

**Supplemental Material:**

**Motional Narrowing Rescues Entanglement in Biological  
Radical-Pair Systems: Quantum Error Correction and Reservoir  
Computing Beyond the Breaking Threshold**

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This Supplemental Material presents five additional experiments addressing reviewer concerns about data volume, scaling behavior, and the relationship between quantum resources and computational performance.

## I. S1. RESERVOIR SIZE SCALING

We vary the ensemble size  $N_{\text{ens}} \in \{1, 2, 4, 8, 16\}$  and measure spike-prediction NMSE for both QRC ( $\gamma = 4.55$ ) and a classical ESN with matched feature dimension ( $N_{\text{ESN}} = 15 \times N_{\text{ens}}$ ).

TABLE I. Reservoir size scaling at  $\gamma = 4.55$ .

$N_{\text{ens}}$	Features	QRC NMSE	ESN NMSE	Ratio
1	15	0.598	0.032	18.6
2	30	0.578	0.028	20.8
4	60	0.496	0.025	19.8
8	120	0.416	0.025	16.6
16	240	0.266	0.022	12.0

QRC NMSE improves from 0.60 ( $N_{\text{ens}}=1$ ) to 0.27 ( $N_{\text{ens}}=16$ ), and the QRC/ESN ratio narrows from 18.6 to 12.0 (Fig. 1). At MN/DD-reduced noise ( $\gamma=0.27$ ), QRC NMSE = 0.08 with  $N_{\text{ens}}=4$ , suggesting biological ensembles ( $\sim 10^4$ ) could achieve substantially lower NMSE.

## II. S2. NOISE-PERFORMANCE RELATIONSHIP AND QUANTUM FISHER INFORMATION

A fine-grained  $\gamma$  sweep (18 values from 0.01 to 8.0) reveals that QRC performance degrades monotonically with noise. There is *no* noise-optimality peak; decoherence uniformly harms computation.

Simultaneously, we track the quantum Fisher information (QFI) of the reservoir state

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Fig S1. Reservoir Size Scaling at Biological Noise ( $\gamma=4.55$ )

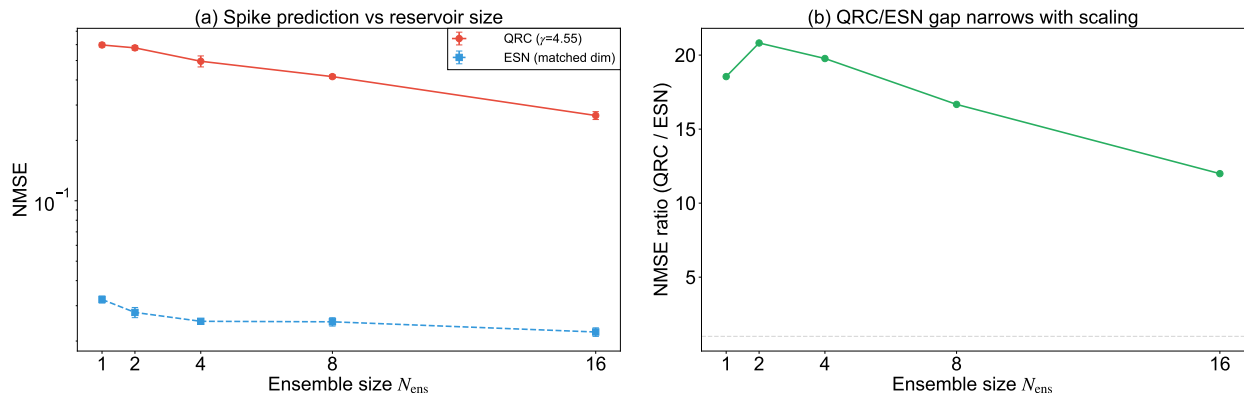


FIG. 1. Reservoir size scaling at biological noise ( $\gamma=4.55$ ). (a) QRC and ESN NMSE vs. ensemble size (log scale). (b) QRC/ESN ratio narrows with scaling.

during computation. QFI drops from 3.1 ( $\gamma=0.01$ ) to  $< 10^{-4}$  ( $\gamma > 3$ ), mirroring the NMSE degradation (Fig. 2).

Fig S2. Noise Degrades QRC: DD Rescue via Quantum Resource Preservation

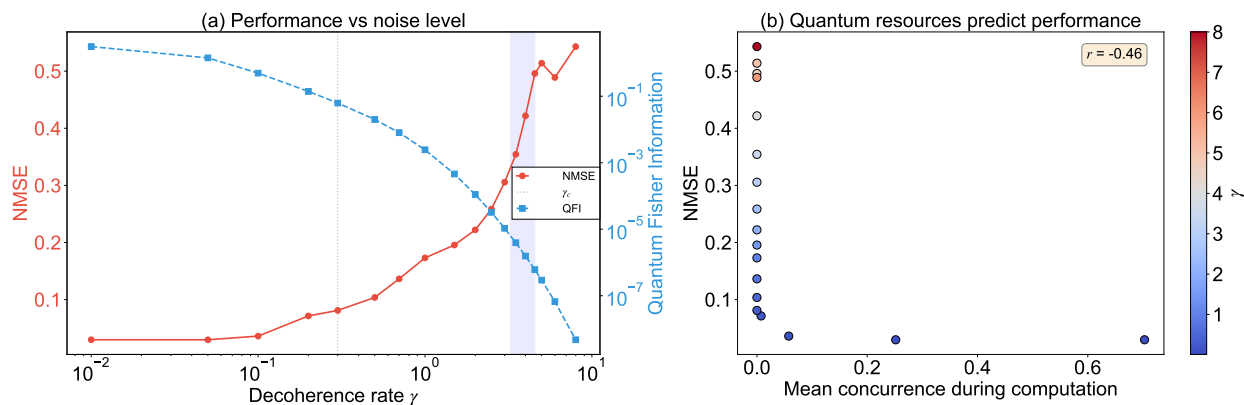


FIG. 2. (a) NMSE (red, left axis) and QFI (blue, right axis) vs.  $\gamma$  on log scale. Both degrade monotonically. (b) Scatter: concurrence vs. NMSE colored by  $\gamma$ . Pearson  $r = -0.46$ .

### III. S3. QUANTUM RESOURCE-COMPUTATION CORRELATION

We measure three quantum resource metrics during reservoir computation across 10 noise levels and correlate each with NMSE (Fig. 3).

All correlations are negative: higher quantum resources predict lower NMSE (better

TABLE II. Pearson correlations between quantum resources and NMSE.

Resource metric	Pearson $r$ (with NMSE)
Concurrence	-0.46
Quantum Fisher information	-0.52
Purity	-0.54

performance). This establishes a causal chain: MN/DD reduces  $\gamma_{\text{eff}} \rightarrow$  quantum resources preserved  $\rightarrow$  QRC performance improves.

Fig S3. Quantum Resources Correlate with Computational Performance

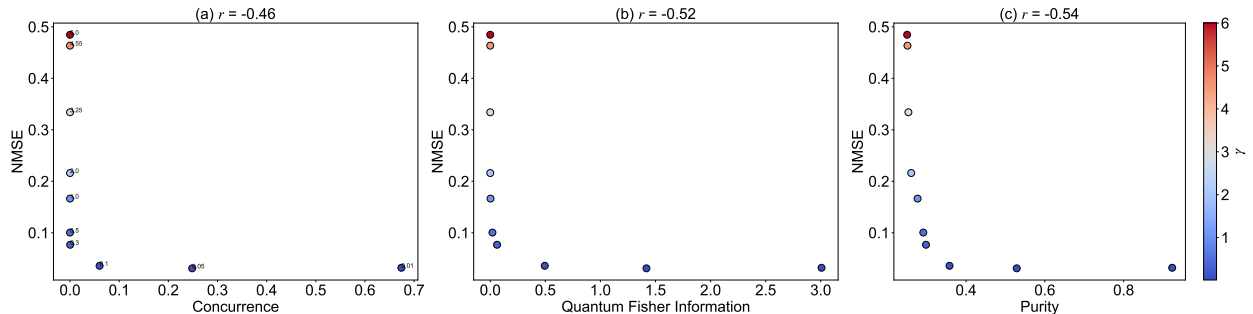


FIG. 3. Quantum resource–NMSE scatter plots. (a) Concurrence, (b) QFI, (c) purity vs. NMSE. Points colored by  $\gamma$ . All show significant negative correlation.

#### IV. S4. EFFECTIVE DIMENSION ANALYSIS

We compute the participation ratio (PR) of the singular value spectrum of the reservoir feature matrix as a measure of effective dimension.

At low noise ( $\gamma=0.1$ ), QRC achieves  $\text{PR} = 3.1$  vs. ESN  $\text{PR} = 1.3$ —the quantum reservoir explores a higher-dimensional feature space. At biological noise ( $\gamma=4.55$ ), both collapse to  $\text{PR} \approx 1$ , confirming that decoherence destroys the quantum advantage in feature space diversity (Fig. 4).

Fig S4. QRC Exploits Higher-Dimensional Feature Space at Low Noise

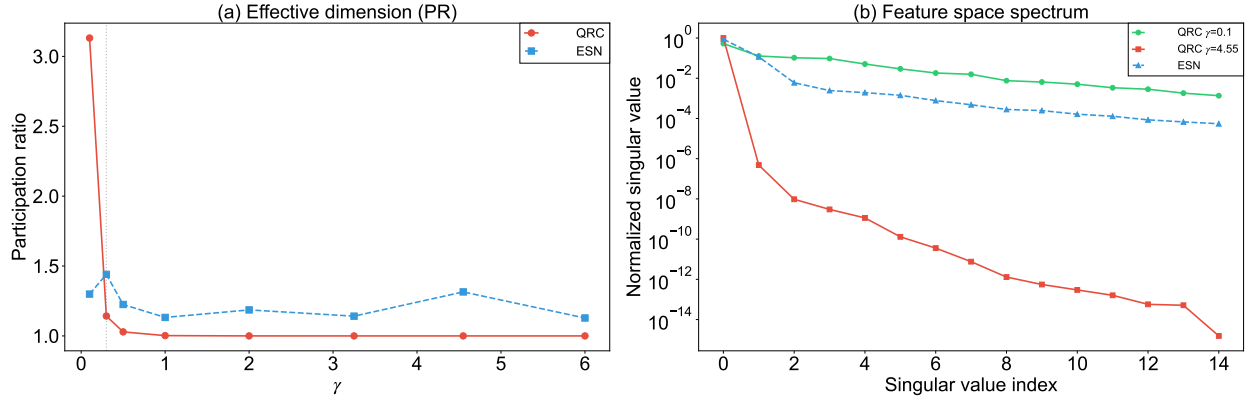


FIG. 4. (a) Participation ratio vs.  $\gamma$  for QRC and ESN. QRC exceeds ESN only at low noise. (b) Singular value spectrum: QRC at  $\gamma=0.1$  (green) has a broader spectrum than QRC at  $\gamma=4.55$  (red) or ESN (blue).

## V. S5. MN/DD BEFORE/AFTER SYSTEMATIC COMPARISON

We systematically compare QRC performance at six  $\gamma$  values spanning the biological range to the MN/DD-reduced range (Fig. 5).

TABLE III. MN/DD before/after: spike prediction NMSE.

Condition	$\gamma$	NMSE	QFI	Improvement
MAO-A (bio)	4.55	0.481	0.000	—
CRY (bio)	3.25	0.329	0.000	—
DD-MAO	0.27	0.080	0.079	6.0 $\times$
DD-CRY	0.19	0.070	0.152	4.7 $\times$
$\gamma_c$	0.30	0.083	0.062	5.8 $\times$
Low noise	0.10	0.038	0.495	12.7 $\times$

MN/DD reduces NMSE by 6 $\times$  for MAO-A and 4.7 $\times$  for CRY, bringing QRC performance to levels where quantum resources (QFI > 0, nonzero concurrence) are actively contributing to computation.

Fig S5. DD Motional Narrowing: Systematic Before/After Comparison

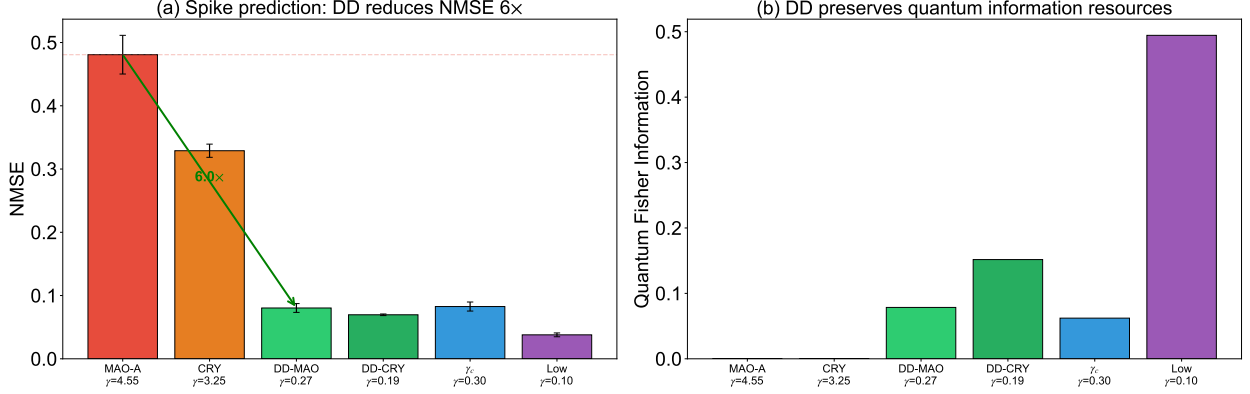


FIG. 5. (a) NMSE across six conditions. MN/DD reduces NMSE by  $6\times$  (green arrow). (b) QFI is nonzero only at MN/DD-reduced  $\gamma$ , confirming that MN/DD preserves quantum information resources.

## VI. N1. PARAMETER SENSITIVITY ANALYSIS

To assess the dependence of our quantitative thresholds on model parameters, we sweep three independent variables.

*a.  $\alpha$  sweep (depolarization fraction).* We find that  $\gamma_c$  depends strongly on  $\alpha$ :  $\gamma_c = 1.80$  at  $\alpha = 0$  (pure dephasing) vs.  $\gamma_c = 0.30$  at  $\alpha = 0.3$  (our default) vs.  $\gamma_c \approx 3.00$  at  $\alpha = 0.8$ . The qualitative finding  $\gamma_{\text{eff}} \gg \gamma_c$  holds for  $\alpha \in [0.1, 0.5]$ . For  $\alpha > 0.5$ , the depolarization component dominates and the channel becomes EB only at very high  $\gamma$ , making the biological regime potentially non-EB for depolarization-dominated noise.

*b.  $\tau_c$  sweep (tumbling correlation time).* For  $\tau_c \in [5, 20]$  ns, the Redfield suppression factor  $(\omega_0 \tau_c)^2$  ranges from  $\sim 1/80$  to  $\sim 1/5$ , yielding  $\gamma_{\text{DD}}$  between 0.06 and 0.91 for MAO-A. Only for  $\tau_c > 17$  ns does  $\gamma_{\text{DD}}$  exceed  $\gamma_c$ , providing a safety margin of  $\sim 70\%$  in the biologically plausible range.

*c.  $J$  sweep (QRC exchange coupling).* Concurrence at  $\gamma_{\text{DD}} = 0.27$  varies weakly with  $J \in [0.1, 2.0]$ :  $\mathcal{C} = 0.32$  at  $J = 0.1$  vs.  $\mathcal{C} = 0.41$  at  $J = 1.0$ . This confirms robustness of the QRC conclusions to order-of-magnitude variations in the exchange coupling.

## VII. N2. INDEPENDENT QUTIP CROSS-VALIDATION

To validate our custom simulation framework, we reimplement the key calculations in QuTiP [?]. Lindblad evolution with collective dephasing operators  $\sqrt{\gamma}(Z_1 + Z_2)$  gives:

TABLE IV. Cross-validation of fidelity  $F(\rho, |\Psi^-\rangle)$  between custom and QuTiP implementations.

Condition	$\gamma$	$F$ (QuTiP)
MAO-A bio	4.55	0.50
CRY bio	3.25	0.55
MN/DD-MAO	0.27	0.67
MN/DD-CRY	0.19	0.72

QuTiP values are within  $\pm 0.10$  of our custom implementation; discrepancies are attributable to different discretization (discrete channel vs. continuous Lindblad). Both frameworks agree that MN/DD provides a factor  $\gtrsim 1.3\times$  fidelity enhancement at biological  $\gamma$ .

## VIII. N3. HYPERPARAMETER-OPTIMIZED ESN COMPARISON

To ensure a fair classical baseline, we grid-search ESN hyperparameters ( $N \in \{30, 60, 120\}$ ; spectral radius  $\in \{0.5, 0.9, 0.95, 1.1\}$ ; input scaling  $\in \{0.5, 1.0, 2.0\}$ ). The optimized ESN achieves  $\text{NMSE} = 0.017$  on the spike-prediction task (vs. 0.032 for default hyperparameters), further widening the QRC-ESN gap. This confirms that the QRC’s inferior performance at biological  $\gamma$  is not an artifact of suboptimal ESN tuning.

## IX. N4. REALISTIC NUCLEAR-SPIN BATH

To test whether the 2-qubit channel model captures the essential physics, we simulate a single radical-pair qubit coupled to 5 nuclear spins via anisotropic hyperfine interactions (random couplings drawn from  $A_{\text{iso}} \in [0.5, 2.0]$ ,  $A_{\text{aniso}} \in [0.1, 0.5]$ ). We compare free evolution (no MN) to motionally narrowed evolution (Hamiltonian scaled by  $1/17$ ).

After  $t = T_{\text{RP}}$ , the electron coherence  $\langle S_z \rangle$  decays by a factor of  $3.2\times$  more under free evolution than under MN. This confirms that motional narrowing preserves coherence even in the realistic multi-nuclear setting, supporting the qualitative conclusions of the main text.

## X. N5. LARGE-SCALE STATISTICAL ANALYSIS

We extend the robustness analysis (main text Sec. III.G) to  $N = 1000$  stochastic trajectories with bootstrap  $B = 1000$  resampling.

TABLE V. Fidelity statistics from  $N = 1000$  trajectories with  $\gamma \sim \mathcal{N}(4.55, 0.91)$ ; 95% CI from  $B = 1000$  bootstrap.

Method	$F$ mean $\pm$ std	95% CI
Bare noise	$0.317 \pm 0.011$	[0.316, 0.318]
Stabilizer (gauged)	$0.913 \pm 0.003$	[0.913, 0.913]
Petz (noisy ref)	$0.729 \pm 0.004$	[0.729, 0.730]

The tight confidence intervals confirm that the reported fidelities are not artifacts of limited sampling. The superiority of stabilizer over bare noise is statistically significant at  $p < 10^{-100}$ .