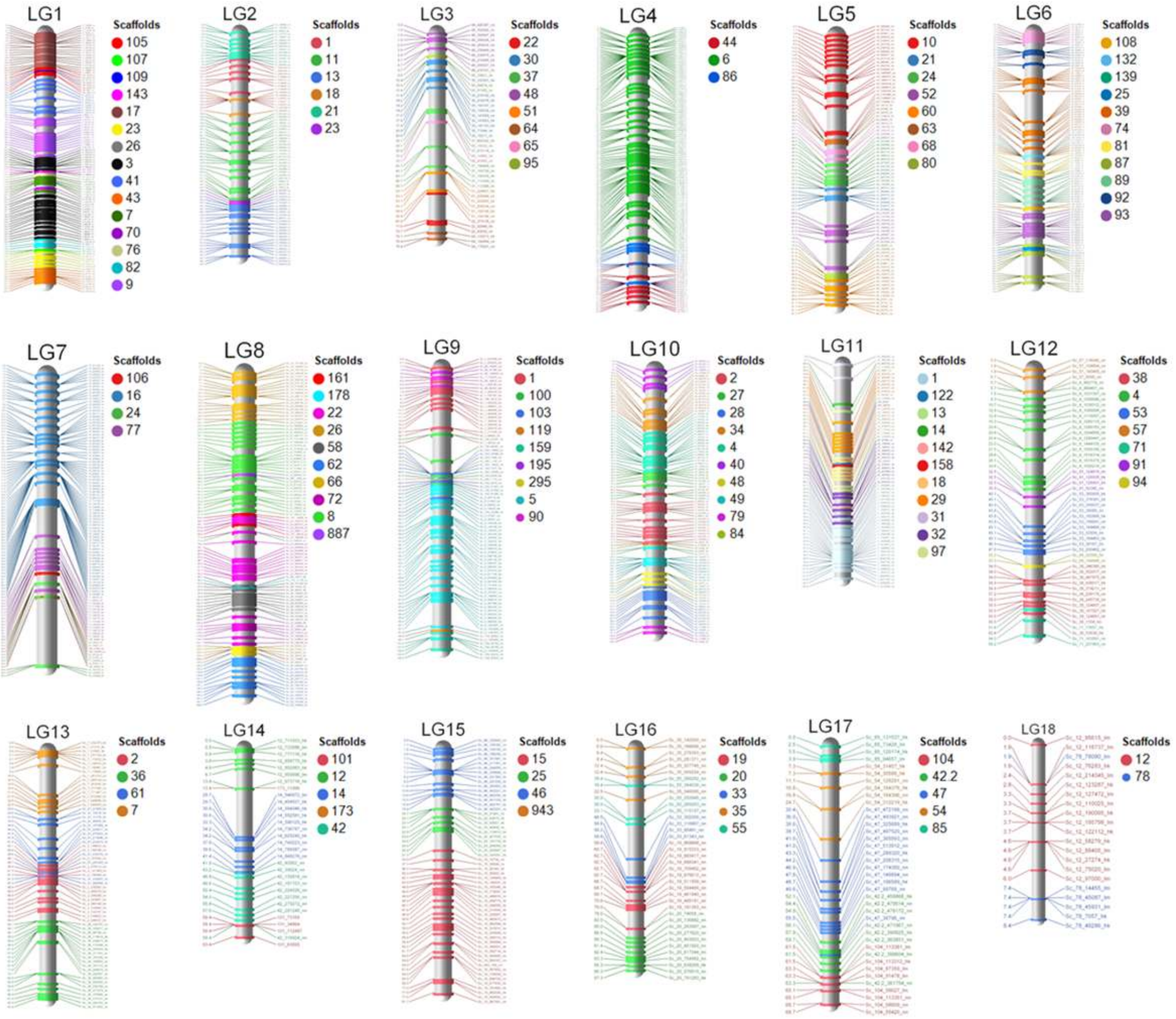


Figure 3_Lamour_MPMI

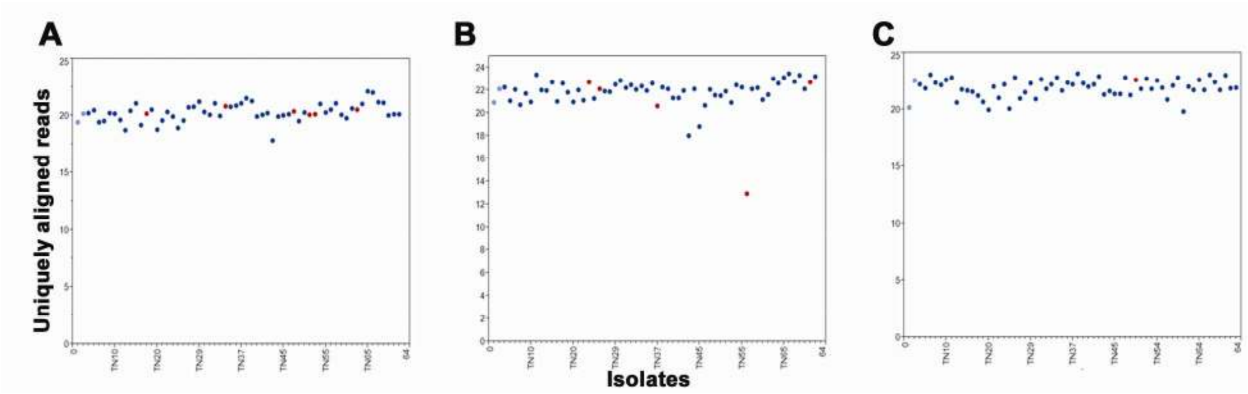
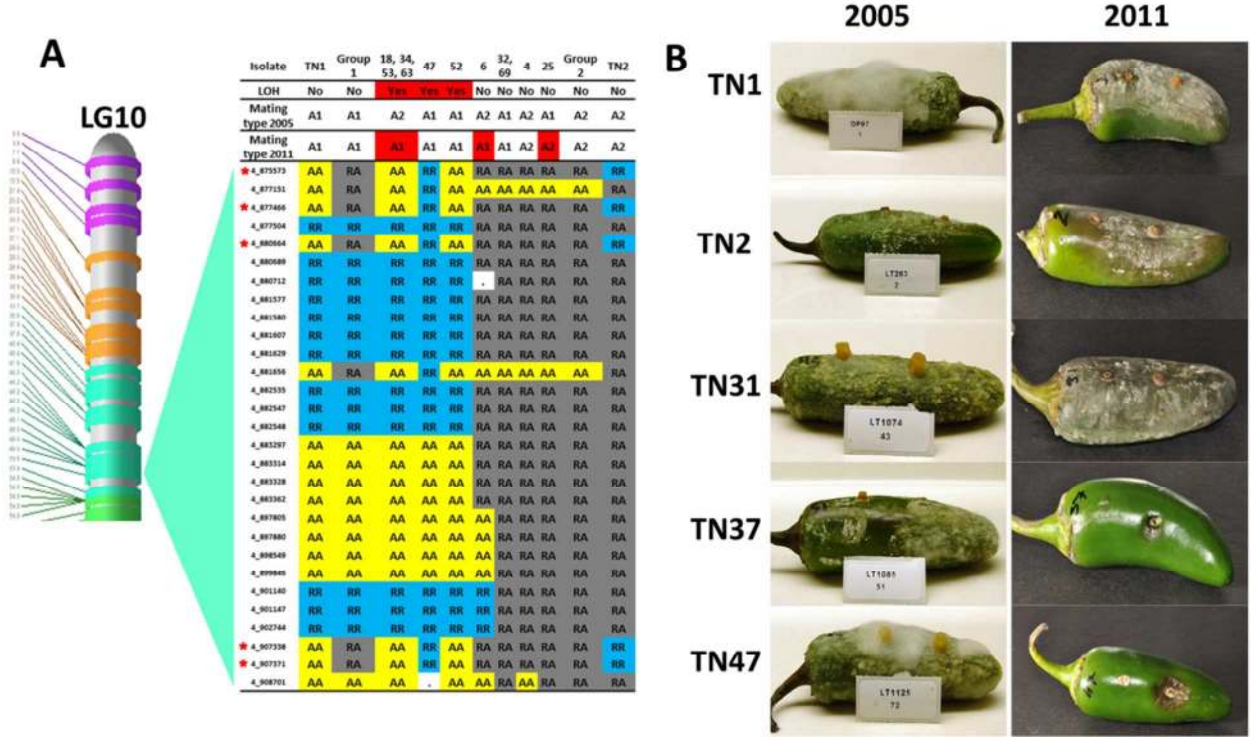

A
Uniquely aligned reads
25
20
15
10
5
0
0
TN10
TN20
TN29
TN37
TN45
TN55
TN65
64
B
24
22
20
18
16
14
12
10
8
6
4
2
0
0
TN10
TN20
TN29
TN37
TN45
TN55
TN65
64
Isolates
C
25
20
15
10
5
0
0
TN10
TN20
TN29
TN37
TN45
TN54
TN64
64

Figure 4

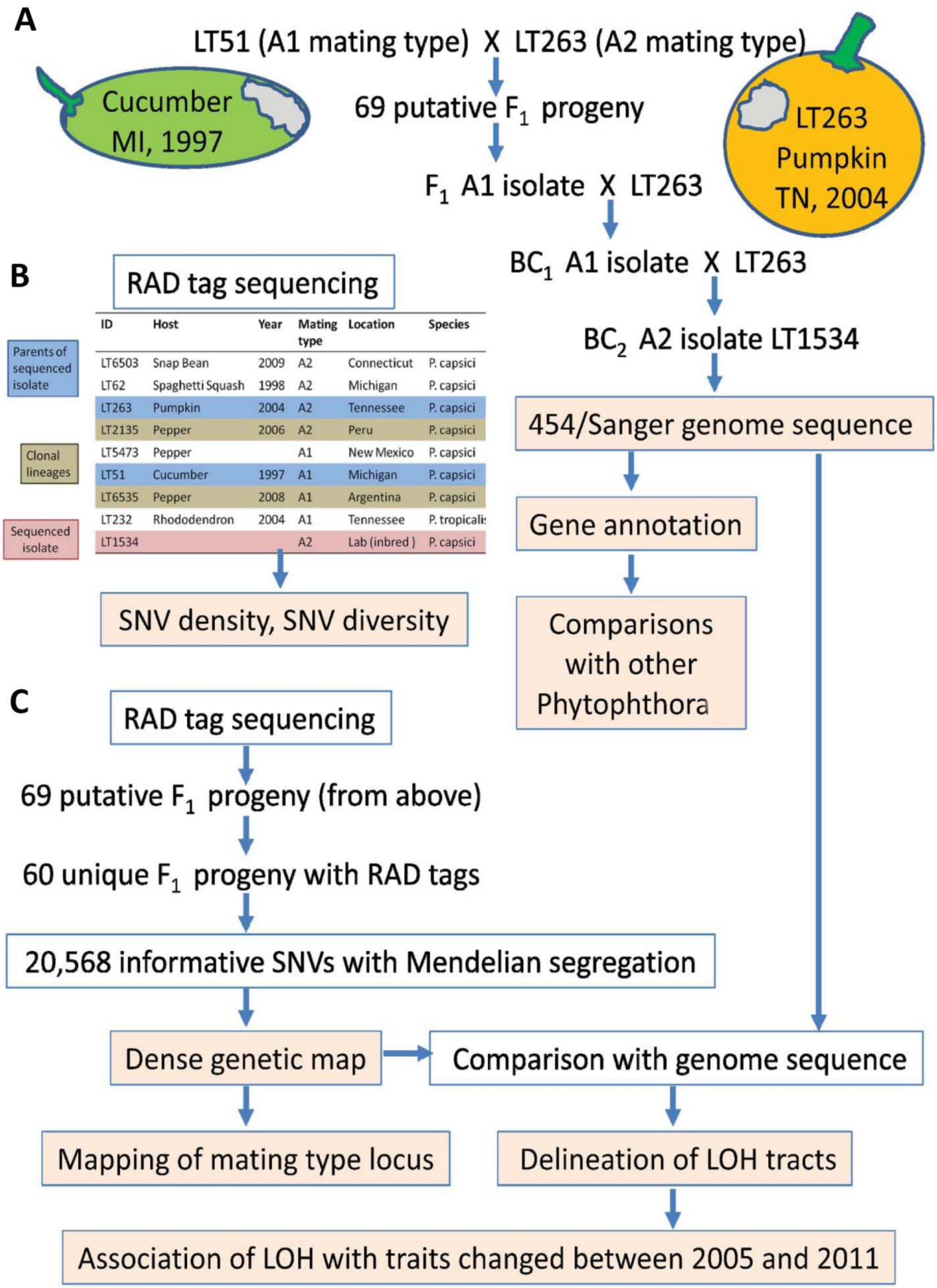


Isolate	TN1	Group 1	18, 34, 53, 63	47	52	6	32, 69	4	25	Group 2	TN2
LOH	No	No	Yes	Yes	Yes	No	No	No	No	No	No
Mating type 2005	A1	A1	A2	A1	A1	A2	A1	A2	A1	A2	A2
Mating type 2011	A1	A1	A1	A1	A1	A1	A1	A2	A2	A2	A2
★ 4_875573	AA	RA	AA	RR	AA	RA	RA	RA	RA	RA	RR
4_877151	AA	RA	AA	RR	AA	AA	AA	AA	AA	AA	RA
★ 4_877466	AA	RA	AA	RR	AA	RA	RA	RA	RA	RA	RR
4_877504	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA	RA
★ 4_880664	AA	RA	AA	RR	AA	RA	RA	RA	RA	RA	RR
4_880689	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA	RA
4_880712	RR	RR	RR	RR	RR	.	RA	RA	RA	RA	RA
4_881577	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA	RA
4_881580	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA	RA
4_881607	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA	RA
4_881629	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA	RA
4_881656	AA	RA	AA	RR	AA	AA	AA	AA	AA	AA	RA
4_882535	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA	RA
4_882547	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA	RA
4_882548	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA	RA
4_883297	AA	AA	AA	AA	AA	RA	RA	RA	RA	RA	RA
4_883314	AA	AA	AA	AA	AA	RA	RA	RA	RA	RA	RA
4_883328	AA	AA	AA	AA	AA	RA	RA	RA	RA	RA	RA
4_883362	AA	AA	AA	AA	AA	RA	RA	RA	RA	RA	RA
4_897805	AA	AA	AA	AA	AA	AA	RA	RA	RA	RA	RA
4_897880	AA	AA	AA	AA	AA	AA	RA	RA	RA	RA	RA
4_898549	AA	AA	AA	AA	AA	AA	RA	RA	RA	RA	RA
4_899846	AA	AA	AA	AA	AA	AA	RA	RA	RA	RA	RA
4_901140	RR	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA
4_901147	RR	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA
4_902744	RR	RR	RR	RR	RR	RR	RA	RA	RA	RA	RA
★ 4_907338	AA	RA	AA	RR	AA	RA	RA	RA	RA	RA	RR
★ 4_907371	AA	RA	AA	RR	AA	RA	RA	RA	RA	RA	RR
4_908701	AA	AA	AA	.	AA	AA	RA	AA	RA	RA	RA

Figure 5

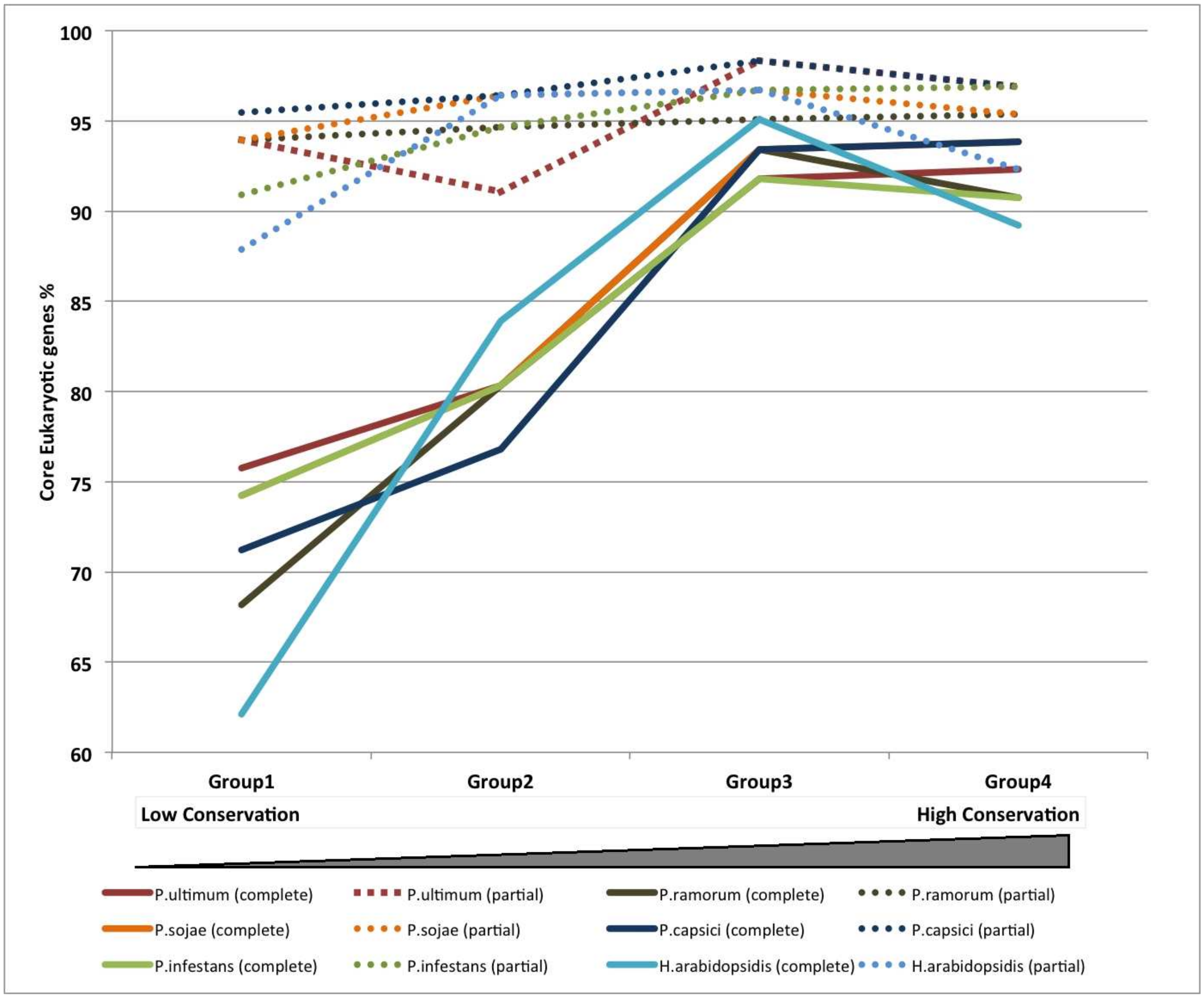
e-Extra supplementary figures and tables

Supplementary Figure 1: Experimental design for molecular and genetic analysis of the vegetable pathogen *P. capsici*. (**A**) Two parental isolates of opposite mating types were crossed. Of 69 putative F_1 progeny, one was backcrossed (BC_1) to parent LT263. A second backcross (BC_2) yielded a moderately inbred isolate (LT1534) for genome sequencing. A hybrid Sanger/454 sequence assembly was performed and gene models were annotated both *ab initio* and using substantial EST and cDNA sequences generated for this project. The *P. capsici* genome and gene content was compared with other Phytophthora species. (**B**) LT1534, the parents, five other *P. capsici* isolates and a *P. tropicalis* isolate underwent reduced representation re-sequencing (RAD, Restriction site-Associated DNA sequencing) by SBS of 72nt tags flanking *Sgr*AI sites. Single nucleotide variants (SNVs) were identified by alignment to the draft reference. SNV density and diversity were calculated. (**C**) *PstI* RAD was performed on 60 unique F_1 progeny from the original cross. 20,568 SNVs had simple Mendelian inheritance and were present in ≥55 of the progeny. The program JoinMap 4.1 was used to test the inheritance of markers from the largest ~100 scaffolds and to generate a genetic map. 18 linkage groups included 90% of the 19,805 predicted genes and covered 84% of the draft genome. Graphical genotypes revealed minimally spanning tracts of LOH in 23 progeny that ranged in length from 299bp to >1Mbp and spanned more than 30% of the genome. LOH was associated with a mating type switch in 4 isolates and with a change in pathogenicity in two isolates over the course of the study.

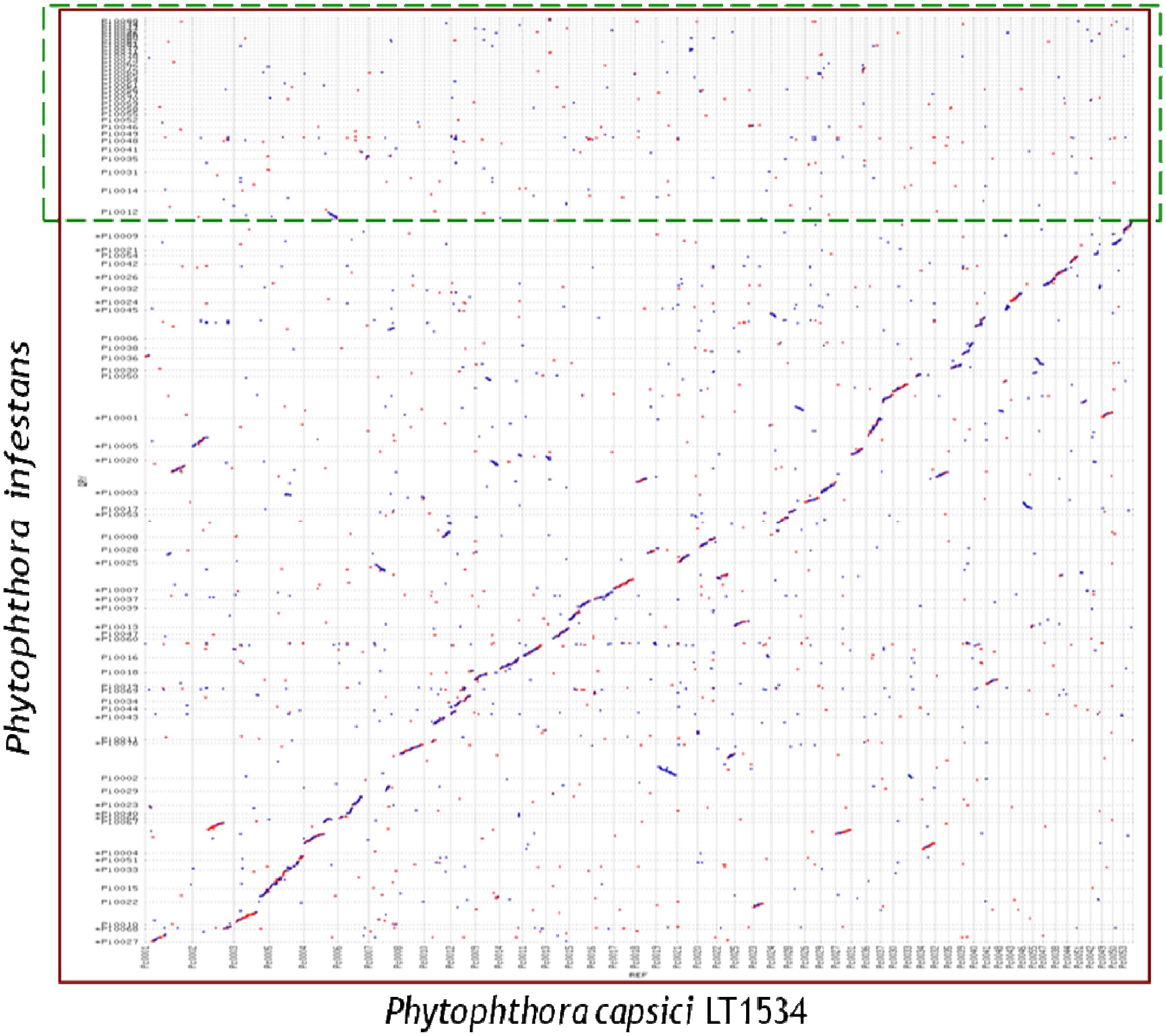


ID	Host	Year	Mating type	Location	Species
LT6503	Snap Bean	2009	A2	Connecticut	P. capsici
LT62	Spaghetti Squash	1998	A2	Michigan	P. capsici
LT263	Pumpkin	2004	A2	Tennessee	P. capsici
LT2135	Pepper	2006	A2	Peru	P. capsici
LT5473	Pepper		A1	New Mexico	P. capsici
LT51	Cucumber	1997	A1	Michigan	P. capsici
LT6535	Pepper	2008	A1	Argentina	P. capsici
LT232	Rhododendron	2004	A1	Tennessee	P. tropicali
LT1534			A2	Lab (inbred)	P. capsici

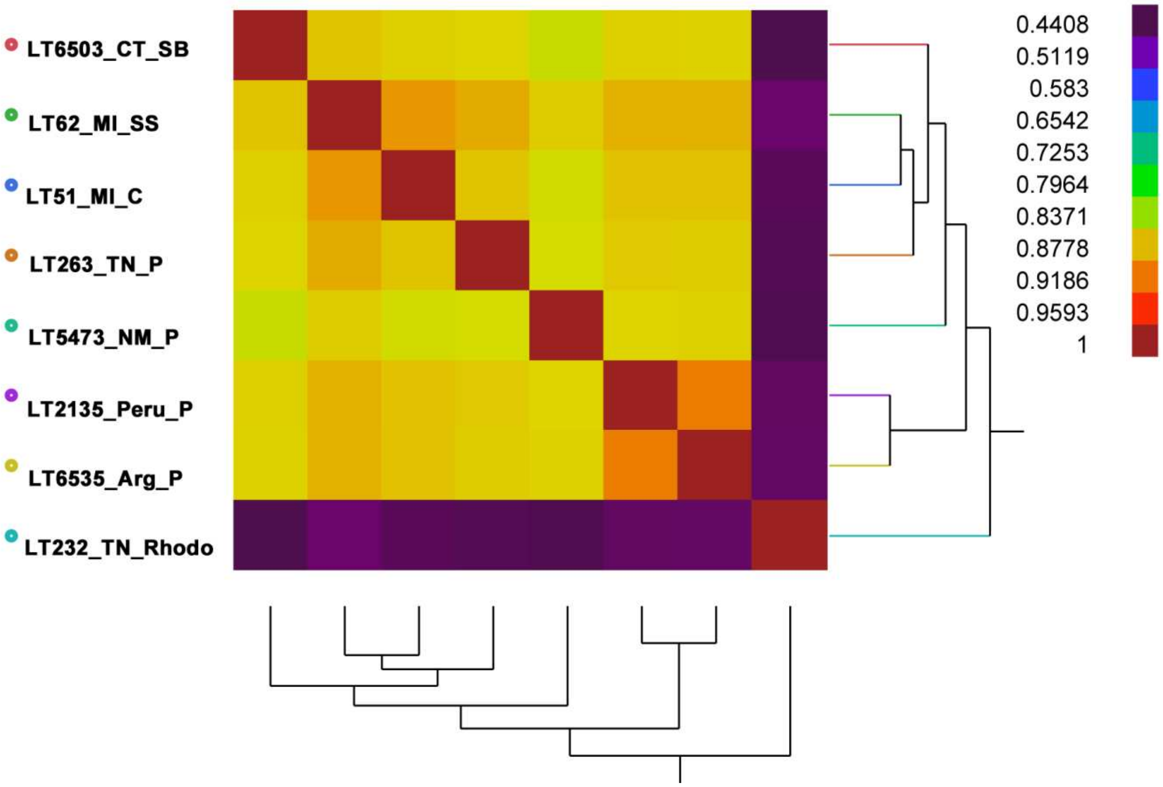
Supplementary Figure 2. Graphical display of CEGMA analyses using standard parameters. *P. capsici* has the highest number of identified core orthologous genes among all oomycete genomes of the *Peronosporaceae* and a comparable amount of fully covered genes. The increase in fully covered genes towards the most conserved ones is a result of the algorithm used for assessing gene completeness in the CEGMA analysis. The high percentage of fully covered genes for CEGMA groups 3 and 4 (most conserved), supports the high continuity of the assembly**.**



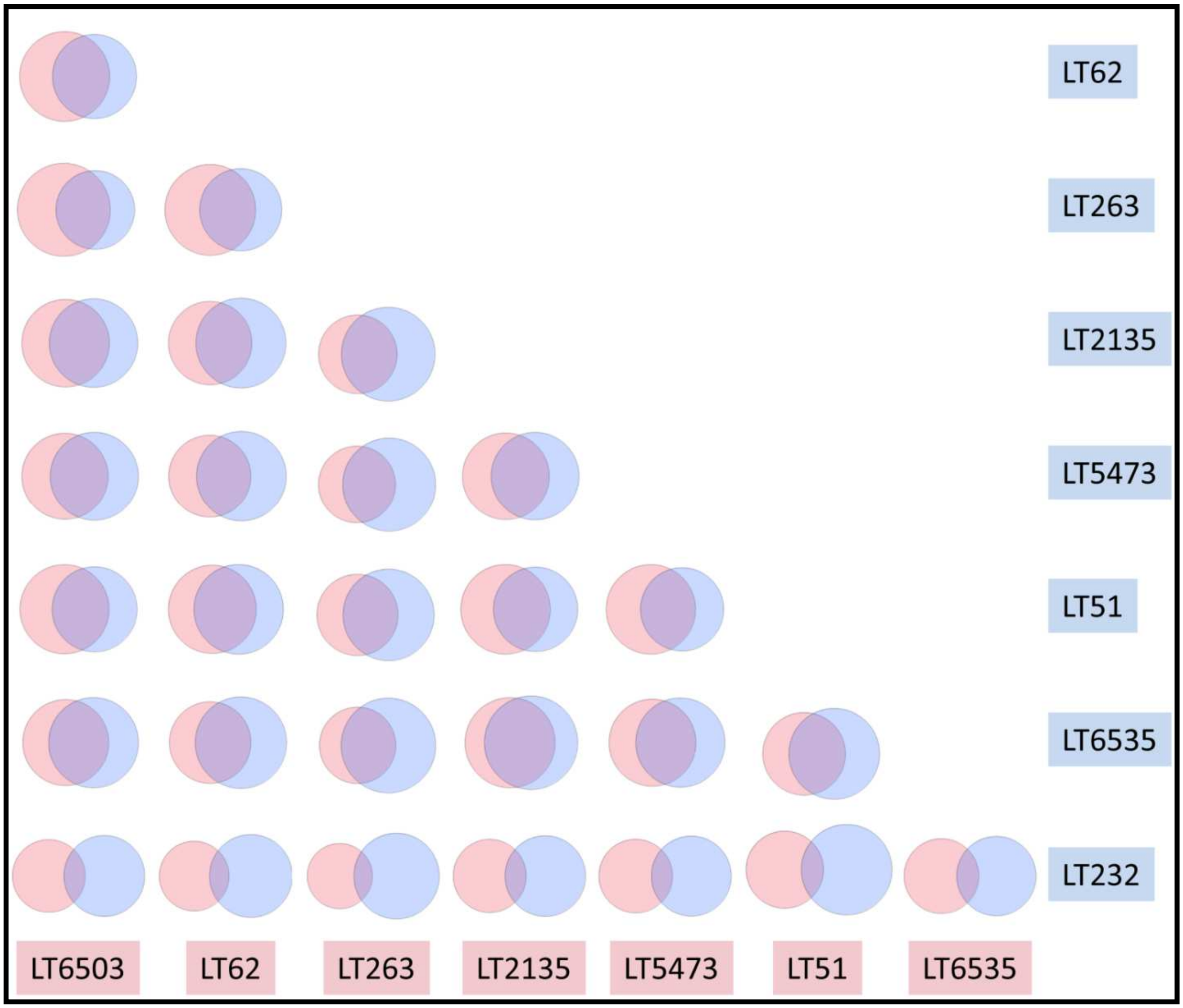
Supplementary Figure 3: Pairwise comparisons of gene models from *P. capsici* with *P. infestans* showed good synteny with some duplications and translocations. Sequences other than gene models were replaced with Ns. Nucleotide sequences were compared using PROmer package of MUMmer, which identifies Maximal Unique Matches in all 6 frames as anchors for amino-acid-based alignment. Large scaffolds (>450 kbp) are shown (155 Mbp for *P. infestans* and 46 Mbp for *P. capsici*). Scaffolds were ordered to maximize the center diagonal. There were some translocations, which possibly were assembly errors. A region (green box) of *P. infestans* had no syntenic genes in *P. capsici.*



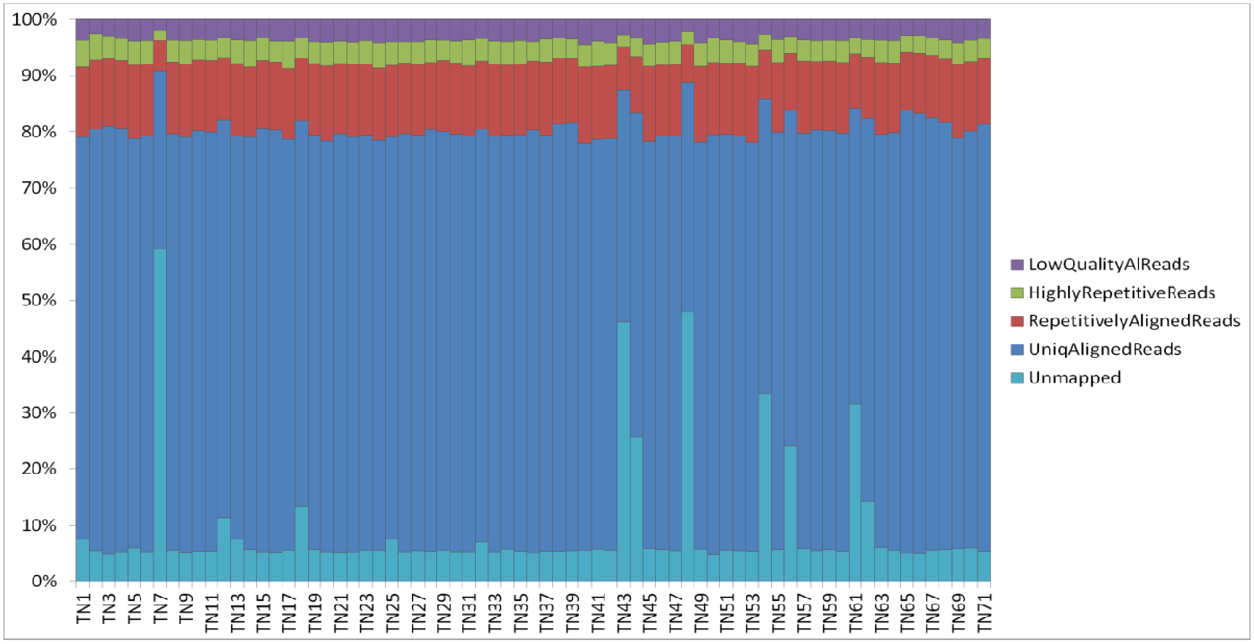
Supplementary Figure 4: Dendrogram and cross correlations for SNVs from 7 *P. capsici* and a *P. tropicalis* (LT232) isolate at regions with 30X coverage in all samples. Left side of the panel indicates isolate origin as abbreviated US state, Peru, or Argentina (Arg) followed by host designated as SB = snap bean, SS = summer squash, C = cucumber, P = pepper, and Rhodo = rhododendron. Branches on the similarity tree on the right side of the panel correspond to isolate directly across. Tree on bottom of panel is identical (isolate LT6503 on the far left) and correlations are designated by color legend on right.



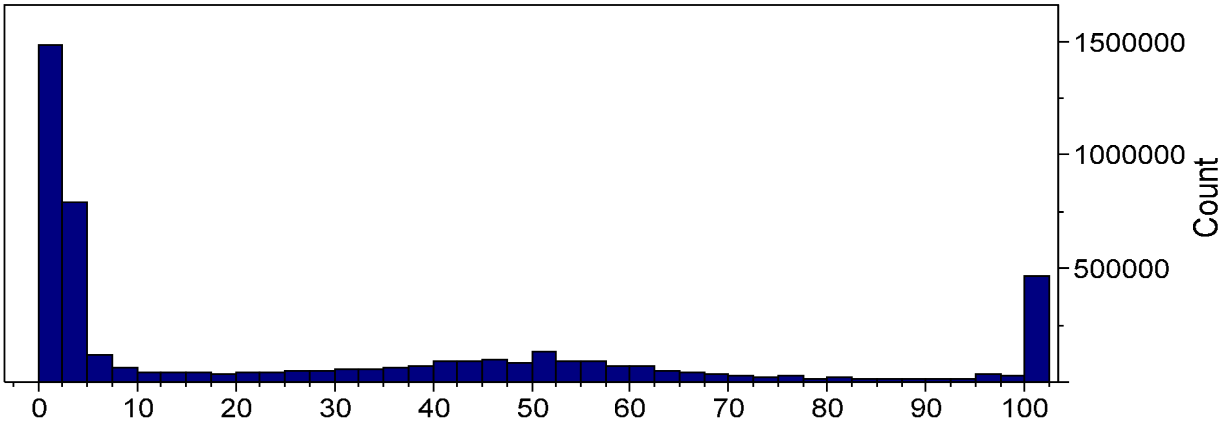
Supplementary Figure 5: Overlap of SNV content of 7 *P. capsici* isolates and one *P. tropicalis* isolate (LT232) sequenced by RAD. SNVs were called at sites with 30X coverage in all samples if supported by ≥ 4 uniquely aligning reads of Q score ≥ 20. Of note, LT263 (recurrent parent of the LT1534) had the fewest SNVs of all *P. capsici* isolates; the two clonal lineages (host = pepper) showed the most overlap; *P. tropicalis* (LT232) showed the least overlap. A total of 64, 537 SNV positions are included. Positions with at least one alternate allele per isolate are LT6503 (20,445), LT62 (17,914), LT263 (14,637), LT2135 (20,869), LT5473 (21,386), LT51 (18,527), LT6535 (22,431), and LT232 (25,308).

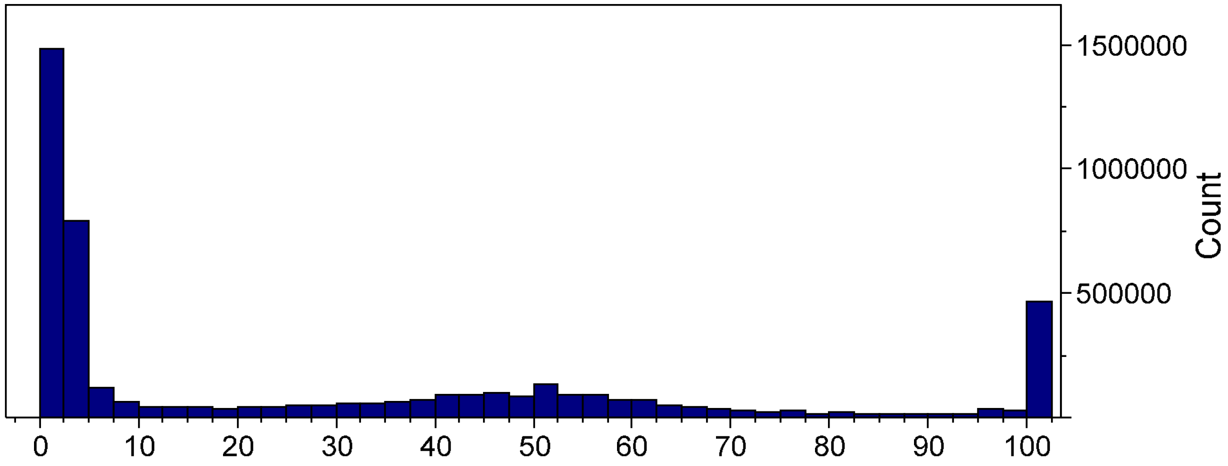


Supplementary Figure 6: Relative abundance of RAD sequences from 69 progeny and two parents based on alignment to the reference *P. capsici* sequence. The X-axis shows isolate ID's and Y-axis shows relative abundance.

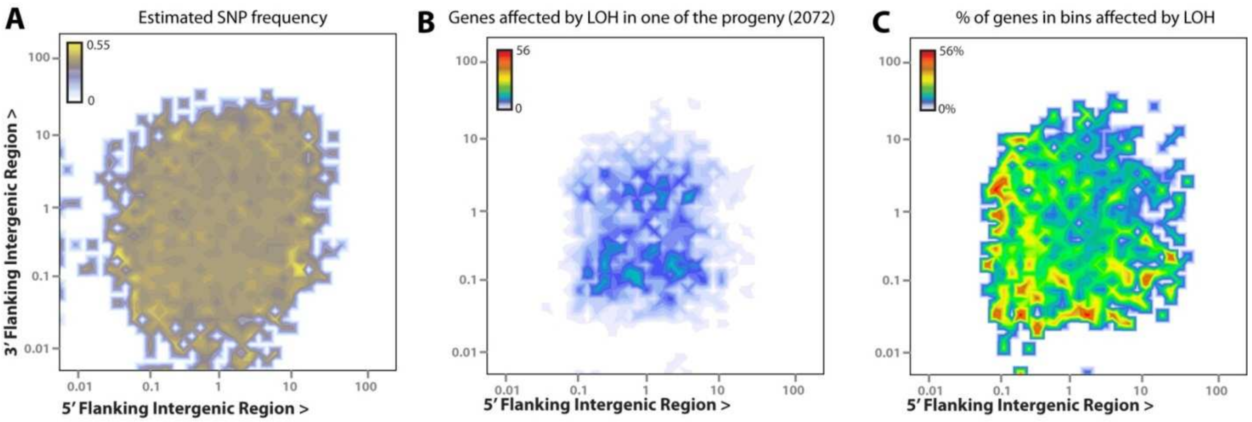


Supplementary Figure 7. Frequencies of alleles based on the requirement for 10X and 20X unique coverage and an average quality of >20 for the alternate alleles. For 10X unique coverage (top) this includes 5,849,663 SNVs and for 20X (bottom) this includes 4,449,193 SNVs across 71 samples.

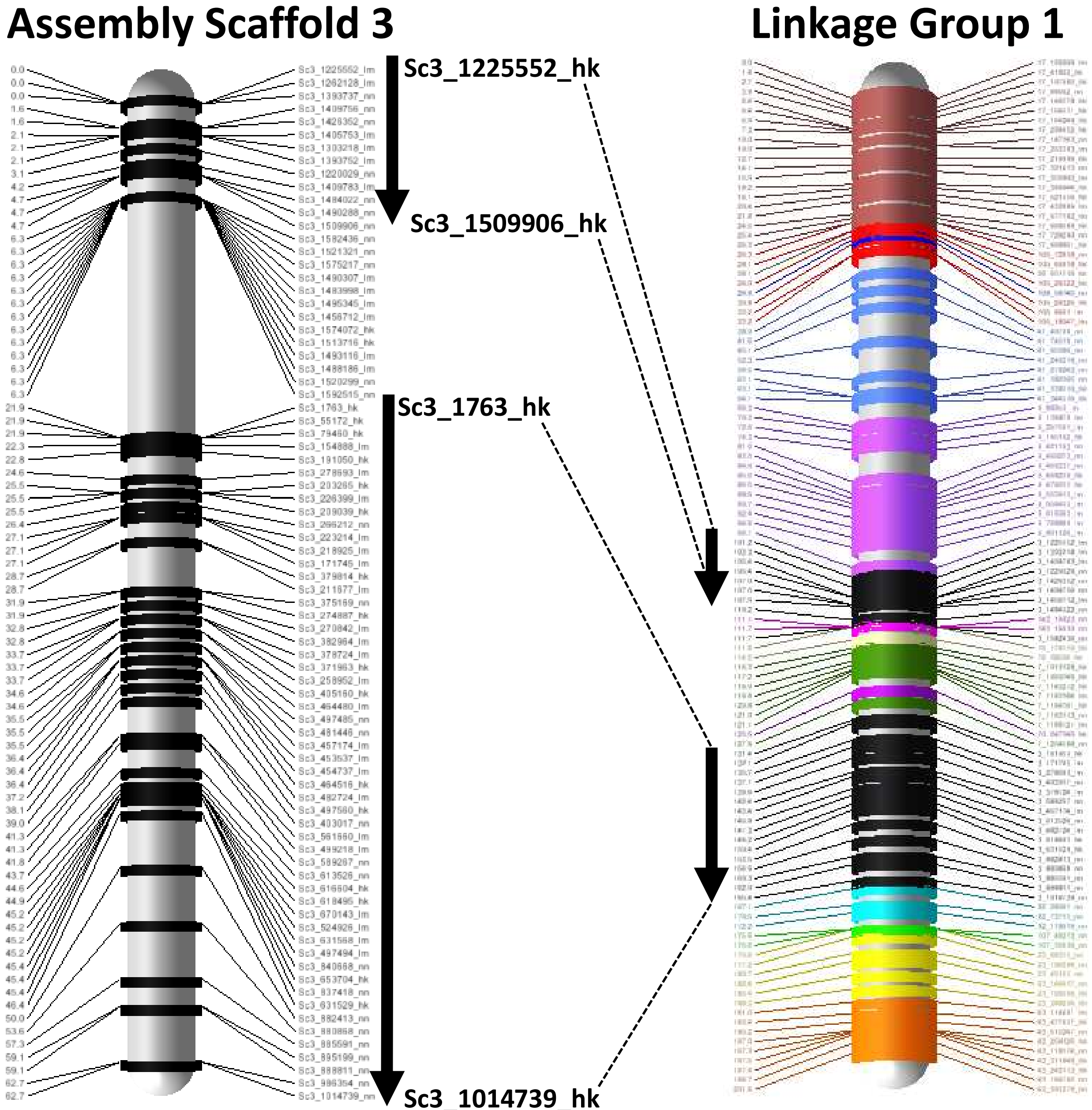




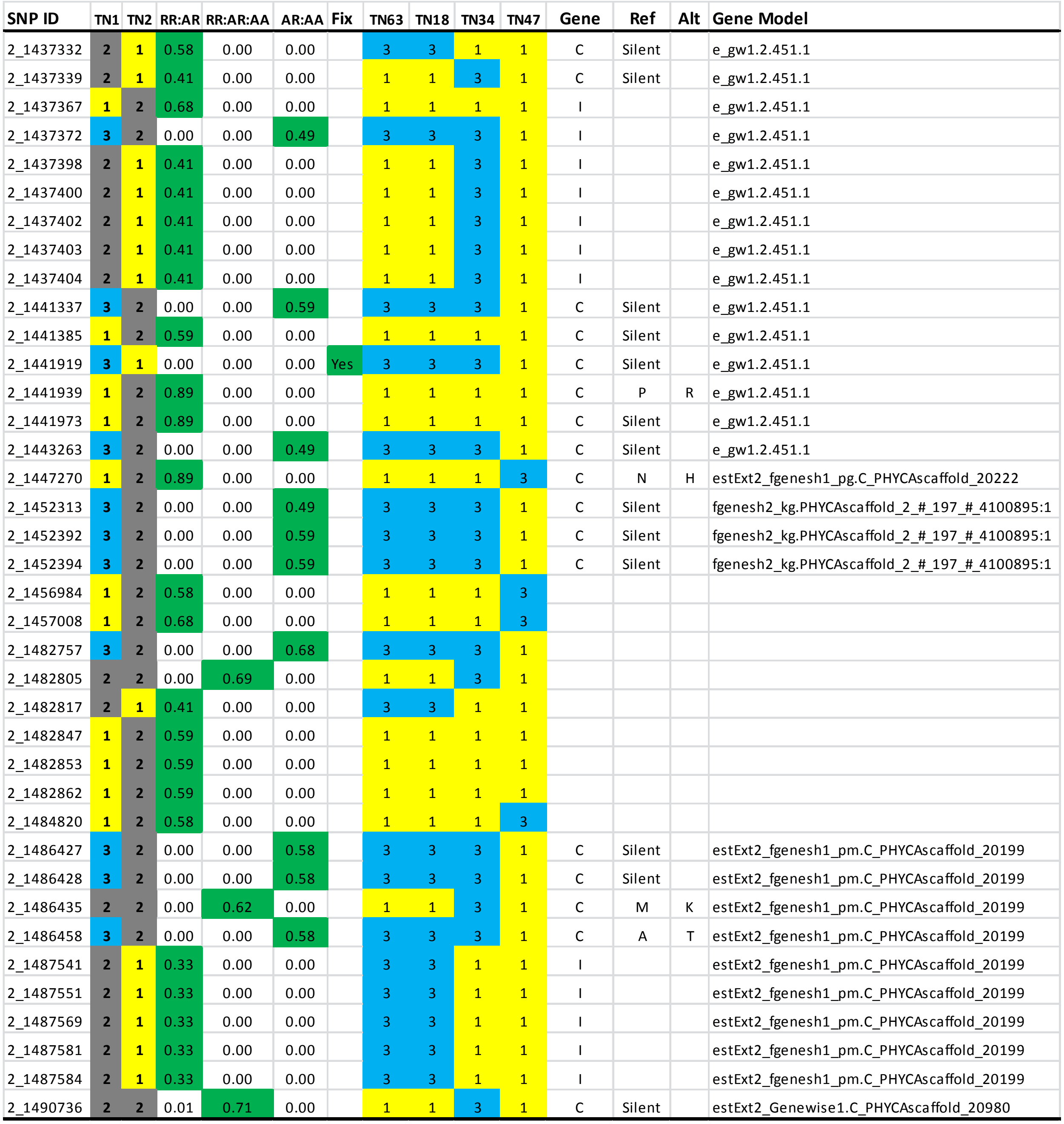
Supplementary Figure 8: Gene-poor environments in *P. capsici* genome show reduced LOH frequency. *P. capsici* genome architecture illustrated by the distribution of all predicted genes according to the length of their 5’ (X-axis) and 3’ (Y-axis) intergenic regions, counted by two-dimensional data binning. (**A**) Estimated SNP frequency is homogenous across the *P. capsici* genome. The SNV frequency was calculated across each individual scaffold (in SNPs per Kbp) and used as an estimate for local SNV frequency of each gene. The average of frequencies for genes in each bin is shown. (**B**) Genome architecture diagram showing only the 2072 genes affected by LOH in at least one re-sequenced strain from the progeny. (**C**)) LOH frequency is reduced for genes residing in a gene-poor environment. The percentage of genes in bins affected by LOH in at least one re-sequenced strain from the progeny.



Supplementary Figure 9: Comparison of the genetic map of *P. capsici* Linkage Group 1 (202cM) with the physical map of Scaffold 3. Two blocks of Scaffold 3 comprising 1.6Mbp contained correctly ordered markers on Linkage Group 1. However, an assembly error occurred between these blocks.

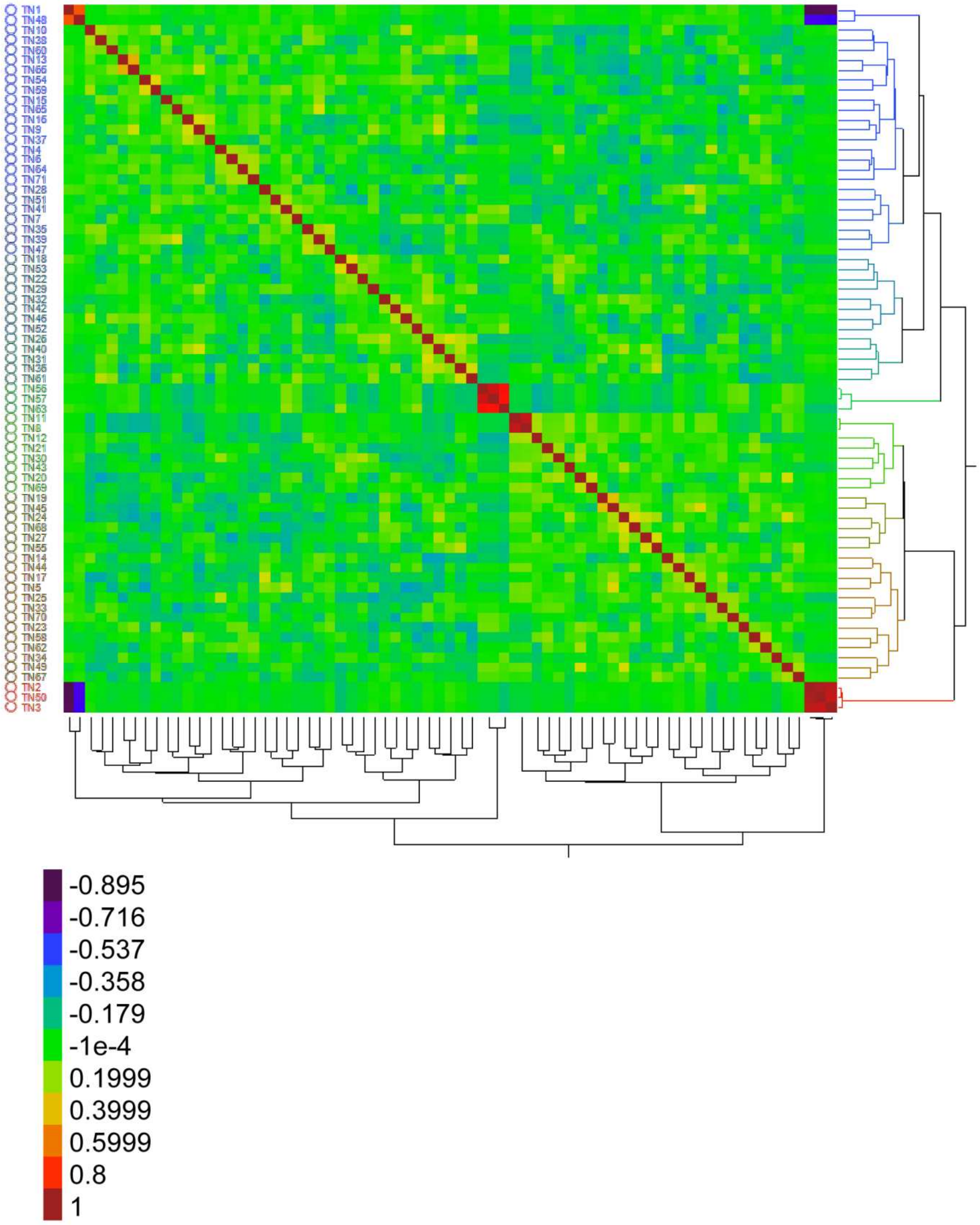


Supplementary Figure 10: Graphical genotypes for four progeny with co-occurring LOH tracts. Genotypes are designated as 1 (yellow) = RR, 2 (gray) = AR, and 3 (blue) = AA (R = reference allele and A = alternate allele). Parent (TN1 and TN2) and progeny (TN63, TN18, TN34, and TN47) genotypes span 38 markers and 53,404 nt on scaffold 2. Columns 4-6 list χ^2 test values (>0.05 in green). Column 7 lists "yes" if all non-LOH progeny are AR for an RR x AA marker. Columns 12 – 15 indicate gene context, the predicted reference amino acid (or "silent" if mutation is synonymous), the alternate amino acid, and the gene model. Note fixation of markers 2_1447270 and 2_1486458 for the reference and alternate allele and the three different composite haplotypes across the entire tract of LOH.



SNP ID	TN1	TN2	RR:AR	RR:AR:AA	AR:AA	Fix	TN63	TN18	TN34	TN47	Gene	Ref	Alt	Gene Model
2_1437332	2	1	0.58	0.00	0.00		3	3	1	1	C	Silent		e_gw1.2.451.1
2_1437339	2	1	0.41	0.00	0.00		1	1	3	1	C	Silent		e_gw1.2.451.1
2_1437367	1	2	0.68	0.00	0.00		1	1	1	1	I			e_gw1.2.451.1
2_1437372	3	2	0.00	0.00	0.49		3	3	3	1	I			e_gw1.2.451.1
2_1437398	2	1	0.41	0.00	0.00		1	1	3	1	I			e_gw1.2.451.1
2_1437400	2	1	0.41	0.00	0.00		1	1	3	1	I			e_gw1.2.451.1
2_1437402	2	1	0.41	0.00	0.00		1	1	3	1	I			e_gw1.2.451.1
2_1437403	2	1	0.41	0.00	0.00		1	1	3	1	I			e_gw1.2.451.1
2_1437404	2	1	0.41	0.00	0.00		1	1	3	1	I			e_gw1.2.451.1
2_1441337	3	2	0.00	0.00	0.59		3	3	3	1	C	Silent		e_gw1.2.451.1
2_1441385	1	2	0.59	0.00	0.00		1	1	1	1	C	Silent		e_gw1.2.451.1
2_1441919	3	1	0.00	0.00	0.00	Yes	3	3	3	1	C	Silent		e_gw1.2.451.1
2_1441939	1	2	0.89	0.00	0.00		1	1	1	1	C	P	R	e_gw1.2.451.1
2_1441973	1	2	0.89	0.00	0.00		1	1	1	1	C	Silent		e_gw1.2.451.1
2_1443263	3	2	0.00	0.00	0.49		3	3	3	1	C	Silent		e_gw1.2.451.1
2_1447270	1	2	0.89	0.00	0.00		1	1	1	3	C	N	H	estExt2_fgenesh1_pg.C_PHYCAscaffold_20222
2_1452313	3	2	0.00	0.00	0.49		3	3	3	1	C	Silent		fgenesh2_kg.PHYCAscaffold_2_#_197_#_4100895:1
2_1452392	3	2	0.00	0.00	0.59		3	3	3	1	C	Silent		fgenesh2_kg.PHYCAscaffold_2_#_197_#_4100895:1
2_1452394	3	2	0.00	0.00	0.59		3	3	3	1	C	Silent		fgenesh2_kg.PHYCAscaffold_2_#_197_#_4100895:1
2_1456984	1	2	0.58	0.00	0.00		1	1	1	3				
2_1457008	1	2	0.68	0.00	0.00		1	1	1	3				
2_1482757	3	2	0.00	0.00	0.68		3	3	3	1				
2_1482805	2	2	0.00	0.69	0.00		1	1	3	1				
2_1482817	2	1	0.41	0.00	0.00		3	3	1	1				
2_1482847	1	2	0.59	0.00	0.00		1	1	1	1				
2_1482853	1	2	0.59	0.00	0.00		1	1	1	1				
2_1482862	1	2	0.59	0.00	0.00		1	1	1	1				
2_1484820	1	2	0.58	0.00	0.00		1	1	1	3				
2_1486427	3	2	0.00	0.00	0.58		3	3	3	1	C	Silent		estExt2_fgenesh1_pm.C_PHYCAscaffold_20199
2_1486428	3	2	0.00	0.00	0.58		3	3	3	1	C	Silent		estExt2_fgenesh1_pm.C_PHYCAscaffold_20199
2_1486435	2	2	0.00	0.62	0.00		1	1	3	1	C	M	K	estExt2_fgenesh1_pm.C_PHYCAscaffold_20199
2_1486458	3	2	0.00	0.00	0.58		3	3	3	1	C	A	T	estExt2_fgenesh1_pm.C_PHYCAscaffold_20199
2_1487541	2	1	0.33	0.00	0.00		3	3	1	1	I			estExt2_fgenesh1_pm.C_PHYCAscaffold_20199
2_1487551	2	1	0.33	0.00	0.00		3	3	1	1	I			estExt2_fgenesh1_pm.C_PHYCAscaffold_20199
2_1487569	2	1	0.33	0.00	0.00		3	3	1	1	I			estExt2_fgenesh1_pm.C_PHYCAscaffold_20199
2_1487581	2	1	0.33	0.00	0.00		3	3	1	1	I			estExt2_fgenesh1_pm.C_PHYCAscaffold_20199
2_1487584	2	1	0.33	0.00	0.00		3	3	1	1	I			estExt2_fgenesh1_pm.C_PHYCAscaffold_20199
2_1490736	2	2	0.01	0.71	0.00		1	1	3	1	C	Silent		estExt2_Genewise1.C_PHYCAscaffold_20980

Supplementary Figure 11: Dendrogram of SNV cross correlations derived 23,809 SNVs from 2 parents and 69 putative progeny *P. capsici* isolates. Isolate names on the left side of the panel correspond to the tree branches directly across on the right side. The same tree is reproduced on the bottom of the panel with isolate TN1 on the far left to create the cross diagonal. Correlations are designated by color legend at bottom of panel.



Supplementary Table 1: Arachne hybrid assembly version11 (20 Aug 2010) of *P. capsici* LT1534 454-Titanium and Sanger gDNA reads.

Scaffold count	917
Contig count	10,760
Scaffold bases total (Mbp)	64
Contig sequence bases total (Mbp)	56
Estimated % sequence bases in gaps	12.5%
Scaffold N50 / L50 (# / kbp)	29 / 706
Contig N50 / L50 (# / kbp)	397 / 35
Number of scaffolds > 50.0 Kb	140
% in scaffolds > 50.0 Kb	91.9%
% assembly masked by repeats	14.4%
# finished cDNAs	1260
% finished cDNAs that align with assembly	97.1%

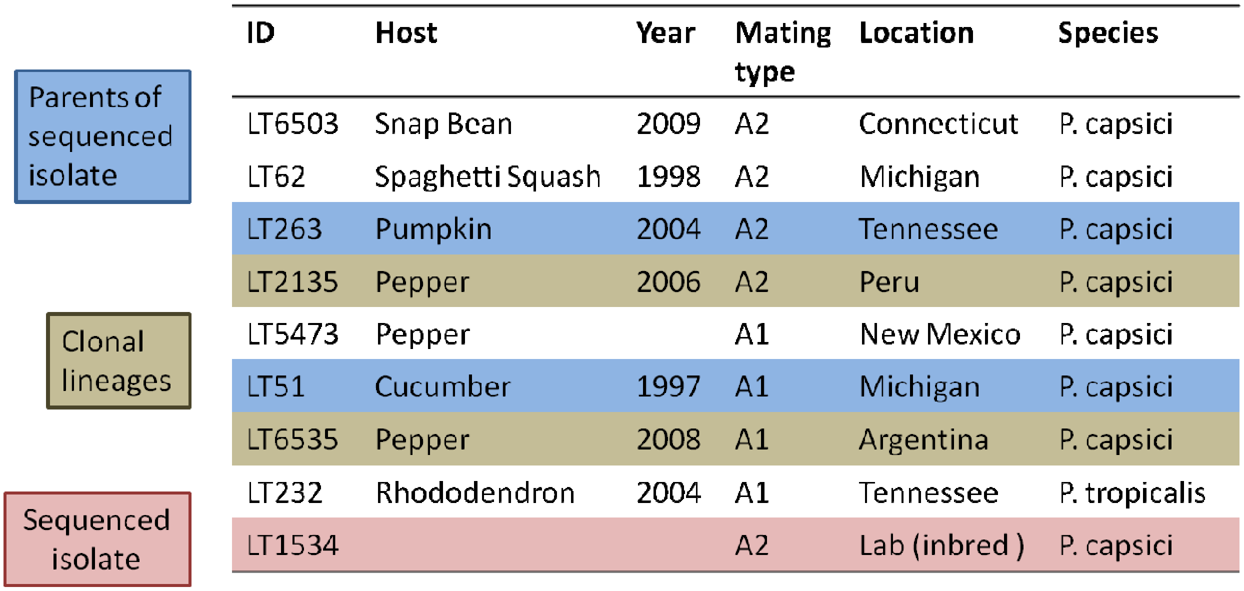
Supplementary Table 2. *Phytophthora capsici* filtered gene models classified by prediction method. Annotation v11 (20 August 2010) was produced by the JGI Annotation Pipeline, using a variety of cDNA-based, protein-based, and *ab initio* gene predictors.

Prediction method	# models
Total	19,805
protein-based	14624 (74%)
cDNA-based	2920 (15%)
ab initio	2261 (11%)

Supplementary Table 3. Properties of the 19,805 *P. capsici* filtered gene models, including genes with homology to transposable elements.

Property	Value
Avg. gene length	1253 nt
Avg. transcript length	1028 nt
Avg. protein length	314 aa
Gene density (per Mbp scaffold)	309
Avg. exon length	467 nt
Avg. intron length	189 nt
Avg. exon frequency	2.2 per gene
Multi-exon genes	9861 (50%)
Genes with similarity to proteins in nr	14925 (75%)
Genes in LT1534 multigene family	15489 (78%)
Genes supported by ESTs	9981 (50%)
Genes with Pfam domain	9234 (47%)
Genes with signal peptide	3162 (16%)
Genes with transmembrane domain	2890 (15%)
Genes with EC number	2821 (14%)
Genes with GO term	8544 (43%)
Complete models (with start and stop codons)	69%

Supplementary Table 4: Field isolates chosen for RAD sequencing (first 8 isolates)



Parents of sequenced isolate

Clonal lineages

Sequenced isolate

ID	Host	Year	Mating type	Location	Species
LT6503	Snap Bean	2009	A2	Connecticut	P. capsici
LT62	Spaghetti Squash	1998	A2	Michigan	P. capsici
LT263	Pumpkin	2004	A2	Tennessee	P. capsici
LT2135	Pepper	2006	A2	Peru	P. capsici
LT5473	Pepper		A1	New Mexico	P. capsici
LT51	Cucumber	1997	A1	Michigan	P. capsici
LT6535	Pepper	2008	A1	Argentina	P. capsici
LT232	Rhododendron	2004	A1	Tennessee	P. tropicalis
LT1534			A2	Lab (inbred)	P. capsici

Supplementary Table 5: RAD sequencing statistics.

Isolate	Reads	Reads Aligned	Reads Uniquely Aligned
LT6503	8.1 M	7.0 M (86%)	6.0 M (73%)
LT62	7.8 M	6.8 M (86%)	5.8 M (74%)
LT263	8.1 M	7.2 M (88%)	6.2 M (76%)
LT2135	7.4 M	6.4 M (86%)	5.4 M (73%)
LT5473	8.4 M	7.2 M (85%)	6.1 M (72%)
LT51	8.5 M	7.4 M (87%)	6.3 M (74%)
LT6535	5.9 M	5.1 M (85%)	4.3 M (72%)
LT232	5.0 M	0.8 M (16%)	0.7 M (14%)

Supplementary Table 6: Single nucleotide variants (SNV) in RAD sequenced isolates.

Sample	Nt with $\geq$ 30X coverage	SNVs	SNVs/kb
LT6503	1,761,096	20,445	24.88
LT62	1,714,370	17,914	22.08
LT263	1,829,566	14,637	16.87
LT2135	1,631,155	20,869	25.52
LT5473	1,760,096	21,386	26.04
LT51	1,903,934	18,527	22.30
LT6535	1,597,281	22,431	25.88
LT232			51.67

SNV detection required at least 30X coverage of that nucleotide in all samples and at least 4 uniquely aligning reads with Q scores of at least 20 to call the variants. The *P. tropicalis* (LT232)/*P. capsici* SNV/kb ratios were identical at both 10X and 30X coverage and in comparisons of all samples. These SNV densities are conservative because the regions had to contain the 6 nt invariant endonuclease site and sufficient reads to align at 90% identity in order to meet the 30X cutoff. Densities were increased to ~26/kb when the coverage requirement was decreased to 10X, and to ~33/kb when the restriction for 30X coverage in the *P. tropicalis* isolate was waived.

Supplementary Table 7: Distribution of SNVs among seven *P. capsici* isolates and one *P. tropicalis* isolate. Bi-allelic SNVs = 59,471; tri-allelic SNVs = 2,413; tetra allelic SNVs = 80; total SNVs = 61,964

# isolates with a given SNP	Number of SNPs
1	34,065
2	8,447
3	5,470
4	4,265
5	3,479
6	3,243
7	4,309
8	1,259

Supplementary Table 8. Summary statistics of RAD sequences generated for the parents and 69 putative progeny.

	Parents and Progeny	Parents	Progeny
Total	158,460,781	9,588,155	148,872,626
Mean	2,231,842	4,794,078	2,157,574
Median	1,655,467	4,794,078	1,646,382
Std. Dev.	1,602,718	138,864	1,563,741
Min.	594,851	4,695,886	594,851
Max.	8,951,606	4,892,269	8,951,606

Supplementary Table 9. **Summary of the markers for each of the linkage groups.** The parental isolates differed at ~25% of the 20,568 loci. TN1 had 5273 RR, 8632 AR, and 6663 AA genotypes, whereas TN2 had 8141 RR, 11767 AR, and 660 AA genotypes (where R = reference allele and A = alternate allele). The smaller proportion of AA genotypes in TN2 reflected its use in backcrosses that produced LT1534, the reference genome.

Linkage Group	SNPs	RR:AR	AR:AR	AR:AA	AA:RR
1	3003	1576	453	519	455
2	1277	625	275	264	113
3	1324	702	204	253	165
4	532	269	139	98	26
5	1621	807	264	333	217
6	839	448	122	156	113
7	448	231	51	92	74
8	1493	865	210	274	144
9	925	465	161	159	140
10	2940	1330	447	684	479
11	1412	704	138	219	351
12	871	386	108	279	98
13	933	493	94	198	148
14	547	217	50	63	217
15	687	319	242	104	22
16	1231	493	43	293	402
17	371	134	80	63	94
18	114	78	22	0	14
Total	**20568**	**10142**	**3103**	**4051**	**3272**

Supplementary Table 10. **Summary of genic and non-genic markers showing simple Mendelian inheritance.**

Linkage Group	Coding Silent	Coding Non-Silent	Intron	3'	5'	Non-Gene	Genes Per Linkage Group	Total Genes in Linkage Groups
1	858	488	382	215	48	1012	716	2,271
2	384	218	107	82	32	454	309	1,016
3	392	187	160	96	27	462	382	1,146
4	176	89	26	24	14	203	140	648
5	450	286	170	97	25	593	371	1,392
6	274	144	43	37	17	324	152	646
7	111	66	44	21	4	202	91	467
8	427	238	114	77	18	619	365	1,087
9	277	157	96	80	16	299	242	1,076
10	800	492	355	196	47	1050	645	1,941
11	378	244	124	75	30	561	357	1,267
12	249	141	51	64	13	353	197	870
13	285	147	57	47	16	381	190	778
14	164	100	36	26	15	206	203	570
15	207	104	63	42	6	265	178	655
16	322	204	130	100	25	450	288	1,194
17	95	62	23	27	6	158	157	546
18	23	15	12	4	1	59	34	119
Total	**5872**	**3382**	**1993**	**1310**	**360**	**7651**	**5017**	**17,689**

Supplementary Table 11. Summary for linkage of scaffolds breaking into blocks with LOD scores ≥7.

Scaffold Block	Lowest Marker	Highest Marker	Total Covered	Linkage Group
Sc1.1	1_53205	1_945508	892303	LG9
Sc1.2	1_1041839	1_1173436	131597	LG2
Sc1.3	1_1283380	1_2077147	793767	LG11
Sc2.1	2_113526	2_546537	433011	LG13
Sc2.2	2_731366	2_1916562	1185196	LG10
Sc4.1	4_87661	4_936084	848423	LG10
Sc4.2	4_953874	4_1526218	572344	LG12
Sc7.1	7_95189	7_945588	850399	LG13
Sc7.2	7_961256	7_1255438	294182	LG1
Sc12.1	12_27274	12_214345	187071	LG18
Sc12.2	12_711003	12_1052066	341063	LG14
Sc13.1	13_112552	13_176739	64187	LG11
Sc13.2	13_290642	13_1028147	737505	LG2
Sc14.1	14_454507	14_856026	401519	LG14
Sc14.2	14_893013	14_991161	98148	LG11
Sc18.1	18_98284	18_475978	377694	LG11
Sc18.2	18_597329	18_965332	368003	LG2
Sc21.1	21_96574	21_533490	436916	LG2
Sc21.2	21_630881	21_910293	279412	LG5
Sc22.1	22_56130	22_491901	435771	LG3
Sc22.2	22_536539	22_839077	302538	LG08
Sc23.1	23_45180	23_357600	312420	LG1
Sc23.2	23_653052	23_764546	111494	LG2
Sc24.1	24_9834	24_190368	180534	LG7
Sc24.2	24_227914	24_769629	541715	LG5
Sc25.1	25_17541	25_427916	410375	LG15
Sc25.2	25_657899	25_803448	145549	LG6
Sc26.1	26_63597	26_631721	568124	LG8
Sc26.2	26_641731	26_706136	64405	LG1
Sc42.1	42_26570	42_320442	293872	LG14
Sc42.2	42_349280	42_479514	130234	LG17
Sc48.1	48_22671	48_192342	169671	LG10
Sc48.2	48_212975	48_350345	137370	LG3

Supplementary Table 12. Summary data for linkage groups and scaffold blocks.

LG/order	Scaffold Block	Scaffold Block Size	LG Total Nts
LG01.01	Sc43	531,961	
LG01.02	Sc23.1	312,420	
LG01.03	Sc82	207,552	
LG01.04	Sc107	135,171	
LG01.05	Sc3	1,611,504	
LG01.06	Sc70	280,435	
LG01.07	Sc7.2	294,182	
LG01.08	Sc9	1,114,135	
LG01.09	Sc41	565,801	
LG01.10	Sc109	125,037	
LG01.11	Sc26.2	64,405	
LG01.12	Sc105	102,149	
LG01.13	Sc17	985,188	**6,329,940**
LG02.01	Sc13.2	737,505	
LG02.02	Sc23.2	111,494	
LG02.03	Sc172	15,116	
LG02.04	Sc11	1,076,090	
LG02.05	Sc18.2	368003	
LG02.06	Sc1.2	131,597	
LG02.07	Sc21.1	436,916	**2,876,721**
LG03.01	Sc48.2	137,370	
LG03.02	Sc95	141,949	
LG03.03	Sc30	669,438	
LG03.04	Sc65	307,771	
LG03.05	Sc37	577,888	
LG03.06	Sc51	529,628	
LG03.07	Sc22.1	435,771	
LG03.08	Sc64	301,055	
LG03.09	Sc102	120,866	
LG03.10	Sc560	6,948	
LG03.11	Sc800	3,230	**3,231,914**
LG04.01	Sc6	1,423,605	
LG04.02	Sc86	162,230	
LG04.03	Sc44	536,020	**2,121,855**
LG05.01	Sc10	1,190,366	
LG05.02	Sc63	355,987	
LG05.03	Sc68	334,182	
LG05.04	Sc24.2	541,715	
LG05.05	Sc50	475,612	
LG05.06	Sc21.2	279,412	
LG05.07	Sc52	444,141	
LG05.08	Sc80	185,445	

LG05.09	Sc60	366,873	
LG05.10	Sc67	292,061	
LG05.11	Sc112	78,237	**4,544,031**
LG06.01	Sc87	182,599	
LG06.02	Sc118	67,328	
LG06.03	Sc139	29,350	
LG06.04	Sc191	15,330	
LG06.05	Sc93	150,113	
LG06.06	Sc108	116,431	
LG06.07	Sc25.2	145,549	
LG06.08	Sc89	163,789	
LG06.09	Sc81	202,973	
LG06.10	Sc132	34,092	
LG06.11	Sc39	591,971	
LG06.12	Sc92	170,487	
LG06.13	Sc74	127,009	**1,997,021**
LG07.01	Sc24.1	180,534	
LG07.02	Sc106	144,267	
LG07.03	Sc77	232,015	
LG07.04	Sc16	1,020,712	**1,577,528**
LG08.01	Sc26.1	568,124	
LG08.02	Sc8	1,194,346	
LG08.03	Sc161	37,761	
LG08.04	Sc22.2	302,538	
LG08.05	Sc58	327,658	
LG08.06	Sc72	230,452	
LG08.07	Sc66	294,895	
LG08.08	Sc62	322,952	**3,278,726**
LG09.01	Sc5	1,593,284	
LG09.02	Sc100	129,988	
LG09.03	Sc103	136,111	
LG09.04	Sc1.1	892,303	
LG09.05	Sc90	152,720	**2,904,406**
LG10.01	Sc34	622,686	
LG10.02	Sc40	570,383	
LG10.03	Sc4.1	848,423	
LG10.04	Sc27	705,730	
LG10.05	Sc2.2	1,185,196	
LG10.06	Sc84	182,275	
LG10.07	Sc49	508,508	
LG10.08	Sc48.1	169,671	
LG10.09	Sc28	757,753	
LG10.10	Sc79	222,129	**5,772,754**
LG11.01	Sc1.3	793,767	
LG11.02	Sc32	608,388	
LG11.03	Sc97	154,197	

LG11.04	Sc18.1	377,694	
LG11.05	Sc29	707,326	
LG11.06	Sc31	686,815	
LG11.07	Sc14.2	98,148	
LG11.08	Sc13.1	64,187	**3,490,522**
LG12.01	Sc71	252,329	
LG12.02	Sc38	550,336	
LG12.03	Sc94	190,298	
LG12.04	Sc53	465,517	
LG12.05	Sc91	167,065	
LG12.06	Sc4.2	572,344	
LG12.07	Sc57	397,303	**2,595,192**
LG13.01	Sc36	679,425	
LG13.02	Sc111	91,577	
LG13.03	Sc2.1	1,925,921	
LG13.04	Sc61	347,729	
LG13.05	Sc7.1	850,399	**3,895,051**
LG14.01	Sc12.2	341,063	
LG14.02	Sc14.1	401,519	
LG14.03	Sc42.1	293,872	
LG14.04	Sc101	136,107	**1,172,561**
LG15.01	Sc15	1,032,281	
LG15.02	Sc25.1	410,375	
LG15.03	Sc46	525,601	**1,968,257**
LG16.01	Sc20	899,172	
LG16.02	Sc19	944,885	
LG16.03	Sc33	640,966	
LG16.04	Sc35	603,175	
LG16.05	Sc55	463,907	**3,552,105**
LG17.01	Sc104	135,144	
LG17.02	Sc42.2	130234	
LG17.03	Sc47	556,112	
LG17.04	Sc54	427,428	
LG17.05	Sc85	206,069	
LG17.06	Sc73	348,431	**1,803,418**
LG18.01	Sc12.1	187,071	
LG18.02	Sc78	194,772	**381,843**
Totals	**125**		**53709626**

Supplementary Table 13. **Flanking markers and tract lengths for isolates with loss of heterozygosity.**

Linkage Group	Isolate	1st LOH	Last LOH	Tract Length
LG01	TN37	3_1774	3_901039	899265
LG01	TN37	3_956368	3_1023899	67531
LG01	TN60	3_1032846	3_1165737	132891
LG01	TN65	3_1032846	3_1165737	132891
LG01	TN37	7_960715	7_1232128	271413
LG01	TN37	9_76547	9_313726	237179
LG01	TN37	17_31860	17_976370	944510
LG01	TN47	17_29488	17_870195	840707
LG01	TN37	23_32662	23_422316	389654
LG01	TN37	26_642307	26_711717	69410
LG01	TN37	41_23637	41_340818	317181
LG01	TN37	43_20676	43_531378	510702
LG01	TN37	70_203860	70_279147	75287
LG01	TN37	82_27984	82_206524	178540
LG01	TN37	105_6822	105_76260	69438
LG01	TN47	105_51382	105_63734	12352
LG01	TN37	107_2162	107_50059	47897
LG01	TN37	109_25479	109_78466	52987
LG03	TN15	30_22501	30_610494	587993
LG03	TN31	30_22501	30_610494	587993
LG03	TN15	48_309043	48_463219	154176
LG03	TN31	48_203358	48_463219	259861
LG03	TN31	65_43166	65_189594	146428
LG03	TN15	95_68974	95_100010	31036
LG03	TN31	95_11127	95_120313	109186
LG04	TN25	6_517600	6_1330434	812834
LG06	TN45	39_45571	39_218172	172601
LG06	TN45	39_269905	39_467526	197621
LG06	TN45	74_57229	74_92332	35103
LG06	TN45	81_83924	81_172214	88290
LG06	TN37	87_72040	87_152869	80829
LG06	TN45	89_41061	89_116125	75064
LG06	TN45	92_10433	92_128655	118222
LG06	TN45	132_10333	132_22914	12581
LG07	TN60	16_155019	16_945332	790313
LG07	TN65	16_134053	16_974846	840793
LG08	TN3	8_159857	8_160156	299
LG08	TN47	8_148811	8_1163217	1014406
LG08	TN13	26_91745	26_340248	248503
LG08	TN3	26_142703	26_609109	466406

LG08	TN47	26_63564	26_620971	557407
LG08	TN37	66_126127	66_190579	64452
LG09	TN50	1_87441	1_742969	655528
LG09	TN50	90_44554	90_110297	65743
LG10	TN18	2_734379	2_1650759	916380
LG10	TN34	2_734379	2_1555552	821173
LG10	TN47	2_932367	2_1752644	820277
LG10	TN53	2_734379	2_1062403	328024
LG10	TN63	2_734379	2_1650759	916380
LG10	TN18	4_86143	4_936679	850536
LG10	TN34	4_86143	4_936679	850536
LG10	TN47	4_42590	4_936704	894114
LG10	TN52	4_86143	4_936679	850536
LG10	TN53	4_86143	4_936679	850536
LG10	TN63	4_86143	4_936679	850536
LG10	TN18	27_8619	27_697509	688890
LG10	TN34	27_8619	27_697509	688890
LG10	TN47	27_1128	27_697509	696381
LG10	TN52	27_8619	27_297350	288731
LG10	TN53	27_8619	27_697509	688890
LG10	TN63	27_8619	27_697509	688890
LG10	TN18	28_38583	28_704354	665771
LG10	TN18	34_47706	34_548650	500944
LG10	TN34	34_47706	34_548650	500944
LG10	TN47	34_27259	34_571709	544450
LG10	TN52	34_47706	34_548650	500944
LG10	TN53	34_47706	34_548650	500944
LG10	TN63	34_47706	34_548650	500944
LG10	TN18	40_53500	40_510721	457221
LG10	TN34	40_53500	40_510721	457221
LG10	TN47	40_53500	40_510721	457221
LG10	TN52	40_53500	40_510721	457221
LG10	TN53	40_53500	40_510721	457221
LG10	TN63	40_53500	40_510721	457221
LG10	TN18	48_66747	48_185568	118821
LG10	TN18	49_163203	49_500583	337380
LG10	TN18	79_90923	79_155337	64414
LG10	TN18	84_57519	84_178288	120769
LG10	TN63	84_57519	84_177335	119816
LG11	TN54	1_1282528	1_2051166	768638
LG11	TN54	18_96129	18_475984	379855
LG11	TN62	31_358469	31_633967	275498
LG11	TN54	32_50547	32_548375	497828
LG11	TN54	97_62889	97_123104	60215
LG12	TN64	4_1416514	4_1526252	109738

LG12	TN64	53_92504	53_418139	325635
LG12	TN64	57_52048	57_123257	71209
LG12	TN64	91_44469	91_134135	89666
LG13	TN63	7_132139	7_207249	75110
LG13	TN63	7_346854	7_427074	80220
LG13	TN66	36_95503	36_626762	531259
LG15	TN17	15_476066	15_890139	414073
LG15	TN44	15_476066	15_838906	362840
LG16	TN25	19_412214	19_765034	352820
LG16	TN37	19_412214	19_765034	352820
LG16	TN70	19_412214	19_765034	352820
LG16	TN25	33_58644	33_570713	512069
LG16	TN37	33_58644	33_570713	512069
LG16	TN58	33_508481	33_570693	62212
LG16	TN70	33_58644	33_570713	512069
LG16	TN23	35_141346	35_556998	415652
LG16	TN25	35_141346	35_556998	415652
LG16	TN37	35_141346	35_556998	415652
LG16	TN58	35_141346	35_556998	415652
LG16	TN70	35_141346	35_556998	415652
LG16	TN23	55_62577	55_381570	318993
LG16	TN25	55_25260	55_381570	356310
LG17	TN47	85_67570	73_215288	147718

Supplementary Table 14. Summary of total nucleotides affected by LOH per isolate.

Isolate	Total LOH Coverage
TN13	248,503
TN62	275,498
TN44	362,840
TN17	414,073
TN03	466,705
TN58	477,864
TN66	531,259
TN64	596,248
TN45	699,482
TN50	721,271
TN23	734,645
TN15	773,205
TN60	923,204
TN65	973,684
TN31	1,103,468
TN70	1,280,541
TN54	1,706,536
TN52	2,097,432
TN25	2,449,685
TN53	2,825,615
TN34	3,318,764
TN63	3,689,117
TN18	4,721,126
TN37	5,556,816
TN47	5,985,033

Supplementary Table 15. Source and version of genomes used for CEGMA analysis.

Organism	Source	Genome version	Reference
Phytophthora ramorum	http://genome.jgi.doe.gov/Phyra1_1/Phyra1_1.download.ftp.html	1.0	Tyler et al. (2006)
Phytophthora sojae	http://genome.jgi-psf.org/Physo3/Physo3.home.html	3.0	Tyler et al. (2006)
Phytophthora capsici	http://genome.jgi-psf.org/PhycaF7/PhycaF7.home.html	11.0	
Phytophthora infestans	http://www.broadinstitute.org/annotation/genome/phytophthora_infestans/MultiDownloads.html	4.1	Haas et al. (2009)
Pythium ultimum	http://pythium.plantbiology.msu.edu/download.html	Release 1	Levesque et al. (2010)
Hyaloperonospora arabidopsis	http://vmd.vbi.vt.edu/download/index.php	8.3.2	Baxter et al. (2010)

Supplementary Table 16. Predicted Crinkler amino acid sequences and gene names.

Gene Name	Amino Acid sequence
>jgi|104199|e_gw1.9.417.1	MVKLFCAIVGEAGSAFSVEVDETDSVDDLKTAIKAVNEDITCPPRKLQLFLAKKADGTWLDGAGAAAVTVDEADRVPLMLDKHGNHHKFVKMNPLLWIKNDQHFGENFRPVHVVVVVPDVAHAQTGLWLVTGFVKNALNTKGIRCKLYWMATLRIGYYDPARRTDKKNVAFWYEDTKLCFHVLFETKDAALLFETDLRIEPQTLGSPLTNQVVETRVAPVNAVSTELQRVFYGDYVPDDSKSPQNSVSSISLTTSGSNLDSSTDEFRFQRIEHEKFFLPYGKAESCHLVSRKQSRNHKREFAKYDRDSNSRLALSRDMHGWFDGMSIEVPIVNMLPGSVKENQSIGNRRKVVEVFVKVLDAGCTDRVFSRLKEGSTTTNDPLMMKTFVHVEDPETFCLCMRWKHDDNAERWRSFWDMTPAVD*
>jgi|106435|e_gw1.12.217.1	MLKLFCVVVGVAGDAFPVNIEPNETVGDMKKKIKHEEMYQFPASELQLFLAKVPKEKHDMAWLSSRSEDVKKLKKGEKTPLIDILTEEDQELQAEDPLDDVLRGMDPPSLCQIHVLVMAPPQDSLRSHLTTLLSVLLCHVLTKAPTTPTDRNVDFKDDVCNFYGCYSPDESCVRCMLLNDAFPSELVVASHLFRCSNEDVSDVMMQITLSDIDDERNGLLLFKPLKYAFDHFQISFIRDDTDVFRLKVFDPSILATPIVDLKDRKGNKVLSTEQTQLLLSRISENPCRFNTQTTFGDVDDSALTFTGLERPFYRCLNLQARVARVMALEKKWIDASYDFQDFWSEVSLDDKMEMFHRSILNS*
>jgi|106457|e_gw1.12.537.1	MKLFCAMVGMAVGIIEVDIDNNAYVTALRDAIATKNEEIKKSALRLKLFLAKKGNAWLTDTEAAGVGGDLESLGFKLMKSVRLLKNPEYFGEDFQTGEGHVHVLVVVPEENMTVGEPVVDVDGVNIYVTSNMTLNPPDLVAFWRAFQAIDTKIEADSVIALPEGTFILGNPKVGSRIYIRPCYPQLWEVCWHIIHHETPNLVILGNPGIGKTYFGYLLLLFLARLGKTVVYESRRTKRRFLFSRNVVIKGSQQDFDDILEQDTTYYVVDAMEPREFQARTILVTSPDRDVWYTFNKISCQTRYMPVWTEQEIFSCREQVYSTIPKSVVQKCFYRWGGIPRYVLQYAQFDNHQALIEKALEVVDFDWLMNAYGKLDDNNSQAHRLLHYRVNERFTCDYFGFASSFVQHEVYQHLHKKEKRKLLEFIGRSVGSGDLSVLRDRLAEEHDHHCARTHKKLKRF*
>jgi|106668|e_gw1.12.123.1	MVKLFCAIVGVEGSVFSVVIGEGQTVEELKKAIKERNDDKINVSWLGLQLFLAKKAKGDGDWLTEKDVQEGVYDMSDLQMLRAARAKLRLVKLSDNDVNEEQKVEGGKSVNVLVVLPGLTTTIKVNERENNALTDELAYYQRIGQEIQSNCQQHCGPILDKIDSIYEKKPYPMPFICVQGSSGMGKSQLAFALGGEGREHPRPWFYWTHGTVSDYDQRIYRNFASIGSAFDSVVWKDEVRKEEEDDILNCTSVLYMTKKLWTYGFIIELLRYCSRSNVGAQMVRVENQTFYVTKSNLEDVIEVRSRMEKNGEVLPFFILDEMPPSRTKKLSAFQLNVFRACGLVVIGMGTDANISNLVGKPEHSRTDPHWWMTVVSCFPPWQSIPFGDPAKEEVWQKVIELHPVVKHIAEHSRGLFSRCFVDAVVKFAMEEVSENETFALADLLDAAFKAVYAELRITKGFMFTEEGRDAQLMALSYTIGSNKPPGTKRPVTDSDSTSEPTPKRRKLDVDVGVASMRAHFANSGYEGIADVDVLQGDLRFRDTSDAWSPICQFPAIEKDVLLYLAVLGGKKFSDYNDTSSTLDVFEEFLERNGNREESNALRRDFTNFIKFENVVAHALFCASRRNGARGIALYEFLSGLVSEFQDEYYQRDEFDASALLKEFDGLKEKFAEKKIPFLAPPNARWPDYILEAGGDCNFGHFERMDGYVMVPGVDGPLFACDCQYWKDDLDSDAMKKIIAGLNGGATGCGDDQQKPKWSNWSLALVFCRKLEEFESEQREDWEFPSTGIATVDCKAWEVNWISKPEAGEKLVIVVQTGRVLCLP*
>jgi|106736|e_gw1.12.192.1	MMKLFCAIVGVAGSAFSVEVNEDQTVEDLKTAIKNQNRMSVDANDLQLFLAKKKNGNRVEWLTQLDVVKGVMDANGFTHLQFADAKLRAVGLKSSELVEVNEEDVAVGKGHVHVLVKIDQTAPNVELMPFTSTCWLVTGSGVNALNTRGVRGQLYRLAHTELGYYDPANVRTDTGNIPRAFWHENNDIQIHVLFKKEEHALYFQSHLVDDFSIPIKSFVSKAPCPTDLQRIFRDHYVADETVSPQLSMFSSEISVFDPSNPVFKYQRIEAERLFGSHGKAESAHLISASHCRNVTSYDEYDKDDNNRLALSREMHGAYDGINCDFPLVNIEVVSASDHPELDHRFKVELQVSVYSHEYVFLLGRLKDGSTKTEDPLVMKTFVYVQDKNIFCTCIQWKYNKNRQLREEFFTTNPRAT*
>jgi|108643|e_gw1.15.666.1	MAKLSLSCVIVGLMGSAFSVDIDADQFVGDLKKIIQKKKNDLHNVDADKLQLFLAKKDKGWLPDKSEAALELKKGEVHEDIQVLINGEEMEATKTLNYWLFEKNQMEEQLSSEQIHVLVVVPEIRDGKKRYRSSLWFAESEPLKKRRVKTDESEDEDDDVSEERTFFQLCGCPPMAHPARKDSKLMERKAYTVIFAQLVEHVKDCFEFNRTSNNPGLSSNVVVTGNPGIGKSW

	FYLYCIFQLIRNREREDIKQLPPYELVMNYDDNFVKYDAARAEFVRLNKEDVDDLMDKPFVLRLVDARSTKLMGWRGVSVLFAVPDAEDLHDFEKVPGPKFIMPAWSLEELQDCNQVLPDDLKLAEDELVSRFDAFGGIPRYVFSKNKTAIENKLKRAMASFSVKEILSYCKRGAAVKESDQSDCVLQMVPSEANFRLKFYLDFLSSDICEKIVFQAEGEDLTMLAKFAMGK*
>jgi|110274|e_gw1.18.174.1	MVKFFCAIIGVAGSAFPVDIDASLSVGDLKNAIKGKNDDIKCTARELQLFLAKKEKGAGAWLTEDEAAAVSLDEGGHLQGFKMMKSSLYLKNPKHFGSNFQSDEDQVHVLVVVPDQAQPQTGLWLVTASVENALNTKGIRCRLYRLMASYLGYYDPVRRTGDKDTALWYEDKTLCIHSIFKSEENALLFDNVLQDECITQTSPLDGHDVSTNVAPVSRQLSELRRIYSRHYAPQDTESPQVSMLSISTNTSIVDVMTDEFKYQRIESEEWFGDVGKAQSCHLMSRDHCRKCPSDRKYDNDPNNRLALSSAMHDWYDGRMYNVPVMNISVESVSERPVIGNRYKVNLIVRALNARYAKWISLILKEGFVASEDSLEMHTCVYVQNPKVFCVCMEWKRKEIDKQWKSYYDMEPAVD*
>jgi|112192|e_gw1.21.161.1	MVKLFCAIVGAMESAISVEVGEGLTVGDLKKAIATDQKFDFAASKLQLFLTETEGGGWLSSEDDAAIAMRTGAIPEQVKKLLKDEIDPAEEIGDKFGSAPTKKTIHVLVVVPEGVTNVTAATVFENNRKRRREDDQPDFWMKAIEDDKVLTLPLTCEELKEHLQRELPVKIPLGGRLSQIVESQNVAGKMNSKLFDTEARHSVTDVTVAILNGVIAPVWIGGESPTEATYHFLWNEVIAKVLMYVSDGTCSRNSSVFTSTGLFRPNLCFYNSANDKVCVFRGEEQARGEMTVPLTDLQRLTWRYDDAPYVFGYAAVAQDVCLVTIRESETNAPGEKRRAKVEIIERYNLRDLRGRLSIFLALLNLSTLFRPVVGRIRPLGIAEYKTIIRPNGVKIAFGENCVVKTYPLTMPSDKIISDLRDLHWQMKENAVPNVVELKSTNMRKRSVELAPVGRQLPLENVHQLLMAMRDILRALVALHTIGLMHRDLRWENVLRYPDEDKWFLIDFDEGASSPAVKVDHLKAETHAPEILSSSTHTTMVDIWSVGYLLETSHVHDLPVALEDIKTQCLQENPSVRPTAQSLLEAVEALIAN*
>jgi|113302|e_gw1.24.271.1	MVFASQDNDFNRCSNPFFSQLPTAEETDEWLEFPSLLPLTRRRSLYIRPSFKSIAAQALLKVDSNRRKYAVVTGTPGIGKSVFLYYVMWKLIKDKKRMLFVTGRPPIYFDGESVLDCYQLPYAGNRNFWSPDLWCLVDATNPCKIAGLPIHHCSVLLASEPRDDYVRHFRKLVPTPQVFYMPIWTEEEMEKIIPLYPSAASVWRDRFETLGGIPRLVLQAVQTDPQEFMRVCFYSLENCMRLVLFHSKTKTGFIDSLYTLEMPRHVHILSQEPYHEYTLAYASETAMRAVIDAKWIVNRAEMLHFLVMNLKSTDSLTQTTCHCIFELYAMQLLELGGTFSYRSLQAGVEQSSETLDEDENDIDIPMSWREIVDRVEADQNEDQLYVPKSAKDVAIDAWMPEVGGFQIALGKEQKIKSQAADELALLGQGGNRLFFLVFPRDFDSFTKQEPLSIEQYALLIPYPEV*
>jgi|114043|e_gw1.25.260.1	MVMVKIFCKIVGEAGSIFSVKIDDSESVEDFMRKIKDRCDGKIVAPWMDLQLFLAKKKDGVWLTKRDVLEVTSELDPLDDTLAPLNSVGLSEEDVRYRMTKEDIKAKKVPVHVLLVVPTEDYLRSPATILLETILPHVLTHATTTLTEDNRDFRHNLCNFYGCYTREQSLVRCMLLDVPLPKSLVLASHLFRRSNEYLSFRMMQISDIDDVKNGLLLFKPLKYAFDHFQISFIRDDTDVFRLKLFDSTIKETPLIDLVDHHGKKVLSEEQTGELLSDVNNDTCLFDVGKTFGDVDGCALAFTGIERPYYHCLNLQARVALMVALKKGWIDESYDFKDFWSEVSLDDKMEMFHRSILNSVADI*
>jgi|117630|e_gw1.33.284.1	MIKLFCAIVGEERNVIEVDISDVESISALKEAIKTKMPITLKYVDANTLQLFPAKMPDDKWLRDDSVAADDLMSGRIHDDIKAMIADSKILRPACRIRDELSAKKTGWKWSLPWSPITPKIKTKQIHVLVKVPDMMTGTLPLCGVAPEAQWRLWQSIVRVTSGTYSGTALVLHRSSRNLYLLTNLHFWLAEYEEEEIFFEHMSAGFKMNVELYLKRNPRKKRSGKQKSDGGELQQTFNGSPVVIVDQLLPGHTTLTEVHSFVFKSDACWCSSVDYDYAVFKVLAPPPRIQLLGVEPSVSHFPTNVYVFGFHDGHEEKKFGHSYAIVPARIKYHRYKCLILSLSTVSLPESGVICTSRGLSIGYLAGSTIDESGNEVNQWLELGFFRRIL*
>jgi|128631|e_gw1.77.29.1	MVKLFCAIVGDPSWSFEVDIDENVSVSELNKAIKTKNKIKLKCVDANDLQLFLAKTDGPSGGKVWLDRAGAAAVETDDLHRFTRMDSTLYVRNPKHFGSGFKPDEGQVHVLVVVPKWAVEAETIGQNVERVGLPRTTALNDPKKYAEEIIALDDWGVNTVHQIPSIWEFMSSLSGCTKTGELFWRLEEKQVASLLLDGWFRESSPGSINQFEDMKSILMGSPGIGKSTLLCVMAFHLVLKYKKNVLVYRQLKGENCLLYLGYEDDEVVYFTVKRCKADRAVSIYEELGYRQGFPNVWLLLDGFRYKEIPEGLETFRMLATSQQVSLKSQESTDAYCCLLPCWSKKDLLSMGSLIYNFTPDEMEERFFYSGGSVREFTYATWEDIQRAMDVAVSGVEDYSKLLTTASCMFTDTSQVVRTFVENTNDRSHYFSSRYWEPMVDSEYAVLALSVRLKADALHRIYTWAKMAGHGSLAGCAFEIYLHRLAIDNRLEL
>jgi|129711|e_g	MMKLFCAVVGEAESVFHVDIEPGETVSDLKDAIKEINKHDPVLKNVTAMNLQLFLAKK

w1.86.23.1	GGAWLSGDDPAVLELEEGEIHPDILEMMDAKPMLDDKTLQFLLFEKNKLPQPSTNQIHVLVEIPAGARAIPYSNRPPKPFVSSEGATWDFQNPLDNEQLSNAIRKHYDAWKRGYYDKILHPLFTCWSGPGTGKSRLLDEFPKLLKDWLFAGKSENPDMIRLLQNAFTFNIAFDKETPHEAGSFSSAAELIGTRMLYQLQDTLKWDPFVQEKSRHSVPSDVMDKLSKILGTRHKDMCVILCVDGMEKLSHENGGKDCEFYKVLTVLSYLIGTSKCWVIAICSATIYSPVKNFLLSSPQWAYEVPTAILSRPTVEGEDIFATFNGDQLIELLIDDMGGFGRALEVLHVMMRKARRKGSLEFMSVLTAVLAELRVLYPRIKKKMASMQEAFLAVVARRPVDKYSRFGKLSLDDVISTGLVRREGRFLTCPYVLYLLLDTPDSPWSKYKCYSSQETRENAKPWQTWEAFNYKLRALKSVACQGKVDWRDIHRGARFGRGCYRVVIEEPRTYSLDVNRKTAKLDGFGEGNIFRCKYDPDQQGYFFEDAFTGVKDAESRAFHEIHQCKKIKDNLSLEDLLEEKKKAAGPHDLFLLYCTSEVEGDIESLENCAVVDRTCWEKYYGPFAARALYVSTVSPPDINTSAIQSLQLVNGIGPAISKRIVEKRPYSSLEEAHEKTGVSMNILSQTSCKRSKVDK*
>jgi|131973|e_gw1.125.9.1	MKLFYVIVGVAGSPFPVDIEPSETVGDLTKAIKKENKCRFKHVDAYDLQLYLAKKDKGNGAWLTEDDVATVRDDAVFQTYKLMKPTLFLNNTEICGESINQCDVHVLVKAPMRLPTIHQLHYRHFTVGSVDIRTKKSMTFDPPPLVRFWRALQGDRTEFKADAVLTLPEGTFLLGNPMLGSRIYIRHCYPRLWQVCLKMINDEAMNTPHLVILGNPGIGKTYFGYVILWLLARSGNTVVYESRVCHRRFLFSQDMVVQGSKKDFIEILEQTTTYYVVDGVEPRYYSAKTILLTSPQREVWYEFNKDDCRSCYMPVWSRDEVLTCRELMYSDIPESVVQDCFRRWGGIPRYVLHYATAGGRQQWLEKAMENITLDSLMDACGDLYENPSEESLHLLHYRVTKEFNTDYFDFASQYVLEEVYRRLYNHNKKKLLEFIDKSGWVGAAAVLRDHLFEVYTVAASLTDEDGDGVAVEQFKANKLL*
>jgi|20879|fgenesh1_pg.PHYCAscaffold_75_#_8	MVKLFCAVVGVQGSAFPVDIDASQSVGDLKDAIKTKNKIKLKNIDASDLQLFLAKPKDGPWLRSDDSDVIRMRSGAIPEQVKKLLNEQIDPAAGIGALFGDAKPTMEIHVLVRVPDYDSDSEVNQQRKLTSFQKLRKESGATGELPVQGDFMKLFDLTDDDIGKVLDIKAIGDIVGFTGSEFYIRKEILTSDQWSGSARLLVAMIAQDNPNWKNIMGELGVINCTQLSLNNDTKVSTTVDASQFIARNNQLQVLPDSD*
>jgi|39322|gw1.83.18.1	MVELSLQCAIVGQIGRSFDVEIDDGKKVSKLKEMIQVKNRETIKCDAKDLRLFLAKMGPPTTTQLLKIWKKESTDGNSPFSFIPEFGEMVKLFYLNNMFIQEEQMELPSTDQIHVLVVVPPPDVGSKRSADIEVAKVLKRLKMIEPKVLTEFIPLPVPEKEFQLDNLSMVQQSDDPIVMTPTLHEFWKKFGEFPLYYFVRMEEVVFWKVIKKLLFGEDRVVIVGSPGVGKSCFLMLLAFYLACIKRKKVLVIRRLK
>jgi|506739|fgenesh2_kg.PHYCAscaffold_21_#_111_#_Contig665.1	MVLVALTCALVGKTGVLGVKIDDSAQVWELKKAITVEKSNDLKDVDADKLELFLAKMEGGTWLDGAGAAAVALDERGHPQGCVQMDPTLWIKNSKHFGDNFKPGEGQVHVLVVVPKDENDRSAAMALGVPSLPPTTFHRHPERLKRWAAINEMIRQKNQDGNEKTGTRDTNKKRKNRDIDKSMPYSSLSWNDLEPILSVEDFDLKASAVPPNVVEALRDRLMQVRKLYGDVYSGKEAKRQVFIVAIIEAVCLMLGDATILVEEEVKGKNVLVHGRFEFVLKRGKNRVSIVEAKRDDIPQGIAQNVAGLEALSDVEGLERTLGIVTNYLEWVFISDDDEKIRRMNTTLKVYGAVPSIQELTEIVGMIYGFLANSS*
>jgi|511381|fgenesh2_kg.PHYCAscaffold_83_#_9_#_Contig727.1	MVKLSLQCAVVDQAGSSFDVEIDDSAKVSKLKKVIKEENPATITCDAKDLQLFLAKKDDAWLDGAGAAAVELDEHGHPQGCVQMDPTLWVKNPKHFGDNFQPGEGQVHVLVVVPEGVVGSASETSKMDFVVDKVSKLYEHSVLSKRTRYVHSEMSSSKGNKLVKELKIRVTPVDAVPFTGGSPTPVEEFEWIKGRTEEQQSGRYRDYVEANIGDVLRNNKLCVFSVEKGANILSVEVPGCDVDLAGRTDMIVLSAIVQKFPHYLPHLPGVKMLIEVKREVKSASEFQALSELIAMDFIVDESVMALLTNLTNHWEFLWVSNKSNNRPIIATTTLTTPGEAFEVIRTLLAQSSTADADIMLPCLAEPVKRRKLNQMLPFIGEASGDGIRESIERYYDIASCLGPDFDMARAVARQVTRSIPTLSYFS*
>jgi|527369|estExt2_fgenesh1_pm.C_PHYCAscaffold_180095	MELRCGVYGEGSVFSVKIARDVKVSALQKKIASVLSTEQHTVFPRLLALYLARKKEGEEVKWLKDDRHAKDFLRGGTITEYEEMRPSWTLDDEELFGPDFQPGQEEIHVLVELPKAAVESASLVKMEKQLDEMYERIAENKRKRYVHSEMSLIKGRALLQDLKMRLTVVDTVPFTTTDASPVQVPAFEWESICDGRGQNIALTEEQQRVRYREYVENNIGDVLTTKKLCVLGVEKGMDILSVAVPGHDIDLAGRSDILMVIEVKRVLKSGCTFQALSELIALDFLVDDPVMALLTNLTDHWQFFWVSDKKKKKHTLLAQSSSADAEINLPCIEEPVKRRKLAEVLPSVSEGGESNGVREAIERYYDIASVLGPDIEMARAVANQVTRSIPIYSSYPS*
>jgi|540976|estExt2_Genewise1P	MTIYCAVVGENESAFGIDIDEGKSVDQLKQAIKERNEDIHVPSHRLKLFLAKKSGVWLTEIDVMEDVSDTTDLELLEAGRATLRSVGLSDEDVGEVDEADAAAGEGPVNVLVVIPEL

lus.C_PHYCAscaffold_50927	YNVPSPVMALFNVMLPHVLTQVPTTESDVVIEFKMELCKFYECYSRHRTWVRCMLLDVAFPKSLVSASHLFRCNNAFMAPLTVQLWDIDDMRNGLLLFKPLKHAFDHFQLSFILDDTNVFRLKLFDPSIYNTRLLDLKDCDNENVLSMEEMGVLFYNTSLTRNPCEFDTQTTFGDVDGSALVFTGLKRPFYRCLNQQARLARVFALKKHWIDESYNFTDFWSEVSLDDKMDMFHRSILEN*
>jgi|556686|estExt2_Genewise1Plus.C_PHYCAscaffold_940014	MVLVALTCALVGKTGVLGVKIDDSAQVWELKKAIKEKSLNKLKNADADELELSLAKKGAGWLSIEDLAAIQKGEDVPGFERVSLVDTEDEAYSASIRDVLKTNGMPPPQTRQIHVLVVVPKDENDRSAMALDVPSLPPTTIHRHPERLKRWAAINEMIRQKNQEGNEKTSTRDTNKKRKNRDIDSSMPYLSLSWTDLEPILTMEDFNLEASAVPQNVVEELRDRLMQVRKLYGDVYSGKEAKRQVFIMPIFEAVCLMLGDATILVEEDVKGKNVHVHGRFEFVLKHGKKRVSIVIAKRDDIPQGIAQNMAGLEALSDVEGLERTLGIVTNYLEWVFISDDDEKIRRMNTTLKVYGAVPSTKELREIVGMICGLLANST*
>jgi|558527|estExt2_Genewise1.C_PHYCAscaffold_11463	MMKLYCAIVGVAGSVFAVEIGEDKTVYDLKDAIKTQNKIKKVDAGDLQLFLAKKKKKGKGMWLTEKDVQKGVNNTSDFNLLGTVGAPLKFVGLLKDDVEFEPTLKDVESMNTPVHVLVAIPQQWTISKKTDAKRLEKEENIPLEMLWQYSEMEITTFPQPDELSSLLQRPLPFQLNLQKFLTPKTIFDPSGPFLVCNELSALIDGFSYSCDYRPDPMASENTWQRMYDQLLDISYRLCRAHGFDVVSNRN
>jgi|559084|estExt2_Genewise1.C_PHYCAscaffold_21063	MIWLYCAIVGKAGGVFGVKINKGDQVWELKKKIKDENQATITCDANELQLFLAKKDGMWLPDEDLVAVDLENGTIHPDIDKMMNAEQQMQDNKTLQFWLFEENEMPKPSTDQIHVLVVVPKQDGTLNETSVAQTPLQDEEASAYSFSELNSAMRDQIVRKMRLVENVPDVKEPEDTSIGGYSWIPKIEENEESQRAGYMAYLQQHLKTLIDRGDFLLDDIADDKSVLDIVDPRLPFAMSGTADVLLINRTSKNPLIKLAGVSLVIELKKKVEPDHVPQAIGQLVSCSMKAPLNCYPLSLLTDLNDRWHFSWFSDNHTLTQVTLKYPKNAFRLIEAAVLRRTESVSLPPSFIPGPFKIIKVDDFLLQPDDGYAEEMMERYELMADVVEPEFLMARRAEYAQHLVQSMPMYAHTFK*
>jgi|563460|estExt2_Genewise1.C_PHYCAscaffold_120265	MMKLFCAIVGARSAFSVEVGEDQTVEDLKLAIKNQNRNKLMSVDANDLQLFLAKKDKGNGMEWLTQLDVVKGVMDANGFAHLLFVDAKLRAVGLDSSELGKVNDKDVAVGKGHVHVLVVVPKTGVSKDGGRSIQKFSAPIEFSEMEHEGGVPSTFRTERKDTVAAIASLLDRIPVVFFRAPPLSGKTAMCHLLYNHIVFSKPDALVASVRANRMARNETFAEYFKKMYGCDFEEFCAYRCDRVLLIDEAQITYNDEQLWRGFVKDTLESQIPGLRLVLFSSYGSFDVYRKQERPGTPILVPTDNTFGLNVTPSKPGLQLSRVELEEMVLNSIGASVSDLIWVLCSGHIGIARAVLVFLRWKFGSTTPNAEDVEMELRSEELLQYVRASYRGIPTADAFQRIVKNNDLSEETILKMSEVLNGVASGKVTSLHDPDGQQTPRSQTAVELLTKFGFLYEDQAKQLQFASNMHLKIWLLSSRTDPIGYMVKDISHGDFIVACVQRMSASRLQKFATENTTRVARERQIQMELYGATTSCLPKGVLVTPEWRTDDGKGFIDLVIRGSGILWFWELLVNGDDAVCHSKRFETGGTNYGSLTRNCRYMLIDFRQNMGVRKRKDGFLYVSFADSFTKAHVFGLDKPTVSVELLS*
>jgi|567378|estExt2_Genewise1.C_PHYCAscaffold_240430	MVNLFCIIVGVAGNAFEVKIDDGASVAALKKEIKQENNIKLKGVDAGDLQLFLAKKDGAWLMSKDLLRMWNEETPEEDERDYMSERLDDPTVRIKEKFPSEYPDRSIHVLVQVPRELLYNQPKPRDSSNEWLAEFFNHKVEPRSLPFVGKLSSFVTQPLPAKIRVKQEWLNEWALSPGLQEKMFVLDDDAPCMEFTSLIFNKRTLNPFRRGKTENAFISMWDSIFRNVLDVLFTQAHIDRDSCNGSSTRQKRPDFLFVLDQVCVFRGEEKPPDVNISVPTEELCSKLVWAYGSVPYVFGYAASGYDIQLHALCPLDPLNVGGVVTKNIGTFNLEVKEHLFQIVLVMLNLSLLFQAIADECPASGRDEFRDITRSSGWPSKPLQTMLISGKNFSTNVGDKRTTTLKRASVPNVDRLTNLHFQKRLAVFKPRGTMVRPSNLLDLFGALKDVLQALVALHRLGWIHRDIRWSNVIRQRTGNSWFLIDFVDAATNPQQYPSGQHLSVEEHAPEIFVENGVHTTAVDIWAVGFLIETSGVEWLDFAGRTSLYRRLIAKDPAARPNAEEVLAELKALEEAAKSEKEACENSRRSETQCRKRKLPDS*
>jgi|570403|estExt2_Genewise1.C_PHYCAscaffold_370147	MEVVKLFCVIVGEAGSAFSVKVGQDQEVDDLKEAIKDRSDGKIDVPRPDLQLFLAKNGNAWLSSDNDDVKALKEGVKTTLIDELTQKEKELQGESGLKKVLAGMLTPSTDQIHVLVVIPDQSKSAPSVSFEGVLDRCRDSFFLQLPTAGEDDSWLMFPQPLPLTERQKLYIRSSYKSIAAQALSKMDPKRRKYAVVTGTPGVGKSVFLFYVMWKLIKEKKRVLLMAEEPAIYFDGESMWEIQQLPYSGNRTFWSVDLWCLVDSVDPTTIAGFPIRKCCVLLASTPRRDCIGEFNKLEPTPDVFYMPLWTKEELSTIAPLYPNAQDQWENRFEGLGGVPRLVLKDLKVTPQELLQTACSNCCLDGDQFEDQNGSDSDSHPQP*

>jgi|573037|estExt2_Genewise1.C_PHYCAscaffold_510047	MVTLFCAIVGIESDAFAVEVNENDSVYALKQAIHARKMYEFSADKLLLFPAKTEGPAWLSNSSEDVVKLEEGEKTPLIEALTTKCQELQAELPVSDMLKEIDPPSLSQIHVLVVLPDLKKRKRGGTTRLSDLLETCSKEGSLPTEGDFLQMFEWDDQDCGKVKDITAIGDIVGFTGFRFFVRKEILCVLENLKHFKANFDRGEVGDQFIFLGSPGTGKSCVLALLCFYVAATSDHPVLWYRSVQYGREMSFTCLFYQKKYYRWNGAEVKIYDRLYDEV
>jgi|573801|estExt2_Genewise1.C_PHYCAscaffold_550284	MIKLFCALVGAQGSAFPVDIDASQSIGDLKDAIKDQKQNDLKNVDADKLQLFLAKKGDGWLASKDLPSIQRDMASPTIFEKLPLVDPTCSIQEVLTENELPDPQTRQIHVLVNVPQVHVLGKRTRADEWFINQIGMKKSRVIVDGNETDRITRYFEMAGFPPLAHPKAEYRKILERNAYIVIFTELMKKAKLSFEKGADCSLVVTGNPGIGKSRFYLYCIFTLFFALTWKLRSSPPSI
>jgi|96357|e_gw1.1.1010.1	MIKLFCVFVGAQGSAFPVDIDASQFVGDLKYAIVEKKKEDPNLKSVTAKNLQLFQTKTENGDGWLSSDDGAVIAMRTGAIPEQVKKLLKDEMDPAEQIGDKFRNAPTKKTIHVLVVVPPAPENERKRKRMEDEVAPDAWIKAIKDEPVTTLPTCEGLKHHLLRALHVKIPINNRLFQIVSAQNSTGELFTVLEKLFEPQPRNVSDITGAVLRPIIDPLLPSGPTTKSSYHHFWDCVIATLLKVVTDGNYHRSTNASASTGAYRPDMCFYSRKSNICVFRGEEKANGELDVPMAELHEKLTWRYDDAPYIFGYAAVGLLVCLVTIQKDEKTSSRAKAEKIETYDLGNLKDRLLFLLALLNLSTLFDPVVDLIRPLGIPEYITRERTNGVRIEFAEDCVIKTYPKNMPSDGIIRNLKSLHRLMKEHSVPNVVELKNANKKKKHVKLAPIGIDRRPVNVDQLLMALCDILKALVALHAINVMHRDLRWENVLKYSTEGDKWFLIDFDEGRLSPAATVTHLKAESHAPEILSSSSHTVKVDIWSVGYLLKTCCLQDLPPELKRIQSQCLQTDPSSRPTAKSLLAGIESLIES*
>jgi|100678|e_gw1.5.1392.1	MVKDIKLRCGAYGEGSVFSVKIKQNADVEALQLAIVNARKGVNNRFNVDPSTLTLYLAGKQEGEEIKWLKDEDSLGDELRGVYPKQYMKMRSSRILDEDYFGENFQPGRHDVHVLVELPEKVSSVQSVVRAVFWLVTGLVENALQTRGVHRLIYRIADAQLGYYDPANMLPDNKPRAFWYTNNDLQFHVLFKEGECVHCTCWCC*
>jgi|102004|e_gw1.6.669.1	CVIGVAGNAFSVNIDENLSVGHLKKAIKGENVNDPTLKNVAAKNLQLFLAKAEGGARLSSLTDEASEDATKVKKGEWLSNLTDDVKKLKKGEKTPLVESLTHENKGLQGESGFKRVLGPFLAKRKEWIWL*
>jgi|106201|e_gw1.12.351.1	IKLSLQCAIVGQTGSSFDVEIDDGEKVSKLKEMITEKNKQDPNLKNVAAKNLQLFLAKKGDAWLPDDDPAAQDLEEGKIHTEIKALIDGNKMKEAWTIEDVLVDNNMTGEGRAPKSRQIHVLAVVPGILTTIERERVDENQD*
>jgi|108281|e_gw1.15.479.1	MKKVSLQCVIVGIGSSFDVEIDDGEKVSKLMRAIKDRKPLTITCEADLLQLFLAKKGNAWLSSSTDDVKALKKGEKTGFIDELMHEKEKMEEEYPLSDYLANMNDPEVKQIHVLVVVP
>jgi|108895|e_gw1.16.149.1	MAKLSLQCAIVGQIGSSFDVEIDDGEKVSKLKDAIKTKNKDDPILKTVAAKNLQLFLAKQGNAWLPDDDPAAQDLNEGKVHTEIQALIPDEHRAALKLVNGESDDYINALTAGEQILASKTIETWLYEKIKMEEPSTAQTHVLVVVP
>jgi|109378|e_gw1.16.566.1	MKLTLQCAIVGQTGSSFDVKIEEGQTVGDLKEAIAVDQKFGFAASKLQLFLAKQPVEDDDGKEVVPVYHPCAEGMKKESFKWLPDKHRAALKLVKGESDDYINSLTAGEPILASKTLTIWLYEKNNMEDPSTQQFHVLVVVPE
>jgi|113678|e_gw1.24.344.1	MNRLERYAALNEIVQEKNQAENGKTSNQDTNHKRKKKALDNSVPFSSLSWDEIEPVLQLNMFHLTAKPVPDEFVRKILAQLADLHQLYGDVSTGKEEKRKMFTMTVLEAVCLHLGDVMIFVDEELTGTKIHMHGSIEFVLQRGAKRVPIVIARRDNVEQGMAQCVACVEVLADAEGLERTFGIVTNYLHWIFIRDEDESIELIDQPLNASMPSFESLKVILGMICGMLESE*
>jgi|114206|e_gw1.25.261.1	PLDDTLAPLNSVGLSEEDVRYRMTKEDIKAKKVPVHVLVVVPPADSPATILLETILPHVLTHATTTFTEDNRDFTHNLCNFYGCYTREQSLVRCMLLDVPLPKSLVLASHLFRRSNEYLSFRMMQISDIDEVKNGLLLFKPLKYAFDHFQISFIRDDTDVFRLKLFDSTIKDTPLIDLSDRYGKKVLSEEQTGELVSVADNGSCLFDVGKTFGDVDGCALAFTGIERPYYRCLNLQARVALMVALKKGWIDESYDFKDFWSEVSLDDKMEMFHRSILNSVAEF*
>jgi|117855|e_gw1.34.341.1	MVTIFCVVAGPGSVFAVDIGITQTIDHLKKQIKENKPNMIRFDADLLKLYLARDGGAWLNSNDDDFKALKRREVPARIKNLMQEQLLLDETAKLNDDDYFGKHFKPGDRDIHVLVELPEDPTEVLHYKSELVCGDCFLAELLVVTNSFRL*
>jgi|120859|e_gw1.42.251.1	MVTVFCAIVGVPGSVFSVKIDENESVAELKKAIKKETPNIFQCNAMDLQLYLTKKGNVWLTEAHVKEGLRDTSGLKLLNSMKTKLKFLGLRDENDEEGEEEEEGMGLVDVLV
>jgi|122221|e_gw1.47.236.1	MVTVFCAIVGVPGSVFSVKIDENESVAELKKAIKKENPNIFQCNAMDCLSDEGGRRVADGGSCEGRLERHQWVEAVGFNEGETKSSGVEERKRRRRR*
>jgi|124124|e_g	MGEELYDPTDKISAKFPSQIPGGTIHVLLVVPEGGKRHLSNEWFTESFHPLKKRRVGED

w1.52.167.1	VNKEKRFFDMRDFPSLLEHPKVEFKTIVEREVYVVIFSQLVQYAKTCFEFVPTSASEPDGKSKPGKDSNIVVTGNPGIGKSRFFLYCIFQLILREREDVALLPPYELVVNHKTNYVKYDAVSKEFVELNKKDVRALQRKPYVIRLVEATSSELTGWRGVSVLFASPGVDGIDNFSKVDGLTFIMPTWTFEELEDYNSLLSDELKLAEDELLSRYDRFGGIPRFVFSQIMDQTEAKIQSAIASFSALDVISYCRKNDAVREKDYSHCVLEMVPTKADFRANFYLDFVSMHIAEAVIDKVHGDSLAKVSEFAV
>jgil125925le_gw1.60.118.1	MTELKLFCALVDTQAVFYVTINGEKTVYDLKKAIKNEKPNDLEKVDTAMLQLYLAKKCDGLWLTENDVKNGVSSTAGLTLLNAAQAPLQDAILGEGLHEPSKEDKVAGNGPVHVLVSVPESVG
>jgil127207le_gw1.67.186.1	MMKLFCSVVGVAGSAFPVDIASDETVGDLKEAIKAKKMYCFPADELRLFLVNTSVKNPDEEEKKAH*
>jgil127255le_gw1.67.176.1	EDEDSSIDPYPWESDLAEDHEGQRKGYMQYLKDNLHGVLSEGGSTTIPPGTSTSGQPKYHLKDTSRMTSLLTCKASSLPFGLKGTADLMIIGEVAHSRNDIFADLQFVIKIKKNQCGPKERKELLLELVAANWKSYSPCAPIGLLSNLNDYWYFMWFTTDRKIARMKLSCPANGLKAM*
>jgil127347le_gw1.68.101.1	MLNLLCAIVGAQGSVFPVLIGESESVGDLKKAIAKMKPLTVTCKADRLQLFLTKTEGGGWLSSKDEVVLATRKGGIPEEINKMLIDEIDPAKEIADVLGAAPTKMVIHVLVVVPRGLYTIHGDHVTARTDGWQSFSPTKLRLTRCRLLEV*
>jgil12764lfgenesh1_pg.PHYCAscaffold_1_#_216	MLLLNCAIIGGGDVISIIIEEWKTVALLKDAIKEKKPIKLNDVDAGDLHLFLAKKDGAWLMSDDLLQMREDGKGERGYMSEELKDPVAKISAKFPSELPDGSIHVLVVQRFRIEDVIDILAELEKIDDVKNMTVILCVDALQQLVNDDAKTRNGQFRRSYHACSDDMAAI*
>jgil128012le_gw1.73.136.1	MKVSLQYVVVGVAGSAFPIDIGKNLLVGHLKEAIKEKHDDIKCPARDLQLFLAKAGGNAWLANSTDHVKKLKKGEKTAYIEALIHENKELPRKDPISKYLERMDEPQMEQIHVLVVVP
>jgil128338le_gw1.75.57.1	MVKLSLQCAIVGQIGSSFDVEIDNGEKVSKLKEMIQVKNRETIKCDAKDLRLFLAKKGDAWLPDDDPAAQDLEEGKVHTAIQALIDGNKMKEAWTIADV*
>jgil128353le_gw1.75.129.1	MVKLFCAVVGVQGSAFPVDIDASLSVGDLKDAIKTKNKIKLKNIDASDLQLFLAKPKDGPWLRSDDSDVIRMRSGAIPEQVKKLLNEQIDPAAGIGALFGDAKPTMEIHVLVRVPDYDSDSEVNQQRKLTSFQKLRKESGATGELPVQGDFMKLFDLTDDDIGKVLNIKAIGDIVGFTGSDFYTFARPN*
>jgil128403le_gw1.75.131.1	GSAFPVDIDVSLSVGDLKKAINVEKTIKLKNVDAADLQLFMTKTKDGQWLRSDASDVINMRSGVIPEQVKKLMNKWTRQMKLANCLVKNHQRRQFTCWWRLQRLI*
>jgil129581le_gw1.85.127.1	MVSITLCCVIVGVVGSEFDVNIAKGKSVHQLKEVIKAKNKKLLENVDTRELQLFLAKTADGTWLSLTDHAVNSLRNGIIPTKVKALLKRE
>jgil129660le_gw1.86.101.1	LWNDEVIVAARIPREKVLMHERISRGGFGEVYVGVYNGRKVAIKMLLPEIRKRIQSVNEFLVEVKLMAALEHPRIVEFIGVAWDSLTDLCVVSELMERGDLRALLSQFQAENHPHGFDHDKVKIALHVAHALTYMHSFSPPIVHRDLKSKNILLTNEFDAKLTDFGASRERVDRTMTAGVGTSLWMAPEIMAGEKYDEKADMFSFAVVLSELDSHVLPYTKLRQETRASDVAILQLVLQGKTQIDFSDACPSSIAALGMACAAKDPTARPTAAQALYELQQTLNSNEFY*
>jgil129685le_gw1.86.155.1	MVKLFCAIAGIAGSVFLVEIEEALEVDDLKNAIQKEKPLTITCDAHQLQLFLAKKDDGKGAWLTEVEVKNGVNDTTGLKPLDAVRAKLKNVQLSDSDVGGVDEADEVAGKGPVNVLVML
>jgil131615le_gw1.108.42.1	MKVSLQCAIVGQTGSSFDVEIDDSEKVSKLKKAIEKQEKISFKDVDAVDLHLFLAKVQKDMTWLYSRSEDVKKLKKGEKTPLIEALTMERHELQGEDPLENVLNGIDPPSVRQIHVLVVVPKG
>jgil131976le_gw1.125.17.1	MDVRYESVAHYFKPINGTRVLKSIENCGEDFEPDEGRVHVLVVAPVTVLMLQDPPYCHFVVDGVNIPITDNMAFNLPGLTGFWKAFQEVDTEIEANTAIKLPEGTFLLGDSNRGSCIYIRSCYLQLWEITQKVVQDEVKKATNLVIDGNSGIGKTYFGYVMLLYLARLGETVVYESYGTKKRVLLSHNVVVEGSQQDFSDILNLPTTFYIVDGVEPMHYQAKTIFLASLDHTLWYTFNEKRDQIRYIPVWSWDELSTCREVLYSDVPESVVEGCFHRWGGIPRYVLQYAQSEEKQILLEKTMEIADFFWLLNGYEKLKANNPEAHRLLHYRVNDHFAKEYFDFASPYVQQEVYDRAYKKDKRVLLGFIGGGDGWKW*
>jgil133238le_gw1.380.5.1	MQLFLAKTEGKWLPDNEDLDTLLLTLHRICTCSHPTSWKLSNPDLFGPGVSLGEDVVHVLVVLKDAEAGVASVELSALPTVKQRHPERLKRWAAINEMVRQRNQERNEKTSTRDT

	NKKRKNRDIDCSIPYSNLSWVDLEPILPMEEDLKLEECRPSKCSSRST*
>jgi|13996|fgenesh1_pg.PHYCAscaffold_5_#_210	MVKLSLQCAIVGQIGSSFDVEIDDGEKVSKLKEAIRTKKHLTITCEADQLQLFLAKQPVEGDDGKEVVPVYHSSAEEVKEESFKWLPDEHRAALNLVNGEPDDYINSLTVGKQILGSKAIATWLYTKNNMELPSNEQIHVLVVHHLTQFK*
>jgi|15135|fgenesh1_pg.PHYCAscaffold_11_#_121	MMHNLHGEAGNLKLTEALESPTRLVTDVVTQWLASMDEMRDEEAAPGRTSPKTQMEKSKDEERDEEVQKKRPKRKFRKSTINVRKEEKAHLLEELSGIAYQDGGDQSSSICHIHALMSEYYLFNSPARGKMKTLTCAIVGVAGSAFPVDIDANKLVGHLKDAIKEKKMYQFPADELQLFLAKKADGAWLSSKDPEVISMRSGDIPEQVKTLMNVEVDPTDDIEDVFEGAPTKKTVHVLVVERR*
>jgi|15224|fgenesh1_pg.PHYCAscaffold_12_#_49	MSDMVFLMLLFEHIVICVSLSSSIFFDAITEKNKKDPILKNVTAKNLKLFLAKTESGWLSYDEDLVNKLLLNRVDTSNTVTATIVDEEREKFDLLLSEKKGCLNVLFICATKYGDNLQEAFGPAKSVIYTEAMQSTEKKATTQYIHEVILLDLTTPQNRAAFFGLAWDDTLQTRLENVIHKAGGGNTAE*
>jgi|20945|fgenesh1_pg.PHYCAscaffold_77_#_13	MVQISLQCAIVGHAGSSFVVGIDDGAKVNKLKKAIQRENPLTITCEADQLQLFLAKDGKHFGSGFKPDEGQVHVLVVVPCAVAGSKAETIGQNVEMNGDGEAGVDIFSL*
>jgi|34764|gw1.83.9.1	MMKLFCVIVGEAGSAFPVGIKPEDTVGDLKEKIKGKNTMTITCDAKDLQLFLAKTHAGWLSDNEDLDTLLQSEIDSSSYLRMRASWKLSKPNLFGPGVSLGEDVVHVLVVVPEG
>jgi|49590|gw1.51.244.1	MLELLCVIVGVTEWAFSVEVDETKSVDNLKGVIKNAKRNALTGINASDLQLFTAKTTDGKWLESNDPDVIKMTSGDIPKQVKKLLKDVIDPVKDIGSVFQDAPTTMTIHVLVVAP
>jgi|502542|fgenesh2_kg.PHYCAscaffold_1_#_2_#_Contig261.1	MVSSPLPSSTLDALAPPFYPSMTWYPSITDDYYLERPHSPGKSGFVIADPVEPMAEIPDEELFDPAFYPLSAMEMQELEQVDEINEILAELDLMESHQELHYKLSEKTRELRSSSDVDAEIYSMMAKASKAKNFSKQHVHLHKNTSFHSKRNMRSALHQPRSVK*
>jgi|505958|fgenesh2_kg.PHYCAscaffold_17_#_43_#_4096633:2	MAASPNKKIREASQLDQLKQFTTVVADTGDFEQINKYKPQDATTNPSLLFKAAQMEQYSALVDDAVAYGKGLSPDLSESERLGYVIDKLSVNFGLEILKVVPGYVSTEVDARLSFDTEGTIARAHRIIELYEKAGIKKDRILIKIASTWEGIQACKHLQKEGISCNMTLLFGFAQAVGCAEAGATLISPFVGRILDWHKAKTGKSSYESHEDPGVVSVTKIYQYYKKYDYKTIVMGASFRNTGEITELAGCDRLTISPNLLEELTKSTAKLDKKLDAETAGKAYTGEKLSYDEKDFRLSMNEDAMATEKLAEGIRGFSADIVKLEQILKAKLSA*
>jgi|508616|fgenesh2_kg.PHYCAscaffold_36_#_69_#_Contig4695.1	MVKLFCAIVGVTGGAFEVKIGYTKSVDHLKDAIKTVNKITLKDVDAPDLQLFLAKPKDGPWLRADNSDVISMRSGAIPEQVKKLMNEEMNPAARIGDLFGDAKPTMEIHVLKVKSVSS
>jgi|50894|gw1.79.118.1	MLKLFCAIVGVAGSVFAVEIGEDKTVYDLKNAIKTQNKIKLKEVDAGDLQLFLTKKKKKGEGMWLTEKDVQKGVNDTSDFNLLGTAGAPLKFVGLLKDDVEFKPTLEDVESMNTPVHVLVAIP
>jgi|509061|fgenesh2_kg.PHYCAscaffold_41_#_57_#_Contig1845.1	MGQGQSSIPTTEVAALVELYDALSGDRWRRRDGWKQPTRDPEQWFGVEVAMGHVVALELPANELSGCLPVASLARLPNLRVLDLSKNQLRGEIPAELGQLTALKRVDLSCNDLSGAIPRQIGACNQLQELNLYQNSLSGTMPKELGKLQSLRTLQLQHNNLCGALPETLCELTQLTKFSVRGNCLTGRIPTDIGRLQSLVFLSLRNNELTGVIPPSLGCCKALEFLNLSSNQLSGPIPETLGELEDLEYLYLFDNALEGRVPGSIARLKFLKESDFRDNRLRGELPNFLDGCSSLEAVMTKWKNRKASYRHAILGDPMPSPDTPPTSSHQFLQTLEDPPSNSSATFLSQSFDHKGSEGLGDGAPEDDPANNSHLVAEFSRKRVFQLPDSVVQAK*
>jgi|509444|fgenesh2_kg.PHYCAscaffold_46_#_29_#_Contig2750.1	MFWSAALDLKTQRAPNRLSYGSFNRSASNSSFHIPQSIPEHQPVSQFTSPLPDKRREEYVERPDTAFARTRASLQLSEHTQTALKMLLQGEREFKKPSLGRTIENKPKPKFAQDMYSMSKISSYSAHRAPMKELPERTPLLKPIARAHGQEEPNPQENSNEHNYWMQELERRRAGLRRSRRRTCTPMSERATTSPLKVGVVMCSVPLVLVLGFVLFIFLFGGGSDASSNVMDVMNNLLGIGRGDDAETIAARHAQDRDRIASTFARPPEKIQLEESIVMQLDVSSDHQKLRGSQKEKAGE*
>jgi|509452|fgen	MESVVPCDLLDELMHGVVILHHEAALVLGTTQFSVETFFPLLAYVLVHCRLPIIHAQLH

esh2_kg.PHYCAscaffold_46_#_37_#_4103400:2	LLENFAITADNANGEESYYVYCVHAAVEYVCNAAGLSGSTNPLGPASSASSAVTTPGGCGLTPVAPMSSTSPPKQAAFSLDLELEMENELDVKVLGLSRDSGEEQPEESGTSALQ*
>jgi|511091|fgenesh2_kg.PHYCAscaffold_75_#_1_#_Contig233.1	MKLFCAIVGVAGSAFSVEVGEDQTVDDLKDAIKVKNDDIKCPARELQLFLAKKDKG
>jgi|52465|gw1.36.563.1	MVELFCVIVGVTGSAFSVKIGNTKSVDHLKDVIKTKNKITLKDVDAPDLQLFLAKPKDGPWLRADNSDVIRMRSG
>jgi|52481|gw1.67.119.1	MAKLFCSVVGVTGSVFLVDIDQAESVRRLKKAIKAKKMYQFPSNELQLFLA
>jgi|530721|estExt2_fgenesh1_pm.C_PHYCAscaffold_750003	MVKLFCAIVGVAGSAFPVTIDEGQSVGDLKEAIQVKNRETIKCDAKDLQLFLAKQPVEGDDGKEVVPVYHRSAEEMKEESFKWLPDEHRAALKLVKGESDNYINSLTAGEQILASKTLTTCKST*
>jgi|532971|estExt2_fgenesh1_pg.C_PHYCAscaffold_90155	MSISEACTCSLQARLHQVENARSREMKAHGTLVQSLEIELESRRICEGESRLALAKLRGVNCKLEAELQAAHGKARQLLEQLEAQRVETSKCEERLKVFCEESDCQLRAAREKSDNLMEEKRQLNVEVSEVKACLEKAKAENKVLHAKYEEKISEANAKTADIVQLTSQITDKQQEIEVATERSQLLLRELTTYRVQQELAQERIKLLEKDVNRTMVTRNRALNWRRKRQELWENQFISHRIFLNWKLRSAQAKFQSAAAMARCNDDTRSRLQLIEMNVLAQCSSAKEELNRVRQACINECVQMQFLRREICQTELPKLLTIVRNHQRSFDNQQRHLEMQLVNQRESFERERERLNMSRQDFEHCVQKAIEEKRLFQKRQHHAMFQVFTSKKKWELHRRVFGAWKEFYLRSIVGHATHTAMVFQSQHLRASTSEVSRPIRRGESHQWTMPAPIRRGESHQWTMPAPIRPISLASQHWRRIDRASS*
>jgi|533583|estExt2_fgenesh1_pg.C_PHYCAscaffold_150061	MMSEEQAATLSEDDGQLQRLETEKRELIDKLKKAVVAGKAMKKQLDDTRAENVLMDEEKQDIVVKLQEVVTRYQAIQQELESKEGELMLAQSKVEAFQVELQAQQEADAKAIKELTTKFSQEEARVMVFQEENNRLTSQVAAMLEDKQQQEKETQTLMQDNQSLQNKVDDLMQQVAGARQLQEDTEQNYLEVASKLNQVLRENDELKNKPGTDASVELQSQLRAVETELAASADKWRQEQLQLEQQIETLTAVNKKNTTELADVADIREKLLVHVGIDLTYASIESLLDTKNNEIQMLTEQLAAAEAPQEQIIREADKTVEDLRAELERVAEEHSLSLVTMENEYRLACEELKTEAEKLTGQLDAAQTQTQQLNDDFSVERIHKSEEENRLLVEKLEECEAALKARASEIEKLVARARTASSDTDKSGSSEMAACKAENLRMIFEVAKTADSVSKLKLDHEELLEAHRKKSSEVDTVLVQLASLESANQTLESDLKKKSEELHNHLETCSMQKEDFESVVANLNNAVIKAEKEKSKIKRDLEDMKTENDVLEEQISELHAVAETKTEPDESQEKDREVEELRSSLVQAKVDFLEQKQQLTALEKKLVAVSKSSGPTCTVNSTSLDAERREFEAALIEMIEMEKKLQVAYEAKQGLESTLQERMEAKTDLETRLSIAEDKITELEQQLEQKVALIATIEEQLSRGKLEEKAIEFETFKTTTNMLKDERSRLFNEIALLKDKIAKSEVQKAAMADSQELANEELEEQLNELADRIAEIEAEKQDLLARLDETVYRSEEDIHQLRERLYMLEEEKSGLDDENFKLERTIEHLESKLDSLEEQKAGLEAANEASSQQLSLLEERVEKATSEIATLSAEKDSLVELQQSLEENVSVLQEDKVKLEQTLDETSSKLRDELDRVTEQMESFQAQLAQSTAEKEEVTIALAELRERSEADKLASGEVTAKLEAQVAENQTLENKISVLKQMAEKALQSLQSSRDELSEAEARASVLVEERDAVKVLLQEKQTAYEQLKTQREELQLRVEQLSSELESSQKKRTEEAAIAEETIQTLKLTEAKLTESLESVKHDLAEAESAVMVLVEERDAARKEITARDLKIEMMTSQQGELDLAAQKLESELSILRSKSSADSEATKEMLRDLEESKAQAEETVRSLQGSSAQAKESLQSIQEQLAESELRVATLEKERDATRTSLNENMSTQETLSALQEDLQKKVDALEAELKELRETSSAELAAANETIENLKNAEAEEAETLAALRQELAEAEGCVMVLVEERDATKKTLSKRDLTLEVLSSEHGELQLKSQSTTTELENLRSKSAADAQAAEEALQSLREELKRATESLESTQNELAESESHVAALTAEYDMVTKAMADVQSERDSLSGLNEELKESVEDLKNEMENRQKQFSSELESAEEAIRTLKTSEVKMTASLDSVEQELCEAKSSSASLTAEYNSILATQKEKEAGISKLTSEIDSLQERIQALESELQELRNQRETEAQTAEETIRSLKESESQTVETLEAIRVKLSETEARVVSADEEREAASKALSEMESHRDAQSTEVESLQERIQALESELQELRNQRETEAQTAEETIRSLKESESQTVETLEAIRVKLSETEARVVSADEEREAASKALSEMESHRDAQSTEVESLQERIQALESELQELRNQRETEAQTAEETIRSLKESESQTVETLEAIRVKLSETEARVVSADEEPLEIGSLQERIQPLESELQELRNQRETEAQAAEETIRSLKESE

	SQTVETLEAIRVKLSETEARVVSADEEREAASKALSEMESHRDAQSTEVESLQERIQALESELQELRNQRETEAQTAEETIRSLKESEAQKVVELDSVKKQVVLLSESSSSALTDLASLREQWVAKDESHAADIASKDEVISTLKSKLEEVMAAYKRLKGHLHELQDRLTQQTSTNDTLKASYEELSGQKIAAVEELEALKIELASSSEHSNTMAEELRQAEEKVAVAEAQRESQMENFKKRVLAYDDELAQMQKQHAVALQEQKETLLKTSAVREEAAATKLLEQKHDQAGTSHEEASQKHEAERMELESQLSSANETIEKLRLASVTSVGLEKEIAELKLQVETETEGANAARAALETYKKRAHTALKKASSENKLNLKKTSEATAKLEKELISAKSRVNTLETELEDTRKRMAEVESAGDLLAQSTREAVESEKRSLEVTLRLEIDSLKAEVNRLEEALENDRQPLEAQINQLSERNAALNQDVITLKEEIRSQTESMEQEVHTKEEEIRDLSKQLQAALAAAASLATNEAGRRSYSPTYSPTEKERRSTASSSRSFDSDGNNSFLHRSSIEEQSEHMAAAVADSCPIPLASKMAPANGVNKSQTDEDEVCRLKLQLNELETASHLFQKKYEDTSALLEEANQQKQRLQELCDGSTQAINIEYLKNVIMKYIESQVPSEKEQLVPVISTLLSFTPQEQQKVMAVHRPNDEGAGLFGGVFSLFGGGAAAAPPPKPLAAPLNFKPSPTTAMSNTTGAALGSKDKNGVLSFGSDPSDDEEFATPLNPFAA*
>jgi|537103|estExt2_fgenesh1_pg.C_PHYCAscaffold_740004	MTVKLFCAVVGFGNIFPVDIDMTDTVEDLKYKIKEKKPNAIYFDASLLKLYLAREGDKWLNSTDEAMRAVKARQCPDRIKNLMQEHLLLDAMNFQTPDGVIHVLVEYPREDELDGSFLENWFPCWSSLQSLFSVEKEKRA*
>jgi|537210|estExt2_fgenesh1_pg.C_PHYCAscaffold_790005	MRPDFLLHYLGMVLLRGEEKSATTEIDEPVKELTAKMSWWNPMFYGDLPYILGYATSGARLRVVMIDRHLHSDAILEFQSIFQQRAEVIKLFYNLAFFFHKMSVLAKRTCPSSLMPFTPDVNRKRKIELMDDVIVRTIKRNQCRDRVDFRRLADIYATLQELNNRVRERTHLQIVRKLRLKKRLLRVQLSPLGTVRPPMNVDEVRVWLQGMLTALKYWHSCDYCHGDLRWSNIVYIPVSSDSGFWVLIDMDESRKSNTTTIDWNHEFQGYTLIFEHDLFQLGQLMNSFTFSLPSDLEDVQKALLTAVHTPAGDLPTILLNQLHD*
>jgi|537308|estExt2_fgenesh1_pg.C_PHYCAscaffold_830012	MKLFCAIVGVAGSAFPVTIDEGQSVGDLKEAIQVKNRETIKCDAKDLQLFLAKQPVEGDDGKEVVPVYHSSAEEVKEDSFKWLPDEHRAALKLVKGEYDDYINALTAREQILASKTIATWLYTKNNMELPSNEQIHVLVVQGKRIEDVIDILAKLEKVDDVKKMTVILCVDGFQKLVNDGEKTFGSTNADQETVDAVDRVCLNKKSKIAKIIRGMYSDLSDEENLFSEP*
>jgi|537717|estExt2_fgenesh1_pg.C_PHYCAscaffold_1080013	MFEKTMKGFGTDEDALSATLVRYHGVLNDIRPVYKKKYGKELRDRPVYKKKYGKELRDRIHGETSGKLLLALPTACAIVGQTGSSFDVEIDDSEKVSKLKKAIEKQEKISFKDVDAVDLQLFLAKVPKEKQGEVERTEEVKDEVQEDMTWLYSRSEDVKKLKKGEKTSLIEALTMERHELQGEDPLEDVLSGIDPPSVLQIHVLVVVPKGEDVVLA*
>jgi|544930|estExt2_Genewise1Plus.C_PHYCAscaffold_160416	MPEPPALQTLDIVDEDGQHQQVVLVGGIEGGKQTVEIANEYGGFTTEEVTAVKTSEGEKLVIEDAQGQATVVEVHELPAEVAATVTEDSQVVNAVTADNQQVQIVVEGEPEHGEQTVQLIDEHGDVTVEQAKAIETSEGVKLEIKTDQGPVSVVVAEVPEEIKEEVIKEQEEHQPGEFGGNPFTEEEPAVLQTVDVVADNGEHQQVVLVGGIEGGKQTVEIANEYGGFTTEEVTAVKTSEGEKLVIEDAQGQATVVEVHELPAEVAATVTEDSQVVNAVTADNQQVQIVVEGEPEHGEQTVQLIDEHGDVTVEQAKAIETSEGVKLEIKTDQGPVSVVVAEVPEEIKEEVIKEQEEHQPGEFGGNPFTEEEPAVLQTVDVVADNGEHQQVVLVGGIEGGKQTVEIANEYGGFTTEEVTAVKTSEGEKLVIEDAQGQATVVEVHELPAEVAATVTEDSQVVNAVTADNQQVQIVVEGEPEHGEQTVQLIDEHGDVTVEQAKAIETSEGVKLEIKTDQGPVSVVVAEVPEEIKEEGPVSVVVAEVPEEIKEEAAEDSMQGSKFMTKPEFREWIRKHYEDRLESLKVEEQKLEDEERANAGRVKGLEDCIEQASNKFGYYGVYEQAPYYQNAVDWVEEECWTAQQWEPESPYEHPNLRR*
>jgi|547387|estExt2_Genewise1Plus.C_PHYCAscaffold_240409	MSERLDDPTVRIKEKFPSEIPDRSIHVLVQVRREFLYNQPKPRDSSNEWLAEFFNHKVEPRSLPFVGNLSSFVTQPLPAKIRVKQEWLNEWALSPGLQEKMFVLDDDAPCMEFTSLIFNKRTLNPFRRGKTENAFISMWDSIFRNVLDVLFTQAHIDRDSCNGSSTRQKRPDFLFVLDQVCVFRGEEKPPDVNISVPTEELCSKLVWAYGSVPYVFGYAASGYDIQLHALYPLDPLKVLTKNIGTFNLEVKEHLFQIVLVMLNLSLLFQAIADECPASGRDEFRDITRSSGVVVRLSPTFVEKIFPDISTFGHLELVYGHLKRASVPNVDRLTNLHFQKRLAVFKPRGTMVRPSNLLDLFGALKDVLQALVALHRLGWIHRDIRWSNVIRQRTGNSWFLIDFVDAATDPQQYPSGQHLSVEEHAPEIFVENGVHTTAVDIWAVGFLIETSGVEWLDFAGRTSLYRRLIAKDPAARPNAEEVLAELMALEESAKSEKEACENSRRSETQCRKRKLPDS*
>jgi|563418|estExt2_Genewise1.	MVKLFCAIVGVAGSVFEVDIDDGASVAALKDAIKNQNPNKLMNVDANDLQLFLAQKDKGNGVEWLTEKDVQGGVSDTSDLKLLARARARLRRVGLSGEDIVEVDEQIEAEGGGPV

C_PHYCAscaffold_120143	NVLVELPPGTNRAPLSDGTDLWLSRFHHARISVLPTLGDLGEYIEHLSL*
>jgi|576078|estExt2_Genewise1.C_PHYCAscaffold_830005	MVTIYCFAVDVEGSSFDVEIDDVAKVSKLKEAIATNQKFDFAASKLQLYLAKKGKGKGVWLTEKDVQEGVSDTNDLKLLGAAGAPLNLVGLSEKDVKFEPTLEDVESMNTPVHVLVVIPSPDVGPKR
>jgi|576081|estExt2_Genewise1.C_PHYCAscaffold_830013	MKLFCAIVGVAGSAFSVEVGEDQTVDDSKLAIKNQKPNDLKDVDREKLQLFLAKQPVEGDEGKEVVPVYHRSAEEMKEESFKWLPDEHRAALKLVKGESDDYINSLTAGEQILASKTFTTWLFKKNKMELPSNEQIHVLVVVPDPSSNAALEYKDPMSNLRKRGAEVMTDVVMEDDAFVAEENRVRVNRVRCIIVGIAGQSFCINIESNARVENLQGAKKSRCRQRLKDVEADDLLIFLAEKADGAWLSADGAF
>jgi|577802|estExt2_Genewise1.C_PHYCAscaffold_4740001	MVELSLQCAIVGQIGSSFDVEIDDGKKVNKLKEMIQVKNRETIKCDAEDLRLFLAKKGNAWLPDDDPAAQDLEEGKVHTAIQALIDGEKMKEARTIADVLDDNNMTGEERAPKSRQIHVLVVVPQQWTVKRVTKPDDDLSRAKRARIVRLEVAYQGPVPTDFYSVPAETIDTYQQLKEAFLSHERLVRPLCLLYGPRRFGKTTIGHRLVSLLDAEPSILVIYCSLTPLSVESEEAFWVALGEFIGEHTRSFQEF
>jgi|59630|gw1.67.177.1	DEMDSSVAPYAWMETNEAVHDQRNAYMQYLKDNLHGVLHQDGSTTTPHAIRQPRYHIKDTSHMKTLLNCTPEALNHGLKGTADLMIVGETAHRMNDVFTDLQLVVEVKKGQCKAYEQQQLTLELVAANLKCEKRCAPIKLLTNLNDYWCFMWFTPDSKKARLTLSCPANGFKAIKDFLAGAVDA
>jgi|60673|gw1.22.466.1	MVKLSCAIVGVPRNVFTVTIEDAASVSALKEAIKTEKKNVMANFAAEDLQLFLAKK
>jgi|70314|gw1.16.564.1	MVKLSLQCAIVGQTGSSFDVEVGESQTVGDLKKAIKTKEPLTITCEADQLQLFLAKQPVGDEGGKEVVPVYHPSVEEMKEESMKWLPDEHRAALKLVKGESDDYINALTAGEQILASKPIATWLYTKNNMELPSNEQIHVLVVVP
>jgi|70333|gw1.32.357.1	MMLSLQCAIVGQTGSSFDVEIDDAEKVTKLKEAIQPKNRQTIKCDAKDLQLYLAKKGNAWLPDDDPAAQDLNEGKVHTEIEALINGNKMKEAWTIADVLVDNKMTGEGLAPKSSQIHVLVVVP
>jgi|71308|gw1.16.631.1	MKLFCAVVGAQGSAFEVKIDNTESVSAFKEAIAAELRYKGRPDMLELFLAKTESGWLSNDDDLITKLLQNRIDTSKLKALWPTWKLNRAKNPQLFGRDVSLGENVVHVLVRFP
>jgi|71310|gw1.13.804.1	MVKLFCAIVGVAGSAFSVEVDQDQTVDDLKDAIKTKNKIKLKKVDASALQLFLAKKGKAWLSNDKTGDTVLQSEDVASFEQMRGSWRLNDPKLFGTSVLLTEKVIHVLVVIP
>jgi|72559|gw1.33.407.1	LVMVSLQCVIVGKEECSFNVKIDDGANVSKLKDVIKEQSGGLITVPPPTMQLFLAKTGREGWLTGDDATAVVSDDLNHFTLMDPTLFVKDPKHFGEGFKPREGQVHVLVV
>jgi|73233|gw1.1.815.1	MVKLFCAIIGEEGSTFPVDIDKGQTVGGLKKKIKEENEDDPTLKTVAAKNLQLFLTKTESDRWLSSNDSVVIAMRKGDVPEQVKKL
>jgi|73236|gw1.1.816.1	MVKLFCTIIGDGSVFVVTIDEGQTVGDLKVAIAAALSYTGRPDLLQLFLAKTEKNAWLTYDKDLVNKL
>jgi|73237|gw1.12.699.1	IMKLFCAIVGVAGSAFSVEVNEDQTVEDLKTAIADNQKFNFANSTLQLFLAKKHEGAWLTQL
>jgi|80099|gw1.10.758.1	MVKLSLQCAIVGQTGSSFDVEVGEGQTVGDLKNAIKTKTLKTVAAKNLQLFLAKQPVGDESGKEVVPVYHPSVEEKKEESIKWLPDEHRAALKLVKGESDDYINALTAGEQILASKTIATWLYTKNNMELPSNEQIHVLVVVP
>jgi|81603|gw1.5.1157.1	MVKLFCAIVGVAGSAFSVEVGEGQSVDDLKEAIKNLKRNDLKGVDRDKLQLFLAKKKNGKGVWLTEKDVQNGVSDTSDLNLLGTMGAPLKFVGLLEKDVKFEPTLKDIESMNTPVHVLVVVPKKRTSTAIVSEEKD
>jgi|81615|gw1.2.1184.1	MVKLFCMIVGEVGTAFSVDIADGDSVDDLKKAIAENQKFGFAASKLQLFLSKKKNDTDEWLTEKDVQGGVIRDTSDLKPLVVARQILSTATDVEVKIETKAFEAETSPVNVLVVVPERDSTA
>jgi|83070|gw1.12.944.1	MMKLFCAIVGAQGTAFSVDIDVSQSVGDLKKAIKHKNEDIKCPHRDLQLFLAKNEKDEWLSSKDPDVIFMRNG

Supplementary Table 17. Predicted RXLR effector amino acid sequences and location in reference genome. Location is scaffold followed by the direction of the first nucleotide based on the reference genome (R = reverse, F = forward).

Location	AA Sequence
>scaffold_1_R314	MKTATAFATVLALIVATNAAQVPPNTPTLRGLRPTADTPSVEDDKEDRKDHHHVKKVKKIAIPVPVPVEVPQFIPVPVSVPSTVVANSNNAVVGPSTNVAGPGAAAPGAPGAPGAVTPAPTTLNGRPAATPAATSTTRSRPTPAPTNFAGARASGAQLPAAPVQAGAPGMTGFPNSAGVGDNTNNNAFGAGIGAAGGFPMAGNGLAGGFGGNPMNRFGGANGMGSGGIFGGAGTGPAMGNGFGGNFGQSMGFGMQDSNGLGGFGGQGMMTNFGQAGNNGFGGGQGGFGGGFNRRERRL*
>scaffold_63_R381	MVNAMTMAIVLCTIVLRCSSRLRAALKQEVRVLRADAAQAAQTASNISSGLGTRLNALIARVSDLEKAFQASQASHHP*
>scaffold_22_F1619	MGPLTGISLTFVACSRLGSWICSSAFLIISLDSTAAASWSRVASRQRNKKGNACMRISKLRLLRSLKTTKTMSYPTS*
>scaffold_52_R1150	MRLGLFLLVALAALFASCDASAARPVNDLPSGRFLRGESFKESLKILPKTYVKELVDDGDKLKAALQSWSDMKLSRKRLAKSLELSTNRIKKLRKIANRHKVNEVFILDQYVKHLKQLKRSPRLPRVVE*
>scaffold_8_F3104	MSLIWRILFVAAILLAGCNAFSDEAPSHLTLTESALMLRLIDTDPDHIGSRDTGKRFLRRDNDEALTDFDTEEGKSSHPSAKMDKAVISPSIQGLSGQIPTALYNFLLKI*
>scaffold_438_R9	MRLFPLFVAIATFLIATDAFLMTGDSNQISNVDSPGGSRQRLLRAHAEVDFEKEAKEMMRMMKNKVTKEDFAKKLKIAEEIDDIINKRAPGMHEFMQTVKYKRYANYMNFLNDMAKTSEYGDLVKEIKAKSRAQVALKTFRKPTTSQSRWQSILASLKGKRIGK*
>scaffold_87_F300	MKSIYRVLLLTVFALLCGLSNAVNSGGRLLRVVDSTDERGGFPSYLKDSFTKWRINSKIKSWVKKQKTDEYVLSKLGLSTLTGKDLVKAPKYSQFQDFKVGMWLKEATPTTTVFNTLGLNKVEGAVEKADDFGTYVKYVMALGEKADDYPLVTWRKLFGGGSLEQLELKRKILLLVKRDEIDISVMLG*
>scaffold_29_F365	MRFAYVVLAAAVAFVASTDSAVASEQAKLTSVVVAENSPLTHSLTAEQEGQRLLRAASDGESSFMERTKFYYWYAMGRTPSYVYEDFFKGMDKSIIAENPNYKVWERYKAYYEKRKAN*
>scaffold_10_F608	MFCPLCVVYLPGLLLCSSDCIIPMYSSVQESAERLPLENRRRPYRNRPTSYITLEIPQGIGRPQVDRHLRLP*
>scaffold_52_R822	MKILRSLTFLLIGTVAQAENSSKLLRGPDPNYDVAGLFPGPADTVVDTPRTKEFEPEVVDEPVIPSTLLNELDENSVERLVTEVTTYDDYTSEYNRHLRSVNDPAFQGQIQLAEPRHPKEHMIPPSPHDDQVPNLRGWT*
>scaffold_27_F834	MQIRVIALALSAALGSVAAVQTTDRSLGTLVGCPAVRSAKSPCLWAGENGEVVDSRALRELFLERHYVAHSDREAYGRNLQEHMTYIEGEDDKAFIGLDTVY*
>scaffold_623_F5	MHLGHLLFVTIVILLASSDGVMSTQNAGKKPIEDTVVGPSNSNGIKKTRALRTDNGSEERGFLSNLVKEAKVRWWLETGKSESQVKKAQLLDELSGKAFETNTKLFQKFATKAYANKLNKWLQDDATTYSVWKILKLENVSSKQLKSSPAYRTYVDYVNQFDELLQRKWGAYKLPEMVGSSKKEMMAKSSIWGEAKRYEAYVKMALDMEGVTGKALKEHKNYAYYNNFLEALKGN*
>scaffold_25_R1072	MCVAPPTICLIFQLCQGSLAEILNDQVCRQNHPARQQLAISIGYMLDAARAVAYLHSFSPAFVHRDINPSNFLVDAECNVQLSGFGESRSTVKRNGRALRPKMKVPELEAKYFTLNATVASPLGTTRTQLDSPCTHMEKNSAEYIAPELIDGLSEPFFYGEAADVYALAITLWDILHPNGDKYPQANDDYVQVHVFECVLQGLRPRINSNLPLKLCSIIERAWQQDPGLRPSAQQIVKSLEDFQDDLCARLVLDLISDFHDCSSGSSLRTTEDLHVRTYTGAFIVDRMIDRRFVRCPAEAIRLGNALMDSSVLHHANHSTSFENNSASRYYFDVDEAQLALPIDSHIERSVRSSSSLSMNESSIAMLNVGHNDAHPRSSFSVGRTRSEPPCRCRQLGQRLINRKSTHFHRQVQFLTALEPTVDGNTLTTALLGGDEASPQNSYNGLDMTPGIAATMA*
>scaffold_25_R336	MYRVLLLTVFALLCGFSNAAKSGGRLLRVVDSAEERGGFPSYLKDSFTKWRINSKINSWVEKQKTDEYVLKKLGLSTLTGKELVKAAKYRQFQDFKVGVWLKEATPTTS
>scaffold_68_F689	MRLNLVVLAAVITLVSRCTAVSAASSTNQINLSNLNQALNTMQNHAGDGNRFLRSAKIVNDDIDSDDDIDRDEEERGGKTWAEKFAKWHARGESADDVYARFALEPVVRQAYKYGQIGRL
>scaffold_24_F444	MRLSFLLLTATFVLLSSGIVASPTTKDESIPSPNQVLSEGRRLRVHKSSIDDVEERGFNPEKFNRLMNERGYRSTRFSNWVNKNYTDRYVYNLLRVDSNPNYKRIFNYYQTYLENFAPRLISS*
>scaffold_11_R2	MAVWIVIAAATALVRVSGGGRILVNCSWIASICVLPRPLRLADVDMAKMAARRRVFNGIAALYDCLTSS*

784	
>scaffold_50_F848	MRFFYFLLLTSAALLSNSNATATVSGEGHVMTSADAPARALETNNGKRSLRYYATDEDVETDKYDQKNGKYDNDDEEERNLQRHNSPNGLKRRRAGSRRIGRREYESDGGR*
>scaffold_46_R1328	MRLSQVLVIAVASFVFASDTVAVATSNQAKISKMEQSPSQRLLRSNHYPVKEEEDESEDSVDFEERGFTTPDEEDLEERSPLSSATVKKLENIAKGWGTTYSSVAMGTSSVSQTKAKALLALRDAYISGIKSEKNAAKMAILMANKS*
>scaffold_24_F1432	MRLLFAVVLILAACLAAADVPALNDAPSKRLLRSTVRVDEEEERGAWDTLSNKFAKVILKPNQFAVRNMDDPKVAKAAKTTLLKTFKSVDPQKFNSVENFFRGKAFNNLENYVLRLNKQDINKQTSVAKVLSTGLGDEKAFHLFLTATQSSDRAVKKSGKFFRDQLLTQWAVEGKTSAEVTKLFPKGLGANYYLHLENKYSGILMDLARDSQKRATRLAKLERARAAAT*
>scaffold_25_R1150	MCVAPPTICLIFQLGQGSLAEILNDQVCRQNHPARQQLAISIGYMLDAARAVAYLHSFSPSFVHRDINPSNFLVDAECNVQLSGFGESRSMVKRNGRALRPKMKVPVLEAKQFALLGTVASPLGTTMTQMDSPCMHMEKNSAEYIAPELIDRQSEHFFYGEAADVYALAITLWDILHPNGDKYPQANDDYVQVHVYECVLQGLRPRINSNLPLKLCSIIERAWQQDPGLRPSAQQIVKSLEDFQDDLCARLVLDLISDFHDCSSRSSLRTTEDPHVRTYTGAFIVDRMIDRRFVRCPAEAIRLGNALMDSSVLHHANHSTSFENNSASRYYFDVDEAQLALPIDSHIERSVRSSSSLSMNESSIAMLNVGSNDAHPPSFSVGRMRSEPPCRCRQLGQRLINRKSTHFHRQVQFLTALEPTVDGNTLTTALLGGEEISPQSAYNDLDVTPGIAATMA*
>scaffold_6_R1884	MRVLSLVTLLAFVSAQLIAANADQTGIAAVDSNTALLPRVLGVESKRTLRRYDPSEFDSEEAVDSDEEADPVEVADSDEEVVSEGEERVGIPGMEKVASKATKADDMVPNAAKGAMKWKILVQKNMGQLVETAKLVKKLKVGSFYSNVELEKMSLSALRQLDDIQQLQKADIKSNVFGTKATANGMRRKMTRTENMKLPPEQFLVSHVGRGAQRLGENGQRLLSAAVISKGDDINSKVLLISSSDTKKGDFLLPKGGWDHGETIEKAVLREVIEEGGVNGQLLHKLGEYPFKKGATAYAYMMKASTVYDDWAESIRYRIWVRTEMLWKY*
>scaffold_10_F2067	MRLSVILLVVAAFVAALDPATAANDANTVVAVPNVHESIATGRFLRAHLEDDYPVKDERDEDDDNEKDEERMFSFFQEKATALSAFKNLVSQSGDDLVEAVSNLTKKEFVALFNQGHTHMAKMVPGFHPGMSLDEFGAVVRAAGLSDDMKNALMVGYGKYLAHLMD*
>scaffold_58_R567	MVFKCWRITLFVVLTVTAPEILKGEEYGTAADWWAFGAVLYELLTGLPPWYSENAREMCKRVLRTPLSVPEYVSTEAKNLLQKLLTRNPYERLGSLLGGPEIKEHPFFQHIDWEMLSFRDAPAPIQPCATSDTVVRPVIIYPYVDFVSNFLPCL*
>scaffold_13_F2050	MVSVSSVYLFSAVLAFATLQGTTATSLSLDPYTTCTSYENFPGRDTDIKDGGSCTVIVPEDPSTSTSKRKLEWVDGNDIADLEAHFGVPMERKLRNLPTSTTHSSPPWSGGNWLVNVDSINYVWDQGQPSAAEKYATAFGLDVKTFMDDVSAQNGIDSVQNATECTEDKECYEDLICAKRAGKSSGRCLPTWWGMGNAWAAAATLEKEPKCPVTFNGVTFQPMDIKALVTDIYDSANVSYVFTGSRYNGYEDSIDDYGRHTDASYRDLNPGFLHIAATNMLGLLNTTFIVDKDPDYVVWNQPVVGFEVREQMNMTPAEAAKKLYGLDTYPWNVNASSIVYVNSYLSWVTESLNGPIVTLNTTETGNYTYLLELNDDEEIIGGEWLYDSNDYHPDFLWLLEAKPAPDTATSFGLSYTNVTMLLEKATEC*
>scaffold_12_F1755	MQTIRAIVTALTLATIVAGDEGATRTLRGAMADNSELDQLEGSGSNNSILWVNASKPEERRPIRPNYHHGHQQLVCQINFPKNCWYVDIFDQ*
>scaffold_81_R75	MRSHALVLLSTALLACIAGVSTTNPFKVTVTETRFLRKSDPKTNEERVIGGSLTSKVGDFIGSTKLQKYKLRWKTLQLDDDLSKVLKSPQVEKIAKYNLNKASGSQVSMFRRIAAKYSDDILARTLVSIERSADDNPALLAMVKQLREDQIANWLKNKETVPRVVSKLKLGSDESIFRSKALDVLEDFIKKYNTARNGDESLLKTLTTIYGGESELVTMISRAYPYAQLNPQSVEKANNIENQLISKWRSENRPDFSVMSKVKFGDDINEALSSGKVRVFFKYSASKTMALKRLNAKYGEGEVAVAMARAKSTLSGHDVAVVVQQKQMTGWLSNGYSMERVFSILRFKEADDFVYKLDALEEYVKLLKSKNPQDTTNILQVLRKGFNGEEDKLAIALSRPLSEEAKGYQALLFKDWMARDMDPMSVAVSVFKIPEADVAAGFSKEITPIMKQYTKFYNGAADIQPLPPAVRNGRS*
>scaffold_81_F103	MLLFRTLLLVAIGTFLVSDSVLAASDDSTFARRFLRTDDSEEKTINLSGLEQSAKLSKVGLKIDNVDWIKLQAKSDTAFKLLNLDQAGEKAFKSPQFKTWISYMSSISEKYPESAIMSTLAARYSDETLVKMIEATKKFEGMEGIAMKMQEAQVKNWMQSGKTADDLFEVLKLDRSMENLLTNPKLDIWSGYLNLFNKYSKPGKETTVVNTFVTFYGDEVVAKALEAAKKVPNTKEKATELQLALFTQWLMEGAKPHQIWKMLQMEKATWMRNPDANIWREYLAFYKLHK*
>scaffold_47_R672	MRLAFALLVLGAVLLSISSVTASTQADKEDDVVPSGEDTRFLRGLETTDSEERWGIRDLFGRKKFEQMLLNNWDELNKFKVDTVISKLKGTKYGAELLTYLNSRPKAVRAAAK*
>scaffold_17_F1	MGVTVLVLSFSVGSGGVKSSTMCPHSDCIFDLHELMYNLQISAISFGGMQQNGSMLTRAVSQRNSNPTFM

914	CVPSLSRMLRILSGKSYREK*
>scaffold_31_F1334	MRLLLWALLVTLVAFVSSINAEFTADSKVTQDSKEEINALTRLLAVDSSDAAKRFLRGDAKDLTTANDDSKELSAEGEERGLIPSSITNLVSKVKTGWANWKAKALEKAFQHMVKNGENPTTLAKRLDIGRTVEGRHHRLYEKFTAWWINYHTVAGT*
>scaffold_143_R10	MRASIVILVAVIAVFTRSGLASASNTAQLQQTVPGATNKVENAEGGRFLREGLKDESDDLTSEERGIWGDLFKKAKPYLNGDIMYARLFKKSNSQLWRREITPDELKSMVIHLEKAGWSGEKLQKLKDKSHGYEKYFYTPIKD*
>scaffold_40_R1065	MAFSSFLKFLAMATLLMVQINAEPSQQTRNLRIQSDDLPQEQARRLGPNWKALIINVKNNPGVSDGVVNLLKKADFVTGTSKKIKEKVKDTAGKVKDKVTGK*
>scaffold_51_F603	MQLTNILWMATVILFSCNDAAASRPELPTISGVDAVQLNPVNQRFLRSDYNSEERAVTLPFAKLDDVAVAKLTTKLFNTEKLKAALGKTKEAYNAREALFKEVNAVNPAVRKAFLAKLAKSGDYNWLLPYWLGFKLKGIRKVETTEIKNAVRAGNAVS*
>scaffold_2_F406	MVVVGVGVCGVASSATYAVPTDPDCAIFSSPQGVWNKYTGILDIPYGRVWNGRCWAVRPIRKRPAKLRKRRSRNQQHRSPRRMLRLNWLEPLIVKTKARAMTQMKFNLLTERRRSRKRDVPRQRPGQYAPGTARSVEEKPAALRPVGQVICYACSKPGHFAKECPDAEANARNDAYLASRIQRSAGKYNGERSL*
>scaffold_107_F190	MRVLSLVTLFTFVSAQLVAVNADRTGIAAGDLNTALLQGVLAVESKRSLRRYDPSEFDERESEEEADSDEEVDSEDEERQIGLPGIEKLDDAVSKFTKTDDVVSQAAKADDVVEKAAKASPKWKALMLKTWMSLLRPEDW*
>scaffold_1_R394	MKTATAFATVLALIVATNGAHVSPNTPALRGLRPTADTPSVEDDKEDRKDHHHVKKVKKIAIPVPVPVEVPQYIPVPVSVPSTVVASSNNAVVGPSTNVAGPGAAAPGAPGAPGAVTPAPTTLNGRPAATPAATSTTRSRPTPAPTNFAGARPSGAQLPAAPAQAGAPGMAGFPNSVGIGDNTNNNAFGAGIGAAGGFPMTGNGLAGGFGGNPTNRFGGANGMGSGGMFGGAGPAMGGRLNGQSMGFGMQGGNGLGGFGGQDMMANFGQTGNNGFAGGQALTQGGFGGGNSFGGGFSRQRRR*
>scaffold_17_R1815	MKACKFLVLLPSQALANHAVLHVVCDRLFRYTAIQRELRKKLVGDYVSMRTEMNQCQQKWLSALRHEHTTTLDRLEKIETRLDSLVEAATISMNKLQ*
>scaffold_11_F1315	MRIGYVTLLATTAILASFGNVSGDTDLDHTQVAKVASLDAVLPINTNRFLRRRENYDDEEAATEERSAFEALAAKLDKSVLPAFLKIANVKDSERAFHILQQYPISLEKRLDILALHGLSKSDRKKVLLLIQ*
>scaffold_14_F2398	MQPTLVIFVNVLLLLVGLIGRSDAVHFDETAQASPSDSTIESKTATNERFLRGNDKTIRTTEEEDRDITVGSLVIASAKAVNMRNKINIMLARGLSPTRVLKKLNVVRMSDKNFNNFARFYARYLDKYSRKKPNLPKTAEDVIVLPKMKDWLAQKLLPFQVEQNLKDLASRNVNRYMQLYFKDADNIIILPRLERWENQKLLPSHFKTNLIEIGVKDTTKYMEWYMRNGGEQVVKAKLQKWLRQGIDPREIGAKLRKIGVTDTAKYVAWYIDAPVVTKLKTWVNTGLRPPQILDELIRAGVTDIQRYYNTISVIYGQRQVRLYRKNLP*
>scaffold_53_F93	MRFTYFVAVALTGLLASNDLVVASTADKTVVHDQVLSDRELIDTGLNDNEKRSLRTNEDLEDDSEDLKKSDEERFSLIQLSNQPRYYVWFEDEMTPKDVRRKFGLTRHSIKLVKRSIYRGYVKYYDEHCSYFENRKKDFCRAQEY*
>scaffold_18_R467	MRLNLVVLATVITLVSRCTAASAASSTNQTNLSKLDQALGYQVGTMQNHAGDGNRFLRRAKTVDGSDDDIDSDDEERGGKTWDEKFAKWHARGETADDIYGRFFLEPIVRRAYKTANIGSLKQHEYYQKWLDYKAFLKAKEK*
>scaffold_25_F810	MRITYILAVTVAATLHSSVTAIPSVKSSKVATENGAVPAVIDSTHAGAGRMLRWVKEYEEDLDDSDDLDDDLDDDLDDDLDDDLDDDLEEERGFGDTLKKANPLKLVKKGTKLTAEQAAKVKEALKDAADYQKMIENANKLIRSD*
>scaffold_6_F3933	MRFCFVVLATVFALLSSETPAIATAEKHSEALSFINGNNYGGTANRSLRSHDKVNAVEEERAIDADKLVKLLNPDDIAAALKNYDDEVVLFTRWWQHEDDVVNKLMEWPNRMKNMPILTKFNDFRTSMHYDQVLTPWLSTKDLDEVATALRASKMNLAKEQFNVWHKSGVKPAEISAAIEKVKNPLKRKGYGALNGLYKMYVSGEAKKTARAAAKKTEEFAAKRAQAKKIAEAAAKRAQEIKTQKETAKKIADAAAKRAAELKAKAAVAA*
>scaffold_193_R7	MSKATPNLLGISWLLGSLVGSHYHLLNRPLCAWNGRLNWPPPRLGVGLRFHQQRRTLIYLEMHRRYLLLLQLTPCFLPPTLHWLRHLRRQRSTKT*
>scaffold_686_R5	MRFHALALLAAFLAFGSGNDAFELTADGAAAYSRFLRKSEPKTNEERVFEGLTSKVDDLIDTTKLQKYKLQWSKLQLGDDLTAVLKSPDVAKIAKFNLNRASGSQVSMFQRITAKYSDDILARTLVSIERSADDNPALLAMVKQLRDDQIANWLKNRETVPGVVSKLKLGTDESIFRSKALDVLEDFIKKYNTARNGDESLLKTLTTIYGGESELVTMVSRARATYPYAQMNPQSVDKASNIENQ
>scaffold_5_F1944	MRLSYALPATIIAVTFLSSGNAVATTDGGTMDLSAMTSPNAVASIDAAVGGGKRSLRYHNKDPEDESDDEALLEEEERKYTNMFSTTKLDEMLDGTKMMSRFKKWKEKGYNTYNLPAETQGDKYTWIRQKYRDYLYHN*
>scaffold_2_F1574	MGCLHLLLLAATTFVACTNAADQLEMPVKRGLRANEERAFGAGVTEGLSNWVARAAPKLLLTDNELEHLAMKVTSTDKVFKMLKLDDGLDGILRNPNLKAFASYIRKVHATNPDQVLITTLITRYGDDTLAKFLFEAKQVRRTE

	ESAKMLQAAQFIKWFDDGKTPNQVFNLLGLKHLTAYEDKFHKLWWEYVVAYAHLASKLKKPLPVEL*
>scaffold_24_R796	MRFTYFLLVATAALLASCNAAAATSNNQNKLSTMTSTDAVVSALESSNDKRFLRSYRKEDDGDDSDDEEERSVMTAEQVAKWTKKVERWVKKGHTPSYIKDKLTALDGTMNAKNREKYRMFGAAWGRANPHELGRM*
>scaffold_10_R1115	MRLSVILLVVAASVAAVGPTAAANEANTVVAAPKLPTARFLRAHLEDDYPVKDERDGEDSDDENDEERMFSIFGEKATALKAFKKLVSESDDDLVMAVSALSKEEFVALFNQGQAAMAKMVPGFRPGMSLDDFATAVSSAGLKPDMQNALMVGYGKYLAHQMG*
>scaffold_3_F2910	MATLVVCASNFALASTVADDLHQEAEGNVDRRLRAAAPANKDNVAKIAGGFLTKIKEGSTLTKAEQMIKNANGDEAAVKKAILLASTAKESAKMSDESIAKLSAMITTAVVKDPKSWPRLQKFVKVTLGAGVGGLALYGAYKLLFNKNSSSGPVTTTTGSADLVAASTSGSGSA*
>scaffold_26_R1068	MLLCVVILAFLNTVILVLCPRIGRVFVSFSTVAAVWFDAGDTVSLSPVLAPSSWFVVIRLAAAFSGEWILGEDSRDLRPDDMDSRSLVTILTEELAEVGGVEAEGRFCSWLVGFLLPSAIVDCEDRMIFELLPAWGRFDTSVSLATCR*
>scaffold_8_R1192	MWLLLCVGFAFSVCVDAVRLGSRVLLCPPSSPPYRTPYCPQQFSHPRPRYEDTPQRGLRAFGAPALDGFVLRCRIVPRSSRLTLQPVLLTV*
>scaffold_93_F91	MRVLNLTMLGAIAFIVNMSAVSSADKPQLAVAGALPISRFLRTHYTDEERAIGLNLLPGSKKISSFMTDKKLSKPQEQQRNRRRFQQTQARQGRRQVVREPEIPRLGSIRGRFQPETPDPELDASHACATVWR*
>scaffold_24_F545	MQSAAYIAAFAAMLAAVKAESGSILQGRQVLRGQLRVHQCADHALGHRGRQAVPAVHEGGRRVLRHLPGSVPVLLHVEDGLPVH*
>scaffold_2_R1164	MHFHSFIFIFLHHTSMTTSAAASCSEAARASRTIELLAPVYEDVCQAIKGGSTTVPVTLERTADDWIQLVFPQTNVRKDVACVNGASGCRCDFVRLLRALLTLTEQLVVKVAATYVLAHRSADVATLEMRVQVHEEARRGTSLRDFDLVLCHLQATVLSVVSRSGKKKIEARHEALESARSSSCHVVGCRLHPWDASSGQFNPSIN*
>scaffold_214_R4	MRLAIKTLVALAAVLLATSTEAAKAVQTGGDVNVVQSSHILPGENKRLLRSEHDEGKLLEDDEEEDDEEERKYGANLFSTAKMEKMLGNDWYRYQVARRWKRDGYTWETLPKDVPVDLVRYFKGFRERHG*
>scaffold_7_R1223	MVKVVRVAVVGAVFMASVDATSMKCGTTQATPLGAPMNDCNPAYGGEIDPNCMPEVAITDAEGCEHATGPAMDEIIGSITGASAATRSLRRMEDASNSDVADLETYFGESLELSFTTLKEQYSSASVPTTPWPGSYWPTYQDGINVIWKTGDVSASEKYAIAFGLDPTDFMNKISAKTGIDSRSSSTKCTADTDCTYRNDGSVCAKRKGVESGYCVPTWYGICHAWAPAALLEAEPQCDVVKNNQTFHVLDIKALMTDVYDGSSISTVFTGARFNGPDIPEEMDAYGRYISAPRRDLGPGFFHIAITNILGKHKKPFILDVTAGSQVWNQPVRSYQVQTMELVDANEASQKYFGVSPYPFNSEMVFLAYVKTTVSWIVEAYADGPLVSSGQVDAYTVSNDYQYVLELDANYAVIGGEWVEGSKTDHPDFLWFPTEKPDASTITSTGLSYAHVKELLELSLACGSSGGTSENASASTSTGGSTSASISGSASSSASKSTNESTSSSNTYSNSASASSSDSSSASSSAGSSASTSTSAAASASTGTSETASASTSSSASGSQTTSSSGYTSSASTSSGSTSSNYVAPGSTGSGSTKTEAPSTAYPSSGTNEDGFLSMSGDGSYPARSASGEESAAGQGSTPASGSAGTTDATSTYTSLTGSTVEDTGASLPSGKDALILTPESTSPSTTGEESTPATTAAPPIGVGYYTPPPTSDGQDLADVLDTTSPIDSRAAVTDEPSEGESTGTTALAHRSC*
>scaffold_568_R2	MRLVIKTLVALAAVVLATSTEAAKAVQTGGDVNAVQSSHILTGENKRLLRSERDEGNLLEDDEENLLEDDEEERKGGANLFSSAKMEKMLGNDWYRYQVARRWKQYGYTWETLPKDVPVDLVRYFKGFRQRHG*
>scaffold_81_R217	MTVRDIVFLAAVVLLVQAQALSVPTDSSTRILRTSVDTEDLFDEQRAGLAESVIKKATAALRPNVTPEKLANWLNKGKSVDDVFARLQLNKASDKILDNPQFATWLTYTDDFVKKNPNTETSAISTLTAHFGTEALTKMIQAAKKVDGTEAIATKLEAAQIQKWLSSGKSADDIFTILKLDQVDDSLLASPVFDAWNNYRKVFAQDNPTNLHKPSVRVLEFVPEPLQQGPTS*
>scaffold_81_F224	MHLQIALFLVVVSLLVNVEAVPAKAQSDSVVSFRHIGRLLRDEREERGVSANAVETITDAVESKINTAQLKSWLESGESADDVFKLLKLDSAADKVLGHAKLDEWIEYMKLFNGQKGSKKTTLIKTLTAHFEDDGVARMIQKALQVDSTAKMAKRLQFEQIQRWLGHEKTPEEVLTLLKLDINRYDLFEKPELLTWVKYLDDWNKMYPDRQTTLFARISPLLEEGILANLLIKAKSVASTEKIALRIQAEQTASWLKAEKTPDDLFTLLRLNRAEDSPLLENPIFDAWVKYADDFREMYPKVSFDPIATISEHYTAAQVATMIVEASKSPSTSSIAHRLNTEQFRDWLNTRQSPVRVFKLLKLDEAGDKLFQSPVITTWLNYATFYNTKREKVSITTLLRKRFGDEVLAGILTEAQQVPATKEEATKLLTSLVGRWPKSRVHPDNVYKWLRVQGREKTDGFRLFYERYAAAYKAARNG*
>scaffold_37_R1044	MRVASLVLLAAVTLLASREVVCATTNTLAKADTDTINAAIPIDDARPLRNLRKKTTSVGYDAEERAAEEELVDVELLDKVISDHAYAKQVFLSWLQNGQTSQDIENRLETLGVQDKYGKVVTQYAHYLTLLEERSA*
>scaffold_18_R1184	MRFSFIVLLAAISSLVTTSHALPALPHEQSTVSKVSSTNPDQSDTGAQPSERRFLRSAGVGSKMLKSESFKDAKFAEWLKQNLSSFTVFESKLGLKEKYRGLYDEYAKLHKASGQYP*
>scaffold_175_F	MWRLSCWAMAETLSVPSLVCSFAVPAVLELPSEVPAAVIVRGSRQVCLRGHRRHRHRRHLRWNCCCSSLR

27	RLRHPFRLRRASLVVLVESSLLPSS*
>scaffold_13_F221	MTALSAWCTAVNSVDAGKCCLLVLMLYCAAQRLVNPSQLLPTGVMGVCRHLRWNHWISRRDTVLQASDTLQDAAYATGVSACEVTKLCELLSSGRSRGDAGSRLCPV*
>scaffold_81_R228	MRVHSLVLLAIAIISATDAVAAQSLPEEQNVSRFLRTNKAKETDSEERVNLAGFELKIGFVDDIIEKMHLSPTFKELLANKGDAKKAFKAFHVDDVADDVFQSAQWKEWAEYVKYVAVKKNENADEALAAAMSVAYNPDGLSKLLAKAAQNPNTKDIATVLENARQSSWINGGFTPGAIFKTLNLDKADDIFDTAPFATWTNFLKAYNEKHPKKAMTEFEVFSSVYGQQKFAKLLASADDGKYAQAMKKELVQSWIDDGVHPTNMFAILKLDKVDDLLTNPVLNLWVRYMKEFNELYPKQATTMIKTFTQSYGDEKVALMIQEAAKSSDEKVVEFAKNLQTAQINQWMVDKKTPKEMLTVLGINSQTLTENPLGNVWRAYNKEYTKKMANGDFAFQP*
>scaffold_50_F1228	MRLTCILLMTAAALVGVLDASAATTGNSVVANAAMVISPLAPESQGRRSLRLVYDDEDDSADEKDEEEEESADEVDEERGWFSDKVALTSLASKFVGKSTDEMGEVIKGLTPAQINTMFESGEDSIQQILPGFKTGMDFTKFDELVQKLPQEQQALVMSAYTKYLHNNGKIL*
>scaffold_38_R261	MRHNFAKVLVAIAFVVTCSAEAEYHTTKSDPLALTLSLRGGVPRTRSLRSDKYAGNEERAAGTSAVESLVKATTNVDDVETWLKRGDTTNKVFKALKLQKAGDNLLDNPQLPTLMRYLRLFNEANPTKKTSLLATLTTHYGNHGLTKIIEAGLASTSKKTVATAKHLQTEQIQYWMARGRSPESVFGVLKLDKLLPFTWISSDLFEKPGLKTWIRYLDEFNAENPKQKTTLISILSKRYNDKTLANMLIAANKAESTSSIAKRIQSEQTLQWLSKGKKPEDIFTLLQLEKAGDSLFQNPLFPAWIKYADDFRLRYSETDLATMSTLINHYSDEAVAKMIMAASEDPNTKMLAKRLQSELQKDWVFSGQTPNDVFIMMNLDKTLDKLLENPLFDIWYQYGLFVNKMSAKANWNPITALLRTYGSEKELSGILMAALKQPSTKAMASKLLQIT*
>scaffold_13_R793	MRLSQVLVIAAASLLFASDTIAVATSNQAKISKMAQSSPNQRLLRSNKYSVKEEDESEDSVDFGKRGFATNDEEDLEERSPLSNAIVAKLDDIAAGWGTTYYKIAMGQSSVSEAKINALLAMRDAFISNNKKEKELARGMLMLANKS*
>scaffold_29_F771	MRLALLFLLVIATLVATGNTLAVEHTEGKITSSDTLLQPTAISNPDTTQTRRLRTPESPNDGEERRLVNVDLAIKDAVHEVRKLTKWKLQFAVWKGLKKSPTKLIQEWGMKYPYTSDPRWAKILAYKAFWGKGPLKYP*
>scaffold_25_F1705	MQRRMSTPFFLMITTIGDAQGEVEWVMIPADNSPLIKSDNFSRNCGATRRTRWATGVALPTSMSQTAPRAAGGRAFPFPIRRCLRFQMICLNRSICSGVLPSASSIWISSILTSSVVALTSGRMAI*
>scaffold_102_R91	MQQHLVFCKVANFILSTVLFFRVALPATHADLNFPQSHEQQLRPLTSSVLDQTRAAVARGRHSQLRRRRLRGWR*
>scaffold_83_R291	MSFTIGVCLVVLLQSEVHIICRKTHKKFSKNSFVNFLVIAKPEGYGQPYGLHHPTQVLRLGRVRLLRRGRERHFYILDSN*
>scaffold_3_F3292	MRLTCILLVAVATLVGVLDASAATTGNTVVANAAMVNSPLVPESQGRRSLRLVYDDEDDSADEKDDEEEESADEVDEERGWFTDKMALSSLASKFVGKSADEMGEVIKGLSPQQINTIFDSGESSIQKLLPGFKTGMEFDKFDDLVRKLPQEQQGVVMSAYSKYLHNNGRFS*
>scaffold_81_F70	MRLHCLLLLAAVALASVDASPLQLNQQSISKANGFLSKRMLRTAESSEDSEDEERMNMPGLDTVTNAISSTVTKGKMKLWLAKGEDADDALKLFNLDNGIEKLRDATNFNTYASYVRQYNAQNPDHEVSMLAAIAARYGDDEAAKLLHTMTRHASTQAVATKLSQEQVDLWMAAKKTPKEVFALLKLNQNVDDLLSSPALYSMDDFLNAYNRQHKNQHTSLMKVVLGSYDNAKVAKALQDGLESASTKSRAWELKERQFDDWIKAGIKPKEN*
>scaffold_46_F862	MVMILIFIIILETGEGFVPDGDNRHYADTNSAQTLKQTDIGEMREQGASGKEIIQKLVENSSTWETKTEFSKQKYLKKKQQKYMPRVRFLRCTAESLCRTYRLKNPAKICNLREDSLGQMLVYGNIFAGGQVLVVDTCMGLVTGAIAERQGGSGRIICPYEGQQPAADILRRFNFGTISSFCEQNGWIVANFLFKNR*
>scaffold_6_R3168	MRLAIKTLVALAAAILATSTEAAKAVQTGGDVHVVQSSHILPGENKRLLRSEHDEGKLLEDDEEEDDEEERKYGANLFSKAKMEKMLGNDWYRYQVARRWKREGYTWEGLPSNVPAALIRYFKGFRERHG*
>scaffold_93_R283	MRSSFLVLLGATLLQSINSTSLAETHITSNVQLHSEDIVRRLRFAPEQVEERGLTVPKFQDIVNNQQLAWWLKRGKTTDDVFAKLKLNLAGSSIFENPKFVAWIKYVDDFNSKHNKGISAIPTLSKQYGDDVLAKMLQKARQDETTKATATRLQTEQMGIWRSQGISSDTVFATFKLDEGIANLLANPGFNIWARYLTEFNPGKKTTIFKTLEDHFSQNILSQLLIAAQKNPRTEKFATSLQNVQLQGFLERGESPTVVFKLLQLDKGADNLFANPQYKTWLNYATSFQKTKSDAAPAPVIDTLTAHYTDISLVKMIATAKATEGTKNMATYVEKSLIGKWATDGKEPTYVSKLLWASATDKKTLEAVYLEQLIIHSTVKVSSNLQLEQISLWMGKKETPDAVFKLLRLNKGSENVFKRPQFDTWLQFANKFKTQNPEQSKSVFATLSAHYDDLPLATMIKTAKEDVNTKKIAEYVERGLLPKWAADGKAPAYVLNKLATDKQDKERVLTLFMKEIRIVEDKITRAES*
>scaffold_118_R15	MQTRYRLLLLVLLAVFLASTRASGASLQETTATSENPRPDGPVPTRSLRESGAVRLLLSPSEEERMGVKEAIGWLWHVVKMKLKIKFWLYRGTTPEQVLEKLKVVSKTDENYKYYARYYFRYYVKYPNKMPKNAPTKTADAIMK

	ARLQDWLDKNLSPPQVFKELGFSGTFASAQGHPDYKYFEQYAKMWSDLQVRISSGHA*
>scaffold_31_R746	MAIFVACSTVATAESVALTLGDNEVRRLRLNQQNIAKAAGDLISKSKESATLTKVINIAKTANGDEAAARRAVMLAAGAK*
>scaffold_8_F2912	MIAPLFLIHCILLLTVCRGRHPPFGLVVVVLQLEQRRRDVRAQVRNLRIHIVTAATNNNQRQYAVLDNIISISNELTA*
>scaffold_18_R689	MSSSTGSQVPSSFLLGSLAGVPFALIAGTHARPLRAVVTVAASNTVPVVSVGMNSPRSPSFAATAISMGVTAFAGICALPAIRAGAVVRPASASLVRNGITIVRPFSPYFTSLRSKSIFAFLSVRKSTPSRNSSVQPEMTHASTQIVSPNTFWNWKRQTPRTSSRNPPIPSTYSTGASRGSLFPYCIHAVPATEYLAQLSSLMNFCSPSIITHAVGNPSSASTYCTASPSPGSPCRCTSLTRANSVSVPGLSPHFRRSCRCRNCSSASVACFSLTASRVSSKVRFSTSLTRSSLERARRTRLRFLILFLRRLRRRACCNCFSGPSSLPVSGLSLSATTSNSASSPILSGSAASPSSEIACTTSSFAGVVRLLPPSAPTPPVASCCAPSPDRASSRTRCSSLAGRCR*
>scaffold_3_F3706	MPRATSPSLVLLSLYNSIGLGGELEPNRSWISVSVGIHAAQKLWWISARRDERVILARKLRPGSVRGLFAGATRLLGWVVRVFGRRHGGGGFFFLELPIFSIRIVERILFRVGSEVGLLRGMLLLVESMVLGDREVTLCRETGSSSANGHCRGCACCRGSRRGLRVRRWERGLERWRVHSEMDSSVLPET*
>scaffold_2_F1382	MRFFWVVLLTVIIVLAGVDTCTARGQSKLSSSDFVRPFVKNAPNTQLESKATRLLRTDVTKYDNDEERAITLPSGLSNMISNVKKWFSNFISKIKLSFGEKRKLNAWLKQGKTPDEVFEILNLHKGTKGLLANKNLRTWSVFMTMYNRKNPTKMVNMLGTLTKYYGNEAVAVLLEVSRQGKTRPLANRLQTQQLHGWARNGLNTDVVFNLLRVGEGSVKTLAQNRALNVWVYYFRQMNFYNKGWEAELTKKLLTVYDDIPMAKAFAVAKTDPGTKYISSQLQRFQFKKWLADKVEPATLLEKLKMDKTKLSFEPTVEVYVAYSSFYKAYSKTVR*
>scaffold_60_F708	MSWMICWICLVTKTISLMQCIRDQCRLHELERTTRNLRQLSFKLVALKSSTDFFRHYYLRCSHDPLLFVGAPKY*
>scaffold_24_F1319	MRLSFIFLLAVTFSSLVATSHALPHEQSTVLKVAATNPDQSVAEGQTSQKRFLRSAGLGSQMLKSESFKKSKFDELLDDNVSSFTFFVDMLKSKKKYRDLYDEYAAIRKARGAYP*
>scaffold_18_F2148	MRPNLVVLAAVIALVSRCTAVSAASSTNQINLSESNQALDTLQNHAGDGNRFLRSANIVDDSVDDIDSDDDIDNDDEERGGKTWAQKFAKWHARGETADDVYKRFKLEPFVRYAYKHRQIGMLKENEYYRKWSITWPS*
>scaffold_5_R1281	MQFTYVLLLALCIAITASAAVQDNEYQAVVSPFAKRSLRSVDTGTESDDEEERGIIPSSLKDIVKKGTSKVSDWSLLRKYKSLQKAGRTDDDIYKLWVRQRKNTDQIYTRWIRLGKSEEEVSQLFLKHGLNAEVLYNILSRQGKSMDDIYSLWKKLKLPEGQIYNIWLKSKTDDQIFSAWYKAKMDPEDIGHVLRLGKDPNTKRNVPFWEKYSEFYRAKKYRTS*
>scaffold_81_R213	MHVRLLFLPVLLLLVGSDTSADKSVPVTTRLLRSQKLLQITTKSECSESTSDPSTTSSKTGSLNRGYPRRSDPTKHDTNESNILFYLKM*
>scaffold_7_R2262	MRLHRTLLAPIAVFLAWNCFDPTTNAQVVAQDLSDKAFAANTNALRSLRSQKSSTSEDDPIINEETRNTMYTQLFPAWYAAGKTPEDAFEELKNPSTGDENWPIYKNYKMYYDTYKTMG*
>scaffold_39_R458	MRTPSFLVLAAALLVNADAASSRHLANPNVQNLAHVNDNWLDTKRFLRVHVEGEERGISAPSVKMLQGWVERGLISDEAVKLISLGDKADDLLSASLLNAWFSYVKVFNKENPSDKMNMIKTLTARFGDEALSTMIETAKRSSKTSAMAEKLQAKQLANWAALKKNPDDIFALLHLNSAKSLLFDQPSVNSWLKYMDDFTLKSSSVEFSAISTLRKYYNDETLAEMIIVALKSSKTSEAAKRVETELLRTWLNSMKSSTDVRRLLNLSTAPQSELSLIWRNYVALLNKVDPKFKTEMLQAWVKKGLITDDTFRLLTLGNAADDLLNGSLLSAWATYIKVFNQQNPTEQLNLIAVLTARFGDEAVSTMLEAAKKVPTYHTIANRVQTEQMKLWLDAGKLPDHIFVALKLNTVKTKLFDQPQLNTWVVYLDEFNKANPNSKTTLFSTLQTRYSEATLAKMLVVAKQNPNLESLAVRIQGEQLQFWIKANRRPGDIFKMLRLNILGSDLMRNQLFTAWVQYTDEFRKLNPGTKLTTLATLRKYYSDETLVTLFLKASQSPNTAKMGKRMESEMLREWFSAGTKPTHPVGVFALLNLGRTGTKVFESPLYNVWTNYVGFMKKAGAFRGDTITLLRGIYGDESLAKVLIAAGKVQSTKNVANTLEKELFALWKAARVHPTQIHKLLRVENVSRNSPIYKFYGDYVLAYTRA*
>scaffold_129_R17	MRLSFVVLLAAAVSSLVATGHALPHEQPTVSKVTATNPDQSVTEGQTSEKRFLRSAGIGRQMLKSDSFKKTKFDEWLADNLSSFTVFIDKLGGKEKYRSLYNEYAALHKASGQYP*
>scaffold_73_R212	MRLLYLAGVAILSFAADATGAKVLVSDDSNHNGAQAASASVVSTTRLLRARSVIDEERAGGISASASDKLAKLFKSSKVTAVAQQGENCGKCLLSHESREHSLYEGI*
>scaffold_46_F1215	MRLSQALVIAAATLLLASDTVAVATSNQAKISKMVQSTPSQRLLRGNKYPIYEEEDESEDSVDLEERGFATPDEEELEERSPLSISQVKKLEGYARRWHTTWEKVALGRSSISEDKVQALLALRNAYISGVKSEKNAAKMLILRANNS*
>scaffold_15_R1282	MRLSQVLVITVASLLFASDTVAVATSNQANLAISKMAPSQRLLRSNKYPIKEEDEEEDLSEDSIDVQERDFTAHDEEDLEERSPLSDAVVKKLNTIANGWGTSYSSVAMGRSSISQAKASALLALRDAYVSGDRGAKAAAKMAILR

	ANKK*
>scaffold_77_F129	MRLSYIFAVVLVAILQSSGTAHPVYEDSKQIVSAGAGDATKVDSGRLLRGVEEKMEAEDEERLFKNLGTYLKKIPQKIKDSWEVKKAKEQLERSRNRRKWIREQNAVPTS*
>scaffold_244_R1	MRLTFVLLAVAASVLTRTDATPATYGEVTSTIESPNRSALKNMAETLKERRPLRRPRCPSTIYRKKSAQTFSETRCSGPACPQSLSRGPSR*
>scaffold_5_R3448	MMRWRLLFILHALMATLTLPSSCWTVEQILTRGPRTRKLRCSTLPRRDNTEVFDCLYEGNATLQRRIATVTWRRKKLVMLKL*
>scaffold_107_F161	MRVLSLVTLFTFVSAQLAAVNADRTGIAAADLNTALLQRVLGVESKRTLRRYDPSERDSEGDADSDDEDEERIITIPGIEKLDDAVSKVTKTDDMVSKAAKASTKWKALIQKNINELAETGKLVKTLKANVLYKDVELEKMSLQGLRQLDDIEQLRKVDIENKVKGTKKTPDGMRRKMEHTANMKLPPAQFLESHIGRDAQLVGESGQRLLSAAVVSKGDDVHGKVLLISSSNPKKGDFLLPKGGWDDGEAIEKAVLREVIEEGGVKSQLI
>scaffold_10_F2271	MRLSVILLVVAAFVAALDPATAANDANTVVAATNVHESIAIARFLRARDEDDYPVKGERDEDDSDNDKEKDEERMFSFFQEKAAALTEKATALSAFKKLVSQSGDDLVTAVSGLSKSEFVALFNQGQAAMAKMVPGFRPGMSLDEFETVVRSAGLSDDLENALMVGYGKYLAHLMPK*
>scaffold_73_F395	MRFGFFLLAAIALFGLCESTVLNTQQKRNLRLSTTNDNEERAIGNISKVDDVADDASKNFAFMINMFKEWDELSQAQIIARMFKQTTPDEFAAMWIMYKVYQKLGADDLIKTLKAKAK*
>scaffold_6_F173	MRLFIKTLVALAVAFLATSTEAAKAVQTGGNVDVVQSSHIVPGENKRLLRSERDEGNLLEDDEENLLEDDEEERKGGLNLFSTAKMEKMLGNDWYKYQVARRWKRDGHTWEHLPQHVPADLVRYFKGFRERHG*
>scaffold_52_R985	MRFAFLLFVAAVSLIASGDALSTQADATSRHLRSHHQTNTYDAEEEERGLDKSIVKSLPEQFKNMYKYPSNMENVLESWRTGLQSVDDAVMYMKSLGMDFDAISHFVDAYRKHINKKGLPY*
>scaffold_78_F77	MHFISSFIAVALPFNVLAEELAWELDCSVPLGFGPGLRLGVDFDRAVTLEFAIGFSFELTDFLEWPRCWRRVLLGHLSSSNLRCWRVSSLRCVLPRGRRQLRRSFTSAEIACIGEPGYTS*
>scaffold_26_F300	MEAQGLFACLLWIRSVFPAGRATVFGDSTIVINQALMLNRCQAPSLRPWVGAIRALGTGRPAFYLQHVRRAYNTASDALCNWMMDTLPASDVILRVPSGLVRHRTRRLRALPR*
>scaffold_431_R1	MKIQLLHLHVLFLVQSLDVLHVLRGYYHAILREVHPVPLGLLPDANNHSLQRPLREILVTRISINRTGRPENHYLAQRRRLLLQHL*
>scaffold_6_F139	MPLPVAVLALELWLDTVSLYHVVCTWSTAIERQQVRPNGFVRVSVGLRSLRWCRRHLCKLRFHIAPVRRQTSVAIPYPLSCQLLSCSCQCFAPGIYCCLLRYSREFVRIPVHEDHFSLSIVLYHRHTAEIAFNHASSYCWWLLDHVKRGVLMHPCKTKEILVTMREFEAVKEIRKVECVEG*
>scaffold_30_R79	MRLKSLKVLSALSACANRVTLQFSPAGTCASAVSALKHYGRAPARVPFVGHPLRHCCKFESRQRRPQQRKLRKTRLKWRMSSDINLE*
>scaffold_11_F1229	MKIYTVGAMLFVAATVSYALESRQLRSQQQQTGARIVAGDGIEETAGDDWNVLLSDRKRGAKQAGTLVRDSGKDEERLVADSRRTQTYPPVQ*
>scaffold_10_R2236	MALGTVVVAHTTLFTHASSACLHFSGCPAVKRTAVEDFDSRYSGASTSPPRVRALRRKRAKRKEISYGVWRLHQMTAHTRGMRWSTGFCGPSPPLLVPFHLVFVLATYVIRCSSAPKPSKR*
>scaffold_29_F661	MRLNCFLFVVAAALVASTNAAASSIQQNHVSQTTPDIQAATQTDSVVKRSLRYVKDEEDSIDTKDEERVQGINVKELNKILSAKRIEIPANIEALSKKAQRDLVHTFKGQDLTKKMFATKLGMRDVDDVANRHYPFFEKWEHLFRPGKKEKKVPEMLIGNHEYYY*
>scaffold_46_R961	MRLAHLFVVLAATFLVSSGALAATNTDSVIKTDSYVKGSKPATHRALRTYKADFEDDDDDDDDDEEERGIKDIPLERLQSLGRKVGVSADDVLSDAAGVMRTMSESQIKQWTKGLNKLKQLYKKAKSPRISDY*
>scaffold_46_R783	MRSSFVLLVAVVALLFRIDAASGSSMKLRSGQNLIPSTETRETEQIGRVLRGEAESDPESEERGITDLAKLLGTKSKTMFDNNALATIVRLKSQFATADDAVQAFMTRNINPDAVYKWLKLYKANNQVVKKTGDAAPEYLLWIRYAKEYKDAHPKWVSKLPKGA*
>scaffold_29_F655	MRLAYVVVVAVVALFASQDAVSAEADVQLGNTLNVNSESTTRFLRVESTIEAEDEERALPSSLTKISEKLKPVGDKVKPLTNKVAPLTEKLTDKTMAIAVRLKPIADTFTGKLKPIADKLMPILKPFAAKLKSAPVVQKIIEKFKTFAEKIKNYKVGGHTLSERYTMAKFENWFKQNKSPDDVKTLLKVGEGATVNTKNYDLSVQYNAFFQWATRDKEMKAKKAAAAATA*
>scaffold_710_F2	MRLTYITIVATAAILACCDGKSAVGDSKPLAVPQSHVQTGNNANRFLRVHDDEEERIGTQFITSLSDKFASAADKLTRSKSLNSISKVDDIAPGRAGKTLGEVLKIDDVAYLKAAGKWSKNLDDVEDAKLVSELSKLDHKEALRVLDEKNAAAFKSIEDMGYSPDGMFKKMKELGKDYFDPFLLKHYTRYWMAKHPTWTSSL*
>scaffold_2_F1679	MRISTLSLLLATVAVVLSSCLASKGEDPSQSIANVDNIRGAGRFLRAQAQVDEERVNLKLSPESEKWLAGLAGKSAAELEKAAQAPKNVNPEKLLAMMKANAEEHFMNLAKSGVTPKIMRKEYNIKRMRKVLSKDALMRNAN

	YQEYERFKEFWNKLPKKLKREFLAKAASLH*
>scaffold_225_R6	MVFSVFFSAILLSVSASFNYNVNLETPRVQYRGWPTTWFRSPIAKILWERYLRNLADSIDIPLNPDIRGWHMSNPPLEVCNRYLLIYPFVEQRIVHSLGQFCSAGDLLRFV*
>scaffold_237_R14	MQRRMSTPFFLMITTIGDAQGEVEWVMIPADNSPLIKSDNFSRNCGATRRTRWAIGVALPTSMSQTAPRPAGGRAFPFPIRRCLRFQMICLKRSICSGVLPSASSIWISSILTSSVVALTSGSMAI*
>scaffold_614_F1	MAFSSFLKFLAMATLLMVQVNAEPSQQTRNLRIQSDDLPQEQARRLGPNWKALIINVKNNPGVSDGVVNLLKKADFVTGTSKKIKEKVKDTAGKVKDKVTGK*
>scaffold_44_R818	MRFSYVLLVAATALLATANAIEADPTSRSLRAHKSHEKSQDEERAFTYTFNFSLWDDLFNSLPEQFQRMRKEPWYLRRIFRSWRSGMGTSDEAVAFMKSQGLSQKAIDQFEDAFLKYRAHKLAKGK*
>scaffold_29_F663	MRFLNILLIIAAVLTAAVSASEDAKPIQIKGANNSPNEVSAHRLLRAHKESDLDAEERVIPDVYHLSKLEKVAIYPKIVGWRLRKFDVNAAMADLGVMAREVGTKNMAIIRWYQKIVKNGGFKHTPKGKYITQRK*
>scaffold_111_R171	MDSTASTAVLIAMTALVDAQRLLRSEASTATDSTVSTADFSTLSSGSGFTPGNVEAQSNFGALDKEGSTGGNRPSGSMQGGAGRGFGGSGHNGMQNVGSGEGLAHGSGSFGGHGGFGRHGGHGRDEGSFSGGDFAGSFGGHDFGGSGFGGNFDRSGNGEMPSIGSGEVPTSGSGEAPTAATTTSSTSSVTASSSA*
>scaffold_443_F6	MRLSVILLVVAAFVAALSPTAAASEANTVVAVPNVHESIATGRFLRARPEDDYPVNDERDEDDSDDDKEKDEERMFSFFQEKKTALKAFKKLVSESDDDLVMAVSALSKEEFVALFNQGQAAMAKMVPGFRPGMSLDEFETVVGRAGLRRDMEDALMVGYGKYPAYVM*
>scaffold_29_R1159	MFPRLYAIALIVVALISTCGGTRMDEKQPLALLTTRSSRHLRSIDDRPRDTKTEERGPNIDIMISDAAKKVKKATWWKVKFAVWKHLLRKDPHDVRGILGMRNMGREALQHKNDEQLAAFWNFYGKGPLKYD*
>scaffold_52_R3	MRICFALLLAVTALTAVVSGSSVNLRASQKIQSGDVAQYKTSGRELRGDLNTDEAAEERVNFGFLKPDPLKSFAKQQMKYAYNERIFNDLLKKFDDPDALYTTLNLSKMKNL*
>scaffold_57_R893	MAFSSFLKILAMITLITFQVNAETSQRARNLRIQDDDFPQEQARRLGGNWKAILINVKNNPGVSDGVVNLIKKVDFVSGTSKKIKEKVKDAKDKVKDATEKVKDKLTGN*
>scaffold_592_F19	MRLNLVVLAAVIALVSRCTAVSAASSTNQINLSNLNQALNTMQNHAGDGNRFLRSAKIVNDDIDSDDDID
>scaffold_73_R384	MRLSYIVLVVVASVFAYCEGASSVSDSERLAVPQSRVQAEQNSNRFLRVHQDDEERAGVEKILTQSASKLKRTVSNVDEGGLISKLWSIRKDNDALFHHIETVMRLDPDGMLLRMRDQGNIDLKLLKHFTKYWAEKYPDWVSKLP*
>scaffold_18_R458	MRLSLVVLAAVIALVSRCTAVSAASSSNQINLSESNQVLDTMQDHAGDVNRFLRSANMVDDSVDDIDSGDAIDDEERGGKTLTFAWWNALGKTADDIYKKYNLKPLVRDAYKYNQVGELKNNKNYQKWAAYSAYLKDRGLN*
>scaffold_16_F1314	MSLLLSWRSRLSSLCLLSLNVSVLCLHGFDIVDFTRCRLRLWFFGHCCFSGRHLRFLSCNRSFLFVHWLNVNFNLRFLNCSLHFFHRLNFSFRVNLVRFSGLLDLRFLVNCIRLHPFRKWESGFQPVVKVFKHRLPFRIVEKRVEISVEHLKLLVTGRQSVVKDLRQFQTRDLVVRAHHHEHRQFA*
>scaffold_63_F287	MKLCHIVALTVALLVACVDPASASKDSKLATQGDNIPTKRLLRTTEDEERGISVSLGLEKISNAFTSGKTKEFKNLVKAGQSADDSFANLGLGHVLNFEKGGEVRTKMVAKFFTSDKFKAWSKYTHKMNQKDADSAMLAGLTRAYGEKNAAVIILLGKDSLSSHTVAKKLETAQFTKWYTVDKIPNADELVKKVLDVPRSKLRKYPREMSIWDNYSKFVGKYVLNPRPGPPVRK*
>scaffold_25_F1242	MRLSFLLPVAMIAIYCATCNANVASNQNKLSMLQARLNDEAGGTRLLRVHHENEEEADREERGLTDLFKTEKAAVKKMAKAIMADPSKADDVYQKWADKGYTLTQLSDFLKSKTRGKYDRVYNGYMTYRDYV*
>scaffold_12_F708	MRALKLLLVTVFLLVSLDATSGYNKLQGTNTEVVDGTQRGVNSERLLRGHPSTVDKVSADDEERASLPTFLKKSTSGATNWLKDKKLAAKLKLRALPMNLDKSVQKTMKDGIDPDRVFTLLNLQKKSNRKINGFRTGEYNLWKELTVEWTKTYPNWVSNISKKPK*
>scaffold_25_R673	MRLSFLLPVAMAAIYCATCNATADSDQNKVSMVQSLDARLNGQADGTRFLRAHHENEEESDREERGLTDLFKTEKAAVKKMAKAIMADPSKADDVYQKWADKGYTLTQLSDFLKSKTRGKYDRVYNGYAIHLDY*
>scaffold_74_F614	MAGRLCVVMAITITLVAASVTTPSQSLLTERQENDTSGRFLRVASTLKEENDEERAAAPVEAVTSLIKNKNVANAAVEAVEKKYPLVIPGVTDLLIKARMKRWFWKRTLPTKVFKKLGLRGHSEDRLKNHPFRKFYAEYLEKWKDAQAHLNVDWGKAPAALPGTITTGNTVLKT*
>scaffold_1_F5431	MKTATAFATVLALIVATNGAHVSPNTPTLRGLRPTADTPSVEDDKEDRKDHHHVKKVKKIAIPVPVPVEVPQYIPVPVSVPSTVVASSNNA
>scaffold_37_F302	MALKIATLLSCLSLWLLFAETFYWKETLSLEVSFAFRPQTSLACVDSTPSNRRSTYRRWLRVNVPWQRLRTQSQCETVQADAQSRFSILGFCMEPTAIWSG*

>scaffold_7_F1370	MRLTYLLLVIATTLFSCNNATASGSSSAKLVISDSADPLHNGDAAEIVGKRILRGSNAEKNKYFDEEEVEEEERALPNLSKLDDEANLKILVDIFKYFDDAGVPGLKVFIKKEAMDLDDLASMMTLYQRYRGAGADDFMDLMKKKIGVAS*
>scaffold_2_R3410	MYKPLLVTVLILLASYTAASLELASETKALDAVPRDRRLLRANTEEGVDGTETQHEERGITTKVGNLIKDWKIKQMFKNGKSFEEIFNKGVTSGDVWDAFKIAKLQNKMSLTDLQFNPKYANWFHYDVWYAWRTAK*
>scaffold_16_F2450	MRICFLLLPVVALIAAVSGSSVNLRASHRIQSRDVAQDNTGGRELRGDLNTGEATEERAKFDFVKKLVSKAKGDPLESFAKKQTRYVFNGRVFNDLYKKFPDPDALYTTLKLSKYENRWDKFGQATPSFKIYGKFRNAYVEKFPDWTSKLNWL*
>scaffold_24_R1723	MASGIFKVIALLVIFAVATTVNAEPVRHLRVEPDHEPVTRKLSRKVPASMLKNFWGIVRTNLENQPTINKAQEMYAKLSHAGHVKPPAFHVPAKAGEDVLKHNYRFLDFA*
>scaffold_21_F1267	MMVVAVRALLVASDLLFLCLHENLGADDWVRNDRCHCLSNSSQDEGLQCRQRTHALGIASRHLRVLQLELQFVEDSVVDRRVTHQYE*
>scaffold_11_F683	MIATATEVLLLISGLTHRGVASAVGTDNAEGVIDTLADLVTPCKSQSFDVRVGVGGLAAFSPTPITKGSSSTAPTRSLRSTGLHKPKPTRASNAPTKAGPKPRQKTAHRDDSAETSTNTKSMLTSSSRLGGGDLRAFRDTVGTKRADVDGVLDRCEASFAKAKRTRALGASDELKQKISSIQAASSGFGGSIMKVMLFLREEN*
>scaffold_475_R2	MRLSFVVLLVATISSLVATSHALPHEQSTVLNVAATNPDQSVTEGQTSEKRFLRSASLGSQLLRSETFKKSKFKDLLDENVSSFTFFVDMLKGKKKYRGIYNEYAAYRKAHNAYP*
>scaffold_50_F314	MRFFLSLAVMILALVADGDAKGSQVLVSNFPNFQQYGASTGVVSTTRLLRARSDEERGGGISVPATDKLSKLLKLPKVTDEQLQQWLSKGKAAESVFYRMDLGNTRITKLFENTQFLRWLQYADDLSDSGKGISAISILSTQYGDDTLYKMIDSAKKTTNTEALGLRLQSEQLKHWVKIGKDPDEVFKLYDLNYAGRRILSTSQFSAWTKYVDDLNAKNEGAFVLIVPTLRKYFSDDELFHIALAAKRSGETEAMGAKLEDAFVQFWTRRKDTPDNVLVELGLKKSMETLLESPLLNILTKYTEVYNVNYAAKKTTVIETLTRTFGDDKVARMLLAGRTESTTKKIAKQFQTDQLEMWLSSGQSVDDVYKLLNLPSRRDLLSDFGNQKLFNTWVTYINTVSLKNPEKTSAMLSTLASSFRDKPMMQILEAANKFPSMEKAATKLQLEKAQNIFSTGISPYEAFMLVALDSVGESVLSSPLFKKWMLYVEDFNKKNPGKEESWYMALRGSYQGGVNKIIDKAMKDPSTMKIASLAQKEQLNEALTRWKYSPEKLFRFLNVGEAGEKVFSAPKFELWVKYLDDWNNAYPSKKTTMIDGLVDNYHISALVPMLAAAEKVPSTKKLASQLQDALVEKWVAEKKTMAYLKPRLKGVPSSDDMLERYTKKLNSA*
>scaffold_111_R154	MKVFSILASAAVLIVMTALVDAQRLLRSEASTVIDSVSTADFSTLSPGSGFTTGNVEAHNNFGALDKEGSTGGPCRAELDAVSVGRALYRIADLDIDTTASNL*
>scaffold_79_R554	MSRFETLSSLLVLWRSMCLVAIPTAAFPPLWRSLRSWTASASGYKPINAAWRTFAFFFTRAPPSTRSWLNISVQALISFTHRSLKMQLSSFRTISRCLPASSMQRRNLWLSRENLSLPHVPASTLHPPFFDRPRSSAVRLVLRPSTTSCCITLPHQQRLRASIL*
>scaffold_22_F1370	MTPLHLVLLFLDLGQIHDPELLVADGAVKDLLQLPIDRSKSACRSFPVAASRALRMLLEHSVLLVQSSSLPSPLSPLLDSAHRPIRQLSGRTRHARLHRQKAASIQRHYRQHPFRSYSFLTAVYLLHPFPPRHLPVPQVFQHSQQRTSRSSPQRCSLPPSRPPARTNLATSAC*
>scaffold_48_R1250	MVKQPFLILVCLDLGFCRVIPVWSADAPAVTNGSVARSLRAAHLELPLHWLLSEPRTLAHCAFCALQSTPAVLAKLERSQTWNRWPFSRK*
>scaffold_12_R1094	MRLSYFVLVAAVCIFACCEQVAAVKDSQGIAATHTDSLRKIDNRFLRGREDVMGDESDDEKDSEAENEERALPKLDVAAEKLMTKAAAKLTRSKSLSSLAKLDDEAFHRAVVTNNFFTLERIEKMGYNPDKMFLKMKEMGKNAPLTDPQKVLLEYYSMFWKIKYPSWVSEVPHMF*
>scaffold_16_R943	MRLSLVVLAAVLFASGTAVSSADPASVAAVHSSRVLSDEDKRFLRRHPTEHDNEERAFGQNMFAALKLSKMKTDAEYRVKVFHRWKKHGYTADDVAKHVPAKLADQYSHHVNTFTTSGWVMNPLRIFSPP*
>scaffold_1_R4569	MRFPIIALAALVAFLSTLDASSLLVQAASDKLNSGRSLRIAAGTGLEQDEERGSLITKIRTTFSKKARVDEWAKAEKSDDFVRKALKLENVADDHLWAMKNYPYYLRFLEKTEAKKINDWLIGDVPTYGAWVKLGLGSIDDIEKVKTTAAFKTYEKFVKEYDDQAIALWKDYKIPIPVAKATSPTEMNARMDILAAAKRGDDYAKKVLGLDNVTGSALISHVNYQYFEHYRRTVKRLQDPKKKLNRLPTITER*
>scaffold_24_R735	MRLQAVVLLVLSAALAVADISAATSGTGGHHVNQNDVSANRLLRSEADVSDGEERAATWLQSLKNLVKPNTAPKTMTKLERENPDVAKLVGKSLDGAFRSLKLNKIKSVDDLFTSKNFETFNGFMIYRNSQSRNKPSTIAKFFTKKLGDEQASKLFSQAAKSSNTKVKKMGESYQTQLLRQWGKEGKTLKQVTKIDASLQTRYQTVLDDLARAAKKKAEQAAAKAKAAANTAT*
>scaffold_1_R252	MKTTGSIMLTAALLLSDSVCTAYYLRGTGIDEDHALDKARVATVQVRYLRKSVEPSFLDSSSTINTSEHHVDNTKAINSSSPVSATKLPDVTLSDLDETERTSTVSPTNVEIGISSGNMVEFMVHPSERSSSVVSDIERRVVPMAGPN

	RARPTERNFWLGSHYPSRYHMKPQHFFMNRQMDRFPVNLPLILPRARQRQHRYFVGV*
>scaffold_29_F1478	MRCILYIALALAAFARSDAVEAFTNADLSSKISHDFAANELVNESSQKRFLRVDYPKSVDTEERMKISSLKKIIKELDVKDAKAKKLAAIKDLAKARKDAQKLATNVVKSKAQRTRTKFSSLEYDNFMRMFKSNLAPEKAKSTGKIKTPEQFTRYEDFYETAKAADILTRMAHA*
>scaffold_93_F127	MRLHCIVVLAVIAFATNGNEVSAGKSRVAITTTGALDTPTTRLLRTQYTDEERAFGLNLLPGSKKISSFMTDKKLSKYLKSNQEFDDVFIKLKLDKAGDKLFENPKFLAWAQYVDDFNQKHQTQNSMLPTLVRQFGGDDLSIMLEKAKQADKTYGVALRLQGEQMKLWRREGLTTDMLFKIYKLDDGATNLLENPGIKIWMRYADELFPGDSTLLFKKLQKTYSDEALSKILINGKTVASSEYGEVGDGFAASSLAEGPCASGESFPVAVTQQGGRCVW*
>scaffold_13_F2760	MLVERDLLATEASQTDLLLLLLLLLGEPRRVCNFHWCSTFLLRCRLLRRCTCITSTRLLLVFLTSLRWFLRLSLLWSL*
>scaffold_8_F3213	MCLQSIFCGAAVLCGEWLVIRAFAVKCRLRSHSLPPAHAALSRGVLPRHLKCLLRYSSYVSTKWHLRYVVQRRRWRNLRHQSRLIFLFVRLPLCQDKSPRDNHQFLVQVWDSIPLRWFGSRSQTTTPL*
>scaffold_18_R428	MIHICTFILLLLSGERDFGVNLNKPFNNHLPLDLPPFSGNHADLLIVCLHKIIVSGYEKLNSVYNCFLTIICNISPYCKKLNMVSAVRLLRLFKLFAQTRYLFDNEANHHLVFFLLETFDNIIQYQYEGNQQVVYAMIQNKNVFYQLNDLQLPPIRASTEGKKEATEKTEEEKATDGEFVPTVEWLSAWKKKLPLTTSLRLLQYLIPQLEDACKKAGGSLDEDAMLYFLRTTTMVGLLPVPHPIVIRKYQINQFTHLWFTTFTWGVIFLRNQVLPLFDGGAITLFTISVL*
>scaffold_8_R1370	MRLSFVVLLAVAVSSLVATGHALPHEQPTVSKVTAANLDQSVTEGQTSEKRFLRSAAGIGRQMLRSESFKKTKFGEWLKDNLSSFTIFVDKLGGKEKYRRLYNEYAALRKASGQYP*
>scaffold_2_F233	MMGSVSAFVVWLKSLLNLPTTCTCSCPCDVQTCYRRELLLLLLPVRACLRRSLLRLLLRLVPRRLEWDLLRFLRADLDLDLS*
>scaffold_4_R236	MRLTFLLPVTMAAIYCATCNATAVSDQGKTPTVHSLDARLNDDTGDRRSLRAFKEKEEFDTEERGFLEKAAVKKVGQGNYERP*
>scaffold_29_R903	MRLASILLVSALLLCGSVFSTEGKQAHTVKNTDGKRLLRSDDYDEERGFNWPWLKKIKQLDETTAIKQLATDFADLKSLNREALDVFHLMREGGMSPKKATYISNLFAKYMENPRLYH*
>scaffold_50_R462	MRFSYFLLLTSAAILSNSNATATVSGEGHVMTSADAPARALETNNGKRSLRYYAADEDDKYDQKNGKYDDDEEEERNFTAAQLAKWTEKAESWVSKNRTPAYIKDKLTGMNGLMTAENRKKYELFTAAYGRANPHALDRL*
>scaffold_25_F487	MRPILLHAEFWTLWLVLAWKACCLREPSGLAFTTTYWSMTKTSYRLTWITSFASTRLSLLRMTTTRRRLRRLLHLLQQTPRMYPLYLKRMRVKRALYRWLQLTCGASTDASARFS*
>scaffold_7_F310	MRSLLALAHHLILCLLPHPAYFHTLMSASRPLDTSMGLGFWLLPSSTSVRSKIQSVWAGDGGTRPLRSILIADSTPPPPEAATLPGDE*
>scaffold_50_R812	MRLTYILAVAVVATLHSSATAFSSVKDSNAADSALAEGGRMLRGEYGNDALIADDDAGKKKVSYGDDALDYDDLDDDDLDDYFEEERTLGDVLKKLNPVRAVKKSAEKTKEHAAKVKEALKDAADYQAMIARAKEMVNKD*
>scaffold_30_R324	MGVWFLLLLDVALVAATSSVRTALFSLPVELCSFVFLTDAGRGLRPVEASLVLAGDAVRGPWSKFCDPFGAKLDSTVRGGNGPL*
>scaffold_111_F98	MKVFSILASAAVLIVMTVLVDAQRRLRSEASTATDSTVSTADFWTLSSGSGFTPGNVEAQSNFGALDKEGSTGGNRPSGSVQGGAGRGFGGSGHNGMQNVGSGEGLAHGSGSFGGHGGFGRHGGHGRGEGSFSGGDFAGSFGGHDIGGGNFGGSGNGEMPSIGSGAVPTTGSGGAPVAATTTSTTSSVAASSSA*
>scaffold_25_R804	MRLTQVLVIAVASLLFARDTVIATSNQAKISKMEQSTPSQRLLRSNKYPIEEEEDEFEDTMDFEEGDYTTTDKEDLEERSPLSSAVVAKLDDIASGWGTSWARVAMGQSSISEDKIKALLALRDAYISGSKKAKQAARMAVLRANNS*
>scaffold_81_F285	MRLNCIVLIAAVASLSTAAATSATTDIKPVRPAINLQPPPLVVGRLLRTVQDEERGFTLPGAGKLADLFESTALKLTQSARINTWLAKGTSTDDAFIKLELNTAGSRIFENPKLLTWAVYVTKVEKKNPEEIILARLSKQFTEGSLAKMIASAKLDSKTEGLATILQAQQRQVWVDAGKSSDEVFKLLQLDEAGTKLFKNQQFSTWTSFVDAFNRKYPEEAVSIFSKLAKTYDDFTLWKMLEAAKKVPKTEIIASKLQAQQIDAWLDAGKSTDEVFNLLKLQRTGDKLFKNSQFLTWVSYVEKFNKKDPDQAIAIFSKLAGIYDQVTLSSMLEAAKHVPSTKRIASYLQGQQNQHWLADGKSTDDIFKLLKLNTPSLENLIGPRLDAWTSFMRAFNMANEGKETTLIATLTTHYKDRGLAQLLQEGTKFASTKKIAEELQTAQFARWLQLGKTEEDIFALLKLKLTTPTTDPEAIVFYRYKLFMDAHM*
>scaffold_50_R1069	MIVSFKKTLFVSAVAVALAVSVEGYSGAVESTYETKRMLRLEAQDVAEEEMADDSECGSLEMAEDDSECGSLEMAEDDSECGSLEMAEESGTGDKGGDNGGNTWTQAPSTGDKGGDNGGNTWTQPPSTGDNGR*
>scaffold_29_F768	MRLVSLFLVIIATLVATGNTLAVEHTEGKITSSDTLLQPTATFNPDTVQTRRLRTPESPKDGEERRLVNLDIAIKDAVHEVRKLTKWKLQFAVWKEIGKKPQKLIQEWGMKYHM*
>scaffold_10_R1	MRLSVILLVVAAFVVALSPTAAASEANTVVAAPKLHESTATARFLRVRPEDDYPVKDERDGEDSDDDKGNDE

133	ERMFSFLEKKTALSAFKKLVSESGDDLVMAVSSLSKAEFVALFNQGQSAMAKLVPGFRPGMSLDDFVTVVKSAGLRRDMEDALMVGYGKYLAHLMD*
>scaffold_50_R934	MHLLYLAGVAILSFAAGATDARVLASDDSNQYRAHAANANIVSTTRLLRARSVIDEERAGGISASASDKLAKLFKSSKVTDEQLQQWLSKGKAAESVFNRMDLGNTRITKLFENTQFLRWLQYADDLSASGKGTSAISILSTQYGDDTLYKMIESAKKTTNTKALGTRLQTEQLKHWVTIGKDPDEVFKLYGLNHVGSHILSESQFSAWTKYVDDLNAKNEGAFVSIIPTLRKHFSDDDLFHIALAAKRVDETKTMGTKLEDAFVQFWIHRKETPDNVLVELGLKKSAETLLENPLLKILTKYTDAYNVKYAAKKTTVIETLTRTFGDDKVARMLQAGRTDSTKKKIAKQFQADQLEMWLNSGQSVDDVYKLLKLPSRRDLLVDFGNQKLFDTWLTFMNAISIKHPEKTSAIFTTLAPTFRDKPMMQILEAANKFPSMEKAATKLQLEKAQSIFSTGISPYEAFKLAALDDVGDSVLSSPLFKKWMLYVEDFNKKNPANKESWFLPLRGNYQGDRLDEIIDKAMKDPSTVKLAKSVERERMKEWLEKWEYSPSTAFRKLHLKTAGEKVFSNPNFELWVKYLDDWNKAYPSNKMTMIDGFRDNYNDLNLVRLFTKAEKTPSSKKLASQLKDALADKWVAEKKTLDYVKSWYSHVPSSDDMLDRFTKKLNNA*
>scaffold_2_F3647	MRLLFWTLLVGLATSGVQPIAALSKVADTSETSTLDHGQSTIIEGTARHLRLAPHEDTSITDVLVERGLKVHDEERGNFAAAAGWTANKAFNGLGKIVGHDNSNKLKTKVAEFFFSILRKKGKTAGDIFAHARKQTDPSQRAKFETVATMYQQYLTKVL*
>scaffold_644_F7	MAGRLCVVMAITITLVAATVTTPSQSLLTERQESDTSGRFLRVTSTLKEENDEERAVAPVEAVTSLIKNKNVANAAVEAVEKKYPLVIPGVTDLIIKARMQRWFWKRTLPTKVFKKLGLRGHSEDRLKNHPFRKFYAEYLEKWKDAQAHLNVDWGKLKATAALPETITTGNTVLKT*
>scaffold_104_R67	MRPNLVVLAAVATLVSRCTVVSATSSTNQINLSNLDQALDIVENHAGNGNRFLRSANIVDDSDDDIDSEDEERGGKTWAQKFAKWNQRGESANDVYMRFGLEPLVRKAYKYGQIGQLQKNEYYRKWAAYSAYLKDKGLN*
>scaffold_36_R1210	MRFFMVAAVAAFAFASSCETASAEAPNAFLIDDNTNAVFSRYLRSTQTDSEERAIAQVLKSEDRTVANVMIKYQSLYRAKITPKQAKLMLGVSDNMVEFTKMTRPIQRFYTGYYSYFTTMEKRKKWKKELKNQVMV*
>scaffold_379_F2	MNIAVLLCFFAFPSGLFFSFRRLRAASLAPFLLSDIRWHVLGGPSLQHFTPKQQQLHALPLQAAYLTSSAAFCSQPLHRRALISLRL*
>scaffold_20_R1237	MLGFLLLVMTVGSTTELILGGWSSAAITPDTRAVLVQALSTTNVCVDSIISVRSQVVAGTNYEFRINGCRGLRGGNCVRASCVAPRTFVVNVFDQPWTRTTRVMSVSEI*
>scaffold_24_F423	MRLSFLLLAATFALLSSGTVASPTTNDEPISSPNTVLSSETEGRHLREHKNSIDDTEERGFNPAKFDRLMNERSYRQTRFGNWVDKPYTDMDVYKLLRVESNPNYRRIFHYYQNYLQEFAPHLITP*
>scaffold_2_R3800	MKFVSTLVFMTVALQSSCSTAQIDFVRSYDHHAIDFSTSSKPTQPSVADVNTVEANQPLRSGNRRLRDGSAAGIVIVGRNGGGFEPLRNGETPD*
>scaffold_11_F1235	MKAKLLLVVLSFLLAVTSVSAERHLRVADDANPLKPYEALNAVIEKFKNKAKGKPERRRLTGEKAFDKFVKAIAVLKEKDHARRVEEAN*
>scaffold_55_R4	MRLFIKTLVALAAVLLATSTEAAKAVQTGGNEDVVQSSHILSRESKRVLRSEYDEEKLLEDDEEELLENDEEERKNGANLFTDAKMKKMLASDWYRYQVARRWKERKYTWQNLPPNVDPNLVAFYKGFRERHG*
>scaffold_55_R623	MFFLVKQLSAVNHMYRFSLASFLGLFKGTLATKMESSSTKDRILRLIPILEHKVLMFVGRALFKEHRPMFGMHLVHGMHPECFDKNEYEFFCGEVVELERGSGGHSTLPEWASPERKEAFTQFVETLPRLTQLCKFESHDMWIRWSKSMECEQNFHPKMDKSGSAGGLSPFQKLLVVQALRPDRLQSAIIQFICGVMQLKSLTPPSLDFKVIGTEEATNTTPVLLLTTAGADPSKELEEVATSVVGKGHYFEVAMGGGQQEKALNLLKSTAEHGEWLCLQNLHLVVAWLPVLEKEFSALNASHKFRLWLTTEPHDAFPLVLLEQSLKITFESPPGMKKNLQRTYAAWNPAFIAKGNSARAQLLFLLAFFHALLQERRTYIPQGWTKFYEFSFGDFRAGSNVMELACQTSGAAIDWQTLHGLMENAIYGGRIDNPYDLRVLRCNLTEYFSQDLLSGHKSLTRGVKLPQSTQHADFLDIIDRFPDIDAPAMFGLPDNIERSMQRSLSGQVIAQLKALSSNEAEATTFDREKWRAQLGPLLETWSKLTTGFQLEGTSLSSSTGKNLQAMTPADAFVALENEYALDLVQQVNSILQALKKVIYGTGLLTPAIQTVAKALLKGIVPTEWAA*
>scaffold_325_F4	MLSVLSLALMLAVVTGAFETSRDVKNGVVTPDSRRLLGFTADQEERKFGGPATGTDHSNSHAWENFKAWFVRTFFFWRKREQTRRLRNYSSM*
>scaffold_50_F43	MGLFYLVCVAILAFVARDATGDRVIVSDGFNQHRENAARASVVSTTRLLRTKSVIDEERVGGIPVSATDKVAKFLKSSKVTDKQLQEWLRKGKTAESVFYRMNLKTSQLFENPQFLRWLQYADDLSASGKGTSAISILSNKYGDEKLYQMIRWAKEKLNTQDLGMRLQTEQLEHWVKVGKDPDEVFKLYYLNHAGGGILSSSQFNAWAKYVDDLSAKNEGATVSIIPTLRKYYSDDNLIKIALAAKEVDETETMGMKLEDALMQFWIHRKESPDNVLVDLGLKKSTGTLLESPLFTILTKYTEAYNAKYPSMKTTMIETLTRTFGDDKVAKVLLAGRTESTTKKIAKQFQADQLDMWLNSGQSVDDVYKLLNLPSRRDLLGDFGGEKLFDTWLTFMNAVSIKTPEKTSTIFSKLATSFEDRPMMQILEAANKFPSMEKAATKLQLEKAQSIFSTGVSPYTAFRMVALDNVGDSVLSSPLFKKWMLYVEDFNKKNPGKEDSWFLSL

	RVNYQGNRLDRVIDKAMKDPSTMKLAKFVEKENMKEWLVRWEHPPSVAFRELHLNKAGEKVFSAPKFELWVKYLDDWNQAYPSKKETMIDGFVDNYHTLDLIPILAAAEKVPSTKKLASQLKDALVDKWVAEKKTLAYVKSWLNGVPSSDDMLKRFATKLNSA*
>scaffold_11_R1430	MRSYHFLLLATAALLSSCNATAAVLCEGQVMTSADAAVPVRALGTSNSKRSLRYYDTEEEDETDKHHQKNDKYDEDEEERTWSAAQIDKWTAKADEWVDLGKTPAYIKAKLTAFNGVMSDKNRKKYELFLAKWGRANPDEFGRR*
>scaffold_22_F208	MALCSCICTGIACFPVSSHFAVYFHLSPHSLLSSLRRLCHTDTAERLLRRVLLIARRTQEQRRVAEWLQVATQRAERSGSRTIQHGHITGAGWTCLLLLHRWVISLFPLRLHSSTGHQLVSL*
>scaffold_29_F1480	MRSVYVVILAVLALLCNDALAATSKTDLAEAELTKNERNRSLRGEVIADEDSYAIDEERVQTSGISKVAKELKLKKANLKKVSAALEKAKSNPSKLAVNAKKMKAIAEKKILAKLSSMENDNFLRLFKANFTPQRAKSTGKIKNPEQFAKYEEFYKLAKLIGLK*
>scaffold_3_R391	MLPTELVLFAFVVGLRQAGYAPPPATTSEWPLLFSPLGGLVNWHTFAFLRINRFLRIVHLRPLSDQLQRFLLYDRRLKRLTPGICYLVRLALDFLLGTHWLSCLFYGVSYLAYDDGEMSWLTTPDMLAFGDGVRDLADIRKVPLLQSYLRTYHFSIGAITTVCYGDIIPMNAQETEVTMAVIFISVALFSMLSGGFYKYFDMELGRRAEYEERVAQVGHFLKFHRFPSDTWRQMQVYFALSWRESRGRRERELLSGLPPSVRQDLAQHVHASLLKNVALFTRCDPTFARAIIAALQHEFFVRNDVIIQRGDMERSLYIVESGIVLISAVRKRQVHAQAGGAEEEQASNDPVGADDNRSPGVSVNEWVRASVGASLRLRKAKKAEKGQANTPRQRQKSLVALMSPTGTITDINNQTEREEKIYKGPFDYFGERSLLFGTPRNATCMALCVTSLFVLTSARFEAILDEFPHERSNSVSAWVMTRTPSLPPDERPIDN*
>scaffold_7_R681	MKACVYLPSLLFLPCPSTSAAEPTDPDEDNSTPHLDALERLLRDRERARQRLVNRLRRPDQEIDTLHDSIRWHVRYGPERIPSPPQSPPTPDFIETYGDSEYAVSDDNSSDSGTESEQSC*
>scaffold_3_F3536	MALVVFFRILLLVCLQIGLDEEAIEDHPTRKTRRQLQAGPHEASSEERVTEETHPEPMARHLRQFPTQHFDIVQSIFGRIGQQIRRAGIDS*
>scaffold_61_F209	MRLLFLLVAIATFLIASEAFSTTGDSNQIYNVDSPVGPRQRFLRAHAEVDLEKEMKKMMKMMKRKVTKEDFAKTLKITDQIDDIINKHAPGMHEFMQTPKYQRYSNYMNFLNDMAKKPEYAALVEEIKAKSRAQVALKTFRKPTTSQNRWQIIFASLKGKRIGK*
>scaffold_23_R490	MQRRMSTPFFLMITTIGDAQGEVEWVMIPADNSPLIKSDNFSRNCGATRRTRWATGVALPTSMSQTAPRAAGGRAFPFPIRRCLRFQMICLNRSICSGVLPSASSIWISSILTSSVVALTSGSTAI*
>scaffold_25_R122	MYRILLLTTFALLCGFSNAVNSDARLLRVVDPTEEKGGFTTYVKDSLTKWRINSKIKSWVKNKKTDEYVLKKLGLSTLTGKDLVNAPKYSQFQDFKVGMWLKEATPTTTVFNTLGLNKVEGAVENADDFGTYVKYVITLGEKADNYPLSQWPRLFGGGSLEQLELKRKILRLQKRNVLEINFMLG*
>scaffold_640_R2	MRICLFCYLLSLTAVVSGSSVNLRASQKIQSLNVVQARMSGRELREDLNTDEATEERVNFGFLKADRLKSFAKQMDETHIRTKSMNHKRN*
>scaffold_38_F1173	MRSYCVLLLVYTAVMSTAGTESTAMDSTQPSTQYDIVLHVRTLRTGEYTVSEERAAGASAVESLGKATTSVDDVETWLKRGDTANKVFKALKLQKAGDNLLDNPQLSTLMRYLRLFNEANPTKKTSLIATVTKHYRNHGLTKIIEAGLASTSKKTVATAKHLQTEQIHYWMAHGRSPESVFGVLIQYTKDALRRSVLLKLDKLLPFTWISSDLFEKPGLKTWIRYLDEFNVRNPKQKTTLISILSKRYNDKTLANMLIAANKAESTSSIAKRIQSEQTLQWLSKGKKTSDLFTMFQLQKAGATLFQNPLFPAWIKYADDFRVIHRDTQLETMTTLMKHFDDDVLAKMIMTAYDVPSTKSLASRLHAELLRGWQWRQETPDDLYILLKLC*
>scaffold_25_F1656	MRLSLLLVAAAALVANSDAAPQSTSSLTKFSTDVAPVRSLRGASKTKTEVDEDDSFDPEEEERGISMYGKLDKVDDILKQLNLADDTVLKKLIAKGKGGVEQLITTDKGVKTLVITSKKTGKKVTFTNIDIENIRKIESTPAIKKQISQWKKLQLSPLAVSRDLRKKGIPRTTDNVMWEAFRLYSATSGRKFNSLRPTGL*
>scaffold_77_R249	MWMTQYHLVVAPALSILTSARDEMGTQEQTAMLKEYLDMAKSYTVDDLKDKPSRCRRLDGKTVQDHLGPEAYQDVARALRVLQVWEKVYPKASIEDELAFLDRLRPQLNSTKS*
>scaffold_1_R407	MRTATAFATVLALIVATNGAHVSPNTPALRGLRPTADTPSVEDDKEDRKDHHHVKKVKKIAIPVPVPVEVPQYIPVPVSVPSTMVASSNNAVIGPSTNVAGPGAAAPGAPGAPGAVTPAPTTLNGRPAATPAATSTTRSRPTPAPTNFAGARPSGAQLPAAPVQAGAPGMAGFPNSVGIGDNTNNNAFGAGIGAAGGFPMTGNGLAGGFGGNPMSGFGGANGMGSGGMFGGAGPAMGGRLNGNDFGGNFGQSMGFGMQGGNGLGGFGGQGMMANFGQTGNNGFAGGQALTQGGFGGGNSFGGGFSRQRRR*
>scaffold_43_F1201	MRWLCIKQQVWLQSHCLMVVSPFLLVCCPCLSDSNVFTSGWTMMLLGSQMWKSSLQNLEWLAAISSACLQMRPRRLLRMQMMLFALVSTSLLS*
>scaffold_6_R2312	MLLRAIVIAVAFVTISLVATGSEASSITVVDPVADRSTQVKRSLRLRNLESVDEDRGPIAGLEKVDDILTKTEKASRKAGKVPSGLKNLLLRNIDEFAEHSKLAKKLSGLKLYKDAGLEKMSLSTLRQLDDIEVKRVSDIKNGITGNKDTP

	GGMRRKMDHVVGDVAPAKYLTSHIGRGDQLYGADGSRLLSSAVVSRPAEQGGGKVLLISSSKPEKGDWLLPKGGWDKGEDIETAALREVMEEGGVRPVLFFLGLSYQYSN*
>scaffold_405_F4	MRLAQILVIAAASLLFAGETVAVATSNQVKISKVAQSSPSQRLLRSNKYPITEEEEDESEDPVDFEERGEEDLEERSPLSSAIVSKLDDIASRWGTTYARVAMGQSTISQNKIDALLSLRDAYVSGSKKAKAAAKIAVLRAND*
>scaffold_9_F155	MPTLLVVIAVSTAMAILDMTRTLRIRISICWYTRSIEFLLSLPLRWCDSRLLINNSILIHVHRDRFIRCHHGRMVWVILFLFSYRTVVSHWRSSGRRVSRVVFIFTMRNSIHR*
>scaffold_42_R191	MSKVFLLLVLSVFALVSCDALSAPVGSKLSLSKTDELNAQPIDAKRMLRAQEEPTNAADEERGMTELANKFKAWAAAIKTWVTNSKLVQSMNNKLASLTQKGRVGQIEKLLKQDNVNVNVLYQNKVKPDELFLALKLDPKLKLIADAPAAWANNPGLSMFYQYATYYAKMTTKA*
>scaffold_73_R270	MRLLYLAGVAILAFIAGDATGAKVLVPDDSDHNRAQAASASVVSTTRLLRTRSVIDEERAGGISASASDKLAKLFKSSKVTDEQLQQWLNKGKTAESVFYRMNLENTLYTRVFKSPQFPRWLQYADDLSASGKGSPAISVLSTKYGDEKLYQMIGWAKKESSTKALGTRLQTEQLEHWVKVGKDPEEVFKLYDLNYAGWRFLSNSQFSAWTKYVDDLNAKNEGAFVSIIPTLRKYFSDDDLFKIALAAKRSGDTEAMGTKLEDAFVQFWVHRKDTPDNVLVELGLKQSTKTLLESPLLSLLTKYTEAYNVRFATKKTTVIETLVRAFDDETVARMLLAGREKSTTKKIAKQFQADQLEMWLNSGQSVDDVYKLLNLPSRRDHLGDFGGEKLFDTWLTFMNAVSIKTPEKTSAIFTTLAPTFKNRPMMQILEAANKFSSMEKAATKLQLEKAQSIFSTGVSPYKAFKMVALDNVGDSVLSSPLFNKWMLYVEEFNKKNPGKEESWFLPLRGNYQGHGLDRVIDKAMKDPSTVKLAKLVQKENMKEWLVRWKYSPSMALRELHLNKAGEKVFSAPKFELWVKYLDDWNQAYPSKKETMIDGFRGNYHDLDLVPMLAAAEKVPSTKKLASELKGALVDKWVAEKKTLAYVKSWLKGISSSDDMLERFTAKLNSV*
>scaffold_300_F13	MTGSTPDHWLCFVISSSLCATTGIKALHCCVSHSLTFQLDFQRLLRLQEQEQSMGVTTAPLKSPMGSPAVPYEPVQTMWEARPRKYKSILFEV
>scaffold_39_R1000	MMLVLLAICETTIHVAAGTSLLFESDFAFGVDSTTSACAIDRPFLDPDKHLLYSNLTNNLIALARCTVLERLEVSCKDMDQRNKFSRLLRSYYLLHVPVALYSTERTSYHQGRNHIHYHVGLI*
>scaffold_7_F1494	MSSKAGLISCALWLLLLVSTLGVDAHKRLLRSEVSHDNLEDRVLDNWKKLSLLVKVGSRTKADKLYAKHVVGKITGNFFDTNAFAAWFVAVQMAYAKTPAKAKVDMVSSLTARYGDQALAKMLATTEDDKFIREMKAIQLDNWQKDKRTVGSVYKLLKLDKEQDELLQSPLIATWIAYATKLDNEDPLGAVFSTLKTQYNGKDFATMLLNVKDTDDSFVVAEKLETLLMKSWQREDKSVVDVYKLLNLDNEGDLFFQHPLIDTLIRYATVVDKKDSFSGVFSLLQARYNEEKMTDMFMTMRDWWPRNILTDQLEDLLLKTWQRQEKTMDDVFKLLKLEQQGDSLFSSKLLSTWVSYVAKVETNPYNVVFSKLKSTYGEETLTSMIIQARDMPTADYVGTGRRIRESSVQGLGEGQVHCP*
>scaffold_17_F940	MQSVTSLACVNGAFLSSVAVIAGSDRSLRVLDVGAGGGGRTMRVVRDAHSRAAHTVALPRPTCYTSHPSNFYDLLLSSAPDSTTHLWDIRADNCVMRFCEHVNRVHTLGVAFSPCMRYVATGSEDRAAYIYDIRTGRRLVKLKGHTDVVTSVAFSPLHPQLATAACDGTVRFYSSTRSD*
>scaffold_21_F492	MSSRLNLLFTGSFLLMARKEIVRIFFHFLLLVNCSAIHATVSSSSGSKSITATRHLRRQAKPSVSRARVDG*
>scaffold_2_R2430	MGLPLMSSVVFPFSLAAGLGGSHATTTWNLADFVSRLTSELPISSLYGVMAGDATHLHHVLAHIGFALFSGVDVPRVTRPSIRTWSQDLVGELRRLLRSHALPTEVLEQVTGSNERRSALGNELLRVVEPFVSELVDFLVRATSASRAAAFGTNSATFLRTMTQQIVRQLRVYARGESTESEDDSDERLKRLLRGLLVWLGMNENMARFVIDSLVCWAEGDNSSIRRGRTRQREENSTDSPAIKRQRE*
>scaffold_30_R1833	MSDSPAKISAVCTALLLLLAPFQWQSTYIPLLPSGLLDFLHSPVPFLVGCHSLSETAEWSDVCFYDIDRDRIAVPAVTRHLGPSSIPNGVELCRLLRKARERFCSLRPTSKPWYELSEEQDTIITLTMQEAEIFLRDLGFDISSQDLAASISGKSSVVLLLREHEVYSRIR*
>scaffold_40_F1027	MVVKKVGRLHLFSFLLELGIDCFADFHCRLLTSRVHSIASSASLRPSRWLQSSRSSLTWTCSRLTRSSGSTRTTRTCMTNCNRCWRTIRRRSRTLCVRRSRYHCRRLRDSAVTLV*
>scaffold_5_F2581	MRFHYLVIIAAFVLSISDTFSTVSATNTVPSRGLRRIFDEERAGGAISVSTSEKLATLFKSSKATDKQLQKWLQKRKPAEDVFYRMNLAKTKTGIFDNPLFIKWVQYADDLSATTSGKGKSAISTLTAQYGDDSLYKMLNVAKQDSKSKELASRLQSDQLEHWVTIGKDPSEVFKLYDLNHVGGSLLRNPQYNSWTKYVDDLNAKHGGEVSMIPTLRKYNYDEDLFAIVGAAKSVDALKSAGVKLENAFVQYWINDKQTPVKVLAELQLGATPKTLESPLFSLLAKYTDVYNVKFPQSKTTMIETFTQAFGIEKVAKMVAAAKETEGKAKKIATELEAAQMQMWIRSSKSVDEVYNLLKLPPKTLVIDLGSSPLFSTWIAYMKILSIKNGDEMLQLIKTLSMQFADRPMMQLLQAMEKFPNIGSTATSLQLRKADDIFATGVTPFRAFKMTALDTVGDSVLSSPVFTKWMSYVDDFNRKNPTKEESWFVSLRSTYEGDFMDKLIETARKSPKTVKIANTVESERMKDWLTRQKAPEHVFHFLKLNKGGEKAFSSPNFQLWAKYLDDFNLQYPGEKTTMIDSIRANYRDIELMPILNEAAKIPSTEKLANKLQNALRDKWVDEKVTVTQLKGLFGHMPSSNDWIQKYAEKL

	NKLS*
>scaffold_39_F70	MRLHCFLLAVATTLAVLNNGITTTEASSLRKVPASAPIDSINAVQPETRRLRSAETVYRHEDSYKRRPFIEEKLHKALTNPKKTKRLYARWYKSGFTKKQVAKGLDQSENRELDVTYENLAKGYAKYVDARRTQQQSV*
>scaffold_48_F1199	MDTSGACVLAVLLFVDPNTDTPQKIVLNVGDCRAIIREAPESSPTGTKLKGKAASGMTFALSEDHCAANTKERMRALRSGAYIQNNRIAGVLEPFRTIGDIDVKGPDMKDWVIPTPEIHQSELLVGRSILVIATDGVWTVLNNNRAMAHAVKELNGGRSSAESAAQAIIKEAREFGSSDDITVVVVSV*
>scaffold_77_R178	MLLCVFTVVIAAIAVSDTTATNAIDDDGVLQTTSRYLLGFNQEERGRVGGPATDGGTDKVSDWWPNFKAWFKRTFYFWKKKETTRRLRDQADY*
>scaffold_15_R3220	MNNLGRSSSVFFTAFFLFFESPCSASFSINAASSASLPLAVTASCPNLENITRKLRFNAKMYSPLLERTPSTAAKITADLDWITLQQ*
>scaffold_18_F2149	MRPNLVVLAAVIALVSRCTAVSAASSTNQINLSESNQALDTLQNHAGDGNRFLRSANIVDDRVDDIDSDDAIDNDDEERGEKNWPKKFAEWHADGKTAEDIYKKYALSHVMRYAYRTGSIQWLKKNEYYRKWAAYSAYRKDRGFD*
>scaffold_9_R771	MRGSQSSQQLCMVLLIRILIVRQLRSLAHQEALLPRAHETSFLEHPARVRHRIVAPHSPQAVGYFGYEPLEWMTVLWEIRSV*
>scaffold_42_R407	MRIYFVLLLAVTALIAAVSGSTANLRASQTIQSGDVVQDNTSGRELRGDLIADEATEERMNFGFLKPDPLKSFAKQQMKYVYNERIFNDLLKKFEDPDALYTTLNLSKIKNRSNVNGVKTSRYNLYENFLISYLDKYPNWRSTLK*
>scaffold_5_F2028	MRLSYTLLIIAVFVSSGNAVATTNGRTTELSAMASPNAVASVDTAVGGEKRSLRYHNNEGLEDESDDEALLEEEERKYTNMFSTTKLDEMLNGTKMMSRFRKWKARGYNTYNLPAVTQKDKYTWIRQKYRDFLYHN*
>scaffold_73_F95	MRCFYLAVILAFVGCGDTKGTTVLASDFSNQHRDHVSSTISITRFLRTADASTGDEDRVGGVSISGTDKIAKLFKSSKVTDEQLQRWLSKGKPAESVFYHGLGEDSLYEVI*
>scaffold_42_F41	MANKHDACQKSLLFLLFLLFSLQLPLSAQSPSCPTESPLPPPSAPDWQAAPPFWPLFSIYDVVTSSSPPAHWTSRTLRPSATQPQP*
>scaffold_5_R2132	MRLSYVVIPAAIAVTFASSGNALAAADGSNTGLSAITSPNVVASIDTAVGGEKRSLRYHTNEDLEDDSDDEGLDDAEEEERRGNNMFSTTKLDEMLDGTQLMSRFKKWQELKYNMYNLPDTILASKYDELRKMYRRFLYYN*
>scaffold_44_F578	MRFSYVLLAAAAALLATANAIEADPRTRSLRAHKSHEKSQDEERAFTYTFNFSLWDDLFNSLPEQFQRMRKEPWYLRRIFRSWRSGMGTSDEAVAYMRSQGLSQKAIDQFEDAYIKYRAHKLAKGK*
>scaffold_6_R3203	MRLAIKTLVALAAAILATSTEAAKAVQTGGDVHVVQSSHILPGENKRLLRSEHDEGKLLEDDEGEDDEEERKYG
>scaffold_11_F1232	MKMTALLTVLTVMLAFVSADNSPRQLRSTLTTSIQDTDGNRLLRSEGLISNLLGGLNSLLNNQQSTNPPTTSTDPTTSEQNPDEIDLLRSRRVS*
>scaffold_31_F1104	MRWYRVLLIAVVSFVISAEQSESSHIRTRSLRGNAVNYSFKDVEDGNADERAGEKEVIKKLTSSKTMKKLSRSVTKAANSFSEKISPALPIKAKLQVWSNTGKSVQFVRQELGLTDLAEAALKKTQSFKYYDDFVTSQLPIWAKKDLTPDEVIEQLGMKGLPAAWFKADPNFKYYDNYLKARVPYWSKNNVEVGDVVKMLNLNTLSGAARREAVNFQYYDDFLVSQLRVWVDKDLPVGTVMAKLDLDKLTGKEILTHPNYEYYKYFVKNRLKAWATEGTSLDDVAVRLGMGDLHGQVLKAHPNFKFLEKYQAKAFQYQQEGWLKQGVTTFDMWNDLQVYRVPMSILRRSNTYNTYKNYVNVVDNYIIRMRKKGVPLDKLPGLTSKDATPHELREKTLIWTSAKRPEWYVKFALGLDGLGENALKEAANYQFYAYYLEAVKFIA*
>scaffold_12_F482	MRAHFLLLAAAAIFLATSDVASANQAELSKVASPQSIETANIAPKRFLRTNKYELDEQEERGIGALDDVIVKAGKTKMSNAELKKLVTPKVLENALSDRNMKLFKDLYAGKVSLKRFAKVMKNNPNKEEVLKSYRWFRNYHISQAKARTAV*
>scaffold_30_R1705	MVSAALASSGSLSGSLVAEPLLLVVLVSRSDSVALDVVDLPDDLPDPDPELLDVVPPLVVLALSSSPPLVTATMIPTAAPMTTRIPTTMRTLRAATIVF*
>scaffold_5_F1718	MQLLRNLVFLALFAGVVAAVQEEQPQQKTHLRGLLDKIVSSDPTPAPVRVLVASWEDGKVGEARKLRPIAEKIVGGETVVMFNDRRLSTADDLESAVVNFDVRSNPNCVVSVCGELTKWYLGSKEQCFDLRIAPKSADQIENGLIRGVSAAYSGLRPVAKNLYLKFDETNFIDGSRCEYEILSGSKTVREEEIASGSQAAMA*
>scaffold_25_F1308	MRLSFLLAAAMATVYCATCNATVDSDQNKVSMVQSRLNGQADGTRFLRTHHENEQESDREERDLTDVFETKKAAVKKLAKEVMADNRRAKDVFQLWKEKGYTLDELNTFLKSAKYQHVYNQYMIFRGYV*
>scaffold_53_F91	MRFFLVAALAAFAFASSCEAAVAEAPNAVQIDDNINAGFSRSLRSTDSEDRAIAQLLSEDRAVASVKVKYQSLYKAKITPNQAKVILGISDDMVELTKTTRSLQRFYTGYLSYYTLMEKRKKRKKELENQVKW*
>scaffold_11_R969	MILSTWLRLSAAFLLAAIACCTTQLGTPRPSMWINVTCSNTFGRSVSRKIMPDTRMYVRTGPSGCCDAGQHKWLIDRILRAHTRRPVSRSTKESIYSRKHTSRPSESFDGGFHSDQRMAAPRNGLSVDGSPVRTAVASAPSPAP

	SAHIRSGPDTRLLPLPACRTGRMSSTWPWTWSCCRRGAPH*
>scaffold_98_R365	MRLSFLVLAATFALLSCDTVASPMTKDECNPSPNQVLSSETEGRRLRVHKSSIDDVEERGFNPEKFNRLMNEQSYRRKRFPNWVSKKYTDRDVYNLLRVDSNPNYKRIFNYYQTYLENFAPRLISS*
>scaffold_66_F274	MRWTSILLVAAAALTGVLDASTSNTVANSGVMESAFSPVIHDHRSLRLVDDDTVDDDEDESVDEVNEERTWFSNAKQALADKLALTAVASNFAGKSTDEMGEVLKKLSRDQINTIFDKGEDSIRQILPGFKSGMDSKKFDDLIKALPQEQQGVLLSAYGKYLFNNGLL*
>scaffold_5_F1702	MTLLAFFLEFGFCVLAMAAKPTFFFSCCTVGPSALLLKPKRELVCTRSNATSSSPSSSELLSSSESSLPSSPSSRRALRFCSSCSSRSVISSRDVTNLRAVPFSRFLRPLPPAAPGFPPGLPLSLIIVF*
>scaffold_10_F1990	MRVSVILLVVAAFAVALNPTAAASDANTVVAVPNVHESIATGRFLRARPVDDYPVKDERDEDDSDDEKDEERMFSFFQEKATALSAFKKLVSQSGDDLVEAVSGLSKGEFQALFNQGKAHMAKMVPGFYPGMSLGEFGTVVRAAGLSDDMENALMVGYGKYLAHLMD*
>scaffold_26_F352	MERVGGLSCIAVAGATVALVEALLSGLEQVRVGHHVSREVQQARKAIAYVLGGARRVEAQHSSASVRSHGLRPRLKAEEGLANCAARSLRLARSLLLRRGRRNCEPRRERGAAERRHCKAAGWDQ*
>scaffold_96_F212	MRLSHFFVVVAAAFLATGAIADSEPNHRNLRKHHDTLVDEERGIPKILDQNIPIERLNSLLKKMDQRKKAELAKLIKLYESSPKFGRTKPSNS*
>scaffold_92_F14	MRFSQVLVVAAVSLLFASETAAVATSNQAKISKVSQSSPSQRLLRSNKYPIKEEEDESEDSVDWEERGFATPDEEELEERSPLSDATVGKLNKIAKGWGTTYGKVAMGQSHISEAKAKALLALRDAYISGDKSAKAAARMAILNANHR*
>scaffold_853_R1	MQRRMSTPFFLMITTIGEAQGEVEWVMIPADNSPLIKSDNFSRNCGATRRTRWATGVALPTSMSQTAPRAAGGRAFPFPIRRCLRFQMICLNRSICSGVLPSASSIWISSILTSSVVALTSGSMAI*
>scaffold_42_R67	MRFCFITLFVATTILASSGNISAATVLNRSVTTSIDAVQPIEAAQTNSNRSLRRRNNYKDEEVAEEERSGIESLAAQLNKKLLPTIRQVAHLDLGRAALTLQQMSLSFDERQAIQALLQLSKKDRKAVLMLIK*
>scaffold_7_R1913	MRLLLWTLLVILVTILSSCDAASVNENKSLQRKLYTKVASHALAADDGFEHDKRALRGASNGVTEARAATVSTKFGSRLMAFFRSIKDKYLAWELKILVPGFEKMAKKGTTYTQVREDFRTRLNWSGLWGTPSGFKRYAKLYRTWLEKNHYSQLAV*
>scaffold_8_R1699	MRVLGAIFSALFLAAGIDVGSSLPNSGVAFPVNPHSLAVETVESKRLLRSYEADSEDEERAGGQLGLVDKFAAKVMQKLYKNPSDVFKRLKLKDVNLENNKVFEGWLVYVNKFRQVKGVENFPDQALFNVIHQSQYYQRDLVPLFQSLTHVQGMKDLARTMQFKLFEAATPATRTLMNKAWLEGFDTSDDVFHILKLQDGVFDHSDKLIQWLKFSDMYKKLPTSQSTSWLDELNLVLKTKKPNQQETKFGLLFQALKEEKGMETIAGKMESQLFERWMKMDSMTPDKVGGMLGGSATTNWKRIFEKLEFTDDRYIFLKAYTEAYAANRGANVLKSVEKLFAENKPVAALERAIKA*
>scaffold_87_R430	MRLSQVLVIAAATFLFASDTVVIATSNQANISKIEQSIPSQRLLRSNKYAVKEEEDESEDSVDFEERGFATPDEEDLEERSPLSAAIVEKLDDIASRWGTTWGRVAMGHSSISDDKIKALIAMRDAFISGKKSDRDVARAMILMANKS*
>scaffold_15_R1164	MRLTSIAFVAAASIFVCFQEASAVSDSKGPESRVQTANSDNRFLRIDQDEEERAGPQPSKSLLEKFTSKVTATKLKRSKAVADLTKLDDVVYLKATPGYNVPLFQRIEKMGFNPDGMLLKMRERGKIDQTLLKHYTNYWKGKYPTWTSNPSV*
>scaffold_17_F1758	MPVFDALLTLTILRAIGCDRVCANQKRRMADIVKRMEDGAFRTGKAWRILRKLNKSEMKNDAERWSTFLELSNVLDPRAFNSRRGRALMNEAEQVISVQQLELAAVRGPIVDVKPEGENVADELWDIAEQIVEFIERKAAPVAEPQDTTNDPTFSFDVVLVTDLEDYLKVEARTAPSGVNGMSDRETHIIDEGIELSVTEQLSRMCSSLKEEEYVISSDILEKGFAELSAIERLDTVSIQVSFLLGMQMRLKSCIIDHCESAKSEFERRIKRVFNQLAGKGQDMDHAASLIVLSAFCPGQVIRECIRGARTGVLHHDLSLKVLQSSPLLLEWREPSEDGSGTLFELELQMTVLDISRNQSSFDRESHNVVSFLLSLVGIDNSTSSIQSSSLMTVSKLITVCINPVWCCPDQSVEMQLNLLTLIQQLFHHFVATSADIDTDTLQISFNLAFRALSSANSNDTKVGALIREKVLLLLKSIMELMPDPVSTIRLEQFDSPLNAPLWTLISLFSDDLGNEELCKGLEDVTAVEAYMQTSSVDEADPLPLPIVISAIQALLWGLLWDSILSENVSVESTKAETWRLLDIIASFEFCGSESPDETIKGSSLIESAVAEMMLECGNVLFRALLCNIIPFLLEYELTENFQEEKLLIPQWAIDKVSENPEIKEQIPCRLVSSHVIMRYVAKCWCLSGVANRQLNAQSDMLVLEALTHVVTAHDQAITASKESLSGTLFCIQWLCFLVSAARELHLDTLSTWSTVRTQLELSFLRLLNQLEHLKAISEAEAKFSQVFVAAWLGYLPDDQFVQVFKYISTKRSN*
>scaffold_22_R974	MILTTNLATWIFLTWAATSSMNLSKCQCTCCLNKCENPRPLRGHLLSSWVSGKQSGWPYQANLLHVHLLEHPRQIRTVGSRK*
>scaffold_65_F381	MRIPCSLLVVIIALLSTTTNAISTEADAGRRSLRSMKAKVQDNQVEEERGGTGTSSLKAFVHDFDFNLLDNIFLPADFKRMTKEPEFLRHMMASWQMGFMSVDDIVLYMTRLNMSEKAINQFKLAYTAYLEYLKAVAKAEKAA

	KLAKASLN*
>scaffold_25_F1318	MRLSFLLAAAMATVYCATCNATADSDQNKVSMVQSRLNGQADGTRFLRTHHENEQESDREERDLTDVFETKKAAVKKLAKEVMADNRRAKDVFQLWKEKGYTLDELNTFLKSAKYQHVYNQYMIFRGYV*
>scaffold_184_R6	MRLSYFVLVAAACIFACGEEVAAVKDSQGIAVSHTDSLRGKDNRFLRGRQDVADEESDDEKNTNVEYEERALPKLDVAAEKLMTRAAAKLTKSKSLSNLAKMDDEAYHRAVVTNNFFTLERIEKMGYNPDKMFLKMKEMGKNAPLTYPQKVLLEYYSMFWKIKYPSWVSEVPRMF*
>scaffold_1_F400	MFVLFNLLSCTRLELSLFLLPRPVAAAAIAAACADGGLGVTRHSPSCRLELSSVTASFVLLHQLRILRST*
>scaffold_6_R2044	MRVLLLVALAVFASSSVNTGVAGIQTKRSLRQYDFKSLTVADSKEEERNFVDKVDDIARVTDDFVTKVKIPTNMNAAVEKVTTMADDIAAVAKTVAKTYPEGLSKGTLAQIKEVEQLRLKDIATYTKKTGDGMRRKISPFPGMKIAPKKYLESHVGRNMQLYGDDGSRLMSSAVVSRSAKDGGGDVLLISSSNPQKNDWLLPKGGWDKGEDIQSAALREVVEEGGVCFFILYM*
>scaffold_60_R842	MFSLPTFVMFLVVPILVMKAEDWSTEGISHSLPNARSLRQERVVDNSDVDSKAQRISGHVATVLGHSAPMDEVGQVVGMLLGV*
>scaffold_8_F3265	MPQTPRCLLLKVLFADVVHCAALYDLLGHSNGSDLKYLMILGHPADLQLSGIQFVRLLRGQSPVALPVAHQLST*
>scaffold_10_R1425	MRLSVILLVVAAFAVALNPTAAASDANTVVAAPNVHESIATGRFLRARPVDDYPVKDERDEDDSDDEKDEERMFSFFQEKATALSAFKKLVSQSGDDLVEAVSGLSKGEFQALFNQGKAHMAKMVPGFYPGMSLGEFGTVVRAAGLSDDMENALMVGYGKYLAHLMD*
>scaffold_81_F233	MRFHALVLLSTALLATTDAFKLTADVTAPQSRLLRKSEPKTNEERVFEGLTSTKLQKYNLLWSKLQLGDDLSAVLKSPDVAKIAKFNLNRAPGSQVSMIQRITAKYGDDVVARTLVSIERDASDNPILLTMVWQLREDQIANWLKNSETVPGVVSKLKLGTDESIFRSRALDVLEDFIKKYNTARNGDESLLKTLTTIYGGESELVKMIAKTRVLGRPPYSNHPASIEKANNIESQLIQKWKSQNLPDFRVMNKLNFDDDVSMALSAGKVGVLLKYSDSKTSAFRRLSAKYGEAEVAIAFAKAEGFLPEATALYRMQMNGWLSKGDTAGRVFSILKMKDTRDFVYKLDALETYVKFLKTKNPDDVTDVFKVLKKGFGAGENKLALAIVRPPEFEITGYHKSLFQDWVARDLDPLSVAVKVFKMSEADVAAAKYSDELKPIIKQYTKFFKETVDLPEMPAVRVGRS*
>scaffold_6_R3191	MRLFIKNLVALAVVLLATSTEATKTIQTSGKVDVVQSSQILTGENKRLLRSEHDEGELLGDDEEGLLEDDEEERKYGANLFSAEKMKKMLGDTDTEKKEEKSCQQ*
>scaffold_67_R406	MWLLVVTLVFSGSIFTYADNSGSDSDNSIDDDYVESTYYYSSNAGLFVGMLVAANTIMHLRCLRTAQLLVAELVNAGVDRLQPPVVMLATTNPTSAV*
>scaffold_636_R1	MQRRMSTPFFLMITTIGDAQGEVEWVMIPADNSPLIKSDSFSRNCGAARRTRWATGVALPTSMSQTAPRAAGGRAFPFPIRRCLRFQMICLNRSICSGVLPSASSIWMSSILTSSVVALTSGSMAI*
>scaffold_12_F1261	MGVWDWILCFTVCEEVGAACPCLTPSIVGRVLLHGKTKKIVSKPPTSNSQTMFCSFILDLIWTTYTTMSKPIQSDSDLDALRKLTRQLRVAKLVTDRDLKQTDRKNATQAVMRKWLPLSTTVLKMVTRVLPSPIAAQVKRAERLCTISSEQLEQSPQHAQVFRSLQSCQTSEDAPLVIYICKVISVEANVLSDYHQSGLAATDEVYVGVGRVYSGVLREGQPVYVMDPKFQGVSGDMDVDTIDPSTVKHVARIDSGLIKTYMMMGRDLHKLDRVPAGNIVGIVGLQEHVLKTATLSSTLACPSLTKMPYQAKPIVRVAVEPEDPRNFGALEAGLQRLYRSDPTVEVHVQETGEHVIVALGELHLERCIKDLKERFAKVAVQVSEPLVGFRESIVDGTISSFQENIVFKELLNPDVTKDDSSEKEDINASAEVQDTKVALGTTPDGTLTLKLRALPLPLETAKLLEESASLLKRIAVSKKANDDMKDKNTVVELEAAASEDVSVFKKKLEKSLQSSESSFLKALPLDQIWSCGPRRVGPNMLINSIPTYRATGCLFPSDSVAETHDSEKDEKIRKLENSIVTGFQMASSAGPLCDEPVWGVAFIIEDVVFHDEKSEEDKSEEEKAEMSKYGPLSGQVISIMRTTCLMSFVKQPVRLVEAVYECTVQCQAEQLGKLYSVISKRRGDIYSEELSDGTALFTVKAHLPVVESFGFATDLLIQTSGAASNPQLIFSHWSIIEMDPFFQPQTEEEREDYGERVYEHNYVRRYIEAVRKRKGLSRDEKVVVHAEKQRTLKR*
>scaffold_81_F90	MRFPFLLLLLVTFLLVNGKADSQSTELRLLRDGNSPREEERALPPPPKVSLFADWLKATGLKVSDKVRARYWLWRKQSAEDVFRLLKLDGGLEKLLGSRKFNTWTSFVNIYNKKNPNEKVTMDGILSKTYGDLELAKALEVAMGSMVKSERKMGTTLSLQQREGWQAAGKTADDVFILLKLDKVGADLFTTPQLNSWYKYVSMQADSKSLMASVLRNHYSDETLSKIFREAKPEIKRMRIIRVQLETAVAKSKPKQILSPEEYFKMLKLDDGVDKFLASSNLDTWIKYVARYNTKNPGQDVSTIKILTKFYGDEELAKVLEAGKKMATTEKVATELQSAQFNQWLSLYSTDDVFRLLKLDNDLDSLLTNPNLITWITYLGQFNANNPGKGTTMIKTFTKFYGEIPLAKMLESSSLVPKTEKVATQFQTAQFKQWLRDGKKPAEIWKALKMEKATWMQNPDAQVWYKYKDWYKLNKPQ*
>scaffold_6_R3137	MPLLILIFIASILATTIYVNTKLLNILPGNSLGVSTYNHSHLDWKMDTAAFETSVGTSIHPTSSFYRRGKTFDRSASRERAVMVCLHDAMLNMGLSLLRELRCLGNHELIQVYHCGNELSDRSVELLFSLDNRVELVDVCSDLSSRGII

	SKEMATKFRSWWIKPLAMYHTDVRHVMLLDVDDVILKDPAVVRTLDGYKNTGTTFFYDRVISNKRFLTGNDTGEMYVHKLLRTFNYTRFNVSEGFNPSQHMLNTFAFNGKSIHEMDSSMVLIDKQRAGKVVMDILLWFITEERFRFTYSWGDKETFWLAFEMARVPYFFSPWGVSVVDSMPNEDLKNHPDTLCGSILQFMPVKGMNDTAEVLYMNGKALIDPYPQGIGFIRKAKQNNLFNTIPTQMTPPQKRRQINTKAYPGKKFNTECLVGMGAVPLPTHFSPNLLRRRVHFLGLAMGVLGSLDHCETYT*
>scaffold_2_R1114	MPVCYFMFLCVSYFASSSCQIKQHVEAFIGDLADAFVPVEGGVLVQRRRNLLTQGLVARQVHTHELEVPAHVARYLRHEEVSRLDADLDAREGAMYDVRREHETELHELREQTCREPHEEQLQLDVALWPLQ*
>scaffold_5_F947	MRTTFLWLLLALVLCVCAAEEPKTPEPTSSANARDNDPVVQEIRGLRNSGMKLNDAKDFKGAIEKLREAITLLHNRVFGEGRHAITDPSEISQDAALYAQILNDYGSVLIRAKQYDEAIEVLEDSVTMVEKIYGDSHPSLGLSLRSLADAYMAKEEYKLAIKKYKTLRKHVKKGLEETHEAYIEASLRIAEGYKKLGNKKKNLKVLRDAVKAQGTEINGLTTGIAELYMELSTAHTAVGEIDDALRAAETASAIFLQRDGEETLSYAFSLNALAGVKMRQKKVDEAVKLLEHAHKIAVKIYGENDPITQASAKTLKEVKEYRLDMHAQKDEL*
>scaffold_48_R1407	MRALCFIFSVLLLLLEIDASSVFNSGAAVTHPHLELTQVTTPTRLLRTSHEEENDERAGASVLDGIVAKAMQLINKNPEDVFKKLKLANTNLQNNAVFEQWLQYVYKFRAAKGEDKFNNHRLFNLLRKSQNHPDDLVPLFQSLTHVQGMEDLARTMQLKLFESGYQSTRNLMNKAWLQGLDTPDDVFHILLLEKNALESQQRLPQWLKFAEMYKTQNKISSWENELSLLLKTPHEKETQFGLLFQSLKKTEGMETIAAKMEAQLFTRWIKTDTMTPDKVGVVLASPTNTNWKRIFEFLPVTEPRHVLLESYTVAYAASRGGKVLKSVEKLFANNQPVAALERAIKV*
>scaffold_59_F711	MRLTYIMIVATAAILACCDGASAVSDSKRLTVPLDRVQTGNNANRFLRVHHDEEEEEEEERTGPQFIKSLSEKFAKAAETGNFAKTVEKLTRSKSLNGISKVDDVVVPGRAGKTLTEVLKIDDVAYLKAAGKWPKNLDDIQEAKLVREISTLDDQATLKLITKENAAEFKKIEDMGFNPDGMLKRMKQLSKNDKDYFDLVLLKHYTQYYMAKHPTWASSL*
>scaffold_29_F1645	MRVFSILLLVAAATLVASASAESESKQRLDVSPAAPQWRTIAENEVPTKRNLRKKEIEEERAITAISLFDDVVKAKGLQALPYPELANLDSKLRTQYLKLLVNNLDRKQIVEITGQVPHYILTHGDKKARRIVQYNKWIWRKEPVDPDWVLKNYPAFFKGYEEFFNNRFTRGYKYA*
>scaffold_2_R1701	MRFSHFVFIAAAILLSSENAIADTPVEGQALMTETDAETPVRALSSNNDKRFLRSYKEEEAYLTEDKYDEEKKREES*
>scaffold_29_R998	MRLLYIAVVAILASTNVYPAAADAEVSSFTFTERPHWDRSLTAATEGDNDGKRFLRKRKKTTTNETIRERSKQGSENTVSYCTACLHYP*
>scaffold_9_F3450	MRFSHVLLLATAALISSCNATAIVPGEGQVTTSADVAVPVRALETRNGKRSLRYYDAEEEDETDKYDQKNGKYDDDEEERVMTAAQIAKWTAKAGEWVEQGKTPAYIKDKLTAFNGVMSDKNKEKYRLFLATWGRAHPNELGRRYLRPEAESSPRSFRKLIVFISNHHLLDVLFCVTR*
>scaffold_6_F3032	MSAFLVAFRCCHVVFAFHWELRSVEFALALGLNRARGSRWLRLVAHLLSLYEAVLDGPSGASTSVAFMPIV*
>scaffold_32_F241	MSRAGSPVALVPPKTVLIVVNVLPLVFERSETSASGWSVSWATGATAMLYRTLVRDADQYSPLFIGCPEVFVAKSEEAALEKQLRALRCVPVFLDPPVAHRYFQGFCKGVLWPVFHNVVDVYNSAELQLDCEENEGKRAKQWFPGQKEDSSGVKSAWCDPVSWNPAAQDMCWSDYCSVNRTVARRVVESYHDGDLVWLHDFHFLMLPSYLLRRLRTALVTMYLHVPFPSSEIFRCLAMRTEILRAMLCADHIGFLTFEHARHFLTSCKRLLGLDYKTCPNGMLVIEYNGRKIHISCSHVEPDVTHLHEMLDKNVAEVNGAALEFAAHVKNAIMAGRDSEQRRIVIGSVDRLEGLTAIPLKLRAFDRFLATHPEKCSSVVLVQIGISLDSRPNDYHRTRDNVLKFTEEINRRYAPPGGVVVYFEEKRKTTCAERVILWRMCDIYLDTCVRGGLSLLPFEYMIAQHRNIQSKAKNSAGTGWSSPRGTIDVGGLDRSFGIMIVSEFSAYSRILSGSLAVNPWKTDDMVGALAKACGMSYYEKHNRFYMNYKFVVGRSDSKPWGERLLTDVEAVTEKMEDASTGEVVQVGFGFDFRVMRFESGFVCLDVDELVKKCANTSRRLFIFDYGGTLSSTANILDEEGARFSHRPGCVEQSAENADSSDRSGGDCTGRSAARYVDGKVRKPISDETRASLRTLCVDPCNIVFVTSNTQRGALEDQFDSIPNLNLIAENGLFIRMGGQTRWECVCEEDKRSFGWKDDVKRVMEAYAARTNGSFLVENAASLLYDYRNSDQEYGEIQSLELCAQLRKIVEVCIKVILSSR*
>scaffold_399_R2	MRLTCILLVAAASLVGVLDASAATTGNTVVANAAMVISPLAPESQGRRSLRLVYDDEDDSADEKDDEEEDSADKVDEERGWLSDKMALTSLASKFVGKSTDEMGEVIKKLTPAQIDTIFDKGEDSIQKMLPGFYSGMDFQKFDDLIRALPQEQQAVMLSAYTKYLHQNGRFS*
>scaffold_7_F1775	MRLVNVWSMLGLVLVLVMVTEAFETTKGAKNGVVTPDARRLLGFAADQEERRFGGPATGTDHSNSHAWENFKAWFKETFFFWRKWEQKRRLRS*
>scaffold_18_F2220	MQRRMSTPFFLMITTIGDAQGEVEWVMIPADNSPLIKSDNFSRNCRATRRTRWATGVALPTSMSQTAPRAAGGRAFPSPIRRCLRFQMICLNRSICSGVLPSASSIWICSILTSSVVALTSGSMAI*

>scaffold_50_F279	MRFLVFLALAIVALVADGEAKDSRLLRARSDEERGGGITVPVADKVAKLFQFSKLTDEQLQQWLSAGKTAESVFYRMGLDNTFVTKVFKSPQFIRWLQYADDLSASGKGTSAISILSTKYGDEQLYKMIGWAKKESSTEALGLRLQSEQLDHWVKVGKDPDEVFKLYDLNYAGSRILSTSQFSAWTKYVDDLNAKNEGAFVSIIPTLRKHFSDDELFHIVLAAKRSGETEAMGMKLEDAFVQFWIHRKETPGNVLVGLGLKKSMETLLESPLLSILTKYTEVYNVNYAAKKTTVIETLTRTFGDDKVARMLLAGRTESTTTKIAKQFQTDQLEMWLSSGQSVDDVYKLLKLPYRDLVADIGTNKLFGTWLTFMNAVSLKNPEKMSAIFTRLEPTFGNRPMMQILEAANKLPSMEKAATKLQLEKAQRIFSTGESPYQLFKLVALDDVGESVLSSPLFKKWMLYVEDFNKKNPSDEVSWFVALRAGYQDDKLGPIIDKAMKDPKTMKLAKLVEKERMKEWLEKWKRPPSMAFRELHLNKAGEKVFSAPKFELWVKYLDDWNQAYPSKKTTMIDAFVDNYHMSTLVPMLAAAEKVPITKKLASQLKDALVDKWIAEKESLAYVKSWLKVVPSSDDMLERFTKKLNSA*
>scaffold_7_R1903	MSVLCLALMLAMVTGAFETSRDVKNGVVTPSSRRLLGFTADQEERRFGGPATGTDHSNSHTWENFKAWFKKTFFFWRKREQTRRLRN*
>scaffold_24_F357	MRLSFLLLVAAVALLSSGTVVSAMTNDEPISTPNQVLSSETEGRKLRMHNIASDDTEERGFNAQKFEQLMDDGTYRSKRFANWVTKRYTDTDIYNKLQISSNPKYKRILNKYQTYIEHFAPGLISP*
>scaffold_17_F359	MAANSCVAVLVLVCGLPGAGKTTLVKQLVATACSISSRLHERISFDDLYEQHVTAEGKPGEFDPEKWKMCQQDMLKRVSNRLKEQNDPVHRNECNQLVLLVDDNFQYRSLRKRFFHLTAKRRRPSGFTLCTTTGMPLMTRSELWFWCALCGCSFRYLSGTECWSKQTRTSTQ*
>scaffold_8_R3193	MRLSFLLPVAMAAIYCATCNATADSDQNKMSTVHSLDARLNDEAGGRRFLRVNQEEEDVDAEERGYFEKAAVKKMAKAIMADPSKADEVYNTWAEKGYTLSKMSEYLKAKKYDQVYNGYALHLDI*
>scaffold_83_F373	MHPPSLVLTLVLSPAALKSSTLHVAALELQDTVEPSSHLASEPSFSPRCRRPLRVASSTCAKAGADPLLAPNGHLK*
>scaffold_25_F1083	MRLSFLLPVAMVAIYCATCNANVDSNQNKASMLQARLNDEAGGTRLLRVHHESDTEERGFLEKAAVKKMAKAIMADPNKADEVYKKWADKGYTLTQMSNFLKSKTAGKYDRVYNGYVIHLDY*
>scaffold_22_F1823	MRLTFLLFAAMLAAFSSTSDAASVDQTTGVRSLRRYQAEDEERGVTSVSTSIDDVLNNLIKQKSSLSKLISQKKLDNMLTKNFIKLLRSNKSYTDEVFTKATLNKMLTSEKFAEKKFVEWYALGLTDKLILQRLNGVGEHFGTLHSQYVTFINRIHGVA*
>scaffold_157_F14	MRVASIALLAVVTALASVTDSSAATTGTVLAKVVSNEAAPSVENEHATRFLRKHKDHHADTEREERNGISLLQGLKSTFEKVADLPFDRAWHHLQMLNLSWDKREALLKLHRLSAKDREAVLKLIT*
>scaffold_7_F2310	MISRSFTLITAGVMASTTLIHASPLQYDPYTPVNISTPLTSSHPAYGAQTEGCIEPIVPEDPNQAKAESMIIQADIYRKLRSMEDTTNSDIQDLETYFGTKMEVNFQTLKQQYSSGHAPATPWASSYWPTFQDSINYVWKTGEPSASEKYATAYGLNVTEFKDKISERSGVDSRRRSTRCTADSDCKDGSVCGKRDGISSGYCIPGWFGICHAWAPAAILEPEPQCDVTKNNVTFHVMDIKGLVTSIYDGAEIKTVFTGARFSGLDSPANKDQYGRFTDAARRDLGPGYFHIAITNVMAKQNRSFVVDVTAGSEVWNQPVRSFNVQSMDLVDTRVASMQYFGVPSYPFNDKMVRLAYVKTTFSWVSESYKDGPLVSSGRIDRYTESKDYEYLLELDADYNIIGGEWVGQSKDEHPDFLWLPTAKPSASAVTSTGLKYADVQELLNLSQSC*
>scaffold_39_R834	MPVLPRLSLAGSSSCSGAQVLSSLLALLDASSAQYASLPSFDELFYPLYLLLHALVKQLEDTKVSEVNAVISKLHNRLETCWNARRPLRLQTFAPTILPTFAPQFDENYTVRKDKTAPKDTAQLKQLQRQVKRARKGAARELRRDAEFIHREKQKEEEARLSAKEEKQKEIRRWLEEQNATFNQQVRKGGHMLKGGGSARGPAPRARTPRK*
>scaffold_104_R20	MRLTSILAAAVVVTLHTSATAFPAVKDTAAIENGAVADIVDSSVTKGGRMLRVNYNNDDDDLDDKKKKTRNSEDPLDNYDEEERVGIVEALKKLNPVTAAKNSAKKLQSTLRRSRK*
>scaffold_61_R521	MKVTKVVVALAALCVALWTSPTDSEDISNILEVSASRHLRQTSAEFAAKPQETGKKRDSTNPLQRRDQALVSAHRVYDPVSGLACSLVGECVACPQSERDESFCRETGYRQELDCPRPNDPKDEALLTKPEDERETRFKACSPADSARPGVAVVKFELLMAAVLAASVVLLRRERRNHMSSFDLRKDPRQRTGLLGGSNSDKSSD*
>scaffold_90_R94	MANLYKLFVTLLVLVSWGSKVSVCCLTSRFLRTQNLKTRYLAKSTSCFQCGSGHHLHPLRHYAVSVSQLASLNLRRLACC*
>scaffold_25_R332	MYRVLLLTVFALLCGFSNAANSGGRLLRVVDSAEERGGFTSYLMDSFTKWRINSKINSWVNKQKTDEYVLAKLGLSTLTGKELVKAAKYPQFQDFKVGVWLKEATPTTSVFSTLGLDKVEGAVEKADDFGTYVKYVMALGEKADDYPITRWRELFGGGSPEQLKLKRQLLFLAKRNAIDIRIMLG*
>scaffold_18_F2130	MRPNLVVLAAVIALVSRCTAVSADSSTNLNQALDTLQNHAGDGNRFLRSANIVDDRVDDIDSDDAIDNDDEERGEKLGLRNLPNGMRAERPQTTSTKGSHSSLTYAKRTNMAKSDGSITTSTIASGPITWPS*
>scaffold_74_F612	MVFIAPKLTAEQALVIISCLLLAARGNRKRFLRTMHFLIASHASVFETHLLGSTQATASTTPLTTRRHGHASILRYLSYDC*
>scaffold_37_F1	MGLLQKVKTMVMIPTVALSLTATRIGVPSVLAARAVPTQTHQPLLPRRAKLIRELRQGINVSRLLVAKSPRIRL

084	QGHLRAVVRYRTRRMIL*
>scaffold_11_F1319	MRIGYVTLLATTAILASFGNVSGDTDLDHTQVVKVASLDAVLPTNTNRLLRGRKNNEEMEERNGFEALAAKLDKSVLPAILKVANLDLGRAALTLQQLRIPFEQRLAIQALLRLSKKDRKAVLLLIK*
>scaffold_11_R2801	MKWCRAASSASLALLACSLAGLQDQAADRWTVHTVQRTRSAEELVHEGTSRWPGDAGAVASVTCPSDLLLALQCREADGQRELRRDDQDLRRLTRMCMCCADHRRIKSGGLFALYMKASVRLTANCDRYELDAPLVSTLTCRSVDKDIHLLPDKEPL*
>scaffold_11_F2657	MQRRMSTPFFLMITTIGDAQGEVEWVMIPADNSPLIKSDNFSRNCGATRRTRWATGVALPTSMSQTAPRAAGGRAFPFPIRRCLRFQMICLNRSICSGVLPSASSIWMSSILTSSVVALTSGSMAI*
>scaffold_50_R1378	MGLFYLVCVAILAFMAGDSTGDRVIVSDGFNQHRENAARASVVSTTRLLRTKSVIDEERVGGIPVSATDKLAKFLKPSKVTDKQLQEWLRNGKTAESVFYRMNLNNPSTKYLFEDLQFTRWLKYADDLSASGKGASAISVLSAKYGDEILYLMIDRAMQEQSKALGIRLQADQLAHWVKVRKDPDEVFKLYDLNYAGRGILSNSQFNAWTKYVDDLSAKNEGAFVSIIPTLRKYYSDDNLIKIALAAKEVDETEAMGMKLEDAFVQFWIHRKETPDNVLVDLGLKKSTKTLLKNPLLNILTKYTEAYNVNYPSMRTTVIETLTRTFSDEVMAKTFLAGRTEYTTKKIAKQFQTDQLEMWLSSGQSVDDVYKLLSLPPRNSLVDFGNQKLFDTWLTFMNAVSIKNPDKTSAIFTTLAPTFNDRPMMQILEAAKKFPSMEKAATKLQLEKAQSIFSTGVSPYTAFRMVALDDVGESVLSSPLFKKWMLRPDRYHLMAHSHLCCRPAAQHFLKRPRRRDVCGGNSCVLPRYVRGRGVAGVALLCRKPNELQLLLLSTTDC*
>scaffold_17_F2587	MIVYTGLTVTTLVAFVATVCLELTEHTACVLSNDLGISSSTAQVLGLSLWSGVHLEQVEQSPFSRQLHGHVVALDQLEDGRYKGHQVFARLLRGALSRNLHNAQRATDHVLVLVRHTLHQYWD*
>scaffold_25_F1282	MRLSFLLPAAMAAIYCATCNATSDQNKMSMVQSLDARLNGQADGTRFLRAHHESEEESDREERGFTDLFKNEKAAVKKMAKAIMADPSKADEVYNTWAAKKYTLTQLSNFLKSKTAGKYDRVYNGYALHLDY*
>scaffold_68_R31	MRLNLAVLAAVIALVSRCTAVSAASSTNQINLSNLNQALNTMPNHAGDGNRLLRTAKIVDDSEDDIDSDDDIDRDEEERGGKTWAEKFAKWHARGESADDVYQRFALEPVVRQAYKYGQIGRLDDNEYYRKWAAYSA
>scaffold_11_F1227	MKLSMLVLALVCISQLGGSSANEATDIMRRQLRVGKAVASLFENQHQSTRELEENIMQDEDNKPNEVQAEPTKFRMRRLRSDYVELIE*
>scaffold_117_F62	MLRSVGGAHFDVHIVSLLFLLHGFSTHTLELLVANVVQSQGIETSECEVVDDQNGNTEPNVARALIDREALELSFALSISVSVTRELRQHIGT*
>scaffold_53_F979	MRLSVILLAVFALSSSSVSATRNHPGETATANTAMQGVDGMRTDTNQMRFLRTEADDDEERLAGKNMFNAEKIEKALQDTSYAKTLFRRWKRYEVEHGAAFDKLIKFNIGKDDKVFGLYKSYVSWLEKHHPLGAETGGGPNLFSKAKLDKAMKDPKYENTMFGRWKRQGFESDAAYNKLLAFNLASDADVYKIYTKYVTWLNIHHPLAKTRKTTAKDFLFNVDRIARAKKDSEFAETLFKKWKTSGLDEKPVYLKLWDMGLKTDDELYKLYKNYVKWLDIHYPLPAKAT*
>scaffold_22_F2097	MGGLRRPALLWIPHFLVADANCNAAVVEIDFKSGRILRDIDYAVISDEFARVAISRLSTFAVVSRPKVFRNDEEGTGIVDRVRLLMLHPTDLSDSSRFGDVKLSFTLVRDVTNYCREAEVRLRQAREEIDGQLPCLTMHSFQLNIRENFSLNLHISEGHRVVFRWPPPTAEVLLTHVEIPLDNLTQESVTYPAFMEIPIHAVVGKTPAQKRTAVNSADTKTPNTEQFLFQRDWAVVIPILRDSKAELDVAPPSPSIIERTSTYLVLDLKTPANEGDPTRMTVEQKEFTPYFYVVEMAIFSPTFWCRYDQTWWFDKTKTKVLDGMYQVVHRGFDTKVMISTSAYAGCVRVARCSIDCLENTVHLFFCHHYPISKAIICLVKISQPTLLKWMPRAADCITYLKSFKLIIPS*
>scaffold_13_R95	MRLLFWTLLVALVAILSSCDAASVDENKALQRKLYTKVASQALAADNRHGKRALRGESSKIAPSSVTEARAATVSTGFGSKIMAFLRAIKEKYLKWEQKILAPSFKEKAEKGTTYSEVLANYRTRLNWSGLWGTPSGFKRYARLYETWLKNNPKYSHLAV*
>scaffold_73_R302	MSSRGHFFSTAFPILAACKFQSVSSSPFPHVALPFGSFLMSIANTFHAPGSLQYLVASLVSAGVMSSGTATSGKSGSDASMRWLSNMMRMLRLRASLTITSRTSR*
>scaffold_25_F1407	MRLSFLLSVAMAVIYCATCNATVDSDQNKVSMVQSLDARLNGQADGTRLLRTHHENEQESDREERGLTDLFKTEKAAVKKMAKAIMADPSKADEVYMKWEAKKYTLTQMSNFLKSKTKGKYDQVYNGYVIHLDH*
>scaffold_60_F366	MLIHATTICHWVWLVQLANGFATFVTMEMKTLTITRLLRRATAKETRNTCTWIASSAGITIWMRTERTRTRRCVPSPIQMAWTCAVSARRPT*
>scaffold_5_R2654	MRPYFLLLVAVLLAISNQLRPADQSIGPLKTRRSLRLAKKSDTSNEKEDERLGLSSLKTEIKKVPLKVKLAWWQHFVGKPSEYVKKKLGANHPLYLKYRHTREGLEMWSWLAEAIRHTKSGKGKGLMAWSHCMNLDQIARQIKKPEGTEPFRVYKRYAKEFDGHRLSSDTYFIDESASVAGRYARAHIWAESKVDKEYVLEFLGLLYMKPIYVKHNPYYQYCSASSSVLVNAMVIKVFVEVHGRVEA*
>scaffold_13_F1424	MLGLPLAILELLHLCHVVLAHMSGLTSQNILVSNTFCKKQKLHVCSRLLRLPDTNSRGGRIGPRTARAQVCAGADQEQGEADPEPTGADPSTYQQAETLGCGEGDLTF*

>scaffold_7_F1378	MSVLCLALMLAMATGAFESTGDAKNGVVTPSSRRLLGFTADQEERKFGGPATGTDVSNSHAWENFKAWFKKTFFFWRKREQTRRLRI*
>scaffold_24_R331	MVLFSFCLVYIIILCCYAEKIRPLTLGQDRRLRCAVIAFPVHEKQRSEDTEVDTIPKVFLAKGSSVEMLWHFCAISADRRLTFLQRGSLRLRLISRPFLFECAWGIPTFLDVVPAAPARWRRRTSRRAQNRAIRPRREVAVRLDQGGLQIGFKEKIKPSPVARTRAKGNDEKECVLHDIRDKFHIQLLHVLQ*
>scaffold_11_F97	MPTSRPCSWLHPAALCPVVFPMMLPLLDCREFSNGPFNLAYVIAVGSDSEPPTPIPITTARMCRSGQTPFCPKFRLGCPFFIFSLNCRGRHPHHRALFHRCLRHFLLHYPRRHCPRRWQCPRSVRTS*
>scaffold_6_R2910	MVSFFLPFFLFLAFVFFTFSCSSPHHDNEPPSRTDRSTPRSSGQPDLHPLRRLRGKSGSGTARRCILPGQTPSDASKDVPLRPPPHAS*
>scaffold_25_R1205	MRITYILAVTVAATLHSSVTAIPSVKSSKVATENGAVPAVIDSTHTGTGRMLRWVNKYEGDLDKYEGDLDDNDDLDDLDDDLEEERGFSDTLKKANPLKLVKKGTKLTAEQAAKVKQALKDAADYQKMIENANKLIRSD*
>scaffold_12_F709	MRASKLLLMTVFLLASLDATSGYNKLQGTNTEVVDGTQRGVNSERLLRGHPSTVDKVSADDEERASLPTFLKKSTSGATNWLKDKKLAAKLKLRALPMNLDKSVQKTMKDGIDPDRVFTLLNLQKKS
>scaffold_12_F2959	MRLISIVLVAVATIFACCQGAPTVSDSKSISVPQHHVQTENNANRLLRVHQDEEERTGAQLVKSLSEKFSKKAAEKLTRSKSFNDFVKLDDVAYKENFHSATQALYQRIEKMGFNPDGMLKTMRKRGDVDLDLLAEYTRYWMKKYPTWTKNQ*
>scaffold_5_F3683	MFCGVLIVALVQSLFFNFLDLSPSEKKVRYLIELEWWEKATRQNAAKLLQTAWRSGNLRRGTDIGDQCHLFSLMRTARRLRIDKPAIELSVEDQVAEMEATILAEVDRMEAQKVKVLQRIQAKATQLATLKHKLQMKKKK*
>scaffold_495_R1	MRLSLLLVAAAVLVANSDAAPQSTSSLTKFSTDVAPVRSLRGASKTKTEVDEDDSFDPEEEERGIAMYGKLDKVDDILKQLNLADDSVIKKLLAKGKGGVEQLITTDKGVKTLVITSKKTGKKVTFTNIDIENIRKIESTPAIK
>scaffold_536_R3	MVLMLVSAVCMCSCLLYCAAQRLVNPSQLLPTGVMEVCRHLRWNHWISRRDTALQASDTLQDATYAKGASACEVTKLCELVSSCRRRGDAGSRLCPA*
>scaffold_5_F1732	MALGVAMAITLGLLSLVSNTTAVGTENAVGPVTRHLRSLLLDQKVSEHGAALDQQPLAASMEATSRRSVPQNPGGPLGGGRTMEAIAPRYEKKAAPETIAEAVAKAEEAEEIAEEALIVALGAENDLQAIEAITEASILSLATNSITEGLGGEEIVIVGEIEDSDDSSDSQEEHTTRKTKAKKHKDW*
>scaffold_1_F4448	MNCSQQSRLLFSLAFCQHSRLIFALVFSQQSRLQCVYDDRILPDEHLRAIRRDVSPLSLYSDRTLRRPSNAP*
>scaffold_53_F92	MRLGYFLLATIVGFLACDNATASVSESTSSKLTAREEHPIHGRIGDFTAGHDNKRALRSEDEDGDADDSDDEERDLILSTIHRPKYWRWFKAGMTPYAVQQVLGLTGVRRLWKPFKRREYKGYVVFYTEQCHKPEYHDFCKKHADP*
>scaffold_12_R42	MRLTSIVLVAAVSIFVCCQGALADSDSKSISVPQHHVHTENNANRLLRVHQDEEERAGPQLVKSLSEKFSKKAAEKLTRSKSFNDFKKLDDVAYKENFHSATQALYQRIEKMGFNPDGMLKTMRKRGDVDLDLLAEYTRYWMRKYPTWTKNQ*
>scaffold_3_R2840	MMALLLVGAPWLLPLMLPLPRFDLAPDVTLTPRERALRFSSLRILPSLISSSLANLFTLLRLPMTAPPRGFLPLR*
>scaffold_68_R530	MKTIIASLLLTAVAVNAANGDVNALSAISTISDAKQVSIRALRAAHGSHEHSSGMGSMEDSHDTTSSTHESTVAGDDDDDHDSHDTSSKSSMAGTAGSAGPSNSTESTQAPDTSSAASITVAAGSIFLAAAAAAFL*
>scaffold_24_F1366	MRLLLVVALTLAAFLAAADVSALNDAPSKRLLRSTVRVDEEEERGMWETLSSKVTKLIKPNQVAIKAMDDPKIAEVAGTSLLTSLKSVNPKKFDSVDGLFSSKAFNNLENYVLRLNKQDINKQTSVAKVFSTGLGDKQAFHLFFTATQSSDSAVEKSGRFFRDQLLTQWATEGKTWTEVSKSVPKGLPATYYPRLENKYFDILFNLAHDTQKRAARLARLEKARMAANTAA*
>scaffold_77_R394	MRLTYILALVIAATLHASGTAISTDKSVKIPAIAADDAGRMLRIVKEKPVSDKEAEREERFANPIKKLGAFLKKKWDKQTLKEAIKRDENRRKWIREQGFEPRD*
>scaffold_5_R2089	MRLSFVVLPAVIAVTFASSGNAVATADGRNTGLSAITPPNVVASIDTAVGGEKRSLRYHNNKDLEDDSDDEGLEDAEEEERRGNNMFSATKLDEMLDGKQVMSRFKKWKAFGYNTYNLPDAIQARKYDELRKMYRKFLYYN*
>scaffold_12_R967	MRLQFAVLFALSVITAANGFSETTAQQFNGELSTGEKQHDEKRILRTEKVDEDDEEGTEGEERVQVSPVSWIIDLFTPKTAEQIAEAAKKAEAVKFYTKLANSPSFRAERFPNWKIDGMQVESVLVHLKLWGLDGEKFKAIATKYTEFLASGKLS*
>scaffold_535_F2	MRLTCILLVAAASLVGVLDASAATTGNTVVANAAMVISPLAPESQGRRSLRLVYDDEDDSADEKDDEEEESADKVDEERGWLSDKMALTSLVSKFVGKSTDEMGEVIKKLTPAQIDTIFDKGEDSIQKMLPGFYSGMDFQKFDDLIRALPQEQQAVMLSAYTKYLHQNGRFS*
>scaffold_29_F1	MRVFSIFLLVAAATLVASASTESESKQRLDNSPAAPQWRTITENEVPTKRNLRKKKIEEERATTAISLFDDAVK

837	AKGWQVLPYAELANLDATVRTQYLKLLVNNLERKQIVELTGQVPRYVLKHGDSKATRLVQYNKWIFNHFKEAVDPAWVLKNYPAFFKGYDKFYQNRFTRGYKYA*
>scaffold_11_F1676	MRLPHFLLVATATFLSSYNSTATVSTEGQMMPSADAAVPVRALEANDGKRFLRYYKKEDMYDENDGDDDVDDDDKYDEEVEERGVMTATQVAKWTDKANKWVRLKETLVTIKEKLTNMKGVISAKNREKYNLFTAVYGRANPHVFERL*
>scaffold_31_F1184	MRFGLFLALLVATFVACSTVANAESVALTLGDNEVRRLRLNQQNIAKAAGDFISKSKESATLTKAINIAKTANGDEAAARRAVMLAAGAKEGAKLSDETMVKLSAMIAESAKKNPKSWPRLKKFVKITLGIQVGGLAIYGAYKLLFDKGSSTAAATTTTTTTTSSGAA*
>scaffold_40_R1072	MAFSSFLKFLAMATLLMVQVNAEPSQQTRNLRIQSDDLPQEQARRLGPNWKALVINVKNNPGVSDGVMKLLKKADLITGTSKKIKEKVKDAAEKVKNSAGKVKDKVTGN*
>scaffold_62_R12	MRVTQTLFAIAVVLFATTDNLTTASKATTSSKVQKDGLYAEIYNVEDGVVTKKMRVPLGDVEQYSDTDFEQLKSTLTTEERAAVHLPFGVDSFFKGLEKFVGFFKFKGRRLRIEEA*
>scaffold_4_R3284	MVKCCAFVVGLVMALASGENNVDVGDVGGNGVKTEAVVRVNATVESLRFPVLFDAIINRSVVLEHSRETRDLRVLSIEREGVVEVEVEVDAATVSSCNATTKACPPEVNDTEIDENSVPPPSLQQTDRLVRVDGENVSTLSFQDVIDSAAGSVAVLPLFKPIGSAHVLSGFARVEILSPKLLEFEPAIPEREQVVMAWIEEKARLKAEREAREREIANNKELQERLEKERLLAEALAKKEEELLAKLDREEYERTRMTPHNLAAGKRRDGWEFRYEVEFKTKGPIGLNWDLNTRDKAVVSHLEPELPAQQLNVIAPRDQIISLNGVDTSKMGPQEVVEVYLSSAIPRKMVFLVQMSAERAAAKSAEKNPVKRVVMNWTLAFDAPEVLRGWEVRLHLASWSVPPQINETNASLPLQFELPTPITGCSSFPVPQSSNETAGVVYLAYRGACTLVEKAKNARTANGSALLIVNNANGEGRFTPSGTVVVERVDVPVTLYESTFVFIRCIWNLICGVCTAG*
>scaffold_211_R6	MRLSQVLVIAVASFVFASDTVATSNQAKISKTVQSSQSQRLLRSNHYPVKEEEDESEDSVDFEERGFTTPDEEDLEERSPLSAAIVEKLDDIASRWGTSWAAVAMGQSSISEDKIKALLALRDAYLSGNKNAKAAAKLAILRANWTRSQQKW*
>scaffold_80_F473	MSFLSLFCFTQLLWSCNFQTVKAVFEAYAQTYVRIPPEGTVVFSTALPTCTWKSTDSVFSFITTRILRF*
>scaffold_62_R723	MIGCKSLISRWPTFFLTLSAADSIWSDFFVACNPQLTLDQARHLNSRERKRYLREYPGIAARHFHRRFKAFFFLQHTLWKRSSSWGNCRLLLAR*
>scaffold_1_F5450	MKTATTFATVLALIVATNAAQVSPHTPALRGLRLTADTPSVEDDKEDRKDHHHVKKVKKIAIPVPVPVEVPQFIPVPVSVPSTVVASSNNAVVGPSTNVAGPGAAAPGAPGAPGAVTPAPTTLNGRPAATPAATSTTRSRPTPAPTNFAGARPSGAQLPAAPVQVGAPGMTGFPNSAGVGDNTNNNAFGAGIGAAGGFPMTGNGLAGGFGRNPMNGFGGANGMGSGGIFGGAGAGPAMGGNGFGGNGLGGFGGQGAAMNFGQAGNNGFGEGQGGFGSGFNRRERHRRR*
>scaffold_26_R1820	MAAIKISWQPGCFFPVALSYLVVWSSELCAANRRMVWIRRSLRFGKTRLRSPYLTEHKLCMFHVFMHFFYLN*
>scaffold_52_R8	MSALRAQIYLFVVARAAVDGQVVCLVAVQQDLVRARAIRLATTNHVHQRRLISTRRPPQSRHQARRRESAHTLQQVQGLFRALRVRHGVQKVLERHHNHERRAANRRFALLRVVFYGILVGQNDGRILLLDR*
>scaffold_33_F296	MGWVFCIAILLIMASMSIPDPYYGDPAMHSIDEEDWTDDQIDSINADAPNSAGKYVVPMMLASFGYLMCELQQMPWWSSTHNENRSNNVAAFKPPFTPSKRRSLRSELLSLRSS*
>scaffold_16_F1464	MRFSQVLVIAAVSLLFANDTVAVATSNHAAISKTVQSSQSQRLLRSNKYLVDEEEDQSEDSVDFEERGGGKSHPLTNRKLRSLKQSLEVGELLIRELLWVSQASRPRRLMRCLPCETRTCFATGLLSRQQR*
>scaffold_2_R3899	MRLQSIVLILVATLVATTQATTKLNAPSSETVDISPQRFLRKHHTQNDEERGAASLIEKAKRVFPSKITDKTLQRWANKKKSPKQALTRLKLDIPGRTSLRSLSSASGPLSWPSATRTTPKKRWSRLYWRNTAMRP*
>scaffold_28_F919	MDTCLSVLLSLYVSACSSQTALPEVLNASVEMASVTVSLYGVGTPSLISRWLRAIAEFYDYPSISQLLDDHFCGLWHRFISASHRPVPQEEENSTGWMKNSQLAPLPNGHSLLQQFPLCILLGEEPGMNTQETHFAKMLDKIVPIGVLHSFISGDMSGENGDRFKFVDEILSCFPVDDMNAERKIDFGAQLTTDLFAFSFMLLVYPDPDLKQLAQQMVDIAEERAHGNTLQLSHLGHIASKMARFTVWNIIQGCDEDLVTQSDLWRDALKMMKEKYSAFDWKLLNIADLLGEFYVLLLRTEHIDPRAVCAVECFKIFVEETRDAVAESSVLQQLLLSICFQSIKRLAVRNRRRIGRVLSLLVRENCEYFMKSTDKFGKYLGFVVQEISDILSKCNASSQTGRNSVGALSVSADDQAELEWVIFAVCNELGSGLGKHALDIDMVSDGISSSLDKLNALIISSRKVVSSETSQSEEERKKNLSQSAMGTRNQAIQQILMFIQREQSRGAQFYNPHPFSGTASAISRETYVNAATQSPAGSLADVRLSAVTTCIDMVRDSSQSTMKLYGKLAQTLLYLSSSGTFGTSRYNCENDAASLANTLGQLGALHASEYEVSPAEQEGELSRLYWRHFHRGALREIKTTFGLVMHENVLTYLSSLLFEGTRFGHVDPTVVEETLKTLQTVLNLEEGLAALARSKDNELKAFLKPFESSSPSNWSSSYSSSGGDWGVKP

	KRTFRQFLKHWTSAEELGFEAWVRSLTACLARESSDPVLKACSALSAMRVDMAVFLFPYALERILRLDNRDVDNPDEEKKSSGVSEPSRIMKAANQGIRFVLTGSTGDALSHHVLASLDGTQRESEFSQPPEAVQLVVHSINFLRETEKAQFVETNGRGPQTVSTIKGKGSRRSSTYTAASIGRQHLNDLAYGCLVDVDFLAVAKAAVRVKMPYSAMQYVEMWLEKKQGGKITSLSSLDRDGMVDTVRDILVEAYSFDSDDDGIYGVNDGRTVKSQLVKYNREGLHARALPLYDVSLQFSSQQLVSTDELTLNTPPRLVEGILTSLQSLGYNHLLTGYLQSLQSGDVAGNKSGTAIAQALEHKYKLAWKSMQWEAVLSGLSASGEHSSHHQMIFQGLRAIAHGNFTRLQGITTKAKEQVLRSVQLSLHSFESTKDSYSALVRLQAIHEIEELANHIRNSVPPTEPLVFSATTTGSGPFLPSLGGTLAAPRQETLTVLPLLEQWHQRRDQIKNDFDKAESLLALEEVLVQVAKPSDNARVVTKLYLDLASLSRKAGRIAIAYRALQKLEHLDERGSLGIYERMQCQIQKAKLLWKQQEARSAIWTGKSVSSELTGYLRDTSISATEVTSLQLLLVKVLTFTGKWIAFQRSESSQVILEDFFQKATEIMSNMDPEAVSERSRDAAKAHFALAEFMAGMYQQVSTRVTSQEWLTGKMVVQARHDELQELQSMEQNMQNENRAHIFALNKEVIYDMNERSKVEASVDQFLIGAICSYGKGLTLSLQAELDMVFRVLSLWFNNQHKPDINRVVIEEVIDMVPSYKVVPLSYQIISRISSASGTFQTALRKLVMKLSEQHPHHTLIQLIALKNSGDVEGKGALQFRTNVGDAKAEGAKVYLTELMKTEQRELLQSLDSIANAYVQLALFDTSEYHGKKKKIPLSTVKIFETNSGRSGGTTFDQCLRARARRGDSVVLPAVLTSQIAPQPDMNYSNVVRMYSFEPQFSITDSGIHRPKIIYCYGSDGEPYKQLVKGQDDTRQDLVIEQVFETMNQFLMEEKATRKRKLRLRTYRVVPLSPIAGVLEWVENTMPWGSYLVSRTSKRLSAHERYHPHEWKHTECRQYLKNAPDKLPAFLEIEANFTPVFHHFFLEKFPDAAVWYQRRLSYVQSAAVTSIVGYILGIGDRHSQNILIHEKTGELVHIDFGVVFDQGMALYTPETVPFRLTRDMVDGMGISGVDGVFSRCCEVTLQLLRKKSASVVTILEVFVHDPLYRWTLSPLKALRIQEGQGHGKPTRSRSSSRSSGSAEYDGTGSMQDTQPADEMHAEPGSTDAAARALIRVKQKLEGYEDPNGSALSIEGQVKQLINAAQDPLNLCKLFPGWAPWL*
>scaffold_29_R308	MTSSSCRCLLPLWSGVSSVYSDAEIPLRRPFLVFLHRGFWYSRCQVPVVSSLCFRIRTFLSEVPWPPARVTRHRVHRSSGRLRFTLLSRRVCCSYRARRSLRSACRLRAFVRSYRWYSIGRLFSTQVLVFTVLRMDHPHLGDVLLLRLLHCRRLLCGALDCGLRLSFSILSDRPIAPISHATIRYIPDAGEFIPNSLWVRENCPVGVSRCRRCRRIHRIPYANTWYYHGVSGSRPNRYRIRHLRSYPLLPDVLHPLSYIIKGVVHLRRLVYRLVKCLRLALSH*
>scaffold_21_F2030	MQRRMSTPFFLMITTIGDAQGEVEWVMIPADNSPLIKSDSFSRNCGATRRTRWATGVALPTSMSQTAPRAAGGRAFPFPIRRCLRFQMICLNRSICTGVLPSASSIWISSILTSSVVALTSGSMAI*
>scaffold_494_F2	MRLLYLAGVAILAFAADAKVLVSDDSVNNRAQAASASVVSTTRLLRTRSVIDEERAGGISASASDKLAKLFKSSKVTDEQLQKWLNNGKTAESVFYRMNLENTLYTRVFESPQFPRWLQYADDLSASGKGASAISVLSTKYGDDTLYKMIGWAKKESSTKALGIRLQTEQLEHWVKIGKDPDEVFKLYKLDYAGNRILGNPQFSAWTKYVDDLNAKNKGAFVSIIPTLRKYISDDDLFKIALAAKRSGETKAMGTKLEDAIVQFWNRAGGPVGNGPT*
>scaffold_100_R322	MRICFVLLLTVAALVTAVSGSSVNLRDSQRIDVVQDKTSSRELRGDLNTDEATEERASFDFVKKLVAKLKGDPLESFAKRQTKYIFSDDIFDEMLKKFPDPDALYTTLKLHVIKNRSNKYGVTTARHKLHQNFLTSYIDKFPNWRSKLN*