

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:23:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240270.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_SRR6240270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240270.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:23:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,451,038
Mapped reads	1,965,359 / 80.18%
Unmapped reads	485,679 / 19.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,045 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	97,313 / 3.97%
Duplication rate	3.36%
Clipped reads	996,363 / 40.65%

2.2. ACGT Content

Number/percentage of A's	35,807,455 / 27.96%
Number/percentage of C's	23,299,272 / 18.2%
Number/percentage of T's	39,503,832 / 30.85%
Number/percentage of G's	29,405,321 / 22.96%
Number/percentage of N's	32,320 / 0.03%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0414

Standard Deviation	0.5291
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2.4. Mapping Quality

Mean Mapping Quality	44.2
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2.5. Mismatches and indels

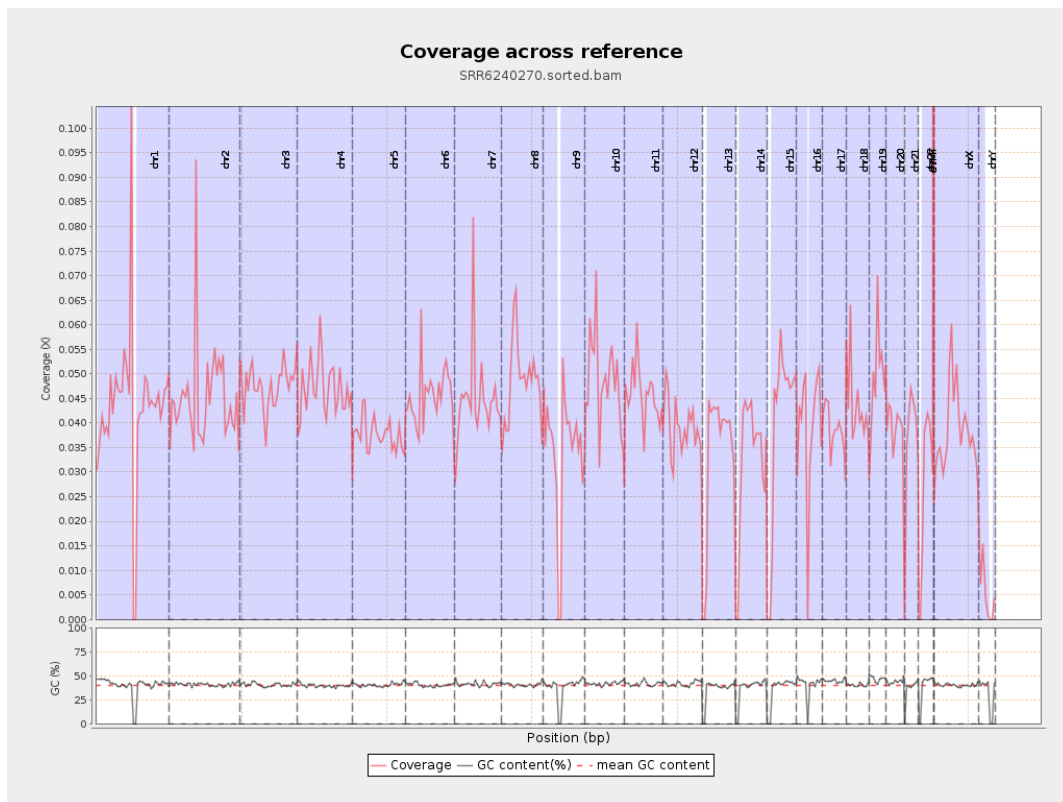
General error rate	0.9%
Mismatches	1,135,759
Insertions	9,415
Mapped reads with at least one insertion	0.47%
Deletions	31,731
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.92%

2.6. Chromosome stats

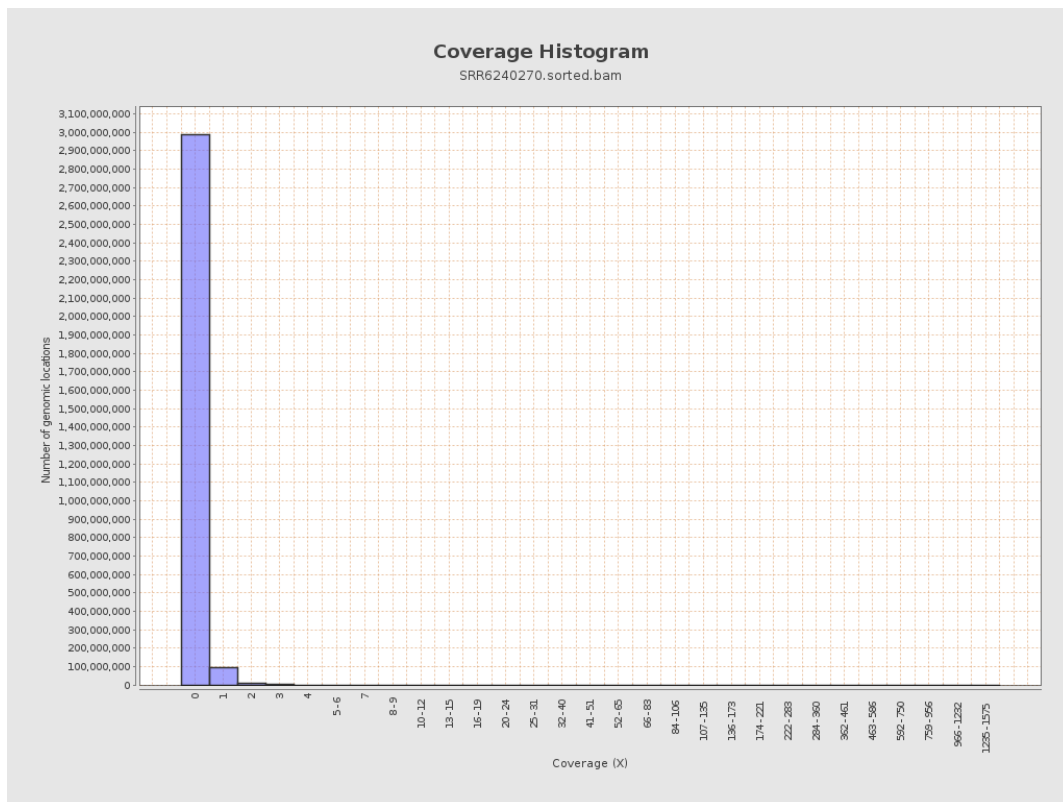
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10828290	0.0434	1.3149
chr2	243199373	10976050	0.0451	0.5402
chr3	198022430	9417145	0.0476	0.2511
chr4	191154276	9014519	0.0472	0.2645
chr5	180915260	6817079	0.0377	0.2276
chr6	171115067	7766067	0.0454	0.3242
chr7	159138663	7158708	0.045	0.5763

chr8	146364022	7072073	0.0483	0.604
chr9	141213431	4789411	0.0339	0.4218
chr10	135534747	6615276	0.0488	0.3714
chr11	135006516	6164982	0.0457	0.3785
chr12	133851895	5241794	0.0392	0.2392
chr13	115169878	3841637	0.0334	0.2106
chr14	107349540	3457808	0.0322	0.2332
chr15	102531392	4068251	0.0397	0.2509
chr16	90354753	3526406	0.039	0.2638
chr17	81195210	3113378	0.0383	0.265
chr18	78077248	3411399	0.0437	0.7711
chr19	59128983	2957202	0.05	0.7913
chr20	63025520	2432380	0.0386	0.2431
chr21	48129895	1768336	0.0367	0.2384
chr22	51304566	1371613	0.0267	0.1866
chrMT	16571	13073	0.7889	1.1441
chrX	155270560	5966802	0.0384	0.2822
chrY	59373566	313199	0.0053	0.1159

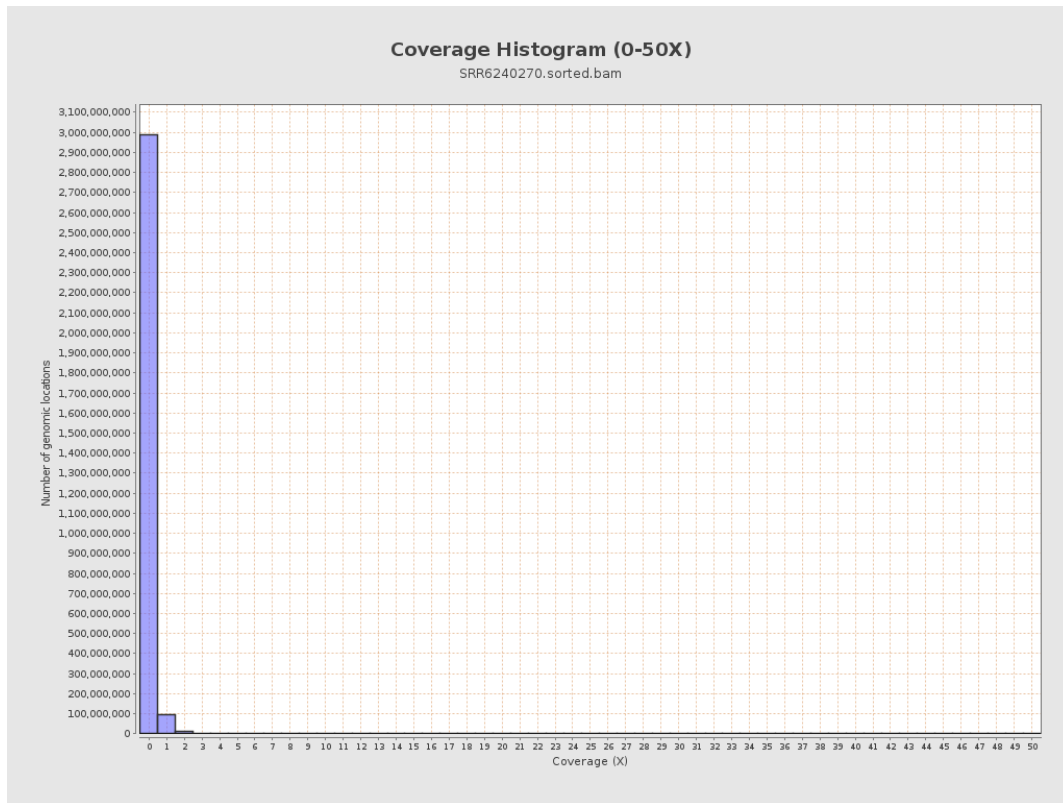
3. Results : Coverage across reference



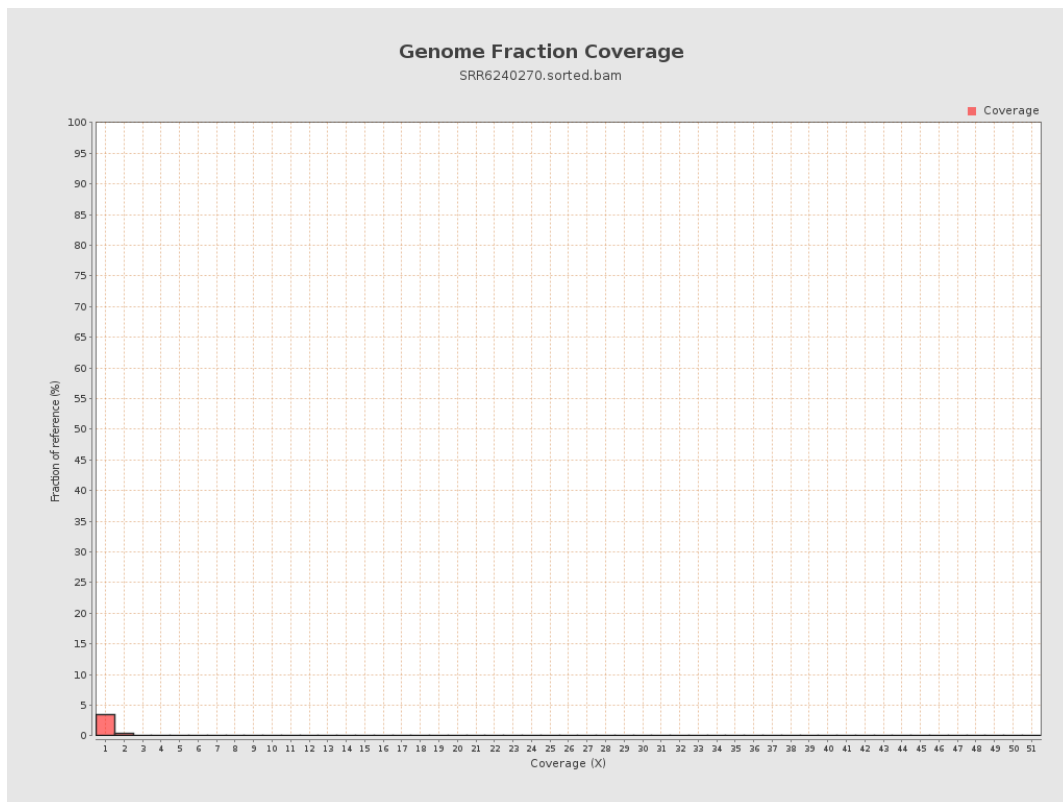
4. Results : Coverage Histogram



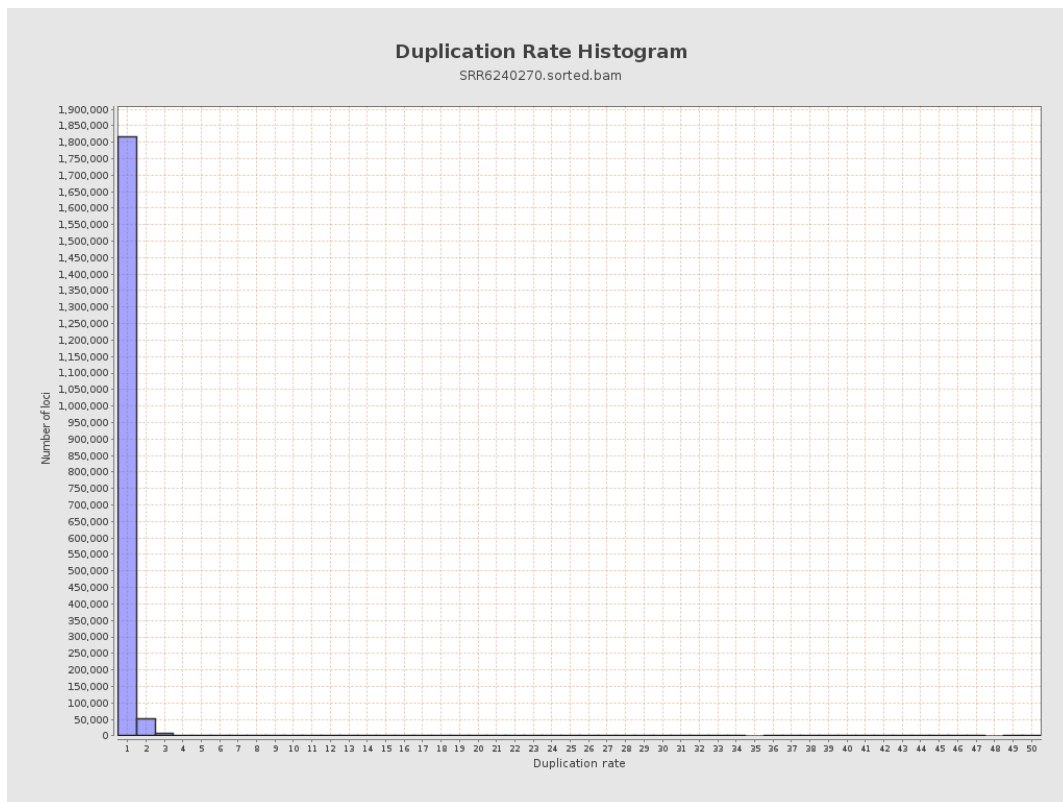
5. Results : Coverage Histogram (0-50X)



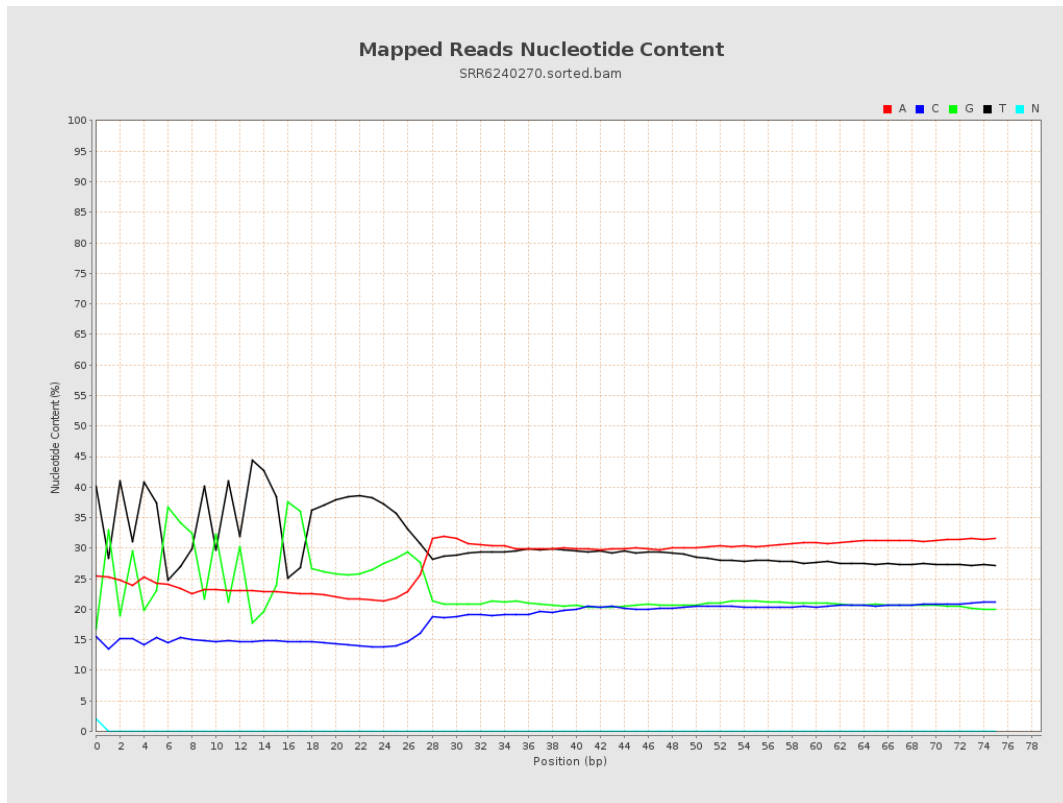
6. Results : Genome Fraction Coverage



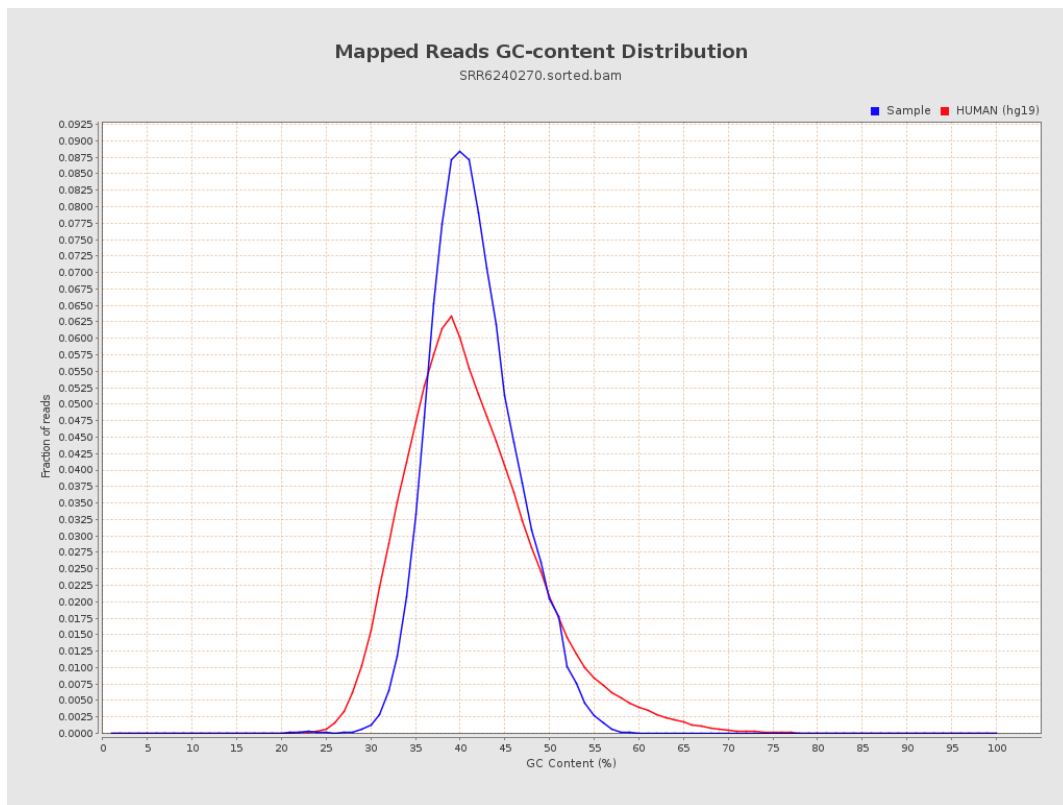
7. Results : Duplication Rate Histogram



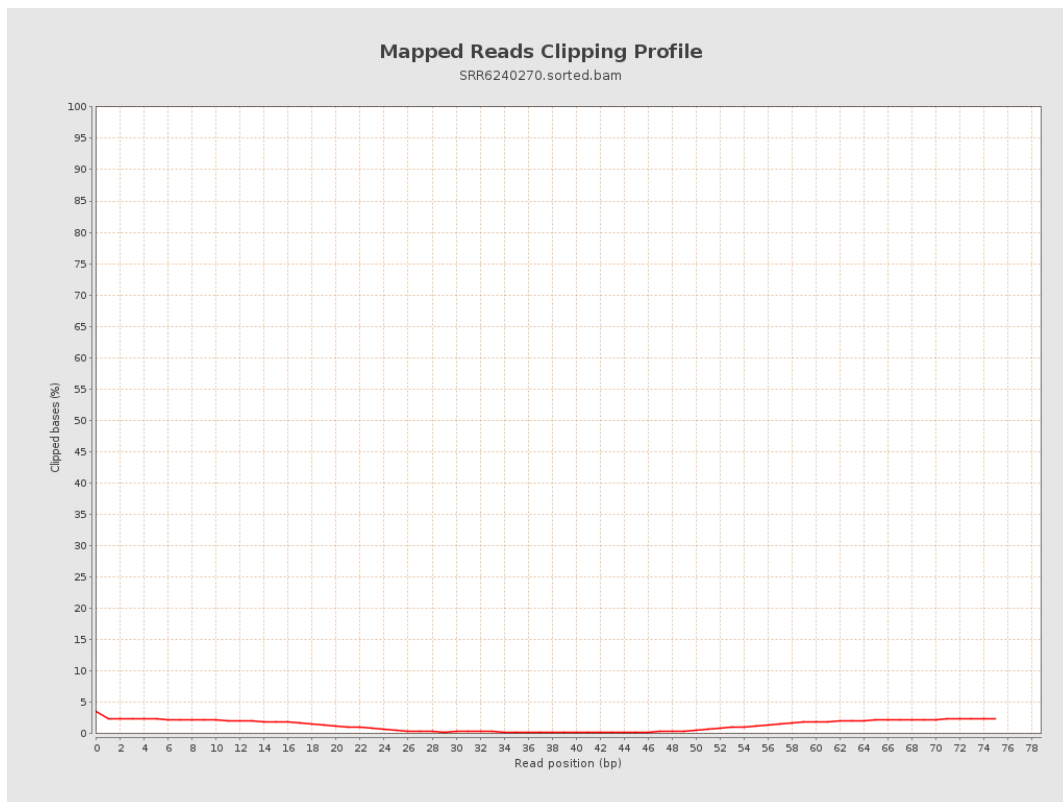
8. Results : Mapped Reads Nucleotide Content



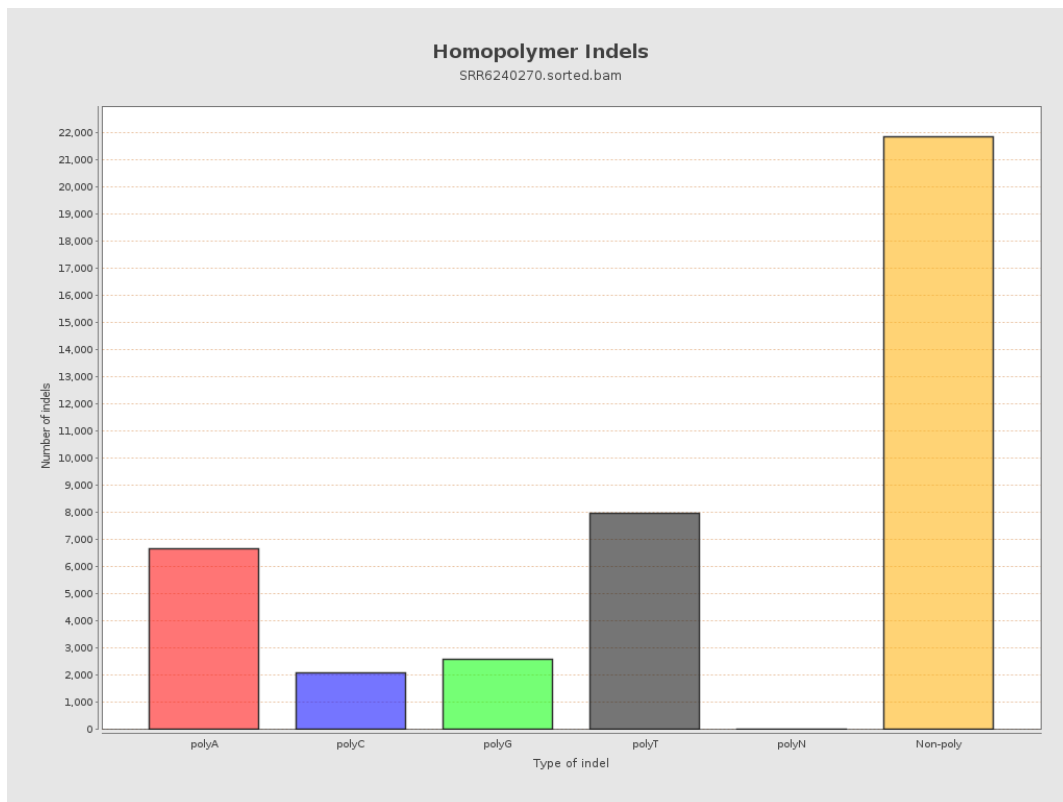
9. Results : Mapped Reads GC-content Distribution



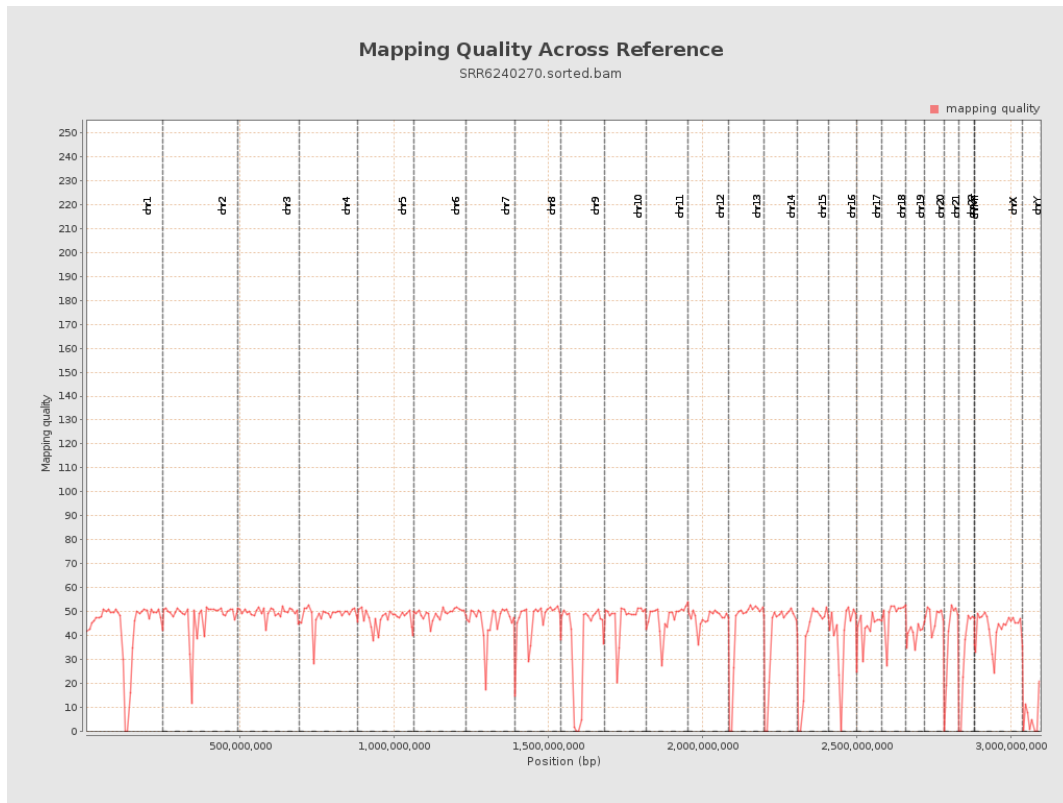
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

