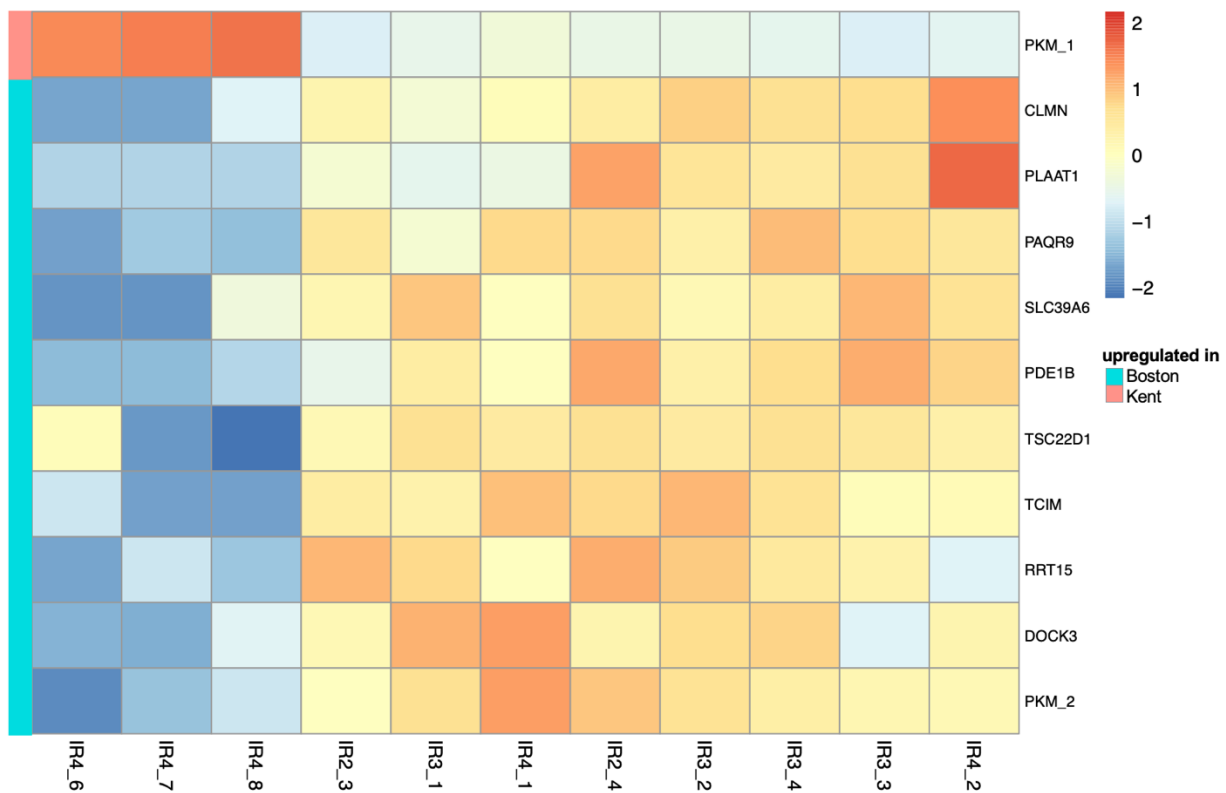
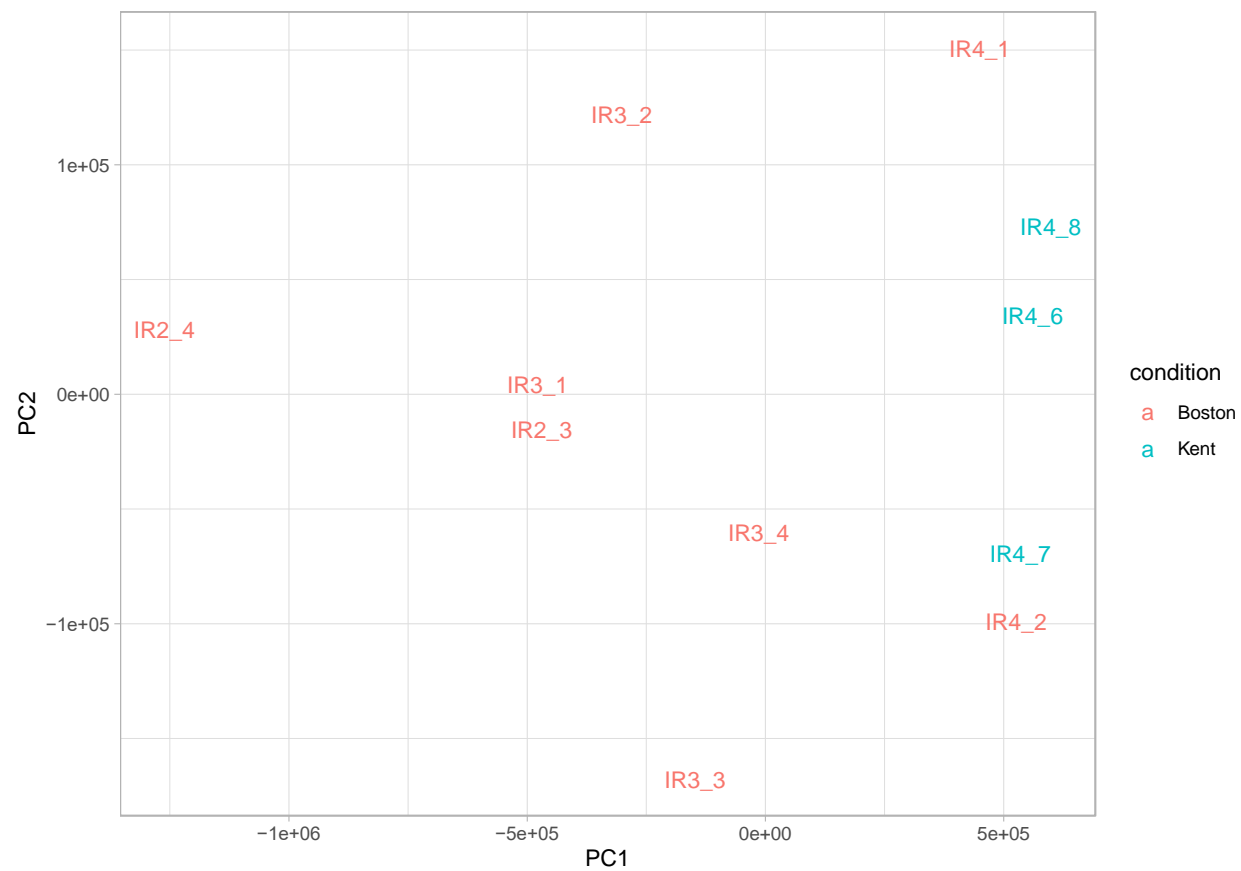


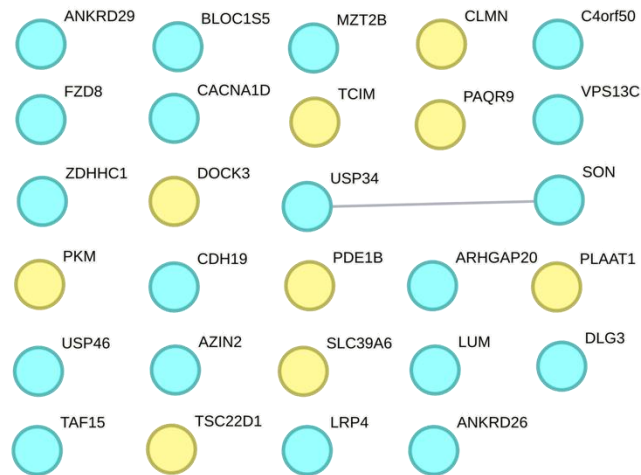
Supplementary Figure 1. Results from BUSCO assessment of 10,844 BUSCOs searched within the transcriptomes assembly of both species, AMGO – American GoldFinch, BCCH – Black capped Chickadees.



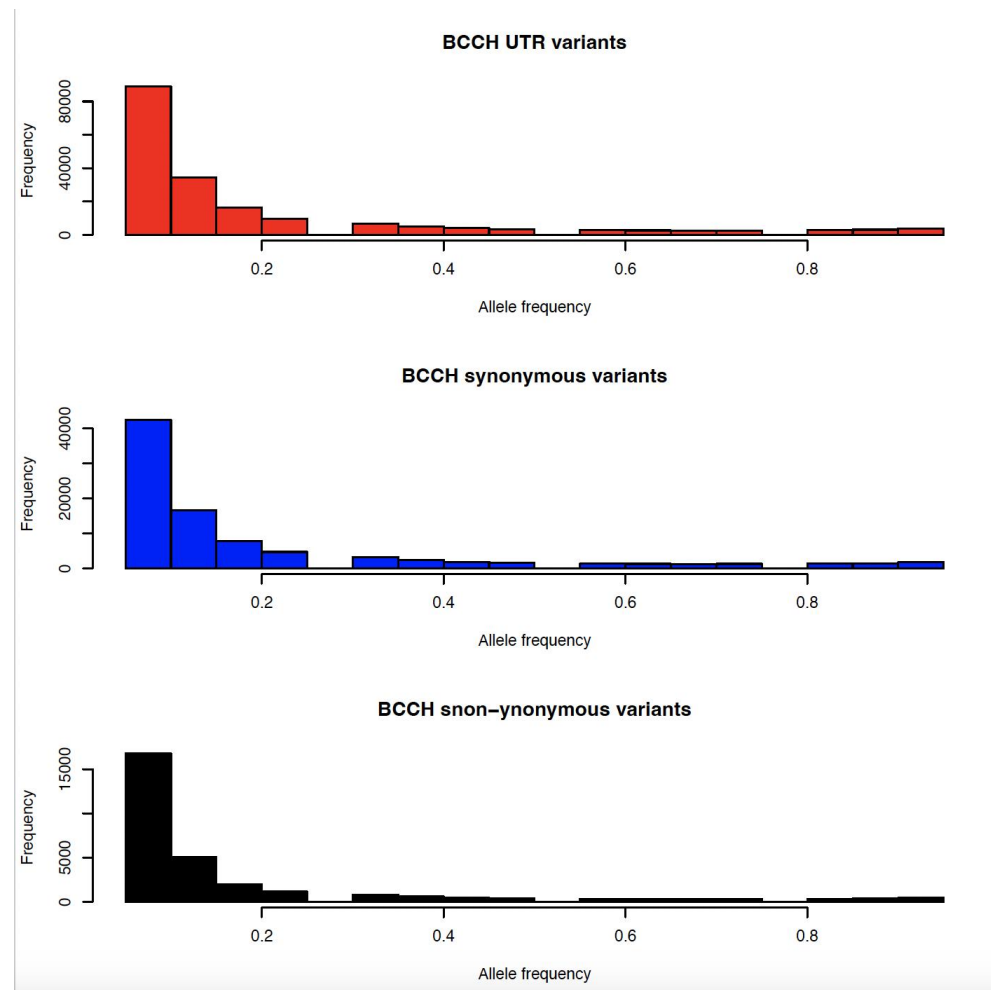
Supplementary Figure 2. A heatmap of the log of transcript per million of all 11 differentially expressed transcripts in American goldfinch brains between Kent and Boston, scaled by row.



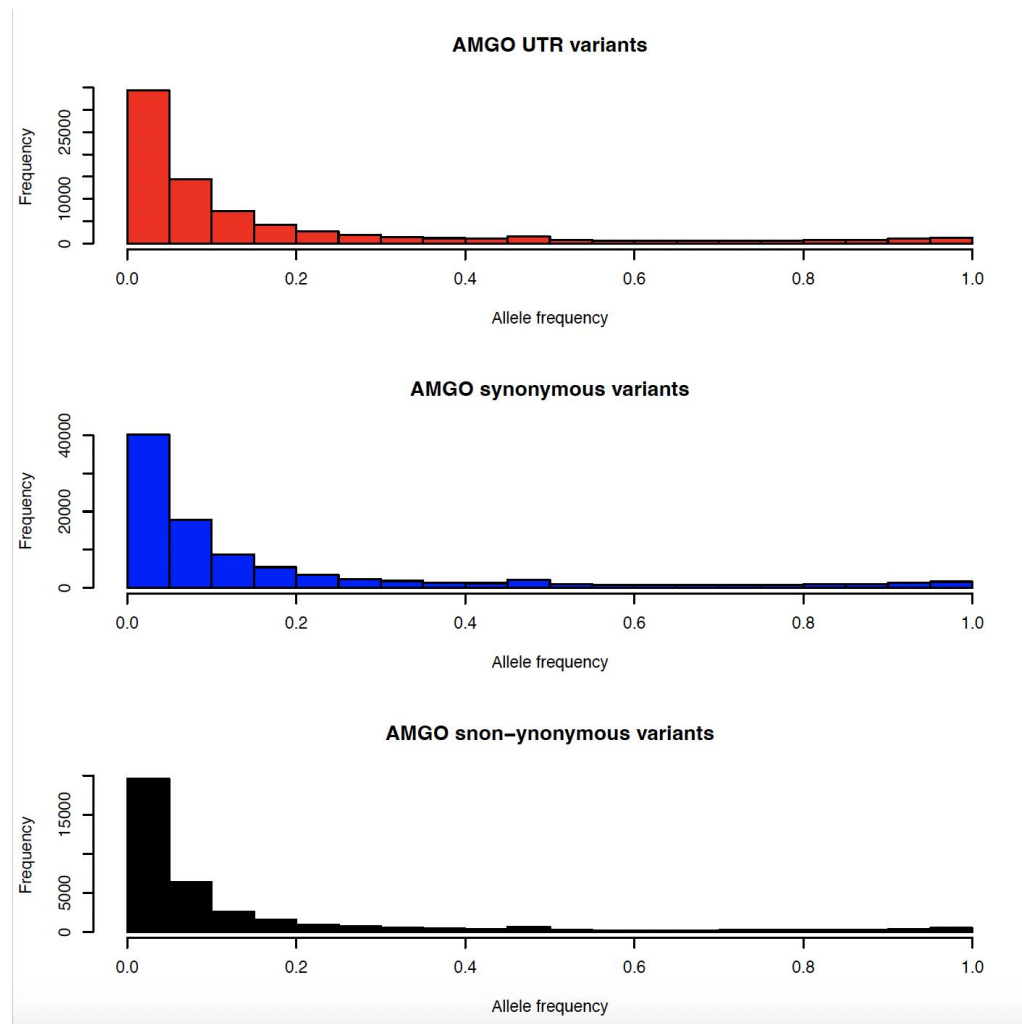
Supplementary Figure 3. Principal component analysis of the estimated transcript abundance of all American goldfinch brain samples. PC1 explains 95.33% of the variance, while PC2 explains 2.43% of the variance.



Supplementary Figure 4. The STRING network of protein-protein interactions between differentially expressed genes (yellow) and genes overlapping highly divergent genetic variants (blue) in American goldfinch brains between Boston and Kent populations.



Supplementary Figure 5. Site frequency distribution of SNPs annotated as UTR, synonymous and non-synonymous in Black-capped chickadees.



Supplementary Figure 6. Site frequency distribution of SNPs annotated as UTR, synonymous and non-synonymous in American goldfinches.

Supplementary Table 1. Details on RNA extraction, RNA quality, and raw RNA sequencing data generated.

Sample ID	Reads ID	Species	Location	Tissue	Tissue weight (mg)	Concentration (ng/μl)	RIN	# Raw Sequencing Reads
18-055	IR1_1	<i>Poecile atricapillus</i>	Boston	Brain	47.2	61.6	9.5	53,431,462
18-056	IR1_2	<i>Poecile atricapillus</i>	Boston	Brain	23.9	>200	9.7	49,814,234
18-059	IR1_3	<i>Poecile atricapillus</i>	Boston	Brain	39.7	152	9.5	44,614,814
18-073	IR2_1	<i>Poecile atricapillus</i>	Boston	Brain	26.7	176	9.6	42,035,660
18-074	IR2_2	<i>Poecile atricapillus</i>	Boston	Brain	21.5	162	9.6	39,774,700
18-047	IR2_3	<i>Spinus tristis</i>	Boston	Brain	31.9	196	9.3	41,253,244
18-057	IR2_4	<i>Spinus tristis</i>	Boston	Brain	22.7	200	9.2	47,072,134
18-058	IR3_1	<i>Spinus tristis</i>	Boston	Brain	28.8	28.4	9.2	45,693,074
18-060	IR3_2	<i>Spinus tristis</i>	Boston	Brain	25.3	>200	9.4	48,687,494
18-072	IR3_3	<i>Spinus tristis</i>	Boston	Brain	30	>200	9.2	45,322,088
18-075	IR3_4	<i>Spinus tristis</i>	Boston	Brain	26.6	>200	9.4	42,080,398
18-077	IR4_1	<i>Spinus tristis</i>	Boston	Brain	20.8	21.4	9.5	50,252,768
18-078	IR4_2	<i>Spinus tristis</i>	Boston	Brain	28.7	43	9	47,901,672
TITR01	IR4_3	<i>Poecile atricapillus</i>	Kent	Brain	28.2	59.4	9.2	43,943,494
TITR02	IR4_4	<i>Poecile atricapillus</i>	Kent	Brain	25.8	150	9.2	42,879,170
TITR03	IR4_5	<i>Poecile atricapillus</i>	Kent	Brain	27.9	>200	9.5	39,870,024
TITR04	IR4_6	<i>Spinus tristis</i>	Kent	Brain	25.4	>200	9.4	49,794,216
TITR05	IR4_7	<i>Spinus tristis</i>	Kent	Brain	24	24.6	9.4	44,225,076
TITR06	IR4_8	<i>S. tristis</i>	Kent	Brain	27.2	73.6	9.7	53,127,520
TITR01	IR5_1	<i>Poecile atricapillus</i>	Kent	Liver	20.8	>200	9.7	42,448,088
TITR02	IR5_2	<i>Poecile atricapillus</i>	Kent	Liver	23.5	>200	10	42,620,364
TITR03	IR5_3	<i>Poecile atricapillus</i>	Kent	Liver	27.8	>200	9.8	50,024,416

TITR04	IR5_4	<i>Spinus tristis</i>	Kent	Liver	21.1	>200	9.7	40,349,998
TITR05	IR5_5	<i>Spinus tristis</i>	Kent	Liver	25.8	>200	9.7	50,106,532
TITR06	IR5_6	<i>Spinus tristis</i>	Kent	Liver	29	>200	9.7	50,195,350

Supplementary Table 2. The annotation of 96 DEGs between black-capped chickadee brains in Kent and Boston. The q-value is the FDR adjusted p-value, and the beta value is the biased estimate of natural log fold change between conditions.

Transcript ID	Gene Name	Annotation Method	q-value	Beta	Upregulated In
TRINITY_DN126_c0_g1_i16	PAK3	Trinotate	2.39E-08	7.4928	Kent
TRINITY_DN1617_c0_g1_i3	SCOC	Trinotate	0.0385	6.6201	Kent
TRINITY_DN2080_c0_g1_i2	TAB3	Trinotate	0.0511	6.1287	Kent
TRINITY_DN3721_c0_g1_i3	EIF4G2	Trinotate	0.0881	6.1053	Kent
TRINITY_DN2461_c0_g1_i7	TXNDC11	Trinotate	0.0881	5.8864	Kent
TRINITY_DN3964_c0_g2_i2	RERE	Trinotate	0.0564	5.5942	Kent
TRINITY_DN4788_c1_g1_i16	KALRN	Trinotate	0.0063	5.4301	Kent
TRINITY_DN4794_c0_g1_i7	NDUFV3	Manual	0.0111	5.4247	Kent
TRINITY_DN3295_c0_g1_i6	LANCL3	Manual	0.0355	5.3633	Kent
TRINITY_DN64343_c0_g1_i1	POLR2G	Trinotate	0.0002	5.2883	Kent
TRINITY_DN298_c0_g1_i25	UBASH3B	Trinotate	0.0440	5.2668	Kent
TRINITY_DN62084_c0_g1_i7	G2E3	Trinotate	0.0222	5.1808	Kent
TRINITY_DN2042_c1_g1_i8	INPP4A	Trinotate	0.0762	5.1251	Kent
TRINITY_DN2345_c3_g1_i3	AGFG2	Trinotate	0.0714	4.8745	Kent
TRINITY_DN1486_c0_g3_i3	FLNB	Trinotate	0.0100	4.7558	Kent
TRINITY_DN3726_c1_g1_i7	GBA2	Trinotate	0.0906	4.6804	Kent
TRINITY_DN760_c0_g1_i9	ABLIM2	Trinotate	0.0082	4.6043	Kent

TRINITY_DN3516_c3_g1_i7	TRPC5	Trinotate	0.0762	4.5913	Kent
TRINITY_DN11246_c0_g1_i1	CSGALNACT2	Trinotate	0.0260	4.5617	Kent
TRINITY_DN21006_c0_g1_i2	ID4	Manual	0.0010	4.5299	Kent
TRINITY_DN4112_c0_g1_i8	CEP85L	Trinotate	0.0440	4.5077	Kent
TRINITY_DN1760_c0_g1_i9	HKDC1	Trinotate	0.0179	4.4620	Kent
TRINITY_DN2722_c0_g1_i9	MXRA7	Manual	0.0386	4.3898	Kent
TRINITY_DN4333_c0_g1_i35	LAML3	Trinotate	0.0762	4.3186	Kent
TRINITY_DN2315_c0_g1_i13	TTC13	Trinotate	0.0260	4.1063	Kent
TRINITY_DN3802_c0_g1_i13	GPAA1	Trinotate	0.0758	4.0900	Kent
TRINITY_DN2716_c1_g1_i2	AHDC1	Manual	0.0987	4.0607	Kent
TRINITY_DN566_c0_g1_i1	TPD52L2	Trinotate	0.0192	4.0606	Kent
TRINITY_DN3078_c0_g1_i3	TIMM29	Trinotate	0.0191	3.8557	Kent
TRINITY_DN321_c0_g1_i17	PNPO	Trinotate	0.0881	3.7583	Kent
TRINITY_DN2047_c0_g1_i1	UGCG_i1	Trinotate	0.0881	3.6511	Kent
TRINITY_DN2751_c0_g3_i18	Y0266	Trinotate	0.0828	3.4782	Kent
TRINITY_DN1114_c2_g1_i5	SOX14	Trinotate	0.0511	3.4336	Kent
TRINITY_DN8264_c0_g1_i2	IRX6	Trinotate	0.0945	3.2928	Kent
TRINITY_DN34206_c0_g1_i1	GATA3_i2	Manual	0.0894	3.0755	Kent
TRINITY_DN2250_c0_g1_i16	PDZD3	Trinotate	0.0161	2.8445	Kent
TRINITY_DN3447_c0_g1_i7	LRRK1	Trinotate	0.0803	2.7167	Kent
TRINITY_DN2741_c0_g2_i1	LEF1	Trinotate	0.0906	2.6887	Kent
TRINITY_DN2675_c0_g2_i1	SP5	Trinotate	0.0707	2.1500	Kent
TRINITY_DN1649_c1_g1_i1	GATA3_i1	Trinotate	0.0234	1.9410	Kent
TRINITY_DN7672_c0_g1_i1	FXYP1	Trinotate	0.0355	1.8264	Kent
TRINITY_DN113_c0_g1_i1	PPDPFL_i1	Trinotate	0.0310	1.6502	Kent
TRINITY_DN2170_c0_g2_i11	IRX1	Trinotate	0.0987	1.6392	Kent
TRINITY_DN11229_c0_g1_i1	PPDPFL_i2	Manual	1.76E-08	1.6364	Kent
TRINITY_DN113_c0_g1_i2	PPDPFL_i3	Trinotate	0.0431	1.5856	Kent
TRINITY_DN3213_c0_g1_i12	FGF13	Trinotate	0.0083	1.5210	Kent

TRINITY_DN597_c1_g2_i4	MYORG	Manual	0.0669	1.4730	Kent
TRINITY_DN398_c1_g1_i1	OFD1	Manual	0.0945	1.1840	Kent
TRINITY_DN17040_c0_g1_i4	BTBD17	Trinotate	0.0082	1.1834	Kent
TRINITY_DN3588_c0_g1_i4	RIPOR2	Trinotate	0.0511	1.1564	Kent
TRINITY_DN1191_c0_g1_i2	GJB6	Trinotate	0.0222	1.0440	Kent
TRINITY_DN1946_c0_g1_i9	PLPP4	Trinotate	0.0030	1.0241	Kent
TRINITY_DN200_c0_g1_i13	ATP1A2	Trinotate	0.0021	0.8941	Kent
TRINITY_DN13996_c0_g1_i2	CHCHD10	Trinotate	0.0931	0.8430	Kent
TRINITY_DN526_c4_g1_i26	RPS6KA6	Trinotate	6.76E-09	-6.2734	Boston
TRINITY_DN340_c0_g1_i24	VGf	Trinotate	0.0881	-5.2737	Boston
TRINITY_DN3162_c0_g2_i8	FAM135A	Trinotate	0.0511	-5.2112	Boston
TRINITY_DN206_c3_g1_i1	USP24	Trinotate	0.0004	-5.1918	Boston
TRINITY_DN208_c3_g1_i3	INSR	Manual	0.0005	-4.8183	Boston
TRINITY_DN4827_c0_g1_i8	HLA-DRA	Trinotate	1.40E-06	-4.7631	Boston
TRINITY_DN3132_c4_g1_i8	CCND3	Trinotate	0.0511	-4.5287	Boston
TRINITY_DN4129_c0_g1_i9	PTPN4	Trinotate	0.0511	-4.3272	Boston
TRINITY_DN4536_c1_g1_i6	FBXO4	Trinotate	0.0021	-4.2774	Boston
TRINITY_DN917_c1_g1_i2	IQGAP1	Trinotate	0.0030	-4.2351	Boston
TRINITY_DN2924_c0_g1_i10	SACS	Trinotate	0.0881	-4.0801	Boston
TRINITY_DN17256_c0_g1_i27	ADCY3	Manual	0.0657	-4.0456	Boston
TRINITY_DN7666_c0_g1_i9	DENND6A	Manual	0.0803	-4.0005	Boston
TRINITY_DN3658_c0_g1_i2	NUMB	Trinotate	0.0540	-3.8167	Boston
TRINITY_DN337_c19_g1_i9	AAK1	Manual	0.0881	-3.7290	Boston
TRINITY_DN2820_c0_g1_i16	BCKDHA	Manual	0.0077	-3.6940	Boston
TRINITY_DN18651_c0_g1_i1	NRN1	Trinotate	0.0987	-3.0896	Boston
TRINITY_DN2047_c1_g1_i8	NLRC3_i1	Trinotate	0.0511	-3.0567	Boston
TRINITY_DN6401_c1_g1_i1	NEMF	Manual	7.49E-07	-2.5076	Boston
TRINITY_DN2047_c1_g1_i3	NLRC3_i2	Trinotate	7.06E-06	-2.4915	Boston
TRINITY_DN2047_c0_g1_i6	UGCG_i2	Trinotate	5.37E-07	-2.2038	Boston

TRINITY_DN270_c0_g1_i13	NACA_i1	Trinotate	7.39E-05	-2.1385	Boston
TRINITY_DN2047_c0_g1_i8	UGCG_i3	Trinotate	6.76E-09	-2.1121	Boston
TRINITY_DN3144_c0_g1_i3	BHLHE22	Trinotate	0.0511	-2.0792	Boston
TRINITY_DN2047_c0_g1_i10	RRT15_i1	Trinotate	1.41E-08	-2.0757	Boston
TRINITY_DN2047_c0_g1_i3	RRT15_i2	Trinotate	1.41E-08	-2.0757	Boston
TRINITY_DN393_c0_g1_i3	CLMN	Trinotate	5.37E-07	-1.8407	Boston
TRINITY_DN2964_c0_g1_i1	PLXNA2	Trinotate	0.0355	-1.6893	Boston
TRINITY_DN175_c9_g1_i16	RASAL2	Trinotate	0.0919	-1.6749	Boston
TRINITY_DN3788_c0_g1_i6	ANKRD11	Trinotate	0.0431	-1.3583	Boston
TRINITY_DN566_c1_g1_i7	IGSF9B	Trinotate	0.0079	-1.3333	Boston
TRINITY_DN270_c0_g1_i9	NACA_i2	Trinotate	0.0762	-1.2659	Boston
TRINITY_DN1650_c0_g1_i10	FBXO34	Trinotate	0.0657	-1.2314	Boston
TRINITY_DN1256_c1_g1_i25	ATP9A	Trinotate	0.0008	-1.0562	Boston
TRINITY_DN4727_c0_g1_i2	DGKH	Manual	0.0954	-1.0544	Boston
TRINITY_DN18_c25_g1_i25	HPCAL1	Trinotate	0.0564	-1.0378	Boston
TRINITY_DN4340_c0_g1_i6	FOSL2	Trinotate	0.0881	-1.0252	Boston
TRINITY_DN16425_c2_g1_i3	GAP43	Trinotate	0.0125	-0.9396	Boston
TRINITY_DN906_c0_g1_i5	SEZ6L	Trinotate	0.0127	-0.8600	Boston
TRINITY_DN1870_c3_g1_i8	MAPKBP1	Trinotate	0.0881	-0.8478	Boston
TRINITY_DN1297_c0_g1_i4	PLCL2	Trinotate	0.0868	-0.7206	Boston
TRINITY_DN97203_c1_g1_i1	NPTXR	Trinotate	0.0987	-0.6876	Boston

Supplementary Table 3. The annotation of 11 DEGs between American goldfinch brains in Kent and Boston. The q-value is the FDR adjusted p-value and the beta value is the biased estimate of natural log fold change between conditions.

Trinity ID	Gene Name	Annotation Method	q-value	Beta	Upregulated In
TRINITY_DN583_c0_g1_i11	PKM_i1	Trinotate	5.30E-06	6.9190	Kent
TRINITY_DN2053_c0_g2_i3	PLAAT1	Trinotate	0.0001	-5.0913	Boston
TRINITY_DN1193_c0_g1_i11	CLMN	Manual	0.0101	-5.0639	Boston
TRINITY_DN4366_c0_g1_i5	SLC39A6	Trinotate	0.0595	-4.9208	Boston
TRINITY_DN386_c1_g1_i25	DOCK3	Trinotate	0.0233	-4.8288	Boston
TRINITY_DN5017_c0_g1_i22	PDE1B	Trinotate	0.0004	-4.4257	Boston
TRINITY_DN2478_c0_g1_i10	TCIM	Trinotate	6.85E-05	-3.5810	Boston
TRINITY_DN359_c1_g2_i2	RRT15	Trinotate	0.0116	-3.2351	Boston
TRINITY_DN1158_c1_g1_i7	PAQR9	Trinotate	2.06E-12	-1.9767	Boston
TRINITY_DN13656_c1_g1_i7	TSC22D1	Trinotate	0.0199	-0.8557	Boston
TRINITY_DN583_c0_g1_i8	PKM_i2	Trinotate	0.0199	-0.7211	Boston

Supplementary Table 4: Annotation based on PANTHER database matches for DEGs between black-capped chickadee brains in Kent and Boston.

Gene ID	PANTHER Family/Subfamily	PANTHER Protein Class
AAK1	PROTEIN KINASE DOMAIN-CONTAINING PROTEIN	non-receptor serine/threonine protein kinase
ABLIM2	ACTIN-BINDING LIM PROTEIN 2	actin or actin-binding cytoskeletal protein
ADCY3	ADENYLATE CYCLASE TYPE 3	adenylate cyclase
AGFG2	ARF-GAP DOMAIN AND FG REPEAT-CONTAINING PROTEIN 2	
AHDC1	AT-HOOK DNA-BINDING MOTIF-CONTAINING PROTEIN 1	
ANKRD11	ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 11	
ATP1A2	SODIUM_POTASSIUM-TRANSPORTING ATPASE SUBUNIT ALPHA-2	primary active transporter
ATP9A	PHOSPHOLIPID-TRANSPORTING ATPASE IIA-RELATED	primary active transporter
BCKDHA	2-OXOISOVALERATE DEHYDROGENASE SUBUNIT ALPHA, MITOCHONDRIAL	dehydrogenase

BHLHE22	CLASS E BASIC HELIX-LOOP-HELIX PROTEIN 22	basic helix-loop-helix transcription factor
BTBD17	BTB_POZ DOMAIN-CONTAINING PROTEIN 17	defense/immunity protein
CCND3	G1_S-SPECIFIC CYCLIN-D3	kinase activator
CEP85L	CENTROSOMAL PROTEIN OF 85 KDA-LIKE	
CHCHD10	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN-CONTAINING PROTEIN 10, MITOCHONDRIAL	
CLMN	CALMIN	
CSGALNACT2	CHONDROITIN SULFATE N-ACETYL GALACTOSAMINYLTRANSFERASE 2	glycosyltransferase
DENND6A	PROTEIN DENND6A	
DGKH	DIACYLGLYCEROL KINASE ETA	kinase
EIF4G2	EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA 2	translation initiation factor
FAM135A	PROTEIN FAM135A	
FBXO34	F-BOX ONLY PROTEIN 34	
FBXO4	F-BOX ONLY PROTEIN 4	
FGF13	FIBROBLAST GROWTH FACTOR 13	growth factor
FLNB	FILAMIN-B	
FOSL2	FOS-RELATED ANTIGEN 2	basic leucine zipper transcription factor
FXYP1	PHOSPHOLEMMAN	primary active transporter
G2E3	G2_M PHASE-SPECIFIC E3 UBIQUITIN-PROTEIN LIGASE	DNA metabolism protein
GAP43	NEUROMODULIN	
GATA3	TRANS-ACTING T-CELL-SPECIFIC TRANSCRIPTION FACTOR GATA-3	DNA-binding transcription factor
GBA2	NON-LYSOSOMAL GLUCOSYLCERAMIDASE	glucosidase
GJB6	GAP JUNCTION BETA-6 PROTEIN	gap junction

GPAA1	GLYCOSYLPHOSPHATIDYLINOSITOL ANCHOR ATTACHMENT 1 PROTEIN	
HKDC1	HEXOKINASE HKDC1	kinase
HLA-DRA	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR ALPHA CHAIN	major histocompatibility complex protein
HPCAL1	HIPPOCALCIN-LIKE PROTEIN 1	calmodulin-related
ID4	DNA-BINDING PROTEIN INHIBITOR ID-4	DNA-binding transcription factor
IGSF9B	PROTEIN TURTLE HOMOLOG B	immunoglobulin superfamily cell adhesion molecule
INPP4A	INOSITOL POLYPHOSPHATE-4-PHOSPHATASE TYPE I A	phosphatase
INSR	INSULIN RECEPTOR	transmembrane signal receptor
IQGAP1	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1	GTPase-activating protein
IRX1	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1	homeodomain transcription factor
IRX6	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-6	homeodomain transcription factor
KALRN	KALIRIN	guanyl-nucleotide exchange factor
LANCL3	LANC-LIKE PROTEIN 3	
LEF1	LYMPHOID ENHANCER-BINDING FACTOR 1	DNA-binding transcription factor
LRRK1	LEUCINE-RICH REPEAT SERINE_THREONINE-PROTEIN KINASE 1	transmembrane signal receptor
MAPKBP1	MITOGEN-ACTIVATED PROTEIN KINASE-BINDING PROTEIN 1	
MXRA7	MATRIX-REMODELING-ASSOCIATED PROTEIN 7	
MYORG	MYOGENESIS-REGULATING GLYCOSIDASE	glucosidase
NACA	NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX SUBUNIT ALPHA, MUSCLE-SPECIFIC FORM	basic helix-loop-helix transcription factor
NDUFV3	NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 3, MITOCHONDRIAL	oxidoreductase

NEMF	RIBOSOME QUALITY CONTROL COMPLEX SUBUNIT NEMF	
NLRC3	NLR FAMILY CARD DOMAIN-CONTAINING PROTEIN 3	scaffold/adaptor protein
NPTXR	NEURONAL PENTRAXIN RECEPTOR	scaffold/adaptor protein
NRN1	NEURITIN	
NUMB	PROTEIN NUMB HOMOLOG	
OFD1	ORAL-FACIAL-DIGITAL SYNDROME 1 PROTEIN	
PAK3	SERINE_THREONINE-PROTEIN KINASE PAK 3	non-receptor serine/threonine protein kinase
PDZD3	NA(+) H(+) EXCHANGE REGULATORY COFACTOR NHE-RF4 (PTHR14191:SF20)	scaffold/adaptor protein
PLCL2	INACTIVE PHOSPHOLIPASE C-LIKE PROTEIN 2	phospholipase
PLPP4	PHOSPHOLIPID PHOSPHATASE 4	phosphatase
PLXNA2	PLEXIN-A2	transmembrane signal receptor
PNPO	PYRIDOXINE-5'-PHOSPHATE OXIDASE	oxidase
POLR2G	DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB7	DNA-directed RNA polymerase
PPDPFL	PANCREATIC PROGENITOR CELL DIFFERENTIATION AND PROLIFERATION FACTOR-LIKE PROTEIN	
PTPN4	TYROSINE-PROTEIN PHOSPHATASE NON- RECEPTOR TYPE 4	protein phosphatase
RASAL2	RAS GTPASE-ACTIVATING PROTEIN NGAP	GTPase-activating protein
RERE	ARGININE-GLUTAMIC ACID DIPEPTIDE REPEATS PROTEIN	
RIPOR2	RHO FAMILY-INTERACTING CELL POLARIZATION REGULATOR 2	non-receptor serine/threonine protein kinase
RPS6KA6	RIBOSOMAL PROTEIN S6 KINASE ALPHA-6	protein modifying enzyme
SACS	SACSIN	
SCOC	SHORT COILED-COIL PROTEIN	

SEZ6L	SEIZURE 6-LIKE PROTEIN	
SOX14	TRANSCRIPTION FACTOR SOX-14	HMG box transcription factor
SP5	TRANSCRIPTION FACTOR SP5	C2H2 zinc finger transcription factor
TAB3	TGF-BETA-ACTIVATED KINASE 1 AND MAP3K7-BINDING PROTEIN 3	
TIMM29	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM29	
TPD52L2	TUMOR PROTEIN D54	
TRPC5	SHORT TRANSIENT RECEPTOR POTENTIAL CHANNEL 5	ion channel
TTC13	TETRATRICOPEPTIDE REPEAT PROTEIN 13	
TXNDC11	THIOREDOXIN DOMAIN-CONTAINING PROTEIN 11	oxidoreductase
UBASH3B	UBIQUITIN-ASSOCIATED AND SH3 DOMAIN-CONTAINING PROTEIN B	
UGCG	CERAMIDE GLUCOSYLTRANSFERASE	glycosyltransferase
USP24	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 24	cysteine protease
VGF	NEUROSECRETORY PROTEIN VGF	intercellular signal molecule

Supplementary Table 5. Annotation based on PANTHER database matches for DEGs between American goldfinch brains in Kent and Boston.

Gene ID	PANTHER Family/Subfamily	Panther Protein Class
PKM	PYRUVATE KINASE PKM	kinase
TSC22D1	TSC22 DOMAIN FAMILY PROTEIN 1	
CLMN	CALMIN	
PLAAT1	PHOSPHOLIPASE A AND ACYLTRANSFERASE 1	acyltransferase
DOCK3	DEDICATOR OF CYTOKINESIS PROTEIN 3	guanyl-nucleotide exchange factor
PDE1B	DUAL SPECIFICITY CALCIUM_CALMODULIN-DEPENDENT 3',5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE 1B	phosphodiesterase
PAQR9	MEMBRANE PROGESTIN RECEPTOR EPSILON	G-protein coupled receptor
SLC39A6	ZINC TRANSPORTER ZIP6	secondary carrier transporter
TCIM	TRANSCRIPTIONAL AND IMMUNE RESPONSE REGULATOR	

Supplementary Table 6. Gene functions enriched in the black-capped chickadee DEGs

upregulated in the Boston population and downregulated in the Kent population. This table contains the TERM ID and a description of that term, a count of genes involved in those processes, and the FDR calculated by either discovery method: STRING or g:Profiler.

Term ID	Go Term Description	Gene Count	FDR	Detected by
GO:0032501	Multicellular organismal process	25	0.0491	g:Profiler
TF:M10026	Factor: PATZ; motif: GGGGNGGGGGMKGGRRNGGNRN	30	0.0054	g:Profiler
TF:M12697_1	Factor: ZNF142; motif: SNSCGCCCGCCCGCSCSS; match class: 1	10	0.0205	g:Profiler
TF:M07436	Factor: WT1; motif: NNGGGNGGGSGN	25	0.0446	g:Profiler
CORUM:1844	APC-IQGAP1 complex	1	0.0498	g:Profiler

Supplementary Table 7. Inbreeding coefficient values (F) for individuals from both species in both locations.

Individual	Species	Location	Observed Homozygous	Expected Homozygous	Number Sites	F
IR2_3	<i>Spinus tristis</i>	Boston	427935	416758.1	518029	0.11037
IR2_4	<i>Spinus tristis</i>	Boston	427951	416758.1	518029	0.11052
IR3_1	<i>Spinus tristis</i>	Boston	423575	416758.1	518029	0.06731
IR3_2	<i>Spinus tristis</i>	Boston	428834	416758.1	518029	0.11924
IR3_3	<i>Spinus tristis</i>	Boston	433642	416758.1	518029	0.16672
IR3_4	<i>Spinus tristis</i>	Boston	421456	416758.1	518029	0.04639
IR4_1	<i>Spinus tristis</i>	Boston	422147	416758.1	518029	0.05321
IR4_2	<i>Spinus tristis</i>	Boston	430728	416758.1	518029	0.13795
IR4_6	<i>Spinus tristis</i>	Kent	420285	416758.1	518029	0.03483
IR4_7	<i>Spinus tristis</i>	Kent	425294	416758.1	518029	0.08429
IR4_8	<i>Spinus tristis</i>	Kent	422230	416758.1	518029	0.05403
IR1_1	<i>Poecile atricapillus</i>	Boston	323007	321036.2	419735	0.01997
IR1_2	<i>Poecile atricapillus</i>	Boston	324304	321036.2	419735	0.03311
IR1_3	<i>Poecile atricapillus</i>	Boston	329817	321036.2	419735	0.08897
IR2_1	<i>Poecile atricapillus</i>	Boston	336465	321036.2	419735	0.15632
IR2_2	<i>Poecile atricapillus</i>	Boston	342188	321036.2	419735	0.21431

IR4_3	<i>Poecile atricapillus</i>	Kent	341876	321036.2	419735	0.21115
IR4_4	<i>Poecile atricapillus</i>	Kent	327956	321036.2	419735	0.07011
IR4_5	<i>Poecile atricapillus</i>	Kent	326634	321036.2	419735	0.05672