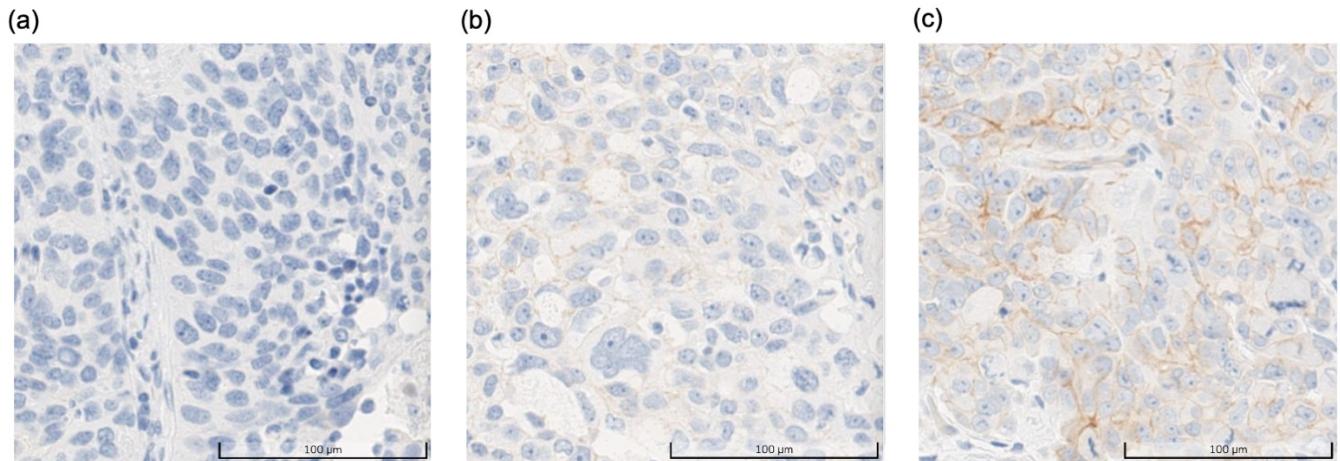
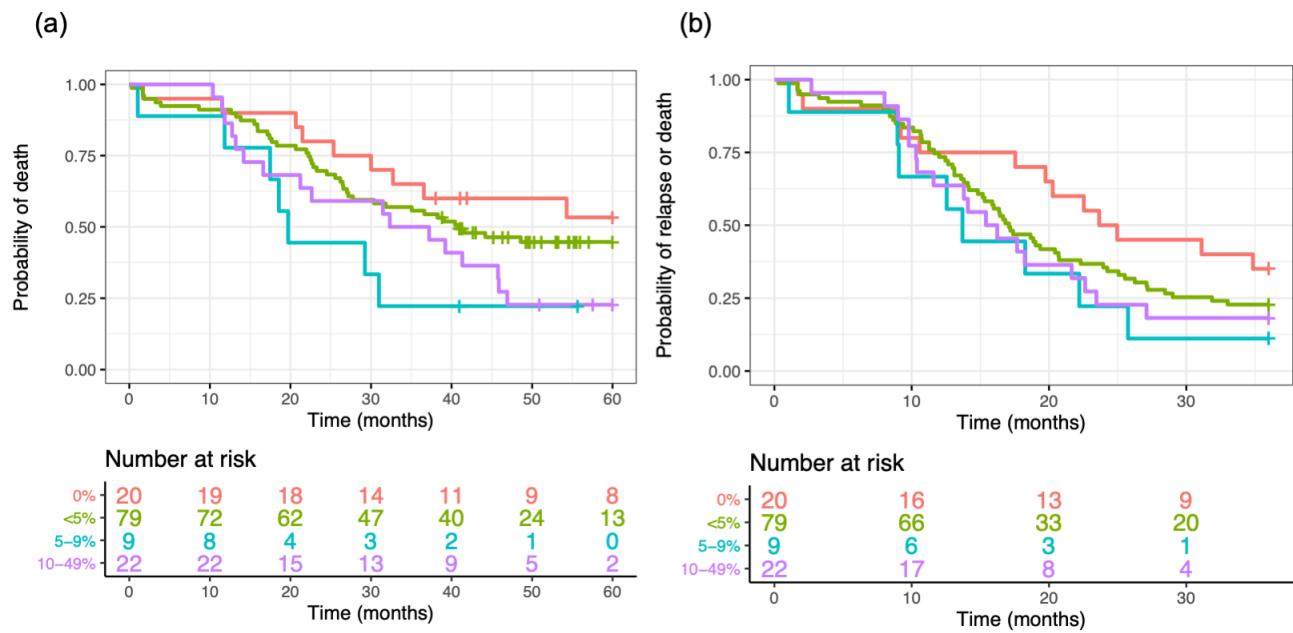


Supplementary material

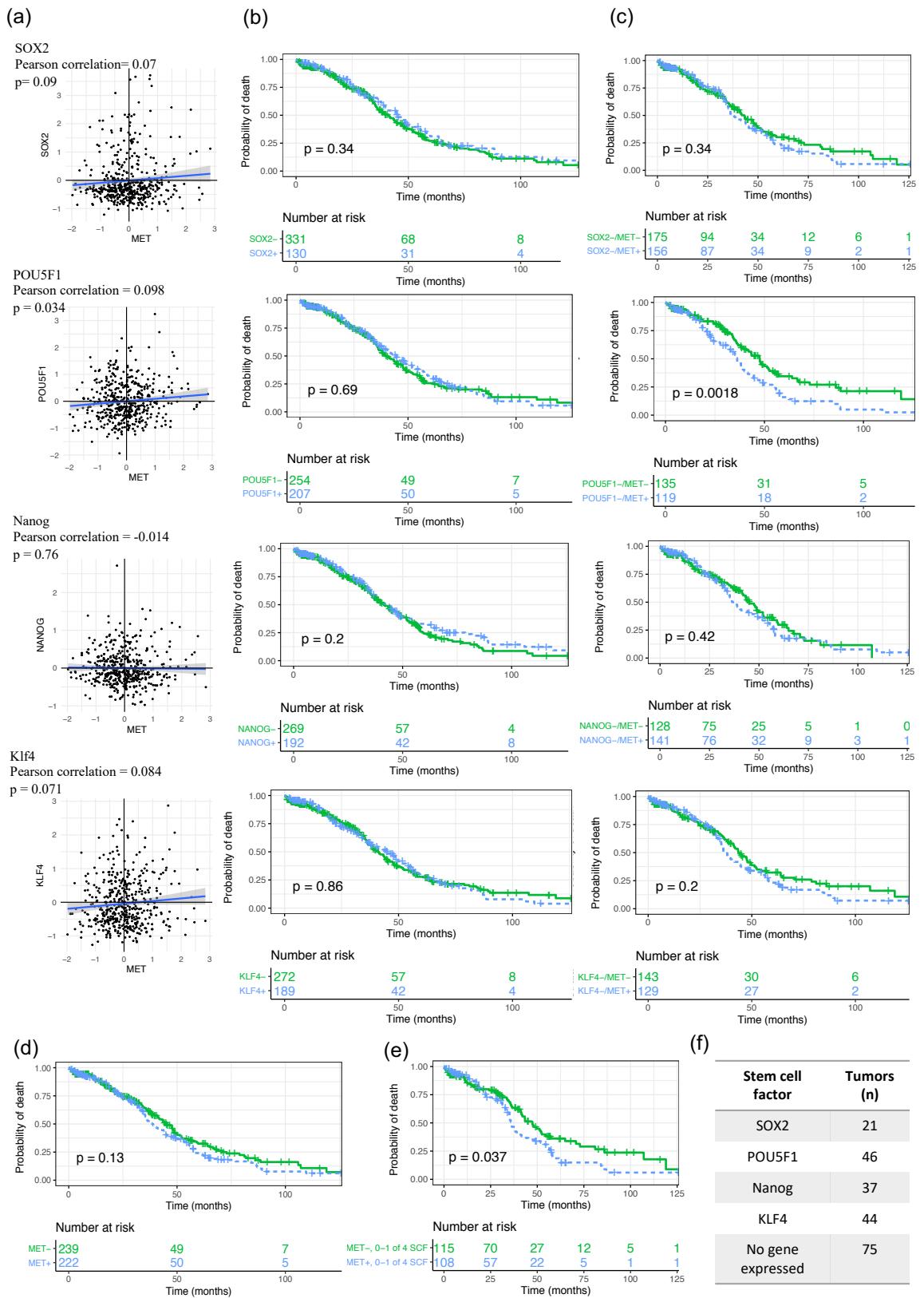


Supplementary Figure 1. Representative images of MET IHC.

TMA core negative for membranous staining (a), membranous staining of weak intensity (b) and membranous staining of moderate intensity (c). Cores were scored as MET positive if $\geq 5\%$ cells had weak or moderate membrane staining. Magnification 20x.



Supplementary Figure 2. Survival outcome for different levels of MET; OS (a) and PFS (b).

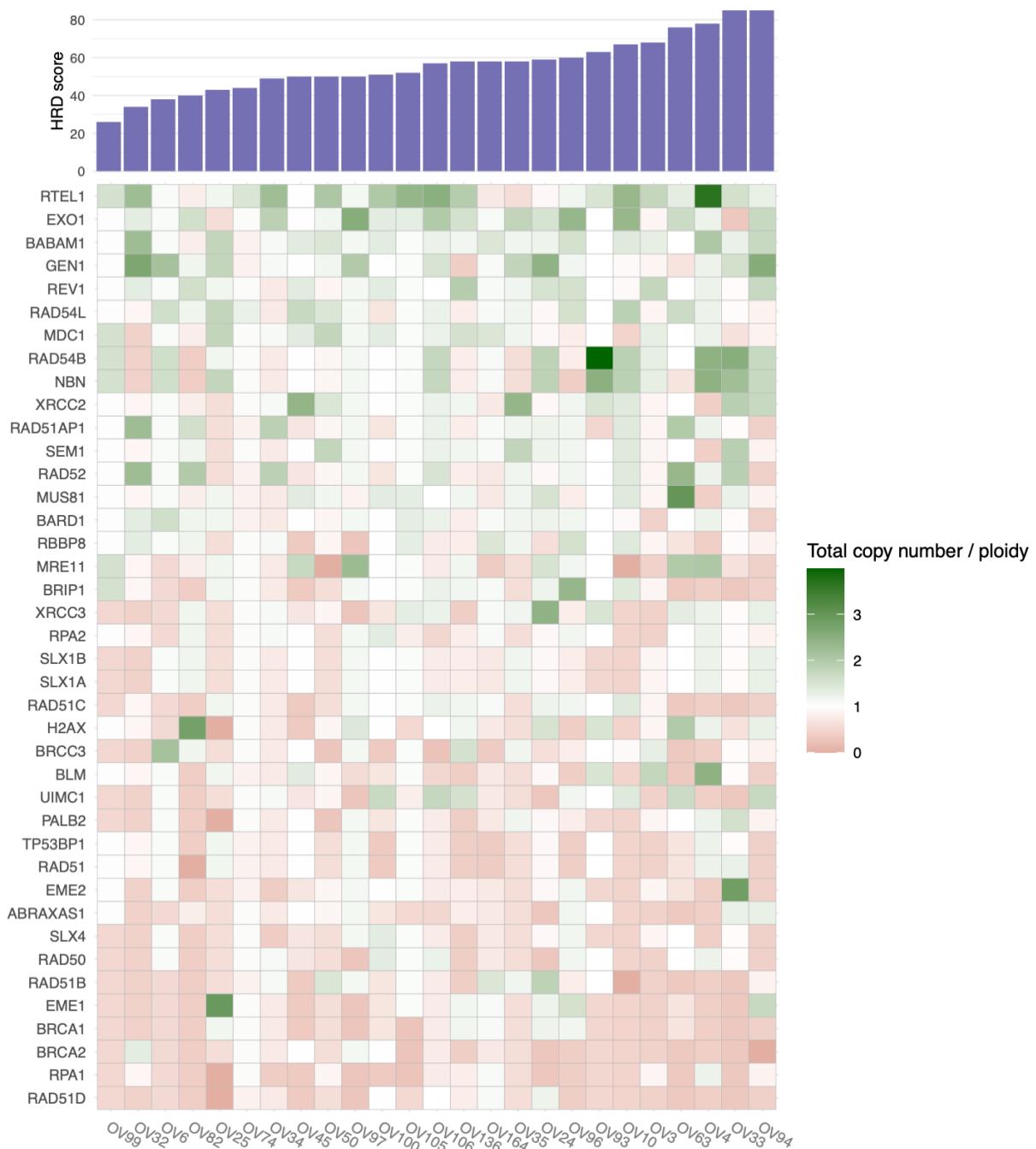


Supplementary Figure 3. Correlations between MET and stem cell factors, and prognostic value of MET in stem cell factor negative tumors. Pearson correlation of mRNA levels of four stem cell factors (and MET (a). Kaplan-Meier analyses of OS for the four stem cell factors (b). Subgroup analyses of OS for MET+- in tumors negative for the respective stem cell factors (c). OS for MET+- in all tumors (d) and in tumors negative for at least three out of the four stem cell factors (e). The number of tumors positive for each stem cell factor in the subgroup analysis (f).

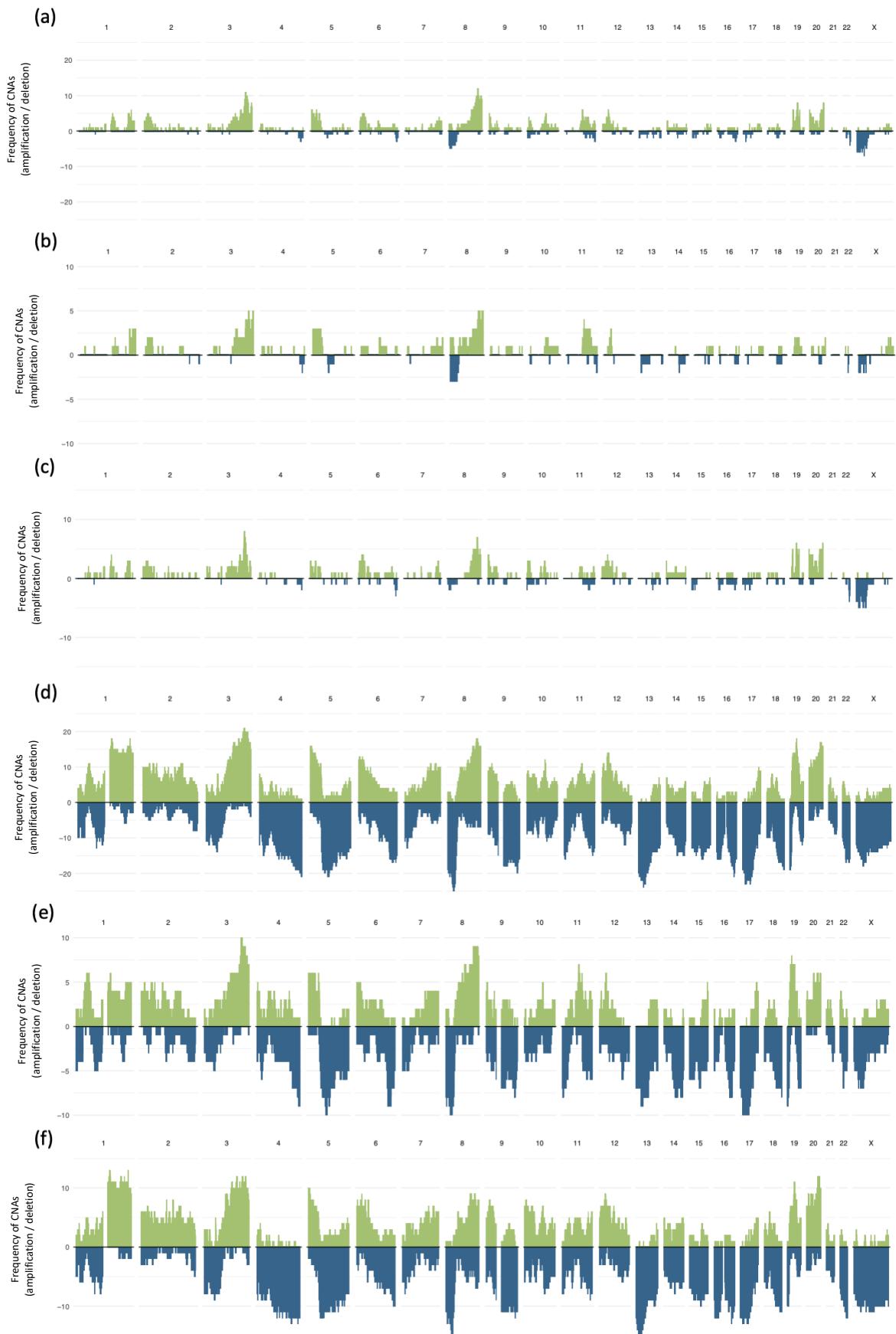
Supplementary Table 1. Clinico-pathological data, cohort 2

	<i>All</i> (n=25)	<i>BRCA1/2</i> <i>mutated</i> (n=10)	<i>BRCA1/2</i> <i>wildtype</i> (n=15)
<i>Age, median (range)¹</i>	60 (42-55)	59 (42-66)	61 (43-78)
<i>Residual disease, n (%)²</i>			
<i>No</i>	21 (84)	6 (60)	15 (100)
<i>Yes</i>	4 (16)	4 (40)	0 (0)
<i>FIGO stage, n (%)</i>			
<i>I-II</i>	2 (8.0)	2 (20)	0 (0)
<i>III</i>	18 (72)	5 (50)	13 (87)
<i>IV</i>	5 (20)	3 (30)	2 (13)
<i>Treatment response, n (%)</i>			
<i>Complete response</i>	23 (92)	9 (90)	14 (93)
<i>Partial response</i>	2 (8.0)	1 (10)	1 (7)
<i>Deceased, n (%)</i>			
<i>Overall survival, months, median (range)³</i>	15 (63)	5 (50)	10 (71)
<i>Progression-free survival, months, median (range)⁴</i>	63 (23-146)	64 (31-119)	49 (23-71)
<i>HRD score, median (range)</i>	21 (14-58)	21 (14-58)	20 (14-43)
	57 (26-85)	63.5 (38-85)	52 (26-76)

¹Age at initial diagnosis. ²Tumor tissue remaining after primary debulking surgery.³Only deceased patients included in OS calculations. ⁴Time to first relapse, before olaparib treatment.

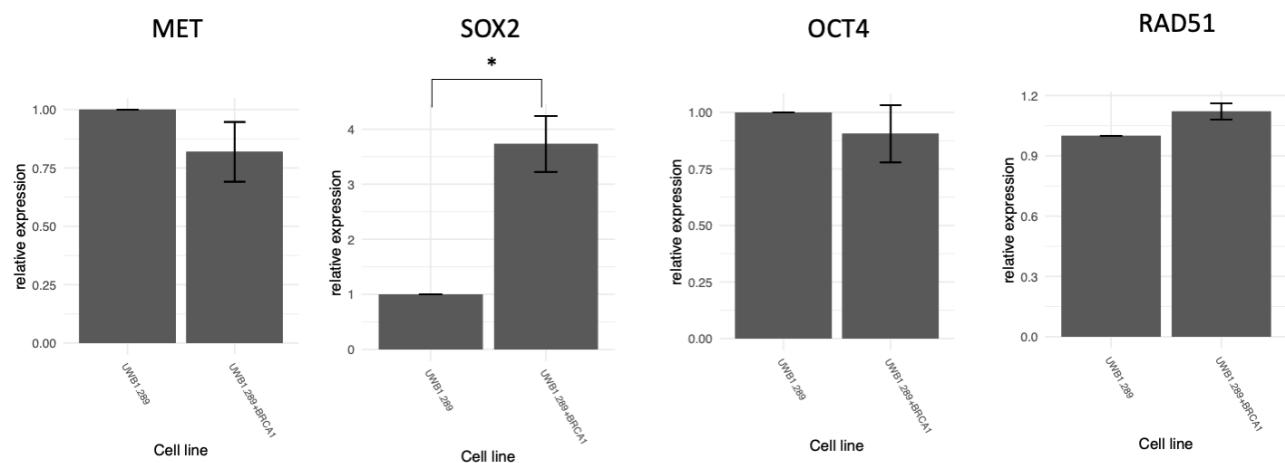


Supplementary Figure 4. Relative gain (total copy number/ploidy) in 40 core HR-associated genes.
Samples sorted by HRD score (x-axis) and genes sorted by mean relative gain (y-axis).



Supplementary Figure 5. Frequency plots of global copy number alterations (CNAs) in cohort 2.

Amplification/Deletion (a-c) and Gain/Loss (d-f). (a) & (d): all patients (n=25), (b) & (e): patients with a *BRCA1/2* mutation (n=10) and (c) & (f): patients with wildtype *BRCA1/2* (n=15).



Supplementary Figure 6. Quantification of Western blot analyses. Analyses were performed with three biological replicates. Means and SE displayed. Relative protein expression for BRCA1 could not be calculated as the protein was not detected in the UWB1.289 cell line.

* significant Student's T-test, p=0.033