

Introduction

- AI-based virtual log file patient-specific QA (PSQA) consists of predicting linear accelerator parameters at delivery for a new treatment plan, based on an AI model trained using delivery-based log files from prior patients.

Methods

- We utilized a Monte Carlo dose calculation algorithm to compare calculated dose distributions from
 - Secondary dose calculation of the Eclipse treatment plan
 - AI-based virtual log files
 - Delivery-based log files recorded during 1st fraction treatment delivery on a Varian TrueBeam linear accelerator.

Conclusion

- AI-based virtual log files can be used to predict the dosimetric results of delivery-based log files and have the potential to become a “delivery-free” pre-treatment analysis to enhance PSQA.

Results

50 IMRT/VMAT plans from various sites

Site	Technique(s)	Range of PTV volume (cm ³)
Single-target SRS	VMAT	7.2 - 51.1
Multi-target SRS	VMAT	1.5 - 17.6
Spine	VMAT	9.2 - 136.9
HN	VMAT	9.6 - 321.6
Lung	VMAT	32.9 - 239.2

Site	Technique(s)	Range of PTV volume (cm ³)
GI	VMAT	24.9 - 3206.8
GU	IMRT/VMAT	40.8 - 879.1
Breast	IMRT/VMAT	140.8 - 1777.9
GYN	VMAT	300.1 - 1947.5
Sarcoma	IMRT/VMAT	354.5 - 996.2

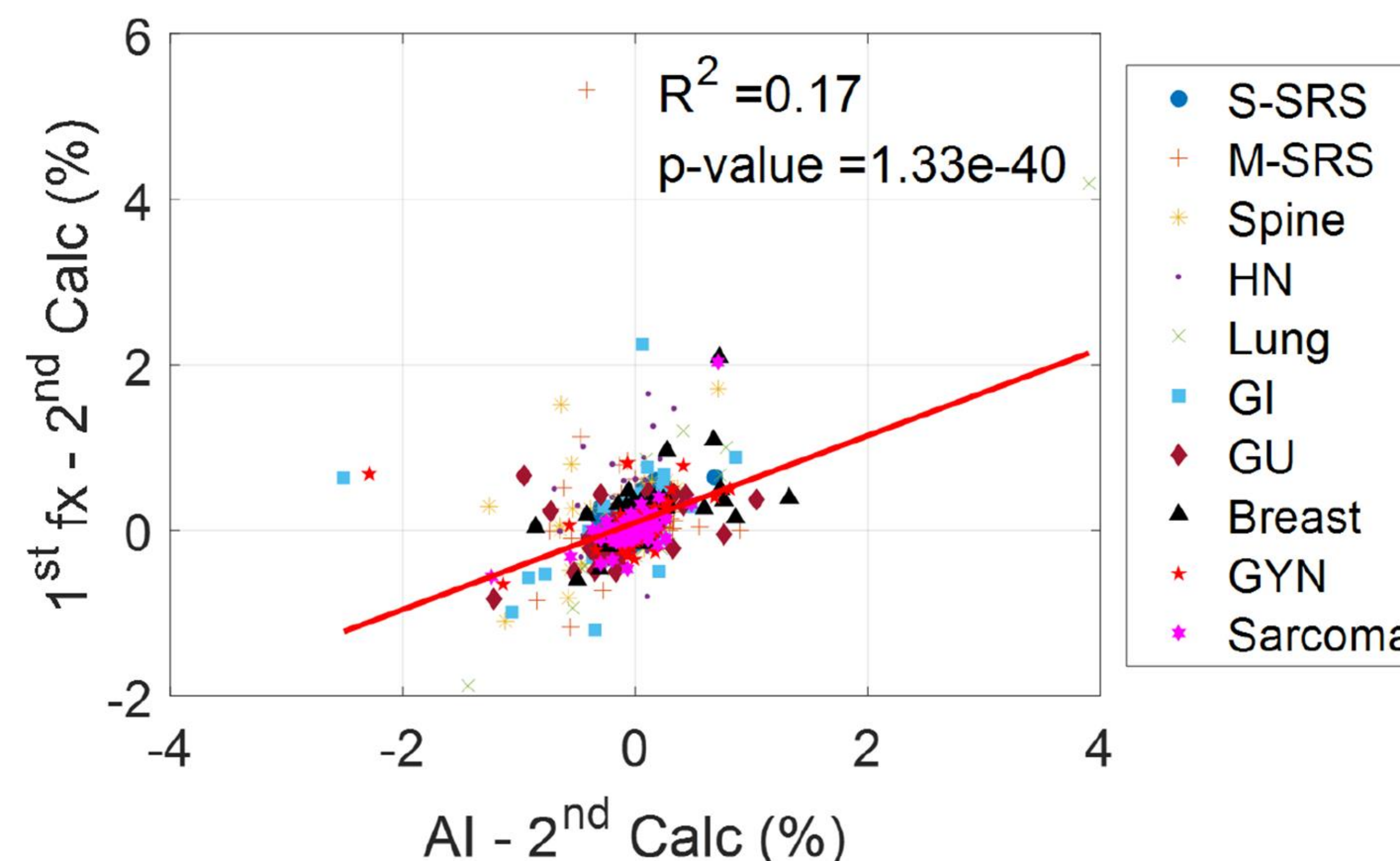


Figure 3 Linear relationship between the differences of AI-based virtual log files versus secondary dose calculations and the differences of delivery-based log files directly from 1st fraction treatment versus secondary dose calculations.

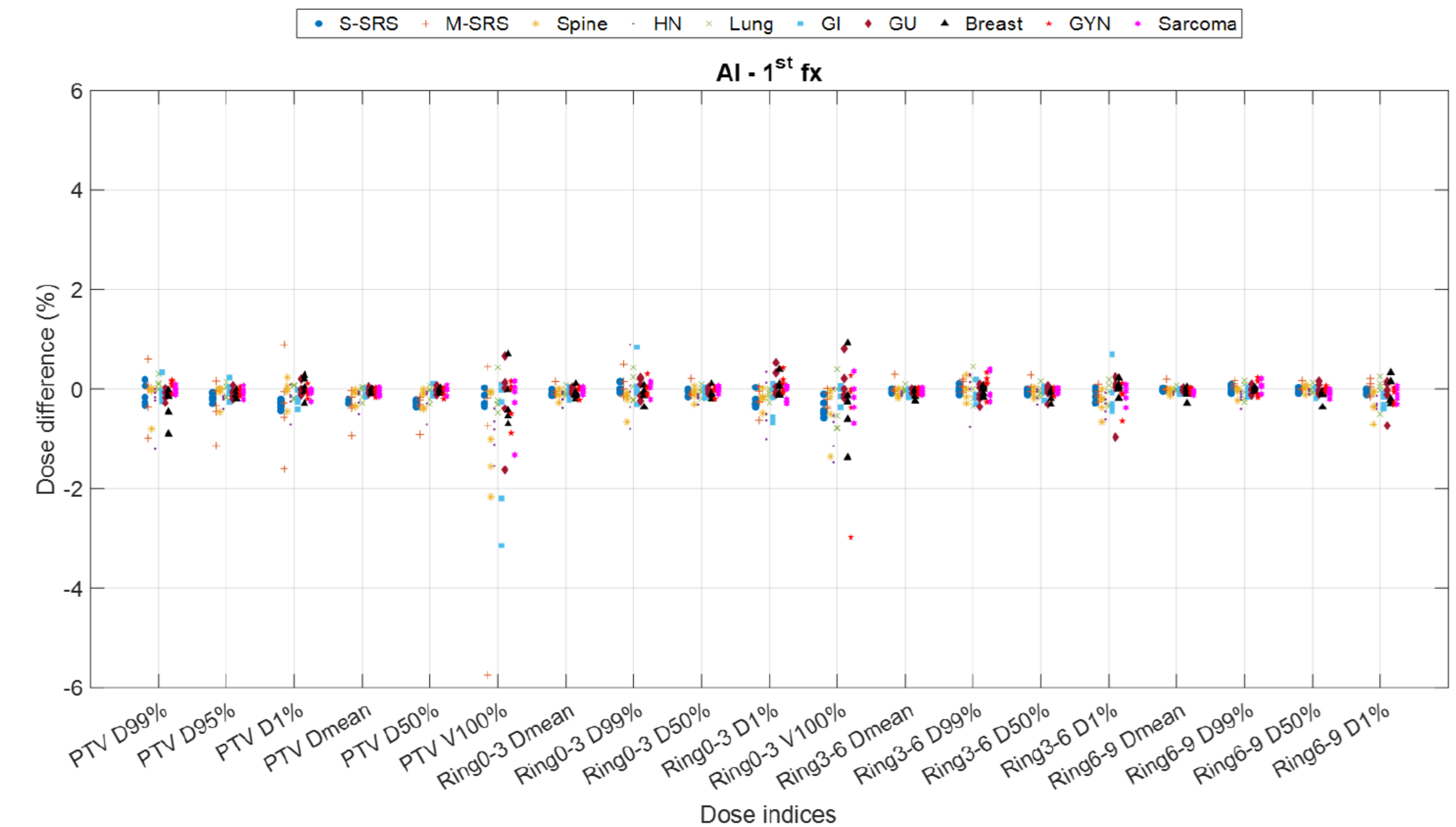


Figure 1 Dose indices differences between doses calculated with AI-based virtual log files and delivery-based log files recorded during the 1st fraction of treatment.

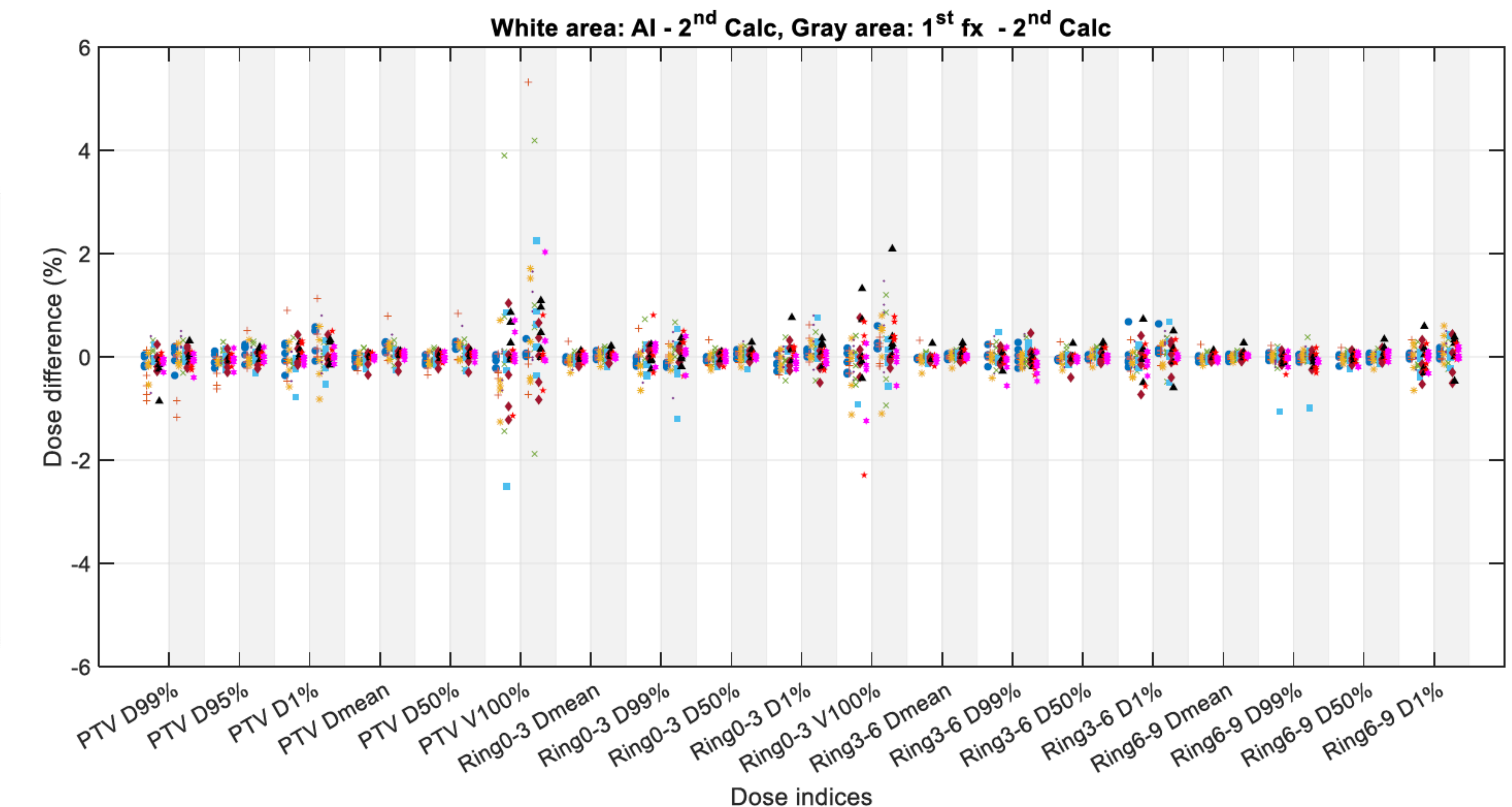


Figure 2 Dose indices differences of AI-based virtual log files versus secondary dose calculations and the differences of delivery-based log files from 1st fraction treatment versus secondary dose calculations.