Supplementary information

Shared mechanisms and interpretable affective predictions in birdsong-to-music transformations

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Supplementary Methods | Sources and rules

This supplement documents a post hoc, deterministic audit of the frozen 13 October experiment. It adds no independent source phrase, participant, neural recording or molecular measurement. The revised primary response analysis retains all 889 declared dimensions; the earlier 202-dimensional present-state assay and all projection audits remain available. Tables S6 onward document the new layer and TAR follow-ups. New examples were selected after inspecting the code and the response archive, rather than preregistered.

Ordered neuromodulator updates

Nuclei run in ascending processing depth, with stable registry order within a depth. The initial vector [DA, NE, OPI, 5HT] is [0, 0.5, 0, 0]. For driving dimension x and weight w, *produce* sets c ← wx; *amplify* sets c ← c + wx(1−c); and *inhibit* sets c ← c − wxc. All channels are clipped to [0,1] after each nucleus. Produce therefore replaces an earlier direct write. The executor supplies acoustic, temporal and upstream C³ outputs to mechanisms, without passing this channel state back into their computation.

The final direct source identities are DA=0.65×ECT[f04:flexibility_index], OPI=0.90×IOTMS[E0:mor_baseline_proxy] and 5HT=0.30×BCH[P0:consonance_signal]. These are bounded source dimensions; no later link modifies these three terminal outputs in the frozen registry. NE retains nine amplify links and one inhibit link; the last is TAR[T2:anxiety_reduction], weight 0.45. Table S3 lists all 52 valid links in execution order. Overwritten direct writes do not exclude indirect influence through the source mechanisms' upstream dependencies.

Ceiling and temporal contrasts

IOTMS[E0:mor_baseline_proxy] is the clipped sum 0.55×pleasantness_mean_1s + 0.45×(1−roughness_skew_1s). Its ceiling of 1 gives an effective OPI ceiling of 0.9. The formula uses acoustic summary inputs; its trait-labelled name is not evidence of a participant trait. The ceiling fraction counts frames exactly equal to float32(0.9), pooled with equal weight across path anchors. MORMR RMS uses only its present-state dimensions and the path origin. For NE, the timing contrast $\delta(t)=NE(u=1,t)-NE(u=0,t)$ uses the same endpoint pair for both signed mean mean[δ] and framewise RMS sqrt(mean[δ²]). No temporal alignment or state carryover is introduced.

Regional sensitivity and contribution accounting

For region r, $RAM_r(t)=\max(0, \Sigma_l w_l Y_l(t))$. A weight-sum control divides each output by $W_r=\Sigma_l |w_l|$, without fitting weights or claiming physiological normalization. Correlations compare the 26 signed endpoint-change means across direct flute and piano paths. Regions share sources and are dependent; these correlations receive no inferential p-values. All four common-RMS endpoints had positive pre-ReLU sums (minimum 0.062835), so their signed changes decompose additively into per-mechanism weighted dimension changes. Tables S1–S2 and complete CSVs retain source counts, weights and signed contributions, including cancellation.

Reconstruction and reproducibility

NumPy float32 replay applied the pinned operators to stored C³ tensors for all 1,146 recordings (484,758 frames). The three terminal identities agreed exactly with this replay. Channel means agreed with archived packed means within 2.9732×10^{-8}; four-endpoint RAM means agreed within 9.4241×10^{-7}. These tolerances compare computational reconstructions; they are not measurement uncertainty. No engine formulas, renderings or stored C³ outputs were changed. Full audit checks and rebuilding instructions accompany the package.

Supplementary Fig. S1 | Regional and channel views

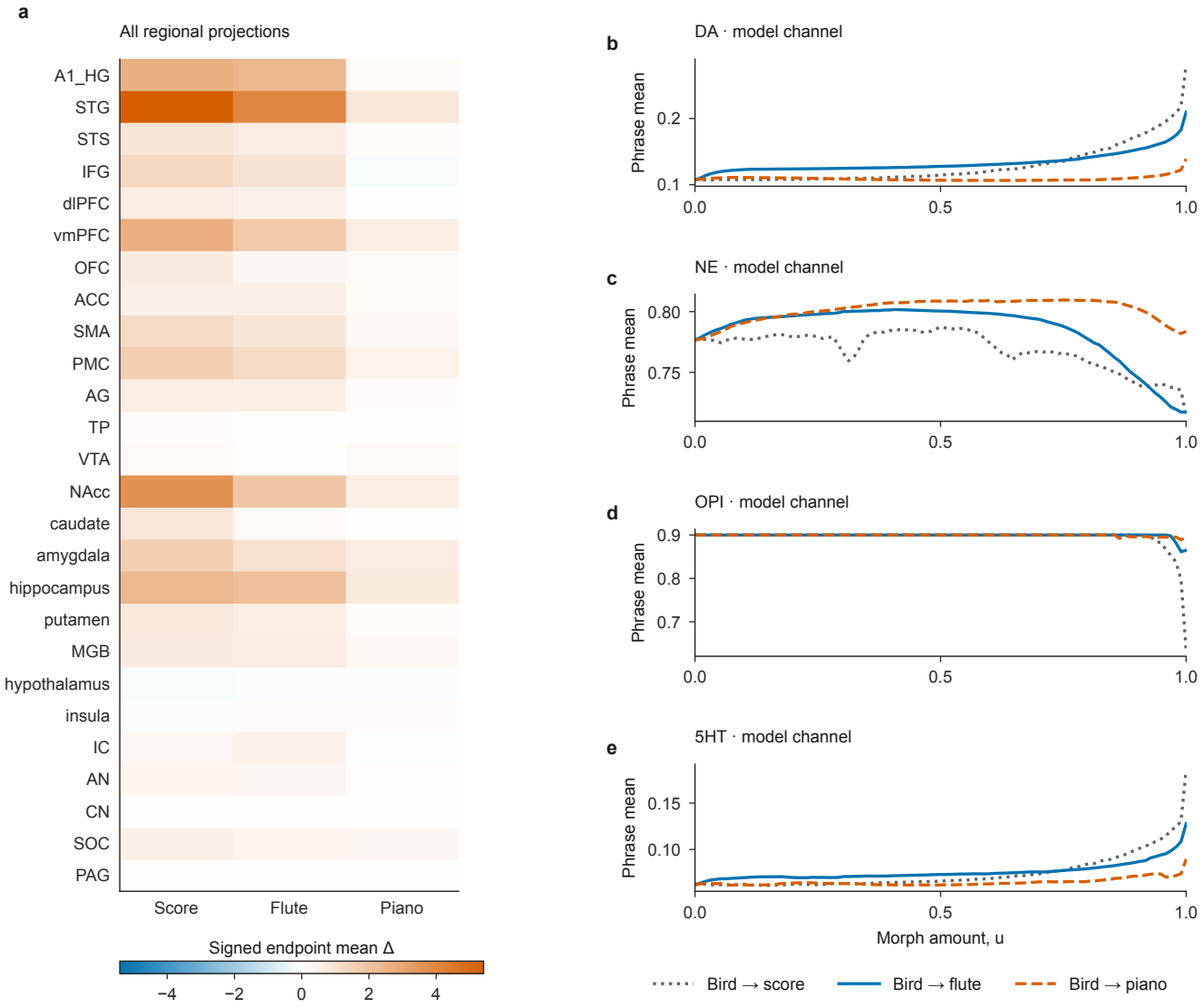

Fig. S1. The original projection analysis is restyled here with every plotted data series retained. Left: all 26 signed regional endpoint changes from the common bird origin. Right: phrase means of the four neuromodulator-labelled channels over 97 anchors on bird→score, bird→flute and bird→piano paths, all at common whole-phrase RMS. These absolute channel means complement, rather than substitute for, source provenance and framewise contrasts in the revised main Fig. 10. Regional labels and channel names designate projections in the model.

Endpoint	DA mean	NE mean	OPI mean	5HT mean
Bird	0.107185	0.776831	0.900000	0.062243
Score	0.280851	0.714486	0.633937	0.185691
Flute	0.209672	0.717187	0.864804	0.127924
Piano	0.138955	0.783752	0.895003	0.089715

From the bird origin, score endpoint changes in STG and A1_HG were 5.411 and 2.640 model units; corresponding flute changes were 3.985 and 2.377. Raw regional magnitudes depend on source count and weights. The 131 weighted aggregates in the original archive are further views of the same model outputs, not independent tests.

Supplementary Fig. S2 | Regional weight control

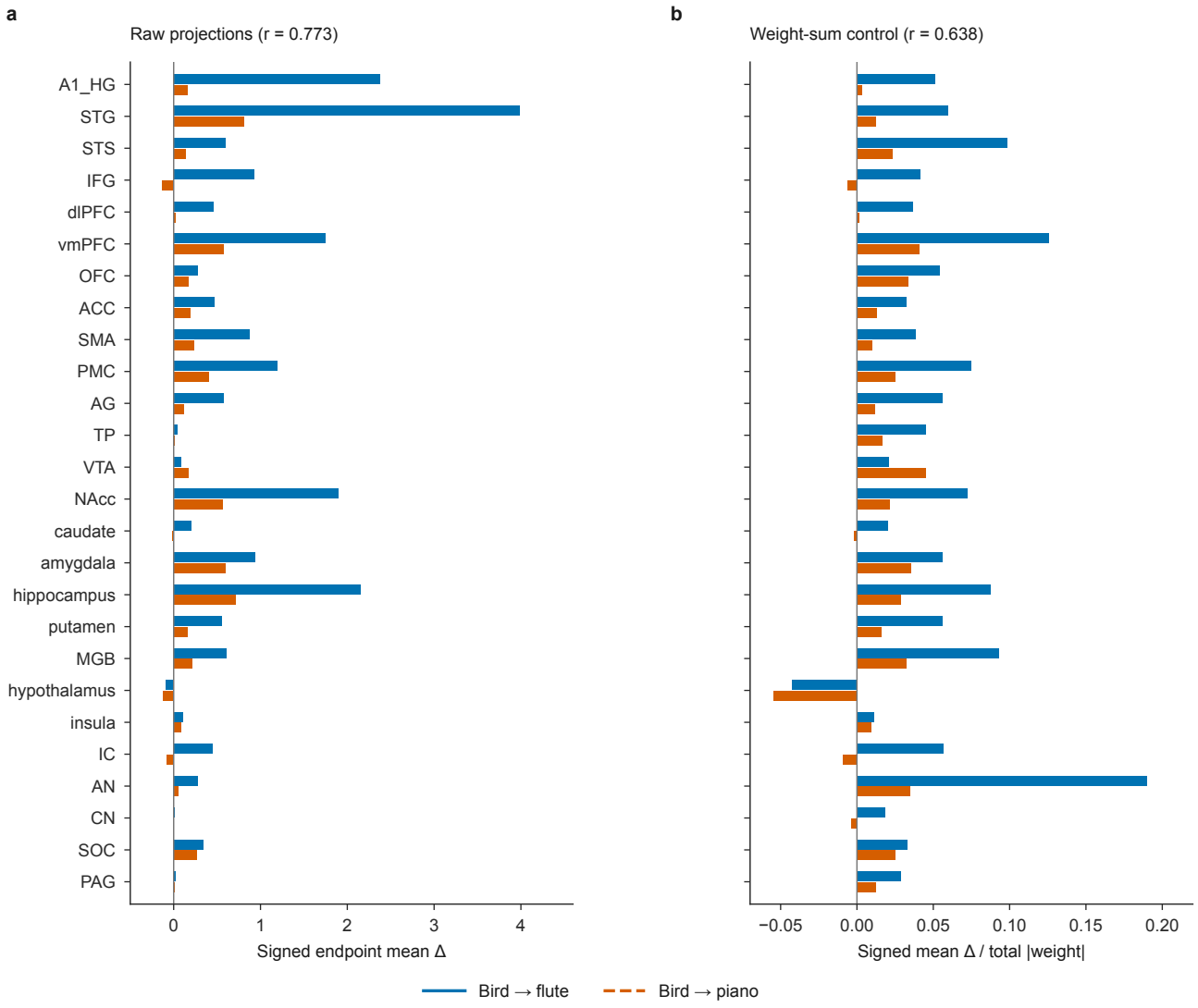

Fig. S2. All 26 signed direct endpoint-change means, with a common bird reference and common-RMS audio. **a,** Frozen RAM output. **b,** The same changes divided by the sum of absolute incoming link weights for each region. Flute and piano vectors correlate at r=0.772922 and r=0.638289, respectively. Signs agree in 22/26 regions; 25 flute and 21 piano changes are positive. Flute exceeds piano in signed change in 25 regions, with VTA the exception. Dividing by positive constants preserves within-region signs and order but changes cross-region scale and correlation. This is a connectivity sensitivity analysis, not physiological calibration or evidence of brain activation. All links and contribution signs are available in Tables S1–S2 and CSVs.

Supplementary Table S1 | Complete regional source inventory

Each row lists the number of dimension links, distinct source mechanisms and total absolute weight W. ΔF and ΔP are signed common-RMS endpoint mean changes from the bird origin. The last two columns divide these changes by W. Regional units are uncalibrated model units.

Region	Links	Mechs	W	ΔF	ΔP	ΔF/W	ΔP/W
A1_HG	63	44	46.65	+2.3774	+0.1595	+0.0510	+0.0034
STG	91	57	66.65	+3.9849	+0.8087	+0.0598	+0.0121
STS	9	6	6.00	+0.5923	+0.1383	+0.0987	+0.0231
IFG	31	24	22.30	+0.9293	-0.1332	+0.0417	-0.0060
dlPFC	17	14	12.45	+0.4558	+0.0180	+0.0366	+0.0014
vmPFC	19	16	13.95	+1.7502	+0.5742	+0.1255	+0.0412
OFC	7	7	5.10	+0.2771	+0.1723	+0.0543	+0.0338
ACC	20	20	14.55	+0.4738	+0.1885	+0.0326	+0.0130
SMA	30	24	22.90	+0.8788	+0.2342	+0.0384	+0.0102
PMC	21	14	16.00	+1.1979	+0.4048	+0.0749	+0.0253
AG	14	13	10.30	+0.5779	+0.1198	+0.0561	+0.0116
TP	1	1	0.90	+0.0404	+0.0149	+0.0449	+0.0165
VTA	5	5	3.85	+0.0816	+0.1749	+0.0212	+0.0454
NAcc	33	26	26.15	+1.9014	+0.5670	+0.0727	+0.0217
caudate	12	10	9.65	+0.1977	-0.0186	+0.0205	-0.0019
amygdala	22	18	16.80	+0.9373	+0.5955	+0.0558	+0.0354
hippocampus	33	27	24.70	+2.1556	+0.7111	+0.0873	+0.0288
putamen	13	12	9.90	+0.5532	+0.1575	+0.0559	+0.0159
MGB	10	8	6.55	+0.6086	+0.2137	+0.0929	+0.0326
hypothalamus	3	2	2.20	-0.0938	-0.1198	-0.0427	-0.0544
insula	12	10	9.00	+0.1036	+0.0860	+0.0115	+0.0096
IC	12	5	7.95	+0.4527	-0.0746	+0.0569	-0.0094
AN	2	1	1.45	+0.2757	+0.0505	+0.1902	+0.0348
CN	1	1	0.70	+0.0128	-0.0024	+0.0183	-0.0035
SOC	14	10	10.40	+0.3440	+0.2635	+0.0331	+0.0253
PAG	1	1	0.75	+0.0214	+0.0094	+0.0285	+0.0125

STG receives 91 dimension links from 57 mechanisms; A1_HG receives 63 from 44. CN, TP and PAG receive one link each. A high raw regional value therefore cannot establish greater biological recruitment. Counts describe the frozen registry. The normalization does not remove shared-input dependence or validate any region mapping. Full link-level weights and dimension names are in data/region-links.csv.

Supplementary Table S2 | Signed contributors: flute

Three largest absolute contributions per region for the direct bird→flute endpoint contrast. Signs are retained: a large negative contributor can oppose positive contributors. Values are means of weighted per-frame C³ dimension changes, summed within each mechanism. Selection ranks absolute contributions separately within each region; it does not rank mechanisms globally.

Region	Largest |contribution|	Second	Third
A1_HG	DAP +0.2667	PCCR +0.2629	SSPS +0.2099
STG	TSCP +0.7563	MIAA +0.4104	ESME +0.3595
STS	CMAT +0.2312	ECT +0.1347	CHPI +0.1001
IFG	ECT +0.3279	CDMR +0.3202	SLEE +0.2463
dlPFC	MEAMR +0.2009	SLEE +0.1563	MSR +0.0620
vmPFC	CMAT +0.2188	DMMS +0.1960	DAP +0.1945
OFC	MORMR +0.1671	CLAM +0.0706	SRP +0.0524
ACC	CSG -0.1657	MEAMN +0.1456	VRIAP +0.1423
SMA	NSCP +0.1432	PEOM +0.1197	RIRI +0.1111
PMC	VRIAP +0.2474	SPH +0.2008	NSCP +0.1181
AG	EDNR +0.1594	TSCP +0.1447	HTP +0.1334
TP	MAD +0.0404	—	—
VTA	RPEM +0.0846	SRP +0.0640	MAD -0.0472
NAcc	DAED +0.4236	MORMR +0.2521	RPEM +0.1894
caudate	VMM +0.1436	SSRI -0.0671	DAED -0.0634
amygdala	DAP +0.2329	MEAMN +0.1606	DMMS +0.1423
hippocampus	DAP +0.2288	DMMS +0.1966	PSH +0.1594
putamen	WMED +0.1114	RIRI +0.1008	SPMC +0.0740
MGB	BCH +0.3400	PSH +0.1001	MORMR +0.0734
hypothalamus	AAC -0.0578	TAR -0.0360	—
insula	CSG -0.1462	VRIAP +0.1224	STC +0.1020
IC	BCH +0.3040	SDNPS +0.1471	SDED -0.1331
AN	BCH +0.2757	—	—
CN	BARM +0.0128	—	—
SOC	CTBB +0.3361	DGTP -0.0986	SPMC +0.0631
PAG	TAR +0.0214	—	—

These contributions sum to the endpoint change before float rounding because the four audited endpoint projections never enter the negative pre-ReLU range. A mechanism may contribute through several linked dimensions. Complete contributions, including those omitted from the top-three display, are in data/region-contributions.csv; all weighted dimension links are in data/region-links.csv. No causal neural attribution is implied.

Supplementary Table S2 | Signed contributors: piano

Three largest absolute contributions per region for the direct bird→piano endpoint contrast. Signs are retained: a large negative contributor can oppose positive contributors. Values are means of weighted per-frame C³ dimension changes, summed within each mechanism. Selection ranks absolute contributions separately within each region; it does not rank mechanisms globally.

Region	Largest |contribution|	Second	Third
A1_HG	SDL -0.1238	AMSS -0.1149	SSPS +0.1041
STG	SDL -0.3389	TSCP +0.2947	ESME +0.1344
STS	CMAT +0.1027	PSCL +0.0327	ECT +0.0273
IFG	PNH -0.1636	MEAMR -0.0792	ECT +0.0748
dlPFC	MEAMR -0.1305	SLEE +0.0438	WMED +0.0344
vmPFC	DAP +0.1269	CMAT +0.1198	VRIAP +0.0903
OFC	MORMR +0.0730	ICEM +0.0243	CLAM +0.0208
ACC	VRIAP +0.0903	VMM +0.0599	PNH -0.0563
SMA	MEAMR -0.0845	NSCP +0.0589	WMED +0.0415
PMC	VRIAP +0.0790	NSCP +0.0759	SPH +0.0516
AG	HTP +0.0329	EDNR +0.0324	SDL -0.0308
TP	MAD +0.0149	—	—
VTA	SSRI +0.0669	SRP +0.0424	RPEM +0.0392
NAcc	RPEM +0.1063	IUCP +0.0994	MORMR +0.0878
caudate	SSRI -0.1132	VMM +0.1015	DAED -0.0828
amygdala	PUPF +0.1181	MEAMN +0.0961	VMM +0.0792
hippocampus	VMM +0.1632	PMIM +0.1477	PUPF +0.1112
putamen	SPMC +0.0258	ASAP +0.0256	RIRI +0.0217
MGB	BCH +0.1162	MORMR +0.0562	PSH +0.0236
hypothalamus	TAR -0.1226	AAC +0.0029	—
insula	STC +0.0504	VRIAP +0.0483	CSG -0.0406
IC	SDED -0.0649	BCH -0.0562	PSH +0.0391
AN	BCH +0.0505	—	—
CN	BARM -0.0024	—	—
SOC	CTBB +0.2650	DGTP -0.0359	SPMC +0.0181
PAG	TAR +0.0094	—	—

These contributions sum to the endpoint change before float rounding because the four audited endpoint projections never enter the negative pre-ReLU range. A mechanism may contribute through several linked dimensions. Complete contributions, including those omitted from the top-three display, are in data/region-contributions.csv; all weighted dimension links are in data/region-links.csv. No causal neural attribution is implied.

Supplementary Table S3 | Ordered channel links (1/2)

All valid NeuroLinks, sorted by processing depth and stable registry order. Dimensions retain their frozen code names. A produce operation replaces the current direct channel value; amplify and inhibit depend on that value. The three terminal producers are marked with an asterisk. NE has no producer.

Order	Depth	Source / dimension	Channel	Effect	Weight
1	0	BCH* / P0:consonance_signal	5HT	produce	0.30
2	0	BCH / P0:consonance_signal	DA	produce	0.15
3	0	CSG / M2:aesthetic_appreciation	DA	produce	0.15
4	0	MIAA / E1:novelty_response	DA	produce	0.10
5	0	MPG / P0:onset_state	NE	amplify	0.15
6	0	ICEM / P0:surprise_signal	NE	amplify	0.75
7	0	ICEM / E1:arousal_response	NE	amplify	0.60
8	0	AAC / E0:emotional_arousal	NE	amplify	0.75
9	0	AAC / I0:chills_intensity	NE	amplify	0.50
10	0	DAED / f01:anticipatory_da	DA	produce	0.90
11	0	DAED / f02:consummatory_da	DA	produce	0.90
12	0	DAED / f03:wanting_index	DA	produce	0.85
13	0	DAED / f04:liking_index	OPI	produce	0.80
14	0	MORMR / f01:opioid_release	OPI	produce	0.95
15	0	MORMR / f02:chills_count	OPI	produce	0.85
16	0	RPEM / current_rpe	DA	produce	0.90
17	0	RPEM / rpe_magnitude	DA	produce	0.85
18	0	EDNR / f01:within_connectivity	DA	produce	0.70
19	0	EDNR / f04:expertise_signature	DA	produce	0.65
20	1	PSCL / P0:pitch_prominence_sig	NE	amplify	0.20
21	1	PUPF / G0:pleasure_P	DA	produce	0.75
22	1	MAD / D1:nacc_music_resp	DA	produce	0.80
23	1	IUCP / P0:current_preference_state	DA	produce	0.70
24	1	MCCN / F0:chills_onset_pred	DA	produce	0.80
25	1	MCCN / E3:chills_magnitude	OPI	produce	0.75
26	1	MCCN / E2:arousal_index	NE	amplify	0.55

The table enumerates 33 DA, 10 NE, 8 OPI and 1 5HT links. “Terminal” refers to direct updates in this execution order; it does not claim isolation from upstream C³ dependencies. Tables and code are frozen-version evidence, not an inference about neurotransmitter concentrations.

Supplementary Table S3 | Ordered channel links (2/2)

All valid NeuroLinks, sorted by processing depth and stable registry order. Dimensions retain their frozen code names. A produce operation replaces the current direct channel value; amplify and inhibit depend on that value. The three terminal producers are marked with an asterisk. NE has no producer.

Order	Depth	Source / dimension	Channel	Effect	Weight
27	1	MEAMR / E3:positive_affect	DA	produce	0.75
28	1	SSRI / P1:endorphin_proxy	OPI	produce	0.80
29	1	SSRI / f01:synchrony_reward	DA	produce	0.75
30	1	SSRI / f02:social_bonding_index	OPI	produce	0.70
31	1	HGSIC / M0:groove_index	DA	produce	0.55
32	1	ASAP / F0:beat_when_pred_0_5s	DA	produce	0.65
33	1	DDSMI / P0:partner_sync	OPI	produce	0.60
34	1	VRMSME / P0:motor_drive	DA	produce	0.70
35	1	SPMC / M0:circuit_flow	DA	produce	0.70
36	1	TSCP / f03:plasticity_magnitude	DA	produce	0.70
37	1	TSCP / F1:cortical_enhancement_pred	DA	produce	0.65
38	1	CDMR / P0:mismatch_signal	DA	produce	0.70
39	1	SLEE / f02:detection_accuracy	DA	produce	0.70
40	1	SLEE / F0:next_probability	DA	produce	0.65
41	2	PCCR / P0:chroma_identity_signal	NE	amplify	0.15
42	2	PWSM / P1:precision_estimate	DA	produce	0.45
43	2	PWSM / P0:weighted_error	NE	amplify	0.50
44	2	TAR / T3:depression_improv	DA	produce	0.75
45	2	TAR / T2:anxiety_reduction	NE	inhibit	0.45
46	2	LDAC / E1:pleasure_gating	DA	produce	0.70
47	2	IOTMS* / E0:mor_baseline_proxy	OPI	produce	0.90
48	2	IOTMS / E2:reward_propensity	DA	produce	0.75
49	2	SSPS / f04:peak_proximity	DA	produce	0.70
50	2	SSPS / optimal_zone_pred	DA	produce	0.65
51	2	ESME / M0:mmn_expertise_function	DA	produce	0.70
52	2	ECT* / f04:flexibility_index	DA	produce	0.65

The table enumerates 33 DA, 10 NE, 8 OPI and 1 5HT links. “Terminal” refers to direct updates in this execution order; it does not claim isolation from upstream C³ dependencies. Tables and code are frozen-version evidence, not an inference about neurotransmitter concentrations.

Supplementary Table S4 | Path summaries and integrity checks

Common-RMS paths. OPI ceiling fraction counts every frame and anchor. NE signed endpoint change is an endpoint mean difference; NE path RMS additionally spans all anchors and is a different estimand. The matched endpoint contrast below provides the direct temporal-averaging demonstration.

Path	Anchors	OPI ceiling fraction	NE endpoint mean Δ	NE path RMS
Bird → score	97	0.935902	-0.062344	0.064391
Score → flute	97	0.210670	+0.002701	0.058826
Score → piano	97	0.540908	+0.069266	0.075631
Pitch only	25	1.000000	-0.002502	0.016069
Timing only	25	1.000000	-0.000073	0.054246
Spectrum only	25	0.960000	-0.057793	0.047798
Bird → flute	97	0.978528	-0.059644	0.059656
Bird → piano	97	0.977261	+0.006922	0.060708

Same endpoint pair: NE(u=1) − NE(u=0)

Operator	Signed frame mean	Framewise RMS
Pitch	-0.00250191	0.01926322
Timing	-0.00007280	0.06331264

Computational integrity

Check	Result
Original waveform / engine hashes	1,146 / 855 checked; zero mismatches in original manuscript audit
Neuro replay	1,146 recordings × 423 frames = 484,758 frames
Terminal identity error vs float32 replay	0 for DA, OPI and 5HT
Maximum archived channel-mean error	2.9731868 × 10−8
RAM endpoint-mean error; minimum pre-ReLU	9.4240157 × 10−7; 0.0628350
Original fresh full-engine reconstruction checks	Four exact endpoint checks; no new engine inference in this revision
Independent biological observations	None; one independent source phrase

The original assay, all primary response tables, and all figure data are preserved; the displays have been redrawn with one visual language. data/readout-audit.json records numerical checks and source hashes; data/readout-traces.npz stores exact plotted frame traces. The executable audit and figure scripts are included. Retained source snippets document the manager, executor and IOTMS extraction formula. The full engine and per-recording tensors remain in the separate experiment archive. README.txt states the rebuild commands and package boundary.

Supplementary Table S5 | Mechanism-name key

Frozen module names used in the main figures and terminal-readout audit. Function codes refer to the architecture registry; names are computational labels and do not establish physiological mechanisms. The full 84-module registry, dimension definitions and source links remain in data/source-metadata.json.

Code	Frozen full name	Function	P dims
BCH	Brainstem Consonance Hierarchy	F1	4
CDMR	Context-Dependent Mismatch Response	F8	3
CSSL	Cross-Species Song Learning	F4	2
ECT	Expertise Compartmentalization Trade-off	F8	2
HTP	Hierarchical Temporal Prediction	F2	3
ICEM	Information Content Emotion Model	F2	2
IOTMS	Individual Opioid Tone Music Sensitivity	F6	1
MEAMR	Music-Evoked Autobiographical Memory Reward	F6	1
MIAA	Musical Imagery Auditory Activation	F1	3
MORMR	mu-Opioid Receptor Music Reward	F6	1
SDL	Salience-Dependent Lateralization	F3	2
SDNPS	Stimulus-Dependent Neural Pitch Salience	F1	3
SLEE	Synaptic Long-term Encoding Engine	F8	3
TAR	Therapeutic Affective Resonance	F5	1
TSCP	Temporal Synaptic Consolidation Processor	F8	3

Function and dimension labels

F1: sensory processing; F2: pattern recognition and prediction; F3: attention and salience; F4: memory; F5: emotion and valence; F6: reward and motivation; F7: motor and timing; F8: learning and plasticity. E/M/P/F dimension prefixes denote extraction, memory, present and forecast. A function code such as F4 is distinct from an F-prefixed dimension. The revised primary response estimand pools each mechanism’s actual declared schema; the retained present-state figures pool P-labelled dimensions only. M can denote memory or temporal integration; TAR uses E/TI/P/F and MSPBA S/M/P/F.

Channel and path abbreviations

DA: dopamine-labelled; NE: noradrenaline-labelled; OPI: opioid-labelled; 5HT: serotonin-labelled output. All are model readouts. B: original bird phrase; S: synthetic score; F: sample-derived flute; P: sample-derived piano. The P path abbreviation denotes piano, while P-layer denotes present-state dimensions. RMS means root mean square. RAM denotes the frozen regional projection readout.

Supplementary Fig. S3 | Exact coordinate views

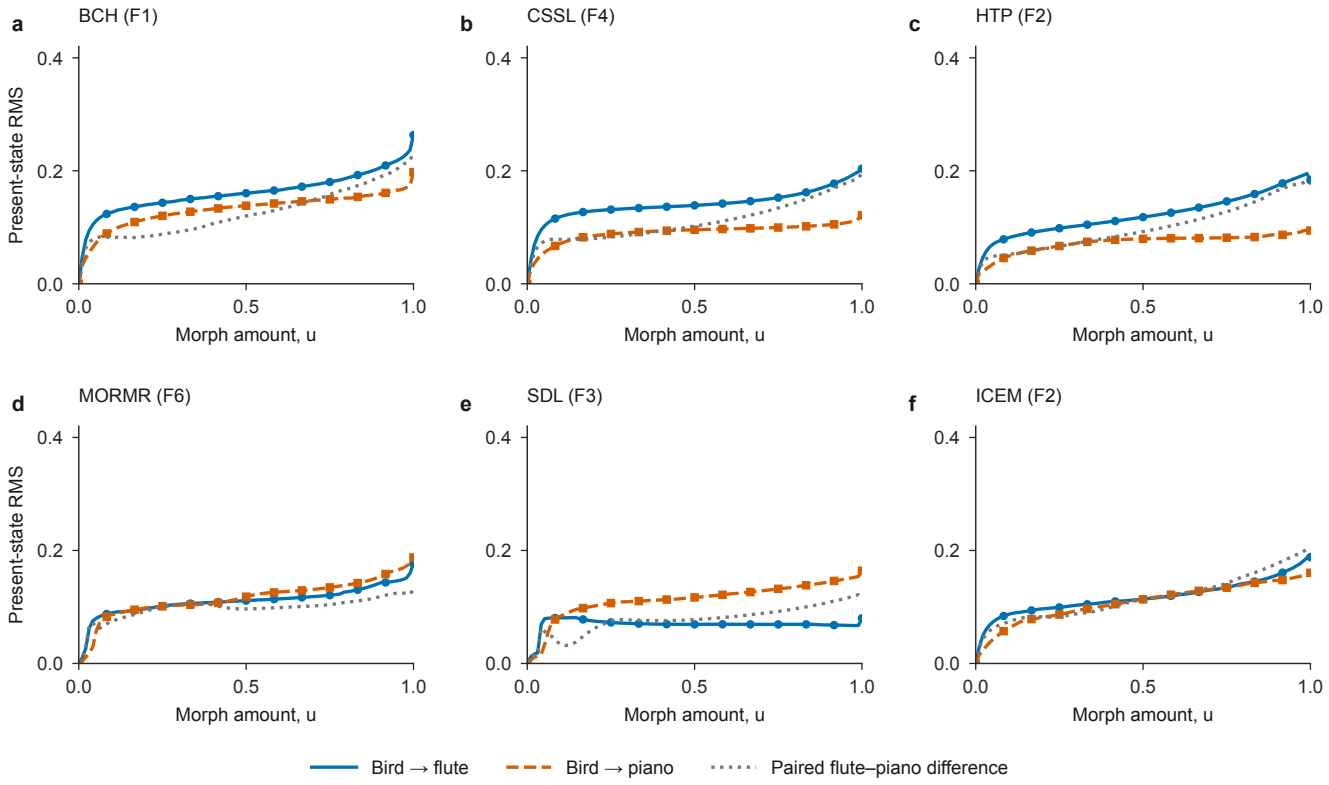

Fig. S3. Exact two-dimensional views of the six coordinates in main Fig. 7. **a–f,** BCH, CSSL, HTP, MORMR, SDL and ICEM. Blue solid and vermilion dashed lines show present-state RMS from the common bird origin; grey dotted lines show RMS between matched flute and piano output tensors. These are distinct estimands. All 97 anchors are retained, with every eighth marked. All panels use the same y limits. Lines connect computed anchors and do not demonstrate resolved responses between them. Function labels refer to Table S5.

Reading the three-dimensional display

Main Fig. 7a groups coordinates a–c; Fig. 7b groups d–f. No principal-component analysis, rescaling or dimensionality reduction is applied. The 3D display exposes joint trajectory shape; these panels retain the relationship of every coordinate to morph amount u. Cross-mechanism units are not perceptually calibrated, and Euclidean separation in the three-coordinate display is not the global 202-dimensional assay metric.

Interactive companion

The retained present-state companion is interactive/index.html in the research package. The offline companion uses the same archived arrays, permits rotation and switches between the two fixed mechanism triplets. Its anchor slider selects one of the 97 computed values without interpolating new model outputs. A separate view shows the 27-setting renderer parameter cube. Hover labels expose the underlying coordinates. The views contain one independent source phrase and no biological measurements.

Supplementary Table S6 | Shared set and route additions

Ranks use all declared output channels, equal-RMS input and full windows. A shared response requires a top-21 rank on every selected route. An asterisk marks the robust five-route set. No output rescaling is applied. B, bird; S, score; F, flute; P, piano.

Mechanism / schema	B→S	S→F	S→P	B→F	B→P
BCH* / E+M+P+F	7	11	14	7	10
PSCL* / E+M+P+F	8	15	12	4	2
SDNPS / E+M+P+F	9	4	5	44	29
IACM* / E+M+P+F	4	16	9	8	11
TAR* / E+TI+P+F	1	3	13	3	1
DAED / E+M+P	14	10	15	11	15
MEAMR / E+P+F	6	12	18	15	12
CDMR / E+M+P+F	16	5	4	36	47
SLEE / E+M+P+F	11	2	2	30	32
ESME / E+M+P+F	20	6	6	46	55

One additional candidate outside the robust set

Route	Candidate	Primary rank	Control range
Bird → score	PCCR	2	2–7
Score → flute	CSG	1	1–1
Score → piano	MSPBA	1	1–2
Bird → flute	PCCR	1	1–2
Bird → piano	PCCR	3	3–4
Pitch only	MPG	1	1–3
Timing only	SDL	1	1–19
Spectrum only	MEAMR	2	1–2
pairedScore	MSPBA	1	1–1
pairedBird	PCCR	2	1–3

Control ranges span native/equal-RMS input, full/trimmed time and grid variants. PairedScore and pairedBird compare existing flute and piano responses at matched u; they are not new flute→piano morph recordings. The extra candidate is selected by response rank, not forced uniqueness. Local maxima and complete non-selected results remain in CSVs.

Supplementary Table S7 | Every TAR endpoint channel

Equal-RMS input and full-phrase averages. Clinical names are literal computational labels. Higher values are not calibrated probabilities, effect sizes or percentages of symptom reduction. Each product or nonlinear term is calculated before averaging.

TAR channel	Bird	Score	Flute	Piano
E0:therapeutic	0.312987	0.480330	0.376044	0.338737
T0:arousal_mod_tgt	0.387676	0.354013	0.342711	0.308711
T1:valence_mod_tgt	0.140196	0.207096	0.168689	0.152672
T2:anxiety_reduction	0.233962	0.349095	0.327338	0.260310
T3:depression_improv	0.050362	0.292997	0.147925	0.095242
I0:rec_tempo_norm	0.120471	0.277929	0.227162	0.192079
I1:rec_consonance	0.674551	0.711750	0.561132	0.518694
P0:therapeutic_reward	0.112320	0.269552	0.100746	0.079502
F0:mood_improv_pred	0.134677	0.189962	0.169008	0.181492
F1:stress_reduc_pred	0.482026	0.425770	0.475034	0.378384

Stress-prediction order under all four controls

Input / time window	Bird	Flute	Score	Piano
matched / full	0.482026	0.475034	0.425770	0.378384
matched / trimmed	0.494172	0.472097	0.435389	0.372126
raw / full	0.510478	0.493316	0.443706	0.367491
raw / trimmed	0.515182	0.489033	0.449949	0.363770

The four conditions preserve bird > flute > score > piano. Trimming removes 0.3 s from each phrase boundary; it does not eliminate the influence of all centered or replicated contexts. The terminal H^3 window is 138 frames (0.801088 s), and incomplete initial windows inherit the first full-window value. No future human observation was used to fit the forecast-labelled output.

Formula coverage

The unique union of all eight path families at two input levels comprises 1,102 recordings. At 423 frames each, the exact TAR terminal audit checks 466,146 frames. Maximum reconstruction error is 1.1920929×10^{-7}; signed mean-term attribution error is 2.1041450×10^{-9}. Archived factorial-only and gain-control recordings outside that union are not counted in this identity check.

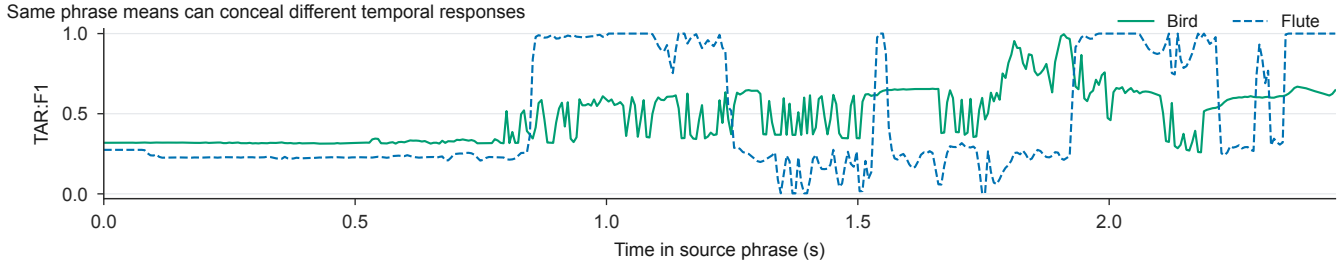

Fig. S4. Every archived F1 frame of the equal-RMS bird and flute endpoints. Their mean difference is −0.006991, but the RMS of their paired frame differences is 0.350864. The signals are compared at the same original frame indices, without time warping. This is model-output variation within one phrase, not a measured listener response.

Supplementary Table S8 | Signed TAR arithmetic

Each row is endpoint minus origin. A=0.20(E0×T2); B=0.20P0; C=0.35(1−r); D=0.25[1−clip(|v|,0,1)]; K is the final clipping residual. All are equal-RMS, full-window means in model units. Sum A+B+C+D+K reproduces net ΔF1 to the stated floating-point tolerance.

Path	A	B	C	D	K	Net
Bird → score	+0.02057	+0.03145	-0.12686	+0.03280	-0.01421	-0.05626
Score → flute	-0.01036	-0.03376	+0.02993	+0.05451	+0.00895	+0.04926
Score → piano	-0.01730	-0.03801	+0.02224	-0.02569	+0.01137	-0.04739
Bird → flute	+0.01020	-0.00231	-0.09694	+0.08731	-0.00525	-0.00699
Bird → piano	+0.00327	-0.00656	-0.10462	+0.00711	-0.00283	-0.10364
Pitch only	+0.00021	+0.00089	+0.01504	+0.00231	+0.00000	+0.01846
Timing only	+0.00019	-0.00005	-0.13877	+0.01763	+0.00000	-0.12100
Spectrum only	+0.01681	+0.02108	+0.10643	+0.00180	-0.01085	+0.13526

Temporal displacement despite similar means

Path	Mean ΔF1	Framewise RMS ΔF1
Bird → score	-0.056256	0.293803
Score → flute	+0.049265	0.431714
Score → piano	-0.047386	0.419005
Bird → flute	-0.006991	0.350864
Bird → piano	-0.103642	0.377487

Interior extrema are retained, not selected as interventions

Path	Minimum F1	At u	Maximum F1	At u
Bird → score	0.232819	0.604167	0.486945	0.041667
Score → flute	0.386345	0.114583	0.709433	0.822917
Score → piano	0.317033	0.739583	0.468831	0.447917
Bird → flute	0.288550	0.750000	0.706517	0.968750
Bird → piano	0.337091	0.135417	0.706528	0.822917

Supplementary Table S9 | Conditional integration

Primary reader: equal-RMS input; ridge α=1; active-subset dimension denominator. Every row uses five contiguous held-out blocks and four-anchor buffers. Gain=best-single MAE−full-profile MAE. The best single layer is chosen after evaluating all single layers on the same held-out blocks, so the comparison is descriptive.

Mechanism	Route	Full MAE	Best layer	Single MAE	Gain
BCH	B→S	0.10738	M	0.09472	-0.01266
BCH	S→F	0.04115	E	0.02470	-0.01645
BCH	S→P	0.03024	P	0.04288	+0.01264
PSCL	B→S	0.06222	E	0.06273	+0.00051
PSCL	S→F	0.03402	F	0.02224	-0.01178
PSCL	S→P	0.06906	M	0.05258	-0.01648
IACM	B→S	0.11980	M	0.11333	-0.00647
IACM	S→F	0.02933	M	0.02062	-0.00871
IACM	S→P	0.07077	P	0.03799	-0.03279
TAR	B→S	0.25306	TI	0.14471	-0.10835
TAR	S→F	0.11303	TI	0.11080	-0.00224
TAR	S→P	0.11840	TI	0.17390	+0.05551
SDNPS	B→S	0.16709	P	0.28546	+0.11837
SDNPS	S→F	0.08212	P	0.05314	-0.02898
SDNPS	S→P	0.05985	P	0.02959	-0.03027
DAED	B→S	0.16807	E	0.12364	-0.04443
DAED	S→F	0.10207	E	0.11158	+0.00951
DAED	S→P	0.12060	E	0.11170	-0.00890
MEAMR	B→S	0.08655	E	0.08690	+0.00035
MEAMR	S→F	0.21151	E	0.19876	-0.01275
MEAMR	S→P	0.06358	E	0.05701	-0.00657
CDMR	B→S	0.37589	E	0.34020	-0.03569
CDMR	S→F	0.12366	P	0.11675	-0.00691
CDMR	S→P	0.14646	F	0.13885	-0.00761
SLEE	B→S	0.35634	E	0.28037	-0.07597
SLEE	S→F	0.13884	P	0.12581	-0.01302
SLEE	S→P	0.16263	P	0.14618	-0.01645
ESME	B→S	0.39685	P	0.38366	-0.01319
ESME	S→F	0.12975	M	0.12525	-0.00450
ESME	S→P	0.15534	E	0.15407	-0.00127

All mechanisms, layer subsets, penalties, input-level conditions and denominator variants remain in integration/ data. Selecting channels for a reader is not an internal architecture ablation. The empty-reader MAE is 0.333803; no human endpoint is used.

Supplementary Table S10 | Full mechanism registry (1/4)

Every frozen mechanism, with its actual layer schema and equal-RMS/full-window rank on five routes. Names are model labels; the table does not identify measured neural mechanisms. S/M/P/F and E/TI/P/F are retained without forced relabelling.

Code / schema	Full mechanism name	B→S	S→F	S→P	B→F	B→P
BCH E+M+P+F	Brainstem Consonance Hierarchy	7	11	14	7	10
CSG E+M+P+F	Consonance-Salience Gradient	24	1	3	60	56
MIAA E+M+P+F	Musical Imagery Auditory Activation	10	27	25	12	16
MPG E+M+P+F	Melodic Processing Gradient	12	26	23	13	6
PCCR E+M+P+F	Pitch Chroma Cortical Representation	2	25	17	1	3
PNH H+M+P+F	Pythagorean Neural Hierarchy	26	18	21	50	43
PSCL E+M+P+F	Pitch Salience in Cortical Lateralization	8	15	12	4	2
SDNPS E+M+P+F	Stimulus-Dependent Neural Pitch Salience	9	4	5	44	29
SDED E+M+P+F	Sensory Dissonance Early Detection	35	22	24	62	40
TPIO E+M+P+F	Timbre Perception-Imagery Overlap	33	44	36	16	20
TPRD T+M+P+F	Tonotopy-Pitch Representation Dissociation	58	45	50	34	42
HTP E+M+P+F	Hierarchical Temporal Prediction	32	29	64	10	30
SPH E+M+P+F	Spatiotemporal Prediction Hierarchy	31	36	35	21	33
ICEM E+M+P+F	Information Content Emotion Model	21	52	43	19	21
PWUP E+M+P+F	Precision-Weighted Uncertainty Processing	23	50	41	14	22
WMED E+M+P+F	Working Memory-Entrainment Dissociation	77	76	78	43	58
UDP E+M+P+F	Uncertainty-Driven Pleasure	43	56	55	33	26
CHPI E+M+P+F	Cross-Modal Harmonic Predictive Integration	52	41	39	58	36
IGFE E+M+P+F	Individual Gamma Frequency Enhancement	41	63	63	18	19
MAA E+M+P+F	Multifactorial Atonal Appreciation	17	40	30	6	9
PSH E+M+P+F	Prediction Silencing Hypothesis	37	74	62	17	52

Supplementary Table S10 | Full mechanism registry (2/4)

Every frozen mechanism, with its actual layer schema and equal-RMS/full-window rank on five routes. Names are model labels; the table does not identify measured neural mechanisms. S/M/P/F and E/TI/P/F are retained without forced relabelling.

Code / schema	Full mechanism name	B→S	S→F	S→P	B→F	B→P
SNEM E+M+P+F	Sensory Novelty and Expectation Model	82	77	83	69	67
IACM E+M+P+F	Inharmonicity-Attention Capture Model	4	16	9	8	11
BARM E+M+P+F	Brainstem Auditory Response Modulation	72	78	80	78	69
STANM E+M+P+F	Spectrotemporal Attention Network Model	66	65	76	39	51
AACM E+M+P+F	Aesthetic-Attention Coupling Model	40	60	60	51	27
AMSS E+M+P+F	Attention-Modulated Stream Segregation	36	47	45	24	17
ETAM E+M+P+F	Entrainment, Tempo and Attention Modulation	62	79	75	42	59
DGTP E+M+P+F	Domain-General Temporal Processing	79	83	82	81	78
SDL E+M+P+F	Salience-Dependent Lateralization	15	62	61	20	8
NEWMD E+M+P+F	Neural Entrainment-Working Memory Dissociation	83	82	81	80	77
PWSM E+M+P+F	Precision-Weighted Salience Model	80	73	71	52	31
MEAMN E+M+P+F	Music-Evoked Autobiographical Memory Network	34	34	31	26	34
MMP R+P+F+C	Musical Mnemonic Preservation	76	72	77	57	61
RASN E+M+P+F	Rhythmic Auditory Stimulation Neuroplasticity	69	81	79	75	49
PMIM P+M+S+F	Predictive Memory Integration Model	47	57	37	48	24
OII E+M+P+F	Oscillatory Intelligence Integration	84	84	84	84	84
HCMC E+M+P+F	Hippocampal-Cortical Memory Circuit	75	75	74	73	71
RIRI E+M+P+F	RAS-Intelligent Rehabilitation Integration	13	38	32	5	5
MSPBA S+M+P+F	Musical Syntax Processing in Broca's Area	44	42	1	23	7
VRIAP E+M+P+F	VR-Integrated Analgesia Paradigm	19	48	42	32	45
CMAPCC E+M+P+F	Cross-Modal Action-Perception Common Code	61	55	58	40	54

Supplementary Table S10 | Full mechanism registry (3/4)

Every frozen mechanism, with its actual layer schema and equal-RMS/full-window rank on five routes. Names are model labels; the table does not identify measured neural mechanisms. S/M/P/F and E/TI/P/F are retained without forced relabelling.

Code / schema	Full mechanism name	B→S	S→F	S→P	B→F	B→P
DMMS E+M+P+F	Developmental Music Memory Scaffold	48	32	26	47	53
CSSL E+M+P+F	Cross-Species Song Learning	53	61	56	27	35
CDEM C+M+P+F	Context-Dependent Emotional Memory	25	80	73	29	60
SRP N+C+T+M+P+F	Striatal Reward Prediction	56	21	28	59	64
AAC E+A+I+P+F	Autonomic-Arousal Circuit	55	51	68	74	57
VMM V+R+P+C	Valence-Mode Mapping	57	23	27	64	62
PUPF E+U+G+P+F	Pleasure-Uncertainty Prediction Function	45	39	47	25	18
CLAM E+B+C+P+F	Closed-Loop Affective Modulation	73	33	48	82	81
MAD E+D+A+P+F	Musical Anhedonia Disconnection	64	37	52	71	68
NEMAC E+M+W+P+F	Nostalgia-Evoked Memory-Affect Circuit	60	46	38	55	44
STAI E+M+P+F	Spectral-Temporal Aesthetic Integration	54	24	29	66	72
DAP E+D+P+F	Developmental Affective Plasticity	22	14	10	22	25
CMAT E+S+T+P+F	Cross-Modal Affective Transfer	49	17	20	65	66
TAR E+TI+P+F	Therapeutic Affective Resonance	1	3	13	3	1
DAED E+M+P	Dopamine Anticipation-Experience Dissociation	14	10	15	11	15
MORMR E+M+P+F	mu-Opioid Receptor Music Reward	38	19	19	49	38
RPEM E+M+P	Reward Prediction Error in Music	29	8	11	35	28
IUCP E+P+F	Inverted-U Complexity Preference	51	30	46	53	39
MCCN E+P+F	Musical Chills Cortical Network	18	28	51	31	23
MEAMR E+P+F	Music-Evoked Autobiographical Memory Reward	6	12	18	15	12
SSRI E+M+P+F	Social Synchrony Reward Integration	42	64	40	28	13

Supplementary Table S10 | Full mechanism registry (4/4)

Every frozen mechanism, with its actual layer schema and equal-RMS/full-window rank on five routes. Names are model labels; the table does not identify measured neural mechanisms. S/M/P/F and E/TI/P/F are retained without forced relabelling.

Code / schema	Full mechanism name	B→S	S→F	S→P	B→F	B→P
LDAC E+P+F	Liking-Dependent Auditory Cortex	46	31	34	63	65
IOTMS E+P	Individual Opioid Tone Music Sensitivity	5	20	22	9	14
SSPS E+P+F	Saddle-Shaped Preference Surface	39	67	57	56	76
PEOM E+M+P+F	Period Entrainment Optimization Model	67	43	44	76	80
MSR E+M+P+F	Musician Sensorimotor Reorganization	59	66	69	54	50
GSSM E+M+P+F	Gait-Synchronized Stimulation Model	81	70	72	83	82
HMCE E+M+P+F	Hierarchical Musical Context Encoding	3	35	33	2	4
HGSIC E+M+P+F	Hierarchical Groove State Integration Circuit	78	59	66	77	79
ASAP E+M+P+F	Action Simulation for Auditory Prediction	70	71	65	72	74
DDSMI E+M+P+F	Dyadic Dance Social Motor Integration	63	54	53	61	63
VRMSME E+M+P+F	VR Music Stimulation Motor Enhancement	65	53	54	68	73
SPMC E+M+P+F	SMA-Premotor-M1 Motor Circuit	74	58	59	79	83
NSCP E+M+P+F	Neural Synchrony Commercial Prediction	50	49	49	41	46
CTBB E+M+P+F	Cerebellar Theta-Burst Balance	68	68	70	67	70
STC E+M+P+F	Singing Training Connectivity	71	69	67	70	75
EDNR E+M+P+F	Expertise-Dependent Network Reorganization	30	13	16	38	37
TSCP E+M+P+F	Temporal Synaptic Consolidation Processor	27	9	8	37	48
CDMR E+M+P+F	Context-Dependent Mismatch Response	16	5	4	36	47
SLEE E+M+P+F	Synaptic Long-term Encoding Engine	11	2	2	30	32
ESME E+M+P+F	Error-Signal Modulated Encoding	20	6	6	46	55
ECT E+M+P+F	Expertise Compartmentalization Trade-off	28	7	7	45	41

Supplementary Table S11 | Reproduction and evidence index

Evidence family	Complete retained record
Original present-state and readout analysis	data/: all mechanisms, dimensions, regions, channels, traces, source contributions and numerical controls
Full-profile mechanism analysis	evidence/mechanisms/data/: sensitivity.csv, channel-sensitivity.csv, ranks.csv, reference-direction.csv, factorial.csv, features.npz and path-curves.npz
All reader outcomes	evidence/mechanisms/data/: original 70,690 readout outcomes, split definitions and saved predictions
Layer integration follow-up	evidence/integration/data/: 41,760 blocked-layer-subsets.csv rows, predictions.npz, integration-gains.csv, response-comparison.csv, validation records
Route signatures	evidence/stages/data/: names-and-ranks.csv, selected-additions.csv, all-local-changes.csv (92,736 rows), peak-intervals.csv (4,080), local-winner-runs.csv (473)
TAR terminal computation	evidence/stages/data/: tar-frames-and-terms.npz, all ten channel curves, signed contrasts, endpoints, extrema and formula validation
Editable scientific artwork	figures/: all 11 main and four supplementary figures, each in PDF, SVG and PNG
Source and revision provenance	preserved-source-manifest.json, FIGURE_CROSSWALK.txt, CLAIMS_AND_SOURCES.txt and SHA256SUMS.txt

Integrity and analysis scope

The 4,050,720 saved follow-up predictions reproduce 41,760 MAE values within 7.21×10^{-8}. A separate 100-fold sklearn comparison agrees within 1.9×10^{-14}. These are numerical verification checks, not confidence intervals. Layer subset and scale failures are retained. The original frozen archive remains external and unchanged; its 1,146 input-waveform hashes and 855 engine-file hashes were verified in the original record. The revision reuses computed evidence and generates no new human or animal measurements.

Interpretation and a decisive next test

Compare preregistered TAR contrasts with ratings and stress-recovery outcomes on independent source phrases, using roughness, envelope dynamics, loudness, pleasantness and arousal baselines. Include challenging interior anchors and plausible-register controls. Test complete TAR versus its terms, and include within-source conditions that match average predictions but differ in temporal pattern. Biological contribution requires held-out predictive value; raw-unit sensitivity or an evocative module name alone does not supply it.

Human evidence motivating the proposed test

Study	Relevant evidence and boundary
Alvarsson et al. (2010)	Four-minute nature-sound recovery; skin conductance and HF-HRV differ in outcome. DOI: 10.3390/ijerph7031036
Stobbe et al. (2022)	Six-minute birdsong conditions; anxiety/paranoia effects, no cognitive-task improvement. DOI: 10.1038/s41598-022-20841-0
You et al. (2026)	Music versus active natural-sound control; recovery and structure-linked network dynamics. Abstract-level use. DOI: 10.1073/pnas.2611584123

These independent studies motivate the comparison; none tests this source phrase, its instrument morphs, or TAR's formula. The new test must evaluate added held-out value beyond the acoustic components and establish its own exposure and outcome protocol.