

Supplementary Table S3 Somatic mutation identified in CCA tissue

CCA tissue	Gene	Consequence	Chrom	Pos	Ref Allele	Alt Allele	AA
KKU-097	KRAS	missense_variant	chr12	12:25245348-25245348	C	A	G/C
KKU-023	BRAF	missense_variant	chr7	7:140808302-140808302	A	C	L/R
KKU-023	PIK3CA	missense_variant	chr3	3:179234297-179234297	A	G	H/R
KKU-023	ARID1A	frameshift_variant	chr1	1:26779439-26779439	-	G	-/X
KKU-452	ARID1A	frameshift_variant	chr1	1:26774936-26774936	-	T	S/SX
KKU-023	ARID2	frameshift_variant	chr12	12:45836771-45836773	TT	-	SL/SX
KKU-023	NCOR1	stop_gained	chr17	17:16117929-16117929	G	A	R/*
KKU-097	TP53	missense_variant	chr17	17:7674212-7674212	T	A	I/F
KKU-452	TP53	stop_gained	chr17	17:7670664-7670664	C	A	E/*
KKU-610	TP53	stop_gained	chr17	17:7670703-7670703	C	A	E/*
KKU-023	MSH6	frameshift_variant	chr2	2:47803552-47803553	T	-	T/X
KKU-097	MSH3	missense_variant	chr5	5:80678960-80678960	G	A	D/N
KKU-023	SMAD4	frameshift_variant	chr18	18:51058143-51058143	-	G	L/LX
KKU-097	SMAD4	frameshift_variant	chr18	18:51048751-51048751	-	A	-/X
KKU-023	AFF4	stop_gained	chr5	5:132934266-132934266	C	A	E/*
KKU-610	CDKN1B	missense_variant	chr12	12:12718114-12718114	C	T	P/L
KKU-023	KMT2C	stop_gained	chr7	7:152152909-152152909	G	A	R/*
KKU-097	KMT2C	frameshift_variant	chr7	7:152205140-152205141	C	-	G/X
KKU-097	ELF3	frameshift_variant	chr1	1:202015320-202015320	-	T	-/X
KKU-023	PDK1	missense_variant	chr2	2:172556161-172556161	C	T	A/V
KKU-023	POLE	stop_gained	chr12	12:132657184-132657184	G	C	Y/*