Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:10:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004057.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_SRR6004057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:10:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,944,485
Mapped reads	1,708,687 / 87.87%
Unmapped reads	235,798 / 12.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,295 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	76,486 / 3.93%
Duplication rate	3.69%
Clipped reads	737,853 / 37.95%

2.2. ACGT Content

Number/percentage of A's	31,461,414 / 27.46%
Number/percentage of C's	21,838,230 / 19.06%
Number/percentage of T's	35,515,505 / 31%
Number/percentage of G's	25,720,317 / 22.45%
Number/percentage of N's	18,433 / 0.02%
GC Percentage	41.52%

2.3. Coverage

Mean	0.037

Standard Deviation	0.3139

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

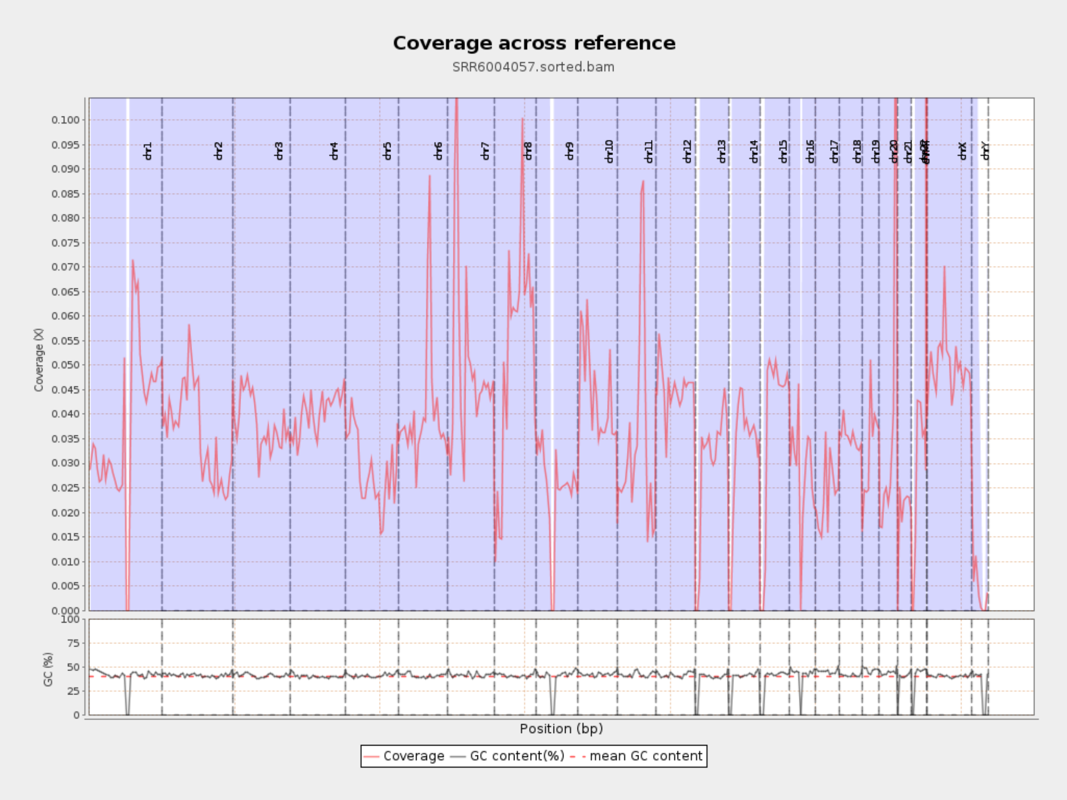
General error rate	0.84%
Mismatches	947,985
Insertions	7,820
Mapped reads with at least one insertion	0.45%
Deletions	25,165
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.56%

2.6. Chromosome stats

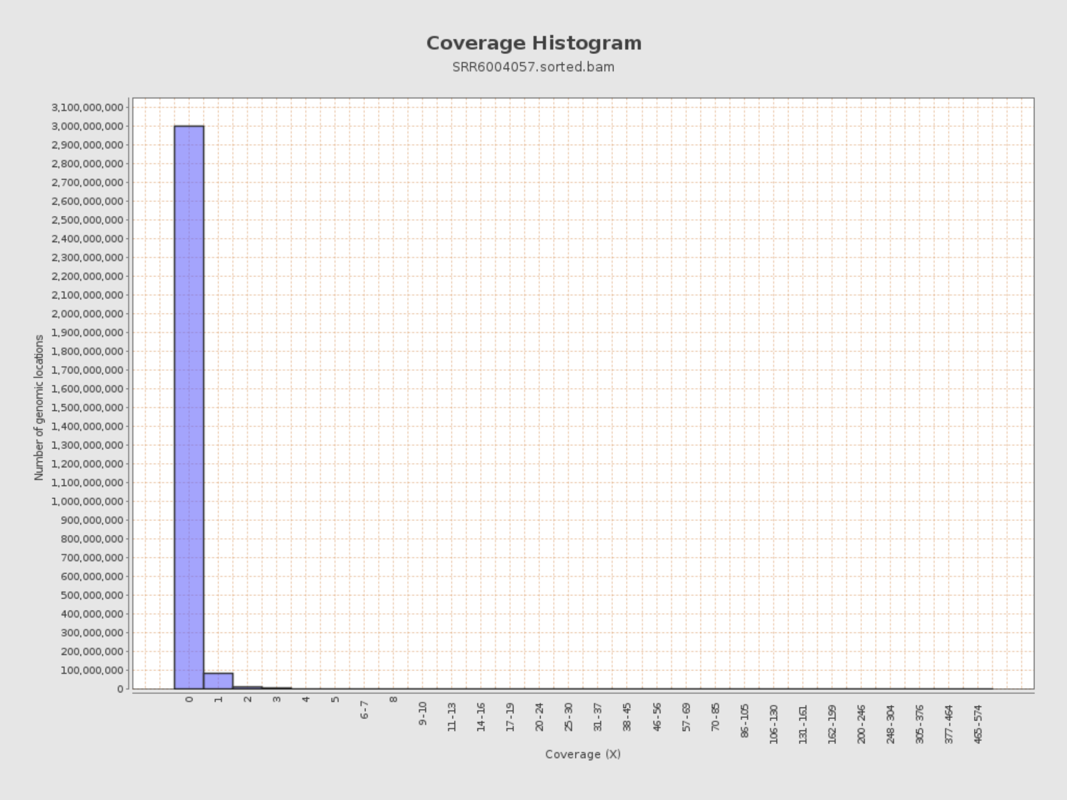
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9311441	0.0374	0.5099
chr2	243199373	8771521	0.0361	0.3566
chr3	198022430	7599037	0.0384	0.2254
chr4	191154276	7718164	0.0404	0.2401
chr5	180915260	5166876	0.0286	0.1964
chr6	171115067	6973052	0.0408	0.2552
chr7	159138663	8049933	0.0506	0.5114

chr8	146364022	7741523	0.0529	0.343
chr9	141213431	3474642	0.0246	0.2684
chr10	135534747	5994217	0.0442	0.3056
chr11	135006516	4720887	0.035	0.2517
chr12	133851895	6035334	0.0451	0.2503
chr13	115169878	3424821	0.0297	0.2052
chr14	107349540	3444835	0.0321	0.2265
chr15	102531392	3911467	0.0381	0.2306
chr16	90354753	2560499	0.0283	0.2107
chr17	81195210	1933029	0.0238	0.1861
chr18	78077248	2762817	0.0354	0.5059
chr19	59128983	1961504	0.0332	0.3743
chr20	63025520	2562865	0.0407	0.2437
chr21	48129895	966312	0.0201	0.1777
chr22	51304566	1385227	0.027	0.1906
chrMT	16571	75888	4.5796	3.4415
chrX	155270560	7774840	0.0501	0.2804
chrY	59373566	276992	0.0047	0.0936

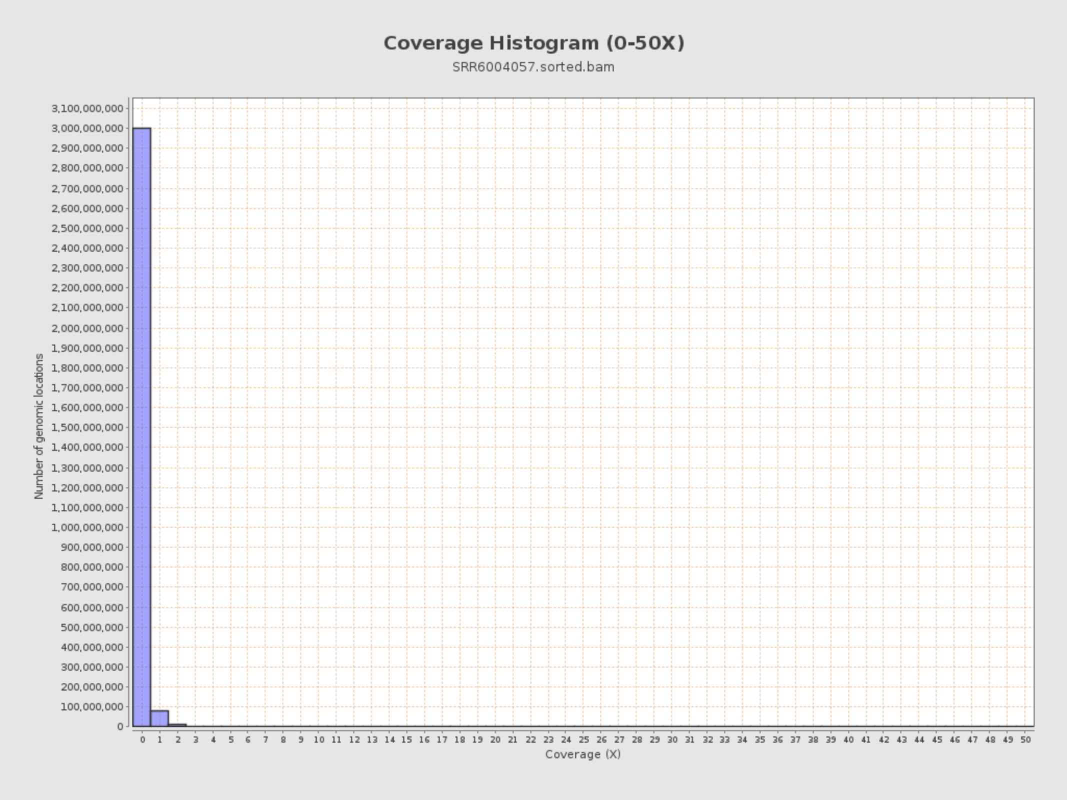
3. Results : Coverage across reference



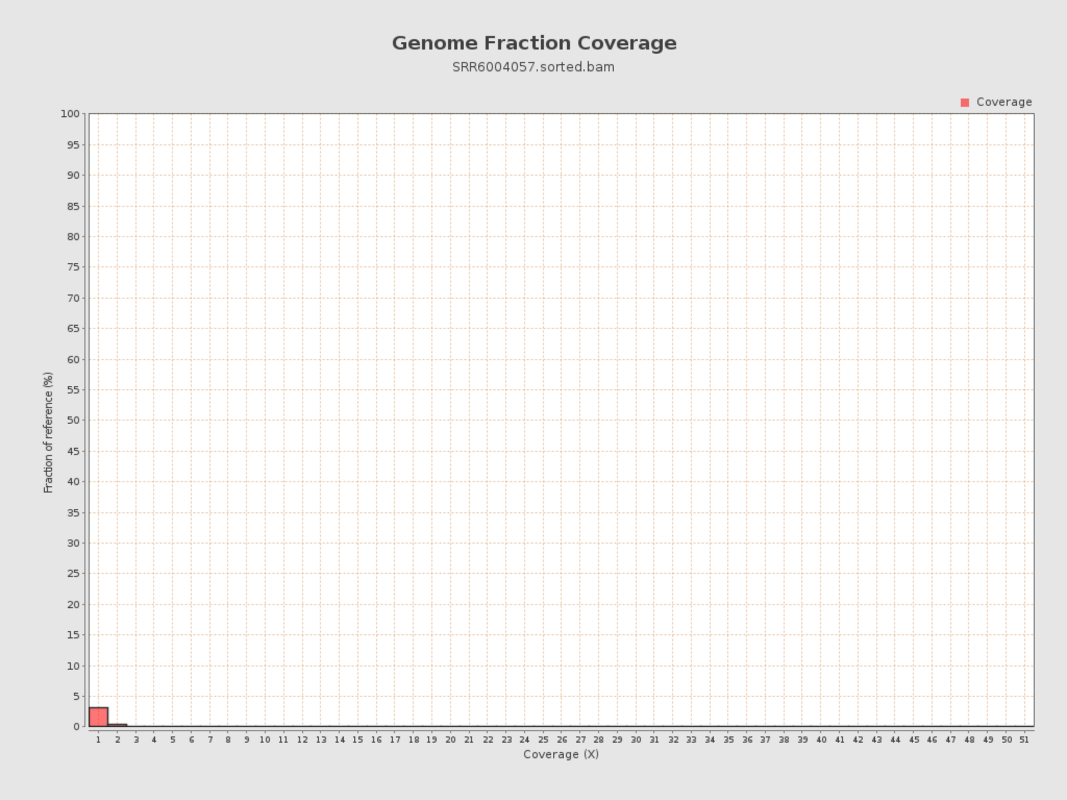
4. Results : Coverage Histogram



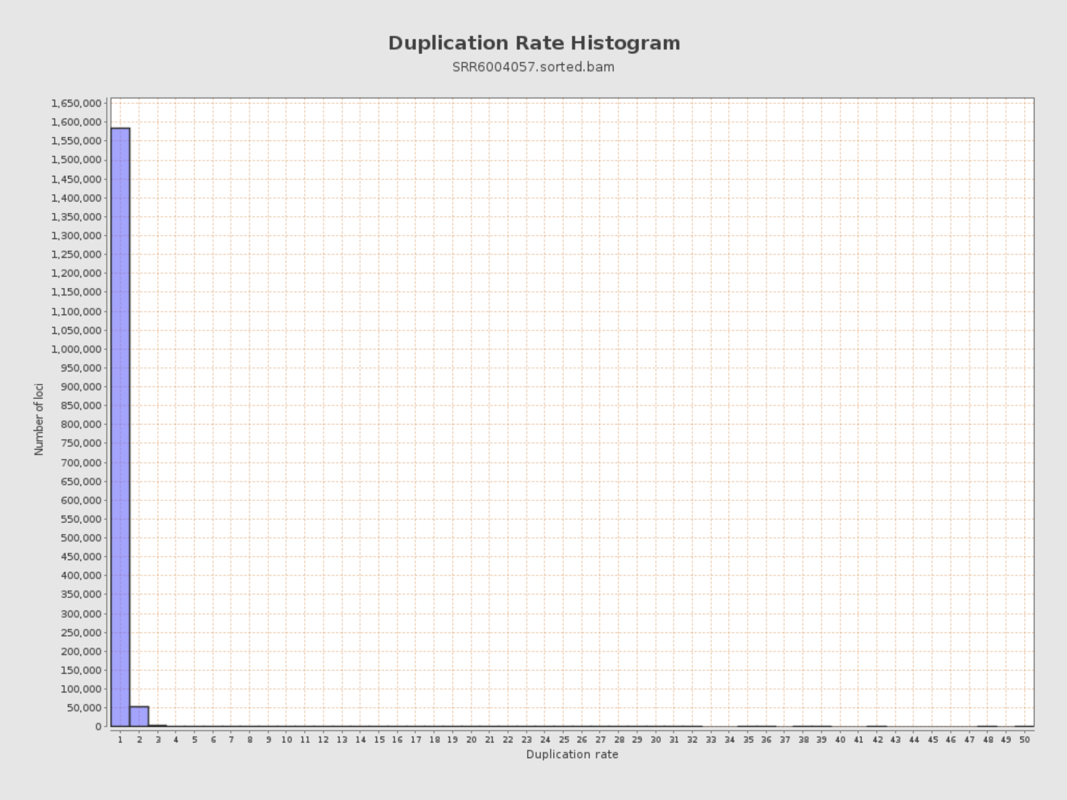
5. Results : Coverage Histogram (0-50X)



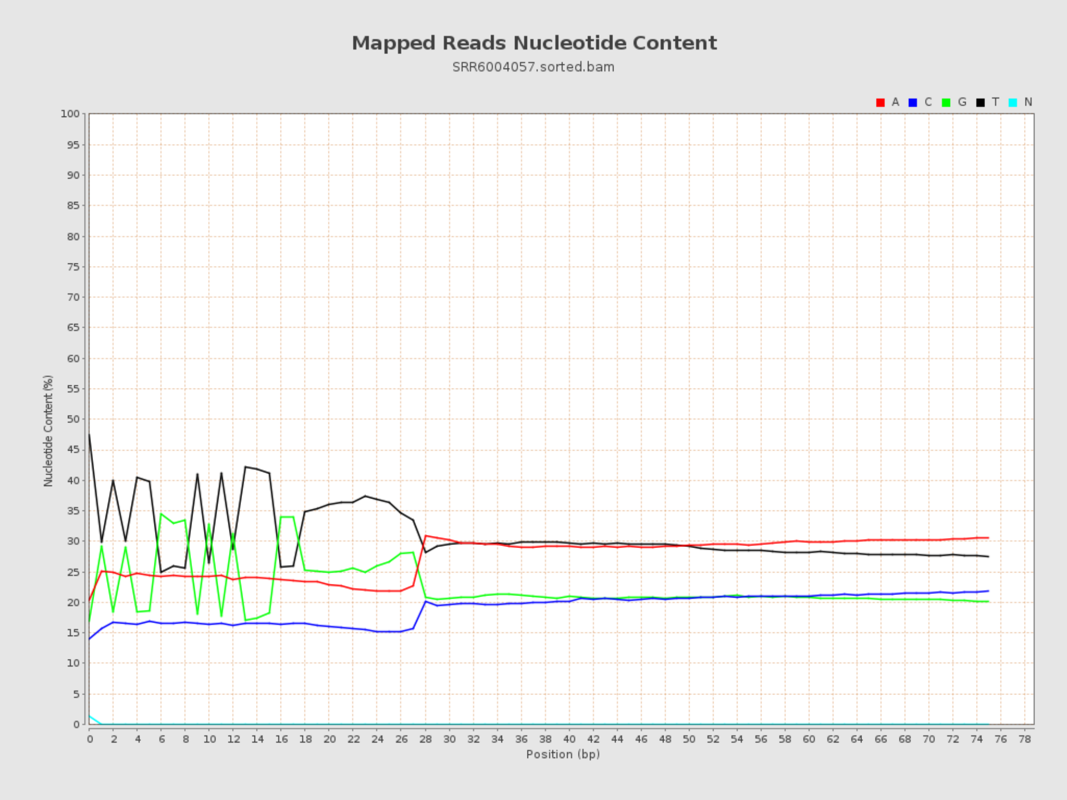
6. Results : Genome Fraction Coverage



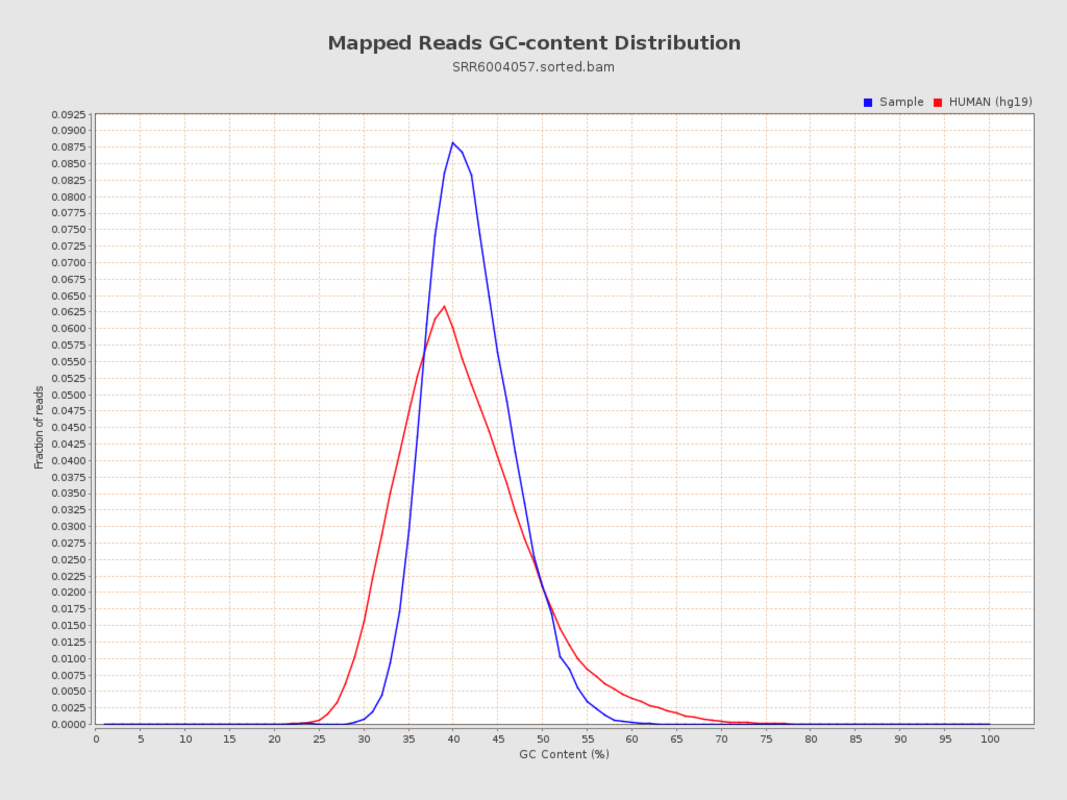
7. Results : Duplication Rate Histogram



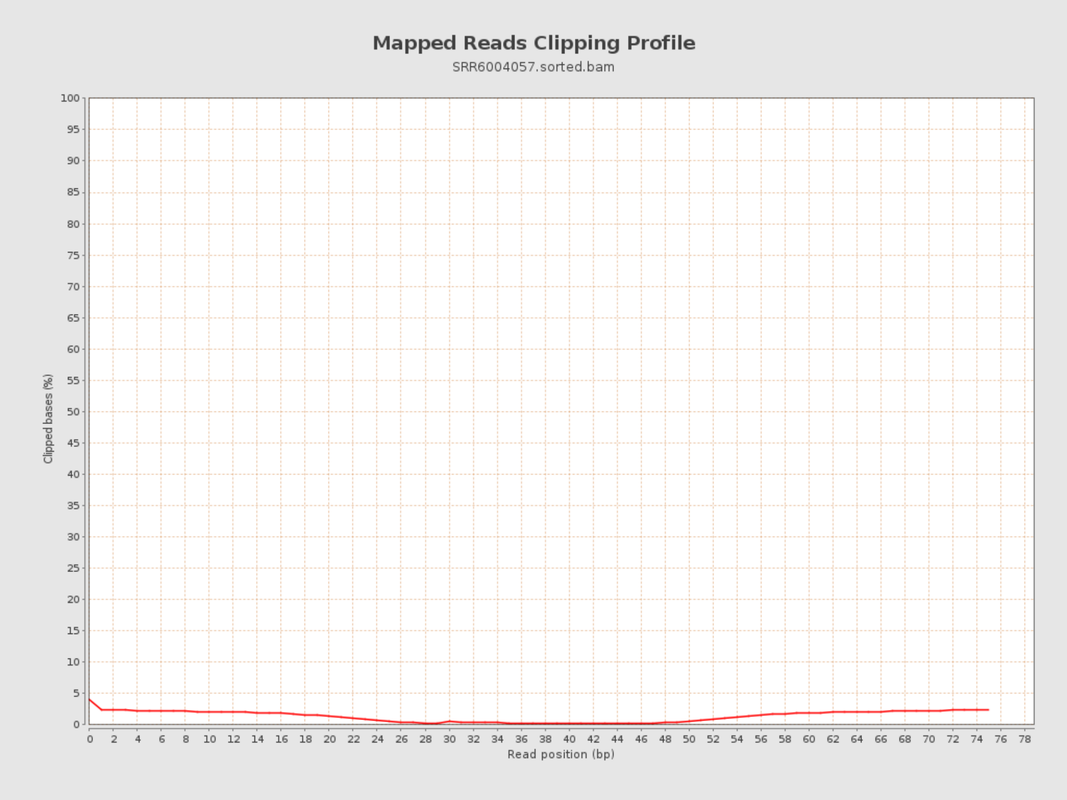
8. Results : Mapped Reads Nucleotide Content



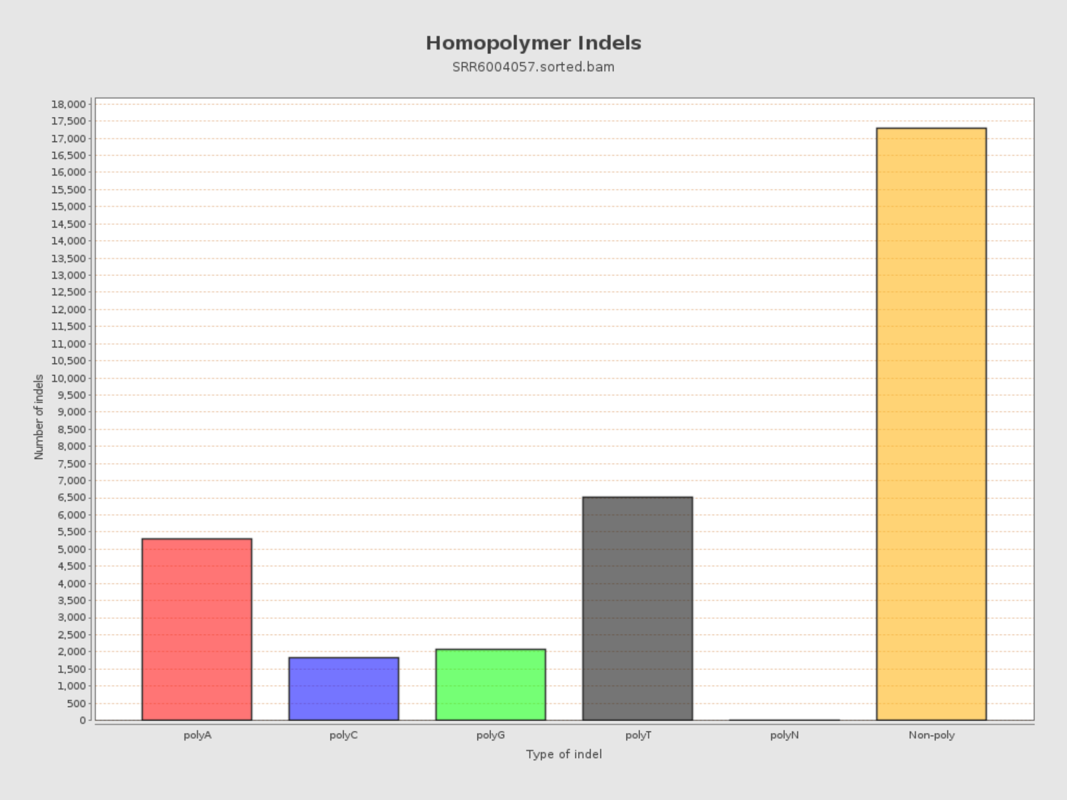
9. Results : Mapped Reads GC-content Distribution



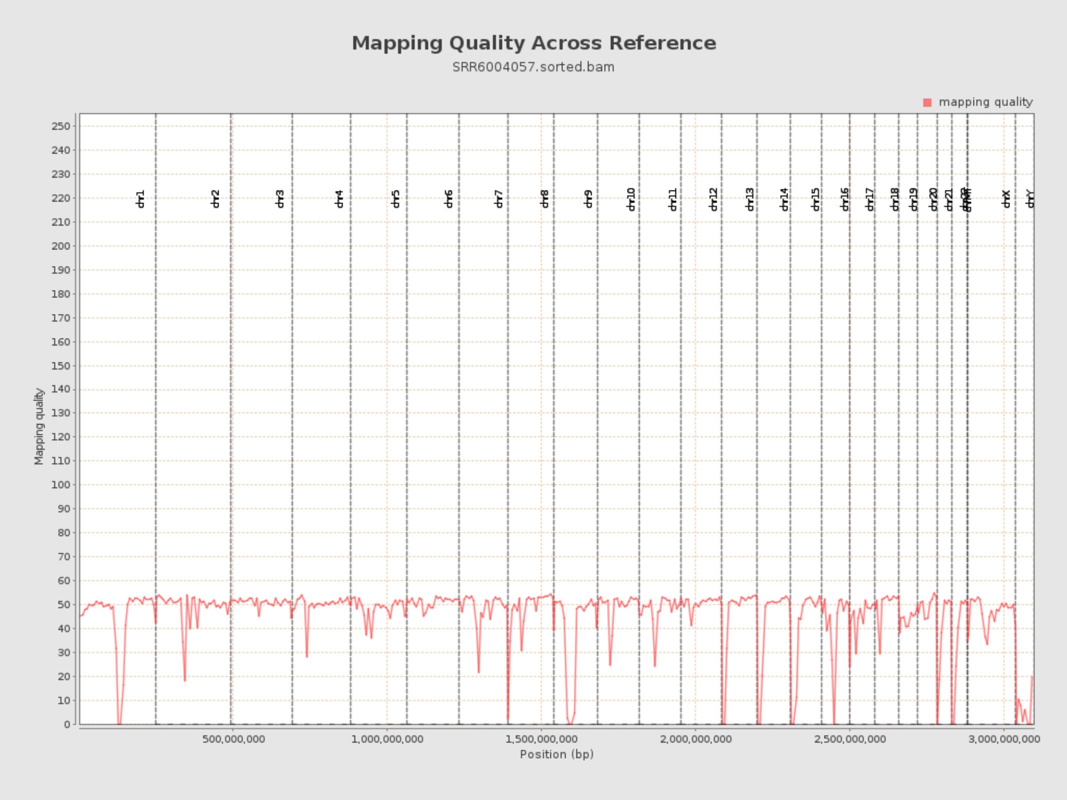
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram