Supplementary Material

Table 1: Animal information

Acq month	center	Rat_id	Weight (g)	Age (weeks)	Breath rate (bpm)	Temperature (°C)
December	GIN	S1	274	7		
December	GIN	S2	258	7		
December	GIN	S3	286	7		
December	GIN	S4	264	7		
December	GIN	S5	300	7		
December	GIN	S6	294	7	70-82	
December	GIN	S7	304	7	75-97	
December	GIN	S8	304	7	82	
December	GIN	S9	288	7	70-80	
December	GIN	S10	296	7	75-97	
December	CRMBM	S11	249,5	7	60	
December	CRMBM	S12	263,6	7	80-88	36,8
December	CRMBM	S13	267	7	30	34
December	CRMBM	S14	269	7	75	37,2
December	CRMBM	S15	273	7	65-75	37
December	CRMBM	S16	279,9	7	90	37,5
December	CRMBM	S17	277	7	80	37,7
December	CRMBM	S18	277	7	75-80	35,6
December	CRMBM	S19	271,3	7	65	34,6
December	CRMBM	S20	274	7	70	35,9
May	GIN	S21	294	10	70	37,7
May	GIN	S22	256	10	70-75	37,8
May	GIN	S23	278	10	70	38,5
May	GIN	S24	282	10	70	37,9
May	GIN	S25	268	10	65	36,8
May	GIN	S26	274	10	70	37,7
May	GIN	S27	314	10	70	37,5
May	GIN	S28		10	75	37,1
May	GIN	S29	262	10	60	36,8
May	GIN	S30	274	10	65	37
May	CRMBM	S31	297,5	7	60	34,8
May	CRMBM	S32	284,9	7	60	34,8
May	CRMBM	S33	302,7	7	55-55	35,3
May	CRMBM	S34	284,8	7	55-60	35,1
May	CRMBM	S35	290,5	7	70-60	35
May	CRMBM	S36	284,3	7	65	34,4
May	CRMBM	S37	275,7	7	60	34,5
May	CRMBM	S38	286,9	7	120-60	34,8
May	CRMBM	S39	285,5	7	120-60	36,2
May	CRMBM	S40	290	7	65	34,3
Mean			279.40 (SD=13.87)		67.13 (SD=11.42)	36.21 (SD=1.36)

Data

Inter subject variability

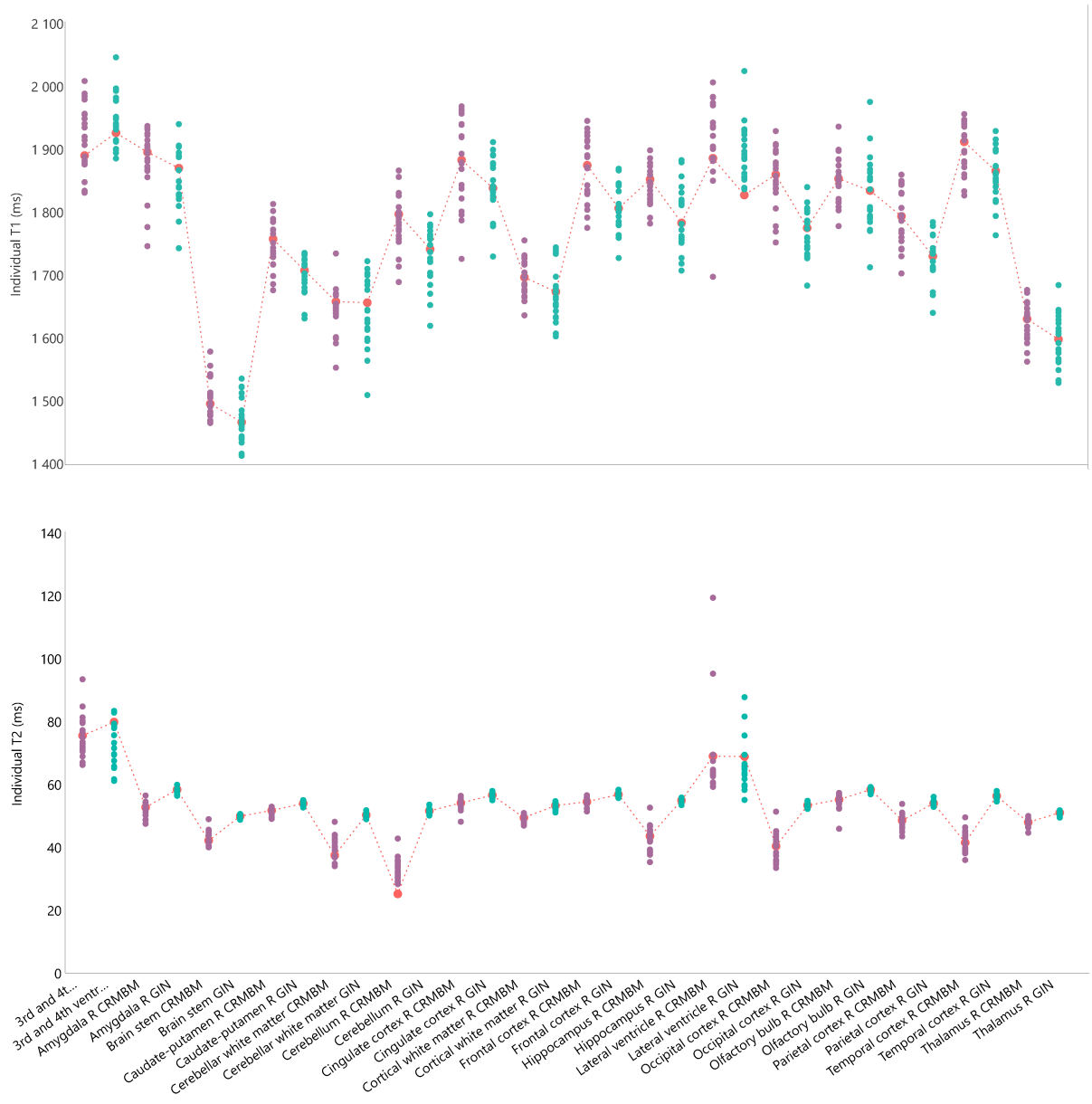

Figure S1: Individual relaxation time values for 13 regions of interest for the left hemisphere. Top: Individual T1 values. **Bottom**: Individual T2 values. Green circles for aC1 values; purple circles for aC2 values and corresponding mean values indicated with a red mark and dash-line. fC2 fitting pipeline and sC3 multi-atlas segmentation were used.

Inter-center variability

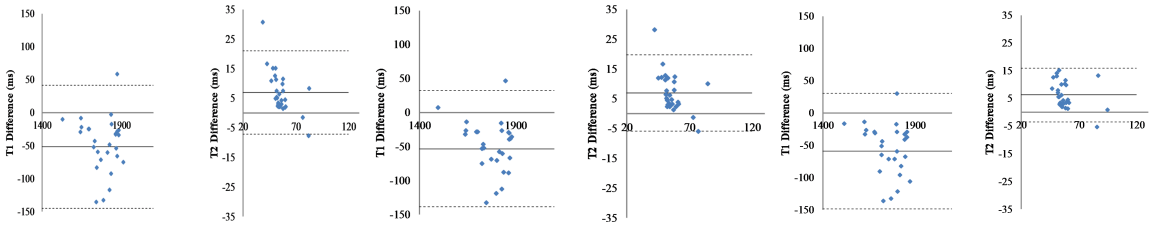

Figure S2: **Inter-center variability**. Differences between T1 (left) and T2 (right) relaxation times computed from data acquired at aC1 (n=20) and aC2 (n=20) for the 29 regions of interest. Fitting pipeline fC1 and Segmentation sC4 (left). Fitting pipeline fC2 and Segmentation sC3 (middle) Fitting pipeline fC3 and Segmentation sC4 (right). Solid line: mean difference. Dash lines: ± 2 standard deviation. X-axis in ms.

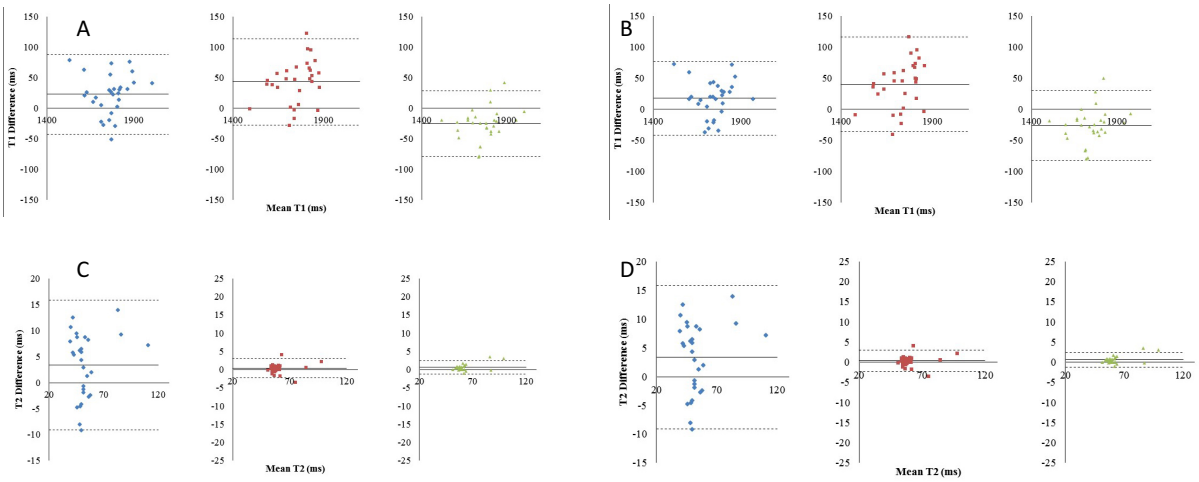

Figure S3. Intra-center reproducibility. Top T1 acquisition: Bland-Altman graph showing the differences in T1 relaxation time (mean values for each ROI) between the two acquisitions versus the corresponding mean T1 value using two processing pipelines. A) Left: S32 (aC2). Middle: S21 (aC1). Right: S22 (aC1). Fitting pipeline fC1, Segmentation sC4. B) Left: S32 (C2). Middle S21 (C1). Right S22 (C1).. Fitting pipeline fC3, Segmentation sC3.

Bottom T2 acquisition: Bland-Altman graph showing the differences in T2 relaxation time (mean values for each ROI) between the two acquisitions versus the corresponding mean T2 value. C) Left: S32 (aC2). Middle: S21 (aC1). Right: S22 (aC1). Fitting pipeline fC1, Segmentation sC4. D) Left: S32 (C2). Middle S21 (C1). Right S22 (C1). Fitting pipeline fC3, Segmentation sC3.

Solid line: mean value, dash lines ± 2 standard deviations.

Pipelines comparison

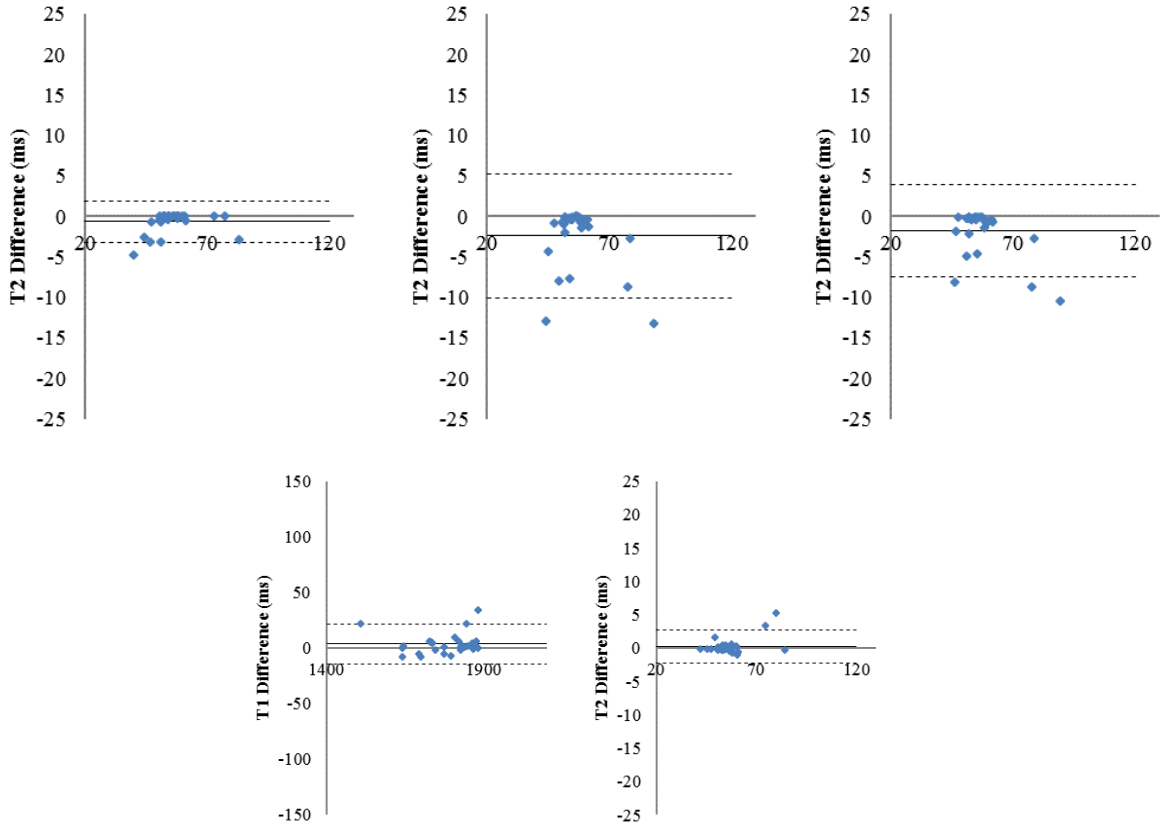

Figure S4: Comparison pipelines. Top: Fitting pipelines. T2 relaxation times values differences computed using different fitting pipelines for all regions of interest (n=29) and average out over the whole set of animals (n=40). Left: T2 values differences for fC1 minus fC2; Middle: T2 values differences for fC1 minus fC3; Right: T2 values differences for fC2 minus fC3. sC4 for segmentation. Solid line: Mean difference. Dash lines: ± 2 standard deviations. **Bottom: Segmentation pipelines.** T1 (left) and T2 (right) relaxation times value differences measured for all regions of interest and average out of the whole set of animals (n=40) using the two different segmentation pipelines sC3 and sC4. fC2 fitting pipeline. Solid line: mean difference. Dash line: ± 2 standard deviations.

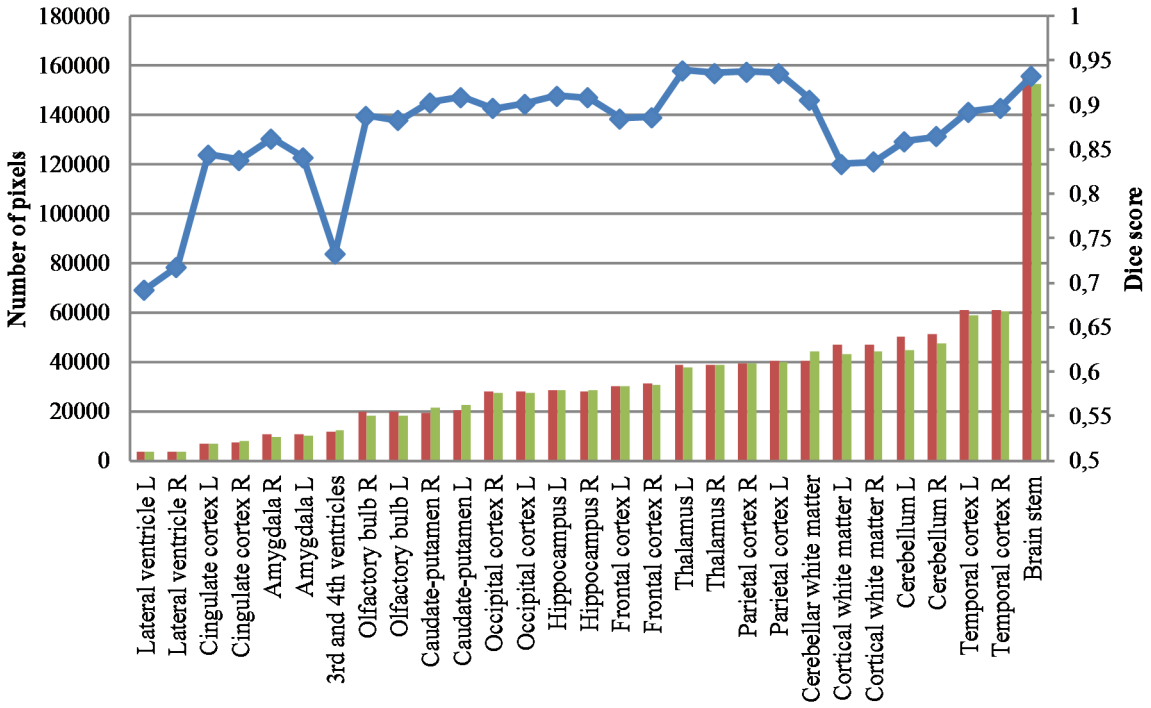

Figure S5: Differences between sC3 (Mircen) and sC4 (ICube) multi-atlas segmentation. Dice score (blue) and number of voxels using sC3 (green) or sC4 (red) in the different regions.