SUPPLEMENTARY INFORMATION

Organization of the inputs and outputs of the mouse superior colliculus

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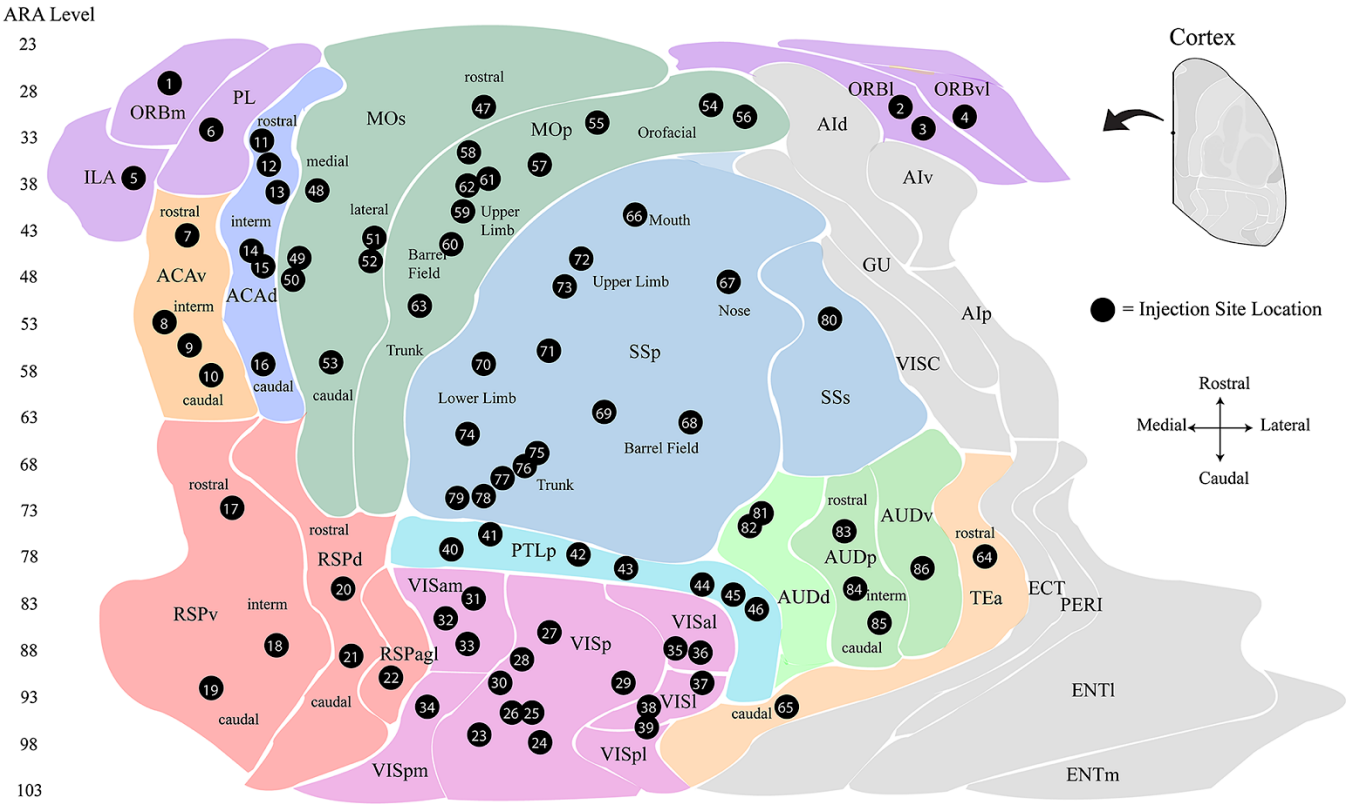


1. ORBm (28) SW110808-04A
2. ORBl (35) SW180117-01A
3. ORBl (37) SW110808-02A
4. ORBvl (33) SW190327-02A
5. ILA (37) SW190315-07A
6. PL (33) SW190315-05A

7. ACAv rostral (44) SW120403-02A
8. ACAv interm (54) SW121031-04B
9. ACAv interm (56) SW110321-04B
10. ACAv caudal (60) SW180228-03A

11. ACAd rostral (36) SW151210-01A
12. ACAd rostral (37) SW151211-01A
13. ACAd interm (42) SW180227-01A
14. ACAd interm (46) SW121031-03B
15. ACAd interm (47) SW180227-02A
16. ACAd caudal (58) SW151211-02A

17. RSPv rostral (73) SW110615-03
18. RSPv interm (88) SW190327-04A
19. RSPv caudal (90) SW151211-01A
20. RSPd rostral (83) SW110613-03B
21. RSPd caudal (88) SW110614-01B
22. RSPagl (91) SW110615-01B

23. VISp caudal (95) SW121221-03A
24. VISp caudolat (96) SW121221-02A
25. VISp caudolat (94) SW180302-05A
26. VISp caudomed (96) SW121221-02A
27. VISp rostromed (87) SW180713-04A
28. VISp rostral (86) SW121221-03A
29. VISp (92) SW151211-01A
30. VISp (90) SW180713-03A
31. VISam (83) SW121031-03B
32. VISam (84) SW151210-02A
33. VISam (86) SW151211-02A
34. VISpm (94) SW190327-04A
35. VISal (90) SW180302-05A
36. VISal (91) SW180302-04A
37. VISl (92) SW180815-01A
38. VISl (92) SW120819-04A
39. VISl/pl (97) SW180522-04A

40. PTLp med (76) SW180717-03A
41. PTLp med (76) SW180717-03A
42. PTLp med (77) SW180424-01A
43. PTLp med (77) SW180424-01A
44. PTLp lat (81) SW180302-05A
45. PTLp lat (82) SW151215-03A
46. PTLp lat (82) SW180302-04A

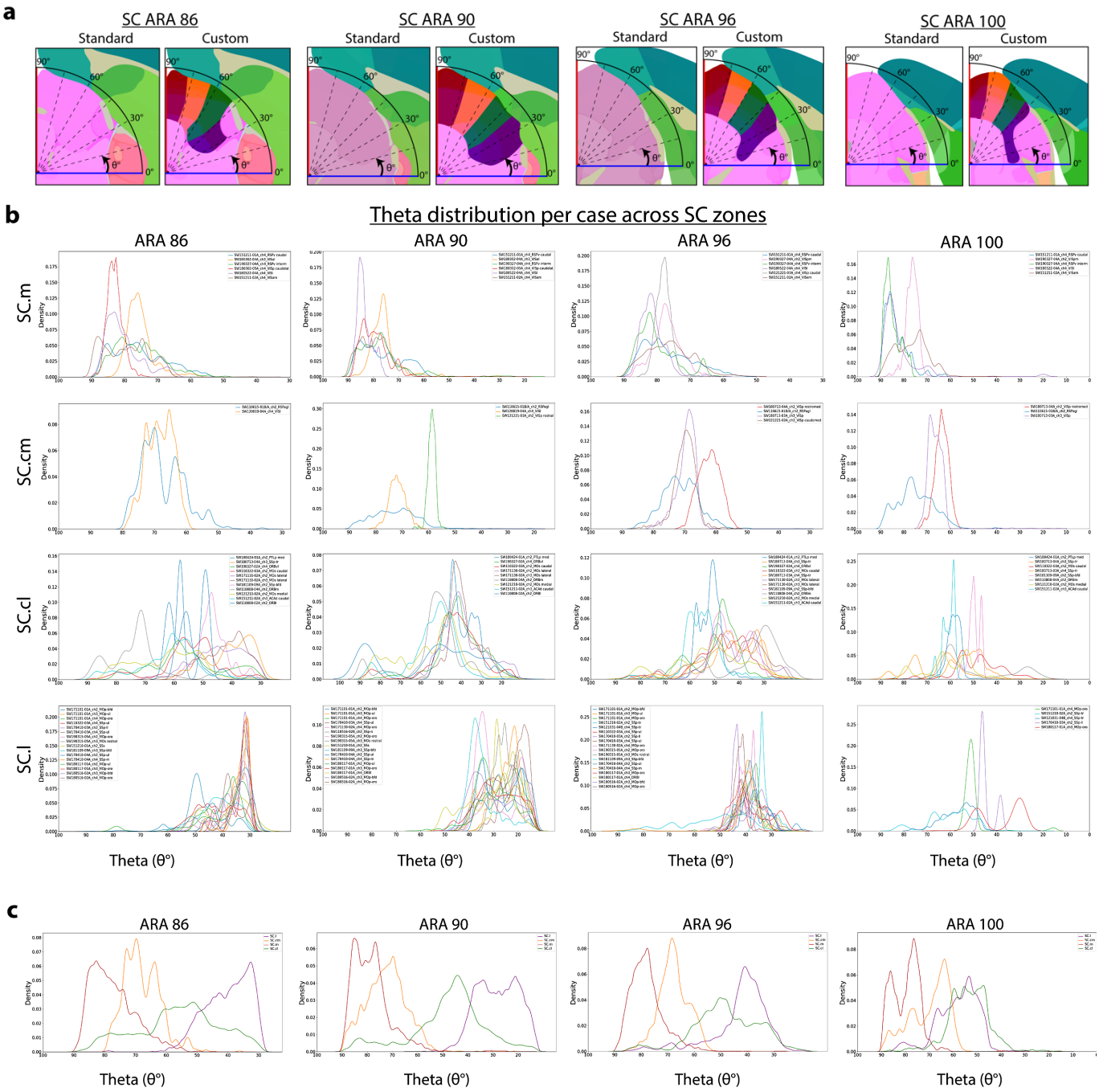
47. MOs rostral (31) SW190315-05A
48. MOs medial (40) SW180227-01A
49. MOs medial (47) SW180227-02A
50. MOs medial (49) SW121210-02A
51. MOs lateral (44) SW171130-02A
52. MOs lateral (46) SW171130-02A
53. MOs caudal (58) SW110322-03A
54. MOp oro (31) SW190315-05A
55. MOp oro (34) SW171101-01A
56. MOp oro (32) SW180516-02A
57. MOp oro (40) SW171130-02A
58. MOp oro (35) SW180117-01A
59. MOp ul (41) SW180117-01A
60. MOp ul (44) SW171101-01A
61. MOp bfd (38) SW171101-01A
62. MOp bfd (40) SW180516-02A
63. MOp tr (52) SW180516-02A

64. TEa rostral (78) SW120125-01A
65. TEa caudal (94) SW120819-04A

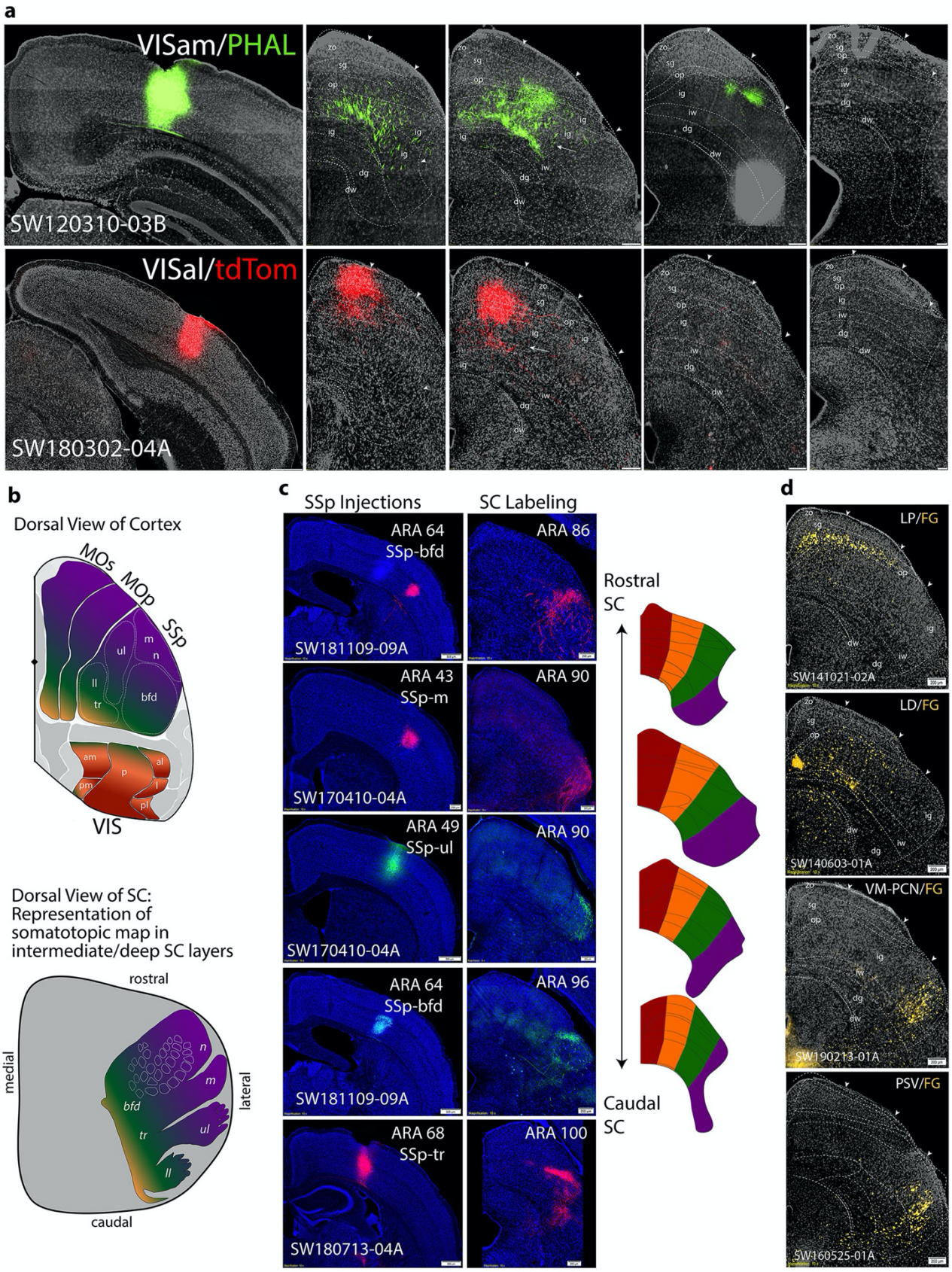
66. SSp-m (43) SW170410-04A
67. SSp-n (50) SW110516-02B
68. SSp-bfd (64) l SW181109-09A
69. SSp-bfd (64) m SW181109-09A
70. SSp-ll (56) SW170410-03A
71. SSp-ul (58) SW110322-03A
72. SSp-ul (47) SW170410-03A
73. SSp-ul (49) SW170410-04A
74. SSp-tr/ll (70) SW121031-03B
75. SSp-tr (68) SW180713-04A
76. SSp-tr (68) SW180713-03A
77. SSp-tr (74) SW121031-04B
78. SSp-tr (74) SW151210-02A
79. SSp-tr (76) SW151211-02A
80. SSs (53) SW151210-01A

81. AUDd (74) SW180713-03A
82. AUDd (74) SW180713-04A
83. AUDp rostral (76) SW190315-09A
84. AUDp interm (84) SW121031-04B
85. AUDp caudal (86) SW190315-09A
86. AUDv (70) SW190315-09A

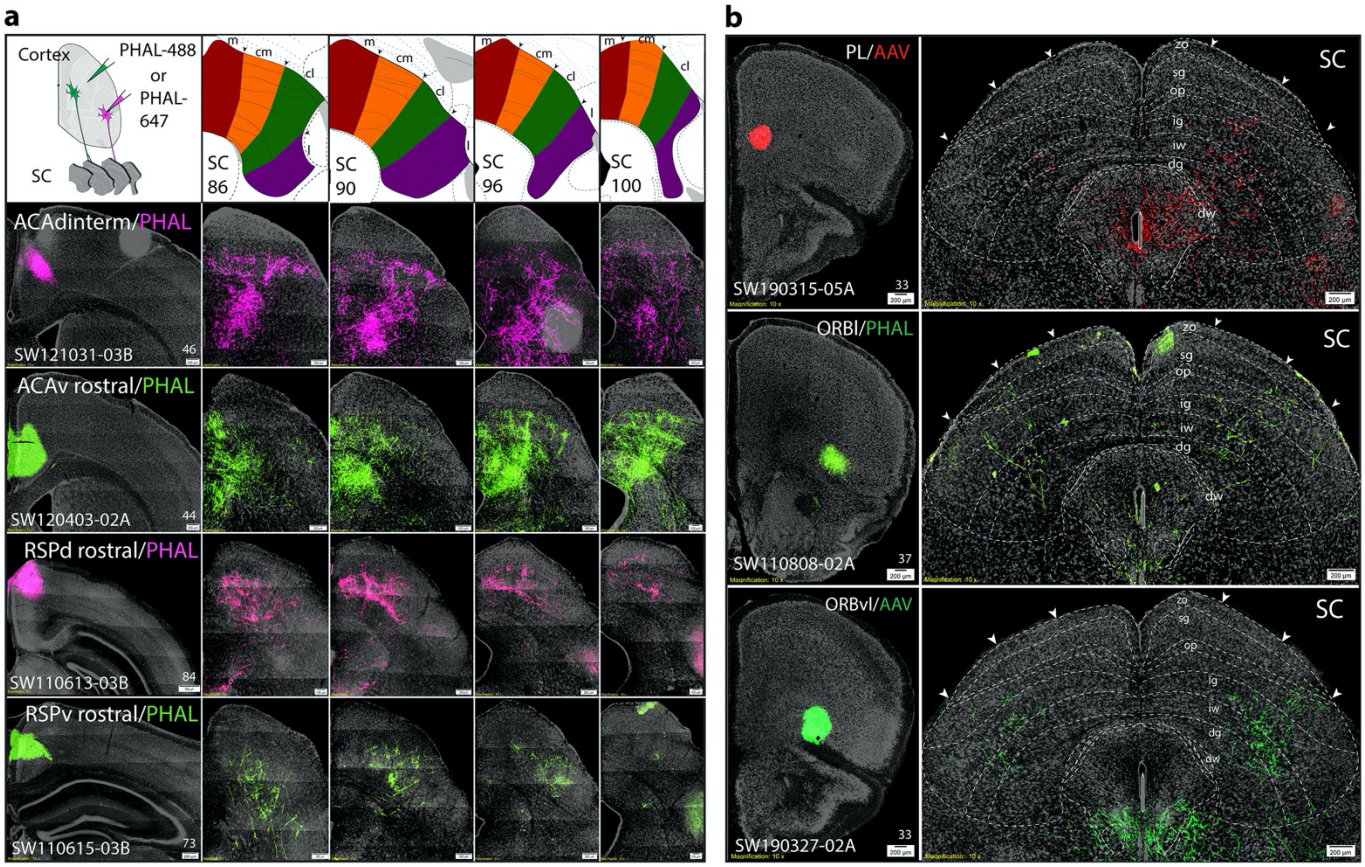
Supplementary Figure 1 | Flat map of mouse cortex with injection sites names.
Shaded brain region corresponds to same shaded color box with corresponding numbers for each case. Generated by expanding the length of each cortical area from the coordinate framework on the Allen Institute Adult Mouse Brain Atlas. Filled circles indicate location of injection site. List of injection sites, coordinates, and location can be cross-referenced by index number with Supplementary Table 2.


a
SC ARA 86
Standard
Custom
SC ARA 90
Standard
Custom
SC ARA 96
Standard
Custom
SC ARA 100
Standard
Custom
90°
60°
30°
0°
θ°
b
Theta distribution per case across SC zones
ARA 86
ARA 90
ARA 96
ARA 100
SC.m
SC.cm
SC.cl
SC.l
Density
Theta (θ°)
c
ARA 86
ARA 90
ARA 96
ARA 100
Density
Theta (θ°)

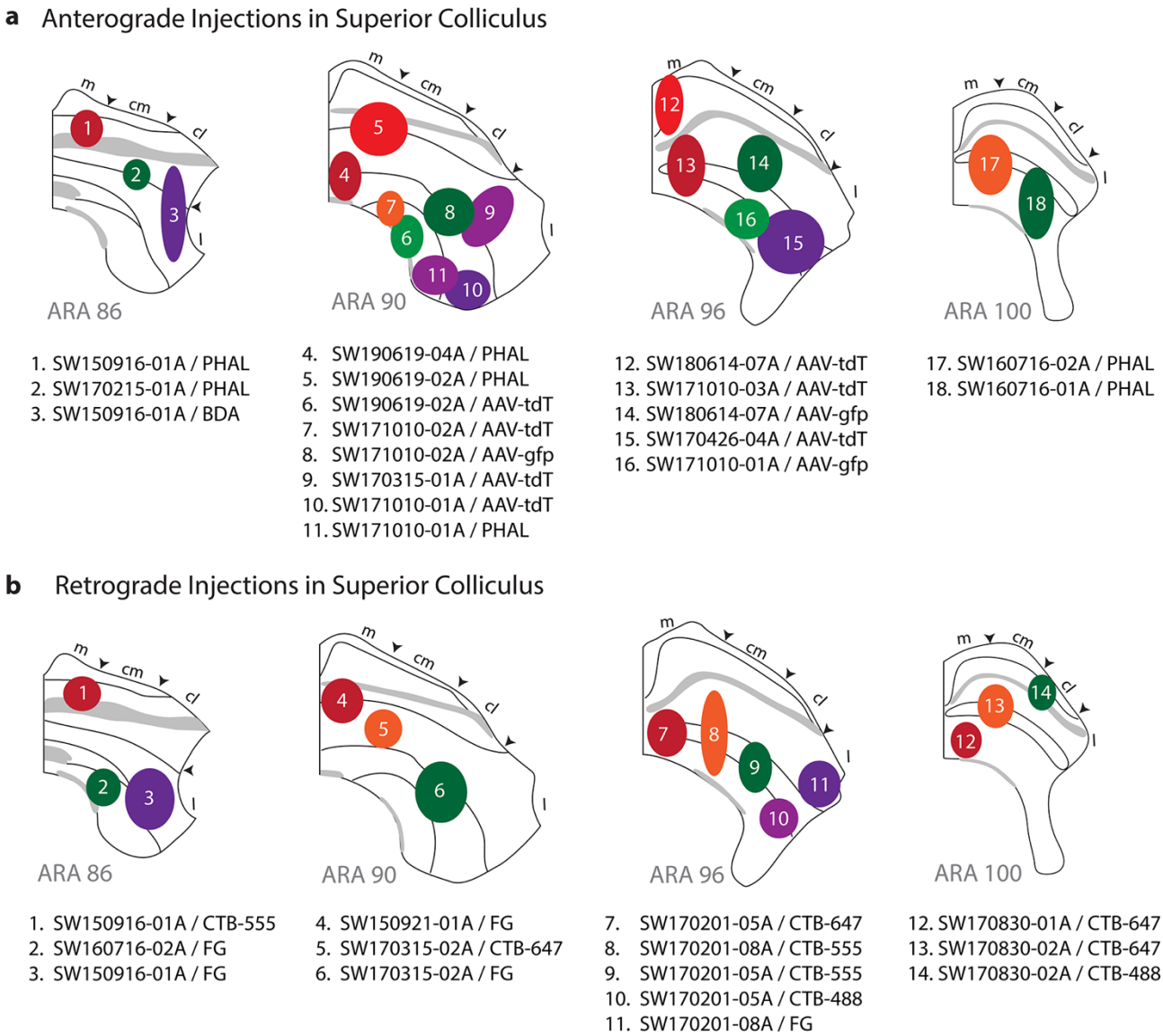
Supplementary Figure 2 | Probability distribution plots.
a) Atlas levels for the SC from rostral to caudal: ARA levels 86, 90, 96, and 100. Left side is polar coordinate ranges used to quantify angular distribution of thresholded pixel labeling in SC. Angles represented by theta (θ°) values where midline starts at 90° and ranges toward 0° at lateral angles. Right side is the custom SC atlas with overlay of angular range showing coarse alignment of manually delineated borders in SC. Color-code associations: red (SC.m), orange (SC.cm), green (SC.cl), purple (SC.l). **b)** Probability distribution plots organized by individual cortical cases that target distinct zones. SC.m, SC.cm, SC.cl, and SC.l. *X*-axis represents pixel density, *y*-axis represents theta angle from medial to lateral. Columns of panels are organized by ARA level displaying plots of individual cases that preferentially target to each SC zone. Top row plots from cases that target SC.m (n=7), next row SC.cm (n=4), next row SC.cl (n=12), and last row SC.l (n=20). **c)** Average of probability distribution plots from multiple cases. Average is based on cases from data in b.


a
VISam/PHAL
SW120310-03B
VISal/tdTom
SW180302-04A
b
Dorsal View of Cortex
MOs
MOp
SSp
m
ul
n
ll
tr
bfd
am
al
p
pm
l
pl
VIS
Dorsal View of SC:
Representation of
somatotopic map in
intermediate/deep SC layers
rostral
medial
lateral
caudal
n
m
bfd
tr
ul
ll
c
SSp Injections
SC Labeling
ARA 64
SSp-bfd
SW181109-09A
ARA 86
ARA 43
SSp-m
SW170410-04A
ARA 90
ARA 49
SSp-ul
SW170410-04A
ARA 90
ARA 64
SSp-bfd
SW181109-09A
ARA 96
ARA 68
SSp-tr
SW180713-04A
ARA 100
Rostral
SC
Caudal
SC
d
LP/FG
SW141021-02A
LD/FG
SW140603-01A
VM-PCN/FG
SW190213-01A
PSV/FG
SW160525-01A

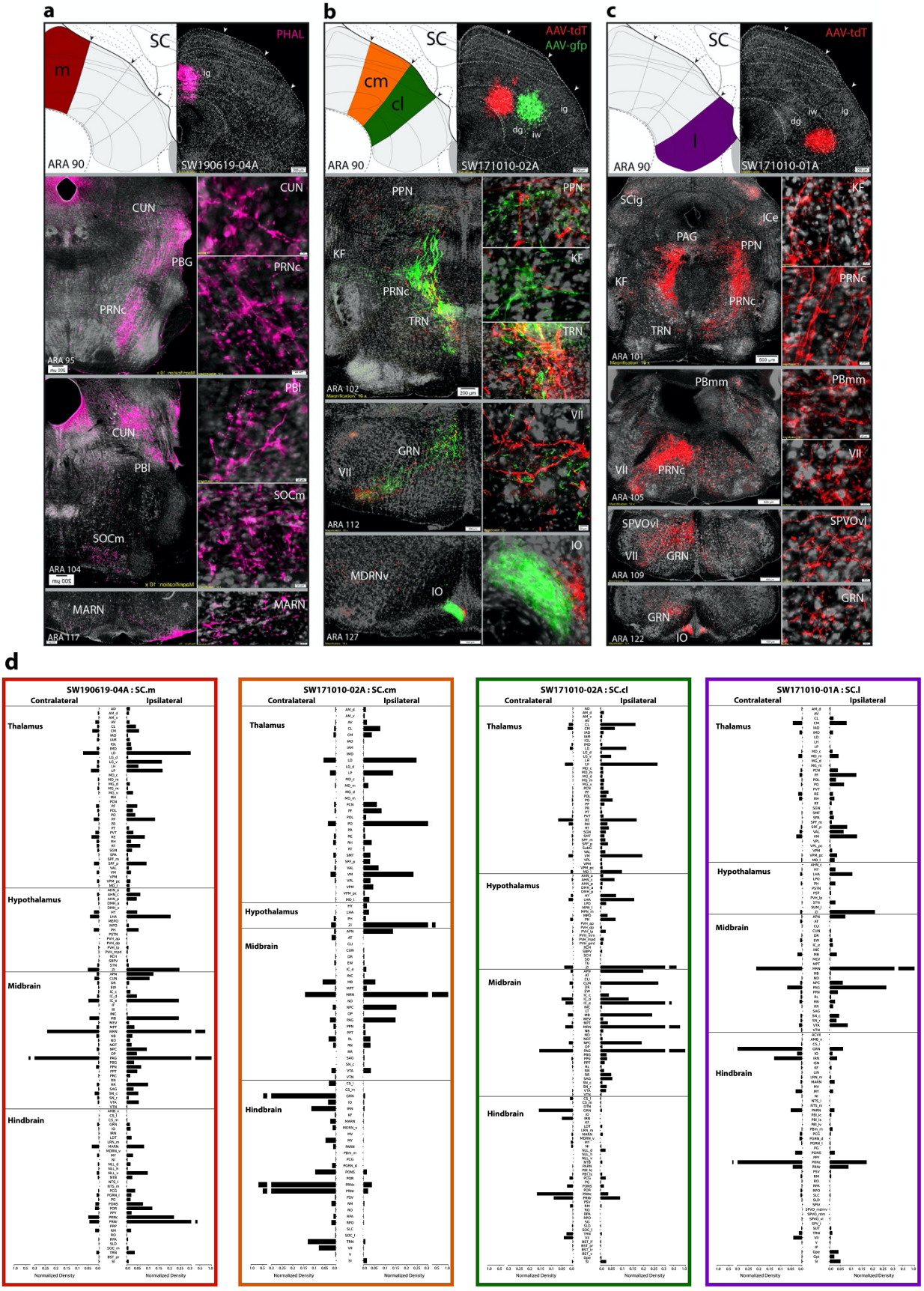
Supplementary Figure 3 | Sensory related connectivity with SC.
a) Raw data of higher order visual areas VISam and VISal. A PHAL injection into VISam (SW120310-03B) projects mainly to intermediate layers in SC.cm, with some terminals in superficial layers. An AAV-tdTomato injection into VISal (SW18080302-04A) projects densely to superficial layers of SC.m with some fibers in the intermediate layers. **b)** Within the cortex, somatic sensorimotor areas are each organized into distinct highly interconnected subnetworks that integrate the somatotopic body map and project subcortically to the SC. Body parts include mouth (m), nose (n), upper limb (ul), lower limb (ll), barrel-field (bfd), and trunk (tr). The dorsal view of the cortical map is color-coded with the dorsal view of the SC body part region it projects to (consistent with the color-coded zones in the SC custom atlas). This organization is conserved topographically as illustrated by dorsal view of SC with overlayed homunculus of somatosensory body representation. **c)** Injection sites into distinct SSp regions project to adjacent and distinct SC.l or SC.cl zones across rostral to caudal levels show adjacent body part projections. Color-code associations: red (SC.m), orange (SC.cm), green (SC.cl), purple (SC.l). Scale bars are 200 µm for all SC panels; 500 µm for injection site panels. **d)** Retrograde labeling of fluorogold (FG)-labeled cells in the SC from four separate injections. First panel: injection into the lateroposterior nucleus of thalamus (LP) back-labeled cells across superficial layers in SC.m and SC.cm zones. Second panel: injection into the laterodorsal nucleus of thalamus (LD) back-labeled cells across superficial and intermediate layers predominantly in SC.cm and SC.m, with sparse cells in SC.cl. Third panel: injection into the ventromedial nucleus (VM) and paracentral nucleus of thalamus (PCN) back-labeled cells in the intermediate and deep layers confined to the SC.l zone.



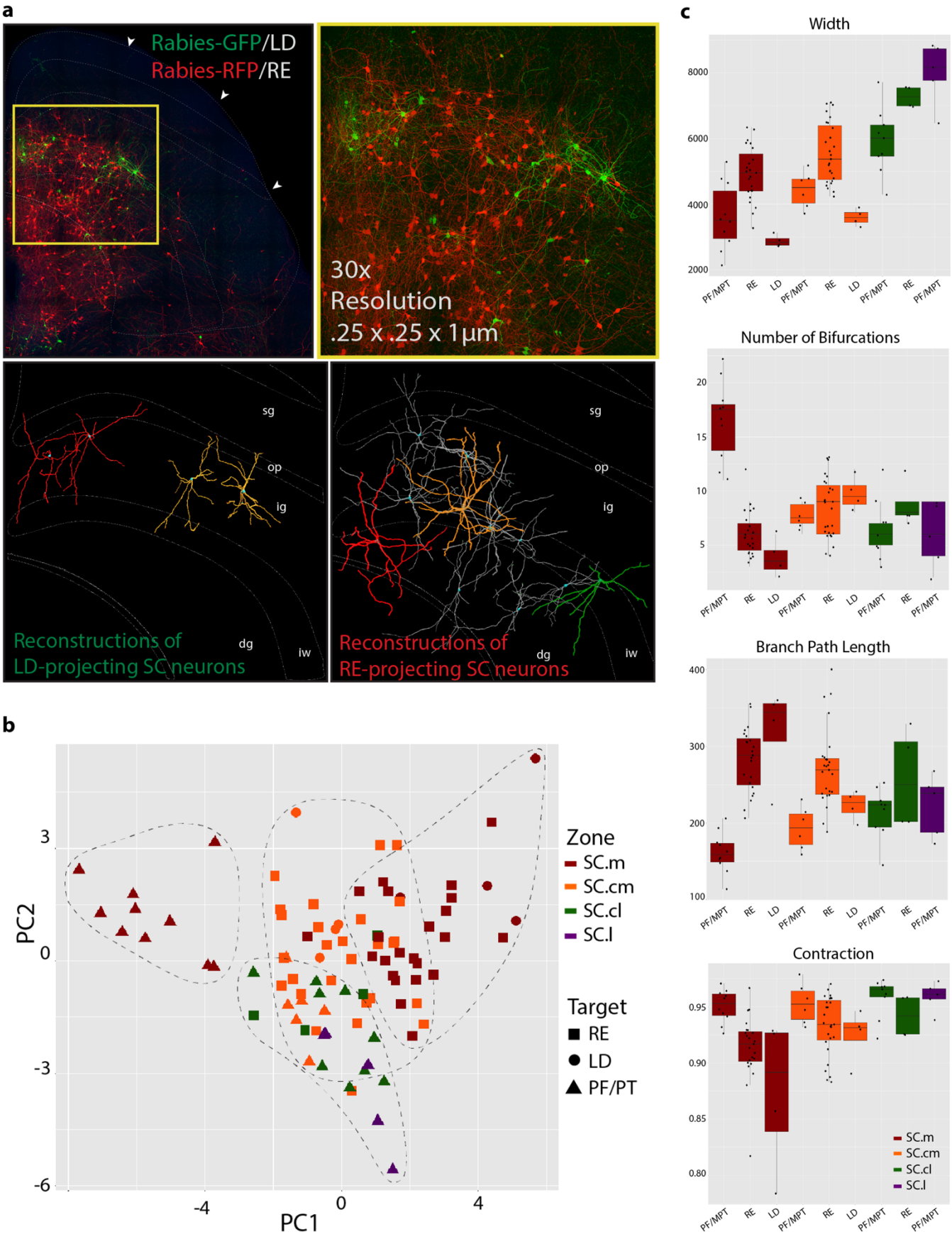
Supplementary Figure 4 | Higher-order cortico-tectal arrays.
a) Data array of individual cases from higher order projections to SC. Injection sites from top to bottom: ACAd-intermediate, ACAv-rostral, RSPd-rostral, RSPv-rostral. **b)** Three cases with single anterograde injections into PL (AAV), ORBl (PHAL), and ORBvl with their respective bilateral projections predominately to SC.cl and SC.l zones at ARA 90. Scale bars are 200 µm.



Supplementary Figure 5 | Injection sites in SC.
a) Anterograde injection sites in superior colliculus. **b)** Retrograde injection sites. The list can be cross-referenced with Supplementary Table 2 for complete details of injection sites, coordinates, and locations. Color-code associations: red (SC.m), orange (SC.cm), green (SC.cl), purple (SC.l). *Abbreviations: AAV, adeno-associated virus; AAV-tdT, AAV-tdTomato; AAV-gfp, AAV-green fluorescent protein; ARA, Allen Reference Atlas; BDA, biotinylated dextran amine; CTB, cholera toxin subunit B conjugates (488, 555, 567); FG, Fluorogold; PHAL, phaseolus vulgaris leucoagglutinin; SC, superior colliculus; m, medial zone; cm, centromedial zone; cl, centrolateral zone; l, lateral zone.*


a
b
c
d
SC
m
cm
cl
l
PHAL
AAV-tdT
AAV-gfp
ig
dg
iw
ARA 90
SW190619-04A
SW171010-02A
SW171010-01A
CUN
PBG
PRNc
PBl
SOCm
MARN
PPN
KF
TRN
GRN
VII
MDRNv
IO
SCig
ICe
PAG
PBmm
SPVOvl
ARA 95
ARA 104
ARA 117
ARA 102
ARA 112
ARA 127
ARA 101
ARA 105
ARA 109
ARA 122
SW190619-04A : SC.m
SW171010-02A : SC.cm
SW171010-02A : SC.cl
SW171010-01A : SC.l
Contralateral
Ipsilateral
Thalamus
Hypothalamus
Midbrain
Hindbrain
Normalized Density

Supplementary Figure 6 | Downstream projections from distinct SC zones to brainstem regions. **a)** PHAL injection into SC.m-ig show prominent ipsilateral projections to midbrain and hindbrain regions. **b)** AAV-tdTomato injection into SC.cm-ig/iw and AAV-gfp injection into SC.cl-ig/iw produce downstream targets similar brainstem regions, with segregated but adjacent outputs in IO. **c)** Downstream projections from AAV-tdTomato injection in SC.l in intermediate white and deep grey layers. See Supplementary Table 1 for complete list of abbreviations. **d)** Quantification of four anterograde injections into each SC zone. Plots represent reconstructed pixel data from output projection terminals of SC throughout the brain. Distributions to contralateral and ipsilateral brain regions are shown, with brain regions organized based on ontological hierarchy in the Allen Reference Atlas (*y*-axis). Data normalization assigns values based on minimum threshold pixel value (0.0006) and maximum threshold pixel value (1) which represents the brain region that receives the highest value of pixels (*x*-axis).


a
Rabies-GFP/LD
Rabies-RFP/RE
30x
Resolution
.25 x .25 x 1µm
sg
op
ig
dg
iw
Reconstructions of
LD-projecting SC neurons
Reconstructions of
RE-projecting SC neurons
b
PC2
PC1
Zone
SC.m
SC.cm
SC.cl
SC.l
Target
RE
LD
PF/PT
c
Width
Number of Bifurcations
Branch Path Length
Contraction
PF/MPT
RE
LD

Supplementary Figure 7 | Characterization of neuronal cell types in the SC based on their anatomical locations, projection targets and neuronal morphology.
a) LD projecting neurons in SC labeled with rabies-GFP in SC.m/cm-ig, and RE projecting neurons labeled with rabies-RFP injected into cells in SC.m/cm-ig/iw/dg. Tissue was processed by the SHIELD clearing protocol and followed by confocal imaging for 3D-reconstruction. Dendrites from LD and RE-projecting SC neurons were reconstructed to visualize differences and dendritic arborizations across SC layers and zones. The LD-projecting SC.m/SC.cm neurons had pyramidal-shaped cell bodies with dendrites that extended dorsally to the superficial optic layers and within the intermediate layers. Of the RE-projecting SC.m/cm neurons, some had dendrites that extended into superficial and intermediate layers, with others that extended into intermediate and deep layers. A subset of neurons extends dendrites horizontally, suggesting they integrate information within the same layer across zones. Other neurons extend vertically, suggesting these receive multimodal information integrated within multiple SC layers. **b)** Principal component analysis (PCA) shows segregation of zone- and target-specific cells based on measured morphological features (see Methods). Number of SC projection neuron reconstructions to RE (n=54), LD (n=8), and PF/MPT (n=31). **c)** Data are presented as whisker plots, where the center line represents the median, box limits show the upper and lower quartiles, and the whiskers represent the minimum and maximum data values. Examples of reports from pairwise tests of morphological parameters that survived the false discovery rate correction tests. Width measures the overall arbor size of neurons. RE-projecting cells in SC.cl and PF/MPT-projecting cells in SC.l are more than twice the width of LD-projecting cells in SC.m. Number of bifurcations compartmentalizes the arborizations into functionally distinct synaptic integration elements. Branch length represents a ratio between the width and number of bifurcations measures, and provides an indication of how they co-vary. It also relates to the number of synapses that can be received on a single computational element. Contraction measures the efficient occupancy of space to reach as many axonal boutons as possible in nearby and further distances. *P*-values for all parameters can be found in Supplementary Table 6. *Abbreviations: LD, laterodorsal nucleus; PF/MPT, parafascicular nucleus of thalamus/midbrain pretectal area; RE, reuniens nucleus of thalamus; SC, superior colliculus; SC layers: zo, zonal; sg, superficial grey; op, optic; ig, intermediate grey; iw, intermediate white; dg, deep grey; dw, deep white.*

Supplementary Table 1 | Brain Region Abbreviation List.

ACAd, Anterior cingulate area cortex, dorsal part
ACAv, Anterior cingulate area cortex, ventral part
AD, Anterodorsal nucleus thalamus
AId, Agranular insular area, dorsal part
AIv, Agranular insular area, ventral part
AIp, Agranular insular area, posterior part
APN, Anterior pretectal nucleus
AUDd, Auditory cortex, dorsal part
AUDp, Primary auditory cortex
AUDv, Auditory cortex, ventral part
AV, Anteroventral nucleus thalamus
BLA, Basolateral amygdalar nucleus
    BLAa, Basolateral amygdalar nucleus, anterior part
    BLAp, Basolateral amygdalar nucleus, posterior part
BMA, Basomedial amygdalar nucleus
    BMAa, Basomedial amygdalar nucleus, anterior part
    BMAp, Basomedial amygdalar nucleus, posterior part
CA1, Field CA1, hippocampal formation
CA3, Field CA3, hippocampal formation
CLA, Claustrum
CM, Centromedial nucleus thalamus
CP, Caudate putamen
        CPc.d, Caudate putamen, caudal, dorsal domain
        CPi.dl, Caudate putamen, intermediate, dorsolateral domain
        CPi.vl, Caudate putamen, intermediate, ventrolateral domain
        CPi.vm, Caudate putamen, intermediate, ventromedial domain
        CPr, Caudate putamen, rostral
CUN, Cuneate nucleus
DN, Dentate nucleus
DG, Dentate gyrus
DTN, Dorsal tegmental nucleus
ENT, Entorhinal cortex
GRN, Gigantocellular reticular nucleus,
GU, Gustatory cortex
Hb, Habenula nucleus thalamus
IAM, Interanteromedial nucleus thalamus
ICe, Inferior colliculus, external part
ILA, Infralimbic area cortex
IO, Inferior olivary nucleus
IRN, Intermediate reticular nucleus
KF, Koelliker-Fuse subnucleus
LA, Lateral amygdalar area
LD, Laterodorsal nucleus thalamus
LG, Lateral geniculate nucleus thalamus
LP, Lateroposterior nucleus thalamus

LM, Lateral mammillary nucleus
MARN, Magnocellular reticular nucleus
MD, Mediodorsal nucleus thalamus
MDRNv, Medullary reticular nucleus, ventral part
MOp, Primary motor cortex
    MOp-oro, Primary motor cortex, orofacial part
MOs, Secondary motor cortex
MOs-fef, Secondary motor cortex, frontal eye field
MRN, Midbrain reticular nucleus
MPT, Midbrain pretectal region
ORBl, Orbitofrontal area cortex, lateral part
ORBm, Orbitofrontal area cortex, medial part
ORBvl, Orbitofrontal area cortex, ventrolateral part
PAG, Periaquaductal gray nucleus
    PAG.dl, Periaquaductal gray nucleus, dorsolateral part
    PAG.vl, Periaquaductal gray nucleus, ventrolateral part
PAR, Parasubiculum
PARN, Parvicellular reticular nucleus
PBG, Parabigeminal nucleus
PBl, Parabrachial nucleus, lateral part
PBmm, Parabrachial nucleus, mediomedial part
PCN, Pericentral nucleus thalamus
PERI, Perirhinal area cortex
PF, Parafascicular nucleus
    PF.ll, Parafascicular nucleus, lower limb
    PF.m, Parafascicular nucleus, mouth domain
    PF.tr, Parafascicular nucleus, trunk domain
    PF.ul, Parafascicular nucleus, upper limb domain
PGRNl, Paragigantocellular reticular nucleus, lateral part
PL, Prelimbic area cortex
PP, Peripenduncular nucleus
PPN, Pedunculopontine nucleus
POST, Postsubiculum
PRE, Presubiculum
PRNc, Pontine reticular nucleus, caudal part
PSV, Principal sensory nucleus of the trigeminal
PTLp, Posterior parietal cortex
RE, Reuniens nucleus thalamus
RSPagl, Retrosplenial area cortex, agranular part
RSPd, Retrosplenial area cortex, dorsal part
RSPv, Retrosplenial area cortex, ventral part
SC, Superior colliculus
    SC.m, Superior colliculus, medial zone
    SC.cm, Superior colliculus, centromedial zone
    SC.cl, Superior colliculus, centrolateral zone
    SC.l, Superior colliculus, lateral zone
SI, Substantia innominate

SNc, Substantia nigra pars compacta
SNr, Substantia nigra pars reticulata
SOCm, Superior olivary complex, medial part
SPFPp, Subparafascicular nucleus, parvicellular part
SPVOl, Spinal motor nucleus of trigeminal, oral lateral part
SPVOvl, Spinal motor nucleus of trigeminal, oral ventrolateral part
SSp, Somatosensory cortex primary
    SSp-bfd, Somatosensory cortex primary, barrel field
    SSp-ll, Somatosensory cortex primary, lower limb
    SSp-m, Somatosensory cortex primary, mouth
    SSp-n, Somatosensory cortex primary, nose
    SSp-tr, Somatosensory cortex primary, trunk
    SSp-ul, Somatosensory cortex primary, upperlimb
SSs, Somatosensory cortex, supplementary
STN, Subthalamic nucleus
SUB, Subiculum
SUBd, Subiculum dorsal
    SUBdd, Subiculum dorsal, dorsal part
    SUBdv, Subiculum dorsal, ventral part
    ProSUB, Prosubiculum
SUBv, Subiculum ventral
    SUBvv, Subiculum ventral, ventral tip
TEa, Temporal association area
TRN, Tegmental reticular nucleus
V, Trigeminal cranial nucleus
VII, Facial motor cranial nucleus
VISC, Visceral cortex
VISal, Visual cortex, anterolateral part
VISam, Visual cortex, anteromedial part
VISl, Visual cortex, lateral part
VISp, Visual cortex, primary
VISpl, Visual cortex, posterolateral part
VISpm, Visual cortex, posteromedial part
VM, Ventromedial nucleus thalamus
vmPFC, Ventromedial prefrontal cortex
VMH, Ventromedial hypothalamic nucleus
    VMH.c, Ventromedial hypothalamic nucleus, central part
    VMH.dm, Ventromedial hypothalamic nucleus, dorsomedial part
    VMH.vl, Ventromedial hypothalamic nucleus, ventrolateral part
ZI, Zona incerta
    ZI.m, Zona incerta, medial part
    ZI.c, Zona incerta, central part
    ZI.l, Zona incerta, lateral part

Supplementary Table 2 | Injection Site List.
Injection site coordinates and tracer information for all cases used throughout the study. Cases are identified by Case ID, Injection Site (ROI, region of interest), Tracer, Tracer Type, Figure reference, ARA Level of injection site, and Coordinates for the injection site based on the Allen Reference Atlas Coordinate Frame. Cortex cases can be cross-referenced to flat map injection site location in Supplementary Figure 1 (n=44 mice with 86 total cortical pathways).

Cortex cases with anterograde projections to Superior Colliculus										
Mouse #	***Pathway #***	**Case ID**	**Injection Site (ROI)**	**Tracer**	**Tracer Type**	**Figure**	**ARA Level**	**ML (X)**	**AP (Y)**	**DV (Z)**
1	***1***	SW110321-04B/A	ACAv interm	PHAL-488	classic / anterograde	3g, 4b	56	0.4	-0.18	-0.75
2	***2***	SW110322-03A	MOs caudal	PHAL-488	classic / anterograde	2g, 4b	58	0.6	-0.38	-0.75
	3	SW110322-03A	SSp-ul	BDA	classic / anterograde	4b	58	2.3	-0.38	-1.5
3	***4***	SW110516-02B/A	SSp-n	PHAL-488	classic / anterograde	2g, 4b	50	3.1	0.45	-2.7
4	***5***	SW110613-03B/A	RSPd rostral	PHAL-488	classic / anterograde	3b, SF4a, 4b	83	0.6	-2.98	-0.25
5	***6***	SW110614-03B/A	RSPd caudal	PHAL-488	classic / anterograde	4b	88	0.6	-3.45	-0.25
6	***7***	SW110615-01B/A	RSPagl	PHAL-488	classic / anterograde	3b, 3g, 4b	91	0.9	-3.78	-0.25
7	***8***	SW110615-03B/A	RSPv rostral	PHAL-488	classic / anterograde	3b, SF4a, 4b	73	0.5	-1.85	-0.75
8	***9***	SW110808-02A	ORBl	PHAL-488	classic / anterograde	SF4b, 4b	37	1.75	1.95	-3.25
9	***10***	SW110808-04A	ORBm	PHAL-488	classic / anterograde	3b, 4b	28	0.6	2.62	-2.4
10	***11***	SW120125-01A	TEa rostral	PHAL-488	classic / anterograde	3b, 4b	78	4.25	-2.35	-3.4
11	***12***	SW120403-02A	ACAv rostral	PHAL-488	classic / anterograde	3b, SF4a, 4b	44	0.5	1.05	-1.8
12	***13***	SW120819-04A	VISl	BDA	classic / anterograde	4b	92	3.5	-3.88	-1.75
	14	SW120819-04A	TEa caudal	PHAL-488	classic / anterograde	3b, 4b	94	4.1	-4.08	-2.5
13	***15***	SW121031-03B/A	SSp-tr/ll	AAV-tdTomato	virus / anterograde	4b	70	1.6	-1.55	-0.75
	16	SW121031-03B/A	ACAd interm	PHAL-647	classic / anterograde	3b, SF4a, 4b	46	0.4	0.85	1.25
	17	SW121031-03B/A	VISam	AAV-GFP	virus / anterograde	4b	83	1.6	-2.98	-0.5
14	***18***	SW121031-04B/A	ACAv interm	PHAL-647	classic / anterograde	3b, 4b	54	0.4	0.2	-1.6
	19	SW121031-04B/A	SSp-tr	AAV-tdTomato	virus / anterograde	2f, 4b	74	2	-1.98	-1
	20	SW121031-04B/A	AUDp interm	AAV-GFP	virus / anterograde	2g, 2f, 3g, 4b	84	4.1	-3.1	-2.5
15	***21***	SW121210-02A	MOs medial	AAV-GFP	virus / anterograde	2g, 4b	49	0.5	0.55	-0.85
16	***22***	SW121221-02A	VISp caudolat	BDA	classic / anterograde	4b	96	2.75	-4.28	-1.25
	23	SW121221-02A	VISp caudomed	PHAL-488	classic / anterograde	2g, 4b	96	2.5	-4.28	-1
17	***24***	SW121221-03A	VISp caudal	BDA	classic / anterograde	2g, 4b	95	1.8	-4.12	-0.75
	25	SW121221-03A	VISp rostral	PHAL-488	classic / anterograde	4b	86	5	-3.28	-1.75
18	***26***	SW151210-01A	ACAd rostral	AAV-tdTomato	virus / anterograde	3b, 3g, 4b	36	0.3	1.85	-1.25
	27	SW151210-01A	SSs	AAV-GFP	virus / anterograde	4b	53	3.25	0.15	-3.25
19	***28***	SW151210-02A	VISam	AAV-tdTomato	virus / anterograde	3e, 3g, 4b	84	1.5	-3.08	-0.75
	29	SW151210-02A	SSp-tr	AAV-GFP	virus / anterograde	3e, 4b	74	2	-1.95	-0.7
20	***30***	SW151211-01A/B	VISp	AAV-GFP	virus / anterograde	3d, 6a, 4b	92	3	-3.88	-1.2
	31	SW151211-01A/B	ACAd rostral	AAV-tdTomato	virus / anterograde	3b, 3d, 6a, 4b	37	0.6	-1.75	-1.25
	32	SW151211-01A/B	RSPv caudal	PHAL-647	classic / anterograde	3b, 3d, 3g, 6a, 4b	90	0.5	-3.68	-0.75
21	***33***	SW151211-02A	ACAd caudal	AAV-tdTomato	virus / anterograde	3e, 4b	58	0.4	-0.38	-1
	34	SW151211-02A	VISam	PHAL-647	classic / anterograde	3e, 4b	86	1.5	-3.28	-0.5
	35	SW151211-02A	SSp-tr	AAV-GFP	virus / anterograde	3g, 4b	76	3	-2.15	-1.2
22	***36***	SW151215-03A	PTLp lat	AAV-tdTomato	virus / anterograde	3b, 4b	82	3.6	-2.88	-1.75
23	***37***	SW170410-03A	SSp-ll	AAV-GFP	virus / anterograde	3g, 4b	56	2.2	-0.18	-1.25
	38	SW170410-03A	SSp-ul	AAV-tdTomato	virus / anterograde	3g, 4b	47	2.5	-0.75	1.5
24	***39***	SW170410-04A	SSp-m	AAV-tdTomato	virus / anterograde	3g,4b, SF3c	43	2.75	1.15	-2.5
	40	SW170410-04A	SSp-ul	AAV-GFP	virus / anterograde	4b, SF3c	49	2.5	0.55	-1.5
25	***41***	SW171101-01A	MOp-oro	PHAL-647	classic / anterograde	3g, 4b	34	2.1	2.1	-2.75
	42	SW171101-01A	MOp-ul	AAV-tdTomato	virus / anterograde	4b	44	1.5	1.1	-1.5
	43	SW171101-01A	MOp-bfd	AAV-GFP	virus / anterograde	3g, 4b	38	1.8	1.65	-1.4
26	***44***	SW171130-02A	MOs lateral	AAV-tdTomato	virus / anterograde	2d, 4b	44	1.1	1.1	-1.5
	45	SW171130-02A	MOs lateral	AAV-GFP	virus / anterograde	2d, 4b	46	1.1	0.85	-1.25
	46	SW171130-02A	MOp-oro	PHAL-647	classic / anterograde	2d, 4b	40	1.4	1.42	-1.6
27	***47***	SW180117-01A	ORBl	PHAL-647	classic / anterograde	3b, 4b	35	1.5	2.1	-3.3
	48	SW180117-01A	MOp-oro	AAV-tdTomato	virus / anterograde	3g, 4b	35	1.5	2.1	-1.75
	49	SW180117-01A	MOp-ul	AAV-GFP	virus / anterograde	3g, 4b	41	1.4	1.35	-1.4
28	***50***	SW180227-01A	ACAd interm	PHAL-647	classic / anterograde	3g, 4b	42	0.5	1.25	-1.4
	51	SW180227-01A	MOs medial	AAV-tdTomato	virus / anterograde	3g, 4b	40	0.6	1.42	-1.25
29	***52***	SW180227-02A	ACAd interm	PHAL-647	classic / anterograde	4b	47	0.3	0.75	-1.2
	53	SW180227-02A	MOs medial	AAV-tdTomato	virus / anterograde	4b	47	0.4	0.75	-0.75
30	***54***	SW180228-03A	ACAv caudal	AAV-tdTomato	virus / anterograde	3b, 4b	58	0.4	-0.38	-1.25
	55	SW180302-04A	VISal	AAV-tdTomato	virus / anterograde	4b	91	3.4	-3.88	-1.6
	56	SW180302-04A	PTLp lat	AAV-GFP	virus / anterograde	4b	82	3.5	-2.88	-1.65
31	***57***	SW180302-05A	VISp caudolat	PHAL-647	classic / anterograde	2c, 4b	94	2.25	-3.88	-1
	58	SW180302-05A	VISal	AAV-tdTomato	virus / anterograde	2c, 4b	90	3.4	-3.68	-1.3
	59	SW180302-05A	PTLp lat	AAV-GFP	virus / anterograde	2c, 4b	81	3.6	-2.88	-1.75
32	***60***	SW180424-01A	PTLp med	AAV-tdTomato	virus / anterograde	3b, 4b	77	2.25	-2.55	-6
	61	SW180424-01A	PTLp med	PHAL-488	classic / anterograde	3g, 4b	77	1.5	-2.55	-6
33	***62***	SW180516-02A	MOp-oro	PHAL-647	classic / anterograde	4b	32	2	2.25	-2.5
	63	SW180516-02A	MOp-bfd	AAV-tdTomato	virus / anterograde	4b	40	1.6	1.42	-1.6
	64	SW180516-02A	MOp-tr	AAV-GFP	virus / anterograde	4b	52	1.6	0.25	-1.3
34	***65***	SW180522-04A	VISl/pl	AAV-tdTomato	virus / anterograde	4b	97	3.5	-4.15	-2
35	***66***	SW180713-03A	VISp	AAV-tdTomato	virus / anterograde	4b	90	2	-3.98	-0.8
	67	SW180713-03A	SSp-tr	PHAL-647	classic / anterograde	4b	68	2	-1.35	-1.25
	68	SW180713-03A	AUDd	AAV-GFP	virus / anterograde	3g	74	4	-1.95	-2.1
36	***69***	SW180713-04A	VISp rostromed	AAV-GFP	virus / anterograde	3g, 6a, 4b	87	2.25	-3.38	-0.75
	70	SW180713-04A	SSp-tr	AAV-tdTomato	virus / anterograde	4b, 6a, SF3c	68	2.5	-1.35	-1.25
	71	SW180713-04A	AUDd	PHAL-647	classic / anterograde	4b, 6a	74	4	-1.95	-2.1
37	***72***	SW180717-03A	PTLp med	PHAL-488	classic / anterograde	3f, 4b	76	1.25	-2.15	-0.6
	73	SW180717-03A	PTLp med	AAV-tdTomato	virus / anterograde	3f, 4b	76	2.1	-2.15	-0.75
38	***74***	SW180815-01A	VISl	AAV-tdTomato	virus / anterograde	3g, 4b	92	3.75	-3.88	-2
39	***75***	SW181109-09A	SSp-bfd	AAV-GFP	virus / anterograde	4b, SF3c	64	3	-0.95	-1.5
	76	SW181109-09A	SSp-bfd	AAV-tdTomato	virus / anterograde	4b, SF3c	64	3.5	-0.95	-2
40	***77***	SW190315-05A	PL	AAV-tdTomato	virus / anterograde	3b, 4b, 6a, SF4b	33	0.4	2.15	-2.3
	78	SW190315-05A	MOs rostral	PHAL-647	classic / anterograde	2e, 4b, 6a	31	1.3	2.35	-1.5
	79	SW190315-05A	MOp-oro	AAV-GFP	virus / anterograde	2e, 4b, 6a	31	2	2.35	-3
41	***80***	SW190315-07A	ILA	PHAL-647	classic / anterograde	3b, 4b	37	0.5	1.75	-3
42	***81***	SW190315-09A	AUDp rostral	AAV-tdTomato	virus / anterograde	4b	76	4.1	-2.15	-2.6
	82	SW190315-09A	AUDp caudal	AAV-GFP	virus / anterograde	4b	86	4.1	-3.28	-2.3
	83	SW190315-09A	AUDv	PHAL-647	classic / anterograde	4b	70	4.2	-1.56	-3.1
43	***84***	SW190327-02A	ORBvl	AAV-GFP	virus / anterograde	3b, 3g, 4b, SF4b	33	1.25	2.15	-3.1
44	***85***	SW190327-04A	RSPv interm	AAV-GFP	virus / anterograde	3b, 4b	88	0.4	-3.45	-0.6
	86	SW190327-04A	VISpm	AAV-tdTomato	virus / anterograde	3g, 4b	94	1.25	-4.08	-0.75

(Supplementary Table 2 : Continued)

Additional cases used throughout study										
Mouse #	***Pathway #***	**Case ID**	**Injection Site (ROI)**	**Tracer**	**Tracer Type**	**Figure**	**ARA Level**	**ML (X)**	**AP (Y)**	**DV (Z)**
45	*87*	SW150916-01A	SC.m	PHAL	classic / anterograde	4b	86	0.5	-3.28	-0.4
	88	SW150916-01A	SC.l	BDA	classic / anterograde	4b	86	1.1	-3.28	-2.5
	89	SW150916-01A	SC.m	CTB-555	classic / retrograde	4b	86	0.5	-3.28	-0.4
	90	SW150916-01A	SC.l	FG	classic / retrograde	4b	86	1.1	-3.28	-2.5
46	*91*	SW150921-01A	SC.m	FG	classic / retrograde	4b	90	0.3	-3.68	-1.6
47	*92*	SW160716-01A	SC.cl/l	PHAL	classic / anterograde	4b	100	0.5	-4.65	-1.3
48	*93*	SW160716-02A	SC.cm	PHAL	classic / anterograde	4b	100	0.3	-4.65	-1.2
	94	SW160716-02A	SC.cm	FG	classic / retrograde	4b	86	0.5	-3.28	-2.3
49	*95*	SW170201-05A	SC.m-iw/dg	CTB-647	classic / retrograde	4b, 5a	96	0.2	-4.28	-1.75
	96	SW170201-05A	SC.cl-dg	CTB-555	classic / retrograde	4b, 5a	96	0.6	-4.28	-2.25
	97	SW170201-05A	SC.l-dg	CTB-488	classic / retrograde	4b, 5a	96	0.9	-4.28	-2.6
50	*98*	SW170201-08A	SC.cm-ig/iw/dg	CTB-555	classic / retrograde	4b, 5a	96	0.6	-4.28	-1.5
	99	SW170201-08A	SC.l-ig	FG	classic / retrograde	4b, 5a	96	1.4	-4.28	-2.4
51	*100*	SW170215-01A	SC.cm	PHAL	classic / anterograde	4b	86	0.5	-3.28	-2.3
52	*101*	SW170315-01A	SC.cl/l	AAV-tdTomato	virus / anterograde	4b	90	1.5	-3.68	-2
53	*102*	SW170315-02A	SC.cm	CTB-647	classic / retrograde	4b	90	0.5	-3.68	-1.5
	103	SW170315-02A	SC.cl	FG	classic / retrograde	4b	90	1.5	-3.68	-2.75
54	*104*	SW170426-04A	SC.l	AAV-tdTomato	virus / anterograde	4b	96	1.1	-4.28	-2.1
55	*105*	SW170830-01A	SC.m	CTB-647	classic / retrograde	4b	100	0.3	-4.65	-1.5
56	*106*	SW170830-02A	SC.cm	CTB-647	classic / retrograde	4b	100	0.25	-4.65	-1.3
	107	SW170830-02A	SC.cl	CTB-488	classic / retrograde	4b	100	0.75	-4.65	-1.3
57	*108*	SW171010-01A	SC.l-ig/iw	AAV-tdTomato	virus / anterograde	4a-b, SF6c	90	1	-3.68	-2.8
	109	SW171010-01A	SC.l-dg	PHAL	virus / anterograde	4a-b	88	1.25	-3.45	-2.75
	110	SW171010-01A	SC.cl-dg	AAV-GFP	virus / anterograde	4a-b	94	1	-4.08	2.5
58	*111*	SW171010-02A	SC.cm	AAV-tdTomato	virus / anterograde	4a-b, SF6b	90	0.55	-3.68	-2.4
	112	SW171010-02A	SC.cl	AAV-GFP	virus / anterograde	4a-b, SF6b	90	0.75	-3.68	-2.5
59	*113*	SW171010-03A	SC.m	AAV-tdTomato	virus / anterograde	4b	96	0.4	-4.28	-1.6
60	*114*	SW180614-07A	SC.m	AAV-tdTomato	virus / anterograde	4b	96	0.25	-4.28	-1.2
	115	SW180614-07A	SC.cl	AAV-GFP	virus / anterograde	4b	96	0.9	-4.28	-1.6
61	*116*	SW190619-02A	SC.m/cm	PHAL	classic / anterograde	4a-b	90	0.5	-3.68	-1.5
	117	SW190619-02A	SC.cl	AAV-tdTomato	virus / anterograde	4a-b	90	0.8	-3.68	-2.1
62	*118*	SW190619-04A	SC.m-iw/dg	PHAL	classic / anterograde	4a-b, SF6a	90	0.25	-3.68	-1.8
63	*119*	SW140603-01A	LD	FG	classic / retrograde	SF3a	69	1.2	-1.45	-2.6
64	*120*	SW140603-03A	MD	FG	classic / retrograde	5c	66	0.3	-1.15	-3.2
65	*121*	SW140916-04A	RE	FG	classic / retrograde	5c	61	0.2	-0.65	-4.7
66	*122*	SW141021-02A	LP	FG	classic / retrograde	SF3a	77	1.6	-2.25	-2.5
67	*123*	SW150716-02A	SNr.cl	PHAL-488	classic / anterograde	5d	84	1.2	-3.08	-5.2
68	*124*	SW171002-03A	SNr.l	PHAL-647	classic / anterograde	5d	84	1	-3.08	-5.25
	125	SW171002-03A	SNr.dl	AAV-RFP	classic / anterograde	5d	84	1.5	-3.08	-5.1
	126	SW171002-03A	SNr.dm	AAV-GFP	classic / anterograde	5d	84	0.75	-3.08	-5.3
69	*127*	SW171213-02A	PF.m	FG	classic / retrograde	5c	75	0.7	-2.05	-3.75
70	*128*	SW180508-04A	SNr.v	PHAL-647	classic / anterograde	5e	84	1.5	-3.08	-5.5
	129	SW180508-04A	SNr.dl	AAV-tdTomato	classic / anterograde	5e	84	1.5	-3.08	-5.1
	130	SW180508-04A	SNr.dm	AAV-GFP	classic / anterograde	5e	84	1	-3.08	-5.5
71	*131*	SW190110-01B	CPc.dm	AAVretro-EF1a-Cre	virus / retrograde	6b	57	1.6	-0.28	-2.5
	132	SW190110-01B	MOs	AAV1.CAG-FLEX-tdTom	virus / anterograde	6b	47	0.5	0.75	-1
72	*133*	SW190207-09A	SNr.m	AAV-RFP	virus / anterograde	5d	84	0.75	-3.08	-5.6
73	*134*	SW190213-01A	VM/PCN	FG	classic / retrograde	SF3a	72	0.6	-1.75	-4
74	*135*	SW190829-03A	ZI.medial	AAV-RFP	virus / anterograde	5b	74	0.6	-1.95	-5
75	*136*	SW190926-10	PF.ul	AAVretro-EF1a-Cre	virus / retrograde	7, 4b	75	0.5	-2.05	-3.4
	137	SW190926-10	SC.l-ig	ıSyn-FLEX-TVA-P2A-GFP-	virus / anterograde	7, 4b	90	1.5	-3.68	-2.5
	138	SW190926-10	SC.l-ig	nvA G-deleted-rabies-mCher	virus / retrograde	7, 4b	90	1.5	-3.68	-2.5
76	*139*	SW191011-01A	ZI.lateral	PHAL-647	classic / anterograde	5b	71	1.75	-1.65	-4.5
77	*140*	SW191011-02A	ZI.central	PHAL-647	classic / anterograde	5b	74	1.25	-1.95	-4.3

Cortex regions which <u>do not</u> send anterograde projections to Superior Colliculus										
78	141	SW121220-05A	AId	BDA	classic / anterograde	n/a	31	2.5	2.35	-3.75
79	142	SW120403-01A	AId	BDA	classic / anterograde	n/a	27	2.3	2.75	-3.75
80	143	SW110321-04B	AIp	BDA	classic / anterograde	n/a	56	4.1	-0.18	-4.6
81	144	SW110906-02A	AIp	PHAL-488	classic / anterograde	n/a	64	4.3	-0.95	-4.5
82	145	SW120118-01A	AId/v	BDA	classic / anterograde	n/a	44	3.4	1.05	-4.5
83	146	SW110906-02A	GU	PHAL-488	classic / anterograde	n/a	38	2.9	1.65	-3.5
84	147	SW120125-03A	GU	PHAL-488	classic / anterograde	n/a	37	2.75	1.75	-3.3
85	148	SW110905-01A	VISC	BDA	classic / anterograde	n/a	54	4	0.02	-4.1
86	149	SW120118-02A	VISC	BDA	classic / anterograde	n/a	66	4.4	-1.15	-4
87	150	SW110906-04A	ECT	BDA	classic / anterograde	n/a	84	4.4	-3.08	-3.95
88	151	SW180815-02A	ENT	AAV-tdTomato	virus / anterograde	n/a	101	4.75	-4.78	-2.75
89	152	SW120403-03A	PERI	BDA	classic / anterograde	n/a	87	4.7	-3.38	-3.9

Supplementary Table 3 | Proportion of labeling values: sensory cortex ROIs to SC zones-layers. Values represent proportion of pixel density for the selected ROI (n=1 per cortical area) distributed across each SC zone across all layers. Far right summations correspond to values used in Figure 2g.

	SC.m							SC.cm							SC.cl							SC.l				Summations			
	SC.m-zo	SC.m-sg	SC.m-op	SC.m-ig	SC.m-iw	SC.m-dg	SC.m-dw	SC.cm-zo	SC.cm-sg	SC.cm-op	SC.cm-ig	SC.cm-iw	SC.cm-dg	SC.cm-dw	SC.cl-zo	SC.cl-sg	SC.cl-op	SC.cl-ig	SC.cl-iw	SC.cl-dg	SC.cl-dw	SC.l-ig	SC.l-iw	SC.l-dg	SC.l-dw	SC.m	SC.cm	SC.cl	SC.l
VISp_caudal	0.45	0.57	0.08	0.00	0.00	0.00	0.00	0.00	0.05	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10	0.06	0.00	0.00
VISam	0.00	0.04	0.13	0.22	0.09	0.03	0.00	0.00	0.07	0.15	0.13	0.07	0.03	0.02	0.00	0.02	0.07	0.02	0.02	0.01	0.02	0.00	0.00	0.00	0.02	0.51	0.47	0.16	0.02
VISal	0.00	0.10	0.12	0.04	0.00	0.00	0.00	0.01	0.34	0.50	0.05	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.26	0.90	0.01	0.00
VISp_caudomed	0.00	0.02	0.03	0.01	0.00	0.00	0.00	0.22	0.53	0.30	0.04	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	1.09	0.01	0.00
VISp_rostromed	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.13	0.13	0.03	0.00	0.00	0.00	0.19	0.44	0.20	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.34	0.85	0.00
AUDp_interm	0.00	0.00	0.00	0.00	0.13	0.07	0.00	0.00	0.00	0.00	0.07	0.20	0.35	0.05	0.00	0.00	0.00	0.00	0.06	0.07	0.02	0.13	0.00	0.02	0.00	0.20	0.67	0.15	0.15
MOs_medial	0.00	0.00	0.02	0.06	0.06	0.01	0.01	0.00	0.00	0.03	0.08	0.05	0.01	0.01	0.00	0.01	0.03	0.13	0.15	0.07	0.06	0.03	0.06	0.08	0.21	0.16	0.18	0.45	0.38
SSp_tr	0.00	0.00	0.01	0.06	0.04	0.00	0.00	0.00	0.00	0.00	0.15	0.05	0.00	0.00	0.00	0.00	0.02	0.25	0.21	0.07	0.01	0.12	0.08	0.08	0.00	0.11	0.20	0.56	0.28
AUDd	0.00	0.00	0.02	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.03	0.00	0.00	0.00	0.00	0.00	0.19	0.13	0.06	0.00	0.09	0.24	0.18	0.00	0.06	0.21	0.38	0.51
MOs_caudal	0.00	0.00	0.00	0.02	0.01	0.01	0.02	0.00	0.00	0.00	0.01	0.03	0.01	0.02	0.00	0.00	0.05	0.12	0.14	0.08	0.06	0.04	0.07	0.07	0.42	0.06	0.07	0.45	0.60
MOs_lateral	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.07	0.26	0.10	0.01	0.00	0.25	0.18	0.10	0.18	0.00	0.02	0.45	0.71
SSp_bfd	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.06	0.00	0.00	0.51	0.30	0.05	0.00	0.00	0.00	0.31	0.86
MOp-bfd	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.15	0.00	0.00	0.00	0.44	0.43	0.02	0.01	0.00	0.00	0.26	0.90
MOp-tr	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.24	0.11	0.02	0.00	0.00	0.66	0.04	0.09	0.00	0.00	0.00	0.38	0.79
MOs_rostral	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.07	0.00	0.00	0.00	0.81	0.19	0.08	0.00	0.00	0.00	0.08	1.08
SSp_ll	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.06	0.01	0.00	0.00	0.50	0.27	0.32	0.00	0.00	0.00	0.09	1.09
MOp-oro	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.01	0.00	0.00	0.50	0.54	0.07	0.00	0.00	0.00	0.06	1.11
SSp_m	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.82	0.32	0.02	0.00	0.00	0.00	0.00	1.16
SSp_n	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.81	0.32	0.04	0.00	0.00	0.00	0.00	1.17
SSp_ul	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.64	0.39	0.14	0.00	0.00	0.00	0.00	1.17
SSs	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.89	0.25	0.03	0.00	0.00	0.00	0.00	1.17

Supplementary Table 4 | Proportion of labeling values: higher order cortex ROIs to SC zones-layers. Values represent proportion of pixel density for the selected ROI (n=1 per cortical area) distributed across each SC zone across all layers. Far right summations correspond to values used in Figure 3b.

	SC.m							SC.cm							SC.cl							SC.l				Summations			
	SC.m-zo	SC.m-sg	SC.m-op	SC.m-ig	SC.m-iw	SC.m-dg	SC.m-dw	SC.cm-zo	SC.cm-sg	SC.cm-op	SC.cm-ig	SC.cm-iw	SC.cm-dg	SC.cm-dw	SC.cl-zo	SC.cl-sg	SC.cl-op	SC.cl-ig	SC.cl-iw	SC.cl-dg	SC.cl-dw	SC.l-ig	SC.l-iw	SC.l-dg	SC.l-dw	SC.m	SC.cm	SC.cl	SC.l
RSPv_caudal	0.01	0.14	0.40	0.25	0.51	0.25	0.04	0.00	0.04	0.16	0.11	0.21	0.03	0.04	0.00	0.01	0.01	0.02	0.01	0.01	0.05	0.00	0.00	0.00	0.00	1.61	0.61	0.12	0.00
RSPv_interm	0.05	0.28	0.57	0.49	0.19	0.04	0.00	0.05	0.10	0.22	0.18	0.03	0.02	0.03	0.00	0.01	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.03	1.64	0.62	0.05	0.03
RSPd_rostral	0.00	0.06	0.30	0.41	0.33	0.06	0.05	0.00	0.02	0.15	0.23	0.30	0.05	0.03	0.00	0.00	0.03	0.01	0.07	0.02	0.04	0.00	0.00	0.01	0.16	1.20	0.79	0.18	0.16
RSPd_caudal	0.00	0.04	0.13	0.22	0.27	0.08	0.00	0.02	0.12	0.25	0.26	0.43	0.22	0.13	0.00	0.01	0.03	0.00	0.03	0.01	0.08	0.00	0.00	0.00	0.00	0.75	1.43	0.16	0.01
RSPagl	0.00	0.02	0.09	0.34	0.37	0.09	0.05	0.00	0.05	0.18	0.28	0.23	0.26	0.19	0.00	0.00	0.01	0.01	0.01	0.04	0.08	0.00	0.00	0.00	0.00	0.98	1.20	0.16	0.00
PTLp_lat	0.00	0.02	0.26	0.58	0.04	0.00	0.00	0.00	0.01	0.12	0.75	0.07	0.00	0.00	0.00	0.00	0.01	0.09	0.17	0.08	0.01	0.01	0.04	0.02	0.05	0.91	0.95	0.37	0.11
TEa_caudal	0.00	0.01	0.06	0.08	0.46	0.25	0.09	0.00	0.01	0.02	0.14	0.21	0.39	0.16	0.00	0.00	0.00	0.03	0.02	0.18	0.23	0.01	0.00	0.00	0.00	0.95	0.92	0.46	0.01
ACAv_caudal	0.00	0.00	0.05	0.30	0.01	0.02	0.01	0.00	0.00	0.16	0.38	0.27	0.21	0.06	0.00	0.02	0.08	0.06	0.28	0.09	0.11	0.00	0.00	0.01	0.23	0.39	1.07	0.63	0.24
ACAv_interm	0.00	0.01	0.05	0.14	0.13	0.10	0.14	0.00	0.01	0.05	0.20	0.26	0.20	0.32	0.00	0.01	0.03	0.04	0.08	0.14	0.23	0.00	0.00	0.03	0.16	0.58	1.03	0.52	0.20
ACAv_rostral	0.00	0.00	0.02	0.08	0.15	0.18	0.15	0.00	0.00	0.01	0.11	0.28	0.26	0.25	0.00	0.00	0.01	0.05	0.14	0.19	0.38	0.00	0.01	0.05	0.01	0.58	0.91	0.77	0.07
RSPv_rostral	0.00	0.00	0.02	0.05	0.01	0.03	0.00	0.00	0.00	0.05	0.30	0.11	0.05	0.03	0.00	0.00	0.04	0.16	0.19	0.19	0.20	0.02	0.01	0.04	0.83	0.11	0.54	0.79	0.90
PTLp_med	0.00	0.00	0.02	0.03	0.36	0.24	0.17	0.00	0.00	0.01	0.03	0.26	0.13	0.18	0.00	0.02	0.07	0.07	0.23	0.20	0.28	0.01	0.01	0.04	0.00	0.82	0.60	0.86	0.06
ACAd_caudal	0.00	0.00	0.00	0.06	0.01	0.02	0.03	0.00	0.00	0.02	0.13	0.10	0.03	0.05	0.00	0.07	0.23	0.21	0.58	0.19	0.29	0.00	0.01	0.04	0.24	0.13	0.34	1.57	0.30
ACAd_interm	0.00	0.00	0.05	0.11	0.05	0.07	0.08	0.00	0.00	0.05	0.15	0.19	0.11	0.32	0.02	0.01	0.10	0.11	0.17	0.17	0.15	0.02	0.06	0.10	0.25	0.36	0.83	0.72	0.42
ACAd_rostral	0.00	0.00	0.00	0.03	0.13	0.06	0.08	0.00	0.00	0.00	0.05	0.27	0.03	0.35	0.00	0.00	0.01	0.10	0.28	0.18	0.10	0.03	0.11	0.28	0.22	0.31	0.70	0.69	0.64
PL	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.02	0.26	0.10	0.17	0.28	0.00	0.00	0.00	0.01	0.25	0.11	0.29	0.00	0.12	0.20	0.52	0.02	0.83	0.65	0.84
ORBm	0.00	0.00	0.01	0.12	0.00	0.00	0.00	0.00	0.00	0.11	0.10	0.12	0.06	0.24	0.00	0.07	0.09	0.07	0.13	0.22	0.50	0.03	0.17	0.32	0.00	0.13	0.62	1.08	0.51
ORBvl	0.00	0.00	0.01	0.04	0.00	0.00	0.00	0.00	0.00	0.02	0.09	0.08	0.03	0.00	0.01	0.00	0.03	0.29	0.41	0.22	0.05	0.06	0.33	0.13	0.55	0.05	0.22	1.01	1.06
ILA	0.00	0.02	0.04	0.09	0.10	0.20	0.08	0.00	0.04	0.09	0.03	0.02	0.01	0.13	0.04	0.12	0.39	0.06	0.05	0.06	0.02	0.13	0.15	0.19	0.26	0.54	0.33	0.74	0.73
TEa_rostral	0.00	0.01	0.09	0.11	0.17	0.20	0.13	0.00	0.00	0.00	0.03	0.14	0.10	0.04	0.00	0.00	0.00	0.03	0.16	0.15	0.16	0.24	0.29	0.23	0.06	0.72	0.30	0.49	0.82
ORBl	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.16	0.11	0.01	0.02	1.00	0.61	0.11	0.14	0.00	0.00	0.30	1.86

Supplementary Table 5 | Morphometric *p*-values.

Table of pairwise comparisons using the Wilcoxon rank sum test. Adjustments for *p*-value were made for multiple comparisons using the false discovery rate (fdr) method. *P*-values are listed for the following neuronal morphometric parameters: contraction, width, number of bifurcations, branch path length, fractal dimension, fragmentation, height, number of branches, and height/width ratio.

Contraction

	PF/MPT - SC.m	RE - SC.m	LD - SC.m	PF/MPT - SC.cm	RE - SC.cm	LD - SC.cm	PF/MPT - SC.cl	RE - SC.cl
RE - SC.m	0.0019	-	-	-	-	-	-	-
LD - SC.m	0.024	0.5253	-	-	-	-	-	-
PF/MPT - SC.cm	0.9578	0.0064	0.049	-	-	-	-	-
RE - SC.cm	0.1386	0.052	0.1172	0.2261	-	-	-	-
LD - SC.cm	0.1439	0.4747	0.2057	0.1412	0.5471	-	-	-
PF/MPT - SC.cl	0.2981	0.0019	0.0503	0.5471	0.0166	0.093	-	-
RE - SC.cl	0.4555	0.1386	0.4747	0.553	0.7076	0.7261	0.1439	-
PF/MPT - SC.l	0.4946	0.0064	0.052	0.7226	0.052	0.093	0.82	0.2981

Width

	PF/MPT - SC.m	RE - SC.m	LD - SC.m	PF/MPT - SC.cm	RE - SC.cm	LD - SC.cm	PF/MPT - SC.cl	RE - SC.cl
RE - SC.m	0.0058	-	-	-	-	-	-	-
LD - SC.m	0.2038	0.00068	-	-	-	-	-	-
PF/MPT - SC.cm	0.0844	0.2038	0.01633	-	-	-	-	-
RE - SC.cm	0.00057	0.03547	0.00057	0.01554	-	-	-	-
LD - SC.cm	0.73327	0.00738	0.03547	0.02743	0.00057	-	-	-
PF/MPT - SC.cl	0.00134	0.01633	0.00719	0.01518	0.35848	0.00719	-	-
RE - SC.cl	0.00599	0.00068	0.03547	0.01633	0.0058	0.03547	0.04028	-
PF/MPT - SC.l	0.00266	0.00057	0.02381	0.00917	0.00188	0.02381	0.00899	0.2038

Number of Bifurcations

	PF/MPT - SC.m	RE - SC.m	LD - SC.m	PF/MPT - SC.cm	RE - SC.cm	LD - SC.cm	PF/MPT - SC.cl	RE - SC.cl
RE - SC.m	0.0003	-	-	-	-	-	-	-
LD - SC.m	0.02569	0.10155	-	-	-	-	-	-
PF/MPT - SC.cm	0.01038	0.06615	0.05382	-	-	-	-	-
RE - SC.cm	0.00037	0.01038	0.02569	0.67932	-	-	-	-
LD - SC.cm	0.03429	0.02823	0.06615	0.14814	0.47941	-	-	-
PF/MPT - SC.cl	0.00514	0.8358	0.14988	0.27131	0.12966	0.10489	-	-
RE - SC.cl	0.03429	0.06615	0.06615	0.67771	0.8358	0.47941	0.17882	-
PF/MPT - SC.l	0.01546	0.9272	0.44167	0.54313	0.17882	0.17241	0.9185	0.48076

Branch Path Length

	PF/MPT - SC.m	RE - SC.m	LD - SC.m	PF/MPT - SC.cm	RE - SC.cm	LD - SC.cm	PF/MPT - SC.cl	RE - SC.cl
RE - SC.m	0.00000072	-	-	-	-	-	-	-
LD - SC.m	0.01028	0.23028	-	-	-	-	-	-
PF/MPT - SC.cm	0.11847	0.00061	0.04699	-	-	-	-	-
RE - SC.cm	0.00000072	0.28913	0.33678	0.00072	-	-	-	-
LD - SC.cm	0.01654	0.03506	0.18701	0.18701	0.06164	-	-	-
PF/MPT - SC.cl	0.01654	0.00148	0.04699	0.30984	0.00548	0.77508	-	-
RE - SC.cl	0.02877	0.51997	0.18701	0.33678	0.82103	0.77143	0.49678	-
PF/MPT - SC.l	0.03796	0.04699	0.18701	0.26623	0.13664	0.90476	0.82103	0.49678

Fractal Dimension

	PF/MPT - SC.m	RE - SC.m	LD - SC.m	PF/MPT - SC.cm	RE - SC.cm	LD - SC.cm	PF/MPT - SC.cl	RE - SC.cl
RE - SC.m	0.00531	-	-	-	-	-	-	-
LD - SC.m	0.06165	0.88571	-	-	-	-	-	-
PF/MPT - SC.cm	0.83907	0.01258	0.08571	-	-	-	-	-
RE - SC.cm	0.12321	0.0526	0.18775	0.15982	-	-	-	-
LD - SC.cm	0.18153	0.40418	0.42562	0.35604	0.76544	-	-	-
PF/MPT - SC.cl	0.08397	0.00012	0.02877	0.18775	0.00088	0.04476	-	-
RE - SC.cl	0.11424	0.42562	0.76544	0.18701	0.63901	0.88571	0.04476	-
PF/MPT - SC.l	0.14259	0.01258	0.04762	0.35532	0.01258	0.04762	0.43636	0.04762

Fragmentation

	PF/MPT - SC.m	RE - SC.m	LD - SC.m	PF/MPT - SC.cm	RE - SC.cm	LD - SC.cm	PF/MPT - SC.cl	RE - SC.cl
RE - SC.m	0.00000026	-	-	-	-	-	-	-
LD - SC.m	0.00621	0.06137	-	-	-	-	-	-
PF/MPT - SC.cm	0.8645	0.000025	0.01805	-	-	-	-	-
RE - SC.cm	0.00000026	0.00621	0.00629	0.000013	-	-	-	-
LD - SC.cm	0.00621	0.51997	0.15238	0.01805	0.1981	-	-	-
PF/MPT - SC.cl	0.0626	0.00000064	0.00629	0.02752	0.00000026	0.00629	-	-
RE - SC.cl	0.00621	0.64756	0.15238	0.01805	0.31541	0.93782	0.00629	-
PF/MPT - SC.l	0.95305	0.0001	0.02597	0.95305	0.00018	0.02597	0.29763	0.02597

Height

	PF/MPT - SC.m	RE - SC.m	LD - SC.m	PF/MPT - SC.cm	RE - SC.cm	LD - SC.cm	PF/MPT - SC.cl	RE - SC.cl
RE - SC.m	0.00000026	-	-	-	-	-	-	-
LD - SC.m	0.0048	0.00057	-	-	-	-	-	-
PF/MPT - SC.cm	0.00327	0.00057	0.02017	-	-	-	-	-
RE - SC.cm	0.0000001	2.7E-12	0.00046	0.0265	-	-	-	-
LD - SC.cm	0.0048	0.03979	0.04472	0.05331	0.06077	-	-	-
PF/MPT - SC.cl	0.00019	0.00103	0.00629	0.30614	0.12993	0.12993	-	-
RE - SC.cl	0.0048	0.00057	0.04472	0.5042	0.0048	0.04472	0.51788	-
PF/MPT - SC.l	0.0024	0.05331	0.04762	0.06679	0.33766	0.55556	0.12993	0.03008

Number of Branches

	PF/MPT - SC.m	RE - SC.m	LD - SC.m	PF/MPT - SC.cm	RE - SC.cm	LD - SC.cm	PF/MPT - SC.cl	RE - SC.cl
RE - SC.m	0.00022	-	-	-	-	-	-	-
LD - SC.m	0.01835	0.10961	-	-	-	-	-	-
PF/MPT - SC.cm	0.00951	0.05037	0.05037	-	-	-	-	-
RE - SC.cm	0.00022	0.00951	0.01835	0.66578	-	-	-	-
LD - SC.cm	0.01835	0.01835	0.06367	0.26852	0.64114	-	-	-
PF/MPT - SC.cl	0.00323	0.74031	0.12302	0.18623	0.12793	0.06367	-	-
RE - SC.cl	0.01835	0.05037	0.06367	1	0.95915	0.4047	0.10961	-
PF/MPT - SC.l	0.0156	1	0.48076	0.23764	0.10961	0.10961	0.95915	0.41544

Height/Width Ratio

	PF/MPT - SC.m	RE - SC.m	LD - SC.m	PF/MPT - SC.cm	RE - SC.cm	LD - SC.cm	PF/MPT - SC.cl	RE - SC.cl
RE - SC.m	0.00000039	-	-	-	-	-	-	-
LD - SC.m	0.00527	0.04482	-	-	-	-	-	-
PF/MPT - SC.cm	0.00527	0.00016	0.01797	-	-	-	-	-
RE - SC.cm	0.00000021	0.00527	0.0058	0.00246	-	-	-	-
LD - SC.cm	0.00527	0.00527	0.04114	0.12857	0.04482	-	-	-
PF/MPT - SC.cl	0.00016	0.01797	0.01185	0.01518	0.84875	0.09375	-	-
RE - SC.cl	0.00527	0.09805	0.04114	0.02981	0.93215	0.12857	0.84875	-
PF/MPT - SC.l	0.00343	0.07907	0.79654	0.00974	0.00016	0.02597	0.0045	0.02597