

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:17:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240268.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_SRR6240268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240268.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:17:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,001,687
Mapped reads	1,559,414 / 77.9%
Unmapped reads	442,273 / 22.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,839 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	139,796 / 6.98%
Duplication rate	6.94%
Clipped reads	1,158,863 / 57.89%

2.2. ACGT Content

Number/percentage of A's	23,829,129 / 25.82%
Number/percentage of C's	15,910,873 / 17.24%
Number/percentage of T's	29,007,999 / 31.43%
Number/percentage of G's	23,528,095 / 25.49%
Number/percentage of N's	21,670 / 0.02%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0298

Standard Deviation	0.2977
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2.4. Mapping Quality

Mean Mapping Quality	41.93
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2.5. Mismatches and indels

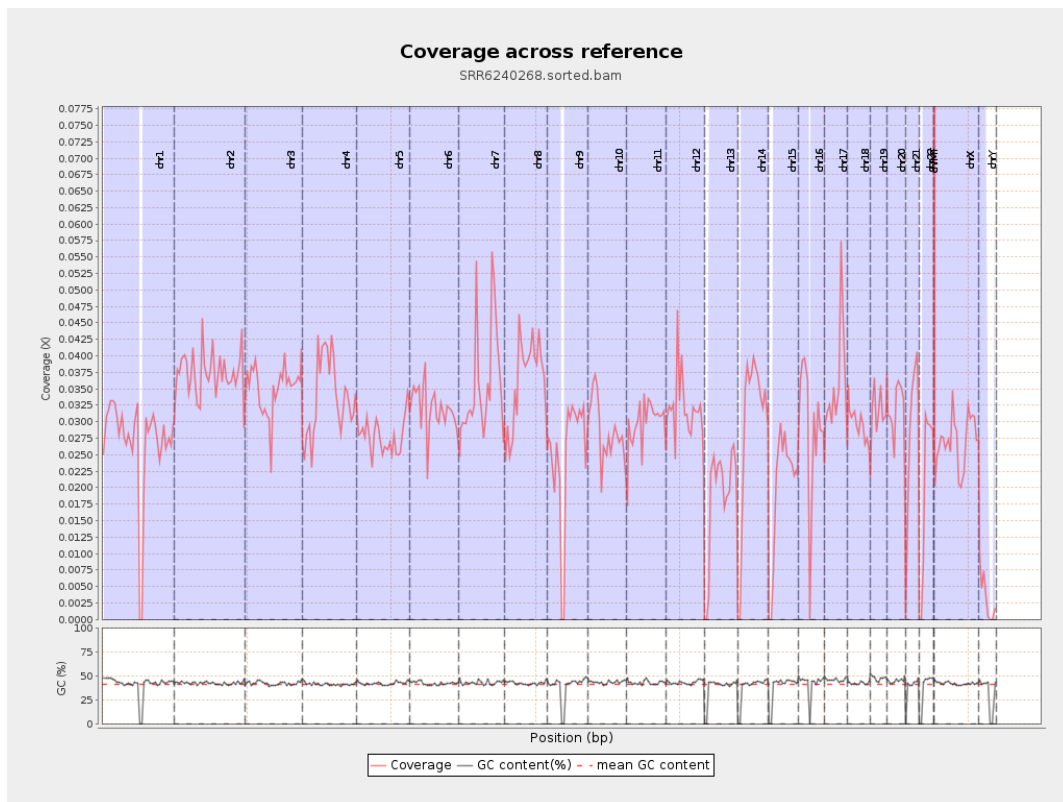
General error rate	1.02%
Mismatches	931,821
Insertions	7,439
Mapped reads with at least one insertion	0.47%
Deletions	32,386
Mapped reads with at least one deletion	2.05%
Homopolymer indels	49.17%

2.6. Chromosome stats

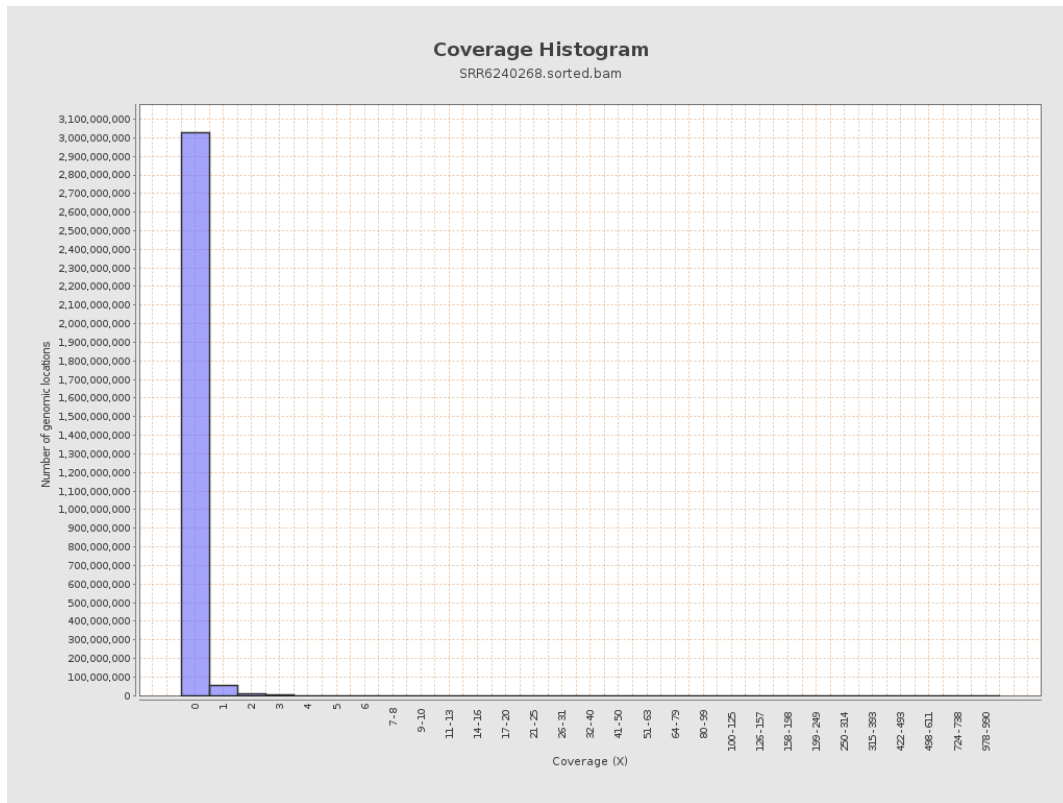
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6704805	0.0269	0.2909
chr2	243199373	9120057	0.0375	0.4962
chr3	198022430	6939764	0.035	0.2504
chr4	191154276	6444525	0.0337	0.2455
chr5	180915260	5035372	0.0278	0.2188
chr6	171115067	5449095	0.0318	0.2698
chr7	159138663	5633865	0.0354	0.5527

chr8	146364022	5334860	0.0364	0.2988
chr9	141213431	3504563	0.0248	0.2343
chr10	135534747	3870374	0.0286	0.2423
chr11	135006516	4065714	0.0301	0.2504
chr12	133851895	4283006	0.032	0.2347
chr13	115169878	2139457	0.0186	0.1847
chr14	107349540	3197874	0.0298	0.2379
chr15	102531392	2053964	0.02	0.2286
chr16	90354753	2590702	0.0287	0.2236
chr17	81195210	2917791	0.0359	0.2571
chr18	78077248	2310654	0.0296	0.3259
chr19	59128983	1885264	0.0319	0.2714
chr20	63025520	1984541	0.0315	0.2344
chr21	48129895	1382799	0.0287	0.2278
chr22	51304566	1037243	0.0202	0.1846
chrMT	16571	64630	3.9002	4.1417
chrX	155270560	4213206	0.0271	0.2329
chrY	59373566	190155	0.0032	0.0803

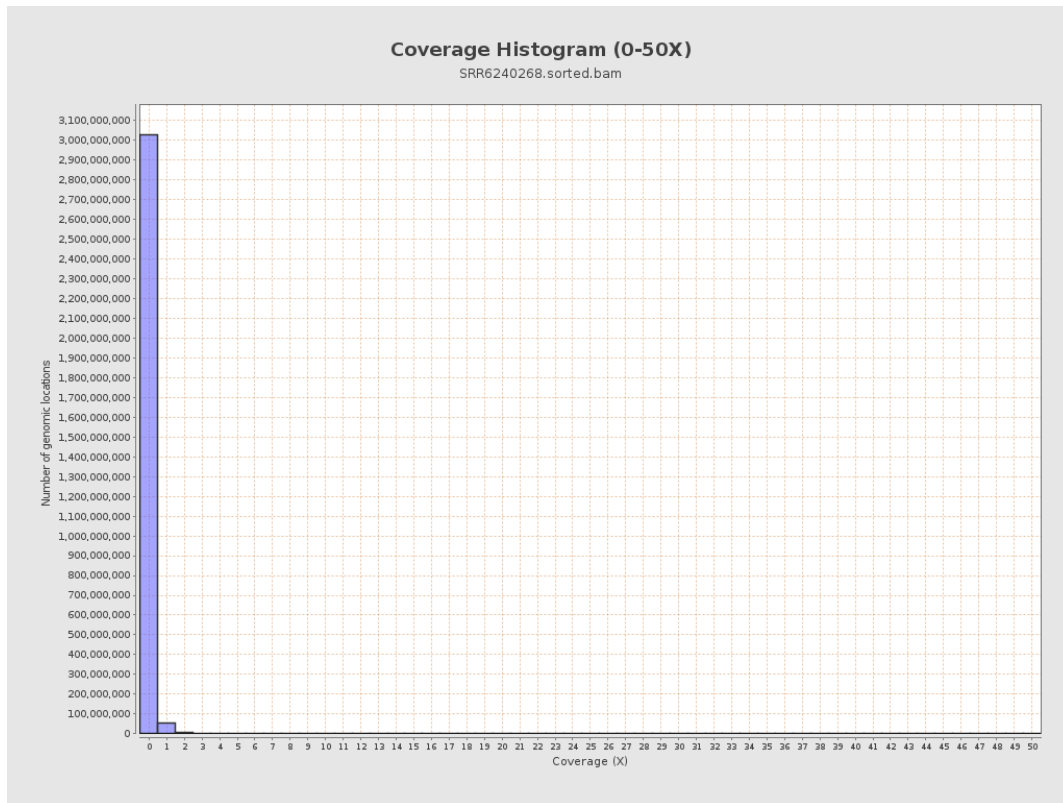
3. Results : Coverage across reference



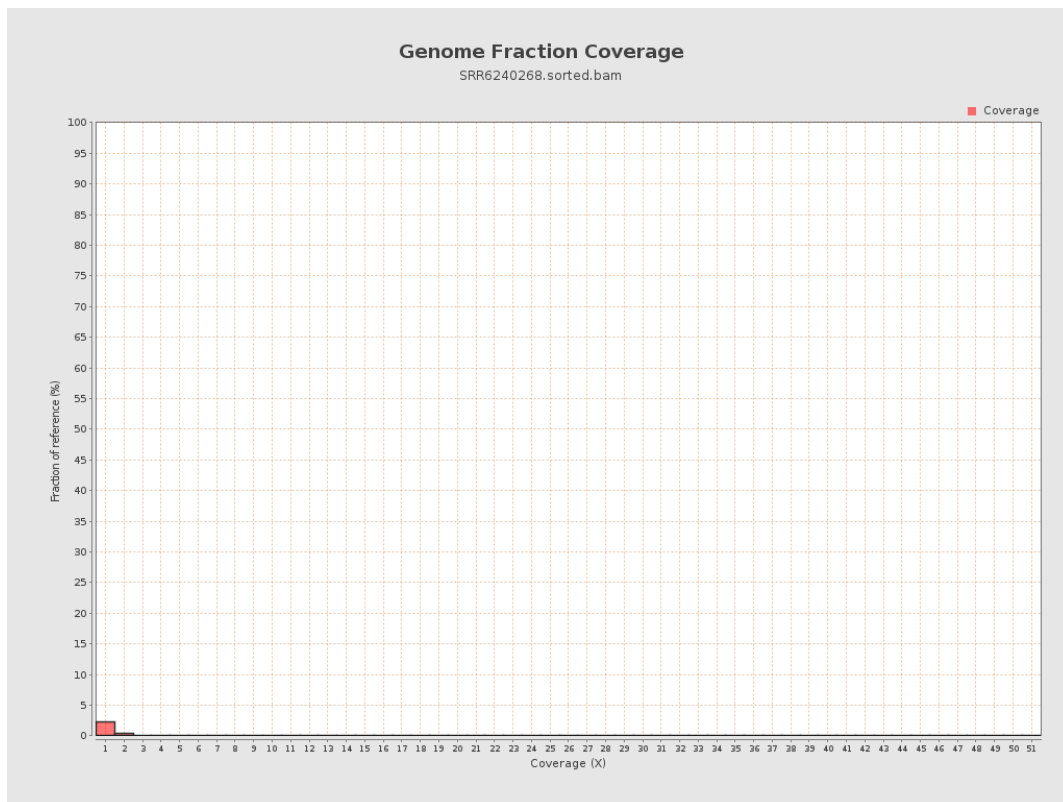
4. Results : Coverage Histogram



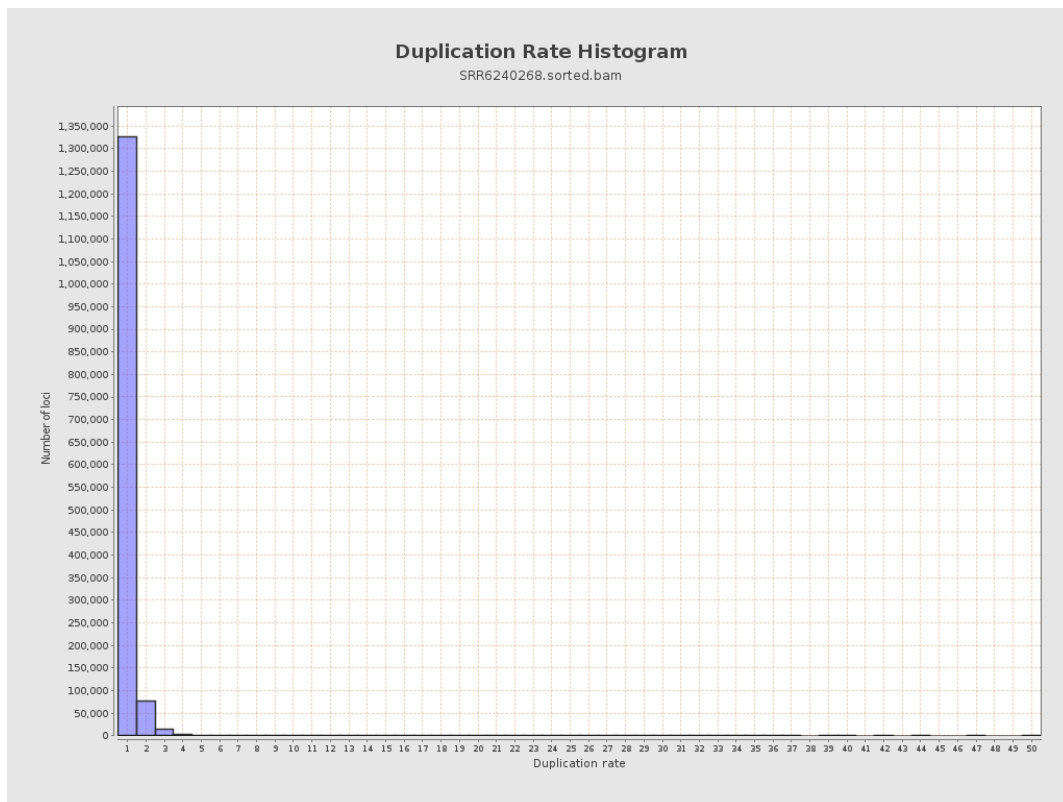
5. Results : Coverage Histogram (0-50X)



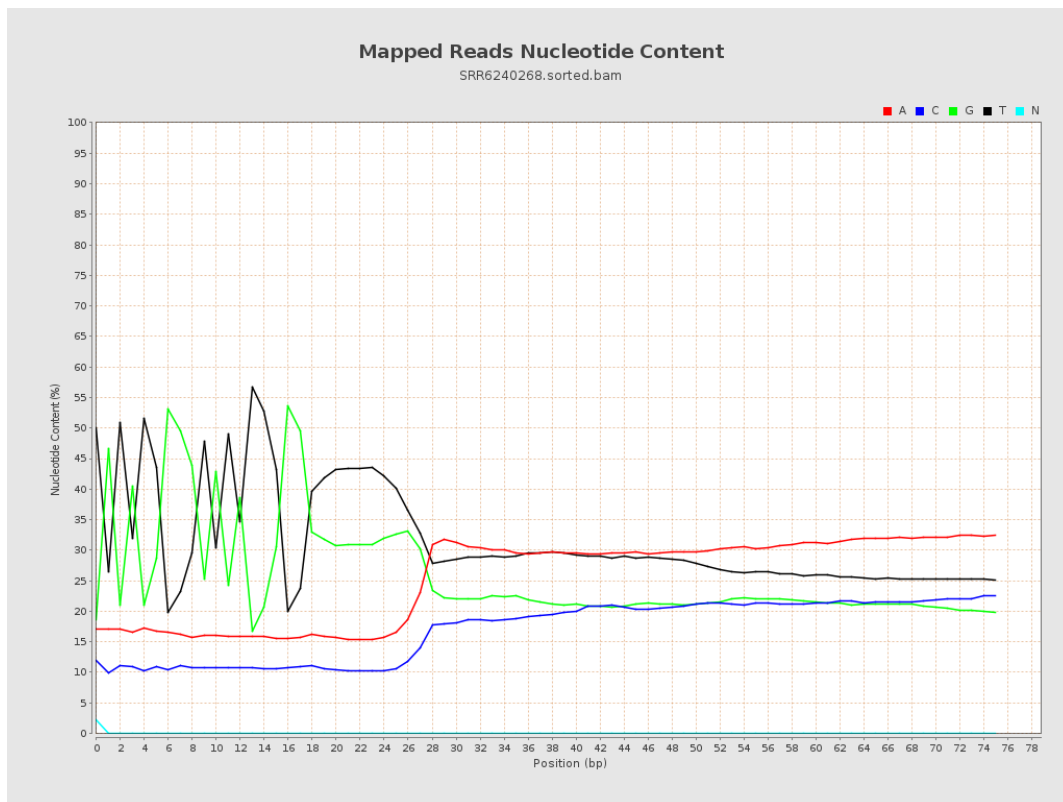
6. Results : Genome Fraction Coverage



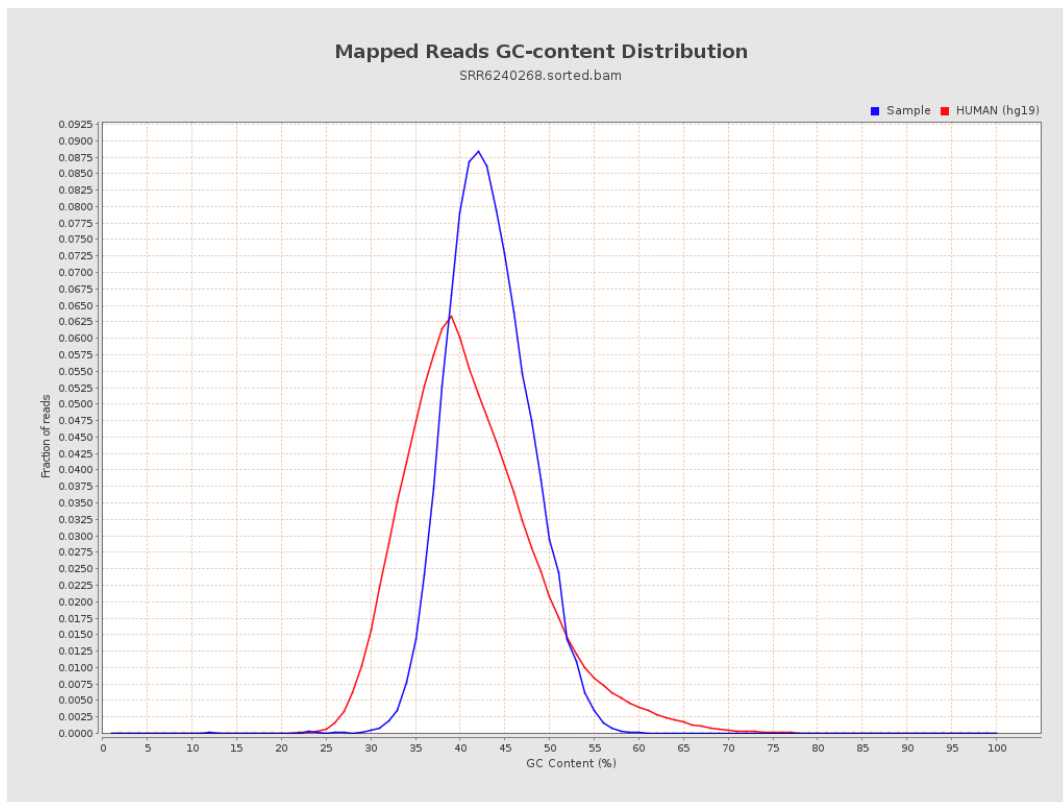
7. Results : Duplication Rate Histogram



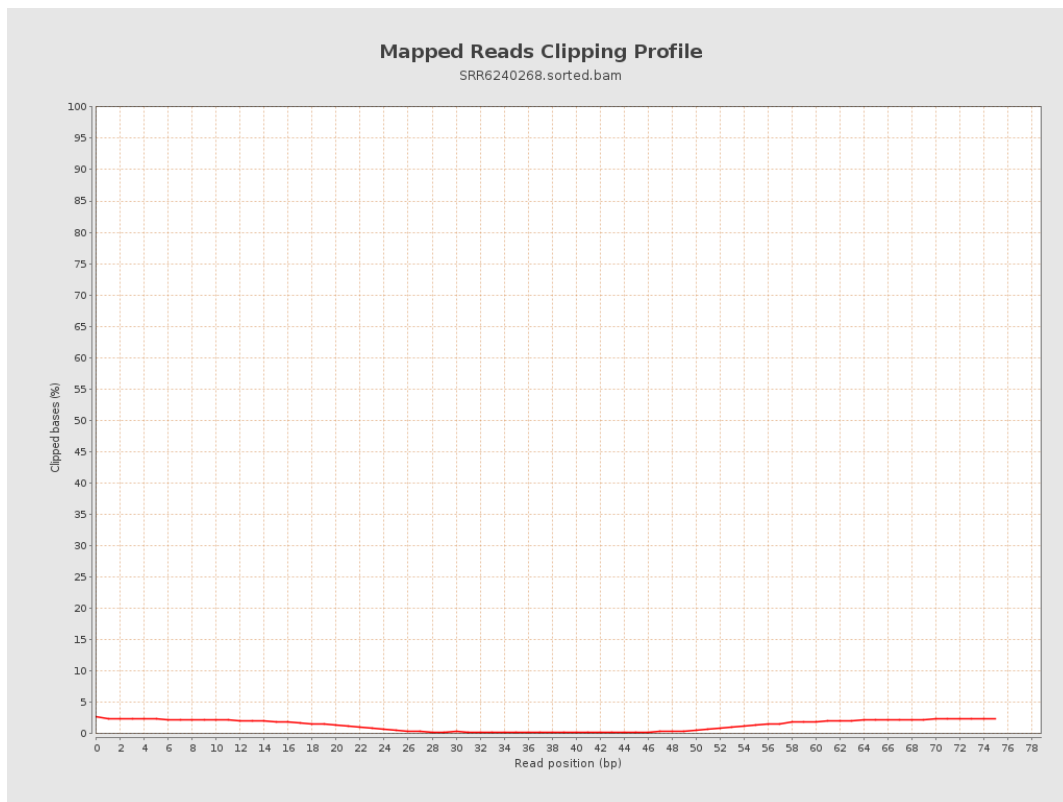
8. Results : Mapped Reads Nucleotide Content



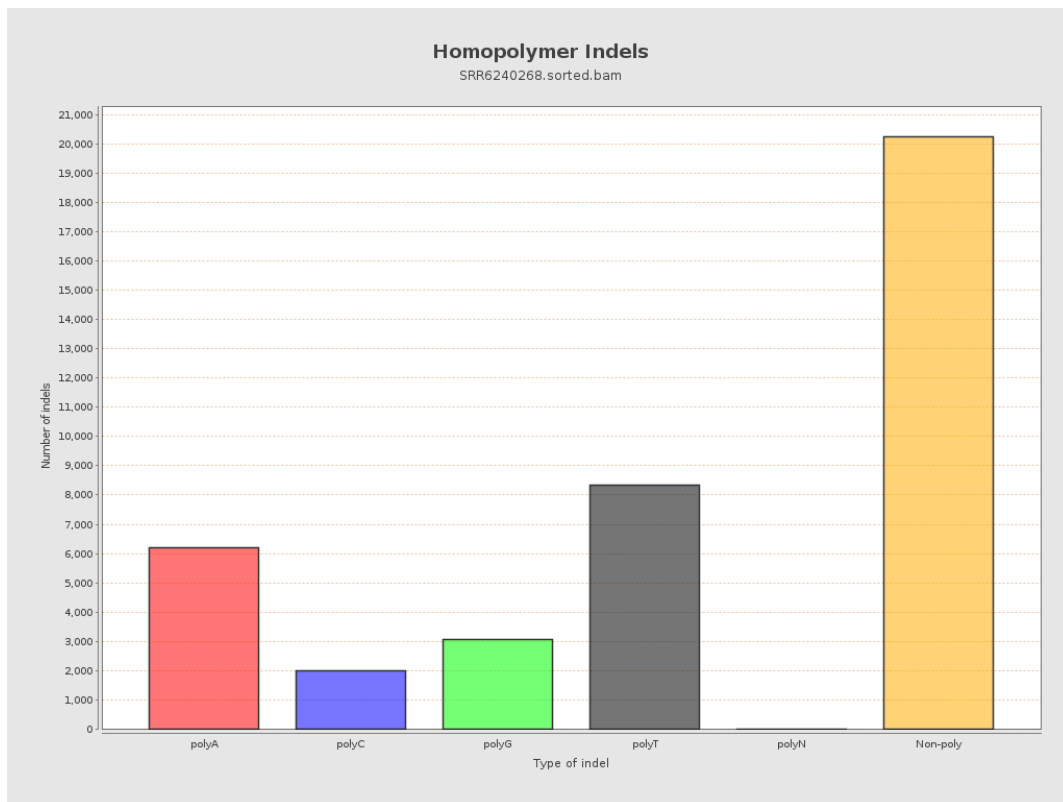
9. Results : Mapped Reads GC-content Distribution



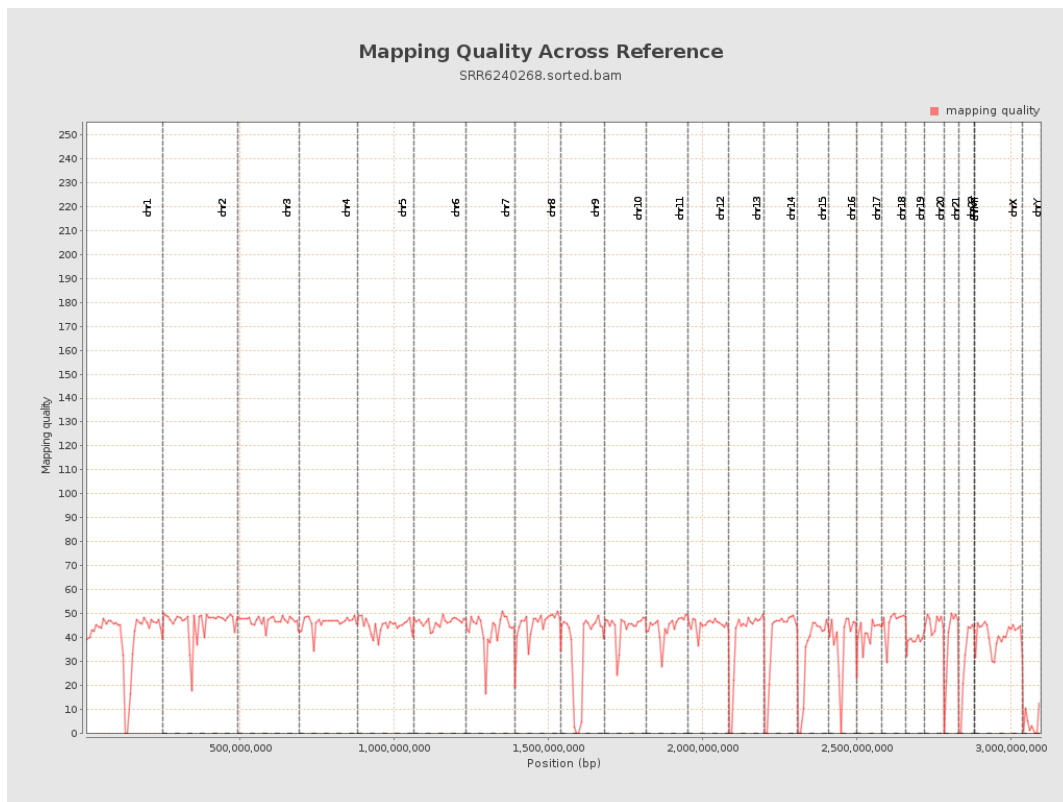
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

