Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 23:31:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779342.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_SRR1779342 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779342_1.fastq.gz SRR1779342_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 23:31:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779342.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	155,871,204
Mapped reads	151,170,143 / 96.98%
Unmapped reads	4,701,061 / 3.02%
Mapped paired reads	151,170,143 / 96.98%
Mapped reads, first in pair	76,246,646 / 48.92%
Mapped reads, second in pair	74,923,497 / 48.07%
Mapped reads, both in pair	149,123,730 / 95.67%
Mapped reads, singletons	2,046,413 / 1.31%
Secondary alignments	0
Supplementary alignments	572,248 / 0.37%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	9,950,578 / 6.38%
Duplication rate	6.3%
Clipped reads	9,194,372 / 5.9%

2.2. ACGT Content

Number/percentage of A's	4,409,741,038 / 29.46%
Number/percentage of C's	3,062,625,989 / 20.46%
Number/percentage of T's	4,392,443,104 / 29.34%
Number/percentage of G's	3,103,549,426 / 20.73%
Number/percentage of N's	967,543 / 0.01%

GC Percentage	41.19%

2.3. Coverage

Mean	4.8366
Standard Deviation	7.108

2.4. Mapping Quality

Mean Mapping Quality	53.85

2.5. Insert size

Mean	48,194.45
Standard Deviation	2,173,767.84
P25/Median/P75	150 / 195 / 253

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	53,202,347
Insertions	1,430,809
Mapped reads with at least one insertion	0.93%
Deletions	1,474,319
Mapped reads with at least one deletion	0.96%
Homopolymer indels	46.82%

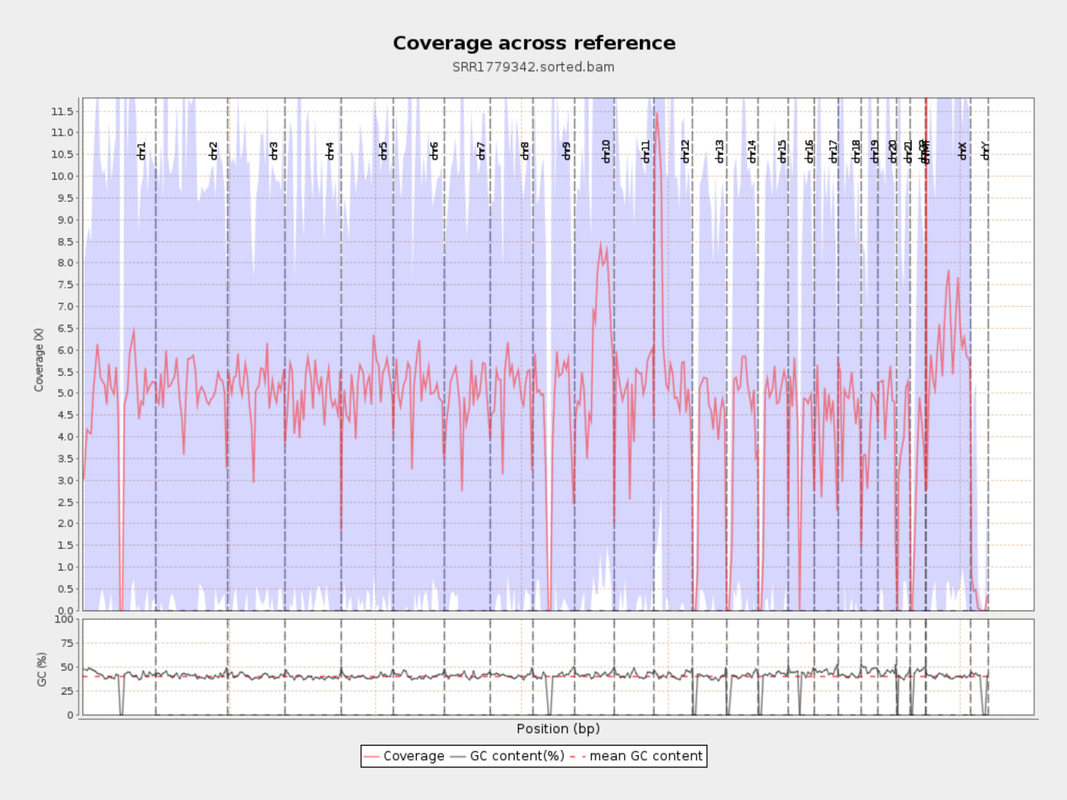
2.7. Chromosome stats

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

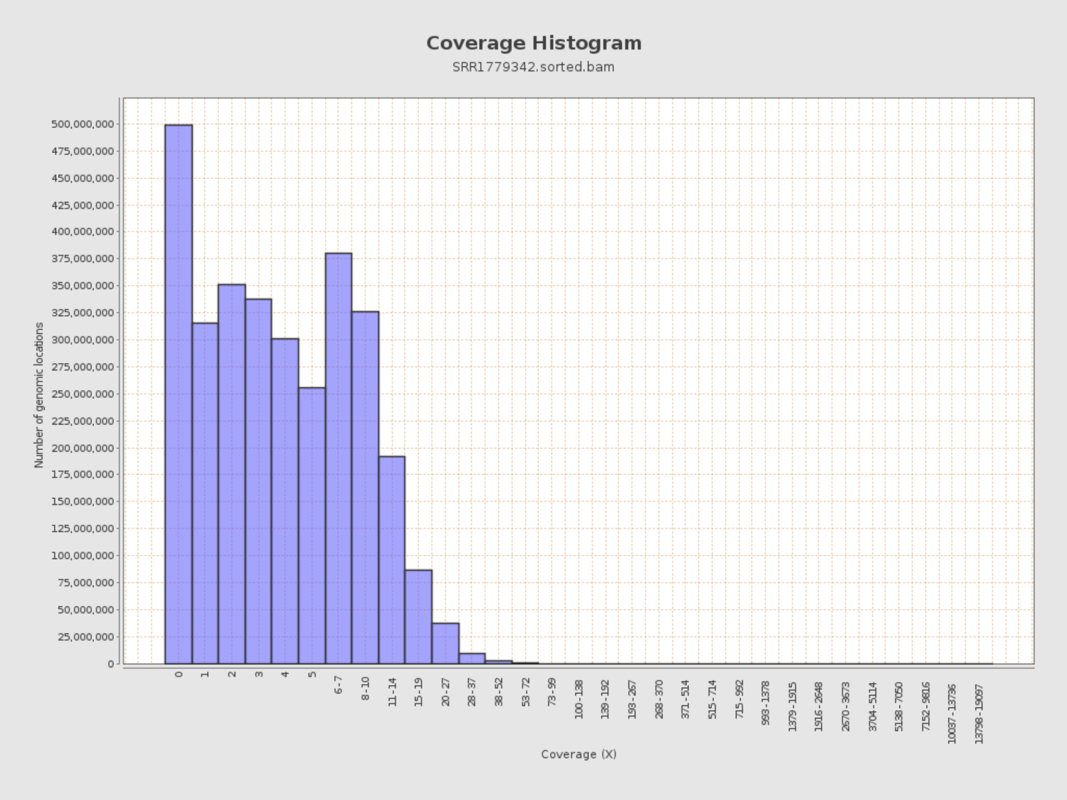
		bases	coverage	deviation
chr1	249250621	1192108344	4.7828	8.3409
chr2	243199373	1238628596	5.0931	15.592
chr3	198022430	1015217826	5.1268	4.6648
chr4	191154276	955125500	4.9966	5.3415
chr5	180915260	929342888	5.1369	4.6254
chr6	171115067	880425961	5.1452	5.4261
chr7	159138663	774620315	4.8676	5.2734
chr8	146364022	744170923	5.0844	4.7917
chr9	141213431	620372948	4.3932	6.0133
chr10	135534747	837058131	6.176	7.9944
chr11	135006516	687539892	5.0926	4.9556
chr12	133851895	857039601	6.4029	6.6199
chr13	115169878	455834576	3.9579	4.2684
chr14	107349540	448587404	4.1788	4.6427
chr15	102531392	422341765	4.1191	4.672
chr16	90354753	370663790	4.1023	4.8072
chr17	81195210	348744652	4.2951	5.2109
chr18	78077248	371883671	4.763	6.0624
chr19	59128983	233504233	3.9491	6.2553
chr20	63025520	302343141	4.7972	5.3699
chr21	48129895	178994169	3.719	7.2943
chr22	51304566	145845941	2.8427	4.0359
chrMT	16571	4215112	254.3668	58.8139
chrX	155270560	943689354	6.0777	5.641

chrY	59373566	14281260	0.2405	2.6325

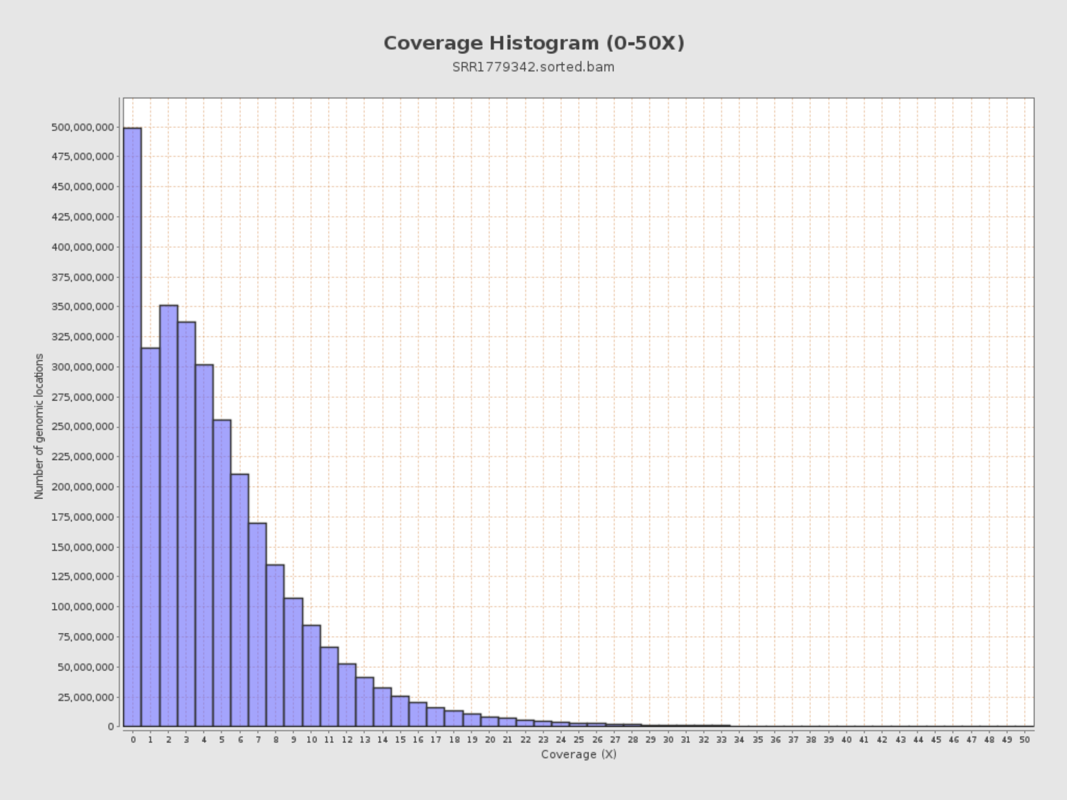
3. Results : Coverage across reference



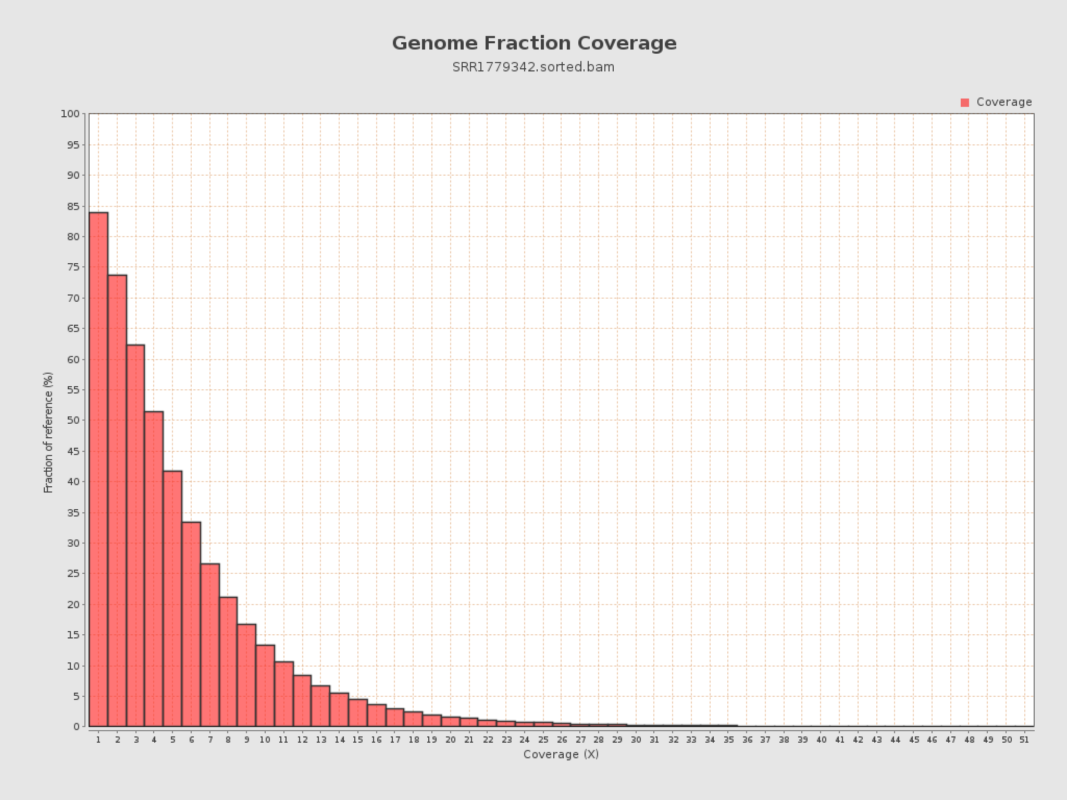
4. Results : Coverage Histogram



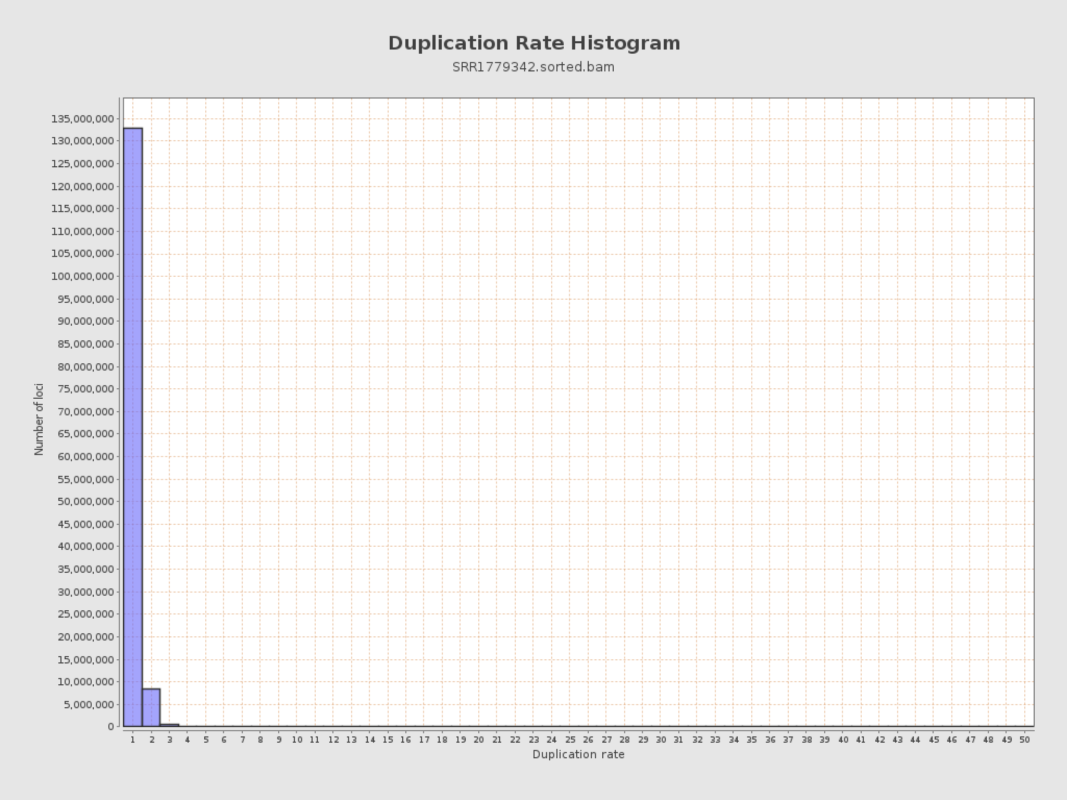
5. Results : Coverage Histogram (0-50X)



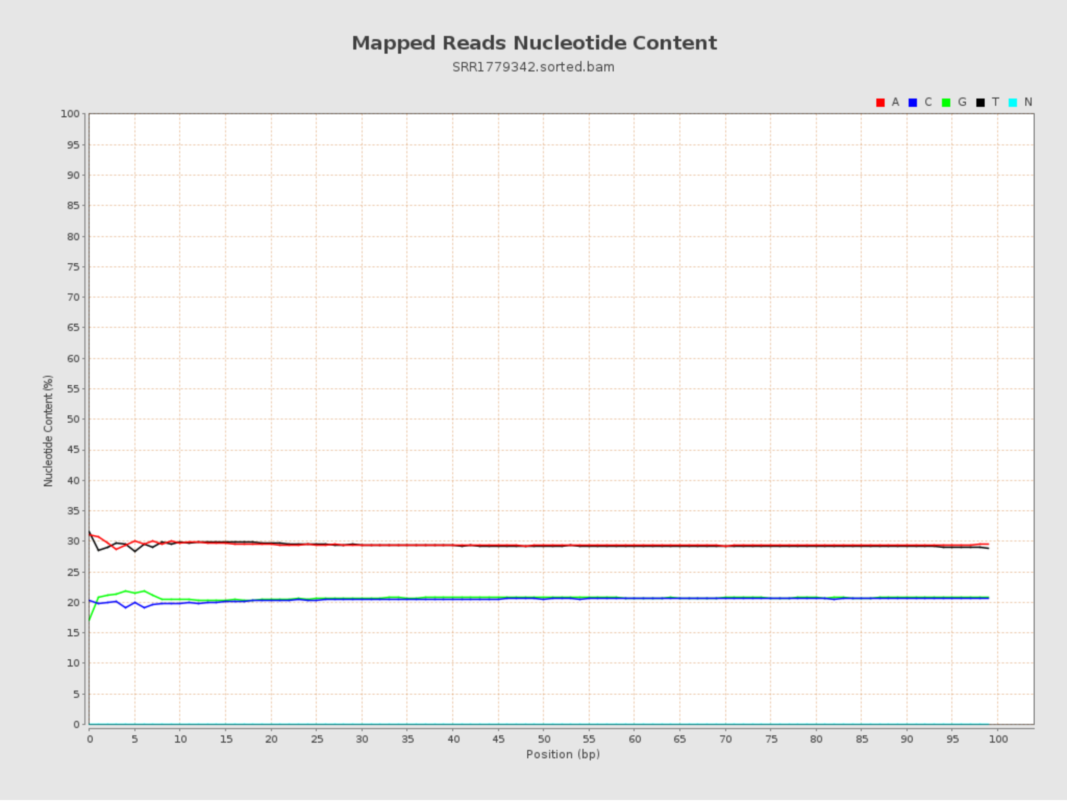
6. Results : Genome Fraction Coverage



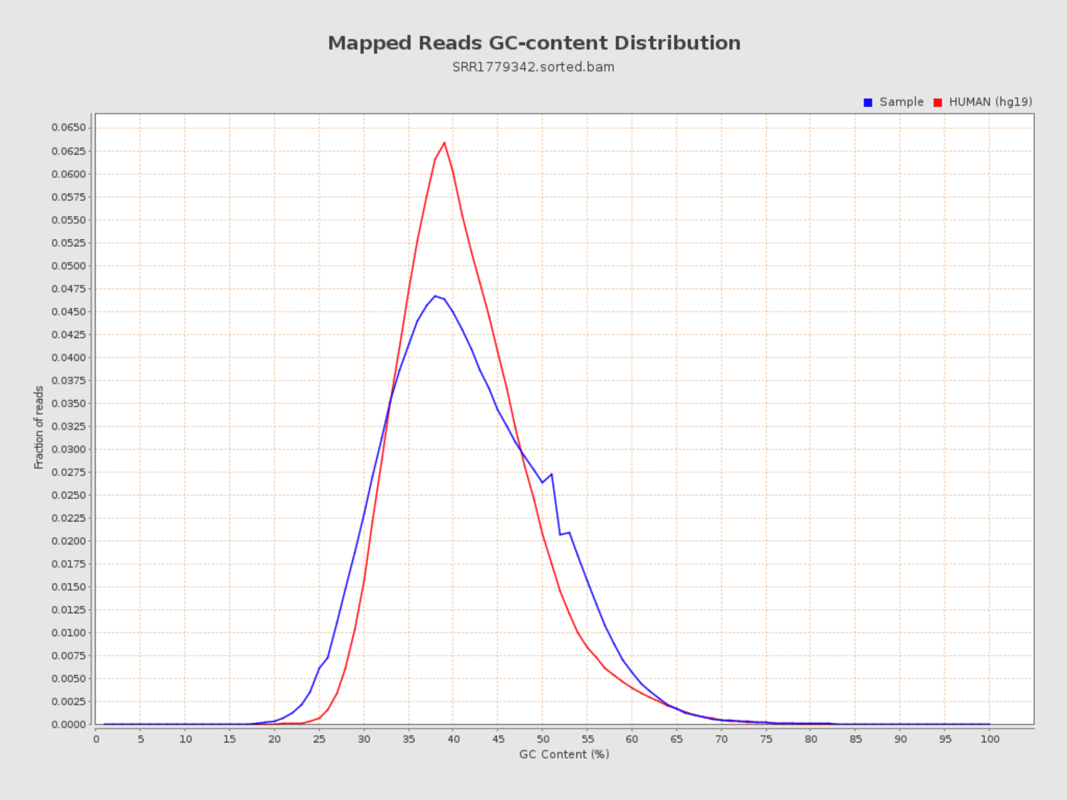
7. Results : Duplication Rate Histogram



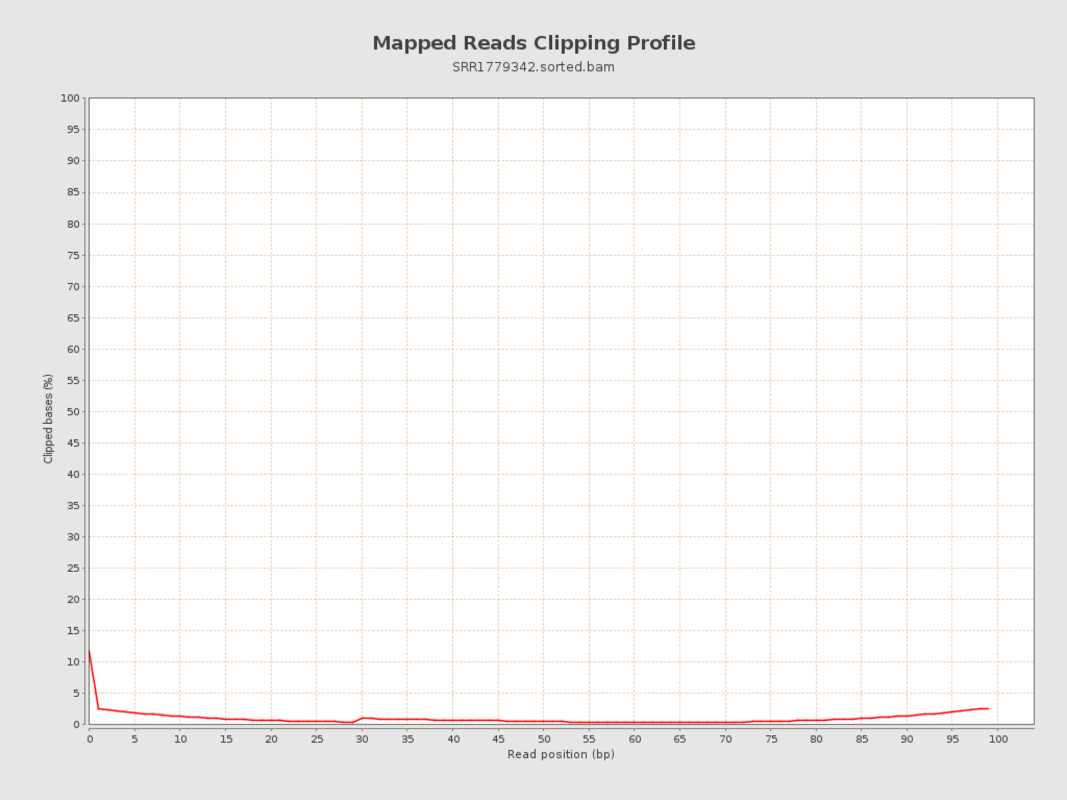
8. Results : Mapped Reads Nucleotide Content



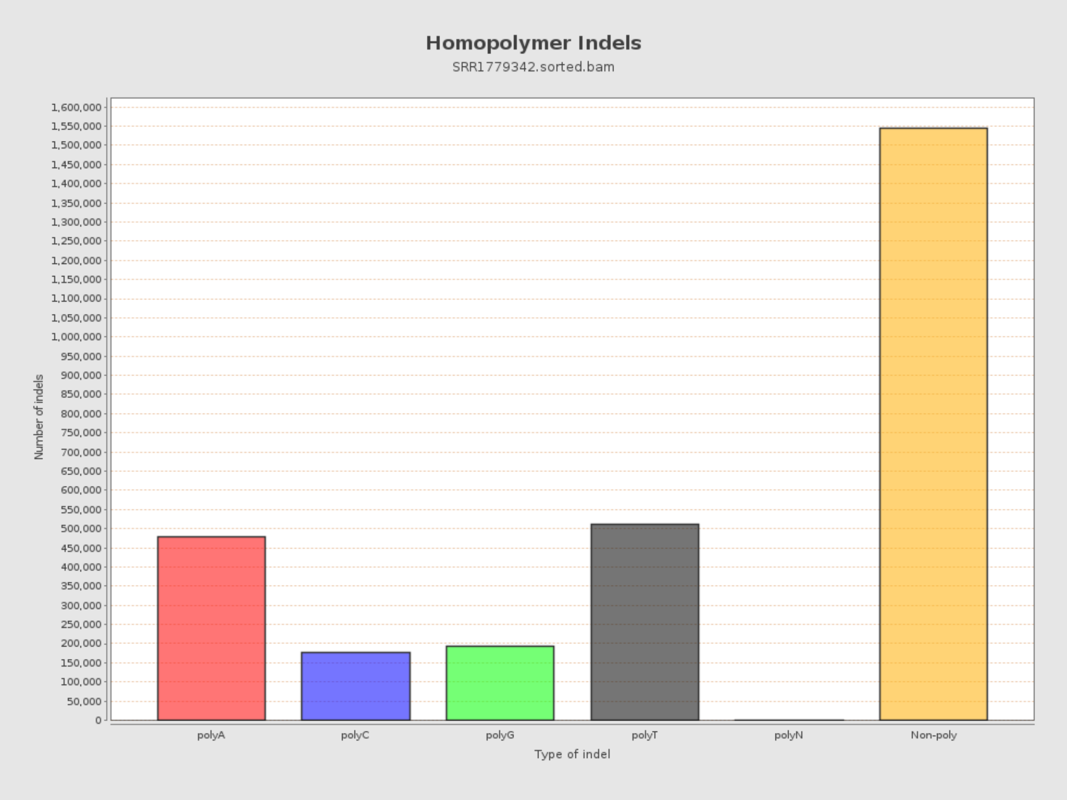
9. Results : Mapped Reads GC-content Distribution



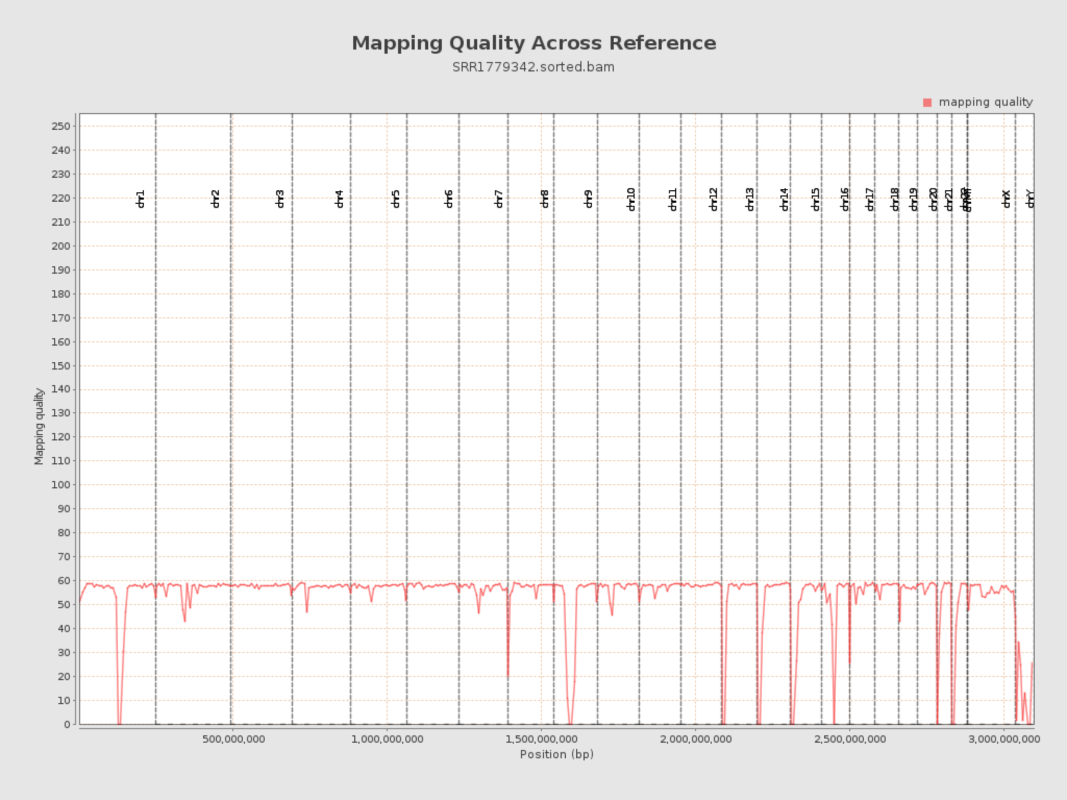
10. Results : Mapped Reads Clipping Profile



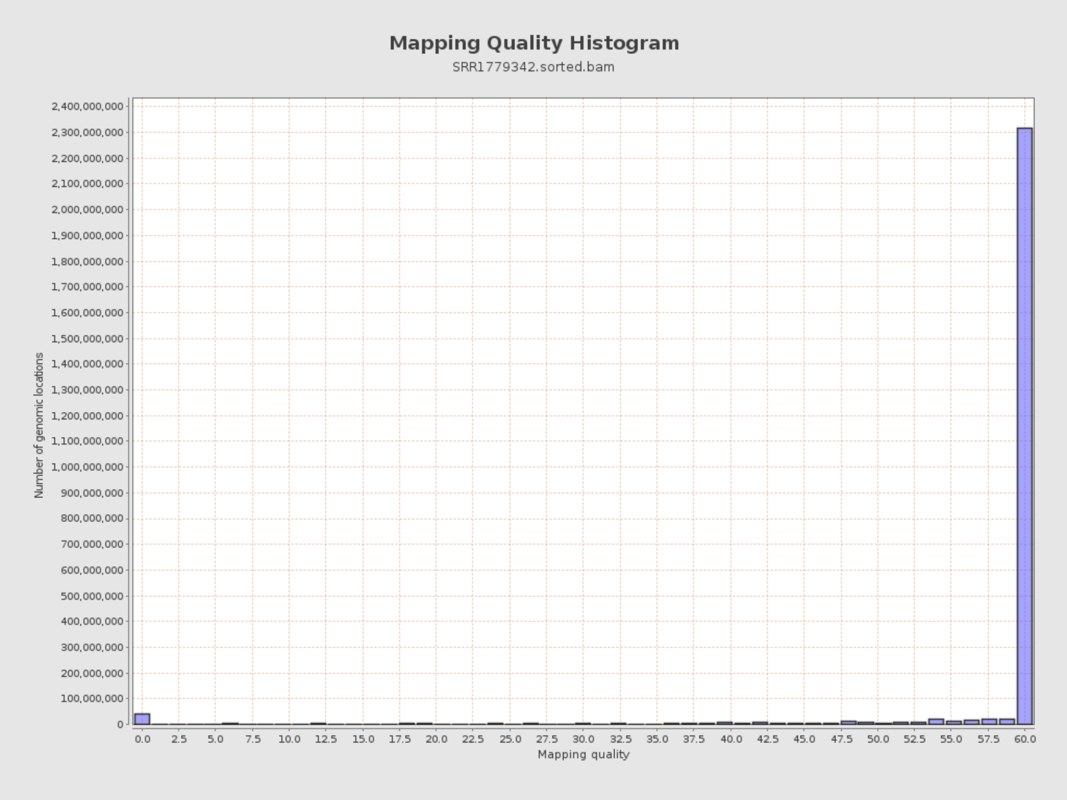
11. Results : Homopolymer Indels



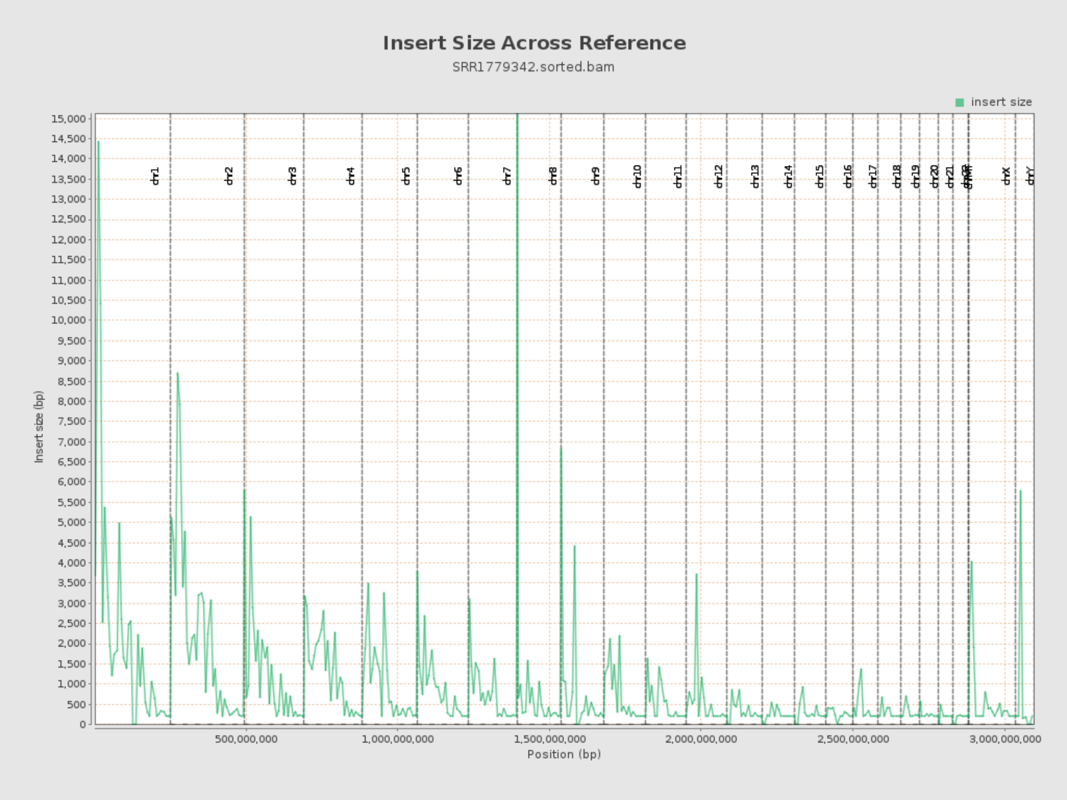
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram