Download HiC files

The files were downloaded directly from ENA (European Nucleotide Archive). To identify the SRR accession from the paper they were searched on NCBI with the project accession number of PRJNA431161 provided by the paper.

```bash
#!/bin/bash -l
#SBATCH --job-name=hic_download_ENA
#SBATCH --output=/scratch/grp/msc_appbio/Group2_ABCC/HiC/logs/%x_%j.out
#SBATCH --error=/scratch/grp/msc_appbio/Group2_ABCC/HiC/logs/%x_%j.err
#SBATCH --time=08:00:00
#SBATCH --cpus-per-task=2
#SBATCH --mem=8G
#SBATCH -p msc_appbio

cd /scratch/grp/msc_appbio/Group2_ABCC/HiC/raw_fastq_HiC

echo "Starting ENA FASTQ downloads..."

# Loop over all SY14 Hi-C SRR accessions used in the paper
for srr in SRR6678863 SRR6678864 SRR6678865 SRR6678866 SRR6678867 SRR6678868 SRR6678869 SRR6678870

# For each accession, the API was queried to retrieve the FTP locations of
# the raw FASTQ files which were then downloaded using wget.
do
  echo "=== Getting URLs for $srr ==="

  urls=$(curl -s
"https://www.ebi.ac.uk/ena/portal/api/filereport?accession=${srr}&result=read_run&fields=fastq_ftp&format=tsv"
     | tail -n 1 | cut -f2)

  # If for some reason ENA didn't return anything, skip
  if [[ -z "$urls" ]]; then
    echo "No URLs found for $srr, skipping."
    continue
  fi

  for url in $(echo "$urls" | tr ';' '\n'); do
    echo "Downloading ftp://$url"
    wget -nc ftp://$url
  done

  echo "=== Done with $srr ==="
done

echo "All ENA downloads completed."
```