Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:25:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240057.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_SRR6240057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:25:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,447,151
Mapped reads	1,148,607 / 79.37%
Unmapped reads	298,544 / 20.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,617 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	118,887 / 8.22%
Duplication rate	8.53%
Clipped reads	678,828 / 46.91%

2.2. ACGT Content

Number/percentage of A's	20,064,201 / 27.57%
Number/percentage of C's	13,052,749 / 17.94%
Number/percentage of T's	23,492,778 / 32.29%
Number/percentage of G's	16,103,885 / 22.13%
Number/percentage of N's	50,401 / 0.07%
GC Percentage	40.07%

2.3. Coverage

Mean	0.0235

Standard Deviation	0.2686

2.4. Mapping Quality

Mean Mapping Quality	46.19

2.5. Mismatches and indels

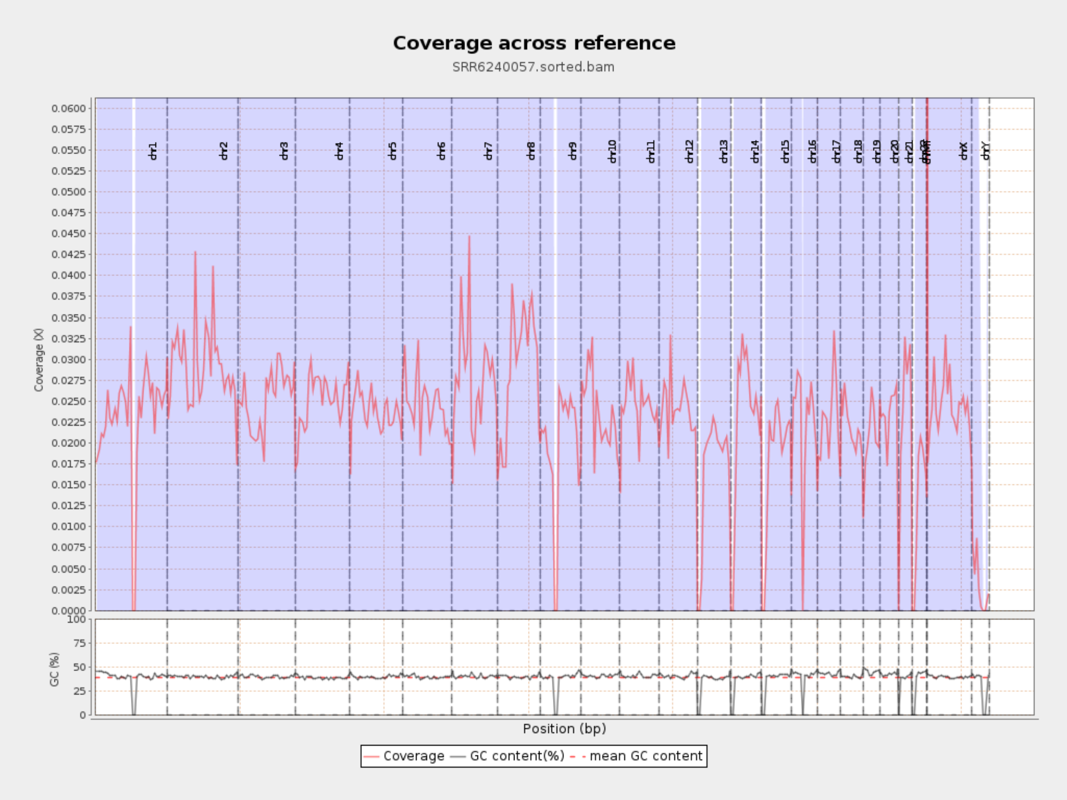
General error rate	1.03%
Mismatches	739,588
Insertions	5,390
Mapped reads with at least one insertion	0.47%
Deletions	25,653
Mapped reads with at least one deletion	2.21%
Homopolymer indels	49.42%

2.6. Chromosome stats

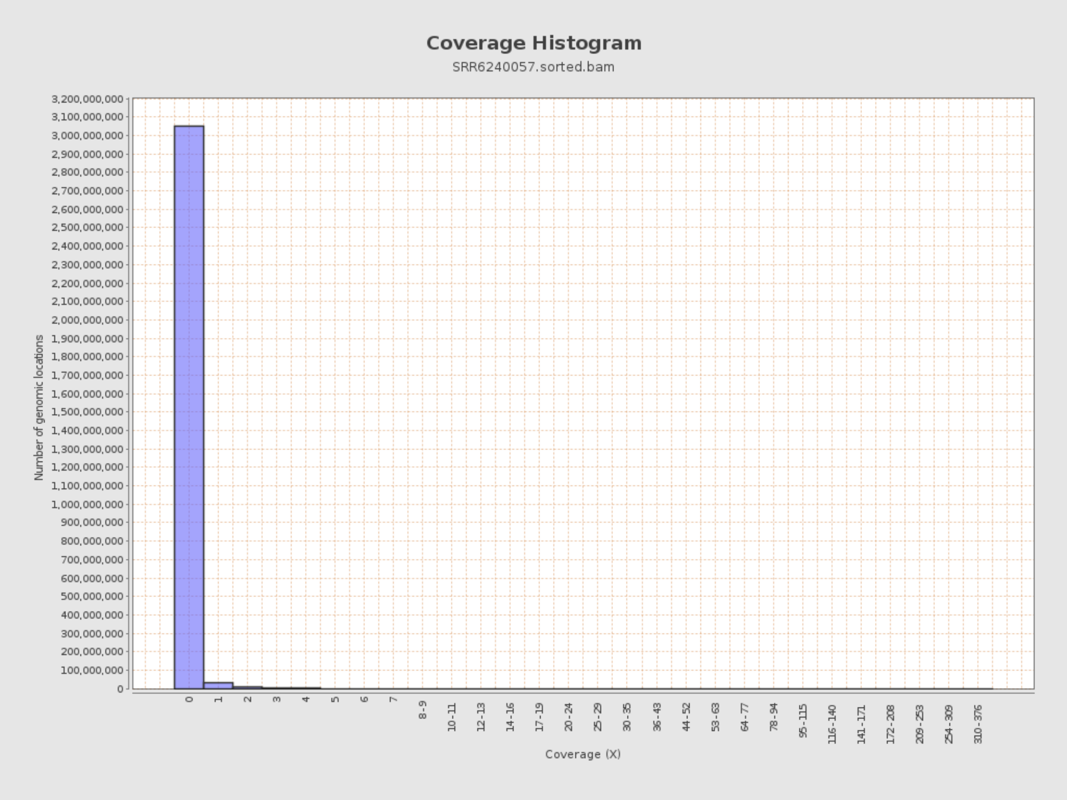
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5738838	0.023	0.3685
chr2	243199373	7122174	0.0293	0.3077
chr3	198022430	4990860	0.0252	0.2313
chr4	191154276	4810225	0.0252	0.2362
chr5	180915260	4341025	0.024	0.2265
chr6	171115067	4209803	0.0246	0.2503
chr7	159138663	4470195	0.0281	0.3947

chr8	146364022	4307182	0.0294	0.3192
chr9	141213431	2764432	0.0196	0.2363
chr10	135534747	3197317	0.0236	0.2474
chr11	135006516	3327304	0.0246	0.2635
chr12	133851895	3221362	0.0241	0.2259
chr13	115169878	1937292	0.0168	0.189
chr14	107349540	2432809	0.0227	0.228
chr15	102531392	1820789	0.0178	0.1956
chr16	90354753	1964228	0.0217	0.2146
chr17	81195210	1858486	0.0229	0.2252
chr18	78077248	1711642	0.0219	0.3577
chr19	59128983	1245915	0.0211	0.2783
chr20	63025520	1456971	0.0231	0.2284
chr21	48129895	1166494	0.0242	0.2329
chr22	51304566	666055	0.013	0.1609
chrMT	16571	49727	3.0008	3.8563
chrX	155270560	3816352	0.0246	0.2349
chrY	59373566	180545	0.003	0.0792

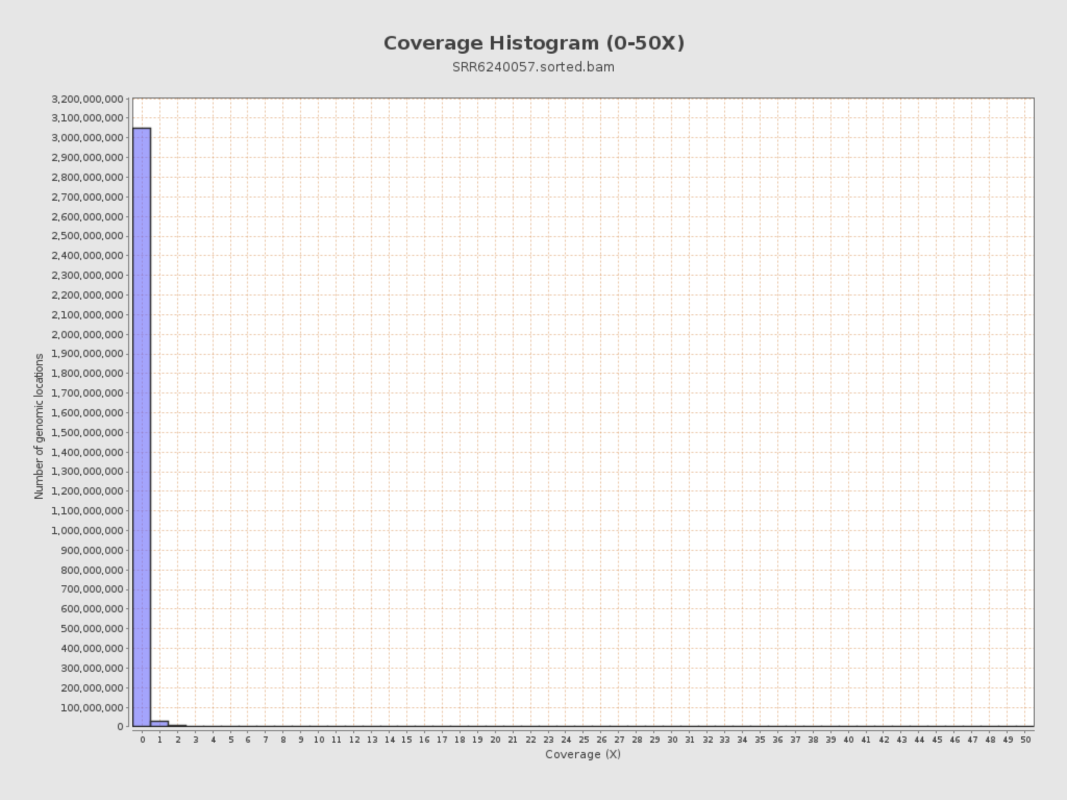
3. Results : Coverage across reference



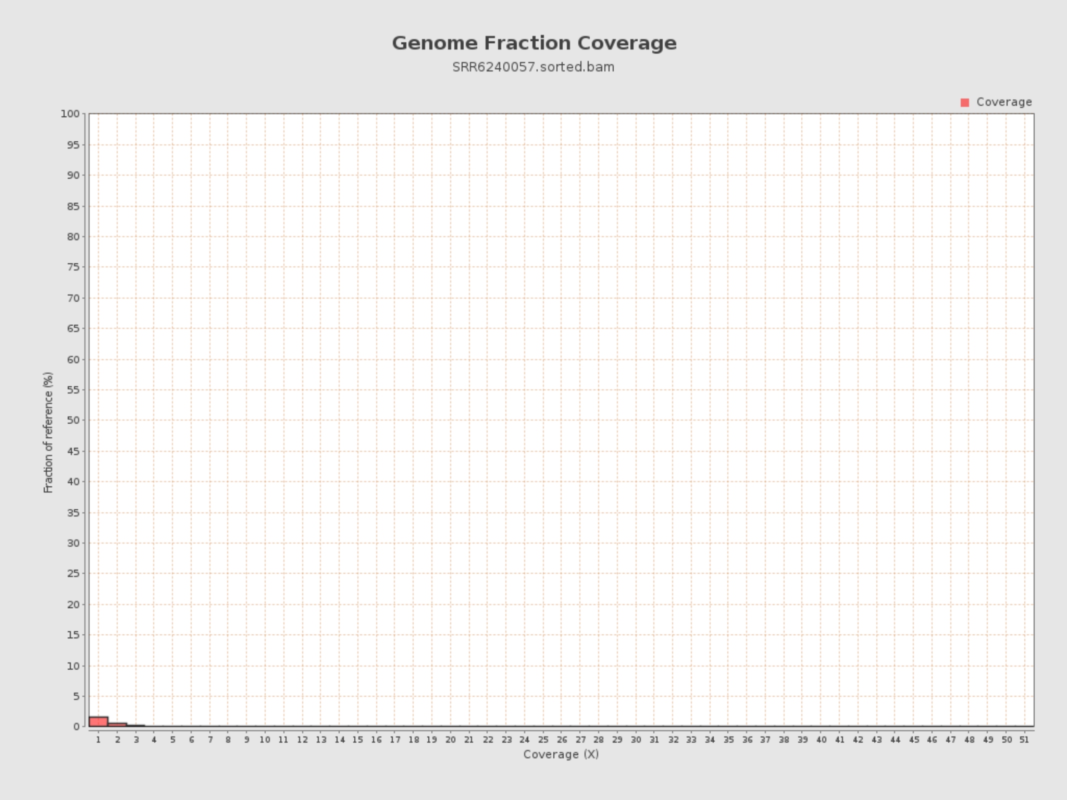
4. Results : Coverage Histogram



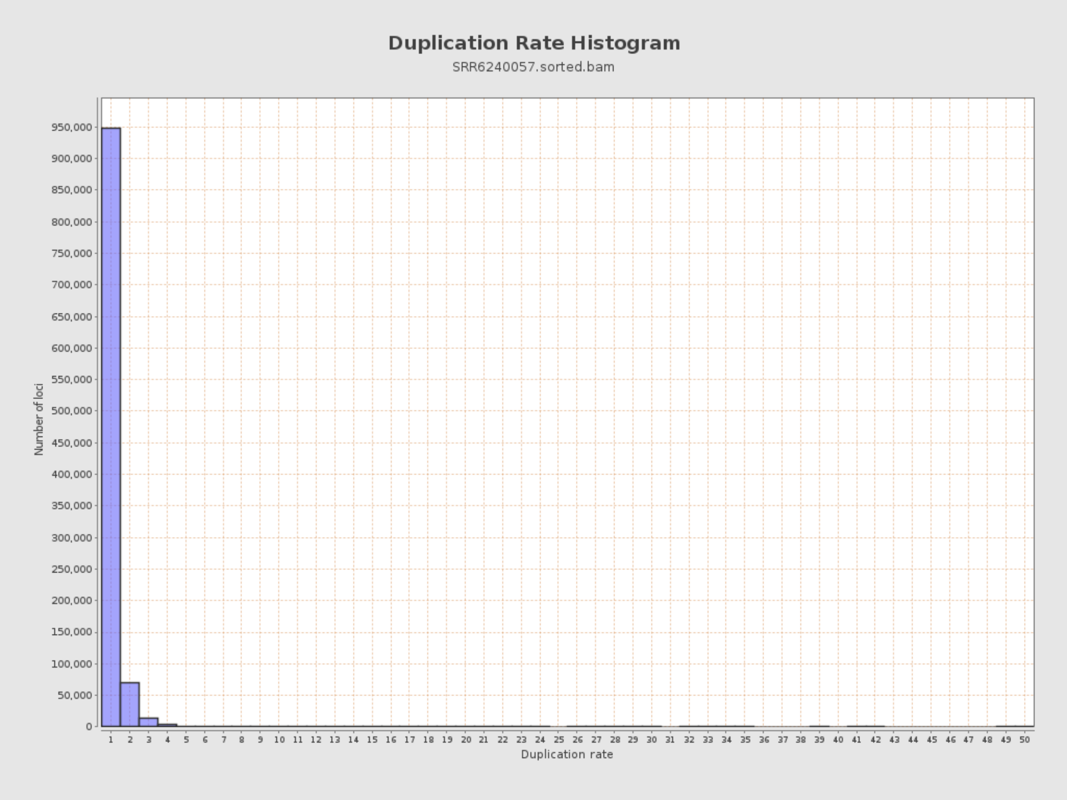
5. Results : Coverage Histogram (0-50X)



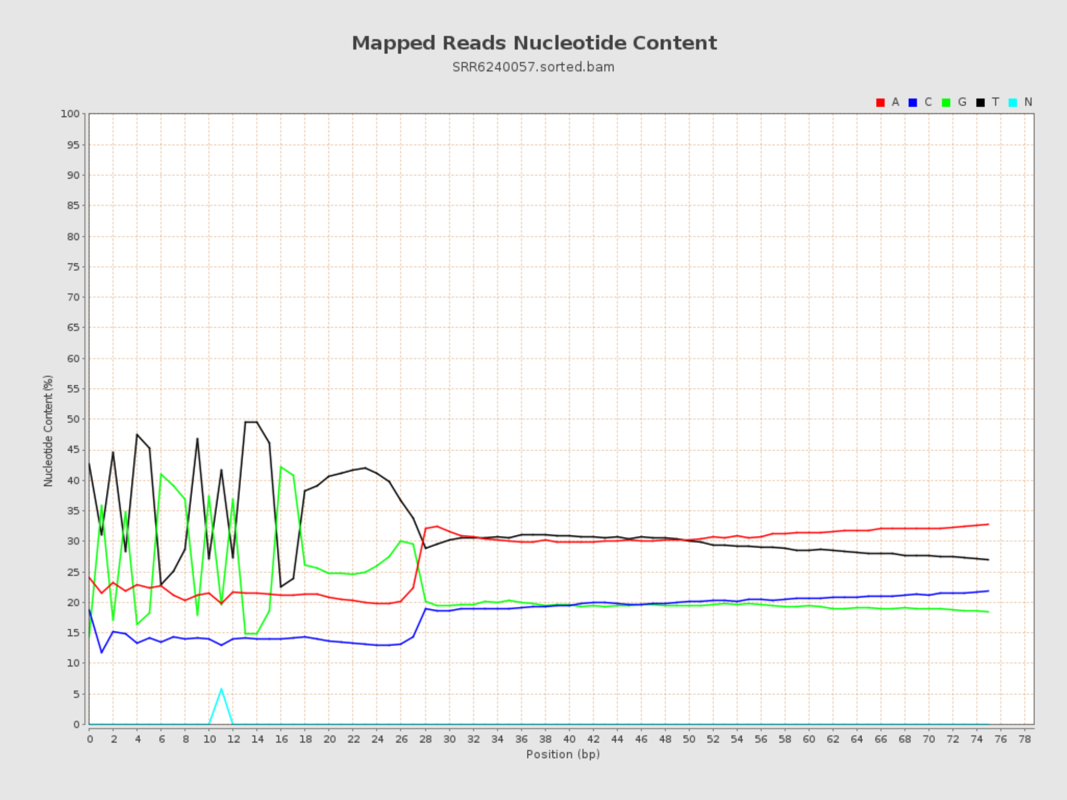
6. Results : Genome Fraction Coverage



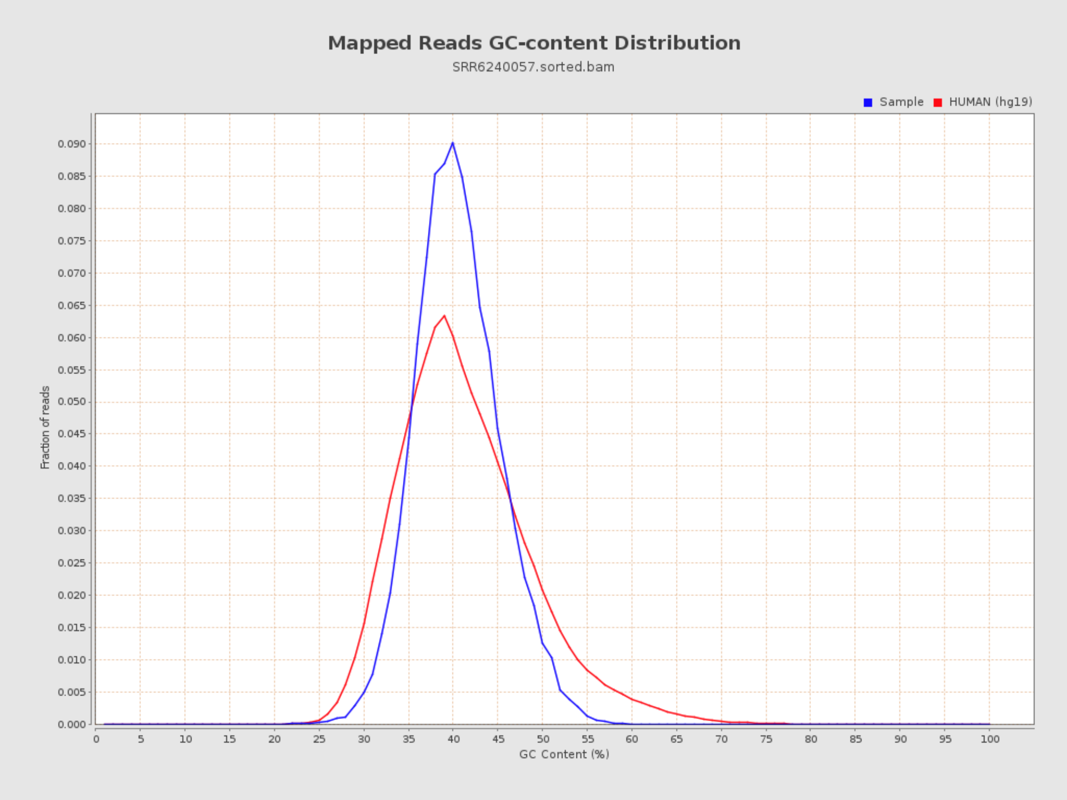
7. Results : Duplication Rate Histogram



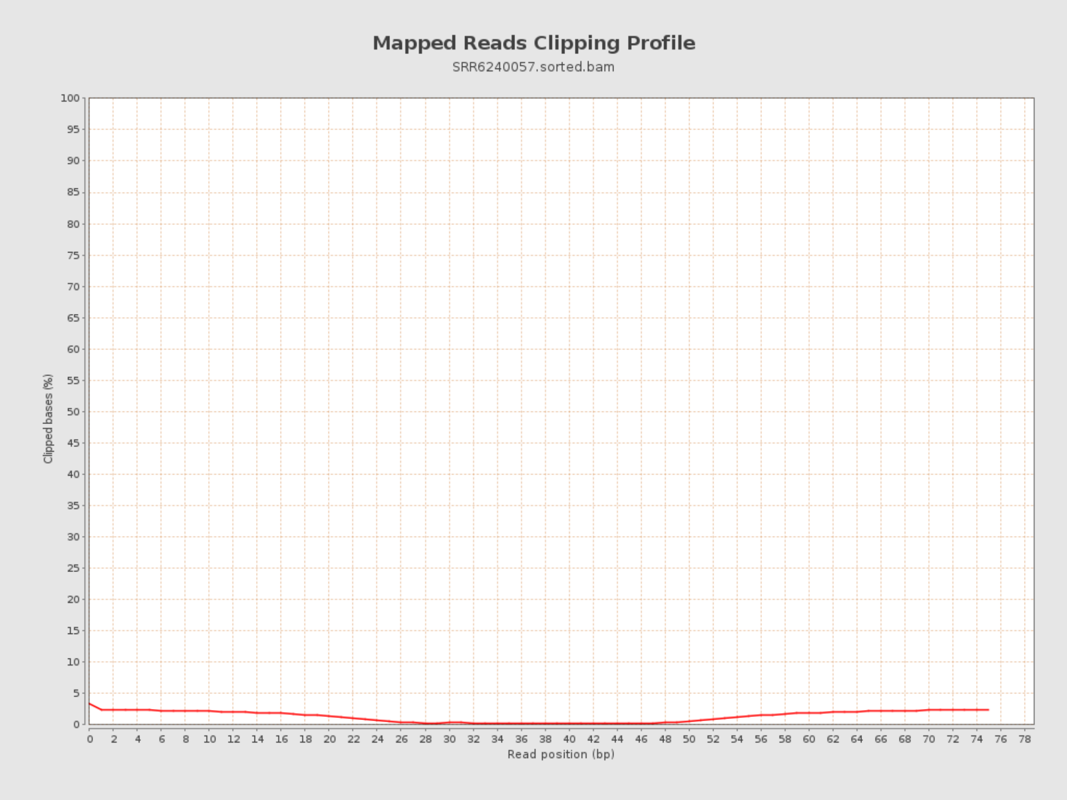
8. Results : Mapped Reads Nucleotide Content



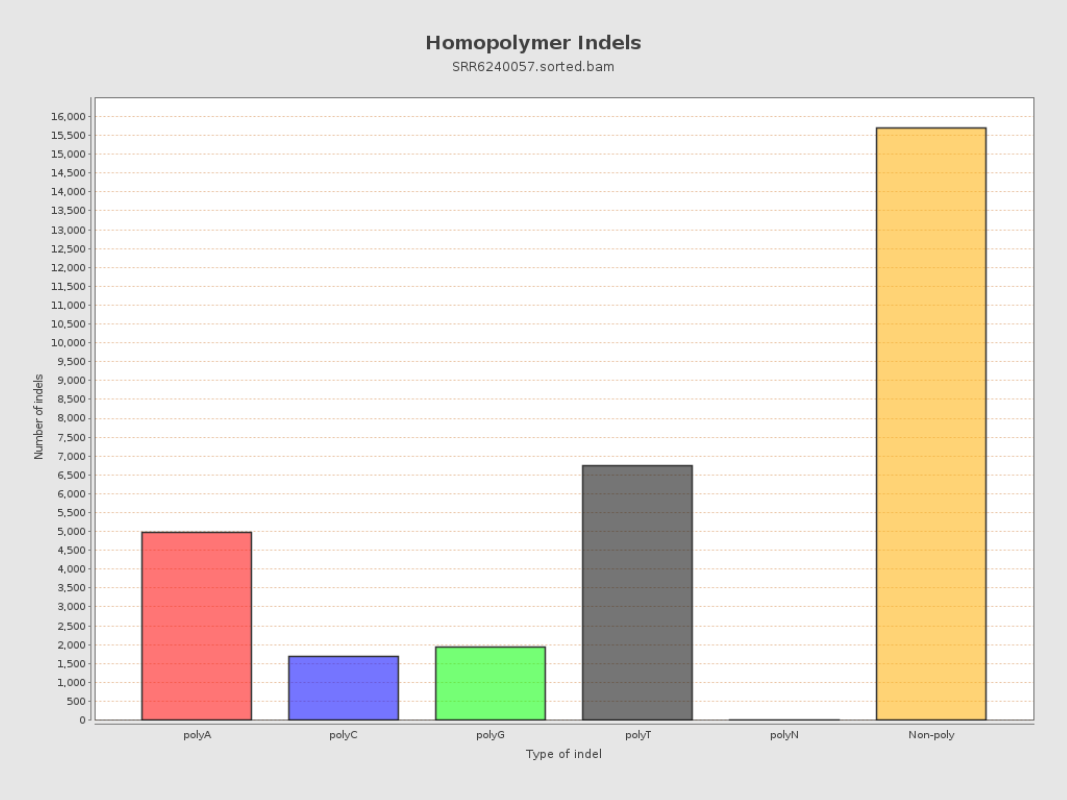
9. Results : Mapped Reads GC-content Distribution



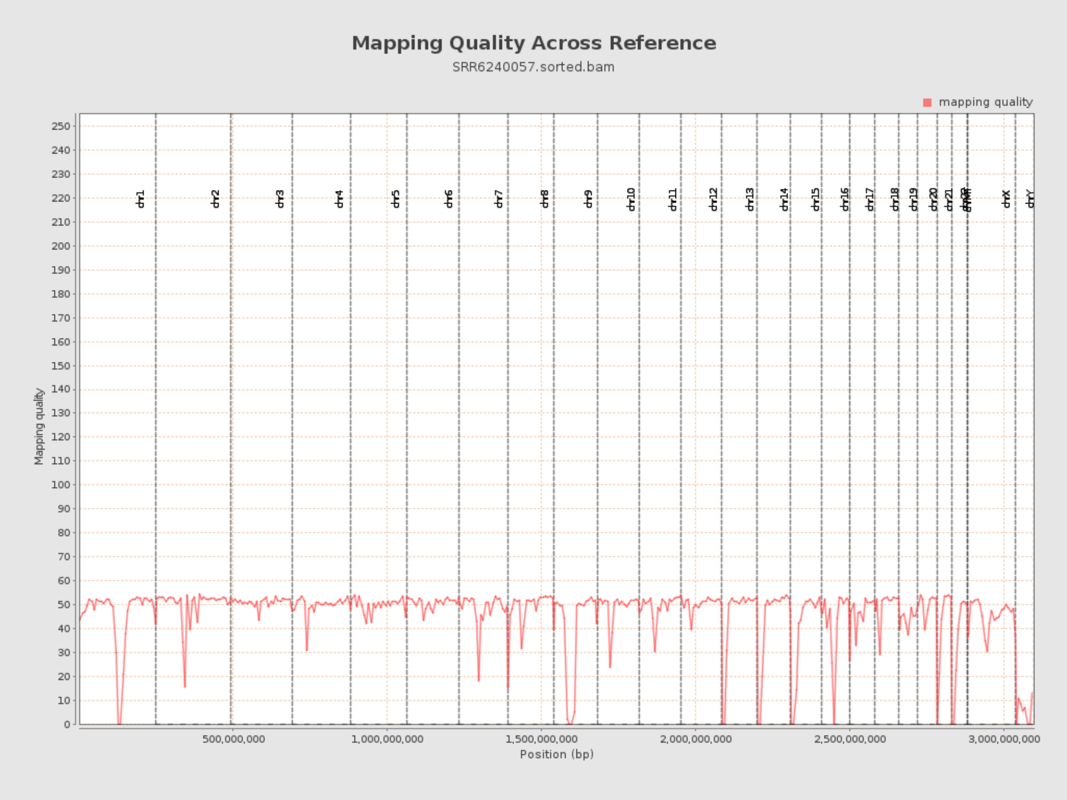
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram