

Variant: NM_001126112.2(TP53):c.214_215delinsTG
(p.Pro72Cys)

Version: 2.0

CA000069 [↗](#)

182953 (ClinVar) [↗](#)

Gene: TP53 ([HGNC:7157](#))
Condition: Li-Fraumeni syndrome ([MONDO:0018875](#))
Inheritance Mode: Autosomal dominant inheritance
UUID: b7e523bb-93f5-4505-943a-3286739499c5
Approved on: 2025/2/6
Published on: 2025/2/7

HGVS expressions

NM_001126112.2(TP53):c.214_215delinsTG (p.Pro72Cys)
NM_001126112.2:c.214_215delinsTG
NC_000017.11:g.7676154_7676155delinsCA
CM000679.2:g.7676154_7676155delinsCA
NC_000017.10:g.7579472_7579473delinsCA
CM000679.1:g.7579472_7579473delinsCA
NC_000017.9:g.7520197_7520198delinsCA
NG_017013.2:g.16396_16397delinsTG
ENST00000503591.2:c.214_215delinsTG
ENST00000508793.6:c.214_215delinsTG
ENST00000509690.6:c.-21-919_-21-918delinsTG
ENST00000514944.6:c.96+227_96+228delinsTG
ENST00000604348.6:c.214_215delinsTG
ENST00000269305.9:c.214_215delinsTG
ENST00000269305.8:c.214_215delinsTG
ENST00000359597.8:c.214_215delinsTG
ENST00000413465.6:c.214_215delinsTG
ENST00000420246.6:c.214_215delinsTG
ENST00000445888.6:c.214_215delinsTG
ENST00000455263.6:c.214_215delinsTG
ENST00000503591.1:c.214_215delinsTG
ENST00000505014.5:n.470_471delinsTG
ENST00000508793.5:c.214_215delinsTG
ENST00000509690.5:c.-21-919_-21-918delinsTG
ENST00000514944.5:c.96+227_96+228delinsTG
ENST00000604348.5:c.214_215delinsTG
ENST00000610292.4:c.97_98delinsTG
ENST00000610538.4:c.97_98delinsTG
ENST00000615910.4:c.214_215delinsTG
ENST00000617185.4:c.214_215delinsTG
ENST00000619485.4:c.97_98delinsTG
ENST00000620739.4:c.97_98delinsTG
ENST00000622645.4:c.97_98delinsTG
ENST00000635293.1:c.97_98delinsTG
NM_000546.5:c.214_215delinsTG
NM_001126113.2:c.214_215delinsTG
NM_001126114.2:c.214_215delinsTG
NM_001126118.1:c.97_98delinsTG
NM_001276695.1:c.97_98delinsTG
NM_001276696.1:c.97_98delinsTG
NM_001276760.1:c.97_98delinsTG
NM_001276761.1:c.97_98delinsTG
NM_001276695.2:c.97_98delinsTG

NM_001276696.2:c.97_98delinsTG
NM_001276760.2:c.97_98delinsTG
NM_001276761.2:c.97_98delinsTG
NM_000546.6:c.214_215delinsTG
NM_001126112.3:c.214_215delinsTG
NM_001126113.3:c.214_215delinsTG
NM_001126114.3:c.214_215delinsTG
NM_001126118.2:c.97_98delinsTG
NM_001276695.3:c.97_98delinsTG
NM_001276696.3:c.97_98delinsTG
NM_001276760.3:c.97_98delinsTG
NM_001276761.3:c.97_98delinsTG

Uncertain Significance

Met criteria codes 1

PM2_Supporting

Not Met criteria codes 20

BA1 BP7 BP4 BP3 BP2 BS1
BS4 BS3 BS2 PP1 PP3
PM6 PS1 PS2 PS3 PS4
PM1 PM5 PM4 PVS1

Evidence Links 0

Expert Panel

TP53 VCEP

Criteria Specification Information

- Criteria Specification: ClinGen TP53 Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for TP53 Version 2.2.0
- Criteria Specification Approval History
- Criteria Specifications for this VCEP

Evidence submitted by expert panel

TP53 VCEP

The NM_000546.6: c.214_215delinsTG variant in TP53 is a deletion/insertion variant predicted to cause substitution of proline by cysteine at amino acid 72 (p.Pro72Cys). Although this variant has been observed in germline cases, to our knowledge, this variant has not been reported in individuals meeting classical LFS or Chompret criteria (PS4 not met; Internal lab contributors). This variant has been observed in 4-7 heterozygous unrelated females from the same data source with no personal history of cancer prior to age 60 years and no personal history of sarcoma at any age (BS2_Moderate; Internal lab contributors). This variant is absent from gnomAD v4.1.0 (PM2_Supporting). In summary, this variant meets the criteria to be classified as variant of uncertain clinical significance for Li Fraumeni syndrome based on the ACMG/AMP criteria applied, as specified by the ClinGen TP53 VCEP: BS2_Moderate, PM2_Supporting. (Bayesian Points: -1; VCEP specifications version 2.2; 2/6/2025).

Met criteria codes

PM2_Supporting   This variant is absent from gnomAD v4.1.0 (PM2_Supporting).

Not Met criteria codes

BA1   No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

BP7   No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

BP4   No predictions available: https://tp53.cancer.gov/mut_details?mut_id=22552 No impact with SpliceAI: https://spliceailookup.broadinstitute.org/#variant=NM_000546.6(TP53)%3Ac.214_215delinsTG%20(p.Pro72Cys)&hg=38&bc=basic&distance=500&r=1000

BP3 

No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline			
BP2		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS1		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS4		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS3		✖	No data
BS2		✖	BS2_MODERATE This variant has been observed in 4-7 heterozygous unrelated females from the same data source with no personal history of cancer prior to age 60 years and no personal history of sarcoma at any age (BS2_Moderate; Internal lab contributors).
PP1		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PP3		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM6		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS1		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS2		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PS3		✖	No data.
PS4		✖	Although this variant has been observed in germline cases, to our knowledge, this variant has not been reported in individuals meeting classical LFS or Chompret criteria (PS4 not met; Internal lab contributors)
PM1		✖	This variant does not reside within a region of TP53 that is defined as a mutational hotspot by the ClinGen TP53 VCEP (PM1 not met).
PM5		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM4		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PVS1		✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

Curation History ↗		
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