Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:42:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004085.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_SRR6004085 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004085.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:42:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,003,430
Mapped reads	1,775,916 / 88.64%
Unmapped reads	227,514 / 11.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,173 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	67,302 / 3.36%
Duplication rate	2.84%
Clipped reads	915,327 / 45.69%

2.2. ACGT Content

Number/percentage of A's	32,981,717 / 28.48%
Number/percentage of C's	20,455,522 / 17.66%
Number/percentage of T's	37,080,465 / 32.02%
Number/percentage of G's	25,255,123 / 21.81%
Number/percentage of N's	44,137 / 0.04%
GC Percentage	39.47%

2.3. Coverage

Mean	0.0374

Standard Deviation	0.3666

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

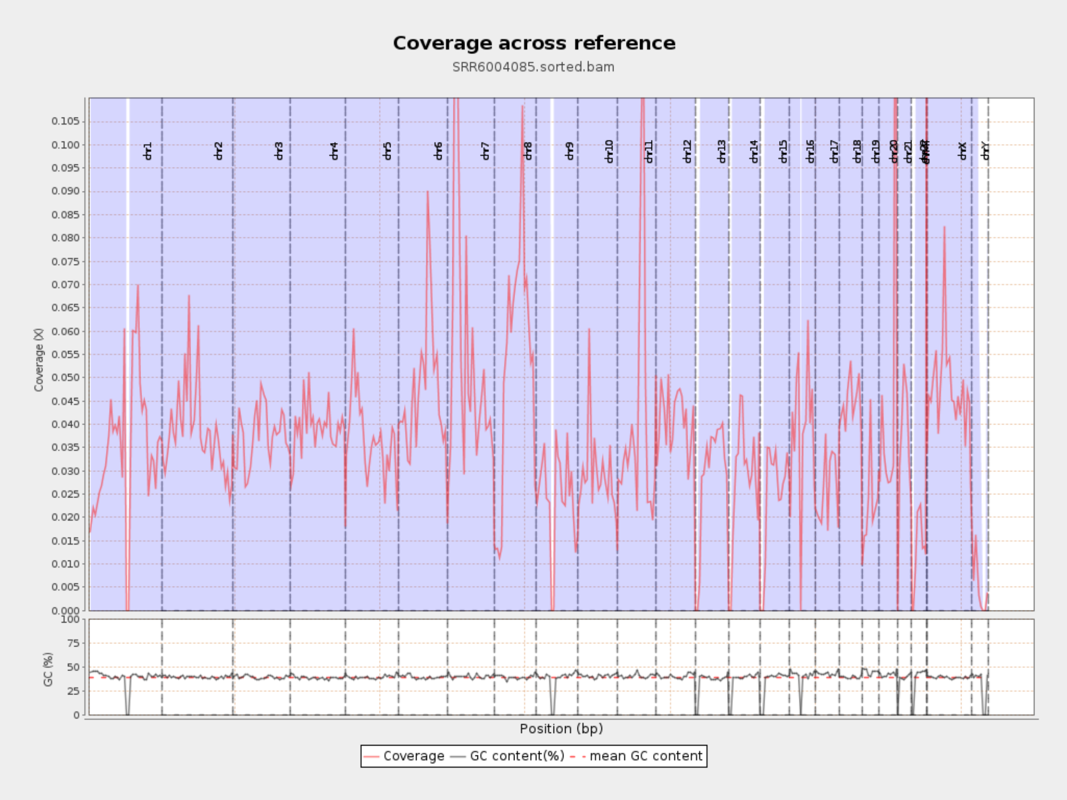
General error rate	0.88%
Mismatches	1,006,751
Insertions	9,314
Mapped reads with at least one insertion	0.52%
Deletions	39,283
Mapped reads with at least one deletion	2.18%
Homopolymer indels	44.07%

2.6. Chromosome stats

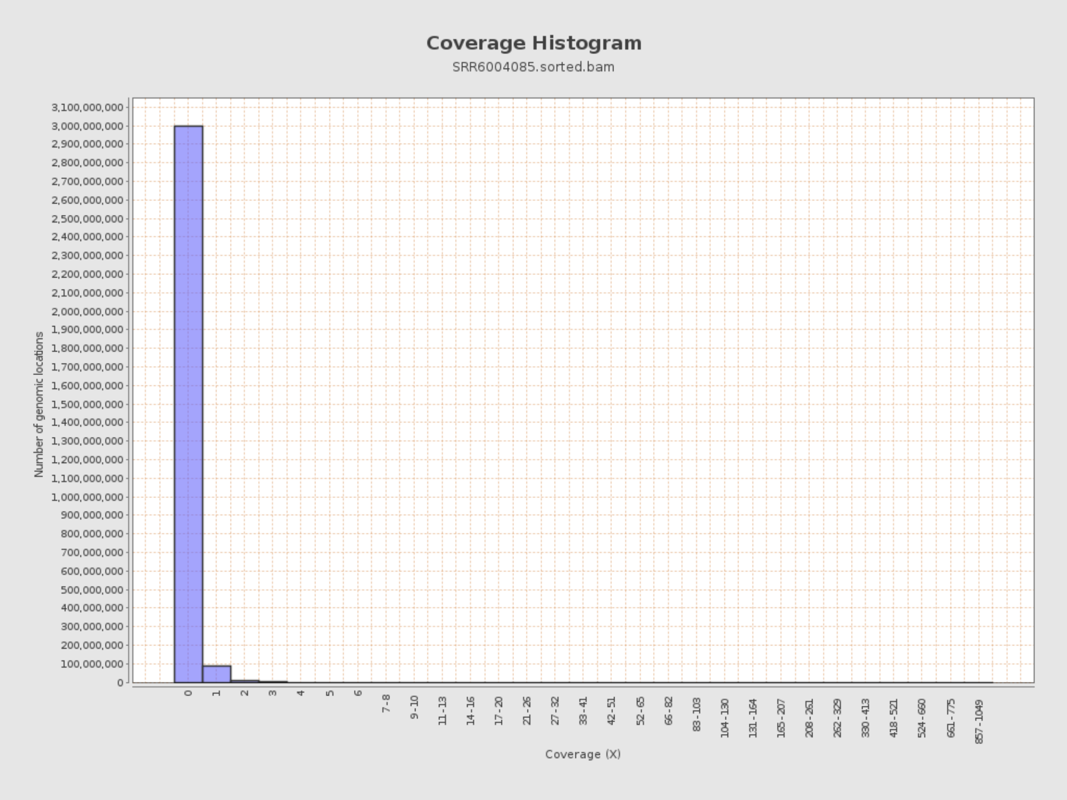
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8724517	0.035	0.63
chr2	243199373	9390879	0.0386	0.3995
chr3	198022430	7460129	0.0377	0.2221
chr4	191154276	7498395	0.0392	0.233
chr5	180915260	6721047	0.0372	0.2203
chr6	171115067	8163489	0.0477	0.2894
chr7	159138663	8917309	0.056	0.5442

chr8	146364022	7870230	0.0538	0.6848
chr9	141213431	3470937	0.0246	0.2755
chr10	135534747	4000988	0.0295	0.3224
chr11	135006516	5658776	0.0419	0.3146
chr12	133851895	5404790	0.0404	0.2325
chr13	115169878	3277612	0.0285	0.189
chr14	107349540	2969694	0.0277	0.2003
chr15	102531392	2517040	0.0245	0.1805
chr16	90354753	3494122	0.0387	0.2538
chr17	81195210	2124772	0.0262	0.2042
chr18	78077248	3492027	0.0447	0.4914
chr19	59128983	1376803	0.0233	0.4481
chr20	63025520	3312894	0.0526	0.2882
chr21	48129895	1684573	0.035	0.2252
chr22	51304566	640833	0.0125	0.123
chrMT	16571	3159	0.1906	0.4937
chrX	155270560	7403434	0.0477	0.2831
chrY	59373566	303946	0.0051	0.1231

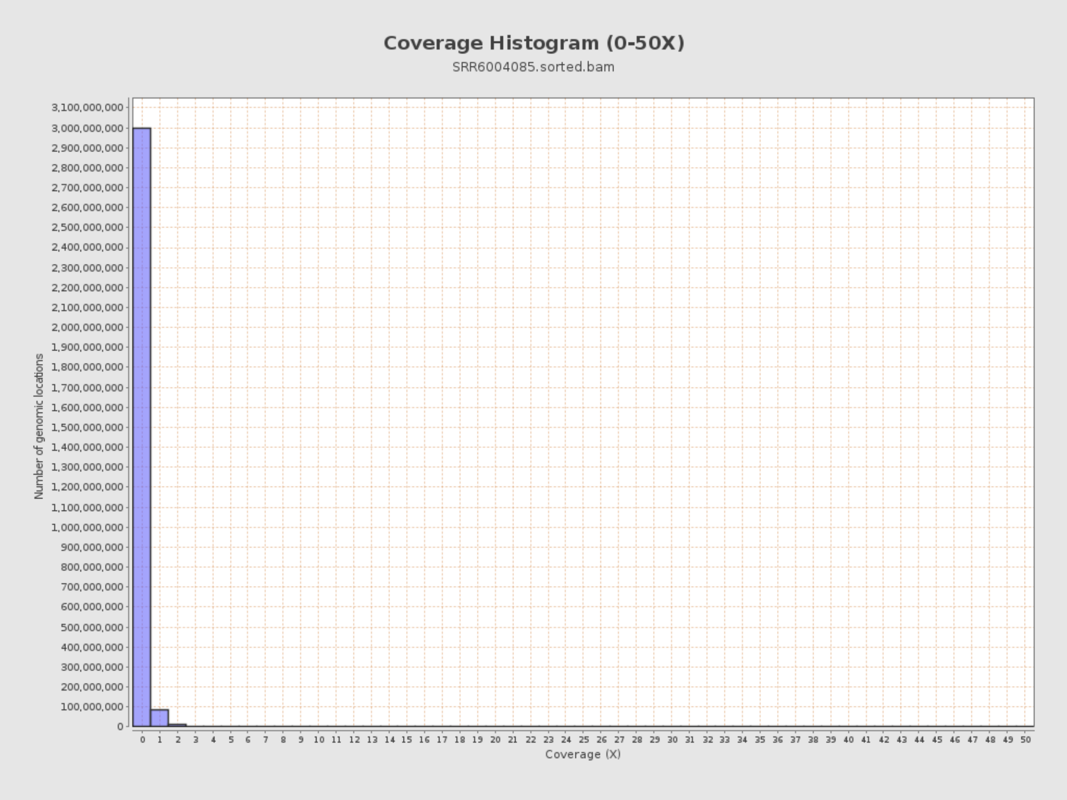
3. Results : Coverage across reference



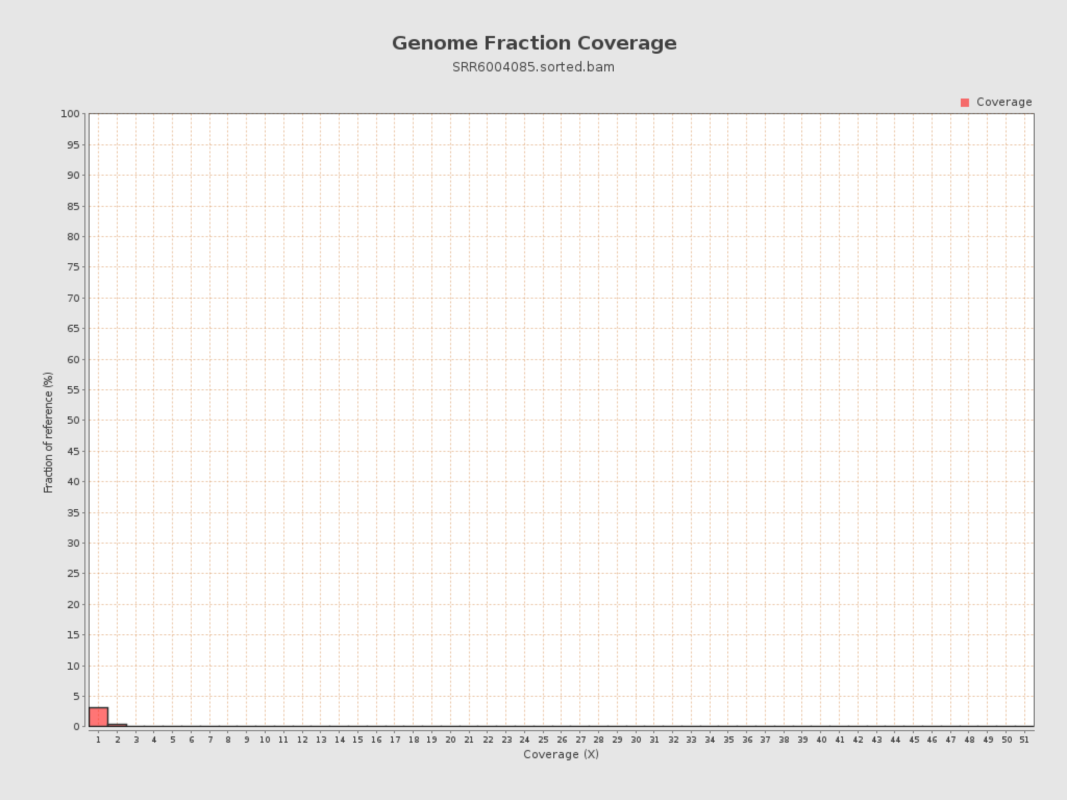
4. Results : Coverage Histogram



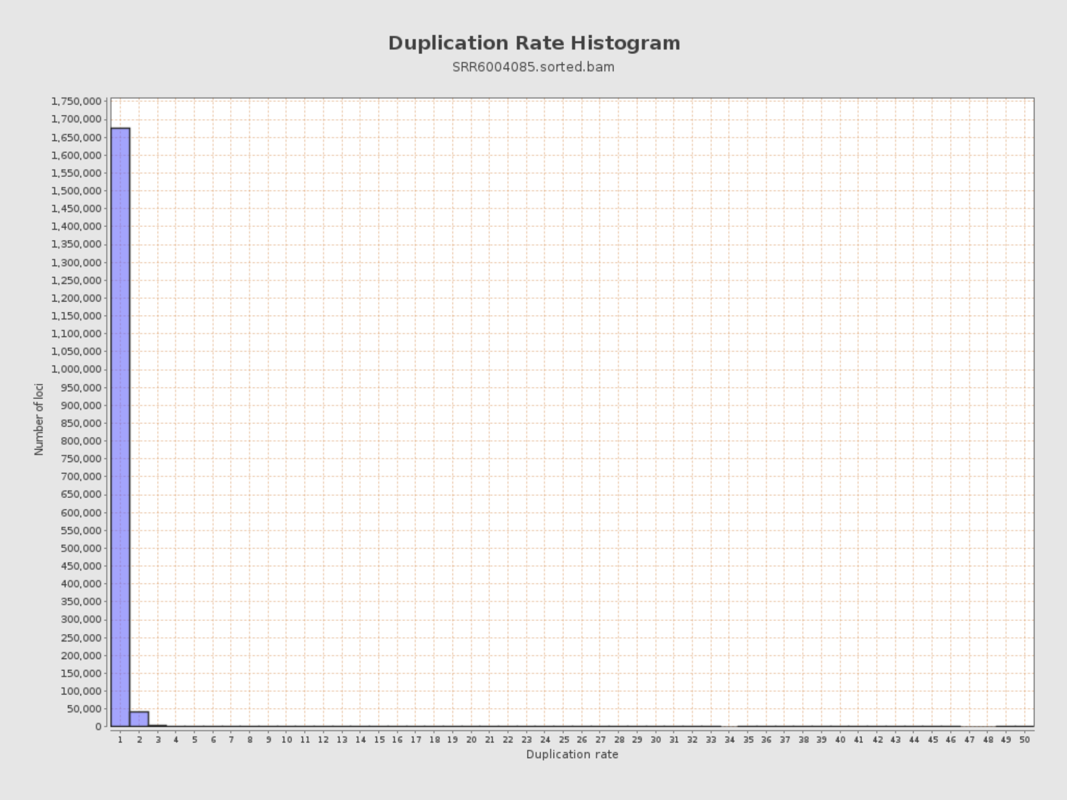
5. Results : Coverage Histogram (0-50X)



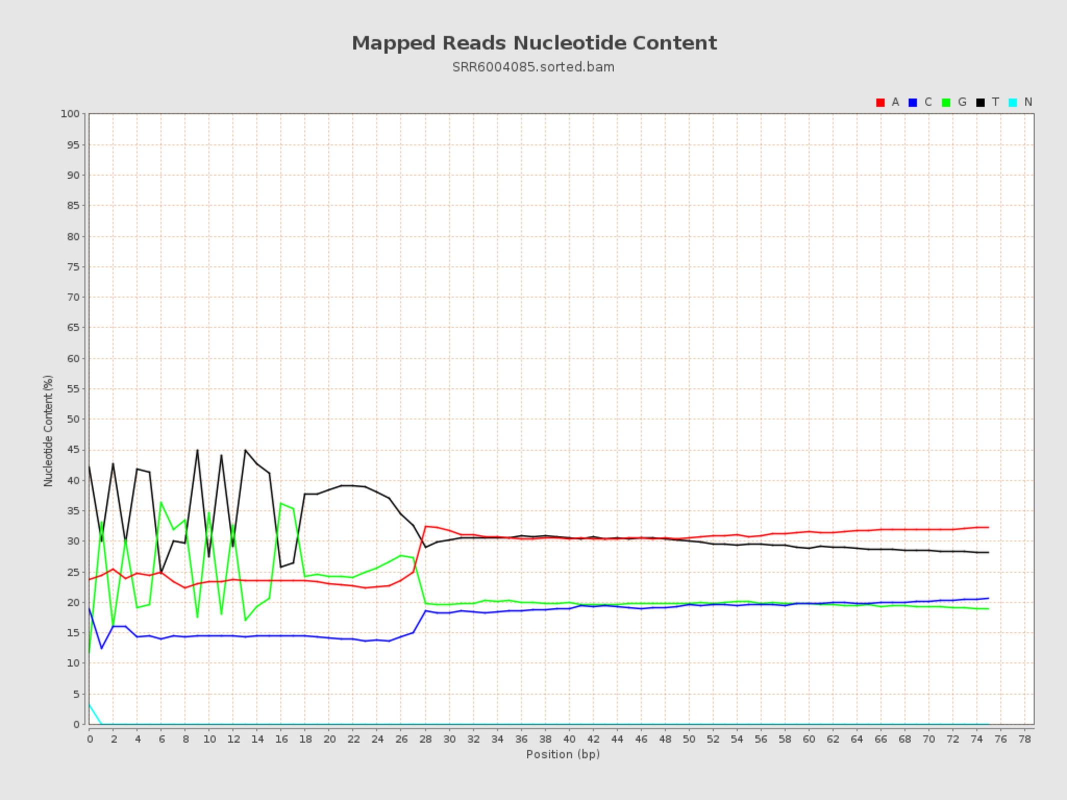
6. Results : Genome Fraction Coverage



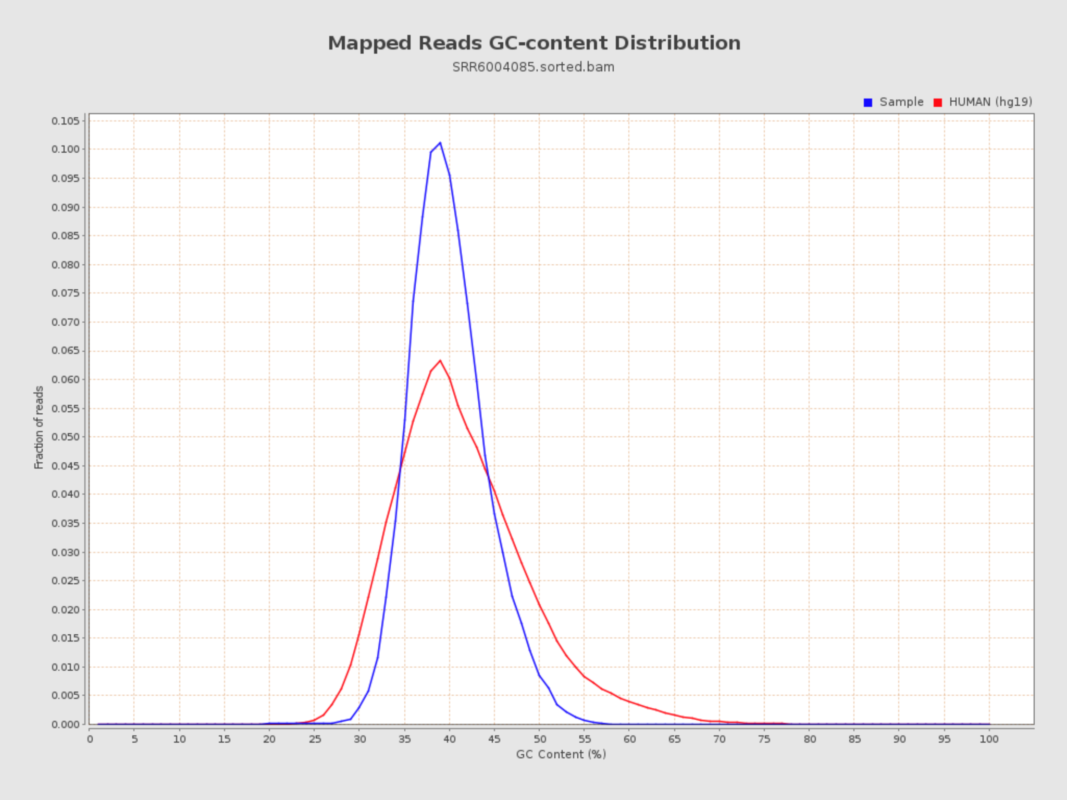
7. Results : Duplication Rate Histogram



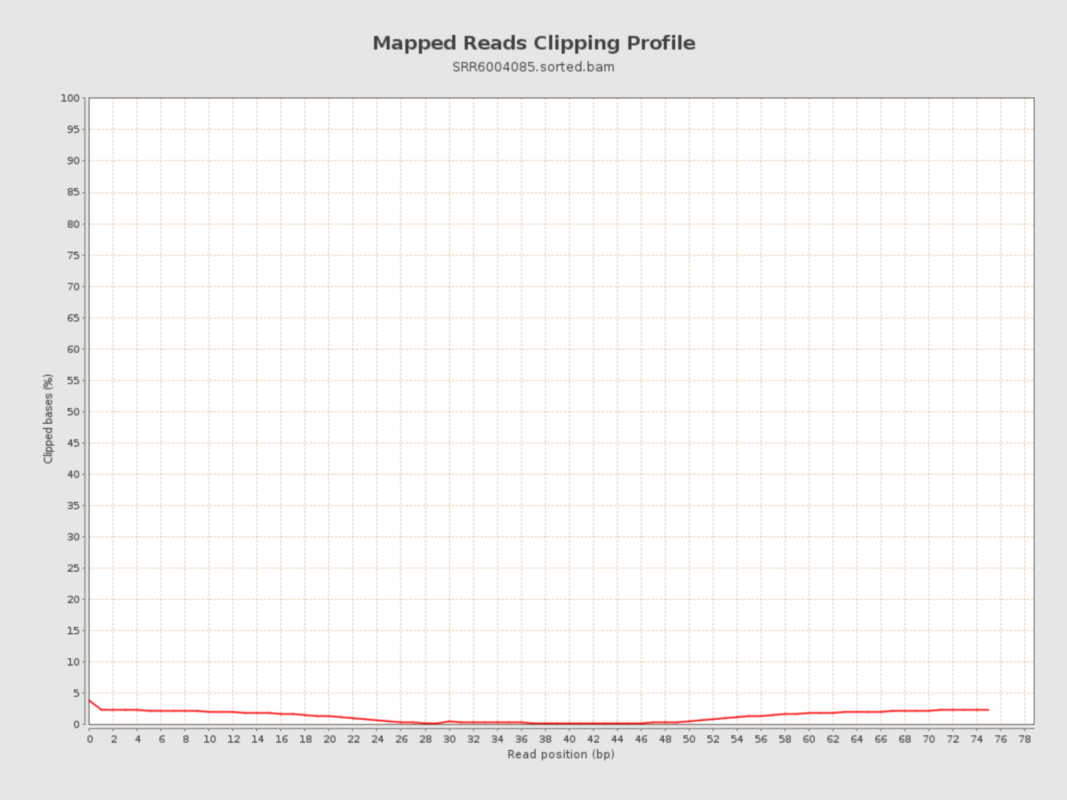
8. Results : Mapped Reads Nucleotide Content



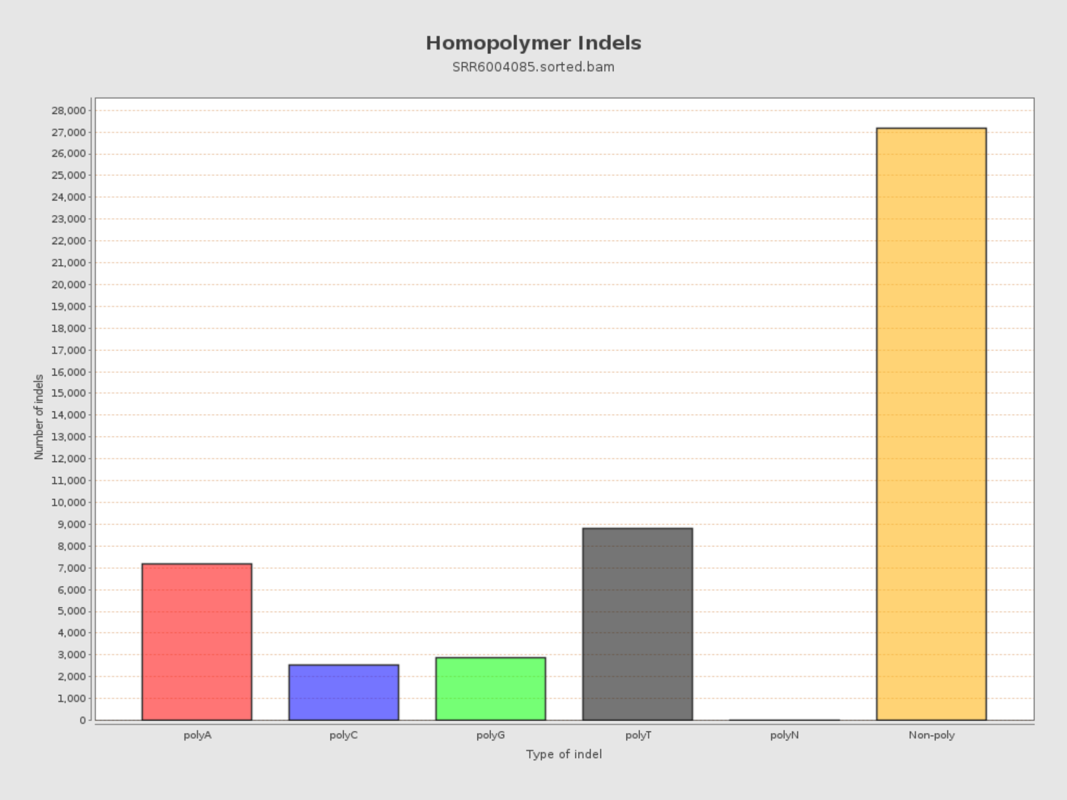
9. Results : Mapped Reads GC-content Distribution



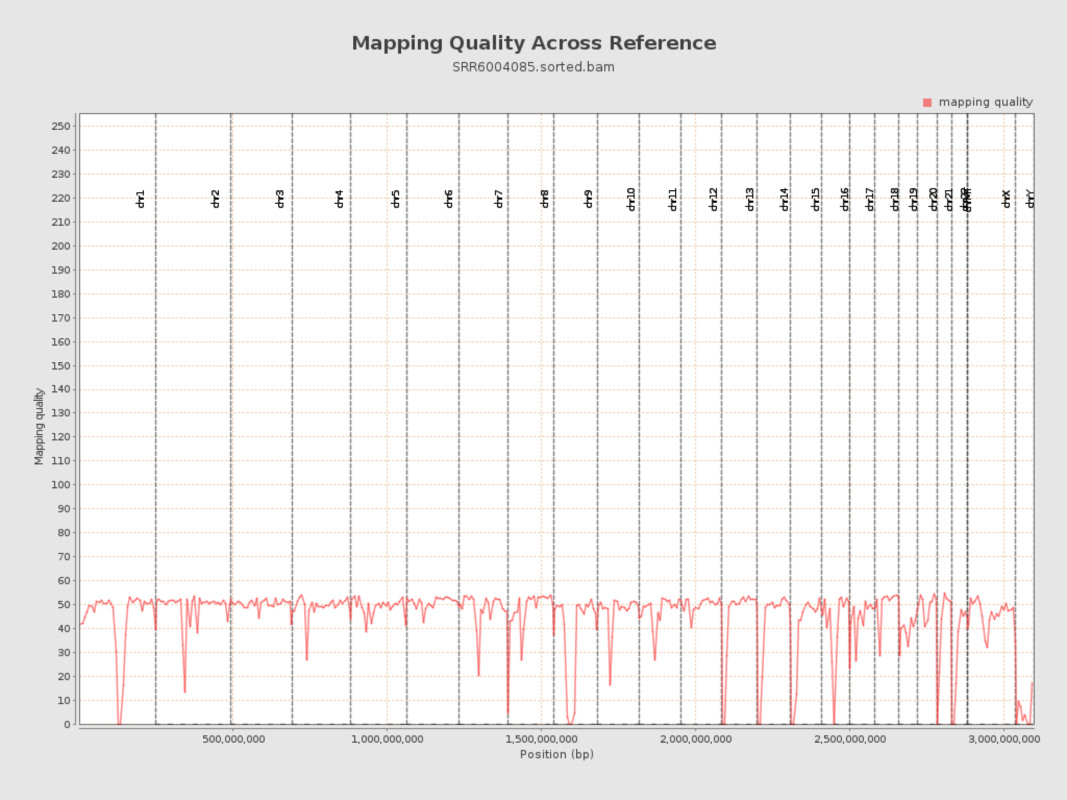
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram