Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:32:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237861.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_SRR6237861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237861.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:32:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,883,121
Mapped reads	1,362,545 / 72.36%
Unmapped reads	520,576 / 27.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,627 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	222,740 / 11.83%
Duplication rate	12.53%
Clipped reads	719,149 / 38.19%

2.2. ACGT Content

Number/percentage of A's	23,881,406 / 27.27%
Number/percentage of C's	15,795,736 / 18.04%
Number/percentage of T's	28,132,579 / 32.13%
Number/percentage of G's	19,675,439 / 22.47%
Number/percentage of N's	80,394 / 0.09%
GC Percentage	40.51%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.369

2.4. Mapping Quality

Mean Mapping Quality	46.91

2.5. Mismatches and indels

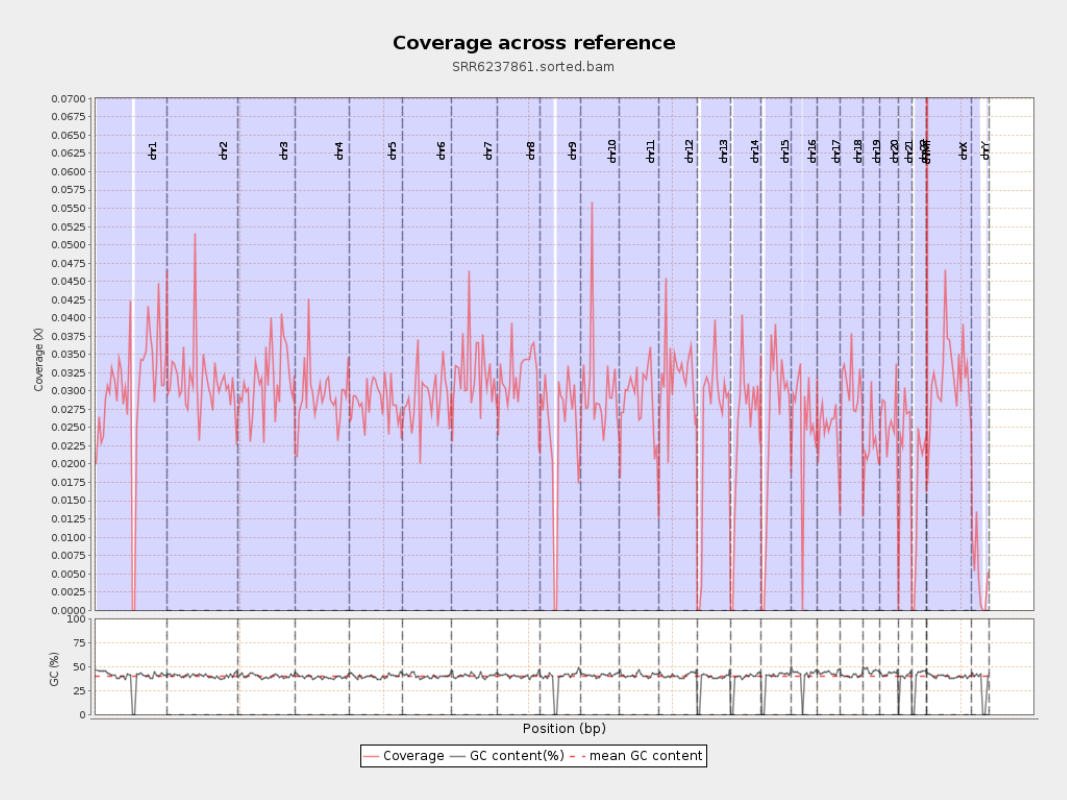
General error rate	0.87%
Mismatches	747,645
Insertions	7,470
Mapped reads with at least one insertion	0.54%
Deletions	29,695
Mapped reads with at least one deletion	2.15%
Homopolymer indels	48.89%

2.6. Chromosome stats

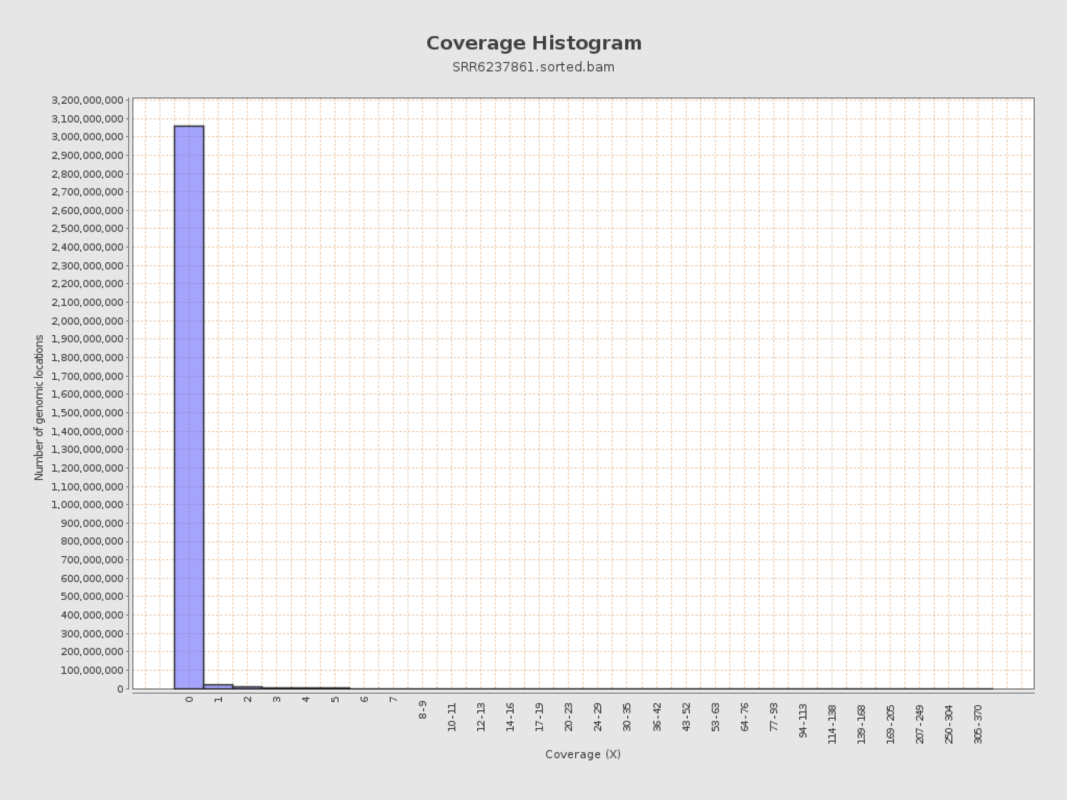
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7412418	0.0297	0.4529
chr2	243199373	7583303	0.0312	0.4011
chr3	198022430	6189093	0.0313	0.3409
chr4	191154276	5598962	0.0293	0.3444
chr5	180915260	5184909	0.0287	0.3367
chr6	171115067	4970251	0.029	0.3504
chr7	159138663	5153222	0.0324	0.4443

chr8	146364022	4667648	0.0319	0.415
chr9	141213431	3464888	0.0245	0.3394
chr10	135534747	4078664	0.0301	0.3956
chr11	135006516	3913403	0.029	0.3889
chr12	133851895	4274529	0.0319	0.3478
chr13	115169878	2935000	0.0255	0.3202
chr14	107349540	2636005	0.0246	0.3178
chr15	102531392	2609708	0.0255	0.3224
chr16	90354753	2276045	0.0252	0.3132
chr17	81195210	1987854	0.0245	0.3216
chr18	78077248	2394362	0.0307	0.4992
chr19	59128983	1327909	0.0225	0.3318
chr20	63025520	1649558	0.0262	0.3233
chr21	48129895	1095351	0.0228	0.296
chr22	51304566	808249	0.0158	0.2416
chrMT	16571	141444	8.5356	6.5545
chrX	155270560	4988043	0.0321	0.3599
chrY	59373566	273085	0.0046	0.126

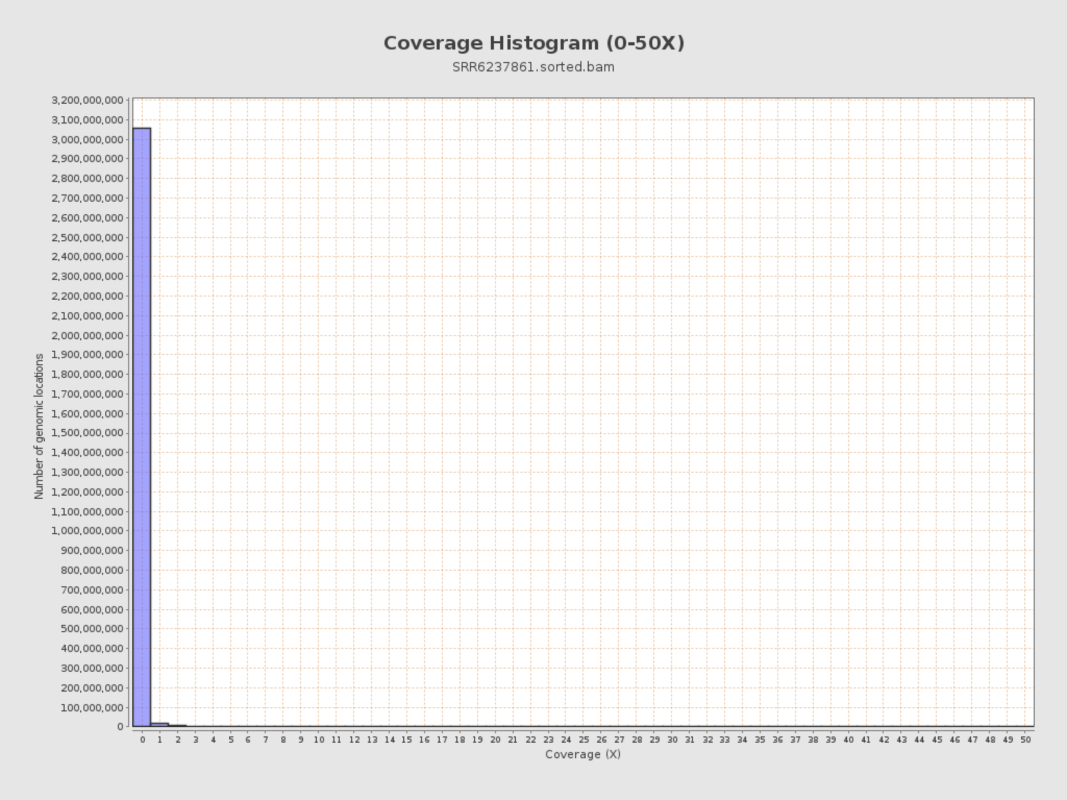
3. Results : Coverage across reference



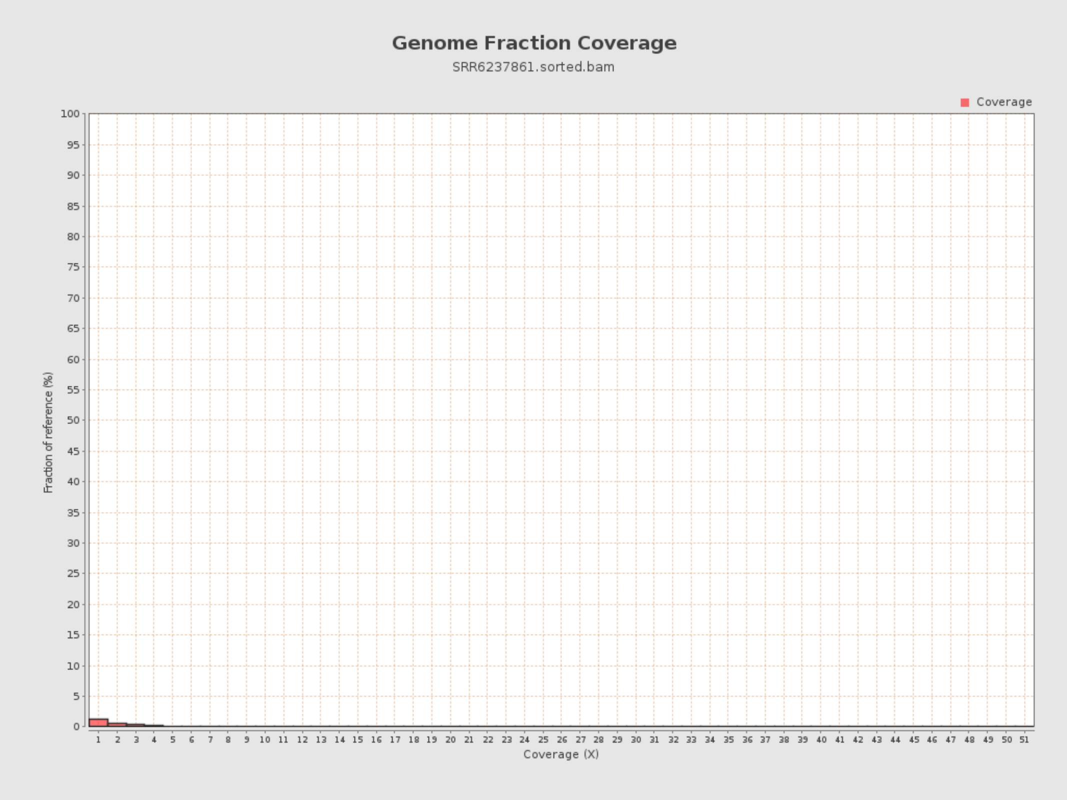
4. Results : Coverage Histogram



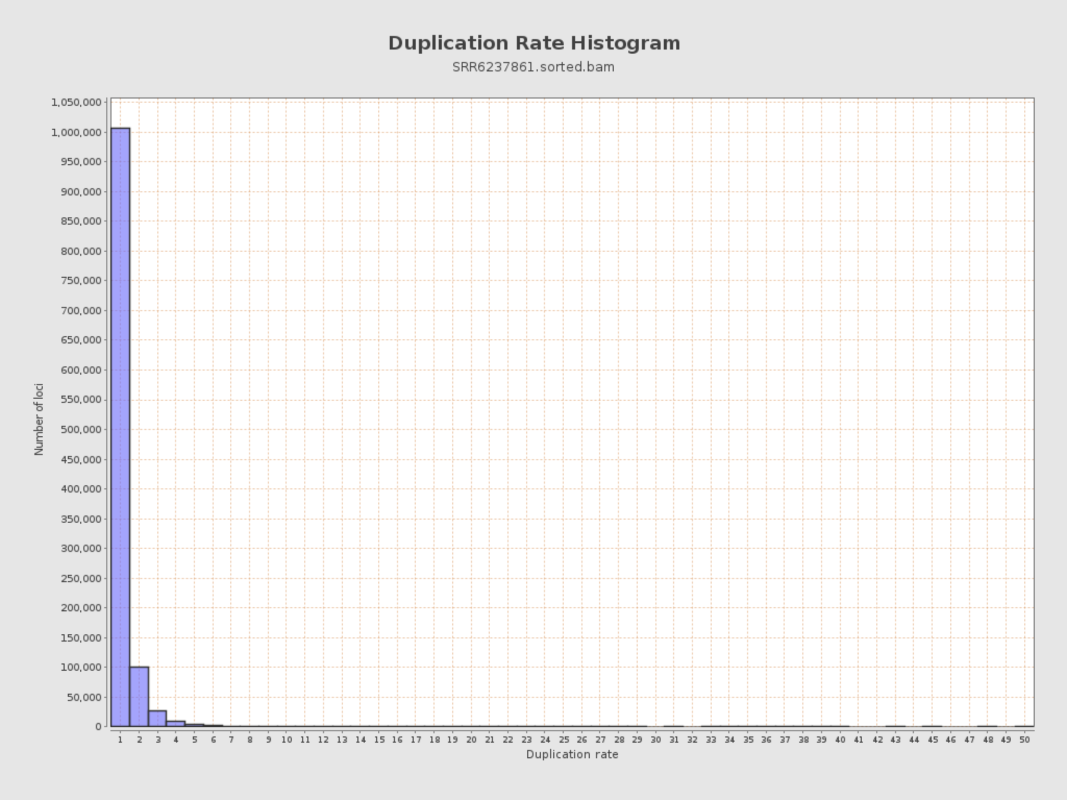
5. Results : Coverage Histogram (0-50X)



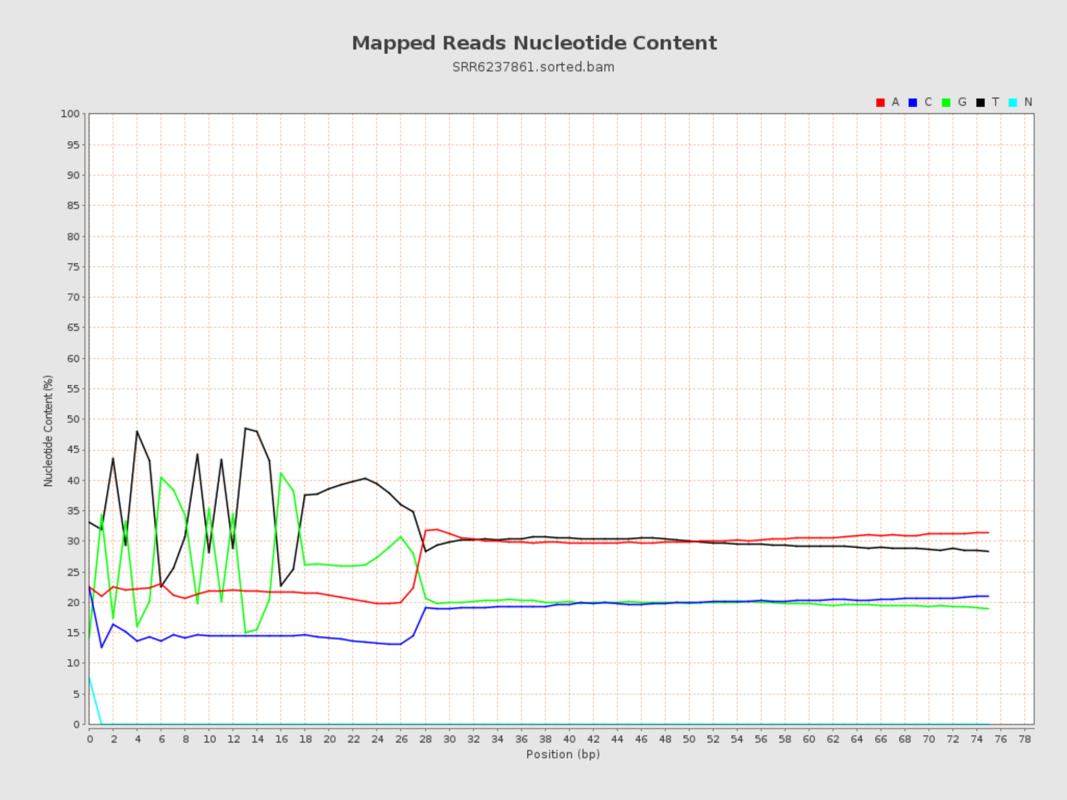
6. Results : Genome Fraction Coverage



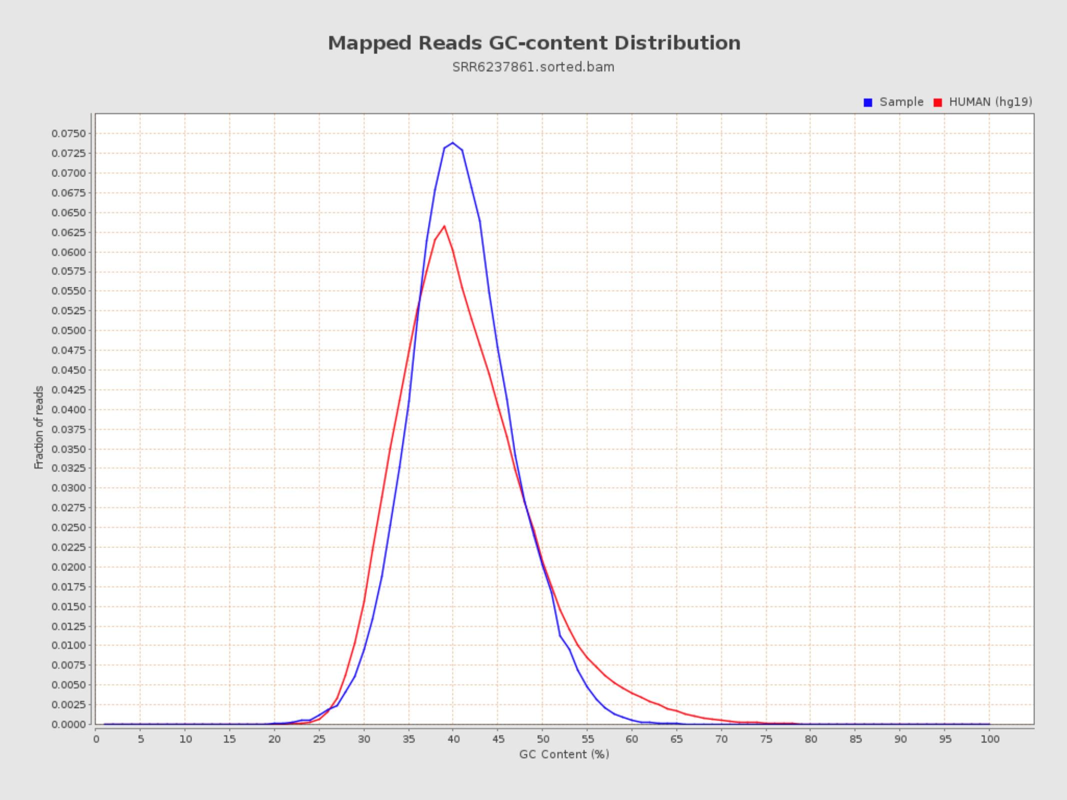
7. Results : Duplication Rate Histogram



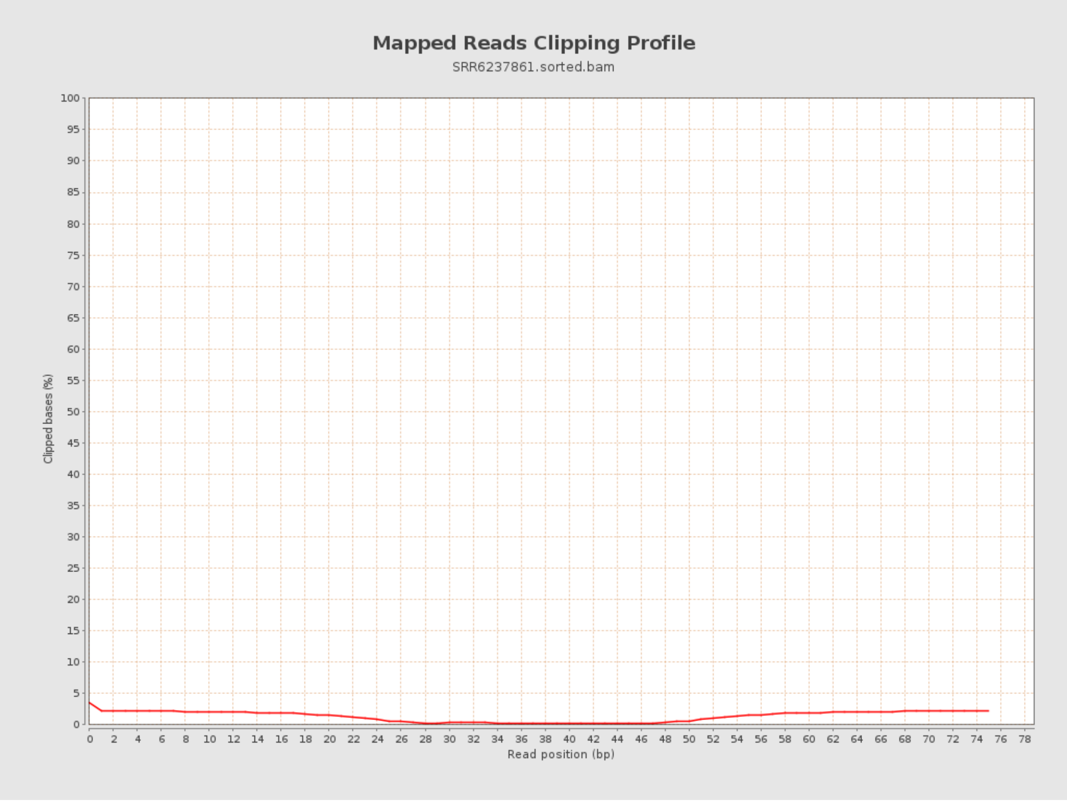
8. Results : Mapped Reads Nucleotide Content



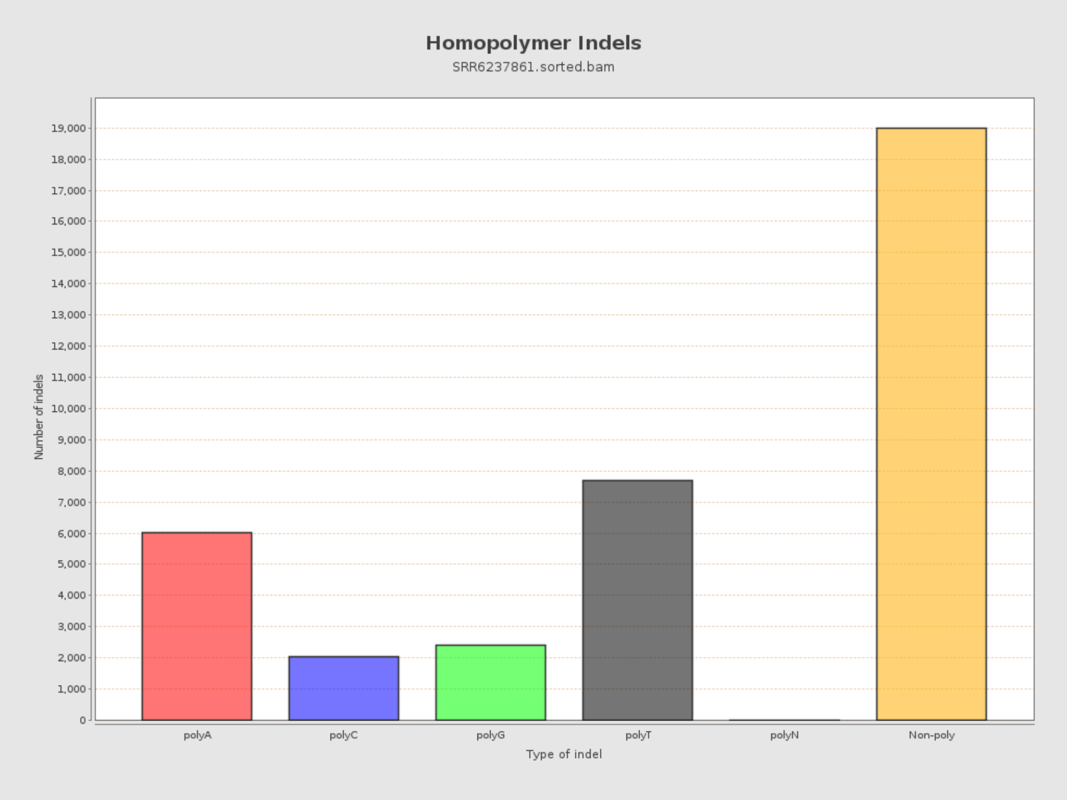
9. Results : Mapped Reads GC-content Distribution



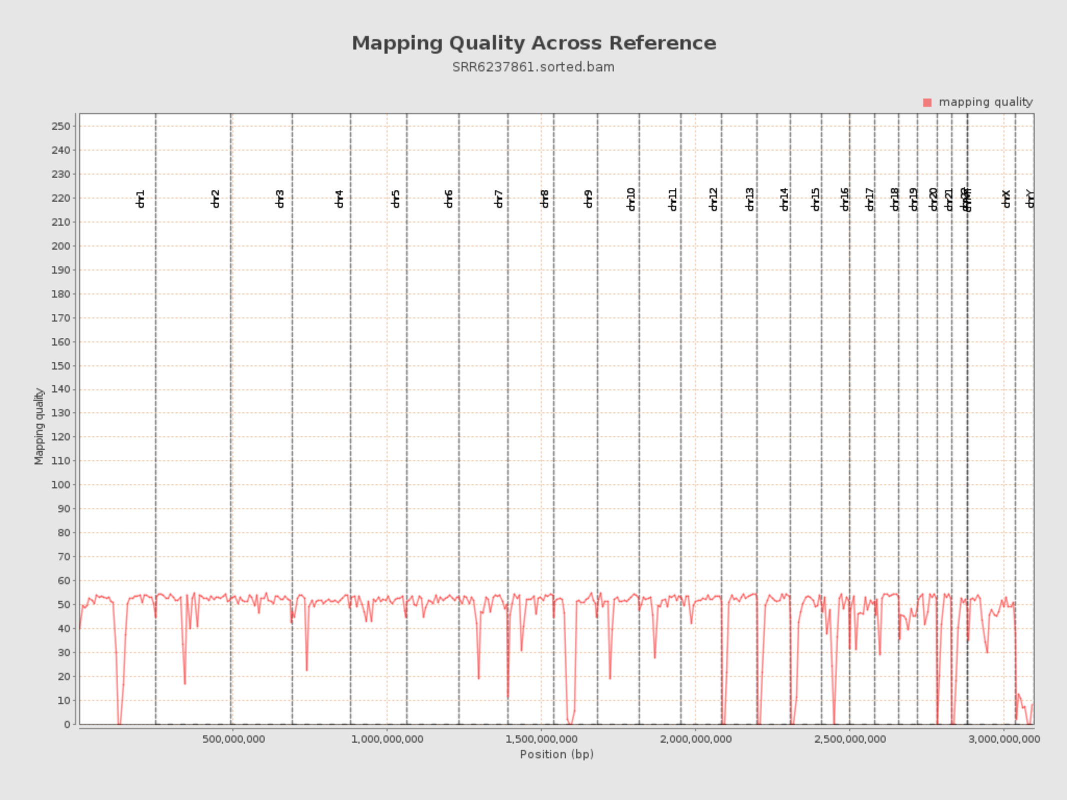
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram