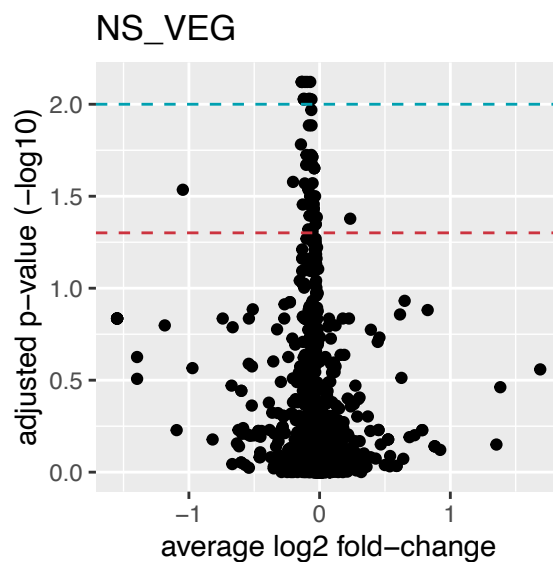


## Pathway analysis

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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

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### Influenza Virus Induced Apoptosis (R-HSA-168277)

	NS_VEG
Regulation	<b>Up</b>
FDR	<b>0.042</b>
Av. FC	0.234
N Genes	2

---

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

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.008</b>
Av. FC	-0.137
N Genes	36

---

### G2/M Checkpoints (R-HSA-69481)

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.008</b>
Av. FC	-0.072
N Genes	138

---

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

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.008</b>
Av. FC	-0.112
N Genes	67

---

### DNA strand elongation (R-HSA-69190)

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.008</b>
Av. FC	-0.137
N Genes	31

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**Cargo concentration in the ER (R-HSA-5694530)**

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.008</b>
Av. FC	-0.132
N Genes	31

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**Homology Directed Repair (R-HSA-5693538)**

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.008</b>
Av. FC	-0.094
N Genes	113

---

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

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.009</b>
Av. FC	-0.12
N Genes	42

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**DNA Double-Strand Break Repair (R-HSA-5693532)**

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.009</b>
Av. FC	-0.079
N Genes	141

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**Cell Cycle Checkpoints (R-HSA-69620)**

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.009</b>
Av. FC	-0.062
N Genes	262

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

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.009</b>
Av. FC	-0.12
N Genes	39

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

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.009</b>
Av. FC	-0.093
N Genes	107

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

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.009</b>
Av. FC	-0.12
N Genes	40

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

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.009</b>
Av. FC	-0.12
N Genes	40

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#### **The role of GTSE1 in G2/M progression after G2 checkpoint (R-HSA-8852276)**

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.011</b>
Av. FC	-0.063
N Genes	69

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#### **DNA Replication (R-HSA-69306)**

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.013</b>
Av. FC	-0.082
N Genes	142

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#### Synthesis of DNA (R-HSA-69239)

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.013</b>
Av. FC	-0.062
N Genes	117

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#### Lagging Strand Synthesis (R-HSA-69186)

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.017</b>
Av. FC	-0.143
N Genes	19

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#### Translesion Synthesis by POLH (R-HSA-110320)

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.019</b>
Av. FC	-0.1
N Genes	17

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#### Mitotic G1 phase and G1/S transition (R-HSA-453279)

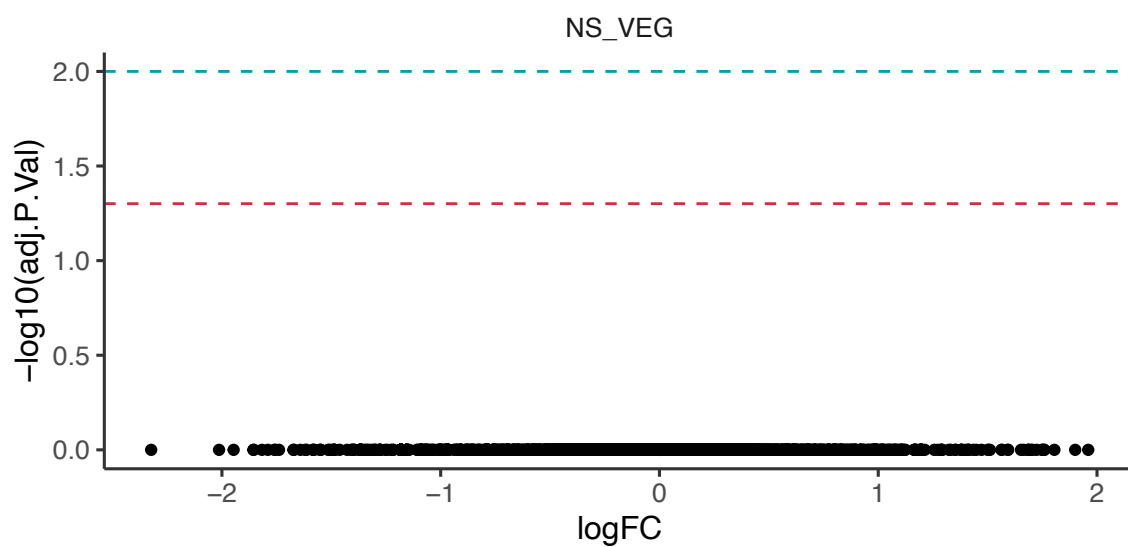
	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.019</b>
Av. FC	-0.063
N Genes	149

---

#### G1/S Transition (R-HSA-69206)

	NS_VEG
Regulation	<b>Down</b>
FDR	<b>0.019</b>
Av. FC	-0.067
N Genes	132

## Protein / Gene level results



### Top up-regulated protein/genes

NS_VEG						
Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
SLC25A6	0.2685962	9.361961	4.799485	0.0006908	0.9997094	-1.860309
ZFP36L2	0.3581939	6.041848	5.263869	0.0003463	0.9997094	-1.867083
MAF	0.4384713	5.742072	5.383939	0.0002911	0.9997094	-1.889156
LHX2	0.3200432	6.111509	4.711786	0.0007898	0.9997094	-2.115520
SIX3	0.2792910	6.028062	4.706035	0.0007968	0.9997094	-2.132885
ZBTB7A	0.2607226	5.986056	4.223140	0.0016987	0.9997094	-2.403156
DPP7	0.2534673	6.923521	3.849959	0.0031151	0.9997094	-2.535871
RPS28	0.3088906	7.804815	3.778941	0.0035030	0.9997094	-2.539751
FOXQ1	0.4786338	5.778067	4.008604	0.0024020	0.9997094	-2.567810
SLC2A6	0.3205818	5.773941	3.979022	0.0025207	0.9997094	-2.584178

**Top down-regulated protein/genes**  
NS\_VEG

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
PRDX1	-0.1867182	7.936443	-2.963134	0.0139689	0.9997094	-3.167697
PSMA5	-0.1663590	6.452867	-3.024798	0.0125610	0.9997094	-3.172141
COPB2	-0.1832717	7.278582	-2.936875	0.0146161	0.9997094	-3.206628
GPN1	-0.1927436	5.180260	-3.154237	0.0100564	0.9997094	-3.213329
PRCP	-0.1532995	7.033625	-2.896532	0.0156699	0.9997094	-3.247856
TGFA	-0.2835301	4.997282	-3.115038	0.0107560	0.9997094	-3.269769
HSP90AB1	-0.1453595	10.469667	-2.761076	0.0198022	0.9997094	-3.325660
PPP1R12B	-0.3055438	5.404214	-2.948709	0.0143208	0.9997094	-3.325996
PLK2	-0.2155063	9.215438	-2.719599	0.0212744	0.9997094	-3.363207
DECR1	-0.1758612	5.684503	-2.852009	0.0169223	0.9997094	-3.365900