Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 15:53:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617556.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_SRR8617556 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617556_1.fastq.gz SRR8617556_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 15:53:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617556.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	53,003,018
Mapped reads	52,222,108 / 98.53%
Unmapped reads	780,910 / 1.47%
Mapped paired reads	52,222,108 / 98.53%
Mapped reads, first in pair	26,290,195 / 49.6%
Mapped reads, second in pair	25,931,913 / 48.93%
Mapped reads, both in pair	51,756,322 / 97.65%
Mapped reads, singletons	465,786 / 0.88%
Secondary alignments	0
Supplementary alignments	1,410,800 / 2.66%
Read min/max/mean length	30 / 150 / 151.29
Duplicated reads (estimated)	20,722,266 / 39.1%
Duplication rate	25.86%
Clipped reads	28,607,203 / 53.97%

2.2. ACGT Content

Number/percentage of A's	2,008,158,671 / 28.83%
Number/percentage of C's	1,318,633,870 / 18.93%
Number/percentage of T's	2,091,186,650 / 30.02%
Number/percentage of G's	1,547,970,781 / 22.22%
Number/percentage of N's	273,265 / 0%

GC Percentage	41.15%

2.3. Coverage

Mean	2.252
Standard Deviation	19.7992

2.4. Mapping Quality

Mean Mapping Quality	53.33

2.5. Insert size

Mean	184,939.37
Standard Deviation	4,176,852.04
P25/Median/P75	218 / 269 / 334

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	77,664,107
Insertions	1,243,394
Mapped reads with at least one insertion	2.24%
Deletions	2,861,025
Mapped reads with at least one deletion	5.26%
Homopolymer indels	46.2%

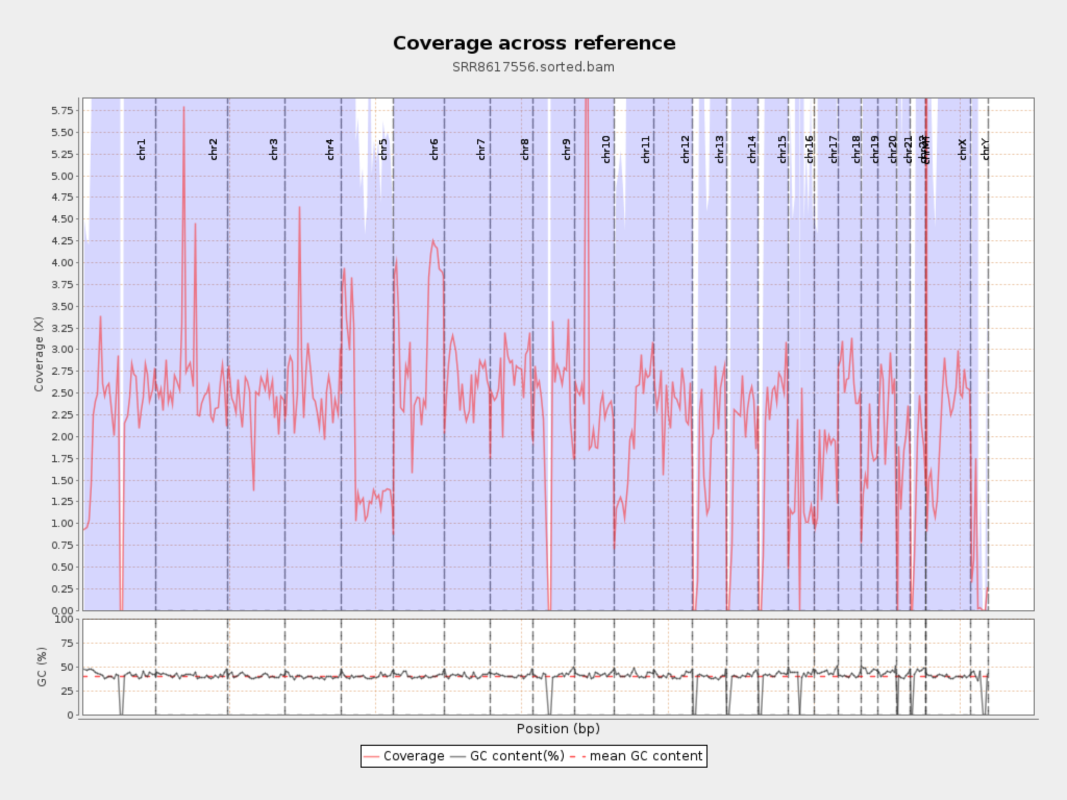
2.7. Chromosome stats

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

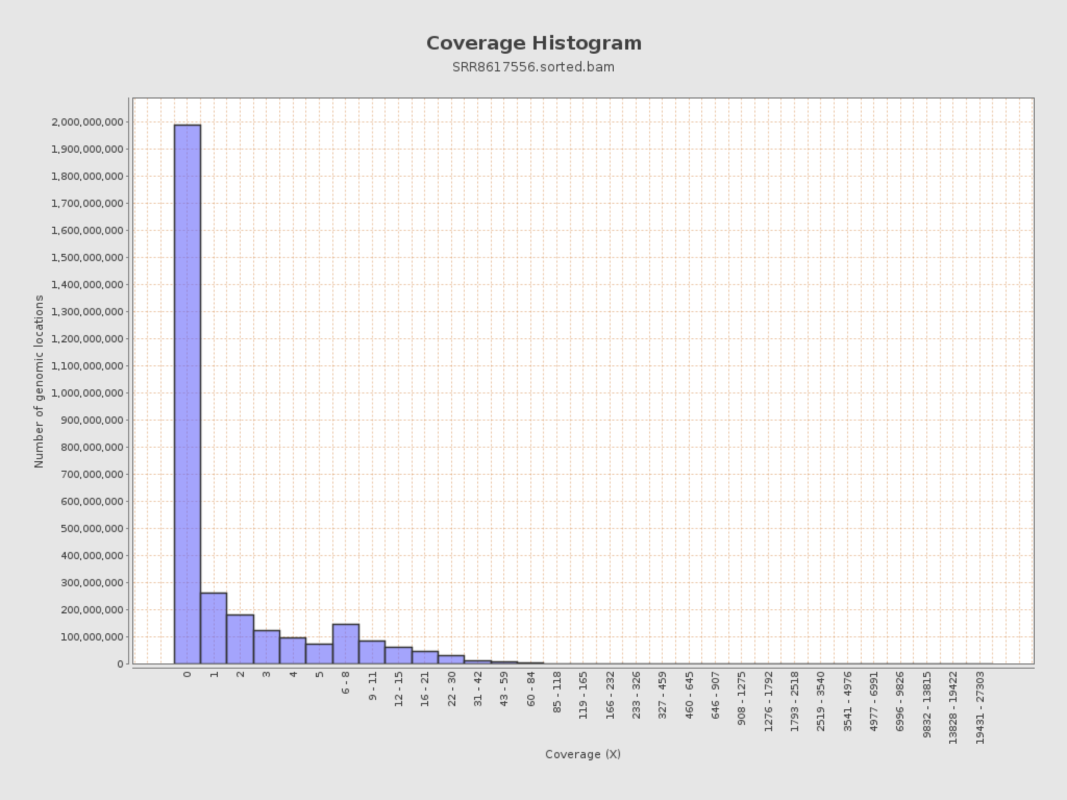
		bases	coverage	deviation
chr1	249250621	547510637	2.1966	13.9275
chr2	243199373	655769550	2.6964	26.3069
chr3	198022430	478568991	2.4167	5.6467
chr4	191154276	496574741	2.5978	17.6595
chr5	180915260	332756531	1.8393	5.2454
chr6	171115067	534263393	3.1222	9.6135
chr7	159138663	417760894	2.6251	15.9371
chr8	146364022	395141883	2.6997	8.2197
chr9	141213431	320461578	2.2693	35.1279
chr10	135534747	356918677	2.6334	58.2384
chr11	135006516	276119780	2.0452	14.1735
chr12	133851895	318949608	2.3829	10.6405
chr13	115169878	205031307	1.7803	4.7868
chr14	107349540	205299116	1.9124	5.4413
chr15	102531392	209943214	2.0476	6.5417
chr16	90354753	107440063	1.1891	17.8261
chr17	81195210	137462178	1.693	17.0473
chr18	78077248	210251943	2.6929	27.5058
chr19	59128983	99139726	1.6767	7.8993
chr20	63025520	152980788	2.4273	7.5006
chr21	48129895	80267631	1.6677	10.1999
chr22	51304566	72673238	1.4165	4.8885
chrMT	16571	3680284	222.0918	108.6906
chrX	155270560	334494921	2.1543	7.5561

chrY	59373566	22163994	0.3733	25.2757

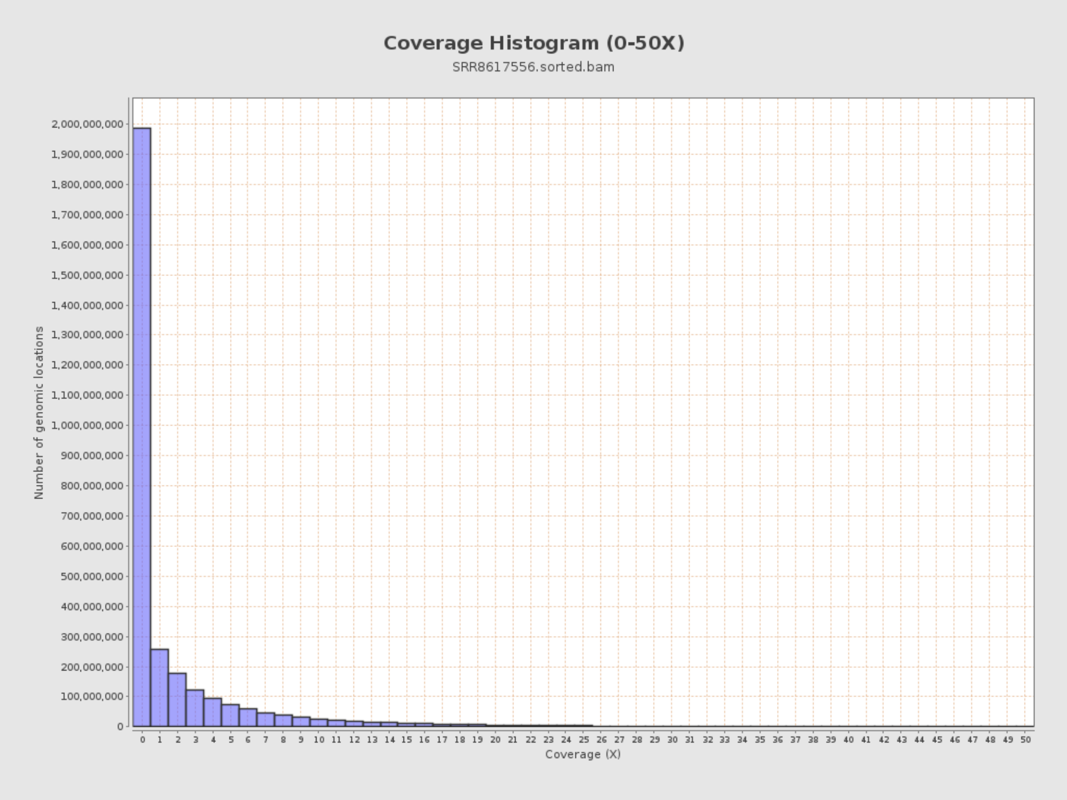
3. Results : Coverage across reference



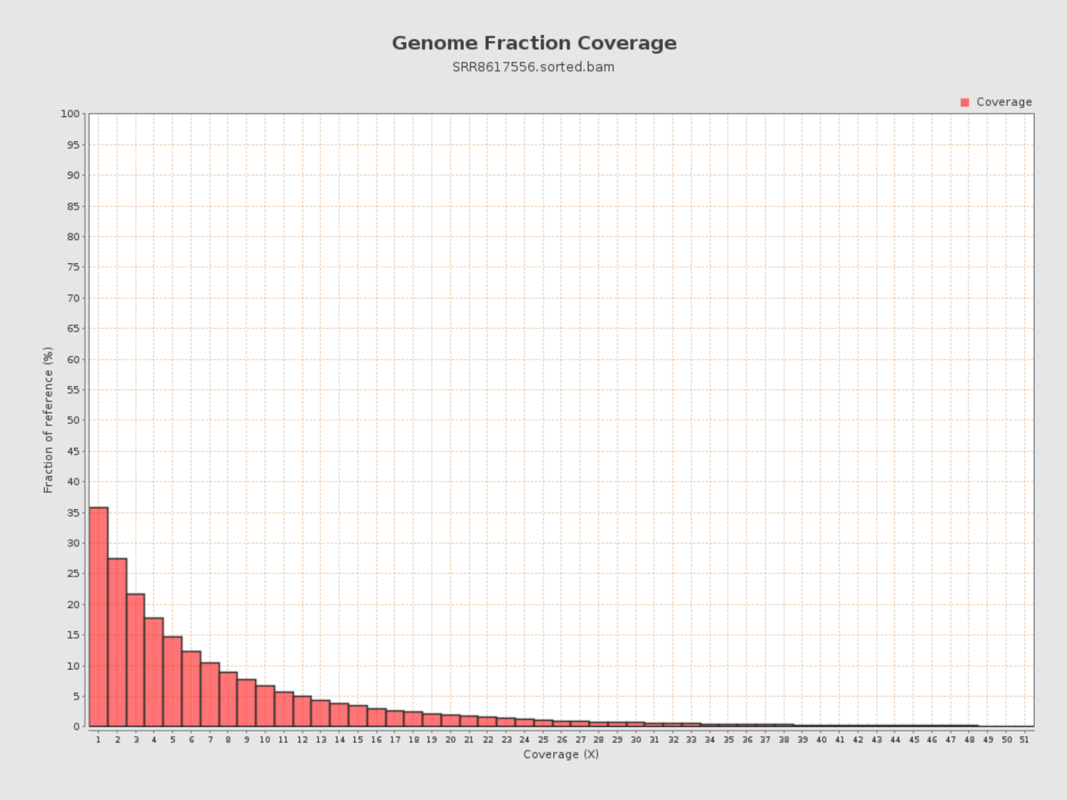
4. Results : Coverage Histogram



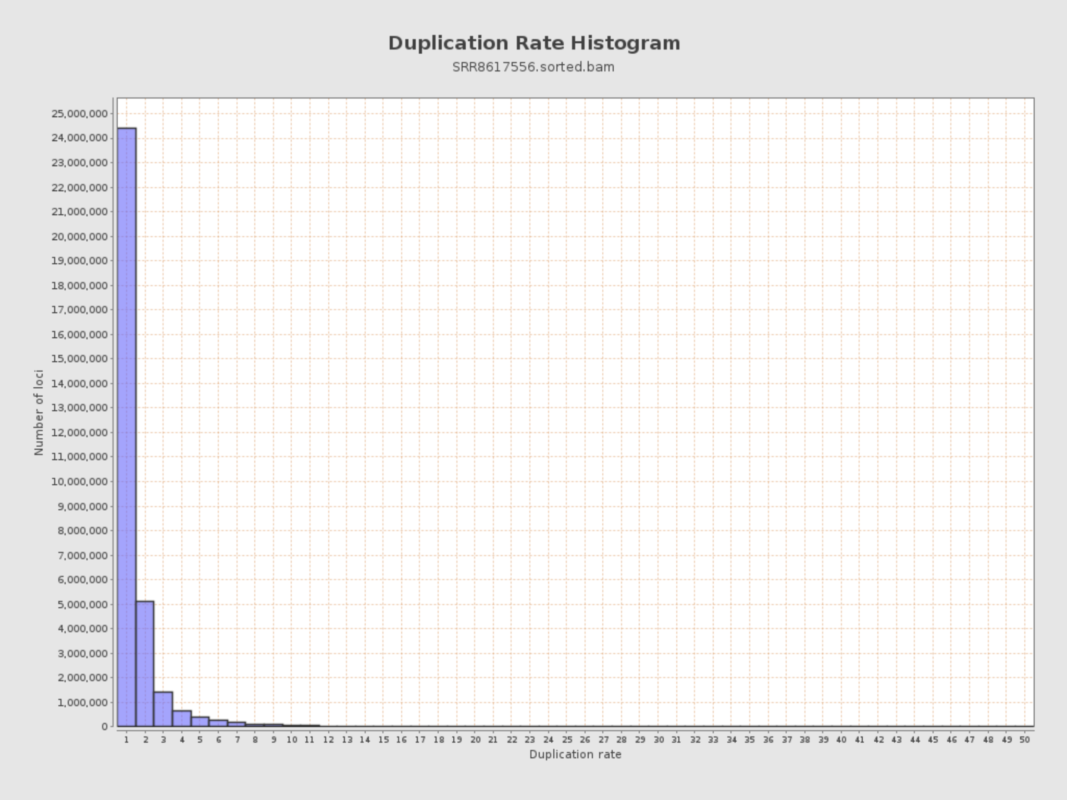
5. Results : Coverage Histogram (0-50X)



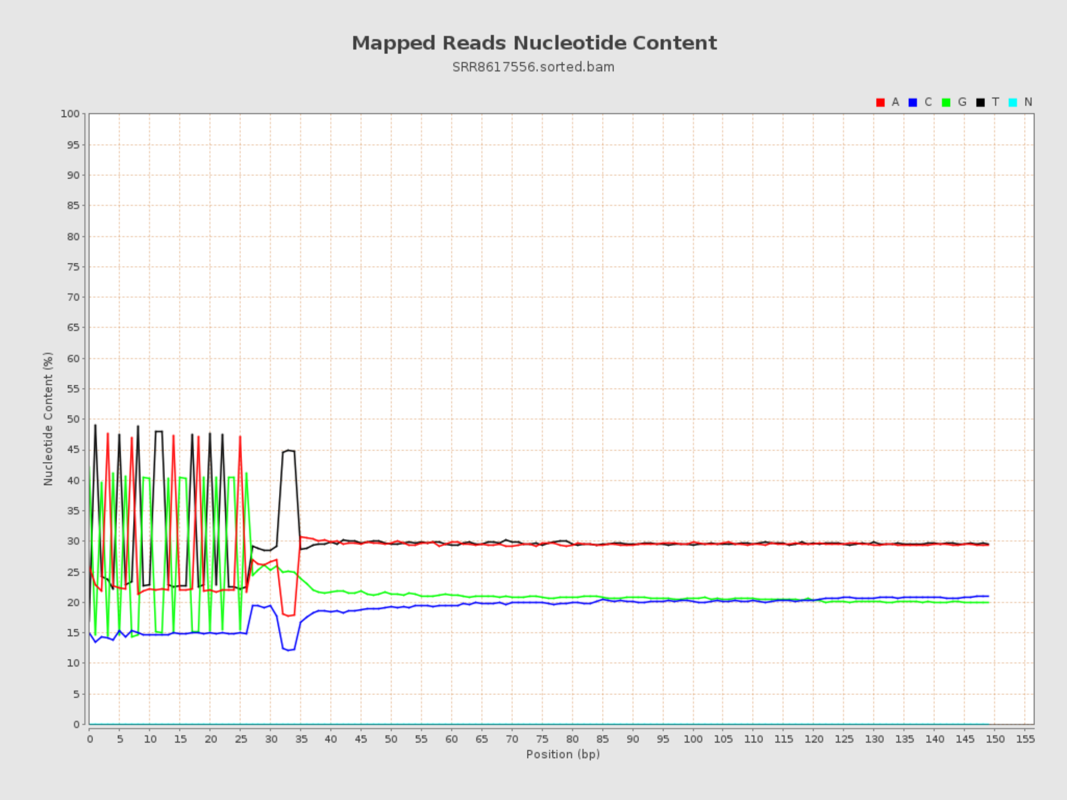
6. Results : Genome Fraction Coverage



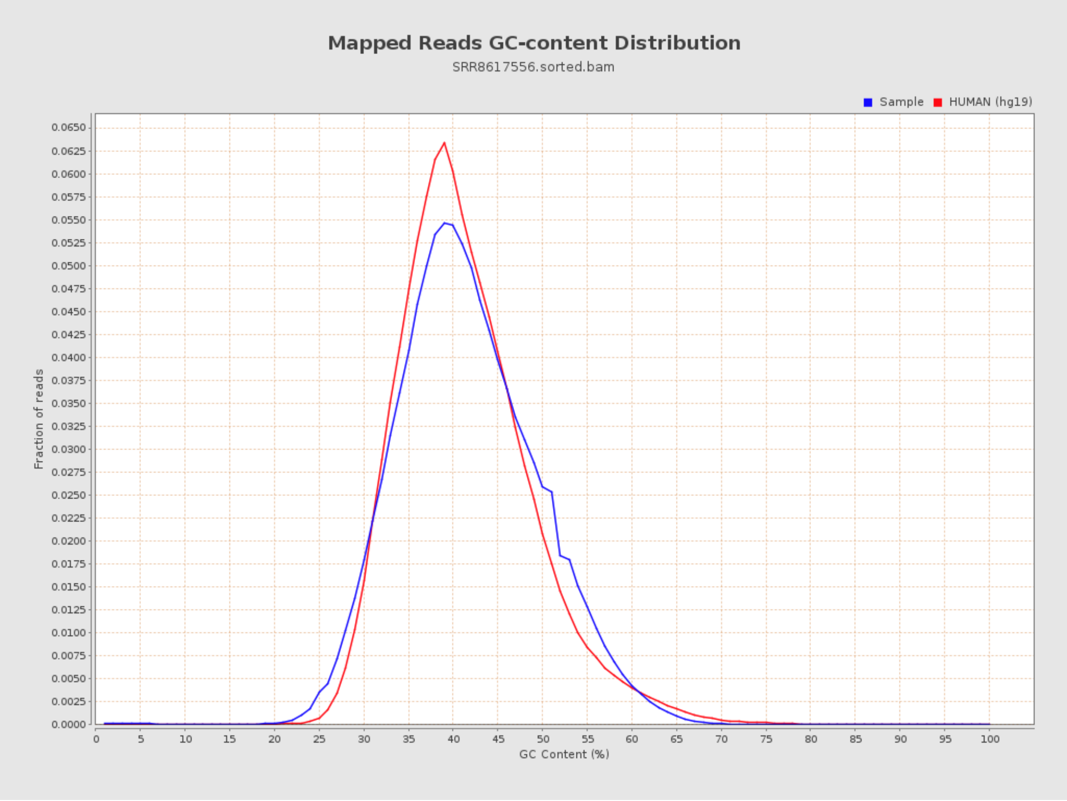
7. Results : Duplication Rate Histogram



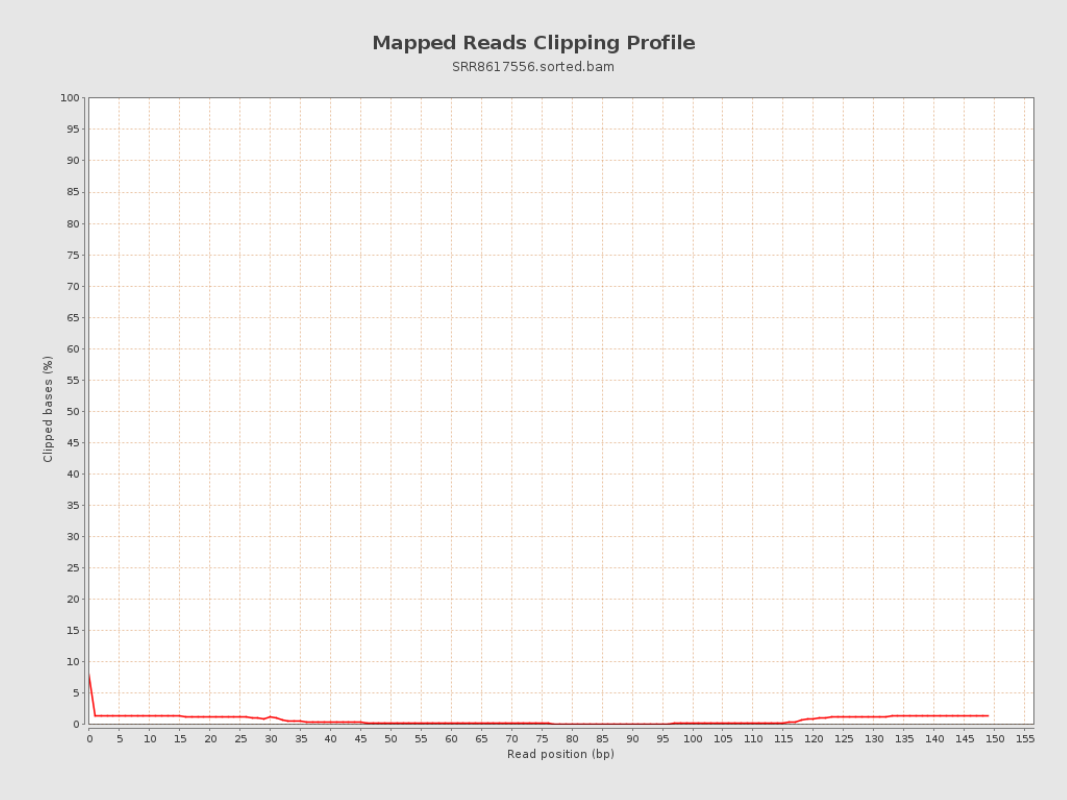
8. Results : Mapped Reads Nucleotide Content



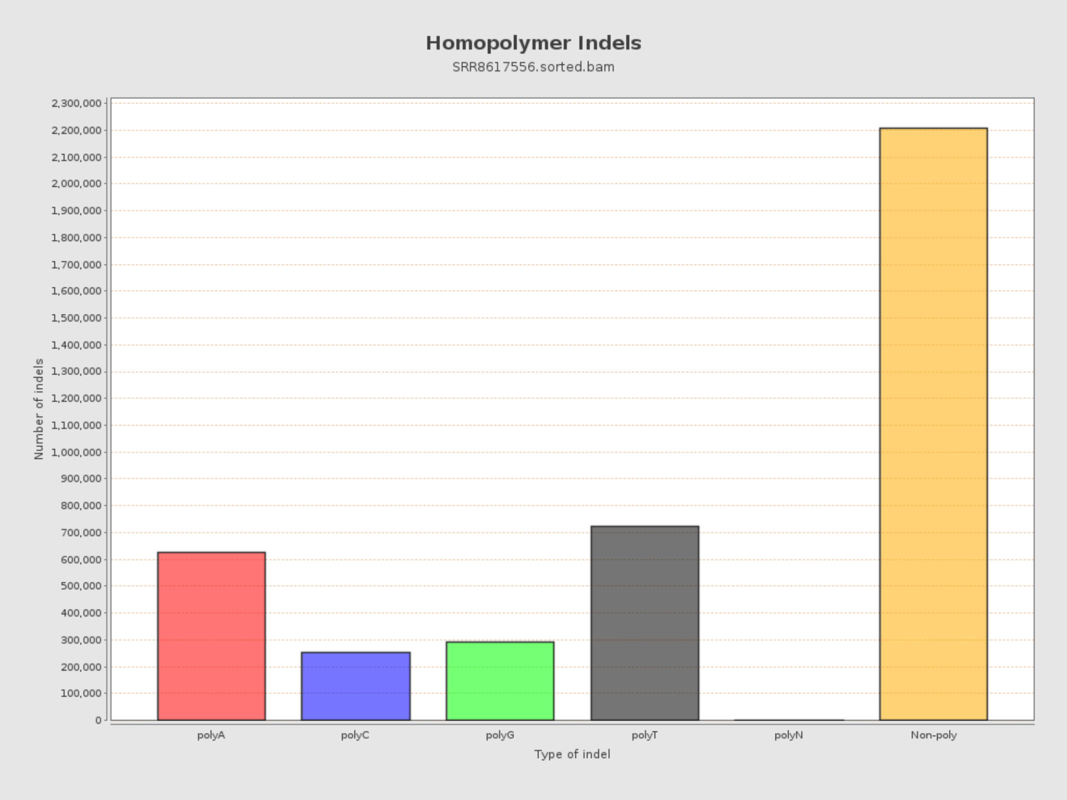
9. Results : Mapped Reads GC-content Distribution



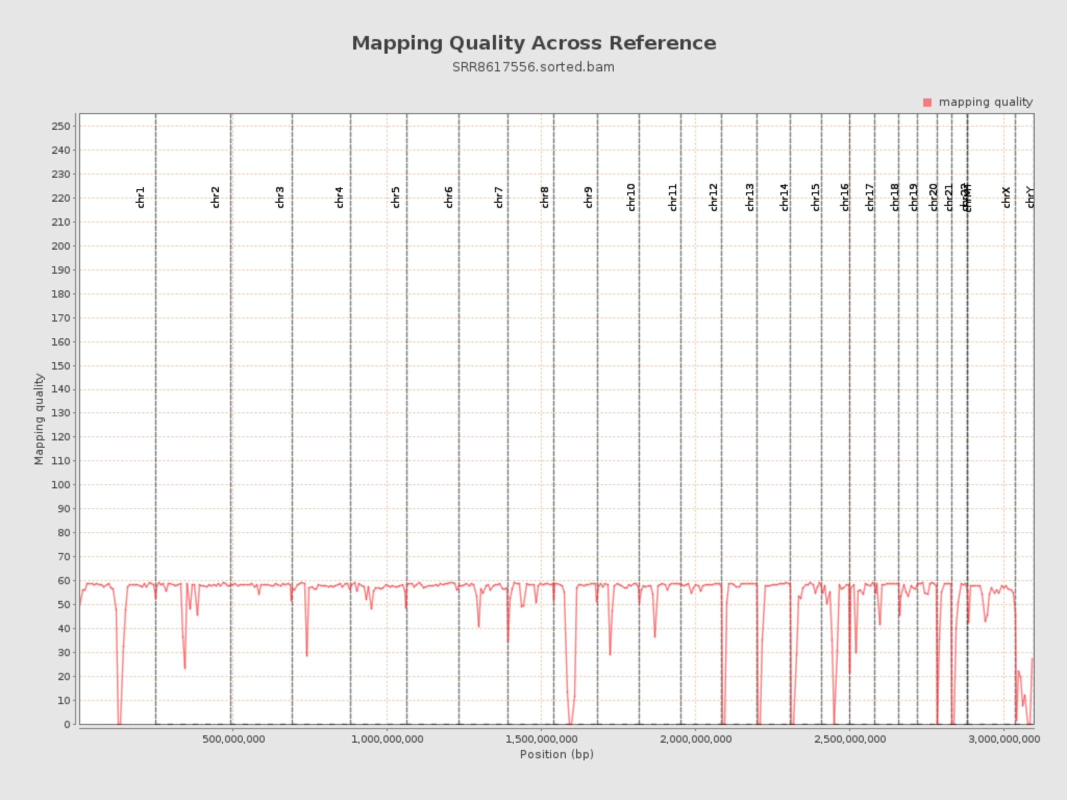
10. Results : Mapped Reads Clipping Profile



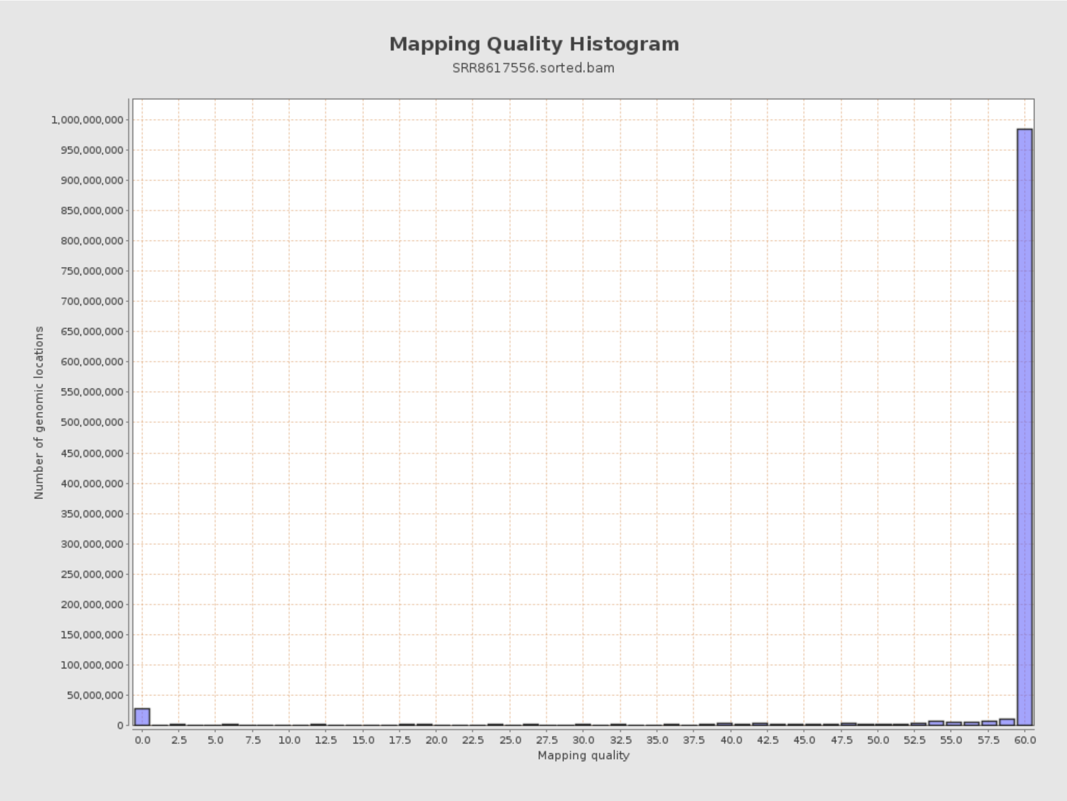
11. Results : Homopolymer Indels



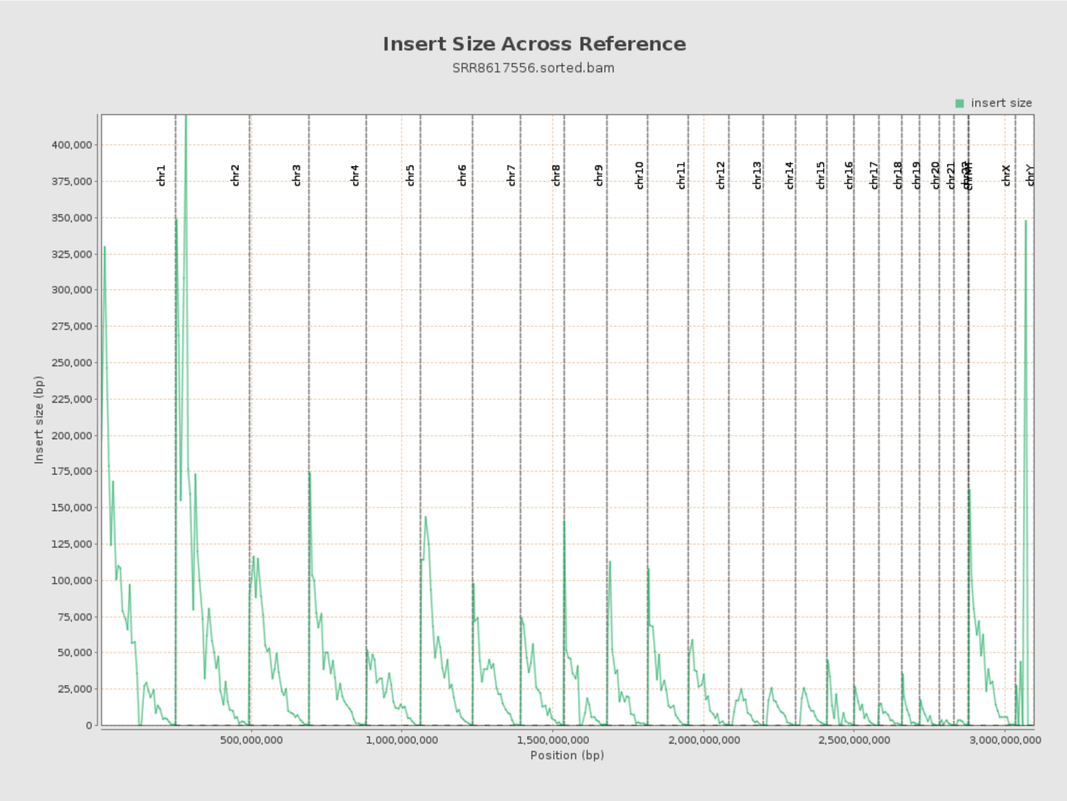
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram