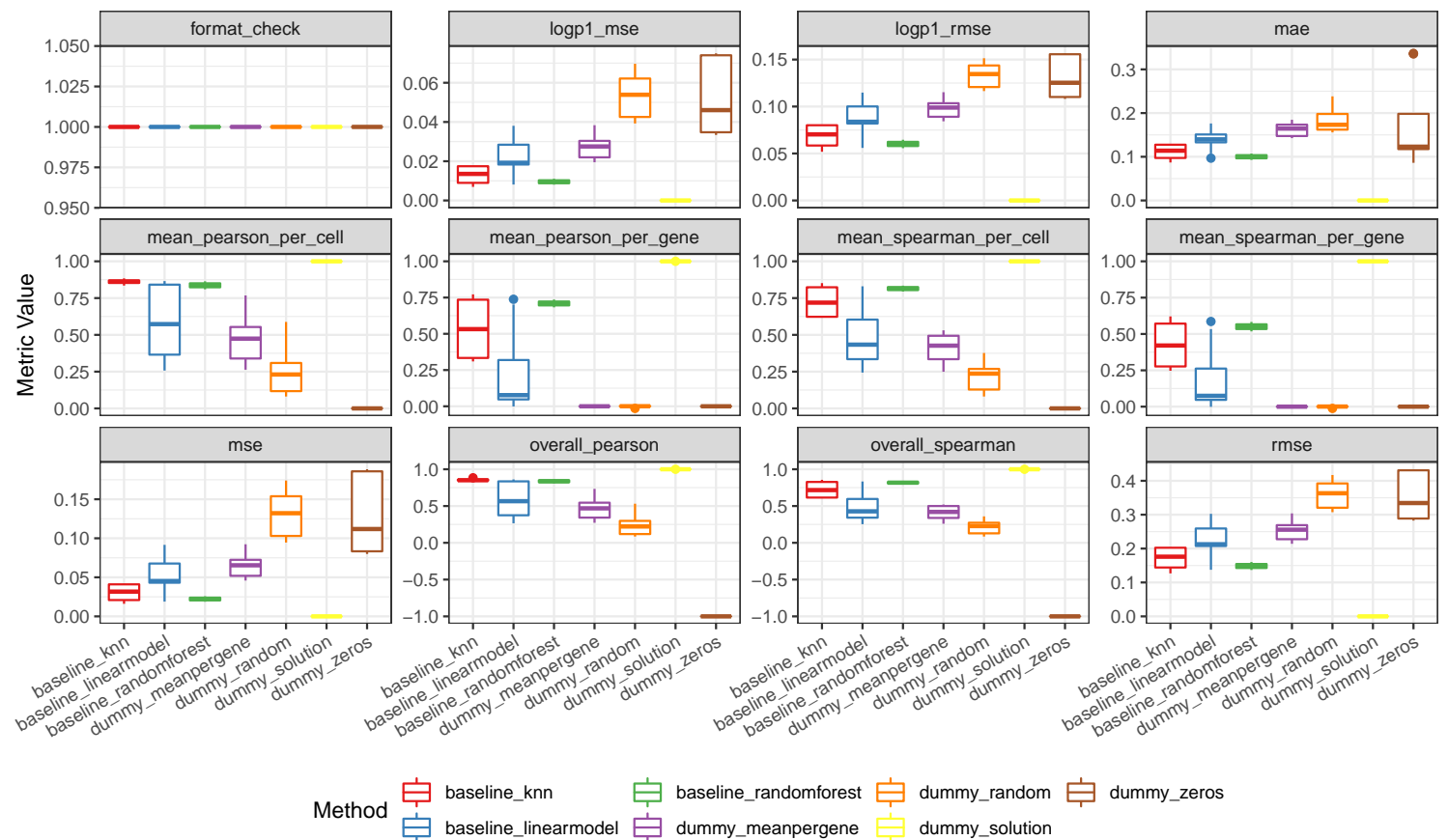
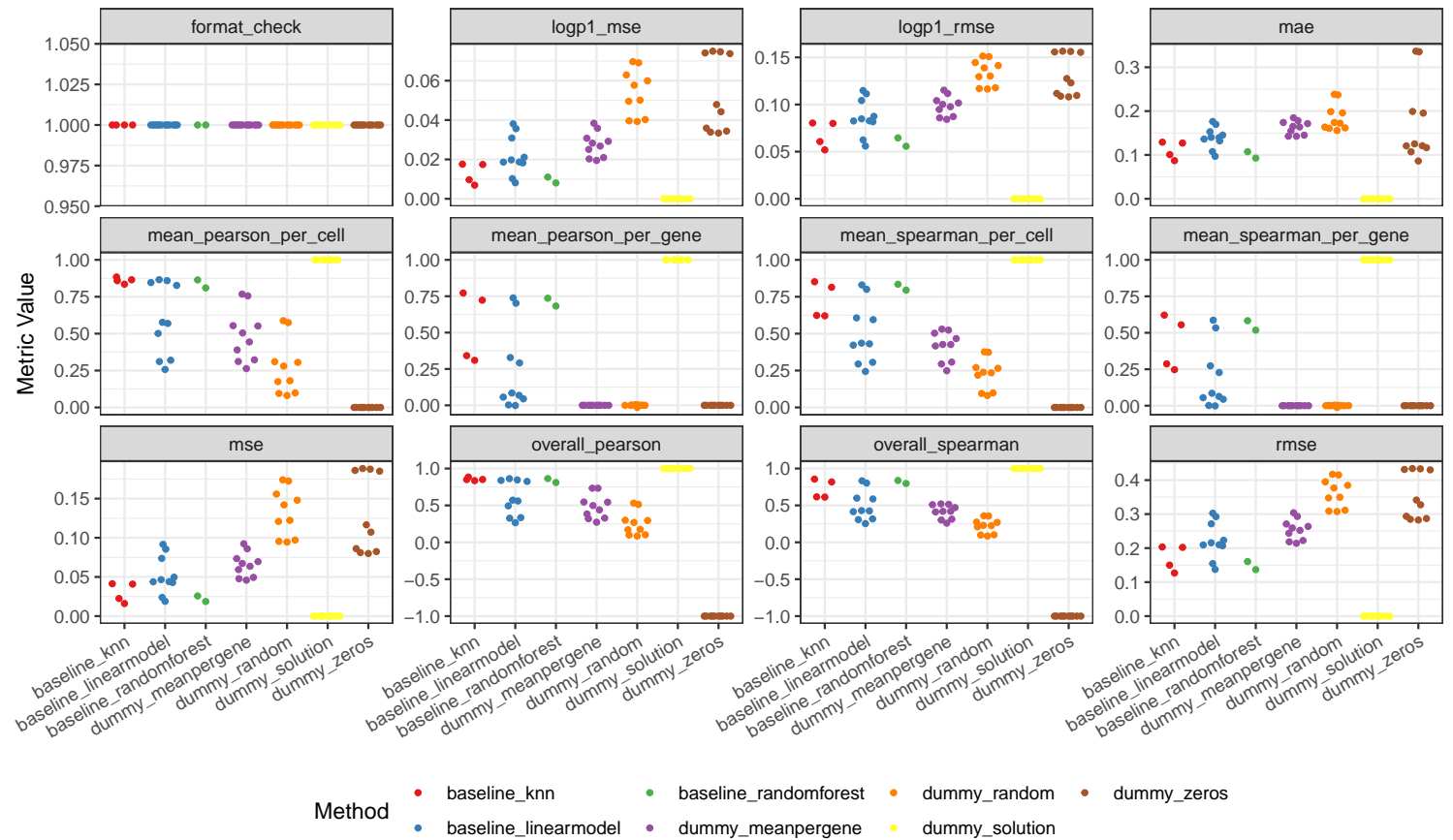


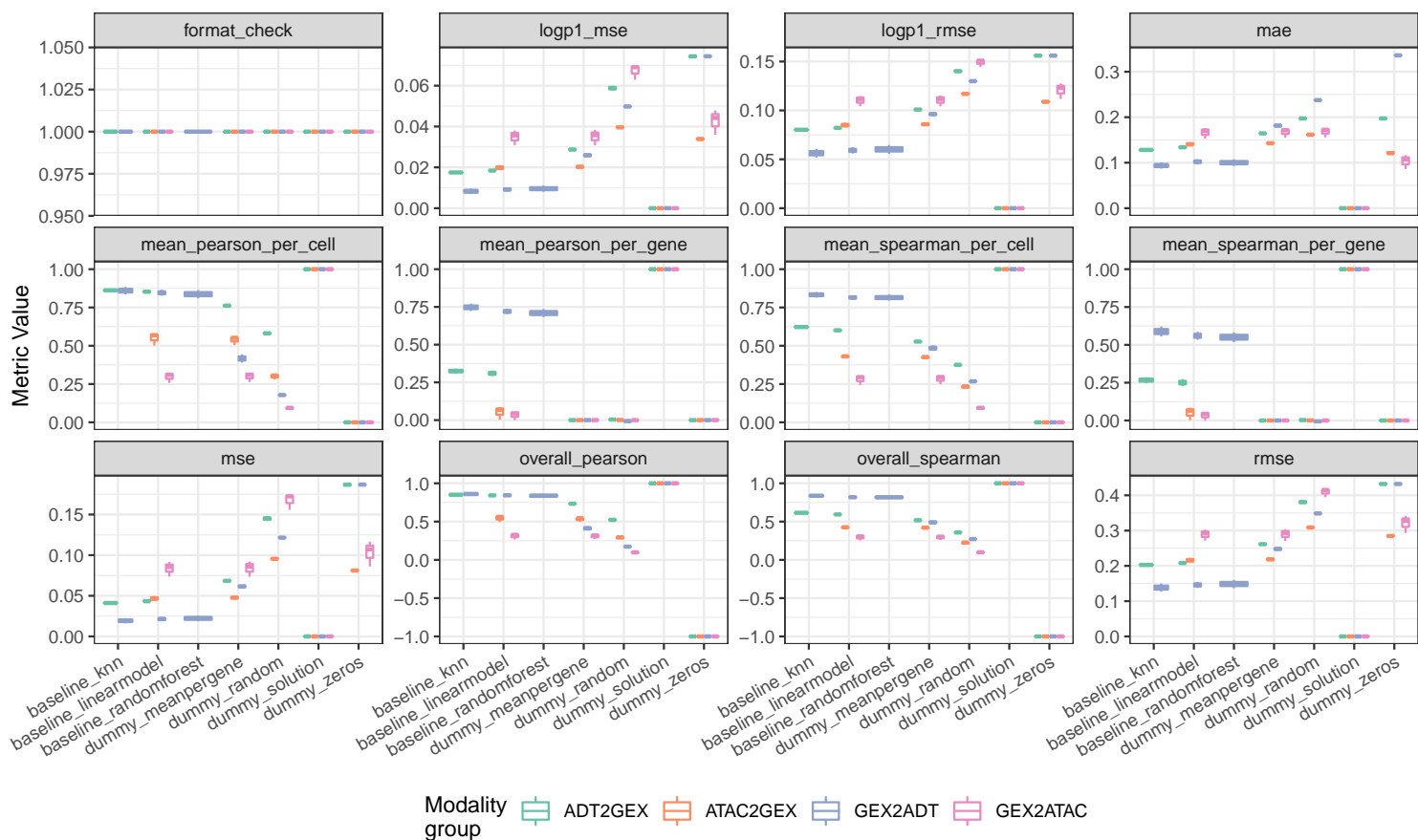
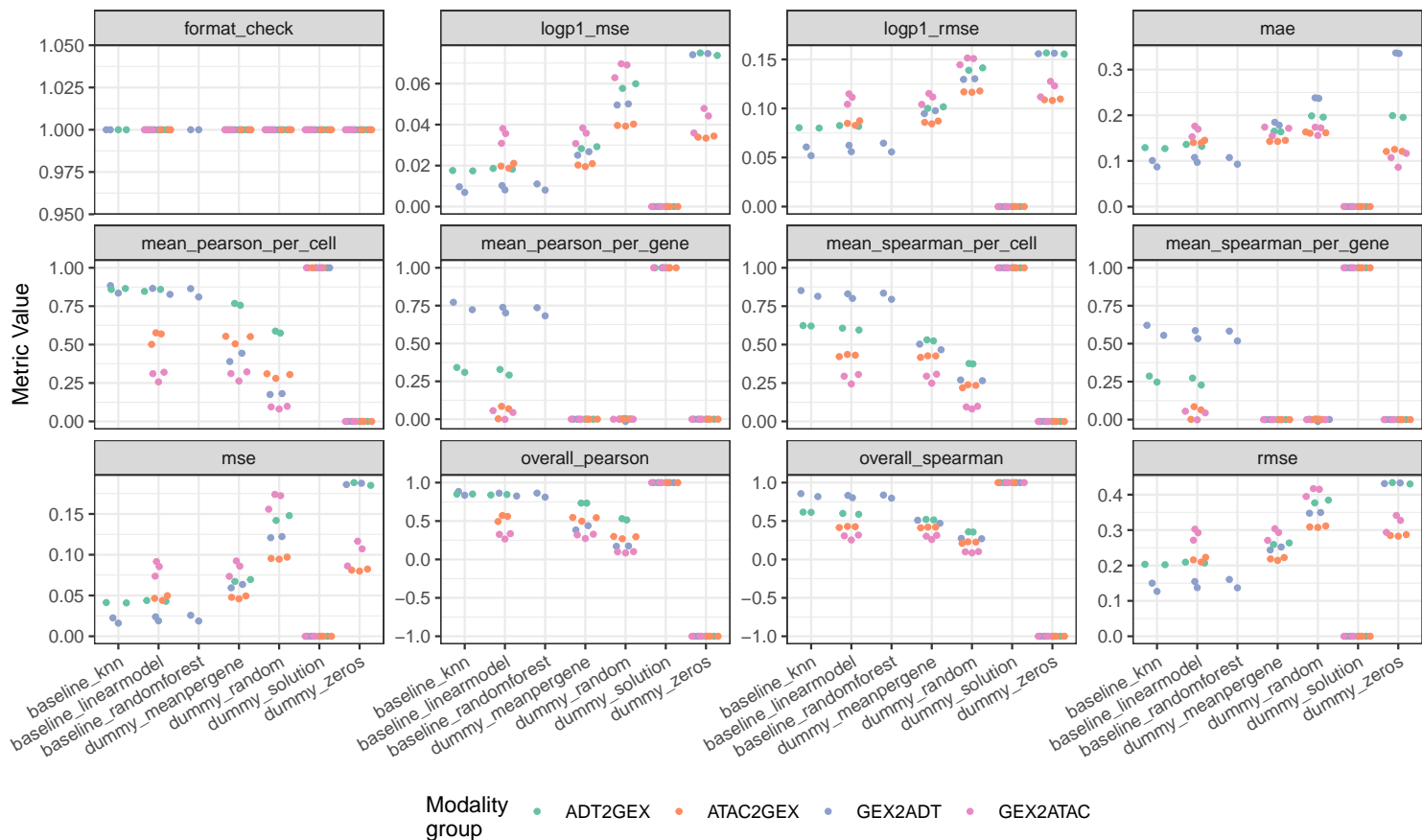
## Predict Modality - Pilot Analysis

## Visualise results

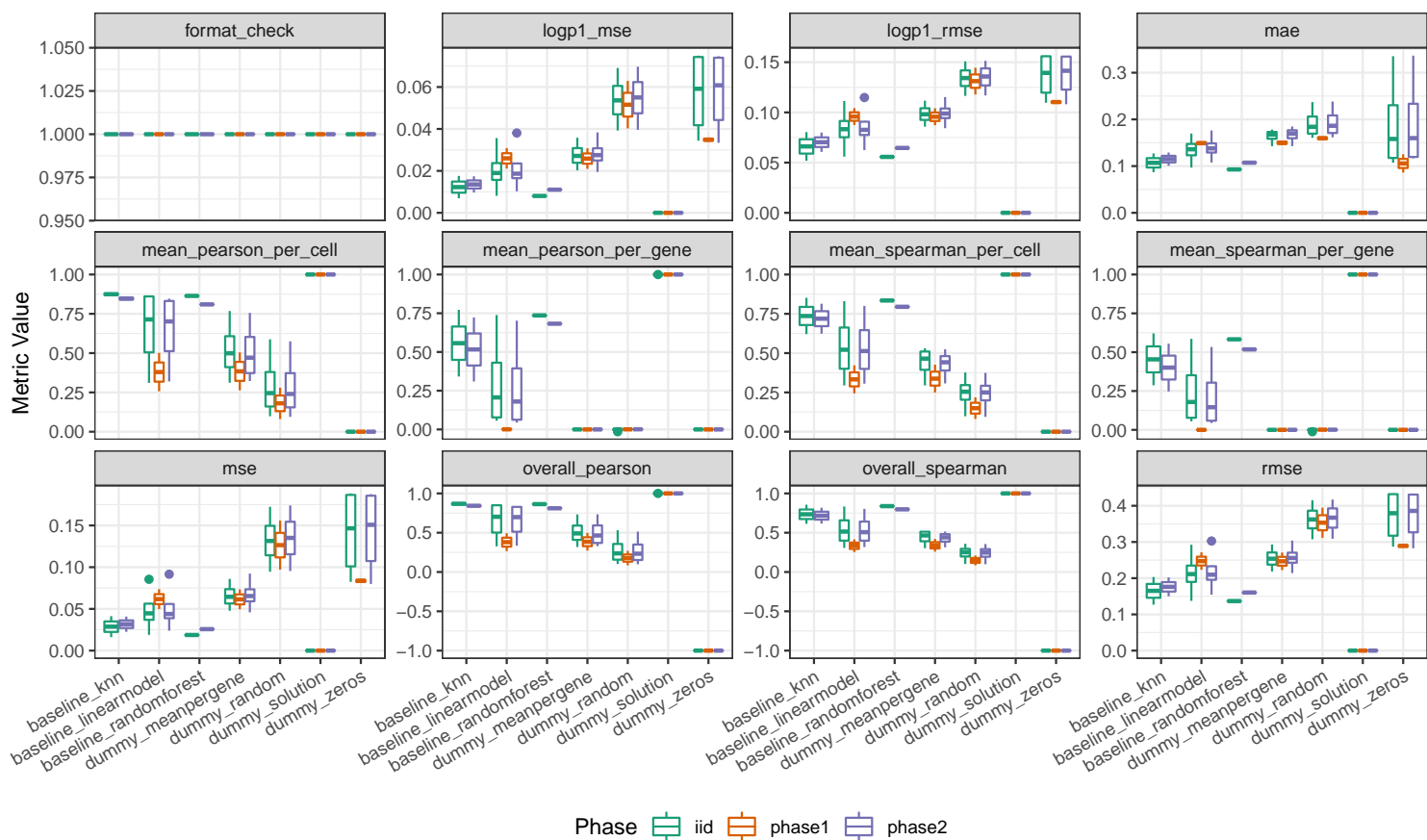
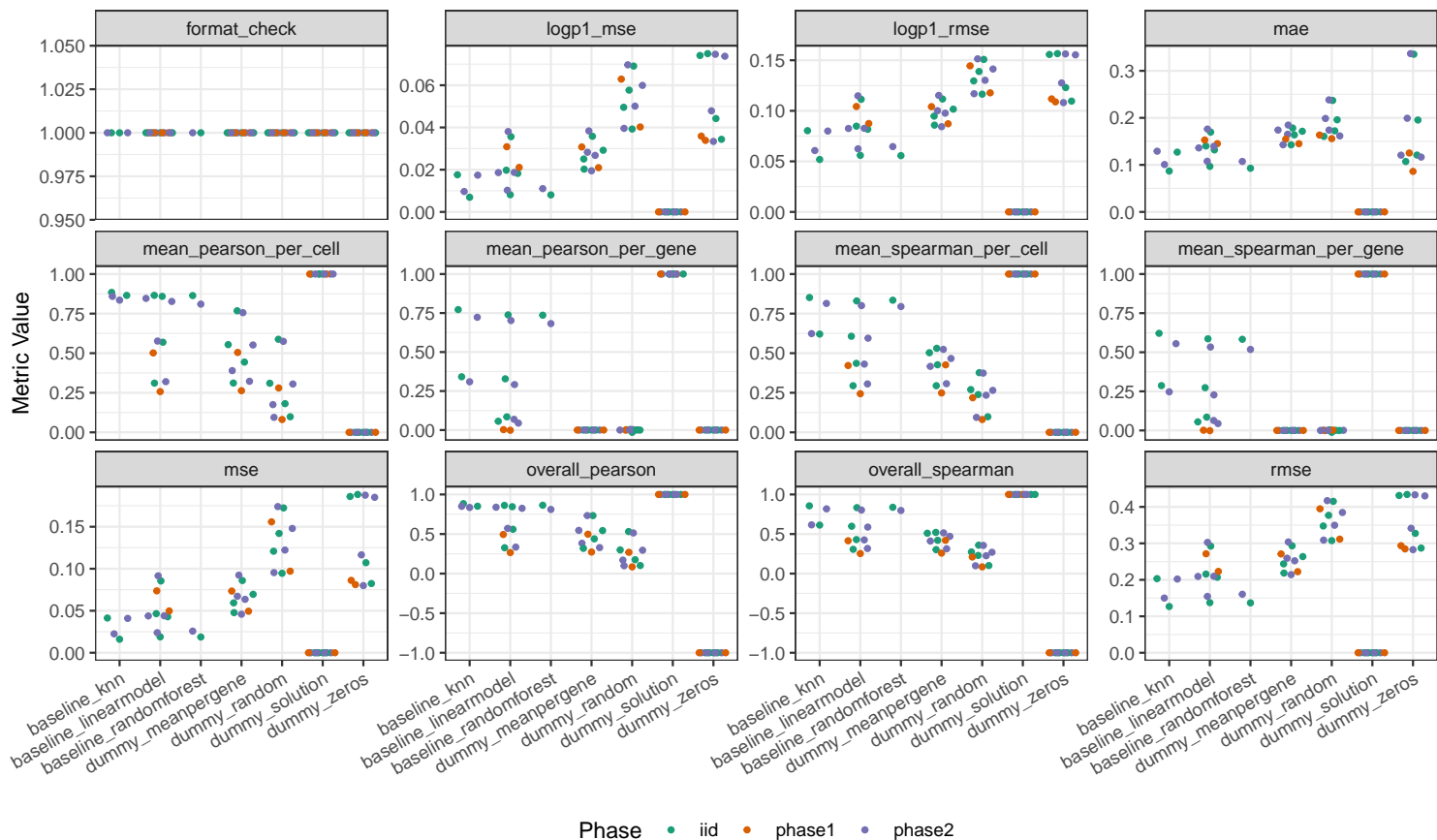
Colour by method.



Colour by modality group.

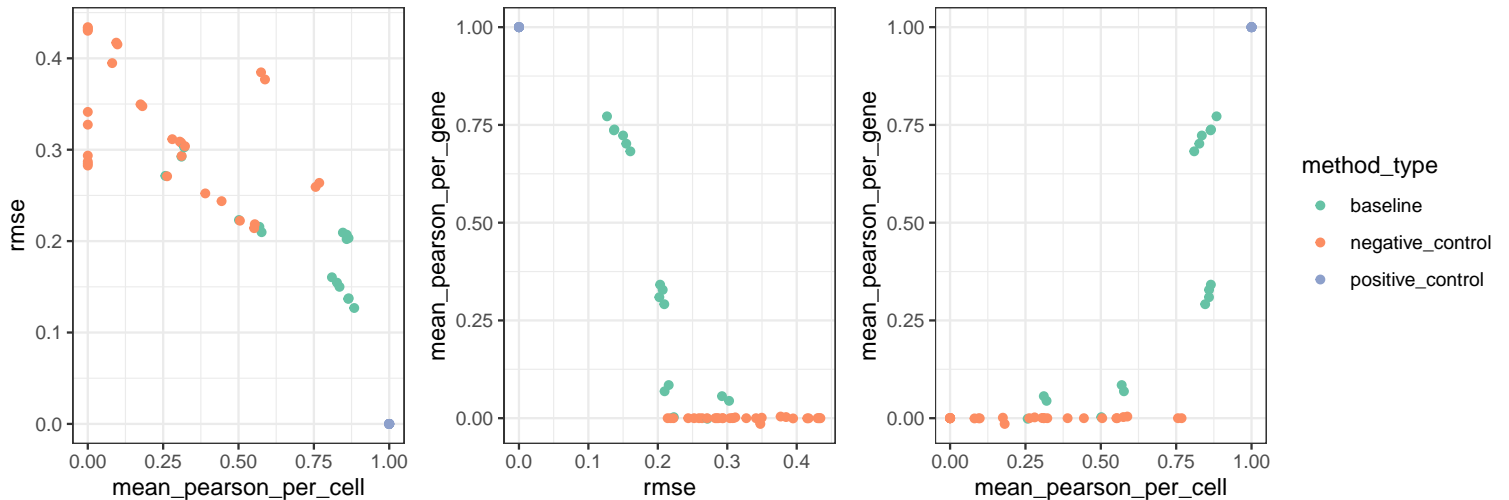


Colour by phase



Comparing most interesting metrics.

```
patchwork::wrap_plots(
  ggplot(df, aes(mean_pearson_per_cell, rmse)) + geom_point(aes(colour = method_type)),
  ggplot(df, aes(rmse, mean_pearson_per_gene)) + geom_point(aes(colour = method_type)),
  ggplot(df, aes(mean_pearson_per_cell, mean_pearson_per_gene)) + geom_point(aes(colour = method_type)),
  nrow = 1,
  guides = "collect"
) & theme_bw() & scale_colour_brewer(palette = "Set2")
```



```
ggplot(dfg %>% filter(metric_id %in% c("mean_spearman_per_cell", "mean_spearman_per_gene", "rmse"))) +
  geom_histogram(aes(value, fill = method_type)) +
  facet_grid(method_type~metric_id, scales = "free_x") +
  theme_bw()
```

## 'stat\_bin()' using 'bins = 30'. Pick better value with 'binwidth'.

