Figure S4. Nuclear p53 expression correlates positively with loss of wild type allele in serous epithelial ovarian carcinomas in p53

mutant mice. A, Single mutants p53mni (a), p53miw (b), or un-injected control ovaries (c) have no significant lesions and no significant
nuclear p53 expression in the ovarian surface epithelium (arrows in a, b, c). Note brown background staining in the cytoplasm of
corpus luteal cells (asterisks in b and c). B, High nuclear p53 expression (brown stain) in K18GT-121pro/Brcal169/p53miw SEOC (a, b)
demonstrating the effect that the loss of the wild type p53 allele has on nuclear p53 expression. A majority of cells in the tumor express
nuclear p53 (higher magnification in b). There is only occasional nuclear p53 expression in K18GT-121pro/Brcal169/p53mni SEOC
(c, d), note small region with nuclear p53 expression (arrow in c) while the majority of the tumor cells are negative (asterisk in c and
in higher magnification in d). Spontaneous loss of the wild type allele can occur in K18GT-121pro/Brcal169/p53mwi SEOC (e, f), note p53
negative region of tumor (asterisk in e) adjacent to the region with high p53 expression (arrow in e). Most of the cells in the p53
expressing tumor have nuclear p53 expression (higher magnification in f, arrow). C, Nuclear p53 expression is increased in tumors that
have both p53 alleles affected (p53mwi) compared to tumors with one mutant and one wild type p53 allele (p53miw). P53mwi mice that
have confirmed loss of wild type p53 allele are shown in green. D, IHC for p53 in non-injected ovary, primary ovarian tumor and

carcinomatosis of the same K18GT-121pro/Brcal169/p53mwi mouse shows stabilization of p53 in carcinomatosis (brown, DAB) due to loss
of wild allele in exon 5 hot spot, as shown by sequence analysis below. Scale bars represent 100 μm.