

cc_cc_g1_mean

UMAP 2

10

5

0

-5

-10

-10

-5

UMAP 1

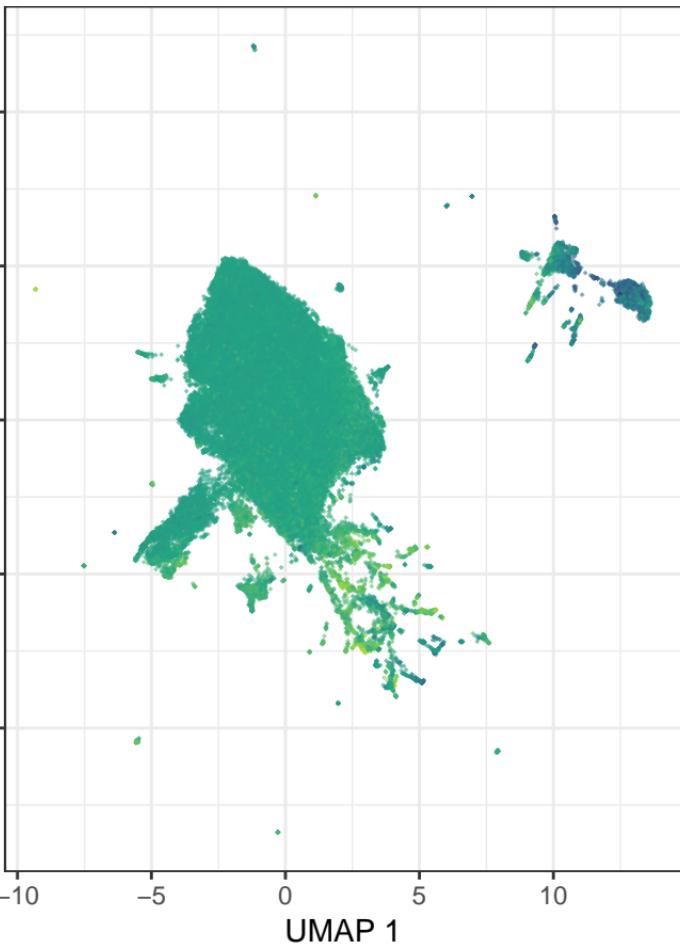
Regression

1

0

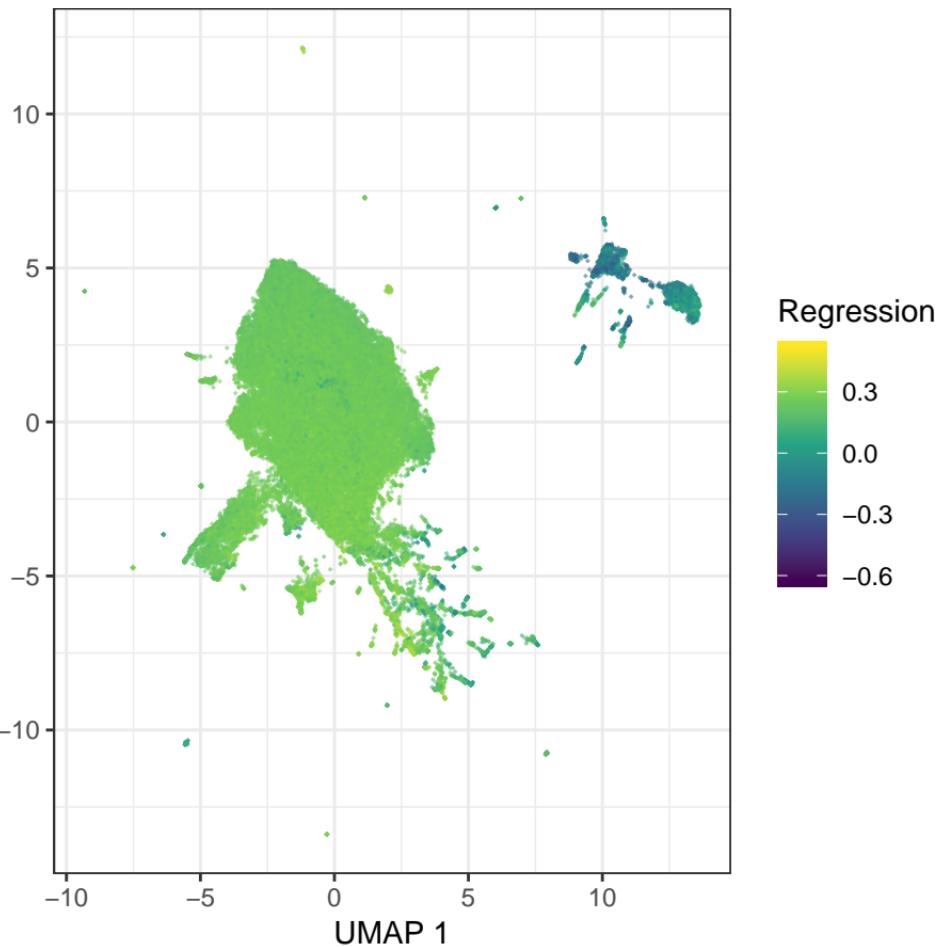
-1

-2



cc_mitosis_ph3_neg_n_spots_mean

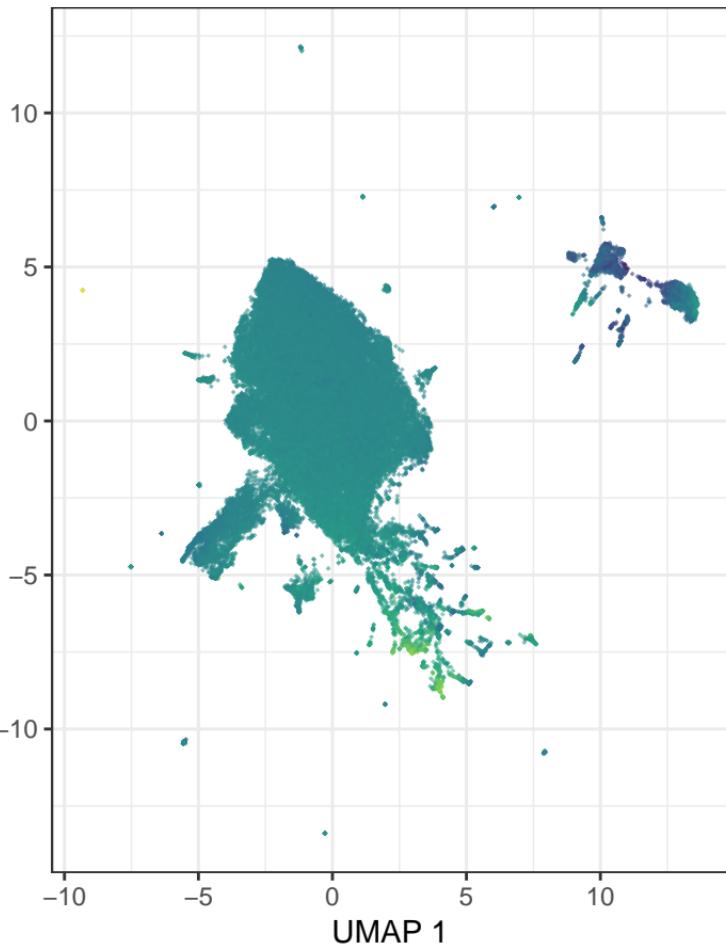
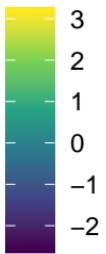
UMAP 2



cc_edu_pos_high_n_spots_h2ax_mean

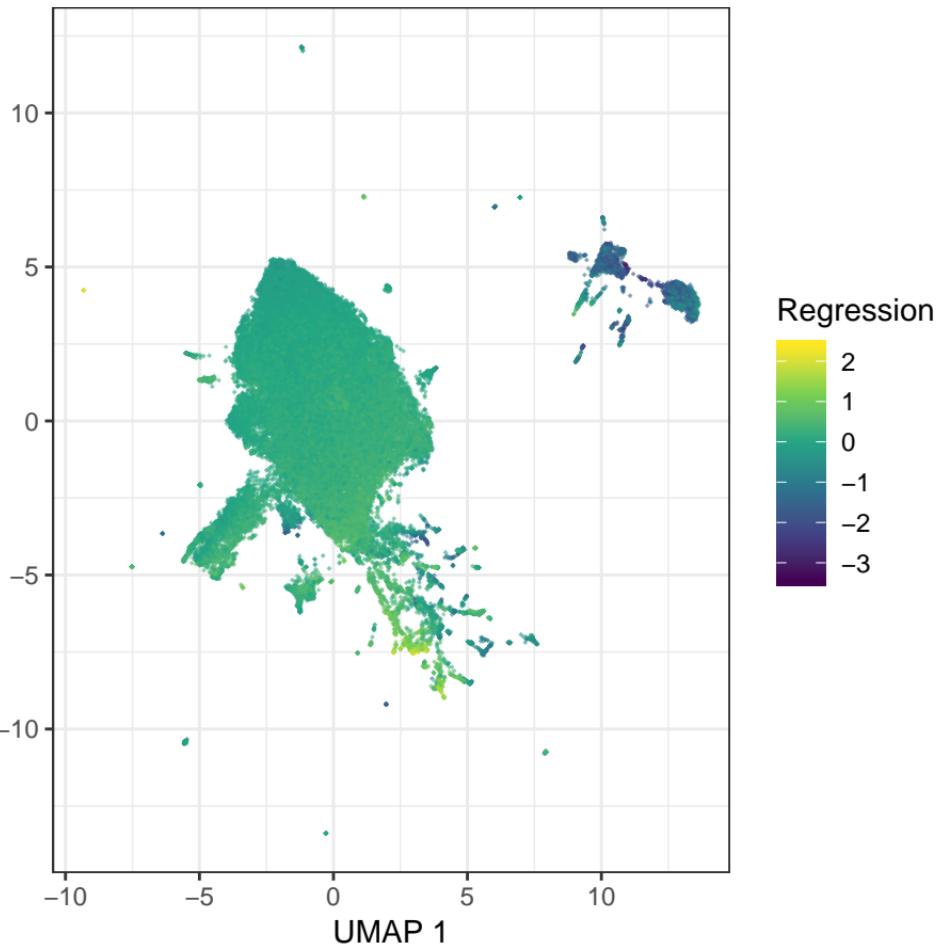
UMAP 2

Regression



cc_polyplloid_n_spots_mean

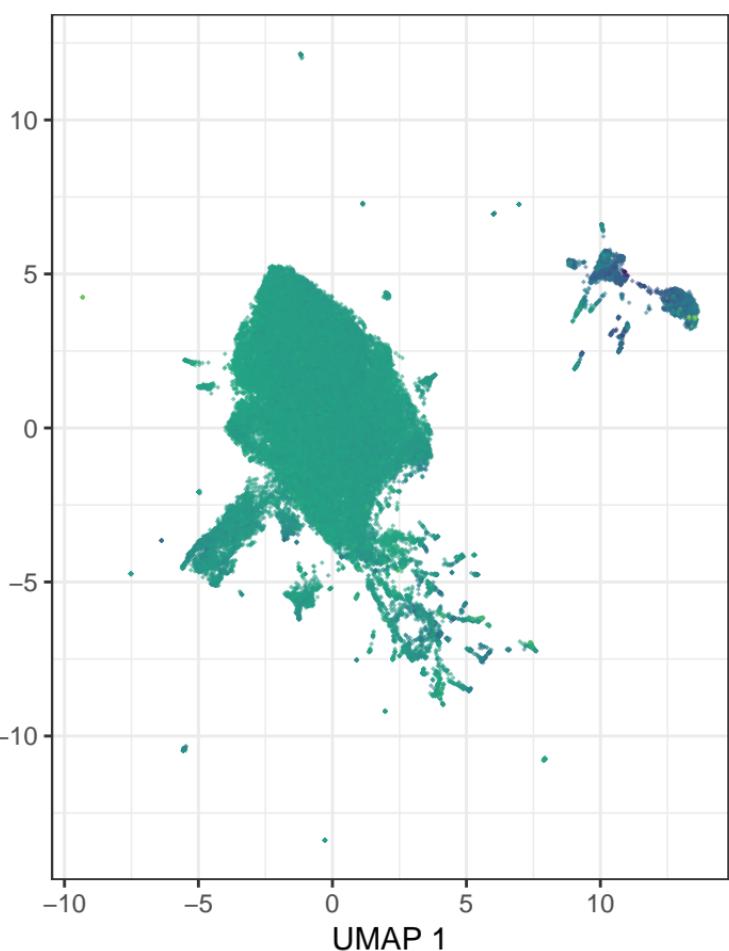
UMAP 2



cc_g2_ph3_neg_n_spots_mean

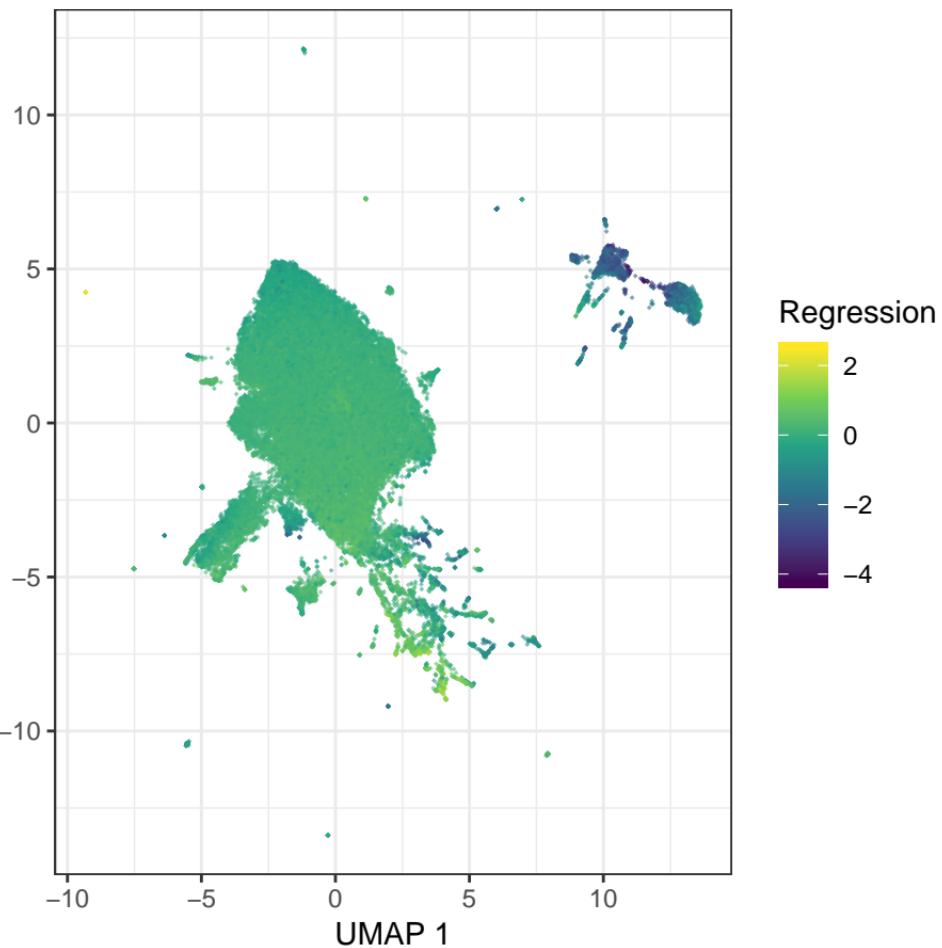
UMAP 2

Regression



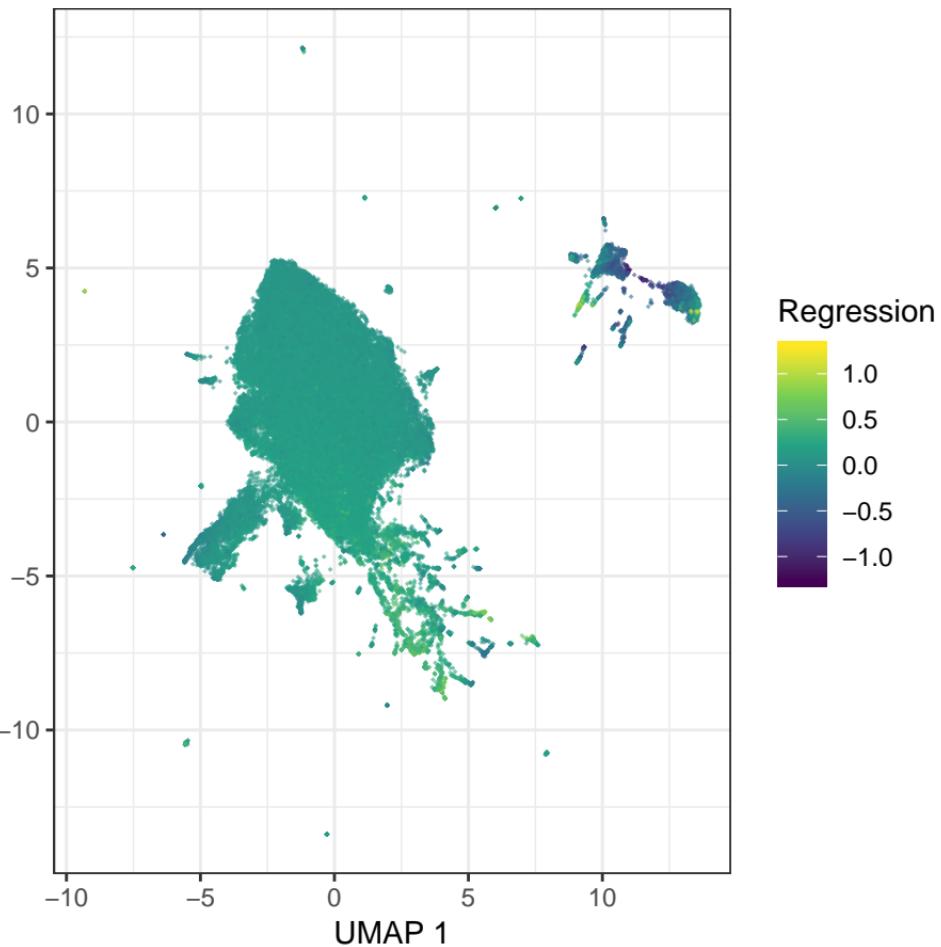
cc_polyplloid_high_n_spots_h2ax_mean

UMAP 2

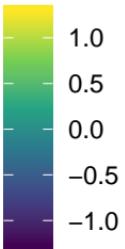


cc_cc_n_spots_per_nucleus_area_mean

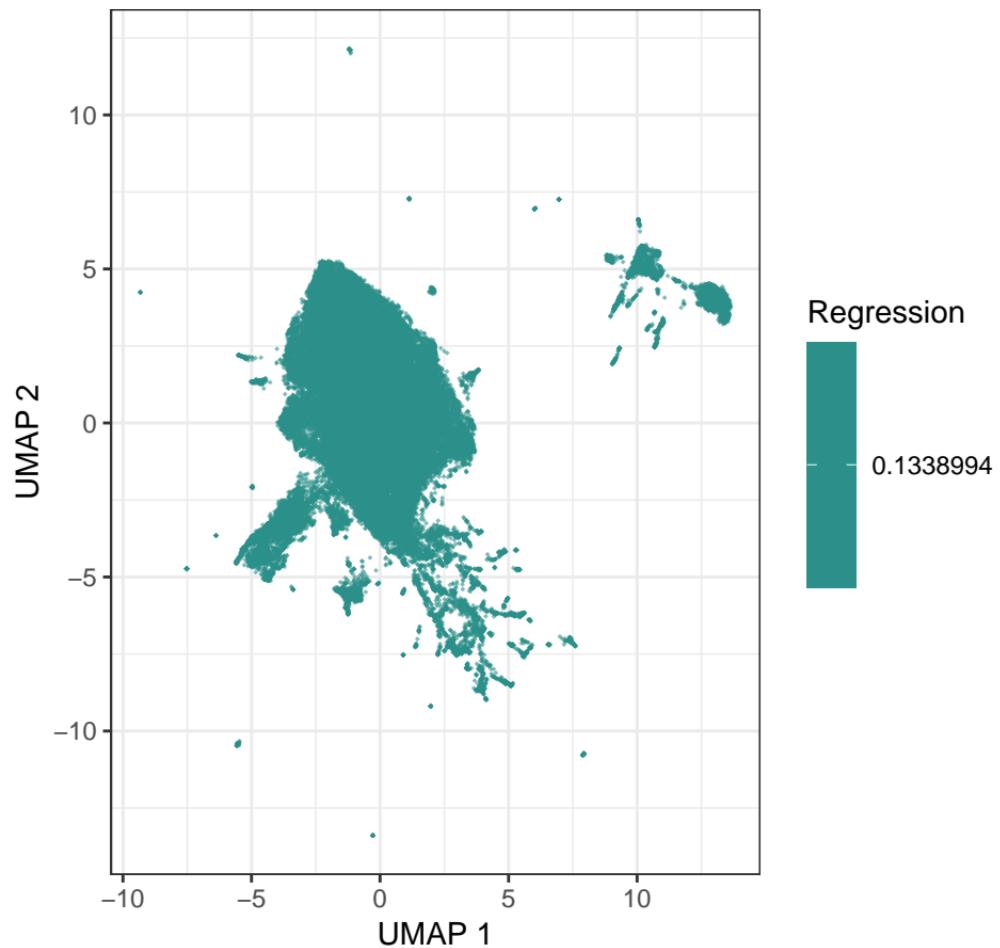
UMAP 2



Regression

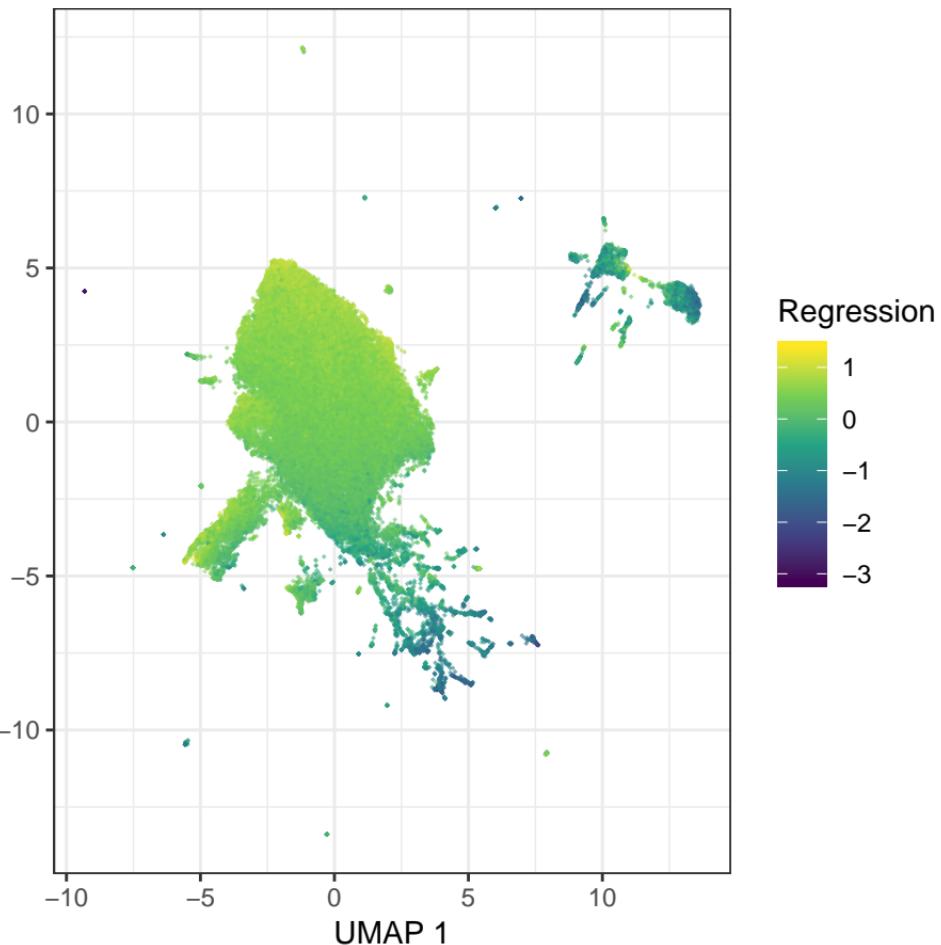


cc_mitosis_ph3_neg_high_n_spots_h2ax_mean



cc_edu_pos_alexa647_intensity_nucleus_area_sum

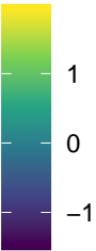
UMAP 2



cc_edu_pos_n_spots_per_nucleus_area_mean

UMAP 2

Regression



10

5

0

-5

-10

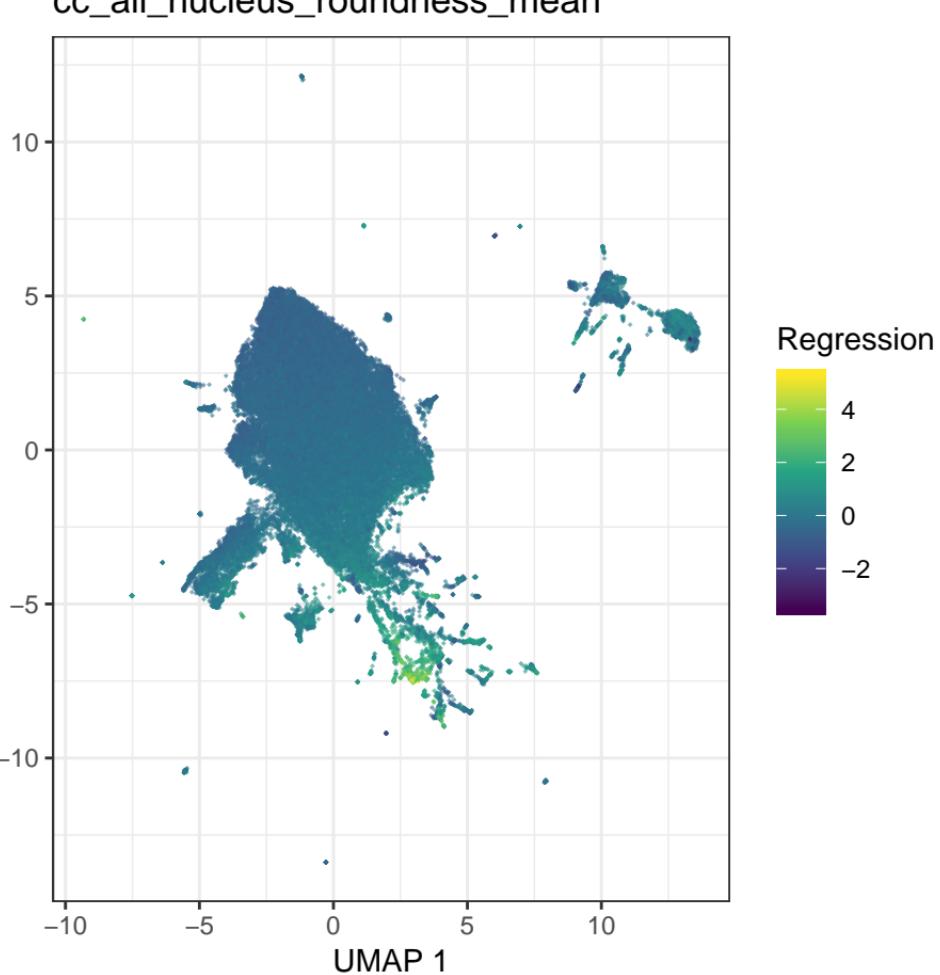
-10

-5

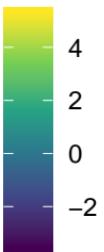
UMAP 1

cc_all_nucleus_roundness_mean

UMAP 2

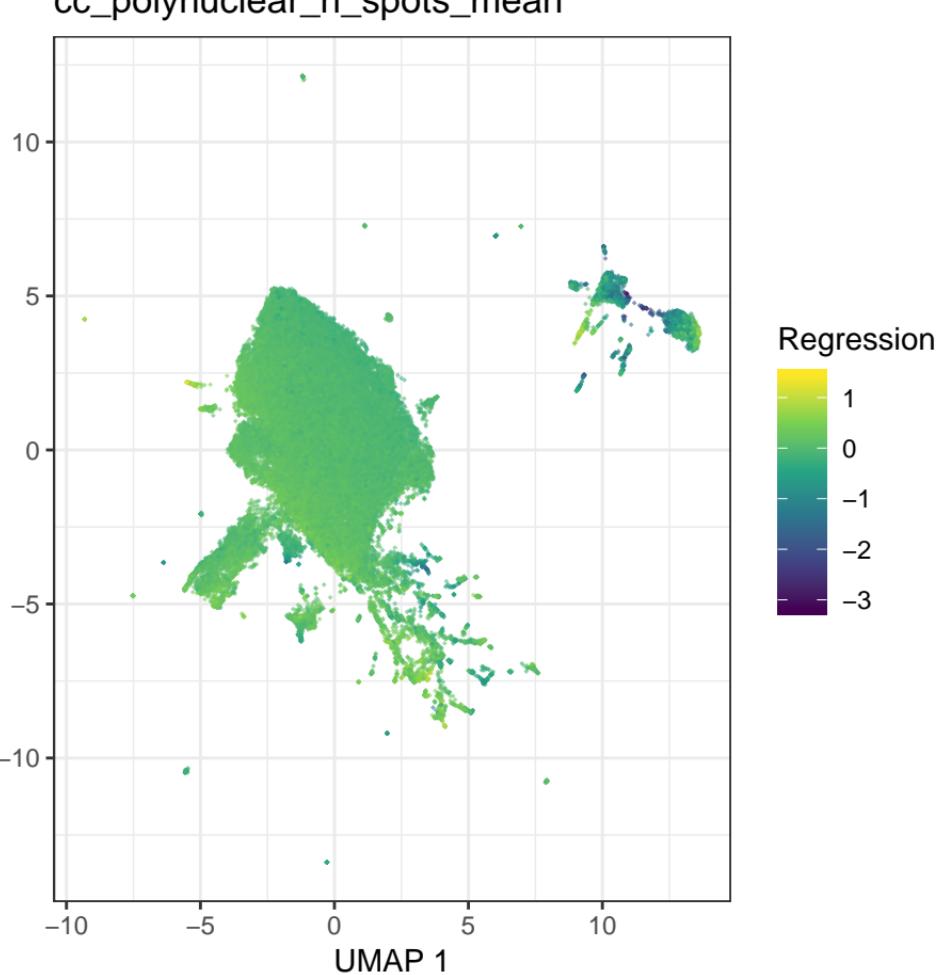


Regression



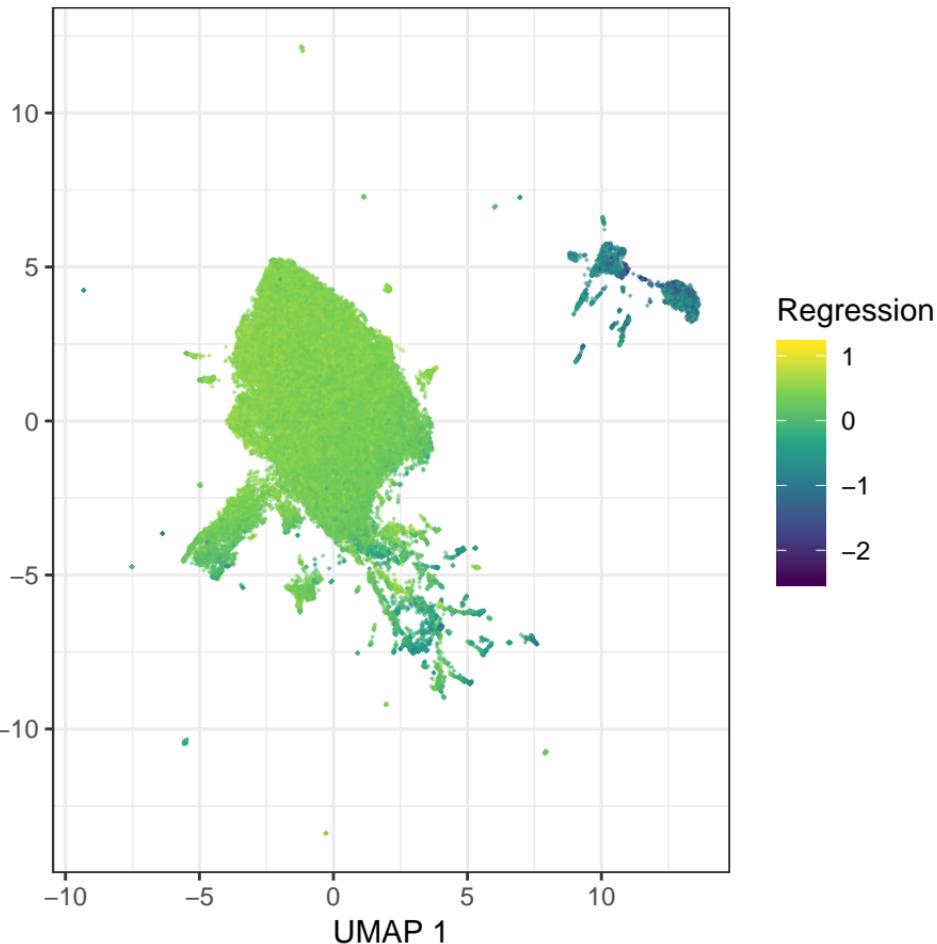
cc_poly-nuclear_n_spots_mean

UMAP 2



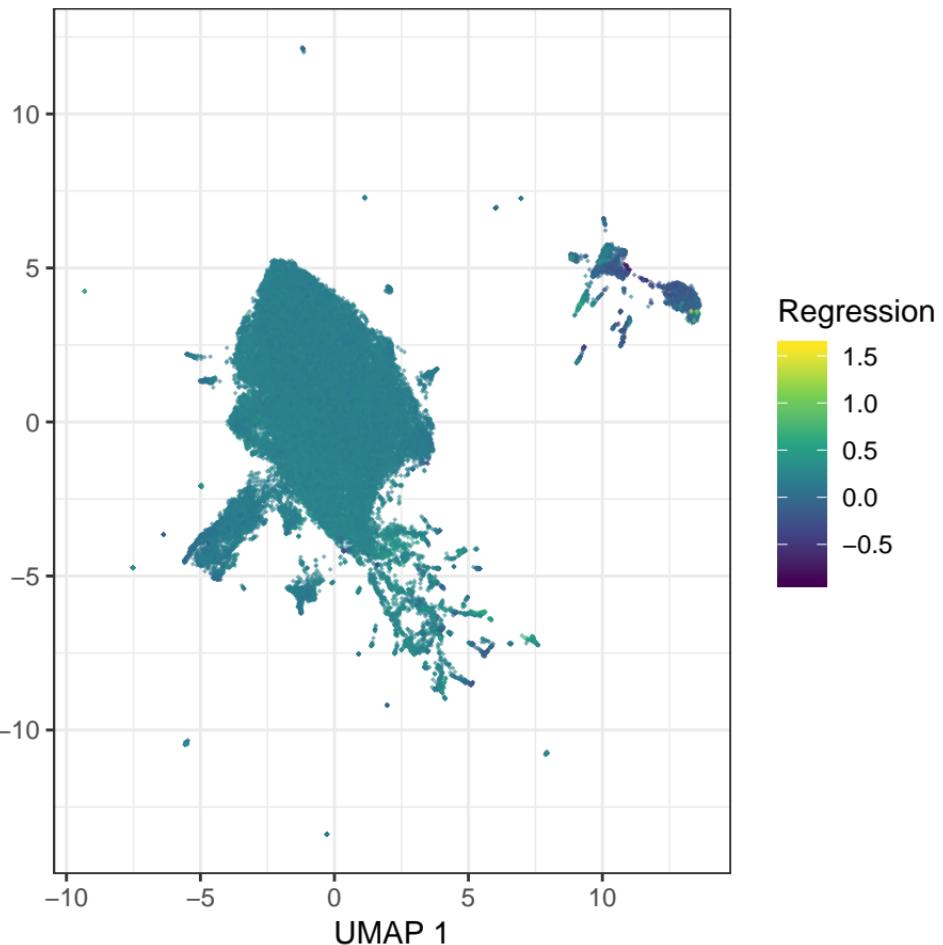
cc_poly-nuclear_n_objects

UMAP 2



cc_g2_ph3_neg_high_n_spots_h2ax_mean

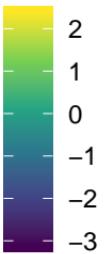
UMAP 2



cc_polyplloid_n_spots_per_nucleus_area_mean

UMAP 2

Regression



10

5

0

-5

-10

-10

-5

UMAP 1

cc_mitosis_ph3_pos_n_objects

UMAP 2

10

5

0

-5

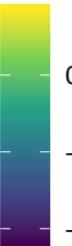
-10

-10

-5

UMAP 1

Regression



cc_all_n_spots_mean

UMAP 2

10

5

0

-5

-10

UMAP 1

Regression

5.0

2.5

0.0

-2.5

-5.0

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

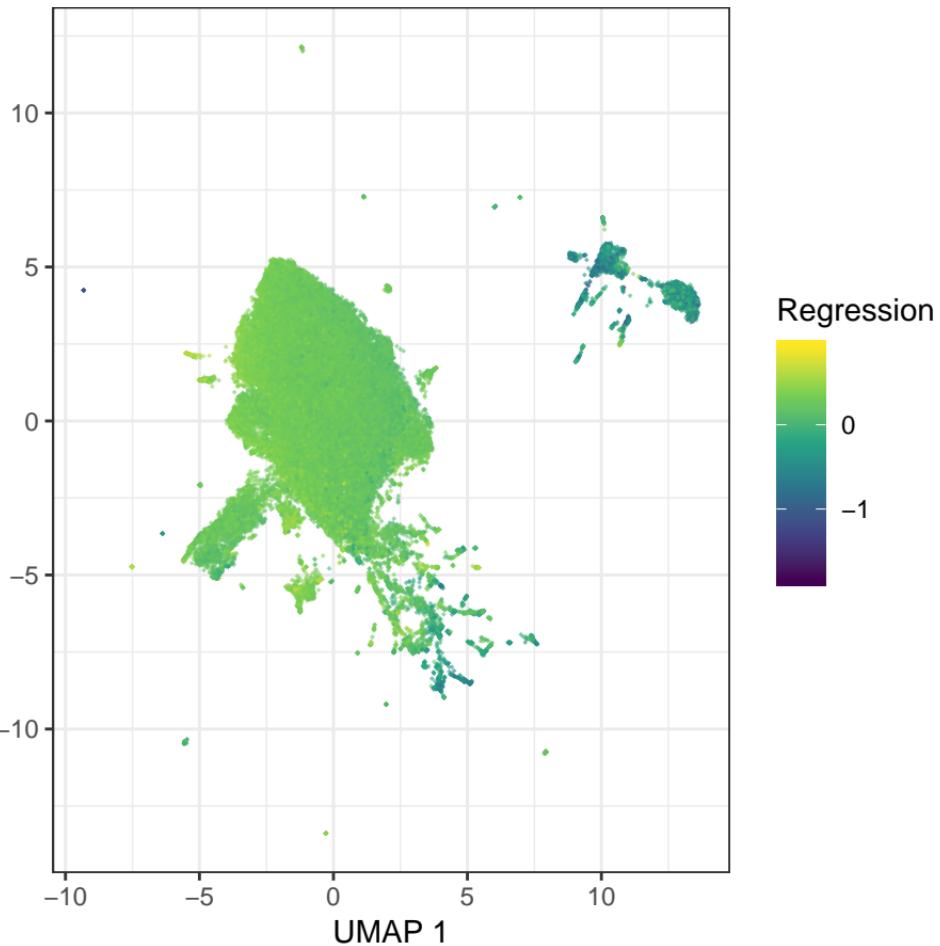
10

-10

-5

cc_polyplloid_n_objects

UMAP 2



Regression

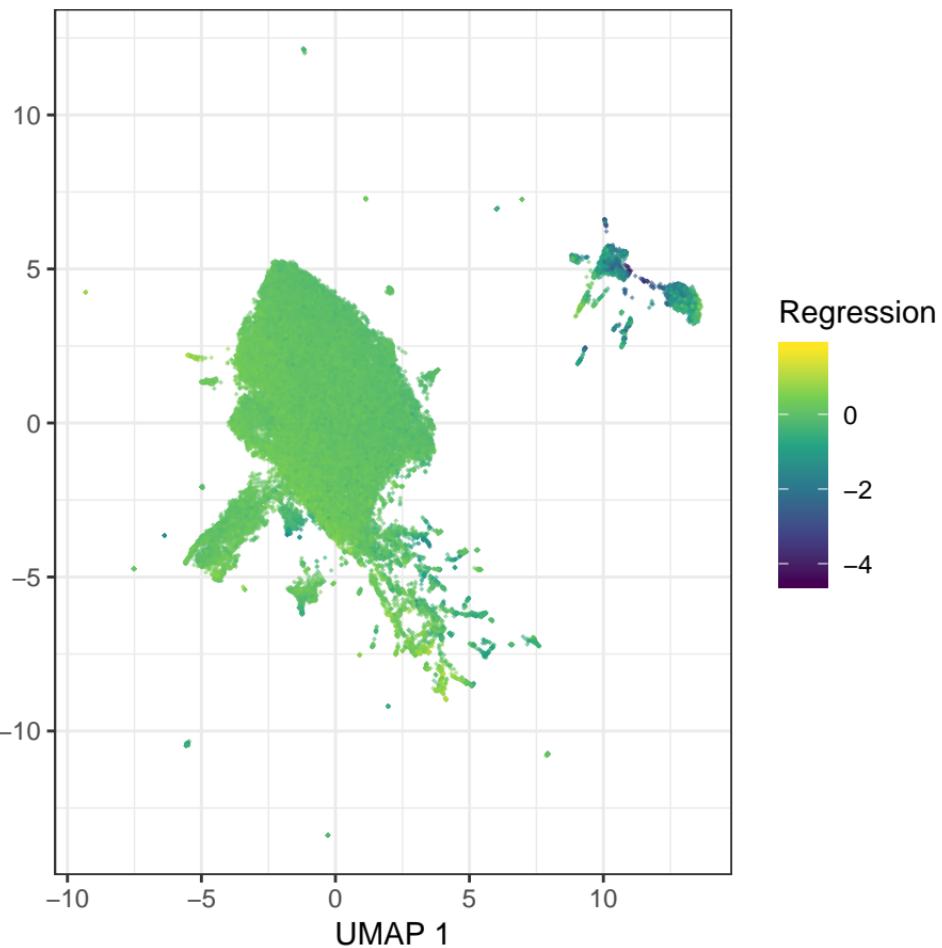


0

-1

cc_poly-nuclear_n_spots_per_nucleus_area_mean

UMAP 2



cc_infection_percentage

UMAP 2

10

5

0

-5

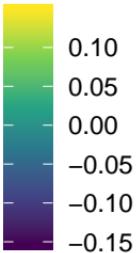
-10

-10

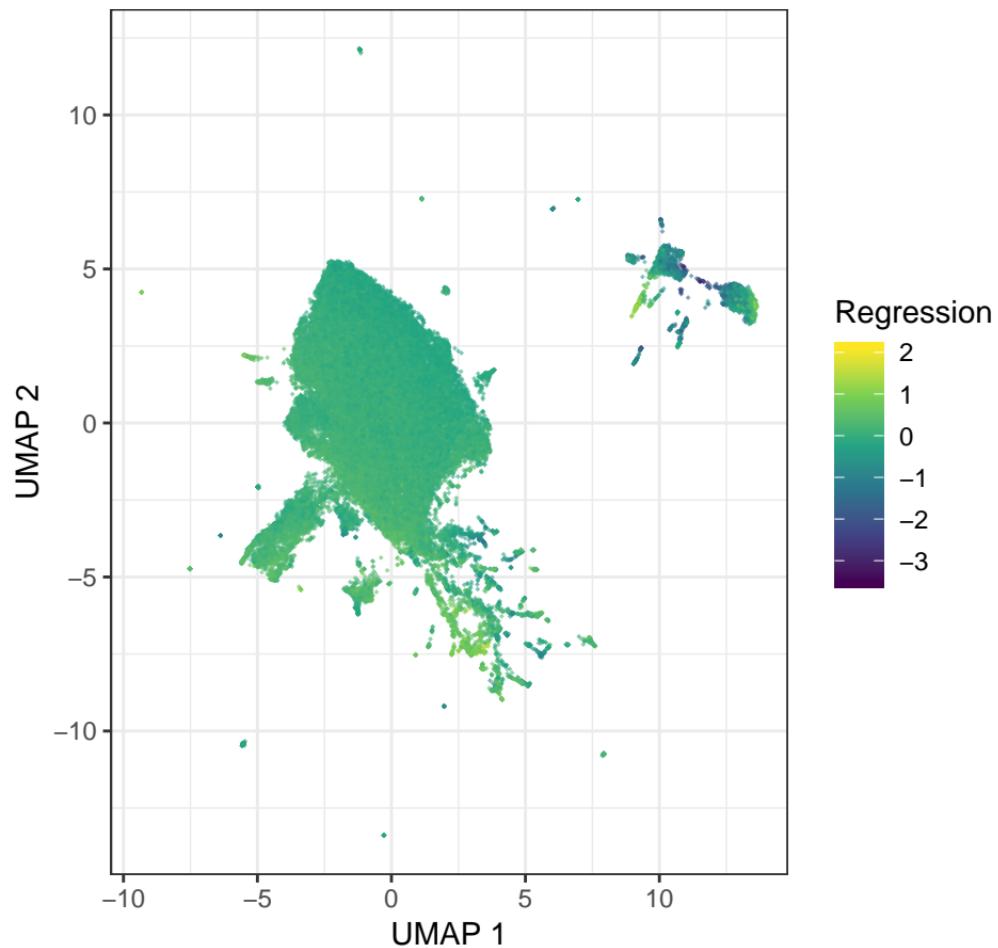
-5

UMAP 1

Regression



cc_poly-nuclear_high_n_spots_h2ax_mean



cc_mitosis_ph3_pos_high_n_spots_h2ax_mean

UMAP 2

10

5

0

-5

-10

-10

-5

UMAP 1

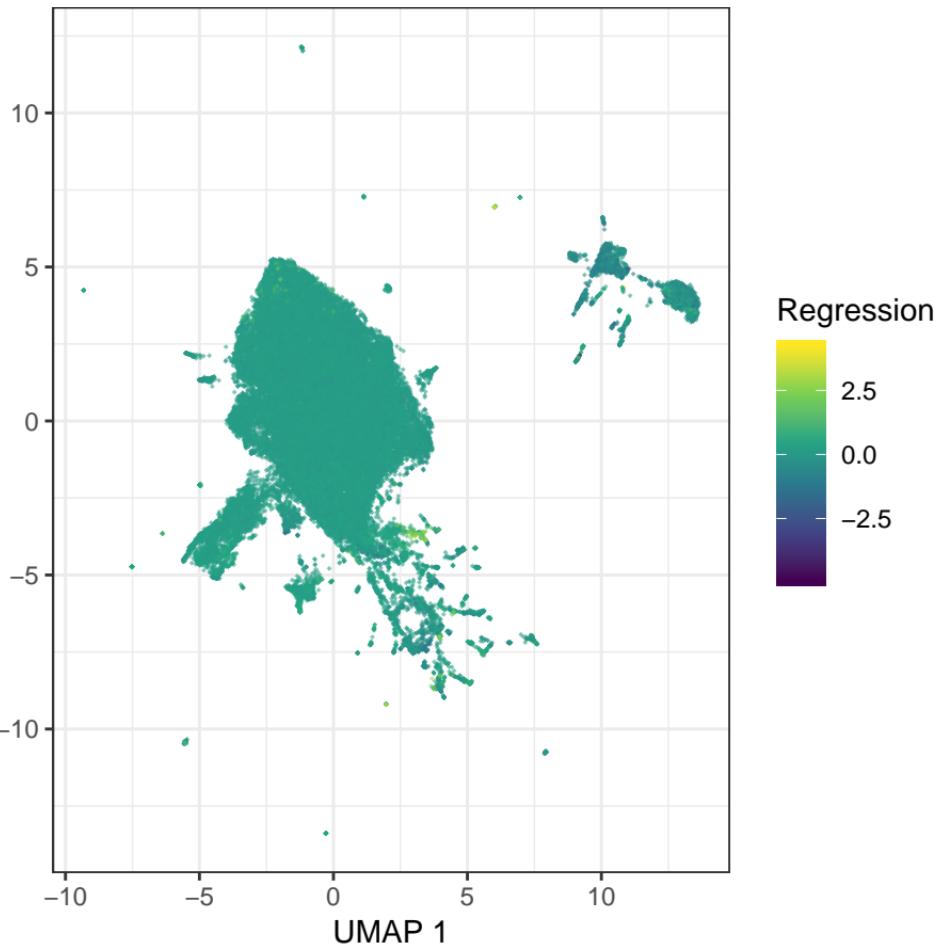
Regression

0.03410795



cc_cc_ph3_pos_hoechst_mitosis_mean

UMAP 2



cc_g2_ph3_pos_n_objects

UMAP 2

10

5

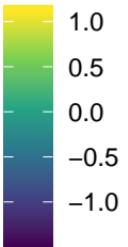
0

-5

-10

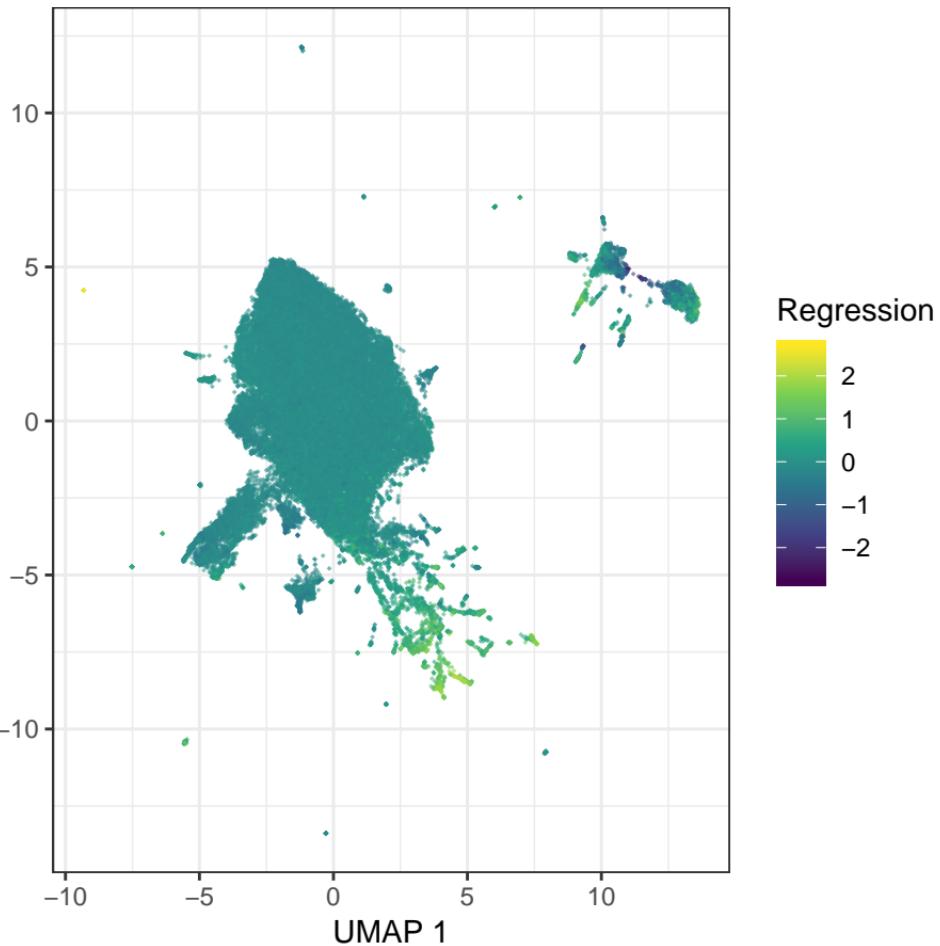
UMAP 1

Regression



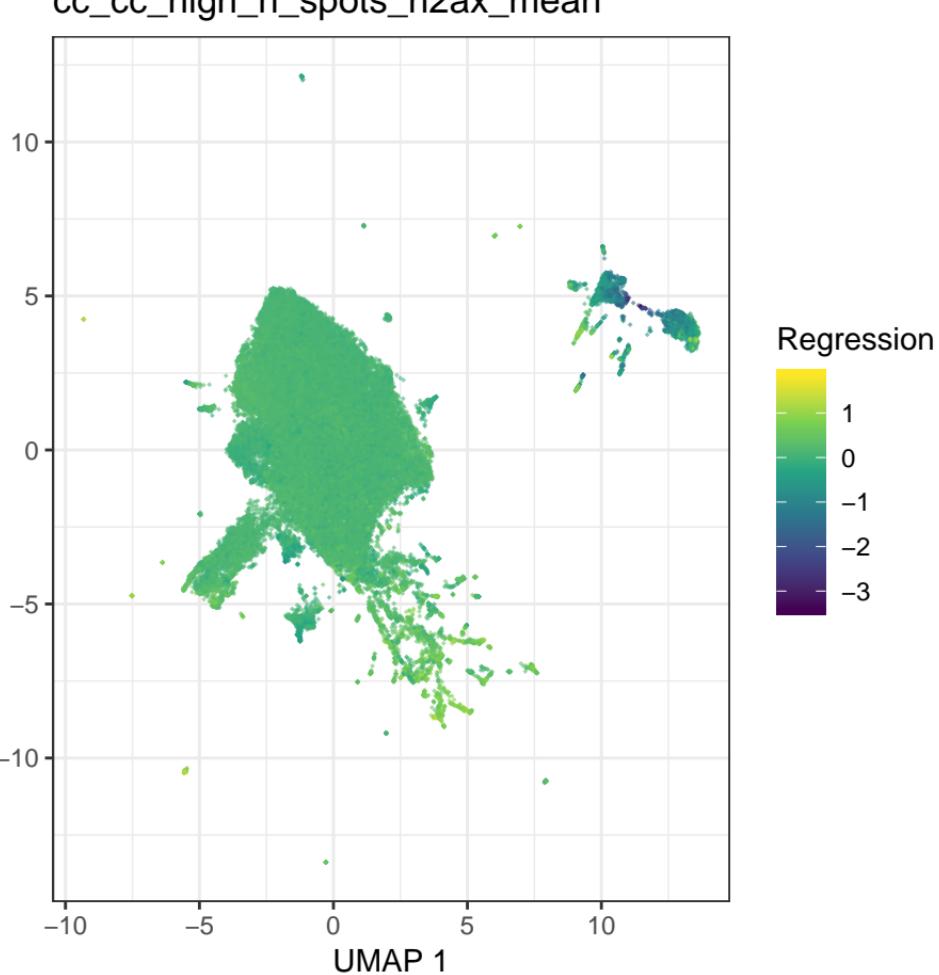
cc_g1_n_spots_mean

UMAP 2



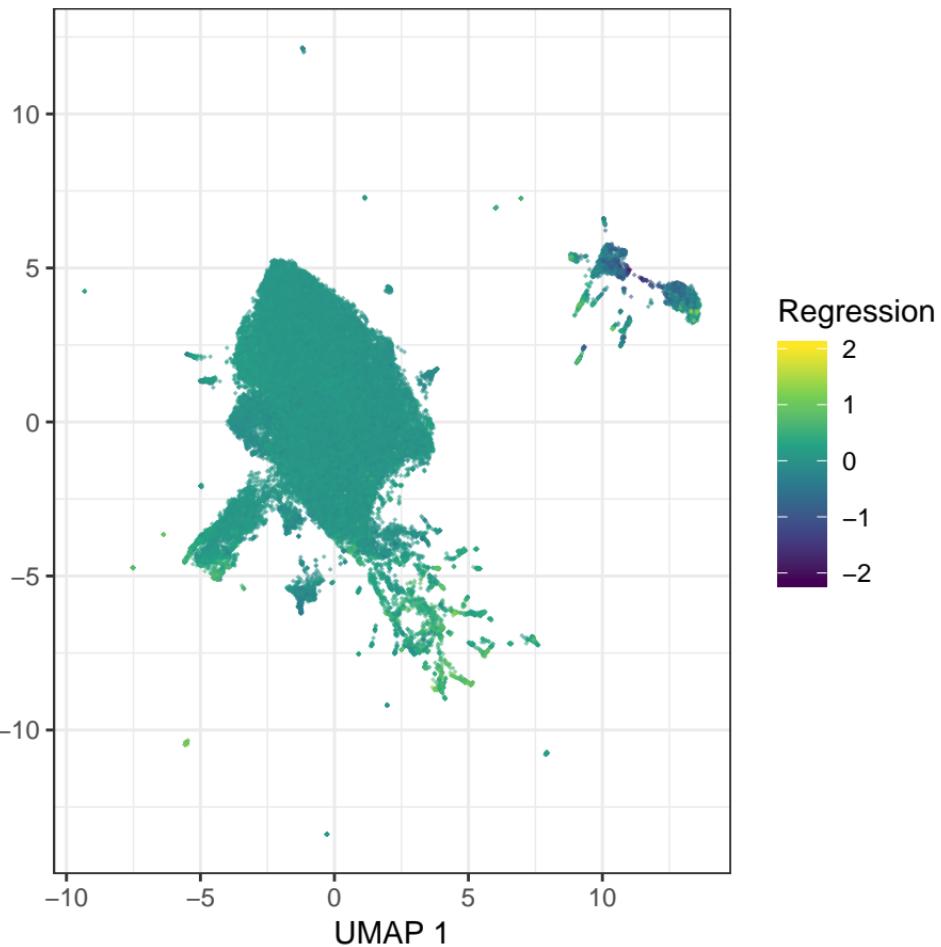
cc_cc_high_n_spots_h2ax_mean

UMAP 2



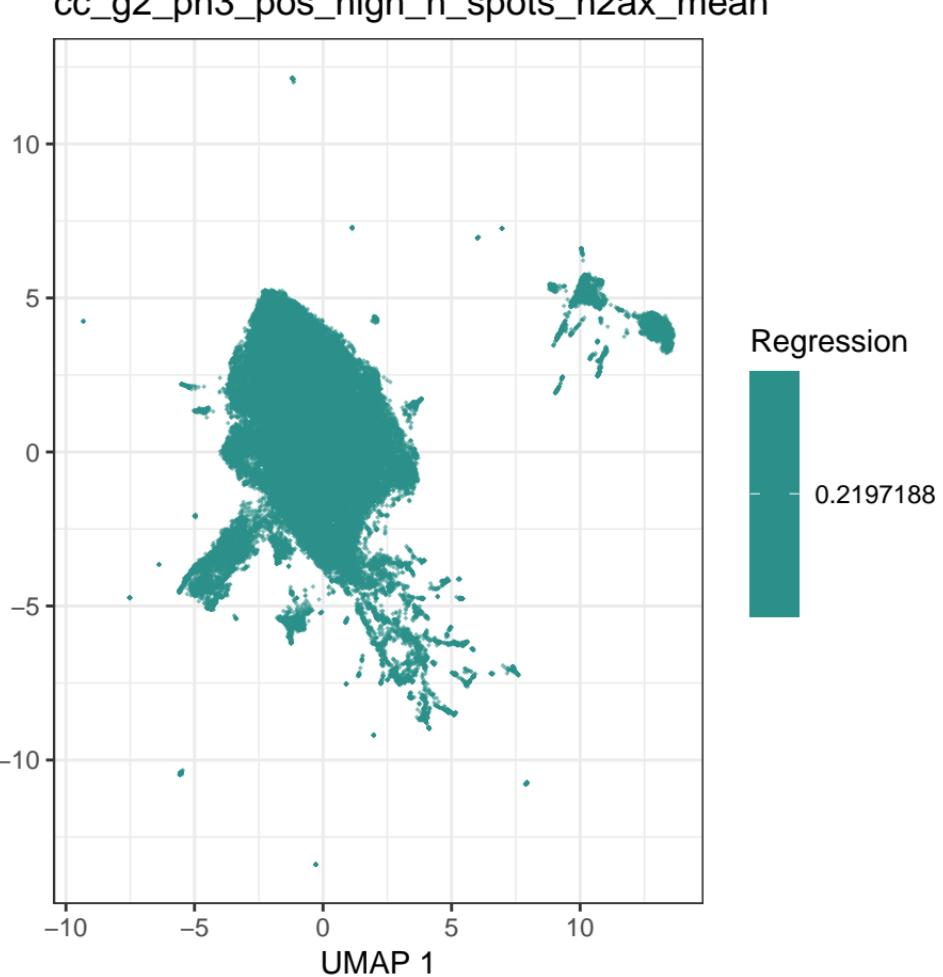
cc_g1_high_n_spots_h2ax_mean

UMAP 2



cc_g2_ph3_pos_high_n_spots_h2ax_mean

UMAP 2



cc_mitosis_ph3_neg_n_spots_per_nucleus_area_mean

UMAP 2

10

5

0

-5

-10

Regression

0.16665844

-10

-5

UMAP 1

cc_cc_g2_ph3_neg_mean

UMAP 2

10

5

0

-5

-10

UMAP 1

Regression

2

0

-2

-4

-10

-5

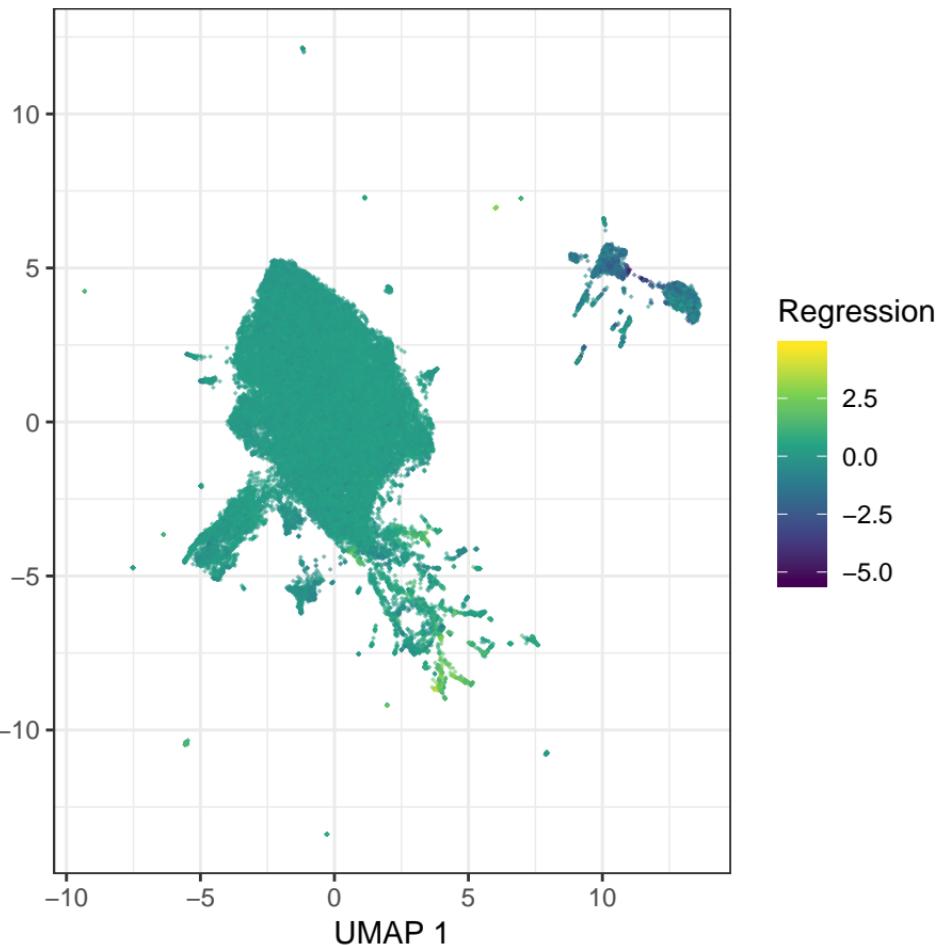
0

5

10

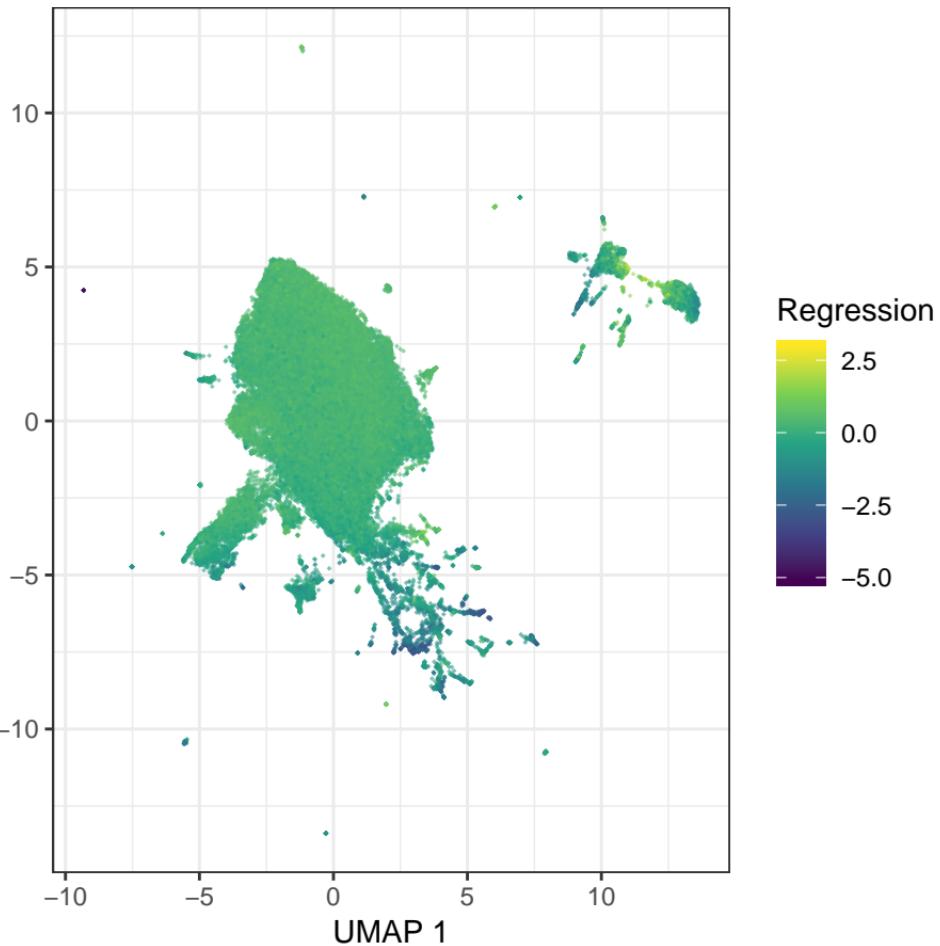
cc_all_large_notround_polynuclear_mean

UMAP 2



cc_cc_edu_pos_mean

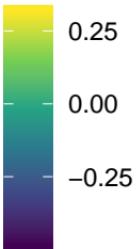
UMAP 2



cc_mitosis_ph3_pos_n_spots_per_nucleus_area_mean

UMAP 2

Regression



10

5

0

-5

-10

-10

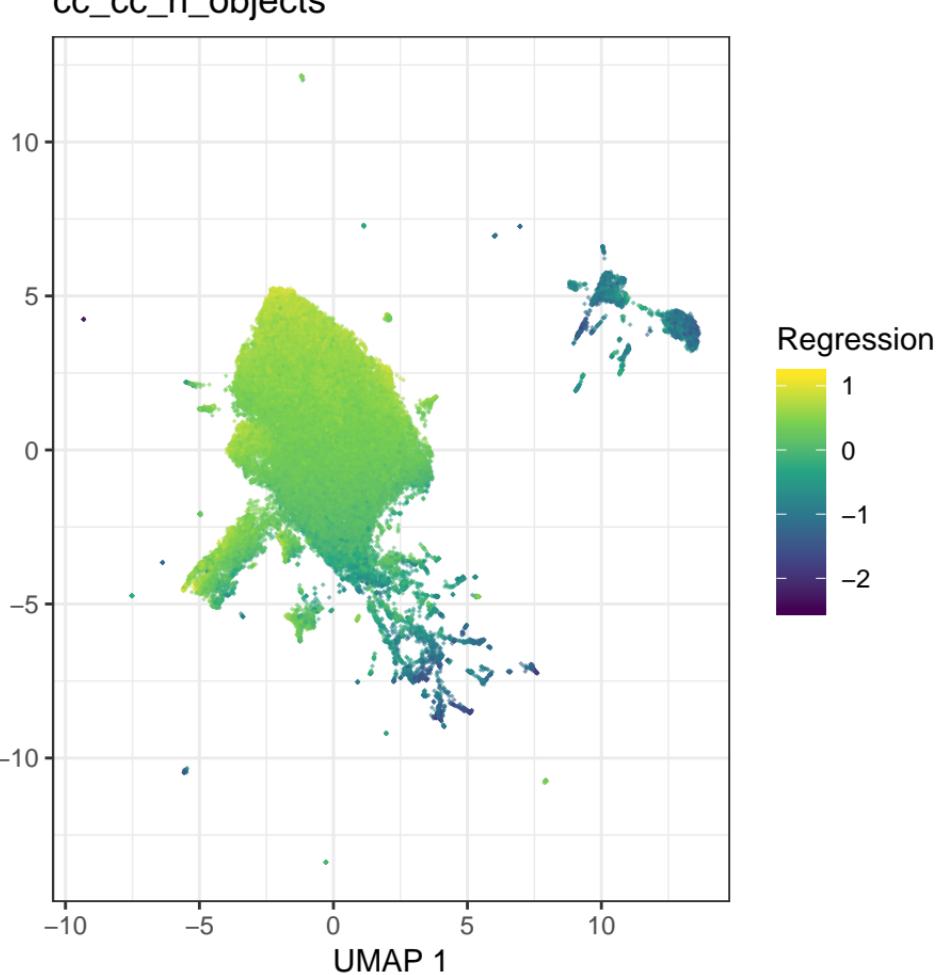
-5

UMAP 1

10

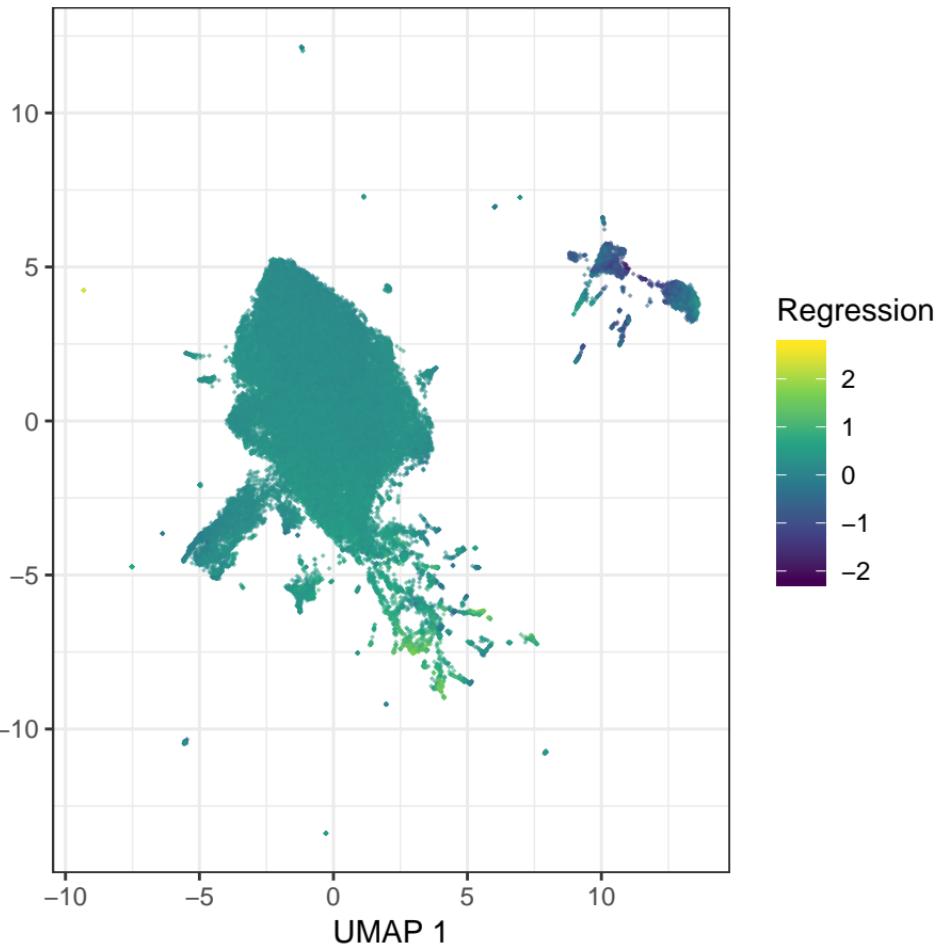
cc_cc_n_objects

UMAP 2



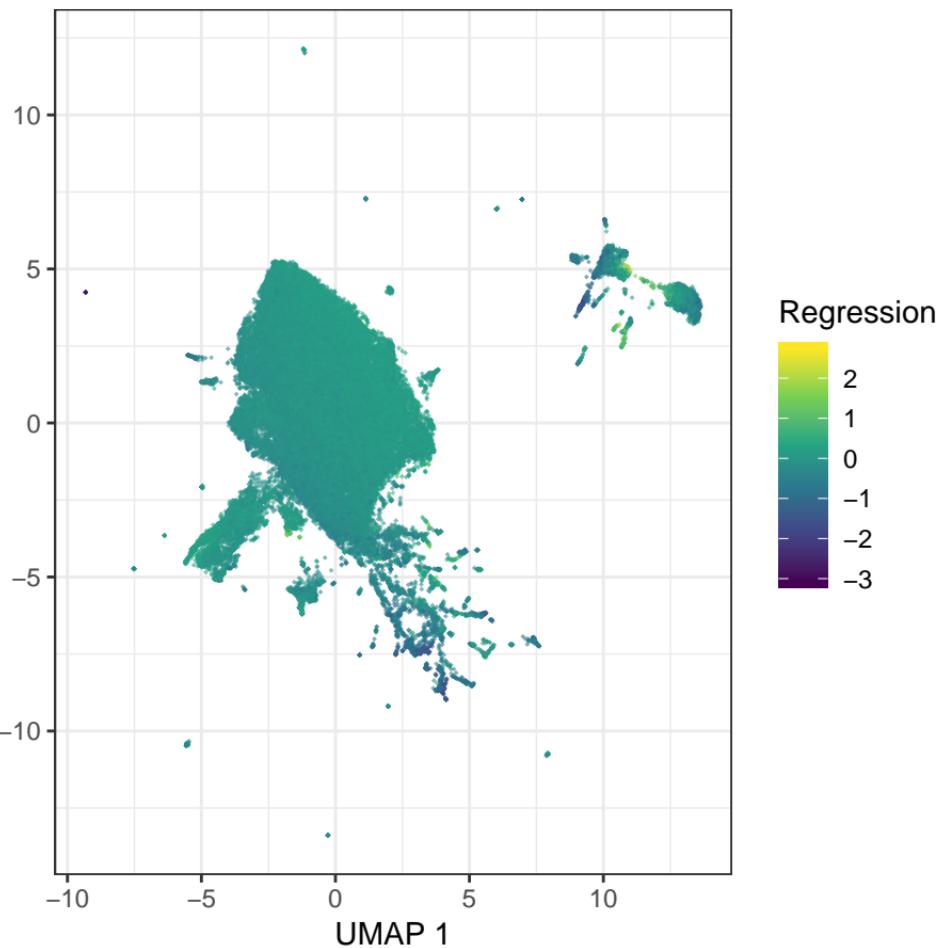
cc_edu_pos_n_spots_mean

UMAP 2

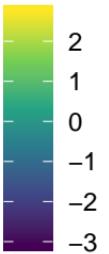


cc_edu_pos_alexa647_intensity_nucleus_area_mean

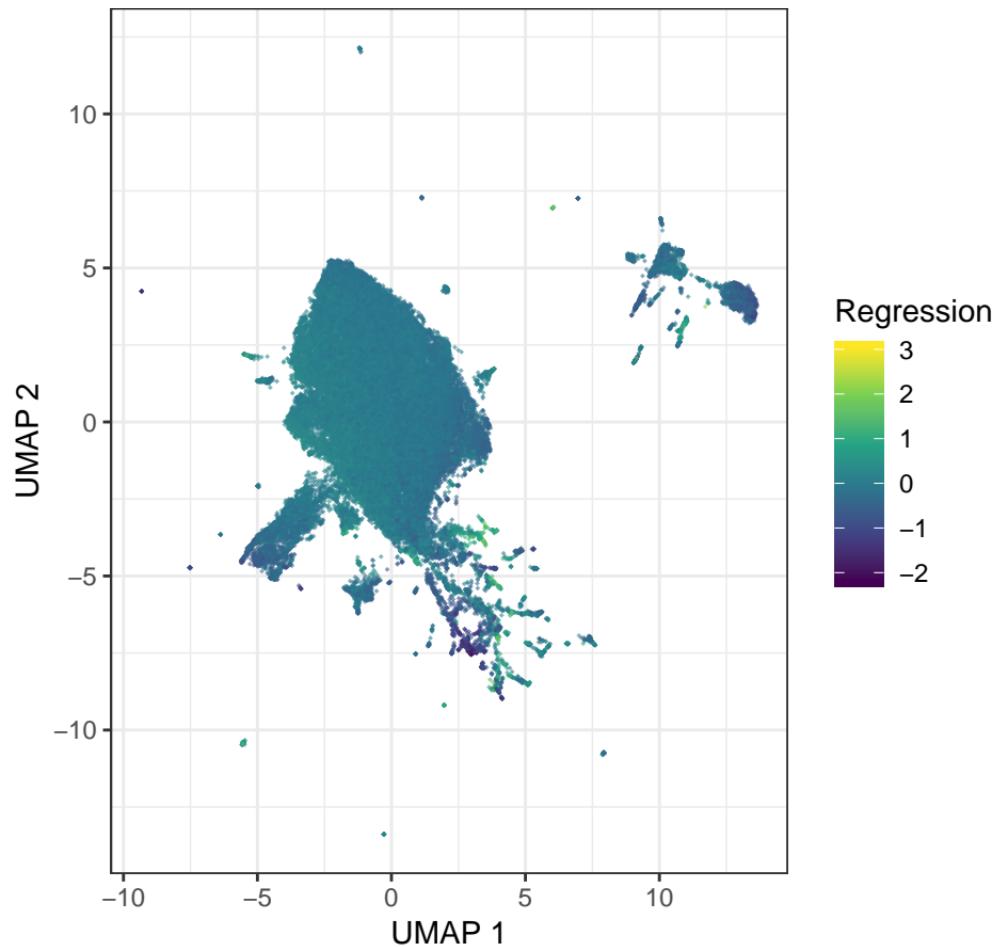
UMAP 2



Regression

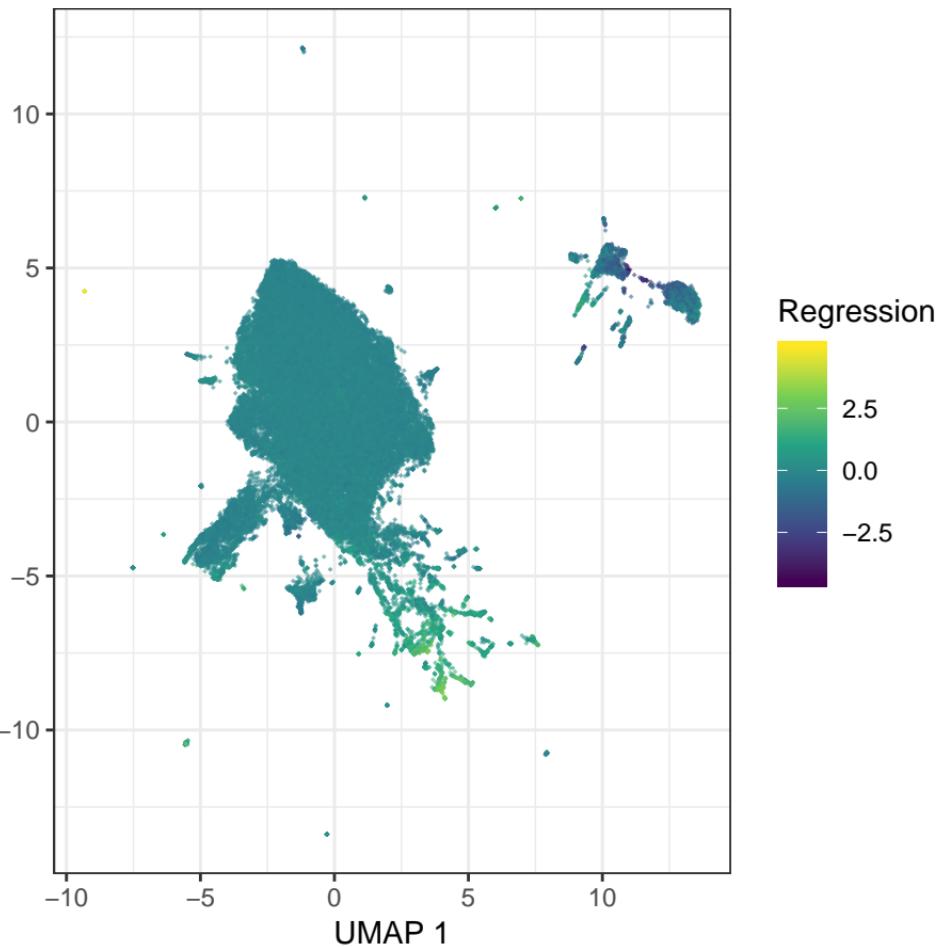


cc_cc_ph3_neg_hoechst_late_mitosis_mean



cc_all_n_spots_per_nucleus_area_mean

UMAP 2



cc_mitosis_ph3_neg_n_objects

UMAP 2

Regression



10

5

0

-5

-10

-10

-5

UMAP 1

cc_g2_g1

UMAP 2

10

5

0

-5

-10

-10

-5

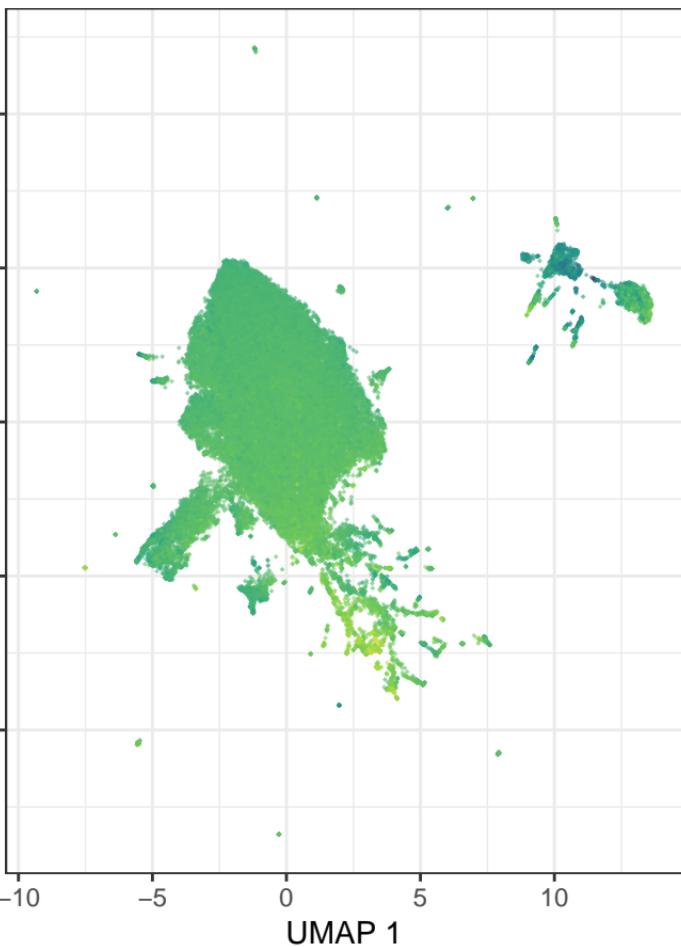
UMAP 1

Regression

0

-1

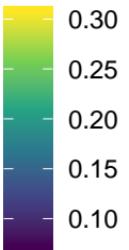
-2



cc_g2_ph3_pos_n_spots_mean

UMAP 2

Regression



10

5

0

-5

-10

-10

-5

0

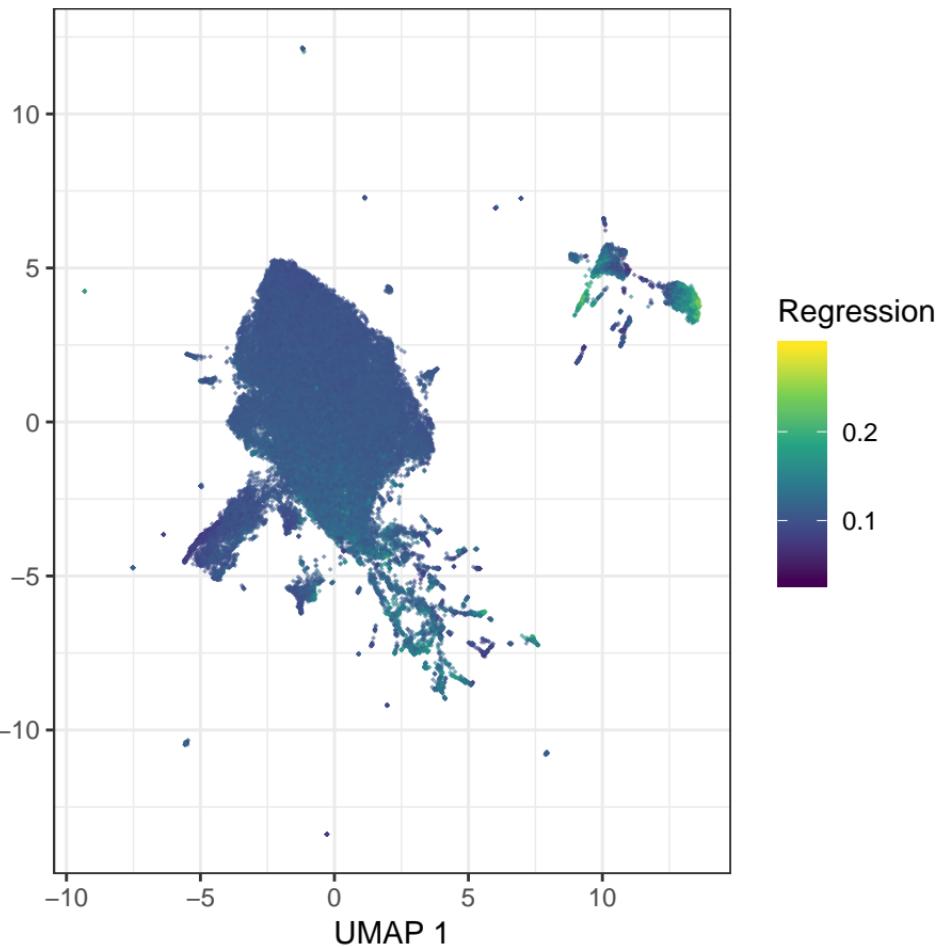
5

10

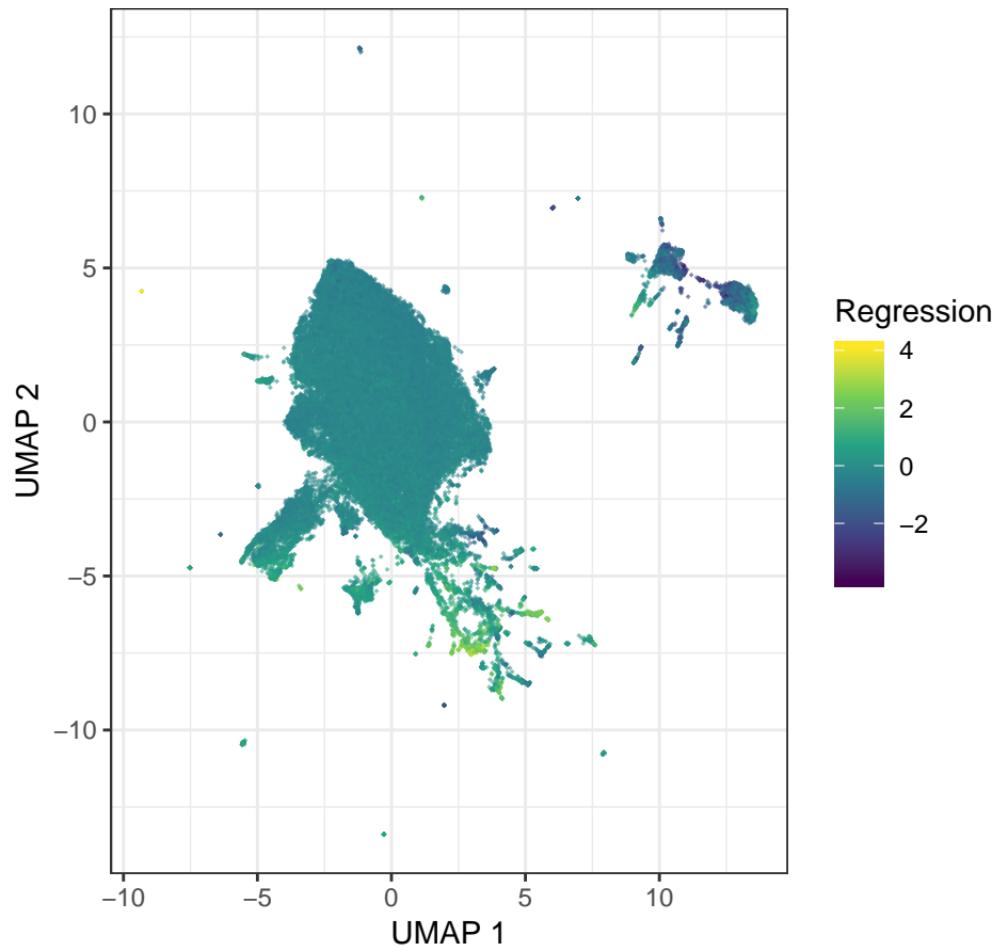
UMAP 1

cc_mitosis_ph3_pos_n_spots_mean

UMAP 2

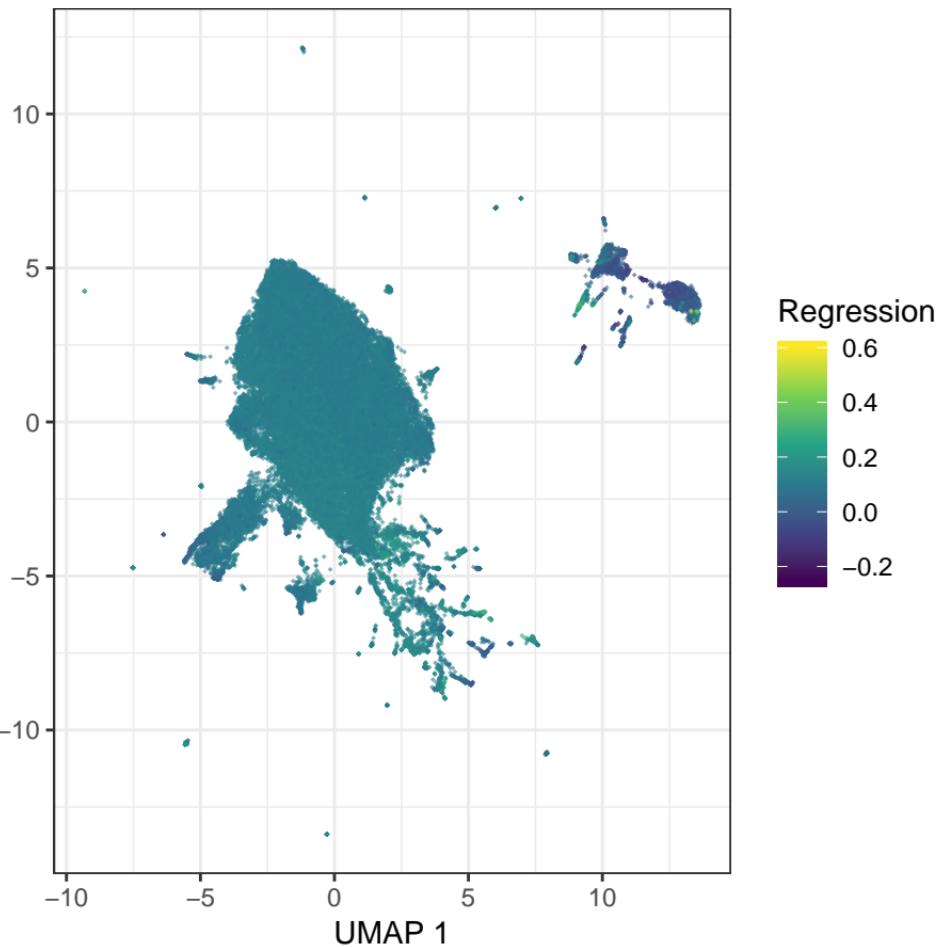


cc_g1_plus_g2



cc_g2_ph3_pos_n_spots_per_nucleus_area_mean

UMAP 2



UMAP 1

cc_g2_plus_all_m

UMAP 2

10

5

0

-5

-10

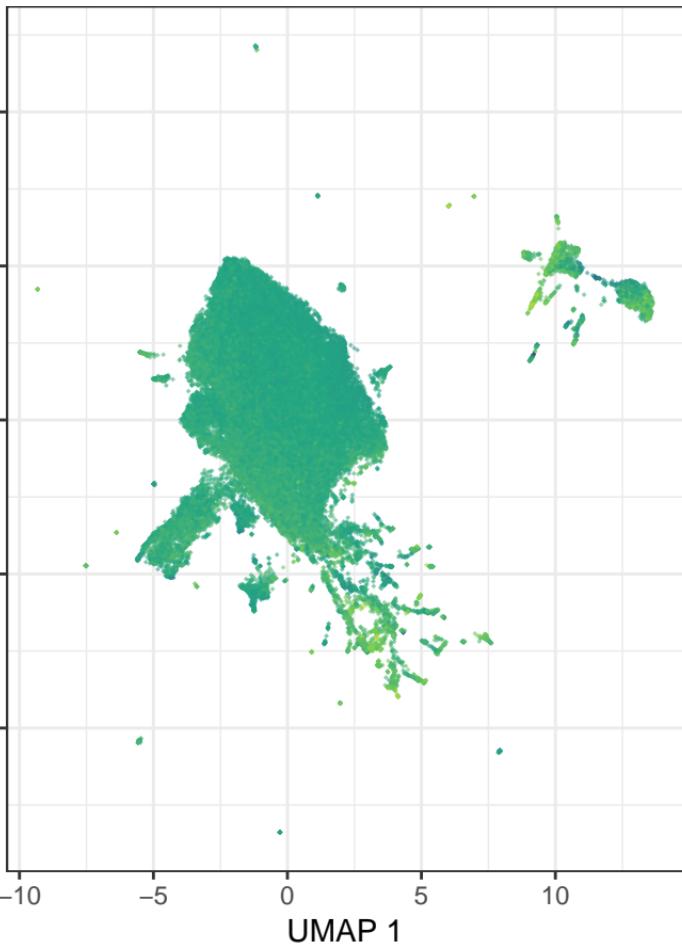
UMAP 1

Regression

2.5

0.0

-2.5



cc_g2_ph3_neg_n_objects

UMAP 2

10

5

0

-5

-10

-10

-5

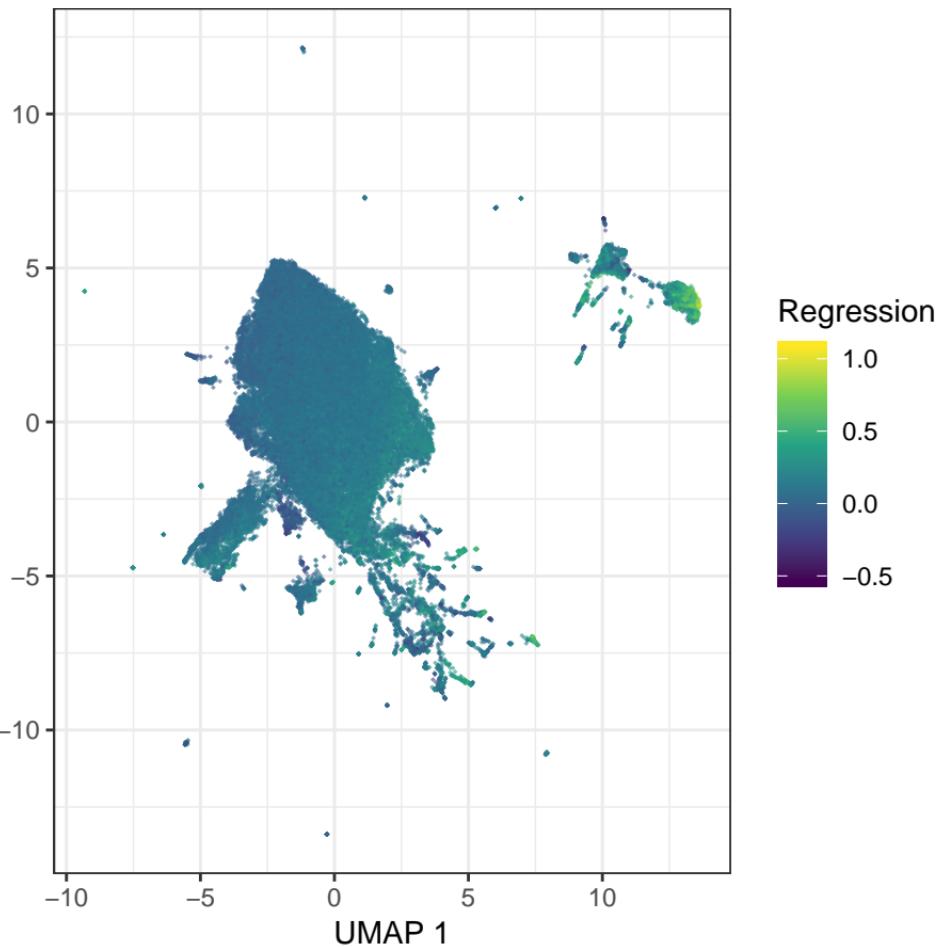
UMAP 1

Regression



cc_cc_g2_ph3_pos_early_mitosis_mean

UMAP 2

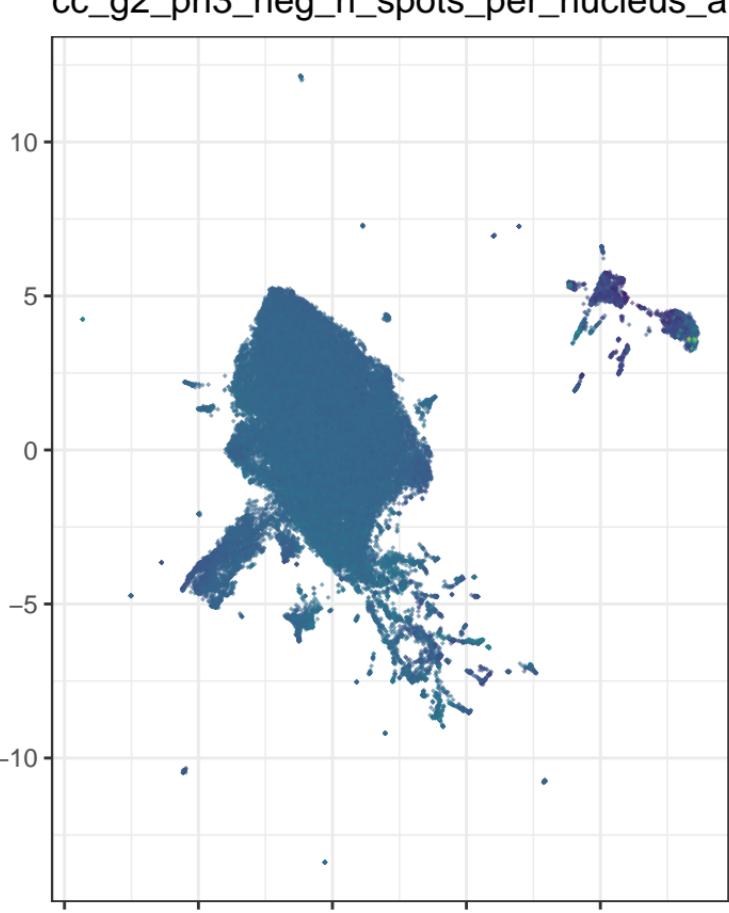


cc_g2_ph3_neg_n_spots_per_nucleus_area_mean

UMAP 2

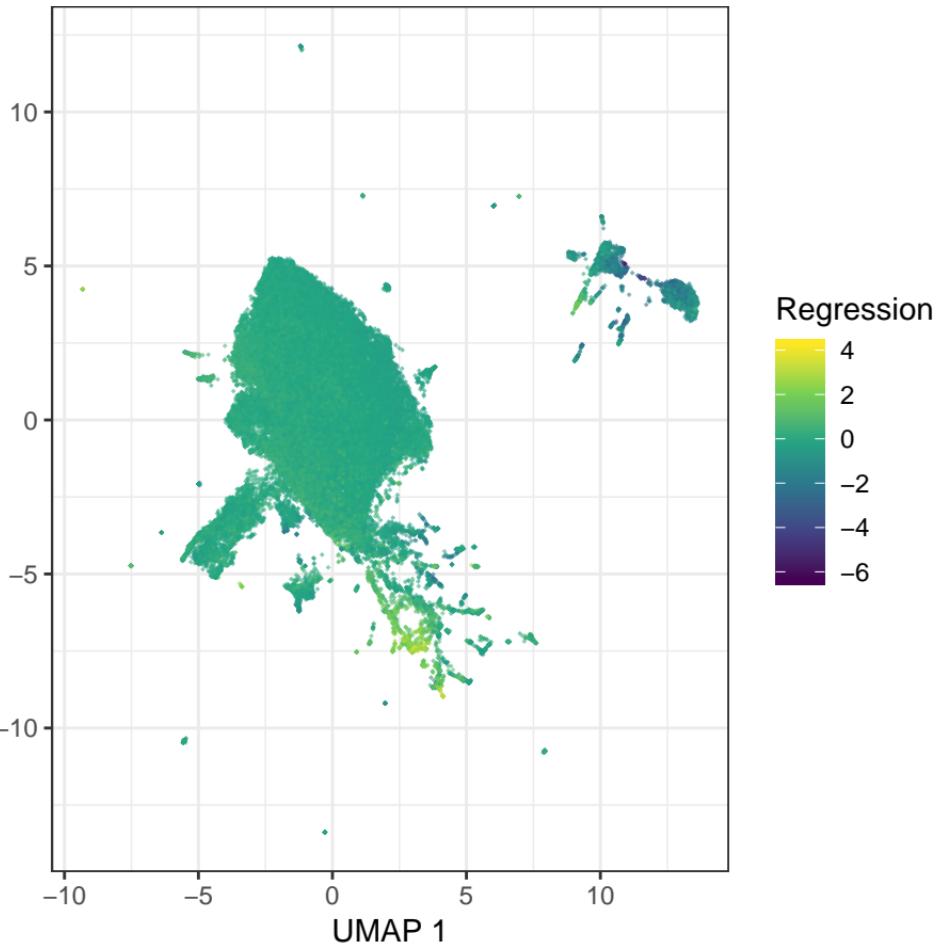
UMAP 1

Regression



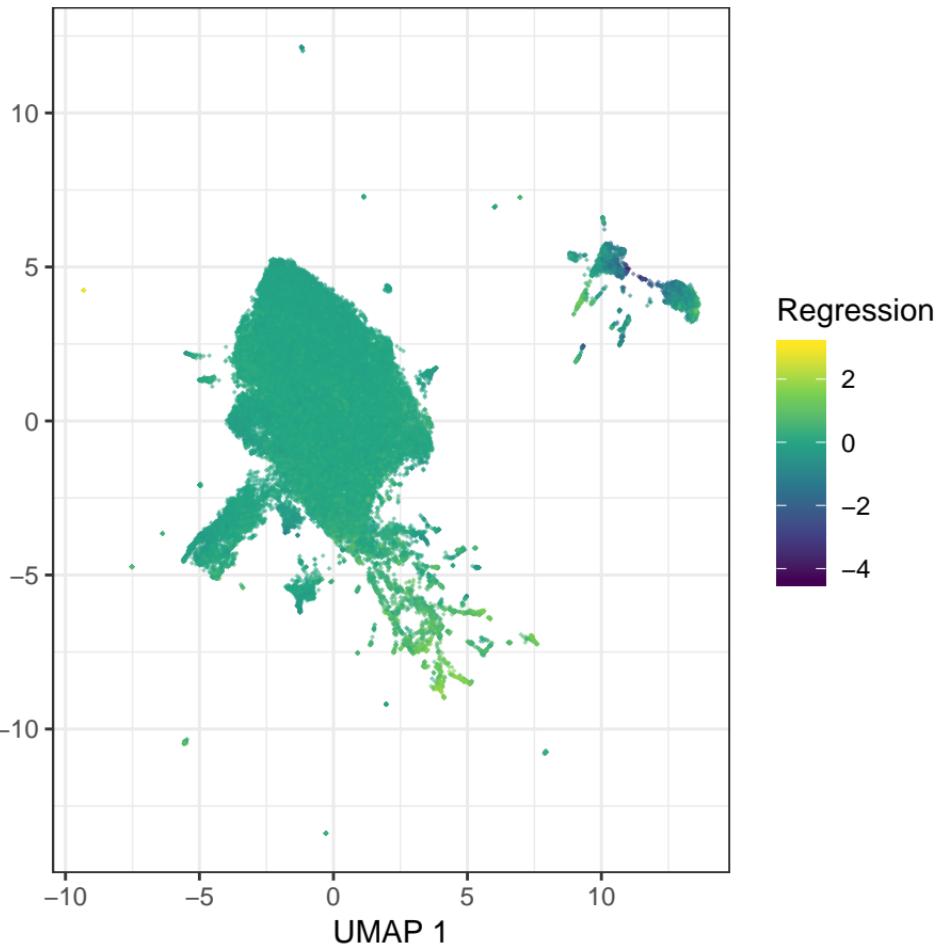
cc_all_nucleus_area_mean

UMAP 2



cc_cc_n_spots_mean

UMAP 2

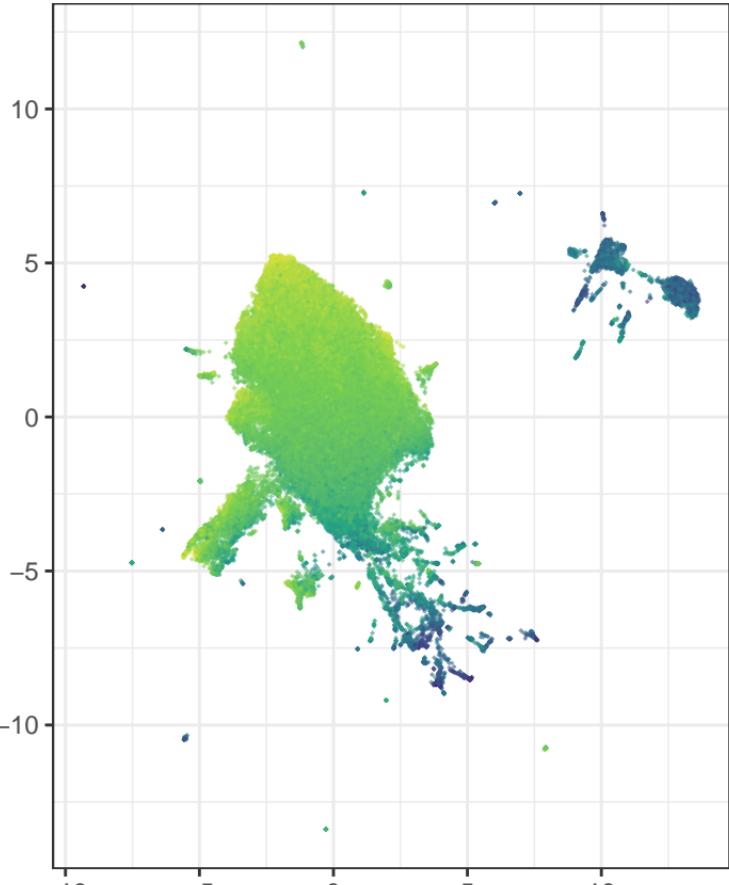
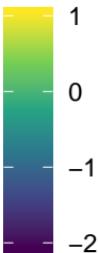


cc_g1_n_objects

UMAP 2

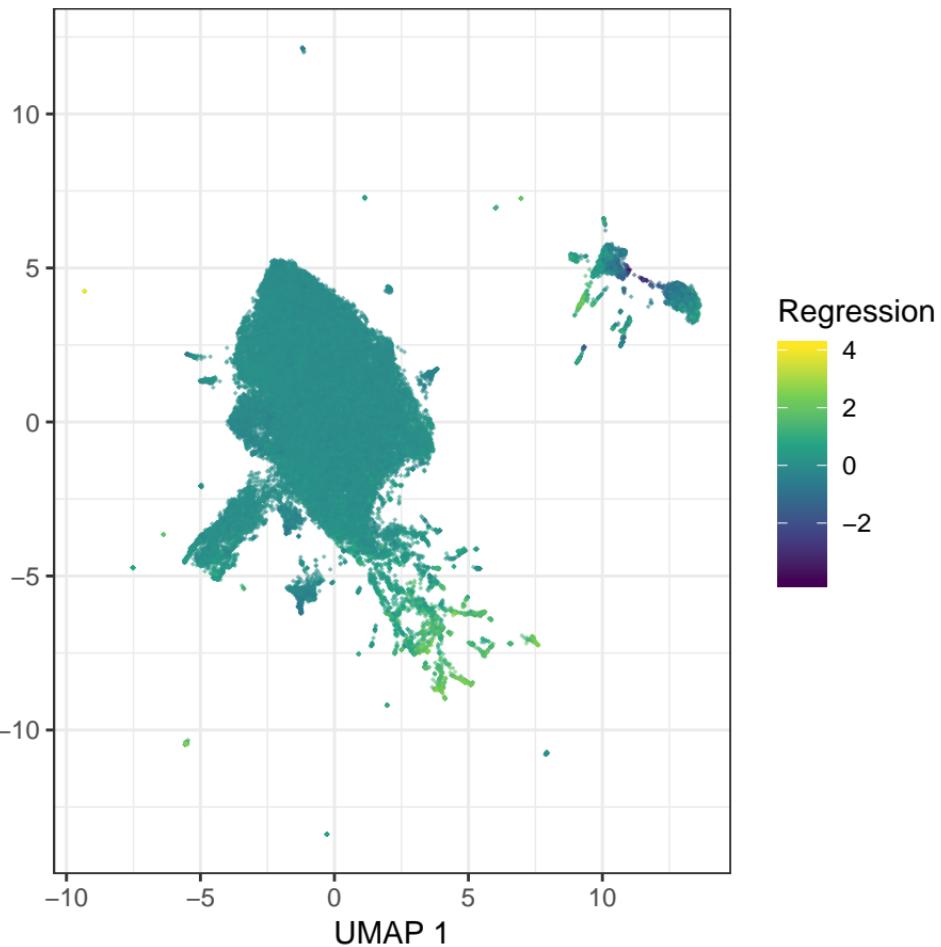
UMAP 1

Regression



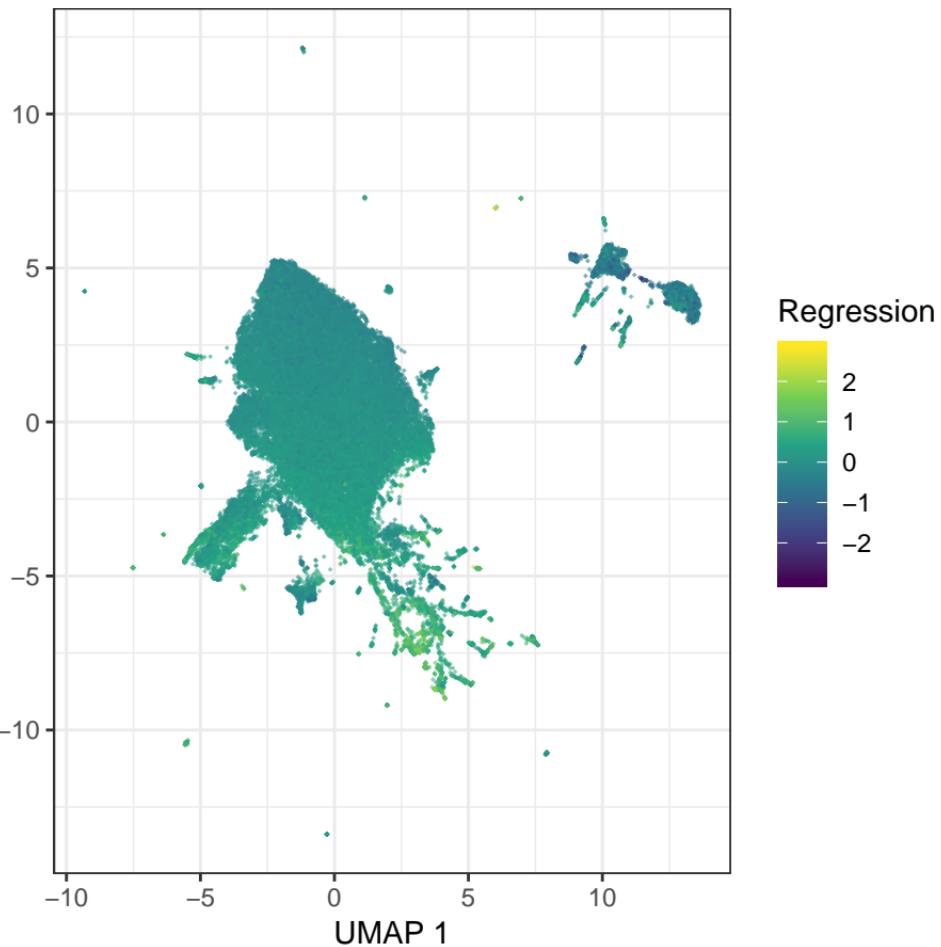
cc_all_high_n_spots_h2ax_mean

UMAP 2



cc_all_large_round_polyplloid_mean

UMAP 2



cc_edu_pos_n_objects

UMAP 2

10

5

0

-5

-10

UMAP 1

Regression

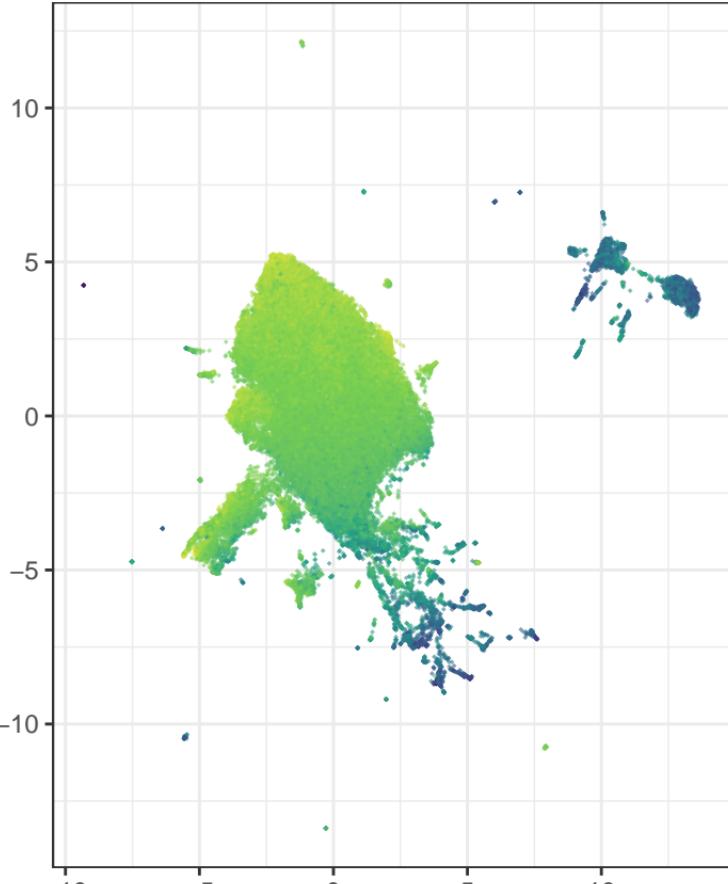
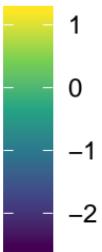


cc_all_n_objects

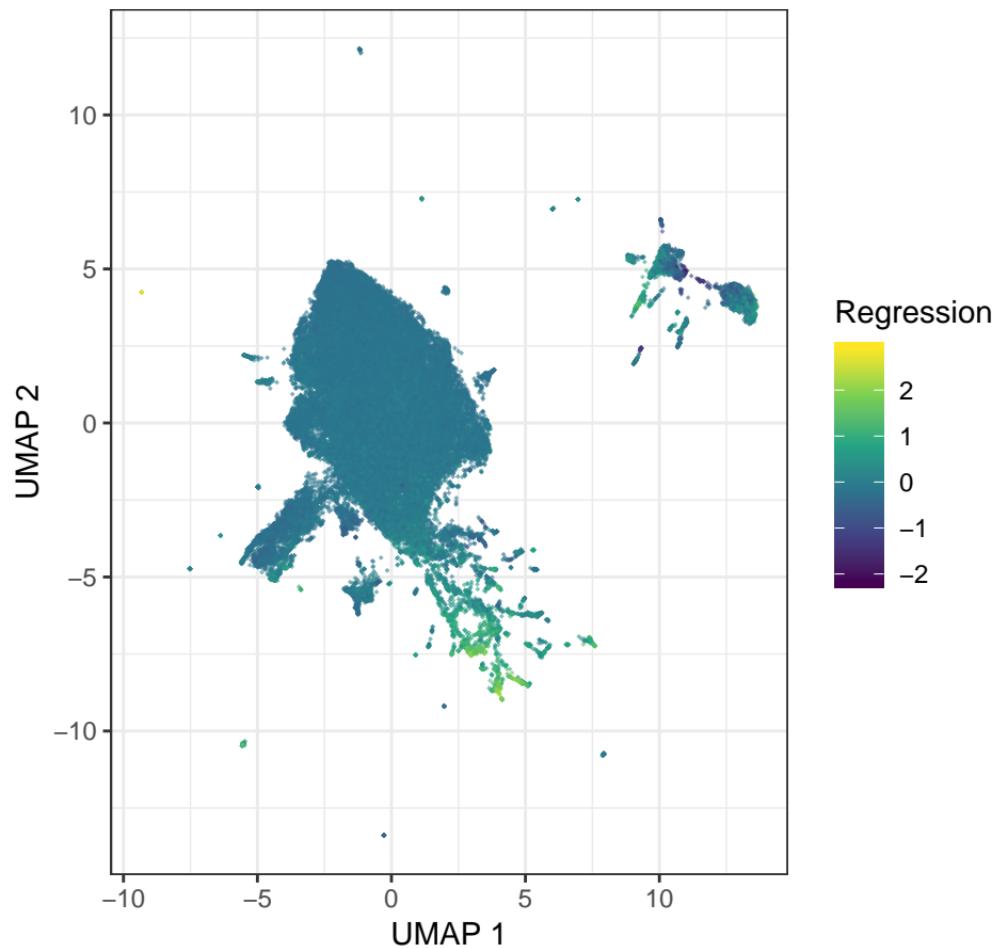
UMAP 2

UMAP 1

Regression

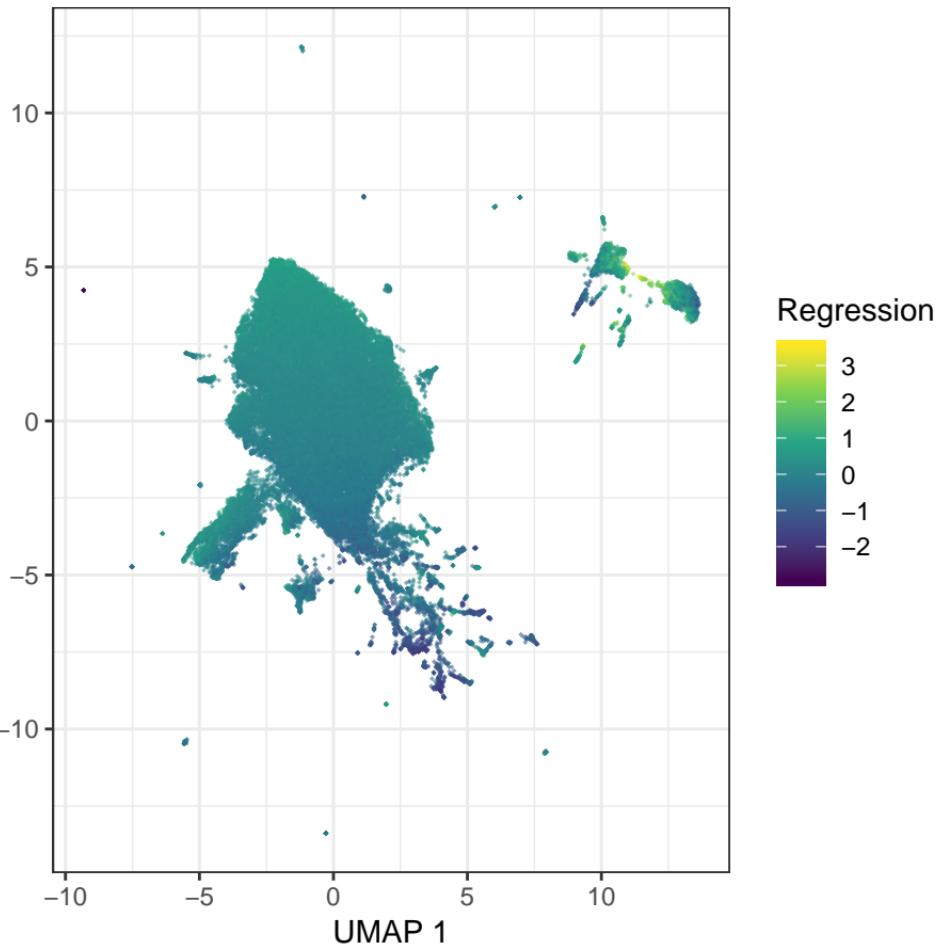


cc_g1_n_spots_per_nucleus_area_mean



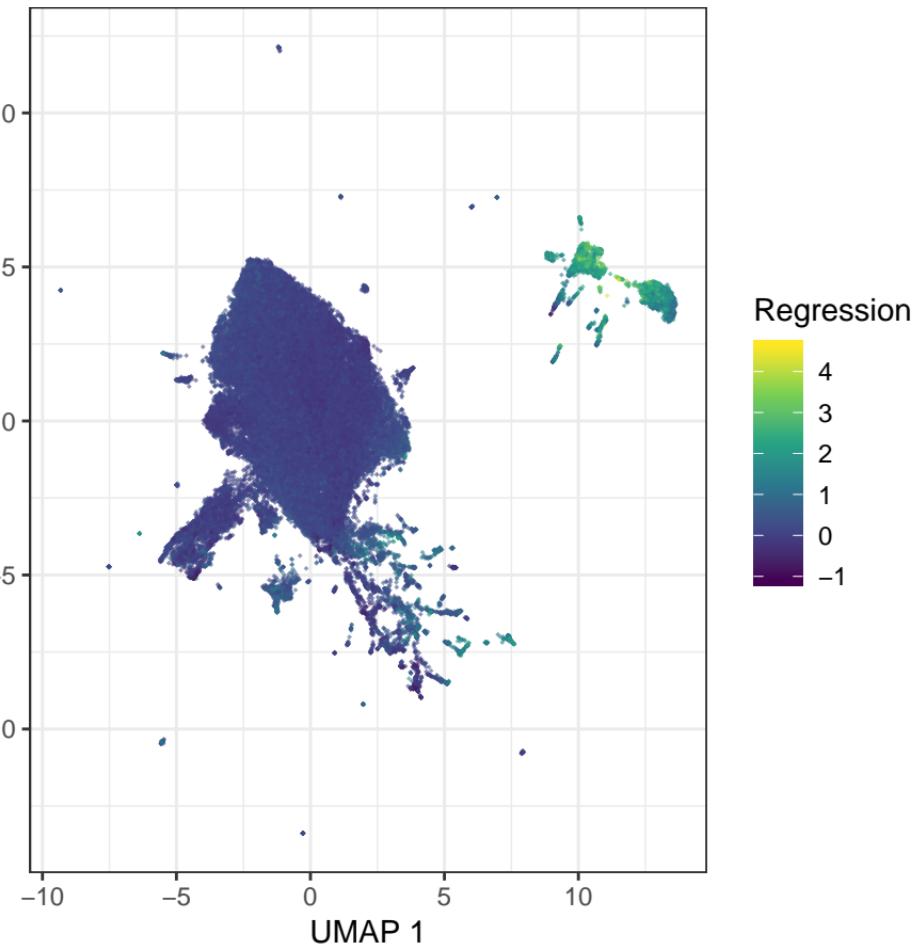
vb_live_cell_roundness

UMAP 2



vb_ros_mean

UMAP 2

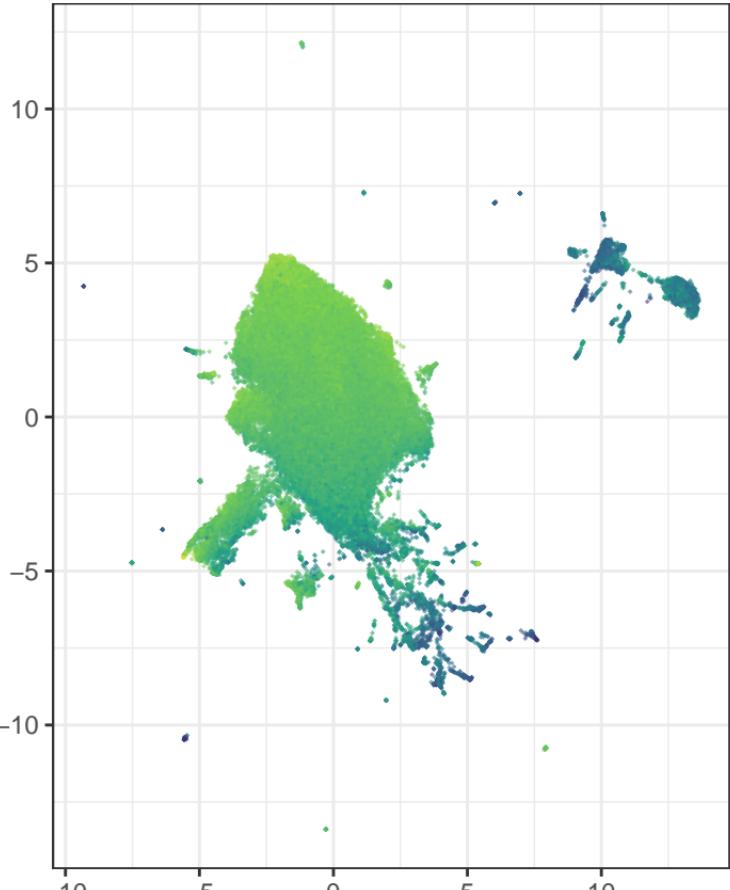
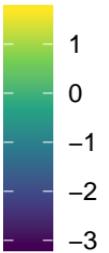


vb_num_live_cells

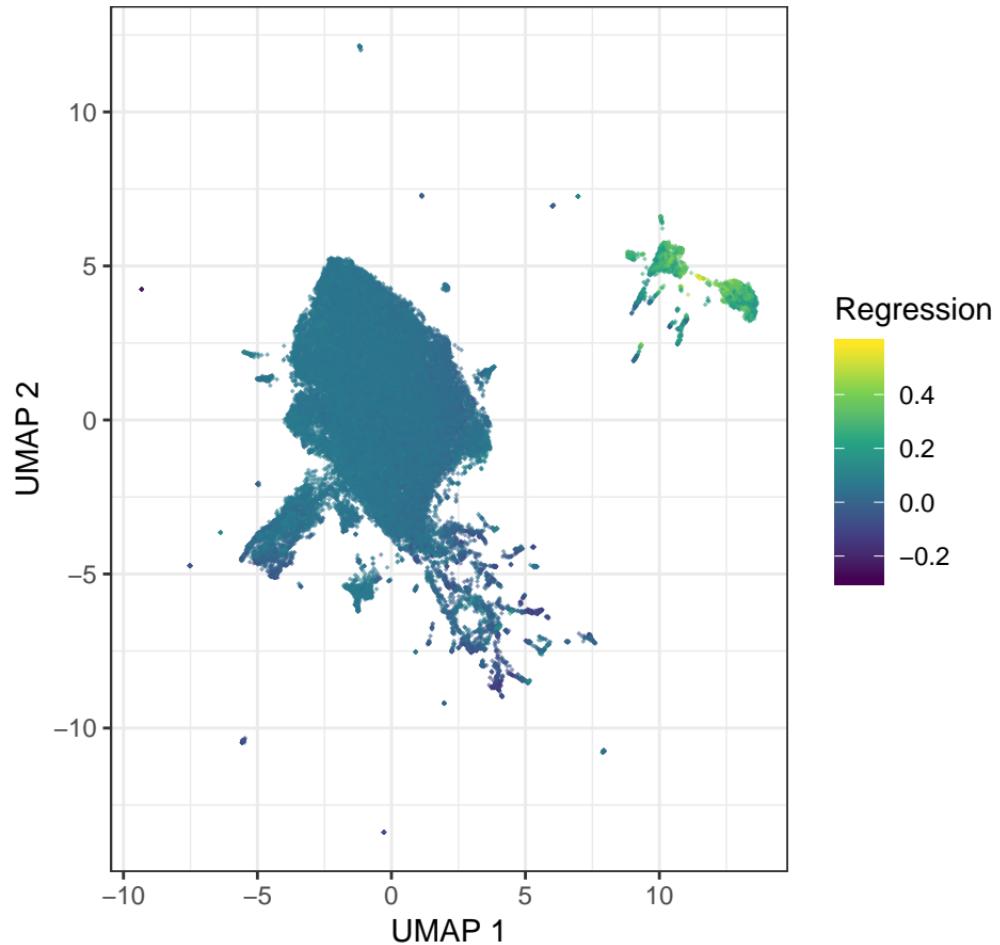
UMAP 2

UMAP 1

Regression



vb_percent_caspase_dead_only



vb_percent_all_early_apoptosis

UMAP 2

10

5

0

-5

-10

-10

-5

0

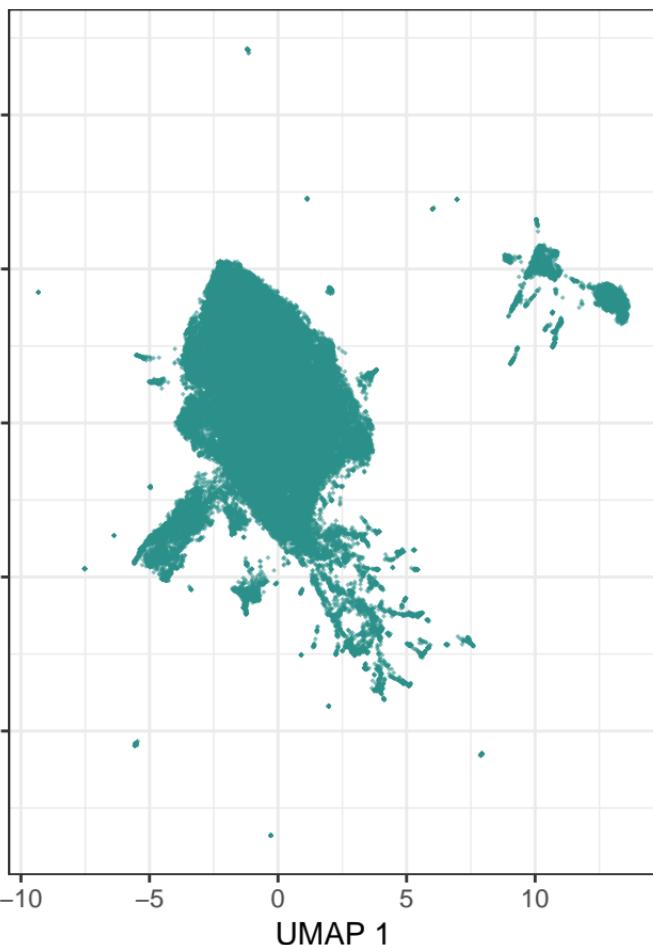
5

10

UMAP 1

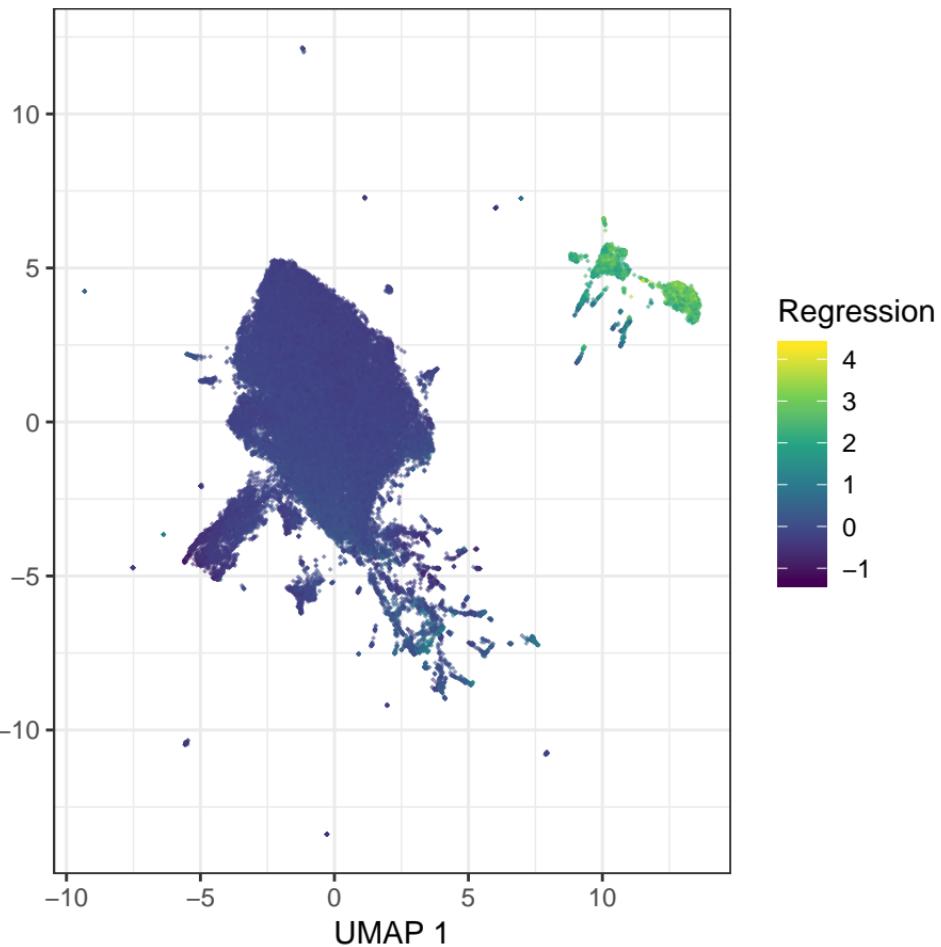
Regression

0.1135548



vb_percent_dead

UMAP 2



vb_live_cell_area

UMAP 2

10

5

0

-5

-10

UMAP 1

Regression

4

2

0

-2

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

-5

0

5

10

-10

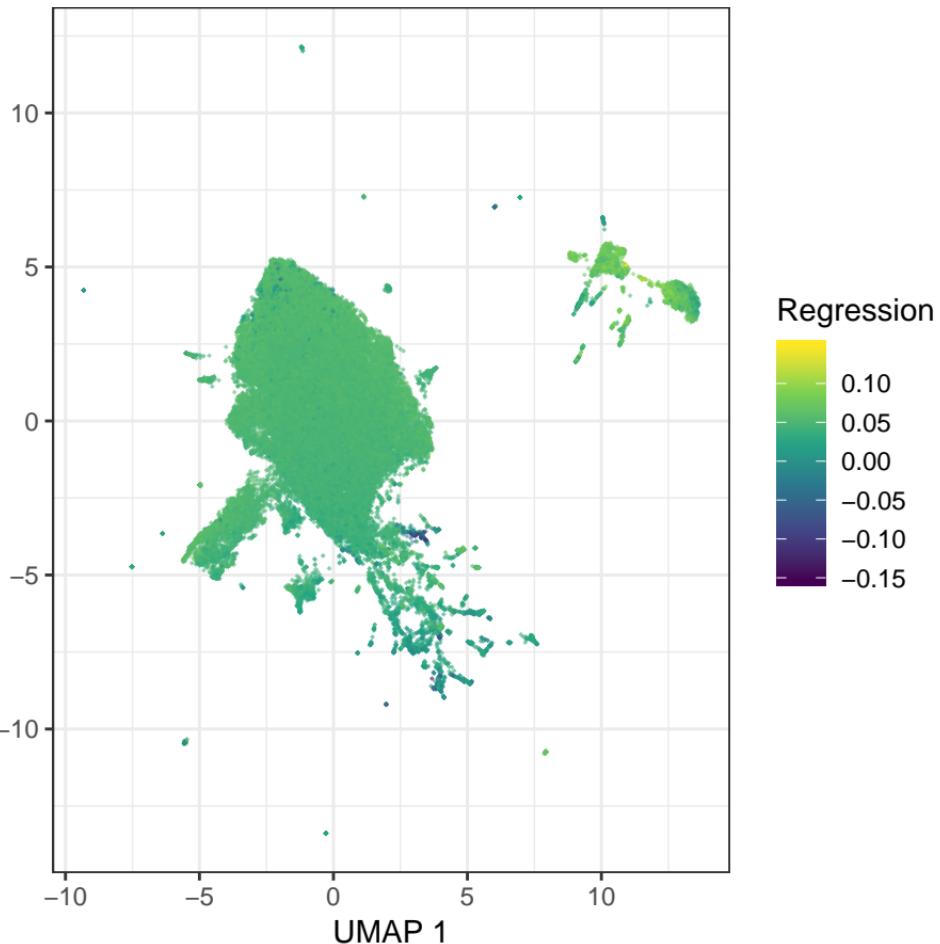
-5

0

<

vb_infection_percentage

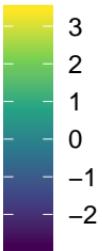
UMAP 2



vb_live_cell_width_length

UMAP 2

Regression



10

5

0

-5

-10

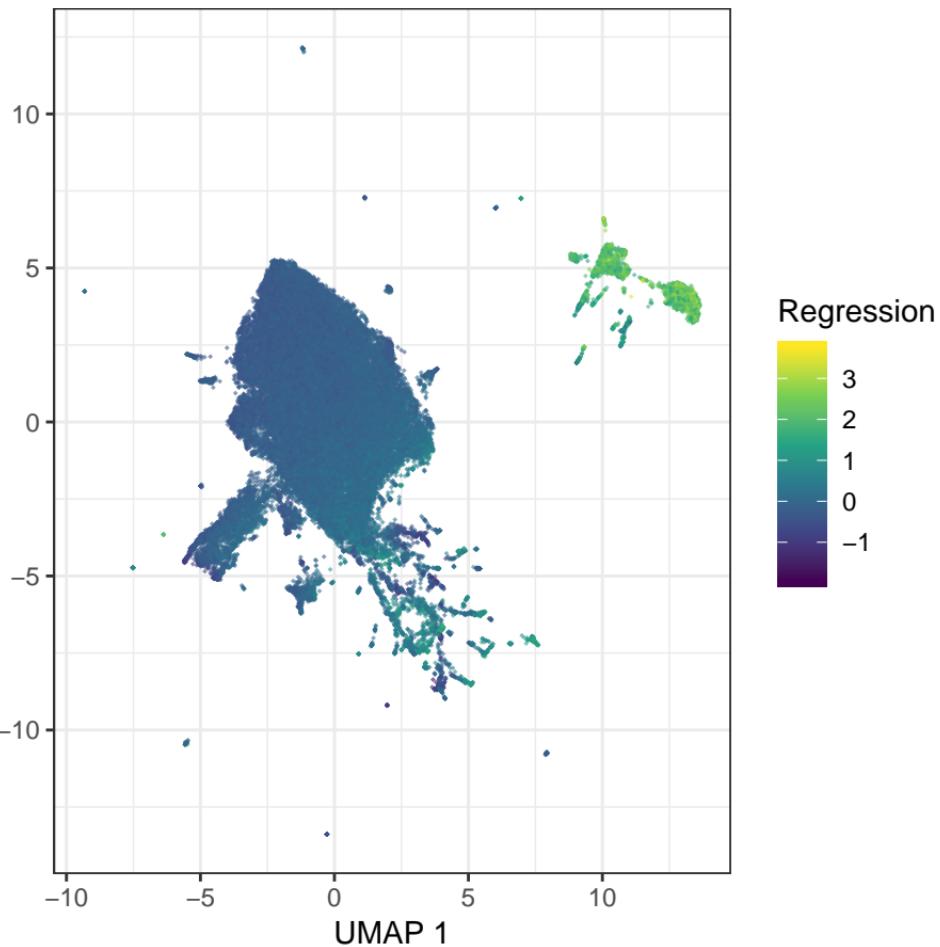
-10

-5

UMAP 1

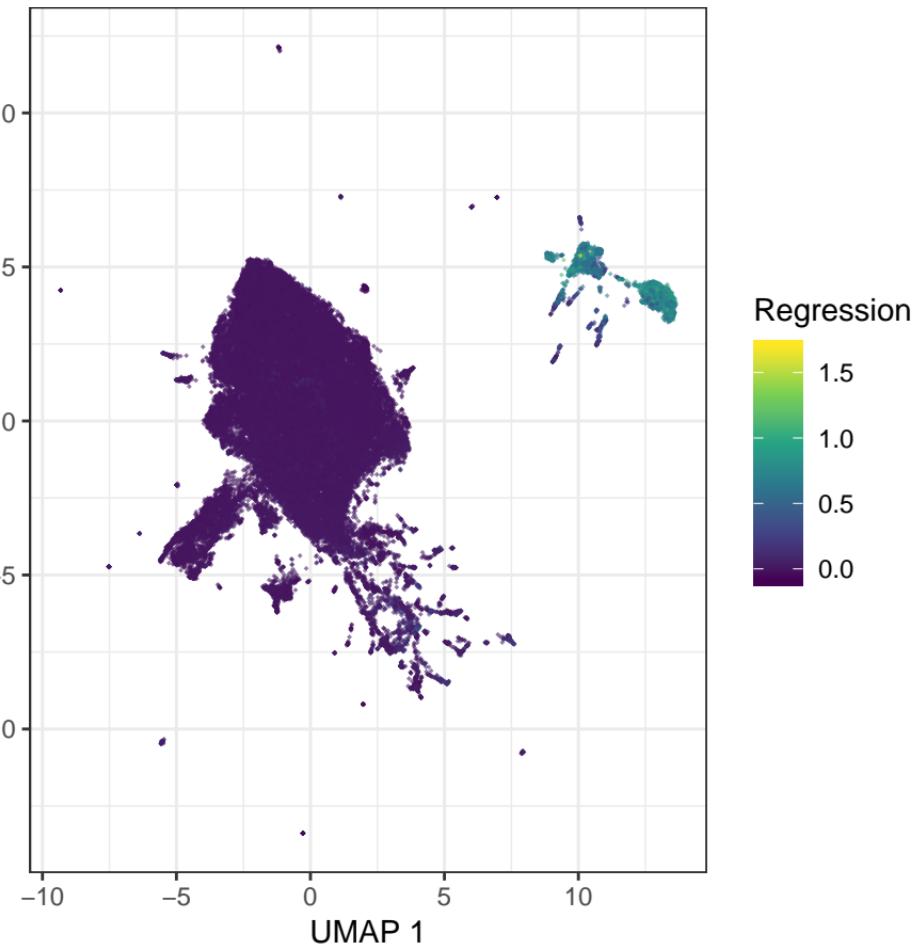
vb_percent_dead_only

UMAP 2



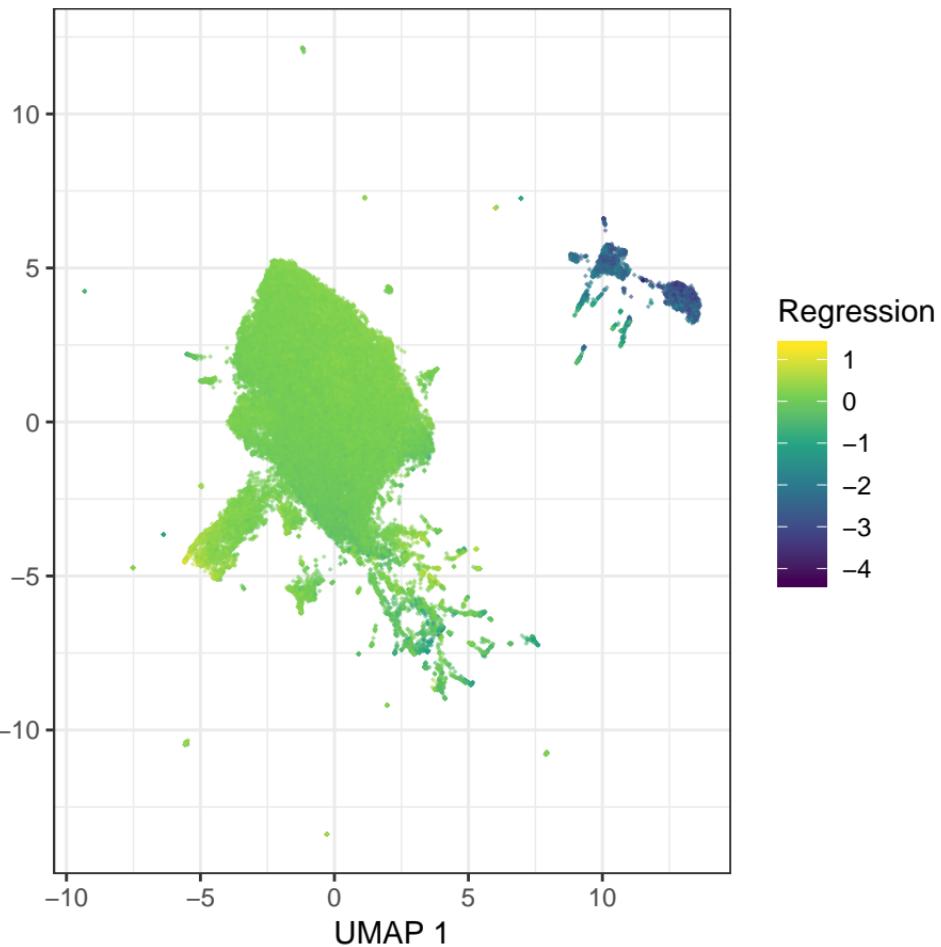
vb_percent_all_late_apoptosis

UMAP 2



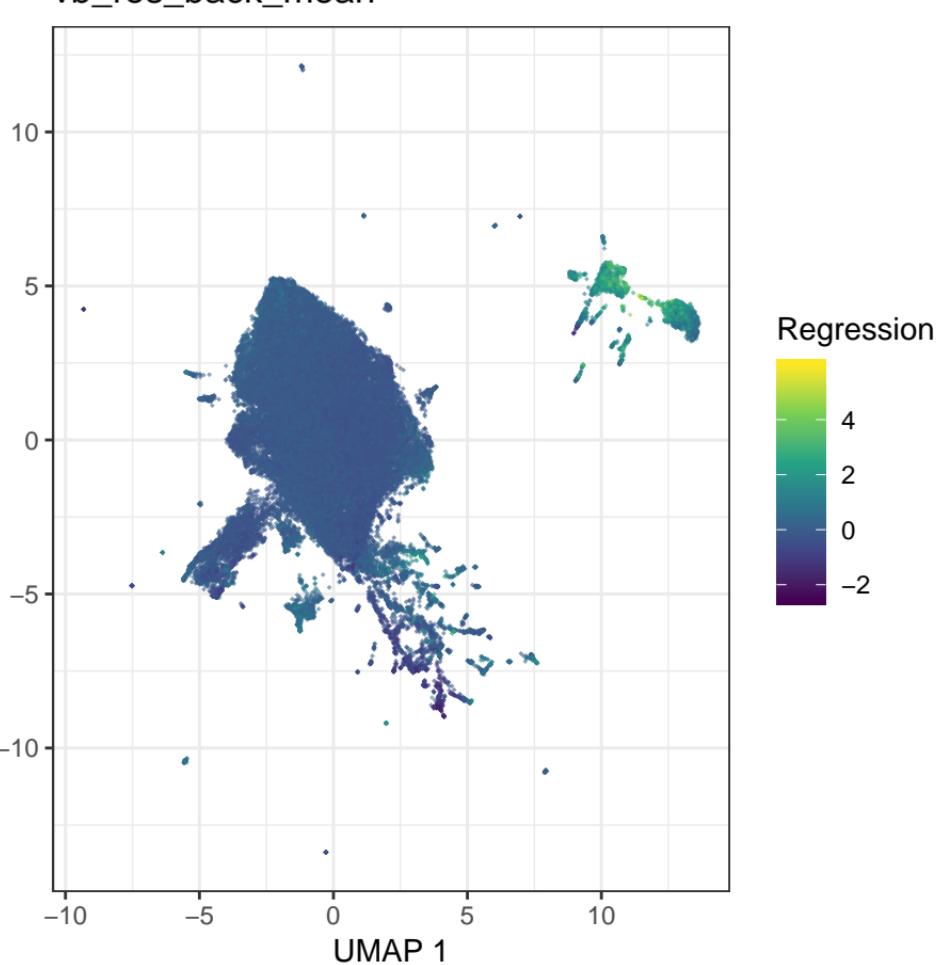
vb_percent_live

UMAP 2



vb_ros_back_mean

UMAP 2



vb_percent_all_apoptosis

UMAP 2

