Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:34:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013240.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_SRR6013240 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013240.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:34:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013240.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,810,671
Mapped reads	1,596,066 / 88.15%
Unmapped reads	214,605 / 11.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,500 / 1.13%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	96,845 / 5.35%
Duplication rate	5.16%
Clipped reads	784,632 / 43.33%

2.2. ACGT Content

Number/percentage of A's	28,697,333 / 27.34%
Number/percentage of C's	19,735,680 / 18.81%
Number/percentage of T's	32,837,588 / 31.29%
Number/percentage of G's	23,650,556 / 22.54%
Number/percentage of N's	26,336 / 0.03%
GC Percentage	41.34%

2.3. Coverage

Mean	0.0339

Standard Deviation	0.2731

2.4. Mapping Quality

Mean Mapping Quality	42.78

2.5. Mismatches and indels

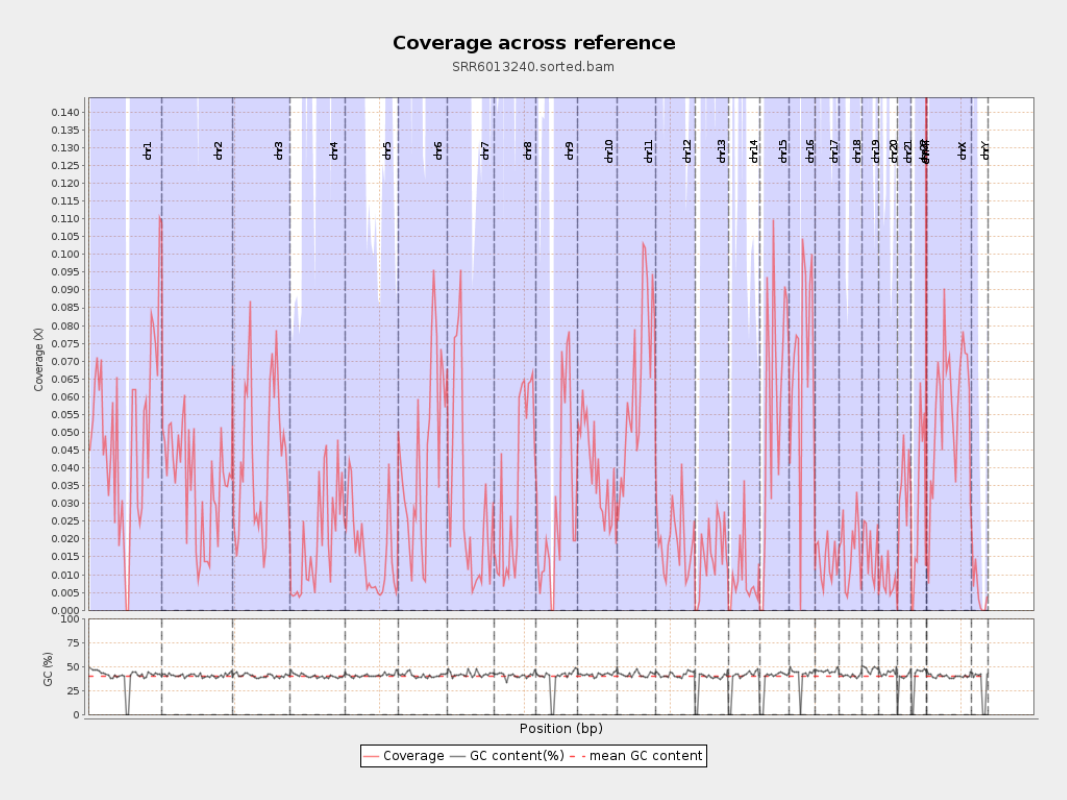
General error rate	0.8%
Mismatches	821,438
Insertions	7,097
Mapped reads with at least one insertion	0.44%
Deletions	27,342
Mapped reads with at least one deletion	1.69%
Homopolymer indels	45.69%

2.6. Chromosome stats

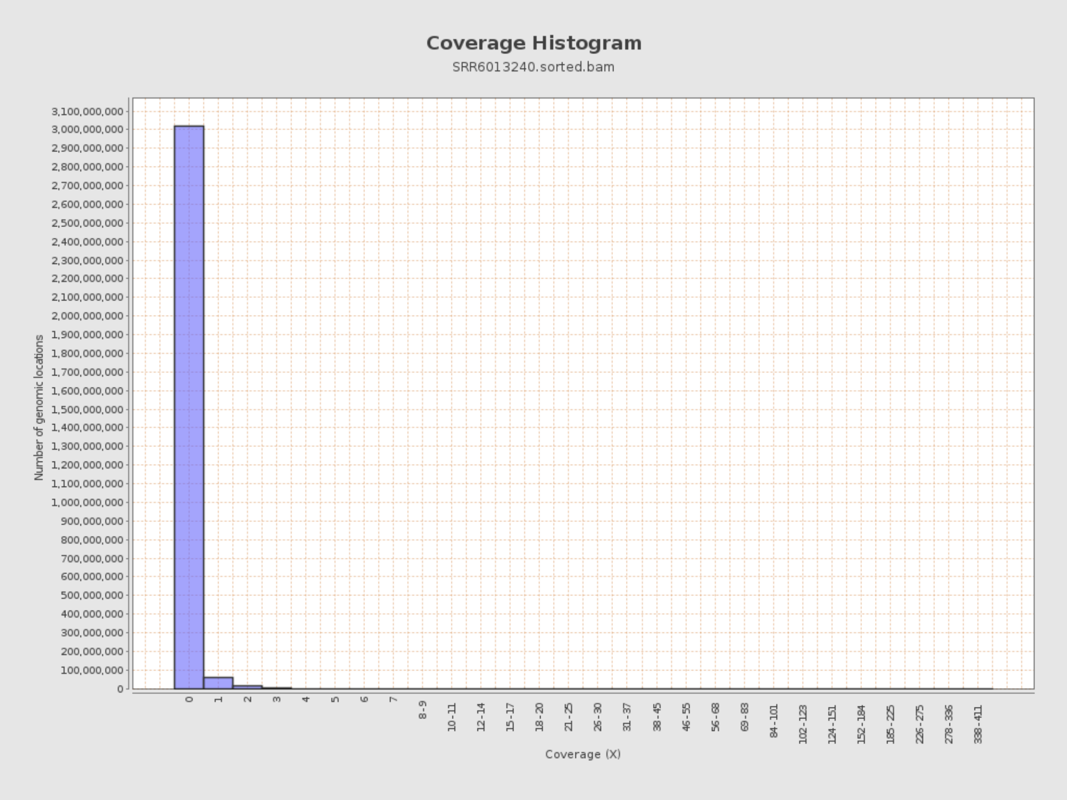
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12173425	0.0488	0.3124
chr2	243199373	8649528	0.0356	0.3179
chr3	198022430	8555190	0.0432	0.2652
chr4	191154276	3699110	0.0194	0.1861
chr5	180915260	2837192	0.0157	0.1602
chr6	171115067	7429310	0.0434	0.2856
chr7	159138663	4961864	0.0312	0.2568

chr8	146364022	5048657	0.0345	0.2977
chr9	141213431	4045442	0.0286	0.248
chr10	135534747	5343732	0.0394	0.3036
chr11	135006516	8488121	0.0629	0.4044
chr12	133851895	2612391	0.0195	0.1772
chr13	115169878	1766201	0.0153	0.1569
chr14	107349540	940075	0.0088	0.1233
chr15	102531392	6015870	0.0587	0.3132
chr16	90354753	6307893	0.0698	0.3812
chr17	81195210	1121675	0.0138	0.1695
chr18	78077248	1361746	0.0174	0.4145
chr19	59128983	992851	0.0168	0.2481
chr20	63025520	552412	0.0088	0.1204
chr21	48129895	1597443	0.0332	0.2425
chr22	51304566	1537177	0.03	0.2205
chrMT	16571	8518	0.514	0.9578
chrX	155270560	8628726	0.0556	0.3295
chrY	59373566	320591	0.0054	0.1203

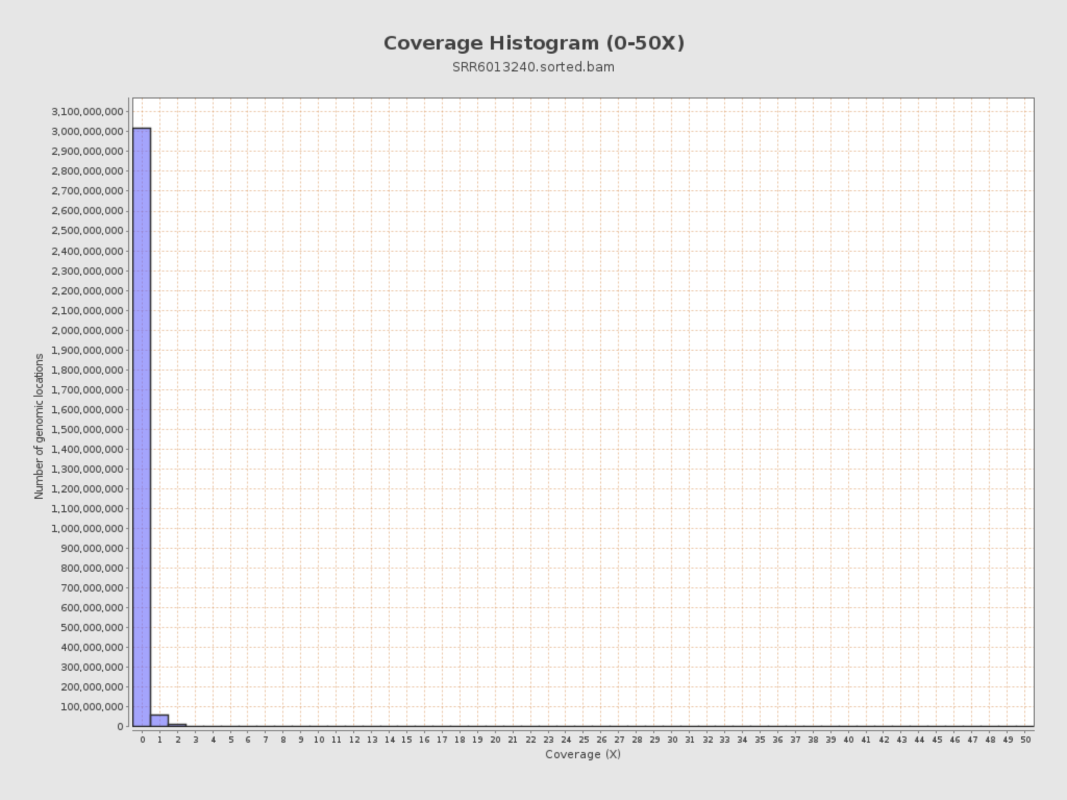
3. Results : Coverage across reference



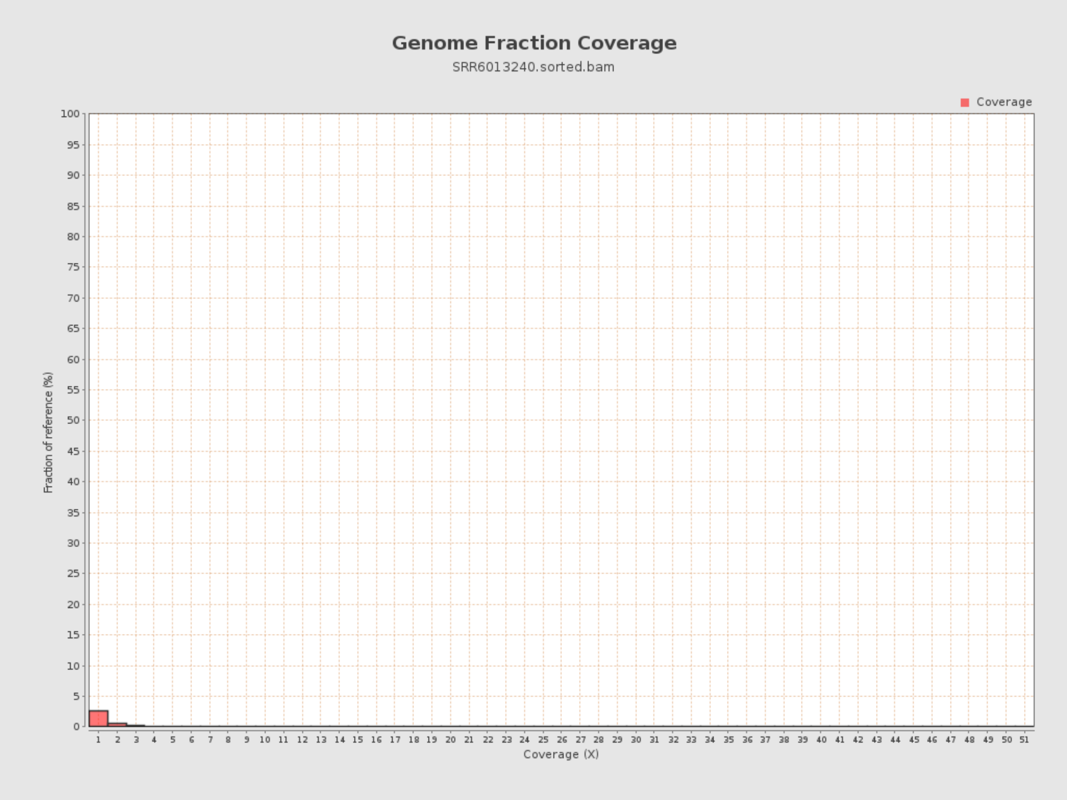
4. Results : Coverage Histogram



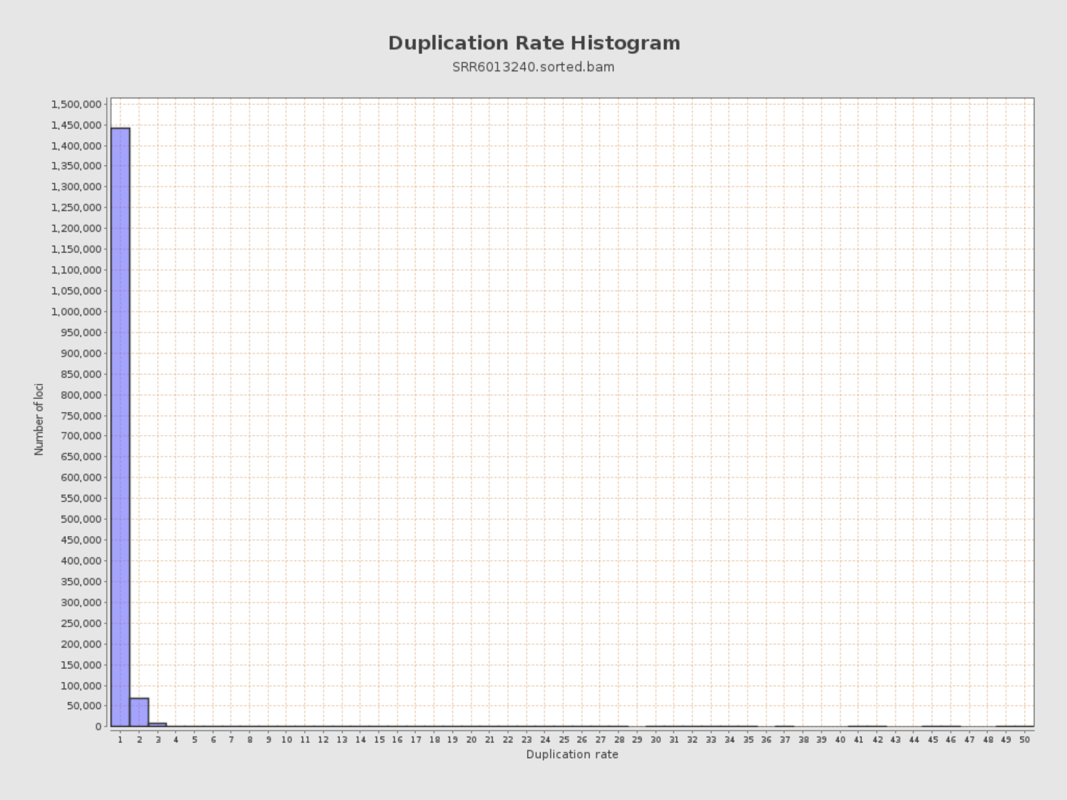
5. Results : Coverage Histogram (0-50X)



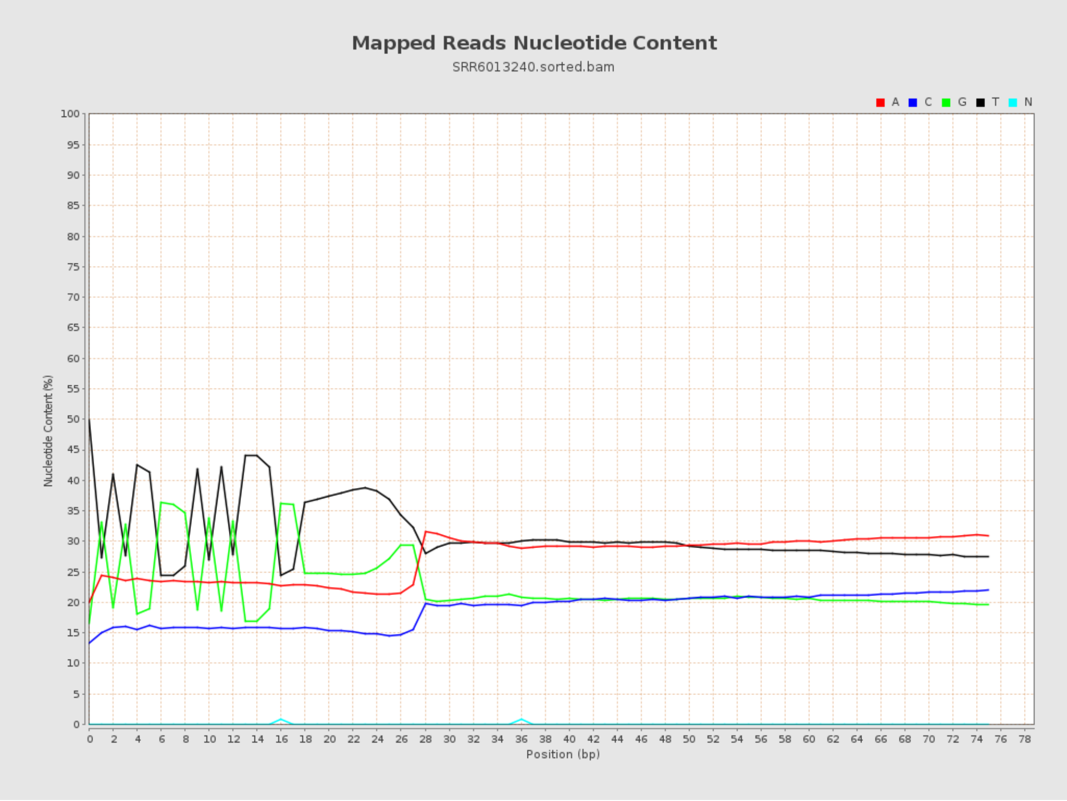
6. Results : Genome Fraction Coverage



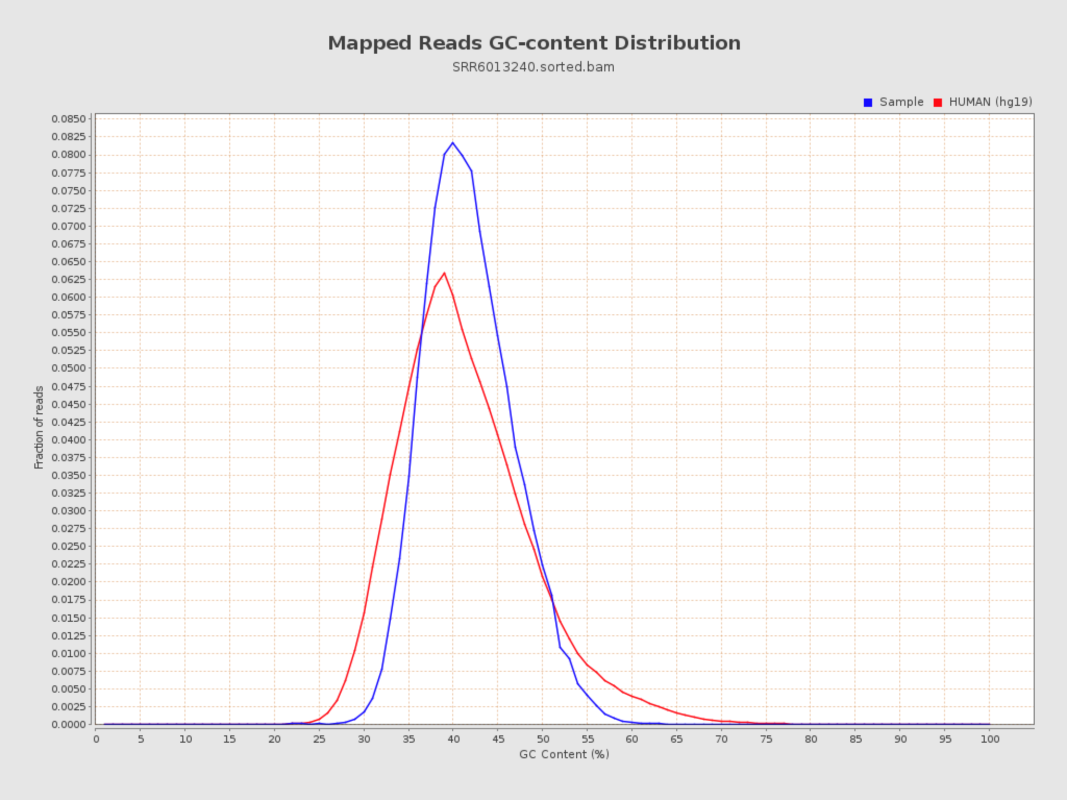
7. Results : Duplication Rate Histogram



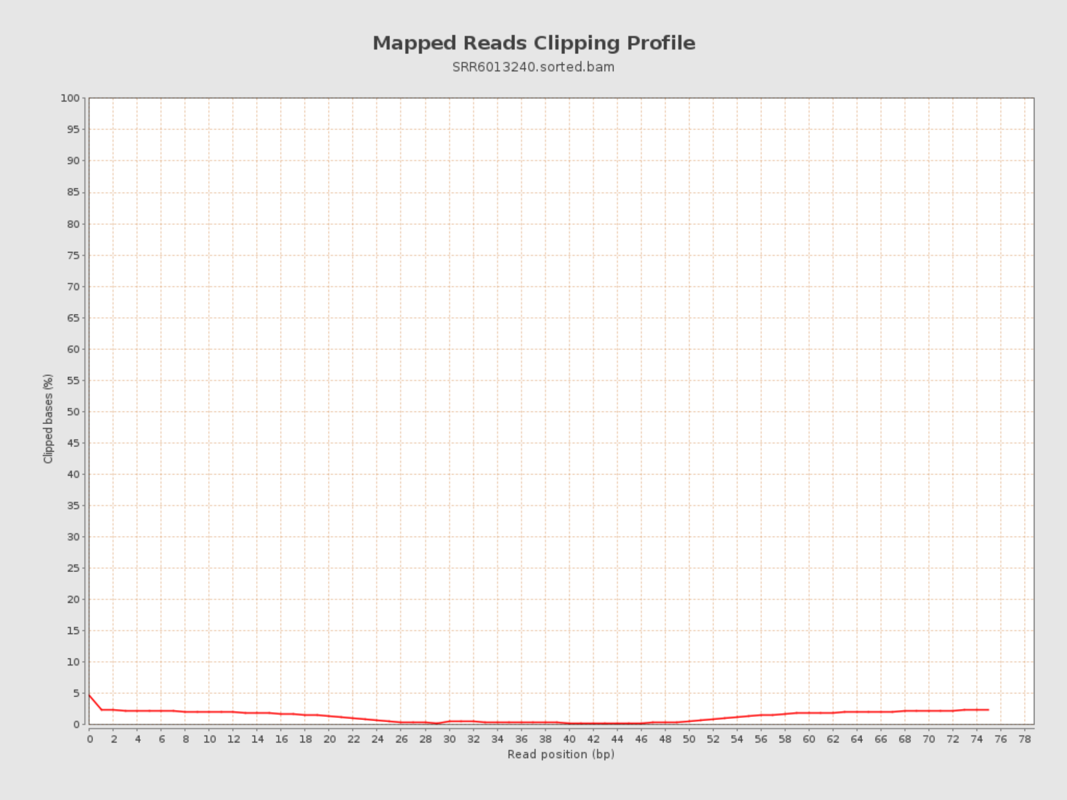
8. Results : Mapped Reads Nucleotide Content



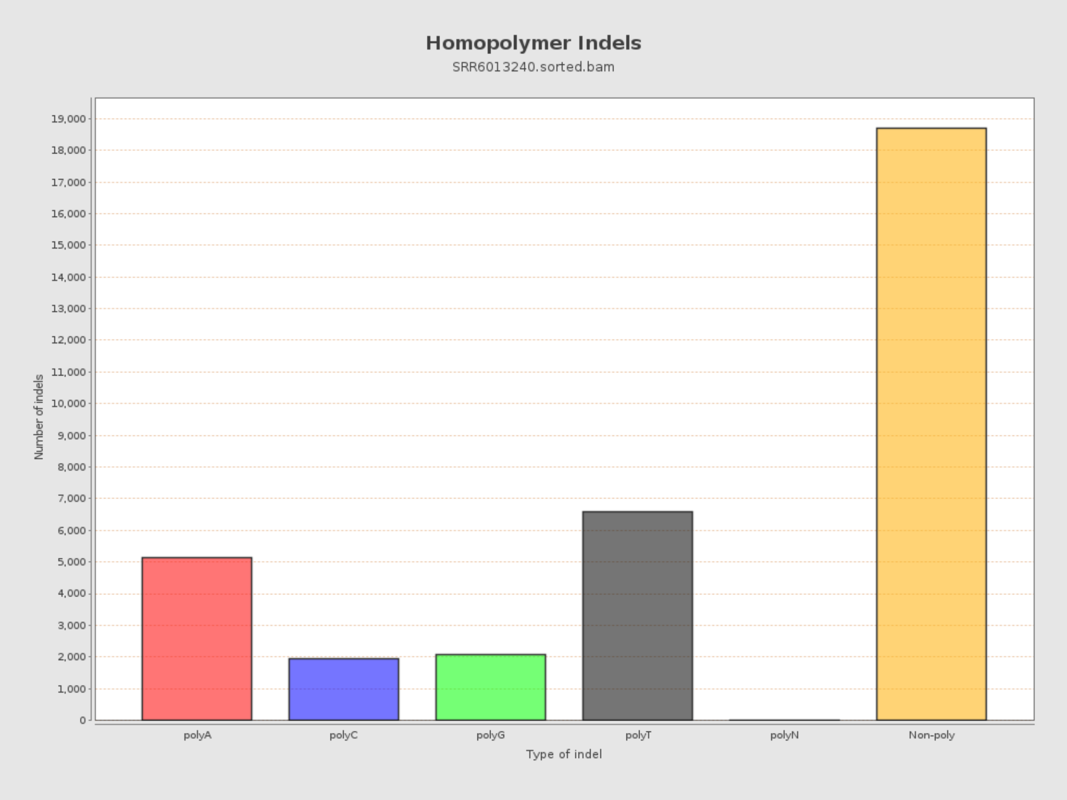
9. Results : Mapped Reads GC-content Distribution



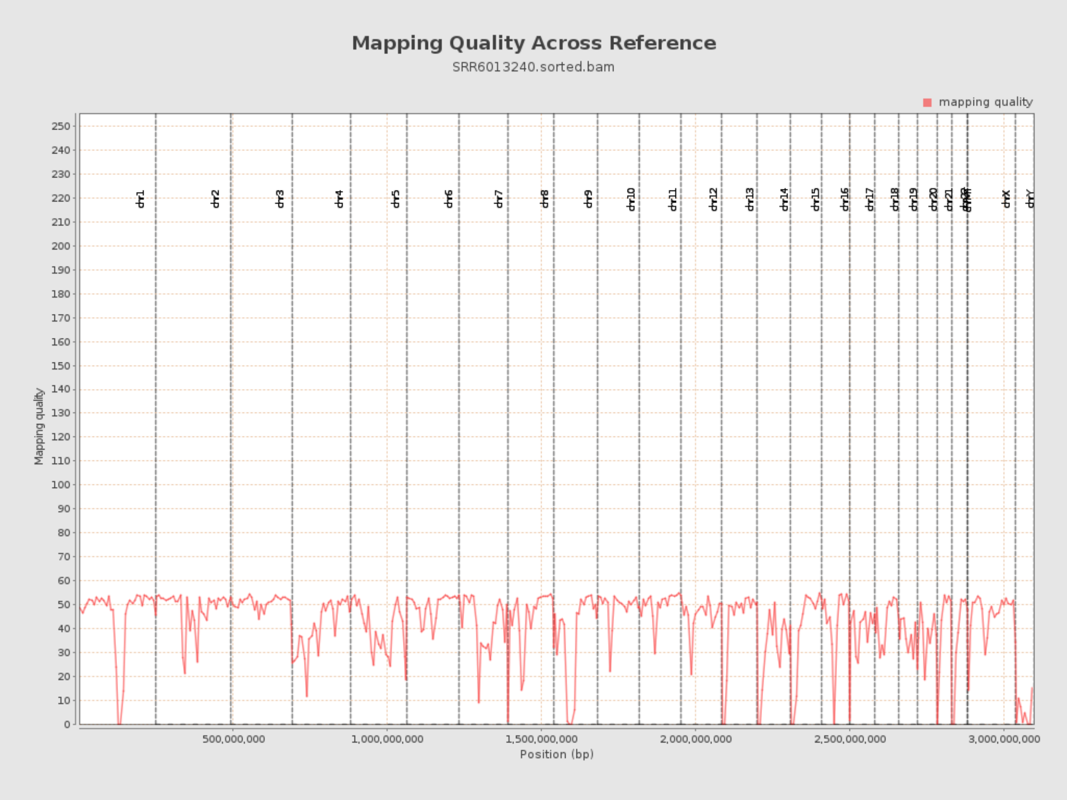
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram