Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:58:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004037.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_SRR6004037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004037.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:58:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,408,275
Mapped reads	2,173,064 / 90.23%
Unmapped reads	235,211 / 9.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,967 / 0.7%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	77,794 / 3.23%
Duplication rate	2.66%
Clipped reads	890,230 / 36.97%

2.2. ACGT Content

Number/percentage of A's	41,444,786 / 28.2%
Number/percentage of C's	27,729,080 / 18.87%
Number/percentage of T's	45,398,780 / 30.89%
Number/percentage of G's	32,279,487 / 21.96%
Number/percentage of N's	113,759 / 0.08%
GC Percentage	40.83%

2.3. Coverage

Mean	0.0475

Standard Deviation	0.4016

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

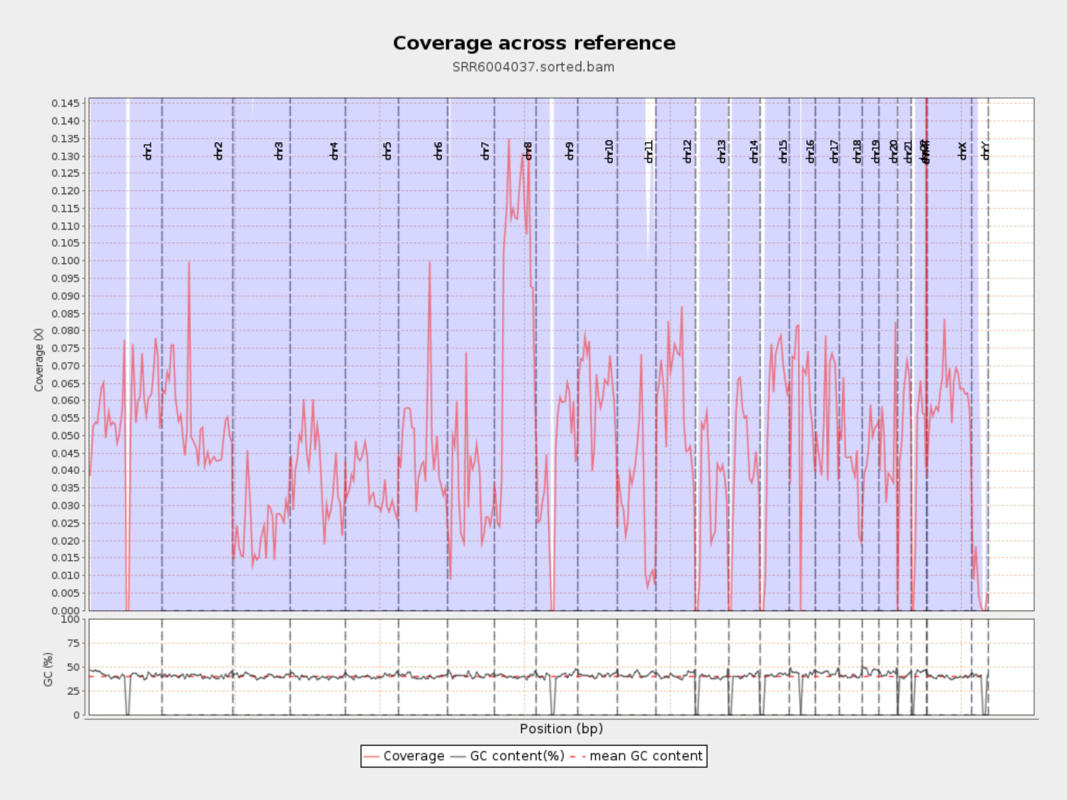
General error rate	0.9%
Mismatches	1,297,193
Insertions	11,514
Mapped reads with at least one insertion	0.52%
Deletions	39,468
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.16%

2.6. Chromosome stats

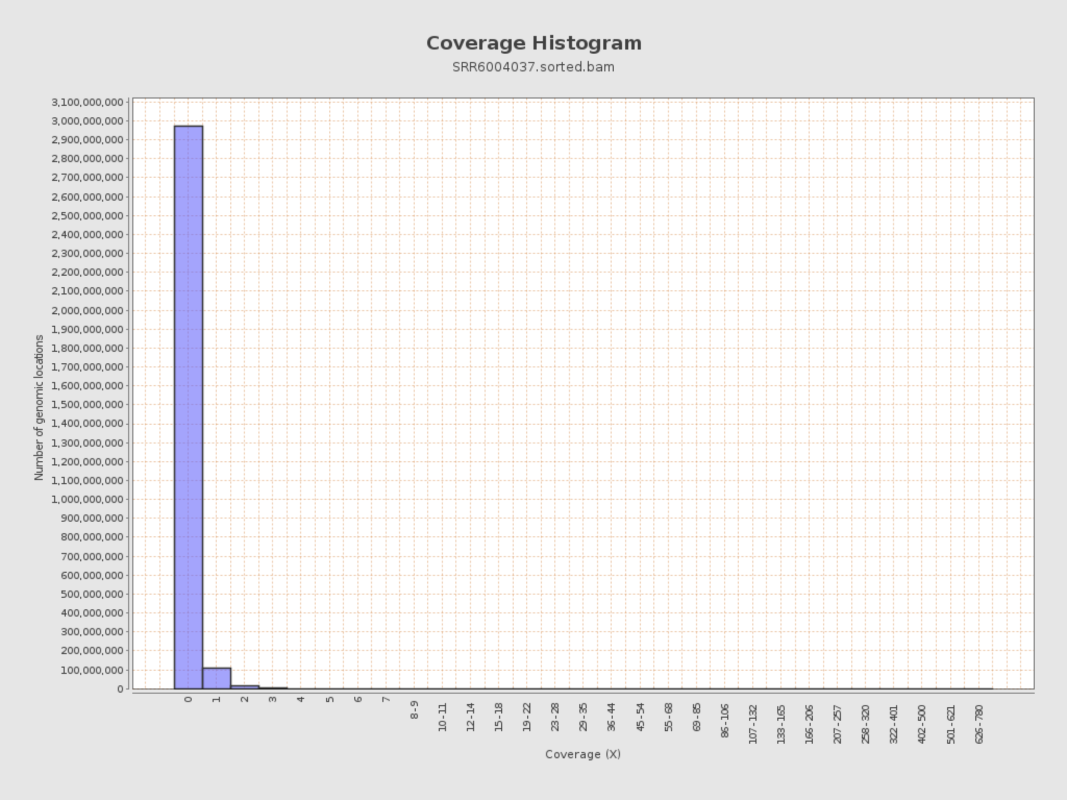
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13822592	0.0555	0.7101
chr2	243199373	13062293	0.0537	0.4748
chr3	198022430	4597843	0.0232	0.173
chr4	191154276	7530271	0.0394	0.24
chr5	180915260	6381455	0.0353	0.2147
chr6	171115067	8089469	0.0473	0.2727
chr7	159138663	5538661	0.0348	0.5443

chr8	146364022	13711120	0.0937	0.564
chr9	141213431	5827357	0.0413	0.3871
chr10	135534747	8693689	0.0641	0.3904
chr11	135006516	4159501	0.0308	0.3021
chr12	133851895	8303889	0.062	0.2835
chr13	115169878	3664088	0.0318	0.1992
chr14	107349540	4541372	0.0423	0.2514
chr15	102531392	5533414	0.054	0.2707
chr16	90354753	5395376	0.0597	0.3388
chr17	81195210	4566655	0.0562	0.3037
chr18	78077248	3326422	0.0426	0.7396
chr19	59128983	2826796	0.0478	0.5032
chr20	63025520	2962235	0.047	0.2544
chr21	48129895	2519774	0.0524	0.2733
chr22	51304566	2033590	0.0396	0.2238
chrMT	16571	6358	0.3837	0.7128
chrX	155270560	9557335	0.0616	0.3175
chrY	59373566	381032	0.0064	0.1308

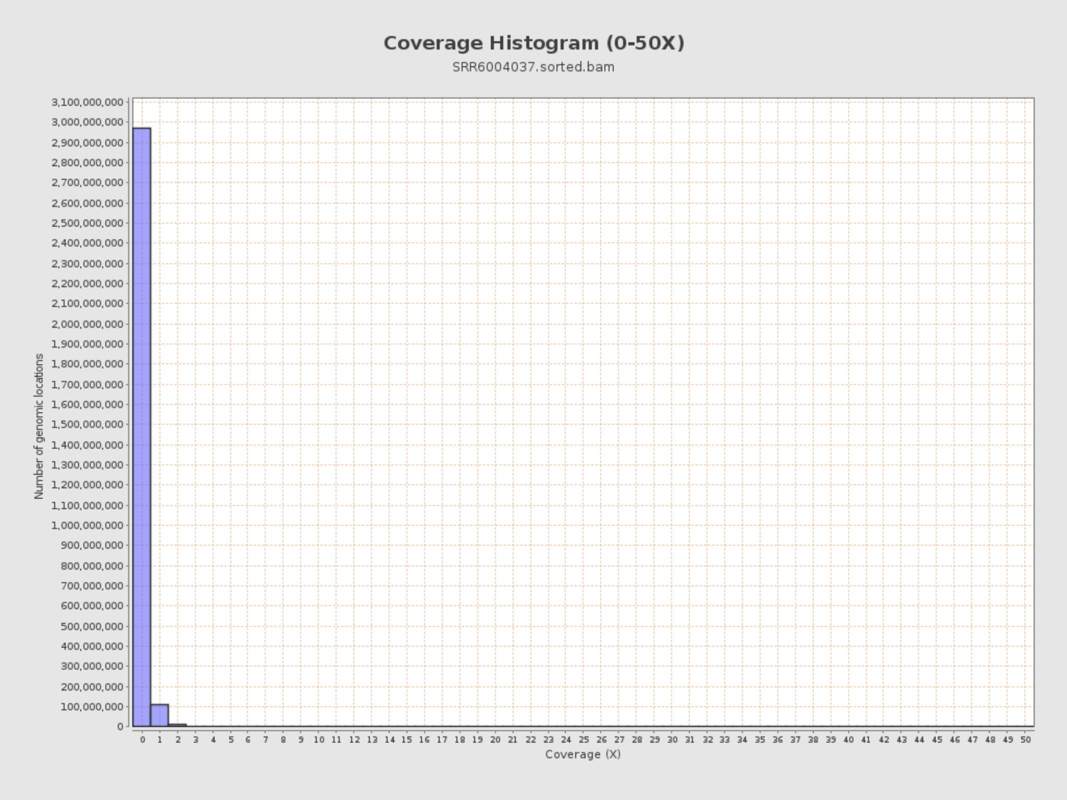
3. Results : Coverage across reference



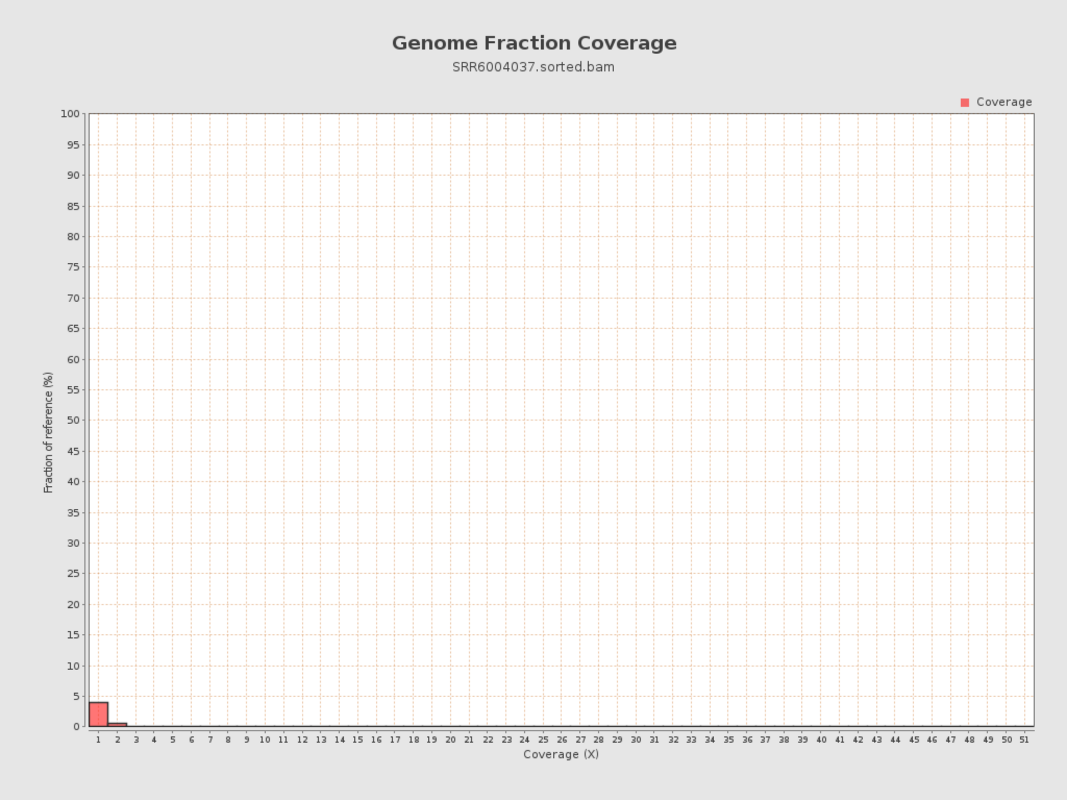
4. Results : Coverage Histogram



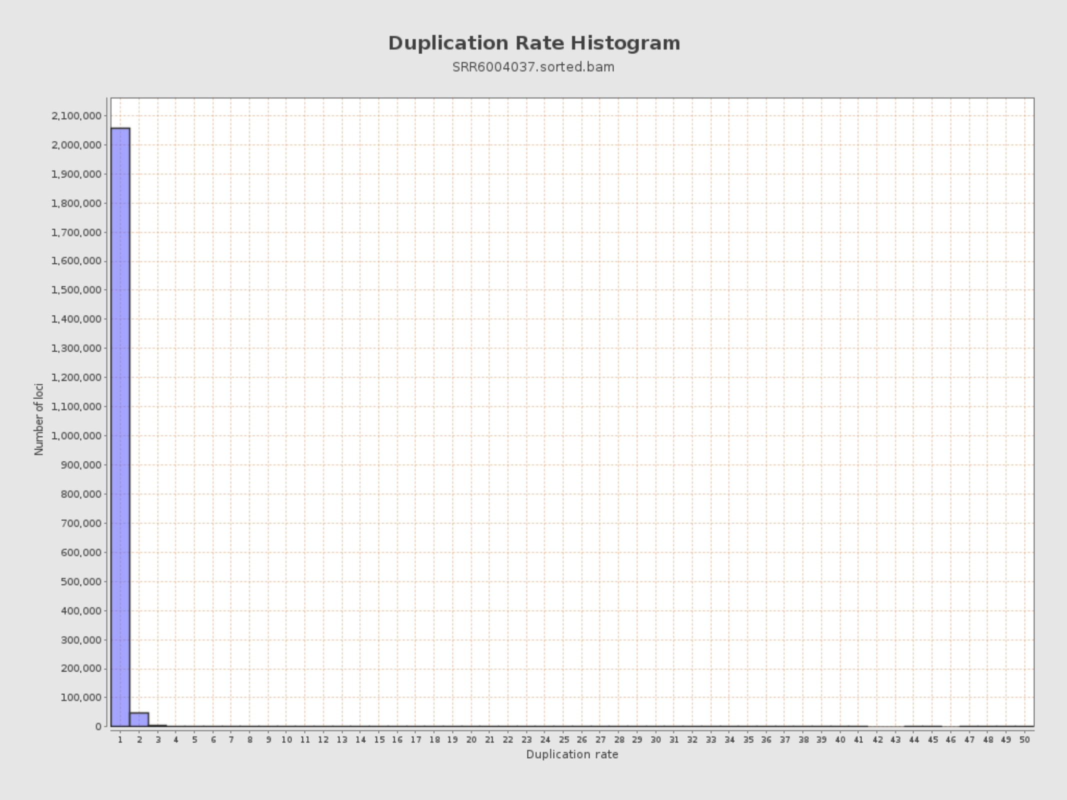
5. Results : Coverage Histogram (0-50X)



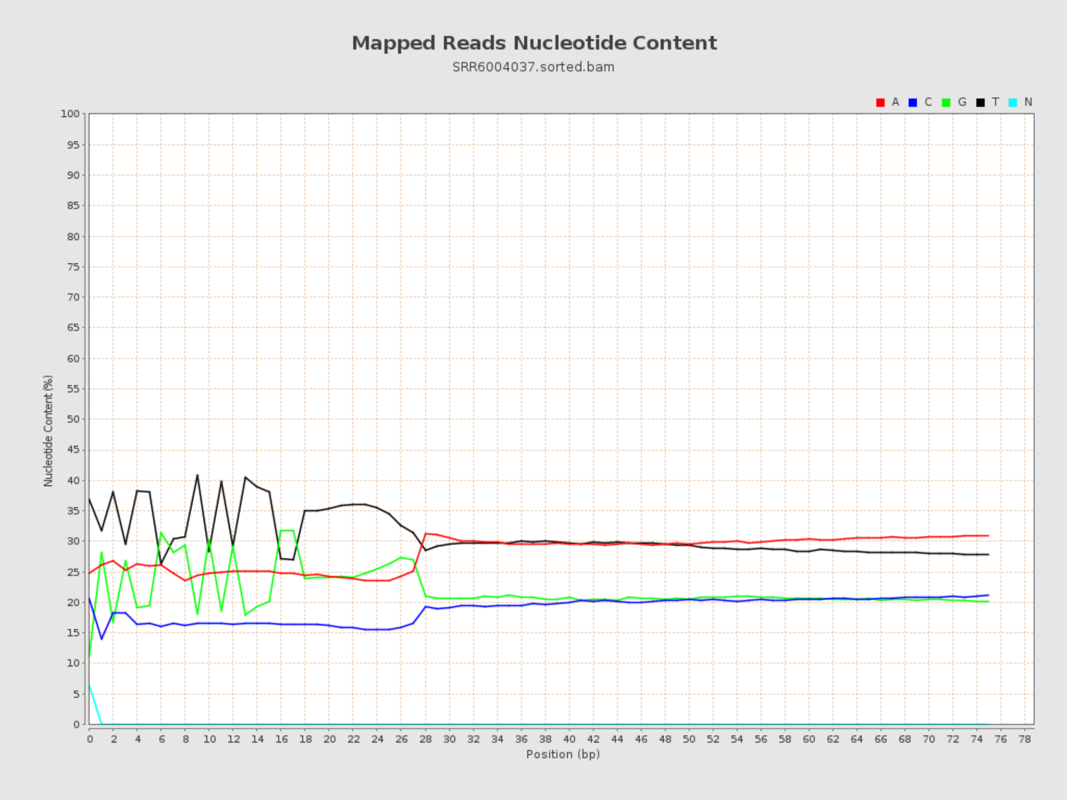
6. Results : Genome Fraction Coverage



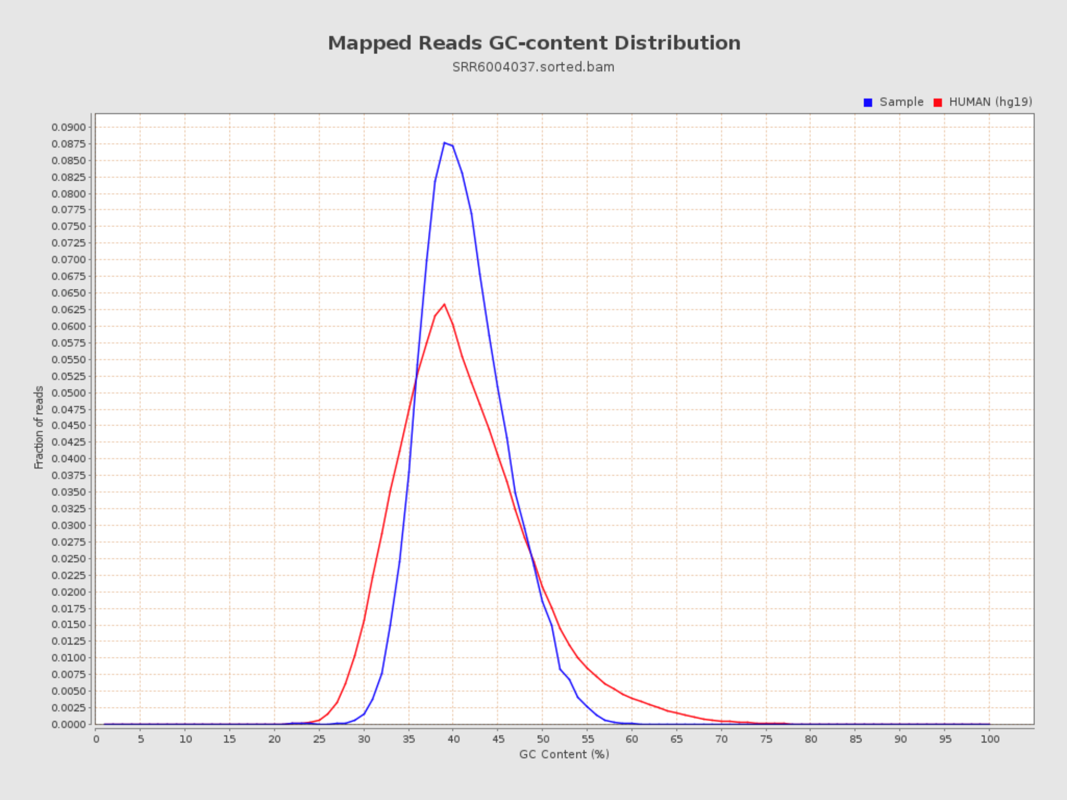
7. Results : Duplication Rate Histogram



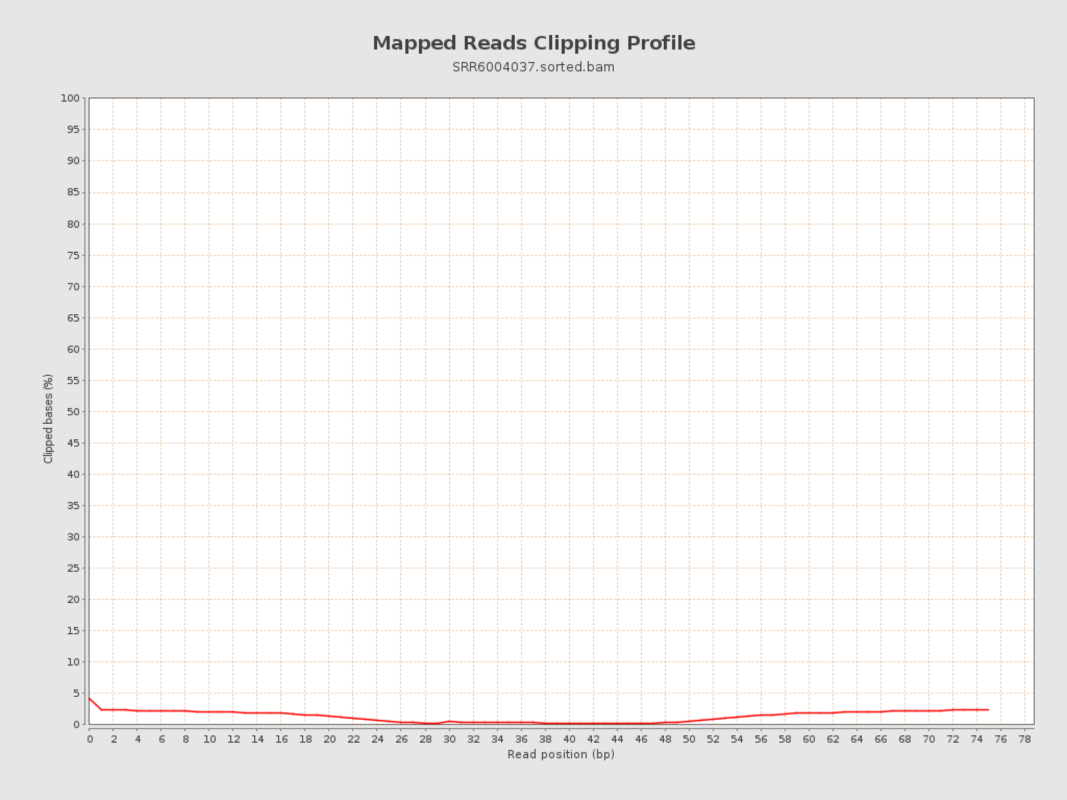
8. Results : Mapped Reads Nucleotide Content



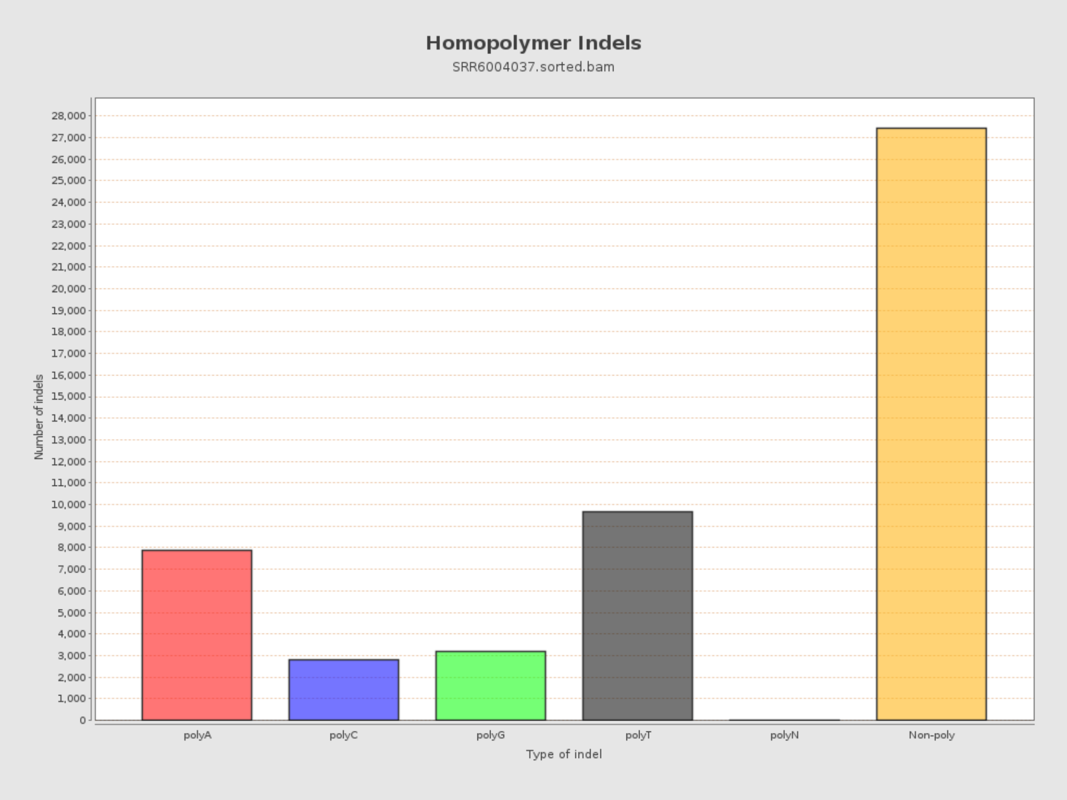
9. Results : Mapped Reads GC-content Distribution



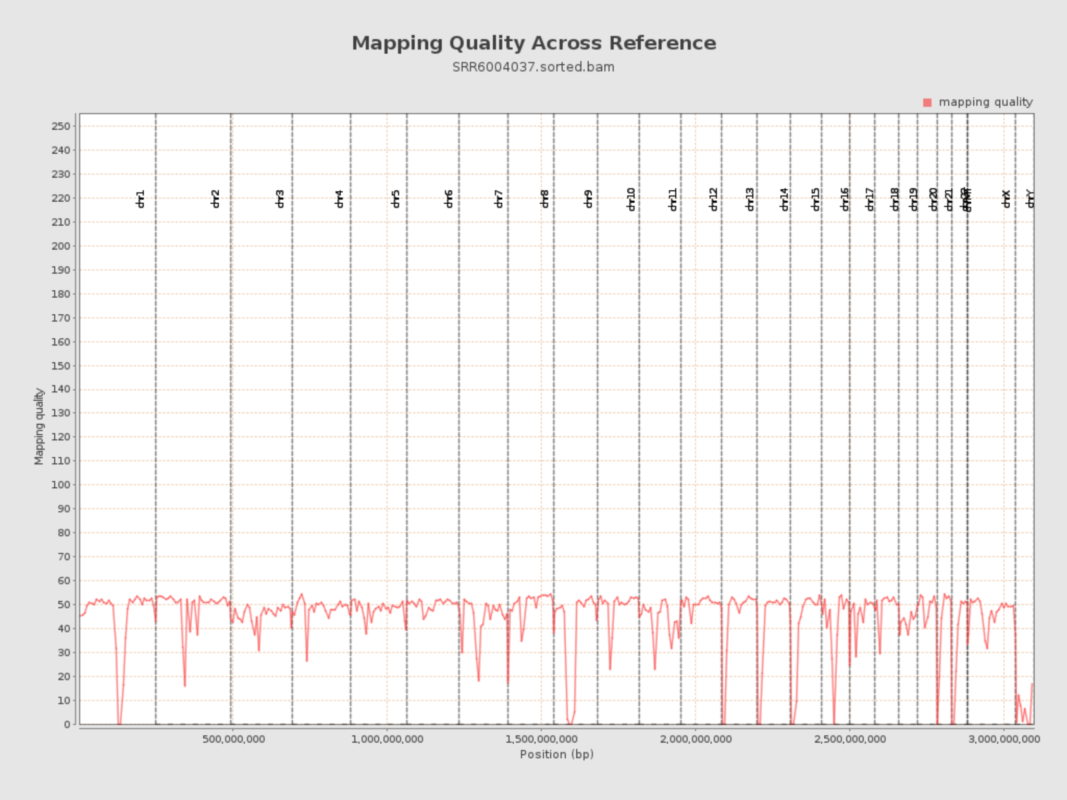
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram