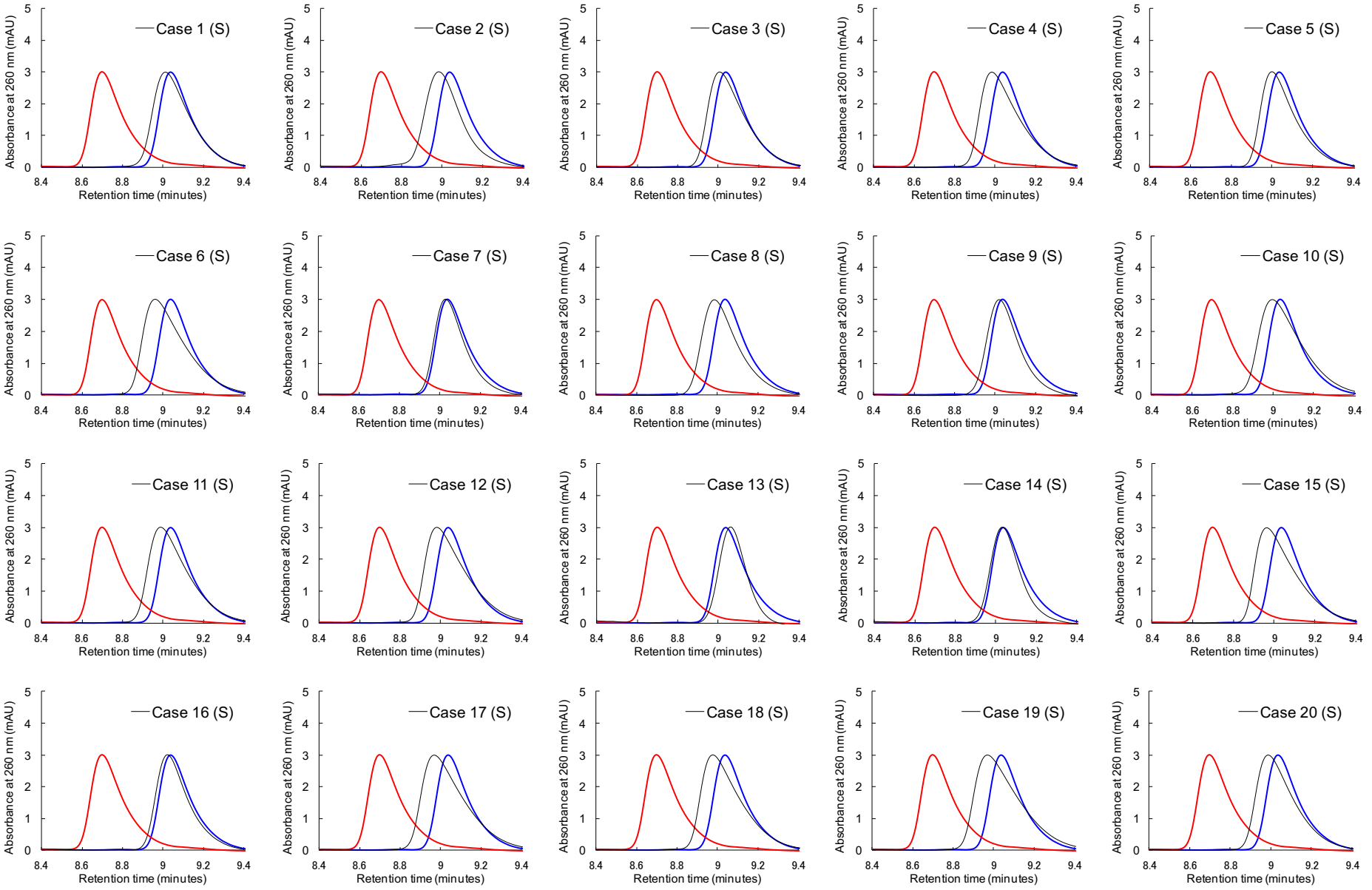
Supporting Information Table S1. Clinicopathological parameters of the clear cell renal cell carcinomas examined.

Clinicopathological parameters		Number of cases or mean ± standard deviation
Age		62.82 ± 10.56
Sex	Male	69
	Female	29
Tumor diameter (cm)		5.72 ± 3.37
Macroscopic configuration	Type 1	34
	Type 2	29
	Type 3	35
Predominant histological grades*	G1	44
	G2	37
	G3	14
	G4	3
Highest histological grades†	G1	7
	G2	41
	G3	26
	G4	24
Vascular involvement	Negative	50
	Positive	48
Renal vein tumor thrombi	Negative	69
	Positive	29
Predominant growth pattern*	Expansive	85
	Infiltrative	13
Most aggressive growth pattern†	Expansive	59
	Infiltrative	39
Tumor necrosis	Negative	67
	Positive	31
Invasion to renal pelvis	Negative	88
	Positive	10
Pathological Tumor-Node-Metastasis stage	Stage I	46
	Stage II	4
	Stage III	24
	Stage IV	24

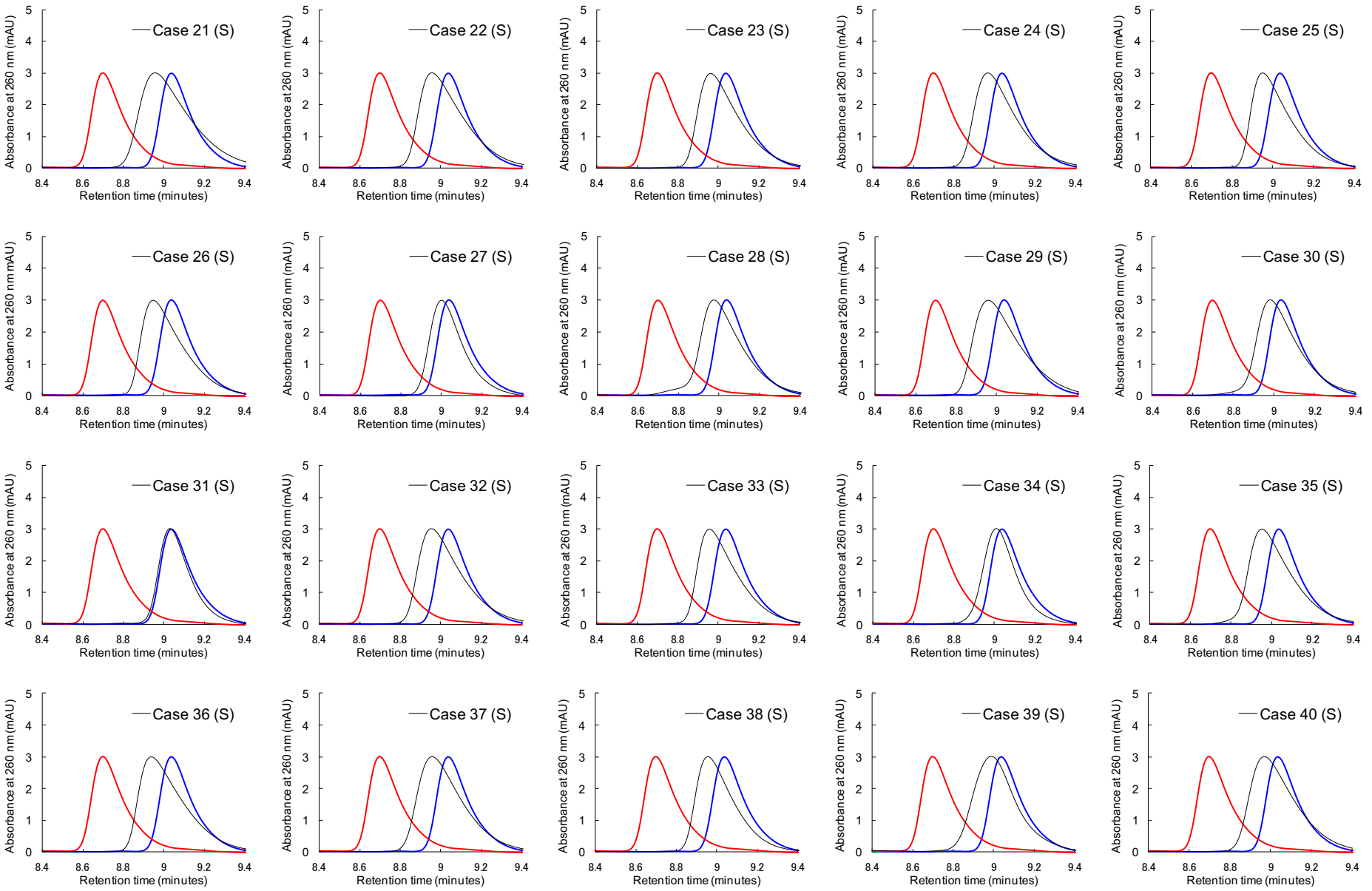
*If the tumor showed heterogeneity, findings in the predominant area were described. †If the tumor showed heterogeneity, the most aggressive features of the tumor were described.

Supporting Information Fig. S1 Chromatograms of all of the 98 clear cell renal cell carcinomas.



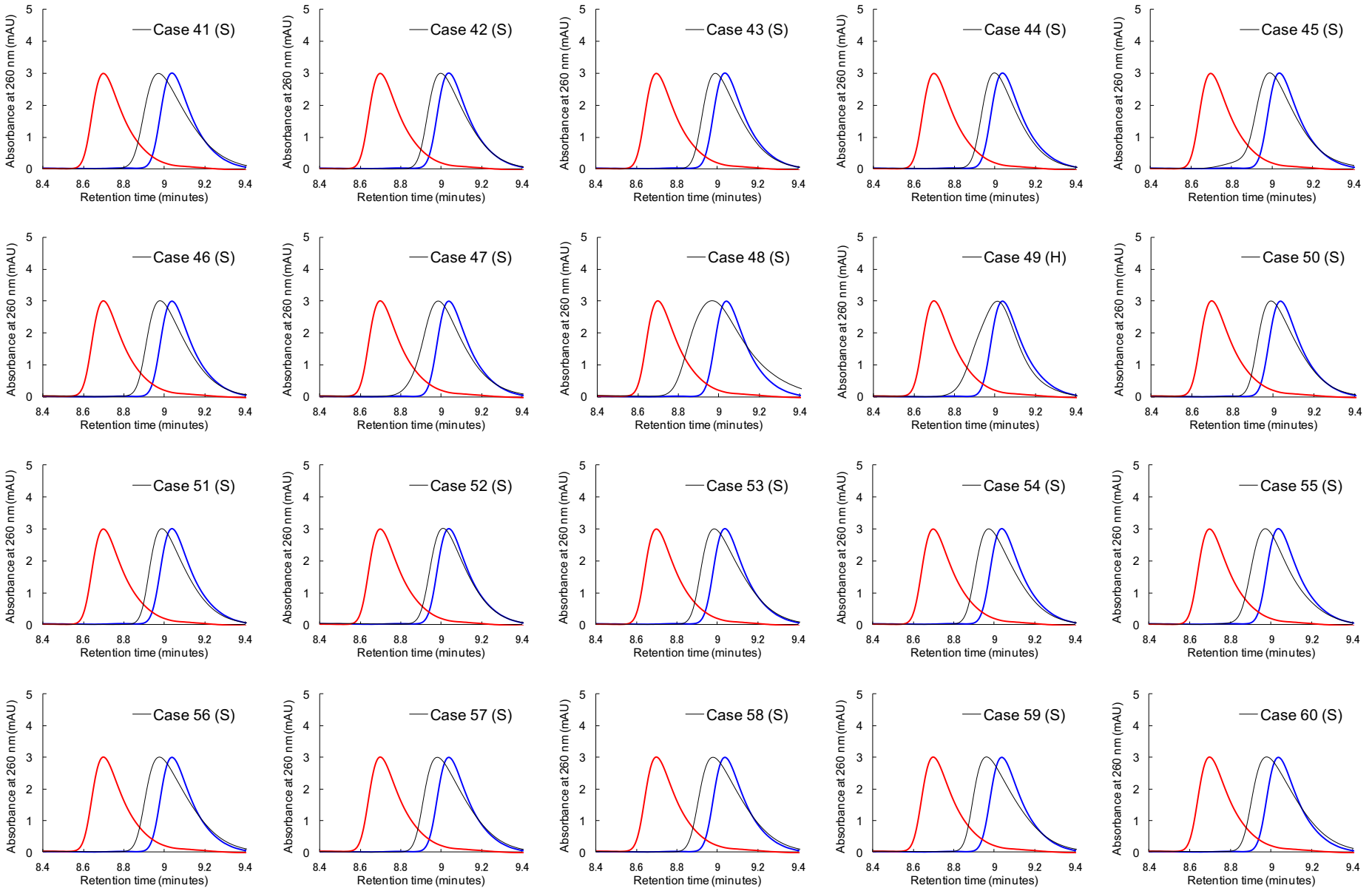
, unmethylated control; , fully methylated control; S, single peak pattern; H, single peak with a shoulder pattern; B, bimodal peak pattern.

Supporting Information Fig. S1 Chromatograms of all of the 98 clear cell renal cell carcinomas (continued).



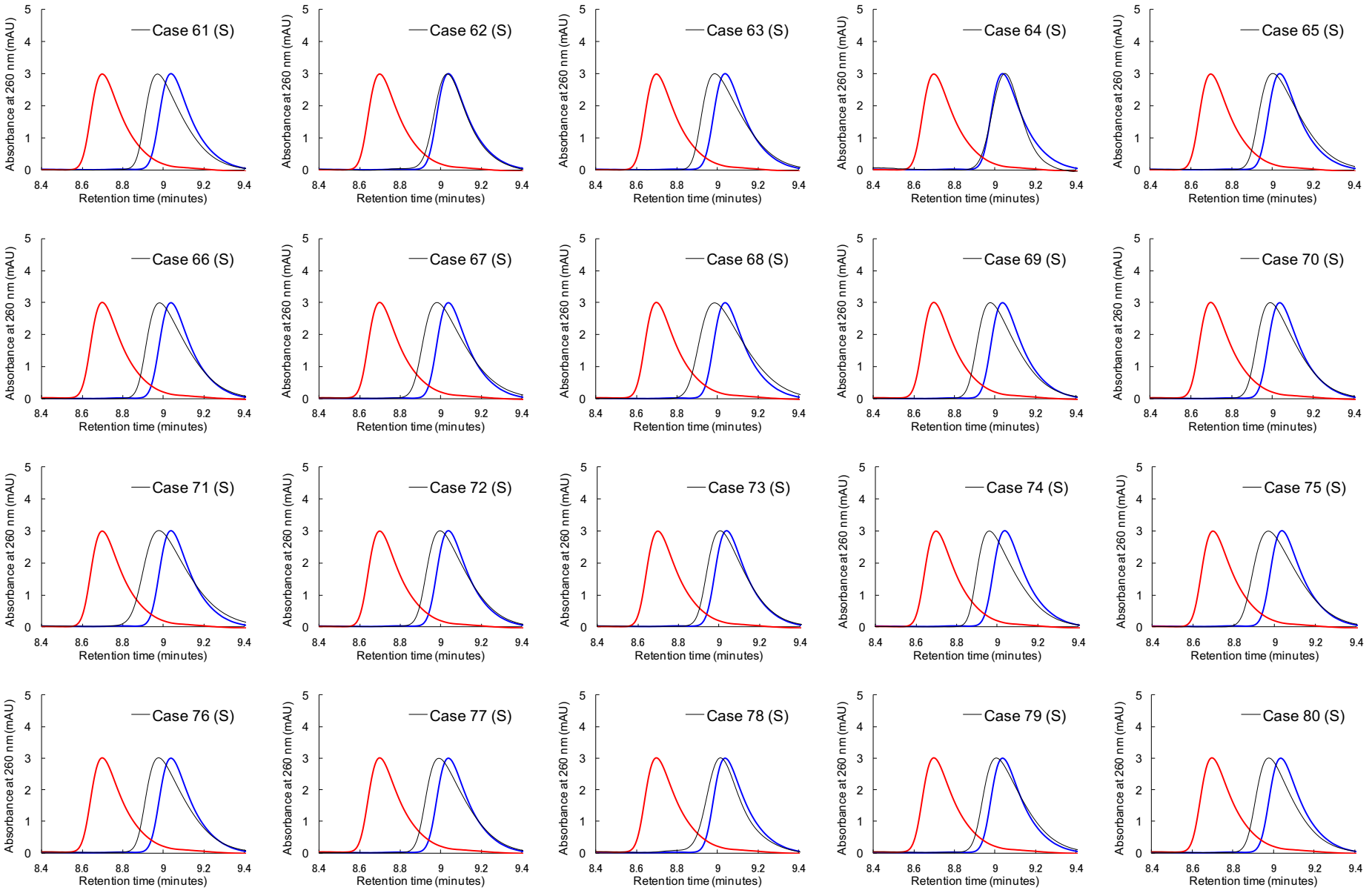
—, unmethylated control; —, fully methylated control; S, single peak pattern; H, single peak with a shoulder pattern; B, bimodal peak pattern.

Supporting Information Fig. S1 Chromatograms of all of the 98 clear cell renal cell carcinomas (continued).



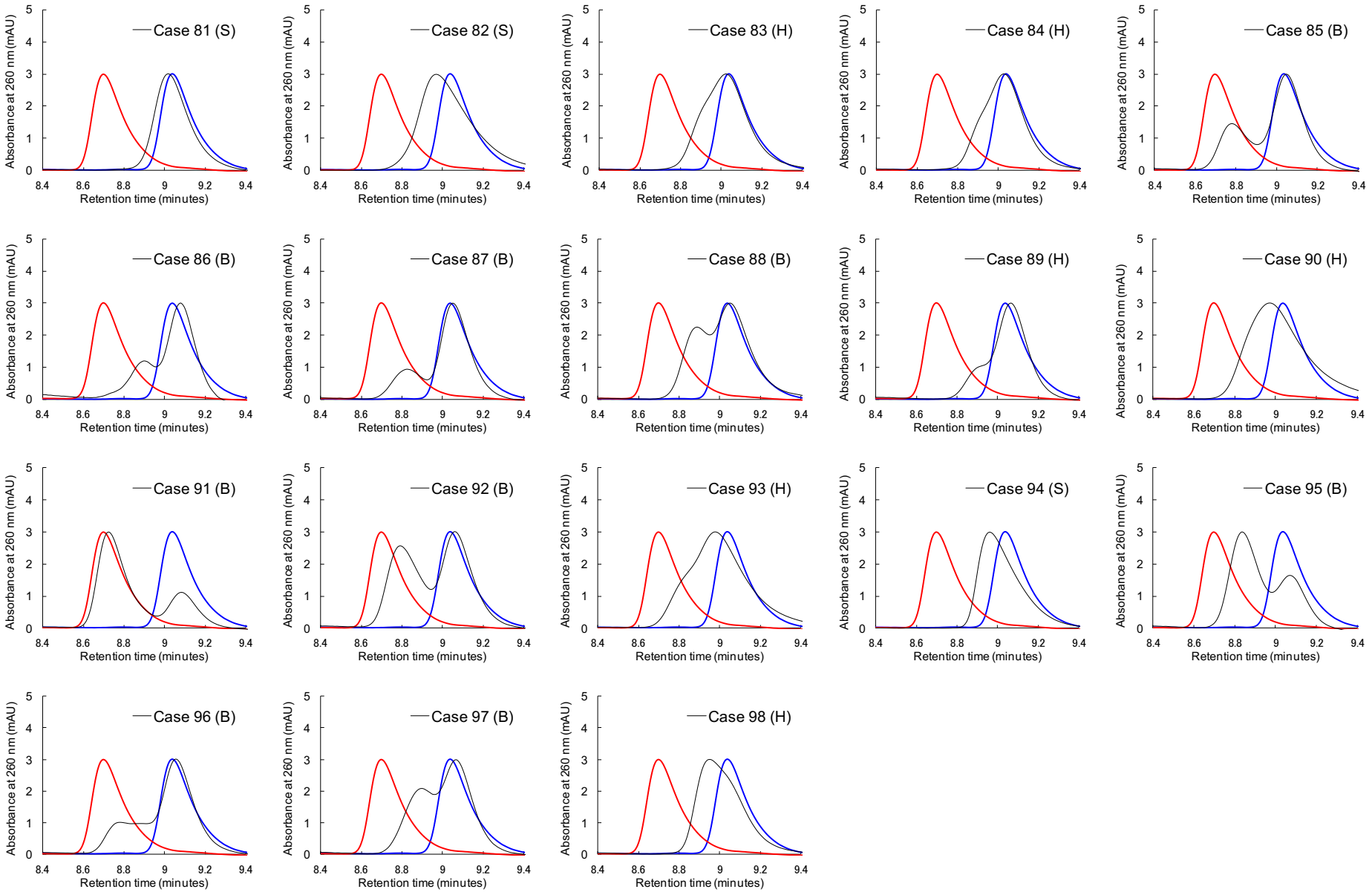
—, unmethylated control; —, fully methylated control; S, single peak pattern; H, single peak with a shoulder pattern; B, bimodal peak pattern.

Supporting Information Fig. S1 Chromatograms of all of the 98 clear cell renal cell carcinomas (continued).



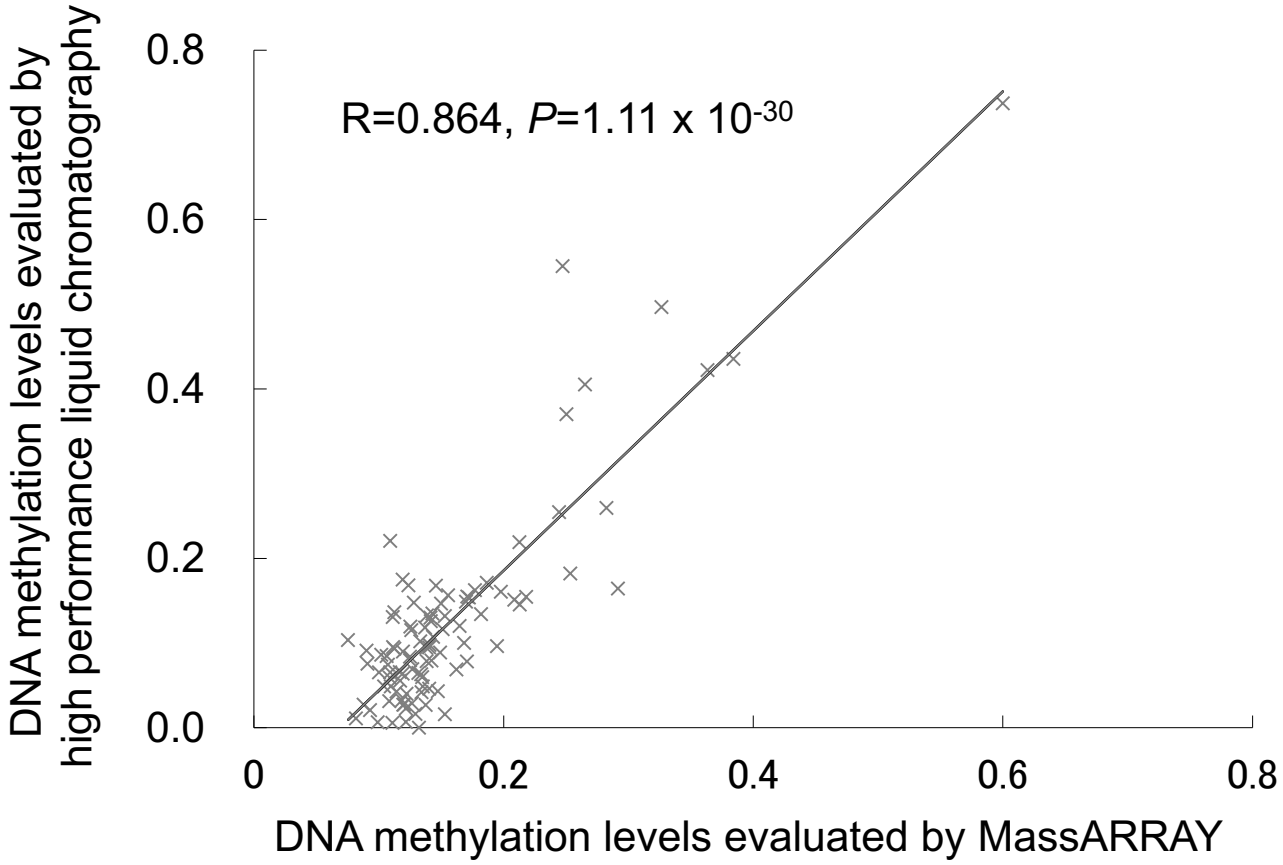
—, unmethylated control; —, fully methylated control; S, single peak pattern; H, single peak with a shoulder pattern; B, bimodal peak pattern.

Supporting Information Fig. S1 Chromatograms of all of the 98 clear cell renal cell carcinomas (continued).



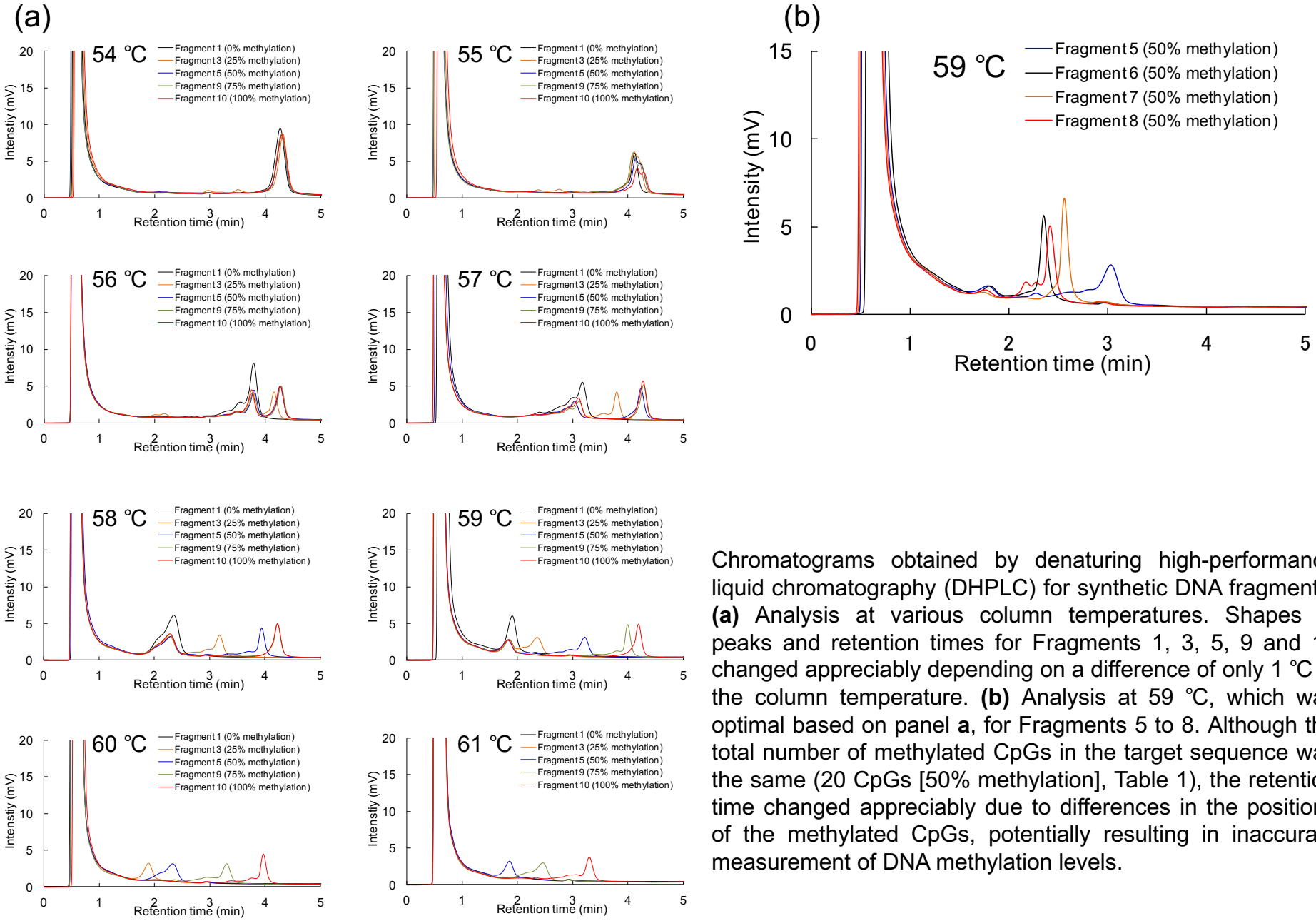
—, unmethylated control; —, fully methylated control; S, single peak pattern; H, single peak with a shoulder pattern; B, bimodal peak pattern.

Supporting Information Fig. S2



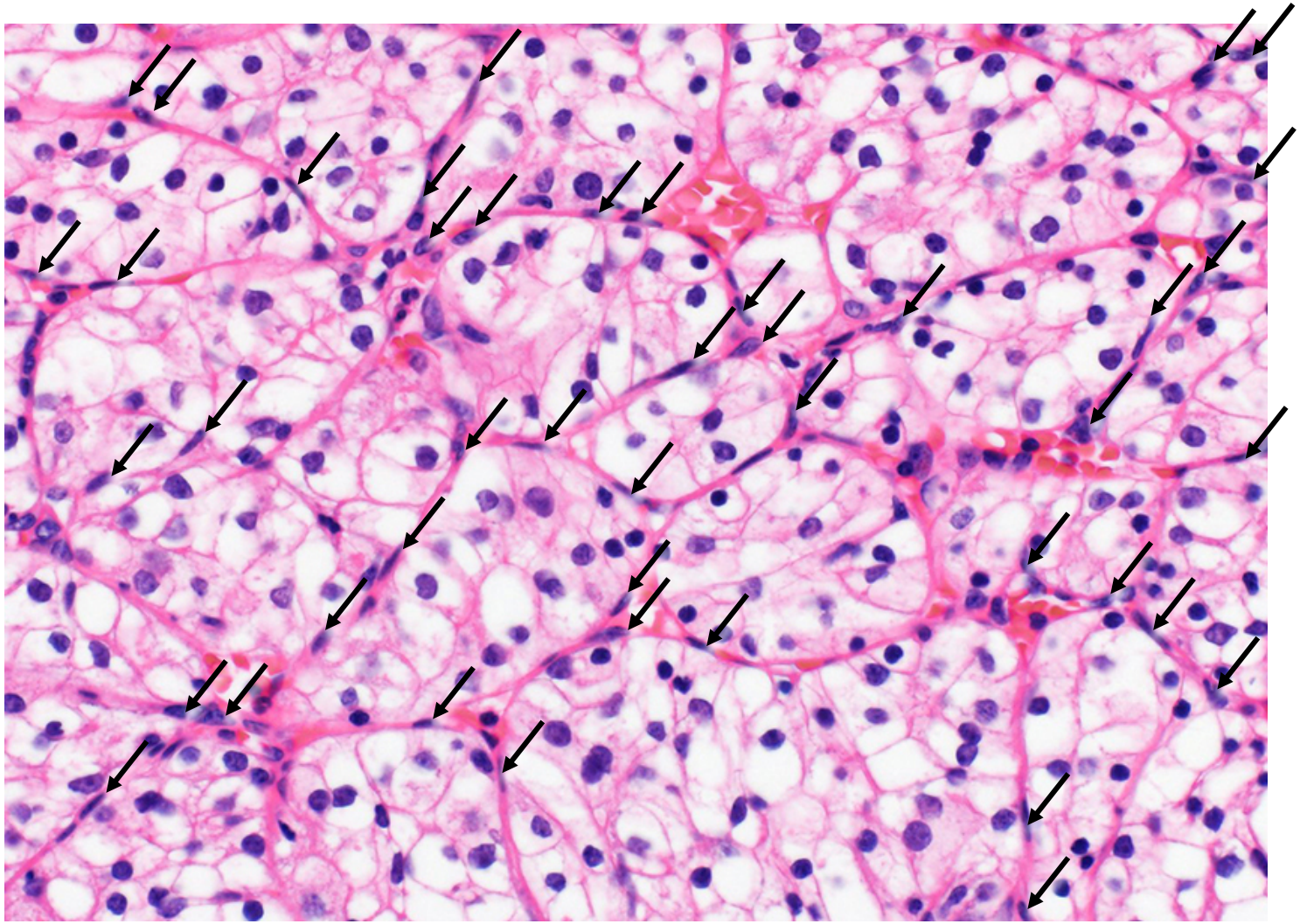
Accordance of DNA methylation levels of the *FAM150A* gene quantified by the newly developed anion-exchange high-performance liquid chromatography method and those evaluated by the conventional MassARRAY method. Excellent accordance was confirmed (R=0.864, P=1.11 x 10^{-30}) for all of the 98 clear cell renal cell carcinomas examined. The sequences of the primer sets and optimized PCR conditions for the MassARRAY method were described in our previous paper (Ref. 16).

Supporting Information Fig. S3



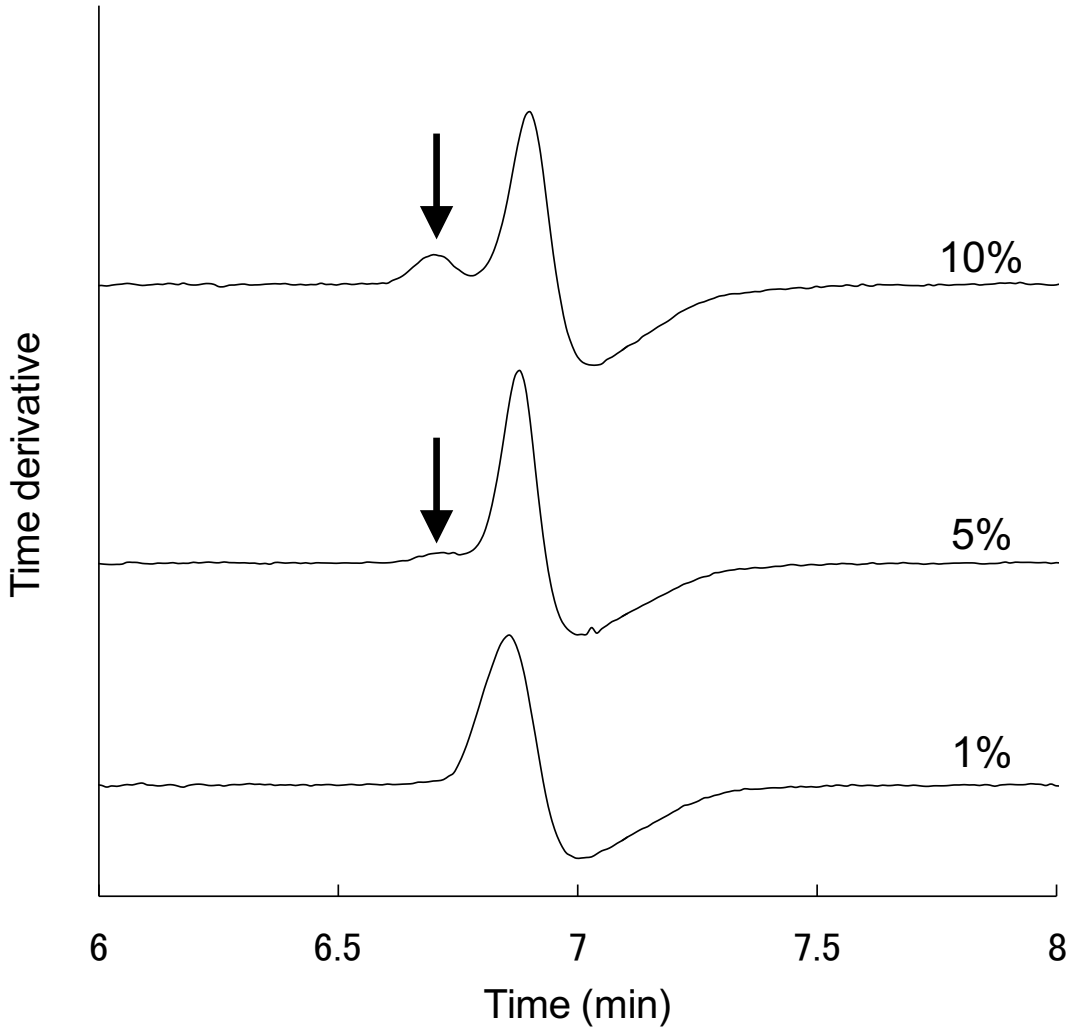
Chromatograms obtained by denaturing high-performance liquid chromatography (DHPLC) for synthetic DNA fragments. **(a)** Analysis at various column temperatures. Shapes of peaks and retention times for Fragments 1, 3, 5, 9 and 10 changed appreciably depending on a difference of only 1 ℃ in the column temperature. **(b)** Analysis at 59 ℃, which was optimal based on panel **a**, for Fragments 5 to 8. Although the total number of methylated CpGs in the target sequence was the same (20 CpGs [50% methylation], Table 1), the retention time changed appreciably due to differences in the positions of the methylated CpGs, potentially resulting in inaccurate measurement of DNA methylation levels.

Supporting Information Fig. S4



A representative microscopic view of clear cell renal cell carcinoma (ccRCC). ccRCCs are hypervascular tumors: considerable numbers of vascular endothelial cells (arrows) are observed among cancer nests. Hematoxylin-eosin staining. Original magnification: ×40.

Supporting Information Fig. S5



Discriminability for a mixture of PCR products from unmethylated (Fragment 1) and fully methylated (Fragment 10) synthetic DNAs. The degree of mixing of the fully methylated DNA template was designed to be 1%, 5% and 10%. At least a 5% mixture of fully methylated DNA (arrows) was confirmed by simply viewing the differential curve.