Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:18:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231724.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_SRR6231724 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231724.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:18:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231724.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,429,704
Mapped reads	1,794,096 / 73.84%
Unmapped reads	635,608 / 26.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,896 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	86,551 / 3.56%
Duplication rate	3.7%
Clipped reads	1,129,230 / 46.48%

2.2. ACGT Content

Number/percentage of A's	29,003,016 / 25.88%
Number/percentage of C's	20,615,783 / 18.39%
Number/percentage of T's	35,007,555 / 31.23%
Number/percentage of G's	27,440,765 / 24.48%
Number/percentage of N's	18,907 / 0.02%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.3392

2.4. Mapping Quality

Mean Mapping Quality	42.14

2.5. Mismatches and indels

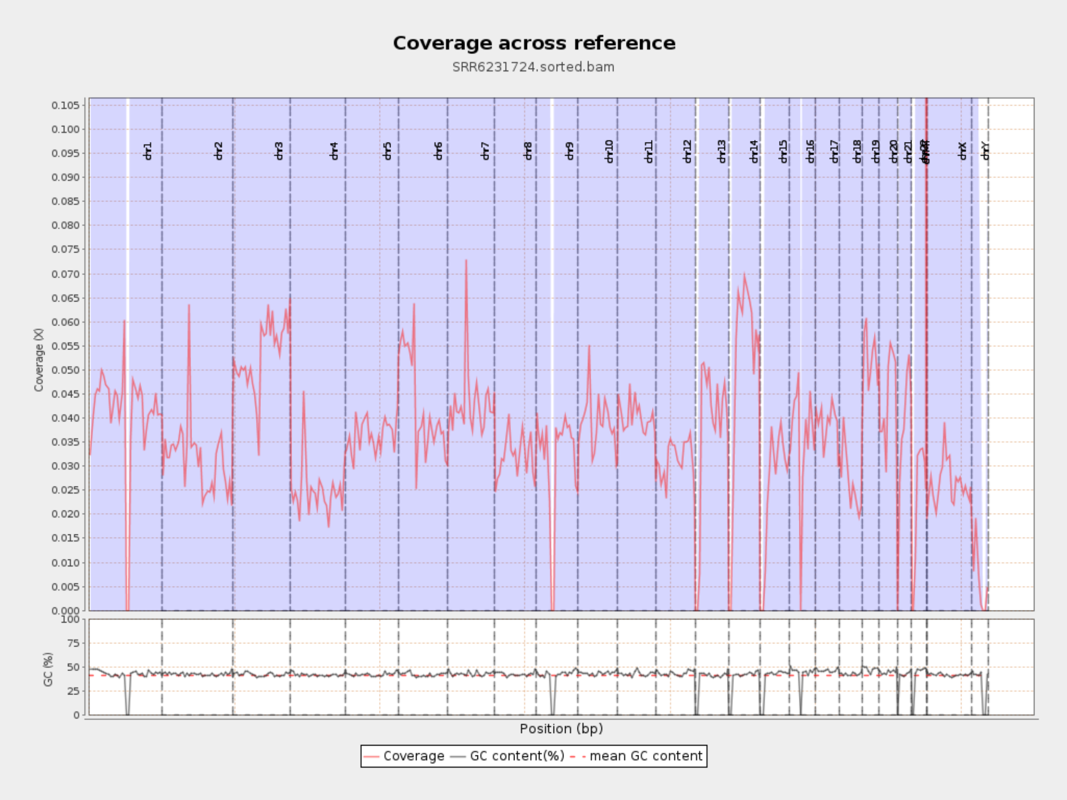
General error rate	0.88%
Mismatches	970,710
Insertions	9,095
Mapped reads with at least one insertion	0.5%
Deletions	39,205
Mapped reads with at least one deletion	2.16%
Homopolymer indels	45.93%

2.6. Chromosome stats

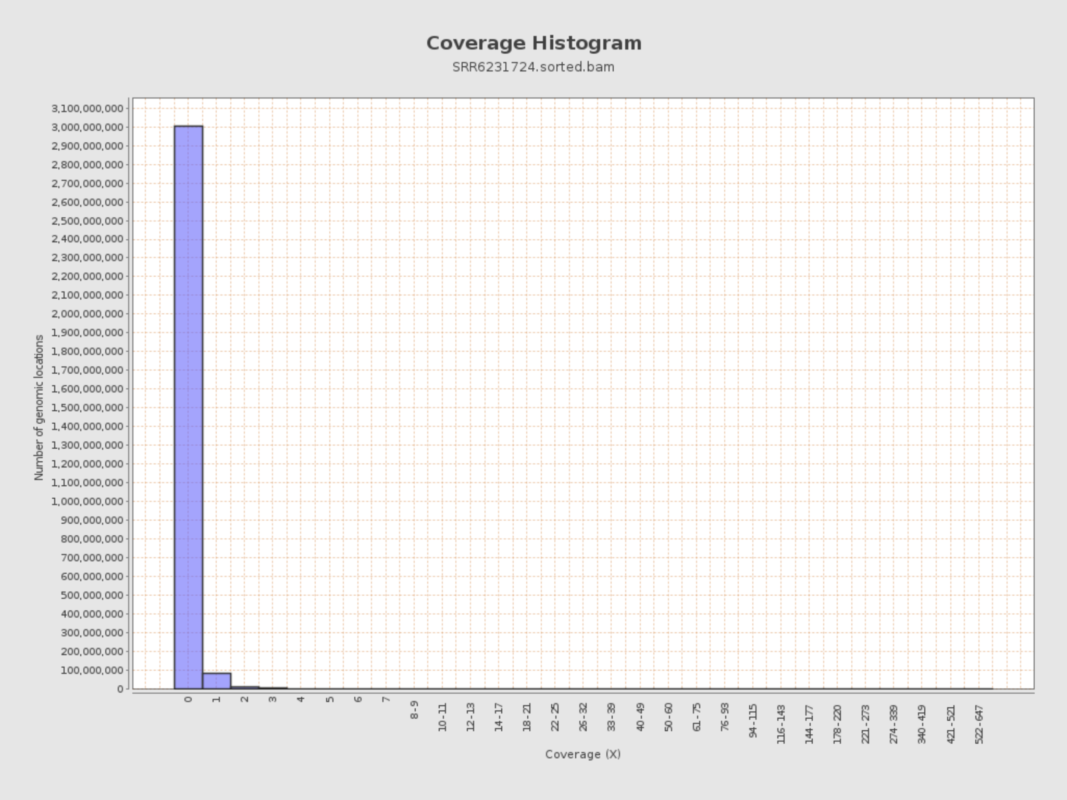
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10158227	0.0408	0.5233
chr2	243199373	7697428	0.0317	0.4165
chr3	198022430	10476035	0.0529	0.2706
chr4	191154276	4737626	0.0248	0.2105
chr5	180915260	6601964	0.0365	0.227
chr6	171115067	7320599	0.0428	0.3044
chr7	159138663	6878158	0.0432	0.5557

chr8	146364022	4682226	0.032	0.3612
chr9	141213431	4418370	0.0313	0.2911
chr10	135534747	5334089	0.0394	0.3037
chr11	135006516	5400242	0.04	0.4034
chr12	133851895	4225622	0.0316	0.2092
chr13	115169878	4274970	0.0371	0.2368
chr14	107349540	5454062	0.0508	0.2814
chr15	102531392	2647119	0.0258	0.2067
chr16	90354753	3246245	0.0359	0.2469
chr17	81195210	3152483	0.0388	0.2725
chr18	78077248	2121092	0.0272	0.4792
chr19	59128983	3094732	0.0523	0.4202
chr20	63025520	2767363	0.0439	0.2669
chr21	48129895	1789192	0.0372	0.2363
chr22	51304566	1139145	0.0222	0.1714
chrMT	16571	73479	4.4342	4.1175
chrX	155270560	4087619	0.0263	0.2169
chrY	59373566	377784	0.0064	0.1227

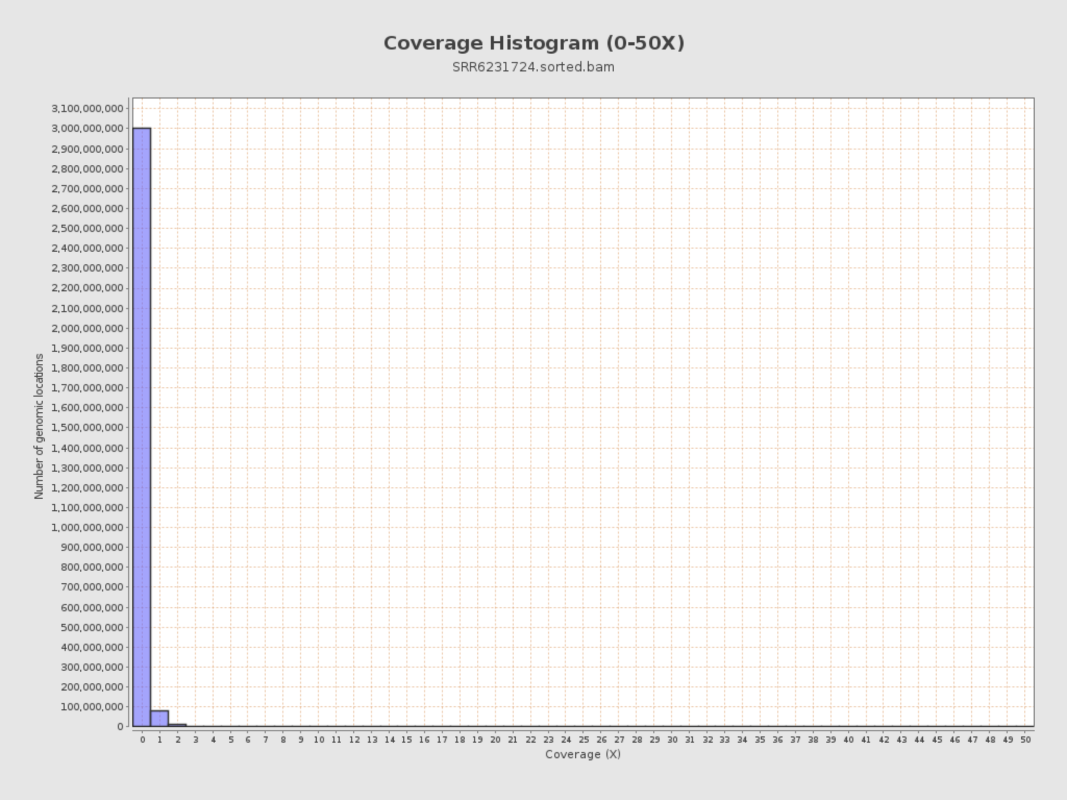
3. Results : Coverage across reference



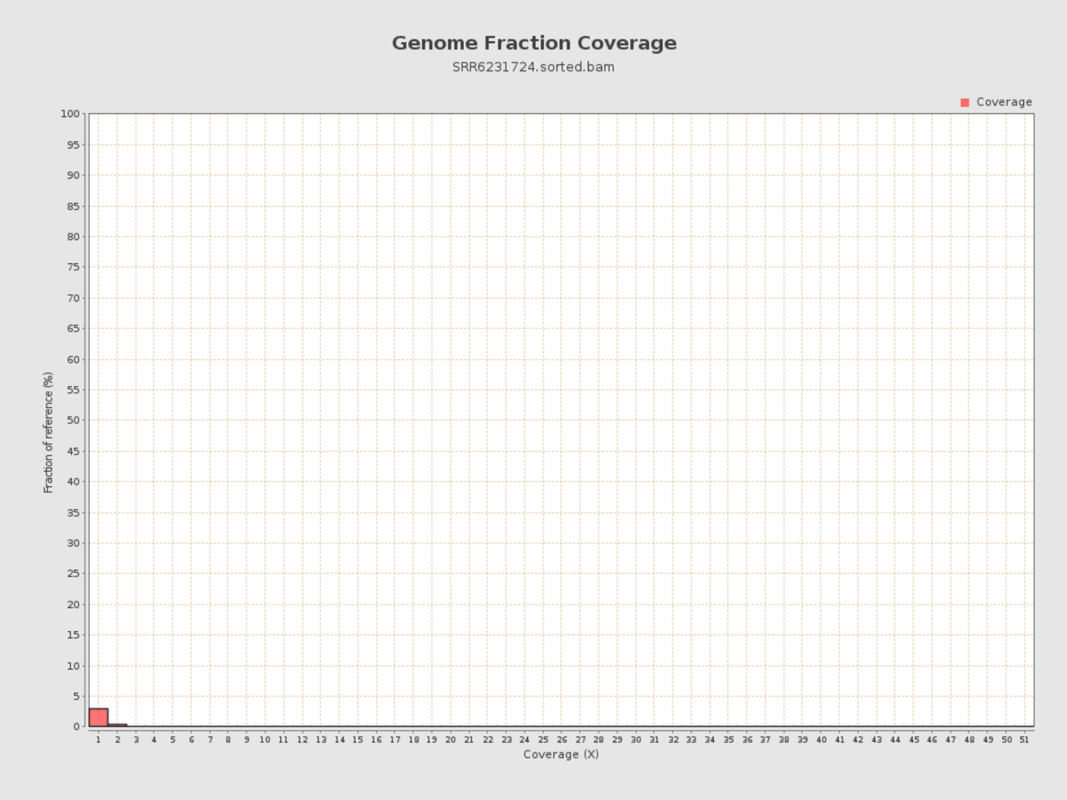
4. Results : Coverage Histogram



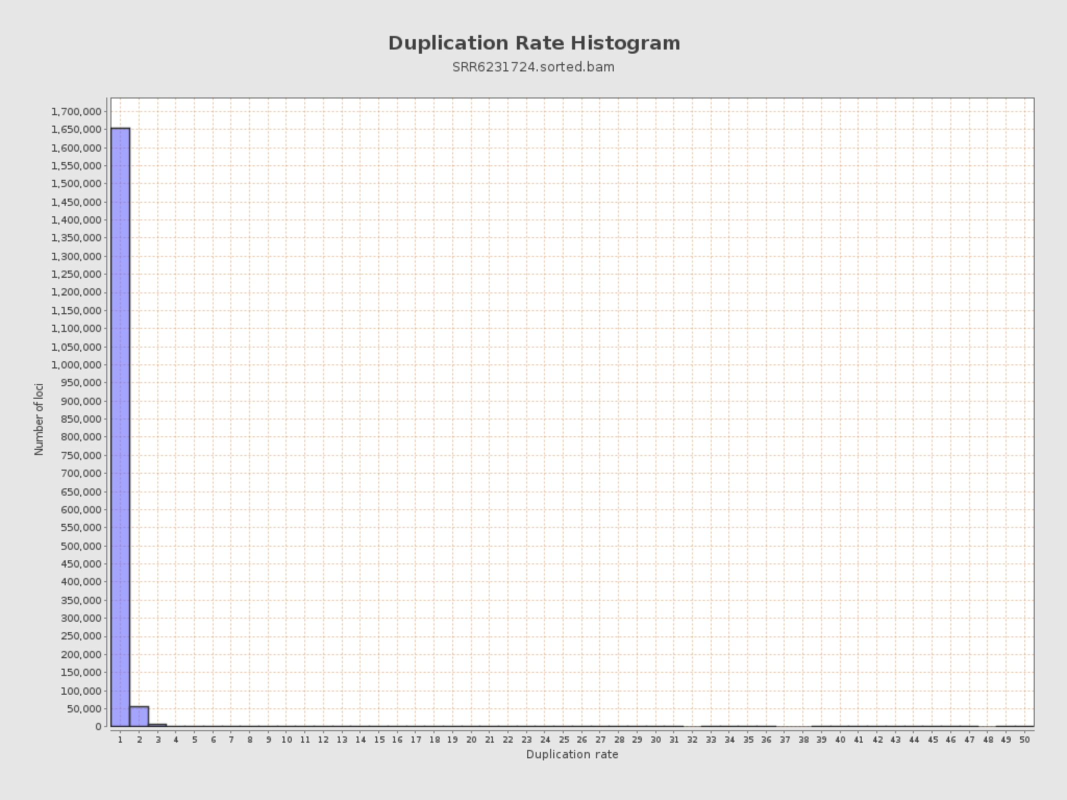
5. Results : Coverage Histogram (0-50X)



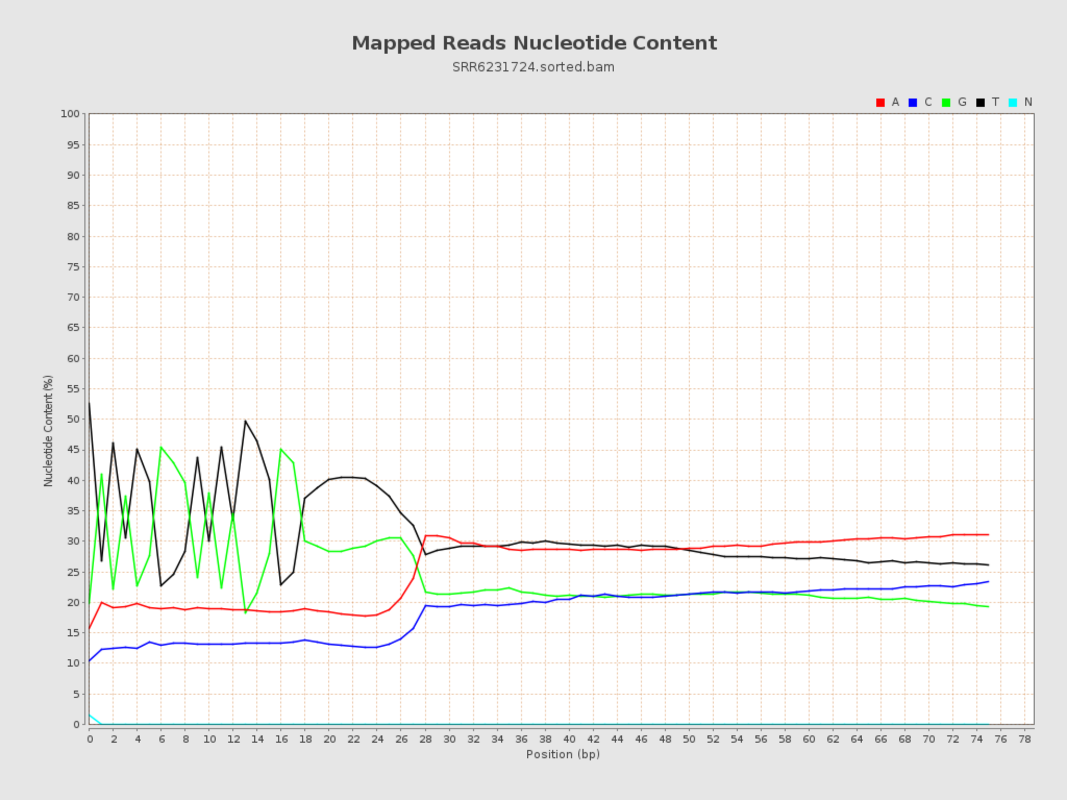
6. Results : Genome Fraction Coverage



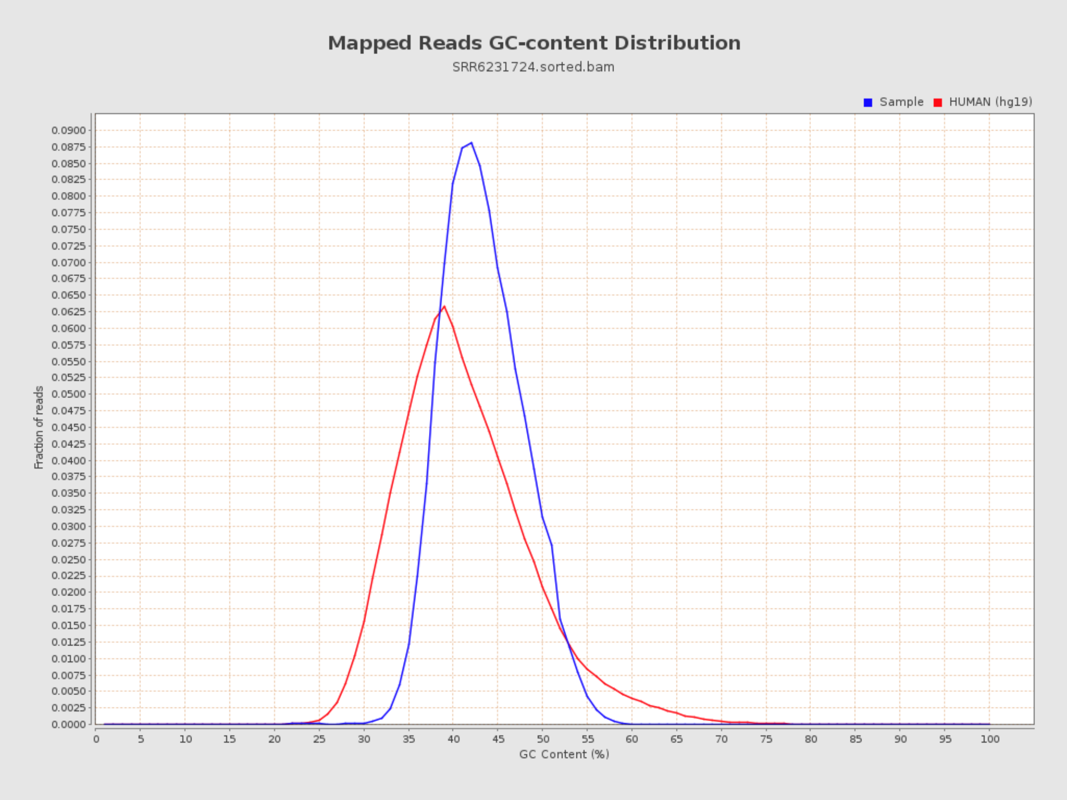
7. Results : Duplication Rate Histogram



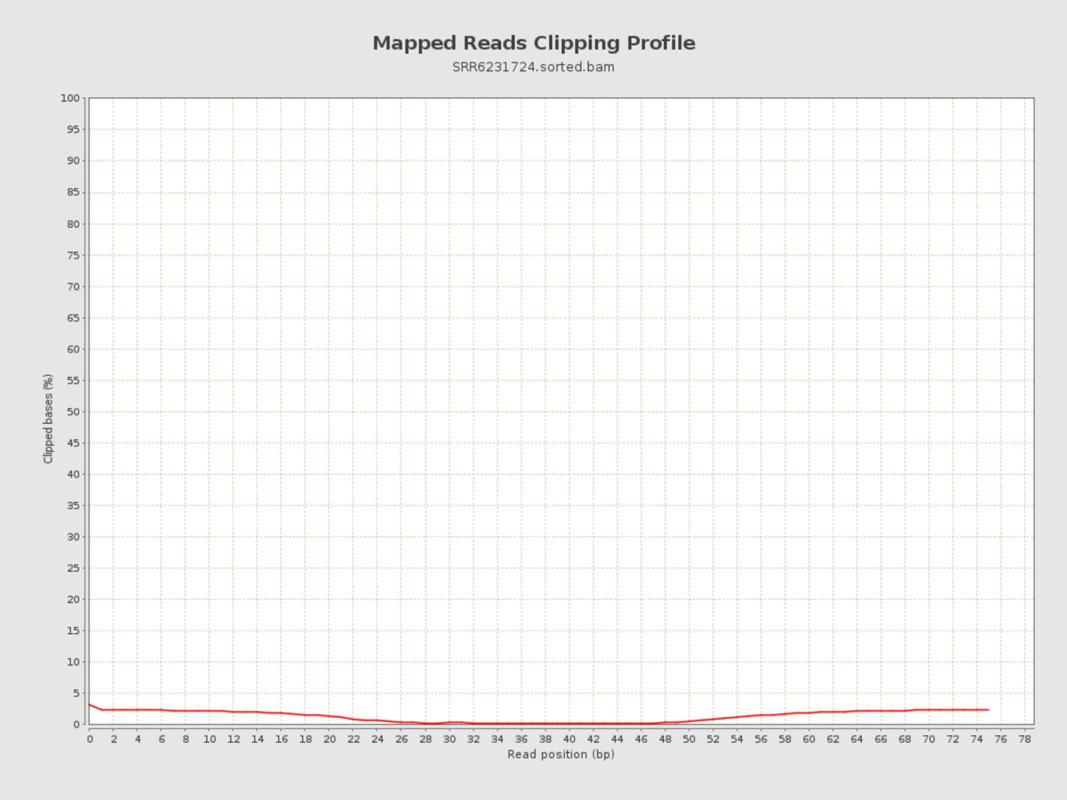
8. Results : Mapped Reads Nucleotide Content



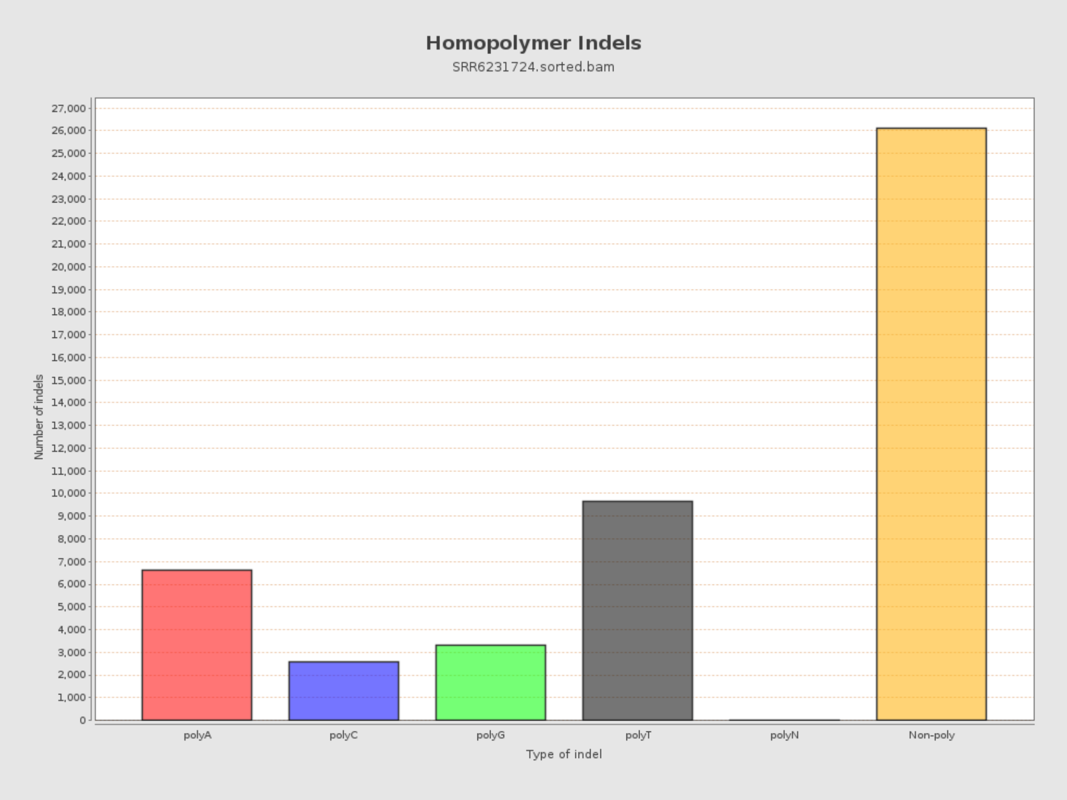
9. Results : Mapped Reads GC-content Distribution



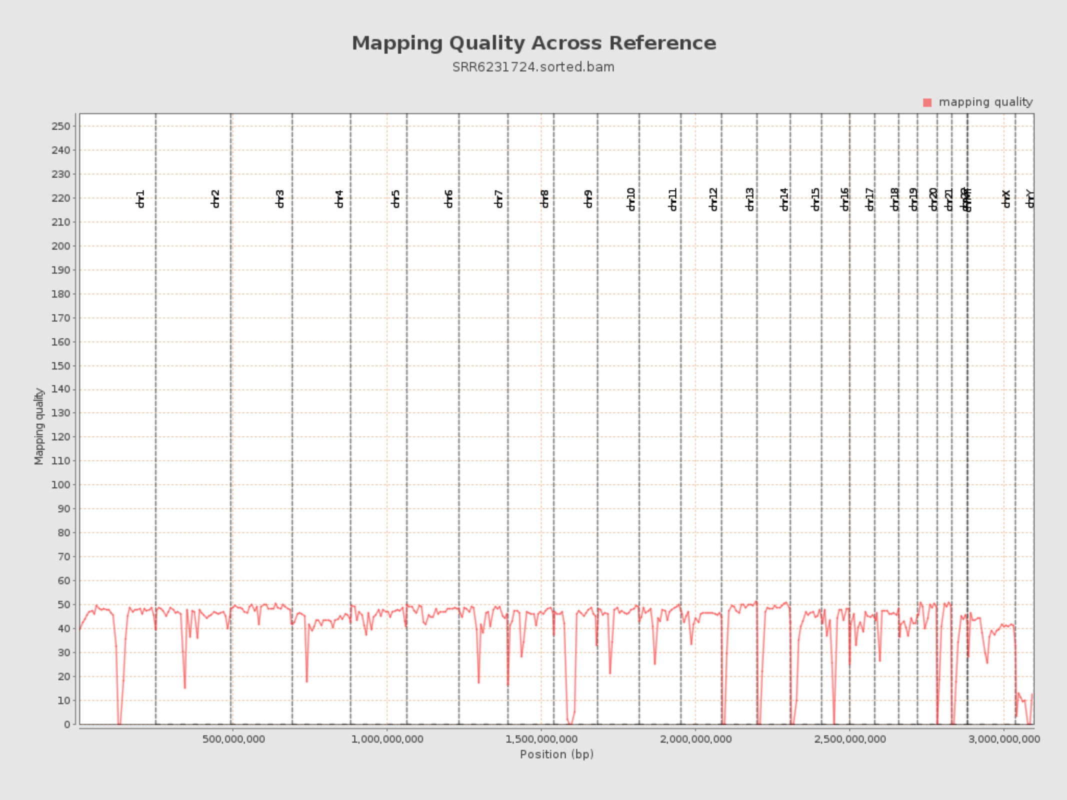
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram