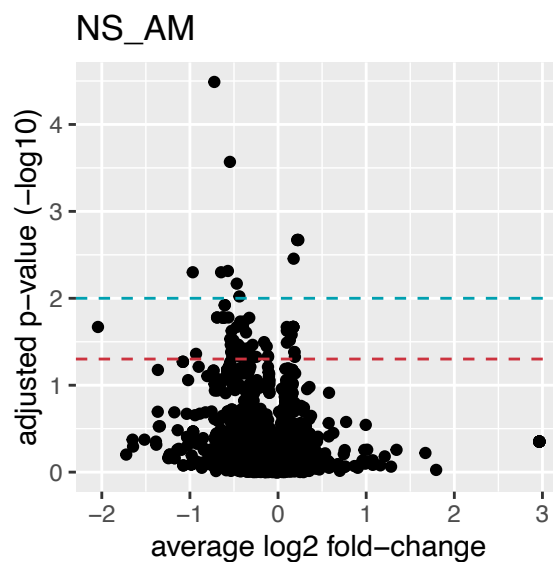


## Pathway analysis

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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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### Mitochondrial translation termination (R-HSA-5419276)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.002</b>
Av. FC	0.23
N Genes	86

---

### Mitochondrial translation elongation (R-HSA-5389840)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.002</b>
Av. FC	0.223
N Genes	86

---

### Mitochondrial translation initiation (R-HSA-5368286)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.002</b>
Av. FC	0.225
N Genes	86

---

### Mitochondrial translation (R-HSA-5368287)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.002</b>
Av. FC	0.217
N Genes	92

---

### rRNA modification in the nucleus and cytosol (R-HSA-6790901)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.004</b>
Av. FC	0.177
N Genes	59

---

**mRNA Splicing - Major Pathway (R-HSA-72163)**

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.021</b>
Av. FC	0.099
N Genes	201

---

**HIV Transcription Initiation (R-HSA-167161)**

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.021</b>
Av. FC	0.172
N Genes	44

---

**RNA Polymerase II HIV Promoter Escape (R-HSA-167162)**

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.021</b>
Av. FC	0.172
N Genes	44

---

**RNA Polymerase II Promoter Escape (R-HSA-73776)**

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.021</b>
Av. FC	0.172
N Genes	44

---

**RNA Polymerase II Transcription Pre-Initiation And Promoter Opening (R-HSA-73779)**

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.021</b>
Av. FC	0.172
N Genes	44

---

**RNA Polymerase II Transcription Initiation (R-HSA-75953)**

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.021</b>
Av. FC	0.172
N Genes	44

---

#### RNA Polymerase II Transcription Initiation And Promoter Clearance (R-HSA-76042)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.021</b>
Av. FC	0.172
N Genes	44

---

#### mRNA Splicing (R-HSA-72172)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.024</b>
Av. FC	0.1
N Genes	210

---

#### RNA polymerase II transcribes snRNA genes (R-HSA-6807505)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.026</b>
Av. FC	0.145
N Genes	75

---

#### Transcription of the HIV genome (R-HSA-167172)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.026</b>
Av. FC	0.155
N Genes	66

---

#### RNA Polymerase II Pre-transcription Events (R-HSA-674695)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.03</b>
Av. FC	0.134
N Genes	77

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#### Processing of Capped Intron-Containing Pre-mRNA (R-HSA-72203)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.032</b>
Av. FC	0.1
N Genes	277

---

#### Formation of the Early Elongation Complex (R-HSA-113418)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.042</b>
Av. FC	0.186
N Genes	33

---

#### Formation of the HIV-1 Early Elongation Complex (R-HSA-167158)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.042</b>
Av. FC	0.186
N Genes	33

---

#### tRNA modification in the nucleus and cytosol (R-HSA-6782315)

	NS_AM
Regulation	<b>Up</b>
FDR	<b>0.047</b>
Av. FC	0.191
N Genes	42

---

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

	NS_AM
Regulation	<b>Down</b>
FDR	<b>&lt; 0.001</b>
Av. FC	-0.723
N Genes	31

---

#### Gluconeogenesis (R-HSA-70263)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>&lt; 0.001</b>
Av. FC	-0.546
N Genes	18

---

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

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.005</b>
Av. FC	-0.569
N Genes	19

---

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

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.005</b>
Av. FC	-0.646
N Genes	33

---

#### Unwinding of DNA (R-HSA-176974)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.005</b>
Av. FC	-0.968
N Genes	12

---

#### Phase II - Conjugation of compounds (R-HSA-156580)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.007</b>
Av. FC	-0.468
N Genes	64

---

#### Mitotic Prometaphase (R-HSA-68877)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.01</b>
Av. FC	-0.438
N Genes	198

---

#### Polymerase switching (R-HSA-69091)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.012</b>
Av. FC	-0.605
N Genes	13

---

#### Leading Strand Synthesis (R-HSA-69109)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.012</b>
Av. FC	-0.605
N Genes	13

---

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

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.017</b>
Av. FC	-0.564
N Genes	122

---

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

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.017</b>
Av. FC	-0.609
N Genes	36

---

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

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.017</b>
Av. FC	-0.691
N Genes	44

---

#### Nucleosome assembly (R-HSA-774815)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.017</b>
Av. FC	-0.691
N Genes	44

---

#### Amplification of signal from the kinetochores (R-HSA-141424)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.017</b>
Av. FC	-0.632
N Genes	94

---

#### Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal (R-HSA-141444)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.017</b>
Av. FC	-0.632
N Genes	94

---

#### G1/S-Specific Transcription (R-HSA-69205)



	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.017</b>
Av. FC	-0.616
N Genes	31

---

#### Post-translational protein phosphorylation (R-HSA-8957275)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.017</b>
Av. FC	-0.327
N Genes	82

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

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.018</b>
Av. FC	-0.385
N Genes	67

---

#### Telomere C-strand (Lagging Strand) Synthesis (R-HSA-174417)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.019</b>
Av. FC	-0.428
N Genes	32

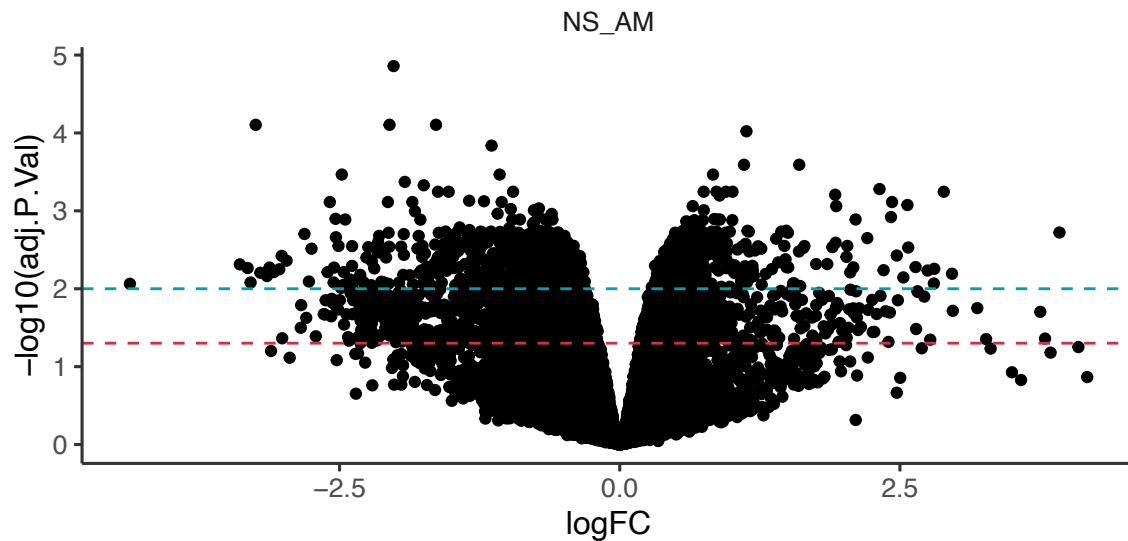
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#### Homologous DNA Pairing and Strand Exchange (R-HSA-5693579)

	NS_AM
Regulation	<b>Down</b>
FDR	<b>0.021</b>
Av. FC	-0.469
N Genes	42

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## Protein / Gene level results



### Top up-regulated protein/genes

NS\_AM

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
OTUD1	1.1303960	7.2386960	15.20617	0e+00	0.0000952	9.435056
ZSCAN18	1.1088877	4.8857968	13.05305	2e-07	0.0002560	8.009787
KDR	1.6012097	5.2563884	13.01513	2e-07	0.0002560	7.993568
DUSP4	0.8321653	8.0360323	12.28296	3e-07	0.0003421	7.471255
PSG2	2.3180686	3.9029677	11.33432	6e-07	0.0005249	6.666070
GATA6	0.8634257	6.2828502	11.09606	7e-07	0.0005686	6.535540
TBC1D5	0.7489512	6.7279952	11.05300	8e-07	0.0005686	6.494170
DKK1	1.0061957	8.6620472	10.71354	1e-06	0.0005686	6.204699
MMP24	0.9469843	7.7144164	10.69693	1e-06	0.0005686	6.186935
OLR1	2.8914695	0.0632745	10.73866	1e-06	0.0005686	4.258767

### Top down-regulated protein/genes

NS\_AM

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
C1S	-2.0177055	4.356335	-22.03271	0e+00	0.0000138	12.033552
MT-CO1	-3.2481497	12.825656	-16.93970	0e+00	0.0000786	10.347998
MT-CO2	-2.0542890	11.424700	-15.90718	0e+00	0.0000786	9.810970

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
MT-TC	-1.6394861	4.757523	-15.88827	0e+00	0.0000786	9.687109
CTSK	-1.1432783	4.763333	-14.25963	1e-07	0.0001453	8.779001
XPOT	-1.0716402	7.167962	-12.21626	3e-07	0.0003421	7.421009
MT-ATP8	-2.4802372	8.348697	-12.18884	3e-07	0.0003421	7.401433
PHGDH	-1.9179260	5.912053	-11.79375	4e-07	0.0004251	7.104665
PAG1	-1.7490834	2.488926	-11.56529	5e-07	0.0004697	6.494018
GCLC	-0.9520169	4.390008	-10.85705	9e-07	0.0005686	6.355989