Extraction plan for APCL18_471-APCL18_564

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_471	APCL18_479	APCL18_486	APCL18_494	APCL18_502	APCL18_510	APCL18_518	APCL18_526	APCL18_533	APCL18_541	APCL18_549	APCL18_557
B	APCL18_472	APCL18_480	APCL18_487	APCL18_495	APCL18_503	APCL18_511	APCL18_519	APCL18_527	APCL18_534	APCL18_542	APCL18_550	APCL18_558
C	APCL18_473	APCL18_481	APCL18_488	APCL18_496	APCL18_504	APCL18_512	APCL18_520	APCL18_528	APCL18_535	APCL18_543	APCL18_551	APCL18_559
D	APCL18_474	XXXX	APCL18_489	APCL18_497	APCL18_505	APCL18_513	APCL18_521	APCL18_529	APCL18_536	APCL18_544	APCL18_552	APCL18_560
E	APCL18_475	APCL18_482	APCL18_490	APCL18_498	APCL18_506	APCL18_514	APCL18_522	XXXX	APCL18_537	APCL18_545	APCL18_553	APCL18_561
F	APCL18_476	APCL18_483	APCL18_491	APCL18_499	APCL18_507	APCL18_515	APCL18_523	APCL18_530	APCL18_538	APCL18_546	APCL18_554	APCL18_562
G	APCL18_477	APCL18_484	APCL18_492	APCL18_500	APCL18_508	APCL18_516	APCL18_524	APCL18_531	APCL18_539	APCL18_547	APCL18_555	APCL18_563
H	APCL18_478	APCL18_485	APCL18_493	APCL18_501	APCL18_509	APCL18_517	APCL18_525	APCL18_532	APCL18_540	APCL18_548	APCL18_556	APCL18_564

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)))
```

```
##   first  last
## 1 E5031 E5126
```

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	E5031	E5039	E5047	E5055	E5063	E5071	E5079	E5087	E5095	E5103	E5111	E5119
B	E5032	E5040	E5048	E5056	E5064	E5072	E5080	E5088	E5096	E5104	E5112	E5120
C	E5033	E5041	E5049	E5057	E5065	E5073	E5081	E5089	E5097	E5105	E5113	E5121
D	E5034	E5042	E5050	E5058	E5066	E5074	E5082	E5090	E5098	E5106	E5114	E5122
E	E5035	E5043	E5051	E5059	E5067	E5075	E5083	E5091	E5099	E5107	E5115	E5123
F	E5036	E5044	E5052	E5060	E5068	E5076	E5084	E5092	E5100	E5108	E5116	E5124
G	E5037	E5045	E5053	E5061	E5069	E5077	E5085	E5093	E5101	E5109	E5117	E5125
H	E5038	E5046	E5054	E5062	E5070	E5078	E5086	E5094	E5102	E5110	E5118	E5126

```
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)
```

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

```
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