THE DEVELOPMENT OF DNA DATABASE FOR *GONYSTYLUS BANCANUS* IN SARAWAK

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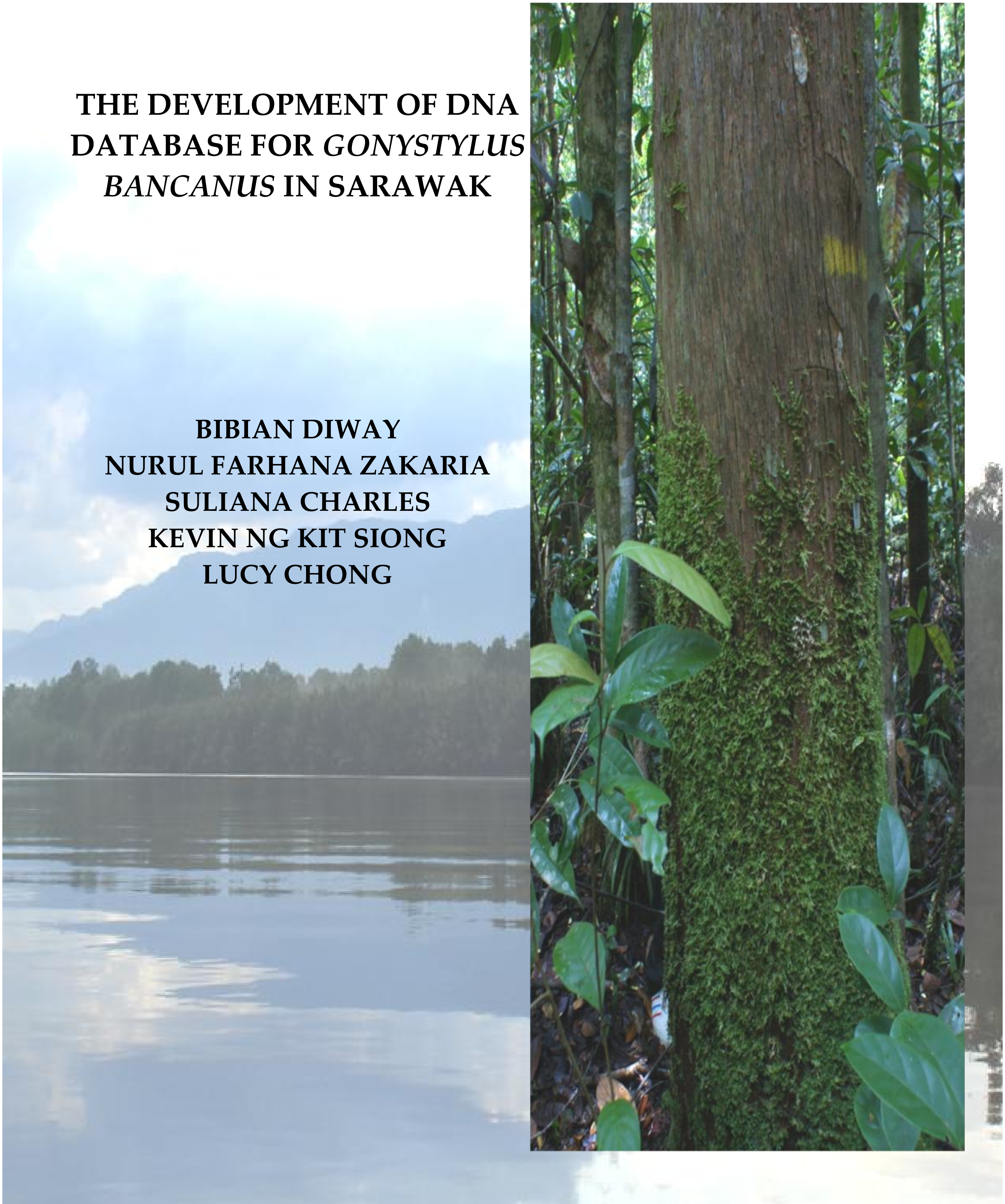

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EXECUTIVE SUMMARY

Gonystylus bancanus popularly known as ramin is an endemic species to Peat Swamp Forest. High demand for the ramin products and depletion of habitat due to land conversion has put ramin in the Appendix II CITES - listed species. Various protection measures has been taken by Sarawak government including imposed on ban on export of ramin log and for export of ramin products will need verification from Customs on the CITES Export Permit. However the control measure by the CITES could not guarantee no illegal trading of ramin. Often the illegal trading happened through false declaration on the species name and origin of the products. This project is to develop the DNA database for *Gonystylus bancanus* in Sarawak to enhance the enhance Sarawak and Malaysia government as well as CITES effort to combat illegal trading. It is an early stage in the effort to use DNA for tracing and tracking of timber origin and verification of species.

The plant materials consisted of leaves and barks samples were collected from nine ramin populations throughout. For extraction of DNA several methods were used including plant extraction kit however only cetyltrimethyl ammonium bromide (CTAB) method with modification yielded a good quality of DNA. From a total of 25 microsatellite markers tested, 18 markers were selected to amplify the DNA and to generate alleles frequencies data for the database. A total of sixty seven unique alleles were detected providing useful information for tracing of timber origin. Genetic diversity measured was generally high for most populations except for Kayangeran Forest Reserve and Loagan Bunut National Park. The expected heterozygosity values ranged from 0.682 to 0.803 indicated that genetic diversity was generally high. The level of genetic diversity of ramin in Sarawak populations was as high as level of genetic diversity for other species of tropical forest.

The genetic identity based on Nei's 1978 identity index, ranged from 0.62994 between populations of Kayangeran and Serapau to 0.982971 between populations of Manggut and Lingga. UPGMA cluster analysis using Nei's 1978 genetic distance clustered the populations into two clusters which positively related to geographical location. Sedilu, Lingga, Serapau, Maludam, Manggut, Betong and Naman were clustered into one group and the isolated populations Kayangeran and Loagan Bunut were clustered in another group. The closest genetic distance was 0.022656 between populations of Manggut and Lingga whereas the furthest was 0.462131 between populations of Kayangeran and Serapau. The high value of *Fst* indicated the ramin populations in Sarawak in former days were connected but now becoming fragmented.

Unique alleles detected within populations and cluster analysis indicated the ability and usefulness of microsatellite markers selected for tracking and tracing of ramin populations in Sarawak. Thus they are effective for the development of DNA database. However for the high accuracy and reliability of microsatellite markers for tracking and tracing timber origin and species identification should base on many loci. In addition, similar project should be extended to other ramin population in other states and neighboring countries in order to enhance implementation of CITES legislation/regulations and the enforcement officials' capacity to curb illegal logging within this region.

1.0 Introduction

Gonystylus bancanus locally know as ramin telur belongs to the family Thymelaeaceae is a native species of fragile Peat Swamp Forest (PSF). The wood is creamy yellow in colour with moderately fine and even texture, is easy to saw, bore and turn and has smooth planned surface. It is one of the most valuable tropical hardwoods and highly sought after for decorative cabinet timber, furniture, squash court flooring and interior decorative work (Lim *et al*., 1999).

The largest importer of ramin sawn timber and products are countries such as China including Hong Kong, United States and Japan (Table 1). From January to November 2009 the production and export of Ramin for Sarawak reported were 2,591 m^3, a decline compared to production in 2008, 2007 and 2006 (Table 2). The decline in ramin production for 2009 as reported by Malaysia during the Fifty-ninth CITES meeting at Doha (Qatar) on 12 March 2010 was the result of global economic recession faced by the timber sector since late 2008.

Table 1 Export destinations for Ramin products (January to November 2009) for Sarawak

Export destination		Ramin products	
Market	Volume (m^3)	Products	Volume (m^3)
China (including Hong Kong)	623	Sawn Timber	1,153
USA	454		
Japan	448	Dowels/Mouldings	1,438
Others	1,066*		
Total	2,591	Total	2,591

Source: CITES, 2010

Table 2 Export of Ramin from 2007 to 2009 (January to November)

	2006	2007	2008	2009
Export Quota (m^3)	22,000	12,875	3,178	3,178
Export volume (m^3)	12,161	10,434.31	3,063.09 (5,112.1214m3)**	2,591
Export performance (%)		81.04	96.38	81.53

Source: CITES 2010 ** including stockpile of year 2007

The reduction in ramin production over the years was also the result of decline in areas covered by peat swamp forest. Based on the 1995/1996 satellite images, 9.2 % or 1.13 million ha of Sarawak's land area was covered by Peat Swamp Forest. However, in 2002, the Landsat and SPOT data showed that 98.5 % of the peat swamp forest has been opened up for various purposes leaving only 18,920.45 ha relatively untouched PSF (Wong 2002). From the total area opened up, 78,260.96 ha has been converted into plantation area. The total area converted to plantation was further increased to 389,483 ha in 2004 (Figure provided by Sarawak Forestry Department GIS unit and reported by Lee 2005).

Due to the reduction in PSF within PFE and the decline in ramin production, Malaysia particularly Sarawak has been reported by Environmental Investigation Agency (EIA) and Telapak of being involved in smuggling and “laundering” of illegal Indonesian ramin into number of importing countries, including US and UK (Traffic 2004, EIA/Telapak 2004). Worse still, Malaysia has also been accused of failing to carry out a proper non-detriment finding for ramin export and has no effective control in place on ramin harvesting (EIA/Telapak 2006). The Malaysian government through Malaysia Timber Council (MTC, 2004) responded that the country does not condone any illegal trade in timber and has implemented various measures to combat the entry of illegal logs.

1.1 Protection of Ramin

Current protection measures taken by Sarawak Government are in accordance with Section 96 (1) of Forest Ordinance 1954 including the ban on export of ramin logs that was enforced in 1980, ban on export of ramin shorts and squares and restriction of export of ramin timber implemented in 1991. At the last points of export, exporters also need to get verification by Customs on the CITES Export Permit (CITES, 2010).

However, there may be cases in which traders circumvent CITES controls by providing false declaration of the species involved. Inspection of timbers is currently done based on wood anatomy which identifies timber into group and is generally not identified to species level and source of timber is not determined. In the case of ramin, the wood anatomy is very similar with *Alstonia*, *Antiaris* spp., *Brosimim aliscastrum*, *Dyera costulata*, *Endospermum* spp., *Chrysophyllum beguei*, *Jacaranda copaia*, *Neolamarckia cadamba*, *Pterygota* spp., *Simarouba amara* and *Terminalia superb*a.

1.2 Use of DNA for timber identification

The application of DNA profiling in human forensic and paternity proof has long been used. The same technique has also been applied in the identification of animals (Butler, 2005). Recently in Peninsular Malaysia, a study using chloroplast DNA proved that the geographical origin of *Neobalanocarpus heimii* can be traced (Tnah *et al.*, 2009), and the comprehensive DNA profiling database developed for *N. heimii* can serve for the random match probability estimation of an illegal logging with its original stumps (Tnah *et al.*, 2010).

2.0 Objective

The aims of the study are; (i) to develop a DNA database as initial stage to enhance efforts of tracing and tracking of *Gonystylus bancanus* timber, (ii) to estimate the genetic diversity of ramin populations in Sarawak, and (iii) to determine extents of genetic differentiation among populations that contribute to baseline information for the tracing and tracking system using DNA markers.

3.0 Methodology

3.1 Study sites and samples collection

Samples were collected from known geographical range of peat swamp forest in Sarawak (Fig. 1). Peat swamp areas in the central part of Sarawak were not surveyed for this project because the areas are earmarked for further development. A total of nine populations were sampled (Table 3). At least 30 individuals were collected from each population, though few areas involved intensive search due to limited stand density remaining.

Figure 1 Distribution of Peat Swamp Forest in Sarawak

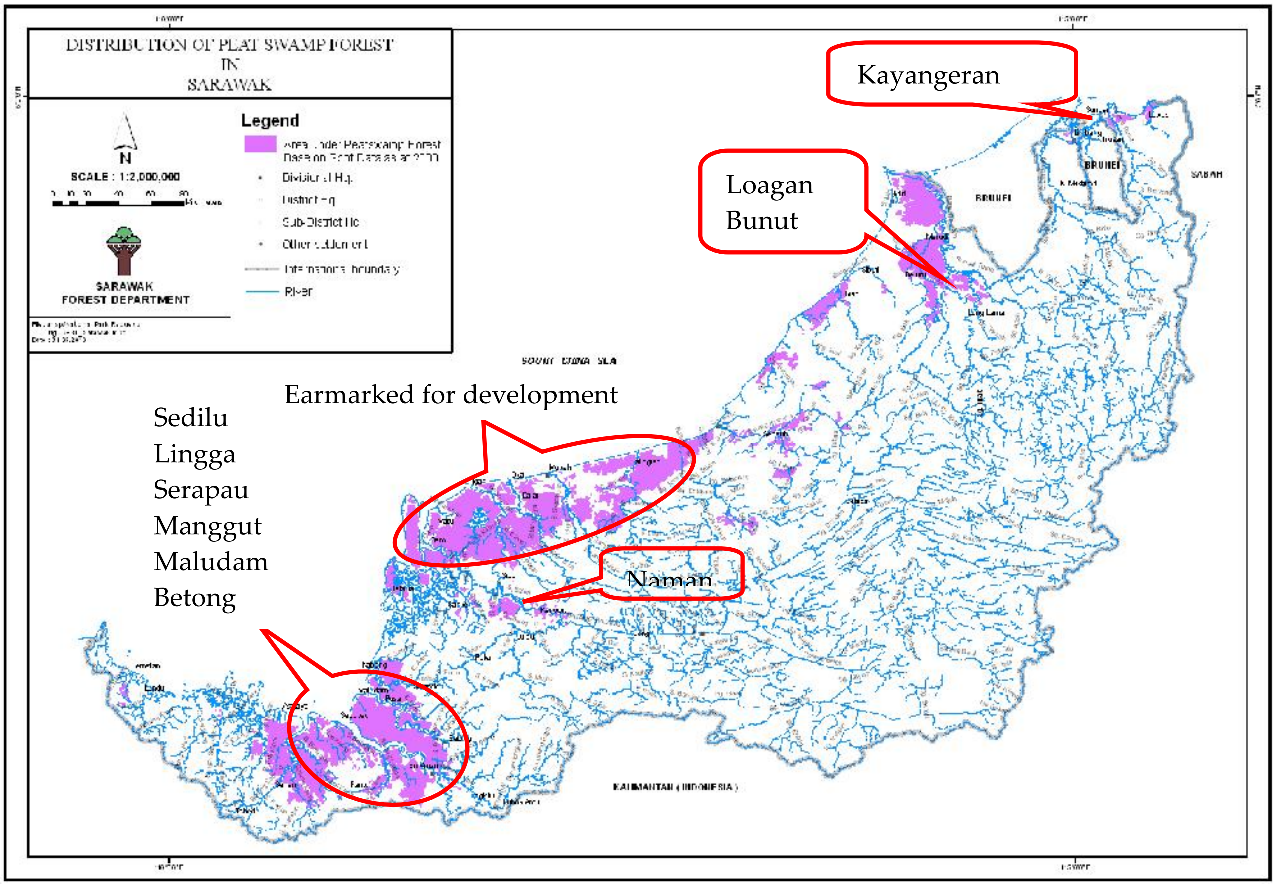


Table 3 Surveyed populations and number of individuals sampled.

Population number	Locality	Nearest town	Latitude	Longitude	No of individuals sampled
1	Sedilu	Simunjan	N01^{0}22'	E110^{0}49'	31
2	Lingga	Sri Aman	N01^{0}21'	E111^{0}10'	30
3	Serapau	Sri Aman	N01^{0}19'	E111^{0}12'	30
4	Loagan Bunut	Miri	N03^{0}47'	E114^{0}14'	101
5	Kayangeran	Lawas	N4^{o}53’	E115^{o}25’	29
6	Maludam	Sebuyau	N01^{o}38’	E111^{o} 03’	36
7	Manggut	Betong	N01^{o}29’	E111^{o} 16’	53
8	Betong	Betong	N01^{o} 25’	E111^{o} 23’	40
9	Naman	Sibu	N02^{o}11’	E111^{o} 50’E	55

3.2 DNA extraction

Genomic DNA was extracted using the prescribed method of Murray and Thompson (1980) with modification. 0.5 g of leaf or inner bark tissues were mixed with 5ml of preheated ($65^{o}C$) CTAB extraction buffer (2% CTAB, 20mM EDTA, 100mM Tris-HCl, 4M NaCl, 1% PVP, 2% β-mercaptoethanol) in 15 ml tube and incubated at $50^{o}C$ for 30 min. After incubation, equal amount of chloroform-isoamyl alcohol (24:1) was added and mixed gently. The mixture was centrifuged at 3500 rpm for 10 min. The aqueous layer was transferred into new 15 ml tube and the DNA was precipitated with 2/3 volumes of isopropanol. The mixture was pelleted by centrifuge at 3500 rpm for 5 minutes. Subsequently, the supernatant was removed and the DNA pellet was washed with 76% ethanol, left to dry and the DNA was redissolved in TE buffer. The DNA was further purified using High Pure PCR Template Preparation Kit (Roche Diagnostics).

3.3 PCR amplification and fragment analysis

PCR amplification was performed using Qiagen multiplex PCR in 8.0 µl reaction mixture, consisting of 2x Type-it multiplex PCR master kit. Eighteen microsatellite markers were utilized. The multiplex PCR was amplified using a GeneAmp PCR System 9700 (Applied Biosystem) at $95^{o}C$ for 5 minutes initial denaturation, 35 cycles of $95^{o}C$ for 30 seconds of denaturation, 50 to $57^{o}C$ for 1 min 30 seconds annealing, $72^{o}C$ for 30 seconds of extension, followed by final extension at $60^{o}C$ for 30 minutes. The amplification product (1 µL PCR product) was combined with 9.9 µL of Hi-Di formamide (Applied Biosystems) and 0.1 µL of 400 HD Rox (Applied Biosystems) to form master mix for fragment analysis. The master mix was assigned against ABI 3130x1 Genetic Analyzer System. The fragment data was edited and genotype profile created using GeneMapper ^{TM} v3.7 software (Applied Biosystems).

3.4 Statistical Analysis

Population variation within and among population was quantified by calculating the allele frequencies, mean number of alleles (MNA) per locus, observed heterozygosity (*Ho*) and expected heterozygosity (*He*) and polymorphic information content (PIC) with The Excel Microsatellite Toolkit software computer program (Park, 2001). A number of polymorphic loci and allelic diversity have been shown to be reliable indicators of a genetic variation and can show the effect of bottlenecks and genetic drift (Nei, 1978).

FSTAT, ver. 2.9.3.2 (Goudet,2002) was used to calculate the allelic richness, Ar (Petit *et al.,* 1998), Wright's (1951) *F* statistics (*F*st, *F*is and *F*it) based on Weir and Cockerham's (1984) to determine the distribution of genetic variation within and among populations and *R*-statistics, Rst, (Slatkin,1995; Goodman,1997) calculation, to estimate a population differentiation. *F*it and *F*is measure heterozygosity of individual relative to the total population and its subpopulations, respectively; *F*st is a measure of genetic differentiation among populations.

Cluster analysis based on genetic distances estimated from Nei's (1978) index of similarity was performed using Genetic Data Analysis (GDA) program (Lewis and Zaykin, 2001). The population dendrograms were performed with the tree drawing software TreeView (Page, 2001).

4.0 Results and Discussions

4.1 Genetic diversity

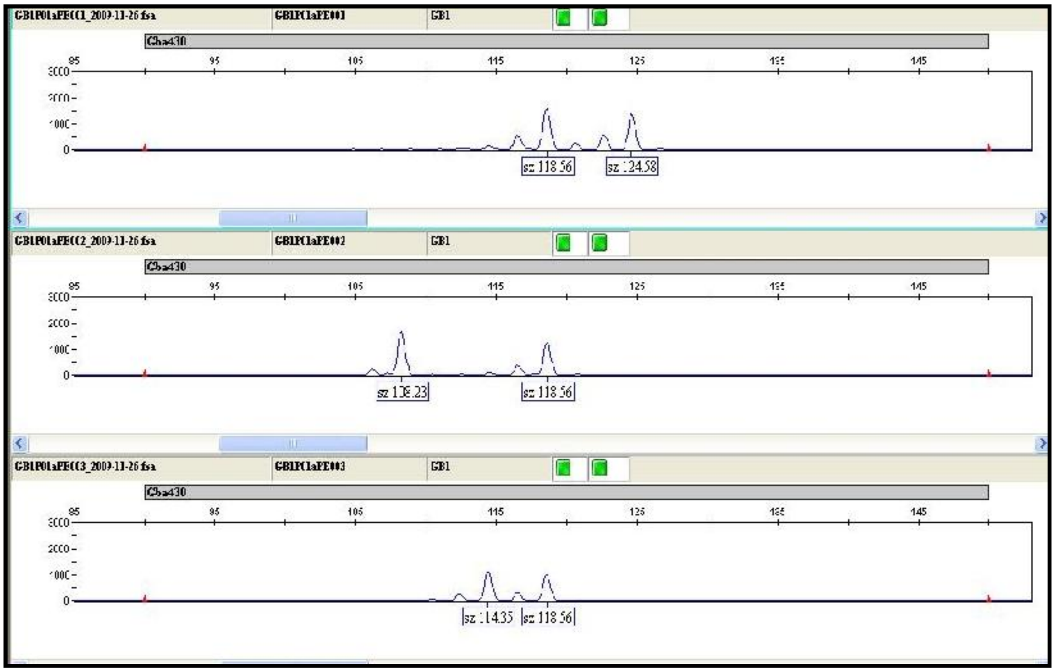
Table 4 Number of alleles per locus

Marker	Sedilu	Lingga	Serapau	Loagan Bunut	Kayangeran	Maludam	Manggut	Betong	Naman	Total
Gba082	19	20	21	16	8	20	22	23	24	32
Gba092	9	11	9	7	4	9	11	7	9	15
Gba100	11	6	9	5	4	10	10	10	12	18
Gba108	21	22	19	14	8	19	21	24	21	35
Gba129	14	15	14	11	10	12	15	16	17	25
Gba147	16	17	16	16	14	20	24	20	21	37
Gba175	2	2	3	2	2	2	2	2	3	3
Gba348	7	7	11	10	6	9	11	11	9	17
Gba430	13	13	11	11	7	11	11	12	18	20
WGb17	13	14	14	16	7	15	17	15	17	24
WGb22	12	11	11	6	2	10	14	11	11	15
WGb24	9	10	7	10	7	10	11	10	9	17
WGb29	12	15	14	9	4	14	15	19	17	27
WGb32	19	17	15	16	10	16	20	17	20	28
WGb37	6	6	6	5	6	6	7	7	7	9
WGb38	7	6	7	5	3	7	6	6	9	11
WGB39	8	8	6	4	4	6	6	7	8	11
Total	207	206	200	168	109	202	227	222	239	356

A total of 356 alleles were detected from 18 polymorphic loci (Table 4). The average number of alleles and allelic richness was relatively high for most populations except for Kayangeran (6.06 and 5.95, respectively) and Loagan Bunut (9.33 and 7.38, respectively) (Table 5). The average number of alleles over all populations was 10.99. Figure 2 shows examples of some observed alleles derived using GeneMapper ver 3.7 software. Polymorphic information content (PIC) was the lowest at Kayangeran (0.621) and the highest at Sedilu (0.76) (Table 5).

Sixty seven of the 356 alleles detected occurred only in one of each of the population. Sedilu had 13 unique alleles that were not detected in other populations, Naman and Manggut had 9 unique alleles, while Lingga and Betong each had 8 unique alleles. Other populations had less than 7 unique alleles. These unique alleles are very informative used for population identification.

Figure 2 Example of some fragment data showing variable alleles size from three individuals of *Gonystylus bancanus*.



Observed and expected heterozygosities, *Ho* and *He* were generally high for all populations with no value less than 0.6. When all populations were compared together, Kayangeran and Loagan Bunut had the lowest value observed. On average, the expected heterozygosity was 0.766, which was within the range observed for other tropical species (Table 6). However, the values of *Fis* were significantly different from zero for three populations, an indication of inbreeding within population (Table 5).

The value of measured genetic diversity at Kayangeran and Loagan Bunut are low, but this may be a function of sampling error. Because the trees at both sites grow in a clump, most of the samples were collected from trees less than 10 meters apart from one to another. Sedilu, Manggut and Naman had high value of genetic diversity but these populations had significant departure from Hardy Weinberg Expectation, with a deficiency of heterozygotes.

Table 5 Estimates of genetic diversities for 9 populations of ramin based on 18 microsatellite loci. *N*, number of individuals sampled from the population; PIC, polymorphic information content; MNA, mean number of alleles; Ar, Allelic richness; *Ho*, observed heterozygosity; *He*, expected heterozygosity; SD, standard deviation; *F*is, Fixation index.

Pop	N	PIC	MNA	Ar	Ho(SD)	He(SD)	*Fis*
Sedilu	31	0.762	11.50	10.96	0.688(0.019)	0.803(0.036)	0.145*
Lingga	30	0.732	11.44	10.8	0.738(0.019)	0.770(0.039)	0.042
Serapau	30	0.738	11.11	10.66	0.747(0.019)	0.775(0.036)	0.037
Loagan Bunut	101	0.677	9.33	7.38	0.706(0.011)	0.719(0.032)	0.018
Kayangeran	29	0.621	6.06	5.95	0.655(0.021)	0.682(0.036)	0.039
Maludam	36	0746	11.22	10.34	0.748(0.017)	0.785(0.030)	0.048
Manggut	53	0.746	12.61	10.33	0.731(0.014)	0.782(0.034)	0.065*
Betong	40	0.748	12.33	10.67	0.745(0.016)	0.787(0.030)	0.053
Naman	55	0.761	13.28	10.96	0.752(0.014)	0.792(0.030)	0.052*
Mean		0.725	10.99	9.78	0.723(0.016)	0.766(0.033)	0.056

*Significantly different from zero ($P<0.05$).

Table 6 Genetic diversity parameters (expected heterozygosities) of other tropical tree species based on microsatellite studies.

Species	No of samples	No of Loci	No of populations	*He*	Reference
Shorea curtisii	40	8	1	0.64	Ujino *et al.*, 1998
Shorea leprosula	173	7	1	0.70	Ng *et al.*, 2004.
Shorea ovalis	156	7	1	0.64	Ng *et al.*, 2004
Neobalanocarpus heimii	30	4	1	0.78	Konuma *et al.*, 2000
Dryobalanops aromatic	90	7	5	0.71	Lim *et al.*, 2002
Shorea macrophylla	32	2	1	0.75	Konishi *et al.*, 2004

4.2 Population differentiation

Table 7 Nei's (1978) genetic identity is above the diagonal, and Nei's (1978) genetic distance coefficients are below the diagonal

	Sedilu	Lingga	Serapau	Loagan Bunut	Kayangeran	Maludam	Manggut	Betong	Naman
Sedilu	-	0.921376	0.912005	0.761285	0.716141	0.926301	0.903312	0.889029	0.861203
Lingga	0.081887	-	0.980047	0.766813	0.660457	0.980337	0.982971	0.956784	0.884990
Serapau	0.092110	0.020154	-	0.750547	0.629940	0.968779	0.977598	0.951722	0.896850
Loagan Bunut	0.272747	0.265513	0.286952	-	0.843882	0.774306	0.757500	0.801043	0.848819
Kayangeran	0.333878	0.414823	0.462131	0.169743	-	0.669202	0.659585	0.717615	0.726191
Maludam	0.076556	0.019859	0.031719	0.255788	0.401670	-	0.976887	0.970750	0.899795
Manggut	0.101687	0.017175	0.022656	0.277732	0.416145	0.023384	-	0.968556	0.883434
Betong	0.117625	0.044177	0.049482	0.221840	0.331823	0.029686	0.031949	-	0.908063
Naman	0.149425	0.122179	0.108867	0.163909	0.319942	0.105589	0.123939	0.096441	-

Genetic identity and distances differed among populations (Table 7). The genetic identity (Nei 1978) ranged from 0.629940 between Kayangeran and Serapau to 0.982971 between Manggut and Lingga. The results show that the populations are divided into at least two geographical regions. Populations from the same geographical region such as Serapau, Maludam, Lingga, Betong, Sedilu and Manggut have high values of more than 0.9. Similarly, when UPGMA cluster analysis derived based on Nei's gentic distance the populations were clustered into two, namely the west cluster consisting of Naman, Sedilu, Betong, Maludam, Serapau, Lingga and Manggut, and the east cluster consisting of Loagan Bunut and Kayangeran (Fig. 3). However it seems that the west cluster was further separated and positively related to geographical location when Lingga, Serapau, Manggut, Maludam and Betong populations showed short genetic distance. The shortest genetic distance was Manggut and Lingga. The five populations were connected through Lupar Rivers. Similar results were obtained when cluster analysis was conducted using structure software ver. 2.3 computer program (Fig. 4).

To determine if populations were significantly distinguishable from each other, the pairwise comparisons of populations was performed. Based on the *Fst* values, the populations were significantly differentiated ($P< 0.05$) from each other except for Manggut, Serapau, Lingga and Maludam. The *Fst* values ranged from 0.0042 between Lingga and Manggut to 0.0939 between Sedilu and Kayangeran (Table 8). The low value of *Fst* observed between Lingga and Serapau, Lingga and Maludam, and Lingga and Manggut indicated that they are similar to each other and is more likely that gene flow would occur along the watercourse.

Figure 3 Dendrogram of genetic distance between populations based on UPGMA generated using GDA

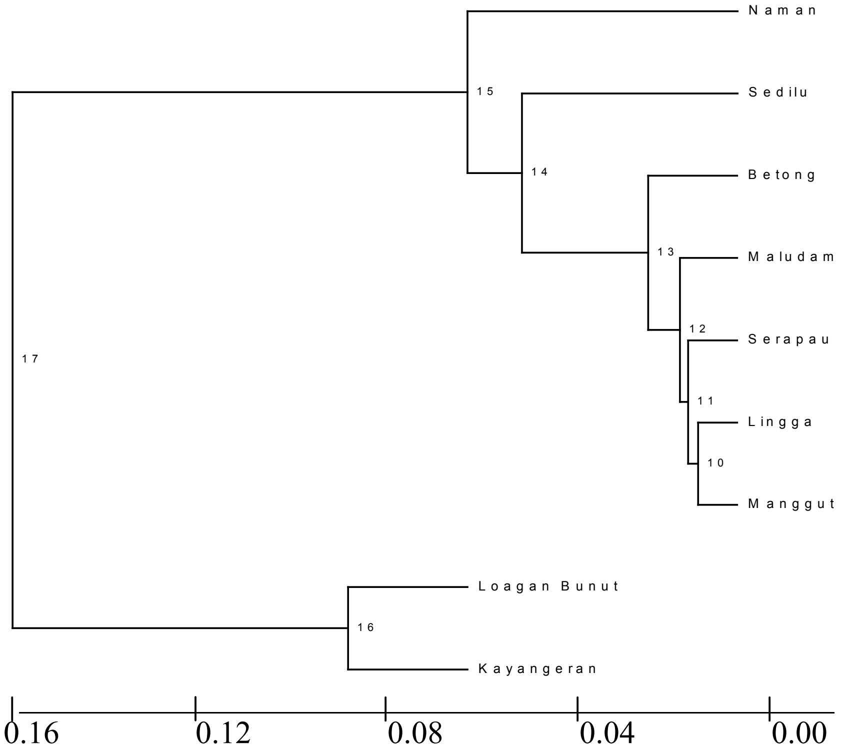
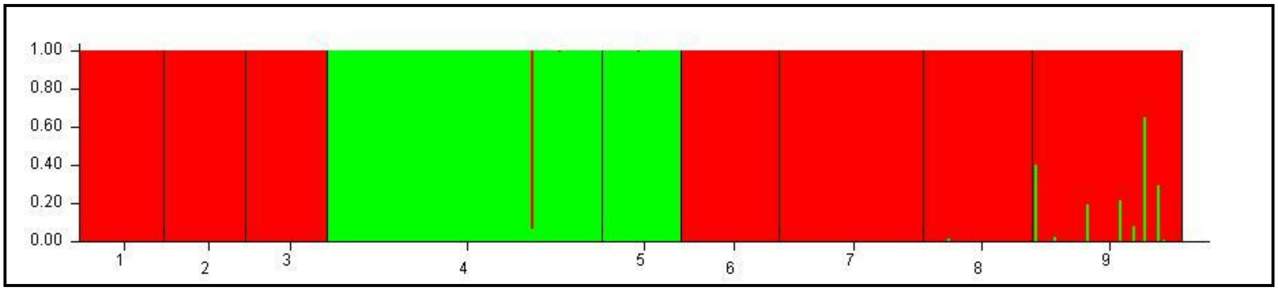


Table 8 Genetic differentiation, as estimated by Fst distance among the analysed populations.

	Sedilu	Lingga	Serapau	Loagan Bunut	Kayangeran	Maludam	Manggut	Betong	Naman
Sedilu	0.0000								
Lingga	0.0200	0.0000							
Serapau	0.0220	0.0052	0.0000						
Loagan Bunut	0.0753	0.0768	0.0811	0.0000					
Kayangeran	0.0939	0.1155	0.1234	0.0619	0.0000				
Maludam	0.0176	0.0050	0.0081	0.0729	0.1096	0.0000			
Manggut	0.0240	0.0042	0.0056	0.0773	0.1113	0.0057	0.0000		
Betong	0.0268	0.0116	0.0127	0.0649	0.0951	0.0072	0.0080	0.0000	
Naman	0.0332	0.0307	0.0271	0.0502	0.0908	0.0256	0.0301	0.0234	0.0000

Figure 4 Cluster of population based on Structure ver. 2.3. Population divided into two clusters: Red and Blue. Population 1: Sedilu; 2: Lingga; 3: Serapau; 4: Loagan Bunut; 5: Kayangeran; 6: Maludam; 7: Manggut; 8: Betong and 9: Naman.



5.0 Conclusions

The effectiveness and efficiency of microsatellite markers to evaluate genetic diversity and population differentiation demonstrated that microsatellite markers are useful for the development of DNA database for ramin. The unique alleles detected in specific populations and signification populations differentiation revealed by cluster analysis and *Fst* value indicated that microsatellite markers could be used for population identification. Thus, microsatellite markers are suitable to generate DNA database for individual timber identification and useful for tracking of wood in production chain (Tnah *et al.*, 2010; Koopman and Diemont 2004; Smulder *et al.*, 2008). However, the use of microsatellite markers for identification should not be based on a limited number of markers but on many loci (Butler 2005). Furthermore, before a marker system can be introduced into forensic casework, a population database must be established for statistical evaluation of identity match proof (Tnah, 2010).

6.0 Recommendations

The current ramin DNA database was developed using leaves and bark samples. For actual timber species identification and tracing and tracking system, samples from wood must be tested. A new proposal entitled “Use of DNA for identification of *Gonystylus* species and geographical origin” has been submitted to ITTO for funding. The unique alleles detected in specific populations in Sarawak based on the 18 markers could be detected in other population outside Sarawak. Thus, the use of more microsatellite markers and sampling across all ramin populations to other states in Malaysia and neighboring countries is important until population specific alleles detected. To implement this, support and commitment from respective countries, local government, policy makers and various NGOs are needed. Once the database is completed, only then it would be reliable in court proceeding to curb illegal logging enhance the implementation of CITES legislation/regulations in this region.

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Long boat is a main transportation used to get to the sampling site.

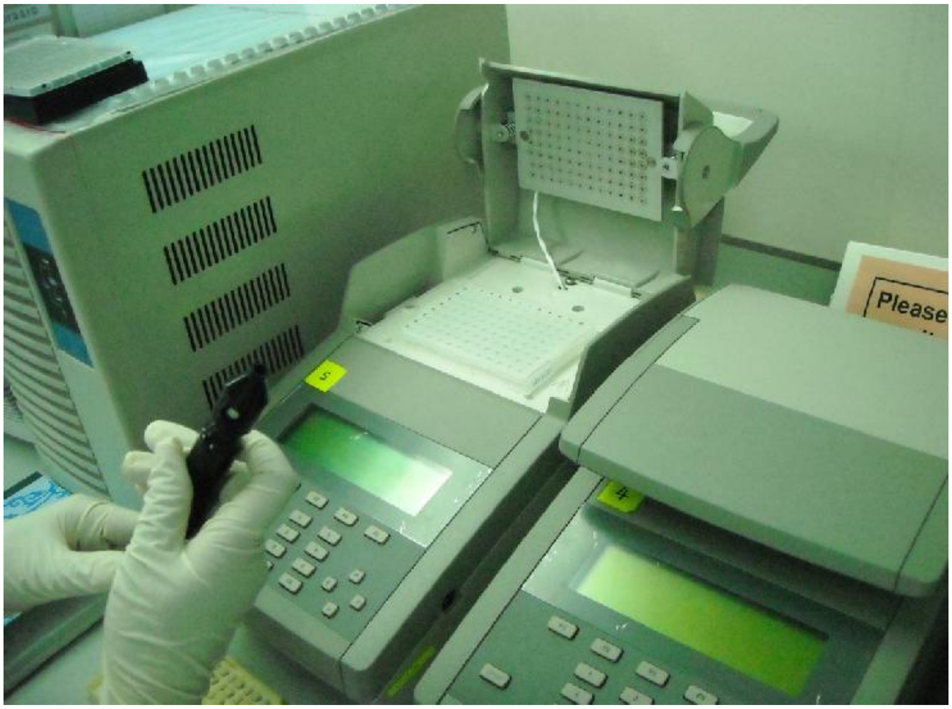
Peat Swamp Forest at Manggut

Peat Swamp Forest at Kayangeran, Lawas

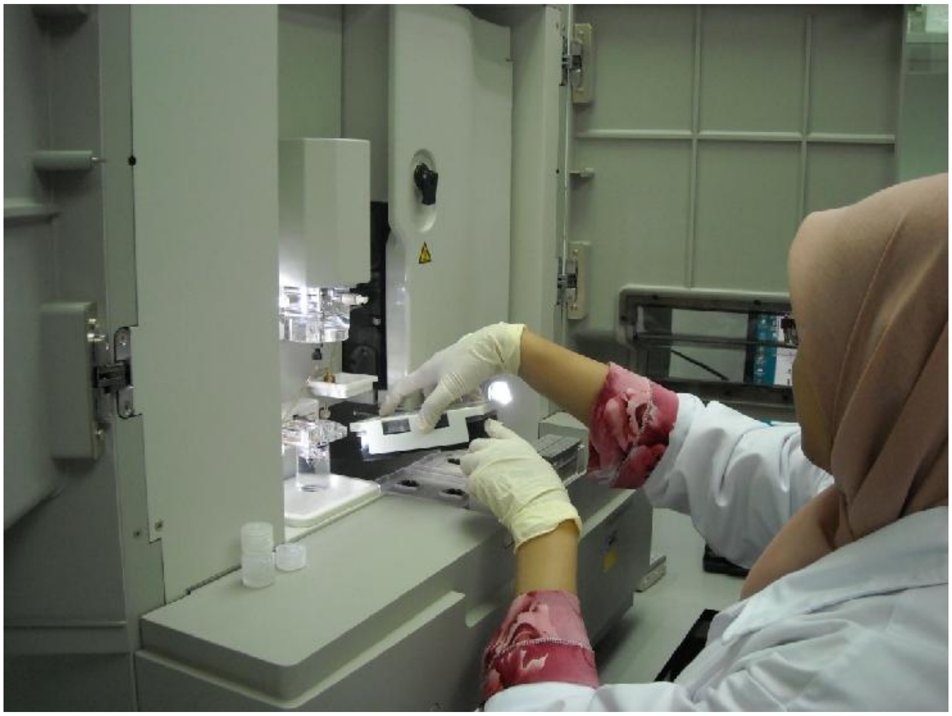
Some remain ramin tree at Naman Forest Reserve

Gonystylus bancanus leaves

Staff preparing the PCR mixed for the DNA amplification



The PCR amplification was conducted using
GeneAmp PCR System 9700 (Applied Biosystem)



Amplified PCR products are load in ABI 3130x1 Genetic Analyzer
System for fragment analysis

Appendix: Genotype Profile of *Gonystylus bancanus* in Sarawak

Individual	**Gba028**		**Gba092**		**Gba100**		**Gba108**		**Gba129**		**Gba147**		**Gba175**		**Gba348**		**Gba430**	
SE001	226	246	88	96	145	163	181	186	155	157	142	156	189	189	106	114	132	140
SE002	250	268	90	104	125	145	189	192	149	149	130	148	186	186	116	122	120	120
SE003	222	250	90	98	145	153	188	196	149	149	142	154	189	189	114	122	106	116
SE004	222	250	88	104	145	155	170	186	149	149	144	148	189	189	126	126	116	120
SE005	214	216	88	88	145	145	182	208	166	168	126	130	189	189	122	126	125	125
SE006	214	214	86	96	144	151	182	182	166	168	130	150	186	189	122	122	114	118
SE007	254	258	90	90	145	162	170	170	149	163	136	136	186	189	114	122	114	116
SE008	226	250	104	104	145	145	178	191	175	175	150	150	189	189	116	116	106	114
SE009	214	228	88	88	145	149	182	223	168	168	126	150	186	189	122	122	0	0
SE010	248	278	88	98	125	125	182	186	149	149	136	150	186	186	114	122	110	122
SE011	214	216	88	88	145	149	192	208	168	168	126	126	189	189	0	0	116	124
SE012	214	214	88	90	143	143	208	223	164	170	126	150	0	0	0	0	125	125
SE013	222	250	88	96	159	159	192	209	149	175	130	144	186	186	122	122	116	122
SE014	264	264	88	88	145	145	182	190	149	149	156	156	186	189	118	126	106	114
SE016	222	226	90	106	145	145	190	194	149	155	122	142	186	189	114	114	114	126
SE017	246	248	90	90	145	145	186	192	149	155	144	156	186	186	116	126	106	114
SE018	222	246	90	90	145	155	200	204	149	149	116	136	186	189	114	126	114	118
SE019	222	256	96	96	155	163	195	196	149	157	142	160	186	186	114	128	112	120
SE020	236	270	88	88	125	125	182	198	149	171	130	136	186	189	106	122	116	120
SE021	236	246	102	104	145	153	180	186	149	170	142	165	186	189	114	114	118	140
SE022	236	236	88	96	125	145	189	209	149	175	142	156	186	189	114	126	114	118
SE023	258	264	90	96	125	145	181	190	165	171	130	142	186	186	114	114	116	120
SE024	244	248	90	108	145	145	186	190	149	170	134	148	189	189	114	116	106	118
SE025	214	214	88	88	149	149	223	223	164	166	126	126	186	186	0	0	125	125
SE026	222	248	90	90	145	153	184	195	149	149	142	148	186	189	114	116	106	116
SE027	246	252	90	104	145	163	186	186	149	157	148	160	189	189	106	128	106	112
SE028	236	244	90	90	145	145	170	188	169	173	142	144	186	186	116	122	116	126
SE029	254	264	90	90	125	125	181	189	149	169	144	148	186	189	114	122	120	126

SE030	222	248	98	106	153	153	184	192	149	157	122	142	186	189	114	114	114	118
SE031	254	290	90	104	145	145	190	190	149	175	136	138	186	189	114	126	116	116
SE032	244	264	90	90	145	155	181	200	157	161	128	142	186	189	122	126	114	126
LI001	250	268	90	98	145	145	186	204	149	149	126	140	186	189	126	126	124	126
LI002	260	266	88	90	125	145	186	192	149	163	142	142	186	189	116	116	116	120
LI003	248	250	90	96	145	155	181	193	149	149	122	142	186	189	122	126	106	134
LI004	250	268	90	90	145	163	178	186	149	149	130	142	189	189	116	130	106	122
LI005	226	228	94	120	145	145	186	188	156	158	138	142	186	186	116	116	0	0
LI006	248	268	90	100	125	125	186	196	149	169	142	146	186	189	122	126	116	118
LI007	236	250	98	100	125	125	184	191	149	169	146	154	186	189	114	126	114	118
LI008	250	254	90	92	145	145	188	194	157	170	118	122	186	189	116	124	108	114
LI009	222	276	90	98	145	147	174	190	149	175	142	150	186	186	122	126	112	118
LI010	248	250	90	90	145	145	186	204	149	169	142	146	186	186	122	130	112	120
LI011	258	264	90	100	145	145	176	186	149	175	140	142	186	189	126	130	114	124
LI012	250	256	90	90	145	145	176	192	153	157	142	146	186	189	124	126	110	124
LI013	252	272	90	104	145	145	179	190	149	171	124	142	189	189	114	116	112	122
LI014	256	264	88	90	145	145	178	188	149	163	142	146	186	189	116	122	106	118
LI015	248	264	90	90	145	145	174	186	149	169	146	168	186	189	126	126	106	120
LI016	222	252	90	100	145	145	182	189	155	161	118	146	186	186	122	126	116	116
LI017	248	248	96	104	145	145	189	190	155	161	118	142	186	189	122	130	116	116
LI018	244	248	90	104	145	145	189	194	161	170	118	146	189	189	122	122	106	116
LI019	246	252	96	102	145	145	184	186	158	165	142	146	186	186	122	122	116	120
LI020	248	252	90	106	145	145	182	189	157	163	138	142	189	189	122	126	106	116
LI021	248	248	88	90	145	145	174	181	149	155	118	144	186	189	122	128	116	118
LI022	248	258	88	90	125	125	180	186	149	175	122	154	186	189	116	130	106	112
LI023	236	246	90	104	145	149	186	188	149	149	138	142	189	189	116	122	106	122
LI024	256	260	96	104	125	145	181	192	149	163	122	132	186	189	114	130	112	120
LI025	214	214	88	96	145	145	202	208	160	166	126	161	186	186	122	130	125	125
LI026	226	250	94	98	145	145	170	186	149	170	122	150	189	189	126	126	118	120
LI027	246	278	90	98	145	145	178	186	149	175	148	150	186	189	122	126	118	120

LI028	248	248	88	98	145	145	186	188	149	149	142	146	186	189	116	126	106	116
LI029	248	248	90	96	145	145	188	189	149	157	142	156	186	186	116	116	106	124
LI030	248	276	90	90	145	145	197	204	170	175	142	142	186	189	122	126	114	118
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SL002	248	258	92	98	145	145	186	195	149	170	146	146	186	189	126	126	116	116
SL003	222	260	96	98	145	145	178	182	149	149	142	142	186	189	116	126	118	118
SL004	248	276	90	100	145	155	170	174	155	174	142	155	189	189	118	126	116	120
SL005	248	252	88	90	125	145	159	174	157	158	122	178	186	189	116	128	112	116
SL006	248	270	100	104	145	145	174	182	149	174	118	124	189	189	114	126	112	116
SL007	248	262	90	90	145	145	174	182	149	174	150	155	186	189	116	126	112	116
SL008	250	274	90	102	125	145	182	190	149	163	136	146	189	189	122	126	114	118
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SL010	250	250	90	100	145	145	170	192	149	149	144	150	189	189	122	130	116	118
SL011	236	260	90	98	145	145	174	182	149	155	144	150	189	189	116	132	106	122
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SL013	238	250	98	104	145	145	193	194	149	155	146	148	189	189	122	128	112	114
SL014	248	278	90	114	125	145	159	190	163	167	138	142	189	189	116	116	118	120
SL015	262	276	90	114	145	145	182	182	157	169	124	150	186	189	124	126	110	116
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SL019	248	264	90	96	145	153	186	186	163	175	142	161	186	186	126	134	0	0
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SL021	214	216	88	88	145	162	202	208	160	166	126	154	186	186	106	106	0	0
SL022	248	272	96	100	125	153	180	192	149	149	142	155	189	189	114	126	116	122
SL023	244	272	88	96	145	153	176	186	149	149	136	144	189	189	122	124	106	122
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SL029	248	248	90	90	156	163	174	192	163	170	126	161	186	186	118	130	118	120
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LB002	226	258	88	90	162	162	186	186	149	153	146	163	189	189	128	128	114	114
LB003	256	270	88	104	145	145	188	203	153	155	136	160	186	189	128	128	118	128
LB004	226	248	90	104	145	162	180	190	153	169	144	144	186	186	126	126	114	114
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LB007	226	258	88	88	125	145	190	190	149	169	136	146	186	186	126	130	114	116
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LB021	256	270	88	102	145	155	188	195	155	173	160	160	189	189	128	132	114	136
LB022	226	258	88	90	125	145	188	192	153	171	132	136	186	189	128	132	114	126
LB023	246	256	90	90	125	143	192	204	149	149	144	160	186	189	126	128	106	114
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LB032	248	270	90	90	143	155	180	180	155	165	142	160	186	189	126	128	120	120
LB033	248	270	90	104	145	162	180	188	155	169	132	150	189	189	126	126	114	136
LB034	226	270	88	90	125	145	188	204	153	155	144	146	186	186	126	128	114	118
LB035	226	246	88	88	145	145	180	184	155	155	144	160	186	189	114	126	116	116
LB036	226	226	88	90	145	145	180	204	165	173	144	155	186	189	126	130	114	128
LB037	226	258	88	98	143	145	188	204	169	173	144	153	186	189	126	126	114	128
LB038	258	270	90	90	145	145	186	188	155	173	132	132	186	186	126	128	106	130
LB039	226	268	88	104	143	145	180	204	173	173	144	144	186	189	126	126	114	116
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LB041	226	226	88	90	145	145	188	188	153	153	146	161	186	189	114	130	106	120
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LB043	250	258	88	102	145	155	188	190	153	155	155	163	186	186	126	128	106	116
LB044	246	250	88	90	145	145	204	204	155	165	144	144	186	186	128	130	114	114
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LB058	270	270	88	90	125	143	190	204	153	155	142	142	189	189	116	130	116	118
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LB062	226	270	90	94	145	162	194	204	153	155	144	160	186	186	122	128	116	116
LB063	226	256	90	90	125	145	188	190	149	157	142	144	186	186	126	130	114	124
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LB071	226	226	88	88	145	145	182	188	165	169	142	160	186	189	126	130	114	130
LB072	236	246	90	104	125	162	184	195	153	173	136	142	186	186	126	128	120	122
LB073	236	276	90	90	125	143	182	184	153	155	136	142	186	186	120	128	120	120
LB074	256	256	88	90	125	145	188	190	149	155	140	162	186	186	130	130	106	128
LB075	226	268	88	90	145	145	188	195	155	165	142	155	186	186	128	128	116	122
LB076	0	0	90	96	125	143	0	0	0	0	0	0	186	186	0	0	0	0
LB077	248	270	90	90	145	145	190	195	165	173	144	150	186	186	114	130	106	118
LB078	256	256	88	90	125	145	190	190	155	173	132	142	189	189	128	130	120	120
LB079	226	256	90	90	143	145	188	190	149	165	140	140	186	186	128	130	106	114
LB080	246	266	90	104	143	155	188	188	153	165	142	144	186	186	130	130	114	118
LB081	246	256	88	90	145	145	192	204	153	169	161	161	186	186	128	130	114	118
LB082	226	256	88	104	143	155	190	195	155	165	144	162	186	186	130	130	114	118
LB083	268	270	90	104	125	145	184	188	155	155	155	160	186	189	108	130	126	130
LB084	270	270	88	90	143	145	180	195	149	169	132	148	186	189	122	128	130	130
LB085	248	256	90	104	145	155	188	188	153	153	160	160	186	186	130	130	114	114
LB086	226	270	90	90	125	145	188	188	149	155	146	155	189	189	108	128	116	118
LB087	246	258	88	90	145	145	184	188	169	169	136	144	186	186	126	128	116	116

LB088	256	256	88	90	125	145	180	195	155	173	132	144	186	186	126	130	118	120
LB089	246	258	88	90	145	145	180	188	149	173	154	160	186	186	130	130	114	124
LB090	226	274	90	90	125	145	188	188	165	169	136	163	186	189	122	128	116	118
LB091	248	258	88	90	143	145	182	188	155	171	144	162	186	186	130	130	114	118
LB092	226	246	90	90	125	145	188	188	155	173	142	160	186	189	114	126	114	122
LB093	266	268	88	90	143	145	184	190	163	165	144	162	186	186	126	128	114	126
LB094	226	248	88	104	143	145	186	188	153	173	132	144	186	186	128	130	116	116
LB095	226	258	90	104	125	145	180	188	149	155	144	160	186	186	124	128	106	114
LB096	226	266	88	98	125	145	190	203	165	173	144	160	186	186	126	130	118	126
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LB098	246	256	88	88	125	125	188	188	149	155	162	162	186	186	128	130	118	128
LB099	246	258	88	88	125	125	180	188	153	169	142	176	189	189	122	128	120	122
LB100	248	256	90	90	125	145	186	188	149	155	144	162	189	189	126	130	120	126
LB101	248	256	88	90	125	125	188	188	149	173	136	144	186	186	128	130	114	116
KG001	246	256	88	90	125	162	180	184	155	155	134	138	186	189	118	130	114	114
KG002	226	248	90	90	145	162	184	188	163	175	138	142	186	186	114	128	116	118
KG003	226	248	90	106	125	145	184	188	169	173	144	146	186	189	126	128	106	118
KG004	246	276	90	98	125	162	188	192	155	163	138	174	186	186	126	128	106	114
KG005	226	248	88	98	145	162	188	190	149	173	138	144	186	186	114	128	118	118
KG006	226	226	88	90	125	145	184	188	155	163	138	138	186	186	128	128	114	118
KG007	246	276	88	106	155	162	186	188	169	173	144	144	186	186	128	128	114	114
KG008	226	226	90	90	125	155	182	192	167	169	118	144	186	189	114	126	114	114
KG009	226	256	88	90	145	155	188	188	169	171	136	177	186	189	116	128	106	118
KG010	226	226	88	88	145	155	184	184	155	169	142	144	186	189	116	128	106	118
KG011	246	248	88	98	145	162	188	194	171	175	144	177	189	189	114	128	114	128
KG013	226	246	98	98	162	162	182	192	155	169	132	138	186	189	128	128	114	114
KG014	248	268	90	98	155	162	188	188	155	155	144	148	186	189	128	130	106	106
KG015	226	266	88	98	125	145	182	184	155	175	142	146	186	186	128	128	118	128
KG016	226	276	88	98	145	155	188	192	163	163	144	144	186	186	114	128	118	122
KG017	226	270	88	90	145	155	188	192	155	155	138	142	186	189	114	128	114	114

KG018	226	226	88	88	125	162	182	188	155	173	136	173	186	186	126	126	114	118
KG019	248	276	98	98	125	145	188	188	155	155	142	144	186	189	114	128	114	118
KG020	226	256	88	98	145	162	182	190	155	155	142	142	186	189	126	128	118	128
KG021	226	270	90	98	125	145	182	192	155	167	138	160	186	186	114	128	118	118
KG022	226	246	88	98	125	145	184	192	157	171	144	150	186	186	114	126	106	122
KG023	246	248	90	90	125	162	188	188	155	165	142	146	186	186	128	128	118	122
KG024	226	246	98	98	155	162	192	192	163	165	134	134	186	186	126	128	106	118
KG025	248	268	88	98	145	145	184	188	155	169	138	144	189	189	116	126	106	106
KG026	226	248	90	98	125	145	188	190	163	165	134	136	186	186	128	128	106	118
KG027	226	246	88	90	145	145	182	184	163	169	142	160	189	189	126	130	118	130
KG028	248	248	88	90	145	155	188	188	167	171	138	144	186	189	114	128	106	122
KG029	226	276	88	98	125	162	182	188	155	165	144	146	186	186	128	128	114	114
KG030	226	226	88	90	145	162	188	188	157	171	142	146	186	186	128	128	106	106
MA001	258	268	90	90	145	145	194	194	149	171	130	142	189	189	114	122	112	118
MA002	228	248	88	98	145	145	182	186	149	151	122	142	189	189	114	126	108	120
MA003	248	280	90	104	125	153	182	206	149	175	126	142	186	186	114	122	112	118
MA004	268	276	98	104	145	145	182	196	149	175	142	146	189	189	114	116	106	112
MA005	248	266	88	88	145	145	182	190	149	149	118	146	186	186	116	130	120	124
MA006	226	266	88	90	145	145	181	190	149	155	142	142	186	186	116	128	106	106
MA007	222	246	90	90	145	145	182	197	149	149	142	148	186	186	116	116	120	128
MA008	248	266	90	114	145	145	174	202	149	155	118	150	189	189	128	128	106	106
MA009	236	264	92	104	125	145	181	186	155	167	140	142	189	189	122	124	116	120
MA010	260	280	88	90	145	153	174	196	153	165	142	146	189	189	118	122	106	112
MA011	236	246	90	90	125	125	188	192	149	151	156	162	189	189	122	130	116	120
MA012	268	276	90	104	125	145	174	192	157	157	142	142	186	186	122	130	106	116
MA013	248	268	90	90	145	145	170	184	153	155	118	142	186	186	116	128	106	124
MA014	222	276	104	104	155	163	184	189	149	153	118	144	189	189	114	124	112	118
MA015	250	272	88	90	145	153	170	192	157	170	142	142	186	186	122	122	114	116
MA016	248	264	90	94	145	167	184	186	149	165	142	142	189	189	116	116	112	116
MA017	250	264	90	98	145	145	182	186	149	155	136	146	186	186	122	130	116	124

MA018	226	238	88	90	125	145	188	191	149	149	138	142	186	186	122	126	108	122
MA019	248	248	90	90	145	153	174	182	155	163	132	150	186	186	124	130	118	120
MA020	222	248	88	90	145	153	174	186	149	163	142	142	186	189	114	116	116	122
MA021	226	260	88	90	125	145	186	191	149	163	144	165	189	189	114	126	108	120
MA022	248	250	88	90	134	145	174	188	163	169	142	144	186	189	122	124	120	122
MA023	248	248	90	98	145	145	170	181	149	155	150	150	186	189	118	130	116	120
MA024	262	264	90	102	145	167	182	186	157	165	112	161	189	189	116	126	112	112
MA025	248	268	90	112	145	155	184	206	153	163	122	146	186	186	114	116	106	126
MA026	250	290	90	98	145	145	186	186	149	153	130	150	189	189	116	118	112	112
MA027	252	262	88	90	134	155	180	184	155	163	118	136	186	189	122	128	120	124
MA028	252	264	88	90	155	155	186	186	155	157	142	150	189	189	122	128	116	124
MA029	264	280	88	98	125	145	181	181	149	153	118	118	186	189	116	122	116	122
MA030	248	264	88	94	145	147	182	193	149	153	142	157	189	189	126	128	114	116
MA031	248	274	88	90	143	145	182	186	149	157	146	150	186	189	116	122	116	120
MA032	250	264	88	104	145	147	186	186	165	175	124	146	189	189	116	126	116	120
MA033	222	248	90	90	125	159	182	193	163	175	138	142	189	189	126	126	112	120
MA034	226	264	88	114	145	145	180	198	149	165	124	130	186	189	116	126	118	124
MA035	248	258	90	90	153	153	170	186	149	165	0	0	189	189	114	114	114	122
MA036	250	264	90	98	125	125	174	192	149	155	142	142	186	186	130	134	116	122
MN001	264	272	88	90	143	143	181	188	149	155	138	150	186	186	118	130	116	120
MN002	246	248	88	96	143	143	186	190	149	163	136	150	189	189	114	122	114	120
MN003	222	266	90	90	125	145	192	198	149	149	124	165	189	189	114	122	106	112
MN004	250	262	88	104	145	155	181	181	149	153	146	153	186	189	114	122	106	120
MN005	244	262	96	108	145	155	181	204	149	149	134	165	189	189	122	122	118	124
MN006	252	268	90	98	155	155	182	184	149	169	126	140	186	186	122	128	112	124
MN007	248	274	88	90	145	145	182	188	153	155	130	140	189	189	116	130	106	122
MN008	222	248	96	98	145	147	184	194	155	167	142	160	186	186	124	126	112	112
MN009	248	256	88	96	145	155	184	190	149	170	126	142	189	189	122	126	120	120
MN010	248	276	90	90	145	155	170	182	149	155	126	142	186	189	102	126	106	118
MN011	248	250	90	90	145	157	184	188	149	157	136	146	186	186	114	122	106	122

MN012	250	252	96	98	145	145	159	195	149	153	142	142	186	186	116	130	120	120
MN013	222	248	90	96	145	153	195	201	158	173	131	142	189	189	124	128	112	122
MN014	248	250	90	96	145	145	182	204	149	151	146	156	189	189	116	124	112	120
MN015	248	262	88	90	147	147	161	174	149	149	148	157	186	186	114	122	106	112
MN016	244	250	92	98	145	145	174	181	155	163	146	155	186	189	122	126	112	124
MN017	250	260	96	96	155	167	182	186	149	170	118	146	186	186	116	130	116	120
MN018	236	250	96	98	125	145	182	184	149	163	142	173	189	189	116	122	106	120
MN019	248	272	90	90	145	145	180	182	153	155	138	138	189	189	114	130	118	120
MN021	248	248	88	104	145	145	190	194	149	155	146	146	189	189	116	130	124	134
MN022	246	250	90	112	145	147	181	195	149	149	136	140	186	186	114	130	116	120
MN023	250	250	90	90	145	163	170	195	163	163	138	140	186	186	116	128	116	122
MN025	248	262	90	106	145	145	182	186	149	161	138	150	189	189	126	126	112	130
MN026	272	276	90	98	125	145	182	182	149	171	134	146	189	189	116	130	118	124
MN027	262	266	88	106	145	145	186	186	153	155	0	0	186	186	116	122	120	134
MN028	250	266	88	98	145	145	186	190	153	170	126	142	186	186	116	122	116	124
MN029	248	262	90	106	147	159	186	186	149	155	118	138	189	189	116	126	116	134
MN030	226	248	88	96	125	125	190	194	157	171	142	146	189	189	130	130	118	134
MN031	254	264	90	96	125	145	181	195	149	149	140	150	189	189	114	122	108	120
MN032	242	248	104	114	143	143	182	186	155	155	126	140	186	189	116	116	108	114
MN033	268	274	88	88	145	145	174	186	149	149	146	165	189	189	116	122	112	116
MN034	250	252	90	104	145	145	174	182	155	161	134	142	189	189	116	122	106	116
MN035	222	264	88	90	125	145	181	186	149	149	142	156	186	186	130	130	112	118
MN036	250	264	90	98	153	155	180	184	163	169	130	146	186	189	114	122	118	120
MN037	248	248	90	112	145	145	170	182	149	170	130	146	189	189	122	122	120	130
MN038	236	276	98	98	145	145	184	184	149	155	118	173	189	189	116	130	120	120
MN039	248	262	90	90	145	145	174	184	149	155	146	173	186	189	108	122	106	116
MN040	250	264	90	96	145	145	182	190	149	149	146	146	186	186	126	137	120	124
MN041	250	268	88	88	125	145	188	192	155	169	138	163	186	186	108	116	116	118
MN042	250	256	90	90	145	163	186	196	163	175	142	150	186	189	122	130	118	118
MN043	226	276	88	90	145	153	159	189	149	155	154	154	189	189	114	137	116	120

MN044	236	248	88	90	145	153	174	194	149	155	142	146	189	189	114	114	114	120
MN045	250	268	88	96	145	145	174	182	149	163	120	146	189	189	114	130	116	124
MN046	248	258	96	98	145	145	182	201	155	162	136	146	186	189	122	122	112	122
MN047	258	280	90	96	125	145	174	201	151	163	136	150	186	186	124	130	106	120
MN048	230	268	90	90	125	145	204	204	155	163	146	150	186	186	114	122	106	122
MN049	262	264	90	90	145	145	178	186	149	149	142	146	189	189	122	122	116	116
MN050	250	250	90	90	145	145	182	182	149	149	142	142	189	189	126	130	118	120
MN051	256	264	88	96	145	167	182	194	149	153	142	146	189	189	122	130	118	120
MN052	250	272	98	102	145	145	174	182	155	171	118	146	189	189	114	126	106	116
MN053	248	248	88	108	145	145	166	201	153	153	144	173	186	189	128	128	118	120
MN054	246	266	90	90	145	145	186	195	153	167	138	140	186	186	124	126	120	122
MN055	262	264	90	106	145	147	186	186	149	155	118	138	186	189	116	126	106	134
BE001	250	264	88	98	145	145	184	186	155	167	130	138	186	189	126	130	116	124
BE002	248	278	90	104	145	155	186	190	153	153	138	140	189	189	122	126	114	116
BE003	248	264	90	90	145	155	186	197	149	170	150	150	186	189	116	130	114	120
BE004	228	248	90	90	125	153	190	196	155	171	134	168	186	189	122	130	106	116
BE005	248	248	90	96	125	125	194	196	153	163	146	150	189	189	126	130	106	116
BE006	248	250	90	104	153	153	159	186	149	155	138	146	189	189	114	126	106	118
BE007	248	250	88	90	145	145	159	194	149	155	148	157	189	189	116	116	116	116
BE008	248	264	90	104	155	155	186	188	149	169	138	144	186	186	116	126	112	116
BE009	244	246	90	98	143	155	186	206	163	163	138	146	186	186	116	126	120	122
BE010	256	258	98	104	145	163	184	186	149	163	136	144	186	186	112	130	116	126
BE011	250	290	88	98	145	155	182	190	149	165	126	150	189	189	126	139	106	116
BE012	248	290	88	90	125	145	188	190	153	169	126	126	189	189	116	139	106	116
BE013	250	250	90	98	125	145	181	184	153	172	138	150	186	189	132	132	116	116
BE014	248	270	90	90	145	145	170	184	149	155	142	146	186	186	116	126	106	126
BE015	222	266	96	98	145	145	181	188	149	163	150	165	189	189	114	132	118	124
BE016	254	276	88	90	125	125	188	204	149	171	126	138	189	189	126	134	112	124
BE017	226	246	90	96	125	167	174	188	149	167	136	142	186	189	116	130	124	124
BE018	248	258	90	90	125	125	174	180	149	167	146	146	186	186	116	126	124	124

BE019	248	272	90	114	125	145	186	194	149	149	116	138	189	189	122	130	116	116
BE020	226	274	90	90	145	145	186	192	159	163	136	146	186	189	122	122	106	112
BE021	250	252	88	90	163	163	186	200	149	169	140	142	186	186	114	114	116	124
BE022	250	258	90	98	145	155	181	191	163	163	142	146	186	186	116	130	108	112
BE023	248	286	90	90	125	145	170	186	153	175	136	146	186	189	114	124	118	118
BE024	262	268	90	90	145	145	180	201	155	155	116	161	189	189	116	124	116	122
BE025	248	252	88	88	145	151	174	181	153	155	142	150	189	189	116	118	106	112
BE026	248	264	90	98	145	161	174	180	145	155	140	144	189	189	114	124	116	118
BE027	248	264	90	90	143	145	189	196	149	167	138	150	186	189	116	122	106	112
BE028	248	250	90	98	145	155	188	192	153	157	146	150	189	189	116	122	118	118
BE029	222	268	96	98	145	145	174	186	155	155	150	161	186	186	116	122	114	116
BE030	248	252	98	98	145	145	174	182	149	162	146	156	186	189	114	122	114	116
BE031	248	258	90	98	145	155	174	174	158	175	140	144	189	189	114	134	114	114
BE032	244	252	96	98	125	145	180	186	155	163	118	140	186	189	122	126	116	118
BE033	252	276	90	90	145	145	197	201	149	149	150	156	186	189	122	130	106	116
BE034	248	276	90	100	125	145	188	192	155	167	146	150	189	189	130	130	116	140
BE035	250	268	88	90	145	145	166	182	155	163	142	146	189	189	116	126	112	118
BE036	248	254	90	98	145	145	170	186	149	155	146	160	186	186	114	122	106	118
BE037	226	250	90	98	145	147	174	194	155	163	142	146	189	189	114	130	104	112
BE038	238	286	90	98	125	145	170	174	149	153	146	146	186	186	114	130	116	116
BE039	238	238	90	98	125	145	174	187	153	170	138	140	186	186	130	130	118	118
BE040	248	250	90	96	125	155	193	198	155	155	124	126	186	189	122	139	112	124
NA001	262	268	90	90	149	149	190	192	149	170	0	0	186	189	126	130	106	130
NA002	270	274	90	104	125	145	190	204	153	171	142	160	186	186	114	116	106	106
NA003	246	262	90	104	145	145	180	188	149	157	122	146	186	190	126	126	116	120
NA004	250	260	88	90	145	145	194	194	149	149	142	160	186	189	126	130	106	122
NA005	248	250	90	90	125	157	190	194	149	155	140	156	186	186	130	130	122	122
NA006	248	256	90	104	145	157	188	190	149	169	142	156	186	186	122	130	122	134
NA007	246	246	90	90	125	145	180	186	149	163	142	142	186	186	126	128	106	116
NA008	248	256	104	104	145	155	159	197	155	175	138	150	189	189	106	116	116	124

NA009	266	272	90	90	125	155	192	206	153	155	136	142	189	189	116	130	116	122
NA010	216	216	88	90	125	125	192	200	160	164	126	130	189	189	0	0	125	125
NA011	236	254	90	104	125	145	192	200	160	164	138	150	189	189	0	0	114	140
NA012	236	236	90	90	145	145	190	204	155	157	146	150	189	189	126	130	122	140
NA013	276	276	90	100	125	155	195	201	149	157	122	142	189	189	116	130	116	140
NA014	248	254	90	90	125	125	194	204	149	157	142	150	189	189	126	130	120	140
NA015	252	270	90	90	145	161	184	195	155	157	142	154	189	189	126	126	114	116
NA016	262	262	90	106	145	161	180	182	149	157	142	144	189	189	114	126	114	114
NA017	268	270	90	98	147	161	187	195	149	170	142	154	189	189	126	130	114	124
NA018	256	272	90	96	145	147	178	186	153	170	144	146	186	189	126	126	122	134
NA019	252	272	88	90	143	143	186	194	149	175	138	146	186	189	114	126	124	140
NA020	246	250	88	104	145	159	182	190	149	149	142	144	186	189	124	126	114	122
NA021	246	272	98	98	0	0	188	188	157	157	142	142	0	0	128	128	0	0
NA022	258	274	98	104	145	155	178	204	149	149	142	150	186	186	106	116	118	122
NA023	262	276	90	104	125	125	187	194	170	175	118	144	189	189	126	126	118	118
NA024	250	274	90	90	145	147	180	187	149	158	144	146	189	189	126	128	118	134
NA025	224	256	90	90	145	151	180	190	155	158	142	144	186	186	126	126	114	128
NA026	250	264	90	104	145	155	186	188	149	157	134	142	186	189	114	122	124	142
NA027	236	264	90	90	125	125	186	194	157	175	160	163	186	189	122	122	116	120
NA028	228	228	88	88	125	145	184	184	149	155	136	160	186	189	114	126	114	116
NA029	246	248	88	92	125	145	178	188	157	165	142	155	189	189	114	122	106	106
NA030	250	250	90	90	125	149	190	194	155	175	144	156	186	186	126	126	112	120
NA031	248	276	90	90	125	145	190	192	149	157	142	144	189	189	114	116	118	120
NA032	248	248	88	104	125	145	180	184	149	167	140	142	186	189	114	122	116	134
NA033	248	256	90	90	145	153	180	190	155	167	140	142	186	189	126	130	116	118
NA034	236	252	90	90	145	149	188	188	163	169	122	134	189	189	122	130	116	120
NA035	246	248	90	90	145	153	187	190	163	163	138	148	186	189	126	126	114	116
NA036	254	272	104	104	145	145	182	188	155	163	142	144	186	189	126	130	122	126
NA037	268	272	90	102	145	155	184	196	155	169	140	156	186	189	106	126	126	142
NA038	250	256	90	102	125	145	188	188	149	175	144	154	186	189	116	126	108	116

NA039	246	274	92	92	125	155	186	190	153	175	142	142	189	189	126	130	110	114
NA040	262	268	90	104	125	145	188	196	161	163	140	142	186	189	114	126	106	136
NA041	248	248	90	90	145	145	194	198	149	157	136	156	189	189	114	126	106	124
NA042	272	276	90	90	125	145	192	200	149	170	134	136	189	189	120	130	114	126
NA043	226	274	90	106	145	153	182	187	153	167	144	144	186	189	122	126	122	122
NA044	246	262	90	90	153	164	170	178	155	171	136	142	189	189	126	126	106	106
NA045	256	264	90	102	145	145	176	190	0	0	124	150	186	186	116	130	108	116
NA046	246	276	88	90	125	145	190	192	149	163	142	142	186	189	114	126	114	120
NA047	246	266	90	104	145	145	188	192	149	155	136	142	189	189	126	126	120	120
NA048	246	250	90	104	149	159	159	190	153	163	144	156	189	189	114	128	114	114
NA049	238	266	88	90	125	145	180	186	155	173	136	142	189	189	120	122	118	120
NA050	246	260	88	98	125	143	182	188	157	170	142	150	189	189	114	122	118	118
NA051	238	248	90	90	125	145	170	184	170	170	144	148	186	189	114	122	118	122
NA052	248	276	90	90	147	151	194	194	155	163	142	144	186	189	122	122	122	122
NA053	228	274	90	104	125	145	188	192	151	170	132	144	189	189	126	130	120	134
NA054	256	272	88	88	145	145	184	204	149	153	142	144	189	189	122	126	108	112
NA055	230	280	88	90	125	164	184	204	153	175	142	158	186	189	116	126	118	122

Ind.	**WGb06**		**WGb17**		**WGb22**		**WGb24**		**WGb29**		**WGb32**		**WGb37**		**WGb38**		**WGb39**	
SE001	196	199	321	333	282	284	332	345	135	146	295	317	169	173	275	275	164	164
SE002	196	199	321	342	276	288	345	349	135	135	303	307	169	171	275	275	154	164
SE003	199	199	318	352	272	284	332	349	118	122	305	315	162	169	281	283	154	160
SE004	187	199	339	342	270	284	345	347	111	137	309	331	171	171	281	283	164	168
SE005	196	196	324	330	272	272	332	332	102	102	293	303	169	175	269	269	0	0
SE006	196	196	324	324	0	0	332	332	104	104	285	293	169	169	269	269	0	0
SE007	187	196	324	358	242	284	332	345	135	135	303	309	173	173	281	283	160	160
SE008	199	199	330	336	270	294	332	332	135	141	309	311	171	173	275	283	160	162
SE009	195	195	321	321	272	272	332	336	102	102	293	293	169	169	269	269	0	0
SE010	187	199	318	339	284	296	332	347	122	135	293	297	162	171	279	283	162	166
SE011	183	198	321	321	0	0	332	332	102	104	293	303	169	169	259	269	0	0
SE012	195	198	321	321	0	0	332	332	104	104	285	293	169	169	269	269	0	0
SE013	199	199	321	339	284	284	323	332	122	122	297	309	169	171	279	281	162	162
SE014	187	199	318	321	284	284	345	351	128	143	305	325	171	173	281	281	160	162
SE016	187	196	318	321	270	284	345	351	135	135	309	333	173	173	281	283	160	164
SE017	199	199	324	339	272	286	332	332	135	141	278	323	162	169	281	283	160	162
SE018	187	196	318	349	242	286	332	349	104	135	297	309	162	173	281	283	160	160
SE019	192	196	318	336	284	284	332	349	122	135	309	319	173	173	275	283	164	164
SE020	190	199	349	370	272	284	332	332	135	135	299	305	169	173	279	281	160	164
SE021	196	199	318	342	282	282	349	349	104	135	297	323	162	169	281	283	160	160
SE022	199	199	318	321	270	282	323	351	143	143	299	305	162	171	283	283	160	162
SE023	199	199	324	330	270	296	332	334	122	135	303	305	169	173	281	283	162	166
SE024	177	199	339	349	270	270	328	345	126	135	278	315	162	169	281	287	160	162
SE025	196	196	324	324	272	272	332	332	104	104	293	303	169	169	269	269	156	168
SE026	199	199	321	352	270	284	332	332	111	135	291	291	162	162	283	283	160	162
SE027	199	199	349	352	272	286	323	345	111	135	291	303	162	173	275	283	162	166
SE028	187	196	330	336	284	292	332	347	135	135	303	307	173	173	283	283	160	164
SE029	196	199	327	330	272	280	332	332	128	135	303	323	169	173	281	283	160	160
SE030	187	199	318	327	270	286	332	351	111	128	305	309	169	173	281	283	162	162

SE031	199	199	321	333	284	284	347	349	126	126	291	309	162	169	275	283	162	171
SE032	187	199	330	339	270	282	332	332	135	135	293	315	162	177	275	287	164	166
LI001	199	199	330	330	270	284	332	345	126	128	303	313	162	171	275	285	160	164
LI002	177	199	327	333	272	284	332	332	120	126	303	319	169	173	281	281	154	160
LI003	177	199	336	367	284	286	332	351	122	122	291	297	162	173	275	275	160	162
LI004	199	199	327	339	284	292	323	332	111	146	303	303	162	173	275	283	160	168
LI005	197	197	324	376	280	284	325	331	111	120	293	293	0	0	283	283	161	173
LI006	199	199	321	327	270	294	332	332	122	135	295	309	162	162	281	287	160	166
LI007	199	199	327	330	284	294	332	349	135	148	311	315	162	171	281	281	166	168
LI008	199	199	321	346	272	284	323	349	122	126	303	305	169	171	275	287	162	162
LI009	199	199	321	376	282	292	323	323	135	148	305	305	169	173	287	287	160	160
LI010	199	199	339	373	270	270	349	349	122	126	317	329	162	162	281	281	160	164
LI011	196	196	321	321	270	284	332	334	135	148	305	311	169	171	281	283	160	160
LI012	196	199	321	339	272	284	334	351	135	135	295	305	162	169	275	275	160	160
LI013	199	199	321	342	284	284	332	349	122	148	307	321	162	171	275	281	162	162
LI014	199	199	321	339	296	296	332	347	139	146	291	315	162	169	275	283	154	166
LI015	199	199	330	339	270	286	347	349	143	148	291	313	169	173	281	283	162	168
LI016	177	199	321	324	284	284	323	323	122	124	293	315	171	171	281	285	160	160
LI017	196	199	321	330	270	290	332	345	122	135	299	299	169	173	281	285	160	162
LI018	199	199	330	349	270	270	345	345	122	148	305	315	169	177	281	281	160	160
LI019	199	199	318	327	272	284	323	332	139	139	307	315	173	181	275	281	160	162
LI020	199	199	324	342	284	294	323	332	126	133	299	317	162	171	281	283	160	162
LI021	199	199	327	336	272	284	332	351	126	126	297	313	162	169	275	283	162	162
LI022	199	199	321	321	284	290	332	334	126	148	297	303	162	171	281	283	160	168
LI023	199	199	324	330	282	284	332	347	148	160	289	297	169	173	283	287	160	168
LI024	199	199	318	349	280	284	323	345	122	126	295	315	171	173	275	281	160	164
LI025	195	195	324	324	284	284	336	336	102	104	293	293	169	171	269	269	0	0
LI026	187	199	321	324	270	284	334	334	133	135	293	309	173	173	281	287	160	162
LI027	187	199	318	318	272	274	332	334	122	139	309	321	162	173	281	281	160	162
LI028	199	199	318	330	270	270	332	332	122	135	305	313	162	177	285	287	162	168

LI029	177	196	330	333	272	294	323	332	135	148	305	305	171	173	281	287	160	166
LI030	196	199	327	330	272	272	332	336	122	124	295	317	173	173	283	285	160	162
SL001	177	199	330	346	272	296	325	349	135	139	297	305	171	173	283	283	160	160
SL002	199	199	321	321	286	286	334	345	122	148	297	307	162	173	281	281	160	164
SL003	199	199	318	321	282	282	332	349	122	148	299	299	171	173	275	287	162	164
SL004	196	199	321	321	272	284	325	349	122	124	293	307	169	171	275	283	154	162
SL005	196	199	318	339	270	282	345	345	122	124	305	311	169	173	281	287	162	164
SL006	199	211	321	336	284	284	349	349	124	124	307	307	169	177	275	281	164	168
SL007	196	199	321	330	284	284	332	332	124	139	303	307	169	173	281	283	154	164
SL008	199	199	321	330	270	296	334	349	122	124	297	307	162	173	275	275	160	168
SL009	199	199	321	370	272	292	349	351	124	126	297	309	162	173	275	285	160	160
SL010	199	199	318	321	270	280	323	349	124	126	295	307	162	173	275	285	164	164
SL011	199	199	327	330	284	292	332	332	111	122	299	315	162	169	281	287	160	164
SL012	199	211	321	330	270	284	334	351	135	146	297	307	162	173	275	283	160	164
SL013	199	199	321	330	270	284	323	349	124	148	295	323	162	179	281	287	160	160
SL014	199	199	318	327	270	284	332	345	118	126	291	323	162	173	281	281	160	164
SL015	199	199	318	349	270	274	332	345	126	126	289	297	162	169	281	289	162	162
SL016	199	199	321	321	270	290	332	332	126	148	307	323	169	179	275	287	160	166
SL017	199	199	318	321	270	296	325	332	122	126	293	305	173	173	281	283	160	162
SL018	196	199	321	339	284	292	332	351	130	148	293	323	169	173	283	283	160	160
SL019	196	199	321	321	270	270	332	351	122	122	293	297	169	171	275	275	160	164
SL020	187	199	321	339	290	292	323	334	126	148	305	325	173	173	281	287	160	160
SL021	195	198	324	324	0	0	332	332	102	102	293	293	169	169	269	269	0	0
SL022	177	199	330	339	284	284	332	332	133	148	293	293	162	173	275	283	162	168
SL023	196	196	330	361	270	282	345	349	124	135	303	305	162	171	285	287	160	160
SL024	199	199	321	330	286	286	323	334	118	122	297	303	162	171	283	287	160	162
SL025	199	199	327	330	270	292	332	334	124	141	299	303	162	171	283	287	160	164
SL026	199	199	330	361	270	272	332	332	126	133	291	299	169	179	283	283	160	164
SL028	196	199	339	364	270	284	332	332	126	135	297	305	171	173	275	285	160	160
SL029	199	199	355	364	284	294	332	332	124	139	295	297	173	173	283	283	160	160

SL030	199	199	318	318	282	284	332	349	122	128	303	305	169	177	283	285	160	162
SL031	199	199	321	367	270	292	323	334	135	148	293	301	169	171	275	283	160	164
LB001	196	199	324	330	270	282	323	353	143	143	295	295	169	173	281	283	164	166
LB002	177	199	324	324	270	270	332	353	135	143	305	319	169	169	283	283	164	166
LB003	196	199	321	324	270	270	332	345	137	141	305	319	169	171	281	287	162	164
LB004	187	199	333	352	270	270	353	353	133	143	289	305	173	177	275	275	164	164
LB005	187	199	318	324	270	270	345	353	143	143	307	313	162	169	281	281	160	162
LB006	177	199	321	324	270	284	334	334	137	143	295	305	169	173	275	281	164	166
LB007	199	199	318	321	270	270	334	351	135	143	295	295	162	169	275	283	160	164
LB008	199	199	318	318	270	286	323	338	135	135	305	319	169	173	283	287	164	164
LB009	196	196	324	324	270	270	323	353	135	135	319	319	162	173	275	281	164	164
LB010	199	199	324	333	270	270	323	347	133	135	295	319	169	173	283	287	160	164
LB011	196	199	318	324	270	286	332	341	135	143	305	313	162	173	281	281	160	160
LB012	199	199	321	339	270	270	323	347	135	135	293	319	169	173	281	283	160	164
LB013	196	196	318	318	270	270	323	341	135	143	289	295	162	173	281	283	162	164
LB014	196	199	324	330	270	270	341	353	122	143	299	319	173	173	281	281	160	160
LB015	196	199	321	333	270	270	341	353	133	133	305	311	169	173	281	283	160	164
LB016	196	199	330	333	270	282	323	345	143	143	295	305	162	173	275	281	160	160
LB017	199	199	330	358	270	270	332	341	135	143	295	317	169	173	283	283	162	164
LB018	199	199	318	324	270	272	332	341	135	143	295	331	162	171	281	283	160	160
LB019	199	199	318	324	270	270	345	351	135	143	295	295	162	173	283	283	164	164
LB020	187	199	318	318	270	270	347	353	135	143	299	313	173	173	281	283	164	164
LB021	187	199	318	330	270	272	341	353	135	143	309	313	162	173	281	281	160	164
LB022	199	199	318	333	270	272	332	353	133	135	299	319	162	173	281	283	160	164
LB023	197	199	318	324	270	272	332	341	133	135	303	331	162	171	281	281	160	160
LB024	197	199	318	318	270	270	332	353	135	143	305	311	171	173	281	281	160	164
LB025	199	199	321	324	270	288	345	353	135	141	297	305	169	169	275	275	162	164
LB026	196	197	318	318	270	286	341	353	135	137	299	331	169	171	275	281	160	160
LB027	199	199	318	342	286	286	341	353	135	135	319	331	169	171	281	281	160	162
LB028	196	197	318	330	270	270	332	353	135	143	299	311	162	162	281	281	162	166

LB029	196	197	318	361	270	286	341	345	133	135	319	331	169	171	281	281	160	160
LB030	199	199	321	352	270	270	332	353	143	143	295	295	162	173	275	281	160	164
LB031	196	196	318	336	270	270	334	334	128	137	295	319	169	173	281	283	160	160
LB032	199	199	324	339	270	284	341	347	141	143	295	319	162	169	283	287	160	164
LB033	196	199	318	355	270	270	332	345	135	137	295	299	169	173	281	283	160	164
LB034	199	199	315	318	270	272	323	332	133	143	301	311	171	173	281	281	160	164
LB035	196	199	321	355	270	272	341	345	135	143	305	311	169	173	281	281	160	164
LB036	196	199	318	321	270	270	341	345	135	143	305	311	169	173	281	283	160	164
LB037	199	199	318	318	270	270	323	347	133	143	295	295	169	173	281	283	164	164
LB038	177	199	318	321	270	270	323	334	141	141	295	295	162	171	281	287	160	162
LB039	199	199	321	321	270	270	323	323	133	143	295	297	169	173	275	281	164	166
LB040	199	199	324	336	270	270	323	353	133	139	295	309	162	169	275	275	164	166
LB041	199	199	318	321	270	272	351	353	137	143	305	313	169	173	275	281	162	164
LB042	199	199	324	324	282	284	332	353	143	143	295	303	169	173	275	283	164	164
LB043	196	199	318	336	270	270	341	351	133	135	293	313	169	173	283	283	164	164
LB044	199	199	318	324	270	284	347	353	133	141	293	305	169	173	283	283	164	164
LB045	196	196	318	318	270	270	323	353	137	141	295	295	169	169	281	287	164	164
LB046	196	199	318	352	284	288	353	353	141	143	289	299	169	173	281	283	164	164
LB047	196	196	318	324	270	284	341	353	141	143	295	313	169	173	275	281	160	164
LB048	196	199	318	318	270	270	323	345	133	135	295	317	173	173	281	283	160	160
LB049	199	199	321	324	272	284	345	353	133	143	295	311	169	173	281	281	164	164
LB050	199	199	324	330	270	272	332	347	133	143	295	295	169	173	275	283	160	160
LB051	199	199	333	336	270	270	323	323	135	143	295	295	173	173	281	283	164	164
LB052	196	199	324	333	270	270	347	353	135	143	295	319	162	169	281	281	162	162
LB053	196	199	324	324	270	270	332	353	137	137	319	321	169	173	281	281	160	160
LB054	187	199	321	324	270	270	332	353	137	137	293	305	169	173	281	287	160	166
LB055	196	199	321	324	270	288	341	353	133	143	305	311	162	173	281	283	160	160
LB056	199	199	318	321	270	272	341	347	133	141	301	311	169	171	281	287	162	166
LB057	196	199	318	361	270	270	323	347	133	135	301	307	162	173	281	283	160	164
LB058	199	199	318	318	270	270	341	353	133	137	295	305	162	173	275	281	160	162

LB059	187	196	318	333	270	272	323	349	139	143	295	319	162	169	275	275	160	164
LB060	199	199	318	324	270	272	332	334	126	141	295	303	162	171	281	281	162	162
LB061	196	199	324	330	270	272	334	353	126	143	289	295	162	169	287	289	160	164
LB062	187	199	318	352	272	272	323	334	133	143	303	319	169	173	275	283	164	164
LB063	196	199	324	333	270	270	347	351	133	133	303	305	173	173	281	281	162	164
LB064	197	199	318	324	272	288	341	347	133	137	295	331	162	162	281	283	162	164
LB065	196	199	318	330	270	270	323	353	133	135	305	305	169	173	281	287	160	160
LB066	199	199	318	333	270	288	351	353	141	143	295	311	173	173	281	283	162	164
LB067	199	199	318	330	270	284	351	351	133	135	299	305	173	173	281	281	160	164
LB068	199	199	318	321	270	270	323	341	126	143	305	321	162	173	275	281	160	164
LB069	197	199	318	318	270	284	332	353	133	135	305	319	162	169	283	283	162	164
LB070	177	199	318	349	270	272	0	0	135	135	299	313	171	173	281	281	162	162
LB071	197	199	324	333	270	272	341	341	122	135	313	317	169	173	283	283	160	164
LB072	199	199	318	318	270	270	347	351	135	137	295	319	169	171	281	283	160	162
LB073	196	199	318	318	270	270	347	347	135	135	295	313	173	173	281	281	164	164
LB074	199	199	318	333	270	270	332	341	135	139	295	313	169	173	281	287	160	160
LB075	196	199	318	324	270	272	334	351	135	135	305	309	169	173	275	281	164	164
LB076	199	199	0	0	284	286	0	0	133	139	0	0	0	0	0	0	160	162
LB077	199	199	318	318	270	272	347	351	128	141	305	309	169	173	281	283	160	160
LB078	177	199	318	367	270	288	323	353	135	143	295	311	162	173	275	281	160	164
LB079	199	199	318	333	270	270	341	353	143	143	295	295	162	173	281	281	160	164
LB080	199	199	318	352	270	284	323	353	135	135	295	299	171	173	281	283	162	164
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LB086	199	199	327	349	270	284	332	347	135	143	299	319	162	173	283	283	162	162
LB087	199	199	318	318	270	272	347	347	135	141	299	311	162	173	275	283	162	164
LB088	196	199	318	324	270	270	332	332	133	143	289	295	169	169	281	281	162	164

LB089	199	199	321	324	270	272	323	341	135	137	295	305	162	173	275	281	160	164
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LB092	199	199	318	330	270	272	332	332	133	135	295	313	162	169	283	283	160	162
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KG002	196	199	324	346	270	272	341	347	137	137	311	311	169	181	283	283	162	164
KG003	177	196	318	346	270	272	345	347	135	137	289	293	169	169	283	283	160	160
KG004	196	196	324	324	270	272	332	332	137	137	303	311	162	181	281	281	164	166
KG005	199	199	324	324	270	272	332	341	135	135	293	303	169	173	281	281	160	164
KG006	196	196	318	318	270	270	332	334	135	137	303	311	169	173	280	281	160	162
KG007	177	199	318	324	272	272	332	341	135	137	303	309	162	169	283	283	160	160
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KG013	196	196	324	333	270	270	332	353	137	137	309	311	173	173	281	283	160	164
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KG015	196	196	343	343	270	270	332	334	135	135	311	315	173	173	281	283	160	162
KG016	196	196	346	352	270	270	332	334	135	137	313	313	162	169	283	283	160	162
KG017	199	199	324	346	270	272	347	347	135	137	291	311	162	162	281	281	160	162
KG018	177	196	318	346	270	270	332	347	135	135	293	313	173	177	281	281	160	162

KG019	196	199	318	324	270	270	323	323	135	137	309	315	169	171	281	283	160	162
KG020	177	196	324	324	270	270	332	334	135	135	309	311	169	169	280	283	160	162
KG021	196	199	318	349	270	270	332	332	135	135	293	295	169	169	281	283	160	164
KG022	177	199	324	324	270	270	332	332	135	135	289	295	162	169	281	281	164	164
KG023	177	196	324	324	270	270	332	334	135	137	293	313	162	162	281	281	162	164
KG024	177	199	324	324	270	270	323	347	124	137	293	313	162	162	281	283	160	160
KG025	196	196	318	324	270	270	323	341	135	135	313	313	162	169	280	283	160	162
KG026	177	196	324	324	270	270	334	334	137	143	295	313	162	173	280	283	160	164
KG027	196	199	318	318	270	270	323	323	135	137	311	311	162	162	281	283	160	162
KG028	196	199	318	324	270	270	332	341	135	137	293	311	169	177	281	281	160	162
KG029	196	199	324	333	270	270	323	341	135	137	289	295	169	173	281	281	160	160
KG030	196	199	324	324	270	270	347	353	135	135	293	313	169	171	281	283	162	162
MA001	196	199	321	327	284	284	332	353	128	135	289	303	171	173	283	287	162	162
MA002	199	199	318	342	284	284	332	353	126	135	305	319	173	173	275	283	160	162
MA003	196	196	321	330	270	270	323	332	135	148	311	315	162	169	275	283	162	162
MA004	196	199	321	333	284	286	323	347	126	139	309	315	173	173	275	285	160	162
MA005	199	199	321	339	270	270	323	332	122	128	293	295	169	177	275	281	162	162
MA006	199	199	321	321	270	270	332	347	122	122	295	303	173	177	275	281	162	164
MA007	196	199	327	358	282	282	323	353	118	148	303	309	162	173	281	283	160	160
MA008	196	199	342	358	270	270	332	347	122	122	295	313	162	177	275	283	162	164
MA009	190	199	321	327	280	284	345	351	122	146	303	305	162	171	275	283	162	162
MA010	187	199	336	367	282	286	323	349	118	122	303	307	173	177	275	281	160	164
MA011	199	199	318	352	270	292	332	334	128	146	295	297	169	169	281	283	160	162
MA012	199	199	318	321	270	272	332	351	122	143	293	299	173	173	275	281	160	164
MA013	199	199	318	349	284	284	323	332	122	128	309	311	162	173	275	281	160	162
MA014	196	199	321	330	274	284	332	332	148	148	295	313	171	173	275	275	162	162
MA015	199	205	324	339	286	286	351	351	111	133	303	303	169	173	275	281	160	164
MA016	177	199	321	330	272	284	332	332	139	143	289	291	173	177	281	287	162	168
MA017	199	199	324	342	284	296	323	332	122	126	297	303	169	171	281	283	160	166
MA018	196	199	321	346	284	286	332	345	135	148	297	305	173	173	275	287	160	162

MA019	199	199	330	346	270	270	323	349	122	126	305	305	171	173	275	279	160	164
MA020	190	196	330	339	270	270	323	332	122	126	305	331	169	169	279	281	160	162
MA021	196	199	318	321	272	286	332	351	126	169	295	297	169	173	275	275	162	168
MA022	190	199	330	342	270	284	332	349	122	135	315	331	169	171	279	287	160	162
MA023	177	199	321	342	284	284	332	334	135	137	297	307	171	177	281	289	166	168
MA024	199	199	330	339	270	284	332	345	124	128	311	315	171	171	281	287	154	162
MA025	199	199	324	346	270	284	349	351	126	126	309	311	169	173	275	275	160	164
MA026	177	196	321	333	282	290	332	349	137	148	303	305	169	181	275	287	160	160
MA027	196	199	321	342	284	296	332	349	135	139	301	311	162	171	275	283	160	168
MA028	187	199	342	342	284	284	345	349	135	139	291	291	162	173	281	283	160	160
MA029	199	199	318	321	284	284	332	345	135	135	291	295	173	173	283	283	160	168
MA030	196	199	318	324	280	284	349	365	122	148	305	309	173	177	283	289	162	162
MA031	196	199	324	330	284	284	323	332	122	128	289	315	173	177	275	285	162	162
MA032	199	199	321	324	284	284	328	332	124	135	295	295	171	171	275	281	162	162
MA033	196	199	309	349	284	296	332	332	122	143	295	297	162	171	275	275	162	166
MA034	199	199	330	330	280	280	349	349	126	135	0	0	171	171	0	0	154	164
MA035	199	199	324	339	270	270	332	353	122	148	305	307	162	171	275	283	164	164
MA036	199	199	321	324	270	274	332	334	122	143	299	319	173	173	275	289	164	164
MN001	199	199	330	330	270	284	332	332	126	148	295	305	162	173	275	285	162	162
MN002	196	199	318	321	266	288	332	345	120	148	287	293	169	173	281	287	154	160
MN003	199	199	333	339	242	292	332	349	122	139	299	301	162	169	281	287	154	160
MN004	199	199	321	333	270	284	332	349	126	126	289	303	162	173	285	287	160	164
MN005	199	199	330	333	270	274	347	349	139	139	303	303	162	173	281	285	162	164
MN006	196	199	330	349	270	284	323	323	118	135	307	327	171	173	281	283	164	164
MN007	199	199	312	330	284	284	332	351	122	148	289	315	173	173	281	283	162	164
MN008	199	199	321	327	270	284	323	323	148	148	278	307	173	173	275	283	160	162
MN009	199	199	321	321	270	292	323	349	122	148	297	303	171	171	285	287	162	162
MN010	199	199	324	339	270	284	332	332	148	148	303	321	173	173	281	285	162	168
MN011	177	199	330	330	282	284	323	355	124	135	299	305	169	171	283	287	160	160
MN012	196	199	321	327	284	286	323	334	135	135	295	295	169	171	275	275	160	162

MN013	196	199	321	324	284	290	345	349	135	135	321	323	162	171	281	285	160	160
MN014	199	199	330	330	270	274	347	351	126	126	303	315	162	169	275	283	162	164
MN015	196	199	318	349	284	284	332	332	126	150	313	315	173	177	275	287	160	160
MN016	196	199	330	333	284	296	323	332	122	148	305	307	171	173	275	283	160	164
MN017	196	196	309	358	272	290	332	353	122	126	295	305	169	171	275	281	160	164
MN018	199	199	321	330	284	284	323	323	124	126	293	303	162	171	287	289	160	162
MN019	199	199	321	330	270	272	323	323	135	135	293	327	162	171	281	287	160	160
MN021	196	199	321	333	284	284	323	345	122	135	311	323	169	173	283	287	162	168
MN022	199	199	318	318	272	284	323	332	126	148	293	301	162	171	281	281	162	168
MN023	199	199	318	318	270	272	332	349	135	148	293	293	162	173	281	281	154	164
MN025	196	199	321	333	284	284	345	349	128	154	297	303	162	162	275	275	160	160
MN026	196	199	318	324	270	286	323	323	124	124	305	321	169	177	275	285	160	164
MN027	199	199	321	333	270	296	332	332	135	135	293	315	171	173	281	287	162	164
MN028	199	199	333	333	272	296	332	332	135	148	293	305	162	171	275	287	160	160
MN029	196	199	318	321	284	294	323	332	122	135	315	321	171	171	281	283	160	162
MN030	196	196	333	361	270	284	323	332	122	143	303	319	169	173	283	287	160	166
MN031	199	199	318	361	282	292	328	349	126	148	305	321	162	177	275	287	162	162
MN032	196	196	321	339	274	284	332	345	111	137	291	291	171	175	275	287	164	168
MN033	199	199	330	330	282	282	349	349	122	124	287	327	171	173	275	283	160	168
MN034	199	199	318	355	270	284	332	345	124	126	307	313	171	173	283	285	162	162
MN035	196	199	321	339	272	290	323	332	124	137	301	301	169	169	275	289	162	168
MN036	199	199	324	342	270	296	323	349	124	148	289	289	173	173	281	285	160	162
MN037	199	199	324	333	272	284	323	323	111	128	291	297	169	171	281	287	160	162
MN038	196	199	342	364	284	290	323	349	126	126	0	0	162	169	283	289	162	162
MN039	199	199	333	364	286	290	323	332	126	135	293	295	162	169	281	289	160	162
MN040	199	199	321	352	270	272	323	323	135	148	293	305	162	169	281	283	160	160
MN041	196	199	321	333	272	284	345	359	122	148	293	297	173	179	275	281	160	164
MN042	177	199	330	330	270	274	332	332	126	148	297	305	173	173	281	281	160	162
MN043	196	199	321	342	272	284	323	332	122	126	278	303	171	173	275	287	160	166
MN044	199	199	318	339	280	284	323	349	137	154	301	303	162	169	275	283	160	160

MN045	199	199	318	327	284	284	323	332	122	126	293	307	171	173	275	283	160	162
MN046	196	199	318	330	274	292	349	351	122	148	297	303	171	173	281	285	154	160
MN047	187	199	318	339	272	272	332	349	124	126	295	297	162	171	281	281	154	162
MN048	199	199	321	358	270	292	323	334	135	148	297	313	162	162	281	283	154	160
MN049	199	199	330	330	270	294	332	345	126	135	297	297	162	171	283	287	154	162
MN050	196	199	318	321	286	290	332	353	124	126	305	305	162	169	283	283	160	162
MN051	196	199	309	367	270	272	323	351	139	158	297	297	162	177	281	281	160	162
MN052	196	196	318	324	284	296	323	332	122	126	305	309	162	169	283	285	160	162
MN053	199	199	321	321	272	284	349	353	122	122	293	297	162	171	281	287	160	164
MN054	199	199	330	333	272	292	332	345	124	135	289	305	162	173	281	281	160	164
MN055	196	196	321	321	270	284	349	349	126	154	303	315	162	173	275	281	160	162
BE001	199	199	321	330	284	284	332	349	122	122	297	313	162	171	281	281	162	162
BE002	196	199	321	321	270	270	323	332	126	135	293	297	173	173	281	281	160	162
BE003	199	199	321	330	272	284	332	353	122	148	295	295	171	177	275	281	162	164
BE004	199	199	318	367	270	272	323	353	126	135	289	321	169	173	275	281	164	168
BE005	196	199	318	339	272	292	323	332	111	137	289	303	169	173	275	289	160	162
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BE007	199	199	321	349	270	284	323	323	122	156	295	303	177	179	275	275	162	166
BE008	187	196	330	330	270	270	323	349	122	158	291	305	169	169	283	283	162	162
BE009	177	187	321	321	284	284	323	323	126	130	291	297	162	173	275	275	160	164
BE010	199	199	318	336	270	284	332	353	126	128	293	301	173	173	281	281	162	162
BE011	199	199	330	330	270	270	323	349	135	135	295	295	162	171	275	289	156	160
BE012	199	199	330	349	270	274	323	334	122	146	295	295	162	169	281	285	156	168
BE013	196	199	330	346	270	272	323	332	135	148	303	305	169	177	281	289	162	162
BE014	199	199	321	324	280	280	332	347	122	135	313	323	162	173	275	289	162	164
BE015	177	199	327	342	284	296	323	332	135	148	297	303	162	171	275	281	162	162
BE016	177	199	318	342	272	290	334	345	118	135	289	293	162	171	281	281	160	164
BE017	196	199	318	330	270	270	349	355	113	148	293	305	169	171	275	285	160	162
BE018	187	199	318	339	270	272	332	349	148	148	305	327	169	169	275	275	160	162
BE019	196	196	318	355	272	272	334	349	135	135	0	0	162	177	275	283	168	168

BE020	177	199	327	330	280	280	323	323	122	133	283	305	162	173	281	283	160	162
BE021	199	199	336	342	270	282	323	323	120	148	291	303	169	173	281	283	160	162
BE022	196	199	318	324	274	284	332	345	126	126	287	327	173	173	275	283	160	162
BE023	199	199	330	355	284	292	332	332	126	126	295	315	171	173	283	287	154	162
BE024	199	199	324	339	274	286	332	351	143	148	299	303	171	171	275	283	162	166
BE025	199	199	330	346	270	284	323	332	120	135	289	307	171	171	275	275	160	166
BE026	196	199	336	364	270	284	332	332	135	135	297	299	169	171	283	283	160	160
BE027	199	199	330	358	270	274	323	349	135	156	291	295	162	169	275	283	160	160
BE028	199	199	339	339	270	272	323	332	122	139	303	305	169	169	275	289	160	160
BE029	177	198	324	327	270	270	332	351	122	135	291	305	173	173	275	281	162	168
BE030	196	199	318	330	272	284	323	332	120	137	295	297	162	169	275	283	160	164
BE031	177	199	327	346	270	270	332	351	122	139	297	305	162	171	275	283	162	164
BE032	196	199	324	352	242	270	332	351	122	135	297	301	162	173	275	275	160	164
BE033	199	199	330	330	272	290	332	332	124	148	301	323	169	177	275	283	160	162
BE034	177	199	318	324	272	272	332	349	122	137	289	305	169	171	275	281	160	162
BE035	199	199	318	339	272	280	323	351	124	135	0	0	162	171	281	281	160	162
BE036	199	199	318	324	272	272	332	332	122	122	297	305	162	171	281	281	160	162
BE037	177	196	321	346	284	290	323	332	122	135	295	303	162	173	281	281	154	160
BE038	199	199	330	339	280	292	332	359	135	137	289	289	171	175	283	287	160	162
BE039	187	199	327	330	272	292	351	353	111	122	293	305	169	177	275	283	162	164
BE040	199	199	318	318	270	270	323	351	135	137	289	323	162	173	283	283	162	164
NA001	199	199	321	352	272	274	332	349	122	126	295	295	169	173	283	283	160	162
NA002	199	199	336	342	270	284	323	332	122	135	295	313	162	169	283	289	162	164
NA003	199	199	324	324	270	272	323	323	122	135	295	315	162	173	281	283	160	164
NA004	196	199	321	324	280	290	341	351	133	135	297	307	169	169	287	289	162	164
NA005	177	177	324	352	270	286	341	349	135	137	305	323	162	169	287	289	162	164
NA006	199	199	321	321	272	286	334	347	124	143	289	299	162	173	283	287	160	164
NA007	199	199	324	330	274	274	347	353	135	154	295	295	171	177	283	285	164	164
NA008	196	199	321	346	242	270	332	345	124	124	293	301	162	171	275	281	154	164
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NA010	195	198	330	346	272	272	332	332	102	104	295	297	169	188	269	271	156	168
NA011	177	196	321	321	270	270	323	332	124	137	319	321	162	177	269	271	164	166
NA012	196	196	321	327	270	284	332	332	113	135	299	321	171	173	275	281	164	168
NA013	196	196	321	321	270	292	332	349	137	146	283	321	173	177	281	289	164	168
NA014	177	199	321	324	270	270	332	332	135	137	295	323	169	171	275	281	162	168
NA015	196	199	349	352	290	292	323	353	122	146	293	293	171	177	279	283	160	164
NA016	199	199	327	352	270	272	323	334	139	146	293	295	169	171	283	289	162	164
NA017	199	199	339	358	270	272	323	323	135	135	293	293	171	173	275	283	162	164
NA018	199	199	321	373	270	290	323	323	133	146	293	295	162	169	275	287	154	166
NA019	177	199	361	373	284	292	323	323	122	146	295	295	169	177	275	283	154	162
NA020	199	199	321	324	270	272	332	334	122	137	295	295	169	169	285	289	162	166
NA021	199	199	318	318	270	272	345	345	104	124	0	0	0	0	0	0	156	160
NA022	199	199	321	342	270	282	347	351	122	124	307	309	162	162	275	287	160	164
NA023	177	199	318	330	270	272	323	334	135	137	299	311	162	169	275	289	154	162
NA024	199	199	318	324	270	270	323	351	128	135	311	329	162	173	281	281	160	162
NA025	177	199	321	330	242	272	332	332	113	137	295	305	169	177	283	289	160	164
NA026	196	199	321	321	270	284	323	347	133	143	293	293	162	171	283	289	160	164
NA027	199	199	321	324	284	294	323	347	135	135	289	295	171	177	275	287	160	164
NA028	199	199	321	327	270	274	323	323	124	137	0	0	162	173	281	281	162	166
NA029	199	199	318	333	270	270	323	341	135	154	289	293	162	177	285	287	160	162
NA030	199	199	321	321	272	292	347	349	135	135	0	0	171	171	285	289	160	162
NA031	177	199	336	355	270	284	323	345	122	135	293	319	171	173	275	281	164	164
NA032	177	199	321	349	270	272	323	349	133	135	295	295	162	169	283	289	160	160
NA033	177	177	324	358	270	270	323	332	133	135	295	309	171	177	283	287	162	164
NA034	177	199	318	321	270	274	341	353	122	124	295	309	162	177	287	287	160	160
NA035	196	199	321	321	284	284	323	351	133	143	305	319	169	177	285	285	164	164
NA036	177	199	318	321	284	284	323	349	135	146	295	305	173	173	283	289	160	162
NA037	199	199	336	352	242	270	323	349	122	124	291	293	169	171	285	285	164	164
NA038	199	199	318	321	270	272	334	349	133	133	293	295	171	171	283	289	164	166
NA039	199	199	318	349	270	294	347	347	135	146	293	303	162	162	275	275	164	164

NA040	196	199	318	318	270	286	323	332	122	135	295	295	162	173	285	289	160	162
NA041	199	199	321	324	270	292	323	332	120	135	305	329	173	177	281	287	160	160
NA042	196	199	321	352	270	284	347	353	135	137	299	311	171	173	283	283	164	166
NA043	199	199	321	321	270	274	332	353	124	135	293	299	169	169	283	285	160	166
NA044	199	199	321	321	270	272	334	349	122	143	295	305	179	179	283	287	162	164
NA045	199	199	321	370	272	284	349	353	128	135	289	311	173	177	281	289	164	164
NA046	196	211	321	321	270	272	323	323	109	109	295	305	169	177	287	289	160	164
NA047	196	199	318	321	270	272	323	351	135	137	293	295	169	171	289	289	164	166
NA048	199	199	321	321	270	270	323	334	122	124	297	305	171	177	283	289	162	168
NA049	177	196	330	358	270	290	347	351	137	152	295	321	171	177	283	283	160	160
NA050	196	196	318	321	272	272	332	349	135	154	303	311	173	177	275	289	160	160
NA051	190	211	324	330	270	272	323	323	135	135	295	311	169	177	281	283	148	166
NA052	177	199	324	330	282	284	323	332	124	137	293	311	169	173	283	289	160	164
NA053	199	199	321	355	270	270	332	332	122	139	293	295	162	162	275	283	154	162
NA054	196	199	318	333	284	284	332	332	122	135	299	313	173	179	281	283	160	164
NA055	199	211	346	358	270	272	345	351	124	135	303	313	177	179	281	283	164	164