InterMEL dataset II dictionary_12/09/2022

Variable	Meaning	Variable type	unit (n/a if not applicable)	Possible data element (examples)
Melanoma_ID	Case identifier (melanoma patient)			1 through 685
Specimen_type	Distinguishes Tm (melanoma tumor) from non-tumor tissue	text	n/a	Tm
Tube_ID	Tube identifier for when tissues where split for extraction in multiple tubes/columns. R suffix added for repeat specimen (new tissue)	alphanumeric	n/a	for tumors: 1-1, 1-2; or 85-R
RNA_Elution	Distinguishes first or main (1), second (2) elutions of RNA form the same column (into a different tube), or not applicable (.)	numeric	n/a	1,2, .
Tumor_RNA_cc	Concentration of RNA obtained from tumor tissue when using a Nanodrop (total RNA), , or not applicable (.)	numeric	nanograms per microliter or ng/µL	35, 744.9
RNA_260_280_ratio	Ratio of absorbance measured at 260 and 280 nm, , or not applicable (.)	numeric	n/a	1.9
RNA_260_230_ratio	Ratio of absorbance measured at 260 and 230 nm, or not applicable (.)	numeric	n/a	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, , or not applicable (.)	numeric	ng	3927
RNA_Total_per_Case	Total amount of RNA, obtained from all tubes for the same case, or , or not applicable (.). Note that total amount of RNA is not repeated for all rows linked to the same case	numeric	ng	4557.2
Tumor_RNA_Tapestation_cc	Concentration of RNA obtained from tumor tissue when using TapeStation, or not applicable (.)	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). <LLOD and n/a when data not reported by the instrument. (.) when not applicable (other tube measured)	numeric	1, 3.6, <LLOD (if undetectable)	2.2
DV200	Proportion of RNA with strands or fragments longer than 200nt; (.) when not applicable	numeric	%	58.78
RNA_Tapestation_per_tube	Amount of RNA obtained in a single extraction tube, as measured by the Tapestation and multiplied by the elution volume; (.) when not applicable	numeric	ng	829.5
RNA_above200nt_per_case	Amount of RNA obtained per case, with fragments/strands above 200nt; (.) when not applicable	numeric	ng	1316.7
RNA_2nd_elution	Amount of RNA obtained in a second elution from the extraction column, as measured by the Nanodrop multiplied by elution volume. (.) when not applicable	numeric	ng	972
DNA_Elution	Distinguishes first or main (1) and second (2) elutions made in separate tubes, from unique (.) elutions of nucleic acids, or when both 1st and 2nd elutions were combined into a single tube (1_2 combo)	numeric	n/a	1,2, ., 1_2 combo
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	n/a	1.64
DNA_260_230_ratio	Ratio of absorbance measured at 260 and 230 nm; (.) when not applicable	numeric	n/a	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	Proportion of dsDNA relative to totDNA [dsDNA x 100/(ss+dsDNA)]; (.) when not applicable	numeric	%	39.9
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	380.30
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	%	33.1
pigmentation_macro	Melanin pigment present / observed macroscopically on tissue and/or pellet of tissue, 'yes' if present/observed, with notes if slight or heavily pigmented; (.) not observed	text	n/a	yes

InterMEL dataset II dictionary_10/11/2022

Variable	Meaning	Variable type	unit (n/a if not applicable)	Possible data element (examples)
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	n/a	4, 2.5, 0 (smear bulk ~ 1kb); [.]
tumor_cells_pc	Tumor cells within targeted tumor area recorded as fraction assessed during initial pathology review; (.) not applicable and/or already provided for case	numeric	%	90, 80
age_of_block	Time in years that transcurred between initial diagnosis/biopsy and extraction of nucleic acids (rounded to the next number for fractions greater or equal to 0.5)	numeric	n/a	12
max_breslow	Tumor thickness based on initial assessment at diagnosis and pathology review (if differs between assessments, thickest measure used); if not assessed/ not available, 999	numeric	mm	3.91
max_ulceration	Defines presence of ulceration as absent (1), present (2), indeterminate (3), or unknown/missing (99)	numeric	n/a	2
tils	Tumor infiltrating lymphocytes absent (3), brisk (1), or non-brisk (2), 99 if not available/possible from the pathology assessment; (.) if not applicable	numeric	n/a	1, 3
mitoses	Absent (0), present (1), cannot assess (.)	numeric	n/a	0, 1
stage_ajcc8	Pathological staging at time of diagnosis based on AJCC ver8: 1, II ; 2, IIA ; 3, IIB ; 4, IIC ; 5, III ; 6, IIIA ; 7, IIIB ; 8, IIIC ; 9, IIID; (.) not available	numeric	n/a	3
age_at_dx	Age at melanoma diagnosis	numeric	n/a	55
Sex	Sex, reported and confirmed genetically on non-tumor specimens unless gDNA not available/not assessable, where 1=male and 2=female	numeric	n/a	1 or 2
RNAmiRNA_testingQC	flagged RNA samples, deemed suboptimal upon miRNA screening/testing at NYU. Blank if tested/ not flagged. NA if not tested.	text	content flag, [.], not_flagged	NA
DNAmethylation_testingQC	flagged DNA samples, deemed suboptimal upon methylation testing at UNC. If not applicable or data not available, [.]	text	failed BMIQ, failed QC, not_flagged, [.]	NA
IGO_DNA_cc	Concentration of DNA determined by IGO (Core) before screening mutations with the MSK-IMPACT assay	numeric	ng/µL	3.9
IGO_tot_DNA	Amount of DNA provided for mutation screening as determined by IGO (Core) before library preparation (IGO DNA cc multiplied by estimated volume)	numeric	ng	159.6
IGO_DNAQC_Recommendation	Recommendation to halt if DNA specimen 'failed' (due to low quantity), 'try' (if suboptimal quantity) or proceed to library synthesis if specimen 'passed' DNA QC, in preparation of MSK-IMPACT assay; (.) if not applicable to this row	text	n/a	Try Library Prep
IGO_LibQC_cc	Concentration of library determined by IGO (Core) before screening mutations with the MSK-IMPACT assay; (.) not applicable to row	numeric	ng/µL	3.18, 4.63
IGO_LibQC_total	Amount of library obtained as determined by IGO (Core) before screening mutations with the MSK-IMPACT assay, derived from LibQC (multiplied by volume); (.) not applicable to row	numeric	ng	218, 287.06
IGO_libQC_Recommendation	Recommendation to halt testing if 'failed' due low quantity, 'try' due to suboptimal quality, or proceed if specimen 'passed' library QC in preparatioon of mutation screening with the MSK-IMPACT assay; NA if not available yet; (.) if not applicable to this row	text	n/a	Try
Sample_coverage	Average number or times a target or known base is 'read or covered';determines degree of confidence at particular base positions; NA if not available yet; (.) if not applicable to this row	numeric	x	314, 728