

**Table S6a. Significantly mutated genes (SMGs) in feline urinary bladder UC.**

<b>Ensembl ID</b>	<b>Gene</b>	<b>q (subs)</b>	<b>q (global)</b>
ENSFCAG00000009623	<i>TP53</i>	2.45E-06	0
ENSFCAG00000015711	<i>BAP1</i>	1.80E-01	7.83E-05
ENSFCAG00000025616	<i>FAT1</i>	3.42E-02	2.96E-04
ENSFCAG00000015718	<i>PBRM1</i>	8.49E-03	8.94E-03
ENSFCAG00000026584	<i>LRP1B</i>	8.49E-03	1.59E-02
ENSFCAG00000001953	<i>JAK1</i>	7.32E-03	3.68E-02
ENSFCAG00000037994	<i>NRAS</i>	1.64E-02	1.37E-01
ENSFCAG00000022826	<i>CDKN2A</i>	3.39E-02	2.81E-01

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 S6b. Significantly mutated genes in feline urinary bladder UC.**

<b>Ensembl ID</b>	<b>Gene</b>	<b>FDR CT</b>
ENSFCAG00000009623	<i>TP53</i>	0.00E+00
ENSFCAG00000025616	<i>FAT1</i>	6.28E-07
ENSFCAG00000015711	<i>BAP1</i>	2.55E-06
ENSFCAG00000019287	<i>SETD2</i>	1.77E-04
ENSFCAG00000026584	<i>LRP1B</i>	5.12E-04
ENSFCAG00000037994	<i>NRAS</i>	1.60E-03
ENSFCAG00000001953	<i>JAK1</i>	2.02E-03

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