

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADBX	PARAMCD	CO	Carbon Monoxide (ppm)	<UK>	<UK>		SDTM	PARAMN=1. If AVAL le 10 then AVALCAT1=<=10', else if AVAL gt 10 then AVALCAT1=>10'
ADBX	PARAMCD	CARBHXGB	Carboxyhemoglobin (%)	<UK>	<UK>		SDTM	PARAMN=2. If AVAL le 2 then AVALCAT1=<=2', else if AVAL gt 2 then AVALCAT1=>2'
ADBX	PARAMCD	COTININE	Cotinine (ng/mL)	<UK>	<UK>		SDTM	PARAMN=3
ADBX	PARAMCD	TRANS3H	Trans-3hydroxycotinine (ng/mL)	<UK>	<UK>		SDTM	PARAMN=4
ADBX	PARAMCD	CYP2A6	CYP2A6 Activity (%)	<UK>	<UK>		Derived	PARAMN=5. AVAL is set equal to (AVAL where PARAMCD = "HCOT")/(AVAL where PARAMCD="COT"). AVALC is set equal to AVAL rounded to 2dp. AVALU set equal to "%".
ADBX	PARAMCD	COT	Cotinine (nmol/L)	<UK>	<UK>		Derived	PARAMN=6. AVAL is set equal to (AVAL where PARAMCD = "COTININE" * 5.675). AVALC is set equal to AVAL. AVALU set equal to "nmol/L".
ADBX	PARAMCD	HCOT	Trans-3hydroxycotinine (nmol/L)	<UK>	<UK>		Derived	PARAMN=7. AVAL is set equal to (AVAL where PARAMCD = "TRANS3H" * 5.202). AVALC is set equal to AVAL. AVALU set equal to "nmol/L".
ADBX	PARAMCD	VOLUME	Volume (mL)	<UK>	<UK>		SDTM	PARAMN=8
ADBX	PARAMCD	U1NA	1-aminonaphthalene (pg/mL)	<UK>	<UK>		SDTM	PARAMN=9
ADBX	PARAMCD	U1NACRE	1-aminonaphthalene (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=10. 1-NA adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="U1NA")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	U1NA24U	1-aminonaphthalene (ng)	<UK>	<UK>		Derived	PARAMN=11. 1-NA quantity excreted over 24 hours. AVAL is set equal to ((AVAL where PARAMCD="U1NA") * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set to AVAL. AVALU set to "ng".
ADBX	PARAMCD	U1OHP	Total 1-hydroxypyrene (pg/mL)	<UK>	<UK>		SDTM	PARAMN=12
ADBX	PARAMCD	U1OHPCRE	Total 1-hydroxypyrene (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=13. 1-OHP adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="U1OHP")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	U1OHP24U	Total 1-hydroxypyrene (ng)	<UK>	<UK>		Derived	PARAMN=14. 1-OHP quantity excreted over 24 hours. AVAL is set equal to ((AVAL where PARAMCD="U1OHP") * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set to AVAL. AVALU set to "ng".
ADBX	PARAMCD	U2NA	2-aminonaphthalene (pg/mL)	<UK>	<UK>		SDTM	PARAMN=15
ADBX	PARAMCD	U2NACRE	2-aminonaphthalene (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=16. 2-NA adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="U2NA")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	U2NA24U	2-aminonaphthalene (ng)	<UK>	<UK>		Derived	PARAMN=17. 2-NA quantity excreted over 24 hours. AVAL is set equal to ((AVAL where PARAMCD="U2NA") * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set to AVAL. AVALU set to "ng".
ADBX	PARAMCD	U3HPMA	3-hydroxypropylmercapturic Acid (ng/mL)	<UK>	<UK>		SDTM	PARAMN=18
ADBX	PARAMCD	U3HPMCRE	3-hydroxypropylmercapturic Acid (ng/mg creat)	<UK>	<UK>		Derived	PARAMN=19. 3-HPMA adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="U3HPMA")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "ng/mg creat".
ADBX	PARAMCD	U3HPM24U	3-hydroxypropylmercapturic Acid (µg)	<UK>	<UK>		Derived	PARAMN=20. 3-HPMA quantity excreted over 24 hours. AVAL is set equal to ((AVAL where PARAMCD="U3HPMA") * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set to AVAL. AVALU set to "µg".
ADBX	PARAMCD	U4ABP	4-Aminobiphenyl (pg/mL)	<UK>	<UK>		SDTM	PARAMN=21
ADBX	PARAMCD	U4ABPCRE	4-Aminobiphenyl (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=22. 4-ABP adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="U4ABP")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	U4ABP24U	4-Aminobiphenyl (ng)	<UK>	<UK>		Derived	PARAMN=23. 4-ABP quantity excreted over 24 hours. AVAL is set equal to ((AVAL where PARAMCD="U4ABP") * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set to AVAL. AVALU set to "ng".
ADBX	PARAMCD	UCEMA	2-cyanoethylmercapturic Acid (ng/mL)	<UK>	<UK>		SDTM	PARAMN=24
ADBX	PARAMCD	UCEMACRE	2-cyanoethylmercapturic Acid (ng/mg creat)	<UK>	<UK>		Derived	PARAMN=25. CEMA adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UCEMA")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "ng/mg creat".
ADBX	PARAMCD	UCEMA24U	2-cyanoethylmercapturic Acid (µg)	<UK>	<UK>		Derived	PARAMN=26. CEMA quantity excreted over 24 hours. AVAL is set equal to ((AVAL where PARAMCD="UCEMA") * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set to AVAL. AVALU set to "µg".
ADBX	PARAMCD	UCOTG	Cotinine-Glucuronide (ng/mL)	<UK>	<UK>		SDTM	PARAMN=27
ADBX	PARAMCD	UCOTGC	Cotinine-Glucuronide (umol/L)	<UK>	<UK>		Derived	PARAMN=28. AVAL is set equal to ((AVAL where PARAMCD = "UCOTG") * 2.838) / 1000. AVALC is set to AVAL. AVALU set to "umol/L".

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ADBX	PARAMCD	CREAT	Creatinine (mg/dL)	<UK>	<UK>		SDTM	PARAMN=29
ADBX	PARAMCD	UFCOT	Free Cotinine (ng/mL)	<UK>	<UK>		SDTM	PARAMN=30
ADBX	PARAMCD	UFCOTC	Free Cotinine (umol/L)	<UK>	<UK>		Derived	PARAMN=31. AVAL is set equal to ((AVAL where PARAMCD = "UFCOT") * 5.675) / 1000. AVALC is set to AVAL. AVALU set to "umol/L".
ADBX	PARAMCD	UFNIC	Free Nicotine (ng/mL)	<UK>	<UK>		SDTM	PARAMN=32
ADBX	PARAMCD	UFNICC	Free Nicotine (umol/L)	<UK>	<UK>		Derived	PARAMN=33. AVAL is set equal to ((AVAL where PARAMCD = "UFNIC") * 6.164) / 1000. AVALC is set to AVAL. AVALU set to "umol/L".
ADBX	PARAMCD	UFTRANSC	Free Trans-3'-Hydroxycotinine (umol/L)	<UK>	<UK>		Derived	PARAMN=34. AVAL is set equal to ((AVAL where PARAMCD = "UFTRANSH") * 5.202) / 1000. AVALC is set to AVAL. AVALU set to "umol/L".
ADBX	PARAMCD	UFTRANSH	Free Trans-3'-Hydroxycotinine (ng/mL)	<UK>	<UK>		SDTM	PARAMN=35
ADBX	PARAMCD	UOHEMA	2-hydroxyethyl Mercapturic Acid (ng/mL)	<UK>	<UK>		SDTM	PARAMN=36. Original HEMA value from SDTM.
ADBX	PARAMCD	UDHEMA	2-hydroxyethyl Mercapturic Acid (Derived) (pg/mL)	<UK>	<UK>		SDTM	PARAMN=37. Derived HEMA. AVAL is set equal to (AVAL where PARAMCD="UOHEMA")*1000. AVALC=STRIP(PUT(AVAL,BEST.)). AVALU is set equal to "pg/mL".
ADBX	PARAMCD	UHEMACRE	2-hydroxyethyl Mercapturic Acid (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=38. Derived HEMA corrected for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UDHEMA") / (AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	UHEMA24U	2-hydroxyethyl Mercapturic Acid (ng)	<UK>	<UK>		Derived	PARAMN=39. Derived HEMA corrected for urine. AVAL is set equal to ((AVAL where PARAMCD="UDHEMA") * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set to AVAL. AVALU set to "ng"
ADBX	PARAMCD	UHMPMA	Hydroxy-1-methylpropylmercapturic Acid (ng/mL)	<UK>	<UK>		SDTM	PARAMN=40
ADBX	PARAMCD	UHMPMCRE	Hydroxy-1-methylpropylmercapturic Acid (ng/mg creat)	<UK>	<UK>		Derived	PARAMN=41. HMPMA corrected for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UHMPMA") / (AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "ng/mg creat".
ADBX	PARAMCD	UHMPM24U	Hydroxy-1-methylpropylmercapturic Acid (µg)	<UK>	<UK>		Derived	PARAMN=42. HMPMA corrected for urine. AVAL is set equal to ((AVAL where PARAMCD="UHMPMA") * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set to AVAL. AVALU set to "µg"
ADBX	PARAMCD	UOMHBMA	Monohydroxybutenyl Mercapturic Acid (ng/mL)	<UK>	<UK>		SDTM	PARAMN=43. Original MHBMA value from SDTM.
ADBX	PARAMCD	UDMHBMA	Monohydroxybutenyl Mercapturic Acid (Derived) (pg/mL)	<UK>	<UK>		SDTM	PARAMN=44. Derived MHBMA. AVAL is set equal to (AVAL where PARAMCD="UOMHBMA")*1000. AVALC=STRIP(PUT(AVAL,BEST.)). AVALU is set equal to "pg/mL".
ADBX	PARAMCD	UMHBMCRE	Monohydroxybutenyl Mercapturic Acid (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=45. MHBMA adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UMHBMA") / (AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	UMHBM24U	Monohydroxybutenyl Mercapturic Acid (ng)	<UK>	<UK>		Derived	PARAMN=46. MHBMA quantity excreted over 24 hours. AVAL is set equal to ((AVAL where PARAMCD="UMHBMA" * (AVAL where PARAMCD="VOLUME")/1000). AVALC is set equal to AVAL. AVALU set equal to "ng".
ADBX	PARAMCD	UNEQCRE	Nicotine Equivalents (mg/g creat)	<UK>	<UK>		Derived	PARAMN=47. NEQ adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="NEQ24U")/((AVAL where PARAMCD="CREAT"))*((AVAL where PARAMCD="VOLUME")/100)))*1000 AVALC is set equal to AVAL. AVALU set equal to "mg/g creat". Please note this uses the UNEQ24U parameter.
ADBX	PARAMCD	UNEQ24U	Nicotine Equivalents (g)	<UK>	<UK>		Derived	PARAMN=48. AVAL is set equal to ((AVAL where PARAMCD = "UFNIC") + (AVAL where PARAMCD = "UNICG") + (AVAL where PARAMCD = "UFCOTC") + (AVAL where PARAMCD = "UCOTGC") + (AVAL where PARAMCD = "UFTRANSC") + (AVAL where PARAMCD = "UTRANSHC") * 162.2 * ((AVAL where PARAMCD = "VOLUME") / 1000))/1000. AVALC is set equal to AVAL.
ADBX	PARAMCD	UNICG	Nicotine-Glucuronide (ng/mL)	<UK>	<UK>		SDTM	PARAMN=49
ADBX	PARAMCD	UNICGC	Nicotine-Glucuronide (umol/L)	<UK>	<UK>		Derived	PARAMN=50. AVAL is set equal to ((AVAL where PARAMCD = "UNICG") * 2.955) / 1000. AVALC is set to AVAL. AVALU set to "umol/L".
ADBX	PARAMCD	UNNAL	NNAL (pg/mL)	<UK>	<UK>		SDTM	PARAMN=51
ADBX	PARAMCD	UNNALCRE	NNAL (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=52. NNAL corrected for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UNNAL") / (AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".

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ADBX	PARAMCD	UNNAL24U	NNAL (ng)	<UK>	<UK>		Derived	PARAMN=53. NNAL corrected for urine. AVAL is set equal to ((AVAL where PARAMCD="UNNAL" * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set equal to AVAL. AVALU set equal to "ng".
ADBX	PARAMCD	UNNN	Total N-nitrosomonocotinine (pg/mL)	<UK>	<UK>		SDTM	PARAMN=54
ADBX	PARAMCD	UNNNCRE	Total N-nitrosomonocotinine (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=55. NNN corrected for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UNNN")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	UNNN24U	Total N-nitrosomonocotinine (ng)	<UK>	<UK>		Derived	PARAMN=56. NNN corrected for urine. AVAL is set equal to ((AVAL where PARAMCD="UNNN" * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set equal to AVAL. AVALU set equal to "ng".
ADBX	PARAMCD	UOTOL	o-toluidine (pg/mL)	<UK>	<UK>		SDTM	PARAMN=57
ADBX	PARAMCD	UOTOLCRE	o-toluidine (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=58. O-TOL corrected for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UOTOL")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	UOTOL24U	o-toluidine (ng)	<UK>	<UK>		Derived	PARAMN=59. O-TOL corrected for urine. AVAL is set equal to ((AVAL where PARAMCD="UOTOL" * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set equal to AVAL. AVALU set equal to "ng".
ADBX	PARAMCD	UOSBMA	S-benzylmercapturic Acid (ng/mL)	<UK>	<UK>		SDTM	PARAMN=60. Original SBMA value in SDTM.
ADBX	PARAMCD	UDSBMA	S-benzylmercapturic Acid (Derived) (pg/mL)	<UK>	<UK>		SDTM	PARAMN=61. Derived SBMA. AVAL is set equal to (AVAL where PARAMCD="UDSBMA")*1000. AVALC=STRIP(PUT(AVAL,BEST.)). AVALU is set equal to "pg/mL".
ADBX	PARAMCD	USBMACRE	S-benzylmercapturic Acid (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=62. S-BMA corrected for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UDSBMA")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	USBMA24U	S-benzylmercapturic Acid (ng)	<UK>	<UK>		Derived	PARAMN=63. S-BMA corrected for urine. AVAL is set equal to ((AVAL where PARAMCD="UDSBMA" * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set equal to AVAL. AVALU set equal to "ng".
ADBX	PARAMCD	UOSPPMA	S-phenylmercapturic Acid (ng/mL)	<UK>	<UK>		SDTM	PARAMN=64. Original value in SDTM.
ADBX	PARAMCD	UDSPMA	S-phenylmercapturic Acid (Derived) (pg/mL)	<UK>	<UK>		SDTM	PARAMN=65. Derived SPMA. AVAL is set equal to (AVAL where PARAMCD="UDSPMA")*1000. AVALC=STRIP(PUT(AVAL,BEST.)). AVALU is set equal to "pg/mL".
ADBX	PARAMCD	USPMACRE	S-phenylmercapturic Acid (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=66. S-PMA corrected for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UDSPMA")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	USPMA24U	S-phenylmercapturic Acid (ng)	<UK>	<UK>		Derived	PARAMN=67. S-PMA corrected for urine. AVAL is set equal to ((AVAL where PARAMCD="UDSPMA" * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set equal to AVAL. AVALU set equal to "ng".
ADBX	PARAMCD	UTRANSHC	Trans-3'-Hydroxycotinineglucuronide (umol/L)	<UK>	<UK>		Derived	PARAMN=68. AVAL is set equal to ((AVAL where PARAMCD = "UTRANSHY") * 2.715) / 1000. AVALC is set to AVAL. AVALU set to "umol/L".
ADBX	PARAMCD	UTRANSHY	Trans-3'-Hydroxycotinineglucuronide (ng/mL)	<UK>	<UK>		SDTM	PARAMN=69
ADBX	PARAMCD	UAMES	Ames Mutagenicity (REV/uL)	<UK>	<UK>		SDTM	PARAMN=70
ADBX	PARAMCD	UAMES24U	Ames Mutagenicity (REV/24h)	<UK>	<UK>		SDTM	PARAMN=71
ADBX	PARAMCD	UPGF2A	Prostaglandin F2 Alpha (pg/mL)	<UK>	<UK>		SDTM	PARAMN=72. PGF adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UPGF2A")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	UPGF2CRE	Prostaglandin F2 Alpha (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=73. PGF adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UPGF2A")/(AVAL where PARAMCD="CREAT"))*100. AVALC is set equal to AVAL. AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	UPGF224U	Prostaglandin F2 Alpha (ng)	<UK>	<UK>		Derived	PARAMN=74. PGF quantity excreted over 24 hours. AVAL is set equal to ((AVAL where PARAMCD="UPGF2A" * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set equal to AVAL. AVALU set equal to "ng".

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ADBX	PARAMCD	UTXB2D11	11-Dehydro-Thromboxane B2 (pg/mL)	<UK>	<UK>		SDTM	PARAMN=75. PGF adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UTXB2D11")/(AVAL where PARAMCD="CREAT"))*100, AVALC is set equal to AVAL, AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	UTXB2CRE	11-Dehydro-Thromboxane B2 (pg/mg creat)	<UK>	<UK>		Derived	PARAMN=76. PGF adjusted for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UTXB2D11")/(AVAL where PARAMCD="CREAT"))*100, AVALC is set equal to AVAL, AVALU set equal to "pg/mg creat".
ADBX	PARAMCD	UTXB224U	11-Dehydro-Thromboxane B2 (ng)	<UK>	<UK>		Derived	PARAMN=77. PARAMN=70. DTX quantity excreted over 24 hours. AVAL is set equal to ((AVAL where PARAMCD="UTXB2D11" * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set equal to AVAL. AVALU set equal to "ng".
ADBX	PARAMCD	CAF	Caffeine (nmol/L)	<UK>	<UK>		Derived	PARAMN=78. AVAL is set equal to (AVAL where PARAMCD = "CAFFEINE" * 5.150). AVALC is set equal to AVAL. AVALU set equal to "nmol/L".
ADBX	PARAMCD	CAFFEINE	Caffeine (ng/mL)	<UK>	<UK>		SDTM	PARAMN=79
ADBX	PARAMCD	CYP1A2	CYP1A2 Activity (%)	<UK>	<UK>		Derived	PARAMN=80. AVAL is set equal to (AVAL where PARAMCD = "PXC")/(AVAL where PARAMCD="CAF"). AVALC is set equal to AVAL. AVALU set equal to "%".
ADBX	PARAMCD	PX	Paraxanthine (ng/mL)	<UK>	<UK>		SDTM	PARAMN=81
ADBX	PARAMCD	PXC	Paraxanthine (nmol/L)	<UK>	<UK>		Derived	PARAMN=82. AVAL is set equal to (AVAL where PARAMCD = "PX" * 5.550). AVALC is set equal to AVAL to 3dp. AVALU set equal to "nmol/L".
ADBX	PARAMCD	ULBALL	All laboratory tests (24H URINE SAMPLE)	<UK>	<UK>		SDTM	PARAMN=94. If LBSCAT="24HR URINE VOLUME" and LBTESTCD="LBALL" then PARAMCD="U"    LBTESTCD. PARAM=LBTEST    ' '    LBSCAT    ' '.
ADBX	PARAMCD	ELBALL1	All laboratory tests (CYTOCHROME 1A2)	<UK>	<UK>		SDTM	PARAMN=95. If LBSCAT="CYTOCHROME 1A2" and LBTESTCD="LBALL" then PARAMCD="E"    LBTESTCD    ' ' 1. PARAM=LBTEST    ' '    LBSCAT    ' '.
ADBX	PARAMCD	ELBALL2	All laboratory tests (CYTOCHROME 2A6)	<UK>	<UK>		SDTM	PARAMN=96. If LBSCAT="CYTOCHROME 2A6" and LBTESTCD="LBALL" then PARAMCD="E"    LBTESTCD    ' ' 2. PARAM=LBTEST    ' '    LBSCAT    ' '.
ADBX	PARAMCD	BELBALL	All laboratory tests (BIOMARKERS OF EXPOSURE)				SDTM	PARAMN=97. If LBSCAT="BIOMARKERS OF EXPOSURE" and LBTESTCD="LBALL" then PARAMCD="BE"    LBTESTCD. PARAM=LBTEST    ' '    LBSCAT    ' '.
ADBX	PARAMCD	BLBALL	All laboratory tests (BIOMARKERS)	<UK>	<UK>		SDTM	PARAMN=98. If LBSCAT="BIOMARKERS" and LBTESTCD="LBALL" then PARAMCD="B"    LBTESTCD. PARAM=LBTEST    ' '    LBSCAT    ' '.
ADBX	PARAMCD	LBALL	All laboratory tests	<UK>	<UK>		SDTM	PARAMN=99. If LBSCAT=" " then PARAMCD=LBTESTCD. PARAM=LBTEST.
ADBX	PARAMCD	UBAP	3-hydroxy(a)benzopyrene (fg/mL)	<UK>	<UK>		SDTM	PARAMN=111. If LBSCAT="BIOMARKERS OF EXPOSURE" and LBTESTCD="BAP" then PARAMCD="UBAP". PARAM=LBTEST    ' '    LBSCAT    ' '.
ADBX	PARAMCD	UBAPCRE	3-hydroxy(a)benzopyrene (fg/mg creat)	<UK>	<UK>		SDTM	PARAMN=112. BaP corrected for creatinine. AVAL is set equal to ((AVAL where PARAMCD="UBAP")/(AVAL where PARAMCD="CREAT"))*100, AVALC is set equal to AVAL, AVALU set equal to "fg/mg creat".
ADBX	PARAMCD	UBAP24U	3-hydroxy(a)benzopyrene (pg)	<UK>	<UK>		SDTM	PARAMN=113. BaP corrected for urine. AVAL is set equal to ((AVAL where PARAMCD="UBAP" * (AVAL where PARAMCD="VOLUME"))/1000. AVALC is set equal to AVAL. AVALU set equal to "pg".
ADDX	PARAMCD	THS2_2	THS 2.2	<UK>	<UK>		Derived	
ADDX	PARAMCD	DTHS2_2	Daily THS 2.2 Administration	<UK>	<UK>		Derived	
ADEG	PARAMCD	HRMEAN	Heart Rate (Beats/min)	<UK>	<UK>		SDTM	
ADEG	PARAMCD	PRMEAN	PR Duration (msec)	<UK>	<UK>		SDTM	
ADEG	PARAMCD	QRS DUR	QRS Duration (msec)	<UK>	<UK>		SDTM	
ADEG	PARAMCD	QTMEAN	QT Duration (msec)	<UK>	<UK>		SDTM	
ADEG	PARAMCD	QTCB	QTcB - Bazett's Correction Formula (msec)	<UK>	<UK>		SDTM	
ADEG	PARAMCD	INTP	Interpretation	<UK>	<UK>		Derived	If EG.EGSTRESC = "NORMAL" and EG.EGTESTCD = "INTP" then AVALC is set equal to "Normal". Else if EG.EGSTRESC = "ABNORMAL" then AVALC is set equal to "Abnormal" and DESC =propcase(scan(EGSTRESC,2,','),'.').

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ADEG	PARAMCD	INTPCM	INTERPRETATION COMMENTS	<UK>	<UK>		SDTM	
ADEG	PARAMCD	QTcF	QTcF - Fridericia's Correction Formula (msec)	<UK>	<UK>		Derived	QTcF=(AVAL where PARAMCD="QT")/((60/(AVAL where PARAMCD="HR"))**1/3).
ADEG	PARAMCD	EGALL	All ECG examinations	<UK>	<UK>		SDTM	
ADEG	PARAMN	HRMEAN		1 <UK>	<UK>		SDTM	
ADEG	PARAMN	PRMEAN		2 <UK>	<UK>		SDTM	
ADEG	PARAMN	QRS DUR		6 <UK>	<UK>		SDTM	
ADEG	PARAMN	QTMEAN		3 <UK>	<UK>		SDTM	
ADEG	PARAMN	QTcB		4 <UK>	<UK>		SDTM	
ADEG	PARAMN	INTP		7 <UK>	<UK>		Derived	
ADEG	PARAMN	INTPCM		8 <UK>	<UK>		SDTM	
ADEG	PARAMN	QTcF		5 <UK>	<UK>		Derived	
ADEG	PARAMN	EGALL		9 <UK>	<UK>		SDTM	
ADEL	PARAMCD	INC01	Subject has signed the informed consent form (ICF) and is able to understand the information provided in the subject information sheet and ICF.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	INC02	Subject is aged from 21 to 65 years (inclusive).	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	INC03	Subject is of Caucasian Origin.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	INC04	Smoking, healthy subject as judged by the Principal Investigator (PI) based on all available assessments in the Screening period / day of admission.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	INC05	Subject smokes at least 10 commercially available CC per day (no brand restrictions) for the last 4 weeks, based on self-reporting and has been smoking for at least the last 3 consecutive years.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	INC06	The subject is a current smoker who does not plan to quit smoking in the next 3 months.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	INC07	The subject is ready to accept 5 days of SA.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	INC08	The subject is ready to accept using the THS 2.2 product.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC01	As per PI judgement, the subject cannot participate in the study for any reason.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC02	A subject who is legally incompetent, physically or mentally incapable of giving consent.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC03	The subject has medical condition requiring smoking cessation, or clinically relevant diseases in the judgement of the PI.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC04	The subject has a body mass index (BMI) <18.5 or >= 32.0 kg/m2.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC05	The subject has medical conditions which require or will require in the course of the study a medical intervention which may interfere with the study participation and/or study results.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC06	The subject has used nicotine-containing products other than commercially available CC as well as electronic cigarettes and similar devices, within 4 weeks prior to assessment.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC07	The subject has received medication within 14 days or within 5 half-lives of the drug prior to the Admission Day that has an impact on CYP1A2 or CYP2A6 activity.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC08	In case subject received medication within 14 days prior to Screening/prior to Admission it will be decided by the PI if these can potentially interfere with the study objectives and subject's safety.	<UK>	<UK>	NY	SDTM	

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADEL	PARAMCD	EXC09	Concomitant use of non-steroidal anti-inflammatory drugs (NSAIDS) or acetylsalicylic acid.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC10	The subject has a positive alcohol test and/or the subject has a history of alcohol abuse that could interfere with subject's participation in the study.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC11	The subject has a positive urine drug test.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC12	Positive serology test for human immunodeficiency virus (HIV)1/2, hepatitis B surface antigen (HbsAg), or hepatitis C virus (HCV).	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC13	Donation or receipt of whole blood or blood products within 3 months prior to Admission.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC14	The subject is a former or current employee of the tobacco industry or of their first-degree relatives (parent, sibling or child).	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC15	The subject is an employee of the investigational site or any other parties involved in the study or of their first-degree relatives (parent, sibling, or child).	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC16	The subject has participated in a clinical study within 3 months prior to the Screening Visit.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC17	The subject has previously participated in the same study at a different time (i.e. each subject can be included in the study population only once).	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC18	For women only: Subject is pregnant (does not have negative pregnancy tests at Screening and at Admission) or is breast feeding.	<UK>	<UK>	NY	SDTM	
ADEL	PARAMCD	EXC19	For women only: Subject does not agree to use an acceptable method of effective contraception.	<UK>	<UK>	NY	SDTM	
ADFA	PARAM	TYIELD	ISO Tar Yield	<UK>	<UK>		Derived	
ADFA	PARAM	NYIELD	ISO Nicotine Yield	<UK>	<UK>		Derived	
ADFA	PARAM	COYIELD	ISO CO Yield	<UK>	<UK>		Derived	
ADFA	PARAM	QUIT	Does the subject plan to quit smoking during the next 3 months?	<UK>	<UK>		Derived	If FAORRES='Yes' then AVAL=1, else if FAORRES='No' then AVAL=2
ADFA	PARAM	CONYR3	Did the subject smoke for at least 3 consecutive years?	<UK>	<UK>		Derived	If FAORRES='Yes' then AVAL=1, else if FAORRES='No' then AVAL=2
ADFA	PARAM	SMOKHIST	How many cigarettes per day has the subject smoked on average during the last 4 weeks?	<UK>	<UK>		Derived	If avals = '<10' then aval = 3; else if avals = '10 to 19' then aval = 4; else if avals = '>19' then aval = 5;
ADFA	PARAM	WKMENT4	Did the subject smoke menthol cigarettes in the last 4 weeks?	<UK>	<UK>		Derived	If FAORRES='Yes' then AVAL=1, else if FAORRES='No' then AVAL=2
ADFA	PARAM	NICOTH	The subject has used nicotine-containing products other than commercially available CC, electronic cigarettes and similar devices, within 4 weeks prior to assessment.	<UK>	<UK>		Derived	If FAORRES='Yes' then AVAL=1, else if FAORRES='No' then AVAL=2
ADFA	PARAM	PERFORM	Was the THS 2.2 product trial performed?	<UK>	<UK>		Derived	If FAORRES='Yes' then AVAL=1, else if FAORRES='No' then AVAL=2
ADFA	PARAM	WILLABL	Is the subject willing and able to use the product during the study?	<UK>	<UK>		Derived	If FAORRES='Yes' then AVAL=1, else if FAORRES='No' then AVAL=2
ADFA	PARAM	NUMSTIC	How many THS 2.2 tobacco sticks used	<UK>	<UK>		Derived	
ADFA	PARAMN	TYIELD		1 <UK>	<UK>		Derived	
ADFA	PARAMN	NYIELD		2 <UK>	<UK>		Derived	
ADFA	PARAMN	COYIELD		3 <UK>	<UK>		Derived	
ADFA	PARAMN	QUIT		4 <UK>	<UK>		Derived	
ADFA	PARAMN	CONYR3		5 <UK>	<UK>		Derived	
ADFA	PARAMN	SMOKHIST		6 <UK>	<UK>		Derived	
ADFA	PARAMN	WKMENT4		7 <UK>	<UK>		Derived	

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Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADFA	PARAMN	NICOTH		8 <UK>	<UK>		Derived	
ADFA	PARAMN	PERFORM		9 <UK>	<UK>		Derived	
ADFA	PARAMN	WILLABL		10 <UK>	<UK>		Derived	
ADFA	PARAMN	NUMSTIC		16 <UK>	<UK>		Derived	
ADLB	PARAMCD	ALB	Albumin	<UK>	<UK>		SDTM	PARAMN = 14; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	ALP	Alkaline Phosphatase	<UK>	<UK>		SDTM	PARAMN = 5; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	ALT	Alanine Aminotransferase	<UK>	<UK>		SDTM	PARAMN = 1; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	AMPHET	Amphetamine	<UK>	<UK>		SDTM	PARAMN = 310; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	AST	Aspartate Aminotransferase	<UK>	<UK>		SDTM	PARAMN = 2; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	BACT	Bacteria	<UK>	<UK>		SDTM	PARAMN = 208; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	BARB	Barbiturates	<UK>	<UK>		SDTM	PARAMN = 311; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	OBASO	Basophils	<UK>	<UK>		SDTM	PARAMN = 173; if LBTESTCD='BASO' and LBORRESU='G/L' then PARAMCD='OJ rim(LBTESTCD), AVAL=input(LBORRES.best.) AVALC=LBORRES, AVALU=LBORRESU. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2;
ADLB	PARAMCD	BASO	Basophils	<UK>	<UK>		SDTM	PARAMN = 113; if LBTESTCD='BASO' and LBSTRESU='G/L' then PARAMCD=LBTESTCD, AVAL=LBSTRESN, AVALU='G/L', AVALC=put(AVAL.best), ANRLO=LBSTNRLO, ANRHI=LBSTNRHI. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2; PARAMTYP=DERIVED, DTYPE=FUNCTION. As a derived variable please make sure all SDTM variables carried over are not retained for this observation
ADLB	PARAMCD	BASOLE	Basophils/Leukocytes	<UK>	<UK>		SDTM	PARAMN = 114; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	BNZDZPN	Benzodiazepine	<UK>	<UK>		SDTM	PARAMN = 312; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	BILDIR	Direct Bilirubin	<UK>	<UK>		SDTM	PARAMN = 4; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'

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Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADLB	PARAMCD	BILI	Bilirubin	<UK>	<UK>		SDTM	PARAMN = 3; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	BUN	Blood Urea Nitrogen	<UK>	<UK>		SDTM	PARAMN = 11; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	CANNAB	Cannabinoids	<UK>	<UK>		SDTM	PARAMN = 313; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	CASTS	Casts	<UK>	<UK>		SDTM	PARAMN = 209; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	CHOL	Cholesterol	<UK>	<UK>		SDTM	PARAMN = 13; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	COCAINE	Cocaine	<UK>	<UK>		SDTM	PARAMN = 314; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	COTININE	Cotinine	<UK>	<UK>		SDTM	PARAMN = 320; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	CREAT	Creatinine	<UK>	<UK>		SDTM	PARAMN = 9; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	CRYSTALS	Crystals	<UK>	<UK>		SDTM	PARAMN = 210; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	CYCAOXA	Calcium Oxalate Crystals	<UK>	<UK>		SDTM	PARAMN = 211; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	DENISTY	Density	<UK>	<UK>		SDTM	PARAMN = 212; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	OEOS	Eosinophils	<UK>	<UK>		SDTM	PARAMN = 171; if LBTESTCD='EOS' and LBORRESU='G/L' then PARAMCD='O' trim(LBTESTCD),AVAL=input(LBORRES,best.) AVALC=LBORRES, AVALU=LBORRESU. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2;
ADLB	PARAMCD	EOS	Eosinophils	<UK>	<UK>		SDTM	PARAMN = 111; if LBTESTCD='EOS' and LBSTRESU='G/L' then PARAMCD=LBTESTCD, AVAL=LBSTRESN, AVALU='G/L', AVALC=LBSTRESC, ANRLO=LBSTRNRLO, ANRHI=LBSTNRHL. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2; PARAMTYP=DERIVED, DTYPE=FUNCTION. As a derived variable please make sure all SDTM variables carried over are not retained for this observation



## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADLB	PARAMCD	EOSLE	Eosinophils/Leukocytes	<UK>	<UK>		SDTM	PARAMN = 112; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	EPIROCE	Round Epithelial Cells	<UK>	<UK>		SDTM	PARAMN = 213; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	EPISQCE	Squamous Epithelial Cells	<UK>	<UK>		SDTM	PARAMN = 214; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	ETHANOL	Ethanol	<UK>	<UK>		SDTM	PARAMN = 330; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	GGT	Gamma Glutamyl Transferase	<UK>	<UK>		SDTM	PARAMN = 6; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	GLUC	Glucose	<UK>	<UK>		SDTM	PARAMN = 8; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	HBSAG	Hepatitis B Virus Surface Antigen	<UK>	<UK>		SDTM	PARAMN = 301; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	HCAB	Hepatitis C Antibody Measurement	<UK>	<UK>		SDTM	PARAMN = 302; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	HCABC	Hepatitis C Antibody Measurement (no units)	<UK>	<UK>		SDTM	PARAMN = 305; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=4;
ADLB	PARAMCD	HBSAGC	Hepatitis B Virus Surface Antigen (no units)	<UK>	<UK>		SDTM	PARAMN = 304; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=4;
ADLB	PARAMCD	HCT	Hematocrit	<UK>	<UK>		SDTM	PARAMN = 103; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	HGB	Hemoglobin	<UK>	<UK>		SDTM	PARAMN = 102; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	HIV12AB	HIV-1 HIV-2 Antibody Measurement	<UK>	<UK>		SDTM	PARAMN = 303; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	HIV12ABC	HIV-1 HIV-2 Antibody Measurement (no units)	<UK>	<UK>		SDTM	PARAMN = 306; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=4;
ADLB	PARAMCD	K	Potassium	<UK>	<UK>		SDTM	PARAMN = 16; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADLB	PARAMCD	LBALL	All laboratory tests	<UK>	<UK>		SDTM	PARAMN = 99 for LBCAT = CLINICAL CHEMISTRY, PARAM = 199 for LBCAT=HAEMATOLOGY,PARAM = 299 for LBCAT=URINALYSIS for others PARAM=399, if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry' and PARCAT1N=1;; if 100 <= PARAMN < 200 then PARCAT1='Hematology' and PARCAT1N=2;; if 200 <= PARAMN <300 then PARCAT1='Urinalysis' and PARCAT1N=3; if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria' and PARCAT1N=4;
ADLB	PARAMCD	LDH	Lactate Dehydrogenase	<UK>	<UK>		SDTM	PARAMN = 7; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria'
ADLB	PARAMCD	OLYM	Lymphocytes	<UK>	<UK>		SDTM	PARAMN = 167; if LBTESTCD='LYM' and LBORRESU='GI/L' then PARAMCD='O' trim(LBTESTCD), AVAL=input(LBORRES,best.) AVALC=LBORRES, AVALU=LBORRESU. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria', PARCAT1N=2;
ADLB	PARAMCD	LYM	Lymphocytes	<UK>	<UK>		SDTM	PARAMN = 107; if LBTESTCD='LYM' and LBSTRESU='GI/L' then PARAMCD=LBTESTCD, AVAL=LBSTRESN, AVALU='G/L', AVALC=LBSTRESC, ANRLO=LBSTNRLO, ANRHI=LBSTNRHI. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria', PARCAT1N=2; PARAMTYP=DERIVED, DTYPE=FUNCTION. As a derived variable please make sure all SDTM variables carried over are not retained for this observation
ADLB	PARAMCD	LYMLE	Lymphocytes/Leukocytes	<UK>	<UK>		SDTM	PARAMN = 108; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria'
ADLB	PARAMCD	MCH	Ery. Mean Corpuscular Hemoglobin	<UK>	<UK>		SDTM	PARAMN = 116; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria'
ADLB	PARAMCD	MCHC	Ery. Mean Corpuscular HGB Concentration	<UK>	<UK>		SDTM	PARAMN = 117; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria'
ADLB	PARAMCD	MCV	Ery. Mean Corpuscular Volume	<UK>	<UK>		SDTM	PARAMN = 118; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria'
ADLB	PARAMCD	OMONO	Monocytes	<UK>	<UK>		SDTM	PARAMN = 169; if LBTESTCD='MONO' and LBORRESU='GI/L' then PARAMCD='O' trim(LBTESTCD), AVAL=input(LBORRES,best.) AVALC=LBORRES, AVALU=LBORRESU. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria', PARCAT1N=2;
ADLB	PARAMCD	MONO	Monocytes	<UK>	<UK>		SDTM	PARAMN = 109; if LBTESTCD='MONO' and LBSTRESU='GI/L' then PARAMCD=LBTESTCD, AVAL=LBSTRESN, AVALU='G/L', AVALC=LBSTRESC, ANRLO=LBSTNRLO, ANRHI=LBSTNRHI. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 =Safety Laboratory Entry Criteria', PARCAT1N=2; PARAMTYP=DERIVED, DTYPE=FUNCTION. As a derived variable please make sure all SDTM variables carried over are not retained for this observation

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADLB	PARAMCD	MONOLE	Monocytes/Leukocytes	<UK>	<UK>		SDTM	PARAMN = 110; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	MUCUS	Mucus	<UK>	<UK>		SDTM	PARAMN = 215; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	ONEUT	Neutrophils	<UK>	<UK>		SDTM	PARAMN = 165; if LBTESTCD='NEUT' and LBORRESU='G/L' then PARAMCD='O' trim(LBTESTCD), AVAL=input(LBORRES.best.) AVALC=LBORRES, AVALU=LBORRESU. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2;
ADLB	PARAMCD	NEUT	Neutrophils	<UK>	<UK>		SDTM	PARAMN = 105; if LBTESTCD='NEUT' and LBSTRESU='G/L' then PARAMCD=LBTESTCD, AVAL=LBSTRESN, AVALU='G/L', AVALC=LBSTRESC, ANRLO=LBSTNRLO, ANRHI=LBSTNRHI. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2; PARAMTYP=DERIVED, DTYPE=FUNCTION. As a derived variable please make sure all SDTM variables carried over are not retained for this observation
ADLB	PARAMCD	NEUTLE	Neutrophils/Leukocytes	<UK>	<UK>		SDTM	PARAMN = 106; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	NITRITE	Nitrite	<UK>	<UK>		SDTM	PARAMN = 205; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	OPIATE	Opiate	<UK>	<UK>		SDTM	PARAMN = 315; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	PH	pH	<UK>	<UK>		SDTM	PARAMN = 201; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	OPLAT	Platelets	<UK>	<UK>		SDTM	PARAMN = 175; if LBTESTCD='PLAT' and LBORRESU='G/L' then LBTESTCD='O' trim(LBTESTCD), AVAL=input(LBORRES.best.) AVALC=LBORRES, AVALU=LBORRESU. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2;
ADLB	PARAMCD	PLAT	Platelets	<UK>	<UK>		SDTM	PARAMN = 115; if LBTESTCD='PLAT' and LBSTRESU='G/L' then PARAMCD=LBTESTCD, AVAL=LBSTRESN, AVALC=LBSTRESC, AVALU='G/L', ANRLO=LBSTNRLO, ANRHI=LBSTNRHI. if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2; PARAMTYP=DERIVED, DTYPE=FUNCTION. As a derived variable please make sure all SDTM variables carried over are not retained for this observation
ADLB	PARAMCD	PREGTEST	Pregnancy Test	<UK>	<UK>		SDTM	PARAMN = 340; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADLB	PARAMCD	PROT	Protein	<UK>	<UK>		SDTM	PARAMN = 10; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	RBC	Erythrocytes	<UK>	<UK>		SDTM	PARAMN = 101; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	SODIUM	Sodium	<UK>	<UK>		SDTM	PARAMN = 15; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	SPGRAV	Specific Gravity	<UK>	<UK>		SDTM	PARAMN = 202; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	TRIG	Triglycerides	<UK>	<UK>		SDTM	PARAMN = 12; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	UBILI	Bilirubin (Urine)	<UK>	<UK>		SDTM	PARAMN = 203; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	UGLUC	Glucose (Urine)	<UK>	<UK>		SDTM	PARAMN = 204; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	UPROT	Protein (Urine)	<UK>	<UK>		SDTM	PARAMN = 207; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	URBC	Erythrocytes (Urine)	<UK>	<UK>		SDTM	PARAMN = 206; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	UWBC	Leukocytes (Urine)	<UK>	<UK>		SDTM	PARAMN = 216; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'
ADLB	PARAMCD	OWBC	Leukocytes	<UK>	<UK>		SDTM	PARAMN = 164; if LBTESTCD='WBC' and LBORRESU='G/L' then PARAMCD='O'   trim(LBTESTCD), AVAL=input(LBORRES.best.) AVALC=LBORRES, AVALU=LBORRESU if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2;
ADLB	PARAMCD	WBC	Leukocytes	<UK>	<UK>		SDTM	PARAMN = 104; if LBTESTCD='WBC' and LBSTRESU='G/L' then PARAMCD=LBTESTCD, AVAL=LBSTRESN, AVALU=G/L, AVALC=LBSTRESC, ANRLO=LBSTNRLO, ANRHI=LBSTNRHI, if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=2; PARAMTYPE=DERIVED, DTYPE=FUNCTION. As a derived variable please make sure all SDTM variables carried over are not retained for this observation
ADLB	PARAMCD	YEAST	Yeast	<UK>	<UK>		SDTM	PARAMN = 217; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1N='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria'

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADLB	PARAMCD	OCCBLD	Occult Blood	<UK>	<UK>		SDTM	PARAMN = 218; if 0 < PARAMN <100 then PARCAT1 = 'Clinical Chemistry', if 100 <= PARAMN < 200 then PARCAT1='Hematology', if 200 <= PARAMN <300 then PARCAT1='Urinalysis', if 300 <= PARAMN <400 then PARCAT1 = 'Safety Laboratory Entry Criteria', PARCAT1N=3;
ADPC	PARAMCD	PCTPT	NUMBER OF PRODUCT USES PER TIMEPOINT	<UK>	<UK>		Derived	
ADPC	PARAMCD	PCDIST	TIME OF DISTRIBUTION	<UK>	<UK>		Derived	
ADPC	PARAMCD	PCBTRET	TIME OF BUTT RETURN	<UK>	<UK>		Derived	
ADPC	PARAMCD	NIC	Nicotine (ng/mL)	<UK>	<UK>		Derived	For non-BLQ samples: PARAMCD=PKMERGE.PARAMCD, PARAMN=PKMERGE.PARAMN, PARAM=PKMERGE.PARAM, AVAL=PKMERGE.AVAL, AVALC=PKMERGE.AVALC, AVALU=PKMERGE.AVALU  For BLQ samples: As above except record will be present twice. For original record, AVAL=null, AVALC=PKMERGE.AVALC, DTYPE=null. For imputed record, AVAL = PKMERGE.AVAL where imputation rules follow SAP section 7.1.If AVAL = 1/2 LLOQ then AVALC = STRIP(PUT(AVAL, BEST.)), DTYPE = "BLQHALF".
ADPC	PARAMCD	COT	Cotinine (ng/mL)	<UK>	<UK>		Derived	PARAMCD=PC.PCTESTCD, PARAMN=2, PARAM=TRIM(PC.PCTEST) ' ( TRIM(PCSTRESU) )'); AVAL=PC.PCSTRESN, AVALC=PC.PCSTRESC, AVALU=PC.PCSTRESU
ADPE	PARAMCD	GAPPEAR	General Appearance	<UK>	<UK>		Derived	Where PE.PETESTCD="GAPPEAR", If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non-missing then AVALC="Abnormal" PARAMN=1
ADPE	PARAMCD	HEENT	Head, Eyes, Ears, Nose, Throat	<UK>	<UK>		Derived	Where PE.PETESTCD="HEENT", If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non-missing then AVALC="Abnormal" PARAMN=2
ADPE	PARAMCD	THYROID	Thyroid Gland	<UK>	<UK>		Derived	Where PE.PETESTCD="THYROID", If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non-missing then AVALC="Abnormal" PARAMN=3
ADPE	PARAMCD	HEART	Heart	<UK>	<UK>		Derived	Where PE.PETESTCD="HEART", If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non-missing then AVALC="Abnormal" PARAMN=4
ADPE	PARAMCD	CHEST	Chest	<UK>	<UK>		Derived	Where PE.PETESTCD="CHEST" and PECAT ne 'CHEST X-RAY'. If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non-missing then AVALC="Abnormal" PARAMN=5
ADPE	PARAMCD	LUNGS	Lungs	<UK>	<UK>		Derived	Where PE.PETESTCD="LUNGS", If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non-missing then AVALC="Abnormal" PARAMN=6
ADPE	PARAMCD	BACK	Back	<UK>	<UK>		Derived	Where PE.PETESTCD="LUNGS", If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non-missing then AVALC="Abnormal" PARAMN=11
ADPE	PARAMCD	CVS	Cardiovascular System	<UK>	<UK>		Derived	Where PE.PETESTCD="CVS", If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non-missing then AVALC="Abnormal" PARAMN=8

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADPE	PARAMCD	GASTRO	Gastrointestinal	<UK>	<UK>		Derived	Where PE.PETESTCD="GASTRO". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" GASTRO = 7
ADPE	PARAMCD	NEURO	Neurologic	<UK>	<UK>		Derived	Where PE.PETESTCD="NEURO". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=9
ADPE	PARAMCD	ABDOMEN	Abdomen	<UK>	<UK>		Derived	Where PE.PETESTCD="GENITO". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=13
ADPE	PARAMCD	SKIN	Skin	<UK>	<UK>		Derived	Where PE.PETESTCD="SKIN". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=10
ADPE	PARAMCD	DENTN	Dentition	<UK>	<UK>		Derived	Where PE.PETESTCD="LYMPH". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=14
ADPE	PARAMCD	MUSCULO	Musculoskeletal	<UK>	<UK>		Derived	Where PE.PETESTCD="MUSCULO". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=12
ADPE	PARAMCD	OTHER	Other	<UK>	<UK>		Derived	Where PE.PETESTCD="OTHER" and SCAN(PESTRESC,2,"-") = null. If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=15
ADPE	PARAMCD	OTHEXTRM	Other - Extremities	<UK>	<UK>		Derived	Where PE.PETESTCD="OTHER" and SCAN(PESTRESC,2,"-") = "EXTREMITIES". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=16
ADPE	PARAMCD	OTHLYMN	Other - Lymph Nodes	<UK>	<UK>		Derived	Where PE.PETESTCD="OTHER" and SCAN(PESTRESC,2,"-") = "LYMPH NODES". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=17
ADPE	PARAMCD	OTHLYMS	Other - Lymphatic System	<UK>	<UK>		Derived	Where PE.PETESTCD="OTHER" and SCAN(PESTRESC,2,"-") = "LYMPHATIC SYSTEM". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=18
ADPE	PARAMCD	OTHVASC	Other - Vascular	<UK>	<UK>		Derived	Where PE.PETESTCD="OTHER" and SCAN(PESTRESC,2,"-") = "VASCULAR". If PE.PESTAT="NOT DONE" then AVALC="Not Examined". Else, if PE.PESTRESC="NORMAL" then AVALC="Normal". Else, if PE.PESTRESC is non- missing then AVALC="Abnormal" PARAMN=19

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADPE	PARAMCD	CHESTX	Chest X-ray	<UK>	<UK>		SDTM	PARAMN=20 AND PECAT= CHEST X-RAY"
ADPE	PARAMCD	PEALL	All Physical Examinations	<UK>	<UK>		SDTM	PARAMN=99
ADPP	PARAMCD	NCAVG	Average Conc (ng/mL) (Nicotine)	<UK>	<UK>		SDTM	PARAMN=1 when PARAMCD='NCAVG', PARCAT1='Nicotine'.
ADPP	PARAMCD	NCMAX	Max Conc (ng/mL) (Nicotine)	<UK>	<UK>		SDTM	PARAMN=2 when PARAMCD='NCMAX', PARCAT1='Nicotine'.
ADPP	PARAMCD	NTMAX	Time of CMAX (h) (Nicotine)	<UK>	<UK>		SDTM	PARAMN=3 when PARAMCD='NTMAX', PARCAT1='Nicotine'.
ADPP	PARAMCD	CCAVG	Average Conc (ng/mL) (Cotinine)	<UK>	<UK>		SDTM	PARAMN=4 when PARAMCD='CCAVG', PARCAT1='Cotinine'.
ADPP	PARAMCD	CCMAX	Max Conc (ng/mL) (Cotinine)	<UK>	<UK>		SDTM	PARAMN=5 when PARAMCD='CCMAX', PARCAT1='Cotinine'.
ADPP	PARAMCD	CTMAX	Time of CMAX (h) (Cotinine)	<UK>	<UK>		SDTM	PARAMN=6 when PARAMCD='CTMAX', PARCAT1='Cotinine'.
ADQSPA	AVAL	NOT AT ALL		1	<UK>	<UK>	SDTM	
ADQSPA	AVAL	VERY LITTLE		2	<UK>	<UK>	SDTM	
ADQSPA	AVAL	LITTLE		3	<UK>	<UK>	SDTM	
ADQSPA	AVAL	MODERATELY		4	<UK>	<UK>	SDTM	
ADQSPA	AVAL	A LOT		5	<UK>	<UK>	SDTM	
ADQSPA	AVAL	QUITE A LOT		6	<UK>	<UK>	SDTM	
ADQSPA	AVAL	EXTREMELY		7	<UK>	<UK>	SDTM	
ADQSPA	PARAMCD	HSSMOK	Is smoking different with the device	<UK>	<UK>		SDTM	If index(QSSTRESC,'STRONGLY AGREE') then AVAL=5,If index(QSSTRESC,'AGREE') then AVAL=4,If index(QSSTRESC,'NEITHER AGREE NOR DISAGREE') then AVAL=3,If index(QSSTRESC,'DISAGREE') then AVAL=2,If index(QSSTRESC,'STRONGLY DISAGREE') then AVAL=1
ADQSPA	PARAMCD	HSENU	How did you enjoy smoking with device	<UK>	<UK>		SDTM	If index(QSSTRESC,'STRONGLY AGREE') then AVAL=5,If index(QSSTRESC,'AGREE') then AVAL=4,If index(QSSTRESC,'NEITHER AGREE NOR DISAGREE') then AVAL=3,If index(QSSTRESC,'DISAGREE') then AVAL=2,If index(QSSTRESC,'STRONGLY DISAGREE') then AVAL=1
ADQSPA	PARAMCD	HSTASTE	Is the taste different with the device	<UK>	<UK>		SDTM	If index(QSSTRESC,'STRONGLY AGREE') then AVAL=5,If index(QSSTRESC,'AGREE') then AVAL=4,If index(QSSTRESC,'NEITHER AGREE NOR DISAGREE') then AVAL=3,If index(QSSTRESC,'DISAGREE') then AVAL=2,If index(QSSTRESC,'STRONGLY DISAGREE') then AVAL=1
ADQSPA	PARAMCD	HSEASY	How was the device to use	<UK>	<UK>		SDTM	If index(QSSTRESC,'STRONGLY AGREE') then AVAL=5,If index(QSSTRESC,'AGREE') then AVAL=4,If index(QSSTRESC,'NEITHER AGREE NOR DISAGREE') then AVAL=3,If index(QSSTRESC,'DISAGREE') then AVAL=2,If index(QSSTRESC,'STRONGLY DISAGREE') then AVAL=1
ADQSPA	PARAMCD	HSDISTU	Was your smoking disturbed by device	<UK>	<UK>		SDTM	If index(QSSTRESC,'STRONGLY AGREE') then AVAL=5,If index(QSSTRESC,'AGREE') then AVAL=4,If index(QSSTRESC,'NEITHER AGREE NOR DISAGREE') then AVAL=3,If index(QSSTRESC,'DISAGREE') then AVAL=2,If index(QSSTRESC,'STRONGLY DISAGREE') then AVAL=1
ADQSPA	PARAMCD	SATISFY	Satisfy	<UK>	<UK>		SDTM	If QSSTRESC='NOT AT ALL' then AVAL=1, if QSSTRESC='VERY LITTLE' then AVAL=2, if QSSTRESC='LITTLE' then AVAL=3, if QSSTRESC='MODERATELY' then AVAL=4, if QSSTRESC='A LOT' then AVAL=5, if QSSTRESC='QUITE A LOT' then AVAL=6, if QSSTRESC='EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	TASTE	Taste	<UK>	<UK>		SDTM	If QSSTRESC='NOT AT ALL' then AVAL=1, if QSSTRESC='VERY LITTLE' then AVAL=2, if QSSTRESC='LITTLE' then AVAL=3, if QSSTRESC='MODERATELY' then AVAL=4, if QSSTRESC='A LOT' then AVAL=5, if QSSTRESC='QUITE A LOT' then AVAL=6, if QSSTRESC='EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	SENSAT	Sensation	<UK>	<UK>		SDTM	If QSSTRESC='NOT AT ALL' then AVAL=1, if QSSTRESC='VERY LITTLE' then AVAL=2, if QSSTRESC='LITTLE' then AVAL=3, if QSSTRESC='MODERATELY' then AVAL=4, if QSSTRESC='A LOT' then AVAL=5, if QSSTRESC='QUITE A LOT' then AVAL=6, if QSSTRESC='EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	CALM	Calm	<UK>	<UK>		SDTM	If QSSTRESC='NOT AT ALL' then AVAL=1, if QSSTRESC='VERY LITTLE' then AVAL=2, if QSSTRESC='LITTLE' then AVAL=3, if QSSTRESC='MODERATELY' then AVAL=4, if QSSTRESC='A LOT' then AVAL=5, if QSSTRESC='QUITE A LOT' then AVAL=6, if QSSTRESC='EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	AWAKE	Awake	<UK>	<UK>		SDTM	If QSSTRESC='NOT AT ALL' then AVAL=1, if QSSTRESC='VERY LITTLE' then AVAL=2, if QSSTRESC='LITTLE' then AVAL=3, if QSSTRESC='MODERATELY' then AVAL=4, if QSSTRESC='A LOT' then AVAL=5, if QSSTRESC='QUITE A LOT' then AVAL=6, if QSSTRESC='EXTREMELY' then AVAL=7

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADQSPA	PARAMCD	IRRITAB	Irritable	<UK>	<UK>		SDTM	If QSSTRESC=NOT AT ALL' then AVAL=1, if QSSTRESC=VERY LITTLE' then AVAL=2, if QSSTRESC=LITTLE' then AVAL=3, if QSSTRESC=MODERATELY' then AVAL=4, if QSSTRESC=A LOT' then AVAL=5, if QSSTRESC=QUITE A LOT' then AVAL=6, if QSSTRESC=EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	CONCEN	Concentrate	<UK>	<UK>		SDTM	If QSSTRESC=NOT AT ALL' then AVAL=1, if QSSTRESC=VERY LITTLE' then AVAL=2, if QSSTRESC=LITTLE' then AVAL=3, if QSSTRESC=MODERATELY' then AVAL=4, if QSSTRESC=A LOT' then AVAL=5, if QSSTRESC=QUITE A LOT' then AVAL=6, if QSSTRESC=EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	HUNGER	Hunger	<UK>	<UK>		SDTM	If QSSTRESC=NOT AT ALL' then AVAL=1, if QSSTRESC=VERY LITTLE' then AVAL=2, if QSSTRESC=LITTLE' then AVAL=3, if QSSTRESC=MODERATELY' then AVAL=4, if QSSTRESC=A LOT' then AVAL=5, if QSSTRESC=QUITE A LOT' then AVAL=6, if QSSTRESC=EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	DIZZY	Dizzy	<UK>	<UK>		SDTM	If QSSTRESC=NOT AT ALL' then AVAL=1, if QSSTRESC=VERY LITTLE' then AVAL=2, if QSSTRESC=LITTLE' then AVAL=3, if QSSTRESC=MODERATELY' then AVAL=4, if QSSTRESC=A LOT' then AVAL=5, if QSSTRESC=QUITE A LOT' then AVAL=6, if QSSTRESC=EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	NAUSEO	Nauseous	<UK>	<UK>		SDTM	If QSSTRESC=NOT AT ALL' then AVAL=1, if QSSTRESC=VERY LITTLE' then AVAL=2, if QSSTRESC=LITTLE' then AVAL=3, if QSSTRESC=MODERATELY' then AVAL=4, if QSSTRESC=A LOT' then AVAL=5, if QSSTRESC=QUITE A LOT' then AVAL=6, if QSSTRESC=EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	CRAVING	Craving	<UK>	<UK>		SDTM	If QSSTRESC=NOT AT ALL' then AVAL=1, if QSSTRESC=VERY LITTLE' then AVAL=2, if QSSTRESC=LITTLE' then AVAL=3, if QSSTRESC=MODERATELY' then AVAL=4, if QSSTRESC=A LOT' then AVAL=5, if QSSTRESC=QUITE A LOT' then AVAL=6, if QSSTRESC=EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	ENJOY	Enjoy	<UK>	<UK>		SDTM	If QSSTRESC=NOT AT ALL' then AVAL=1, if QSSTRESC=VERY LITTLE' then AVAL=2, if QSSTRESC=LITTLE' then AVAL=3, if QSSTRESC=MODERATELY' then AVAL=4, if QSSTRESC=A LOT' then AVAL=5, if QSSTRESC=QUITE A LOT' then AVAL=6, if QSSTRESC=EXTREMELY' then AVAL=7
ADQSPA	PARAMCD	MCEQA	Aversion Subscale	<UK>	<UK>		Derived	If at least 1 of PARAMCD in ('DIZZY' 'NAUSEO') is non-missing then MCEQA is set equal to the average of AVAL when PARAMCD IN ('DIZZY' 'NAUSEO')
ADQSPA	PARAMCD	MCEQCR	Craving Reduction Subscale	<UK>	<UK>		Derived	Set equal to AVAL when PARAMCD='CRAVING'
ADQSPA	PARAMCD	MCEQERTS	Enjoyment Respiratory Tract Sensations	<UK>	<UK>		Derived	Set equal to AVAL when PARAMCD='SENSAT'
ADQSPA	PARAMCD	MCEQPR	Psychological Reward Subscale	<UK>	<UK>		Derived	If at least 50% of PARAMCD in ('CALM' 'AWAKE' 'IRRITAB' 'CONCEN' 'HUNGER') are non-missing then MCEQPR is set to the average of AVAL when PARAMCD IN ('CALM' 'AWAKE' 'IRRITAB' 'CONCEN' 'HUNGER')
ADQSPA	PARAMCD	MCEQSS	Smoking Satisfaction Subscale	<UK>	<UK>		Derived	If at least 50% of PARAMCD in ('SATISFY' 'TASTE' 'ENJOY') are non-missing then MCEQSS is set to the average of AVAL when PARAMCD in ('SATISFY' 'TASTE' 'ENJOY')
ADQSPA	PARAMCD	QSALL	All questionnaire tests	<UK>	<UK>		SDTM	
ADQSPA	PARAMN	HSSMOK		1 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	HSENJ		2 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	HSTASTE		3 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	HSEASY		4 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	HSDISTU		5 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	SATISFY		6 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	TASTE		7 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	SENSAT		8 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	CALM		9 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	AWAKE		10 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	IRRITAB		11 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	CONCEN		12 <UK>	<UK>		SDTM	
ADQSPA	PARAMN	HUNGER		13 <UK>	<UK>		SDTM	



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Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADQSPA	PARAMN	DIZZY		14	<UK>	<UK>	SDTM	
ADQSPA	PARAMN	NAUSEO		15	<UK>	<UK>	SDTM	
ADQSPA	PARAMN	CRAVING		16	<UK>	<UK>	SDTM	
ADQSPA	PARAMN	ENJOY		17	<UK>	<UK>	SDTM	
ADQSPA	PARAMN	MCEQA		18	<UK>	<UK>	Derived	
ADQSPA	PARAMN	MCEQCR		19	<UK>	<UK>	Derived	
ADQSPA	PARAMN	MCEQERTS		20	<UK>	<UK>	Derived	
ADQSPA	PARAMN	MCEQPR		21	<UK>	<UK>	Derived	
ADQSPA	PARAMN	MCEOSS		22	<UK>	<UK>	Derived	
ADQSPA	PARAMN	QSALL		99	<UK>	<UK>	SDTM	
ADQSND	PARAMCD	MNWS01	Angry, Irritable, Frustrated		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS02	Anxious, Tense		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS03	Depressed Mood, Sad		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS04	Desire or Craving to Smoke		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS05	Difficulty Concentrating		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS06	Increase Appetite, Hungry, Weight Gain		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS07	Insomnia, Sleep Problems, Awakening at Night		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS08	Restless		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS09	Impatient		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS10	Constipation		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS11	Dizziness		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS12	Coughing		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS13	Dreaming or Nightmares		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS14	Nausea		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWS15	Sore Throat		<UK>	<UK>	SDTM	!QSSTRESC="NONE" then AVAL=0, if QSSTRESC="SLIGHT" then AVAL=1, if QSSTRESC="MILD" then AVAL=2, if QSSTRESC="MODERATE" then AVAL=3, if QSSTRESC="SEVERE" then AVAL=4
ADQSND	PARAMCD	MNWRWDS1	MNWS-R Withdrawal Score 1		<UK>	<UK>	Derived	If less than 50% are non-missing then set to the average of AVAL where PARAMCD in (MNWS01-MNWS09), else set to missing
ADQSND	PARAMCD	MNWRWDS2	MNWS-R Withdrawal Score 2		<UK>	<UK>	Derived	If less than 50% are non-missing then set to the average of AVAL where PARAMCD in (MNWS01-MNWS15), else set to missing

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Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADQSNB	PARAMCD	FTND01		<UK>	<UK>		SDTM	If QSSTRESC = 'WITHIN 5 MINUTES' then AVAL = 3, if QSSTRESC = '6-30 MINUTES' then AVAL = 2, if QSSTRESC = '31-60 MINUTES' then AVAL = 1, if QSSTRESC = 'AFTER 60 MINUTES' then AVAL = 0
ADQSNB	PARAMCD	FTND02		<UK>	<UK>		SDTM	If QSSTRESC = 'YES' then AVAL = 1, if QSSTRESC = 'NO' then AVAL = 0
ADQSNB	PARAMCD	FTND03		<UK>	<UK>		SDTM	If QSSTRESC = 'THE FIRST ONE IN THE MORNING' then AVAL = 1, if QSSTRESC = 'ANY OTHER' then AVAL = 0
ADQSNB	PARAMCD	FTND04		<UK>	<UK>		SDTM	If QSSTRESC = '10 OR LESS' then AVAL = 0, if QSSTRESC = '11-20' then AVAL = 1, if QSSTRESC = '21-30' then AVAL = 2, if QSSTRESC = '31 OR MORE' then AVAL = 3
ADQSNB	PARAMCD	FTND05		<UK>	<UK>		SDTM	If QSSTRESC = 'YES' then AVAL = 1, if QSSTRESC = 'NO' then AVAL = 0
ADQSNB	PARAMCD	FTND06		<UK>	<UK>		SDTM	If QSSTRESC = 'YES' then AVAL = 1, if QSSTRESC = 'NO' then AVAL = 0
ADQSNB	PARAMCD	FTNDSC	Fagerstrom Score	<UK>	<UK>		Derived	If all items of AVAL where PARAMCD IN (FTND01-FTND06) are non-missing then set to sum of FTND01-FTND06, else set to missing. If 0 <= FTNDSC <= 3 then AVALCAT1='Mild', if 4 <= FTNDSC <= 6 then AVALCAT1='Moderate', if 7 <= FTNDSC <= 10 then AVALCAT1='Severe'
ADQSNB	PARAMN	MNWS01		1 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS02		2 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS03		3 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS04		4 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS05		5 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS06		6 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS07		7 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS08		8 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS09		9 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS10		10 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS11		11 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS12		12 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS13		13 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS14		14 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWS15		15 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	MNWRWDS1		17 <UK>	<UK>		Derived	
ADQSNB	PARAMN	MNWRWDS2		18 <UK>	<UK>		Derived	
ADQSNB	PARAMN	FTND01		19 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	FTND02		20 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	FTND03		21 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	FTND04		22 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	FTND05		23 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	FTND06		24 <UK>	<UK>		SDTM	
ADQSNB	PARAMN	FTNDSC		25 <UK>	<UK>		Derived	
ADQSSU	PARAMCD	QSU01	Desire for Cigarette	<UK>	<UK>		SDTM	If QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7
ADQSSU	PARAMCD	QSU02	Nothing Better than Smoking	<UK>	<UK>		SDTM	If QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7
ADQSSU	PARAMCD	QSU03	Probably Smoke Now	<UK>	<UK>		SDTM	If QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADQSSU	PARAMCD	QSU04	Control Things Better	<UK>	<UK>		SDTM	if QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7
ADQSSU	PARAMCD	QSU05	Cigarette Right Now	<UK>	<UK>		SDTM	if QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7
ADQSSU	PARAMCD	QSU06	Urge for a Cigarette	<UK>	<UK>		SDTM	if QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7
ADQSSU	PARAMCD	QSU07	Cigarette Taste Good	<UK>	<UK>		SDTM	if QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7
ADQSSU	PARAMCD	QSU08	Do Anything for a Cigarette	<UK>	<UK>		SDTM	if QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7
ADQSSU	PARAMCD	QSU09	Less Depressed	<UK>	<UK>		SDTM	if QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7
ADQSSU	PARAMCD	QSU10	Smoke as Soon as Possible	<UK>	<UK>		SDTM	if QSSTRESC='STRONGLY DISAGREE' then AVAL = 1, if QSSTRESC='DISAGREE' then AVAL=2, if QSSTRESC='SOMEWHAT DISAGREE' then AVAL=3, if QSSTRESC='DO NOT AGREE OR DISAGREE' then AVAL=4, if QSSTRESC='SOMEWHAT AGREE' then AVAL=5, if QSSTRESC='AGREE' then AVAL=6, if QSSTRESC='STRONGLY AGREE' then AVAL=7
ADQSSU	PARAMCD	QSUFACT1	Reward	<UK>	<UK>		Derived	Factor 1 is the average of non-missing AVAL where PARAMCD IN ('QSU01', 'QSU03', 'QSU06', 'QSU07', 'QSU10') if at least 50% of item scores are non-missing. If less than 50% of item scores are missing then = missing
ADQSSU	PARAMCD	QSUFACT2	Relief	<UK>	<UK>		Derived	Factor 2 is the average of non-missing AVAL where PARAMCD IN ('QSU02', 'QSU04', 'QSU05', 'QSU08', 'QSU09') and if at least 50% of item scores are non-missing. If less than 50% of item scores are missing then = missing
ADQSSU	PARAMCD	QSU010	Total Score	<UK>	<UK>		Derived	Average of all non-missing AVAL where PARAMCD in ('QSU01' to 'QSU10') and if at least 50% of item scores are non-missing. If less than 50% of item scores are non-missing then = missing
ADQSSU	PARAMN	QSU01		1	<UK>	<UK>	SDTM	
ADQSSU	PARAMN	QSU02		2	<UK>	<UK>	SDTM	
ADQSSU	PARAMN	QSU03		3	<UK>	<UK>	SDTM	
ADQSSU	PARAMN	QSU04		4	<UK>	<UK>	SDTM	
ADQSSU	PARAMN	QSU05		5	<UK>	<UK>	SDTM	
ADQSSU	PARAMN	QSU06		6	<UK>	<UK>	SDTM	
ADQSSU	PARAMN	QSU07		7	<UK>	<UK>	SDTM	

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADQSSU	PARAMN	QSU08		8	<UK>	<UK>	SDTM	
ADQSSU	PARAMN	QSU09		9	<UK>	<UK>	SDTM	
ADQSSU	PARAMN	QSU10		10	<UK>	<UK>	SDTM	
ADQSSU	PARAMN	QSUFACT1		11	<UK>	<UK>	Derived	
ADQSSU	PARAMN	QSUFACT2		12	<UK>	<UK>	Derived	
ADQSSU	PARAMN	QSUTOTAL		13	<UK>	<UK>	Derived	
ADQSSYM	PARAMCD	COUGH24	Regular Need to Cough		<UK>	<UK>	SDTM	
ADQSSYM	PARAMCD	COUIMP	Cough Impact Scale		<UK>	<UK>	SDTM	
ADQSSYM	PARAMCD	COUINT	Cough Intensity Scale		<UK>	<UK>	SDTM	If QSSTRESC='VERY MILD' then AVAL=1, if QSSTRESC='MILD' then AVAL=2, if QSSTRESC='MODERATE' then AVAL=3, if QSSTRESC='SEVERE' then AVAL=4, if QSSTRESC='VERY SEVERE' then AVAL=5
ADQSSYM	PARAMCD	COURFEQ	Cough Frequency Scale		<UK>	<UK>	SDTM	If QSSTRESC='RARELY' then AVAL=1, if QSSTRESC='SOMETIMES' then AVAL=2, if QSSTRESC='FAIRLY OFTEN' then AVAL=3, if QSSTRESC='OFTEN' then AVAL=4, if QSSTRESC='ALMOST ALWAYS' then AVAL=5
ADQSSYM	PARAMCD	COUSPUT	Sputum Production		<UK>	<UK>	SDTM	If QSSTRESC='NO SPUTUM' then AVAL=0, if QSSTRESC='A MODERATE AMOUNT OF SPUTUM' then AVAL=1, if QSSTRESC='A LARGE AMOUNT OF SPUTUM' then AVAL=2, if QSSTRESC='A VERY LARGE AMOUNT OF SPUTUM' then AVAL=3
ADQSSYM	PARAMCD	COUOTH	Other Observation		<UK>	<UK>	SDTM	
ADQSSYM	PARAMN	COUGH24		1	<UK>	<UK>	SDTM	
ADQSSYM	PARAMN	COUIMP		2	<UK>	<UK>	SDTM	
ADQSSYM	PARAMN	COUINT		3	<UK>	<UK>	SDTM	
ADQSSYM	PARAMN	COURFEQ		4	<UK>	<UK>	SDTM	
ADQSSYM	PARAMN	COUSPUT		5	<UK>	<UK>	SDTM	
ADQSSYM	PARAMN	COUOTH		6	<UK>	<UK>	SDTM	
ADSP	PARAMCD	ATMPCORR	Atmospheric Pressure Correction		<UK>	<UK>	SDTM	
ADSP	PARAMCD	ATMPSPAN	Atmospheric Pressure Span		<UK>	<UK>	SDTM	
ADSP	PARAMCD	CONSMON	Consumption since morning		<UK>	<UK>	SDTM	
ADSP	PARAMCD	DFI	Sum of Ii and Di		<UK>	<UK>	SDTM	
ADSP	PARAMCD	DI	Puff Duration		<UK>	<UK>	SDTM	
ADSP	PARAMCD	FILESTAT	File Status		<UK>	<UK>	SDTM	
ADSP	PARAMCD	FLAG	Flag		<UK>	<UK>	SDTM	
ADSP	PARAMCD	FLWSPAN	Flow Span		<UK>	<UK>	SDTM	
ADSP	PARAMCD	FLWTHLD	Flow Threshold		<UK>	<UK>	SDTM	
ADSP	PARAMCD	FNEGFZ	Force negative flow to zero		<UK>	<UK>	SDTM	
ADSP	PARAMCD	II	Inter Puff Interval		<UK>	<UK>	SDTM	
ADSP	PARAMCD	INTPFMIN	Inter-Puff min time		<UK>	<UK>	SDTM	
ADSP	PARAMCD	INTRFER	Interference Time		<UK>	<UK>	SDTM	
ADSP	PARAMCD	KCOEFF	K Coefficient		<UK>	<UK>	SDTM	
ADSP	PARAMCD	MODEFLOW	Mode of Flow Correction		<UK>	<UK>	SDTM	
ADSP	PARAMCD	MODEVOL	Mode of Volume Correction		<UK>	<UK>	SDTM	
ADSP	PARAMCD	PCI	Peak Pressure Drop		<UK>	<UK>	SDTM	
ADSP	PARAMCD	PDSPAN	PD Span		<UK>	<UK>	SDTM	
ADSP	PARAMCD	PDTHSLD	PD Threshold		<UK>	<UK>	SDTM	
ADSP	PARAMCD	PFFMINTM	Puff min time		<UK>	<UK>	SDTM	
ADSP	PARAMCD	PMI	Average Pressure Drop		<UK>	<UK>	SDTM	
ADSP	PARAMCD	PN	Number of interpuffs peaks		<UK>	<UK>	SDTM	
ADSP	PARAMCD	POSQCI	PosQci		<UK>	<UK>	SDTM	
ADSP	PARAMCD	QCI	Peak Flow Qci		<UK>	<UK>	SDTM	
ADSP	PARAMCD	QMI	Average Flow		<UK>	<UK>	SDTM	
ADSP	PARAMCD	RCI	Peak Resistance		<UK>	<UK>	SDTM	
ADSP	PARAMCD	REASON	Reason		<UK>	<UK>	SDTM	
ADSP	PARAMCD	RMI	Average Resistance		<UK>	<UK>	SDTM	
ADSP	PARAMCD	RTDBTHD	RTD base threshold		<UK>	<UK>	SDTM	
ADSP	PARAMCD	SMPLAQ	Sample Acquisition		<UK>	<UK>	SDTM	
ADSP	PARAMCD	S_PI	S.PI		<UK>	<UK>	SDTM	
ADSP	PARAMCD	VI	Puff Volume		<UK>	<UK>	SDTM	
ADSP	PARAMCD	VOLTHLD	Volume Threshold		<UK>	<UK>	SDTM	

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADSP	PARAMCD	WI	Work	<UK>	<UK>		SDTM	
ADSP	PARAMCD	HSTNI	Daily Average - Puff Number	<UK>	<UK>		Derived	For each value of USUBJID, AVISIT, ADTM find the maximum value of XTSPID, call this temp1. AVAL is set to the average of temp1 within each USUBJID, AVISIT, ADT. AVALC = AVAL with 1 decimal places, AVALU is missing
ADSP	PARAMCD	HSTVI	Daily Average - Puff Volume	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='VI'), AVALC = AVAL with 1 dp, AVALU = mL
ADSP	PARAMCD	HSTDI	Daily Average - Puff Duration	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='DI'), AVALC = AVAL with 1 dp, AVALU = s
ADSP	PARAMCD	HSTQMI	Daily Average - Average Flow	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='QMI'), AVALC = AVAL with 1 dp, AVALU = mL/s
ADSP	PARAMCD	HSTQCI	Daily Average - Peak Flow Qci	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='QCI'), AVALC = AVAL with 1 dp, AVALU = mL/s
ADSP	PARAMCD	HSTII	Daily Average - Inter Puff Interval	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='II'), AVALC = AVAL with 1 dp, AVALU = s
ADSP	PARAMCD	HSTDFI	Daily Average - Sum of Ii and Di	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='DFI'), AVALC = AVAL with 1 dp, AVALU = s
ADSP	PARAMCD	HSTWI	Daily Average - Work	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='WI'), AVALC = AVAL with 1 dp, AVALU = mJ
ADSP	PARAMCD	HSTPMI	Daily Average - Average Pressure Drop	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='PMI'), AVALC = AVAL with 1 dp, AVALU = mm wg
ADSP	PARAMCD	HSTPCI	Daily Average - Peak Pressure Drop	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='PCI'), AVALC = AVAL with 1 dp, AVALU = mm wg
ADSP	PARAMCD	HSTRMI	Daily Average - Average Resistance	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='RMI'), AVALC = AVAL with 1 dp, AVALU = mm wg/mL/s
ADSP	PARAMCD	HSTRCI	Daily Average - Peak Resistance	<UK>	<UK>		Derived	AVAL = the average of (AVAL where PARAMCD='RCI'), AVALC = AVAL with 1 dp, AVALU = mm wg/mL/s
ADVS	PARAMCD	SUSYSBP	SUPINE SYSTOLIC BLOOD PRESSURE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	SUDIABP	SUPINE DIASTOLIC BLOOD PRESSURE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	SUPULSE	SUPINE PULSE RATE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	SURESP	SUPINE RESPIRATORY RATE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	INTP	INTERPRETATION OF EXAMINATION	<UK>	<UK>		Derived	If VS.VSSTRESC = "NORMAL" and VS.VSTESTCD = "INTP" then AVALC is set equal to "Normal". Else if VS.VSSTRESC = "ABNORMAL CLINICALLY NOT RELEVANT" and VS.VSTESTCD = "INTP" then AVALC is set equal to "Abnormal, CNR". Else, if VS.VSSTRESC = "ABNORMAL CLINICALLY RELEVANT" and VS.VSTESTCD = "INTP" then AVALC is set equal to "Abnormal, CR".
ADVS	PARAMCD	HEIGHT	HEIGHT	<UK>	<UK>		SDTM	
ADVS	PARAMCD	WEIGHT	WEIGHT	<UK>	<UK>		SDTM	
ADVS	PARAMCD	BMI	BODY MASS INDEX	<UK>	<UK>		SDTM	if VSTESTCD='BMI' then do; If 0 < VSSTRESN < 18.5 then AVALCAT1 = "Underweight", If 18.5 <= VSSTRESN < 25 then AVALCAT1 = "Normal weight", If 25 <= VSSTRESN < 30 then AVALCAT1 = "Overweight", If VSSTRESN >= 30 then AVALCAT1 = "Obese"; end;
ADVS	PARAMCD	DBMI	BODY MASS INDEX (Derived)	<UK>	<UK>		SDTM	Derive as VSSTRESN where VSTESTCD=WEIGHT / ((VSSTRESN where VSTESTCD=HEIGHT/100)**2). If 0 < VSSTRESN < 18.5 then AVALCAT1 = "Underweight", If 18.5 <= VSSTRESN < 25 then AVALCAT1 = "Normal weight", If 25 <= VSSTRESN < 30 then AVALCAT1 = "Overweight", If VSSTRESN >= 30 then AVALCAT1 = "Obese";
ADVS	PARAMCD	INTPCM	COMMENT	<UK>	<UK>		SDTM	
ADVS	PARAMCD	SISYSBP	SITTING SYSTOLIC BLOOD PRESSURE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	SIDIABP	SITTING DIASTOLIC BLOOD PRESSURE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	SIPULSE	SITTING PULSE RATE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	SIRESP	SITTING RESPIRATORY RATE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	STSYSBP	STANDING SYSTOLIC BLOOD PRESSURE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	STDIABP	STANDING DIASTOLIC BLOOD PRESSURE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	STPULSE	STANDING PULSE RATE	<UK>	<UK>		SDTM	
ADVS	PARAMCD	STRESP	STANDING RESPIRATORY RATE	<UK>	<UK>		SDTM	

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADVS	PARAMCD	VSALL	All Vital Signs	<UK>	<UK>		SDTM	
ADVS	PARAMCD	SUVSALL	All Supine Vital Signs	<UK>	<UK>		SDTM	
ADVS	PARAMCD	SIVSALL	All Sitting Vital Signs	<UK>	<UK>		SDTM	
ADVS	PARAMCD	STVSALL	All Standing Vital Signs	<UK>	<UK>		SDTM	
ADVS	PARAMN	SUSYSBP		1	<UK>	<UK>	SDTM	
ADVS	PARAMN	SUDIABP		2	<UK>	<UK>	SDTM	
ADVS	PARAMN	SUPULSE		3	<UK>	<UK>	SDTM	
ADVS	PARAMN	SURESP		4	<UK>	<UK>	SDTM	
ADVS	PARAMN	INTP		13	<UK>	<UK>	Derived	
ADVS	PARAMN	HEIGHT		14	<UK>	<UK>	SDTM	
ADVS	PARAMN	WEIGHT		15	<UK>	<UK>	SDTM	
ADVS	PARAMN	BMI		16	<UK>	<UK>	SDTM	
ADVS	PARAMN	DBMI		22	<UK>	<UK>	SDTM	
ADVS	PARAMN	INTPCM		17	<UK>	<UK>	SDTM	
ADVS	PARAMN	SISYSBP		5	<UK>	<UK>	SDTM	
ADVS	PARAMN	SIDIABP		6	<UK>	<UK>	SDTM	
ADVS	PARAMN	SIPULSE		7	<UK>	<UK>	SDTM	
ADVS	PARAMN	SIRESP		8	<UK>	<UK>	SDTM	
ADVS	PARAMN	STSYSBP		9	<UK>	<UK>	SDTM	
ADVS	PARAMN	STDIABP		10	<UK>	<UK>	SDTM	
ADVS	PARAMN	STPULSE		11	<UK>	<UK>	SDTM	
ADVS	PARAMN	STRESP		12	<UK>	<UK>	SDTM	
ADVS	PARAMN	SYSBP		18	<UK>	<UK>	SDTM	
ADVS	PARAMN	DIABP		19	<UK>	<UK>	SDTM	
ADVS	PARAMN	PULSE		20	<UK>	<UK>	SDTM	
ADVS	PARAMN	VSALL		21	<UK>	<UK>	SDTM	
ADVS	PARAMN	SUVSALL		23	<UK>	<UK>	SDTM	
ADVS	PARAMN	SIVSALL		24	<UK>	<UK>	SDTM	
ADVS	PARAMN	STVSALL		25	<UK>	<UK>	SDTM	
ADXP	PARAMCD	FEVMEAS	Best measured FEV1 value	<UK>	<UK>		SDTM	
ADXP	PARAMCD	FVCMEAS	Best measured FVC value	<UK>	<UK>		SDTM	
ADXP	PARAMCD	WBRONCHO	Name of bronchodilator (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	WDOSE	Dose (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	FEVFVC	Calculated ratio between FEV1/FVC	<UK>	<UK>		SDTM	
ADXP	PARAMCD	FEVPCT	Percent of predicted FEV1 value	<UK>	<UK>		SDTM	
ADXP	PARAMCD	FVCPCT	Percent of predicted FVC value	<UK>	<UK>		SDTM	
ADXP	PARAMCD	FEVPRED	Predicted FEV1 value	<UK>	<UK>		SDTM	
ADXP	PARAMCD	FVCPRED	Predicted FVC value	<UK>	<UK>		SDTM	
ADXP	PARAMCD	INTP	Interpretation	<UK>	<UK>		SDTM	
ADXP	PARAMCD	DFEVFVC	Ratio between FEV1/FVC (Derived)	<UK>	<UK>		Derived	If PARAMN=FEVFVC and XPSTRESN is missing then AVAL=round (XPSTRESN where XPTESTCD="FEV1MEAS")/(XPSTRESN where XPTESTCD="FVCMEAS"),0.01). AVALC=put(AVAL,5,2). PARAMTYP=DERIVED, DTYPE=RATIO, AVALU=RATIO
ADXP	PARAMCD	WFEVMEAS	Best measured FEV1 value (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	WFVCMESAS	Best measured FVC value (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	WFEVFVC	Calculated ratio between FEV1/FVC (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	WFEVPCT	Percent of predicted FEV1 value (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	WFVCPCT	Percent of predicted FVC value (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	WFEVPRED	Predicted FEV1 value (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	WFVCPRED	Predicted FVC value (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	WINTP	Interpretation (with bronchodilator)	<UK>	<UK>		SDTM	
ADXP	PARAMCD	XPALL	All Spirometry examinations	<UK>	<UK>		SDTM	
ADXP	PARAMN	WFEVMEAS		6	<UK>	<UK>	Derived	
ADXP	PARAMN	WFVCMESAS		4	<UK>	<UK>	Derived	
ADXP	PARAMN	WBRONCHO		1	<UK>	<UK>	Derived	
ADXP	PARAMN	WDOSE		2	<UK>	<UK>	Derived	
ADXP	PARAMN	WFEVFVC		9	<UK>	<UK>	Derived	

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADXP	PARAMN	WFEVPCT		8	<UK>	<UK>	Derived	
ADXP	PARAMN	WFVCPCT		5	<UK>	<UK>	Derived	
ADXP	PARAMN	WFEVPRED		7	<UK>	<UK>	Derived	
ADXP	PARAMN	WFVCPRED		3	<UK>	<UK>	Derived	
ADXP	PARAMN	WINTP		10	<UK>	<UK>	Derived	
ADXP	PARAMN	FEVMEAS		15	<UK>	<UK>	Derived	
ADXP	PARAMN	FVCMEAS		13	<UK>	<UK>	Derived	
ADXP	PARAMN	FEVFVC		18	<UK>	<UK>	Derived	
ADXP	PARAMN	FEVPCT		17	<UK>	<UK>	Derived	
ADXP	PARAMN	FVCPCT		14	<UK>	<UK>	Derived	
ADXP	PARAMN	FEVPRED		16	<UK>	<UK>	Derived	
ADXP	PARAMN	FVCPRED		12	<UK>	<UK>	Derived	
ADXP	PARAMN	DFEVFVC		20	<UK>	<UK>	Derived	
ADXP	PARAMN	INTP		19	<UK>	<UK>	Derived	
ADXP	PARAMN	XPALL		30	<UK>	<UK>	Derived	
ADDV	PARAMCD	MISRND	Being administered the wrong product according to the randomization schedule.				Derived	PARAMCD = 1
ADDV	PARAMCD	PCOMP	Use of any nicotine or tobacco-containing product other than the assigned product. Exhaled CO breath test >10 ppm for subjects from the SA arm				Derived	PARAMCD = 2
ADDV	PARAMCD	VIOLATN	Violation of inclusion/exclusion criteria.				Derived	PARAMCD = 3
ADDV	PARAMCD	URDUR	Start and end times not within the 30 min window.				Derived	PARAMCD = 4
ADDV	PARAMCD	CONMED	Use of drugs which are known to affect CYP2A6 activity.				Derived	PARAMCD=5
ADDV	PARAMCD	TDQS	Assessments not taken at the correct time or within the allowed time window				Derived	PARAMCD=6
ADDV	PARAMCD	TDBLOOD	Assessments not taken at the correct time or within the allowed time window				Derived	PARAMCD=7
ADDV	PARAMCD	TD CYP1A	Assessments not taken at the correct time or within the allowed time window				Derived	PARAMCD=8
ADDV	PARAMCD	TD CYP2A	Assessments not taken at the correct time or within the allowed time window				Derived	PARAMCD=9
ADDV	PARAMCD	TD COUGH	Assessments not taken at the correct time or within the allowed time window				Derived	PARAMCD=10
ADDV	PARAMCD	TD COBT	Assessments not taken at the correct time or within the allowed time window				Derived	PARAMCD=11
ADDV	PARAMCD	TDHST	Assessments not taken at the correct time or within the allowed time window				Derived	PARAMCD=12
ADDV	PARAMCD	TIMEMISS	Assessment date or time is missing				Derived	PARAMCD=13
ADDV	PARAMCD	ASSMISS	Assessment is missing				Derived	PARAMCD=14
ADDV	PARAMCD	VISMISS	Scheduled visit not done				Derived	PARAMCD=15
ADXT	PARAMCD	NPC	Total number of puffs				Derived	PARAMN=1
ADXT	PARAMCD	TVOL	Total puff volume (mL)				Derived	PARAMN=2
ADXT	PARAMCD	AVGVI	Average puff volume (mL)				Derived	PARAMN=3
ADXT	PARAMCD	AVGDI	Average puff duration (s)				Derived	PARAMN=4
ADXT	PARAMCD	TDI	Total puff duration (s)				Derived	PARAMN=5
ADXT	PARAMCD	AVGOMI	Average flow (mL/s)				Derived	PARAMN=6
ADXT	PARAMCD	AVGQCI	Average Peak flow (mL/s)				Derived	PARAMN=7
ADXT	PARAMCD	TII	Total inter puff interval (s)				Derived	PARAMN=8
ADXT	PARAMCD	AVGLI	Average inter puff interval (s)				Derived	PARAMN=9
ADXT	PARAMCD	TDFI	Total smoking duration (s)				Derived	PARAMN=10
ADXT	PARAMCD	TWI	Total Work (mJ)				Derived	PARAMN=11
ADXT	PARAMCD	AVGWI	Average Work (mJ)				Derived	PARAMN=12
ADXT	PARAMCD	AVGPMI	Average pressure drop (mmWg)				Derived	PARAMN=13
ADXT	PARAMCD	AVGPCI	Average Peak pressure drop (mmWg)				Derived	PARAMN=14
ADXT	PARAMCD	SMINT	Smoking Intensity (mL/s)				Derived	PARAMN=15
ADXT	PARAMCD	PTI	Puffing Time Index (%)				Derived	PARAMN=16

## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADXT	PARAMCD	PFEQ	Puff Frequency (puffs/min)				Derived	PARAMN=17
ADXT	PARAMCD	NI	Puff Number				SDTM	PARAMN=18
ADXT	PARAMCD	VI	Puff volume (mL)				SDTM	PARAMN=19
ADXT	PARAMCD	DI	Puff Duration (S)				SDTM	PARAMN=20
ADXT	PARAMCD	QMI	Average Flow [Vi/Di] (mL/s)				SDTM	PARAMN=21
ADXT	PARAMCD	QCI	Peak Flow (mL/s)				SDTM	PARAMN=22
ADXT	PARAMCD	II	Inter Puff Interval (S)				SDTM	PARAMN=23
ADXT	PARAMCD	DFI	Sum of Ii and Di (S)				SDTM	PARAMN=24
ADXT	PARAMCD	WI	Work [INT Pmi*FinalFlow*dt] (mJ)				SDTM	PARAMN=25
ADXT	PARAMCD	PMI	Average Pressure Drop (mmWG)				SDTM	PARAMN=26
ADXT	PARAMCD	PCI	Peak Pressure Drop (mmWG)				SDTM	PARAMN=27
ADXT	PARAMCD	RMI	Average Resistance [Pmi/Qmi] (mmWG/mL/s)				SDTM	PARAMN=28
ADXT	PARAMCD	RCI	Peak Resistance [Pci/Qci] (mmWG/mL/s)				SDTM	PARAMN=29
ADXT	PARAMCD	PN	Number of Interpuffs Peaks				SDTM	PARAMN=30
ADXT	PARAMCD	POSQCI	Position of the peak flow in the puff (%)				SDTM	PARAMN=31
ADXT	PARAMCD	SPI	Total Pressure Drop (mmWG)				SDTM	PARAMN=32
ADXT	PARAMCD	FNICOF	Analysis Full Filter Nicotine Amount per filter (mg/filter)				SDTM	PARAMN=33
ADXT	PARAMCD	FNICO	Analysis Full Filter Nicotine Amount per mL (mg/mL)				SDTM	PARAMN=34
ADXT	PARAMCD	FABUVTAB	Analysis Full Filter Absolute UV TAR Absorbance				SDTM	PARAMN=35
ADXT	PARAMCD	FNMUVABS	Analysis Full Filter Normalized UV Absorbance (per filter)				SDTM	PARAMN=36
ADXT	PARAMCD	MNICOF	Analysis Mouthpiece Nicotine Amount per filter (mg/filter)				SDTM	PARAMN=37
ADXT	PARAMCD	MNICO	Analysis Mouthpiece Nicotine Amount per mL (mg/mL)				SDTM	PARAMN=38
ADXT	PARAMCD	MABUVTAB	Analysis Mouthpiece Absolute UV TAR Absorbance				SDTM	PARAMN=39
ADXT	PARAMCD	MNMUVABS	Analysis Mouthpiece Normalized UV Absorbance (per filter)				SDTM	PARAMN=40
ADXT	PARAMCD	PNICOF	Analysis PLA + Hat Nicotine Amount per filter (mg/filter)				SDTM	PARAMN=41
ADXT	PARAMCD	PNICO	Analysis PLA + Hat Nicotine Amount per mL (mg/mL)				SDTM	PARAMN=42
ADXT	PARAMCD	PABUVTAB	Analysis PLA + Hat Absolute UV TAR Absorbance				SDTM	PARAMN=43
ADXT	PARAMCD	PNMUVABS	Analysis PLA + Hat Normalized UV Absorbance (per filter)				SDTM	PARAMN=44
ADXT	PARAMCD	DILU_VOL	Dilution Volume (mL)				SDTM	PARAMN=45
ADXT	PARAMCD	EXTR_VOL	Extraction Volume (mL)				SDTM	PARAMN=46
ADXT	PARAMCD	SMP_L_VOL	Sample Volume (mL)				SDTM	PARAMN=47
ADXT	PARAMCD	TOTL_VOL	Total Volume (mL)				SDTM	PARAMN=48
ADXT	PARAMCD	VITP_L	Visual Inspection (Level)				SDTM	PARAMN=49
ADXT	PARAMCD	ANPC	Total number of puffs (average over visit)				Derived	PARAMN=50
ADXT	PARAMCD	ATVOL	Total puff volume (mL) (average over visit)				Derived	PARAMN=51
ADXT	PARAMCD	AAVGVI	Average puff volume (mL) (average over visit)				Derived	PARAMN=52
ADXT	PARAMCD	AAVGDI	Average puff duration (s) (average over visit)				Derived	PARAMN=53
ADXT	PARAMCD	ATDI	Total puff duration (s) (average over visit)				Derived	PARAMN=54
ADXT	PARAMCD	AAVGQMI	Average flow (mL/s) (average over visit)				Derived	PARAMN=55
ADXT	PARAMCD	AAVGQCI	Average Peak flow (mL/s) (average over visit)				Derived	PARAMN=56
ADXT	PARAMCD	ATII	Total inter puff interval (s) (average over visit)				Derived	PARAMN=57
ADXT	PARAMCD	AAVGII	Average inter puff interval (s) (average over visit)				Derived	PARAMN=58
ADXT	PARAMCD	ATDFI	Total smoking duration (s) (average over visit)				Derived	PARAMN=59
ADXT	PARAMCD	ATWI	Total Work (mJ) (average over visit)				Derived	PARAMN=60
ADXT	PARAMCD	AAVGWI	Average Work (mJ) (average over visit)				Derived	PARAMN=61
ADXT	PARAMCD	AAVGPMI	Average pressure drop (mmWg) (average over visit)				Derived	PARAMN=62



## ValueLevelMetadata

Dataset	Variable	Value	Label	Type	Length	Controlled Terms or Format	Origin	Comment
ADXT	PARAMCD	AAVGPCI	Average Peak pressure drop (mmHg) (average over visit)				Derived	PARAMN=63
ADXT	PARAMCD	ASMINT	Smoking Intensity (mL/s) (average over visit)				Derived	PARAMN=64
ADXT	PARAMCD	APTI	Puffing Time Index (%) (average over visit)				Derived	PARAMN=65
ADXT	PARAMCD	APFEQ	Puff Frequency (puffs/min) (average over visit)				Derived	PARAMN=66
ADXT	PARAMCD	TFNICOF	Analysis Full Filter Nicotine Amount per filter (mg/filter) (total over visit)				Derived	PARAMN=67
ADXT	PARAMCD	TFNICO	Analysis Full Filter Nicotine Amount per mL (mg/mL) (total over visit)				Derived	PARAMN=68
ADXT	PARAMCD	TFABUVTA	Analysis Full Filter Absolute UV TAR Absorbance (total over visit)				Derived	PARAMN=69
ADXT	PARAMCD	TFNMUVAB	Analysis Full Filter Normalized UV Absorbance (per filter) (total over visit)				Derived	PARAMN=70
ADXT	PARAMCD	TMNICOF	Analysis Mouthpiece Nicotine Amount per filter (mg/filter) (total over visit)				Derived	PARAMN=71
ADXT	PARAMCD	TMNICO	Analysis Mouthpiece Nicotine Amount per mL (mg/mL) (total over visit)				Derived	PARAMN=72
ADXT	PARAMCD	TMABUVTA	Analysis Mouthpiece Absolute UV TAR Absorbance (total over visit)				Derived	PARAMN=73
ADXT	PARAMCD	TMNMUVAB	Analysis Mouthpiece Normalized UV Absorbance (per filter) (total over visit)				Derived	PARAMN=74
ADXT	PARAMCD	TPNICOF	Analysis PLA + Hat Nicotine Amount per filter (mg/filter) (total over visit)				Derived	PARAMN=75
ADXT	PARAMCD	TPNICO	Analysis PLA + Hat Nicotine Amount per mL (mg/mL) (total over visit)				Derived	PARAMN=76
ADXT	PARAMCD	TPABUVTA	Analysis PLA + Hat Absolute UV TAR Absorbance (total over visit)				Derived	PARAMN=77
ADXT	PARAMCD	TPNMUVAB	Analysis PLA + Hat Normalized UV Absorbance (per filter) (total over visit)				Derived	PARAMN=78
ADXT	PARAMCD	HSTALL	All HST Tests				SDTM	PARAMN=99