

Supplementary tables

Table S1: Comparison of FCN and Deeplab3 network performances in distinct tasks. Performances were determined by comparing analysis results the test data to the ground truth data (provided by manual labeling). The following quality measures were assessed separately for each class: pixel error rate, rates for true positive (TP), true negative (TN), false positive (FP), false negative (FN) detection as well as specificity (spec.) [defined as $TN/(TN+FP)$] and sensitivity (sens.) [defined as $TP/(TP+FN)$].

D-LAP algorithm		Error [%]	class name	TP [%]	TN [%]	FP [%]	FN [%]	Spec [%]	Sens [%]
1	FCN	5.08	mRNA	0.3	98.9	0.7	0.0	99.3	92.5
			neuron	10.3	84.7	4.1	0.8	95.3	92.7
	DeepLab3	4.39	mRNA	0.0	99.7	0.0	0.3	100.0	0.0
			neuron	11.0	84.6	4.2	0.2	95.2	98.3
2 (human)	FCN	4.13	mRNA	0.2	98.9	0.9	0.0	99.1	94.7
			neuron	5.2	91.0	2.5	1.4	97.3	80.8
	DeepLab3	2.49	mRNA	0.0	99.8	0.0	0.2	100.0	0.0
			neuron	6.1	91.4	2.1	0.4	97.8	95.6
3	FCN	0.64	nucleus	0.0	99.4	0.0	0.6	100.0	1.7
	DeepLab3	0.61	nucleus	0.5	98.9	0.5	0.1	99.5	85.5
4	FCN	0.31	nucleus	0.2	99.5	0.3	0.0	99.7	46.7
	DeepLab3	0.26	nucleus	0.1	99.7	0.2	0.0	99.8	59.8
5	FCN	7.08	nucleus	1.0	97.3	1.5	0.2	98.4	80.9
			cytoplasm	3.7	90.8	4.9	0.7	94.8	83.8
	DeepLab3	3.3	nucleus	0.9	98.5	0.3	0.3	99.7	74.5
			cytoplasm	4.1	92.9	2.2	0.8	97.7	83.7
6	FCN	8.34	nucleus	9.4	87.9	1.2	1.5	98.7	87.2
			cytoplasm	12.4	82.8	4.1	0.8	95.3	93.4
			membrane	2.3	94.2	1.7	1.7	98.2	58.9
	DeepLab3	5.49	nucleus	3.0	93.5	2.5	1.0	97.4	75.6
			cytoplasm	9.7	89.0	0.8	0.5	99.1	95.0
			membrane	11.7	85.2	2.2	0.9	97.5	92.4

Table S2: Details of RNAscope probes. RNAscope target probes were obtained from the Advanced Cell Diagnostics (ACD) library. All probes detected but did not discriminate between known splice variants of the respective target genes. Abbreviations: NCBI: National Center for Biotechnology Information.

Species	Gene	ACD Cat No.	Assay target region according to NCBI Genbank gene accession no. (NM)
mouse	Tyrosine hydroxylase (<i>Th</i>)	317621	483 – 1603 of NM_009377.1 (exon 3-13)
	Cav1.3 (<i>Cacna1d</i>)	502591	522 – 1994 of NM_001302637.1 (exon 1-10)
	Cav2.3 (<i>Cacna1e</i>)	449211	2319 – 3317 of NM_009782.3 (exon 20-22)
human	Tyrosine hydroxylase (<i>TH</i>)	441651	596 – 1681 of NM_199292.2 (exon 4-14)
	Cav1.3 (<i>CACNA1D</i>)	502591	522 – 1994 of NM_001302637.1 (exon 1-10)

Table S3: Mean mRNA molecule numbers in individual mouse SN DA neurons, determined manually and via DLAP algorithm 1. Data and statistics for graphs in Fig. 3b. Number of total analyzed neurons is given by n, N represents the number of analyzed mice. P-values according to Two-way ANOVA followed by Tukey's multiple comparison (significant values in bold red).

		manual				automated				p-value
	n N	median	10-90 %	mean	±SD	median	10-90 %	mean	±SD	
Cav1.3	449	22	9-41	24	12	23	9-41	24	12	0.9988
	3	24	22-24	24	1	24	23-24	24	1	
Cav2.3	372	66	32-113	70	31	65	31-117	70	32/	0.9995
	3	67	66-75	69	5	67	65-75	69	5	
Cav1.3 M vs Cav2.3 M, <0.0001 ; Cav1.3 A vs Cav2.3 A, <0.0001										

Table S4: Single cell correlation analyses between manually and DLAP algorithm 1 determined results. Data and statistics for graphs in Fig. 3c and S1a, according to Pearson correlation (slope of the linear regression with its own 95% confidence interval).

	Cav1.3	Cav2.3
all mice (N = 3)		
Pearson r (95% confidence interval)	0.959 (0.950-0.966)	0.959 (0.950-0.967)
R squared	0.919	0.920
p-value	<0.0001	<0.0001
No. of XY pairs	444	372
Slope (95% confidence interval)	0.998 (0.971-1.026)	0.989 (0.960-1.020)
Proportionality constant α	1.01 ± 0.16	1.00 ± 0.14
mouse 1		
Pearson r (95% confidence interval)	0.964 (0.952-0.973)	0.963 (0.951-0.973)
R squared	0.929	0.928
p-value	<0.0001	<0.0001
No. of XY pairs	168	167
Slope (95% confidence interval)	1.005 (0.962-1.047)	1.004 (0.961-1.047)
Proportionality constant α	1.01 ± 0.15	1.00 ± 0.13
mouse 2		
Pearson r (95% confidence interval)	0.954 (0.936-0.967)	0.964 (0.947-0.976)
R squared	0.910	0.930
p-value	<0.0001	<0.0001
No. of XY pairs	131	96
Slope (95% confidence interval)	0.997 (0.943-1.052)	1.011 (0.954-1.068)
Proportionality constant α	1.00 ± 0.17	1.00 ± 0.14
mouse 3		
Pearson r (95% confidence interval)	0.956 (0.939-0.968)	0.943 (0.917-0.960)
R squared	0.913	0.888
p-value	<0.0001	<0.0001
No. of XY pairs	145	109
Slope (95% confidence interval)	0.991 (0.941-1.042)	0.935 (0.871-0.998)
Proportionality constant α	1.02 ± 0.16	1.01 ± 0.15

Table S5: Details of human *postmortem* midbrain samples. Samples were provided by the German BrainBank. The mean age of the aged cohort was significantly higher compared to that of the adult cohort (** = 0.0012; t-test), the mean RIN was significantly lower (*0.038; t-test), PMI was not significantly different. Abbreviations: AD: Alzheimer's disease; CERAD: Consortium to establish a registry for Alzheimer's disease; f: female; LB: Lewy Body; m: male; NFT: neurofibrillary tangles; PD: Parkinson's disease; PMI: post mortem interval, RIN: RNA integrity number.

Cohort	Age, gender	PMI [h]	RIN	Braak AD/NFT, PD	CERA-stage	LB-pathology
adult	46, f	27	8.5	- , 0	0	no
	34, m	10	8.3	- , 0	0	no
	46, m	19	8.4	- , 0	0	no
<i>mean±SD</i>	42 ± 7**	19 ± 9	8.4 ± 0.1*			
aged	76, m	24	6.9	I, -	A	no
	76, f	11	6.4	0, -	0	no
	81, f	18	4.0	II, -	0	no
<i>mean±SD</i>	78 ± 3	18 ± 7	5.8 ± 1.6			

Table S6: mRNA molecule numbers per human SN DA neuron, determined manually and via DLAP algorithm 2. Data and statistics for graphs in Fig. 4b and c. Number of total analyzed neurons is given by n, N represents the number of analyzed brain samples. P-values according to Two-way ANOVA followed by Tukey's multiple comparison (significant values in bold red).

Cav1.3 mRNA-derived dots/cell										
		manual				automated				p-value
	n N	median	10-90 %	mean	±SD	median	10-90 %	mean	±SD	
adult	223	36	11-68	39	23	37	13-78	42	25	0.6376
	3	38	34-43	38	5	39	34-47	40	7	
aged	258	10	2-32	13	12	12	2-38	17	15	0.2982
	3	16	10-16	14	3	19	13-20	17	4	
adult M vs aged M, <0.0001 ; adult A vs aged A, <0.0001										
rel. BF signal intensity/cell										
		manual				automated				p-value
	n N	median	10-90 %	mean	±SD	median	10-90 %	mean	±SD	
adult	223	16.4	10.8-22.3	16.4	4.5	16.7	11.0-23.1	16.7	4.7	0.9964
	3	16.2	14.5-18.9	16.5	2.2	16.6	14.7-19.0	16.7	2.2	
aged	258	20.4	15.4-26.8	21.2	5.4	20.7	15.6-26.5	21.1	5.1	>0.9999
	3	21.6	20.7-22.2	21.5	0.8	21.5	20.6-22.2	21.4	0.8	
adult M vs aged M, <0.0001 ; adult A vs aged A, <0.0001										
BF-adjusted Cav1.3 mRNA-derived dots/cell										
		manual				automated				p-value
	n N	median	10-90 %	mean	±SD	median	10-90 %	mean	±SD	
adult	180	31	18-50	32	12	31	17-49	32	12	>0.9999
	3	33	30-34	32	2	33	29-34	32	3	
aged	224	17	9-30	19	9	20	11-35	21	10	0.0436
	3	18	14-21	17	3	21	16-22	20	3	
adult M vs aged M, <0.0001 ; adult A vs aged A, <0.0001										

Table S7: Single cell correlation analyses between manually and DLAP algorithm 2 determined results. Data and statistics for graphs in Fig. 4d and S1b and c, according to Pearson correlation (slope of the linear regression with its own 95% confidence interval).

	Cav1.3 mRNA dot counts / cell	rel. BF intensity / cell	Cav1.3 molecules, NM/BF-adjusted according to model
all human samples (N = 6)			
Pearson r (95% confidence interval)	0.964 (0.957-0.970)	0.992 (0.990-0.993)	0.897 (0.877-0.915)
R squared	0.928	0.983	0.805
p-value	<0.0001	<0.0001	<0.0001
No. of XY pairs	481	481	404
Slope (95% confidence interval)	1.034 (1.008-1.060)	0.968 (0.957-0.979)	0.867 (0.827-0.910)
Proportionality constant α	1.28 $\pm$ 1.18	1.01 $\pm$ 0.03	1.10 $\pm$ 0.25
adult samples (N = 3)			
Pearson r (95% confidence interval)	0.975 (0.967-0.980)	0.996 (0.995-0.997)	0.876 (0.837-0.906)
R squared	0.950	0.992	0.767
p-value	<0.0001	<0.0001	<0.0001
No. of XY pairs	223	223	180
Slope (95% confidence interval)	1.044 (1.012-1.076)	1.033 (1.021-1.046)	0.851 (0.781-0.920)
Proportionality constant α	1.23 $\pm$ 1.51	1.01 $\pm$ 0.02	1.01 $\pm$ 0.18
aged samples (N = 3)			
Pearson r (95% confidence interval)	0.890 (0.861-0.913)	0.988 (0.984-0.990)	0.872 (0.836-0.900)
R squared	0.792	0.976	0.872
p-value	<0.0001	<0.0001	<0.0001
No. of XY pairs	258	258	224
Slope (95% confidence interval)	1.130 (1.059-1.201)	0.940 (0.9221-0.958)	0.977 (0.905-1.050)
Proportionality constant α	1.33 $\pm$ 0.78	1.00 $\pm$ 0.03	1.17 $\pm$ 0.27

Table S8: SN DA neuron numbers determined via unbiased stereology and via DLAP algorithm 3 on DAB-stained sections. Data and statistics for graphs in Fig. 5b. Given are the numbers of all TH-positive SN neurons, unilaterally determined for each mouse by stereology or algorithm. N represents the number of analyzed mice. P-values according to Mann-Whitney test (significant values in bold red).

	manual (Stereology)					automated			
	N	median	10-90 %	mean	$\pm$ SD	median	10-90 %	mean	$\pm$ SD
	10	4789	3561-6444	4951	1079	4199	3100-6297	4317	911.8
p-value	Mann-Whitney test: 0.2176								

Table S9: SN DA neuron numbers determined via unbiased stereology and via DLAP algorithm 4 on DAB- and hematoxylin-stained sections. Data and statistics for graphs in Fig. 6b. Given are the numbers of all TH-positive SN neurons/mouse, unilaterally determined by stereology or algorithm. N represents the number of analyzed mice. P-values according to Two-way ANOVA followed by Tukey's multiple comparison (significant values in bold red).

	saline					PD-drug					p-value
	N	median	10-90 %	mean	±SD	N	median	10-90 %	mean	±SD	
manual (stereology)	9	3826	2666-4919	3959	643	12	2556	1209-3587	2504	922	0.022
automated (Aiforia)		6881	5749-8418	7048	823		4619	1680-5913	4108	1596	<0.0001
automated (Wolution)		4797	3442-5084	4614	500		2768	1314-4230	2708	975	0.0010
p-values	saline M vs. saline A (W), 0.7441; drug M vs. drug A (W), 0.9963; saline M vs. saline A (A), <0.0001 ; drug M vs. drug A (A), 0.0036 ; saline A (W) vs saline A (A), <0.0001 ; drug A (W) vs drug A (A), 0.0156										

Table S10: Remaining SN DA neurons after PD-drug (MPTP) treatment determined via unbiased stereology and via DLAP algorithm 4. Data and statistics for graphs in Fig. 6b. Given are the percentages of remaining TH-positive SN neurons/mouse after drug treatment relative to saline, unilaterally determined by stereology or algorithm. N represents the number of analyzed mice. P-values according to Kruskal-Wallis with Dunn's multiple comparison (significant values in bold red).

group	N	median	10-90 %	mean	±SD
manual (Stereology)	12	64.6	30.5-90.6	63.3	23.3
automated (Aiforia)		65.5	23.8-83.9	58.3	22.7
automated (Wolution)		60.0	28.5-91.7	58.7	21.1
p-values	M vs A (W), >0.9999; M vs A (A), >0.9999, A (W) vs A (A), >0.9999				

Table S11: Single cell correlation analyses between manually and DLAP algorithm 3 and 4 determined results Data and statistics for graphs in Fig. 5c/6c, according to Pearson correlation (slope of the linear regression with its own 95% confidence interval).

	juvenile	adult (Aiforia)	adult (Wolution)
Individual sections			
Pearson r (95% confidence interval)	0.796 (0.753-0.832)	0.742 (0.688-0.787)	0.791 (0.746-0.829)
R squared	0.634	0.5500	0.626
p-value	<0.0001	<0.0001	<0.0001
No. of XY pairs	332	3189	319
Slope (95% confidence interval)	2.134 (1.959-2.310)	3.613 (3.251-3.974)	2.389 (2.185-2.593)
Proportionality constant α	2.60 ± 1.00	6.48 ± 8.43	3.86 ± 2.34
Individual sections: PD-drug			
Pearson r (95% confidence interval)		0.860 (0.833-0.882)	0.815 (0.781-0.845)
R squared		0.739	0.665
p-value		<0.0001	<0.0001

No. of XY pairs		433	433
Slope (95% confidence interval)		4.042 (3.814-4.269)	2.383 (2.223-2.544)
Proportionality constant α		5.00 $\pm$ 3.16	3.46 $\pm$ 2.12
Mean (for all animals) per section			
Pearson r (95% confidence interval)	0.889 (0.828-0.929)	0.946 (0.917-0.965)	0.897 (0.844-0.933)
R squared	0.790	0.895	0.805
p-value	<0.0001	<0.0001	<0.0001
No. of XY pairs	73	80	80
Slope (95% confidence interval)	2.383 (2.092-2.674)	4.771 (4.402-5.139)	2.913 (2.590-3.236)
Proportionality constant α	2.58 $\pm$ 0.58	4.81 $\pm$ 1.01	3.20 $\pm$ 0.74
Mean per animal			
Pearson r (95% confidence interval)	0.619 (-0.018-0.898)	0.901 (0.768-0.960)	0.919 (0.808-0.967)
R squared	0.383	0.812	0.845
p-value	0.0564	<0.0001	<0.0001
No. of XY pairs	10	21	21
Slope (95% confidence interval)	0.5229 (-0.018-1.064)	1.639 (1.260-2.018)	1.057 (0.8396-1.275)
Proportionality constant α	0.89 $\pm$ 0.15	1.71 $\pm$ 0.29	1.13 $\pm$ 0.15

Table S12: Number of SN neurons analyzed via DLAP-5. Data and statistics for graphs in Fig. 7c, d, S5b and S6. Given are the numbers of all TH-positive SN neurons/mouse, bilaterally determined by the algorithm, the number of neurons excluded/included neurons for further DAT analysis (criteria specified in Figure S5a), and the determined number of TH-positive DAT-positive/DAT-negative SN neurons. Rostral, medial and caudal locations were determined according to the respective stereotaxic coordinates (bregma: -2.7 mm to -3.1 mm (rostral); -3.1 to -3.5 (medial); -3.5 to -3.9 (caudal)). N represents the number of analyzed mice. P-values according to Wilcoxon or Mann-Whitney tests (significant values in bold red).

	N	mean	$\pm$ SD	%	mean	$\pm$ SD	%	mean	$\pm$ SD	%
		all detected TH+ SN neurons			excluded TH+ neurons from further DAT analysis			included TH+ neurons for further DAT analysis		
whole axis	7	4187	439	100	1171	152	28 $\pm$ 3.3	3015	374	72 $\pm$ 3.3
p-value		MWU: all vs analyzed TH+ neurons 0.006								
		identified TH+ DAT+			identified TH+ DAT-			all included TH+ neurons		
whole axis		2876	340	95.5 $\pm$ 1.5	139	54	4.5 $\pm$ 1.5	3015	374	100
rostral		941	199	98.8 $\pm$ 0.6	12	8	1.2 $\pm$ 0.6	953	203	100
medial		1067	208	94.7 $\pm$ 2.2	60	29	5.3 $\pm$ 2.2	1127	225	100
caudal		838	120	92.6 $\pm$ 2.4	67	25	7.4 $\pm$ 2.4	905	129	100
p-value		Wilcoxon: all analyzed TH+ vs analyzed TH+ DAT+ 0.0156 Chi-square: rostral vs medial, 0.0973 , rostral vs caudal, 0.0304 , caudal vs medial, 0.5515								

Table S13: Semi-quantitative DAT immunofluorescence per mouse SN DA neuron, determined via DLAP algorithm 5. Data and statistics for graphs in Fig. S5c. n represents the number of total analyzed SN DA neurons or the number background images.

mouse No	SN DA neurons					background					threshold
	n	median	10-90 %	mean	±SD	median	n	10-90 %	mean	±SD	BG-RF+2SD
1	3407	3.4	2.2-4.5	3.3	0.9	1.0	56	0.5-1.5	1.0	0.4	1.8
2	2945	3.6	2.4-4.9	3.6	1.0	0.9	58	0.5-1.4	1.0	0.4	1.8
3	2969	3.6	2.3-4.8	3.6	1.0	0.9	56	0.5-1.6	1.0	0.4	1.8
4	3129	3.4	2.1-4.7	3.4	1.0	0.9	60	0.5-1.6	1.0	0.5	1.9
											BG-RF+1.5SD
5	2715	2.9	2.1-3.7	2.9	0.6	1.1	58	0.4-1.6	1.0	0.4	1.9
6	2314	2.6	1.8-3.6	2.6	0.7	0.9	54	0.6-1.6	1.0	0.4	1.8
7	3417	2.6	1.8-3.5	2.6	0.7	0.9	54	0.5-1.6	1.0	0.4	1.9

Table S14: SN neuron size and calbindin_{d28k} (CB) co-expression. Data and statistics for graphs in Fig. 7e and 9b. Sizes were determined for all DAT-pos, and DAT-neg. TH-pos. SN neurons according to via DLAP-5 determined cell body areas. For CB, the mean numbers of CB-pos. and CB-neg. neurons / animal, and the relative % of CB and TH co-expression are given. N represents the number of analyzed mice, n represents the number of analyzed neurons. P-values according to Two-way ANOVA followed by Tukey's multiple comparison (cell size) or Chi-square (CB) test (significant values in bold red).

DAT / CB co-expression of TH+ neurons	n N	relative % (co-expression-type)		cell size [μm ²]		p-value (cell size)
		mean	±SD	mean	±SD	
TH+ DAT+	20211 7	95.4	1.6	213.6 213.8	78.1 12.9	<0.0001
TH+ DAT-	972 7	4.6	1.6	144.5 143.7	60.8 13.2	
TH+ CB+	845 3	10.0	1.0	170.9 170.0	70.1 12.5	<0.0001
TH+ CB-	7601 3	90.0	1.0	204.6 203.7	72.8 10.4	
		% of all DAT+				
TH+ DAT+ CB+	703 3	8.7	0.8	183.2 181.9	67.8 8.5	<0.0001
TH+ DAT+ CB-	7348 3	91.3	0.8	206.3 205.4	72.6 10.1	
		% of all DAT-				
TH+ DAT- CB+	142 3	37.4	7.3	109.7 109.8	44.3 9.7	0.0117
TH+ DAT- CB-	253 3	62.6	7.3	154.9 153.0	58.8 13.6	

Table S15: Semi-quantitative immunofluorescence per mouse SN DA neuron, determined manually and via DLAP algorithm 6. Data and statistics for graphs in Fig. 10b. Number of total analyzed neurons is given by n, N represents the number of analyzed mice. P-values according to Kruskal-Wallis with Dunn's multiple comparison and Mann-Whitney test (significant values in bold red).

TH										
		manual				automated				p-value
ROI	n	median	10-90 %	mean	±SD	median	10-90 %	mean	±SD	
cell body	94	272.8	125.6-534.1	307.9	145.4	284.4	134.4-542.0	317.8	147.3	0.6029
membrane		181.2	81.44-357.1	203.4	101.8	162.0	79.78-316.2	180.3	86.10	0.1707
nucleus		39.52	24.33-75.87	45.78	22.51	46.93	26.80-88.50	52.00	24.14	0.0334
p-values	Kruskal-Wallis: M; cell body vs nucleus, <0.0001; cell body vs membrane, <0.0001; A; cell body vs nucleus, <0.0001; cell body vs membrane, <0.0001;									
Kv4.3										
		manual				automated				p-value
ROI	n	median	10-90 %	mean	±SD	median	10-90 %	mean	±SD	
cell body	94	2.3	1.4-3.8	2.5	1.0	2.3	1.3-3.9	2.6	1.1	0.5862
membrane		9.0	5.1-15.7	9.9	4.0	6.6	3.9-11.5	7.2	3.0	<0.0001
nucleus		0.6	0.3-1.2	0.6	0.4	0.6	0.3-1.1	0.7	0.4	0.9270
p-values	Kruskal-Wallis: M; membrane vs cell body, <0.0001; membrane vs nucleus, <0.0001; A; membrane vs cell body, <0.0001; membrane vs nucleus, <0.0001;									
DAPI										
		manual				automated				p-value
ROI	n	median	10-90 %	mean	±SD	median	10-90 %	mean	±SD	
cell body	94	1.9	1.0-3.2	2.1	1.1	1.6	0.9-2.8	1.8	0.9	0.0765
membrane		0.8	0.5-2.0	1.0	0.6	0.8	0.5-3.4	1.3	1.0	0.3500
nucleus		9.3	6.3-13.5	9.8	2.8	9.3	6.3-13.7	9.7	2.8	0.8212
p-values	Kruskal-Wallis: M; nucleus vs membrane, <0.0001; nucleus vs cell body, <0.0001; A; nucleus vs membrane, <0.0001; nucleus vs cell body, <0.0001;									

Table S16: Single cell correlation analyses between manually and DLAP-6 determined results. Data and statistics for graphs in Fig. 10c., according to Pearson correlation (slope of the linear regression with its own 95% confidence interval).

	Cytoplasm: TH	Membrane: Kv4.3	Nucleus: DAPI
Pearson r (95% confidence interval)	0.995 (0.992-0.997)	0.966 (0.949-0.977)	0.996 (0.994-0.008)
R squared	0.990	0.933	0.993
p-value	<0.0001	<0.0001	<0.0001
No. of XY pairs	94	94	94
Slope (95% confidence interval)	1.01 (0.989-1.029)	0.737 (0.696-0.777)	0.986 (0.969-1.00)
Proportionality constant α	0.96 ± 0.05	1.38 ± 0.15	1.01 ± 0.03

Table S17: Relative immunofluorescence-signal quantification for Kv4.3 in SN DA neuron membranes from WT and Kv4.3 KO mice, determined via DLAP-6. Data and statistics for graphs in Fig. 10e & S7. Number of analyzed neurons is given by n, N represents the number of analyzed mice. P-values according Mann-Whitney test (significant values in bold red).

WT					Kv4.3 KO					p-value
n	median	10-90 %	mean	±SD	n	median	10-90 %	mean	±SD	
N					N					
179	7.2	4.4-11.5	7.7	2.9	200	0.7	0.21-1.5	0.8	0.5	<0.0001
2	7.7	7.2-8.2	7.7	0.7	2	0.9	0.5-1.3	0.9	0.6	