Supp. Table S2 - Distribution of *TP53* variants by protein domains

	Pathogenic (P)	**Likely Pathogenic (LP)**	**Possibly Pathogenic (PP)**	**Likely Benign (LB)**		**Uncertain Significance (VUS)**	**Total**	
Variant Category	Non synonymous	Non synonymous	Non synonymous	Synonymous	Non synonymous	Non synonymous	**Non synonymous**	**Synonymous**
Protein domain								
Transcriptional activation	0	0	5	16	4	2	11	16
Proline Rich	0	1	0	8	4	1	6	8
Proline Rich/DNA-binding transition	0	0	2	2	0	0	2	2
DNA Binding	18	10	14	23	7	4	53	23
DNA Binding/Oligomerization transition	0	2	3	9	6	1	12	9
Oligomerization	1	1	3	3	7	0	12	3
Oligom./C-Terminal Reg. transition	0	0	1	0	0	0	1	0
C-Terminal Regulatory	0	1	0	1	3	2	6	1
Total	19	15	28	62	31	10	103	62

Tabular representation of Figure 2. According to the NM_000546.5 reference, domains of TP53 were divided in: transcriptional activation (residues 1 to 62), proline-rich region (residues 63-97), DNA-binding domain (residues 109-288), oligomerization domain (residues 319-359), and C-terminal regulatory domain (residues 363-393). Numbers do not include duplicate values for variants detected in more than one database. Nonsynonymous variants include 1 nonframeshift deletion and 1 nonsense variant. Abbreviations: P, pathogenic; LP, likely pathogenic; PP, possibly pathogenic; LB, likely benign; VUS, variant of uncertain significance.

Supp. Table S3 - Distribution of *TP53* variants across different population ancestries

			Variant Classification									
			Pathogenic (P)		Likely Pathogenic (LP)		Possibly Pathogenic (PP)		Likely Benign (LB)		Uncertain Significance (VUS)	
Database	**Ancestry**	**Total Individuals**	**Number of Individuals**	**Prevalence**	**Number of Individuals**	**Prevalence**	**Number of Individuals**	**Prevalence**	**Number of Individuals**	**Prevalence**	**Number of Individuals**	**Prevalence**
ExAC non-TCGA	African/African American	4,533	2	0.0004	1	0.0002	8	0.0018	32	0.0071	1	0.0002
	Latino	5,608	4	0.0007	5	0.0009	6	0.0011	32	0.0057	1	0.0002
	East Asian	3,933	2	0.0005	4	0.0010	2	0.0005	28	0.0071	5	0.0013
	Finnish	3,307	2	0.0006	6	0.0018	4	0.0012	12	0.0036	1	0.0003
	Non-Finnish European	27,173	19	0.0007	56	0.0021	14	0.0005	75	0.0028	0	0.0000
	Other	347	0	0.0000	0	0.0000	0	0.0000	0	0.0000	0	0.0000
	South Asian	8,204	5	0.0006	5	0.0006	15	0.0018	151	0.0184	0	0.0000
	Total	53,105	34	0.0006	77	0.0014	49	0.0009	330	0.0062	8	0.0002
FLOSSIES	African American	2,559	0	0.0000	2	0.0008	8	0.0031	18	0.0070	2	0.0008
	European American	7,325	1	0.0001	14	0.0019	6	0.0008	26	0.0035	1	0.0001
	Total	9,884	1	0.0001	16	0.0016	14	0.0014	44	0.0045	3	0.0003
WES Controls	European	994	1	0.0010	2	0.0020	1	0.0010	3	0.0030	0	0.0000

Variant distribution across ancestries comprised in each database. Prevalence calculated by the number of individuals within a certain category divided by the total number of individuals of a given ancestry. Abbreviations: WES, Whole-Exome-Sequencing; P, pathogenic; LP, likely pathogenic; PP, possibly pathogenic; LB, likely benign; VUS, variant of uncertain significance.