Log-rank test	Dataset	HbA1c levels	< 6.5%		\geq 6.5% and < 8.0%		$\geq 8.0\%$	
(Mantel-Cox)			Chi-square	p-value	Chi-square	p-value	Chi-square	p-value
TTFT (overall	Unmatched	< 6.5%	-	-	2.123	0.145	0.547	0.460
p > 0.05)	(complete) dataset	$\geq 6.5\%$ and $< 8.0\%$	2.123	0.145	-	-	0.126	0.723
		$\geq 8.0\%$	0.547	0.460	0.126	0.723	-	-
	Propensity score-	< 6.5%	-	-	2.391	0.122	1.185	0.276
	matched (1:1)	$\geq 6.5\%$ and $< 8.0\%$	2.391	0.122	-	-	0.003	0.959
	dataset ^{a)}	$\geq 8.0\%$	1.185	0.276	0.003	0.959	-	-
CSS (overall	Unmatched	< 6.5%	-	-	3.381	0.066	7.843	0.005
p < 0.05)	(complete) dataset	$\geq 6.5\%$ and $< 8.0\%$	3.381	0.066	-	-	0.524	0.469
		$\geq 8.0\%$	7.843	0.005	0.524	0.469	-	-
	Propensity score-	< 6.5%	-	-	4.240	0.039	5.937	0.015
	matched (1:1)	$\geq 6.5\%$ and $< 8.0\%$	4.240	0.039	-	-	0.051	0.821
	dataset ^{a)}	$\geq 8.0\%$	5.937	0.015	0.051	0.821	-	-

S7 Table. Pairwise comparisons among different HbA1c subgroups in diabetic patients for TTFT and CSS

TTFT, time-to-first-treatment; CSS, cancer-specific survival; HbA1c, hemoglobin A1c; β 2-MG, β 2-microglobulin; *IGHV*, immunoglobulin heavy chain variable region. ^{a)}Propensity score-matched (1:1) analyses were performed with a small caliper of 0.1 for matching potential cofounders including age, Binet stage, β_2 -MG levels, *TP53* disruption, *IGHV* mutational status, etc.