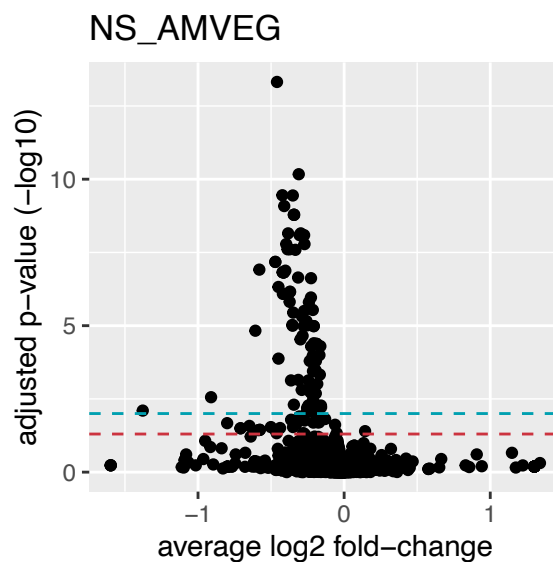


Pathway analysis



Volcano plot summarising the GSEA analysis. Contains all the pathways mapped to the Reactome database each point represents one pathway with its position on the x-axis determined by its average log2 fold change within the pathway. The y-axis position is determined by the pathways' p-value (FDR adjusted) with lower p-values positioned higher on the plot due to the inverse log ($-\log_{10}$); The red line indicates the position on the y-axis where the adjusted p-value = 0.05, the blue line 0.01.

Top-regulated pathways

Translation of Replicase and Assembly of the Replication Transcription Complex (R-HSA-9694676)

	NS_AMVEG
Regulation	Up
FDR	0.04
Av. FC	0.143
N Genes	14

DNA strand elongation (R-HSA-69190)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.46
N Genes	31

HDR through Homologous Recombination (HRR) (R-HSA-5685942)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.31
N Genes	67

Activation of ATR in response to replication stress (R-HSA-176187)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.423
N Genes	36

Homologous DNA Pairing and Strand Exchange (R-HSA-5693579)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.351
N Genes	42

Activation of the pre-replicative complex (R-HSA-68962)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.41
N Genes	33

Presynaptic phase of homologous DNA pairing and strand exchange (R-HSA-5693616)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.342
N Genes	39

Diseases of DNA Double-Strand Break Repair (R-HSA-9675136)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.344
N Genes	40

Defective homologous recombination repair (HRR) due to BRCA2 loss of function (R-HSA-9701190)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.344
N Genes	40

Mitotic Prometaphase (R-HSA-68877)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.297
N Genes	198

Lagging Strand Synthesis (R-HSA-69186)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.383
N Genes	19

Diseases of DNA repair (R-HSA-9675135)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.305
N Genes	51

Homology Directed Repair (R-HSA-5693538)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.274
N Genes	113

HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA) (R-HSA-5693567)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.271
N Genes	107

Resolution of D-loop Structures through Holliday Junction Intermediates (R-HSA-5693568)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.396
N Genes	35

Resolution of D-Loop Structures (R-HSA-5693537)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.387
N Genes	36

Resolution of Sister Chromatid Cohesion (R-HSA-2500257)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.372
N Genes	122

Impaired BRCA2 binding to RAD51 (R-HSA-9709570)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.334
N Genes	34

Deposition of new CENPA-containing nucleosomes at the centromere (R-HSA-606279)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.471
N Genes	44

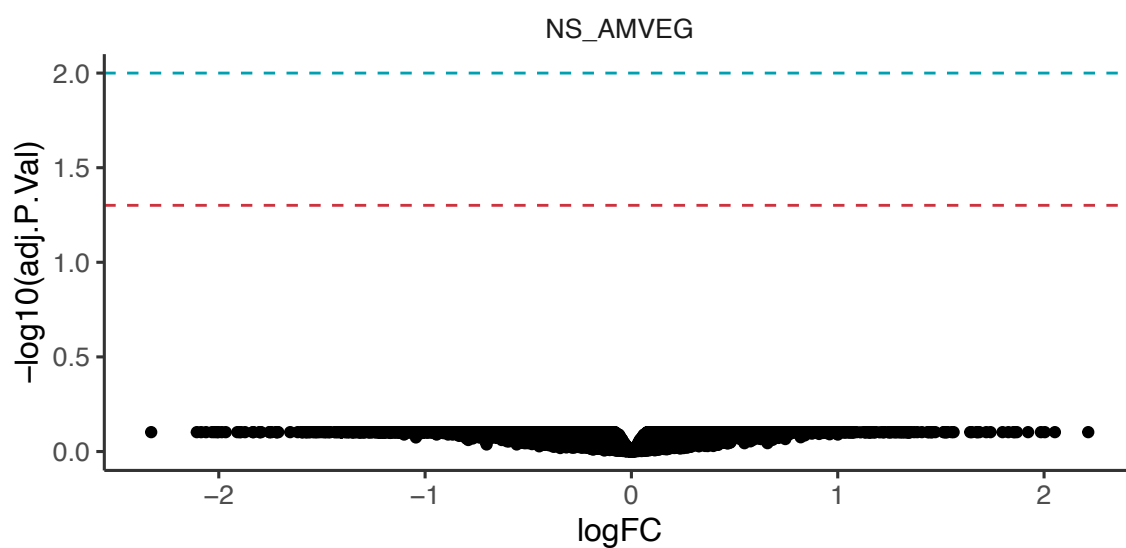
Nucleosome assembly (R-HSA-774815)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.471
N Genes	44

Unwinding of DNA (R-HSA-176974)

	NS_AMVEG
Regulation	Down
FDR	< 0.001
Av. FC	-0.58
N Genes	12

Protein / Gene level results



Top up-regulated protein/genes

NS_AMVEG

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
DUSP7	0.2842325	5.495068	3.798817	0.0036850	0.7899135	-3.010968
CA11	0.2497568	5.765293	3.356655	0.0075894	0.7899135	-3.209616
MYO1D	0.2667145	6.263798	3.244050	0.0091515	0.7899135	-3.227707

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
KLF13	0.2783400	5.548920	3.154137	0.0106348	0.7899135	-3.351531
CDK20	0.3045652	4.315730	3.570426	0.0053377	0.7899135	-3.357297
HS6ST1	0.4210735	7.023031	2.967247	0.0145582	0.7899135	-3.375150
ADAMTS2	0.3473689	5.328595	3.147039	0.0107619	0.7899135	-3.383144
GAA	0.4213517	6.248476	2.985578	0.0141154	0.7899135	-3.392726
HSPB8	0.2965447	8.226608	2.927032	0.0155800	0.7899135	-3.416992
PLD3	0.2523913	7.447696	2.901477	0.0162669	0.7899135	-3.417803

Top down-regulated protein/genes
NS_AMVEG

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
TPR	-0.2713207	7.421897	-3.800563	0.0036747	0.7899135	-2.862736
ECT2	-0.4726716	6.315891	-3.816777	0.0035802	0.7899135	-2.895845
MIS18BP1	-0.4426055	5.226915	-3.907177	0.0030978	0.7899135	-3.007733
TMPO	-0.5633611	6.485768	-3.512812	0.0058661	0.7899135	-3.053348
KIF18A	-0.6697231	4.323038	-4.345431	0.0015595	0.7899135	-3.067502
CACYBP	-0.2539173	6.239450	-3.505981	0.0059322	0.7899135	-3.073647
ASPM	-0.9396228	5.417113	-3.593999	0.0051360	0.7899135	-3.137262
AKAP12	-0.6062608	5.729690	-3.380306	0.0072979	0.7899135	-3.202614
SEM1	-0.2644065	5.374267	-3.458262	0.0064166	0.7899135	-3.204009
DNMT1	-0.3778757	6.694972	-3.234601	0.0092968	0.7899135	-3.208680