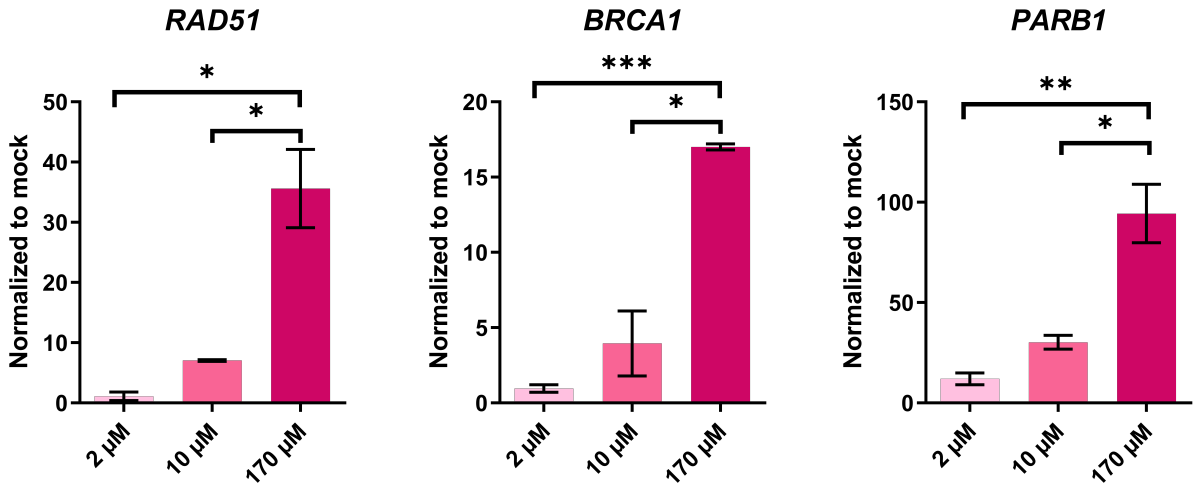
Appendix

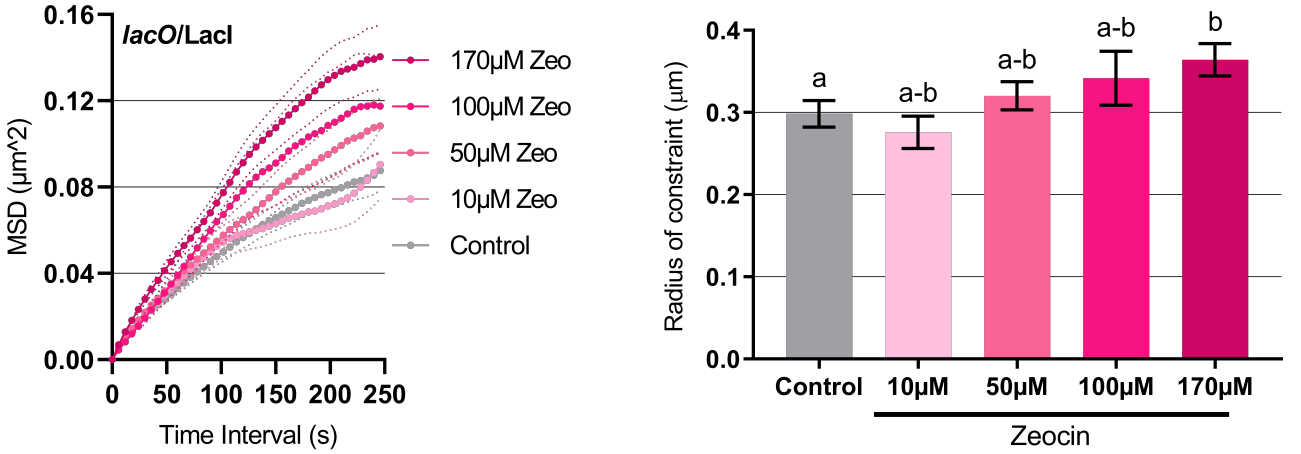
Table of content

A

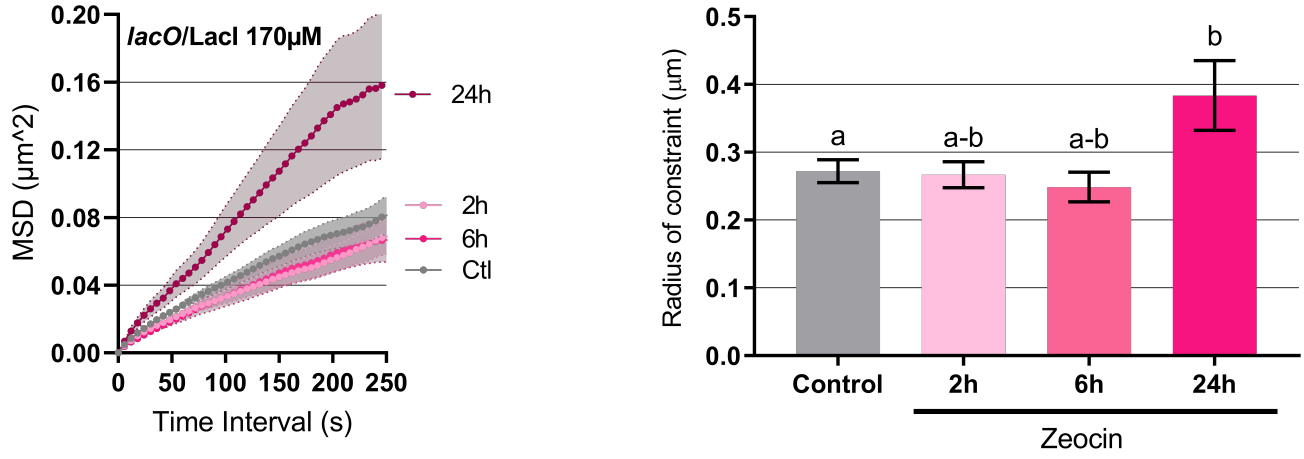


Appendix Figure S1: Zeocin induces expression of DDR genes in a dose-dependent manner. Expression analysis of DDR responsive genes *RAD51, BRCA1* and *PARB1* in 7-day-old Arabidopsis seedlings treated with different zeocin concentrations. Two to three independent biological replicates were performed. Values represent means ± SEM. Student t-test, *P < 0.05 **P < 0.01 ***P < 0.001.

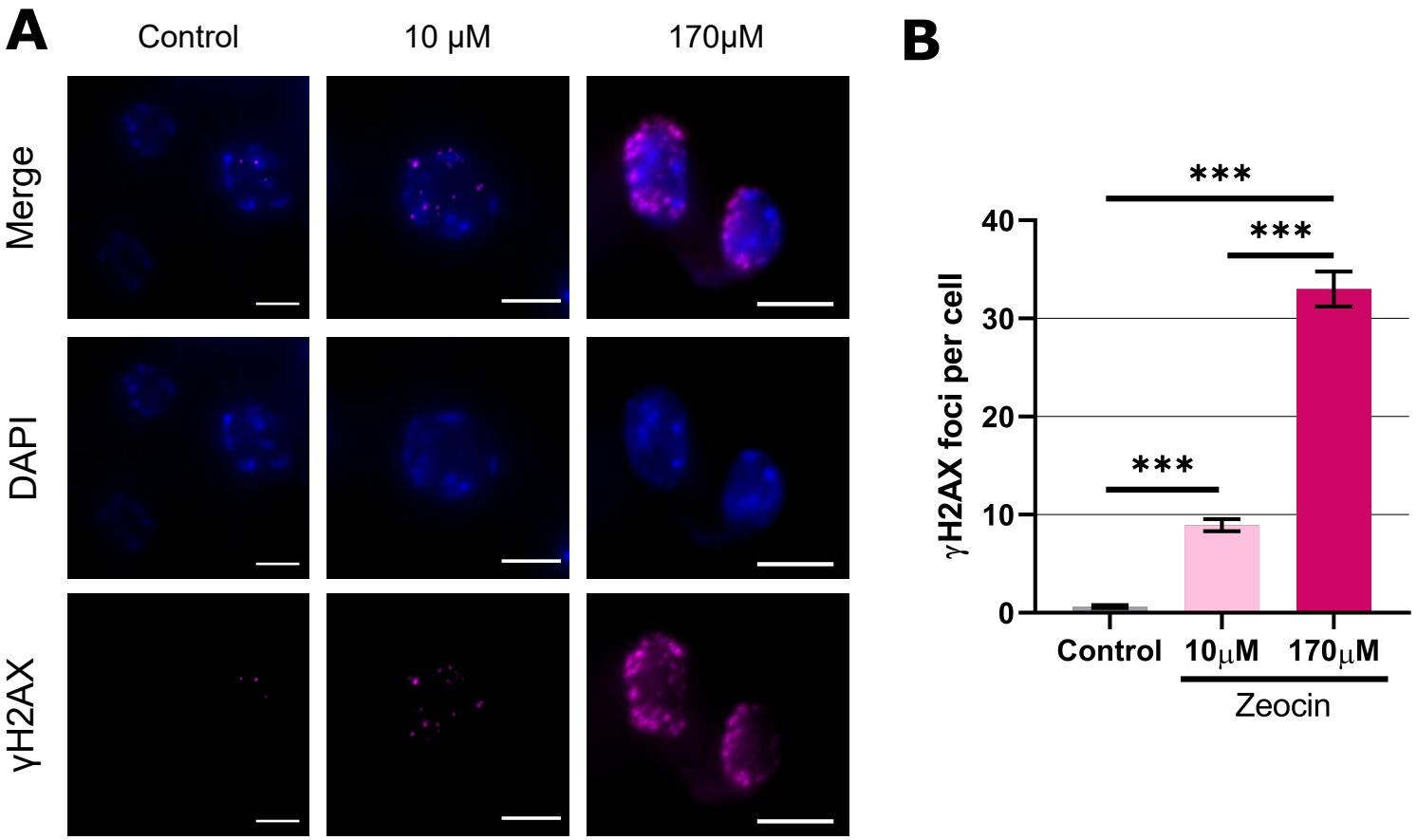
A



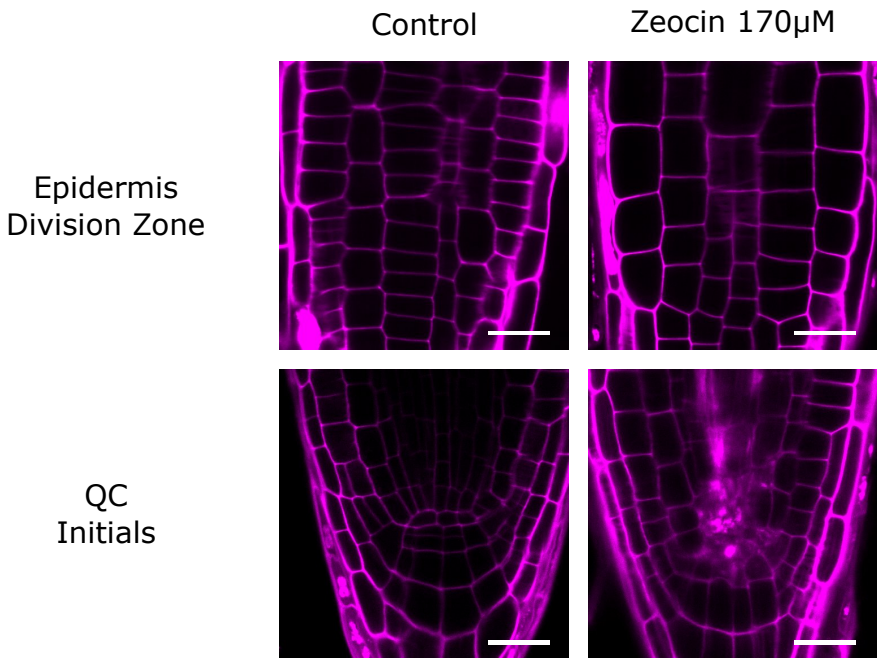
B



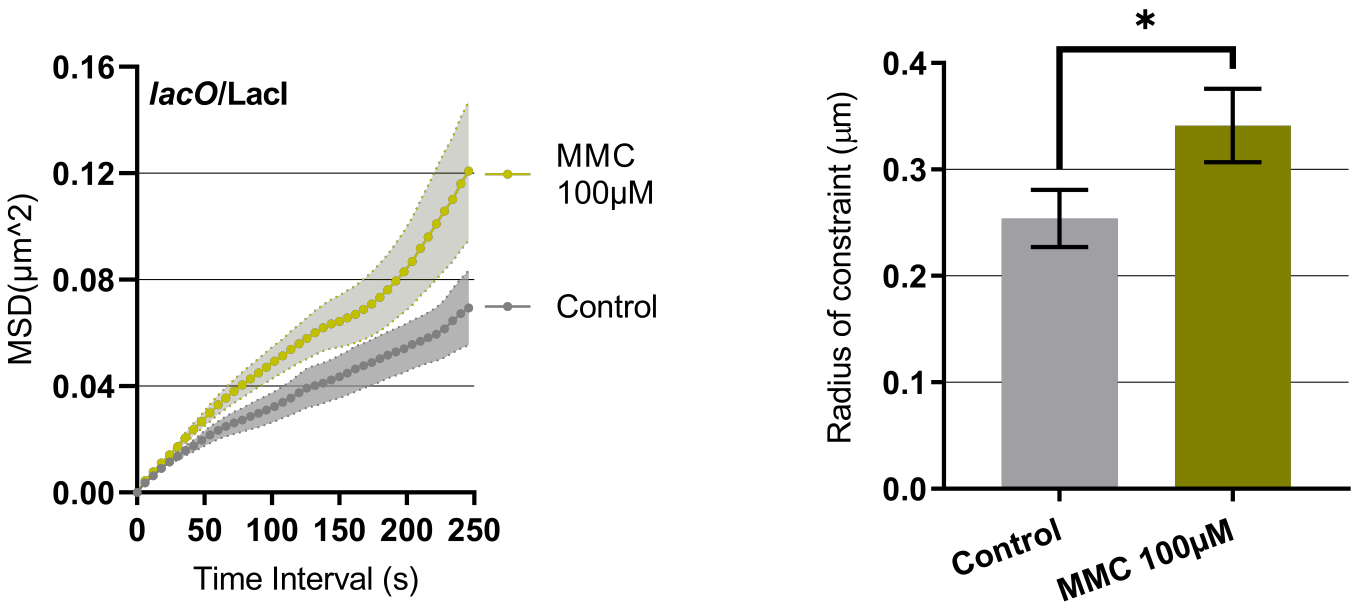
Appendix Figure S2: Treatment with high concentrations of zeocin results in increased chromatin mobility. (A-B) MSD curves and corresponding Rc histograms for: (A) Arabidopsis *lacO*/LacI line 112 in control conditions and upon treatment with different zeocin concentrations (10µM n=97; 50µM n=111; 100µM n=29; and 170µM n=93 nuclei); (B) *lacO*/LacI line 112 in control conditions and different times of zeocin treatment (2h n=39; 6h n=45; and 24h n=20); Values represent means ± SEM. Letters indicate one-way ANOVA followed by Bonferroni's correction ($p < 0.05$)



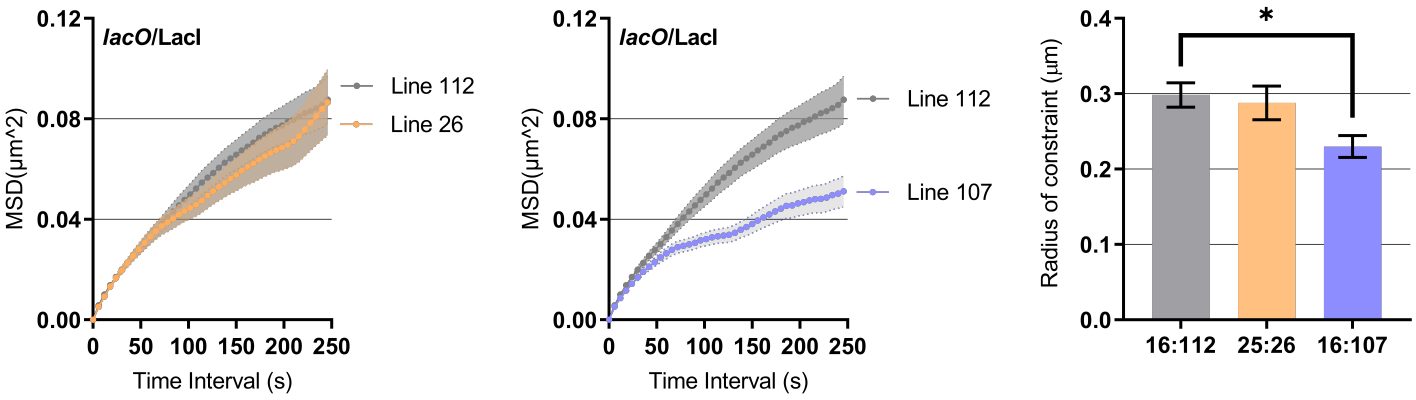
Appendix Figure S3: Zeocin induces γH2AX foci in a dose-dependent manner. (A) Representative images of immunolabeling of Arabidopsis nuclei with an antibody against γH2AX. 7-day-old Col-0 seedlings were treated for 24h with zeocin (10µM and 170µM). γH2AX foci (purple). DNA labelled with DAPI (blue). Scale bar, 5 µm. (B) Quantification of γH2AX foci per cell treated with different zeocin concentrations (Control n=137 10.M n=136 and 170.M n=106 nuclei). Values represent means ± SEM. Student t-test, *P < 0.05 **P < 0.01 ***P < 0.001.



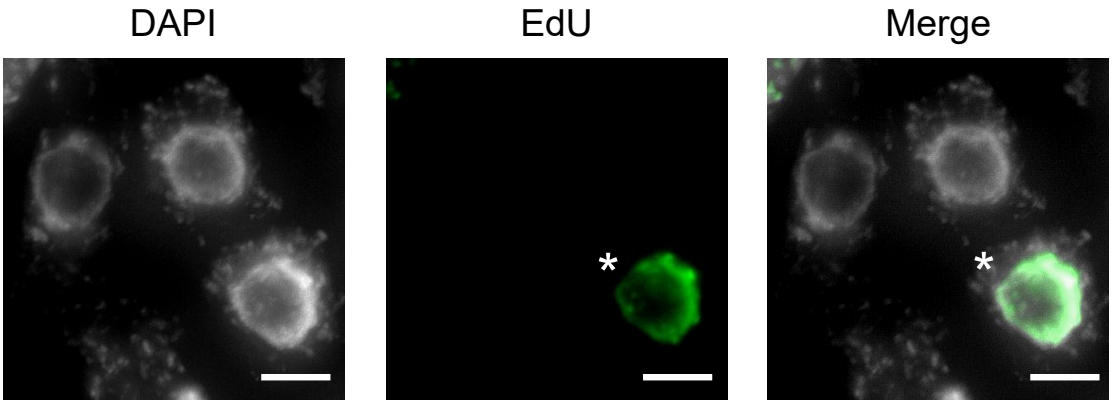
Appendix Figure S4: Genotoxic stress upon zeocin induces cell death in quiescent center cells but not in epidermal cells from Arabidopsis roots. Representative images of roots stained with PI (magenta), which marks the outline of living cells but enters dead cells. Images show epidermal cells from the division zone and the stem cell niche (quiescent center cells and initials) from 7-day-old Col-0 seedling after 24 h of zeocin treatment compared to non-treated samples (Control). Scale bar, 20 µm.



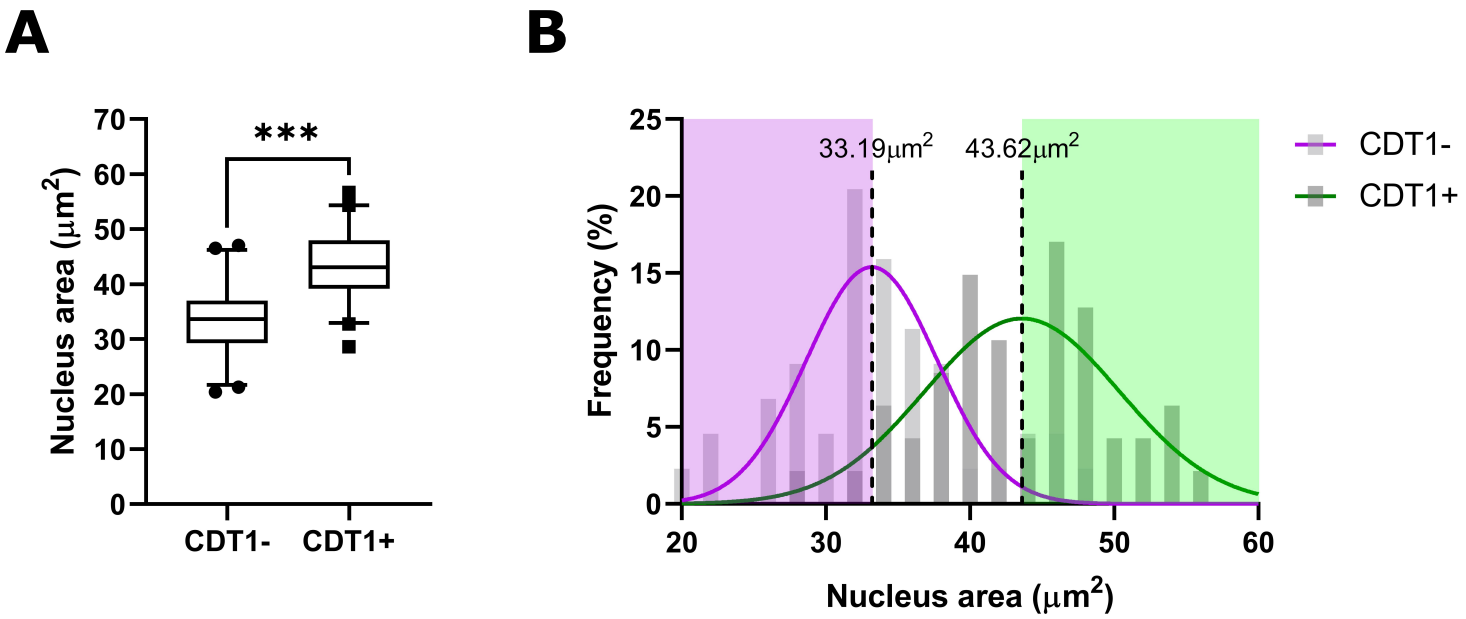
Appendix Figure S5: Chromatin mobility increase upon MMC treatment. MSD analysis of Arabidopsis *lacO*/LacI lines based on time-lapse experiments of nuclei upon treatment with 100µM MMC. Radius of constraint was calculated from MSD curves. Control n=32; 100µM MMC n=30 nuclei. Values represent means ± SEM. Student t-test, *P < 0.05.



Appendix Figure S6: Chromatin mobility for additional *lacO*/LacI lines in control conditions. MSD analysis of Arabidopsis *lacO*/LacI line 112 (n=116 nuclei) compared to line 26 (n=52 nuclei) and 107 (n=53 nuclei). Radius of constraint was calculated from MSD curves. Values represent means ± SEM. Student t-test, *P < 0.05



Appendix Figure S7: Quantitative analysis of EdU incorporation on *Arabidopsis thaliana* roots. DAPI-stained (DNA) and EdU-labelled cells from the meristem region after roots were incubated for 6h in EdU. Asterisk indicates cells showing EdU signal. Scale bar, 10 μm.



Appendix Figure S8: Nucleus area in S/G2 versus G1 cells. (A) Quantification of nuclear area in Arabidopsis nuclei with and without CDT1 signal. Nuclei from epidermal trichoblast root cells from *lacO*/LacI lines were measured from optical slices obtained from confocal microscopy imaging. (B) Frequency distribution in percent for the nuclear area (µm2) of nuclei with (dark gray) or without (light gray) CDT1 signal. Each curve was fitted by a Gaussian function (CDT1- in purple; CDT1+ in green). The median value of CDT1-/+ distribution has been used as thresholds to determine cells in G1 or S/G2 phase. Values represent means ± SEM. Student t-test, ***P < 0.001.

Appendix Table S1: Primers Used in This Study

qPCR	
RAD51-F	GCGCAAGTAGATGGTTCAGC
RAD51-R	TTCCTCAACGCCAACCTTGT
PARP2-F	GGTACGCTAAACCGCAAACC
PARP2-R	GGGTTTCTTCTCTTTCGCTTAAA
BRCA1-F	ACGAAGTCCCACCGAGAAAC
BRCA1-R	TCCATGCGGTTGTGTAGCTT
PP2A-F	TAACGTGGCCAAAATGATGC
PP2A-R	GTTCTCCACAACCGCTTGGT

Genotyping	
sog1 dCAPS F	CTCCCAGGACCAACCAAGTGAG
sog1 dCAPS R	GATTCCGATCAGGATTTTGCTAG