

Population structure and individual movement of southern right whales around New Zealand and Australia

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Supplement. Additional information on the definition of southern right whale mitochondrial control region haplotypes in the context of other studies (Tables S1 & S2). We also provide details on the microsatellite genotype matches between the 2 New Zealand calving grounds (Table S4) and provide microsatellite allele frequency data on a region and stock level (Table S5)

Table S1. *Eubalaena australis*. Polymorphic sites for mitochondrial control region found in the southern right whale. Three different frames of reference for the base pair positions of polymorphic sites have been given, corresponding to: 1. Portway (1998), 2. Baker et al. (1999), 3. Malik et al. (2000). Patenaude & Harcourt (2006), Carroll (2006) and Patenaude et al. (2007) use the same frame of reference as Baker et al. (1999) and Rosenbaum et al. (2000) uses a similar frame of reference to Baker et al. (1999). As Malik et al. (2000) aligned their sequences with the bowhead whale *Balaena mysticetus*, there is an apparent indel event in comparison with other publications. However, this indel event only occurs in comparison to the bowhead whale, and not within the right whale haplotypes. As some of these data (Portway 1998, Baker et al. 1999, Patenaude & Harcourt 2006 and Patenaude et al. 2007) were obtained from tables of polymorphic sites from the respective publications, there was not base information for every polymorphic site listed in this table. The sites missing (in relation to the Ref 2 reference frame) for Portway (1998) were 7, 18, 33, 66 and 69. For Baker et al. (1999) they were 18, 58, 59, 64, 65, 66, 81, 93, 111, 114, 144, 225, 236, 248, 255, 265 and 266. For Patenaude & Harcourt (2006) they were 58, 59, 64, 65, 66, 81, 93, 114, 144, 236, 248, 255, 265, 266 and 271. For Patenaude et al. (2007), the only polymorphic site without information is at 18 bp. The largest number of sequences with a variant at these sites was 3, so the missing bases were assumed to correspond to BakHapA (as defined by Carroll 2006) for the purposes of this table. Numbering differs from the associated publication (Baker et al. 1999, Carroll 2006) by 1 bp owing to an insertion in haplotype SHeaY relative to all other haplotypes.

References for base pair positions	1 2 3	26 7 80	36 17 90	38 19 92	53 34 107	78 59 132	79 60 133	80 61 134	84 65 138	85 66 139	86 67 140	87 68 141	88 69 142	89 70 143	96 77 150	97 78 151	101 82 155	104 85 158	105 86 159	112 93 166	
Haplotype	Ref																				
BakHapA	2	A	-	A	A	A	T	C	T	A	A	T	T	C	G	T	C	T	G	G	
BakHapA+	2	G	.	.	G
BakHapB	2	C	C	T	A	.	
BakHapC	2	C	.	.	.	C	.	C	.	.	
BakHapD	2	T	.	.	.	C	.	.	A	C	.	C	.	.	
BakHapE	2	T	C	.	C	A	.	
BakHapF	2	T	C	.	C	A	A	
CarHapJ	5	T	C	A	.	
MalHapF	3	C	A	.	
PatBakHapC	6	C	.	C	.	.	
PatHap01	6	C	
PatHap02	6	C	
PatHap03	6	C	
PatHap04	6	C	
PatHap05	6	C	C	A	.	
PatHap06	6	C	C	
PatHap07	6	C	C	A	.	
PatHap08	6	T	C	C	A	.	
PatHap09	6	T	C	C	
PatHap10	6	T	C	C	A	.	
PatHap11	6	T	C	C	A	.	
PatHap12	6	C	C	C	.	A	C	.	C	.	
PatHap13	6	C	.	.	.	C	.	C	.	
PatHap14	6	C	.	C	A	.	
PatHap15	6	C	A	.	
PatHap16	6	C	.	.	A	.	
PatHap17	6	C	A	.	
PatHap18	6	C	.	.	A	C	.	C	.	.	
PatHap19	6	C	C	.	.	
PatHap21	6	T	.	.	.	C	.	.	.	C	T	C	A	A	
PatHap22	6	G	.	T	C	G	.	C	C	A	.	

PatHap23	6	T	.	.	.	C	C	A	.
PatHap24	6	T	C
PatHap25	6	C	.	.	A	.
PatHap26	6	C	C
PatHap27	6	C	C
PatHap28	6	C	C	.	.	.	C	A
PatMalHapA	6	G	.	C	C	A	.
PatMalHapB	6	C	C
PorHap21	1	C
SHeaY	7	.	A	.	.	.	T	C	.	C	A	.
SWPI	4 ^a	.	.	T	.	.	T	C	A	.
SWPJ	4 ^a	T	.	.	.	C	.	.	C	.	C	A	A

Table S1 continued

References	1	113	131	134	144	164	207	229	245	247	252	256	259	266	268	275	285	286	287	291	293	
for base pair	2	94	112	115	125	145	188	210	226	228	233	237	240	247	249	256	266	267	268	272	274	
positions	3	167	185	188	198	219	262	284	300	302	307	311	314	321	323	330	340	341	342	346	348	
Haplotype	Ref																					
BakHapA	2	G	T	T	C	C	T	T	T	A	G	A	A	C	T	A	A	C	C	T	T	
BakHapA+	2
BakHapB	2
BakHapC	2	.	.	.	T	.	C	C	.	G	A	.	G	T	
BakHapD	2	.	.	.	T	.	C	C	.	.	A	.	G	T	.	.	
BakHapE	2	.	.	.	T	.	C	C	.	G	A	.	G	
BakHapF	2	.	.	.	T	.	C	C	.	G	A	.	G	T	C	
CarHapJ	5	.	C	C	C	
MalHapF	3	.	.	C	T	.	C	C	.	G	A	.	G	T	T	.	C	
PatBakHapC	6	.	.	.	T	.	C	C	.	G	A	.	G	T	
PatHap01	6	T	.	C	
PatHap02	6	C	
PatHap03	6	.	C	C	
PatHap04	6	
PatHap05	6	C	
PatHap06	6	
PatHap07	6	T	.	C	
PatHap08	6	C	
PatHap09	6	C	C	
PatHap10	6	C	.	.	.	G	
PatHap11	6	C	
PatHap12	6	.	.	.	T	.	.	C	.	G	A	.	G	T	.	.	
PatHap13	6	.	.	.	T	.	C	C	.	G	A	.	G	.	.	.	G	.	T	.	.	
PatHap14	6	.	.	.	T	.	C	C	.	G	A	.	G	T	T	.	.	
PatHap15	6	.	.	C	T	.	C	C	.	G	A	.	G	.	C	.	.	T	T	.	C	
PatHap16	6	.	.	.	T	.	C	C	.	G	A	.	G	T	T	.	.	
PatHap17	6	.	.	.	T	.	C	C	C	G	A	.	G	T	
PatHap18	6	.	.	.	T	.	C	C	.	.	A	.	G	T	.	.	
PatHap19	6	.	.	C	T	.	C	C	.	G	A	.	G	T	T	.	C	
PatHap21	6	.	.	.	T	.	C	C	.	G	A	.	G	T	.	G	C	
PatHap22	6	A	.	.	T	.	C	C	.	G	A	.	G	

PatHap23	6	A	.	.	T	.	C	C	.	G	A	.	G
PatHap24	6	C
PatHap25	6	.	.	.	T	.	C	C	.	G	A	.	G	.	.	.	G	.	T	C
PatHap26	6	C
PatHap27	6	.	.	C	T	.	C	C	.	G	A	.	G	T	T	C
PatHap28	6	.	.	C	T	.	.	C	.	G	A	.	G	T	T	.
PatMalHapA	6	T	.	C
PatMalHapB	6
PorHap21	1	C	C
SHeaY	7	.	.	.	T	.	C	C	.	G	A	.	G
SWPI	4 ^a	.	C	C
SWPJ	4 ^a	.	.	.	T	.	C	C	.	G	A	.	G	T	T	C

^aIt is assumed that these haplotypes have a C at site 67, rather than a T, as in Patenaude & Harcourt (2006); T is listed as a variable site for SWPD in relation to the other haplotypes

Table S2. *Eubalaena australis*. Synonyms from different publications for each of those haplotypes presented in Table S1. Haplotypes are named with the same label as the oldest publication that defined them, with a couple of exceptions: haplotypes other than Portway's (1998), denoted by PorHap##, which were defined differently in the Patenaude et al. (2007) paper compared with the original publication, have been given the prefix 'Pat' in front of the original code, e.g. PatBakHapC, PatMalHapA. To reflect the number of inconsistencies between the Patenaude et al. (2007) definition of Portway's (1998) haplotypes, and how they were originally defined by Portway (1998), the haplotypes coded PorHap## in Patenaude et al. (2007) and Carroll (2006) have been renamed PatHap## in this table. Beside each haplotype or synonym is a number denoting the reference that the haplotype was taken from: 1. Portway (1998), 2. Baker et al. (1999), 3. Malik et al. (2000), 4. Patenaude & Harcourt (2006), 5. Carroll (2006), 6. Patenaude et al. (2007), 7. Rosenbaum et al. (2000). PorHap26 is highlighted in orange as this haplotype has not been verified from the original source

Haplotype	Ref	Synonym	Ref	Synonym	Ref	Synonym	Ref	Synonym	Ref	Synonym	Ref		
BakHapA	2			SHeaV	7			SWPA	4 ^a	BakHapA	5	BakHapA	6
BakHapA+	2							SWPA+	4 ^a			BakHapA+	6
BakHapB	2			SHeaU	7			SWPB	4 ^a	BakHapB	5	BakHapB	6
BakHapC	2			SHeaZ	7			SWPC	4 ^a	BakHapC	5		
BakHapD	2							SWPD	4	BakHapD	5	BakHapD	
BakHapE	2	PorHap10	1	SHeaX	7	MalHapG	3	SWPE	4 ^a	BakHapE	5	BakHapE	6
BakHapF	2							SWPF	4 ^a			BakHapF	
CarHapJ	5												
MalHapF	3											MalHapF	6
PatBakHapC	6												
PatHap01	6	PorHap09	1										
PatHap02	6	PorHap16	1			MalHapC/D	3 ^b						
PatHap03	6	PorHap17	1										
PatHap04	6	PorHap12	1	SHeaT	7	MalHapB	3			PatHap4.1/4.2	5		
PatHap05	6	PorHap18	1										
PatHap06	6	PorHap19	1										
PatHap07	6	PorHap20	1			MalHapA	3						
PatHap08	6	PorHap08	1										
PatHap09	6												
PatHap10	6	PorHap07	1										
PatHap11	6	PorHap11	1										
PatHap12	6	PorHap22	1										
PatHap13	6	PorHap01	1										
PatHap14	6	PorHap14	1			MalHapH	3						
PatHap15	6	PorHap23	1										
PatHap16	6	PorHap13	1										

PatHap17	6	PorHap02	1			SWPK	4 ^a	PatHap17	5
PatHap18	6	PorHap15	1	MalHapJ	3				
PatHap19	6	PorHap03	1						
PatHap21	6	PorHap04	1						
PatHap22	6	PorHap05	1	MalHapI	3				
PatHap23	6	PorHap06	1						
PatHap24	6	PorHap24	1	MalHapE	3				
PatHap25	6	PorHap25	1						
PatHap26	6	PorHap26	1						
PatHap27	6								
PatHap28	6								
PatMalHapA	6								
PatMalHapB	6								
PorHap21	1								
SHeaY	7								
SWPI	4 ^a								
SWPJ	4 ^a								

^aIt is assumed that these haplotypes have a C at site 67, rather than a T, as in Patenaude & Harcourt (2006); T is listed as a variable site for SWPD in relation to the other haplotypes

^bNot resolved over 289 bp

Table S3. *Eubalaena australis*. Thirteen microsatellite loci used for genotyping of southern right whales. Primer sequences and repeats units from the reference are indicated. TA is the annealing temperature, mM Mg is the concentration of magnesium used in the reactions. Each 10 μ l PCR reaction contained 1 \times PCR buffer, MgCl₂ at concentration specified below, 0.4 μ M each primer, 0.2 mM dNTPs, 0.25 units thermostable Platinum *Taq* DNA polymerase (Invitrogen) and 10 to 20 ng μ l⁻¹ DNA template. The PCR reactions have cycling conditions of (1) an initial denaturing step at 94°C for 3 min; (2) 30 cycles at 94°C for 30 s, TA for 30 s and 72°C for 30 s; and (3) a final extension step at 72°C for 10 min

Locus	Primers	Label	TA (°C)	mM Mg	Repeat Unit	Reference
RW31	F: TATTCATGGAGTGCTTTGG R: CCTAGAGTCCAGTGTGGTA	FAM	54	2.0	(TG)n	Waldick et al. (1999)
RW48	F: CCAATGACTTTTCCCTGTA R: GATACCGCAGTGTGCTCTG	NED	50	2.5	(TG)n	Waldick et al. (1999)
RW410	F: ATGGCATTACTTCATTCTTT R: GCCAAACTTACCAAATTGTG	VIC	50	2.5	(GT)n	Waldick et al. (1999)
RW18	F: AGAGGGAAGCAAAGTGG R: GAAGGNTGCCAGACACCC	FAM	60	2.5	(TG)TA(TG)n	Waldick et al. (1999)
GATA28	F: AAAGACTGAGATCTATAGTTA R: CGCTGATAGATTAGTCTAGG	NED	50	2.5	(GATA)n	Palsbøll et al. (1997)
GATA98	F: TGTACCCTGGATGGATAGATT R: ATGTCTCTCTCACACCTCACC	VIC	50	2.5	(GATA)n	Palsbøll et al. (1997)
TR3G1	F: CTCCGCAACAAGAGAGGC R: CTTCTGGGTACAAGCCC	FAM	A ^a	2.5	(GATA)n	Frasier et al. (2006)
TR3G2	F: CTGCGGTGTTGGTTAATAGC R: CCTGACATTTTCTGTGTCCC	VIC	50	2.5	(GATA)n	Frasier et al. (2006)
TR3F4	F: TGCTCTGCAACAAGAGAAGC R: GCCAAGGTTTTAGAGAGAGTG	FAM	59	2.0	(GATA)n	Frasier et al. (2006)
EV1	F: CCCTGCTCCCCATTCTC R: ATAAACTCTAATACACITCCTCCAAC	NED	60	2.5	(AC)n	Valsecchi & Amos (1996)
EV37	F: AGCTTGATTTGGAAGTCATGA R: TAGTAGAGCCGTGATAAAGTGC	NED	54	2.5	(AC)n	Valsecchi & Amos (1996)
EV14	F: TAAACATCAAAGCAGACCCC R: CCAGAGCCAAGGTCAAGAG	VIC	51	2.5	(GT)n	Valsecchi & Amos (1996)
GT23	F: GTTCCCAGGCTCTGCACTCTG R: CATTTCTACCCACCTGTCAT	VIC	58	2.0	(GT)n	Bérubé et al. (2000)

^aThe letter A indicates this primer pair had a touchdown PCR protocol; for the cycling, each annealing temperature is used for 5 cycles before stepping down to the next annealing temperature; the final annealing temperature is used for 10 cycles, resulting in a total of 30 cycles. Annealing temperatures are 68°C, 64°C, 61°C, 58°C and 55°C

Table S4. *Eubalaena australis*. Genetic profiles of southern right whales sampled at both the New Zealand (NZ) subantarctic and mainland NZ calving grounds. Profiles consist of mtDNA control region haplotype (500 bp, mtDNA), genetically identified sex and microsatellite genotype. Dashed lines indicate the sample was not successfully genotyped at that locus. For each match, the probability of identity (PID; Paetkau & Strobeck 1994) and number of matching loci is listed (N loci match)

Sample code	Sex	mtDNA	PID/ N loci match	EV1	EV 14	EV3 7	GAT A 28	GAT A 98	GT2 3	RW 18	RW 31	RW 410	RW 48	TR3 F4	TR3 G1	TR3 G2
Eau03NZ03	M	BakHapB'	1.10E	124/ 126	122/ 135	189/ 199	166/ 180	116/ 116	-/-	199/ 217	125/ 125	195/ 203	118/ 120	301/ 305	222/ 222	168/ 184
Eau06AI068	M	BakHapB'	- 12/11	124/ 126	122/ 135	189/ 199	166/ 180	116/ 116	114/ 116	199/ 217	125/ 125	195/ 203	118/ 120	301/ 305	-/-	168/ 184
Eau03NZ04	F	BakHapB+	5.64E	126/ 144	133/ 137	189/ 201	166/ 166	112/ 116	-/-	187/ 199	117/ 125	205/ 209	118/ 120	301/ 305	-/-	176/ 184
Eau06AI035	F	BakHapB+	- 14/11	126/ 144	133/ 137	189/ 201	166/ 166	112/ 116	116/ 116	187/ 199	117/ 125	-/-	118/ 120	301/ 305	-/-	176/ 184
Eau05NZ05	F	BakHapA	4.51E	138/ 142	133/ 133	203/ 207	174/ 178	112/ 116	-/-	193/ 231	121/ 123	195/ 211	118/ 126	333/ 333	230/ 238	176/ 180
Eau07AI050	F	BakHapA	- 18/12	138/ 142	133/ 133	203/ 207	174/ 178	112/ 116	110/ 120	193/ 231	121/ 123	195/ 211	118/ 126	333/ 333	230/ 238	176/ 180
Eau07NZ04	F	BakHapB+	9.93E	122/ 126	133/ 133	199/ 205	166/ 178	112/ 112	-/-	193/ 195	123/ 125	203/ 209	118/ 124	301/ 329	206/ 206	172/ 184
Eau08AI043	F	BakHapB+	- 15/12	122/ 126	133/ 133	199/ 205	166/ 178	112/ 112	118/ 120	193/ 195	123/ 125	203/ 209	118/ 124	301/ 329	206/ 206	172/ 184
U09090	F	BakHapC	1.37E	132/ 136	-/-	199/ 207	174/ 178	112/ 116	112/ 112	187/ 199	123/ 123	199/ 211	108/ 146	333/ 337	202/ 222	180/ 184
Eau07AI038	F	BakHapC	- 19/10	132/ 136	-/-	199/ 207	-/-	-/-	112/ 112	187/ 199	123/ 123	199/ 211	108/ 146	333/ 337	202/ 222	180/ 184
U09141	F	BakHapA	1.10E	-/-	122/ 133	-/-	174/ 178	104/ 120	-/-	193/ 209	117/ 125	-/-	118/ 122	301/ 301	222/ 222	172/ 176
Eau07AI172	F	BakHapA	-12/9	136/ 140	122/ 133	193/ 195	174/ 178	104/ 120	114/ 114	193/ 209	117/ 125	195/ 201	118/ 122	301/ 301	222/ 222	172/ 176
U09148	M	BakHapB+	1.92E	126/ 126	133/ 133	187/ 191	178/ 178	112/ 112	112/ 116	195/ 195	123/ 125	203/ 207	118/ 124	305/ 305	234/ 238	176/ 180
Eau06AI100	M	BakHapB+	- 17/13	126/ 126	133/ 133	187/ 191	178/ 178	112/ 112	112/ 116	195/ 195	123/ 125	203/ 207	118/ 124	305/ 305	234/ 238	176/ 180

Table S5. *Eubalaena australis*. Microsatellite diversity of southern right whale calving grounds and one migratory corridor across NZ and Australia. NZSA and MNZ are pooled for NZ data set, VIC and NSW (not shown here due to small sample size, 2N = 8) are pooled for SEA data set, and SA and WA are pooled for SWA data set (for location abbreviations see Table 1). The following indices are listed by loci: k , number of alleles; H_o , observed heterozygosity; H_e , expected heterozygosity. Allelic richness is calculated over all loci (AR). *indicates that this locus is out of Hardy-Weinberg equilibrium

Locus	NZSA	MNZ	VIC	SA	WA	SEA	SWA	NZ
EV1								
2N	1080	76	18	38	26	26	64	1146
Size range	118–158	122–148	120–148	122–148	122–148	120–148	122–148	118–158
k	17	14	10	13	11	12	13	17
H_o	0.88	0.89	0.78	0.79	1.00	0.85	0.88	0.88
H_e	0.87	0.85	0.86	0.91	0.83	0.90	0.88	0.87
EV14								
2N	984	54	18	40	2	26	42	1030
Size range	120–147	120–143	122–141	122–147	131–133	120–141	122–147	120–147
k	14	10	7	8	2	8	8	14
H_o	0.79	0.74	0.89	0.85	1.00	0.77	0.86	0.79
H_e	0.78	0.75	0.88	0.80	1.00	0.82	0.80	0.78
EV37								
2N	1054	76	16	40	24	24	64	1120
Size range	187–207	187–207	193–207	187–207	185–207	189–207	185–207	187–207
k	11	11	6	10	9	9	11	11
H_o	0.84	0.89	0.76	0.85	0.92	0.83	0.88	0.84
H_e	0.87	0.85	0.73	0.85	0.80	0.85	0.83	0.87
GATA28								
2N	1048	78	16	40	26	24	66	1128
Size range	162–186	162–186	162–178	162–178	162–186	162–178	162–186	162–186
k	10	7	6	5	6	6	6	10
H_o	0.79	0.74	0.88	0.90	0.62	0.92	0.80	0.79
H_e	0.78	0.74	0.80	0.77	0.69	0.76	0.75	0.77
GATA98								
2N	1068	78	18	40	26	24	66	1138
Size range	104–140	104–124	104–120	104–124	108–120	104–120	104–124	104–140
k	8	6	5	6	4	5	6	8

H_o	0.67	0.82	0.88	0.70	0.69	0.83	0.70	0.68
H_e	0.71	0.79	0.80	0.80	0.70	0.77	0.77	0.72
GT23								
2N	1048	22	18	32	26	26	58	1068
Size range	106–120	105–116	108–120	110–120	106–120	108–120	106–120	106–120
k	8	5	7	6	7	7	7	8
H_o	0.82	0.73	1.00	0.88	0.77	1	0.83	0.82
H_e	0.82	0.79	0.87	0.83	0.81	0.84	0.81	0.82
RW18								
2N	992	76	18	34	26	26	60	1058
Size range	187–245	187–241	187–217	187–239	187–239	187–231	187–239	187–245
k	20	12	6	10	7	8	11	20
H_o	0.82	0.76	0.89	0.71	0.85	0.85	0.77	0.82
H_e	0.82	0.83	0.82	0.82	0.77	0.81	0.80	0.82
RW31								
2N	1086	78	18	42	26	26	68	1154
Size range	117–137	117–137	117–127	117–127	117–131	117–127	117–131	117–137
k	10	6	5	5	7	5	7	10
H_o	0.72	0.72	0.56	0.71	0.77	0.70	0.74	0.72
H_e	0.70	0.68	0.61	0.70	0.78	0.76	0.73	0.70
RW410								
2N	1106	74	16	38	26	24	64	1170
Size range	187–211	191–211	197–211	191–211	191–211	195–211	191–211	187–211
k	13	9	5	8	9	7	10	13
H_o	0.88	0.87	0.63	0.79	0.77	0.67	0.78	0.88
H_e	0.87	0.88	0.84	0.86	0.87	0.84	0.86	0.87
RW48								
2N	1030	74	18	40	26	24	66	1094
Size range	106–146	108–146	108–126	106–120	108–146	108–126	106–146	106–146
k	10	7	6	7	7	6	8	10
H_o	0.85	0.79	0.78	0.70	0.92	0.75	0.79	0.84
H_e	0.82	0.80	0.84	0.82	0.80	0.83	0.82	0.81
TR3F4								
2N	1062	74	18	38	26	26	64	1126
Size range	301–353	301–353	301–333	301–345	301–337	301–333	301–345	301–353

k	18	14	7	12	8	7	12	18
H_o	0.85	0.84	0.89	0.84	0.85	0.92	0.84	0.85
H_e	0.85	0.83	0.86	0.89	0.87	0.86	0.88	0.85
TR3G1								
2N	954	72	16	42	24	24	66	1018
Size range	202–250	202–250	210–242	202–242	206–238	206–242	202–242	202–250
k	13	12	7	10	6	10	11	13
H_o	0.63	0.67	1.00	0.76	0.42	0.83	0.64	0.63
H_e	0.84*	0.86	0.88	0.85	0.73	0.92	0.81	0.84
TR3G2								
2N	1088	76	18	42	26	26	66	1154
Size range	168–188	168–188	168–184	168–188	168–184	168–184	168–188	168–188
k	6	6	5	6	5	5	6	6
H_o	0.78	0.87	0.89	0.85	0.85	0.92	0.85	0.78
H_e	0.78	0.79	0.84	0.78	0.73	0.82	0.75	0.78
All Loci								
Mean 2N	1046	70	17	39	24	26	62	1108
Overall AR	6.8	6.8	6.3	6.9	6.2	6.9	6.7	6.8
Mean k	12.07	9.29	6.14	8.29	6.93	7.31	8.9	12.07
Mean H_o	0.79	0.80	0.83	0.80	0.80	0.83	0.79	0.79
Mean H_e	0.81	0.81	0.81	0.83	0.80	0.83	0.81	0.81

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