Table S13. Commonly amplified or deleted cancer genes from a comparison of focal amplifications and deletions across human, canine and feline urinary bladder invasive UC.

Regions compared	Human vs dog		Human vs cat	Dog vs cat		
	Amplified	Deleted	Amplified	Deleted	Amplified	Deleted
5Mb (cat, dog), focal targets (human)	MDM2	-	PPARG	СКЕВВР	-	-
10Mb (cat, dog), focal targets (human)	MDM2	RB1	PPARG	CREBBP, NCOR1	-	-
20Mb (cat, dog), focal targets (human)	MDM2	RB1	PPARG	CREBBP, NCOR1	-	-
5Mb (cat, dog), wide peak (human)	MDM2, ZFHX3	FSTL3, STK11, TCF3	PPARG, RNF213	CREBBP	-	-
10Mb (cat, dog), wide peak (human)	MDM2, ZFHX3	FSTL3, STK11, TCF3, RB1	PPARG, RNF213	CREBBP, NCOR1, ARHGEF10	-	-
20Mb (cat, dog), wide peak (human)	MDM2, ZFHX3	FSTL3, STK11, TCF3, RB1, CASP3, FSTL3, ARHGEF10	PPARG, RNF213	CREBBP, NCOR1, ARHGEF10	-	ARHGEF10

Significantly amplified or deleted focal regions in feline, canine and human UC were compared to identify commonly amplified or deleted Cancer Gene Census (CGC) or bladder cancer (BLCA) genes. For each pairwise comparison, syntenic regions and common genes within focal regions were identified. For feline and canine UC, focal regions with a maximum size of 5Mb, 10Mb and 20Mb (see Methods) were compared to focal target regions identified in human MIBC and wider peak regions from GISTIC analysis.