Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:11:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548984.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_SRR1548984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548984.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:11:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,013,827
Mapped reads	2,173,506 / 43.35%
Unmapped reads	2,840,321 / 56.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	44,897 / 0.9%
Duplication rate	1.5%
Clipped reads	218,884 / 4.37%

2.2. ACGT Content

Number/percentage of A's	26,008,638 / 30.32%
Number/percentage of C's	16,803,684 / 19.59%
Number/percentage of T's	26,128,296 / 30.46%
Number/percentage of G's	16,821,269 / 19.61%
Number/percentage of N's	4,464 / 0.01%
GC Percentage	39.21%

2.3. Coverage

Mean	0.0277
Standard Deviation	0.2387

2.4. Mapping Quality

Mean Mapping Quality	43.09

2.5. Mismatches and indels

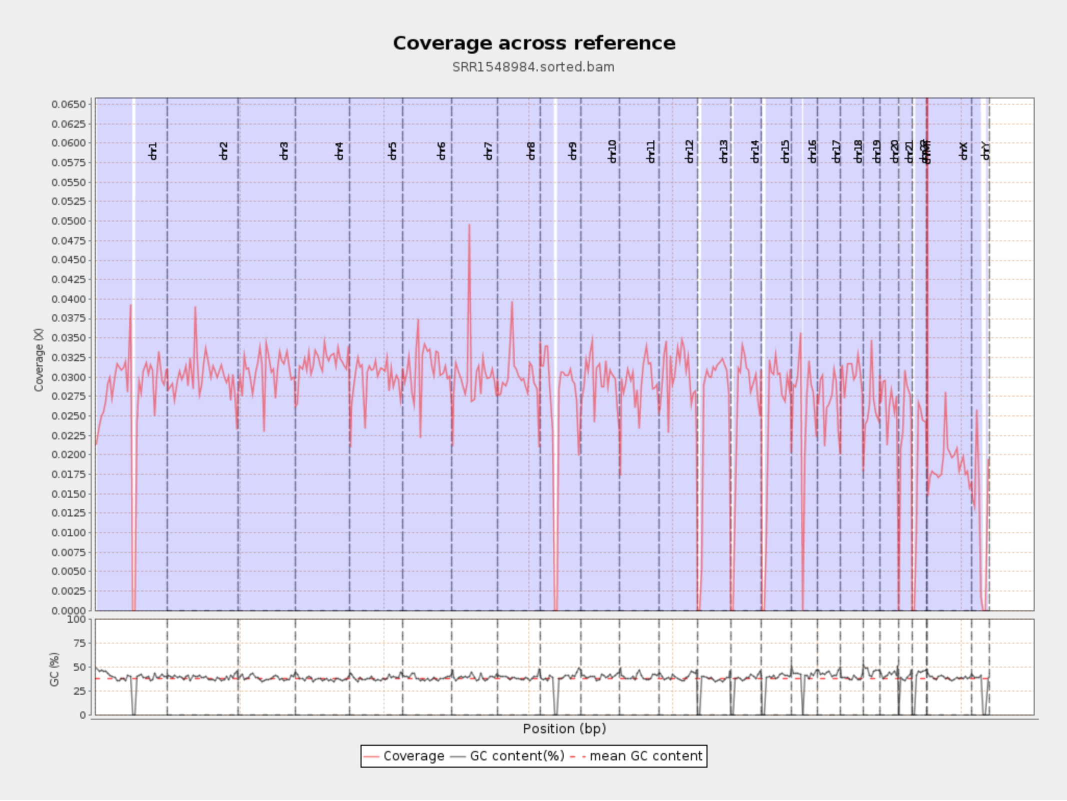
General error rate	0.31%
Mismatches	265,578
Insertions	3,896
Mapped reads with at least one insertion	0.18%
Deletions	9,348
Mapped reads with at least one deletion	0.43%
Homopolymer indels	45.12%

2.6. Chromosome stats

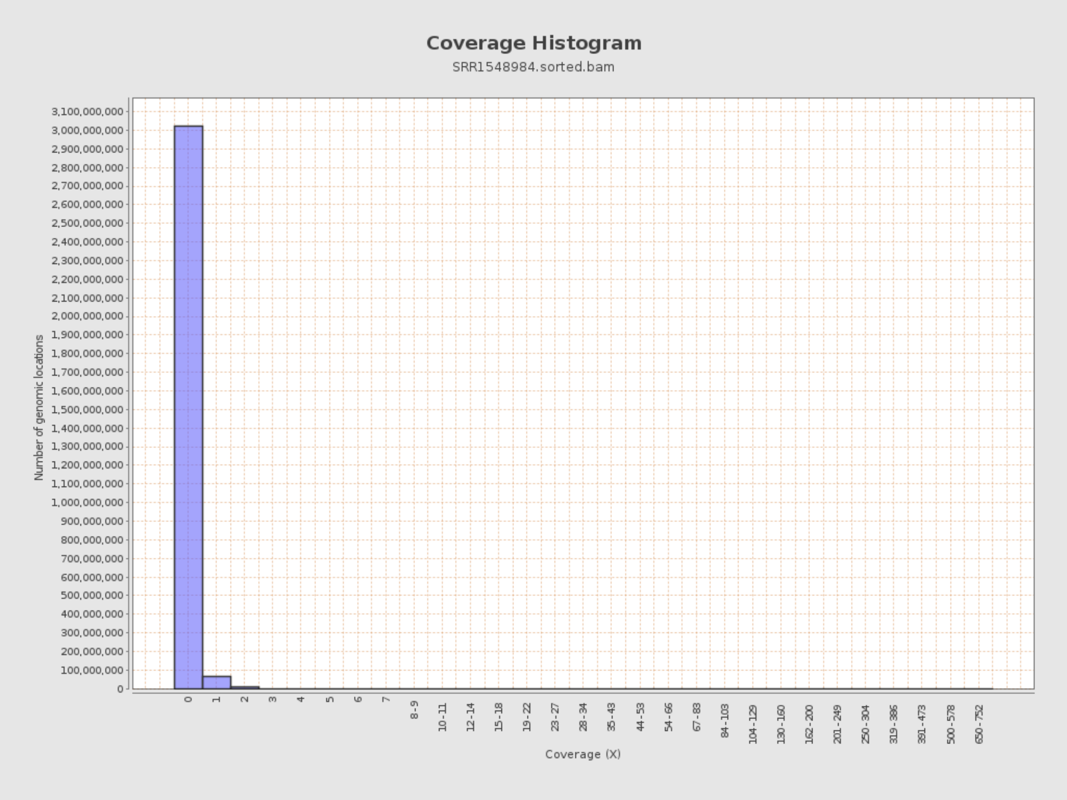
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6843780	0.0275	0.3499
chr2	243199373	7328974	0.0301	0.2299
chr3	198022430	6084100	0.0307	0.194
chr4	191154276	6068513	0.0317	0.1992
chr5	180915260	5425306	0.03	0.1921
chr6	171115067	5315816	0.0311	0.2111
chr7	159138663	4816269	0.0303	0.3187
chr8	146364022	4381273	0.0299	0.4157

chr9	141213431	3691843	0.0261	0.2075
chr10	135534747	4026322	0.0297	0.2073
chr11	135006516	3931486	0.0291	0.2132
chr12	133851895	4056419	0.0303	0.1967
chr13	115169878	2923146	0.0254	0.1766
chr14	107349540	2691552	0.0251	0.1894
chr15	102531392	2482317	0.0242	0.1721
chr16	90354753	2299421	0.0254	0.1809
chr17	81195210	2172761	0.0268	0.1875
chr18	78077248	2393184	0.0307	0.2927
chr19	59128983	1557141	0.0263	0.3047
chr20	63025520	1654315	0.0262	0.1821
chr21	48129895	1134370	0.0236	0.1801
chr22	51304566	898032	0.0175	0.1659
chrMT	16571	4636	0.2798	0.5721
chrX	155270560	2923898	0.0188	0.1646
chrY	59373566	673099	0.0113	0.1448

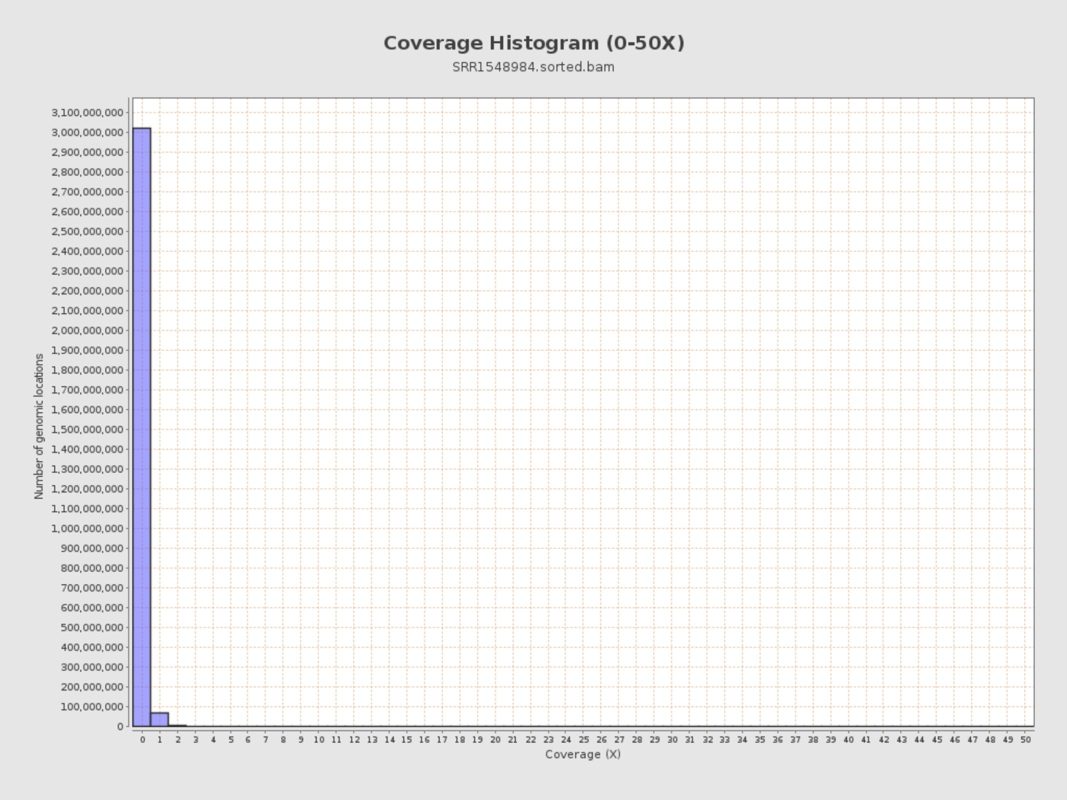
3. Results : Coverage across reference



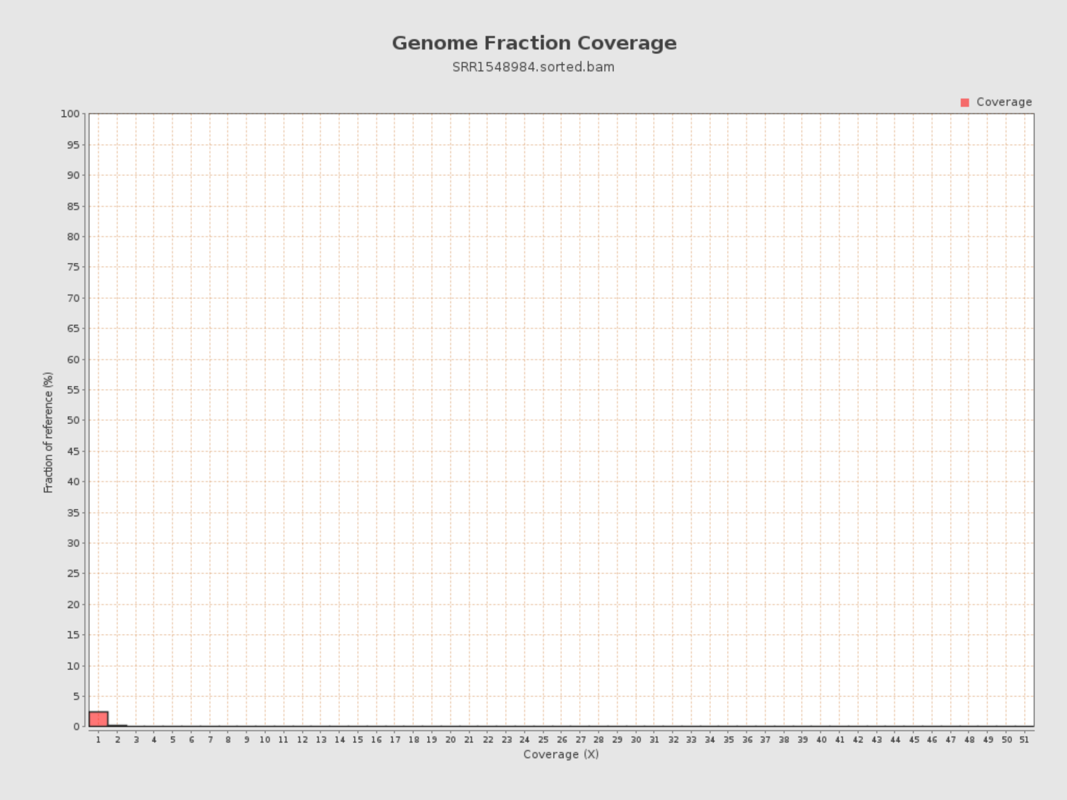
4. Results : Coverage Histogram



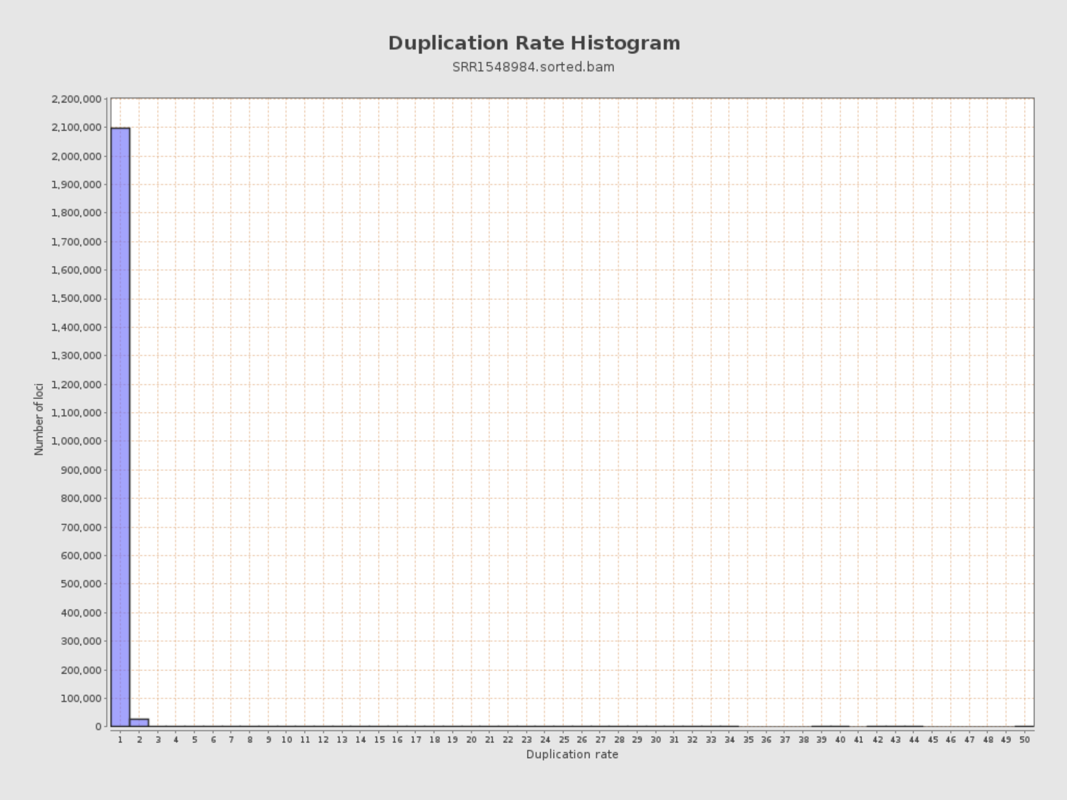
5. Results : Coverage Histogram (0-50X)



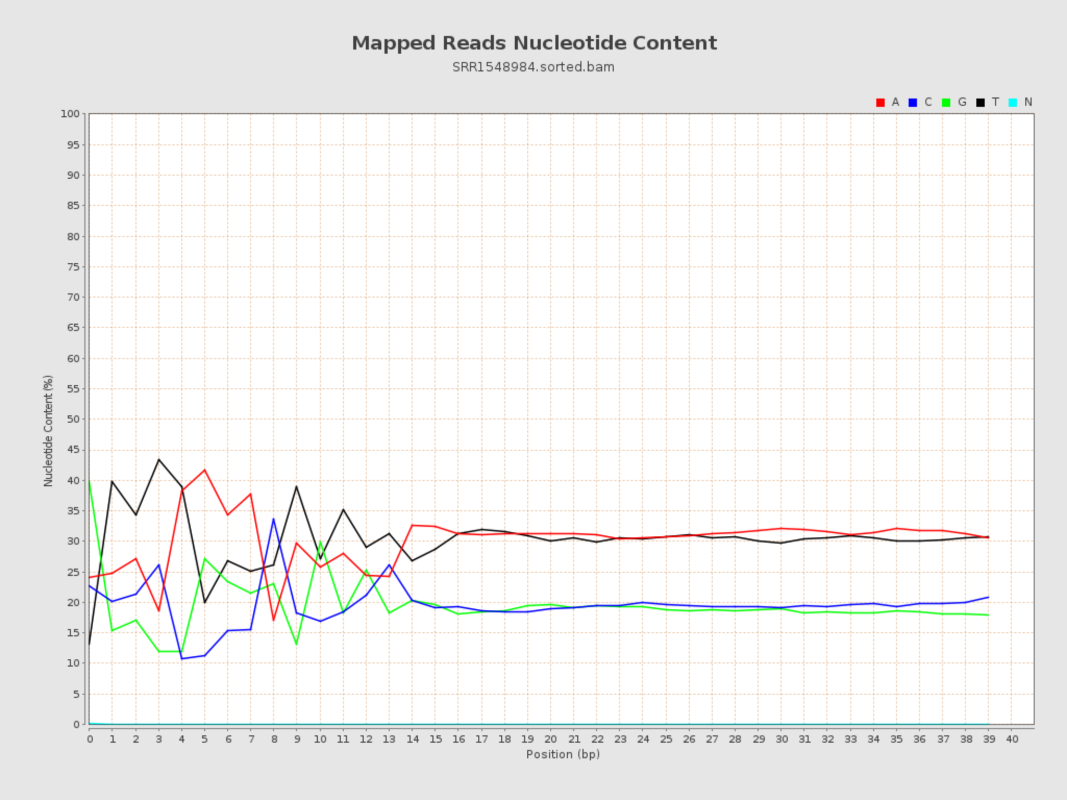
6. Results : Genome Fraction Coverage



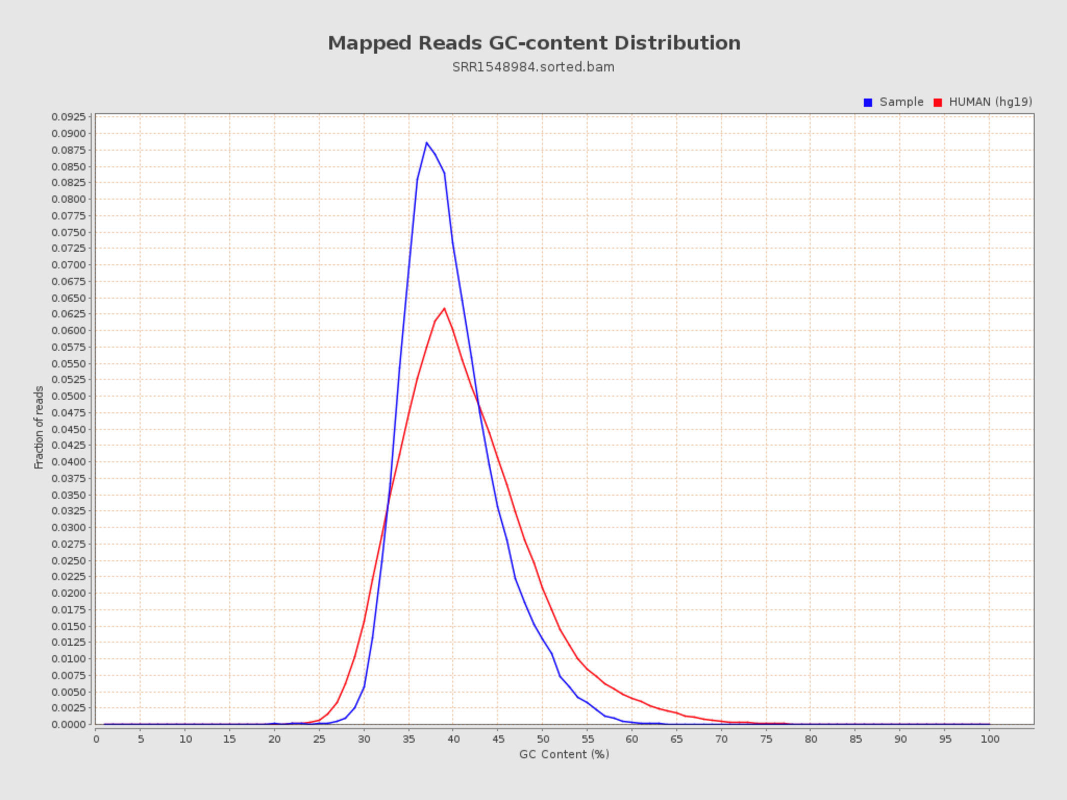
7. Results : Duplication Rate Histogram



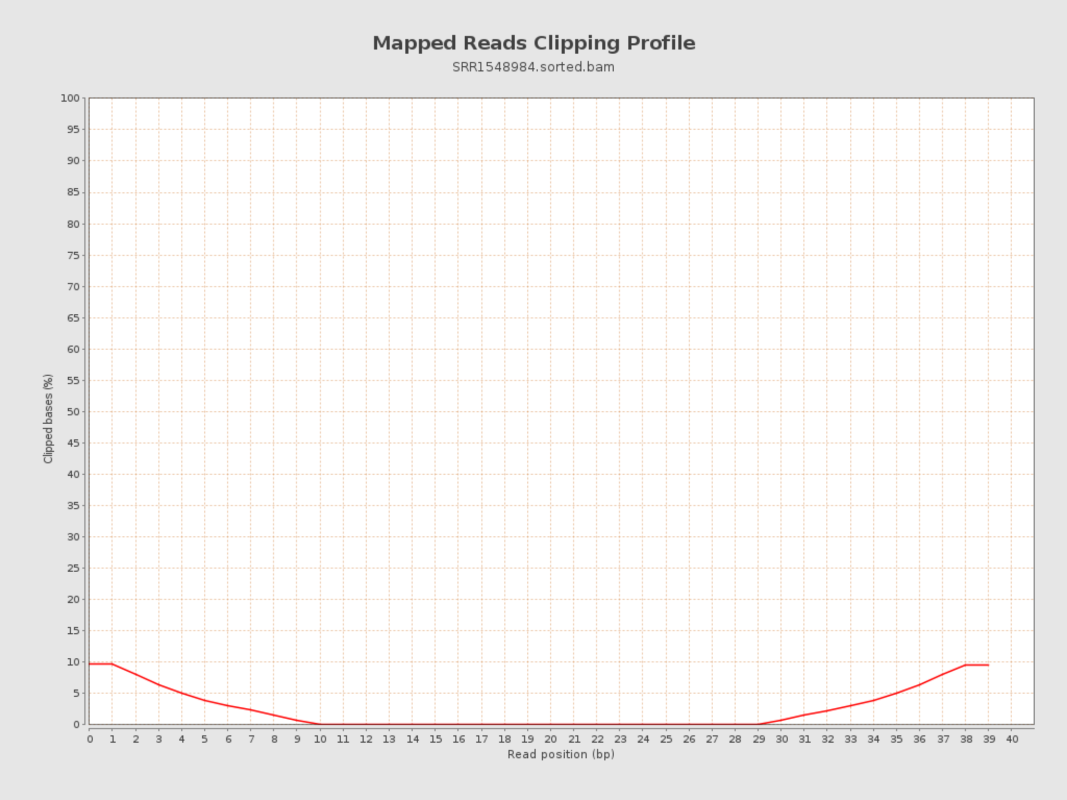
8. Results : Mapped Reads Nucleotide Content



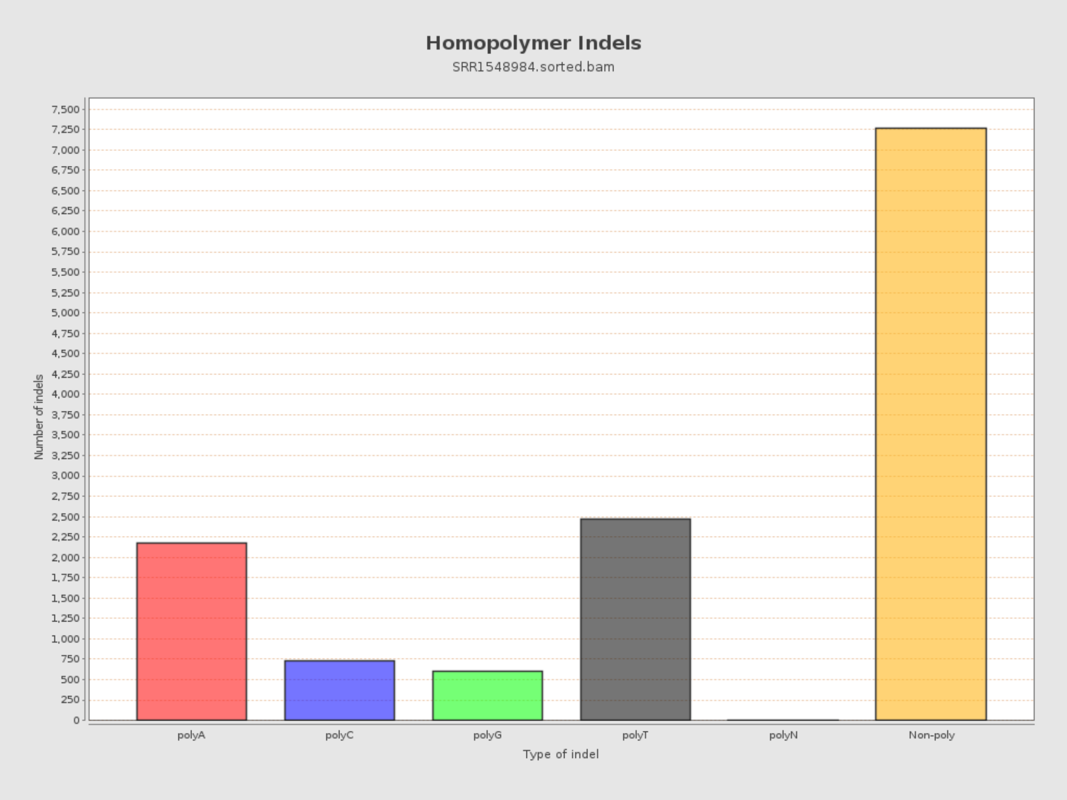
9. Results : Mapped Reads GC-content Distribution



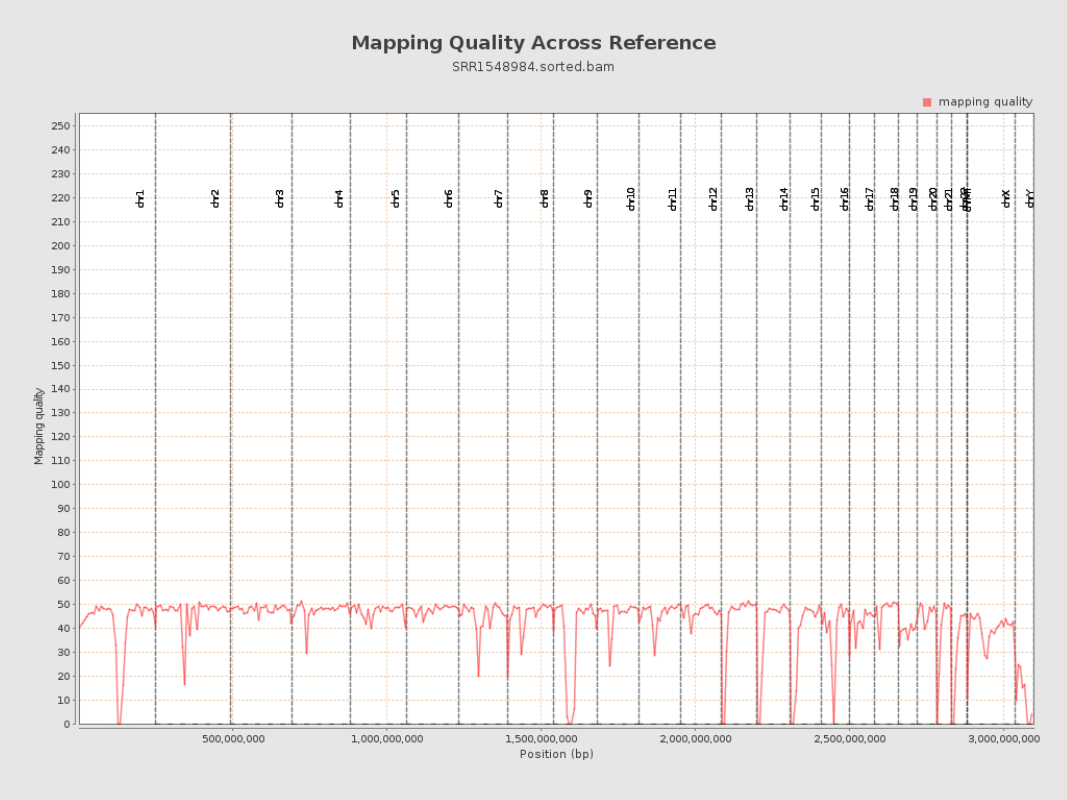
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram