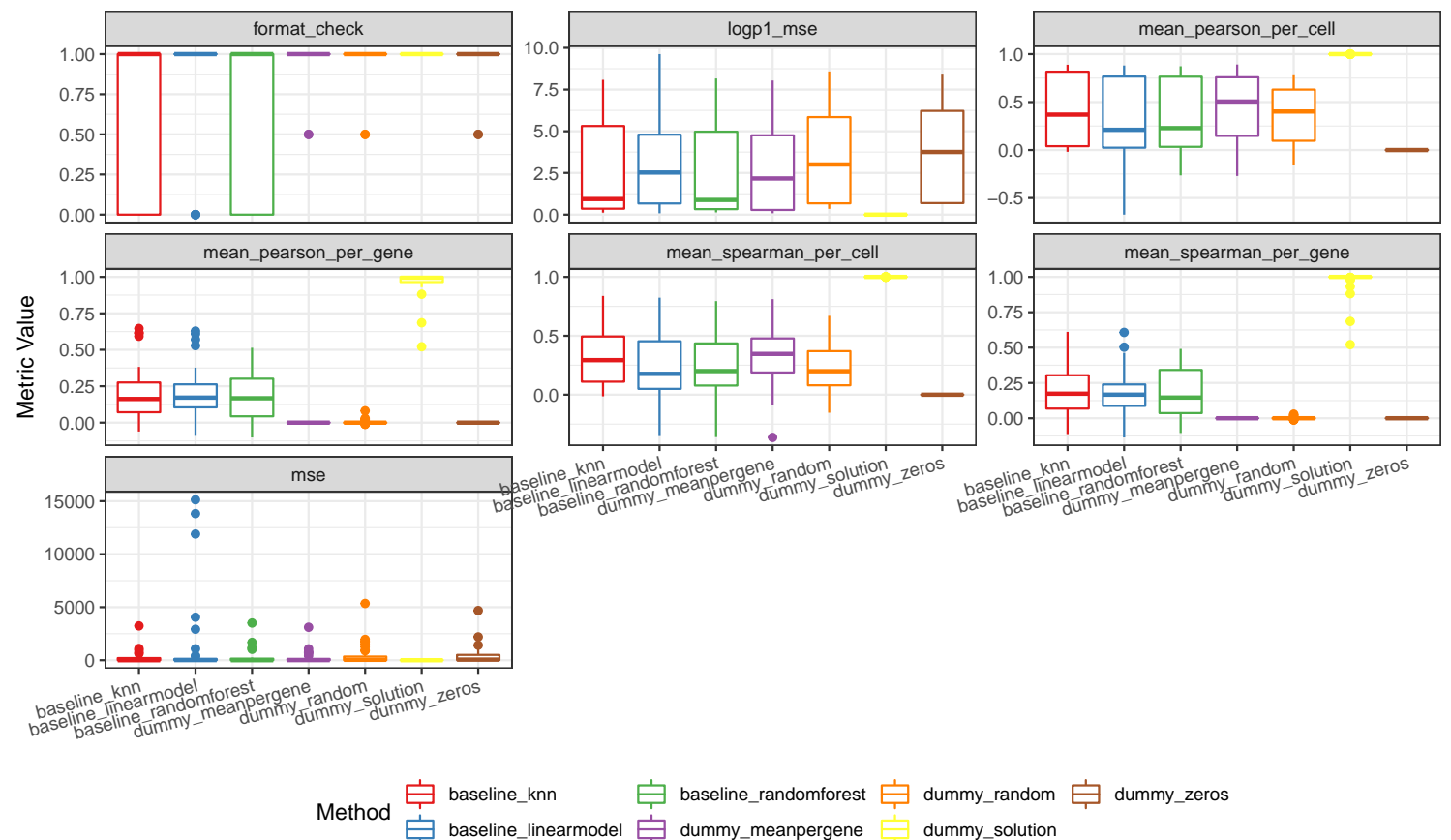
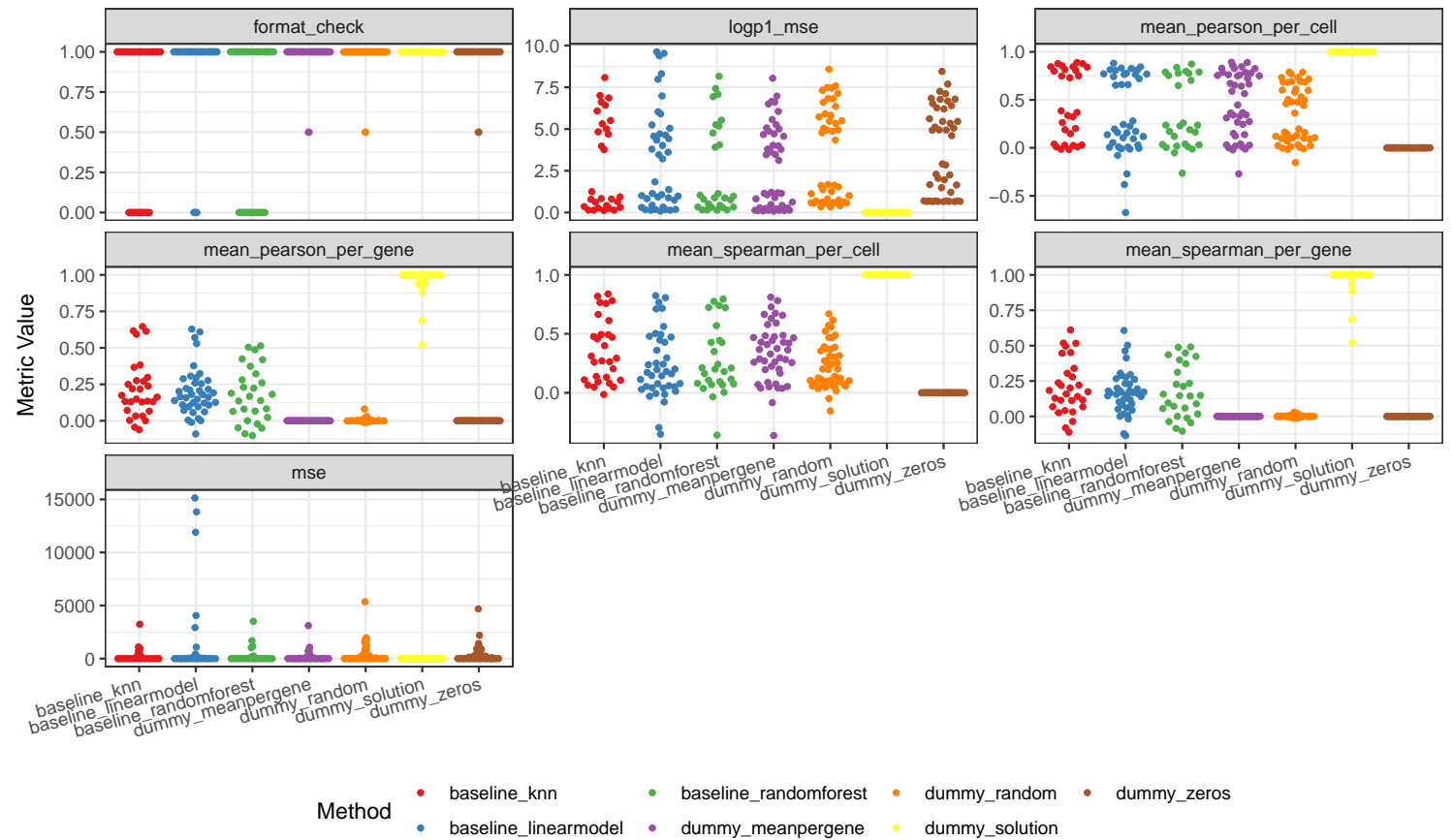


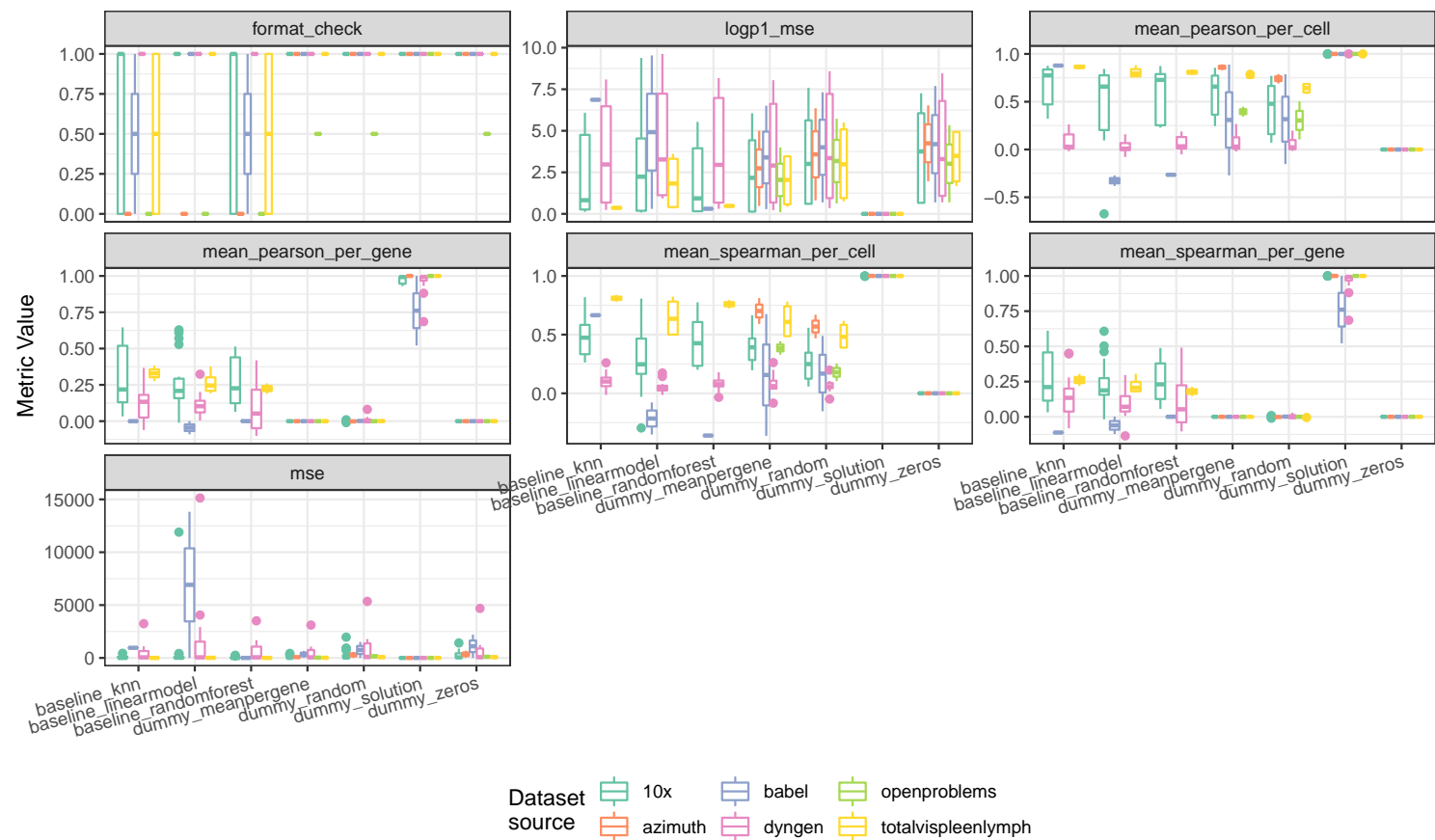
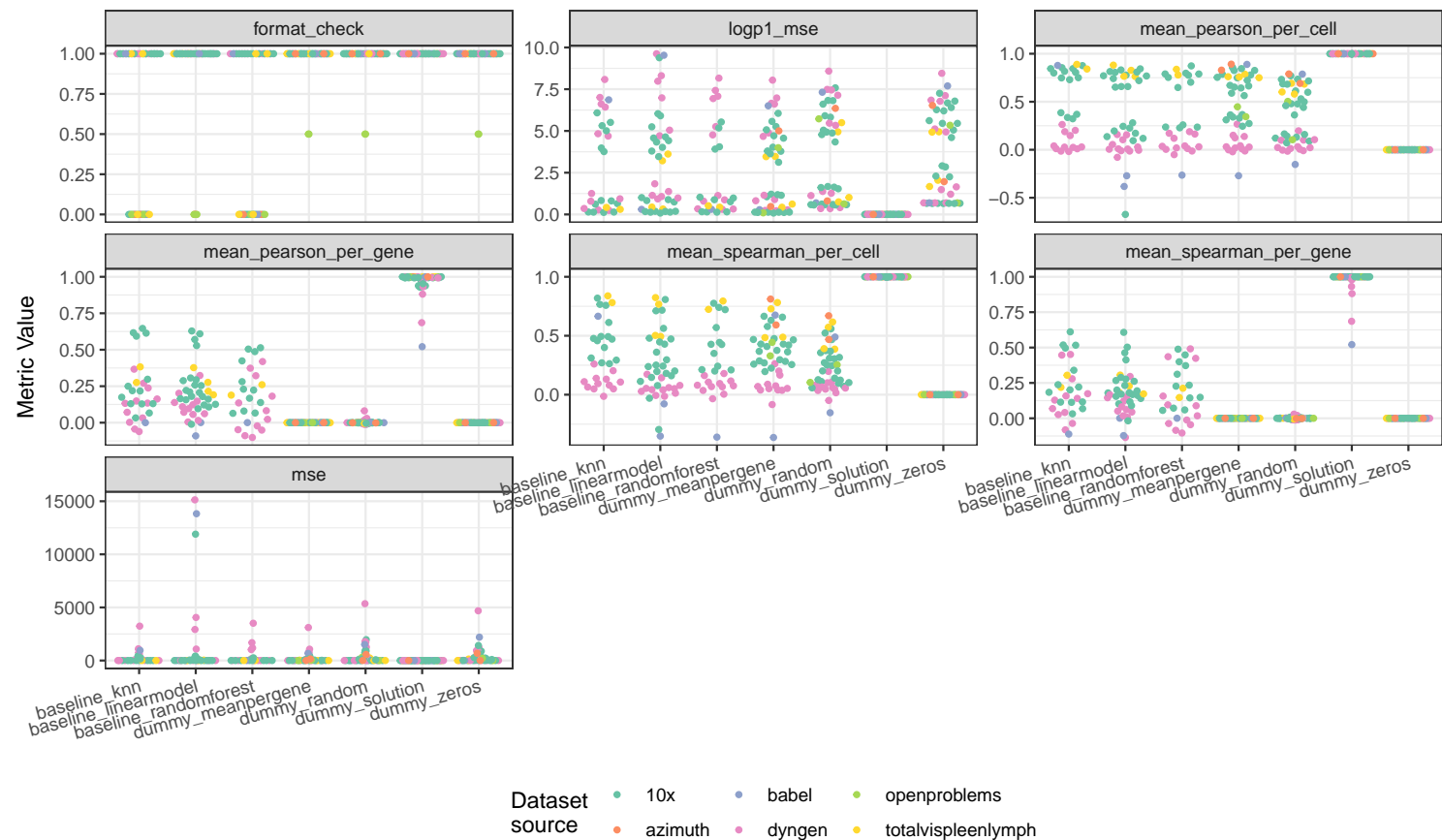
Predict Modality - Pilot Analysis

Visualise results

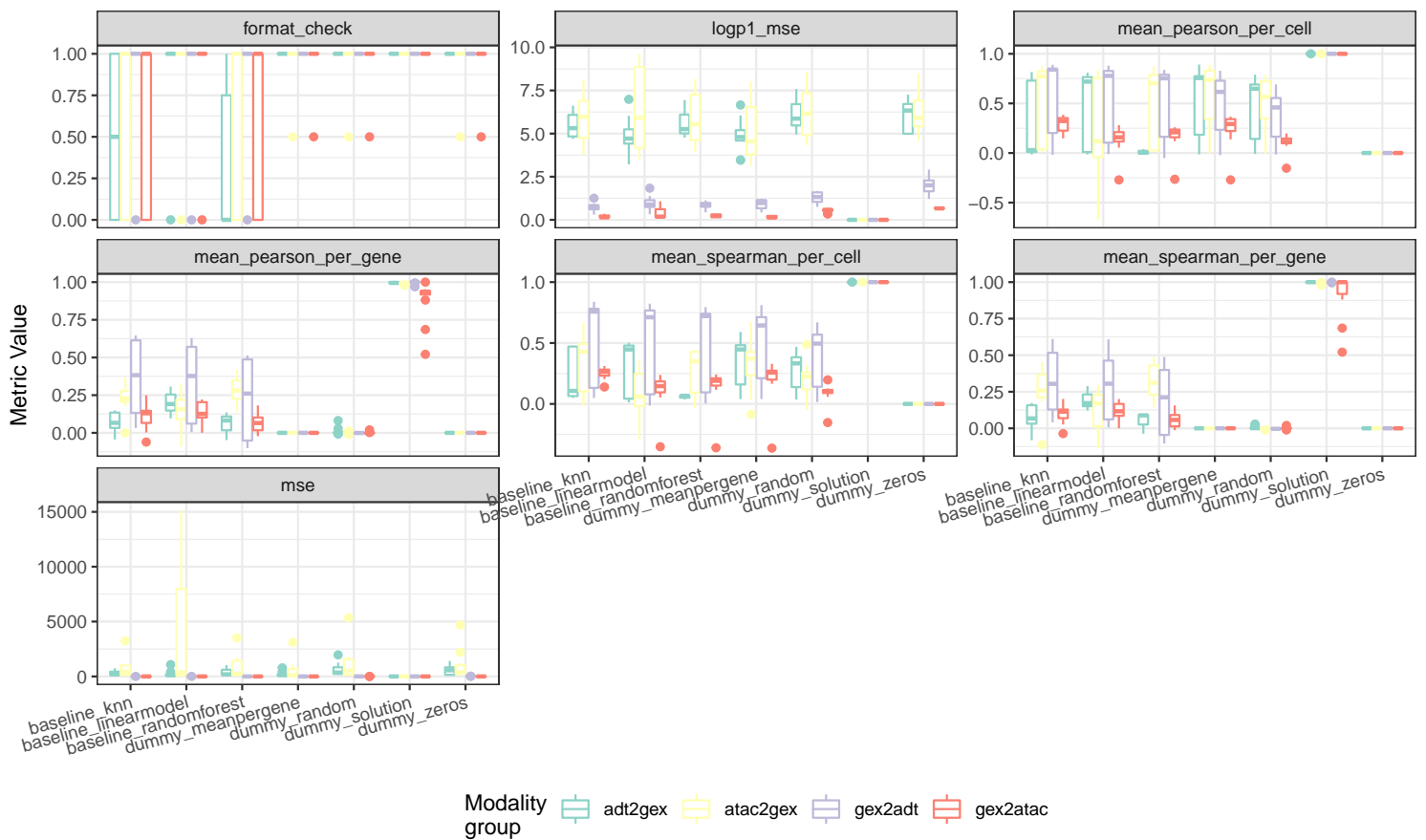
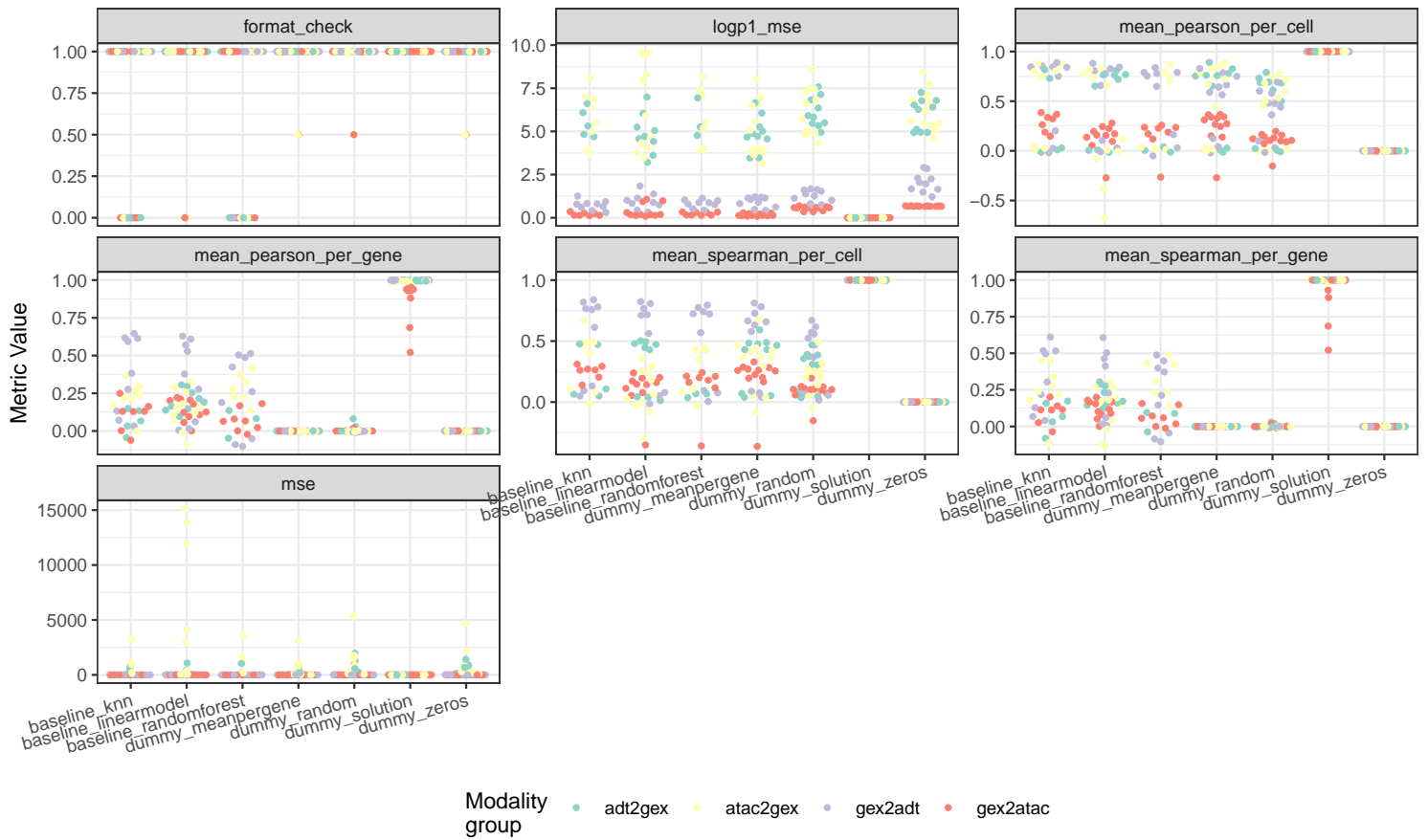
Colour by method.



Colour by dataset source.

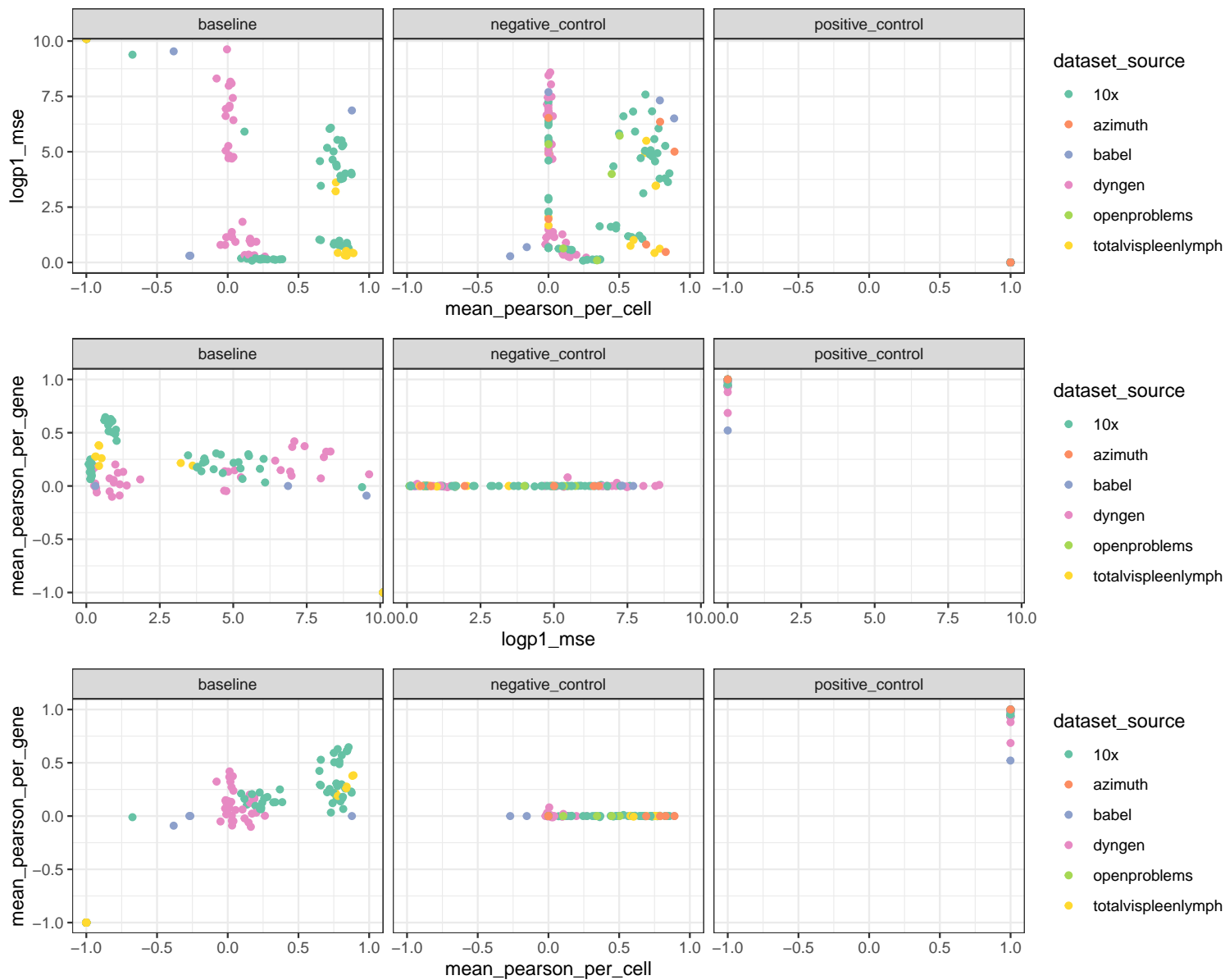


Colour by modality group.

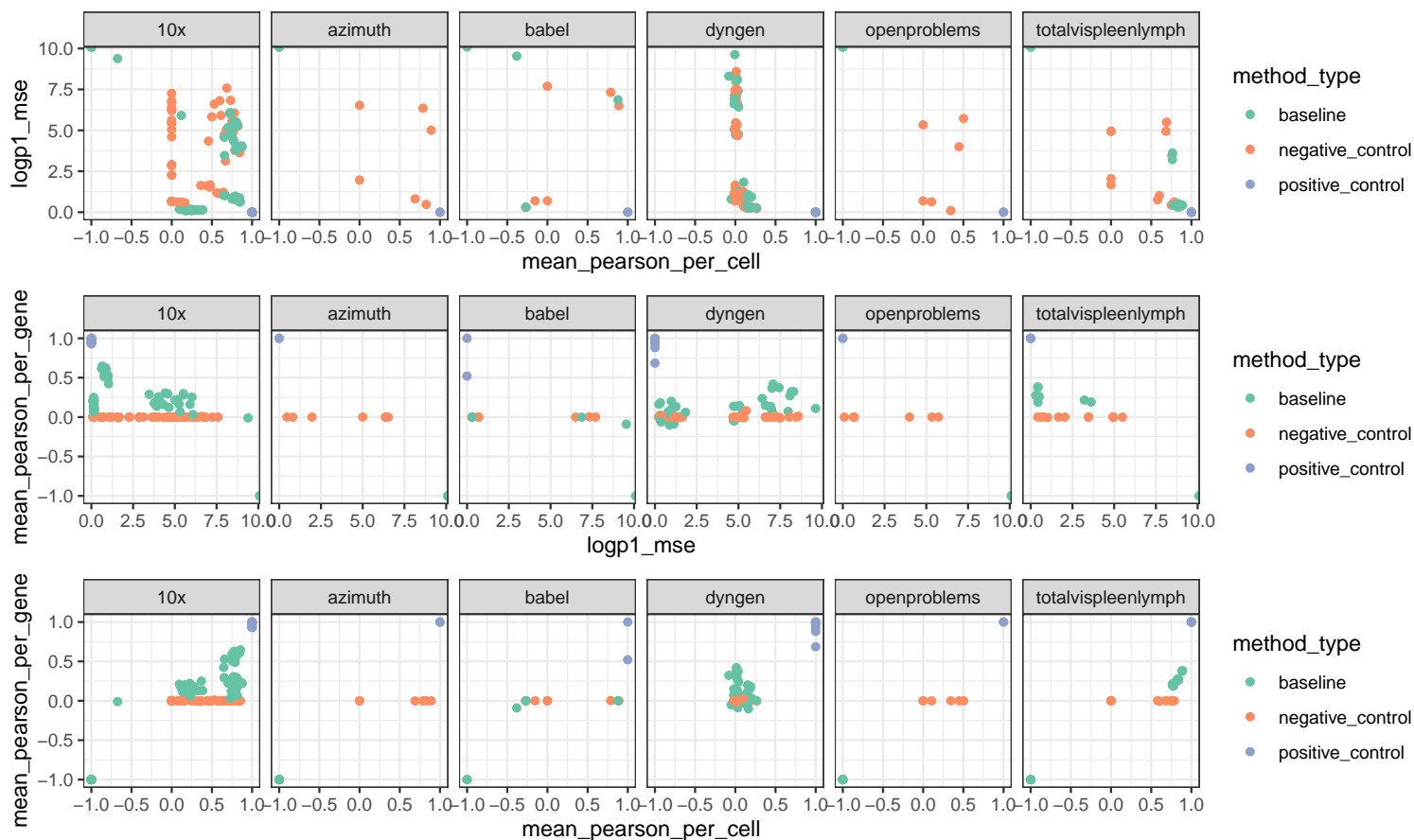


Comparing most interesting metrics.

```
patchwork::wrap_plots(
  ggplot(df, aes(mean_pearson_per_cell, logp1_mse)) + geom_point(aes(colour = dataset_source)) + facet_wrap(~method_type, ncol = 1)
  ggplot(df, aes(logp1_mse, mean_pearson_per_gene)) + geom_point(aes(colour = dataset_source)) + facet_wrap(~method_type, ncol = 1)
  ggplot(df, aes(mean_pearson_per_cell, mean_pearson_per_gene)) + geom_point(aes(colour = dataset_source)) + facet_wrap(~method_type, ncol = 1)
) & theme_bw() & scale_colour_brewer(palette = "Set2")
```



```
patchwork::wrap_plots(
  ggplot(df, aes(mean_pearson_per_cell, logp1_mse)) + geom_point(aes(colour = method_type)) + facet_wrap(~dataset_source, ncol = 1)
  ggplot(df, aes(logp1_mse, mean_pearson_per_gene)) + geom_point(aes(colour = method_type)) + facet_wrap(~dataset_source, ncol = 1)
  ggplot(df, aes(mean_pearson_per_cell, mean_pearson_per_gene)) + geom_point(aes(colour = method_type)) + facet_wrap(~dataset_source, ncol = 1)
) & theme_bw() & scale_colour_brewer(palette = "Set2")
```



```
ggplot(dfg %>% filter(metric_id %in% c("mean_pearson_per_cell", "mean_pearson_per_gene", "log1_mse"))) +
  geom_histogram(aes(value, fill = method_type)) +
  facet_wrap(~metric_id, scales = "free_x") +
  theme_bw()
```

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

