q4C Data analysis steps

	• Data (Fastq) from sequencing facility: demultiplexed by barcode
Trim	• remove low quality reads and linker sequences
Digest	• digest NlaIII in silico fragments to break composite reads
Align	• align against combined reference (human + viral)
Extraction	• identify and quantify ligation sites
Filter	• remove barcode errors, decrease noise by selecting convergent reads
Peak calling	• identify reproducible contacts.