Effects of habitat loss on the genetic diversity of *Embiratermes neotenicus* (Isoptera) in a fragmented landscape of the Atlantic Forest, Brazil

Running title: Effects of habitat loss on genetic diversity

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Data Availability Statement

The data that supports the findings of this study are available in the supplementary material of this article.

Abstract

1. Connectivity loss during habitat fragmentation poses a serious threat to global biodiversity. The effects of this process depend on factors such as the dispersal ability and breeding systems of each species, the type of land use surrounding the habitat remnants and the position of fragments in the landscape.
2. Termites are abundant in tropical ecosystems, and within this group, soil-feeding species are the most sensitive to environmental degradation.
3. We investigated whether the fragmentation of the Atlantic Forest that occurred approximately 110 years ago because of sugarcane plantations in Northeast Brazil affected the genetic diversity of a population of *Embiratermes neotenicus* (Termitidae: Syntermitinae) in 14 fragments separated by 3 m to 104 m over an extent of 20 km.
4. For 10 nests in each fragment, 10 individuals (*n* = 1400) were genotyped at five microsatellite loci. Our results show that the population exhibits weak genetic structure, with no relations between genetic variability and fragment features.
5. This result may be explained by the extraordinarily long lifespan of individual colonies, given this species' peculiar breeding system, offering several opportunities for dispersal events and patch colonization.
6. Landscape features such as the arrangement of forest fragments and seasonal nature of the sugarcane matrix could enable this species to maximize dispersal success and avoid local extinction.

Keywords: connectivity; isolation; microsatellites; population genetic structure; termites.

Introduction

Habitat fragmentation poses a serious threat to biodiversity and ecological processes in ecosystems worldwide (Fletcher et al. 2018; Haddad et al. 2015). This process decreases the size of populations and limits dispersal. Consequences include a reduction in gene flow, the loss of genetic variability and adaptive potential, and inbreeding depression (Fahrig 2001; Keyghobadi 2007). However, the magnitude of fragmentation effects depends on several factors such as the dispersal ability and breeding system of each species (Fahrig 2001; Fougeyrollas et al. 2018), the type of land use surrounding the habitat remnants (Debinski 2006; Jules & Shahani 2009; Ricketts 2001) and the position of fragments in the landscape (Sauders, Hobbs & Margules 1991).

Tropical rainforests are the biome that has suffered the most from environmental fragmentation (Taubert et al. 2018). Among such rainforests, the Atlantic Forest stands out as one of the largest on the planet, originally covering 148.194.638 ha and occupying most of the Brazilian coast, northeastern Argentina and northeastern Paraguay (Carlson, Mitchell & Rodriguez 2011; Izquierdo, De Angelo & Aide 2008; Ribeiro et al. 2009). It harbors 1 to 8% of the world's biodiversity and is one of the most important hotspots for biodiversity conservation (Marchese 2015; Silva & Casteleti 2005). It is also one of the most degraded ecosystems, with only 11.4 to 16% of its original surface remaining, and is subdivided into thousands of fragments, mainly because of the expansion of agricultural frontiers and urbanization (Joly, Metzger & Tabarelli 2014; Reis et al. 2002; Ribeiro et al. 2009).

Termites (Blattodea: Isoptera) are abundant in humid tropical ecosystems, such as the Atlantic Forest, and are key players in nutrient cycling and energy flow (Dangerfield, McCarthy & Ellery 1998; Vasconcellos 2010). Soil-feeding termites are particularly numerous and diversified in humid forests, where they contribute significantly to soil humification (Martius 1994; Vasconcellos 2010). Soil-feeding termites are also the most sensitive types of termites to environmental changes, presenting the potential to be used as model organisms for fragmentation studies (Davies 2002; Dupont et al. 2009).

Among soil-feeding species, *Embiratermes neotenicus* (Holmgren, 1906) is widely distributed and abundant in rainforests and has been frequently recorded in the Atlantic Forest (Cancello et al. 2014; Ernesto et al. 2014; Souza, Alves & Vasconcellos 2012). This species constructs well-defined epigeal nests, and colonies are initiated by a pair of primary reproductives (king and queen). The dispersal and mating strategies include long-distance flights resulting in outbreeding (Fougeyrollas et al. 2018). Therefore, we selected *E. neotenicus* as a suitable model to study the effect of environmental fragmentation. In the present study, we investigated whether the fragmentation of the Atlantic Forest that occurred approximately 110 years ago because of sugarcane plantations in Northeast Brazil impacted the genetic variability and genetic structure of a population of *E. neotenicus* in 14 fragments. For 10 nests in each fragment, 10 individuals (n = 1400) were genotyped at five microsatellite loci. Considering that the type of matrix that surrounds a fragment can affect the isolation of populations (i.e., during dispersal events), we tested whether the distance between fragments impacts gene flow and whether genetic diversity correlates with the size, shape or forest cover around the fragments.

Material and methods

Study area and biological material

Collections of *E. neotenicus* were carried out between May 2016 and June 2017 in 14 forest fragments located at Usina São José, Igarassu, Pernambuco (S7º49'07" and W35º00'45"), in the northern portion of the Atlantic Forest in Northeast Brazil. The climate is hot and humid. The average annual temperature is 26.3 ºC, the relative air humidity is 83.9%, and the average monthly rainfall is 121.3 mm (data collected at the meteorological station of the Usina São José between January and December of 2016). The average wind speed is 18.29 km/h, predominantly in the east-southeast direction (Weatherspark 2018). The soil originates from sediments of the Barreira Group and is classified as a deep sandstone clay ranging from sandy to clayey clay with low to medium fertility. The relief varies from flat to smooth undulating, and the original vegetation is classified as subperenifolia forest (Koffler et al. 1986). Sugarcane was planted in 1906 (Gaspar 2009) and currently has a total planting area of 280 km^2 and isolates 110 Atlantic Forest fragments with different sizes and shapes (Silva et al. 2012), 14 of which were selected for this study (Fig. 1). The fragments were located 3 m to 104 m from other fragments over an extent of 20 km. For each fragment, the total area, shape (i.e. the ratio between the perimeter of the fragment and the minimum perimeter of the fragment in terms of the number of cell surfaces (Bogaert et al. 2000; Milne 1991)) and forest cover within a radius of 1 km around the fragments were measured (Table 1). The values of these attributes were obtained by accessing data from the Geographic Information System (GIS) developed for the study area by Trindade et al. (2008) using multispectral satellite images. In each of the 14 fragments, workers and soldiers from 10 nests of *E. neotenicus* were collected and stored in absolute ethanol (*n* = 140 nests in total).

DNA extraction, amplification and genotyping

Total genomic DNA was extracted from the head of five soldiers and five workers from each of the sampled nests, totaling 1400 samples. Extraction was performed using a Chelex-based method (Walsh, Metzger & Higuchi 1991). Individuals were genotyped at 5 microsatellite loci with dinucleotide repeat motifs (En-08, En-10, En-11, En-15 and En-19) previously used to investigate the colony genetic structure in a population of *E. neotenicus* from French Guiana (Fougeyrollas et al. 2015).

DNA amplification was performed in two PCR multiplexes, each with a total volume of 25 μL and containing 0.2 μL (1 U) of FastStart Taq DNA Polymerase (Roche Diagnostics), 2.5 μL of 10X PCR buffer, 1.5 μL of 25 mM $MgCl_2$, 0.6 μL of 10 mM dNTP mix, 0.2 μM each forward and reverse primer (En-08 and En-10 in multiplex 1; En-11, En-15 and En-19 in multiplex 2; Table S1), 2 μL of template DNA and PCR-grade water (q.s.).

The following cycling conditions were used: an initial denaturing step at 95°C for 10 min; 40 cycles of denaturation at 95°C for 30 s, annealing at 60°C for 30 s, and extension at 72°C for 60 s; and a final extension step at 72°C for 10 min. Amplicons were visualized on an ABI 3730XL sequencer (Applied Biosystems). Fragment lengths were manually checked on chromatograms, and genotypes were scored using Peak Scanner v1.0 software (Applied Biosystems).

Statistical analyses

Microsatellite characteristics

We investigated microsatellite marker characteristics in the population by randomly choosing one individual per nest (*n* = 140; Supporting Table S2) and checking for the presence of null alleles or scoring errors owing to large allelic dropout using Micro-Checker v2.2.3 software

(Van Oosterhout et al. 2004). Deviations from Hardy-Weinberg equilibrium were tested using GENEPOP 4.2 (http://genepop.curtin.edu. au; Raymond & Rousset 1995; Rousset 2008).

Genetic structure of colonies

We evaluated colony breeding systems by calculating the number of alleles and genotypes at each locus across all genotyped individuals (*n* = 1400; Supporting Table S2). Furthermore, average within-colony relatedness (r_{nest}) *sensu* Queller & Goodnight (1989) was calculated using the “grouprel” function in the R package 'related' v1.0 (Pew et al. 2015), and within-colony inbreeding coefficients (F_{IC}; Weir & Cockerham 1984) were computed using GENEPOP4.2.

Genetic diversity analyses

The genetic diversity in each investigated fragment of the Atlantic Forest was assessed by randomly choosing one individual per nest (*n* = 140), the same dataset used to investigate the microsatellite characteristics. We calculated the number of alleles, the observed and expected heterozygosities and the fixation index using GenAlEx 6.5 software (Peakall & Smouse 2012). These parameters of genetic diversity were compared between fragments using one-way analysis of variance (ANOVA) with R software v3.5.3 (R Core Team 2018).

The relations between landscape features and genetic diversity were tested using generalized linear models, adopting a Gaussian family distribution (Dobson 1990). Two models were created. The first model included the number of alleles as the response variable and landscape features as explanatory variables, and the second model included observed heterozygosity as the response variable and landscape features as explanatory variables. The models were run in R v3.5.3.

Population genetic structure and landscape genetic analyses

Population genetic structure and landscape genetic analyses were performed by randomly choosing one individual per nest (n = 140), the same dataset used to investigate the microsatellite characteristics and genetic diversity analyses. The relationship between geographic and genetic distances was assessed using a Mantel test with 9999 permutations, and the pairwise F_{ST} and the relative probability were calculated using GenAlEx 6.5 (Peakall & Smouse 2012). Population genetic structure was estimated with a Bayesian model-based clustering method. The number of population clusters (K) was obtained using STRUCTURE v2.3.4 software (Pritchard, Stephens & Donnelly 2000) under an admixture model with correlated allelic frequencies among populations. Simulations were run 20 times for K=1-14 with a burn-in of 50000 and 100000 Markov chain Monte Carlo (MCMC) repetitions. The optimal K value was determined with STRUCTURE HARVESTER v0.6.94 (Earl & vonHoldt 2012) using the delta K method (Evanno, Regnaut & Goudet 2005). CLUMPP v1.1.2 (Jakobsson & Rosenberg 2007) was used to align simulations for the optimal K and eliminate label switching among clusters using the *Greedy* algorithm with 200000 replicates. Graphical results were obtained using DISTRUCT v1.1 (Rosenberg 2003). Genetic structure was also tested by calculating the genetic divergence between populations (F_{ST}), and hierarchical F-statistics were estimated at different levels, specifically, the degree of inbreeding among nestmates (F_{IC}) and differentiation between colonies within the population of fragment (F_{CP}), using the R package 'hierfstat' (Goudet 2005).

To test the effect of landscape features on population genetic structure, site-specific genetic differentiation (population-specific F_{ST} value) was estimated and related to landscape features using generalized linear models by applying a hierarchical Bayesian method in GESTE 2.0 software (Foll & Gaggiotti 2006). We used the reversible jump MCMC method and 10 pilot runs with a length of 5000 as a burn-in prior to drawing samples from a chain with a length of 50000, separated by a thinning interval of 20. We ran seven models with a single landscape variable or combination of the landscape variables: size; shape; forest cover; size and shape; size and forest cover; shape and forest cover; and size, shape and forest cover.

Results

Microsatellite characteristics

No sign of null alleles was detected at the population level except at locus En-10 (frequency of 0.29), as suggested by the general excess of homozygotes. There was no evidence of scoring error due to large allele dropout. Therefore, the locus En-10 was not included in subsequent analyses.

All microsatellite loci were polymorphic. The number of alleles per locus varied from 3 (En-19) to 23 (En-11). The loci En-08 and En-11 showed significant deviation from Hardy-Weinberg equilibrium ($P < 0.05$). The microsatellite characteristics are summarized in Supporting Table S1.

Genetic structure of colonies

The genotypes of the individuals are presented in Supporting Table S2. All genotyped individuals were heterozygous for at least one marker (Table S3). Most of the colonies (70%; 98 nests) were compatible with a simple family design, i.e., individuals were derived from a single pair of primary reproductives and displayed a maximum of four alleles and genotypes at a given locus. However, 40 colonies (28.5%) exhibited a maximum of four alleles but more than four different genotypes, which is consistent with an extended family design. The remaining two colonies presented more than four alleles, therefore being consistent with a mixed family design. The within-colony pairwise relatedness ($r_{nest;}$ mean ± sd: -0.260 ± 0.170) and inbreeding coefficients ($F_{IC;}$ mean ± sd: -0.262 ± 0.169) within colonies are shown in Table S3.

Genetic diversity analyses

Over the four retained loci, the mean number of alleles per fragment ranged from 4 to 6 (Table 2). The fragments with the largest number of private alleles were VV and ZB (two alleles). Across all investigated sites, En-11 presented the largest number of private alleles (five alleles; Table S4). The observed heterozygosity ranged from 0.40 to 0.70, the expected heterozygosity ranged from 0.46 to 0.58, and the fixation index ranged from -0.22 to 0.11 (Table 2). Genetic diversity did not differ among fragments: there was no difference in the number of alleles ($F_{13,42}$ =0.113; P > 0.05), observed heterozygosity ($F_{13,42}$ =0.258; P > 0.05) or expected heterozygosity ($F_{13,42}$ = 0.108; P > 0.05). Moreover, there was no difference between expected heterozygosity and observed heterozygosity ($F_{1,26}$ = 0.151; P > 0.05).

Population genetic structure and landscape genetic analyses

No significant correlation was found between genetic differentiation and geographical distance (Mantel test: r = 0.0186, P = 0.196; Fig. S1). The pairwise F_{ST} between fragments and the relative probability are presented in Supplementary Table S5.

STRUCTURE analysis revealed that K = 7 was the optimal number of genetic clusters. No differentiation of the genetic profiles was observed among the sampled populations, and the seven clusters were represented in all individuals at similar proportions (Fig. S2). The populations exhibited moderate genetic structure (F_{ST} = 0.076), while the pairwise F_{ST} between fragments (Table S5) indicated low to moderate genetic structure according to the classification of Wright (1978). Accordingly, hierarchical *F*-statistics showed differentiation between colonies within the same site ($F_{Nest/Site}$ = 0.519), while sites did not differ from each other for the investigated population ($F_{Site/Pop}$ = 0.027). There were no relations between landscape features and either genetic diversity (Table 3) or population genetic structure (the models including only the constant showed the highest probability for all combinations of landscape features; Table 4).

Discussion

Our results revealed moderate genetic structuring of *E. neotenicus* among the 14 Atlantic Forest fragments investigated, indicating that gene flow probably occurs between them or that the fragments have not been isolated long enough to promote genetic differentiation.

Flying high is an important feature of dispersal for tropical rainforest termites. Although alates of ground-dwelling species spend more time in lower strata than in upper strata, some species can fly at a height up to 28 m, such as *Embiratermes chagresi* (Bourguignon et al. 2009). Flying above the canopy would allow the termites to take advantage of winds and maximize their dispersal. In fact, the seasonal nature of sugarcane cultivation exposes the surrounding forest fragments to increased wind action in the postharvest period (Ferrante et al. 2017). In the northeastern part of Brazil, the sugarcane harvest occurs mainly between September and March, while the vast majority of the species belonging to the Termitidae in the Atlantic Forest swarm between March and May (Medeiros, Bandeira & Martius 1999), as is also the case for *E. neotenicus* in our study sites (pers. obs.).

Thus, during the swarming period, the matrix consists of uncovered soil or small and young plants, which could facilitate the dispersal of alates among forest remnants by wind action. In addition, the preharvest practice of burning sugarcane is still commonly applied and leads population declines of natural predators of termites such as small mammals (Griffiths & Brook 2014) and arthropods such as ants (Vasconcelos et al. 2009). Therefore, swarming shortly after harvest would allow winged reproductives to achieve higher dispersal success.

Long-distance dispersal increases local genetic diversity and decreases levels of population differentiation, effectively avoiding the effects of fragmentation. Other studies support the idea that termites are able to disperse over long distances (Mona et al. 2013). The population genetic structure of *Nasutitermes takasagoensis* (Termitidae: Nasutitermitinae) was investigated among oceanic islands separated by 200 m to 443 km. Populations presented moderate genetic structure when separated by a distance up to 46 km, indicating the occurrence of gene flow (Garcia et al. 2002; García et al. 2004). García et al. (2006) studied the genetic diversity of *Nasutitermes coxipoensis* in Cerrado fragments in Brazil and observed no restriction to gene flow and no genetic differentiation between fragments separated by less than 60 km, which may be partly explained by the seasonal production and release of thousands of alates by each nest.

The dispersal and mating strategies of *E. neotenicus* were studied in a connected rainforest of French Guiana (Fougeyrollas et al. 2018). The results suggest that long-distance flights are the rule for this species, leading to no or low genetic differentiation between study sites separated by up to 10 km. In a population in French Guiana, colonies of *E. neotenicus* were determined to be simple families and were shown to undergo asexual queen succession (AQS; Fougeyrollas et al. 2015, 2018). In this breeding system, nondispersing (neotenic) queens are parthenogenetically produced, while workers, soldiers and alates are produced sexually by mating between the primary king and the primary queen or neotenic queens. In *E. neotenicus*, the primary queen is replaced by multiple neotenic queens (up to almost 200) early in the colony's life cycle (Fougeyrollas et al. 2015). As these neotenic queens are parthenogenetically produced, their matings with the primary king do not change the colony's genetic structure, and no inbreeding occurs. The AQS breeding system was also described in other soil-feeding termites at the same study site in French Guiana: *Silvestritermes minutus* (Termitidae: Syntermitinae) and several species belonging to the *Termes* group (Termitidae: Termitinae) (Fougeyrollas et al. 2017; Fournier et al. 2016; Hellemans et al. 2019). As in *E. neotenicus*, most colonies of *S. minutus* and *Cavitermes tuberosus* were founded by unrelated reproductives as a result of long-distance dispersal, and no population genetic structure was observed (Fougeyrollas et al. 2018; Fournier et al. 2016).

The main advantages of AQS appear to be the expansion of colony reproductive potential through the reproduction of many more queens and an increase in lifespan via the ability of replacement queens to produce subsequent generations of parthenogens (Matsuura 2017). Therefore, through an enhanced lifespan, colonies have several opportunities to produce alates. It follows that such mechanisms may contribute to maximizing the odds of colonizing a neighboring patch over the years and maintaining gene flow between the investigated Atlantic Forest fragments.

Our study suggests that gene flow prevents genetic differentiation between the fragments investigated, resulting in a small number of private alleles between fragments and no relationships between genetic diversity and fragment features. The same observation was made in other studies on invertebrate populations with low genetic structure in fragmented habitats (Garcia et al. 2006; Ramirez & Haakonsen 1999). Therefore, depending on the circumstances, a fragmentation event will not necessarily lead to a loss of genetic diversity

(Young, Boyle & Brown 1996). Our work demonstrates that agricultural practices can be maintained in a landscape context where the deleterious effects of natural habitat loss are mitigated by the functional connectivity of forest fragments. In the context of the landscape studied here, the proximity of fragments acts in synergy with the dispersal capacity of *E. neotenicus* and favors gene flow between the populations, and such a landscape context may also be favorable for other insects providing ecosystem services.

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Conflict of interest

The authors declare that there is no conflict of interest.

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Table 1. Attributes and genetic diversity of *E. neotenicus* populations in 14 fragments of the Atlantic Forest in Northeast Brazil (Abbr.: abbreviation; FC: forest cover within a 1 km radius around the fragment).

Fragment	*Abbr.*	*Coordinates*	*Size (ha)*	*Shape*	*FC (ha)*
Vizinho de Vespa	VV	S 7°44.75' W 34°59.00'	5.96	1.506	93.06
Santa Helena	SH	S 7°47.20’ W 34°56.60'	11.78	1.253	127.72
Vespa	VE	S 7°45.07' W 34°58.90'	13.81	3.258	151.99
Chico Dias	CD	S 7°49.02' W 34°59.65'	32.87	1.468	210.13
Dedo de Deus	DD	S 7°45.50' W 35°00.90'	51.15	2.184	306.59
Chave	CH	S 7°49.40' W 34°58.60'	89.29	2.418	294.12
Vizinho de Chave	VC	S 7°50.12' W 34°58.77'	112.13	3.133	126.65
Vizinho de Avião	VA	S 7°47.82’ W 34°57.80’	184.06	3.057	166.12
Perto de Cruzinha	PC	S 7°41.30’ W 34°58.02’	239.05	2.099	150.33
Piedade	PD	S 7°50.02’ W 35°00.05’	308.98	3.337	98.27
Vizinho de Dedo Deus	VDD	S 7°45.70' W 35°00.60'	322.71	3.733	556.25
Macacos	MC	S 7°46.70' W 35°00.50'	356.94	3.231	235.7
Zambana	ZB	S 7°42.50’ W 34°59.70’	387.85	2.21	222.63
Campo do Avião	CA	S 7°48.48' W 34°58.78'	410.46	3.942	475.76

Table 2. Basic population statistics estimated from microsatellite datasets for the total population and for each sample from Atlantic Forest fragments (N_{ind}: number of individuals; N_A: number of alleles; H_O: observed heterozygosity; H_E: expected heterozygosity; *F*: fixation index).

Fragment	N_{ind}	N_A *(mean ± se)*	H_O *(mean ± se)*	H_E *(mean ± se)*	F *(mean ± se)*
All	140	4.2 (±0.3)	0.52 (±0.04)	0.51 (±0.04)	-0.031 (±0.03)
VV	10	4.5 (±1.04)	0.60 (±0.17)	0.52 (±0.15)	-0.14 (±0.06)
SH	10	3.5 (±0.96)	0.42 (±0.05)	0.58 (±0.09)	0.25 (±0.04)
VE	10	4.5 (±1.70)	0.57 (±0.19)	0.52 (±0.17)	-0.10 (±0.09)
CD	10	3.7 (±1.03)	0.45 (±0.13)	0.46 (±0.13)	0.01 (±0.06)
DD	10	4.5 (±1.5)	0.5 (±0.16)	0.50 (±0.15)	0.05 (±0.08)
CH	10	4.2 (±1.31)	0.70 (±0.15)	0.58 (±0.13)	-0.225 (±0.07)
VC	10	3.5 (±1.04)	0.50 (±1.19)	0.45 (±0.16)	-0.08 (±0.08)
VA	10	4.7 (±1.7)	0.6 (±0.14)	0.58 (±0.11)	-0.04 (±0.23)
PC	10	4.0 (±1.41)	0.52 (±0.15)	0.51 (±0.16)	-0.06 (±0.07)
PD	10	4.7 (±1.16)	0.45 (±0.13)	0.53 (±0.15)	0.11 (±0.10)
VDD	10	4.3 (±1.11)	0.55 (±0.10)	0.53 (±0.13)	-0.08 (±0.09)
MC	10	4.2 (±1.11)	0.52 (±0.19)	0.55 (±0.16)	0.01 (±0.10)
ZB	10	5.2 (±2.72)	0.55 (±0.20)	0.50 (±0.20)	-0.14 (±0.09)
CA	10	4.0 (±1.41)	0.40 (±0.17)	0.41 (±0.18)	-0.01 (±0.05)

Table 3. Generalized linear models used to predict the number of alleles and observed heterozygosity for *E. neotenicus* populations in 14 fragments of the Atlantic Forest in Northeast Brazil. N_A – number of alleles; H_O – observed heterozygosity; FC – forest cover within a 1 km radius around the fragment.

Response variable	Explanatory variables	Coefficient	Standard error	Z	p
N_A	Intercept	4.6084629	0.4319720	10.668	<0.01
	Size	0.0023589	0.0012452	1.894	0.0874
	Shape	-0.2771388	0.2345261	-1.182	0.2647
	FC	-0.0003018	0.0011540	-0.262	0.7990
H_O	Intercept	5.882e-01	7.186e-02	8.186	<0.01
	Size	-1.663e-05	2.071e-04	-0.080	0.938
	Shape	-4.853e-02	3.901e-02	-1.244	0.242
	FC	2.409e-04	1.920e-04	1.255	0.238

Table 4. Results of different models tested in GESTE. The first column shows the landscape variable(s) tested in the model. The second and third columns correspond to the model that best explains the data and its probability (P), respectively. The remaining four columns show the probability of each individual variable in the highest-probability model, with the factor in the first column corresponding to labels G1, G2 and/or G3 in subsequent columns and G1*G2 referring to the interaction between factors G1 and G2 (FC: forest cover within a 1 km radius around the fragment).

Factor(s) in model	Highest-probability model	P (model)	P (G1)	P (G2)	P (G1*G2)	P (G3)
Size	Constant	0.794	0.206			
Shape	Constant	0.748	0.252			
FC	Constant	0.764	0.236			
Size, Shape	Constant	0.334	0.306	0.339	0.142	
Size, FC	Constant	0.380	0.332	0.318	0.0898	
Shape, FC	Constant	0.521	0.263	0244	0.0386	
Size, Shape, FC	Constant	0.387	0.323	0.259	-	0.296

Table S1. Microsatellite loci used for the genetic study and their characteristics in 10 individuals from 140 colonies collected in 14 Atlantic Forest fragments (N_A: number of alleles; H_O: observed heterozygosity; H_E: expected heterozygosity).

Locus	*Motif*	*Primer sequence (5'-3')*	*Label*	N_A	*Allele size range (bp)*	H_O	H_E
Multiplex 1							
En-11	$(ac)_{14}$	F: CCAACTCGTAGGTGTAGAGGAT R: CCGTCTCTTGTGAGTGTTGTG	VIC	23	154–198	0.77	0.77
En-15	$(ca)_{15}$	F: CGATGAGATTCCGTAGACACC R: AACCCTAGCACCTCACATGC	NED	9	286–292	0.47	0.44
En-19	$(tg)_{17}$	F: TACATTCAAATTAGTCTTGTGCCC R: TTGGTCGAGCCTATCTGGTC	PET	3	177–181	0.13	0.13
Multiplex 2							
En-08	$(ac)_{13}$	F: CTGAGCGGTTGCAGAGTACC R: TTCCCGGCCAAAGTACTAAC	6' FAM	10	170–188	0.66	0.70
En-10	$(tg)_{14}$	F: CGTCCAGAAGATTCCTACCG R: TCTCTACCTCGTGTCTGCCT	NED	11	116–142	0.12	0.50

Table S2. Genotypes of individuals of *E. neotenicus* from 14 Atlantic Forest fragments in Northeast Brazil (Pop – population; Ind – individual). Samples in bold correspond to randomly choosing one individual per nest used to access the microsatellite characteristics, Genetic diversity analyses, population genetic structure and landscape genetic analyses.

Pop	Colony	Ind	En-08		En-11		En-15		En-19	
VV	VV_1	VV_1_W1	180	180	164	190	286	286	179	179
VV	VV_1	VV_1_W2	180	180	164	164	286	286	179	179
VV	**VV_1**	**VV_1_W3**	**178**	**180**	**164**	**190**	**286**	**286**	**179**	**179**
VV	VV_1	VV_1_W4	180	180	164	190	278	286	179	179
VV	VV_1	VV_1_W5	178	178	182	190	278	286	179	179
VV	VV_1	VV_1_S1	178	180	164	164	286	286	179	179
VV	VV_1	VV_1_S2	178	180	164	190	286	286	179	179
VV	VV_1	VV_1_S3	178	180	164	164	286	286	179	179
VV	VV_1	VV_1_S4	0	0	164	164	286	286	179	179
VV	VV_1	VV_1_S5	0	0	164	182	278	286	179	179
VV	VV_2	VV_2_W1	176	178	164	194	278	286	179	179
VV	VV_2	VV_2_W2	178	184	176	178	278	286	0	0
VV	**VV_2**	**VV_2_W3**	**176**	**178**	**164**	**164**	**278**	**286**	**179**	**179**
VV	VV_2	VV_2_W4	178	184	164	164	278	278	179	179
VV	VV_2	VV_2_W5	176	178	164	194	278	286	179	179
VV	VV_2	VV_2_S1	176	176	164	164	278	286	179	179
VV	VV_2	VV_2_S2	0	0	164	194	278	286	179	179
VV	VV_2	VV_2_S3	176	176	164	194	278	278	179	179
VV	VV_2	VV_2_S4	176	178	164	194	278	286	179	179
VV	VV_2	VV_2_S5	0	0	164	194	278	278	179	179
VV	VV_3	VV_3_W1	178	178	182	190	286	286	179	179
VV	VV_3	VV_3_W2	178	178	164	182	278	286	179	179
VV	**VV_3**	**VV_3_W3**	**180**	**180**	**182**	**190**	**278**	**286**	**179**	**179**
VV	VV_3	VV_3_W4	178	180	182	190	286	286	179	179
VV	VV_3	VV_3_W5	178	180	182	190	278	286	179	179
VV	VV_3	VV_3_S1	180	180	164	190	286	286	179	179
VV	VV_3	VV_3_S2	178	180	164	190	278	286	179	179
VV	VV_3	VV_3_S3	178	180	164	190	286	286	179	179
VV	VV_3	VV_3_S4	180	180	164	190	286	286	179	179
VV	VV_3	VV_3_S5	180	180	164	182	286	286	179	179
VV	VV_4	VV_4_W1	178	184	162	164	278	290	179	179
VV	VV_4	VV_4_W2	178	184	162	164	278	290	179	179
VV	**VV_4**	**VV_4_W3**	**178**	**184**	**164**	**186**	**278**	**290**	**179**	**179**

VV	VV_4	VV_4_W4	178	184	164	186	278	290	179	179
VV	VV_4	VV_4_W5	178	184	164	164	278	290	179	179
VV	VV_4	VV_4_S1	178	184	164	164	278	290	179	179
VV	VV_4	VV_4_S2	178	184	162	186	278	290	179	179
VV	VV_4	VV_4_S3	178	184	162	186	278	290	179	179
VV	VV_4	VV_4_S4	178	184	164	164	278	290	179	179
VV	VV_4	VV_4_S5	178	184	164	164	278	278	179	179
VV	VV_5	VV_5_W1	176	178	164	186	278	278	179	179
VV	VV_5	VV_5_W2	176	178	164	186	278	286	179	179
VV	**VV_5**	**VV_5_W3**	**178**	**182**	**164**	**190**	**278**	**286**	**179**	**179**
VV	VV_5	VV_5_W4	176	178	164	186	278	286	179	179
VV	VV_5	VV_5_W5	176	178	164	186	278	286	179	179
VV	VV_5	VV_5_S1	178	182	164	186	278	286	179	179
VV	VV_5	VV_5_S2	176	180	162	186	278	286	179	179
VV	VV_5	VV_5_S3	176	180	164	186	278	278	179	179
VV	VV_5	VV_5_S4	176	178	164	186	278	278	179	179
VV	VV_5	VV_5_S5	182	182	162	190	278	286	179	179
VV	VV_6	VV_6_W1	178	178	154	190	286	286	179	179
VV	VV_6	VV_6_W2	178	182	154	190	278	278	179	179
VV	**VV_6**	**VV_6_W3**	**178**	**182**	**154**	**164**	**286**	**286**	**179**	**179**
VV	VV_6	VV_6_W4	176	178	154	190	278	278	179	179
VV	VV_6	VV_6_W5	176	178	154	190	278	286	179	179
VV	VV_6	VV_6_S1	178	178	154	164	278	286	179	179
VV	VV_6	VV_6_S2	176	182	154	164	286	286	179	179
VV	VV_6	VV_6_S3	178	182	154	190	278	286	179	179
VV	VV_6	VV_6_S4	178	182	154	164	278	286	179	179
VV	VV_6	VV_6_S5	178	178	154	164	286	286	179	179
VV	VV_7	VV_7_W1	178	182	154	164	278	286	179	179
VV	VV_7	VV_7_W2	178	178	154	190	278	278	179	179
VV	**VV_7**	**VV_7_W3**	**178**	**178**	**154**	**190**	**278**	**286**	**179**	**179**
VV	VV_7	VV_7_W4	178	182	154	190	278	278	179	179
VV	VV_7	VV_7_W5	178	182	154	164	278	286	179	179
VV	VV_7	VV_7_S1	176	178	154	190	278	286	179	179
VV	VV_7	VV_7_S2	178	182	154	190	278	286	179	179
VV	VV_7	VV_7_S3	178	182	154	190	278	286	179	179
VV	VV_7	VV_7_S4	178	182	154	164	278	278	179	179
VV	VV_7	VV_7_S5	178	178	154	190	278	278	179	179
VV	VV_8	VV_8_W1	180	180	180	184	286	286	177	179
VV	VV_8	VV_8_W2	180	180	180	184	286	286	179	179
VV	**VV_8**	**VV_8_W3**	**180**	**184**	**164**	**186**	**286**	**286**	**177**	**179**
VV	VV_8	VV_8_W4	180	180	180	186	286	286	177	179

VV	VV_8	VV_8_W5	180	180	180	186	286	286	177	179
VV	VV_8	VV_8_S1	180	180	164	186	286	286	179	179
VV	VV_8	VV_8_S2	180	184	180	184	286	286	177	179
VV	VV_8	VV_8_S3	184	184	164	186	286	286	179	179
VV	VV_8	VV_8_S4	180	180	164	186	286	286	177	179
VV	VV_8	VV_8_S5	180	180	164	186	286	286	177	179
VV	VV_9	VV_9_W1	178	180	154	184	278	286	179	179
VV	VV_9	VV_9_W2	180	180	154	184	278	286	179	179
VV	**VV_9**	**VV_9_W3**	**178**	**178**	**174**	**184**	**278**	**286**	**179**	**179**
VV	VV_9	VV_9_W4	178	180	164	174	286	286	177	179
VV	VV_9	VV_9_W5	178	180	174	184	278	286	179	179
VV	VV_9	VV_9_S1	178	180	174	184	278	286	179	179
VV	VV_9	VV_9_S2	180	180	164	164	278	286	179	179
VV	VV_9	VV_9_S3	180	180	164	174	286	286	177	179
VV	VV_9	VV_9_S4	180	180	164	174	286	286	179	179
VV	VV_9	VV_9_S5	180	180	154	164	286	286	179	179
VV	VV_10	VV_10_W1	178	180	164	182	284	286	179	179
VV	VV_10	VV_10_W2	178	180	164	164	286	286	179	179
VV	**VV_10**	**VV_10_W3**	**178**	**180**	**164**	**182**	**284**	**286**	**179**	**179**
VV	VV_10	VV_10_W4	180	180	164	182	286	286	179	179
VV	VV_10	VV_10_W5	178	180	164	164	286	286	179	179
VV	VV_10	VV_10_S1	180	180	164	182	284	284	179	179
VV	VV_10	VV_10_S2	180	180	164	182	284	286	179	179
VV	VV_10	VV_10_S3	178	180	164	182	286	286	179	179
VV	VV_10	VV_10_S4	178	180	164	164	284	286	179	179
VV	VV_10	VV_10_S5	178	178	164	182	284	286	179	179
SH	SH_1	SH_1_W1	178	180	162	164	278	286	179	179
SH	SH_1	SH_1_W2	0	0	162	164	278	286	179	179
SH	**SH_1**	**SH_1_W3**	**178**	**178**	**162**	**162**	**278**	**286**	**179**	**179**
SH	SH_1	SH_1_W4	178	178	162	164	278	286	179	179
SH	SH_1	SH_1_W5	178	180	162	164	278	286	177	179
SH	SH_1	SH_1_S1	178	178	162	164	278	286	177	179
SH	SH_1	SH_1_S2	178	180	162	164	278	286	177	179
SH	SH_1	SH_1_S3	178	180	162	162	278	286	179	179
SH	SH_1	SH_1_S4	0	0	162	162	278	286	179	179
SH	SH_1	SH_1_S5	0	0	162	162	278	286	179	179
SH	SH_2	SH_2_W1	178	178	162	186	278	278	179	179
SH	SH_2	SH_2_W2	180	180	164	186	278	286	179	179
SH	**SH_2**	**SH_2_W3**	**178**	**180**	**162**	**164**	**286**	**286**	**179**	**179**
SH	SH_2	SH_2_W4	0	0	162	164	278	286	179	179
SH	SH_2	SH_2_W5	178	178	186	186	278	286	179	179

SH	SH_2	SH_2_S1	180	180	162	164	278	286	179	179
SH	SH_2	SH_2_S2	180	180	186	186	278	286	179	179
SH	SH_2	SH_2_S3	178	180	186	186	278	286	179	179
SH	SH_2	SH_2_S4	178	178	162	186	278	286	179	179
SH	SH_2	SH_2_S5	178	178	164	186	278	286	179	179
SH	SH_3	SH_3_W1	172	180	162	162	278	286	177	179
SH	SH_3	SH_3_W2	178	180	162	162	278	286	179	179
SH	**SH_3**	**SH_3_W3**	**172**	**184**	**162**	**186**	**278**	**278**	**179**	**179**
SH	SH_3	SH_3_W4	172	184	162	162	278	286	179	179
SH	SH_3	SH_3_W5	172	184	162	162	278	286	179	179
SH	SH_3	SH_3_S1	180	184	162	162	278	286	177	179
SH	SH_3	SH_3_S2	180	180	162	162	278	286	177	179
SH	SH_3	SH_3_S3	172	180	162	162	278	278	177	179
SH	SH_3	SH_3_S4	178	184	162	186	278	278	177	177
SH	SH_3	SH_3_S5	180	184	162	162	278	278	179	179
SH	SH_4	SH_4_W1	180	184	162	184	278	278	179	179
SH	SH_4	SH_4_W2	180	184	162	184	278	278	179	179
SH	SH_4	SH_4_W3	178	180	162	186	0	0	179	179
SH	**SH_4**	**SH_4_W4**	**180**	**184**	**162**	**186**	**278**	**278**	**179**	**179**
SH	SH_4	SH_4_W5	180	184	162	186	278	278	179	179
SH	SH_4	SH_4_S1	178	180	182	184	278	278	179	179
SH	SH_4	SH_4_S2	178	180	182	186	278	278	179	179
SH	SH_4	SH_4_S3	180	184	182	184	278	278	179	179
SH	SH_4	SH_4_S4	180	184	162	186	278	278	179	179
SH	SH_4	SH_4_S5	178	180	182	186	278	278	179	179
SH	SH_5	SH_5_W1	172	178	164	184	278	278	179	179
SH	SH_5	SH_5_W2	172	172	164	164	278	278	179	179
SH	**SH_5**	**SH_5_W3**	**172**	**172**	**164**	**164**	**278**	**286**	**179**	**179**
SH	SH_5	SH_5_W4	172	178	164	164	278	286	179	179
SH	SH_5	SH_5_W5	172	178	162	184	286	286	179	179
SH	SH_5	SH_5_S1	172	178	162	164	286	286	179	179
SH	SH_5	SH_5_S2	178	178	162	184	286	286	179	179
SH	SH_5	SH_5_S3	172	178	162	184	278	278	179	179
SH	SH_5	SH_5_S4	172	178	162	164	286	286	179	179
SH	SH_5	SH_5_S5	172	178	164	184	278	286	179	179
SH	SH_6	SH_6_W1	180	182	162	162	278	286	179	179
SH	**SH_6**	**SH_6_W2**	**178**	**180**	**182**	**182**	**278**	**286**	**177**	**179**
SH	SH_6	SH_6_W3	178	180	182	182	278	278	0	0
SH	SH_6	SH_6_W4	172	180	0	0	0	0	179	179
SH	SH_6	SH_6_W5	180	182	162	164	278	278	179	179
SH	SH_6	SH_6_S1	178	180	162	182	278	286	177	179

SH	SH_6	SH_6_S2	180	182	162	164	278	278	177	179
SH	SH_6	SH_6_S3	0	0	162	182	278	278	177	177
SH	SH_6	SH_6_S4	178	180	162	164	278	278	177	179
SH	SH_6	SH_6_S5	180	182	182	182	278	278	179	179
SH	SH_7	SH_7_W1	0	0	162	184	0	0	179	179
SH	SH_7	SH_7_W2	178	178	162	184	278	286	179	179
SH	**SH_7**	**SH_7_W3**	**178**	**180**	**184**	**184**	**278**	**286**	**179**	**179**
SH	SH_7	SH_7_W4	178	180	184	184	278	286	179	179
SH	SH_7	SH_7_W5	178	180	162	184	278	286	179	179
SH	SH_7	SH_7_S1	178	178	162	184	278	286	179	179
SH	SH_7	SH_7_S2	178	180	162	184	278	286	179	179
SH	SH_7	SH_7_S3	178	178	162	162	278	286	179	179
SH	SH_7	SH_7_S4	178	180	184	184	278	286	179	179
SH	SH_7	SH_7_S5	180	180	162	162	278	286	179	179
SH	SH_8	SH_8_W1	180	184	162	196	278	278	177	179
SH	SH_8	SH_8_W2	0	0	184	196	278	278	177	179
SH	**SH_8**	**SH_8_W3**	**184**	**184**	**184**	**196**	**278**	**278**	**177**	**179**
SH	SH_8	SH_8_W4	184	184	162	162	278	286	177	179
SH	SH_8	SH_8_W5	180	184	162	184	278	286	179	179
SH	SH_8	SH_8_S1	184	184	162	162	278	278	179	179
SH	SH_8	SH_8_S2	180	184	162	196	278	278	179	179
SH	SH_8	SH_8_S3	0	0	162	162	278	278	0	0
SH	SH_8	SH_8_S4	180	184	162	162	278	286	177	179
SH	SH_8	SH_8_S5	180	180	196	196	278	278	179	179
SH	SH_9	SH_9_W1	178	178	162	162	278	286	179	179
SH	SH_9	SH_9_W2	178	180	162	184	278	286	179	179
SH	**SH_9**	**SH_9_W3**	**178**	**178**	**162**	**184**	**278**	**278**	**177**	**179**
SH	SH_9	SH_9_W4	178	180	162	162	286	286	177	179
SH	SH_9	SH_9_W5	178	178	162	162	286	286	179	179
SH	SH_9	SH_9_S1	180	180	162	184	278	278	179	179
SH	SH_9	SH_9_S2	180	180	162	162	278	286	179	179
SH	SH_9	SH_9_S3	178	178	162	162	278	286	177	179
SH	SH_9	SH_9_S4	178	180	162	184	278	286	177	179
SH	SH_9	SH_9_S5	178	180	162	162	284	286	177	179
SH	SH_10	SH_10_W1	180	180	162	162	286	286	177	177
SH	SH_10	SH_10_W2	180	180	162	186	278	286	177	177
SH	**SH_10**	**SH_10_W3**	**180**	**180**	**162**	**162**	**286**	**286**	**177**	**177**
SH	SH_10	SH_10_W4	180	180	162	186	278	286	177	177
SH	SH_10	SH_10_W5	180	180	162	162	286	286	177	179
SH	SH_10	SH_10_S1	180	180	162	186	286	286	177	179
SH	SH_10	SH_10_S2	180	180	162	162	278	286	177	179

SH	SH_10	SH_10_S3	180	180	162	162	286	286	177	177
SH	SH_10	SH_10_S4	180	180	162	186	286	286	177	177
SH	SH_10	SH_10_S5	180	180	162	162	286	286	177	179
VE	VE_1	VE_1_W1	176	178	162	162	278	286	179	179
VE	VE_1	VE_1_W2	176	178	162	164	278	282	179	179
VE	**VE_1**	**VE_1_W3**	**176**	**184**	**164**	**164**	**278**	**286**	**179**	**179**
VE	VE_1	VE_1_W4	176	184	162	162	278	286	179	179
VE	VE_1	VE_1_W5	176	184	164	164	278	282	179	179
VE	VE_1	VE_1_S1	176	184	162	164	278	286	179	179
VE	VE_1	VE_1_S2	176	178	164	164	278	286	179	179
VE	VE_1	VE_1_S3	176	184	164	164	278	286	179	179
VE	VE_1	VE_1_S4	176	184	162	162	278	282	179	179
VE	VE_1	VE_1_S5	176	178	162	164	278	286	179	179
VE	VE_2	VE_2_W1	180	184	162	186	286	286	179	179
VE	VE_2	VE_2_W2	180	184	162	164	286	286	179	179
VE	**VE_2**	**VE_2_W3**	**180**	**184**	**164**	**186**	**278**	**286**	**179**	**179**
VE	VE_2	VE_2_W4	180	184	162	186	278	286	179	179
VE	VE_2	VE_2_W5	172	180	164	186	278	286	179	179
VE	VE_2	VE_2_S1	184	184	164	164	278	286	179	179
VE	VE_2	VE_2_S2	0	0	162	186	278	286	179	179
VE	VE_2	VE_2_S3	0	0	164	164	278	286	179	179
VE	VE_2	VE_2_S4	180	184	162	164	278	286	179	179
VE	VE_2	VE_2_S5	184	184	162	164	286	286	179	179
VE	VE_3	VE_3_W1	176	176	162	164	278	278	179	179
VE	VE_3	VE_3_W2	176	180	162	164	282	286	179	179
VE	**VE_3**	**VE_3_W3**	**176**	**180**	**162**	**164**	**282**	**286**	**179**	**179**
VE	VE_3	VE_3_W4	176	180	162	164	278	278	179	179
VE	VE_3	VE_3_W5	0	0	164	164	278	278	179	179
VE	VE_3	VE_3_S1	176	180	164	164	278	282	179	179
VE	VE_3	VE_3_S2	176	180	162	164	278	286	179	179
VE	VE_3	VE_3_S3	180	180	164	164	282	286	179	179
VE	VE_3	VE_3_S4	176	176	162	164	282	286	179	179
VE	VE_3	VE_3_S5	176	180	164	164	278	278	179	179
VE	VE_4	VE_4_W1	176	178	162	182	278	282	179	179
VE	VE_4	VE_4_W2	178	178	164	182	286	286	179	179
VE	**VE_4**	**VE_4_W3**	**178**	**180**	**162**	**162**	**282**	**286**	**179**	**179**
VE	VE_4	VE_4_W4	178	180	164	182	286	286	179	179
VE	VE_4	VE_4_W5	178	180	162	162	282	286	179	179
VE	VE_4	VE_4_S1	0	0	162	182	282	286	179	179
VE	VE_4	VE_4_S2	176	180	162	162	286	286	179	179
VE	VE_4	VE_4_S3	180	180	162	164	278	286	179	179

VE	VE_4	VE_4_S4	176	180	162	164	282	286	179	179
VE	VE_4	VE_4_S5	0	0	162	182	286	286	179	179
VE	VE_5	VE_5_W1	176	180	162	164	278	286	179	179
VE	VE_5	VE_5_W2	176	180	154	162	278	286	179	179
VE	**VE_5**	**VE_5_W3**	**176**	**182**	**162**	**164**	**278**	**278**	**179**	**179**
VE	VE_5	VE_5_W4	176	180	162	164	278	278	179	179
VE	VE_5	VE_5_W5	176	176	162	164	278	286	179	179
VE	VE_5	VE_5_S1	176	176	154	182	278	286	179	179
VE	VE_5	VE_5_S2	0	0	164	182	278	286	179	179
VE	VE_5	VE_5_S3	178	180	164	182	278	278	179	179
VE	VE_5	VE_5_S4	176	180	164	182	278	278	179	179
VE	VE_5	VE_5_S5	182	182	154	182	278	278	179	179
VE	VE_6	VE_6_W1	180	180	154	188	278	286	179	179
VE	VE_6	VE_6_W2	178	178	154	188	278	278	179	179
VE	**VE_6**	**VE_6_W3**	**180**	**180**	**154**	**162**	**278**	**278**	**179**	**179**
VE	VE_6	VE_6_W4	180	180	162	166	278	288	179	179
VE	VE_6	VE_6_W5	180	180	162	166	278	288	179	179
VE	VE_6	VE_6_S1	180	180	154	188	278	286	179	179
VE	VE_6	VE_6_S2	180	180	166	188	278	286	179	179
VE	VE_6	VE_6_S3	178	180	166	188	278	286	179	179
VE	VE_6	VE_6_S4	0	0	166	188	278	286	179	179
VE	VE_6	VE_6_S5	180	180	162	166	286	288	179	179
VE	VE_7	VE_7_W1	0	0	164	164	278	286	179	179
VE	VE_7	VE_7_W2	180	180	164	178	278	286	179	179
VE	**VE_7**	**VE_7_W3**	**180**	**180**	**164**	**178**	**278**	**286**	**179**	**179**
VE	VE_7	VE_7_W4	176	180	164	188	278	286	179	179
VE	VE_7	VE_7_W5	0	0	164	178	286	286	179	179
VE	VE_7	VE_7_S1	180	180	164	188	286	286	179	179
VE	VE_7	VE_7_S2	176	176	164	188	278	286	179	179
VE	VE_7	VE_7_S3	176	180	164	178	286	286	179	179
VE	VE_7	VE_7_S4	176	176	164	178	286	286	179	179
VE	VE_7	VE_7_S5	176	180	164	178	278	286	179	179
VE	VE_8	VE_8_W1	0	0	178	182	278	286	179	179
VE	VE_8	VE_8_W2	178	180	178	182	278	286	179	179
VE	**VE_8**	**VE_8_W3**	**178**	**180**	**182**	**188**	**278**	**286**	**179**	**179**
VE	VE_8	VE_8_W4	178	180	178	182	278	286	179	179
VE	VE_8	VE_8_W5	178	178	178	182	278	286	179	179
VE	VE_8	VE_8_S1	178	180	182	188	278	286	179	179
VE	VE_8	VE_8_S2	178	180	178	182	286	286	179	179
VE	VE_8	VE_8_S3	180	180	182	188	278	286	179	179
VE	VE_8	VE_8_S4	178	178	182	188	278	286	179	179

VE	VE_8	VE_8_S5	178	180	182	188	286	286	179	179
VE	VE_9	VE_9_W1	180	184	162	190	278	278	179	179
VE	VE_9	VE_9_W2	180	184	182	190	278	286	179	179
VE	**VE_9**	**VE_9_W3**	**0**	**0**	**162**	**190**	**278**	**286**	**179**	**179**
VE	VE_9	VE_9_W4	180	184	162	182	278	286	179	179
VE	VE_9	VE_9_W5	182	184	190	190	278	278	177	179
VE	VE_9	VE_9_S1	184	184	182	190	278	286	177	179
VE	VE_9	VE_9_S2	176	180	190	190	286	286	179	179
VE	VE_9	VE_9_S3	180	184	190	190	278	286	177	179
VE	VE_9	VE_9_S4	176	182	162	182	278	286	179	179
VE	VE_9	VE_9_S5	176	182	182	190	286	286	179	179
VE	VE_10	VE_10_W1	176	178	164	166	278	282	179	179
VE	VE_10	VE_10_W2	178	178	164	166	278	278	179	179
VE	**VE_10**	**VE_10_W3**	**176**	**176**	**164**	**184**	**278**	**282**	**179**	**179**
VE	VE_10	VE_10_W4	172	178	164	184	278	278	179	179
VE	VE_10	VE_10_W5	180	180	164	166	278	282	179	179
VE	VE_10	VE_10_S1	176	180	166	184	0	0	179	179
VE	VE_10	VE_10_S2	176	180	164	166	278	282	179	179
VE	VE_10	VE_10_S3	176	180	164	184	278	282	179	179
VE	VE_10	VE_10_S4	176	180	164	184	278	282	179	179
VE	VE_10	VE_10_S5	176	180	154	184	278	282	179	179
CD	CD_1	CD_1_W1	178	178	162	162	286	286	179	179
CD	CD_1	CD_1_W2	180	184	162	162	286	286	179	179
CD	**CD_1**	**CD_1_W3**	**178**	**178**	**162**	**162**	**286**	**286**	**179**	**179**
CD	CD_1	CD_1_W4	178	178	162	162	278	286	179	179
CD	CD_1	CD_1_W5	178	178	162	162	286	286	179	179
CD	CD_1	CD_1_S1	178	182	162	164	278	286	179	179
CD	CD_1	CD_1_S2	178	184	162	164	286	286	179	179
CD	CD_1	CD_1_S3	0	0	162	164	286	286	179	179
CD	CD_1	CD_1_S4	178	180	162	164	278	286	179	179
CD	CD_1	CD_1_S5	0	0	162	162	286	286	179	179
CD	CD_2	CD_2_W1	178	180	154	162	278	278	179	179
CD	CD_2	CD_2_W2	174	178	154	162	278	286	179	179
CD	**CD_2**	**CD_2_W3**	**174**	**178**	**154**	**162**	**278**	**278**	**179**	**179**
CD	CD_2	CD_2_W4	180	184	154	162	278	278	179	179
CD	CD_2	CD_2_W5	174	184	154	162	278	286	179	179
CD	CD_2	CD_2_S1	0	0	162	162	278	286	179	179
CD	CD_2	CD_2_S2	174	174	154	162	278	278	179	179
CD	CD_2	CD_2_S3	178	178	162	162	278	278	179	179
CD	CD_2	CD_2_S4	0	0	154	162	278	278	179	179
CD	CD_2	CD_2_S5	0	0	154	162	278	278	179	179

CD	CD_3	CD_3_W1	178	180	162	164	278	286	179	179
CD	CD_3	CD_3_W2	178	178	162	162	278	286	179	179
CD	**CD_3**	**CD_3_W3**	**178**	**180**	**162**	**164**	**286**	**286**	**179**	**179**
CD	CD_3	CD_3_W4	178	180	162	164	278	286	179	179
CD	CD_3	CD_3_W5	178	178	162	164	278	286	179	179
CD	CD_3	CD_3_S1	178	178	162	164	278	286	179	179
CD	CD_3	CD_3_S2	178	180	162	164	278	278	179	179
CD	CD_3	CD_3_S3	178	180	162	164	278	278	179	179
CD	CD_3	CD_3_S4	178	178	162	162	278	286	179	179
CD	CD_3	CD_3_S5	178	178	162	164	286	286	179	179
CD	CD_4	CD_4_W1	184	184	162	162	278	278	177	179
CD	CD_4	CD_4_W2	178	180	162	164	278	278	177	179
CD	**CD_4**	**CD_4_W3**	**180**	**184**	**162**	**162**	**278**	**278**	**177**	**179**
CD	CD_4	CD_4_W4	184	184	162	162	278	278	177	179
CD	CD_4	CD_4_W5	178	184	162	162	278	278	179	179
CD	CD_4	CD_4_S1	178	180	162	164	278	278	177	179
CD	CD_4	CD_4_S2	0	0	164	164	278	278	179	179
CD	CD_4	CD_4_S3	178	184	162	162	278	278	177	179
CD	CD_4	CD_4_S4	0	0	162	164	278	278	179	179
CD	CD_4	CD_4_S5	178	180	162	164	278	278	179	179
CD	CD_5	CD_5_W1	178	180	162	164	278	286	179	179
CD	CD_5	CD_5_W2	178	184	162	164	278	286	179	179
CD	**CD_5**	**CD_5_W3**	**178**	**184**	**162**	**162**	**278**	**286**	**179**	**179**
CD	CD_5	CD_5_W4	180	180	162	162	278	286	179	179
CD	CD_5	CD_5_W5	178	184	162	164	278	286	179	179
CD	CD_5	CD_5_S1	180	180	162	164	278	278	179	179
CD	CD_5	CD_5_S2	178	184	162	162	278	278	179	179
CD	CD_5	CD_5_S3	178	184	162	164	278	278	179	179
CD	CD_5	CD_5_S4	0	0	162	162	278	286	179	179
CD	CD_5	CD_5_S5	178	184	162	162	278	278	179	179
CD	CD_6	CD_6_W1	178	180	162	162	278	278	177	179
CD	CD_6	CD_6_W2	178	180	162	162	278	278	177	179
CD	**CD_6**	**CD_6_W3**	**178**	**180**	**162**	**162**	**278**	**278**	**179**	**179**
CD	CD_6	CD_6_W4	178	180	162	162	278	278	179	179
CD	CD_6	CD_6_W5	178	180	162	162	278	278	179	179
CD	CD_6	CD_6_S1	0	0	162	162	278	286	179	179
CD	CD_6	CD_6_S2	0	0	162	162	278	278	177	179
CD	CD_6	CD_6_S3	0	0	162	162	278	278	179	179
CD	CD_6	CD_6_S4	178	180	162	162	278	278	179	179
CD	CD_6	CD_6_S5	178	180	162	162	278	278	179	179
CD	CD_7	CD_7_W1	176	184	154	164	278	286	179	179

CD	CD_7	CD_7_W2	178	184	154	172	278	286	179	179
CD	**CD_7**	**CD_7_W3**	**176**	**176**	**154**	**172**	**278**	**286**	**179**	**179**
CD	CD_7	CD_7_W4	178	184	162	164	278	286	179	179
CD	CD_7	CD_7_W5	178	184	162	172	278	286	179	179
CD	CD_7	CD_7_S1	176	176	162	164	278	286	179	179
CD	CD_7	CD_7_S2	178	184	162	164	278	286	179	179
CD	CD_7	CD_7_S3	178	184	154	172	278	286	179	179
CD	CD_7	CD_7_S4	0	0	154	172	278	286	179	179
CD	CD_7	CD_7_S5	0	0	154	172	278	286	179	179
CD	CD_8	CD_8_W1	178	184	160	162	278	286	179	179
CD	CD_8	CD_8_W2	178	184	162	178	278	286	179	179
CD	**CD_8**	**CD_8_W3**	**178**	**184**	**162**	**178**	**278**	**286**	**179**	**179**
CD	CD_8	CD_8_W4	174	178	162	178	278	278	179	179
CD	CD_8	CD_8_W5	178	184	160	162	278	278	179	179
CD	CD_8	CD_8_S1	178	184	162	178	278	278	179	179
CD	CD_8	CD_8_S2	178	184	160	162	278	278	179	179
CD	CD_8	CD_8_S3	178	184	162	162	278	278	179	179
CD	CD_8	CD_8_S4	0	0	162	178	278	286	179	179
CD	CD_8	CD_8_S5	178	184	162	178	278	286	179	179
CD	CD_9	CD_9_W1	178	180	154	162	278	278	179	179
CD	CD_9	CD_9_W2	174	180	162	186	278	278	179	179
CD	**CD_9**	**CD_9_W3**	**178**	**184**	**154**	**162**	**278**	**286**	**179**	**179**
CD	CD_9	CD_9_W4	178	184	154	162	278	286	179	179
CD	CD_9	CD_9_W5	178	184	154	162	278	278	179	179
CD	CD_9	CD_9_S1	180	180	162	162	278	278	179	179
CD	CD_9	CD_9_S2	0	0	154	162	278	278	179	179
CD	CD_9	CD_9_S3	180	184	162	186	278	286	179	179
CD	CD_9	CD_9_S4	0	0	162	162	278	286	179	179
CD	CD_9	CD_9_S5	178	184	162	162	286	286	179	179
CD	CD_10	CD_10_W1	180	180	162	162	278	278	179	179
CD	CD_10	CD_10_W2	180	184	162	168	278	278	179	179
CD	**CD_10**	**CD_10_W3**	**180**	**180**	**162**	**168**	**278**	**278**	**179**	**179**
CD	CD_10	CD_10_W4	178	184	162	162	278	278	179	179
CD	CD_10	CD_10_W5	180	180	162	162	278	278	179	179
CD	CD_10	CD_10_S1	0	0	162	162	278	278	179	179
CD	CD_10	CD_10_S2	178	180	162	162	278	278	179	179
CD	CD_10	CD_10_S3	0	0	162	162	278	278	179	179
CD	CD_10	CD_10_S4	0	0	162	162	278	278	179	179
CD	CD_10	CD_10_S5	0	0	162	162	278	278	179	179
DD	DD_1	DD_1_W1	180	180	162	184	278	286	179	179
DD	DD_1	DD_1_W2	178	180	162	164	278	286	179	179

DD	**DD_1**	**DD_1_W3**	**180**	**180**	**162**	**164**	**278**	**286**	**179**	**179**
DD	DD_1	DD_1_W4	180	180	162	184	278	286	179	179
DD	DD_1	DD_1_W5	178	180	162	184	278	286	179	179
DD	DD_1	DD_1_S1	180	180	162	184	278	286	179	179
DD	DD_1	DD_1_S2	184	184	162	184	278	286	179	179
DD	DD_1	DD_1_S3	180	180	162	164	278	286	179	179
DD	DD_1	DD_1_S4	180	180	162	164	278	286	179	179
DD	DD_1	DD_1_S5	184	184	162	184	278	286	179	179
DD	DD_2	DD_2_W1	174	178	162	164	278	286	179	179
DD	DD_2	DD_2_W2	176	180	162	182	278	278	179	179
DD	**DD_2**	**DD_2_W3**	**174**	**176**	**162**	**164**	**278**	**286**	**179**	**179**
DD	DD_2	DD_2_W4	174	178	162	182	278	286	179	179
DD	DD_2	DD_2_W5	180	180	182	186	278	286	179	179
DD	DD_2	DD_2_S1	176	178	162	164	278	286	179	179
DD	DD_2	DD_2_S2	176	180	162	182	278	278	179	179
DD	DD_2	DD_2_S3	176	180	162	164	278	286	179	179
DD	DD_2	DD_2_S4	176	178	162	164	278	278	179	179
DD	DD_2	DD_2_S5	176	178	162	164	278	278	179	179
DD	DD_3	DD_3_W1	180	180	164	164	278	280	179	179
DD	DD_3	DD_3_W2	178	180	162	164	278	280	179	179
DD	**DD_3**	**DD_3_W3**	**178**	**180**	**164**	**164**	**278**	**278**	**179**	**179**
DD	DD_3	DD_3_W4	176	180	162	164	278	278	179	179
DD	DD_3	DD_3_W5	178	178	162	164	278	278	179	179
DD	DD_3	DD_3_S1	178	180	162	162	278	278	179	179
DD	DD_3	DD_3_S2	180	180	164	164	278	278	179	179
DD	DD_3	DD_3_S3	180	180	162	164	278	278	179	179
DD	DD_3	DD_3_S4	0	0	162	164	278	278	179	179
DD	DD_3	DD_3_S5	180	180	164	164	278	278	179	179
DD	DD_4	DD_4_W1	180	184	164	164	278	286	179	179
DD	DD_4	DD_4_W2	180	184	164	186	286	286	179	179
DD	**DD_4**	**DD_4_W3**	**178**	**184**	**164**	**186**	**286**	**286**	**179**	**179**
DD	DD_4	DD_4_W4	178	184	164	164	278	286	179	179
DD	DD_4	DD_4_W5	180	184	164	186	278	286	179	179
DD	DD_4	DD_4_S1	0	0	164	164	278	286	179	179
DD	DD_4	DD_4_S2	0	0	164	186	278	286	179	179
DD	DD_4	DD_4_S3	178	184	164	164	286	286	179	179
DD	DD_4	DD_4_S4	0	0	164	164	0	0	179	179
DD	DD_4	DD_4_S5	0	0	164	164	0	0	0	0
DD	DD_5	DD_5_W1	180	180	162	164	278	286	179	179
DD	DD_5	DD_5_W2	178	180	154	164	278	278	179	179
DD	**DD_5**	**DD_5_W3**	**180**	**180**	**162**	**164**	**278**	**286**	**179**	**179**

DD	DD_5	DD_5_W4	180	180	162	164	278	286	179	179
DD	DD_5	DD_5_W5	180	180	162	164	278	286	179	179
DD	DD_5	DD_5_S1	178	180	154	164	278	280	179	179
DD	DD_5	DD_5_S2	178	180	154	162	278	286	179	179
DD	DD_5	DD_5_S3	180	180	164	164	278	286	179	179
DD	DD_5	DD_5_S4	178	180	164	164	278	280	179	179
DD	DD_5	DD_5_S5	0	0	154	162	278	286	179	179
DD	DD_6	DD_6_W1	176	180	162	190	278	278	179	179
DD	DD_6	DD_6_W2	176	180	162	190	278	278	177	179
DD	DD_6	DD_6_W3	0	0	160	188	278	278	177	179
DD	**DD_6**	**DD_6_W4**	**180**	**180**	**162**	**188**	**278**	**278**	**177**	**179**
DD	DD_6	DD_6_W5	180	180	162	188	278	278	179	179
DD	DD_6	DD_6_S1	176	180	162	190	278	280	177	179
DD	DD_6	DD_6_S2	0	0	162	190	278	278	177	179
DD	DD_6	DD_6_S3	180	180	160	190	278	278	177	179
DD	DD_6	DD_6_S4	176	180	160	190	278	278	179	179
DD	DD_6	DD_6_S5	180	180	162	190	278	278	179	179
DD	DD_7	DD_7_W1	180	180	0	0	278	286	0	0
DD	DD_7	DD_7_W2	178	178	164	180	278	278	179	179
DD	**DD_7**	**DD_7_W3**	**182**	**182**	**180**	**184**	**278**	**278**	**179**	**179**
DD	DD_7	DD_7_W4	178	178	168	180	278	278	179	179
DD	DD_7	DD_7_W5	178	182	168	180	278	278	179	179
DD	DD_7	DD_7_S1	0	0	168	184	0	0	179	179
DD	DD_7	DD_7_S2	182	182	168	184	278	278	179	179
DD	DD_7	DD_7_S3	180	182	0	0	0	0	0	0
DD	DD_7	DD_7_S4	180	182	180	184	278	278	179	179
DD	DD_7	DD_7_S5	178	182	168	184	278	278	179	179
DD	DD_8	DD_8_W1	180	180	164	176	278	286	177	179
DD	DD_8	DD_8_W2	178	180	164	164	278	286	179	179
DD	**DD_8**	**DD_8_W3**	**180**	**180**	**162**	**176**	**286**	**286**	**179**	**179**
DD	DD_8	DD_8_W4	180	180	164	176	286	286	179	179
DD	DD_8	DD_8_W5	178	180	162	176	278	286	179	179
DD	DD_8	DD_8_S1	180	180	162	176	286	286	179	179
DD	DD_8	DD_8_S2	180	180	162	164	278	286	179	179
DD	DD_8	DD_8_S3	178	178	162	176	278	286	179	179
DD	DD_8	DD_8_S4	180	180	164	164	274	286	179	179
DD	DD_8	DD_8_S5	178	178	162	176	286	286	179	179
DD	DD_9	DD_9_W1	180	180	182	184	278	286	179	179
DD	DD_9	DD_9_W2	178	180	164	186	278	278	179	179
DD	**DD_9**	**DD_9_W3**	**174**	**180**	**184**	**186**	**278**	**286**	**179**	**179**
DD	DD_9	DD_9_W4	178	180	164	186	278	286	179	179

DD	DD_9	DD_9_W5	174	180	164	182	278	278	179	179
DD	DD_9	DD_9_S1	180	184	184	186	278	278	179	179
DD	DD_9	DD_9_S2	184	184	184	186	278	278	179	179
DD	DD_9	DD_9_S3	180	184	184	186	278	278	179	179
DD	DD_9	DD_9_S4	180	184	184	186	278	286	179	179
DD	DD_9	DD_9_S5	180	184	184	184	278	286	179	179
DD	DD_10	DD_10_W1	180	180	164	186	278	286	179	179
DD	DD_10	DD_10_W2	180	180	164	186	278	286	179	179
DD	**DD_10**	**DD_10_W3**	**178**	**180**	**164**	**190**	**278**	**286**	**179**	**179**
DD	DD_10	DD_10_W4	180	180	162	190	278	278	179	179
DD	DD_10	DD_10_W5	180	180	164	190	278	278	179	179
DD	DD_10	DD_10_S1	180	180	0	0	0	0	179	179
DD	DD_10	DD_10_S2	178	180	164	186	278	278	179	179
DD	DD_10	DD_10_S3	178	180	164	190	278	278	179	179
DD	DD_10	DD_10_S4	0	0	164	186	278	278	179	179
DD	DD_10	DD_10_S5	0	0	164	190	278	286	179	179
CH	CH_1	CH_1_W1	178	180	162	184	278	286	179	179
CH	CH_1	CH_1_W2	180	180	162	162	278	278	179	179
CH	**CH_1**	**CH_1_W3**	**178**	**178**	**164**	**184**	**278**	**286**	**177**	**179**
CH	CH_1	CH_1_W4	178	180	162	162	278	286	177	179
CH	CH_1	CH_1_W5	178	180	0	0	0	0	0	0
CH	CH_1	CH_1_S1	178	180	162	162	278	278	179	179
CH	CH_1	CH_1_S2	178	180	162	164	278	278	179	179
CH	CH_1	CH_1_S3	180	180	162	184	278	278	177	179
CH	CH_1	CH_1_S4	178	180	162	164	278	278	177	179
CH	CH_1	CH_1_S5	178	180	162	184	278	286	179	179
CH	CH_2	CH_2_W1	182	184	162	186	278	278	179	179
CH	CH_2	CH_2_W2	176	184	162	186	278	278	179	179
CH	**CH_2**	**CH_2_W3**	**182**	**184**	**162**	**164**	**278**	**286**	**179**	**179**
CH	CH_2	CH_2_W4	184	184	162	186	278	278	179	179
CH	CH_2	CH_2_W5	184	184	162	186	278	286	179	179
CH	CH_2	CH_2_S1	184	184	162	186	278	278	179	179
CH	CH_2	CH_2_S2	182	184	162	186	278	286	179	179
CH	CH_2	CH_2_S3	184	184	162	186	278	286	179	179
CH	CH_2	CH_2_S4	0	0	162	186	278	278	179	179
CH	CH_2	CH_2_S5	184	184	162	186	278	286	179	179
CH	CH_3	CH_3_W1	180	184	162	164	278	278	177	179
CH	CH_3	CH_3_W2	184	184	162	186	286	286	179	179
CH	**CH_3**	**CH_3_W3**	**180**	**184**	**162**	**186**	**278**	**286**	**179**	**179**
CH	CH_3	CH_3_W4	180	184	162	186	278	286	179	179
CH	CH_3	CH_3_W5	180	184	162	186	278	286	179	179

CH	CH_3	CH_3_S1	180	184	162	164	278	278	179	179
CH	CH_3	CH_3_S2	184	184	164	186	278	286	177	179
CH	CH_3	CH_3_S3	184	184	162	164	278	286	179	179
CH	CH_3	CH_3_S4	184	184	162	164	278	278	179	179
CH	CH_3	CH_3_S5	0	0	162	186	278	286	179	179
CH	CH_4	CH_4_W1	178	184	162	190	286	286	177	179
CH	CH_4	CH_4_W2	178	180	162	162	278	286	177	179
CH	**CH_4**	**CH_4_W3**	**178**	**184**	**184**	**190**	**286**	**286**	**177**	**179**
CH	CH_4	CH_4_W4	180	184	162	184	278	286	177	179
CH	CH_4	CH_4_W5	178	184	162	184	278	288	179	179
CH	CH_4	CH_4_S1	0	0	162	184	290	290	179	179
CH	CH_4	CH_4_S2	184	184	184	190	286	288	177	179
CH	CH_4	CH_4_S3	184	184	162	184	286	288	179	179
CH	CH_4	CH_4_S4	184	184	162	190	290	290	177	179
CH	CH_4	CH_4_S5	178	180	162	190	278	288	177	179
CH	CH_5	CH_5_W1	180	184	164	186	278	278	179	179
CH	CH_5	CH_5_W2	180	184	164	184	278	286	179	179
CH	**CH_5**	**CH_5_W3**	**184**	**184**	**164**	**186**	**278**	**286**	**179**	**179**
CH	CH_5	CH_5_W4	180	180	164	186	278	286	177	179
CH	CH_5	CH_5_W5	180	184	162	186	278	278	177	179
CH	CH_5	CH_5_S1	184	184	162	186	278	286	177	179
CH	CH_5	CH_5_S2	184	184	162	184	278	278	177	179
CH	CH_5	CH_5_S3	184	184	162	184	278	278	177	179
CH	CH_5	CH_5_S4	184	184	164	186	278	278	177	179
CH	CH_5	CH_5_S5	180	184	162	186	278	278	177	179
CH	CH_6	CH_6_W1	180	184	162	190	278	286	179	179
CH	CH_6	CH_6_W2	182	184	162	190	278	286	179	179
CH	**CH_6**	**CH_6_W3**	**180**	**184**	**162**	**190**	**278**	**286**	**179**	**179**
CH	CH_6	CH_6_W4	180	184	162	184	278	286	179	179
CH	CH_6	CH_6_W5	182	184	162	184	278	286	179	179
CH	CH_6	CH_6_S1	182	184	162	184	278	286	179	179
CH	CH_6	CH_6_S2	180	184	162	190	278	286	179	179
CH	CH_6	CH_6_S3	180	184	162	190	278	278	179	179
CH	CH_6	CH_6_S4	180	184	162	190	278	286	179	179
CH	CH_6	CH_6_S5	182	184	162	190	278	278	179	179
CH	CH_7	CH_7_W1	178	180	160	162	278	278	179	179
CH	CH_7	CH_7_W2	178	180	162	164	278	278	179	179
CH	**CH_7**	**CH_7_W3**	**178**	**180**	**160**	**162**	**278**	**278**	**179**	**179**
CH	CH_7	CH_7_W4	178	184	162	164	278	278	179	179
CH	CH_7	CH_7_W5	180	184	160	162	278	278	179	179
CH	CH_7	CH_7_S1	0	0	160	186	278	278	179	179

CH	CH_7	CH_7_S2	180	184	160	186	278	278	179	179
CH	CH_7	CH_7_S3	0	0	160	162	278	278	179	179
CH	CH_7	CH_7_S4	180	184	160	186	278	278	179	179
CH	CH_7	CH_7_S5	184	184	164	186	278	278	177	179
CH	CH_8	CH_8_W1	0	0	162	186	278	278	179	179
CH	CH_8	CH_8_W2	178	180	162	186	278	278	179	179
CH	**CH_8**	**CH_8_W3**	**178**	**180**	**162**	**186**	**278**	**278**	**179**	**179**
CH	CH_8	CH_8_W4	180	180	162	164	278	278	179	179
CH	CH_8	CH_8_W5	180	180	186	186	278	278	179	179
CH	CH_8	CH_8_S1	178	178	162	186	278	278	179	179
CH	CH_8	CH_8_S2	178	180	162	164	278	278	179	179
CH	CH_8	CH_8_S3	180	180	162	164	278	278	179	179
CH	CH_8	CH_8_S4	178	180	162	186	278	278	179	179
CH	CH_8	CH_8_S5	180	180	162	186	278	278	179	179
CH	CH_9	CH_9_W1	0	0	162	162	278	278	179	179
CH	CH_9	CH_9_W2	180	184	162	184	278	286	177	179
CH	**CH_9**	**CH_9_W3**	**180**	**184**	**184**	**186**	**278**	**286**	**177**	**179**
CH	CH_9	CH_9_W4	178	184	184	186	278	278	177	179
CH	CH_9	CH_9_W5	180	184	184	186	278	286	177	179
CH	CH_9	CH_9_S1	180	184	162	162	278	278	177	179
CH	CH_9	CH_9_S2	180	184	162	186	278	286	177	179
CH	CH_9	CH_9_S3	180	184	162	186	278	286	177	179
CH	CH_9	CH_9_S4	184	184	162	186	278	286	179	179
CH	CH_9	CH_9_S5	184	184	0	0	278	286	179	179
CH	CH_10	CH_10_W1	180	188	162	166	278	286	179	179
CH	CH_10	CH_10_W2	178	180	162	186	278	286	179	179
CH	**CH_10**	**CH_10_W3**	**170**	**188**	**162**	**166**	**278**	**286**	**179**	**179**
CH	CH_10	CH_10_W4	180	188	162	166	278	286	179	179
CH	CH_10	CH_10_W5	180	188	162	186	278	286	179	179
CH	CH_10	CH_10_S1	170	178	186	186	278	278	179	179
CH	CH_10	CH_10_S2	170	178	186	186	278	286	179	179
CH	CH_10	CH_10_S3	170	178	162	166	278	278	179	179
CH	CH_10	CH_10_S4	180	188	166	166	278	286	179	179
CH	CH_10	CH_10_S5	170	188	166	186	278	286	179	179
VC	VC_1	VC_1_W1	178	180	162	164	278	286	179	179
VC	VC_1	VC_1_W2	180	184	162	164	278	286	179	179
VC	**VC_1**	**VC_1_W3**	**178**	**180**	**162**	**164**	**278**	**286**	**179**	**179**
VC	VC_1	VC_1_W4	180	184	164	182	278	286	179	179
VC	VC_1	VC_1_W5	178	184	164	182	278	286	179	179
VC	VC_1	VC_1_S1	180	184	164	182	278	286	179	179
VC	VC_1	VC_1_S2	180	184	164	182	278	286	179	179

VC	VC_1	VC_1_S3	180	184	162	162	278	286	179	179
VC	VC_1	VC_1_S4	178	180	164	182	278	286	179	179
VC	VC_1	VC_1_S5	178	180	162	164	278	286	179	179
VC	VC_2	VC_2_W1	178	184	160	164	278	290	177	179
VC	VC_2	VC_2_W2	178	178	160	164	278	290	179	179
VC	**VC_2**	**VC_2_W3**	**178**	**184**	**162**	**164**	**278**	**290**	**179**	**179**
VC	VC_2	VC_2_W4	178	184	160	164	278	280	177	179
VC	VC_2	VC_2_W5	178	180	162	164	278	290	177	179
VC	VC_2	VC_2_S1	178	184	162	164	278	288	179	179
VC	VC_2	VC_2_S2	178	180	162	164	278	278	177	179
VC	VC_2	VC_2_S3	178	184	160	164	278	278	177	179
VC	VC_2	VC_2_S4	178	180	160	164	278	288	177	179
VC	VC_2	VC_2_S5	178	184	162	164	278	278	177	179
VC	VC_3	VC_3_W1	174	180	154	166	278	278	179	179
VC	VC_3	VC_3_W2	178	180	158	184	278	278	179	179
VC	**VC_3**	**VC_3_W3**	**178**	**180**	**154**	**166**	**278**	**278**	**179**	**179**
VC	VC_3	VC_3_W4	178	178	154	158	278	278	179	179
VC	VC_3	VC_3_W5	178	178	158	184	0	0	179	179
VC	VC_3	VC_3_S1	178	180	154	158	278	278	179	179
VC	VC_3	VC_3_S2	180	184	154	166	278	278	179	179
VC	VC_3	VC_3_S3	178	180	166	184	278	278	179	179
VC	VC_3	VC_3_S4	178	180	158	166	278	278	179	179
VC	VC_3	VC_3_S5	178	178	166	184	278	278	179	179
VC	VC_4	VC_4_W1	180	184	162	186	278	292	179	179
VC	VC_4	VC_4_W2	180	184	162	186	286	292	179	179
VC	**VC_4**	**VC_4_W3**	**180**	**184**	**162**	**186**	**278**	**278**	**179**	**179**
VC	VC_4	VC_4_W4	174	184	162	186	278	292	179	179
VC	VC_4	VC_4_W5	174	184	186	186	278	278	179	179
VC	VC_4	VC_4_S1	180	184	162	186	278	278	179	179
VC	VC_4	VC_4_S2	180	184	162	162	278	292	179	179
VC	VC_4	VC_4_S3	180	184	162	162	278	292	179	179
VC	VC_4	VC_4_S4	180	184	182	186	278	292	179	179
VC	VC_4	VC_4_S5	174	184	162	186	286	292	179	179
VC	VC_5	VC_5_W1	172	180	162	182	278	286	179	179
VC	VC_5	VC_5_W2	178	178	154	182	278	286	179	179
VC	VC_5	VC_5_W3	172	178	0	0	0	0	0	0
VC	**VC_5**	**VC_5_W4**	**172**	**180**	**162**	**182**	**278**	**286**	**179**	**179**
VC	VC_5	VC_5_W5	172	178	162	182	278	286	179	179
VC	VC_5	VC_5_S1	172	172	162	182	278	278	177	179
VC	VC_5	VC_5_S2	172	180	154	162	278	286	179	179
VC	VC_5	VC_5_S3	172	180	162	182	278	278	179	179

VC	VC_5	VC_5_S4	178	180	162	182	278	278	179	179
VC	VC_5	VC_5_S5	178	180	154	182	278	286	177	179
VC	VC_6	VC_6_W1	178	178	162	162	278	278	179	179
VC	VC_6	VC_6_W2	178	180	162	164	278	278	179	179
VC	**VC_6**	**VC_6_W3**	**178**	**178**	**162**	**164**	**278**	**278**	**179**	**179**
VC	VC_6	VC_6_W4	178	178	162	164	278	278	179	179
VC	VC_6	VC_6_W5	174	180	164	182	278	286	179	179
VC	VC_6	VC_6_S1	178	178	162	162	278	278	179	179
VC	VC_6	VC_6_S2	178	178	162	182	278	286	179	179
VC	VC_6	VC_6_S3	178	180	164	182	278	286	179	179
VC	VC_6	VC_6_S4	178	180	162	164	278	278	179	179
VC	VC_6	VC_6_S5	178	178	162	182	278	278	179	179
VC	VC_7	VC_7_W1	178	178	162	166	278	286	179	179
VC	VC_7	VC_7_W2	178	180	162	166	278	278	179	179
VC	**VC_7**	**VC_7_W3**	**178**	**180**	**162**	**162**	**278**	**286**	**179**	**179**
VC	VC_7	VC_7_W4	178	178	162	166	278	278	179	179
VC	VC_7	VC_7_W5	178	178	162	162	278	286	179	179
VC	VC_7	VC_7_S1	180	180	162	162	278	278	179	179
VC	VC_7	VC_7_S2	180	180	162	166	278	286	179	179
VC	VC_7	VC_7_S3	178	180	162	166	278	278	179	179
VC	VC_7	VC_7_S4	178	180	162	166	278	286	179	179
VC	VC_7	VC_7_S5	178	178	162	166	278	286	179	179
VC	VC_8	VC_8_W1	178	178	154	162	278	278	179	179
VC	VC_8	VC_8_W2	178	178	154	162	278	286	179	179
VC	**VC_8**	**VC_8_W3**	**178**	**178**	**154**	**162**	**286**	**286**	**179**	**179**
VC	VC_8	VC_8_W4	178	178	154	162	278	286	179	179
VC	VC_8	VC_8_W5	178	178	162	164	278	286	179	179
VC	VC_8	VC_8_S1	178	178	162	164	278	286	179	179
VC	VC_8	VC_8_S2	178	178	162	164	278	278	179	179
VC	VC_8	VC_8_S3	178	178	162	164	278	286	179	179
VC	VC_8	VC_8_S4	178	178	162	164	278	286	179	179
VC	VC_8	VC_8_S5	178	178	154	162	286	286	177	179
VC	VC_9	VC_9_W1	178	180	162	182	278	286	179	179
VC	VC_9	VC_9_W2	178	180	182	182	278	278	179	179
VC	**VC_9**	**VC_9_W3**	**178**	**180**	**162**	**182**	**278**	**278**	**179**	**179**
VC	VC_9	VC_9_W4	178	180	182	182	278	286	179	179
VC	VC_9	VC_9_W5	0	0	154	182	278	286	179	179
VC	VC_9	VC_9_S1	180	180	162	182	278	286	179	179
VC	VC_9	VC_9_S2	180	180	154	182	278	286	179	179
VC	VC_9	VC_9_S3	178	178	154	162	278	286	179	179
VC	VC_9	VC_9_S4	178	180	182	182	278	278	179	179

VC	VC_9	VC_9_S5	178	180	162	182	278	278	179	179
VC	VC_10	VC_10_W1	180	180	164	164	278	278	179	179
VC	VC_10	VC_10_W2	0	0	164	164	278	278	179	179
VC	**VC_10**	**VC_10_W3**	**180**	**184**	**164**	**164**	**278**	**278**	**179**	**179**
VC	VC_10	VC_10_W4	178	184	164	164	278	278	179	179
VC	VC_10	VC_10_W5	178	180	162	164	278	278	179	179
VC	VC_10	VC_10_S1	178	184	162	164	278	278	179	179
VC	VC_10	VC_10_S2	178	184	162	164	278	278	179	179
VC	VC_10	VC_10_S3	178	184	162	164	278	278	179	179
VC	VC_10	VC_10_S4	178	184	162	164	278	278	179	179
VA	VA_1	VA_1_W1	182	182	154	186	286	286	177	179
VA	VA_1	VA_1_W2	178	182	186	186	278	278	177	179
VA	**VA_1**	**VA_1_W3**	**178**	**182**	**186**	**186**	**278**	**286**	**177**	**179**
VA	VA_1	VA_1_W4	178	180	154	186	278	278	177	179
VA	VA_1	VA_1_W5	178	180	154	186	286	286	179	179
VA	VA_1	VA_1_S1	178	184	154	154	286	286	179	179
VA	VA_1	VA_1_S2	182	184	186	186	286	286	179	179
VA	VA_1	VA_1_S3	178	184	154	154	286	286	179	179
VA	VA_1	VA_1_S4	178	180	154	154	278	286	177	179
VA	VA_1	VA_1_S5	184	184	154	186	278	286	177	179
VA	VA_2	VA_2_W1	180	180	162	162	278	286	179	179
VA	VA_2	VA_2_W2	176	180	162	178	278	286	177	179
VA	**VA_2**	**VA_2_W3**	**176**	**180**	**162**	**162**	**278**	**286**	**179**	**179**
VA	VA_2	VA_2_W4	176	180	162	178	286	286	177	179
VA	VA_2	VA_2_W5	176	180	162	178	286	286	179	179
VA	VA_2	VA_2_S1	176	180	162	162	286	286	179	179
VA	VA_2	VA_2_S2	176	180	162	178	278	286	179	179
VA	VA_2	VA_2_S3	176	180	162	178	286	286	179	179
VA	VA_2	VA_2_S4	176	180	162	162	278	286	177	179
VA	VA_2	VA_2_S5	176	180	162	162	286	286	177	179
VA	VA_3	VA_3_W1	180	180	162	164	286	286	179	179
VA	VA_3	VA_3_W2	180	180	162	186	278	286	179	179
VA	**VA_3**	**VA_3_W3**	**180**	**180**	**164**	**186**	**286**	**286**	**179**	**179**
VA	VA_3	VA_3_W4	180	180	162	164	278	286	177	179
VA	VA_3	VA_3_W5	172	180	164	188	278	286	179	179
VA	VA_3	VA_3_S1	172	180	186	188	286	286	177	179
VA	VA_3	VA_3_S2	180	180	186	188	278	286	179	179
VA	VA_3	VA_3_S3	180	180	164	186	286	286	177	179
VA	VA_3	VA_3_S4	172	180	164	186	282	290	0	0
VA	VA_3	VA_3_S5	0	0	162	186	278	286	179	179
VA	VA_4	VA_4_W1	178	184	158	164	278	286	177	179

VA	VA_4	VA_4_W2	178	180	164	190	278	278	179	179
VA	**VA_4**	**VA_4_W3**	**180**	**182**	**158**	**190**	**278**	**286**	**179**	**179**
VA	VA_4	VA_4_W4	182	184	164	164	278	286	177	179
VA	VA_4	VA_4_W5	180	182	158	164	278	286	179	179
VA	VA_4	VA_4_S1	0	0	158	164	286	286	179	179
VA	VA_4	VA_4_S2	178	180	164	190	278	278	179	179
VA	VA_4	VA_4_S3	178	184	164	190	282	282	177	179
VA	VA_4	VA_4_S4	180	182	164	164	278	286	177	179
VA	VA_4	VA_4_S5	0	0	164	164	278	278	179	179
VA	VA_5	VA_5_W1	178	180	188	188	278	278	179	179
VA	VA_5	VA_5_W2	180	180	0	0	0	0	0	0
VA	**VA_5**	**VA_5_W3**	**180**	**180**	**154**	**180**	**278**	**286**	**179**	**179**
VA	VA_5	VA_5_W4	178	184	154	190	278	278	179	179
VA	VA_5	VA_5_W5	178	184	188	188	278	278	179	179
VA	VA_5	VA_5_S1	178	184	154	180	278	286	179	179
VA	VA_5	VA_5_S2	178	180	188	190	278	278	179	179
VA	VA_5	VA_5_S3	0	0	154	180	278	286	179	179
VA	VA_5	VA_5_S4	178	184	154	190	278	278	179	179
VA	VA_5	VA_5_S5	180	180	154	190	278	286	179	179
VA	VA_6	VA_6_W1	180	184	182	190	286	286	179	179
VA	VA_6	VA_6_W2	0	0	162	162	0	0	179	179
VA	**VA_6**	**VA_6_W3**	**180**	**184**	**162**	**190**	**278**	**286**	**179**	**179**
VA	VA_6	VA_6_W4	180	184	162	190	278	286	179	179
VA	VA_6	VA_6_W5	180	180	162	190	286	286	179	179
VA	VA_6	VA_6_S1	180	184	162	190	286	286	179	179
VA	VA_6	VA_6_S2	180	184	162	190	286	286	179	179
VA	VA_6	VA_6_S3	180	180	162	190	286	286	179	179
VA	VA_6	VA_6_S4	180	184	162	190	278	286	179	179
VA	VA_6	VA_6_S5	180	180	160	182	278	286	179	179
VA	VA_7	VA_7_W1	180	180	162	162	278	286	179	179
VA	VA_7	VA_7_W2	172	180	162	162	286	286	179	179
VA	**VA_7**	**VA_7_W3**	**180**	**182**	**162**	**162**	**286**	**286**	**177**	**179**
VA	VA_7	VA_7_W4	180	180	162	162	286	286	179	179
VA	VA_7	VA_7_W5	178	180	162	162	278	286	179	179
VA	VA_7	VA_7_S1	172	180	162	162	286	286	179	179
VA	VA_7	VA_7_S2	180	180	162	162	286	286	179	179
VA	VA_7	VA_7_S3	180	180	162	162	286	286	179	179
VA	VA_7	VA_7_S4	172	180	162	162	278	286	177	179
VA	VA_7	VA_7_S5	180	180	162	162	278	286	179	179
VA	VA_8	VA_8_W1	180	180	164	186	278	278	177	179
VA	VA_8	VA_8_W2	0	0	164	186	0	0	0	0

VA	**VA_8**	**VA_8_W3**	**180**	**184**	**164**	**182**	**278**	**286**	**177**	**177**
VA	VA_8	VA_8_W4	180	180	162	186	278	278	177	179
VA	VA_8	VA_8_W5	180	180	162	186	278	286	177	177
VA	VA_8	VA_8_S1	180	180	162	182	286	286	177	177
VA	VA_8	VA_8_S2	180	184	162	186	278	286	177	179
VA	VA_8	VA_8_S3	180	180	162	182	278	286	177	177
VA	VA_8	VA_8_S4	180	184	164	182	278	286	177	179
VA	VA_8	VA_8_S5	180	184	162	186	278	286	177	179
VA	VA_9	VA_9_W1	172	184	162	162	278	286	179	179
VA	VA_9	VA_9_W2	176	176	162	162	278	286	179	179
VA	**VA_9**	**VA_9_W3**	**172**	**176**	**162**	**162**	**278**	**286**	**179**	**179**
VA	VA_9	VA_9_W4	176	184	160	162	286	286	179	179
VA	VA_9	VA_9_W5	172	184	160	162	278	286	179	179
VA	VA_9	VA_9_S1	172	176	162	162	278	286	179	179
VA	VA_9	VA_9_S2	172	184	162	162	278	278	179	179
VA	VA_9	VA_9_S3	176	184	162	162	278	286	179	179
VA	VA_9	VA_9_S4	172	184	162	162	278	286	179	179
VA	VA_9	VA_9_S5	0	0	162	162	278	278	179	179
VA	VA_10	VA_10_W1	176	178	158	188	278	286	179	179
VA	VA_10	VA_10_W2	180	182	158	164	278	286	179	179
VA	**VA_10**	**VA_10_W3**	**176**	**182**	**186**	**188**	**278**	**286**	**179**	**179**
VA	VA_10	VA_10_W4	176	182	158	188	278	278	179	179
VA	VA_10	VA_10_W5	176	178	158	164	278	278	179	179
VA	VA_10	VA_10_S1	182	182	186	188	278	286	179	179
VA	VA_10	VA_10_S2	176	182	164	186	278	286	179	179
VA	VA_10	VA_10_S3	176	178	186	188	286	286	179	179
VA	VA_10	VA_10_S4	180	182	164	186	278	278	179	179
VA	VA_10	VA_10_S5	180	180	158	188	278	286	179	179
PC	PC_1	PC_1_W1	178	180	184	190	278	286	179	179
PC	PC_1	PC_1_W2	176	180	162	164	278	278	179	179
PC	**PC_1**	**PC_1_W3**	**178**	**180**	**164**	**190**	**278**	**286**	**179**	**179**
PC	PC_1	PC_1_W4	178	180	184	190	278	286	179	179
PC	PC_1	PC_1_W5	178	180	162	164	278	286	179	179
PC	PC_1	PC_1_S1	178	180	184	190	278	286	179	179
PC	PC_1	PC_1_S2	178	180	162	184	278	278	179	179
PC	PC_1	PC_1_S3	0	0	164	164	278	286	179	179
PC	PC_1	PC_1_S4	178	180	184	190	278	286	179	179
PC	PC_1	PC_1_S5	178	180	184	190	278	286	179	179
PC	PC_2	PC_2_W1	172	184	162	186	278	286	179	179
PC	PC_2	PC_2_W2	172	184	162	162	278	286	179	179
PC	**PC_2**	**PC_2_W3**	**176**	**180**	**162**	**162**	**278**	**286**	**179**	**179**

PC	PC_2	PC_2_W4	0	0	162	186	278	286	179	179
PC	PC_2	PC_2_W5	172	184	162	186	278	286	179	179
PC	PC_2	PC_2_S1	176	180	186	186	278	286	179	179
PC	PC_2	PC_2_S2	176	180	162	186	278	286	179	179
PC	PC_2	PC_2_S3	184	184	162	186	278	278	179	179
PC	PC_2	PC_2_S4	172	184	186	186	278	286	179	179
PC	PC_2	PC_2_S5	176	184	162	186	278	286	179	179
PC	PC_3	PC_3_W1	178	178	162	166	278	278	179	179
PC	PC_3	PC_3_W2	178	178	162	166	278	286	179	179
PC	**PC_3**	**PC_3_W3**	**178**	**178**	**162**	**182**	**278**	**278**	**179**	**179**
PC	PC_3	PC_3_W4	178	180	162	166	278	286	179	179
PC	PC_3	PC_3_W5	178	178	162	182	278	278	179	179
PC	PC_3	PC_3_S1	178	178	162	182	278	278	179	179
PC	PC_3	PC_3_S2	178	180	162	182	278	286	179	179
PC	PC_3	PC_3_S3	178	178	162	166	278	278	179	179
PC	PC_3	PC_3_S4	178	178	162	166	278	278	179	179
PC	PC_3	PC_3_S5	180	180	182	186	278	278	179	179
PC	PC_4	PC_4_W1	178	180	168	188	278	278	179	179
PC	PC_4	PC_4_W2	178	180	154	154	278	278	179	179
PC	**PC_4**	**PC_4_W3**	**180**	**180**	**154**	**168**	**278**	**286**	**179**	**179**
PC	PC_4	PC_4_W4	180	180	154	182	286	286	179	179
PC	PC_4	PC_4_W5	180	180	168	188	278	286	179	179
PC	PC_4	PC_4_S1	180	180	182	188	278	278	179	179
PC	PC_4	PC_4_S2	178	180	168	168	278	286	177	179
PC	PC_4	PC_4_S3	180	180	154	168	286	286	179	179
PC	PC_4	PC_4_S4	178	178	154	168	278	278	179	179
PC	PC_4	PC_4_S5	0	0	182	188	278	278	179	179
PC	PC_5	PC_5_W1	176	178	164	186	278	278	179	179
PC	PC_5	PC_5_W2	176	178	164	186	278	278	179	179
PC	**PC_5**	**PC_5_W3**	**176**	**178**	**164**	**186**	**278**	**278**	**179**	**179**
PC	PC_5	PC_5_W4	0	0	182	186	278	278	179	179
PC	PC_5	PC_5_W5	176	178	164	182	278	278	179	179
PC	PC_5	PC_5_S1	178	178	164	186	278	278	179	179
PC	PC_5	PC_5_S2	176	178	186	186	278	278	179	179
PC	PC_5	PC_5_S3	178	178	164	186	278	278	179	179
PC	PC_5	PC_5_S4	176	178	164	186	278	278	179	179
PC	PC_5	PC_5_S5	176	178	164	182	278	278	179	179
PC	PC_6	PC_6_W1	0	0	164	182	286	286	177	179
PC	PC_6	PC_6_W2	172	172	164	164	278	286	177	179
PC	**PC_6**	**PC_6_W3**	**172**	**178**	**164**	**186**	**286**	**286**	**177**	**179**
PC	PC_6	PC_6_W4	180	180	182	186	286	286	179	179

PC	PC_6	PC_6_W5	172	178	164	164	286	286	177	179
PC	PC_6	PC_6_S1	178	180	164	182	286	286	179	179
PC	PC_6	PC_6_S2	172	178	186	186	286	286	177	179
PC	PC_6	PC_6_S3	178	180	164	164	286	286	177	179
PC	PC_6	PC_6_S4	172	172	164	182	286	286	177	179
PC	PC_6	PC_6_S5	172	172	164	164	286	286	177	179
PC	PC_7	PC_7_W1	178	180	162	166	286	286	179	179
PC	PC_7	PC_7_W2	178	180	166	186	278	286	179	179
PC	**PC_7**	**PC_7_W3**	**178**	**178**	**162**	**186**	**278**	**286**	**179**	**179**
PC	PC_7	PC_7_W4	178	178	166	186	286	286	179	179
PC	PC_7	PC_7_W5	178	180	166	186	286	286	179	179
PC	PC_7	PC_7_S1	178	178	166	186	278	286	179	179
PC	PC_7	PC_7_S2	0	0	186	186	278	278	179	179
PC	PC_7	PC_7_S3	176	178	166	186	286	286	179	179
PC	PC_7	PC_7_S4	178	178	162	166	278	286	179	179
PC	PC_7	PC_7_S5	178	178	166	186	278	278	179	179
PC	PC_8	PC_8_W1	178	180	186	186	278	286	179	179
PC	PC_8	PC_8_W2	176	180	186	186	286	286	179	179
PC	**PC_8**	**PC_8_W3**	**180**	**180**	**186**	**186**	**278**	**286**	**179**	**179**
PC	PC_8	PC_8_W4	180	180	186	186	278	286	179	179
PC	PC_8	PC_8_W5	176	176	186	186	278	286	179	179
PC	PC_8	PC_8_S1	176	180	186	186	278	278	179	179
PC	PC_8	PC_8_S2	176	180	186	186	286	286	179	179
PC	PC_8	PC_8_S3	176	176	186	186	278	286	179	179
PC	PC_8	PC_8_S4	176	176	186	186	278	286	179	179
PC	PC_8	PC_8_S5	178	178	186	186	0	0	179	179
PC	PC_9	PC_9_W1	178	178	164	166	278	278	179	179
PC	PC_9	PC_9_W2	178	178	164	166	278	286	179	179
PC	**PC_9**	**PC_9_W3**	**178**	**180**	**164**	**166**	**278**	**286**	**179**	**179**
PC	PC_9	PC_9_W4	178	178	186	186	278	286	179	179
PC	PC_9	PC_9_W5	0	0	164	186	278	278	179	179
PC	PC_9	PC_9_S1	182	182	164	166	278	286	179	179
PC	PC_9	PC_9_S2	178	180	164	186	278	286	179	179
PC	PC_9	PC_9_S3	176	182	164	166	278	278	179	179
PC	PC_9	PC_9_S4	176	178	186	186	278	286	179	179
PC	PC_9	PC_9_S5	180	180	186	186	278	286	179	179
PC	PC_10	PC_10_W1	178	178	162	182	278	278	179	179
PC	PC_10	PC_10_W2	172	178	162	182	278	286	179	179
PC	**PC_10**	**PC_10_W3**	**172**	**178**	**164**	**186**	**278**	**278**	**179**	**179**
PC	PC_10	PC_10_W4	178	178	164	186	278	286	179	179
PC	PC_10	PC_10_W5	172	178	182	186	278	286	179	179

PC	PC_10	PC_10_S1	172	178	162	182	278	278	179	179
PC	PC_10	PC_10_S2	178	178	0	0	278	278	177	179
PC	PC_10	PC_10_S3	172	178	162	182	278	278	179	179
PC	PC_10	PC_10_S4	178	178	164	186	278	278	179	179
PC	PC_10	PC_10_S5	172	178	164	186	278	278	179	179
PD	PD_1	PD_1_W1	182	186	164	186	278	286	179	179
PD	PD_1	PD_1_W2	182	186	164	186	278	278	179	179
PD	**PD_1**	**PD_1_W3**	**180**	**180**	**162**	**164**	**278**	**286**	**179**	**179**
PD	PD_1	PD_1_W4	180	180	164	186	278	286	179	179
PD	PD_1	PD_1_W5	180	186	164	186	278	278	179	179
PD	PD_1	PD_1_S1	0	0	162	186	278	278	179	179
PD	PD_1	PD_1_S2	0	0	164	186	278	278	179	179
PD	PD_1	PD_1_S3	182	186	162	164	278	278	179	179
PD	PD_1	PD_1_S4	182	186	162	164	278	278	179	179
PD	PD_1	PD_1_S5	0	0	162	164	278	278	179	179
PD	PD_2	PD_2_W1	180	184	162	186	278	278	0	0
PD	PD_2	PD_2_W2	176	178	178	186	278	278	179	179
PD	**PD_2**	**PD_2_W3**	**176**	**180**	**178**	**186**	**278**	**278**	**179**	**179**
PD	PD_2	PD_2_W4	180	184	178	186	278	278	179	179
PD	PD_2	PD_2_W5	180	184	178	186	278	278	179	179
PD	PD_2	PD_2_S1	0	0	168	178	278	278	179	179
PD	PD_2	PD_2_S2	0	0	162	168	278	278	179	179
PD	PD_2	PD_2_S3	176	176	168	178	278	278	179	179
PD	PD_2	PD_2_S4	0	0	178	186	278	278	179	179
PD	PD_2	PD_2_S5	0	0	178	186	278	278	179	179
PD	PD_3	PD_3_W1	178	184	164	178	278	286	179	179
PD	PD_3	PD_3_W2	180	180	162	162	278	286	179	179
PD	**PD_3**	**PD_3_W3**	**180**	**180**	**164**	**178**	**278**	**286**	**179**	**179**
PD	PD_3	PD_3_W4	178	184	162	178	278	286	179	179
PD	PD_3	PD_3_W5	178	184	162	162	278	286	179	179
PD	PD_3	PD_3_S1	180	180	160	164	278	286	179	179
PD	PD_3	PD_3_S2	0	0	160	164	278	286	179	179
PD	PD_3	PD_3_S3	0	0	160	162	278	286	179	179
PD	PD_3	PD_3_S4	180	180	162	178	278	286	179	179
PD	PD_3	PD_3_S5	0	0	160	164	278	286	179	179
PD	PD_4	PD_4_W1	176	188	162	162	278	278	179	179
PD	PD_4	PD_4_W2	176	188	162	184	278	278	179	179
PD	**PD_4**	**PD_4_W3**	**176**	**182**	**162**	**182**	**278**	**278**	**177**	**179**
PD	PD_4	PD_4_W4	176	182	162	182	278	278	179	179
PD	PD_4	PD_4_W5	176	182	162	182	278	278	179	179
PD	PD_4	PD_4_S1	182	182	162	184	278	278	179	179

PD	PD_4	PD_4_S2	0	0	182	184	278	278	177	179
PD	PD_4	PD_4_S3	180	180	182	184	278	286	179	179
PD	PD_4	PD_4_S4	176	182	182	184	278	278	177	179
PD	PD_4	PD_4_S5	0	0	162	182	278	278	179	179
PD	PD_5	PD_5_W1	180	184	164	184	278	286	179	179
PD	PD_5	PD_5_W2	178	180	160	160	278	286	179	179
PD	**PD_5**	**PD_5_W3**	**180**	**184**	**162**	**184**	**286**	**286**	**179**	**179**
PD	PD_5	PD_5_W4	178	180	164	184	278	286	179	179
PD	PD_5	PD_5_W5	178	180	162	162	278	278	179	179
PD	PD_5	PD_5_S1	0	0	162	184	278	286	0	0
PD	PD_5	PD_5_S2	180	180	162	162	286	286	179	179
PD	PD_5	PD_5_S3	178	180	162	162	278	286	179	179
PD	PD_5	PD_5_S4	180	180	162	184	278	278	179	179
PD	PD_5	PD_5_S5	178	178	162	164	286	286	179	179
PD	PD_6	PD_6_W1	178	180	164	166	278	278	179	179
PD	PD_6	PD_6_W2	178	178	164	182	278	278	179	179
PD	**PD_6**	**PD_6_W3**	**178**	**178**	**164**	**166**	**278**	**278**	**179**	**179**
PD	PD_6	PD_6_W4	178	178	164	166	278	278	179	179
PD	PD_6	PD_6_W5	178	178	164	166	278	278	179	179
PD	PD_6	PD_6_S1	0	0	164	182	278	278	179	179
PD	PD_6	PD_6_S2	178	180	164	182	278	278	179	179
PD	PD_6	PD_6_S3	178	180	164	182	278	278	179	179
PD	PD_6	PD_6_S4	0	0	166	166	278	278	179	179
PD	PD_6	PD_6_S5	0	0	164	182	278	278	179	179
PD	PD_7	PD_7_W1	178	180	154	184	278	278	179	179
PD	PD_7	PD_7_W2	180	180	162	184	278	278	179	179
PD	**PD_7**	**PD_7_W3**	**178**	**178**	**184**	**184**	**278**	**278**	**179**	**179**
PD	PD_7	PD_7_W4	180	182	184	184	278	278	179	179
PD	PD_7	PD_7_W5	178	182	154	184	278	278	179	179
PD	PD_7	PD_7_S1	0	0	154	184	278	278	179	179
PD	PD_7	PD_7_S2	178	178	154	162	278	278	179	179
PD	PD_7	PD_7_S3	0	0	154	184	278	278	179	179
PD	PD_7	PD_7_S4	178	182	162	184	278	278	179	179
PD	PD_7	PD_7_S5	178	178	184	184	278	278	179	179
PD	PD_8	PD_8_W1	176	180	164	164	278	286	179	179
PD	PD_8	PD_8_W2	174	180	164	164	278	278	179	179
PD	**PD_8**	**PD_8_W3**	**174**	**176**	**164**	**164**	**278**	**278**	**179**	**179**
PD	PD_8	PD_8_W4	180	180	164	164	278	286	179	179
PD	PD_8	PD_8_W5	180	180	164	164	278	278	179	179
PD	PD_8	PD_8_S1	180	180	164	166	278	286	179	179
PD	PD_8	PD_8_S2	176	180	164	166	278	286	179	179

PD	PD_8	PD_8_S3	180	180	164	164	278	286	179	179
PD	PD_8	PD_8_S4	0	0	164	166	278	286	179	179
PD	PD_8	PD_8_S5	0	0	164	166	278	286	179	179
PD	PD_9	PD_9_W1	182	184	164	186	278	278	179	179
PD	PD_9	PD_9_W2	178	184	164	186	278	278	179	179
PD	**PD_9**	**PD_9_W3**	**172**	**178**	**164**	**186**	**278**	**286**	**179**	**179**
PD	PD_9	PD_9_W4	178	184	0	0	0	0	0	0
PD	PD_9	PD_9_W5	178	180	166	190	278	286	179	179
PD	PD_9	PD_9_S1	178	180	164	190	278	278	179	179
PD	PD_9	PD_9_S2	182	184	164	190	278	278	179	179
PD	PD_9	PD_9_S3	180	182	164	190	278	286	179	179
PD	PD_9	PD_9_S4	182	182	164	186	278	286	179	179
PD	PD_9	PD_9_S5	180	182	166	186	278	278	179	179
PD	PD_10	PD_10_W1	174	178	164	190	278	286	179	179
PD	PD_10	PD_10_W2	174	178	164	190	278	278	179	179
PD	**PD_10**	**PD_10_W3**	**178**	**178**	**162**	**190**	**278**	**278**	**177**	**179**
PD	PD_10	PD_10_W4	178	178	162	190	278	278	179	179
PD	PD_10	PD_10_W5	174	178	162	190	278	286	179	179
PD	PD_10	PD_10_S1	178	178	164	166	278	286	177	179
PD	PD_10	PD_10_S2	0	0	164	166	278	278	179	179
PD	PD_10	PD_10_S3	174	174	162	190	278	286	177	179
PD	PD_10	PD_10_S4	178	178	164	166	278	286	179	179
PD	PD_10	PD_10_S5	174	178	162	166	278	278	179	179
VDD	VDD_1	VDD_1_W1	182	182	168	168	278	286	179	181
VDD	VDD_1	VDD_1_W2	180	182	168	182	278	286	179	179
VDD	**VDD_1**	**VDD_1_W3**	**182**	**182**	**168**	**182**	**278**	**286**	**179**	**181**
VDD	VDD_1	VDD_1_W4	182	182	168	168	278	286	179	181
VDD	VDD_1	VDD_1_W5	182	182	168	168	278	286	179	179
VDD	VDD_1	VDD_1_S1	180	180	182	186	278	278	179	179
VDD	VDD_1	VDD_1_S2	180	180	182	182	278	278	179	179
VDD	VDD_1	VDD_1_S3	180	182	168	168	278	286	177	179
VDD	VDD_1	VDD_1_S4	180	182	182	182	278	278	179	179
VDD	VDD_1	VDD_1_S5	180	182	168	182	278	286	179	179
VDD	VDD_2	VDD_2_W1	180	180	162	164	278	286	179	179
VDD	VDD_2	VDD_2_W2	178	180	162	186	278	278	179	179
VDD	VDD_2	VDD_2_W3	0	0	162	162	278	286	179	179
VDD	**VDD_2**	**VDD_2_W4**	**178**	**180**	**162**	**164**	**278**	**278**	**179**	**179**
VDD	VDD_2	VDD_2_W5	180	184	162	164	278	278	179	179
VDD	VDD_2	VDD_2_S1	178	180	162	186	278	286	179	179
VDD	VDD_2	VDD_2_S2	178	180	162	186	278	286	179	179
VDD	VDD_2	VDD_2_S3	180	180	162	162	278	286	179	179

VDD	VDD_2	VDD_2_S4	180	180	162	162	278	278	179	179
VDD	VDD_2	VDD_2_S5	178	180	162	162	278	286	179	179
VDD	VDD_3	VDD_3_W1	174	180	154	186	278	278	179	179
VDD	VDD_3	VDD_3_W2	180	180	164	178	278	286	179	179
VDD	**VDD_3**	**VDD_3_W3**	**180**	**182**	**178**	**186**	**278**	**286**	**179**	**179**
VDD	VDD_3	VDD_3_W4	180	180	154	186	278	286	179	179
VDD	VDD_3	VDD_3_W5	180	180	154	164	278	278	179	179
VDD	VDD_3	VDD_3_S1	180	180	154	186	278	286	179	179
VDD	VDD_3	VDD_3_S2	180	180	164	178	278	278	179	179
VDD	VDD_3	VDD_3_S3	180	180	154	186	278	286	179	179
VDD	VDD_3	VDD_3_S4	180	180	154	164	278	278	179	179
VDD	VDD_3	VDD_3_S5	0	0	164	178	278	286	179	179
VDD	VDD_4	VDD_4_W1	174	182	154	170	278	286	179	179
VDD	VDD_4	VDD_4_W2	176	182	154	170	278	286	179	179
VDD	**VDD_4**	**VDD_4_W3**	**176**	**184**	**154**	**164**	**278**	**286**	**179**	**179**
VDD	VDD_4	VDD_4_W4	0	0	154	164	278	286	179	179
VDD	VDD_4	VDD_4_W5	182	182	154	164	278	286	179	179
VDD	VDD_4	VDD_4_S1	176	184	154	170	278	286	179	179
VDD	VDD_4	VDD_4_S2	174	182	164	180	278	286	179	179
VDD	VDD_4	VDD_4_S3	174	184	170	180	278	286	179	179
VDD	VDD_4	VDD_4_S4	0	0	154	170	0	0	179	179
VDD	VDD_4	VDD_4_S5	0	0	154	164	278	286	179	179
VDD	VDD_5	VDD_5_W1	0	0	178	178	278	286	177	179
VDD	VDD_5	VDD_5_W2	178	180	178	180	278	278	177	179
VDD	**VDD_5**	**VDD_5_W3**	**178**	**180**	**178**	**178**	**278**	**286**	**177**	**179**
VDD	VDD_5	VDD_5_W4	176	178	178	180	278	286	179	179
VDD	VDD_5	VDD_5_W5	176	178	178	180	278	286	179	179
VDD	VDD_5	VDD_5_S1	176	180	178	180	278	278	179	179
VDD	VDD_5	VDD_5_S2	176	178	178	180	278	278	179	179
VDD	VDD_5	VDD_5_S3	176	180	178	180	278	286	177	179
VDD	VDD_5	VDD_5_S4	176	180	178	180	278	286	179	179
VDD	VDD_5	VDD_5_S5	176	178	178	180	278	278	177	179
VDD	VDD_6	VDD_6_W1	178	182	164	164	278	286	179	179
VDD	VDD_6	VDD_6_W2	182	182	164	164	278	286	179	179
VDD	**VDD_6**	**VDD_6_W3**	**178**	**182**	**162**	**164**	**278**	**278**	**179**	**179**
VDD	VDD_6	VDD_6_W4	178	182	164	164	278	286	179	179
VDD	VDD_6	VDD_6_W5	178	182	164	164	278	278	179	179
VDD	VDD_6	VDD_6_S1	178	178	162	164	278	278	179	179
VDD	VDD_6	VDD_6_S2	178	182	162	164	278	286	179	179
VDD	VDD_6	VDD_6_S3	178	182	162	164	278	286	177	179
VDD	VDD_6	VDD_6_S4	178	182	162	164	278	286	179	179

VDD	VDD_6	VDD_6_S5	178	182	164	164	278	278	179	179
VDD	VDD_7	VDD_7_W1	178	180	166	186	278	278	179	179
VDD	VDD_7	VDD_7_W2	180	180	164	166	278	278	179	179
VDD	**VDD_7**	**VDD_7_W3**	**178**	**180**	**162**	**186**	**278**	**278**	**179**	**179**
VDD	VDD_7	VDD_7_W4	180	186	162	164	278	278	179	179
VDD	VDD_7	VDD_7_W5	178	180	162	164	278	278	179	179
VDD	VDD_7	VDD_7_S1	180	182	164	164	278	278	0	0
VDD	VDD_7	VDD_7_S2	180	180	164	166	278	278	179	179
VDD	VDD_7	VDD_7_S3	178	180	166	186	278	278	179	179
VDD	VDD_7	VDD_7_S4	178	180	166	186	278	278	179	179
VDD	VDD_7	VDD_7_S5	180	180	162	164	278	278	179	179
VDD	VDD_8	VDD_8_W1	180	180	162	164	278	286	179	181
VDD	VDD_8	VDD_8_W2	180	184	164	168	278	286	179	179
VDD	**VDD_8**	**VDD_8_W3**	**180**	**180**	**164**	**168**	**278**	**286**	**179**	**179**
VDD	VDD_8	VDD_8_W4	180	180	162	164	278	278	179	181
VDD	VDD_8	VDD_8_W5	180	180	0	0	0	0	0	0
VDD	VDD_8	VDD_8_S1	180	184	162	164	278	286	179	181
VDD	VDD_8	VDD_8_S2	180	184	164	168	278	278	179	181
VDD	VDD_8	VDD_8_S3	180	184	162	164	278	278	179	181
VDD	VDD_8	VDD_8_S4	180	184	162	168	278	278	177	179
VDD	VDD_8	VDD_8_S5	178	184	162	168	278	286	177	179
VDD	VDD_9	VDD_9_W1	178	180	164	164	278	278	177	179
VDD	VDD_9	VDD_9_W2	176	178	164	164	278	278	179	179
VDD	**VDD_9**	**VDD_9_W3**	**176**	**178**	**164**	**164**	**278**	**278**	**177**	**179**
VDD	VDD_9	VDD_9_W4	0	0	164	182	278	278	179	179
VDD	VDD_9	VDD_9_W5	178	180	164	182	278	278	179	179
VDD	VDD_9	VDD_9_S1	176	180	164	182	278	278	179	179
VDD	VDD_9	VDD_9_S2	178	180	164	164	278	278	179	179
VDD	VDD_9	VDD_9_S3	178	180	164	164	278	278	179	179
VDD	VDD_9	VDD_9_S4	176	180	164	182	278	278	179	179
VDD	VDD_9	VDD_9_S5	180	180	164	182	278	278	179	179
VDD	VDD_10	VDD_10_W1	180	180	164	164	278	278	179	179
VDD	VDD_10	VDD_10_W2	180	180	186	192	278	278	179	179
VDD	**VDD_10**	**VDD_10_W3**	**180**	**180**	**164**	**164**	**278**	**278**	**179**	**179**
VDD	VDD_10	VDD_10_W4	178	180	164	192	278	278	179	179
VDD	VDD_10	VDD_10_W5	180	180	162	186	278	278	179	179
VDD	VDD_10	VDD_10_S1	180	180	164	192	278	278	179	179
VDD	VDD_10	VDD_10_S2	180	180	162	164	278	278	179	179
VDD	VDD_10	VDD_10_S3	180	180	162	164	278	278	179	179
VDD	VDD_10	VDD_10_S4	180	180	186	192	278	278	179	179
VDD	VDD_10	VDD_10_S5	180	180	164	192	278	278	179	179

MC	MC_1	MC_1_W1	176	178	164	186	278	278	179	179
MC	MC_1	MC_1_W2	176	178	164	186	278	278	179	179
MC	**MC_1**	**MC_1_W3**	**176**	**178**	**184**	**186**	**278**	**278**	**177**	**179**
MC	MC_1	MC_1_W4	176	180	184	186	278	278	179	179
MC	MC_1	MC_1_W5	176	178	162	184	278	278	179	179
MC	MC_1	MC_1_S1	0	0	162	164	278	278	179	179
MC	MC_1	MC_1_S2	0	0	164	186	278	278	179	179
MC	MC_1	MC_1_S3	0	0	162	164	278	278	177	179
MC	MC_1	MC_1_S4	0	0	184	186	278	278	177	179
MC	MC_1	MC_1_S5	180	180	162	184	278	278	177	179
MC	MC_2	MC_2_W1	178	184	162	164	278	278	179	179
MC	MC_2	MC_2_W2	178	178	162	190	278	278	179	179
MC	**MC_2**	**MC_2_W3**	**178**	**184**	**162**	**164**	**278**	**278**	**179**	**179**
MC	MC_2	MC_2_W4	178	178	162	164	278	278	179	179
MC	MC_2	MC_2_W5	178	184	162	164	278	278	179	179
MC	MC_2	MC_2_S1	178	184	162	164	278	278	179	179
MC	MC_2	MC_2_S2	178	184	164	164	278	278	179	179
MC	MC_2	MC_2_S3	178	184	162	164	278	278	179	179
MC	MC_2	MC_2_S4	178	178	162	164	278	278	179	179
MC	MC_2	MC_2_S5	184	184	162	190	278	278	179	179
MC	MC_3	MC_3_W1	176	184	186	190	278	278	179	179
MC	MC_3	MC_3_W2	176	178	186	186	278	278	179	179
MC	**MC_3**	**MC_3_W3**	**176**	**184**	**186**	**190**	**278**	**278**	**179**	**179**
MC	MC_3	MC_3_W4	176	184	186	186	278	278	179	179
MC	MC_3	MC_3_W5	176	184	180	190	278	278	179	179
MC	MC_3	MC_3_S1	178	184	186	186	278	278	179	179
MC	MC_3	MC_3_S2	0	0	180	186	278	278	179	179
MC	MC_3	MC_3_S3	176	184	186	190	278	278	179	179
MC	MC_3	MC_3_S4	176	178	186	186	278	278	179	179
MC	MC_3	MC_3_S5	176	178	180	190	278	278	179	179
MC	MC_4	MC_4_W1	180	182	164	184	278	278	179	179
MC	MC_4	MC_4_W2	178	180	182	184	278	286	179	179
MC	**MC_4**	**MC_4_W3**	**178**	**180**	**182**	**184**	**278**	**286**	**179**	**179**
MC	MC_4	MC_4_W4	180	184	182	184	278	286	179	179
MC	MC_4	MC_4_W5	178	184	164	184	278	278	179	179
MC	MC_4	MC_4_S1	178	184	164	182	278	286	179	179
MC	MC_4	MC_4_S2	0	0	164	182	0	0	179	179
MC	MC_4	MC_4_S3	180	184	182	182	278	286	179	179
MC	MC_4	MC_4_S4	0	0	164	182	278	286	179	179
MC	MC_4	MC_4_S5	178	184	164	182	278	278	179	179
MC	MC_5	MC_5_W1	176	178	162	164	278	278	179	179

MC	MC_5	MC_5_W2	176	178	162	164	278	278	179	179
MC	**MC_5**	**MC_5_W3**	**178**	**178**	**162**	**164**	**278**	**278**	**179**	**179**
MC	MC_5	MC_5_W4	176	178	162	164	278	278	179	179
MC	MC_5	MC_5_W5	176	178	162	164	278	278	179	179
MC	MC_5	MC_5_S1	178	180	162	164	278	278	179	179
MC	MC_5	MC_5_S2	178	178	162	164	278	278	179	179
MC	MC_5	MC_5_S3	178	180	162	164	278	288	179	179
MC	MC_5	MC_5_S4	176	178	162	164	278	278	179	179
MC	MC_5	MC_5_S5	176	180	164	164	278	278	179	179
MC	MC_6	MC_6_W1	178	180	162	162	278	286	177	179
MC	MC_6	MC_6_W2	174	180	162	164	278	286	177	179
MC	**MC_6**	**MC_6_W3**	**180**	**180**	**162**	**164**	**278**	**286**	**179**	**179**
MC	MC_6	MC_6_W4	178	180	162	164	278	286	177	179
MC	MC_6	MC_6_W5	178	178	162	162	278	286	179	179
MC	MC_6	MC_6_S1	172	178	162	162	278	286	177	179
MC	MC_6	MC_6_S2	172	178	162	162	278	286	177	179
MC	MC_6	MC_6_S3	174	180	162	162	278	286	179	179
MC	MC_6	MC_6_S4	180	180	162	162	278	286	177	179
MC	MC_6	MC_6_S5	180	180	162	164	278	286	177	179
MC	MC_7	MC_7_W1	172	176	164	186	286	286	179	179
MC	MC_7	MC_7_W2	172	180	164	186	278	286	179	179
MC	**MC_7**	**MC_7_W3**	**172**	**180**	**162**	**186**	**286**	**286**	**179**	**179**
MC	MC_7	MC_7_W4	172	172	164	186	278	278	179	179
MC	MC_7	MC_7_W5	172	180	162	186	278	286	179	179
MC	MC_7	MC_7_S1	172	178	162	186	278	278	179	179
MC	MC_7	MC_7_S2	172	180	162	186	286	286	179	179
MC	MC_7	MC_7_S3	176	178	162	186	278	286	179	179
MC	MC_7	MC_7_S4	172	176	164	186	278	286	179	179
MC	MC_7	MC_7_S5	172	176	162	186	278	286	179	179
MC	MC_8	MC_8_W1	178	178	162	164	278	278	179	179
MC	MC_8	MC_8_W2	178	178	162	164	278	278	179	179
MC	**MC_8**	**MC_8_W3**	**178**	**178**	**162**	**164**	**278**	**278**	**179**	**179**
MC	MC_8	MC_8_W4	178	180	162	164	278	278	179	179
MC	MC_8	MC_8_W5	178	178	162	164	278	278	179	179
MC	MC_8	MC_8_S1	178	180	162	164	278	278	179	179
MC	MC_8	MC_8_S2	178	180	162	164	278	278	179	179
MC	MC_8	MC_8_S3	176	178	162	164	278	278	179	179
MC	MC_8	MC_8_S4	180	180	162	162	278	282	179	179
MC	MC_8	MC_8_S5	178	178	162	164	278	278	179	179
MC	MC_9	MC_9_W1	180	182	164	164	278	282	179	179
MC	MC_9	MC_9_W2	180	182	164	164	286	288	179	179

MC	**MC_9**	**MC_9_W3**	**180**	**180**	**164**	**184**	**286**	**288**	**179**	**179**
MC	MC_9	MC_9_W4	180	182	164	184	278	288	179	179
MC	MC_9	MC_9_W5	180	180	164	184	286	288	179	179
MC	MC_9	MC_9_S1	180	182	164	184	286	286	179	179
MC	MC_9	MC_9_S2	178	180	164	164	282	286	179	179
MC	MC_9	MC_9_S3	178	180	164	184	278	288	179	179
MC	MC_9	MC_9_S4	172	180	164	184	278	282	179	179
MC	MC_9	MC_9_S5	180	180	164	164	282	286	179	179
MC	MC_10	MC_10_W1	176	178	164	164	278	278	179	179
MC	MC_10	MC_10_W2	176	178	164	164	278	278	179	179
MC	**MC_10**	**MC_10_W3**	**176**	**178**	**162**	**188**	**278**	**286**	**179**	**179**
MC	MC_10	MC_10_W4	176	178	164	188	278	286	179	179
MC	MC_10	MC_10_W5	176	178	164	188	278	286	179	179
MC	MC_10	MC_10_S1	174	176	164	188	286	286	179	179
MC	MC_10	MC_10_S2	176	178	162	188	286	286	179	179
MC	MC_10	MC_10_S3	178	178	164	164	286	286	179	179
MC	MC_10	MC_10_S4	178	178	162	164	278	278	179	179
MC	MC_10	MC_10_S5	174	178	164	186	278	286	179	179
ZB	ZB_1	ZB_1_W1	178	180	164	184	278	278	179	179
ZB	ZB_1	ZB_1_W2	178	180	164	184	278	278	179	179
ZB	**ZB_1**	**ZB_1_W3**	**178**	**180**	**180**	**184**	**278**	**286**	**179**	**179**
ZB	ZB_1	ZB_1_W4	180	180	164	180	278	286	179	179
ZB	ZB_1	ZB_1_W5	178	180	180	184	278	286	179	179
ZB	ZB_1	ZB_1_S1	178	180	180	184	278	278	179	179
ZB	ZB_1	ZB_1_S2	178	180	180	184	278	286	179	179
ZB	ZB_1	ZB_1_S3	180	180	164	180	278	286	179	179
ZB	ZB_1	ZB_1_S4	180	180	0	0	278	278	179	179
ZB	ZB_1	ZB_1_S5	0	0	164	180	278	278	179	179
ZB	ZB_2	ZB_2_W1	178	180	166	190	278	286	179	179
ZB	ZB_2	ZB_2_W2	0	0	166	198	278	286	179	179
ZB	**ZB_2**	**ZB_2_W3**	**178**	**180**	**166**	**198**	**278**	**278**	**179**	**179**
ZB	ZB_2	ZB_2_W4	178	180	164	166	278	278	179	179
ZB	ZB_2	ZB_2_W5	0	0	166	198	0	0	179	179
ZB	ZB_2	ZB_2_S1	178	180	166	190	278	286	179	179
ZB	ZB_2	ZB_2_S2	178	178	166	190	278	286	179	179
ZB	ZB_2	ZB_2_S3	178	180	166	190	278	286	179	179
ZB	ZB_2	ZB_2_S4	178	178	166	190	278	278	179	179
ZB	ZB_2	ZB_2_S5	178	180	166	190	278	278	179	179
ZB	ZB_3	ZB_3_W1	172	180	186	186	278	286	179	179
ZB	ZB_3	ZB_3_W2	178	180	162	186	278	278	179	179
ZB	**ZB_3**	**ZB_3_W3**	**180**	**180**	**162**	**186**	**278**	**286**	**179**	**179**

ZB	ZB_3	ZB_3_W4	178	180	162	162	278	286	179	179
ZB	ZB_3	ZB_3_W5	180	184	162	186	278	286	179	179
ZB	ZB_3	ZB_3_S1	178	180	186	186	278	278	179	179
ZB	ZB_3	ZB_3_S2	180	184	186	186	278	286	179	179
ZB	ZB_3	ZB_3_S3	180	184	162	186	278	278	179	179
ZB	ZB_3	ZB_3_S4	180	184	162	186	278	278	179	179
ZB	ZB_3	ZB_3_S5	172	178	162	186	278	286	179	179
ZB	ZB_4	ZB_4_W1	178	180	196	198	278	286	179	179
ZB	ZB_4	ZB_4_W2	178	180	196	198	278	286	179	179
ZB	**ZB_4**	**ZB_4_W3**	**178**	**180**	**190**	**196**	**278**	**286**	**179**	**179**
ZB	ZB_4	ZB_4_W4	172	178	196	198	278	286	179	179
ZB	ZB_4	ZB_4_W5	178	180	188	198	278	286	179	179
ZB	ZB_4	ZB_4_S1	178	180	188	190	278	286	179	179
ZB	ZB_4	ZB_4_S2	178	180	190	196	278	286	179	179
ZB	ZB_4	ZB_4_S3	180	180	188	190	278	286	179	179
ZB	ZB_4	ZB_4_S4	178	178	196	198	278	286	179	179
ZB	ZB_4	ZB_4_S5	178	180	184	190	278	286	179	179
ZB	ZB_5	ZB_5_W1	180	180	162	186	278	278	179	179
ZB	ZB_5	ZB_5_W2	180	180	164	186	278	278	179	179
ZB	**ZB_5**	**ZB_5_W3**	**176**	**184**	**186**	**186**	**278**	**278**	**179**	**179**
ZB	ZB_5	ZB_5_W4	176	184	162	186	278	278	179	179
ZB	ZB_5	ZB_5_W5	176	180	164	186	278	286	179	179
ZB	ZB_5	ZB_5_S1	180	180	162	164	278	286	179	179
ZB	ZB_5	ZB_5_S2	180	184	186	186	278	278	179	179
ZB	ZB_5	ZB_5_S3	176	184	162	186	278	278	179	179
ZB	ZB_5	ZB_5_S4	180	180	186	186	278	278	179	179
ZB	ZB_5	ZB_5_S5	176	184	162	186	278	278	179	179
ZB	ZB_6	ZB_6_W1	178	180	156	164	278	278	179	179
ZB	ZB_6	ZB_6_W2	178	180	154	164	278	278	179	179
ZB	**ZB_6**	**ZB_6_W3**	**180**	**180**	**156**	**164**	**278**	**278**	**179**	**179**
ZB	ZB_6	ZB_6_W4	178	178	154	164	278	278	179	179
ZB	ZB_6	ZB_6_W5	178	178	156	162	278	278	179	179
ZB	ZB_6	ZB_6_S1	180	180	156	162	278	278	179	179
ZB	ZB_6	ZB_6_S2	180	180	156	162	278	278	179	179
ZB	ZB_6	ZB_6_S3	178	180	154	164	278	278	179	179
ZB	ZB_6	ZB_6_S4	180	180	154	164	278	278	179	179
ZB	ZB_6	ZB_6_S5	178	178	156	164	278	278	179	179
ZB	ZB_7	ZB_7_W1	176	176	176	186	278	278	179	179
ZB	ZB_7	ZB_7_W2	178	178	188	198	278	278	179	179
ZB	**ZB_7**	**ZB_7_W3**	**176**	**182**	**188**	**198**	**278**	**286**	**179**	**179**
ZB	ZB_7	ZB_7_W4	176	178	188	198	278	286	179	179

ZB	ZB_7	ZB_7_W5	178	178	188	198	278	278	179	179
ZB	ZB_7	ZB_7_S1	178	182	188	198	278	278	179	179
ZB	ZB_7	ZB_7_S2	0	0	188	198	278	278	179	179
ZB	ZB_7	ZB_7_S3	176	182	188	198	278	286	179	179
ZB	ZB_7	ZB_7_S4	176	182	188	198	278	286	179	179
ZB	ZB_7	ZB_7_S5	178	178	188	198	278	286	179	179
ZB	ZB_8	ZB_8_W1	176	180	162	184	278	278	179	181
ZB	ZB_8	ZB_8_W2	176	182	162	184	278	278	179	179
ZB	**ZB_8**	**ZB_8_W3**	**176**	**180**	**164**	**166**	**278**	**278**	**179**	**179**
ZB	ZB_8	ZB_8_W4	178	182	162	166	278	278	179	179
ZB	ZB_8	ZB_8_W5	178	180	164	184	278	278	179	181
ZB	ZB_8	ZB_8_S1	176	180	164	184	278	278	179	181
ZB	ZB_8	ZB_8_S2	176	180	164	184	278	278	179	181
ZB	ZB_8	ZB_8_S3	178	180	162	164	278	278	179	179
ZB	ZB_8	ZB_8_S4	178	180	164	184	278	278	179	181
ZB	ZB_8	ZB_8_S5	178	182	164	184	278	278	179	181
ZB	ZB_9	ZB_9_W1	182	184	166	186	278	286	179	179
ZB	ZB_9	ZB_9_W2	178	180	166	186	278	286	179	179
ZB	**ZB_9**	**ZB_9_W3**	**182**	**184**	**154**	**186**	**278**	**286**	**179**	**179**
ZB	ZB_9	ZB_9_W4	180	182	154	186	278	286	179	179
ZB	ZB_9	ZB_9_W5	180	182	154	186	278	286	179	179
ZB	ZB_9	ZB_9_S1	180	182	166	186	278	286	179	179
ZB	ZB_9	ZB_9_S2	182	184	166	186	278	286	179	179
ZB	ZB_9	ZB_9_S3	178	180	154	186	278	286	179	179
ZB	ZB_9	ZB_9_S4	178	182	154	186	278	286	179	179
ZB	ZB_9	ZB_9_S5	178	182	154	186	278	286	179	179
ZB	ZB_10	ZB_10_W1	176	180	162	186	278	286	179	181
ZB	ZB_10	ZB_10_W2	176	178	180	182	278	286	179	179
ZB	**ZB_10**	**ZB_10_W3**	**176**	**178**	**180**	**182**	**278**	**278**	**179**	**179**
ZB	ZB_10	ZB_10_W4	176	180	162	186	278	286	179	179
ZB	ZB_10	ZB_10_W5	176	180	180	182	278	286	179	181
ZB	ZB_10	ZB_10_S1	176	180	180	186	278	286	179	179
ZB	ZB_10	ZB_10_S2	180	180	162	186	278	286	179	179
ZB	ZB_10	ZB_10_S3	178	180	162	180	278	286	179	179
ZB	ZB_10	ZB_10_S4	178	180	162	186	278	286	179	179
ZB	ZB_10	ZB_10_S5	176	178	162	180	278	286	179	179
CA	CA_1	CA_1_W1	180	180	178	182	278	278	179	179
CA	CA_1	CA_1_W2	180	180	178	182	278	278	179	179
CA	**CA_1**	**CA_1_W3**	**178**	**180**	**178**	**186**	**278**	**278**	**179**	**179**
CA	CA_1	CA_1_W4	178	180	162	182	278	278	179	179
CA	CA_1	CA_1_W5	180	180	178	186	278	278	179	179

CA	CA_1	CA_1_S1	178	180	162	186	278	278	179	179
CA	CA_1	CA_1_S2	178	180	178	182	278	278	179	179
CA	CA_1	CA_1_S3	180	180	162	182	278	278	179	179
CA	CA_1	CA_1_S4	180	180	162	182	278	278	179	179
CA	CA_1	CA_1_S5	178	180	178	182	278	278	179	179
CA	CA_2	CA_2_W1	178	180	162	186	278	278	179	179
CA	CA_2	CA_2_W2	178	180	162	186	278	278	179	179
CA	**CA_2**	**CA_2_W3**	**178**	**178**	**162**	**186**	**278**	**278**	**179**	**179**
CA	CA_2	CA_2_W4	178	180	162	186	278	278	179	179
CA	CA_2	CA_2_W5	178	180	162	186	278	278	179	179
CA	CA_2	CA_2_S1	178	180	162	186	278	278	179	179
CA	CA_2	CA_2_S2	178	180	162	186	278	278	179	179
CA	CA_2	CA_2_S3	178	178	162	186	278	278	179	179
CA	CA_2	CA_2_S4	178	178	162	186	278	278	179	179
CA	CA_2	CA_2_S5	178	180	162	186	278	278	179	179
CA	CA_3	CA_3_W1	180	180	166	184	278	286	179	179
CA	CA_3	CA_3_W2	176	180	166	184	278	278	179	179
CA	**CA_3**	**CA_3_W3**	**180**	**180**	**162**	**184**	**278**	**278**	**179**	**179**
CA	CA_3	CA_3_W4	180	180	164	166	278	286	179	179
CA	CA_3	CA_3_W5	180	180	162	184	278	286	179	179
CA	CA_3	CA_3_S1	180	180	162	184	278	286	179	179
CA	CA_3	CA_3_S2	0	0	164	166	278	278	179	179
CA	CA_3	CA_3_S3	178	180	166	184	278	286	179	179
CA	CA_3	CA_3_S4	178	180	164	184	278	286	179	179
CA	CA_3	CA_3_S5	180	180	166	184	278	278	179	179
CA	CA_4	CA_4_W1	178	180	162	186	278	278	179	179
CA	CA_4	CA_4_W2	178	180	162	186	278	278	179	179
CA	**CA_4**	**CA_4_W3**	**178**	**180**	**162**	**188**	**278**	**278**	**179**	**179**
CA	CA_4	CA_4_W4	178	180	162	186	278	278	179	179
CA	CA_4	CA_4_W5	178	180	162	186	278	278	179	179
CA	CA_4	CA_4_S1	178	180	162	186	278	278	179	179
CA	CA_4	CA_4_S2	178	180	162	186	278	278	179	179
CA	CA_4	CA_4_S3	180	180	162	186	278	278	179	179
CA	CA_4	CA_4_S4	178	180	162	186	278	278	179	179
CA	CA_4	CA_4_S5	178	180	162	186	278	278	179	179
CA	CA_5	CA_5_W1	178	184	162	166	282	286	177	179
CA	CA_5	CA_5_W2	178	184	162	192	282	286	177	179
CA	**CA_5**	**CA_5_W3**	**178**	**184**	**164**	**166**	**278**	**278**	**177**	**179**
CA	CA_5	CA_5_W4	178	180	164	166	278	286	177	179
CA	CA_5	CA_5_W5	180	180	164	166	278	286	177	179
CA	CA_5	CA_5_S1	184	184	162	166	278	282	177	177

CA	CA_5	CA_5_S2	180	184	164	166	278	278	179	179
CA	CA_5	CA_5_S3	178	184	162	166	278	282	177	177
CA	CA_5	CA_5_S4	180	184	164	192	278	282	177	179
CA	CA_5	CA_5_S5	178	180	164	192	278	278	177	179
CA	CA_6	CA_6_W1	178	180	162	164	278	286	179	179
CA	CA_6	CA_6_W2	0	0	164	164	278	278	179	179
CA	**CA_6**	**CA_6_W3**	**178**	**180**	**164**	**164**	**278**	**286**	**179**	**179**
CA	CA_6	CA_6_W4	178	180	162	162	278	278	179	179
CA	CA_6	CA_6_W5	178	180	162	164	278	286	179	179
CA	CA_6	CA_6_S1	178	180	164	164	278	278	179	179
CA	CA_6	CA_6_S2	178	180	162	162	278	286	179	179
CA	CA_6	CA_6_S3	180	184	164	192	278	278	177	179
CA	CA_6	CA_6_S4	178	180	164	164	278	278	179	179
CA	CA_6	CA_6_S5	178	180	162	162	278	278	179	179
CA	CA_7	CA_7_W1	178	180	162	162	278	286	179	179
CA	CA_7	CA_7_W2	178	180	162	186	278	278	179	179
CA	**CA_7**	**CA_7_W3**	**180**	**180**	**164**	**186**	**278**	**278**	**179**	**179**
CA	CA_7	CA_7_W4	180	180	162	164	278	286	179	179
CA	CA_7	CA_7_W5	178	180	162	186	278	286	179	179
CA	CA_7	CA_7_S1	180	180	162	164	278	278	179	179
CA	CA_7	CA_7_S2	180	180	162	164	278	286	179	179
CA	CA_7	CA_7_S3	178	180	162	164	280	280	179	179
CA	CA_7	CA_7_S4	178	180	162	164	280	280	179	179
CA	CA_7	CA_7_S5	180	180	162	162	280	286	179	179
CA	CA_8	CA_8_W1	174	178	162	186	278	278	179	179
CA	CA_8	CA_8_W2	178	184	154	164	278	278	179	179
CA	**CA_8**	**CA_8_W3**	**178**	**184**	**154**	**164**	**278**	**278**	**179**	**179**
CA	CA_8	CA_8_W4	174	178	162	164	278	278	179	179
CA	CA_8	CA_8_W5	174	178	0	0	0	0	0	0
CA	CA_8	CA_8_S1	178	184	162	162	278	278	179	179
CA	CA_8	CA_8_S2	174	178	164	164	278	278	179	179
CA	CA_8	CA_8_S3	178	184	154	164	278	278	179	179
CA	CA_8	CA_8_S4	174	178	154	164	278	278	179	179
CA	CA_8	CA_8_S5	178	184	162	186	278	278	179	179
CA	CA_9	CA_9_W1	172	180	162	162	278	278	179	179
CA	CA_9	CA_9_W2	172	180	162	164	278	278	179	179
CA	**CA_9**	**CA_9_W3**	**172**	**180**	**162**	**162**	**278**	**278**	**179**	**179**
CA	CA_9	CA_9_W4	180	182	162	164	278	278	179	179
CA	CA_9	CA_9_W5	180	182	162	164	278	278	179	179
CA	CA_9	CA_9_S1	172	178	162	162	278	278	179	179
CA	CA_9	CA_9_S2	172	180	164	186	278	278	179	179

CA	CA_9	CA_9_S3	180	180	162	164	278	278	179	179
CA	CA_9	CA_9_S4	180	182	162	186	278	278	179	179
CA	CA_9	CA_9_S5	180	182	162	186	278	278	179	179
CA	CA_10	CA_10_W1	180	180	186	186	278	278	179	179
CA	CA_10	CA_10_W2	178	184	186	186	278	278	179	179
CA	**CA_10**	**CA_10_W3**	**180**	**184**	**186**	**186**	**278**	**278**	**179**	**179**
CA	CA_10	CA_10_W4	178	184	186	186	278	278	179	179
CA	CA_10	CA_10_W5	180	184	186	186	278	278	179	179
CA	CA_10	CA_10_S1	180	180	186	188	278	278	179	179
CA	CA_10	CA_10_S2	178	184	186	186	278	278	179	179
CA	CA_10	CA_10_S3	178	184	186	186	278	278	179	179
CA	CA_10	CA_10_S4	178	184	186	188	278	278	179	179
CA	CA_10	CA_10_S5	178	180	186	188	278	278	179	17 9

Table S3. Number of alleles and genotypes per colony of *E. neotenicus* from 14 Atlantic Forest fragments in Northeast Brazil (N_A – number of alleles; N_G – number of genotypes; F_{IC} – within-colony inbreeding coefficient; r_{nest} - average within-colony relatedness; FD – family design).

	En-08		**En-11**		**En-15**		**En-19**		F_{IC}	r_{nest}	FD
	N_A	N_G	N_A	N_G	N_A	N_G	N_A	N_G			
VV_1	2	3	3	4	2	2	1	1	-0.089	0.59	S
VV_2	3	3	4	3	2	2	1	1	-0.304	0.50	S
VV_3	2	3	3	3	2	2	1	1	-0.182	0.52	S
VV_4	2	1	3	4	2	2	1	1	-0.573	0.67	S
VV_5	4	4	4	4	2	2	1	1	-0.385	0.36	S
VV_6	3	4	3	2	2	3	1	1	-0.215	0.47	S
VV_7	3	3	3	2	2	2	1	1	-0.484	0.63	S
VV_8	2	3	4	3	1	1	2	2	-0.213	0.63	S
VV_9	2	3	4	5	2	2	2	2	-0.145	0.37	E
VV_10	2	3	2	2	2	3	1	1	-0.246	0.63	S
SH_1	2	2	2	2	2	1	2	2	-0.533	0.50	S
SH_2	2	3	3	4	2	3	1	1	-0.028	0.29	S
SH_3	4	6	2	2	2	2	2	3	-0.160	0.40	E
SH_4	3	2	4	4	1	1	1	1	-0.429	0.55	S
SH_5	2	3	3	4	2	3	1	1	0.000	0.40	S
SH_6	4	3	3	4	2	2	2	3	-0.113	0.10	S
SH_7	2	3	2	3	2	1	1	1	-0.336	0.60	S
SH_8	2	3	3	5	2	2	2	2	-0.022	0.37	E
SH_9	2	3	2	2	3	4	2	2	-0.052	0.34	S
SH_10	1	1	2	2	2	2	2	2	-0.179	0.81	S
VE_1	3	2	2	3	3	2	1	1	-0.290	0.43	S
VE_2	3	3	3	4	2	2	1	1	-0.322	0.43	S
VE_3	2	3	2	2	3	4	1	1	-0.156	0.46	S
VE_4	3	5	3	4	3	4	1	1	-0.127	0.38	E
VE_5	4	5	4	4	2	2	1	1	-0.195	0.32	E
VE_6	2	3	4	4	3	4	1	1	-0.153	0.40	S
VE_7	2	3	3	3	2	2	1	1	-0.231	0.57	S
VE_8	2	3	3	2	2	2	1	1	-0.509	0.62	S
VE_9	4	5	3	4	2	3	2	2	-0.150	0.25	E
VE_10	4	6	4	4	2	2	1	1	-0.294	0.40	E
CD_1	4	5	2	2	2	2	1	1	-0.077	0.66	E
CD_2	4	6	2	2	2	2	1	1	-0.241	0.60	E
CD_3	2	2	2	2	2	3	1	1	-0.357	0.57	S
CD_4	3	4	2	3	1	1	2	2	-0.121	0.49	S

CD_5	3	3	2	2	2	2	1	1	-0.244	0.48	S
CD_6	2	1	1	1	2	2	2	2	-0.535	0.84	S
CD_7	3	3	4	4	2	1	1	1	-0.420	0.40	S
CD_8	3	2	3	3	2	2	1	1	-0.545	0.62	S
CD_9	4	5	3	3	2	3	1	1	-0.154	0.40	E
CD_10	3	4	2	2	1	1	1	1	0.036	0.85	S
DD_1	3	3	3	2	2	1	1	1	-0.347	0.46	S
DD_2	4	5	4	3	2	2	1	1	-0.331	0.27	E
DD_3	3	4	2	3	2	2	1	1	0.020	0.57	S
DD_4	3	2	2	2	2	2	1	1	-0.389	0.71	S
DD_5	2	2	3	4	3	3	1	1	-0.357	0.42	S
DD_6	2	2	4	4	2	2	2	2	-0.328	0.49	S
DD_7	3	5	4	4	2	2	1	1	0.008	0.35	E
DD_8	2	3	3	4	3	3	2	2	0.006	0.35	S
DD_9	4	5	4	5	2	2	1	1	-0.245	0.35	E
DD_10	2	2	4	3	2	2	1	1	-0.325	0.57	S
CH_1	2	3	3	4	2	2	2	2	-0.250	0.39	S
CH_2	3	3	3	2	2	2	1	1	-0.481	0.68	S
CH_3	2	2	3	3	2	3	2	2	-0.333	0.49	S
CH_4	3	4	3	4	4	5	2	2	-0.140	0.12	E
CH_5	2	3	4	4	2	2	2	2	-0.250	0.32	S
CH_6	3	2	3	2	2	2	1	1	-0.610	0.59	S
CH_7	3	4	4	4	1	1	2	2	-0.286	0.54	S
CH_8	2	3	3	3	1	1	1	1	-0.228	0.68	S
CH_9	3	3	3	4	2	2	2	2	-0.390	0.29	S
CH_10	4	4	3	5	2	2	1	1	-0.275	0.30	E
VC_1	3	3	3	3	2	1	1	1	-0.586	0.43	S
VC_2	3	3	3	2	4	4	2	2	-0.467	0.28	S
VC_3	4	4	4	5	1	1	1	1	-0.244	0.55	E
VC_4	3	2	3	4	3	3	1	1	-0.354	0.48	S
VC_5	3	5	3	3	2	2	2	2	-0.341	0.30	E
VC_6	3	3	3	4	2	2	1	1	-0.130	0.47	S
VC_7	2	3	2	2	2	2	1	1	-0.205	0.53	S
VC_8	1	1	3	2	2	3	1	1	-0.348	0.70	S
VC_9	2	3	3	4	2	3	2	2	-0.289	0.50	S
VC_10	3	4	3	3	1	1	1	1	-0.297	0.72	S
VA_1	4	6	2	3	2	3	2	2	0.055	0.23	E
VA_2	2	2	2	2	2	2	2	2	-0.428	0.61	S
VA_3	2	2	4	5	4	3	2	2	-0.217	0.33	E
VA_4	4	4	3	4	3	4	2	2	-0.122	0.12	S
VA_5	3	3	4	4	2	2	1	1	-0.038	0.26	S

VA_6	2	2	4	4	2	2	1	1	-0.375	0.60	S
VA_7	4	4	1	1	2	2	2	2	-0.158	0.73	S
VA_8	2	2	4	4	2	3	2	2	-0.296	0.37	S
VA_9	3	4	2	2	2	3	1	1	-0.283	0.64	S
VA_10	4	5	4	4	2	3	1	1	-0.180	0.25	E
PC_1	3	2	4	5	2	2	1	1	-0.481	0.38	E
PC_2	4	4	2	3	2	2	1	1	-0.350	0.50	S
PC_3	2	3	4	3	2	2	1	1	-0.154	0.54	S
PC_4	2	3	4	6	2	3	2	2	0.136	0.28	E
PC_5	2	2	3	4	1	1	1	1	-0.494	0.77	S
PC_6	3	4	3	5	2	2	2	2	-0.065	0.52	E
PC_7	3	3	3	4	2	3	1	1	-0.142	0.49	S
PC_8	3	5	1	1	2	3	1	1	0.110	0.63	E
PC_9	4	6	3	3	2	2	1	1	0.000	0.26	E
PC_10	2	2	4	3	2	2	2	2	-0.267	0.49	S
PD_1	3	3	3	3	2	2	1	1	-0.261	0.47	S
PD_2	4	4	4	4	1	1	1	1	-0.287	0.67	S
PD_3	3	2	4	5	2	1	1	1	-0.219	0.24	E
PD_4	4	4	3	4	2	2	2	2	-0.165	0.45	S
PD_5	3	4	4	5	2	3	1	1	0.031	0.22	E
PD_6	2	2	3	3	1	1	1	1	-0.309	0.73	S
PD_7	3	5	3	4	1	1	1	1	-0.014	0.66	E
PD_8	3	4	2	2	2	2	1	1	-0.242	0.63	S
PD_9	5	6	4	4	2	2	1	1	-0.231	0.20	M
PD_10	2	3	4	4	2	2	2	2	-0.187	0.30	S
VDD_1	2	3	3	4	2	2	3	3	0.000	0.40	S
VDD_2	3	3	3	3	2	2	1	1	-0.323	0.50	S
VDD_3	3	3	4	4	2	2	1	1	-0.286	0.50	S
VDD_4	4	5	4	4	2	1	1	1	-0.447	0.51	E
VDD_5	3	3	2	2	2	2	2	2	-0.456	0.48	S
VDD_6	2	3	2	2	2	2	2	2	-0.395	0.61	S
VDD_7	4	4	4	5	1	1	1	1	-0.236	0.55	E
VDD_8	3	3	3	3	2	2	3	3	-0.355	0.26	S
VDD_9	3	4	2	2	1	1	2	2	-0.274	0.67	S
VDD_10	2	2	4	5	1	1	1	1	-0.095	0.73	E
MC_1	3	3	4	4	1	1	2	2	-0.245	0.42	S
MC_2	2	3	3	3	1	1	1	1	-0.364	0.73	S
MC_3	3	3	3	4	1	1	1	1	-0.274	0.69	S
MC_4	4	4	3	4	2	2	1	1	-0.381	0.44	S
MC_5	3	4	2	2	2	2	1	1	-0.493	0.71	S
MC_6	4	5	2	2	2	1	2	2	-0.365	0.35	E

MC_7	4	5	3	2	2	3	1	1	-0.305	0.41	E
MC_8	3	4	2	2	2	2	1	1	-0.306	0.70	S
MC_9	4	4	2	2	4	5	1	1	-0.261	0.47	E
MC_10	3	4	4	5	2	3	1	1	-0.082	0.37	E
ZB_1	2	2	3	3	2	2	1	1	-0.414	0.54	S
ZB_2	2	2	4	3	2	2	1	1	-0.489	0.60	S
ZB_3	4	5	2	3	2	2	1	1	-0.299	0.43	E
ZB_4	3	4	5	5	2	1	1	1	-0.513	0.48	M
ZB_5	3	4	3	4	2	2	1	1	-0.051	0.44	S
ZB_6	2	3	4	3	1	1	1	1	-0.013	0.52	S
ZB_7	3	5	4	2	2	2	1	1	-0.244	0.55	E
ZB_8	4	4	4	5	1	1	2	2	-0.356	0.39	E
ZB_9	4	4	3	2	2	1	1	1	-0.602	0.53	S
ZB_10	3	4	4	4	2	2	2	2	-0.410	0.20	S
CA_1	2	2	4	4	1	1	1	1	-0.317	0.67	S
CA_2	2	2	2	1	1	1	1	1	-0.759	0.9	S
CA_3	3	3	4	4	2	2	1	1	-0.323	0.49	S
CA_4	2	2	3	2	1	1	1	1	-0.809	0.90	S
CA_5	3	5	4	4	3	4	2	3	-0.244	0.11	E
CA_6	3	2	3	4	2	2	2	2	-0.125	0.36	S
CA_7	2	2	3	4	3	4	1	1	-0.084	0.35	S
CA_8	3	2	4	5	1	1	1	1	-0.294	0.57	E
CA_9	4	4	3	4	1	1	1	1	-0.288	0.61	S
CA_10	3	4	2	2	1	1	1	1	-0.144	0.72	S

Table S4. Private alleles by population of *E. neotenicus* from 14 Atlantic Forest fragments in Northeast Brazil.

Population	*Locus*	*Allele*	*Frequency*
VV	En-11	174	0.030
VV	En-11	194	0.030
CD	En-11	172	0.030
DD	En-15	274	0.005
CH	En-08	170	0.027
VC	En-15	292	0.036
VDD	En-11	170	0.025
ZB	En-11	156	0.030
ZB	En-11	198	0.086

Table S5. Pairwise F_{ST} (below the diagonal) and probability (above diagonal) values by population of *E. neotenicus* from 14 Atlantic Forest fragments in Northeast Brazil.

	DD	*PC*	*CH*	*VA*	*VE*	*SH*	*VDD*	*VC*	*CA*	*ZB*	*CD*	*PD*	*VV*	*MC*
DD	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
PC	0.022	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
CH	0.030	0.029	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
VA	0.031	0.047	0.026	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
VE	0.019	0.033	0.047	0.050	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
SH	0.042	0.037	0.014	0.033	0.062	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
VDD	0.026	0.027	0.037	0.053	0.038	0.038	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001
VC	0.037	0.025	0.046	0.080	0.041	0.048	0.038	0	0.001	0.001	0.001	0.001	0.001	0.001
CA	0.065	0.051	0.072	0.117	0.069	0.074	0.038	0.038	0	0.001	0.001	0.001	0.001	0.001
ZB	0.033	0.028	0.050	0.071	0.035	0.066	0.031	0.038	0.040	0	0.001	0.001	0.001	0.001
CD	0.043	0.035	0.033	0.055	0.045	0.038	0.054	0.024	0.073	0.055	0	0.001	0.001	0.001
PD	0.026	0.017	0.028	0.056	0.036	0.028	0.010	0.027	0.031	0.026	0.039	0	0.001	0.001
VV	0.039	0.030	0.044	0.055	0.050	0.064	0.060	0.062	0.111	0.068	0.066	0.053	0	0.001
MC	0.020	0.009	0.023	0.051	0.025	0.028	0.023	0.017	0.037	0.024	0.025	0.008	0.040	0

Fig. 1. A – Location of the study area. Dark gray - Atlantic Forest; B - Atlantic Forest fragments of the Usina São José, Igarassu, Pernambuco, Brazil. Light gray - Atlantic Forest fragments sampled.

Fig. S1. Relation between pairwise F_{ST} and geographical distance (km) for *E. neotenicus* populations from 14 fragments of the Atlantic Forest in Northeast Brazil.

Fig. S2. Genetic structure analysis of *E. neotenicus* populations from 14 fragments of the Atlantic Forest in Northeast Brazil based on one individual per colony and four microsatellite loci. A - The most likely *K* value corresponds to the uppermost hierarchical level among runs. B **-** Population genetic structure as inferred using the Bayesian clustering algorithm in STRUCTURE for *K*=7. The colored segments represent the proportion of each genetic cluster. The identification of populations is indicated above.

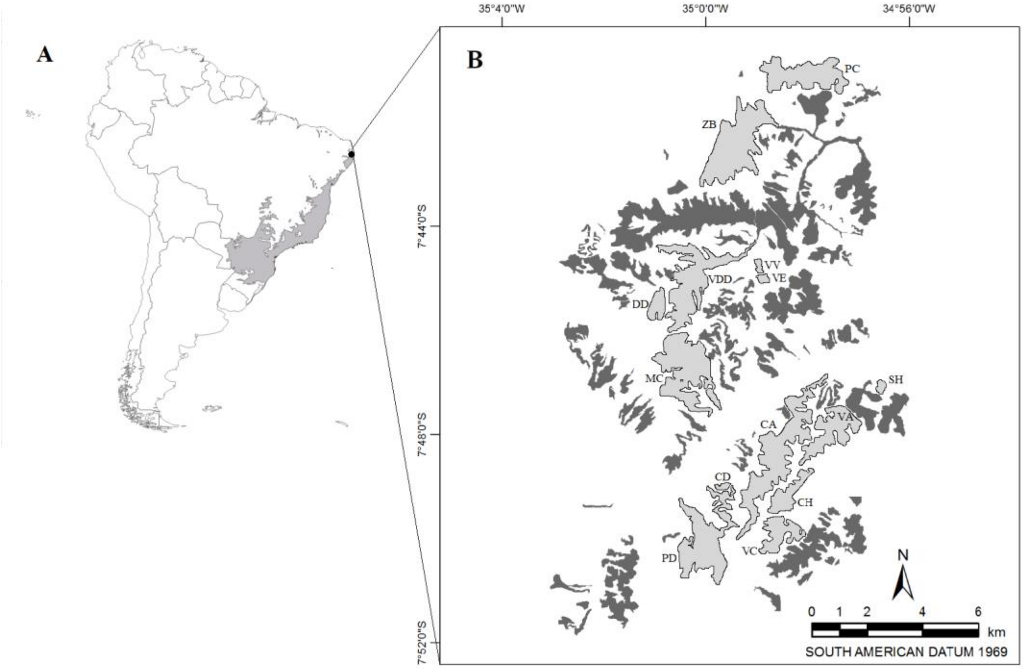
A
B
35°4'0"W
35°0'0"W
34°56'0"W
7°44'0"S
7°48'0"S
7°52'0"S
PC
ZB
VV
VDD
VE
DD
MC
SH
CA
VA
CD
CH
VC
PD
N
0
1
2
4
6
km
SOUTH AMERICAN DATUM 1969

Fig. 1

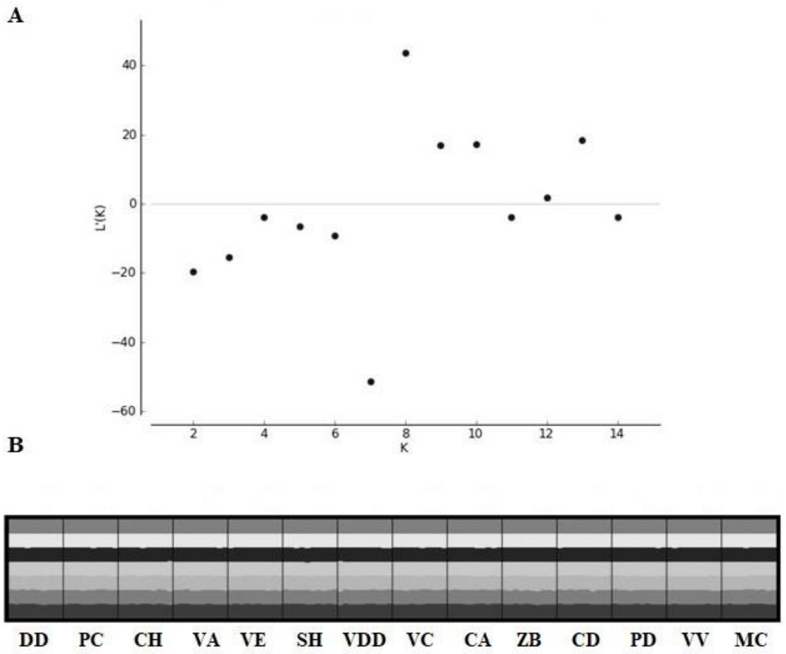
A
40
20
0
−20
−40
−60
L'(K)
2
4
6
8
10
12
14
K
B
DD
PC
CH
VA
VE
SH
VDD
VC
CA
ZB
CD
PD
VV
MC

Fig. S1

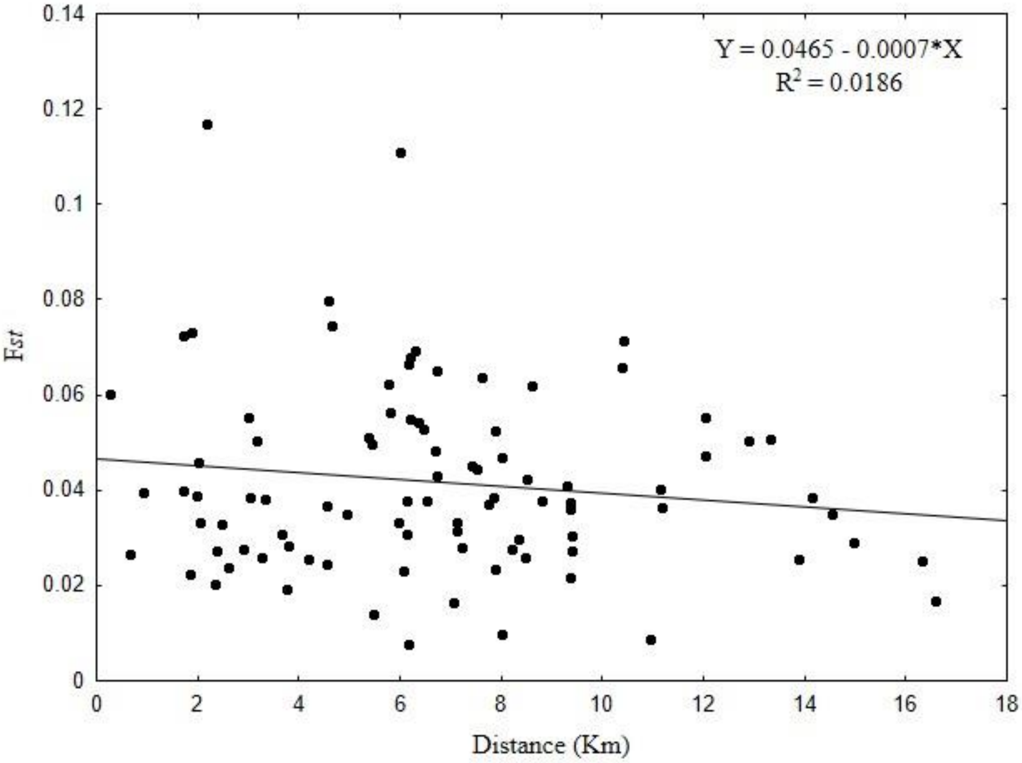
Y = 0.0465 - 0.0007*X
R^2 = 0.0186
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
F*st*
0
2
4
6
8
10
12
14
16
18
Distance (Km)

Fig. S2