

Heatmap showing z-score expression of 20 genes across 8 samples. The color scale ranges from -2 (blue) to 6 (red). Genes are clustered on the y-axis, and samples are clustered on the x-axis. A dendrogram is shown at the top.

Gene	Ctrl_S7	Ctrl_S13	Ctrl_S1	Ctrl_S2	RS_S16	RS_S6	RS_S12	RS_S9
HNRNPU	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5
SMARCA5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5
SMC4	2.5	2.5	2.5	2.5	0.5	0.5	0.5	0.5
CENPF	1.5	1.5	1.5	1.5	-1.5	0.5	-1.5	0.5
STAG1	-1.5	-1.5	-1.5	-1.5	0.5	0.5	0.5	0.5
DYNC1LI1	-1.5	-1.5	-1.5	-1.5	0.5	0.5	0.5	0.5
RCC1	-1.5	-1.5	-1.5	-1.5	0.5	0.5	0.5	0.5
CDC20	1.5	1.5	1.5	1.5	-1.5	-1.5	-1.5	-1.5
CENPE	0.5	0.5	0.5	0.5	-1.5	-1.5	-1.5	-1.5
BUB1	0.5	0.5	0.5	0.5	-1.5	-1.5	-1.5	-1.5
NCAPG	0.5	0.5	0.5	0.5	-1.5	-1.5	-1.5	-1.5
KIF2C	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5
MAD2L1	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5
CDCA8	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5
KIF14	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5	-1.5
NSL1	-2.5	-2.5	-2.5	-2.5	-1.5	-1.5	-1.5	-1.5
CEP97	-2.5	-2.5	-2.5	-2.5	-1.5	-1.5	-1.5	-1.5
GEN1	-2.5	-2.5	-2.5	-2.5	-1.5	-1.5	-1.5	-1.5
NUF2	-2.5	-2.5	-2.5	-2.5	-1.5	-1.5	-1.5	-1.5
NCAPH	-2.5	-2.5	-2.5	-2.5	-1.5	-1.5	-1.5	-1.5
NEK2	-2.5	-2.5	-2.5	-2.5	-1.5	-1.5	-1.5	-1.5
KIF15	-2.5	-2.5	-2.5	-2.5	-1.5	-1.5	-1.5	-1.5
ABRAXAS1	-3.5	-3.5	-3.5	-3.5	-1.5	-1.5	-1.5	-1.5
PSRC1	-3.5	-3.5	-3.5	-3.5	-1.5	-1.5	-1.5	-1.5
SPC25	-3.5	-3.5	-3.5	-3.5	-1.5	-1.5	-1.5	-1.5

4

4

2

0

0

-2