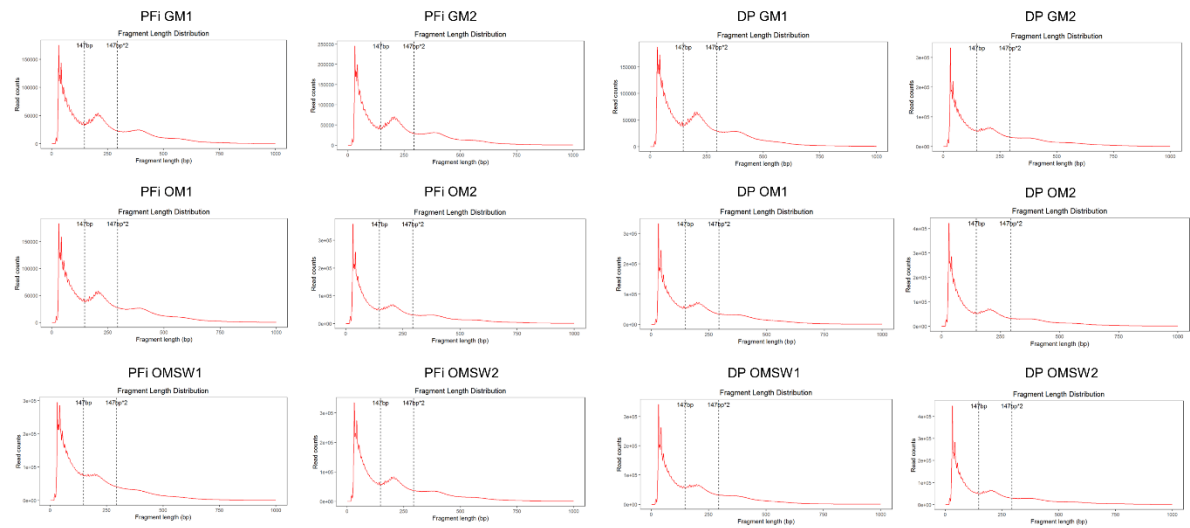
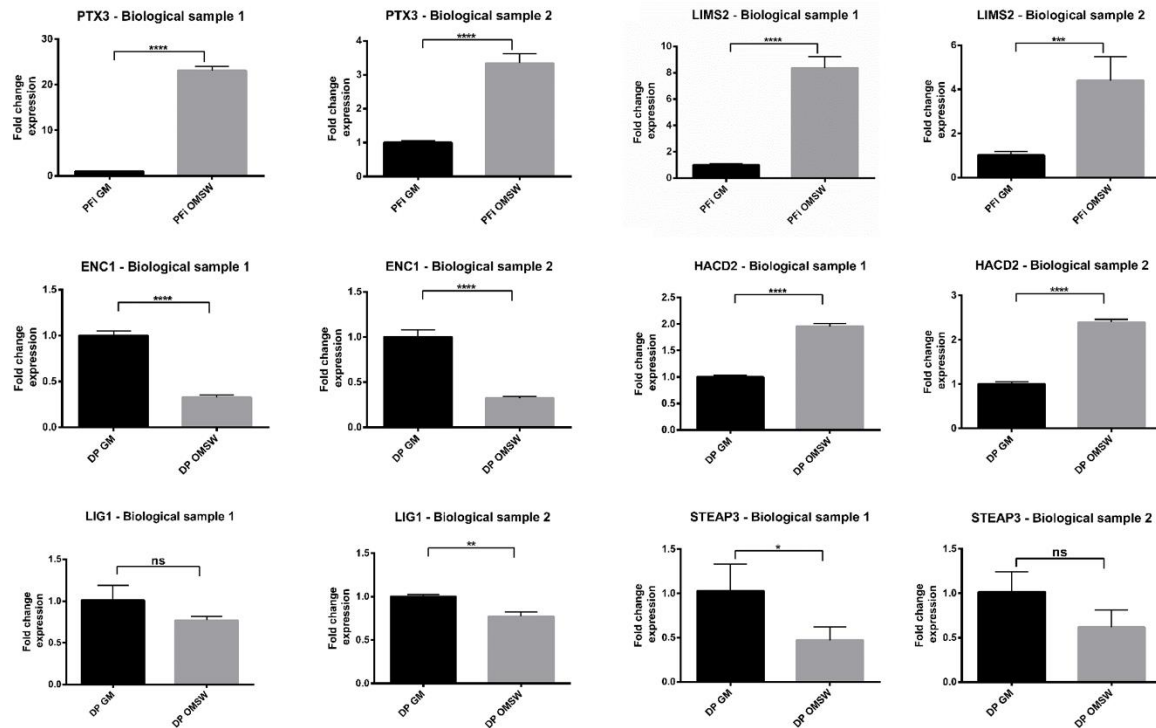


SUPPLEMENTARY INFORMATION

Figures and Tables



**Figure S1: ATAC-seq nucleosome banding.** Each prepared library is shown, with clear banding indicating good quality libraries.



**Figure S2: RT-PCR data validating RNA-seq results.** Gene names are shown above graphs, in addition to the biological replicate in which the validation was performed. In all cases, the trend was the same as that observed in the RNA-seq results. Significance shown on graphs calculated using technical repeats (ns= $p > 0.05$ , \*= $p < 0.05$ , \*\*= $p < 0.01$ , \*\*\*= $p < 0.001$ , \*\*\*\*= $p < 0.0001$ ).

| Primer name | Sequence (5' to 3')     | Annealing temperature (°C) |
|-------------|-------------------------|----------------------------|
| GAPDH-F     | CGTCTTCACCACCATGGAGA    | 60                         |
| GAPDH-R     | CGGCCATCACGCCACAGTTT    |                            |
| PTX3-F      | CATCTCCTTGCGATTCTGTTTTG | 60                         |
| PTX3-R      | CCATTCCGAGTGCTCCTGA     |                            |
| LIMS2-F     | GCACCGGCACTATGAGAAGAA   | 60                         |
| LIMS2-R     | ACGGGCTTCATGTCGAACTC    |                            |
| ENC1-F      | GCCAGCCATCTATCTCATGGA   | 60                         |
| ENC1-R      | GGTTACCACACCGTCATTCTG   |                            |
| HACD2-F     | GCAGTAACACATAGCGTCAAAGA | 60                         |
| HACD2-R     | TGATGAGGTAAGGCAGATGGTT  |                            |
| LIG1-F      | GCCCTGCTAAAGGCCAGAAG    | 60                         |
| LIG1-R      | CATGGGAGAGGTGTCAGAGAG   |                            |
| STEAP3-F    | CAGCCCTATGTGCAGGAAAG    | 60                         |
| STEAP3-R    | GCAAGTACACGAGTGACAGCA   |                            |

**Table. S1. Primer sequences used in validation.** GAPDH taken from Farshdousti Hagh et al [47]. Other primers designed against sequences in the UCSC database