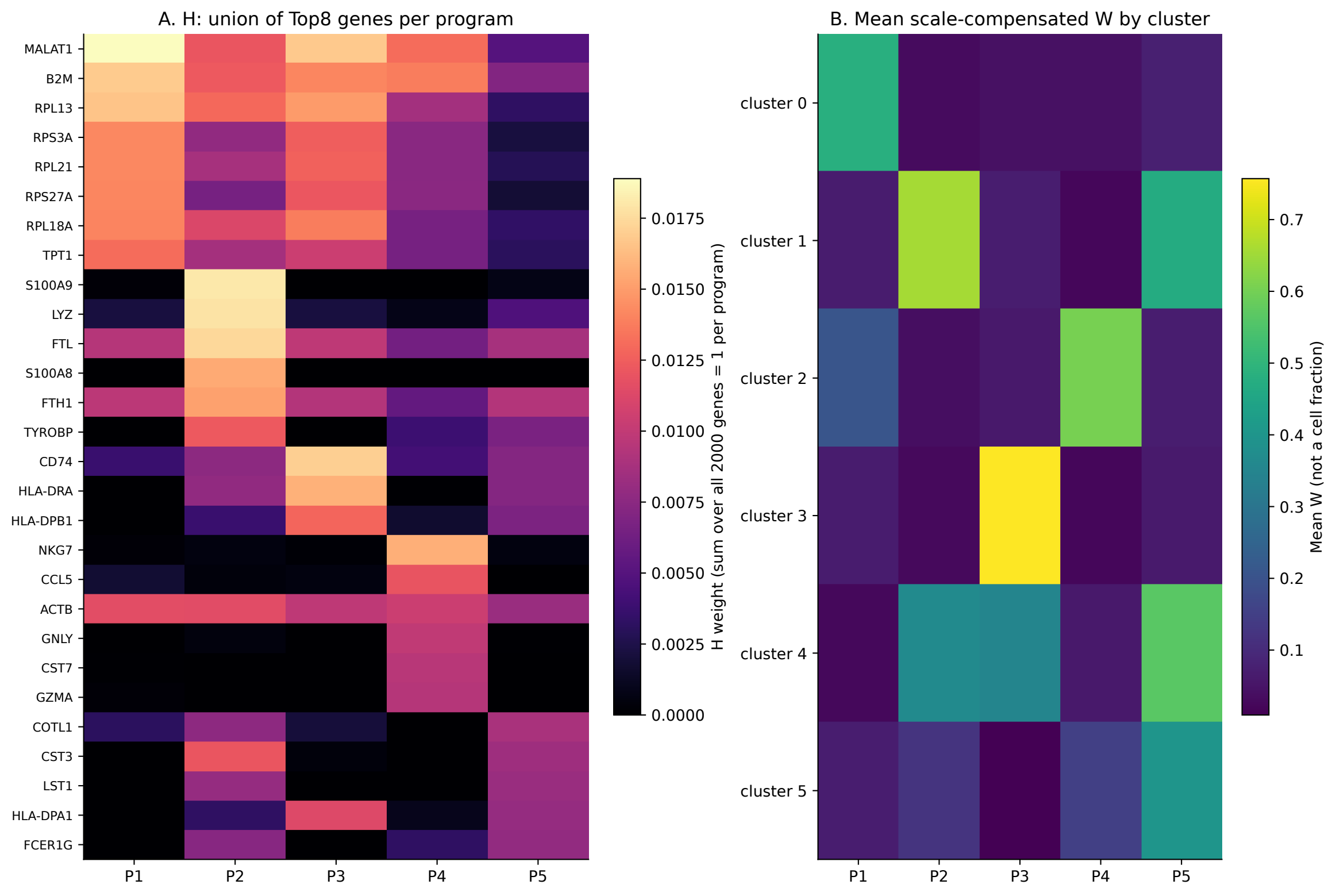
A. H: union of Top8 genes per program
MALAT1
B2M
RPL13
RPS3A
RPL21
RPS27A
RPL18A
TPT1
S100A9
LYZ
FTL
S100A8
FTH1
TYROBP
CD74
HLA-DRA
HLA-DPB1
NKG7
CCL5
ACTB
GNLY
CST7
GZMA
COTL1
CST3
LST1
HLA-DPA1
FCER1G
P1
P2
P3
P4
P5
0.0175
0.0150
0.0125
0.0100
0.0075
0.0050
0.0025
0.0000
H weight (sum over all 2000 genes = 1 per program)
B. Mean scale-compensated W by cluster
cluster 0
cluster 1
cluster 2
cluster 3
cluster 4
cluster 5
P1
P2
P3
P4
P5
0.7
0.6
0.5
0.4
0.3
0.2
0.1
Mean W (not a cell fraction)