

Supplementary Material 1

Regional Heterogeneity of Sensorimotor BOLD Lateralisation During Unilateral Hand Movement

Brain Topography | Supplementary Material 1

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Contents: supplementary methods and analysis revision; Tables S1–S8; Figs. S1–S3. Numerical source tables are supplied as Supplementary Material 2.

S1 Analysis scope and revision

The initial programme included physiological-noise modelling (PNM), cortical connectivity and spinal analyses. These branches were withdrawn from the current study because valid re-estimation had not been established within the available-data scope. Their models and results remain in the historical records, outside the evidence supporting this regional activation manuscript.

The current study uses qualified non-PNM regional activation inputs, corrected anatomical-mask mapping and refitted first-level models. HCP regional results are reused from their completed analysis. This restricted scope was adopted on methodological grounds, not to retain statistically supported findings. Detailed technical histories of the withdrawn branches are not needed to reproduce the present measures.

The signed hand-aligned regional measure, equal four-region composite, original atlas labels, 80% coverage threshold and five regional contrast definitions were retained. Eligibility and the repair/validation plan were recorded before new group inference on 29 September 2026, after historical findings were known. Thus, this is a revision-stage analysis, not prospective preregistration. The covariance-aware WTS was introduced earlier during methodological revision and was reapplied without method selection. Paired mask/model-change inference and the non-PNM extension of activation run-order sensitivity were explicitly recorded as new revision-stage sensitivities.

The historical ROI-label permutation procedure required exchangeability beyond equality of regional means. Agreement with WTS does not establish that assumption or retrospectively validate the historical confirmatory gate. The current report presents the retained five contrasts with their original Holm family, alongside covariance-aware sensitivity evidence; it does not claim confirmation under the original gate. No new S1 – PMd comparison was added to convert the descriptive mean pattern into a strict ordering.

S2 Inputs and eligibility

Forty-four nominal CoSpine runs were assessed for paired regional measures. Sub-03 motorL was kept out because correspondence of its image series to the independent task/event records remained unresolved. Sub-04's two runs had conflicting sidecar/series associations and incomplete independent hand/event binding. Neither hand labels nor onset shifts were inferred from activation or correlation peaks. Sub-03 motorR was not used alone. For the other runs, the public BIDS task labels and event files were the authority in the absence of a specific conflict. This distinction accepts the public task records without asserting an unavailable independent acquisition-log verification.

Sub-08 motorL had usable raw imaging, reversed-phase-encoding field maps and events, but lacked its previous local cortical preprocessing because of a physiological-recording dependency. For the present non-PNM analysis, distortion correction, slice-timing correction, motion correction and EPI-to-T1 registration were rebuilt from the public images. The anatomical input matched the historical structural file's SHA256 identity. The paired right-hand upstream image was reused. Both activation models were fitted with the corrected masks and inspected anatomically. No missing hand was replaced or imputed.

Each regional measure required four valid hand-by-hemisphere measurements with at least 80% atlas coverage. All 20 final participants qualified for all four regions. Table S1 lists participant disposition and Table S2 the minimum coverage across each region's four cells. The complete 320-cell coverage table and 44-run disposition table are included in Supplementary Material 2. Figure S1 visualises the same coverage minima.

For each region r , hand h and hemisphere H , the effective mask was the intersection of the atlas label and that run's final analysis mask. Coverage used the full atlas parcel as the denominator, not only the portion

overlapping the acquired signal. The mean COPE was calculated within the effective mask with equal voxel weights. The regional measure and equally weighted composite were defined as follows, with RH/LH indicating the moving hand and L/R the anatomical hemisphere. Missing hemispheres or hand runs were not replaced by zeros or by the opposite side.

$$D_r = \frac{(C_{r,RH,L} - C_{r,RH,R}) + (C_{r,LH,R} - C_{r,LH,L})}{2}$$

$$D_{motor} = \frac{D_{M1} + D_{S1} + D_{PMd} + D_{PMv}}{4}$$

Table S1 CoSpine participant disposition

Participant	Included runs	Observed order	Disposition
sub-01	2	R_before_L	Qualified paired data; four regions complete
sub-02	2	R_before_L	Qualified paired data; four regions complete
sub-03	0	Not analysed	motorL correspondence unresolved; motorR unpaired
sub-04	0	Not analysed	Both runs: acquisition-to-task correspondence unresolved
sub-05	2	L_before_R	Qualified paired data; four regions complete
sub-06	2	L_before_R	Qualified paired data; four regions complete
sub-07	2	L_before_R	Qualified paired data; four regions complete
sub-08	2	R_before_L	Qualified paired data; four regions complete
sub-09	2	L_before_R	Qualified paired data; four regions complete
sub-10	2	R_before_L	Qualified paired data; four regions complete
sub-11	2	R_before_L	Qualified paired data; four regions complete
sub-12	2	L_before_R	Qualified paired data; four regions complete
sub-13	2	L_before_R	Qualified paired data; four regions complete
sub-14	2	L_before_R	Qualified paired data; four regions complete
sub-15	2	R_before_L	Qualified paired data; four regions complete
sub-16	2	R_before_L	Qualified paired data; four regions complete
sub-17	2	L_before_R	Qualified paired data; four regions complete
sub-18	2	L_before_R	Qualified paired data; four regions complete
sub-19	2	L_before_R	Qualified paired data; four regions complete
sub-20	2	L_before_R	Qualified paired data; four regions complete
sub-21	2	R_before_L	Qualified paired data; four regions complete
sub-22	2	L_before_R	Qualified paired data; four regions complete

^a Both hands were required. Included participants contribute all four regions. L_before_R and R_before_L denote left-first and right-first, respectively. No participant was excluded by effect magnitude or significance.

Table S2 Minimum four-cell regional coverage

Participant	M1 (%)	S1 (%)	PMd (%)	PMv (%)
sub-01	98.24	96.56	99.15	100.00
sub-02	95.03	87.31	98.87	99.26
sub-05	99.52	96.02	99.72	97.48
sub-06	95.67	90.86	97.32	94.81
sub-07	99.84	95.27	99.15	99.85
sub-08	100.00	96.56	100.00	100.00
sub-09	95.69	97.09	98.17	99.85
sub-10	89.26	88.58	95.63	98.67
sub-11	93.75	88.17	97.32	96.59
sub-12	99.52	84.38	99.32	99.11
sub-13	100.00	98.06	100.00	99.85
sub-14	100.00	98.71	99.58	99.85
sub-15	100.00	98.71	100.00	100.00
sub-16	96.31	98.49	96.33	99.56
sub-17	100.00	90.97	99.66	99.70
sub-18	99.36	97.63	99.58	100.00
sub-19	91.99	91.83	98.19	99.70
sub-20	98.40	95.27	99.72	100.00
sub-21	99.68	96.02	99.66	99.41
sub-22	100.00	85.05	99.66	99.26

^a Each entry is the minimum of the two hands $\times$ two hemispheres. The unchanged threshold is 80%. Complete run-by-region values accompany Supplementary Material 2.

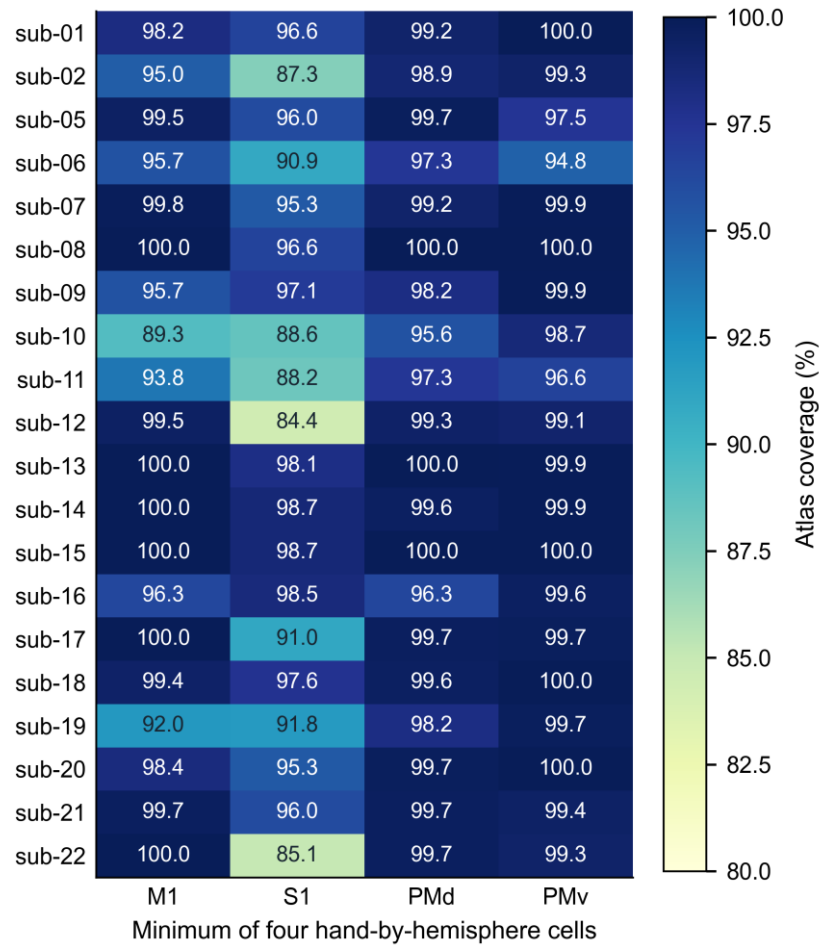


Fig. S1 Minimum atlas coverage for each participant and region. Each cell is the smallest coverage percentage across the two hands and two hemispheres. All 20 participants meet the unchanged 80% threshold for every region; the underlying 320 run-by-unilateral-region values are supplied in Supplementary Material 2

S3 Processing and first-level specification

The current non-PNM branch used local preprocessed BOLD data derived without physiological precleaning. Dependency checks distinguished these images from similarly named physiological-regression products. Public events matched the model event files and observed run lengths; there was no additional deletion of saved volumes or fitted time offset. Slice-timing offsets were converted to TR fractions for FSL slicetimer. This interface is separate from the slice-dependent physiological-model input implicated in the withdrawn branch.

Released CoSpine events defined the participant-specific movement blocks, and the observed time-series length defined each run's model grid. Temporal derivatives accommodated small response-timing differences within the specified HRF model; they did not alter event onsets or change the movement contrast into a temporal-derivative test. Spatial correspondence checks required matching atlas, COPE and final-mask dimensions, orientation and affine before extraction. No new atlas interpolation or activation-based voxel selection was introduced at that stage.

The earlier anatomical-mask builder attempted different coordinate interpretations of an FSL registration and selected a world-affine fallback, omitting the estimated EPI/T1 alignment. The corrected mask used `convert_xfm` to invert the saved EPI-to-T1 transform and `flirt` with nearest-neighbour sampling into the mean EPI reference. An independent scaled-millimetre-coordinate calculation checked the transformation. Binary-mask agreement exceeded the prespecified 99.99% tolerance in the technical checks. Native anatomical support was intersected with finite, nonzero sampling in at least 95% of time points, warped with nearest-neighbour interpolation and intersected with the standard MNI brain mask. Effective regions retained the original atlas labels and coverage rule.

All 40 activation models were refitted because mask changes can affect intensity normalisation, FILM neighbourhood support and extraction. The first technical pair was selected by run properties, including unequal run lengths, not by effects. All final models passed checks for finite estimates, design rank, positive residual degrees of freedom, task contrast, motion/spike consistency, spatial correspondence and completed FILM output. Anatomical review covered all runs at four axial levels, with additional paired structural/EPI views for sub-08. This was targeted image-level quality control, not exhaustive voxelwise registration validation.

CoSpine movement models used the FSL double-gamma response and its temporal derivative, 12 motion/derivative columns, retained frame impulses at $FD > 0.5$ mm, 100-s high-pass filtering and FILM prewhitening. No smoothing or physiological-regression step was added. FEAT grand-median scaling targeted 10,000. The movement COPE selected the canonical task coefficient. Old and corrected matched models retained task and nuisance definitions; numerical writing precision differed slightly (maximum absolute design-matrix difference 0.00000001). Paired changes therefore describe the corrected mask and dependent model implementation rather than an isolated extraction-mask experiment.

For reconstructed sub-08 motorL, `applytopup` explicitly used Jacobian modulation and spline interpolation; the T1-support transform and mask warp explicitly used nearest-neighbour interpolation. The recorded `mcflirt` and `BOLD applywarp` calls did not set an interpolation override. Historical stage-specific interpolation/build records for reused upstream images were incomplete, so no unverified historical default is asserted here. The current first-level models used FSL 6.0.7.22. Recorded analysis libraries were Python 3.13.5, NumPy 2.3.5, SciPy 1.16.3, NiBabel 5.3.2 and statsmodels 0.14.6. The full executed configurations remain in the analysis records.

HCP inputs were the official S1200 minimally preprocessed MNI-volume products (Glasser et al. 2013). Separate LR/RL models included the hand, foot, tongue and cue regressors and their derivatives, 100-s filtering and FILM prewhitening, without additional smoothing. The 12 motion columns were supplied translations, rotations and derivatives. FD was calculated from backward differences of the first six columns with translations in millimetres, rotations converted from degrees to radians and a 50-mm head radius; the first difference was zero. Each $FD > 0.5$ -mm frame received an impulse without neighbour expansion. COPE 1 represented left hand and COPE 2 right hand. Regional values were averaged across LR/RL within each participant. The upstream preprocessing build and exact analysed-sample demographics were unavailable in the retained records; the local first-level version was FSL 6.0.7.22.

S4 Statistical implementation and complete regional results

Let x be the four-region participant vector, $\bar{x}$ its sample mean and S its sample covariance. With $C = [I_3, -I_3]$, the covariance-aware statistic was:

$$W = n(C\bar{x})^T (CSC^T)^{-1} (C\bar{x})$$

Parametric null draws used the full observed covariance, with covariance re-estimated for every draw, following covariance-aware repeated-measures methodology (Bathke et al. 2018; Friedrich et al. 2019). Table S3 reports the current full-sample WTS results, and Table S4 the complete composite and region-versus-zero statistics. No ROI-label omnibus p value is substituted for these results.

The composite was one measure. Four regional tests formed one Holm family per cohort, and the five retained paired regional comparisons formed another family per cohort (Holm 1979). CoSpine exact mean sign flips enumerated 2^n assignments with inclusive comparison tolerance $10^{-12} \times \max(1, |\text{observed mean}|)$; exact p was the extreme proportion. HCP individual-region/composite tests used the exact binomial sign test; its regional contrasts used 100,000 Monte Carlo mean sign flips. Zero Monte Carlo exceedances were reported using $(b + 1)/(B + 1)$, never $p = 0$. Bootstrap intervals were unadjusted percentile intervals, not inversions of the sign-flip tests (Winkler et al. 2014). All tests retained their assumptions; an insignificant assumption check was not used to establish them.

The five regional weight vectors, in M1/S1/PMd/PMv order, were (1, 0, 0, -1), (0, 1, 0, -1), (0, 0, 1, -1), (0.5, 0.5, -0.5, -0.5) and (1, -1, 0, 0). Each participant's regional vector was transformed before calculating a group estimate. The four-region composite used (0.25, 0.25, 0.25, 0.25). Current core estimates use all 20 complete participants; the measure-specific matched-processing samples are identified separately in Section S5. An anatomical left-right contrast within a phase-encoding run is not interchangeable with the hand-aligned contrast, and HCP LR/RL labels do not identify the moving hand.

For CoSpine composite/ROI summaries and paired processing changes, 10,000 participant bootstrap draws used seed 20260727. HCP composite/ROI summaries used seed 20260731. Regional-contrast interval seeds were 20260801 through 20260805 in the displayed contrast order. WTS used 99,999 replicates with seeds 2026092102 for current CoSpine and 2026092103 for HCP. The HCP contrast sign-flip count was 100,000, distinct from its 10,000-resample interval count. Descriptive mean rankings do not introduce additional pairwise tests.

Table S3 Covariance-aware regional heterogeneity sensitivity

Cohort	n	WTS	Draws	Exceedances	Plus-one p
CoSpine	20	246.377647	99,999	0	0.000010
HCP	100	1072.556964	99,999	0	0.000010

^a Both tests use the rank-three equality-of-regional-means contrast, full within-participant covariance and parametric bootstrap with covariance re-estimation. These are revision-stage sensitivities, not retrospective validation of the original ROI-label gate. Zero exceedances produce $p = 1/100,000$, not zero.

Table S4 Additional composite and regional summaries

Cohort	Measure	n	SD	Positive n	Median	Raw p	Holm p
CoSpine	Composite	20	10.313	20	26.610	<0.001	—
CoSpine	M1	20	24.239	20	51.070	<0.001	<0.001
CoSpine	S1	20	14.236	20	46.663	<0.001	<0.001
CoSpine	PMd	20	8.125	20	7.612	<0.001	<0.001
CoSpine	PMv	20	6.170	12	0.979	0.917	0.917
HCP	Composite	100	11.263	100	35.771	<0.001	—
HCP	M1	100	22.481	100	69.273	<0.001	<0.001
HCP	S1	100	17.090	100	53.383	<0.001	<0.001
HCP	PMd	100	9.848	96	16.016	<0.001	<0.001
HCP	PMv	100	12.305	61	3.983	0.035	0.035

^a Mean estimates, pointwise intervals and standardised effects appear in main Table 2. SD and median retain cohort-specific COPE units. Positive counts are descriptive in CoSpine and supply the HCP binomial sign tests. Full-precision results are included in Supplementary Material 2.

S5 Sample and processing changes

Four sets separate interpretation of the revision: A, the historical non-PNM sample; B, the old model restricted to the intersection of old and current measure eligibility; C, the corrected model in exactly the B participants; and the final corrected sample, including all current eligible participants. Table S5 gives these means and sample sizes. B – A and final – C describe overlapping-sample composition changes; neither is an independent-group comparison. Table S6 and Fig. S2 report the within-participant C – B changes, using the additional five-measure family fixed before new results. Table S7 retains all five regional contrasts in B and C; the final contrasts are in the main manuscript, Table 3.

The matched complete-case sample comprised 17 participants: sub-01, sub-02, sub-05, sub-07, sub-09, sub-10, sub-11, sub-13, sub-14, sub-15, sub-16, sub-17, sub-18, sub-19, sub-20, sub-21 and sub-22. M1, PMd and PMv matched samples additionally included sub-06 and sub-12 (n = 19). The final complete-case sample also included sub-08, whose missing upstream non-PNM branch was newly completed. Correct mapping raised the previously limiting S1 coverage cells in sub-06 and sub-12 above the original 80% threshold. Their eligibility was not obtained by changing the threshold.

In the 17 matched complete cases, composite lateralisation increased by 0.530486 units, with a percentile interval of 0.000158–1.195909, exact sign-flip $p = 0.098572$ and Holm $p = 0.394287$. The interval and test are different inferential constructions; the small positive unadjusted interval lower bound is retained without rounding it to zero or treating it as a corrected rejection. None of the five paired changes survived Holm correction. This lack of corrected support is not an equivalence result. New and old matched WTS sensitivities both had plus-one $p = 0.000010$ ($W = 192.550$ and 207.513 , respectively).

Table S5 Separating sample composition and model changes

Measure	A mean (n)	B mean (n)	C mean (n)	Final mean (n)
Composite	27.387 (19)	28.284 (17)	28.814 (17)	28.059 (20)
M1	50.573 (21)	51.381 (19)	53.415 (19)	52.686 (20)
S1	47.442 (19)	48.673 (17)	49.401 (17)	49.033 (20)
PMd	10.506 (21)	10.708 (19)	10.999 (19)	10.661 (20)
PMv	−0.595 (21)	0.331 (19)	0.331 (19)	−0.144 (20)

^a A: historical non-PNM available cases. B: old models in matched eligible participants. C: corrected models in the same participants as B. Final: all currently eligible corrected models. All values are CoSpine COPE units. B – A and Final – C describe sample composition, not independent-group effects.

Table S6 Paired corrected-minus-previous model changes

Measure	n	Mean change [95% CI]	Raw p	Holm p
Composite	17	0.530486 [0.000158, 1.195909]	0.098572	0.394287
M1	19	2.033535 [0.291734, 4.298529]	0.047222	0.236111
S1	17	0.727983 [−0.186704, 2.054312]	0.263763	0.527527
PMd	19	0.291082 [−0.109720, 0.653955]	0.158001	0.474003
PMv	19	−0.000192 [−0.162861, 0.163538]	0.998619	0.998619

^a The composite and four ROI changes form one additional revision-stage five-measure Holm family. Exact two-sided mean sign flips; 10,000 participant percentile-bootstrap resamples. These pointwise intervals are not inversions of the tests. Six decimals preserve the near-zero composite lower bound. All changes are CoSpine COPE units.

Table S7 Regional contrasts under matched old and corrected models

Set	Contrast	n	Difference [95% CI]	Raw p	Holm p
B	M1 – PMv	19	51.050 [41.153, 62.459]	<0.001	<0.001
B	S1 – PMv	17	48.689 [42.323, 55.335]	<0.001	<0.001
B	PMd – PMv	19	10.377 [6.916, 13.868]	<0.001	<0.001
B	Mean(M1, S1) – Mean(PMd, PMv)	17	45.446 [38.623, 52.671]	<0.001	<0.001
B	M1 – S1	17	4.667 [−4.714, 15.134]	0.412	0.412
C	M1 – PMv	19	53.084 [43.261, 64.133]	<0.001	<0.001
C	S1 – PMv	17	49.443 [42.622, 56.442]	<0.001	<0.001
C	PMd – PMv	19	10.668 [7.248, 14.154]	<0.001	<0.001
C	Mean(M1, S1) – Mean(PMd, PMv)	17	46.276 [39.119, 53.736]	<0.001	<0.001
C	M1 – S1	17	5.102 [−4.547, 15.694]	0.373	0.373

^a B and C use the same participants for a given contrast. Each set retains all five regional comparisons with its own five-item Holm family; these are within-set results, not paired tests of between-implementation change. Final expanded-sample results are in main Table 3. Values are CoSpine COPE units.

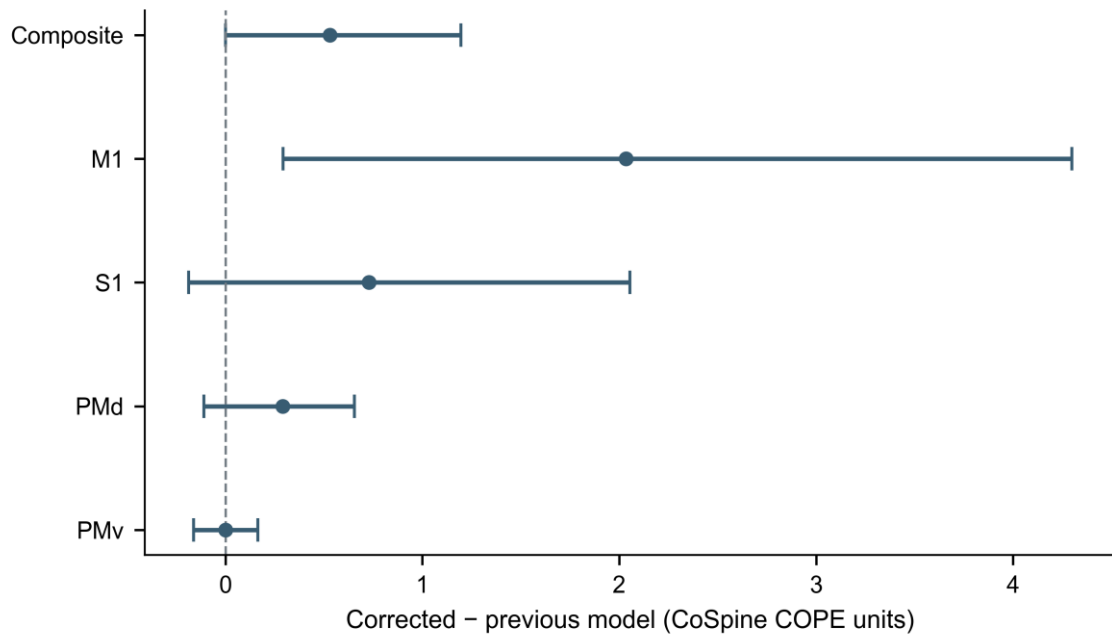


Fig. S2 Paired change after correction of anatomical-mask mapping and dependent model refitting. Points and bars are mean corrected-minus-previous differences and pointwise 95% percentile-bootstrap intervals (10,000 resamples). Samples are 17 for the composite and S1 and 19 for M1, PMd and PMv. These five changes form a separate Holm family; none survives correction. The dashed line marks zero. Changes include mask-dependent scaling and model fitting, not only extraction support

S6 Run order and HCP phase encoding

CoSpine order sensitivity retained right-hand-first = 0 and left-hand-first = 1. The composite coefficient was estimated by ordinary least squares with HC3 uncertainty. Regional-profile-by-order sensitivity used the existing repeated-measures interaction F statistic, permuting participant-level order labels 100,000 times while retaining each participant's four regional values (seed 20260801). This extension to the current non-PNM sample was a revision-stage sensitivity. All 20 participants were retained. Table S8 reports both results. The observed, non-random order and assumptions of the corresponding label permutation limit causal interpretation.

Figure S3 shows participant-level LR and RL regional contrasts in HCP. Both phase-encoding runs included both hand conditions. The participant measure was their equal average, and no new run-comparison significance test was performed for this display. The cohort-specific tests and effect scales used in the main analysis are unchanged.

Table S8 Activation run-order sensitivity

Analysis	n	Estimate or statistic	95% CI	p
Composite order coefficient	20	4.322252	[-4.776172, 13.420675]	0.351807
ROI × order interaction	20	F(3, 54) = 0.055147	Not applicable	0.971850

^a Composite coding: right-hand-first = 0; left-hand-first = 1; coefficient is left-first minus right-first in CoSpine COPE units, with HC3 uncertainty. Order groups: 12 left-first and 8 right-first.

^b The regional-profile interaction uses 100,000 participant-order-label permutations and plus-one p. Both analyses are revision-stage sensitivities of observed, non-random order, not causal tests.

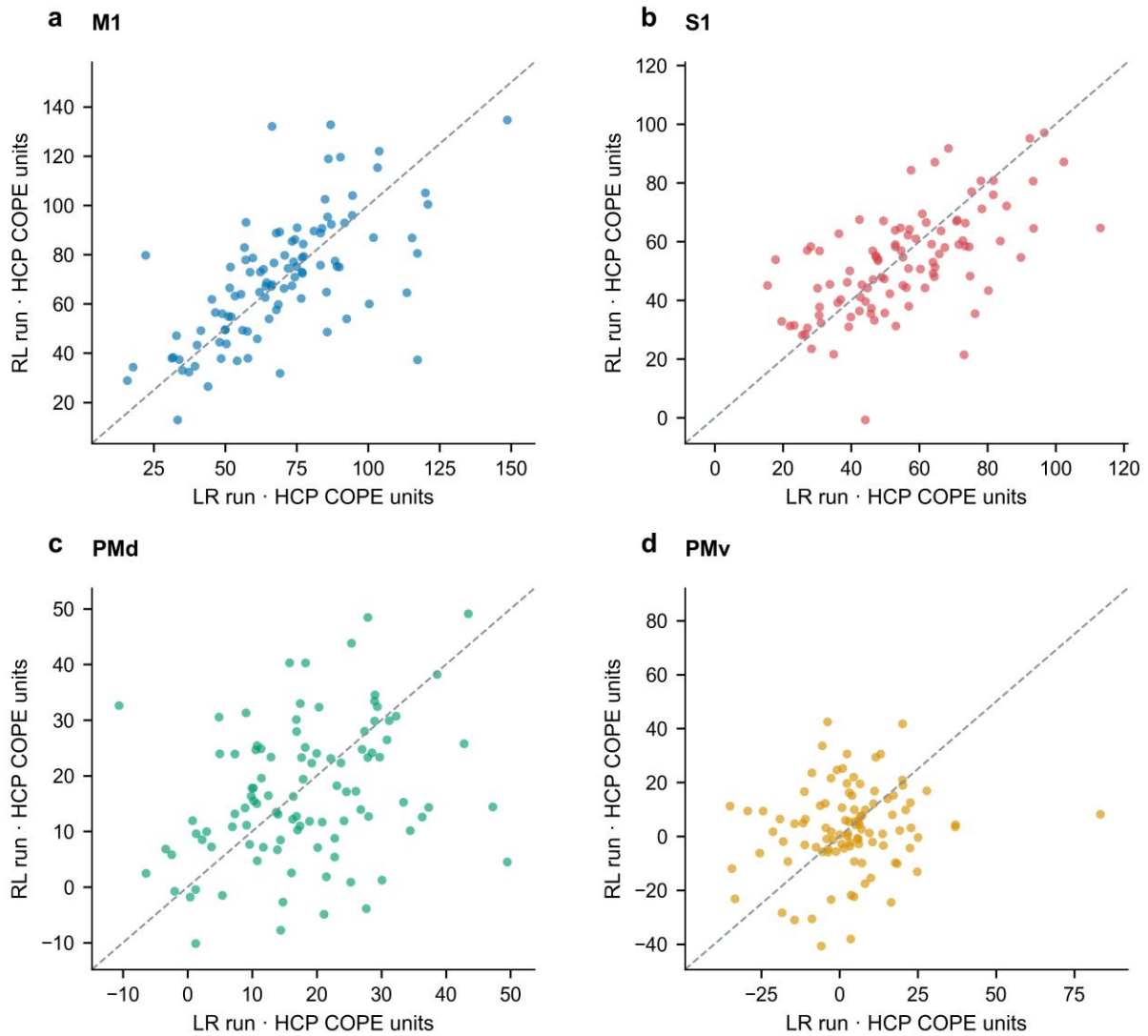


Fig. S3 HCP regional contrasts in paired LR and RL phase-encoding runs. Each point is one participant ($n = 100$ per region); the dashed line denotes equal run values. Panels show M1 (a), S1 (b), PMd (c) and PMv (d). Both runs contain both hand conditions. Values are hand-aligned contrasts in HCP COPE units. This descriptive display introduces no additional test

S7 Data and reporting notes

The final 20-person CoSpine age and sex summary was recalculated from the released participants.tsv after joining to the final measure list: 52.55 ± 9.96 years, range 37–74; 10 male and 10 female participants. For context, the original 22-person table yields 52.36 ± 10.63 years, whereas the source publication reports 52.30 years (Wei et al. 2025). The current sample statistics use the participant table, not either original cohort mean. No participant is included solely to reproduce a previous sample count.

Supplementary Material 2 supplies complete current regional estimates and numerical comparison tables, including all five contrasts and all matched processing changes. Metadata distinguishes current core estimates from historical non-PNM processing references. Individual HCP records and identifiers are not redistributed in this supplement; group results are included, and source access remains governed by HCP terms.

The public numerical supplement is `Supplementary_Material_2.zip`. Files `activation_group_results.csv` and `five_contrast_results.csv` distinguish FINAL_corrected from B_old_matched and C_corrected_matched; the latter two identify the processing sensitivity sets, not alternative core samples. `CoSpine_WTS_results.csv` uses the same set labels. `HCP_reused_ROI_results.csv`, `06b3_hcp_primary_composite_results.csv`, `HCP_five_contrasts.csv` and `HCP_WTS_results.csv` contain the corresponding existing HCP summaries. Participant endpoints, run disposition and coverage files document the current CoSpine sample. Numerical files are retained in their machine-readable form; Supplementary Material 1 supplies their methods and interpretation.

Main figures use saved participant-level and group results. Figure 1 identifies the four atlas parcels. In Figure 2, each cohort's regional mean is assigned to both homologous parcels for display on an fsaverage5 reference surface. The displayed geometry is a weighted blend of 35% pial and 65% inflated coordinates; sampling uses the original pial/white geometry. This is anatomical presentation of a regional statistic, not vertex-wise analysis. Half-violins use Scott-bandwidth kernel densities restricted to the observed range and scaled to equal peak width. In Figure 3, participant columns follow fixed identifier order without clustering; contrast heatmaps retain signed, cohort-specific COPE units. No new inference was introduced by these displays.

Figure 1 reuses schematic AI-generated hand illustrations. Cortical surfaces, atlas parcels and numerical plots use anatomical resources and saved analysis results. AI assistance is disclosed under “Use of artificial intelligence” in the main manuscript's Statements and Declarations; the hand-image tool/model and production record remain subject to author confirmation.

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