Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:32:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240186.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_SRR6240186 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240186.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:32:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240186.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,036,916
Mapped reads	823,471 / 79.42%
Unmapped reads	213,445 / 20.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,796 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	66,845 / 6.45%
Duplication rate	6.54%
Clipped reads	359,003 / 34.62%

2.2. ACGT Content

Number/percentage of A's	15,854,779 / 28.64%
Number/percentage of C's	10,256,480 / 18.53%
Number/percentage of T's	17,564,713 / 31.73%
Number/percentage of G's	11,633,199 / 21.02%
Number/percentage of N's	45,597 / 0.08%
GC Percentage	39.54%

2.3. Coverage

Mean	0.0179

Standard Deviation	0.2472

2.4. Mapping Quality

Mean Mapping Quality	47.08

2.5. Mismatches and indels

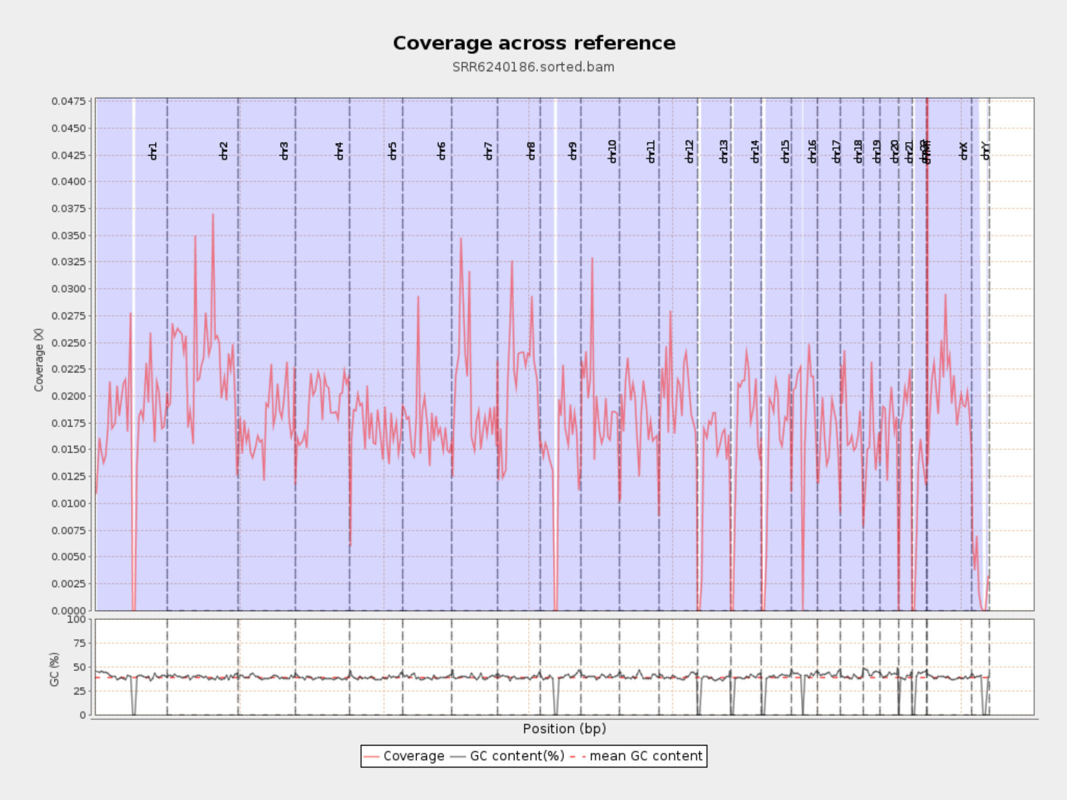
General error rate	0.93%
Mismatches	506,967
Insertions	3,885
Mapped reads with at least one insertion	0.47%
Deletions	15,311
Mapped reads with at least one deletion	1.84%
Homopolymer indels	48.24%

2.6. Chromosome stats

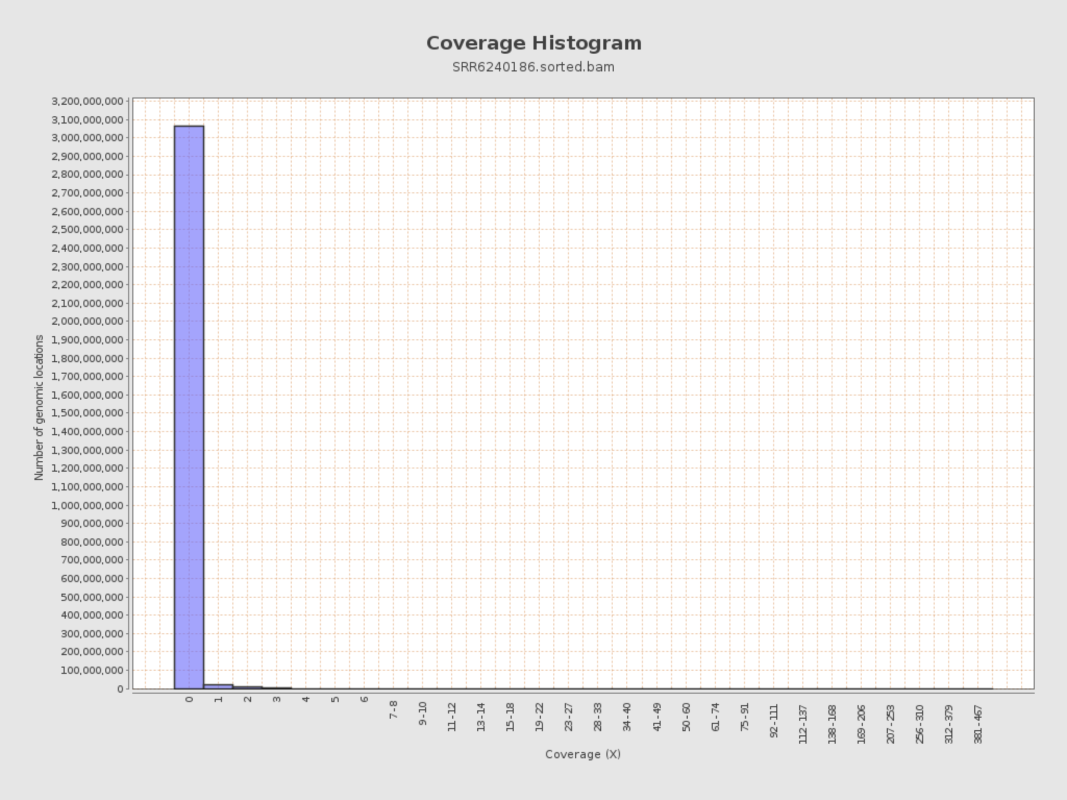
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4333231	0.0174	0.3491
chr2	243199373	5732004	0.0236	0.2744
chr3	198022430	3449590	0.0174	0.2044
chr4	191154276	3656987	0.0191	0.2168
chr5	180915260	3089112	0.0171	0.2056
chr6	171115067	2958191	0.0173	0.2278
chr7	159138663	3211022	0.0202	0.2807

chr8	146364022	3179195	0.0217	0.3657
chr9	141213431	2063373	0.0146	0.2144
chr10	135534747	2610679	0.0193	0.2497
chr11	135006516	2450017	0.0181	0.2336
chr12	133851895	2720505	0.0203	0.2215
chr13	115169878	1582069	0.0137	0.1861
chr14	107349540	1786579	0.0166	0.2043
chr15	102531392	1548802	0.0151	0.1929
chr16	90354753	1651538	0.0183	0.213
chr17	81195210	1290288	0.0159	0.1934
chr18	78077248	1355107	0.0174	0.321
chr19	59128983	910891	0.0154	0.2507
chr20	63025520	1080692	0.0171	0.2001
chr21	48129895	838548	0.0174	0.2018
chr22	51304566	501964	0.0098	0.1485
chrMT	16571	10908	0.6583	1.084
chrX	155270560	3211399	0.0207	0.2353
chrY	59373566	158935	0.0027	0.0747

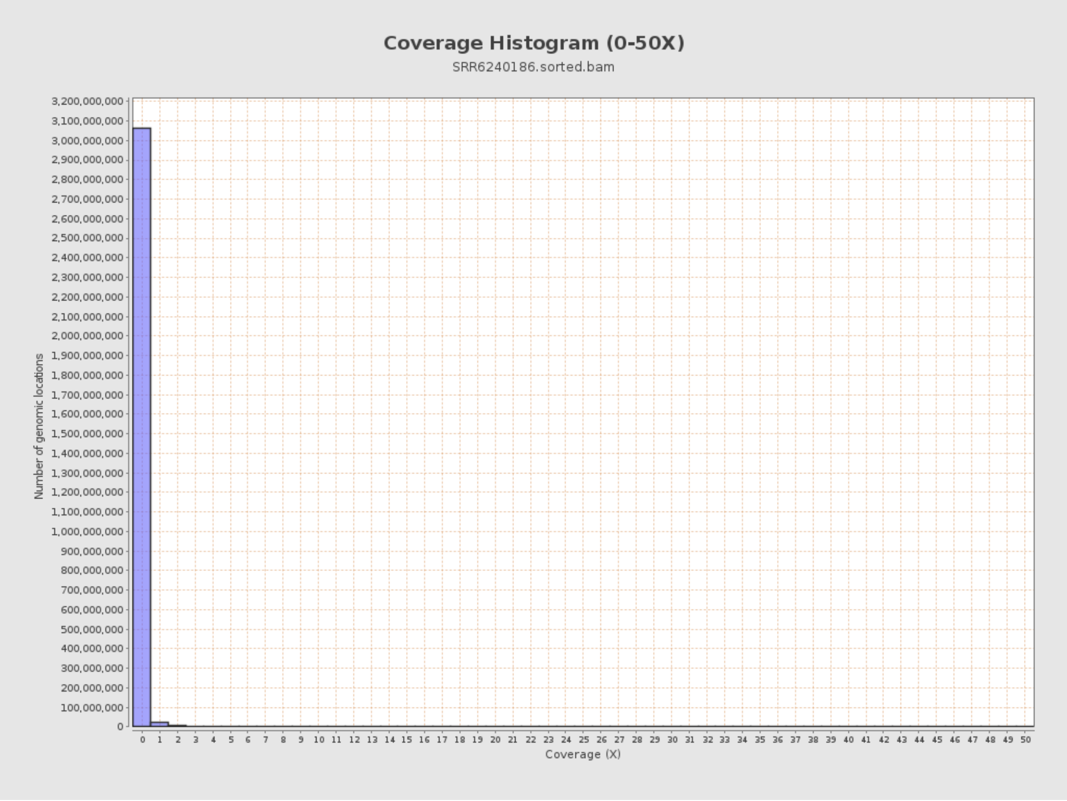
3. Results : Coverage across reference



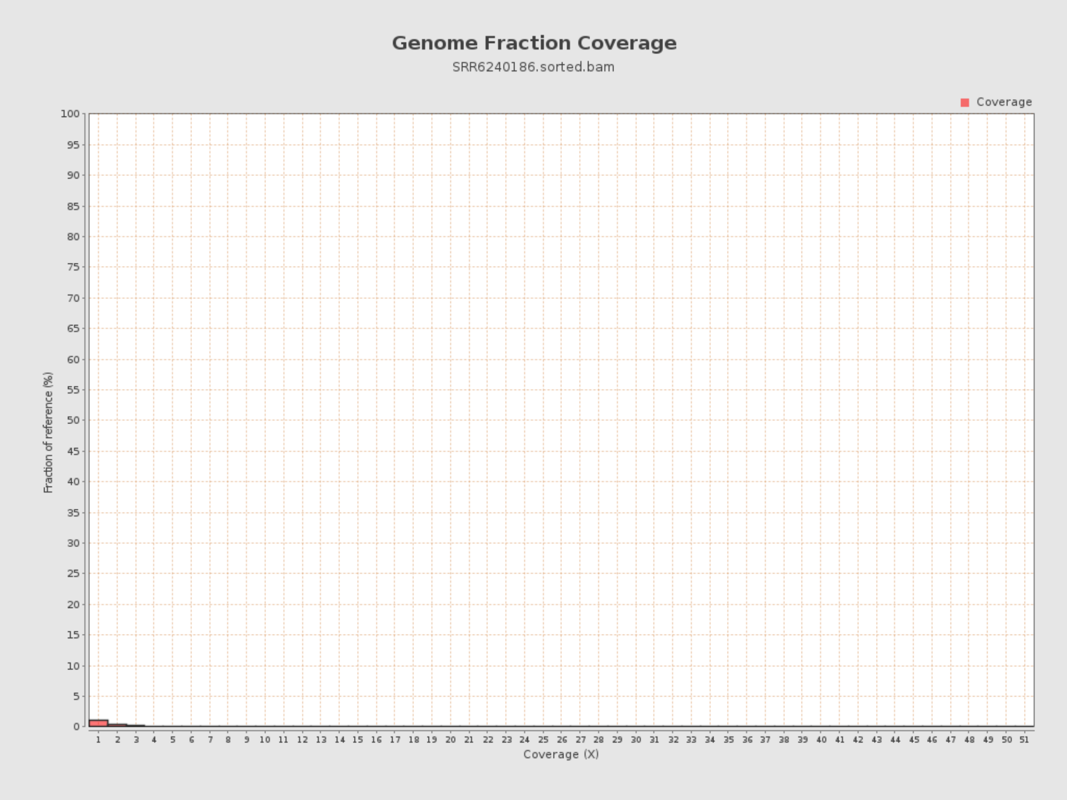
4. Results : Coverage Histogram



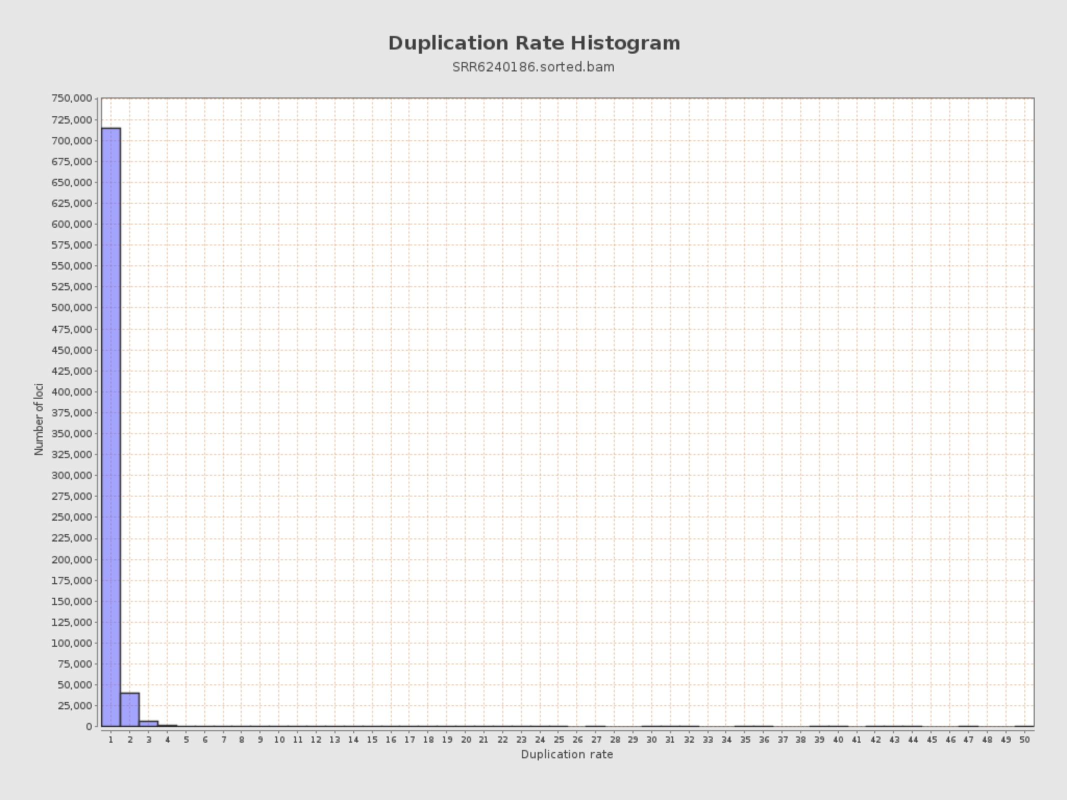
5. Results : Coverage Histogram (0-50X)



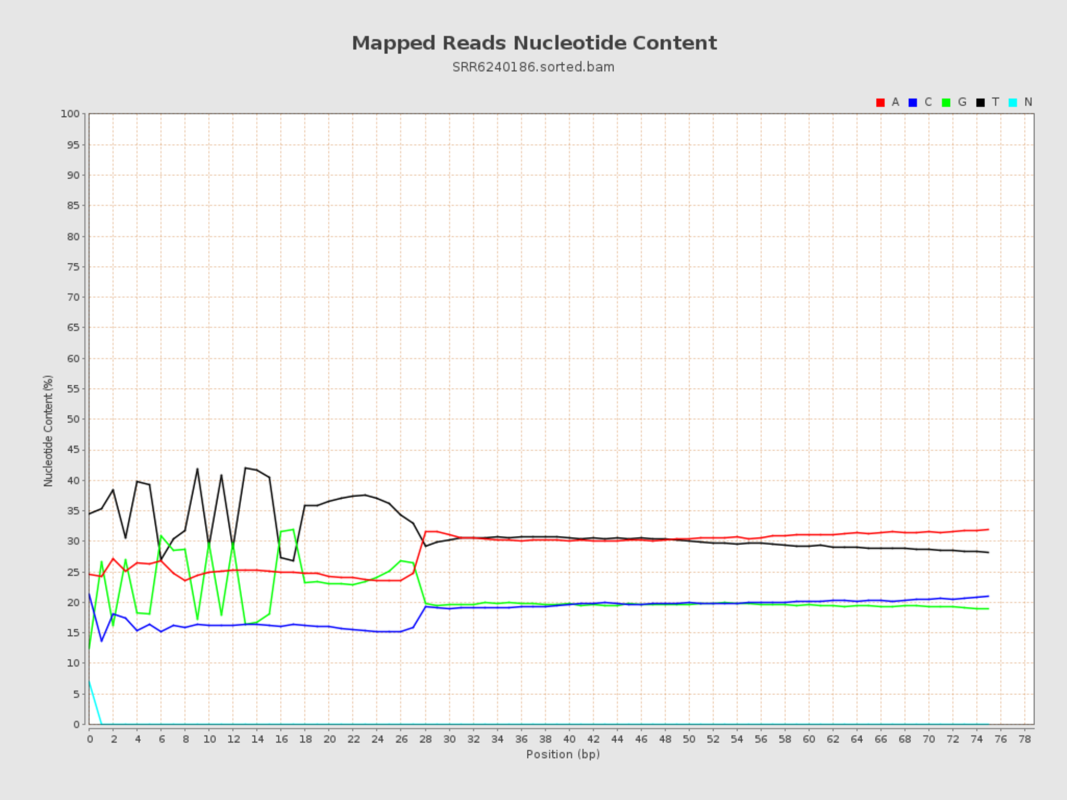
6. Results : Genome Fraction Coverage



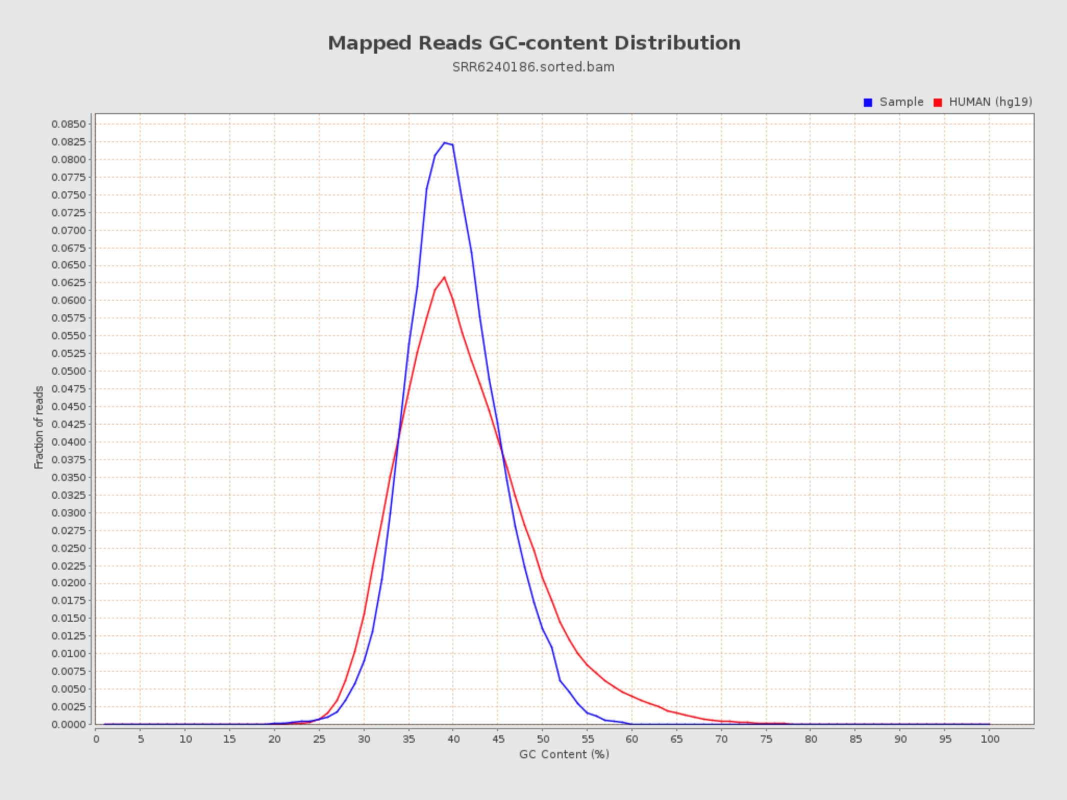
7. Results : Duplication Rate Histogram



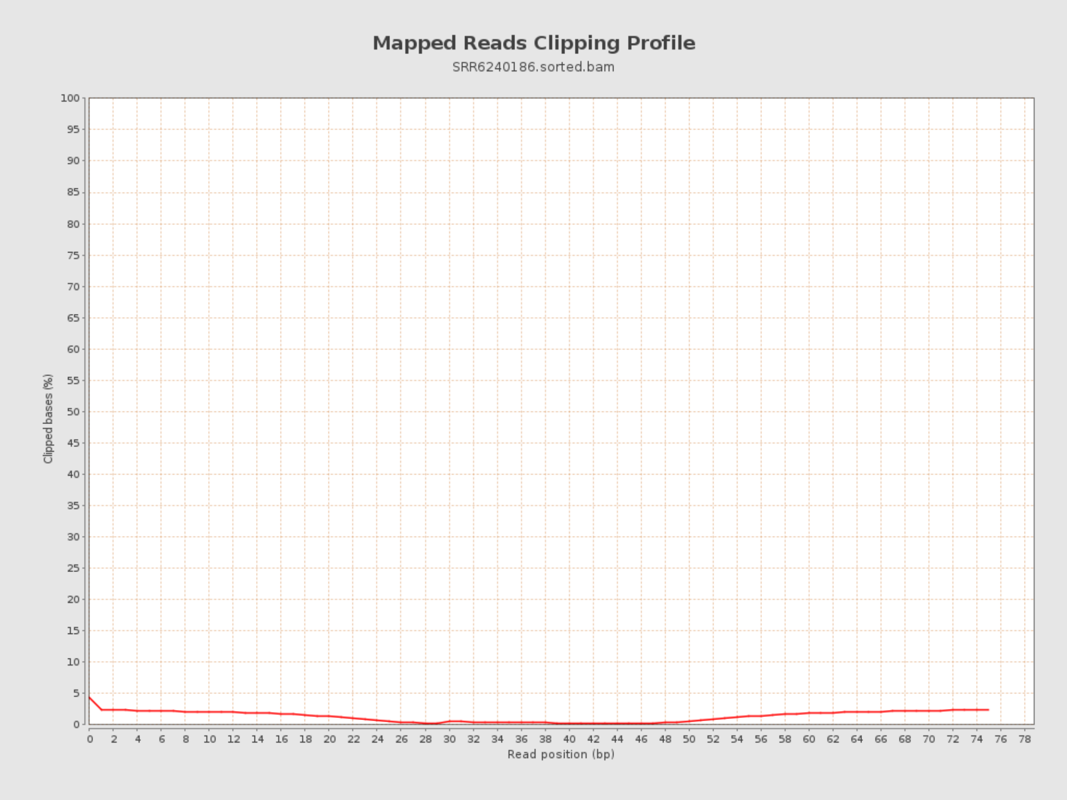
8. Results : Mapped Reads Nucleotide Content



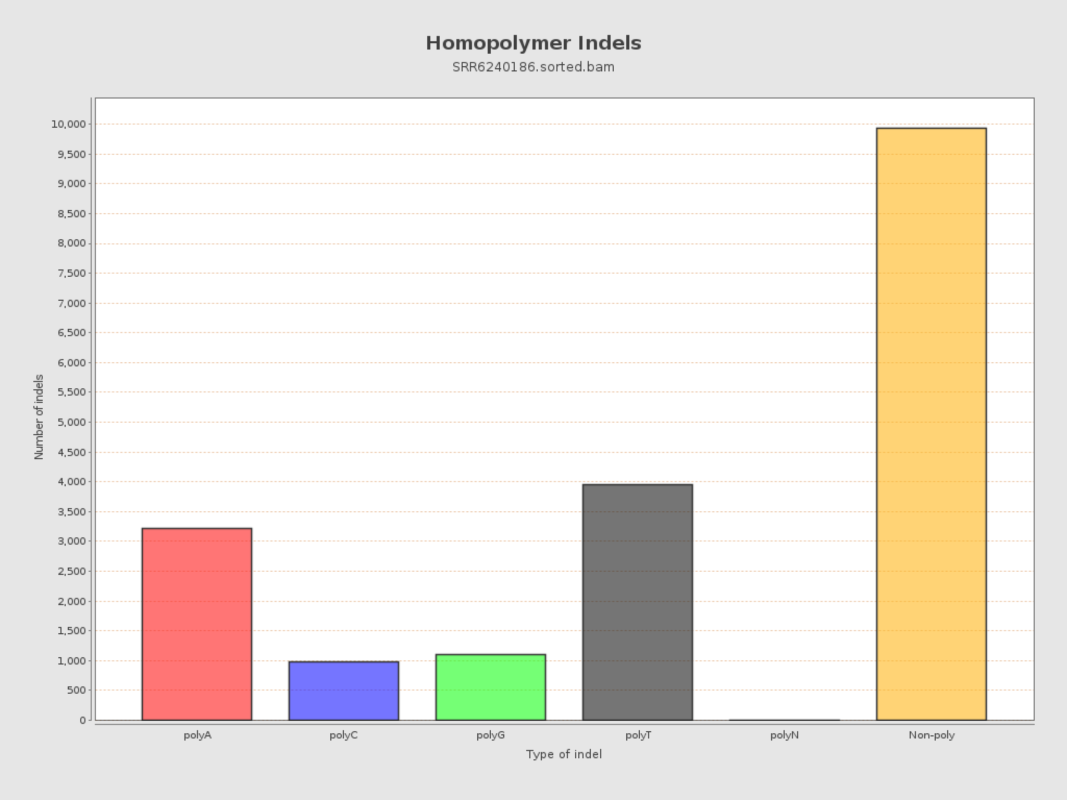
9. Results : Mapped Reads GC-content Distribution



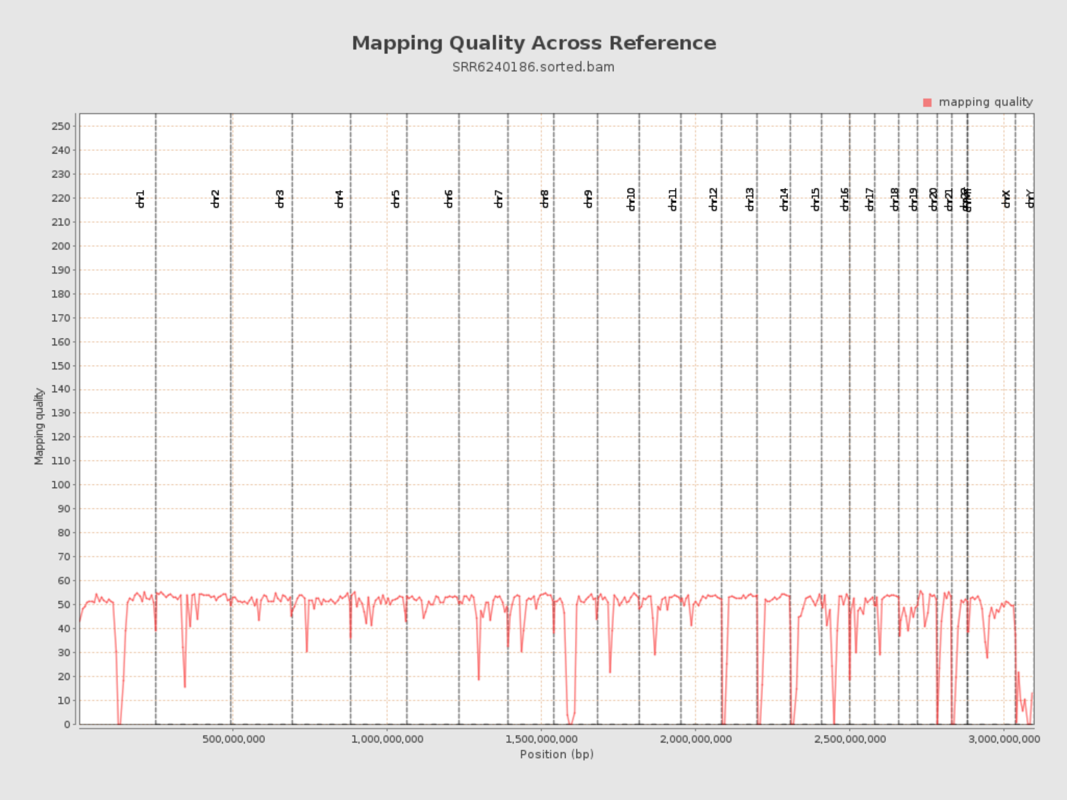
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram