

Table S5a. Significantly mutated genes (SMGs) in canine urinary bladder canine UC.

Ensembl ID	Gene	<i>q</i> (subs)	<i>q</i> (global)
ENSCAFG00000003907	<i>BRAF</i>	0.00E+00	0.00E+00
ENSCAFG00000019028	<i>CDH12</i>	4.08E-02	3.41E-02
ENSCAFG00000012314	<i>ARID1A</i>	9.96E-01	4.73E-02
ENSCAFG00000014589	<i>KDM6A</i>	9.96E-01	8.36E-02

SMGs identified using dNdScv. A gene was considered a SMG if the *q* value based on substitutions only (subs) or the *q* value based on all mutation types (global) was < 0.1.

Table S5b. Significantly mutated genes in canine urinary bladder canine UC.

Ensembl ID	Gene	FDR CT
ENSCAFG00000003907	<i>BRAF</i>	0.00E+00
ENSCAFG00000019028	<i>CDH12</i>	3.92E-06
ENSCAFG00000017775	<i>GPRASP1</i>	1.12E-04
ENSCAFG00000004870	<i>PCDH17</i>	1.08E-03
ENSCAFG00000012314	<i>ARID1A</i>	1.72E-03
ENSCAFG00000004944	<i>PCDH9</i>	1.72E-03
ENSCAFG00000000786	<i>CSMD3</i>	1.72E-03
ENSCAFG00000014589	<i>KDM6A</i>	8.25E-03
ENSCAFG00000001862	<i>ZNF804B</i>	8.25E-03

SMGs identified using MuSiC2 with FDR CT < 0.01, where CT is the convolution test.