Remove samples from plate where fin had degraded and there was no ethanol

Access database.

Find the range of rows to be changed

```
# pull in all table
dat <- dbReadTable(write, params$type)

samples <- c("APCL18_369", "APCL18_349", "APCL18_500", "APCL18_529", "APCL18_557")
change <- dat %>%
  filter(sample_id %in% samples) %>%
  mutate(sample_id = "XXXX",
    notes = "fin clip originally assigned to this space was not extracted because it was degraded in the


dat <- change_rows(dat, change, params$id)
```

Write to database

```
dbWriteTable(write, params$type, dat, row.names = F, overwrite = T)
```

```
## [1] TRUE
```

```
dbDisconnect(write)
```

```
## [1] TRUE
```