Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:31:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238488.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_SRR6238488 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238488.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:31:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238488.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,314,696
Mapped reads	3,910,229 / 90.63%
Unmapped reads	404,467 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,197 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	918,785 / 21.29%
Duplication rate	18.38%
Clipped reads	2,580,549 / 59.81%

2.2. ACGT Content

Number/percentage of A's	57,716,245 / 24.23%
Number/percentage of C's	41,643,480 / 17.48%
Number/percentage of T's	80,130,035 / 33.64%
Number/percentage of G's	58,699,375 / 24.64%
Number/percentage of N's	15,837 / 0.01%
GC Percentage	42.12%

2.3. Coverage

Mean	0.077

Standard Deviation	0.9378

2.4. Mapping Quality

Mean Mapping Quality	43.06

2.5. Mismatches and indels

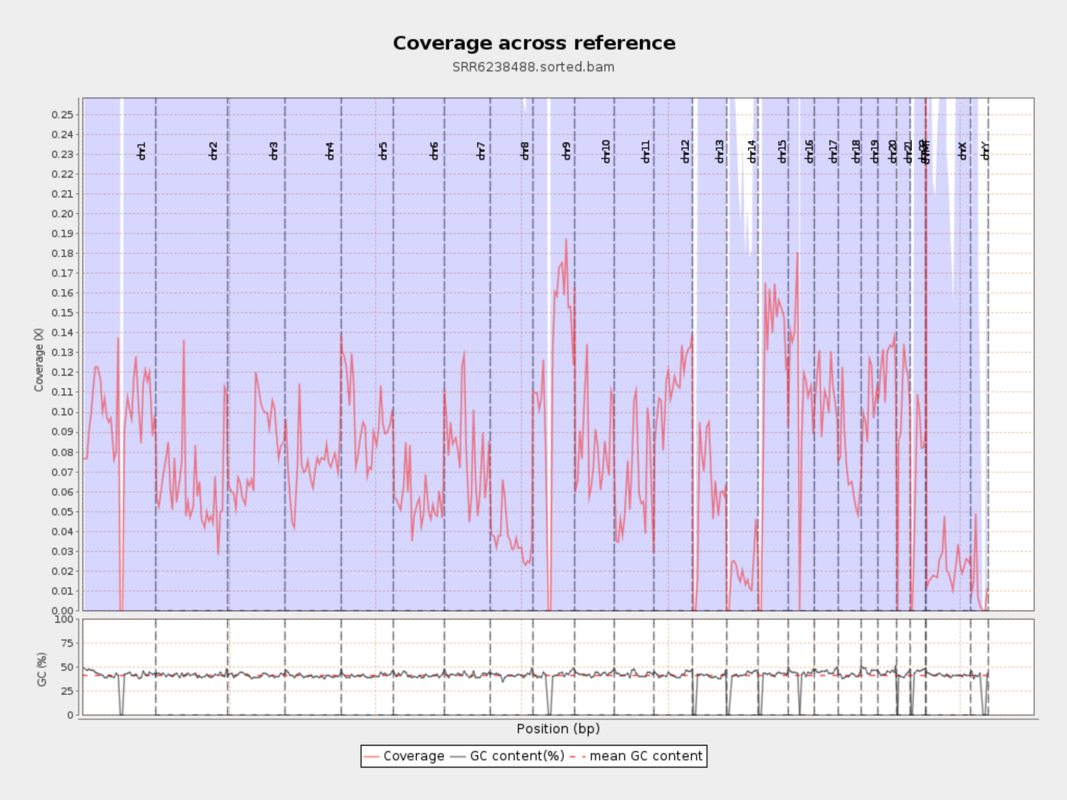
General error rate	0.64%
Mismatches	1,501,766
Insertions	16,767
Mapped reads with at least one insertion	0.42%
Deletions	75,044
Mapped reads with at least one deletion	1.9%
Homopolymer indels	41.28%

2.6. Chromosome stats

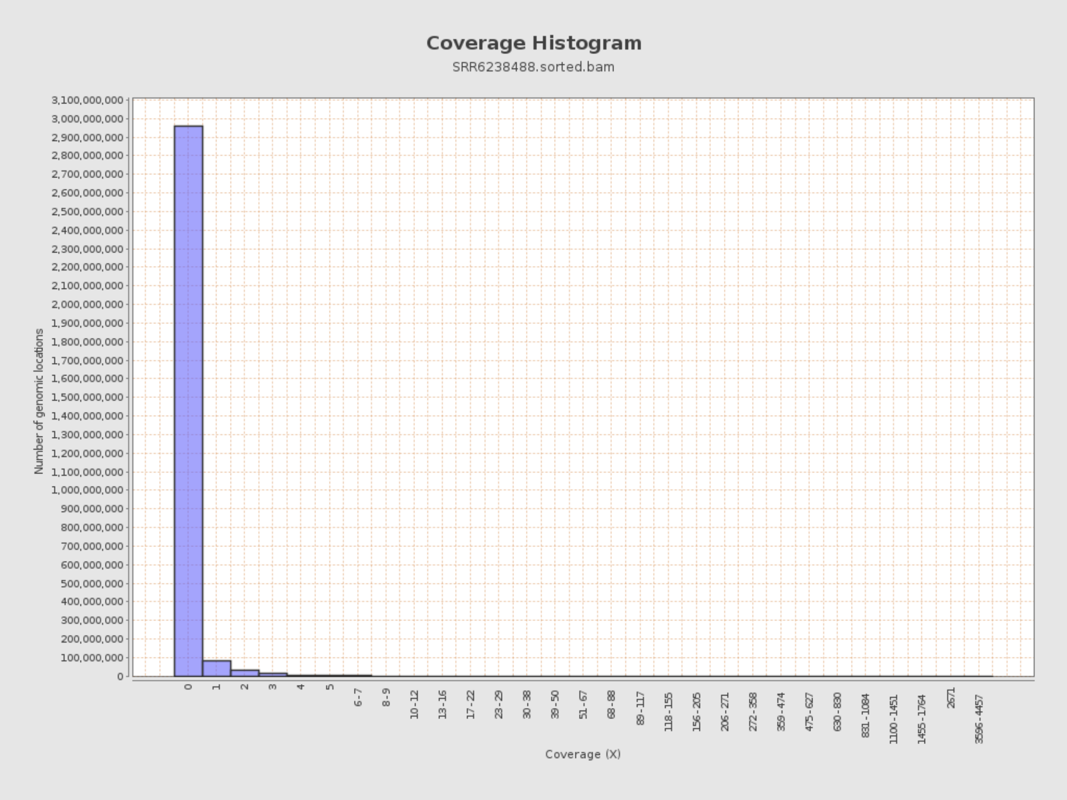
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24074418	0.0966	1.1252
chr2	243199373	15246039	0.0627	2.0409
chr3	198022430	15854950	0.0801	0.4627
chr4	191154276	13986041	0.0732	0.4863
chr5	180915260	17422066	0.0963	0.5122
chr6	171115067	9461065	0.0553	0.7744
chr7	159138663	12899177	0.0811	0.83

chr8	146364022	5192532	0.0355	1.0072
chr9	141213431	17413552	0.1233	0.9291
chr10	135534747	11067674	0.0817	0.7786
chr11	135006516	8408018	0.0623	0.5034
chr12	133851895	15240009	0.1139	0.5895
chr13	115169878	6729842	0.0584	0.5463
chr14	107349540	1955314	0.0182	0.3473
chr15	102531392	12488539	0.1218	0.6608
chr16	90354753	10025585	0.111	0.6788
chr17	81195210	8990939	0.1107	0.5847
chr18	78077248	5585717	0.0715	2.0299
chr19	59128983	6146179	0.1039	0.921
chr20	63025520	7927987	0.1258	0.6106
chr21	48129895	4761494	0.0989	0.5781
chr22	51304566	3361184	0.0655	0.4168
chrMT	16571	4852	0.2928	0.6507
chrX	155270560	3397722	0.0219	0.3297
chrY	59373566	694389	0.0117	0.4468

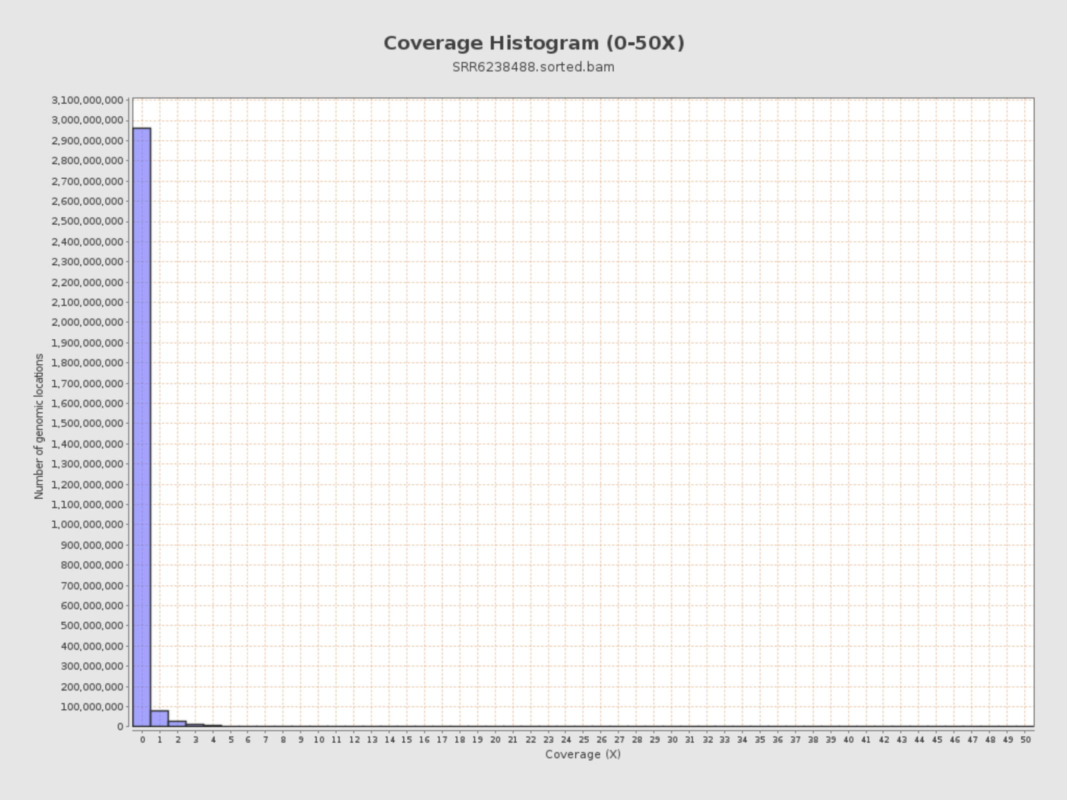
3. Results : Coverage across reference



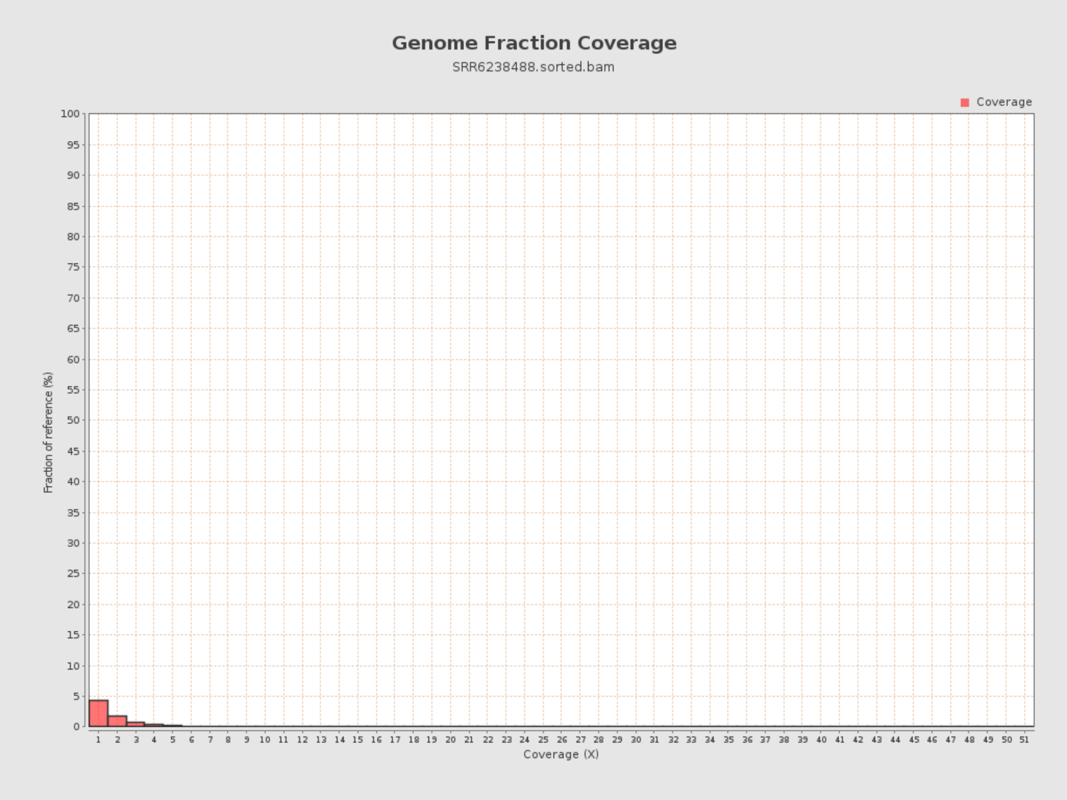
4. Results : Coverage Histogram



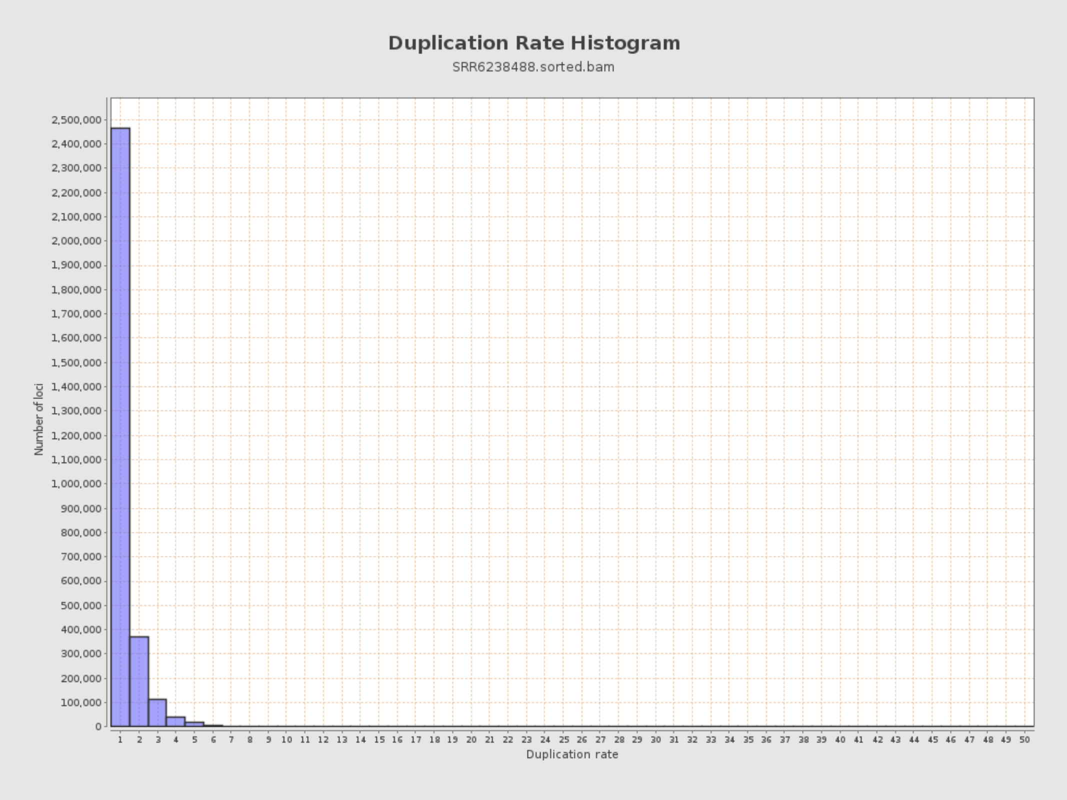
5. Results : Coverage Histogram (0-50X)



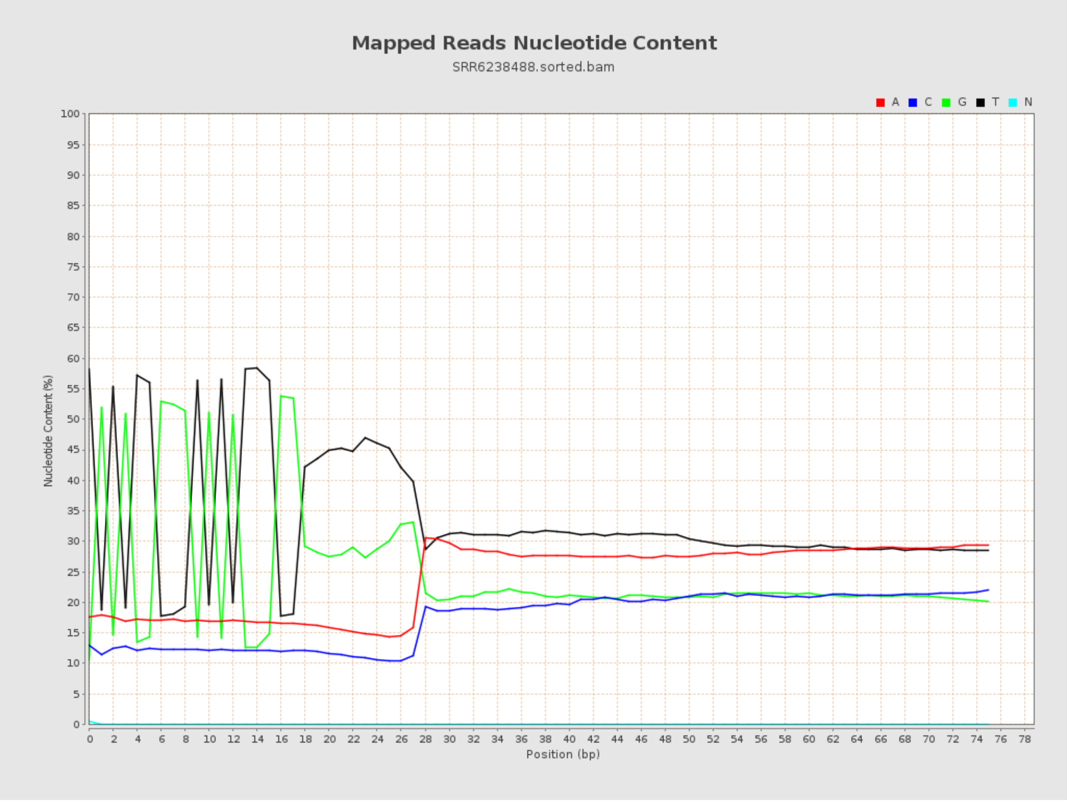
6. Results : Genome Fraction Coverage



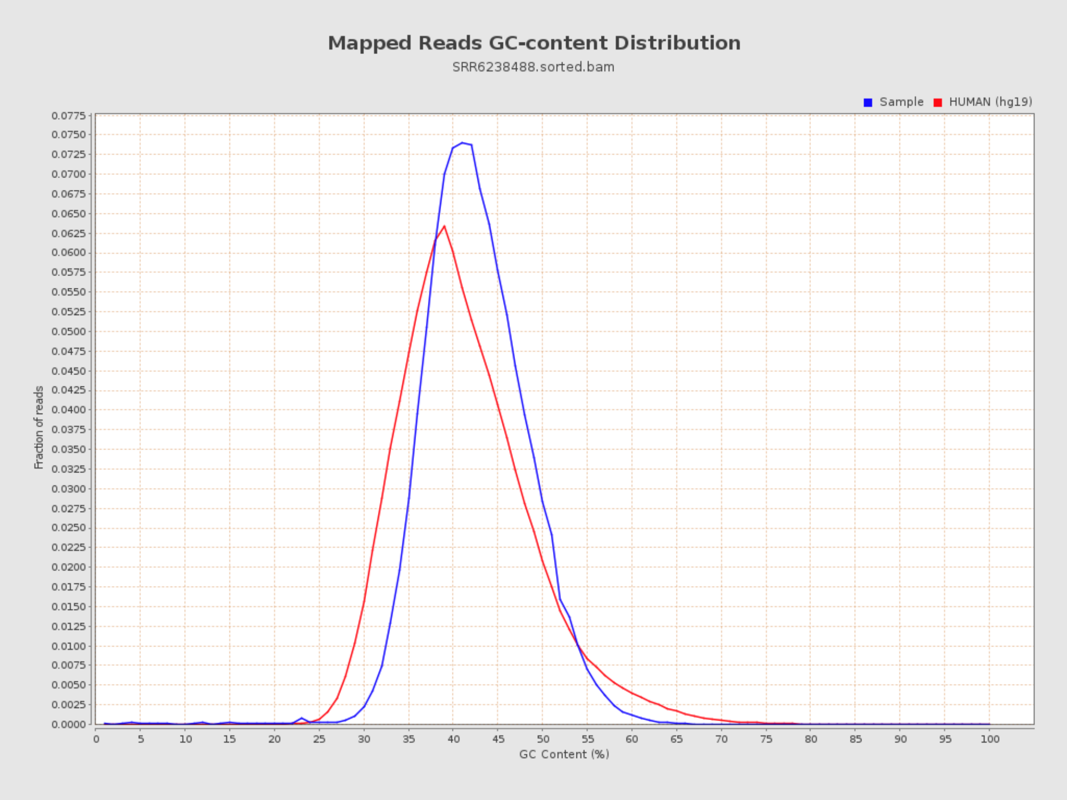
7. Results : Duplication Rate Histogram



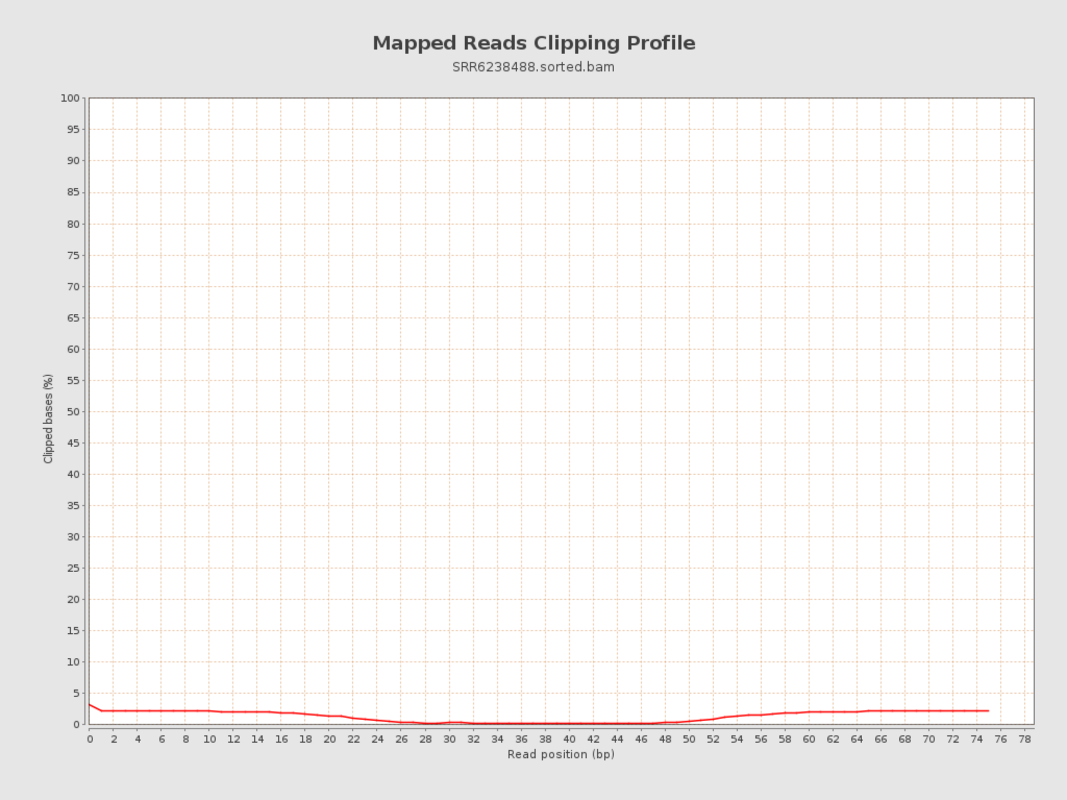
8. Results : Mapped Reads Nucleotide Content



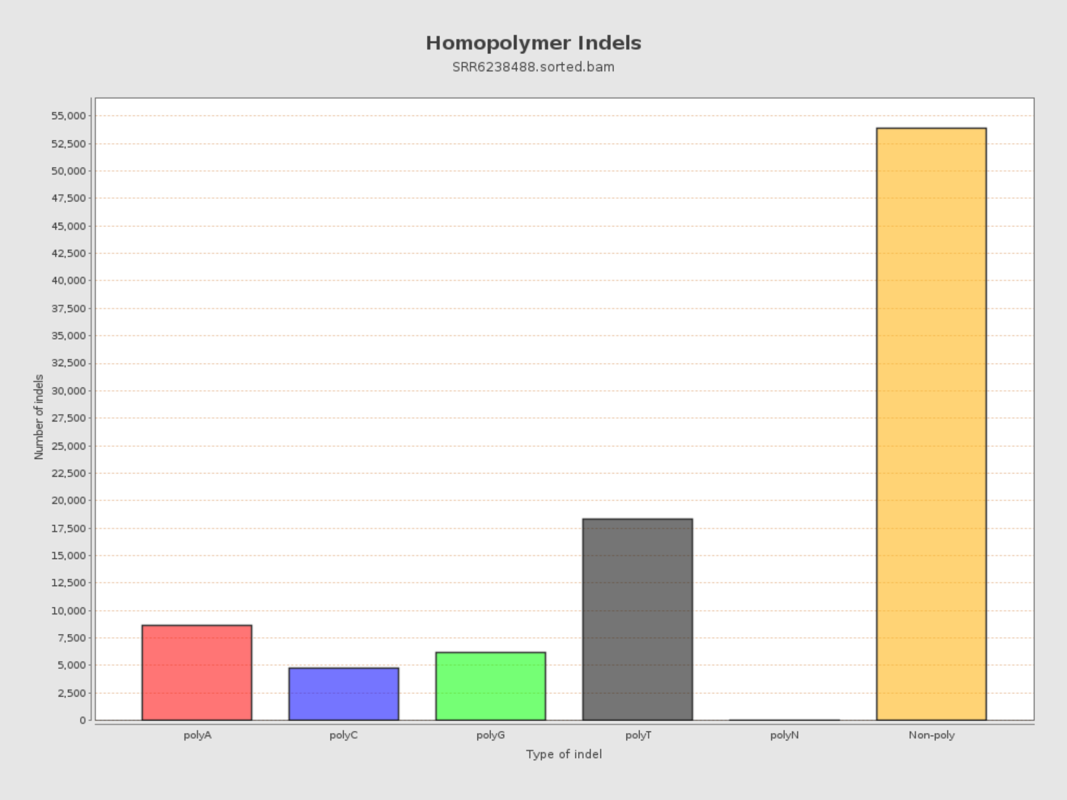
9. Results : Mapped Reads GC-content Distribution



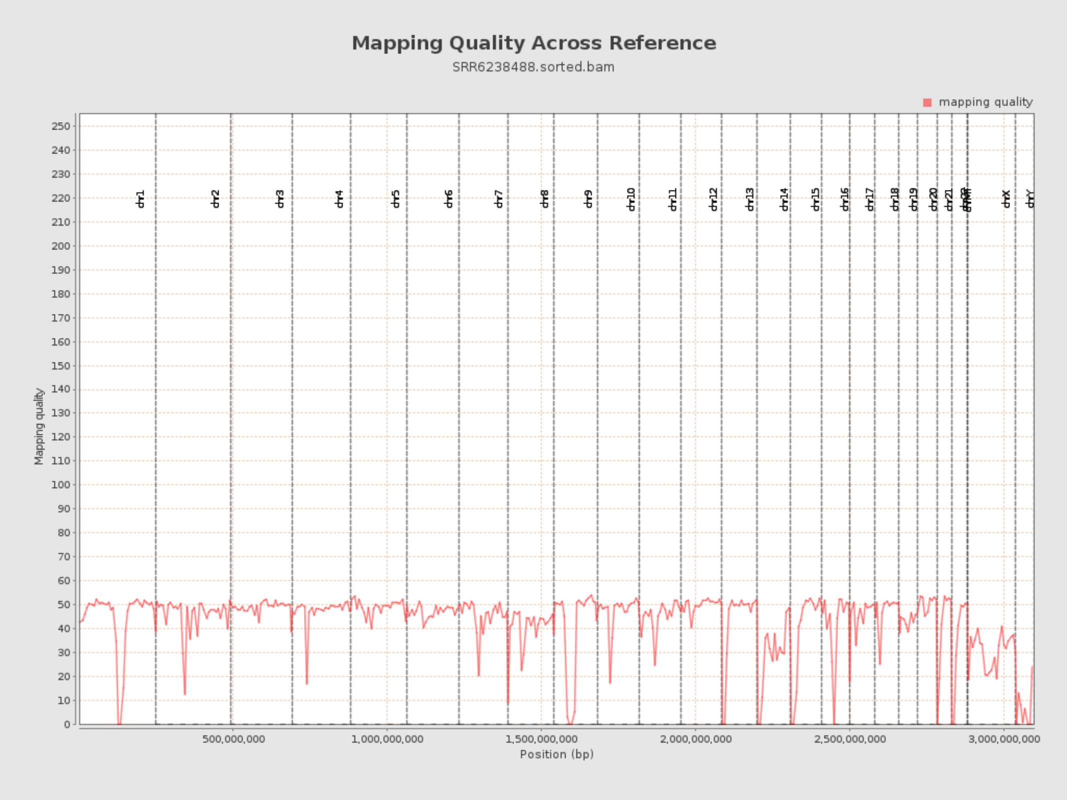
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram