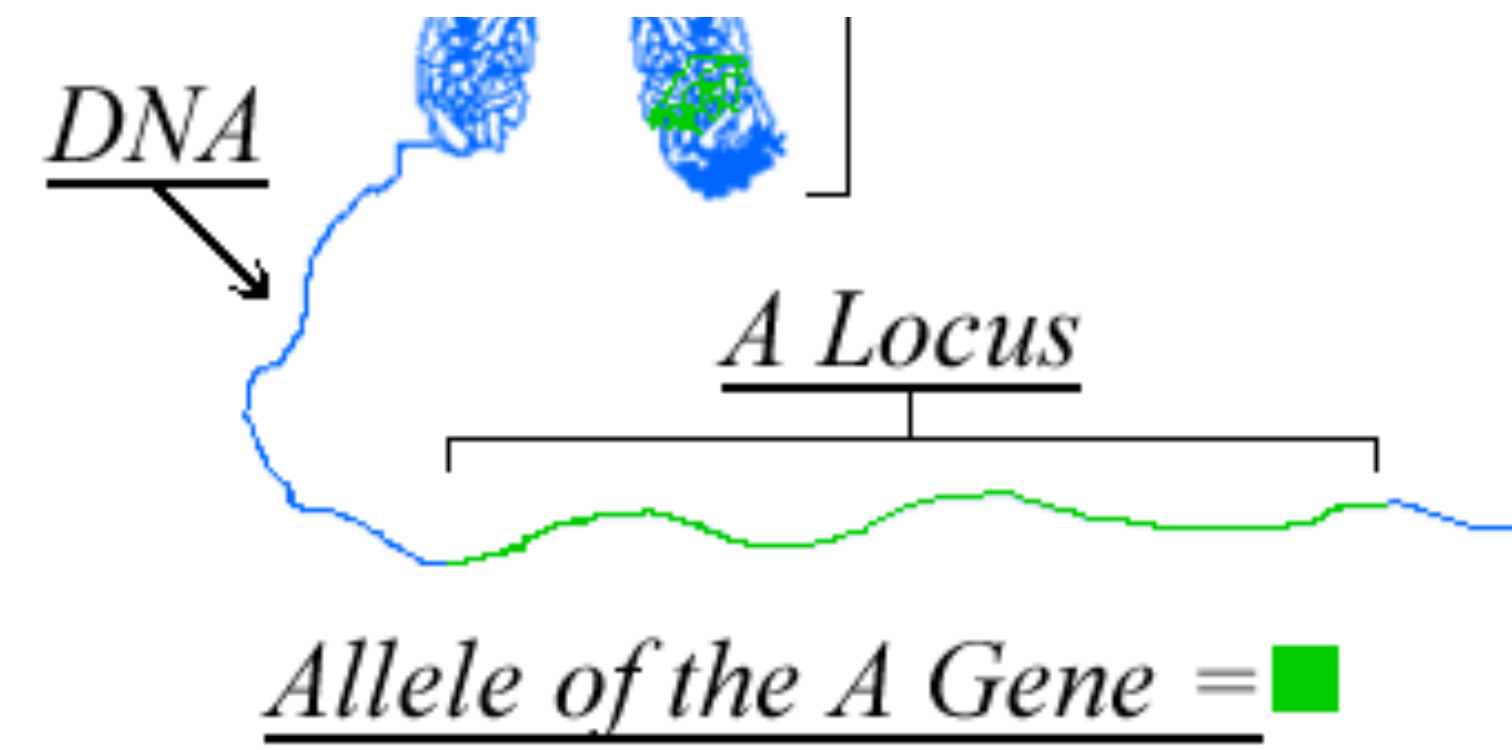
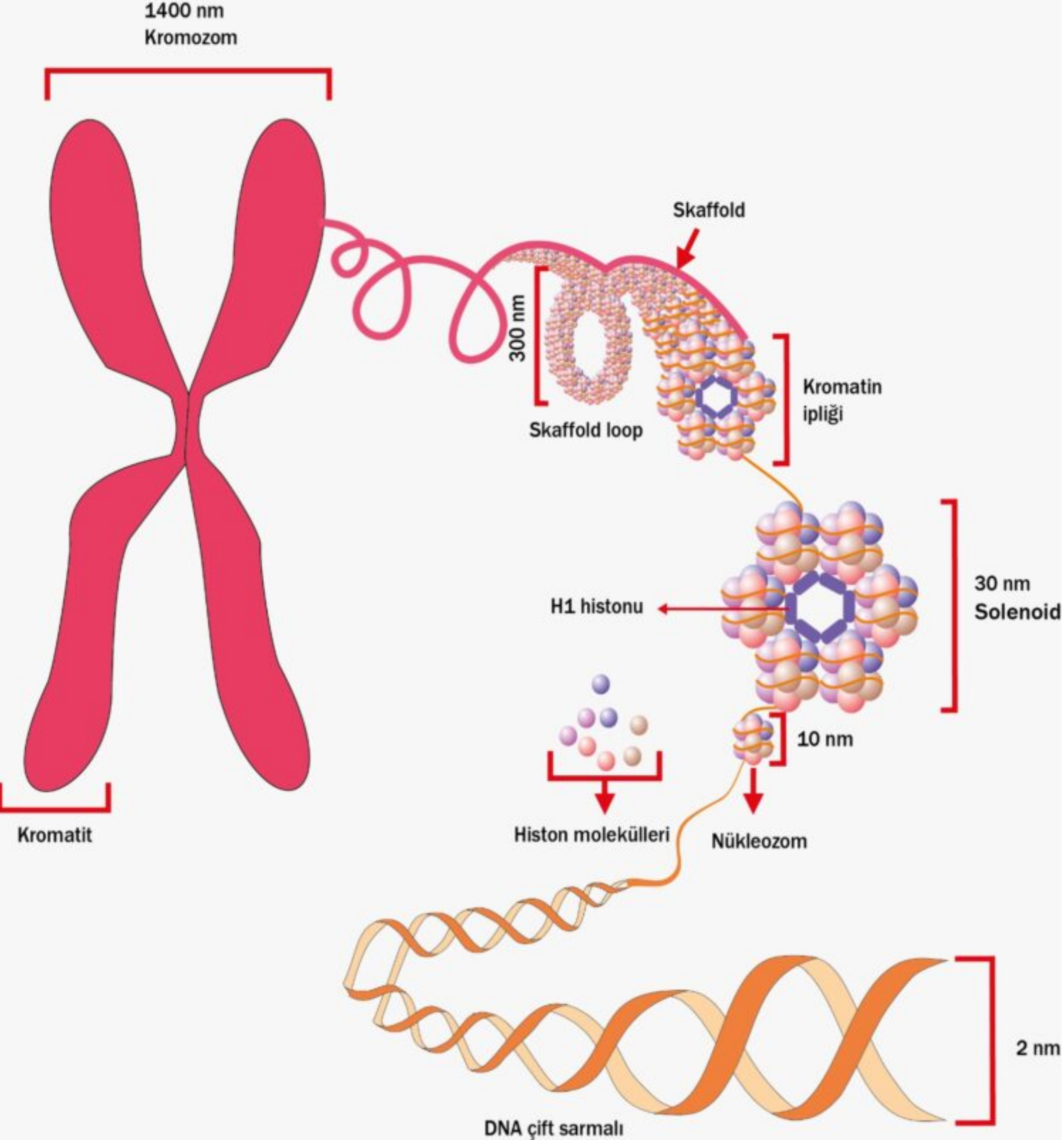
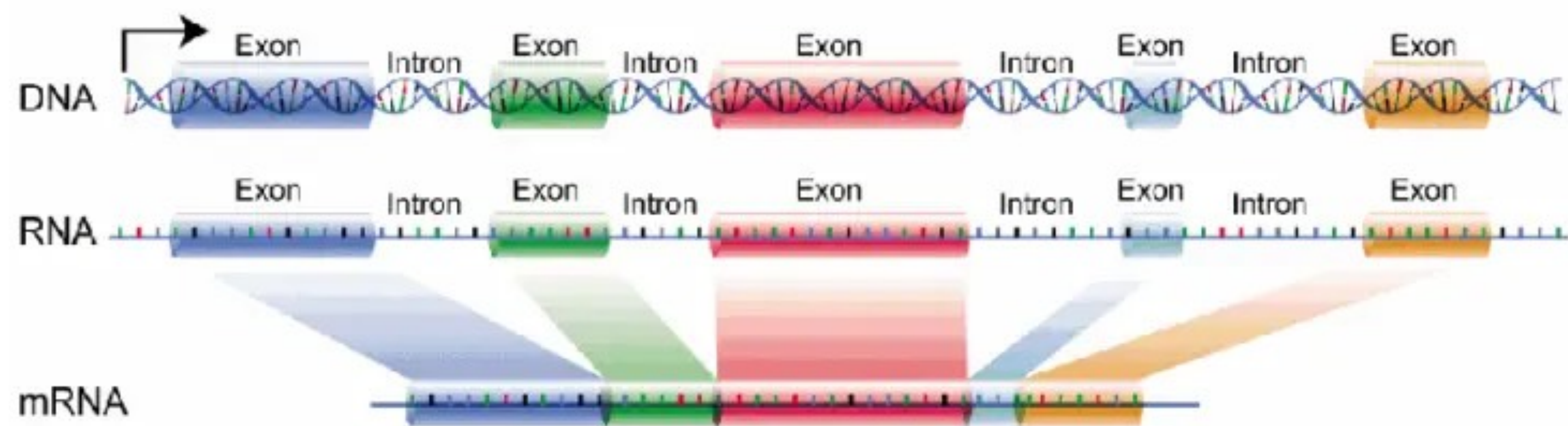
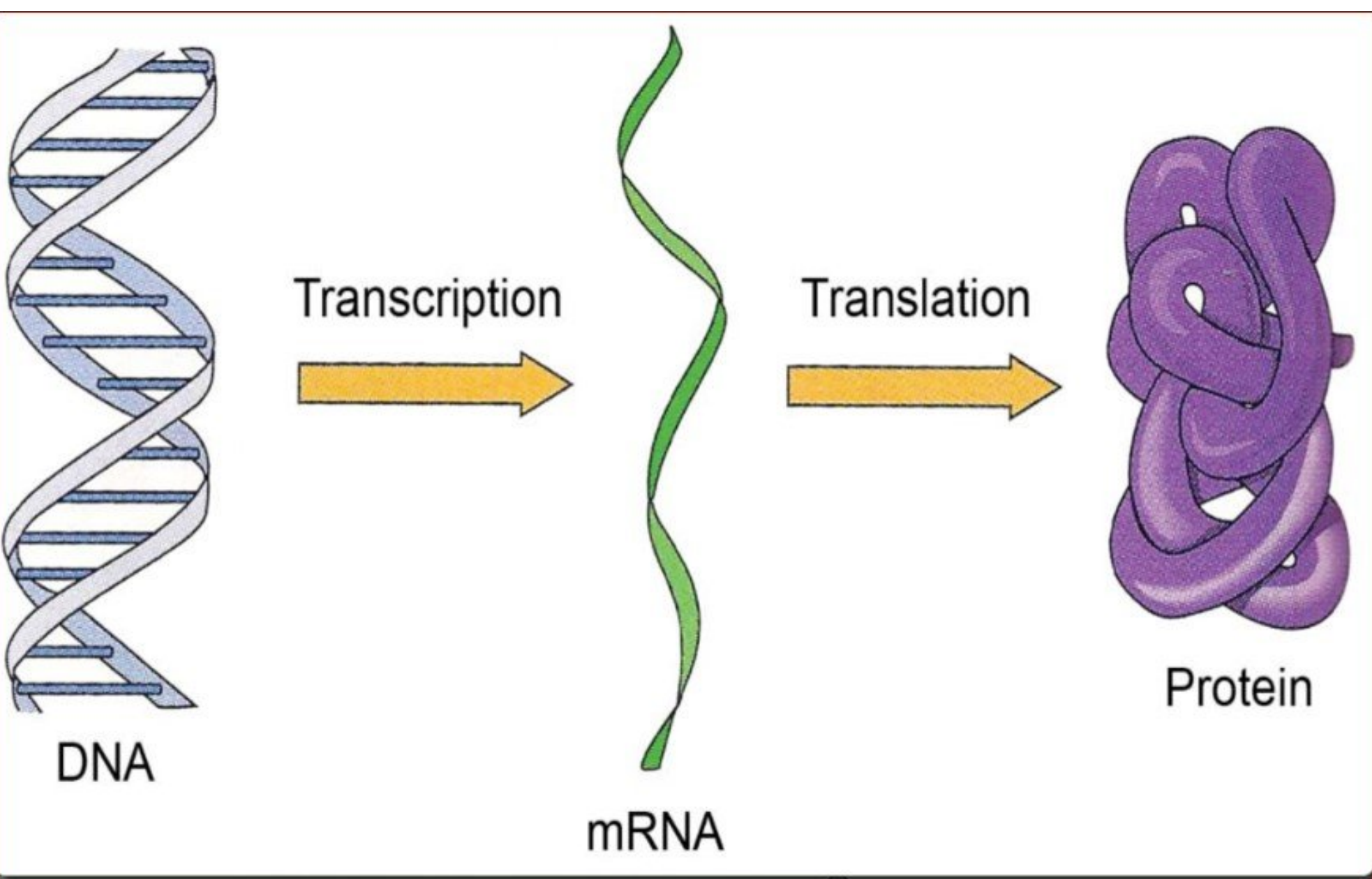


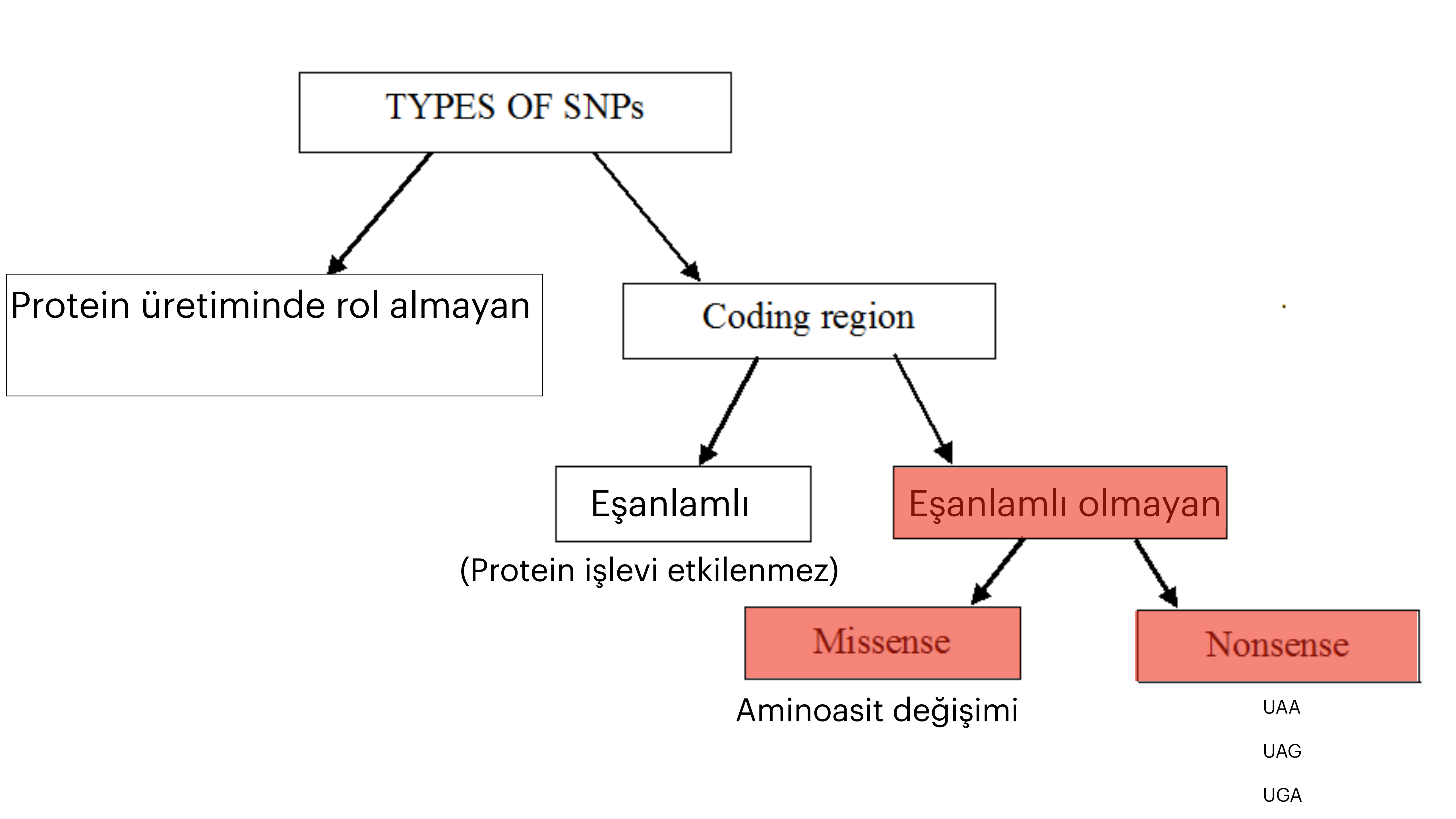
SNP ve GENETİK

SNP'lerin Oluşumu ve Genetikteki Yeri





TYPES OF SNPs



```
graph TD; A[TYPES OF SNPs] --> B[Protein üretiminde rol almayan]; A --> C[Coding region]; C --> D[Eş anlamlı]; C --> E[Eş anlamlı olmayan]; D --> F["(Protein işlevi etkilenmez)"]; E --> G[Missense]; E --> H[Nonsense]; G --> I[Aminoasit değişimi]; H --> J["UAA<br/>UAG<br/>UGA"]
```

The diagram is a hierarchical flowchart titled 'TYPES OF SNPs'. It starts with a root box 'TYPES OF SNPs' which branches into two boxes: 'Protein üretiminde rol almayan' (left) and 'Coding region' (right). The 'Coding region' box further branches into 'Eş anlamlı' (left) and 'Eş anlamlı olmayan' (right). The 'Eş anlamlı' box has a sub-label '(Protein işlevi etkilenmez)' below it. The 'Eş anlamlı olmayan' box branches into 'Missense' and 'Nonsense'. Below 'Missense' is the text 'Aminoasit değişimi'. Below 'Nonsense' are the stop codons 'UAA', 'UAG', and 'UGA' listed vertically. The boxes for 'Eş anlamlı olmayan', 'Missense', and 'Nonsense' are shaded red, while the others are white.

Protein üretiminde rol almayan

Coding region

Eş anlamlı

(Protein işlevi etkilenmez)

Eş anlamlı olmayan

Missense

Aminoasit değişimi

Nonsense

UAA

UAG

UGA

Gene

Gene



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TP53 tumor protein p53 [*Homo sapiens* (human)]

Gene ID: 7157, updated on 12-Nov-2024

Download Datasets

Table of contents

- Summary
- Genomic context
- Genomic regions, transcripts, and products
- Expression
- Bibliography
- Phenotypes
- Variation
- HIV-1 interactions
- Pathways from PubChem
- Interactions
- General gene information
 - Markers, Clone Names, Homology, Gene Ontology
- General protein information
- NCBI Reference Sequences (RefSeq)
- Related sequences
- Additional links
 - Locus-specific Databases

Genome Browsers

- Genome Data Viewer
- Variation Viewer (GRCh37.p13)
- Variation Viewer (GRCh38)
- 1000 Genomes Browser (GRCh37.p13)
- Ensembl
- UCSC

Related information

- 3D structures
- BioAssay by Target (List)

Summary

- Official Symbol** TP53 provided by HGNC
- Official Full Name** tumor protein p53 provided by HGNC
- Primary source** [HGNC:HGNC:11998](#)
- See related** [Ensembl:ENSG00000141510](#) [MIM:191170](#); [AllianceGenome:HGNC:11998](#)
- Gene type** protein coding
- RefSeq status** REVIEWED
- Organism** [Homo sapiens](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
- Also known as** P53; BCC7; LFS1; BMFS5; TRP53
- Summary** This gene encodes a tumor suppressor protein containing transcriptional activation, DNA binding, and oligomerization domains. The encoded protein responds to diverse cellular stresses to regulate expression of target genes, thereby inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism. Mutations in this gene are associated with a variety of human cancers, including hereditary cancers such as Li-Fraumeni syndrome. Alternative splicing of this gene and the use of alternate promoters result in multiple transcript variants and isoforms. Additional isoforms have also been shown to result from the use of alternate translation initiation codons from identical transcript variants (PMIDs: 12032546, 20937277). [provided by RefSeq, Dec 2016]
- Expression** Ubiquitous expression in spleen (RPKM 13.2), lymph node (RPKM 13.1) and 25 other tissues [See more](#)
- Orthologs** [mouse](#) [all](#)
- NEW** Try the new [Gene table](#)
- Try the new [Transcript table](#)

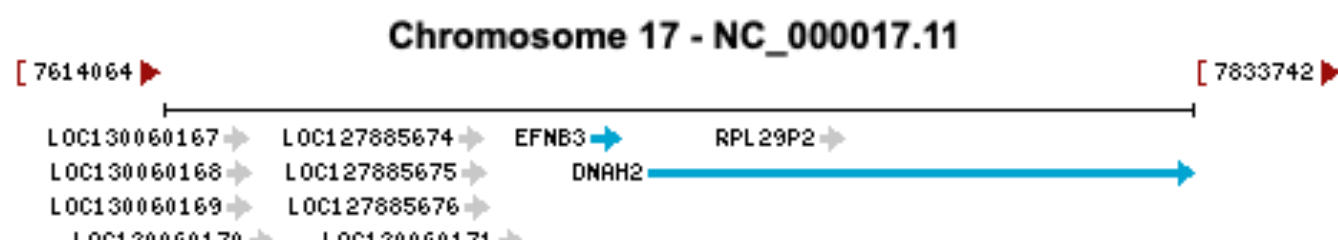
Genomic context

Location: 17p13.1

See TP53 in [Genome Data Viewer](#)

Exon count: 13

Annotation release	Status	Assembly	Chr	Location
RS_2024_08	current	GRCh38.p14 (GCF_000001405.40)	17	NC_000017.11 (7668421..7687490, complement)
RS_2024_08	current	T2T-CHM13v2.0 (GCF_009914755.1)	17	NC_060941.1 (7572544..7591594, complement)
RS_2024_09	previous assembly	GRCh37.p13 (GCF_000001405.25)	17	NC_000017.10 (7571739..7590808, complement)



SNV

Single Nucleotide Variation

- <1%
- Nadir görülür
- Aile veya belirli bireylerle sınırlıdır

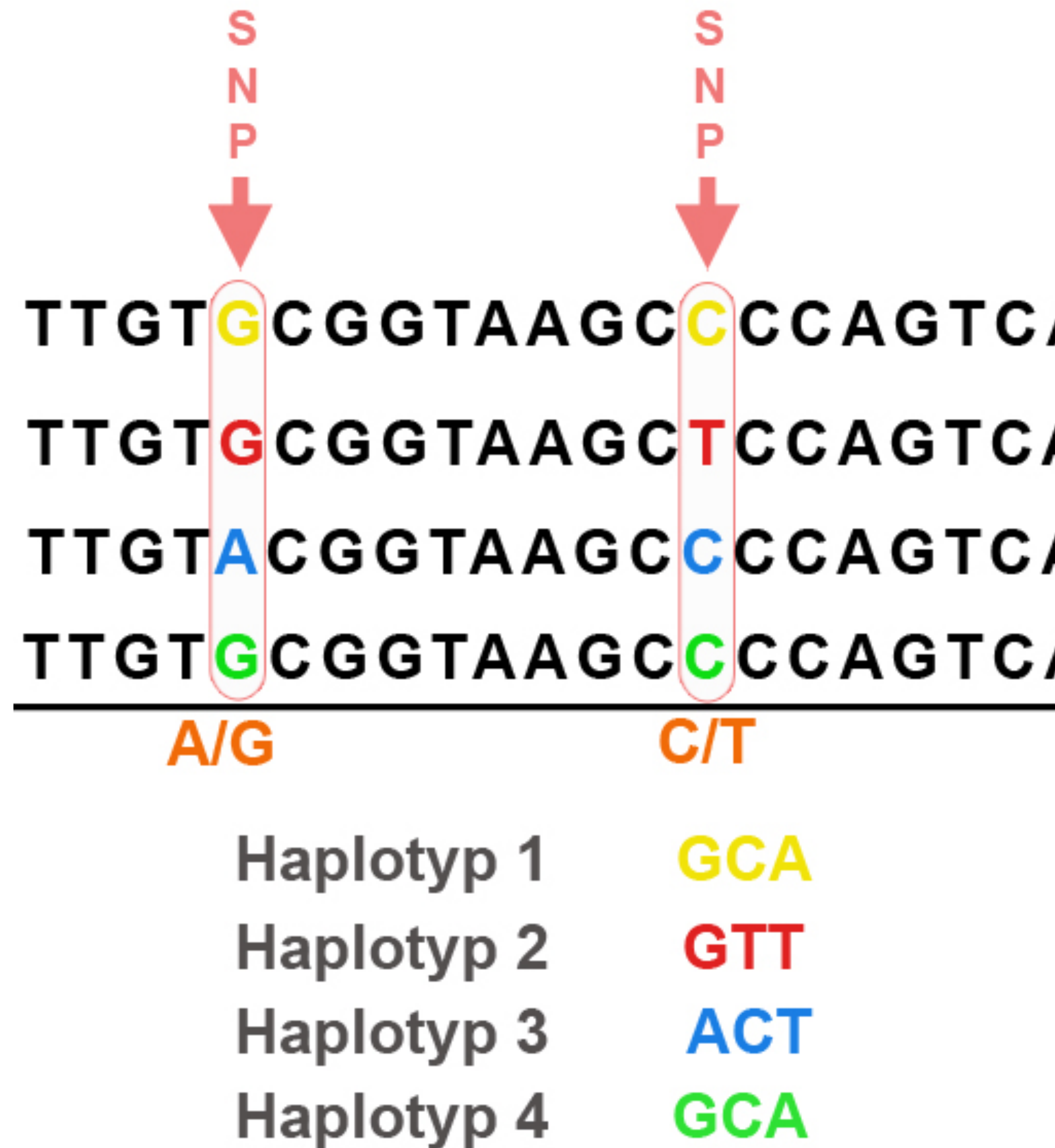
Single Nucleotide Variation

Reference Genome	A	T	C	G	C	A	G
Example Sequence	A	T	C	G	C	C	T

SNP

Tek Nükleotid Polimorfizmi

- %1>
- İki insan arasında benzerlik %99,9 olmasına rağmen SNP 30 - 300 milyon vardır.
- Her **SNP** ayrıca **SNV**'dir.



2^{10,000,000,000}

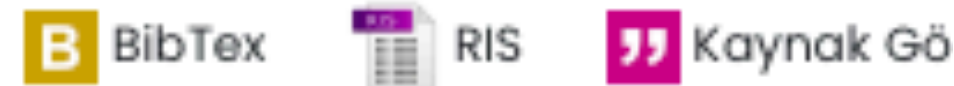
Evrendeki atom sayısı 2^{66}

Genetik Varyasyon

- Genetik çeşitlilik
- Kişiselleştirilmiş Tıp
- **Karmaşık**
- **SNP - SNP etkileşimi**



TR	EM
----	----



Yıl 2016, Cilt: 2 Sayı: 1, 28 - 31, 31.01.2016

<https://doi.org/10.30934/kusbed.358489>

● Cited By: 1

Amaç: TP53 geni temel olarak DNA tamiri, apoptozis, hücre yaşlanması ve hücre döngü kontrolünde görev alan en önemli tümör baskılayıcı genlerden biridir. TP53 rs10425 (Arg72Pro) polimorfizmi tümör baskılama sırasında P53 protein yapısında değişikliğe neden olan bir polimorfizmdir. Bu verilere dayanarak, bu çalışmanın amacı TP53 rs10425 polimorfizmi ve meme kanseri riski arasındaki ilişkiyi araştırmaktır.

Yöntem: TP53 rs1042522 polimorfizmi için 508 meme kanserli kadın hastadan ve 367 sağ kadından alınan periferik kanlardan DNA izole edilerek PCR-RELP yöntemi ile genotipler

SNP

rs1042522

Create alert Advanced

Display Settings: Summary, 20 rows, 1 page, Sorted by SNP_ID

Items: 8

rs1042522 [*Homo sapiens*]

Variant: SNV
Alleles: G>A,C,T [\[Show Flanks\]](#)
Chromosome: 17:7676154 (GRCh38)
17:7579472 (GRCh37)
Canonical SPDI: NC_000017.11:7676153:G:A,NC_000017.11:7676153:G:C,NC_000017.11:7676153:G:T
Gene: TP53 ([Varview](#))
Functional Consequence: coding_sequence_variant,upstream_transcript_variant,missense_variant,genic_upstream_variant
Clinical significance: pathogenic,uncertain-significance,benign,likely-benign
Validated: by frequency,by alfa,by cluster
MAF: G=0.285663/30142 ([ALFA](#))
T=0./0 (KOREAN)
G=0.107143/6 (PRJEB36033)

HGVS: NC_000017.11:g.7676154G>A, NC_000017.11:g.7676154G>C,
NC_000017.11:g.7676154G>T, NC_000017.10:g.7579472G>A,
NC_000017.10:g.7579472G>C, NC_000017.10:g.7579472G>T,
NC_013013.2:-16307C>G, NC_013013.2:-16307C>A, NM_001163013.2:c.16307C>G, NM_001163013.2:c.16307C>A

PubMed

☐ rs60388830 has merged into rs1042522 [*Homo sapiens*]
2.

Variant type: SNV
Alleles: G>A,C,T [\[Show Flanks\]](#)
Chromosome: 17:7676154 (GRCh38)
17:7579472 (GRCh37)

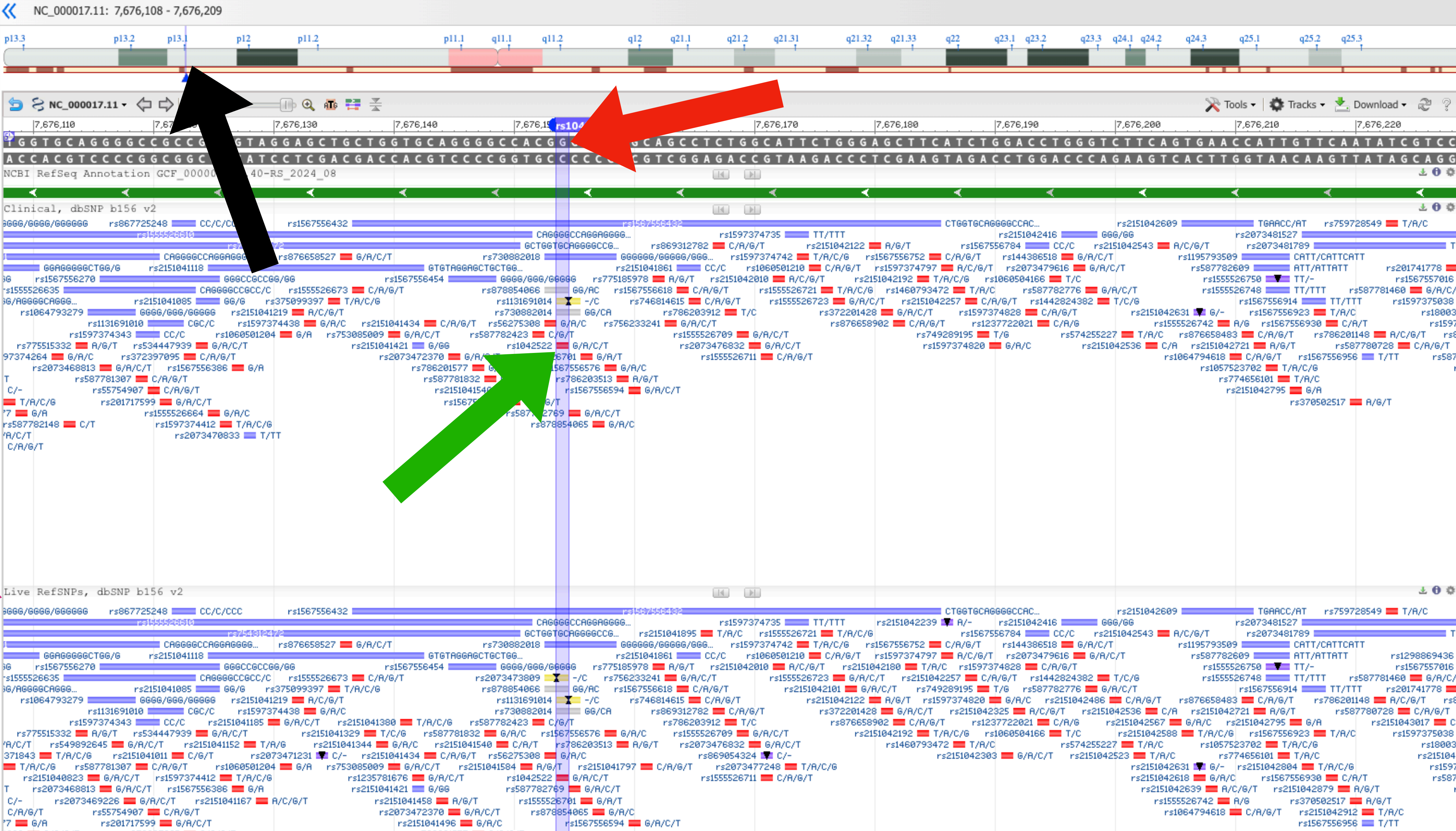
Canonical SPDI: NC_000017.11:7676153:G:A,NC_000017.11:7676153:G:C,NC_000017.11:7676153:G:T,NC_000017.11:7676153:G:G

Homo sapiens
(human)

Assembly: GRCh38.p14 (GCF_000001405.40) Chr 17 (NC_000017.11)

Search assembly
rs1042522

Pick Assembly
Tracks
History
Assembly Region



Welcome to the Reference SNP (rs) Report
All alleles are reported in the [Forward orientation](#). Click on the [Variant Details](#) tab for details on Genomic Placement, Gene, and Amino Acid changes. HGVS names are in the [HGVS](#) tab.

Reference SNP (rs) Report

[Download](#) [f](#) [t](#) [g+](#) [?](#)

Current Build 156
Released September 21, 2022

rs1042522

Organism *Homo sapiens*
Position chr17:7676154 (GRCh38.p14) [?](#)
Alleles G>A / G>C / G>T
Variation Type SNV Single Nucleotide Variation
Frequency G=0.382621 (101276/264690, TOPMED)
G=0.331835 (83136/250534, GnomAD_exome)
G=0.373457 (52281/139992, GnomAD) ([+ 23 more](#))

Clinical Significance Not reported in [ClinVar](#)
Gene : Consequence TP53 : Missense Variant
Publications [390 citations](#)
[LitVar²](#) 2054
Genomic View [See rs on genome](#)

Nokta Mutasyonu

%38

- Frequency
- Variant Details
- Clinical Significance
- HGVS
- Submissions
- History
- Publications
- Flanks

ALFA Allele Frequency

The ALFA project provide aggregate allele frequency from dbGaP. More information is available on the project [page](#) including descriptions, data access, and terms of use.

Release Version: 20231103111315

Search:

Population	Group	Sample Size	Ref Allele	Alt Allele	Ref HMOZ	Alt HMOZ	HTRZ	HWEP
Total	Global	105516	G=0.285663	C=0.714337, T=0.000000	0.094659	0.523333	0.382008	32
European	Sub	90388	G=0.26336	C=0.73664, T=0.00000	0.073439	0.54671	0.379851	11
African	Sub	2988	G=0.6854	C=0.3146, T=0.0000	0.523427	0.15261	0.323963	32

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RefSen nrn


```
2151085896.fasta dosyası masaüstüne indirildi.  
2151085754.fasta dosyası masaüstüne indirildi.  
2151085636.fasta dosyası masaüstüne indirildi.  
2151085616.fasta dosyası masaüstüne indirildi.  
2151085508.fasta dosyası masaüstüne indirildi.  
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2151085436.fasta dosyası masaüstüne indirildi.  
2151085294.fasta dosyası masaüstüne indirildi.  
(base) sahil@sahil-3 ~ %
```



a.py



```
1 from Bio import Entrez  
2 import os  
3  
4 Entrez.email = "dogukansahil@gmail.  
5 Entrez.api_key = "a6190b141aea42289  
6  
7 desktop_path = os.path.join(os.path.expanduser("~"), "Desktop")  
8  
9 def fetch_snp_fasta(gene_name):  
10     # SNP'leri bulmak için arama yap  
11     search_handle = Entrez.esearch(db="snp", term=gene_name, retmax=10)
```

```
ACCCTCTTTTCTTATCATTTGACATTTTAAACTCTGGGGCAGGTCCTCGCGTAGAACGCGGGCT  
GCCACTTCCCCTGCCGAGCGGGCGGTGAGAAGTGTGGGAACCGGGCGCTGCCAGGCTCACCTG  
CCTCCGCTCCCAGGTAACCGCCCCGGGCTCCGGCCCCCGGGCCCGGCTCGGGGGCCCGCGGGGCC  
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TCCGTACCCGCGCCTGGAGCGCTTAAAGACACCCTGCCGCGGGGTCGGGGCGAGGTGCAGCAC  
CGCGCTTCCAAAGCTCCAGATCCGCTCCAGCGGCAAGCAAGCTCTAGACATCCGCGCTTCCGCT
```

- <https://www.ncbi.nlm.nih.gov/snp/>
- <https://pmc.ncbi.nlm.nih.gov/articles/PMC1235544/>
- <https://pmc.ncbi.nlm.nih.gov/articles/PMC24792/>