Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 19:10:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779400.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_SRR1779400 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779400_1.fastq.gz SRR1779400_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 19:10:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779400.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,206,876
Mapped reads	17,398,072 / 95.56%
Unmapped reads	808,804 / 4.44%
Mapped paired reads	17,398,072 / 95.56%
Mapped reads, first in pair	8,766,848 / 48.15%
Mapped reads, second in pair	8,631,224 / 47.41%
Mapped reads, both in pair	17,227,090 / 94.62%
Mapped reads, singletons	170,982 / 0.94%
Secondary alignments	0
Supplementary alignments	59,483 / 0.33%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	697,679 / 3.83%
Duplication rate	3.57%
Clipped reads	754,565 / 4.14%

2.2. ACGT Content

Number/percentage of A's	414,390,304 / 29.97%
Number/percentage of C's	275,371,605 / 19.92%
Number/percentage of T's	412,272,268 / 29.82%
Number/percentage of G's	280,177,007 / 20.27%
Number/percentage of N's	303,744 / 0.02%

GC Percentage	40.18%

2.3. Coverage

Mean	0.4467
Standard Deviation	1.8582

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	47,050.91
Standard Deviation	2,046,419.47
P25/Median/P75	141 / 183 / 234

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	4,624,412
Insertions	124,792
Mapped reads with at least one insertion	0.71%
Deletions	147,685
Mapped reads with at least one deletion	0.84%
Homopolymer indels	47.2%

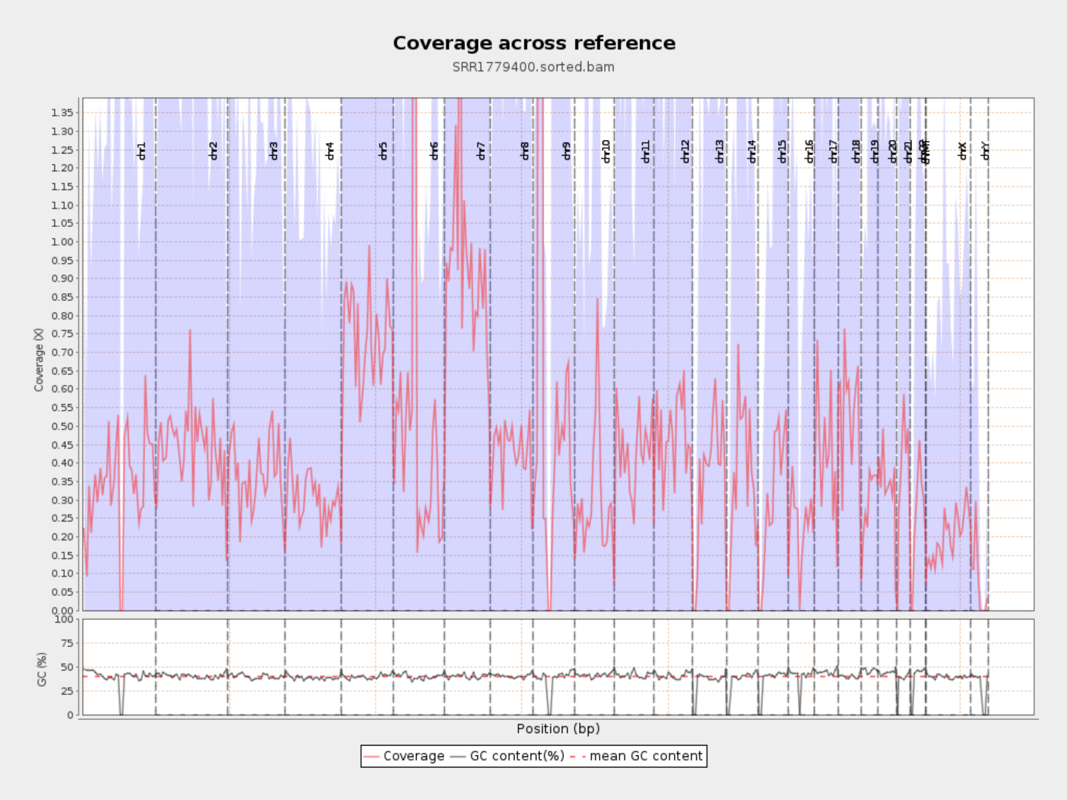
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

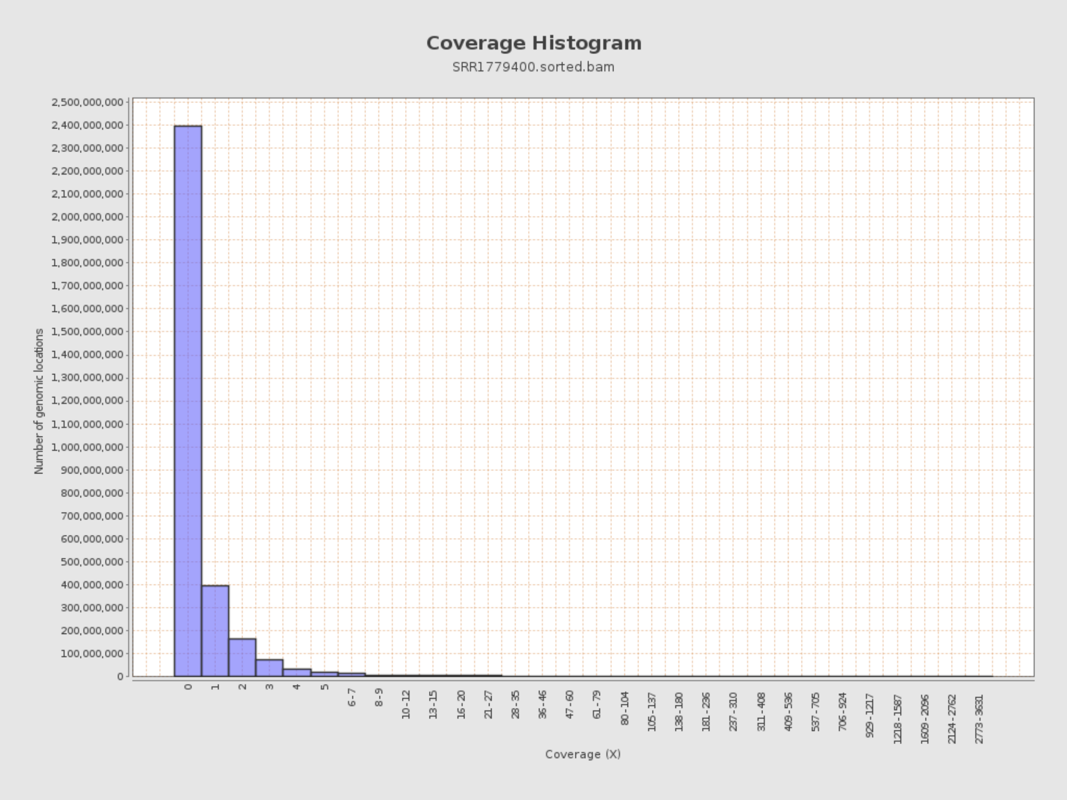
		bases	coverage	deviation
chr1	249250621	85294615	0.3422	3.7261
chr2	243199373	108596020	0.4465	1.1076
chr3	198022430	72702386	0.3671	0.9009
chr4	191154276	58641606	0.3068	0.8084
chr5	180915260	133094474	0.7357	1.3096
chr6	171115067	93096458	0.5441	2.2114
chr7	159138663	150945043	0.9485	2.6777
chr8	146364022	63184941	0.4317	1.0044
chr9	141213431	138480507	0.9806	4.0746
chr10	135534747	40668184	0.3001	1.6103
chr11	135006516	57720646	0.4275	1.115
chr12	133851895	63262322	0.4726	1.0301
chr13	115169878	41631849	0.3615	0.9036
chr14	107349540	38542698	0.359	0.8848
chr15	102531392	31693710	0.3091	0.8403
chr16	90354753	20690176	0.229	0.7502
chr17	81195210	35209853	0.4336	1.0795
chr18	78077248	42760242	0.5477	1.4761
chr19	59128983	17679897	0.299	2.2171
chr20	63025520	22068158	0.3501	0.9211
chr21	48129895	17507188	0.3637	0.9457
chr22	51304566	13128902	0.2559	0.7766
chrMT	16571	1102	0.0665	0.2851
chrX	155270560	31288276	0.2015	0.6684

chrY	59373566	4933811	0.0831	0.4543

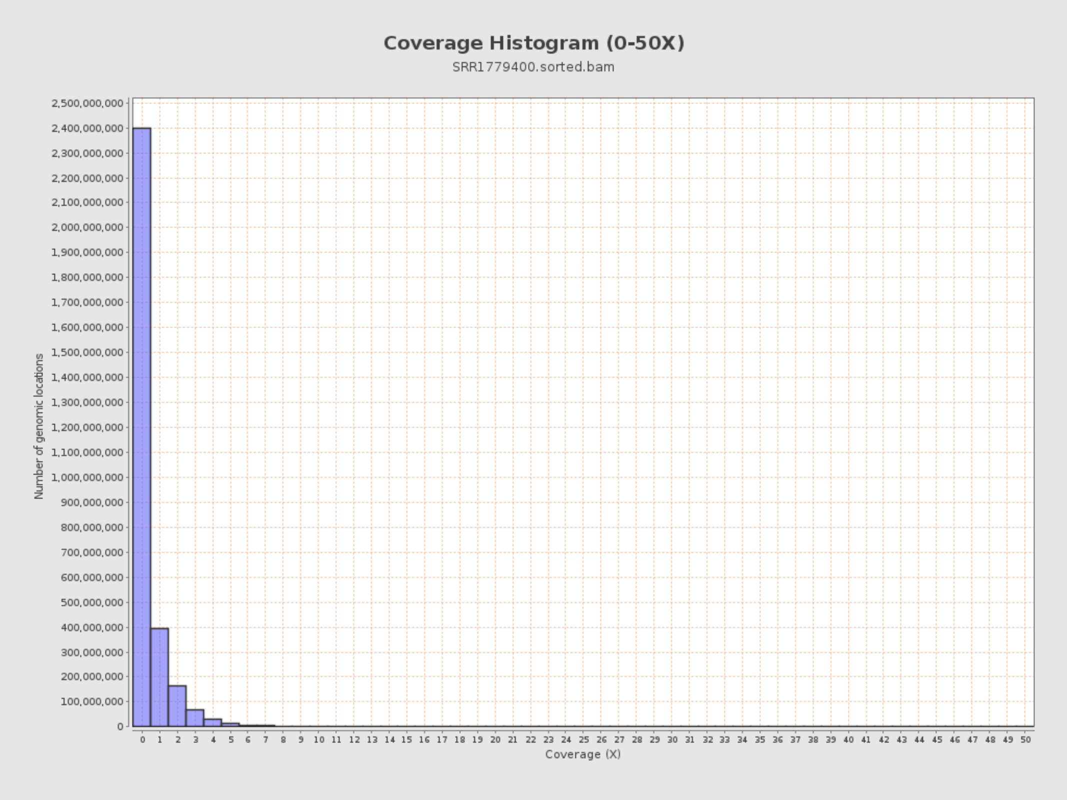
3. Results : Coverage across reference



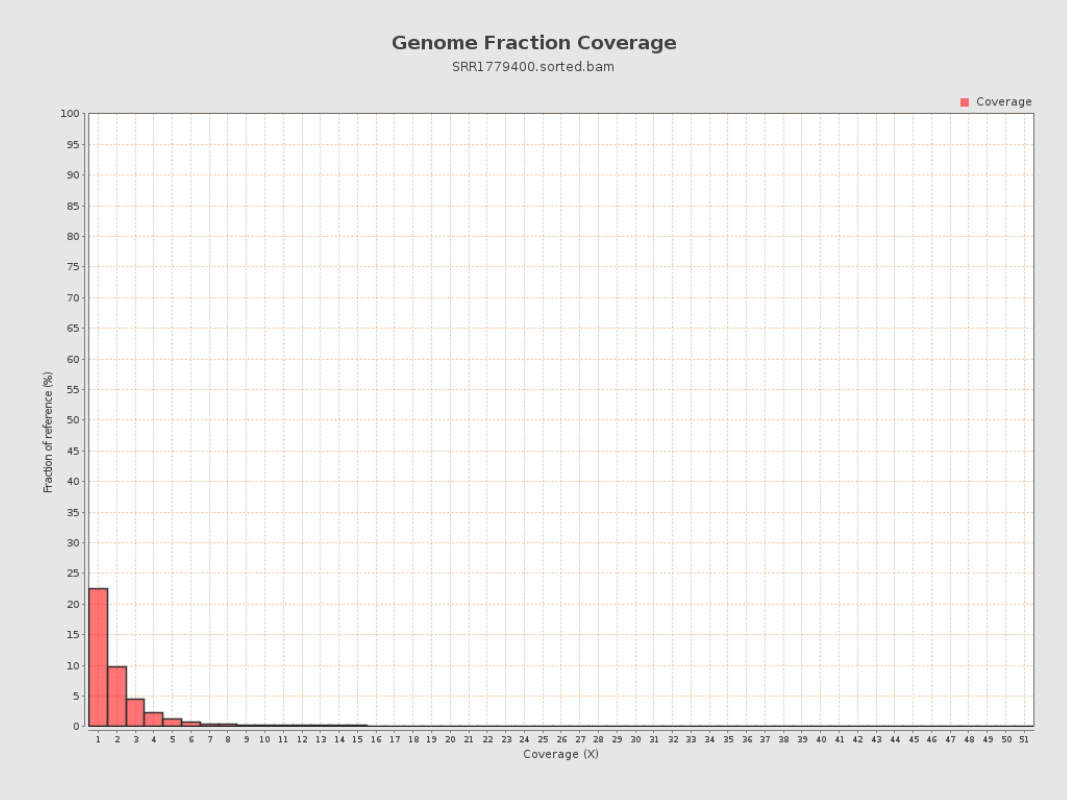
4. Results : Coverage Histogram



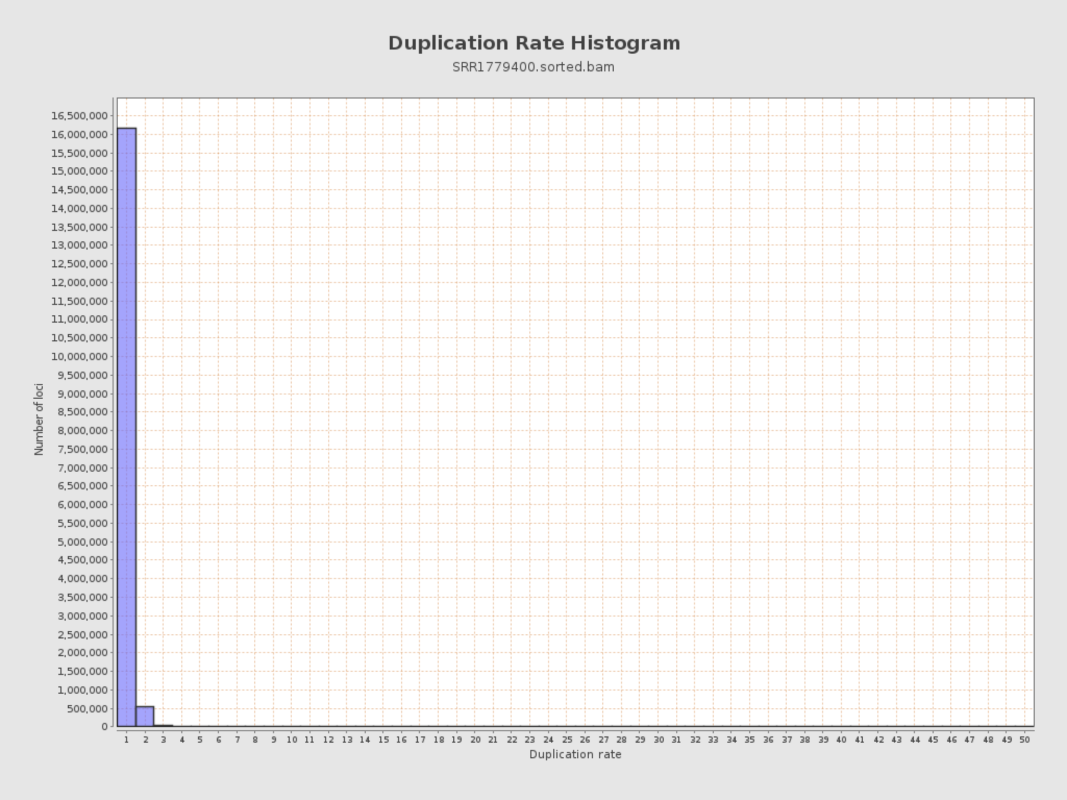
5. Results : Coverage Histogram (0-50X)



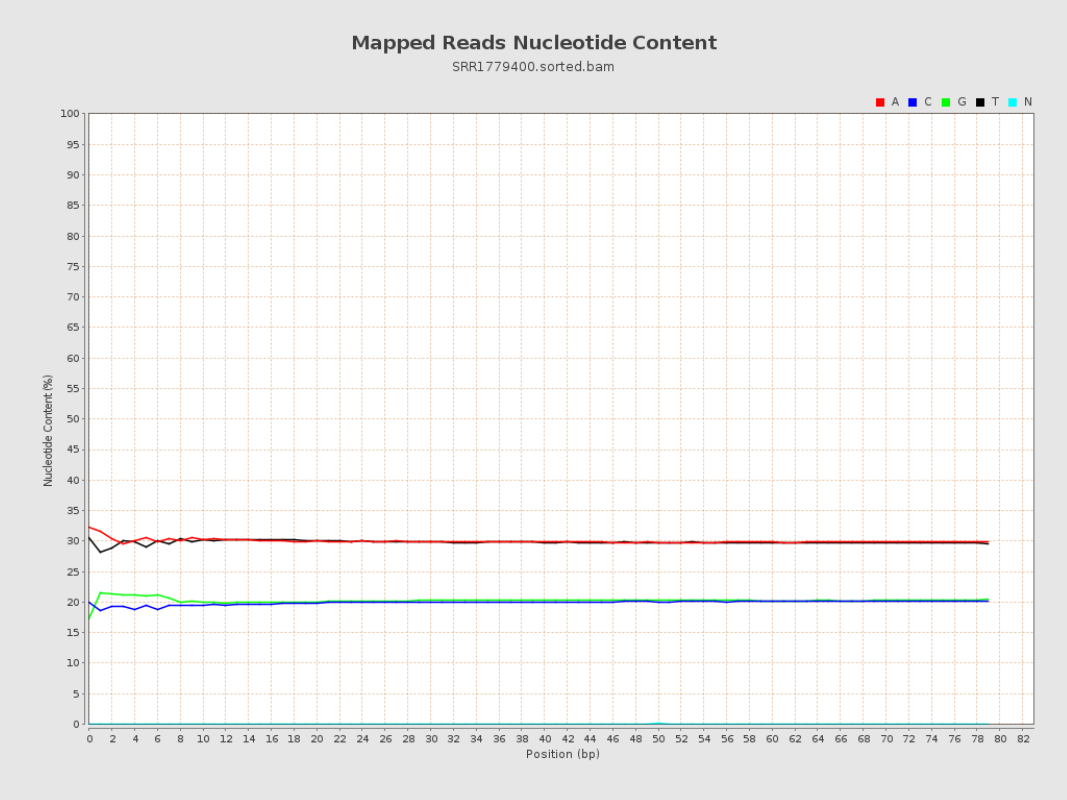
6. Results : Genome Fraction Coverage



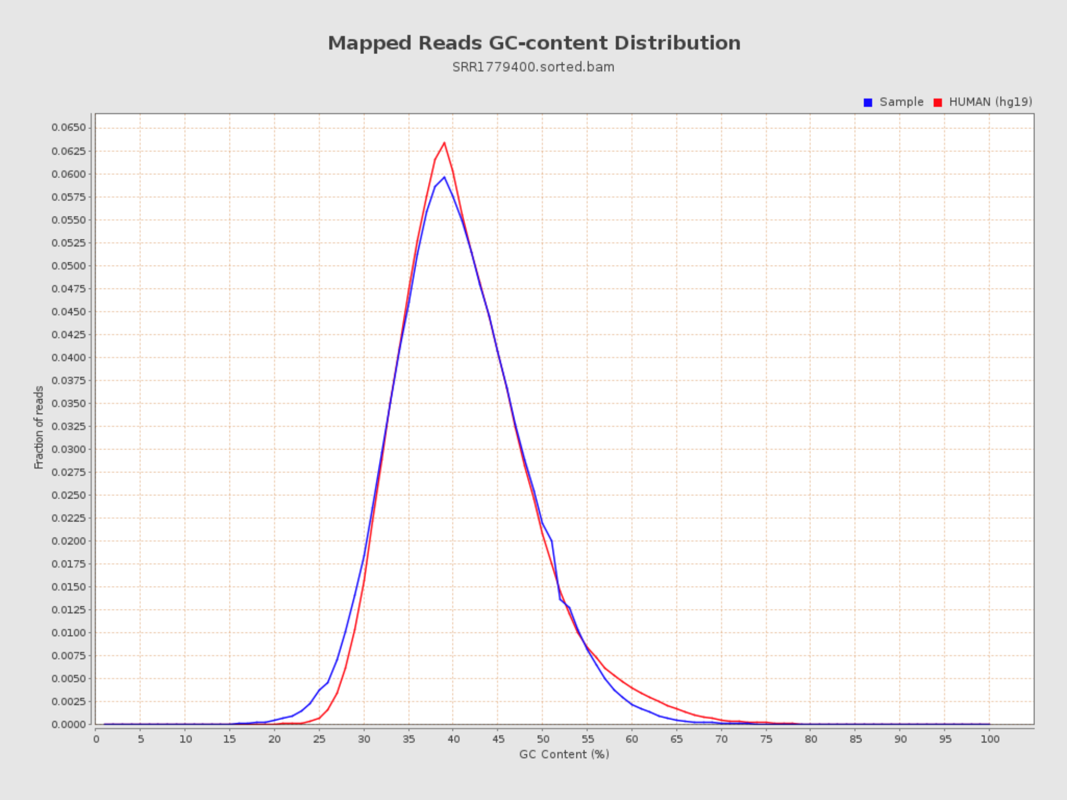
7. Results : Duplication Rate Histogram



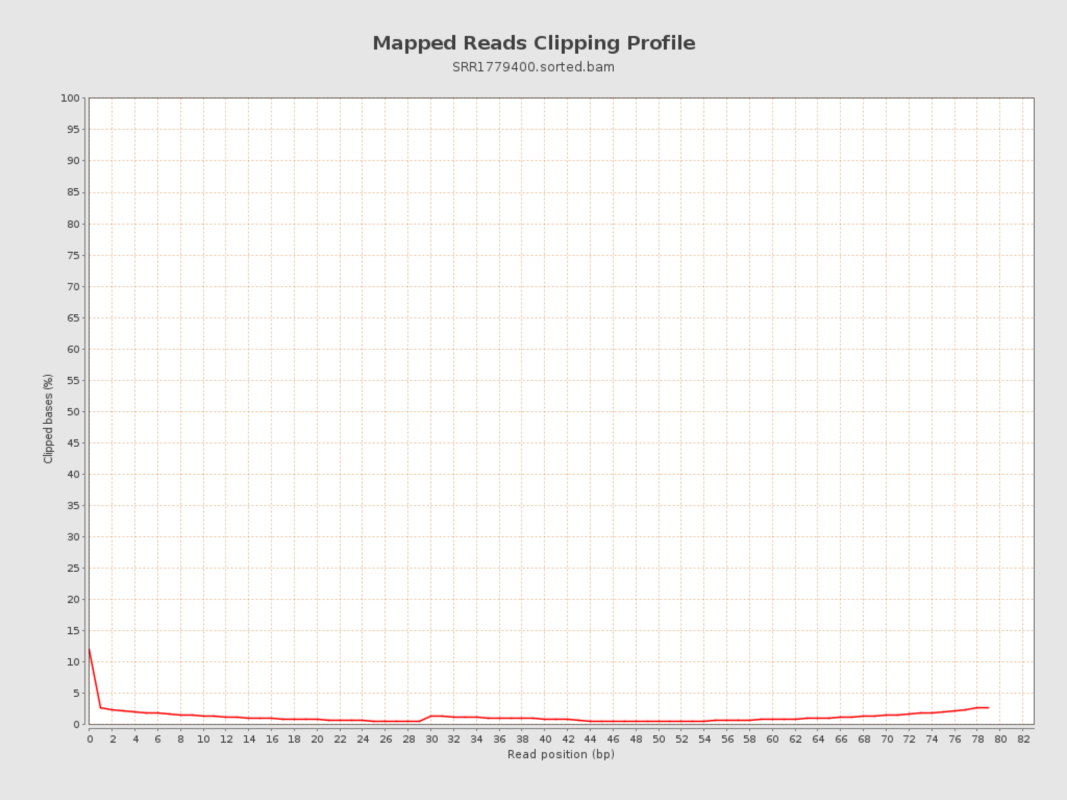
8. Results : Mapped Reads Nucleotide Content



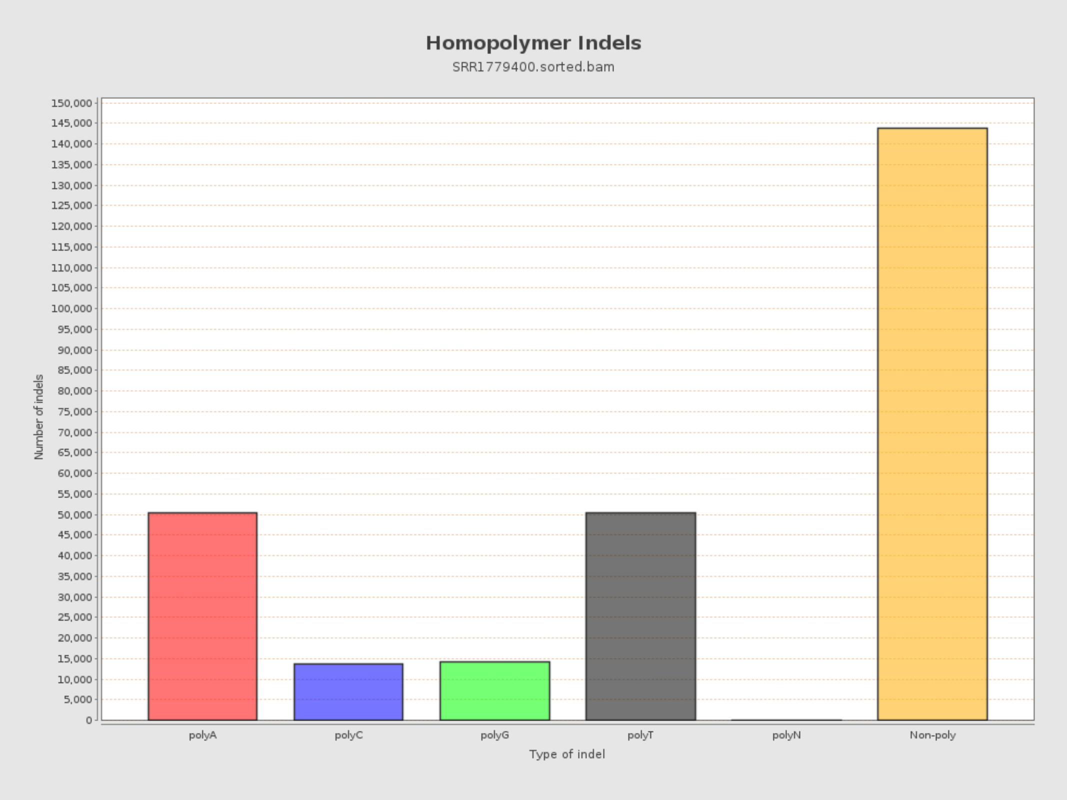
9. Results : Mapped Reads GC-content Distribution



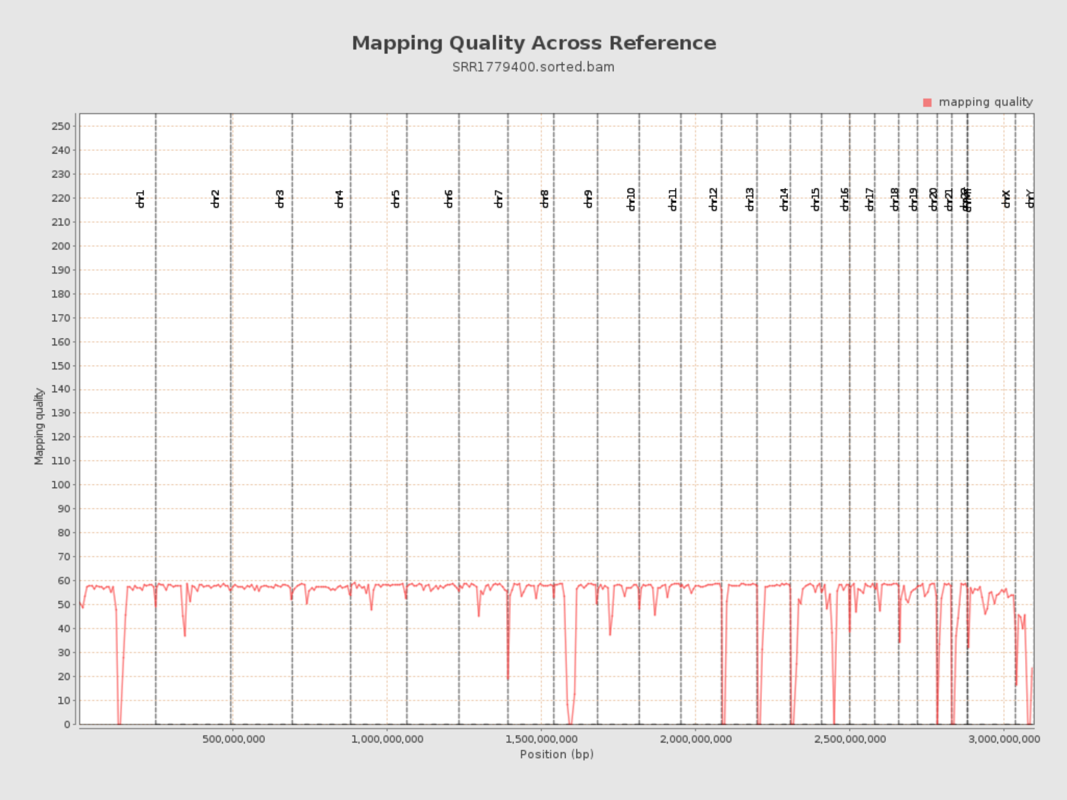
10. Results : Mapped Reads Clipping Profile



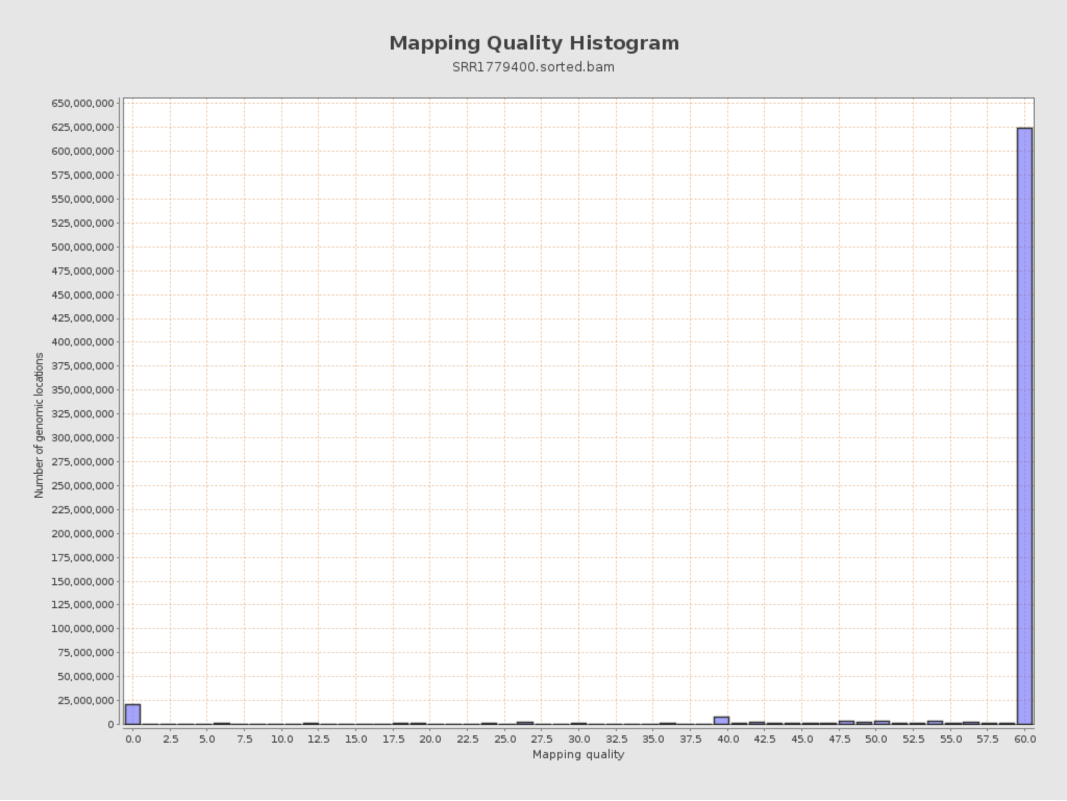
11. Results : Homopolymer Indels



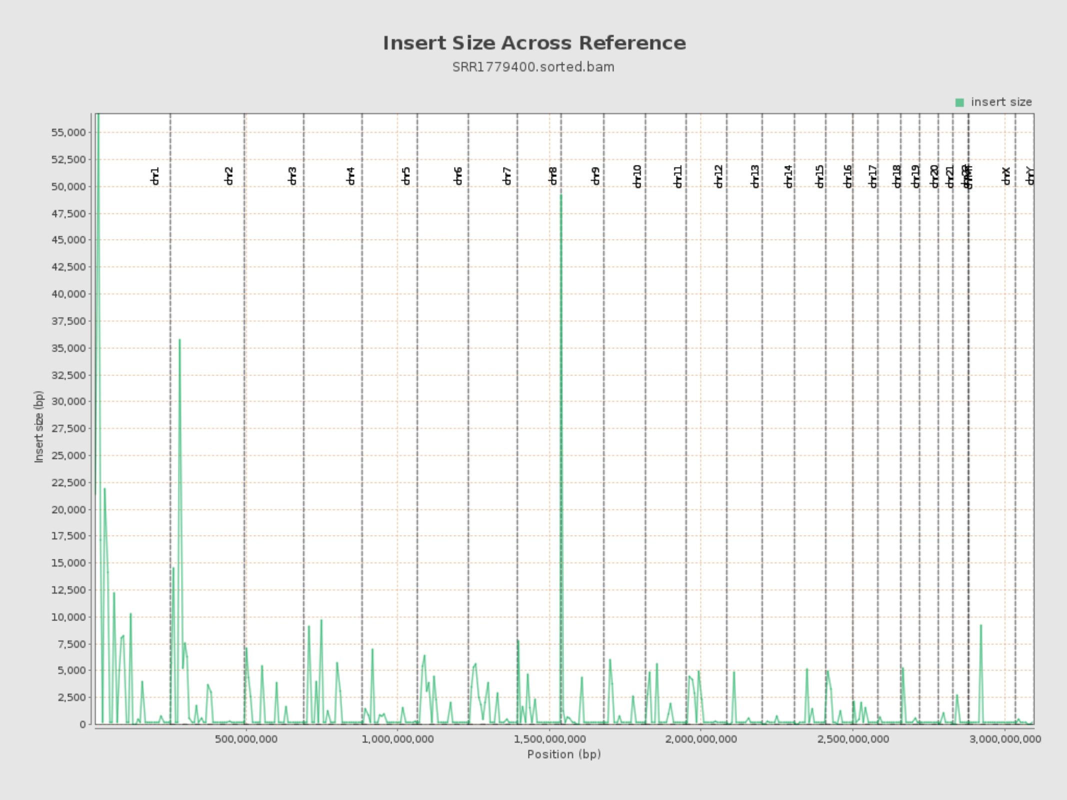
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram