Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:04:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240071.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_SRR6240071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:04:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,568,199
Mapped reads	1,126,585 / 71.84%
Unmapped reads	441,614 / 28.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,325 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	231,896 / 14.79%
Duplication rate	14.84%
Clipped reads	723,415 / 46.13%

2.2. ACGT Content

Number/percentage of A's	18,532,718 / 26.61%
Number/percentage of C's	11,922,826 / 17.12%
Number/percentage of T's	23,319,076 / 33.48%
Number/percentage of G's	15,877,282 / 22.79%
Number/percentage of N's	5,547 / 0.01%
GC Percentage	39.91%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.3112

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

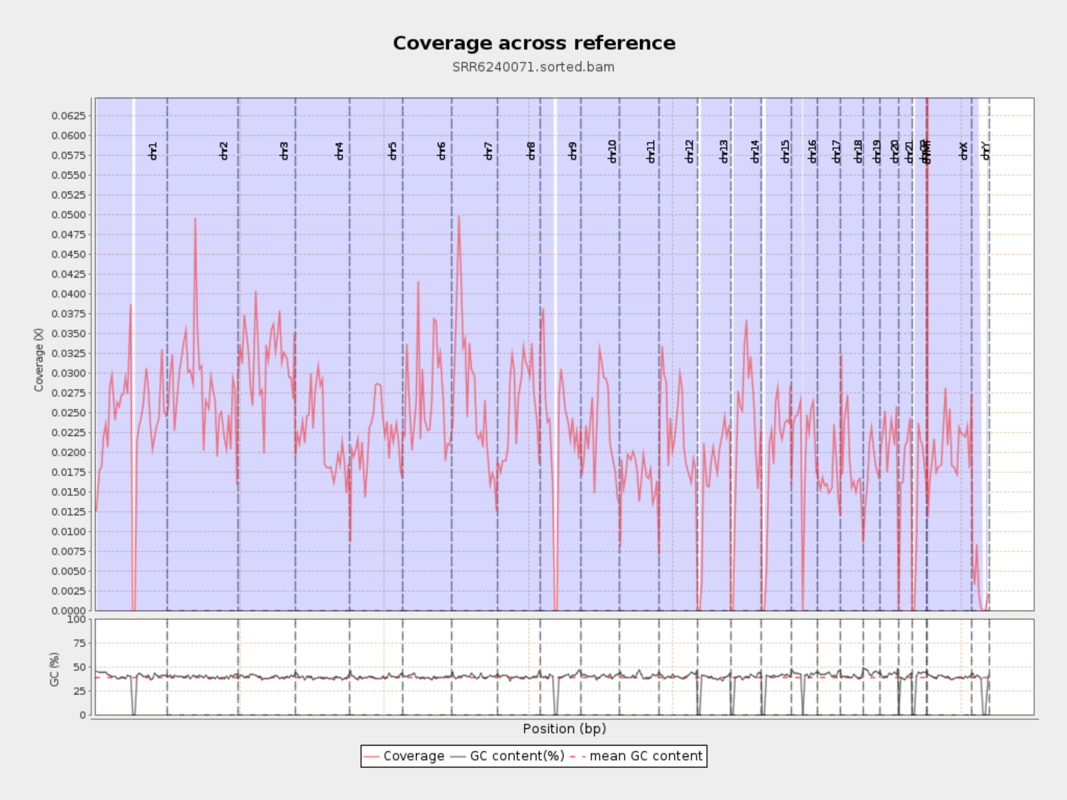
General error rate	0.97%
Mismatches	669,342
Insertions	5,027
Mapped reads with at least one insertion	0.44%
Deletions	22,380
Mapped reads with at least one deletion	1.97%
Homopolymer indels	49.6%

2.6. Chromosome stats

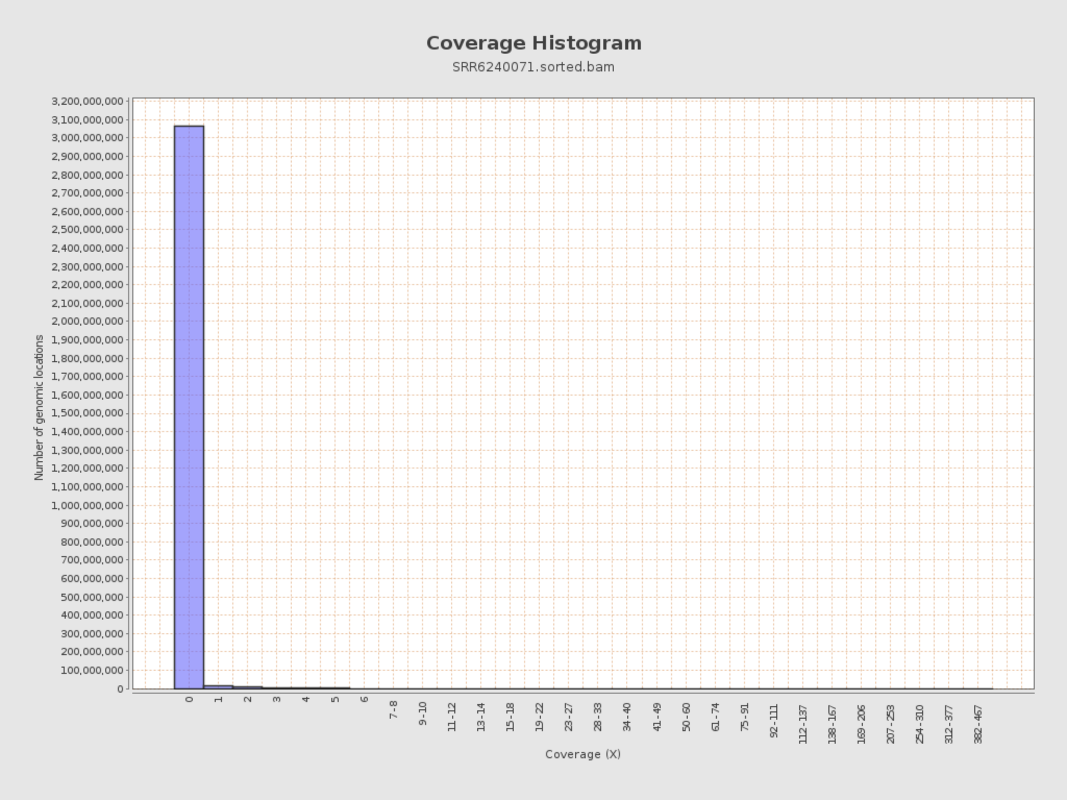
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5826964	0.0234	0.4014
chr2	243199373	6811069	0.028	0.3616
chr3	198022430	6310422	0.0319	0.3352
chr4	191154276	4167951	0.0218	0.279
chr5	180915260	3971405	0.022	0.2773
chr6	171115067	4577335	0.0268	0.326
chr7	159138663	4268820	0.0268	0.354

chr8	146364022	3795881	0.0259	0.4093
chr9	141213431	3205826	0.0227	0.3043
chr10	135534747	3082652	0.0227	0.304
chr11	135006516	2292961	0.017	0.2551
chr12	133851895	3076868	0.023	0.2808
chr13	115169878	1929461	0.0168	0.2425
chr14	107349540	2391189	0.0223	0.282
chr15	102531392	1920856	0.0187	0.2559
chr16	90354753	1880203	0.0208	0.2553
chr17	81195210	1343963	0.0166	0.2308
chr18	78077248	1461529	0.0187	0.3605
chr19	59128983	1059967	0.0179	0.2783
chr20	63025520	1372773	0.0218	0.2787
chr21	48129895	850880	0.0177	0.2568
chr22	51304566	726514	0.0142	0.2105
chrMT	16571	39055	2.3568	3.3188
chrX	155270560	3176606	0.0205	0.2688
chrY	59373566	154664	0.0026	0.0822

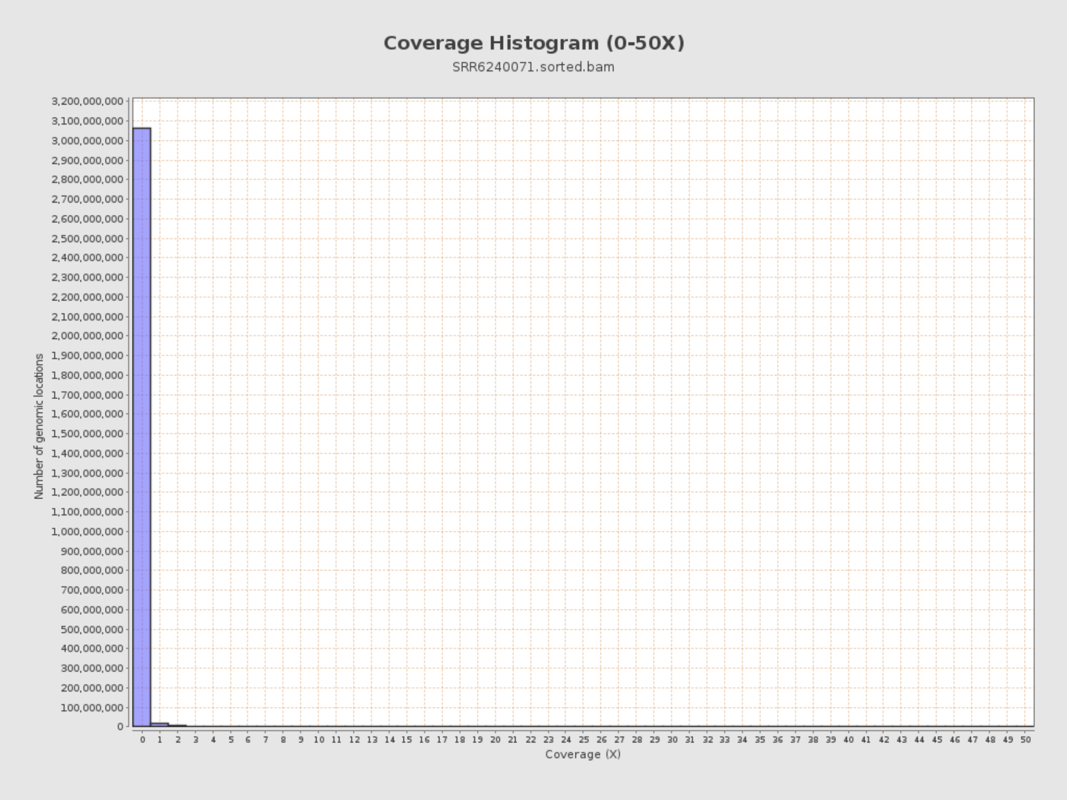
3. Results : Coverage across reference



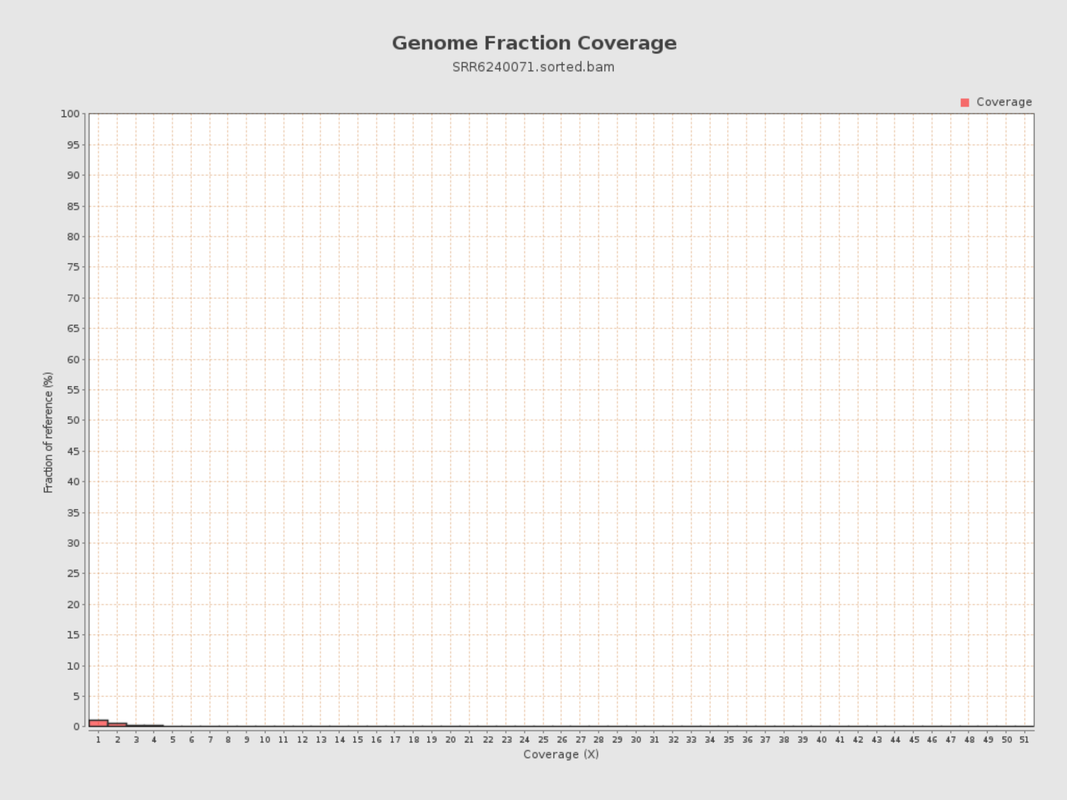
4. Results : Coverage Histogram



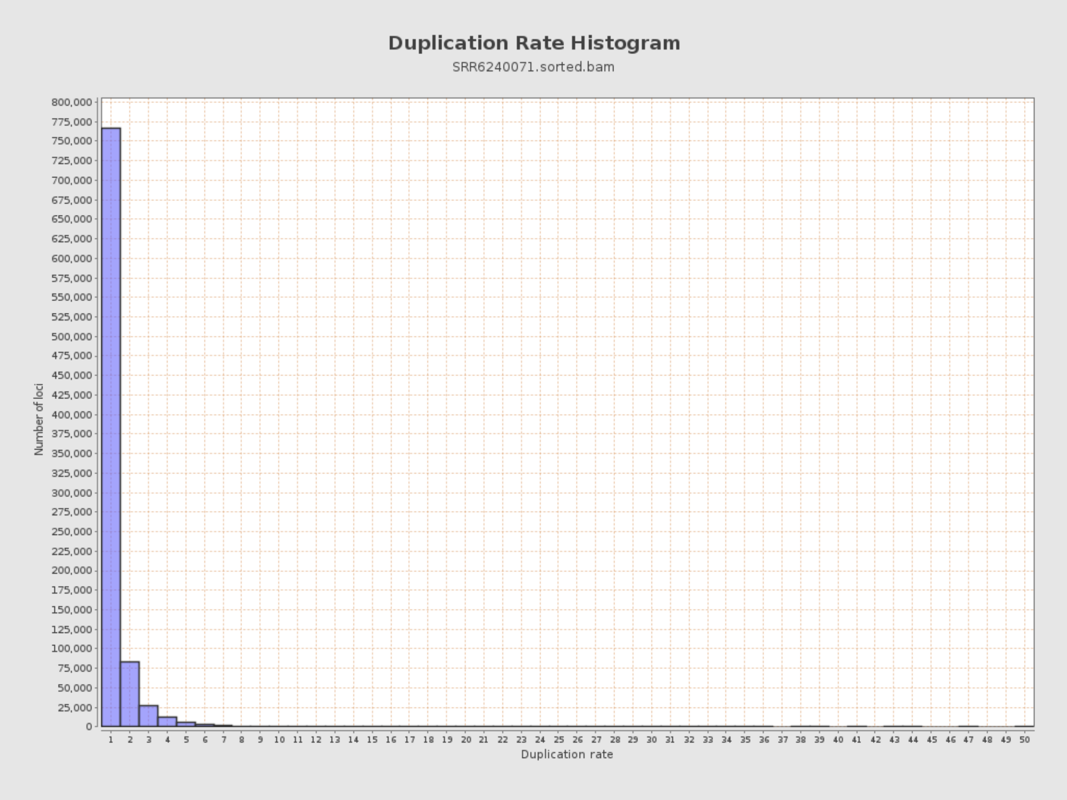
5. Results : Coverage Histogram (0-50X)



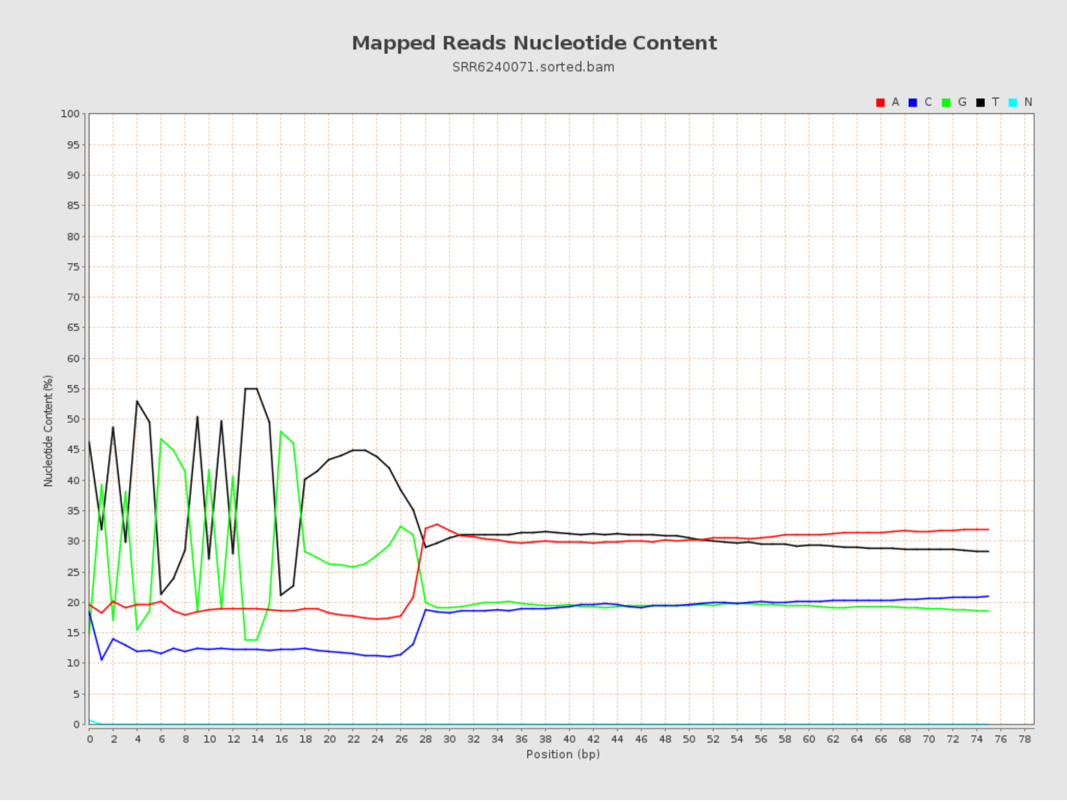
6. Results : Genome Fraction Coverage



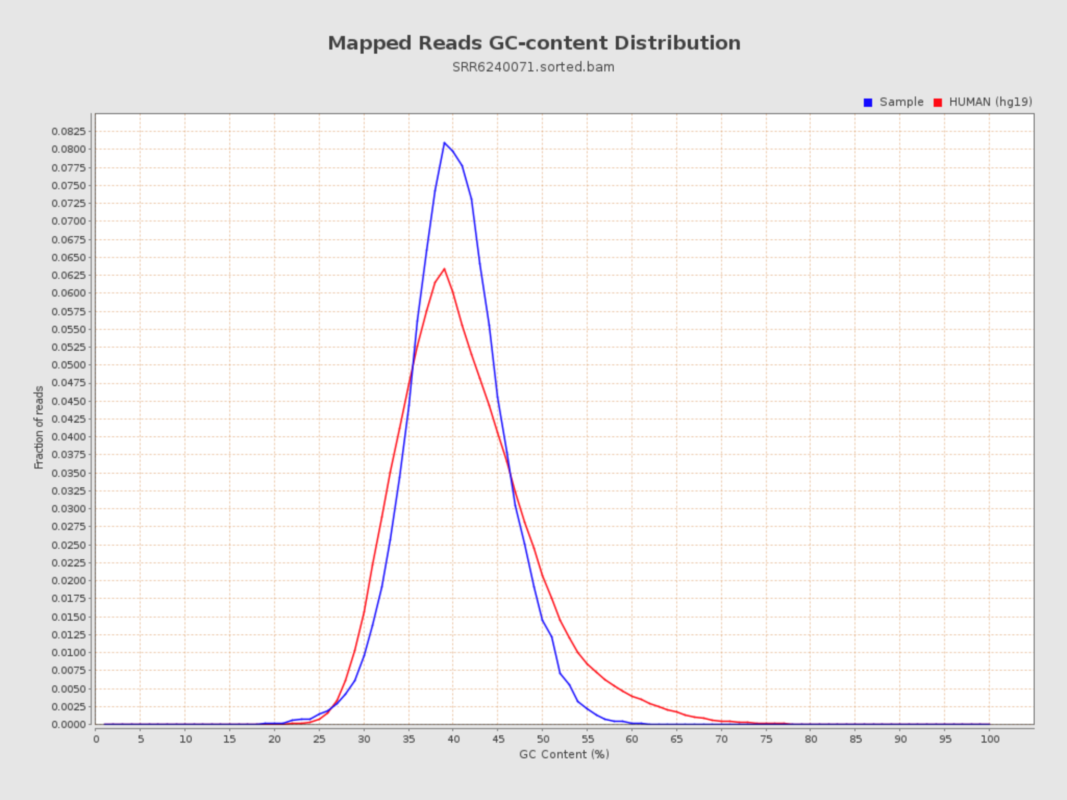
7. Results : Duplication Rate Histogram



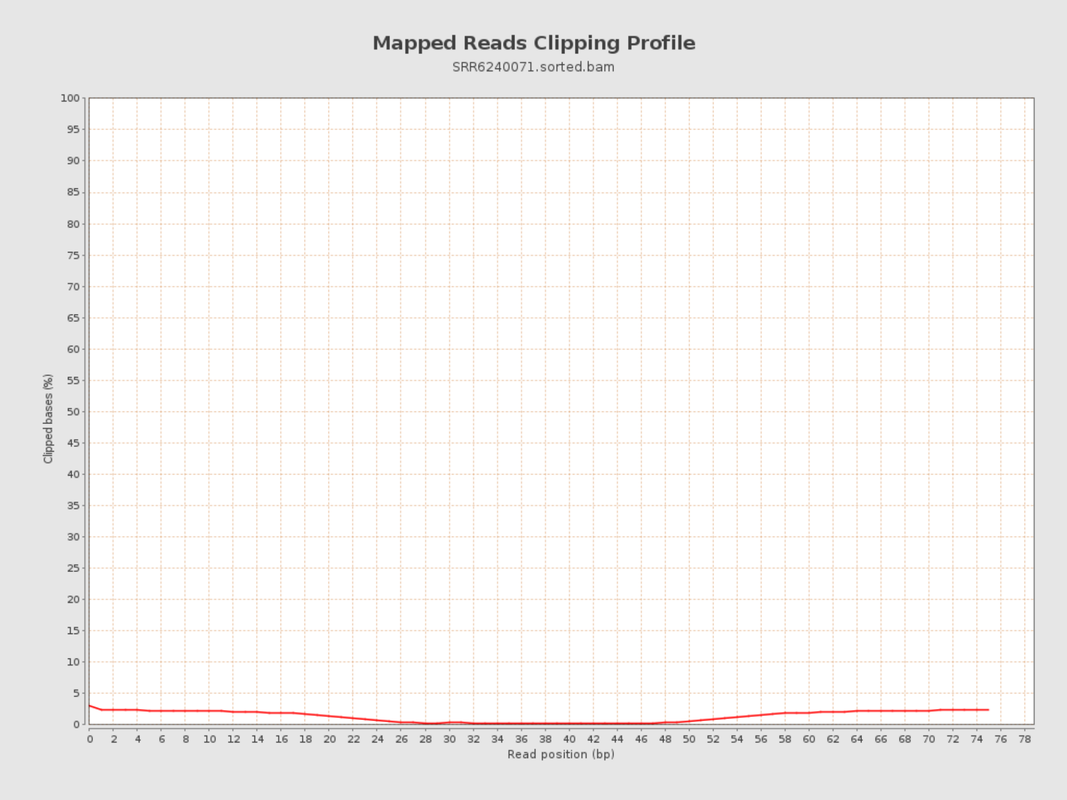
8. Results : Mapped Reads Nucleotide Content



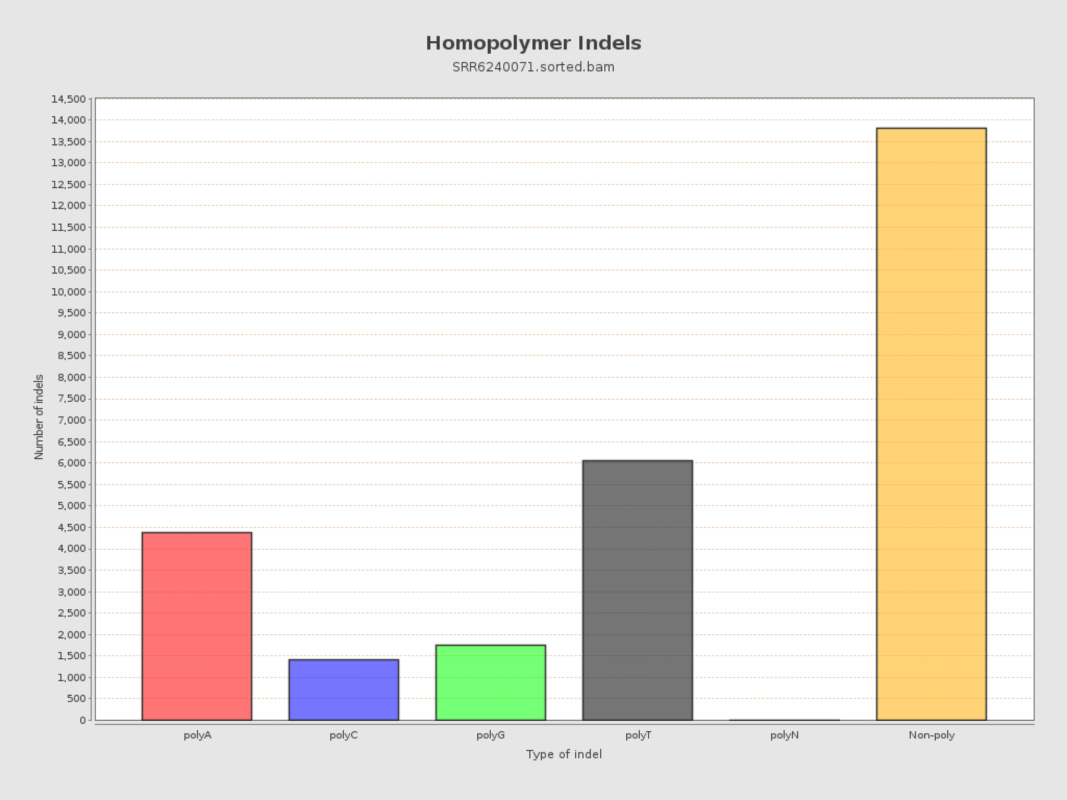
9. Results : Mapped Reads GC-content Distribution



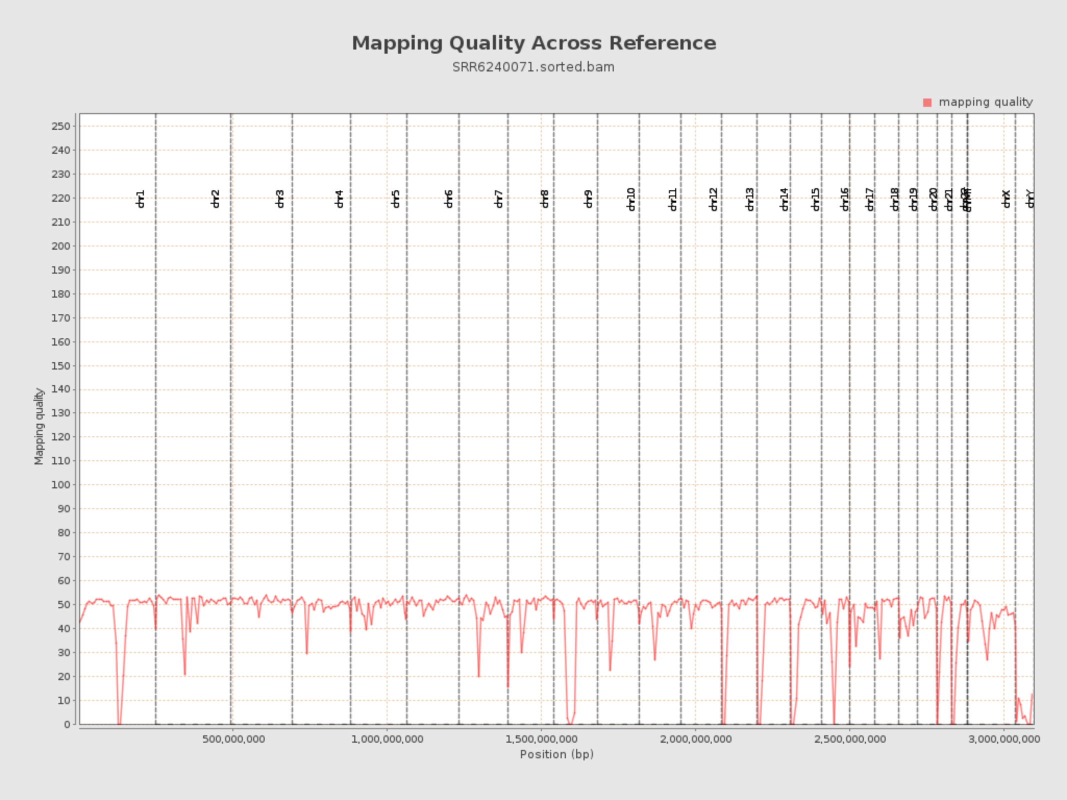
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram