Supplementary Materials

1.1 Validation analyses controlling for nodal distance, sample size and temporal signal-to-noise ratio (tSNR)

**Nodal Distance.** The tool processing nodes in the human adults were left-lateralized, whereas the face processing nodes were bilateral, which might result in greater distances between the tool and face processing nodes (i.e. between-domain path) compared to the distances among tool processing nodes in all three groups. Indeed, when the path length (i.e., the Euclidean distance of two nodes) was calculated by averaging the Euclidean distance between every voxel pair with each from one node, longer path length for the between-domain connections than that for the within-tool-domain connections was evident in all three groups (human adults: $t_{36} = 2.1, p = 0.047, \text{Cohen's } d = 0.92$; human neonates: $t_{36} = 2.1, p = 0.046, \text{Cohen's } d = 0.92$; macaques: $t_{36} = 2.6, p = 0.01, \text{Cohen's } d = 1.2$). Such differences in nodal distance might contribute to greater within-tool-domain rsFC compared to the between-domain rsFC observed in the current study. To circumvent this issue, the network effects (i.e., greater within-domain than between-domain rsFC) were further evaluated when the same analyses were carried out with tool and face processing nodes in the left hemisphere only, where the distance of within-tool-domain connections and of between-domain connections were comparable (human adults: $t_{16} = 0.05, p = 0.96$; human neonates: $t_{16} = 0.05, p = 0.96$; macaques: $t_{16} = 0.03, p = 0.98$). The resulting patterns for both the tool and face processing networks remained similar to those in the main analysis. Namely, significantly stronger within-tool-domain rsFC in comparison to between-domain rsFC was still evident in human adults ($t_{99} = 12.0, p_{\text{corrected}} < 0.001, \text{Cohen's } d = 1.2$) and human neonates (for homologous regions, $t_{117} = 7.6, p_{\text{corrected}} < 0.001, \text{Cohen's } d = 0.70$), but not in macaques (for homologous regions, $t_{24} = -6.5, p_{\text{corrected}} < 0.001$; i.e., in the reverse direction of tool-network presence, Figure 2B). Significantly stronger within-face-domain rsFC compared with between-domain rsFC was observed in human adults ($t_{99} = 5.6, p_{\text{corrected}} < 0.001, \text{Cohen's } d = 0.56$) and macaques (for homologous regions, $t_{24} = 6.3, p_{\text{corrected}} < 0.001, \text{Cohen's } d = 1.3$), but not in human neonates (for homologous regions, $t_{117} = -0.09, p = 0.93$, Figure 2B, see result replications based on subgroups of human neonates and macaques in Figure S1B).

**Sample size.** We further considered the potential influences of sample size differences, as the macaque dataset was much smaller ($n = 25$) than the two human datasets ($n \geq 100$) and this was the dataset in which we did not observe the tool homologous network. This concern is assuaged by the fact that we observed the face homologous network in macaques and not in human neonates (i.e., a form of dissociation between the two populations). Nevertheless, a bootstrapping analysis was conducted to evaluate the network effects among groups with balanced samples ($n = 25$). To do this, the subsamples of human adults and neonates with the subject sizes equal to that of macaque sample were created by randomly sampling 25 data from the HCP and dHCP datasets, respectively. These resting-state images were submitted to the same network analyses as described in the main analysis for comparisons of within-domain and between-domain rsFC. This process was repeated 10,000 times, producing group-specific distributions of within-domain minus between-domain rsFC. The network effect obtained based on the macaque dataset was then compared against these distributions of the network effects derived from the subsamples of human adults and neonates with equal sample sizes. As shown in Figure 2C, the distributions of rsFC differences for the tool (homologous) networks in human adults and neonates are greater than 0. As such, the presence of the tool (homologous) network in human adults and neonates is robust across bootstrapping samplings. Note
that the bootstrapping results for the face processing network evinced this network’s reliability in human adults (i.e., rsFC differences $> 0$), but not in human neonates (Figure 2C), by corroborating the results based on the full sample.

$tSNR$. A tSNR map was generated for each individual (Murphy et al., 2007). Specifically, a tSNR map was first computed for each run by dividing the mean value of time series in each voxel by its standard deviation, which were then averaged across all runs for each participant. All groups showed relative high quality in both the tool and face processing nodes ($> 30$). The mean tSNR of each ROI pair was then regressed out from the corresponding rsFC using a linear regression model within each subject. The residual term from the model, representing the ROI wise functional connectivity independent of the tSNR influence, was then applied in the network analyses. The same result patterns were observed for the three groups (Figure S4). Both tool and face processing networks were present in human adults (tool processing network, both hemispheres: $t_{99} = 11.4$, $p_{corrected} < 0.001$, Cohen’s $d = 1.1$, left hemisphere: $t_{99} = 10.0$, $p_{corrected} < 0.001$, Cohen’s $d = 1.0$; face processing network, both hemispheres: $t_{99} = 18.1$, $p_{corrected} < 0.001$, Cohen’s $d = 1.8$, left hemisphere: $t_{99} = 7.0$, $p_{corrected} < 0.001$, Cohen’s $d = 0.70$); the human neonates only showed intrinsic functional network for tool processing nodes (both hemispheres: $t_{117} = 10.9$, $p_{corrected} < 0.001$, Cohen’s $d = 1.0$, left hemisphere: $t_{117} = 5.9$, $p_{corrected} < 0.001$, Cohen’s $d = 0.55$), but not for face processing nodes (both hemispheres: $t_{117} = -0.93$, $p = 0.35$, left hemisphere: $t_{117} = 2.3$, $p_{corrected} = 0.051$), while the opposite pattern was observed in macaques (tool processing network, both hemispheres: $t_{24} = -4.0$, $p_{corrected} < 0.001$, left hemisphere: $t_{24} = -6.4$, $p_{corrected} < 0.001$; i.e., in the reverse direction of tool-network presence; face processing network, both hemispheres: $t_{24} = 4.1$, $p_{corrected} < 0.001$, Cohen’s $d = 0.83$, left hemisphere: $t_{24} = 6.1$, $p_{corrected} < 0.001$, Cohen’s $d = 1.2$).

1.2 Validation of the tool processing network effect using anatomically-defined ROIs

The results in the main text used ROIs derived from meta-analyses based on human adult functional activations, with the human neonate and macaque ROIs obtained through cross-population transformation. This approach may be subject to potential errors specifically introduced by the transformation process and/or the specific functional ROI selection method (fully left lateralized based on the meta-analysis method using Neurosynth). We thus performed a set of validation analyses using tool processing ROIs derived from the anatomically-defined atlas available for each population, approximating the corresponding functional ROIs, and using nodes in both hemispheres, to validate the results obtained based on the human adult-specific functional ROI approach. The automated anatomical labeling atlas (AAL, Tzourio-Mazoyer et al., 2002) was used for the human adult group. The LPreG and LIFG functional nodes corresponded to the Precentral_L and Frontal_Inf_Tri_L areas in the AAL atlas; The LIPL/SPL node corresponded to the combination of the Parietal_Sup_L and Parietal_Inf_L areas (analyses treating them as separate nodes were also performed, which did not alter the result patterns); The LOTC node corresponded to the posterior 1/3 portion of the MTG area (Temporal_Mid_L). For the human neonate group, the tool processing ROIs were similarly defined based on the neonate AAL atlas (Shi et al., 2011). For macaques, we used the National Institute of Mental Health Macaque Template (NMT, version 2.0, Jung et al., 2021) atlas. The LPreG node corresponded to the left premotor cortex area available in the NMT atlas; The LIPL/SPL node corresponded to the combination of the left inferior and superior parietal lobules in NMT; The LIFG node corresponded to the rostral ventrolateral prefrontal cortex in NMT; The LOTC node corresponded to the TEO in NMT. We re-evaluated the tool processing network effects
using these anatomically-defined ROIs, and the same result pattern was obtained. Significantly stronger within-tool-domain rsFC in comparison to the between-domain rsFC was still evident in both human adults (both hemispheres: \( t_{99} = 24.9, p_{\text{corrected}} < 0.001 \), Cohen’s \( d = 2.5 \), left hemisphere: \( t_{99} = 18.2, p_{\text{corrected}} < 0.001 \), Cohen’s \( d = 1.8 \)) and human neonates (both hemispheres: \( t_{117} = 7.3, p_{\text{corrected}} < 0.001 \), Cohen’s \( d = 0.67 \), left hemisphere: \( t_{117} = 3.9, p_{\text{corrected}} < 0.001 \), Cohen’s \( d = 0.36 \)), and not in macaques (both hemispheres: \( t_{24} = -1.3, \ p = 0.22 \), left hemisphere: \( t_{24} = -4.6, p_{\text{corrected}} < 0.001 \); i.e., in the reverse direction of tool-network presence).

We further examined the tool processing network considering nodes in both hemispheres. Anatomically-based ROI selection approach as described in the paragraph above was used to define the bilateral tool processing nodes based on the group-specific atlases (i.e., the AAL atlas for human adults, the neonatal AAL atlas for human neonates, and the NMT atlas for macaques). Similar to the original results based on the left-hemispheric nodes, the within-tool-domain rsFC were significantly higher than the between-domain rsFC in both human adults (\( t_{99} = 20.6, p_{\text{corrected}} < 0.001 \), Cohen’s \( d = 2.1 \)) and neonates (\( t_{117} = 11.4, p_{\text{corrected}} < 0.001 \), Cohen’s \( d = 1.0 \)), but not in the macaques (\( t_{24} = 0.39, p = 0.70 \)).

1.3 Validation of the topology similarity results for the tool processing network with more data points

We first split the time series equally into 10 bins (with a minimum of 25 data points) for each participant. Pearson correlations were calculated for each of the six ROI pairs for every time bin, which were normalized to Fisher Z scores. This resulted in a tool-network vector of 60 data points (6 paths * 10 bins) for each individual. Topological similarity analyses were thus computed by Pearson correlations on this tool vector for each subject pair across all three groups. Fisher Z scores derived from the between-group correlation results were then subjected to the one-sample and two-sample \( t \)-tests to examine whether the between-group similarities were significantly above zero and differed among different group pairs, respectively. This validation analysis revealed the same result pattern as reported in the main text. Specifically, the topological patterns of the tool (homologous) networks in human adults and neonates were significantly correlated with moderate effect sizes \( (r = 0.25 \pm 0.23, \text{one-sample } t_{11799} = 118.8, p_{\text{corrected}} < 0.001, \text{Cohen’s } d = 1.1) \); the similarities between the macaque group and either human group were, although statistically significant, very low (human adults-macaques: \( r = 0.01 \pm 0.25 \), one-sample \( t_{14299} = 2.8, p_{\text{corrected}} = 0.03 \), Cohen’s \( d = 0.06 \); human neonates-macaques, \( r = 0.02 \pm 0.19 \), one-sample \( t_{2949} = 5.5, p_{\text{corrected}} < 0.001 \), Cohen’s \( d = 0.10 \)), and significantly lower than the similarity between the two human groups (human adults-human neonates vs. human adults-macaques: \( t_{14298} = 46.2, p_{\text{corrected}} < 0.001 \), Cohen’s \( d = 1.02 \); human adults-human neonates vs. human neonates-macaque: \( t_{14748} = 50.6, p_{\text{corrected}} < 0.001 \), Cohen’s \( d = 1.04 \)).

Reference
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Shi, F., Yap, P.-T., Wu, G., Jia, H., Gilmore, J.H., Lin, W., Shen, D., 2011. Infant brain atlases from neonates to 1-and 2-year-olds. PloS One 6, e18746.

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Table S1. A full list of the macaque subject IDs included in the current analysis.

| ID in the current project | Dataset  | Original subject ID |
|--------------------------|----------|---------------------|
| Macaque 001              | Newcastle| 32097               |
| Macaque 002              | Newcastle| 32100               |
| Macaque 003              | Newcastle| 32104               |
| Macaque 004              | Newcastle| 32105               |
| Macaque 005              | Newcastle| 32106               |
| Macaque 006              | Newcastle| 32107               |
| Macaque 007              | Newcastle| 32108               |
| Macaque 008              | Newcastle| 32109               |
| Macaque 009              | Newcastle| 32110               |
| Macaque 010              | Oxford   | 32163               |
| Macaque 011              | Oxford   | 32165               |
| Macaque 012              | Oxford   | 32166               |
| Macaque 013              | Oxford   | 32167               |
| Macaque 014              | Oxford   | 32169               |
| Macaque 015              | Oxford   | 32171               |
| Macaque 016              | Oxford   | 32172               |
| Macaque 017              | Oxford   | 32173               |
| Macaque 018              | Oxford   | 32174               |
| Macaque 019              | Oxford   | 32175               |
| Macaque 020              | Oxford   | 32176               |
| Macaque 021              | Oxford   | 32177               |
| Macaque 022              | Oxford   | 32178               |
| Macaque 023              | Oxford   | 32179               |
| Macaque 024              | Oxford   | 32180               |
| Macaque 025              | Oxford   | 32181               |
Table S2. A list of the human adult ROIs generated based on the Neurosynth database.

| Area                                         | Abbreviation | Peak Voxel (Z value) | Cluster Size (Voxels) | Peak Coordinates (MNI) |
|----------------------------------------------|--------------|----------------------|-----------------------|------------------------|
| **Tool**                                     |              |                      |                       |                        |
| Left lateral occipitotemporal cortex         | LOTC         | 8.39                 | 462                   | -52 -58 -2            |
| Left inferior frontal gyrus                 | LIFG         | 6.67                 | 57                    | -52 40 6             |
| Left inferior and superior parietal lobe     | LIPL/SPL     | 9.89                 | 745                   | -68 -22 32           |
| Left premotor area                           | LPreG        | 5.35                 | 107                   | -54 8 34             |
| Left fusiform face area                      | LFFA         | 17.41                | 342                   | -40 -52 -22          |
| Right fusiform face area                     | RFFA         | 26.82                | 479                   | 40 -50 -20           |
| Left occipital face area                     | LOFA         | 13.34                | 233                   | -38 -86 -14          |
| Right occipital face area                    | ROFA         | 16.86                | 145                   | -44 -76 -14          |
| Left superior temporal gyrus                 | LSTG         | 5.74                 | 117                   | -54 -56 8            |
| Right superior temporal gyrus                | RSTG         | 8.24                 | 212                   | 54 -40 6             |
| Right anterior temporal lobe                 | RATL         | 8.34                 | 151                   | 36 -8 -32            |
| Right inferior frontal gyrus                 | RIFG         | 6.97                 | 185                   | 42 16 24             |

**Face**

| Area                                         | Abbreviation | Peak Voxel (Z value) | Cluster Size (Voxels) | Peak Coordinates (MNI) |
|----------------------------------------------|--------------|----------------------|-----------------------|------------------------|
| Left superior temporal gyrus                 | LSTG         | 5.74                 | 117                   | -54 -56 8            |
| Right superior temporal gyrus                | RSTG         | 8.24                 | 212                   | 54 -40 6             |
| Right anterior temporal lobe                 | RATL         | 8.34                 | 151                   | 36 -8 -32            |
| Right inferior frontal gyrus                 | RIFG         | 6.97                 | 185                   | 42 16 24             |
Table S3. Statistical results of cross-population comparisons for path-specific functional connectivity

|                      | LPreG-LIFG        | LPreG-LOTC       | LPreG-LIPL/SPL   |
|----------------------|------------------|------------------|------------------|
|                      | Dif   | t     | p     | Cohen’s d | Dif   | t     | p     | Cohen’s d | Dif   | t     | p     | Cohen’s d |
| Human adults VS. Neonates | 0.13  | 3.8   | **    | 0.51  | 0.37  | 12.5  | ***   | 1.7    | 0.07  | 1.9    | (0.054) | 0.26   |
| Human neonates VS. Macaques | 0.09  | 1.6   | (0.11)| 0.35  | 0.15  | 3.2   | **    | 0.71   | 0.58  | 9.9    | ***    | 2.2    |
|                      | LIFG-LOTC | Dif   | t     | p     | Cohen’s d |
| Human adults VS. Neonates | 0.23  | 8.7   | ***   | 1.2   | 0.07  |
| Human neonates VS. Macaques | -0.01 | -0.26 | (0.80)| -0.06 | 0.10  |
|                      | LIFG-LIPL/SPL | Dif   | t     | p     | Cohen’s d |
| Human adults VS. Neonates | 0.12  | 2.4   | (0.02)| 0.33  | 0.36  |
| Human neonates VS. Macaques | -0.01 | -0.26 | (0.80)| -0.06 | 0.10  |
|                      | LOTC-LIPL/SPL | Dif   | t     | p     | Cohen’s d |
| Human adults VS. Neonates | 0.46  | 11.7  | ***   | 6.2   | 0.31  |
| Human neonates VS. Macaques | -0.01 | -0.26 | (0.80)| -0.06 | 0.10  |

Note. * indicates $p_{corrected} < 0.05$ after Bonferroni correction. For non-significant results, the uncorrected $p$ is presented in parentheses.

Dif: differences in mean values; LOTC: left lateral occipitotemporal cortex; LIPL/SPL: left inferior and superior parietal lobule; LPreG: left premotor gyrus; LIFG: left inferior frontal gyrus.

* $p_{corrected} < 0.05$, ** $p_{corrected} < 0.01$, *** $p_{corrected} < 0.001$. 

Table S4. Interaction effects of group (human neonates vs. other groups) × path (LPreG-LIPL/SPL vs. other paths)

| Path Comparison                      | LPreG-LIFG | LPreG-LOTC | LIFG-LOTC | LIFG-LIPL/SPL | LOTC-LIPL/SPL | df  |
|--------------------------------------|------------|------------|-----------|---------------|---------------|-----|
|                                      | F          | p           | partial η² | F             | p             | partial η² | F          | p             | partial η² | F            | p           | partial η² | df  |
| Human adults VS. Neonates            |            |             |           |               |               |           |            |             |               |               |             |           |     |
| 1.1                                  | 1.1 (0.29) | 0.005       | 76.7 *     | 14.4 *        | 0.01 (0.92)   | 0          | 55.7 *     | 0.21          | 1, 216       |               |             |           |     |
| Human neonates VS. Macaques          | 35.8       | *           | 73.7 *     | 105.3 *       | 80.0 *        | 0.36       | 21.6 *     | 0.13          | 1, 141       |               |             |           |     |

Note. * indicates $p_{corrected} < 0.05$ after Bonferroni correction. For non-significant results, the uncorrected $p$ is presented in parentheses.

LOTC: left lateral occipitotemporal cortex; LIPL/SPL: left inferior and superior parietal lobule; LPreG: left premotor gyrus; LIFG: left inferior frontal gyrus
Figure S1. Resting-state functional connectivity (rsFC) results when the pre-term neonates, full-term neonates, awake macaques, and anesthetized macaques were analyzed separately. A. Bar graphs illustrate the rsFC values for within- and between- domain functional connectivity in the pre-term neonate, full-term neonate, awake macaque, and anesthetized subgroups. B. Bar graphs show replication results for the network analysis restricted to the left-hemispheric nodes with balanced within-tool-domain and between-domain nodal distances. Within-domain rsFC values were greater than between-domain rsFC values in pre-term ($t_{11} = 3.6, p_{corrected} = 0.008, \text{cohen's } d = 1.0$) and full-term neonates ($t_{105} = 6.9, p_{corrected} < 0.001, \text{cohen's } d = 0.67$) for the tool processing network, but not for the face processing network (pre-term: $t_{11} = -1.1, p = 0.28$; full-term: $t_{105} = 0.20, p = 0.84$). Within-domain FC values were greater than between-domain FC values in awake ($t_{8} = 4.6, p_{corrected} = 0.004, \text{cohen's } d = 1.5$) and anesthetized macaques ($t_{15} = 4.7, p_{corrected} < 0.001, \text{cohen's } d = 1.2$) for the face processing network, but not for the tool processing network (awake: $t_{8} = -3.2, p_{corrected} = 0.03$; anesthetized: $t_{15} = -5.7, p_{corrected} < 0.001$). Effect sizes (Cohen’s $d$) are shown for comparisons in which significantly greater within-domain than between-domain rsFC was observed. Error bars indicate standard errors.
Figure S2. Network topology similarity results in subgroups of pre-term (A) and full-term (B) neonates, as well as awake (C) and anesthetized (D) macaques. The results of subgroups remained unchanged in each analysis. Bar graphs illustrate the network topological pattern similarities for participants belonging to different subgroups. Effect sizes (Cohen’s $d$) are shown for comparisons showing significant differences in the between-group pattern similarities between different group pairs (all $p_{corrected} < 0.05$). Error bars indicate standard errors.
Figure S3. Replication results based on data from 17 macaques with at least 50% ROI coverage. Bar graphs illustrate rsFC values for within-domain and between-domain connectivity in the macaque group (with at least 50% ROI coverage) based on nodes in both hemispheres (bi-hemispheric, left column) or the left-hemisphere only (right column). Effect sizes (Cohen’s $d$) are shown for comparisons in which significantly greater within-domain than between-domain rsFC was observed (all $p_{corrected} < 0.01$). Error bars indicate standard errors.
Figure S4. Resting-state functional connectivity (rsFC) result after regressing tSNR. A. Bar graphs illustrate the rsFC values for within- and between-domain functional connectivity in human adults, human neonates, and macaques. Within-domain rsFC values were significantly greater than between-domain rsFC values in human adults for both the face and tool processing networks, in human neonates only for the tool processing network, and in macaques only for the face processing network (all $p_{corrected} < 0.05$). B. Bar graphs show replication results for the network analysis using only the left-hemispheric nodes. Effect sizes (Cohen’s $d$) are shown for comparisons in which significantly greater within-domain than between-domain rsFC was observed (all $p_{corrected} < 0.05$). Error bars indicate standard error.
Figure S5. The topological pattern for the face (homologous) network. A. Path-specific connectivity strengths (Fisher Z scores) of the face (homologous) network in all three groups. All group comparisons between human adults and human neonates were significant (all $t > 5$, $p_{corrected} < 0.001$). Most of the paths were comparable between human neonates and monkeys, except LFFA-LSTG ($t = -7.8$, $p_{corrected} < 0.001$, Cohen’s $d = -1.7$), LOFA-RFFA ($t = -3.4$, $p_{corrected} = 0.03$, Cohen’s $d = -0.74$), RFFA-ROFA ($t = -4.8$, $p_{corrected} < 0.001$, Cohen’s $d = -1.1$), LFFA-RSTG ($t = -4.8$, $p_{corrected} < 0.001$, Cohen’s $d = -1.0$), LOFA-RSTG ($t = -3.3$, $p_{corrected} = 0.03$, Cohen’s $d = -0.73$), LSTG-RSTG ($t = 3.4$, $p_{corrected} = 0.001$, Cohen’s $d = 0.74$). B. The correlational matrix for the face (homologous) network topology similarity among all three population groups. C. Bar graphs show face network topology similarities for participants belonging to different groups. Effect sizes.
(Cohen’s $d$) are shown for comparisons in which significant differences in between-group pattern similarities was observed between different group pairs (all $p_{\text{corrected}} < 0.001$). Error bars indicate standard errors.
Figure S6. Nodal and path (functional connection) contributions to the tool processing network in human adults. A. Bar graphs illustrate network effects, calculated as within-domain minus between-domain rsFC, for the full tool processing network and when each constituent node (left column) or each constituent path (right column) is removed. Between-domain rsFC was computed from nodes in both hemispheres (Bilateral). Results show that no matter which node or path was removed, the within-domain rsFC strengths based on the remaining tool processing nodes or paths were still significantly higher than the between-domain rsFC strengths. Effect sizes (Cohen’s $d$) are shown above each bar. Error bars indicate standard errors. B. Bar graphs illustrate network effects, calculated as within-domain minus between-domain rsFC, for the full tool processing network and when each constituent node (left column) or each constituent path (right column) is removed. Between-domain rsFC was computed from nodes in the left hemisphere. Results show that no matter which node or path was removed, the within-domain rsFC strengths based on the remaining tool processing nodes or paths were still significantly higher than the between-domain rsFC strengths. Effect sizes (Cohen’s $d$) are shown above each bar (all $p_{corrected} < 0.05$). Error bars indicate standard errors.

LOTC: left lateral occipitotemporal cortex; LIPL/SPL: left inferior and superior parietal lobule; LPreG: left premotor gyrus; LIFG: left inferior frontal gyrus.
Figure S7. Critical contributions of the premotor node and its connectivity with the parietal region to the formation of the intrinsic tool processing network in pre-term and full-term neonate subgroups, as revealed by leave-one-node/path-out analyses. Bar graphs illustrate
network effects, calculated as within-domain minus between-domain rsFC, for the full tool processing network and when each constituent node (left column) or path (right column) is removed. Between-domain rsFC was computed based on nodes in both hemispheres (bi-hemispheric, A for pre-term; C for full-term) or the left-hemisphere only (B for pre-term; D for full-term). Effect sizes (Cohen’s $d$) are shown when the rsFC strengths of the remaining tool network were significantly higher than the between-domain rsFC strengths (all $p_{corrected} < 0.05$, Bonferroni corrected). Error bars indicate standard errors.
Figure S8. Overlaps (red) between the tool homologous nodes (green) in the macaque brain and the manually-drawn lateral grasping network (blue) available in Howells et al. (2020). The left premotor gyrus (LPreG) and F5 are presented in the top panel, the left inferior and superior parietal lobule (LIPL/SPL) and AIP in the middle panel, and the left inferior frontal gyrus and m46v/m12r in the bottom panel.