Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:36:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240188.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_SRR6240188 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240188.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:36:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240188.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,715,629
Mapped reads	1,477,067 / 86.09%
Unmapped reads	238,562 / 13.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,310 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	76,579 / 4.46%
Duplication rate	4.17%
Clipped reads	713,042 / 41.56%

2.2. ACGT Content

Number/percentage of A's	28,531,470 / 29.09%
Number/percentage of C's	18,357,862 / 18.72%
Number/percentage of T's	30,717,755 / 31.32%
Number/percentage of G's	20,395,919 / 20.8%
Number/percentage of N's	74,246 / 0.08%
GC Percentage	39.51%

2.3. Coverage

Mean	0.0317

Standard Deviation	0.3527

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

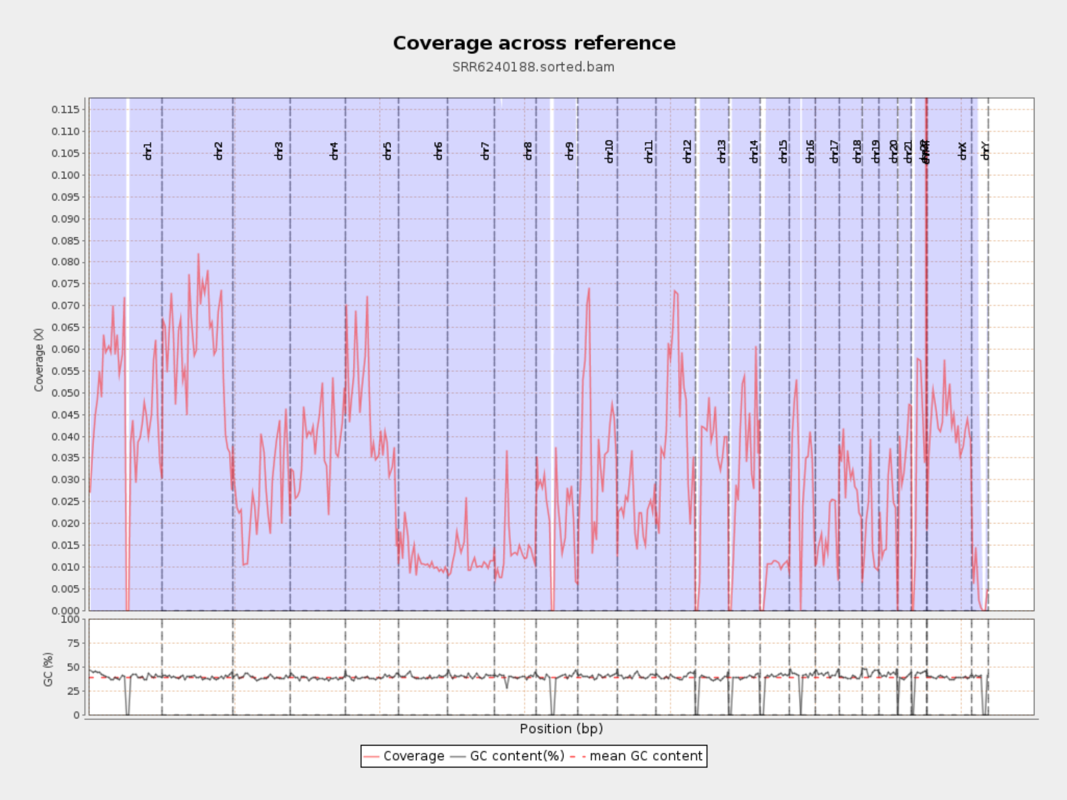
General error rate	0.98%
Mismatches	951,425
Insertions	6,921
Mapped reads with at least one insertion	0.46%
Deletions	35,745
Mapped reads with at least one deletion	2.39%
Homopolymer indels	44.86%

2.6. Chromosome stats

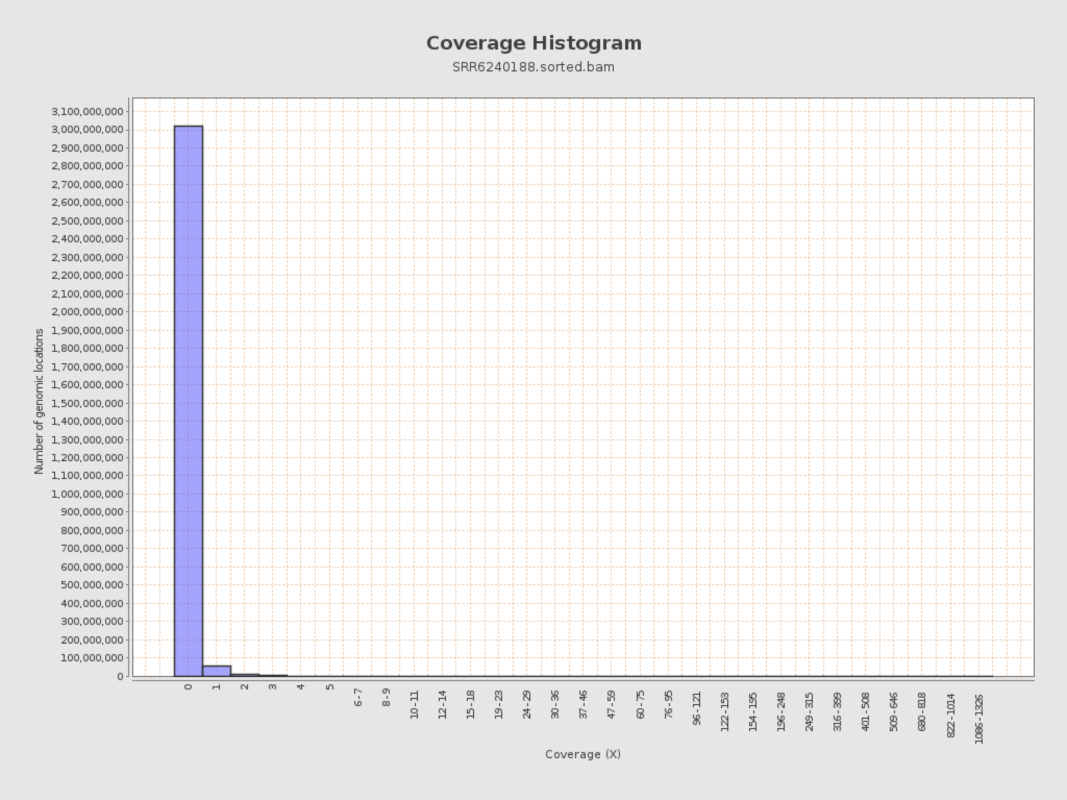
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11597651	0.0465	0.5799
chr2	243199373	14893499	0.0612	0.3718
chr3	198022430	5351451	0.027	0.2084
chr4	191154276	7235969	0.0379	0.2523
chr5	180915260	8086326	0.0447	0.2677
chr6	171115067	2005861	0.0117	0.1434
chr7	159138663	1952441	0.0123	0.2075

chr8	146364022	1963290	0.0134	0.83
chr9	141213431	3014762	0.0213	0.2731
chr10	135534747	5278674	0.0389	0.3847
chr11	135006516	3105288	0.023	0.2606
chr12	133851895	6020055	0.045	0.2716
chr13	115169878	3870778	0.0336	0.2283
chr14	107349540	3502245	0.0326	0.2455
chr15	102531392	903597	0.0088	0.1201
chr16	90354753	2955863	0.0327	0.2534
chr17	81195210	1328283	0.0164	0.1732
chr18	78077248	2403197	0.0308	0.5222
chr19	59128983	1049783	0.0178	0.3729
chr20	63025520	1375307	0.0218	0.1951
chr21	48129895	1682501	0.035	0.2481
chr22	51304566	1677202	0.0327	0.2239
chrMT	16571	19118	1.1537	1.3725
chrX	155270560	6587994	0.0424	0.2775
chrY	59373566	278236	0.0047	0.1084

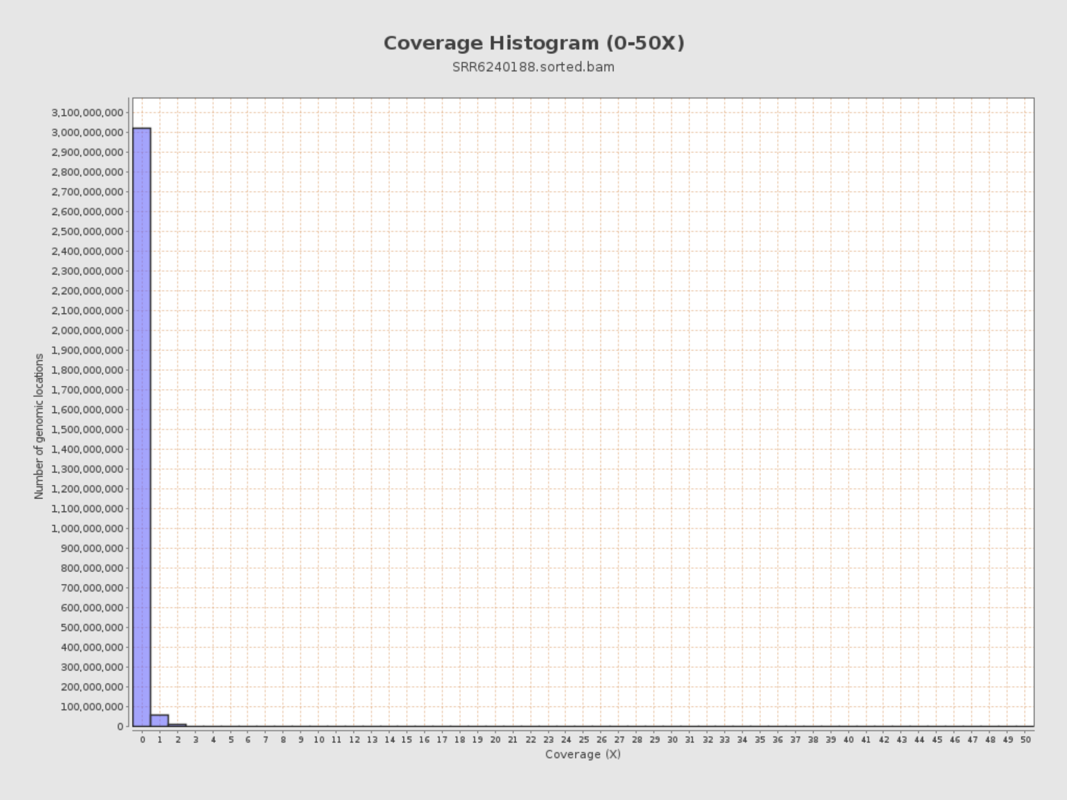
3. Results : Coverage across reference



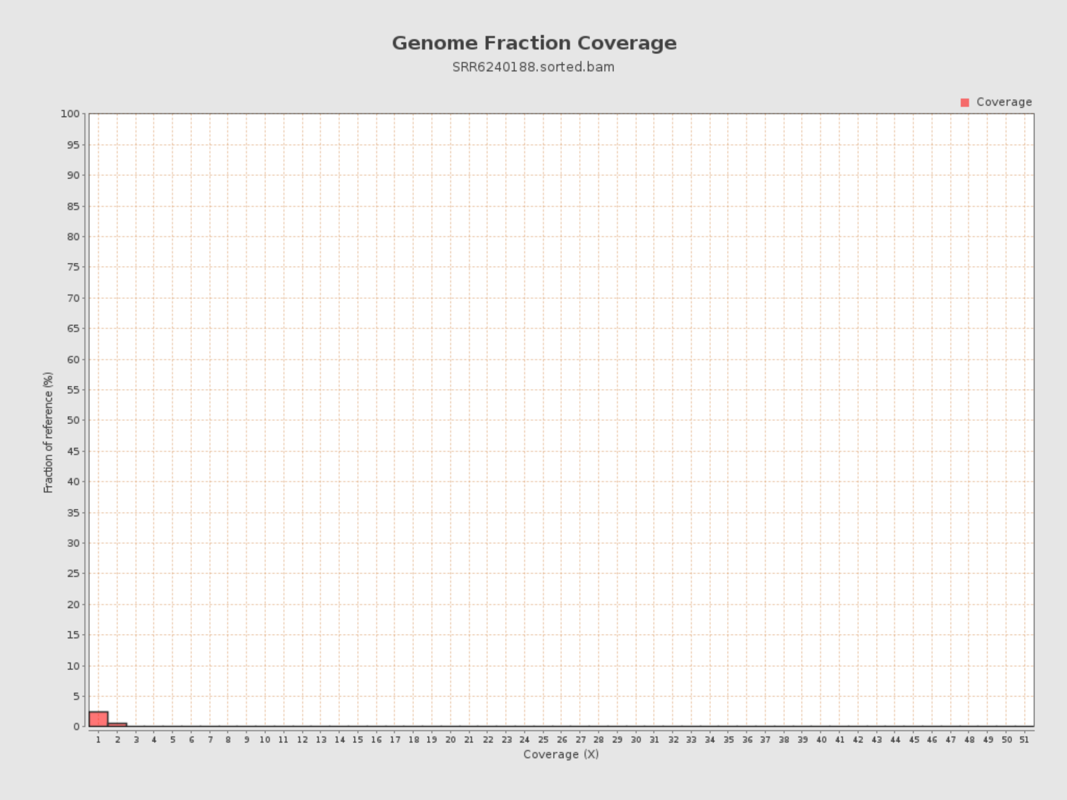
4. Results : Coverage Histogram



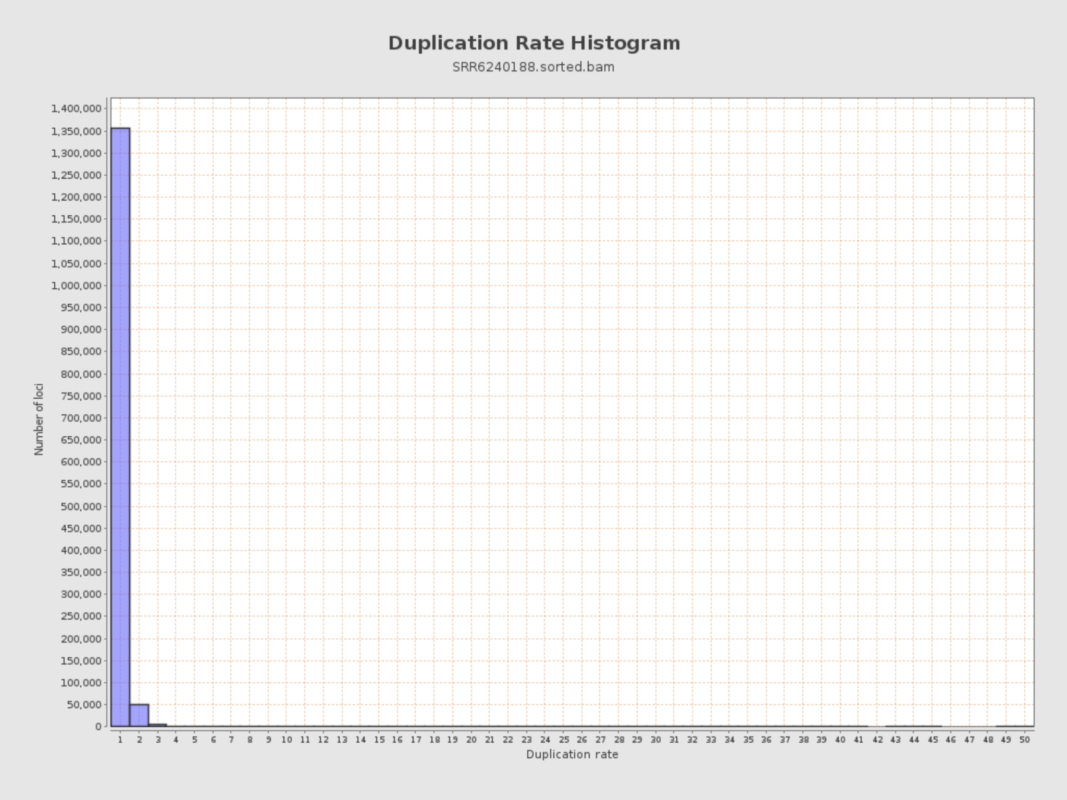
5. Results : Coverage Histogram (0-50X)



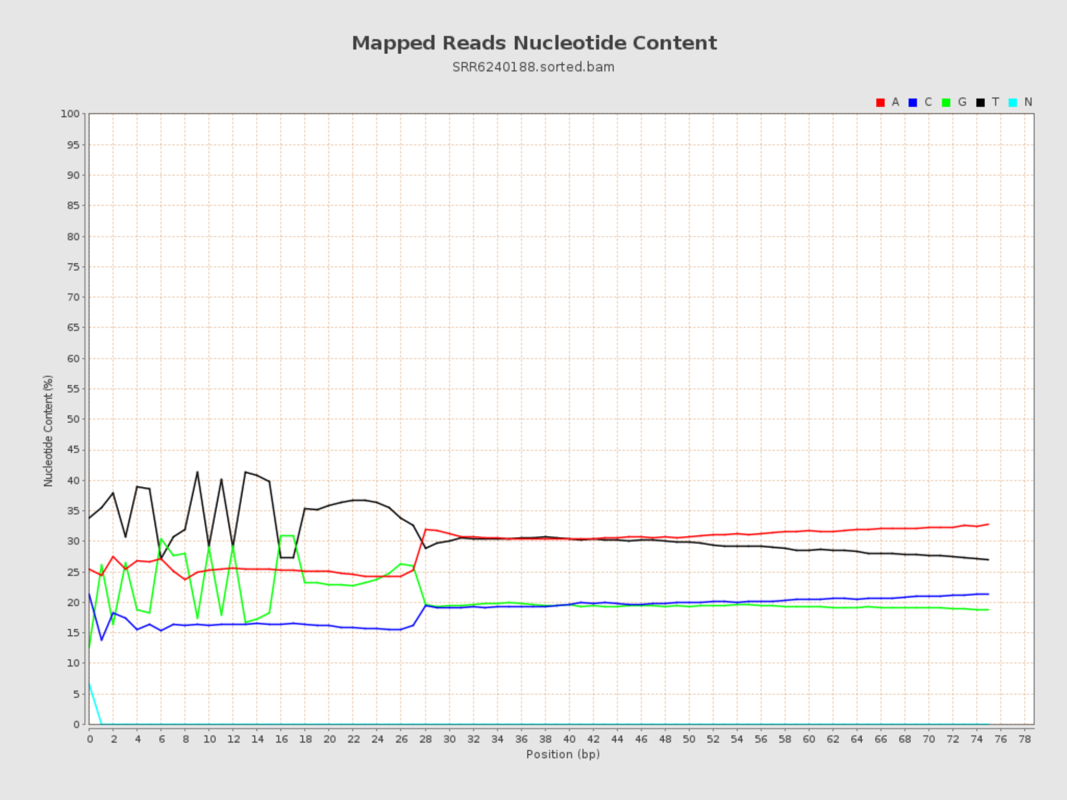
6. Results : Genome Fraction Coverage



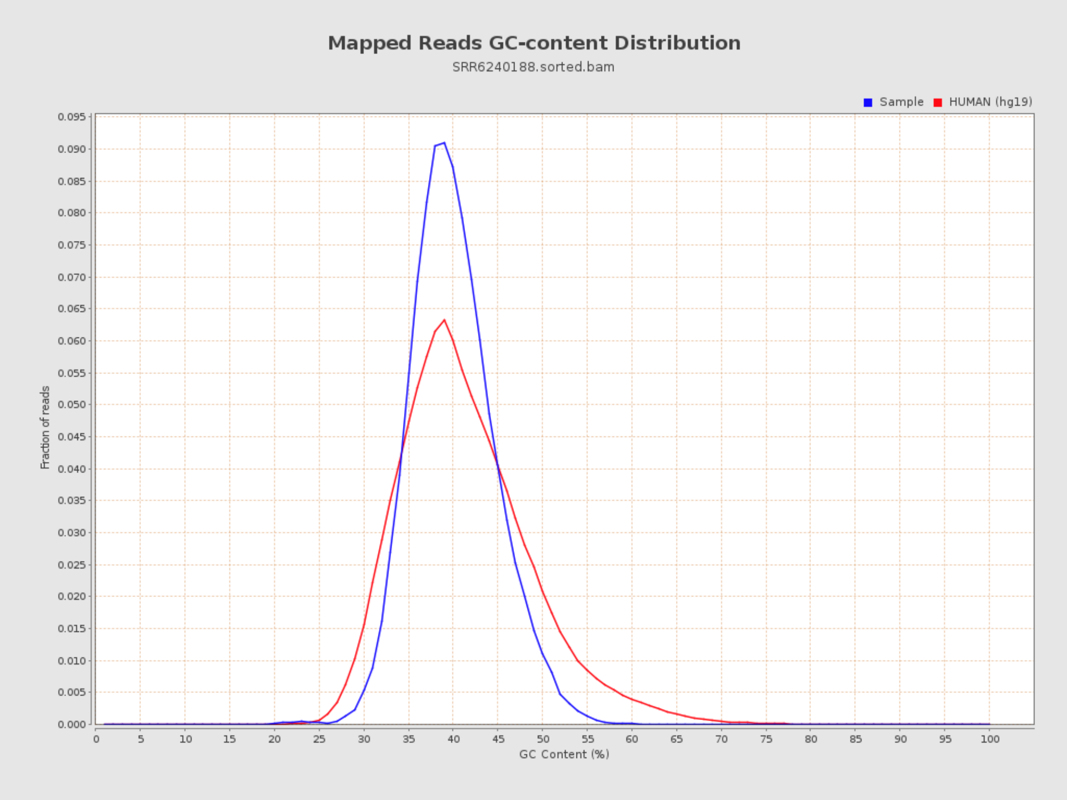
7. Results : Duplication Rate Histogram



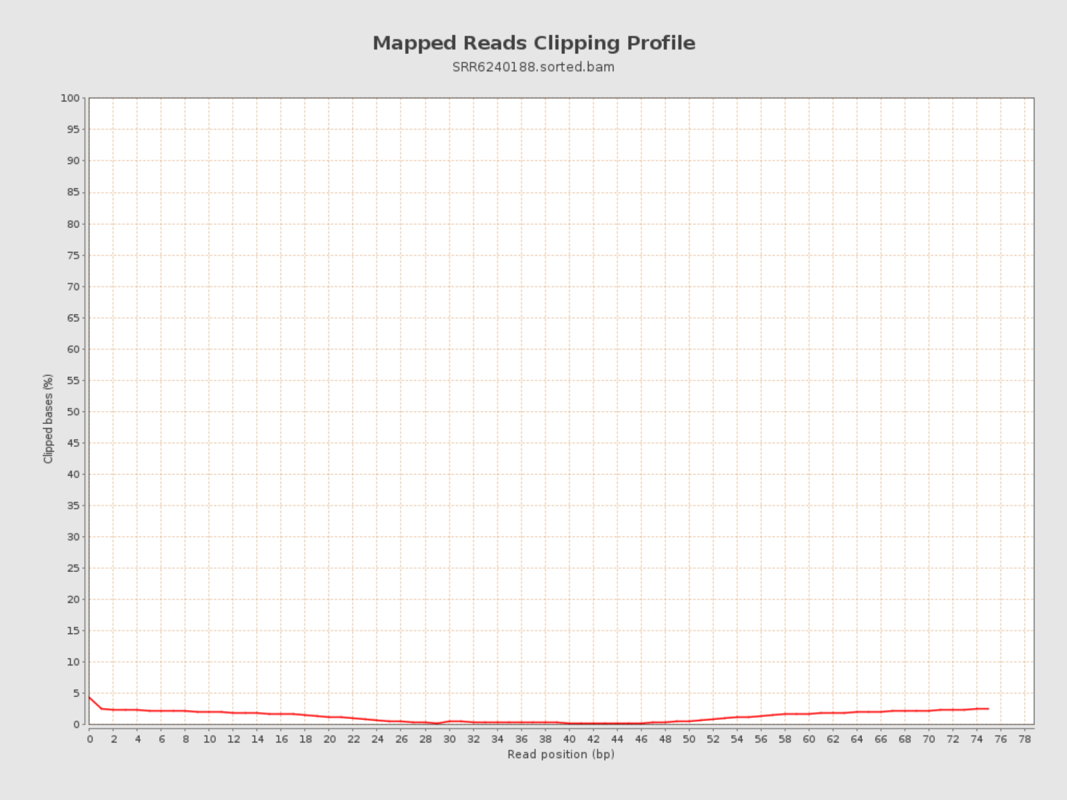
8. Results : Mapped Reads Nucleotide Content



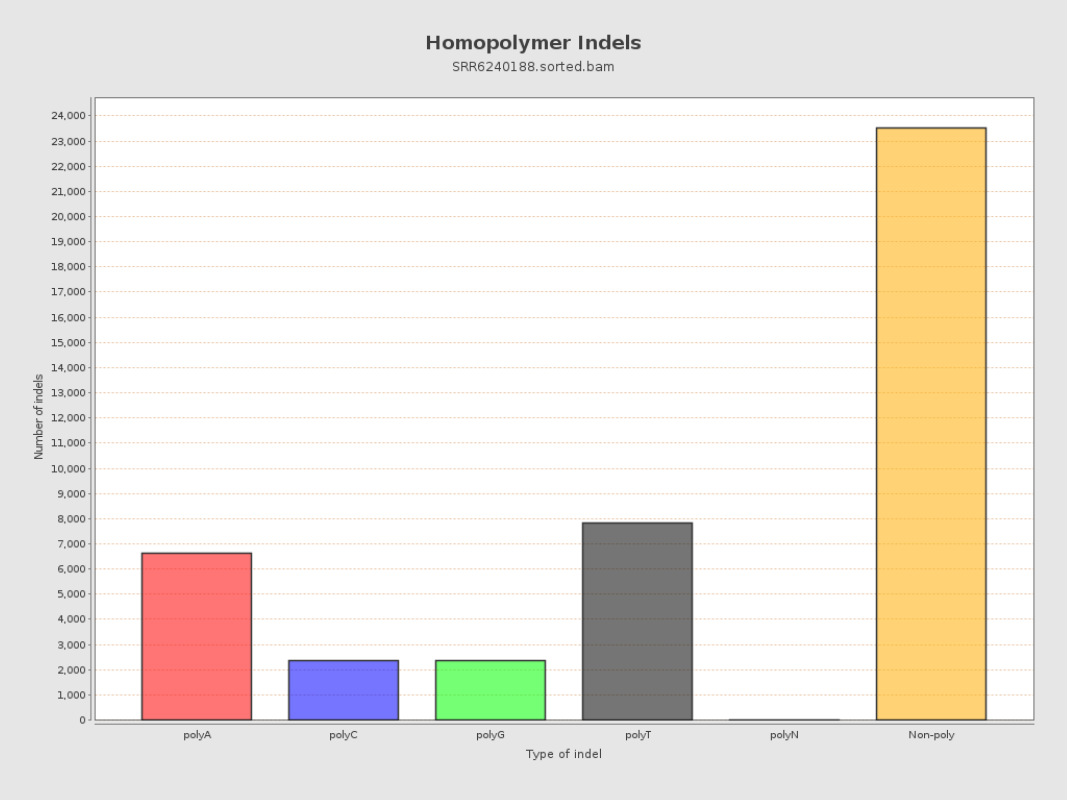
9. Results : Mapped Reads GC-content Distribution



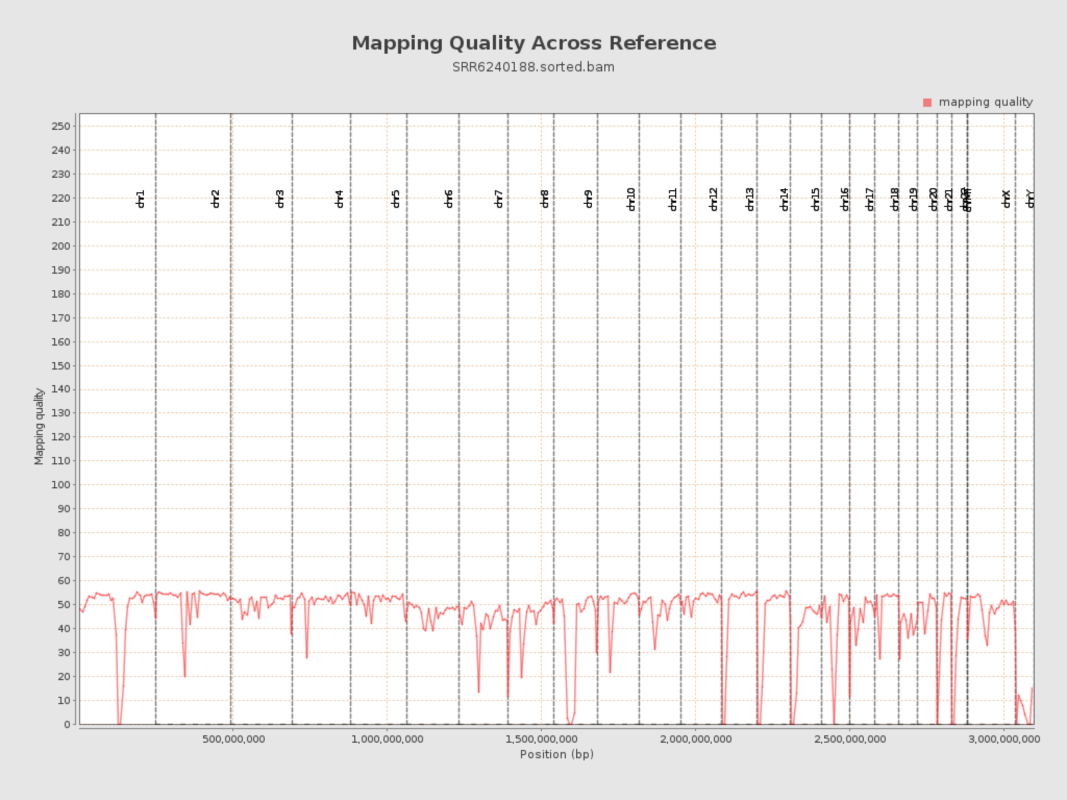
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram