

Additional file 1 of 1

Supplementary Information

Figure S1 - Best-k for Bayesian clustering analysis of EF1a SNP data of *Pyura chilensis*

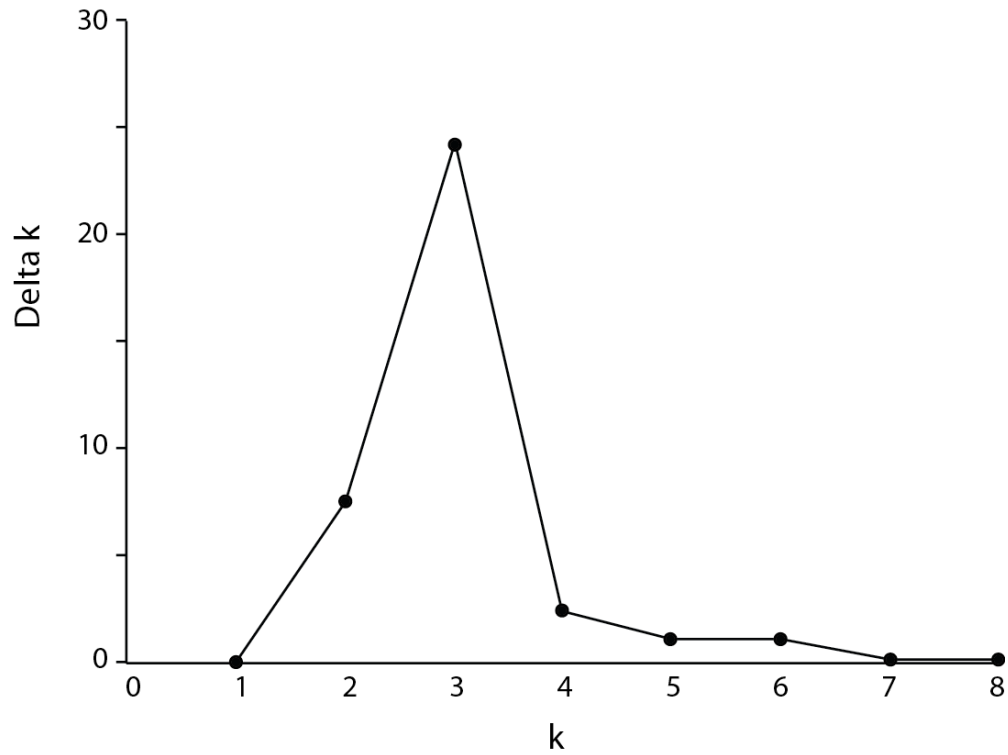


Figure S2 – Number of individuals of each COI haplogroup of *Pyura chilensis* assigned with highest probability to each of the three Bayesian k-clusters.

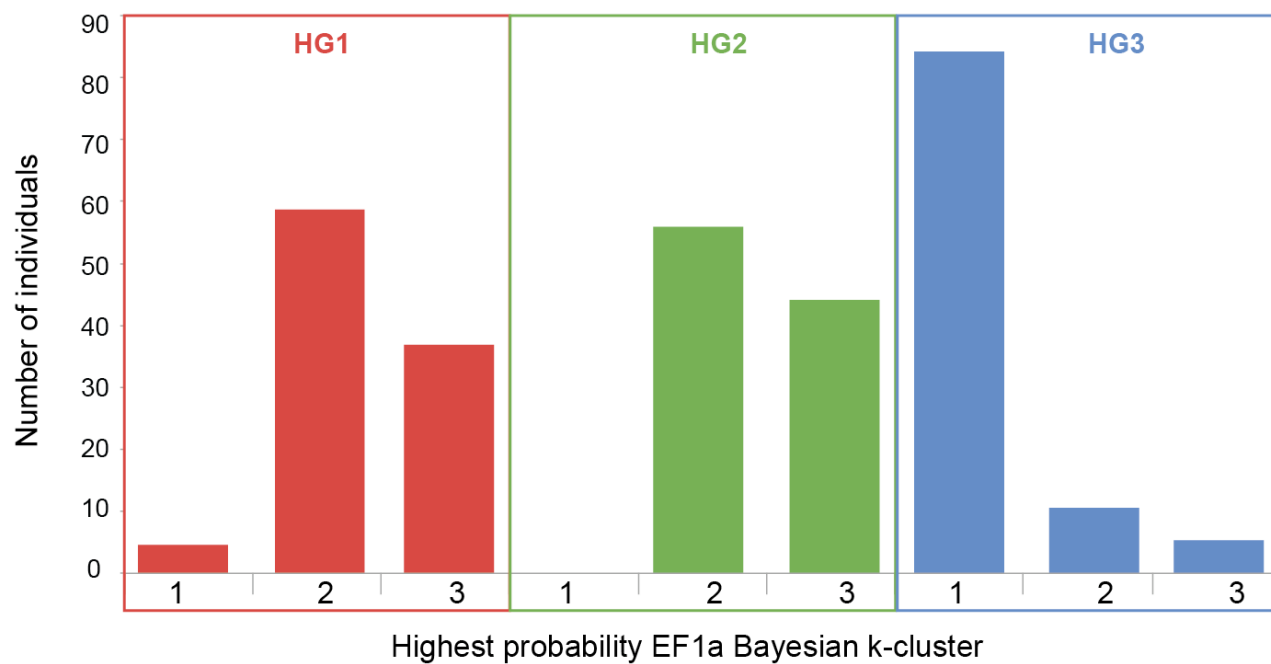


Figure S3 - Geographic distribution of the diversity of three COI haplogroups and EF1a haplotypes of *Pyura chilensis*

COI haplotypes are shown organized per haplogroup (HG1-HG3) and EF1a data corresponds to haplotypes generated with Phase. Portions in white represent haplotypes unique to one site; colors represent each haplotype and their frequency is proportional to the number of individuals that bared it.

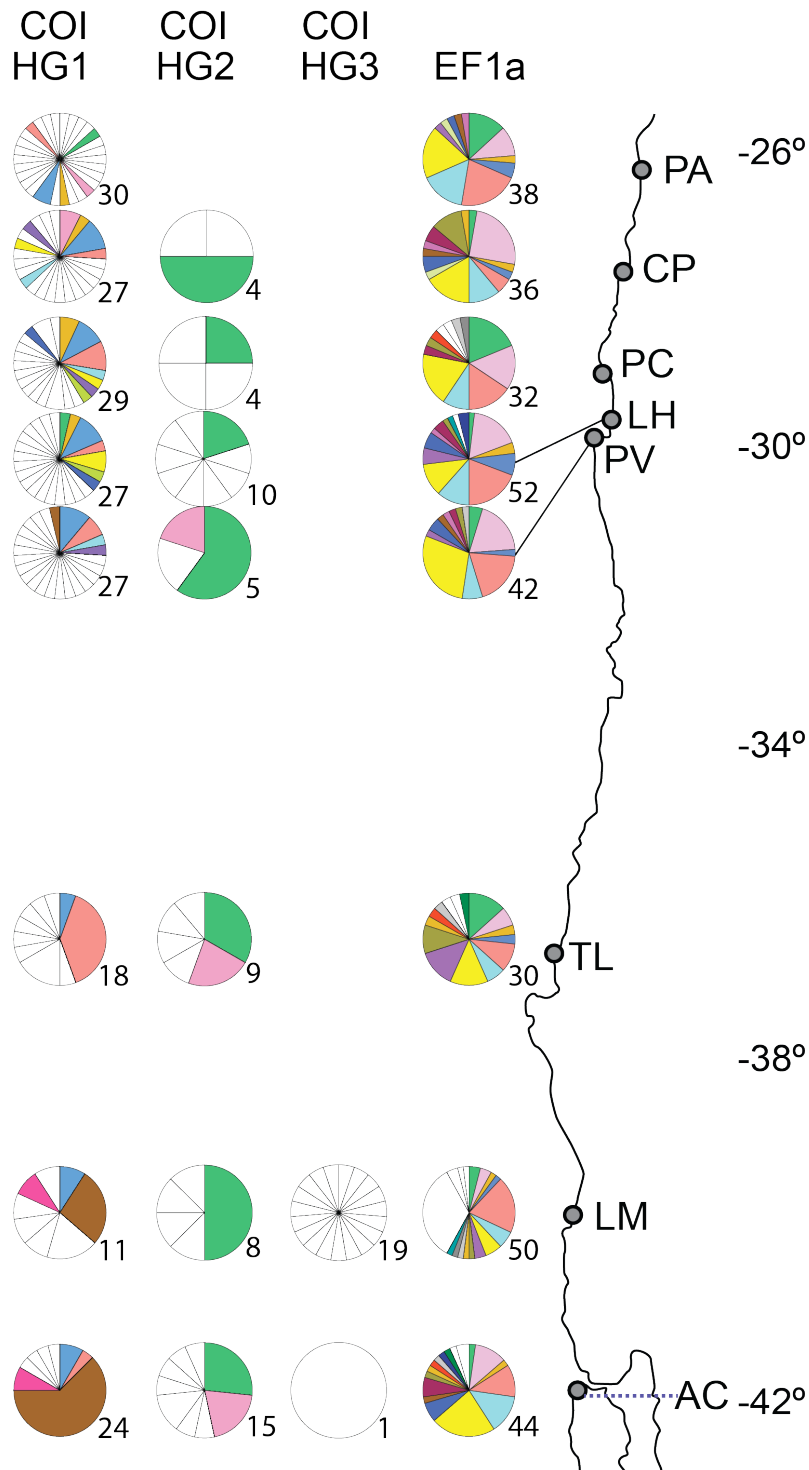


Figure S4 - Mismatch frequency distributions of COI haplogroups and EF1a haplotypes of *Pyura chilensis*

Number of observed (bars) and expected (lines) pairwise differences between sequences under a geographic expansion model.

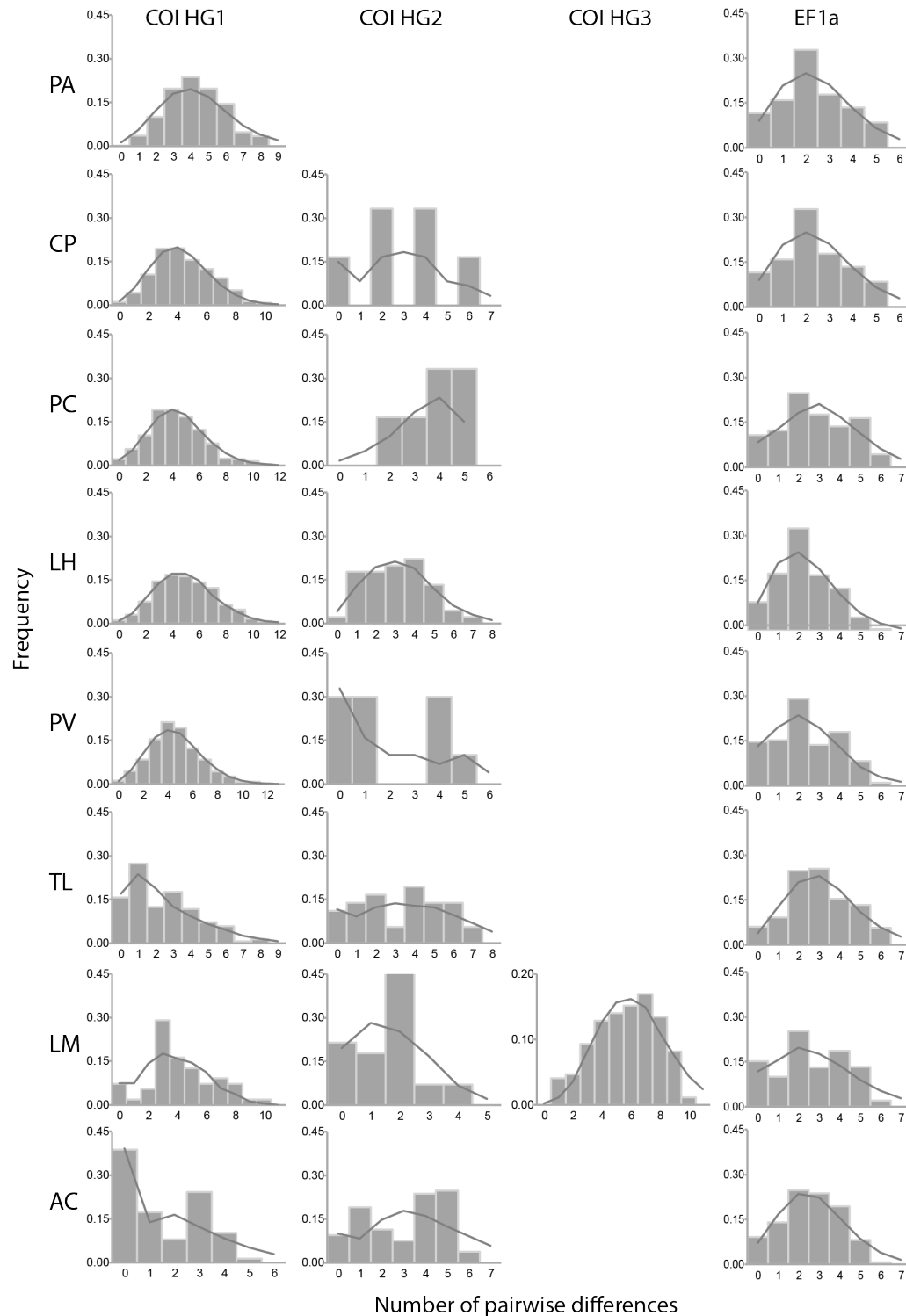
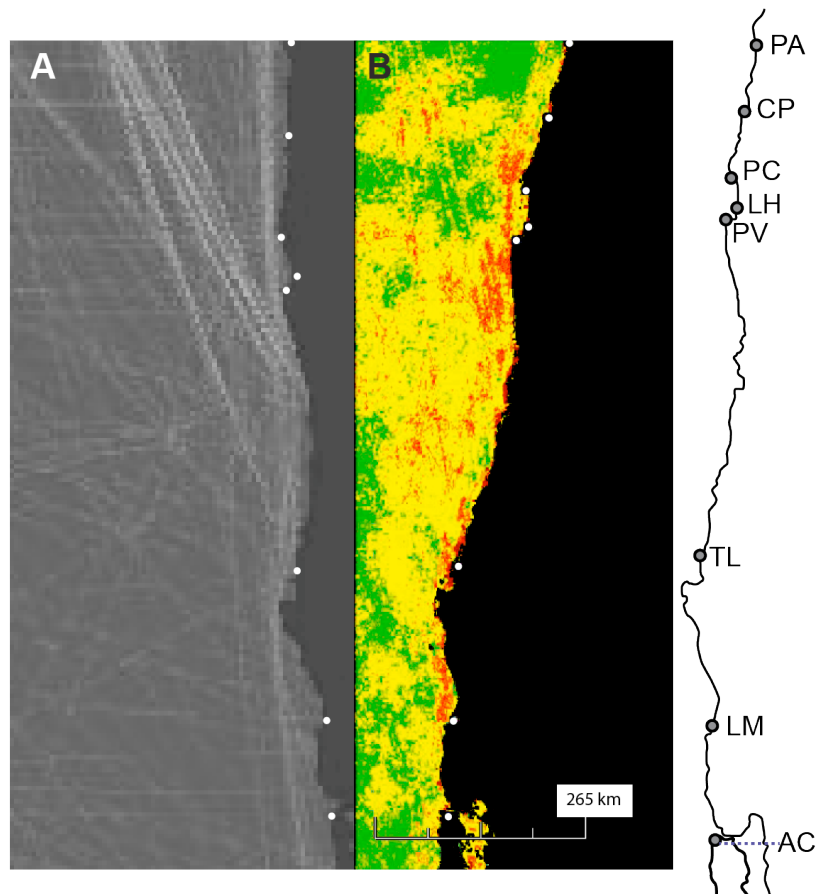


Figure S5 - Maps of marine transport and human impact on the study area

A) Marine commercial activity (shipping) map modified after the downloadable worldwide version of provided at <http://www.nceas.ucsb.edu/globalmarine/impacts> (Halpern et al. 2008). B) Map of the model of Halpern et al. (2008) of global map of human impact on marine ecosystems, modified in Google Earth after the open access version of the model (<http://www.nceas.ucsb.edu/globalmarine/models>). White dots represent sampling sites.



REFERENCE:

Halpern B, Walbridge S, Selkoe KA, Kappel CV, Micheli F, D'Agrosa C, Bruno JF, Casey KS, Ebert C, Fox HE, et al.: **A global map of human impact on marine ecosystems.** *Science* 2008, **319**:948–952

Table S1 - Locus by locus probability of Hardy-Weinberg equilibrium for EF1a SNPs of *Pyura chilensis*.

Significant departures after Bonferroni correction in bold ($P < 0.05$).

	PA	CP	PC	LH	PV	TL	LM	AC
EF1a52	0.898	0.914	0.635	0.831	0.810	0.004	0.868	0.900
EF1a58	0.440	0.586	0.464	0.526	0.733	0.790	0.003	0.431
EF1a113	M	0.909	0.865	0.900	M	M	0.007	M
EF1a114	M	M	M	M	M	M	0.008	M
EF1a115	0.621	0.919	0.495	0.01	0.398	0.854	0.004	0.171
EF1a136	0.323	0.231	0.115	0.552	0.619	0.863	0.005	0.722
EF1a169	0.873	0.509	0.890	0.677	0.785	0.855	0.006	0.747
EF1a184	0.560	0.571	0.256	0.903	0.396	0.197	0.319	0.950
EF1a271	0.171	0.911	0.811	0.003	0.724	0.341	0.191	0.790

Table S2 - Locus by locus F_{IS} inbreeding coefficients for EF1a SNPs of *Pyura chilensis*

Significant values in bold.

	PA	CP	PC	LH	PV	TL	LM	AC
EF1a52	0.000	-0.057	-0.073	-0.018	-0.021	0.618	-0.094	0.037
EF1a58	-0.125	-0.083	-0.128	-0.098	-0.043	-0.030	0.478	-0.130
EF1a113	NA	0.000	0.000	0.000	NA	NA	0.805	NA
EF1a114	NA	NA	NA	NA	NA	NA	0.863	NA
EF1a115	-0.071	0.034	-0.117	0.456	-0.147	0.000	0.507	-0.242
EF1a136	0.201	-0.209	0.343	0.125	-0.076	0.064	0.721	-0.047
EF1a169	0.000	-0.106	0.000	-0.057	-0.021	0.064	0.178	-0.040
EF1a184	-0.089	0.125	0.254	0.028	0.186	0.325	-0.154	0.019
EF1a271	-0.237	0.003	-0.023	0.563	-0.047	0.247	0.242	0.066
All	-0.089	-0.029	0.060	0.233	-0.019	0.195	0.476	-0.050

Table S3 - Pairwise multi-locus F_{ST} for EF1a SNPs of *Pyura chilensis*
Significant values in bold ($P < 0.05$).

	PA	CP	PC	LH	PV	TL	LM
PA							
CP	0.05248						
PC	-0.00014	0.01542					
LH	0.01595	0.01004	0.00934				
PV	-0.00898	0.01943	-0.01311	0.00609			
TL	0.02002	0.03403	-0.00049	0.03528	0.00262		
LM	0.1471	0.15236	0.14322	0.11485	0.14456	0.14842	
AC	0.02026	-0.00039	-0.00944	0.00401	0.00066	0.00584	0.13826

Table S4 - SAMOVA groupings for COI haplogroups and EF1a haplotypes of *Pyura chilensis*

	<i>K</i>	2	3	4	5	6	7
ALL COI	F_{CT}	0.449	0.340	0.284	0.259	0.247	0.236
	<i>P</i>	0.124	0.042	0.019	0.012	0.019	0.032
	Groups	1. LM	1. LM	1. LM	1. LM	1. LM	1. LM
		2. rest	2. PA	2. TA	2. PA	2. PA	2. PA
			3. rest	3. AC	3. TA	3. TA	3. TA
				4. rest	4. AC	4. AC	4. AC
					5. rest	5. LH	5. LH
						6. rest	6. PV
							7. CP,PC
COI HG1	F_{CT}	0.105	0.078	0.061	0.049	0.044	0.043
	<i>P</i>	0.122	0.036	0.018	0.016	0.005	0.028
	Groups	1. AC	1. AC	1. AC	1. AC	1. AC	1. AC
		2. rest	2. LM	2. LM	2. LM	2. LM	2. LM
			3. rest	3. TA	3. TA	3. TA	3. TA
				4. rest	4. LH	4. LH	4. LH
					5. rest	5. PA,LV	5. PA
						6. CP,PC	6. LV
							7. CP,PV
COI HG2	F_{CT}	0.053	0.058	0.068	0.086	0.084	-
	<i>P</i>	0.140	0.042	0.005	0.022	0.065	-
	Groups	1. LM	1. LM	1. LM	1. LM	1. LM	
		2. rest	2. PC	2. PC	2. PC	2. PC	
			3. rest	3. CP,LH	3. TA	3. TA	
				4. rest	4. AC	4. AC	
					5. rest	5. LH	
						6. PV,TA	
ALL EF1a	F_{CT}	0.075	0.061	0.053	0.048	0.046	0.049
	<i>P</i>	0.123	0.046	0.014	0.002	0.025	0.049
	Groups	1. LM	1. LM	1. LM	1. LM	1. LM	1. LM
		2. rest	2. PA,CP	2. CP	2. CP	2. CP	2. CP
			3. rest	3. TL	3. TL	3. TL	3. TL
				4. rest	4. LH,AC	4. LH	4. LH
					5. rest	5. AC	5. AC
						6. rest	6. PA
							6. PC,PV

Table S5 - Signals of past demographic events and estimated times of expansion of two COI haplogroups of *Pyura chilensis*

Sum of square deviation of the mismatch frequency distribution of the number of pairwise nucleotide differences (SDD); probability associated to SDD ($P(\text{SDD})$); Harpending's raggedness index (r); probability associated to r ($P(r)$). Values of SDD and r calculated for mismatch distribution expectations according to the demographic expansion model and the geographic expansion model. Approximate coalescent time (τ); lower (τ_{lb}) and upper (τ_{ub}) boundaries calculated with the percentile method based on 1000 bootstrap replicates at $\alpha = 0.05$; estimated time of expansion in million years calculated with a mutation rate of $1.5\% \text{ Mya}^{-1}$ ($t_{\text{exp-1.5}}$); estimated time of expansion in million years was calculated with a mutation rate of $3\% \text{ Mya}^{-1}$ ($t_{\text{exp-3}}$); confidence limit of expansion time, lower boundary (CL_{lb}); confidence limit of expansion time, upper boundary (CL_{ub}).

Model		COI HG1 Northern sites	COI HG2
Demographic expansion	SDD	0.00029	0.00550
	$P(\text{SDD})$	0.53000	0.64000
	r	0.01669	0.01801
	$P(r)$	0.39000	0.88000
	τ	4.557	3.854
	τ_{lb}	3.555	0.486
	τ_{ub}	5.182	7.592
	$t_{\text{exp-1.5}}$	0.247	0.209
	$\text{CL}_{\text{lb-1.5}}$	0.193	0.026
	$\text{CL}_{\text{ub-1.5}}$	0.281	0.412
	$t_{\text{exp-3}}$	0.124	0.105
	$\text{CL}_{\text{lb-3}}$	0.096	0.013
	$\text{CL}_{\text{ub-3}}$	0.141	0.206
Geographic expansion	SDD	0.00028	0.00771
	$P(\text{SDD})$	0.61000	0.64000
	r	0.01669	0.01801
	$P(r)$	0.42000	0.92000
	τ	4.560	2.545
	τ_{lb}	2.822	0.745
	τ_{ub}	5.358	5.484
	$t_{\text{exp-1.5}}$	0.248	0.138
	$\text{CL}_{\text{lb-1.5}}$	0.153	0.040
	$\text{CL}_{\text{ub-1.5}}$	0.291	0.298
	$t_{\text{exp-3}}$	0.124	0.069
	$\text{CL}_{\text{lb-3}}$	0.077	0.020
	$\text{CL}_{\text{ub-3}}$	0.145	0.149