Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:41:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819009.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_SRR1819009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819009.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:41:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	672,238
Mapped reads	657,052 / 97.74%
Unmapped reads	15,186 / 2.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,189 / 1.52%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	170,156 / 25.31%
Duplication rate	22.21%
Clipped reads	665,075 / 98.93%

2.2. ACGT Content

Number/percentage of A's	17,626,351 / 29.07%
Number/percentage of C's	12,940,284 / 21.34%
Number/percentage of T's	17,180,418 / 28.34%
Number/percentage of G's	12,879,096 / 21.24%
Number/percentage of N's	2,989 / 0%
GC Percentage	42.59%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.3048

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

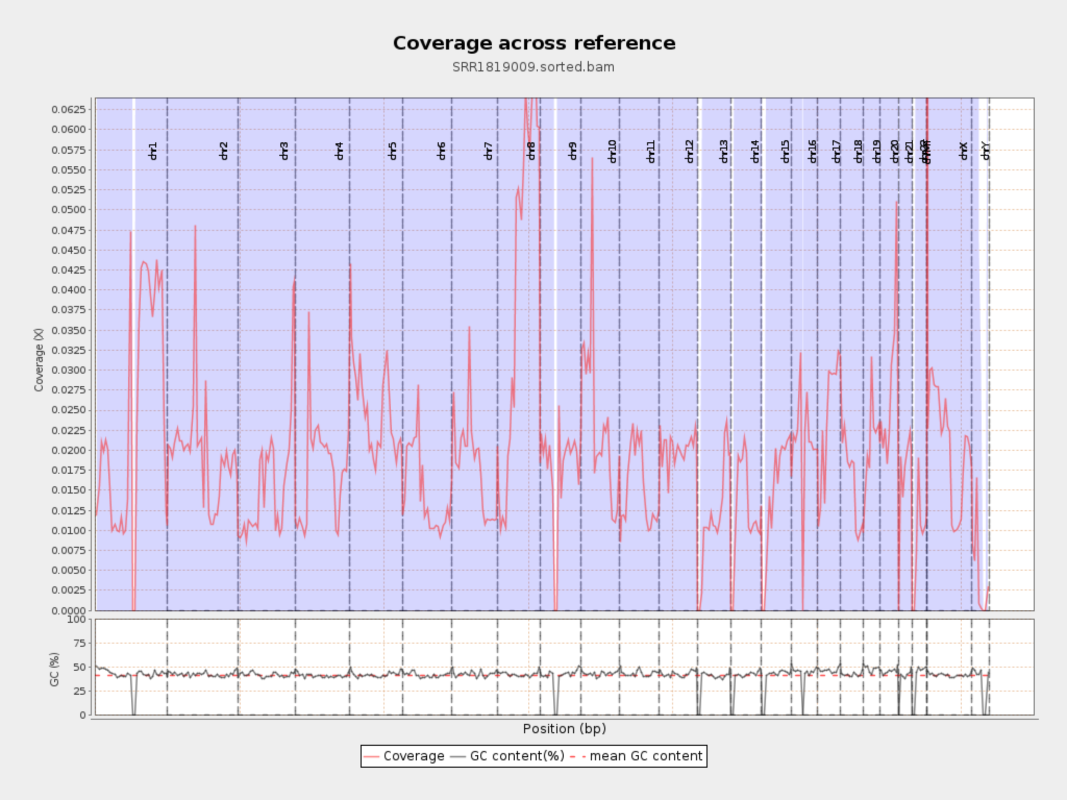
General error rate	0.72%
Mismatches	414,589
Insertions	8,744
Mapped reads with at least one insertion	1.29%
Deletions	20,208
Mapped reads with at least one deletion	3%
Homopolymer indels	41.78%

2.6. Chromosome stats

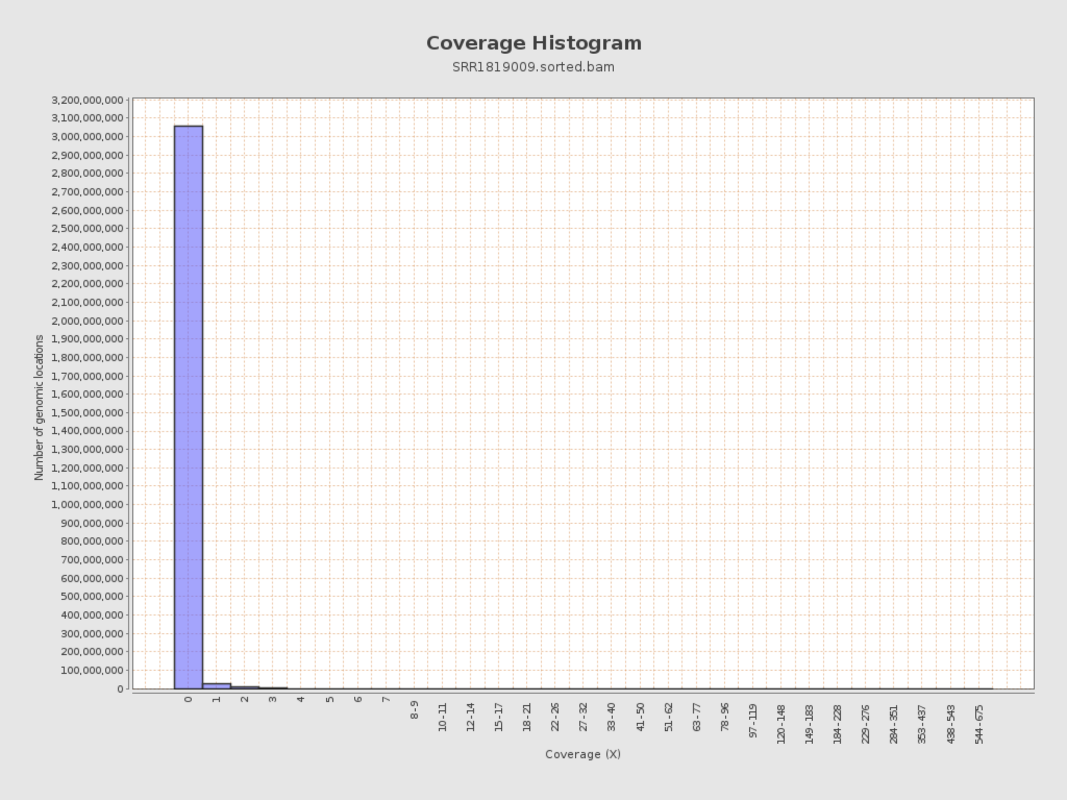
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5958052	0.0239	0.6036
chr2	243199373	4757681	0.0196	0.3668
chr3	198022430	3073834	0.0155	0.1721
chr4	191154276	3339467	0.0175	0.2157
chr5	180915260	4492786	0.0248	0.222
chr6	171115067	2513740	0.0147	0.1926
chr7	159138663	2914850	0.0183	0.328

chr8	146364022	6091450	0.0416	0.3133
chr9	141213431	2455840	0.0174	0.2557
chr10	135534747	3240770	0.0239	0.3795
chr11	135006516	2076895	0.0154	0.2002
chr12	133851895	2713898	0.0203	0.2022
chr13	115169878	1326050	0.0115	0.1463
chr14	107349540	1316903	0.0123	0.1633
chr15	102531392	1488705	0.0145	0.1658
chr16	90354753	1867529	0.0207	0.2984
chr17	81195210	1932285	0.0238	0.2285
chr18	78077248	1270495	0.0163	0.3182
chr19	59128983	1248350	0.0211	0.4842
chr20	63025520	1787313	0.0284	0.244
chr21	48129895	823524	0.0171	0.199
chr22	51304566	466164	0.0091	0.1363
chrMT	16571	21660	1.3071	1.7547
chrX	155270560	3236385	0.0208	0.2448
chrY	59373566	252162	0.0042	0.2795

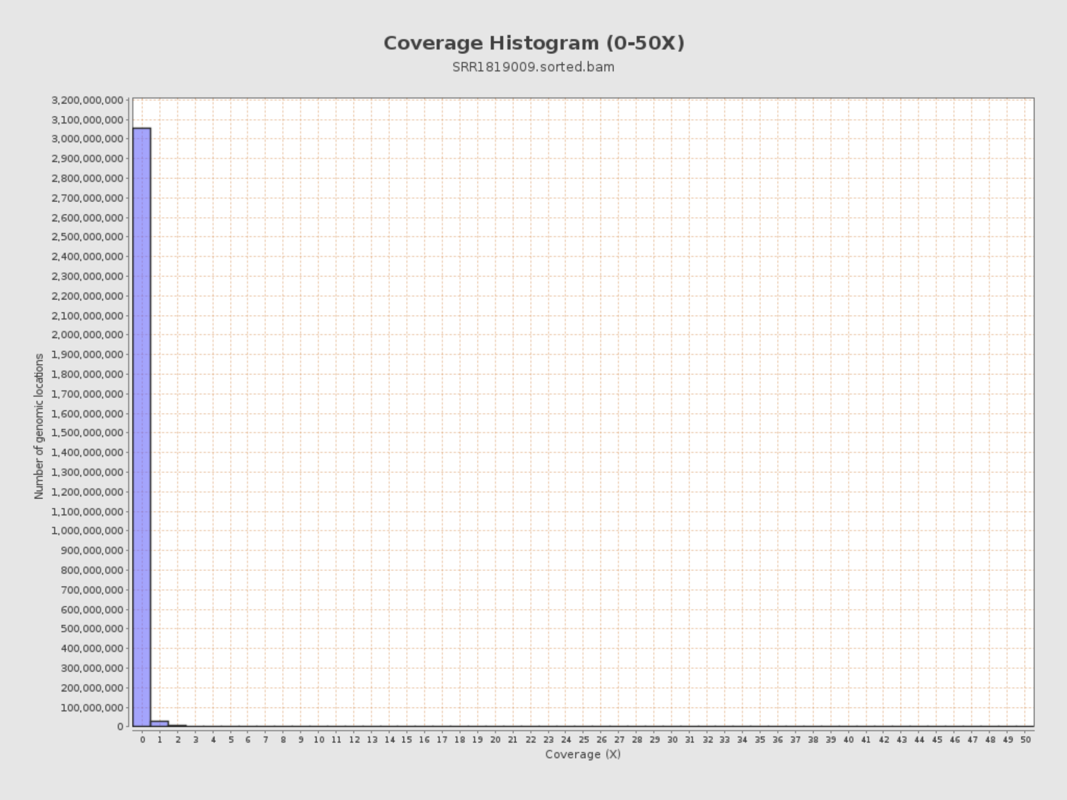
3. Results : Coverage across reference



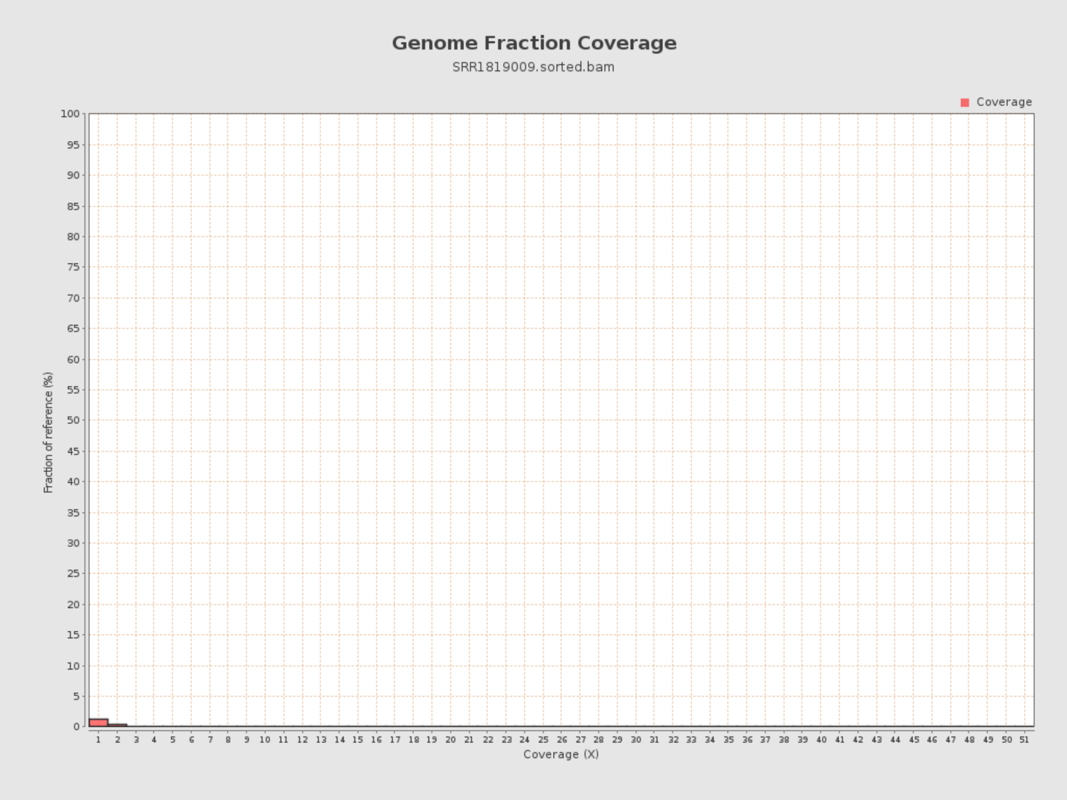
4. Results : Coverage Histogram



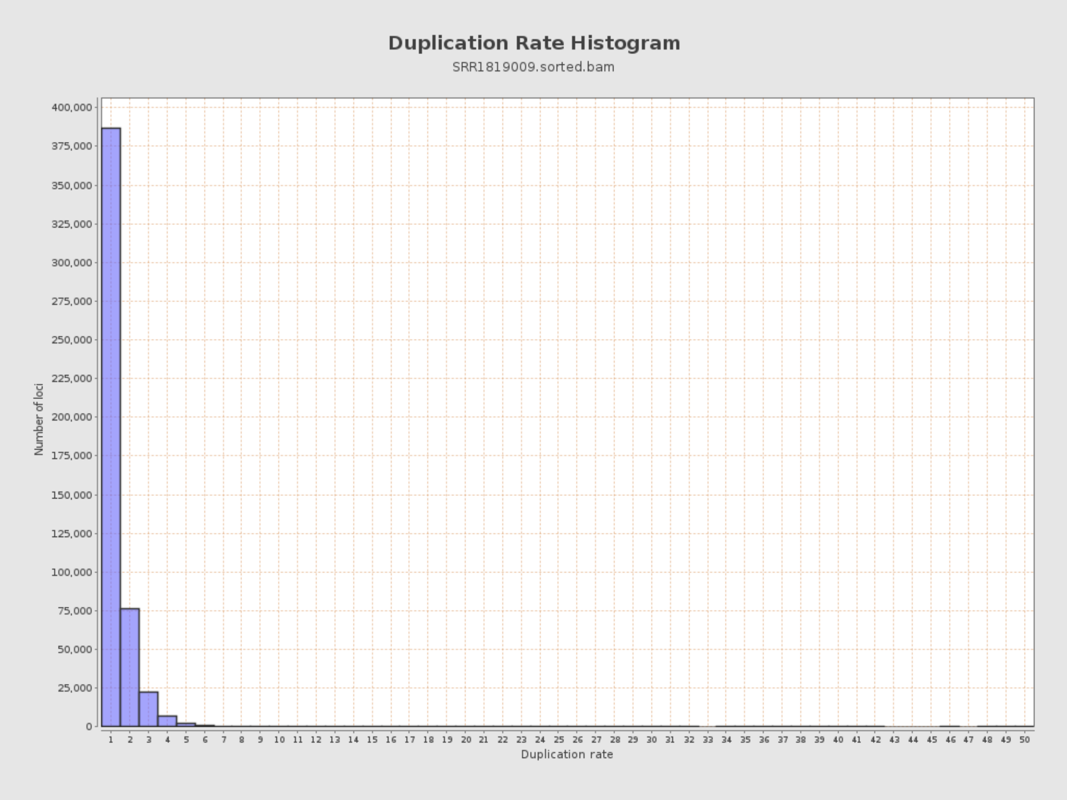
5. Results : Coverage Histogram (0-50X)



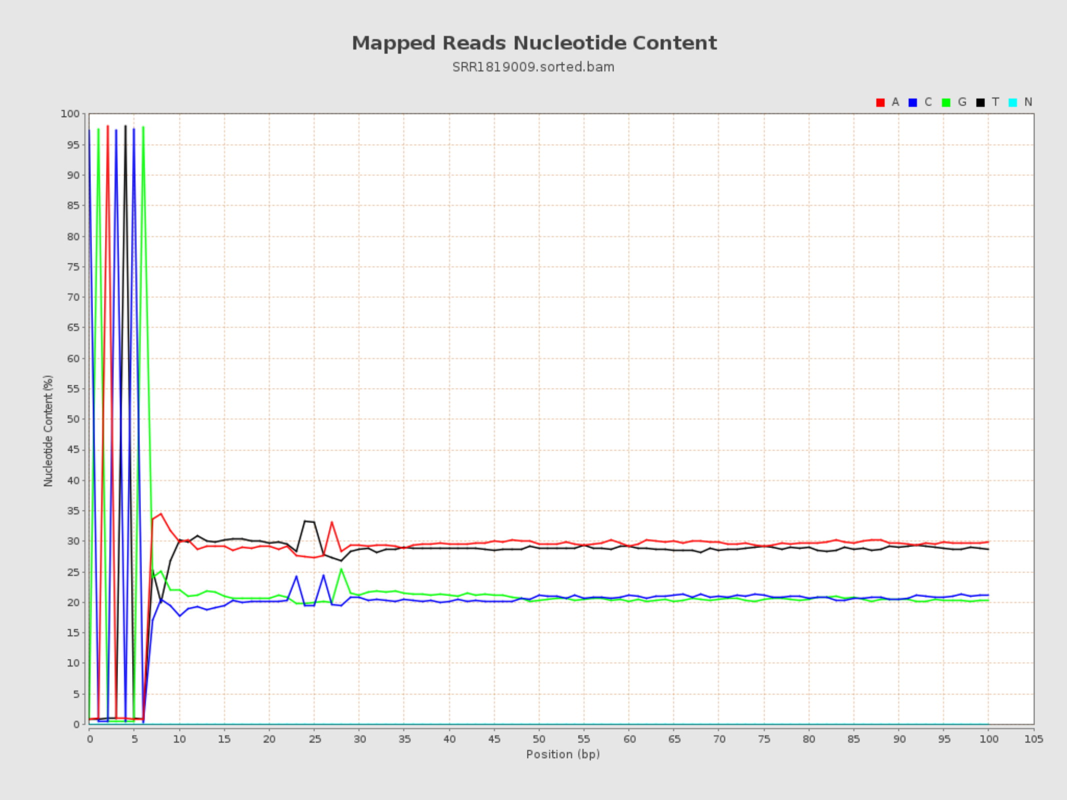
6. Results : Genome Fraction Coverage



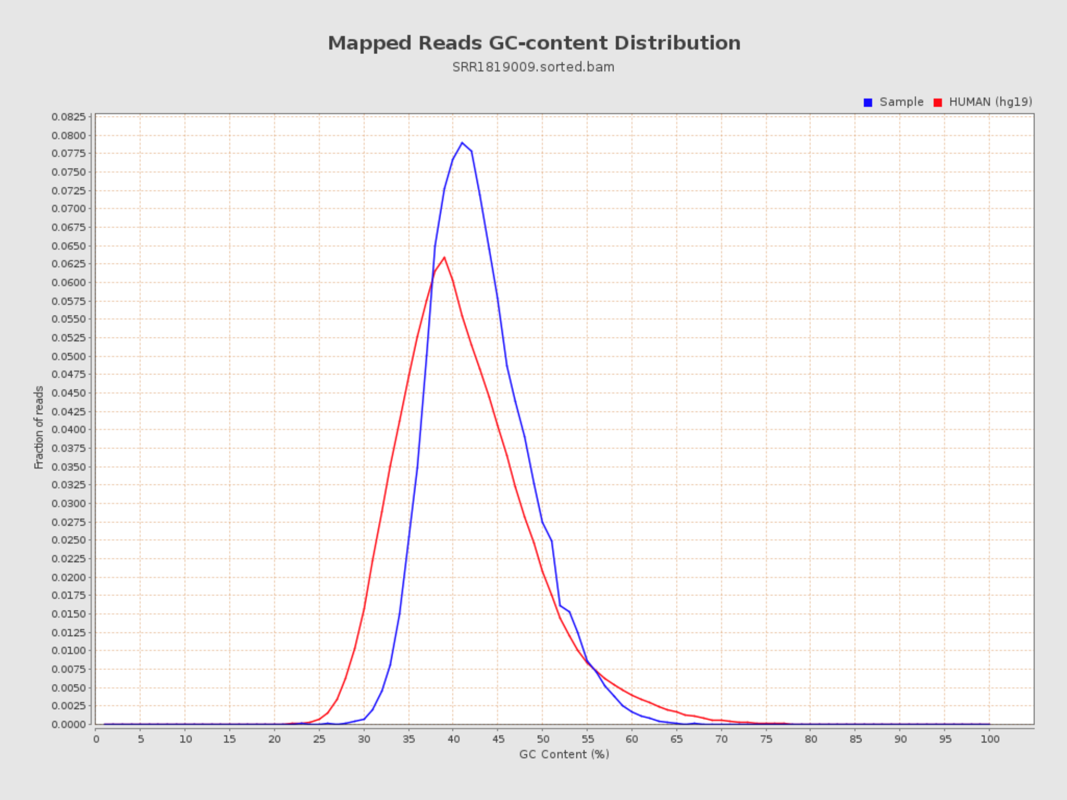
7. Results : Duplication Rate Histogram



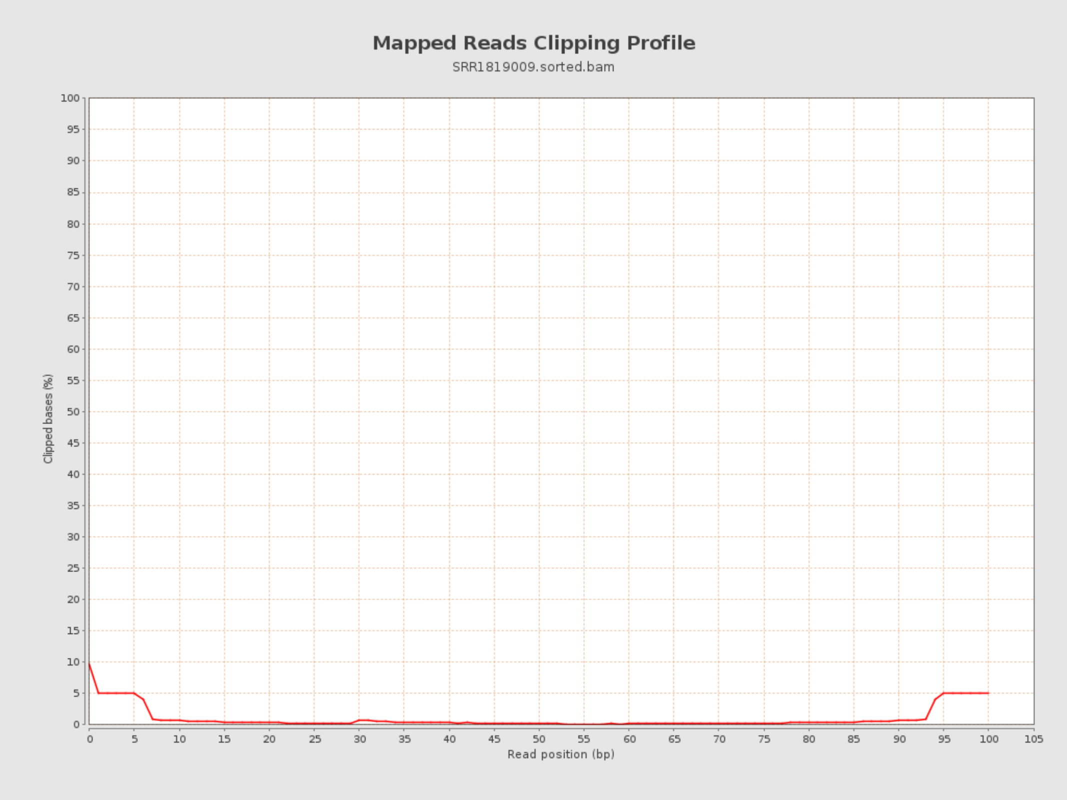
8. Results : Mapped Reads Nucleotide Content



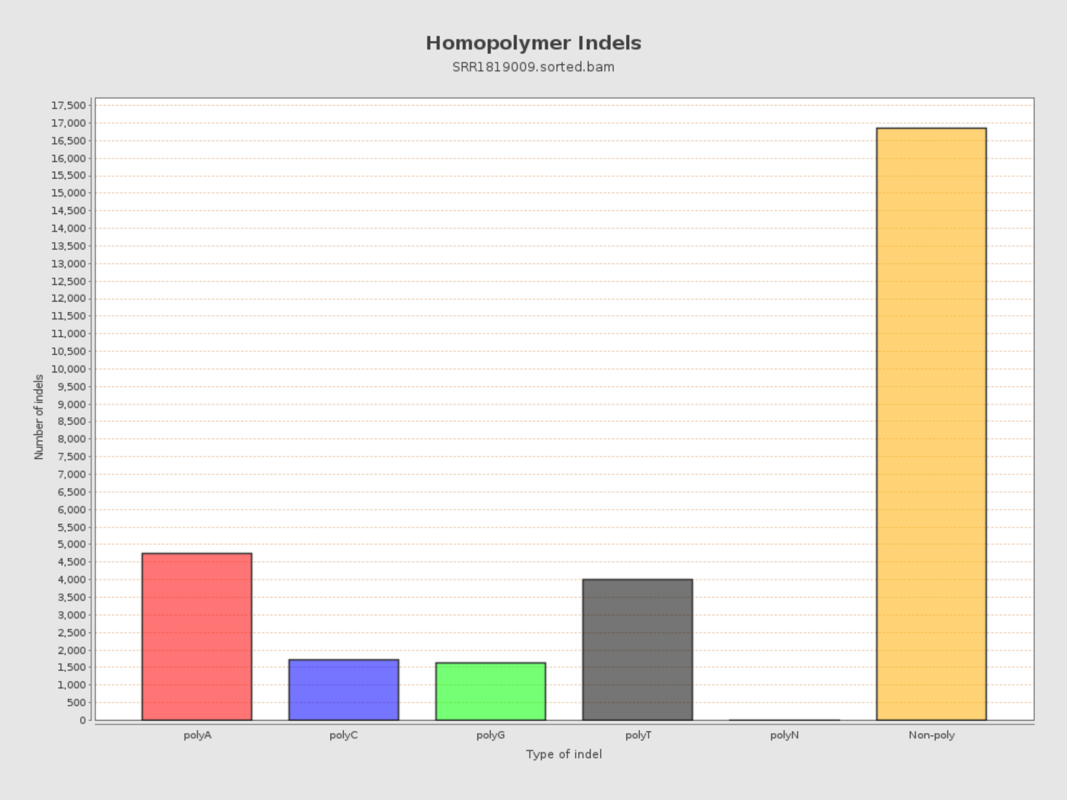
9. Results : Mapped Reads GC-content Distribution



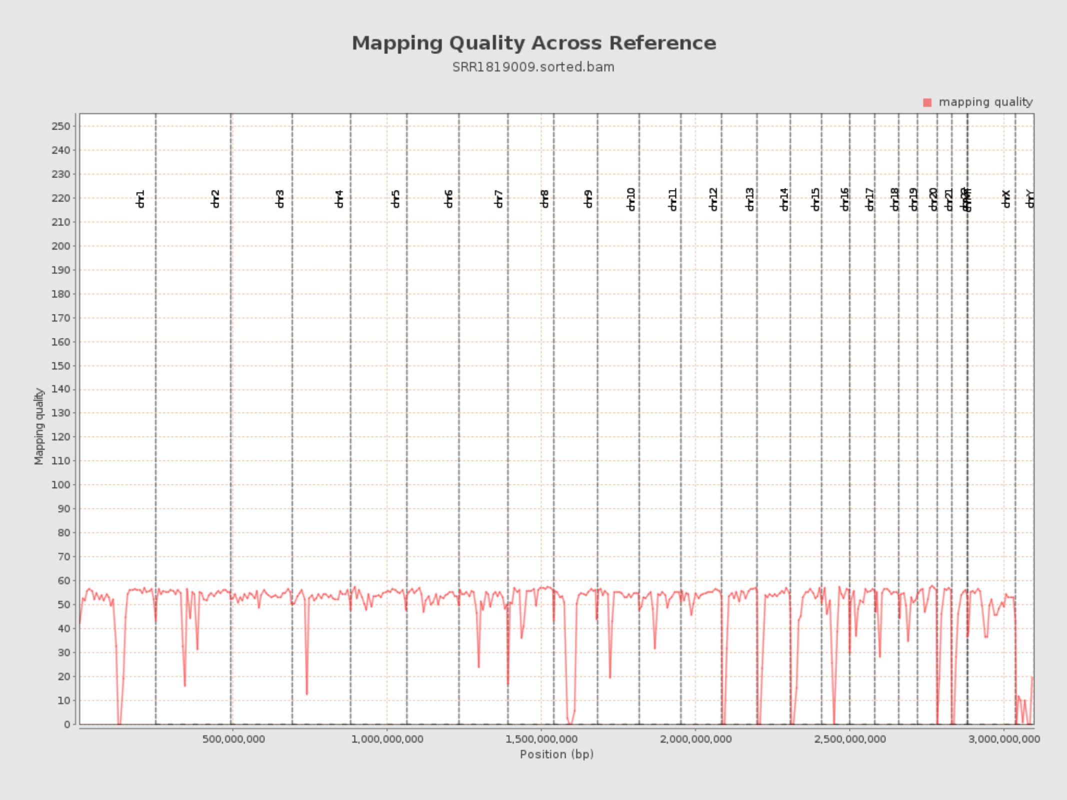
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram