Table S3. Variants identified in the mutational analysis of hereditary cancer genes in case 29

Variant calling				Coverage		rs ID	MAF	*In silico* predictions					ClinVar Classification
									Protein function				
Gene	Transcript	cDNA change	Predicted protein change	Allele Frequency (%)	Read Depth		genomAD (%)	Splicing	SIFT	Mutation Taster	Polyphen2 /HumDiv	Polyphen2 /HumVar	
XRCC2	NM_005431.1	c.115G>A	p.V39M	45,19	104	rs730882040	0,01	No changes	Deleterious	Disease causing	Possibly damaging	Possibly damaging	Uncertain significance**