Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 07:02:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054609.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_SRR054609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054609.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 07:02:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,401,510
Mapped reads	12,117,376 / 69.63%
Unmapped reads	5,284,134 / 30.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	313 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,756,932 / 15.84%
Duplication rate	15.9%
Clipped reads	1,194,565 / 6.86%

2.2. ACGT Content

Number/percentage of A's	175,278,745 / 30.71%
Number/percentage of C's	104,137,653 / 18.25%
Number/percentage of T's	177,119,518 / 31.03%
Number/percentage of G's	113,997,221 / 19.97%
Number/percentage of N's	179,316 / 0.03%
GC Percentage	38.22%

2.3. Coverage

Mean	0.1844

Standard Deviation	1.3509

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

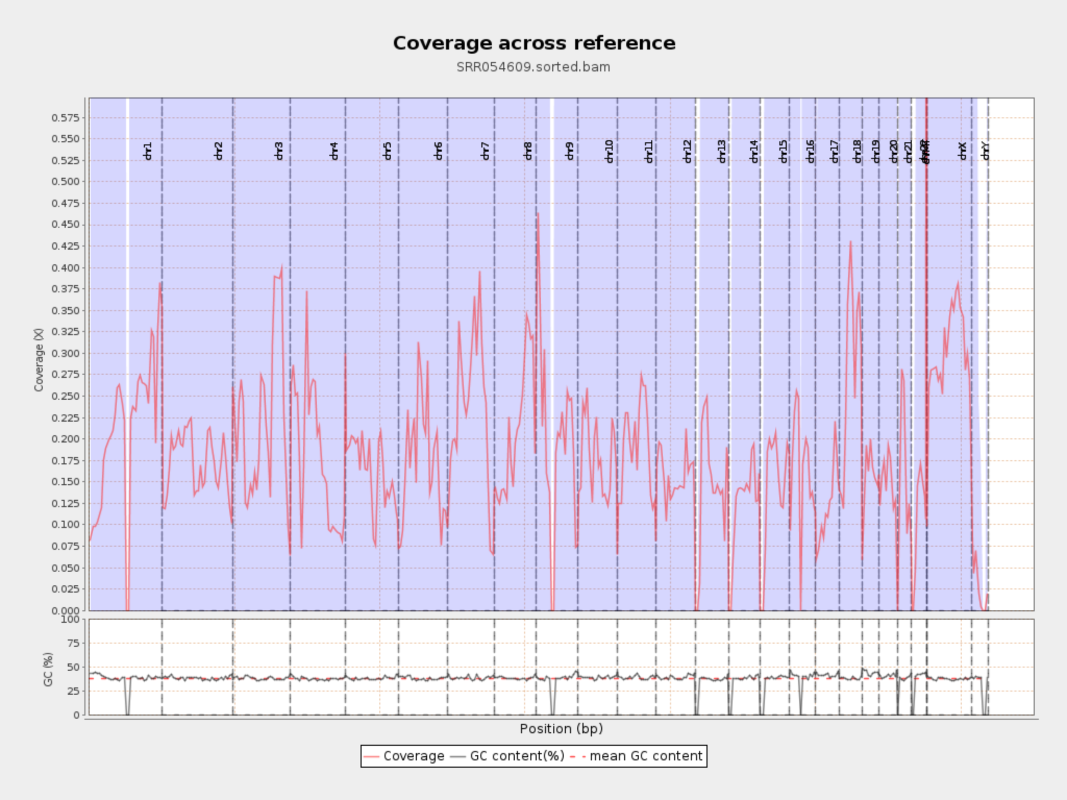
General error rate	0.59%
Mismatches	3,354,299
Insertions	24,087
Mapped reads with at least one insertion	0.2%
Deletions	81,674
Mapped reads with at least one deletion	0.67%
Homopolymer indels	48.7%

2.6. Chromosome stats

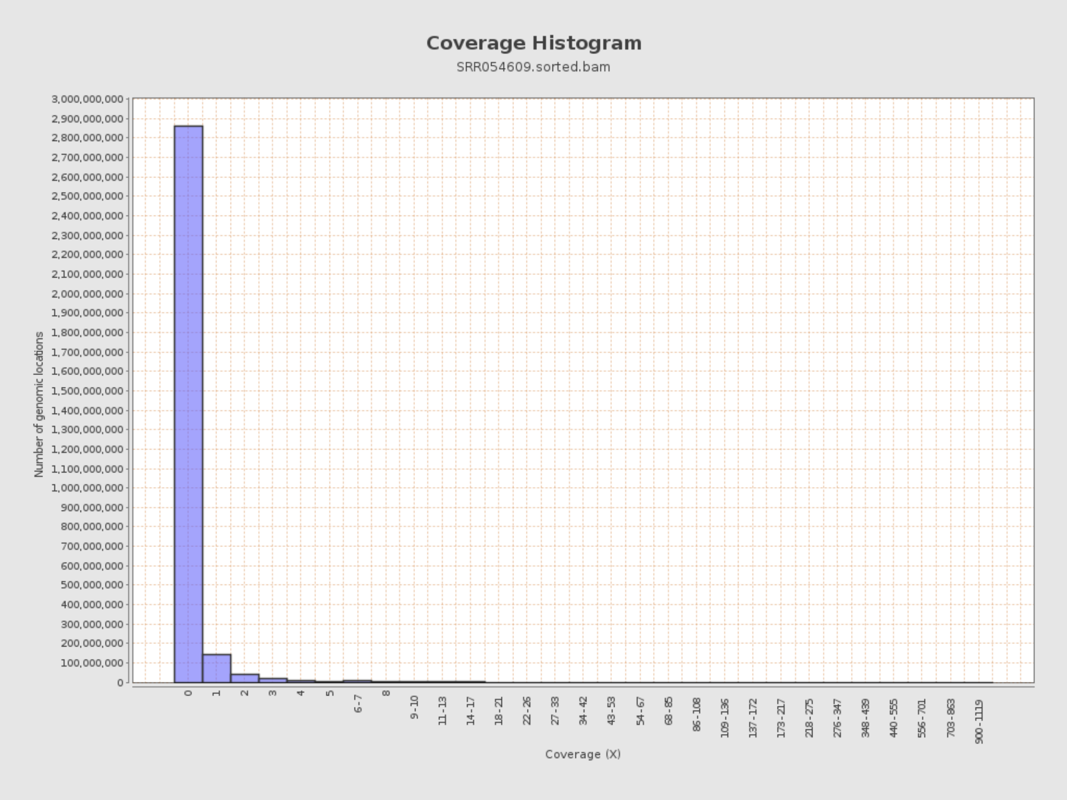
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	51875251	0.2081	1.4975
chr2	243199373	41975826	0.1726	1.3669
chr3	198022430	44298628	0.2237	1.4279
chr4	191154276	34299105	0.1794	1.2842
chr5	180915260	29520361	0.1632	1.1017
chr6	171115067	29514154	0.1725	1.2681
chr7	159138663	38227459	0.2402	1.6939

chr8	146364022	31030199	0.212	1.4783
chr9	141213431	28673265	0.203	1.4703
chr10	135534747	24417400	0.1802	1.3158
chr11	135006516	25779967	0.191	1.3588
chr12	133851895	20905600	0.1562	1.1188
chr13	115169878	16114106	0.1399	1.0411
chr14	107349540	13181048	0.1228	1.1506
chr15	102531392	14435760	0.1408	1.0117
chr16	90354753	14948405	0.1654	1.323
chr17	81195210	9846834	0.1213	0.9135
chr18	78077248	22042489	0.2823	1.8879
chr19	59128983	9422222	0.1594	1.2715
chr20	63025520	9328366	0.148	1.133
chr21	48129895	7442704	0.1546	1.2608
chr22	51304566	5222316	0.1018	0.8165
chrMT	16571	45904	2.7701	6.981
chrX	155270560	46658748	0.3005	1.7916
chrY	59373566	1626349	0.0274	0.5736

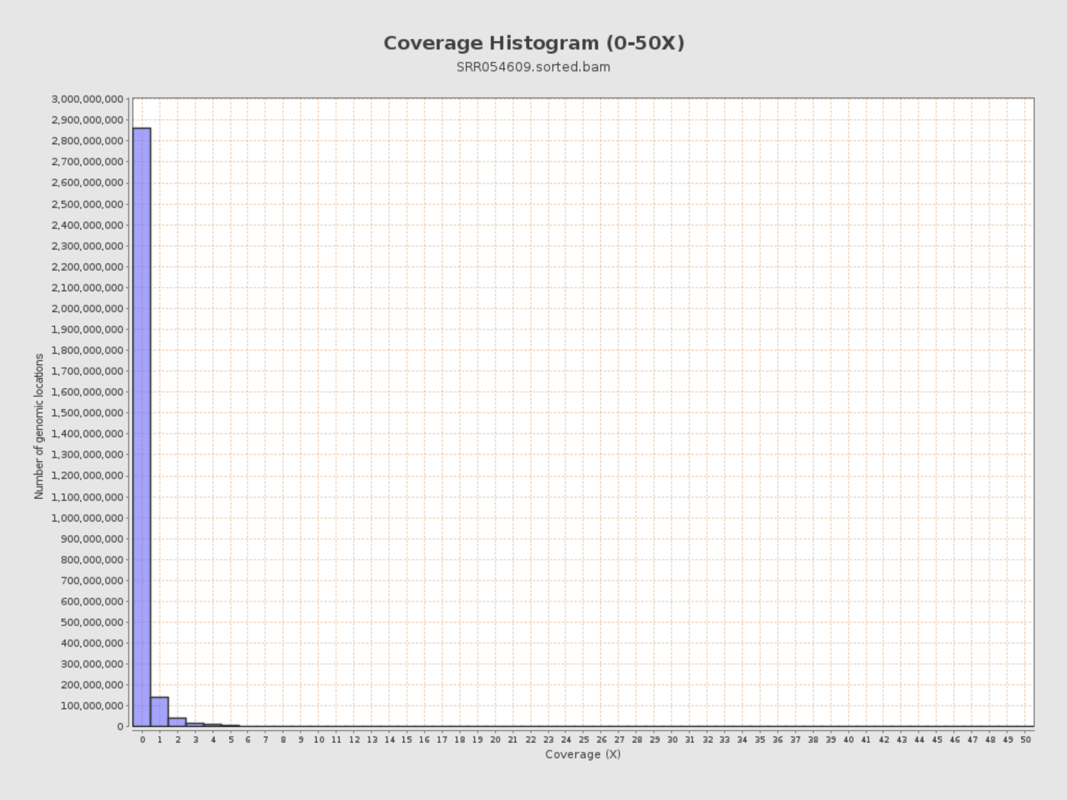
3. Results : Coverage across reference



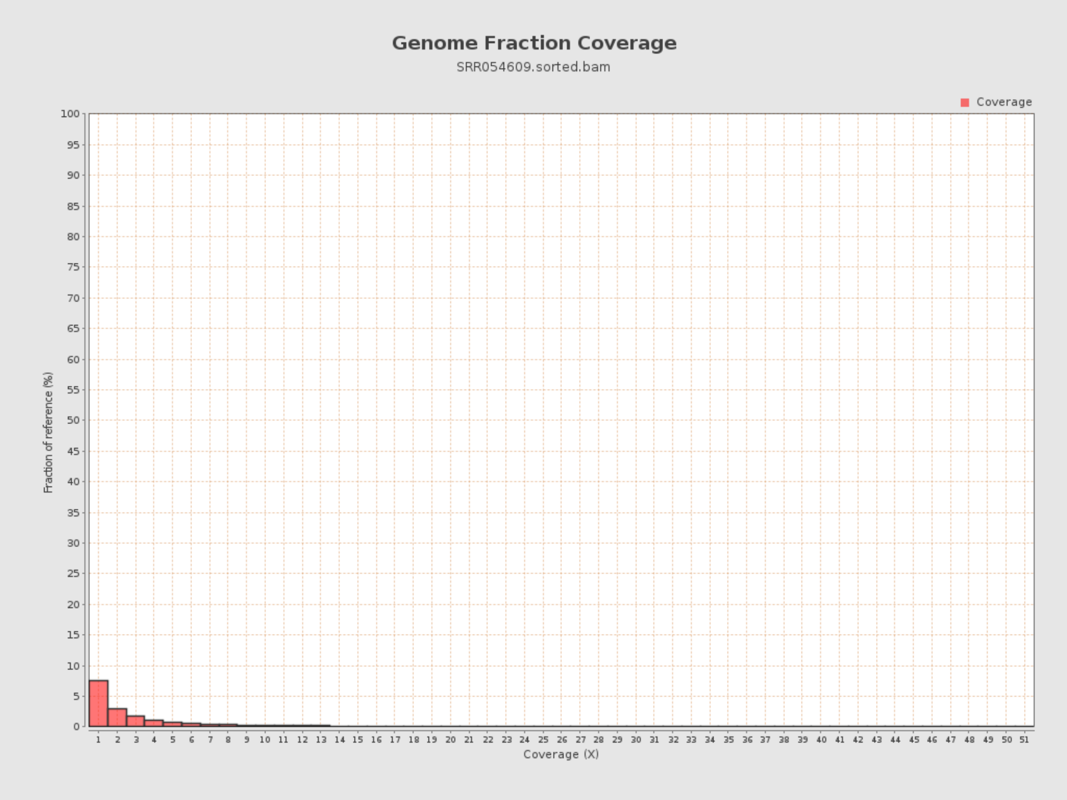
4. Results : Coverage Histogram



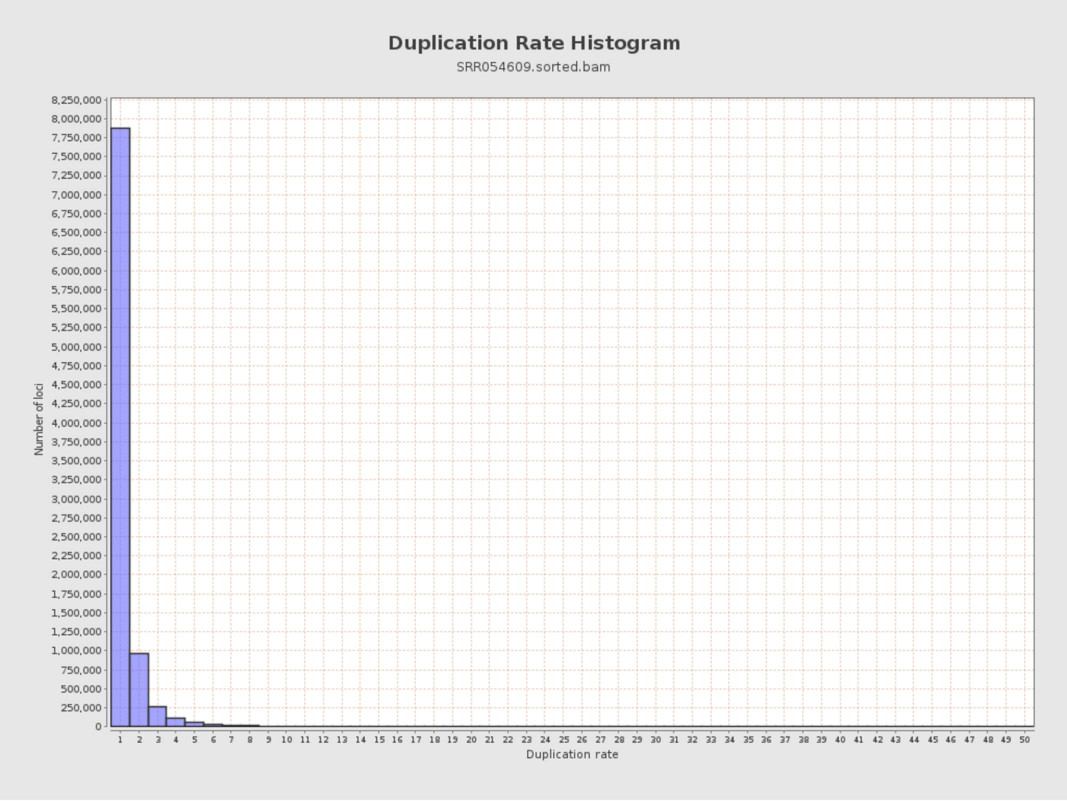
5. Results : Coverage Histogram (0-50X)



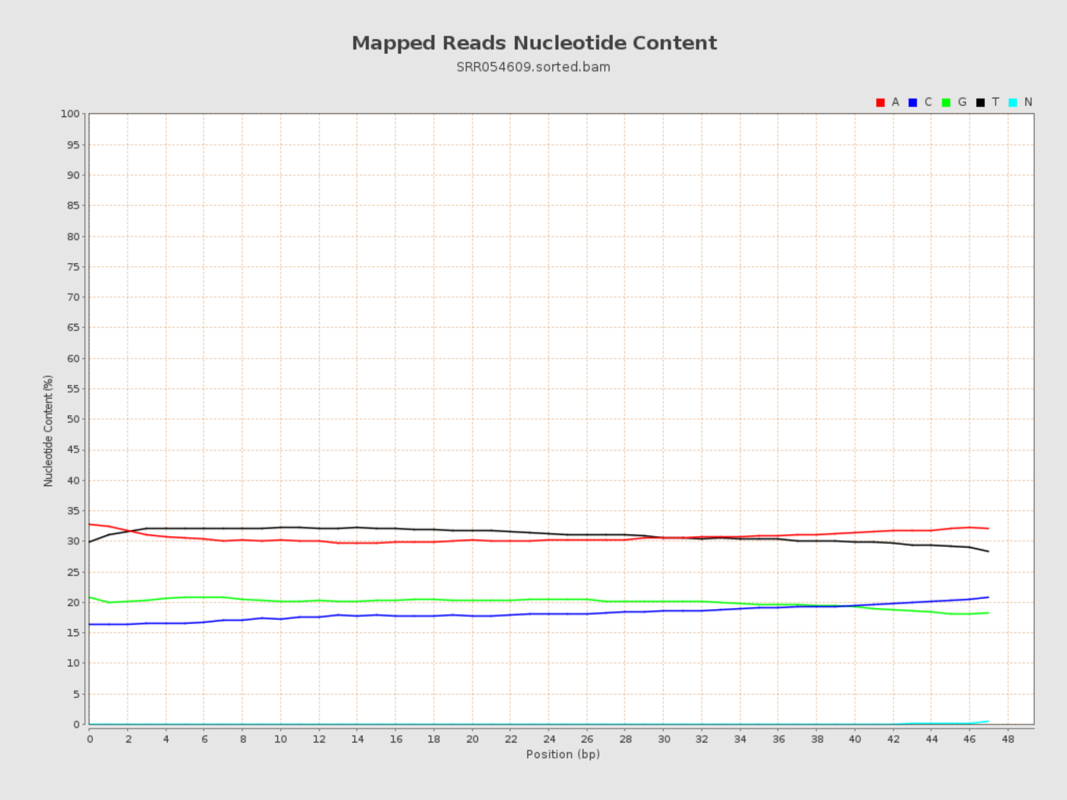
6. Results : Genome Fraction Coverage



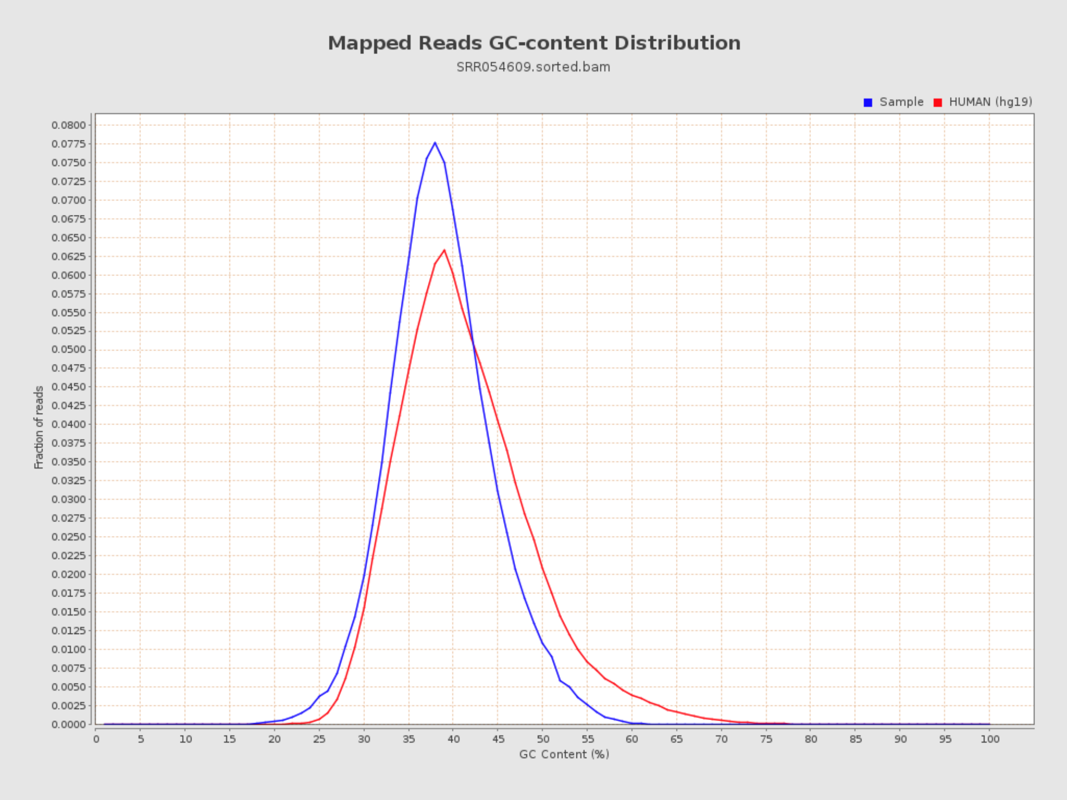
7. Results : Duplication Rate Histogram



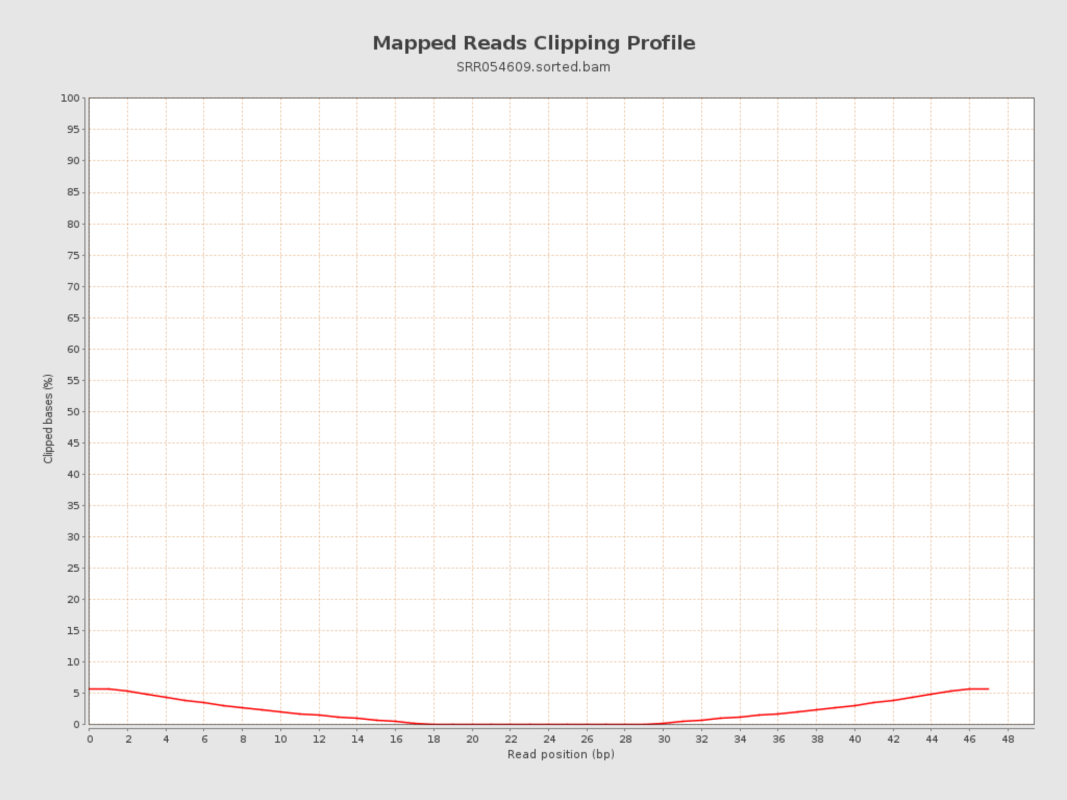
8. Results : Mapped Reads Nucleotide Content



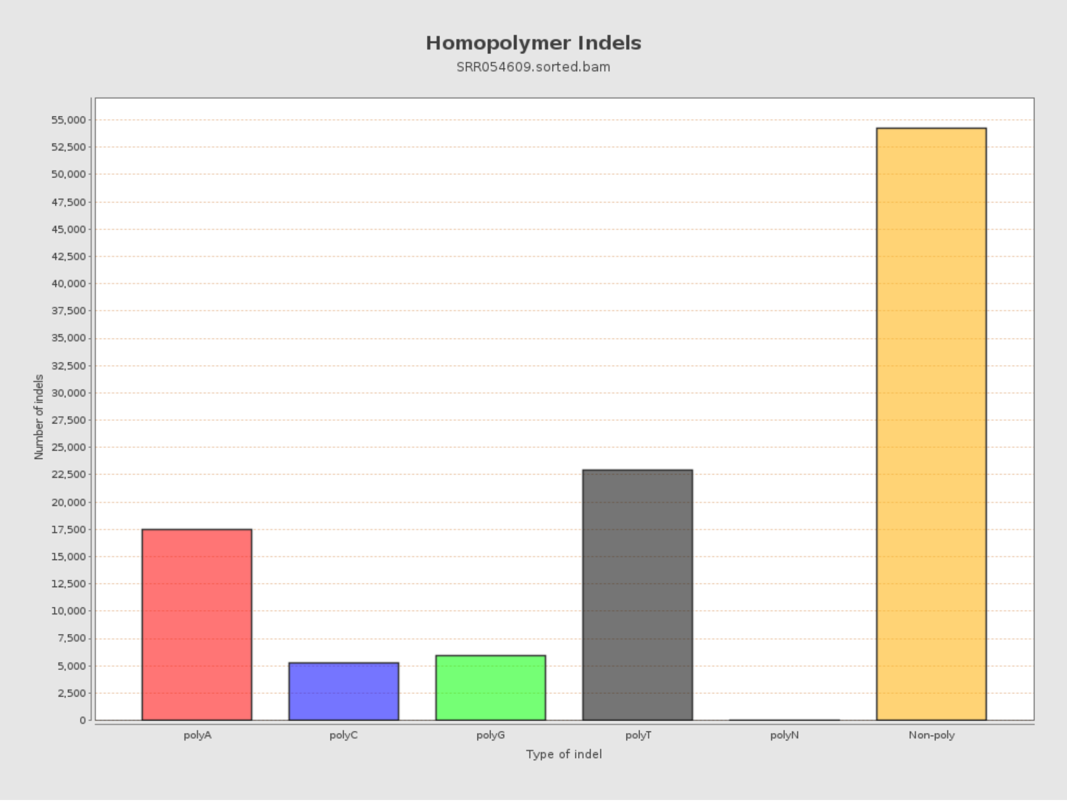
9. Results : Mapped Reads GC-content Distribution



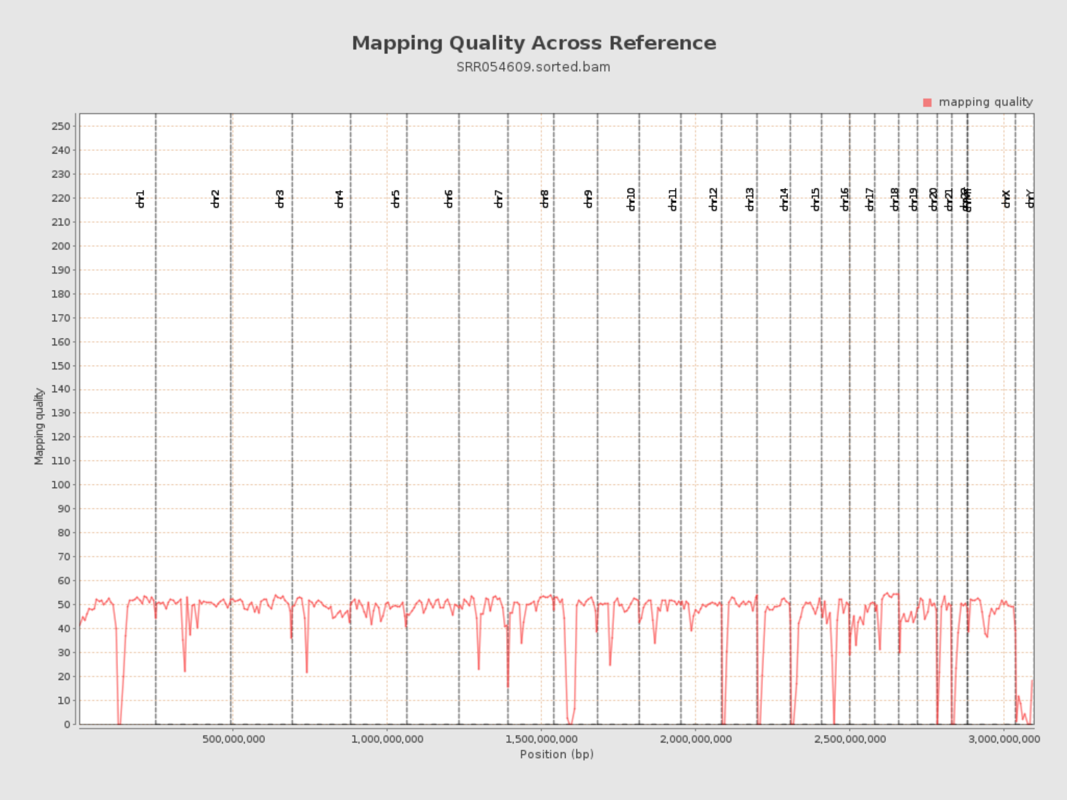
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram