

Figure 1: A plot showing the number of genes in a cluster (Y-axis) versus the Gene List Index (X-axis). The X-axis ranges from 0 to 15,000. The Y-axis ranges from 0 to 100. A red line represents the number of genes in a cluster, which starts at approximately 20, rises to a peak of about 100 at index 4383, and then decreases, crossing the zero line at index 8765. A green shaded area represents the number of genes in a cluster, which starts at approximately 100 and decreases to about 10 at index 15,000. A horizontal dashed line is drawn at Y=20. A vertical dotted red line marks the peak at index 4383, and a vertical dotted green line marks the zero crossing at index 8765. The plot is divided into two regions: "clus3" (left) and "NON.clus3" (right).

A density plot showing the probability density function (PDF) of ES values. The x-axis is labeled 'ES' and ranges from approximately -1.0 to 1.0. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 1.5. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks around -0.5 and 0.5. A vertical black line represents the 'Observed Gene Set ES value' at approximately 0.528. The area under the red curve to the right of this line is shaded in light red. Text labels on the x-axis indicate 'Neg. ES "NON.clus3"' for negative values and 'Pos. ES: "clus3"' for positive values. Below the x-axis, summary statistics are provided: ES = 0.528, NES = 1.28, Norm. p-val = 0.243, FWER = 0.982, and FDR = 0.45.

ES = 0.528 NES = 1.28 Norm. p-val = 0.243 FWER = 0.982 FDR = 0.45

Class	clus3	NON.clus3
XRCC2		
RAD51		
RAD54B		
BLM		
RAD54L		
RPA3		
POLD2		
POLD1		
EME1		
SSBP1		
RAD50		
SHFM1		
XRCC3		
BRCA2		
RPA1		
TOP3B		
RPA2		
MUS81		
TOP3A		
POLD3		
NBN		
RAD52		
MRE11A		
RAD51L1		
RPA4		
RAD51L3		
POLD4		