

Supplementary Table 1. Genes included into RADzeta and centroids

Genes	logFC	t	Centroid of 12	Centroid of 12
			sensitive cells	resistant cells
NUP210	-0.875	-5.192	0.673	-0.201
PPAT	-0.528	-5.235	1.179	0.652
CEP76	-0.480	-5.121	0.551	0.071
PAICS	-0.466	-5.406	2.166	1.700
FCHO1	-0.350	-4.826	-0.602	-0.951
HMG1	-0.318	-4.829	2.447	2.129
ILK	0.419	5.838	0.397	0.816
NEDD4L	1.027	5.066	-0.265	0.762
EPS8	1.532	4.862	-0.240	1.292

Supplementary Table 2. Statistical description and coefficients from univariate linear regression

	BRCA (n=45)	OV (n=30)	GBM (n=33)	Kruskal Wallis <i>P</i>
IC50 of olaparib (Median, IQR)	4.044 (3.494-4.614)	4.191 (3.047-4.702)	3.596 (2.985-4.140)	0.057
IC50 of talazoparib (Median, IQR)	3.425 (2.190-4.368)	1.911 (0.951-2.943)	1.973 (1.042-2.726)	<0.001
Coefficient of olaparib (<i>p</i>)	-1.486±0.979 (0.136)	-7.456±2.047 (0.001)	-4.000±2.020 (0.057)	-2.935±0.743 (<0.001)
Coefficient of talazoparib (<i>p</i>)	-5.045±1.663 (0.004)	-6.269±2.655 (0.025)	-2.087±3.534 (0.559)	-6.372±1.164 (<0.001)

Supplementary Table 3. GSEA results in BRCA showing top 10 enrichment Reactome pathways and in GBM showing top 20 significantly enriched Reactome pathways

BRCA Olaparib				
ID	Description	NES	pvalue	p.adjust
R-HSA-72312	rRNA processing	2.499	0.002	0.101
R-HSA-6791226	Major pathway of rRNA processing in the nucleolus and cytosol	2.498	0.002	0.101
R-HSA-8868773	rRNA processing in the nucleus and cytosol	2.482	0.002	0.101
R-HSA-6790901	rRNA modification in the nucleus and cytosol	2.432	0.002	0.101
R-HSA-381753	Olfactory Signaling Pathway	2.074	0.001	0.101
R-HSA-73863	RNA Polymerase I Transcription Termination	1.976	0.002	0.101
R-HSA-418555	G alpha (s) signalling events	1.961	0.001	0.101
R-HSA-191273	Cholesterol biosynthesis	1.950	0.002	0.101
R-HSA-75205	Dissolution of Fibrin Clot	1.880	0.004	0.107
R-HSA-1650814	Collagen biosynthesis and modifying enzymes	1.876	0.002	0.101
GBM Olaparib				
ID	Description	NES	pvalue	p.adjust

R-HSA-141424	Amplification of signal from the kinetochores	3.005	0.002	0.020
R-HSA-141444	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	3.005	0.002	0.020
R-HSA-68877	Mitotic Prometaphase	2.944	0.002	0.020
R-HSA-2500257	Resolution of Sister Chromatid Cohesion	2.912	0.002	0.020
R-HSA-69618	Mitotic Spindle Checkpoint	2.890	0.002	0.020
R-HSA-5663220	RHO GTPases Activate Formins	2.603	0.002	0.020
R-HSA-69620	Cell Cycle Checkpoints	2.563	0.002	0.020
R-HSA-2555396	Mitotic Metaphase and Anaphase	2.554	0.002	0.020
R-HSA-68886	M Phase	2.547	0.002	0.020
R-HSA-68882	Mitotic Anaphase	2.547	0.002	0.020
R-HSA-72702	Ribosomal scanning and start codon recognition	2.543	0.002	0.020
R-HSA-72649	Translation initiation complex formation	2.503	0.002	0.020
R-HSA-2467813	Separation of Sister Chromatids	2.496	0.002	0.020
R-HSA-72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	2.495	0.002	0.020
R-HSA-8868773	rRNA processing in the nucleus and cytosol	2.464	0.002	0.020
R-HSA-72695	Formation of the ternary complex, and subsequently, the 43S complex	2.435	0.002	0.020
R-HSA-168273	Influenza Viral RNA Transcription and Replication	2.433	0.002	0.020
R-HSA-72312	rRNA processing	2.422	0.002	0.020
R-HSA-68962	Activation of the pre-replicative complex	2.420	0.002	0.020