

MAP-BASED CLONING OF THE *NIP* GENE IN

MODEL LEGUME *Medicago truncatula*

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Large amounts of industrial fertilizers are used to maximize crop yields. Unfortunately, they are not completely consumed by plants; consequently, this leads to soil pollution and negative effects on aquatic systems. An alternative to industrial fertilizers can be found in legume plants that provide a nitrogen source that is not harmful for the environment. Legume plants, through their symbiosis with soil bacteria called rhizobia, are able to reduce atmospheric nitrogen into ammonia, a biological nitrogen source. Establishment of the symbiosis requires communication on the molecular level between the two symbionts, which leads to changes on the cellular level and ultimately results in nitrogen-fixing nodule development. Inside the nodules hypoxic environment, the bacterial enzyme nitrogenase reduces atmospheric nitrogen to ammonia. *Medicago truncatula* is the model legume plant that is used to study symbiosis with mycorrhiza and with the bacteria *Sinorhizobium meliloti*. The focus of this work is the *M. truncatula* nodulation mutant *nip* (numerous infections and polyphenolics). The *NIP* gene plays a role in the formation and differentiation of nodules, and development of lateral roots. Studying this mutant will contribute knowledge to understanding the plant response to infection and how the invasion by rhizobia is regulated. Previous genetic mapping placed *NIP* at the top of linkage group 1 of the *M. truncatula* genome. A *NIP* mapping population was established with the purpose of performing fine mapping in the region containing *NIP*. DNA from two *M. truncatula* ecotypes A17 and A20 can be distinguished through polymorphisms.

Positional mapping of the *NIP* gene is based on the A17/A20 genetic map of *M. truncatula*. The *NIP* mapping population of 2277 plants was scored for their nodulation phenotype and genotyped with flanking molecular genetic markers 146o17 and 23c16d, which are located ~1.5 cM apart and on either side of *NIP*. This resulted in the identification of 170 recombinant plants, These plants' DNAs were tested further with different available genetic markers located in the region of interest, to narrow the genetic interval that contains the *NIP* gene. Segregation data from genotyping analysis of recombinant plants placed *NIP* in the region between 4L4 and 807 genetic markers.

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TABLE OF CONTENTS

	Page
ACKNOWLEDGEMENTS	iii
LIST OF TABLES.....	v
LIST OF FIGURES.....	vi
LIST OF ABBREVIATIONS.....	vii
Chapter	
1. INTRODUCTION	1
2. IDENTIFICATION OF RECOMBINANT PLANTS	22
3. ISOLATION OF RECOMBINANT PLANTS AND TESTING THEIR DNA WITH DIFFERENT GENETIC MARKERS.....	29
4. DISCUSSION	35
5. MATERIAL AND METHODS	38
APPENDIX.....	48
BIBLIOGRAPY	105

LIST OF TABLES

	Page
1. Phenotyping and Genotyping Data for the NIP Mapping Population (F2 Generation)	50
2. Phenotyping and Genotyping Data for F3 Generation of the <i>NIP</i> Mapping Population	64
3. Phenotyping and Genotyping Data for Recombinant Plants from F2 and F3 Generations from <i>NIP</i> Mapping Population	98
4. Recombinant Plants that were Selected for Further Testing	103

LIST OF FIGURES

	Page
1. Nodulated roots of <i>M. truncatula</i> , and nitrogen fixing legume nodule	4
2. Schematic representation of a nodule	10
3. Phenotype of wild-type plants (A17) vs. phenotype of <i>nip</i> plants at 15 dpi.....	13
4. Cross between F1 progeny to obtain F2 generation.....	15
5. Crossing-over and recombination during meiosis.....	16
6. Schematic representation of the top Linkage Group 1.....	18
7. Genotyping with 23c16d and 146o17 genetic markers.....	24
8. Genotyping with ENBP genetic marker	26
9. Genotyping with 2D12 genetic marker.....	31
10. Genotyping with 164n9 genetic marker	31
11. Genotyping with 4L4 genetic marker	32
12. Genotyping with 807 genetic marker	33

LIST OF ABBREVIATIONS

BME	β -mercaptoethanol
bp	base pair
$^{\circ}\text{C}$	degree centigrade
CCaMK	Ca ⁺⁺ /calmodulin-dependent protein kinase
cm	centimeter
CTAB	hexadecyl trimethylammonium bromide
dNTP	dideoxyribonucleotide
ddH ₂ O	reverse osmosis and deionized water
DIH ₂ O	deionized water
DNA	deoxyribonucleic acid
EDTA	ethylenediamine tetraacetic acid
EtOH	ethanol
g	gram
h	hour
KCl	potassium chloride
min	minutes
mix (F+R)	mixture of a forward and a reverse primer
MgSO ₄	magnesium sulfate
mL	milliliter
mM	millimolar

CHAPTER 1

INTRODUCTION

Legumes and Their Importance

In the third world regions poor nutrition and hunger are major issues. Soils there have low amount of nutrients, in addition, bad management of soil resources and inefficient use of fertilizers lead to very low yields of food crops. Use of mineral fertilizers is very expensive. For example, prices for fertilizers in some developing regions on average are two to six times more expensive when compared to prices in Europe, Asia and North America. Genetically modified crops containing higher amounts of nutritionally important compounds like vitamins, and amino acids can help with malnutrition. However, nitrogen depleted soils are the main problem for growing genetically engineered crops (Sanchez, 2002).

Use of nitrogen-fixing legume plants, the Leguminosae, can help to solve issues of poor nutrition, hunger, and can increase depleted soils with nitrogen. Legumes are second after cereal crops in their importance for human use. A large number of legume plants are used as important grain cultivars, some are valuable as feed for animals, and are cultivated on vast pasture areas. High quality protein content of legume seeds makes soybeans, beans, peas, and chickpeas major food staples. Soybeans and peanuts are valuable sources of vegetable oil worldwide. Many plants from the *Leguminosae* family develop tubercules. Plants such as alfalfa, clover and lupin are widely cultivated as food for animals (www.ildis.org).

Legume plants also utilized for nontraditional purposes. Obtaining tannins, gums and medicines are good examples. Species like *Derris* and *Lonchocarpus* are used to obtain rotenone, an insecticide used as a poison for fish and also as a molluscicide. Legume trees are used for timber and for collection of resins; other legume plants (genera *Indigofera* and *Copaifera*) are used as dye sources (www.ildis.org).

Many legume plants can utilize N₂ from air and are able to reduce it into nitrogenous compounds that are useful for the plant. This is because plants in the Leguminosae can form a symbiotic relationship with soil bacteria called rhizobia. During the symbiosis the bacteria can reduce atmospheric nitrogen for the plants, which enables legume plants to live in low nitrogen conditions. Legume plants form root nodules, which are the place where nitrogen fixing bacteria reduce nitrogen. Plants provide the bacteria with a hypoxic environment, which is a necessary condition for optimal functioning of the bacterial enzyme nitrogenase. Also, plants supply bacteria with fixed carbon that is generated by plants through process of photosynthesis (www.ildis.org).

The ability of the legume plants to enter into a symbiotic nitrogen fixation relationship with bacteria reduces fertilizer use. The inclusion of legume plants in crop rotation systems can increase nitrogen levels in soils formerly depleted of nitrogen. The use of aerial plant parts as fertilizer further contributes to increasing soil nitrogen content. Nitrogen obtained through symbiosis contributes to increased amounts of protein in the foliage, and seeds of the legume plants when compared to protein content of the plants that are not able to get additional nitrogen through symbiosis. Higher

protein content makes legume plants valuable crops for agriculture (www.en.wikipedia.org).

Legume species present great value for humans. Nitrogen-fixing plants are well adapted for growth in low nitrogen environments. Their unique ability to form a symbiosis offers great scientific value. A deep understanding of symbiosis and the mechanisms that control it may enable future generations to apply knowledge and transform non-nitrogen-fixing plants like cereal crops with the ability to utilize an alternative environmentally friendly source of nitrogen.

Benefits of Symbiotic Nitrogen Fixation

Fixing atmospheric nitrogen inside nodules by the means of symbiosis provides legume plants with the ability to live in the environments that are depleted in nitrogen. It allows plants to thrive without nitrogen fertilizers. Soils become enriched in nitrogen through fixation in nodules and the decomposition of foliage when the aerial parts of legumes are used as green fertilizers. Every year soils are being enriched by fifty million tons of nitrogen that is fixed by bacteria, and this source of nitrogen is not harmful for the environment (Udvardi and Scheible, 2005).

Nodule Development

Nodules develop on the roots of the legume plants. Photographs of nodulated roots and a nodule are presented in Figure 1.

A. Nodulated roots of *Medicago truncatula*



B. Nitrogen-fixing nodule

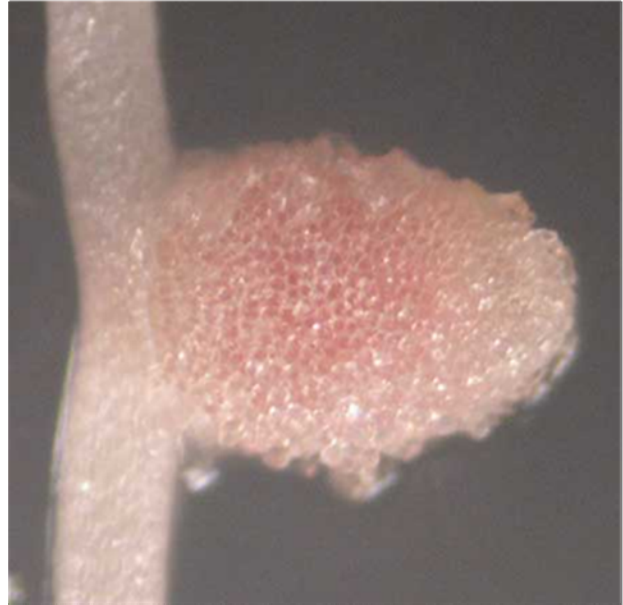
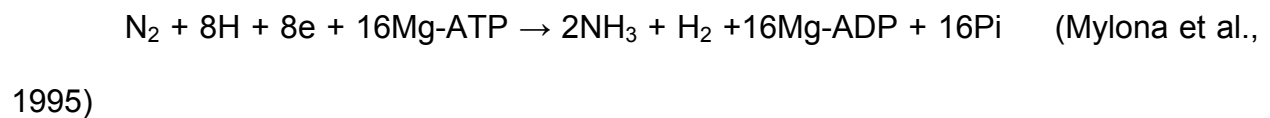


Figure 1. A. Nodulated roots of *M. truncatula*; B. Nitrogen fixing legume nodule

Nitrogen fixation takes place inside nodules where atmospheric nitrogen is reduced to ammonia by the bacterial enzyme nitrogenase.



Ammonia is used to make amino acids, which in turn are used to make other nitrogen-containing compounds (Hirsch, 1992). Conversion of nitrogen to ammonia is an oxygen-sensitive process and can be done only by some prokaryotic organisms (Mylona et al., 1995).

Legume plants will enter into the symbiosis with bacteria only if they grow in the nitrogen deficient conditions and if the correct type of bacteria are present (Hirsch, 1992). The process of nodule development can be divided into three steps: pre-

infection, nodule initiation and differentiation (Hirsch, 1992). During pre-infection the plant releases flavonoids into the rhizosphere. Flavonoids act as attractant for specific bacteria species, and they stimulate bacteria *nod* genes (nodulation genes) that are responsible for Nod factors synthesis (Mylona et al., 1995). Nod factors are lipochitooligosaccharides, a type of glycolipid, that generally have a 3-5 β -1, 4-linked N-acetylglucosamines with a fatty acid on the nonreducing sugar residue backbone (Mylona et al., 1995). Nod factors are important for initiating the symbiotic response in legume plant. The symbiotic response includes the recognition of bacteria by root-hair cells, curling of root hairs, initiation and propagation of infection threads, and the formation of root nodules (Cullimore and Denarie, 2003).

Nod factor binds on the roots to the receptor called Nod factor perception protein (NFP). *Nod Factor Perception (NFP)* is a putative Nod factor receptor gene. It was determined that NFP is a lysine motif (LysM)-receptor-like kinase (RLK) (Arrighi et al., 2006). In *L. japonicus* two transmembrane LysM-RLKs, *NFR1* and *NFR5*, were cloned. It is postulated that when activated as a heteroduplex complex NRF1/NRF5 they trigger calcium influx and cause swelling of root hair tips. The activated NFR1/NFR5 heteroduplex is necessary for activation of a putative receptor complex NORK/DMI2. NORK/DMI2 is responsible for plant symbiotic responses (Arrighi et al., 2006). In *M. truncatula* the LysM-RLKs LYK3 and LYK4 play a postulated role in recognition of Nod factors. It was shown that *LYK3* and *LYK4* genes are necessary for Nod factor induced infection of root hair cells by rhizobia (Cullimore and Denarie, 2003).

LYK3 is predicted to be a putative Nod factor receptor, and it shows 72% sequence identity with *NFR5 L. japonicus* and 86% sequence identity with *SYM10* a

postulated Nod factor receptor from a pea (Arrighi et al., 2006). From studying mutants it was determined that *NFP* plays important role in Nod factor perception during early steps of the symbiotic interaction. *NFP* was placed upstream of the genes *DMI1*, *DMI2*, *DMI3*, *NSP1*, and *NSP2* that control symbiotic responses and nodulation (Arrighi et al., 2006).

From LYK3 and LYK4 the signal is transduced to another receptor like kinase DMI2 and a putative cation channel DMI1 that regulates calcium spiking in the perinuclear region of root hair cells (Smit et al., 2005). The receptor like kinase DMI2 and the putative cation channel DMI1 are predicted to be upstream of both Ca⁺⁺ spiking and DMI3 in the nodulation signaling pathway (Gleason et al., 2006). The initial detectable response to the Nod factor is the rise in cytosolic calcium in root hair epidermal cells that leads to the depolarization of the plasma membrane (Brewin, 2004). Cytosolic calcium spiking that is associated with the nucleus of epidermal root cells affects DMI3, a calcium/calmodulin-dependent protein kinase (Kalo et al., 2005). The DMI3 kinase is located in the nucleus of epidermal cells, and it is believed to interact with transcription factors that control the host plant gene expression (Smit et al., 2005). Nodulation signaling pathway genes *NSP1* and *NSP2* are located downstream of *DMI3*, and they are important for their role in the nodulation pathway (Smit et al., 2005). *NSP1* and *NSP2* are putative transcription factors belonging to the GRAS family. They are located in the nucleus of the plant root cells. *NSP1* and *NSP2* connect Nod factor to changes in expression of the plant genes that are necessary for nodule development. They are believed to be activated through phosphorylation by DMI3, which encodes the protein kinase Ca⁺⁺/calmodulin-dependent protein kinase (CCaMK) (Gleason et al.,

2006). When in the active state, NSP1 and NSP2 promote transcription of the early nodulation genes (Udvardi and Scheible, 2005). Activation of NSP2 leads to production of a plant hormone cytokinin, which is important for nodule development. Increased amounts of cytokinin can induce nodule formation. Consequently, it was shown that inhibition of a *M. truncatula* receptor for cytokinin decreased nodulation (Oldroyd, 2007). Activation of *L. japonicus* cytokinin receptor histidine kinase1 (LHK1), is both necessary and sufficient for nodule organogenesis. LHK1 mutants abolished nodule primordium formation (Murray et al., 2007).

After the plant and bacteria recognize each other, bacteria attach to the root hair tip where the cell wall is thin. Specific recognition between the lectins, which are located on the surface of the plant root cells, and adhesins, which are located on the bacterial surface, aids in the attachment of the specific kind of the bacteria to the root cells. The signal produced by the bacteria increases as the numbers of bacteria increase (Brewin, 2004). After 6-18h from the initial contact with the bacteria, the plant root hair shape changes. Rhizobium *nod* genes are necessary for hair deformation (Hirsch, 1992). Under the action of the Nod factor, root hairs deform, yet the only shape that will lead to the future nodule development is a shepherd's crook. Shepherd's crook is when the root hair forms a 360 degree curl (Hirsch, 1992) and living rhizobia are required for its formation. It is thought that where rhizobia attach to the root surface they secrete Nod factor that causes change in local cell wall biosynthesis, and prolonged presence of the Nod factor results in change in the direction of the root tip growth towards bacteria (Brewin, 2004). As the root hair curls, bacteria become trapped inside the curl and bacteria multiply inside of the hair curl pocket. Inside of the curl a local hydrolysis of the

plant cell wall happens, plasma membrane invaginates, and new plant cell wall is deposited around it (Mylona et al., 1995; Brewin, 2004).

A plant cell wall presents an obstacle for the bacteria to enter inside the plant. Modifications at the cellular level need to take place in order for the rhizobia to get inside a host plant, but it is not known how these occur. Nod factor produced by the bacteria causes cell cycle activation. Cell cycle activation in the outer cortex is accompanied by the relocation of the nucleus from the periphery to the center of the cell. Cells of the outer cortex do not progress further than the G2 phase of the cell cycle. These cells form aligned transcellular cytoplasmic strands that are known as the preinfection threads. Over time the infection threads will develop in the place of the preinfection threads (Brewin, 2004). Bacteria enter the plant through the infection threads (Mylona et al., 1995). Infection threads are the tubelike structures that have invading bacteria embedded into the plant extracellular matrix and they are bounded by the plant cell wall material (Brewin, 2004). A matrix that surrounds bacteria inside the infection thread is made from the compounds produced by a plant and bacteria (Mylona et al., 1995). Infection thread formation is thought to involve a reconstruction of plant cell walls as they grow and move across several layers of the cortical cells (Brewin, 2004). A number of changes occur at the cellular level not only in the outer cortex, but also in the inner cortex as the rhizobia enter the plant. Nodule organogenesis is initiated by dedifferentiation of root cortical cells that is followed by cell proliferation, establishing a cluster of meristematic cells that give rise to the nodule primordium (Tirichine et al., 2007). The nodule primordium is the place where plant cells initially become invaded by rhizobia. After activation of the cell cycle, cells of the endodermis and pericycle give rise

to the nodule vasculature, and the outer side of the non infected cortex of the mature nodule (Brewin, 2004). Bacterial invasion of primordia occurs through infection threads progression through root hairs into the root cortex (Gage, 2004).

When the infection thread reaches the nodule primordium, bacteria are released into the cytoplasm of nodule primordium cells. By a process similar to endocytosis, the rhizobia become surrounded by the plasma membrane (Brewin, 2004), forming a symbiosome. The symbiosome includes the symbiosome membrane, the symbiosome space, and bacteroid. Many symbiosomes can be found in each nodule cell (Catalano et al., 2006). The symbiosome membrane is initially derived from a plasma membrane, and during maturation it becomes biochemically different from the plant plasma membrane. The symbiosome membrane becomes enriched with additional proteins and lipids, differentiating it from a plasma membrane (Catalano et al., 2006). The symbiosome membrane forms a permeable barrier between a plant cell and rhizobia. Through the symbiosome membrane, an exchange of different signals and metabolites, e.g., ammonium, carbon sources, takes place. Once inside the symbiosome, the internalized bacteria are called bacteroids. The symbiosome membrane also protects the bacteroids from plant defense response (Mylona et al., 1995). Bacteroids grow, divide and elongate inside of the host cell until they mostly fill the host cell.

Differentiation of nodule primordia into mature nodules that are able to fix nitrogen occurs after rhizobia are initially released from infection threads into the infected cells. Secondary signals of unknown origin are believed to cause morphological cell changes and tissue differentiation. Two kinds of nodules are known: determinate nodules and indeterminate nodules. They are distinguished based on their growth

patterns (Mylona et al., 1995). In determinate nodules, the meristem stops dividing during the early stage of nodule development; therefore, all cells in the central tissue stay at the same developmental stage (Mylona et al., 1995). In contrast, in indeterminate nodules, different regions can be clearly identified. An indeterminate nodule can be divided into following regions: the invasion region is where infection threads can be observed, and initial symbiosis takes place in the prefixing zone II. Here the continual release of rhizobia from infection thread takes place and bacteroids divide and elongate. Zone III is divided into nitrogen-fixation zone and inefficient zone where nitrogenase activity is low. An interzone can be found between zones II and III and bacteroids that have reached their full elongated size are located here (Vasse et al., 1990). The senescent zone IV is the last zone (Hirsch, 1992). The locations of the four nodule zones are depicted in the Figure 2.

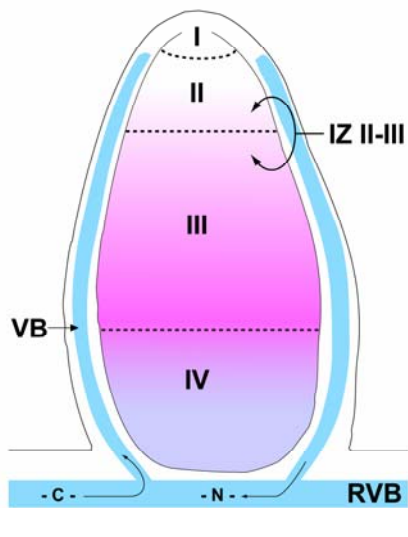


Figure 2. Schematic representation of a nodule.

I, II, III, and IV show location of the four major zones inside a nodule

IZ II-III shows position of the interzone region

VB indicates location of a vascular bundle

RVB indicates position of a root vascular bundle

(Adapted from Coque, 2006. PhD dissertation University of North Texas, Denton, Texas)

Medicago truncatula as a Model Legume

Medicago truncatula is of particular interest for use in molecular genetics. It is an annual diploid $2n=16$ plant that is largely cultivated as a foraging crop (Young et al., 2005). *M. truncatula* is self fertile, is easily transformed, and has a short reproductive cycle. Its genome is small, consisting of 500 Mb of DNA. Different ecotypes are available which allows for genetic studies. As a member of the *Galegoid* phylum *M. truncatula* is phylogenetically related to many agriculturally valuable legume crops, like pea, chickpea, faba bean, alfalfa and clover. This relatedness opens a possibility for useful findings from *Medicago* to be applied to related legumes that are useful for humanity. *M. truncatula* enters into the symbiotic relationship with well studied species of bacteria *Sinorhizobium meliloti*, whose genome is sequenced (Galibert et al., 2001). *M. truncatula* plants are also used to study symbiosis with mycorrhiza. Many different tools are presently available for genetic studies. These include cDNA libraries, a BAC library and numerous mutant lines (Thoquet et al., 2002). Also, microarray and DNA chips, as well as detailed physical and genetic maps are available for scientists to conduct their work (Young et al., 2005).

nip Mutant

In our laboratory we study *M. truncatula*, and we are interested in gaining more knowledge about genes that are involved in the nodulation process. The goal is to identify genes that are important for nodulation. Several genes that are important for signal transduction pathways for nodule formation have been cloned (Mitra et al., 2004). We study mutants with defective nodulation phenotypes. Two mutants that we work

with are *nip* (numerous infections and polyphenolics) (Veereshlingam et al., 2004), and *sli* (sluggish mutation invasion) (Haynes et al., 2004), both of which have defects in the infection and invasion processes of nodule development. Studying these mutants will help to understand how plants respond to infection and how the invasion by the rhizobia is regulated. A primary goal of current research is to map and clone the *NIP* gene that is responsible for mutant phenotype, and later to map and clone *SLI* gene.

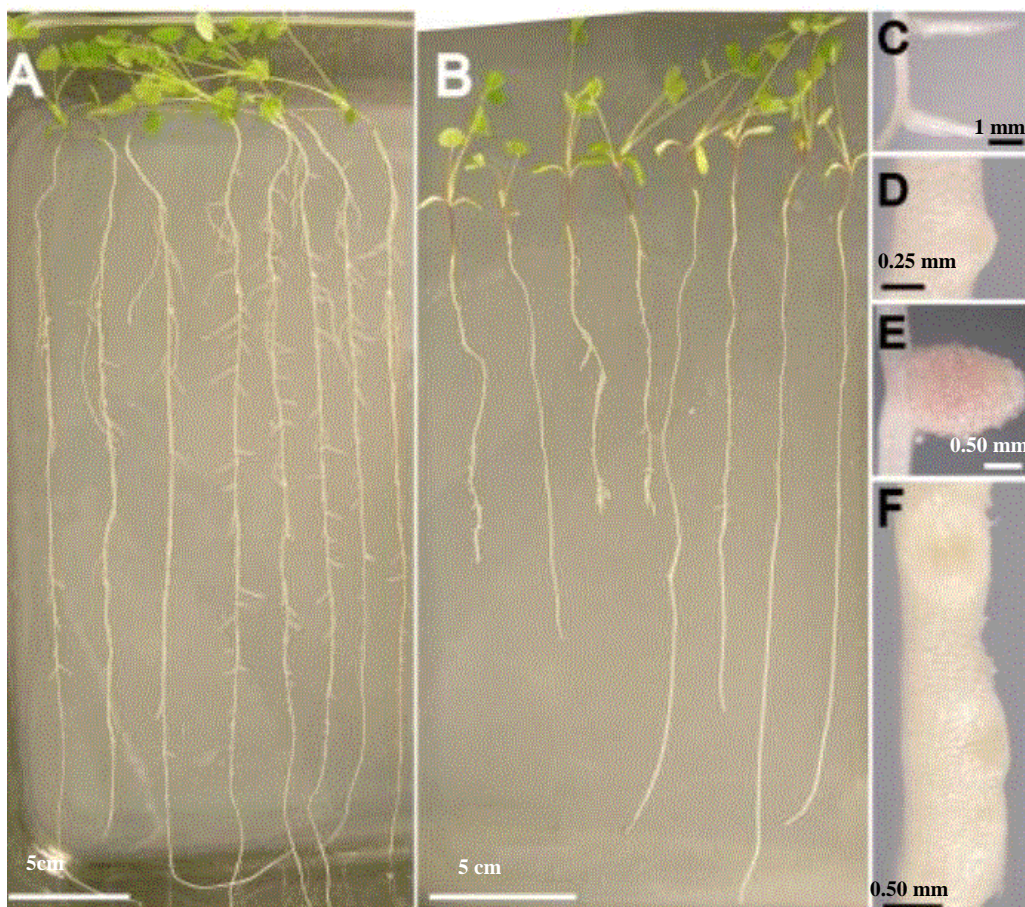
This project focuses on working with *nip* mutant plants. *nip* mutant plants are phenotypically different from wild type plants, and thus can be easily identified. Wild type plants are healthy and robust. They have a well developed root system. Wild-type plants have long primary roots, along with many developed lateral roots. Big pink nodules can be clearly seen on the wild-type plant roots. Pink nodules are indication of presence of leghemoglobin and an effective symbiosis with rhizobia.

nip mutant plants show nitrogen starvation symptoms when grown in media without nitrogen and in the presence of *S. meliloti*. When examining *nip* mutant plants, it can be seen that plants overall are weaker and smaller in size. They show signs of nitrogen deficiency. The root system of these plants is less developed. Generally, the main root is shorter when compared to wild-type plants, and *nip* plants have abnormal lateral roots. *nip* mutant plants have small nodule bumps— small white and brown nodules that fail to develop completely. *nip* nodules are stopped at an early developmental stage, and they show defective development of infection threads inside nodules. Abnormal infection threads can be explained as rhizobia not getting inside the plant host cells efficiently. Also, *nip* nodules have a brown pigment, and show accumulation of polyphenolics compounds, which is an indication of a plant defense

response (Veereshlingam et al., 2004). *NIP* is important for regulation in development of roots and nodules, since when it is defective, the mutant shows abnormal nodule development, abnormal progression of infection threads, and abnormal development of lateral roots. Accumulation of phenolic compounds also suggests that it might be involved in the defense response (Veereshlingam et al., 2004). Phenotypic differences between wild-type plants and *nip* plants are presented in Figure 3.

Figure 3 Phenotype of wild-type plants (A17) vs. phenotype of *nip* plants at 15 dpi.

A, Wild-type plants; B, *nip* plants; C, Wild-type primary root with emergent lateral roots;
D, *nip* lateral root;
E, Wild-type nodule; F, *nip* nodules/bumps.



(Veereshlingam et al., 2004)

Positional Mapping of the *NIP* Gene

nip mutant plants, also called C90, with abnormal nodulation phenotype were isolated from a *M. truncatula* population that had been mutagenized with ethyl methane sulfonate (Penmetsa and Cook, 2000). The *nip* mutation was shown to be recessive and behaved as a single gene. The gene responsible for mutant phenotype was named *NIP*. Mutant *nip* is in the A17 background (*nip/nip*). To create a genetic mapping population, *nip* was crossed to wild-type *M. truncatula* of the ecotype A20. This ecotype pair, A17 and A20, is the basis for a genetic map of *M. truncatula* and many genetic markers are readily available for this cross. Positional mapping of the *NIP* gene is based on linkage analysis and the A17/A20 genetic map. The first generation of plants from this cross (F1) was obtained and found to be wild-type. These had a *NIP/nip* genotype. The F1s were selfed to create the F2 generation. In the F2 generation, segregation for the phenotype occurs and *NIP:nip* phenotype plants were observed to occur in a ratio of approximately 3:1, which is consistent with a recessive gene behavior (Veereshlingam et al., 2004). In figure 4, the cross of heterozygous individuals from F1 to obtain F2, it can be seen that 25% of the F2 progeny should have mutant phenotype. Plants with *nip/nip* genotype will have *nip* phenotype, and plants with genotype *NIP/NIP* and *NIP/nip* will have wild-type phenotype (Griffiths et al., 1999).

Figure 4 Cross between F1 progeny to obtain F2 generation

♀/♂	<i>NIP</i>	<i>nip</i>
<i>NIP</i>	<i>NIP/NIP</i>	<i>NIP/nip</i>
<i>nip</i>	<i>NIP/nip</i>	<i>nip/nip</i>

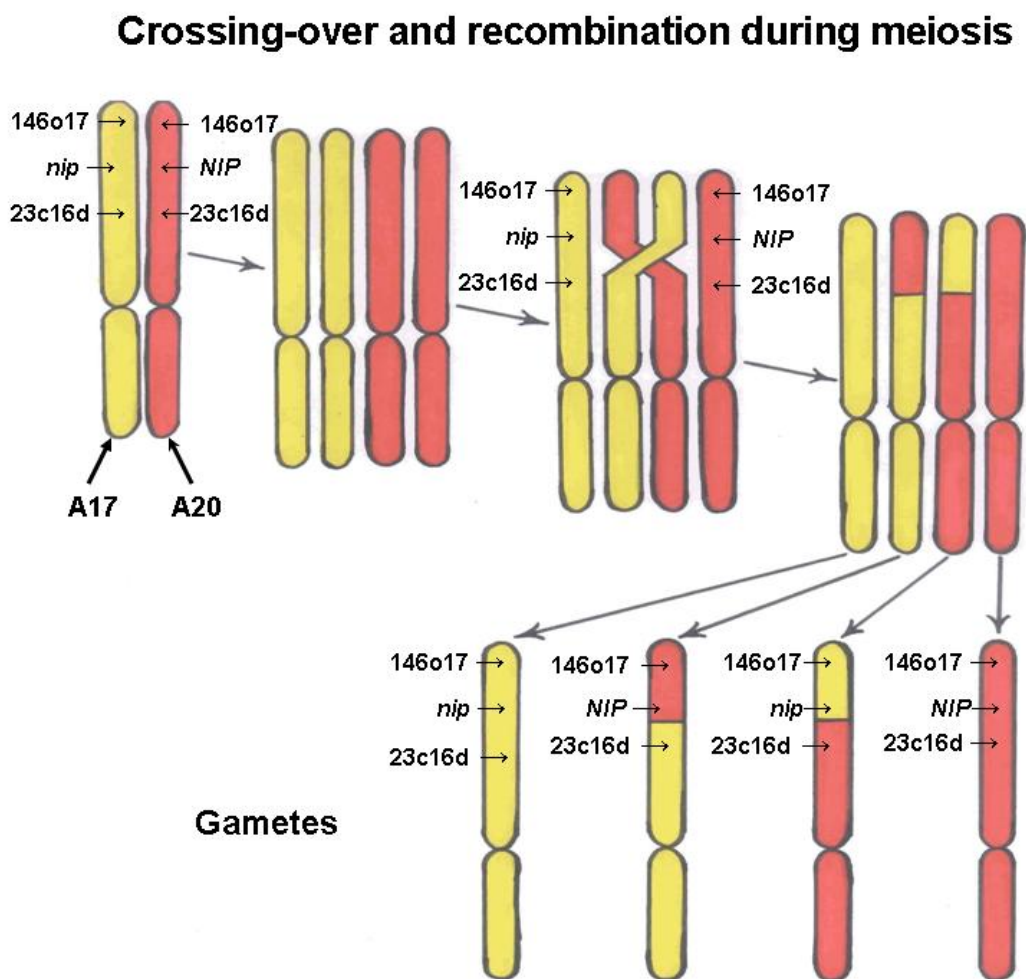
The progeny from these plants made the F2 *NIP* mapping population. Initially, the F2 progeny are evaluated by nodulation phenotype. The leaf material was collected for genomic DNA extraction, and when plants became mature their seeds were collected. The genomic DNA is extracted from plants that make up the F2 *NIP* mapping population. Then extracted DNA is used for the genotyping of the plants. Through the genotyping studies, plants of interest were identified for future propagation. Plants of interest showed a recombination event in the genetic interval that contains *NIP* or *nip*.

The A17 and A20 DNA are polymorphic; therefore, A17 DNA can be distinguished from A20 DNA due to the DNA difference of the different loci.

Having A17, A20 homozygote DNA and A17/A20 heterozygote DNA allowed us to utilize genetic studies to construct a genetic map. Genetic map relies on linkage analysis. Genes that are located closer to each other tend to segregate together. Genes that are further apart are at higher risk to be subjected to the crossing over event during

meiosis (Griffiths et al., 1999). Recombination also occurs during propagation from F1 to F2 between the A17 and A20 genotypes. Because the grandparents of the F2 generation were originally *nip/nip* in the A17 ecotype background and *NIP/NIP* in the A20 ecotype background, A17 DNA can be expected to co-segregate with *nip* and A20 DNA with *NIP*. The A17/A20 heterozygote plants were selfed to form F3's providing additional possible recombination events. Figure 5 is the schematic representation of the crossing-over and recombination during meiosis.

Figure 5 Crossing-over and recombination during meiosis



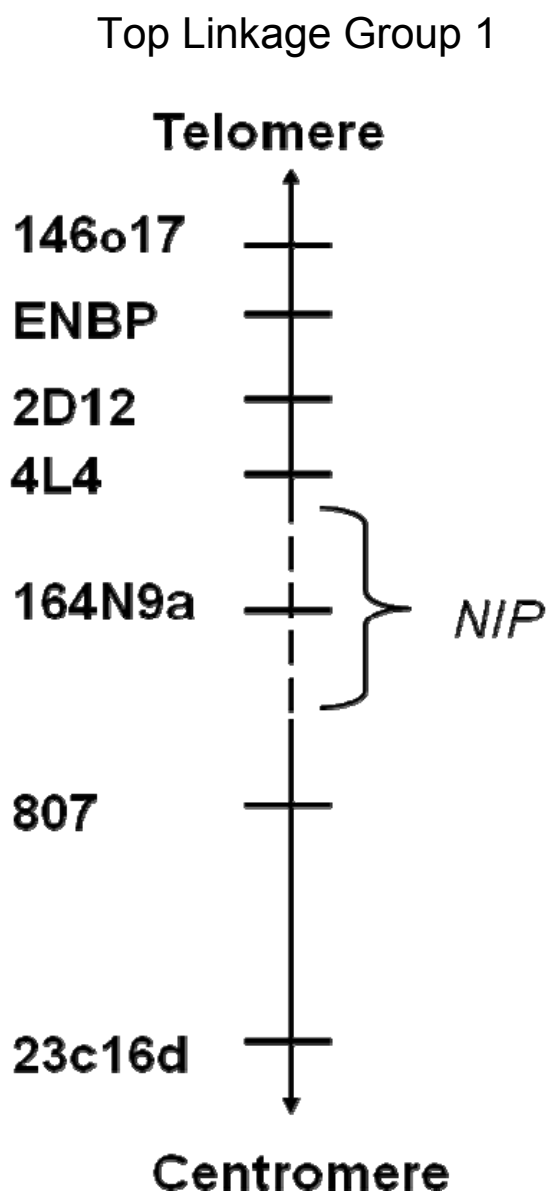
Adapted from www.accessexcellence.org

The current goal is to screen for recombinant plants by determining a genotype of each F2 plant at two loci located approximately 1.5 cM apart at the top of the chromosome 1. The loci 146o17 and 23c16d were amplified by PCR. The two loci chosen flank the *NIP* gene and are polymorphic in A17 and A20. Markers 146o17 and 23c16 can be used in a duplex PCR reaction because they have a significant difference in product sizes. Marker 146o17 is telomeric, while 23c16d is located on the centromeric side of the region where the *NIP* gene is located. Duplex PCR with these two markers gives us an opportunity to identify recombinant plants more quickly.

By analyzing the genotyping data, it is possible to isolate events of informative recombination within the mutant population. Each locus can be identified as either an A17 homozygote, an A20 homozygote or, a heterozygote. Recombinant plants are isolated, and their DNA material is further tested with other genetic markers.

At present, we have seven genetic markers (146o17, ENBP, 002D12, 4L4, 164n9, 807, and 23c16d) across the narrow genetic interval containing *NIP*. The position of the markers is presented in the Figure 6. These markers were developed from available BAC sequences and show polymorphisms in the different A17 and A20 ecotypes. When working with the genetic markers, studies will pinpoint the location of crossing over and the location of the *NIP*. Future genetic markers are being developed as the physical interval containing *NIP* is delimited.

Figure 6 Schematic representation of the top part of Linkage Group 1



Objective and Means

Objective

My contribution to the research conducted in Dr. Dickstein laboratory was to identify genetically important plants, and to genotype them with currently available genetic markers. The primary objective of this work was identification of recombinant plants in the *NIP* mapping population. These are then genotyped at multiple loci with various genetic markers. Information gathered from recombinant plant analysis will allow us to localize *NIP* with respect to the known polymorphic markers on the *M. truncatula* genetic map.

Means

During transfer of plants from hydroponic chamber into soil an individual number was assigned to each plant. A total of 1766 F2 plants compose the primary *NIP* mapping population. Second generation plants 1-953 were genotyped by Heath Wessler. I genotyped all plants with assigned individual numbers 954 to 1766, using leaf material for DNA extraction and further genetic studies.

Each plant was evaluated for the nodulation phenotype, which allowed observation whether genetic markers segregate together with *NIP* gene. Leaf material was collected from each plant for DNA extraction. Genomic DNA was extracted using the CTAB method (<http://iprotocol.mit.edu/protocol/120.htm/>), from F2 generation plants.

The next step was to determine each plant's genotype. Knowing the genotype at several marker loci was a main criterion for the identification of recombinant plants. Plants from F2 mapping population were genotyped with two flanking markers 146o17, and 23c16d, and with the ENBP marker. Therefore, recombinant plants were identified.

To make sure that no mistakes occurred, and that signal received from the PCR reaction was not false, the DNA from leaves of the plants that tested once for recombination were re-extracted. Re-extracted DNA was tested again with the markers to confirm that particular plant is truly recombinant. Plants that tested a second time for recombination were selected for “recombinants pool”. This means that DNA material was placed and kept in a special box for F2 generation recombinant plants only, DNA was placed on DNA microtiter plate for recombinant DNA only (20x dilution) – ready to be used in PCR reaction with any genetic markers of interest. Also, tubes with leaf material were isolated, and placed into the box containing leaf material that originates from recombinant plants. This box is retained in case more DNA is needed for tests in the future.

Another part of the objective was to assist with keeping track of several F3 generation plants, which have been generated from heterozygous plants in the main mapping population with the purpose to identify more recombinant plants. DNA was extracted from F3 plants generation, and transferred to 96 well microtiter DNA plates. Plants from F3 generation were also evaluated for their nodulation phenotypes. The F3 generation of plants was genotyped, and screened only with two flanking markers 146o17, and 23c16d, for the purpose of quick identification of recombinant plants. Recombinant plants were identified, tested a second time for verification of the recombination event, and then placed into the F3 “recombinant pool”.

Microtiter DNA plates with F3 and F2 recombinant DNA were tested with available genetic markers: 146o17, ENBP, 2d12, 4L4, 164n9, 807 and 23c16d. Analyzing all the data from genotyping with genetic markers helped to determine in what

place recombination took place; it also helped to evaluate position of the *NIP* gene that is surrounded by A17 DNA with respect to recombination. This analysis helped to delimit the region where it is believed *NIP* gene is located.

CHAPTER 2

IDENTIFICATION OF RECOMBINANT PLANTS

Introduction

The *nip* (numerous infections and polyphenolics) mutant (Veereshlingam et al., 2004), was identified from the EMS generated *Medicago truncatula* mutants (Penmetsa and Cook, 2000). The goal of the work described here was to genotype the *NIP* mapping population F2 generation, and to identify recombinant plants. To accomplish the goal plants were phenotyped with respect to nodulation. DNA was extracted and regions of interest were amplified by PCR. PCR products were analyzed on 8% polyacrylamide gels, and DNA was stained with SYBR Green stain.

NIP Mapping Population F2 Generation and Screening for Recombinant Plants

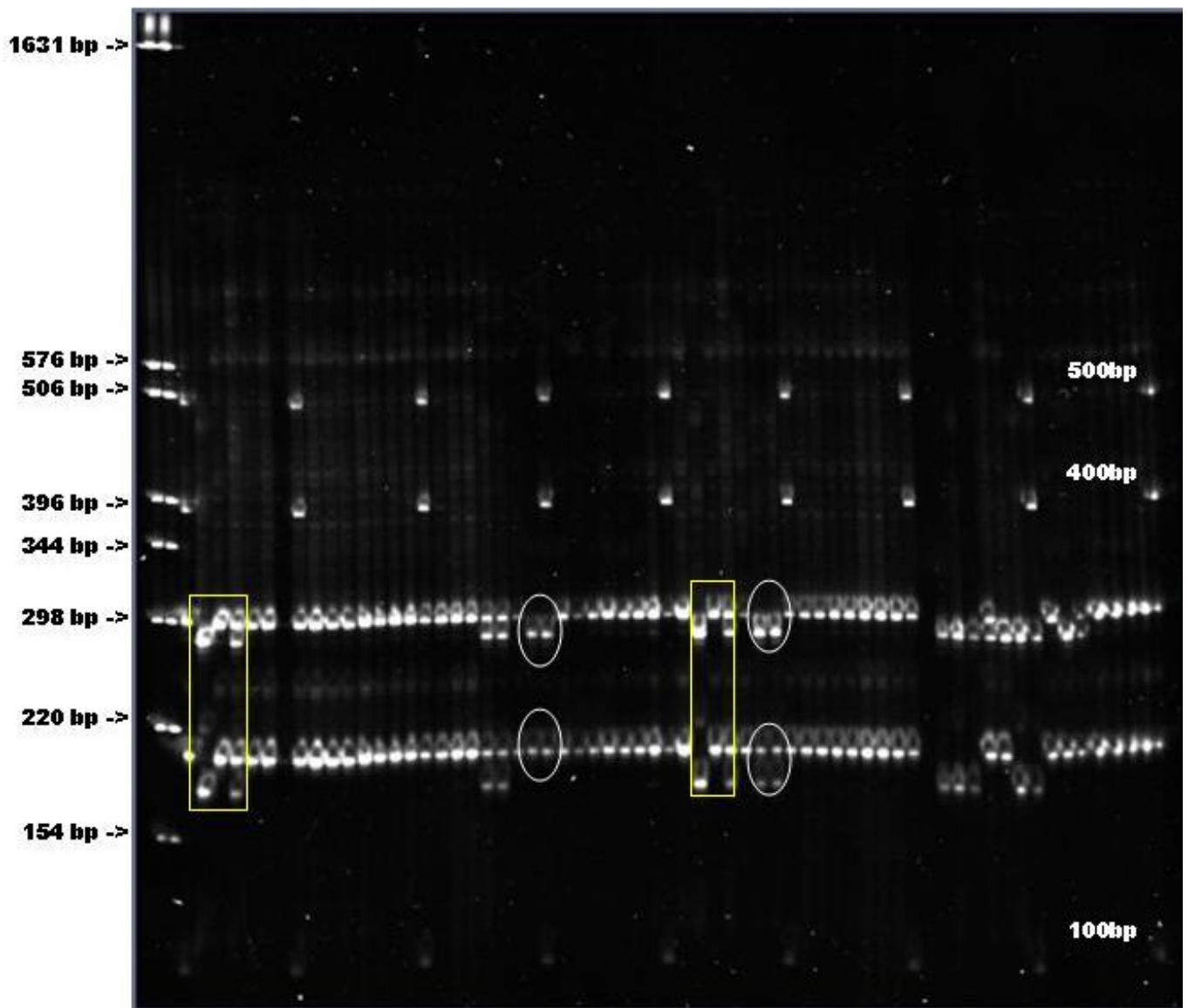
nip mutant plants were created in the A17 ecotype of *Medicago truncatula*. Mutant plants were crossed into different ecotype of *Medicago truncatula*, the A20 ecotype, that has wild-type alleles of the *NIP* gene. The progeny obtained from these plants made the F2 *nip* mapping population. The *NIP* mapping population F2 generation includes a total of 1766 plants. All plants composing the *NIP* mapping population were assigned individual identification numbers starting from 1 and ending at 1766. Plants from 1 to 953 were genotyped by Heath Wessler. I genotyped plants from 954 to 1766, a total of 812 plants. Of 812 plants, 126 plants were initially too small and later died, therefore we could not collect leaf material for the DNA extraction and genotyping.

Total of 686 plants from the *NIP* mapping population F2 generation have been genotyped at two flanking markers 23c16d and 146o17. Figure7 a typical 8% polyacrylamide gel stained with SYBR green with the duplex PCR reaction for the

genetic markers 23c16d and 146o17. A significant difference in the PCR product sizes, and similar PCR conditions for the amplification of these two genetic markers allowed duplex PCR reactions. Duplex PCR reactions provided faster genotyping at two the 23c16d and 146o17 loci that flank the region of the *NIP* location, and allowed for easy scoring of the recombinant plants on the same gel.

Figure 7 Genotyping with 23c16d and 146o17 genetic markers

The amplicon derived from the genetic marker 23c16d forms top row located in the 298 bp region, and 146o17 amplicon forms the bottom row in the region slightly below 220 bp. The control DNAs for A17, A20 and H (heterozygote) are highlighted in the boxes. The A17 DNA yields a single lower band, the A20 DNA yields a higher band with respect to A17 band, and the H DNA gives two bands. Recombinant DNA samples are highlighted in the circles.

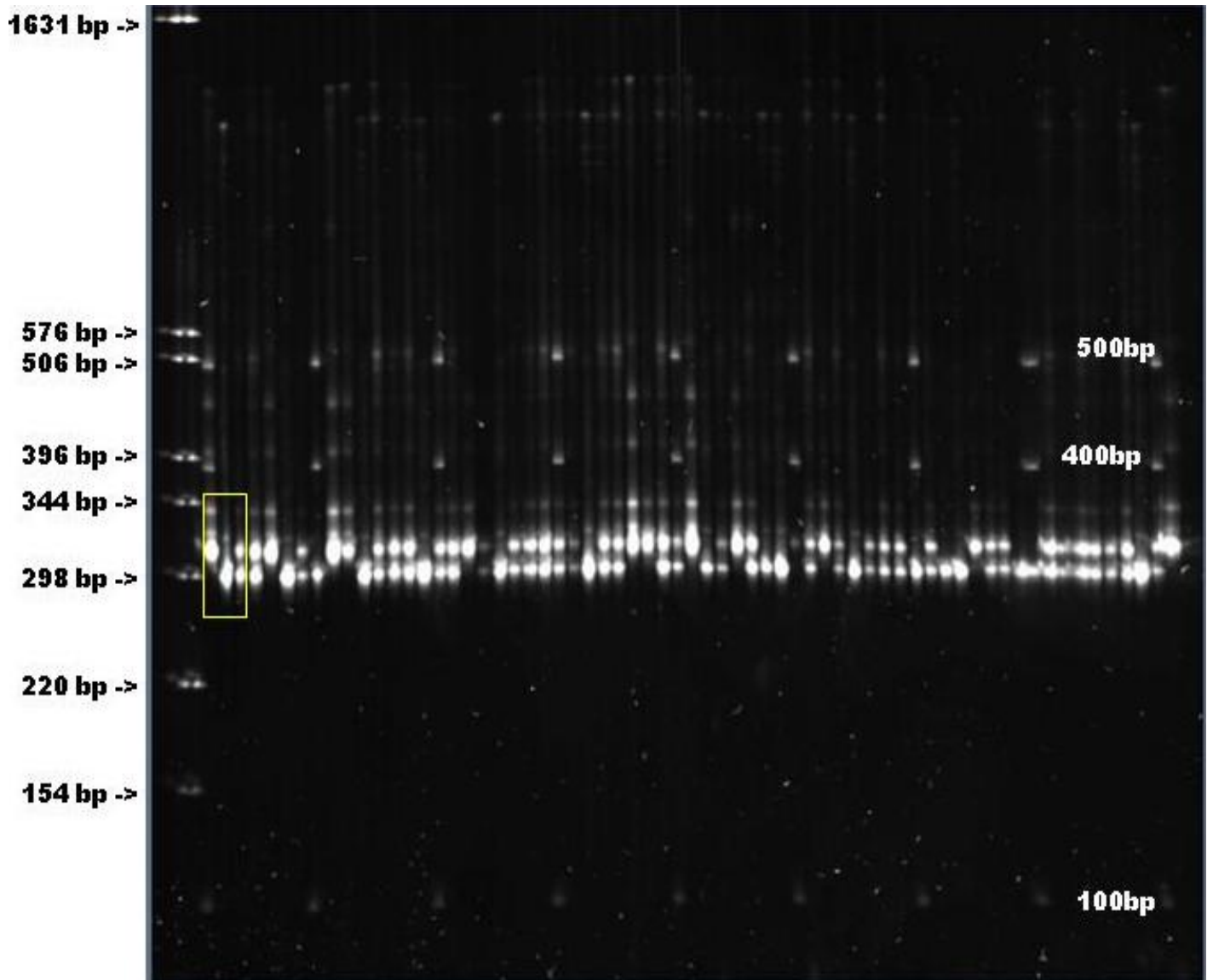


Genotyping with ENBP Genetic Marker

The F2 *NIP* mapping population was genotyped with the 23c16d and 146o17 genetic markers, but also plants from F2 generation were genotyped with the ENBP marker that is located near 146o17 genetic marker. ENBP is one of the first genetic markers that we had and it is located in the region between two flanking markers. Genotyping with ENBP allowed us to isolate plants with recombination in the area between ENBP and 23c16d markers. Plants that had recombination in the area between 146o17 and ENBP markers were not of interest for further testing. *NIP* is between ENBP and 23c16d. Most of the identified recombinant plants showed that in plants with wild-type nodulation phenotype heterozygous DNA was segregating with 23c16d marker and in some cases with ENBP marker too. Plants that had *nip* mutant nodulation phenotype showed that A17 DNA was segregating with 23c16d marker. From segregation data, we concluded that the *NIP* gene is located in the area between the ENBP and 23c16d markers. Figure 8 presents a picture of the 8% polyacrylamide gel with the PCR products for the ENBP genetic marker.

Figure 8 Genotyping with ENBP genetic marker

The genetic marker ENBP yields amplicons of approximately 300 bp sizes. The control DNA A17, A20 and H are highlighted in the box. The A17 DNA forms a higher band with respect to the A20 DNA that forms a lower band, and the H DNA forms two bands.



Data for phenotyping and genotyping with 23c16d, 146o17 and ENBP genetic markers of the plants from the *NIP* mapping population from F2 generation are presented in Table 1 in the appendix. From genotyping data from 686 plants from F2 generation it was possible to identify 67 recombinant plants, generated from 17 parental lines.

NIP Mapping Population F3 Generation and Screening for Recombinant Plants

Genotyping of the plants from *NIP* mapping population F2 generation did not yield a lot of recombinant plants. Identified recombinant plants had either A20 DNA at one locus and H DNA at another locus, or A17 DNA for one locus and H DNA for second locus. In order to determine the location of the A17 DNA it was necessary to further propagate progeny of the recombinant plants to obtain segregation data. Also, to obtain more recombinant plants the heterozygous plants were propagated because of the higher probability of recombination event to occur. Therefore, heterozygous plants and recombinant plants were propagated to create *NIP* mapping population from F3 generation. Each plant in the *NIP* mapping population F3 generation was assigned an individual identification number, starting at 3000 to avoid confusion with F2 generation plants. I have genotyped plants in the F3 generation starting from individual plant number 3000 and ending at individual plant number 4836. This makes total number of F3 generation plants 1836, and out of this total number 245 plants died before any leaf material could be collected for DNA extraction and genotyping. Therefore, the number of plants that was actually genotyped is 1591. Plants from F3 generation have been genotyped with two flanking markers 23c16d and 146o17 for fast identification of recombinant plants. From 1591 plants, 103 recombinant plants were identified, and

these plants originated from 36 different parental lines. Results on genotyping and phenotyping plants from the F3 generation are presented in the Table 2 in the appendix.

CHAPTER 3

ISOLATION OF RECOMBINANT PLANTS AND TESTING THEIR DNA WITH DIFFERENT GENETIC MARKERS

Introduction

As described in the previous chapter, plants from F2 and F3 generations from *NIP* mapping population were genotyped with two flanking markers 23c16d and 146o17. The main goal of the genotyping was to identify recombinant plants. From the second generation of plants 67, recombinant plants were identified, and they originate from 17 parental lines. Currently, from the F3 generation of plants, 103 recombinant plants were identified and these plants originate from 36 different parental lines. More work is being done by other members of the Dr. Dickstein lab to obtain more recombinant plants, test them with various genetic markers, and to develop new genetic markers to the region of interest.

All identified recombinant plants from F2 and F3 generations were isolated, and their DNA was genotyped at multiple loci with available genetic markers ENBP, 2D12, 164n9, 4L4 and 807. Main purpose of this work was to determine the region where recombination took place and what markers co-segregate with A17 DNA or A20 DNA relative to location of the *NIP* gene.

Figure 9 Genotyping with 2D12 genetic marker

The genetic marker 2D12 forms bands in the range between 300 bp and 225 bp sizes. The control DNA A17, A20 and H are highlighted in the box. The A17 DNA forms two bands that are positioned lower with the respect to two bands formed by A 20 DNA. A20 DNA forms to bands that are positioned higher with respect bands formed by A17 DNA. Heterozygote (H) DNA forms four bands.

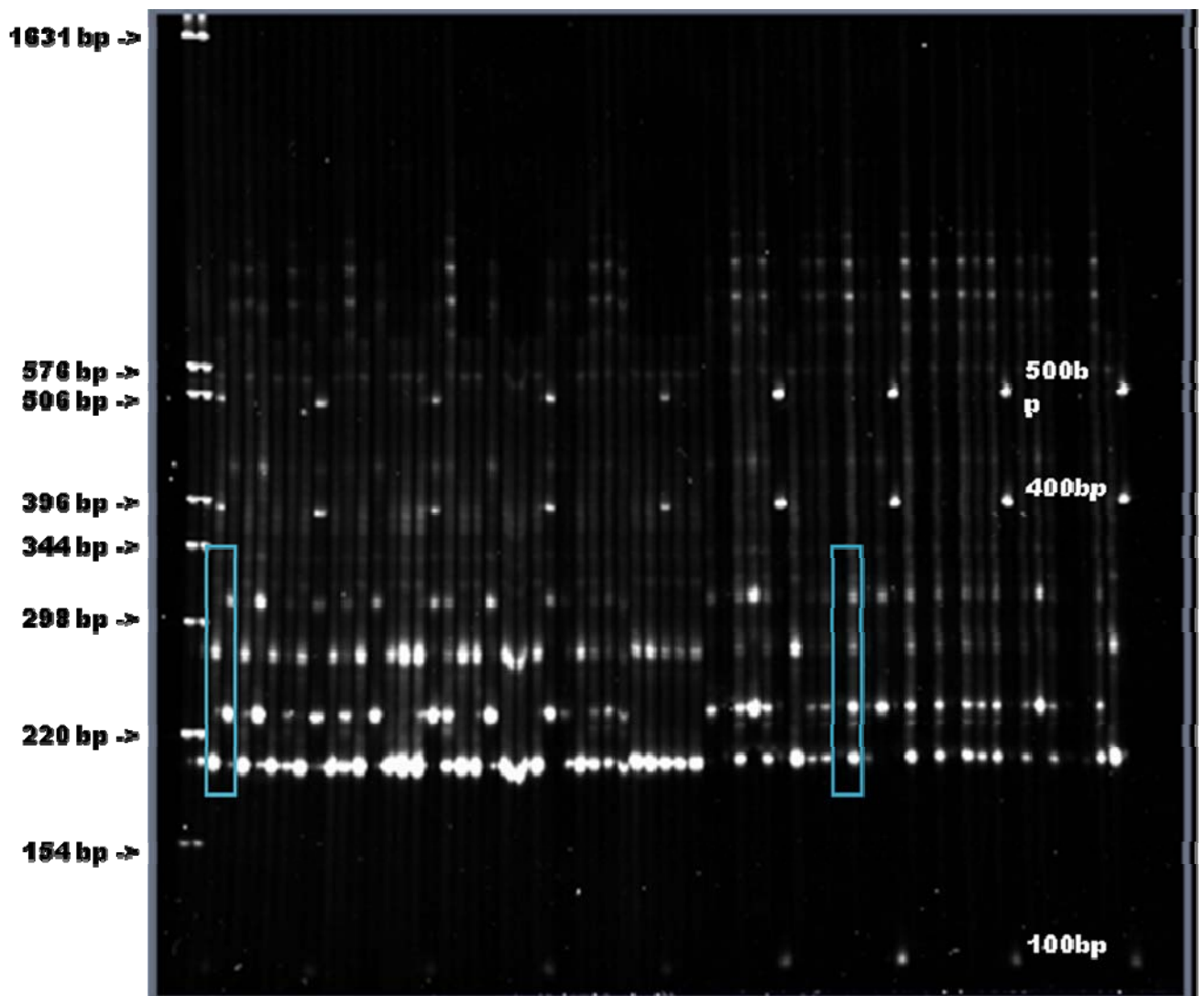


Figure 10 Genotyping with 164n9 genetic marker

The genetic marker 164n9 forms bands of 220 bp sizes. The control DNA A17, A20 and H are highlighted in the boxes. The A17 DNA forms a higher band with respect to the A20 DNA that forms a lower band, and the H DNA forms two bands.

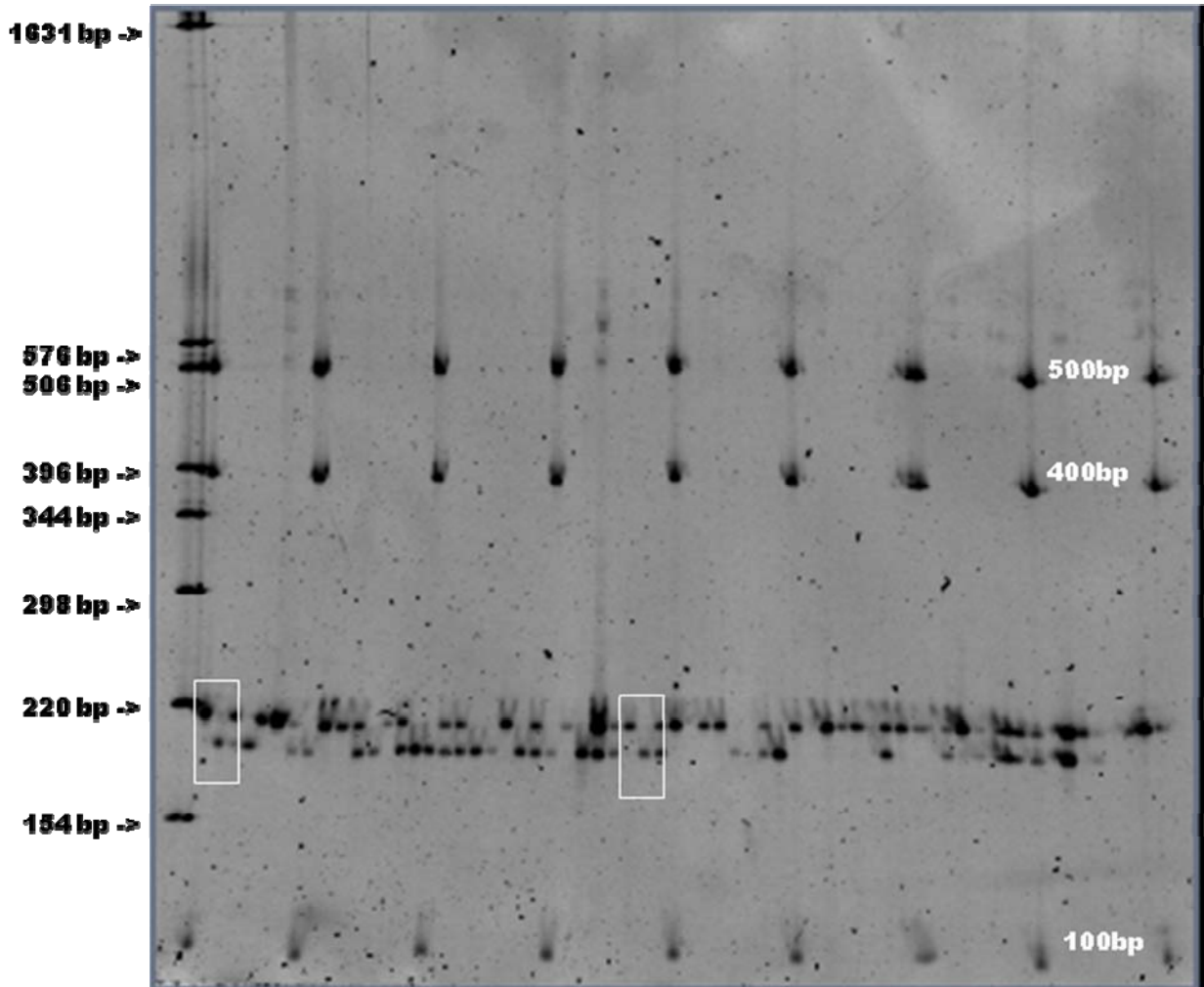


Figure 11 Genotyping with 4L4 genetic marker

The genetic marker 4L4 forms bands of 640bp and 720bp sizes. The control DNA A17, A20 and H are highlighted in the boxes. The A17 DNA yields a lower band with respect to the A20 DNA that yields a higher band, and the H DNA yields two bands.

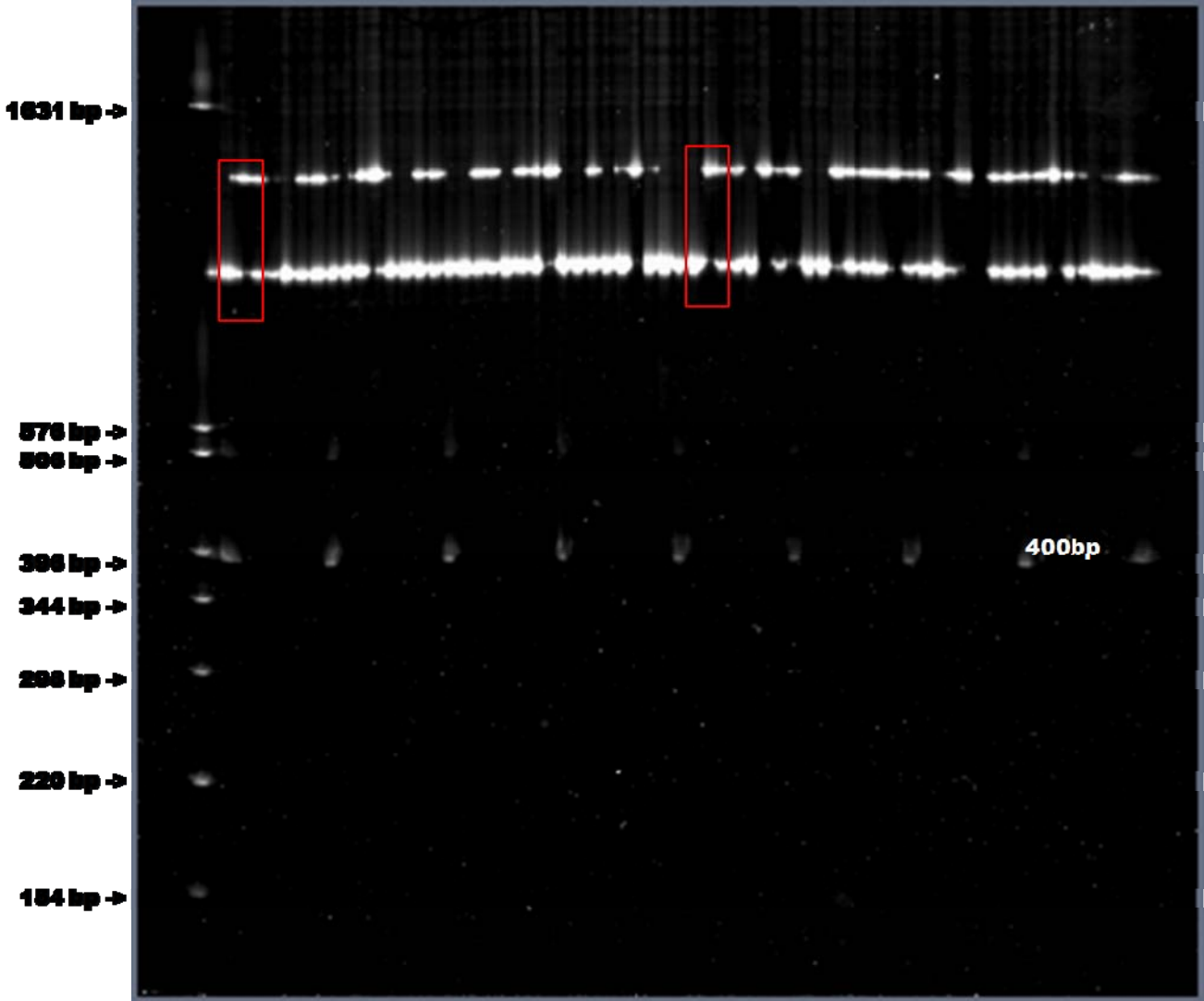
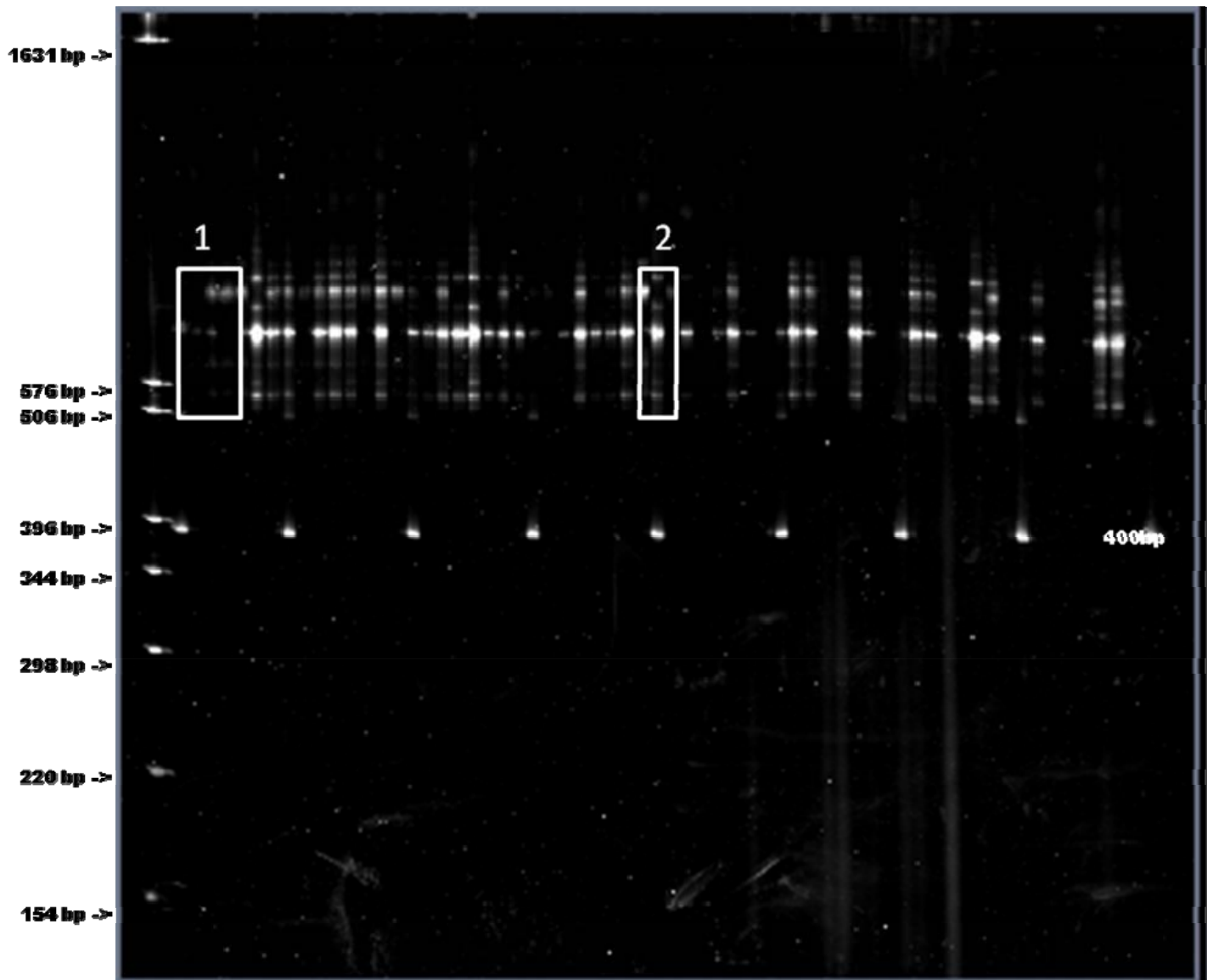


Figure 12 Genotyping with 807 genetic marker

The genetic marker 807 forms bands of 640bp and 720bp sizes. The control DNA A17, A20 and H are highlighted in the box 1, and A17, A20DNA only are highlighted in the box 2. The A17 DNA forms a higher band with respect to the A20 DNA that forms a lower band, and the H DNA forms two bands.



Results for genotyping with various available genetic markers of identified recombinant plants from F2 and F3 generations are presented in Table 3 in the appendix.

Key for the Table 3 is the same as for the Table 2

Note that not all plants presented in the table 3 were tested with all 7 genetic markers. From the available data in Table 3 that presents all identified recombinant plants it was decided to choose only 2-3 recombinant plants from each line to represent each recombination event and have recombination in the region of interest. These plants will be a subject for further testing with newly developed markers. Currently work is being done by other members of Dr. Dickstein's lab to obtain new markers in the region of interest. Table 4 presents a data that includes only few plants that were chosen to be representatives of a particular plant parental line.

Key for the Table 4 is the same as for the Table 2.

CHAPTER 4

DISCUSSION

Earlier genetic mapping has placed *nip* on linkage group 1 of *M. truncatula* and fine mapping of the *nip* locus is the central focus of this work. Genomics project of *M. truncatula* that is currently in progress has generated genetic map between A17 and A20 cultivars (Choi et al., 2004). Previous studies showed that *nip* did not complement *latd*, and it is believed that *nip* is allelic to *latd*. Genetic markers NCAS, DK140 and R15J11L placed *latd* on the top of linkage group1 (Bright et al., 2005). Molecular markers located on the top of the chromosome one were used to see if *nip* was linked to them. Markers 003C01 and DK140L were used by Veereshlingham, and results showed that *nip* homozygous plants co-segregated with both markers. It placed *nip* on the upper arm of the chromosome 1.

With the purpose to map-based clone *NIP* the mapping population was established. To create a mapping population, and for purposes of genetic characterization male sterile C90 plants were crossed into the background of the different ecotype the wild-type genotype A20 (Penmetsa and Cook, 2000; Kuppusamy et al., 2004). F1 from the cross between *nip* and A20 showed a wild type phenotype for nodulation, consistent with the recessive nature of the mutant. This F2 segregating population was scored for its nodulation phenotype and collected as the mapping population. In F2 generation from 686 plants that were phenotyped 177 plants had *nip* phenotype and 509 plants had wild type nodulation phenotype, which makes up a ratio of 1:2.9 *nip*:wild-type. Frequency of phenotypes positive for nodulation and phenotypes negative for nodulation in the F2 generation was consistent with segregation as a single

recessive allele. From F2 generation 686 plants were genotyped with three markers 146017, ENBP and 23c16d. From genotyping 67 recombinant plants were identified.

Twenty two of the sixty seven recombination events were in the *nip* homozygous background, thus permitting location of the recombinants relative to *nip* and the markers based on F2 data. The remaining 45 recombinants occurred in phenotypically wild-type plants. Mapping these recombinants relative to *nip* would be accomplished by phenotyping and genotyping of F3 progeny, placing *nip* between 23c16d and 146o17 markers. From F2 generation the A17/A20 heterozygote plants were selfed to form F3 plants providing additional possible recombination events. From F3 generation of *NIP* mapping population 1591 individuals were evaluated for nodulation phenotype and genotyped with two flanking genetic markers 146o17 and 23c16d. From genotyping plant from F3 generation 103 recombinant plants were identified. 38 of the 103 recombination events were in plants with *nip* nodulation phenotype. Other 63 recombinants occurred in phenotypically wild-type plants. Progeny from these plants will be needed in order to map these recombinants relative to *nip*. The other two recombinant plant had no identified phenotype because plants were small and had no nodules and it was hard to distinguish if it was wild-type or *nip* nodulation phenotype.

Recombinant plants were isolated and their DNA was placed on the DNA microtiter plate are summarized in the Table 3. Some of these plants were tested with ENBP, 2D12, 4L4 164n9, 807 genetic markers. Based on the segregation data it was decided not to test all of the plants presented in the Table 3 with all available markers. Plants with recombination between 146o17 and ENBP (plant line #133) were not of interest to us because both markers are telomeric to *NIP*. For some lines it was decided

to choose only a couple plants that were representatives of the particular line, and test them with markers. From the genotyping results we obtained three plant lines that have recombination between 4L4 and 164n9 markers. Plants originating from lines #133#3 and line #390 had wild-type nodulation phenotype. And plants originating from the line #368 had *nip* nodulation phenotype. Other 12 lines showed recombination event between markers 164n9 and 807. Plants originating from lines #278, #368, #683 had *nip* nodulation phenotype. Plants originating from lines # 133#1, #511, #660, #531, #155, #698, #850, and #683 had wild-type nodulation phenotype. These data points that *nip* is located in the interval between 4L4 and 807 genetic markers. Several plants from these lines were chosen for further testing with available genetic markers. For plants with wild-type phenotype we need to obtain progeny to know if they are homozygous or heterozygous. Plants that were chosen for further testing are listed in Table 4.

In summary, this work has resulted in genotyping 2277 plants, and the identification of 170 plants in the *NIP* mapping population with recombination events between 146o17 and 23c16d genetic markers. These are listed in Table 3. The recombinants have helped us narrow the genetic interval that contains the *NIP* gene to that between markers 4L4 and 807. Further efforts towards for fine mapping of the *NIP* gene are being pursued by other members of the lab.

CHAPTER 5

MATERIAL AND METHODS

DNA extraction protocol from plant tissues:

DNA extraction protocol was adapted from Aldrich and Cullis, 1993. The initial preparation step for DNA extraction was to warm up extraction buffer in 65°C water bath. Extraction buffer is composed of 2X CTAB and 0.2% β -mercaptoethanol (BME).

100ml stock 2XCTAB:

of 2%(v/v) CTAB:2G

100mM Tris: 10ml of 1M Tris, pH8.0

20mM EDTA: 4ml of 0.5M EDTA, pH 8.0

1.4M NaCl: 8.2g

2% PVP: 2g

In order to determine the necessary volume of 2XCTAB, we multiplied number of samples by 0.7. Obtained number indicated what volume of 2X CTAB (ml) to use. Then the BME was added in proportion of 20 μ l per 10ml of CTAB solution.

One large leaf or small trifoliolate was grinded in 1.5ml Eppendorf tube in the presence of liquid nitrogen. Frozen leaf was grinded to a powder with a pestle. Then, 700 μ l of the warm extraction buffer was added to the tube with leaf powder, and content was grinded more until the uniform green solution was made. Tube was placed in to the 65°C water bath for incubation for minimum 30min, but no longer than 2 h.

After incubation, 570 μ l of the solution of Chloroform:Isoamylalcol (24:1 v/v) was added.

Then, samples were shake fast for 1min. For extraction of genomic DNA the use of the

vortex is not recommended, because it can break large DNA. Next, samples were centrifuged for 5min at 13000rpm. After centrifugation three layers formed. The top clear layer, which contains DNA, was transferred to the clean Eppendorf tube. DNA was precipitated with 2/3 volume of 100% isopropanol for at least 5min. Then, samples were centrifuged for 10min at 13000rpm. Supernatant was removed, and the pellet was washed twice with 400µl of 70% EtOH. After each wash samples were centrifuged for 3min at 13000rpm. Finally, 70% EtOH was removed from the tube, and the pellet was left to air dry until it was clear. DNA was re-suspended in 20µl of the TE buffer pH8 (10mM TrisHCl, pH 8.0 and 1mMEDTA, pH 8.0). DNA was stored in -80°C.

DNA Dilution

20X diluted DNA were used for PCR reactions. DNA dilution was done in the 96 well microtiter DNA plates (GeneMate). Sterile double distilled water was added to each well in the amount of 76µl, and then 4µl of DNA was added into each well. Microtiter DNA plates were sealed with adhesive sealing film for PCR (GeneMate, Kaysville,UT), and strip of parafilm around the edges of the DNA microtiter plates, and they were kept at -20°C.

Polymerase Chain Reaction

PCR markers that had polymorphisms for A17 and A20 DNA were chosen for genotyping. Each PCR reaction was a 22µl reaction per well. Each PCR reaction included 2µl of 10X Thermopol buffer (1X ThermoPol Reaction Buffer: 10mM KCl, 10 mM (NH₄)₂SO₄, 20mM Tris-HCl, 2mM MgSO₄, 0.1% Triton X-100, pH 8.8 @ 25°C) (NE Biolabs), 2 µl of 2.5mM dNTP, 0.8µl of 5mM each forward and reverse primer (for some primers amounts had to be adjusted), 0.15µl of Taq DNA polymerase (NE Biolabs),

sterile distilled water to reach volume of 20µl, and then 2µl of 1:20 diluted DNA was added last. PCR conditions were as follows: 94°C for 4min or 94°C for 7min if amplified pieces were more than 500bp, cycling was accomplished at 94°C for 30sec, 52-57°C (depending on primer sets) for 25sec, elongation at 72°C for 30-50sec. (depending on the size of the product), this was run for 30-35 cycles, and then kept at 4°C. PCR products were run on the polyacrylamide gels.

Primers and Conditions Used for PCR Reaction

Primers were designed based on the sequence information available at NCBI (<http://www.ncbi.nlm.nih.gov>).

h2_23c16d-F (Tm55.9C)

5'-TTTCCCAATAGATCCACATGC-3'

h2_23c16d-R (Tm 57.3C)

5'-CACTCATGGTCTCAAGCCAA-3'

146o17-01F (Tm 58.4C)

5'-GTCCGTGGATTGATTAACAGTC-3'

146o17-01R (Tm 56.5C)

5'-TTGGAATGTGTTCTGCATCAAG-3'

Duplex PCR reaction master mix for 1 reaction: 2.25ul 10X ThermoPol buffer, 1.8ul 2.5mM dNTPs, 0.9ul of 146o17 primer mix(F+R) 5mM, 0.7ul of 23c16d primer mix (F+R) 5mM, 0.15 Taq, 14.3ul dd H₂O

Duplex PCR protocol (30 cycles): 94C-4min, 94C-30sec,-54.5C-30sec, 72C-30sec, 72C-7min, 4C-hold

ENBP1F (Tm 64.4C)

5'-CACTTCCCCTGTCCTAGTCCTAC-3'

ENBP1R (Tm 62.7C)

5'-GACTCGTCATCACCAAGTTTCATCC-3'

Master mix for 1reaction: 2.2ul 10X ThermoPol buffer, 1.8ul 2.5mM dNTPs, primer mix

ENBP (F+R) 5mM 3ul, Taq 0.15ul, 12.9ul ddH₂O

PCR protocol: 94C-3min, 94C-30sec, 52-30sec, 72-40sec, 34cycles, 72-5min, 4hold

2D12-F

5'-GGCGTGGACAATATTTGAGTG-3'

2D12-R

5'-CGTACGTACCCTTGTCTCC-3'

Master mix for 1reaction: 2.25ul 10X ThermoPol buffer, 1.8ul 2.5mM dNTPs, 0.9ul of

2D12 primer mix(F+R) 5mM, 0.15 Taq, 14.9ul dd H₂O

PCR protocol (32 cycles): 94C-5min, 94C-30sec, 53.9C-30sec, 72C-30sec, 72C-10min
and 4C-hold

h2 164n9a-F (Tm59.4C)

5'-CCACTTCCCACAACCTCTGT-3'

h2 164n9a-R (Tm 57.3C)

5'-CACCTTTCTGGGTTGAGAA-3

Master mix for 1reaction: 2ul 10X ThermoPol buffer, 2ul 2.5mM dNTPs, 0.9ul of 164n9
primer mix (F+R) 5mM, 0.15 Taq, 14.9ul dd H₂O

PCR protocol: 94C-7min, 94C-30sec, 52C-25sec, 72C-40sec, 35cycles, 72C10min, 4C
hold.

4L4-S-1F (Tm55.3C)

5'-CCC GAG AAC GAA CAA AAG AA-3'

4L4-S-1R (Tm 57.3C)

5'-TAA GGT ACC GTT TGG CCT GA-3'

PCR protocol (4L4) (30cycles): 94C-7min, 94C-30sec, 51C-25sec, 72C-50sec, 72C-10min, 4C-hold

Master mix for 1PCR reaction: 2ul of 10X ThermoPol Buffer, 2ul of 2.5mM dNTPs, 1ul of primer mix (F+R) 5mM, 0.15ul Taq, 14.9ul ddH₂O

807-20F (Tm 59.7C)

5'-AAC TTG TGT GTT CCT TTC CAA CTA G-3'

807-20R (Tm 62.4C)

5'-CCG GCC CCG AGT ATG ATA ATT TC-3'

807-21R (Tm 69.5C)

5'-AGG GCT GAC CCC TGA TGT CAA GAG ACT TAA AG-3'

Master mix for 1reaction: 2ul of 10X ThermoPol Buffer, 2ul of 2.5mM dNTPs, 2ul of primer mix (F+R) 5mM, 0.15ul Taq, 13.9ul ddH₂O

PCR protocol: 94C-7min, 94C-30sec, 57C-25sec, 72C-40sec, 72-7min, 4C hold

Polymerase Chain Reaction

PCR markers that amplified polymorphic regions in A17 and A20 DNA were chosen for genotyping. Each PCR reaction was a 22ul reaction per 1 well. PCR reaction included 2ul of 10X Thermopol buffer (1X ThermoPol Reaction Buffer: 10mM KCl, 10mM (NH₄)₂SO₄, 20mM Tris-HCL, 2mM MgSO₄, 0.1% Triton X-100, pH 8.8 @ 25°C) (NE Biolabs), 2ul of 2.5mM dNTPs, 0.8ul of 5mM each forward and reverse primer (for

some primers amounts had to be adjusted), 0.15ul of Taq DNA polymerase (NE Biolabs), sterile distilled water to reach volume of 20ul, and then 2ul of 1:20 diluted DNA was added last. PCR conditions were as follows: 94°C for 4minutes or 94°C for 7min if amplified pieces were more than 500bp, cycling was accomplished at 94°C for 30 seconds, 52-57°C (depending on primer sets) for 25 sec, elongation at 72°C for 30-50 sec (depending on the size of the product), this was run for 30-35 cycles, then 72°C for 7min and kept at 4°C. PCR products were electrophoresed on the polyacrylamide gels.

Preparation of the 8% polyacrylamide gel

Two glass plates, bigger plate with dimensions 8" by 9" and smaller 8" by 8" plates, were cleaned withalconox powder detergent. They were dried with a paper towel and cleaned on both sides with 70% EtOH. Plastic spacer strips were cleaned with 70% EtOH also. Plastic spacer strips (3 long & thin, and 1 short & wide).

Kimwipe folded 3 times were used under the hood to apply 5% DichlorodimethylSilane (ALDRICH, Dichlorodimethylsilane,99%) in Heptane (Kodak) solution on the surface of the plates that would be in contact with the gel.

On the leveled bench area 4 large stoppers were placed for support of the glass plates. Large glass plate was placed facing up with the side that was covered with the 5% Dichlorodimethyl Silane in Heptane solution. Short (1.3cm by 20.5cm) plastic spacer strip was placed on the bottom edge of the plate, and two longer (1.3cm by 25cm) spacer strips were placed on the sides of the plate. Then the smaller glass plate was placed on top of the larger glass plate and the spacer strips. It is important that the area covered with 5% Dichlorodimethyl Silane in Heptane solution faces inside to where it would be in contact with the gel. Glass plates and spacers were adjusted so that all

edges were evenly aligned. Four large paperclips were used per each side of the gel chamber to fix plates together.

Gel preparation:

For 8% polyacrylamide gel, 50ml total volume uses the following ingredients:
10ml of 5% TBE buffer (pH 8.13-8.23) (Tris-Borate-EDTA 10X : 1000ml water, Tris base 108g, Boric acid 55g, 0.5 M EDTA pH 8.0 40ml)
8ml of Long Ranger Gel solution (CambrexBioscience, Rockland, ME, USA)
Distilled water to the volume of 50ml

The Aspirator Pump Model 7049-00 Cole-Parmer Instruments Company was used to filter the above solution through Filter Paper (Fisherbrand, Qualitative P5, porosity-medium, flow rate-slow, diameter 5.5cm).

After filtering, 0.06g of Ammonium persulfate electrophoresis grade (FisherScientific) was added, and then the solution was mixed and degassed. 12 μ l of SIGMA TEMED (N,N,N',N'-Tetramethylethylenediamine) 99% was added to the degassed mixture. A 60ml syringe was filled with the gel solution. It is important that air bubbles are present inside the syringe. The gel solution was poured slowly in between the glass plates. The gel solution needs to be poured in the continuous manner to avoid introducing air bubbles into the gel. Short (2.5cm by 17.5cm) plastic spacer was placed on the top part of the gel in between glass plates, and the 3 large paper clips were clipped on the top part of the gel chamber. It takes 15min for the gel solution to assume gel consistency. Yet, it is better to use the gel after 12 hours which provides for a better polymerization.

Running polyacrylamide gel:

After gel polymerization took place all paperclips were removed, and the short plastic spacer on the bottom of the gel and short wide plastic spacer on the top part of the gel were removed also. Gel was washed under the tap water, and a brush was used to remove excess polyacrylamide from the glass plates. Glass plates were dried with a paper towels.

A vertical electrophoresis unit was set up. The bottom chamber of the electrophoresis unit was filled with 250ml of 1X TBE buffer first. Glass plates were placed inside the electrophoresis unit. Spacer blocks (LifeTechnologies) and the side plastic spacers of the gel chamber need to be lined up. The spacer blocks need to be tightly adjacent to the short glass plate to prevent leaking of the buffer. Large paperclips were used to attach glass plates to the electrophoresis unit, and thus create a top chamber. 250-300ml of 1X TBE buffer was added to the top electrophoresis chamber. Syringe was utilized to remove air bubbles between two glass plates in both electrophoresis chambers. An aluminum plate 8" by 4" to dissipate heat was attached behind the glass plates with two large paper clips.

Gel was warmed up prior to loading PCR samples on the gel. Vertical electrophoresis unit was connected to the power supply (BioRad Model 3000Xi Computer Controlled Electrophoresis Power Supply) and run the empty gel was running for 12min at 250-300V.

Next, the power supply was turned off, and a rubber tube was used to remove buffer from the top electrophoresis chamber. With a paper towel the area between glass

plates was dried from the buffer. The space between two plates was filled with a Ficoll solution, and a layer of the Ficoll was placed on the top edge of the short glass plate.

20% Ficoll loading solution is prepared as follows:

20g of Ficoll 400 powder was mixed with deionized water, and brought to a final volume of 100ml. The solution was kept on a hot plate (50°C), while stirring with a magnetic stir bar, for several hours until Ficoll went into the solution. Water needs to be added on the consistent basis to maintain a total volume of 100ml. Next, 1.2ml of a 50mg/ml stock of Blue Dextran was added. Then, a 5g of BioRad AG501-X8 deionizing resin was added to the solution, and it was stirred for additional 60-90minutes

The solution was decanted off the deionizing resin and filtered through a 0.45 micron filter into a sterile vessel. The solution was stored at 4.0°C (www.Gelcompany.com).

Eight channel multichannel pipettor 0.5-10ul was used to load 2ul of PCR sample into the 64 well membrane tray (The Gel Company #TAM64). It is recommended to use platinum low retention tips (Gene Mate 10ul, cat# P-3296-1) to load PCR samples.

PCR samples need to be mixed with the loading dye mix of Orange G and blue (Xylene Cyanol) prior to loading them on the gel. Loading dye (50ml) is composed of 2.5ml of 0.5M EDTA pH8, 7.5g Ficoll, 0.25g Xylene Cyanol or OrangeG (Sambrook et al.,1989). Blue Xylene Cyanol can be used alone. Unlaminated comb membrane (The Gel Company) was used to soak up the PCR samples from each well. The membrane comb was air dried, and then it was placed in between two glass plates on the surface of the gel. 1X TBE buffer was added into the top electrophoresis chamber to the level where buffer slightly covers top edge of the short glass plate. Then, the power unit was turned on to 500V for 2-3min, or until all samples traveled from membrane into the gel. After all

samples migrated inside the gel the power supply was turned off, and the membrane was removed. 1X TBE buffer was added to fill the top electrophoresis chamber. Pasteur pipette was used to flush out the Ficoll solution from the space in between the glass plates. Finally, the power supply was set to 350-400V, and the gel was run for 1h 30min to up to 2h depending on the size of the PCR product.

DNA STAINING:

DNA staining was done by using SYBR Green dye. 500ml of 1X TBE buffer was poured into the rectangular plastic container and 30 μ l of 10000X concentrated SYBR Green dye (Invitrogen) was added. Container was wrapped in the aluminum foil, because SYBR Green dye is light sensitive, and kept at -4°C. Gel was kept in the staining solution for 30min, and then scanned using BioRad FX laser scanner. One gel staining solution was used to stain 4-5 gels.

APPENDIX

Key for Table 1

+

Plants with wild-type nodulation phenotype

nip

Plants with *nip* nodulation phenotype

?

Plants with undetermined nodulation phenotype

A17

Plants with A17 genotype at a particular locus

A20

Plants with A20 genotype at a particular locus

H

Plants with both A20 and A17 genotypes at a particular locus

redo

Plants that tested positive for recombination event once, and no leaf material was found to retest them for recombination

confirmed

Recombinant plants that tested positive for recombination second time

Note: plants that died before leaf material could be collected, and therefore before they could yield any genotyping data, are not shown in the table.

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 155#	#954	+	4	A20	A20	A20	
C90 X A20 51#	#955	<i>nip</i>	4	H	H	H	
C90 X A20 74#	#958	<i>nip</i>	4	A17	A17	A17	
C90 X A20 51#	#959	<i>nip</i>	4	A17	A17	A17	
C90 X A20 51#	#960	+	4,12,38	H	H	H	
C90 X A20 51#	#961	+	4	A20	A20	A20	
C90 X A20 51#	#962	+	4,23	H	H	H	
C90 X A20 148#	#963	+	4	A20	A20	A20	
C90 X A20 133#	#964	+	6,31	A20	H	H	redo
C90 X A20 133#	#965	+	6,31	A20	H	H	redo
C90 X A20 133#	#966	+	6	A20	A20	A20	
C90 X A20 133#	#967	+	6,31	A20	H	H	confirmed
C90 X A20 133#	#968	+	6	A20	A20	A20	
C90 X A20 133#	#969	+	6	A20	A20	A20	
C90 X A20 133#	#970	+	6,31	A20	H	H	confirmed
C90 X A20 133#	#971	+	6,31	A20	H	H	
C90 X A20 133#	#972	+	4	A20	A20	A20	
C90 X A20 133#	#973	+	4,31	A20	H	H	confirmed
C90 X A20 133#	#974	+	4,31	A20	H	H	confirmed
C90 X A20 133#	#975	+	4,31	A20	H	H	redo
C90 X A20 133#	#976	?	4,31	A20	H	H	
C90 X A20 133#	#977	<i>nip</i>	4	A17	A17	A17	
C90 X A20 133#	#978	+	4	A20	A20	A20	
C90 X A20 133#	#979	+	4	H	H	H	
C90 X A20 133#	#980	<i>nip</i>	4	A17	A17	A17	
C90 X A20 133#	#981	<i>nip</i>	4	A17	A17	A17	
C90 X A20 133#	#982	+	4	H	H	H	
C90 X A20 133#	#984	+	4	H	H	H	
C90 X A20 133#	#985	+	4	H	H	H	
C90 X A20 133# 3.	#986	+	12	A20	A20	A20	
C90 X A20 133# 3.	#987	<i>nip</i>	4	A17	A17	A17	
C90 X A20 133# 3.	#989	+	4	A20	A20	A20	
C90 X A20 133# 3.	#990	<i>nip</i>	4	A17	A17	A17	
C90 X A20 133# 3.	#991	<i>nip</i>	4	A17	A17	A17	
C90 X A20 133# 3.	#992	+	4,16	H	H	H	
C90 X A20 133# 3.	#993	+	4,16	H	H	H	
C90 X A20 133# 3.	#994	+	4,16	H	H	H	
C90 X A20 133# 3.	#996	<i>nip</i>	4	A17	A17	A17	
C90 X A20 281#5.	#997	<i>nip</i>	6	A17	A17	A17	
C90 X A20 281#5.	#998	+	6	H	H	H	
C90 X A20 281#5.	#999	<i>nip</i>	9	H	H	H	
C90 X A20 281#5.	#1000	+	9	A20	A20	A20	
C90 X A20 281#5.	#1001	+	9	H	H	H	
C90 X A20 281#5.	#1002	<i>nip</i>	9	A17	A17	A17	
C90 X A20 281#5.	#1004	<i>nip</i>	9	A17	A17	A17	
C90 X A20 281#5.	#1005	+	9	H	H	H	
C90 X A20 281#5.	#1006	+	31	H	H	H	
C90 X A20 281#2.	#1007	+	9	A20	H	A20	redo
C90 X A20 281#2.	#1008	+	4	H	H	H	
C90 X A20 281#2.	#1009	+	4	H	H	H	
C90 X A20 281#2.	#1010	+	4,16	H	H	H	
C90 X A20 281#2.	#1011	+	4	H	H	H	
C90 X A20 281#2.	#1012	+	4,16	A20	A20	A20	
C90 X A20 281#2.	#1013	+	4	H	H	H	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 281#2.	#1014	+	4,16	H	H	H	
C90 X A20 281#2.	#1016	+	4	H	H	H	
C90 X A20 281#2.	#1017	+	4	A20	A20	A20	
C90 X A20 281#2.	#1018	+	4	H	H	H	
C90 X A20 281#2.	#1019	<i>nip</i>	4	A17	A17	A17	
C90 X A20 281#2.	#1020	+	4,31	H	H	H	
C90 X A20 281#2.	#1021	+	9,31	A20	A20	A20	
C90 X A20 281#2.	#1022	+	9	H	H	H	
C90 X A20 281#2.	#1023	<i>nip</i>	9	A17	A17	A17	
C90 X A20 281#	#1024	+	9	H	H	H	
C90 X A20 281#	#1025	+	9	H	H	H	
C90 X A20 281#	#1026	+	12	H	H	H	
C90 X A20 281#	#1027	+	9	A20	A20	A20	
C90 X A20 281#	#1028	+	9	A20	A20	A20	
C90 X A20 281#	#1029	?	9	H	H	H	
C90 X A20 281#	#1030	+	9	H	H	H	
C90 X A20 281#	#1031	+	9	H	H	H	
C90 X A20 281#	#1032	+	9	H	H	H	
C90 X A20 281#	#1033	+	9	H	H	H	
C90 X A20 281#	#1034	+	9	H	H	H	
C90 X A20 281#	#1035	<i>nip</i>	9	A17	A17	A17	
C90 X A20 281#	#1036	+	9	A20	A20	A20	
C90 X A20 278#	#1038	<i>nip</i>	9,16	A17	A17	H	confirmed
C90 X A20 278#	#1039	<i>nip</i>	9,31	A17	A17	A17	
C90 X A20 278#	#1040	<i>nip</i>	9,16	A17	A17	H	confirmed
C90 X A20 278#	#1041	<i>nip</i>	9,16	A17	A17	H	confirmed
C90 X A20 278#	#1042	<i>nip</i>	4,16	A17	A17	H	confirmed
C90 X A20 278#	#1043	<i>nip</i>	4,16	A17	A17	H	confirmed
C90 X A20 278#	#1044	<i>nip</i>	12,4	A17	A17	A17	
C90 X A20 278#	#1045	<i>nip</i>	4,31	A17	A17	H	confirmed
C90 X A20 278#	#1046	<i>nip</i>	4	A17	A17	H	redo
C90 X A20 278#	#1047	<i>nip</i>	4,16,31	A17	A17	H	confirmed
C90 X A20 278#	#1048	<i>nip</i>	4,31	H	A17	H	redo
C90 X A20 278#	#1049	<i>nip</i>	5,31	A17	A17	H	redo
C90 X A20 278#	#1050	<i>nip</i>	5,31	A17	A17	H	redo
C90 X A20 278#	#1051	<i>nip</i>	5	A17	A17	H	redo
C90 X A20 278#	#1052	<i>nip</i>	5,31	A17	A17	H	confirmed
C90 X A20 133#1.	#1053	+	12,5	H	H	H	
C90 X A20 133#1.	#1054	<i>nip</i>	5	A17	A17	A17	
C90 X A20 133#1.	#1055	<i>nip</i>	5	A20	A20	A20	
C90 X A20 133#1.	#1056	?	5	H	H	H	
C90 X A20 133#1.	#1057	<i>nip</i>	5	H	H	H	
C90 X A20 133#1.	#1058	<i>nip</i>	5	H	H	H	
C90 X A20 133#1.	#1059	<i>nip</i>	5	H	H	H	
C90 X A20 133#1.	#1060	<i>nip</i>	5	H	H	H	
C90 X A20 148#4.	#1061	<i>nip</i>	5	H	H	H	
C90 X A20 148#4.	#1062	?	5	A17	A17	A17	
C90 X A20 148#4.	#1063	+	5	H	H	H	
C90 X A20 148#4.	#1065	+	5	A20	A20	A20	
C90 X A20 148#4.	#1066	+	12,5	H	H	H	
C90 X A20 148#4.	#1067	+	5	H	H	H	
C90 X A20 148#4.	#1068	+	5	A20	A20	A20	
C90 X A20 100#	#1069	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1070	<i>nip</i>	5	A17	A17	A17	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 100#	#1071	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1072	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1073	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1074	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1075	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1076	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1077	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1078	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1079	<i>nip</i>	5	A17	A17	A17	
C90 X A20 100#	#1080	<i>nip</i>	5	A17	A17	A17	
C90 X A20 133 #3	1081	+	2	A20	A20	A20	
C90 X A20 133 #3	1082	+	2	H	H	H	
C90 X A20 133 #3	1083	<i>nip</i>	12,2,31	A17	A17	A17	
C90 X A20 133 #3	1084	+	2,16	H	H	H	
C90 X A20 133 #3	1085	+	2	A20	A20	A20	
C90 X A20 133 #3	1087	+	2	H	H	H	
C90 X A20 133 #3	1088	+	2	A17	A17	A17	
C90 X A20 133 #3	1089	<i>nip</i>	2	A17	A17	A17	
C90 X A20 133 #3	1090	+	2	H	H	H	
C90 X A20 133 #3	1091	+	2,12,31	H	H	A20	confirmed
C90 X A20 133 #3	1092	+	2,31	A20	A20	A20	
C90 X A20 133 #3	1093	+	2	H	H	H	
C90 X A20 133 #3	1094	+	2	A17	A17	A17	
C90 X A20 133 #3	1095	+	2,31	H	H	H	
C90 X A20 133 #3	1096	+	2	H	H	H	
C90 X A20 133 #3	1097	<i>nip</i>	2	A17	A17	A17	
C90 X A20 133 #3	1098	+	2	H	H	H	
C90 X A20 133 #3	1100	+	2	A17	A17	A17	
C90 X A20 133 #3	1101	+	2	H	H	H	
C90 X A20 133 #3	1102	+	2	H	H	H	
C90 X A20 133 #3	1103	+	2	H	H	H	
C90 X A20 133 #3	1104	+	2	H	H	H	
C90 X A20 133 #3	1105	+	2	A20	A20	A20	
C90 X A20 133 #3	1106	+	2	H	H	H	
C90 X A20 133 #3	1107	+	2	H	H	H	
C90 X A20 133 #3	1108	+	2	H	H	H	
C90 X A20 133 #3	1109	+	31	A20	A20	A20	
C90 X A20 133 #3	1110	+	2	H	H	H	
C90 X A20 133 #3	1111	+	2	H	H	H	
C90 X A20 133 #3	1112	+	2	H	H	H	
C90 X A20 133 #3	1113	+	2	H	H	H	
C90 X A20 133 #3	1114	+	2	A20	A20	A20	
C90 X A20 133 #3	1115	+	2,16	A20	A20	A20	
C90 X A20 133 #3	1116	<i>nip</i>	2,12	A17	A17	A17	
C90 X A20 133 #3	1117	<i>nip</i>	2,12	A17	A17	A17	
C90 X A20 133 #3	1118	<i>nip</i>	2,31	A17	A17	A17	
C90 X A20 133 #3	1119	<i>nip</i>	2	A17	A17	A17	
C90 X A20 133 #3	1120	<i>nip</i>	2	A17	A17	A17	
C90 X A20 133 #3	1121	<i>nip</i>	2	A17	A17	A17	
C90 X A20 133 #3	1122	<i>nip</i>	2	A17	A17	A17	
C90 X A20 133 #3	1123	<i>nip</i>	2,12	A17	A17	A17	
C90 X A20 133 #3	1124	<i>nip</i>	2	A17	A17	A17	
C90 X A20 133 #3	1125	+	2,30	H	H	H	
C90 X A20 133 #3	1126	+	2,30	A20	A20	A20	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 133 #3	1127	+	12,30	H	H	H	
C90 X A20 133 #3	1128	+	27	A20	A20	A20	
C90 X A20 133 #3	1129	+	27	H	H	H	
C90 X A20 133 #3	1130	+	27	H	H	H	
C90 X A20 133 #3	1131	+	27	H	H	H	
C90 X A20 133 #3	1132	+	27	H	H	H	
C90 X A20 133 #3	1133	+	27,30	A20	A20	H	redo
C90 X A20 133 #3	1134	+	27	H	H	H	
C90 X A20 133 #3	1135	+	27	A20	A20	A20	
C90 X A20 133 #3	1136	+	27	A20	A20	A20	
C90 X A20 133 #3	1137	+	27	H	H	H	
C90 X A20 133 #3	1138	+	30,27	H	H	H	
C90 X A20 133 #3	1139	+	2,30	H	H	H	
C90 X A20 133 #3	1142	+	2	H	H	H	
C90 X A20 133 #3	1144	+	2	A20	A20	A20	
C90 X A20 133 #3	1145	+	2,30	H	H	H	
C90 X A20 133 #1	1147	<i>nip</i>	2,30	A17	A17	A17	
C90 X A20 133 #1	1149	<i>nip</i>	2,30	A17	A17	A17	
C90 X A20 133 #1	1150	<i>nip</i>	3	A17	A17	A17	
C90 X A20 133 #1	1151	<i>nip</i>	6,3,30	A17	A17	A17	
C90 X A20 133 #1	1152	<i>nip</i>	3	A17	A17	A17	
C90 X A20 133 #1	1153	<i>nip</i>	3	A17	A17	A17	
C90 X A20 133 #1	1154	<i>nip</i>	3	A17	A17	A17	
C90 X A20 133 #1	1155	<i>nip</i>	3	A17	A17	A17	
C90 X A20 133 #1	1156	<i>nip</i>	12,6,3	A17	A17	A17	
C90 X A20 133 #1	1157	<i>nip</i>	3	A17	A17	A17	
C90 X A20 133 #1	1158	<i>nip</i>	6,3	A17	A17	A17	
C90 X A20 133 #1	1159	<i>nip</i>	6,3	A17	A17	A17	
C90 X A20 133 #1	1161	<i>nip</i>	3	A17	A17	A17	
C90 X A20 133 #1	1163	+	6,3	H	H	H	
C90 X A20 133 #1	1164	+	3	A20	A20	A20	
C90 X A20 133 #1	1166	+	3	A20	A20	A20	
C90 X A20 133 #1	1167	+	3	A20	A20	A20	
C90 X A20 133 #1	1168	+	6,3	H	H	H	
C90 X A20 133 #1	1169	+	16,3	H	H	H	
C90 X A20 133 #1	1170	+	3	H	H	H	
C90 X A20 133 #1	1171	+	3	H	H	H	
C90 X A20 133 #1	1172	+	3,31	A20	A20	H	confirmed
C90 X A20 133 #1	1173	+	1	A20	A20	A20	
C90 X A20 133 #1	1174	+	1	A20	A20	A20	
C90 X A20 133 #1	1175	+	1	H	H	H	
C90 X A20 133 #1	1176	+	12,3,1	H	H	H	
C90 X A20 133 #1	1177	+	3,1	H	H	H	
C90 X A20 133 #1	1178	+	1	H	H	H	
C90 X A20 133 #1	1179	+	1	H	H	H	
C90 X A20 133 #1	1180	+	12,3,1	H	H	H	
C90 X A20 133 #1	1182	+	1	A20	A20	A20	
C90 X A20 133 #1	1185	+	1	A20	A20	A20	
C90 X A20 133 #1	1186	+	1	H	H	H	
C90 X A20 133 #1	1187	+	1	A20	A20	A20	
C90 X A20 133 #1	1188	+	1	H	H	H	
C90 X A20 133 #1	1189	+	1	A20	A20	A20	
C90 X A20 133 #1	1190	+	1	H	H	H	
C90 X A20 133 #1	1191	+	12,3,1	H	H	H	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 133 #1	1192	+	12,1	A20	A20	A20	
C90 X A20 133 #1	1193	+	1	A20	A20	A20	
C90 X A20 133 #1	1194	+	1	A20	A20	A20	
C90 X A20 133 #1	1195	+	20,1	A17	A17	A17	
C90 X A20 133 #1	1196	+	20,1	H	H	H	
C90 X A20 133 #1	1197	+	20,1	A20	A20	A20	
C90 X A20 133 #1	1198	+	3,1	H	H	H	
C90 X A20 133 #1	1199	+	3,1	H	H	H	
C90 X A20 133 #1	1200	+	20,1	A20	A20	A20	
C90 X A20 133 #1	1201	+	20,1	A20	A20	A20	
C90 X A20 133 #1	1203	+	3,20,1	H	H	H	
C90 X A20 133 #1	1204	+	3,1	H	H	H	
C90 X A20 133 #1	1205	+	20,1	A20	A20	A20	
C90 X A20 133 #2	1206	+	20,1	H	H	H	
C90 X A20 133 #2	1207	+	20,1	H	H	H	
C90 X A20 133 #2	1208	+	20,1	H	H	H	
C90 X A20 133 #2	1209	+	20,1	H	H	H	
C90 X A20 133 #2	1210	+	20,1	H	H	H	
C90 X A20 133 #2	1211	+	6,3	A20	A20	A20	
C90 X A20 133 #2	1212	+	3,1	A20	A20	A20	
C90 X A20 133 #2	1214	+	16,1	A20	A20	A20	
C90 X A20 133 #2	1215	+	20,1	H	H	H	
C90 X A20 133 #2	1216	+	20,1	H	H	H	
C90 X A20 133 #2	1217	+	20,1	H	H	H	
C90 X A20 133 #2	1218	+	20,1	H	H	H	
C90 X A20 133 #2	1219	+	20,1	H	H	H	
C90 X A20 133 #2	1220	+	20,1	A20	A20	A20	
C90 X A20 133 #2	1221	+	20,1	A20	A20	A20	
C90 X A20 133 #2	1222	+	20,1	H	H	H	
C90 X A20 133 #2	1223	+	20,1	H	H	H	
C90 X A20 133 #2	1224	+	20,1	A20	A20	A20	
C90 X A20 133 #2	1225	+	20,1	H	H	H	
C90 X A20 133 #2	1226	+	20,1	A20	A20	A20	
C90 X A20 133 #2	1227	+	20,1	A20	A20	A20	
C90 X A20 133 #2	1228	+	20,1	H	H	H	
C90 X A20 133 #2	1229	+	20,1	A20	A20	A20	
C90 X A20 133 #2	1230	+	20,1	A20	A20	A20	
C90 X A20 133 #2	1231	+	20,1	H	H	H	
C90 X A20 133 #2	1232	+	20,1	A20	A20	A20	
C90 X A20 133 #2	1233	+	20,1	H	H	H	
C90 X A20 133 #2	1234	+	20,1	H	H	H	
C90 X A20 133 #2	1236	+	20,1	H	H	H	
C90 X A20 133 #2	1237	<i>nip</i>	20,1	A17	A17	A17	
C90 X A20 133 #2	1238	<i>nip</i>	20,1	A17	A17	A17	
C90 X A20 133 #2	1239	<i>nip</i>	20,1	A17	A17	A17	
C90 X A20 133 #2	1240	<i>nip</i>	20,1	A17	A17	A17	
C90 X A20 133 #2	1241	<i>nip</i>	1	A17	A17	A17	
C90 X A20 133 #2	1243	<i>nip</i>	1	A17	A17	A17	
C90 X A20 133 #2	1244	<i>nip</i>	20,1,31	A17	A17	A17	
C90 X A20 133 #2	1246	<i>nip</i>	12,1	A17	A17	A17	
C90 X A20 133 #4	1251	<i>nip</i>	20,1,31	A20	A17	A17	confirmed
C90 X A20 133 #4	1252	<i>nip</i>	20,1,27	A20	A17	A17	confirmed
C90 X A20 133 #4	1254	<i>nip</i>	16,1,27	A20	A17	A17	confirmed
C90 X A20 133 #4	1255	<i>nip</i>	20,1,27	A20	A17	A17	confirmed

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 133 #4	1256	<i>nip</i>	20,1,27,38	A20	A17	A17	confirmed
C90 X A20 133 #4	1258	<i>nip</i>	20,1,27	A20	A17	A17	confirmed
C90 X A20 133 #4	1259	<i>nip</i>	12,1	A20	A17	A17	confirmed
C90 X A20 133 #4	1261	<i>nip</i>	20,1,27	A20	A17	A17	confirmed
C90 X A20 133 #4	1262	<i>nip</i>	12,1	A17	A17	A17	
C90 X A20 133 #4	1264	+	20,1,27	A20	H	H	confirmed
C90 X A20 133 #4	1265	+	16,1	A20	A20	A20	
C90 X A20 133 #4	1266	+	16,1	A20	H	H	confirmed
C90 X A20 133 #4	1267	+	1,27	A20	H	H	confirmed
C90 X A20 133 #4	1268	+	20,1,27	A20	H	H	confirmed
C90 X A20 133 #4	1270	+	12,15,1,30	A20	H	H	confirmed
C90 X A20 133 #4	1271	+	12,16,1,30	A20	H	H	confirmed
C90 X A20 133 #4	1272	+	1,30	A20	H	H	confirmed
C90 X A20 133 #4	1273	+	16,1,30	A20	H	H	confirmed
C90 X A20 133 #4	1275	+	12,1,30	A20	H	H	confirmed
C90 X A20 133 #4	1276	+	1	A20	A20	A20	
C90 X A20 133 #4	1278	+	16,1,30	A20	H	H	confirmed
C90 X A20 133 #4	1279	+	2,16,30	A20	H	H	confirmed
C90 X A20 133 #4	1280	+	2,16,30	A20	A20	H	confirmed
C90 X A20 133 #4	1281	+	2,16,30	A20	H	H	confirmed
C90 X A20 133 #4	1286	+	31	A20	H	H	
C90 X A20 133 #4	1287	+	31	A20	A20	A20	
C90 X A20 133 #4	1289	+	31	A20	A20	A20	
C90 X A20 133 #4	1292	+	12,31,27	A20	H	H	confirmed
C90 X A20 133 #4	1293	+	31	A20	H	H	
C90 X A20 133 #4	1294	+	31	A20	H	H	
C90 X A20 133 #4	1297	+	31	A20	H	H	redo
C90 X A20 133 #4	1298	+	31	A20	H	H	redo
C90 X A20 133 #4	1299	+	31	A20	A20	A20	
C90 X A20 #356	1300	+	2	H	H	H	
C90 X A20 #356	1301	+	31	H	H	H	
C90 X A20 #356	1302	<i>nip</i>	2	A17	A17	A17	
C90 X A20 #356	1303	<i>nip</i>	2	A17	A17	A17	
C90 X A20 #356	1304	<i>nip</i>	2	A17	A17	A17	
C90 X A20 #356	1305	<i>nip</i>	2	A17	A17	A17	
C90 X A20 #356	1306	<i>nip</i>	2	A17	A17	A17	
C90 X A20 #356	1307	+	31	H	H	H	
C90 X A20 #356	1308	+	2,30	H	H	H	
C90 X A20 #356	1309	+	2	H	H	H	
C90 X A20 #356	1310	+	2	H	H	H	
C90 X A20 #356	1311	+	2	H	H	H	
C90 X A20 #356	1312	+	2	H	H	H	
C90 X A20 #356	1313	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #356	1314	+	31	H	H	H	
C90 X A20 # 316	1315	+	2	H	H	H	
C90 X A20 # 316	1316	<i>nip</i>	31	A17	A17	A17	
C90 X A20 # 316	1317	+	2	H	H	H	
C90 X A20 # 316	1318	+	30	A20	A20	A20	
C90 X A20 # 316	1319	+	2	H	H	H	
C90 X A20 # 316	1320	+	2	H	H	H	
C90 X A20 # 316	1321	+	2	H	H	H	
C90 X A20 # 316	1322	+	2,30	H	H	H	
C90 X A20 # 351	1323	<i>nip</i>	2,30	A17	A17	A17	
C90 X A20 # 351	1324	<i>nip</i>	2	A17	A17	A17	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 # 351	1325	+	30	H	H	H	
C90 X A20 # 351	1326	+	30	H	H	H	
C90 X A20 # 351	1327	+	30	H	H	H	
C90 X A20 # 351	1328	+	30	H		H	
C90 X A20 #326	1329	+	30	H	H	H	
C90 X A20 #326	1330	+	30	A20	A20	A20	
C90 X A20 #326	1331	+	30	H	H	H	
C90 X A20 #326	1332	+	30	H	H	H	
C90 X A20 #326	1333	+	30	H	H	H	
C90 X A20 #326	1334	+	30	H	H	H	
C90 X A20 #326	1335	+	30	H	H	H	
C90 X A20 #326	1336	<i>nip</i>	30	A17	A17	A17	
C90 X A20 #326	1337	<i>nip</i>	30	A17	A17	A17	
C90 X A20 #326	1338	<i>nip</i>	30	A17	A17	A17	
C90 X A20 #326	1339	+	30	H	H	H	
C90 X A20 #326	1340	+	30	A20	A20	A20	
C90 X A20 #326	1342	+	31	H	H	H	
C90 X A20 #326	1343	+	31	H	H	H	
C90 X A20 #326	1344	+	31	H	H	H	
C90 X A20 #326	1345	+	31	H	H	H	
C90 X A20 #326	1346	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #326	1347	+	2	A20	A20	A20	
C90 X A20 #326	1348	<i>nip</i>	2	A17	A17	A17	
C90 X A20 #326	1349	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #326	1351	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #326	1353	+	12,2	A20	A20	A20	
C90 X A20 #326	1354	+	31	H	H	H	
C90 X A20 #326	1355	+	12,2	H	H	H	
C90 X A20 #326	1356	+	2,12	A20	A20	A20	
C90 X A20 #326	1357	+	12,2,30	H	H	H	
C90 X A20 #326	1358	+	12,2	A20	A20	A20	
C90 X A20 #326	1359	+	2	H	H	H	
C90 X A20 #325	1360	+	2	A20	A20	A20	
C90 X A20 #325	1361	+	2	A17	A17	A17	
C90 X A20 #325	1362	<i>nip</i>	2,31	A17	A17	A17	
C90 X A20 #325	1363	+	2,31	H	H	H	
C90 X A20 #325	1364	+	2,30,38	A20	A20	A20	
C90 X A20 #325	1365	+	2	A20	A20	A20	
C90 X A20 #325	1366	+	2	H	H	H	
C90 X A20 #325	1367	+	2	A20	A20	A20	
C90 X A20 #325	1368	<i>nip</i>	3	A17	A17	A17	
C90 X A20 #325	1369	+	3	A20	A20	A20	
C90 X A20 #325	1370	+	3	H	H	H	
C90 X A20 #325	1371	+	3,31	A20	A20	A20	
C90 X A20 #325	1372	+	3	H	H	H	
C90 X A20 #325	1373	+	3	A20	A20	A20	
C90 X A20 #325	1374	+	3	A20	A20	A20	
C90 X A20 #325	1375	<i>nip</i>	6,3	A17	A17	A17	
C90 X A20 #325	1376	+	3	A20	A20	A20	
C90 X A20 #325	1377	+	3	A17	A17	A17	
C90 X A20 #325	1378	+	3,31	A20	A20	A20	
C90 X A20 #325	1379	<i>nip</i>	3	A17	A17	A17	
C90 X A20 #325	1380	+	3,31	A20	A20	A20	
C90 X A20 #353	1381	+	3	H	H	H	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 #353	1382	+	6,3	H	H	H	
C90 X A20 #353	1383	+	3	H	H	H	
C90 X A20 #353	1384	+	3	A20	A20	A20	
C90 X A20 #353	1385	+	3	A20	A20	A20	
C90 X A20 #353	1386	<i>nip</i>	3	A17	A17	A17	
C90 X A20 #353	1387	+	3,31	H	H	H	
C90 X A20 #353	1388	+	6,3	H	H	H	
C90 X A20 #353	1389	+	6,3	H	H	H	
C90 X A20 #353	1391	<i>nip</i>	3	A17	A17	A17	
C90 X A20 #353	1392	+	3	H	H	H	
C90 X A20 #317	1393	+	31	H	H	H	
C90 X A20 #317	1394	+	3,31	A20	A20	A20	
C90 X A20 #317	1395	<i>nip</i>	3	A17	A17	A17	
C90 X A20 #319	1402	+	3	A20	A20	A20	
C90 X A20 #319	1403	<i>nip</i>	3	H	H	H	
C90 X A20 #319	1405	+	3	H	H	H	
C90 X A20 #319	1406	+	3,30	A20	A20	A20	
C90 X A20 #319	1407	+	3	H	H	H	
C90 X A20 #319	1408	+	3	H	H	H	
C90 X A20 #319	1409	+	3	H	H	H	
C90 X A20 #319	1410	<i>nip</i>	3	A17	A17	A17	
C90 X A20 #319	1411	<i>nip</i>	3	A17	A17	A17	
C90 X A20 #319	1412	+	3	A20	A20	A20	
C90 X A20 #319	1413	+	3	H	H	H	
C90 X A20 #319	1414	+	3	H	H	H	
C90 X A20 #319	1415	<i>nip</i>	3	A17	A17	A17	
C90 X A20 #319	1416	+	3	H	H	H	
C90 X A20 #319	1418	+	3	H	H	H	
C90 X A20 #319	1419	+	3,31	H	H	H	
C90 X A20 #319	1420	+	31	H	H	H	
C90 X A20 #319	1421	+	3	H	H	H	
C90 X A20 #319	1422	+	3	A20	A20	A20	
C90 X A20 #319	1423	+	3	H	H	H	
C90 X A20 #319	1424	+	3	H	H	H	
C90 X A20 #319	1425	+	3,31	H	H	H	
C90 X A20 #319	1426	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #319	1427	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #327	1428	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #327	1429	+	3	H	H	H	
C90 X A20 #327	1430	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #327	1431	+	3,31	H	H	H	
C90 X A20 #327	1432	+	3	H	H	H	
C90 X A20 #327	1433	+	3	A20	A20	A20	
C90 X A20 #327	1434	+	3	A20	A20	A20	
C90 X A20 #327	1435	+	3	A20	A20	A20	
C90 X A20 #327	1436	+	3,30	A20	A20	A20	
C90 X A20 #327	1437	+	30	A20	A20	A20	
C90 X A20 #327	1438	+	30,38	H		H	
C90 X A20 #327	1439	+	30	H	H	H	
C90 X A20 #327	1441	+	30	?	H	H	
C90 X A20 #327	1442	+	30	A20	A20	A20	
C90 X A20 #327	1443	+	30	H	H	H	
C90 X A20 #327	1444	+	30	A20	A20	A20	
C90 X A20 #327	1445	?	30	H	H	H	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 #327	1446	+	30,38	A20	A20	A20	
C90 X A20 #327	1447	+	30	A20	A20	A20	
C90 X A20 #327	1448	+	30	A20	A20	A20	
C90 X A20 #327	1452	+	20	H	H	H	
C90 X A20 #327	1454	<i>nip</i>	12	H	H	H	
C90 X A20 #511	1457	+	6	A20	A20	A20	
C90 X A20 #511	1458	+	6,20,27	A20	A20	H	confirmed
C90 X A20 #511	1462	+	6	H	H	H	
C90 X A20 #511	1464	+	6,20	H	H	H	
C90 X A20 #511	1465	+	6,20,27	A20	A20	H	confirmed
C90 X A20 #511	1466	+	6	H	H	H	
C90 X A20 #511	1468	+	6	A20	A20	A20	
C90 X A20 #511	1470	+	6	A20	A20	A20	
C90 X A20 #511	1471	+	6	H	H	H	
C90 X A20 #511	1472	+	6	H	H	H	
C90 X A20 #362	1478	+	6,20,30	H	H	H	
C90 X A20 #362	1479	<i>nip</i>	30	A17	A17	A17	
C90 X A20 #362	1481	+	6	A20	A20	A20	
C90 X A20 #362	1484	+	6	H	A20	A20	redo
C90 X A20 #362	1485	+	6,27	A20	A20	H	confirmed
C90 X A20 # 526	1486	+	6,12	H	H	H	
C90 X A20 # 526	1488	<i>nip</i>	12	A17	A17	A17	
C90 X A20 # 526	1489	+	6,20,31	H	H	H	
C90 X A20 # 526	1490	+	6	A20	A20	A20	
C90 X A20 # 526	1491	+	6,38	H	?	H	
C90 X A20 #530	1492	+	6,27	A20	A20	H	confirmed
C90 X A20 #530	1493	+	6	H	H	H	
C90 X A20 #530	1497	+	12	H	H	H	
C90 X A20 #530	1498	+	6	A20	A20	A20	
C90 X A20 #530	1499	<i>nip</i>	12	A17	A17	A17	
C90 X A20 #530	1502	<i>nip</i>	16	A17	A17	A17	
C90 X A20 #530	1505	+	12	H	H	H	
C90 X A20 #530	1506	+	31	H	H	H	
C90 X A20 #530	1509	+	30	H	H	H	
C90 X A20 #530	1510	+	30	H	H	H	
C90 X A20 #533	1511	+	16,30	H	H	H	
C90 X A20 #533	1513	+	31	H	H	H	
C90 X A20 #533	1514	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #533	1515	+	31	H	H	H	
C90 X A20 #533	1516	+	31	H	H	H	
C90 X A20 #533	1517	<i>nip</i>	12	A17	A17	A17	
C90 X A20 #389	1518	+	31	H	H	H	
C90 X A20 #389	1519	+	31	H	H	H	
C90 X A20 #389	1520	+	30	A20	A20	A20	
C90 X A20 #389	1521	<i>nip</i>	30	A17	A17	A17	
C90 X A20 #389	1522	<i>nip</i>	30	A17	A17	A17	
C90 X A20 #389	1523	+	30	H	H	H	
C90 X A20 #389	1524	+	30	H	H	H	
C90 X A20 #389	1525	<i>nip</i>	30	A17	A17	A17	
C90 X A20 #389	1526	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #389	1527	+	30	A20	A20	A20	
C90 X A20 #389	1528	+	30	A20	A20	A20	
C90 X A20 #389	1532	+	6	H	H	H	
C90 X A20 #389	1533	+	6	A20	A20	A20	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 #391	1534	+	6	A20	A20	A20	
C90 X A20 #391	1535	+	6	H	H	H	
C90 X A20 #391	1537	<i>nip</i>	6	A17		A17	
C90 X A20 #391	1538	+	6	A20	A20	A20	
C90 X A20 #391	1539	+	6	H	H	H	
C90 X A20 #391	1540	+	6	H	H	H	
C90 X A20 #391	1542	<i>nip</i>	6,20,30	A17	A17	A17	
C90 X A20 #391	1543	+	6,20,30	H	H	H	
C90 X A20 #391	1544	+	6	H	H	H	
C90 X A20 #391	1545	+	6	H	H	H	
C90 X A20 #391	1547	<i>nip</i>	6	A17	A17	A17	
C90 X A20 #391	1548	+	6	H	H	H	
C90 X A20 #391	1549	+	6,20	A20	A20	A20	
C90 X A20 #391	1550	+	6	A20	A20	A20	
C90 X A20 #361	1551	+	6	H	H	H	
C90 X A20 #361	1552	+	6,20	A20	A20	A20	
C90 X A20 #361	1553	+	6	H	H	H	
C90 X A20 #361	1554	+	6	H	H	H	
C90 X A20 #361	1555	+	20,30	H	H	H	
C90 X A20 #361	1556	+	20	H	H	H	
C90 X A20 #361	1557	+	30	H	H	H	
C90 X A20 #361	1558	?	20	H	H	H	
C90 X A20 #361	1559	+	23	H	H	H	
C90 X A20 #361	1560	+	20	A20	A20	A20	
C90 X A20 #361	1561	<i>nip</i>	23	A17	A17	A17	
C90 X A20 #361	1562	+	23	A20	A20	A20	
C90 X A20 #361	1563	+	23	H	H	H	
C90 X A20 #361	1564	+	20,30	H	H	H	
C90 X A20 #361	1565	+	20	H	H	H	
C90 X A20 #361	1566	+	20	H	H	H	
C90 X A20 #361	1567	+	20	A20	A20	A20	
C90 X A20 #361	1568	+	23	H	H	H	
C90 X A20 #361	1569	+	23	A20	A20	A20	
C90 X A20 #361	1570	+	23	H	H	H	
C90 X A20 #358	1572	+	23	H	H	H	
C90 X A20 #358	1573	+	23	H	H	H	
C90 X A20 #358	1574	+	20,30	A20	A20	H	redo
C90 X A20 #358	1575	+	23,30	H	H	H	
C90 X A20 #527	1576	+	20	A20	A20	A20	
C90 X A20 #527	1577	+	20	H	H	H	
C90 X A20 #527	1578	<i>nip</i>	12	A17	A17	A17	
C90 X A20 #527	1579	+	20,30	H	H	H	
C90 X A20 #527	1580	+	20	H	H	H	
C90 X A20 #527	1582	+	16	H		H	
C90 X A20 #527	1583	+	20,30	H	H	H	
C90 X A20 #527	1584	+	12	A20	A20	A20	
C90 X A20 #527	1586	+	23	H	H	H	
C90 X A20 #527	1587	+	23	A20	A20	A20	
C90 X A20 #527	1588	+	23	A20	A20	A20	
C90 X A20 #527	1589	<i>nip</i>	12	A17	A17	A17	
C90 X A20 #527	1590	+	20,30	A20	A20	A20	
C90 X A20 #527	1591	+	12,30	A20	A20	H	confirmed
C90 X A20 #527	1592	+	23	H	H	H	
C90 X A20 #527	1593	+	20	H	H	H	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 #527	1594	+	20	H	H	H	
C90 X A20 #512	1595	+	20	A20	A20	A20	
C90 X A20 #512	1596	<i>nip</i>	23	A17	A17	A17	
C90 X A20 #512	1597	+	23	H	H	H	
C90 X A20 #512	1598	+	20	H	H	H	
C90 X A20 #512	1599	+	23	H	H	H	
C90 X A20 #512	1600	<i>nip</i>	20	A17	A17	A17	
C90 X A20 #512	1601	+	20	H	H	H	
C90 X A20 #512	1602	+	20	H	H	H	
C90 X A20 #512	1603	+	20	H	H	H	
C90 X A20 #512	1604	+	20	H	H	H	
C90 X A20 #512	1605	+	20,9	A20	A20	A20	
C90 X A20 #512	1606	+	20	H	H	H	
C90 X A20 #512	1607	+	20	H	H	H	
C90 X A20 #512	1608	+	20	H	H	H	
C90 X A20 #512	1609	+	20	H	H	H	
C90 X A20 #512	1610	<i>nip</i>	23	A17	A17	A17	
C90 X A20 #512	1611	+	20	A20	A20	H	redo
C90 X A20 #512	1612	+	20	H	H	H	
C90 X A20 #512	1613	+	20	H	H	H	
C90 X A20 #512	1614	+	21	H	H	H	
C90 X A20 #512	1616	+	21,30	A20	A20	A20	
C90 X A20 #512	1617	+	23	A20	A20	A20	
C90 X A20 #512	1618	<i>nip</i>	23	A17	A17	A17	
C90 X A20 #512	1619	+	21	A20	A20	A20	
C90 X A20 #512	1620	+	23	H	H	H	
C90 X A20 #512	1621	+	21	H	H	H	
C90 X A20 #509	1622	+	21	H	H	H	
C90 X A20 #509	1624	<i>nip</i>	23	A17	A17	A17	
C90 X A20 #509	1625	+	21,38	A20	A20	A20	
C90 X A20 #509	1626	+	21	H	H	H	
C90 X A20 #509	1627	+	21	H	H	H	
C90 X A20 #509	1628	+	21	A20	A20	A20	
C90 X A20 #509	1629	+	21	H	H	H	
C90 X A20 #509	1630	+	21	H	H	H	
C90 X A20 #509	1632	<i>nip</i>	23	A17	A17	A17	
C90 X A20 #568	1634	+	6	H	H	H	
C90 X A20 #568	1635	+	21,30,27	H	H	H	
C90 X A20 #568	1641	+	21	A20	A20	A20	
C90 X A20 #568	1642	+	21	H	H	H	
C90 X A20 #540	1644	+	21	H	H	H	
C90 X A20 #540	1650	+	21,31,27	H	H	H	
C90 X A20 #540	1651	+	21,31,27	H	H	H	
C90 X A20 #540	1652	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #540	1653	+	21	H	H	H	
C90 X A20 #540	1654	+	21	H	H	H	
C90 X A20 #540	1655	+	23	A20	A20	A20	
C90 X A20 #540	1656	<i>nip</i>	31	A17	A17	A17	
C90 X A20 #540	1657	+	21	H	?	H	
C90 X A20 #539	1658	+	21,31	A20	A20	A20	
C90 X A20 #539	1659	+	21	A20	A20	A20	
C90 X A20 #539	1660	+	21	A20	A20	A20	
C90 X A20 #539	1661	+	21	A20	A20	A20	
C90 X A20 #539	1662	+	6	A20	A20	A20	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 #539	1663	+	21	A20	A20	A20	
C90 X A20 #539	1664	+	21	A20	A20	A20	
C90 X A20 #539	1666	+	21,31	A20	A20	A20	
C90 X A20 #539	1667	+	21	A20	A20	A20	
C90 X A20 #539	1668	+	21	A20	A20	A20	
C90 X A20 #539	1669	+	6	A20	A20	A20	
C90 X A20 #539	1670	+	21	A20	A20	A20	
C90 X A20 #539	1671	+	6	A20	A20	A20	
C90 X A20 #590	1675	+	6	A20	A20	A20	
C90 X A20 #590	1676	+	6	H	H	H	
C90 X A20 #590	1677	+	23	H	H	H	
C90 X A20 #590	1678	<i>nip</i>	6	A17	A17	A17	
C90 X A20 #590	1679	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #590	1681	<i>nip</i>	6	A17	A17	A17	
C90 X A20 #590	1682	+	6,21	A17	H	H	confirmed
C90 X A20 #590	1683	<i>nip</i>	6,21	A17	A17	A17	
C90 X A20 #590	1687	+	6,23,21	A20	H	H	confirmed
C90 X A20 #590	1688	+	6	H	H	H	
C90 X A20 #590	1689	+	6	H	H	H	
C90 X A20 #590	1690	+	6	H	H	H	
C90 X A20 #590	1691	<i>nip</i>	6	A17	A17	A17	
C90 X A20 #590	1692	<i>nip</i>	6	A17	A17	A17	
C90 X A20 #590	1693	<i>nip</i>	6	A17	A17	A17	
C90 X A20 #590	1694	+	6	A20	A20	A20	
C90 X A20 #590	1695	<i>nip</i>	6	A17	A17	A17	
C90 X A20 #590	1696	<i>nip</i>	6	A17	A17	A17	
C90 X A20 #590	1697	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #590	1698	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #561	1699	+	21	H	H	H	
C90 X A20 #561	1701	+	21	H	H	H	
C90 X A20 #561	1702	+	21	H	H	H	
C90 X A20 #561	1703	+	21,27	A20	A20	H	confirmed
C90 X A20 #561	1704	+	21,27	A20	A20	H	confirmed
C90 X A20 #561	1705	+	21	H	H	H	
C90 X A20 #561	1706	+	21	H	H	H	
C90 X A20 #561	1707	+	21	H	H	H	
C90 X A20 #555	1708	+	21	H	H	H	
C90 X A20 #555	1709	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #555	1710	+	21	H	H	H	
C90 X A20 #555	1711	+	21	H	H	H	
C90 X A20 #550	1712	+	21	H	H	H	
C90 X A20 #550	1714	+	21	A20	A20	A20	
C90 X A20 #550	1715	+	21	H	H	H	
C90 X A20 #550	1716	+	21	H	H	H	
C90 X A20 #550	1717	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #550	1718	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #550	1719	+	21	A20	A20	A20	
C90 X A20 #550	1720	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #560	1721	+	21,30	H	H	H	
C90 X A20 #560	1722	+	21,30	H	H	H	
C90 X A20 #560	1723	+	21	H	H	H	
C90 X A20 #560	1724	+	21	H	H	H	
C90 X A20 #560	1725	+	23	A20	A20	A20	
C90 X A20 #560	1726	+	21	H	H	H	

Table 1

Phenotyping And Genotyping Data For The <i>Nip</i> Mapping Population (F2 Generation)							
Parents	Plant #	Phenotype	Plate #	146o17	ENBP	23c16	Comments
C90 X A20 #560	1727	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #560	1728	+	21	H	H	H	
C90 X A20 #560	1729	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #560	1731	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #552	1733	+	21	H	H	H	
C90 X A20 #552	1734	+	21	H	H	H	
C90 X A20 #552	1735	+	21	H	H	H	
C90 X A20 #552	1737	+	23,27	H	H	A20	confirmed
C90 X A20 #552	1739	+	21,27	A20	A20	A20	
C90 X A20 #542	1740	+	21	H	H	H	
C90 X A20 #542	1741	+	21	H	H	H	
C90 X A20 #542	1742	+	21	H	H	H	
C90 X A20 #542	1743	<i>nip</i>	21	A17	A17	A17	
C90 X A20 #567	1746	+	21,27	H	A20	A20	confirmed
C90 X A20 #567	1747	+	21	H	H	H	
C90 X A20 #567	1748	+	21	A20	A20	A20	
C90 X A20 #567	1749	+	21	H	H	H	
C90 X A20 #567	1750	+	21	A20	A20	A20	
C90 X A20 #567	1751	+	21	A20	A20	A20	
C90 X A20 #567	1752	+	21	H	H	H	
C90 X A20 #567	1753	<i>nip</i>	27,21	A17	A17	A17	
C90 X A20 #567	1754	+	21	H	H	H	
C90 X A20 #567	1755	<i>nip</i>	27,21	A17	A17	A17	
C90 X A20 #567	1756	<i>nip</i>	27,21	A17	A17	A17	
C90 X A20 #567	1757	+	27,21	H	H	H	
C90 X A20 #567	1758	+	27,21	A20	A20	A20	
C90 X A20 #567	1759	<i>nip</i>	27	A17	A17	A17	
C90 X A20 #567	1760	<i>nip</i>	27,21	A17	A17	A17	
C90 X A20 #567	1761	+	23	A20	A20	A20	
C90 X A20 #559	1762	+	23	H	H	H	
C90 X A20 #559	1763	<i>nip</i>	23	A17	A17	A17	
C90 X A20 #559	1764	<i>nip</i>	23,27	H	H	A17	confirmed
C90 X A20 #559	1765	<i>nip</i>	27	A17	A17	A17	

Key for the Table 2

WT	Plants with wild-type nodulation phenotype
<i>nip</i>	Plants with <i>nip</i> nodulation phenotype
?	Plants with undetermined nodulation phenotype
A17	Plants with A17 genotype at a particular locus
A20	Plants with A20 genotype at a particular locus
H	Plants with both A20 and A17 genotypes at a particular locus
redo	Plants that tested positive for recombination event once, and no leaf material was found to retest them for recombination
confirmed	Recombinant plants that tested positive for recombination a second time

Note: plants that died before leaf material could be collected, and therefore before they could yield any genotyping data, are not shown in the table.

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #517	3000	WT		7	A20	A20
C90XA20 #517	3001	WT		7	A20	A20
C90XA20 #517	3002	WT		7	A20	A20
C90XA20 #517	3003	WT		7	A20	A20
C90XA20 #517	3004	WT		7	A20	A20
C90XA20 #517	3005	WT		7	A20	A20
C90XA20 #517	3006	WT		7	A20	A20
C90XA20 #517	3007	WT		7	A20	A20
C90XA20 #517	3008	WT		7	A20	A20
C90XA20 #517	3009	WT		7	A20	A20
C90XA20 #517	3010	WT		7	A20	A20
C90XA20 #517	3011	WT		7	A20	A20
C90XA20 #517	3012	WT		7	A20	A20
C90XA20 #517	3013	WT		7	A20	A20
C90XA20 #517	3014	WT		7	A20	A20
C90XA20 #401	3015	WT		7	A20	A20
C90XA20 #133#4	3016	WT	confirmed	11,7,16	A20	A17
C90XA20 #133#4	3017	<i>nip</i>		11,12,7	A20	A20
C90XA20 #133#4	3018	WT	confirmed	11,7,16	A20	A17
C90XA20 #133#4	3019	<i>nip</i>	confirmed	11,7,16	A20	A17
C90XA20 #133#4	3020	WT	Confirmed	7,18	A20	H
C90XA20 #133#4	3021	<i>nip</i>	confirmed	11,7,16	A20	A17
C90XA20 #162	3022	<i>nip</i>		7	A17	A17
C90XA20 #162	3023	<i>nip</i>		7	A17	A17
C90XA20 #162	3024	<i>nip</i>		7	A17	A17
C90XA20 #162	3025	<i>nip</i>		7	A17	A17
C90XA20 #279	3026	<i>nip</i>		7	A17	A17
C90XA20 #279	3027	<i>nip</i>		7	A17	A17
C90XA20 #279	3028	<i>nip</i>		7	A17	A17
C90XA20 #655	3030	WT		7	A20	A20
C90XA20 #655	3031	WT		7	A17	A17
C90XA20 #655	3032	?		17	A17	A17
C90XA20 #655	3033	WT		7	A20	A20
C90XA20 #368	3035	<i>nip</i>	Confirmed	12,18	A20	A17
C90XA20 #368	3037	<i>nip</i>		11	A17	A17
C90XA20 #521	3038	WT		11	A20	A20
C90XA20 #521	3039	WT		11	A20	A20
C90XA20 #521	3040	WT		11	A20	A20
C90XA20 #521	3041	WT		11	A20	A20
C90XA20 #521	3042	WT		11	A20	A20
C90XA20 #521	3043	WT		11	A20	A20
C90XA20 #521	3044	WT		12	A20	A20
C90XA20 #521	3045	WT		11	A20	A20
C90XA20 #521	3046	WT		11	A20	A20
C90XA20 #521	3048	WT		11	A20	A20
C90XA20 #515	3049	WT		7	A20	A20
C90XA20 #515	3050	WT		7	A20	A20

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #515	3053	WT		7	A20	A20
C90XA20 #515	3054	WT		7	A20	A20
C90XA20 #515	3055	WT		7	A20	A20
C90XA20 #515	3056	WT		7	A20	A20
C90XA20 #515	3057	WT		7	A20	A20
C90XA20 #515	3058	WT		7	A20	A20
C90XA20 #515	3059	WT		7	A20	A20
C90XA20 #515	3060	WT		7	A20	A20
C90XA20 #514	3062	<i>nip</i>		17	A17	A17
C90XA20 #514	3069	WT		17,18	A17	A17
C90XA20 #514	3074	WT		17	H	H
C90XA20 #514	3075	<i>nip</i>		17,18	A17	A17
C90XA20 #514	3076	WT		17	A20	A20
C90XA20 #514	3079	WT		17	A20	A20
C90XA20 #514	3080	WT		7	A20	A20
C90XA20 #514	3082	WT		7	A20	A20
C90XA20 #514	3083	WT		7	H	H
C90XA20 #514	3084	WT		7	H	H
C90XA20 #514	3088	WT		7	A20	A20
C90XA20 #368	3090	<i>nip</i>	confirmed	11,12	H	A17
C90XA20 #368	3091	<i>nip</i>	confirmed	11,7,16	H	A17
C90XA20 #368	3093	<i>nip</i>	confirmed	11,7,16	H	A17
C90XA20 #827	3094	<i>nip</i>		17	A17	A17
C90XA20 #827	3095	<i>nip</i>		17	A17	A17
C90XA20 #520	3096	WT		7	A20	A20
C90XA20 #520	3097	WT		11	A20	A20
C90XA20 #520	3098	WT		11	A20	A20
C90XA20 #520	3099	WT		11	A20	A20
C90XA20 #520	3100	WT		11	A20	A20
C90XA20 #520	3101	WT		11	A20	A20
C90XA20 #520	3102	WT		11	A20	A20
C90XA20 #520	3103	WT		11,7	A20	A20
C90XA20 #520	3104	WT		11,7	A20	A20
C90XA20 #520	3105	WT		11	A20	A20
C90XA20 #520	3106	WT		11	A20	A20
C90XA20 #520	3108	WT		11	A20	A20
C90XA20 #520	3109	WT		11	A20	A20
C90XA20 #520	3110	WT		11	A20	A20
C90XA20 #520	3111	WT		17	A20	A20
C90XA20 #520	3113	WT		11	A20	A20
C90XA20 #520	3114	WT		12,7	A20	A20
C90XA20 #520	3118	WT		11,7	A20	A20
C90XA20 #520	3119	WT		11,7	A20	A20
C90XA20 #520	3120	WT		11,7	A20	A20
C90XA20 #520	3122	WT		11	A20	A20
C90XA20 #520	3123	WT		11	A20	A20
C90XA20 #520	3124	WT		11	A20	A20
C90XA20 #520	3125	WT		11	A20	A20

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #520	3126	WT		11	A20	A20
C90XA20 #520	3130	WT		17	A20	A20
C90XA20 #520	3131	WT		11	A20	A20
C90XA20 #520	3132	WT		8	A20	A20
C90XA20 #520	3133	WT		17	A20	A20
C90XA20 #520	3134	WT		17	A20	A20
C90XA20 #520	3137	WT		8	A20	A20
C90XA20 #520	3138	WT		11	H	H
C90XA20 #520	3139	WT		8	A20	A20
C90XA20 #520	3140	WT		17	H	H
C90XA20 #520	3141	WT		8	A20	A20
C90XA20 #675	3150	<i>nip</i>		17	A17	A17
C90XA20 #675	3151	WT		8	A20	A20
C90XA20 #675	3152	WT		8	A20	A20
C90XA20 #675	3153	WT		8	A20	A20
C90XA20 #675	3154	WT		8,12	H	H
C90XA20 #675	3155	WT		8,12	H	H
C90XA20 #675	3157	WT		8	A20	A20
C90XA20 #675	3158	WT		11	H	H
C90XA20 #675	3159	WT		12	A17	A17
C90XA20 #755	3161	WT		8	A20	A20
C90XA20 #755	3163	<i>nip</i>		8	A17	A17
C90XA20 #755	3164	WT		17	A17	A17
C90XA20 #755	3166	WT		8	H	H
C90XA20 #755	3167	WT		17	A17	A17
C90XA20 #755	3169	WT		17	A20	A20
C90XA20 #755	3172	WT		8	A20	A20
C90XA20 #755	3173	<i>nip</i>		8	A20	A20
C90XA20 #755	3174	WT		8	H	H
C90XA20 #755	3175	WT		8	H	H
C90XA20 #755	3178	WT		8	A20	A20
C90XA20 #937	3184	WT		8	A20	A20
C90XA20 #401	3190	WT		8	H	H
C90XA20 #401	3191	WT		11,12	A20	A20
C90XA20 #401	3193	WT		16,17	H	H
C90XA20 #401	3194	WT		8	H	H
C90XA20 #401	3196	WT		17	H	H
C90XA20 #401	3198	<i>nip</i>		9	A17	A17
C90XA20 #401	3201	<i>nip</i>		17	A17	A17
C90XA20 #390	3205	WT		17	A17	A17
C90XA20 #390	3207	WT	confirmed	9,16	A17	H
C90XA20 #390	3208	WT	confirmed	9,18	A17	H
C90XA20 #390	3209	WT	confirmed	9,18	A17	A20
C90XA20 #390	3210	WT	confirmed	9,18	A17	A20
C90XA20 #390	3212	WT	confirmed	9,23	A17	A20
C90XA20 #390	3213	WT	confirmed	11,15	A17	H
C90XA20 #390	3214	WT	confirmed	9,16	A17	H
C90XA20 #390	3215	<i>nip</i>		17	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #390	3216	<i>nip</i>		17	A17	A17
C90XA20 #390	3217	<i>nip</i>		17,18	A17	A17
C90XA20 #390	3219	WT	confirmed	9,23	A17	A20
C90XA20 #390	3220	WT	confirmed	9,23	A17	A20
C90XA20 #390	3221	WT	confirmed	9,12,16	A17	H
C90XA20 #390	3222	WT	confirmed	11,15,16	A17	A20
C90XA20 #390	3225	WT		9	H	H
C90XA20 #390	3231	WT	redo	9	A17	H
C90XA20 #390	3239	WT	confirmed	9	A17	A20
C90XA20 #390	3241	<i>nip</i>		9	A17	A17
C90XA20 #390	3242	WT	redo	9	A17	A20
C90XA20 #390	3243	WT	confirmed	9	A17	H
C90XA20 #390	3245	WT	redo	9	A17	H
C90XA20 #390	3248	WT		9	H	H
C90XA20 #390	3255	WT	redo	9	A17	H
C90XA20 #390	3259	<i>nip</i>		11	A17	A17
C90XA20 #390	3261	WT	confirmed	11,15	A17	H
C90XA20 #660	3265	WT	confirmed	11,15	A20	H
C90XA20 #660	3266	WT	confirmed	11,15	A20	H
C90XA20 #660	3267	WT	confirmed	11,15	A20	H
C90XA20 #660	3269	WT	confirmed	11,12,18	A20	A17
C90XA20 #660	3270	WT	confirmed	11,12,15	A20	H
C90XA20 #660	3271	WT	confirmed	11,12,15	A20	H
C90XA20 #517	3274	WT		17	A20	A20
C90XA20 #517	3275	WT		17	A20	A20
C90XA20 #517	3276	WT		17,18	A20	A20
C90XA20 #517	3287	WT		17	A20	A20
C90XA20 #517	3293	WT		9	A20	A20
C90XA20 #517	3294	WT		9	A20	A20
C90XA20 #517	3298	WT		9	A20	A20
C90XA20 #517	3299	WT		9	A20	A20
C90XA20 #517	3300	WT		9	A20	A20
C90XA20 #517	3302	WT		16	A20	A20
C90XA20 #517	3303	WT		9	A20	A20
C90XA20 #517	3304	WT		9	A20	A20
C90XA20 #517	3305	WT		9	A20	A20
C90XA20 #517	3306	WT		9	A20	A20
C90XA20 #517	3308	WT		9	A20	A20
C90XA20 #517	3309	WT		9	A20	A20
C90XA20 #517	3310	WT		9	A20	A20
C90XA20 #517	3311	WT		9	A20	A20
C90XA20 #517	3314	WT		9	A20	A20
C90XA20 #517	3320	WT		9	A20	A20
C90XA20 #517	3323	WT		9	A20	A20
C90XA20 #517	3325	WT		9	A20	A20
C90XA20 #531	3328	WT	Confirmed	17,18,23	A20	A17
C90XA20 #531	3329	WT	Confirmed	11,12,18	H	A17
C90XA20 #531	3333	WT		23	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #521	3341	WT			A20	A20
C90XA20 #521	3342	WT			A20	A20
C90XA20 #521	3345	WT			A20	A20
C90XA20 #521	3346	WT			A20	A20
C90XA20 #521	3348	WT			A20	A20
C90XA20 #521	3349	WT		12	A20	A20
C90XA20 #521	3351	WT		11,12	A20	A20
C90XA20 #521	3352	WT		11,12	A20	A20
C90XA20 #162	3355	<i>nip</i>			A17	A17
C90XA20 #162	3362	<i>nip</i>		17	A17	A17
C90XA20 #515	3369	WT		12	A20	A20
C90XA20 #515	3370	WT			A20	A20
C90XA20 #515	3373	WT			A20	A20
C90XA20 #515	3374	WT			A20	A20
C90XA20 #515	3376	WT			A20	A20
C90XA20 #515	3377	WT			A20	A20
C90XA20 #655	3382	<i>nip</i>		17	A17	A17
C90XA20 #655	3383	WT		17	H	H
C90XA20 #655	3384	<i>nip</i>			H	H
C90XA20 #278	3393	<i>nip</i>	Confirmed	18	A17	A20
C90XA20 #278	3396	<i>nip</i>			A17	A17
C90XA20 #278	3399	<i>nip</i>	Confirmed	17,18	A17	A20
C90XA20 #133#4	3405	WT	Confirmed	17,18	A20	H
C90XA20 #133#4	3406	<i>nip</i>	Confirmed	17,18	A20	A17
C90XA20 #133#4	3408	WT	Confirmed	17,18	A20	H
C90XA20 #133#4	3409	WT	Confirmed	17,18	A20	H
C90XA20 #133#4	3411	WT	Confirmed	17,18	A20	H
C90XA20 #133#4	3412	WT	confirmed	17,18	A20	H
C90XA20 #133#4	3414	WT		16	A20	A20
C90XA20 #133#4	3415	WT		17,18	A20	A20
C90XA20 #368	3418	<i>nip</i>		17	A17	A17
C90XA20 #368	3422	<i>nip</i>	Confirmed	17,18	H	A17
C90XA20 #279	3423	WT			A17	A17
C90XA20 #279	3424	<i>nip</i>			A17	A17
C90XA20 #279	3425	WT		16	A17	A17
C90XA20 #279	3426	?		12	A17	A17
C90XA20 #279	3428	<i>nip</i>			A17	A17
C90XA20 #279	3430	<i>nip</i>		17	A17	A17
C90XA20 #279	3432	<i>nip</i>			A17	A17
C90XA20 #279	3433	<i>nip</i>		12	A17	A17
C90XA20 #279	3435	<i>nip</i>		12,18	A17	A17
C90XA20 #279	3437	<i>nip</i>			A17	A17
C90XA20 #279	3439	<i>nip</i>			A17	A17
C90XA20 #279	3441	<i>nip</i>		12	A17	A17
C90XA20 #155	3442	WT		11,12	H	H
C90XA20 #155	3443	WT			H	H
C90XA20 #155	3444	WT		12	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #155	3445	WT			H	H
C90XA20 #155	3446	WT			A17	A17
C90XA20 #155	3447	WT	confirmed	16,17	A20	H
C90XA20 #155	3448	WT		17	A20	A20
C90XA20 #155	3449	WT		17	H	H
C90XA20 #155	3450	WT		17	H	H
C90XA20 #155	3451	WT		17	H	H
C90XA20 #155	3452	WT		17	A17	A17
C90XA20 #155	3453	WT		17	H	H
C90XA20 #155	3455	WT		17	H	H
C90XA20 #155	3456	WT		17	H	H
C90XA20 #155	3458	WT		17	H	H
C90XA20 #155	3459	<i>nip</i>		17	A17	A17
C90XA20 #155	3460	<i>nip</i>		17	A17	A17
C90XA20 #525	3461	WT		17	A20	A20
C90XA20 #525	3462	WT		17	A20	A20
C90XA20 #525	3463	WT		17	A20	A20
C90XA20 #525	3464	WT		17	A20	A20
C90XA20 #525	3465	WT		17	A20	A20
C90XA20 #525	3466	WT		17	A20	A20
C90XA20 #525	3467	WT		17	A20	A20
C90XA20 #525	3468	WT		17	A20	A20
C90XA20 #525	3471	WT			A20	A20
C90XA20 #525	3472	WT		12,18	A20	A20
C90XA20 #525	3475	WT		17	A20	A20
C90XA20 #525	3476	WT			A20	A20
C90XA20 #525	3477	WT			A20	A20
C90XA20 #525	3478	WT			A20	A20
C90XA20 #525	3480	WT		12	A20	A20
C90XA20 #525	3481	WT		11,12	A20	A20
C90XA20 #525	3482	WT			A20	A20
C90XA20 #525	3483	WT		12	A20	A20
C90XA20 #525	3484	WT			H	H
C90XA20 #525	3485	<i>nip</i>			A17	A17
C90XA20 #525	3486	WT			H	H
C90XA20 #525	3487	WT		17	A20	A20
C90XA20 #525	3488	WT			A20	A20
C90XA20 #525	3489	WT			A20	A20
C90XA20 #525	3490	WT			A20	A20
C90XA20 #525	3491	WT		12	H	H
C90XA20 #665	3492	WT			A20	A20
C90XA20 #665	3493	WT		12,18	H	H
C90XA20 #665	3494	WT		11,12	H	H
C90XA20 #665	3495	WT		17	H	H
C90XA20 #368	3497	<i>nip</i>	Confirmed	11,18	H	A17
C90XA20 #368	3498	<i>nip</i>	Confirmed	11,16	H	A17
C90XA20 #368	3500	<i>nip</i>		11	A17	A17
C90XA20 #368	3511	<i>nip</i>	confirmed	11,16	H	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #368	3512	<i>nip</i>		11	A17	A17
C90XA20 #368	3513	<i>nip</i>	confirmed	11,16	H	A17
C90XA20 #368	3514	<i>nip</i>	confirmed	12,18	H	A17
C90XA20 #368	3515	<i>nip</i>	confirmed	11,16	A20	A17
C90XA20 #368	3516	<i>nip</i>	confirmed	17,18	H	A17
C90XA20 #368	3518	<i>nip</i>	confirmed	11,16	H	A17
C90XA20 #368	3519	<i>nip</i>	confirmed	11,16	H	A17
C90XA20 #368	3520	<i>nip</i>	confirmed	12,18	H	A17
C90XA20 #368	3521	<i>nip</i>	confirmed	11,15	A20	A17
C90XA20 #848	3522	<i>nip</i>		14	A17	A17
C90XA20 #848	3523	<i>nip</i>		14	A17	A17
C90XA20 #848	3524	WT		15	H	H
C90XA20 #848	3525	<i>nip</i>		14	A17	A17
C90XA20 #848	3526	WT		14	H	H
C90XA20 #848	3527	WT		14	H	H
C90XA20 #848	3528	WT		14	H	H
C90XA20 #848	3529	<i>nip</i>		14	A17	A17
C90XA20 #848	3530	WT		14	H	H
C90XA20 #848	3531	WT		14	A20	A20
C90XA20 #848	3532	<i>nip</i>		14	A17	A17
C90XA20 #848	3533	WT		14	H	H
C90XA20 #848	3534	WT		14	H	H
C90XA20 #848	3535	WT		14	H	H
C90XA20 #848	3536	WT		14	H	H
C90XA20 #848	3537	<i>nip</i>		14	A17	A17
C90XA20 #848	3538	WT		14	H	H
C90XA20 #848	3539	<i>nip</i>		14	A17	A17
C90XA20 #749	3540	WT		16	A20	A20
C90XA20 #749	3541	WT		14	A20	A20
C90XA20 #749	3542	WT			A20	A20
C90XA20 #749	3543	WT			A20	A20
C90XA20 #749	3544	WT			A20	A20
C90XA20 #749	3545	WT			A20	A20
C90XA20 #749	3546	WT			A20	A20
C90XA20 #749	3547	WT			A20	A20
C90XA20 #749	3548	WT			A20	A20
C90XA20 #749	3549	WT			A20	A20
C90XA20 #749	3550	WT			A20	A20
C90XA20 #749	3551	WT		16	A20	A20
C90XA20 #749	3552	WT		16	A20	A20
C90XA20 #749	3553	WT		14	A20	A20
C90XA20 #749	3554	WT		13	A20	A20
C90XA20 #749	3555	WT		14	A20	A20
C90XA20 #749	3556	WT		14	A20	A20
C90XA20 #754	3557	WT		14	A17	A17
C90XA20 #754	3558	WT		14	A20	A20
C90XA20 #754	3559	WT		14,16	H	H
C90XA20 #754	3560	WT		14	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #754	3561	WT		14	A20	A20
C90XA20 #921	3562	WT		14	A20	A20
C90XA20 #921	3563	WT		14	H	H
C90XA20 #921	3564	WT		15	A20	A20
C90XA20 #921	3565	WT		13	H	H
C90XA20 #921	3566	WT		14	H	H
C90XA20 #921	3567	WT		14	A20	A20
C90XA20 #921	3568	WT		14	A20	A20
C90XA20 #921	3569	WT		14	H	H
C90XA20 #921	3570	WT		14	H	H
C90XA20 #921	3571	WT		14	H	H
C90XA20 #921	3572	WT		14	H	H
C90XA20 #921	3573	WT		14	H	H
C90XA20 #921	3574	WT		14	A20	A20
C90XA20 #921	3575	WT		15	A20	A20
C90XA20 #921	3576	WT		15	H	H
C90XA20 #921	3577	WT		14	H	H
C90XA20 #921	3578	WT		14	H	H
C90XA20 #921	3579	WT		15	H	H
C90XA20 #921	3580	<i>nip</i>		15	A17	A17
C90XA20 #921	3581	<i>nip</i>		15	A17	A17
C90XA20 #921	3582	<i>nip</i>		15	A17	A17
C90XA20 #921	3583	<i>nip</i>		15	A17	A17
C90XA20 #921	3584	<i>nip</i>		15	A17	A17
C90XA20 #921	3585	<i>nip</i>		15	A17	A17
C90XA20 #921	3586	<i>nip</i>		15	A17	A17
C90XA20 #681	3587	WT		15	A17	A17
C90XA20 #681	3588	WT		15	H	H
C90XA20 #681	3589	WT		15	A20	A20
C90XA20 #681	3590	WT		15	A20	A20
C90XA20 #681	3591	WT		15	H	H
C90XA20 #681	3592	WT		15	H	H
C90XA20 #681	3593	WT		15	H	H
C90XA20 #681	3594	WT		15	H	H
C90XA20 #681	3595	WT		15	A20	A20
C90XA20 #681	3596	WT		15	A20	A20
C90XA20 #681	3597	WT		15	H	H
C90XA20 #681	3598	WT		15	A20	A20
C90XA20 #681	3599	WT		15	A20	A20
C90XA20 #681	3600	WT		15	H	H
C90XA20 #681	3601	WT		15	A20	A20
C90XA20 #681	3602	WT		14	H	H
C90XA20 #681	3603	WT		14	H	H
C90XA20 #681	3604	WT		14	H	H
C90XA20 #681	3605	WT		14	H	H
C90XA20 #948	3606	WT		14	H	H
C90XA20 #948	3607	WT		14	H	H
C90XA20 #948	3608	WT		14	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #948	3609	WT		14	H	H
C90XA20 #948	3610	WT		14	H	H
C90XA20 #948	3611	WT		13	A20	A20
C90XA20 #948	3612	WT		13	H	H
C90XA20 #948	3613	WT		13	A20	A20
C90XA20 #948	3614	WT		13	H	H
C90XA20 #948	3615	WT		15	H	H
C90XA20 #948	3616	WT		13	H	H
C90XA20 #948	3617	WT		16	H	H
C90XA20 #948	3618	WT		16	A20	A20
C90XA20 #948	3619	WT		14	H	H
C90XA20 #948	3620	WT		14	H	H
C90XA20 #948	3621	<i>nip</i>		14	A17	A17
C90XA20 #948	3622	<i>nip</i>		14	A17	A17
C90XA20 #948	3623	<i>nip</i>		16	A17	A17
C90XA20 #754	3624	WT		14	A20	A20
C90XA20 #754	3625	WT		14	H	H
C90XA20 #754	3626	WT		14	A20	A20
C90XA20 #754	3627	WT		13	H	H
C90XA20 #754	3628	WT		13	H	H
C90XA20 #754	3629	WT		13	A20	A20
C90XA20 #754	3630	WT		13	H	H
C90XA20 #754	3631	WT		13	H	H
C90XA20 #754	3632	WT		13	A20	A20
C90XA20 #754	3633	WT		13	H	H
C90XA20 #754	3634	<i>nip</i>		13	A17	A17
C90XA20 #754	3635	<i>nip</i>		13	A17	A17
C90XA20 #698	3636	WT		13	H	H
C90XA20 #698	3637	WT		15	A20	A20
C90XA20 #698	3638	WT		13	H	H
C90XA20 #698	3639	WT		13	A20	A20
C90XA20 #698	3640	WT		15	H	H
C90XA20 #698	3641	WT		13	H	H
C90XA20 #698	3642	WT		13	A20	A20
C90XA20 #698	3643	WT		13	H	H
C90XA20 #698	3644	WT		13	H	H
C90XA20 #698	3645	WT		13	A20	A20
C90XA20 #698	3646	WT		13	H	H
C90XA20 #698	3647	WT		13	H	H
C90XA20 #698	3648	WT		13	A20	A20
C90XA20 #698	3649	WT		13	A20	A20
C90XA20 #698	3650	WT		13	H	H
C90XA20 #698	3651	WT	confirmed	13,15,16	H	A20
C90XA20 #698	3652	WT		13	A20	A20
C90XA20 #698	3653	<i>nip</i>		13	A17	A17
C90XA20 #698	3654	<i>nip</i>		13	A17	A17
C90XA20 #698	3655	<i>nip</i>		13	A17	A17
C90XA20 #698	3656	<i>nip</i>		13	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #698	3657	<i>nip</i>		13	A17	A17
C90XA20 #698	3658	<i>nip</i>		13,15	A17	A17
C90XA20 #731	3659	WT		14	A20	A20
C90XA20 #731	3660	WT		14	H	H
C90XA20 #731	3661	WT		14	H	H
C90XA20 #731	3662	WT		14	H	H
C90XA20 #731	3663	WT		14	H	H
C90XA20 #731	3664	WT		14	H	H
C90XA20 #731	3665	WT		14	H	H
C90XA20 #731	3666	WT		14	H	H
C90XA20 #731	3667	WT		14	H	H
C90XA20 #731	3668	<i>nip</i>		14	A17	A17
C90XA20 #731	3669	<i>nip</i>		14	A17	A17
C90XA20 #731	3670	<i>nip</i>		16	A17	A17
C90XA20 #731	3671	<i>nip</i>		14	A17	A17
C90XA20 #731	3672	<i>nip</i>		14	A17	A17
C90XA20 #850	3673	WT		14	A20	A20
C90XA20 #850	3674	WT		14	H	H
C90XA20 #850	3675	WT		15	A20	A20
C90XA20 #850	3676	WT		14	A20	A20
C90XA20 #850	3677	WT		14	A20	A20
C90XA20 #850	3678	<i>nip</i>		14	A17	A17
C90XA20 #850	3679	<i>nip</i>		14	A17	A17
C90XA20 #850	3680	<i>nip</i>		14	A17	A17
C90XA20 #850	3681	WT		14	H	H
C90XA20 #850	3682	WT		14	A20	A20
C90XA20 #850	3683	WT		15	A20	A20
C90XA20 #850	3684	WT		15	A20	A20
C90XA20 #850	3685	WT		15	A20	A20
C90XA20 #850	3686	WT		15	H	H
C90XA20 #850	3687	WT		15	H	H
C90XA20 #850	3688	WT	confirmed	15,16	H	A20
C90XA20 #850	3689	WT		15	H	H
C90XA20 #850	3690	WT		15	H	H
C90XA20 #850	3691	<i>nip</i>		15	A17	A17
C90XA20 #850	3692	<i>nip</i>		15	A17	A17
C90XA20 #850	3693	<i>nip</i>		15	A17	A17
C90XA20 #850	3694	<i>nip</i>		15	A17	A17
C90XA20 #850	3695	<i>nip</i>		15	A17	A17
C90XA20 #683	3696	WT		15	A20	A20
C90XA20 #683	3697	WT		13	H	H
C90XA20 #683	3698	WT		13	H	H
C90XA20 #683	3699	WT		13	A20	A20
C90XA20 #683	3700	WT		13	A20	A20
C90XA20 #683	3701	WT		13	H	H
C90XA20 #683	3702	WT		13	A20	A20
C90XA20 #683	3703	WT		13	H	H
C90XA20 #683	3704	WT		13	A20	A20

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #683	3705	WT	Confirmed	13,15,16	H	A17
C90XA20 #683	3706	WT		13	A20	A20
C90XA20 #683	3707	WT		13	A20	A20
C90XA20 #683	3708	WT		13	A20	A20
C90XA20 #683	3709	WT		13	A20	A20
C90XA20 #683	3710	WT		13	A20	A20
C90XA20 #683	3711	<i>nip</i>		15	A17	A17
C90XA20 #683	3712	<i>nip</i>	confirmed	13,15,16	A17	H
C90XA20 #683	3713	<i>nip</i>		15	A17	A17
C90XA20 #683	3714	<i>nip</i>		13	A17	A17
C90XA20 #681	3715	WT		13	H	H
C90XA20 #681	3716	<i>nip</i>		13	A17	A17
C90XA20 #1111	3717	WT		22	A20	A20
C90XA20 #993	3718	WT		22	A20	A20
C90XA20 #993	3719	WT	Confirmed	22,24	H	A20
C90XA20 #993	3720	WT		22	H	H
C90XA20 #993	3721	?		22	A17	A17
C90XA20 #993	3723	?		22	A17	A17
C90XA20 #993	3724	WT		22,23,24	H	H
C90XA20 #993	3725	WT		22	H	H
C90XA20 #993	3726	WT		22	H	H
C90XA20 #993	3729	WT		22,23	H	H
C90XA20 #816	3730	WT		22,23	A20	A20
C90XA20 #816	3731	WT	Confirmed	22,23,24	A17	H
C90XA20 #816	3732	WT		22	H	H
C90XA20 #816	3733	?		23	H	H
C90XA20 #816	3734	?		23	H	H
C90XA20 #1013	3735	?		23	H	H
C90XA20 #1013	3736	WT		22	A20	A20
C90XA20 #1013	3737	WT		22	H	H
C90XA20 #1030	3742	WT		22	H	H
C90XA20 #1030	3743	WT		22	H	H
C90XA20 #1030	3744	WT		22	A20	A20
C90XA20 #1030	3745	WT		22	H	H
C90XA20 #1030	3746	?		23	A17	A17
C90XA20 #1030	3747	WT		22,23	A20	A20
C90XA20 #1030	3748	<i>nip</i>		22	A17	A17
C90XA20 #1030	3749	<i>nip</i>	Confirmed	22,23	A20	H
C90XA20 #1030	3750	?		22	H	H
C90XA20 #1030	3751	WT		22	H	H
C90XA20 #1030	3752	WT		22	A20	A20
C90XA20 #1030	3753	<i>nip</i>		23	H	H
C90XA20 #1030	3755	WT		22	A20	A20
C90XA20 #1030	3756	<i>nip</i>		22	A20	A20
C90XA20 #1163	3757	WT		22	H	H
C90XA20 #1163	3758	WT		22	H	H
C90XA20 #1163	3759	WT		22	A20	A20
C90XA20 #1163	3760	WT		22	A20	A20

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #1163	3761	WT		22	A20	A20
C90XA20 #1163	3762	WT		22	H	H
C90XA20 #1163	3763	WT		22	H	H
C90XA20 #1163	3764	WT		22	H	H
C90XA20 #1163	3765	<i>nip</i>		22	A17	A17
C90XA20 #1163	3766	WT		22	A20	A20
C90XA20 #1163	3767	WT		22	A20	A20
C90XA20 #1163	3768	WT		22	H	H
C90XA20 #1163	3769	WT		22	H	H
C90XA20 #1163	3770	WT		22	H	H
C90XA20 #1163	3771	WT		22	H	H
C90XA20 #1163	3772	WT		22	A20	A20
C90XA20 #1163	3773	?		22	H	H
C90XA20 #1163	3774	WT		22	A20	A20
C90XA20 #1163	3775	?		22	H	H
C90XA20 #1163	3776	WT		22	A17	A17
C90XA20 #1163	3777	WT		22	A20	A20
C90XA20 #1163	3778	WT		22	A17	A17
C90XA20 #1163	3779	?		22	H	H
C90XA20 #1163	3780	WT		22	A20	A20
C90XA20 #1163	3781	?		22	A17	A17
C90XA20 #1163	3782	WT		22	H	H
C90XA20 #1163	3783	WT		22	H	H
C90XA20 #1179	3784	WT		22	H	H
C90XA20 #1179	3785	WT		22,23	H	H
C90XA20 #1179	3786	WT		22	H	H
C90XA20 #1179	3787	WT		22	A20	A20
C90XA20 #1179	3788	WT		22	A20	A20
C90XA20 #1179	3789	WT		22	H	H
C90XA20 #1179	3790	WT		22	A20	A20
C90XA20 #1018	3791	<i>nip</i>		22	A20	A20
C90XA20 #1018	3794	<i>nip</i>		22	H	H
C90XA20 #1018	3795	?		22	A20	A20
C90XA20 #1018	3796	?		22	A17	A17
C90XA20 #1106	3798	<i>nip</i>		22	A17	A17
C90XA20 #1106	3799	WT		22	H	H
C90XA20 #1106	3800	WT		22	H	H
C90XA20 #1106	3801	<i>nip</i>		22	H	H
C90XA20 #1106	3802	WT		22	H	H
C90XA20 #1106	3803	WT		22	H	H
C90XA20 #1106	3804	<i>nip</i>		22	A17	A17
C90XA20 #1106	3805	?		22	A17	A17
C90XA20 #1106	3806	<i>nip</i>		22	A17	A17
C90XA20 #1106	3807	WT		22,23	H	H
C90XA20 #1106	3808	<i>nip</i>		22	A17	A17
C90XA20 #1106	3809	WT		22	H	H
C90XA20 #1106	3810	<i>nip</i>		22	A17	A17
C90XA20 #1106	3811	WT		22	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20 #1106	3812	?		22	H	H
C90XA20 #1106	3813	?		23	H	H
C90XA20 #1106	3814	WT		22	H	H
C90XA20 #1106	3815	WT		22	H	H
C90XA20 #1106	3816	?		22	H	H
C90XA20 #1106	3817	<i>nip</i>		22	A17	A17
C90XA20 #1106	3818	?		22	H	H
C90XA20 #1106	3819	WT		22	A20	A20
C90XA20 #1106	3820	?		22	A20	A20
C90XA20 #1106	3821	?	Confirmed	22,23	H	A20
C90XA20 #1106	3822	<i>nip</i>		22	H	H
C90XA20#1112	3823	WT		25	H	H
C90XA20#1112	3824	WT		25	A20	A20
C90XA20#1112	3825	WT		25	A20	A20
C90XA20#1112	3826	<i>nip</i>		25	A17	A17
C90XA20#1112	3827	WT		25	H	H
C90XA20#1112	3828	<i>nip</i>	Confirmed	25,27	A17	H
C90XA20#1112	3829	<i>nip</i>		25	A20	A20
C90XA20#1112	3830	WT		24,26	H	H
C90XA20#1112	3831	WT		24	A20	A20
C90XA20#1112	3832	WT		24	H	H
C90XA20#1112	3833	WT		24	H	H
C90XA20#1112	3834	WT		24	A20	A20
C90XA20#1082	3835	WT		24,26	A17	A17
C90XA20#1082	3836	WT		24	H	H
C90XA20#1082	3837	?		24	A20	A20
C90XA20#1082	3838	?		24	A20	A20
C90XA20#1082	3839	WT		24	A20	A20
C90XA20#1082	3840	WT		24,26	H	H
C90XA20#1082	3841	WT		24	H	H
C90XA20#1082	3842	WT		24,26	H	H
C90XA20#1082	3843	WT		24,26	H	H
C90XA20#1082	3844	WT	Confirmed	24,26	H	A20
C90XA20#1082	3845	WT		24	H	H
C90XA20#1082	3846	?		24	H	H
C90XA20#1082	3847	WT		24	A20	A20
C90XA20#1082	3848	WT		24	H	H
C90XA20#1082	3849	WT		24	A17	A17
C90XA20#1082	3850	WT		24	H	H
C90XA20#1082	3851	WT		24	H	H
C90XA20#1082	3852	WT		24	A20	A20
C90XA20#1082	3853	WT		24,26	H	H
C90XA20#1082	3854	WT		24	H	H
C90XA20#1082	3855	WT		24	H	H
C90XA20#1082	3856	WT		24,26	H	H
C90XA20#1082	3857	<i>nip</i>		24	A17	A17
C90XA20#1082	3858	WT		24	H	H
C90XA20#1082	3859	WT		24	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1082	3860	WT		24	H	H
C90XA20#1082	3861	WT		24,26,27	H	H
C90XA20#1082	3862	WT		24	H	H
C90XA20#1082	3863	WT		24	H	H
C90XA20#1082	3864	WT		24	A20	A20
C90XA20#1082	3865	<i>nip</i>		24	H	H
C90XA20#1082	3866	WT		24,26,27	H	H
C90XA20#1186	3867	WT		24	A20	A20
C90XA20#1186	3868	WT		24	H	H
C90XA20#1186	3869	WT		24,26	H	H
C90XA20#1186	3870	WT		24	H	H
C90XA20#1186	3871	WT		24	A20	A20
C90XA20#1186	3872	<i>nip</i>		24	H	H
C90XA20#1186	3873	<i>nip</i>		24	H	H
C90XA20#1186	3874	WT		24	H	H
C90XA20#1186	3875	WT		24	A20	A20
C90XA20#1186	3876	<i>nip</i>		24	A17	A17
C90XA20#1186	3877	WT		24,26	H	H
C90XA20#1013	3878	WT		24	H	H
C90XA20#1013	3879	WT		24	H	H
C90XA20#1013	3880	WT		24	H	H
C90XA20#1013	3881	WT		24	H	H
C90XA20#1013	3882	WT		24,26,27	A20	A20
C90XA20#1013	3883	WT		24	H	H
C90XA20#1013	3884	WT		24	H	H
C90XA20#1013	3885	<i>nip</i>		24,26,27	A17	A17
C90XA20#1013	3886	WT		24,26,27	A20	A20
C90XA20#1013	3887	<i>nip</i>		24	H	H
C90XA20#1013	3888	WT		24,26	A20	A20
C90XA20#1013	3889	WT		24	A20	A20
C90XA20#1013	3890	WT		24	H	H
C90XA20#1013	3891	WT		24	A20	A20
C90XA20#1013	3892	WT		24	H	H
C90XA20#1013	3893	WT		24	H	H
C90XA20#1013	3894	WT		24	A20	A20
C90XA20#1013	3895	WT		24,26	H	H
C90XA20#1013	3896	WT		24,26	A20	A20
C90XA20#1013	3897	<i>nip</i>		24	A17	A17
C90XA20#1013	3898	WT		24	H	H
C90XA20#1013	3899	<i>nip</i>		24	A17	A17
C90XA20#1013	3900	<i>nip</i>		24,26	A20	A20
C90XA20#1013	3901	<i>nip</i>		24	A17	A17
C90XA20#1013	3902	WT		24	A20	A20
C90XA20#1013	3903	<i>nip</i>		24	A17	A17
C90XA20#1013	3904	WT		24	H	H
C90XA20#1013	3905	WT		24	A20	A20
C90XA20#1013	3906	WT		24,26	A20	A20
C90XA20#1102	3907	WT		24	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1102	3908	WT		24,26	A20	A20
C90XA20#1102	3909	WT		24	H	H
C90XA20#1102	3910	<i>nip</i>		24	A17	A17
C90XA20#1102	3911	WT		24	A17	A17
C90XA20#1102	3912	WT		24	A20	A20
C90XA20#1102	3913	WT		24	H	H
C90XA20#1102	3914	WT	Confirmed	24,26,27	H	A20
C90XA20#1102	3915	WT	Confirmed	24,26,27	H	A17
C90XA20#1102	3916	WT		24	A20	A20
C90XA20#1101	3917	WT		24	H	H
C90XA20#1101	3918	WT		25,26,27	A20	A20
C90XA20#1101	3919	<i>nip</i>		25	A17	A17
C90XA20#1101	3920	<i>nip</i>		25	A17	A17
C90XA20#1101	3921	WT		25	H	H
C90XA20#1101	3922	WT		25	H	H
C90XA20#1101	3923	WT		25	H	H
C90XA20#1101	3924	WT		25	A20	A20
C90XA20#1101	3925	WT		25	H	H
C90XA20#1101	3926	WT		25	H	H
C90XA20#1101	3927	WT		25,26	H	H
C90XA20#1101	3928	WT		25,26,27	H	H
C90XA20#1101	3929	WT		25	H	H
C90XA20#1101	3930	WT		25	H	H
C90XA20#1101	3931	WT		26	H	H
C90XA20#1101	3932	<i>nip</i>		25	A17	A17
C90XA20#1101	3933	WT		25	H	H
C90XA20#1101	3934	WT		25	H	H
C90XA20#1101	3935	WT		25	H	H
C90XA20#1043	3936	<i>nip</i>		25	A17	A17
C90XA20#1043	3937	<i>nip</i>		27	A17	A17
C90XA20#1043	3938	<i>nip</i>		27	A17	A17
C90XA20#1043	3939	<i>nip</i>		25	A17	A17
C90XA20#1043	3940	<i>nip</i>		25	A17	A17
C90XA20#1043	3941	<i>nip</i>		25	A17	A17
C90XA20#1043	3942	<i>nip</i>	Confirmed	25,26,27	A17	H
C90XA20#1043	3943	<i>nip</i>	Confirmed	25,26	A17	H
C90XA20#1043	3944	<i>nip</i>	Confirmed	25,26,27	A17	H
C90XA20#1043	3945	<i>nip</i>		25	A17	A17
C90XA20#1043	3946	<i>nip</i>	confirmed	25,26	A17	A20
C90XA20#1043	3947	<i>nip</i>	confirmed	25,26	A17	H
C90XA20#1043	3948	<i>nip</i>	Confirmed	25,26	A17	H
C90XA20#1043	3949	<i>nip</i>		25	A17	A17
C90XA20#1043	3950	<i>nip</i>	confirmed	25,26	A17	H
C90XA20#1043	3951	<i>nip</i>	confirmed	25,26	A17	H
C90XA20#1043	3953	<i>nip</i>	Confirmed	25,27	A17	H
C90XA20#1178	3954	WT		25	H	H
C90XA20#1178	3955	WT		25	H	H
C90XA20#1178	3956	WT		25	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1178	3957	WT		25	H	H
C90XA20#1178	3958	WT		25	A20	A20
C90XA20#1178	3959	WT		25	H	H
C90XA20#1178	3960	WT		25,26,27	H	H
C90XA20#1178	3961	WT		25	H	H
C90XA20#1178	3962	WT		25	A20	A20
C90XA20#1178	3963	WT		25	H	H
C90XA20#1178	3964	WT		25	H	H
C90XA20#1178	3965	?	Confirmed	25,26,27	A17	H
C90XA20#1178	3966	?		25	H	H
C90XA20#1178	3967	<i>nip</i>		25	A17	A17
C90XA20#1178	3968	<i>nip</i>		25	A17	A17
C90XA20#1178	3969	<i>nip</i>		25	A17	A17
C90XA20#1178	3970	<i>nip</i>		25	A17	A17
C90XA20#1178	3971	WT		25	H	H
C90XA20#1178	3972	WT		25	H	H
C90XA20#1178	3973	WT		25	H	H
C90XA20#1178	3974	WT		25	H	H
C90XA20#1178	3975	WT		25	H	H
C90XA20#1178	3976	WT		25	A20	A20
C90XA20#1178	3977	WT		25,27	H	H
C90XA20#1178	3978	WT		25,27	H	H
C90XA20#1016	3979	<i>nip</i>	Confirmed	25,27	A17	H
C90XA20#1016	3980	WT		25	H	H
C90XA20#1016	3981	<i>nip</i>		25	A17	A17
C90XA20#1016	3982	WT		25	H	H
C90XA20#1016	3983	WT		25	H	H
C90XA20#1016	3984	<i>nip</i>		25	A17	A17
C90XA20#1016	3985	WT		25	H	H
C90XA20#1016	3986	WT		25	A20	A20
C90XA20#1016	3987	<i>nip</i>		25	A17	A17
C90XA20#1016	3988	WT		27	H	H
C90XA20#1016	3989	WT		26,27	H	H
C90XA20#1016	3990	<i>nip</i>		26	A17	A17
C90XA20#1016	3991	<i>nip</i>		26	A17	A17
C90XA20#1016	3992	WT		26	H	H
C90XA20#1016	3993	WT		26	A20	A20
C90XA20#1016	3994	WT		26	H	H
C90XA20#1016	3995	<i>nip</i>		26	A17	A17
C90XA20#1016	3996	WT		26	H	H
C90XA20#1016	3997	WT		26	H	H
C90XA20#1016	3998	<i>nip</i>		26	A17	A17
C90XA20#1016	3999	<i>nip</i>		26	A17	A17
C90XA20#1016	4000	WT		26	H	H
C90XA20#1016	4001	WT		26	H	H
C90XA20#1016	4002	WT		26	H	H
C90XA20#1016	4003	WT		27	H	H
C90XA20#1016	4004	WT		26	A20	A20

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1016	4005	<i>nip</i>		26,27	A17	A17
C90XA20#1016	4006	WT		26	H	H
C90XA20#1016	4007	WT		26	A20	A20
C90XA20#1016	4008	WT		26	H	H
C90XA20#1016	4009	WT		26	H	H
C90XA20#1016	4010	WT		26	A20	A20
C90XA20#1016	4011	WT		27	H	H
C90XA20#1016	4012	WT		27	H	H
C90XA20#1016	4013	WT		26,27	A20	A20
C90XA20#1016	4014	WT		26	A20	A20
C90XA20#1016	4015	WT		26	H	H
C90XA20#1113	4016	<i>nip</i>		28	A17	A17
C90XA20#1113	4017	WT		28,32	A20	A20
C90XA20#1113	4018	WT		28,32	H	H
C90XA20#1113	4019	WT		28,32	H	H
C90XA20#1113	4020	WT		28,32	H	H
C90XA20#1113	4021	<i>nip</i>		28	A17	A17
C90XA20#1113	4022	WT		28	H	H
C90XA20#1113	4023	WT		28,32	H	H
C90XA20#1113	4024	WT		28	H	H
C90XA20#1113	4025	WT		28	H	H
C90XA20#1113	4026	WT		28,32	A20	A20
C90XA20#1113	4027	WT		28,32	H	H
C90XA20#1113	4028	WT		28	A20	A20
C90XA20#1113	4029	<i>nip</i>		28	A17	A17
C90XA20#1113	4030	<i>nip</i>		28	A17	A17
C90XA20#1113	4031	<i>nip</i>		28	A17	A17
C90XA20#1113	4032	<i>nip</i>		28	A17	A17
C90XA20#1113	4033	<i>nip</i>		28	H	H
C90XA20#1113	4034	WT		28,32	H	H
C90XA20#1113	4035	<i>nip</i>		28	A17	A17
C90XA20#1113	4036	<i>nip</i>		28	A17	A17
C90XA20#1113	4037	WT		28	A20	A20
C90XA20#1113	4038	WT		28	A20	A20
C90XA20#1113	4039	WT		28	H	H
C90XA20#1113	4040	WT		28	H	H
C90XA20#1113	4041	WT		28	H	H
C90XA20#1113	4042	WT		28	H	H
C90XA20#1113	4043	<i>nip</i>		28	A17	A17
C90XA20#1113	4044	<i>nip</i>		28,32	A17	A17
C90XA20#1113	4045	WT		28	H	H
C90XA20#1113	4046	WT		28	H	H
C90XA20#1113	4047	WT		28	H	H
C90XA20#1113	4048	WT		28	A20	A20
C90XA20#1113	4049	<i>nip</i>		28	A17	A17
C90XA20#1113	4050	WT		28	A20	A20
C90XA20#1113	4051	WT		28	A20	A20
C90XA20#1113	4052	<i>nip</i>		28	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1113	4053	<i>nip</i>		28	A17	A17
C90XA20#1113	4054	WT		28	H	H
C90XA20#1113	4055	WT		28,32	H	H
C90XA20#1113	4056	WT		28,32	H	H
C90XA20#1113	4057	WT		28	H	H
C90XA20#1113	4058	<i>nip</i>		28	A17	A17
C90XA20#1113	4059	WT		28	A20	A20
C90XA20#1113	4060	WT		28	H	H
C90XA20#1113	4061	WT		28,32	A20	A20
C90XA20#1113	4062	WT		28,32	H	H
C90XA20#1113	4063	<i>nip</i>		28,32	A17	A17
C90XA20#1113	4064	<i>nip</i>		28	A17	A17
C90XA20#1113	4065	WT		28,32	H	H
C90XA20#1113	4066	<i>nip</i>		28	H	H
C90XA20#1113	4067	WT		28	H	H
C90XA20#1113	4068	<i>nip</i>		28	A17	A17
C90XA20#1113	4069	<i>nip</i>		28	H	H
C90XA20#1113	4070	<i>nip</i>		28,32	A17	A17
C90XA20#1113	4071	WT		28	A17	A17
C90XA20#1113	4072	WT		28	A17	A17
C90XA20#1113	4073	WT		28	H	H
C90XA20#1113	4074	<i>nip</i>	Confirmed	28,38	A17	H
C90XA20#1163	4075	WT		28	H	H
C90XA20#1163	4076	WT		28	A17	A17
C90XA20#1163	4077	<i>nip</i>		28	A17	A17
C90XA20#1163	4078	WT		28	A20	A20
C90XA20#1163	4079	WT		28	A20	A20
C90XA20#1163	4080	WT		28	H	H
C90XA20#1163	4081	WT		28	H	H
C90XA20#1163	4082	<i>nip</i>		28	A17	A17
C90XA20#1163	4083	WT		28	H	H
C90XA20#1163	4084	WT		28	H	H
C90XA20#1163	4085	WT		28	H	H
C90XA20#1163	4086	WT		28	H	H
C90XA20#1163	4087	WT		28	A20	A20
C90XA20#1163	4088	WT		28	A20	A20
C90XA20#1163	4089	WT		28	A20	A20
C90XA20#1163	4090	WT		28	H	H
C90XA20#1163	4091	WT		28	H	H
C90XA20#1163	4092	WT	Confirmed	28,38	H	A20
C90XA20#1163	4093	<i>nip</i>		28,32	A17	A17
C90XA20#1163	4094	WT		28	H	H
C90XA20#1163	4095	<i>nip</i>		28	A17	A17
C90XA20#1163	4096	WT		28	H	H
C90XA20#1163	4097	<i>nip</i>		33	A17	A17
C90XA20#1163	4098	<i>nip</i>		33	A17	A17
C90XA20#1180	4099	WT		28	A20	A20
C90XA20#1180	4100	WT		28	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1180	4101	WT		28	H	H
C90XA20#1180	4102	WT		28	A20	A20
C90XA20#1180	4103	WT		28,32	H	H
C90XA20#1180	4104	WT		28	H	H
C90XA20#1180	4105	WT		28	A20	A20
C90XA20#1180	4106	WT		28	H	H
C90XA20#1180	4107	WT		28	H	H
C90XA20#1180	4108	WT		28	H	H
C90XA20#1180	4109	<i>nip</i>		28,32	A17	A17
C90XA20#1180	4110	<i>nip</i>		29	A17	A17
C90XA20#1180	4111	<i>nip</i>		29	A17	A17
C90XA20#1180	4112	WT		29	H	H
C90XA20#1180	4113	WT		29	H	H
C90XA20#1180	4114	<i>nip</i>		29	H	H
C90XA20#1180	4115	WT		29	H	H
C90XA20#1180	4116	<i>nip</i>		33	H	H
C90XA20#1180	4117	WT	Confirmed	33,38	A20	H
C90XA20#1180	4118	<i>nip</i>		33	A17	A17
C90XA20#1180	4119	WT		33	H	H
C90XA20#1180	4120	WT		33	H	H
C90XA20#1180	4121	WT		33	H	H
C90XA20#1180	4122	WT		33,37	H	H
C90XA20#1180	4123	WT	Confirmed	33,38	A20	H
C90XA20#1180	4124	WT		33	H	H
C90XA20#1180	4125	WT		33	H	H
C90XA20#1180	4126	WT		33	H	H
C90XA20#1180	4127	<i>nip</i>		33	A17	A17
C90XA20#1180	4128	WT		33	A20	A20
C90XA20#1179	4129	WT		33	A20	A20
C90XA20#1179	4130	<i>nip</i>		33	A17	A17
C90XA20#1179	4131	WT		33	H	H
C90XA20#1179	4132	WT		33	A20	A20
C90XA20#1179	4133	<i>nip</i>		33	A17	A17
C90XA20#1179	4134	<i>nip</i>		33	A17	A17
C90XA20#1179	4135	WT	Confirmed	34,38	H	A20
C90XA20#1179	4136	<i>nip</i>		29	A17	A17
C90XA20#1179	4137	<i>nip</i>		29	A17	A17
C90XA20#1179	4138	<i>nip</i>		29	A17	A17
C90XA20#1179	4139	WT		29	H	H
C90XA20#1179	4140	<i>nip</i>		29	A17	A17
C90XA20#1179	4141	WT		29	H	H
C90XA20#1179	4142	WT		29	H	H
C90XA20#1179	4143	WT		29	H	H
C90XA20#1179	4144	WT		29	H	H
C90XA20#1179	4145	<i>nip</i>		29	A17	A17
C90XA20#1179	4146	WT		29	H	H
C90XA20#1179	4147	<i>nip</i>		29	A17	A17
C90XA20#1179	4148	WT		29	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1179	4149	WT		29	H	H
C90XA20#1179	4150	WT		29	H	H
C90XA20#1179	4151	WT		29	H	H
C90XA20#1179	4152	WT		29	H	H
C90XA20#1188	4153	<i>nip</i>		29	H	H
C90XA20#1188	4154	WT		29,33	H	H
C90XA20#1188	4155	WT		29	H	H
C90XA20#1188	4156	WT		29	H	H
C90XA20#1188	4157	WT		29	H	H
C90XA20#1188	4158	<i>nip</i>		29	A17	A17
C90XA20#1188	4159	<i>nip</i>		29	A17	A17
C90XA20#1188	4160	WT		29	H	H
C90XA20#1188	4161	WT		29	H	H
C90XA20#1188	4162	<i>nip</i>		29	A17	A17
C90XA20#1188	4163	WT		29	A20	A20
C90XA20#1188	4164	<i>nip</i>		29	A17	A17
C90XA20#1188	4165	<i>nip</i>		29	A17	A17
C90XA20#1188	4166	WT		29	H	H
C90XA20#1188	4167	WT		29	A20	A20
C90XA20#1188	4168	WT		29	H	H
C90XA20#1188	4169	WT		29	A20	A20
C90XA20#1188	4170	<i>nip</i>		29	A17	A17
C90XA20#1188	4171	WT		29,33	H	H
C90XA20#1188	4172	WT		29	H	H
C90XA20#1188	4173	WT		29	H	H
C90XA20#1188	4174	WT		29	H	H
C90XA20#1177	4175	WT	Confirmed	29,34	A20	H
C90XA20#1177	4176	WT		39	H	H
C90XA20#1177	4177	WT		36	H	H
C90XA20#1177	4178	<i>nip</i>		36	H	H
C90XA20#1177	4179	<i>nip</i>		36	A17	A17
C90XA20#1177	4180	WT		36	H	H
C90XA20#1177	4181	WT		36	H	H
C90XA20#1177	4182	WT		36	A20	A20
C90XA20#1177	4183	?		36	H	H
C90XA20#1177	4184	WT		36,39	H	H
C90XA20#1177	4185	WT		36	A20	A20
C90XA20#1177	4186	<i>nip</i>		36	A17	A17
C90XA20#1177	4187	WT		36	A20	A20
C90XA20#1177	4188	<i>nip</i>		36	A17	A17
C90XA20#1177	4189	<i>nip</i>		36	A17	A17
C90XA20#1177	4190	<i>nip</i>		36	A17	A17
C90XA20#1177	4191	WT		36	H	H
C90XA20#1177	4192	WT		36,39	H	H
C90XA20#1177	4193	<i>nip</i>		36	A17	A17
C90XA20#1177	4194	<i>nip</i>		36	A17	A17
C90XA20#1177	4195	WT		36	A20	A20
C90XA20#1177	4196	WT		29	A20	A20

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1177	4197	WT	Confirmed	29,33	H	A17
C90XA20#1177	4198	WT		29	A20	A20
C90XA20#1177	4199	<i>nip</i>		29	A17	A17
C90XA20#1177	4200	WT		32	H	H
C90XA20#1177	4201	<i>nip</i>		29	A17	A17
C90XA20#1177	4202	<i>nip</i>		29	A17	A17
C90XA20#1177	4203	<i>nip</i>		29	A17	A17
C90XA20#1177	4204	WT		32	H	H
C90XA20#1177	4205	WT		29	H	H
C90XA20#1177	4206	WT		29	A20	A20
C90XA20#1177	4207	<i>nip</i>		32	A17	A17
C90XA20#1177	4208	WT		29	H	H
C90XA20#1176	4209	WT		33	H	H
C90XA20#1176	4210	WT		33	A20	A20
C90XA20#1176	4211	WT		33	A20	A20
C90XA20#1176	4212	WT		33	H	H
C90XA20#1176	4213	WT		33	H	H
C90XA20#1176	4214	WT		33	H	H
C90XA20#1176	4215	<i>nip</i>		33	A17	A17
C90XA20#1176	4216	WT		33	H	H
C90XA20#1176	4217	WT		33	H	H
C90XA20#1176	4218	<i>nip</i>		33	A17	A17
C90XA20#1176	4219	<i>nip</i>		33	A17	A17
C90XA20#1176	4220	WT		33	A20	A20
C90XA20#1176	4221	WT		33	H	H
C90XA20#1176	4222	<i>nip</i>		33	A17	A17
C90XA20#1176	4223	WT		33	H	H
C90XA20#1186	4224	WT		37	H	H
C90XA20#1186	4225	<i>nip</i>		33	A17	A17
C90XA20#1186	4226	WT		33	A20	A20
C90XA20#1186	4227	<i>nip</i>	Confirmed	33,38,40	A17	H
C90XA20#1186	4228	<i>nip</i>		33	A17	A17
C90XA20#1186	4229	<i>nip</i>		33	A17	A17
C90XA20#1186	4230	<i>nip</i>		33,37	A17	A17
C90XA20#1186	4231	<i>nip</i>		33	A17	A17
C90XA20#1186	4232	WT		29,34	H	H
C90XA20#1186	4233	WT		29	H	H
C90XA20#1186	4234	WT		29	H	H
C90XA20#1186	4235	WT		29	H	H
C90XA20#1186	4236	WT		29	H	H
C90XA20#1186	4237	WT		29	H	H
C90XA20#1186	4238	WT	Confirmed	29,34	A20	H
C90XA20#1186	4239	WT		29	A20	A20
C90XA20#1186	4240	WT		29	H	H
C90XA20#1186	4241	WT		29	A20	A20
C90XA20#1186	4242	WT		29	A20	A20
C90XA20#1199	4243	WT		29	H	H
C90XA20#1199	4244	WT		29	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1199	4245	WT		29	H	H
C90XA20#1199	4246	<i>nip</i>		29	A17	A17
C90XA20#1199	4247	<i>nip</i>		37,39	A17	A17
C90XA20#1199	4248	WT	Confirmed	32,38	H	A17
C90XA20#1199	4249	WT		32	H	H
C90XA20#1199	4250	WT		37	H	H
C90XA20#1199	4251	<i>nip</i>		32	A17	A17
C90XA20#1199	4252	<i>nip</i>		37	A17	A17
C90XA20#1199	4253	WT		32	H	H
C90XA20#1199	4254	WT		32	H	H
C90XA20#1199	4255	WT	Confirmed	32,38	H	A20
C90XA20#1199	4256	WT		32	H	H
C90XA20#1199	4257	WT		32	H	H
C90XA20#1199	4258	WT		32	H	H
C90XA20#1199	4259	WT		32	H	H
C90XA20#1199	4260	WT		32	H	H
C90XA20#1199	4261	<i>nip</i>		32	A17	A17
C90XA20#1199	4262	WT		32	H	H
C90XA20#1199	4263	<i>nip</i>		37	A17	A17
C90XA20#1199	4264	WT		32	H	H
C90XA20#1199	4265	WT		37	A20	A20
C90XA20#1199	4266	WT		32	H	H
C90XA20#1199	4267	<i>nip</i>		32	A17	A17
C90XA20#1207	4268	WT		37	A20	A20
C90XA20#1207	4269	<i>nip</i>		37	A17	A17
C90XA20#1207	4270	<i>nip</i>		37	A17	A17
C90XA20#1207	4271	WT		37	H	H
C90XA20#1207	4272	WT		37,39	H	H
C90XA20#1207	4273	<i>nip</i>		37	A17	A17
C90XA20#1207	4274	<i>nip</i>		37	A17	A17
C90XA20#1207	4275	WT		37	H	H
C90XA20#1207	4276	WT		37	H	H
C90XA20#1207	4277	WT		37,39	H	H
C90XA20#1207	4278	WT		37	H	H
C90XA20#1207	4279	WT		37	H	H
C90XA20#1207	4280	WT		37	H	H
C90XA20#1207	4281	WT		37	A20	A20
C90XA20#1207	4282	WT		37	A20	A20
C90XA20#1207	4283	WT		37	H	H
C90XA20#1207	4284	WT		37	H	H
C90XA20#1207	4285	WT		37	H	H
C90XA20#1207	4286	WT		37	H	H
C90XA20#1207	4287	WT	Confirmed	37,38	A20	H
C90XA20#1207	4288	WT		37	A20	A20
C90XA20#1207	4289	WT		37	A20	A20
C90XA20#1207	4290	<i>nip</i>		37	A17	A17
C90XA20#1207	4291	<i>nip</i>		37	A17	A17
C90XA20#1207	4292	<i>nip</i>		37	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1207	4293	WT		37	H	H
C90XA20#1207	4294	WT		37	A20	A20
C90XA20#1207	4295	<i>nip</i>		37	A17	A17
C90XA20#1207	4296	WT		37	A20	A20
C90XA20#1207	4297	WT		37	H	H
C90XA20#1207	4298	WT		37	H	H
C90XA20#1207	4299	WT		37	H	H
C90XA20#1207	4300	WT		37	A20	A20
C90XA20#1207	4301	WT		37	H	H
C90XA20#1207	4302	WT		37	H	H
C90XA20#1207	4303	<i>nip</i>		37	A17	A17
C90XA20#1207	4304	WT		37	H	H
C90XA20#1207	4305	WT		37	H	H
C90XA20#1207	4306	WT		37	A20	A20
C90XA20#1207	4307	WT		37	H	H
C90XA20#1207	4308	WT		36	H	H
C90XA20#1207	4309	WT		36	H	H
C90XA20#1207	4310	<i>nip</i>		36	A17	A17
C90XA20#1207	4311	WT		36	H	H
C90XA20#1207	4312	<i>nip</i>		36	A17	A17
C90XA20#1207	4313	WT		36	H	H
C90XA20#1207	4314	<i>nip</i>		36	A20	A20
C90XA20#1207	4315	<i>nip</i>		36	A17	A17
C90XA20#1207	4316	WT		36	H	H
C90XA20#1207	4317	WT		36	H	H
C90XA20#1207	4318	<i>nip</i>		36	A17	A17
C90XA20#1207	4319	WT		36	A20	A20
C90XA20#1207	4320	<i>nip</i>		36	A17	A17
C90XA20#1207	4321	<i>nip</i>		36	A17	A17
C90XA20#1207	4322	WT		36	A20	A20
C90XA20#1207	4323	<i>nip</i>		36	H	H
C90XA20#1207	4324	WT		36	A20	A20
C90XA20#1359	4325	WT		36	H	H
C90XA20#1359	4326	WT		36	H	H
C90XA20#1359	4327	WT		37	H	H
C90XA20#1359	4328	WT		37	H	H
C90XA20#1359	4329	<i>nip</i>		37	A17	A17
C90XA20#1359	4330	WT		37	H	H
C90XA20#1359	4331	WT		37	H	H
C90XA20#1359	4332	WT		37	H	H
C90XA20#1359	4333	WT		37	H	H
C90XA20#1359	4334	WT		37	H	H
C90XA20#1359	4335	WT		37	H	H
C90XA20#1359	4336	<i>nip</i>		37	A17	A17
C90XA20#1359	4337	WT		37	H	H
C90XA20#1359	4338	<i>nip</i>		37	A17	A17
C90XA20#1359	4339	WT		37	A20	A20
C90XA20#1359	4340	<i>nip</i>		37	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1359	4341	WT		37	H	H
C90XA20#1359	4342	WT		37	H	H
C90XA20#1366	4343	<i>nip</i>		37	A17	A17
C90XA20#1366	4344	WT		37	H	H
C90XA20#1366	4346	WT		32	A20	A20
C90XA20#1366	4347	WT		32	H	H
C90XA20#1366	4348	WT		32,37	H	H
C90XA20#1366	4349	<i>nip</i>		32	A17	A17
C90XA20#1366	4350	WT		32	H	H
C90XA20#1366	4351	WT		32	H	H
C90XA20#1366	4352	<i>nip</i>		32	A17	A17
C90XA20#1366	4353	WT		32	H	H
C90XA20#1366	4354	WT		32	A20	A20
C90XA20#1366	4355	WT		32	H	H
C90XA20#1366	4356	WT		32	H	H
C90XA20#1366	4357	WT		32	A20	A20
C90XA20#1366	4358	WT		32	H	H
C90XA20#1366	4359	WT		32	H	H
C90XA20#1366	4360	WT		32	H	H
C90XA20#1366	4361	WT		32	A17	A17
C90XA20#1366	4362	<i>nip</i>		32	A17	A17
C90XA20#1366	4363	WT		32	A20	A20
C90XA20#1366	4364	WT		32	H	H
C90XA20#1366	4365	<i>nip</i>		32	H	H
C90XA20#1366	4366	WT		33	H	H
C90XA20#1366	4367	WT		33	H	H
C90XA20#1366	4368	WT		33	H	H
C90XA20#1366	4369	WT		33	H	H
C90XA20#1366	4370	<i>nip</i>		33	A17	A17
C90XA20#1366	4371	WT		33	A20	A20
C90XA20#1366	4372	WT		33	H	H
C90XA20#1366	4373	<i>nip</i>		33	A17	A17
C90XA20#1366	4374	WT		33	A20	A20
C90XA20#1366	4375	<i>nip</i>		33	A17	A17
C90XA20#1366	4376	WT		33	H	H
C90XA20#1366	4377	WT		33	A20	A20
C90XA20#1366	4378	WT		33	A20	A20
C90XA20#1366	4379	WT		33	H	H
C90XA20#1366	4380	WT		33	H	H
C90XA20#1366	4381	<i>nip</i>		33	A17	A17
C90XA20#1366	4382	WT		33	H	H
C90XA20#1366	4383	<i>nip</i>		33	A17	A17
C90XA20#1366	4384	WT		33	H	H
C90XA20#1366	4385	WT		33	A20	A20
C90XA20#1366	4386	WT		34,37	H	H
C90XA20#1366	4387	WT		34,37	A20	A20
C90XA20#1366	4388	WT		34,37	A20	A20
C90XA20#1366	4389	WT		34,37	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1366	4390	WT		34	A20	A20
C90XA20#1366	4391	<i>nip</i>		34,37	A17	A17
C90XA20#1366	4392	<i>nip</i>		34	A17	A17
C90XA20#1366	4393	<i>nip</i>		37	A17	A17
C90XA20#1366	4394	WT		34	H	H
C90XA20#1366	4395	<i>nip</i>		34	A17	A17
C90XA20#1366	4396	WT		34,37	A20	A20
C90XA20#1366	4397	<i>nip</i>		34	A17	A17
C90XA20#1366	4398	WT		34	H	H
C90XA20#1366	4399	WT		34,37	H	H
C90XA20#1204	4400	<i>nip</i>		34,37	A17	A17
C90XA20#1204	4401	<i>nip</i>		34	A17	A17
C90XA20#1204	4403	WT		34,37,39	H	H
C90XA20#1204	4404	WT		34,37	H	H
C90XA20#1204	4405	WT		34	A20	A20
C90XA20#1204	4406	WT		36	A20	A20
C90XA20#1204	4407	WT		36	A20	A20
C90XA20#1204	4408	WT		36	H	H
C90XA20#1204	4409	WT		36	H	H
C90XA20#1204	4410	WT		36	H	H
C90XA20#1204	4411	WT		36	H	H
C90XA20#1204	4412	WT		36,39	H	H
C90XA20#1204	4413	WT		36	A20	A20
C90XA20#1204	4414	<i>nip</i>		36	A17	A17
C90XA20#1204	4415	WT		37,39	H	H
C90XA20#1204	4416	<i>nip</i>		37	A17	A17
C90XA20#1204	4417	WT		37,39	H	H
C90XA20#1204	4418	WT		37	H	H
C90XA20#1204	4419	WT	confirmed	37,39,44	A17	H
C90XA20#1204	4420	WT		37	H	H
C90XA20#1204	4421	WT		37	H	H
C90XA20#1204	4423	<i>nip</i>		37,39	A17	A17
C90XA20#1204	4424	<i>nip</i>		39	A17	A17
C90XA20#1204	4425	<i>nip</i>		39	A17	A17
C90XA20#1204	4426	WT		39,42	A20	A20
C90XA20#1204	4427	WT		39	A20	A20
C90XA20#1204	4428	WT		39	H	H
C90XA20#1204	4429	WT		39	A20	A20
C90XA20#1204	4430	<i>nip</i>		39	A17	A17
C90XA20#1204	4431	WT		39	A20	A20
C90XA20#1176	4433	WT		39	H	H
C90XA20#1176	4434	WT		39	H	H
C90XA20#1176	4435	WT		39	H	H
C90XA20#1176	4436	WT		39	H	H
C90XA20#1176	4437	<i>nip</i>		39	A17	A17
C90XA20#1176	4438	<i>nip</i>		39	A17	A17
C90XA20#1176	4439	WT		39,42	H	H
C90XA20#1176	4440	WT		39	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1176	4441	WT		39	H	H
C90XA20#1176	4442	WT		39	A20	A20
C90XA20#1176	4443	WT		39	A20	A20
C90XA20#1176	4444	<i>nip</i>		39	A17	A17
C90XA20#1176	4445	<i>nip</i>		39	A17	A17
C90XA20#1216	4446	<i>nip</i>		32	A17	A17
C90XA20#1216	4447	WT		32	H	H
C90XA20#1216	4448	WT		32	H	H
C90XA20#1216	4449	<i>nip</i>		32	A17	A17
C90XA20#1216	4450	WT		39	H	H
C90XA20#1216	4451	WT		39	H	H
C90XA20#1216	4452	WT		39	H	H
C90XA20#1216	4453	WT		39,42	H	H
C90XA20#1216	4454	<i>nip</i>		39	A17	A17
C90XA20#1216	4455	<i>nip</i>		39	A17	A17
C90XA20#1216	4456	WT		39	H	H
C90XA20#1216	4457	WT		39	H	H
C90XA20#1216	4458	WT		39	H	H
C90XA20#1216	4459	WT		39	H	H
C90XA20#1216	4460	WT		39	H	H
C90XA20#1216	4461	WT		39	A20	A20
C90XA20#1216	4462	WT		39	H	H
C90XA20#1216	4464	WT		39,42	H	H
C90XA20#1216	4465	WT		39	H	H
C90XA20#1216	4466	<i>nip</i>		39	A17	A17
C90XA20#1216	4467	<i>nip</i>		39	A17	A17
C90XA20#1216	4468	WT		39,42	H	H
C90XA20#1216	4469	<i>nip</i>		39	A17	A17
C90XA20#1216	4470	WT		39	H	H
C90XA20#1216	4471	WT		39	H	H
C90XA20#1216	4473	WT	confirmed	39,44	H	A17
C90XA20#1216	4474	WT		39	H	H
C90XA20#1216	4475	<i>nip</i>		39	A17	A17
C90XA20#1216	4476	WT		39	H	H
C90XA20#1216	4477	WT		39	A20	A20
C90XA20#1216	4478	WT		39	H	H
C90XA20#1216	4479	WT		39	H	H
C90XA20#1216	4480	<i>nip</i>		33	A17	A17
C90XA20#1216	4481	WT		33	A20	A20
C90XA20#1216	4482	WT		33	A17	A17
C90XA20#1216	4483	WT		33	H	H
C90XA20#1216	4484	WT		33	H	H
C90XA20#1216	4485	WT		33	H	H
C90XA20#1216	4486	WT		33	A20	A20
C90XA20#1216	4487	WT		33	A20	A20
C90XA20#1216	4488	WT		33	H	H
C90XA20#1216	4489	WT		33	A20	A20

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1216	4490	<i>nip</i>		33	A17	A17
C90XA201208	4491	<i>nip</i>		33	A17	A17
C90XA201208	4492	<i>nip</i>		33	A20	A20
C90XA201208	4493	WT		33	A17	A17
C90XA201208	4494	<i>nip</i>		33	A17	A17
C90XA201208	4495	WT		33,37	H	H
C90XA201208	4496	WT		33	H	H
C90XA201208	4497	WT		33	H	H
C90XA201208	4498	WT		33,37	A20	A20
C90XA201208	4499	WT		33,38	H	H
C90XA201208	4500	WT		33	H	H
C90XA201208	4501	WT		33	H	H
C90XA201208	4502	WT		33	H	H
C90XA201208	4503	WT		33	A20	A20
C90XA201208	4504	WT		33	H	H
C90XA201208	4505	?		33	H	H
C90XA201208	4506	WT		44	H	H
C90XA201208	4507	<i>nip</i>		44	A17	A17
C90XA201208	4508	WT		39	A20	A20
C90XA201208	4509	WT		39	A20	A20
C90XA201208	4510	WT		39	A20	A20
C90XA201208	4511	<i>nip</i>		39	A17	A17
C90XA201208	4512	WT		39,42	H	H
C90XA201208	4513	WT		39	H	H
C90XA201208	4514	WT		39,42	H	H
C90XA201208	4515	WT		39	H	H
C90XA201208	4516	<i>nip</i>		39	A20	A20
C90XA201208	4517	WT		39	A17	A17
C90XA201208	4518	WT		39	H	H
C90XA201208	4519	WT		39,44	H	H
C90XA201208	4520	WT		39	H	H
C90XA20#1308	4521	WT	confirmed	39,44	H	A17
C90XA20#1308	4522	<i>nip</i>		39	A17	A17
C90XA20#1308	4524	WT		39,42	H	H
C90XA20#1308	4525	WT		39	H	H
C90XA20#1308	4526	WT		39	H	H
C90XA20#1308	4527	WT		39	H	H
C90XA20#1308	4528	WT		39	H	H
C90XA20#1308	4529	<i>nip</i>		39	H	H
C90XA20#1308	4530	WT		39,42	H	H
C90XA20#1308	4531	WT		39	H	H
C90XA20#1308	4532	WT		39	H	H
C90XA20#1308	4533	WT		39	H	H
C90XA20#1308	4534	WT	confirmed	39,44	A20	H
C90XA20#1308	4535	<i>nip</i>		39	A17	A17
C90XA20#1308	4536	WT		39	A20	A20
C90XA20#1308	4537	WT		39	H	H
C90XA20#1308	4538	<i>nip</i>		40	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1308	4539	WT		40	H	H
C90XA20#1309	4540	WT		40	A17	A17
C90XA20#1309	4541	<i>nip</i>		40	H	H
C90XA20#1309	4542	WT		40	A17	A17
C90XA20#1309	4543	WT		40	H	H
C90XA20#1309	4544	WT		40	H	H
C90XA20#1309	4545	WT		40	H	H
C90XA20#1309	4546	WT		40,42	H	H
C90XA20#1309	4547	WT		40	H	H
C90XA20#1309	4548	WT		40	H	H
C90XA20#1309	4549	<i>nip</i>		40	A17	A17
C90XA20#1309	4550	WT		40	H	H
C90XA20#1309	4551	WT	confirmed	38,44	A20	H
C90XA20#1309	4552	WT	confirmed	38,44	A20	H
C90XA20#1309	4553	WT		38	H	H
C90XA20#1309	4554	WT		38	H	H
C90XA20#1309	4555	<i>nip</i>		38	A17	A17
C90XA20#1309	4556	<i>nip</i>		38	A17	A17
C90XA20#1309	4557	WT		38	H	H
C90XA20#1309	4558	WT		38	H	H
C90XA20#1309	4559	<i>nip</i>		38	A17	A17
C90XA20#1309	4560	WT		38	H	H
C90XA20#1309	4561	WT		38	H	H
C90XA20#1309	4562	WT		38	H	H
C90XA20#1309	4563	WT		38	H	H
C90XA20#1309	4564	<i>nip</i>		38	A17	A17
C90XA20#1309	4565	WT		38,44	H	H
C90XA20#1309	4566	WT		38,44	H	H
C90XA20#1309	4567	<i>nip</i>		38	A17	A17
C90XA20#1309	4568	WT		38,42	H	H
C90XA20#1309	4569	<i>nip</i>		38	A17	A17
C90XA20#1309	4570	WT		38	H	H
C90XA20#1309	4571	WT		40	H	H
C90XA20#1309	4572	WT		40	H	H
C90XA20#1309	4573	WT		40	H	H
C90XA20#1309	4574	WT		40	H	H
C90XA20#1309	4575	WT		40	H	H
C90XA20#1309	4576	WT		40	H	H
C90XA20#1203	4577	WT		40,42	H	H
C90XA20#1203	4578	WT		40	H	H
C90XA20#1203	4579	WT		40	A17	A17
C90XA20#1203	4580	WT		40	H	H
C90XA20#1203	4581	WT		40	H	H
C90XA20#1203	4582	WT		40	H	H
C90XA20#1203	4583	WT		40	H	H
C90XA20#1203	4584	WT		40	H	H
C90XA20#1203	4585	WT		40	H	H
C90XA20#1203	4586	<i>nip</i>		40	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1203	4587	WT		40	A20	A20
C90XA20#1203	4588	<i>nip</i>		40	H	H
C90XA20#1203	4589	WT		40	A17	A17
C90XA20#1203	4590	WT		40	H	H
C90XA20#1203	4591	WT		40	H	H
C90XA20#1203	4592	WT		40	H	H
C90XA20#1203	4593	<i>nip</i>		40	A17	A17
C90XA20#1383	4594	WT		34	H	H
C90XA20#1383	4595	WT		34	H	H
C90XA20#1383	4596	WT		34	H	H
C90XA20#1383	4597	WT		34	H	H
C90XA20#1383	4598	WT		34	H	H
C90XA20#1383	4599	WT		34	H	H
C90XA20#1383	4600	WT		34	H	H
C90XA20#1383	4601	WT		34	H	H
C90XA20#1383	4602	WT		34	A20	A20
C90XA20#1383	4603	WT		34,38	A20	A20
C90XA20#1383	4604	WT		34	A20	A20
C90XA20#1383	4605	<i>nip</i>		34	A17	A17
C90XA20#1383	4606	WT		34	H	H
C90XA20#1383	4607	WT		34	H	H
C90XA20#1383	4608	WT		34	A20	A20
C90XA20#1383	4609	WT?		34	A20	A20
C90XA20#1383	4610	<i>nip</i>		34	A17	A17
C90XA20#1383	4611	WT		34	H	H
C90XA20#1383	4612	<i>nip</i>		34	A17	A17
C90XA20#1383	4613	WT		34	A20	A20
C90XA20#1383	4614	WT		36	H	H
C90XA20#1383	4615	<i>nip</i>		36	A17	A17
C90XA20#1383	4616	WT		36	H	H
C90XA20#1383	4617	WT		36	H	H
C90XA20#1383	4618	WT		36	H	H
C90XA20#1383	4619	WT		36	A20	A20
C90XA20#1383	4620	<i>nip</i>		36	A17	A17
C90XA20#1383	4621	WT		36	A20	A20
C90XA20#1383	4622	WT		36	A20	A20
C90XA20#1383	4623	WT		36	A20	A20
C90XA20#1383	4624	WT		36	H	H
C90XA20#1383	4625	WT		36	H	H
C90XA20#1381	4626	?		36	A20	A20
C90XA20#1381	4627	WT		36	H	H
C90XA20#1381	4628	WT		36	H	H
C90XA20#1381	4629	WT		36	H	H
C90XA20#1381	4630	<i>nip</i>		36,40	A17	A17
C90XA20#1381	4631	WT		36	A20	A20
C90XA20#1381	4632	WT		36	H	H
C90XA20#1381	4633	WT		36	H	H
C90XA20#1381	4634	<i>nip</i>		34	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1381	4635	<i>nip</i>		34	A17	A17
C90XA20#1381	4636	WT		34	H	H
C90XA20#1381	4637	WT		34	H	H
C90XA20#1381	4638	WT		34	H	H
C90XA20#1381	4639	<i>nip</i>		34	A17	A17
C90XA20#1381	4640	<i>nip</i>		34	A17	A17
C90XA20#1381	4641	WT	Confirmed	34,38	H	A20
C90XA20#1381	4642	WT		34	H	H
C90XA20#1381	4643	WT		34	A17	A17
C90XA20#1381	4644	WT		34	H	H
C90XA20#1381	4645	WT		34	H	H
C90XA20#1381	4646	WT		34	H	H
C90XA20#1381	4647	WT		34	H	H
C90XA20#1381	4648	WT		34	A17	A17
C90XA20#1381	4649	WT		34	H	H
C90XA20#1381	4650	WT		34	A20	A20
C90XA20#1381	4651	WT		34	H	H
C90XA20#1381	4652	WT		34	H	H
C90XA20#1381	4653	<i>nip</i>		34	A17	A17
C90XA20#1381	4654	WT		34	H	H
C90XA20#1381	4655	WT		34	H	H
C90XA20#1381	4656	<i>nip</i>		34	A17	A17
C90XA20#1381	4657	WT		34	A20	A20
C90XA20#1381	4658	WT		34	A20	A20
C90XA20#1381	4659	WT		34	A20	A20
C90XA20#1381	4660	WT		34	H	H
C90XA20#1381	4661	<i>nip</i>		34	A17	A17
C90XA20#1381	4662	WT		34	H	H
C90XA20#1381	4663	<i>nip</i>		34	A17	A17
C90XA20#1381	4664	<i>nip</i>		34	A20	A20
C90XA20#1381	4665	WT		34	H	H
C90XA20#1381	4666	WT		34	H	H
C90XA20#1381	4667	WT		34	A20	A20
C90XA20#1381	4668	WT		34	H	H
C90XA20#1381	4669	WT		34	H	H
C90XA20#1381	4670	WT		34	H	H
C90XA20#1381	4671	WT		34	H	H
C90XA20#1381	4672	WT		34	A20	A20
C90XA20#1381	4673	WT		34	H	H
C90XA20#1381	4674	WT		36	A20	A20
C90XA20#1381	4675	WT		36	H	H
C90XA20#1381	4676	WT		36	A20	A20
C90XA20#1381	4677	WT		36	H	H
C90XA20#1381	4678	WT		36	A20	A20
C90XA20#1381	4679	<i>nip</i>		36,40	A17	A17
C90XA20#1389	4680	WT	Confirmed	36,38	H	A17
C90XA20#1389	4681	WT		36	A20	A20
C90XA20#1389	4682	<i>nip</i>		36	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1389	4683	WT		36	H	H
C90XA20#1389	4684	WT		36	H	H
C90XA20#1389	4685	WT		36	H	H
C90XA20#1389	4686	WT		36	A20	A20
C90XA20#1389	4687	<i>nip</i>		36	A17	A17
C90XA20#1389	4688	WT		36	H	H
C90XA20#1389	4689	WT		36	H	H
C90XA20#1389	4690	WT		36	H	H
C90XA20#1389	4691	WT		36	H	H
C90XA20#1389	4692	WT		36	H	H
C90XA20#1389	4693	<i>nip</i>		36	A17	A17
C90XA20#1389	4694	<i>nip</i>		38	A17	A17
C90XA20#1389	4695	WT		38	H	H
C90XA20#1389	4696	WT		38	A20	A20
C90XA20#1389	4697	WT		38	H	H
C90XA20#1389	4698	WT		38	H	H
C90XA20#1389	4699	<i>nip</i>		38	A17	A17
C90XA20#1126	4700	WT		38	A20	A20
C90XA20#1126	4701	WT		38	A20	A20
C90XA20#1126	4702	WT		38	A20	A20
C90XA20#1126	4703	WT		38,42	A20	A20
C90XA20#1126	4704	WT		38	A20	A20
C90XA20#1126	4705	?		38	A20	A20
C90XA20#1126	4706	WT		38	A20	A20
C90XA20#1126	4707	WT		38	A20	A20
C90XA20#1126	4708	WT		38	A20	A20
C90XA20#1126	4709	WT		38	A20	A20
C90XA20#1126	4710	WT		38	A20	A20
C90XA20#1126	4711	WT		38	A20	A20
C90XA20#1126	4712	WT		38	A20	A20
C90XA20#1126	4713	WT		38	A20	A20
C90XA20#1126	4714	WT		34	A20	A20
C90XA20#1126	4715	WT		34	A20	A20
C90XA20#1126	4716	WT		34	A20	A20
C90XA20#1126	4717	WT		40	A20	A20
C90XA20#1126	4718	WT		40	A20	A20
C90XA20#1126	4719	WT		40	A20	A20
C90XA20#1126	4720	?		40	A17	A17
C90XA20#1126	4721	WT		34,38,42	A20	A20
C90XA20#1126	4722	WT		34	A20	A20
C90XA20#1126	4723	WT		34	A20	A20
C90XA20#1126	4724	WT		34	A20	A20
C90XA20#1126	4725	WT		34	A20	A20
C90XA20#1126	4726	?		34	A20	A20
C90XA20#1126	4727	<i>nip</i>		35	A20	A20
C90XA20#1126	4728	WT		35	A17	A17
C90XA20#1126	4729	WT		35	A20	A20
C90XA20#1126	4731	WT		35	A20	A20

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1126	4732	WT		35	A20	A20
C90XA20#1126	4733	WT		35	H	H
C90XA20#1126	4734	WT		35	A20	A20
C90XA20#1126	4735	WT		35	A20	A20
C90XA20#1126	4736	WT		35	A20	A20
C90XA20#1126	4737	WT		35,38,44	A20	A20
C90XA20#1126	4738	WT		35	A20	A20
C90XA20#1219	4739	WT		35	A20	A20
C90XA20#1219	4740	?		35	A20	A20
C90XA20#1219	4741	WT		35	H	H
C90XA20#1219	4742	WT		35	H	H
C90XA20#1219	4743	<i>nip</i>		35	A17	A17
C90XA20#1219	4744	WT		35	H	H
C90XA20#1219	4745	WT		35	A20	A20
C90XA20#1219	4746	WT		35	A20	A20
C90XA20#1219	4747	WT		35	H	H
C90XA20#1219	4748	WT		35	A20	A20
C90XA20#1219	4749	<i>nip</i>		35	A17	A17
C90XA20#1219	4750	WT		38,40	H	H
C90XA20#1219	4751	WT		35	H	H
C90XA20#1219	4752	WT		35	H	H
C90XA20#1219	4753	WT	Confirmed	35,40	H	A17
C90XA20#1219	4754	WT		35	H	H
C90XA20#1219	4755	WT		35	A20	A20
C90XA20#1219	4756	WT		35	A20	A20
C90XA20#1219	4757	WT		35	H	H
C90XA20#1219	4758	WT		35	A20	A20
C90XA20#1219	4759	WT		35	A20	A20
C90XA20#1219	4760	WT		35	H	H
C90XA20#1219	4761	WT		35	A20	A20
C90XA20#1219	4762	WT		35	A20	A20
C90XA20#1219	4763	WT		35	H	H
C90XA20#1219	4764	<i>nip</i>	Confirmed	35,38	H	A17
C90XA20#1219	4765	WT		35	H	H
C90XA20#1219	4766	WT		35,38,40	A20	A20
C90XA20#1219	4767	WT		35,38,40	A20	A20
C90XA20#1219	4768	WT		35	A20	A20
C90XA20#1219	4769	<i>nip</i>	Confirmed	35,38	A17	H
C90XA20#1219	4770	WT		35	H	H
C90XA20#1209	4771	<i>nip</i>		35,38,40	A17	A17
C90XA20#1209	4772	WT		35	A20	A20
C90XA20#1209	4773	WT		35	H	H
C90XA20#1209	4774	<i>nip</i>		35	A17	A17
C90XA20#1209	4775	WT		35	A20	A20
C90XA20#1209	4776	WT		35	A20	A20
C90XA20#1209	4777	<i>nip</i>		35	A17	A17
C90XA20#1209	4778	WT		35	H	H
C90XA20#1209	4779	WT		35	H	H

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1209	4780	WT		35	A20	A20
C90XA20#1209	4781	WT		35	H	H
C90XA20#1209	4782	<i>nip</i>		35	A17	A17
C90XA20#1209	4783	<i>nip</i>		35	A17	A17
C90XA20#1209	4784	WT		42	H	H
C90XA20#1209	4785	WT		35	H	H
C90XA20#1209	4786	WT		35	H	H
C90XA20#1209	4787	WT		35,38	A20	A20
C90XA20#1209	4788	WT		35	H	H
C90XA20#1209	4789	WT		35	H	H
C90XA20#1209	4790	WT		35	H	H
C90XA20#1209	4791	WT		35	H	H
C90XA20#1209	4792	WT		35	A20	A20
C90XA20#1209	4793	WT		35	H	H
C90XA20#1388	4794	WT		35	H	H
C90XA20#1388	4795	<i>nip</i>		35	A17	A17
C90XA20#1388	4796	WT		35	H	H
C90XA20#1388	4797	WT		35	H	H
C90XA20#1388	4798	WT		35	H	H
C90XA20#1388	4799	<i>nip</i>		35	A17	A17
C90XA20#1388	4800	WT		35	H	H
C90XA20#1388	4801	WT		35	H	H
C90XA20#1388	4802	<i>nip</i>		35	H	H
C90XA20#1388	4803	<i>nip</i>		35	A17	A17
C90XA20#1388	4804	WT		35	A20	A20
C90XA20#1388	4805	WT		35	H	H
C90XA20#1388	4806	WT		35	H	H
C90XA20#1388	4807	WT		35	H	H
C90XA20#1388	4808	WT		35	H	H
C90XA20#1388	4809	WT		35	A20	A20
C90XA20#1388	4810	<i>nip</i>		35	A17	A17
C90XA20#1388	4811	<i>nip</i>		35	A17	A17
C90XA20#1388	4812	WT		35	H	H
C90XA20#1388	4813	<i>nip</i>		35	A17	A17
C90XA20#1388	4814	<i>nip</i>		35	A17	A17
C90XA20#1388	4815	<i>nip</i>		35	A17	A17
C90XA20#1388	4816	WT		35,38	H	H
C90XA20#1388	4817	<i>nip</i>		35	A17	A17
C90XA20#1388	4818	WT		35,38	H	H
C90XA20#1388	4819	WT		42	H	H
C90XA20#1388	4820	WT		38	A20	A20
C90XA20#1388	4821	WT		38	H	H
C90XA20#1388	4822	WT		38	H	H
C90XA20#1388	4823	WT		38	A20	A20
C90XA20#1388	4824	WT		38	H	H
C90XA20#1388	4825	<i>nip</i>		38	A17	A17
C90XA20#1388	4826	WT		38	H	H
C90XA20#1388	4827	<i>nip</i>		38	A17	A17

Table 2.

Phenotyping And Genotyping Data For F3 Generation Of The *NIP* Mapping Population

Parents	Plant #	Phenotype	Notes	Plate #	146o17	23c16
C90XA20#1388	4828	WT		38	A20	A20
C90XA20#1388	4829	<i>nip</i>		38	A17	A17
C90XA20#1388	4830	WT		38	A20	A20
C90XA20#1388	4831	WT		38	A20	A20
C90XA20#1388	4832	WT	Confirmed	38,44	H	A20
C90XA20#1388	4833	<i>nip</i>		38	A17	A17
C90XA20#1388	4834	<i>nip</i>		36	A17	A17
C90XA20#1388	4835	<i>nip</i>		40	A17	A17
C90XA20#1388	4836	WT		38	H	H

Table 3. Phenotype And Genotyping Data For Recombinant Plants From F2 and F3 Generations
From *NIP* Mapping Population

Genotype	Phenotype	Plant#	Notes	146o17	ENBP	2D12	4L4	164n9	80720	23c16d
Recombinant Plants Obtained From F2 Generation of The <i>Nip</i> Mapping Population										
C90XA20#133	WT	964	REDO	A20	H					H
C90XA20#133	WT	965	REDO	A20	H					H
C90XA20#133	WT	967	REDO	A20	H					H
C90XA20#133	WT	970	confirmed	A20	H					H
C90XA20#133	WT	973	confirmed	A20	H		H	H	H	H
C90XA20#133	WT	974	confirmed	A20	H		H	H	H	H
C90XA20#133	WT	975	REDO	A20	H					H
C90XA20 281#2	WT	1007	REDO	A20	H					A20
C90XA20 278#	<i>nip</i>	1038	confirmed	A17	A17					H
C90XA20 278#	<i>nip</i>	1040	confirmed	A17	A17					H
C90XA20 278#	<i>nip</i>	1041	confirmed	A17	A17					H
C90XA20 278#	<i>nip</i>	1042	confirmed	A17	A17		A17	A17	H	H
C90XA20 278#	<i>nip</i>	1043	confirmed	A17	A17		A17	A17	H	H
C90XA20 278#	<i>nip</i>	1045	confirmed	A17	A17					H
C90XA20 278#	<i>nip</i>	1046	REDO	A17	A17					H
C90XA20 278#	<i>nip</i>	1047	confirmed	A17	A17					H
C90XA20 278#	<i>nip</i>	1048	REDO	H	A17					H
C90XA20 278#	<i>nip</i>	1049	REDO	A17	A17					H
C90XA20 278#	<i>nip</i>	1050	REDO	A17	A17					H
C90XA20 278#	<i>nip</i>	1051	REDO	A17	A17					H
C90XA20 278#	<i>nip</i>	1052	confirmed	A17	A17					H
C90XA20 133#3	WT	1091	confirmed	H	H		A20	A20	A20	A20
C90XA20 133#3	WT	1133	REDO	A20	A20		A20	H	H	H
C90XA20 133#1	WT	1172	confirmed	A20	A20		A20	A20	H	H
C90XA20 133#4	WT	1264	confirmed	A20	H					H
C90XA20 133#4	WT	1266	confirmed	A20	H					H
C90XA20 133#4	WT	1267	confirmed	A20	H					H
C90XA20 133#4	WT	1268	confirmed	A20	H					H
C90XA20 133#4	WT	1270	confirmed	A20	H			H		H
C90XA20 133#4	WT	1271	confirmed	A20	H		H	H	H	H
C90XA20 133#4	WT	1272	confirmed	A20	H					H

Table 3. Phenotype And Genotyping Data For Recombinant Plants From F2 and F3 Generations
From *NIP* Mapping Population

Genotype	Phenotype	Plant#	Notes	146o17	ENBP	2D12	4L4	164n9	80720	23c16d
C90XA20 133#4	<i>WT</i>	1273	confirmed	A20	H					H
C90XA20 133#4	<i>WT</i>	1275	confirmed	A20	H					H
C90XA20 133#4	<i>WT</i>	1278	confirmed	A20	H					H
C90XA20 133#4	<i>WT</i>	1279	confirmed	A20	H					H
C90XA20 133#4	<i>WT</i>	1280	confirmed	A20	A20					H
C90XA20 133#4	<i>WT</i>	1281	confirmed	A20	H					H
C90XA20 133#4	<i>WT</i>	1292	confirmed	A20	H					H
C90XA20 133#4	<i>WT</i>	1297	REDO	A20	H					H
C90XA20 133#4	<i>WT</i>	1298	REDO	A20	H					H
C90XA20 #511	<i>WT</i>	1458	Confirmed	A20	A20		A20	A20	H	H
C90XA20 #511	<i>WT</i>	1465	confirmed	A20	A20		A20	A20	H	H
C90XA20 #362	<i>WT</i>	1484	REDO	H	A20			A20		A20
C90XA20 #362	<i>WT</i>	1485	confirmed	A20	A20		H	H	H	H
C90XA20 #530	<i>WT</i>	1492	confirmed	A20	A20		H	H		H
C90XA20 #358	<i>WT</i>	1574	REDO	A20	A20		A20	A20		H
C90XA20#527	<i>WT</i>	1591	confirmed	A20	A20		H	H		H
C90XA20# 512	<i>WT</i>	1611	REDO	A20	A20			H		H
C90XA20#590	<i>WT</i>	1682	confirmed	A17	H		H	H		H
C90XA20#590	<i>WT</i>	1687	confirmed	A20	H		H	H		H
C90XA20#561	<i>WT</i>	1703	confirmed	A20	A20		H	H		H
C90XA20#561	<i>WT</i>	1704	confirmed	A20	A20		A20	A20		H
C90XA20#552	<i>WT</i>	1737	confirmed	H	H		A20	A20	A20	A20
C90XA20#567	<i>WT</i>	1746	confirmed	H	A20		A20	A20	A20	A20
C90XA20#559	<i>nip</i>	1764	confirmed	H	H					A17

Table 3. Phenotype And Genotyping Data For Recombinant Plants From F2 and F3 Generations
From *NIP* Mapping Population

Genotype	Phenotype	Plant#	Notes	146o17	ENBP	2D12	4L4	164n9	80720	23c16d
Recombinant Plants Obtained From F3 Generation of The <i>Nip</i> Mapping Population										
C90XA20#133#4	<i>wt</i>	3016	confirmed	A20		A17	A17	A17	A17	A17
C90XA20#133#4	<i>wt</i>	3018	confirmed	A20		A17	A17	A17	A17	A17
C90XA20#133#4	<i>nip</i>	3019	confirmed	A20		A17	A17	A17	A17	A17
C90XA20#133#4	<i>wt</i>	3020	confirmed	A20	H	H	H	H	H	H
C90XA20#133#4	<i>nip</i>	3021	confirmed	A20		A17	A17	A17	A17	A17
C90XA20#133#4	<i>wt</i>	3405	confirmed	A20	H	H	H	H	H	H
C90XA20#133#4	<i>nip</i>	3406	confirmed	A20	A17	A17	A17	A17	A17	A17
C90XA20#133#4	<i>wt</i>	3408	confirmed/dead, pods	A20	H	H	H	H	H	H
C90XA20#133#4	<i>wt</i>	3409	confirmed/dead, pods	A20	H	H	H	H	H	H
C90XA20#133#4	<i>wt</i>	3411	confirmed/dead, pods	A20	H	H	H	H	H	H
C90XA20#133#4	<i>wt</i>	3412	confirmed/dead, pods	A20	H	H	H	H		H
C90XA20 #368	<i>nip</i>	3035	confirmed/dead , pods	A20	A20	A20	A20	A17		A17
C90XA20 #368	<i>nip</i>	3090	confirmed	H		H	H	A17	A17	A17
C90XA20 #368	<i>nip</i>	3091	confirmed	H		H	H	A17	A17	A17
C90XA20 #368	<i>nip</i>	3093	confirmed	H		H	H	A17	A17	A17
C90XA20 #368	<i>nip</i>	3422	confirmed/dead,pods	H	H		H	A17	A17	A17
C90XA20 #368	<i>nip</i>	3497	confirmed	H	H	H	H	H	A17	A17
C90XA20 #368	<i>nip</i>	3498	Confirmed/dead 1 pod	H	H	H	H	A17	A17	A17
C90XA20 #368	<i>nip</i>	3511	confirmed	H	H		H	A17	A17	A17
C90XA20 #368	<i>nip</i>	3513	Confirmed	H	H	H	H	A17	A17	A17
C90XA20 #368	<i>nip</i>	3514	dead/3 pods, Redo	H	H					A17
C90XA20 #368	<i>nip</i>	3515	Confirmed	A20	A20	A20	A20	A17	A17	A17
C90XA20 #368	<i>nip</i>	3516	confirmed	H	H	H	H	A17	A17	A17
C90XA20 #368	<i>nip</i>	3518	confirmed	H	H	H	H	A17	A17	A17
C90XA20 #368	<i>nip</i>	3519	confirmed	H		H	H	H	A17	A17
C90XA20 #368	<i>nip</i>	3520	REDO	H	H					A17
C90XA20 #368	<i>nip</i>	3521	confirmed/dead,pods	A20	A20	A20	A20	A17	A17	A17
C90XA20 #390	<i>wt</i>	3207	confirmed	A17		A17	A17	H	H	H
C90XA20 #390	<i>wt</i>	3208	confirmed/dead pods	A17	A17	A17	A17	H	H	H
C90XA20 #390	<i>wt</i>	3209	confirmed	A17	A17	A17	A17	A20	A20	A20
C90XA20 #390	<i>wt</i>	3210	confirmed	A17	A17	A17	A17	A20	A20	A20

Table 3. Phenotype And Genotyping Data For Recombinant Plants From F2 and F3 Generations
From *NIP* Mapping Population

Genotype	Phenotype	Plant#	Notes	146o17	ENBP	2D12	4L4	164n9	80720	23c16d
C90XA20 #390	<i>wt</i>	3212	confirmed	A17		A17	A17	A20	A20	A20
C90XA20 #390	<i>wt</i>	3213	confirmed	A17	A17	A17	A17	H	H	H
C90XA20 #390	<i>wt</i>	3214	confirmed/dead,pods	A17		A17	A17	H	H	H
C90XA20 #390	<i>wt</i>	3219	confirmed	A17		A17	A17	A20	A20	A20
C90XA20 #390	<i>wt</i>	3220	confirmed	A17		A17	A17	A20	A20	A20
C90XA20 #390	<i>wt</i>	3221	confirmed	A17	A17	A17	A17	H	H	H
C90XA20 #390	<i>wt</i>	3222	confirmed	A17		H	H	H	H	A20
C90XA20 #390	<i>wt</i>	3231	DEAD	A17						H
C90XA20 #390	<i>wt</i>	3239	REDO	A17						A20
C90XA20 #390	<i>wt</i>	3242	DEAD	A17						A20
C90XA20 #390	<i>wt</i>	3243	REDO	A17						H
C90XA20 #390	<i>wt</i>	3245	DEAD	A17						H
C90XA20 #390	<i>wt</i>	3255	DEAD	A17						H
C90XA20 #390	<i>wt</i>	3261	Confirmed/DEAD 8PODS	A17		A17	A17	H	H	H
C90XA20 #660	<i>wt</i>	3265	confirmed/dead 3pods	A20		A20	A20	A20	H	H
C90XA20 #660	<i>wt</i>	3266	confirmed	A20		A20	A20	A20	H	H
C90XA20 #660	<i>wt</i>	3267	confirmed	A20		A20	A20	A20	H	H
C90XA20 #660	<i>wt</i>	3269	confirmed	A20	A20	A20	A20	A20	A17	17
C90XA20 #660	<i>wt</i>	3270	confirmed/dead 6pods	A20	A20	A20	A20	A20	H	H
C90XA20 #660	<i>wt</i>	3271	confirmed	A20	A20	A20	A20	A20	H	H
C90XA20 #531	<i>wt</i>	3329	confirmed/dead16pods	H	H	H	H	H	A17	A17
C90XA20 #531	<i>wt</i>	3328	confirmed	A20	A20					A17
C90XA20 #278	<i>nip</i>	3393	confirmed	A17	A17	A17	A17	A17	A20	A20
C90XA20 #278	<i>nip</i>	3399	confirmed/dead,pods	A17	A17	A17	A17	A17	A20	A20
C90XA20 #155	<i>wt</i>	3447	confirmed/dead,pods	A20	A20	A20	A20	A20	H	H
C90XA20 #698	<i>wt</i>	3651	confirmed	H	H	H	H	H	A20	A20
C90XA20 #850	<i>wt</i>	3688	confirmed	H	H	H	H	H	A20	A20
C90XA20 #683	<i>wt</i>	3705	confirmed	H	H	H	H	H	A17	A17
C90XA20 #683	<i>nip</i>	3712	confirmed	A17		A17	A17	A17	H	H
C90XA20 #993	<i>wt</i>	3719		H			A20		A20	A20
C90XA20 #816	<i>wt</i>	3731		A17			H		H	H
C90XA20 #1030	<i>nip</i>	3749		A20			A20		H	H

Table 3. Phenotype And Genotyping Data For Recombinant Plants From F2 and F3 Generations
From *NIP* Mapping Population

Genotype	Phenotype	Plant#	Notes	146o17	ENBP	2D12	4L4	164n9	80720	23c16d
C90XA20 #1106	<i>wt?</i>	3821		H			H		A20	A20
C90XA20 #1112	<i>nip</i>	3828		A17			H		H	H
C90XA20 #1082	<i>wt</i>	3844		H			A20		A20	A20
C90XA20 #1102	<i>wt</i>	3914		H			H		A20	A20
C90XA20 #1102	<i>wt</i>	3915		H			H		A17	A17
C90XA20 #1043	<i>nip</i>	3942		A17			A17		H	H
C90XA20 #1043	<i>nip</i>	3943		A17			A17		H	H
C90XA20 #1043	<i>nip</i>	3944		A17			A17		H	H
C90XA20 #1043	<i>nip</i>	3946		A17			A17		A20	A20
C90XA20 #1043	<i>nip</i>	3947		A17			A17		H	H
C90XA20 #1043	<i>nip</i>	3948		A17			A17		H	H
C90XA20 #1043	<i>nip</i>	3950		A17			A17		H	H
C90XA20 #1043	<i>nip</i>	3951		A17			A17		H	H
C90XA20 #1043	<i>nip</i>	3953		A17			A17		H	H
C90XA20 #1178	?	3965		A17					A17	H
C90XA20 #1016	<i>nip</i>	3979		A17			A17		H	H

TABLE 4 RECOMBINANT PLANTS THAT WERE SELECTED FOR FURTHER TESTING

F2 GENERATION RECOMBINANT PLANTS										
Genotype	Phenotype	plant#	146o17	ENBP	2D12	4L4	164N9	80720	23c16d	NOTES
C90XA20 281#2	WT	1007	A20	H					A20	Confirm, progeny, genotype
C90XA20 278#	nip	1043	A17	A17		A17	A17	H	H	see 3946, progeny of this plant
C90XA20 133#3	WT	1133	A20	A20		A20	H	H	H	progeny and genotype
C90XA20 133#1	WT	1172	A20	A20		A20	A20	H	H	progeny and genotype
C90XA20 #511	WT	1458	A20	A20		A20	A20	H	H	progeny and genotype, 78L20
C90XA20 #511	WT	1465	A20	A20		A20	A20	H	H	progeny and genotype, 78L21
C90XA20 #358	WT	1574	A20	A20		A20	A20		H	get 8o7 data
C90XA20# 512	WT	1611	A20	A20		H	H		H	get 4L4 phenotype
C90XA20#561	WT	1704	A20	A20		A20	A20		H	get 8o7 data
C90XA20#559	nip	1764	H	H		A17	A17		A17	get 4L4, 164n9, 8o7 data
F3 GENERATION RECOMBINANT PLANTS										
Genotype	Phenotype	plant#	146o17	ENBP	2D12	4L4	164N9	80720	23c16d	
C90XA20 #368	nip	3035	A20	A20	A20	A20	A17		A17	further genotyping between 4L4 and 164n9
C90XA20 #368	nip	3090	H		H	H	A17	A17	A17	further genotyping between 4L4 and 164n10
C90XA20 #368	nip	3515	A20	A20	A20	A20	A17	A17	A17	further genotyping between 4L4 and 164n10
C90XA20 #368	nip	3521	A20	A20	A20	A20	A17	A17	A17	use if problems with 3035, 3090, 3515
C90XA20 #390	wt	3209	A17	A17	A17	A17	A20	A20	A20	further genotyping between 4L4 and 164n10
C90XA20 #390	wt	3210	A17	A17	A17	A17	A20	A20	A20	further genotyping between 4L4 and 164n10
C90XA20 #390	wt	3212	A17		A17	A17	A20	A20	A20	further genotyping between 4L4 and 164n10
C90XA20 #660	wt	3265	A20		A20	A20	A20	H	H	could be back-up for 3269
C90XA20 #660	wt	3266	A20		A20	A20	A20	H	H	could be back-up for 3269
C90XA20 #660	wt	3267	A20		A20	A20	A20	H	H	could be back-up for 3269
C90XA20 #660	wt	3269	A20	A20	A20	A20	A20	A17	17	78L20*
C90XA20 #660	wt	3270	A20	A20	A20	A20	A20	H	H	could be back-up for 3269
C90XA20 #660	wt	3271	A20	A20	A20	A20	A20	H	H	could be back-up for 3269
C90XA20 #531	wt	3329	H	H	H	H	H	A17	A17	78L20* progeny and genotype
C90XA20 #531	wt	3328	A20	A20		A20			A17	rest of genotype
C90XA20 #278	nip	3393	A17	A17	A17	A17	A17	A20	A20	78L20*
C90XA20 #278	nip	3399	A17	A17	A17	A17	A17	A20	A20	back up for 3393

TABLE 4 RECOMBINANT PLANTS THAT WERE SELECTED FOR FURTHER TESTING

F2 GENERATION RECOMBINANT PLANTS										
Genotype	Phenotype	plant#	146o17	ENBP	2D12	4L4	164N9	80720	23c16d	NOTES
C90XA20 #155	wt	3447	A20	A20	A20	A20	A20	H	H	progeny and 78L20 2nd priority 78L20
C90XA20 #698	wt	3651	H	H	H	H	H	A20	A20	progeny and 78L20 2nd priority 78L20
C90XA20 #850	wt	3688	H	H	H	H	H	A20	A20	progeny and 78L20 2nd priority 78L20
C90XA20 #683	wt	3705	H	H	H	H	H	A17	A17	78L20*
C90XA20 #683	nip	3712	A17		A17	A17	A17	H	H	78L20*
C90XA20 #1030	nip	3749	A20			A20		H	H	do 164N9, maybe 78L20, progeny needed
C90XA20 #1106	wt?	3821	H			H	H	A20	A20	do 164N9, maybe 78L20, progeny needed
C90XA20 #1112	nip	3828	A17			H	H	H	H	do 164N9, maybe 78L20, progeny needed
C90XA20 #1082	wt	3844	H			A20		A20	A20	maybe progeny
C90XA20 #1102	wt	3914	H			H	H	A20	A20	do 164N9, maybe 78L20, progeny needed
C90XA20 #1102	wt	3915	H			H	H	A17	A17	do 164N9, definitely 78L20*
C90XA20 #1043	nip	3942	A17			A17	H	H	H	back up for 3946
C90XA20 #1043	nip	3943	A17			A17	A17	H	H	back up for 3947
C90XA20 #1043	nip	3944	A17			A17		H	H	back up for 3948
C90XA20 #1043	nip	3946	A17			A17	A17	A20	A20	do 164N9, definitely 78L20*
C90XA20 #1043	nip	3947	A17			A17		H	H	back up for 3946
C90XA20 #1043	nip	3948	A17			A17		H	H	back up for 3947
C90XA20 #1043	nip	3950	A17			A17		H	H	back up for 3948
C90XA20 #1043	nip	3951	A17			A17		H	H	back up for 3949
C90XA20 #1043	nip	3953	A17			A17		H	H	back up for 3950
C90XA20 #1016	nip	3979	A17			A17	A17	H	H	do 164N9, definitely 78L20*

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