Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:41:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013266.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_SRR6013266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013266.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:41:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,724,462
Mapped reads	1,492,028 / 86.52%
Unmapped reads	232,434 / 13.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,094 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	115,423 / 6.69%
Duplication rate	6.25%
Clipped reads	693,746 / 40.23%

2.2. ACGT Content

Number/percentage of A's	26,854,715 / 27.13%
Number/percentage of C's	17,923,646 / 18.11%
Number/percentage of T's	32,009,408 / 32.34%
Number/percentage of G's	22,168,395 / 22.4%
Number/percentage of N's	20,774 / 0.02%
GC Percentage	40.51%

2.3. Coverage

Mean	0.032

Standard Deviation	0.3882

2.4. Mapping Quality

Mean Mapping Quality	43.7

2.5. Mismatches and indels

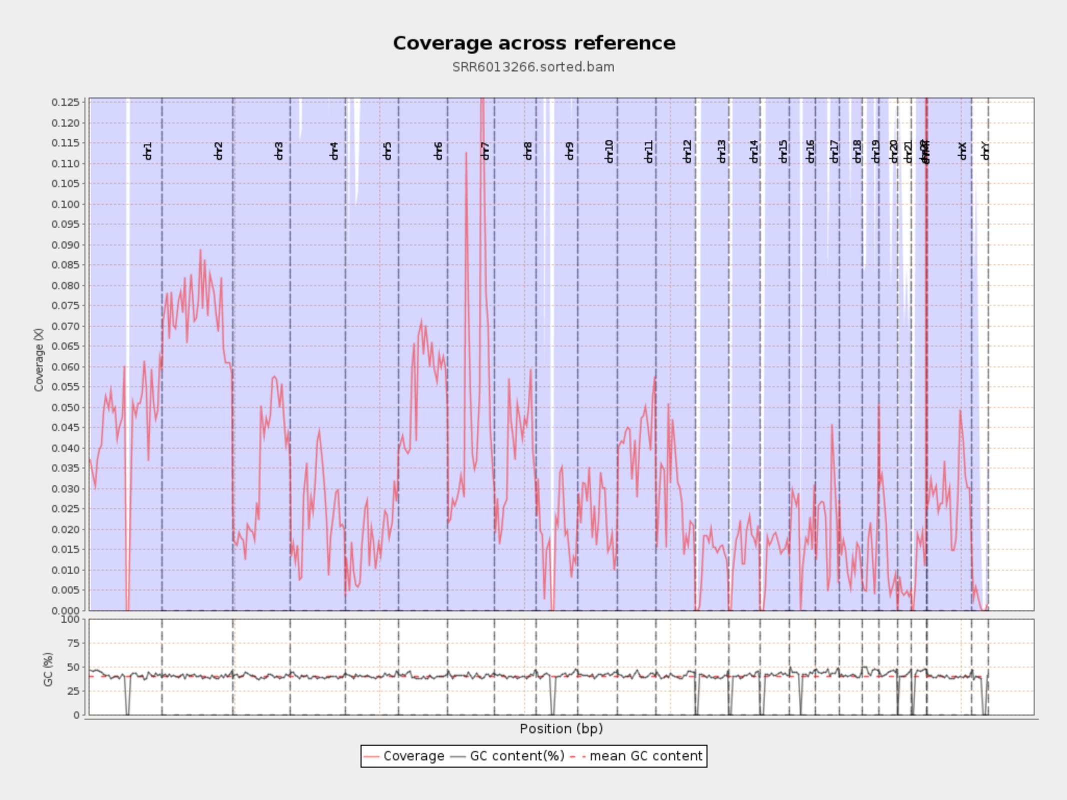
General error rate	0.8%
Mismatches	775,597
Insertions	6,788
Mapped reads with at least one insertion	0.45%
Deletions	23,872
Mapped reads with at least one deletion	1.58%
Homopolymer indels	46.37%

2.6. Chromosome stats

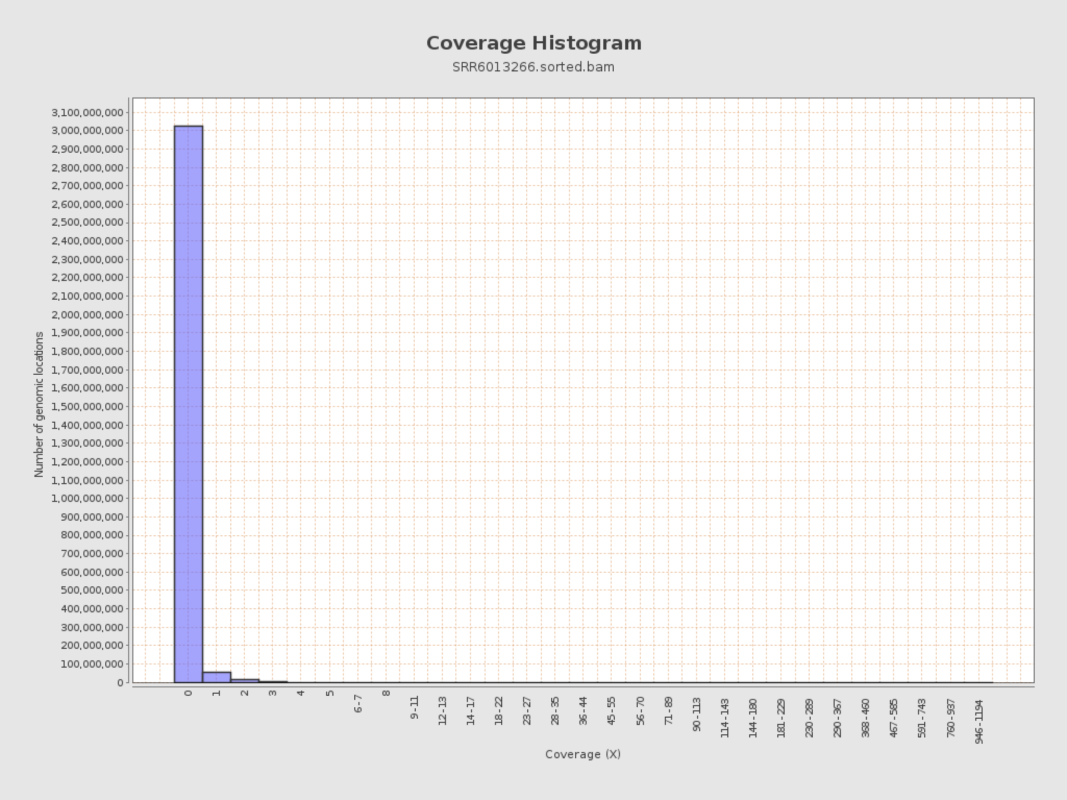
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11106010	0.0446	0.4583
chr2	243199373	17938528	0.0738	0.5963
chr3	198022430	6860481	0.0346	0.2444
chr4	191154276	4512899	0.0236	0.1989
chr5	180915260	3067231	0.017	0.1666
chr6	171115067	9616950	0.0562	0.3601
chr7	159138663	8646631	0.0543	1.1185

chr8	146364022	5668532	0.0387	0.3151
chr9	141213431	2405089	0.017	0.1931
chr10	135534747	3214922	0.0237	0.2597
chr11	135006516	5819783	0.0431	0.2842
chr12	133851895	3740295	0.0279	0.2187
chr13	115169878	1463315	0.0127	0.1511
chr14	107349540	1623461	0.0151	0.1618
chr15	102531392	1372348	0.0134	0.1491
chr16	90354753	1852595	0.0205	0.1876
chr17	81195210	1752350	0.0216	0.1973
chr18	78077248	1039540	0.0133	0.2275
chr19	59128983	836715	0.0142	0.3023
chr20	63025520	1043478	0.0166	0.1672
chr21	48129895	218001	0.0045	0.0817
chr22	51304566	583705	0.0114	0.1325
chrMT	16571	38249	2.3082	2.2882
chrX	155270560	4450075	0.0287	0.2243
chrY	59373566	145929	0.0025	0.0633

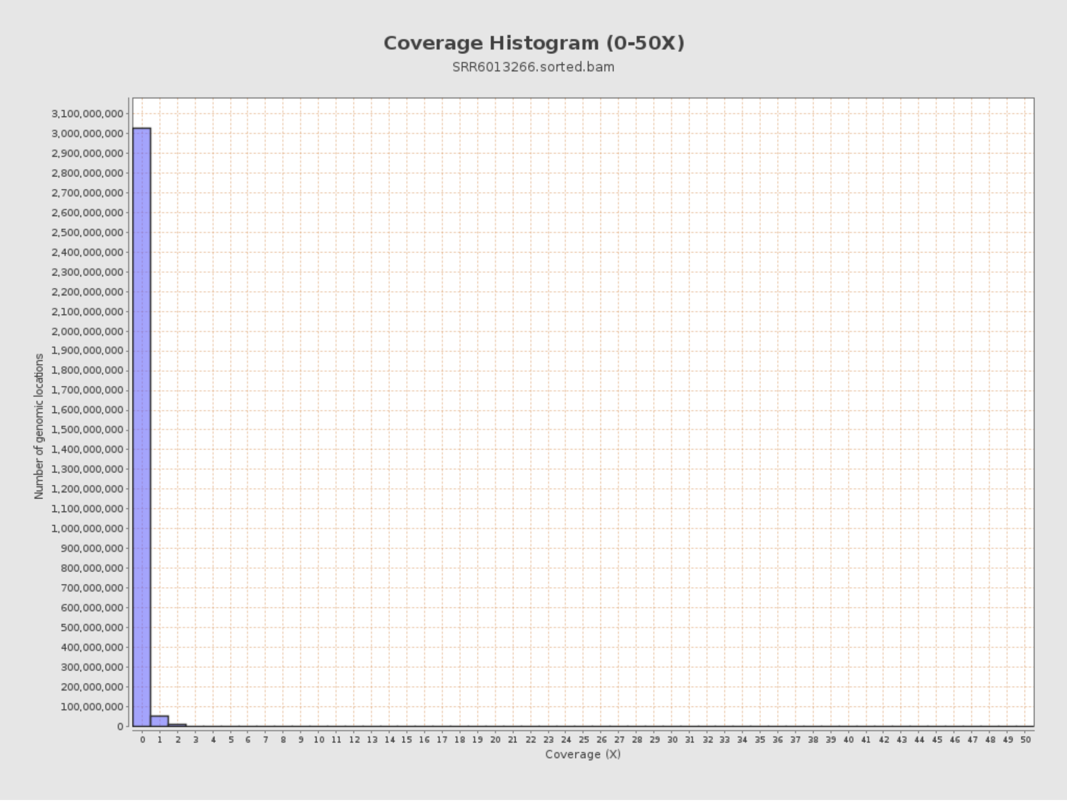
3. Results : Coverage across reference



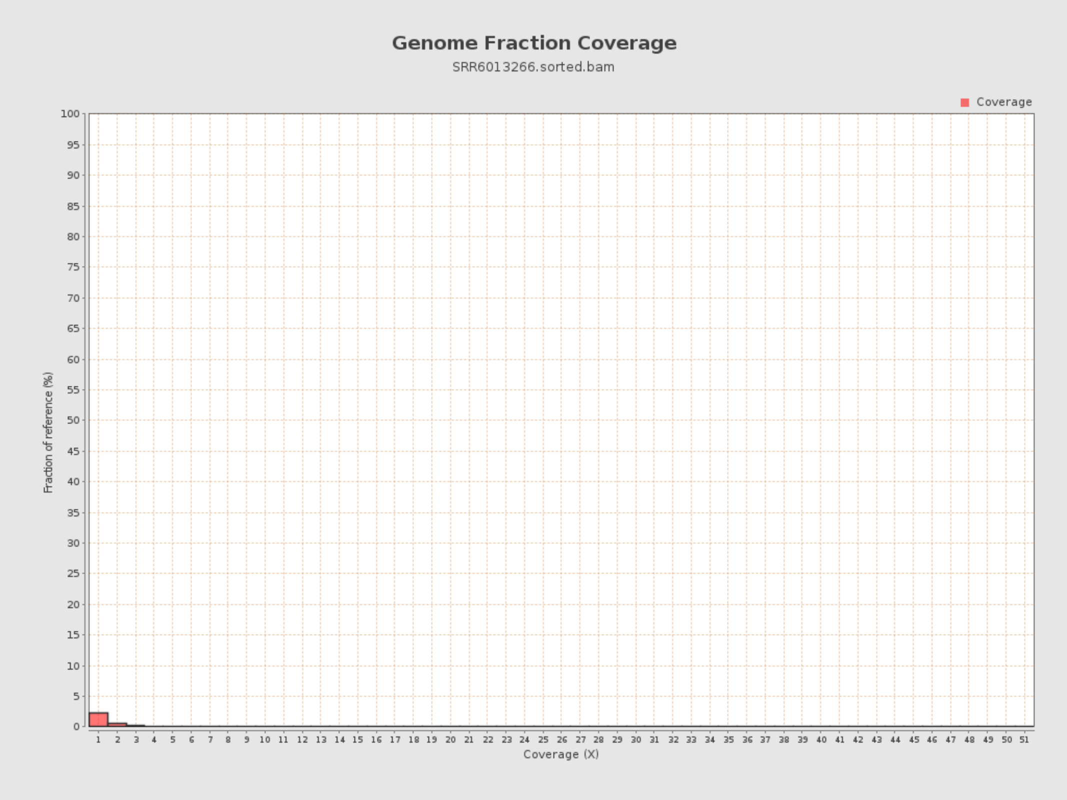
4. Results : Coverage Histogram



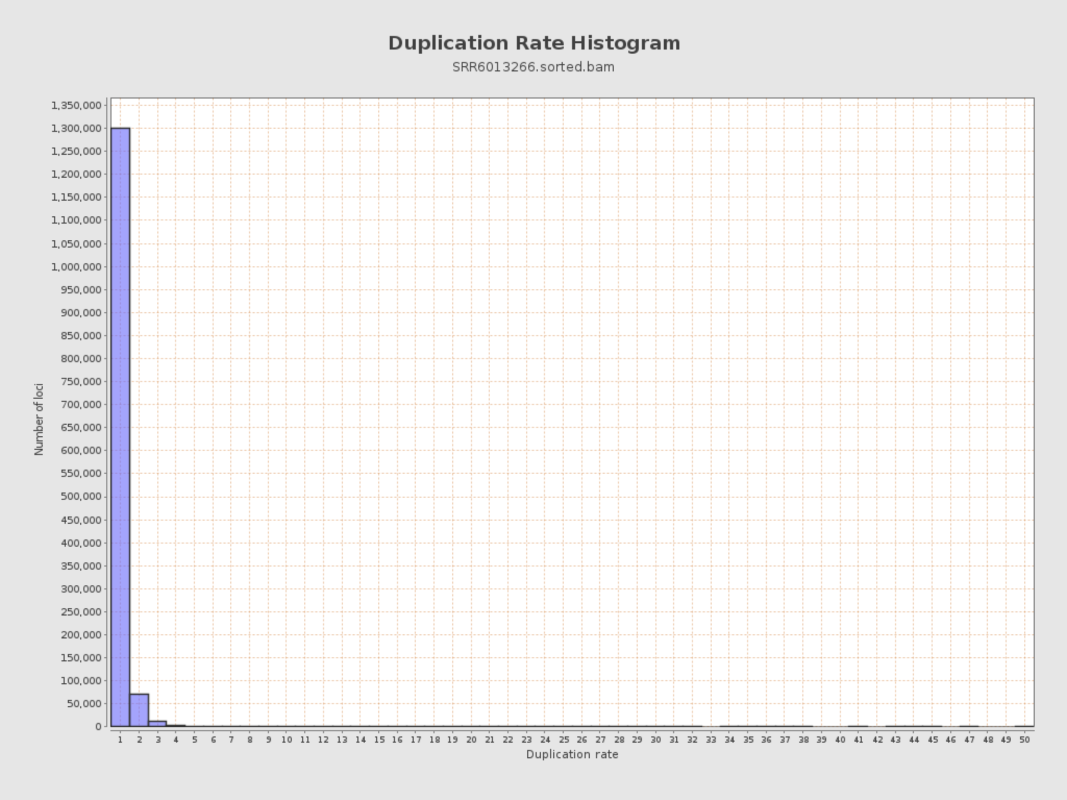
5. Results : Coverage Histogram (0-50X)



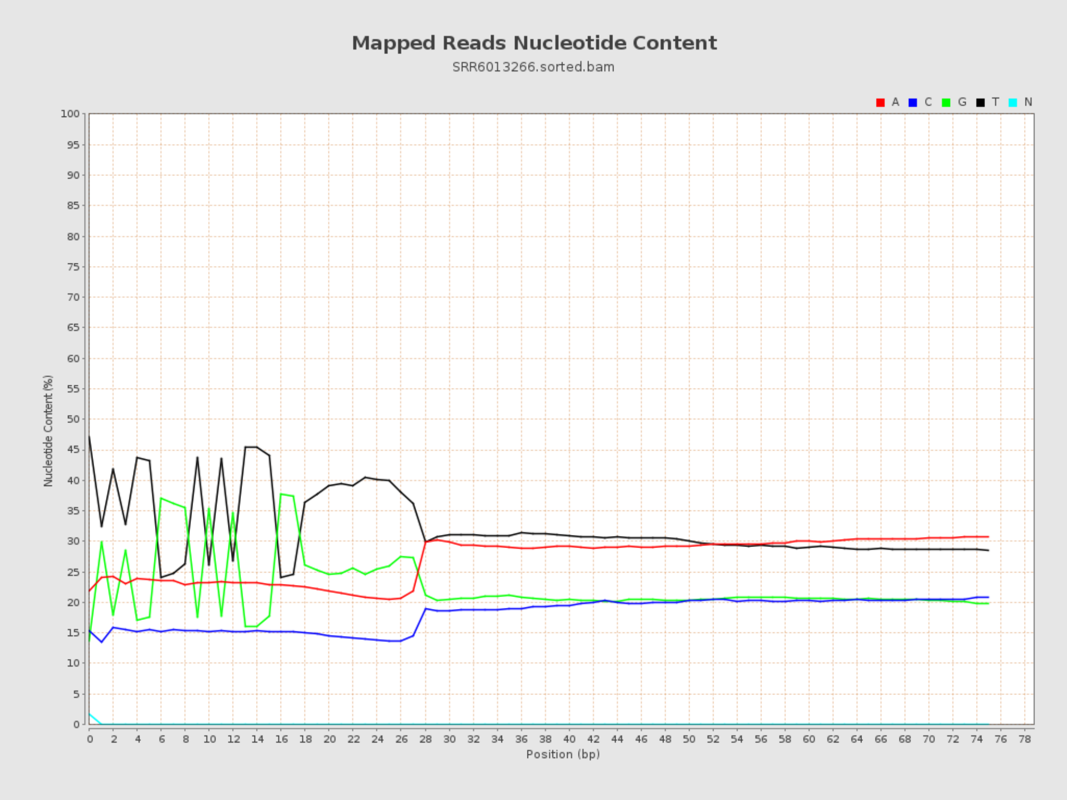
6. Results : Genome Fraction Coverage



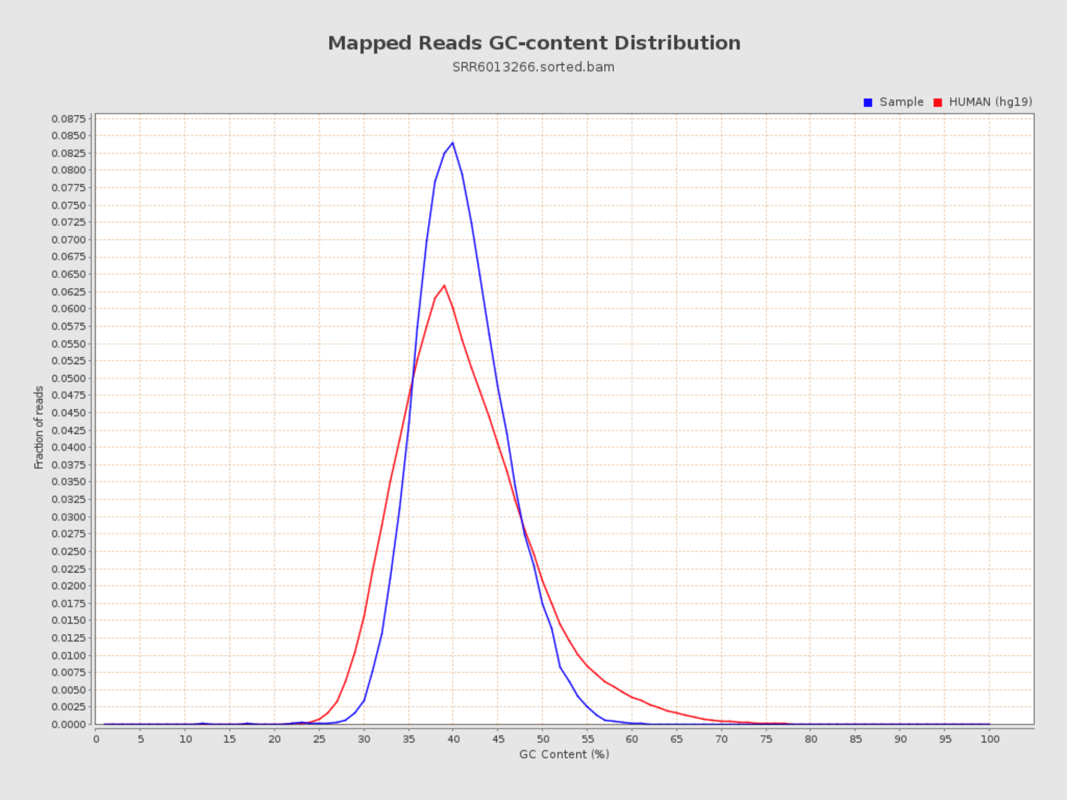
7. Results : Duplication Rate Histogram



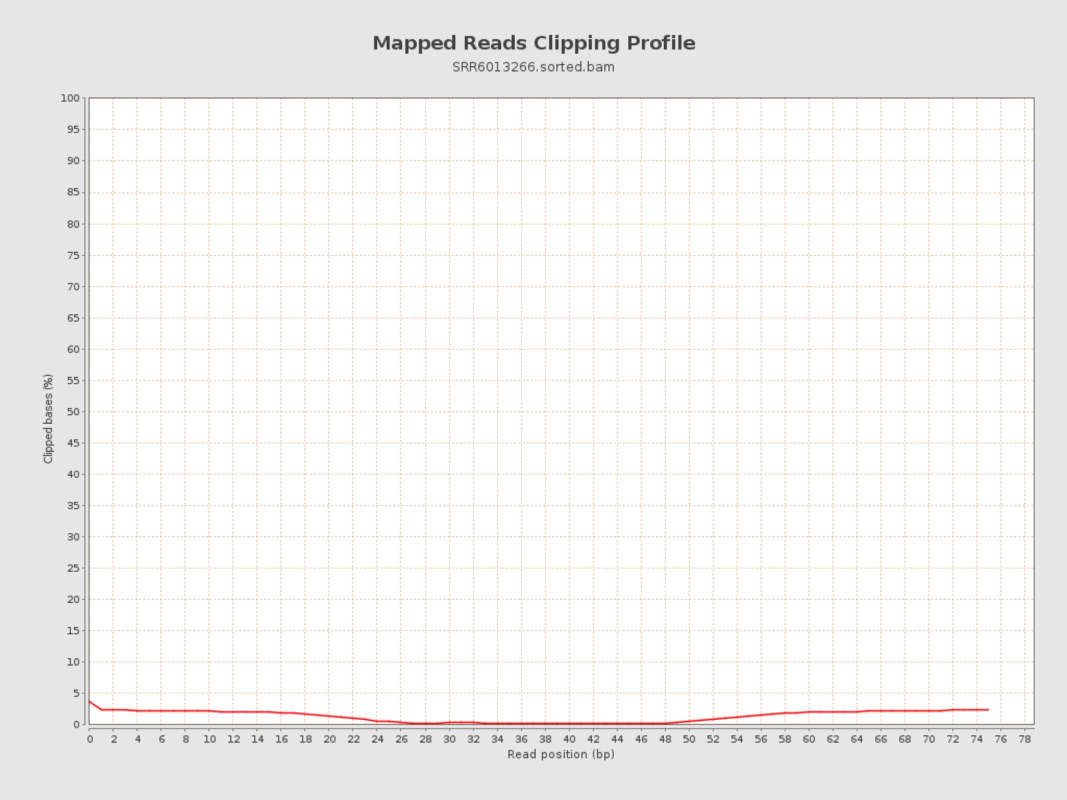
8. Results : Mapped Reads Nucleotide Content



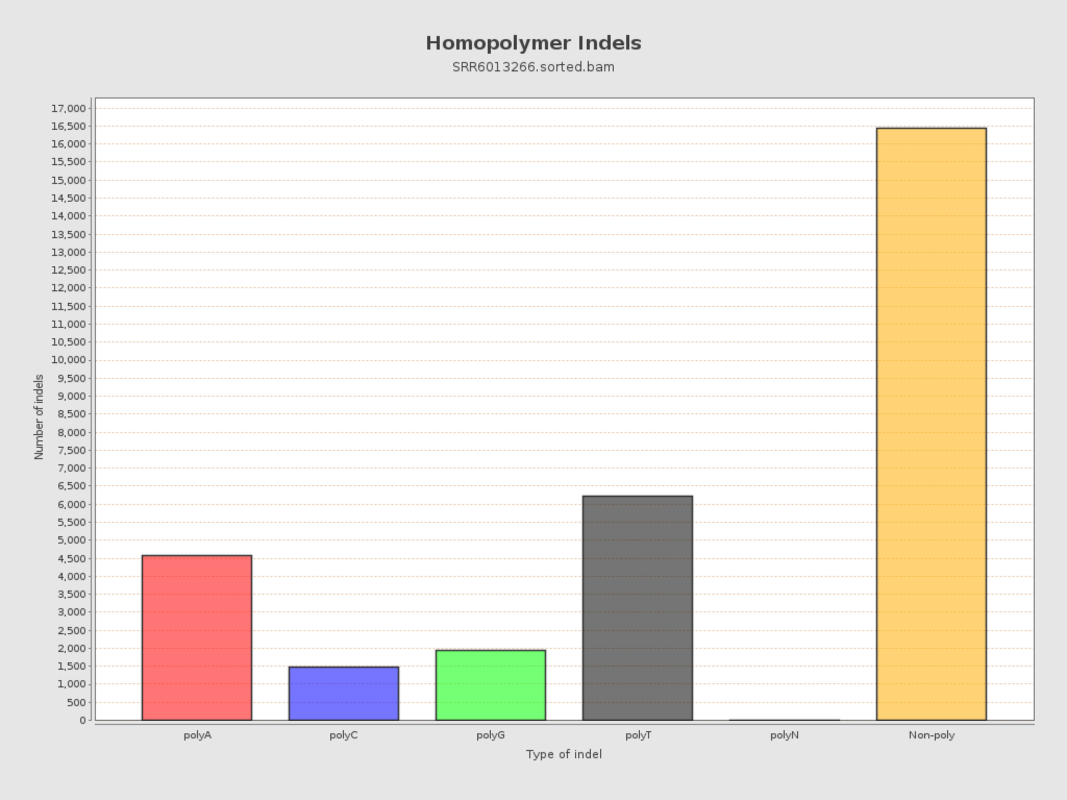
9. Results : Mapped Reads GC-content Distribution



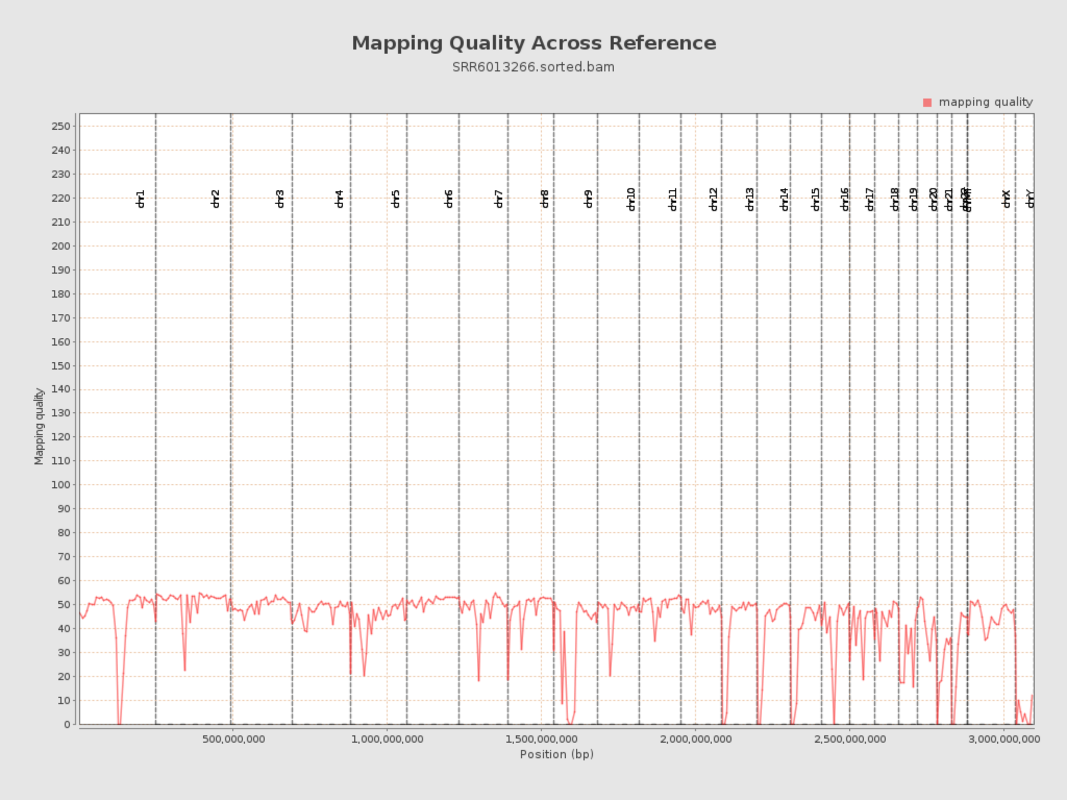
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram