Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:08:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008714.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_SRR6008714 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008714.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:08:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008714.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,345,377
Mapped reads	1,244,585 / 92.51%
Unmapped reads	100,792 / 7.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,159 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	39,107 / 2.91%
Duplication rate	2.27%
Clipped reads	582,383 / 43.29%

2.2. ACGT Content

Number/percentage of A's	22,006,327 / 26.92%
Number/percentage of C's	15,537,831 / 19.01%
Number/percentage of T's	25,249,938 / 30.89%
Number/percentage of G's	18,841,591 / 23.05%
Number/percentage of N's	106,122 / 0.13%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.277

2.4. Mapping Quality

Mean Mapping Quality	43.96

2.5. Mismatches and indels

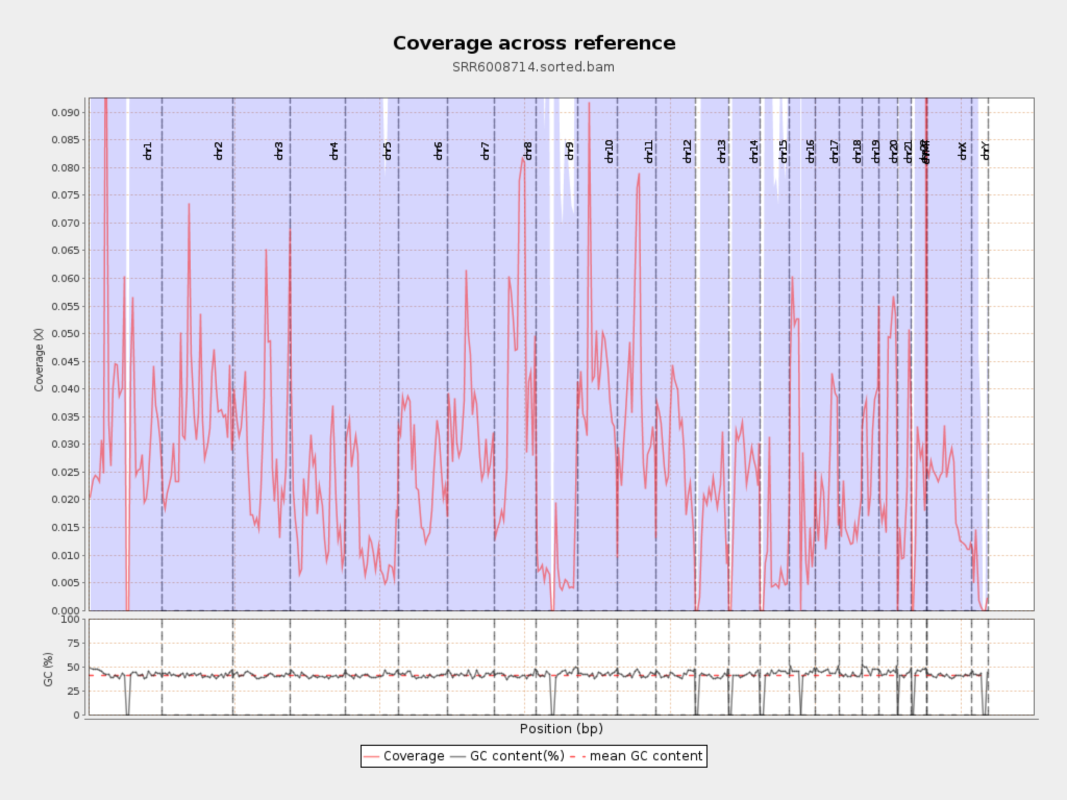
General error rate	0.85%
Mismatches	681,385
Insertions	5,603
Mapped reads with at least one insertion	0.45%
Deletions	25,441
Mapped reads with at least one deletion	2.02%
Homopolymer indels	44.87%

2.6. Chromosome stats

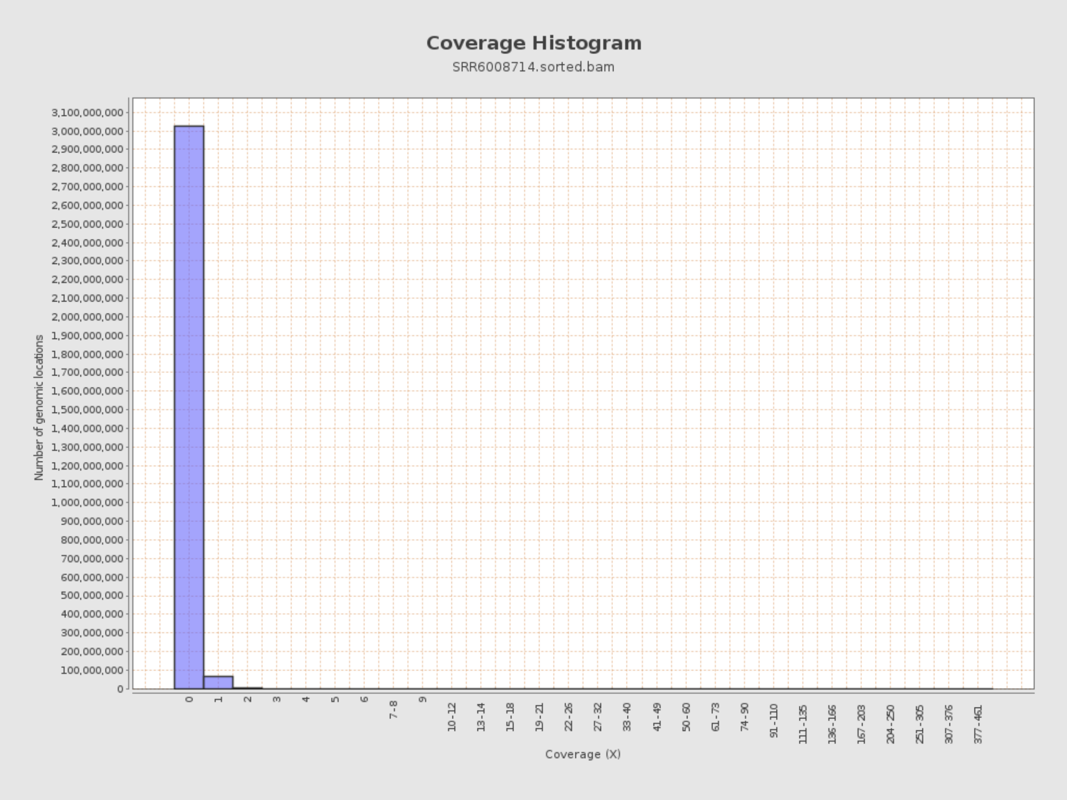
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8308452	0.0333	0.4315
chr2	243199373	8503345	0.035	0.3269
chr3	198022430	6016665	0.0304	0.2118
chr4	191154276	3666675	0.0192	0.1605
chr5	180915260	2649308	0.0146	0.1323
chr6	171115067	4362911	0.0255	0.1925
chr7	159138663	5478628	0.0344	0.4084

chr8	146364022	6151055	0.042	0.3358
chr9	141213431	984298	0.007	0.1649
chr10	135534747	5817971	0.0429	0.5305
chr11	135006516	5202045	0.0385	0.2853
chr12	133851895	3989991	0.0298	0.1888
chr13	115169878	1918595	0.0167	0.1398
chr14	107349540	2551896	0.0238	0.1719
chr15	102531392	757832	0.0074	0.0958
chr16	90354753	2514205	0.0278	0.2384
chr17	81195210	1997074	0.0246	0.1974
chr18	78077248	1207559	0.0155	0.3361
chr19	59128983	1939050	0.0328	0.3118
chr20	63025520	2244432	0.0356	0.2104
chr21	48129895	998994	0.0208	0.1651
chr22	51304566	965124	0.0188	0.1497
chrMT	16571	14370	0.8672	1.1931
chrX	155270560	3302574	0.0213	0.1752
chrY	59373566	244097	0.0041	0.1547

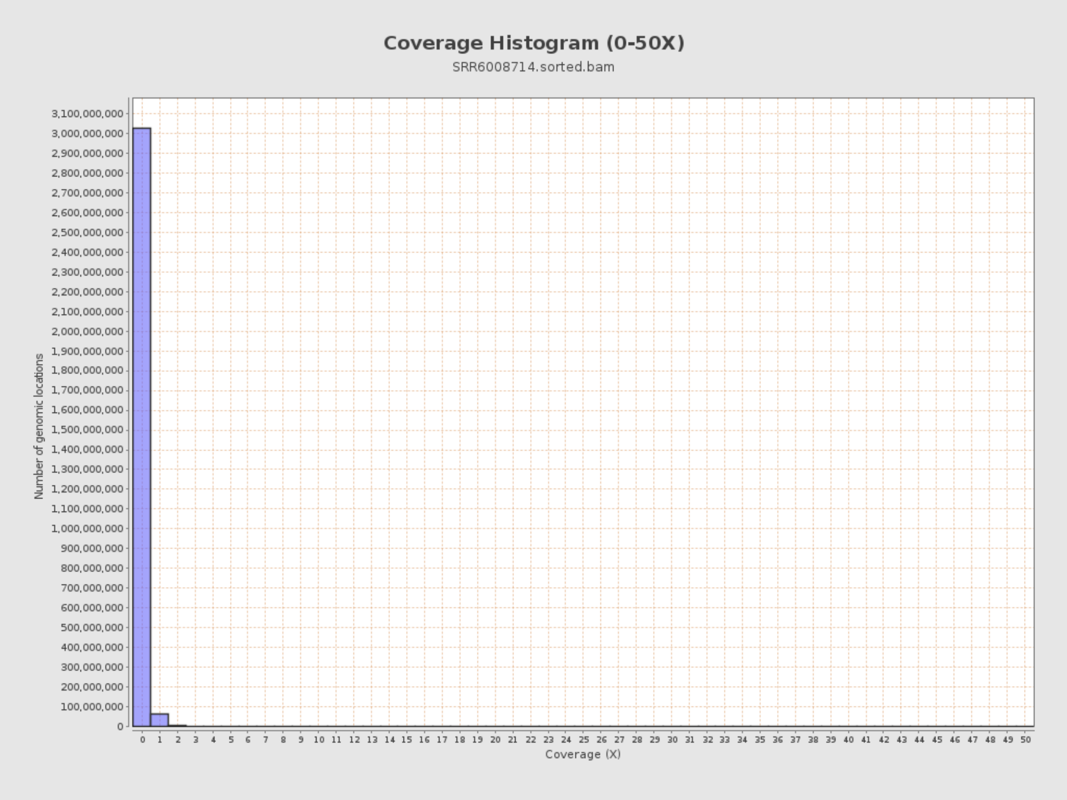
3. Results : Coverage across reference



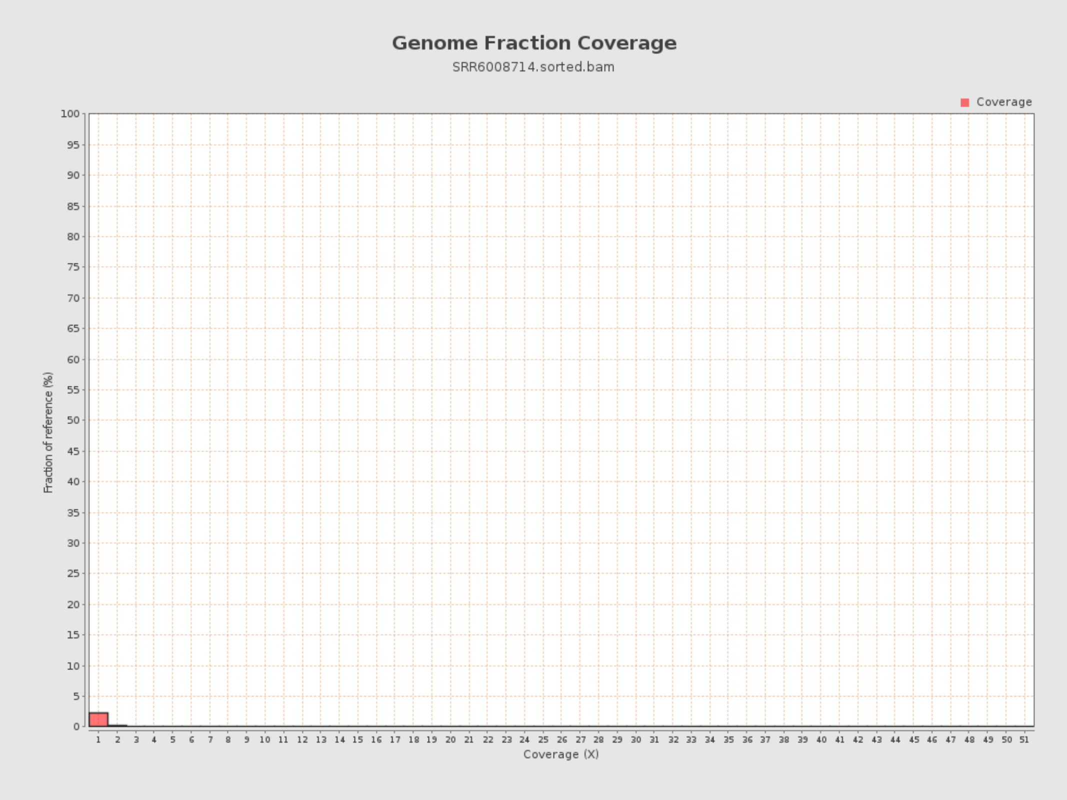
4. Results : Coverage Histogram



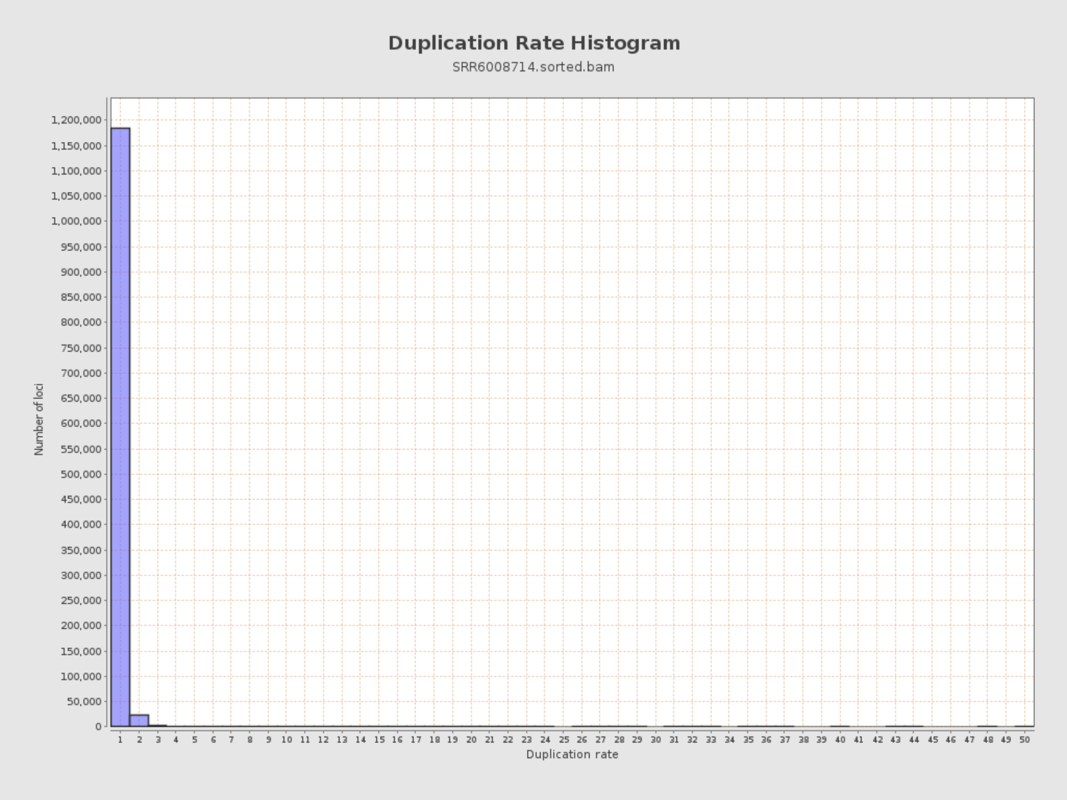
5. Results : Coverage Histogram (0-50X)



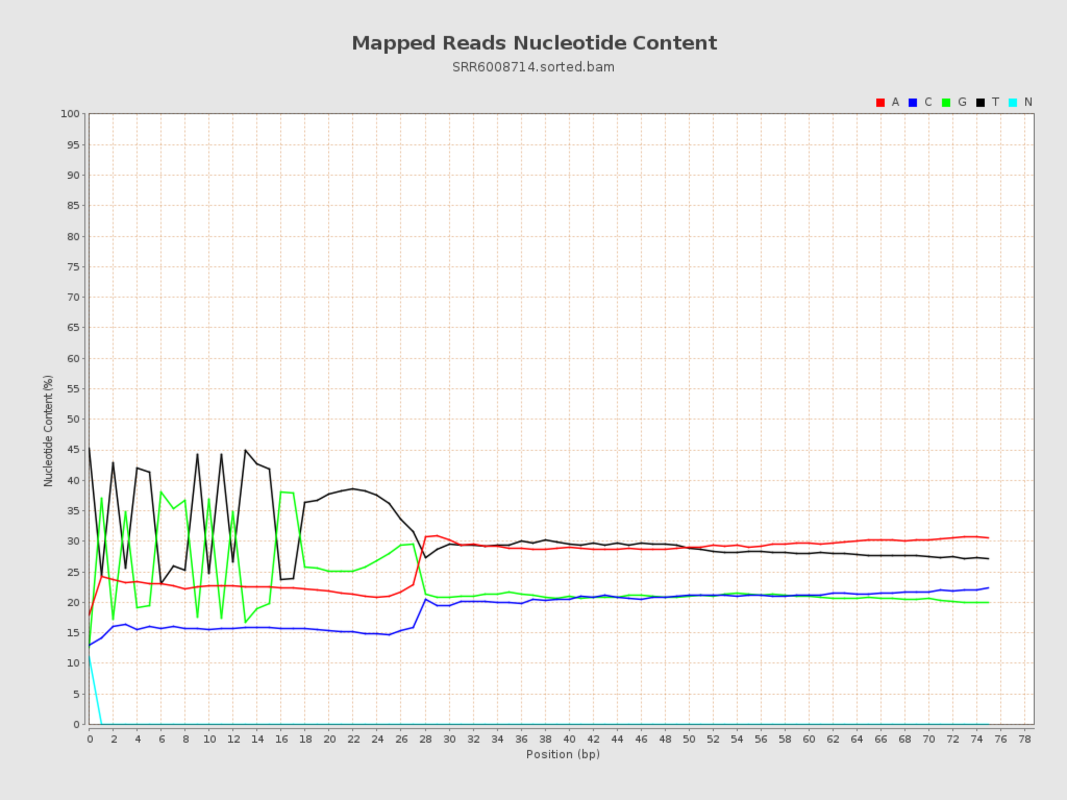
6. Results : Genome Fraction Coverage



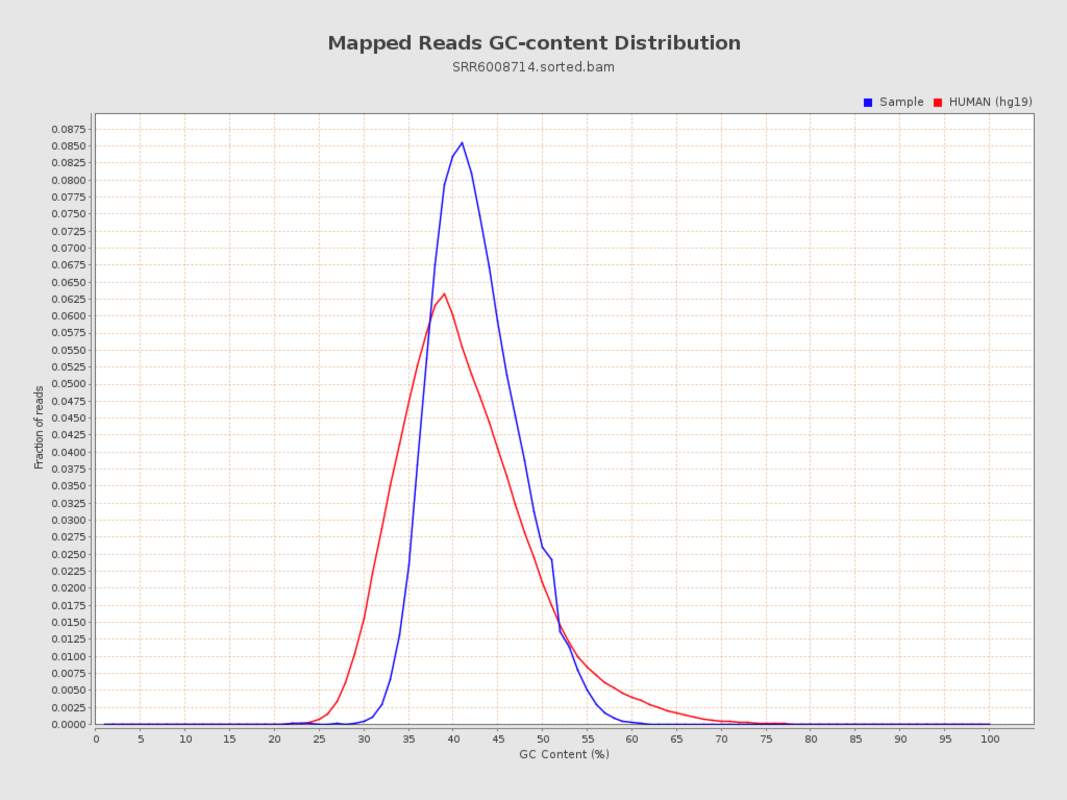
7. Results : Duplication Rate Histogram



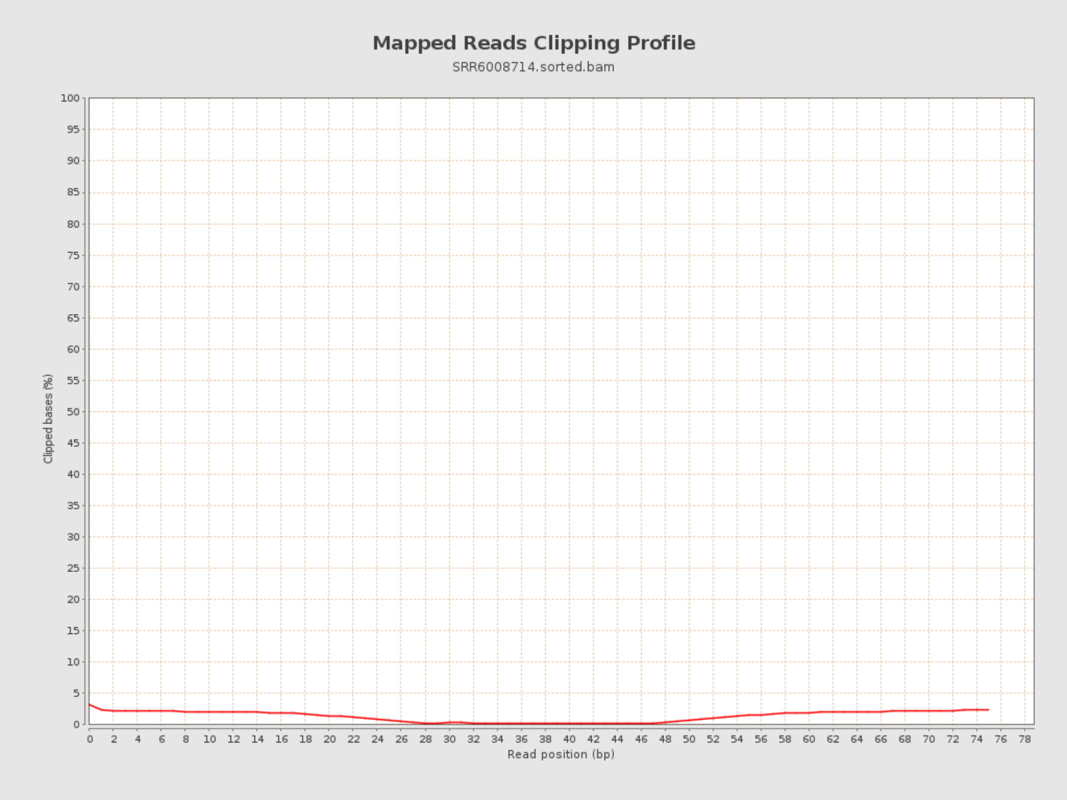
8. Results : Mapped Reads Nucleotide Content



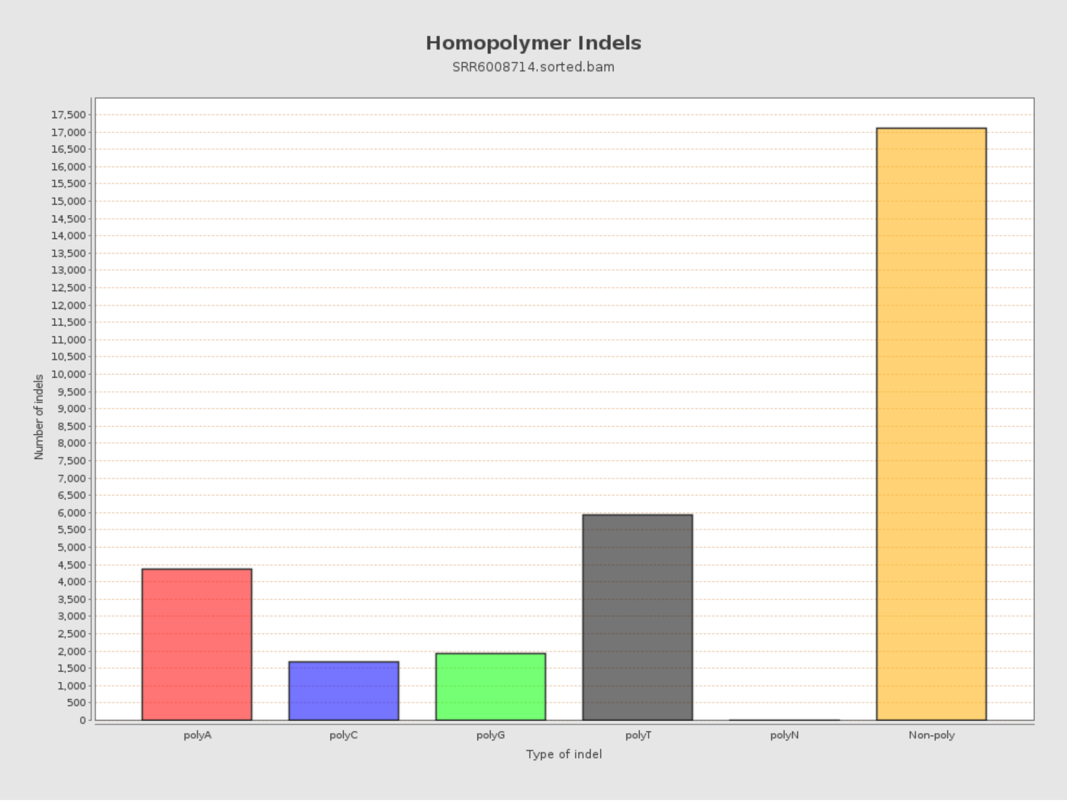
9. Results : Mapped Reads GC-content Distribution



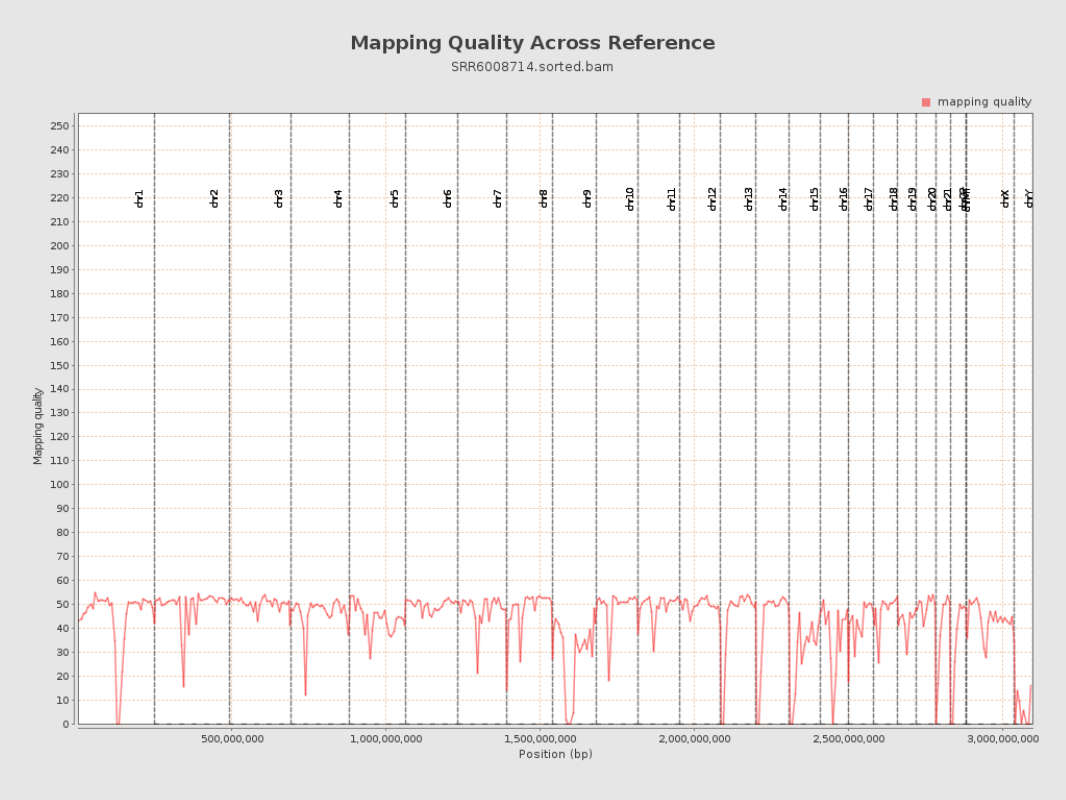
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram