Genetic Dissection of Internode Length Above the Uppermost Ear in Four RIL Populations of Maize (Zea mays L.)

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ABSTRACT The internode length above the uppermost ear (ILAU) is an important influencing factor for canopy architecture in maize. Analyzing the genetic characteristics of internode length is critical for improving plant population structure and increasing photosynthetic efficiency. However, the genetic control of ILAU has not been determined. In this study, quantitative trait loci (QTL) for internode length at five positions above the uppermost ear were identified using four sets of recombinant inbred line (RIL) populations in three environments. Genetic maps and initial QTL were integrated using meta-analyses across the four populations. Seventy QTL were identified: 16 in population 1; 14 in population 2; 25 in population 3; and 15 in population 4. Individual effects ranged from 5.36% to 26.85% of phenotypic variation, with 27 QTL >10%. In addition, the following common QTL were identified across two populations: one common QTL for the internode length of all five positions; one common QTL for the internode length of three positions; and one common QTL for the internode length of one position. In addition, four common QTL for the internode length of four positions were identified in one population. The results indicated that the ILAU at different positions above the uppermost ear could be affected by one or several of the same QTL. The traits may also be regulated by many different QTL. Of the 70 initial QTL, 46 were integrated in 14 meta-QTL (mQTLs) by meta-analysis, and 17 of the 27 initial QTL with R² >10% were integrated in 7 mQTLs. Four of the key mQTLs (mQTL2-2, mQTL3-2, mQTL5-1, mQTL5-2, and mQTL9) in which the initial QTL displayed $R^2 > 10\%$ included four to 11 initial QTL for an internode length of four to five positions from one or two populations. These results may provide useful information for marker-assisted selection to improve canopy architecture.

KEYWORDS

maize RIL population internode length QTL mapping major QTL

Maize is a globally important food and feed crop, and improving maize yield per unit area is a major goal of maize breeding. Plant architecture breeding to improve the plant type and photosynthetic efficiency per unit area is a primary approach for achieving high yield in maize. Plant architecture influences solar radiation capture within the canopy,

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nitrogen reservoirs for grain filling, abiotic stress tolerance, and biological and economic output per unit area. By selecting leaf architecture, root architecture, stem architecture, and ear architecture, among others, an ideal plant architecture can be created to allow maize to fully capture and use solar energy at all growth stages and maximize maize yields per unit area. The remarkable importance of plant architecture in maize is clear when hybrids are retrospectively analyzed (Duvick 1977, 2005; Duvick and Cassman1999; Russell 1985, 1991; Sakamoto *et al.* 2006; Tollenaar and Wu 1999; Troyer 2001). The genetic controls underlying stem architecture are of particular interest for maize plant architecture improvement. The stem architecture includes the plant height, ear height, stem diameter, and internode length. Plant and ear heights have been studied extensively (Austin *et al.* 2001; Beavis *et al.* 1991; Berke and Rocheford 1995; Koester *et al.* 1993; Li *et al.* 2007); however, limited studies have been conducted on internode length, which is one

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of the decisive factors affecting plant and ear height. In grass, internode length is attributed to the development of intercalary meristems at the base of the growing internode, which is capable of cell division and cell elongation (Sauter and Kende 1992; Van Der Knaap *et al.* 2000). Internode length in maize, particularly internode length above the uppermost ear (ILAU), is an important index that reflects optimal canopy architecture. Therefore, establishing equitable ILAU is critical for improving plant architecture, population quality, photosynthetic efficiency, and grain yield.

In maize, internode length affects lodging resistance as well as yield per unit area. Shortening the internode length below the ear enhances resistance to lodging (Cao *et al.* 2006; Lü *et al.* 2008). Increasing three consecutive internode lengths (the first leaf above the uppermost ear, the leaf of the ear, and the first leaf below the ear) improves female spike differentiation, resulting in larger ears and increased grain weight (Cao *et al.* 2006). Increasing the ILAU decreases the canopy height, improves ventilation and light penetration, and enhances photosynthesis in the middle and lower leaves as well as the efficiency of light energy utilization for the entire plant (Guo *et al.* 2005). In general, as the ILAU increases, the middle and upper leaves capture more light and conductive photosynthetic activity is enhanced.

With the rapid development of high-density molecular marker linkage maps and quantitative trait loci (QTL) detection approaches, a large amount of data are currently available for maize QTL, such as yield, plant height, ear height, and resistance. However, QTL studies of ILAU have not been performed, and the genetic basis of ILAU remains unclear. To dissect the genetic basis for ILAU in maize, QTL were mapped using four sets of recombinant inbred line (RIL) populations derived from crosses (Yu82×Yu87-1, Yu82×Shen137, Yu87-1×Zong3, and Yu537×Shen137). The objectives were to identify additional genomic regions of QTL for internode length above the uppermost ear, to estimate the magnitude and type of their genetic effects, and to provide information for fine mapping and markerassisted selection.

MATERIALS AND METHODS

Population development

The four sets of study populations consisted of 208, 197, 223, and 212 RILs derived from the crosses Yu82×Yu87-1, Yu82×Shen137, Yu87-1×Zong3, and Yu537A×Shen137, respectively. The four populations were designated Population 1 (Pop. 1), Population 2 (Pop. 2), Population 3 (Pop. 3), and Population 4 (Pop. 4).

The parents of four populations were chosen based on distinct maize germplasm groups. Inbred lines Yu82, Yu537A, and Zong3 were derived from a Chinese Stiff Stalk germplasm, which is a heterotic group used broadly in China, whereas inbred lines Shen137 and Yu87-1 were derived from a non-Stiff Stalk germplasm, which is also a heterotic group used broadly in China.

Field trial and trait evaluation

The four populations of five parents were evaluated in three environments in 2011 and 2012: Pop. 1 was planted in Zhengzhou, Anyang, and Zhumadian of Henan Province in 2011; Pop. 2 was planted in Shangqiu, Wenxian, and Nanyang of Henan Province in 2011; Pop. 3 was planted in Zhengzhou, Puyang, and Shangqiu of Henan Province in 2012; and Pop. 4 was planted in Wenxian, Nanyang, and Anyang of Henan Province in 2012. Each field experiment followed a randomized complete block design with three replicates. Each plot included one row that was 4 m long and 0.67 m wide and had a total of 17 plants at a density of 60,000 plants/ha. Ten days after pollen shed, five consecutive plants from the middle of each plot were chosen to evaluate the ILAU (ILFir, ILSec, ILThi, ILFor, and ILFif, the first, second, third, fourth, and fifth internode length above the uppermost ear, respectively), and each internode length was defined as the length from node to node (Figure 1). Family trait values were reported as the average from five plants in each replicate. The overall performance was determined by calculating the average over the three experimental environments. Descriptive statistics and simple Pearson correlation coefficients (r) were calculated between traits using SPSS 12.0 software (SPSS Inc., Chicago, IL).

Molecular linkage construction and QTL analysis

Young leaf samples at the seedling stage from the four RIL populations were collected, and genomic DNA was extracted using the cetyltrimethylammonium bromide (CTAB) method (Saghai-Maroof *et al.* 1984). The genotype data for each single nucleotide polymorphism (SNP) marker were analyzed using maize SNP3K (Illumina Inc., San Diego, CA), which generated homozygous and heterozygous genotype clusters. A total of 3072 SNP markers were selected as



Figure 1 Schematic explanation of ILFir, ILSec, ILThi, ILFor, and ILFif. IL indicates the length from node to node; ILFir, the first internode length above the uppermost ear; ILSec, the second internode length above the uppermost ear; ILThi, the third internode length above the uppermost ear; ILFor, the fourth internode length above the uppermost ear; and ILFif, the fifth internode length above the uppermost ear.

per the manufacturer's recommendation to analyze the four populations and corresponding parents. Ultimately, the four linkage maps were created using Joinmap version 4.0 software and consisted of 1179, 1116, 1243, and 1102 SNP markers. The parameters included a logarithm of odds (LOD) threshold >3.0, total length of 1873.02 cM for Pop. 1 with an average interval of 1.59 cM, total length of 1839.75 cM for Pop. 2 with an average interval of 1.65 cM, total length of 1863.00 cM for Pop. 3 with an average interval of 1.50 cM, and total length of 1629.48 cM for Pop. 4 with an average interval of 1.48 cM.

QTL mapping was conducted using the composite-interval mapping method (CIM) of the software Windows QTL cartographer version 2.5 (Zeng 1994). For the CIM, Model 6 of the Zmaoqtl module was used to detect QTL and estimate their effects. The genome was scanned every 2 cM between markers and putative QTL with a window size of 10 cM. The maximum number of cofactors was used to control the genetic background for each trait. Five control markers were identified by forward and backward regression. Empirical threshold levels for declaring QTL significance at the 5% genome-wide type I error level were independently set for each trait by performing 1000 random permutations. The phenotypic variation and additive effect explained by each QTL were estimated from the value expressed by the QTL peaks obtained from the CIM.

QTL integration and meta-analysis

To integrate the QTL information on the ILAU for the four RIL populations in this study, the four linkage maps were integrated and the number and positions of consensus QTL were estimated by meta-analysis (Goffinet and Gerber 2000; Arcade *et al.* 2004; Chardon *et al.* 2004). The initial QTL identified in the four populations were projected onto the integrated map using their positions and the confidence intervals shared by the four genetic linkage maps. A modified Akaike's information criterion (AIC) was calculated to select the QTL models with varying numbers of mQTLs, and the model with the lowest AIC value was selected as significant and used to identify the number of mQTLs on each chromosome.

RESULTS

Phenotypic performance of the internode length of five parents and four RIL populations

The five parental lines have 5–7 internodes above the uppermost ear, and all five trait values were markedly lower for Yu82, Zong3, and Yu537A than for Yu87-1 and Shen137 (Table 1). For the RIL populations, the trait values exhibited high variability and transgressive segregation, with trait values exceeding the range of the parental lines. All traits were normally distributed in the four RIL populations (Table 1). The variances of genotype were significant at P = 0.01, and the variance interactions between genotype and environment were not significant for the measured traits (Table 2).

The broad-sense heritability (h^2) for ILAU was high and ranged from 65.73% to 83.45% in the four RIL populations (Table 1). The phenotypic correlations among the five traits were calculated based on the combined data for the three environments (Table 3). The correlation coefficients between internode lengths among positions were significant (P = 0.01) and ranged from 0.27 to 0.85 in four RIL populations.

Table 1 Phenotypic pe	erformance of the five	parental lines and	d four RIL populations
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Population	Parameter	ILFir (cm)	ILSec (cm)	ILThi (cm)	ILFor (cm)	ILFif (cm)
Yu82	$Mean \pm SD$	25.42 ± 1.86	13.74 ± 1.23	12.60 ± 1.33	11.99 ± 1.53	11.21 ± 1.32
Zong3	$Mean \pm SD$	26.44 ± 2.57	13.32 ± 1.43	11.21 ± 1.42	10.87 ± 1.22	10.23 ± 1.42
Yu537	$Mean \pm SD$	25.68 ± 2.45	12.48 ± 1.63	11.50 ± 1.21	10.52 ± 1.33	10.00 ± 1.67
Yu87-1	$Mean \pm SD$	30.14 ± 2.23	14.79 ± 1.45	14.60 ± 1.36	13.75 ± 1.44	12.77 ± 1.42
Shen137	$Mean \pm SD$	29.29 ± 1.89	15.00 ± 1.65	14.57 ± 1.38	14.06 ± 1.32	13.70 ± 1.52
Yu82×Yu87-1	$Mean \pm SD$	26.15 ± 2.27	14.33 ± 1.11	13.97 ± 1.12	13.43 ± 1.14	12.70 ± 1.15
	Range	16.78-39.00	11.47-18.67	10.58-18.44	8.91–17.86	7.92 ± 18.00
	Skewness	0.01	0.40	0.24	0.19	0.18
	Kurtosis	0.57	-0.09	-0.19	-0.23	-0.23
	h² (%)	79.34	80.09	76.52	81.26	69.86
		70.51-84.87	69.44-82.65	65.83-83.72	66.75-84.01	60.35-78.44
Yu82×Shen137	$Mean \pm SD$	28.00 ± 3.16	13.9 ± 2.11	13.72 ± 2.23	13.80 ± 2.12	12.10 ± 2.12
	Range	20.30-34.09	9.81-17.81	8.74-17.35	8.49-16.59	8.06-16.72
	Skewness	0.07	0.03	0.24	0.19	-0.02
	Kurtosis	0.65	0.57	0.71	-0.25	-0.18
	h² (%)	83.45	78.79	77.61	78.32	67.97
		72.54-87.46	65.06-82.35	67.38-85.29	65.69-87.52	59.52-79.88
Zong3×Yu87-1	$Mean \pm SD$	26.95 ± 4.25	14.29 ± 2.18	12.88 ± 2.17	12.38 ± 2.18	11.62 ± 2.22
	Range	18.03-37.03	6.50-29.33	7.44—20.67	6.33-20.67	2.50-19.33
	Skewness	0.09	1.02	0.31	0.41	0.21
	Kurtosis	0.62	0.74	0.76	1.03	0.72
	h² (%)	80.67	82.56	78.63	79.43	68.72
		65.34-86.29	70.03-87.60	60.79-84.32	68.57-86.35	61.87-80.35
Yu537×Shen137	$Mean \pm SD$	25.86 ± 3.42	12.87 ± 2.14	12.15 ± 2.32	11.83 ± 1.89	11.56 ± 2.01
	Range	18.72-35.00	9.44-21.50	5.17-19.78	5.92-17.50	6.94-20.50
	Skewness	0.27	0.39	0.59	0.37	1.00
	Kurtosis	1.40	0.60	0.92	0.83	0.87
	h² (%)	82.59	76.83	78.54	77.05	65.73
		71.30-87.45	65.09-82.44	69.72-84.69	64.33-82.18	54.62-80.33

ILFir, the first internode length above the uppermost ear; ILSec, the second internode length above the uppermost ear; ILThi, the third internode length above the uppermost ear; ILFif, the fifth internode length above the uppermost ear.

Table 2 Analysis of variance for the studied traits in four RIL populations (F-test)

Population	Variation Source	ILFir	ILSec	ILThi	ILFor	ILFif
Yu82×Shen137	Family	4.19 [†]	4.99†	3.45 ⁺	4.18 [†]	4.00 ⁺
	Location	1.08	1.80	1.19	1.18	1.23
	Family imes location	0.61	0.36	0.25	0.63	0.63
Yu82×Yu87-1	Family	9.80†	7.65 ⁺	8.39 ⁺	9.30 ⁺	8.23†
	Location	0.98	1.66	1.83	1.90	1.93
	Family imes location	0.95	1.22	1.12	1.04	1.11
Zong3×Yu87-1	Family	2.25 ⁺	3.27 ⁺	2.40 ⁺	3.22 ⁺	3.00 ⁺
-	Location	0.86	1.04	1.01	1.19	1.22
	Family imes location	0.82	0.93	0.86	0.67	0.62
Yu537×Shen137	Family	3.35 ⁺	2.37 ⁺	3.68 ⁺	4.14 ⁺	3.66†
	Location	0.86	1.04	1.01	1.19	1.22
	Family imes location	0.82	0.93	0.86	0.67	0.62

ILFir, the first internode length above the uppermost ear; ILSec, the second internode length above the uppermost ear; ILThi, the third internode length above the uppermost ear; ILFif, the fifth internode length above the uppermost ear.

[†]Significant at P = 0.01.

QTL identification for leaf width in the four populations

Seventy QTL for ILFir, ILSec, ILThi, ILFor, and ILFif were mapped to all maize chromosomes in the four RIL populations, with 16 QTL in Pop. 1, 14 QTL in Pop. 2, 25 QTL in Pop. 3, and 15 QTL in Pop. 4 (Table 4). The contributions to phenotypic variation for a single QTL ranged from 5.36% to 26.85%, with 27 QTL >10%.

The 16 QTL affecting internode lengths above the uppermost ear were located on chromosomes 1, 4, 5, and 7 in Pop. 1, with four QTL for ILFir, three QTL for ILSec, four QTL for ILThi, three QTL for ILFor, and two QTL for ILFif. The contributions of the QTL to phenotypic variation ranged from 5.36% to 16.65%, with four QTL >10%. All positive alleles with the exception of q11LFir1, q11LThi1, and q11LThi7 were contributed by Yu87-1. The QTL q11LFir4, q11LSec4, q11LThi4, and q11LFor4 were located in the same region between PZE-104005295 and PZE-104005482. The QTL q11LFir5-2, q11LSec5-2, q11LThi5, q11LFor5, and q11LFif5 were located in the same region between PZE-105141173 and PZE-1051414651.

Table 3 Correlation coefficients of ILAU in the four RIL populations

Population	Trait	ILSec	ILThi	ILFor	ILFif
Yu82×Yu87-1	ILFir	0.51 ⁺	0.52 ⁺	0.43 ⁺	0.30 ⁺
	ILSec		0.80 [†]	0.67†	0.51 ⁺
	ILThi			0.85†	0.67†
	ILFor				0.82 ⁺
Yu82×Shen137	ILFir	0.28†	0.29†	0.25†	0.36†
	ILSec		0.40 ⁺	0.58†	0.35 ⁺
	ILThi			0.42 ⁺	0.53 ⁺
	ILFor				0.61 ⁺
Zong3×Yu87-1	ILFir	0.39†	0.41 ⁺	0.36†	0.27 ⁺
	ILSec		0.71 ⁺	0.63†	0.54†
	ILThi			0.76†	0.67†
	ILFor				0.80 ⁺
Yu537×Shen137	ILFir	0.52 ⁺	0.57†	0.48†	0.36 ⁺
	ILSec		0.78†	0.76†	0.60 ⁺
	ILThi			0.84†	0.66†
	ILFor				0.75 [†]

ILFir, the first internode length above the uppermost ear; ILSec, the second internode length above the uppermost ear; ILThi, the third internode length above the uppermost ear; ILFor, the fourth internode length above the uppermost ear. TSignificant at P = 0.01.

The 14 QTL in Pop. 2 were located on all chromosomes except chromosomes 2, 4, and 8. Among the detected QTL, three were associated with ILFir, three were associated with ILSec, one was associated with ILFir, three were associated with ILFor, and four were associated with ILFif. Individual QTL explained 7.54%–26.85% of the total phenotypic variance. Eight positive alleles of the 14 QTL were derived from Shen137 and contributed to increased internode lengths above the uppermost ear. The QTL q2ILFir7 and q2ILFif7 were detected at the same marker interval, PZE-107002330–SYN20419, with two QTL accounting for >20% of the phenotypic variation. The QTL q2ILSec9, q2ILThi9, and q2ILFor9 were detected at the same marker interval, PZE-109086476. The QTL q2ILFor6 and q2ILFif6 were detected at the same marker interval, PZE-106104150–PZE-106105801.

Twenty-five QTL in Pop. 3 were associated with internode lengths above the uppermost ear, including five QTL for ILFir, five QTL for ILSec, five QTL for ILThi, six QTL for ILFor, and four QTL for ILFif. These QTL were distributed across the entire genome with the exception of chromosomes 4, 6, and 7, and they accounted for 6.10%-16.76% of the phenotypic variation. Positive alleles of 14 QTL were derived from Yu87-1 and contributed to increased internode length values above the uppermost ear. The QTL q3ILFir3, q3ILSec3, q3ILThi3, and q3ILFor3 were detected in the same region between PZE-103110355 and PZE-103115618, with two QTL accounting for >10% of the phenotypic variation. The QTL q3ILFir5-2, q3ILThi5-2, q3ILFor5-2, and q3ILFif5 were detected in the same region between PZE-105123635 and PZE-105128217. The QTL q3ILThi9 and q3ILFor9 were located in the same chromosomal regions between PZE-109075481 and PZE-109079845 and accounted for 8.86% and 11.15% of the total phenotypic variation, respectively.

The 15 QTL associated with internode lengths above the uppermost ear in Pop. 4 were identified on chromosomes 2, 3, 4, 5, and 6, with two QTL for ILFir, three QTL for ILSec, two QTL for ILThi, four QTL for ILFor, and four QTL for ILFif, accounting for 6.71%–18.36% of the phenotypic variance. The positive alleles of eight QTL were derived from Shen137 and contributed to increases in the trait values. The QTL q4ILSec2-1, q4ILThi2, q4ILFor2-1, and q4ILFif2 were identified in the same region between PZE-102136708 and PZE-102137972, with all QTL accounting for >10% of the phenotypic variation. The QTL q4ILSec6 and q4ILFor6-2 were detected in the same region between PZE-106062631 and PZE-106062790.

Table 4 QTL detected ¹	for internode	length above	e the uppermost	t ear in the	four recombinant	inbred line (RIL) populations across
three environments							

Tu82 Y 192-1 III Firit III Firit Sta 453,173-42,011,928 PZE 101071898-PZE 101071142 2.80 4.88 0.70 III Firit III Firit 3,895,283-406,729 PZE 101071898-PZE 104005492 3.45 4.08 -0.71 III Firit 5 163,789,771-64,011,38 PZE 101071187-PZE 105141445 4.84 -0.54 III Firit 31105-05 115,68,7073-00,98,395 SW11061-SYN20306 3.25 7.64 -0.46 III Firit 1111565 119,646,7073-00,98,395 SW11061-SYN20306 4.88 9.44 -0.54 III Thii 1111565 119,4485,001-19,987,101 PZE 10100529F-PZE 104005482 2.30 5.36 -0.40 III Thii 1111565 119,4486,001-19,987,101 PZE 1010105482 2.30 -0.46 1111167 151,346,600-19,987,610 PZE 101011007-PZE 10514270 6.22 1.6,30 -0.46 1111167 19,498,500-19,987,610 PZE 100101368-PZE 107011480 2.57 -0.46 1111167 119,498,500-19,987,610 PZE 1010101480 2.57 -0.46 -0.56 <th>Trait</th> <th>QTL</th> <th>Chr</th> <th>Ph (bp)</th> <th>Marker Interval</th> <th>LOD</th> <th>R² (%)</th> <th>А</th>	Trait	QTL	Chr	Ph (bp)	Marker Interval	LOD	R ² (%)	А
Likir q1lLFird 1 54,433,173-e2011928 PZE-101007398-PZE-10400542 2.45 6.08 0.70 q1lLFird 5 163,198,379-166,411,388 PZE-10005295-PZE-10400542 3.45 6.08 -0.47 LLSec q1lLFird 5 163,68,717-96,106,672 PZE-101017131-PZE-105114165 4.88 9.44 -0.54 LLSec q1lLSec-52 5 195,68,7317-96,106,672 PZE-10511173-PZE-105141445 4.88 9.44 -0.54 q1lLTh4 4 3,955,258-4,066,729 PZE-10514173-PZE-105141445 4.88 9.44 -0.55 q1lLTh4 4 3,955,258-4,066,729 PZE-105140772-10514720 6.55 16.24 -0.46 q1lLTh7 7 17,979,797-12,253,343 PZE-101002559-PZE-104005422 2.33 6.87 -0.46 q1lLFro7 7 7,979,797-12,253,342 PZE-10101254-PZE-10101154 2.57 6.66 -0.42 LFr q1lLFro7 7 7,979,797-12,253,342 PZE-10101254-PZE-10101154 2.5 6.67 -0.52 VB2 <t< td=""><td>Yu82×Yu87-1</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>	Yu82×Yu87-1							
qillEndi 4 3.952,283-4.064,729 PZE.101002529-FZE.10400542 3.43 1.6.6 -0.70 qillEndi-2 5 10.378,379-166,471,3 PZE.10101173-FZE-105101445 4.84 9.44 -0.54 LSoc qillEndi-2 5 19.568,7817-169,106,672 PZE.10101273-FZE-101017188 2.325 7.66 -0.46 LIDhi qillEndi-2 5 19.568,7817-169,106,677 PZE.1011173-FZE-1051141455 4.88 9.44 -0.54 LIDhi qillEndi<1	ILFir	q1ILFir1	1	54,453,173-62,011,928	PZE-101071898-PZE-101071162	2.80	6.88	0.70
a) b) b)<		q1ILFir4	4	3,895,258–4,086,729	PZE-104005295-PZE-104005482	3.45	6.08	-0.77
cite q11.5ec 19.568.781-7.96.106.672 PZE:105141173-PZE:105141465 488 9.44 -0.54 LiSac q11.5ec5-1 5 19.64.7073-20493.395 PZE:10003095-PZE:10010482 2.25 7.64.84 -0.54 LIThi q11.5m45 5 19.64.7073-2049.335 PZE:101040291-PZE:101011496 4.88 -0.44 -0.54 q11.5m4 43.855254-0.06.72 PZE:101040291-PZE:101014270 6.56 16.24 -0.88 q11.5m5 194.848,500-196.987.410 PZE:103100575-PZE:104005482 2.90 5.36 -0.46 q11.5m7 7 5.958.486.50-196.987.410 PZE:103101007-PZE:10314270 6.62 1.46 -0.69 q11.5m7 7 9.799.796-1252.3342 PZE:103101346-PZE:107015480 2.93 7.45 -0.52 YU22x Shar137 7 7.797.797.797.797.797.797 PZE:103013346-PZE:107015480 2.95 9.44 -0.54 LEri q11.5m7 7 7.979.796.1252.3342 PZE:10004072-PZE:10015480 2.85 6.127 -0.52 YU22x Shar137 PZE:100040100-PZE:10510		q1ILFir5-1	5	163,198,379–166,411,388	PZE-105107181-PZE-105109134	8.47	16.65	-1.41
LiSec q1LSec1 3.895,258-4.096,729 PZE 104005295-FZE-104005482 2.55 7.66 -0.45 q1LSec5-2 5 19.667,073-20.493,75 SW1610-157N20306 0.05 15.66 -0.55 q1LThi 149,515,795-54,45,13 PZE-105101178-PZE-1011486 2.71 7.10 0.65 q1LThi 149,515,795-54,45,13 PZE-105104027-PZE-10107154 3.73 6.7 -0.40 q1LThi 7 151,536,567-156,448,103 PZE-10510579-524,040,729 PZE-10510542209 6.56 1.66,7 -0.66 q1LFori 7 9.79,796-12,523,342 PZE-107003546-PZE-107015480 2.57 6.66 -0.55 Yu22x5han137 111474 7 9.79,796-12,523,342 PZE-107002330-SYR2019 10.83 2.685 -1.87 Q1LFir 7 9.79,79,796-12,523,342 PZE-107002330-SYR2019 10.83 2.685 -1.87 Q1LFir 9.101,406,206-104,373,477 PZE-107002330-SYR2019 10.83 2.685 -1.87 Q1LFir 9.101,406,206-104,373,477 PZE-107002330-SYR2019 10.83		q1ILFir5-2	5	19,568,7817-196,106,672	PZE-105141173-PZE-105141465	4.88	9.44	-0.54
q11LSec5-1 5 195,647,072-0094329 SVN1601-SVN20306 6.05 15.66 -0.55 LLThi q11LThi 1 49,515,795-544,05,73 PZE-10164221 PZE-10164221 2.00 5.3 -0.40 q11LThi 5 194,843,500-196,987,610 PZE-101640257-PZE-10405422 2.00 5.3 -0.40 q11LThi 5 194,843,500-196,987,610 PZE-105141007-PZE-105142709 6.42 1.46 -0.46 q11LFord 7 9,799,796-12523,342 PZE-105101007-PZE-10514209 2.3 6.45 -0.46 q11LFord 7 9,799,796-12523,342 PZE-107013546-PZE-107015480 2.5 6.65 -0.52 V282x5ben137 1 9,799,796-12523,342 PZE-107013546-PZE-107015480 2.5 1.87 -0.76 LEFr Q2LFr10 1 142,494,350-149,871,402 PZE-10703354-PZE-107015480 2.5 1.87 Q2LFr10 1 142,494,350-149,270,277 PZE-10703354-PZE-10015480 2.5 1.6 1.87 Q2LFr11 1 142,445,350-149,250,509	ILSec	q1ILSec4	4	3,895,258–4,086,729	PZE-104005295-PZE-104005482	3.25	7.68	-0.46
att att< att< </td <td></td> <td>q1ILSec5-1</td> <td>5</td> <td>18,667,073-20,693,395</td> <td>SYN1601-SYN20306</td> <td>6.05</td> <td>15.68</td> <td>-0.55</td>		q1ILSec5-1	5	18,667,073-20,693,395	SYN1601-SYN20306	6.05	15.68	-0.55
LLThi q1(LThi 49,515,795-54,453,173 PZE-101066291-PZE-10107198 2.71 7.10 0.65 q1(LThi5 5 194,848,500-196,987,410 PZE-105141200-272E-105142709 6.56 16.24 -0.86 q1(LThi7) 7 151,536,567-156,461,00 PZE-101005295-PZE-104005482 2.90 7.22 0.47 LEFor q1(LFor 7 9,799,796-12,523,342 PZE-10400529-PZE-104005482 2.57 6.69 -0.69 q1(LFor 7 9,799,796-12,523,342 PZE-107013546-PZE-107015480 2.65 6.67 -0.55 v282×56m-137 Q2[LFir0 1 1.279,234-47,09,247 PZE-107012330-5VR20419 1.083 2.6.85 -1.87 Q2[LFir0 1 1.42,484,350-169,6420-92 PZE-107012330-5VR20410 4.85 1.21 0.63 Q3[LFir0 1 1.42,484,350-169,6240-109 PZE-10702330-5VR20419 4.85 0.42 UEFir Q3[LFir1 0 1.33,745,032-135,152,250 PZE-101096242-PZE00480110 4.86 0.57 Q3[LFir1 0 3.34,745,032-135,15		q1ILSec5-2	5	195,687,817–196,106,672	PZE-105141173-PZE-105141465	4.88	9.44	-0.54
interface interface <t< td=""><td>ILThi</td><td>q1ILThi1</td><td>1</td><td>49,515,795–54,453,173</td><td>PZE-101066291-PZE-101071898</td><td>2.71</td><td>7.10</td><td>0.65</td></t<>	ILThi	q1ILThi1	1	49,515,795–54,453,173	PZE-101066291-PZE-101071898	2.71	7.10	0.65
and LLThis 5 194,848,500-196,987,410 PZE-105141007-PZE-105142709 6.56 16.24 -0.38 LLFor allLFord 4 3,985,258.4,086,729 PZE-104005429-PZE-104005420 6.56 16.24 -0.46 allLFor 7 9,797,746-12,523,342 PZE-104005429-PZE-104005420 2.57 6.69 -0.69 allLFor 7 9,797,746-12,523,342 PZE-107013546-PZE-107015480 2.65 6.67 -0.55 V022×Shen137 CllLFir 9 101,463,000-106,907,471 PZE-10700230-SVN20419 10.83 2.6.55 -1.67 ap2LLFir0 10 122,464,330-143,114,064 PZE-10700230-SVN20419 10.83 2.6.85 -1.63 LLSee ap2LLSer9 9 133,745,032-135,152,250 PZE-10096229-PZE-100984010 4.08 0.50 ap2LLSer10 123,745,032-135,152,250 PZE-100970207-PZE-10984047 2.81 7.84 0.42 LLFir ap1LFir0 133,745,032-135,152,250 PZE-100990207-PZE-109082474 2.85 7.84 0.43 LLSee ap1LFir1 <		a11LThi4	4	3,895,258-4,086,729	PZE-104005295-PZE-104005482	2.90	5.36	-0.40
chr chr <td></td> <td>a11LThi5</td> <td>5</td> <td>194,848,500–196,987,610</td> <td>PZE-105141007-PZE-105142709</td> <td>6.56</td> <td>16.24</td> <td>-0.88</td>		a11LThi5	5	194,848,500–196,987,610	PZE-105141007-PZE-105142709	6.56	16.24	-0.88
LiFor q1UFrof 4 3,295,258-4,066,729 PZE-104005295-PZE-104005295-PZE-10514107-PZE-105141050-PZE-10514107-PZE-1		a11LThi7	7	151,536,567-156,648,103	PZE-107105855-PZE-107107154	3.79	7.22	0.47
a a b 194,246,300-196,987,410 PZE-105141007-PZE-105112480 2.62 1.64 -0.62 LIFIF a ILFIF 5 194,248,300-196,987,410 PZE-10701334-PZE-107112480 2.65 6.67 -0.52 YU82 x Shen137 a 7 7,979,794-12,523,342 PZE-107013346-PZE-107101480 2.65 1.67 -0.52 YU82 x Shen137 a 1,979,634-4,709,247 PZE-107002330-SYN20419 10.83 2.68.5 1.12 0.63 G2LIFIT0 10 142,484,530-143,114,064 PZE-109062229-PZB02480.1 10.83 2.68.5 1.81 -0.76 LISec q2LISecf 9 133,745,032-145,152,250 PZE-109062229-PZE-109313818-276 2.81 7.83 0.42 LIFor q2LIFI6 10 123,745,032-135,152,250 PZE-109090207-PZE-10908476 2.81 7.54 0.43 LIFor q2LIFI6 153,609-243-156,368,157 PZE-1010105112 3.84 7.75 0.82 Q2LIFI6 153,609-243-156,268,157 PZE-10101015012 3.89 4.14	ILFor	a11LFor4	4	3,895,258-4,086,729	PZE-104005295-PZE-104005482	3.33	6.87	-0.46
child		g1ILFor5	5	194,848,500-196,987,610	PZE-105141007-PZE-105142709	6.62	14.69	-0.69
LiFif q1LFif5 5 194,846,500-166,987,400 PZE-105141007-PZE-10701542070 2.93 7.45 -0.55 Yu82xShen137 - 9,799,796-12,523,342 PZE-107013546-PZE-107015480 2.65 6.67 -0.55 Yu82xShen137 - 101,408,206-104,373,477 PZE-107003230-SYNL20419 10.83 2.685 -1.87 q2LFir0 9 103,445,300-43,114,044 PZE-107003230-SYNL20419 10.83 2.685 -1.87 LiSec q2LISec5 9 93,745,002-135,152,250 PZE-107003230-SYNL20419 10.83 2.685 -1.87 LiFor q2LISec7 9 133,745,002-135,152,250 PZE-100086110 4.08 10.15 0.52 LiFor q2LIFor6 6 156,609,243-156,366,157 PZE-100086170 2.87 8.18 0.53 q2LIFor 9 133,745,022-135,152,250 PZE-10104510-PZE-1050801 3.07 7.88 0.53 q2LIFor 9 133,745,022-135,152,250 PZE-10104510518 3.34 7.75 0.82 q2LIFif 1 <td></td> <td>g1ILFor7</td> <td>7</td> <td>9,799,796–12,523,342</td> <td>PZE-107013546-PZE-107015480</td> <td>2.57</td> <td>6.69</td> <td>-0.62</td>		g1ILFor7	7	9,799,796–12,523,342	PZE-107013546-PZE-107015480	2.57	6.69	-0.62
q1LFir/ V82X5hen137 7 9,799,796-12,523,342 PZE-107013846-PZE-107015480 2.65 6.67 -0.52 ILFir q2LFir/ q2LFir/9 9 101,408,206-104,373,477 PZE-107002330-SYN20419 10.83 26.85 -1.87 ILSec q2LFir/9 9 101,408,206-104,373,477 PZE-1007062229-PZE02401. 4.55 11.21 0.63 q2LSec5 5 1895,371,160-193,310,292 PZE-100703235-SYN12154 3.10 8.18 -0.76 q2LSec10 10 123,635,404-124,526,091 SYN15051-PZE-100086476 4.88 10.15 0.52 ILTror q2LFor3 3 19,645,756-20,022,149 PZE-100092027-PZE-109086476 3.08 8.35 0.52 ILFir q2LFor3 13,745,032-135,152,250 PZE-101099263-PZE-10101581 3.34 7.75 0.82 q2LFirf 7 1,979,634-4709,247 PZE-101099263-PZE-10101581 3.34 7.75 0.82 q2LFirf 7 1,979,634-4709,247 PZE-1010192157 3.88 8.10 0.57 q2LFirf 7	ILFif	q1ILFif5	5	194,848,500-196,987,610	PZE-105141007-PZE-105142709	2.93	7.45	-0.55
Yu82xShen137 Image: Constraint of the constr		a11LFif7	7	9.799.796-12.523.342	PZE-107013546-PZE-107015480	2.65	6.67	-0.52
ILFir Q2 LFir7 7 1.979,434-4,709,247 PZE-107002330-SYN20119 10.83 26.85 -1.87 Q2 LFir10 10 104,482,60-104,373,477 PZE-10302229-PZ802480.1 4.55 1.21 0.63 Q2 LSec7 5 199,537,160-193,310,222 PZE-10313386-PZE-10308477 2.81 7.83 0.421 Q2 LSec7 10 123,645,324-04-124,526,091 SYN15051-PZE-110086476 2.81 7.84 0.421 Q2 LFor3 3 19,654,756-20.022,149 PZE-1030026528-PZE-1010086476 2.85 7.88 0.53 Q2 LFor3 3 19,654,756-20.022,149 PZE-103026528-PZE-101010518 3.34 7.88 0.53 Q2 LFor4 6 155,609,243-156,386,157 PZE-104014150-PZE-106105801 3.07 8.83 0.57 Q2 LFir6 6 155,609,243-117,684,380 PZE-109102578 3.08 8.18 0.57 Q2 LFir6 1 19,952,438-19,4527,599 PZE-101146525-PZE-101105715 3.08 8.10 0.58 Z0 LFir6 1 189,522,438-19,4527,599 <	Yu82×Shen137	1		, , - ,- ,-				
cip/LFir9 9 101.408.206-104.373.477 PZE-100906229-PZE0240.1 4.55 11.21 0.63 ILSec q2LEir(7) 10 142.484.530-143.114.064 PZE-10097035-SYN12154 3.10 8.18 -0.76 q2LEsec9 7 133.745.032-135,152.250 PZE-1097090207-PZE-10086476 2.81 7.83 0.42 q2LESec1 10 132.635.040-124.52.09 PZE-109709027-PZE-10086476 2.85 7.54 0.43 LIFin q2LErof.3 19.654.756-20.022.149 PZE-103025244 3.67 7.88 0.53 q2LErof.9 9 133.745.032-135,152.250 PZE-100090207-PZE-100086476 2.88 8.86 0.57 q2LErof 6 155.609.243-156.368.157 PZE-100104150-PZE-101008176 3.08 8.057 q2LErof 7 13.745.032-145.568.157 PZE-101001507-PZE-101001571 2.88 8.18 0.57 q2LErof 7 1.979.634-47.09.247 PZE-101106150-PZE-101012157 3.08 7.75 0.82 q2LErof 7 144.500.83.56.163-80.802.797 SYN26664-PZE	ILFir	g2ILFir7	7	1,979,634-4,709,247	PZE-107002330-SYN20419	10.83	26.85	-1.87
april ILSec april 10 142,484,530-443,114,064 PZE-1010096735-SYN12154 3.10 8.18 -0.76 april LSec 9 189,537,160-193,310,292 PZE-105133858-PZE-105138181 3.95 9.49 0.50 april LSec 9 10 123,345,324-24,252,091 SYN15051-PZE-10908476 2.81 7.54 0.42 LThi april LFor3 3 19,654,756-20,022,149 PZE-10900207-PZE-109086476 2.86 7.54 0.43 quil For6 6 155,607,243-156,386,157 PZE-1010105728-10066476 3.08 8.35 0.52 quil For6 6 155,607,243-156,386,157 PZE-1010101518 3.34 7.75 0.82 quil Fir6 6 155,607,243-155,248,107 PZE-1010102330-SYN2419 10.33 25.63 -1.44 quil Fir6 19,522,638-19,4527,599 PZE-101101518 3.14 6.22 -0.97 guil Fir6 18,9522,638-19,4527,599 PZE-101102527 3.08 8.10 0.65 Zong3 × Yu8-1 11 189,522,638-19,4527,599 PZE-1011002157		a2ILFir9	9	101.408.206-104.373.477	PZE-109062229-PZB02480.1	4.55	11.21	0.63
ILSec q2ILSec5 5 189/537/160-193/310/292 PZE-105133858-PZE-105138182 3.95 9.49 0.50 q2ILSec10 10 123,435,04-124,522,50 PZE-109090207-PZE-10908476 2.81 7.83 0.42 q2ILFer7 9 133,745,032-135,152,250 PZE-10090207-PZE-109086476 2.85 7.54 0.43 ILFor q2ILFor6 6 155,609,243-155,152,250 PZE-100090207-PZE-109086476 2.08 8.35 0.53 Q2ILFor6 6 155,609,243-156,368,157 PZE-100090207-PZE-1001065801 3.07 7.88 0.53 Q2ILFir7 1,979,634-4,709,247 PZE-101099263-PZE-1011001518 3.14 7.75 0.82 Q2ILFir7 1,979,634-4,709,247 PZE-101002330-SNL20419 10.33 25.63 -1.64 q2ILFir3 149,008,365-175,554,472 PZE-101110355-PZE-101150712 5.89 1.4.41 -1.44 Q3ILFir1 1 189,522,638-19,452,7599 PZE-10110325-PZE-101150712 5.89 1.4.41 -1.44 Q3ILFir1 1 189,008,365-175,554,472 PZE-10100		a2ILFir10	10	142,484,530-143,114,064	PZE-110096735-SYN12154	3.10	8.18	-0.76
q2LSec9 9 133/745/032-135.152/250 PZE-109090207-PZE-109086476 2.81 7.83 0.42 LILThi q2LLSec10 10 123,635,404-124,526,091 SYN15051-PZE-1100068110 4.08 10.15 0.52 LILToi q2LLFor3 3 19,654,755-20,022,149 PZE-103026528-PZE-103027544 3.67 8.86 0.57 q2LLFor6 6 155,609,243-156,368,157 PZE-100709207-PZE-109066476 3.08 8.35 0.52 q2LLFif4 19,361,3551-97,628,360 PZE-101099263-PZE-10101518 3.47,75 0.82 q2LLFif7 7 1,979,634-4,709,247 PZE-101099263-PZE-101010518 3.47,75 0.82 q2LFif7 7 1,979,634-4,709,247 PZE-1011450-PZE-106105801 2.67 8.18 0.57 q3LFir3 3 169,008,365-175,554,472 PZE-101150712 3.08 8.10 -0.65 Cong3×Yu87-1 1144,508,722,599 PZE-10114552-PZE-101150712 3.08 8.10 -1.44 q3LFir3 3 169,008,365-175,554,472 PZE-101145022-PZE-100315618 3.15	ILSec	a2ILSec5	5	189.537.160-193.310.292	PZE-105133858-PZE-105138182	3.95	9.49	0.50
q2lLSec10 10 123,635,404-124,526,091 SYN15051-PZE-100906470 2.08 10.15 0.52 ILFri q2lLFn93 33,745,032-135,152,250 PZE-103026528-PZE-1030025754 3.67 7.54 0.43 ILFor q2lLFor6 6 155,609,243-155,386,157 PZE-103026528-PZE-1003025744 3.67 7.88 0.53 q2lLFor6 6 155,609,243-155,386,157 PZE-1010090207-PZE-10906476 3.08 8.35 0.52 q2lLFi6 6 155,609,243-155,6380 PZE-101099263-PZE-10110518 3.34 7.75 0.82 q2lLFi7 1,979,634,47,09,247 PZE-10000230-SYN20419 10.33 25.63 -1.64 q2lLFi7 1,979,634,47,09,247 PZE-101102330-SYN20419 10.38 8.10 0.65 Cong3×YU87.1 1 189,522,638-19,4527,599 PZE-1011105712 5.89 14.41 -1.44 q3lLFi7-1 1 189,522,638-19,4527,599 YN28646-PZE-105073970 4.32 9.13 -1.15 q3lLFir1 1 189,522,638-19,4527,599 YN28464-PZE-103073568 <td< td=""><td></td><td>a2ILSec9</td><td>9</td><td>133,745,032-135,152,250</td><td>PZE-109090207-PZE-109086476</td><td>2.81</td><td>7.83</td><td>0.42</td></td<>		a2ILSec9	9	133,745,032-135,152,250	PZE-109090207-PZE-109086476	2.81	7.83	0.42
ILThi Q2LThi9 9 133,745,032-135,152,250 PZE-100090207-PZE-109086476 2.85 7.54 0.43 ILFor Q2LFor3 3 19,654,756-20.022,149 PZE-103026528-PZE-103027544 3.67 8.86 0.57 Q2LFor6 6 155,609,243-156,368,157 PZE-1001005801 3.07 7.88 0.53 Q2LFif6 6 155,609,243-156,368,157 PZE-101009263-PZE-106105801 3.08 8.35 0.52 Q2LFif7 7 1,979,634-4,709,247 PZE-100104150-PZE-106105801 2.07 8.18 0.67 Q2LFif9 144,508,752-141,768,418 PZE-101002330-SVRU20419 10.33 25.63 -1.64 Q3LFir3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 3.15 6.82 -0.97 Q3LFir5-1 5 63,405,163-80.802,797 SYN2864-PZE-105073970 4.32 -1.17 Q3LFir51 10 128,463,363-130,267,668 PZE-101072556 4.73 9.67 1.17 ULFir 15 63,405,163-80.802,797 SYN2864-PZE-103173576 4.73		a2ILSec10	10	123.635.404-124.526.091	SYN15051-PZE-110068110	4.08	10.15	0.52
ILFor q2LEFor3 3 19,654,756-20,022,149 PZE-103024528-PZE-103027544 3.67 8.86 0.57 q2LEFor9 6 155,609,243-155,368,157 PZE-106104150-PZE-106108501 3.07 7.88 0.53 q2LEFor9 9 133,745,032-135,152,57 PZE-101099263-PZE-109086476 3.08 8.35 0.52 q2LEFif6 6 155,609,243-155,368,157 PZE-101092530-PZE-109086476 3.08 8.10 0.56 q2LEFif6 6 155,609,243-155,368,157 PZE-101092330-SYN20419 10.33 25.63 -1.64 q2LEFif7 7 1,979,634-4,709,247 PZE-101002330-SYN20419 10.33 25.63 -1.64 q3LEFir3 3 169,008,365-175,554,472 PZE-10114525-PZE-103115618 3.15 6.82 -0.97 q3LEFir5-1 5 63,405,163-80,802,797 SYN26864-PZE-105073970 4.32 9.13 -1.15 q3LEFir5-1 5 63,405,163-80,802,797 SYN26864-PZE-105128589 3.08 9.77 1.23 q3LEFir5-1 5 63,405,163-80,802,797	ILThi	a2ILThi9	9	133.745.032-135.152.250	PZE-109090207-PZE-109086476	2.85	7.54	0.43
q2lLFor6 6 155,609,243-156,368,157 PZE-106104150-PZE-109086476 3.07 7.88 0.53 LLFif q2lLFif 1 33,745,032-133,152,250 PZE-109090207-PZE-109086476 3.08 8.35 0.52 q2lLFif 1 33,615,197,262,80 PZE-101019518 3.34 7.75 0.82 q2lLFif 7 1,979,634-4,709,247 PZE-106104150-PZE-108105801 2.87 8.18 0.57 q2lLFif 7 1,979,634-4,709,247 PZE-101009253-PZE-108105801 2.87 8.18 0.55 Zong3×Yu87-1 ILFir q3lLFir1 1 189,522,638-19,4527,599 PZE-101145525-PZE-101150712 5.89 14.41 -1.44 q3lLFir5-1 5 63,405,163-80,802,797 SYN2864-PZE-105128589 3.08 7.7 1.23 q3lLFir5-2 178,63,383-184,840,77 SYN38466-PZE-105128589 3.88 8.14 -0.60 q3lLSec3 169,008,365-175,554,472 PZE-100902437-PZE-1009074370 3.19 7.36 0.53 lLSec 133,269,052 105,251,0472 <th< td=""><td>ILFor</td><td>a2ILFor3</td><td>3</td><td>19.654.756-20.022.149</td><td>PZE-103026528-PZE-103027544</td><td>3.67</td><td>8.86</td><td>0.57</td></th<>	ILFor	a2ILFor3	3	19.654.756-20.022.149	PZE-103026528-PZE-103027544	3.67	8.86	0.57
q2 LFor9 9 133,745,032-135,152,250 PZE-109090207-PZE-109008476 3.08 8.35 0.52 ILFif q2 LFif4 1 93,613,551-97,628,380 PZE-100109223-PZE-101101518 3.34 7.75 0.82 q2 LFif4 6 155,609,243-156,368,517 PZE-106104150-PZE-106105801 2.87 8.18 0.57 q2 LFif7 7 1,979,634-4,709,247 PZE-107002330-SYN20419 10.33 25.63 -1.64 q2 LFir3 3 169,008,365-175,554,472 PZE-101146525-PZE-101150712 5.89 14.41 -1.44 q3 LFir5-1 5 63,405,163-80,802,797 SYN2864-PZE-105073970 4.32 9.13 -1.15 q3 LFir5-1 5 63,405,163-80,802,797 SYN2864-PZE-105128589 3.08 9.77 1.23 q3 LFir10 10 128,463,363-130,267,668 PZE-103110355-PZE-103115618 3.28 8.14 -0.60 q3 LSec3 3 169,008,365-175,554,472 PZE-100723700 3.19 7.36 0.58 q3 LFir10 128,764,337-201,018,022 PZE-1010073270<		a2ILFor6	6	155.609.243-156.368.157	PZE-106104150-PZE-106105801	3.07	7.88	0.53
ILFif q2ILFif1 1 93,613,551-97,628,380 PZE-101099263-PZE-101101518 3.34 7.75 0.82 q2ILFif6 6 155,609,243-156,368,157 PZE-107002330-SYN20419 10.33 25.63 -1.64 q2ILFif6 7 1,979,634-4,709,247 PZE-107002330-SYN20419 10.33 25.63 -1.64 Q3ILFir3 3 149,008,365-175,554,472 PZE-101146525-PZE-101150712 5.89 14.41 -1.44 q3ILFir5-1 5 63,005,163-80,802,797 SYN28646-PZE-100573970 4.32 9.13 -1.73 q3ILFir5-1 5 63,405,163-80,802,797 SYN28646-PZE-100573970 3.19 7.36 0.58 q3ILSec5.1 5 63,405,163-80,802,797 SYN28644-PZE-105105391 3.15 8.82 -0.58 q3ILSec5.1 5 63,405,163-80,802,797 SYN2864-PZE-10073576 4.73 9.87 1.17 ILSec q3ILSec5.1 5 63,405,163-80,802,797 SYN2864-PZE-100573970 3.19 7.36 0.58 q3ILSec5.1 5 63,405,163-80,802,79		a2ILFor9	9	133.745.032-135.152.250	PZE-109090207-PZE-109086476	3.08	8.35	0.52
q2 LFif6 6 155,609,243156,368,157 PZE-106104150-PZE-106105801 2.87 8.18 0.57 q2 LFif7 7 1,979,634.4,709,247 PZE-106104150-PZE-109102157 3.08 8.10 0.65 Zong3×Yu87-1 ILFir q3 LFir1 1 189,522,638-19,4527,599 PZE-1011145525-PZE-101150712 5.89 14.41 -1.44 q3 LFir5 1 6,3,405,163.80,802,777 SYN28644-PZE-1001150712 5.89 14.41 -1.44 q3 LFir5 5 6,3,405,163.80,802,797 SYN28644-PZE-1051037370 4.32 9.13 -1.15 q3 LFir5 5 6,3,405,163.80,802,797 SYN28644-PZE-10073370 3.19 7.36 0.58 q3 LFir5 1 6,3,405,163.80,802,797 SYN28644-PZE-100073970 3.19 7.36 0.58 q3 LSec5-1 5 6,3,405,163.80,802,797 SYN26864-PZE-100073970 3.19 7.36 0.58 q3 LSec5-1 5 6,3,405,163.80,802,797 SYN26864-PZE-100073970 3.19 7.36 0.58 q3 LSec5-1 5 6,3,405	ILFif	a2ILFif1	1	93.613.551–97.628.380	PZE-101099263-PZE-101101518	3.34	7.75	0.82
q2 LFif7 q2 LFif7 q2 LFif7 7 t44,508,752-141,768,418 PZE-107002330-SYN20419 10.33 t0.33 25.63 t0.65 -1.64 Zong3×Yu87-1 1 144,508,752-141,768,418 PZE-109099670-PZE-109102157 3.08 8.10 0.65 LlFir q31LFir1 1 189,522,638-19,4527,599 PZE-101146525-PZE-101150712 5.89 14.41 -1.44 q31LFir5-1 5 63,405,163-80,802,797 SYN2864-PZE-105073970 4.32 9.13 -1.15 q31LFir5-1 5 63,405,163-80,802,797 SYN28646-PZE-105128589 3.08 9.77 1.23 g31LSec5 1 649,008,365-175,554,472 PZE-103110355-PZE.103115618 3.28 8.14 -0.60 q31LSec5 5 63,405,163-80,802,797 SYN28646-PZE-105073970 3.19 7.36 0.58 q31LSec5 5 63,405,163-80,802,797 SYN28646-PZE-105103931 3.44 10.39 0.75 q31LSec5 1 56,920-140,436,979 PZE-105073970 3.19 7.36 0.58 q31LSec70 1 122,764,555-123,364,763		a2ILFif6	6	155.609.243-156.368.157	PZE-106104150-PZE-106105801	2.87	8.18	0.57
q2 LFiif9 144,500,752-141,768,418 PZE-10909970-PZE-109102157 3.08 8.10 0.65 Zong3×Yu87-1 ILFir q31LFir1 1 189,522,638-19,4527,599 PZE-101146525-PZE-101150712 5.89 14.41 -1.44 Q31LFir5-1 5 63,405,163-80,802,797 SYN2884-PZE-105128589 3.08 9.77 1.15 Q31LFir5-1 5 63,405,163-80,802,797 SYN28844-PZE-105073970 4.32 9.13 -1.15 Q31LSec53 3 169,008,365-175,554,472 PZE-101072576 4.73 9.87 1.17 ILSec Q31LSec5-1 63,405,163-80,802,797 SYN28844-PZE-105073970 3.18 8.84 -0.60 Q31LSec5-2 5 200,776,837-201,018,062 PZE-101079253-PZE-10007375 3.74 1.039 0.75 Q31LSec10 102,274,55554,472 PZE-105073970 3.18 8.85 -0.58 Q31LSec79 9 135,296,920-140,436,979 PZE-105073970 3.13 18.85 -0.58 Q31LThi 31 69,008,365-175,554,472 PZE-105074181-PZE-105073970		a21LFif7	7	1.979.634–4.709.247	PZE-107002330-SYN20419	10.33	25.63	-1.64
Zong3×Yu87-1 Image: Constraint of the constr		a2ILFif9		144.508.752–141.768.418	PZE-109099670-PZE-109102157	3.08	8.10	0.65
ILFir q3ILFir1 1 189,522,638-19,4527,599 PZE-101146525-PZE-101150712 5.89 14.41 -1.44 q3ILFir3 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 3.15 6.82 -0.97 q3ILFir5-1 5 63,405,163-80,802,797 SYN26864-PZE-105128589 3.08 9.77 1.23 q3ILFir5-2 5 178,630,838-184,840,977 SYN38466-PZE-105128589 3.08 9.77 1.23 q3ILSec3 3 169,008,365-175,554,472 PZE-103110355-PZE-101512618 3.28 8.14 -0.60 q3ILSec5 5 63,405,163-80,802,797 SYN28664-PZE-105073970 3.19 7.36 0.58 q3ILSec7 9 135,296,920-140,436,979 PZE-109092637-PZE-109094331 3.15 8.85 -0.58 q3ILSec10 1 122,764,555-123,364,763 PZE-1010066732-PZE-1010067110 2.70 7.53 0.53 ILThi q3ILThi2 17,397,718-17,903,733 SYN18094-PZE-102037260 2.58 6.10 0.54 q3ILThi2 17,397,718-17,903,733 SYN18094-PZE-1015128217 3.62 10.93 0.89 0.81 0.44<	Zona3×Yu87-1	1						
q3ILFir3 3 169,008,355-175,554,472 PZE-103110355-PZE-103115618 3.15 6.82 -0.97 q3ILFir5-1 5 63,405,163-80,802,797 SYN28664-PZE-105073970 4.32 9.13 -1.15 q3ILFir5-2 5 178,630,838-184,840,977 SYN38466-PZE-105128589 3.08 9.77 1.23 q3ILFir50 10 128,445,363-130,267,668 PZE-110072258-PZE-103115618 3.28 8.14 -0.60 q3ILSec5-1 5 63,405,163-80,802,797 SYN28664-PZE-105073970 3.19 7.36 0.58 q3ILSec5-2 5 200,776,837-201,018,062 PZE-105150110-PZE-105150391 3.44 -0.60 q3ILSec5-1 5 63,405,163-80,802,797 SYN18064-PZE-105073970 3.19 7.36 0.58 q3ILSec5-2 5 200,776,837-201,018,062 PZE-1051510110-PZE-10510311 2.70 7.53 0.53 q3ILThi 31 169,008,365-175,554,472 PZE-100173550 2.58 6.10 0.54 q3ILThi 3 169,008,365-175,554,472 PZE-105073870 4.13 <td>ILFir</td> <td>a3ILFir1</td> <td>1</td> <td>189.522.638-19.4527.599</td> <td>PZE-101146525-PZE-101150712</td> <td>5.89</td> <td>14.41</td> <td>-1.44</td>	ILFir	a3ILFir1	1	189.522.638-19.4527.599	PZE-101146525-PZE-101150712	5.89	14.41	-1.44
q31LFir5-1 5 63,405,163-80,802,797 SYN26864-PZE-105073970 4.32 9.13 -1.15 q31LFir5-2 5 178,630,838-184,840,977 SYN38466-PZE-105128589 3.08 9.77 1.23 q31LFir10 10 128,463,363-130,267,668 PZE-110072258-PZE-103115618 3.28 8.14 -0.60 q31LSec3 3 69,008,365-175,554,472 PZE-103110355-PZE-103115618 3.28 8.14 -0.60 q31LSec5-1 5 63,405,163-80,802,797 SYN26864-PZE-105073970 3.19 7.36 0.58 q31LSec5-1 5 63,405,163-80,802,797 SYN26864-PZE-105073970 3.19 7.36 0.58 q31LSec10 122,764,555-123,364,763 PZE-101006732-PZE-100094331 3.15 8.85 -0.58 q31LThi2 2 17,397,718-17,903,733 SYN18094-PZE-105073970 4.13 10.38 -0.71 q31LThi3 169,008,365-175,554,472 PZE-105074181-PZE-105073970 4.13 10.38 -0.71 q31LFor2 179,626,240-184,744,673 PZE-105074181-PZE-105128217 3.62 <t< td=""><td></td><td>a3ILFir3</td><td>3</td><td>169.008.365-175.554.472</td><td>PZE-103110355-PZE-103115618</td><td>3.15</td><td>6.82</td><td>-0.97</td></t<>		a3ILFir3	3	169.008.365-175.554.472	PZE-103110355-PZE-103115618	3.15	6.82	-0.97
q3lLFir5-2 5 179,630,838-184,840,977 SYN38466-PZE-105128589 3.08 9.77 1.23 q3lLFir10 10 128,463,363-130,267,668 PZE-110072258-PZE-110073576 4.73 9.87 1.17 ILSec q3lLSec5-1 5 63,405,153-80,802,77 SYN26864-PZE-105073970 3.19 7.36 0.58 q3lLSec5-2 5 200,776,837-201,018,062 PZE-105150110-PZE-105150391 3.44 10.39 0.75 q3lLSec10 10 122,764,555-123,364,763 PZE-1000702727-PZE-109094331 3.15 8.85 -0.58 q3lLThi2 2 17,397,718-17,903,733 SYN18094-PZE-102037260 2.58 6.10 0.54 q3lLThi3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 4.40 11.54 -0.73 q3lLThi5-1 5 80,223,529-80,802,797 PZE-1050734970 4.13 10.38 -0.71 q3lLFor1 1 220,106,564-219,701,709 SYN18094-PZE-10507385-PZE-103115618 4.40 11.54 -0.62 q3lLFor3 169,008,365-175,554,472 PZE-1010745305		a3ILFir5-1	5	63.405.163-80.802.797	SYN26864-PZE-105073970	4.32	9.13	-1.15
q3lLFir10 10 128,463,363-130,267,668 PZE-11007258-PZE-110073576 4.73 9.87 1.17 ILSec q3lLSec3 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 3.28 8.14 -0.60 q3lLSec5-2 5 200,776,837-201,018,062 PZE-105150110-PZE-105150391 3.14 10.39 0.75 q3lLSec5-2 5 200,776,4555-123,364,763 PZE-1009094331 3.15 8.85 -0.58 q3lLSec10 10 122,764,555-123,364,763 PZE-10006732-PZE-10007110 2.70 7.53 0.53 q3lLThi<3		a3ILFir5-2	5	178,630,838–184,840,977	SYN38466-PZE-105128589	3.08	9.77	1.23
ILSec q3ILSec3 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 3.28 8.14 -0.60 q3ILSec5-1 5 63,405,163-80,802,797 SYN26864-PZE-105073970 3.19 7.36 0.58 q3ILSec5-2 5 200,776,837-201,018,062 PZE-105150110-PZE-109094331 3.15 8.85 -0.58 q3ILSec10 10 122,764,555-123,364,763 PZE-110066732-PZE-110067110 2.70 7.53 0.53 ILThi q3ILThi2 2 17,397,718-17,903,733 SYN18094-PZE-102037260 2.58 6.10 0.54 q3ILThi5-1 5 80,223,529-80,802,797 PZE-105173635-PZE-105128217 3.62 10.93 0.89 q3ILThi5-2 5 179,626,240-184,744,673 PZE-109074509-PZE-109079845 3.61 8.86 -0.65 ILFor q3ILFor3 169,008,365-175,554,472 PZE-105123635-PZE-103115618 5.79 17.45 -1.22 q3ILFor3 169,008,365-175,554,472 PZE-105073970 3.61 8.86 -0.65 q3ILFor3 169,008,365-175,554,472 PZE-105123635-PZE-105128217 3.25 9.27 0.91		a3ILFir10	10	128.463.363-130.267.668	PZE-110072258-PZE-110073576	4.73	9.87	1.17
indistriction indistribute indistrindistrindi indistribute indist	ILSec	q3ILSec3	3	169,008,365-175,554,472	PZE-103110355-PZE-103115618	3.28	8.14	-0.60
q3lLSec5-2 5 200,776,837-201,018,062 PZE-105150110-PZE-105150391 3.44 10.39 0.75 q3lLSec9 9 135,296,920-140,436,979 PZE-109092637-PZE-109094331 3.15 8.85 -0.58 q3lLSec10 10 122,764,555-123,364,763 PZE-110066732-PZE-10007110 2.70 7.53 0.53 q3lLThi2 2 17,397,718-17,903,733 SYN18094-PZE-102037260 2.58 6.10 0.54 q3lLThi3 166,008,365-175,554,472 PZE-103115618 4.40 11.54 -0.73 q3lLThi5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 4.13 10.38 -0.71 q3lLThi5-2 5 179,626,240-184,744,673 PZE-105128217 3.62 10.93 0.89 q3lLFor1 1 220,106,564-219,701,709 SYN2411-SYN19847 4.25 7.48 -0.65 q3lLFor3 169,008,365-175,554,472 PZE-105128217 3.62 9.27 0.91 q3lLFor3 169,008,365-175,554,472 PZE-100110355-PZE-103115618 5.79 7.48 -0.92 <td></td> <td>a3ILSec5-1</td> <td>5</td> <td>63,405,163-80,802,797</td> <td>SYN26864-PZE-105073970</td> <td>3.19</td> <td>7.36</td> <td>0.58</td>		a3ILSec5-1	5	63,405,163-80,802,797	SYN26864-PZE-105073970	3.19	7.36	0.58
q3lLSec9 9 135,296,920-140,436,979 PZE-109092637-PZE-109094331 3.15 8.85 -0.58 q3lLSec10 10 122,764,555-123,364,763 PZE-110066732-PZE-110067110 2.70 7.53 0.53 ILThi q3lLThi2 2 17,397,718-17,903,733 SYN18094-PZE-102037260 2.58 6.10 0.54 q3lLThi5 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 4.40 11.54 -0.73 q3lLThi5-1 5 80,223,529-80,802,797 PZE-105123635-PZE-105128217 3.62 10.93 0.89 q3lLThi5-2 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 3.62 10.93 0.89 q3lLFor1 1 220,106,564-219,701,709 SYN2411-SYN19847 4.25 7.48 -0.92 q3lLFor2 2 17,397,718-19,905,537 SYN18094-PZE-102039914 3.25 9.27 0.91 q3lLFor3 3 169,008,365-175,554,472 PZE-103110355-PZE-105128217 3.29 6.92 0.70 q3lLFor5-1 5 80,223,529-80,802,797 <td></td> <td>q3ILSec5-2</td> <td>5</td> <td>200,776,837-201,018,062</td> <td>PZE-105150110-PZE-105150391</td> <td>3.44</td> <td>10.39</td> <td>0.75</td>		q3ILSec5-2	5	200,776,837-201,018,062	PZE-105150110-PZE-105150391	3.44	10.39	0.75
q3ILSec10 10 122,764,555-123,364,763 PZE-110066732-PZE-110067110 2.70 7.53 0.53 ILThi q3ILThi2 2 17,397,718-17,903,733 SYN18094-PZE-102037260 2.58 6.10 0.54 q3ILThi3 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 4.40 11.54 -0.73 q3ILThi5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 4.13 10.38 -0.71 q3ILThi5-2 5 179,626,240-184,744,673 PZE-105074509-PZE-105128217 3.62 10.93 0.89 q3ILThi9 9 116,763,031-127,820,710 PZE-109074509-PZE-109079845 3.61 8.86 -0.65 ILFor q3ILFor1 1 220,106,564-219,701,709 SYN2411-SYN19847 4.25 7.48 -0.92 q3ILFor3 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 5.79 17.45 -1.22 q3ILFor3 3 169,008,365-175,554,472 PZE-105123635-PZE-103115618 5.79 17.45 -1.22 q3ILFor5 5		a3ILSec9	9	135,296,920–140,436,979	PZE-109092637-PZE-109094331	3.15	8.85	-0.58
ILThi d3ILThi2 2 17,397,718-17,903,733 SYN18094-PZE-102037260 2.58 6.10 0.54 q3ILThi3 3 169,008,365-175,554,472 PZE-103115518 4.40 11.54 -0.73 q3ILThi5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 4.13 10.38 -0.71 q3ILThi5-2 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 3.62 10.93 0.89 q3ILThi9 9 116,763,031-127,820,710 PZE-109074509-PZE-109079845 3.61 8.86 -0.65 q3ILFor1 1 220,106,564-219,701,709 SYN2411-SYN19847 4.25 7.48 -0.92 q3ILFor2 2 17,397,718-19,905,537 SYN18094-PZE-102039914 3.25 9.27 0.91 q3ILFor3 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 5.79 17.45 -1.22 q3ILFor5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 5.08 14.04 -1.21 q3ILFor5-2 5 17,962,6240-184,744,673 PZE-105123635-PZE-105128217 3.29 6.92 0.70 q3ILFor5-2 5 17,962,6240-184,744,673 PZE-105123635-PZE-105128217 3.29 6.92 0.70 q3ILFor5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 3.29 6.92 0.70 q3ILFif5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 3.29 6.92 0.70 q3ILFif5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 3.94 6.1 1.01 q3ILFif5 9 9 117,976,872-127,820,710 PZE-109075481-PZE-109079845 4.58 11.15 -0.90 ILFif q3ILFif2 2 24,585,454-34,305,177 PZE-102047066-PZE-102056295 3.19 8.61 1.01 q3ILFif5 9 12,822,604-135,146,198 PZE-109078269-PZE-105128217 2.99 7.04 0.82 q3ILFif9 9 121,822,604-135,146,198 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 ILFir q4ILFir3-1 3 8,270,856-9,886,045 PZE-103015388-SYN36244 3.54 12.01 -0.88 q4ILFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544 2.85 8.71 -0.72		a3ILSec10	10	122,764,555–123,364,763	PZE-110066732-PZE-110067110	2.70	7.53	0.53
q3lLThi3 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 4.40 11.54 -0.73 q3lLThi5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 4.13 10.38 -0.71 q3lLThi5-2 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 3.62 10.93 0.89 q3lLThi9 9 116,763,031-127,820,710 PZE-109074509-PZE-109079845 3.61 8.86 -0.65 lLFor q3lLFor1 1 220,106,564-219,701,709 SYN2411-SYN19847 4.25 7.48 -0.92 q3lLFor2 2 17,397,718-19,905,537 SYN18094-PZE-102039914 3.25 9.27 0.91 q3lLFor3 3 169,008,365-175,554,472 PZE-105173618 5.79 17.45 -1.22 q3lLFor5-1 5 80,223,529-80,802,797 PZE-105073970 5.08 14.04 -1.21 q3lLFor5-2 5 17,962,6240-184,744,673 PZE-105073970 5.08 14.04 -1.21 q3lLFor5-2 5 17,962,6240-184,744,673 PZE-105073970 5.08 14.04 -1.21 q3lLFif5 17,	ILThi	q3ILThi2	2	17,397,718–17,903,733	SYN18094-PZE-102037260	2.58	6.10	0.54
q3ILThi5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 4.13 10.38 -0.71 q3ILThi5-2 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 3.62 10.93 0.89 q3ILThi9 9 116,763,031-127,820,710 PZE-109074509-PZE-109079845 3.61 8.86 -0.65 ILFor q3ILFor1 1 220,106,564-219,701,709 SYN2411-SYN19847 4.25 7.48 -0.92 q3ILFor2 2 17,397,718-19,905,537 SYN18094-PZE-102039914 3.25 9.27 0.91 q3ILFor3 3 169,008,365-175,554,472 PZE-1051723635-PZE-103115618 5.79 17.45 -1.22 q3ILFor5-1 5 80,223,529-80,802,797 PZE-1050734181-PZE-105073970 5.08 14.04 -1.21 q3ILFor5-2 5 17,962,6240-184,744,673 PZE-105128617 3.29 6.92 0.70 q3ILFor9 9 117,976,872-127,820,710 PZE-105128617 3.29 6.92 0.70 q3ILFif 3 179,626,240-184,744,673 PZ		a3ILThi3	3	169,008,365-175,554,472	PZE-103110355-PZE-103115618	4.40	11.54	-0.73
q3lLThi5-2 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 3.62 10.93 0.89 q3lLThi9 9 116,763,031-127,820,710 PZE-109074509-PZE-109079845 3.61 8.86 -0.65 ILFor q3lLFor1 1 220,106,564-219,701,709 SYN2411-SYN19847 4.25 7.48 -0.92 q3lLFor2 2 17,397,718-19,905,537 SYN18094-PZE-102039914 3.25 9.27 0.91 q3lLFor3 3 169,008,365-175,554,472 PZE-105123635-PZE-103115618 5.79 17.45 -1.22 q3lLFor5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 5.08 14.04 -1.21 q3lLFor5-2 5 17,962,6240-184,744,673 PZE-105123635-PZE-105128217 3.29 6.92 0.70 q3lLFor5-2 5 17,962,6240-184,744,673 PZE-109075481-PZE-109079845 4.58 11.15 -0.90 ILFif q3lLFor9 9 117,976,872-127,820,710 PZE-102047066-PZE-102056295 3.19 8.61 1.01 q3lLFor9 9 127,976,872-127,820,710 PZE-105123635-PZE-105128217 2.99 7.04		q3ILThi5-1	5	80,223,529-80,802,797	PZE-105074181-PZE-105073970	4.13	10.38	-0.71
q3ILThi9 9 116,763,031-127,820,710 PZE-109074509-PZE-109079845 3.61 8.86 -0.65 ILFor q3ILFor1 1 220,106,564-219,701,709 SYN2411-SYN19847 4.25 7.48 -0.92 q3ILFor2 2 17,397,718-19,905,537 SYN18094-PZE-102039914 3.25 9.27 0.91 q3ILFor3 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 5.79 17.45 -1.22 q3ILFor5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 5.08 14.04 -1.21 q3ILFor5-2 5 17,962,6240-184,744,673 PZE-109075481-PZE-105128217 3.29 6.92 0.70 q3ILFor5 5 17,962,6240-184,744,673 PZE-109075481-PZE-109079845 4.58 11.15 -0.90 ILFif q3ILFif2 2 24,585,454-34,305,177 PZE-102047066-PZE-102056295 3.19 8.61 1.01 q3ILFif5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 179,626,240-138,146,198 PZE-109078269-PZE-109086475 6.38 16.76 -		a3ILThi5-2	5	179,626,240-184,744,673	PZE-105123635-PZE-105128217	3.62	10.93	0.89
ILFor q3ILFor1 1 220,106,564–219,701,709 SYN2411–SYN19847 4.25 7.48 -0.92 q3ILFor2 2 17,397,718–19,905,537 SYN18094–PZE-102039914 3.25 9.27 0.91 q3ILFor3 3 169,008,365–175,554,472 PZE-103110355–PZE-103115618 5.79 17.45 -1.22 q3ILFor5-1 5 80,223,529–80,802,797 PZE-105074181–PZE-105073970 5.08 14.04 -1.21 q3ILFor5-2 5 17,962,6240–184,744,673 PZE-105123635–PZE-105128217 3.29 6.92 0.70 q3ILFor5 5 17,962,6240–184,744,673 PZE-109075481–PZE-109079845 4.58 11.15 -0.90 ILFif q3ILFif2 2 24,585,454–34,305,177 PZE-102047066–PZE-102056295 3.19 8.61 1.01 q3ILFif5 5 179,626,240–184,744,673 PZE-105123635–PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 179,626,240–184,744,673 PZE-109078269–PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 9 11.13 -1.00 -1.15 -1.15 -1.15 -0.88		q3ILThi9	9	116,763,031-127,820,710	PZE-109074509-PZE-109079845	3.61	8.86	-0.65
q3ILFor2 2 17,397,718-19,905,537 SYN18094-PZE-102039914 3.25 9.27 0.91 q3ILFor3 3 169,008,365-175,554,472 PZE-103110355-PZE-103115618 5.79 17.45 -1.22 q3ILFor5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 5.08 14.04 -1.21 q3ILFor5-2 5 17,962,6240-184,744,673 PZE-105123635-PZE-105128217 3.29 6.92 0.70 q3ILFor5-2 5 17,962,6240-184,744,673 PZE-109075481-PZE-109079845 4.58 11.15 -0.90 ILFif q3ILFif2 2 24,585,454-34,305,177 PZE-102047066-PZE-102056295 3.19 8.61 1.01 q3ILFif5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 179,626,240-184,744,673 PZE-109078269-PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 179,626,240-135,146,198 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 9 121,822,604-135,146,198 PZE-109078269-PZE-109086475 6.38 16.76 -1.1	ILFor	q3ILFor1	1	220,106,564-219,701,709	SYN2411-SYN19847	4.25	7.48	-0.92
q3ILFor3 3 169,008,365–175,554,472 PZE-103110355–PZE-103115618 5.79 17.45 -1.22 q3ILFor5-1 5 80,223,529–80,802,797 PZE-105074181–PZE-105073970 5.08 14.04 -1.21 q3ILFor5-2 5 17,962,6240–184,744,673 PZE-105123635–PZE-105128217 3.29 6.92 0.70 q3ILFor5-2 5 17,962,6240–184,744,673 PZE-109075481–PZE-109079845 4.58 11.15 -0.90 ILFif q3ILFif2 2 24,585,454–34,305,177 PZE-102047066–PZE-102056295 3.19 8.61 1.01 q3ILFif5 5 179,626,240–184,744,673 PZE-105123635–PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 179,626,240–184,744,673 PZE-109078269–PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 179,626,240–135,146,198 PZE-109078269–PZE-105128217 2.99 7.04 0.82 q3ILFif9 9 121,822,604–135,146,198 PZE-109078269–PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 ILFir q4ILFir3-1 3 8,270,856–9,886,045 PZE-103015388–SYN36244		a3ILFor2	2	17,397,718–19,905,537	SYN18094-PZE-102039914	3.25	9.27	0.91
q3ILFor5-1 5 80,223,529-80,802,797 PZE-105074181-PZE-105073970 5.08 14.04 -1.21 q3ILFor5-2 5 17,962,6240-184,744,673 PZE-105123635-PZE-105128217 3.29 6.92 0.70 q3ILFor5-2 5 17,962,6240-184,744,673 PZE-109075481-PZE-109079845 4.58 11.15 -0.90 ILFif q3ILFif2 2 24,585,454-34,305,177 PZE-102047066-PZE-102056295 3.19 8.61 1.01 q3ILFif5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 179,626,240-184,744,673 PZE-108092173-PZA03698.1 3.94 11.13 -1.00 q3ILFif8 8 149,193,811-155,571,435 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 9 121,822,604-135,146,198 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 1LFir q4ILFir3-1 3 8,270,856-9,886,045 PZE-103015388-SYN36244 3.54 12.01 -0.88 q4ILFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544		q3ILFor3	3	169,008,365–175,554,472	PZE-103110355-PZE-103115618	5.79	17.45	-1.22
q3ILFor5-2 5 17,962,6240-184,744,673 PZE-105123635-PZE-105128217 3.29 6.92 0.70 q3ILFor9 9 117,976,872-127,820,710 PZE-109075481-PZE-109079845 4.58 11.15 -0.90 ILFif q3ILFif2 2 24,585,454-34,305,177 PZE-102047066-PZE-102056295 3.19 8.61 1.01 q3ILFif5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 179,626,240-184,744,673 PZE-108092173-PZA03698.1 3.94 11.13 -1.00 q3ILFif8 8 149,193,811-155,571,435 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 9 121,822,604-135,146,198 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 ILFir q4ILFir3-1 3 8,270,856-9,886,045 PZE-103015388-SYN36244 3.54 12.01 -0.88 q4ILFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544 2.85 8.71 -0.72		a3ILFor5-1	5	80,223,529-80,802,797	PZE-105074181-PZE-105073970	5.08	14.04	-1.21
q3ILFor9 9 117,976,872-127,820,710 PZE-109075481-PZE-109079845 4.58 11.15 -0.90 ILFif q3ILFif2 2 24,585,454-34,305,177 PZE-102047066-PZE-102056295 3.19 8.61 1.01 q3ILFif5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 179,626,240-184,744,673 PZE-108092173-PZA03698.1 3.94 11.13 -1.00 q3ILFif8 8 149,193,811-155,571,435 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 9 121,822,604-135,146,198 PZE-103015388-SYN36244 3.54 12.01 -0.88 q4ILFir3-1 3 8,270,856-9,886,045 PZE-103026528-PZE-103027544 3.54 12.01 -0.88 q4ILFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544 2.85 8.71 -0.72		a3ILFor5-2	5	17,962,6240–184,744,673	PZE-105123635-PZE-105128217	3.29	6.92	0.70
ILFif q3ILFif2 2 24,585,454-34,305,177 PZE-102047066-PZE-102056295 3.19 8.61 1.01 q3ILFif5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 2.99 7.04 0.82 q3ILFif8 8 149,193,811-155,571,435 PZE-108092173-PZA03698.1 3.94 11.13 -1.00 q3ILFif9 9 121,822,604-135,146,198 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 ILFir q4ILFir3-1 3 8,270,856-9,886,045 PZE-103015388-SYN36244 3.54 12.01 -0.88 q4ILFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544 2.85 8.71 -0.72		, q3ILFor9	9	117,976,872-127,820,710	PZE-109075481-PZE-109079845	4.58	11.15	-0.90
q3ILFif5 5 179,626,240-184,744,673 PZE-105123635-PZE-105128217 2.99 7.04 0.82 q3ILFif5 5 149,193,811-155,571,435 PZE-108092173-PZA03698.1 3.94 11.13 -1.00 q3ILFif9 9 121,822,604-135,146,198 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 ILFir q4ILFir3-1 3 8,270,856-9,886,045 PZE-103015388-SYN36244 3.54 12.01 -0.88 q4ILFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544 2.85 8.71 -0.72	ILFif	a3ILFif2	2	24,585,454-34,305,177	PZE-102047066-PZE-102056295	3.19	8.61	1.01
q3lLFif8 8 149,193,811-155,571,435 PZE-108092173-PZA03698.1 3.94 11.13 -1.00 q3lLFif9 9 121,822,604-135,146,198 PZE-109078269-PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 ILFir q4lLFir3-1 3 8,270,856-9,886,045 PZE-103015388-SYN36244 3.54 12.01 -0.88 q4lLFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544 2.85 8.71 -0.72		a3ILFif5	5	179,626,240–184.744.673	PZE-105123635-PZE-105128217	2.99	7.04	0.82
q3ILFif9 9 121,822,604–135,146,198 PZE-109078269–PZE-109086475 6.38 16.76 -1.15 Yu537×Shen137 ILFir q4ILFir3-1 3 8,270,856–9,886,045 PZE-103015388–SYN36244 3.54 12.01 -0.88 q4ILFir3-2 3 19,654,756–20,022,149 PZE-103026528–PZE-103027544 2.85 8.71 -0.72		g3ILFif8	8	149,193,811–155.571.435	PZE-108092173-PZA03698.1	3.94	11.13	-1.00
Yu537×Shen137 q4ILFir3-1 3 8,270,856-9,886,045 PZE-103015388-SYN36244 3.54 12.01 -0.88 q4ILFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544 2.85 8.71 -0.72		q3ILFif9	9	121,822,604–135.146.198	PZE-109078269-PZE-109086475	6.38	16.76	-1.15
ILFir q4ILFir3-1 3 8,270,856-9,886,045 PZE-103015388-SYN36244 3.54 12.01 -0.88 q4ILFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544 2.85 8.71 -0.72	Yu537×Shen137							-
q4ILFir3-2 3 19,654,756-20,022,149 PZE-103026528-PZE-103027544 2.85 8.71 -0.72	ILFir	q4ILFir3-1	3	8,270,856–9,886.045	PZE-103015388-SYN36244	3.54	12.01	-0.88
		, q4ILFir3-2	3	19,654,756-20,022,149	PZE-103026528-PZE-103027544	2.85	8.71	-0.72

(continued)

Table 4, continued

Trait	QTL	Chr	Ph (bp)	Marker Interval	LOD	R² (%)	А
ILSec	q4ILSec2-1	2	182,674,225–190,259,082	PZE-102136708-PZE-102137972	3.79	11.34	0.47
	q4ILSec2-2	2	217,295,349–220,397,345	SYN27033-PZA01991.3	3.76	14.58	0.79
	q4ILSec6	6	113,705,211–128,207,560	PZA00182.4-PZE-106072609	2.53	8.10	-0.40
ILThi	q4ILThi2	2	182,674,225–190,259,082	PZE-102136708-PZE-102137972	4.66	14.06	0.60
	q4lLThi5	5	179,270,149–180,440,398	PZE-105122012-PZE-105123697	3.70	10.88	0.71
ILFor	q4ILFor2-1	2	182,674,225–190,259,082	PZE-102136708-PZE-102137972	7.32	18.36	0.75
	q4ILFor2-2	2	206,357,621–210,816,696	PZE-102165687-PZE-102168198	2.70	6.71	-0.45
	q4ILFor6-1	6	82,616,403-86,257,528	PZE-106036132-PZE-106038001	2.82	6.46	0.45
	q4ILFor6-2	6	113,738,213–11,4026,921	PZE-106062631-PZE-106062790	3.92	9.61	-0.54
ILFif	q4ILFif2	2	182,674,225–190,259,082	PZE-102136708-PZE-102137972	4.32	13.10	0.78
	q4ILFif3	3	124,139,760–132,620,186	PZE-103077185-PZE-103082258	4.05	13.83	-0.84
	q4ILFif4	4	175,440,362–243,222,942	PZE-104099080-PZE-104152506	3.09	10.36	-0.77
	q4ILFif6	6	161,570,136–161,844,331	PZE-106115356-PZE-106116148	2.64	7.06	-0.64

A, additive effect; ILFir, the first internode length above the uppermost ear; ILSec, the second internode length above the uppermost ear; ILThi, the third internode length above the uppermost ear; ILFir, the fourth internode length above the uppermost ear; ILFir, the fifth internode length above the uppermost ear. Additive effect: positive values indicate that Yu82, Zong3, or Yu537 carries the allele for an increase in the traits, whereas negative values indicate that Shen137 or Yu87-1 carries the allele for an increase in the trait value.

Genetic map integration and mQTL analysis

The mQTL analysis was a superior method for identifying true and consistent QTL for the measured traits from the four RIL populations, and the genetic map and initial QTL were integrated by meta-analysis. The integrated genetic map included 2439 SNP markers and was 1933.74 cM long, with an average of 0.79 cM between markers based on the four populations. After integration, 46 initial QTL were captured by 14 mQTLs located on all chromosomes except for chromosome 8 (Table 5). The mean phenotypic variation of the initial QTL synthesized into the corresponding mQTLs was 5.36%–26.85%, with 17 QTL >10%. One mQTL included an average of 3.29 initial QTL, with a range of 2 to 11 for 2 to 4 traits.

The initial QTL included in mQTL5-2 with four QTL >10% were identified for five internode lengths above the uppermost ear in two populations; the initial QTL in mQTL9 with two QTL >10% were demonstrated for three traits in two populations; the initial QTL in mQTL3-1 were identified for one trait in two populations; the initial QTL in mQTL2-2, mQTL3-2, mQTL4, and mQTL5-1 were identified for four traits in one population; and the QTL identified in the remaining mQTLs were identified for two traits in one population.

DISCUSSION

Increasing grain yield per unit area is one of most important objectives of maize breeding. In recent decades, numerous approaches (improved photosynthesis, nutrient use efficiency, tolerance to biotic and abiotic stress) have been proposed to increase grain yield per unit area (Bertin and Gallais 2001; Tuberosa et al. 2002; Hund et al. 2004; Grance et al. 1987; Louwerse and Zweerde 1997). The effect of changes in growth processes and plant traits on yield at the canopy level is unclear (Zhu et al. 2012; Evans 2013). However, canopy morphology is an important and complicated agronomic trait, and research has focused on leaf area, leaf angle, leaf length, tassel morphology, and QTL mapping (Mickelson et al. 2002; Ku et al. 2010, 2012; Li et al. 2008; Tian et al. 2011). The QTL responsible for ILAU have not been identified. In this study, the QTL for each ILAU were mapped using four sets of RIL populations evaluated in three environments, which resulted in the identification of 70 QTL: 16 QTL in Pop. 1, 14 QTL in Pop. 2, 25 QTL in Pop. 3, and 15 QTL in Pop. 4 (Table 4). Individual effects ranged from 5.36% to 26.85% of the phenotypic variation, with 27 QTL contributing >10%. Forty-six initial QTL were included in 14 mQTLs by meta-analysis, and 17 of the 27 initial QTL with $R^2 > 10\%$ were included in 7 mQTLs. These results could provide useful information for marker-assisted selection (MAS) to improve canopy architecture.

Comparison of the mapping results across five traits measured in the four RIL populations

We verified three common QTL located in the same or similar chromosome regions, one for ILAU at all positions in bin 5.06, one for three measured traits in bin 9.06, and one for ILSec in bin 10.04 across two RIL populations (Table 5). Although four common QTL were identified for four measured traits in one population, six common QTL were identified for two measured traits in one population, and additional QTL were identified for one measured trait in different populations. The position consistency of the QTL demonstrated that all internode lengths above the uppermost ear may be affected by one or several of the same QTL. In addition, the position-specific QTL demonstrated that internode length at different positions above the uppermost ear may be regulated by many different QTL. In terms of different populations, one QTL for five measured traits in bin 5.06, one QTL for three measured traits in bin 9.06, and one QTL for one measured trait in bin 10.04 were located across two RIL populations. These QTL were consistent across the two populations and merit further study via the construction of isogenic lines (NILs). Although the two populations exhibited certain similarities because they shared a parental line, population-specific QTL (e.g., QTL in bin 2.07, QTL in bin 4.01, QTL in bin 5.03) were also identified. Population-specific QTL were attributed to differences in the genetic background between the two populations because they shared only one common parental line.

Synthesis of initial QTL for five traits across four populations and comparison of QTL related to plant height in previous studies

To determine if the loci identified in different QTL mapping studies are identical, the chromosomal regions of a common subset of markers were compared across different studies or indirectly compared by evaluating each mapping population according to a reference map (Tuberosa *et al.* 2002). mQTL analyses are a superior method for combining data from independent studies to identify consensus QTL and for revealing genetic correlations among traits.

	Candidate Gene/Previous Studies About Plant Height in Maize	Peiffer et al. (2014)		q4ILFif2 GRMZM2G001977		^c or3 Ajmone-Marsan et al. 1994;	Kozumplik <i>et al.</i> 1996; Lübberstedt	et al. 1997; Melchinger et al. 1998;	Tang et al. 2007; Elisabetta et al.	2007; Gonzalo <i>et al.</i> 2010	For4	q3lLFor5-1	11 ILFor5, Ajmone-Marsan <i>et al.</i> 1994;	3ILThi5-2, Lübberstedt et al. 1997; Tang	et al. 2007; Gonzalo et al. 2010	GRMZM2G097132			GRMZM2G115357	.Thi9, Peiffer et al. (2014)		
nant inbred line (RIL) populations	Integrated QTL	q1lLFir1, q1lLThi1	q3lLThi2, q3lLFor2	q4ILSec2-1, q4ILThi2, q4ILFor2-1, c	q4ILFir3-2, q2ILFor3	q3ILSec3, q3ILFir3, q3ILThi3, q3ILF					q11LFir4, q11LSec4, q11LThi4, q11LF	q3ILFir5-1, q3ILSec5-1, q3ILThi5-1,	a11LFir5-2, a11LSec5-2, a11LThi5, a	a11LFif5, a21LSec5, a31LFir5-2, a	q3ILFor5-2, q3ILFif5, q4ILThi5	q4ILSec6, q4ILFor6-2	q2ILFor6, q2ILFif6	q2ILFir7, q2ILFif7	q1ILFor7, q1ILFif7	q2ILSec9, q2ILThi9, q2ILFor9, q3IL	q3ILFor9, q3ILFif9	q2ILSec10, q3ILSec10
s of recombir	No. of QTL	2	2	4	2	4					4	4	11			2	2	2	2	9		2
ie uppermost ear in four set	Physical Intervals (pb)	54,453,173-62,011,928	17,397,718–17,903,733	182,674,225-190,259,082	19,654,756–20,022,149	169,008,365-175,554,472					3,895,258–4,086,729	80,223,529-80,802,797	184,744,673–194,848,500			113,738,213-128,207,560	155,609,243-156,368,157	1,979,634–4,709,247	9,799,796–12,523,342	127,820,710-133,745,032		122,764,555-123,635,404
OTLs for internode length above th	Flanking Markers	PZE-101071898-PZE-101071162	SYN18094-PZE-102037260	PZE-102136708-PZE-102137972	PZE-103026528-PZE-103027544	PZE-103110355-PZE-103115618					PZE-104005295-PZE-104005482	PZE-105074181-PZE-105073970	PZE-105128217-PZE-105141007			PZE-106062631-PZE-106072609	PZE-106104150-PZE-106105801	PZE-107002330-SYN20419	PZE-107013546-PZE-107015480	PZE-109079845-PZE-109090207		PZE-110066732-SYN15051
The m	Chr	1	7	2	ო	m					4	ß	Ŋ			9	9	7	7	6		10
📕 Table 5	mQTL	mQTL1	mQTL2-1	mQTL2-2	mQTL3-1	mQTL3-2					mQTL4	mQTL5-1	mQTL5-2			mQTL6-1	mQTL6-2	mQTL7-1	mQTL7-2	mQTL9		mQTL10

In maize, mQTLs for drought tolerance, flowering, grain yield components, ear rot resistance, leaf architecture, and silage quality have been reported (Danan et al. 2011; Truntzler et al. 2010; Hao et al. 2010; Chardon et al. 2004; Li et al. 2011; Xiang et al. 2012, 2010; Ku et al. 2012). In the present study, we identified 14 mQTLs from a total of 70 QTL in the four populations for each ILAU using mQTL analyses, and 62.96% of the QTL showed $R^2 < 10\%$. mQTL5-2 included 11 initial QTL for internode length at five positions from two populations that explained 6.92%-16.24% of the phenotypic variation. mQTL9 included six QTL for internode length at three positions from two populations that explained 7.54%-16.76% of the phenotypic variation. mQTL10 included two QTL for internode length at one position from two populations that explained 10.15% and 7.53% of the phenotypic variation. mQTL2-2, mQTL3-2, and mQTL5-1 included four QTL for internode length at four positions from one population, with at least two initial QTL with R² <10%. These mQTLs, particularly mQTL2-2, mQTL5-1, and mQTL9, may merit further analysis via the construction of secondary mapping populations, such as fine mapping, MAS, and map-based cloning. Studies of mQTL2-2, mQTL5-1, and mQTL9 are currently underway in our laboratory. In short, the analysis of each ILAU at the molecular level revealed mQTLs associated with these traits in the four populations, potentially enabling their simultaneous improvement through MAS.

Plant height was determined by internode length and internode number. Plant height has been widely studied, although internode length has not been researched. In studies on QTL of plant height, numerous common QTL have been identified across different populations and different environments (Table 5). These mOTLs include shared alleles identified in the present study and studies on plant height (Peiffer et al. 2014) between PZE-101071898 and PZE-101071162 on chromosome 1 for ILAU; shared alleles identified in the present study and studies on plant height (Zhang 2010; Ajmone-Marsan et al. 1994; Kozumplik et al. 1996; Lübberstedt et al. 1997; Melchinger et al. 1998; Tang et al. 2007; Elisabetta et al. 2007; Gonzalo et al. 2010) between PZE-103110355 and PZE-103115618 on chromosome 3 for ILAU as well as for other generations (RIL and F2:3 generations); shared alleles identified in the present study and studies on plant height (Ajmone-Marsan et al. 1994; Lübberstedt et al. 1997; Tang et al. 2007; Gonzalo et al. 2010) between PZE-105128217 and PZE-105141007 on chromosome 5 detected in the present study for ILAU; and shared alleles identified in the present study and studies on plant height (Peiffer et al. 2014) between PZE-109079845 and PZE-109090207 on chromosome 9 for ILAU. These results showed that mQTLs affected plant height by acting on internode length. In addition, ILAU-specific mQTLs (e.g., mQTL3-1, mQTL 2-1, etc.) were also identified.

Associations with genes in the hormonal pathways of plant height

The studies showed that plant height was affected by plant hormones and other factors that affect cell division, cell elongation, or both (Wang and Li 2008; Komorisono et al. 2005). More than 100 genes/ loci affect plant height through gibberellin, brassinosteroid, and auxin signaling, transport and synthesis pathways, as well as through cell proliferation (Multani et al. 2003; Komorisono et al. 2005). To further assess the genetic basis of ILAU variation, the association between mQTLs and genes known to be involved in plant height in Arabidopsis, rice, and maize were investigated through a bioinformatics approach in maize. Three candidate genes controlling plant height were located in three mQTL intervals for ILAU (Table 5). GRMZM2G001977 was

Table 5 The mOTLs for internode length above the uppermost ear in four sets of recombinant inbred line (RIL) populations

located in the mQTL2-2 interval on chromosome 2. The candidate gene is involved in the GA-signaling pathway and putative gibberellin receptor GID1L2 (Alexandrov et al. 2009). The gene affects stem growth and the autonomous flowering time pathway (Zhang et al. 2012; Griffiths et al. 2006). GRMZM2G097132 was mapped to the mQTL6-1 interval on chromosome 6, and the gene belongs to the 2OG-Fe (II) oxygenase superfamily and was 2-oxoglutaratedependent dioxygenase, which catalyzes subsequent reactions in the GA biosynthesis pathway (Hedden and Phillips 2000). A loss of function in this gene in plants can generate a dwarf phenotype in Arabidopsis. GRMZM2G115357 was mapped to the mQTL7-2 interval on chromosome 7, and the gene is a member of the auxininduced Aux/IAA family (SHY2/IAA3). A gain-of-function mutation in SHY2/IAA3 causes enlarged cotyledons, short hypocotyls, and altered auxin-regulated root development in Arabidopsis. Therefore, the gene causes pleiotropic auxin-related phenotypes, which indicates that the Aux/IAA gene plays a central role in auxin signaling (Reed 2001). The consistency of the mQTLs and candidate genes identified in this study provided valuable information that was used to fine-map and determine quantitative trait genes and reveal the molecular mechanisms responsible for ILAU.

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