Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:06:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237580.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_SRR6237580 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237580.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:06:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237580.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,569,942
Mapped reads	1,279,904 / 81.53%
Unmapped reads	290,038 / 18.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,849 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	75,344 / 4.8%
Duplication rate	4.11%
Clipped reads	817,767 / 52.09%

2.2. ACGT Content

Number/percentage of A's	20,183,750 / 25.29%
Number/percentage of C's	14,850,504 / 18.61%
Number/percentage of T's	24,209,195 / 30.34%
Number/percentage of G's	20,526,713 / 25.72%
Number/percentage of N's	34,050 / 0.04%
GC Percentage	44.33%

2.3. Coverage

Mean	0.0258

Standard Deviation	0.2662

2.4. Mapping Quality

Mean Mapping Quality	39.42

2.5. Mismatches and indels

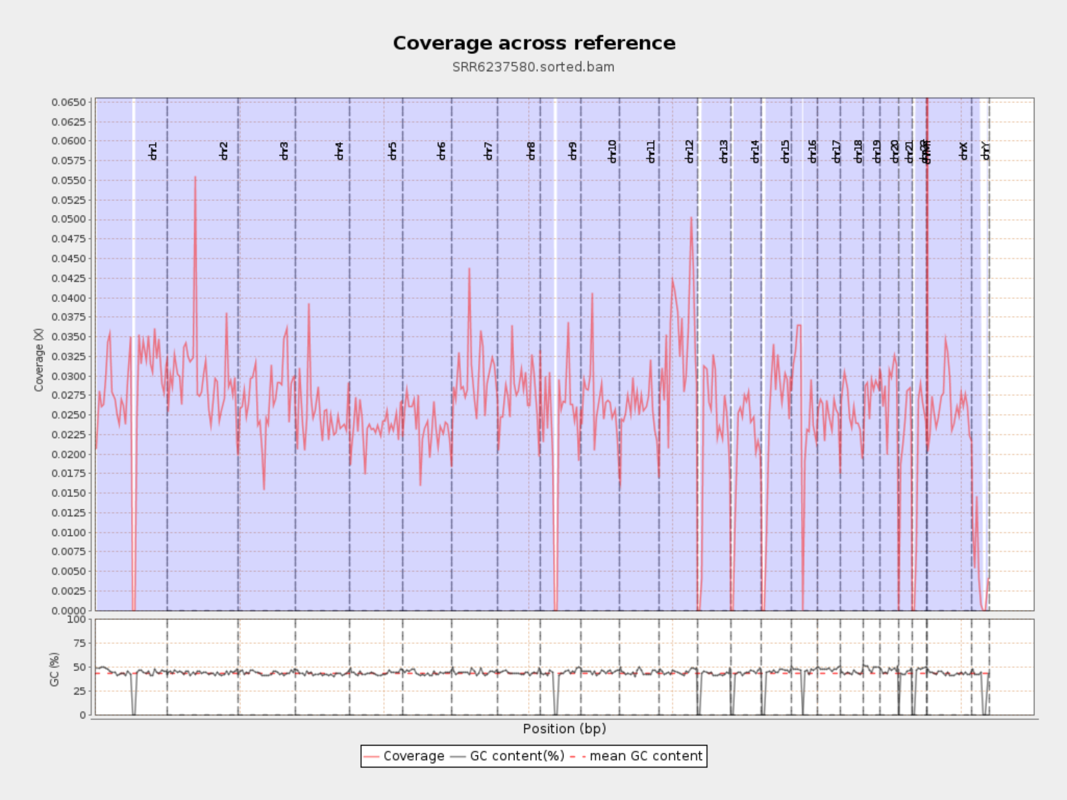
General error rate	0.97%
Mismatches	759,357
Insertions	7,354
Mapped reads with at least one insertion	0.57%
Deletions	28,202
Mapped reads with at least one deletion	2.17%
Homopolymer indels	45.87%

2.6. Chromosome stats

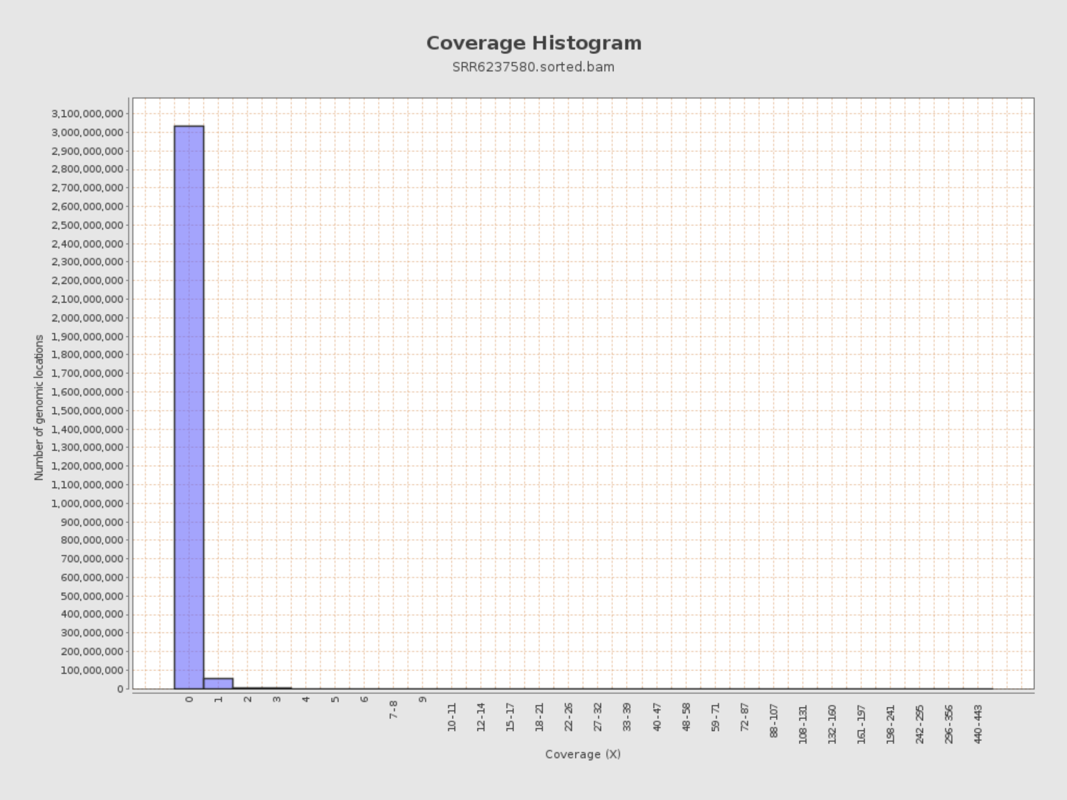
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6956188	0.0279	0.3128
chr2	243199373	7292333	0.03	0.3735
chr3	198022430	5371081	0.0271	0.2148
chr4	191154276	4803587	0.0251	0.2191
chr5	180915260	4277692	0.0236	0.1937
chr6	171115067	4036385	0.0236	0.2097
chr7	159138663	4781293	0.03	0.387

chr8	146364022	4029424	0.0275	0.2571
chr9	141213431	3302206	0.0234	0.2876
chr10	135534747	3616140	0.0267	0.2547
chr11	135006516	3493525	0.0259	0.3002
chr12	133851895	4628204	0.0346	0.251
chr13	115169878	2538156	0.022	0.1944
chr14	107349540	2188264	0.0204	0.212
chr15	102531392	2405903	0.0235	0.2063
chr16	90354753	2294070	0.0254	0.2271
chr17	81195210	2026232	0.025	0.223
chr18	78077248	1988405	0.0255	0.3806
chr19	59128983	1653889	0.028	0.2786
chr20	63025520	1777680	0.0282	0.2207
chr21	48129895	1045561	0.0217	0.2056
chr22	51304566	931961	0.0182	0.1771
chrMT	16571	61741	3.7258	3.4694
chrX	155270560	4068415	0.0262	0.2223
chrY	59373566	281850	0.0047	0.1193

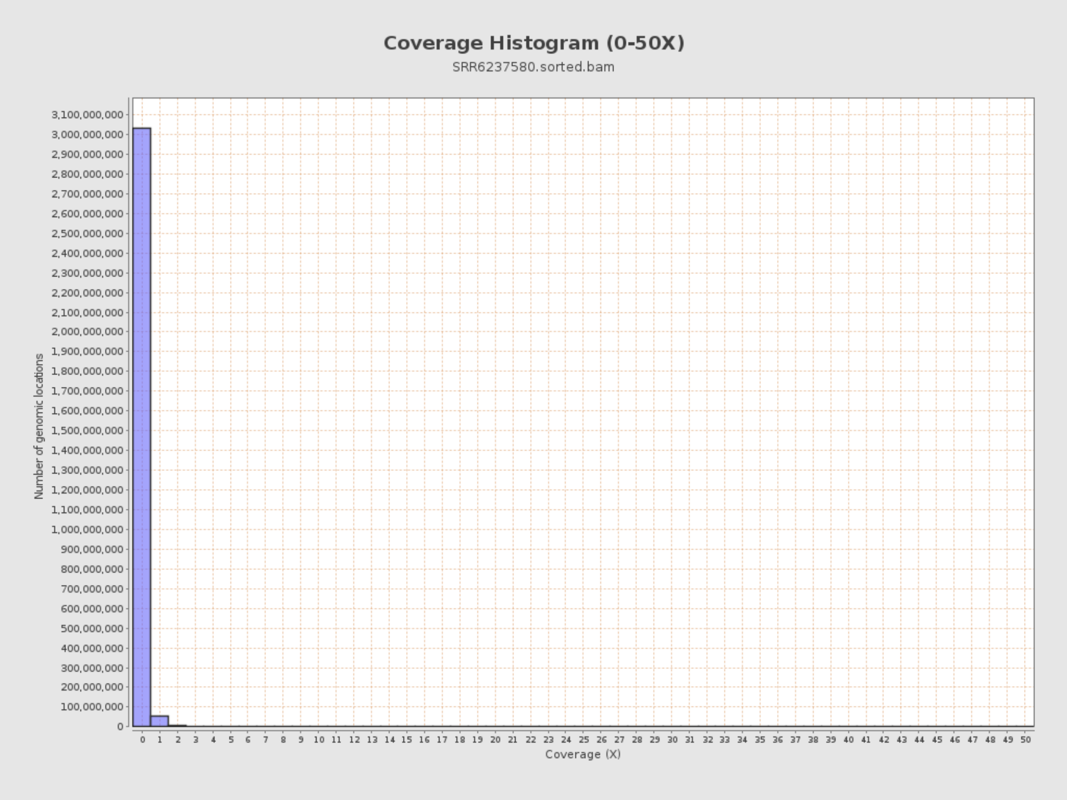
3. Results : Coverage across reference



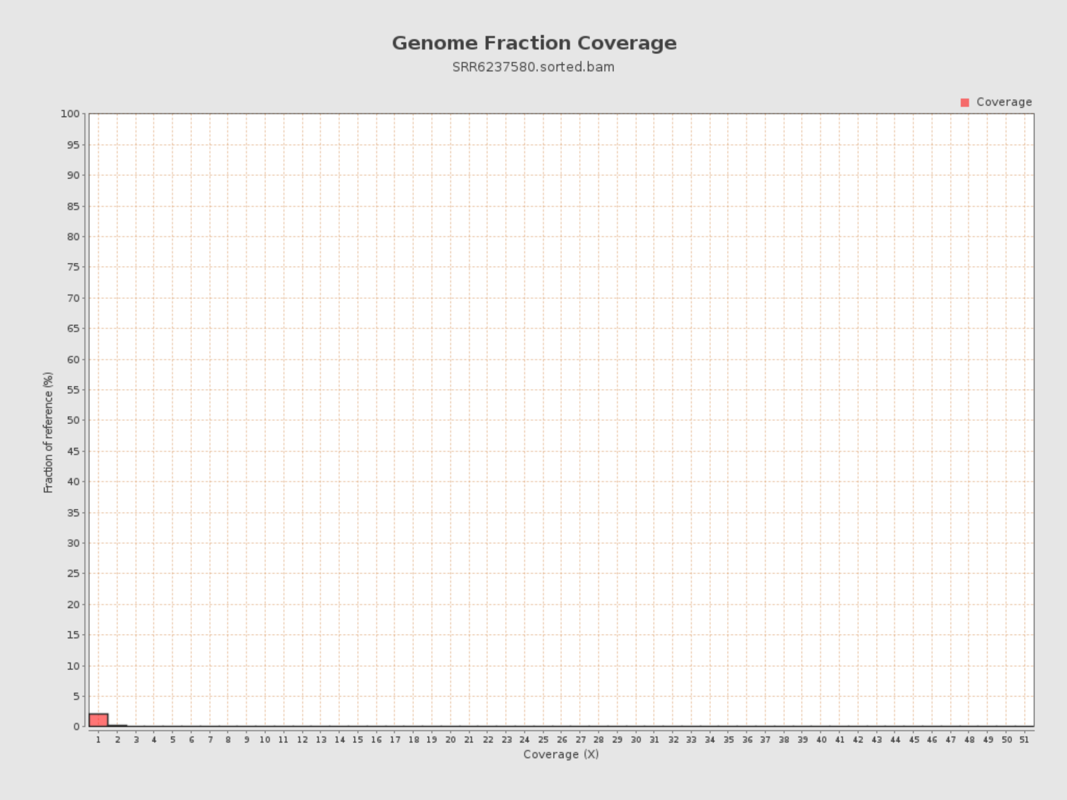
4. Results : Coverage Histogram



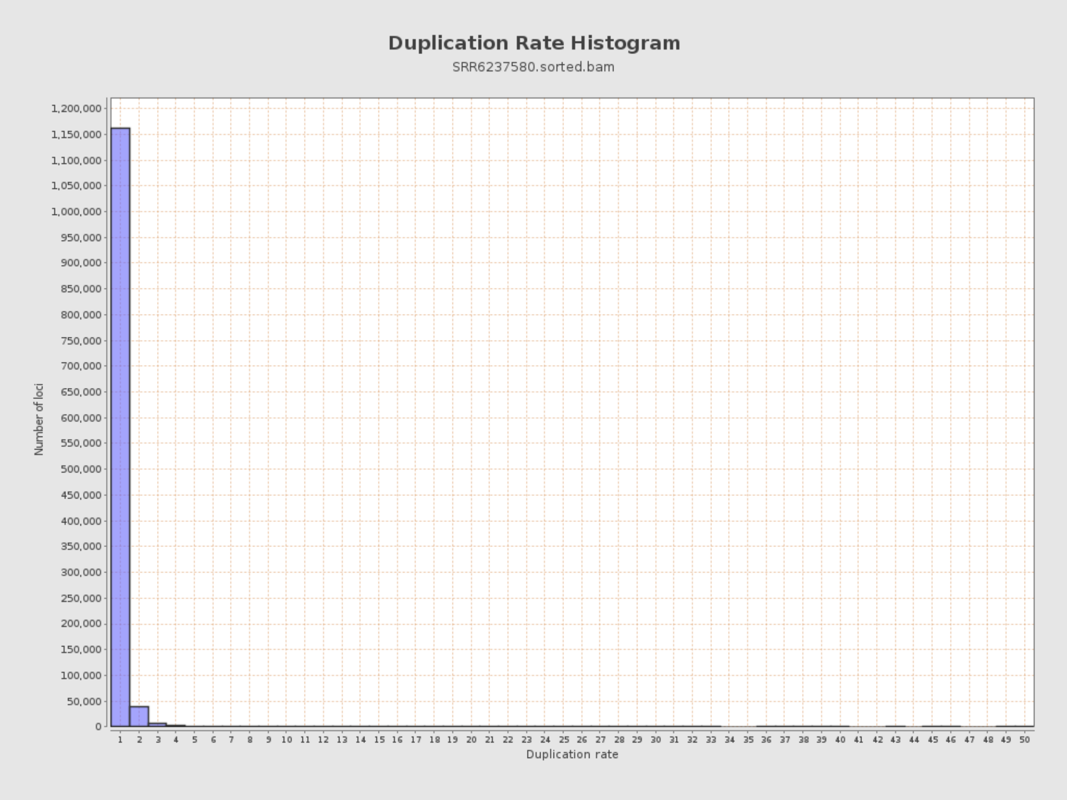
5. Results : Coverage Histogram (0-50X)



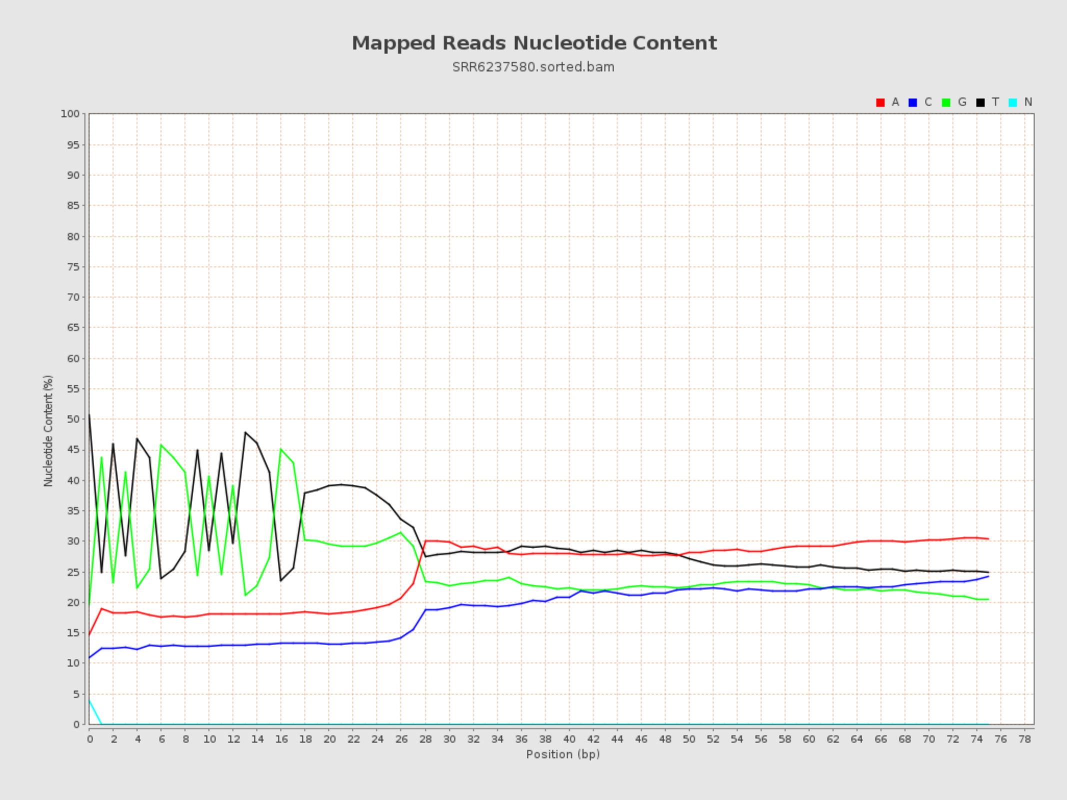
6. Results : Genome Fraction Coverage



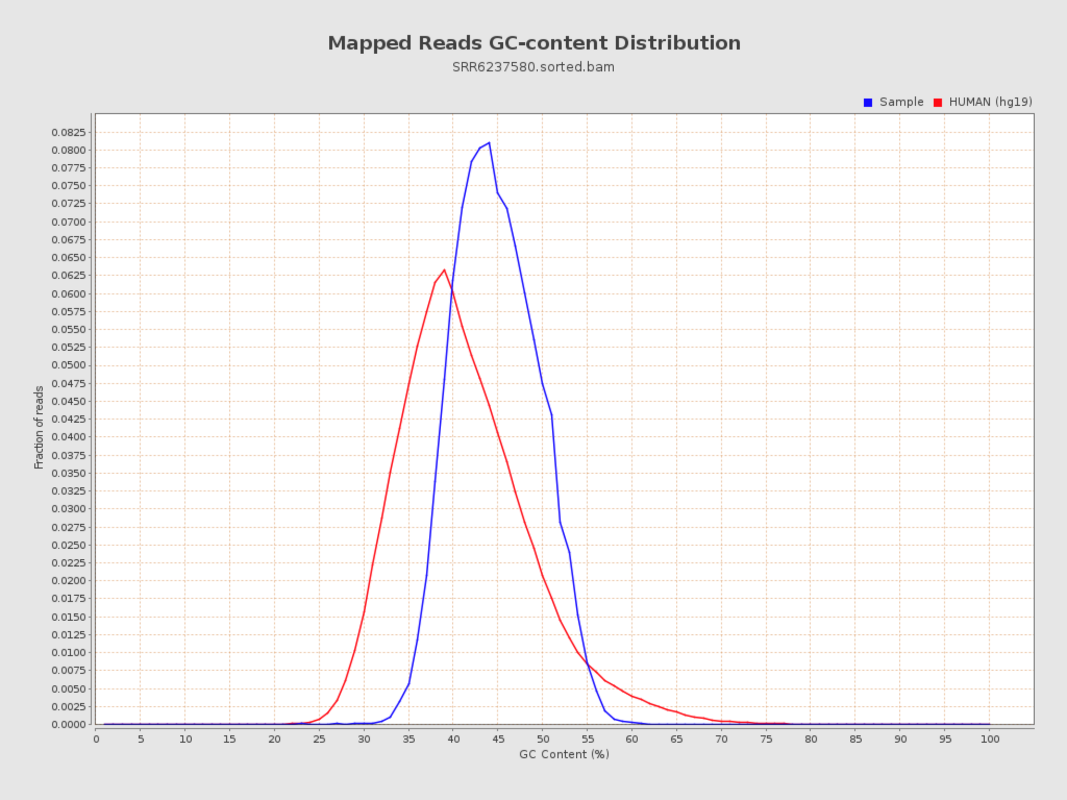
7. Results : Duplication Rate Histogram



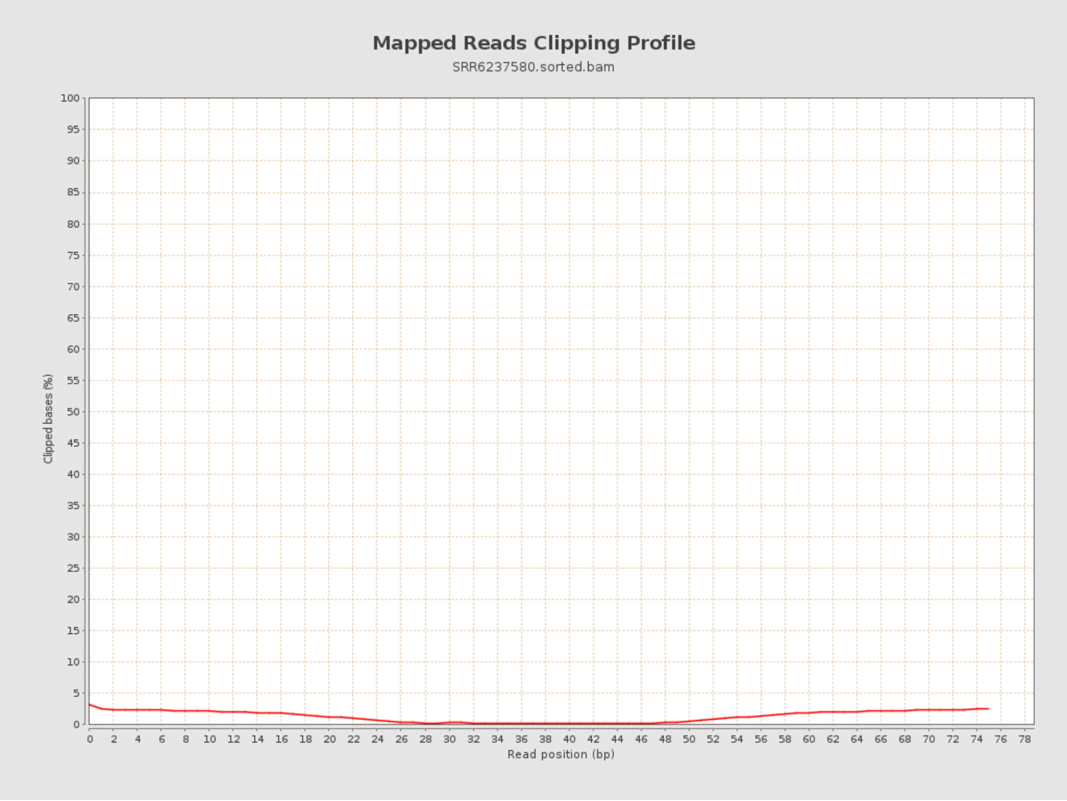
8. Results : Mapped Reads Nucleotide Content



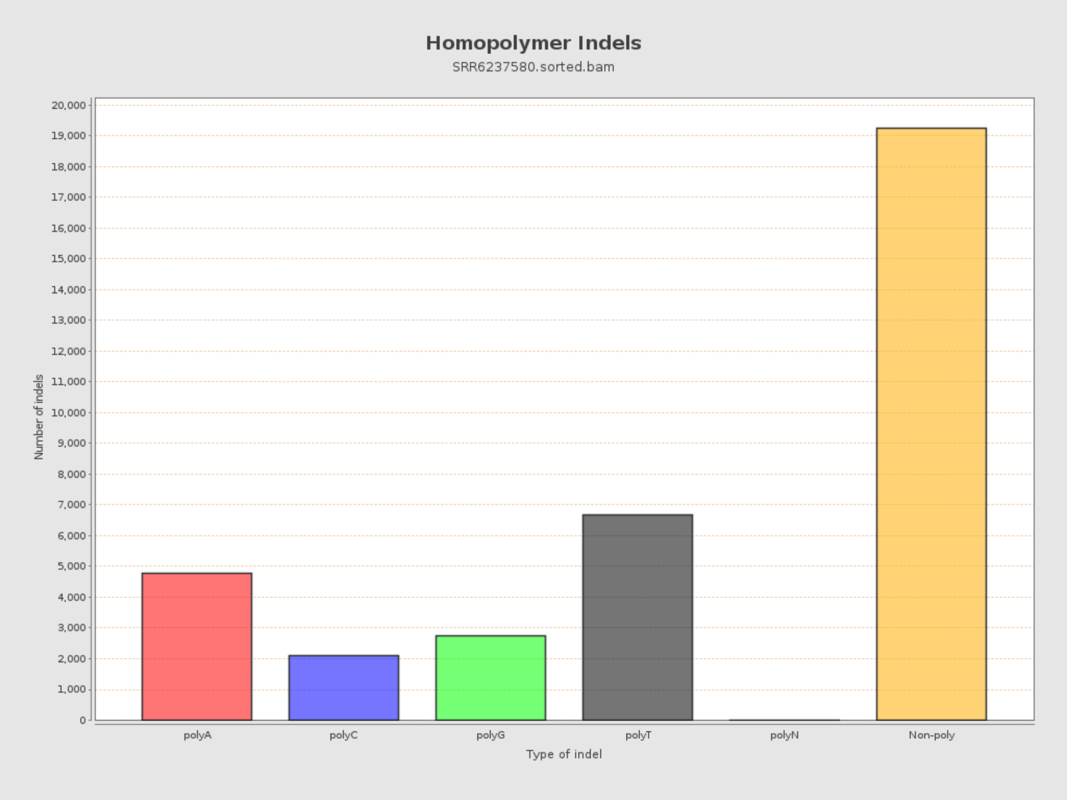
9. Results : Mapped Reads GC-content Distribution



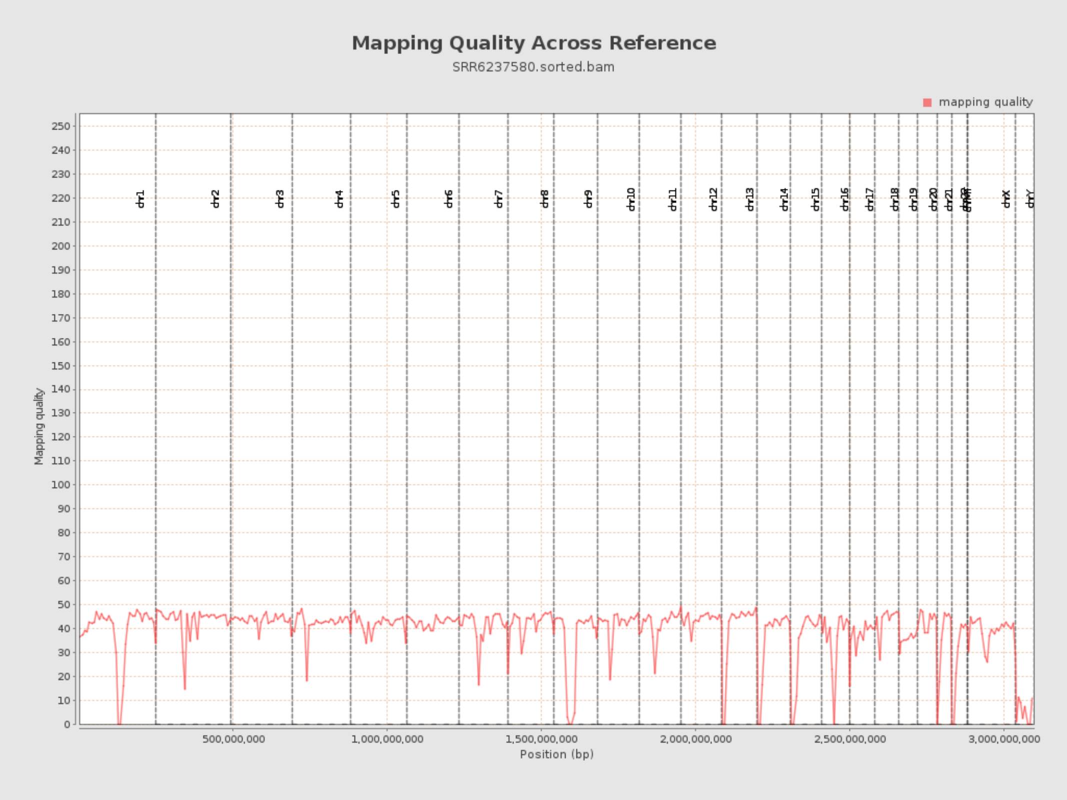
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram