Sample Name	% Dups	% GC	Length	% Failed	M Seqs
GSM461177_1_subsampled_fastqsanger	23.6%	53%	37 bp	0%	1.1
GSM461177_2_subsampled_fastqsanger	25.2%	53%	37 bp	9%	1.1
GSM461180_1_subsampled_fastqsanger	23.8%	54%	37 bp	9%	1.2
GSM461180_2_subsampled_fastqsanger	8.1%	55%	37 bp	9%	1.2

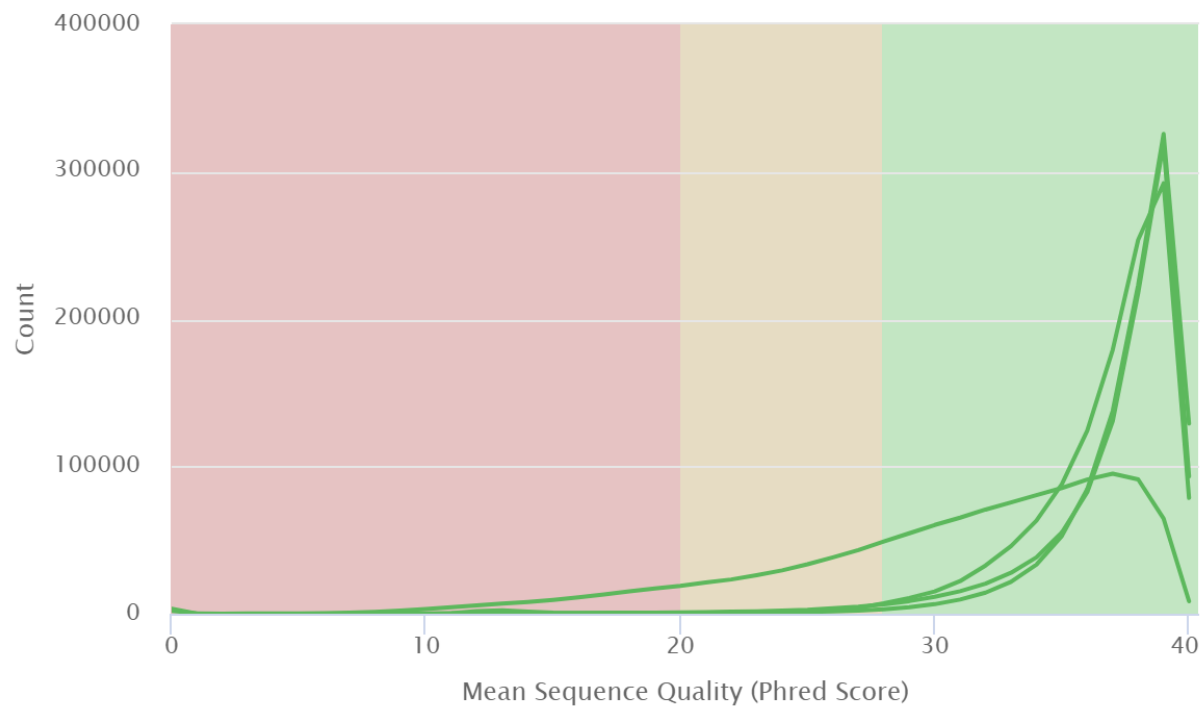## FastQC: Sequence Counts

Created with MultiQC
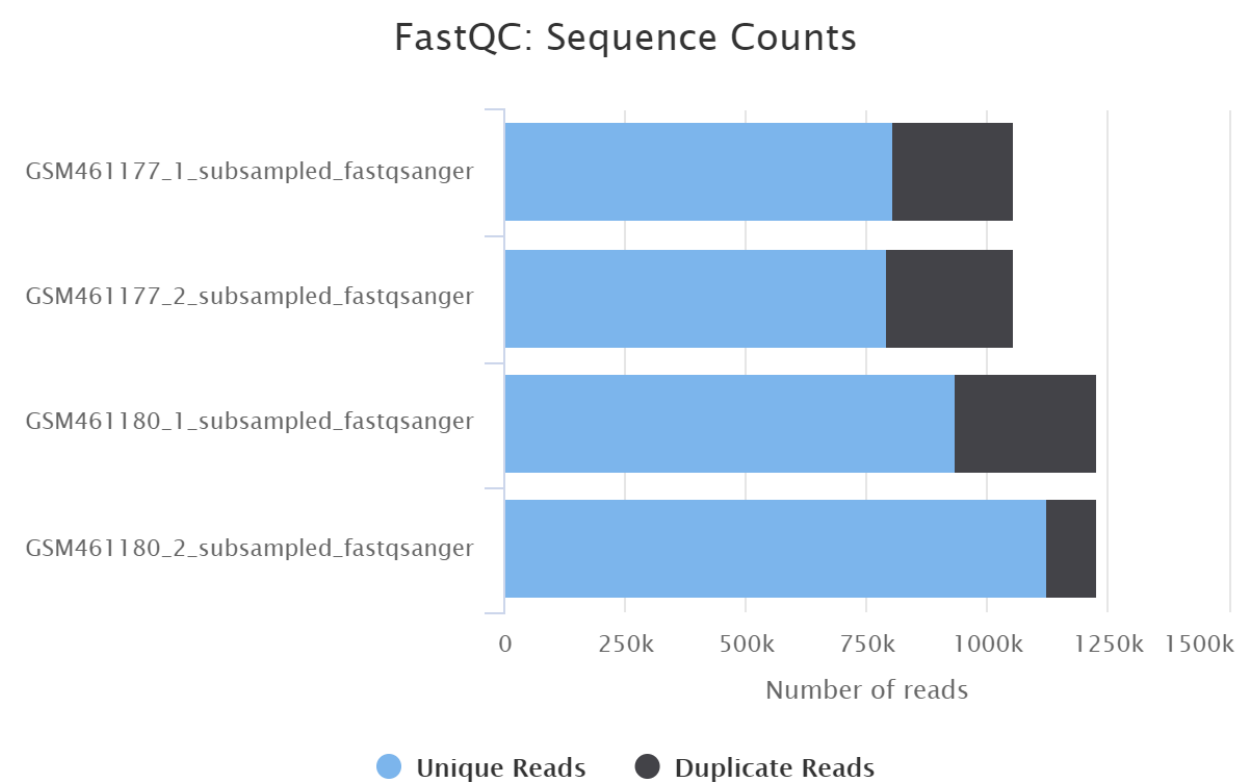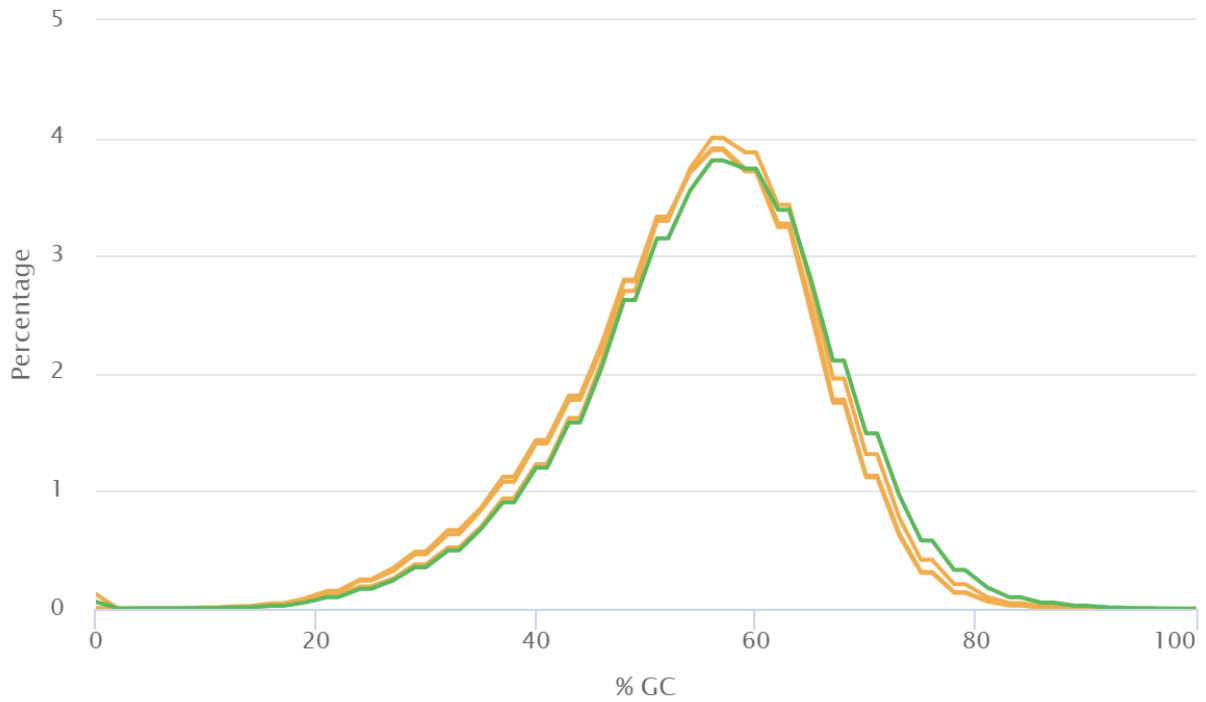
FastQC: Mean Quality Scores
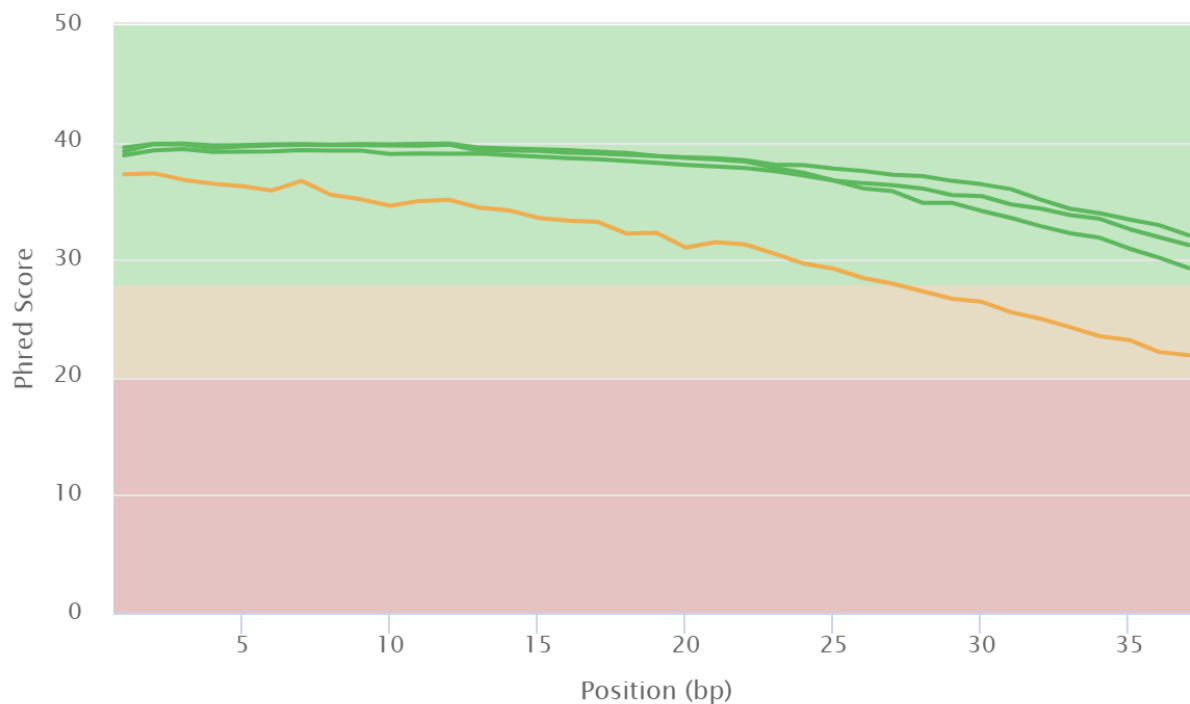
Created with MultiQC

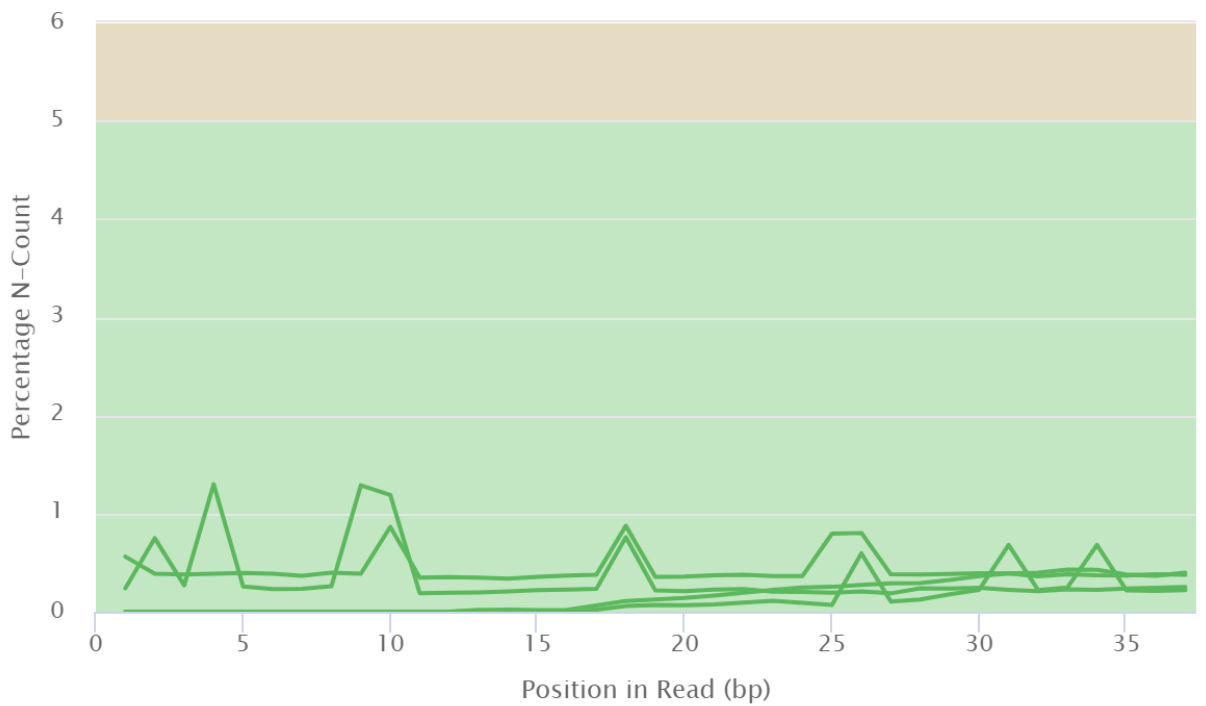# FastQC: Per Sequence Quality Scores

Created with MultiQC

FastQC: Per Sequence GC Content

Created with MultiQC

FastQC: Per Base N Content

Created with MultiQC

FastQC: Status Checks

GSM461177_1_subsampl

GSM461177_2_subsampl

GSM461180_1_subsampl

GSM461180_2_subsampl

Basi...
Per Base Seque...
Per Tile Sequence Qu
Per Sequence Quality
Per Sequence Co
Per Sequence GC Cont
Per Base N Content
Sequence Length Dist
Sequence Duplication
Overrepresented Sequ
Adapter Content

Section Name

Created with MultiQC