Supplementary Experimental Data File

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Arrangement of CLASH dataset (Helwak et al. 2013)

CLASH dataset was retrieved from PubMed

```
clashelwak <- read.table("mmc1.txt", comment.char = "#",
    header = TRUE, skip = 1)

# hg19
```

Query of Human Genome 19.

```
# HG19
listEnsemblArchives()
listMarts(host = "http://grch37.ensembl.org")
ensemblgrch37 = useMart(host = "http://grch37.ensembl.org",
    biomart = "ENSEMBL_MART_ENSEMBL", dataset = "hsapiens_gene_ensembl")
hg19 <- getBM(attributes = c("ensembl_transcript_id",
    "ensembl_gene_id", "chromosome_name", "start_position",
    "end_position", "hgnc_symbol", "entrezgene_id",
    "strand"), mart = ensemblgrch37)
```

Adding miRNA and gene information

```
clashelwak <- clashelwak %>% separate(microRNA_name,
    c("Barcode", "Database", "mirna_name", "type"),
    sep = "_") %>% separate(mRNA_name, c("Ensembl_Gene_Id",
    "Ensembl_Transcript_Id", "Hugo_Symbol", "mRNA_Type"),
    sep = "_")
```

MiRNA releases are obtained from miRBase. In this step, release 21 (in Human genome 38) is utilised.

```
mirbasehg38 <- read.table("mirbasehg38.txt", comment.char = "#") %>%
    filter(V3 != "miRNA_primary_transcript") %>% separate(V9,
    c("ID", "Alias", "Name", "Precusor"), sep = ";") %>%
    mutate(ID = substr(ID, 4, length(ID)), Alias = substr(Alias,
        7, length(Alias)), Name = substr(Name, 6, length(Name)),
        Precusor = substr(Precusor, 14, length(Precusor))) %>%
    dplyr::select(chr = V1, start = V4, end = V5, strand = V7,
        ID, Alias, Name, Precusor)
```

CLASH dataset is published in miRBase erlease 15 and Human Genome 19 version.

```
clashelwakfinal <- read_tsv("mirna_mature.txt", col_names = FALSE) %>%
    filter(startsWith(X2, "hsa")) %>% dplyr::select(mirna_ID = X2,
    mirbase_ID = X3) %>% inner_join(mirbasehg38 %>%
    dplyr::select(ID, Name), by = c(mirbase_ID = "ID")) %>%
    dplyr::select(mirbase_ID, Name) %>% distinct() %>%
    inner_join(clashelwak, by = c(mirbase_ID = "Barcode")) %>%
    dplyr::select(Name, miRNA_seq, Ensembl_Gene_Id,
        Ensembl_Transcript_Id, Hugo_Symbol, mRNA_seq_extended,
        chimeras_decompressed, seed_type, seed_basepairs,
        folding_class, seq_ID, folding_energy, X5.UTR,
        CDS, X3.UTR) %>% inner_join(hg19, by = c(Ensembl_Gene_Id = "ensembl_gene_id",
    Ensembl_Transcript_Id = "ensembl_transcript_id",
    Hugo_Symbol = "hgnc_symbol")) %>% mutate(region1 = ifelse(X5.UTR ==
    "1", "5UTR", " "), region2 = ifelse(X3.UTR == "1",
    "3UTR", " "), region3 = ifelse(CDS == "1", "CDS",
    " ")) %>% unite(region, c(region1, region2, region3),
    sep = "||") %>% dplyr::select(chromosome_name,
    start_position, end_position, strand, Hugo_Symbol,
    Ensembl_Gene_Id, Ensembl_Transcript_Id, mRNA_seq_extended,
    Name, miRNA_seq, seq_ID, seed_type, seed_basepairs,
    folding_class, folding_energy, region) %>% as_tibble()
```

Converting CLASH data to human genome 38 build.

```
lift19 <- clashelwakfinal %>% dplyr::select(1, 2, 3) %>%
    unite(start_end, c("start_position", "end_position"),
        sep = "-") %>% mutate(Chromosome = paste0("chr",
    chromosome_name, "")) %>% unite(chromosome_name,
    c("Chromosome", "start_end"), sep = ":")

write_tsv(lift19, "lift19.txt")

# Lift over process is made via UCSC liftover tool.
# (https://genome.ucsc.edu/cgi-bin/hgLiftOver)

lift19_del <- read_tsv("deleted_lift19.txt")
colnames(lift19_del)[1] <- "chromosome_loc"

lift19_del <- lift19_del %>% dplyr::filter(startsWith(chromosome_loc,
    "chr")) %>% separate(chromosome_loc, c("Chr", "End"),
    "-", remove = TRUE) %>% separate(Chr, c("Chr",
    "Start"), ":", remove = TRUE)

lift19_del$Start <- as.numeric(lift19_del$Start)
lift19_del$End <- as.numeric(lift19_del$End)

clashelwakfinal <- clashelwakfinal %>% mutate(Chromosome = paste0("chr",
    chromosome_name, "")) %>% dplyr::anti_join(lift19_del,
    by = c(Chromosome = "Chr", start_position = "Start",
        end_position = "End"))
```

```
hg38clash <- read.delim("hg38clashcomp.txt", header = FALSE)

clashelwakfinal <- clashelwakfinal %>% bind_cols(hg38clash)

colnames(clashelwakfinal)[18] <- "HG38build_loc"

clashelwakfinal <- clashelwakfinal %>% dplyr::mutate(Genom_build = rep("hg19"))
str(clashelwakfinal)


# Arrangement in dataset

clashelwakfinal <- clashelwakfinal %>% dplyr::select(cluster = seq_ID,
    chromosome = Chromosome, start_position, end_position,
    strand, hgnc_symbol = Hugo_Symbol, Ensembl_Gene_Id,
    Ensembl_Transcript_Id, target_seq = mRNA_seq_extended,
    miRNA = Name, miR_seq = miRNA_seq, seed_type, seed_type2 = seed_basepairs,
    seed_type3 = folding_class, Energy = folding_energy,
    HG38build_loc, Genom_build, region)

clashelwakfinal$cluster <- as.character(clashelwakfinal$cluster)
clashelwakfinal$strand <- as.character(clashelwakfinal$strand)
clashelwakfinal$target_seq <- as.character(clashelwakfinal$target_seq)
clashelwakfinal$miR_seq <- as.character(clashelwakfinal$miR_seq)
clashelwakfinal$seed_type <- as.character(clashelwakfinal$seed_type)
clashelwakfinal$HG38build_loc <- as.character(clashelwakfinal$HG38build_loc)
clashelwakfinal$seed_type2 <- as.numeric(clashelwakfinal$seed_type2)
clashelwakfinal$seed_type3 <- as.character(clashelwakfinal$seed_type3)
```

Interpreting the CLASH seed structures in dataset

```
clashelwakfinal <- clashelwakfinal %>% mutate(seed_type = ifelse(seed_type ==
    "noncanonical_seed" & seed_type2 > 4 & seed_type3 ==
    "I", paste0(seed_type2, "-mer"), seed_type), seed_type = ifelse(seed_type ==
    "noncanonical_seed" & seed_type2 > 4 & seed_type3 ==
    "II", paste0(seed_type2, "-mer_noncanonical"),
    seed_type), seed_type = ifelse(seed_type == "noncanonical_seed" &
    seed_type2 > 4 & seed_type3 == "III", paste0(seed_type2,
    "-mer_noncanonical"), seed_type), seed_type = ifelse(seed_type ==
    "noncanonical_seed" & seed_type2 > 4 & seed_type3 ==
    "IV", paste0(seed_type2, "-mer_noncanonical"),
    seed_type), seed_type = ifelse(startsWith(seed_type,
    "no"), "none", seed_type)) %>% dplyr::select(-seed_type2,
    -seed_type3)
```

Arrangement of CLEAR-CLiP Dataset (Moore et al. 2015)

CLASH dataset was retrieved from Nature web page

```
clearclip <- read_xlsx("CLEAR-CLIP.xlsx")

# Clearclip hg18
```

Query of Human Genome 18

```
# HG18
listEnsemblArchives()
listMarts(host = "may2009.archive.ensembl.org")
ensembl54 = useMart(host = "may2009.archive.ensembl.org",
    biomart = "ENSEMBL_MART_ENSEMBL", dataset = "hsapiens_gene_ensembl")

hg18 <- getBM(attributes = c("ensembl_transcript_id",
    "ensembl_gene_id", "chromosome_name", "start_position",
    "end_position", "hgnc_symbol", "entrezgene", "strand"),
    mart = ensembl54)
```

Adding Genome Information to dataset

```
clearclipfinal <- hg18 %>% inner_join(clearclip, by = c(entrezgene = "gene.id",
    hgnc_symbol = "gene.symbol")) %>% distinct()
```

Converting human genome build

```
lift18 <- clearclipfinal %>% unite(start_end, c("start_position",
    "end_position"), sep = "-") %>% unite(location,
    c("chr", "start_end"), sep = ":") %>% dplyr::select(location)

write_tsv(lift18, "lift18.txt")

deleted_lift18 <- read_tsv("deleted_lift18.txt")

colnames(deleted_lift18)[1] <- "Chromosome_loc"

deleted_lift18 <- deleted_lift18 %>% dplyr::filter(startsWith(Chromosome_loc,
    "chr")) %>% separate(Chromosome_loc, c("Chr", "End"),
    "-", remove = TRUE) %>% separate(Chr, c("Chr",
    "Start"), ":", remove = TRUE)

deleted_lift18$Start <- as.numeric(deleted_lift18$Start)
deleted_lift18$End <- as.numeric(deleted_lift18$End)

clearclipfinal <- clearclipfinal %>% dplyr::anti_join(deleted_lift18,
    by = c(chr = "Chr", start_position = "Start", end_position = "End"))

hg38clearclip <- read.delim("hg38clearclip.txt", header = FALSE)
```

```
clearclipfinal <- clearclipfinal %>% bind_cols(hg38clearclip)

colnames(clearclipfinal)[28] <- "HG38build_loc"

clearclipfinal <- clearclipfinal %>% dplyr::mutate(Genom_build = rep("hg18"))

clearclipfinal <- clearclipfinal %>% dplyr::select(cluster = cluster.ID,
    chromosome = chr, start_position, end_position,
    strand = strand.y, hgnc_symbol, Ensembl_Gene_Id = ensembl_gene_id,
    Ensembl_Transcript_Id = ensembl_transcript_id,
    target_seq = target.map, miRNA, miR_seq = miR.map,
    seed_type = "seed match", Energy = MFE, HG38build_loc,
    Genom_build, region)
```

Seed type manipulation

```
clipdata_seed <- data_frame(seed_type = c("5mer_1",
    "5mer_2", "5mer_3", "6mer", "6mer.indel", "6mer.mm",
    "6mer_off.mm", "6merA1", "6merA1.indel", "6merA1.mm",
    "7merA1", "7merA1.indel", "7merA1.mm", "7merm8",
    "7merm8.indel", "7merm8,mm", "8mer", "8mer.indel",
    "8mer.mm", "NA"), seed_type_com = c("5-mer", "5-mer_noncanonical",
    "5-mer_noncanonical", "6-mer", "6-mer_noncanonical",
    "6-mer_noncanonical", "6-mer_noncanonical", "6-merA1",
    "6-merA1_noncanonical", "6-merA1_noncanonical",
    "7-merA1", "7-merA1_noncanonical", "7-merA1_noncanonical",
    "7-mer-8m", "7-mer-8m_noncanonical", "7-mer-8m_noncanonical",
    "8-mer", "8-mer_noncanonical", "8-mer_noncanonical",
    "none"))

clearclipfinal <- clearclipfinal %>% inner_join(clipdata_seed,
    by = "seed_type") %>% dplyr::select(1:11, seed_type = seed_type_com,
    Energy, HG38build_loc, Genom_build, region)


clearclipfinal$HG38build_loc <- as.character(clearclipfinal$HG38build_loc)
```

Integration of two experimental dataset

```
experimentalmirnagene <- bind_rows(clashelwakfinal,
    clearclipfinal) %>% distinct()
```

Adding Coefficients of Interaction factors

Numeric valuesof interaction factors are shown at Table S2-3 in Supplementary Tables file.

```
experimentalmirnagene <- experimentalmirnagene %>%
    mutate(region2 = str_replace_all(region, "NA",
        ""), region3 = str_replace_all(region2, "\\|",
        ""), region = str_replace_all(region3, c(`3'UTR` = "3UTR",
        `5'UTR` = "5UTR"))) %>% dplyr::select(-region2,
    -region3) %>% mutate(region_effect = as.double(ifelse(region %in%
    c("3UTRCDS", "CDS3UTR", "5UTR3UTR", "CDS5UTR3UTR",
        "CDS3UTRintron"), "0.93", ifelse(region %in%
    c("CDS", "CDSintron"), "0.42", ifelse(region %in%
    c("3UTR", "3UTRintron"), "0.84", ifelse(region %in%
    c("5UTR", "5UTRintron"), "0.01", ifelse(region %in%
    c("5UTRCDS", "CDS5UTR"), "0.42", ifelse(region %in%
    c("intron", ""), "0.01", ifelse(region %in% c("exon_unclassified",
    ""), "0.2", NA)))))))))
```

```
seed_type_effect <- data_frame(seed_type = c("5-mer",
    "5-mer_noncanonical", "6-mer", "6-mer_noncanonical",
    "6-merA1", "6-merA1_noncanonical", "7-mer", "7-mer_noncanonical",
    "7-merA1", "7-merA1_noncanonical", "7-mer-8m",
    "7-mer-8m_noncanonical", "8-mer", "8-mer_noncanonical",
    "9-mer", "9-mer_noncanonical", "none"), seed_type_effect = c(0.05,
    0.04, 0.07, 0.05, 0.07, 0.05, 0.23, 0.19, 0.19,
    0.16, 0.25, 0.21, 0.43, 0.35, 0.43, 0.35, 0.01))

experimentalmirnagene <- experimentalmirnagene %>%
    inner_join(seed_type_effect, by = "seed_type")
```

```
## Saving dataset
saveRDS(experimentalmirnagene, "data/experimentalmirnagene.RDS")
```

```
experimentalmirnagene <- readRDS("data/experimentalmirnagene.RDS")
experimentalmirnagene
```

```
## # A tibble: 45,340 x 18
##    cluster chromosome start_position end_position strand hgnc_symbol
##    <chr>   <chr>               <int>        <int> <chr>  <chr>
##  1 0727A-~ chr5            162864575    162873157 1      CCNG1
##  2 L1HS-1~ chr14            95552565     95624347 -1     DICER1
##  3 L2HS-8~ chr6            109307640    109416022 -1     SESN1
##  4 L2HS-1~ chr5             36876861     37066515 1      NIPBL
##  5 L2-407~ chr4            106603784    106817143 -1     INTS12
##  6 L1HS-7~ chr5            130977407    131132710 -1     FNIP1
##  7 L1HS-4~ chr11           134123389    134135749 1      ACAD8
##  8 0727A-~ chr15            59397277     59417244 1      CCNB2
##  9 L2HS-1~ chr19            37001597     37019562 -1     ZNF260
## 10 L2HS-9~ chr11            64889252     64902004 -1     SYVN1
## # ... with 45,330 more rows, and 12 more variables: Ensembl_Gene_Id <chr>,
## #   Ensembl_Transcript_Id <chr>, target_seq <chr>, miRNA <chr>,
## #   miR_seq <chr>, seed_type <chr>, Energy <dbl>, HG38build_loc <chr>,
## #   Genom_build <chr>, region <chr>, region_effect <dbl>,
## #   seed_type_effect <dbl>
```

REFERENCES

Helwak, Aleksandra, Grzegorz Kudla, Tatiana Dudnakova, and David Tollervey. 2013. "Mapping the Human miRNA Interactome by CLASH Reveals Frequent Noncanonical Binding." *Cell* 153 (3): 654–65. https://doi.org/10.1016/j.cell.2013.03.043.

Moore, Michael J., Troels K. H. Scheel, Joseph M. Luna, Christopher Y. Park, John J. Fak, Eiko Nishiuchi, Charles M. Rice, and Robert B. Darnell. 2015. "miRNA-Target Chimeras Reveal miRNA 3'-End Pairing as a Major Determinant of Argonaute Target Specificity." *Nature Communications* 6 (November): 8864. https://doi.org/10.1038/ncomms9864.