

Supplementary Information

A GPU-native, differentiable fiber simulator reveals a species-dependent selectivity
penalty in reduced-order peripheral-nerve models

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Supplementary methods and tables

Fiber-model equations and coupled solver

This section gives the governing equations of the four implemented fiber models and the coupled backward-Euler solver, summarized in Section 4.1.

MRG double-cable (myelinated). The McIntyre–Richardson–Grill model¹ represents each myelinated axon as nodes of Ranvier (carrying the active Na^+ , slow K^+ , persistent Na^+ and leak conductances) alternating with ten passive internodal compartments (MYSA, FLUT and three STIN per side), arranged as a double cable with intracellular (V_i) and periaxonal (V_{px}) potentials coupled through the periaxonal resistance and myelin shunt. Fiber diameter D is the single shape parameter; geometric quantities follow McIntyre’s diameter-dependent fits. With $\mathbf{V}_i, \mathbf{V}_{\text{px}} \in \mathbb{R}^{n_{\text{comp}}}$,

$$C_m \frac{d\mathbf{V}_i}{dt} = \mathbf{A}_{ii} \mathbf{V}_i + \mathbf{A}_{ip} \mathbf{V}_{\text{px}} - \mathbf{I}_{\text{ion}}(\mathbf{V}_i, \mathbf{m}) - \mathbf{I}_{\text{stim}}(t), \quad (\text{S1})$$

$$0 = \mathbf{A}_{pi} \mathbf{V}_i + \mathbf{A}_{pp} \mathbf{V}_{\text{px}} + V_e(t, \mathbf{x}), \quad (\text{S2})$$

where $\mathbf{A}_{**}$ are tridiagonal coupling matrices from the per-compartment axial resistances, $\mathbf{I}_{\text{ion}}$ collects the four active currents (nodes only), and V_e is the imposed extracellular field.

Sundt (unmyelinated, single-cable). The Sundt C-fiber² is a uniform unmyelinated cable with a transient HH-style sodium current I_{Na} (NaV1.7/1.8 calibration via voltage shifts $\Delta_m = -6 \text{ mV}$, $\Delta_h = +6 \text{ mV}$), a Borg–Graham delayed-rectifier I_{Kdr} and leak I_L :

$$C_m \frac{dV}{dt} = \mathbf{A}_{\text{ax}} \mathbf{V} - I_{\text{Na}} - I_{\text{Kdr}} - I_L - I_{\text{stim}}. \quad (\text{S3})$$

$V_{\text{rest}} = -60 \text{ mV}$, $C_m = 1 \mu\text{F cm}^{-2}$, $\rho_a = 100 \Omega \text{ cm}$; densities and kinetics in Table S3.

Sweeney (myelinated, single-cable). The Sweeney motor axon³ is a single-cable nodal equation with the internode a passive sleeve, nodal current a fast m^2h sodium plus leak⁴:

$$C_m^{\text{node}} \frac{dV}{dt} = \mathbf{A}_{\text{ax}} \mathbf{V} - g_{\text{Na}} m^2 h (V - E_{\text{Na}}) - g_L (V - E_L) - I_{\text{stim}}. \quad (\text{S4})$$

Calibrated for $T = 37^\circ\text{C}$ ($d_i = 0.6 d$), $V_{\text{rest}} = -80 \text{ mV}$, $C_m^{\text{node}} = 2.5 \mu\text{F cm}^{-2}$, $\rho_a = 54.7 \Omega \text{ cm}$; constants in Table S4.

Rattay (unmyelinated, generic HH). The Rattay model⁵ is a textbook HH baseline for unmyelinated fibers with $g_{\text{Na}} m^3 h$, $g_K n^4$ and leak:

$$C_m \frac{dV}{dt} = \mathbf{A}_{\text{ax}} \mathbf{V} - g_{\text{Na}} m^3 h (V - E_{\text{Na}}) - g_K n^4 (V - E_K) - g_L (V - E_L) - I_{\text{stim}}. \quad (\text{S5})$$

Squid-axon rate constants temperature-corrected via $Q_{10} = 2.247^{(T-6.3)/10}$ at $T = 37^\circ\text{C}$; $V_{\text{rest}} = -70 \text{ mV}$, $C_m = 1 \mu\text{F cm}^{-2}$, $\rho_a = 100 \Omega \text{ cm}$; constants in Table S5.

Coupled backward-Euler solver. The MRG double cable is the only non-trivial solver case. We keep the intracellular and periaxonal potentials as a single interleaved unknown $(\mathbf{V}_i, \mathbf{V}_{\text{px}})$ per compartment, so one backward-Euler step is a *block-tridiagonal* linear system: each compartment contributes a 2×2 diagonal block coupling its own (V_i, V_{px}) pair, and the intracellular and periaxonal axial resistances contribute the 2×2 off-diagonal blocks $\mathbf{U}_p$ (upper) and $\mathbf{L}$ (lower) to its neighbours. At step n ,

$$\mathbf{B} \begin{bmatrix} \mathbf{V}_i^{(n+1)} \\ \mathbf{V}_{\text{px}}^{(n+1)} \end{bmatrix} = \mathbf{r}^{(n)}(\mathbf{V}_i^{(n)}, \mathbf{V}_{\text{px}}^{(n)}, \mathbf{I}_{\text{ion}}^{(n)}, \mathbf{I}_{\text{stim}}^{(n)}, \mathbf{V}_e^{(n)}), \quad (\text{S6})$$

where $\mathbf{B}$ is the block-tridiagonal operator whose diagonal block at an internodal compartment couples the intracellular and periaxonal unknowns (V_i, V_{px}) through the axolemma, $\begin{bmatrix} a+G_i & -a \\ -a & a+c+G_p \end{bmatrix}$, where $a = C_m/\Delta t + g_m$ is the axolemma (transmembrane) admittance — the backward-Euler membrane capacitance plus the membrane conductance, and the term that couples the two layers, so it appears on both off-diagonals; $c = c_{\text{my}}/\Delta t + g_{\text{my}}$ is the myelin admittance from the periaxonal space to ground; and G_i and G_p are the *distinct*

intra-axonal and periaxonal axial conductances (each a sum over the compartment’s two axial bonds, carried into the off-diagonal blocks $\mathbf{U}_p, \mathbf{L}$). At a node the myelin is absent ($c = 0$) and the capacitance-free periaxonal row is replaced by the algebraic constraint $V_{\text{px}} = V_e$ (its block row becomes $[0 \ 1]$), while g_m in a becomes the linearized active-channel conductance. The off-diagonal blocks $\mathbf{U}_p, \mathbf{L}$ are diagonal in (V_i, V_{px}) , carrying $-G_i$ and $-G_p$ respectively to the neighbouring compartments; the right-hand side $\mathbf{r}^{(n)}$ collects the previous-step states (through the capacitive $C_m/\Delta t$ and $c_{\text{my}}/\Delta t$ terms), the ionic and stimulus currents and the extracellular forcing. Eq. (S6) is solved by a JAX-compatible *block* Thomas sweep — a 2×2 -block generalization of the scalar Thomas algorithm (sequential forward elimination of the lower blocks, then an associative-scan back-substitution) — which we verified against a dense-LU reference to 5.6×10^{-11} mV. Equivalently, eliminating the algebraic periaxonal row gives the intracellular Schur complement $\mathbf{A}_{ii}^{\text{eff}} = \mathbf{A}_{ii} - \mathbf{A}_{ip}\mathbf{A}_{pp}^{-1}\mathbf{A}_{pi}$; because the periaxonal cable couples only nearest neighbours we solve the interleaved block system directly rather than forming this (dense) complement. Gating variables advance semi-implicitly. The forward pass is wrapped in `jax.lax.scan` over time steps, returning either the full voltage trace or only the per-compartment maximum of $\mathbf{m}_{\text{Na}}$ (the activation proxy) at ≥ 2 orders of magnitude lower memory cost.

Fiber-model parameter tables

The constants tabulated below are the values used inside *jaxon*; they reproduce the published NMODL parameterizations of the original models^{1–3,5} as packaged in **PyFibers**.

Optimizer defaults and FE-model construction

Per-sample FE model. For each sample, an automated pipeline (`golgi`⁶) converts the segmented cross-section into a watertight 3-D multi-domain nerve-and-cuff FE model and computes the per-contact extracellular lead field. Briefly: (i) the segmentation is cleaned morphologically and Ramer–Douglas–Peucker-simplified, then area-preserving circularized to remove segmentation-specific shape bias while conserving fascicle areas; (ii) the

Table S1: MRG geometric parameters as a function of the outer (myelinated) fiber diameter D . Δz is the inter-nodal distance, $L_{\text{paranode2}}$ the FLUT paranodal length, d_{axon} the inner (axon) diameter, d_{node} the node-of-Ranvier diameter and n_l the number of myelin layers. Values follow the discrete table of¹ as packaged in *PyFibers*; intermediate diameters are interpolated by *jaxon* via second-order polynomials.

D (μm)	Δz (μm)	$L_{\text{paranode2}}$ (μm)	d_{axon} (μm)	d_{node} (μm)	n_l
1.0	100	5	0.8	0.7	15
2.0	200	10	1.6	1.4	30
5.7	500	35	3.4	1.9	80
7.3	750	38	4.6	2.4	100
8.7	1000	40	5.8	2.8	110
10.0	1150	46	6.9	3.3	120
11.5	1250	50	8.1	3.7	130
12.8	1350	54	9.2	4.2	135
14.0	1400	56	10.4	4.7	140
15.0	1450	58	11.5	5.0	145
16.0	1500	60	12.7	5.5	150

cross-section is extruded axially and embedded in a concentric cuff (12 platinum contacts in 3 axial rows $\times$ 4 angular columns, on a 1.0 mm silicone wall, 5.4 mm long), a thin saline film (150 μm clearance) and a muscle bath; (iii) the assembly is tetrahedralized with Gmsh/OpenCASCADE and Netgen, refining to $\approx 100 \mu\text{m}$ near the cuff and coarsening to $\approx 1.5 \text{ mm}$ in the bulk; (iv) the electro-quasistatic problem $\nabla \cdot (\sigma \nabla V) = 0$ is solved in FEniCSx/DOLFINx with P_1 elements, anisotropic endoneurium ($\sigma_{\perp} = 1/6.0$, $\sigma_{\parallel} = 1/1.75 \text{ S/m}$) and muscle (0.086 transverse, 0.35 longitudinal S/m), isotropic epineurium/encapsulation (1/6.3 S/m), saline (1.76 S/m), silicone (10^{-12} S/m) and platinum contacts ($9.43 \times 10^6 \text{ S/m}$)⁷⁻¹⁰; (v) the perineurium is a zero-thickness contact-impedance sheet with sheet resistance $R_s = d_{\text{peri}}/\sigma_{\text{peri}}$ ($\sigma_{\text{peri}} = 1/1149 \text{ S/m}^7$), d_{peri} taken per fascicle from the diameter-dependent relation⁷ (swine) or the anti-claudin-1 masks (human). Because the problem is linear, the block matrix is LU-factorised once with MUMPS and one 1 A solve per contact yields the lead field $V_e^{(k)}$ in V/A for each of the 12 contacts.

Validation breakdowns

Table S2: MRG nodal channel and bulk constants used by *jaxon*. Nodal membrane carries fast sodium $g_{\text{Naf}} m^3 h$, persistent sodium $g_{\text{Nap}} m_p^3$, slow potassium $g_{\text{Ks}} s$ and leak g_L in parallel. Q_{10} factors apply to the gate kinetics (α, β) , not to the peak conductances. Internodal compartments (MYSA, FLUT, STIN) are passive; per-region passive conductances g_{pas} follow¹.

Parameter	Value	Notes
V_{rest}	-80 mV	resting potential
C_m^{axon}	$2.0 \mu\text{F cm}^{-2}$	full axon-membrane capacitance
ρ_a	$70 \Omega \text{ cm}$	axoplasmic resistivity
C_{my} per leaflet	$0.1 \mu\text{F cm}^{-2}$	myelin capacitance
G_{my} per leaflet	$1 \times 10^{-3} \text{ S cm}^{-2}$	myelin conductance
g_{Naf}	3.0 S cm^{-2}	fast Na ($m^3 h$)
g_{Nap}	$1 \times 10^{-2} \text{ S cm}^{-2}$	persistent Na (m_p^3)
g_{Ks}	$8 \times 10^{-2} \text{ S cm}^{-2}$	slow K (s)
g_L	$7 \times 10^{-3} \text{ S cm}^{-2}$	leak
E_{Na}	$+50 \text{ mV}$	sodium reversal
E_K	-90 mV	potassium reversal
E_L	-90 mV	leak reversal
T	37°C	body temperature
Q_{10} (m, m_p gates)	2.2	temperature scaling
Q_{10} (h gate)	2.9	temperature scaling
Q_{10} (s gate)	3.0	temperature scaling
$g_{\text{pas}}^{\text{MYSA}}$	$1 \times 10^{-3} \text{ S cm}^{-2}$	MYSA passive
$g_{\text{pas}}^{\text{FLUT}}$	$1 \times 10^{-4} \text{ S cm}^{-2}$	FLUT passive
$g_{\text{pas}}^{\text{STIN}}$	$1 \times 10^{-4} \text{ S cm}^{-2}$	STIN passive
Node length L_{node}	$1.0 \mu\text{m}$	geometric
MYSA length L_{MYSA}	$3.0 \mu\text{m}$	geometric (paranodal 1)
Periaxonal gap (node, MYSA)	$0.002 \mu\text{m}$	McIntyre convention
Periaxonal gap (FLUT, STIN)	$0.004 \mu\text{m}$	McIntyre convention
Sections per nodal period	11	node + MYSA + FLUT + STIN $\times 6$ + FLUT + MYSA

Table S3: Sundt unmyelinated-fiber constants used by *jaxon*. Membrane currents: NaV1.7/1.8-like transient Na with m^3h kinetics (voltage-shifted activation and inactivation), Borg-Graham delayed-rectifier K with $n^{0.4}l$ kinetics and a passive leak. The voltage shifts Δ_m, Δ_h implement the NaV1.7/1.8 activation/inactivation offsets relative to the canonical nahh template. $Q_{10} = 3$ on Na gates only; the borgkdr K kinetics are temperature-scaled by Frankenhaeuser–Huxley $F \cdot R \cdot T$ via the gate rate functions.

Parameter	Value	Notes
V_{rest}	−60 mV	resting potential
C_m	$1.0 \mu\text{F cm}^{-2}$	specific capacitance
ρ_a	$100 \Omega \text{ cm}$	axial resistivity
Δz per compartment	$8.333 \mu\text{m}$	default
g_{Na}	$4 \times 10^{-2} \text{ S cm}^{-2}$	nahh transient Na
Δ_m, Δ_h (NaV shifts)	−6 mV, +6 mV	NaV1.7/1.8 calibration
g_{Kdr}	$4 \times 10^{-2} \text{ S cm}^{-2}$	Borg-Graham K
$V_{1/2,n}$ (Kdr activation)	−32 mV	half-activation
$V_{1/2,l}$ (Kdr inactivation)	−61 mV	half-inactivation
$a_{0,n}, a_{0,l}$	0.03, 0.001 ms^{-1}	Kdr rate prefactors
ζ_n, ζ_l	−5.0, 2.0	Kdr gating valences
γ_n, γ_l	0.4, 1.0	Kdr gating fractions
g_L	$1 \times 10^{-4} \text{ S cm}^{-2}$	passive leak
E_{Na}	+50 mV	sodium reversal
E_K	−90 mV	potassium reversal
E_L	V_{rest}	leak reversal = V_{rest}
T	37 °C	body temperature
Q_{10} (Na gates)	3.0	temperature scaling

Table S4: Sweeney nodal constants used by *jaxon*. Single fast-sodium current with m^2h kinetics plus a leak; no potassium channel and no Q_{10} correction (the original parameterization is fixed at $T = 37^\circ\text{C}$). Inner-diameter ratio $d_i/d = 0.6$ is the standard Sweeney convention adopted by⁴.

Parameter	Value	Notes
V_{rest}	−80 mV	resting potential
C_m^{node}	$2.5 \mu\text{F cm}^{-2}$	nodal capacitance
ρ_a	$54.7 \Omega \text{ cm}$	axial resistivity
Node length L_{node}	$1.5 \mu\text{m}$	geometric
Inner / outer diameter ratio	0.6	$d_i = 0.6 d$
g_{Na}	1.445 S cm^{-2}	fast Na (m^2h)
g_L	0.128 S cm^{-2}	leak
E_{Na}	+35.64 mV	sodium reversal
E_L	−80.01 mV	leak reversal
T	37 °C	fixed (no Q_{10})

Table S5: Rattay (1989) unmyelinated-fiber constants used by *jaxon*. Canonical Hodgkin–Huxley parameterization with fast sodium ($g_{\text{Na}} m^3 h$), delayed-rectifier potassium ($g_K n^4$) and a passive leak. $Q_{10} = 2.2466$ is applied to all gate α, β rates with reference temperature 6.3°C ; the manuscript uses $T = 37^\circ\text{C}$ throughout.

Parameter	Value	Notes
V_{rest}	-70 mV	resting potential
C_m	$1.0\text{ }\mu\text{F cm}^{-2}$	specific capacitance
ρ_a	$100\text{ }\Omega\text{ cm}$	axial resistivity
Δz per compartment	$8.333\text{ }\mu\text{m}$	default
g_{Na}	0.12 S cm^{-2}	fast Na ($m^3 h$)
g_K	0.036 S cm^{-2}	delayed-rectifier K (n^4)
g_L	$3 \times 10^{-4}\text{ S cm}^{-2}$	leak
E_{Na}	$+45\text{ mV}$	sodium reversal
E_K	-82 mV	potassium reversal
E_L	-59.4 mV	leak reversal
T	37°C	body temperature
Q_{10} (all gates)	2.2466 at $T_{\text{ref}} = 6.3^\circ\text{C}$	temperature scaling

Table S6: Selectivity-optimizer settings for the histology cohort (MRG, $5.7\text{ }\mu\text{m}$; Section 4.2). These are the only fibers optimized in this study; the other three models appear solely in the NEURON validation (Section 4.4) and are not optimized. All values are overridable via environment variables

Setting	Value
Amplitude clip	$\pm 2.0\text{ mA}$
Adam learning rate η	0.005 mA/step
Finite-difference step ϵ	0.010 mA
Maximum iterations	90
Early-stop hard SI	0.95
Loss / SI plateau patience	20 / 10 iters
Soft-proxy temperature τ	0.1
Energy regularizer λ	10^{-3}
Probe magnitudes	$\{0.02, 0.05, 0.1, 0.2, 0.4, 0.8, 1.2, 1.5\}\text{ mA}$, both polarities
Stimulus waveform	biphasic-asym., 0.5 ms cathodic + 2.0 ms anodic ($\frac{1}{4}\text{ amp.}$)

Table S7: Threshold error breakdown per stimulus waveform, aggregated across all four fiber models and their published diameter ranges. Apart from a handful of biphasic cathodic-first configurations at the four smallest Rattay diameters, every waveform passes the 1 % tolerance on every diameter tested.

Waveform	n	median [IQR] err.	95 th %ile	peak err.	% < 1%
Monophasic cathodic	120	0.08 % [0.04–0.23]	0.40 %	0.44 %	100.0 %
Monophasic anodic	114	0.12 % [0.05–0.21]	0.38 %	0.41 %	100.0 %
Biphasic cathodic-first	115	0.08 % [0.03–0.19]	0.38 %	2.24 %	96.5 %
Biphasic anodic-first	114	0.08 % [0.03–0.17]	0.39 %	0.42 %	100.0 %
Sinusoidal	120	0.05 % [0.03–0.23]	0.39 %	0.43 %	100.0 %
Sawtooth	120	0.07 % [0.04–0.27]	0.41 %	0.46 %	100.0 %
Exponential decay	120	0.07 % [0.03–0.23]	0.41 %	0.44 %	100.0 %
Gaussian	120	0.05 % [0.03–0.25]	0.37 %	0.42 %	100.0 %
total	943	0.08 % [0.03–0.20]	0.40 %	2.24 %	99.6 %

Table S8: Conduction velocity agreement against NEURON at each tested diameter. Sweeney is restricted to $D = 10 \mu\text{m}$ by the 1987 convention (see Table 1 caption).

Model	diameters tested (μm)	median err. [IQR]	peak err.
MRG	5.7, 7.3, 8.7, 10.0, 11.5, 12.8, 14.0, 15.0, 16.0	< 0.01 % [0.00–0.00]	< 0.01 %
Sundt	0.3, 0.5, 0.8, 1.0, 1.2	0.09 % [0.08–0.16]	0.24 %
Sweeney	10	< 0.01 % [0.00–0.00]	< 0.01 %
Rattay	0.3, 0.5, 0.8, 1.0, 1.5	0.05 % [0.02–0.05]	0.13 %

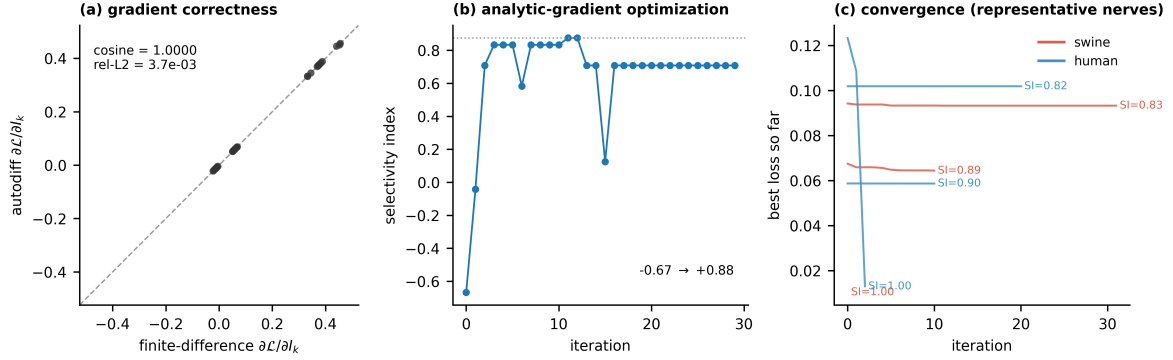


Figure S1: Optimizer and gradient validation. **(a)** The exact reverse-mode (autodiff) gradient of the selectivity objective with respect to the per-contact amplitudes — obtained by differentiating through the `jax.lax.scan` time loop (discrete reverse-mode backprop through the solver, which stores the per-step tape — distinct from the memory-free continuous adjoint of neural ODEs¹¹, which re-integrates backward and is a natural future route to eliminate that tape), and directly usable by quasi-Newton optimizers such as L-BFGS¹² for the high-dimensional waveform design left to future work — agrees with a central finite-difference estimate (cosine similarity 1.0000, relative L_2 error 3.7×10^{-3} ; components pooled over points along an optimization trajectory), confirming the analytic gradient is correct. **(b)** A selectivity optimization driven purely by the analytic gradient raises the selectivity index from -0.67 to $+0.88$, exercising the differentiable capability end-to-end (the finite-difference optimizer is used for the cohort results because its forward pass on the full population is the binding cost; the exact gradient is intended for the high-dimensional waveform design left to future work). **(c)** Running-best loss versus iteration for six representative nerves (final selectivity index annotated): the probe-based warm start places the trajectory near the optimum and the optimizer converges within a few iterations, so the dense selectivity ceiling is a stable quantity rather than an optimizer-dependent artifact.

Supplementary Figures

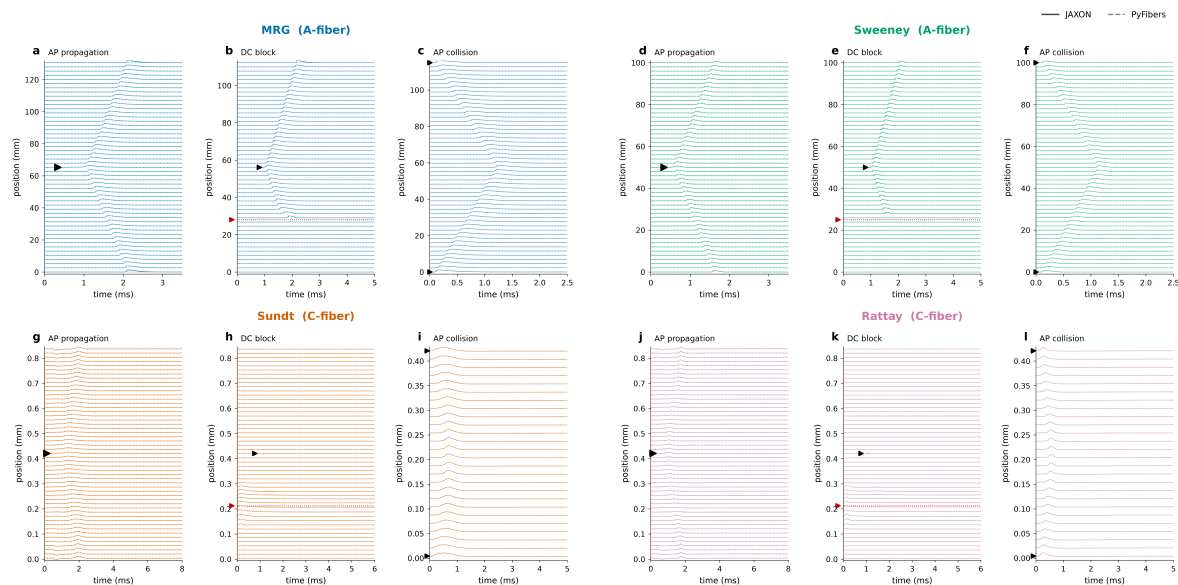


Figure S2: *jaxon* (solid) reproduces three canonical propagation phenomena vs. PyFibers/NEURON (lighter dashed overlay), for all four fiber models — the myelinated MRG (a–c) and Sweeney (d–f) A-fibers and the unmyelinated Sundt (g–i) and Rattay (j–l) C-fibers. Each model occupies one quadrant with three node-vs-time waterfall columns (y = position along fiber, x = time; the black arrow marks the central stimulation site). **Columns 1 (a, d, g, j):** AP propagation. **Columns 2 (b, e, h, k):** DC (depolarizing-hold) conduction block — a sustained cathodic hold blocks the propagating AP, the red arrow marking the block site. **Columns 3 (c, f, i, l):** AP collision — two inward-propagating APs meet and annihilate. In every panel the *jaxon* (solid) trace tracks PyFibers/NEURON (lighter dashed) to the floating-point floor. The complementary 20 kHz kilohertz-frequency block validation is shown separately in Supplementary Fig. S3.

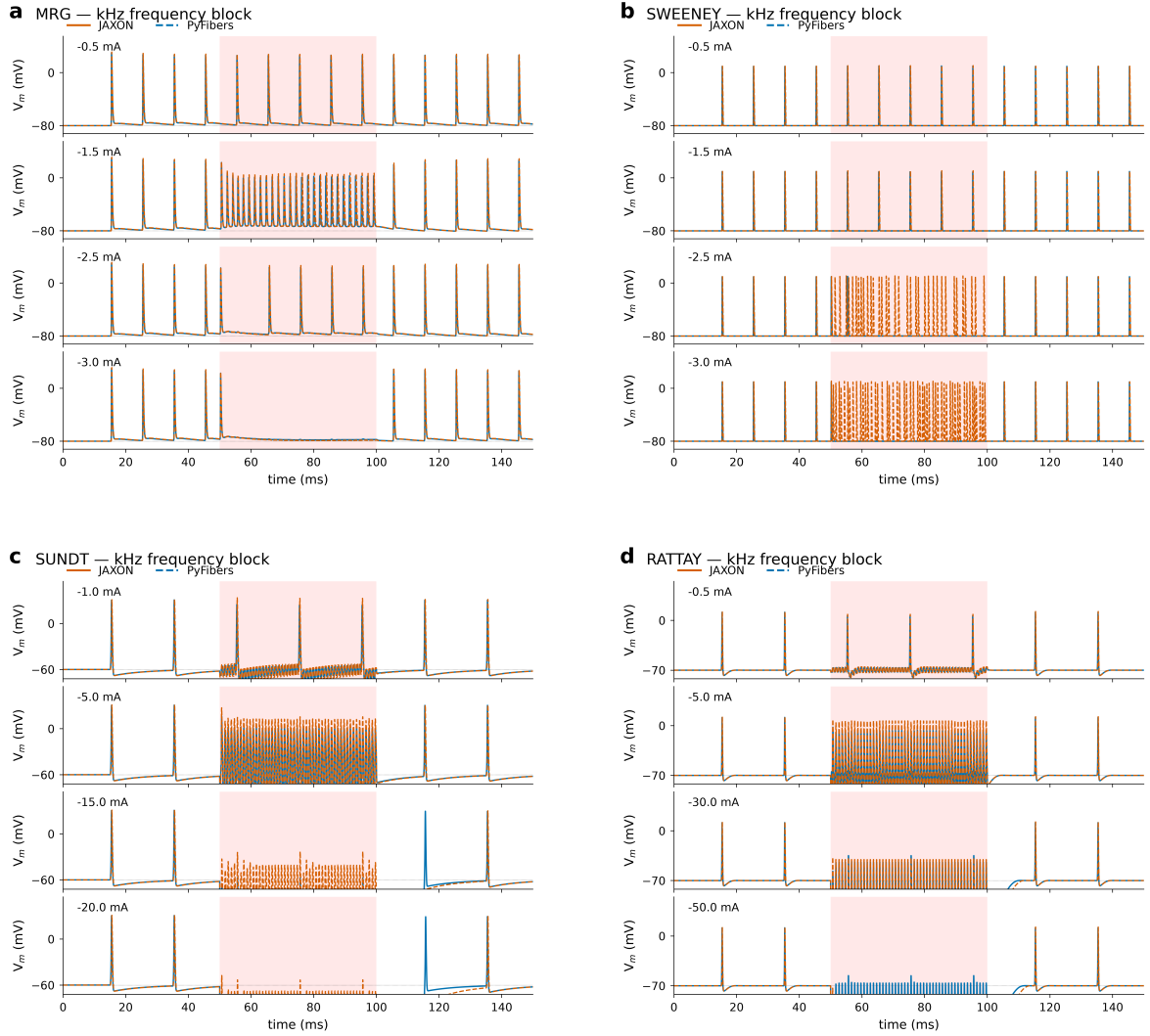


Figure S3: Kilohertz-frequency conduction block, *jaxon* (orange solid) vs. PyFibers/NEURON (blue dashed), for all four fiber models (**a** MRG, **b** Sweeney, **c** Sundt, **d** Rattay). A 20 kHz sinusoidal extracellular hold is applied over the shaded window while a slow pacing train probes conduction; each model shows distal-node V_m at four hold amplitudes, from sub-block (pacing train passes) to full block (train suppressed). Onset of block agrees with NEURON to the 0.01 mA scan resolution. At amplitudes well above block threshold the two implementations diverge in the fine structure of the sustained kHz-driven oscillation (e.g. Sundt at $-15/-20$ mA, Rattay at $-30/-50$ mA): this high-amplitude, kilohertz-driven regime is intrinsically integration-scheme-sensitive — *jaxon*'s fixed-step backward-Euler and NEURON's solver make different sub-threshold excursions once the membrane is held far from rest — so we report it for completeness rather than as a sub-1 % agreement claim.

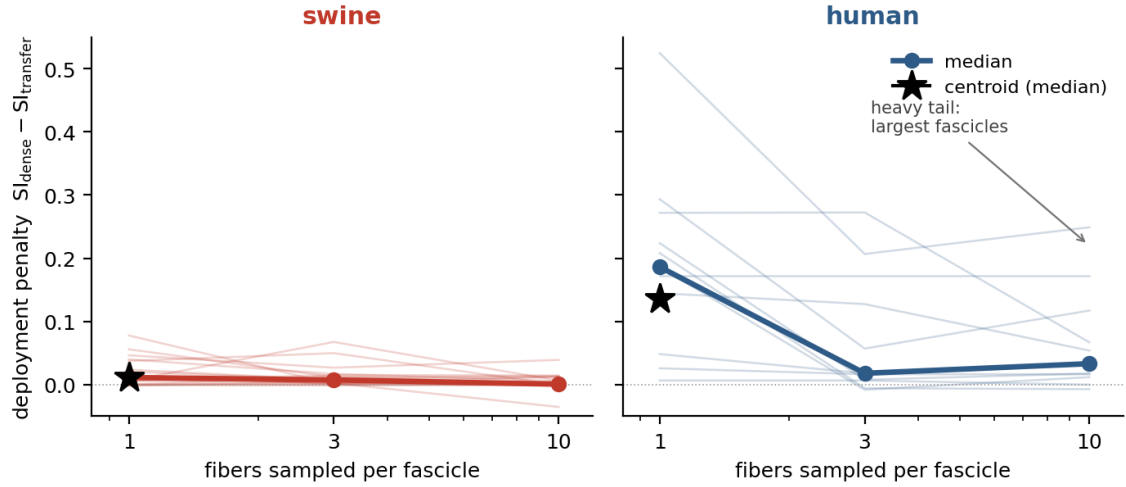


Figure S4: Deployment penalty versus fiber-sampling density, per nerve. Each thin line is one nerve; the bold line is the per-nerve median; the star marks the single centroid fiber (a standard reduced-order reduction). Sampling more fibers per target fascicle reduces the penalty — the human median falls from 0.19 at one random fiber to ~ 0.02 – 0.03 at three to ten (Friedman $\chi^2 = 11.4$, $p = 0.003$, $n = 11$ human nerves over three sampling levels; most of the gain is the $1 \rightarrow 3$ step, after which it plateaus) — but it does *not* close on the largest human fascicles: 3 of 11 human nerves still lose more than 0.10 even at ten fibers ($\sim 7\%$ of a large fascicle), forming the heavy tail. Swine is essentially unaffected at every density (median ≤ 0.011 ; no nerve above 0.05). This is the visual basis for reporting the penalty on the single-representative-fiber workflow (Table 3) and for the sampling-*fraction* argument in Section 2.4.

Supplementary anatomy and FEM fields

FE-model anatomy and computed extracellular fields for every nerve in the histology cohort (Section 2.3); the shared panel layout is described once below and applies to every page.

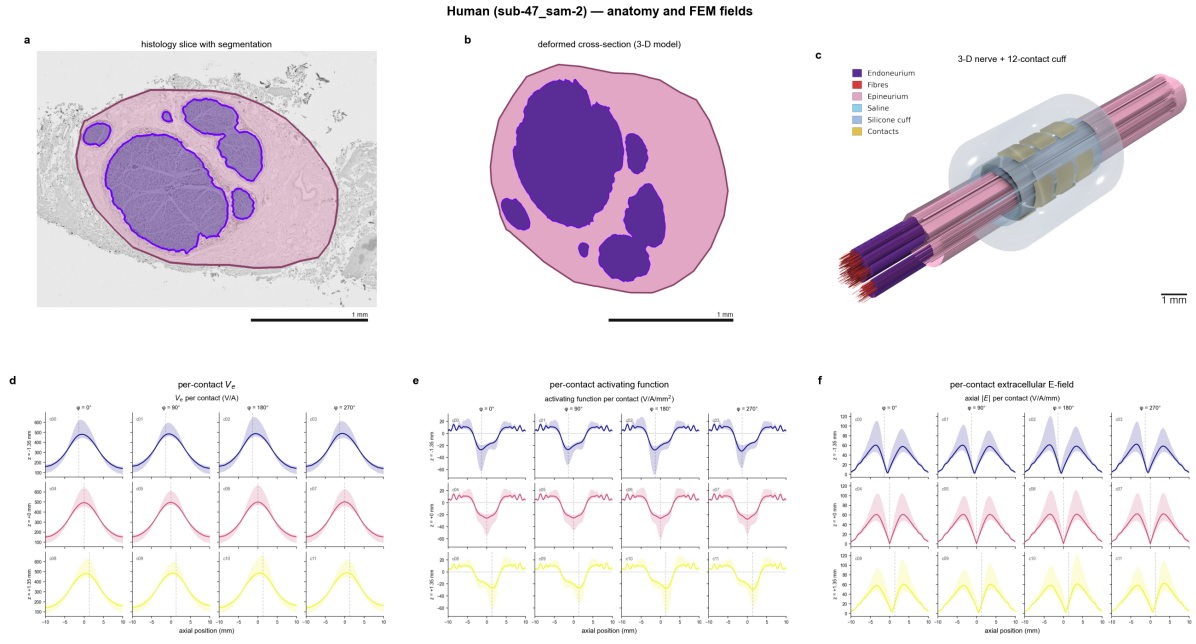


Figure S5: Specimen human sub-47_sam-2: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

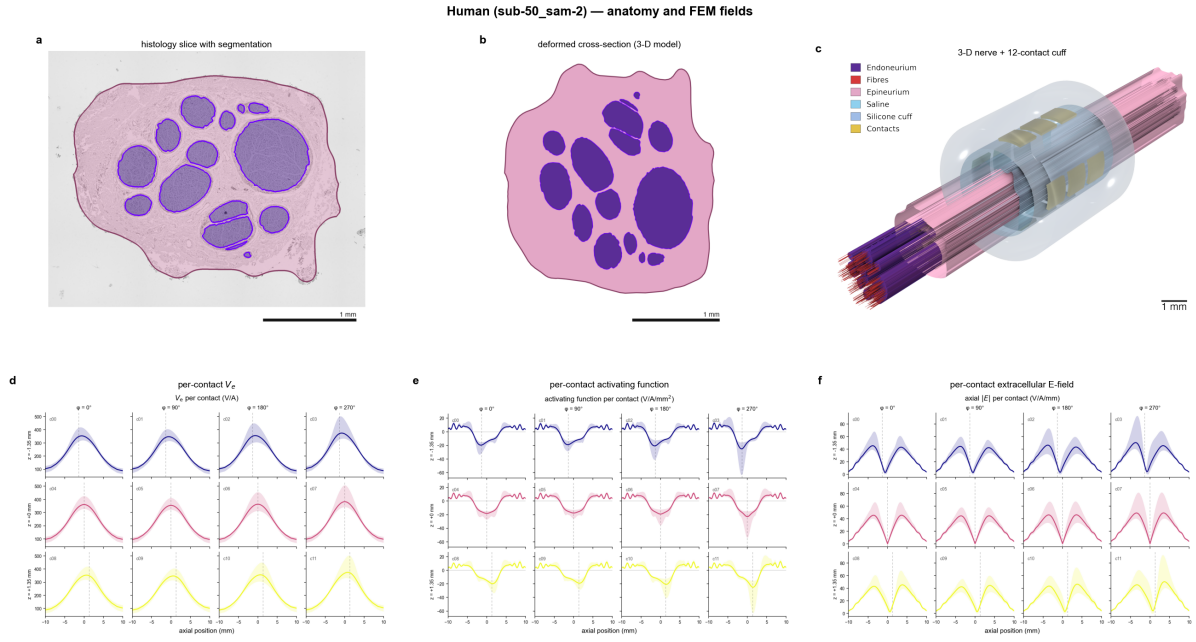


Figure S6: Specimen human sub-50_sam-2: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

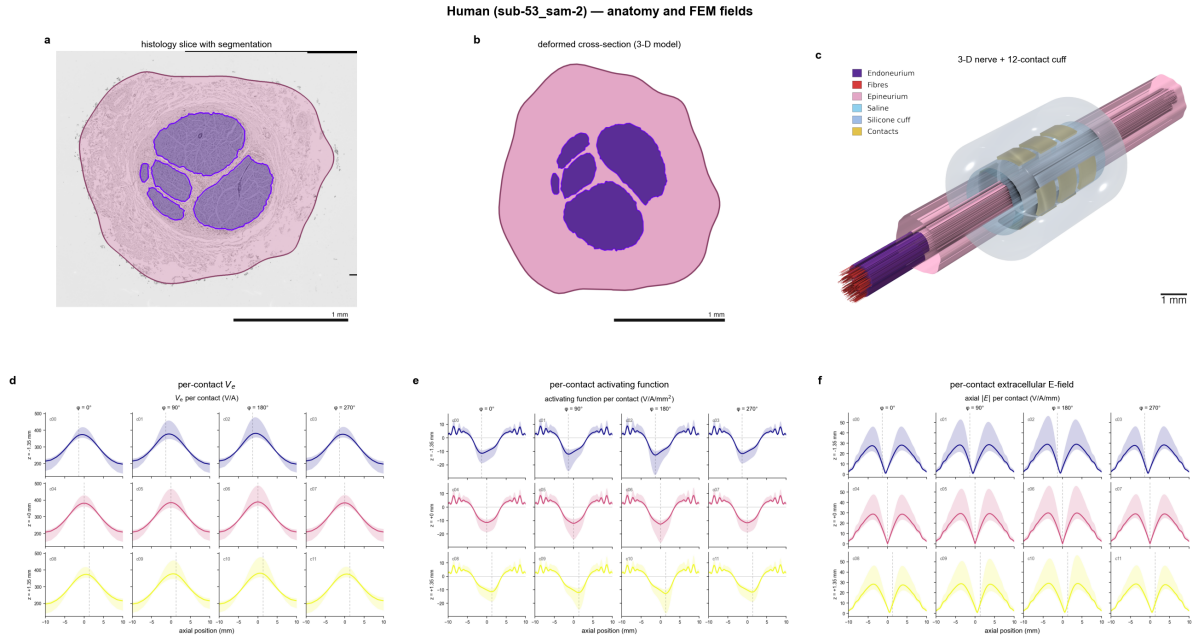


Figure S7: Specimen human sub-53_sam-2: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

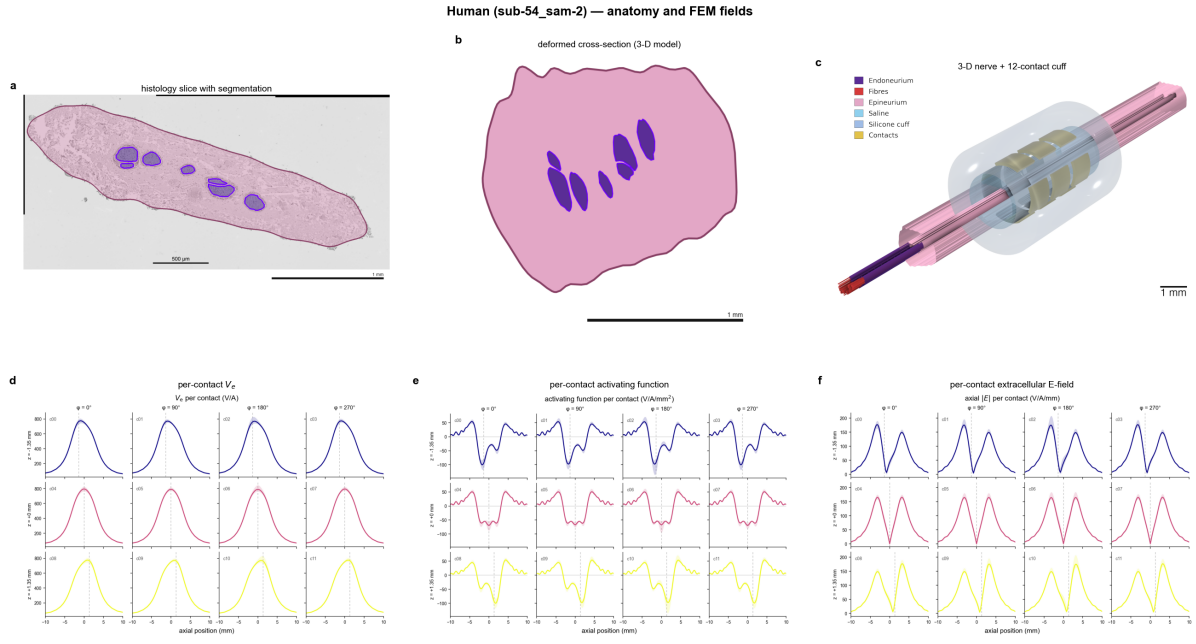


Figure S8: Specimen human sub-54_sam-2: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

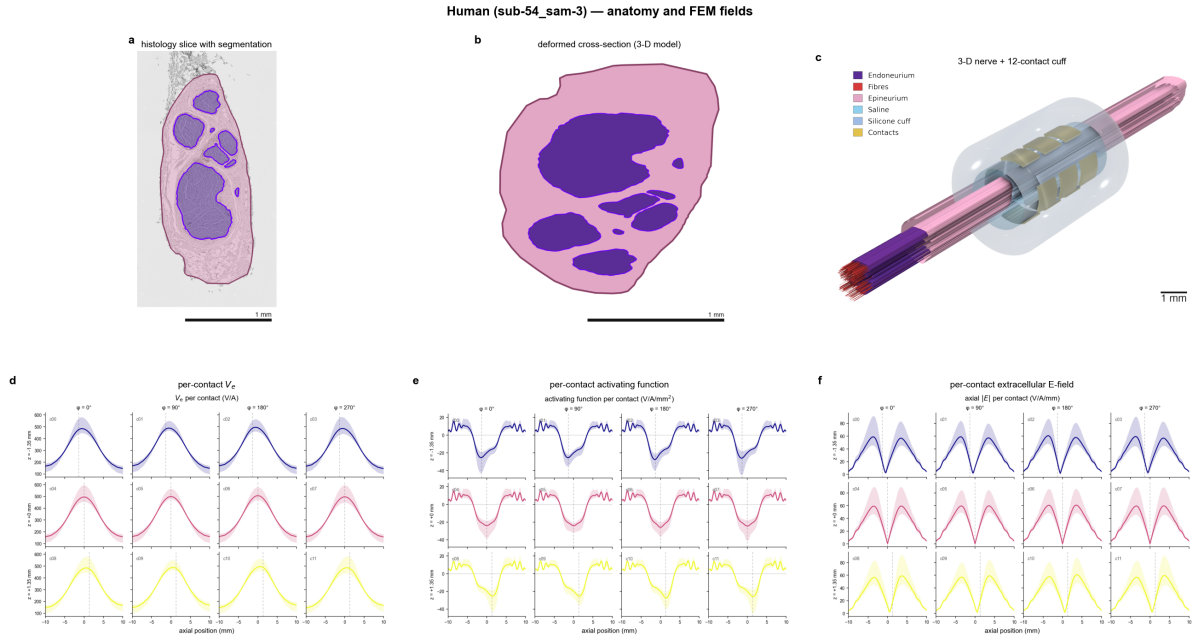


Figure S9: Specimen human sub-54_sam-3: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

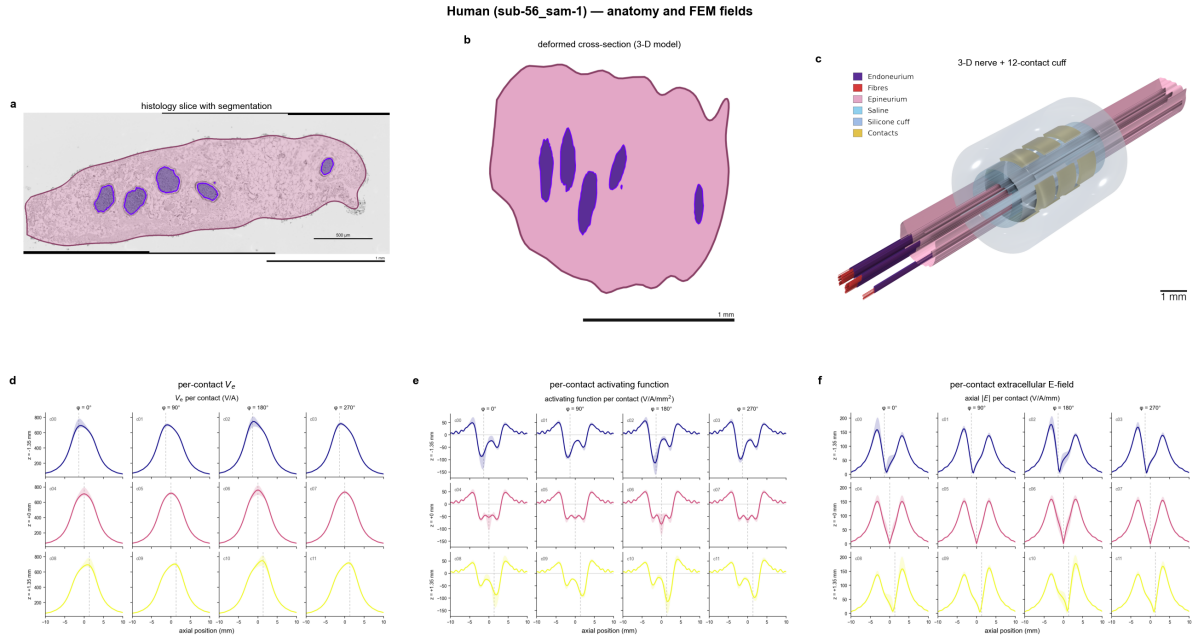


Figure S10: Specimen human sub-56_sam-1: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

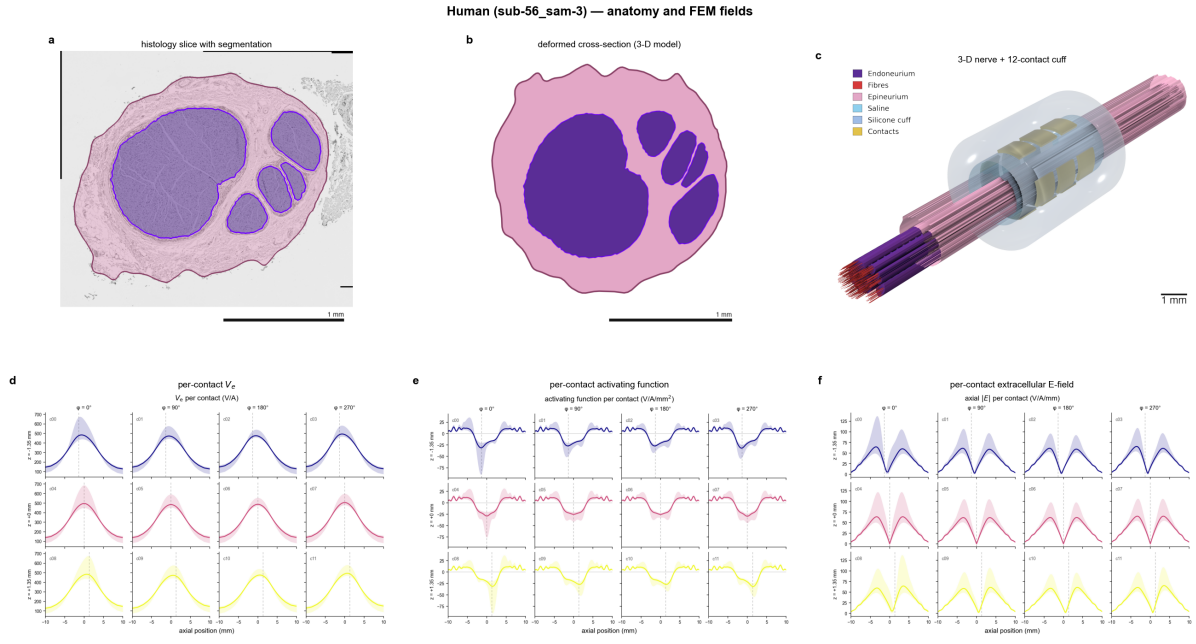


Figure S11: Specimen human sub-56_sam-3: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

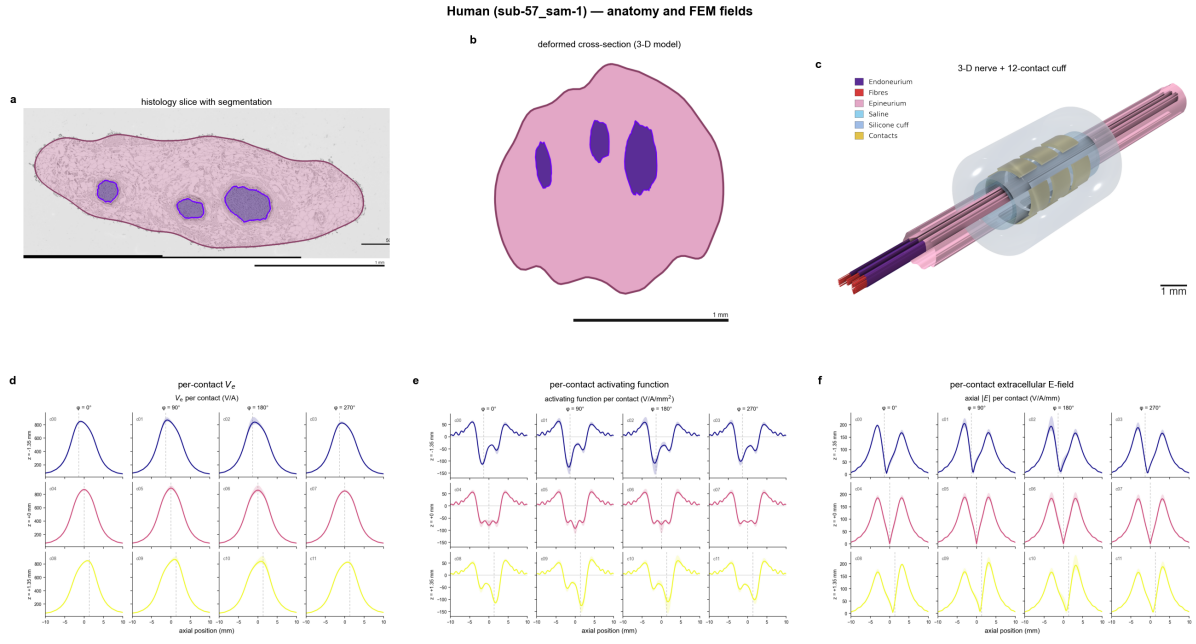


Figure S12: Specimen human sub-57_sam-1: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

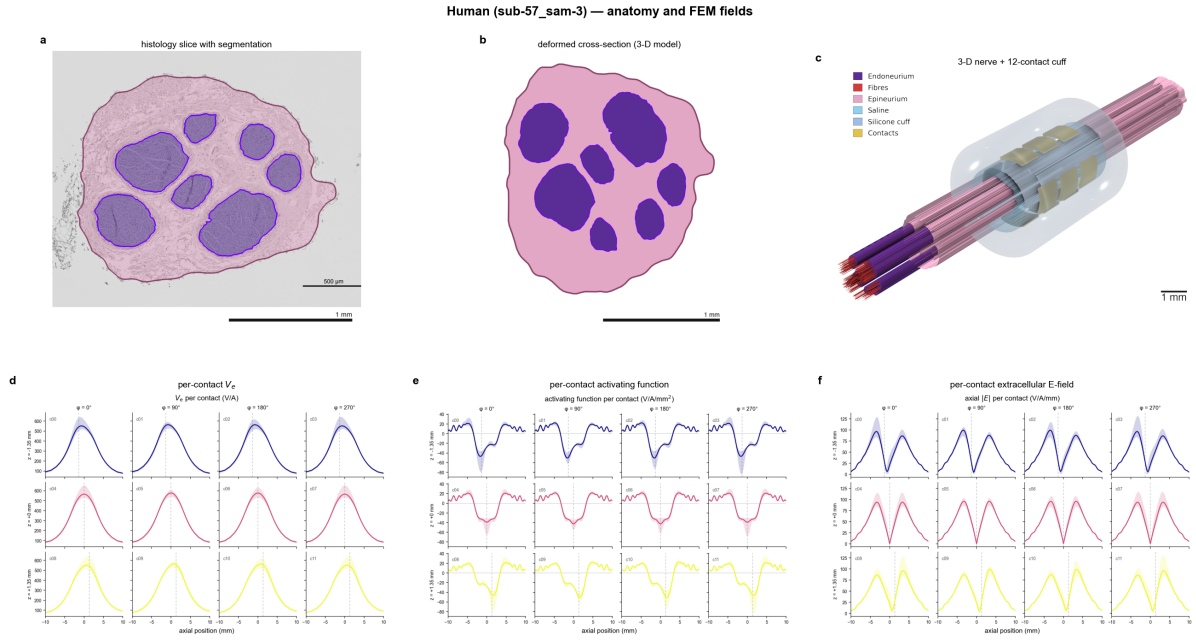


Figure S13: Specimen human sub-57_sam-3: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

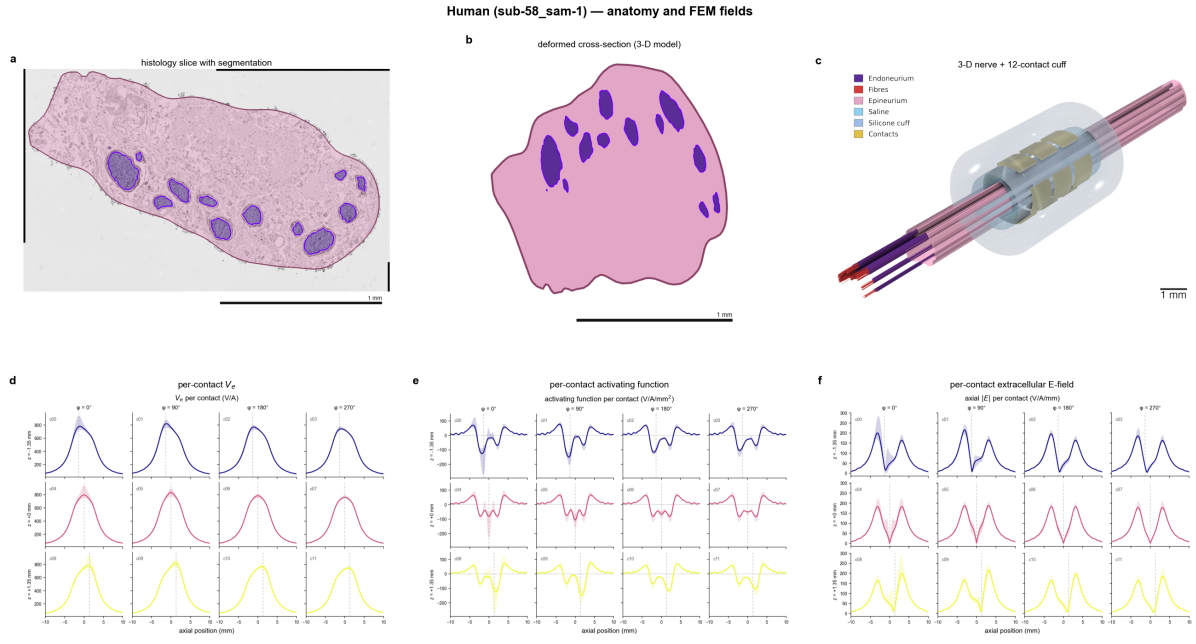


Figure S14: Specimen human sub-58_sam-1: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

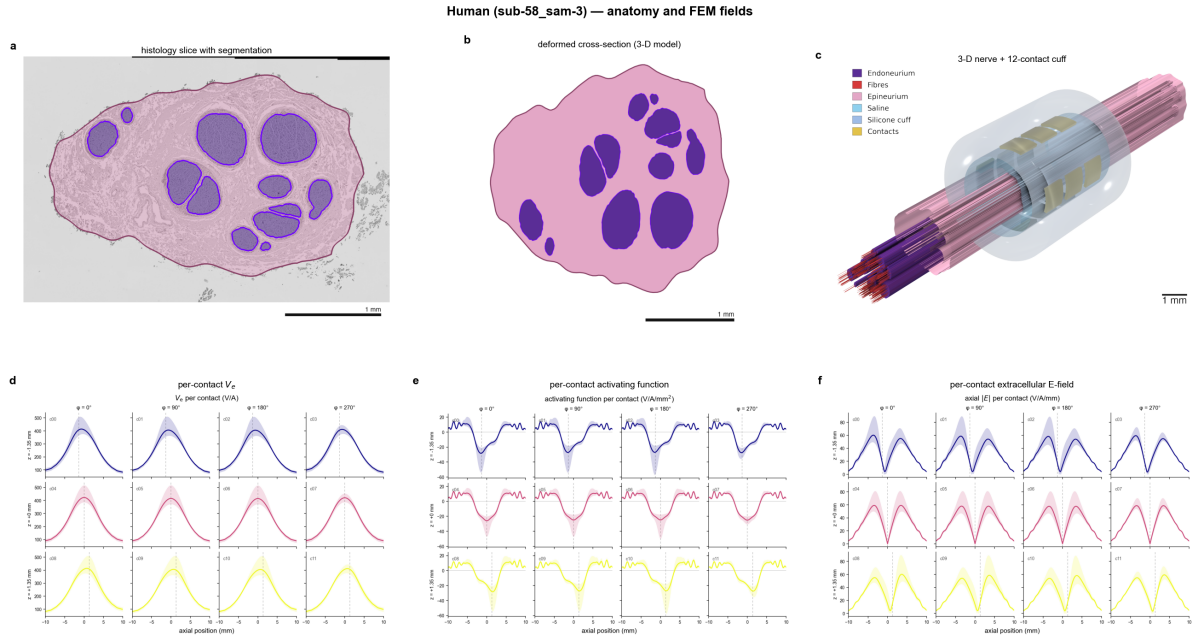


Figure S15: Specimen human sub-58_sam-3: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

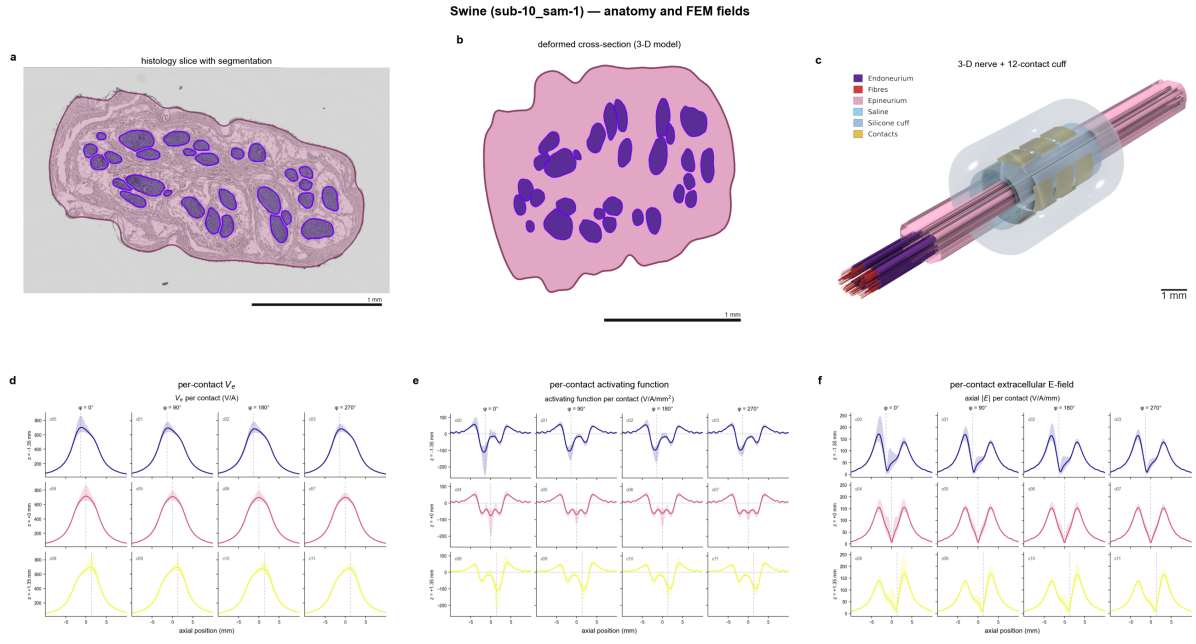


Figure S16: Specimen **swine sub-10_sam-1**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

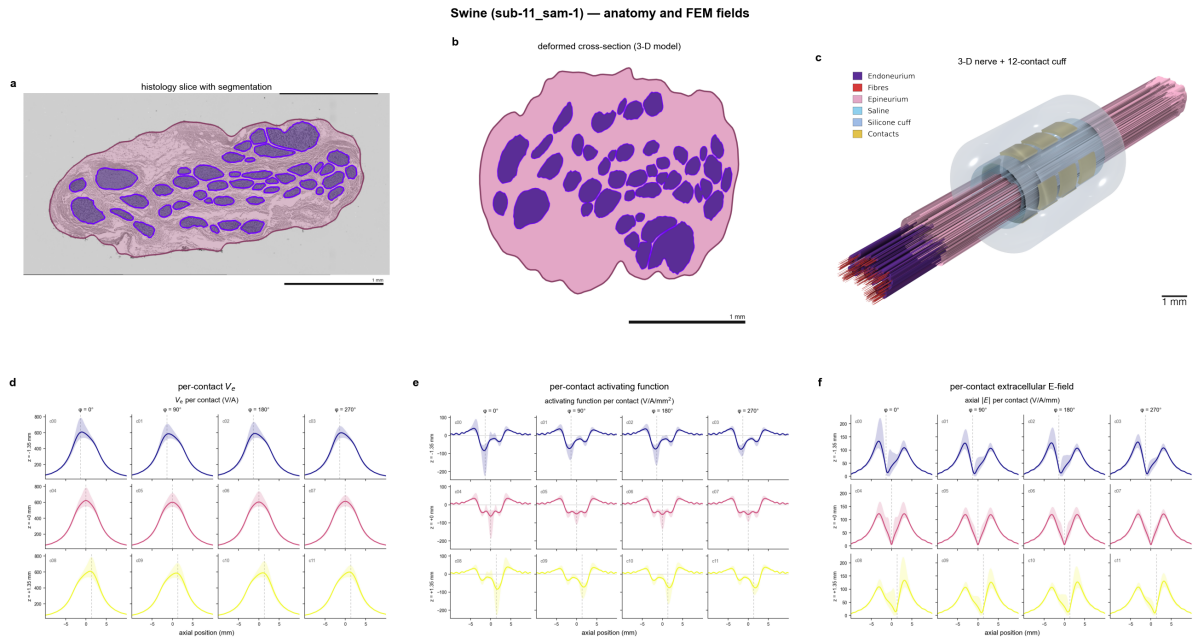


Figure S17: Specimen **swine sub-11_sam-1**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

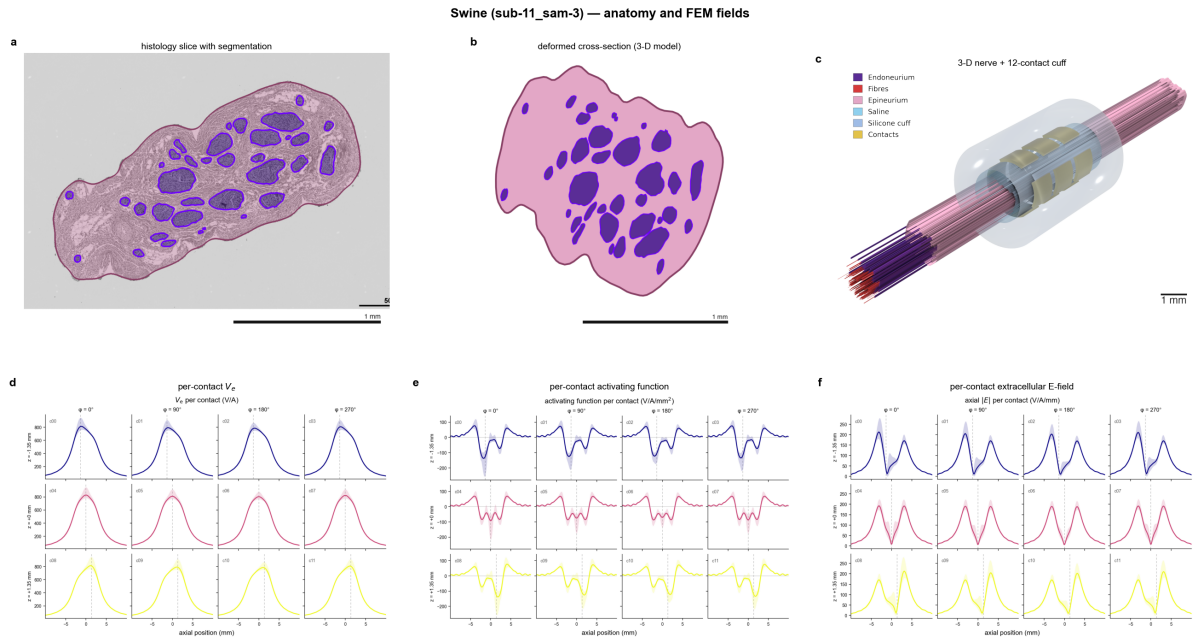


Figure S18: Specimen **swine sub-11_sam-3**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

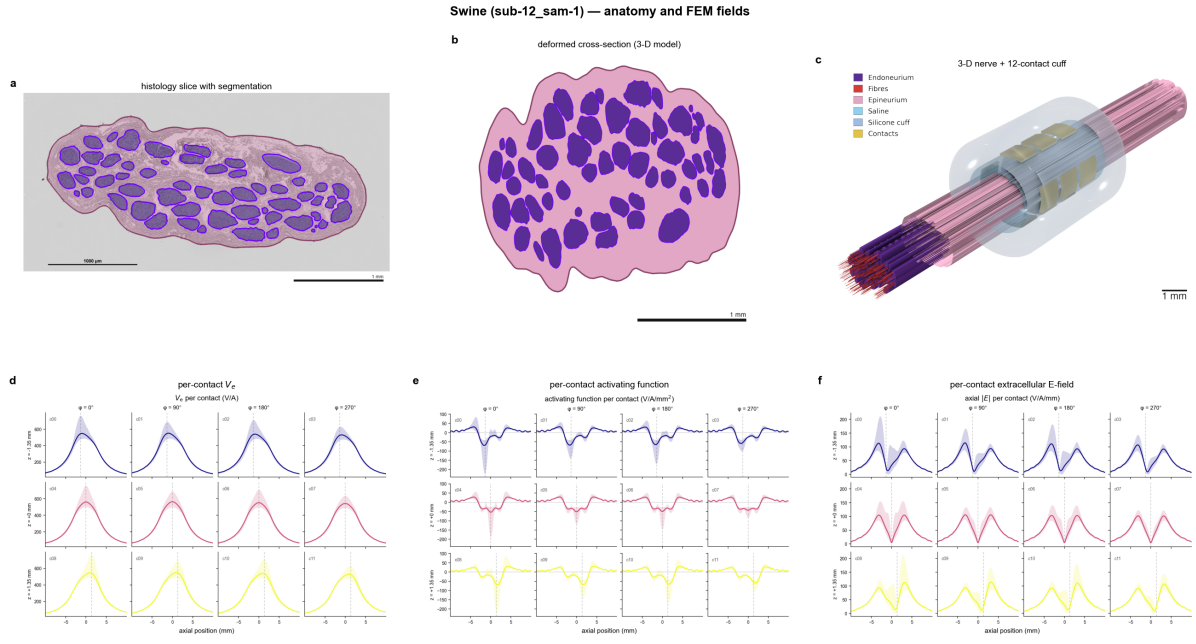


Figure S19: Specimen **swine sub-12_sam-1**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

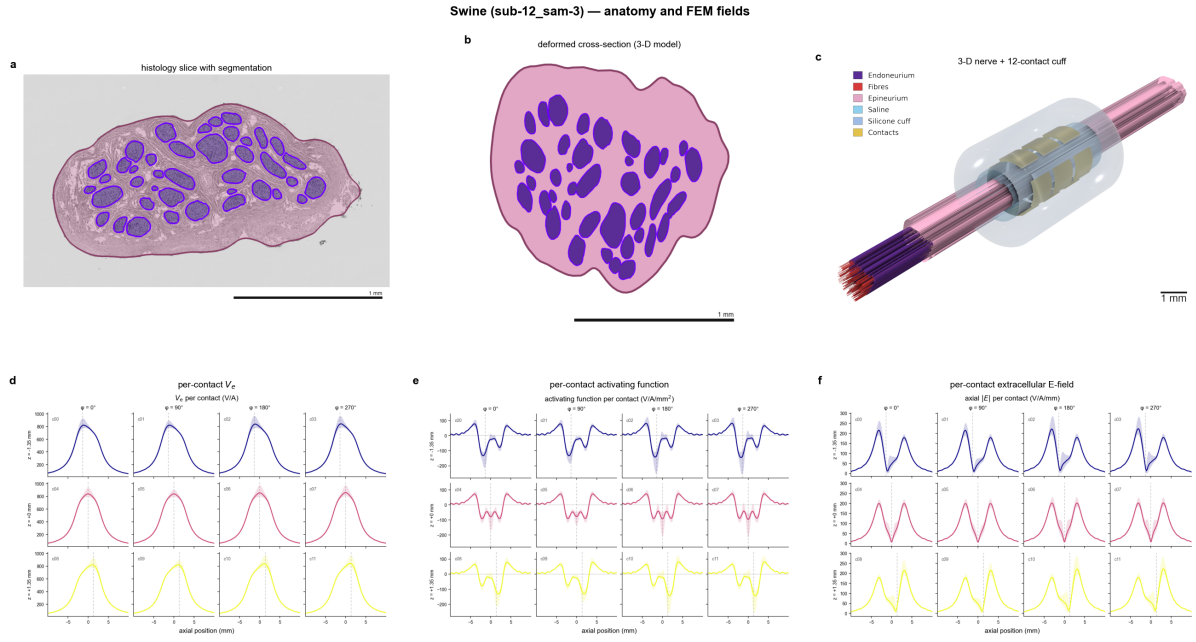


Figure S20: Specimen **swine sub-12_sam-3**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

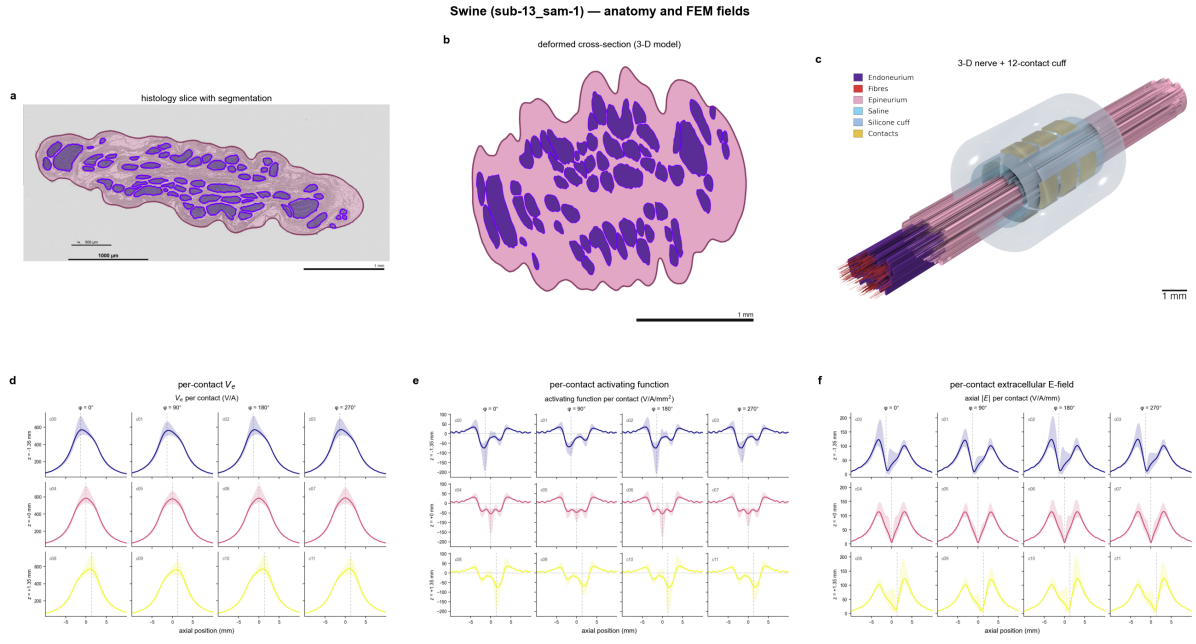


Figure S21: Specimen **swine sub-13_sam-1**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

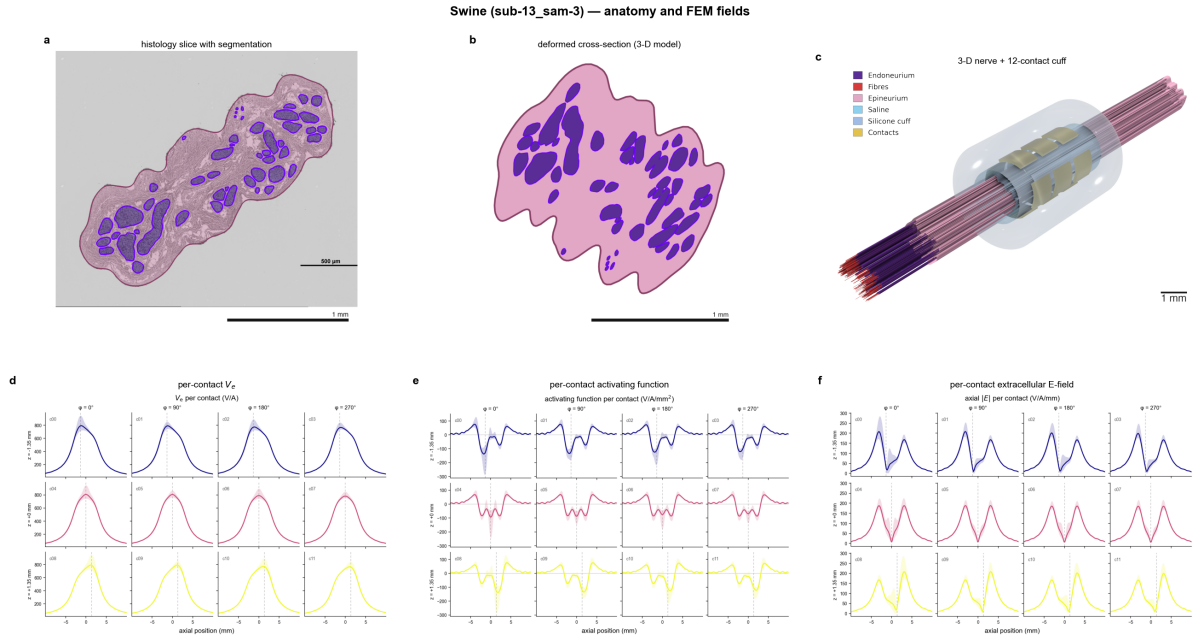


Figure S22: Specimen **swine sub-13_sam-3**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

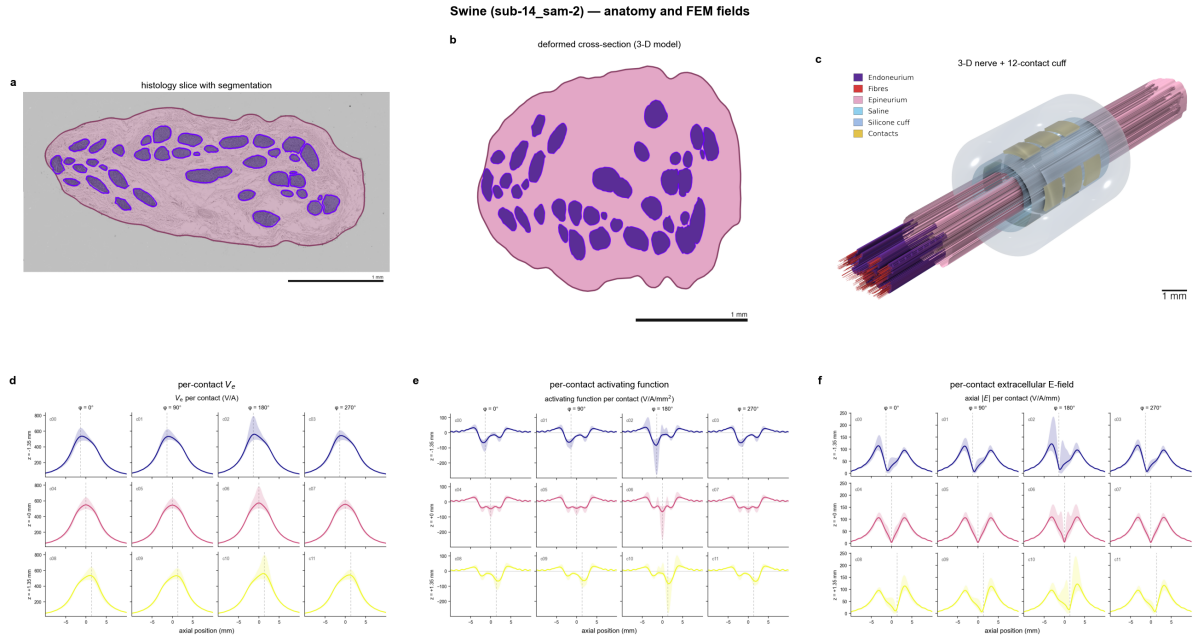


Figure S23: Specimen **swine sub-14_sam-2**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

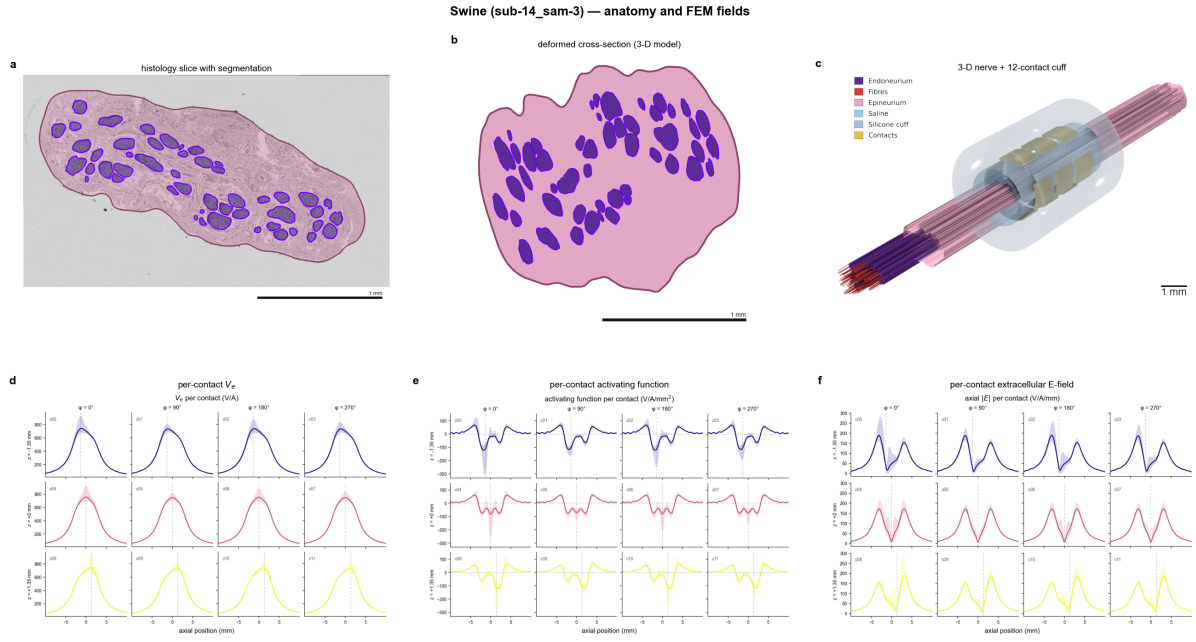


Figure S24: Specimen **swine sub-14_sam-3**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

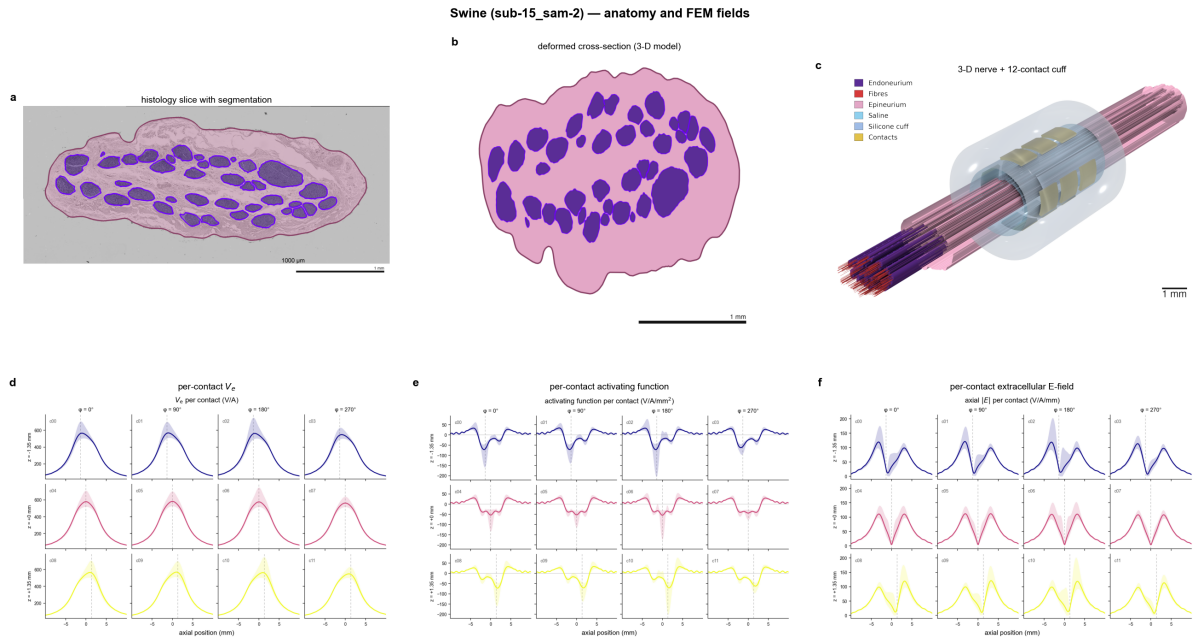


Figure S25: Specimen **swine sub-15_sam-2**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

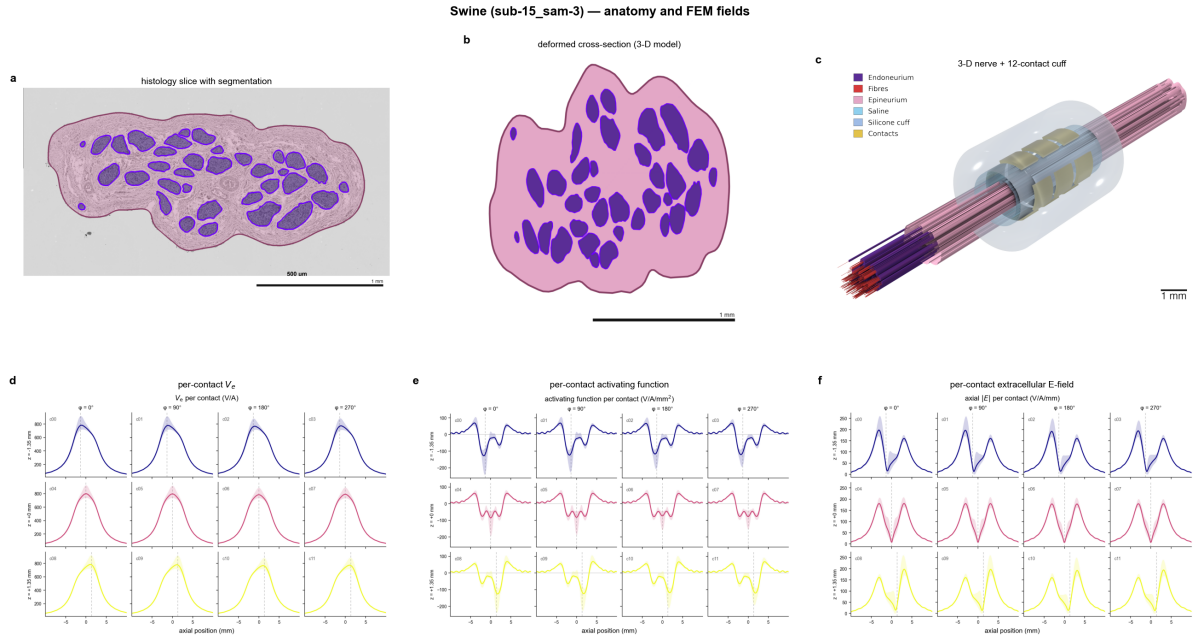


Figure S26: Specimen **swine sub-15_sam-3**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

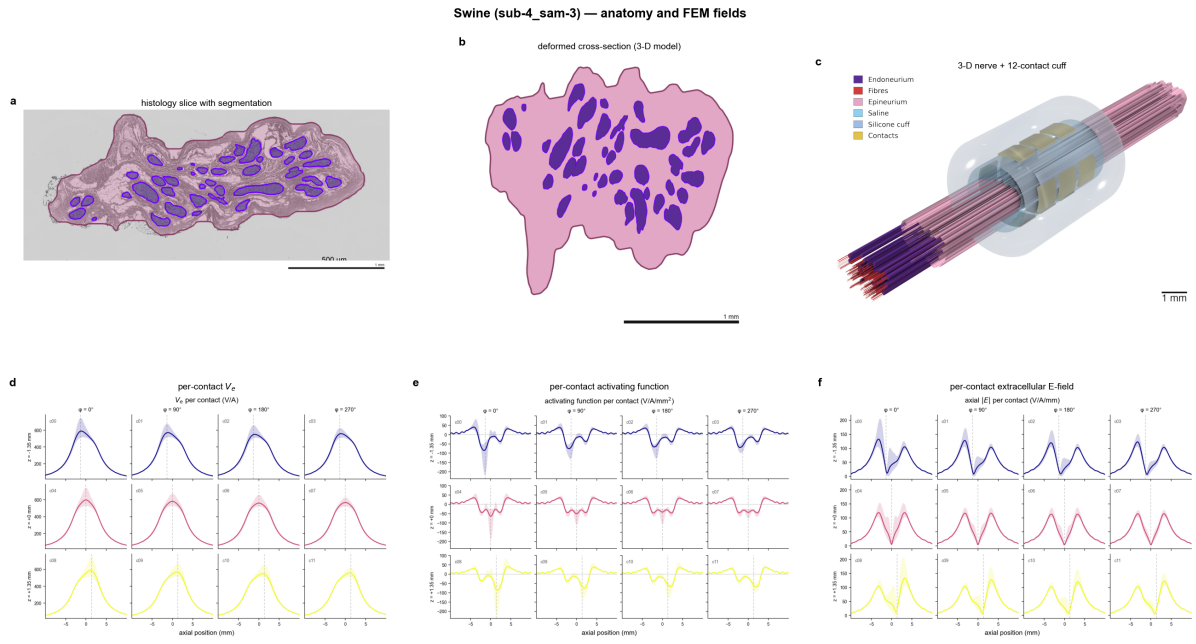


Figure S27: Specimen **swine sub-4_sam-3**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

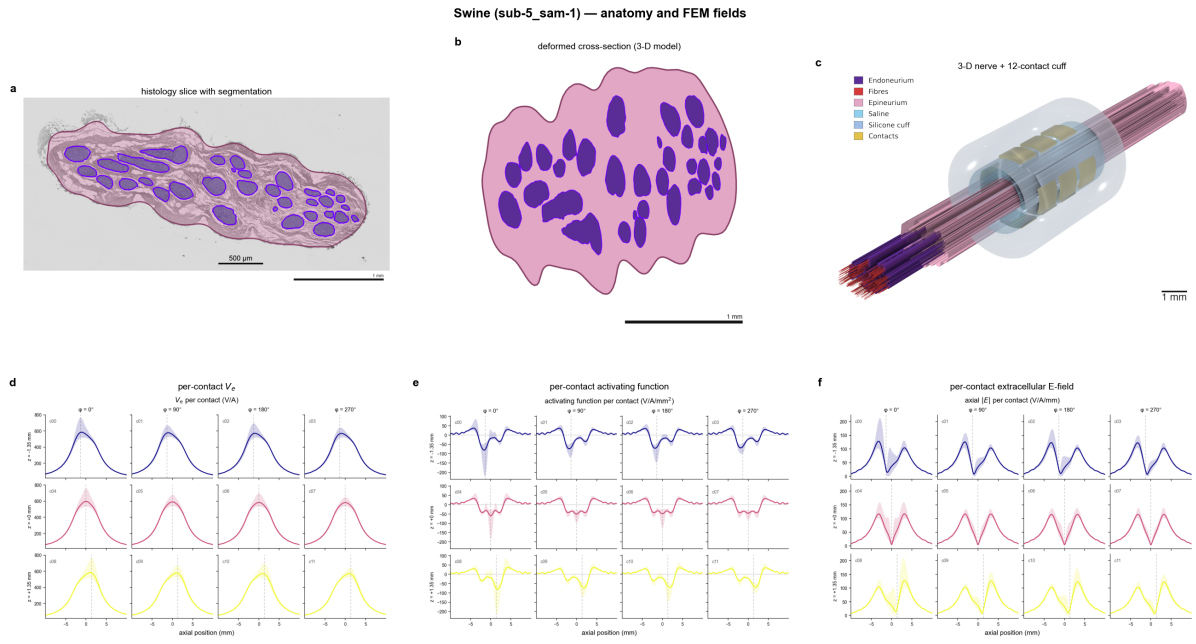


Figure S28: Specimen **swine sub-5_sam-1**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

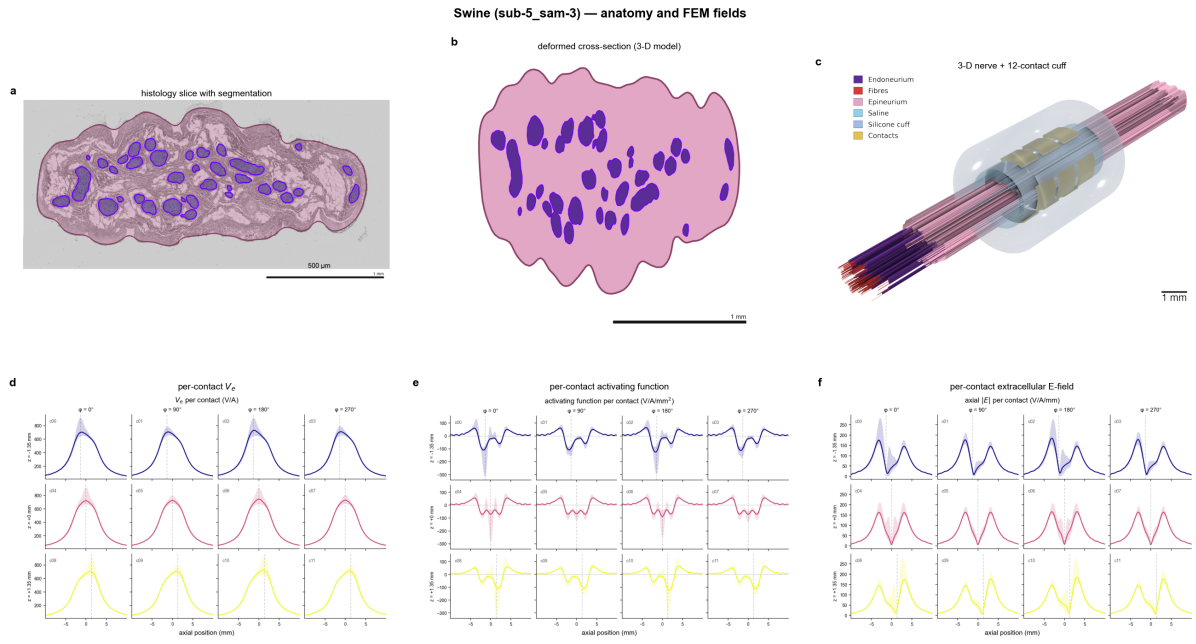


Figure S29: Specimen **swine sub-5_sam-3**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

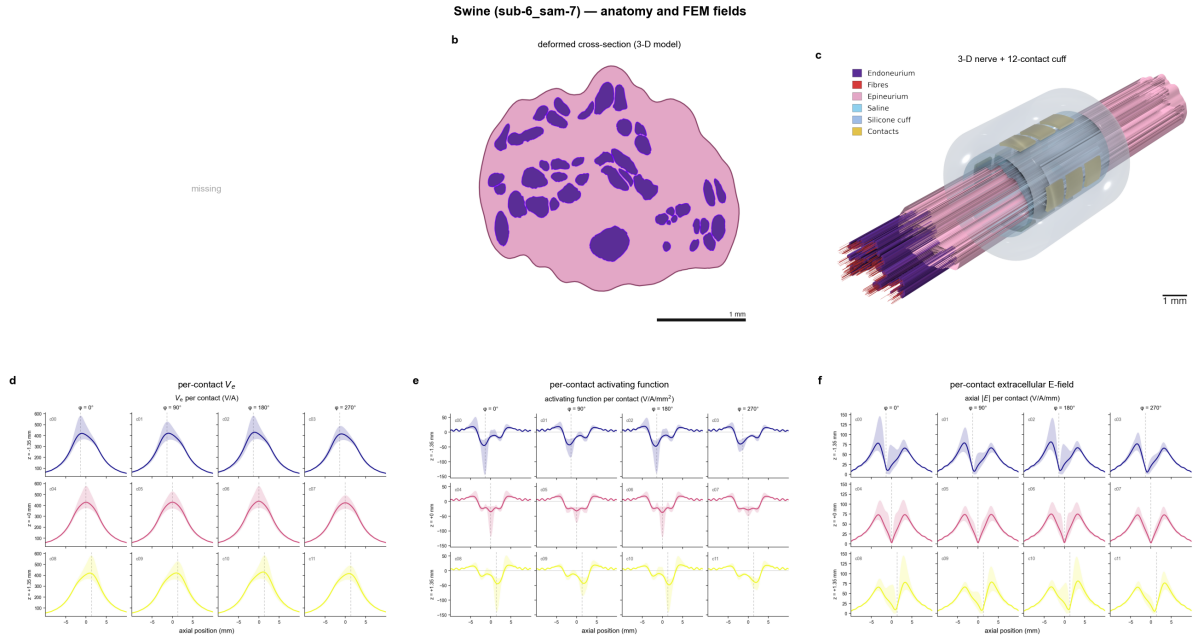


Figure S30: Specimen **swine sub-6_sam-7**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

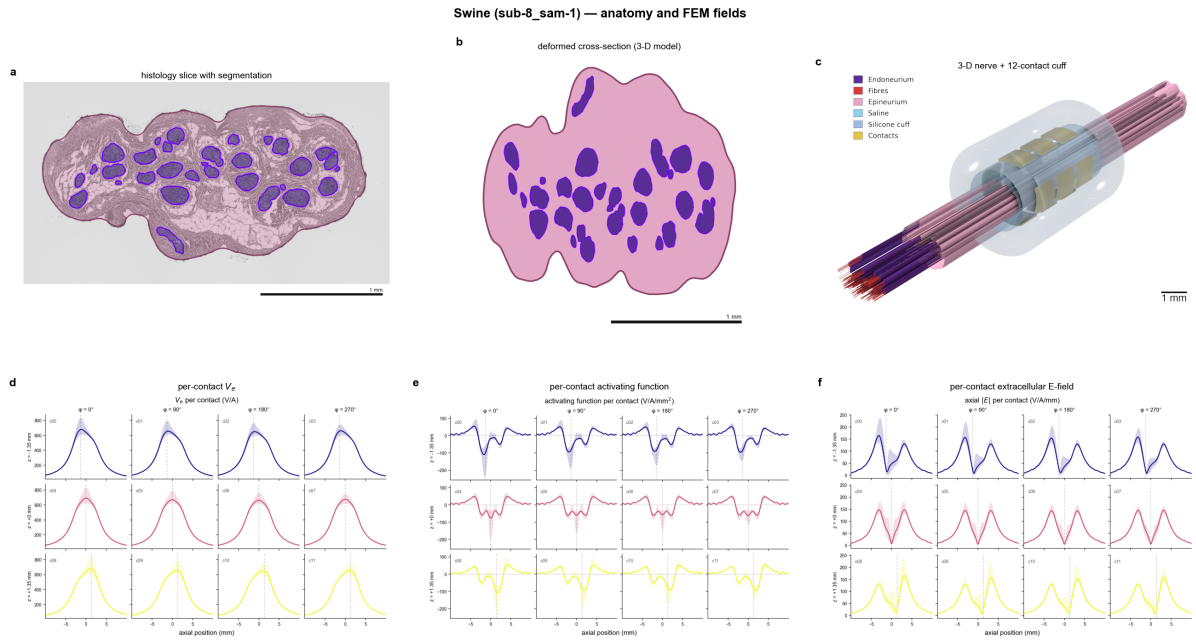


Figure S31: Specimen **swine sub-8_sam-1**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

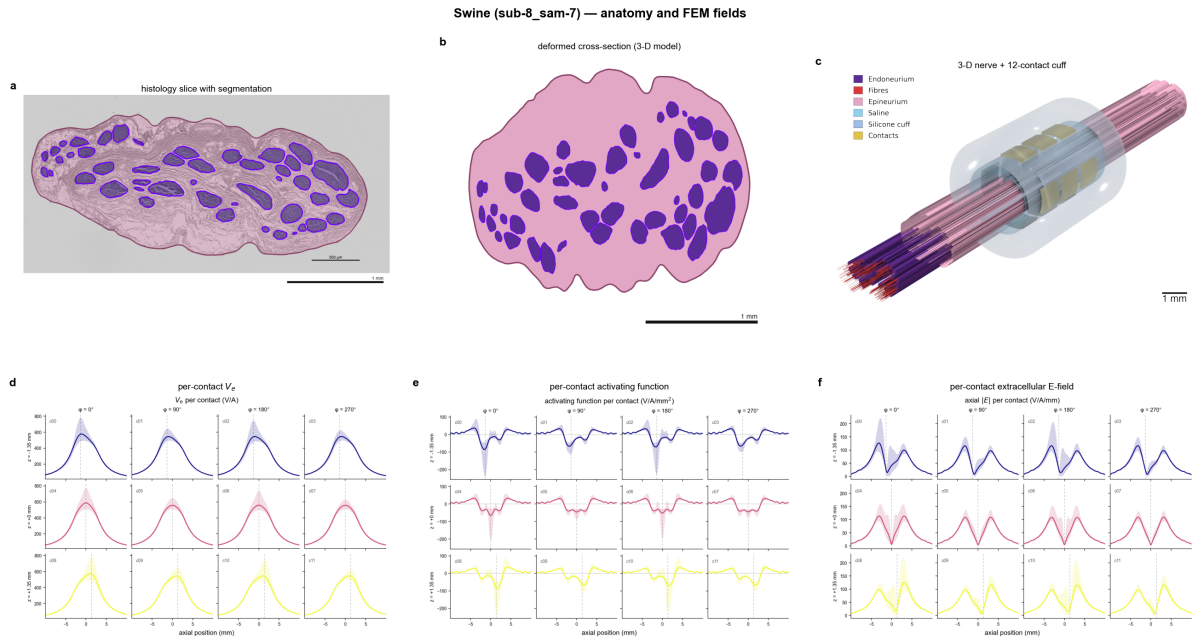


Figure S32: Specimen **swine sub-8_sam-7**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

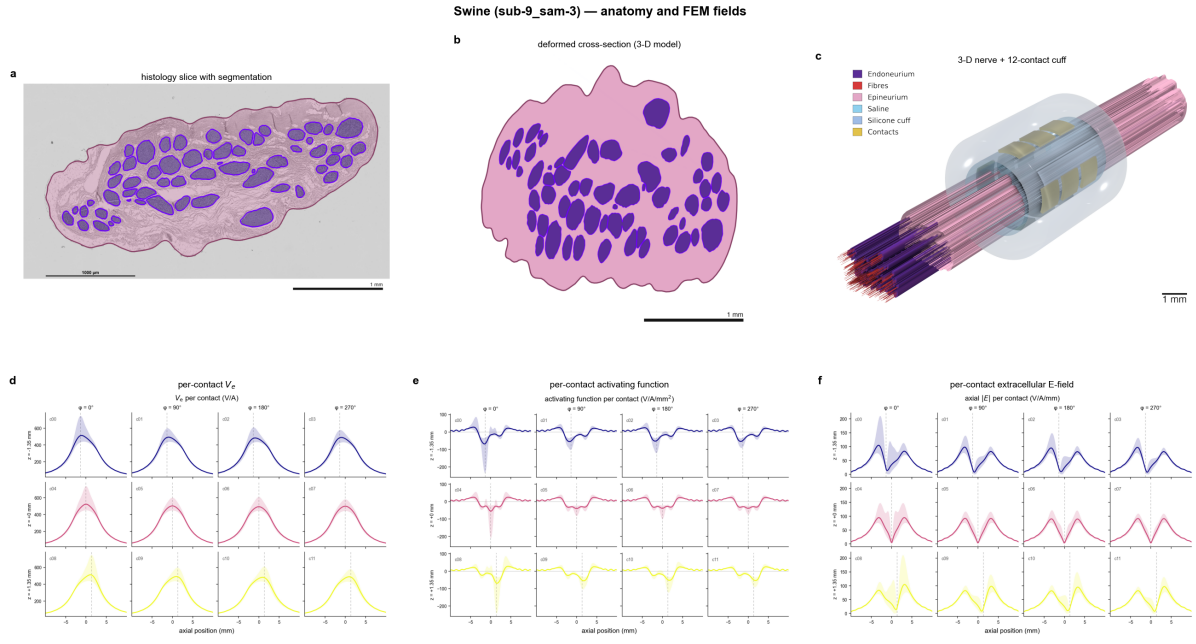


Figure S33: Specimen **swine sub-9_sam-3**: anatomy and FEM fields. **(a)** histology slice with manual segmentation; **(b)** area-preserving deformed cross-section used to build the 3-D model; **(c)** 3-D nerve and 12-contact cuff (component legend inset); **(d)** per-contact extracellular potential V_e ; **(e)** per-contact activating function; **(f)** per-contact extracellular E-field magnitude.

Per-specimen selectivity-optimization outcomes for the full histology-derived vagus-nerve cohort (Section 2.3). Each figure collects all target-cluster seeds for one nerve; the shared layout and color scheme are described once below and apply to every panel.

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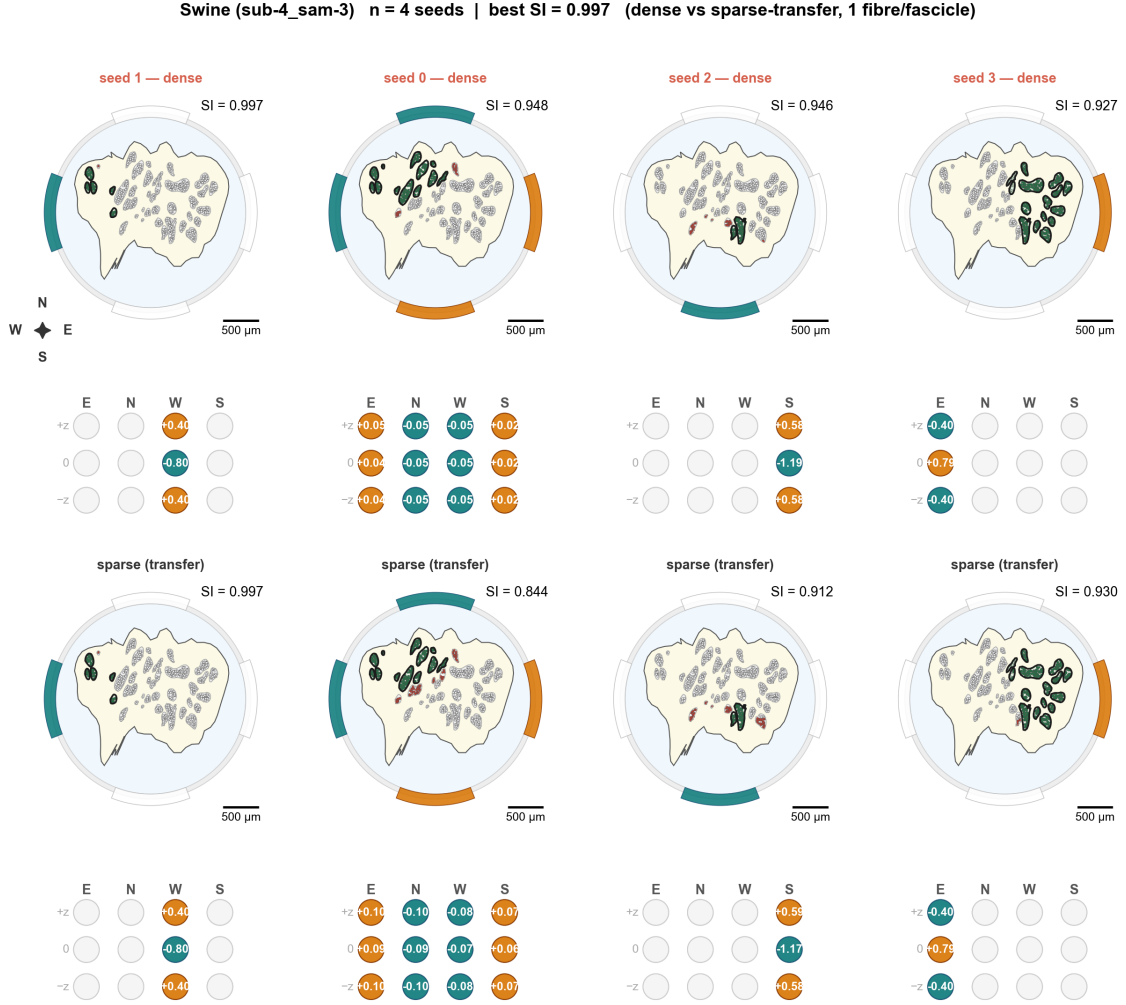


Figure S34: Specimen **swine sub-4_sam-3**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

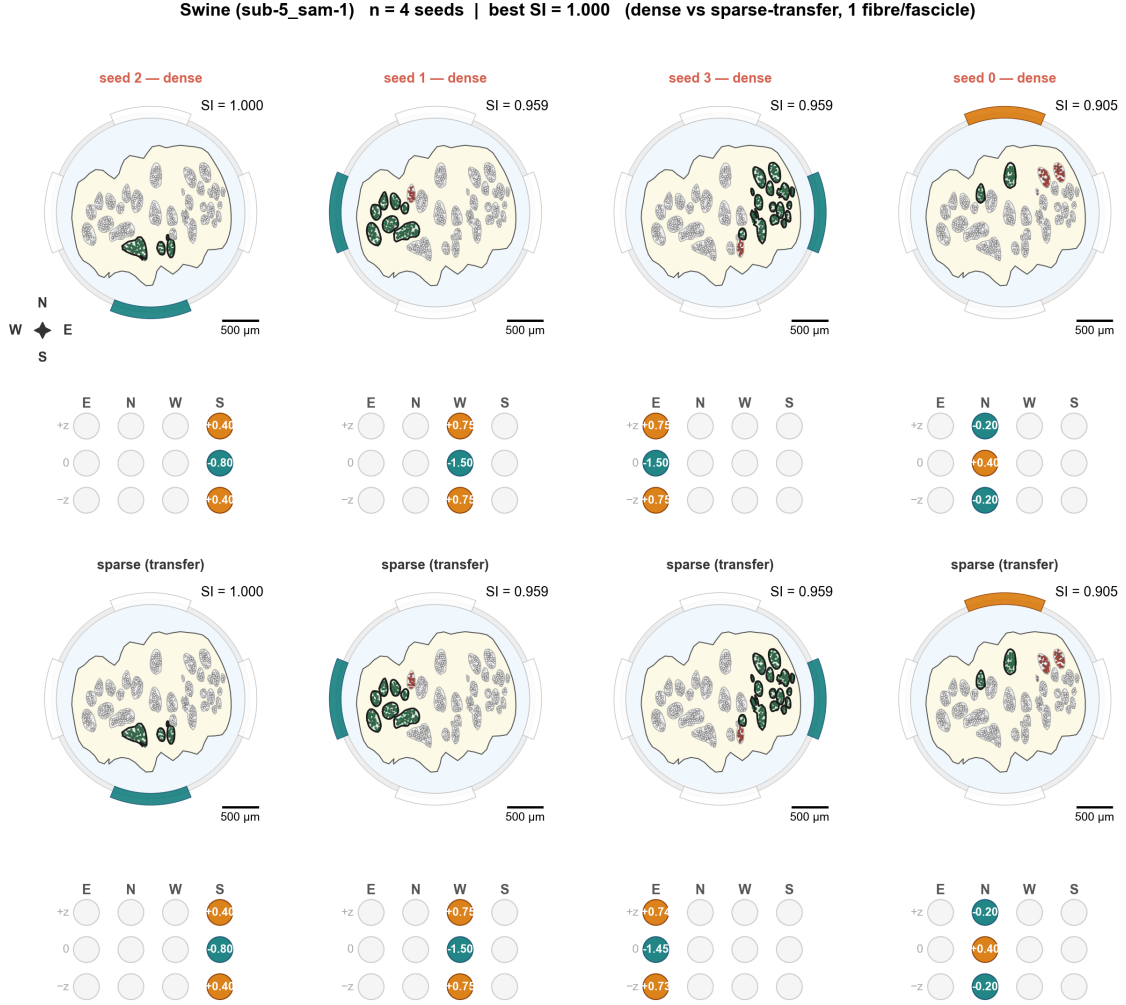


Figure S35: Specimen **swine sub-5_sam-1**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

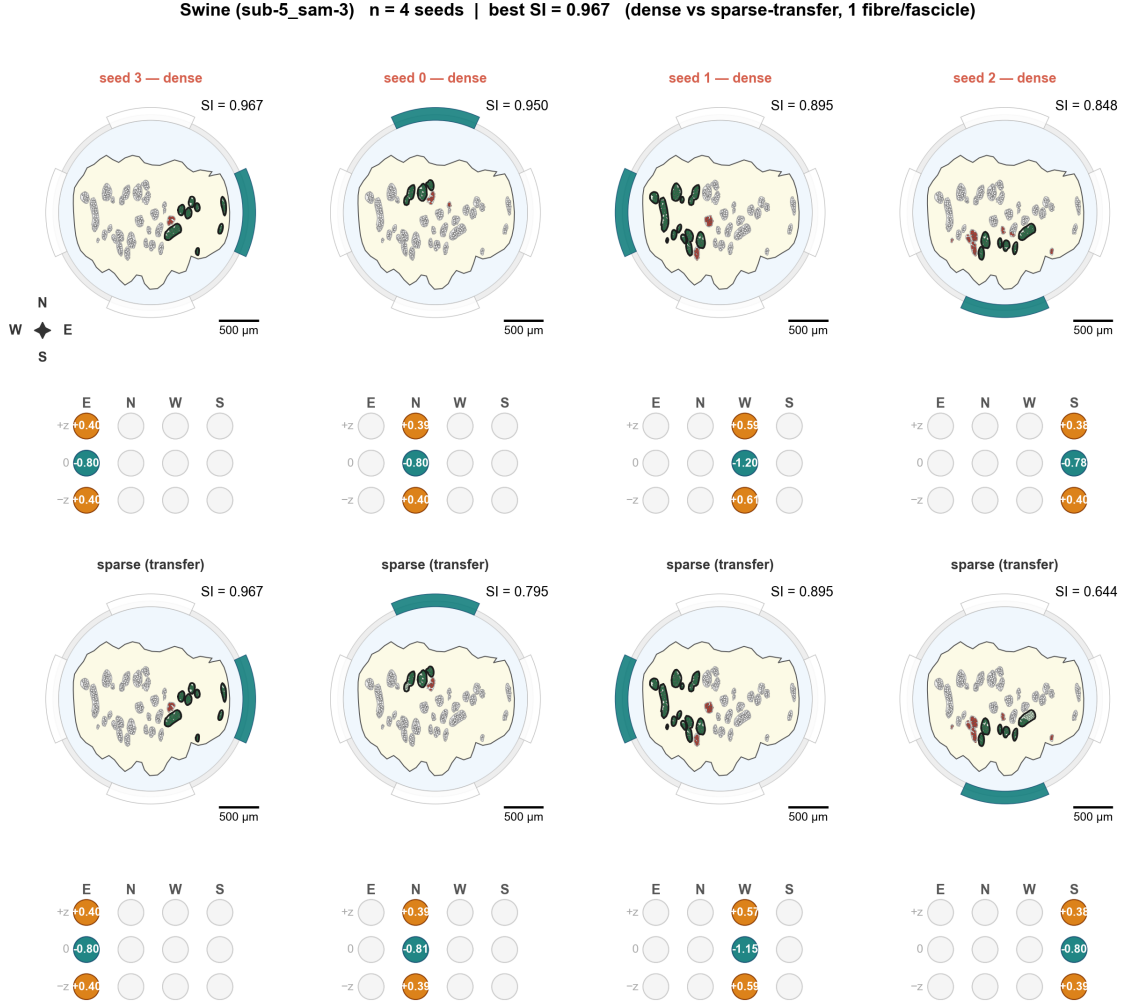


Figure S36: Specimen **swine sub-5_sam-3**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

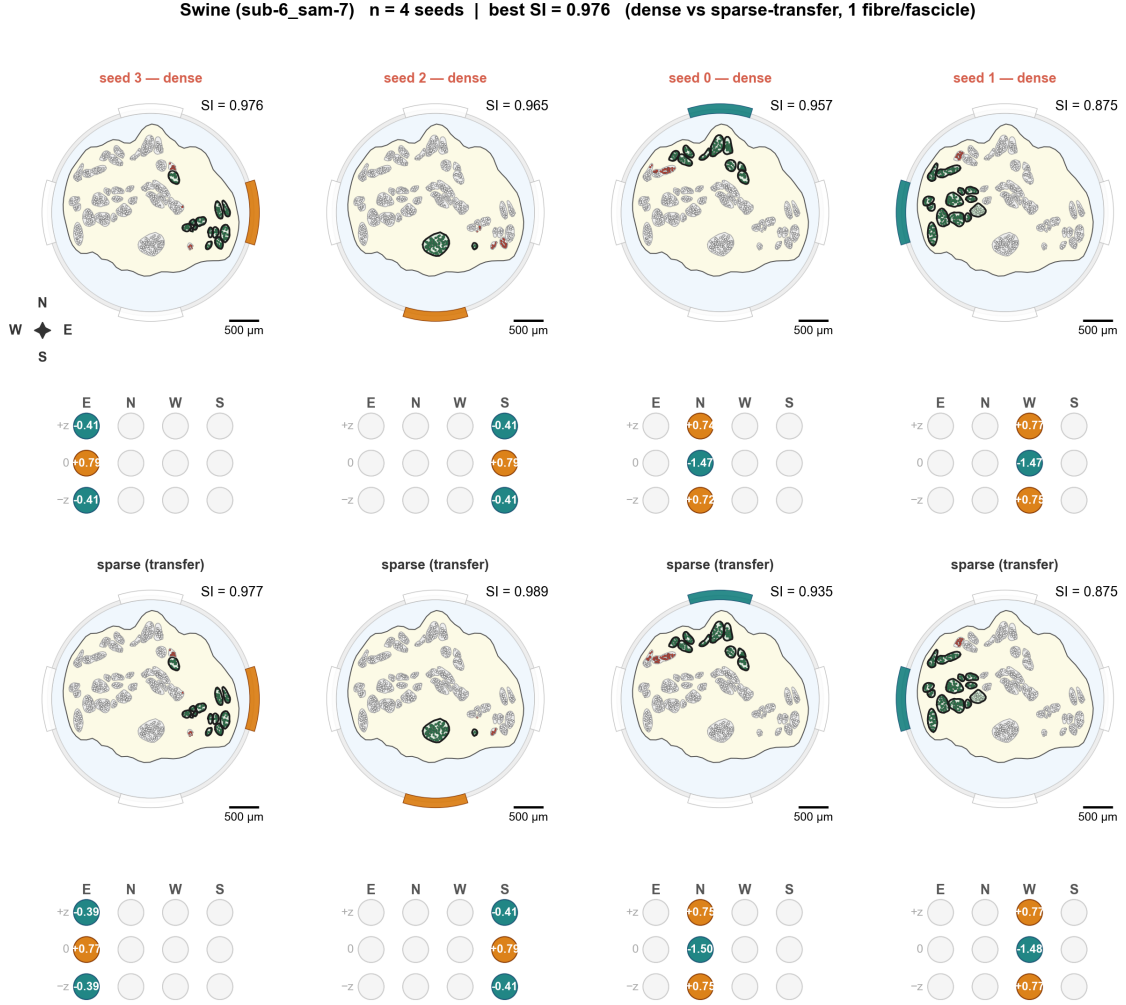


Figure S37: Specimen **swine sub-6_sam-7**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

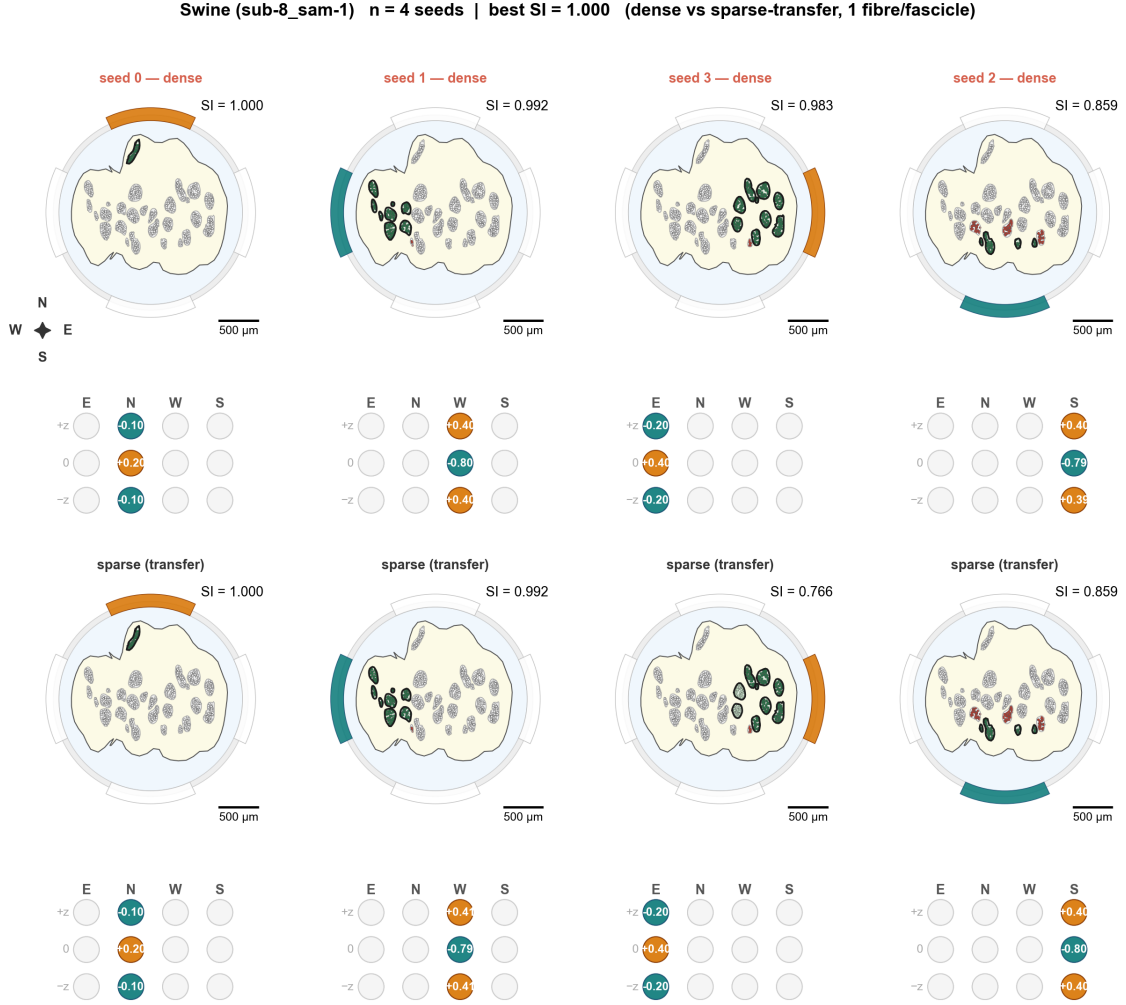


Figure S38: Specimen **swine sub-8_sam-1**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).



Figure S39: Specimen **swine sub-8_sam-7**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).



Figure S40: Specimen **swine sub-9_sam-3**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

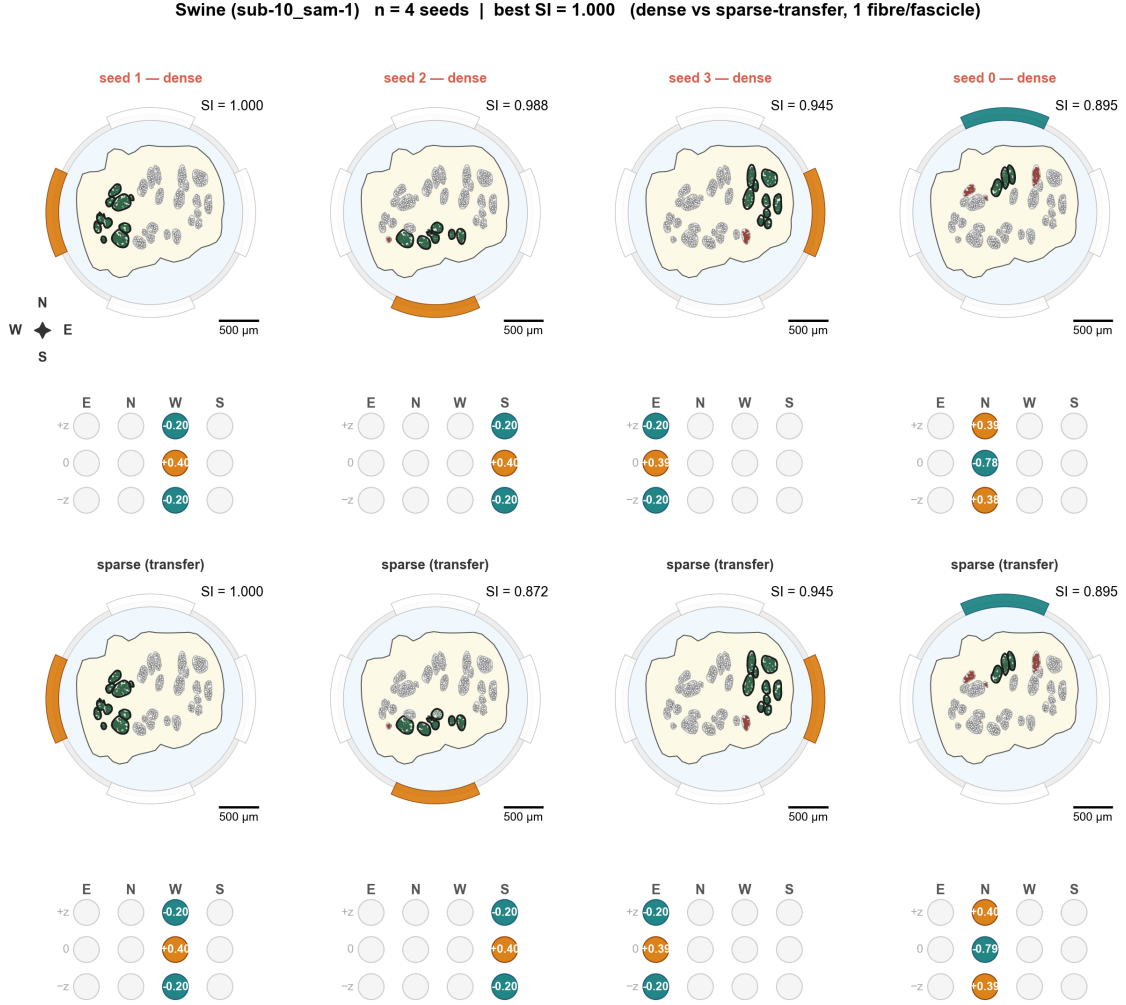


Figure S41: Specimen **swine sub-10_sam-1**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

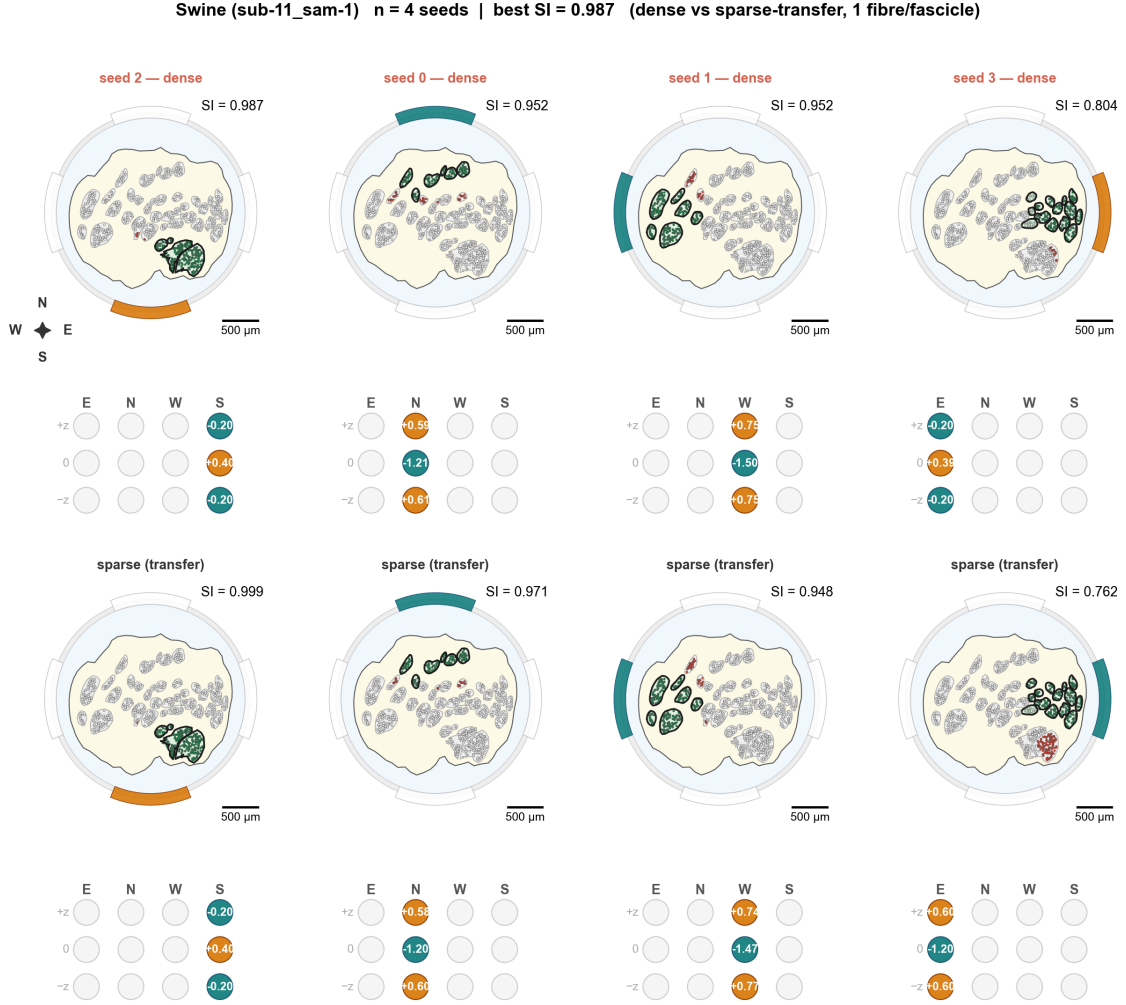


Figure S42: Specimen **swine sub-11_sam-1**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

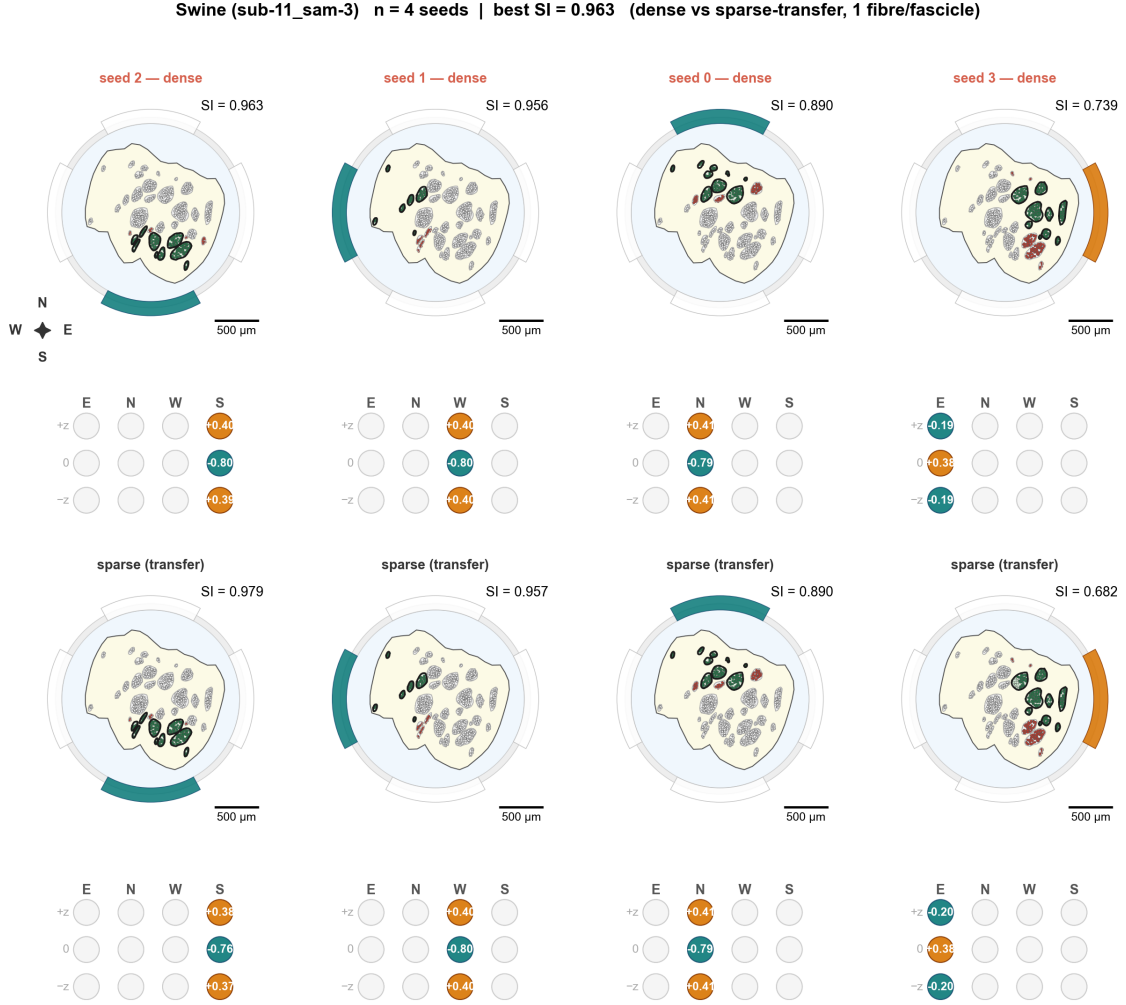


Figure S43: Specimen **swine sub-11_sam-3**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).



Figure S44: Specimen **swine sub-12_sam-1**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

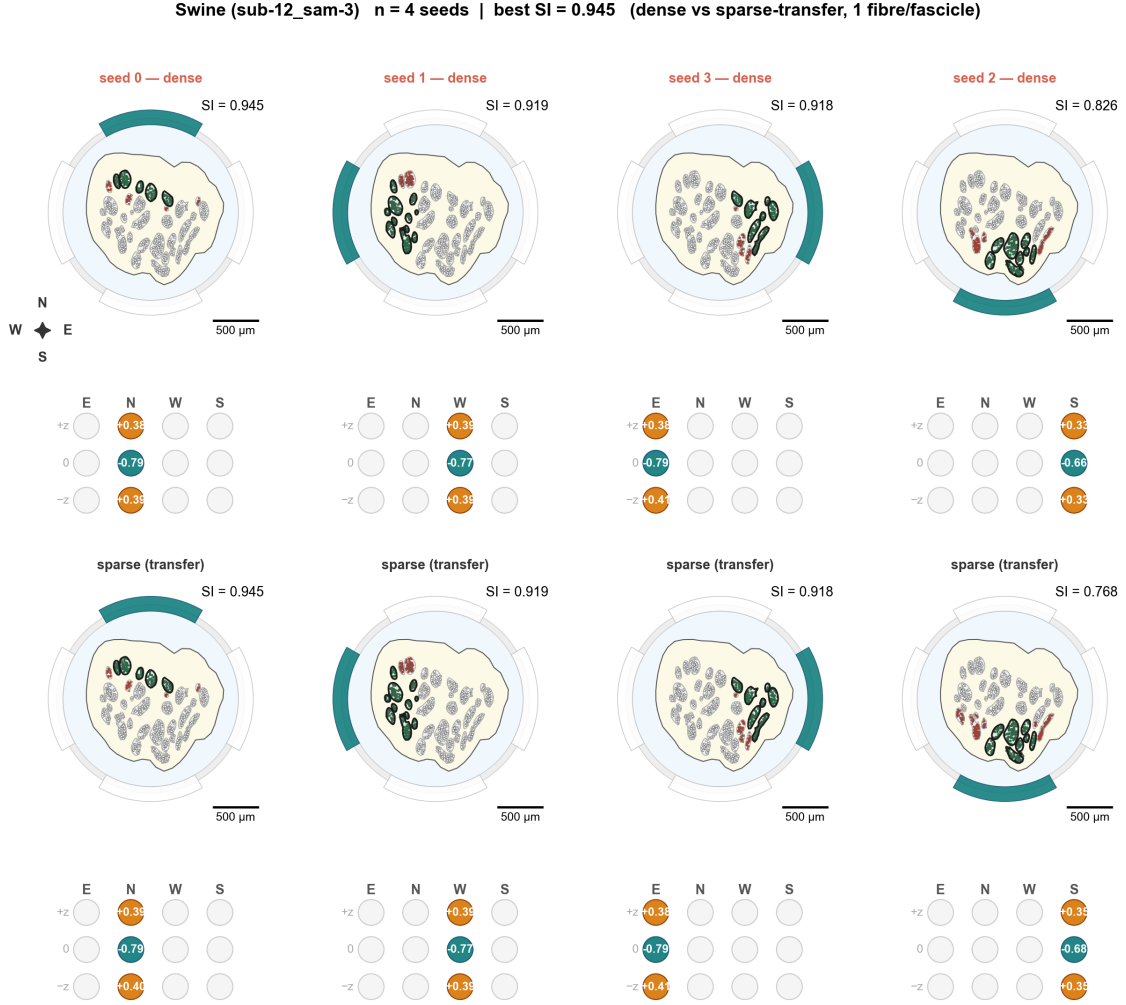


Figure S45: Specimen **swine sub-12_sam-3**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

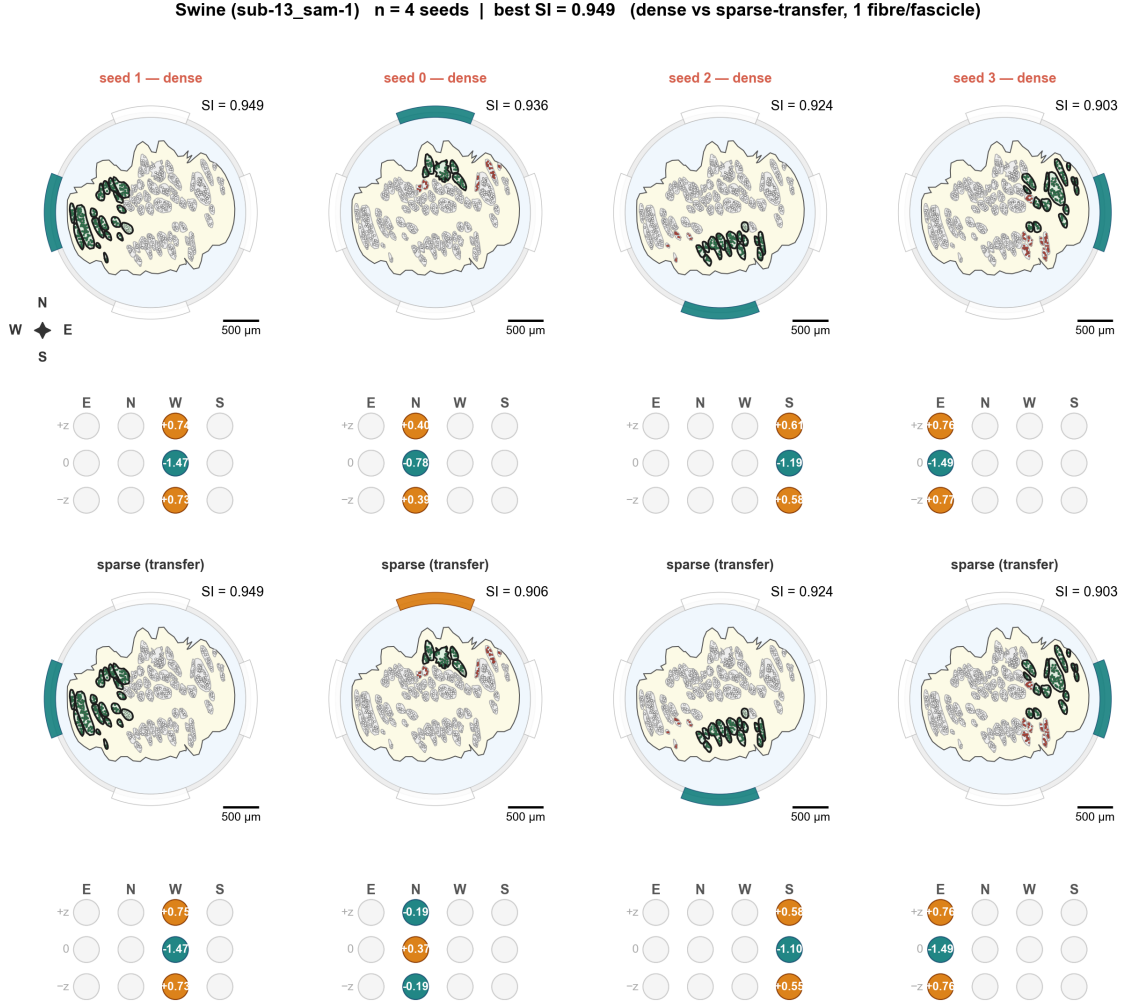


Figure S46: Specimen **swine sub-13_sam-1**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

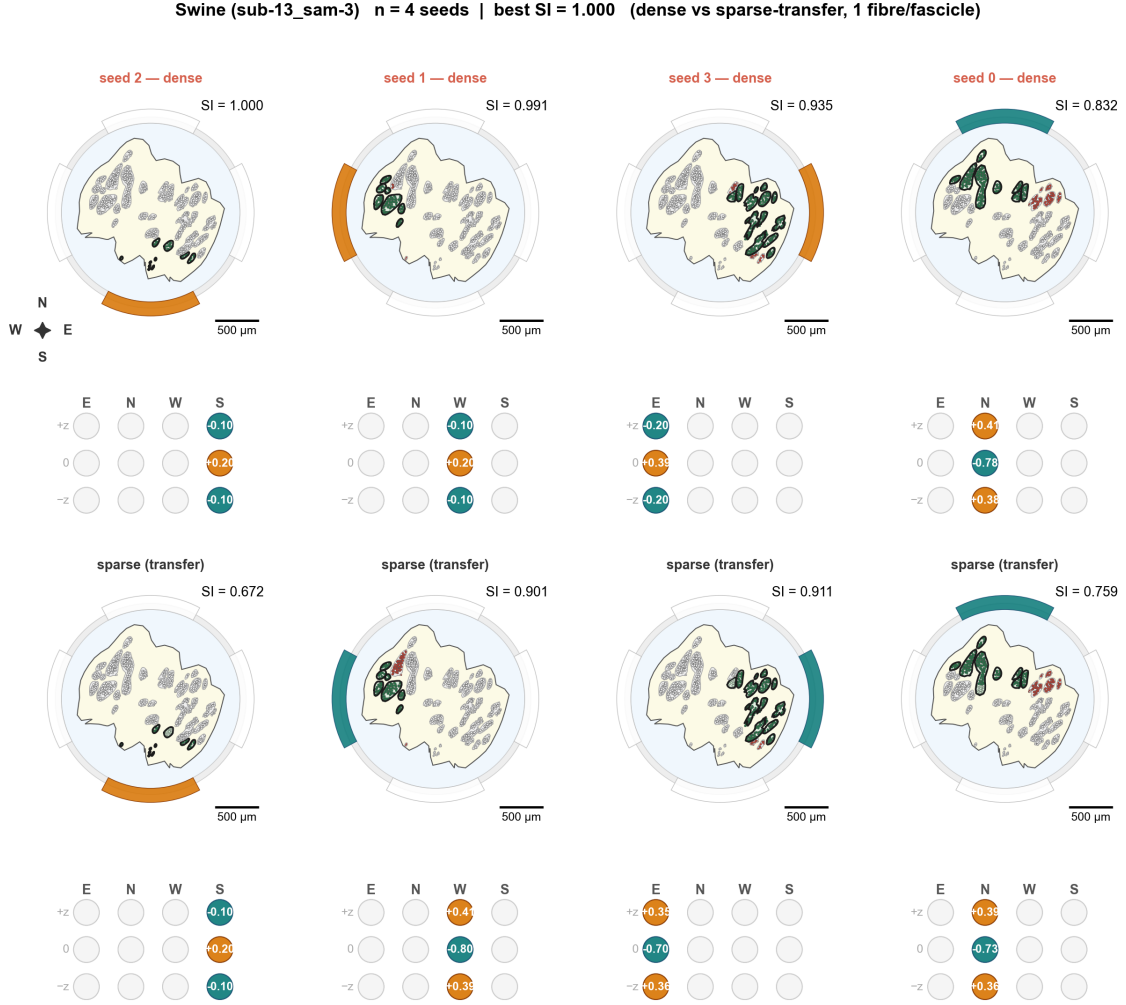


Figure S47: Specimen **swine sub-13_sam-3**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).



Figure S48: Specimen **swine sub-14_sam-2**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

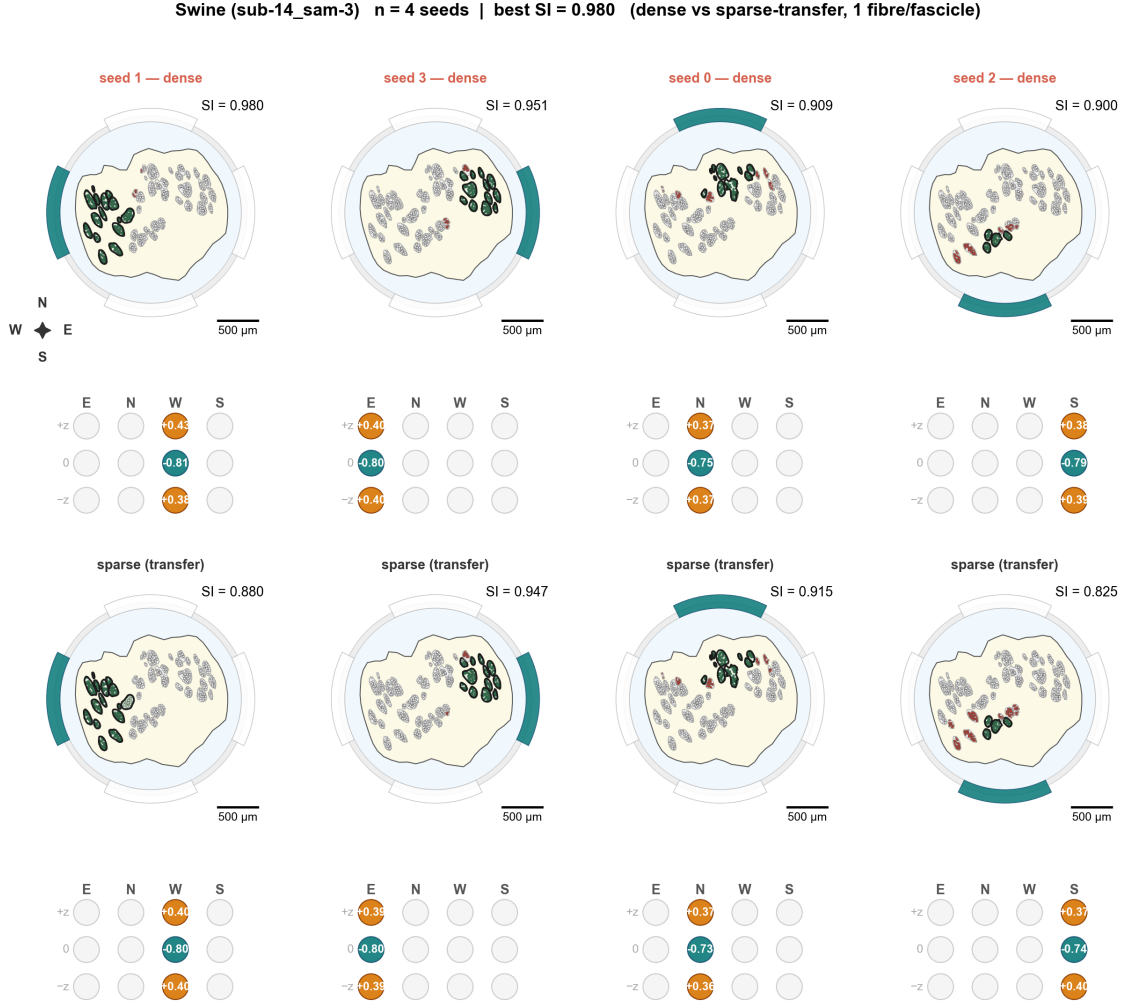


Figure S49: Specimen **swine sub-14_sam-3**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).



Figure S50: Specimen **swine sub-15_sam-2**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

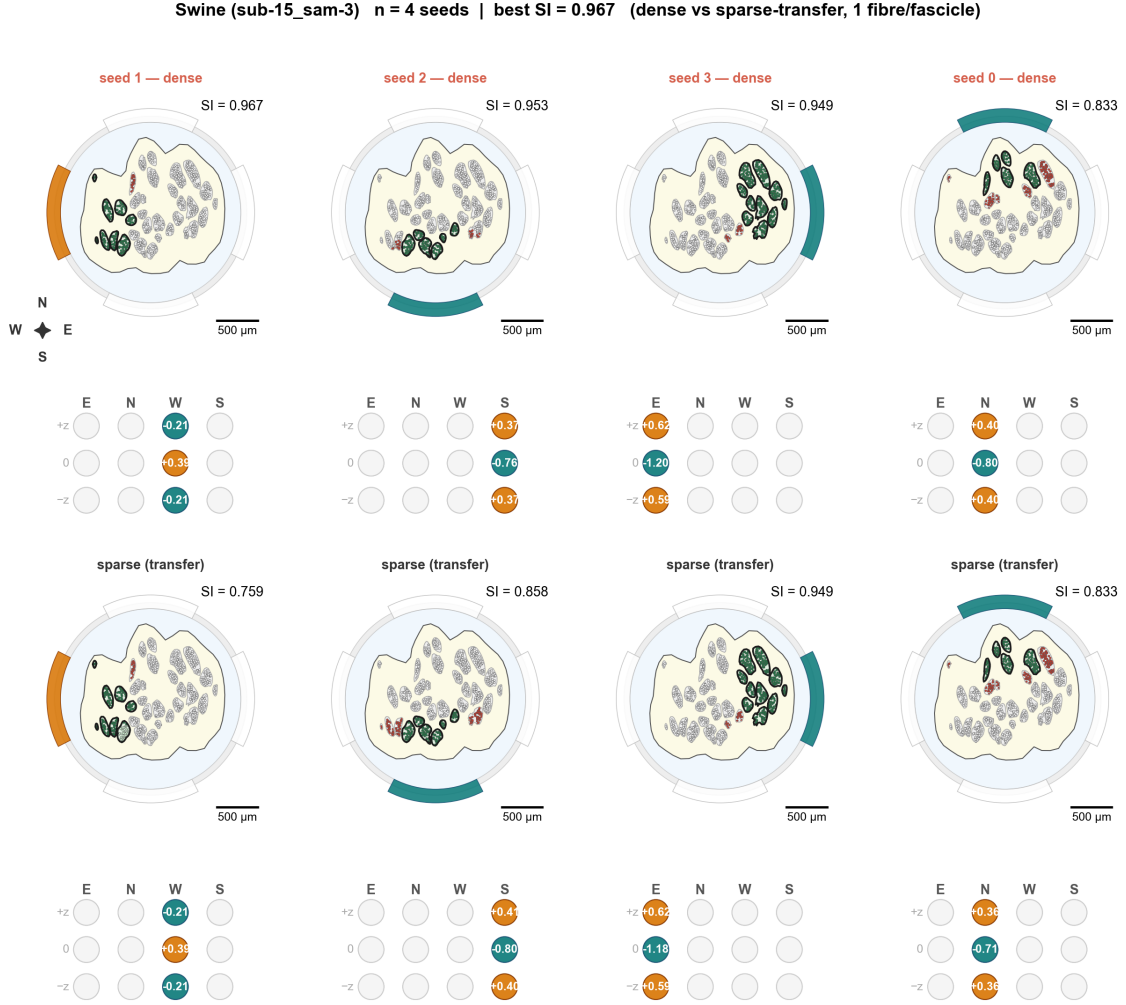


Figure S51: Specimen **swine sub-15_sam-3**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

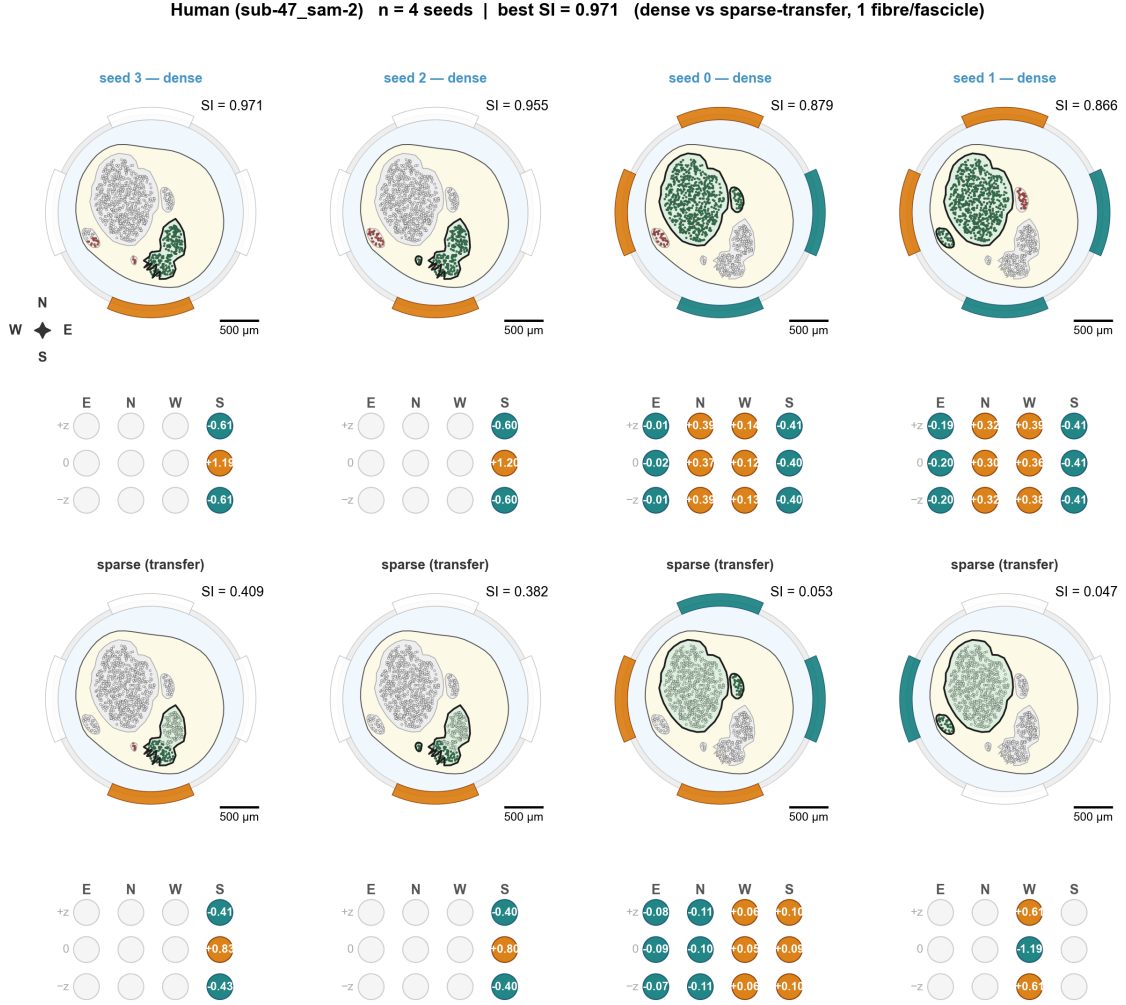


Figure S52: Specimen **human sub-47_sam-2**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

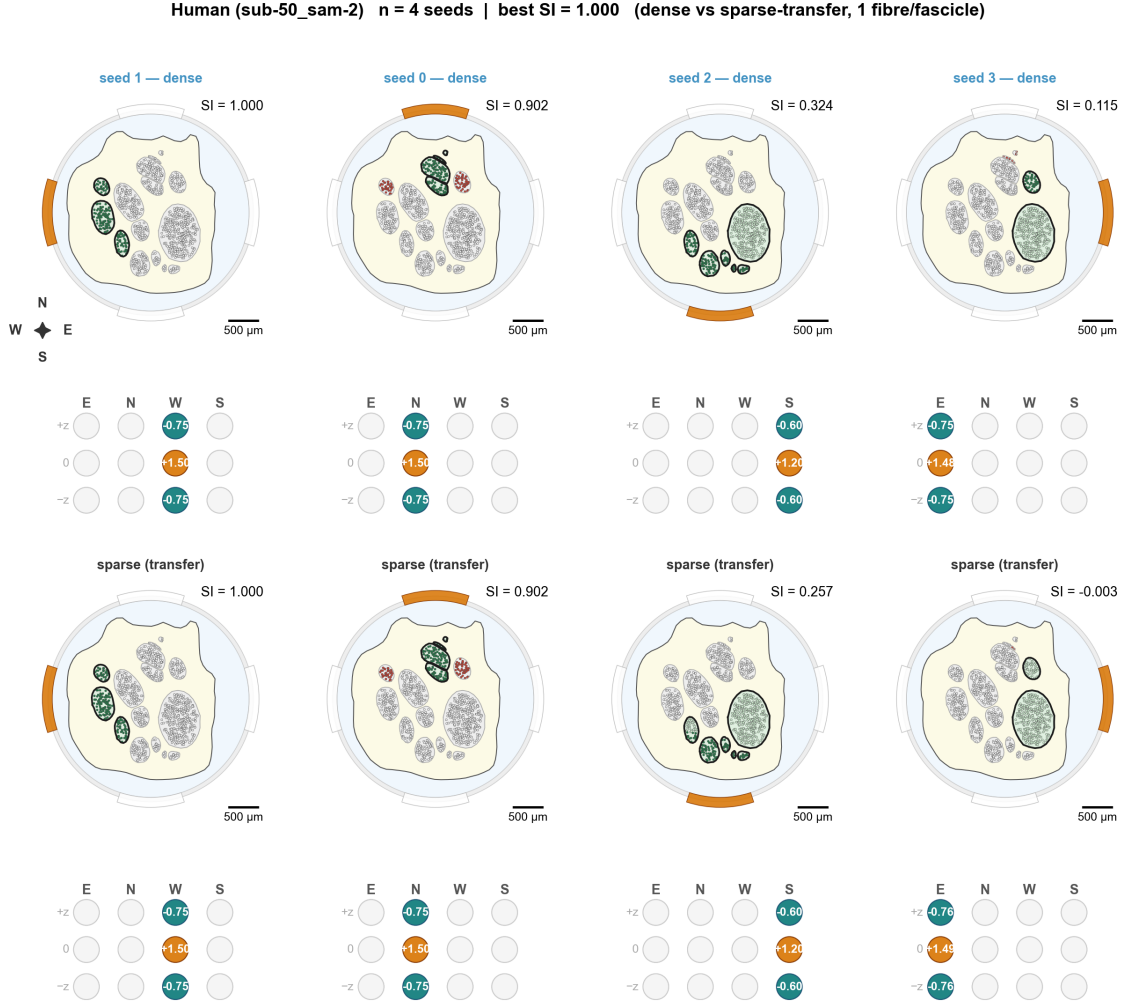


Figure S53: Specimen human sub-50_sam-2. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

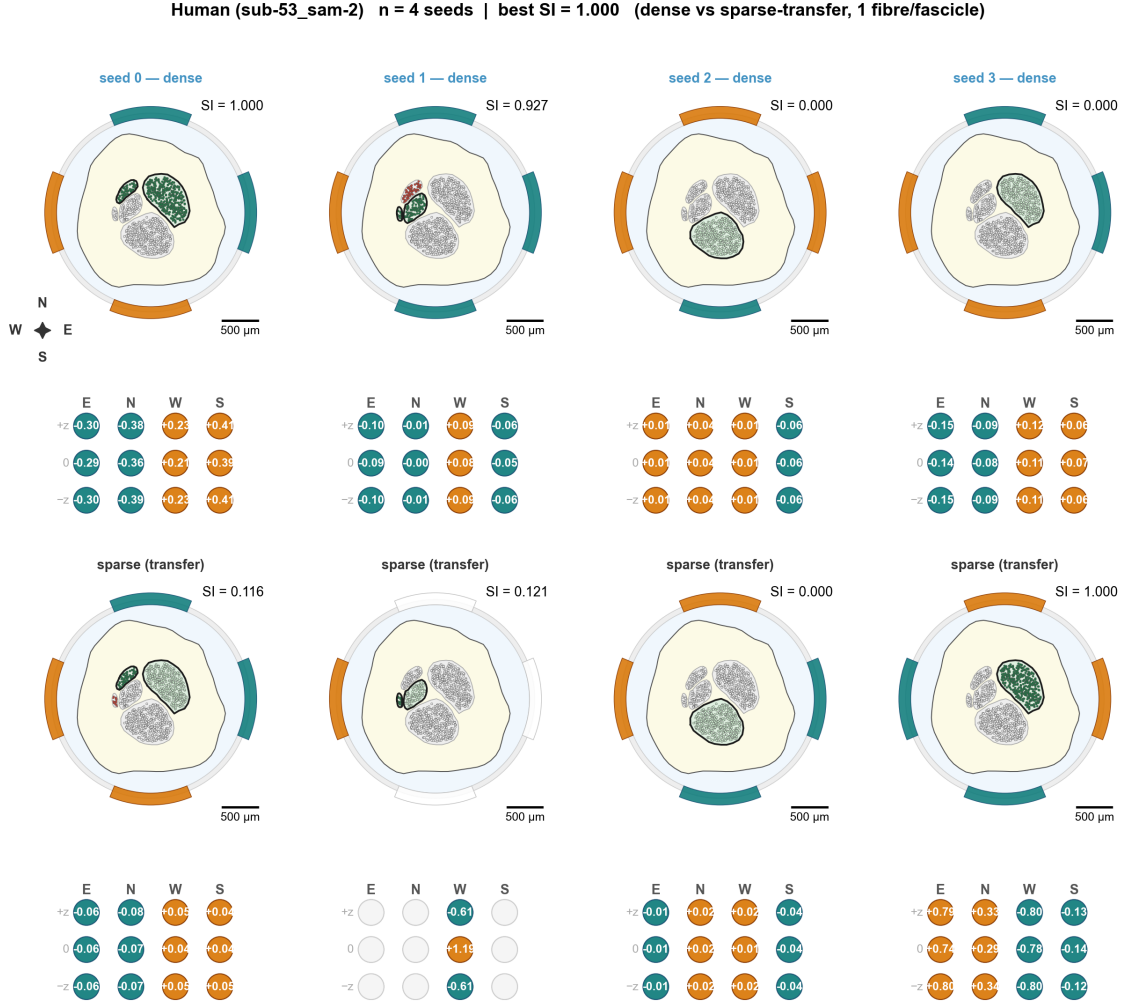


Figure S54: Specimen **human sub-53_sam-2**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

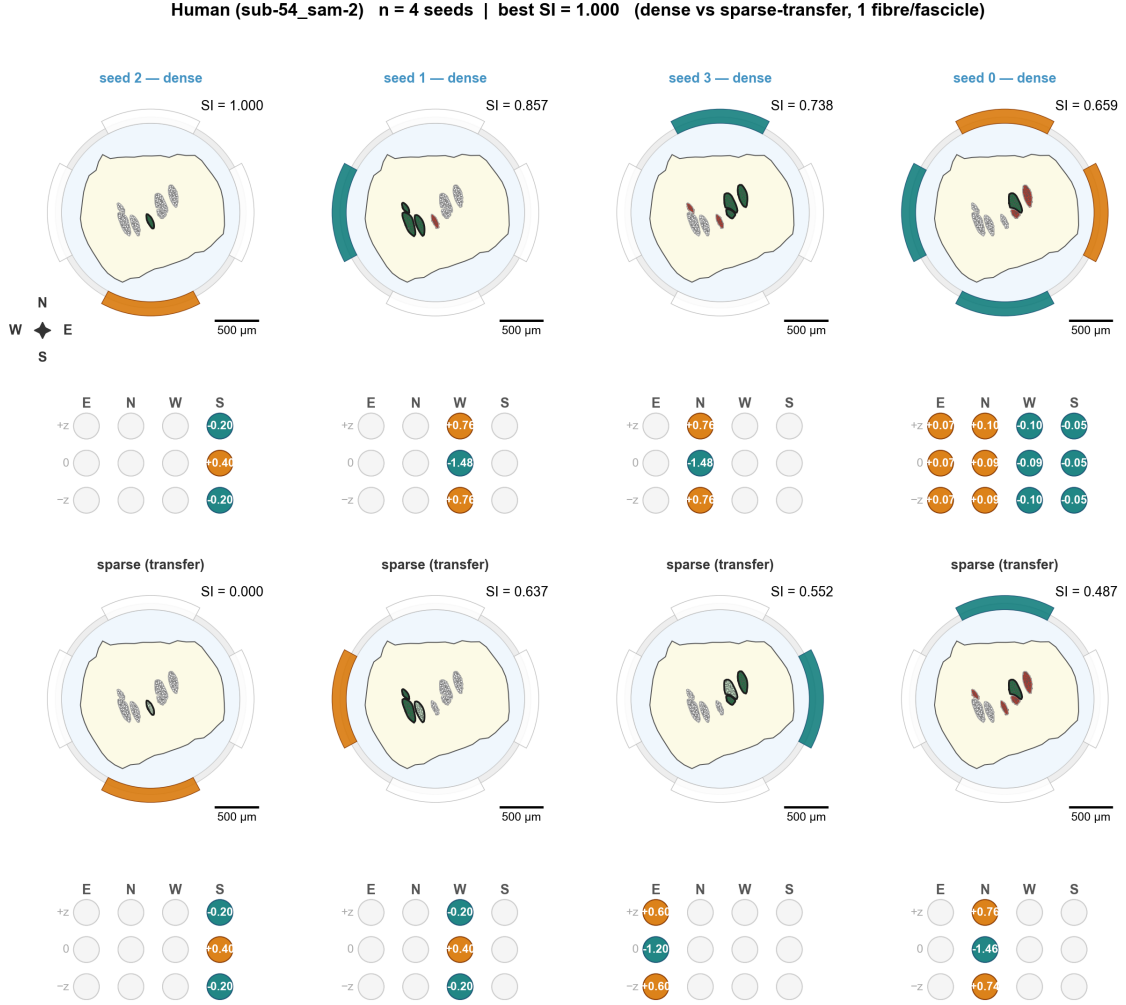


Figure S55: Specimen **human sub-54_sam-2**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

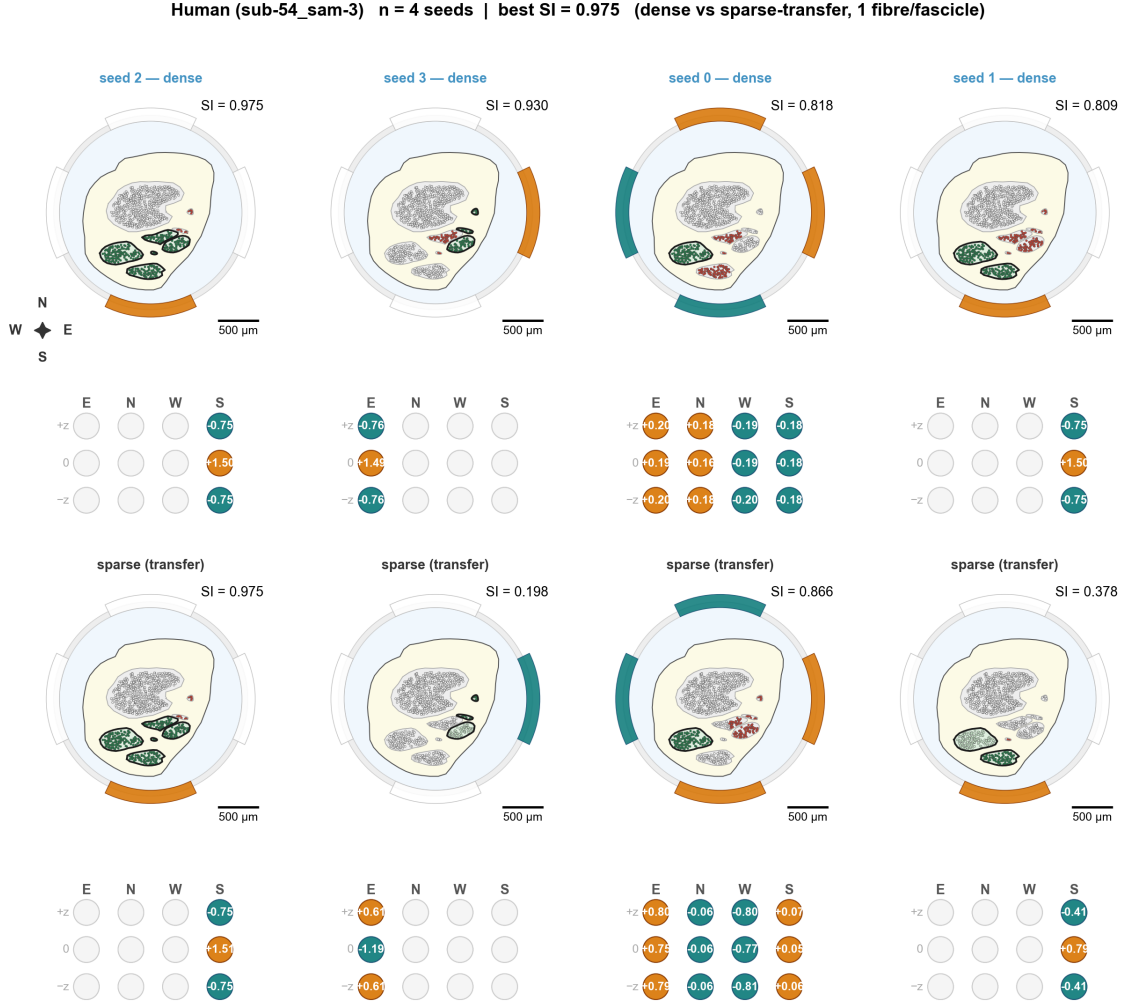


Figure S56: Specimen human sub-54_sam-3. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

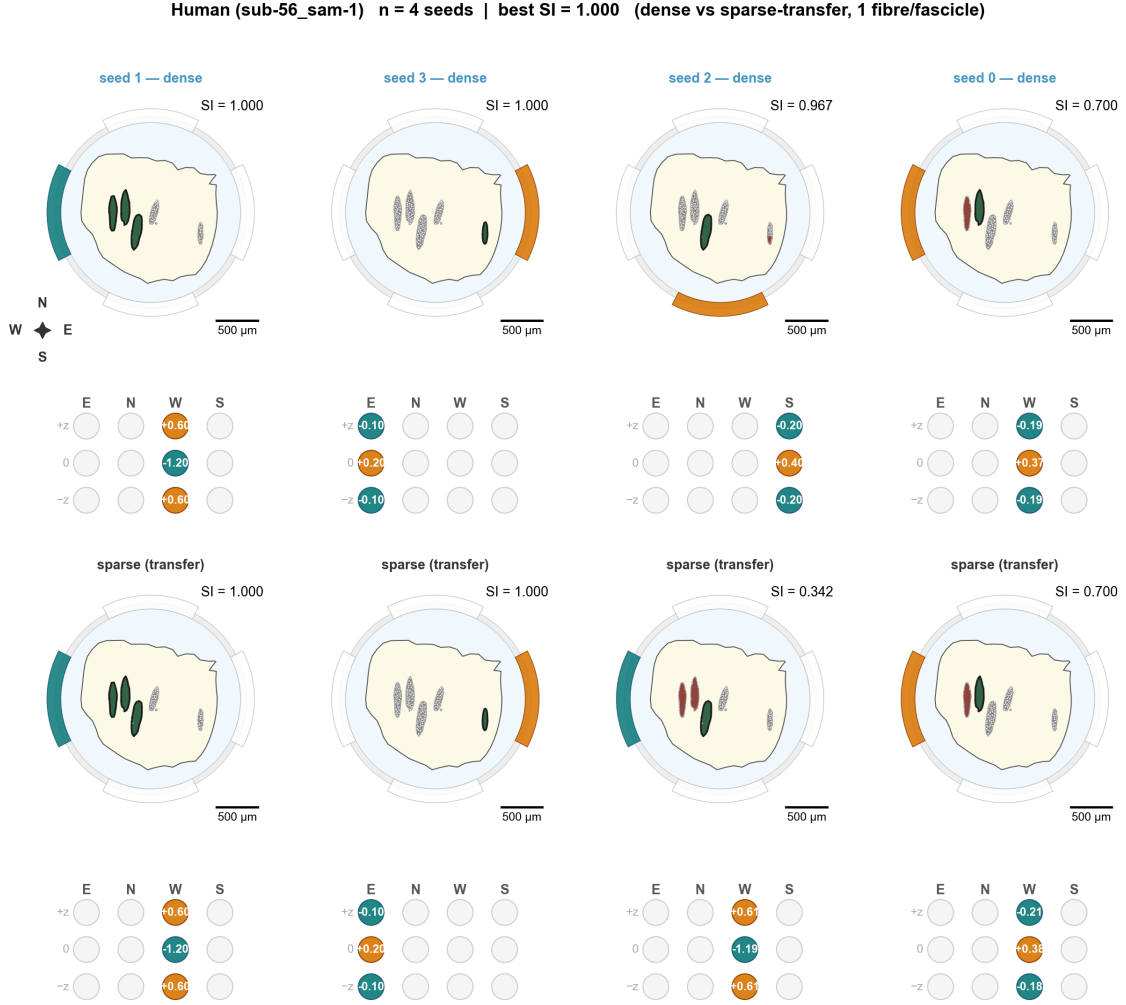


Figure S57: Specimen human sub-56_sam-1. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

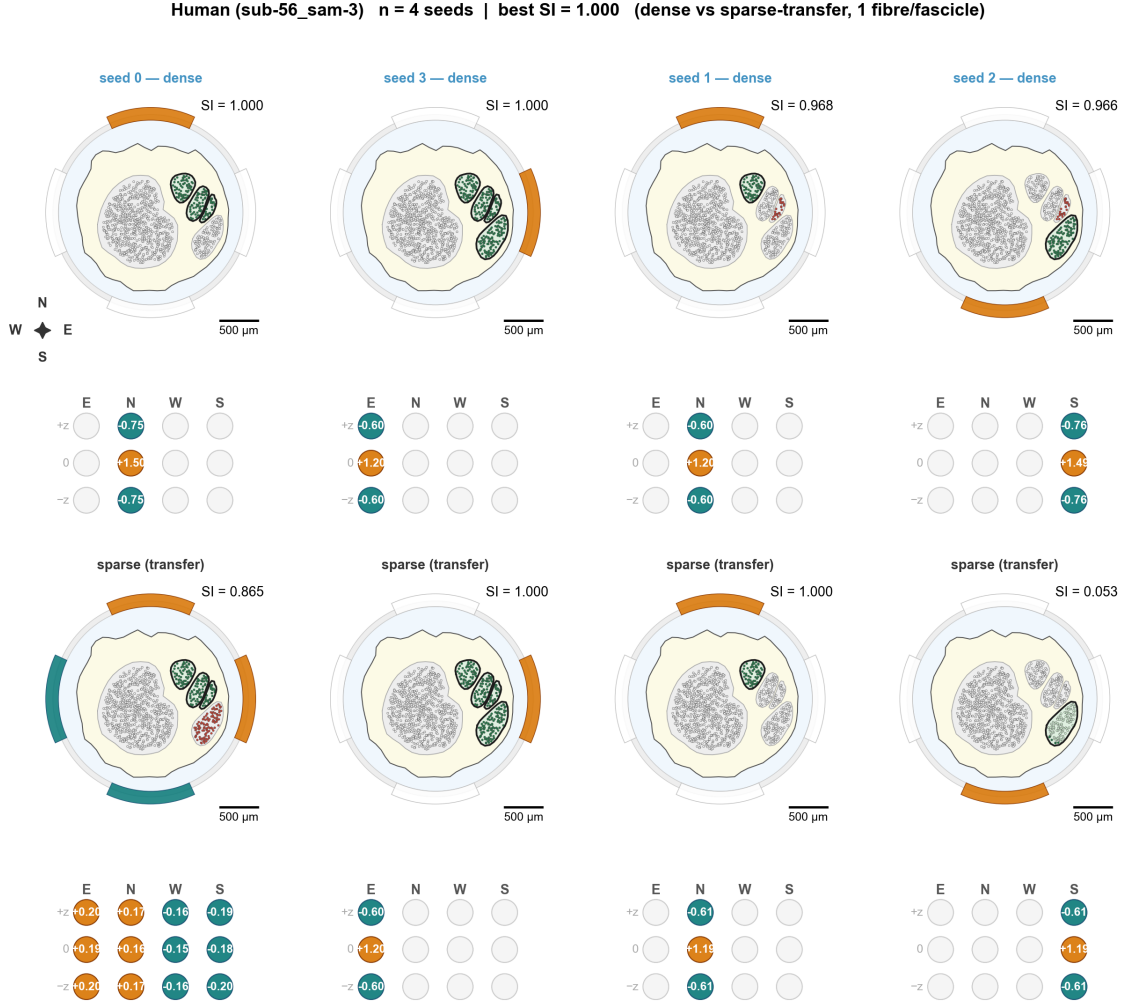


Figure S58: Specimen human sub-56_sam-3. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

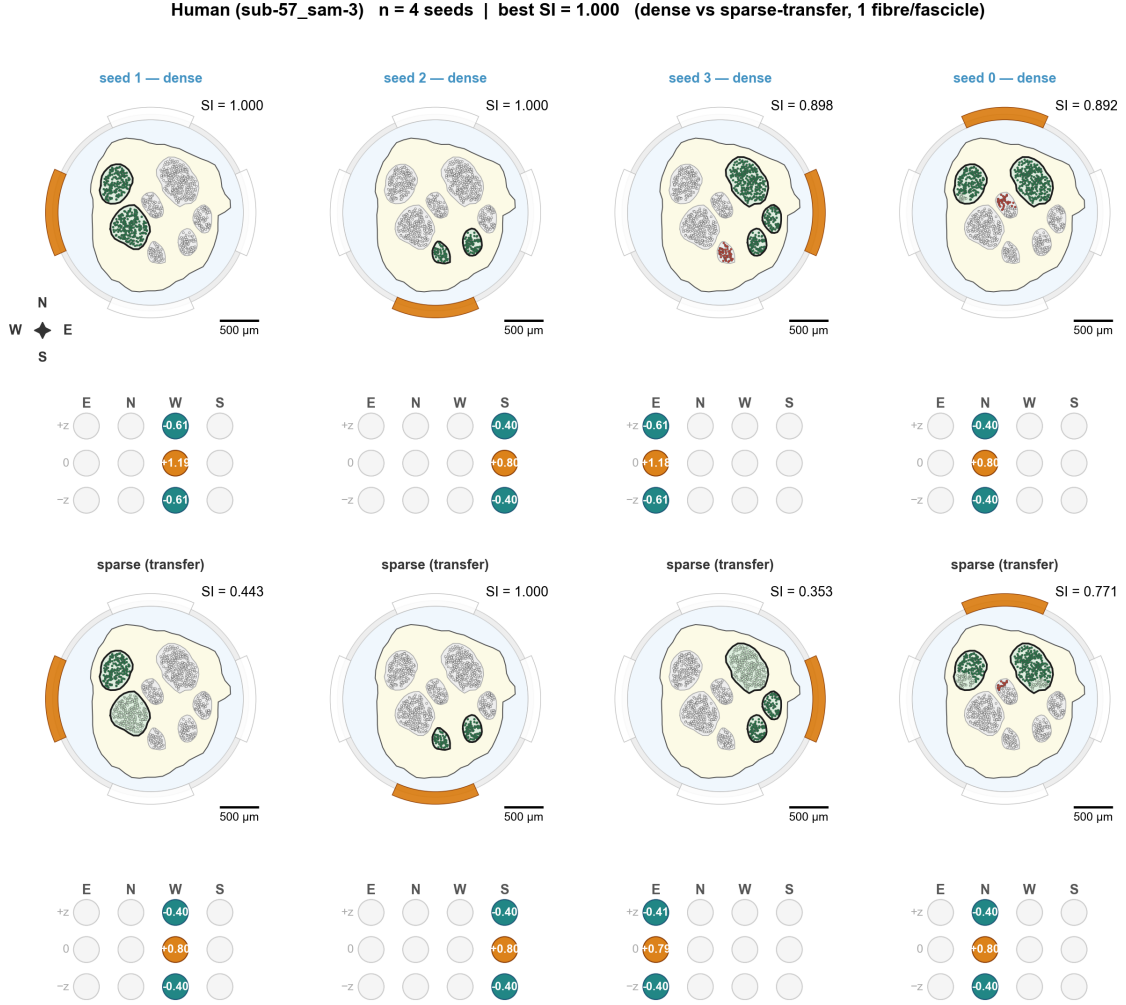


Figure S59: Specimen **human sub-57_sam-3**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

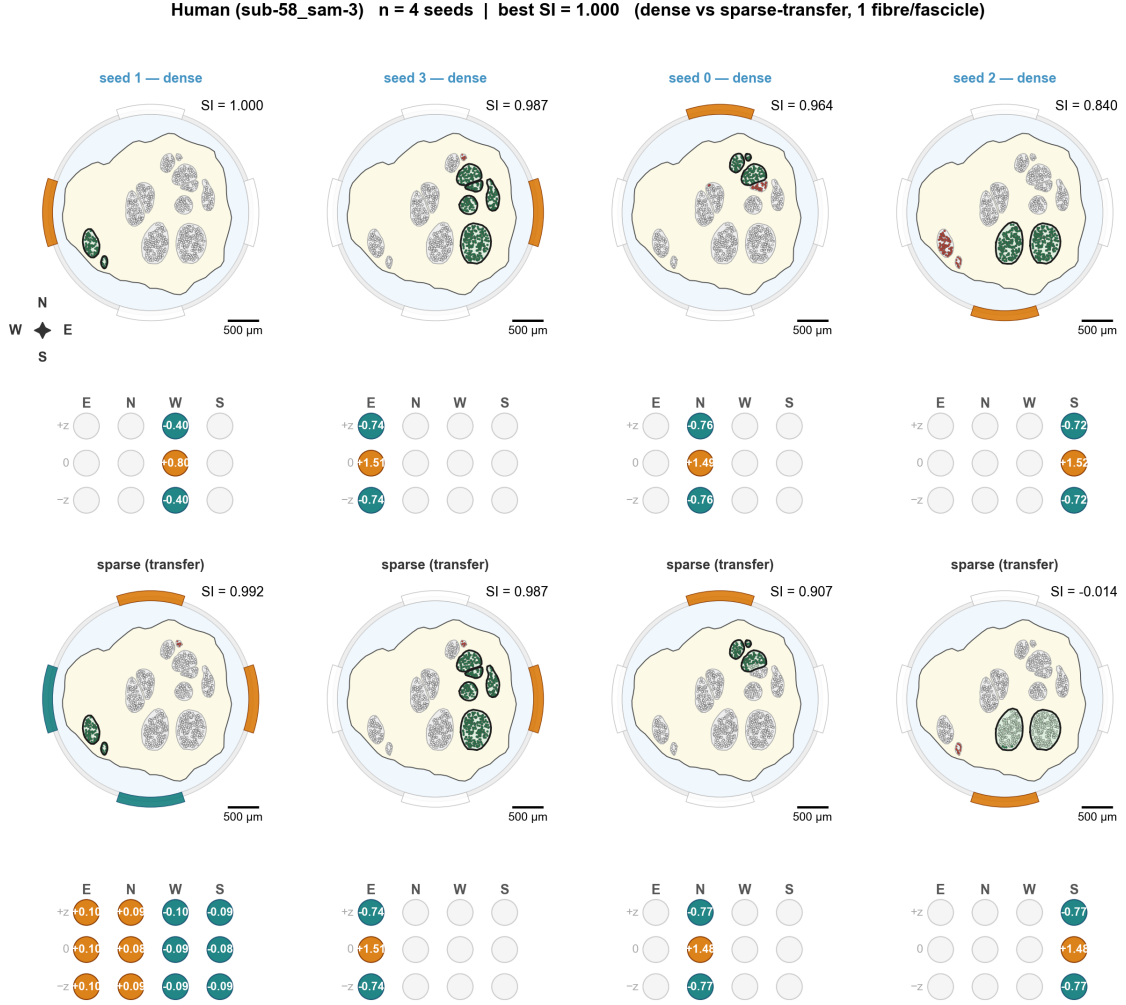


Figure S60: Specimen human sub-58_sam-3. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

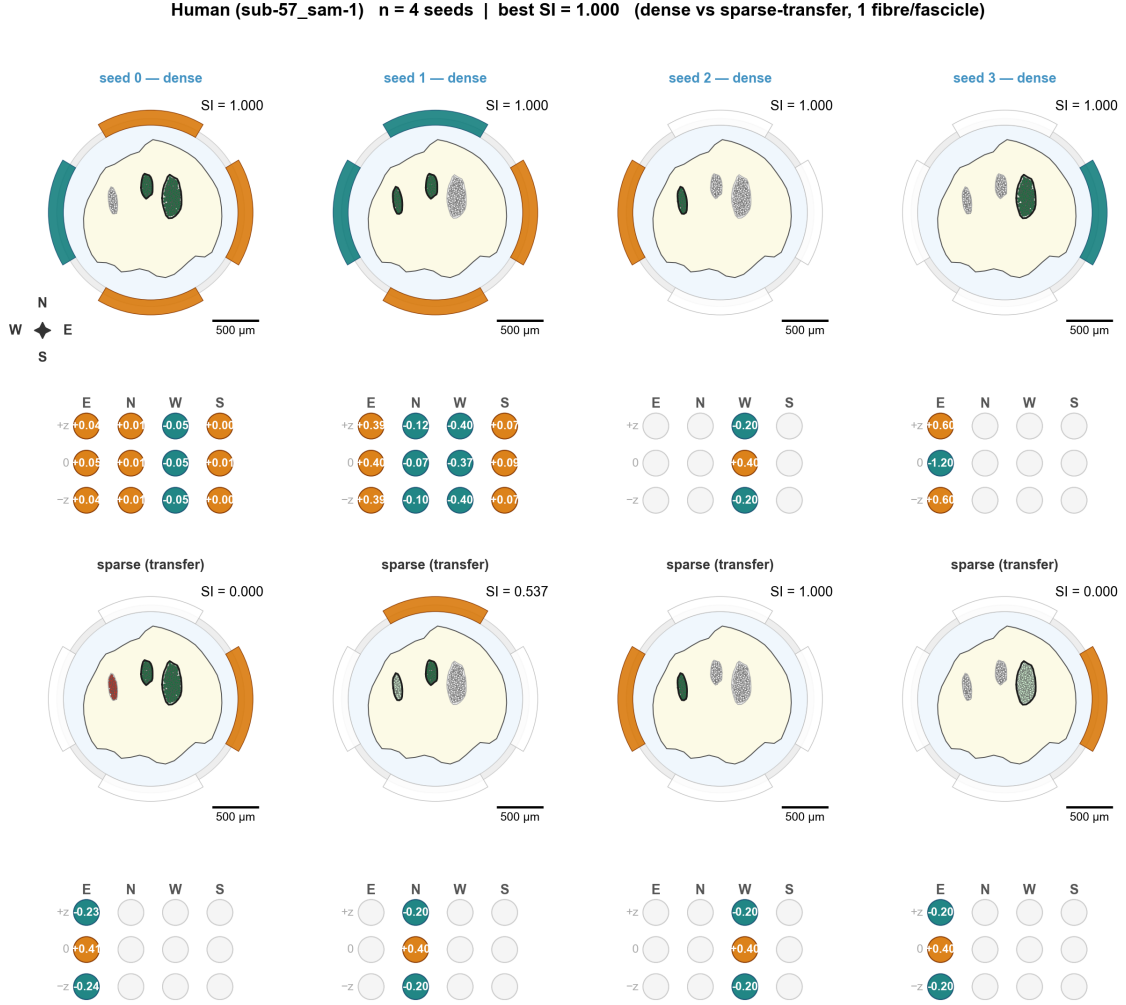


Figure S61: Specimen **human sub-57_sam-1**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

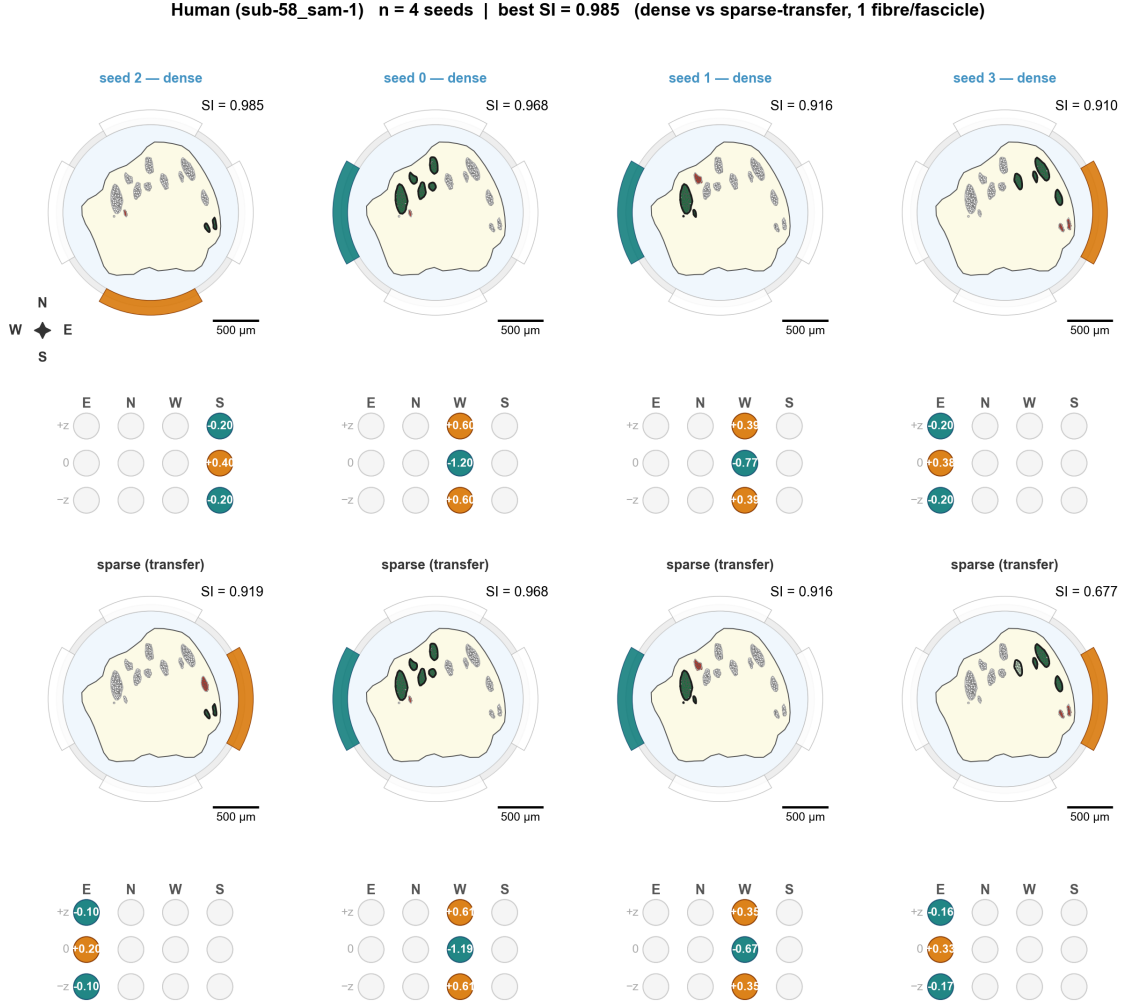


Figure S62: Specimen **human sub-58_sam-1**. All target-cluster seeds for this nerve, ordered left-to-right by achievable selectivity index SI. Each seed shows the nerve cross-section (top) with fibers colored by post-optimization recruitment (target fired / target silent / off-target fired / off-target silent) and the peripheral target-fascicle cluster outlined, above the optimized 12-contact cuff pattern (bottom; cathode blue, anode orange, inactive white, marker size $\propto |I_k|$, over four angular columns $\times$ three axial rows).

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