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SUPPLEMENTARY INFORMATION

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Generalizable representations of pain, cognitive control, and negative emotion in medial frontal cortex

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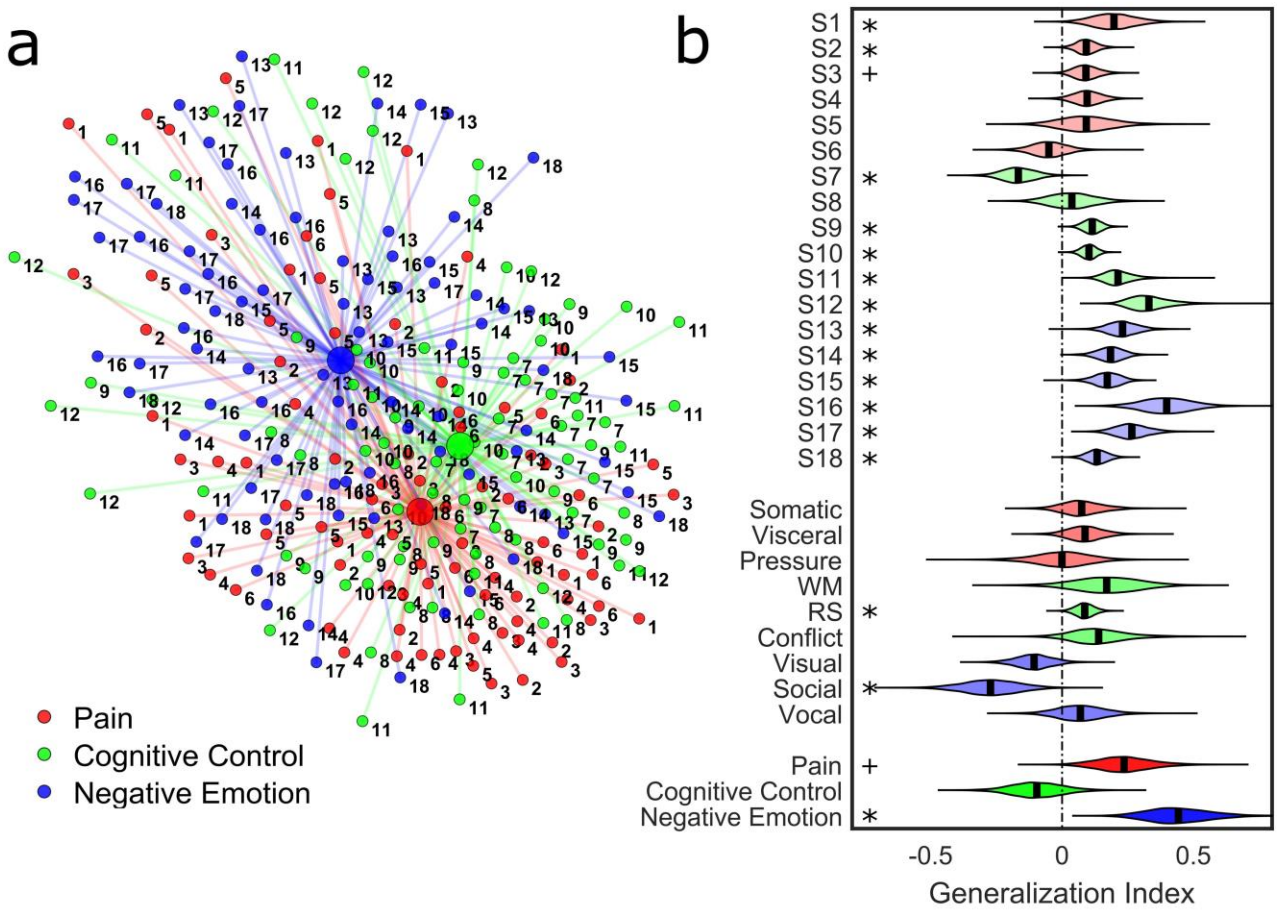
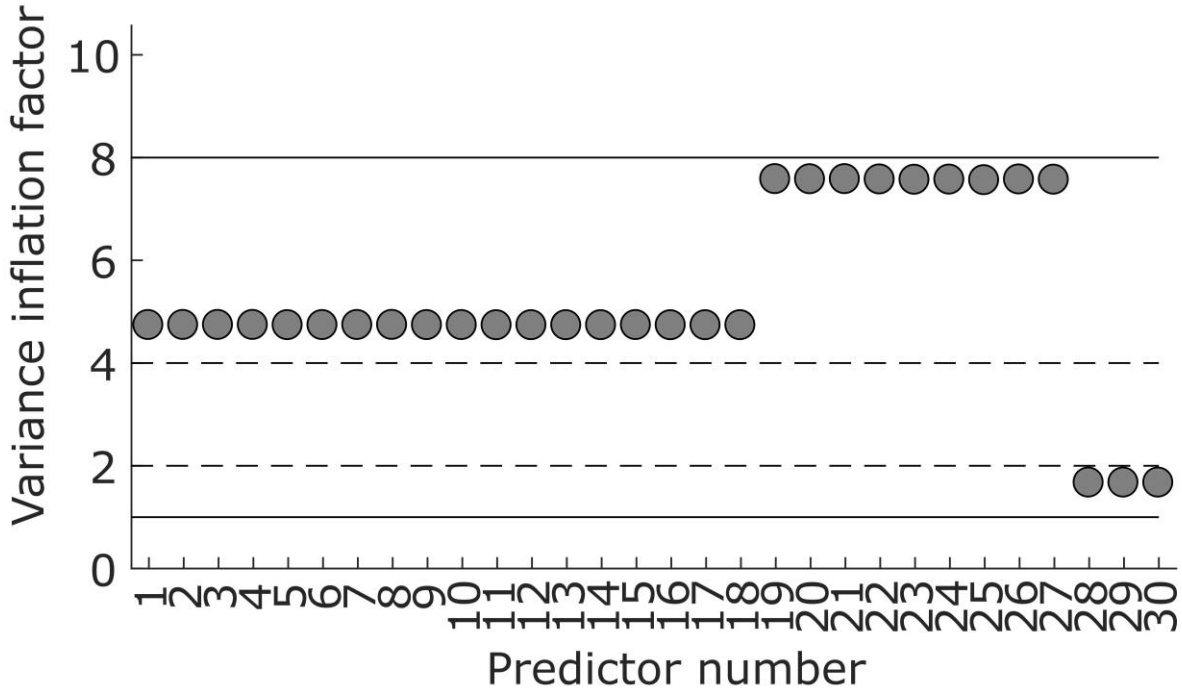


Supplementary Figure 1

Generalizability of MFC activation.

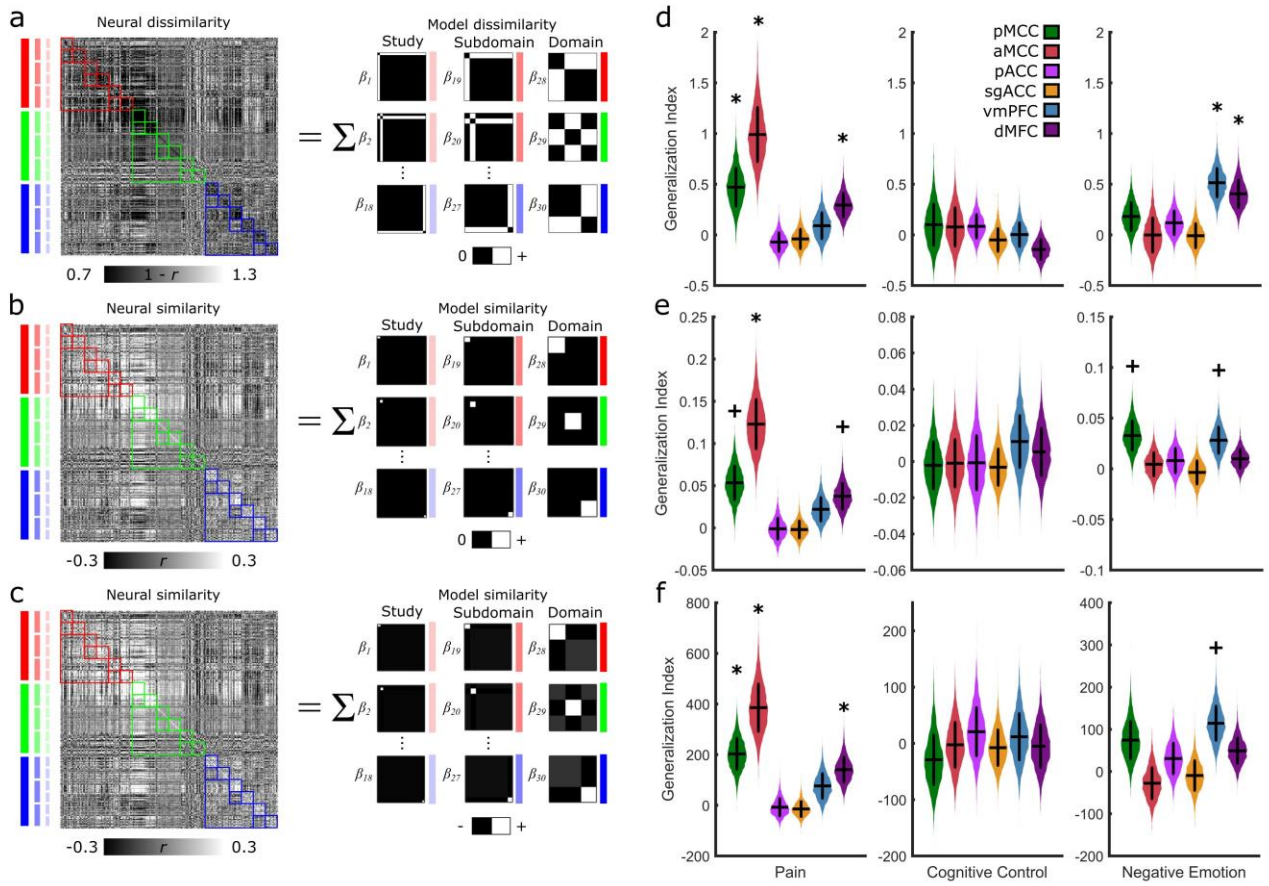
(**a**) Force-directed graph conveying the observed similarity of brain activation across MFC (see Figure 1b) using the Fruchterman-Reingold algorithm. Each small circle corresponds to a brain activation pattern from a single subject. The number next to each circle indicates the study it came from, and the color of each circle indicates domain membership of each study. Large circles depict the mean location of contrasts from each domain. (**b**) Results from modeling the similarity of activation patterns spanning the full MFC. The model explains clustering of brain activation patterns as a combination of study (top 18 rows), subdomain (middle nine rows), and domain-specific effects (bottom three rows). Smoothed bootstrap distributions of the generalization index (b = 5,000 bootstrap samples, drawn by random resampling of n = 270 participants) are plotted for each term and indicate the extent to which contrasts that share this feature are more (or less) similar. In general, there is greater clustering of domains and individual studies. For example, the domain of negative emotion is distinct from the domains of pain and cognitive control, yet the subdomain of social emotion does not form a clear cluster, because studies 15 and 16 are dissimilar from one another. *FDR q < .05; + P < .05 uncorrected.



Supplementary Figure 2

Variance Inflation Factors (VIFs) for representational similarity-based models.

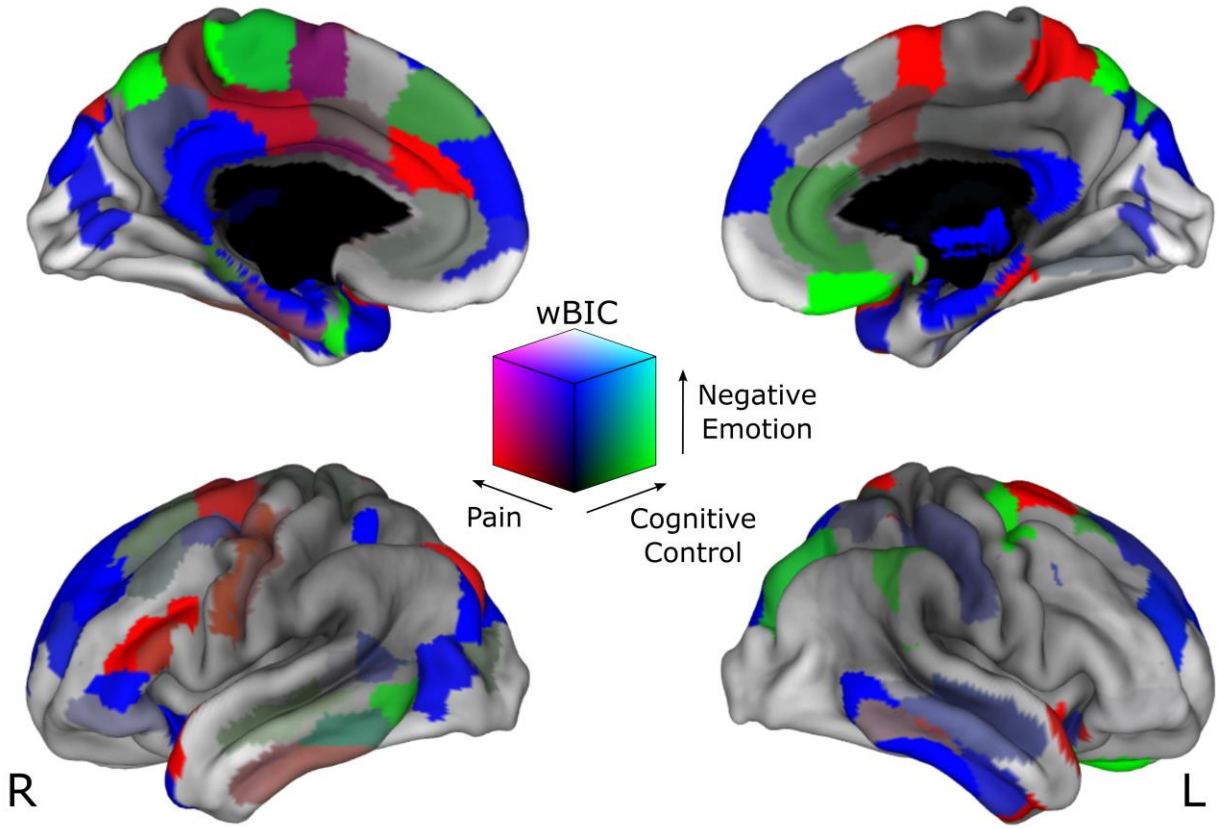
VIFs indicate how much multicollinearity in a design matrix has inflated the variance of parameter estimates. All values here are below the standard cutoff of 10 (see Ray, W.D. Applied Linear Statistical-Models, 3rd Edition - Neter,J, Wasserman,W, Kutner,Mh. *J Oper Res Soc* **42**, 815-815 (1991).).



Supplementary Figure 3

Regional analyses using different model parameterizations yield similar results.

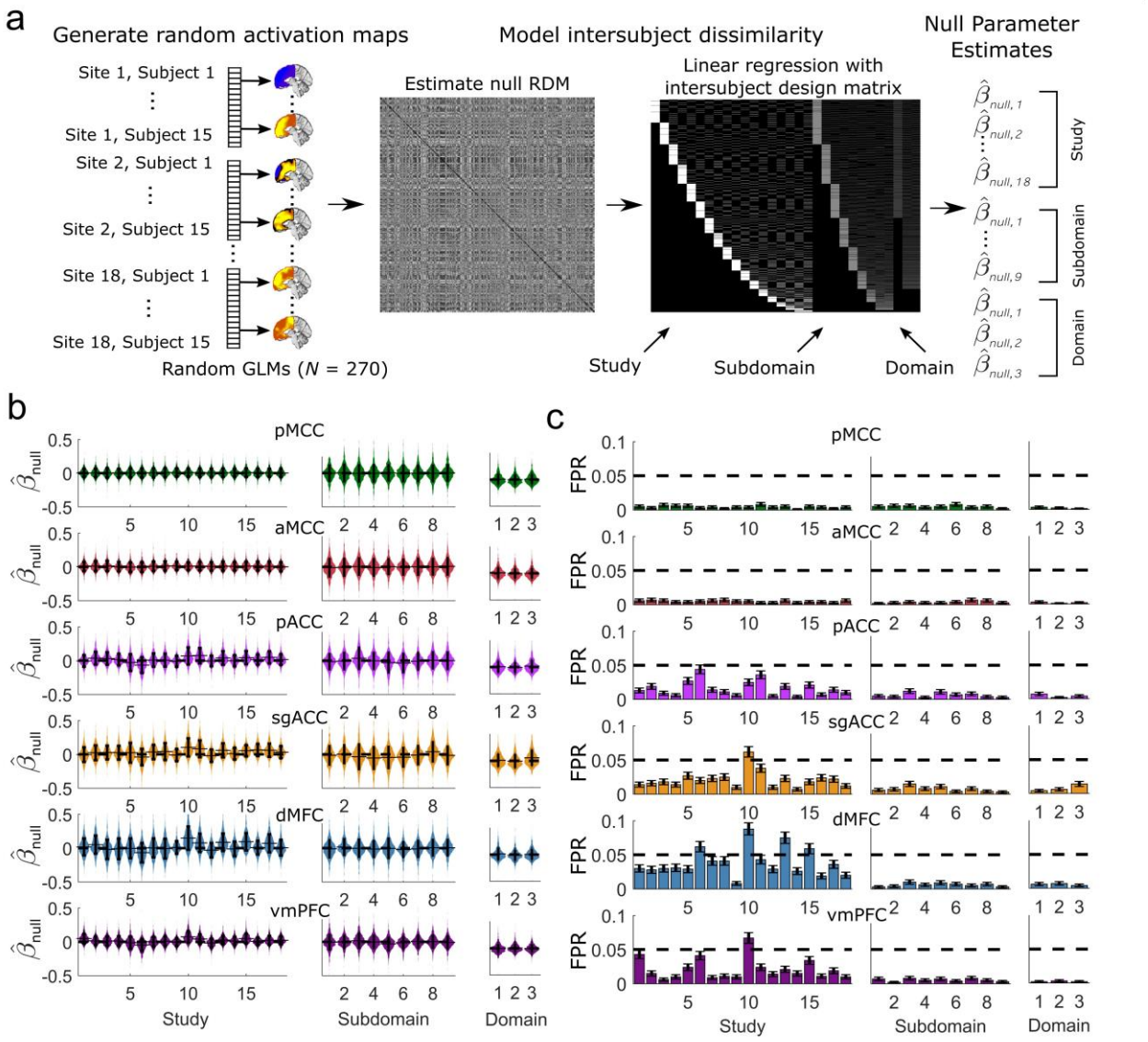
(**a**) Model parameterized to capture increases in dissimilarity (1 – Pearson's *r, n* = 270 participants) for patterns of brain activity observed in subjects engaged in different studies, subdomains, or domains. The average within study dissimilarity serves as a reference and is modeled with a constant term. (**b**) Model parameterized to capture increases in similarity (Pearson's *r, n* = 270 participants) for patterns of brain activity from the same study, subdomain, or domain. The average between domain similarity serves as a reference and is modeled with a constant term. (**c**) Model parameterized to capture differences in similarity (Pearson's *r, n* = 270 participants) for patterns of brain activity from the same study, subdomain, or domain versus those that come from different studies, subdomains, or domains. The average overall similarity serves as a reference and is modeled with a constant term. (**d-f**) Bootstrap distributions (b = 5,000 bootstrap samples, drawn by random resampling of *n* = 270 participants) of the generalization index for terms modeling 'pain', 'cognitive control', and 'negative emotion'. *FDR $q < .05$ corrected. + $P < .05$ uncorrected.



Supplementary Figure 4

Results of model comparisons conducted using the Brainnetome Atlas.

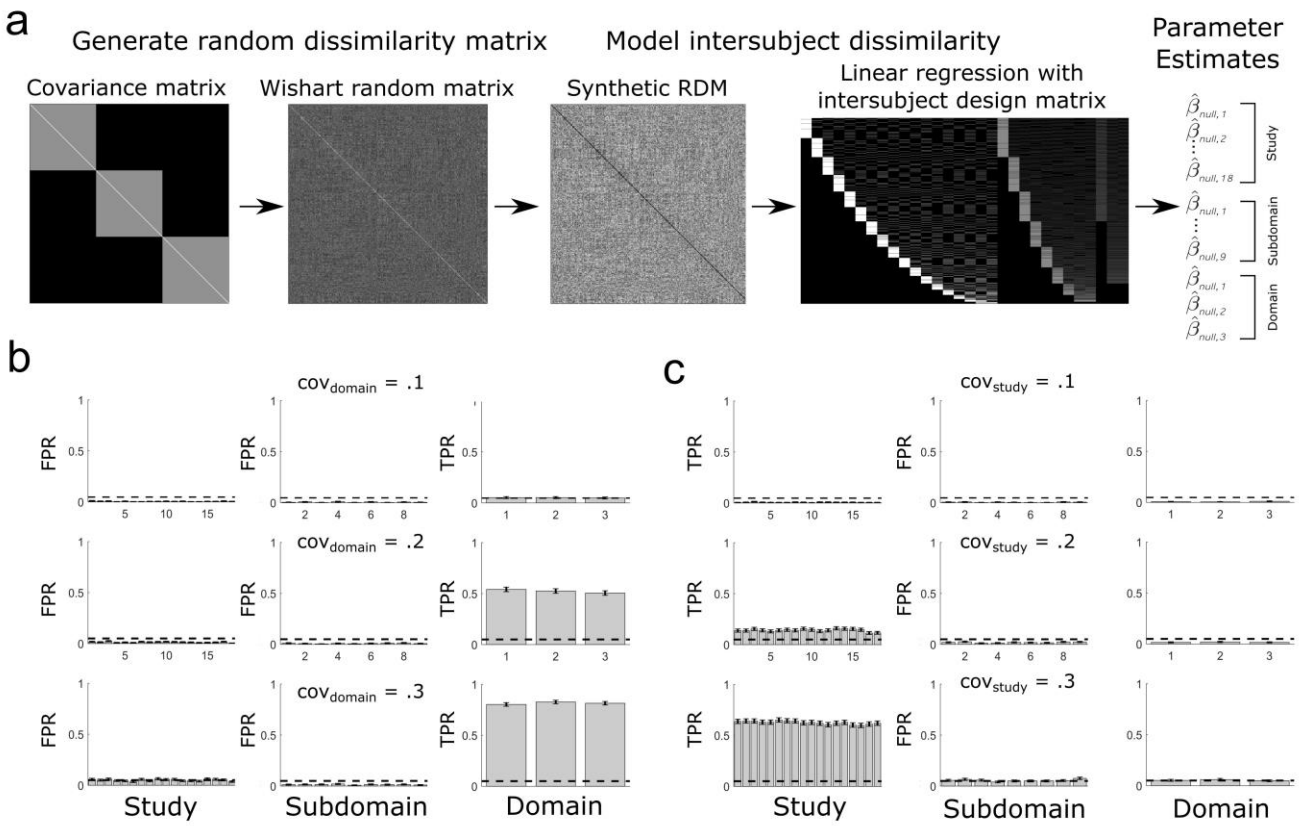
Colors indicate Bayesian information criterion weights, which reflect the relative evidence in favor of generalizable representation of pain (red), cognitive control (green), and negative emotion (blue). The colormap ranges from values of 0 to 1 for each model and the colors are additive. Purple regions indicate brain regions that exhibit equivocal evidence for representation of pain and negative emotion, and transparent (gray) regions do not exhibit evidence for the representation of a single domain. For full details see Table S6.



Supplementary Figure 5

Evaluation of model bias and variance, as well as false positive rates using resting-state fMRI (rsfMRI) data.

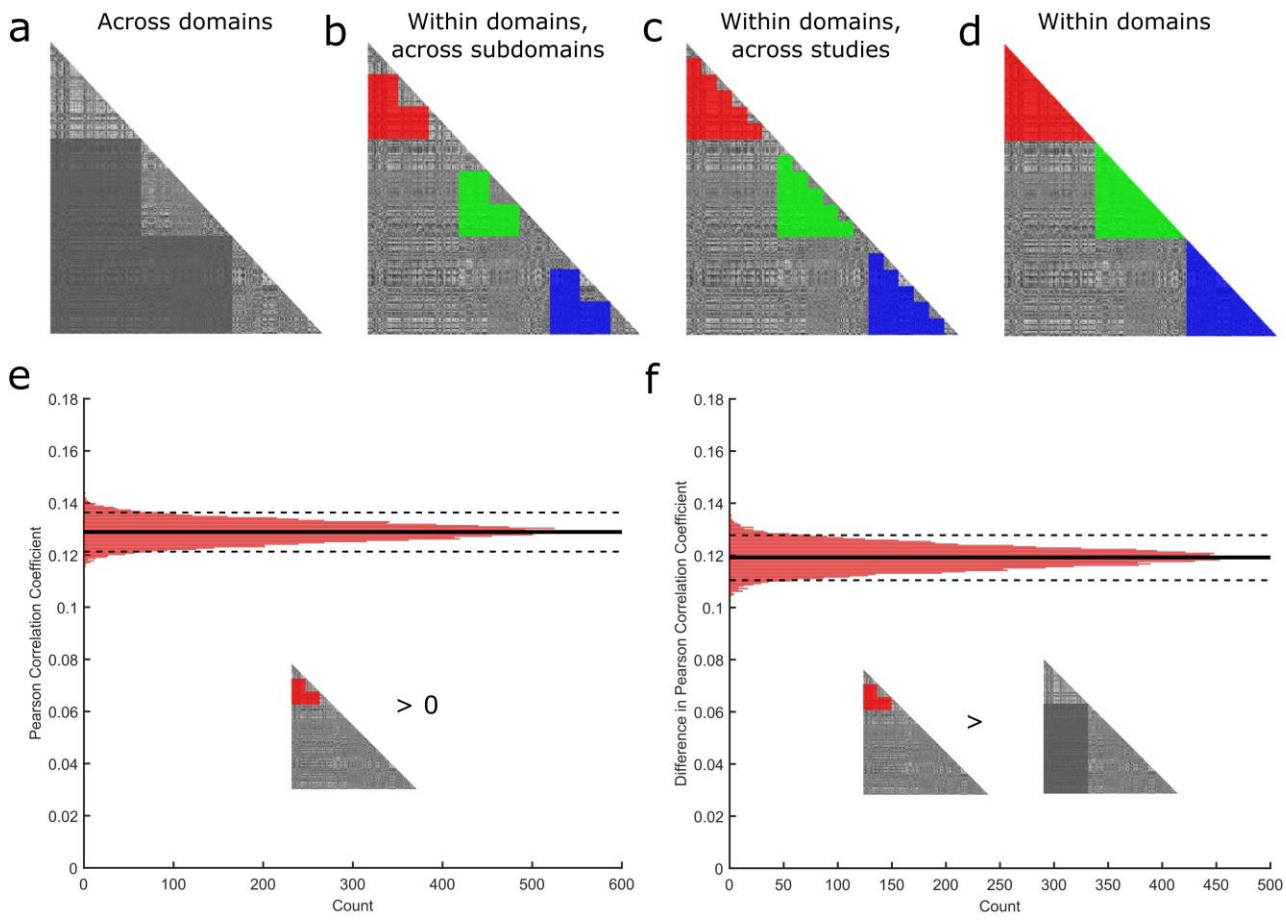
(**a**) Null-hypothesis representational similarity analysis (RSA) modeling procedure for a single Monte Carlo iteration (this procedure was repeated 1,000 times). Mirroring our experimental procedure, rsfMRI data was sampled from 18 sites from the 1,000 functional connectomes project[70] (15 subjects per site, total *n* = 270). In each iteration, a random GLM was fit for each subject, producing 270 independent activation maps. These maps were used to estimate a 'null' representational dissimilarity matrix that served as the outcome for RSA-based models. The mean and standard deviation of parameter estimates from these models (β_{null}) were computed to index the bias and variance of our modeling procedure. To provide an estimate of the false positive rate (FPR), *P*-values were calculated on each iteration using bootstrap resampling. The FPR was calculated as the proportion of significant effects across the 1,000 iterations. (**b**) Bias and variance of the modeling procedure. Violin plots indicate the distribution of parameter estimates from null models (across 1,000 MC iterations), error bars indicate the mean and bootstrap standard error. Results show little bias, with all bootstrap distributions centered near the expected value of zero. (**c**) Estimated FPR for each region of interest. Significant effects were identified using a threshold α = .05 on each MC iteration. Dashed lines indicate the nominal rate of 0.05, which is the expected frequency for a single test using a threshold of α = .05. Error bars reflect standard error of the mean based on a binomial distribution. The conservative false positive rates are likely due to the dependence structure in the dissimilarity measurements that we do not explicitly account for, but none the less is evidence of a valid statistical procedure.



Supplementary Figure 6

Evaluation of model sensitivity and false positive rates by generating synthetic data with Wishart noise.

(**a**) Mirroring our experimental procedure, synthetic data was generated with a covariance structure with unique effects for each of 270 "subjects" and either 3 domains or 18 studies (not shown). On each of 500 Monte Carlo (MC) iterations, a Wishart random matrix was generated from a pre-specified covariance structure and converted to a representational dissimilarity matrix that served as the outcome for representational similarity analysis-based models. *P*-values were calculated on each iteration using bootstrap resampling to provide estimates of the true and the false positive rates. This procedure was repeated three times with different levels of signal (the covariance across studies and domains was set to values of 0.1, 0.2, and 0.3). (**b**) Estimates of true and false positive rates for simulations where domain effects are present. Error bars reflect standard error of the mean based on a binomial distribution. (**c**) Estimates of true and false positive rates for simulations where study effects are present. Significant effects were identified using a threshold α = .05 on each MC iteration. Error bars reflect standard error of the mean based on a binomial distribution. Sensitivity increases monotonically with the true effect size, and false positives are at or below the nominal value.



Supplementary Figure 7

Methods for comparing the similarity of patterns of brain activity within and across studies, using bootstrap resampling to derive P-values and make inferences.

Unique pairwise correlations between patterns of brain activity from 270 subjects are displayed in each panel. This illustration shows actual data from the anterior midcingulate cortex. (**a**) Full inter-subject correlation matrix where the shaded dark region indicates across-domain correlations. The average similarity across domains is estimated as the average inter-subject correlation in this area. (**b**) Regions of the inter-subject correlation matrix averaged to compute domain-general effects of pain (red), cognitive control (green), negative emotion (blue). These effects are computed by averaging correlations within domains but across different subdomains. (**c**) Regions used to compute the average correlation within domains but across different studies. (**d**) Regions used to compute the average correlation within domains. (**e**) For bootstrap tests, we resampled individual correlation coefficients from all 10 regions of the correlation matrix (here shown for the region with pairs of contrasts that are within the pain domain, but from different subdomains). The solid line indicates the sample mean correlation coefficient; the dashed lines indicate 95% confidence intervals of the mean, computed by bootstrap resampling (full bootstrap distribution shown). (**f**) Comparisons of the means between different regions reveal generalizable domain effects (**b** > **a**), average effects of subdomain (**c** > **b**), and average effects of study (**d** > **c**). Differences in the means of two regions of the correlation matrix are compared against zero using the same bootstrap procedure (here showing a comparison of the average similarity within the pain domain and from different subdomains versus the similarity between pain and other domains).

Supplementary Table 1.
Bootstrap mean (standard error) of generalization indices for each region of interest.

	pMCC	aMCC	pACC	sgACC	vmPFC	dMFC
Constant	.891 (.012)*	.893 (.014)*	.938 (.013)*	.968 (.014)*	.892 (.010)*	.852 (.009)*
S1	.110 (.084)	.054 (.131)	.149 (.118)	.150 (.116)	.106 (.072)	.194 (.080)
S2	.085 (.072)	-.034 (.097)	.061 (.078)	.119 (.106)	.100 (.078)	.061 (.044)
S3	.004 (.090)	.029 (.110)	.056 (.063)	.074 (.058)	.160 (.049)*	.131 (.06)
S4	-.0005 (.088)	-.084 (.076)	.147 (.100)	.070 (.064)	.253 (.070)*	.105 (.060)
S5	.015 (.076)	-.108 (.134)	.089 (.098)	-.006 (.070)	.003 (.134)	.150 (.120)
S6	.0005 (.066)	-.204 (.100)	.039 (.101)	.012 (.066)	-.148 (.089)	.013 (.076)
S7	.185 (.137)	.070 (.095)	-.062 (.065)	.041 (.102)	.157 (.070)	-.196 (.070)*
S8	-.003 (.089)	.028 (.093)	.216 (.097)	.031 (.102)	.585 (.104)*	-.080 (.088)
S9	.153 (.045)*	.116 (.040)*	-.017 (.044)	.020 (.043)	.077 (.037)	.135 (.031)*
S10	.181 (.050)*	.163 (.045)*	-.014 (.045)	.026 (.039)	.021 (.033)	.138 (.032)*
S11	.262 (.076)*	.139 (.058)	.195 (.109)	.090 (.074)	.178 (.056)*	.218 (.045)*
S12	.283 (.113)	.275 (.084)*	.121 (.062)	.077 (.069)	.242 (.082)*	.366 (.070)*
S13	.250 (.074)*	.242 (.086)*	-.017 (.073)	.137 (.105)	.091 (.060)	.248 (.077)*
S14	.229 (.081)*	.249 (.092)*	.079 (.098)	.132 (.101)	.180 (.061)*	.175 (.052)*
S15	.181 (.093)	.319 (.101)*	-.053 (.061)	-.011 (.094)	-.027 (.069)	.253 (.050)*
S16	.360 (.128)*	.433 (.130)*	.099 (.091)	.012 (.106)	.251 (.114)	.392 (.092)*
S17	.108 (.066)	.302 (.098)*	.112 (.069)	.095 (.066)	-.002 (.052)	.317 (.071)*
S18	.132 (.077)	.096 (.063)	.078 (.050)	.061 (.063)	.086 (.085)	.146 (.045)*
Thermal	-.013 (.119)	-.0127 (.155)	.013 (.160)	-.097 (.200)	.071 (.098)	.032 (.067)
Visceral	.093 (.146)	-.009 (.142)	-.013 (.107)	-.002 (.107)	-.042 (.080)	.075 (.083)
Mechanical	.121 (.104)	.107 (.163)	-.066 (.131)	.084 (.123)	.140 (.172)	-.057 (.123)
Working Memory	.067 (.192)	.055 (.134)	-.163 (.123)	.078 (.195)	-.544 (.127)*	.332 (.135)
Response Selection	.237 (.112)	.112 (.084)	.117 (.072)	.069 (.070)	.197 (.053)*	.052 (.035)
Conflict	-.097 (.166)	.033 (.128)	.053 (.175)	-.037 (.122)	-.004 (.112)	.189 (.115)
Visual Negative	-.164 (.115)	-.103 (.136)	-.019 (.142)	-.153 (.189)	-.047 (.092)	-.093 (.090)
Social Negative	-.339 (.164)	-.330 (.183)	.067 (.136)	.119 (.209)	-.154 (.133)	-.286 (.095)*
Auditory Negative	.085 (.117)	-.129 (.111)	.043 (.114)	.010 (.108)	.315 (.127)	.022 (.104)
Pain	.470 (.186)*	.990 (.266)*	-.072 (.091)	-.041 (.095)	.090 (.127)	.294 (.116)*
Cognitive Control	.100 (.202)	.078 (.188)	.084 (.115)	-.051 (.111)	.002 (.116)	-.145 (.096)
Negative Emotion	.181 (.138)	-.002 (.167)	.118 (.115)	-.009 (.118)	.514 (.140)*	.404 (.133)*

* FDR $q < .05$ corrected. Mean and standard error based on 5,000 bootstrap iterations.

Supplementary Table 2.
Mean (standard error) of pattern similarity in each region of interest.

Brain Region	Domain	Pain	Cognitive Control	Negative Emotion
pMCC	Pain	.0838 (.0029)	-.0005 (.0019)	.0144 (.0021)
	Cognitive Control	-.0005 (.0019)	.0171 (.0026)	.0002 (.0019)
	Negative Emotion	.0144 (.0021)	.0002 (.0019)	.0400 (.0031)
	Within domain and across subdomains	.0713 (.0035)	-.0029 (.0030)	.0379 (.0036)
aMCC	Pain	.1342 (.0031)	.0083 (.0018)	.0111 (.0023)
	Cognitive Control	.0083 (.0018)	.0300 (.0023)	.0128 (.0025)
	Negative Emotion	.0111 (.0023)	.0128 (.0018)	.0200 (.0031)
	Within domain and across subdomains	.1289 (.0038)	.0195 (.0025)	.0157 (.0037)
pACC	Pain	.0256 (.0030)	.0208 (.0020)	.0208 (.0021)
	Cognitive Control	.0208 (.0020)	.0314 (.0026)	.0124 (.0019)
	Negative Emotion	.0208 (.0021)	.0124 (.0019)	.0316 (.0029)
	Within domain and across subdomains	.0202 (.0036)	.0233 (.0030)	.0268 (.0035)
sgACC	Pain	.0001 (.0034)	.0029 (.0021)	.0005 (.0024)
	Cognitive Control	.0029 (.0021)	.0083 (.0028)	.0012 (.0023)
	Negative Emotion	.0005 (.0024)	.0012 (.0023)	.0017 (.0037)
	Within domain and across subdomains	-.0003 (.0041)	-.0024 (.0031)	-.0024 (.0045)
vmPFC	Pain	.0605 (.0025)	.0351 (.0016)	.0117 (.0016)
	Cognitive Control	.0351 (.0016)	.0397 (.0022)	.0072 (.0014)
	Negative Emotion	.0117 (.0016)	.0072 (.0014)	.0584 (.0022)
	Within domain and across subdomains	.0511 (.0029)	.0308 (.0025)	.0474 (.0026)
dMFC	Pain	.0958 (.0021)	.0565 (.0013)	.0243 (.0013)
	Cognitive Control	.0565 (.0013)	.0726 (.0020)	.0302 (.0013)
	Negative Emotion	.0243 (.0013)	.0302 (.0013)	.0570 (.0018)
	Within domain and across subdomains	.0871 (.0026)	.0443 (.0021)	.0481 (.0021)
MFC	Pain	.0918 (.0019)	.0566 (.0012)	.0231 (.0012)
	Cognitive Control	.0566 (.0012)	.0735 (.0020)	.0278 (.0012)
	Negative Emotion	.0231 (.0012)	.0278 (.0012)	.0563 (.0016)
	Within domain and across subdomains	.0811 (.0023)	.0500 (.0021)	.0489 (.0018)

Mean and standard error based on 10,000 bootstrap iterations. pMCC = posterior midcingulate cortex, aMCC = anterior midcingulate cortex, pACC = perigenual anterior cingulate cortex, sgACC = subgenual anterior cingulate cortex, vmPFC = ventromedial prefrontal cortex, dMFC = dorsal medial frontal cortex, MFC = medial frontal cortex.

Supplementary Table 3.

Mean Pearson correlation [95% CI] within each region of interest and the full MFC, for contrasts involving pain.

Region	Between domains (Background noise, *n = 32,400 pairwise correlations*)	Within domain, across subdomains (Generalizable domain effect, *n = 2,700 pairwise correlations*)	Within domain, between studies (Effect of subdomain, *n = 3,375 pairwise correlations*)	Within domain (Effect of study, *n = 4,005 pairwise correlations*)
pMCC	.0069 [.0003 .0109]	.0713 [.0644 .0781]*	.0751 [.0691 .0810]*	.0838 [.0781 .0893]*
aMCC	.0097 [.0056 .0136]	.1289 [.1214 .1364]*	.1304 [.1235 .1370]	.1342 [.1278 .1403]*
pACC	.0208 [.0168 .0248]	.0202 [.0133 .0271]	.0191 [.0130 .0254]	.0257 [.0197 .0314]*
sgACC	.0017 [-.0027 .0062]	-.0029 [-.0111 .0050]	-.0033 [-.0103 .0038]	.0001 [-.0066 .0068]*
vmPFC	.0234 [.0202 .0267]	.0511 [.0456 .0569]*	.0539 [.0486 .0590]	.0605 [.0557 .0653]*
dMFC	.0404 [.0379 .0431]	.0871 [.0816 .0920]*	.0879 [.0834 .0925]	.0958 [.0917 .1000]*
MFC	.0399 [.0375 .0422]	.0811 [.0765 .0855]*	.0841 [.0800 .0881]*	.0918 [.0880 .0956]*

* Correlation coefficient is significantly greater than the preceding column at $P < .05$, based on bias-corrected and accelerated bootstrap confidence intervals. Descriptors in parenthesis explain the effect being tested.

Supplementary Table 4.

Mean Pearson correlation [95% CI] within each region of interest and the full MFC, for contrasts involving negative emotion.

Region	Between domains (Background noise, *n = 32,400 pairwise correlations*)	Within domain, across subdomains (Generalizable domain effect, *n = 2,700 pairwise correlations*)	Within domain, between studies (Effect of subdomain, *n = 3,375 pairwise correlations*)	Within domain (Effect of study, *n = 4,005 pairwise correlations*)
pMCC	.0073 [.0034 .0112]	.0379 [.0307 .0450]*	.0302 [.0237 .0366]	.0400 [.0339 .0459]
aMCC	.0119 [.0080 .0160]	.0157 [.0085 .0229]	.0053 [-.0012 .0119]	.0200 [.0138 .0260]
pACC	.0166 [.0127 .0206]	.0268 [.0202 .0339]*	.0286 [.0225 .0350]	.0316 [.0258 .0372]
sgACC	.0008 [-.0036 .0055]	-.0024 [-.0113 .0061]	-.0027 [-.0105 .0051]	.0017 [-.0054 .0089]
vmPFC	.0095 [.0064 .0125]	.0474 [.0424 .0526]*	.0495 [.0449 .0542]	.0584 [.0541 .0628]
dMFC	.0273 [.0247 .0298]	.0481 [.0439 .0521]*	.0415 [.0379 .0451]	.0570 [.0536 .0604]
MFC	.0255 [.0232 .0278]	.0489 [.0455 .0524]*	.0432 [.0401 .0463]	.0563 [.0534 .0595]

* Correlation coefficient is significantly greater than the preceding column at $P < .05$, based on the bias corrected and accelerated percentile method

Supplementary Table 5.

Mean Pearson correlation [95% CI] within each region of interest and the full MFC, for contrasts involving cognitive control.

Region	Between domains (Background noise, *n = 32,400 pairwise correlations*)	Within domain, across subdomains (Generalizable domain effect, *n = 2,700 pairwise correlations*)	Within domain, between studies (Effect of subdomain, *n = 3,375 pairwise correlations*)	Within domain (Effect of study, *n = 4,005 pairwise correlations*)
pMCC	-.0002 [-.0040 .0035]	-.0029 [-.0089 .0025]	.0010 [-.0044 .0060]*	.0171 [.0119 .0220]*
aMCC	.0105 [.0071 .0142]	.0195 [.0145 .0245]*	.0232 [.0186 .0278]*	.0300 [.0256 .0344]*
pACC	.0166 [.0127 .0203]	.0233 [.0175 .0291]	.0232 [.0179 .0287]	.0314 [.0263 .0365]*
sgACC	.0020 [-.0022 .0063]	-.0024 [-.0084 .0036]	-.0003 [-.0060 .0052]	.0083 [.0028 .0136]*
vmPFC	.0211 [.0181 .0241]	.0308 [.0260 .0357]*	.0242 [.0199 .0286]	.0397 [.0352 .0439]*
dMFC	.0433 [.0409 .0459]	.0443 [.0402 .0482]	.0549 [.0511 .0585]*	.0726 [.0687 .0763]*
MFC	.0422 [.0399 .0446]	.0496 [.0453 .0537]*	.0568 [.0531 .0605]*	.0735 [.0695 .0774]*

* Correlation coefficient is significantly greater than the preceding column at $P < .05$, based on the bias corrected and accelerated percentile method

Supplementary Table 6.
Bayesian Information Criterion (BIC) weights for the full Brainnetome Atlas.

Hemisphere	Region	Study and Subdomain (28)	Pain (29)	Cognitive Control (29)	Negative Emotion (29)	Full Model (31)
R	vmPu, ventromedial putamen	0.824	0.067	0.054	0.054	0.000
R	Otha, occipital thalamus	0.806	0.055	0.085	0.053	0.000
L	A37dl, dorsolateral area37	0.785	0.057	0.050	0.107	0.001
R	A24rv, rostroventral area 24	0.779	0.055	0.050	0.116	0.001
L	A4t, area 4(trunk region)	0.776	0.048	0.122	0.053	0.001
L	A32sg, subgenual area 32	0.755	0.052	0.134	0.058	0.001
L	A1/2/3tru, area1/2/3(trunk region)	0.753	0.050	0.150	0.046	0.001
R	A28/34, area 28/34 (EC, entorhinal cortex)	0.752	0.050	0.106	0.091	0.001
L	A21c, caudal area 21	0.750	0.082	0.115	0.051	0.001
R	cTtha, caudal temporal thalamus	0.712	0.059	0.104	0.122	0.002
R	GP, globus pallidus	0.701	0.050	0.047	0.200	0.001
R	A7pc, postcentral area 7	0.677	0.046	0.207	0.069	0.002
L	A8vl, ventrolateral area 8	0.659	0.039	0.151	0.147	0.004
L	mOccG, middle occipital gyrus	0.643	0.071	0.225	0.057	0.003
L	A8dl, dorsolateral area 8	0.612	0.079	0.268	0.038	0.004
R	A20cl, caudolateral of area 20	0.575	0.245	0.048	0.129	0.002
L	A20il, intermediate lateral area 20	0.513	0.402	0.032	0.051	0.002
L	A20cv, caudoventral of area 20	0.454	0.437	0.078	0.027	0.003
L	A5m, medial area 5(PEm)	0.448	0.477	0.033	0.037	0.004
L	GP, globus pallidus	0.312	0.250	0.258	0.051	0.128
R	A6dl, dorsolateral area 6	0.000	0.995	0.000	0.000	0.005
R	TH, area TH (medial PPHC)	0.001	0.993	0.000	0.000	0.006
R	A20r, rostral area 20	0.000	0.990	0.000	0.000	0.010
L	IFS, inferior frontal sulcus	0.000	0.989	0.000	0.000	0.011
L	A38l, lateral area 38	0.000	0.982	0.000	0.000	0.018
R	A6m, medial area 6	0.011	0.981	0.001	0.001	0.006
R	vId/vIg, ventral dysgranular and granular insula	0.000	0.972	0.000	0.000	0.028
L	A32p, pregenual area 32	0.000	0.969	0.000	0.000	0.031
L	A44d, dorsal area 44	0.000	0.953	0.000	0.000	0.047
R	A5m, medial area 5(PEm)	0.061	0.920	0.005	0.005	0.009
L	lsOccG, lateral superior occipital gyrus	0.117	0.861	0.011	0.007	0.004
R	A38l, lateral area 38	0.000	0.832	0.000	0.000	0.168
L	A20iv, intermediate ventral area 20	0.114	0.820	0.007	0.049	0.009
R	A1/2/3ll, area1/2/3 (lower limb region)	0.000	0.805	0.000	0.000	0.195
L	A23c, caudal area 23	0.126	0.723	0.008	0.120	0.023
L	A6dl, dorsolateral area 6	0.000	0.717	0.000	0.000	0.283
L	A45c, caudal area 45	0.108	0.662	0.063	0.010	0.157
R	A5l, lateral area 5	0.211	0.578	0.022	0.179	0.010
R	A21c, caudal area 21	0.373	0.562	0.031	0.026	0.007

L	A4hf, area 4(head and face region)	0.006	0.545	0.118	0.000	0.332
L	A6m, medial area 6	0.009	0.456	0.001	0.364	0.171
L	A24rv, rostroventral area 24	0.239	0.440	0.017	0.292	0.012
R	A35/36c, caudal area 35/36	0.388	0.414	0.142	0.026	0.030
L	A28/34, area 28/34 (EC, entorhinal cortex)	0.308	0.374	0.029	0.253	0.036
L	A1/2/3ll, area1/2/3 (lower limb region)	0.000	0.000	0.996	0.000	0.004
R	A7m, medial area 7(PEp)	0.003	0.000	0.992	0.000	0.004
R	A13, area 13	0.000	0.000	0.989	0.000	0.011
R	mPFtha, medial pre-frontal thalamus	0.005	0.000	0.976	0.002	0.018
L	A7m, medial area 7(PEp)	0.016	0.001	0.941	0.023	0.018
R	dlPu, dorsolateral putamen	0.035	0.013	0.941	0.004	0.008
R	A6cdl, caudal dorsolateral area 6	0.015	0.003	0.844	0.004	0.133
L	TI, area TI (temporal agranular insular cortex)	0.000	0.000	0.837	0.000	0.163
L	A4ll, area 4, (lower limb region)	0.005	0.000	0.725	0.134	0.136
L	A37vl, ventrolateral area 37	0.172	0.012	0.709	0.047	0.061
R	lsOccG, lateral superior occipital gyrus	0.002	0.000	0.694	0.113	0.191
R	A40c, caudal area 40(PFm)	0.000	0.000	0.545	0.000	0.455
R	A8dl, dorsolateral area 8	0.389	0.034	0.523	0.041	0.013
L	A9m, medial area 9	0.319	0.043	0.518	0.065	0.055
R	A32sg, subgenual area 32	0.437	0.028	0.499	0.034	0.002
L	TH, area TH (medial PPHC)	0.382	0.124	0.434	0.031	0.030
L	A20cl, caudolateral of area 20	0.349	0.031	0.365	0.249	0.007
L	A23v, ventral area 23	0.000	0.000	0.000	0.996	0.004
L	A23d, dorsal area 23	0.000	0.000	0.000	0.996	0.004
L	A5l, lateral area 5	0.000	0.000	0.000	0.996	0.004
L	A9/46d, dorsal area 9/46	0.000	0.000	0.000	0.995	0.005
R	A10m, medial area 10	0.000	0.000	0.000	0.995	0.005
R	A23v, ventral area 23	0.000	0.000	0.000	0.993	0.007
L	A38m, medial area 38	0.000	0.000	0.000	0.992	0.008
R	msOccG, medial superior occipital gyrus	0.000	0.000	0.000	0.992	0.008
L	A9l, lateral area 9	0.000	0.000	0.000	0.992	0.008
L	A39c, caudal area 39(PGp)	0.000	0.000	0.000	0.991	0.009
R	A20cv, caudoventral of area 20	0.000	0.000	0.000	0.990	0.010
R	lPFtha, lateral pre-frontal thalamus	0.000	0.000	0.000	0.989	0.011
R	A37dl, dorsolateral area37	0.000	0.000	0.000	0.988	0.012
R	mPMtha, pre-motor thalamus	0.000	0.000	0.000	0.987	0.013
L	rHipp, rostral hippocampus	0.000	0.000	0.000	0.982	0.018
R	A37vl, ventrolateral area 37	0.000	0.000	0.000	0.981	0.019
R	A7c, caudal area 7	0.000	0.000	0.000	0.978	0.022
L	msOccG, medial superior occipital gyrus	0.000	0.000	0.000	0.978	0.022
R	rHipp, rostral hippocampus	0.013	0.001	0.001	0.974	0.011
R	dmPOS, dorsomedial parietooccipital sulcus (PEr)	0.000	0.000	0.000	0.968	0.032

L	vmPu, ventromedial putamen	0.000	0.000	0.000	0.960	0.040
L	vIa, ventral agranular insula	0.000	0.000	0.000	0.957	0.043
L	A45r, rostral area 45	0.000	0.000	0.000	0.945	0.055
L	dCa, dorsal caudate	0.000	0.000	0.000	0.943	0.057
L	A10m, medial area 10	0.000	0.000	0.000	0.937	0.063
R	PPtha, posterior parietal thalamus	0.000	0.000	0.000	0.906	0.094
L	A35/36c, caudal area 35/36	0.001	0.000	0.000	0.890	0.110
L	A35/36r, rostral area 35/36	0.064	0.030	0.004	0.888	0.014
R	A38m, medial area 38	0.000	0.000	0.000	0.877	0.123
L	V5/MT+, area V5/MT+	0.089	0.011	0.009	0.866	0.024
L	rCunG, rostral cuneus gyrus	0.023	0.006	0.002	0.858	0.111
R	A46, area 46	0.020	0.002	0.091	0.844	0.043
L	A14m, medial area 14	0.000	0.000	0.000	0.813	0.187
L	A46, area 46	0.029	0.003	0.036	0.790	0.142
R	A20il, intermediate lateral area 20	0.011	0.002	0.004	0.773	0.210
R	A9l, lateral area 9	0.000	0.000	0.006	0.732	0.262
R	rCunG, rostral cuneus gyrus	0.001	0.000	0.000	0.727	0.271
L	TL, area TL (lateral PPHC, posterior parahippocampal gyrus)	0.000	0.000	0.000	0.717	0.283
R	vIa, ventral agranular insula	0.000	0.000	0.000	0.594	0.406
R	IFJ, inferior frontal junction	0.000	0.000	0.000	0.559	0.441
R	A9m,medial area 9	0.009	0.001	0.006	0.554	0.430
R	A20iv, intermediate ventral area 20	0.000	0.000	0.000	0.536	0.464
R	aSTS, anterior superior temporal sulcus	0.419	0.044	0.084	0.431	0.021
L	cHipp, caudal hippocampus	0.000	0.000	0.000	0.000	1.000
L	rLinG, rostral lingual gyrus	0.000	0.000	0.000	0.000	1.000
L	mPMtha, pre-motor thalamus	0.000	0.000	0.000	0.000	1.000
L	PPtha, posterior parietal thalamus	0.000	0.000	0.000	0.000	1.000
R	cHipp, caudal hippocampus	0.000	0.000	0.000	0.000	1.000
R	A11l, lateral area 11	0.000	0.000	0.000	0.000	1.000
L	vmPOS,ventromedial parietooccipital sulcus	0.000	0.000	0.000	0.000	1.000
R	A7r, rostral area 7	0.000	0.000	0.000	0.000	1.000
L	A7c, caudal area 7	0.000	0.000	0.000	0.000	1.000
L	A12/47o, orbital area 12/47	0.000	0.000	0.000	0.000	1.000
R	A37elv, extreme lateroventral area37	0.000	0.000	0.000	0.000	1.000
R	cLinG, caudal lingual gyrus	0.000	0.000	0.000	0.000	1.000
L	iOccG, inferior occipital gyrus	0.000	0.000	0.000	0.000	1.000
R	dIa, dorsal agranular insula	0.000	0.000	0.000	0.000	1.000
R	A39rd, rostrodorsal area 39(Hip3)	0.000	0.000	0.000	0.000	1.000
L	A22r, rostral area 22	0.000	0.000	0.000	0.000	1.000
R	A8m, medial area 8	0.000	0.000	0.000	0.000	1.000
L	A37mv, medioventral area37	0.000	0.000	0.000	0.000	1.000
L	A22c, caudal area 22	0.000	0.000	0.000	0.000	1.000
L	vId/vIg, ventral dysgranular and granular insula	0.000	0.000	0.000	0.000	1.000

L	A4tl, area 4(tongue and larynx region)	0.000	0.000	0.000	0.000	1.000
R	A37mv, medioventral area37	0.000	0.000	0.000	0.000	1.000
L	A40c, caudal area 40(PFm)	0.000	0.000	0.000	0.000	1.000
R	A45c, caudal area 45	0.000	0.000	0.000	0.000	1.000
L	A1/2/3tonIa, area 1/2/3(tongue and larynx region)	0.000	0.000	0.000	0.000	1.000
R	A1/2/3ulhf, area 1/2/3(upper limb, head and face region)	0.000	0.000	0.000	0.000	1.000
R	A22r, rostral area 22	0.000	0.000	0.000	0.000	1.000
L	A41/42, area 41/42	0.000	0.000	0.000	0.000	1.000
L	cLinG, caudal lingual gyrus	0.000	0.000	0.000	0.000	1.000
R	A37lv, lateroventral area37	0.000	0.000	0.000	0.000	1.000
L	A37lv, lateroventral area37	0.000	0.000	0.000	0.000	1.000
R	A40rd, rostrodorsal area 40(PFt)	0.000	0.000	0.000	0.000	1.000
L	A6cvl, caudal ventrolateral area 6	0.000	0.000	0.000	0.000	1.000
R	A41/42, area 41/42	0.000	0.000	0.000	0.000	1.000
R	dId, dorsal dysgranular insula	0.000	0.000	0.000	0.000	1.000
R	dIg, dorsal granular insula	0.000	0.000	0.000	0.000	1.000
L	TE1.0 and TE1.2	0.000	0.000	0.000	0.000	1.000
R	TE1.0 and TE1.2	0.000	0.000	0.000	0.000	1.000
R	A4tl, area 4(tongue and larynx region)	0.000	0.000	0.000	0.000	1.000
R	A6cvl, caudal ventrolateral area 6	0.000	0.000	0.000	0.000	1.000
L	A40rd, rostrodorsal area 40(PFt)	0.000	0.000	0.000	0.000	1.000
R	G, hypergranular insula	0.000	0.000	0.000	0.000	1.000
L	G, hypergranular insula	0.000	0.000	0.000	0.000	1.000
L	dIg, dorsal granular insula	0.000	0.000	0.000	0.000	1.000
L	A40rv, rostroventral area 40(PFop)	0.000	0.000	0.000	0.000	1.000
R	IFS, inferior frontal sulcus	0.000	0.000	0.000	0.000	1.000
R	A45r, rostral area 45	0.000	0.000	0.000	0.000	1.000
L	A44op, opercular area 44	0.000	0.000	0.000	0.000	1.000
R	A44op, opercular area 44	0.000	0.000	0.000	0.000	1.000
R	A44v, ventral area 44	0.000	0.000	0.000	0.000	1.000
R	A12/47o, orbital area 12/47	0.000	0.000	0.000	0.000	1.000
R	A40rv, rostroventral area 40(PFop)	0.000	0.000	0.000	0.000	1.000
R	A1/2/3tonIa, area 1/2/3(tongue and larynx region)	0.000	0.000	0.000	0.000	1.000
R	mAmyg, medial amygdala	0.000	0.000	0.000	0.000	1.000
L	A44v, ventral area 44	0.000	0.000	0.000	0.000	1.000
L	A7pc, postcentral area 7	0.000	0.000	0.000	0.000	1.000
L	dIa, dorsal agranular insula	0.000	0.000	0.000	0.000	1.000
R	A9/46v, ventral area 9/46	0.000	0.000	0.000	0.000	1.000
L	A9/46v, ventral area 9/46	0.000	0.000	0.000	0.000	1.000
R	A23d, dorsal area 23	0.000	0.000	0.000	0.000	1.000
R	cpSTS, caudoposterior superior temporal sulcus	0.000	0.000	0.000	0.000	1.000
R	A21r, rostral area 21	0.000	0.000	0.000	0.000	1.000

L	A20rv, rostroventral area 20	0.000	0.000	0.000	0.000	1.000
L	Otha, occipital thalamus	0.000	0.000	0.000	0.000	1.000
R	A4ll, area 4, (lower limb region)	0.000	0.000	0.000	0.000	1.000
R	iOccG, inferior occipital gyrus	0.000	0.000	0.000	0.000	1.000
R	A1/2/3tru, area1/2/3(trunk region)	0.000	0.000	0.000	0.000	1.000
L	rTtha, rostral temporal thalamus	0.000	0.000	0.000	0.000	1.000
L	A37elv, extreme lateroventral area37	0.000	0.000	0.000	0.000	1.000
L	A21r, rostral area 21	0.000	0.000	0.000	0.000	1.000
L	A10l, lateral area10	0.000	0.000	0.000	0.000	1.000
L	lPFtha, lateral pre-frontal thalamus	0.000	0.000	0.000	0.000	1.000
R	lAmyg, lateral amygdala	0.000	0.000	0.000	0.000	1.000
R	TL, area TL (lateral PPHC, posterior parahippocampal gyrus)	0.000	0.000	0.000	0.000	1.000
R	V5/MT+, area V5/MT+	0.000	0.000	0.000	0.000	1.000
L	A7ip, intraparietal area 7(hIP3)	0.000	0.000	0.000	0.000	1.000
L	A8m, medial area 8	0.000	0.000	0.000	0.000	1.000
R	A20rv, rostroventral area 20	0.000	0.000	0.000	0.000	1.000
L	IFJ, inferior frontal junction	0.000	0.000	0.000	0.000	1.000
L	A11m, medial area 11	0.000	0.000	0.000	0.000	1.000
L	OPC, occipital polar cortex	0.000	0.001	0.000	0.000	0.999
L	A39rd, rostrodorsal area 39(Hip3)	0.000	0.001	0.000	0.000	0.999
R	mOccG, middle occipital gyrus	0.000	0.000	0.001	0.000	0.999
R	OPC, occipital polar cortex	0.000	0.001	0.000	0.000	0.999
L	A11l, lateral area 11	0.000	0.000	0.000	0.001	0.999
L	A4ul, area 4(upper limb region)	0.000	0.000	0.001	0.000	0.999
R	vmPOS,ventromedial parietooccipital sulcus	0.000	0.000	0.000	0.002	0.998
R	A32p, pregenual area 32	0.000	0.002	0.000	0.000	0.998
R	A4ul, area 4(upper limb region)	0.000	0.002	0.000	0.000	0.997
R	rTtha, rostral temporal thalamus	0.000	0.000	0.000	0.003	0.997
R	A22c, caudal area 22	0.000	0.003	0.000	0.000	0.997
L	A2, area 2	0.000	0.003	0.000	0.000	0.997
R	A4t, area 4(trunk region)	0.000	0.002	0.002	0.000	0.996
R	A39c, caudal area 39(PGp)	0.000	0.000	0.000	0.008	0.992
R	A31, area 31 (Lc1)	0.000	0.000	0.000	0.008	0.992
R	A11m, medial area 11	0.000	0.000	0.000	0.008	0.992
L	A13, area 13	0.000	0.000	0.009	0.000	0.991
L	mPFtha, medial pre-frontal thalamus	0.000	0.000	0.009	0.000	0.991
R	A4hf, area 4(head and face region)	0.000	0.010	0.000	0.000	0.990
L	A39rv, rostroventral area 39(PGa)	0.000	0.000	0.011	0.000	0.989
R	A10l, lateral area10	0.000	0.001	0.000	0.010	0.988
R	NAC, nucleus accumbens	0.000	0.000	0.000	0.012	0.988
L	cCunG, caudal cuneus gyrus	0.000	0.032	0.000	0.000	0.968
R	A6vl, ventrolateral area 6	0.000	0.000	0.000	0.035	0.965
R	A44d,dorsal area 44	0.000	0.003	0.000	0.038	0.959

L	dmPOS, dorsomedial parietooccipital sulcus(PEr)	0.000	0.000	0.000	0.042	0.958
R	TI, area TI(temporal agranular insular cortex)	0.000	0.001	0.000	0.045	0.954
L	A20r, rostral area 20	0.000	0.049	0.000	0.000	0.951
R	A8vl, ventrolateral area 8	0.000	0.000	0.000	0.050	0.950
R	A23c, caudal area 23	0.000	0.000	0.045	0.021	0.934
L	dId, dorsal dysgranular insula	0.000	0.072	0.000	0.000	0.928
R	A39rv, rostroventral area 39(PGa)	0.000	0.000	0.000	0.076	0.924
R	A12/47l, lateral area 12/47	0.000	0.000	0.000	0.083	0.917
R	cCunG, caudal cuneus gyrus	0.000	0.000	0.000	0.085	0.915
R	A9/46d, dorsal area 9/46	0.001	0.000	0.005	0.106	0.889
L	rpSTS, rostroposterior superior temporal sulcus	0.000	0.000	0.000	0.118	0.882
R	vCa, ventral caudate	0.000	0.000	0.000	0.133	0.867
R	Stha, sensory thalamus	0.000	0.000	0.000	0.135	0.865
R	A14m, medial area 14	0.000	0.000	0.000	0.139	0.861
L	A7r, rostral area 7	0.000	0.000	0.000	0.140	0.860
L	vCa, ventral caudate	0.000	0.000	0.000	0.178	0.822
L	NAC, nucleus accumbens	0.000	0.187	0.000	0.000	0.813
L	Stha, sensory thalamus	0.000	0.000	0.000	0.201	0.798
R	rpSTS, rostroposterior superior temporal sulcus	0.000	0.000	0.000	0.206	0.794
L	A24cd, caudodorsal area 24	0.000	0.220	0.001	0.000	0.779
L	dlPu, dorsolateral putamen	0.000	0.263	0.000	0.000	0.737
R	A7ip, intraparietal area 7(hIP3)	0.000	0.000	0.000	0.280	0.720
R	A35/36r, rostral area 35/36	0.000	0.000	0.000	0.281	0.719
L	A12/47l, lateral area 12/47	0.000	0.000	0.000	0.332	0.668
L	mAmyg, medial amygdala	0.000	0.000	0.000	0.337	0.663
L	A1/2/3ulhf, area 1/2/3(upper limb, head and face region)	0.000	0.354	0.000	0.000	0.646
L	A31, area 31 (Lc1)	0.000	0.000	0.000	0.375	0.625
R	A2, area 2	0.000	0.000	0.000	0.382	0.618
L	aSTS, anterior superior temporal sulcus	0.046	0.074	0.265	0.010	0.604
L	lAmyg, lateral amygdala	0.000	0.000	0.026	0.378	0.596
L	A6vl, ventrolateral area 6	0.001	0.000	0.001	0.443	0.555
L	A6cdl, caudal dorsolateral area 6	0.005	0.450	0.009	0.000	0.535
R	A24cd, caudodorsal area 24	0.000	0.476	0.000	0.000	0.524
R	rLinG, rostral lingual gyrus	0.108	0.051	0.123	0.196	0.523
L	cTtha, caudal temporal thalamus	0.031	0.015	0.017	0.432	0.504
R	dCa, dorsal caudate	0.046	0.015	0.045	0.435	0.459
L	cpSTS, caudoposterior superior temporal sulcus	0.058	0.020	0.066	0.398	0.458

The number of free parameters in each model is listed in parenthesis.

Supplementary Table 7.

Experimental parameters for each study.

Study Number	*Reference*	*Subdomain*	*Domain*	*Stimulus/ Paradigm*	*Contrast*†	*Number of Runs*	*Run Length*	*Number of Trials*	*Stimulus Duration*	*Max t-statistic*††	*N (female)*	*Mean Age*	*IRB/Ethics Approval Committee*	*MRI System*
1	Atlas et al. 2010	Cutaneous Somatic Pain	Pain	Thermal stimulation	High vs low pain	8	6'18"	64	10 s	3.384	19 (9)	25.5	Columbia University	1.5T GE Signa TwinSpeed Excite HD
2	Wager et al. 2013	Cutaneous Somatic Pain	Pain	Thermal stimulation	49.3° C vs baseline	10	~6'40"	8	12.5 s	5.257	33 (22)	27.9	Columbia University	1.5T GE Signa TwinSpeed Excite HD
3	Kano et al. 2017	Visceral Pain	Pain	Rectal distention	Distension vs baseline	6	12'	36	18 s	6.606	29 (15)	22.5	Tohoku University School of Medicine	3T Siemens TrioTIM
4	Rubio et al. 2015	Visceral Pain	Pain	Rectal distention	Distension vs baseline	6	12'	36	18 s	13.128	15 (9)	24*	Comité de Protection des Personnes Sud Est V, France	3T Philips Achieva TX
5	MPA1***	Mechanical Pain	Pain	Pressure Stimulation	7 kg/cm^2 vs baseline	4	6’37”	8	10 s	4.038	15 (4)	26.9	University of Colorado Boulder	3T Siemens TrioTIM
6	MPA2***	Mechanical Pain	Pain	Pressure Stimulation	4, 5, 6 and 7 kg/cm^2 vs baseline	6	7'3”	24	10 s	5.022	15 (8)	24.2	University of Colorado Boulder	3T Siemens Prisma
7	DeYoung et al. 2009	Working Memory	Cognitive Control	N-back (faces and words)	3-back blocks vs baseline	6	5'52"	348	2 s	7.798	104 (59)	22.7	Washington University Medical Center	3T Siemens Allegra
8	van Ast et al. 2016	Working Memory	Cognitive Control	N-back (words)	N-back blocks vs baseline	4	~5'	306	2 s	12.100	21 (10)	22.2	Columbia University	3T Philips Achieva
9	Aron et al. 2007	Response Selection	Cognitive Control	Stop signal Task	All trials vs baseline	6	5'32"	768	~1 s	7.989	15 (5)	28.1	UCLA	3T Siemens Allegra

10	Xue et al. 2008	Response Selection	Cognitive Control	Stop signal Task	All trials vs baseline	6	6'4"	768	~1 s	6.605	15 (9)	23.6	UCLA	3T Siemens Allegra
11	ds101***	Response Conflict	Cognitive Control	Simon Task	Incongruent vs Congruent Trials	2	5'	24	1 s	3.265	21 (9)	30.5	New York University	3T Siemens Allegra
12	Kelly et al. 2008	Response Conflict	Cognitive Control	Eriksen Flanker Task	Incongruent vs Congruent Trials	2	10'	12	2 s	2.358	26 (10)	28.3	New York University	3T Siemens Allegra
13	Gianaros et al. 2014	Visual Emotion	Negative Emotion	Images from IAPS	Negative pictures vs baseline	1	11'28"	15	7 s	4.494	183 (88)	42.7	University of Pittsburgh	3T Siemens TrioTIM
14	Yarkoni et al. 2011**	Visual Emotion	Negative Emotion	Images from IAPS	Negative vs neutral pictures	NR	NR	NR	~4 s	5.278	108 (NR)	NR	Stanford University, Columbia University	1.5 and 3T GE Signa LX Horizon Echospeed, 1.5T GE Signa Twin Speed Excite HD scanner
15	Kross et al. 2011	Social Emotion	Negative Emotion	Images of ex-partners	Images of ex-partner vs friend	2	~13'30"	16	15 s	7.157	40 (21)	20.8	Columbia University	1.5T GE Signa TwinSpeed
16	Krishnan et al. 2016	Social Emotion	Negative Emotion	Images of others in pain	High pain pictures vs baseline	9	8'	27	11 s	5.870	30 (12)	25.2	University of Colorado Boulder	3T Siemens TrioTIM
17	BMRK5***	Auditory Emotion	Negative Emotion	Sounds from IADS	Unpleasant Sounds vs baseline	4	10'	12	8 s	5.432	15 (7)	31.1	University of Colorado Boulder	3T Siemens TrioTIM
18	PM01***	Auditory Emotion	Negative Emotion	Sounds from IADS	Unpleasant Sounds vs baseline	4	9'18"	12	8 s	5.306	15 (9)	24.4	University of Colorado Boulder	3T Siemens TrioTIM

Note. Informed consent was provided for each study listed.
* Median age
** Data are collapsed across four separate studies
*** Data not previously published
† Baseline involved eyes open fixation for all studies
†† Maximum statistic from one-sample t-test in MFC (n = 15)
NR = Data not reported
IAPS = International Affective Picture System
IADS = International Affective Digital Sounds