Supplemental Material

A Pipeline for Automated Voxel Dosimetry: Application in Patients with Multi-SPECT/CT Imaging After 177Lu-Peptide Receptor Radionuclide Therapy

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Supplemental Table 1. *Patient baseline characteristics and cycle 1 mean absorbed dose estimate from the DPM Monte Carlo calculation with voxel-level dose-rate fitting. The standard deviation estimated from contour perturbations is in parenthesis. Healthy liver standard deviation is not included as not all liver lesions were segmented. Tumor volumes are indicated. Median (range) of organ volumes: L kidney, 162(78-275)mL; R kidney, 163(118-258)mL; Healthy liver, 1821(1166-3369)mL.*

								Mean Absorbed Dose (Gy)							
Patient Code	**Sex**	**Age (y)**	**Weight (kg)**	**Grade**	**Ki-67**	**eGFR^{+} (mL/min)**	**Admin Activity (GBq)**	**L Kidney**	**R Kidney**	**Healthy Liver**	**Tumor 1**	**Tumor 2**	**Tumor 3**	**Tumor 4**	**Tumor 5**
2	M	71	96	na	na	82	7.14	2.6 (0.2)	2.8 (0.1)	1.0	52.2(11.0) 2.9 mL*	36.1 (5.5) 4.3 mL*	31.7 (5.2) 3.5 mL	22.3 (5.6) 2.5 mL	
4	M	64	98	na	na	81	7.13	2.2 (0.1)	2.2 (0.1)	1.5	23.5 (2.4) 106.1 mL	67.8(12.0) 3.1 mL			
5	F	72	55	G2	11%	96	7.34	2.8 (0.1)	3.1 (0.3)	5.4	31.0 (3.1) 12.1 mL	13.6 (0.9) 55.4 mL	28.4 (2.5) 11.2 mL	9.6 (0.7) 58.2 mL	9.8 (0.7) 59 mL
6	F	62	52	G1	< 2%	43	7.33	3.7 (0.2)	4.8 (0.3)	1.5	4.2 (0.3) 11.7 mL	63.5(13.6) 3.0 mL	3.1 (0.2) 68.1 mL*	4.7 (0.6) 22.2 mL**	
7	F	39	129	G3	15%-20%	81	7.48	1.8 (0.1)	2.3 (0.3)	7.9	16.0 (0.8) 373 mL	17.1 (0.7) 207 mL	23.0 (1.4) 22.7 mL	19.0 (1.2) 13.7 mL	24.8 (2.0) 10.2 mL
8	M	56	90	na	na	109	7.07	2.2 (0.1)	2.4 (0.1)	0.3	4.1 (0.5) 569 mL***				
10	F	66	94	na	na	25	3.69^{++}	3.8 (0.2)	4.0 (0.3)	3.1	16.7 (1.2) 272 mL***	6.6 (0.4) 128 mL	9.7 (0.3) 296 mL	5.8 (0.5) 18.5 mL	12.4 (1.0) 90 mL
11	M	70	72	G2	3%	68	7.34	3.1 (0.2)	2.9 (0.2)	6.8	22.1 (1.3) 155 mL	21.1 (2.8) 12.6 mL	25.2 (1.3) 49.4 mL	25.0 (2.2) 22.8 mL	21.9 (1.2) 104 mL
12	M	57	90	G2	5%	91	7.20	2.2 (0.1)	2.3 (0.1)	1.6	18.5 (2.0) 142 mL	9.3 (1.3) 65.6 mL	9.2 (0.9) 10.9 mL	7.1 (1.1) 17.8 mL	14.5 (2.0) 15.5 mL
13	M	66	87	G2	10%-15%	91	7.31	2.5 (0.1)	2.7 (0.2)	4.0	7.0 (0.2) 29.8 mL	17.7 (1.6) 10.0 mL	7.8 (0.6) 28.3 mL	10.3 (0.7) 33.5 mL	12.1 (1.4) 5.6 mL*
14	M	56	113	G1	<2%	67	7.35	5.3 (0.3)	6.3 (0.6)	2.4	19.8 (1.2) 1039 mL	1.8 (0.2) 8.0 mL	21.5 (2.0) 22.7 mL	22.4 (2.6) 23.4 mL	15.4 (1.4) 99.7 mL*
15	M	72	79	G2	9 per 10 hpf	55	7.14	3.7 (0.2)	4.0 (0.1)	1.7	13.7 (0.9) 80.0 mL	30.0 (3.1) 13.4 mL	43.2(17.6) 2.1 mL		
16	M	74	86	G1	na	88	7.37	2.2 (0.1)	2.3 (0.1)	2.6	20.1 (1.7) 91.4 mL	16.5 (1.8) 8.3 mL	41.5 (4.0) 35.3 mL	36.0 (9.1) 2.4 mL	15.0 (1.3) 16.5 mL****
18	M	71	68	G2	10%	91	3.75^{++}	1.4 (0.1)	1.6 (0.1)	1.7	12.4 (1.1) 233 mL	7.0 (0.5) 256 mL	7.4 (0.3) 268 mL	11.5 (0.9) 208 mL	
20	M	70	97	G2	12%, 20%	66	7.38	5.5 (0.3)	5.7 (0.3)	1.5	44.9 (4.0) 28.8 mL				
22	M	67	74	G1	<2%	92	7.31	4.4 (0.2)	4.5 (0.3)	1.5	30.5 (2.5) 9.2 mL	15.7 (2.3) 3.9 mL	75.8 (7.3) 11.6 mL	21.2(2.1) 7.0 mL**	
23	F	74	69	G1	<2%	48	7.15	6.5 (0.3)	6.7 (0.2)	1.2					
25	M	66	77	G2	na	91	7.22	2.5 (0.1)	2.7 (0.1)	1.1	8.3 (0.7) 77.0 mL	21.96(2.0) 46.2 mL	56.8 (4.8) 7.5 mL*	31.9 (2.8) 10.9 mL*	
26	F	76	79	G2	5%-10%	55	6.81	3.4 (0.2)	5.1 (0.9)	9.3	34.5 (2.3) 24.0 mL	36.6 (2.1) 20.5 mL	41.0 (2.6) 10.3 ml	36.9 (3.3) 21.4 mL	49.6 (4.0) 9.9 mL
c02	F	76	89	G2	7%	49	7.30	3.7 (0.1)	4.4 (0.2)	2.4	9.1 (0.7) 7.3 mL	12.7 (1.6) 4.6 mL	9.7 (1.1) 3.9 mL	5.3 (0.6) 7.1 mL	5.0 (0.5) 71.5 mL****

$^{+}$Estimated glomerular filtration rate.

$^{++}$ Reduced activity due to concern of renal or marrow toxicity

*Lymph node lesion; ** Body wall lesion; ***Pancreas lesion; **** Mesenteric lesion; All other lesions are in the liver

Supplemental Table 2*. Performance of deep learning kidney segmentation (without and with fine tuning) relative to manual segmentation for the first 14 patients (27 kidney*[*]*). In general, fine tuning of CNN-generated contours did not result in large changes in similarity measures or absorbed dose, but in one case the Dice score improved from 0.77 to 0.91 and mean absorbed dose agreement improved from -21% to 4%.*

	Manual vs. Fully Automated CNN-segmentation					**Manual vs. CNN Segmentation with Manual Fine Tuning**[*]				
	Volume Absolute Difference	Mean Dose Absolute Difference	Dice	HD (mm)	MDA (mm)	Volume Absolute Difference	Mean Dose Absolute Difference	Dice	HD (mm)	MDA (mm)
L Kidney										
Mean	5%	2%	0.92	10.7	0.92	4%	1%	0.93	8.3	0.80
Median	4%	1%	0.93	8.5	0.78	3%	1%	0.93	8.2	0.76
Min	0%	0%	0.85	6.0	0.68	0%	0%	0.86	6.0	0.68
Max	18%	5%	0.94	36.0	2.04	17%	5%	0.94	12.2	1.19
R Kidney										
Mean	8%	3%	0.91	11.4	0.99	5%	2%	0.93	9.9	0.81
Median	6%	2%	0.93	9.2	0.84	6%	1%	0.93	8.8	0.81
Min	0%	0%	0.77	4.5	0.68	0%	0%	0.91	4.5	0.68
Max	27%	21%	0.94	24.4	2.05	11%	4%	0.94	24.4	0.99

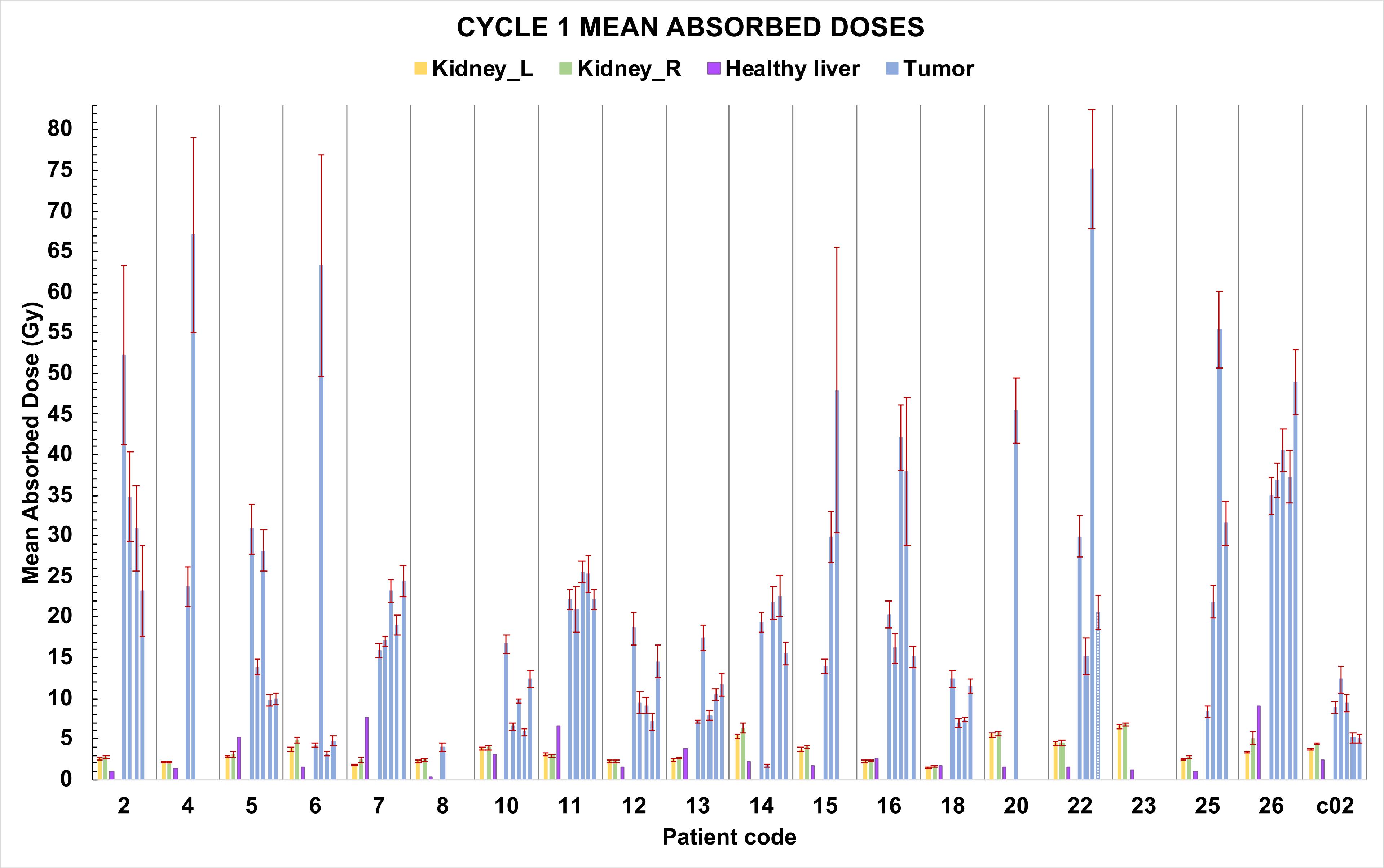
[*] CNN failed to locate right kidney in one case due to unusual location

Supplemental Table 3. *Effective half-life and mean absorbed dose statistics across all patients from DPM MC dose estimation with voxel-level dose-rate fitting. Effective half-life values in parenthesis correspond to organ level dose-rate fitting.*

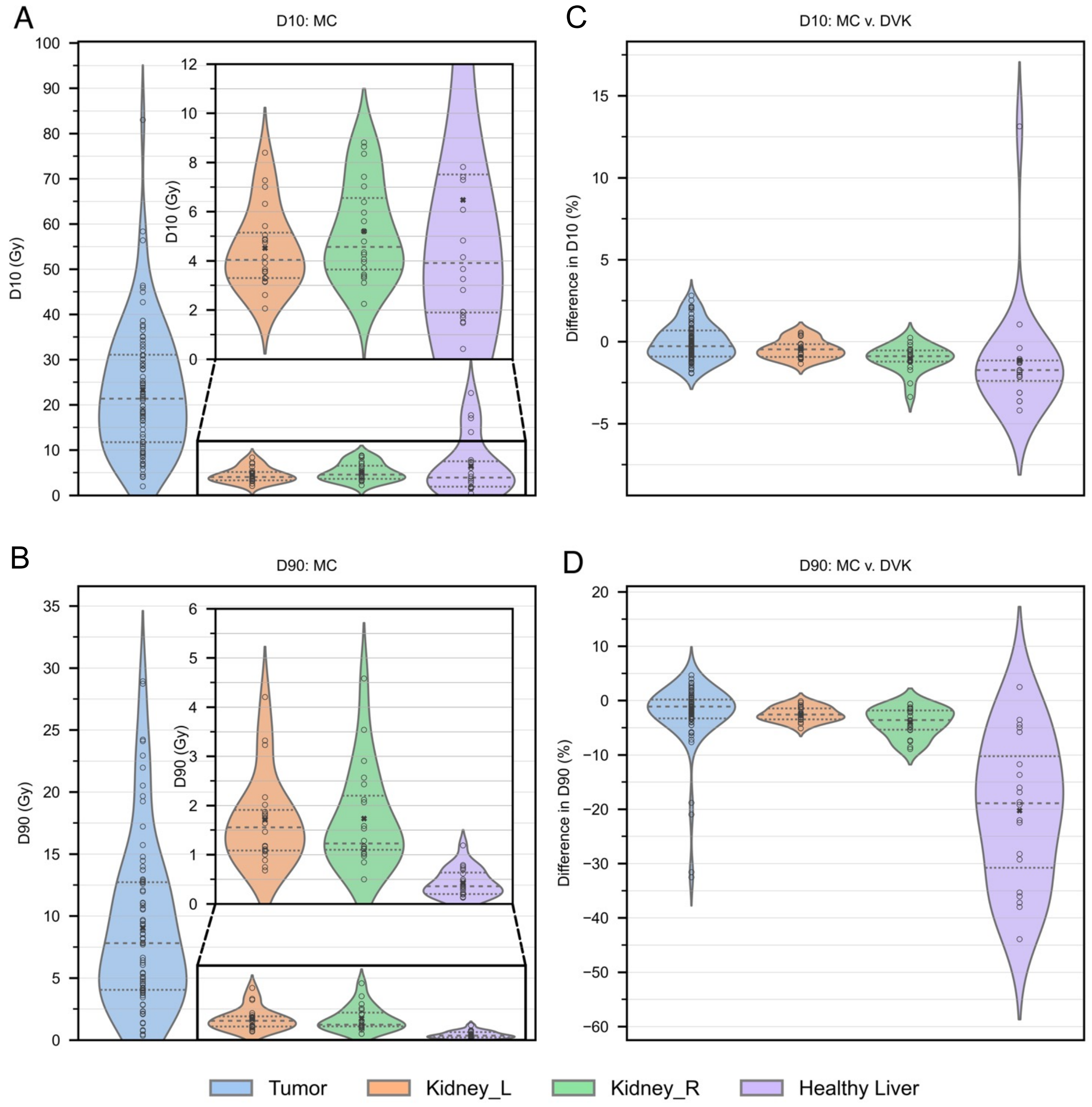
	Tumor	**L Kidney**	**R Kidney**	**Healthy Liver**
Sample size	77	20	20	20
Effective Half Life (h)[*]				
Average	84.4 (88.6)	52.4 (55.9)	51.9 (56.2)	67.1 (75.5)
Median	80.4 (84.2)	49.1 (51.7)	48.6 (50.3)	64.1 (74.1)
Min	8.0 (46.3)	8.0 (42.4)	8.0 (42.7)	8.0 (33.1)
Max[**]	159.5 (159.5)	159.5 (108.2)	159.5 (116.4)	159.5 (123.5)
STD	20.6 (25.3)	20.6 (15.2)	21.6 (17.0)	36.7 (18.8)
Mean Absorbed Dose				
Average (Gy)	21.7	3.3	3.6	2.9
(Gy/GBq)	3.16	0.49	0.54	0.44
Median (Gy)	17.7	3.0	3.0	1.7
(Gy/GBq)	2.72	0.41	0.43	0.28
Min. (Gy)	1.8	1.4	1.6	0.3
(Gy/GBq)	0.24	0.24	0.31	0.04
Max. (Gy)	75.8	6.5	6.7	9.3
(Gy/GBq)	10.37	1.02	1.07	1.36
STD (Gy)	15.8	1.3	1.5	2.5
(Gy/GBq)	2.16	0.21	0.23	0.36

[*] Corresponding to the main component of the exponential fit

[**] *A constraint that T_{eff} is less than or equal to physical half-life was used in curve-fitting.*



Supplemental Figure 1. *Cycle 1 organ and lesion mean absorbed doses for all patients calculated using the MC voxel-level option. The error bars indicate 1 standard deviation estimated from the contour perturbation approach. Healthy liver standard deviation is not included as not all liver lesions were segmented. See supplemental Table 1 for administered activities.*



Supplemental Figure 2. *DVH statistics A) D10, B) D90 from DPM MC dose estimation. Difference in C) D10 and D) D90 estimated from MC vs. DVK convolution. Difference = 100*(MC-DVK)/MC. These metrics are reported without PVC, because RCs were used only as a mean value correction.*