Supplementary Tables

Title: A foundation model for three-dimensional anatomical reconstruction from sparse X-ray projections

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Contents. Supplementary Tab. 1–34. Unless stated otherwise, every statistic is a mean over the full test set with a 95% confidence interval from a bootstrap over patients (10,000 resamples); differences between methods use paired resampling of the same patients (Methods, Confidence intervals and statistical tests). PSNR and SSIM are computed over $[-1{,}024, 1{,}024]$ HU.

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Supplementary Tab. 1 | Reconstruction fidelity with four projections. All methods were trained under the same training budget and early-stopping rule.

Dataset	n	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**
PSNR (dB)							
CT-RATE	602	23.29 [23.15, 23.43]	23.50 [23.34, 23.64]	25.60 [25.43, 25.77]	25.17 [25.07, 25.26]	27.16 [26.99, 27.31]	29.41 [29.25, 29.56]
TotalSegmentator	79	22.70 [22.45, 22.94]	22.74 [22.50, 22.97]	24.73 [24.39, 25.06]	24.93 [24.70, 25.15]	26.63 [26.25, 27.01]	29.37 [28.98, 29.76]
MSD	209	24.04 [23.86, 24.21]	24.16 [23.97, 24.34]	26.50 [26.23, 26.76]	26.29 [26.13, 26.44]	28.44 [28.15, 28.71]	30.27 [29.98, 30.55]
AbdomenCT-1K	158	23.76 [23.54, 23.96]	23.64 [23.42, 23.85]	25.65 [25.39, 25.90]	26.00 [25.81, 26.18]	28.04 [27.75, 28.32]	29.74 [29.44, 30.04]
AMOS	75	23.63 [23.43, 23.81]	23.69 [23.50, 23.88]	25.35 [25.12, 25.57]	25.71 [25.55, 25.87]	28.00 [27.72, 28.26]	29.65 [29.37, 29.91]
CQ500	71	23.18 [22.51, 23.74]	24.16 [23.70, 24.50]	26.53 [26.12, 26.85]	26.29 [25.92, 26.56]	29.49 [28.95, 29.93]	30.86 [30.42, 31.24]
ToothFairy3	77	24.16 [23.87, 24.41]	24.19 [23.90, 24.45]	26.51 [26.06, 26.93]	26.29 [26.08, 26.49]	29.36 [28.98, 29.71]	30.82 [30.47, 31.16]
VerSe	50	22.15 [21.76, 22.56]	21.93 [21.52, 22.35]	22.34 [21.92, 22.76]	24.12 [23.63, 24.63]	25.53 [24.75, 26.36]	27.61 [26.75, 28.50]
SSIM ($\times$100)							
CT-RATE	602	62.85 [62.10, 63.56]	72.00 [71.48, 72.49]	78.27 [77.70, 78.84]	77.61 [77.19, 78.03]	83.46 [83.02, 83.90]	87.15 [86.76, 87.53]
TotalSegmentator	79	60.98 [59.01, 62.73]	67.33 [65.76, 68.89]	73.57 [72.01, 75.17]	72.68 [71.61, 73.65]	81.27 [80.19, 82.38]	87.46 [86.74, 88.17]
MSD	209	67.15 [66.50, 67.80]	72.48 [71.60, 73.36]	81.35 [80.33, 82.34]	81.48 [80.82, 82.11]	84.68 [83.85, 85.49]	86.98 [86.51, 87.42]
AbdomenCT-1K	158	75.32 [74.47, 76.16]	72.63 [71.48, 73.76]	78.68 [77.56, 79.79]	80.05 [79.38, 80.70]	84.22 [83.39, 85.03]	88.45 [87.90, 88.99]
AMOS	75	69.15 [67.63, 70.49]	64.08 [62.89, 65.29]	70.17 [69.01, 71.35]	82.29 [81.81, 82.75]	86.43 [85.91, 86.92]	90.18 [89.78, 90.57]
CQ500	71	71.23 [69.11, 72.76]	78.75 [76.58, 80.35]	87.57 [85.76, 89.00]	88.10 [86.70, 89.04]	93.46 [91.78, 94.66]	95.59 [94.65, 96.21]
ToothFairy3	77	78.04 [77.18, 78.82]	85.37 [84.26, 86.35]	90.73 [89.45, 91.85]	88.06 [87.47, 88.59]	94.25 [93.54, 94.86]	95.46 [95.09, 95.80]
VerSe	50	54.02 [51.03, 56.81]	61.83 [58.17, 65.48]	64.95 [60.26, 69.59]	73.33 [70.64, 76.00]	77.25 [74.18, 80.35]	81.43 [79.33, 83.52]

Supplementary Tab. 2 | Reconstruction fidelity with eight projections. All methods were trained under the same training budget and early-stopping rule.

Dataset	n	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**
PSNR (dB)							
CT-RATE	602	24.85 [24.75, 24.95]	24.77 [24.61, 24.93]	27.39 [27.24, 27.54]	26.01 [25.93, 26.08]	29.32 [29.18, 29.45]	31.39 [31.25, 31.54]
TotalSegmentator	79	24.50 [24.28, 24.72]	23.52 [23.31, 23.74]	26.67 [26.36, 26.97]	26.53 [26.33, 26.73]	28.76 [28.45, 29.07]	31.37 [31.03, 31.72]
MSD	209	25.48 [25.33, 25.63]	25.58 [25.42, 25.73]	28.25 [27.98, 28.49]	27.32 [27.19, 27.44]	30.86 [30.59, 31.11]	32.74 [32.43, 33.03]
AbdomenCT-1K	158	24.57 [24.44, 24.71]	25.04 [24.87, 25.20]	27.64 [27.42, 27.85]	27.12 [26.99, 27.24]	30.65 [30.37, 30.92]	32.23 [31.91, 32.53]
AMOS	75	25.16 [24.98, 25.33]	25.09 [24.92, 25.25]	27.32 [27.10, 27.53]	26.94 [26.81, 27.07]	30.85 [30.55, 31.11]	31.67 [31.40, 31.93]
CQ500	71	25.02 [24.63, 25.32]	25.70 [25.34, 25.95]	28.33 [27.84, 28.68]	27.08 [26.70, 27.32]	31.96 [31.40, 32.38]	33.06 [32.66, 33.40]
ToothFairy3	77	24.77 [24.45, 25.05]	25.14 [24.91, 25.36]	28.38 [27.98, 28.74]	27.29 [27.12, 27.44]	31.60 [31.25, 31.94]	33.30 [32.94, 33.66]
VerSe	50	23.85 [23.39, 24.31]	23.11 [22.74, 23.49]	23.58 [23.23, 23.94]	25.82 [25.46, 26.18]	27.26 [26.72, 27.83]	29.48 [28.73, 30.25]
SSIM ($\times$100)							
CT-RATE	602	72.32 [71.67, 72.92]	76.91 [76.39, 77.39]	82.04 [81.59, 82.49]	80.03 [79.65, 80.40]	80.69 [80.22, 81.14]	89.18 [88.85, 89.50]
TotalSegmentator	79	75.86 [74.87, 76.88]	63.81 [61.88, 65.80]	77.44 [76.11, 78.82]	77.99 [76.97, 79.04]	83.39 [82.32, 84.49]	90.46 [89.86, 91.05]
MSD	209	80.09 [79.52, 80.66]	80.79 [80.13, 81.44]	84.73 [83.87, 85.55]	80.46 [80.05, 80.86]	90.07 [89.52, 90.59]	92.09 [91.66, 92.50]
AbdomenCT-1K	158	68.30 [67.22, 69.39]	77.63 [76.77, 78.48]	83.11 [82.20, 83.99]	82.92 [82.47, 83.37]	86.94 [86.17, 87.71]	90.17 [89.82, 90.50]
AMOS	75	76.27 [74.73, 77.63]	70.50 [69.29, 71.76]	76.69 [75.55, 77.82]	85.20 [84.75, 85.62]	89.76 [89.35, 90.14]	92.18 [91.84, 92.50]
CQ500	71	79.84 [78.21, 81.12]	83.67 [82.16, 84.85]	89.72 [88.00, 90.99]	88.83 [87.44, 89.72]	94.70 [93.26, 95.67]	96.89 [96.14, 97.37]
ToothFairy3	77	82.64 [81.67, 83.55]	87.87 [86.93, 88.69]	92.58 [91.57, 93.46]	90.07 [89.62, 90.47]	95.82 [95.32, 96.24]	96.64 [96.35, 96.90]
VerSe	50	70.73 [68.59, 72.79]	66.36 [62.46, 70.22]	68.86 [64.76, 72.95]	77.84 [76.07, 79.52]	80.30 [77.66, 82.92]	86.23 [84.48, 87.90]

Supplementary Tab. 3 | Paired reconstruction differences between SPARC and the strongest competing method. The comparator is the competing method with the highest mean in that dataset, number of projections and metric. Differences are SPARC minus comparator, with paired 95% confidence intervals in brackets from a bootstrap over patients (10,000 resamples of the same patients). Improved: the percentage of volumes in which SPARC scored higher. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

			PSNR (dB)				SSIM (×100)			
Projections	Dataset	n	Comparator	Difference	*P*	Improved	Comparator	Difference	*P*	Improved
4	CT-RATE	602	DeepSparse	+2.25 [2.16, 2.35]	<0.001	100.0%	DeepSparse	+3.69 [3.55, 3.83]	<0.001	100.0%
	TotalSegmentator	79	DeepSparse	+2.74 [2.59, 2.89]	<0.001	100.0%	DeepSparse	+6.19 [5.64, 6.72]	<0.001	98.7%
	MSD	209	DeepSparse	+1.84 [1.76, 1.92]	<0.001	100.0%	DeepSparse	+2.29 [1.78, 2.85]	<0.001	66.0%
	AbdomenCT-1K	158	DeepSparse	+1.70 [1.62, 1.79]	<0.001	100.0%	DeepSparse	+4.23 [3.83, 4.64]	<0.001	100.0%
	AMOS	75	DeepSparse	+1.65 [1.49, 1.81]	<0.001	100.0%	DeepSparse	+3.75 [3.49, 4.03]	<0.001	100.0%
	CQ500	71	DeepSparse	+1.37 [1.19, 1.56]	<0.001	100.0%	DeepSparse	+2.13 [1.50, 2.94]	<0.001	100.0%
	ToothFairy3	77	DeepSparse	+1.46 [1.34, 1.58]	<0.001	100.0%	DeepSparse	+1.21 [0.89, 1.60]	<0.001	98.7%
	VerSe	50	DeepSparse	+2.07 [1.88, 2.27]	<0.001	100.0%	DeepSparse	+4.18 [2.82, 5.50]	<0.001	68.0%
8	CT-RATE	602	DeepSparse	+2.07 [2.01, 2.14]	<0.001	100.0%	C^2RV	+7.13 [6.88, 7.40]	<0.001	100.0%
	TotalSegmentator	79	DeepSparse	+2.62 [2.50, 2.73]	<0.001	100.0%	DeepSparse	+7.06 [6.25, 7.91]	<0.001	98.7%
	MSD	209	DeepSparse	+1.88 [1.81, 1.96]	<0.001	100.0%	DeepSparse	+2.02 [1.83, 2.22]	<0.001	98.1%
	AbdomenCT-1K	158	DeepSparse	+1.58 [1.49, 1.67]	<0.001	100.0%	DeepSparse	+3.23 [2.68, 3.78]	<0.001	80.4%
	AMOS	75	DeepSparse	+0.83 [0.72, 0.94]	<0.001	98.7%	DeepSparse	+2.43 [2.16, 2.70]	<0.001	97.3%
	CQ500	71	DeepSparse	+1.10 [0.94, 1.30]	<0.001	100.0%	DeepSparse	+2.19 [1.66, 2.91]	<0.001	94.4%
	ToothFairy3	77	DeepSparse	+1.70 [1.57, 1.82]	<0.001	100.0%	DeepSparse	+0.82 [0.63, 1.08]	<0.001	100.0%
	VerSe	50	DeepSparse	+2.21 [1.98, 2.46]	<0.001	100.0%	DeepSparse	+5.93 [4.66, 7.18]	<0.001	90.0%

Supplementary Tab. 4 | Hounsfield-unit error by intensity band. Mean absolute error and mean signed error between each method's reconstruction and the ground-truth CT, per volume and then averaged, on the full CT-RATE and TotalSegmentator test sets; a negative signed error means the reconstruction underestimates attenuation. The last block gives SPARC's paired difference in mean absolute error from the strongest competing method, that is, the competing method with the lowest mean absolute error in that band. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

Projections	Method	All voxels	Air	Lung	Soft tissue	Bone
Mean absolute error (HU)						
CT-RATE (602 volumes)						
4	DIF-Net	59.9 [58.7, 61.2]	31.7 [30.8, 32.6]	137.1 [132.9, 141.3]	80.6 [76.6, 85.2]	353.9 [345.3, 363.6]
	DIF-Gaussian	53.3 [51.6, 55.1]	23.0 [21.6, 24.7]	129.1 [125.1, 133.3]	78.7 [74.7, 83.5]	326.4 [318.1, 336.0]
	C^2RV	46.3 [44.8, 47.7]	16.8 [15.9, 17.8]	122.1 [117.4, 127.1]	71.6 [68.7, 75.3]	292.5 [286.1, 299.2]
	SVCT	53.3 [52.3, 54.4]	31.6 [30.8, 32.4]	105.5 [102.0, 109.3]	73.0 [70.6, 75.8]	277.4 [270.7, 284.5]
	DeepSparse	37.9 [36.9, 39.0]	11.5 [10.9, 12.1]	99.9 [96.4, 103.5]	66.1 [63.5, 69.2]	254.7 [247.8, 262.4]
	SPARC	29.5 [28.7, 30.4]	9.3 [8.9, 9.7]	78.9 [76.4, 81.5]	48.4 [47.7, 49.1]	186.3 [183.1, 189.6]
8	DIF-Net	45.4 [44.6, 46.3]	21.2 [20.7, 21.7]	107.5 [104.5, 110.7]	63.4 [61.5, 65.5]	243.3 [238.5, 248.4]
	DIF-Gaussian	44.0 [42.1, 46.3]	19.2 [17.2, 21.7]	100.9 [98.1, 103.9]	62.3 [60.6, 64.4]	236.8 [231.1, 242.8]
	C^2RV	37.7 [36.7, 38.8]	12.8 [12.2, 13.4]	98.7 [95.0, 102.6]	60.2 [58.4, 62.5]	242.0 [237.1, 247.2]
	SVCT	48.8 [48.0, 49.7]	30.5 [29.8, 31.2]	93.2 [91.0, 95.5]	63.6 [62.4, 64.9]	237.4 [233.1, 241.7]
	DeepSparse	34.1 [33.5, 34.8]	14.7 [14.4, 15.0]	80.4 [77.9, 83.2]	51.6 [50.5, 52.9]	196.6 [193.2, 200.2]
	SPARC	25.2 [24.6, 25.9]	8.6 [8.3, 8.9]	65.0 [63.1, 67.1]	41.3 [40.8, 41.8]	142.9 [140.4, 145.5]
TotalSegmentator (79 volumes)						
4	DIF-Net	69.6 [66.8, 72.7]	40.8 [38.2, 43.6]	175.1 [165.9, 184.9]	87.7 [81.9, 93.9]	352.5 [340.7, 364.4]
	DIF-Gaussian	63.8 [60.2, 67.6]	29.4 [26.2, 32.8]	159.5 [151.1, 168.5]	106.3 [99.0, 113.9]	419.7 [408.7, 430.7]
	C^2RV	53.1 [49.7, 56.7]	25.2 [21.9, 28.7]	174.5 [162.7, 187.1]	78.3 [73.0, 83.9]	351.2 [341.1, 361.4]
	SVCT	58.9 [56.6, 61.3]	39.5 [37.4, 41.8]	146.9 [139.4, 154.7]	69.3 [65.9, 72.8]	287.0 [276.7, 297.5]
	DeepSparse	42.8 [40.0, 45.7]	18.1 [16.0, 20.5]	136.7 [128.5, 145.4]	64.7 [60.9, 68.8]	249.5 [239.1, 260.4]
	SPARC	29.7 [27.9, 31.6]	11.2 [10.2, 12.2]	92.9 [88.1, 97.7]	47.5 [45.1, 50.1]	179.1 [170.5, 188.5]
8	DIF-Net	46.5 [43.6, 49.5]	21.1 [19.2, 23.2]	144.1 [137.3, 151.2]	67.4 [64.1, 71.0]	233.9 [227.3, 240.6]
	DIF-Gaussian	60.0 [56.2, 63.8]	29.1 [25.9, 32.5]	169.6 [163.4, 175.8]	94.1 [88.8, 99.7]	334.3 [325.6, 343.2]
	C^2RV	44.1 [41.3, 46.9]	19.1 [16.8, 21.4]	137.8 [129.0, 147.0]	71.3 [67.0, 75.7]	255.4 [249.2, 261.9]
	SVCT	46.5 [44.5, 48.5]	31.5 [29.7, 33.2]	111.0 [105.9, 116.3]	59.1 [55.8, 62.5]	196.3 [187.3, 205.6]
	DeepSparse	35.5 [33.3, 37.7]	14.0 [12.4, 15.6]	97.0 [92.2, 101.9]	62.2 [59.8, 64.6]	214.1 [207.2, 221.0]
	SPARC	23.8 [22.4, 25.3]	8.7 [8.0, 9.5]	72.6 [69.4, 75.8]	39.0 [37.3, 40.9]	132.7 [126.9, 138.6]
Mean signed error, reconstruction minus CT (HU)						
CT-RATE (602 volumes)						
4	DIF-Net	8.8 [7.2, 10.3]	26.5 [25.6, 27.5]	47.1 [42.2, 52.4]	−41.7 [−47.9, −36.5]	−347.1 [−356.9, −338.4]
	DIF-Gaussian	4.0 [1.8, 6.1]	14.9 [13.5, 16.6]	42.1 [37.1, 47.2]	−33.1 [−39.9, −27.6]	−316.8 [−326.5, −308.1]
	C^2RV	2.7 [0.7, 4.4]	8.7 [8.0, 9.5]	39.9 [34.6, 45.2]	−20.8 [−26.5, −16.6]	−275.9 [−283.0, −269.1]
	SVCT	5.2 [4.2, 6.1]	24.7 [24.1, 25.3]	31.1 [27.5, 34.9]	−39.7 [−43.6, −36.5]	−263.5 [−271.0, −256.3]
	DeepSparse	−4.3 [−5.2, −3.5]	5.6 [5.2, 6.1]	22.1 [18.7, 25.5]	−34.4 [−38.3, −31.0]	−235.2 [−243.3, −227.9]
	SPARC	0.8 [0.7, 1.0]	4.8 [4.6, 5.1]	16.2 [14.5, 17.8]	−10.8 [−11.4, −10.1]	−148.2 [−152.1, −144.4]
8	DIF-Net	4.5 [3.3, 5.5]	14.8 [14.2, 15.4]	15.7 [12.7, 18.7]	−22.3 [−25.6, −19.5]	−218.3 [−223.7, −213.2]
	DIF-Gaussian	4.7 [2.4, 7.3]	11.7 [9.7, 14.2]	16.3 [12.7, 19.8]	−17.2 [−21.0, −14.1]	−211.0 [−217.6, −204.4]
	C^2RV	−4.2 [−5.6, −3.0]	4.3 [3.9, 4.8]	8.5 [4.3, 12.7]	−26.2 [−29.9, −23.4]	−218.3 [−223.9, −212.8]
	SVCT	7.2 [6.7, 7.8]	25.5 [24.9, 26.1]	30.2 [27.8, 32.6]	−31.9 [−33.8, −30.2]	−216.9 [−221.5, −212.3]
	DeepSparse	2.1 [1.4, 2.8]	10.8 [10.5, 11.1]	6.7 [4.1, 9.2]	−20.6 [−22.8, −18.8]	−169.9 [−173.6, −166.4]
	SPARC	1.1 [1.0, 1.3]	4.6 [4.4, 4.8]	6.1 [5.0, 7.3]	−7.9 [−8.4, −7.4]	−100.6 [−103.7, −97.6]
TotalSegmentator (79 volumes)						
4	DIF-Net	11.4 [8.0, 15.2]	29.3 [26.5, 32.3]	45.6 [35.0, 57.2]	−27.6 [−34.7, −20.5]	−348.5 [−360.5, −336.6]
	DIF-Gaussian	−20.5 [−23.4, −17.3]	9.4 [7.2, 11.9]	30.5 [20.7, 40.9]	−82.7 [−90.6, −74.9]	−418.8 [−429.7, −407.9]
	C^2RV	−6.0 [−8.6, −3.3]	8.3 [6.0, 11.0]	51.1 [38.2, 65.6]	−38.5 [−43.9, −33.1]	−346.2 [−356.5, −336.0]
	SVCT	8.8 [6.8, 11.0]	28.4 [26.6, 30.4]	49.5 [40.3, 59.1]	−27.5 [−31.0, −24.2]	−276.2 [−286.9, −266.0]
	DeepSparse	3.2 [1.3, 5.3]	12.3 [10.6, 14.3]	35.1 [26.1, 45.2]	−16.9 [−21.3, −12.7]	−230.2 [−241.2, −220.0]
	SPARC	2.1 [1.6, 2.6]	8.0 [7.2, 8.8]	21.5 [17.3, 25.8]	−8.6 [−10.0, −7.2]	−146.8 [−157.0, −137.6]
8	DIF-Net	0.5 [−1.0, 2.2]	9.1 [7.8, 10.4]	28.8 [21.3, 36.3]	−16.4 [−19.5, −13.4]	−214.5 [−221.7, −207.4]
	DIF-Gaussian	−24.0 [−26.4, −21.4]	−6.6 [−8.3, −5.0]	13.1 [3.5, 23.2]	−61.2 [−66.8, −55.4]	−333.0 [−341.7, −324.3]
	C^2RV	−13.7 [−15.3, −12.0]	0.7 [−0.5, 2.0]	10.8 [1.0, 21.7]	−43.6 [−47.4, −39.7]	−240.6 [−247.4, −233.8]
	SVCT	1.0 [−0.3, 2.2]	17.0 [16.0, 18.1]	10.2 [3.6, 16.8]	−23.9 [−26.8, −20.8]	−167.8 [−177.1, −158.7]
	DeepSparse	−12.6 [−13.9, −11.3]	3.4 [2.3, 4.5]	5.5 [−0.5, 11.8]	−45.0 [−47.6, −42.5]	−199.7 [−206.4, −193.1]
	SPARC	0.8 [0.3, 1.1]	5.4 [4.9, 5.9]	4.8 [2.0, 7.6]	−7.0 [−7.9, −6.0]	−95.9 [−102.0, −90.0]

Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples). Intensity bands are defined on the ground-truth CT: air below −900 HU, lung −900 to −500 HU, soft tissue −100 to below 300 HU, bone at least 300 HU. HU values are clipped to [−1,024, 1,024] before comparison, so errors in dense bone are underestimated.

Supplementary Tab. 4 | Hounsfield-unit error by intensity band (continued).

Projections	Intensity band	Comparator	Difference (HU)	*P*
SPARC minus strongest competing method, mean absolute error (HU)				
CT-RATE (602 volumes)				
4	All voxels	DeepSparse	−8.4 [−8.9, −7.9]	< 0.001
	Air	DeepSparse	−2.2 [−2.5, −1.9]	< 0.001
	Lung	DeepSparse	−20.9 [−23.1, −18.9]	< 0.001
	Soft tissue	DeepSparse	−17.8 [−20.5, −15.4]	< 0.001
	Bone	DeepSparse	−68.4 [−75.0, −62.6]	< 0.001
8	All voxels	DeepSparse	−8.9 [−9.2, −8.6]	< 0.001
	Air	C^2RV	−4.2 [−4.6, −3.9]	< 0.001
	Lung	DeepSparse	−15.4 [−16.7, −14.2]	< 0.001
	Soft tissue	DeepSparse	−10.4 [−11.6, −9.4]	< 0.001
	Bone	DeepSparse	−53.7 [−56.3, −51.3]	< 0.001
TotalSegmentator (79 volumes)				
4	All voxels	DeepSparse	−13.1 [−14.3, −11.9]	< 0.001
	Air	DeepSparse	−7.0 [−8.4, −5.6]	< 0.001
	Lung	DeepSparse	−43.8 [−48.8, −39.2]	< 0.001
	Soft tissue	DeepSparse	−17.2 [−19.3, −15.3]	< 0.001
	Bone	DeepSparse	−70.4 [−75.6, −65.5]	< 0.001
8	All voxels	DeepSparse	−11.7 [−12.6, −10.7]	< 0.001
	Air	DeepSparse	−5.3 [−6.3, −4.3]	< 0.001
	Lung	DeepSparse	−24.4 [−27.3, −21.7]	< 0.001
	Soft tissue	SVCT	−20.0 [−22.0, −18.1]	< 0.001
	Bone	SVCT	−63.6 [−68.5, −59.0]	< 0.001

Supplementary Tab. 5 | Hounsfield-unit accuracy inside each segmented structure. TotalSegmentator test set (79 volumes), with eight and four projections, measured inside the ground-truth organ masks used for the segmentation experiments, on the same exported reconstructions as Supplementary Tab. 4.

Structure	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**
Mean absolute error (HU)						
Eight projections						
Abdominal organs						
Liver	48.5 [42.7, 55.8]	78.1 [72.0, 85.4]	57.9 [52.0, 65.0]	35.3 [31.3, 40.4]	54.6 [50.9, 58.8]	25.1 [20.5, 32.6]
Spleen	56.7 [52.4, 61.0]	83.4 [77.6, 89.1]	75.4 [70.2, 80.7]	41.6 [38.6, 44.7]	74.6 [70.3, 79.0]	30.8 [28.7, 33.0]
Left kidney	81.1 [70.1, 94.0]	107.3 [95.1, 121.1]	107.5 [87.2, 132.4]	70.1 [59.0, 83.9]	87.3 [81.6, 93.1]	47.5 [44.4, 50.7]
Right kidney	71.9 [62.5, 82.7]	99.2 [89.1, 111.0]	95.1 [78.0, 116.2]	65.0 [52.0, 83.5]	86.2 [72.8, 106.9]	47.5 [41.8, 55.2]
Aorta	101.8 [92.1, 112.3]	142.5 [129.2, 156.4]	135.7 [121.7, 150.9]	76.1 [68.9, 84.4]	100.5 [91.9, 109.5]	56.6 [51.8, 61.8]
Lung lobes						
Left upper lobe	136.0 [124.3, 148.7]	159.4 [148.7, 170.9]	128.0 [115.2, 141.9]	121.0 [107.9, 136.5]	96.6 [88.3, 106.2]	70.7 [66.5, 75.0]
Left lower lobe	142.8 [128.9, 158.2]	168.2 [158.3, 179.2]	153.3 [136.4, 171.4]	106.3 [96.5, 117.9]	99.2 [89.3, 110.2]	76.0 [70.3, 81.9]
Right upper lobe	123.5 [107.3, 142.9]	151.4 [137.4, 167.3]	112.3 [95.4, 133.4]	99.6 [89.0, 113.5]	87.3 [79.1, 98.1]	67.4 [62.7, 72.4]
Right middle lobe	110.1 [101.3, 120.0]	131.0 [123.1, 138.8]	105.8 [93.9, 119.1]	98.4 [90.8, 106.4]	79.9 [74.2, 85.8]	64.5 [59.8, 69.3]
Right lower lobe	133.8 [122.5, 146.0]	165.6 [156.5, 175.7]	144.8 [127.5, 163.6]	102.6 [93.2, 114.8]	94.0 [84.7, 105.8]	73.4 [67.4, 80.4]
Four projections						
Abdominal organs						
Liver	57.4 [49.8, 67.3]	84.4 [74.3, 96.6]	57.3 [52.3, 62.9]	49.5 [43.5, 56.8]	39.9 [34.9, 47.0]	27.4 [23.7, 32.7]
Spleen	62.7 [55.8, 70.0]	100.8 [90.3, 111.3]	71.0 [64.7, 77.5]	63.7 [58.1, 69.8]	55.4 [50.9, 60.2]	39.1 [36.0, 42.5]
Left kidney	80.0 [70.9, 89.2]	108.0 [96.0, 119.9]	108.2 [92.4, 128.8]	105.3 [92.3, 120.9]	72.2 [66.3, 78.1]	56.1 [51.9, 60.3]
Right kidney	81.7 [71.1, 93.3]	112.9 [99.2, 127.5]	101.7 [88.0, 117.0]	97.8 [84.2, 114.4]	78.3 [64.3, 98.2]	60.1 [50.5, 74.5]
Aorta	125.8 [109.2, 143.2]	177.2 [158.0, 197.0]	134.0 [118.5, 150.3]	103.2 [91.6, 115.4]	92.8 [82.6, 104.1]	66.6 [59.9, 74.0]
Lung lobes						
Left upper lobe	198.3 [178.1, 219.6]	139.9 [129.0, 151.3]	213.7 [183.2, 244.7]	174.1 [152.4, 199.0]	137.5 [123.4, 153.8]	93.9 [87.4, 100.9]
Left lower lobe	179.3 [163.3, 196.9]	156.9 [143.3, 172.0]	187.8 [166.4, 210.5]	147.6 [134.2, 162.6]	128.6 [113.8, 145.8]	97.0 [87.9, 106.8]
Right upper lobe	146.1 [129.6, 163.9]	134.2 [119.4, 150.5]	139.9 [116.2, 169.7]	130.9 [116.7, 148.8]	114.2 [98.3, 136.8]	82.5 [75.6, 89.8]
Right middle lobe	159.5 [142.1, 178.9]	130.1 [117.2, 144.6]	145.2 [126.7, 164.9]	138.3 [124.1, 154.4]	113.8 [103.2, 126.0]	86.4 [78.2, 95.6]
Right lower lobe	167.3 [151.2, 185.2]	160.0 [143.8, 177.2]	178.1 [155.5, 202.4]	137.8 [124.3, 153.5]	118.0 [104.3, 134.0]	96.0 [84.2, 112.4]

Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples).

Supplementary Tab. 5 | Hounsfield-unit accuracy inside each segmented structure (continued).

Structure	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**
Mean signed error, reconstruction minus CT (HU)						
Eight projections						
Abdominal organs						
Liver	−25.6 [−33.2, −19.2]	−59.6 [−67.5, −48.5]	−47.1 [−53.6, −40.8]	−19.5 [−23.3, −15.4]	−49.1 [−53.2, −44.7]	−14.7 [−22.4, −10.1]
Spleen	−45.6 [−51.5, −39.2]	−76.6 [−83.6, −69.1]	−70.2 [−76.5, −63.4]	−26.8 [−31.5, −22.0]	−72.2 [−77.1, −67.0]	−20.9 [−23.3, −18.5]
Left kidney	−64.8 [−79.7, −50.9]	−94.6 [−109.9, −80.8]	−95.1 [−121.3, −74.4]	−52.9 [−67.7, −41.0]	−78.9 [−86.2, −71.1]	−31.2 [−34.9, −27.6]
Right kidney	−54.1 [−66.3, −42.5]	−83.3 [−94.7, −69.2]	−75.7 [−97.3, −56.6]	−45.9 [−65.0, −33.4]	−79.5 [−100.5, −66.1]	−30.4 [−39.2, −23.6]
Aorta	−70.5 [−82.8, −58.5]	−124.1 [−139.1, −109.5]	−124.8 [−140.0, −110.3]	−50.1 [−58.4, −42.6]	−90.0 [−99.6, −80.7]	−32.4 [−38.0, −26.8]
Lung lobes						
Left upper lobe	53.2 [37.5, 69.2]	69.6 [52.9, 86.1]	37.4 [21.2, 53.9]	52.8 [35.1, 73.0]	31.5 [19.8, 44.1]	10.3 [5.4, 14.9]
Left lower lobe	46.3 [29.7, 64.2]	69.4 [52.0, 87.0]	61.0 [37.0, 85.6]	23.9 [12.0, 37.7]	33.7 [21.8, 47.0]	14.2 [9.6, 19.3]
Right upper lobe	43.6 [25.8, 63.1]	48.4 [27.1, 70.9]	3.3 [−17.5, 28.0]	19.5 [3.9, 38.4]	19.1 [6.2, 34.6]	4.0 [−0.2, 8.4]
Right middle lobe	23.1 [8.5, 37.7]	28.5 [13.8, 43.6]	29.7 [14.2, 46.6]	34.9 [25.5, 44.6]	17.6 [9.1, 26.2]	4.2 [−0.4, 8.6]
Right lower lobe	30.4 [17.7, 44.4]	61.1 [45.7, 77.0]	42.3 [16.2, 67.9]	23.0 [11.3, 38.3]	27.2 [15.3, 41.9]	9.5 [3.5, 17.1]
Four projections						
Abdominal organs						
Liver	−20.0 [−31.1, −6.3]	−66.4 [−79.5, −49.7]	−40.5 [−47.8, −32.1]	−35.0 [−42.9, −27.5]	−23.6 [−31.9, −17.0]	−14.6 [−20.5, −10.6]
Spleen	−45.1 [−55.5, −34.5]	−96.7 [−108.3, −85.3]	−60.7 [−69.3, −51.9]	−58.1 [−65.0, −51.5]	−45.0 [−51.6, −38.4]	−28.8 [−33.2, −24.7]
Left kidney	−60.2 [−72.6, −46.8]	−94.4 [−108.9, −79.8]	−91.8 [−114.3, −72.5]	−96.0 [−112.4, −82.2]	−51.2 [−60.3, −41.7]	−41.6 [−46.1, −37.2]
Right kidney	−57.0 [−71.7, −41.4]	−95.7 [−111.6, −77.1]	−81.8 [−98.9, −62.1]	−80.2 [−96.4, −63.3]	−59.4 [−81.3, −43.2]	−42.8 [−58.5, −32.0]
Aorta	−94.4 [−114.8, −74.2]	−165.4 [−186.6, −144.3]	−115.7 [−133.6, −97.7]	−82.5 [−96.1, −69.4]	−58.1 [−72.1, −44.8]	−36.3 [−44.4, −28.6]
Lung lobes						
Left upper lobe	132.6 [106.8, 159.8]	37.5 [22.3, 52.6]	152.0 [114.1, 190.7]	125.0 [99.8, 153.8]	72.4 [53.3, 93.9]	35.6 [27.9, 43.6]
Left lower lobe	91.7 [72.6, 113.0]	39.0 [17.7, 61.1]	119.4 [93.7, 146.8]	88.3 [72.9, 105.7]	52.4 [35.2, 72.7]	33.1 [24.7, 42.8]
Right upper lobe	55.6 [35.6, 78.4]	23.6 [3.8, 45.3]	41.0 [14.1, 75.0]	71.9 [54.5, 93.2]	22.4 [0.4, 51.1]	13.9 [7.4, 20.9]
Right middle lobe	84.7 [63.1, 108.6]	17.7 [−1.9, 38.0]	72.3 [49.7, 96.3]	85.2 [68.4, 103.8]	40.8 [27.0, 55.9]	21.8 [15.5, 28.6]
Right lower lobe	60.0 [38.6, 83.4]	23.5 [−1.8, 48.0]	99.8 [73.8, 127.5]	72.1 [56.3, 90.4]	25.7 [8.8, 45.5]	28.5 [16.2, 47.2]

Supplementary Tab. 6 | Reconstruction error of SPARC by intensity band and by location. Eight projections, except the last block, which compares four and eight projections. MAE is in HU. NRMSE is the root-mean-square error within an intensity band divided by the standard deviation of ground-truth HU values in that band; Pearson r is the voxel-wise correlation within the band. r is the distance from the central axis of the volume and R the body radius (Methods).

Dataset	Metric	Air	Lung	Soft tissue	Bone
Error within each intensity band, eight projections (Supplementary Fig. 7b–d)					
CT-RATE (602)	MAE (HU)	8.8 [8.4, 9.1]	65.0 [63.0, 67.0]	41.3 [40.8, 41.8]	142.9 [140.4, 145.5]
	NRMSE	0.69 [0.67, 0.72]	0.99 [0.96, 1.01]	0.92 [0.90, 0.95]	0.97 [0.95, 0.98]
	Pearson r	0.83 [0.83, 0.84]	0.66 [0.65, 0.67]	0.68 [0.67, 0.68]	0.69 [0.68, 0.69]
TotalSegmentator (79)	MAE (HU)	8.6 [7.9, 9.4]	72.6 [69.4, 75.8]	39.0 [37.3, 40.9]	132.9 [127.0, 138.7]
	NRMSE	0.76 [0.71, 0.83]	1.03 [0.98, 1.07]	0.79 [0.75, 0.83]	0.94 [0.90, 0.98]
	Pearson r	0.81 [0.79, 0.83]	0.67 [0.65, 0.69]	0.73 [0.71, 0.75]	0.73 [0.71, 0.74]
MSD (209)	MAE (HU)	6.1 [5.7, 6.5]	65.9 [63.9, 67.9]	37.3 [36.6, 38.1]	140.9 [136.2, 146.1]
	NRMSE	0.62 [0.59, 0.65]	0.96 [0.93, 0.98]	0.70 [0.67, 0.72]	1.10 [1.07, 1.14]
	Pearson r	0.87 [0.86, 0.88]	0.69 [0.68, 0.70]	0.78 [0.77, 0.79]	0.65 [0.63, 0.66]
AbdomenCT-1K (158)	MAE (HU)	8.2 [7.8, 8.7]	73.0 [70.5, 75.7]	38.2 [37.4, 39.0]	142.4 [138.9, 145.9]
	NRMSE	0.69 [0.65, 0.74]	1.06 [1.03, 1.09]	0.71 [0.69, 0.73]	1.10 [1.07, 1.13]
	Pearson r	0.85 [0.83, 0.86]	0.66 [0.65, 0.67]	0.77 [0.76, 0.78]	0.66 [0.65, 0.68]
AMOS (75)	MAE (HU)	6.8 [6.4, 7.2]	78.1 [74.7, 81.7]	35.8 [34.6, 37.0]	123.3 [117.3, 129.6]
	NRMSE	0.74 [0.68, 0.81]	1.12 [1.08, 1.16]	0.78 [0.74, 0.81]	0.95 [0.91, 0.99]
	Pearson r	0.82 [0.80, 0.83]	0.66 [0.64, 0.67]	0.75 [0.74, 0.77]	0.70 [0.68, 0.72]
CQ500 (71)	MAE (HU)	3.9 [3.2, 5.1]	104.5 [97.3, 113.1]	33.2 [30.4, 36.4]	114.5 [105.9, 124.4]
	NRMSE	0.90 [0.80, 1.00]	1.40 [1.32, 1.49]	1.24 [1.17, 1.31]	0.76 [0.72, 0.81]
	Pearson r	0.78 [0.76, 0.81]	0.59 [0.57, 0.61]	0.65 [0.63, 0.67]	0.78 [0.76, 0.80]
ToothFairy3 (77)	MAE (HU)	2.0 [1.8, 2.1]	91.4 [85.1, 97.9]	48.3 [46.8, 49.9]	110.7 [106.9, 114.6]
	NRMSE	1.21 [1.09, 1.34]	1.50 [1.43, 1.58]	0.97 [0.95, 1.00]	0.65 [0.63, 0.67]
	Pearson r	0.74 [0.72, 0.77]	0.61 [0.59, 0.63]	0.66 [0.65, 0.67]	0.82 [0.81, 0.83]
VerSe (50)	MAE (HU)	11.0 [9.3, 12.8]	105.6 [99.4, 112.2]	53.3 [50.5, 56.4]	195.7 [186.7, 205.2]
	NRMSE	1.31 [1.18, 1.45]	1.47 [1.40, 1.55]	1.06 [0.99, 1.14]	1.28 [1.23, 1.33]
	Pearson r	0.66 [0.63, 0.69]	0.52 [0.50, 0.55]	0.60 [0.57, 0.63]	0.59 [0.57, 0.61]

Radial zones (Fig. 3c; Supplementary Fig. 7a) and body width (Supplementary Fig. 7e), eight projections

Dataset	Central ($r/R < 0.5$)	Peripheral ($0.5 \leq r/R < 1$)	Outside ($r/R \geq 1$)	Pearson r, PSNR vs body width
CT-RATE	52.6 [51.6, 53.6]	27.7 [27.3, 28.2]	8.3 [7.8, 8.8]	−0.40 [−0.46, −0.33]
TotalSegmentator	48.6 [46.1, 51.1]	26.3 [24.9, 27.6]	9.3 [8.2, 10.4]	−0.43 [−0.61, −0.19]
MSD	39.3 [37.3, 41.3]	24.5 [23.4, 25.6]	6.9 [6.5, 7.4]	−0.39 [−0.50, −0.27]
AbdomenCT-1K	42.5 [40.3, 44.7]	26.5 [25.4, 27.7]	9.0 [8.5, 9.6]	−0.33 [−0.47, −0.19]
AMOS	49.4 [47.5, 51.4]	26.8 [25.6, 28.1]	6.2 [5.6, 6.8]	−0.07 [−0.35, 0.24]
CQ500	23.6 [21.6, 25.9]	19.8 [18.0, 22.1]	3.8 [2.5, 6.1]	−0.53 [−0.81, 0.16]
ToothFairy3	24.5 [23.0, 26.0]	16.8 [15.5, 18.4]	2.1 [1.9, 2.2]	−0.12 [−0.30, 0.05]
VerSe	66.2 [61.8, 70.8]	39.5 [36.5, 42.4]	11.2 [9.1, 13.5]	−0.86 [−0.91, −0.79]

HU bands are defined from the ground-truth CT as in Supplementary Tab. 4; the names denote intensity bands, not segmented tissues. A two-voxel rim is excluded here, rather than the one-voxel rim in Supplementary Tab. 4 and 5.

Supplementary Tab. 6 | Reconstruction error of SPARC by intensity band and by location (continued).

r/R bin centre	CT-RATE (602)	TotalSegmentator (79)	MSD (209)	AbdomenCT-1K (158)	AMOS (75)	CQ500 (71)	ToothFairy3 (77)	VerSe (50)
Mean absolute error (HU) against the distance from the axis, eight projections (Supplementary Fig. 7a)								
0.05	60.5	53.5	45.8	48.2	54.3	21.9	16.7	77.6
0.15	58.1	53.6	44.8	47.4	54.8	22.8	17.4	75.4
0.25	58.1	51.9	41.7	44.6	50.1	22.3	21.3	71.5
0.35	53.4	49.0	38.8	42.3	48.7	23.1	26.1	65.4
0.45	46.2	44.2	35.7	39.1	47.2	25.0	28.2	59.7
0.55	40.7	38.7	33.0	35.5	42.1	27.1	25.5	54.9
0.65	35.9	32.6	30.2	32.1	34.8	27.2	22.9	48.5
0.75	30.0	27.1	25.8	28.2	27.7	23.0	19.2	41.4
0.85	23.1	22.2	21.0	22.9	21.9	15.9	13.6	35.0
0.95	16.7	17.5	17.6	19.3	16.1	11.5	8.6	26.7
1.05	11.2	12.5	11.6	13.1	10.6	7.7	3.8	17.5
1.15	7.2	8.1	5.4	7.7	5.2	3.4	1.5	9.7
1.25	5.3 (600)	6.7	3.2	5.3	3.5	2.6	1.4	5.8
1.35	4.0 (569)	6.5 (75)	2.5 (206)	4.0 (153)	4.2	1.6 (70)	1.4	5.6
1.45	3.2 (450)	11.1 (62)	2.2 (181)	3.1 (125)	3.3 (72)	1.7 (70)	2.2	6.7 (40)
1.55	2.6 (303)	9.8 (42)	2.0 (121)	2.4 (85)	3.8 (60)	3.4 (69)	2.3 (69)	7.7 (29)
1.65	2.4 (147)	11.3 (24)	2.1 (75)	1.7 (54)	2.8 (39)	1.9 (66)	1.8 (64)	7.9 (22)
1.75	2.3 (57)	22.1 (16)	2.1 (31)	1.5 (23)	3.8 (21)	1.9 (64)	6.4 (42)	2.1 (15)
1.85	2.4 (25)	18.7 (7)	2.5 (19)	1.5 (8)	4.1 (10)	2.3 (56)	10.7 (10)	1.8 (14)
1.95	2.3 (11)	6.6 (3)	2.1 (6)	0.9 (4)	4.0 (6)	3.7 (44)	5.8 (3)	2.6 (14)

Dataset	Four projections	Eight projections	Eight minus four	Volumes higher with eight
PSNR (dB) with the two-voxel rim excluded, four against eight projections (Supplementary Fig. 7f)				
CT-RATE (602)	29.36 [29.20, 29.51]	31.36 [31.21, 31.50]	+2.00 [1.96, 2.04]	100%
TotalSegmentator (79)	29.71 [29.28, 30.15]	32.05 [31.63, 32.46]	+2.33 [2.22, 2.46]	100%
MSD (209)	30.13 [29.84, 30.41]	32.60 [32.30, 32.90]	+2.47 [2.41, 2.53]	100%
AbdomenCT-1K (158)	29.61 [29.31, 29.91]	32.11 [31.80, 32.42]	+2.50 [2.44, 2.56]	100%
AMOS (75)	29.60 [29.32, 29.87]	31.95 [31.66, 32.22]	+2.35 [2.24, 2.46]	100%
CQ500 (71)	31.10 [30.63, 31.51]	33.70 [33.25, 34.11]	+2.61 [2.45, 2.77]	100%
ToothFairy3 (77)	30.90 [30.53, 31.25]	33.45 [33.07, 33.82]	+2.55 [2.43, 2.68]	100%
VerSe (50)	27.96 [26.96, 29.01]	30.02 [29.12, 30.99]	+2.07 [1.92, 2.22]	100%

In the radial profile, a number in parentheses gives the volumes that reach that bin when fewer than all volumes of the test set do (test-set size in the header). Differences between four and eight projections are descriptive; no tests are applied.

Supplementary Tab. 7 | Reconstruction accuracy against computational cost (eight projections). Mean PSNR averages the eight test sets, each weighted equally (Supplementary Tab. 2). Time per volume and peak GPU memory, the peak allocated while the network runs, are for a 256^3 output, means over the CT-RATE test set (Methods). Supplementary Tab. 8 breaks the time down and adds floating-point operations and SPARC at other output grids.

Method	Mean PSNR over the eight test sets (dB)	Time per volume (s)	Peak memory (GiB)	Parameters (M)
DIF-Net	24.78	1.12	6.06	31.1
DIF-Gaussian	24.75	2.29	6.25	31.7
C^2RV	27.19	9.52	6.14	50.8
SVCT	26.76	0.03	1.39	27.4
DeepSparse	30.16	2.23	2.41	6.0
SPARC	31.91	3.89	5.67	136.1

Supplementary Tab. 8 | Computational cost of reconstruction. Every CT-RATE test volume with eight projections (Methods). Input preparation turns the projections and acquisition geometry into the network's inputs; network, the model's forward pass (for SPARC, the backbone and point decoder; mean ± s.d. over volumes); reconstruction time, the two together. Peak memory is the peak allocated while the network runs.

Method	Output resolution	Parameters (M)	Input preparation (s)	Network (s)	Reconstruction time (s)	Peak memory (GiB)	GFLOPs[a]
DIF-Net	256^3	31.1	0.031	1.084 ± 0.001	1.115	6.06	5,144
DIF-Gaussian	256^3	31.7	0.036	2.251 ± 0.002	2.288	6.25	6,595
C^2RV	256^3	50.8	0.047	9.473 ± 0.006	9.519	6.14	97,783
SVCT	256^3	27.4	0.003	0.032 ± 0.004	0.034	1.39	2,126
DeepSparse	256^3	6.0	0.036	2.192 ± 0.003	2.228	2.41	6,355
SPARC	256^3	136.1	0.005	3.883 ± 0.049	3.888	5.67	134,538
SPARC at other output resolutions (the decoder is resolution-free)							
SPARC	128^3	136.1	0.003	0.601 ± 0.007	0.604	5.29	19,476
SPARC	384^3	136.1	0.010	12.668 ± 0.155	12.678	6.71	446,849
SPARC	512^3	136.1	0.021	29.729 ± 0.379	29.750	8.74	1,055,033

[a] Counted with PyTorch FlopCounterMode. Operators without a registered formula, such as grid sampling (used thousands of times per volume by DIF-Net, DIF-Gaussian, C^2RV and DeepSparse), are not counted, so these are lower bounds and under-count those methods most.

Supplementary Tab. 9 | Where SPARC's reconstruction time goes. Input preparation, the backbone and the point decoder, timed one by one on every test volume (Methods).

Setting	Input preparation (ms)	Backbone (ms)	Point decoder (s)	Sum (s)
Output resolution, CT-RATE test set with eight projections; plotted in Fig. 3e,f				
96^3	3.6	124.4	0.23	0.35
128^3	4.3	124.4	0.52	0.65
160^3	4.9	123.8	1.01	1.13
192^3	5.8	123.9	1.68	1.81
256^3	8.8	123.2	3.97	4.10
320^3	13.6	121.5	7.70	7.83
384^3	20.9	120.3	13.62	13.76
448^3	32.5	121.0	21.72	21.88
512^3	45.6	121.5	31.87	32.04
Number of projections, AMOS test set with a 256^3 *output; plotted in Supplementary Fig. 8d*				
2 projections (bi-planar)	10.2	79.0	2.18	2.27
4 projections	10.2	94.8	2.82	2.93
8 projections	10.1	124.3	4.23	4.37
16 projections	9.9	178.6	7.04	7.23

Timing the steps one by one adds synchronisation, so their sum is slightly longer than the reconstruction time in Supplementary Tab. 8, and keeps more tensors in memory, so memory is reported only there and in Supplementary Fig. 8.

Supplementary Tab. 10 | Training cost. Pretraining ran on 16 GPUs; every reconstruction run used one GPU. Not included: evaluation, export and task-network runs; the reconstruction models with two and sixteen projections; and the finetuning on all patients from the other two initialisations of Supplementary Tab. 28.

Stage or method	Runs	GPUs	Wall time (h)	GPU-hours
Stage 1: CT encoder (masked autoencoding)	1	16	65.2	1,043
Stage 2: SPARC	1	16	41.3	660
SPARC pretraining (Stages 1 and 2)	2	16	–	1,703
Stage 2: reconstruction loss only (ablation)	1	16	34.3	549
Reconstruction models for eight datasets and two numbers of projections				
DIF-Net	16	1	–	161
DIF-Gaussian	16	1	–	167
C^2RV	16	1	–	219
SVCT	16	1	–	151
DeepSparse	16	1	–	152
SPARC	16	1	–	338
SPARC adaptation per dataset (included in the SPARC row above)				
CT-RATE, 4 projections	1	1	49.6	50
CT-RATE, 8 projections	1	1	63.9	64
TotalSegmentator, 4 projections	1	1	26.1	26
TotalSegmentator, 8 projections	1	1	38.1	38
MSD, 4 projections	1	1	17.3	17
MSD, 8 projections	1	1	28.4	28
AbdomenCT-1K, 4 projections	1	1	16.0	16
AbdomenCT-1K, 8 projections	1	1	22.7	23
AMOS, 4 projections	1	1	8.4	8
AMOS, 8 projections	1	1	13.6	14
CQ500, 4 projections	1	1	9.0	9
CQ500, 8 projections	1	1	13.3	13
ToothFairy3, 4 projections	1	1	8.7	9
ToothFairy3, 8 projections	1	1	14.1	14
VerSe, 4 projections	1	1	3.3	3
VerSe, 8 projections	1	1	4.8	5
Reconstruction with fewer adaptation patients	24	1	–	266
Total	123	–	–	**3,706**

Counted from 123 runs that have a training log.

Supplementary Tab. 11 | Robustness to acquisition errors, PSNR (8 projections). Mean PSNR (dB) of each trained model on the perturbed test sets, without retraining; the unperturbed rows give the reference. The last three columns give the competing method with the highest mean under that condition and SPARC's paired difference from it, with its 95% CI in brackets, so a negative value means that method achieved a higher value than SPARC. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

		Mean PSNR (dB)						SPARC minus strongest competing method		
Perturbation	Dataset	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**	Comparator	Difference	*P*
Unperturbed										
–	CT-RATE	24.85	24.77	27.39	26.01	29.32	31.39		–	
	TotalSegmentator	24.50	23.52	26.67	26.53	28.76	31.37		–	
	CQ500	25.02	25.70	28.33	27.08	31.96	33.06		–	
	VerSe	23.85	23.11	23.58	25.82	27.26	29.48		–	
Photon noise, incident photons per detector pixel										
10^6	CT-RATE	24.86	24.77	27.38	26.01	29.32	31.38	DeepSparse	+2.06 [2.00, 2.13]	<0.001
	TotalSegmentator	24.50	23.53	26.68	26.53	28.76	31.36	DeepSparse	+2.60 [2.49, 2.71]	<0.001
	CQ500	25.03	25.71	28.34	27.08	31.96	33.06	DeepSparse	+1.10 [0.93, 1.29]	<0.001
	VerSe	23.84	23.11	23.58	25.82	27.26	29.47	DeepSparse	+2.21 [1.98, 2.46]	<0.001
10^5	CT-RATE	24.61	24.48	27.06	25.99	29.14	31.16	DeepSparse	+2.03 [1.97, 2.09]	<0.001
	TotalSegmentator	24.23	23.46	26.37	26.40	28.32	30.96	DeepSparse	+2.64 [2.52, 2.75]	<0.001
	CQ500	23.89	25.71	28.34	27.08	31.93	33.05	DeepSparse	+1.11 [0.96, 1.30]	<0.001
	VerSe	23.66	23.06	23.58	25.69	27.15	29.35	DeepSparse	+2.20 [1.97, 2.44]	<0.001
3×10^4	CT-RATE	23.64	23.59	25.92	25.79	28.26	30.31	DeepSparse	+2.05 [1.99, 2.11]	<0.001
	TotalSegmentator	23.54	23.04	25.24	25.92	26.50	29.82	DeepSparse	+3.33 [3.15, 3.51]	<0.001
	CQ500	21.67	25.66	28.23	27.08	31.58	32.96	DeepSparse	+1.38 [1.24, 1.55]	<0.001
	VerSe	21.66	22.84	23.22	25.17	26.46	28.80	DeepSparse	+2.33 [2.12, 2.56]	<0.001
10^4	CT-RATE	22.01	21.87	22.94	25.14	26.30	28.43	DeepSparse	+2.14 [2.08, 2.20]	<0.001
	TotalSegmentator	22.70	22.29	22.94	24.73	22.90	28.00	SVCT	+3.27 [3.08, 3.47]	<0.001
	CQ500	19.44	24.93	27.10	27.06	29.91	32.47	DeepSparse	+2.56 [2.43, 2.70]	<0.001
	VerSe	19.30	22.36	22.12	24.17	24.36	27.53	DeepSparse	+3.17 [2.93, 3.42]	<0.001
Angular jitter per projection (SD)										
0.5°	CT-RATE	24.71	24.62	27.08	25.87	28.81	30.58	DeepSparse	+1.77 [1.70, 1.84]	<0.001
	TotalSegmentator	24.40	23.47	26.48	26.38	28.42	30.79	DeepSparse	+2.36 [2.24, 2.48]	<0.001
	CQ500	25.00	25.67	28.28	27.05	31.78	32.85	DeepSparse	+1.06 [0.90, 1.26]	<0.001
	VerSe	23.81	23.08	23.54	25.76	27.14	29.22	DeepSparse	+2.08 [1.84, 2.32]	<0.001
1°	CT-RATE	24.40	24.29	26.46	25.54	27.86	29.23	DeepSparse	+1.37 [1.30, 1.44]	<0.001
	TotalSegmentator	24.21	23.34	26.12	26.17	27.86	29.82	DeepSparse	+1.96 [1.82, 2.10]	<0.001
	CQ500	24.93	25.58	28.12	26.95	31.36	32.34	DeepSparse	+0.98 [0.82, 1.17]	<0.001
	VerSe	23.68	22.99	23.42	25.57	26.75	28.58	DeepSparse	+1.83 [1.60, 2.07]	<0.001
2°	CT-RATE	23.68	23.54	25.23	24.71	26.13	27.01	DeepSparse	+0.89 [0.83, 0.95]	<0.001
	TotalSegmentator	23.62	22.95	25.13	25.28	26.39	27.69	DeepSparse	+1.30 [1.16, 1.44]	<0.001
	CQ500	24.73	25.34	27.71	26.74	30.39	31.16	DeepSparse	+0.76 [0.62, 0.93]	<0.001
	VerSe	23.31	22.72	23.09	24.96	25.89	27.26	DeepSparse	+1.37 [1.14, 1.61]	<0.001
Source-to-detector distance error										
1%	CT-RATE	23.25	23.14	24.70	24.65	25.40	25.92	DeepSparse	+0.52 [0.47, 0.57]	<0.001
	TotalSegmentator	23.50	22.92	24.95	25.31	26.01	26.72	DeepSparse	+0.71 [0.59, 0.83]	<0.001
	CQ500	24.32	24.80	26.72	26.20	28.64	29.11	DeepSparse	+0.46 [0.28, 0.67]	<0.001
	VerSe	23.36	22.76	23.11	24.98	25.75	26.91	DeepSparse	+1.16 [0.91, 1.44]	<0.001
2%	CT-RATE	21.19	21.07	21.95	22.42	22.18	22.26	SVCT	−0.16 [−0.25, −0.07]	0.005
	TotalSegmentator	21.84	21.71	22.69	23.05	23.07	23.15	DeepSparse	+0.08 [0.02, 0.14]	0.060
	CQ500	23.03	23.31	24.51	24.60	25.32	25.41	DeepSparse	+0.09 [0.00, 0.19]	0.15
	VerSe	22.40	22.03	22.21	23.53	23.79	24.14	DeepSparse	+0.34 [0.16, 0.54]	0.002
5%	CT-RATE	18.12	18.03	18.47	18.63	18.55	18.52	SVCT	−0.11 [−0.14, −0.07]	<0.001
	TotalSegmentator	18.91	19.08	19.37	19.42	19.44	19.33	DeepSparse	−0.11 [−0.15, −0.08]	<0.001
	CQ500	20.32	20.41	20.90	21.17	21.20	21.17	DeepSparse	−0.04 [−0.11, 0.06]	0.37
	VerSe	20.03	20.03	20.02	20.53	20.64	20.55	DeepSparse	−0.09 [−0.17, 0.01]	0.15
Detector offset (SD)										
1 mm	CT-RATE	24.59	24.51	26.92	25.78	28.62	30.34	DeepSparse	+1.72 [1.66, 1.79]	<0.001
	TotalSegmentator	24.35	23.42	26.40	26.35	28.34	30.60	DeepSparse	+2.26 [2.15, 2.38]	<0.001
	CQ500	24.73	25.35	27.77	26.78	30.61	31.52	DeepSparse	+0.91 [0.74, 1.11]	<0.001
	VerSe	23.77	23.06	23.51	25.73	27.10	29.21	DeepSparse	+2.11 [1.88, 2.34]	<0.001
2 mm	CT-RATE	24.03	23.94	26.02	25.24	27.38	28.68	DeepSparse	+1.30 [1.24, 1.37]	<0.001
	TotalSegmentator	23.92	23.14	25.76	25.83	27.36	29.12	DeepSparse	+1.76 [1.61, 1.91]	<0.001
	CQ500	24.15	24.67	26.70	26.11	28.61	29.31	DeepSparse	+0.69 [0.53, 0.88]	<0.001
	VerSe	23.54	22.88	23.30	25.45	26.57	28.36	DeepSparse	+1.79 [1.57, 2.03]	<0.001
4 mm	CT-RATE	22.89	22.79	24.36	23.95	25.20	26.03	DeepSparse	+0.83 [0.78, 0.88]	<0.001
	TotalSegmentator	23.04	22.46	24.46	24.59	25.61	26.73	DeepSparse	+1.13 [0.97, 1.29]	<0.001
	CQ500	22.72	23.09	24.46	24.15	25.54	25.86	DeepSparse	+0.32 [0.18, 0.52]	0.001
	VerSe	22.96	22.42	22.73	24.58	25.31	26.52	DeepSparse	+1.21 [1.02, 1.43]	<0.001
Angular range of the acquisition										
180°	CT-RATE	22.81	22.51	23.07	23.93	25.26	26.18	DeepSparse	+0.92 [0.84, 1.00]	<0.001
	TotalSegmentator	23.17	22.30	23.61	24.76	25.74	28.39	DeepSparse	+2.65 [2.53, 2.78]	<0.001
	CQ500	23.60	23.73	26.33	26.23	29.29	30.42	DeepSparse	+1.13 [0.97, 1.31]	<0.001
	VerSe	23.25	22.60	22.28	24.51	25.46	27.18	DeepSparse	+1.72 [1.61, 1.82]	<0.001
120°	CT-RATE	20.57	20.20	20.47	21.50	22.40	22.78	DeepSparse	+0.38 [0.34, 0.42]	<0.001
	TotalSegmentator	22.05	21.45	21.98	23.20	24.08	24.80	DeepSparse	+0.72 [0.63, 0.81]	<0.001
	CQ500	20.75	20.26	22.51	23.36	24.77	25.27	DeepSparse	+0.50 [0.36, 0.67]	<0.001
	VerSe	22.36	21.56	21.15	23.10	24.12	25.41	DeepSparse	+1.29 [1.18, 1.40]	<0.001
90°	CT-RATE	16.92	16.71	16.86	17.88	18.28	18.05	DeepSparse	−0.23 [−0.28, −0.19]	<0.001
	TotalSegmentator	18.15	18.12	17.95	18.85	19.38	19.21	DeepSparse	−0.17 [−0.23, −0.11]	<0.001
	CQ500	18.78	18.36	19.66	20.64	21.55	21.71	DeepSparse	+0.16 [0.03, 0.32]	0.12
	VerSe	19.46	18.87	18.42	19.78	20.79	21.38	DeepSparse	+0.59 [0.49, 0.68]	<0.001

Supplementary Tab. 12 | Robustness to acquisition errors, PSNR (4 projections). Mean PSNR (dB) of each trained model on the perturbed test sets, without retraining; the unperturbed rows give the reference. The last three columns give the competing method with the highest mean under that condition and SPARC's paired difference from it, with its 95% CI in brackets, so a negative value means that method achieved a higher value than SPARC. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

		Mean PSNR (dB)						SPARC minus strongest competing method		
Perturbation	Dataset	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**	Comparator	Difference	*P*
Unperturbed										
–	CT-RATE	23.29	23.50	25.60	25.17	27.16	29.41		–	
	TotalSegmentator	22.70	22.74	24.73	24.93	26.63	29.37		–	
	CQ500	23.18	24.16	26.53	26.29	29.49	30.86		–	
	VerSe	22.15	21.93	22.34	24.12	25.53	27.61		–	
Photon noise, incident photons per detector pixel										
10^6	CT-RATE	23.29	23.47	25.60	25.16	27.15	29.40	DeepSparse	+2.25 [2.16, 2.35]	<0.001
	TotalSegmentator	22.65	22.76	24.75	24.94	26.62	29.36	DeepSparse	+2.74 [2.59, 2.89]	<0.001
	CQ500	23.15	24.17	26.53	26.25	29.48	30.85	DeepSparse	+1.37 [1.19, 1.56]	<0.001
	VerSe	22.15	21.93	22.35	24.14	25.52	27.60	DeepSparse	+2.08 [1.89, 2.28]	<0.001
10^5	CT-RATE	23.14	23.23	25.38	25.13	27.00	29.24	DeepSparse	+2.25 [2.16, 2.34]	<0.001
	TotalSegmentator	22.24	22.67	24.53	24.87	26.33	29.03	DeepSparse	+2.69 [2.55, 2.84]	<0.001
	CQ500	22.16	24.18	26.51	24.82	29.38	30.85	DeepSparse	+1.47 [1.28, 1.66]	<0.001
	VerSe	21.98	21.85	22.33	24.03	25.41	27.51	DeepSparse	+2.10 [1.90, 2.30]	<0.001
3×10^4	CT-RATE	22.56	22.48	24.48	24.83	26.44	28.64	DeepSparse	+2.20 [2.11, 2.29]	<0.001
	TotalSegmentator	21.62	22.10	23.70	24.43	25.32	28.14	DeepSparse	+2.82 [2.67, 2.97]	<0.001
	CQ500	19.18	24.12	26.37	23.54	28.84	30.79	DeepSparse	+1.96 [1.79, 2.14]	<0.001
	VerSe	21.59	21.46	21.98	23.56	24.76	27.13	DeepSparse	+2.37 [2.13, 2.61]	<0.001
10^4	CT-RATE	21.42	20.75	22.59	23.60	25.20	27.35	DeepSparse	+2.15 [2.07, 2.24]	<0.001
	TotalSegmentator	20.43	20.79	22.16	23.41	23.13	26.67	SVCT	+3.27 [3.10, 3.45]	<0.001
	CQ500	18.66	23.50	25.05	22.13	26.03	30.47	DeepSparse	+4.43 [4.15, 4.76]	<0.001
	VerSe	20.54	20.76	20.62	22.79	23.19	26.35	DeepSparse	+3.17 [2.86, 3.46]	<0.001
Angular jitter per projection (SD)										
0.5°	CT-RATE	23.20	23.39	25.39	25.03	26.79	28.76	DeepSparse	+1.97 [1.88, 2.07]	<0.001
	TotalSegmentator	22.66	22.70	24.62	24.86	26.42	28.87	DeepSparse	+2.45 [2.30, 2.61]	<0.001
	CQ500	23.16	24.14	26.49	26.26	29.37	30.72	DeepSparse	+1.35 [1.17, 1.55]	<0.001
	VerSe	22.14	21.91	22.32	24.10	25.48	27.45	DeepSparse	+1.98 [1.79, 2.17]	<0.001
1°	CT-RATE	23.02	23.17	24.97	24.72	26.11	27.69	DeepSparse	+1.58 [1.48, 1.68]	<0.001
	TotalSegmentator	22.59	22.61	24.45	24.70	26.09	28.19	DeepSparse	+2.10 [1.92, 2.27]	<0.001
	CQ500	23.13	24.09	26.42	26.17	29.10	30.36	DeepSparse	+1.26 [1.09, 1.45]	<0.001
	VerSe	22.09	21.86	22.26	23.99	25.22	27.04	DeepSparse	+1.82 [1.63, 2.01]	<0.001
2°	CT-RATE	22.58	22.68	24.16	24.02	24.93	26.02	DeepSparse	+1.09 [1.00, 1.20]	<0.001
	TotalSegmentator	22.34	22.34	23.92	24.14	25.26	26.65	DeepSparse	+1.39 [1.18, 1.60]	<0.001
	CQ500	23.03	23.96	26.18	25.93	28.49	29.64	DeepSparse	+1.15 [0.98, 1.33]	<0.001
	VerSe	21.93	21.68	22.08	23.64	24.63	26.08	DeepSparse	+1.45 [1.26, 1.66]	<0.001
Source-to-detector distance error										
1%	CT-RATE	22.41	22.51	23.94	24.13	24.74	25.58	DeepSparse	+0.84 [0.77, 0.93]	<0.001
	TotalSegmentator	22.19	22.24	23.79	24.19	24.96	26.07	DeepSparse	+1.11 [0.96, 1.27]	<0.001
	CQ500	22.86	23.71	25.63	25.61	27.46	28.18	DeepSparse	+0.71 [0.52, 0.92]	<0.001
	VerSe	21.93	21.71	22.08	23.71	24.71	25.90	DeepSparse	+1.19 [0.99, 1.40]	<0.001
2%	CT-RATE	20.95	20.94	21.74	22.26	22.08	22.28	SVCT	+0.02 [−0.08, 0.12]	0.84
	TotalSegmentator	21.20	21.26	22.25	22.63	22.72	23.05	DeepSparse	+0.33 [0.23, 0.43]	<0.001
	CQ500	22.12	22.76	24.07	24.21	24.89	25.15	DeepSparse	+0.26 [0.14, 0.39]	<0.001
	VerSe	21.43	21.20	21.53	22.80	23.34	23.86	DeepSparse	+0.52 [0.34, 0.70]	<0.001
5%	CT-RATE	18.17	18.14	18.46	18.67	18.62	18.59	SVCT	−0.08 [−0.12, −0.04]	<0.001
	TotalSegmentator	18.81	18.93	19.24	19.46	19.38	19.36	SVCT	−0.09 [−0.19, 0.02]	0.33
	CQ500	20.09	20.42	21.02	21.15	21.24	21.20	DeepSparse	−0.04 [−0.12, 0.06]	0.84
	VerSe	19.85	19.70	19.76	20.28	20.44	20.53	DeepSparse	+0.10 [−0.02, 0.22]	0.33
Detector offset (SD)										
1 mm	CT-RATE	23.11	23.30	25.27	24.90	26.58	28.55	DeepSparse	+1.97 [1.88, 2.06]	<0.001
	TotalSegmentator	22.61	22.66	24.58	24.77	26.33	28.73	DeepSparse	+2.40 [2.26, 2.55]	<0.001
	CQ500	23.00	23.88	26.15	25.90	28.44	29.63	DeepSparse	+1.20 [1.03, 1.38]	<0.001
	VerSe	22.11	21.90	22.30	24.06	25.39	27.41	DeepSparse	+2.02 [1.84, 2.21]	<0.001
2 mm	CT-RATE	22.71	22.86	24.62	24.31	25.54	27.13	DeepSparse	+1.59 [1.51, 1.68]	<0.001
	TotalSegmentator	22.35	22.41	24.16	24.34	25.55	27.39	DeepSparse	+1.83 [1.67, 2.00]	<0.001
	CQ500	22.63	23.30	25.38	25.11	26.78	27.73	DeepSparse	+0.95 [0.78, 1.13]	<0.001
	VerSe	21.98	21.78	22.19	23.89	25.02	26.80	DeepSparse	+1.77 [1.59, 1.96]	<0.001
4 mm	CT-RATE	21.82	21.91	23.31	23.04	23.71	24.84	DeepSparse	+1.13 [1.06, 1.20]	<0.001
	TotalSegmentator	21.73	21.81	23.25	23.32	24.18	25.33	DeepSparse	+1.16 [0.97, 1.34]	<0.001
	CQ500	21.62	22.02	23.65	23.36	24.34	25.00	DeepSparse	+0.65 [0.51, 0.82]	<0.001
	VerSe	21.64	21.44	21.84	23.31	24.06	25.40	DeepSparse	+1.34 [1.15, 1.55]	<0.001
Angular range of the acquisition										
180°	CT-RATE	18.28	18.76	19.03	20.38	20.90	21.67	DeepSparse	+0.77 [0.70, 0.83]	<0.001
	TotalSegmentator	18.62	19.25	20.01	20.65	21.19	23.35	DeepSparse	+2.16 [2.03, 2.30]	<0.001
	CQ500	20.71	21.62	23.64	23.48	24.73	25.27	DeepSparse	+0.54 [0.40, 0.69]	<0.001
	VerSe	19.69	19.84	19.98	20.83	21.59	23.43	DeepSparse	+1.84 [1.63, 2.05]	<0.001
120°	CT-RATE	19.08	18.74	18.93	19.40	20.02	21.94	DeepSparse	+1.92 [1.85, 2.00]	<0.001
	TotalSegmentator	19.65	19.92	20.23	20.69	21.50	24.15	DeepSparse	+2.65 [2.52, 2.78]	<0.001
	CQ500	20.01	19.53	22.19	21.90	22.64	24.37	DeepSparse	+1.73 [1.61, 1.86]	<0.001
	VerSe	20.27	19.97	20.31	20.78	21.75	23.98	DeepSparse	+2.23 [2.02, 2.45]	<0.001
90°	CT-RATE	16.43	16.52	16.85	17.26	17.49	18.12	DeepSparse	+0.63 [0.59, 0.66]	<0.001
	TotalSegmentator	17.27	17.47	17.98	18.24	18.85	19.89	DeepSparse	+1.04 [0.94, 1.13]	<0.001
	CQ500	18.70	17.93	20.15	20.46	21.20	22.24	DeepSparse	+1.04 [0.93, 1.16]	<0.001
	VerSe	18.56	18.02	18.79	19.05	19.91	21.60	DeepSparse	+1.69 [1.54, 1.86]	<0.001

Supplementary Tab. 13 | Robustness to acquisition errors, SSIM (8 projections). Mean SSIM (×100) of each trained model on the perturbed test sets, without retraining; the unperturbed rows give the reference. The last three columns give the competing method with the highest mean under that condition and SPARC's paired difference from it, with its 95% CI in brackets, so a negative value means that method achieved a higher value than SPARC. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

		Mean SSIM (×100)						SPARC minus strongest competing method		
Perturbation	Dataset	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**	Comparator	Difference	*P*
Unperturbed										
–	CT-RATE	72.32	76.91	82.04	80.03	80.69	89.18		–	
	TotalSegmentator	75.86	63.81	77.44	77.99	83.39	90.46		–	
	CQ500	79.84	83.67	89.72	88.83	94.70	96.89		–	
	VerSe	70.73	66.36	68.86	77.84	80.30	86.23		–	
Photon noise, incident photons per detector pixel										
10^6	CT-RATE	72.44	76.90	82.04	80.03	80.94	89.17	C^2RV	+7.13 [6.88, 7.40]	< 0.001
	TotalSegmentator	75.40	63.76	77.43	77.97	83.35	90.44	DeepSparse	+7.09 [6.27, 7.93]	< 0.001
	CQ500	79.96	83.73	89.72	88.83	94.71	96.89	DeepSparse	+2.18 [1.64, 2.89]	< 0.001
	VerSe	70.84	66.34	68.86	77.88	80.29	86.23	DeepSparse	+5.94 [4.68, 7.20]	< 0.001
10^5	CT-RATE	71.63	76.02	81.46	79.97	81.83	88.88	DeepSparse	+7.05 [6.63, 7.52]	< 0.001
	TotalSegmentator	72.38	62.84	76.40	77.46	81.62	89.79	DeepSparse	+8.18 [7.24, 9.13]	< 0.001
	CQ500	79.03	83.81	89.67	88.84	94.76	96.88	DeepSparse	+2.12 [1.59, 2.83]	< 0.001
	VerSe	70.34	65.87	68.60	77.42	79.85	86.00	DeepSparse	+6.15 [4.89, 7.40]	< 0.001
3×10^4	CT-RATE	70.06	73.15	79.02	79.42	83.16	87.61	DeepSparse	+4.45 [4.33, 4.57]	< 0.001
	TotalSegmentator	67.33	59.89	72.72	75.82	75.33	87.44	SVCT	+11.62 [10.88, 12.38]	< 0.001
	CQ500	77.91	83.77	89.42	88.87	94.49	96.80	DeepSparse	+2.31 [1.75, 3.09]	< 0.001
	VerSe	66.51	64.14	66.49	75.79	77.06	84.16	DeepSparse	+7.11 [5.70, 8.50]	< 0.001
10^4	CT-RATE	67.32	66.98	71.93	77.57	79.76	84.41	DeepSparse	+4.65 [4.45, 4.86]	< 0.001
	TotalSegmentator	61.50	55.91	65.66	72.48	66.02	82.66	SVCT	+10.17 [9.45, 10.92]	< 0.001
	CQ500	77.02	82.71	87.80	88.90	92.39	96.35	DeepSparse	+3.96 [3.27, 4.94]	< 0.001
	VerSe	62.01	61.35	62.67	72.89	70.53	78.75	SVCT	+5.86 [5.02, 6.70]	< 0.001
Angular jitter per projection (SD)										
0.5°	CT-RATE	71.89	76.45	81.51	79.64	80.07	88.50	C^2RV	+6.99 [6.74, 7.24]	< 0.001
	TotalSegmentator	75.56	63.62	77.09	77.63	82.89	89.95	DeepSparse	+7.06 [6.24, 7.91]	< 0.001
	CQ500	79.79	83.63	89.68	88.79	94.63	96.82	DeepSparse	+2.19 [1.66, 2.90]	< 0.001
	VerSe	70.56	66.23	68.74	77.71	80.09	85.92	DeepSparse	+5.83 [4.58, 7.08]	< 0.001
1°	CT-RATE	70.96	75.48	80.47	78.67	78.75	87.09	C^2RV	+6.63 [6.39, 6.87]	< 0.001
	TotalSegmentator	74.96	63.17	76.40	77.12	82.01	88.92	DeepSparse	+6.91 [6.08, 7.75]	< 0.001
	CQ500	79.68	83.49	89.56	88.69	94.44	96.63	DeepSparse	+2.19 [1.66, 2.88]	< 0.001
	VerSe	70.11	65.80	68.27	77.19	79.27	85.03	DeepSparse	+5.76 [4.50, 7.01]	< 0.001
2°	CT-RATE	68.70	73.15	78.01	76.23	75.76	83.93	C^2RV	+5.92 [5.71, 6.14]	< 0.001
	TotalSegmentator	73.21	61.88	74.29	74.97	79.34	85.99	DeepSparse	+6.64 [5.84, 7.48]	< 0.001
	CQ500	79.37	83.15	89.21	88.40	93.97	96.12	DeepSparse	+2.16 [1.66, 2.79]	< 0.001
	VerSe	68.96	64.85	67.25	75.75	77.57	83.14	DeepSparse	+5.57 [4.34, 6.79]	< 0.001
Source-to-detector distance error										
1%	CT-RATE	67.81	72.27	77.15	76.40	74.86	82.42	C^2RV	+5.27 [5.03, 5.53]	< 0.001
	TotalSegmentator	73.07	61.89	74.13	75.11	79.08	85.05	DeepSparse	+5.97 [5.15, 6.82]	< 0.001
	CQ500	78.70	82.36	88.37	87.74	93.01	95.03	DeepSparse	+2.02 [1.47, 2.74]	< 0.001
	VerSe	69.09	65.04	67.37	75.81	77.38	82.52	DeepSparse	+5.14 [3.97, 6.30]	< 0.001
2%	CT-RATE	60.88	65.18	69.76	69.56	66.60	72.98	C^2RV	+3.22 [3.00, 3.45]	< 0.001
	TotalSegmentator	67.88	57.97	68.65	69.37	72.41	77.02	DeepSparse	+4.61 [3.81, 5.45]	< 0.001
	CQ500	76.55	80.15	85.95	85.55	90.09	91.65	DeepSparse	+1.56 [1.18, 1.99]	< 0.001
	VerSe	65.86	62.27	64.38	71.73	72.46	76.57	DeepSparse	+4.11 [3.04, 5.18]	< 0.001
5%	CT-RATE	49.69	53.71	58.41	55.98	54.34	59.40	C^2RV	+0.99 [0.80, 1.20]	< 0.001
	TotalSegmentator	58.22	50.40	59.13	58.00	61.30	64.48	DeepSparse	+3.17 [2.30, 4.11]	< 0.001
	CQ500	71.25	74.94	80.31	79.68	83.80	84.82	DeepSparse	+1.01 [0.67, 1.41]	< 0.001
	VerSe	58.34	55.84	57.94	62.78	64.10	66.68	DeepSparse	+2.59 [1.60, 3.59]	< 0.001
Detector offset (SD)										
1 mm	CT-RATE	71.51	76.10	81.23	79.49	79.80	88.26	C^2RV	+7.04 [6.78, 7.30]	< 0.001
	TotalSegmentator	75.39	63.46	76.92	77.61	82.82	89.81	DeepSparse	+6.99 [6.17, 7.84]	< 0.001
	CQ500	79.36	83.13	89.24	88.51	94.08	96.28	DeepSparse	+2.19 [1.67, 2.90]	< 0.001
	VerSe	70.43	66.12	68.59	77.63	79.95	85.88	DeepSparse	+5.93 [4.66, 7.18]	< 0.001
2 mm	CT-RATE	69.80	74.36	79.47	78.15	77.88	86.31	C^2RV	+6.84 [6.59, 7.09]	< 0.001
	TotalSegmentator	73.99	62.42	75.46	76.45	81.14	88.14	DeepSparse	+7.00 [6.18, 7.86]	< 0.001
	CQ500	78.47	82.20	88.29	87.77	92.94	95.06	DeepSparse	+2.12 [1.62, 2.75]	< 0.001
	VerSe	69.56	65.31	67.82	77.03	78.91	84.69	DeepSparse	+5.78 [4.50, 7.04]	< 0.001
4 mm	CT-RATE	66.11	70.67	75.74	74.61	73.64	82.02	C^2RV	+6.28 [6.05, 6.52]	< 0.001
	TotalSegmentator	71.27	60.17	72.53	73.56	77.78	84.64	DeepSparse	+6.86 [6.00, 7.75]	< 0.001
	CQ500	75.97	79.64	85.68	85.15	89.90	91.88	DeepSparse	+1.98 [1.48, 2.67]	< 0.001
	VerSe	67.62	63.52	65.92	75.03	76.35	81.83	DeepSparse	+5.48 [4.20, 6.76]	< 0.001
Angular range of the acquisition										
180°	CT-RATE	67.75	68.02	73.41	72.51	73.74	85.47	DeepSparse	+11.73 [11.21, 12.30]	< 0.001
	TotalSegmentator	73.50	59.72	72.94	72.63	78.39	87.26	DeepSparse	+8.87 [7.85, 9.92]	< 0.001
	CQ500	76.77	79.03	86.86	87.38	93.06	95.58	DeepSparse	+2.52 [2.00, 3.18]	< 0.001
	VerSe	70.08	64.96	67.05	73.73	77.02	83.21	DeepSparse	+6.19 [4.95, 7.42]	< 0.001
120°	CT-RATE	64.70	62.97	69.13	68.61	71.80	80.57	DeepSparse	+8.77 [8.25, 9.35]	< 0.001
	TotalSegmentator	72.55	58.62	71.37	71.18	76.84	83.81	DeepSparse	+6.97 [6.06, 7.91]	< 0.001
	CQ500	72.65	72.17	81.48	83.09	90.21	92.85	DeepSparse	+2.64 [2.15, 3.27]	< 0.001
	VerSe	69.05	62.98	65.50	71.83	75.61	81.61	DeepSparse	+5.99 [4.70, 7.28]	< 0.001
90°	CT-RATE	57.21	54.31	59.80	60.38	63.36	69.89	DeepSparse	+6.53 [6.04, 7.10]	< 0.001
	TotalSegmentator	64.30	52.68	62.36	63.37	69.09	72.94	DeepSparse	+3.85 [3.11, 4.60]	< 0.001
	CQ500	69.04	67.34	76.71	78.27	86.02	88.61	DeepSparse	+2.59 [2.12, 3.13]	< 0.001
	VerSe	63.05	56.57	59.44	65.18	69.55	74.43	DeepSparse	+4.88 [3.72, 6.04]	< 0.001

Supplementary Tab. 14 | Robustness to acquisition errors, SSIM (4 projections). Mean SSIM ($\times 100$) of each trained model on the perturbed test sets, without retraining; the unperturbed rows give the reference. The last three columns give the competing method with the highest mean under that condition and SPARC's paired difference from it, with its 95% CI in brackets, so a negative value means that method achieved a higher value than SPARC. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

		Mean SSIM ($\times 100$)						SPARC minus strongest competing method		
Perturbation	Dataset	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**	Comparator	Difference	*P*
Unperturbed										
–	CT-RATE	62.85	72.00	78.27	77.61	83.46	87.15		–	
	TotalSegmentator	60.98	67.33	73.57	72.68	81.27	87.46		–	
	CQ500	71.23	78.75	87.57	88.10	93.46	95.59		–	
	VerSe	54.02	61.83	64.95	73.33	77.25	81.43		–	
Photon noise, incident photons per detector pixel										
10^6	CT-RATE	62.68	71.81	78.27	77.62	83.44	87.14	DeepSparse	+3.70 [3.56, 3.84]	< 0.001
	TotalSegmentator	60.52	67.33	73.57	72.70	81.19	87.44	DeepSparse	+6.25 [5.70, 6.78]	< 0.001
	CQ500	71.25	78.68	87.57	88.00	93.46	95.59	DeepSparse	+2.14 [1.50, 2.95]	< 0.001
	VerSe	53.96	61.90	64.94	73.38	77.20	81.43	DeepSparse	+4.23 [2.87, 5.57]	< 0.001
10^5	CT-RATE	61.79	70.90	77.81	77.65	82.96	86.89	DeepSparse	+3.93 [3.79, 4.09]	< 0.001
	TotalSegmentator	58.51	66.35	72.80	72.54	79.82	86.78	DeepSparse	+6.96 [6.31, 7.58]	< 0.001
	CQ500	69.79	78.52	87.55	85.38	93.31	95.58	DeepSparse	+2.27 [1.60, 3.14]	< 0.001
	VerSe	53.39	61.23	64.55	73.11	76.36	81.17	DeepSparse	+4.82 [3.34, 6.29]	< 0.001
3×10^4	CT-RATE	59.26	68.40	75.80	76.72	81.11	85.79	DeepSparse	+4.68 [4.52, 4.86]	< 0.001
	TotalSegmentator	54.36	62.87	69.72	71.47	74.63	84.49	DeepSparse	+9.85 [8.74, 11.01]	< 0.001
	CQ500	67.12	78.26	87.35	81.91	92.62	95.51	DeepSparse	+2.89 [2.19, 3.80]	< 0.001
	VerSe	51.41	58.71	62.78	71.88	72.97	79.54	DeepSparse	+6.57 [4.64, 8.51]	< 0.001
10^4	CT-RATE	54.01	63.26	70.20	70.24	76.78	82.90	DeepSparse	+6.12 [5.94, 6.32]	< 0.001
	TotalSegmentator	47.08	57.01	63.63	68.87	65.94	79.80	SVCT	+10.93 [9.73, 12.30]	< 0.001
	CQ500	64.41	77.21	85.10	77.90	89.64	95.12	DeepSparse	+5.48 [4.81, 6.23]	< 0.001
	VerSe	46.46	54.98	58.80	69.76	66.82	75.55	SVCT	+5.79 [5.14, 6.47]	< 0.001
Angular jitter per projection (SD)										
0.5°	CT-RATE	62.53	71.64	77.83	77.21	82.83	86.40	DeepSparse	+3.56 [3.43, 3.70]	< 0.001
	TotalSegmentator	60.83	67.14	73.28	72.48	80.87	86.85	DeepSparse	+5.98 [5.45, 6.49]	< 0.001
	CQ500	71.20	78.71	87.52	88.06	93.39	95.52	DeepSparse	+2.13 [1.50, 2.93]	< 0.001
	VerSe	53.93	61.76	64.88	73.29	77.13	81.20	DeepSparse	+4.07 [2.74, 5.37]	< 0.001
1°	CT-RATE	61.90	70.92	76.93	76.32	81.58	84.90	DeepSparse	+3.32 [3.19, 3.46]	< 0.001
	TotalSegmentator	60.53	66.82	72.88	72.07	80.25	85.91	DeepSparse	+5.66 [5.16, 6.17]	< 0.001
	CQ500	71.11	78.63	87.44	87.96	93.21	95.32	DeepSparse	+2.11 [1.50, 2.89]	< 0.001
	VerSe	53.70	61.46	64.61	72.97	76.51	80.40	DeepSparse	+3.89 [2.62, 5.17]	< 0.001
2°	CT-RATE	60.34	69.20	74.98	74.16	78.90	81.84	DeepSparse	+2.94 [2.81, 3.07]	< 0.001
	TotalSegmentator	59.58	65.75	71.52	70.55	78.42	83.21	DeepSparse	+4.80 [4.34, 5.25]	< 0.001
	CQ500	70.91	78.41	87.20	87.67	92.81	94.94	DeepSparse	+2.13 [1.52, 2.91]	< 0.001
	VerSe	53.23	60.86	63.99	72.11	75.28	78.79	DeepSparse	+3.51 [2.29, 4.74]	< 0.001
Source-to-detector distance error										
1%	CT-RATE	59.98	68.82	74.72	74.67	78.87	81.49	DeepSparse	+2.63 [2.50, 2.75]	< 0.001
	TotalSegmentator	59.39	65.62	71.38	70.78	78.16	82.88	DeepSparse	+4.72 [4.25, 5.19]	< 0.001
	CQ500	70.57	77.98	86.64	87.28	92.10	94.00	DeepSparse	+1.89 [1.26, 2.67]	< 0.001
	VerSe	53.21	60.98	64.04	72.30	75.47	78.39	DeepSparse	+2.92 [1.82, 4.04]	< 0.001
2%	CT-RATE	55.16	63.57	68.81	68.87	71.75	73.03	DeepSparse	+1.28 [1.18, 1.38]	< 0.001
	TotalSegmentator	56.18	62.32	67.45	66.72	73.06	76.07	DeepSparse	+3.01 [2.59, 3.42]	< 0.001
	CQ500	69.33	76.50	84.80	85.27	89.60	91.09	DeepSparse	+1.49 [0.93, 2.16]	< 0.001
	VerSe	51.53	59.12	62.12	69.67	71.96	73.87	DeepSparse	+1.91 [0.96, 2.88]	< 0.001
5%	CT-RATE	45.64	53.30	58.38	55.92	59.59	59.76	DeepSparse	+0.18 [0.09, 0.26]	< 0.001
	TotalSegmentator	48.90	54.97	59.24	57.29	63.33	64.39	DeepSparse	+1.06 [0.68, 1.43]	< 0.001
	CQ500	65.13	72.23	80.17	79.90	84.18	84.70	DeepSparse	+0.52 [0.01, 1.10]	0.12
	VerSe	46.55	54.38	57.02	62.46	64.63	64.96	DeepSparse	+0.33 [−0.64, 1.31]	0.51
Detector offset (SD)										
1 mm	CT-RATE	62.25	71.34	77.59	76.95	82.48	86.13	DeepSparse	+3.65 [3.51, 3.79]	< 0.001
	TotalSegmentator	60.66	67.02	73.20	72.29	80.78	86.75	DeepSparse	+5.97 [5.42, 6.51]	< 0.001
	CQ500	70.88	78.29	87.16	87.65	92.78	94.93	DeepSparse	+2.15 [1.51, 2.95]	< 0.001
	VerSe	53.86	61.67	64.77	73.15	76.91	81.09	DeepSparse	+4.18 [2.84, 5.51]	< 0.001
2 mm	CT-RATE	60.96	69.97	76.14	75.42	80.46	84.04	DeepSparse	+3.58 [3.45, 3.72]	< 0.001
	TotalSegmentator	59.76	66.08	72.10	71.20	79.21	84.85	DeepSparse	+5.64 [5.09, 6.17]	< 0.001
	CQ500	70.26	77.49	86.38	86.78	91.58	93.71	DeepSparse	+2.13 [1.51, 2.90]	< 0.001
	VerSe	53.37	61.16	64.30	72.73	76.13	80.05	DeepSparse	+3.92 [2.62, 5.21]	< 0.001
4 mm	CT-RATE	58.15	66.93	73.01	71.93	76.33	79.75	DeepSparse	+3.41 [3.28, 3.55]	< 0.001
	TotalSegmentator	57.88	64.16	69.91	68.73	76.39	81.31	DeepSparse	+4.91 [4.41, 5.40]	< 0.001
	CQ500	68.40	75.34	84.21	84.21	88.72	90.83	DeepSparse	+2.11 [1.50, 2.88]	< 0.001
	VerSe	52.09	59.90	63.09	71.36	74.08	77.64	DeepSparse	+3.55 [2.27, 4.84]	< 0.001
Angular range of the acquisition										
180°	CT-RATE	49.67	56.31	61.35	63.16	68.99	73.48	DeepSparse	+4.50 [4.35, 4.64]	< 0.001
	TotalSegmentator	51.63	58.46	62.62	61.47	70.00	74.86	DeepSparse	+4.86 [4.35, 5.37]	< 0.001
	CQ500	64.02	71.05	82.72	83.50	88.76	91.47	DeepSparse	+2.71 [2.14, 3.36]	< 0.001
	VerSe	47.59	57.28	59.82	64.90	67.83	72.43	DeepSparse	+4.59 [3.11, 6.06]	< 0.001
120°	CT-RATE	51.90	55.69	59.81	60.23	66.53	75.16	DeepSparse	+8.63 [8.38, 8.87]	< 0.001
	TotalSegmentator	54.36	59.21	62.98	60.68	70.49	78.31	DeepSparse	+7.82 [7.08, 8.54]	< 0.001
	CQ500	61.55	64.11	79.48	80.16	85.35	90.11	DeepSparse	+4.76 [4.21, 5.41]	< 0.001
	VerSe	49.05	58.35	60.86	64.85	68.21	73.37	DeepSparse	+5.16 [3.53, 6.76]	< 0.001
90°	CT-RATE	46.17	49.64	55.13	56.40	63.18	66.88	DeepSparse	+3.70 [3.49, 3.92]	< 0.001
	TotalSegmentator	49.84	53.58	59.00	56.48	66.39	71.04	DeepSparse	+4.65 [4.11, 5.19]	< 0.001
	CQ500	61.21	60.36	76.28	77.25	84.41	87.90	DeepSparse	+3.49 [2.96, 4.15]	< 0.001
	VerSe	46.58	53.89	57.91	61.95	65.66	70.37	DeepSparse	+4.72 [3.17, 6.25]	< 0.001

Supplementary Tab. 15 | SPARC under acquisition errors, in detail (8 projections): photon noise, angular jitter and combined perturbations. Paired change in PSNR (dB) from the same trained model's unperturbed evaluation on the same volumes; SPARC only, with no retraining. Levels that also appear in Supplementary Tab. 11 are repeated here so that each family forms one curve.

Perturbation	CT-RATE	TotalSegmentator	CQ500	VerSe
Photon noise, incident photons per detector pixel				
10^6	−0.01 [−0.01, −0.01]	−0.02 [−0.03, −0.01]	0.00 [0.00, 0.00]	0.00 [−0.01, 0.00]
3×10^5	−0.05 [−0.06, −0.04]	−0.09 [−0.13, −0.06]	0.00 [−0.01, 0.00]	−0.02 [−0.04, −0.01]
10^5	−0.23 [−0.26, −0.20]	−0.42 [−0.53, −0.32]	−0.02 [−0.02, −0.01]	−0.12 [−0.17, −0.08]
3×10^4	−1.08 [−1.18, −0.98]	−1.55 [−1.80, −1.31]	−0.10 [−0.11, −0.08]	−0.68 [−0.85, −0.51]
10^4	−2.96 [−3.15, −2.78]	−3.38 [−3.74, −3.02]	−0.59 [−0.68, −0.52]	−1.94 [−2.32, −1.57]
3×10^3	−5.96 [−6.19, −5.72]	−5.85 [−6.27, −5.43]	−3.37 [−3.65, −3.10]	−4.09 [−4.62, −3.54]
10^3	−8.82 [−9.05, −8.59]	−8.60 [−9.05, −8.14]	−8.17 [−8.54, −7.79]	−7.39 [−7.81, −6.94]
Angular jitter per projection (SD)				
0.25°	−0.24 [−0.26, −0.22]	−0.14 [−0.17, −0.11]	−0.06 [−0.08, −0.05]	−0.06 [−0.08, −0.03]
0.5°	−0.81 [−0.86, −0.76]	−0.59 [−0.69, −0.49]	−0.21 [−0.26, −0.18]	−0.26 [−0.32, −0.20]
1°	−2.16 [−2.27, −2.06]	−1.56 [−1.82, −1.31]	−0.72 [−0.87, −0.59]	−0.89 [−1.06, −0.74]
2°	−4.38 [−4.53, −4.23]	−3.68 [−4.13, −3.25]	−1.90 [−2.15, −1.67]	−2.22 [−2.53, −1.91]
3°	−5.81 [−5.96, −5.65]	−5.19 [−5.66, −4.71]	−3.28 [−3.64, −2.94]	−3.06 [−3.44, −2.69]
Photon noise with angular jitter				
10^5, 0.5°	−1.03 [−1.08, −0.97]	−0.93 [−1.10, −0.77]	−0.23 [−0.28, −0.19]	−0.36 [−0.47, −0.27]
10^5, 1°	−2.33 [−2.44, −2.23]	−2.12 [−2.44, −1.82]	−0.76 [−0.86, −0.66]	−0.94 [−1.12, −0.76]
10^5, 2°	−4.39 [−4.54, −4.24]	−3.80 [−4.17, −3.44]	−1.99 [−2.24, −1.76]	−2.40 [−2.72, −2.08]
10^4, 0.5°	−3.39 [−3.56, −3.22]	−3.63 [−4.00, −3.26]	−0.77 [−0.87, −0.69]	−2.14 [−2.52, −1.77]
10^4, 1°	−4.22 [−4.38, −4.05]	−4.17 [−4.54, −3.78]	−1.22 [−1.35, −1.10]	−2.46 [−2.85, −2.07]
10^4, 2°	−5.62 [−5.78, −5.46]	−5.40 [−5.84, −4.94]	−2.30 [−2.55, −2.08]	−3.30 [−3.74, −2.86]
Photon noise with a source-to-detector distance error				
10^4, 2%	−9.44 [−9.58, −9.31]	−8.72 [−9.12, −8.32]	−7.71 [−8.10, −7.30]	−5.77 [−6.24, −5.30]

Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples). Angular jitter is drawn independently for each projection.

Supplementary Tab. 16 | SPARC under acquisition errors, in detail (8 projections): geometry and angular range. Paired change in PSNR (dB) from the same trained model's unperturbed evaluation on the same volumes; SPARC only, with no retraining. Levels shared with Supplementary Tab. 11 are repeated so that each family forms one curve.

Perturbation	CT-RATE	TotalSegmentator	CQ500	VerSe
Source-to-detector distance error, random sign				
0.5%	−2.37 [−2.44, −2.30]	−1.83 [−2.01, −1.66]	−1.47 [−1.60, −1.33]	−0.82 [−0.99, −0.67]
1%	−5.47 [−5.59, −5.35]	−4.65 [−4.97, −4.33]	−3.96 [−4.23, −3.67]	−2.56 [−2.90, −2.24]
2%	−9.14 [−9.27, −9.01]	−8.22 [−8.61, −7.82]	−7.66 [−8.06, −7.24]	−5.34 [−5.79, −4.89]
3%	−10.91 [−11.04, −10.79]	−10.03 [−10.40, −9.63]	−9.75 [−10.20, −9.29]	−7.02 [−7.47, −6.57]
5%	−12.87 [−13.00, −12.75]	−12.05 [−12.41, −11.68]	−11.90 [−12.36, −11.40]	−8.92 [−9.34, −8.50]
10%	−15.51 [−15.64, −15.39]	−14.57 [−14.92, −14.23]	−14.50 [−14.96, −14.01]	−11.57 [−12.00, −11.12]
Source-to-detector distance error, fixed sign				
−5%	−12.80 [−12.93, −12.68]	−12.36 [−12.74, −11.97]	−11.77 [−12.23, −11.29]	−9.36 [−9.80, −8.91]
−2%	−9.13 [−9.26, −9.00]	−8.51 [−8.90, −8.10]	−7.64 [−8.03, −7.22]	−5.53 [−5.97, −5.09]
+2%	−9.14 [−9.27, −9.01]	−7.93 [−8.29, −7.55]	−7.64 [−8.05, −7.22]	−5.20 [−5.66, −4.75]
+5%	−12.96 [−13.08, −12.83]	−11.74 [−12.07, −11.40]	−12.06 [−12.52, −11.57]	−8.78 [−9.18, −8.37]
Detector offset (SD)				
1 mm	−1.05 [−1.13, −0.98]	−0.77 [−0.95, −0.61]	−1.54 [−1.85, −1.25]	−0.26 [−0.35, −0.19]
2 mm	−2.71 [−2.84, −2.57]	−2.26 [−2.62, −1.92]	−3.76 [−4.28, −3.24]	−1.11 [−1.39, −0.85]
4 mm	−5.36 [−5.57, −5.16]	−4.64 [−5.23, −4.06]	−7.20 [−7.97, −6.41]	−2.95 [−3.50, −2.43]
8 mm	−8.24 [−8.48, −8.01]	−7.38 [−8.00, −6.76]	−10.06 [−10.88, −9.21]	−5.11 [−5.88, −4.37]
Angular range of the acquisition				
270°	−4.90 [−4.98, −4.82]	−2.57 [−2.74, −2.40]	−4.97 [−5.31, −4.63]	−3.11 [−3.39, −2.83]
180°	−5.21 [−5.29, −5.14]	−2.99 [−3.24, −2.75]	−2.64 [−2.85, −2.44]	−2.30 [−2.58, −2.02]
120°	−8.61 [−8.74, −8.48]	−6.57 [−6.89, −6.26]	−7.79 [−8.21, −7.35]	−4.07 [−4.38, −3.76]
90°	−13.34 [−13.50, −13.19]	−12.16 [−12.53, −11.80]	−11.35 [−11.82, −10.85]	−8.10 [−8.55, −7.64]
60°	−16.76 [−16.89, −16.62]	−16.17 [−16.56, −15.77]	−14.35 [−14.78, −13.88]	−12.25 [−12.60, −11.88]

Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples). Fixed-sign distance errors have the same sign for every volume; a positive error means that the true source-to-detector distance is longer than the distance given to the model. Random-sign errors have their sign drawn for each volume.

Supplementary Tab. 17 | A fixed photon budget divided among different numbers of projections (AMOS). AMOS test set (75 volumes); each number of projections is a separately trained model, and two projections are bi-planar. The change is paired against the same model's noise-free evaluation. Changes are descriptive; no tests are applied.

Projections	Incident photons per pixel per projection	PSNR (dB)	Noise-free PSNR (dB)	Change (dB)
8×10^4 *incident photons per detector pixel in total*				
2	40,000	27.36 [27.12, 27.59]	27.70 [27.44, 27.95]	−0.34 [−0.40, −0.28]
4	20,000	27.72 [27.48, 27.96]	29.65 [29.37, 29.91]	−1.93 [−2.13, −1.72]
8	10,000	26.25 [25.90, 26.60]	31.67 [31.40, 31.93]	−5.43 [−5.82, −5.03]
16	5,000	22.34 [21.83, 22.89]	33.97 [33.71, 34.21]	−11.64 [−12.17, −11.06]
8×10^5 *incident photons per detector pixel in total*				
2	400,000	27.69 [27.43, 27.94]	27.70 [27.44, 27.95]	−0.01 [−0.01, 0.00]
4	200,000	29.61 [29.33, 29.87]	29.65 [29.37, 29.91]	−0.04 [−0.05, −0.03]
8	100,000	31.49 [31.22, 31.75]	31.67 [31.40, 31.93]	−0.18 [−0.25, −0.12]
16	50,000	32.47 [32.17, 32.75]	33.97 [33.71, 34.21]	−1.50 [−1.74, −1.28]

Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples).

Supplementary Tab. 18 | Classification with the classifier trained on full CT (AUROC). Each method's test reconstructions were given, unchanged, to the classifier trained on full CT; the reference column is that classifier on the full CT. CT-RATE test set, 602 volumes. AUROC is computed on the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples).

	Reconstruction given to the classifier trained on full CT						Reference
Finding	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**	Full CT
Eight projections							
Macro average	0.725 [0.701, 0.748]	0.717 [0.693, 0.740]	0.730 [0.705, 0.752]	0.745 [0.720, 0.768]	0.741 [0.715, 0.764]	0.756 [0.730, 0.779]	0.772 [0.746, 0.795]
Medical material	0.813 [0.729, 0.886]	0.788 [0.703, 0.872]	0.840 [0.762, 0.906]	0.793 [0.710, 0.870]	0.807 [0.735, 0.875]	0.788 [0.693, 0.872]	0.768 [0.663, 0.861]
Arterial wall calcification	0.862 [0.814, 0.906]	0.826 [0.773, 0.876]	0.850 [0.801, 0.896]	0.852 [0.803, 0.896]	0.862 [0.816, 0.905]	0.881 [0.838, 0.920]	0.897 [0.858, 0.932]
Cardiomegaly	0.848 [0.785, 0.903]	0.849 [0.789, 0.902]	0.889 [0.839, 0.931]	0.869 [0.813, 0.918]	0.859 [0.797, 0.911]	0.877 [0.821, 0.925]	0.871 [0.810, 0.922]
Pericardial effusion	0.777 [0.654, 0.871]	0.770 [0.626, 0.880]	0.767 [0.626, 0.876]	0.798 [0.667, 0.904]	0.774 [0.635, 0.885]	0.765 [0.602, 0.890]	0.766 [0.592, 0.897]
Coronary artery wall calcification	0.834 [0.784, 0.883]	0.808 [0.752, 0.862]	0.840 [0.787, 0.888]	0.842 [0.789, 0.891]	0.850 [0.800, 0.896]	0.868 [0.821, 0.911]	0.883 [0.841, 0.922]
Hiatal hernia	0.690 [0.584, 0.790]	0.666 [0.564, 0.764]	0.687 [0.589, 0.779]	0.699 [0.595, 0.793]	0.712 [0.615, 0.803]	0.722 [0.626, 0.812]	0.764 [0.675, 0.847]
Lymphadenopathy	0.715 [0.645, 0.779]	0.716 [0.648, 0.778]	0.695 [0.617, 0.764]	0.742 [0.677, 0.800]	0.713 [0.644, 0.775]	0.740 [0.673, 0.801]	0.730 [0.658, 0.795]
Emphysema	0.682 [0.603, 0.761]	0.650 [0.570, 0.728]	0.661 [0.581, 0.740]	0.704 [0.628, 0.780]	0.665 [0.587, 0.746]	0.708 [0.631, 0.784]	0.754 [0.684, 0.822]
Atelectasis	0.701 [0.627, 0.770]	0.688 [0.615, 0.755]	0.698 [0.625, 0.765]	0.702 [0.631, 0.766]	0.698 [0.626, 0.764]	0.718 [0.648, 0.782]	0.730 [0.662, 0.792]
Lung nodule	0.613 [0.546, 0.679]	0.600 [0.533, 0.664]	0.594 [0.525, 0.661]	0.607 [0.537, 0.676]	0.615 [0.548, 0.679]	0.635 [0.570, 0.698]	0.605 [0.539, 0.670]
Lung opacity	0.557 [0.478, 0.639]	0.570 [0.492, 0.651]	0.589 [0.504, 0.672]	0.652 [0.574, 0.726]	0.621 [0.552, 0.688]	0.664 [0.598, 0.727]	0.814 [0.762, 0.862]
Pulmonary fibrotic sequela	0.656 [0.576, 0.729]	0.631 [0.550, 0.705]	0.664 [0.586, 0.737]	0.657 [0.576, 0.732]	0.670 [0.592, 0.741]	0.660 [0.582, 0.733]	0.659 [0.584, 0.728]
Pleural effusion	0.901 [0.835, 0.952]	0.923 [0.867, 0.966]	0.903 [0.828, 0.958]	0.918 [0.846, 0.968]	0.896 [0.808, 0.959]	0.906 [0.817, 0.968]	0.897 [0.784, 0.972]
Mosaic attenuation pattern	0.736 [0.639, 0.825]	0.724 [0.638, 0.807]	0.762 [0.672, 0.843]	0.749 [0.650, 0.839]	0.750 [0.657, 0.836]	0.764 [0.670, 0.850]	0.764 [0.672, 0.846]
Peribronchial thickening	0.736 [0.635, 0.823]	0.696 [0.595, 0.785]	0.710 [0.612, 0.796]	0.741 [0.652, 0.817]	0.748 [0.656, 0.827]	0.763 [0.681, 0.835]	0.730 [0.628, 0.818]
Consolidation	0.566 [0.471, 0.674]	0.616 [0.538, 0.697]	0.626 [0.538, 0.723]	0.675 [0.587, 0.766]	0.701 [0.618, 0.777]	0.719 [0.640, 0.793]	0.819 [0.741, 0.887]
Bronchiectasis	0.630 [0.458, 0.777]	0.607 [0.439, 0.759]	0.625 [0.463, 0.766]	0.638 [0.450, 0.796]	0.638 [0.457, 0.793]	0.636 [0.446, 0.794]	0.622 [0.443, 0.773]
Interlobular septal thickening	0.736 [0.584, 0.857]	0.780 [0.646, 0.887]	0.737 [0.578, 0.862]	0.767 [0.625, 0.879]	0.767 [0.621, 0.879]	0.793 [0.666, 0.891]	0.822 [0.718, 0.907]
Four projections							
Macro average	0.702 [0.679, 0.724]	0.699 [0.675, 0.722]	0.716 [0.692, 0.737]	0.731 [0.705, 0.753]	0.734 [0.711, 0.754]	0.741 [0.715, 0.764]	0.772 [0.746, 0.795]
Medical material	0.803 [0.702, 0.883]	0.781 [0.674, 0.873]	0.809 [0.699, 0.898]	0.805 [0.722, 0.881]	0.821 [0.737, 0.891]	0.790 [0.704, 0.867]	0.768 [0.663, 0.861]
Arterial wall calcification	0.859 [0.804, 0.906]	0.822 [0.767, 0.874]	0.815 [0.760, 0.867]	0.857 [0.809, 0.903]	0.863 [0.817, 0.907]	0.871 [0.824, 0.915]	0.897 [0.858, 0.932]
Cardiomegaly	0.867 [0.808, 0.917]	0.858 [0.804, 0.907]	0.887 [0.838, 0.929]	0.877 [0.825, 0.922]	0.877 [0.825, 0.923]	0.875 [0.820, 0.923]	0.871 [0.810, 0.922]
Pericardial effusion	0.751 [0.629, 0.846]	0.708 [0.575, 0.819]	0.748 [0.611, 0.855]	0.764 [0.623, 0.876]	0.782 [0.641, 0.889]	0.762 [0.605, 0.884]	0.766 [0.592, 0.897]
Coronary artery wall calcification	0.848 [0.798, 0.893]	0.809 [0.748, 0.866]	0.813 [0.758, 0.866]	0.851 [0.800, 0.898]	0.838 [0.787, 0.886]	0.852 [0.800, 0.901]	0.883 [0.841, 0.922]
Hiatal hernia	0.658 [0.553, 0.756]	0.649 [0.548, 0.744]	0.661 [0.565, 0.750]	0.706 [0.608, 0.796]	0.702 [0.604, 0.794]	0.711 [0.616, 0.798]	0.764 [0.675, 0.847]
Lymphadenopathy	0.693 [0.612, 0.767]	0.695 [0.624, 0.761]	0.711 [0.642, 0.775]	0.698 [0.627, 0.761]	0.719 [0.652, 0.782]	0.738 [0.673, 0.796]	0.730 [0.658, 0.795]
Emphysema	0.614 [0.532, 0.696]	0.611 [0.534, 0.689]	0.647 [0.569, 0.726]	0.683 [0.604, 0.762]	0.672 [0.591, 0.751]	0.699 [0.620, 0.777]	0.754 [0.684, 0.822]
Atelectasis	0.695 [0.622, 0.763]	0.684 [0.610, 0.752]	0.682 [0.608, 0.748]	0.707 [0.638, 0.770]	0.707 [0.638, 0.770]	0.710 [0.639, 0.776]	0.730 [0.662, 0.792]
Lung nodule	0.593 [0.526, 0.657]	0.606 [0.540, 0.672]	0.596 [0.526, 0.665]	0.603 [0.534, 0.670]	0.606 [0.539, 0.671]	0.631 [0.565, 0.695]	0.605 [0.539, 0.670]
Lung opacity	0.523 [0.442, 0.604]	0.520 [0.436, 0.603]	0.568 [0.484, 0.649]	0.600 [0.514, 0.682]	0.557 [0.480, 0.633]	0.588 [0.518, 0.654]	0.814 [0.762, 0.862]
Pulmonary fibrotic sequela	0.635 [0.555, 0.712]	0.635 [0.554, 0.712]	0.675 [0.599, 0.744]	0.655 [0.572, 0.730]	0.655 [0.577, 0.727]	0.658 [0.582, 0.729]	0.659 [0.584, 0.728]
Pleural effusion	0.867 [0.793, 0.927]	0.883 [0.814, 0.941]	0.886 [0.822, 0.939]	0.884 [0.791, 0.948]	0.911 [0.843, 0.958]	0.903 [0.814, 0.967]	0.897 [0.784, 0.972]
Mosaic attenuation pattern	0.764 [0.672, 0.844]	0.742 [0.660, 0.819]	0.754 [0.661, 0.839]	0.759 [0.665, 0.842]	0.741 [0.651, 0.825]	0.770 [0.675, 0.856]	0.764 [0.672, 0.846]
Peribronchial thickening	0.676 [0.589, 0.759]	0.668 [0.583, 0.748]	0.668 [0.588, 0.744]	0.747 [0.671, 0.816]	0.743 [0.664, 0.814]	0.754 [0.678, 0.824]	0.730 [0.628, 0.818]
Consolidation	0.533 [0.424, 0.656]	0.541 [0.439, 0.658]	0.576 [0.477, 0.685]	0.580 [0.481, 0.687]	0.617 [0.522, 0.717]	0.641 [0.543, 0.724]	0.819 [0.741, 0.887]
Bronchiectasis	0.561 [0.405, 0.696]	0.603 [0.442, 0.745]	0.632 [0.469, 0.776]	0.610 [0.436, 0.771]	0.631 [0.455, 0.785]	0.626 [0.441, 0.782]	0.622 [0.443, 0.773]
Interlobular septal thickening	0.696 [0.552, 0.814]	0.756 [0.633, 0.856]	0.753 [0.609, 0.872]	0.770 [0.626, 0.883]	0.770 [0.630, 0.878]	0.765 [0.619, 0.878]	0.822 [0.718, 0.907]

Supplementary Tab. 19 | Paired differences in macro-AUROC with the classifier trained on full CT. Same 602 test volumes, paired 95% confidence intervals from a bootstrap over patients (10,000 resamples). *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

Projections	Comparison	Difference	*P*
8	DIF-Net minus full CT	−0.047 [−0.063, −0.029]	< 0.001
	DIF-Gaussian minus full CT	−0.055 [−0.073, −0.037]	< 0.001
	C^2RV minus full CT	−0.042 [−0.059, −0.025]	< 0.001
	SVCT minus full CT	−0.027 [−0.042, −0.013]	0.001
	DeepSparse minus full CT	−0.031 [−0.046, −0.016]	< 0.001
	SPARC minus full CT	−0.016 [−0.027, −0.005]	0.016
	SPARC minus DIF-Net	+0.031 [0.016, 0.045]	< 0.001
	SPARC minus DIF-Gaussian	+0.039 [0.023, 0.054]	< 0.001
	SPARC minus C^2RV	+0.026 [0.011, 0.041]	0.003
	SPARC minus SVCT	+0.011 [0.000, 0.023]	0.18
	SPARC minus DeepSparse	+0.015 [0.005, 0.024]	0.012
4	DIF-Net minus full CT	−0.070 [−0.091, −0.048]	< 0.001
	DIF-Gaussian minus full CT	−0.074 [−0.097, −0.049]	< 0.001
	C^2RV minus full CT	−0.056 [−0.077, −0.035]	< 0.001
	SVCT minus full CT	−0.041 [−0.058, −0.025]	< 0.001
	DeepSparse minus full CT	−0.038 [−0.055, −0.022]	< 0.001
	SPARC minus full CT	−0.031 [−0.046, −0.016]	< 0.001
	SPARC minus DIF-Net	+0.039 [0.018, 0.059]	0.001
	SPARC minus DIF-Gaussian	+0.043 [0.022, 0.062]	< 0.001
	SPARC minus C^2RV	+0.026 [0.008, 0.042]	0.015
	SPARC minus SVCT	+0.010 [−0.002, 0.023]	0.22
	SPARC minus DeepSparse	+0.007 [−0.006, 0.019]	0.24

Supplementary Tab. 20 | Further classification metrics with the classifier trained on full CT. The classifier of Supplementary Tab. 18 on each input. Macro-AUPRC is the average precision averaged over the 18 findings. Sensitivity and specificity use, for each finding, the threshold that maximised Youden's index for that classifier on the full-CT validation set (303 volumes, 130 patients), applied unchanged to every input; the macro values average them over the findings. CT-RATE test set, 602 volumes. The metrics are computed on the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples). SPARC minus input is the difference between SPARC and the input of that row, paired by patient. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

	Macro-AUPRC			Macro-sensitivity			Macro-specificity		
Input	Value	SPARC minus input	*P*	Value	SPARC minus input	*P*	Value	SPARC minus input	*P*
Eight projections									
DIF-Net	0.368 [0.336, 0.417]	+0.035 [0.010, 0.059]	0.078	0.707 [0.663, 0.747]	−0.029 [−0.068, 0.003]	1.00	0.601 [0.567, 0.636]	+0.075 [0.057, 0.094]	< 0.001
DIF-Gaussian	0.355 [0.327, 0.403]	+0.049 [0.024, 0.070]	0.001	0.670 [0.617, 0.716]	+0.008 [−0.029, 0.043]	1.00	0.622 [0.588, 0.655]	+0.055 [0.037, 0.073]	< 0.001
C^2RV	0.377 [0.347, 0.423]	+0.026 [0.003, 0.048]	0.27	0.716 [0.665, 0.760]	−0.038 [−0.069, −0.011]	0.13	0.613 [0.581, 0.644]	+0.064 [0.049, 0.080]	< 0.001
SVCT	0.393 [0.365, 0.437]	+0.010 [−0.007, 0.029]	1.00	0.626 [0.565, 0.680]	+0.052 [0.029, 0.074]	< 0.001	0.703 [0.672, 0.733]	−0.026 [−0.040, −0.013]	0.003
DeepSparse	0.379 [0.350, 0.429]	+0.024 [0.011, 0.035]	0.002	0.641 [0.578, 0.694]	+0.037 [0.020, 0.055]	< 0.001	0.683 [0.652, 0.714]	−0.006 [−0.019, 0.007]	1.00
SPARC	0.403 [0.371, 0.453]	–		0.678 [0.619, 0.729]	–		0.677 [0.644, 0.709]	–	
Full CT (reference)	0.430 [0.400, 0.478]	−0.027 [−0.046, −0.010]	0.048	0.672 [0.610, 0.725]	+0.006 [−0.020, 0.032]	1.00	0.733 [0.696, 0.768]	−0.056 [−0.073, −0.039]	< 0.001
Four projections									
DIF-Net	0.343 [0.316, 0.390]	+0.041 [0.012, 0.065]	0.044	0.704 [0.663, 0.739]	−0.011 [−0.053, 0.026]	1.00	0.545 [0.516, 0.575]	+0.096 [0.072, 0.121]	< 0.001
DIF-Gaussian	0.339 [0.315, 0.381]	+0.045 [0.014, 0.072]	0.039	0.688 [0.644, 0.727]	+0.006 [−0.030, 0.037]	1.00	0.554 [0.522, 0.585]	+0.087 [0.068, 0.107]	< 0.001
C^2RV	0.362 [0.332, 0.409]	+0.022 [−0.007, 0.048]	1.00	0.652 [0.601, 0.697]	+0.042 [0.006, 0.075]	0.23	0.611 [0.580, 0.642]	+0.031 [0.013, 0.048]	0.009
SVCT	0.379 [0.347, 0.425]	+0.005 [−0.012, 0.023]	1.00	0.631 [0.574, 0.681]	+0.062 [0.032, 0.091]	< 0.001	0.670 [0.642, 0.697]	−0.028 [−0.043, −0.013]	0.004
DeepSparse	0.372 [0.347, 0.417]	+0.012 [−0.006, 0.024]	1.00	0.638 [0.583, 0.686]	+0.055 [0.032, 0.079]	< 0.001	0.682 [0.651, 0.712]	−0.040 [−0.055, −0.025]	< 0.001
SPARC	0.384 [0.353, 0.431]	–		0.693 [0.636, 0.742]	–		0.641 [0.610, 0.672]	–	
Full CT (reference)	0.430 [0.400, 0.478]	−0.046 [−0.071, −0.025]	0.002	0.672 [0.610, 0.725]	+0.021 [−0.007, 0.050]	1.00	0.733 [0.696, 0.768]	−0.091 [−0.114, −0.068]	< 0.001

Supplementary Tab. 21 | Grad-CAM maps: agreement with the map on full CT and share inside the involved organ. Every positive CT-RATE test volume for ten findings with an anatomical location (1,311 volume–finding pairs, 203 patients). Upper block: Pearson correlation, inside the body, between the Grad-CAM map of the classifier trained on full CT (seed 0) on each method's reconstruction and its map on the CT itself, SPARC's paired difference, and the percentage of volume–finding pairs in which the map on SPARC's reconstruction was closer to the map on CT. Lower block: for the same ten findings, the share of the seed-0 Grad-CAM map (inside the body) that lies in the involved organ (in parentheses; TotalSegmentator on the CT, dilated by 3 voxels, or by a 16-mm margin for the effusions), for the classifier trained on full CT (on the CT), SPARC* (the classifier trained on SPARC's reconstructions) and SPARC† (SPARC's finetuned encoder with a classification head). Brackets, 95% confidence intervals from a bootstrap over patients (10,000 resamples). *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

Reconstruction	Correlation with the map on CT	SPARC minus method	*P*	SPARC closer (% of pairs)
Eight projections				
DIF-Net	0.507 [0.484, 0.528]	+0.162 [0.150, 0.175]	<0.001	99%
DIF-Gaussian	0.515 [0.492, 0.536]	+0.155 [0.140, 0.171]	<0.001	99%
C^2RV	0.549 [0.526, 0.569]	+0.120 [0.112, 0.129]	<0.001	97%
SVCT	0.569 [0.548, 0.589]	+0.100 [0.091, 0.110]	<0.001	96%
DeepSparse	0.585 [0.567, 0.603]	+0.084 [0.078, 0.091]	<0.001	94%
SPARC	0.669 [0.649, 0.688]	–		–
Four projections				
DIF-Net	0.417 [0.394, 0.439]	+0.163 [0.146, 0.181]	<0.001	97%
DIF-Gaussian	0.433 [0.407, 0.456]	+0.148 [0.131, 0.166]	<0.001	98%
C^2RV	0.463 [0.444, 0.482]	+0.118 [0.107, 0.128]	<0.001	96%
SVCT	0.491 [0.472, 0.510]	+0.089 [0.079, 0.100]	<0.001	90%
DeepSparse	0.510 [0.491, 0.528]	+0.071 [0.062, 0.080]	<0.001	89%
SPARC	0.581 [0.559, 0.600]	–		–

Share of the Grad-CAM map inside the involved organ, eight projections					
Finding (organ)	Full CT	SPARC*	SPARC†	SPARC† minus SPARC*	*P*
Cardiomegaly (heart; n = 65)	0.018 [0.014, 0.023]	0.072 [0.050, 0.099]	0.098 [0.079, 0.120]	+0.026 [0.006, 0.045]	0.015
Coronary artery wall calcification (heart; n = 153)	0.021 [0.019, 0.024]	0.013 [0.012, 0.014]	0.045 [0.039, 0.050]	+0.032 [0.027, 0.037]	<0.001
Pericardial effusion (heart, 16-mm margin; n = 30)	0.082 [0.063, 0.098]	0.153 [0.071, 0.236]	0.135 [0.110, 0.155]	−0.017 [−0.094, 0.060]	0.66
Arterial wall calcification (aorta; n = 160)	0.021 [0.018, 0.023]	0.019 [0.017, 0.021]	0.029 [0.027, 0.032]	+0.010 [0.008, 0.012]	<0.001
Pleural effusion (lungs, 16-mm margin; n = 54)	0.198 [0.161, 0.231]	0.238 [0.184, 0.289]	0.355 [0.292, 0.401]	+0.117 [0.050, 0.171]	<0.001
Consolidation (lungs; n = 102)	0.399 [0.351, 0.440]	0.130 [0.101, 0.155]	0.250 [0.221, 0.279]	+0.120 [0.094, 0.150]	<0.001
Lung opacity (lungs; n = 223)	0.385 [0.362, 0.408]	0.082 [0.067, 0.098]	0.248 [0.226, 0.268]	+0.166 [0.143, 0.189]	<0.001
Atelectasis (lungs; n = 135)	0.390 [0.369, 0.412]	0.434 [0.408, 0.459]	0.157 [0.144, 0.171]	−0.277 [−0.304, −0.252]	<0.001
Emphysema (lungs; n = 116)	0.491 [0.455, 0.521]	0.581 [0.541, 0.617]	0.284 [0.257, 0.308]	−0.297 [−0.324, −0.272]	<0.001
Lung nodule (lungs; n = 273)	0.448 [0.429, 0.467]	0.566 [0.535, 0.595]	0.228 [0.213, 0.244]	−0.338 [−0.357, −0.317]	<0.001

Supplementary Tab. 22 | Segmentation with the segmentation model trained on full CT (Dice). Each method's test reconstructions were given, unchanged, to the segmentation model trained on full CT; the reference column is that segmentation model on the full CT. TotalSegmentator test set, 79 volumes. Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples).

	Reconstruction given to the segmentation model trained on full CT						Reference
Structure	DIF-Net	DIF-Gaussian	C^2RV	SVCT	DeepSparse	**SPARC**	Full CT
Eight projections							
Abdominal organs (mean)	0.487 [0.452, 0.519]	0.389 [0.357, 0.419]	0.536 [0.496, 0.573]	0.680 [0.639, 0.718]	0.668 [0.628, 0.704]	0.740 [0.705, 0.772]	0.860 [0.831, 0.884]
Liver	0.688 [0.637, 0.733]	0.562 [0.513, 0.607]	0.735 [0.684, 0.781]	0.809 [0.759, 0.850]	0.806 [0.756, 0.847]	0.850 [0.804, 0.885]	0.896 [0.851, 0.931]
Spleen	0.601 [0.552, 0.647]	0.546 [0.500, 0.590]	0.614 [0.564, 0.660]	0.763 [0.727, 0.794]	0.717 [0.674, 0.755]	0.812 [0.786, 0.834]	0.924 [0.909, 0.936]
Left kidney	0.341 [0.291, 0.390]	0.246 [0.204, 0.290]	0.412 [0.352, 0.472]	0.571 [0.498, 0.639]	0.551 [0.484, 0.614]	0.635 [0.566, 0.699]	0.795 [0.735, 0.850]
Right kidney	0.362 [0.308, 0.414]	0.254 [0.203, 0.305]	0.444 [0.385, 0.501]	0.624 [0.553, 0.688]	0.608 [0.542, 0.667]	0.682 [0.616, 0.740]	0.829 [0.762, 0.885]
Aorta	0.443 [0.408, 0.477]	0.336 [0.298, 0.375]	0.473 [0.424, 0.519]	0.634 [0.584, 0.680]	0.656 [0.610, 0.698]	0.723 [0.683, 0.759]	0.854 [0.822, 0.882]
Lung lobes (mean)	0.695 [0.658, 0.728]	0.607 [0.566, 0.647]	0.697 [0.651, 0.737]	0.732 [0.695, 0.765]	0.784 [0.750, 0.814]	0.819 [0.788, 0.846]	0.881 [0.853, 0.906]
Left upper lobe	0.645 [0.583, 0.704]	0.569 [0.504, 0.633]	0.666 [0.603, 0.725]	0.709 [0.654, 0.760]	0.745 [0.689, 0.797]	0.786 [0.733, 0.835]	0.852 [0.799, 0.898]
Left lower lobe	0.698 [0.640, 0.752]	0.648 [0.586, 0.705]	0.679 [0.609, 0.743]	0.752 [0.694, 0.804]	0.796 [0.743, 0.843]	0.832 [0.784, 0.873]	0.894 [0.851, 0.928]
Right upper lobe	0.748 [0.694, 0.796]	0.648 [0.583, 0.706]	0.744 [0.689, 0.791]	0.748 [0.697, 0.790]	0.833 [0.788, 0.869]	0.854 [0.802, 0.895]	0.922 [0.881, 0.953]
Right middle lobe	0.647 [0.599, 0.690]	0.500 [0.449, 0.550]	0.669 [0.618, 0.717]	0.686 [0.641, 0.727]	0.747 [0.698, 0.789]	0.790 [0.746, 0.828]	0.854 [0.803, 0.897]
Right lower lobe	0.735 [0.670, 0.794]	0.673 [0.605, 0.737]	0.724 [0.650, 0.792]	0.765 [0.697, 0.826]	0.799 [0.736, 0.855]	0.831 [0.773, 0.882]	0.885 [0.836, 0.927]
Four projections							
Abdominal organs (mean)	0.312 [0.285, 0.339]	0.310 [0.287, 0.332]	0.403 [0.368, 0.436]	0.467 [0.428, 0.503]	0.553 [0.516, 0.586]	0.685 [0.651, 0.716]	0.860 [0.831, 0.884]
Liver	0.562 [0.515, 0.605]	0.591 [0.541, 0.637]	0.689 [0.637, 0.736]	0.704 [0.648, 0.754]	0.750 [0.701, 0.792]	0.825 [0.780, 0.862]	0.896 [0.851, 0.931]
Spleen	0.339 [0.292, 0.386]	0.400 [0.356, 0.440]	0.428 [0.374, 0.480]	0.551 [0.493, 0.605]	0.607 [0.554, 0.655]	0.742 [0.709, 0.769]	0.924 [0.909, 0.936]
Left kidney	0.193 [0.158, 0.228]	0.145 [0.116, 0.173]	0.272 [0.223, 0.323]	0.303 [0.247, 0.358]	0.405 [0.350, 0.458]	0.567 [0.501, 0.627]	0.795 [0.735, 0.850]
Right kidney	0.183 [0.147, 0.219]	0.136 [0.110, 0.163]	0.232 [0.189, 0.274]	0.286 [0.233, 0.339]	0.422 [0.372, 0.469]	0.603 [0.544, 0.658]	0.829 [0.762, 0.885]
Aorta	0.284 [0.254, 0.312]	0.277 [0.244, 0.309]	0.393 [0.352, 0.433]	0.489 [0.440, 0.535]	0.580 [0.534, 0.622]	0.689 [0.649, 0.723]	0.854 [0.822, 0.882]
Lung lobes (mean)	0.538 [0.492, 0.581]	0.553 [0.511, 0.592]	0.613 [0.568, 0.654]	0.633 [0.592, 0.670]	0.715 [0.674, 0.751]	0.775 [0.742, 0.805]	0.881 [0.853, 0.906]
Left upper lobe	0.516 [0.457, 0.573]	0.517 [0.454, 0.579]	0.574 [0.510, 0.635]	0.623 [0.565, 0.678]	0.685 [0.625, 0.740]	0.755 [0.701, 0.805]	0.852 [0.799, 0.898]
Left lower lobe	0.544 [0.481, 0.604]	0.594 [0.531, 0.653]	0.617 [0.549, 0.680]	0.661 [0.597, 0.721]	0.729 [0.669, 0.785]	0.793 [0.741, 0.839]	0.894 [0.851, 0.928]
Right upper lobe	0.548 [0.485, 0.606]	0.574 [0.511, 0.630]	0.637 [0.576, 0.688]	0.651 [0.603, 0.691]	0.735 [0.680, 0.782]	0.800 [0.748, 0.842]	0.922 [0.881, 0.953]
Right middle lobe	0.504 [0.449, 0.556]	0.454 [0.408, 0.499]	0.582 [0.531, 0.630]	0.550 [0.499, 0.599]	0.679 [0.629, 0.724]	0.737 [0.691, 0.779]	0.854 [0.803, 0.897]
Right lower lobe	0.579 [0.511, 0.643]	0.625 [0.560, 0.687]	0.657 [0.585, 0.724]	0.680 [0.611, 0.744]	0.747 [0.679, 0.807]	0.790 [0.723, 0.849]	0.885 [0.836, 0.927]

Supplementary Tab. 23 | Paired differences in mean Dice with the segmentation model trained on full CT. Same 79 test volumes, paired 95% confidence intervals from a bootstrap over patients (10,000 resamples). *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

		Abdominal organs		Lung lobes	
Projections	Comparison	Difference	*P*	Difference	*P*
8	DIF-Net minus full CT	−0.373 [−0.397, −0.349]	< 0.001	−0.187 [−0.205, −0.170]	< 0.001
	DIF-Gaussian minus full CT	−0.471 [−0.495, −0.447]	< 0.001	−0.274 [−0.299, −0.250]	< 0.001
	C^2RV minus full CT	−0.324 [−0.352, −0.298]	< 0.001	−0.185 [−0.210, −0.162]	< 0.001
	SVCT minus full CT	−0.180 [−0.205, −0.158]	< 0.001	−0.149 [−0.170, −0.131]	< 0.001
	DeepSparse minus full CT	−0.192 [−0.216, −0.171]	< 0.001	−0.097 [−0.109, −0.086]	< 0.001
	SPARC minus full CT	−0.119 [−0.136, −0.105]	< 0.001	−0.063 [−0.071, −0.054]	< 0.001
	SPARC minus DIF-Net	+0.253 [0.236, 0.271]	< 0.001	+0.124 [0.110, 0.139]	< 0.001
	SPARC minus DIF-Gaussian	+0.351 [0.332, 0.371]	< 0.001	+0.211 [0.190, 0.234]	< 0.001
	SPARC minus C^2RV	+0.205 [0.186, 0.225]	< 0.001	+0.122 [0.103, 0.143]	< 0.001
	SPARC minus SVCT	+0.060 [0.049, 0.072]	< 0.001	+0.087 [0.073, 0.102]	< 0.001
	SPARC minus DeepSparse	+0.073 [0.062, 0.083]	< 0.001	+0.035 [0.028, 0.042]	< 0.001
4	DIF-Net minus full CT	−0.548 [−0.571, −0.523]	< 0.001	−0.343 [−0.377, −0.311]	< 0.001
	DIF-Gaussian minus full CT	−0.550 [−0.572, −0.527]	< 0.001	−0.328 [−0.355, −0.303]	< 0.001
	C^2RV minus full CT	−0.457 [−0.484, −0.431]	< 0.001	−0.268 [−0.297, −0.241]	< 0.001
	SVCT minus full CT	−0.393 [−0.421, −0.366]	< 0.001	−0.248 [−0.274, −0.223]	< 0.001
	DeepSparse minus full CT	−0.307 [−0.330, −0.286]	< 0.001	−0.166 [−0.188, −0.146]	< 0.001
	SPARC minus full CT	−0.175 [−0.194, −0.158]	< 0.001	−0.106 [−0.121, −0.093]	< 0.001
	SPARC minus DIF-Net	+0.373 [0.351, 0.394]	< 0.001	+0.237 [0.213, 0.261]	< 0.001
	SPARC minus DIF-Gaussian	+0.375 [0.352, 0.397]	< 0.001	+0.222 [0.203, 0.243]	< 0.001
	SPARC minus C^2RV	+0.282 [0.262, 0.303]	< 0.001	+0.162 [0.142, 0.183]	< 0.001
	SPARC minus SVCT	+0.218 [0.201, 0.237]	< 0.001	+0.142 [0.126, 0.158]	< 0.001
	SPARC minus DeepSparse	+0.132 [0.121, 0.145]	< 0.001	+0.060 [0.049, 0.072]	< 0.001

Supplementary Tab. 24 | Further segmentation metrics with the segmentation model trained on full CT, eight projections. The segmentation model of Supplementary Tab. 22 on each input; TotalSegmentator test set, 79 volumes. Metrics are averaged over test volumes and over the five abdominal organs or the five lung lobes. NSD, normalised surface Dice: the share of both boundaries within the stated tolerance of the other; HD95, 95th percentile of the symmetric boundary distance; ASD, mean distance from the predicted to the reference boundary; ASSD, its symmetric version; volume error, predicted minus reference volume relative to the reference, only for structures lying wholly inside the scan (272 of 641 volume–structure pairs), because for a structure cut by the scan's coverage a few reference voxels give errors of thousands of per cent. Higher is better for Dice and NSD, lower for the distances and the absolute volume error. Structures absent from a reference volume are skipped. A structure the segmentation model did not predict at all counts as Dice 0 and NSD 0 and volume error -100% and is left out of the distances (eight projections: DIF-Net 25, DIF-Gaussian 39, C^2RV 30, SVCT 17, DeepSparse 20, **SPARC** 15, Full CT 12 of 1,923 structure predictions, three per volume–structure pair from the three training seeds). Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples). The lower block gives SPARC minus each input, paired over the same patients. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods); for the signed volume error, *P* tests the difference from zero.

Input	Dice	NSD, 2 mm	NSD, 3 mm	HD95 (mm)	ASD (mm)	ASSD (mm)	Abs. volume error (%)	Signed volume error (%)	*P* (signed error vs 0)
Abdominal organs									
DIF-Net	0.487 [0.452, 0.519]	0.240 [0.220, 0.260]	0.327 [0.301, 0.353]	48.0 [40.7, 56.5]	18.67 [13.87, 24.72]	17.38 [13.46, 22.25]	34.6 [31.1, 38.3]	−27.0 [−32.0, −21.2]	< 0.001
DIF-Gaussian	0.389 [0.357, 0.419]	0.186 [0.169, 0.204]	0.259 [0.235, 0.282]	70.9 [63.3, 79.6]	28.45 [23.29, 34.76]	24.66 [20.40, 29.91]	42.5 [39.4, 46.2]	−38.4 [−43.0, −34.1]	< 0.001
C^2RV	0.536 [0.496, 0.573]	0.261 [0.238, 0.283]	0.355 [0.325, 0.385]	43.4 [36.1, 51.8]	17.71 [12.51, 24.10]	17.33 [12.47, 23.29]	28.5 [23.7, 33.3]	−16.8 [−22.8, −10.2]	< 0.001
SVCT	0.680 [0.639, 0.718]	0.369 [0.338, 0.398]	0.495 [0.456, 0.531]	29.9 [23.7, 37.2]	13.44 [8.62, 19.67]	12.76 [8.54, 18.06]	22.8 [15.3, 29.8]	−6.9 [−15.4, 3.4]	0.76
DeepSparse	0.668 [0.628, 0.704]	0.372 [0.343, 0.400]	0.490 [0.454, 0.524]	30.6 [24.0, 38.8]	11.99 [7.69, 17.64]	11.22 [7.72, 15.72]	23.0 [18.1, 27.5]	−6.1 [−12.0, 1.4]	0.66
SPARC	0.740 [0.705, 0.772]	0.471 [0.440, 0.500]	0.596 [0.561, 0.629]	22.4 [17.8, 27.9]	9.13 [6.27, 12.67]	8.60 [6.04, 11.77]	15.5 [12.2, 18.9]	+0.9 [−3.9, 6.1]	1.00
Full CT (reference)	0.860 [0.831, 0.884]	0.776 [0.743, 0.806]	0.843 [0.811, 0.871]	16.8 [12.5, 21.9]	6.78 [4.29, 10.02]	5.80 [3.66, 8.60]	8.1 [6.1, 10.5]	+1.2 [−1.2, 4.2]	1.00
Lung lobes									
DIF-Net	0.695 [0.658, 0.728]	0.475 [0.446, 0.504]	0.561 [0.530, 0.592]	55.0 [45.2, 66.0]	21.45 [16.58, 26.92]	16.63 [12.68, 21.08]	14.2 [11.9, 16.5]	−2.7 [−4.6, −1.0]	0.049
DIF-Gaussian	0.607 [0.566, 0.647]	0.377 [0.349, 0.404]	0.456 [0.425, 0.486]	93.3 [79.6, 108.3]	36.31 [28.60, 45.02]	27.89 [21.71, 34.84]	16.4 [14.1, 18.8]	−1.6 [−4.0, 0.9]	0.85
C^2RV	0.697 [0.651, 0.737]	0.471 [0.433, 0.507]	0.558 [0.518, 0.596]	47.8 [38.4, 58.1]	20.54 [14.98, 26.79]	16.03 [11.69, 20.87]	12.4 [10.3, 14.6]	−2.3 [−5.3, 0.4]	0.76
SVCT	0.732 [0.695, 0.765]	0.545 [0.514, 0.574]	0.638 [0.604, 0.668]	33.1 [27.6, 39.3]	12.17 [9.28, 15.62]	10.22 [7.73, 13.17]	13.7 [11.7, 15.8]	−10.1 [−13.1, −7.0]	< 0.001
DeepSparse	0.784 [0.750, 0.814]	0.602 [0.574, 0.629]	0.693 [0.664, 0.721]	30.5 [24.1, 37.8]	11.56 [8.19, 15.62]	9.27 [6.42, 12.78]	8.1 [6.2, 10.4]	−1.7 [−3.5, 0.0]	0.54
SPARC	0.819 [0.788, 0.846]	0.682 [0.654, 0.708]	0.754 [0.726, 0.779]	23.5 [17.5, 31.0]	8.78 [5.62, 12.86]	7.28 [4.61, 10.77]	7.3 [5.3, 9.7]	−1.9 [−4.1, 0.4]	0.76
Full CT (reference)	0.881 [0.853, 0.906]	0.828 [0.801, 0.851]	0.870 [0.844, 0.894]	14.4 [9.4, 20.4]	4.97 [2.75, 7.97]	4.45 [2.56, 6.94]	3.2 [2.0, 4.7]	−0.7 [−2.2, 0.8]	1.00

	Dice		NSD, 2 mm		HD95 (mm)		ASSD (mm)		Abs. volume error (%)	
SPARC minus	Difference	*P*	Difference	*P*	Difference	*P*	Difference	*P*	Difference	*P*
Abdominal organs										
DIF-Net	+0.253 [0.236, 0.271]	< 0.001	+0.231 [0.216, 0.245]	< 0.001	−25.6 [−30.9, −20.8]	< 0.001	−8.78 [−11.45, −6.71]	< 0.001	−19.2 [−21.9, −16.2]	< 0.001
DIF-Gaussian	+0.351 [0.332, 0.371]	< 0.001	+0.285 [0.265, 0.305]	< 0.001	−48.5 [−54.7, −42.9]	< 0.001	−16.06 [−19.12, −13.68]	< 0.001	−27.0 [−31.0, −23.3]	< 0.001
C^2RV	+0.205 [0.186, 0.225]	< 0.001	+0.210 [0.194, 0.226]	< 0.001	−21.0 [−26.1, −16.1]	< 0.001	−8.73 [−12.75, −5.52]	< 0.001	−13.1 [−16.1, −9.6]	< 0.001
SVCT	+0.060 [0.049, 0.072]	< 0.001	+0.102 [0.092, 0.112]	< 0.001	−7.5 [−10.8, −4.5]	< 0.001	−4.16 [−6.94, −2.11]	0.012	−7.3 [−12.5, −1.4]	0.11
DeepSparse	+0.073 [0.062, 0.083]	< 0.001	+0.099 [0.090, 0.107]	< 0.001	−8.2 [−12.9, −4.1]	0.004	−2.62 [−4.76, −0.89]	0.10	−7.6 [−9.8, −3.9]	< 0.001
Full CT	−0.119 [−0.136, −0.105]	< 0.001	−0.305 [−0.322, −0.287]	< 0.001	+5.6 [3.1, 8.4]	< 0.001	+2.80 [1.52, 4.27]	0.001	+7.3 [5.4, 9.3]	< 0.001
Lung lobes										
DIF-Net	+0.124 [0.110, 0.139]	< 0.001	+0.206 [0.191, 0.222]	< 0.001	−31.4 [−39.5, −24.2]	< 0.001	−9.35 [−12.46, −6.52]	< 0.001	−6.9 [−9.4, −3.9]	< 0.001
DIF-Gaussian	+0.211 [0.190, 0.234]	< 0.001	+0.305 [0.284, 0.326]	< 0.001	−69.7 [−82.2, −58.5]	< 0.001	−20.60 [−26.17, −15.77]	< 0.001	−9.1 [−11.6, −6.4]	< 0.001
C^2RV	+0.122 [0.103, 0.143]	< 0.001	+0.211 [0.189, 0.234]	< 0.001	−24.3 [−32.2, −17.0]	< 0.001	−8.75 [−12.19, −5.61]	< 0.001	−5.1 [−7.1, −2.9]	< 0.001
SVCT	+0.087 [0.073, 0.102]	< 0.001	+0.137 [0.125, 0.149]	< 0.001	−9.6 [−13.3, −5.7]	< 0.001	−2.94 [−4.82, −1.06]	0.033	−6.4 [−8.4, −4.2]	< 0.001
DeepSparse	+0.035 [0.028, 0.042]	< 0.001	+0.079 [0.072, 0.087]	< 0.001	−6.9 [−10.4, −3.7]	0.001	−1.98 [−3.57, −0.58]	0.11	−0.8 [−1.8, 0.1]	0.76
Full CT	−0.063 [−0.071, −0.054]	< 0.001	−0.146 [−0.160, −0.132]	< 0.001	+9.1 [5.9, 12.4]	< 0.001	+2.84 [1.75, 4.32]	< 0.001	+4.2 [3.0, 5.5]	< 0.001

Supplementary Tab. 25 | Further segmentation metrics with the segmentation model trained on full CT, four projections. As Supplementary Tab. 24, with four projections and without the paired differences; structures not predicted at all: DIF-Net 26, DIF-Gaussian 41, C^2RV 44, SVCT 52, DeepSparse 28, **SPARC** 19, Full CT 12 of 1,923 structure predictions. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods); for the signed volume error, *P* tests the difference from zero.

Input	Dice	NSD, 2 mm	NSD, 3 mm	HD95 (mm)	ASD (mm)	ASSD (mm)	Abs. volume error (%)	Signed volume error (%)	*P* (signed error vs 0)
Abdominal organs									
DIF-Net	0.312 [0.285, 0.339]	0.144 [0.131, 0.158]	0.200 [0.182, 0.219]	73.6 [65.9, 82.4]	30.01 [24.60, 36.23]	28.30 [23.75, 33.68]	53.5 [49.0, 58.0]	−49.0 [−54.5, −42.8]	< 0.001
DIF-Gaussian	0.310 [0.287, 0.332]	0.131 [0.120, 0.143]	0.184 [0.168, 0.200]	79.6 [71.6, 88.8]	32.40 [26.97, 38.87]	29.81 [25.34, 35.22]	51.6 [45.3, 57.4]	−42.5 [−51.1, −33.2]	< 0.001
C^2RV	0.403 [0.368, 0.436]	0.180 [0.163, 0.197]	0.248 [0.225, 0.271]	57.7 [50.4, 66.0]	23.22 [18.22, 29.13]	22.40 [18.10, 27.48]	43.1 [39.3, 46.9]	−37.5 [−42.3, −32.1]	< 0.001
SVCT	0.467 [0.428, 0.503]	0.202 [0.182, 0.221]	0.282 [0.255, 0.308]	55.9 [47.6, 65.3]	24.15 [18.08, 31.71]	23.49 [18.05, 30.22]	40.5 [35.4, 45.2]	−34.0 [−39.2, −27.6]	< 0.001
DeepSparse	0.553 [0.516, 0.586]	0.264 [0.243, 0.285]	0.356 [0.329, 0.382]	39.9 [33.3, 47.7]	15.91 [11.89, 20.84]	14.51 [11.25, 18.41]	30.8 [25.8, 35.9]	−13.9 [−20.0, −5.9]	< 0.001
SPARC	0.685 [0.651, 0.716]	0.374 [0.349, 0.399]	0.487 [0.457, 0.517]	25.5 [20.2, 32.2]	10.75 [7.26, 15.17]	10.13 [7.04, 13.99]	21.6 [17.3, 27.1]	+2.5 [−3.4, 10.1]	1.00
Full CT (reference)	0.860 [0.831, 0.884]	0.776 [0.743, 0.806]	0.843 [0.811, 0.871]	16.8 [12.5, 21.9]	6.78 [4.29, 10.02]	5.80 [3.66, 8.60]	8.1 [6.1, 10.5]	+1.2 [−1.2, 4.2]	1.00
Lung lobes									
DIF-Net	0.538 [0.492, 0.581]	0.308 [0.278, 0.337]	0.384 [0.350, 0.417]	125.4 [110.2, 141.8]	49.62 [41.40, 58.60]	36.94 [30.37, 44.08]	21.9 [17.7, 26.2]	−14.2 [−20.9, −7.6]	< 0.001
DIF-Gaussian	0.553 [0.511, 0.592]	0.301 [0.276, 0.326]	0.380 [0.350, 0.409]	90.0 [76.7, 104.5]	36.11 [28.59, 44.49]	28.29 [22.24, 35.00]	19.8 [17.5, 22.2]	−4.6 [−7.3, −1.8]	0.006
C^2RV	0.613 [0.568, 0.654]	0.361 [0.328, 0.394]	0.449 [0.412, 0.486]	60.5 [48.6, 73.7]	26.17 [19.17, 34.04]	20.87 [15.34, 27.00]	17.5 [14.7, 20.2]	−10.0 [−14.1, −5.8]	< 0.001
SVCT	0.633 [0.592, 0.670]	0.413 [0.384, 0.442]	0.511 [0.477, 0.543]	56.0 [46.9, 65.9]	20.91 [16.12, 26.28]	16.99 [13.06, 21.45]	23.7 [19.7, 27.5]	−21.4 [−26.2, −16.2]	< 0.001
DeepSparse	0.715 [0.674, 0.751]	0.481 [0.449, 0.511]	0.583 [0.549, 0.616]	38.0 [30.5, 46.7]	14.03 [9.84, 19.43]	11.35 [8.12, 15.45]	12.5 [10.3, 14.9]	−4.2 [−7.1, −1.3]	0.024
SPARC	0.775 [0.742, 0.805]	0.593 [0.563, 0.621]	0.684 [0.653, 0.712]	26.1 [21.0, 31.9]	10.08 [7.10, 13.79]	8.03 [5.80, 10.76]	9.6 [7.4, 11.8]	−3.6 [−6.4, −0.7]	0.054
Full CT (reference)	0.881 [0.853, 0.906]	0.828 [0.801, 0.851]	0.870 [0.844, 0.894]	14.4 [9.4, 20.4]	4.97 [2.75, 7.97]	4.45 [2.56, 6.94]	3.2 [2.0, 4.7]	−0.7 [−2.2, 0.8]	1.00

Supplementary Tab. 26 | SPARC and DeepSparse with 2, 4, 8 and 16 projections on CT-RATE and TotalSegmentator. Each number of projections is a separately trained reconstruction model (two projections bi-planar, the others uniformly spaced). Classification and segmentation use the classifier and segmentation model trained on full CT, applied unchanged to each reconstruction, as in Fig. 5 and 6 (full CT: macro-AUROC 0.772 [0.746, 0.795]; mean Dice 0.860 [0.831, 0.884] for the abdominal organs and 0.881 [0.853, 0.906] for the lung lobes). CT-RATE test set 602 volumes (261 patients), TotalSegmentator 79. PSNR, SSIM and Dice are means over the full test set and AUROC is computed on it; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples). The SPARC minus DeepSparse column is paired over the same patients. Rows for four and eight projections repeat Supplementary Tab. 1–3, 18, 19, 22 and 23. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods), so a comparison repeated from another table can carry a different *P* value there.

Projections	DeepSparse	SPARC	SPARC minus DeepSparse	*P*
CT-RATE, reconstruction PSNR (dB)				
2	24.26 [24.09, 24.43]	27.77 [27.61, 27.92]	+3.50 [3.39, 3.62]	< 0.001
4	27.16 [26.99, 27.31]	29.41 [29.25, 29.56]	+2.25 [2.16, 2.35]	< 0.001
8	29.32 [29.18, 29.45]	31.39 [31.25, 31.54]	+2.07 [2.01, 2.14]	< 0.001
16	30.70 [30.57, 30.83]	32.86 [32.72, 33.00]	+2.15 [2.09, 2.22]	< 0.001
CT-RATE, reconstruction SSIM (×100)				
2	76.30 [75.77, 76.81]	85.02 [84.58, 85.47]	+8.72 [8.50, 8.95]	< 0.001
4	83.46 [83.02, 83.90]	87.15 [86.76, 87.53]	+3.69 [3.55, 3.83]	< 0.001
8	80.69 [80.22, 81.14]	89.18 [88.85, 89.50]	+8.48 [7.89, 9.13]	< 0.001
16	88.00 [87.74, 88.25]	90.79 [90.49, 91.08]	+2.79 [2.66, 2.93]	< 0.001
CT-RATE, classification macro-AUROC				
2	0.715 [0.692, 0.736]	0.734 [0.706, 0.757]	+0.019 [0.001, 0.035]	0.053
4	0.734 [0.711, 0.754]	0.741 [0.715, 0.764]	+0.007 [−0.006, 0.019]	0.24
8	0.741 [0.715, 0.764]	0.756 [0.730, 0.779]	+0.015 [0.005, 0.024]	0.008
16	0.759 [0.734, 0.782]	0.767 [0.740, 0.790]	+0.007 [0.001, 0.013]	0.049
TotalSegmentator, reconstruction PSNR (dB)				
2	23.87 [23.50, 24.22]	27.66 [27.25, 28.06]	+3.79 [3.55, 4.03]	< 0.001
4	26.63 [26.25, 27.01]	29.37 [28.98, 29.76]	+2.74 [2.59, 2.89]	< 0.001
8	28.76 [28.45, 29.07]	31.37 [31.03, 31.72]	+2.62 [2.50, 2.73]	< 0.001
16	30.17 [29.87, 30.47]	32.83 [32.51, 33.16]	+2.66 [2.55, 2.78]	< 0.001
TotalSegmentator, reconstruction SSIM (×100)				
2	72.40 [70.93, 73.92]	85.25 [84.30, 86.22]	+12.85 [11.99, 13.70]	< 0.001
4	81.27 [80.19, 82.38]	87.46 [86.74, 88.17]	+6.19 [5.64, 6.72]	< 0.001
8	83.39 [82.32, 84.49]	90.46 [89.86, 91.05]	+7.06 [6.25, 7.91]	< 0.001
16	85.37 [84.48, 86.28]	92.53 [92.03, 93.04]	+7.16 [6.47, 7.86]	< 0.001
TotalSegmentator, abdominal organs, mean Dice				
2	0.449 [0.415, 0.480]	0.641 [0.605, 0.673]	+0.192 [0.176, 0.208]	< 0.001
4	0.553 [0.516, 0.586]	0.685 [0.651, 0.716]	+0.132 [0.121, 0.145]	< 0.001
8	0.668 [0.628, 0.704]	0.740 [0.705, 0.772]	+0.073 [0.062, 0.083]	< 0.001
16	0.708 [0.667, 0.745]	0.780 [0.745, 0.811]	+0.072 [0.062, 0.084]	< 0.001
TotalSegmentator, lung lobes, mean Dice				
2	0.625 [0.577, 0.669]	0.723 [0.687, 0.755]	+0.098 [0.079, 0.120]	< 0.001
4	0.715 [0.674, 0.751]	0.775 [0.742, 0.805]	+0.060 [0.049, 0.072]	< 0.001
8	0.784 [0.750, 0.814]	0.819 [0.788, 0.846]	+0.035 [0.028, 0.042]	< 0.001
16	0.807 [0.774, 0.837]	0.847 [0.818, 0.874]	+0.040 [0.034, 0.047]	< 0.001

Supplementary Tab. 27 | Reconstruction with fewer adaptation patients (CT-RATE, 8 projections). Rows are nested subsets of the 913 patients in the training set of the CT-RATE validation cohort; each subset contains the smaller ones. For every selected patient, the simulated projections are paired with the full CT as the reconstruction target. The protocol and the 602-volume test set are identical at every budget. From scratch is SPARC's architecture trained without pretraining; with all 913 patients it is the No pretraining model of Supplementary Tab. 28. Differences are paired by patient. Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples). *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

		Mean				SPARC minus comparator					
						From scratch		DeepSparse		SVCT	
Patients	Volumes	**SPARC**	From scratch	DeepSparse	SVCT	Difference	*P*	Difference	*P*	Difference	*P*
PSNR (dB)											
10	28	28.17 [28.03, 28.30]	23.95 [23.83, 24.08]	24.77 [24.59, 24.94]	23.54 [23.42, 23.66]	+4.21 [4.15, 4.28]	<0.001	+3.40 [3.31, 3.49]	<0.001	+4.62 [4.55, 4.69]	<0.001
25	64	28.68 [28.54, 28.81]	25.37 [25.23, 25.50]	26.05 [25.89, 26.20]	24.38 [24.26, 24.49]	+3.32 [3.26, 3.38]	<0.001	+2.64 [2.56, 2.71]	<0.001	+4.31 [4.24, 4.37]	<0.001
50	127	29.06 [28.93, 29.19]	26.50 [26.36, 26.64]	27.01 [26.84, 27.17]	24.84 [24.74, 24.94]	+2.56 [2.50, 2.62]	<0.001	+2.05 [1.98, 2.13]	<0.001	+4.22 [4.16, 4.28]	<0.001
100	252	29.48 [29.35, 29.60]	27.68 [27.53, 27.82]	27.85 [27.69, 28.01]	25.21 [25.11, 25.30]	+1.80 [1.75, 1.85]	<0.001	+1.62 [1.56, 1.69]	<0.001	+4.27 [4.21, 4.33]	<0.001
225	531	29.94 [29.81, 30.06]	28.74 [28.60, 28.87]	28.56 [28.42, 28.70]	25.58 [25.50, 25.67]	+1.20 [1.16, 1.25]	<0.001	+1.38 [1.32, 1.43]	<0.001	+4.35 [4.30, 4.41]	<0.001
450	1,079	30.40 [30.27, 30.53]	29.62 [29.48, 29.76]	28.94 [28.79, 29.08]	25.71 [25.62, 25.78]	+0.78 [0.74, 0.82]	<0.001	+1.47 [1.40, 1.53]	<0.001	+4.70 [4.64, 4.76]	<0.001
913 (all)	2,134	31.39 [31.25, 31.54]	30.56 [30.41, 30.70]	29.32 [29.18, 29.45]	26.01 [25.93, 26.08]	+0.84 [0.81, 0.87]	<0.001	+2.07 [2.01, 2.14]	<0.001	+5.39 [5.31, 5.46]	<0.001
SSIM ($\times 100$)											
10	28	84.59 [84.18, 84.99]	67.65 [67.19, 68.09]	74.30 [73.84, 74.75]	68.24 [67.78, 68.68]	+16.94 [16.73, 17.16]	<0.001	+10.29 [10.08, 10.50]	<0.001	+16.35 [16.15, 16.56]	<0.001
25	64	85.82 [85.43, 86.20]	72.08 [71.68, 72.47]	77.71 [77.21, 78.22]	71.60 [71.23, 71.96]	+13.74 [13.53, 13.96]	<0.001	+8.11 [7.84, 8.40]	<0.001	+14.21 [13.99, 14.45]	<0.001
50	127	86.33 [85.96, 86.70]	77.32 [76.82, 77.81]	80.08 [79.70, 80.46]	74.83 [74.44, 75.22]	+9.02 [8.79, 9.24]	<0.001	+6.25 [5.98, 6.53]	<0.001	+11.50 [11.28, 11.74]	<0.001
100	252	87.02 [86.66, 87.38]	80.66 [80.21, 81.09]	83.52 [83.10, 83.94]	76.43 [76.03, 76.81]	+6.36 [6.17, 6.56]	<0.001	+3.50 [3.34, 3.66]	<0.001	+10.59 [10.36, 10.88]	<0.001
225	531	87.66 [87.32, 88.00]	83.83 [83.41, 84.24]	84.79 [84.39, 85.18]	77.78 [77.40, 78.16]	+3.84 [3.69, 4.00]	<0.001	+2.88 [2.75, 3.01]	<0.001	+9.88 [9.78, 9.99]	<0.001
450	1,079	88.52 [88.18, 88.86]	85.56 [85.17, 85.95]	81.12 [80.89, 81.36]	77.17 [76.86, 77.47]	+2.96 [2.85, 3.08]	<0.001	+7.40 [7.10, 7.71]	<0.001	+11.35 [11.24, 11.47]	<0.001
913 (all)	2,134	89.18 [88.85, 89.50]	87.38 [87.02, 87.74]	80.69 [80.22, 81.14]	80.03 [79.65, 80.40]	+1.80 [1.72, 1.88]	<0.001	+8.48 [7.89, 9.13]	<0.001	+9.15 [9.06, 9.24]	<0.001

Supplementary Tab. 28 | Contribution of the pretraining losses, adapting the same architecture from three initialisations (8 projections). No pretraining (random initialisation), pretraining with the reconstruction loss only, or SPARC's pretraining with both losses, each adapted to CT-RATE and to TotalSegmentator with the same adaptation protocol. No pretraining on CT-RATE is the From scratch model with all 913 patients in Supplementary Tab. 27. The reconstructions were given, unchanged, to the classifier and segmentation model trained on full CT; the Full CT column gives these two on the CT itself. Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples). Differences are paired by patient. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

					SPARC minus reconstruction loss only		Reconstruction loss only minus no pretraining	
	No pretraining	Reconstruction loss only	SPARC	Full CT	Difference	*P*	Difference	*P*
Reconstruction, CT-RATE								
PSNR (dB)	30.56 [30.41, 30.70]	30.85 [30.72, 30.98]	31.39 [31.25, 31.54]	–	+0.54 [0.52, 0.56]	< 0.001	+0.30 [0.26, 0.33]	< 0.001
SSIM ($\times 100$)	87.38 [87.02, 87.74]	88.70 [88.38, 89.02]	89.18 [88.85, 89.50]	–	+0.48 [0.46, 0.50]	< 0.001	+1.32 [1.24, 1.40]	< 0.001
Reconstruction, TotalSegmentator								
PSNR (dB)	30.22 [29.84, 30.60]	31.30 [30.95, 31.66]	31.37 [31.03, 31.72]	–	+0.07 [0.05, 0.09]	< 0.001	+1.09 [0.99, 1.19]	< 0.001
SSIM ($\times 100$)	87.37 [86.55, 88.20]	90.37 [89.75, 90.99]	90.46 [89.86, 91.05]	–	+0.09 [0.02, 0.15]	0.034	+3.00 [2.65, 3.37]	< 0.001
Classifier trained on full CT, CT-RATE								
Macro-AUROC	0.753 [0.728, 0.776]	0.754 [0.728, 0.777]	0.756 [0.730, 0.779]	0.772 [0.746, 0.795]	+0.002 [−0.002, 0.005]	0.78	+0.001 [−0.003, 0.006]	0.78
Segmentation model trained on full CT, TotalSegmentator								
Dice, ten structures	0.742 [0.713, 0.768]	0.777 [0.748, 0.801]	0.779 [0.751, 0.804]	0.870 [0.848, 0.890]	+0.003 [0.001, 0.005]	0.052	+0.035 [0.031, 0.038]	< 0.001
Dice, abdominal organs	0.682 [0.646, 0.714]	0.733 [0.697, 0.765]	0.740 [0.705, 0.772]	0.860 [0.831, 0.884]	+0.007 [0.005, 0.011]	< 0.001	+0.051 [0.045, 0.058]	< 0.001
Dice, lung lobes	0.802 [0.770, 0.830]	0.820 [0.789, 0.848]	0.819 [0.788, 0.846]	0.881 [0.853, 0.906]	−0.002 [−0.005, 0.001]	0.67	+0.018 [0.014, 0.022]	< 0.001

Supplementary Tab. 29 | Classification with the three ways of using SPARC. Eight projections; CT-RATE test set, 602 volumes; probabilities averaged over three training seeds. SPARC, SPARC's reconstruction given to the classifier trained on full CT; SPARC*, given to a classifier of the same architecture trained on SPARC's reconstructions; SPARC†, a task head on SPARC's pretrained encoder, frozen or finetuned, without reconstruction (Supplementary Fig. 2a). The reference is the classifier trained on full CT, on the full CT. Macro values average the 18 findings. AUROC and AUPRC (average precision) are computed on the full test set, not averaged over its volumes; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples).

	Reference	SPARC's reconstruction		SPARC†, no reconstruction	
Finding	Full CT	SPARC	SPARC*	Frozen	Finetuned
Macro-AUROC	0.772 [0.746, 0.795]	0.756 [0.730, 0.779]	0.749 [0.725, 0.772]	0.752 [0.728, 0.775]	0.759 [0.735, 0.782]
Macro-AUPRC	0.430 [0.400, 0.478]	0.403 [0.371, 0.453]	0.378 [0.356, 0.425]	0.395 [0.371, 0.437]	0.414 [0.385, 0.458]
AUROC per finding					
Medical material	0.768 [0.663, 0.861]	0.788 [0.693, 0.872]	0.791 [0.681, 0.884]	0.751 [0.631, 0.864]	0.775 [0.640, 0.882]
Arterial wall calcification	0.897 [0.858, 0.932]	0.881 [0.838, 0.920]	0.890 [0.849, 0.928]	0.891 [0.841, 0.935]	0.896 [0.850, 0.938]
Cardiomegaly	0.871 [0.810, 0.922]	0.877 [0.821, 0.925]	0.883 [0.829, 0.930]	0.899 [0.852, 0.940]	0.901 [0.852, 0.943]
Pericardial effusion	0.766 [0.592, 0.897]	0.765 [0.602, 0.890]	0.766 [0.600, 0.888]	0.778 [0.653, 0.878]	0.787 [0.646, 0.897]
Coronary artery wall calcification	0.883 [0.841, 0.922]	0.868 [0.821, 0.911]	0.878 [0.832, 0.920]	0.873 [0.824, 0.918]	0.870 [0.822, 0.914]
Hiatal hernia	0.764 [0.675, 0.847]	0.722 [0.626, 0.812]	0.732 [0.642, 0.813]	0.726 [0.642, 0.803]	0.758 [0.679, 0.828]
Lymphadenopathy	0.730 [0.658, 0.795]	0.740 [0.673, 0.801]	0.693 [0.615, 0.763]	0.706 [0.633, 0.773]	0.707 [0.635, 0.775]
Emphysema	0.754 [0.684, 0.822]	0.708 [0.631, 0.784]	0.724 [0.655, 0.791]	0.742 [0.673, 0.811]	0.713 [0.639, 0.785]
Atelectasis	0.730 [0.662, 0.792]	0.718 [0.648, 0.782]	0.730 [0.661, 0.792]	0.729 [0.659, 0.793]	0.726 [0.656, 0.790]
Lung nodule	0.605 [0.539, 0.670]	0.635 [0.570, 0.698]	0.614 [0.546, 0.683]	0.613 [0.544, 0.682]	0.601 [0.534, 0.669]
Lung opacity	0.814 [0.762, 0.862]	0.664 [0.598, 0.727]	0.666 [0.596, 0.732]	0.669 [0.588, 0.746]	0.690 [0.610, 0.766]
Pulmonary fibrotic sequela	0.659 [0.584, 0.728]	0.660 [0.582, 0.733]	0.653 [0.582, 0.720]	0.665 [0.589, 0.736]	0.667 [0.587, 0.743]
Pleural effusion	0.897 [0.784, 0.972]	0.906 [0.817, 0.968]	0.887 [0.782, 0.958]	0.887 [0.785, 0.956]	0.897 [0.809, 0.958]
Mosaic attenuation pattern	0.764 [0.672, 0.846]	0.764 [0.670, 0.850]	0.768 [0.671, 0.858]	0.732 [0.646, 0.810]	0.745 [0.661, 0.825]
Peribronchial thickening	0.730 [0.628, 0.818]	0.763 [0.681, 0.835]	0.758 [0.659, 0.843]	0.764 [0.653, 0.856]	0.770 [0.661, 0.865]
Consolidation	0.819 [0.741, 0.887]	0.719 [0.640, 0.793]	0.650 [0.539, 0.761]	0.691 [0.599, 0.780]	0.680 [0.580, 0.785]
Bronchiectasis	0.622 [0.443, 0.773]	0.636 [0.446, 0.794]	0.623 [0.447, 0.772]	0.672 [0.514, 0.806]	0.689 [0.516, 0.831]
Interlobular septal thickening	0.822 [0.718, 0.907]	0.793 [0.666, 0.891]	0.784 [0.652, 0.887]	0.756 [0.609, 0.871]	0.788 [0.649, 0.894]

Supplementary Tab. 30 | Segmentation with the three ways of using SPARC. Eight projections; TotalSegmentator test set, 79 volumes; three training seeds; structures absent from a volume are skipped. SPARC, SPARC's reconstruction given to the segmentation model trained on full CT; SPARC*, given to a segmentation model of the same architecture trained on SPARC's reconstructions; SPARC†, a task head on SPARC's pretrained encoder, frozen or finetuned, without reconstruction (Supplementary Fig. 2a). The reference is the segmentation model trained on full CT, on the full CT. Values are means over the full test set; brackets give 95% confidence intervals from a bootstrap over patients (10,000 resamples).

	Reference	SPARC's reconstruction		SPARC†, no reconstruction	
Structure	Full CT	SPARC	SPARC*	Frozen	Finetuned
Abdominal organs (mean)	0.860 [0.831, 0.884]	0.740 [0.705, 0.772]	0.752 [0.718, 0.782]	0.679 [0.643, 0.711]	0.726 [0.690, 0.758]
Liver	0.896 [0.851, 0.931]	0.850 [0.804, 0.885]	0.856 [0.811, 0.892]	0.825 [0.775, 0.865]	0.853 [0.803, 0.893]
Spleen	0.924 [0.909, 0.936]	0.812 [0.786, 0.834]	0.808 [0.782, 0.832]	0.765 [0.736, 0.791]	0.793 [0.764, 0.817]
Left kidney	0.795 [0.735, 0.850]	0.635 [0.566, 0.699]	0.654 [0.589, 0.713]	0.573 [0.509, 0.632]	0.610 [0.542, 0.673]
Right kidney	0.829 [0.762, 0.885]	0.682 [0.616, 0.740]	0.694 [0.628, 0.753]	0.608 [0.549, 0.663]	0.670 [0.606, 0.727]
Aorta	0.854 [0.822, 0.882]	0.723 [0.683, 0.759]	0.746 [0.708, 0.780]	0.621 [0.576, 0.662]	0.704 [0.664, 0.739]
Lung lobes (mean)	0.881 [0.853, 0.906]	0.819 [0.788, 0.846]	0.833 [0.804, 0.858]	0.781 [0.748, 0.811]	0.830 [0.802, 0.854]
Left upper lobe	0.852 [0.799, 0.898]	0.786 [0.733, 0.835]	0.798 [0.745, 0.847]	0.732 [0.671, 0.789]	0.803 [0.757, 0.845]
Left lower lobe	0.894 [0.851, 0.928]	0.832 [0.784, 0.873]	0.843 [0.794, 0.884]	0.796 [0.742, 0.844]	0.835 [0.785, 0.878]
Right upper lobe	0.922 [0.881, 0.953]	0.854 [0.802, 0.895]	0.884 [0.844, 0.917]	0.836 [0.788, 0.874]	0.871 [0.820, 0.906]
Right middle lobe	0.854 [0.803, 0.897]	0.790 [0.746, 0.828]	0.802 [0.759, 0.841]	0.750 [0.704, 0.790]	0.799 [0.756, 0.837]
Right lower lobe	0.885 [0.836, 0.927]	0.831 [0.773, 0.882]	0.836 [0.777, 0.888]	0.792 [0.732, 0.846]	0.840 [0.786, 0.887]

Supplementary Tab. 31 | Paired differences between the ways of using SPARC. Eight projections; the same 602 CT-RATE and 79 TotalSegmentator test volumes, with paired 95% confidence intervals from a bootstrap over patients (10,000 resamples). Approaches as in Supplementary Tab. 29 and 30; SPARC minus full CT is in Supplementary Tab. 19 and 23. *P* values are two-sided, derived from the confidence intervals and Holm-adjusted within this table (Methods).

	Macro-AUROC, CT-RATE		Dice, abdominal organs		Dice, lung lobes	
Comparison	Difference	*P*	Difference	*P*	Difference	*P*
SPARC* minus SPARC	−0.007 [−0.021, 0.009]	0.79	+0.012 [0.006, 0.017]	< 0.001	+0.014 [0.006, 0.022]	0.005
SPARC† (finetuned) minus SPARC*	+0.009 [−0.004, 0.023]	0.54	−0.026 [−0.034, −0.018]	< 0.001	−0.003 [−0.013, 0.007]	0.79
SPARC* minus full CT	−0.023 [−0.035, −0.011]	0.001	−0.108 [−0.123, −0.095]	< 0.001	−0.049 [−0.057, −0.041]	< 0.001
SPARC† (frozen) minus full CT	−0.020 [−0.037, −0.003]	0.12	−0.181 [−0.202, −0.164]	< 0.001	−0.100 [−0.111, −0.090]	< 0.001
SPARC† (finetuned) minus full CT	−0.013 [−0.029, 0.003]	0.42	−0.134 [−0.154, −0.117]	< 0.001	−0.051 [−0.062, −0.041]	< 0.001

Supplementary Tab. 32 | Pretraining settings for the two stages.

	Stage 1 (CT encoder)	Stage 2 (SPARC)
Architecture	ViT-L/16	ConvNeXt pyramid + 3D transformer
Input	CT 256^3	2–16 projections, 512^2; CT 256^3
Grid / token dim	16^3, 1024	16^3, 768
Objective	normalised-pixel MSE on masked patches	reconstruction loss (MSE) + CT-feature supervision (smooth-L_1)
λ (CT-feature weight)	–	1
Training data	CT-RATE training split, 47,149 volumes	
Volume sampling	256^3 voxels at an isotropic spacing drawn between 1.0 and 2.0 mm	
Volume centre	random point in the body's bounding box	centre of the body's bounding box
Geometry randomisation	–	Supplementary Tab. 33
Optimiser	AdamW	AdamW
LR (max / min)	1.5e−4 / 1e−6	1e−4 / 1e−6
Weight decay	0.05	0.04
Warm-up / schedule	8k / cosine	4k / cosine
Iterations	200k	150k
Global batch	64	16
Query points per step	–	16,384
Gradient clip	–	1.0
Masking ratio	0.75	–
Compute	4×4 GH200	
Stage 2 architecture		
2D encoder	ConvNeXt pyramid, 4 stages; 5 scales from 512^2 to 32^2 pixels	
Pyramid channels	64, 128, 256, 512 and 1,024 (1,984 in total)	
2D transformer	6 layers on the 32^2 scale (1,024 tokens)	
Geometry input	Plücker rays, 6 values per pixel; patch mean + MLP, added to the 32^2 tokens	
Fusion	maximum over projections at the 16^3 grid points; 8-layer 3D transformer; $\mathbf{F}$: $16^3 \times 768$	
CT-feature head	4 transformer blocks + linear layer (pretraining only)	
Point decoder	residual MLP, hidden layers of 512, 512 and 256 with batch normalisation; input $768 + 1{,}984 = 2{,}752$	

Supplementary Tab. 33 | Acquisition geometry. Projections are digitally reconstructed radiographs rendered from each CT, with geometry matched to the physical extent of each anatomy.

Setting	Torso[a]	Head (CQ500)	Maxillofacial (ToothFairy3)
Reconstruction grid (voxels)	256^3	256^3	256^3
Voxel spacing (mm)	1.6	1.2	0.625
Field of view (mm)	409.6	307.2	160.0
Source-to-axis distance (mm)	800	600	312
Source-to-detector / source-to-axis ratio	1.5	1.5	1.5
Detector resolution (pixels)	512^2	512^2	512^2
Detector pixel	2.4 mm	sized to the patient	sized to the patient
Projections at evaluation	4 or 8, uniformly spaced; one model per number of projections		
Further analyses	2 (bi-planar) and 16 projections		
Metric range	PSNR and SSIM over $[-1{,}024, 1{,}024]$ HU, normalised to $[0, 1]$		
Randomisation during pretraining			
Number of projections	2 to 16		
Angular pattern	uniform, random, limited arc, bi-planar, clustered		
Source-to-axis distance (mm)	600 to 2,000		
Source-to-detector / source-to-axis ratio	1.05 to 2.5		
Out-of-plane source angle	-5° to 5°, the same for all projections of a sample		
Detector pixel	sized to the patient		

[a] CT-RATE, TotalSegmentator, MSD, AbdomenCT-1K, AMOS and VerSe.

Supplementary Tab. 34 | Settings for the task networks and for the task heads on the pretrained encoder.

	Classification	Segmentation
Task networks (trained on full CT or on reconstructions)		
Architecture	3D CNN with the encoder of the U-Net	3D U-Net
Levels	4; two $3 \times 3 \times 3$ convolutions per level, each with instance normalisation and GELU	
Channels	16, 32, 64 and 128; max pooling by 2 between levels	
Output	global mean, then MLP $128 \to 128 \to 18$ (GELU, dropout 0.1)	transposed convolutions with skip concatenation; $1 \times 1 \times 1$ convolution to 11 classes
Input	256^3 volume, HU clipped to $[-1{,}024, 1{,}024]$ and scaled to $[0, 1]$; trained from random initialisation	
Loss	binary cross-entropy	cross-entropy + soft Dice
Optimiser / lr / weight decay	AdamW / $5\text{e}{-4}$ / $1\text{e}{-4}$	AdamW / $1\text{e}{-3}$ / $1\text{e}{-4}$
Batch	4 volumes	2 volumes
Length	20k–60k iterations, early stopping	6k iterations
Checkpoint	best validation macro-AUROC	best validation mean Dice
Seeds	3	
Task heads on the pretrained encoder		
Input	mean of $\mathbf{F}$ over the 16^3 grid (768)	$\mathbf{F}$ at point q (768) + 2D features at the projections of q (5 scales, maximum over projections; 1,984) = 2,752
Layers	LayerNorm, $768 \to 512$, GELU, dropout 0.1, $512 \to 18$	$2{,}752 \to 256 \to 256 \to 11$ with GELU, shared by all points
Parameters	0.40 M (404,498)	0.77 M (773,387)
Loss	sigmoid + binary cross-entropy	softmax + cross-entropy + soft Dice
Inference	–	all 256^3 grid points, argmax
Frozen encoder: lr / schedule	$1\text{e}{-3}$ / 4k iterations	$5\text{e}{-5}$ / ≤ 120 epochs, early stopping
Finetuned encoder: length	frozen-encoder schedule, then 6 epochs	≤ 120 epochs, early stopping
Finetuned encoder: head-only epochs	epoch 1 (lr $1\text{e}{-4}$)	epochs 1–4 (lr $1\text{e}{-3}$)
Finetuned encoder: head / encoder lr	$1\text{e}{-4}$ / $1\text{e}{-6}$	$1\text{e}{-4}$ / $5\text{e}{-6}$
Weight decay	$1\text{e}{-4}$	$1\text{e}{-4}$
Batch	16 (frozen); 1×4 accum. (finetuned)	1 volume, 65,536 points
Repeats / CI	3 seeds; patient-level bootstrap 95% CI	