Supplementary Material

Table S1. Complete mutations set found in subject A: 4 premolar teeth analyzed at different PMI/ADDs, with mutations found at specific PMIs or PMI/ADD ranges. Case 7—LRFP at PMI 16; case 3: ULFP at PMI 23; case 9: URFP at PMI 28; case 4: LLFP at PMI 30. Coloured boxes represent the occurrence of mutations; clear boxes represent the absence of mutations.

PMI (Days)		16	23	28	30
ADD (°C)		369.2	551.2	678.3	581.5
GENES	MUTATIONS				
ABL1	c.*1363G>A	■	■		
AKT3	c.*3909T>C	■	■		
ALK	c.4338C>T	■	■	■	
ANKRD26	c.-140C>G	■	■		
	c.212-1110A>G				■
APC	c.1162G>A				■
	c.1749G>A				■
	c.1840G>T				■
	c.2176T>C				■
	c.407C>T				■
	c.5034G>A	■	■	■	
	c.5268T>G	■	■	■	
	c.5465T>A	■	■	■	
	c.5880G>A	■	■	■	
ATR	c.7274G>A	■	■		
	c.1953G>A				■
	c.2211C>T				■
	c.2550A>C				■
AXIN1	c.1284G>A	■	■		
	c.1827T>C	■	■		
	c.1549G>A	■	■		
	c.4563A>G				■
	c.6668C>T				■
	c.2742A>G				■
AXIN2	c.331=				■
	c.402T>C				■
BAP1	c.501G>A	■			
BLM	c.3102G>A	■			
	c.3531C>A	■			
	c.3945C>T	■			
BRAF	c.*1363G>A				■
	c.*1483A>G				■
	c.*813T>C				■
	c.*922G>C				■
	c.3324A>G				■
	c.5094C>T				■
	c.6555C>T				■
	c.75+60C>T				■
BRCA1	c.3113A>G	■	■	■	
	c.3119G>A	■	■	■	

	c.3548A>G	■	■	■	
	c.4308T>C	■	■	■	
	c.4837A>G	■	■	■	
	c.5075-237C>A	■	■	■	
	c.18C>T				■
	c.2783-181G>A				■
	c.2989A>G				■
	c.3183T>A				■
	c.320-2491 A>T				■
	c.320-4481 A>G				■
	c.3333C>T				■
CD276	c.540+7405G>A				■
	c.58+1134C>T				■
CHD2	c.1389A>G				■
	c.1638_1650delinsTGGGCAGGATGCA				■
	c.1782A>G				■
	c.783C>T				■
	c.2049A>G	■	■	■	
	c.2718A>G	■	■	■	
	c.3564C>T	■	■		
	c.5416A>C	■	■		
CIC	c.3052G>A			■	
	c.6018T>C			■	
	c.7260C>T			■	
CRLF2	c.33C>G			■	
E2F3	c.1000-110G>A	■	■	■	
	c.1136-736A>C	■	■	■	
	c.2169+1275A>G				■
	c.2169+1465T>C				■
	c.2169+54A>G				■
	c.2169+934G>T				■
	c.330A>T				■
	c.5061+1034A>G				■
	c.5062-523T>C				■
EGFR	c.1839C>T c.1880+55C>T	■	■	■	
	c.1881-1267C>A	■	■	■	
	c.1881-1585A>G	■	■	■	
	c.1881-2094A>G	■	■	■	
	c.1881-404T>G	■	■	■	
	c.1881-721G>A	■	■	■	
	c.1887T>A	■	■	■	
	c.2283+125T>C	■	■	■	
	c.2283+1296C>T	■	■	■	
	c.2283+1901G>A	■	■	■	
	c.2283+2225C>T	■	■	■	
	c.2283+269T>C	■	■	■	
	c.2283+2994A>G	■	■	■	
	c.274T>C				■
	c.2868T>C				■
	c.2983C>T				■
	c.3014G>A				■

	c.3127T>C				
	c.489C>T				
	c.563G>A				
	c.622-248G>A				
	c.686T>C				
	c.738C>T				
ESR1	c.1096+21499_1096+21500				
	c.1236-18935G>A				
	c.236-12072G>A				
	c.236-12121T>C				
	c.236-12350A>G				
	c.236-5004G>A				
	c.236-6047A>T				
	c.236-9376C>G				
	c.236-9652G>T				
ETV1	c.182-3581A>G				
	c.182-3990C>T				
	c.182-4016G>C				
	c.182-4229 182-4228delinsGC				
	c.235+113A>G				
	c.235+11542C>T				
FLI1	c.203G>T				
GRM3	c.879C>T				
H3F3C	c.*2T>G				
KRAS	c.*512T>C				
	c.-12+2376_-12+2391dup				
	c.2049A>G				
	c.2225G>C				
	c.2547=				
	c.2629A>T				
	c.2718A>G				
	c.387G>A				
	c.3906T>C				
	c.451-5617G>A				
	c.451-7404A>C				
MAP3K1	c.-6-2208A>C				
	c.-6-7161G>A				
	c.951G>T				
MSH6	c.1189+2922T>C				
	c.1189+699C>T				
	c.1190-1609C>T				
	c.186C>A				
	c.276A>G				
	c.540T>C				
	c.956C>T				
PAX3	c.1173+3075T>G				
	c.1173+4667C>T				
	c.1173+5515C>T				
	c.1173+8919A>C				
	c.1174-10G>C				
	c.2412A>G				

	c.67-11872T>C				
	c.804T>C				
	c.-8-11265C>T				
	c.-8-12925A>G				
	c.-8-16713T>C				
	c.-8-18084G>T				
	c.-8-18602A>G				
	c.-8-18729C>T				
	c.-8-23811A>G				
	c.-8-24615G>A				
	c.-8-24969C>T				
	c.-8-25230del				
	c.-8-9088G>A				
PDGFRA	c.1701 A>G				
	c.1787-269G>A				
	c.3222T>C				
PTEN	c.80-3023C>T				
RET	c.2136+182G>A				
	c.2136+271T>C				
	c.2136+374C>T				
	c.2137-167T>C				
	c.2137-324A>G				
	c.2284+430C>T				
	c.2284+47C>T				
	c.450+4044C>T				
	c.463+1398C>G				
	c.463+2405G>T				
	c.463+3246A>G				
	c.463+4241C>T				
	c.463+49G>A				
	c.463+5025G>A				
	c.463+5273				
	463+5277delinsAG				
	c.463+5558G>C				
	c.463+6186T>C				
	c.463+6306A>G				
	c.463+6694A>G				
	c.463+6797G>A				
	c.463+7077G>A				
	c.463+7117_463+7131delinsATTATTTGGTTGTTTC				
	c.463+848G>C				
ROS1	c.5231-1578A>G				
	c.5231-191C>T				
	c.5231-2516A>G				
	c.5231-2735T>C				
	c.5231-3291C>T				
	c.5231-3311T>C				
	c.5231-415C>T				
	c.5231-735T>C				
	c.5348+1319G>A				
	c.5348+361T>A				

	c.5624-1461G>T				
	c.5624-876A>G				
	c.5759+351 del				
	c.5759+468A>C				
	c.5759+603A>C				
	c.5760-137G>A				
	c.5760-281C>T				
	c.5760-53G>T				
	c.5922+434G>C				
TP53	c.-28-1184T>C				
	c.-28-3073G>C				
	c.-28-3143C>T				
	c.-29+2135T>C				
	c.-29+2225T>A				
ZFHX3	c.4446A>T				
	c.8823A>G				

Table S2. Complete mutations set found in subject B, two premolar teeth analyzed at different PMI/ADDs, with mutations found at specific PMI/ADDs. Case 10: LRSP at PMI 17; case 2: URSP at PMI 30. Coloured boxes represent the occurrence of mutations; clear boxes represent the absence of mutations.

PMI (Days)		**17**	**30**
ADD (°C)		**440.9**	**738.1**
GENES	**MUTATIONS**		
ABRAXAS1	c.1117G>A		
ADGRA2	c.3660C>T		
AKT2	c.-84-5059-84-5052		
AKT3	c.*3694G>A		
	c.*3909T>C		
	c.*3731C>T		
ALK	c.1500A>G		
	c.3067+365C>T		
	c.3068-329G>A		
	c.3068-415G>C		
	c.3359+24G>C		
	c.3375C>A		
	c.4472A>G		
	c.3068-574C>A		
	c.4338C>T		
AMER1	c.135C>T		
ATR	c.7274G>A		
APC	c.7504G>A		
AR	c.1616+10462G>A		
AURKB	c.893T>C		
AXIN1	c.1045C>T		
	c.1284G>A		
	c.1549G>A		
	c.1827T>C		

BARD1	c.70C>T		
BCL10	c.13G>T		
BCL2L11	c.394+3056G>C		
	c.394+3849C>T		
BCL2L2	c.128A>G		
BCL6	c.492G>T		
BCR	c.2387A>G		
	c.2708-193G>A		
	c.2782+182		
BLM	c.1046G>A		
BMPR1A	c.1140C>T		
	c.1140+2755_1140+2776		
	c.1140+2850G>A		
	c.1140+757A>G		
BRAF	c.1140+2430C>T		
	c.1140+2755_1140+2776		
	c.1140+2850G>A		
	c.1140+757A>G		
BRCA1	c.-19-216A>G		
	c.2311T>C		
	c.2612C>T		
	c.3119G>A		
	c.3548A>G		
	c.4308T>C		
	c.4837A>G		
	c.5075-237C>A		
	c.134+1967T>C		
	c.134+2983_134+3004delinsAAACCCCTACTGATGAA		
	c.-19-115T>C		
	c.3113A>G		
	c.399T>C		
CCND1	c.723+571		
	c.723G>A		
CCND2	c.493C>T		
CCNE1	c.1215C>T		
	c.399T>C		
DOT1L	c.4156G>A		
EGFR	c.2284-1652C>T		
	c.2284-199T>C		
	c.2284-2766G>A		
	c.2284-498G>A		
	c.2284-60T>C		
	c.2284-755A>G		
	c.89-25201A>G		
	c.1881-781C>T		
	c.747+548C>T		
	c.748-235C>T		
	c.1881-721G>A		
EML4	c.*1941A>G		
ETV1	c.181+1867T>A		
	c.181+1883G>A		

	c.181+536G>A		
	c.181+623C>T		
	c.181+735G>T		
	c.181+789T>C		
	c.181+852A>C		
	c.181+894A>G		
	c.181+946T>C		
ETV6	c.463+7490C>A		
	c.463+7929G>A		
	c.463+848G>C		
	c.464-6175G>T		
	c.464-6269C>T		
FAT1	c.8523C>T		
FLI1	c.203G>T		
	c.942C>G		
HNF1A	c.1375C>T		
	c.1460G>A		
KAT6A	c.401T>C		
	c.4455C>T		
KDM5A	c.2594T>C		
	c.4149C>T		
ROS1	c.5624-1340T>C		
RPS6KB2	c.1259C>T		
	c.807C>T		
RPTOR	c.1269C>T		
TNFRSF14	c.50A>G		
TP53	c.1100+154C>G		
ZFHX3	c.1212C>T		
	c.1282A>C		
	c.1602C>T		

Table S3. Mutations found in teeth extracted from different subjects and analyzed at same PMI/ADDs. Column 2 reports the results obtained from a sample analyzed at PMI 8 in the 2022 pilot study and compared with the results obtained from sample 8 (Column 1) from this study. Columns 3 to 11 compare the samples analyzed in this study. Coloured boxes represent the occurrence of mutations; clear boxes represent the absence of mutations.

PMI (Days)		8	8	16	16	17	23	28	30	30	35	35
ADD (°C)		157,4	183,1	369,2	388,2	440,9	551,2	678,3	581,5	738,1	753,8	753,8
GENES	MUTATIONS											
ABRAXAS1	c.1117G>A											
AKT3	c.*3909T>C											
ALK	c.3067+365C>T											
	c.3068-415G C											
	c.3068-574C>A											
	c.3359+24G>C											
	c.3375C>A											
	c.4338C>T											
	c.4472A>G											
AMER1	c.135C>T											
ANKRD26	c.4204C>T											
ATR	c.7274G>A											
AXIN1	c.1284G>A											
	c.1549G>A											
	c.1827T>C											
BAP1	c.501G>A											
BCL2L11	c.394+3056G>C											
	c.394+3849C>T											

BCL2L2	c.128A>G									■	■	■
BCL6	c.492G>T									■	■	■
BLM	c.1046G>A									■	■	■
	c.3102G>A	■	■	■	■							
	c.3531C>A	■	■	■	■							
	c.3945C T	■	■	■	■							
BMPR1A	c.1140C>T									■	■	■
BRAF	c.1140+757A>G									■	■	■
	c.1141-1305T>C									■	■	■
BRCA1	c.134+1967T>C	■	■	■	■	■	■	■	■			
	c.134+2983_134+3004delinsAAACCC CTACTGATGAA	■	■	■	■	■	■	■	■			
	c.-19-115T>C	■	■	■	■	■	■	■	■			
	c.-19-216A>G	■	■	■	■	■	■	■	■			
	c.3113A>G			■	■	■	■	■				
	c.3119G>A			■	■	■	■	■				
	c.3548A>G	■	■	■	■	■	■	■				
	c.4308T>C	■	■	■	■	■	■	■				
	c.4837A>G	■	■	■	■	■	■	■				
	c.5075-237C>A	■	■	■	■	■	■	■				
CCND1	c.723+571			■	■	■	■	■	■	■	■	■
	c.723G>A			■	■	■	■	■	■	■	■	■
EGFR	c.1881-721G>A			■	■	■	■	■				
	c.1881-781C>T									■	■	■
	c.747+548C>T									■	■	■
	c.748-235C>T									■	■	■
	c.89-25201A>G									■	■	■
EML4	c.*1941A>G									■	■	■
ERBB2	c.2086-29G>A	■	■									
	c.2273delA	■	■									
FAT1	c.8523C>T									■	■	■
FGFR3	c.2393delC	■	■									
	c.840C>T	■	■									
	c.843A>C	■	■									
FLI1	c.203G>T					■	■	■				
	c.942C>G					■	■	■				
HNF1A	c.1375C>T									■	■	■
	c.1460G>A									■	■	■
KAT6A	c.401T>C									■	■	■
	c.4455C>T									■	■	■
KDM5A	c.2594T>C									■	■	■
	c.4149C>T									■	■	■
PDGFRA	c.2003-11delT	■	■									
PTEN	c.802-18delC	■	■									
	c.802-19dupT	■	■									
	c.802-23C>T	■	■									
	c.802-29C>T	■	■									
	c.80-3023C>T			■	■	■	■	■				
ROS1	c.5624-1340T>C			■	■	■	■	■				
TNFRSF14	c.50A>G	■	■	■	■	■	■	■	■			