Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/06 05:36:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1778057.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_SRR1778057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1778057_1.fastq.gz SRR1778057_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Oct 06 05:36:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1778057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	172,300,986
Mapped reads	162,733,539 / 94.45%
Unmapped reads	9,567,447 / 5.55%
Mapped paired reads	162,733,539 / 94.45%
Mapped reads, first in pair	82,177,317 / 47.69%
Mapped reads, second in pair	80,556,222 / 46.75%
Mapped reads, both in pair	160,450,044 / 93.12%
Mapped reads, singletons	2,283,495 / 1.33%
Secondary alignments	0
Supplementary alignments	153,225 / 0.09%
Read min/max/mean length	30 / 76 / 70.02
Duplicated reads (estimated)	104,913,681 / 60.89%
Duplication rate	51.6%
Clipped reads	13,637,018 / 7.91%

2.2. ACGT Content

Number/percentage of A's	2,840,157,073 / 25.17%
Number/percentage of C's	2,813,713,406 / 24.94%
Number/percentage of T's	2,838,028,741 / 25.15%
Number/percentage of G's	2,790,275,498 / 24.73%
Number/percentage of N's	1,342,083 / 0.01%

GC Percentage	49.67%

2.3. Coverage

Mean	3.6452
Standard Deviation	36.6008

2.4. Mapping Quality

Mean Mapping Quality	52.1

2.5. Insert size

Mean	19,395.83
Standard Deviation	1,387,185.33
P25/Median/P75	86 / 103 / 127

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	56,565,640
Insertions	302,726
Mapped reads with at least one insertion	0.18%
Deletions	443,360
Mapped reads with at least one deletion	0.27%
Homopolymer indels	37.7%

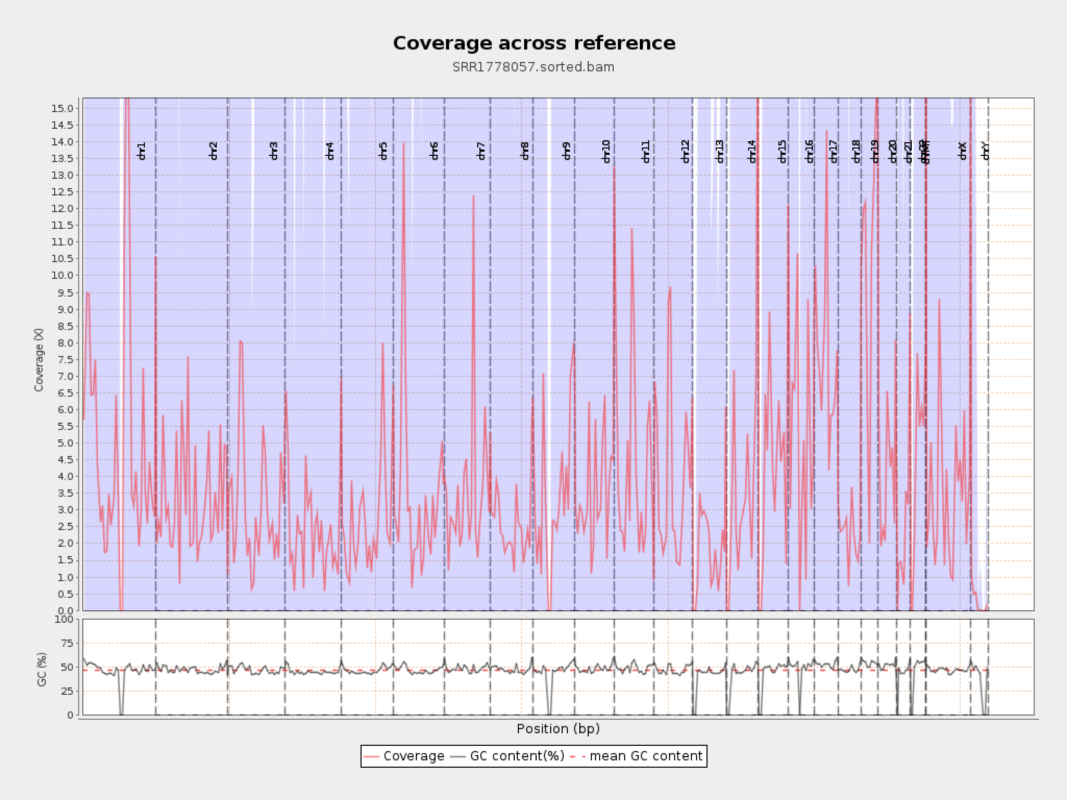
2.7. Chromosome stats

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

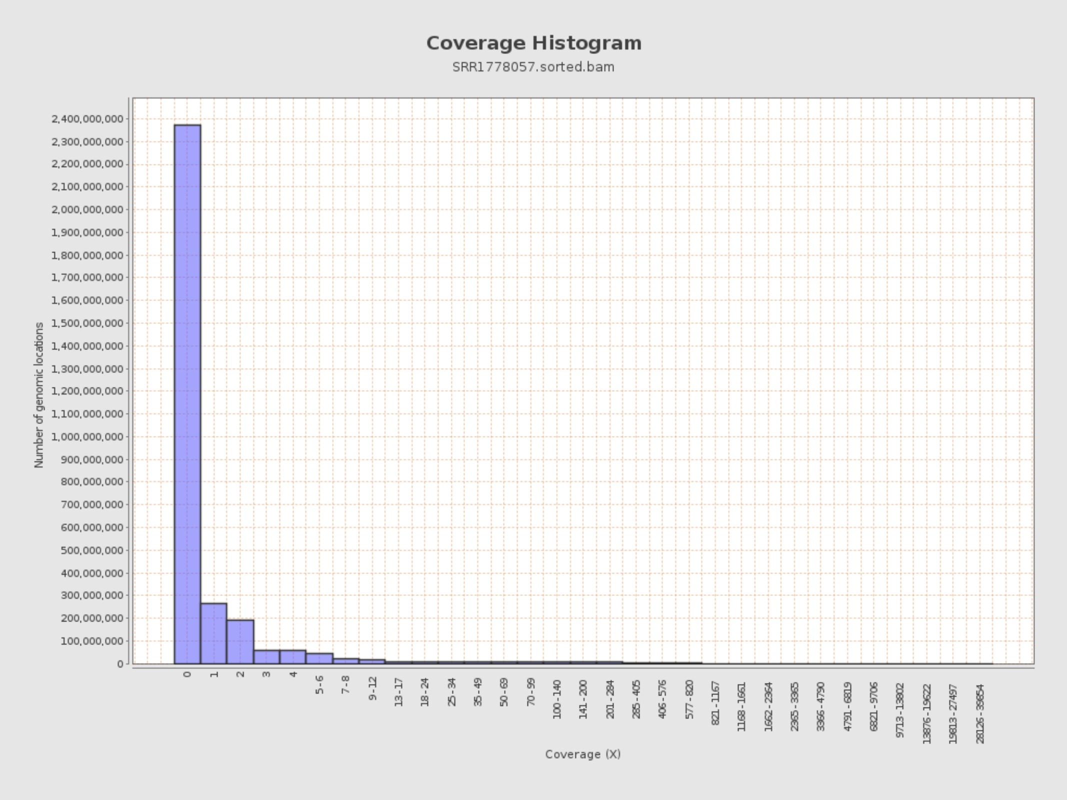
		bases	coverage	deviation
chr1	249250621	1256038525	5.0393	49.1197
chr2	243199373	815912657	3.3549	34.1841
chr3	198022430	614310682	3.1022	36.6509
chr4	191154276	455875450	2.3849	25.9515
chr5	180915260	508923642	2.813	27.0934
chr6	171115067	574032707	3.3547	38.248
chr7	159138663	561584992	3.5289	40.9748
chr8	146364022	372669426	2.5462	25.6943
chr9	141213431	468560537	3.3181	31.3029
chr10	135534747	475241448	3.5064	31.8674
chr11	135006516	601730640	4.457	37.4504
chr12	133851895	547946638	4.0937	33.5039
chr13	115169878	204733402	1.7777	22.8258
chr14	107349540	357724891	3.3323	32.6041
chr15	102531392	413968290	4.0375	36.5405
chr16	90354753	470448751	5.2067	40.4417
chr17	81195210	621978927	7.6603	56.7059
chr18	78077248	176880969	2.2655	25.1152
chr19	59128983	611485691	10.3416	58.81
chr20	63025520	249370370	3.9567	31.4634
chr21	48129895	123879489	2.5739	28.7926
chr22	51304566	222986382	4.3463	34.3803
chrMT	16571	523492	31.5909	14.7908
chrX	155270560	562494571	3.6227	46.5029

chrY	59373566	15146323	0.2551	20.5065

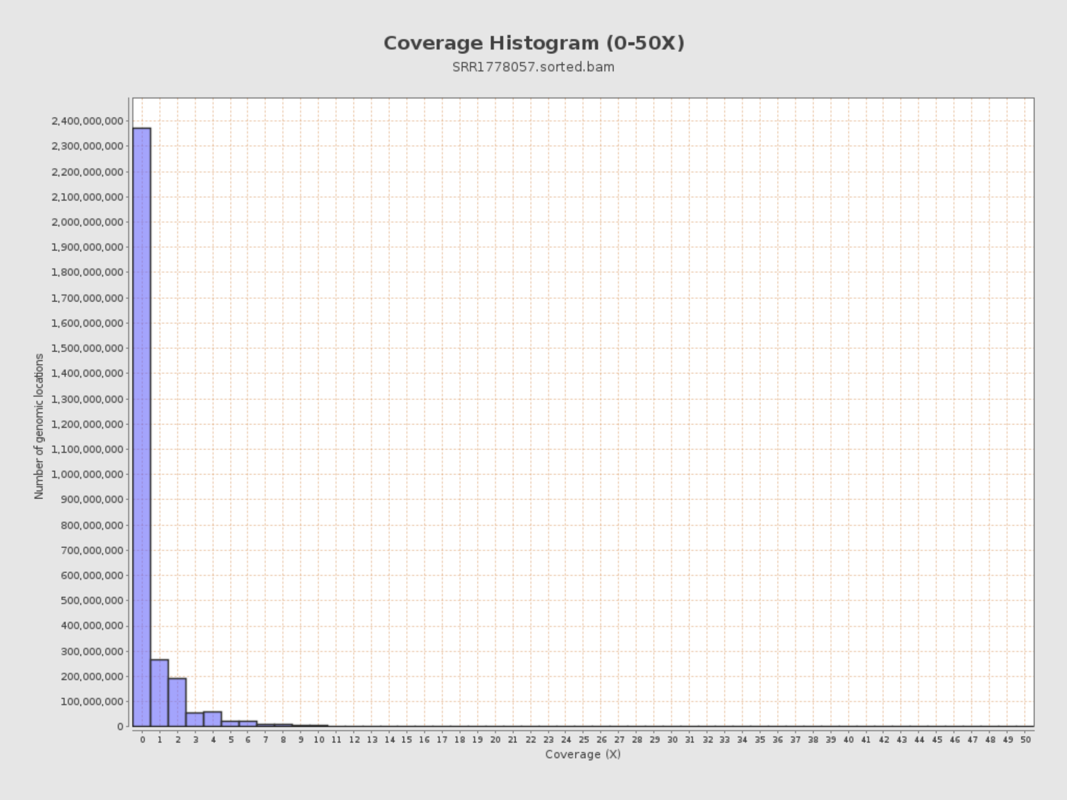
3. Results : Coverage across reference



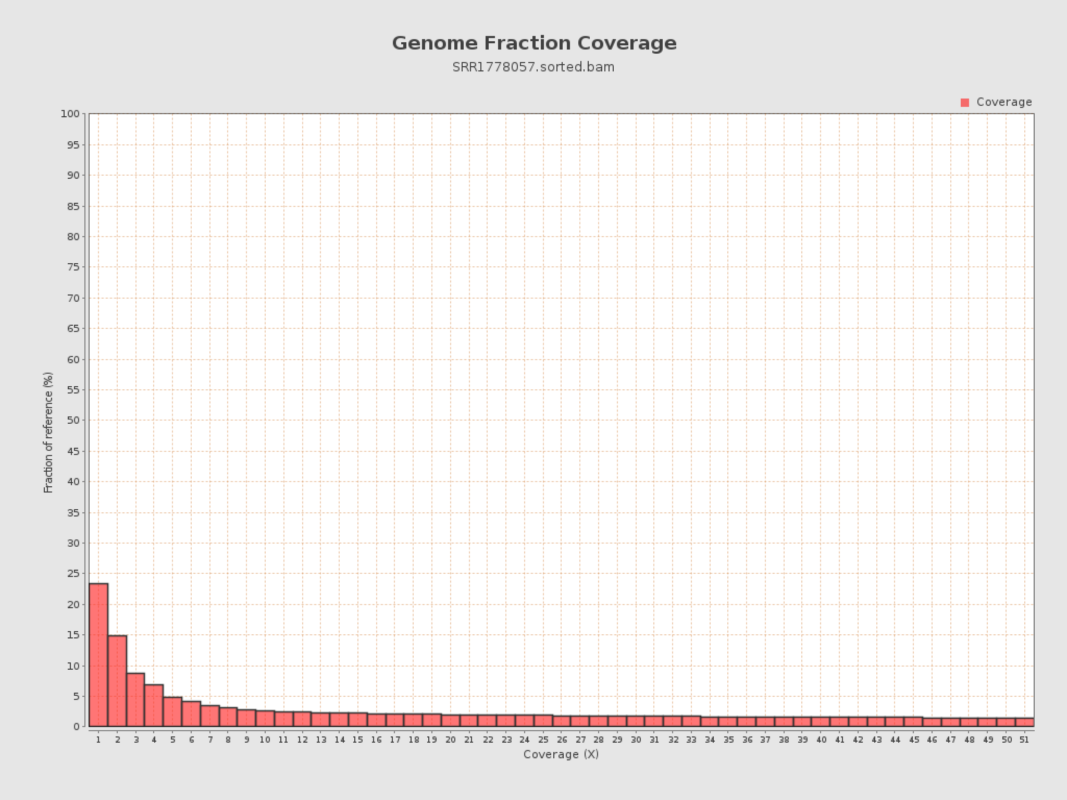
4. Results : Coverage Histogram



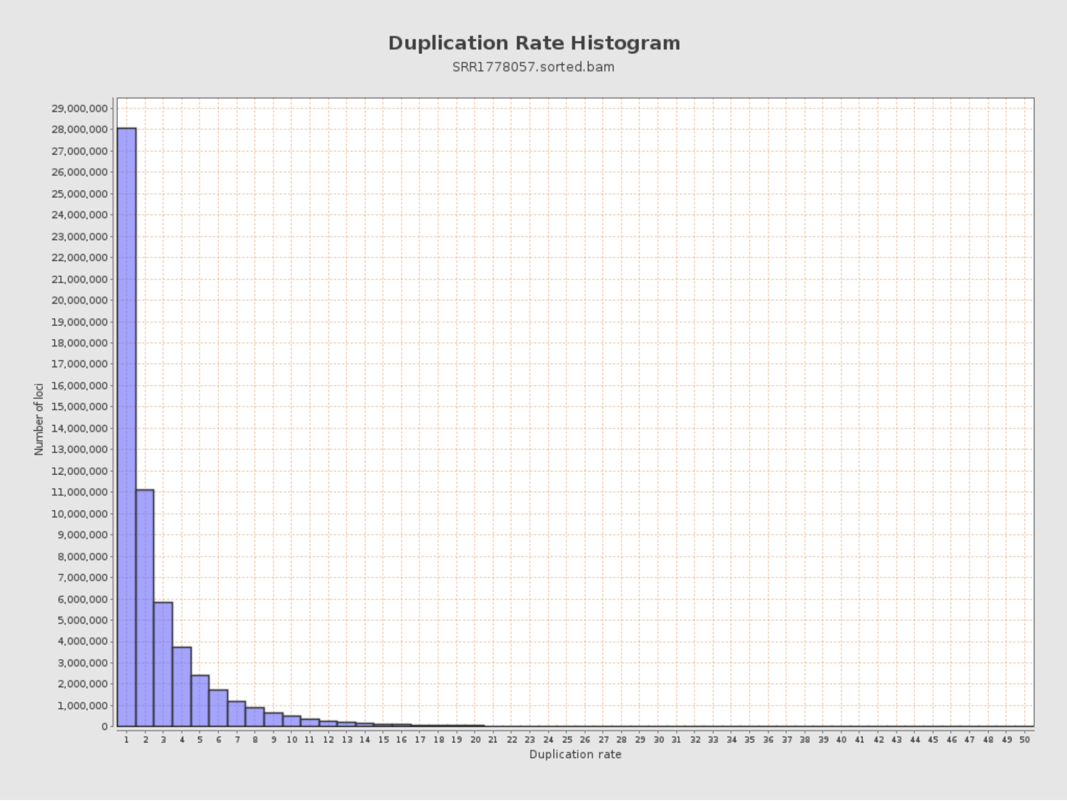
5. Results : Coverage Histogram (0-50X)



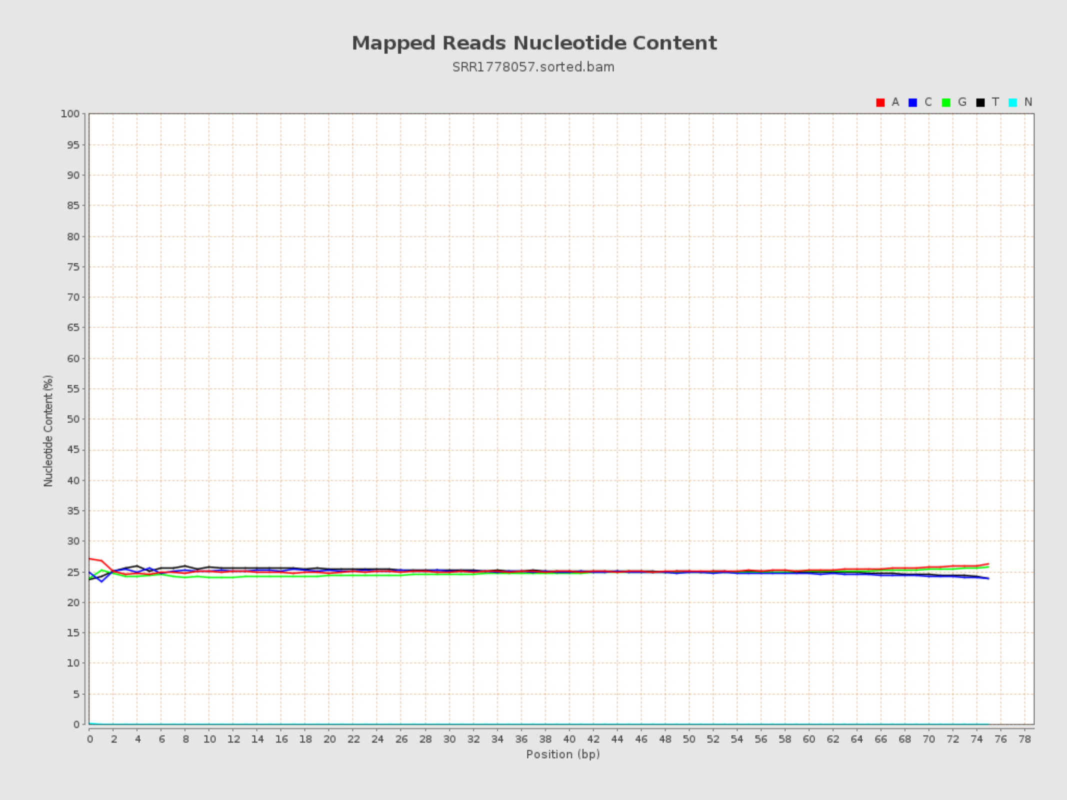
6. Results : Genome Fraction Coverage



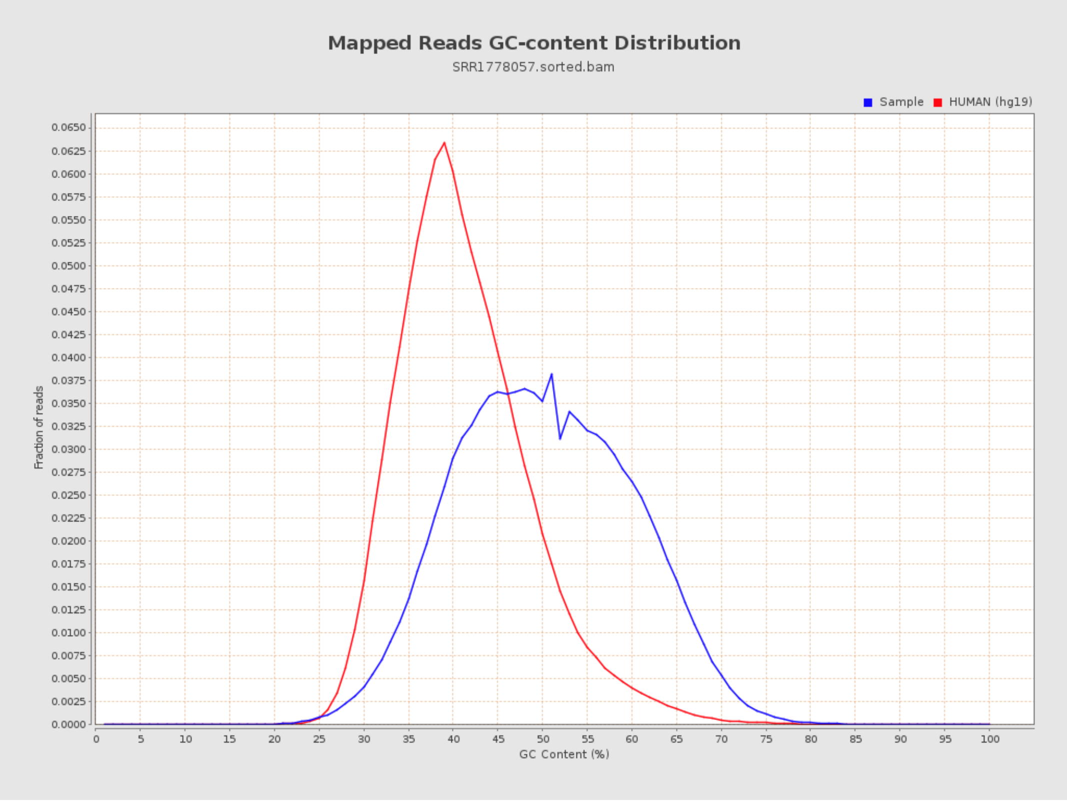
7. Results : Duplication Rate Histogram



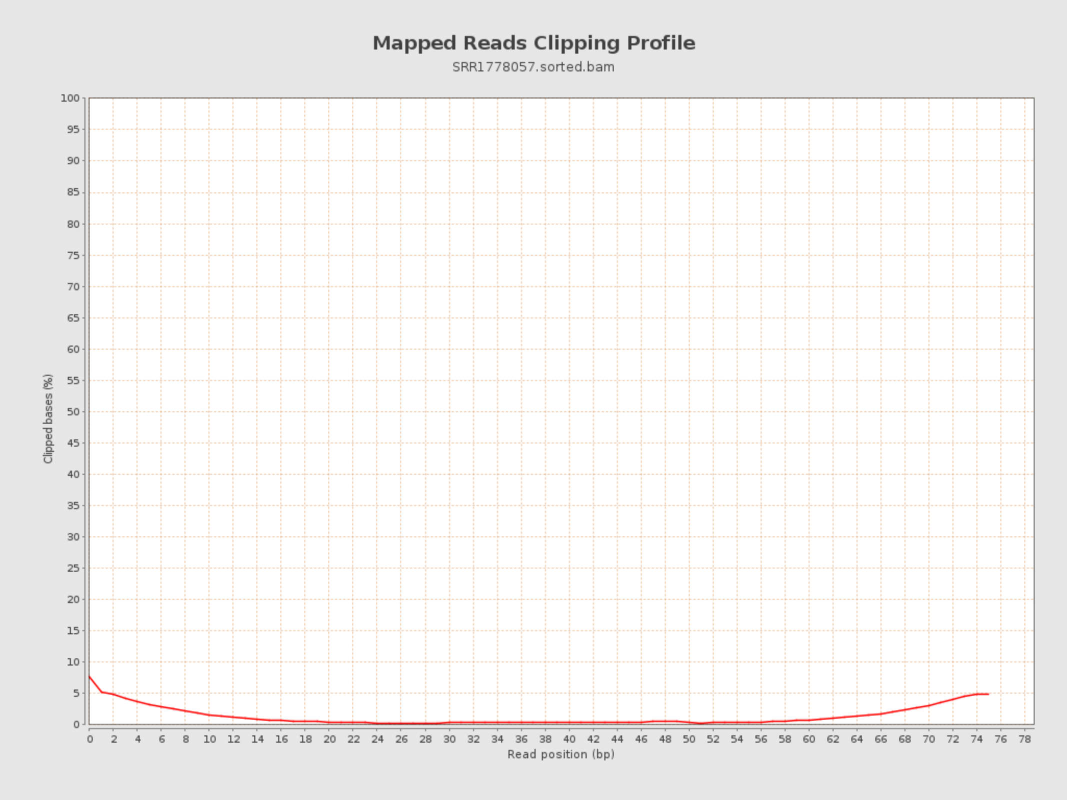
8. Results : Mapped Reads Nucleotide Content



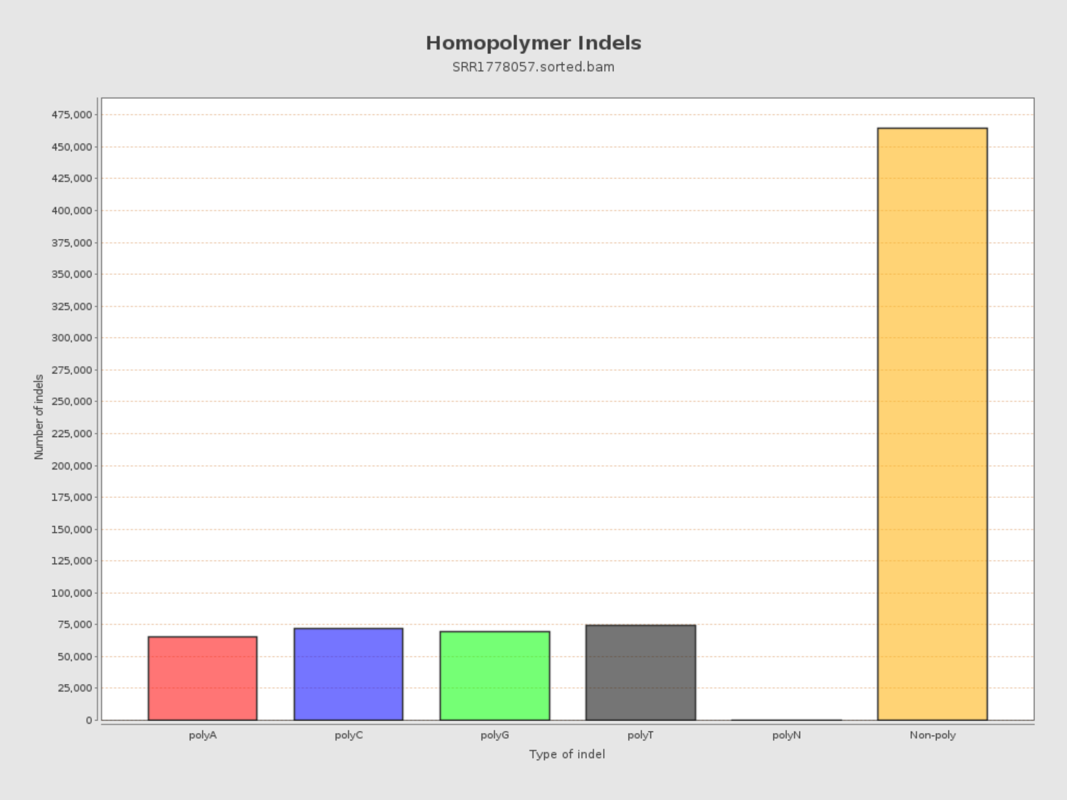
9. Results : Mapped Reads GC-content Distribution



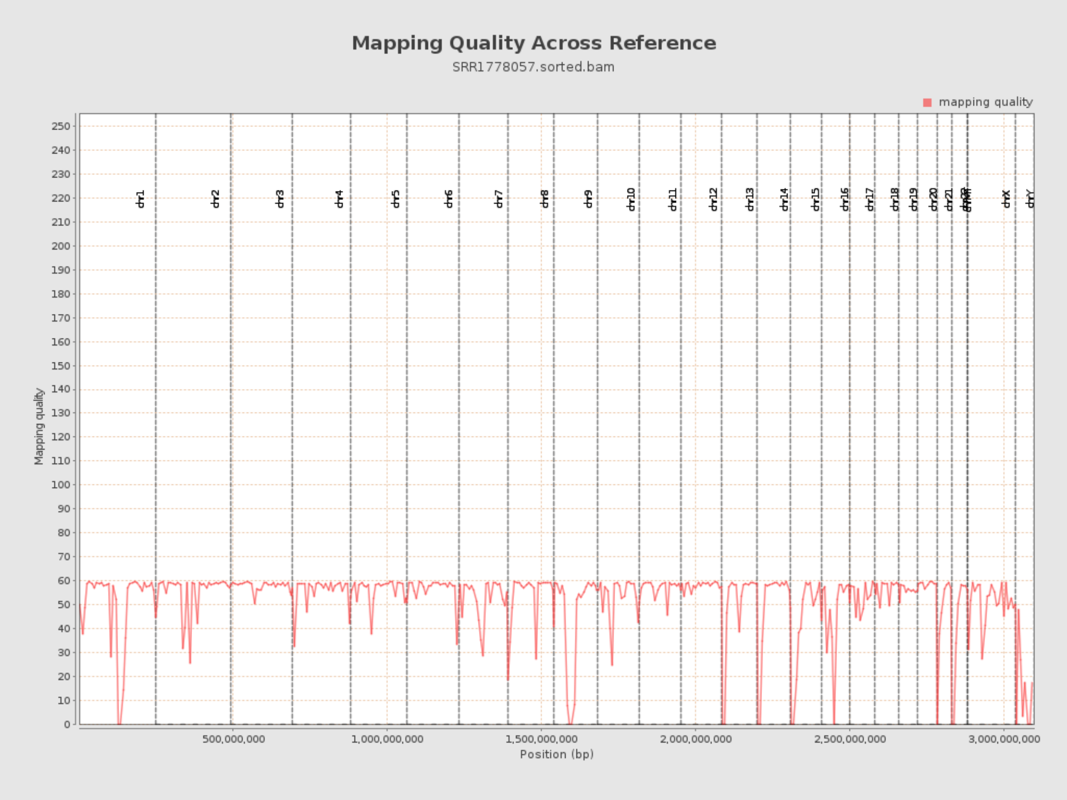
10. Results : Mapped Reads Clipping Profile



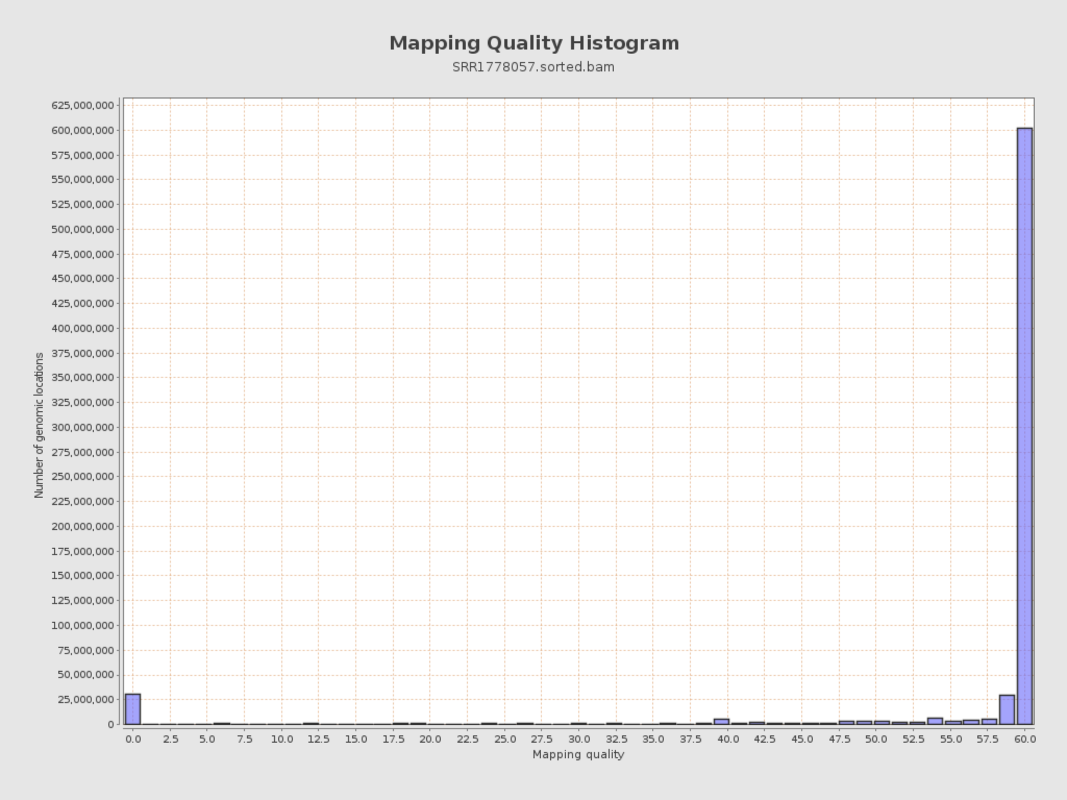
11. Results : Homopolymer Indels



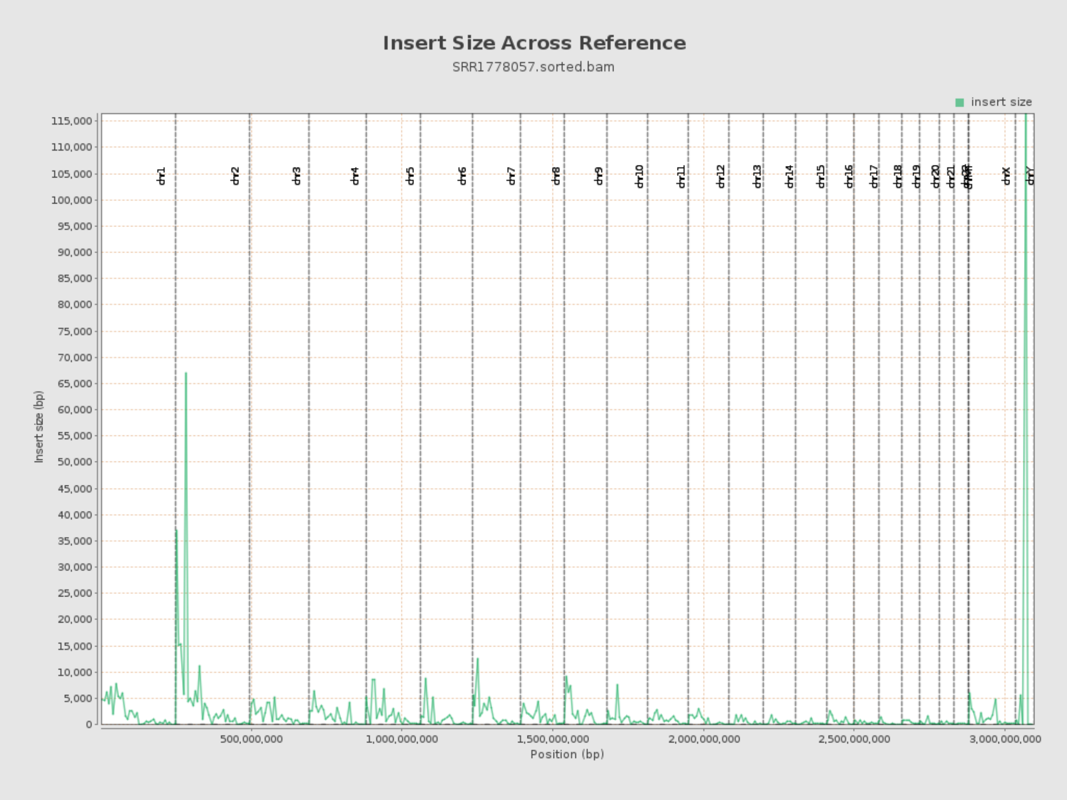
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram