

Table S7. Mutations at 3' untranslated regions (UTRs) of *UGT* genes in TCGA tumors. Mutations in functional miRNA seed target sites are in bold.

1As	2As	2A3	2B4	2B7	2B10	2B11	2B15	2B28	3A1	3A2	UGT8
c.*1G>C c.*37T>C c.*46A>G c.*65G>T <b>c.*70A&gt;T</b> <b>c.*74T&gt;A</b> c.*78A>C c.*85T>C	c.*15G>A c.*15G>A c.*20A>G c.*21T>C c.*27_*28insA c.*45T>C	c.*5T>A c.*26G>C c.*58G>A c.*63dupT c.*67G>T c.*67G>A c.*96T>C c.*97C>A c.*123C>G c.*138C>A c.*163C>A	c.*4C>T c.*5G>A c.*16G>A c.*23G>T c.*24G>A c.*38G>T c.*38G>T c.*41C>A c.*43C>T c.*43C>T c.*69G>T c.*83G> <b>T</b> <b>c.*83G&gt;A</b> c.*90T>G c.*110C>T c.*114C>G c.*118A>T c.*124C>A c.*124C>A c.*131A>C c.*209dupA c.*267T>C	c.*14T>C c.*35G>T c.*35G>A c.*57C>T c.*58C>A c.*61C>T c.*64G>A c.*75A>G c.*86C>A c.*106A>G c.*108A>G c.*111A>G c.*136T>G c.*151A>C c.*236delA	c.*4T>A c.*8T>G c.*9G>C c.*11G>A c.*26_*42del c.*58C>A c.*78C>A c.*84T>G c.*86C>T c.*93C>T c.*109dupA c.*109delA c.*109delA c.*109delA c.*116C>T c.*116C>T c.*117G>A c.*117G>A c.*120G>A	c.*5G>A c.*23G>A c.*64G>A c.*73G>T c.*73G>T c.*75T>C c.*86G>T c.*99C>A	c.*7C>T c.*7_*14dupCAAAAGCC c.*16G>A c.*16G>A c.*29T>C c.*29T>C c.*30G>A c.*34G>C c.*46C>T c.*54T>G c.*62G>A c.*76G>A c.*76G>A c.*78G>A c.*79G>A c.*79G>A c.*84C>T c.*84C>T c.*84C>T c.*89T>G c.*91C>T c.*95T>C c.*109T>G c.*128A>G c.*136T>C c.*139A>G c.*233G>T	c.*8T>G c.*23G>A c.*31G>A c.*35G>A c.*122C>G c.*167C>G c.*171C>T c.*194G>A c.*205G>T	c.*7G>A c.*7G>T c.*17G>T c.*18G>T c.*23G>A c.*25G>T c.*26G>T c.*33T>G c.*34C>T c.*34C>T c.*35C>T c.*36C>T c.*37T>C c.*39G>T c.*41C>G c.*42C>T c.*50G>A c.*57C>A c.*58C>T c.*60C>A c.*61C>G c.*61C>A c.*62C>T c.*70C>T c.*78C>T c.*126C>T c.*135C>A c.*141C>A c.*190dupT	c.*6G>T c.*20G>A c.*20G>A c.*21G>A c.*23dupG c.*28T>C c.*35G>T c.*35G>A c.*37C>T c.*37C>T c.*38G>A c.*43C>T c.*56G>A c.*62C>T c.*91G>T c.*113T>G c.*118G>T c.*127G>A c.*132delA c.*159C>A c.*184A>C	c.*13G>C c.*20G>T c.*38C>G c.*75A>G c.*274G>C c.*379G>T

\*: stop codon