Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:07:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240263.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_SRR6240263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240263.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:07:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,528,148
Mapped reads	2,110,900 / 83.5%
Unmapped reads	417,248 / 16.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,390 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	175,876 / 6.96%
Duplication rate	6.87%
Clipped reads	1,276,679 / 50.5%

2.2. ACGT Content

Number/percentage of A's	35,801,433 / 27.07%
Number/percentage of C's	23,199,356 / 17.54%
Number/percentage of T's	43,288,787 / 32.73%
Number/percentage of G's	29,938,339 / 22.64%
Number/percentage of N's	32,648 / 0.02%
GC Percentage	40.18%

2.3. Coverage

Mean	0.0427

Standard Deviation	0.3896

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

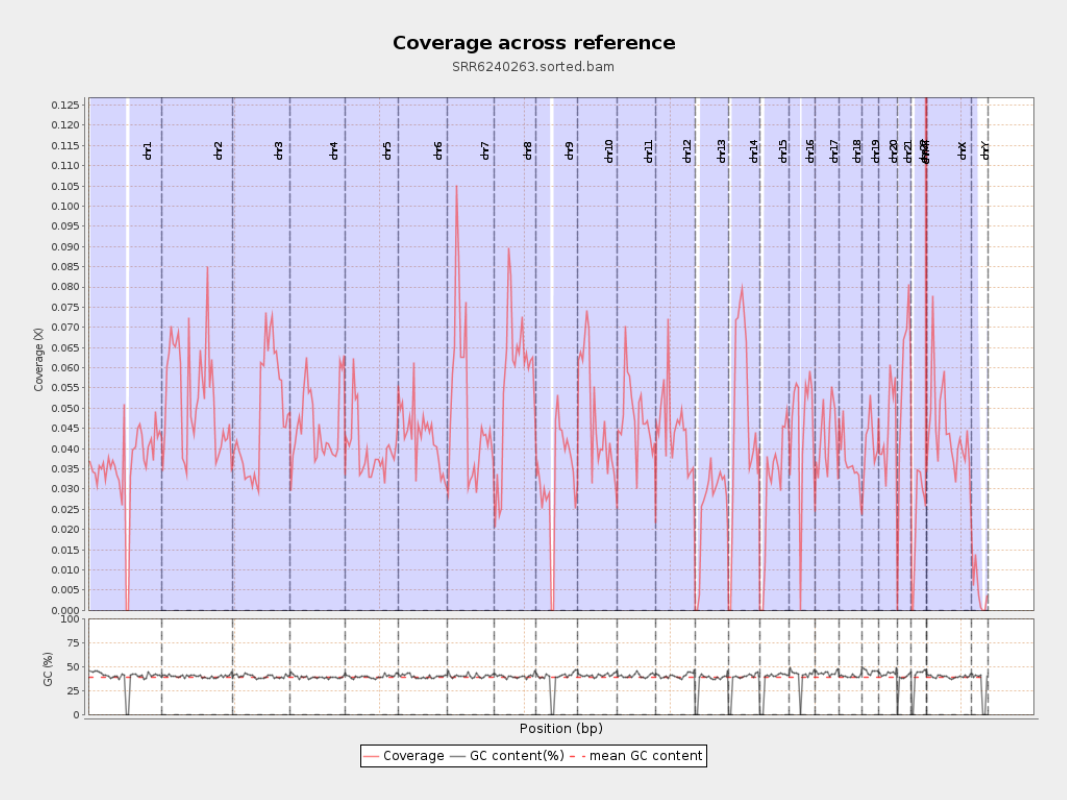
General error rate	0.9%
Mismatches	1,177,197
Insertions	9,524
Mapped reads with at least one insertion	0.45%
Deletions	41,863
Mapped reads with at least one deletion	1.96%
Homopolymer indels	48.46%

2.6. Chromosome stats

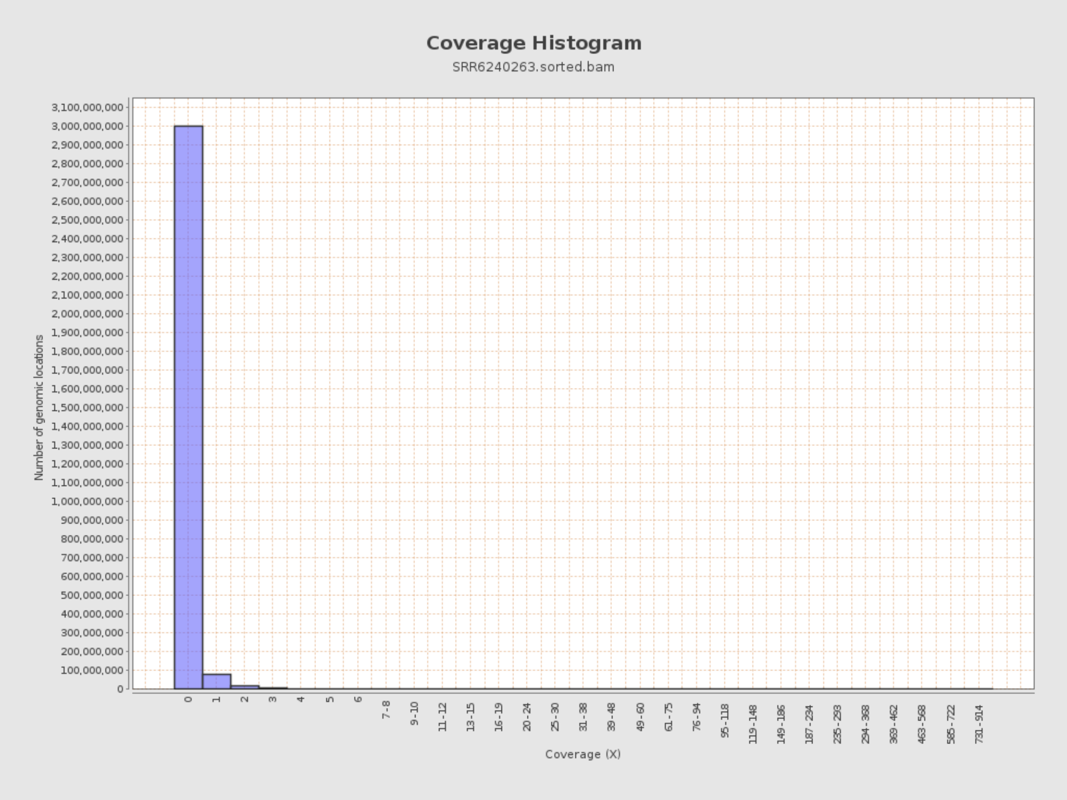
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8897065	0.0357	0.578
chr2	243199373	12697911	0.0522	0.4629
chr3	198022430	9482652	0.0479	0.2776
chr4	191154276	8765890	0.0459	0.2784
chr5	180915260	7213222	0.0399	0.2546
chr6	171115067	7393896	0.0432	0.3428
chr7	159138663	8004033	0.0503	0.6154

chr8	146364022	8290281	0.0566	0.6191
chr9	141213431	4610302	0.0326	0.3396
chr10	135534747	6578623	0.0485	0.3589
chr11	135006516	6428436	0.0476	0.3714
chr12	133851895	5989141	0.0447	0.275
chr13	115169878	2937230	0.0255	0.1997
chr14	107349540	5117414	0.0477	0.2937
chr15	102531392	3183850	0.0311	0.234
chr16	90354753	4111591	0.0455	0.2857
chr17	81195210	3441187	0.0424	0.2917
chr18	78077248	2880934	0.0369	0.5509
chr19	59128983	2462039	0.0416	0.4177
chr20	63025520	2835302	0.045	0.2736
chr21	48129895	2678795	0.0557	0.316
chr22	51304566	1152565	0.0225	0.1842
chrMT	16571	31861	1.9227	2.1363
chrX	155270560	6860238	0.0442	0.2978
chrY	59373566	287777	0.0048	0.1014

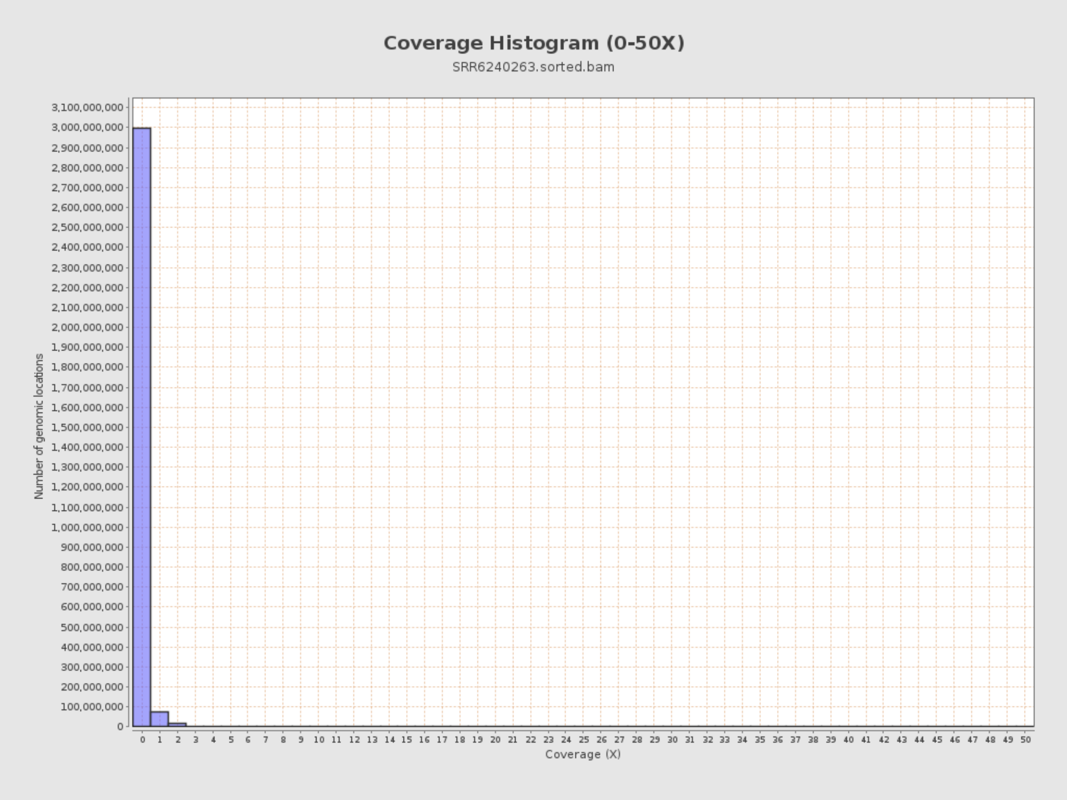
3. Results : Coverage across reference



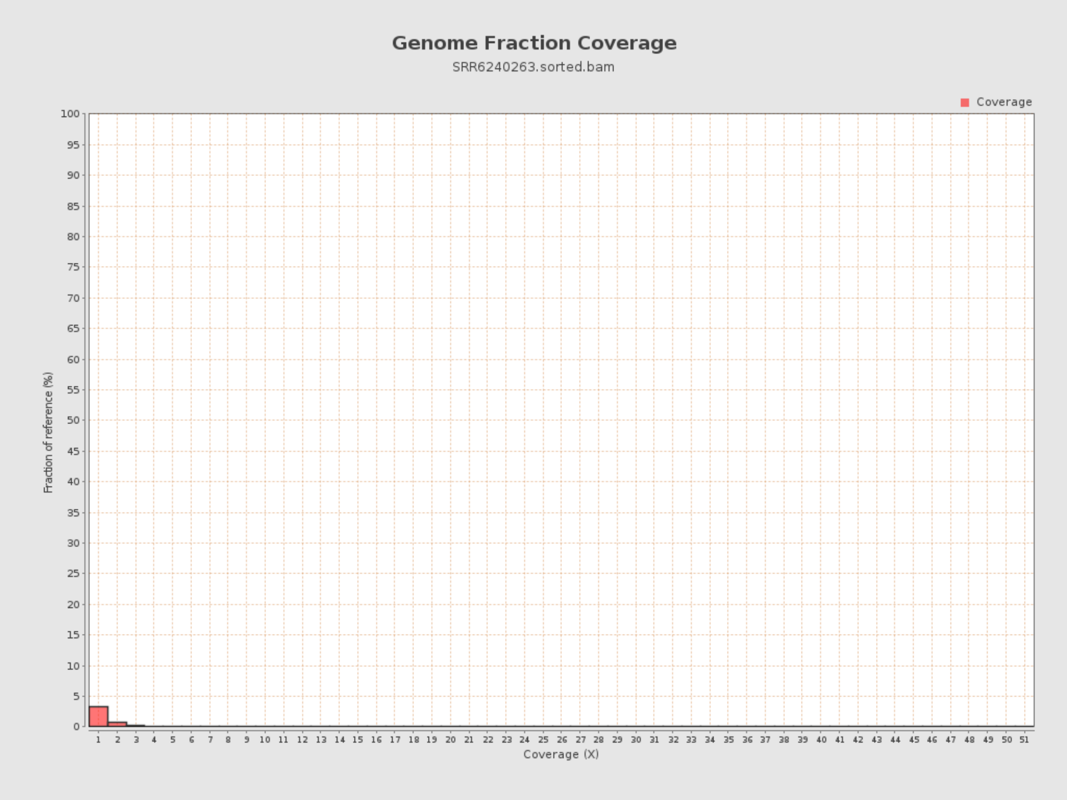
4. Results : Coverage Histogram



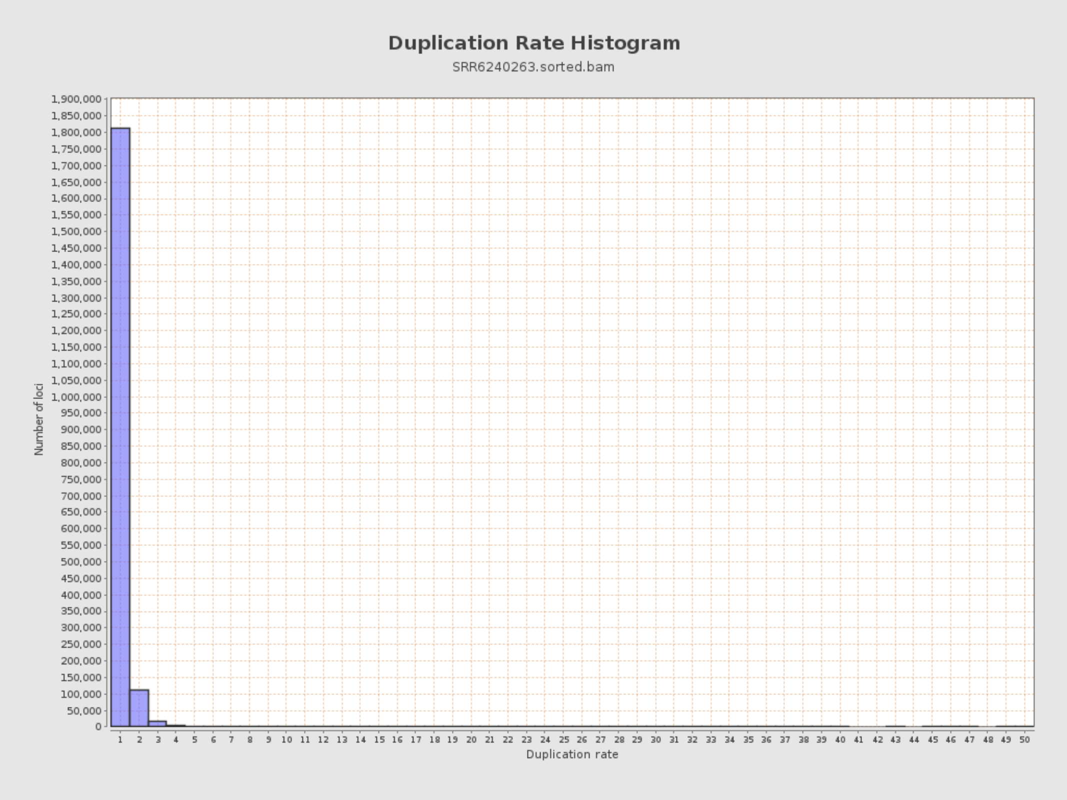
5. Results : Coverage Histogram (0-50X)



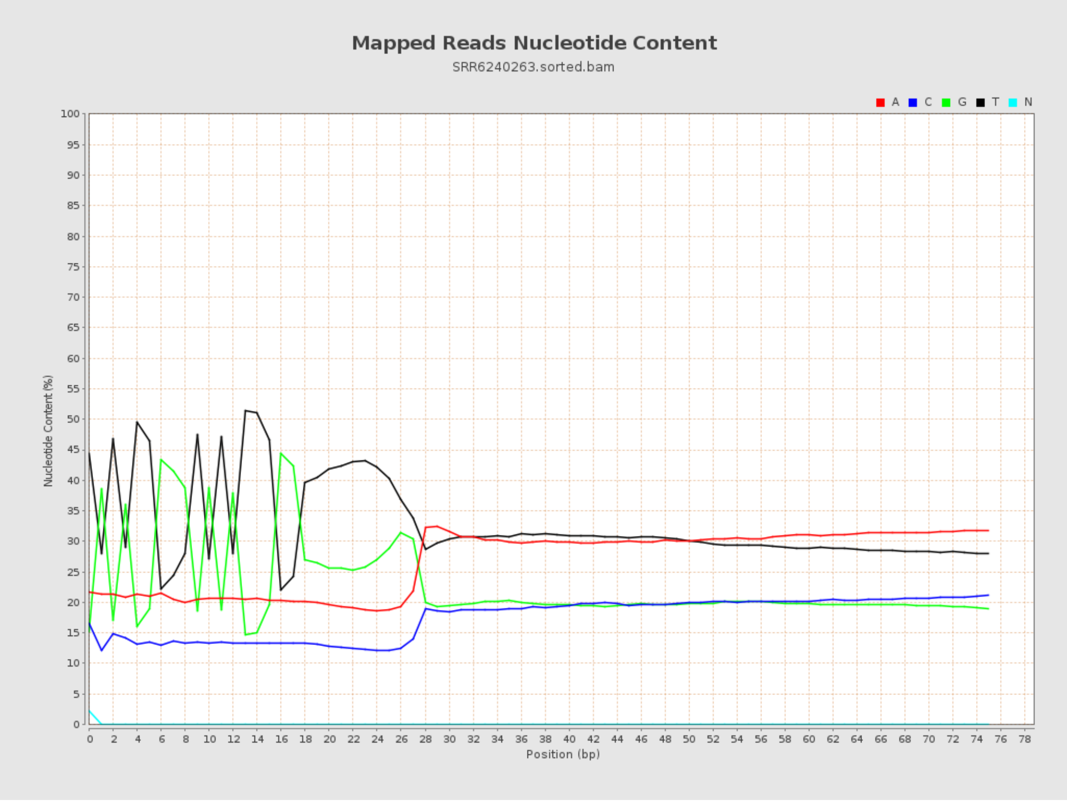
6. Results : Genome Fraction Coverage



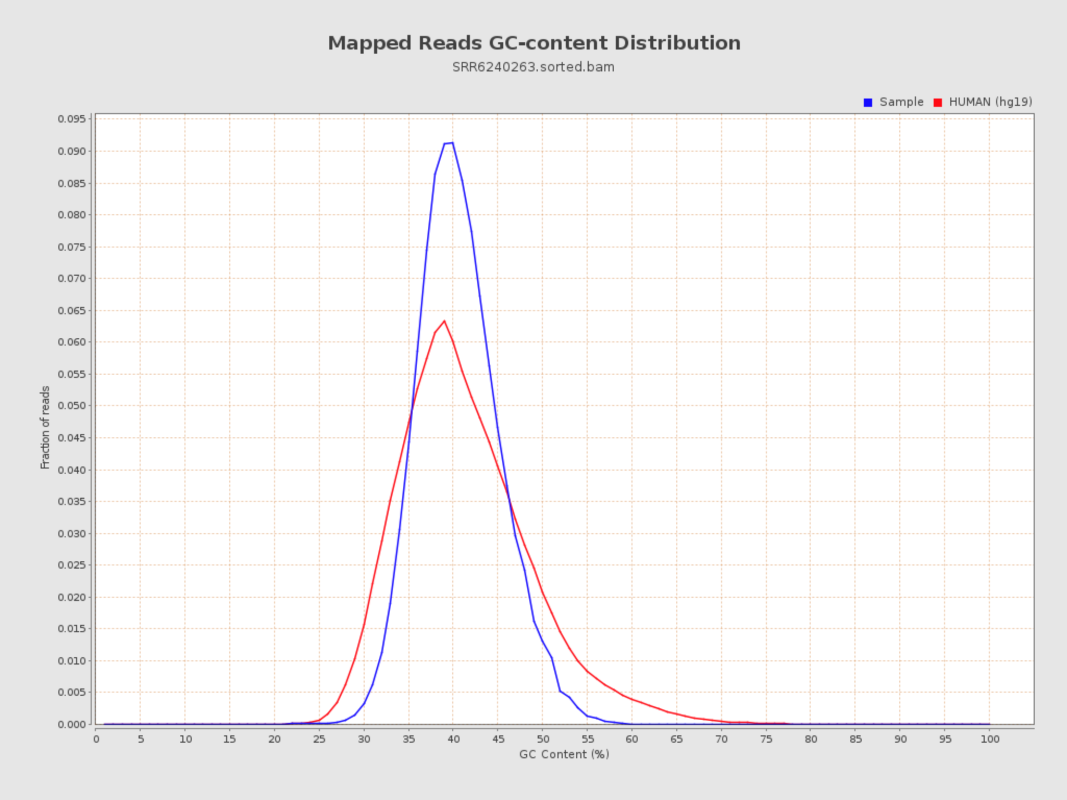
7. Results : Duplication Rate Histogram



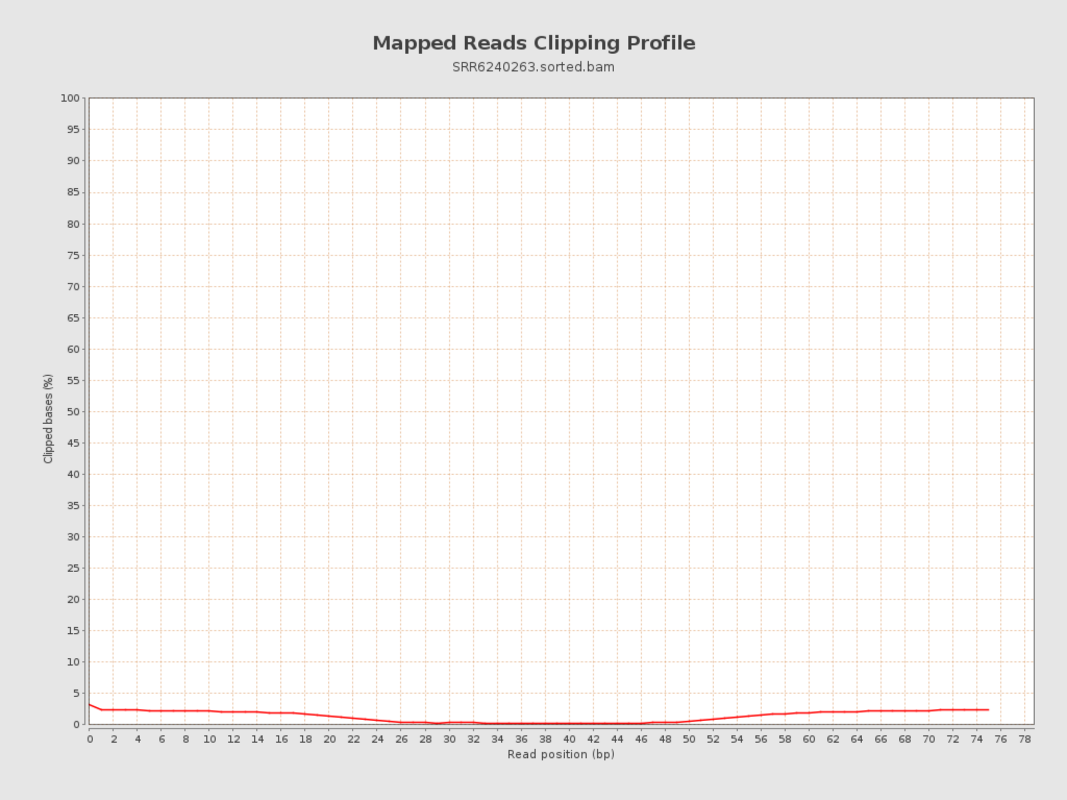
8. Results : Mapped Reads Nucleotide Content



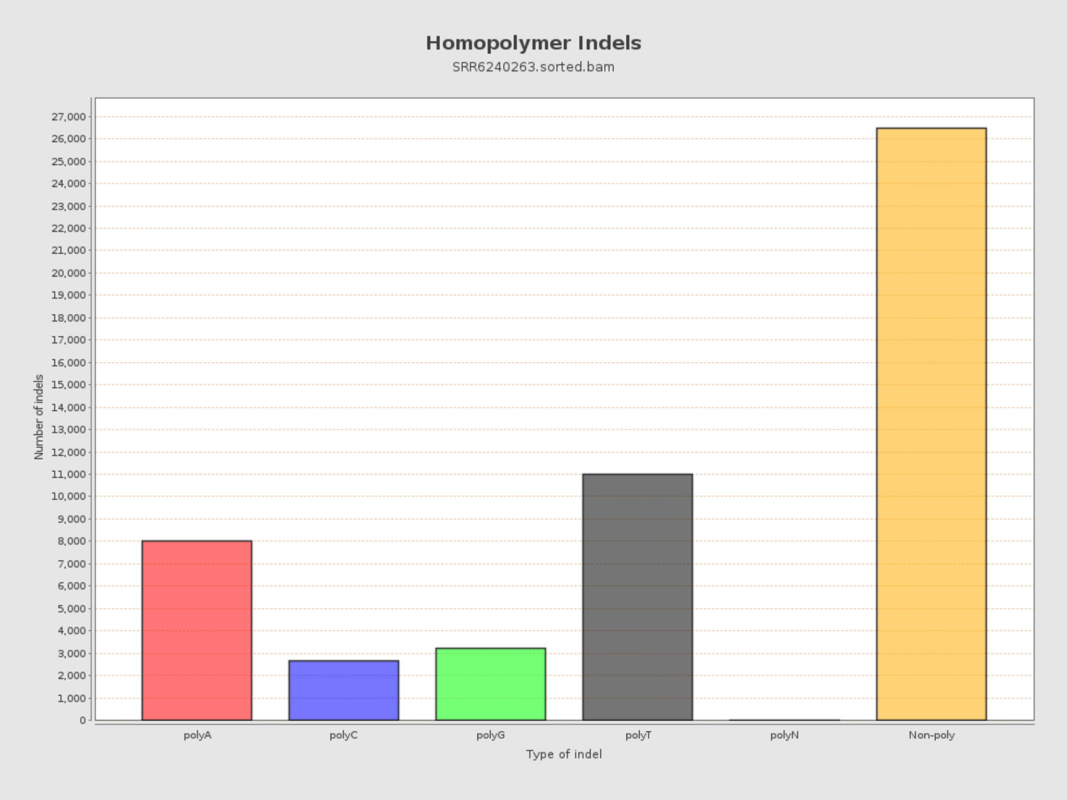
9. Results : Mapped Reads GC-content Distribution



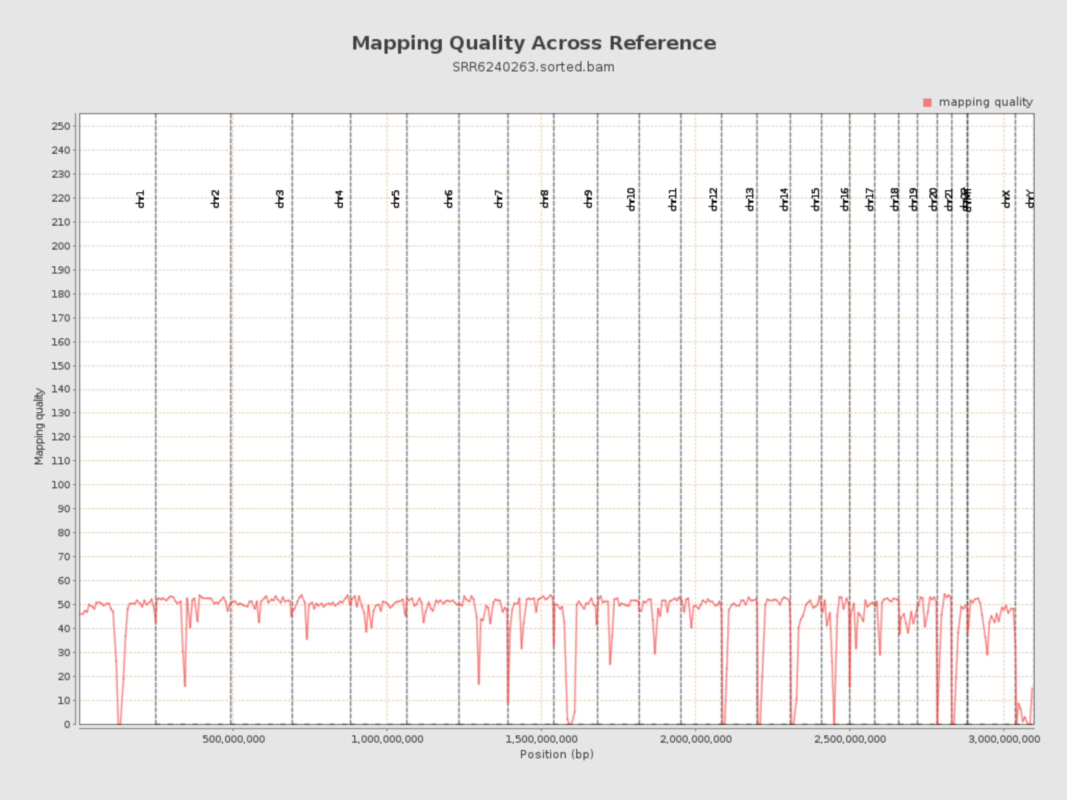
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram