Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:40:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238521.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_SRR6238521 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238521.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:40:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238521.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,337,528
Mapped reads	1,140,540 / 85.27%
Unmapped reads	196,988 / 14.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,288 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	171,024 / 12.79%
Duplication rate	12.49%
Clipped reads	734,661 / 54.93%

2.2. ACGT Content

Number/percentage of A's	16,699,743 / 24.05%
Number/percentage of C's	12,106,469 / 17.43%
Number/percentage of T's	23,649,484 / 34.05%
Number/percentage of G's	16,987,032 / 24.46%
Number/percentage of N's	4,031 / 0.01%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.4259

2.4. Mapping Quality

Mean Mapping Quality	42.87

2.5. Mismatches and indels

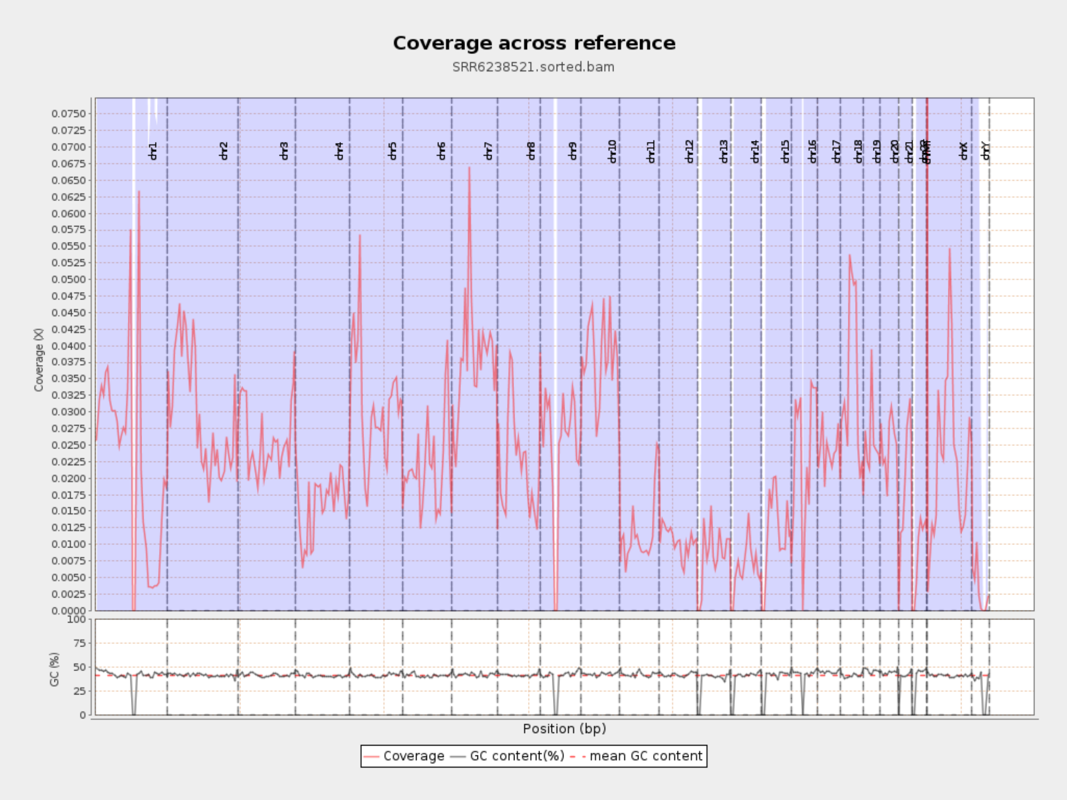
General error rate	0.71%
Mismatches	485,471
Insertions	4,442
Mapped reads with at least one insertion	0.39%
Deletions	24,922
Mapped reads with at least one deletion	2.16%
Homopolymer indels	39.81%

2.6. Chromosome stats

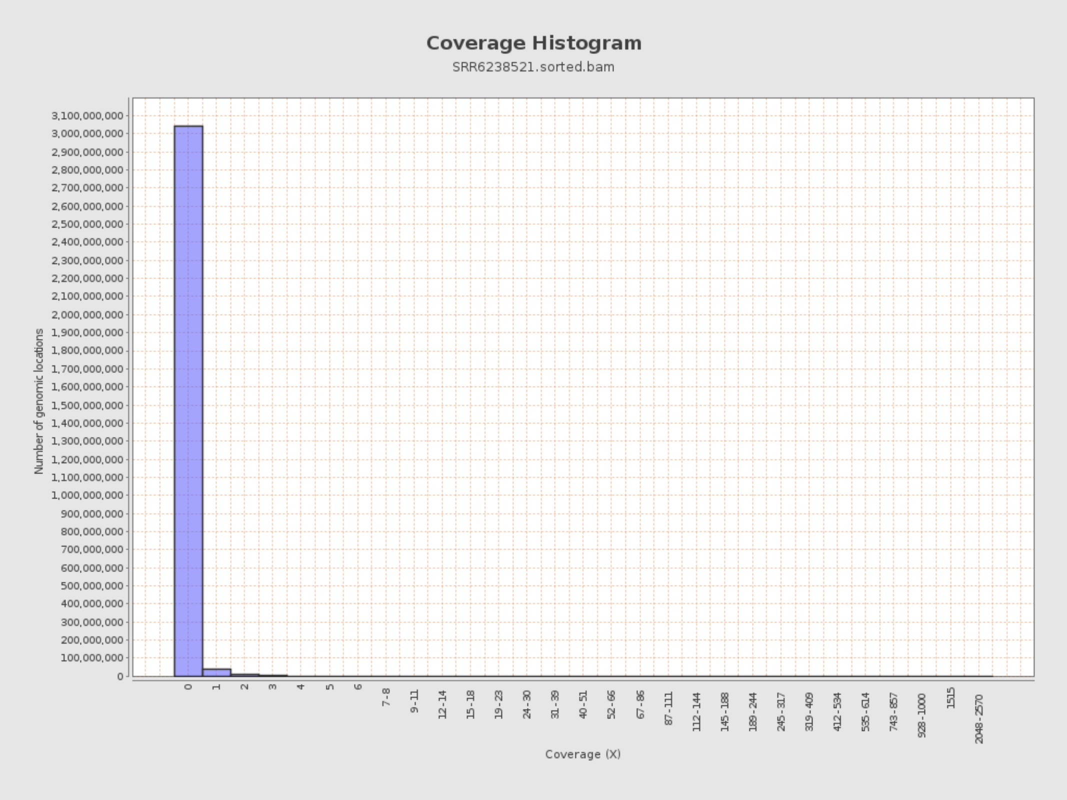
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5670648	0.0228	0.5375
chr2	243199373	7228910	0.0297	1.1175
chr3	198022430	5083024	0.0257	0.2125
chr4	191154276	3096680	0.0162	0.1679
chr5	180915260	5668840	0.0313	0.2334
chr6	171115067	3739831	0.0219	0.3666
chr7	159138663	6146967	0.0386	0.5111

chr8	146364022	3292542	0.0225	0.2298
chr9	141213431	3524707	0.025	0.2559
chr10	135534747	5225442	0.0386	0.2974
chr11	135006516	1547826	0.0115	0.1443
chr12	133851895	1412413	0.0106	0.1416
chr13	115169878	953516	0.0083	0.1831
chr14	107349540	694868	0.0065	0.1152
chr15	102531392	1207127	0.0118	0.2194
chr16	90354753	2058634	0.0228	0.2116
chr17	81195210	1951632	0.024	0.206
chr18	78077248	2801116	0.0359	0.5416
chr19	59128983	1516560	0.0256	0.3889
chr20	63025520	1555839	0.0247	0.2075
chr21	48129895	927561	0.0193	0.1873
chr22	51304566	449469	0.0088	0.1183
chrMT	16571	4947	0.2985	0.5682
chrX	155270560	3542698	0.0228	0.2057
chrY	59373566	186689	0.0031	0.1413

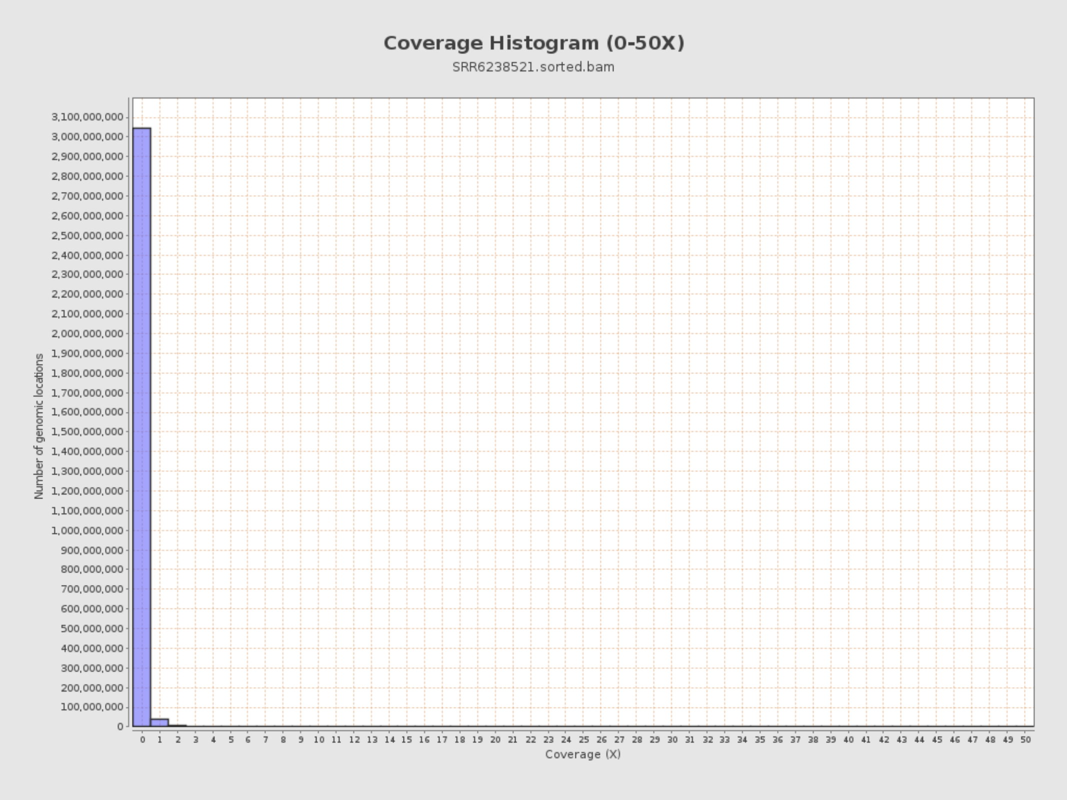
3. Results : Coverage across reference



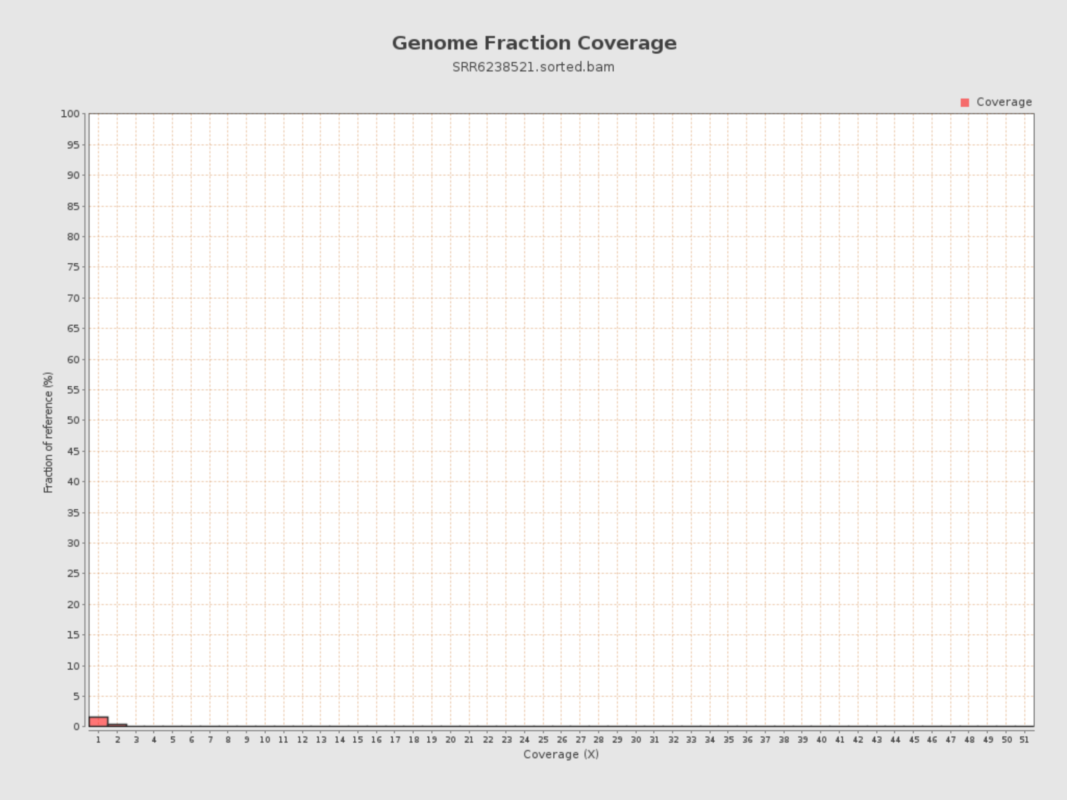
4. Results : Coverage Histogram



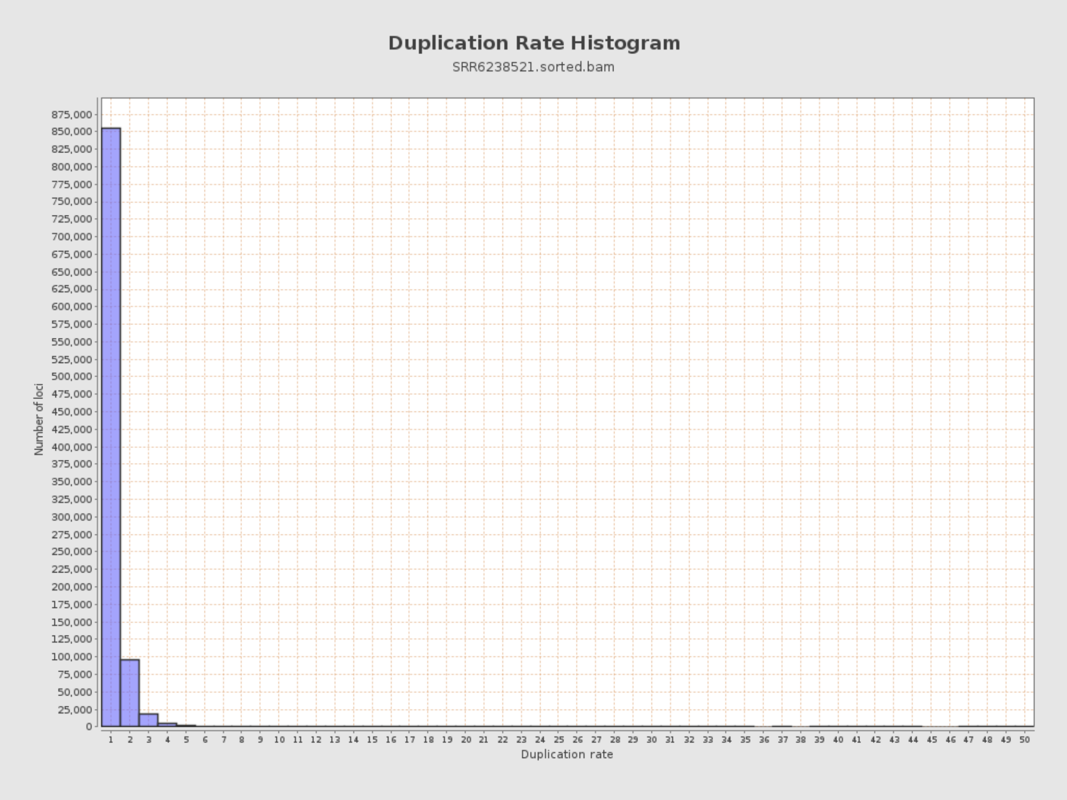
5. Results : Coverage Histogram (0-50X)



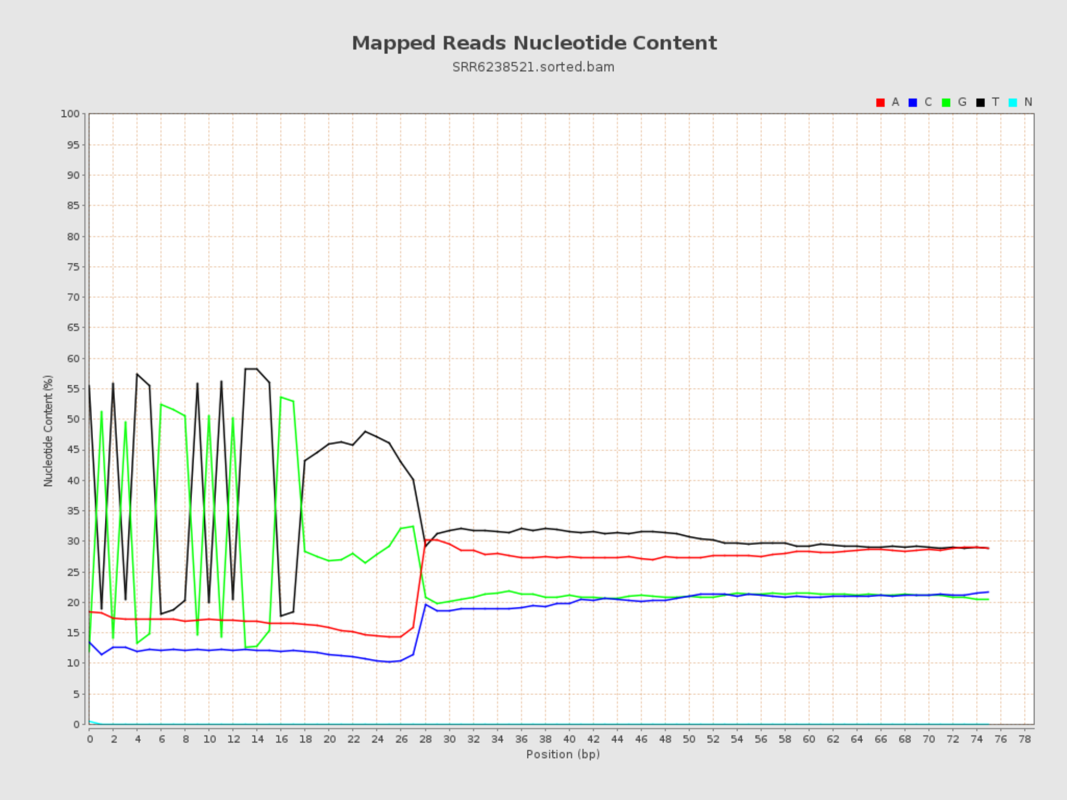
6. Results : Genome Fraction Coverage



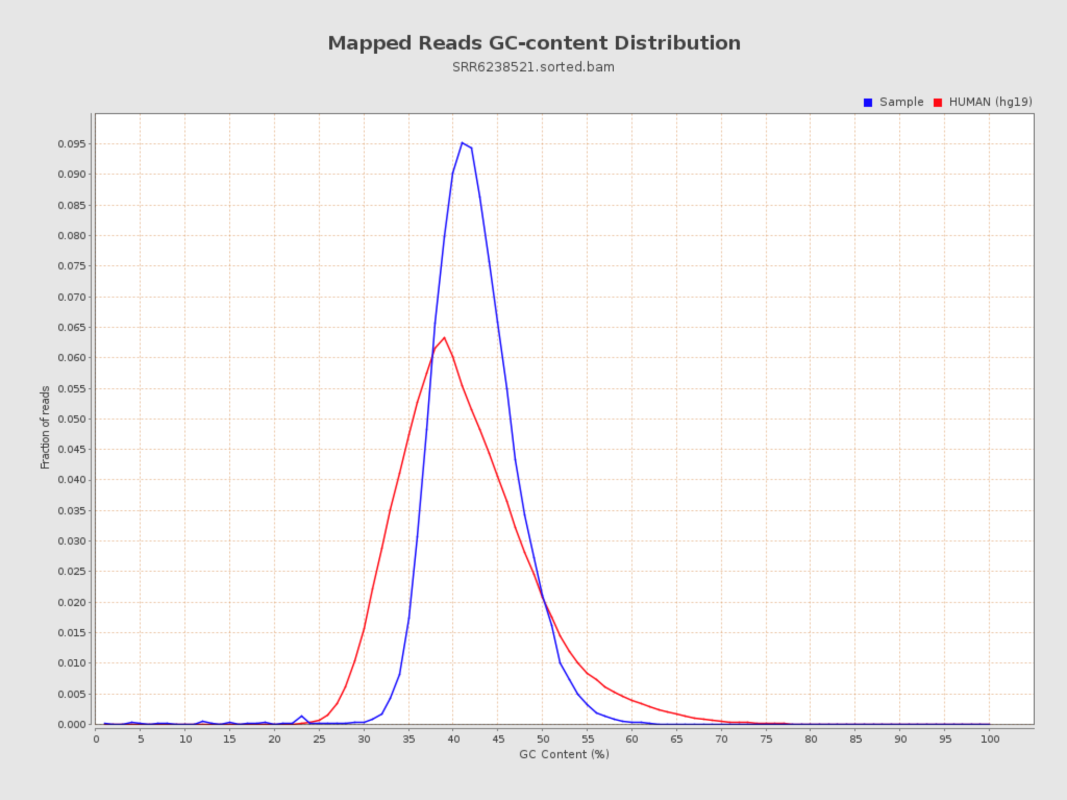
7. Results : Duplication Rate Histogram



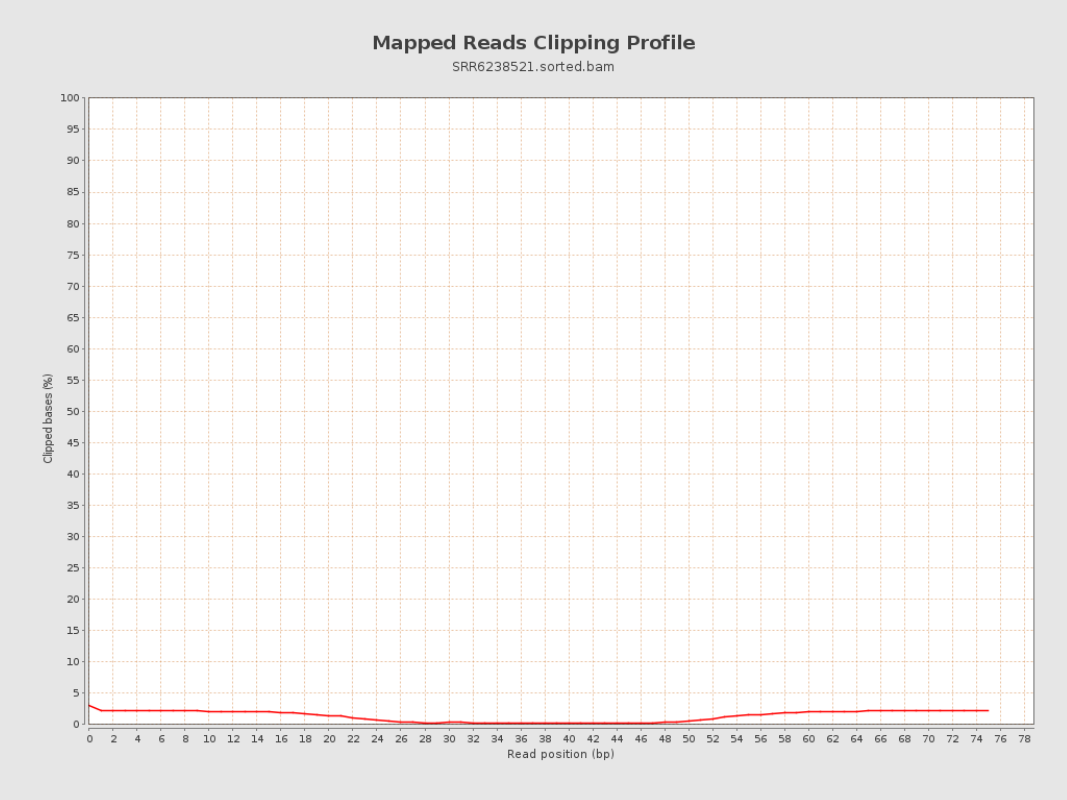
8. Results : Mapped Reads Nucleotide Content



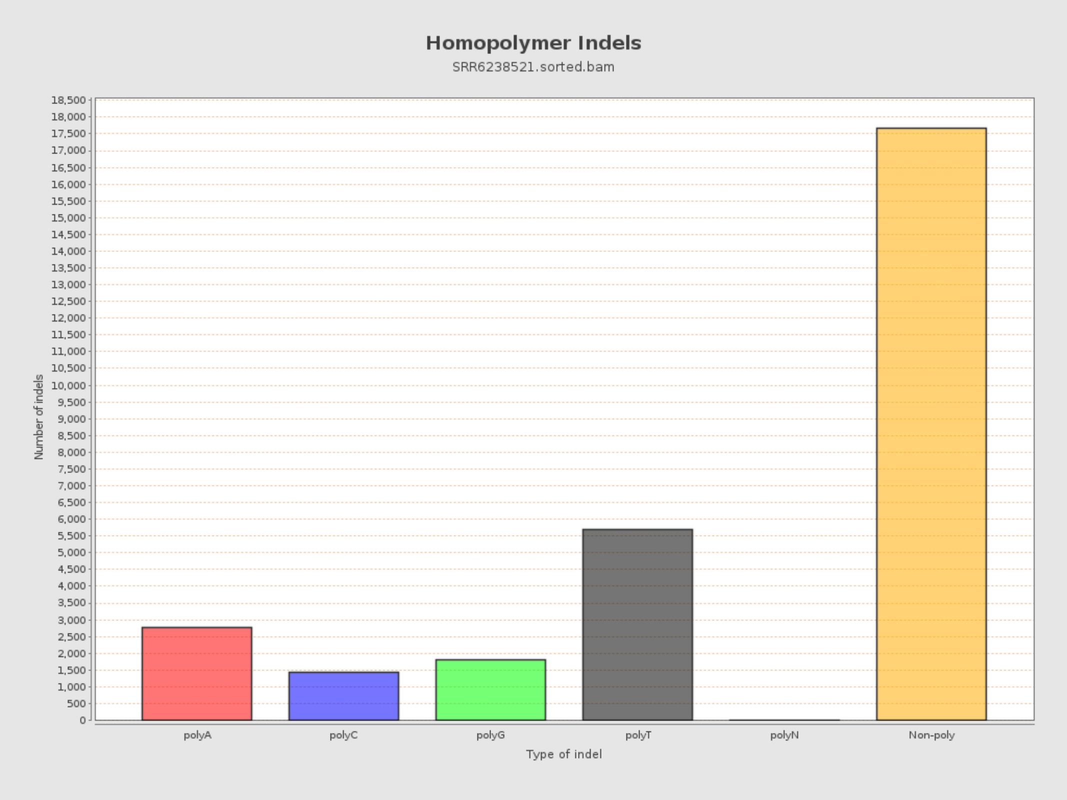
9. Results : Mapped Reads GC-content Distribution



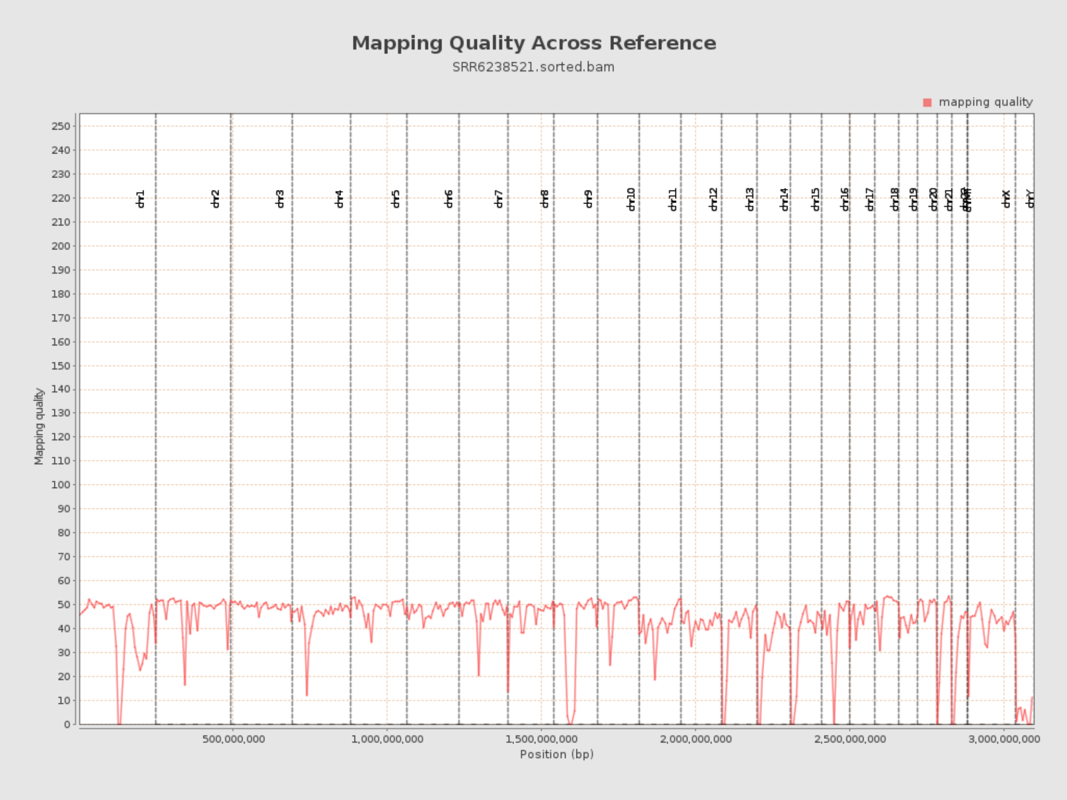
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram