

```

data[, .SD[sample(.N, 1)],
      by=c("pathogen"),
      .SDcols=c("replicate", "sirna", "plate_idx", "well_idx",
                "image_idx", "cell_idx", "infection_index")] %>%
tableGrob(rows=NULL, theme = ttheme_default(base_size=10)) %>%
grid.arrange

```

pathogen	replicate	sirna	plate_idx	well_idx	image_idx	cell_idx	infection_index
listeria	1	s186587	2	58	6	762	97.70050
salmonella	1	s678948	148	52	6	219	104.00808
rhino	1	s652097	130	95	8	384	102.17730
shigella	2	s925080	137	14	8	559	110.75163
vaccinia	1	s962170	114	96	6	847	91.84849
brucella	2	s31472	111	67	9	561	120.74844
adeno	1	s375666	137	45	2	488	85.07430

Figure 1: