Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:20:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240269.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_SRR6240269 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240269.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:20:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240269.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,895,509
Mapped reads	1,468,840 / 77.49%
Unmapped reads	426,669 / 22.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,603 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	152,502 / 8.05%
Duplication rate	8.52%
Clipped reads	1,029,474 / 54.31%

2.2. ACGT Content

Number/percentage of A's	23,716,531 / 26.69%
Number/percentage of C's	14,958,645 / 16.83%
Number/percentage of T's	29,542,285 / 33.25%
Number/percentage of G's	20,617,809 / 23.2%
Number/percentage of N's	19,574 / 0.02%
GC Percentage	40.04%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2795

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

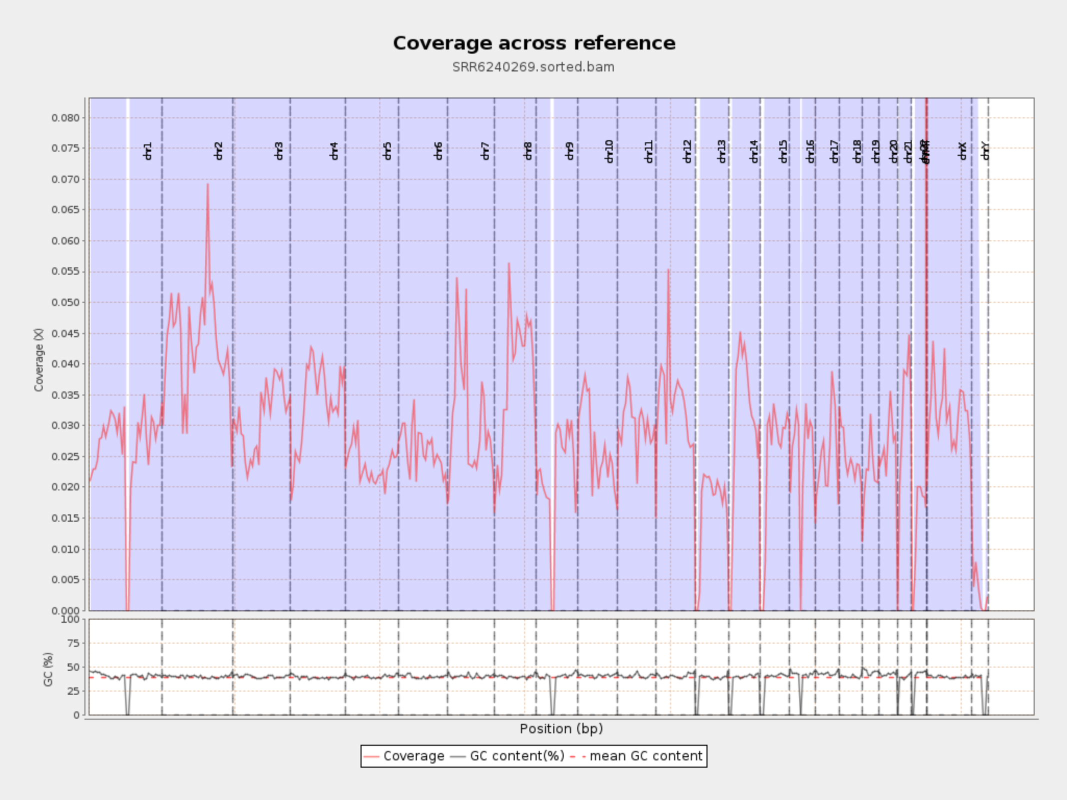
General error rate	0.98%
Mismatches	857,300
Insertions	6,278
Mapped reads with at least one insertion	0.42%
Deletions	29,135
Mapped reads with at least one deletion	1.96%
Homopolymer indels	50.59%

2.6. Chromosome stats

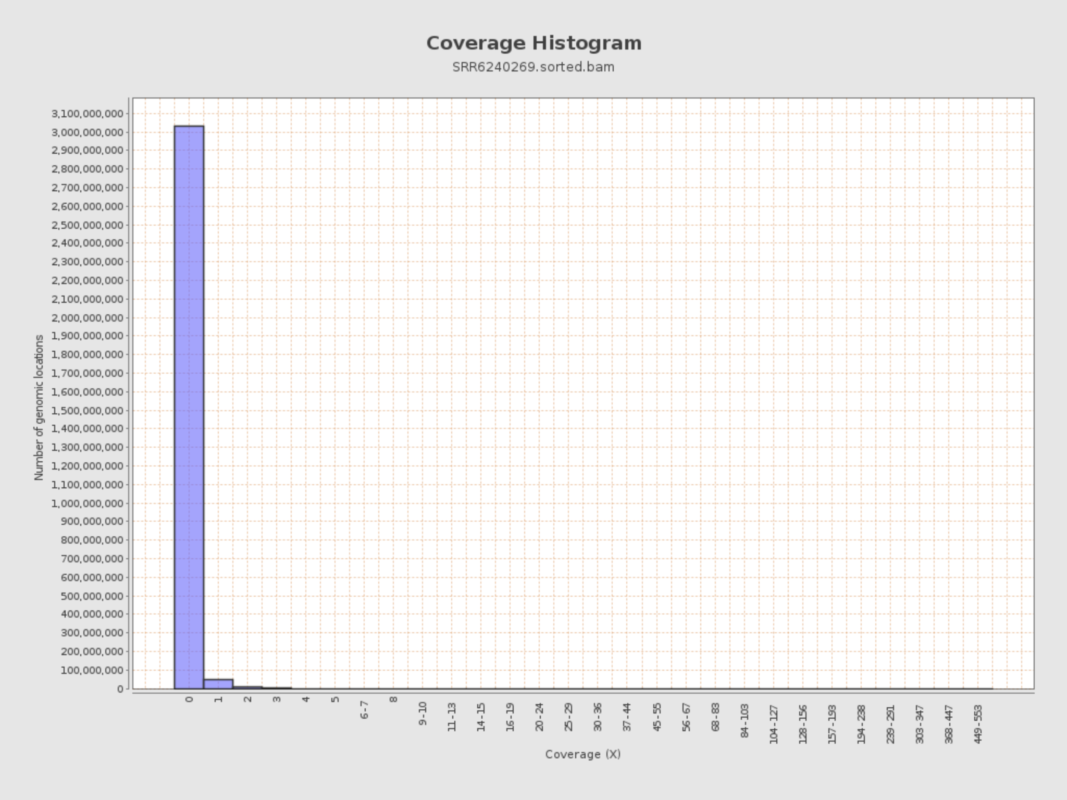
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6596341	0.0265	0.3206
chr2	243199373	10619497	0.0437	0.3695
chr3	198022430	6207171	0.0313	0.2348
chr4	191154276	6440921	0.0337	0.2502
chr5	180915260	4299792	0.0238	0.2032
chr6	171115067	4465703	0.0261	0.2372
chr7	159138663	5058771	0.0318	0.5074

chr8	146364022	5607358	0.0383	0.3402
chr9	141213431	3092614	0.0219	0.2475
chr10	135534747	3666559	0.0271	0.2408
chr11	135006516	4070767	0.0302	0.2708
chr12	133851895	4546108	0.034	0.2391
chr13	115169878	1883971	0.0164	0.168
chr14	107349540	3251444	0.0303	0.2301
chr15	102531392	2460367	0.024	0.2139
chr16	90354753	2259770	0.025	0.2038
chr17	81195210	2040899	0.0251	0.2194
chr18	78077248	1944745	0.0249	0.3265
chr19	59128983	1348376	0.0228	0.2547
chr20	63025520	1682049	0.0267	0.2173
chr21	48129895	1476215	0.0307	0.2343
chr22	51304566	690813	0.0135	0.1454
chrMT	16571	64857	3.9139	4.8666
chrX	155270560	4945987	0.0319	0.2514
chrY	59373566	183030	0.0031	0.0708

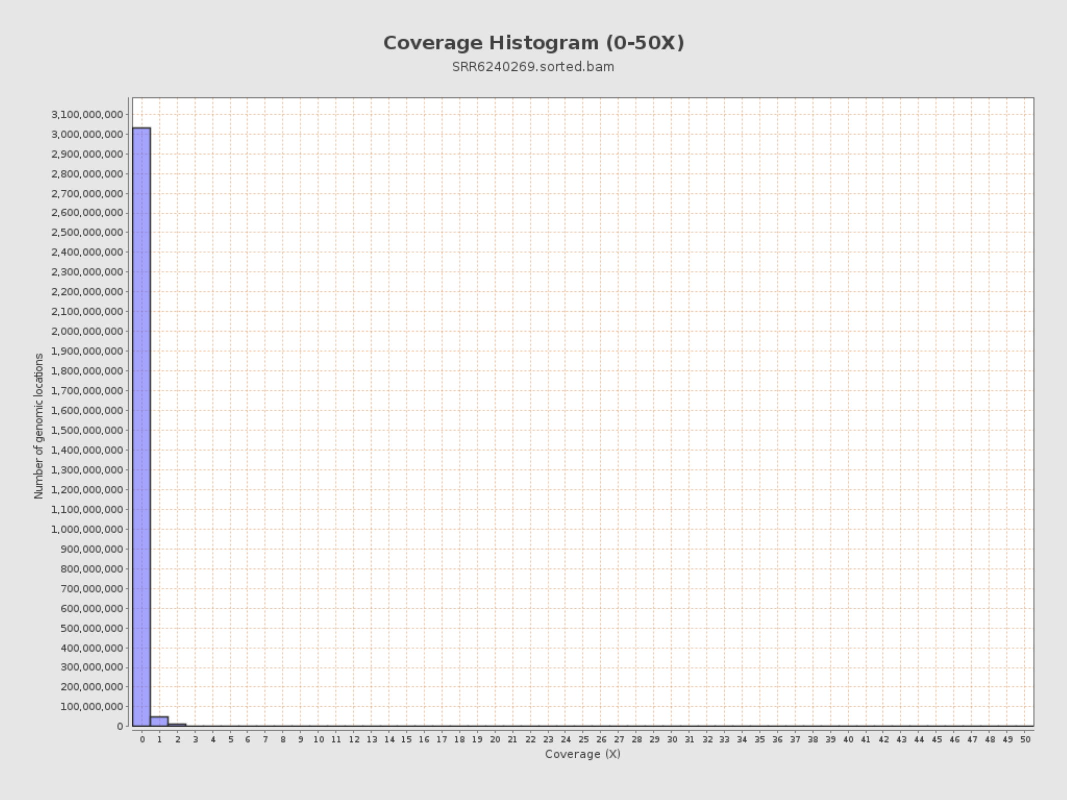
3. Results : Coverage across reference



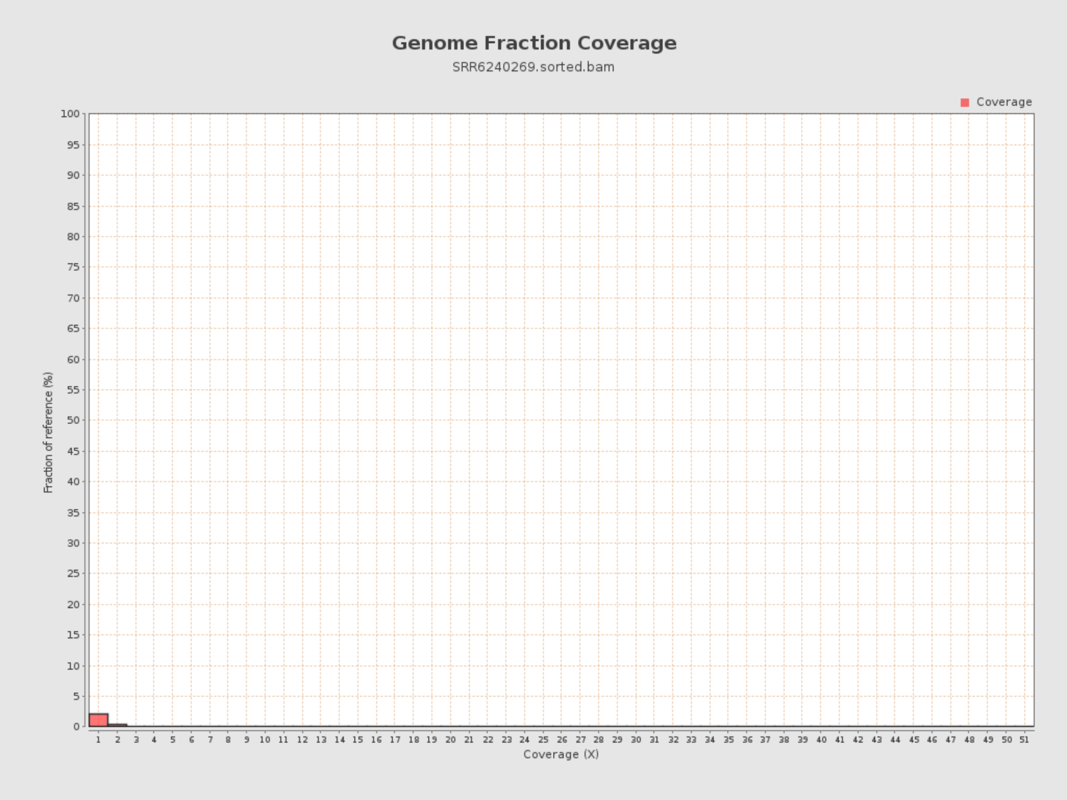
4. Results : Coverage Histogram



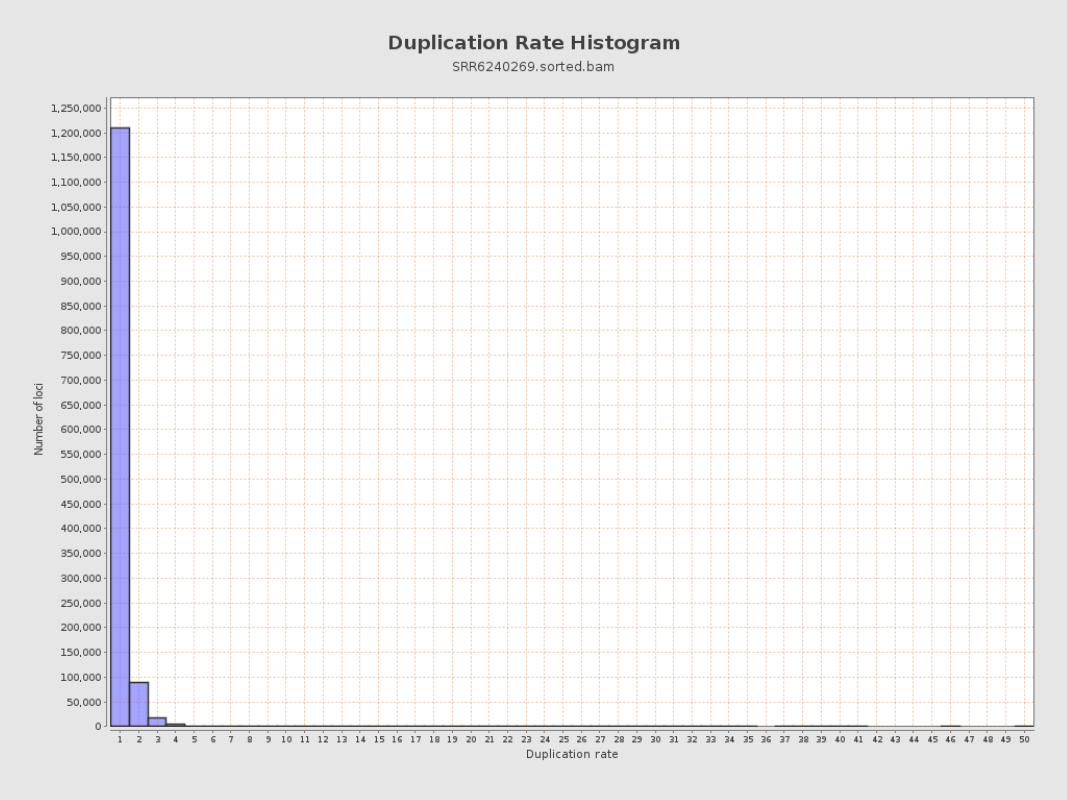
5. Results : Coverage Histogram (0-50X)



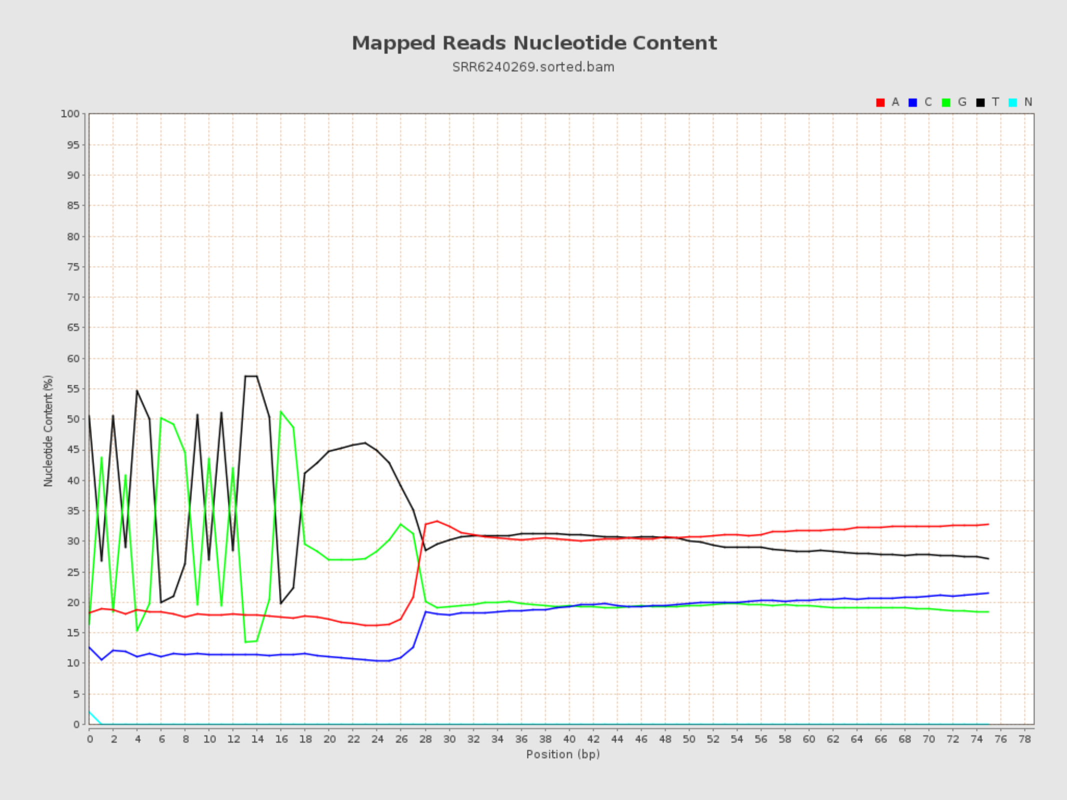
6. Results : Genome Fraction Coverage



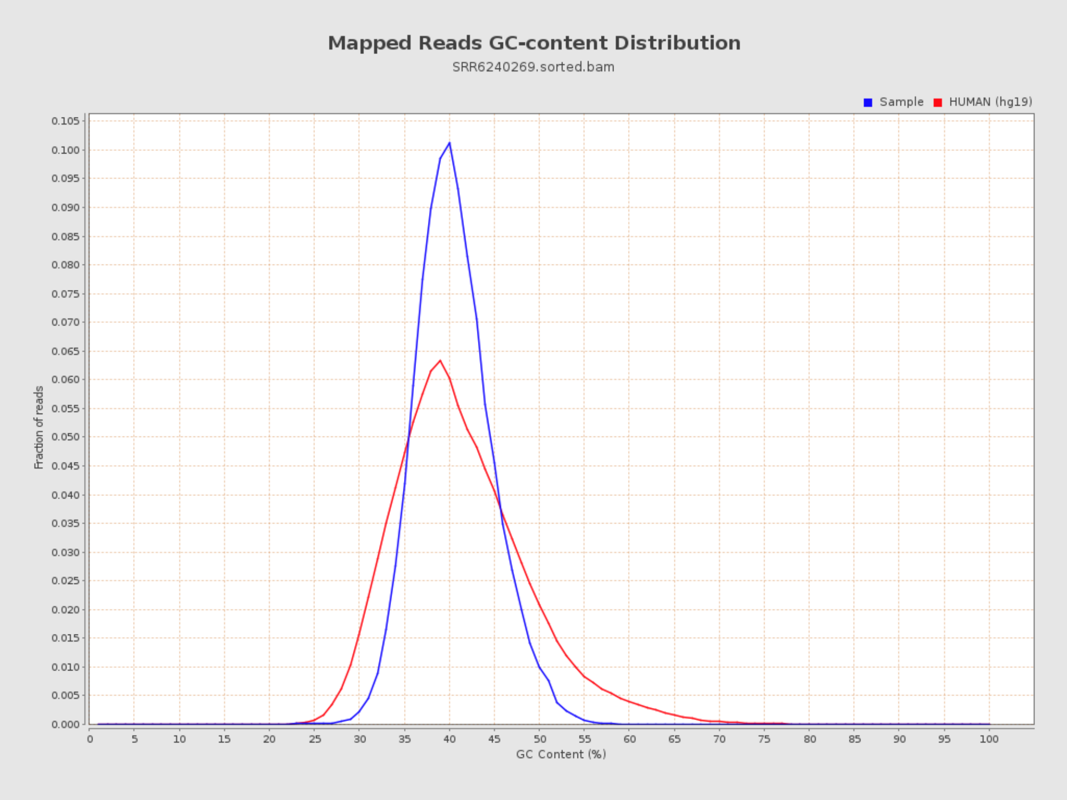
7. Results : Duplication Rate Histogram



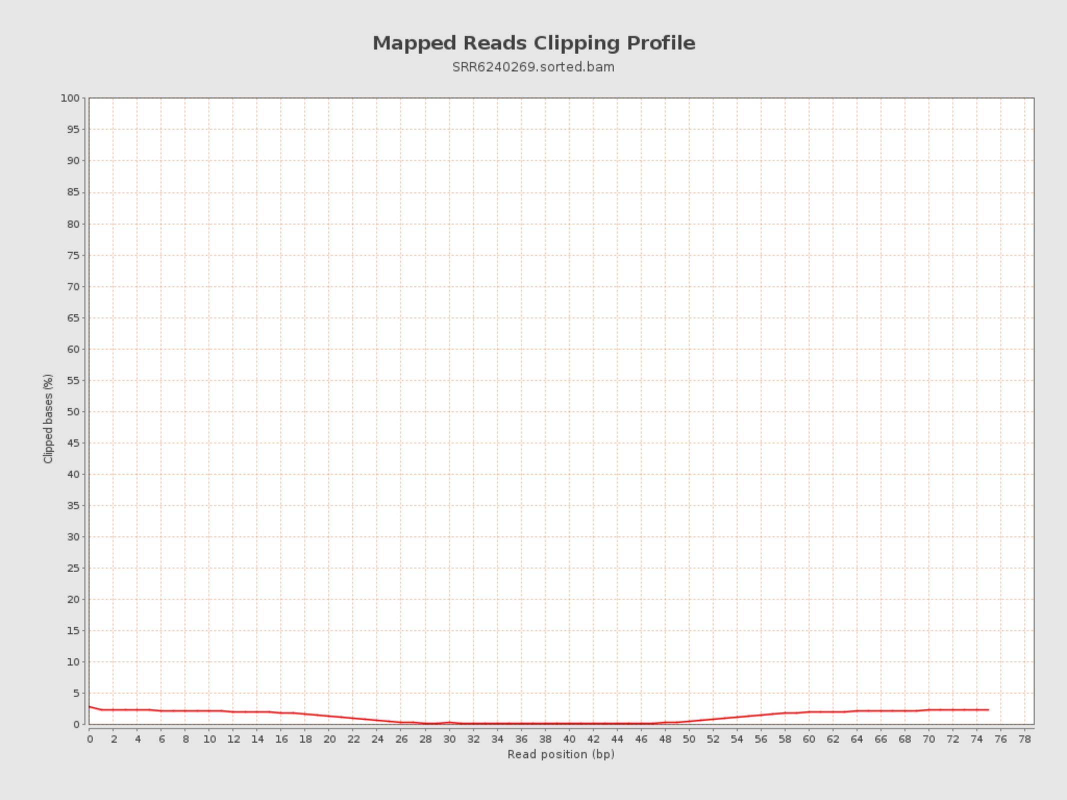
8. Results : Mapped Reads Nucleotide Content



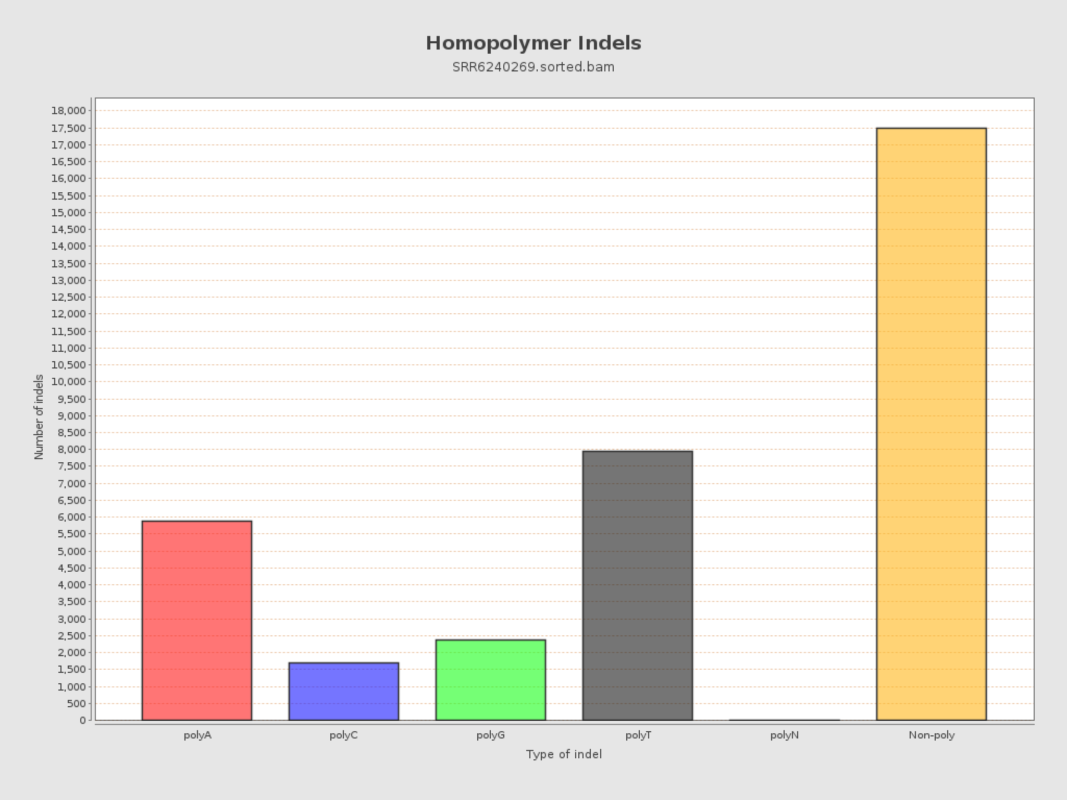
9. Results : Mapped Reads GC-content Distribution



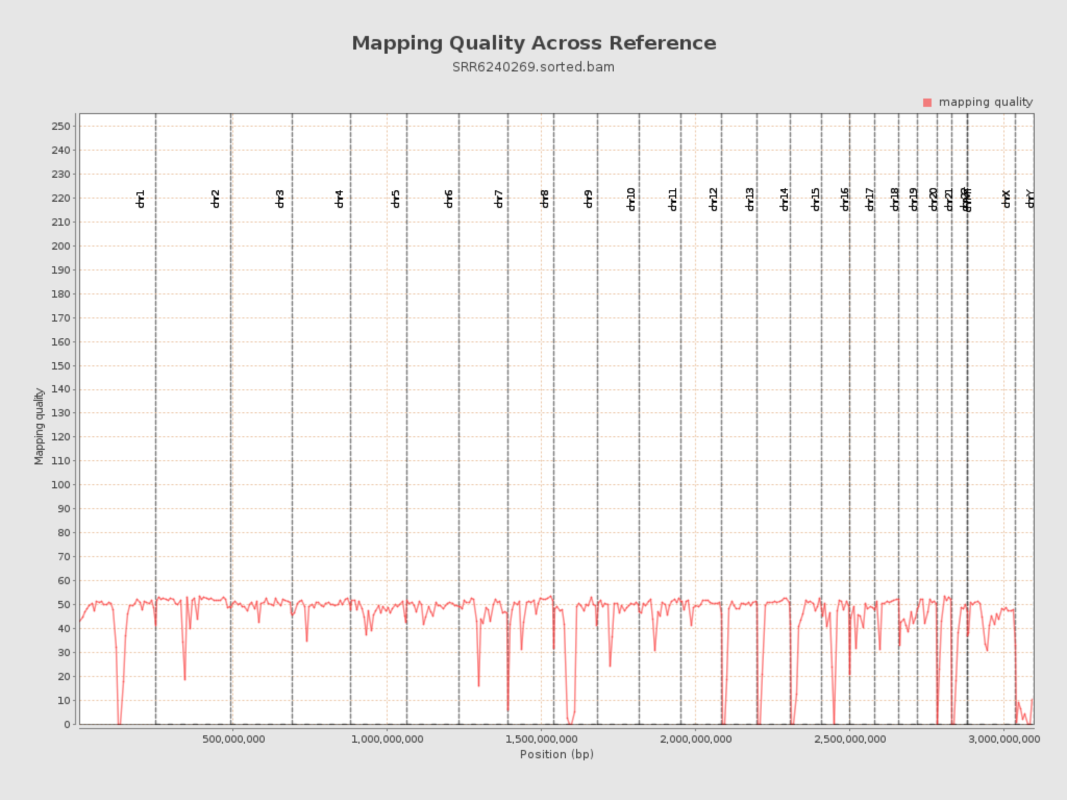
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram