Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 09:59:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777289.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1777289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777289.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 09:59:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	541,491
Mapped reads	514,934 / 95.1%
Unmapped reads	26,557 / 4.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	176 / 0.03%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	5,791 / 1.07%
Duplication rate	0.67%
Clipped reads	34,015 / 6.28%

2.2. ACGT Content

Number/percentage of A's	7,766,646 / 29.97%
Number/percentage of C's	5,251,077 / 20.26%
Number/percentage of T's	7,565,559 / 29.19%
Number/percentage of G's	5,330,514 / 20.57%
Number/percentage of N's	1,747 / 0.01%
GC Percentage	40.83%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.1174

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

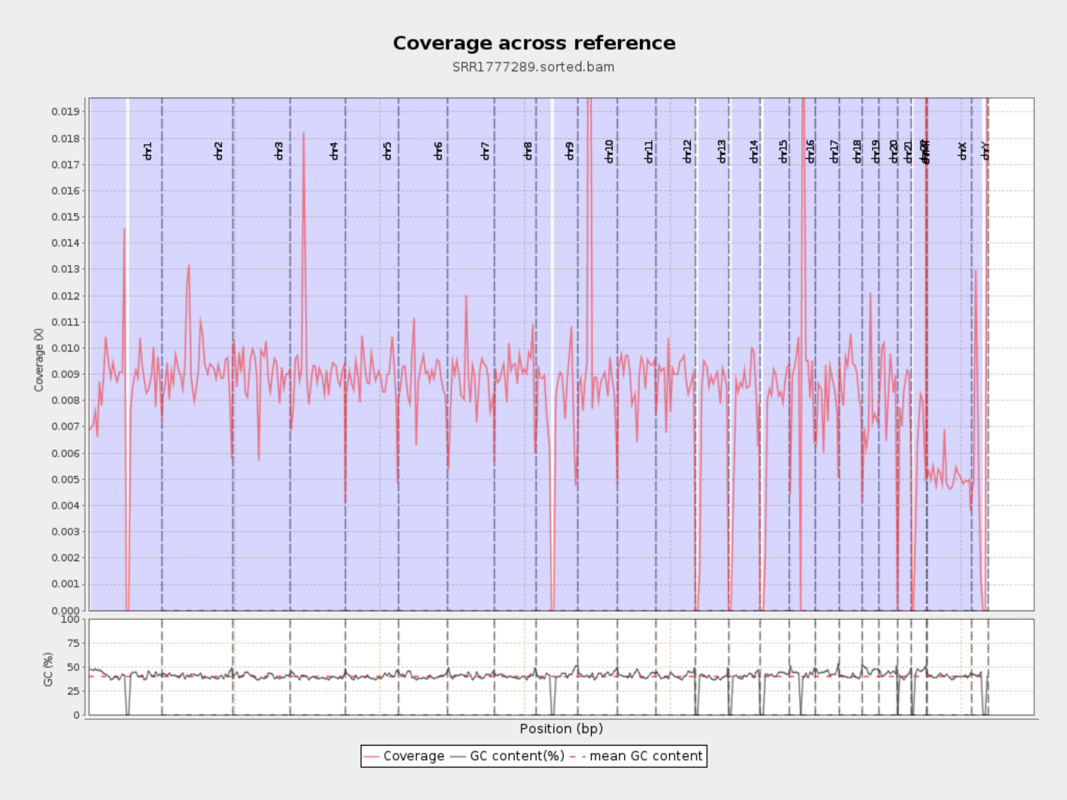
General error rate	0.34%
Mismatches	81,962
Insertions	4,065
Mapped reads with at least one insertion	0.79%
Deletions	2,026
Mapped reads with at least one deletion	0.39%
Homopolymer indels	47.56%

2.6. Chromosome stats

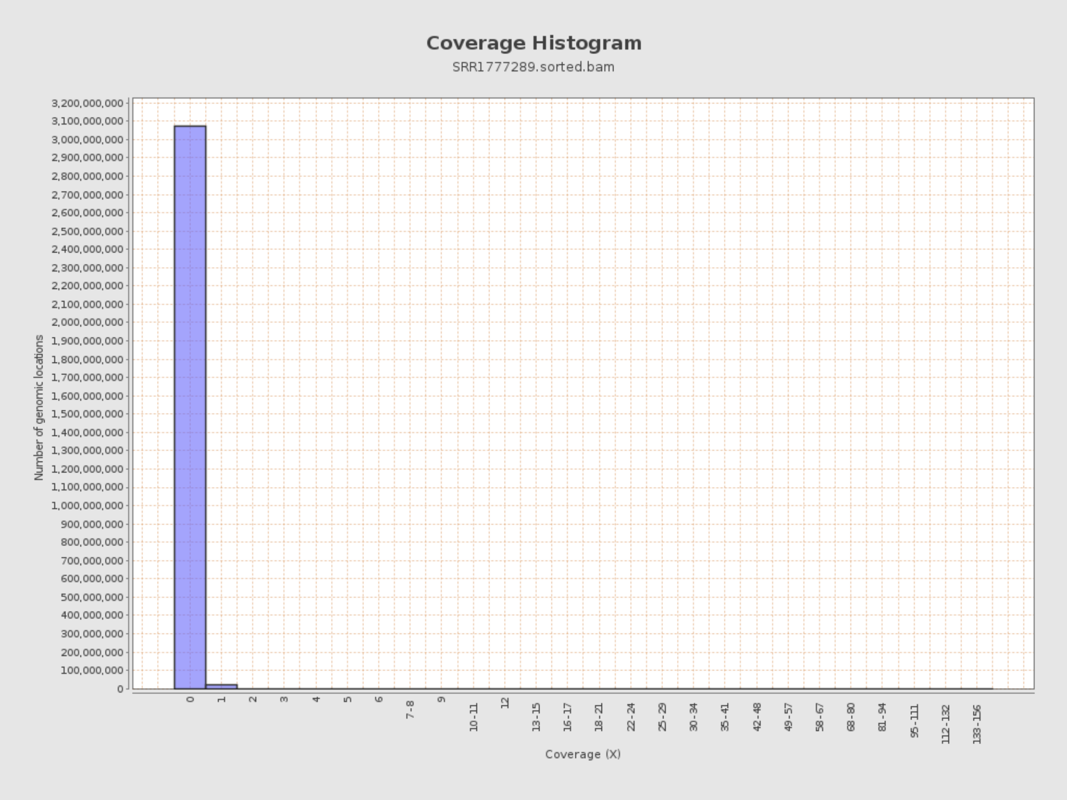
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2078637	0.0083	0.1562
chr2	243199373	2251445	0.0093	0.1196
chr3	198022430	1800730	0.0091	0.1006
chr4	191154276	1763612	0.0092	0.1074
chr5	180915260	1607432	0.0089	0.0964
chr6	171115067	1517382	0.0089	0.0988
chr7	159138663	1397403	0.0088	0.1072

chr8	146364022	1337860	0.0091	0.1033
chr9	141213431	1047144	0.0074	0.0926
chr10	135534747	1384715	0.0102	0.2288
chr11	135006516	1206485	0.0089	0.0998
chr12	133851895	1182806	0.0088	0.0965
chr13	115169878	838301	0.0073	0.0867
chr14	107349540	771464	0.0072	0.0875
chr15	102531392	703482	0.0069	0.0842
chr16	90354753	864669	0.0096	0.1589
chr17	81195210	638944	0.0079	0.0927
chr18	78077248	703486	0.009	0.1219
chr19	59128983	445878	0.0075	0.1282
chr20	63025520	541148	0.0086	0.0967
chr21	48129895	347822	0.0072	0.0952
chr22	51304566	251959	0.0049	0.0777
chrMT	16571	70746	4.2693	2.5021
chrX	155270560	792476	0.0051	0.0753
chrY	59373566	373157	0.0063	0.1383

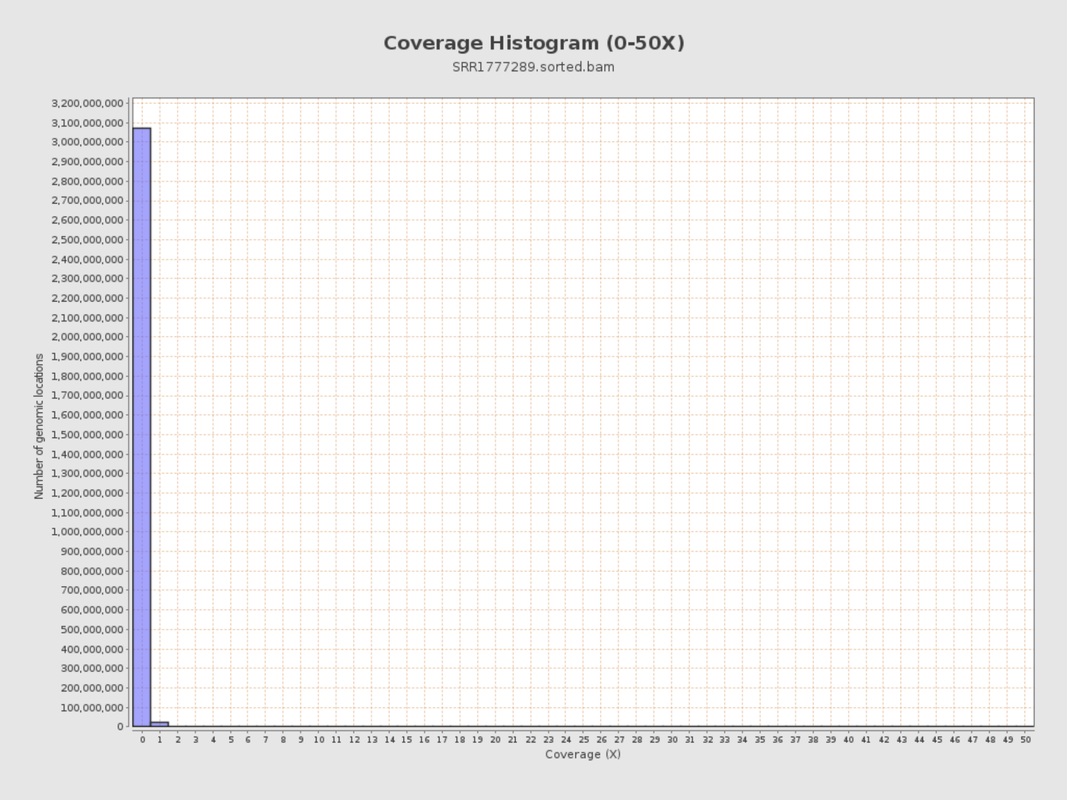
3. Results : Coverage across reference



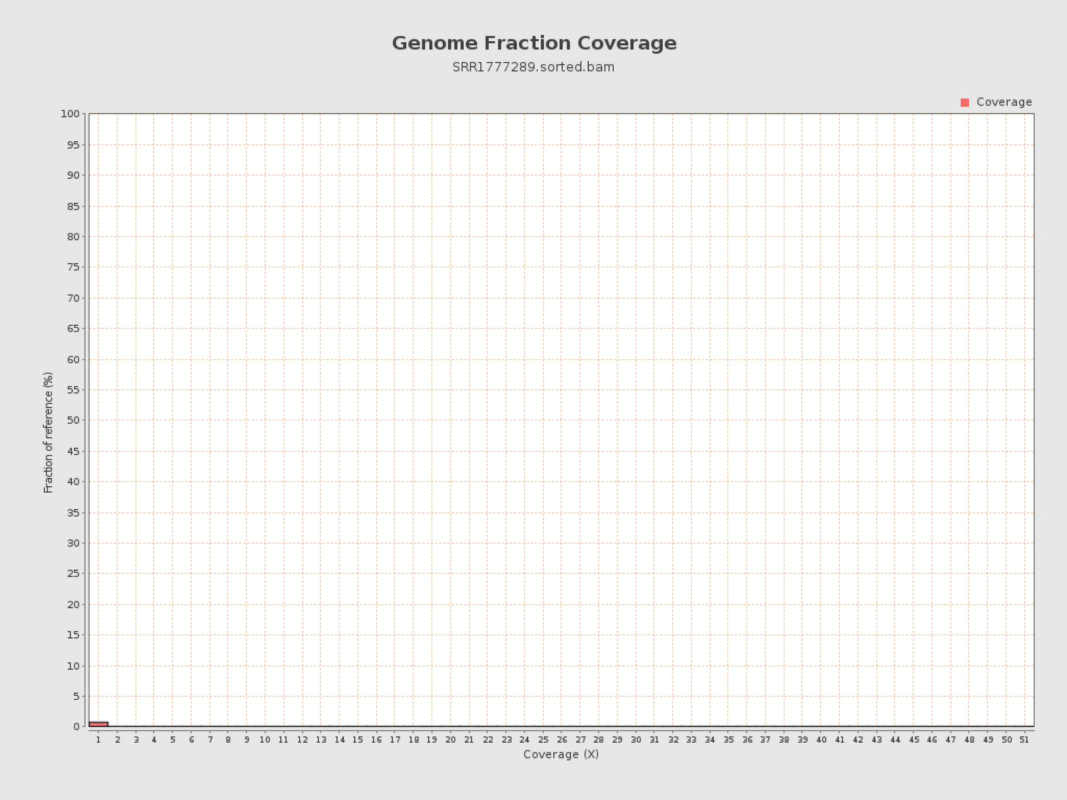
4. Results : Coverage Histogram



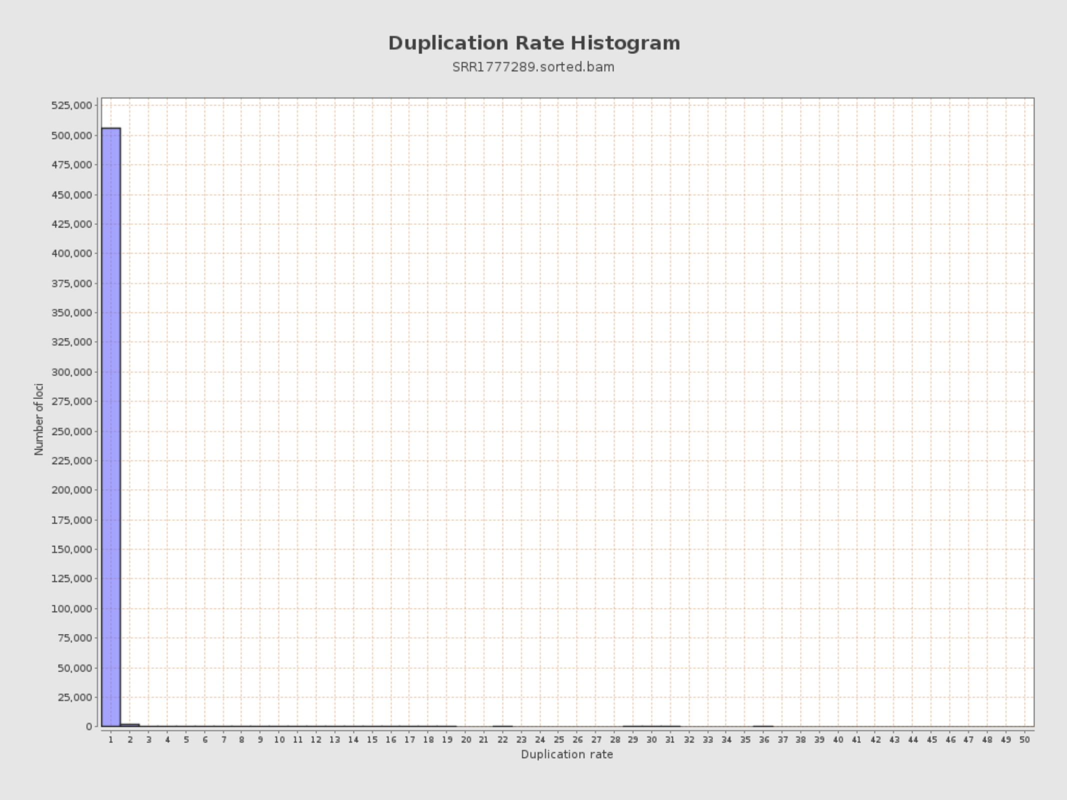
5. Results : Coverage Histogram (0-50X)



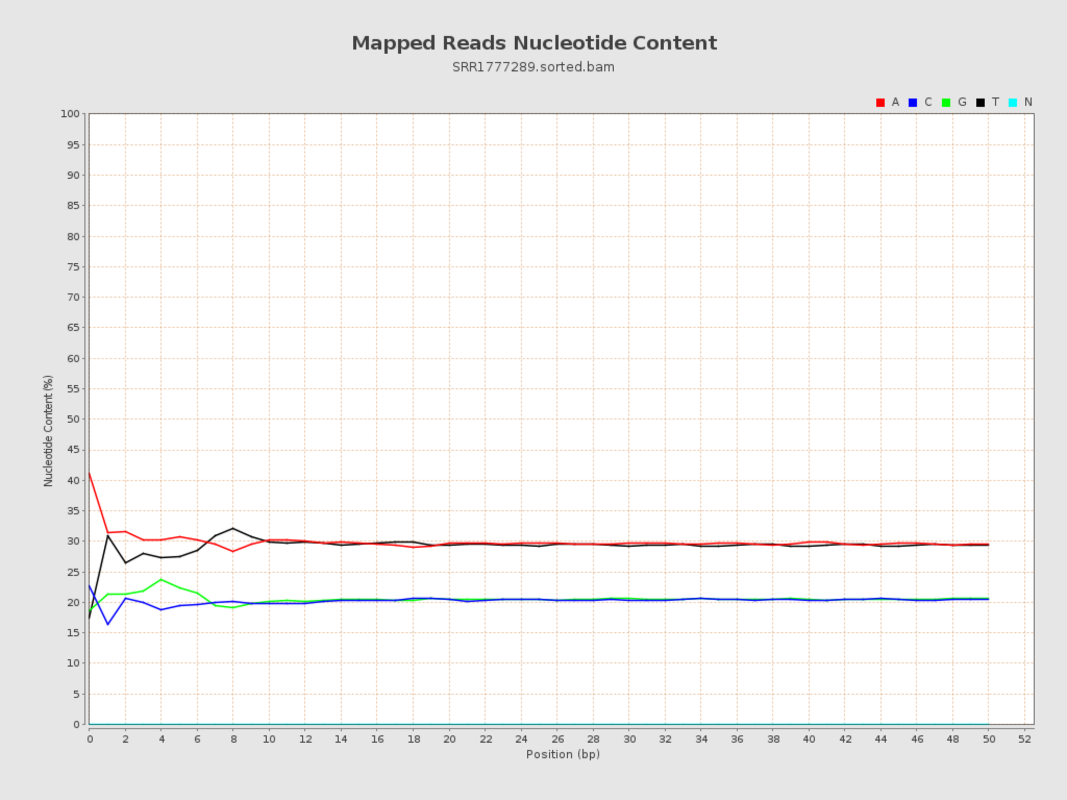
6. Results : Genome Fraction Coverage



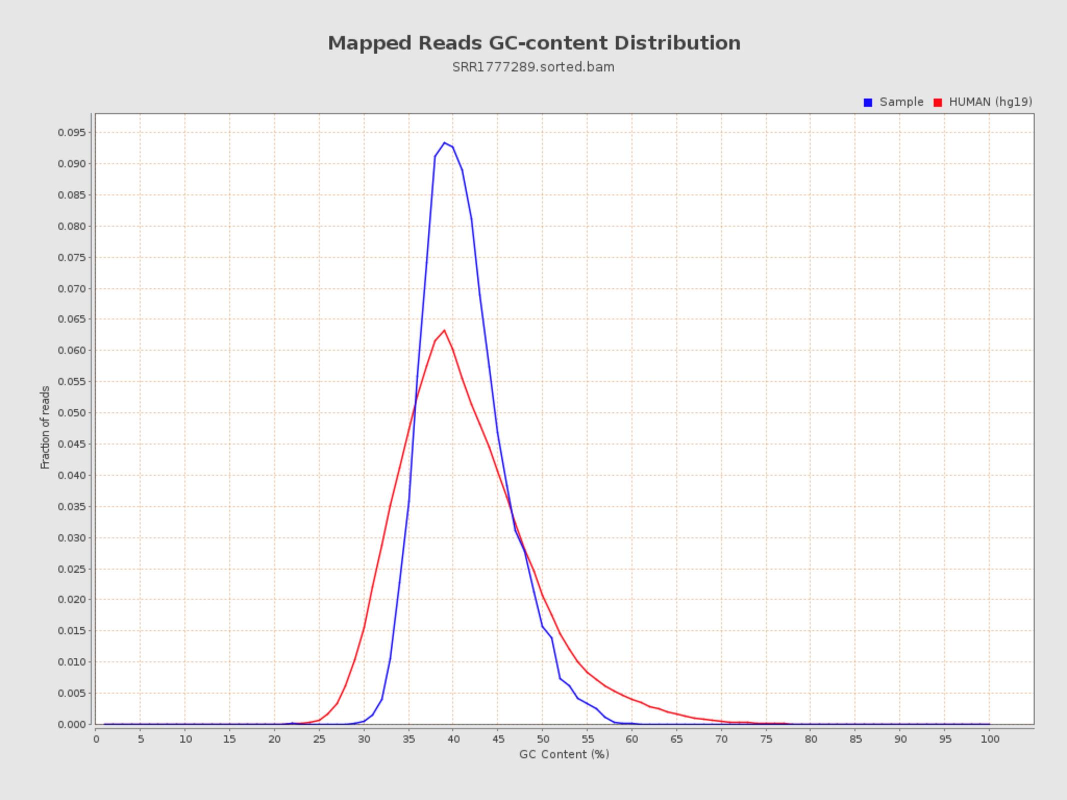
7. Results : Duplication Rate Histogram



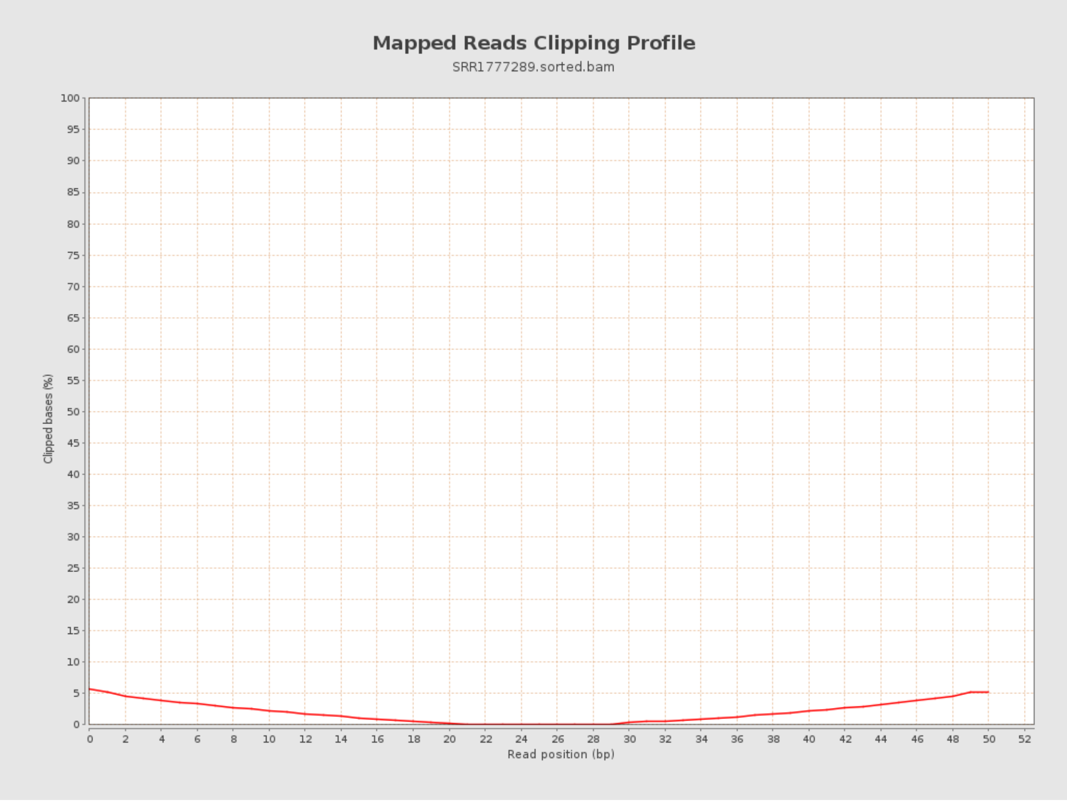
8. Results : Mapped Reads Nucleotide Content



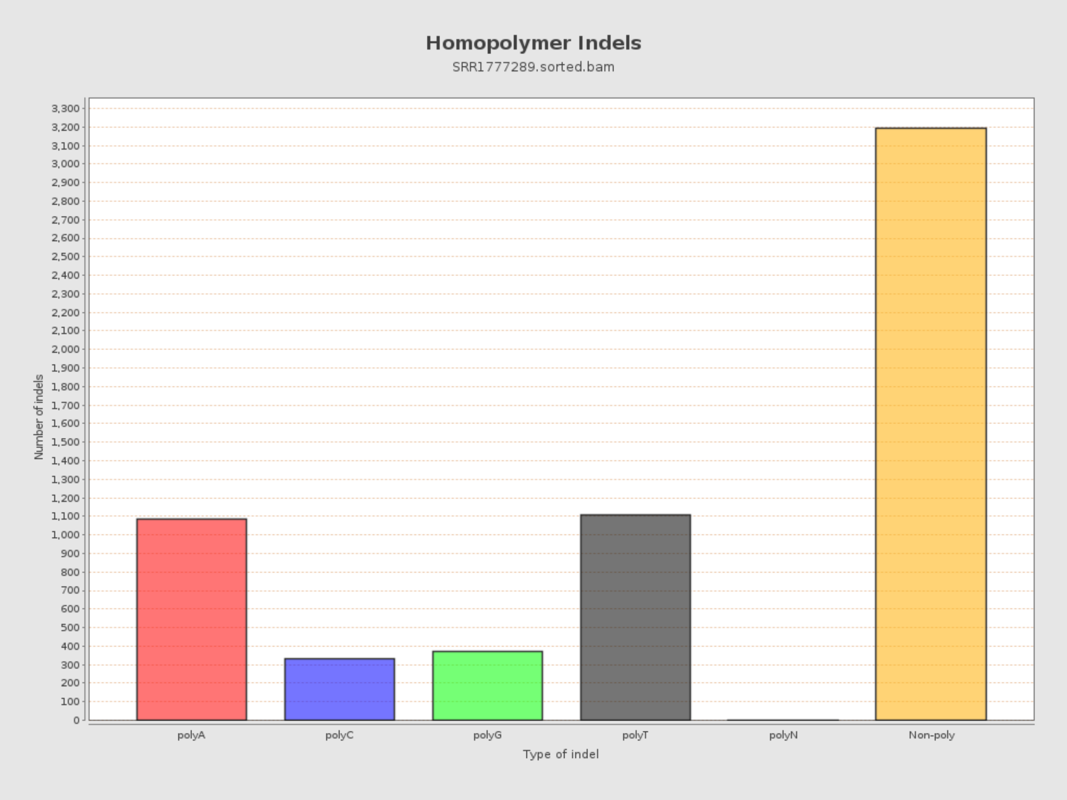
9. Results : Mapped Reads GC-content Distribution



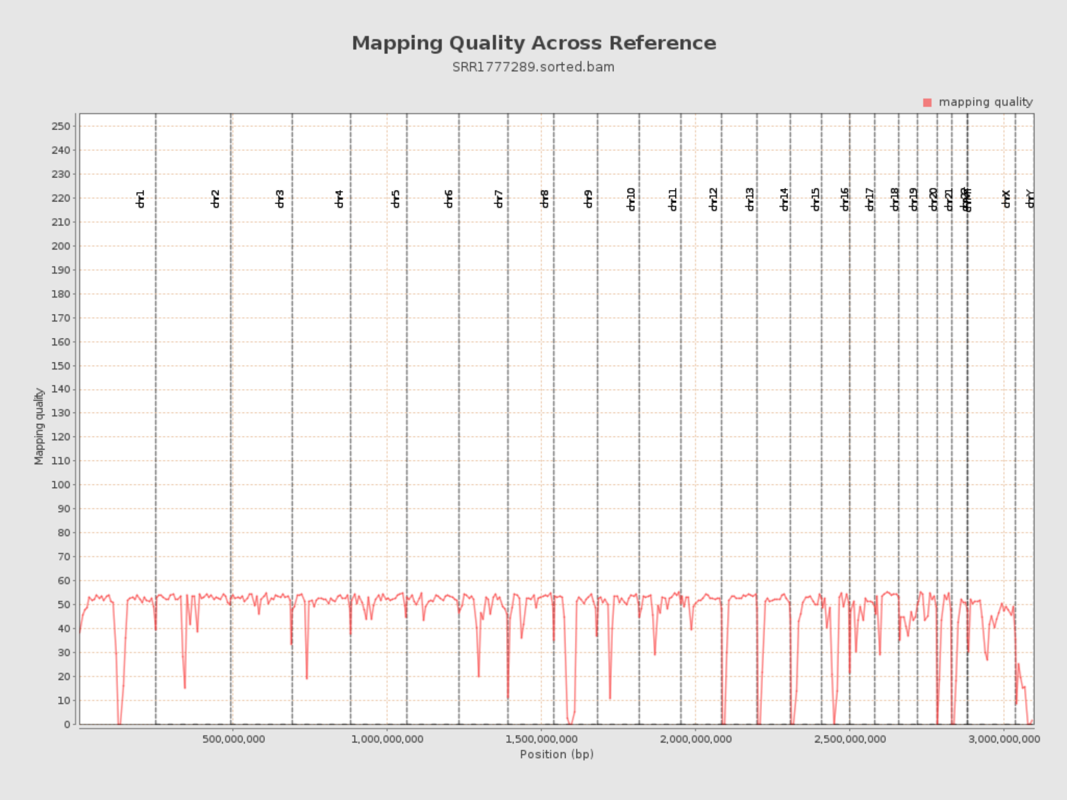
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram