Supplementary Material

Rapid morphological divergence following a human-mediated introduction: The role of drift and directional selection

Library preparation

100 ng of genomic DNA from each individual was digested with 2.4 U of restriction enzyme SbfI-HF (New-England Biolabs Inc., Beverly MA, USA) at 37_oC for 60 minutes, followed by an inactivation step of 80_oC for 20 minutes. BestRAD Sbf1 adapters were then ligated to the overhanging ends of the products of the restriction reactions by adding 50 nM to each sample with 320 U T4 DNA Ligase (New-England Biolabs Inc.). Barcoding of samples was achieved with a set of index nucleotides within the BestRAD Sbf1 adapter sequences. Reactions were incubated at 20_°C for 16 hours and then heat-inactivated by holding at 65°C for 20 minutes. The reactions were then pooled, cleaned with AMPure XP beads, and the products randomly sheared to a mean size of 500 bp by sonication, using a BioRuptor NGS (Diagenode). Following sonication, Dynabeads M-280 streptavidin magnetic beads (Life Technologies) were used to bind the biotinylated ends of the BestRAD Sbf1 adaptors. Sbf1-HF was used once more to release adapter bound fragments and AMPure XP beads were used to clean the samples. After the bead clean up, ends were treated with Blunt End-Repair Mix found in the NEBNext Ultra DNA Library Prep Kit (New-England Biolabs Inc.) to remove overhangs. NEBNext Adaptors for Illumina sequencing were then ligated to blunt ends following a twostep incubation; first incubated at 20_oC for 15 minutes with Blunt/TA Ligase Master Mix (New-England Biolabs Inc.) and then at 37°C for 15 minutes with USER Enzyme (New-England Biolabs Inc.). Following size selection using AMPure XP beads to isolate fragments within the size range 300-700 bp, the library was PCR enriched using 10 uM of P1 index primer and 10 uM of Universal PCR Primer (NEB). First a test PCR was run using 5 ul of DNA with 15 PCR cycles. Depending on the brightness of the band produced, the final PCR cycle number was adjusted from 9-12 cycles. PCR products were cleaned using AMPure XP beads. Libraries were sequenced on three Illumina HiSeq4000 lanes (Illumina, San Diego, CA, USA) at the UC Davis Genome Center using paired-end 150-bp sequence reads.

Table S1: Principal components analysis of morphological data. Coefficients of correlation between morphological variables and the derived principal components extracted by principal components analysis.

Mannhalagical trait	Factor loadings					
Morphological trait	PC1	PC2				
Wing length	0.265	0.719				
Tail length	0.487	0.429				
Tarsus length	0.297	-				
Culmen length (P)	0.525	-0.419				
Culmen depth (A)	0.571	-0.284				
Culmen width (A)	-	0.182				
Variance explained	29.38%	21.75%				

Table S2: Explained variance (% of total variance) of PC1 and PC2 from principle component analysis of morphological traits. Also shown are results from ANOVAs of PC scores. The differences in mean PC scores between South Island (New Zealand) silvereyes and French Polynesian silvereyes were explored using Turkey's post-hoc tests. Statistical significance is indicated by asterisks: *** P < 0.001; ** P < 0.01; * P < 0.05; NS = non-significant.

Explained		ANOVA		Difference from SNZ						
PC Axis	Variance (%)	F 6, 441	P-value	All FP	TAH	MOO	HUA	RAI	MAU	
PC1	29.38	28.59	< 0.001	1.67***	1.77***	1.70***	1.10**	1.89***	1.38***	
PC2	21.75	10.66	< 0.001	-0.93***	-0.73**	-1.163***	-0.33 NS	-0.91**	-1.01**	

Table S3: Known, novel or predicted genes occurring within 10kb of outlier SNPs identified, using *PCAdapt*, between New Zealand and French Polynesian islands. Population codes as follows: NZ = South Island, New Zealand; FP = all French Polynesian islands; TAH = Tahiti, MOO = Mo'orea; HUA = Huahine; RAI = Raiatea; MAU = Maupiti.

Gene stable ID	Gene description	Gene start (bp)	Gene end (bp)	Chromosome	Gene name	NZ vs.
ENSTGUG00000006887	dystrophin	9154708	10148444	1	DMD	HUA
ENSTGUG00000010796		35582832	35585680	1		HUA
ENSTGUG00000010849	KDEL motif containing 1	37962335	37970867	1	KDELC1	RAI
ENSTGUG00000011664		49704389	49861236	1		MOO
ENSTGUG00000011735	FRY microtubule binding protein	50626080	50796176	1	FRY	HUA
ENSTGUG00000011967	FRAS1 related extracellular matrix protein 2	53819513	53939566	1	FREM2	HUA
ENSTGUG00000012117	Taeniopygia guttata SPRY domain containing 7 (SPRYD7), mRNA	55948726	55958266	1	SPRYD7	MOO
ENSTGUG00000012422	mitochondrial translation release factor 1	59579943	59591090	1	MTRF1	HUA
ENSTGUG00000012549		69793105	69992841	1		MOO
ENSTGUG00000013001	asparaginyl-tRNA synthetase 2, mitochondrial	86711122	86758565	1	NARS2	TAH
ENSTGUG00000013496	EPH receptor A6	101653625	102054107	1	EPHA6	RAI
ENSTGUG00000000764	zinc finger MYND-type containing 11	10897250	11003676	2	ZMYND11	HUA
ENSTGUG00000001094	mohawk homeobox	17223251	17392565	2	MKX	HUA
ENSTGUG00000001311	cubilin	21974685	22109468	2	CUBN	RAI
ENSTGUG00000001501	VPS50, EARP/GARPII complex subunit	25251229	25335000	2	VPS50	MAU
ENSTGUG00000004189	NIMA related kinase 11	62221688	62308845	2	NEK11	HUA
ENSTGUG00000004894	transglutaminase 4	64731646	64741764	2	TGM4	MOO
ENSTGUG00000007906	von Willebrand factor C domain containing 2	85435608	85489383	2	VWC2	HUA
ENSTGUG00000008631		93799185	93925718	2		HUA
ENSTGUG00000010074		106598017	106623803	2		RAI
ENSTGUG00000011815	Taeniopygia guttata 2,4-dienoyl-CoA reductase 1 (DECR1), mRNA	130703700	130717968	2	DECR1	HUA

ENSTGUG00000011869	pyruvate dehyrogenase phosphatase catalytic subunit 1	132302035	132307232	2	PDP1	HUA
ENSTGUG00000011966	phosphatidylserine synthase 1	133397397	133422104	2	PTDSS1	HUA
ENSTGUG00000011987	lysosomal protein transmembrane 4 beta	133895664	133963069	2	LAPTM4B	HUA
ENSTGUG00000011992	matrilin 2	134004617	134048324	2	MATN2	HUA
ENSTGUG00000012027	odd-skipped related transciption factor 2	134428506	134431204	2	OSR2	HUA
ENSTGUG00000012030	vacuolar protein sorting 13 homolog B	134494587	134931563	2	VPS13B	HUA
ENSTGUG00000012148	collagen triple helix repeat containing 1	136194280	136200691	2	CTHRC1	HUA
ENSTGUG00000003612	pleckstrin homology, MyTH4 and FERM domain containing H2	16425219	16471280	3	PLEKHH2	MAU
ENSTGUG00000010902	ARFGEF family member 3	50723474	50824543	3	ARFGEF3	ТАН
ENSTGUG00000011615	monooxygenase DBH like 1	59131319	59181152	3	MOXD1	HUA
ENSTGUG00000011773		61861362	61921523	3		HUA
ENSTGUG00000012218	blood vessel epicardial substance	71122911	71252155	3	BVES	HUA
ENSTGUG00000013229	phospholipase A2 group VII	108349385	108357841	3	PLA2G7	HUA
ENSTGUG00000002514		10348610	10684047	4		HUA
ENSTGUG00000004549		25456400	25591830	4		HUA
ENSTGUG00000005716	catalase	6271419	6285186	5	CAT	MOO
ENSTGUG00000005980	lysine demethylase 2A	6538590	6567985	5	KDM2A	HUA
ENSTGUG00000006012	G protein-coupled receptor kinase 2	6571621	6577897	5	GRK2	HUA
ENSTGUG00000006094	ankyrin repeat domain 13D	6582669	6585026	5	ANKRD13D	HUA
ENSTGUG00000008025		8537039	8729742	5		HUA
ENSTGUG00000009146	nucleosome assembly protein 1 like 4	12881930	13003509	5	NAP1L4	HUA
ENSTGUG00000012373	thyroid stimulating hormone receptor	41137345	41175645	5	TSHR	HUA
ENSTGUG00000012820	REST corepressor 1	51054854	51135675	5	RCOR1	HUA
ENSTGUG00000012959	protein phosphatase 2 regulatory subunit B'epsilon	55239178	55306635	5	PPP2R5E	HUA
ENSTGUG00000013194	valosin containing protein lysine methyltransferase	60520695	60523997	5	VCPKMT	HUA

ENSTGUG00000004487	C-type lectin domain family 2 member B-like	3175115	3314084	6		HUA
ENSTGUG00000004592	phosphatase domain containing paladin 1	3250009	3269651	6	PALD1	HUA
ENSTGUG00000007660	SEC31 homolog B, COPII coat complex component	16443466	16474660	6	SEC31B	MOO
ENSTGUG00000007917		16864802	16865718	6		MOO
ENSTGUG00000003583		2408013	2681518	7		HUA
ENSTGUG00000004748	contactin associated protein like 5	7834568	8039714	7	CNTNAP5	RAI
ENSTGUG00000007152		13113900	13170539	7		HUA, TAH
ENSTGUG00000007262	cysteine and serine rich nuclear protein 3	13252086	13272166	7	CSRNP3	MOO
ENSTGUG00000007583	ceramide synthase 6	13965237	14081484	7	CERS6	HUA
ENSTGUG00000010653		23648780	23744147	7		MAU
ENSTGUG00000011260	lanosterol synthase	28607527	28615834	7	LSS	HUA, MOO
ENSTGUG00000011322		28963908	29034843	7		HUA, MAU, TAH
ENSTGUG00000011444	carbamoyl-phosphate synthase 1	29360824	29444139	7	CPS1	MAU
ENSTGUG00000003826		2916739	2967087	8		HUA
ENSTGUG00000018373	zinc finger and BTB domain containing 37	3334159	3339163	8	ZBTB37	HUA
ENSTGUG00000005495	dihydropyrimidine dehydrogenase	8944758	9180702	8	DPYD	MAU
ENSTGUG00000006332	Taeniopygia guttata selenoprotein F (SELENOF), mRNA	12485119	12513156	8	SELENOF	RAI
ENSTGUG00000006382		12638237	12741483	8		HUA
ENSTGUG00000007625	ring finger protein 220	17464143	17689061	8	RNF220	HUA
ENSTGUG00000009063	zyg-11 family member A, cell cycle regulator	22081785	22093628	8	ZYG11A	MAU
ENSTGUG00000009700	hook microtubule tethering protein 1	24544351	24566662	8		MAU
ENSTGUG00000009745	nuclear factor I A	24945852	25164582	8	NFIA	HUA, MAU
ENSTGUG00000005665	heparan sulfate 6-O-sulfotransferase 1	3776452	3976275	9	HS6ST1	MAU
ENSTGUG00000007084	protein phosphatase 2 regulatory subunit B"alpha	6573476	6609786	9	PPP2R3A	RAI
ENSTGUG00000008270		10768020	10786905	9		RAI

ENSTGUG00000009820		17638634	17660277	9		HUA
ENSTGUG00000010675	G protein subunit beta 4	20069493	20079705	9	GNB4	HUA
ENSTGUG00000006654	myosin VA	8523659	8598997	10	MYO5A	HUA
ENSTGUG00000008476	solute carrier organic anion transporter family member 3A1	14621964	14731878	10	SLCO3A1	MOO
ENSTGUG00000009006		18257909	18275693	10		HUA
ENSTGUG00000017715	microRNA 184	20485775	20485848	10	MIR184	HUA
ENSTGUG00000010006	zinc finger protein 710	20492147	20493497	10	ZNF710	HUA
ENSTGUG00000010009	semaphorin 4B	20501862	20505986	10	SEMA4B	HUA
ENSTGUG00000005417	E2F transcription factor 4	4815708	4825887	11	E2F4	HUA, MOO, RAI
ENSTGUG00000005428	engulfment and cell motility 3	4827918	4834507	11	ELMO3	HUA, MOO, RAI
ENSTGUG00000005766	tubulin polymerization promoting protein family member 3	5056834	5058661	11	TPPP3	HUA
ENSTGUG00000008994	URI1, prefoldin like chaperone	14711166	14741310	11		MAU
ENSTGUG00000008404	coiled-coil domain containing 174	11785828	11797268	12	CCDC174	MAU
ENSTGUG00000010102	contactin 4	19614606	19766886	12		HUA
ENSTGUG00000000209	interleukin 12B	1338072	1344091	13	IL12B	HUA
ENSTGUG00000000776	FAT atypical cadherin 2	6519325	6562614	13	FAT2	RAI
ENSTGUG00000000816		6633705	6783751	13		HUA
ENSTGUG00000001246	core histone macro-H2A.1	9525620	9569022	13	H2AFY	HUA
ENSTGUG00000004540	KIAA0556	3169643	3207271	14	KIAA0556	HUA
ENSTGUG00000008135		12554331	12555206	14		MAU
ENSTGUG00000009821		11316478	11424936	15		MOO
ENSTGUG00000009830		11366499	11374215	15		MOO
ENSTGUG00000009905	sodium/glucose cotransporter 1	11507233	11538464	15		HUA
ENSTGUG00000003398		5138627	5267364	17		MAU

ENSTGUG00000003550		5370218	5372236	17		MAU
ENSTGUG00000003552	dolichyl-phosphate mannosyltransferase subunit 2, regulatory	5374125	5374580	17	DPM2	MAU
ENSTGUG00000003554	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	5376833	5488169	17	ST6GALNAC4	HUA, MAU, TAH
ENSTGUG00000003556		5380700	5381723	17		MAU
ENSTGUG00000003559	adenylate kinase 1	5383752	5387428	17	AK1	MAU
ENSTGUG00000003704	TruB pseudouridine synthase family member 2	5499738	5503313	17	TRUB2	HUA, TAH
ENSTGUG00000007364	PBX homeobox 3	10940614	11046375	17	PBX3	HUA
ENSTGUG00000007428	Ral GEF with PH domain and SH3 binding motif 1	11515416	11577459	17	RALGPS1	MAU
ENSTGUG00000003385	transmembrane channel like 6	1691137	1696099	18	TMC6	MAU
ENSTGUG00000003410	hepatocyte growth factor-regulated tyrosine kinase substrate	1699283	1707780	18	HGS	MAU
ENSTGUG00000003446	mitochondrial ribosomal protein L12	1708980	1712466	18	MRPL12	MAU
ENSTGUG00000006238	myosin-3	5544437	5559002	18		MAU
ENSTGUG00000006545		5571232	5573803	18		MAU
ENSTGUG00000006551	myosin heavy chain, skeletal muscle, adult	5585671	5600256	18		MAU
ENSTGUG00000007675	chromosome 18 open reading frame, human C17orf62	6697273	6703781	18	CYBC1	HUA
ENSTGUG00000007809	jumonji domain containing 6, arginine demethylase and lysine hydroxylase	7731908	7741193	18	JMJD6	HUA
ENSTGUG00000007819	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	7751042	7828425	18	ST6GALNAC2	HUA
ENSTGUG00000007923	ubiquitin conjugating enzyme E2 O	7960889	7981633	18	UBE2O	MAU
ENSTGUG00000008958		11474946	11478895	19		HUA, MOO
ENSTGUG00000008962		11481381	11485166	19		HUA, MOO
ENSTGUG00000008966	PITPNM family member 3	11496529	11534638	19	PITPNM3	HUA, MOO
ENSTGUG00000002039	zinc finger and BTB domain containing 17	109799	116290	21	ZBTB17	TAH
ENSTGUG00000004728		2773733	2777396	22		HUA

ENSTGUG00000004741	ASH2 like, histone lysine methyltransferase complex subunit	2784936	2792494	22	ASH2L	HUA
ENSTGUG00000001038		2978316	2979139	23		HUA
ENSTGUG00000001039		2987758	2989220	23		HUA
ENSTGUG00000001130	runt related transcription factor 3	3280382	3312215	23	RUNX3	HUA
ENSTGUG00000001160	myomesin 3	3534172	3567527	23	MYOM3	HUA
ENSTGUG00000001176	fatty acid-binding protein, liver-like	3568981	3570931	23		HUA
ENSTGUG00000001265	hes related family bHLH transcription factor with YRPW motif-like	3743972	3744625	23	HEYL	HUA
ENSTGUG00000001266	poly(A) binding protein cytoplasmic 4	3755982	3768257	23	PABPC4	HUA
ENSTGUG00000001438	leucine zipper protein 1	4294754	4297891	23	LUZP1	HUA
ENSTGUG00000001329		2526723	2529254	26		MAU
ENSTGUG00000001330	troponin T2, cardiac type	2537936	2542499	26	TNNT2	MAU
ENSTGUG00000001345	transmembrane protein 9	2697635	2701249	26	TMEM9	HUA
ENSTGUG00000001363	PTPRF interacting protein alpha 4	2749706	2780727	26	PPFIA4	MOO
ENSTGUG00000001381	adenosine receptor A1	2801182	2823090	26	ADORA1	HUA
ENSTGUG00000001511	plexin A2	3571959	3682353	26	PLXNA2	HUA
ENSTGUG00000002482		2319216	2319366	27		HUA
ENSTGUG00000002515		2388654	2627252	27		HUA
ENSTGUG00000002656	vacuolar protein sorting 25 homolog	2509069	2631604	27	VPS25	HUA
ENSTGUG00000002727	tubulin gamma 1	2596517	2601876	27	TUBG1	HUA
ENSTGUG00000002735	contactin associated protein 1	2609963	2615943	27	CNTNAP1	HUA
ENSTGUG00000002970		2944147	2950604	27		HUA
ENSTGUG00000000551		2758875	2784928	28		MAU
ENSTGUG00000000664	WD repeat domain 18	3047464	3054358	28	WDR18	RAI
ENSTGUG00000000667		3061236	3072627	28		RAI
ENSTGUG00000002908	LHFPL tetraspan subfamily member 3	12508602	12668585	1A	LHFPL3	RAI

ENSTGUG00000007680	otogelin like	39135461	39219032	1A	OTOGL	MAU
ENSTGUG00000012520	adenosine deaminase 2	70536304	70554685	1A	ADA2	TAH
ENSTGUG00000005324	chloride voltage-gated channel 5	16132112	16150679	4A	CLCN5	HUA, RAI

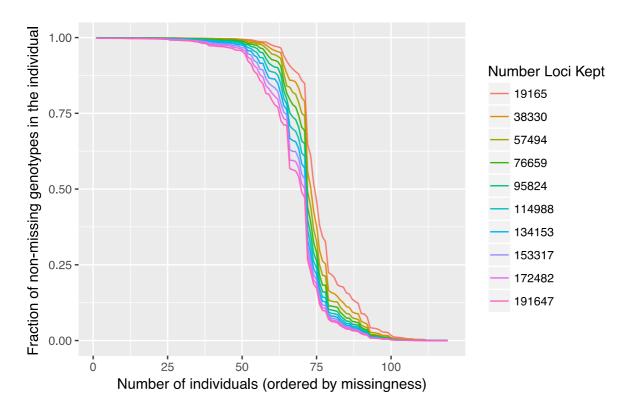


Figure S1: Missingness plot generated using *genoscapeRtools* used to determine the optimal number of samples and SNPs to retain for downstream analyses.