IML Dataset-I Dictionary

Variable	Meaning	Variable type	unit (if applicable)	Possible data element (examples)
Melanoma_ID	Case identifier (melanoma patient)	numeric		1
NL_or_Tm	Distinguishes Tm (melanoma tumor) and non-tumor tissue (NL)	text		Tm
Specimen_type	Tm (melanoma tumor) and non-tumor tissue: bening nevus, unafected skin (skin), blood, buffy coat (buffy), benign lymphnode (LN), or saliva	text		skin, buffy, LN
Specimen_format	How tissue was provided: sections, curls, saliva collection kit, tube	text		sections
FFPE_thickness_H&Es	Thickness of tissue stained with hematoxylin-eosine. (.) not applicable; unk, if information not provided by the contributing Center.	numeric (unless unk or .)	microns or µm	4
Purity_tumor_cells_iPath	Percent of tumor cells within targeted tumor area assessed during iPath/ initial pathology review (diagnostic confirmation and usefulness of tissue for downstream testing). Not applicable for non-tumor tissue ('.').	numeric	%	80, 90
pigmentation_macro	Assessment of brownish pigment (melanin) observed with the naked eye. When visible on the tissue or pellet, might include a comment on color and/or intensity. Blank when no pigmentation noticed. Not applicable ('.')	text		yes; yes_slight
Ave_Target_Tissue_Lenght_for_scraping	Length of tissue suitable for NA extractions, as marked on the H&E slide upon initial pathology review and diagnostic confirmation of melanoma (iPath). Informed as an average to account for shape and potential variation between first and last H&E. (.) not applicable	numeric	milimeters or mm	10, 4.5, 30.5
Ave_target_tissue_width_for_scraping	Width of tissue suitable for NA extractions, as marked on the H&E upon iPath. Informed as an average to account for shape and potential variation between first and last H&E. (.) not applicable	numeric	milimeters or mm	7, 1.5, 4.8
FFPE_thickness_for_NA	Thickness of tissue sectioned and placed on glass slides, for the extraction of nucleic acids. (.) not applicable; unk, not available/unknown (not provided by study center)	numeric	microns or µm	10
Nr_sections_for_NA	Number of tissue sections placed on glass slides for scraping and extraction of nucleic acids. Not applicable ('.').	numeric		9
Total_derived_target_area_per_case	Estimated total area of tissue suitable for NA extractions, obtained by multiplying ave length, ave width, and number of available sections for NA extractions. (.) not applicable; unk, not available/unknown (not provided by study center)	numeric	mm2	131, 2230, 145
Curls_nr_sections	If curls provided, indicates the number of sections procurred for nucleic acid extraction, per tube and case. Not applicable if not curls ('.'); not available ('unk')	numeric (unless unk or .)		4, ., unk
Curls_thickness	Thickness of tissue provided as curls. Not applicable if not curls ('.'); not available ('unk')	numeric (unless unk or .)	microns or µm	10
Elution	Distinguishes first or main (1), second (2), and unique (.) elutions from columns during RNA/DNA co-extractions	numeric		1,2, .
Tube_ID	Tube identifier for when tissues where split for extraction in multiple tubes/columns. Non-tumor tissue distinguished from tumor with suffix-NL	alphanumeric		1-1, 1-2; or 9-NL-1, 9-NL-2, etc
Tumor_RNA_cc	Concentration of RNA obtained from tumor tissue when using a Nanodrop (total RNA)	numeric	nanograms per microliter or ng/µL	35, 744.9
RNA_260_280_ratio	Ratio of absorbance measured at 260 and 280 nm	numeric		1.9
RNA_260_230_ratio	Ratio of absorbance measured at 260 and 230 nm	numeric		1.8
RNA_Total_per_tube_ng	Total amount of RNA, obtained in a single extraction tube, as measured with the Nanodrop and multiplied by the elution volume	numeric	ng	3927
RNA_Total_per_Case	Total amount of RNA as measured with the Nanodrop, per case (sum of RNA obtained from all tubes and elutions)	numeric	ng	4557.2

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Tumor_RNA_Tapestation_cc_ng_micro	Concentration of RNA obtained from tumor tissue when using TapeStation. (.), not applicable; n/a, not available.	numeric	nanograms per microliter or ng/µL	39.5
RNA_RIN	RNA integrity number, measure of RNA robustness upon separation in an electrophoretic field (min 1, max 10). (.), not applicable; n/a, not available; <LLOD, below the level of detection.	numeric	1, 3.6, <LLOD (if undetectable)	2.2
DV200	Proportion of RNA with strands or fragments longer than 200nt. (.) if not applicable.	numeric	%	58.78
RNA_Tapestation_per_tube	Amount of total RNA obtained in a single extraction tube, as measured by the Tapestation and multiplied by the elution volume. (.), not applicable	numeric	ng	829.5
RNAabove200nt_per_tube	Amount of RNA above 200nt (=total RNA * DV200/100), obtained from all tubes and elutions, per tube. (.), not applicable.	numeric	ng	1316.7
DNA_Nanodrop_cc	Concentration of DNA obtained from tumor tissue when using a Nanodrop. Refers to concentration of all DNA (single and double stranded); (.) when not applicable	numeric	nanograms per microliter or ng/µL	36.32
DNA_260_280_ratio	Ratio of absorbance measured at 260 and 280 nm; (.) when not applicable	numeric		1.64
DNA_260_230_ratio	Ratio of absorbance measured at 260 and 230 nm; (.) when not applicable	numeric		0.77
totDNA_per_tube	Amound of total DNA obtained (single and double stranded, or ss + dsDNA) per extraction tube; (.) when not applicable	numeric	ng	2251.8
totDNA_per_case	Amound of total DNA obtained (single and double stranded, or ss + dsDNA) per case, includes all extraction tubes for the same tissue and case; (.) when not applicable	numeric	ng	40802.2
dsDNA_cc	Measure of concentration of double stranded DNA (dsDNA) obtained with the Qubit broad range kit, and Qubit instrument; (.) when not applicable	numeric	nanograms per microliter or ng/µL	14.5
dsDNA_per_elution	Amount of dsDNA obtained in a single elution (elution volume multiplied by cc of dsDNA); (.) when not applicable	numeric	ng	899
dsDNA_per_sample	Amount of dsDNA obtained across all elutions for the same tissue and extraction tube; (.) when not applicable	numeric	ng	899
Percent_dsDNA_per tube	Proportion of dsDNA relative to totDNA [dsDNA x 100/(ss+dsDNA)]	numeric	%	39.9
Ave_percent_dsDNA_per_case	Average of %dsDNA obtained across all extraction tubes -from the same tissue/case (when tissue is large enough to be split); (n/a or [.]) not applicable if already provided on another row for the same case.	numeric	ng	28.5, 31.9
dsDNA_per_case	Amount of dsDNA obtained across all extraction tubes and elutions for the same case; (.) when not applicable. Note that total per case is provided in some, not all rows of tube IDs for the same case.	numeric	ng	380, 2827.2
QC_PCR_bands	Number of bands obtained when checking amplifiability (as DNA integrity and impurities measure or presence of inhibitors). Range: 0 to 4 bands, 100 to 400bp each. Smearing denoted as text or after the comma, with values proportional to intensity observed that is relative to the band). Smearing can be observed when DNA is overloaded in the PCR reaction; (.) not applicable if reported on another row for the same specimen, or if not assessible due to limited amount of material/ aved for testing.	alphanumeric		4, 2.5, 0 (smear bulk ~ 1kb)
Time_elapsed	Time in days that transcurred between melanoma block sectioning/cutting at the centers, and extraction of nucleic acid(s); (.) not available	numeric	days	150