

Nick's lncRNA in Lynch RNAseq

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Background

To check the expression of lncRNAs identified by Nick's team in our Lynch cohort.

Details of the transcripts is shared by Nick's team (Dr Wojciech Barczak) in the email on 31st March 2024.

1. **ENST00000400362.2** BX322557.10 (now LINC00205-201)
2. ENST00000685281.1 AC079135.1 (now GBX2-AS1)
3. **ENST00000562866.1** VPS9D1-AS1
4. **ENST00000529369.1** RP11-660L16.2 (now DHCR7-DT)
5. **ENST00000585075.1** RP11-649A18.12 (now MIF4GD-DT)
6. **ENST00000544868.1** **ENST00000534336.1** MALAT1
7. **ENST00000430633.1**, **ENST00000550853.1** LINC00094 (now BRD3OS but non-protein transcript)

```
library(dplyr)
library(tidyverse)
```

```
# A tibble: 6 x 5
  tx          Sample      TPM Tissue Patient
<chr>      <chr>      <dbl> <chr>   <fct>
1 ENST00000430633 S1_6310_Poly 1.83   Polyp   6310
2 ENST00000430633 S11_6344_Pol 0.639   Polyp   6344
3 ENST00000430633 S12_6344_Nor 0.470   Normal  6344
4 ENST00000430633 S13_6346_Pol 0.902   Polyp   6346
5 ENST00000430633 S14_6346_Nor 1.46    Normal  6346
6 ENST00000430633 S15_6794_Pol 1.02    Polyp   6794
```

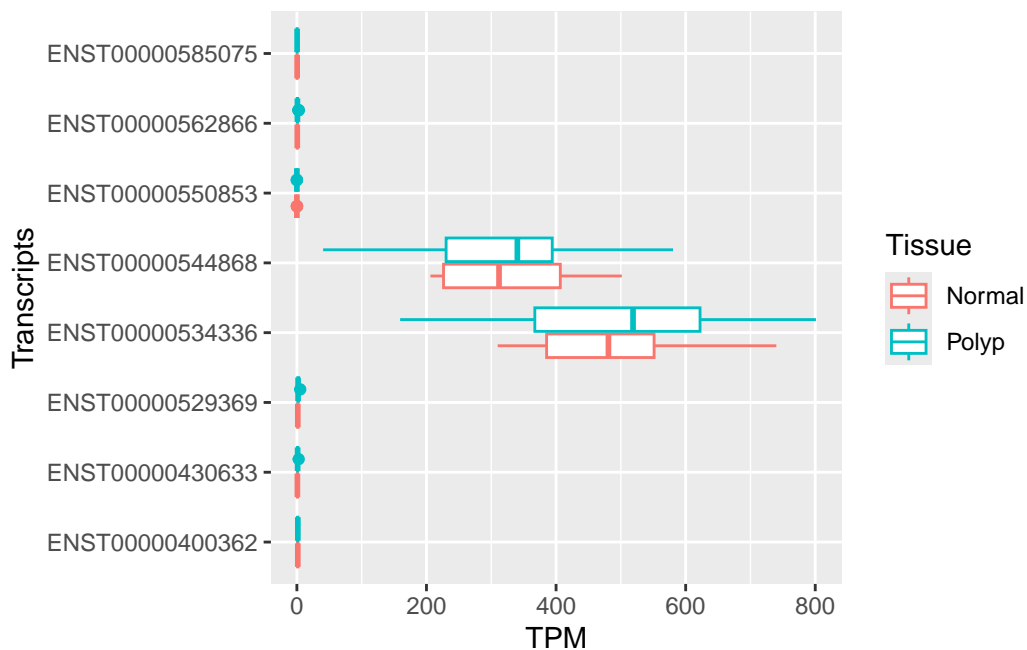
In our cohort, we have 16 Lynch patients, polyps and paired neighboring normal tissues were collected and sent for RNA sequencing.

ENST00000400362	ENST00000430633	ENST00000529369	ENST00000534336	ENST00000544868
42	42	42	42	42
ENST00000550853	ENST00000562866	ENST00000585075		
42	42	42		

in our data, Transcript ENST00000685281.1 is **NOT** found, the other 8 has been detected in all tissues.

Now take a look at the level of expression (in TPM) in **Normal vs Polyps tissues** from Lynch patients.

```
lncRNA_anno %>% ggplot(aes(x = tx, y = TPM, colour = Tissue)) + geom_boxplot() + coord_flip()
```



You have two transcripts expressed in the RNAseq, although their expression levels do not seem to differ significantly between polyps and normal tissues.

```
sessionInfo()
```

```

R version 4.3.2 (2023-10-31)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Sonoma 14.2.1

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib;

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/London
tzcode source: internal

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods    base

other attached packages:
[1] lubridate_1.9.3 forcats_1.0.0  stringr_1.5.1  purrr_1.0.2
[5] readr_2.1.5     tidyr_1.3.1    tibble_3.2.1   ggplot2_3.5.0
[9] tidyverse_2.0.0 dplyr_1.1.4

loaded via a namespace (and not attached):
[1] gtable_0.3.5      jsonlite_1.8.8    compiler_4.3.2    tidyselect_1.2.1
[5] scales_1.3.0      yaml_2.3.8        fastmap_1.1.1     R6_2.5.1
[9] labeling_0.4.3    generics_0.1.3    knitr_1.45        munsell_0.5.1
[13] pillar_1.9.0      tzdb_0.4.0        rlang_1.1.3       utf8_1.2.4
[17] stringi_1.8.3     xfun_0.43         timechange_0.3.0  cli_3.6.2
[21] withr_3.0.0       magrittr_2.0.3    digest_0.6.35     grid_4.3.2
[25] rstudioapi_0.15.0 hms_1.1.3         lifecycle_1.0.4   vctrs_0.6.5
[29] evaluate_0.23     glue_1.7.0        farver_2.1.1      fansi_1.0.6
[33] colorspace_2.1-0  rmarkdown_2.26    tools_4.3.2       pkgconfig_2.0.3
[37] htmltools_0.5.8.1

```