Extraction plan for APCL18_095-APCL18_188

2018-07-11

This is a script for adding samples that are not in the laboratory database and have not been extracted. This is set up to handle one plate at a time.

Obtain a list of all clownfish sample ids from the Leyte database

```
# connect to leyte fieldwork db
leyte <- read_db("Leyte")
# import fish table
# select down to only sample_id numbers and remove any rows without a sample
fish <- leyte %>% tbl("clownfish") %>%
  # select only the column sample_id
  select(sample_id) %>%
  # remove any non-sample observations
  filter(!is.na(sample_id)) %>%
  distinct(sample_id) %>%
  # remove any repeat sample_ids (this should not be needed)
  collect()

# make sure each sample_id is only represented once
fish <- distinct(fish)
```

Select the range of samples in the plate

```
work <- fish %>%
  filter(sample_id >= params$first, sample_id <= params$last)

# define wells
plate <- data.frame(row = rep(LETTERS[1:8], 12), col = unlist(lapply(1:12, rep, 8))) %>%
  mutate(sample_id = ifelse(row == "D" & col == 2, "XXXX", NA),
    sample_id = ifelse(row == "E" & col == 8, "XXXX", sample_id))

samples <- plate %>%
  filter(is.na(sample_id)) %>%
  select(-sample_id)

plate <- anti_join(plate, samples, by = c("row", "col"))

samples <- cbind(samples, work)

plate <- rbind(plate, samples) %>%
  arrange(col, row)
```

Make a plate map of sample IDs (for knowing where to place fin clips)

```
platemap <- as.matrix(reshape2::acast(plate, plate[,1] ~ plate[,2]), value.var = plate[,3])
knitr::kable(platemap, booktabs = T) %>%
  # use scale_down to get map to fit within the bounds of the pdf
  kable_styling(latex_options = "scale_down")
```

	1	2	3	4	5	6	7	8	9	10	11	12
A	APCL18_095	APCL18_103	APCL18_110	APCL18_118	APCL18_126	APCL18_134	APCL18_142	APCL18_150	APCL18_157	APCL18_165	APCL18_173	APCL18_181
B	APCL18_096	APCL18_104	APCL18_111	APCL18_119	APCL18_127	APCL18_135	APCL18_143	APCL18_151	APCL18_158	APCL18_166	APCL18_174	APCL18_182
C	APCL18_097	APCL18_105	APCL18_112	APCL18_120	APCL18_128	APCL18_136	APCL18_144	APCL18_152	APCL18_159	APCL18_167	APCL18_175	APCL18_183
D	APCL18_098	XXXX	APCL18_113	APCL18_121	APCL18_129	APCL18_137	APCL18_145	APCL18_153	APCL18_160	APCL18_168	APCL18_176	APCL18_184
E	APCL18_099	APCL18_106	APCL18_114	APCL18_122	APCL18_130	APCL18_138	APCL18_146	XXXX	APCL18_161	APCL18_169	APCL18_177	APCL18_185
F	APCL18_100	APCL18_107	APCL18_115	APCL18_123	APCL18_131	APCL18_139	APCL18_147	APCL18_154	APCL18_162	APCL18_170	APCL18_178	APCL18_186
G	APCL18_101	APCL18_108	APCL18_116	APCL18_124	APCL18_132	APCL18_140	APCL18_148	APCL18_155	APCL18_163	APCL18_171	APCL18_179	APCL18_187
H	APCL18_102	APCL18_109	APCL18_117	APCL18_125	APCL18_133	APCL18_141	APCL18_149	APCL18_156	APCL18_164	APCL18_172	APCL18_180	APCL18_188

ONLY DO THIS ONCE

Generate extract numbers for database

```
lab <- read_db("Laboratory")
extracted <- lab %>% tbl("extraction") %>%
  summarise(last = max(extraction_id, na.rm = T)) %>%
  collect() %>%
  mutate(last = substr(last, 2,5))

plate <- plate %>%
  mutate(well = 1:nrow(plate)) %>%
  mutate(extraction_id = paste("E", well + as.numeric(extracted$last), sep = "")) %>%
  mutate(well = paste(row, col, sep = "")) %>%
  mutate(method = "DNeasy96",
    final_vol = "200")

plate_name <- plate %>%
  summarise(first = min(extraction_id),
    last = max(extraction_id, na.rm = T))
```

Make a platemap with extraction ids

```
map <- plate %>%
  select(row, col, extraction_id)
  platemap <- as.matrix(reshape2::acast(map, map[,1] ~ map[,2]), value.var = map[,3])
```

```
## Using extraction_id as value column: use value.var to override.
```

```
knitr::kable(platemap, booktabs = T) %>%
  kable_styling()
```

	1	2	3	4	5	6	7	8	9	10	11	12
A	E4743	E4751	E4759	E4767	E4775	E4783	E4791	E4799	E4807	E4815	E4823	E4831
B	E4744	E4752	E4760	E4768	E4776	E4784	E4792	E4800	E4808	E4816	E4824	E4832
C	E4745	E4753	E4761	E4769	E4777	E4785	E4793	E4801	E4809	E4817	E4825	E4833
D	E4746	E4754	E4762	E4770	E4778	E4786	E4794	E4802	E4810	E4818	E4826	E4834
E	E4747	E4755	E4763	E4771	E4779	E4787	E4795	E4803	E4811	E4819	E4827	E4835
F	E4748	E4756	E4764	E4772	E4780	E4788	E4796	E4804	E4812	E4820	E4828	E4836
G	E4749	E4757	E4765	E4773	E4781	E4789	E4797	E4805	E4813	E4821	E4829	E4837
H	E4750	E4758	E4766	E4774	E4782	E4790	E4798	E4806	E4814	E4822	E4830	E4838

```
plate <- plate %>%
  mutate(plate = paste(plate_name$first, plate_name$last, sep = "-")) %>%
  select(-row, -col)
```

Import the extract list into the database

Make sure you have created your output PDF for this labwork before sending to the database

```
rm(lab)
lab <- write_db("Laboratory")
```

```
## Loading required package: DBI
```

```
# dbWriteTable(lab, "extraction", plate, row.names = F, overwrite = F, append = T)

dbDisconnect(lab)
```

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

```
rm(lab)
```

Load fin clips

Calculate the amount of lysis buffer to make

```
num_samples <- params$num_samples

w_error <- num_samples *1.1

mix <- readr::read_csv("num_samples_w_error, ul_prot_k, ml_ATL_buff
0,0,0") %>%
mutate(num_samples_w_error = w_error,
ul_prot_k = w_error * 20 * 0.001,
ml_ATL_buff = w_error * 180 * 0.001)

kable(mix)
```

num_samples_w_error	ul_prot_k	ml_ATL_buff
105.6	2.112	19.008

1. Set up tubes of fin clips into the plate formation on tube holder block according to plate map.
2. Create the lysis mix in a 50mL falcon tube, **do not vortex (foamy)**, and pour into 50mL reservoir.
3. Place an 8 well strip of collection tubes (H position labeled with the column number) onto the loading plate and fill with 200uL of lysis mix.
4. Double check that the next column of tubes matches the plate map
5. Place the fins in the collection tubes
6. Cap the tubes
7. When the entire plate is done, place in the incubator overnight.
8. Allow the plate to cool and check the caps to make sure they are on securely.
9. Follow the Qiagen protocol for plate extraction.

Next follow the protocol for gel and pico_plate to check quality and quantity of extracts