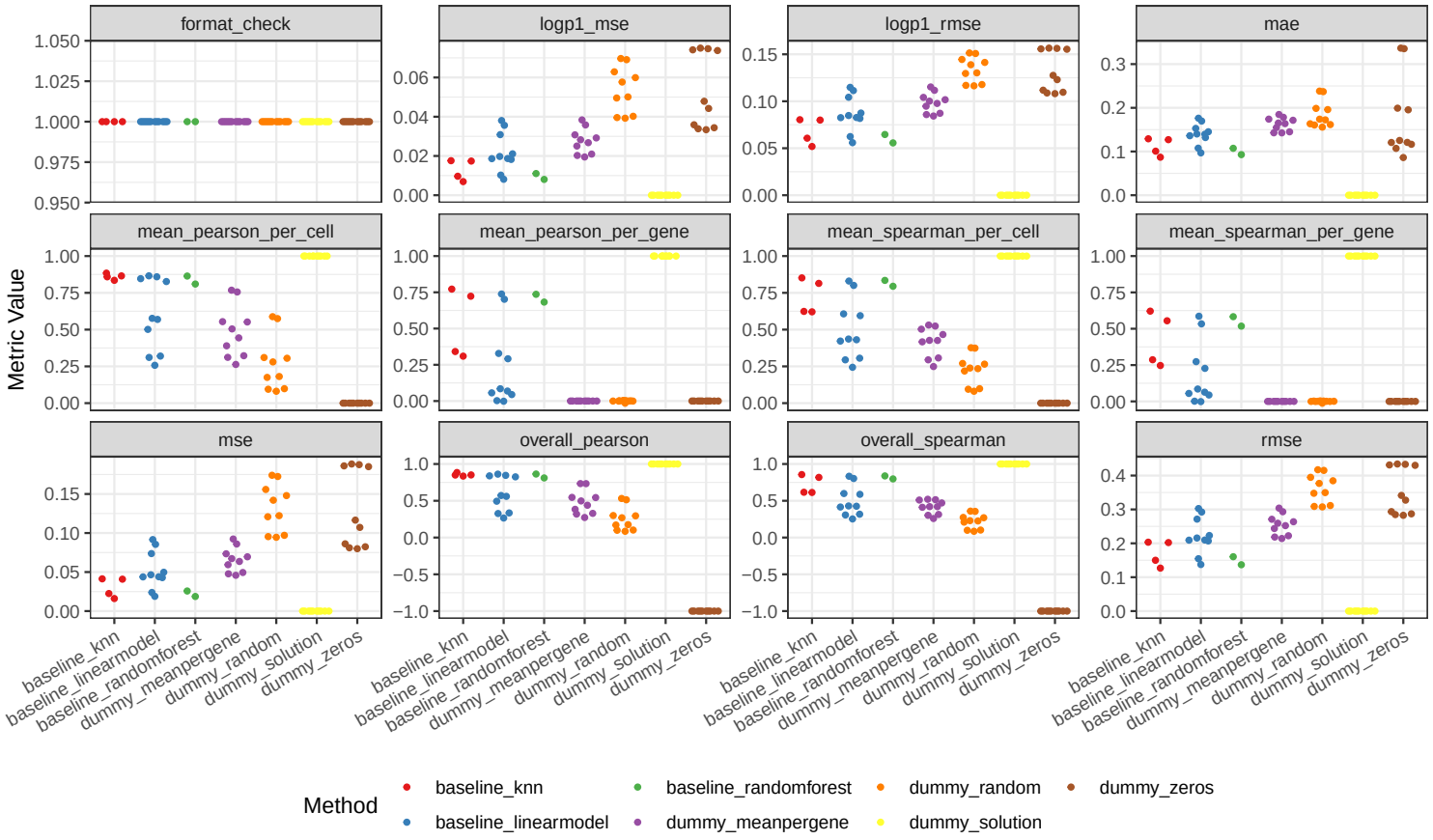
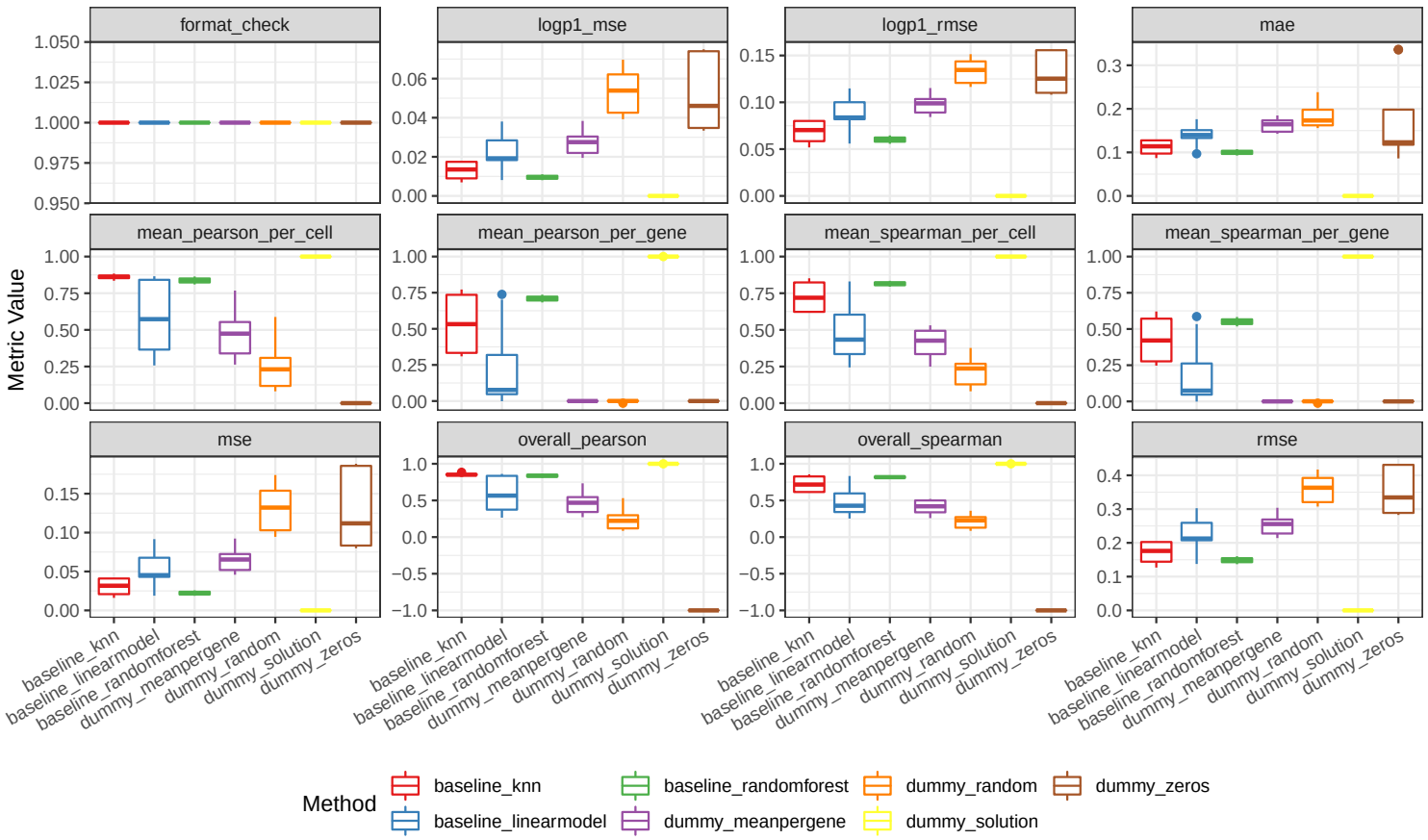
Predict Modality - Pilot Analysis

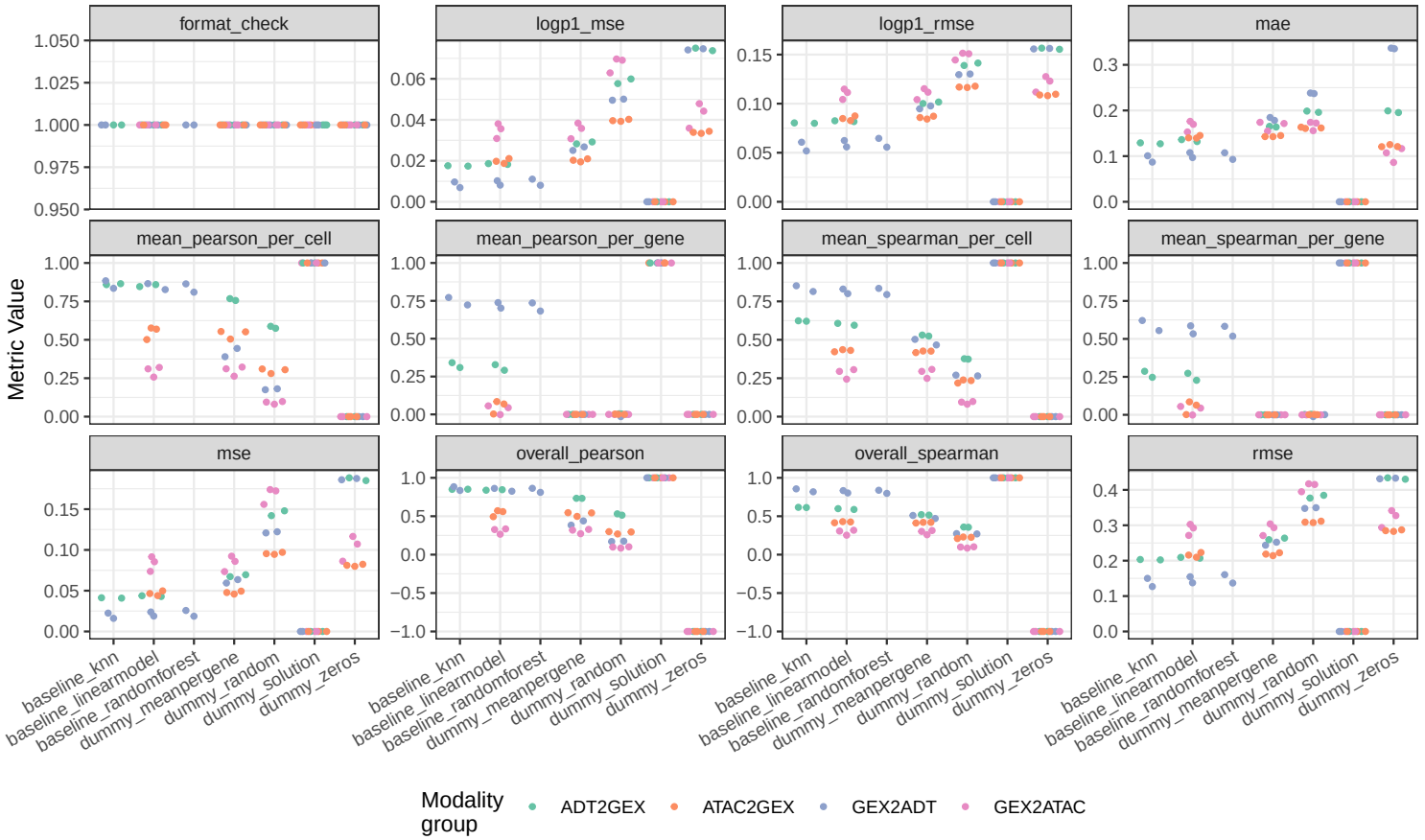
Visualise results

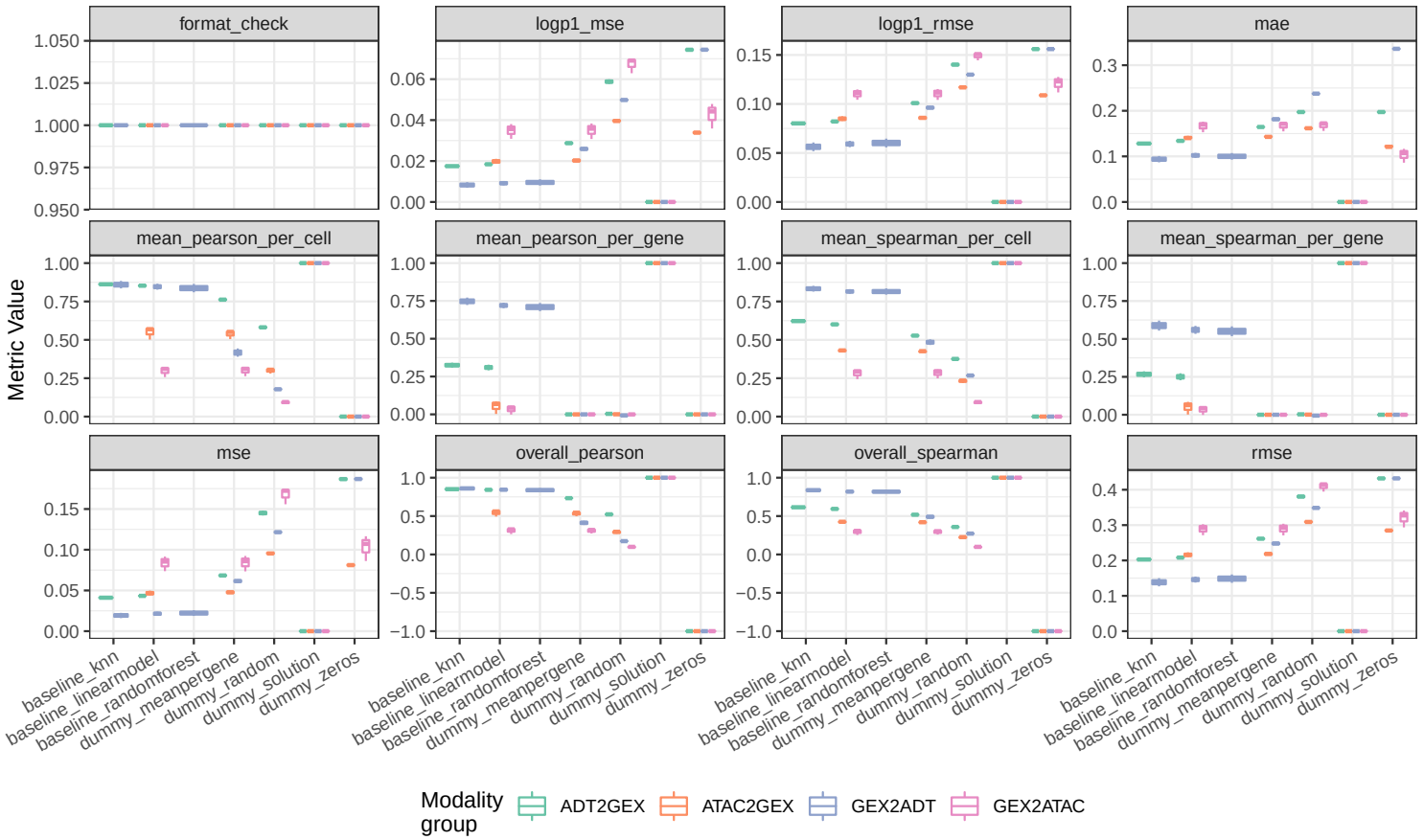
Colour by method.



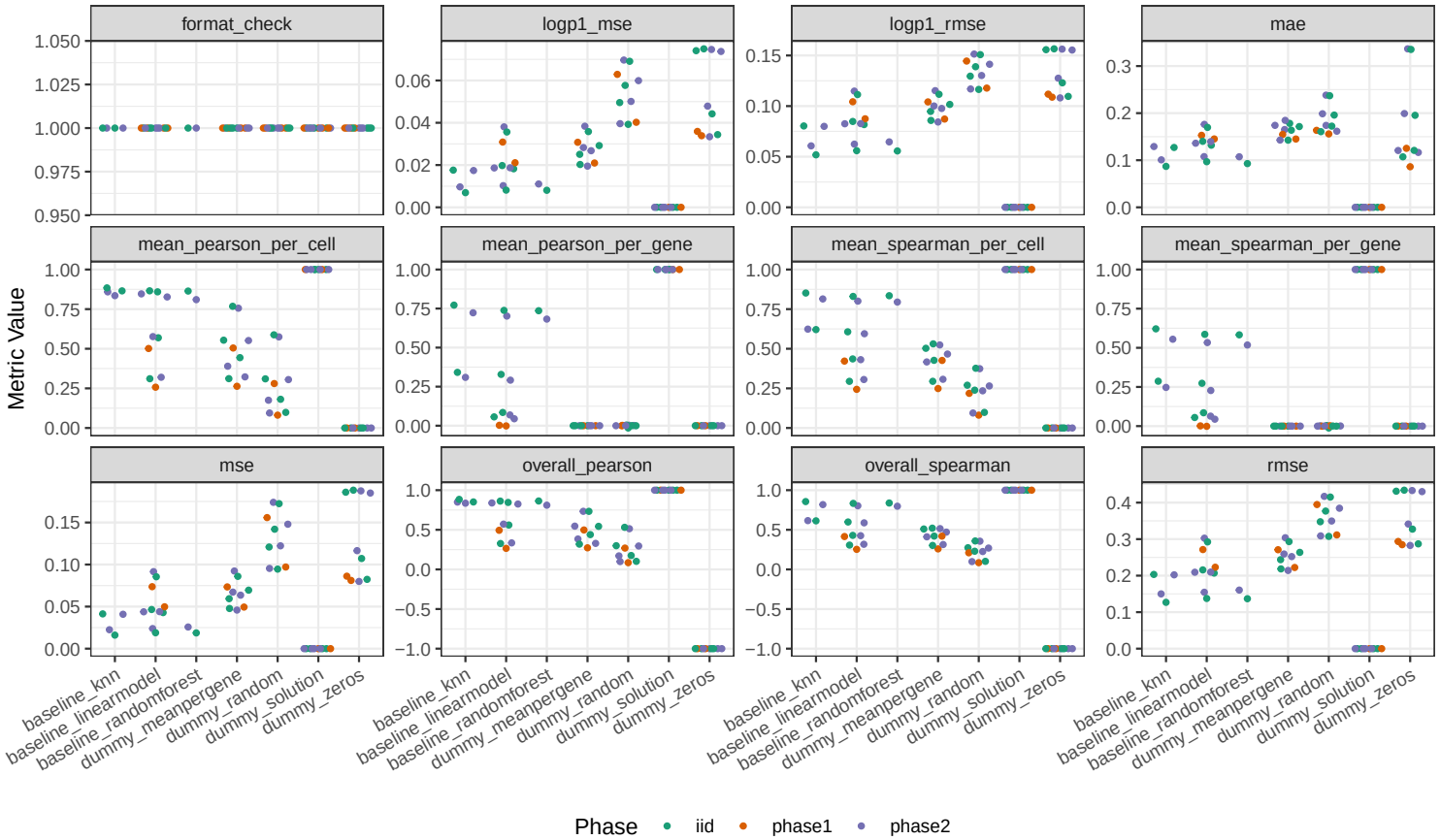


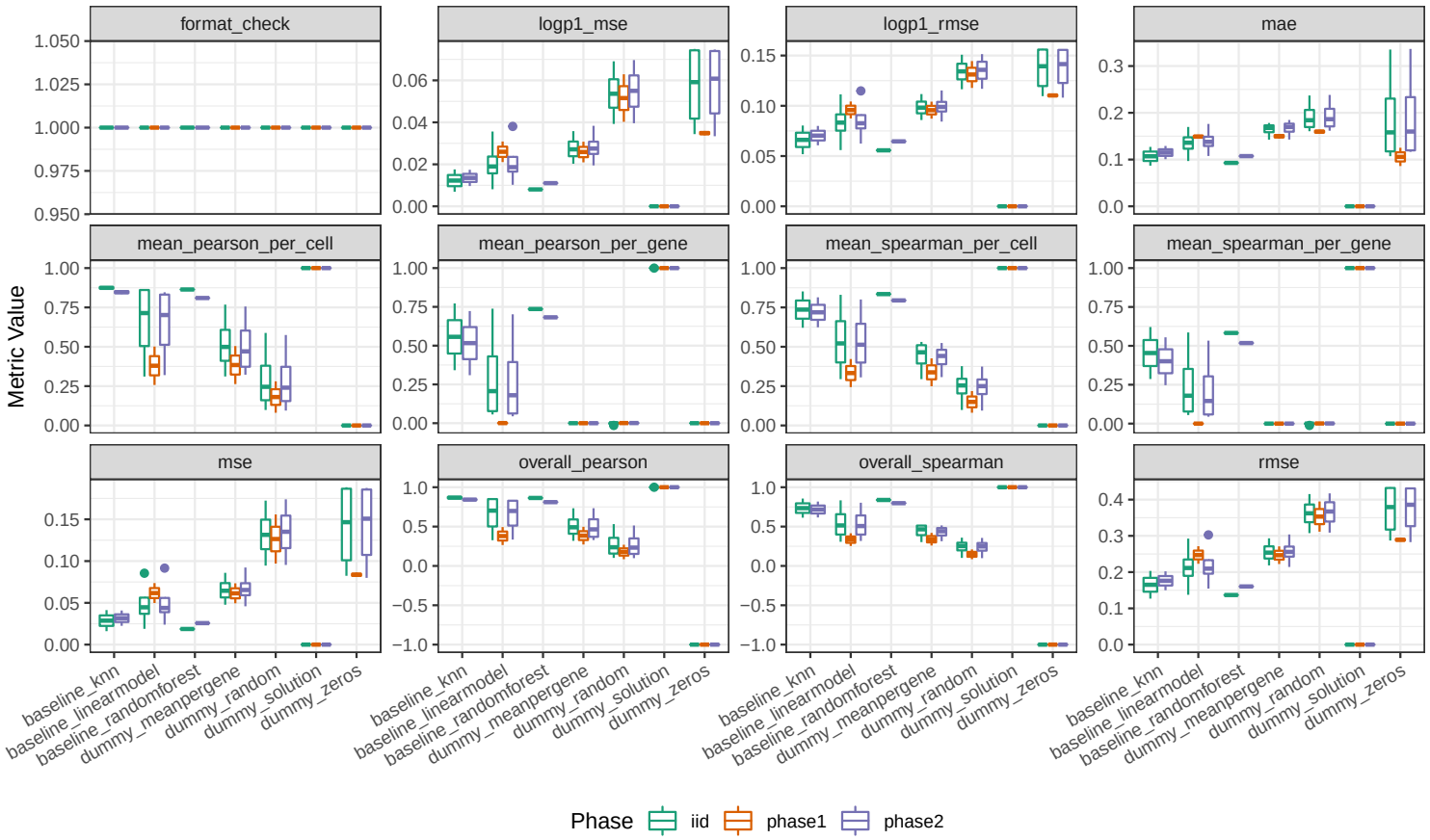
Colour by modality group.





Colour by phase





Comparing most interesting metrics.

```
selected_metrics <- c("rmse", "mae", "mean_spearman_per_cell", "mean_spearman_per_gene")

plots <-
  crossing(x = selected_metrics, y = selected_metrics) %>%
  filter(x > y) %>%
  pmap(function(x, y) {
    ggplot(df, aes_string(x, y)) + geom_point(aes(colour = method_type)) + labs(x = x, y = y)
  })
GGally::ggpairs(
  df,
  mapping = aes(colour = method_type, fill = method_type),
  columns = selected_metrics,
  diag = list(continuous = "barDiag", discrete = "barDiag", na = "naDiag")
) & theme_bw() &
  scale_colour_brewer(palette = "Set2") &
  scale_fill_brewer(palette = "Set2")
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
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```

rmse
mae
mean_spearman_per_cell
mean_spearman_per_gene
Corr: 0.892***
baseline: 0.987***
negative_control: 0.563**
positive_control: NA
Corr: −0.925***
baseline: −0.954***
negative_control: −0.597***
positive_control: NA
Corr: −0.911***
baseline: −0.901***
negative_control: −0.019
positive_control: NA
Corr: −0.752***
baseline: −0.956***
negative_control: −0.021
positive_control: NA
Corr: −0.843***
baseline: −0.936***
negative_control: −0.153
positive_control: NA
Corr: 0.894***
baseline: 0.969***
negative_control: 0.036
positive_control: NA
10.0
7.5
5.0
2.5
0.0
0.3
0.2
0.1
0.0
1.00
0.75
0.50
0.25
0.00
0.0
0.1
0.2
0.3
0.4
0.00
0.25
0.50
0.75
1.00