Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:14:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013297.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_SRR6013297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013297.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:14:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013297.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,198,919
Mapped reads	1,619,592 / 73.65%
Unmapped reads	579,327 / 26.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,237 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	151,720 / 6.9%
Duplication rate	7.63%
Clipped reads	906,768 / 41.24%

2.2. ACGT Content

Number/percentage of A's	27,620,275 / 26.54%
Number/percentage of C's	19,356,479 / 18.6%
Number/percentage of T's	32,965,073 / 31.68%
Number/percentage of G's	24,105,118 / 23.16%
Number/percentage of N's	21,174 / 0.02%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0336

Standard Deviation	0.3255

2.4. Mapping Quality

Mean Mapping Quality	43.22

2.5. Mismatches and indels

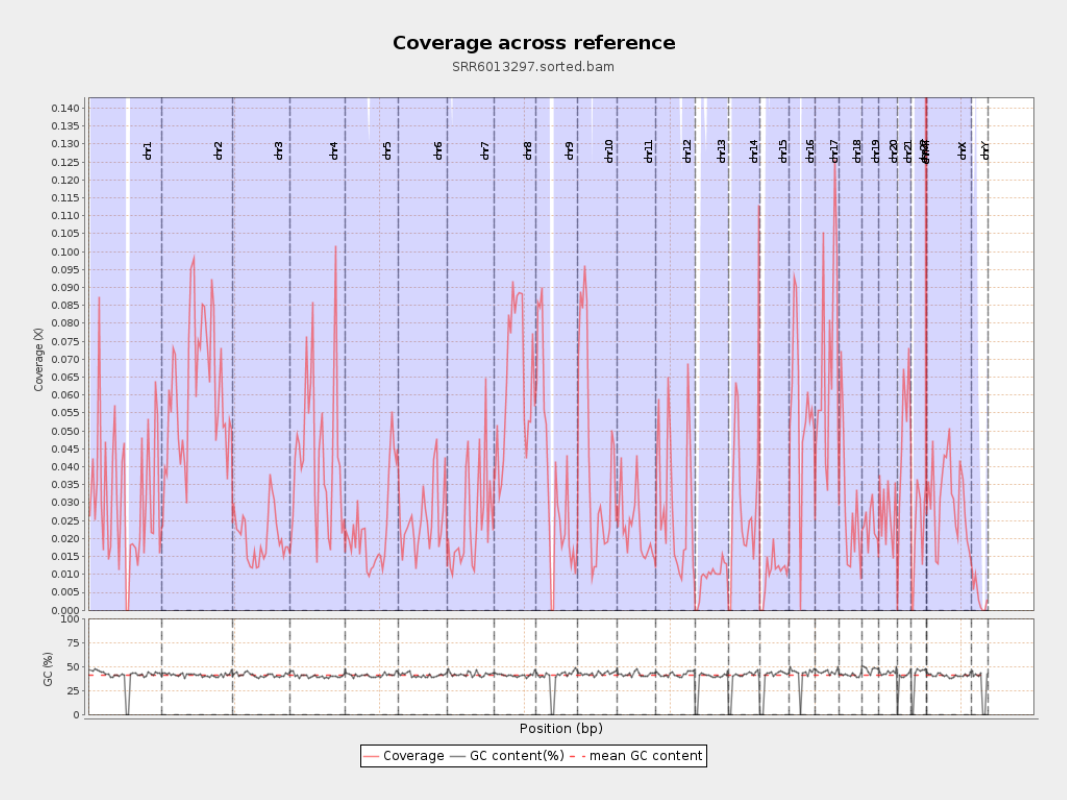
General error rate	0.89%
Mismatches	914,589
Insertions	7,561
Mapped reads with at least one insertion	0.46%
Deletions	24,787
Mapped reads with at least one deletion	1.52%
Homopolymer indels	46.2%

2.6. Chromosome stats

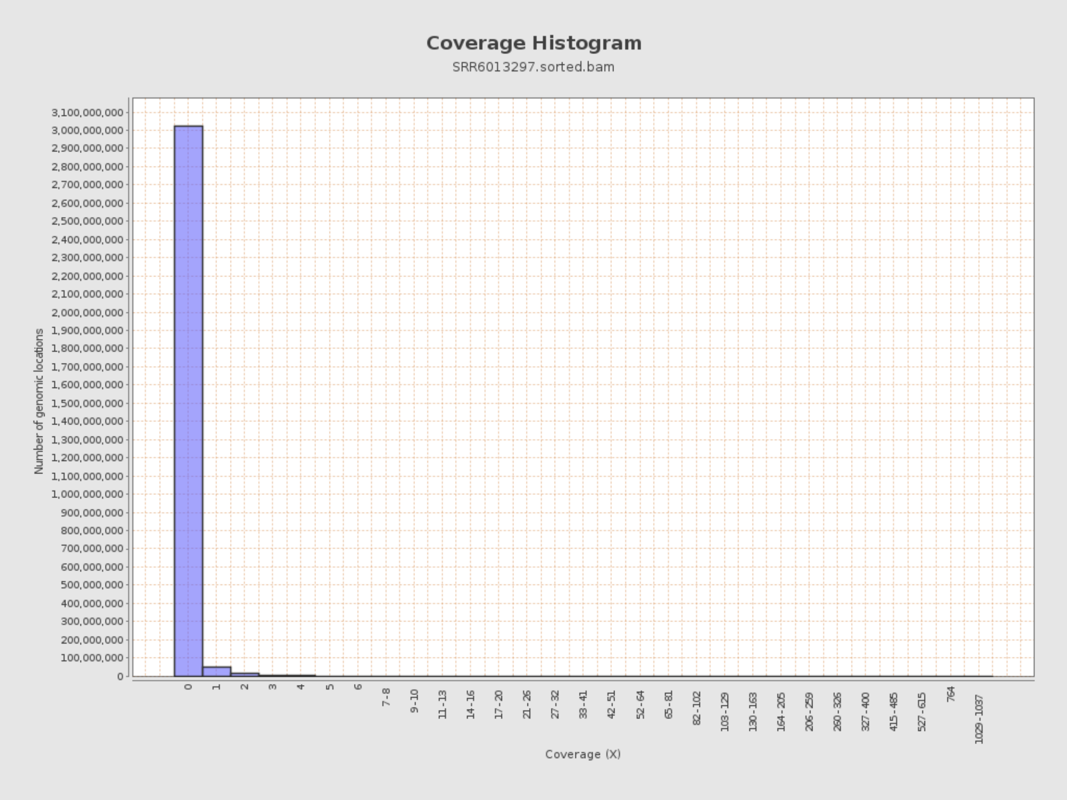
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7662986	0.0307	0.3124
chr2	243199373	14894510	0.0612	0.5619
chr3	198022430	4081858	0.0206	0.1927
chr4	191154276	8220846	0.043	0.2858
chr5	180915260	4062279	0.0225	0.2058
chr6	171115067	4397818	0.0257	0.2616
chr7	159138663	3943843	0.0248	0.354

chr8	146364022	9194385	0.0628	0.4972
chr9	141213431	4929277	0.0349	0.3221
chr10	135534747	5778816	0.0426	0.3473
chr11	135006516	3081705	0.0228	0.2398
chr12	133851895	4053472	0.0303	0.2459
chr13	115169878	1060566	0.0092	0.1328
chr14	107349540	3047930	0.0284	0.2492
chr15	102531392	1054499	0.0103	0.1533
chr16	90354753	5159232	0.0571	0.3396
chr17	81195210	5651515	0.0696	0.422
chr18	78077248	2278775	0.0292	0.4746
chr19	59128983	1399813	0.0237	0.3132
chr20	63025520	1737390	0.0276	0.2334
chr21	48129895	2283447	0.0474	0.3065
chr22	51304566	1089208	0.0212	0.1988
chrMT	16571	59825	3.6102	3.2946
chrX	155270560	4759942	0.0307	0.2619
chrY	59373566	225549	0.0038	0.0825

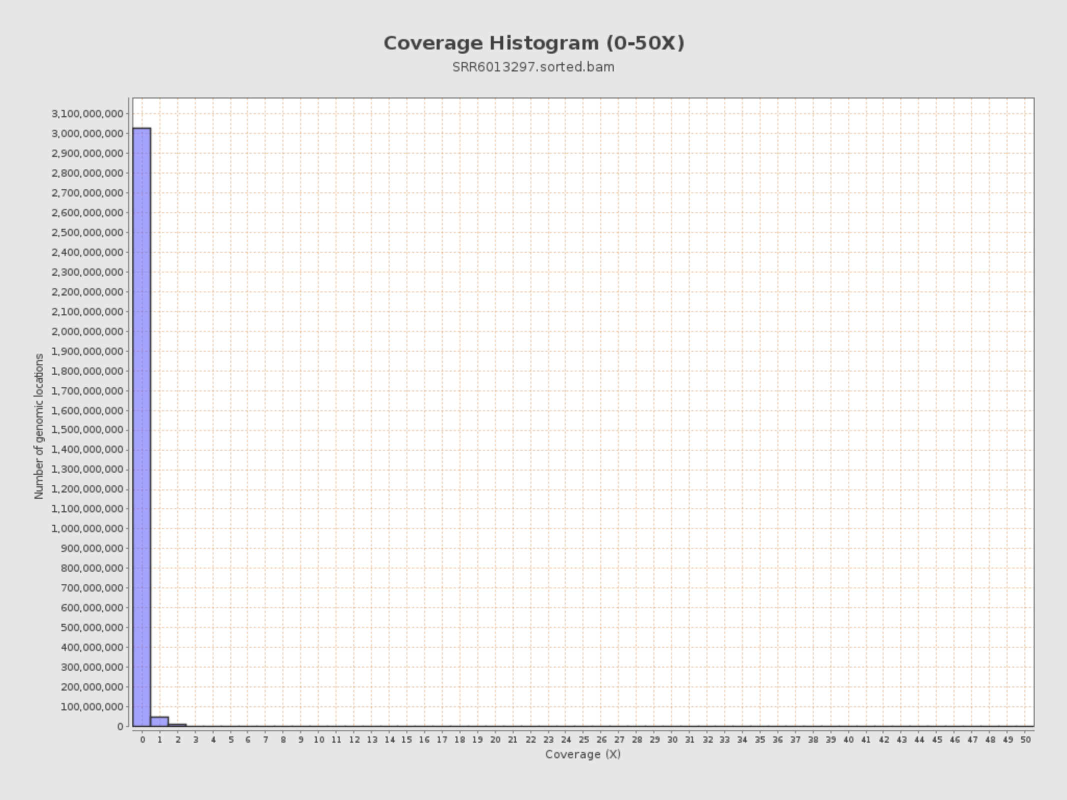
3. Results : Coverage across reference



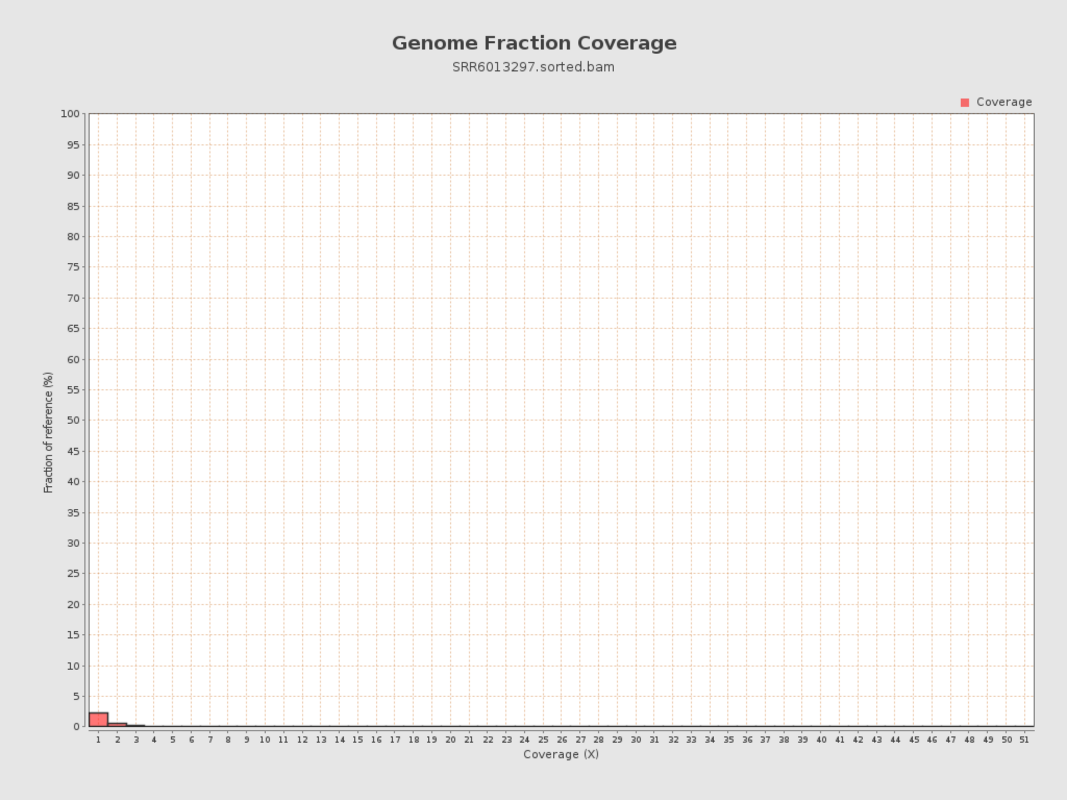
4. Results : Coverage Histogram



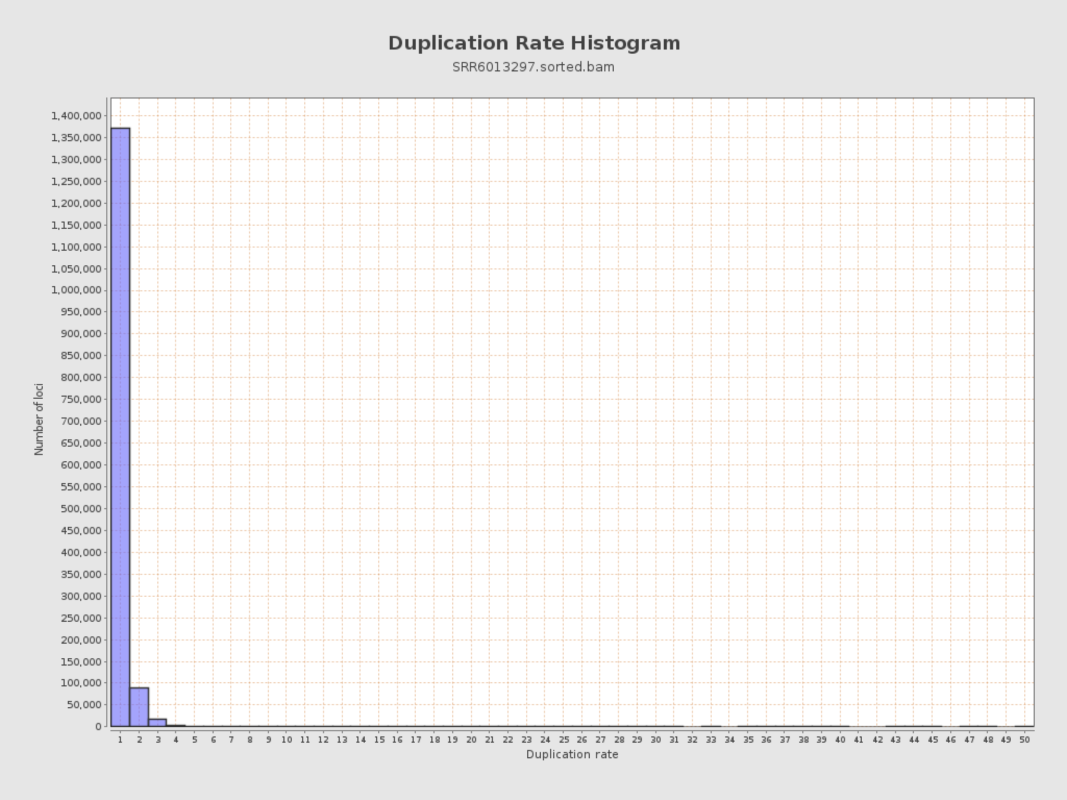
5. Results : Coverage Histogram (0-50X)



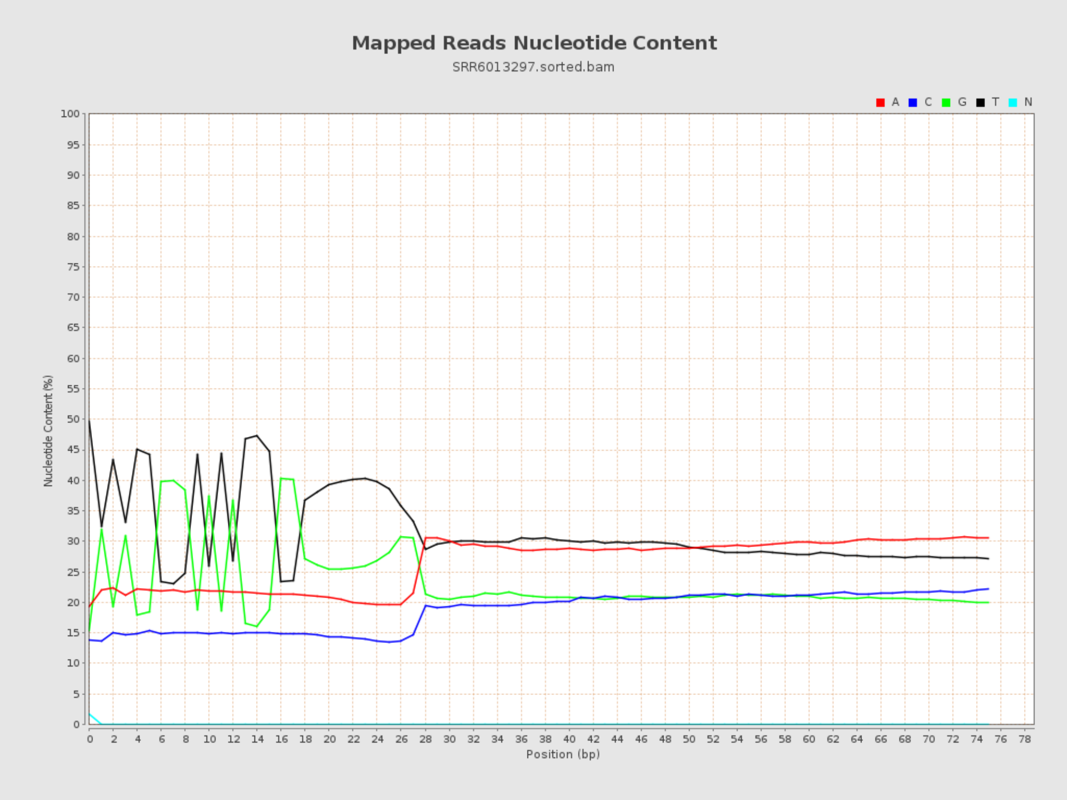
6. Results : Genome Fraction Coverage



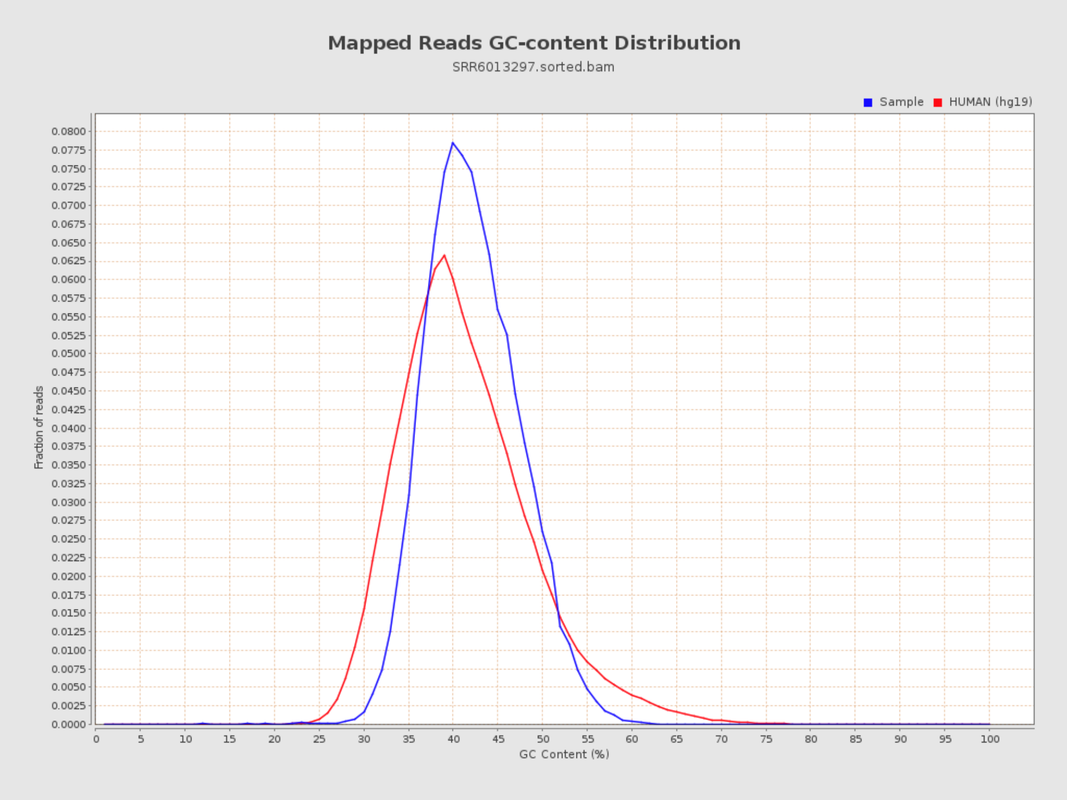
7. Results : Duplication Rate Histogram



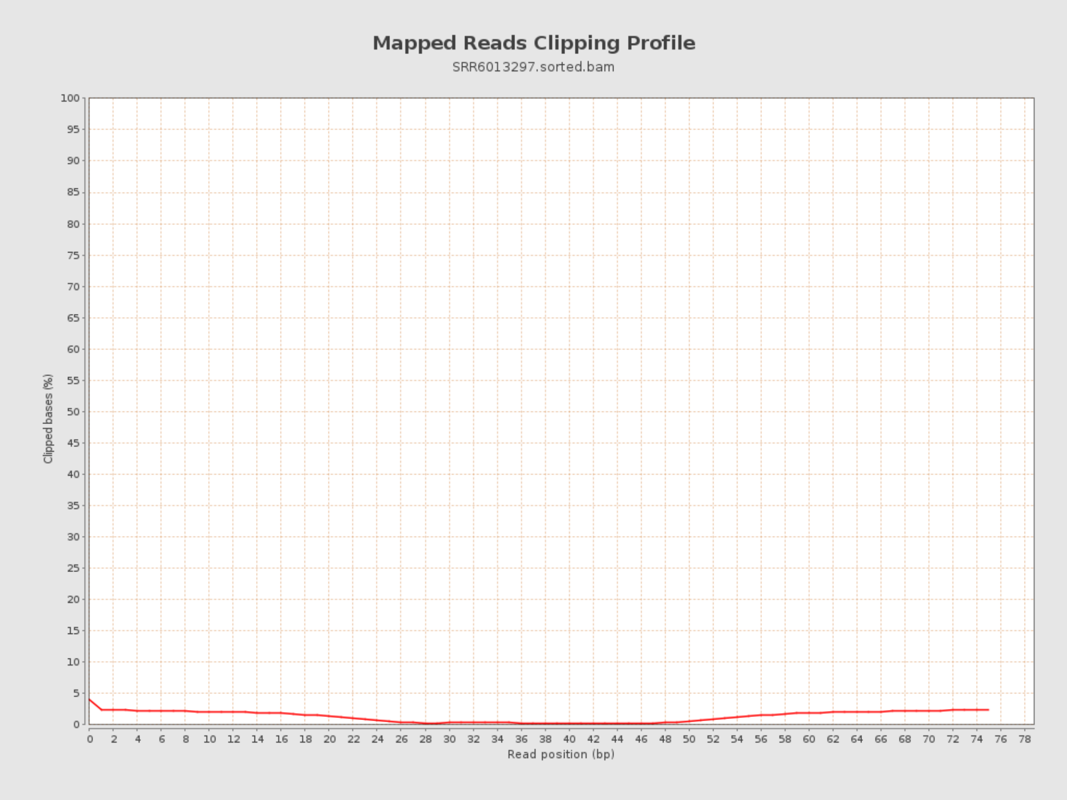
8. Results : Mapped Reads Nucleotide Content



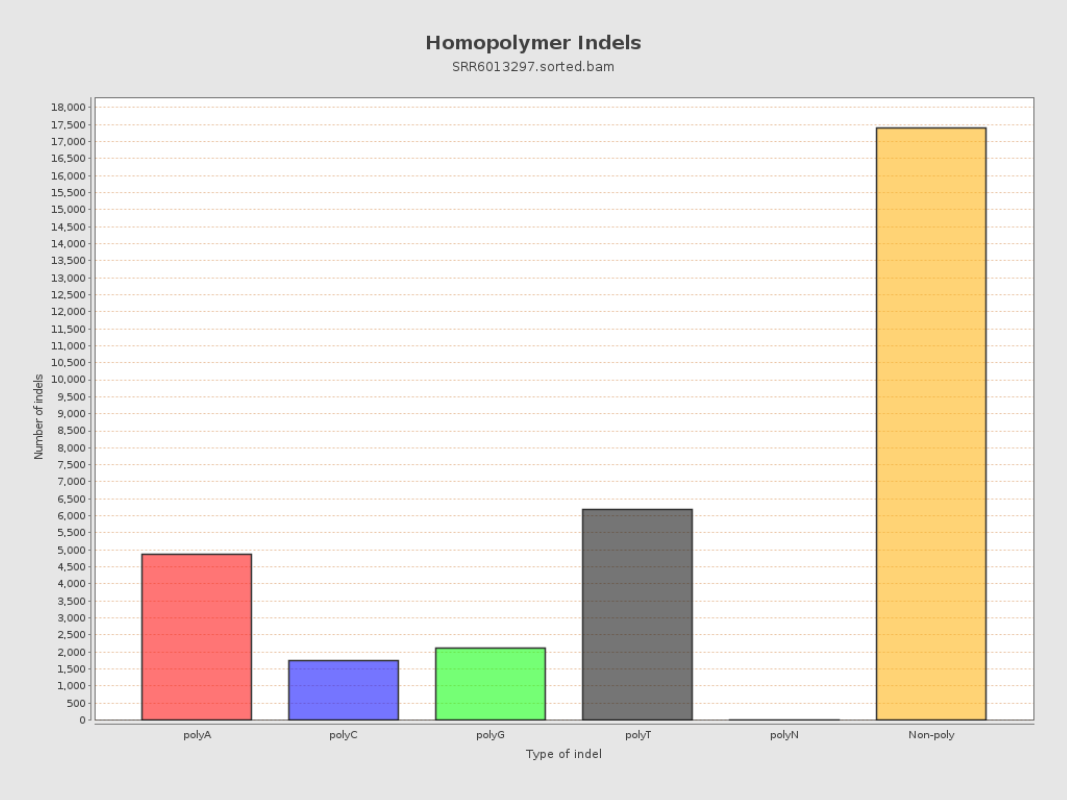
9. Results : Mapped Reads GC-content Distribution



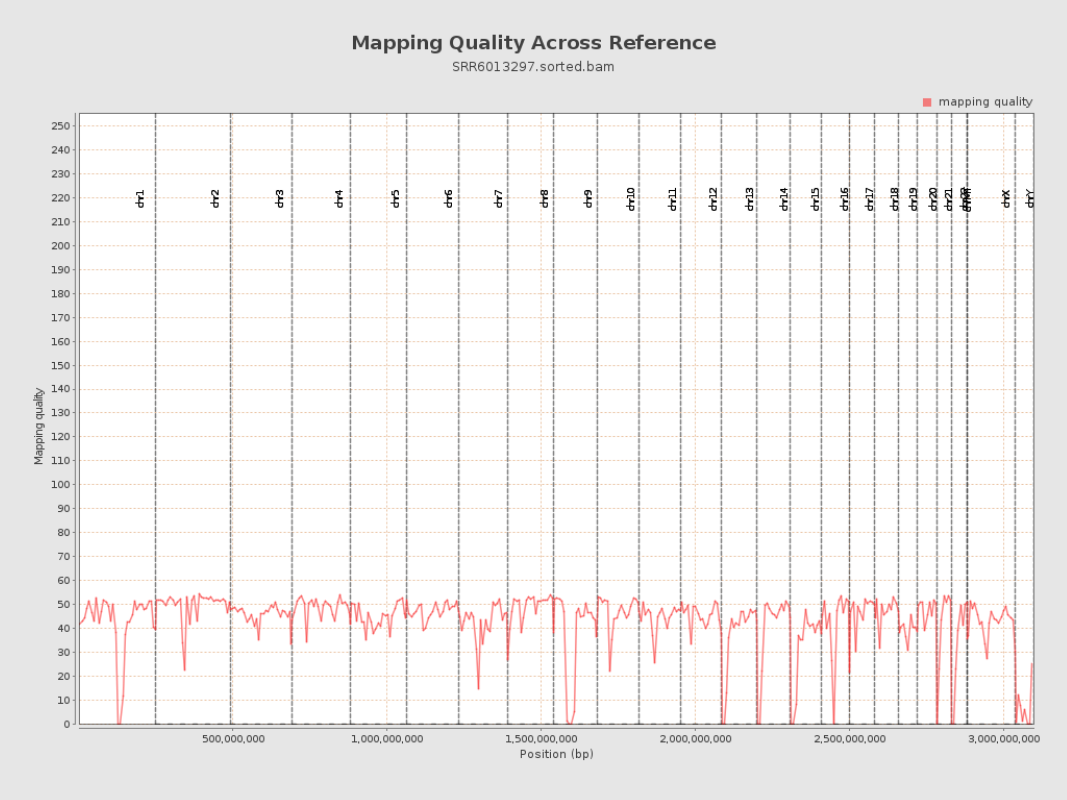
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram