Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 04:17:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617701.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_SRR8617701 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617701_1.fastq.gz SRR8617701_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 04:17:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617701.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,262,156
Mapped reads	41,123,477 / 97.31%
Unmapped reads	1,138,679 / 2.69%
Mapped paired reads	41,123,477 / 97.31%
Mapped reads, first in pair	20,785,804 / 49.18%
Mapped reads, second in pair	20,337,673 / 48.12%
Mapped reads, both in pair	40,433,446 / 95.67%
Mapped reads, singletons	690,031 / 1.63%
Secondary alignments	0
Supplementary alignments	2,118,737 / 5.01%
Read min/max/mean length	30 / 150 / 152.56
Duplicated reads (estimated)	9,838,866 / 23.28%
Duplication rate	13.74%
Clipped reads	22,199,022 / 52.53%

2.2. ACGT Content

Number/percentage of A's	1,562,774,328 / 28.21%
Number/percentage of C's	1,123,530,428 / 20.28%
Number/percentage of T's	1,579,422,681 / 28.51%
Number/percentage of G's	1,274,107,881 / 23%
Number/percentage of N's	88,683 / 0%

GC Percentage	43.28%

2.3. Coverage

Mean	1.7908
Standard Deviation	29.2984

2.4. Mapping Quality

Mean Mapping Quality	52.05

2.5. Insert size

Mean	442,645.05
Standard Deviation	6,588,732.82
P25/Median/P75	214 / 286 / 374

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	75,809,047
Insertions	1,000,830
Mapped reads with at least one insertion	2.26%
Deletions	1,729,280
Mapped reads with at least one deletion	4.02%
Homopolymer indels	42.64%

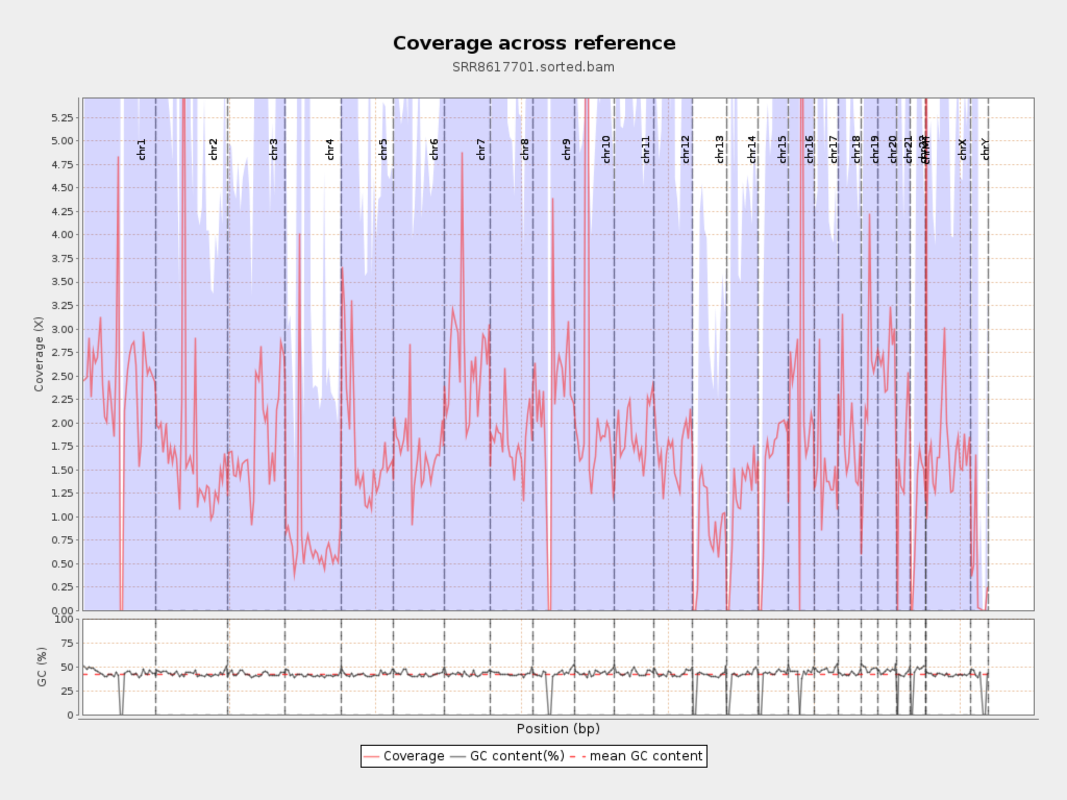
2.7. Chromosome stats

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

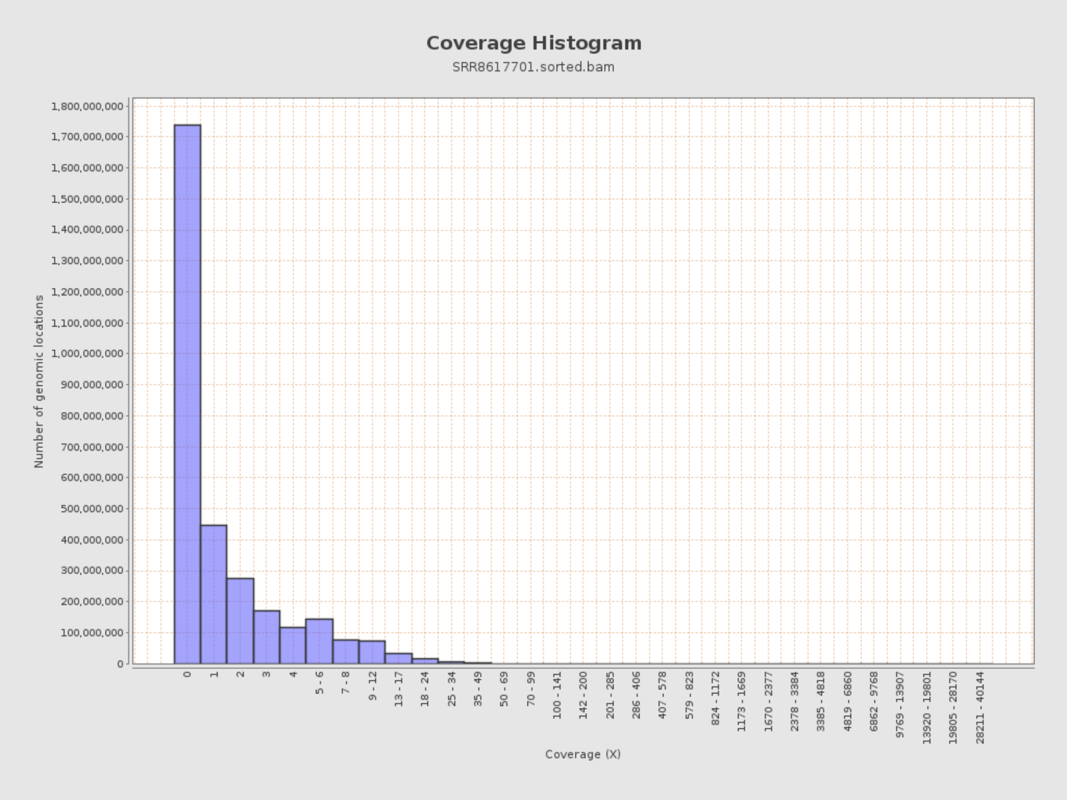
		bases	coverage	deviation
chr1	249250621	597140593	2.3957	40.6249
chr2	243199373	426369684	1.7532	35.1806
chr3	198022430	362847325	1.8324	4.3653
chr4	191154276	148649753	0.7776	21.3313
chr5	180915260	317328013	1.754	4.411
chr6	171115067	288740187	1.6874	14.0602
chr7	159138663	429937274	2.7017	42.358
chr8	146364022	264184901	1.805	9.0369
chr9	141213431	313063303	2.217	48.5639
chr10	135534747	305317433	2.2527	72.4497
chr11	135006516	253713130	1.8793	15.0617
chr12	133851895	229612969	1.7154	6.7242
chr13	115169878	97196061	0.8439	2.0996
chr14	107349540	124354846	1.1584	3.2974
chr15	102531392	152490005	1.4873	4.7862
chr16	90354753	237773829	2.6316	48.3983
chr17	81195210	120868592	1.4886	21.3755
chr18	78077248	144719158	1.8535	34.211
chr19	59128983	144346373	2.4412	24.9226
chr20	63025520	169395713	2.6877	7.8737
chr21	48129895	76500619	1.5895	11.1726
chr22	51304566	54456407	1.0614	3.2156
chrMT	16571	849361	51.2559	29.6909
chrX	155270560	263013612	1.6939	9.0968

chrY	59373566	20808260	0.3505	23.6076

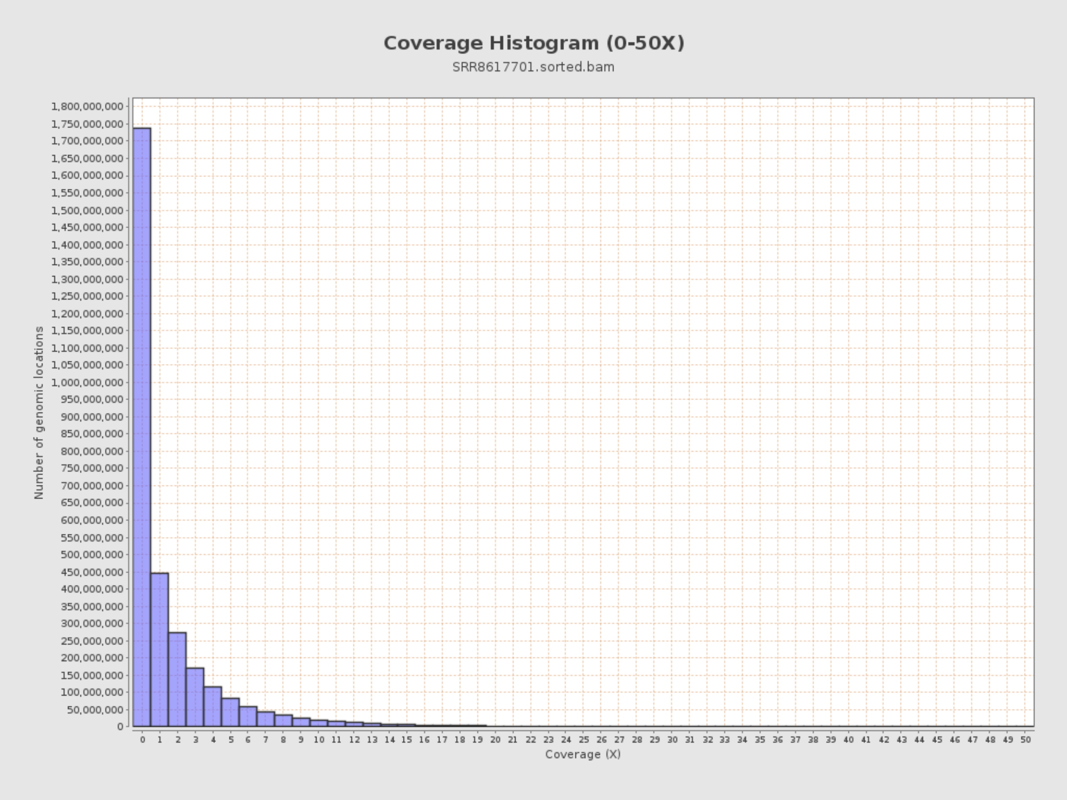
3. Results : Coverage across reference



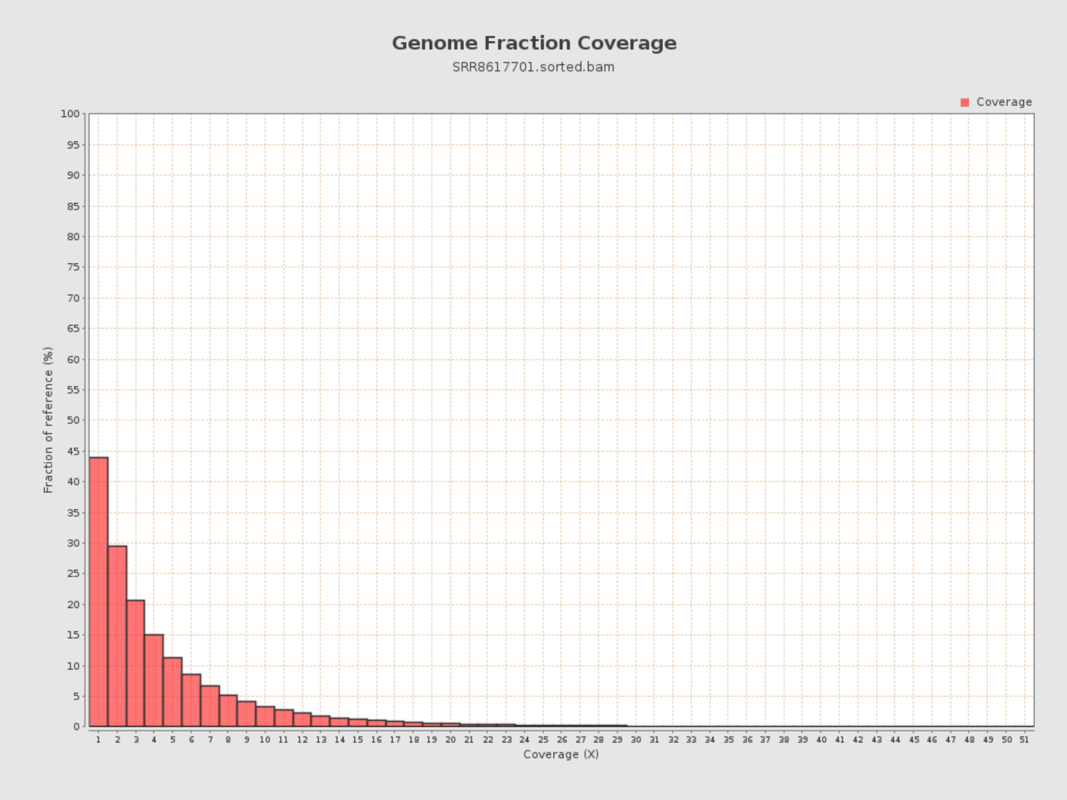
4. Results : Coverage Histogram



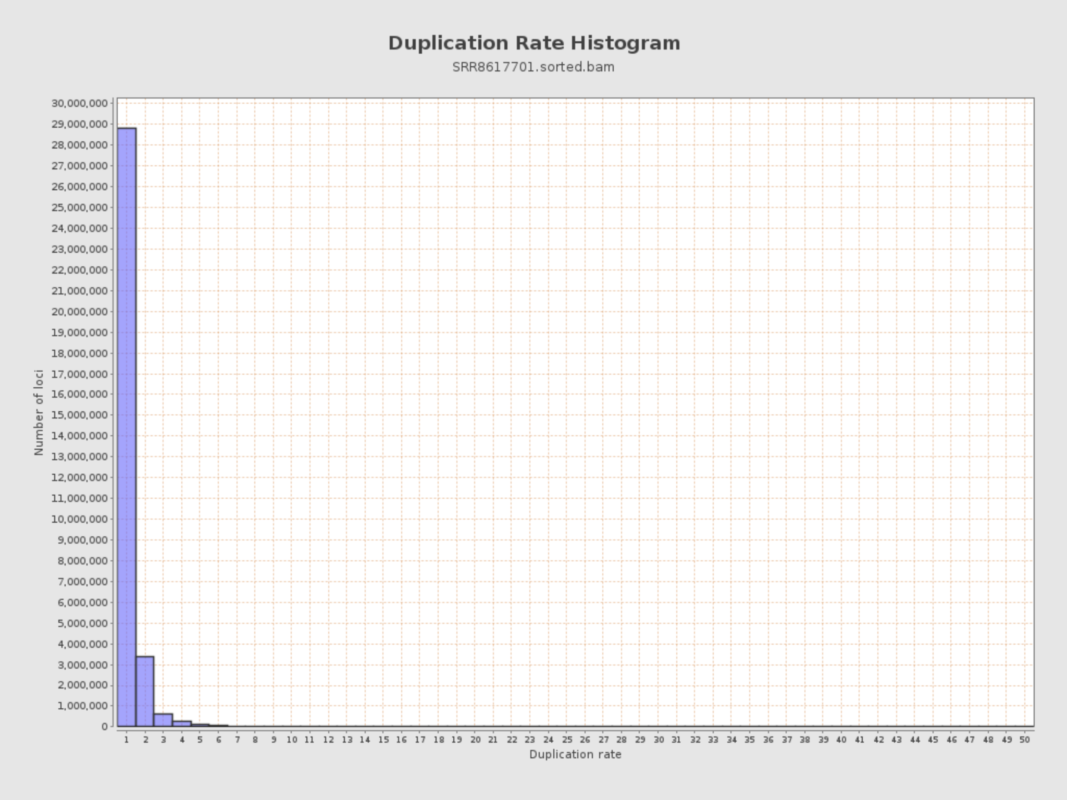
5. Results : Coverage Histogram (0-50X)



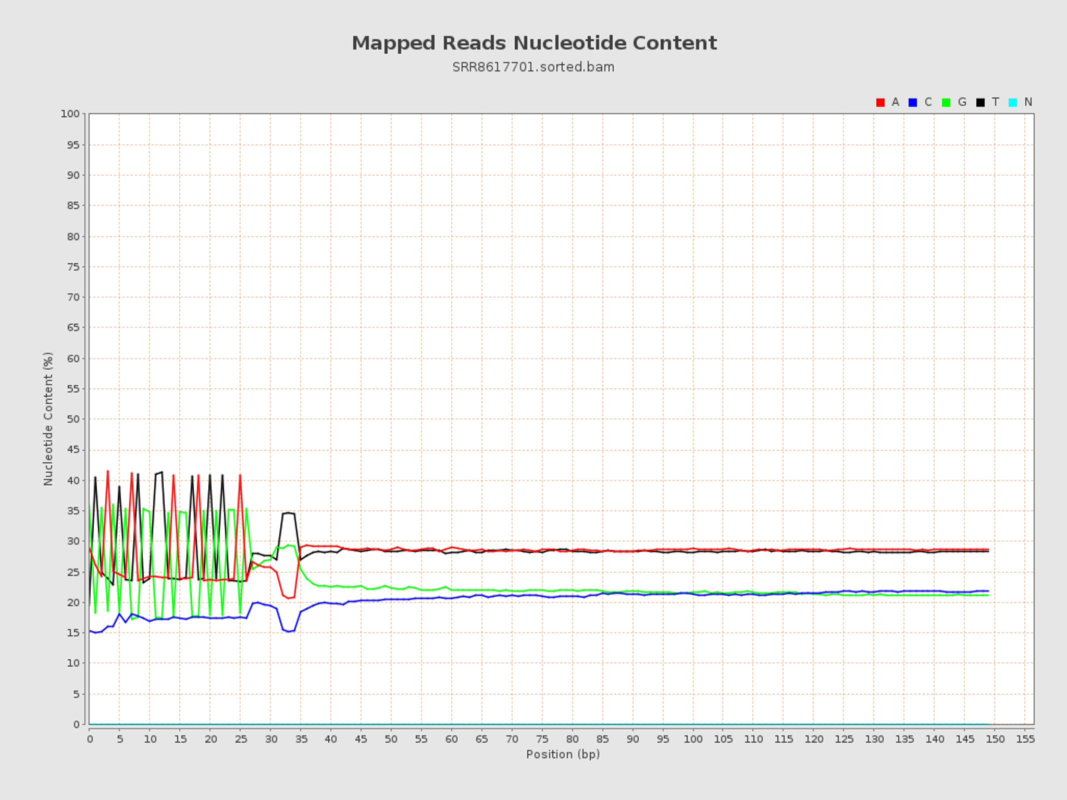
6. Results : Genome Fraction Coverage



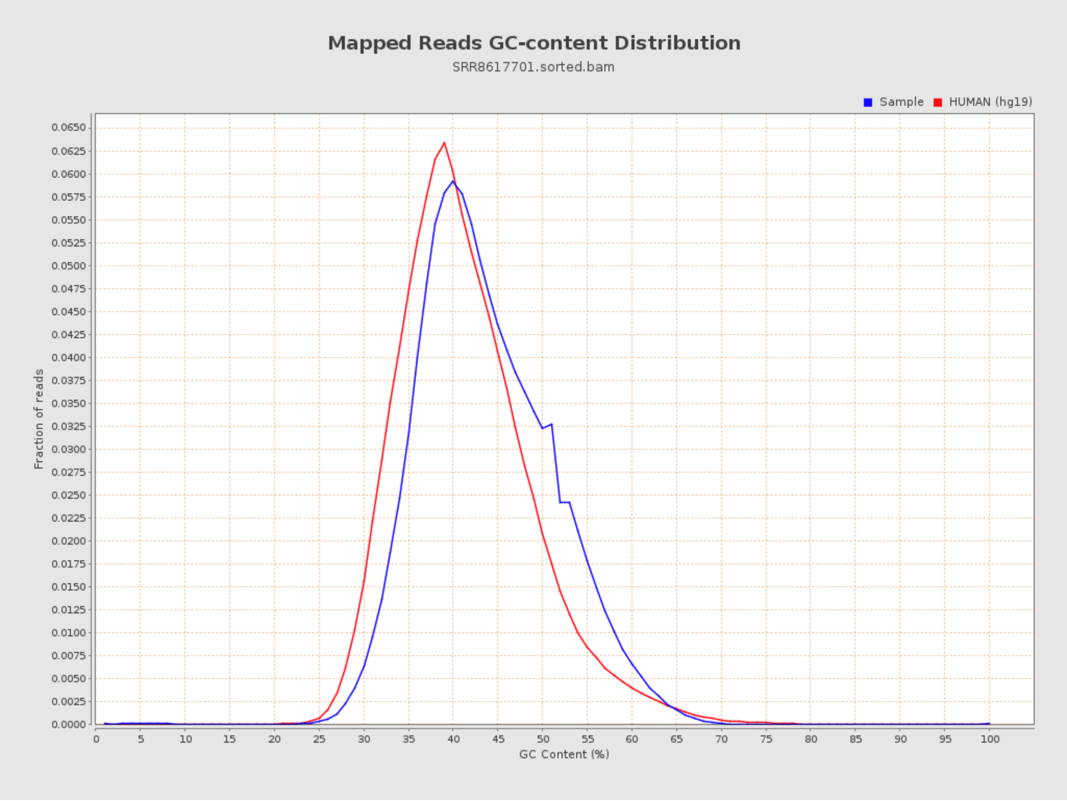
7. Results : Duplication Rate Histogram



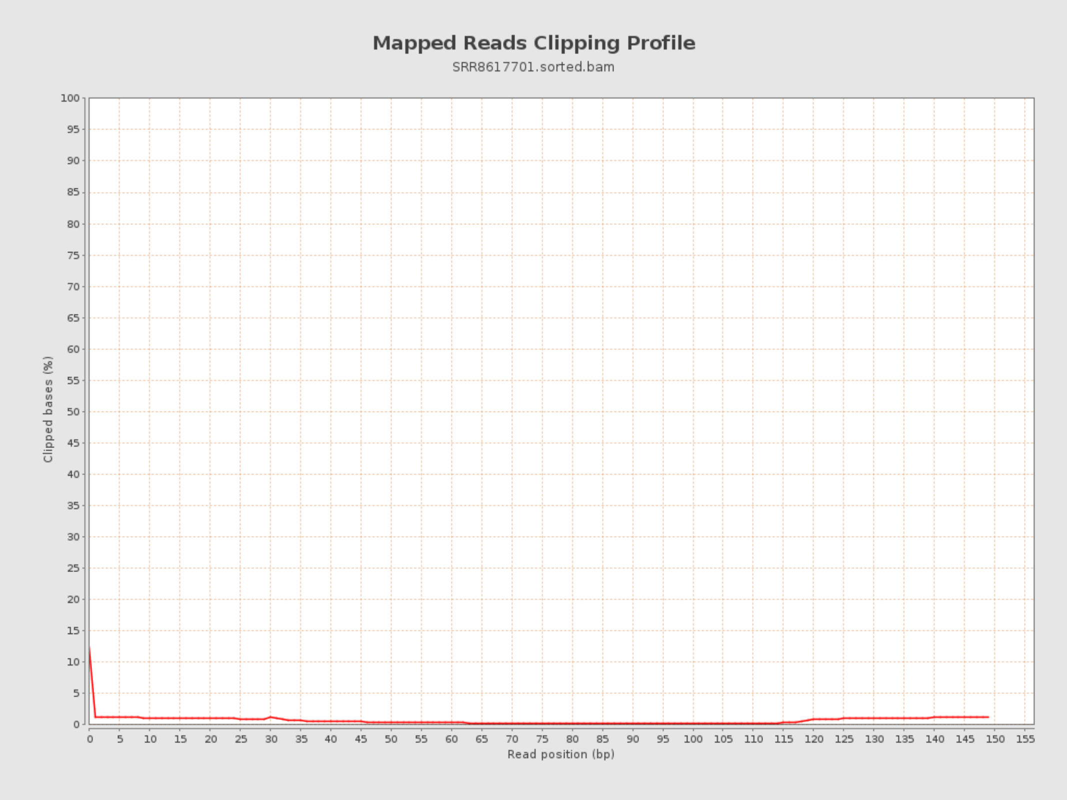
8. Results : Mapped Reads Nucleotide Content



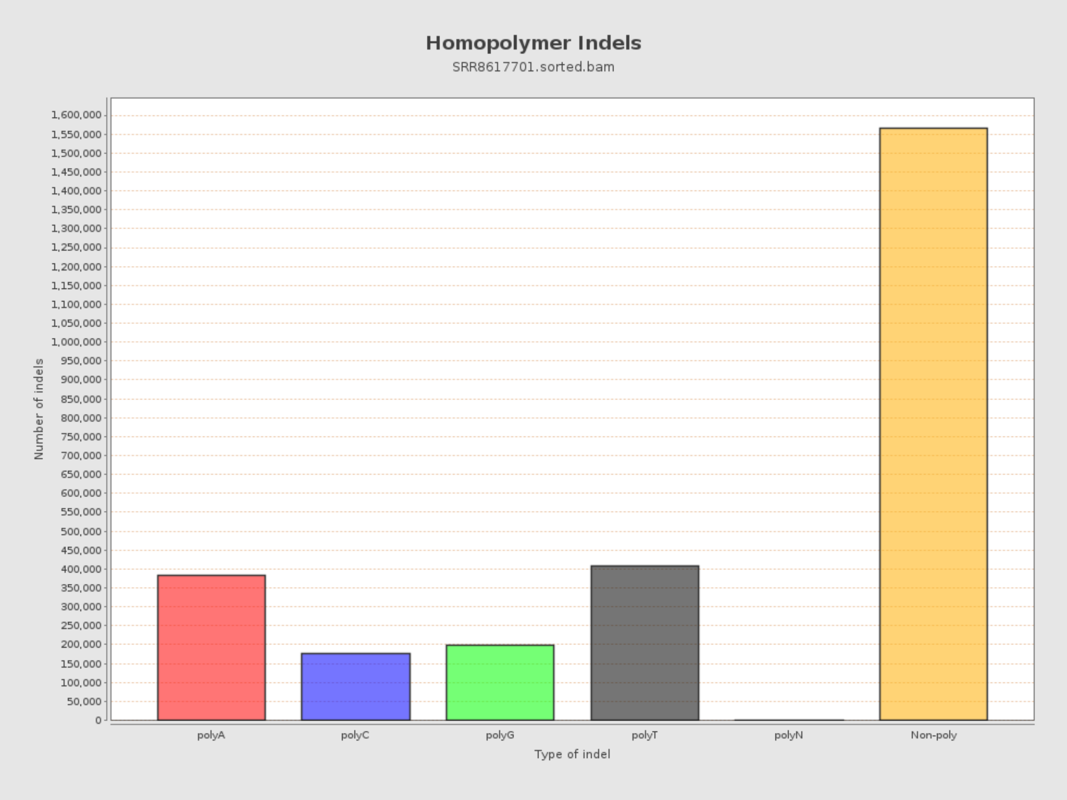
9. Results : Mapped Reads GC-content Distribution



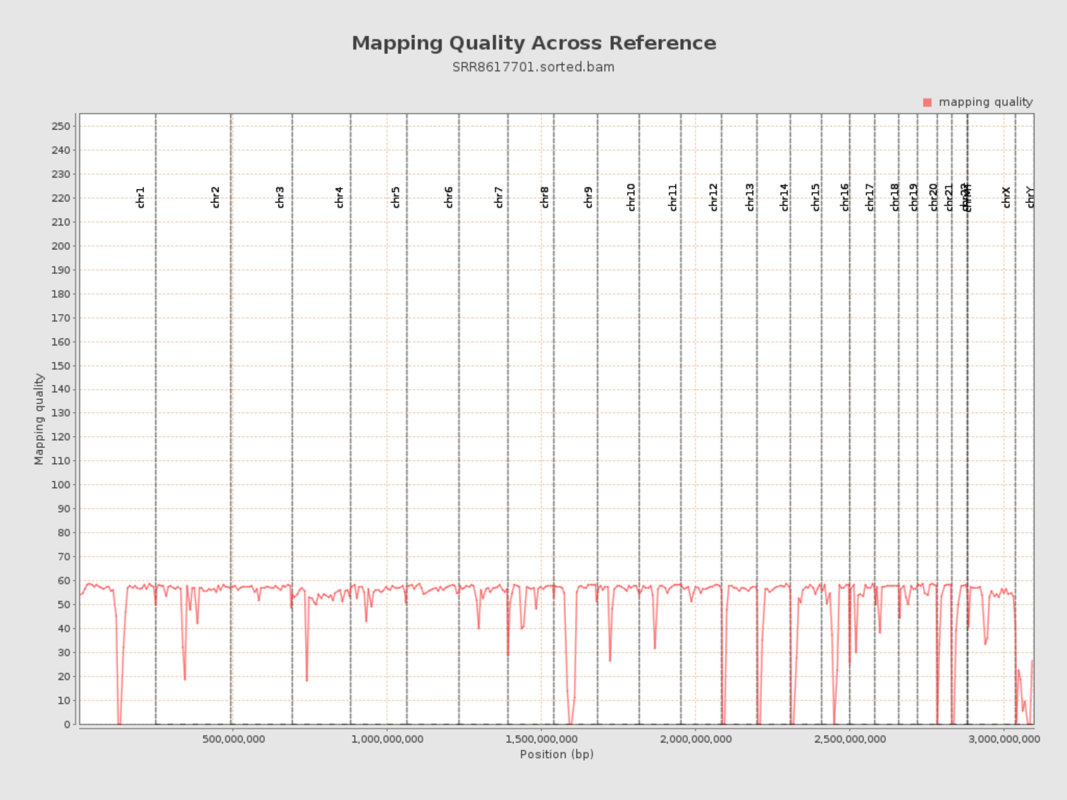
10. Results : Mapped Reads Clipping Profile



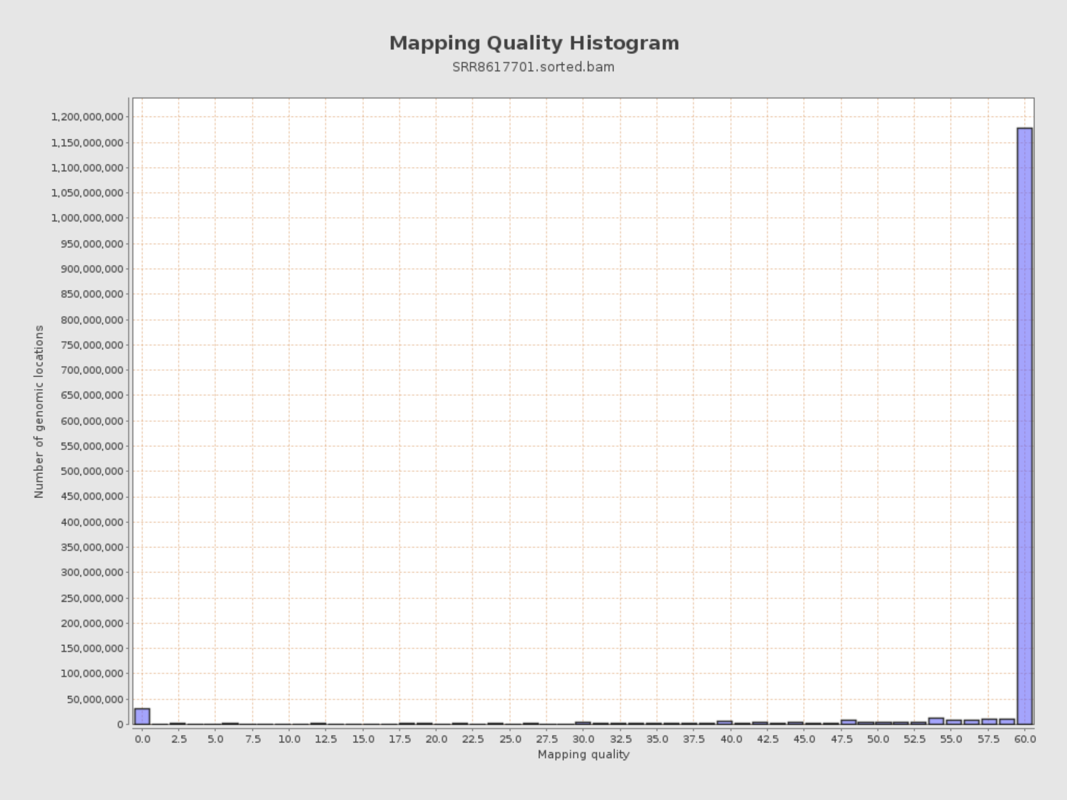
11. Results : Homopolymer Indels



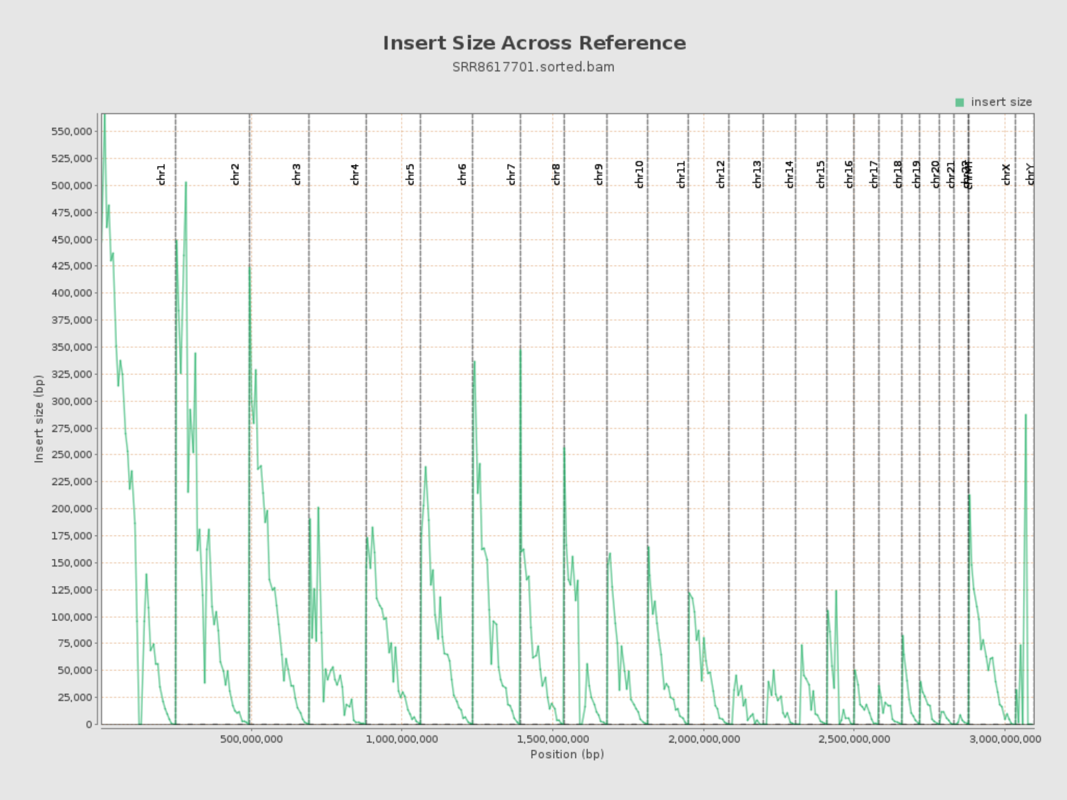
12. Results : Mapping Quality Across Reference



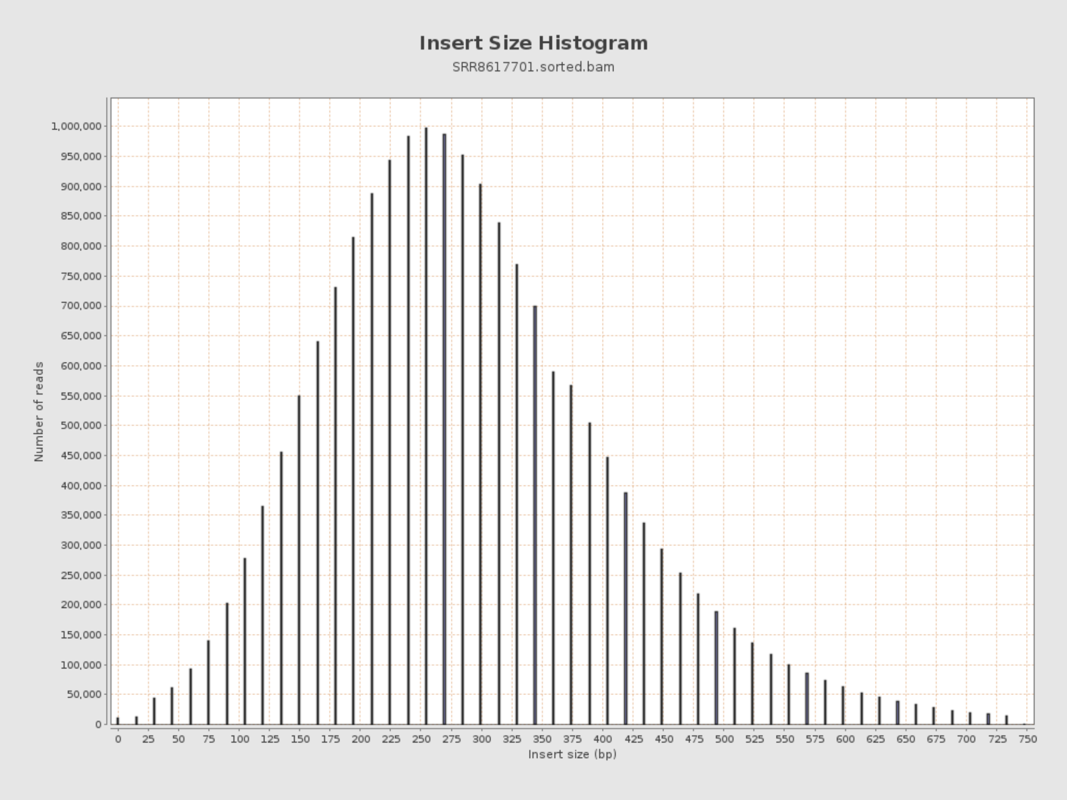
13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram



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