Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:44:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013267.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_SRR6013267 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013267.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:44:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013267.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,127,917
Mapped reads	1,886,177 / 88.64%
Unmapped reads	241,740 / 11.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,824 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	90,039 / 4.23%
Duplication rate	3.98%
Clipped reads	835,292 / 39.25%

2.2. ACGT Content

Number/percentage of A's	34,457,438 / 27.43%
Number/percentage of C's	22,977,219 / 18.29%
Number/percentage of T's	40,328,129 / 32.11%
Number/percentage of G's	27,817,841 / 22.15%
Number/percentage of N's	27,372 / 0.02%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0406

Standard Deviation	0.3214

2.4. Mapping Quality

Mean Mapping Quality	43.24

2.5. Mismatches and indels

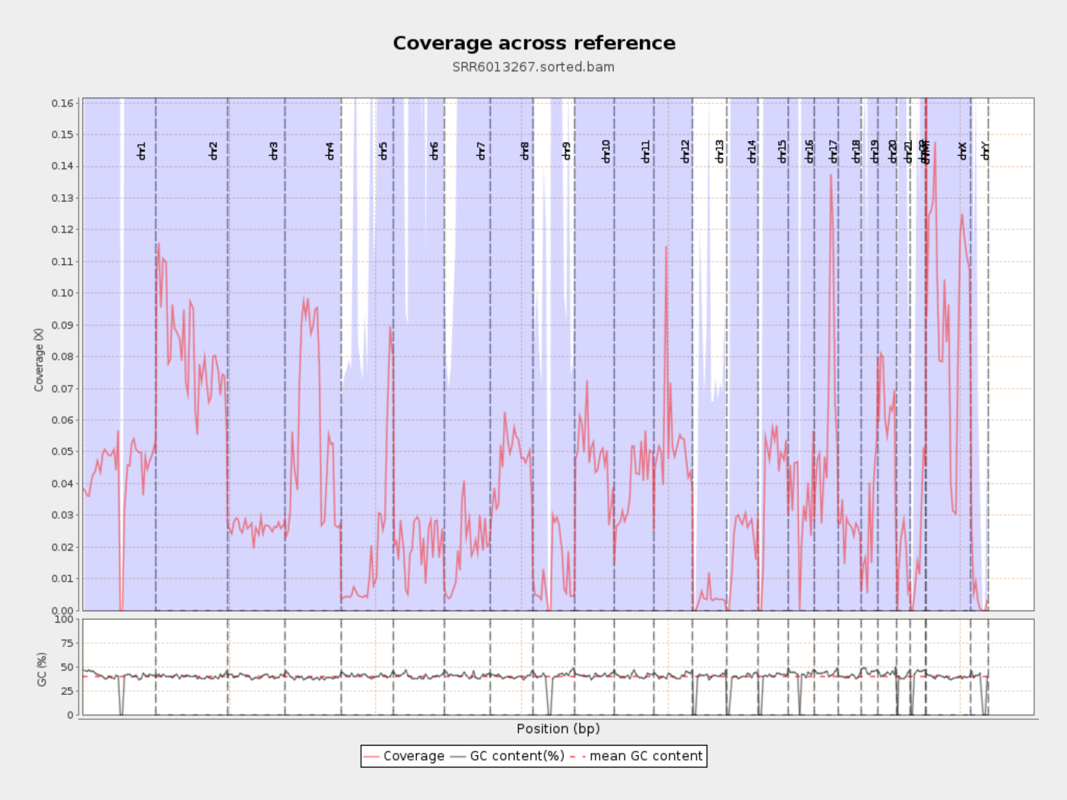
General error rate	0.81%
Mismatches	998,013
Insertions	8,406
Mapped reads with at least one insertion	0.44%
Deletions	32,329
Mapped reads with at least one deletion	1.7%
Homopolymer indels	46.21%

2.6. Chromosome stats

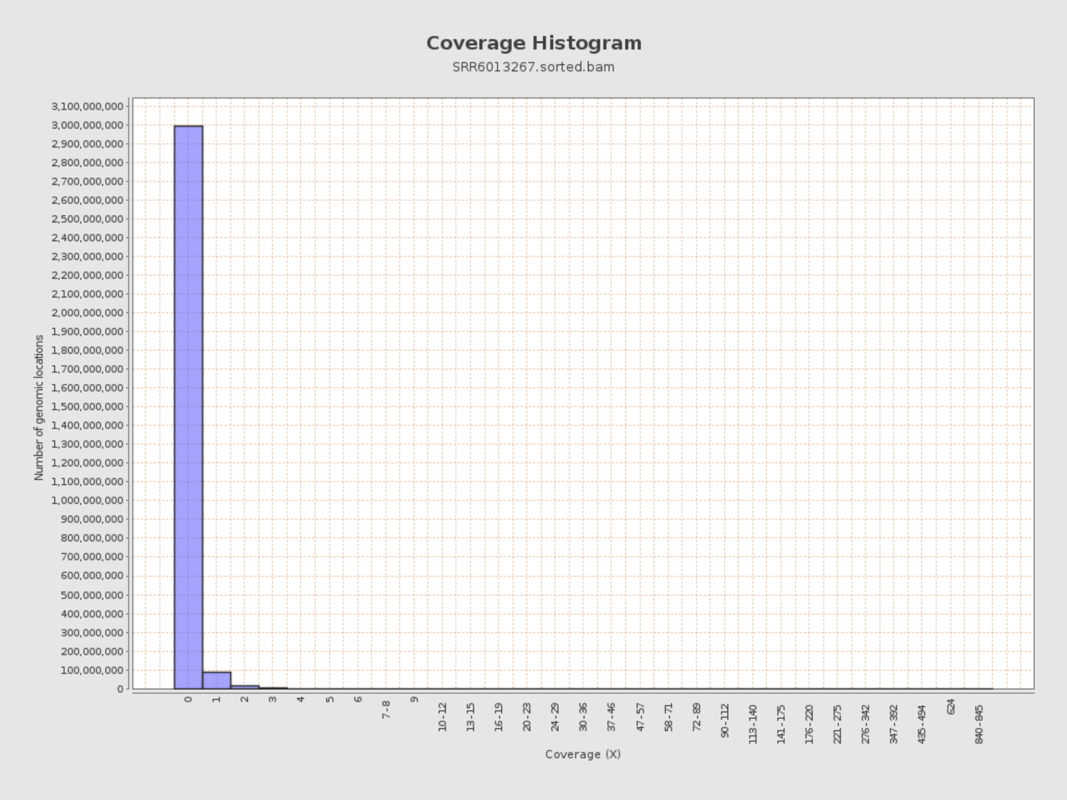
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10825794	0.0434	0.3815
chr2	243199373	19959314	0.0821	0.5328
chr3	198022430	5213502	0.0263	0.1882
chr4	191154276	11176757	0.0585	0.2833
chr5	180915260	3682426	0.0204	0.1705
chr6	171115067	3547818	0.0207	0.2158
chr7	159138663	2998602	0.0188	0.2184

chr8	146364022	6862014	0.0469	0.3898
chr9	141213431	1648626	0.0117	0.2561
chr10	135534747	6617165	0.0488	0.3735
chr11	135006516	5400630	0.04	0.2635
chr12	133851895	7186370	0.0537	0.2724
chr13	115169878	424098	0.0037	0.0788
chr14	107349540	2373488	0.0221	0.1855
chr15	102531392	4251179	0.0415	0.2348
chr16	90354753	3054046	0.0338	0.2229
chr17	81195210	5235951	0.0645	0.3174
chr18	78077248	2048178	0.0262	0.4628
chr19	59128983	1626109	0.0275	0.3445
chr20	63025520	4094830	0.065	0.3899
chr21	48129895	739415	0.0154	0.1519
chr22	51304566	998872	0.0195	0.1599
chrMT	16571	447674	27.0155	15.345
chrX	155270560	14948535	0.0963	0.4003
chrY	59373566	301610	0.0051	0.0915

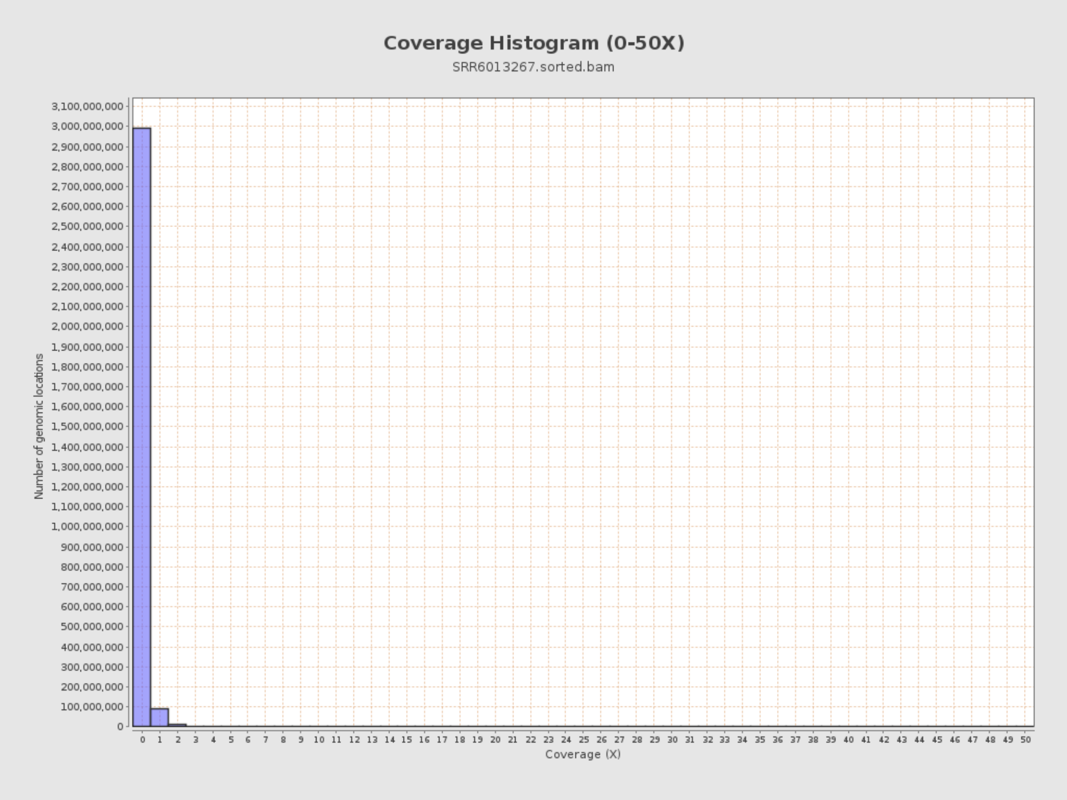
3. Results : Coverage across reference



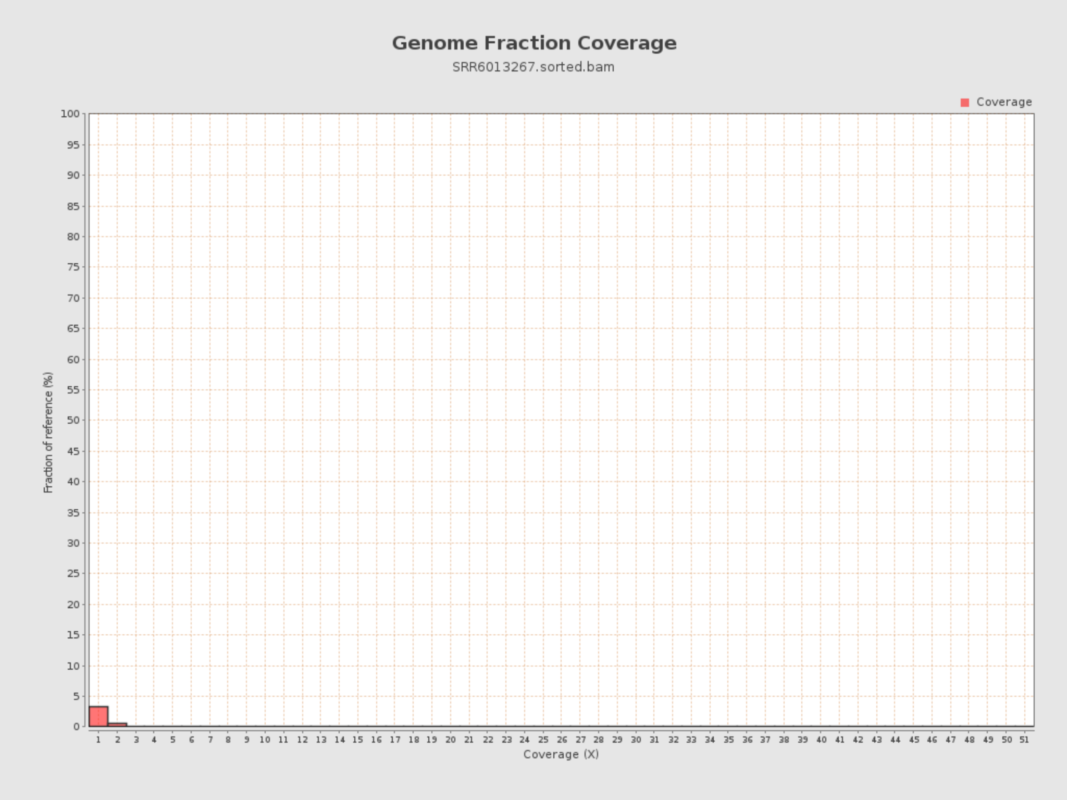
4. Results : Coverage Histogram



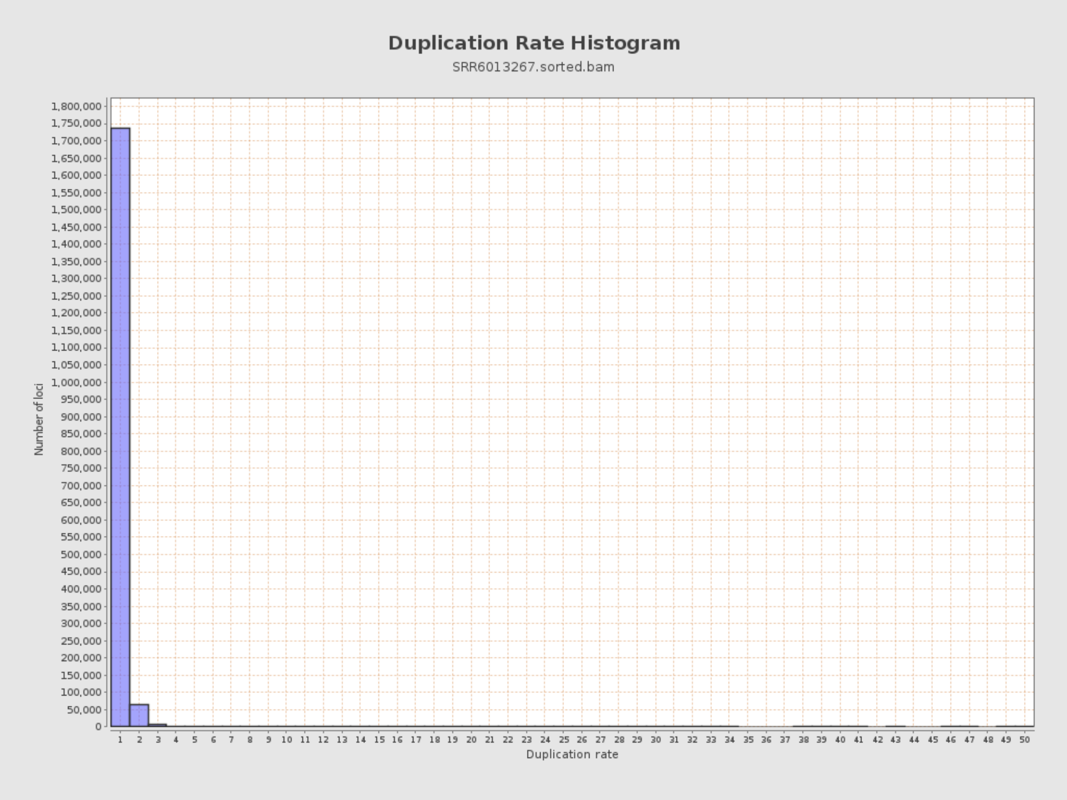
5. Results : Coverage Histogram (0-50X)



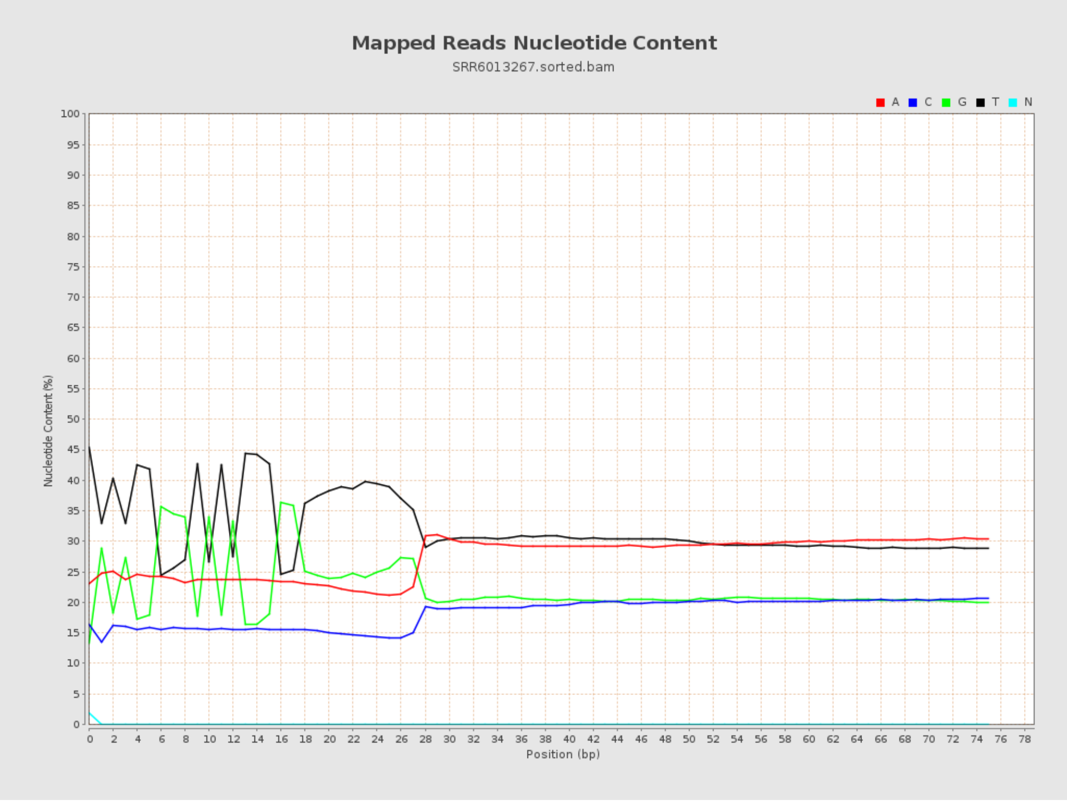
6. Results : Genome Fraction Coverage



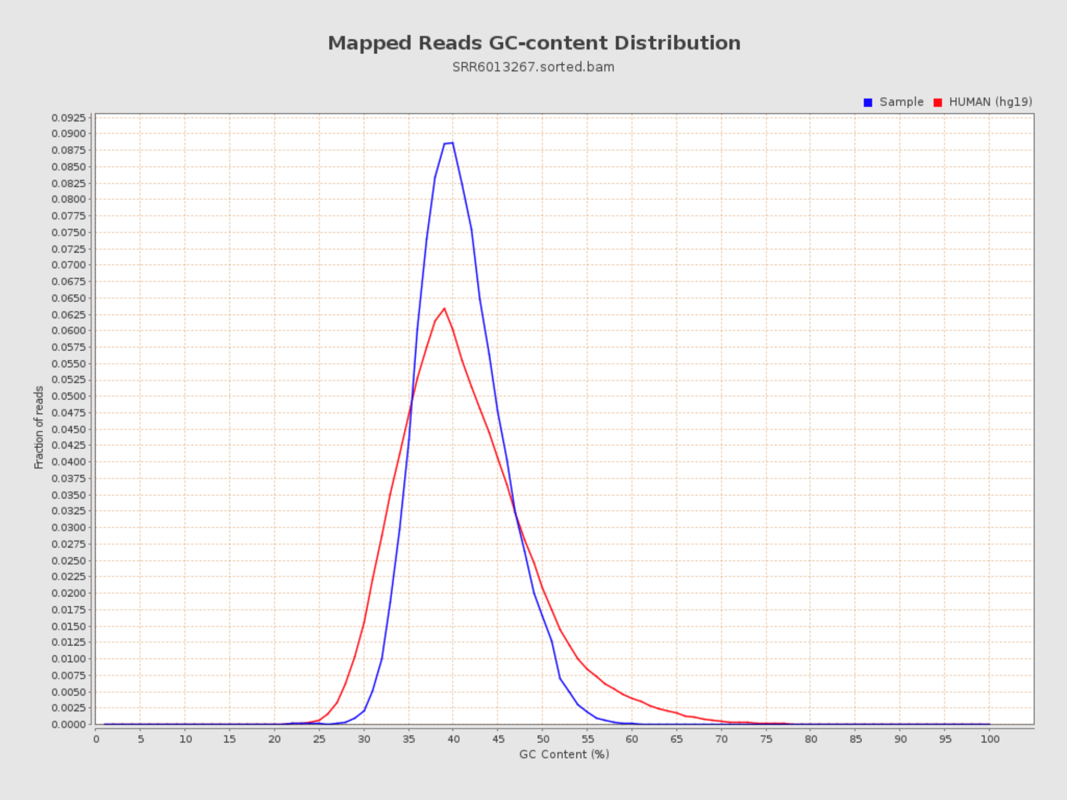
7. Results : Duplication Rate Histogram



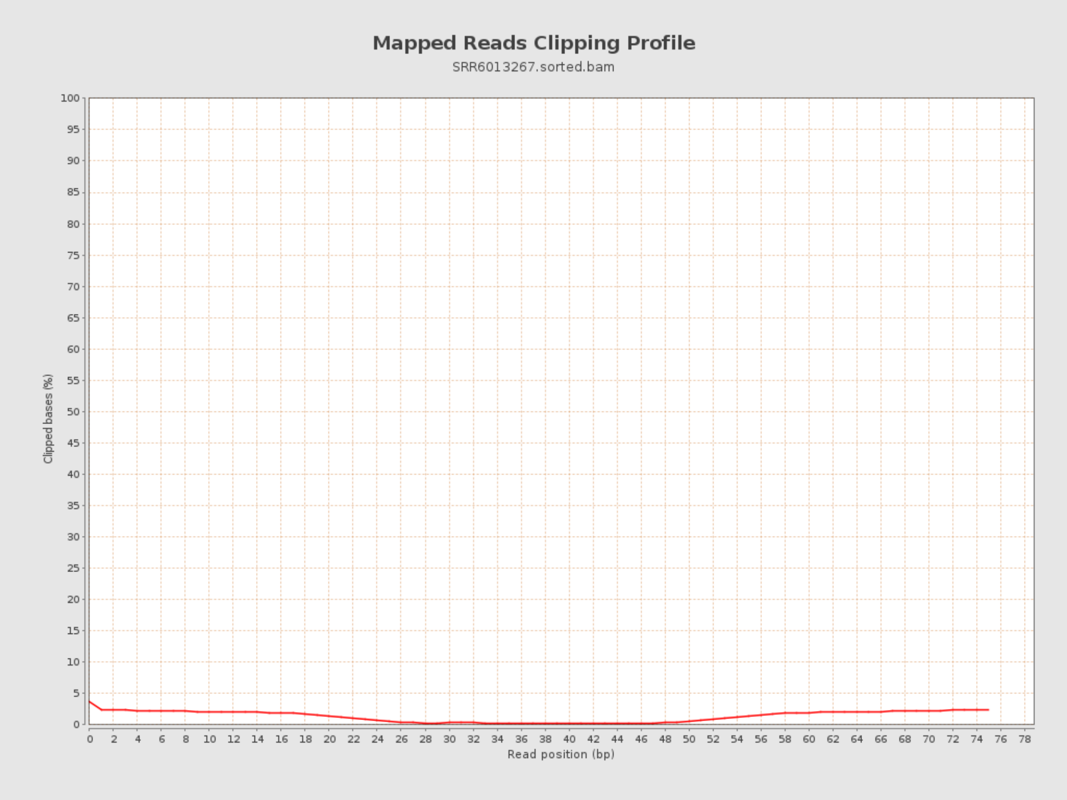
8. Results : Mapped Reads Nucleotide Content



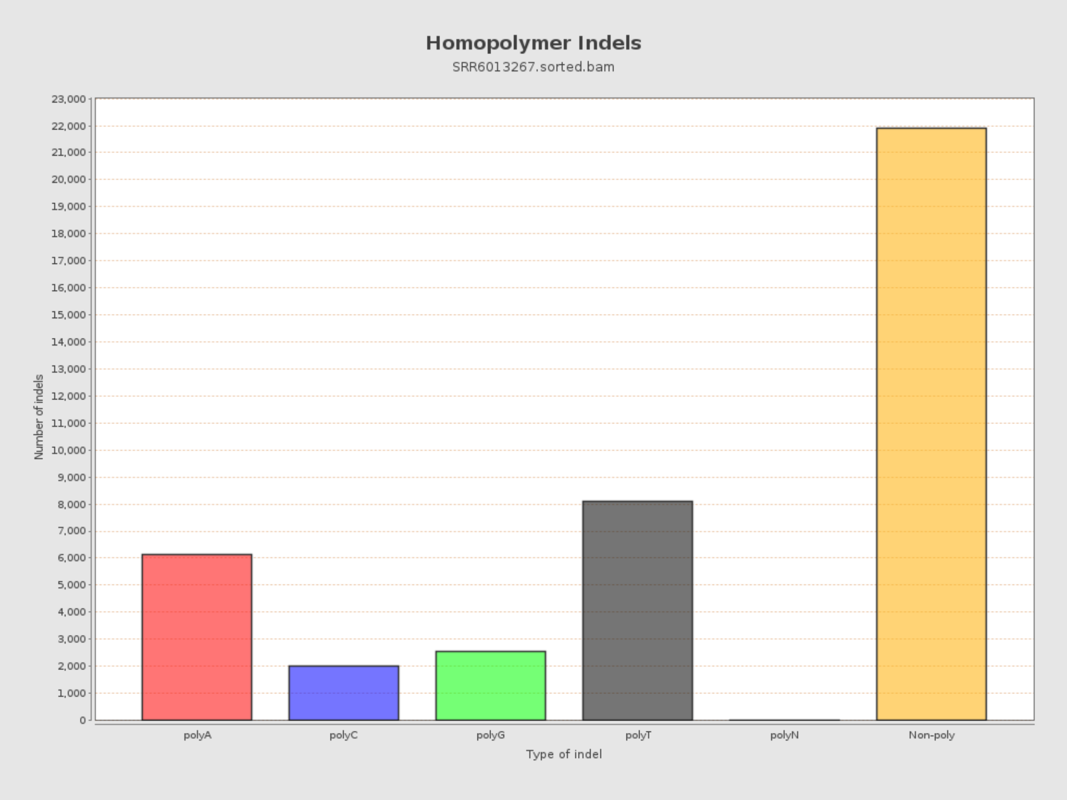
9. Results : Mapped Reads GC-content Distribution



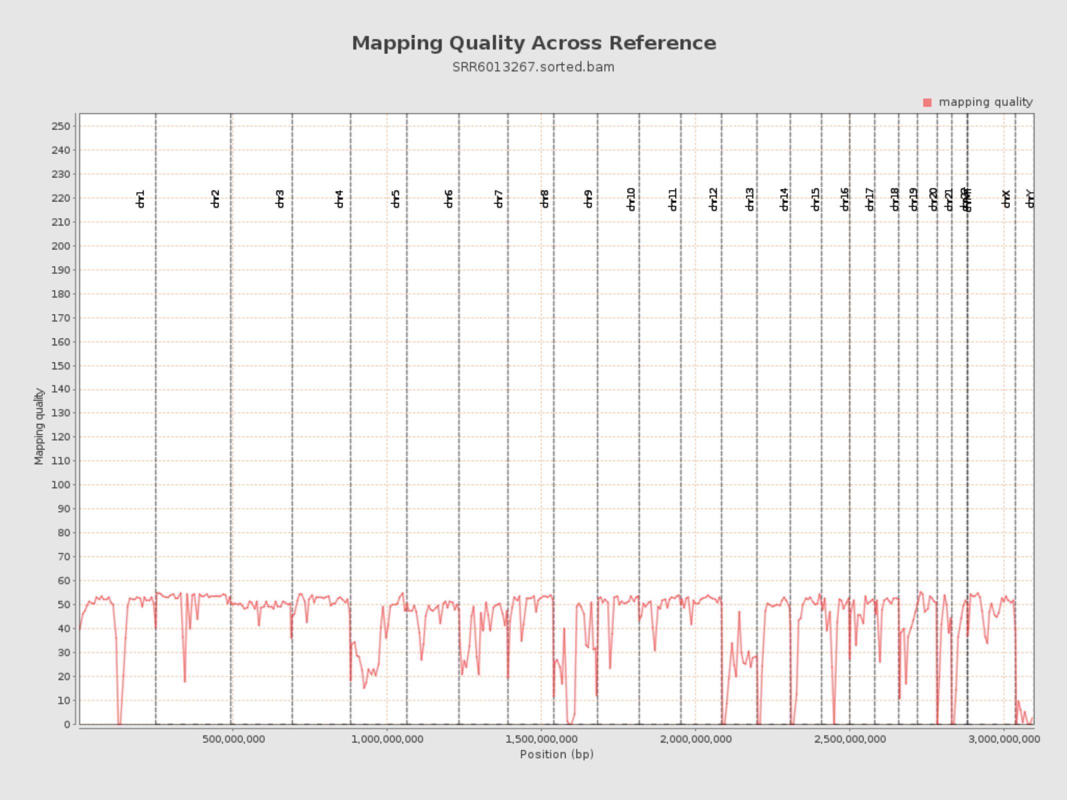
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram