Blood biomarkers

BRHS 30 year follow-up (Q30)

2010 – 2012

Fasting blood samples

At the 30 year follow-up physical examination in 2010-2012 (Q30), the BRHS study participants were asked to fast for a minimum of 6 hours, during which they were instructed to drink only water and to attend for measurement at a prespecified time between 0800 and 1800 h.

All men were asked to provide a blood sample, collected using the BD Vacutainer system. The filled tubes were gently agitated and placed in a rack. Serum gel tubes stood for a minimum of 30 minutes before being centrifuged on site to preserve the sample during transit. The blood collection tubes were delivered overnight from the examination centres to the Department of Chemical Pathology at the Royal Free Hospital in London. Plasma samples were centrifuged and both plasma and serum gel samples were aliquoted and then frozen for longer term storage at −70°C.

The blood sampling procedure is described in section 4.6 of the Physical examination protocol (BRHS 2010-12 (Q30) 30yr follow-up Physical examination protocol.pdf).

The handling of the blood specimens is described in Appendix C of the physical examination protocol (BRHS 2010-12 (Q30) 30yr follow-up Physical examination protocol.pdf).

Blood marker adjustments

* Adjusted blood markers: A number of blood markers (Glucose, insulin, triglycerides, LDL, HDL, cholesterol, HbA1c) were adjusted for examination time and fasting duration (using the time the BRHS participants reported as having something to eat or drink other than water) which was recorded on the physical examination data collection form**.** These blood markers are available both in unadjusted and adjusted form. The methods for adjustments used are the same as those described in Emberson et al[1] which were used for the 20-year follow-up examination blood markers. Additional notes are in BRHS Q30 Blood marker Adjustment Report by C Sartini 2014 (Appendix 1)[2].

1. *Emberson J,Whincup PH, Walker M , Thomas M,Alberti KGMM. Biochemical measures in a population-based study: effect of fasting duration and time of day. Ann Clin Biochem 2002; 39: 493- 501* and

2. BRHS Q30 Blood marker Adjustment Report by C Sartini 2014 (Appendix A)

Blood biomarkers

A list of all available BHRS bloods biomarkers for 2010-2012(Q30) can be found in the table below followed by the laboratory methods in methodological summaries used for each blood marker where available (section 1).

A double star (**) against a blood marker indicates that the blood marker has been adjusted for examination/sample time and fasting duration. The corresponding unadjusted(raw data) variable is indicated with a single star (*).

Blood biomarkers - BRHS 30 year follow-up (Q30) 2010-12

Blood marker (Q30 2010-12)	Units	Methods section	BRHS variable name	Mean	SD	Min	Max	N	N Miss	Data access
Adiponectin	ug/ml	B.38	q30adiponectin	9.05	6.23	0.42	30.00	1603	119	yes
Albumin	g/l	B.8	q30alb	44.81	2.47	35.00	54.00	1638	84	yes
Alanine Aminotransferase (ALT)	u/l	B.12	q30alt	20.36	9.81	4.00	178.00	1635	87	yes
Alkaline Phosphatase (ALP)?	mmol/l	B.10	q30aphos	73.59	28.57	12.00	564.00	1638	84	yes
Aspartame Transaminase (AST)	u/l	B.11	q30ast	23.65	7.77	5.00	110.00	1630	92	yes
Basophils Absolute Value		B.23	q30baso_abs	0.03	0.02	0.00	0.30	1590	132	yes
Calcium	mmol/L	B.1	q30calc	2.29	0.09	2.00	2.78	1638	84	yes
Corrected Calcium			q30ccalc	2.19	0.09	1.92	2.72	1638	84	yes
CHDR (Cholesterol/HDL ratio)	ratio		q30chdr	3.38	1.04	1.10	8.40	1638	84	yes
*Cholesterol (raw/unadjusted)	mmol/l	B.13	q30chol	4.63	1.03	2.20	8.50	1638	84	yes
** Cholesterol (adjusted)	mmol/l		q30chol_adj	4.63	1.03	2.20	8.50	1638	84	yes
Carboxymethyl lysine (CML)	uM	B.40	q30cml	2.72	1.38	0.23	16.76	1553	169	yes
Lysine Percentage of lysine that is glycated (CML to Lysine ratio)	ratio	B.40	q30cml_per_lys	0.07	0.03	0.02	0.43	1553	169	yes
Creatinine	µ mol/l	B.7/B.6	q30creat	98.61	28.79	50.00	365.00	1636	86	yes
C-Reactive protein (CRP)	mg/L	B.26	q30crp	3.19	9.51	0.05	239.84	1601	121	yes
Cystatin C	mg/L	B.32	q30cystatinc	1.06	0.37	0.20	3.59	1604	118	yes
D-dimer	ng/ml	B.27	q30ddimer	303.59	302.27	25.00	2000.00	1610	112	yes
eGFR [q30egfr=32788 x q30creat $^{(-1.154)}$ x q30xage$^{(-0.203)}$]		B.41	q30egfr	72.71	18.10	14.91	146.01	1636	86	yes
Eosinophils Absolute Value	10^9 /l	B.23	q30eosin_abs	0.18	0.14	0.00	1.35	1590	132	yes
Gamma-Glutamyl transferase (gamma-GT, GGT)	u/l	B.20	q30ggt	32.51	35.93	6.00	420.00	1636	86	yes
*Glucose (raw/unadjusted)	mmol/l	B.21	q30gluc	5.79	1.74	3.20	24.50	1536	186	yes
**Glucose (adjusted)	mmol/l	B.21	q30gluc_adj	5.77	1.58	2.75	22.15	1536	186	yes
Haemoglobin(hb)	g/l	B.23	q30hb	14.13	1.36	8.10	18.20	1610	112	yes
*Glycated Haemoglobin (HbA1c) (raw/unadjusted)	%	B.22	q30hba1c	5.85	0.68	3.70	11.50	1597	125	yes
** Glycated Haemoglobin (HbA1c) (adjusted)	%	B.22	q30hba1c_adj	5.85	0.67	3.71	12.35	1597	125	yes
Haematocrit	l/l	B.23	q30hct	0.43	0.04	0.27	0.56	1610	112	yes
*HDL High Density Lipoprotein cholesterol (raw/unadjusted)	mmol/l	B.15	q30hdlc	1.45	0.42	0.50	4.50	1638	84	yes
** HDL High Density Lipoprotein cholesterol (adjusted)	mmol/l	B.15	q30hdlc_adj	1.45	0.42	0.47	4.48	1638	84	yes

* Raw data. Not adjusted

** Adjusted for fasting duration

Blood marker (Q30 2010-12) (cont. 1)	Units	Methods section	BRHS variable name	Mean	SD	Min	Max	N	N Miss	Data access
High-Sensitivity Troponin T (hs cTnT) - pg/ml or ng/L equivalent	pg/ml	B.35	q30hstnt	14.51	16.08	1.50	407.10	1603	119	yes
Insulin-like growth factor 1 (IGF-1)	ng/ml	B.31	q30igf_1	75.81	24.00	16.43	200.25	1604	118	yes
Interleukin-6 (IL-6)	pg/ml	B.28	q30il6	4.32	4.61	0.15	30.00	1618	104	yes
*Insulin (raw/unadjusted)	mU/L	B.24	q30rawinsulin	10.30	10.58	0.33	136.88	1619	103	yes
** Insulin (adjusted)	mU/L	B.24	q30insulin_adj	10.35	9.37	0.36	110.99	1612	110	yes
*LDL Low Density Lipoprotein Cholesterol (direct) (raw/unadjusted)	mmol/l	B.16	q30ldlc	2.60	0.94	0.30	6.40	1632	90	yes
** LDL Low Density Lipoprotein Cholesterol (direct) (adjusted)	mmol/l	B.16	q30ldlc_adj	2.60	0.93	0.31	6.53	1632	90	yes
Leptin	ng/ml	B.39	q30leptin	9.93	10.08	0.41	130.58	1603	119	yes
Lymphocytes Absolute Value	10^9 /l	B.23	q30lymph_abs	1.79	2.46	0.31	71.74	1590	132	yes
Lysine concentration	uM	B.40	q30lys	39186.1	6731.5	8343.7	58231.3	1565	157	yes
Magnesium (Mg)	mmol/L	B.18	q30magn	0.82	0.07	0.44	1.14	1637	85	yes
Mean Cell Haemoglobin (MCH)	pg	B.23	q30mch	30.67	1.72	21.70	38.50	1610	112	yes
Mean Cell Haemoglobin Concentration (MCHC)	g/dl	B.23	q30mchc	32.50	1.43	26.40	36.20	1610	112	yes
Mean Cell volume (MCV)	fl	B.23	q30mcv	94.48	5.83	77.10	130.80	1610	112	yes
Monocytes Absolute Value	10^9 /l	B.23	q30monocy_abs	0.59	0.21	0.00	2.19	1590	132	yes
Mean Platelet volume (MPV)	fl	B.23	q30mpv	11.28	0.97	8.70	14.90	1605	117	yes
Neutrophils Absolute Value	10^9 /l	B.23	q30neutro_abs	4.30	1.46	0.44	13.18	1590	132	yes
NT-proBNP (units: pg/ml or ng/L equivalent)	pg/ml	B.34	q30ntprobnp	393.9	946.0	2.5	15899.0	1603	119	yes
Phosphate	mmol/l	B.2	q30phosph	1.09	0.16	0.47	3.30	1637	85	yes
Platelets	10^9 /l	B.23	q30plat	225.2	59.2	64.0	646.0	1608	114	yes
Potassium	mmol/l	B.5	q30potass	4.39	0.40	2.70	6.50	1628	94	yes
Proinsulin	pmol/L	B.36	q30proinsulin	18.2	20.3	1.8	132.0	1604	118	yes
Rage (sRage)	pg/ml	B.33	q30rage	1213.9	758.0	157.0	7411.0	1604	118	yes
Red blood cell count (RBC)	10^{12}/l	B.23	q30rbc	4.61	0.44	2.48	6.09	1610	112	yes
Red Blood Cell Distribution Width	%	B.33	q30rdw	14.12	1.21	11.60	28.90	1610	112	yes
Sodium	mmol/l	B.4	q30sodium	141.24	3.06	126.00	162.00	1637	85	yes
Total Bilirubin	µ mol/l	B.9	q30tbili	12.24	5.34	3.00	42.00	1634	88	yes
Tissue plasminogen activator(tPA)	ng/ml	B.29	q30tpa	10.05	5.43	1.50	50.00	1610	112	yes
Protein (Total Protein)	g/l	B.19	q30tprot	69.99	4.05	56.00	91.00	1638	84	yes

* Adjusted for fasting duration

** Raw data. Not adjusted

Blood marker (Q30 2010-12) (cont. 2)	**Units**	**Methods section**	**BRHS variable name**	**Mean**	**SD**	**Min**	**Max**	**N**	**N Miss**	**Data access**
**Triglycerides (raw/unadjusted)	mmol/l	B.14	q30trig	1.30	0.67	0.40	8.90	1638	84	yes
* Triglycerides (adjusted)	mmol/l	B.14	q30trig_adj	1.30	0.66	0.36	8.73	1638	84	yes
Urate	mmol/l	B.17	q30urat	0.36	0.08	0.12	0.77	1570	152	yes
Urea	mmol/l	B.3	q30urea	6.84	2.45	2.60	30.40	1638	84	yes
Vitamin D	ng/ml	B.37	q30vitd	22.36	13.18	1.50	70.00	1582	140	yes
Von Willebrand factor (VWF)	IU/dl	B.30	q30vwf	134.91	73.74	19.45	433.17	1610	112	yes
White blood cell count (WBC)	10^9 /l	B.23	q30wbc	6.91	3.09	1.99	87.49	1610	112	yes

* Adjusted for fasting duration

** Raw data. Not adjusted

1. Methodological Summaries

Routine Biochemistry

Measured at the Department of Clinical Biochemistry, Royal Free Hospital, London. (Prof Mike Thomas).

B.1 Calcium mmol/L
Principal: The method is based on a blanked colorimetric endpoint assay using o-cresolphthalein complexone which produces a purple coloured complex whose intensity is directly proportional to the calcium concentration.

Between batch Imprecision: <2%

Reference: Gindler EM & King JD. 1972 “Rapid colorimetric determination of calcium in biologic fluids with methythymol blue.” Am JClin Pathol 58: 376 - 382

B.2 Phosphate mmol/l
Principal: A colorimetric assay with endpoint determination and sample blanking. Inorganic phosphate forms an ammonium phosphomolybdate complex with ammonium molybdate in the presence of sulphuric acid. The complex is determined photometrically in the ultraviolet region (340 nm).

Between batch Imprecision: <2%

Reference: Weissman N, Pileggi VJ. 1974 “Inorganic anions.” In: Henry RJ, Cannon DC, Winkelman JW, eds. “Clinical chemistry: principles and techniques” 2nd ed. New York: Harper and Row:723 - 727

B.3 Urea mmol/l
Principal: A kinetic UV assay. Urea is enzymatically converted via urease to ammonium ions which are utilised by the enzyme glutamate dehydrogenase. This enzyme consumes NADH, the decrease of which is measured kinetically.

Between batch Imprecision: 3.4%

Reference: Kaplan, L.A., 1984. Urea. In: Clinical Chemistry; Theory, Analysis and Correlation, Kaplan, L.A. and A.J. Pesce (Eds.). CV Mosby Co., St. Louis, pp: 1257-1261.

B.4 Sodium mmol/l
Principal: Sodium is measured by an ion selective electrode. A membrane composed of crown ether with a neutral PVC carrier forms a selective membrane for sodium ions, creating an electrical potential as sodium ions traverse the membrane. The electrical potential can be compared to a reference electrode to determine the sodium ion concentration.

Between batch Imprecision: <2%

Reference: GB Levy,. 1981. “Determination of Sodium with Ion-Selective Electrodes.” Clin Chem. 27: 1435-1438.

B.5 Potassium mmol/l
Principal: Potassium is measured by an ion selective electrode. A selective membrane composed of valinomycin creates an electrical potential as only potassium ions traverse the membrane. The electrical potential can be compared to a reference electrode to determine the potassium ion concentration.
Between batch Imprecision: <2%

Reference: Fiedler U, Růžička J. 1973. “Selectrode—the universal ion-selective electrode: Part VII. A valinomycin-based potassium electrode with nonporous polymer membrane and solid-state inner reference system”. Analytica Chimica Acta. 67: 179-193.

B.6 Creatinine - Jaffe μ mol/l
Principal: Rate blanked kinetic assay. Creatinine reacts with picric acid in alkaline conditions to produce an orange-red product which can be measured photometrically. The rate blank step is introduced to minimise interferences from bilirubin. A negative factor of -26 µmol/L is applied to reduce non specific interferences.

Between batch Imprecision: 2.3%

Reference: Peake M, Whiting M. 2006. “Measurement of Serum Creatinine – Current Status and Future Goals” Clin Biochem Rev. 27: 173-184.

B.7 Creatinine - Enymatic μ mol/l
Principal: Enzymatic colorimetric assay. Creatinine is converted via a series of enzymes to hydrogen peroxide, which can be measured spectrophotometrically at 546nm following a modified Trinder reaction with absorbance blanking at 700nm.

Between batch Imprecision: 2.1%

Reference: Peake M, Whiting M. 2006. “Measurement of Serum Creatinine – Current Status and Future Goals” Clin Biochem Rev. 27: 173-184.

B.8 Albumin g/l
Principal: Endpoint colorimetric assay. In acidic conditions, albumin can bind bromocrescol green to produce a coloured complex, the intensity of which is directly proportionate to the concentration of albumin.

Between batch Imprecision: <2%

Reference: Hill PG, 1985. “The measurement of albumin in serum and plasma.” Ann Clin Biochem 22:565–78

B.9 Total Bilirubin μ mol/l
Principal: Colorimetric assay. Indirect/Unconjugated bilirubin is liberated following interaction with detergents. After this step, the bilirubin reacts with diazonium ions under strongly acidic conditions to produce azobilirubin, which can be measured spectrophotometrically.

Between batch Imprecision: <2%

Reference: Watson D, Rogers JA. 1961 “A study of six representative methods of plasma bilirubin analysis” J Clin Pathol. 14: 271-278.

B.10 Alkaline Phosphatase mmol/l
Principal: Enzymatic colorimetric assay. In the presence of zinc and magnesium, ALP is able to convert p-nitrophenyl phosphate into p-nitrolphenol, the concentration of which is measured spectrophotometrically and is proportionate to the concentration of ALP.

Between batch Imprecision: <2%

Reference: Bowers GN Jr, McComb RB. 1975 “Measurement of total alkaline phosphatase activity in human serum.” Clin Chem 21: 1988-1995.

B.11 Aspartate Transaminase (AST) u/l
Principal: Kinetic enzymatic assay. AST is able to produce oxaloacetate when L-aspartate and alpha-ketoglutarate are present. Oxaloacetate can then be utilised by malate dehydrogenase along with NADH and H+ to produce L-Malate and NAD+. The rate of consumption of NADH is measured spectrophotometrically and the decrease in absorbance is directly proportionate to the rate of production of oxaloacetate and therefore the AST concentration.

Between batch Imprecision: 3.2%

Reference: Bergmeyer HU, Horder M, Rej R. 1986 “Approved Recommendation (1985) on IFCC Methods for the Measurement of Catalytic Concentration of Enzymes” J. Clin. Chem. Clin. Biochem. 24: 497-510.

B.12 Alanine Aminotransferase (ALT) u/l
Principal: Kinetic enzymatic assay. ALT is able to form pyruvate and L-Glutamate from alpha-ketoglutarate and L-aspartate. Pyruvate can then be utilised with NADH and H+ by lactate dehydrogenase to produce L-Malate and NAD+. The rate of consumption of NADH can be measured spectrophotometrically and is proportionate to the concentration of ALT.

Between batch Imprecision: 3.2%

Reference: Bergmeyer HU, Horder M, Rej R. 1986 “Approved Recommendation (1985) on IFCC Methods for the Measurement of Catalytic Concentration of Enzymes” J. Clin. Chem. Clin. Biochem. 24: 481-495.

B.13 Cholesterol mmol/l
Principal: Enzymatic colorimetric assay. Cholesterol and cholesterol esters are converted via a series of enzymatic reactions to hydrogen peroxide which is then utilised to produce a red dye via a peroxidase enzyme. The colour intensity of the dye is directly proportionate to the concentration of cholesterol.

Between batch Imprecision: <2%

Reference: Deeg R, Ziegenhorn J. 1983 “Kinetic enzymic method for automated determination of total cholesterol in serum.” Clin Chem 29: 1798-1802.

B.14 Triglycerides mmol/l
Principal: Enzymatic colorimetric assay. Triglycerides are converted via a series of enzymatic reactions to produce hydrogen peroxide, which is then utilised in a Trinder endpoint reaction to form a red dye. The concentration of the dye is used to determine the concentration of triglyceride.

Between batch Imprecision: <2%

Reference: Wahlefeld, A. W. 1974. Triglycerides. Determination after enzymatic hydrolysis. In: “Methods of Enzymatic Analysis.” H. U. Bergmeyer, editor. Academic Press, New York, NY.

B.15 High Density Lipoprotein Cholesterol (HDL) mmol/l

Principal: Homogenous enzymatic colorimetric assay. A detergent containing a sugar compound in conjunction with magnesium is used to favour the conversion of HDL cholesterol esters to cholesterol over other sources of cholesterol such as LDL-cholesterol. This liberated HDL-cholesterol is further converted to hydrogen peroxide which can react with a dye via peroxidase to form a purple-blue pigment which can be detected spectrophotometrically. The concentration of the purple-blue pigment is directly proportionate to the concentration of HDL-Cholesterol.

Between batch Imprecision: <2%

Reference: Nauck M, März W, Jarausch J, Cobbaert C, Sägers A, Bernard D, Delanghe J, Honauer G, Lehmann P, Oestrich E, von Eckardstein A, Walch S, Wieland H, Assmann G. 1997 “Multicenter evaluation of a homogeneous assay for HDL-cholesterol without sample pretreatment.” Clin Chem. 43: 1622-1629.

B.16 Low Density Lipoprotein Cholesterol (direct) (LDL) mmol/l

Principal: Homogenous enzymatic colorimetric assay. A detergent containing a sugar compound in conjunction with magnesium is used to favour the conversion of LDL cholesterol esters to cholesterol over other sources of cholesterol such as HDL-cholesterol. This liberated LDL-cholesterol is further converted to hydrogen peroxide which can react with a dye via peroxidase to form a purple-blue pigment which can be detected spectrophotometrically. The concentration of the purple-blue pigment is directly proportionate to the concentration of LDL-Cholesterol.

Between batch Imprecision: <2%

Reference: Esteban-Salán M, Guimón-Bardesi A, de La Viuda-Unzueta JM, Azcarate-Ania MN, Pascual-Usandizaga P, Amoroto-Del-Río E. 2000 “Analytical and clinical evaluation of two homogeneous assays for LDL-cholesterol in hyperlipidemic patients.” Clin Chem 46:1121¬1131.

B.17 Urate mmol/l

Principal: Enzymatic colorimetric assay. Uric acid is converted via uricase to hydrogen peroxide which can react via a peroxidase to a quinone-diimine dye which can be measured spectrophotometrically. The concentration of the dye is proportionate to the urate concentration.

Between batch Imprecision: <2%

Reference: Zhao Y, Yang X, Lu W, Liao H, Liao F. 2009 “Uricase based methods for determination of uric acid in serum” Microchimica Acta 164: 1-6.

B.18 Magnesium mmol/L

Principal: Colorimetric endpoint assay. The sample is incubated with EGTA to minimise calcium interference and an alkaline buffer, after which xylidyl blue is added which will react with magnesium to produce a purple product. The decrease in absorbance at 600nm by xylidyl blue is measured and used to determine the magnesium concentration.

Between batch Imprecision: <2%

Reference: D. Stankov, T. Jovanović, M. Jelikić-Stankov. 1997 “Spectrophotometric Determination of Magnesium in Serum Using Xylidyl Blue Reagent in Micellar Medium” In: “Magnesium: Current Status and New Developments” p51-52. Kluwer Academic Publishers.

B.19 Total Protein g/l
Principal: Colorimetric assay. In alkaline conditions protein can complex with copper ions to produce a copper protein complex, the concentration of which is determined spectrophotometrically and is directly proportionate to the concentration of protein in the sample.

Between batch Imprecision: <2%

Reference: Savory J, Heintges MG, Sonowane M, Cross RE. 1976 "Measurement of total protein and albumin in serum with a centrifugal analyzer" Clin Chem. 22: 1102-1104.

B.20 Gamma-Glutamyltransferase (GGT) u/l
Principal: Enzymatic colorimetric assay. Following addition of substrate, GGT catalyses the conversion of reagent into 5-amino-2-nitrobenzoate which can be measured via spectrophotometry at 410nm.

Between batch Imprecision: <2%

Reference: Tietz, N.W., 1986. "Fundamentals of Clinical Chemistry", 3rd Edition, W.B. Saunders,

B.21 Glucose mmol/l
Principal: Enzymatic colorimetric method. Glucose is enzymatically converted into hydrogen peroxidase which can be utilised by a peroxidase enzyme to produce a red dye which is read via spectrophotometry at 505nm. The concentration of the dye is directly proportionate to the concentration of glucose in the sample.

Between batch Imprecision: 3.8%

Reference: Trinder P. 1969 "Determination of blood glucose using 4-amino phenazone as oxygen acceptor."

B.22 Glycated Haemoglobin (HbA1c) %

HbA1c was analysed using the TOSOH G11 analyser, method principle HPLC.

Routine Haematology markers

B.23 Routine Haematology markers

Routine haematology analyses were carried out at the Department of Haematology, Royal Free Hospital, London (Dr Chris McNamara)

Available haematology markers include:

	units
Haemoglobin	g/l
White Blood Cell Count	10^9 /l
Platelets Red Blood Cell Count	10^9 /l
Red blood cell count (RBC)	10^{12}/l
Red Blood Cell Distribution Width	%
Haematocrit	l/l
Mean Cell Volume (MCV)	fl
Mean Cell Hemoglobin (MCH)	pg
Mean Cell Hemoglobin Concentration (MCHC)	g/dl
Neutrophils Absolute Value	10^9 /l
Lymphocytes Absolute Value	10^9 /l
Monocytes Absolute Value	10^9 /l
Eosinophils Absolute Value	10^9 /l
Basophils Absolute Value	
Mean Platelet Volume (MPV)	fl

OTHER BLOOD MARKERS

B.24 Insulin mU/L

Measured at the Institute of Cellular Medicine, Newcastle University. (Prof Sally Marshall)

Serum insulin was measured using an enzyme-linked immunosorbent assay ELISA which does not cross-react with proinsulin.

B.26 C-Reactive protein (CRP) mg/L

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh) Measured using ultrasensitive assay on an automated analyser (Cobas c311, Roche Diagnostics, Burgess Hill, UK) with the manufacturers calibrators and quality controls.

	Limits of detection and assigned values			
	Lower limit[1]	Assigned value[1]	Upper limit[2]	Assigned value[2]
C-Reactive protein(CRP)	<0.1 mg/L	0.05	n/a	n/a

[1] A laboratory reported result of "< than the lower limit of detection" was assigned the value of ½ of the lowest limit of detection.

[2] A laboratory reported result of "> than the upper limit of detection" was assigned the value the upper limit of detection.

Laboratory notes: C reactive protein (CRP): There are a few outliers >200mg/L at upper end. These outliers are to be expected for CRP, and have been checked. *Paul Welsh*

B.27 D-dimer ng/ml

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using high-sensitivity enzyme-linked immunosorbent assay (ELISA) (Asserachrom , Stago, Theale, UK).

	Limits of detection and assigned values			
	Lower limit[1]	Assigned value[1]	Upper limit[2]	Assigned value[2]
D-dimer	<50 ng/ml	25	>200	200

[1] A laboratory reported result of "< than the lower limit of detection" was assigned the value of ½ of the lowest limit of detection.

[2] A laboratory reported result of "> than the upper limit of detection" was assigned the value the upper limit of detection.

B.28 Interleukin-6 (IL-6) pg/mL

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using a high-sensitivity enzyme-linked immunosorbent assays (ELISA) (R&D Systems, Abingdon, UK)

	Limits of detection and assigned values			
	Lower limit[1]	Assigned value[1]	Upper limit[2]	Assigned value[2]
Interleukin-6 (IL-6)	n/a	n/a	>30	30

[1] A laboratory reported result of "< than the lower limit of detection" was assigned the value of ½ of the lowest limit of detection.

[2] A laboratory reported result of "> than the upper limit of detection" was assigned the value the upper limit of detection.

B.29 Tissue plasminogen activator(tPA) ng/mL

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using high-sensitivity enzyme-linked immunosorbent assay (ELISA) (Asserachrom , Stago, Theale, UK).

	Limits of detection and assigned values			
	Lower limit[1]	Assigned value[1]	Upper limit[2]	Assigned value[2]
Tissue plasminogen activator(tPA)	<3 ng/ml	1.5	>50	50

[1] A laboratory reported result of "< than the lower limit of detection" was assigned the value of ½ of the lowest limit of detection.

[2] A laboratory reported result of "> than the upper limit of detection" was assigned the value the upper limit of detection.

B.30 Von Willebrand factor (VWF) IU/dL

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using high-sensitivity enzyme-linked immunosorbent assays (ELISA) (Technozym , Pathway Diagnostics, Dorking, UK)

B.31 Insulin-like growth factor 1 (IGF-1) ng/ml

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using an enzyme-linked immunosorbent assays (ELISA) R&D Systems, Abingdon, UK)

B.32 Cystatin C mg/L
Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using an automated analyser (Cobas c311, Roche Diagnostics, Burgess Hill, UK) with the manufacturers calibrators and quality controls.

B.33 Rage pg/ml
Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using an enzyme-linked immunosorbent assays (ELISA) (R&D Systems, Abingdon, UK)

Reference: Wannamethee SG, Welsh P, Papacosta O, Ellins EA, Halcox JPJ, Whincup PH, et al. Circulating soluble receptor for advanced glycation end product: Cross-sectional associations with cardiac markers and subclinical vascular disease in older men with and without diabetes. Atherosclerosis. 2017;264:36-43 Epub 2017/08/02

B.34 NT-proBNP ng/L or pg/ml (equivalent)
Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using an automated immunoassay analyser (Cobas e411, Roche Diagnostics, Burgess Hill, UK) with the manufacturers' calibrators and quality controls. The lower limit of sensitivity was 5 pg/ml

	Limits of detection and assigned values			
	Lower limit[1]	Assigned value[1]	Upper limit[2]	Assigned value[2]
NT - proBNP	< 5 pg/ml	2.5	n/a	n/a

[1] A laboratory reported result of "< than the lower limit of detection" was assigned the value of ½ of the lowest limit of detection.
[2] A laboratory reported result of "> than the upper limit of detection" was assigned the value the upper limit of detection.

Laboratory note:
NT-proBNP outlier checks

- NTproBNP values of 15899 and 12627 were confirmed to be correct (Dr Paul Welsh)

B.35 High-Sensitivity Troponin T (hsTnT) ng/L or pg/ml (equivalent)
Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using an automated immunoassay analyser (Cobas e411, Roche Diagnostics, Burgess Hill, UK) with the manufacturers' calibrators and quality controls. The lower limit of sensitivity was 3 pg/ml

	Limits of detection and assigned values			
	Lower limit[1]	Assigned value[1]	Upper limit[2]	Assigned value[2]
High sensitivity troponin T(hsTnT)	<3 pg/ml	1.5	n/a	n/a

[1] A laboratory reported result of "< than the lower limit of detection" was assigned the value of ½ of the lowest limit of detection.
[2] A laboratory reported result of "> than the upper limit of detection" was assigned the value the upper limit of detection.

Laboratory note:
hsTnT outlier checks:

- hsTnT value of 407.1 was confirmed to be true/correct value (Dr Paul Welsh)

B.36 Proinsulin pmol/L

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using an enzyme-linked immunosorbent assays (ELISA) (Mercodia, Diagenics Milton Keynes, UK)

	Limits of detection and assigned values			
	Lower limit[1]	Assigned value[1]	Upper limit[2]	Assigned value[2]
Proinsulin	<3.5 pmol/L	1.75	>132	132

[1] A laboratory reported result of "< than the lower limit of detection" was assigned the value of ½ of the lowest limit of detection.

[2] A laboratory reported result of "> than the upper limit of detection" was assigned the value the upper limit of detection.

B.37 Vitamin D ng/mL

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using an automated analyser (Cobas e411, Roche Diagnostics, Burgess Hill, UK) with the manufacturers calibrators and quality controls.

	Limits of detection and assigned values			
	Lower limit[1]	Assigned value[1]	Upper limit[2]	Assigned value[2]
Vitamin D	< 3 ng/ml	1.5	>70	70

[1] A laboratory reported result of "< than the lower limit of detection" was assigned the value of ½ of the lowest limit of detection.

[2] A laboratory reported result of "> than the upper limit of detection" was assigned the value the upper limit of detection.

Laboratory note: Values not measurable.
* 22 with insufficient blood have been set to MISSING value =.
* 38 were recorded as <3 ng/mL. These were assigned the value of 1/2 of 3 --> 1.5 ng/mL
* 9 were recorded as >70 ng/mL. These were assigned to the value of 70 ng/mL

B.38 Adiponectin ug/ml

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using an enzyme-linked immunosorbent assays (ELISA) (R&D Systems, Abingdon, UK)

	Limits of detection and assigned values			
	Lower limit[1]	Assigned value[1]	Upper limit[2]	Assigned value[2]
Adiponectin	n/a	n/a	>30 ug/ml	30

[1] A laboratory reported result of "< than the lower limit of detection" was assigned the value of ½ of the lowest limit of detection.

[2] A laboratory reported result of "> than the upper limit of detection" was assigned the value the upper limit of detection.

Laboratory note: Values Not measurable.
Adiponectin values recorded as ">30" were assigned the value of 30. There are 19 such values

B.39 Leptin ng/ml

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Measured using an enzyme-linked immunosorbent assays (ELISA) (R&D Systems, Abingdon, UK)

B.40 Carboxymethyl lysine (CML) uM, Lysine uM, CML to Lysine ratio

Measured at the University of Glasgow, Institute of Cardiovascular & Medical Sciences (Dr Paul Welsh)
Isotope dilution Mass spectrometry Chromatography was carried out on a Dionex UltiMate 3000 RSLC system (Thermo Fisher Scientific, Hemel Hempstead, UK)
https://journals.sagepub.com/doi/10.1177/0004563219830432

B.41 eGFR (estimated glomerular filtration rate)

The following formula was used to calculate eGFR:

$$\text{q30egfr} = 32788 \times \text{q30creat}^{(-1.154)} \times \text{q30xage}^{(-0.203)}$$

where q30creat **is creatinine** and q30xage is **age.**

Note: Above formula is equivalent to formula: $\text{eGFR}=\mathbf{186}*((\text{q30creat}/\mathbf{88.4})^{-1.154})\text{x}(\text{q30xage}^{-0.203})$

Biomarkers adjustments for fasting duration and time of appointment – Q30

Claudio Sartini – 27/06/2014

SUMMARY

The biomarkers we took in to account for possible adjustment are listed below

- Total cholesterol (Q30chol)
- HDL cholesterol (Q30hdlc)
- LDL cholesterol (Q30ldlc)
- Triglycerides (Q30trig)
- HBA (Q30hba1c)
- Glucose (Q30gluc)
- Insulin previously adjusted by batch (q30insulin_adj). See document "Analysis decision insulin.doc".

A data cleaning was necessary to adjust the hour of examination and time last eaten in a small number of cases. With Lucy Lennon we manually examined the data sheets and I corrected the incoherent information inside my do file.

```
doedit "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\READ Q30_5DEC13_Claudio.do"
```
(APPENDIX 1)

In cases where the subjects reported the day of last eaten (today/yesterday), but gave no actual time, the fasting time was calculated as the median fasting time of the population for the specific hour of examination the subject reported and day last eaten.
A cut off point of 6 hours was used to define a successful faster from a non-successful faster, precisely the categories are <6 and 6+
A fasting time >20 hours was recoded as equal to 20 hours, for transformation purposes and because of the small number of subjects having fasting time >20 hours.

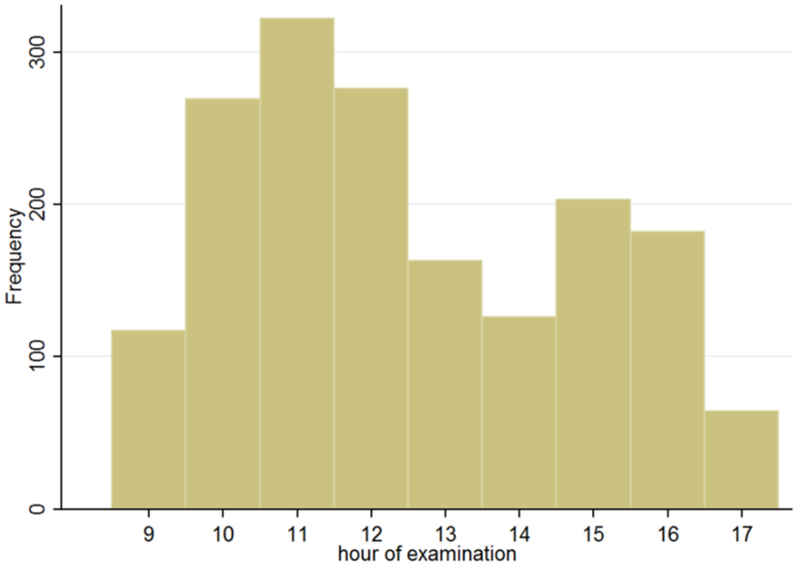
I redefined diabetes status following Peter's comment:

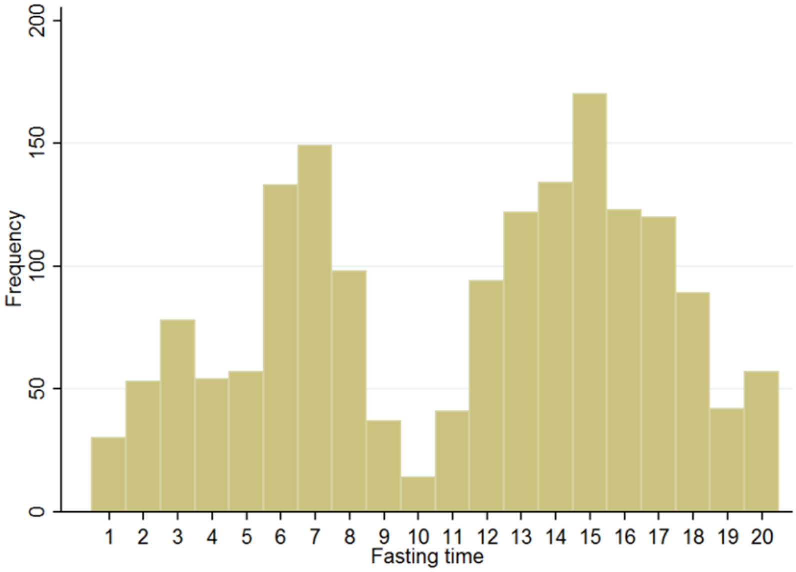
A) Information from Q30 questionnaire
B) information from the datasheet

Characteristics of the population:

We have 264 diabetics' participants out of 1722 (15%).
Fasting time were available for 1695 subjects out of 1722 (98%). 27 missing data.

We have 272 out of 1695 participants (16%) with fasting time <6h.
For non-diabetics the mean fasting time is 12 hours (SD=5). For Diabetics is 7 (SD=5).
156 out of 264 diabetics with fasting time available (59.1%) have fasting time <6h
116 out of 1431 non-diabetics with fasting time available (0.8%) have fasting time <6h





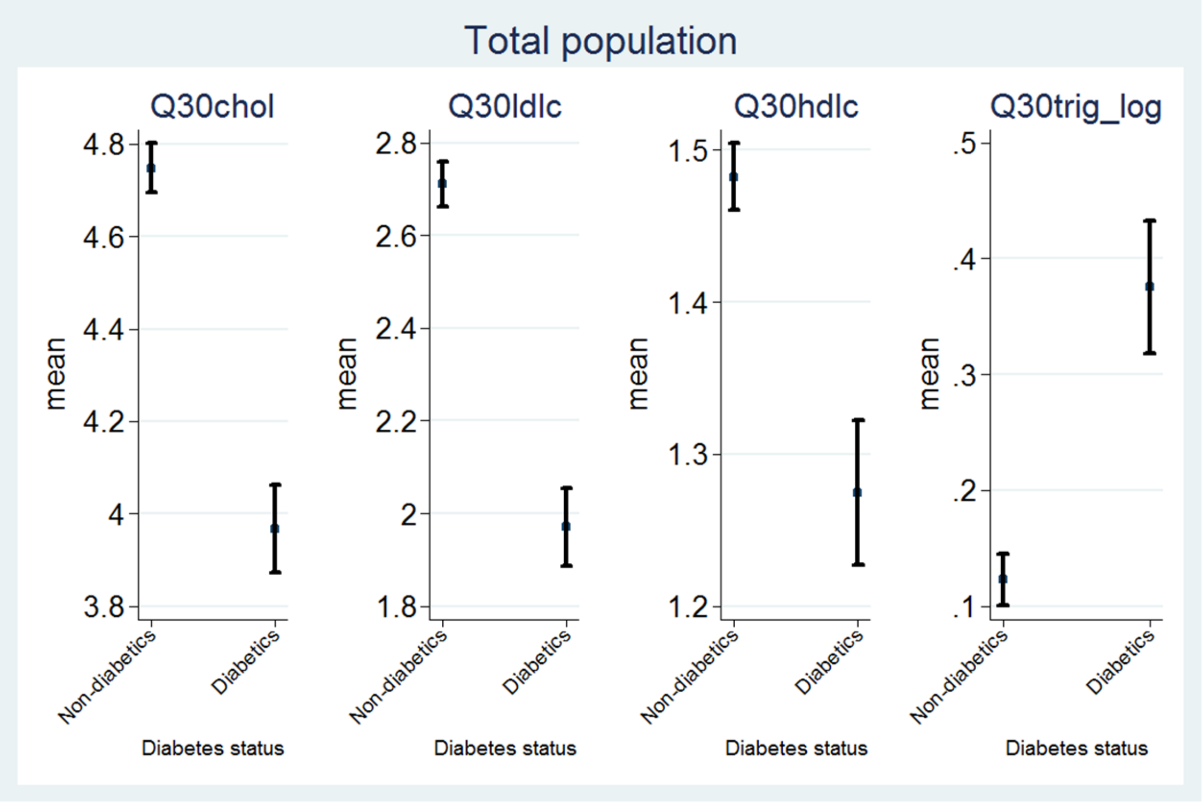
DISTRIBUTIONS AND TRANSFORMATIONS

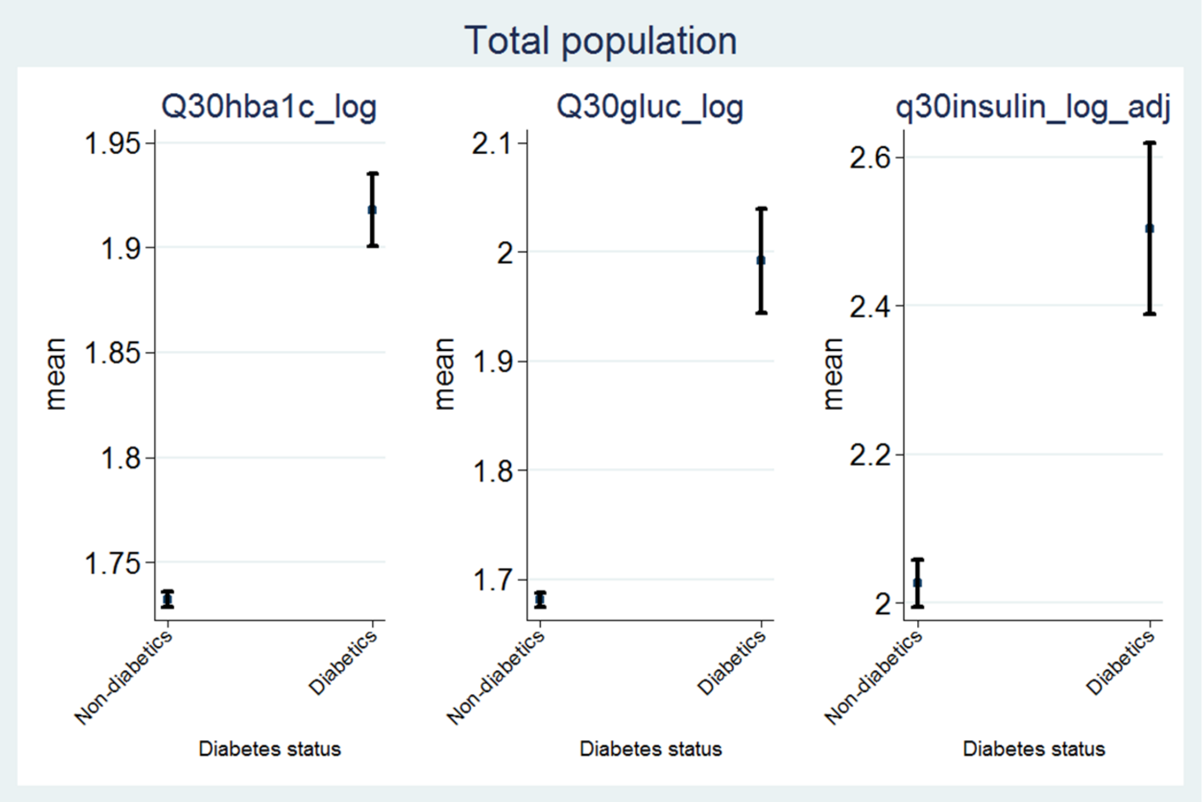
Triglycerides, HBA, glucose, and insulin were log transformed before any kind of adjustments. New variable are:

- Triglycerides (Q30trig_log), log transformed
- HBA (Q30hba1c_log), log transformed
- Glucose (Q30gluc_log), log transformed
- Insulin previously adjusted by batch (q30insulin_log_adj), log transformed

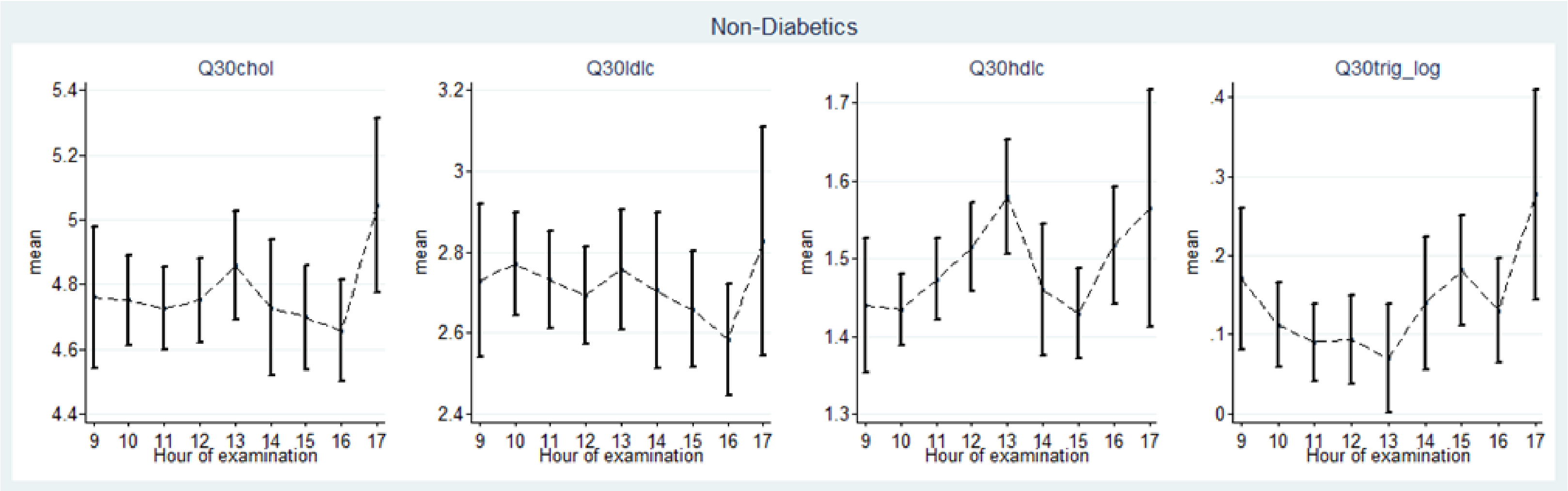
VARIABLES OF INTEREST: DIABETES STATUS

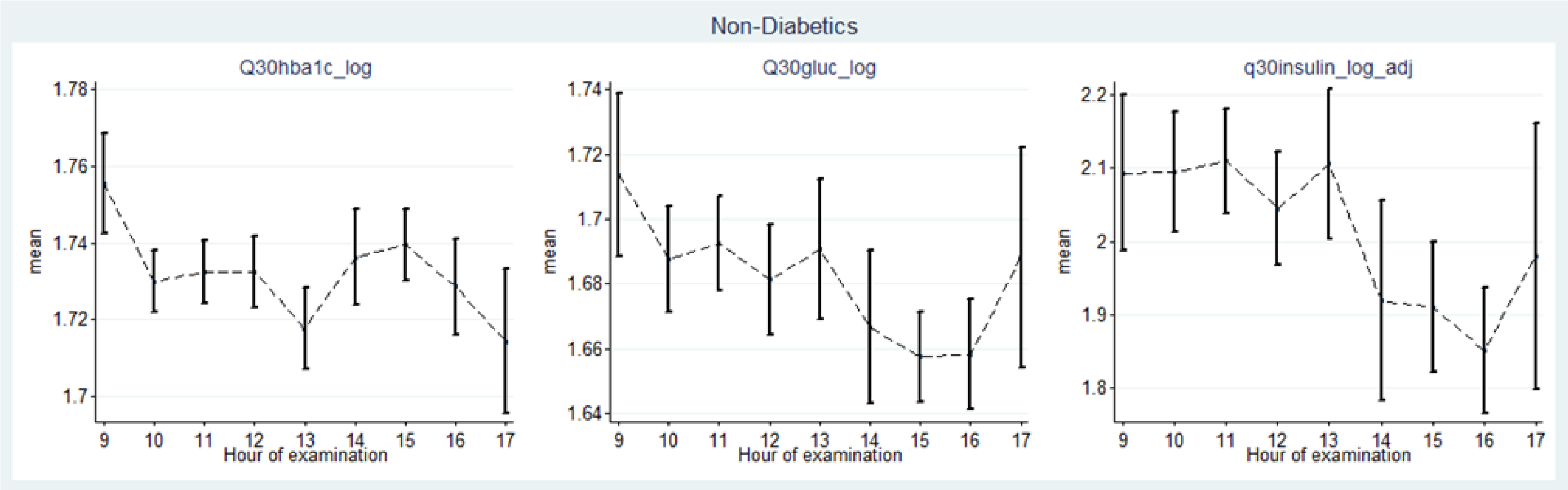
Overall population: Mean and confidence intervals by diabetic status



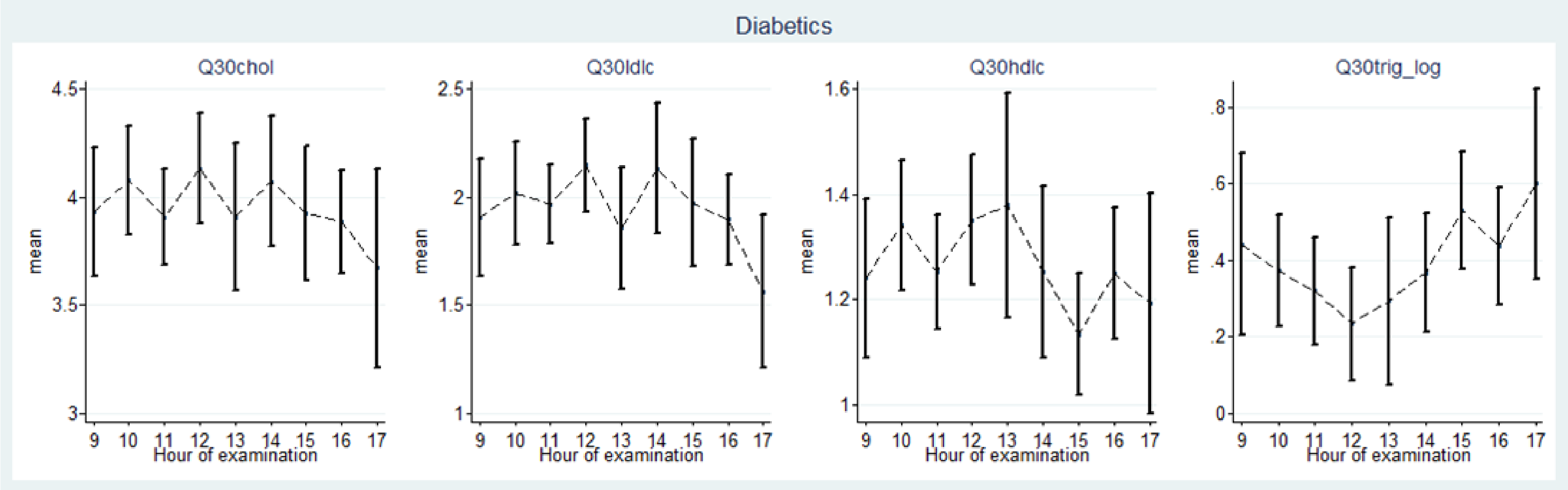


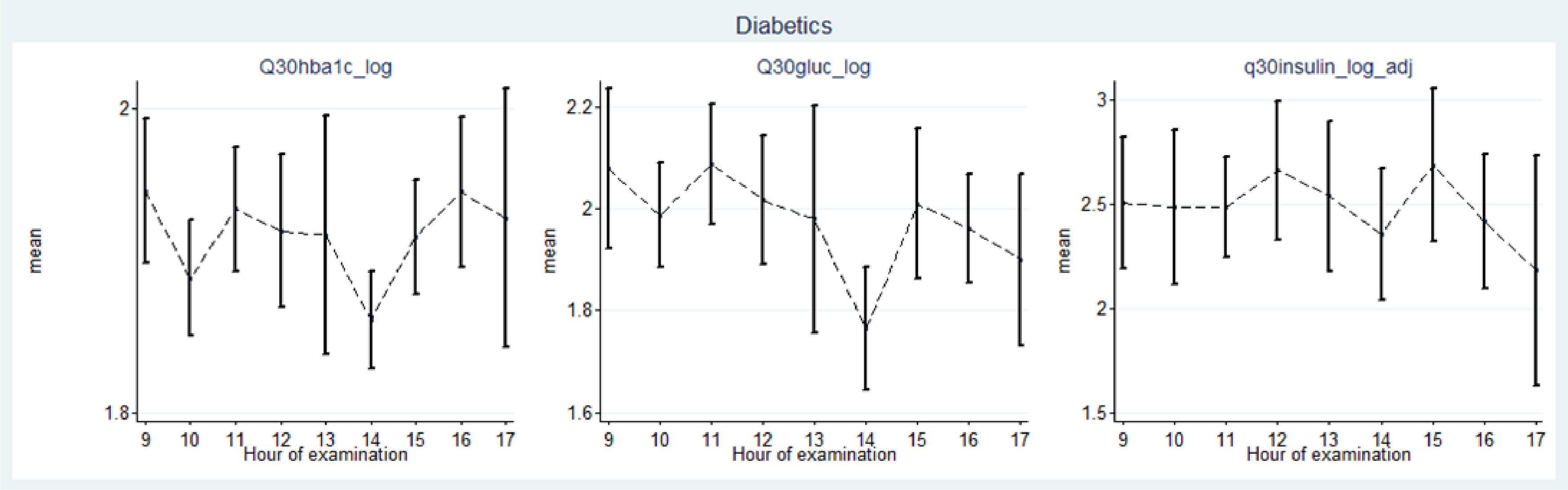
VARIABLES OF INTEREST: HOUR OF THE DAY – NON DIABETICS



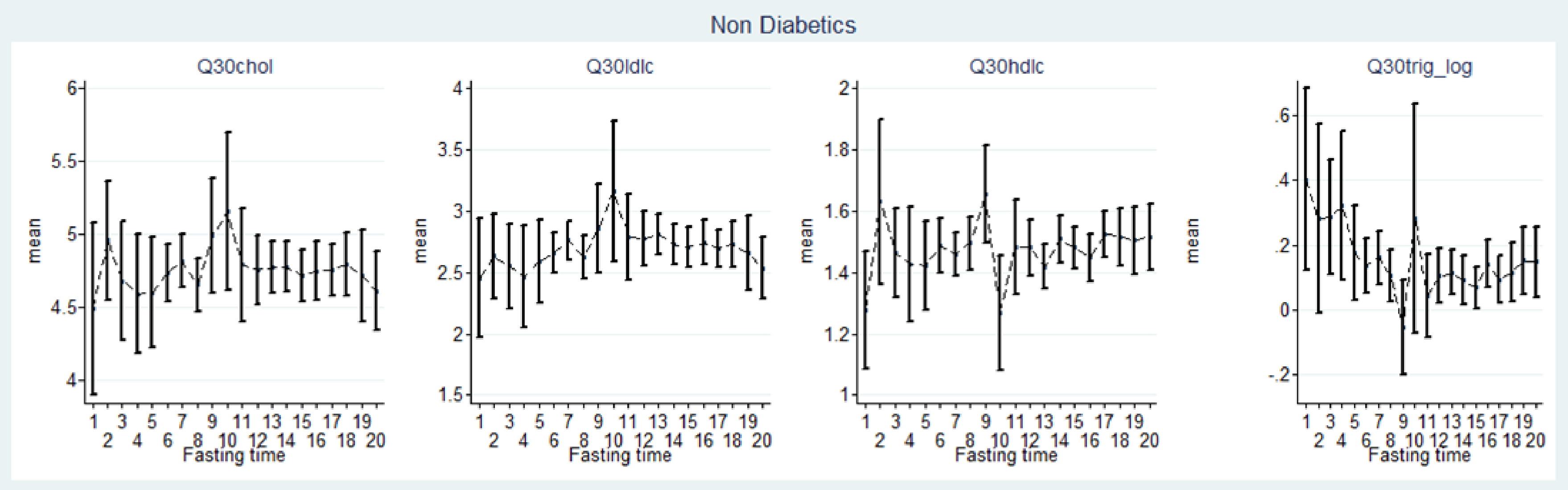


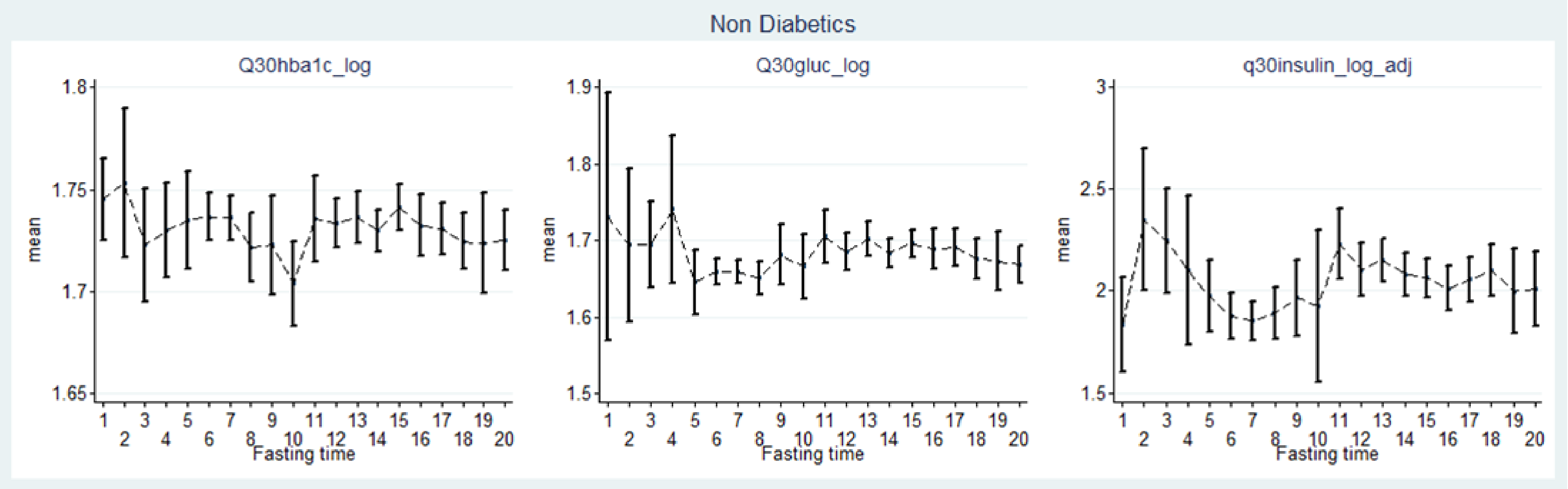
VARIABLES OF INTEREST: HOUR OF THE DAY – DIABETICS



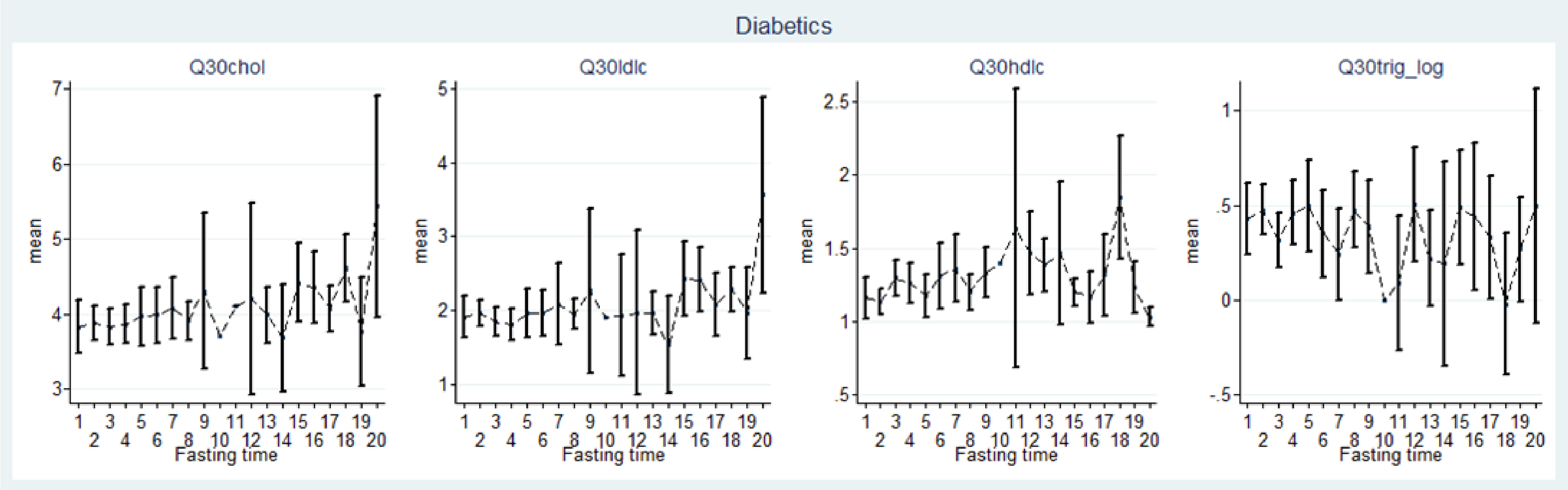


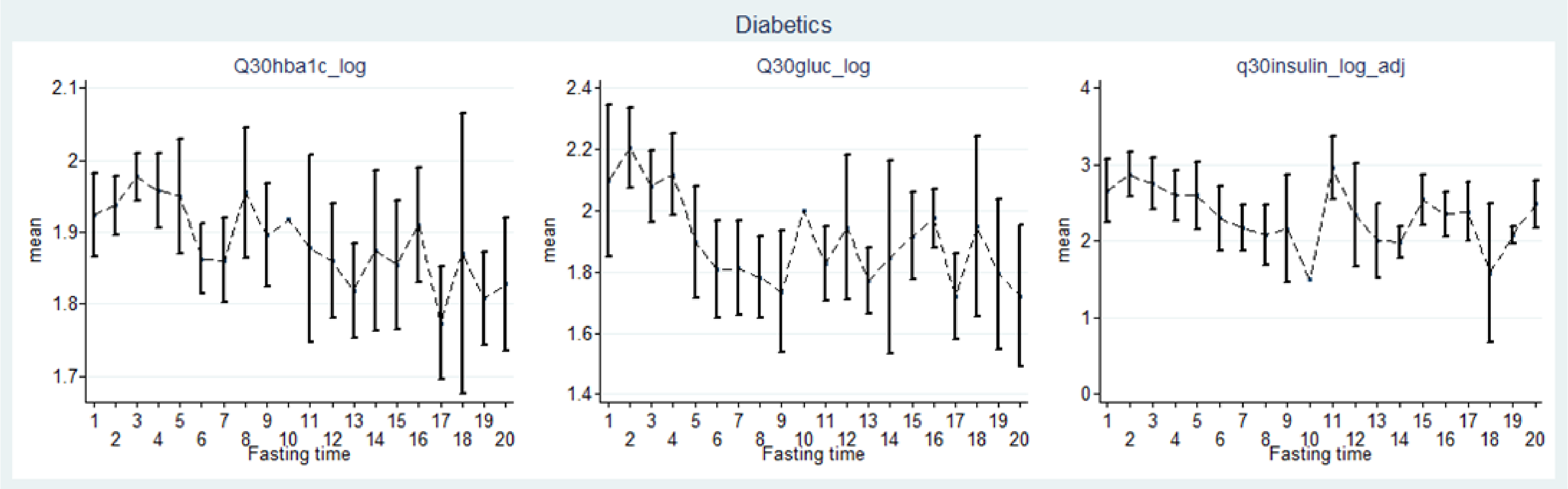
VARIABLES OF INTEREST: FASTING TIME – NON DIABETICS





VARIABLES OF INTEREST: FASTING TIME – DIABETICS





ADJUSTMENTS PROCEDURE

The variables considered to potentially vary by fasting duration times were analysed separately for non-diabetic first and diabetics, as the diabetics group is the only one group of subjects that were not asked to fast.

TRANSFORMATION OF FASTING DURATION AND APPOINTMENT TIME

Fasting time was categorized in two intervals, [0,6) or [6,20], creating a dichotomous variable. The fasting time was divided creating a continuous variable as it shows below

Fasting time	Fasting dummy variable	Fasting time continuous
1	0	1
2	0	2
3	0	3
4	0	4
5	0	5
6	1	1
7	1	2
8	1	3
9	1	4
10	1	5
11	1	6
12	1	7
13	1	8
14	1	9
15	1	10
16	1	11
17	1	12
18	1	13
19	1	14
20	1	15

For time of appointment a similar procedure was adopted. All appointments were categorised as either morning or afternoon appointments, where afternoon appointments began art 2p.m.

Hour of examination	part of the day	Hour of examination continuous
9	0	1
10	0	2
11	0	3
12	0	4
13	0	5
14	1	1
15	1	2
16	1	3
17	1	4

ADJUSTMENTS CHOICE SUMMARY (FULL MODELS DETAILS ARE REPORTED INTO THE NEXT PAGE):

TOTAL CHOLESTEROL:

Non Diabetics: NO adjustment required

Diabetics: Choice is model 1

HDL CHOLESTEROL:

Non Diabetics: Choice is model 3

Diabetics: Choice is model 3

LDL CHOLESTEROL:

Non Diabetics: Choice is model 3

Diabetics: Choice is model 1

TRYGLICERIDES:

Non Diabetics: Choice is model 3

Diabetics: NO adjustment required

HBA:

Non Diabetics: Choice is model 2

Diabetics: Choice is model 1

GLUCOSE:

Non Diabetics: Choice is model 2

Diabetics: Choice is model 3

INSULINE:

Non Diabetics: Choice is model 3

Diabetics: Choice is model 1

DO FILES I USED TO GENERATE THE ADJUSTED VARIABLES → Path: S:\Pop_Health\BRHS_Winter_Deaths\scripts CS

22. Non Diabetics - Total Cholesterol, LDL, HDL, triglycerides, insulin, glucose, HBA.do (APPENDIX 2)
23. Diabetics - Total Cholesterol, LDL, HDL, triglycerides, insulin, glucose, HBA.do (APPENDIX 3)

<u>ADJUSTMENTS FORMULA AFTER I RUN THE MODELS</u>

MARKER ADJUDSTED = MEAN(MARKER) +(MARKER ORIGINAL VALUE – PREDICTED VALUE)

NON DIABETICS SENSITIVITY ANALYSIS – PLEASE NOTE THE RED COLOUR IS THE FINAL ADJUSTMENT CHOICE.

	NON DIABETICS			
	Model1	**Model2**	**Model3**	**Model4**
	Q30chol	**Q30chol**	**Q30chol**	**Q30chol**
	Coeff(LB,UB)	Coeff(LB,UB)	Coeff(LB,UB)	Coeff(LB,UB)
Fasting time (>=6h vs <6)	0.1181(-0.0846,0.3208)		0.1179(-0.0852,0.3210)	0.0719(-0.4668,0.6106)
Fasting time continuous (transformed)	-0.0044(-0.0179,0.0090)		-0.0087(-0.0244,0.0069)	-0.0207(-0.1604,0.1189)
Hour of the day (>13 vs <=13)		0.0116(-0.1324,0.1556)	-0.0225(-0.1810,0.1359)	-0.0297(-0.2808,0.2215)
Hour of the day continuous (transformed)		0.0258(-0.0226,0.0742)	0.0256(-0.0231,0.0742)	0.0243(-0.0316,0.0803)
(fasting_interval==1)*Fasting time continuous (transformed)				0.0125(-0.1289,0.1539)
(hour_interval==1)*Hour of the day continuous (transformed)				0.0065(-0.1151,0.1281)
R-Square	0.0011	0.001	0.0025	0.0025
Adj. R-Square	-0.0004	-0.0004	-0.0004	-0.0018
	Q30hdlc	**Q30hdlc**	**Q30hdlc**	**Q30hdlc**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	0.0346(-0.0488,0.1180)		**0.0278(-0.0554,0.1110)**	-0.0129(-0.2336,0.2077)
Fasting time continuous (transformed)	0.0015(-0.0040,0.0070)		**0.0010(-0.0054,0.0074)**	-0.0102(-0.0674,0.0470)
Hour of the day (>13 vs <=13)		0.0595(0.0006,0.1185)	**0.0650(0.0001,0.1299)**	0.0664(-0.0365,0.1692)
Hour of the day continuous (transformed)		0.0384(0.0186,0.0582)	**0.0377(0.0178,0.0576)**	0.0377(0.0148,0.0607)
(fasting_interval==1)*Fasting time continuous (transformed)				0.0114(-0.0465,0.0694)
(hour_interval==1)*Hour of the day continuous (transformed)				0.0009(-0.0489,0.0507)
R-Square	0.0009	0.0104	**0.0107**	0.0109
Adj. R-Square	-0.0006	0.009	**0.0079**	0.0066
	Q30ldlc	**Q30ldlc**	**Q30ldlc**	**Q30ldlc**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	0.1850(0.0005,0.3695)		**0.1940(0.0092,0.3788)**	0.3375(-0.1513,0.8263)
Fasting time continuous (transformed)	-0.0031(-0.0152,0.0091)		**-0.0094(-0.0236,0.0048)**	0.0283(-0.0988,0.1554)
Hour of the day (>13 vs <=13)		-0.0837(-0.2144,0.0471)	**-0.1199(-0.2636,0.0238)**	-0.0986(-0.3262,0.1290)
Hour of the day continuous (transformed)		-0.0060(-0.0499,0.0380)	**-0.0070(-0.0511,0.0370)**	-0.0034(-0.0542,0.0473)
(fasting_interval==1)*Fasting time continuous (transformed)				-0.0392(-0.1678,0.0895)
(hour_interval==1)*Hour of the day continuous (transformed)				-0.0197(-0.1300,0.0905)
R-Square	0.0028	0.0014	**0.005**	0.0054
Adj. R-Square	0.0014	0	**0.0021**	0.0011

	Q30trig_log	**Q30trig_log**	**Q30trig_log**	Q30trig_log
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	Coeff(LB,UB)
Fasting time (>=6h vs <6)	-0.1496(-0.2324,-0.0668)		**-0.1525(-0.2353,-0.0697)**	-0.3598(-0.5788,-0.1409)
Fasting time continuous (transformed)	-0.0017(-0.0072,0.0038)		**0.0024(-0.0040,0.0088)**	-0.0493(-0.1060,0.0075)
Hour of the day (>13 vs <=13)		0.0447(-0.0142,0.1037)	**0.0525(-0.0120,0.1171)**	-0.0144(-0.1165,0.0876)
Hour of the day continuous (transformed)		-0.0106(-0.0304,0.0092)	**-0.0084(-0.0283,0.0114)**	-0.0189(-0.0417,0.0038)
(fasting_interval==1)*Fasting time continuous (transformed)				0.0546(-0.0029,0.1120)
(hour_interval==1)*Hour of the day continuous (transformed)				0.0516(0.0022,0.1010) **pvalue = 0.041**
R-Square	0.0105	0.0058	**0.0151**	0.021
Adj. R-Square	0.009	0.0044	**0.0122**	0.0168
	Q30hba1c_log	**Q30hba1c_log**	**Q30hba1c_log**	**Q30hba1c_log**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	-0.0018(-0.0150,0.0113)		-0.0008(-0.0139,0.0124)	-0.0065(-0.0412,0.0282)
Fasting time continuous (transformed)	-0.0003(-0.0011,0.0006)		-0.0002(-0.0013,0.0008)	-0.0020(-0.0110,0.0070)
Hour of the day (>13 vs <=13)		**-0.0100(-0.0193,-0.0007)**	-0.0112(-0.0214,-0.0010)	-0.0082(-0.0244,0.0079)
Hour of the day continuous (transformed)		**-0.0060(-0.0092,-0.0029)**	-0.0060(-0.0091,-0.0028)	-0.0056(-0.0092,-0.0019)
(fasting_interval==1)*Fasting time continuous (transformed)				0.0017(-0.0073,0.0108)
(hour_interval==1)*Hour of the day continuous (transformed)				-0.0016(-0.0094,0.0062)
R-Square	0.0004	**0.0105**	0.0107	0.0109
Adj. R-Square	-0.0011	**0.0091**	0.0078	0.0065
	Q30gluc_log	**Q30gluc_log**	**Q30gluc_log**	**Q30gluc_log**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	-0.0143(-0.0382,0.0095)		-0.0116(-0.0354,0.0123)	-0.0617(-0.1249,0.0015)
Fasting time continuous (transformed)	0.0020(0.0004,0.0035)		0.0005(-0.0013,0.0023)	-0.0124(-0.0286,0.0038)
Hour of the day (>13 vs <=13)		**-0.0330(-0.0498,-0.0163)**	-0.0308(-0.0491,-0.0124)	-0.0406(-0.0695,-0.0117)
Hour of the day continuous (transformed)		**-0.0027(-0.0083,0.0029)**	-0.0026(-0.0082,0.0030)	-0.0042(-0.0107,0.0022)
(fasting_interval==1)*Fasting time continuous (transformed)				0.0134(-0.0030,0.0298)
(hour_interval==1)*Hour of the day continuous (transformed)				0.0085(-0.0056,0.0226)
R-Square	0.0052	**0.0137**	0.0142	0.0174
Adj. R-Square	0.0036	**0.0122**	0.0111	0.0129
	q30insulin_log_adj	**q30insulin_log_adj**	**q30insulin_log_adj**	**q30insulin_log_adj**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	-0.1254(-0.2429,-0.0079)		**-0.1138(-0.2307,0.0032)**	-0.1476(-0.4565,0.1613)
Fasting time continuous (transformed)	0.0150(0.0072,0.0228)		**0.0047(-0.0043,0.0137)**	-0.0031(-0.0832,0.0771)
Hour of the day (>13 vs <=13)		-0.1991(-0.2826,-0.1156)	**-0.1818(-0.2733,-0.0902)**	-0.2028(-0.3482,-0.0573)
Hour of the day continuous (transformed)		-0.0054(-0.0335,0.0226)	**-0.0047(-0.0329,0.0235)**	-0.0079(-0.0402,0.0245)
(fasting_interval==1)*Fasting time continuous (transformed)				0.0084(-0.0727,0.0896)
(hour_interval==1)*Hour of the day continuous (transformed)				0.0149(-0.0558,0.0855)
R-Square	0.0115	0.0224	**0.0253**	0.0254
Adj. R-Square	0.01	0.0209	**0.0224**	0.0211

DIABETICS SENSITIVITY ANALYSIS – PLEASE NOTE THE RED COLOUR IS THE FINAL CHOICE

	DIABETICS			
	Model1	**Model2**	**Model3**	**Model4**
	Q30chol	**Q30chol**	**Q30chol**	**Q30chol**
	Coeff(LB,UB)	Coeff(LB,UB)	Coeff(LB,UB)	Coeff(LB,UB)
Fasting time (>=6h vs <6)	**0.1662(-0.0429,0.3753)**		0.1693(-0.0424,0.3810)	0.2116(-0.2332,0.6564)
Fasting time continuous (transformed)	**0.0345(0.0033,0.0657)**		0.0342(0.0015,0.0669)	0.0469(-0.0672,0.1610)
Hour of the day (>13 vs <=13)		-0.1560(-0.4009,0.0889)	-0.1245(-0.3679,0.1188)	0.0572(-0.3811,0.4956)
Hour of the day continuous (transformed)		-0.0327(-0.1173,0.0519)	-0.0439(-0.1275,0.0396)	-0.0198(-0.1242,0.0847)
(fasting_interval==1)*Fasting time continuous (transformed)				-0.0143(-0.1343,0.1057)
(hour_interval==1)*Hour of the day continuous (transformed)				-0.1004(-0.2855,0.0847)
R-Square	**0.047**	0.0064	0.0523	0.057
Adj. R-Square	**0.0392**	-0.0017	0.0366	0.0334
	Q30hdlc	**Q30hdlc**	**Q30hdlc**	**Q30hdlc**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	0.1066(0.0005,0.2127)		**0.1241(0.0175,0.2307)**	0.1917(-0.0325,0.4160)
Fasting time continuous (transformed)	0.0077(-0.0081,0.0235)		**0.0022(-0.0142,0.0187)**	0.0213(-0.0362,0.0789)
Hour of the day (>13 vs <=13)		-0.0761(-0.1983,0.0461)	**-0.0778(-0.2004,0.0447)**	-0.0557(-0.2767,0.1654)
Hour of the day continuous (transformed)		0.0188(-0.0234,0.0610)	**0.0176(-0.0245,0.0596)**	0.0170(-0.0357,0.0696)
(fasting_interval==1)*Fasting time continuous (transformed)				-0.0210(-0.0815,0.0395)
(hour_interval==1)*Hour of the day continuous (transformed)				-0.0199(-0.1132,0.0734)
R-Square	0.0306	0.0218	**0.05**	0.0525
Adj. R-Square	0.0227	0.0137	**0.0343**	0.0288
	Q30ldlc	**Q30ldlc**	**Q30ldlc**	**Q30ldlc**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	**0.1322(-0.0524,0.3167)**		0.1343(-0.0522,0.3208)	0.0513(-0.3377,0.4403)
Fasting time continuous (transformed)	**0.0280(0.0006,0.0555)**		0.0284(-0.0003,0.0572)	0.0063(-0.0936,0.1062)
Hour of the day (>13 vs <=13)		-0.1568(-0.3721,0.0585)	-0.1314(-0.3461,0.0834)	0.1871(-0.1968,0.5711)
Hour of the day continuous (transformed)		-0.0427(-0.1172,0.0319)	-0.0527(-0.1265,0.0211)	-0.0008(-0.0929,0.0913)
(fasting_interval==1)*Fasting time continuous (transformed)				0.0235(-0.0815,0.1285)
(hour_interval==1)*Hour of the day continuous (transformed)				-0.1572(-0.3194,0.0051)
R-Square	**0.0399**	0.0089	0.0488	0.064
Adj. R-Square	**0.032**	0.0007	0.0329	0.0404

	Q30trig_log	**Q30trig_log**	**Q30trig_log**	**Q30trig_log**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	-0.0969(-0.2248,0.0311)		-0.1229(-0.2508,0.0050)	-0.0830(-0.3509,0.1850)
Fasting time continuous (transformed)	-0.0047(-0.0238,0.0144)		0.0034(-0.0164,0.0231)	0.0138(-0.0549,0.0825)
Hour of the day (>13 vs <=13)		0.1268(-0.0188,0.2725)	0.1346(-0.0124,0.2816)	-0.0421(-0.3062,0.2219)
Hour of the day continuous (transformed)		-0.0179(-0.0682,0.0324)	-0.0184(-0.0689,0.0321)	-0.0465(-0.1094,0.0164)
(fasting_interval==1)*Fasting time continuous (transformed)				-0.0111(-0.0834,0.0612)
(hour_interval==1)*Hour of the day continuous (transformed)				0.0877(-0.0238,0.1992)
R-Square	0.0148	0.0296	0.0449	0.0548
Adj. R-Square	0.0067	0.0216	0.0291	0.0312
	Q30hba1c_log	**Q30hba1c_log**	**Q30hba1c_log**	**Q30hba1c_log**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	**-0.0837(-0.1206,-0.0467)**		-0.0818(-0.1191,-0.0445)	-0.0534(-0.1321,0.0254)
Fasting time continuous (transformed)	**-0.0026(-0.0082,0.0029)**		-0.0033(-0.0092,0.0025)	0.0045(-0.0155,0.0245)
Hour of the day (>13 vs <=13)		0.0094(-0.0354,0.0542)	0.0066(-0.0364,0.0497)	-0.0387(-0.1157,0.0383)
Hour of the day continuous (transformed)		0.0075(-0.0079,0.0228)	0.0087(-0.0059,0.0233)	0.0004(-0.0178,0.0187)
(fasting_interval==1)*Fasting time continuous (transformed)				-0.0084(-0.0296,0.0127)
(hour_interval==1)*Hour of the day continuous (transformed)				0.0201(-0.0122,0.0524)
R-Square	**0.1097**	0.004	0.1155	0.1237
Adj. R-Square	**0.1021**	-0.0044	0.1004	0.1012
	Q30gluc_log	**Q30gluc_log**	**Q30gluc_log**	**Q30gluc_log**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	-0.2687(-0.3701,-0.1672)		**-0.2530(-0.3545,-0.1515)**	-0.4375(-0.6502,-0.2248)
Fasting time continuous (transformed)	0.0000(-0.0152,0.0153)		**-0.0057(-0.0216,0.0102)**	-0.0574(-0.1118,-0.0029)
Hour of the day (>13 vs <=13)		-0.1072(-0.2302,0.0157)	**-0.1121(-0.2291,0.0049)**	-0.1532(-0.3615,0.0551)
Hour of the day continuous (transformed)		0.0009(-0.0409,0.0427)	**0.0040(-0.0355,0.0435)**	0.0085(-0.0404,0.0573)
(fasting_interval==1)*Fasting time continuous (transformed)				0.0570(-0.0003,0.1143)
(hour_interval==1)*Hour of the day continuous (transformed)				0.0441(-0.0431,0.1313)
R-Square	0.1246	0.0196	**0.146**	0.1635
Adj. R-Square	0.117	0.0111	**0.1311**	0.1413
	q30insulin_log_adj	**q30insulin_log_adj**	**q30insulin_log_adj**	**q30insulin_log_adj**
	Coeff(LB,UB)	**Coeff(LB,UB)**	**Coeff(LB,UB)**	**Coeff(LB,UB)**
Fasting time (>=6h vs <6)	**-0.4900(-0.7382,-0.2417)**		-0.4714(-0.7230,-0.2198)	-0.6438(-1.1717,-0.1158)
Fasting time continuous (transformed)	**-0.0120(-0.0493,0.0254)**		-0.0181(-0.0576,0.0214)	-0.0640(-0.1996,0.0715)
Hour of the day (>13 vs <=13)		-0.0923(-0.3907,0.2061)	-0.1025(-0.3937,0.1887)	0.1847(-0.3423,0.7118)
Hour of the day continuous (transformed)		0.0033(-0.0994,0.1059)	0.0103(-0.0894,0.1101)	0.0613(-0.0633,0.1858)
(fasting_interval==1)*Fasting time continuous (transformed)				0.0508(-0.0917,0.1934)
(hour_interval==1)*Hour of the day continuous (transformed)				-0.1277(-0.3474,0.0920)
R-Square	**0.0799**	0.0027	0.0837	0.0907
Adj. R-Square	**0.0722**	-0.0056	0.0683	0.0676

APPENDIX 1: READ Q30_5DEC13_Claudio.do

```
/************************************************************************************************************************/
/* READ ALL Q30  DATA  - LINES 1-7 Qr data 8-10 Data sheets 11 Biochemistry and Haematology 12 ECG 13 Test Your Memory(TYM)            */
/************************************************************************************************************************/
clear

infix 1:                  /*
*/      serial 1-8 coder 9-10 q3010d 11-12 q3010m 13-14 q3010y 15-18 q3011d 19-20 q3011m 21-22 q3011y 23-26 /*
*/      q3020a 27 q3020ay 28-31 q3020b 32 q3020by 33-36 q3020c 37 q3020cy 38-41 q3020d 42 q3020dy 43-46 q3020e 47 q3020ey 48-51 /*
*/      q3020f 52 q3020fy 53-56 q3020g 57 q3020gy 58-61 q3020h 62 q3020hy 63-66 q3020i 67 q3020iy 68-71 q3020j 72 q3020jy 73-76 /*
*/      q3020k 77 q3020ky 78-81 q3021 82 q3021y 83-86 q3021a 87 q3030 88 q3030y 89-92 q3030a 93 q3030b 94 q3030c 95      /*
*/      q3040a 96 q3040ay 97-100 q3040b 101 q3040by 102-105 q3040c 106 q3040cy 107-110 q3040d 111 q3040dy 112-115 q3040e 116    /*
*/      q3040ey 117-120 q3040f 121 q3040fy 122-125 q3040g 126 q3040gy 127-130 q3040h 131 q3050 132 q3050y 133-136  /*
*/      q3051feet 137 q3051kidney 138 q3051eyes 139 q3051nerves 140 q3060 141 q3060y 142-145 q3061site1 146-148 q3061site2 149-151     /*
*/      2:          /*
*/      q3070a 1 q3070b 2 q3070c 3 q3070d 4 q3070e 5 q3070f 6 q3070g 7 q3070h 8 q3070i 9 q3070j 10 q3070k 11 q3070l 12 q3070m 13      /*
*/      q3070n 14 q3070o 15 q3070p 16 q3070q 17 q3070r 18 q3070s 19 q3070t 20 q3070u1 21-23 q3070u2 24-26   /*
*/      q3080 27 q3080y 28-31 q3081 32 q3081o 33 q3082knees 34 q3082hips 35 q3082feet 36 q3082wrist 37 q3082back 38 q3082neck 39 q3082shoulder
40      /*
*/      q3082oth 41 q3082ou 42 q3090knees 43 q3090hips 44 q3090feet 45 q3090wrist 46 q3090back 47 q3090neck 48 q3090shoulder 49 q3090other 50 /*
*/      q30100 51 q30101 52 q30110 53 q30111 54 q30111y 55-58 q30112 59 q30112y 60-63 q30113 64 q30114 65-66 q30115 67 q30120 68 q30121 69   /*
*/      q30130 70 q30131 71 q30132 72 q30140 73 q30141 74 q30142 75 q30143 76 q30150 77 q30151 78 q30152 79 q30153 80 q30154 81 q30155 82    /*
*/      q30160 83 q30161 84 q30162 85 q30170 86 q30171 87 q30172 88 q30173 89 q30180 90 q30180a 91 q30180b 92 q30182 93 q30183 94 q30184 95  /*
*/      q30185 96 q30186l 97 q30186r 98 q30190st 99-100 q30190lb 101-102 q30190kg 103-105 q30191 106 q30192 107 q30193ydiet 108 q30193yexer 109
        /*
*/      q30194 110 q30195 111 q30196pc 112 q30196ma 113 q30196ih 114 q30200 115 q30201 116-117 q30202 118 q30203 119 q30204 120 q30210 121   /*
*/      q30211 122 q30212 123-124 q30213beer 125 q30213wine 126 q30213spirits 127 q30213combi 128 q30213lowalc 129 q30214ww 130 q30214wwgl 131-
132     /*
*/      q30215rw 133 q30215rwgl 134-135 q30216bmeal 136 q30216wmeal 137 q30216ameal 138 q30216smeal 139 q30217 140 q30218pc 141 q30218da 142  /*
*/      q30218ih 143 q30218or 144 q30219 145 q302110 146 q302111 147 q302112 148        /*
*/      3:                              /*
*/      q30220 1 q30221 2-3 q30222 4 q30223 5-6 q30224 7 q30225 8 q30226 9-10 q30227 11-12 q30228 13-14 q30229 15 q302210 16-17 /*
*/      q30230 18 q30231 19 q30232 20 q30233 21 q30234 22 q30235 23-25 q30240 26 q30240a 27 q30240b 28 q30241a 29 q30241b 30 q30241c 31 q30241d
32      /*
*/      q30241e 33 q30241f 34 q30242a 35 q30242b 36 q30242c 37 q30242d 38 q30242e 39 q30250 40 q30251 41 q30252 42 q30260a 43 q30260b 44
q30260c 45    /*
*/      q30260d 46 q30260e 47 q30260f 48 q30260g 49 q30260h 50 q30260i 51 q30260j 52 q30260k 53 q30260l 54 q30260m 55 q30260n 56 q30260o 57
q30260p 58    /*
*/      q30260q 59 q30260r 60 q30260s 61 q30270 62 q30271 63 q30272 64 q30273 65 q30274 66 q30275 67 q30280 68 q30280ws 69 q30280wf 70
q30280wch 71  /*
*/      q30290 72 q30291 73-76 q30292 77-80 q30293 81 q30294 82 q30295bath 83 q30295cou 84 q30295arth 85 q30295leg 86 q30295thir 87    /*
*/      q30295wor 88 q30295oth 89 q30295ou 90 q30296 91 q30297 92 q30298 93 q30299 94   /*
*/      q30300 95 q30301 96 q30302 97-98 q30302dk 99 q30303 100-101 q30303dk 102 q30304 103 q30305 104      /*
*/      q30306a 105 q30306b 106 q30306c 107 q30306d 108 q30306e 109 q30306f 110   /*
*/      q30307a 111 q30307b 112 q30307c 113 q30307d 114 q30307e 115 q30307f 116 q30307g 117 q30307h 118      /*
*/      q30310a 119 q30310b 120 q30310c 121 q30310d 122 q30310e 123 q30310f 124 q30310g 125 q30310h 126 q30310i 127 q30310j 128 q30310k 129   /*
*/      q30320 130 q30321 131 q30330 132 q30331 133-136 q30332 137 q30333 138 q30334 139 q30335 140   /*
```

```
*/     4:                    /*
*/     q30340a 1  q30340ah 2-3   q30340b 4  q30340bh 5-6   q30340c 7 q30340ch 8-9    q30340d 10 q30340dh 11-12 q30340e 13 q30340eh 14-15    /*
*/     q30340f 16 q30340fh 17-18 q30340g 19 q30340gh 20-21 q30340h 22 q30340hh 23-24 q30340i 25 q30340ih 26-27 q30340j 28 q30340jh 29-30    /*
*/     q30340k 31 q30340kh 32-33 q30340l 34 q30340lh 35-36 q30340m 37 q30340mh 38-39 q30340n 40 q30340nh 41-42 q30340o 43 q30340oh 44-45    /*
*/     q30340p 46 q30340ph 47-48 q30340q 49 q30340qh 50-51 q30340r 52 q30340rh 53-54 q30340s 55 q30340sh 56-57    /*
*/     q30350  58 q30351  59 q30360  60 q30370  61 q30371  62 q30372  63 q30373  64 q30374  65 q30375  66 q30376  67 q30377  68 q30378 69   /*
*/     q30380a 70 q30380b 71 q30380c 72 q30380d 73 q30380e 74 q30380f 75 q30380g 76 q30380h 77 q30380i 78 q30380j 79 q30380k 80 q30390 81   /*
*/     q30390a 82 q30390b 83 q30390c 84 q30390d 85 q30390e 86 q30390f 87 q30400a 88 q30400b 89 q30410 90   /*
*/     q30420a 91 q30420b 92 q30420c 93 q30420d 94 q30420e 95 q30420f 96 q30420g 97 q30420h 98      /*
*/     q30430 99-100 q30431 101-104 q30432 105 q30433 106 q30440 107 q30441 108 q30441yr 109-112 q30442 113 q30442yr 114-117 q30443 118-120 /*
*/     q30444 121 q30444yr 122-125 q30445 126 q30446 127 q30447 128-130 q30448 131 q30449 132 /*
*/     5:             /*
*/     q3045medyr1  1-4     q3045medpr1  5   q3045bnf12_1 6-7     q3045bnf34_1  8-9      q3045bnf5_1 10 q3045bnf6_1 11   q3045icd1   12-14  /*
*/     q3045medyr2  15-18   q3045medpr2  19  q3045bnf12_2 20-21    q3045bnf34_2  22-23   q3045bnf5_2 24 q3045bnf6_2 25   q3045icd2   26-28  /*
*/     q3045medyr3  29-32   q3045medpr3  33  q3045bnf12_3 34-35    q3045bnf34_3  36-37   q3045bnf5_3 38 q3045bnf6_3 39   q3045icd3   40-42  /*
*/     q3045medyr4  43-46   q3045medpr4  47  q3045bnf12_4 48-49    q3045bnf34_4  50-51   q3045bnf5_4 52 q3045bnf6_4 53   q3045icd4   54-56  /*
*/     q3045medyr5  57-60   q3045medpr5  61  q3045bnf12_5 62-63    q3045bnf34_5  64-65   q3045bnf5_5 66 q3045bnf6_5 67   q3045icd5   68-70  /*
*/     q3045medyr6  71-74   q3045medpr6  75  q3045bnf12_6 76-77    q3045bnf34_6  78-79   q3045bnf5_6 80 q3045bnf6_6 81   q3045icd6   82-84  /*
*/     q3045medyr7  85-88   q3045medpr7  89  q3045bnf12_7 90-91    q3045bnf34_7  92-93   q3045bnf5_7 94 q3045bnf6_7 95   q3045icd7   96-98  /*
*/     q3045medyr8  99-102  q3045medpr8  103 q3045bnf12_8 104-105  q3045bnf34_8  106-107 q3045bnf5_8 108 q3045bnf6_8 109 q3045icd8   110-112/*
*/     q3045medyr9  113-116 q3045medpr9  117 q3045bnf12_9 118-119  q3045bnf34_9  120-121 q3045bnf5_9 122 q3045bnf6_9 123 q3045icd9   124-126/*
*/     q3045medyr10 127-130 q3045medpr10 131 q3045bnf12_10 132-133 q3045bnf34_10 134-135 q3045bnf5_10 136 q3045bnf6_10 137 q3045icd10 138-140
       /*
*/     6:     /*
*/     q30460 1 q30461 2 q30462 3 q30463 4 q30464 5-7 /*
*/     q30465a_name 8  q30465a_often 9  q30465a_long 10 q30465b_name 11 q30465b_often 12 q30465b_long 13 q30465c_name 14 q30465c_often 15
q30465c_long 16     /*
*/     q30465d_name 17 q30465d_often 18 q30465d_long 19 q30465e_name 20 q30465e_often 21 q30465e_long 22 q30465f_name 23 q30465f_often 24
q30465f_long 25     /*
*/     q30465g_name 26 q30465g_often 27 q30465g_long 28 q30465h_name 29 q30465h_often 30 q30465h_long 31 q30465i_name 32 q30465i_often 33
q30465i_long 34     /*
*/     q30465j_name 35 q30465j_often 36 q30465j_long 37 q30465k_name 38 q30465k_often 39 q30465k_long 40 q30465l_name 41 q30465l_often 42
q30465l_long 43     /*
*/     q30466a_name 44-45 q30466a_often 46 q30466a_long 47 q30466b_name 48-49 q30466b_often 50 q30466b_long 51    /*
*/     q30466c_name 52-53 q30466c_often 54 q30466c_long 55 q30466d_name 56-57 q30466d_often 58 q30466d_long 59    /*
*/     q30466e_name 60-61 q30466e_often 62 q30466e_long 63
                                                       /*
*/     d3010 64 d3011 65 d3020 66 d3021 67 d3022 68 d3023 69 d3024 70 d3025 71 d3026 72 d3027 73 d3028 74 d3030 75 d3031 76 d3032 77  /*
*/     d3040 78 d3041 79 d3042 80 d3043 81 d3044 82 d3045 83 d3046 84 d3047 85 d3048 86 d3049 87 d30410 88 d30411 89 d30412 90 d30413 91
d30414 92    /*
*/     d3050 93 d3051 94 d3052 95-96 d3053 97-98 d3054 99-100 d3055 101-102 d3056ou1 103-104 d3056ou2 105-106 d3056ou3 107-108 d3056ou4 109-
110 d3056ou5 111-112       /*
*/     d3060 113 d3061 114 d3070 115 d3071 116 d3073 117 d3074 118 d3075 119    /*
*/     d3077slices 120-121 d3077thick 122 d3078slices 123-124 d3078thick 125 d3079slices 126-127 d3079thick 128 d30710slices 129-130
d30710thick 131     /*
*/     d3080 132 d3081 133 d3082 134 d3083 135 d3084 136 d3090 137 d3091 138 d3092 139 d3093 140 d3094 141 d3095 142 d3096 143 d3097 144 d3098
145    /*
*/     d30100 146 d30101 147 d30110 148 d30111 149 d30112 150 d30113 151 d30114 152    /*
*/     7:                         /*
*/     d30120 1 d30121 2 d30122 3 d30130 4 d30130o 5 d30131 6 d30132 7 d30140 8 d30141 9      /*
```

```
*/     d30150but 10 d30150ffmarg 11 d30150ffmarg_ou 12 d30150lfmarg 13 d30150lfmarg_ou 14 d30150hmarg 15   /*
*/     d30151 16 d30152 17 d30152_br 18 d30153 19 d30153_br 20     /*
*/     d30160nadul 21-22 d30160nch1to4 23-24 d30160nch5to16 25-26 d30160nch_u1yr 27-28 /*
*/     d30161lbs 29-30 d30161ozs 31-32 d30161gr 33-35 /*
*/     d30162lbs 36-37 d30162ozs 38-39 d30162gr 40-42 /*
*/     d30163lbs 43-44 d30163ozs 45-46 d30163gr 47-49 /*
*/                     d30164ozs 50-51 d30164ml 52-54 /*
*/                     d30165ozs 55-56 d30165ml 57-59 /*
*/                     d30166ozs 60-61 d30166ml 62-64 /*
*/     d30167lbs 65-66 d30167ozs 67-68 d30167gr 69-71 /*
*/     d30168lbs 72-73 d30168ozs 74-75 d30168gr 76-78 /*
*/     d30169lbs 79-80 d30169ozs 81-82 d30169gr 83-85 /*
*/     d30170 86-87 d30171 88 d30172 89 d30173 90-91 d30174 92-93 d30175 94-95 d30177 96-97   /*
*/     d30180 98 d30181 99 /*
*/     d30181mon_i 100-101 d30181mon_ii 102-103 d30181mon_iii 104-105 d30181mon_iv 106-107 d30181mon_v 108-109    /*
*/     d30181tue_i 110-111 d30181tue_ii 112-113 d30181tue_iii 114-115 d30181tue_iv 116-117 d30181tue_v 118-119    /*
*/     d30181wed_i 120-121 d30181wed_ii 122-123 d30181wed_iii 124-125 d30181wed_iv 126-127 d30181wed_v 128-129    /*
*/     d30181thu_i 130-131 d30181thu_ii 132-133 d30181thu_iii 134-135 d30181thu_iv 136-137 d30181thu_v 138-139    /*
*/     d30181fri_i 140-141 d30181fri_ii 142-143 d30181fri_iii 144-145 d30181fri_iv 146-147 d30181fri_v 148-149    /*
*/     d30181sat_i 150-151 d30181sat_ii 152-153 d30181sat_iii 154-155 d30181sat_iv 156-157 d30181sat_v 158-159    /*
*/     d30181sun_i 160-161 d30181sun_ii 162-163 d30181sun_iii 164-165 d30181sun_iv 166-167 d30181sun_v 168-169    /*
*/     d30182 170 d30183 171      /*
*/     8:                         /*
*/     serial2 1-8 q30batch 9-11 str Q30obs  12-13 Q30time_hour 14-15 Q30time_min 16-17 Q30sitstand5 18 Q30sitstand5_secs 19-23
Q30sitstand5t_n 24  /*
*/     str Q30sitstand5t_h  25 Q30walk3m 26 Q30walk3m_secs 27-31 Q30walk3m_inc 32 Q30height 33-37  str Q30ht_p  38 Q30weight 39-43 str Q30wt_p
44     /*
*/     Q30weight2 45-49 Q30waistc1 50-54 Q30waistc2 55-59 str Q30waist_p  60 Q30hip1 61-65 Q30hip2 66-70 str Q30hip_p  71 Q30armc 72-75      /*
*/     str Q30armc_p  76 Q30tricep1 77-80 Q30tricep2 81-84  str Q30tricep_p 85 Q30subscap1 86-89 Q30subscap2 90-93 str Q30subscap_p  94      /*
*/     Q30sbpsit1 95-97 Q30sbpsit2 98-100 Q30sbpstand1 101-103 Q30sbpstand2 104-106 Q30dbpsit1 107-109 Q30dbpsit2 110-112 Q30dbpstand1 113-115
       /*
*/     Q30dbpstand2 116-118 Q30hratesit1 119-121 Q30hratesit2 122-124 Q30hratestand1 125-127 Q30hratestand2 128-130      /*
*/     Q30bp_cuff 131 Q30bp_instr 132 str Q30bp_instr_p  133 Q30faintness 134 Q30breathless 135 Q30room_temp 136-139 Q30ethnicity 140
Q30spir_instr 141   /*
*/     Q30inh24h 142 Q30time_inh_h 143-144 Q30time_inh_m 145-146 Q30btv_dsheet 147-151 Q30ci 152 str Q30ci_p  153 /*
*/     9:                                /*
*/     Q30grip_instr 1 Q30grip_r1 2-3 Q30grip_r2 4-5 Q30grip_r3 6-7 Q30grip_dom_r 8 str Q30grip_rp 9 Q30grip_l1 10-11 Q30grip_l2 12-13
Q30grip_l3 14-15    /*
*/     Q30grip_dom_l 16 str Q30grip_lp  17 Q30spir_ref 18-20 Q30spir_nblows 21-22 Q30spir_btv 23-27 Q30fvc 28-31 Q30fev05 32-35 Q30fev1 36-39
Q30pef 40-42  /*
*/     Q30fef2575 43-46 Q30fef7585 47-50 Q30fef25 51-54 Q30fef50 55-58 Q30fef75 59-62 Q30bc_dated 63-64 Q30bc_datem 65-66 Q30bc_datey 67-70
Q30bc_timeh 71-72   /*
*/     Q30bc_timem 73-74 Q30bc_bodytype 75-75 Q30bc_gender 76 Q30bc_age 77-78 Q30bc_height 79-81 Q30bc_weight 82-86 Q30bc_bmi 87-90
Q30bc_BMR_kj 91-95  /*
*/     Q30bc_bmr_kcal 96-100 Q30bc_fat_pc 101-104 Q30bc_fatmass 105-108 Q30bc_ffm 109-112 Q30bc_tbw 113-116 Q30bc_VFR 117-118
Q30bc_drange_fatpc_min 119-120    /*
*/     Q30bc_drange_fatpc_max 121-122 Q30bc_drange_fmass_min 123-126 Q30bc_drange_fmass_max 127-130 Q30imp_wb 131-134    /*
*/     Q30imp_rl 135-138 Q30imp_ll 139-142 Q30imp_ra 143-146 Q30imp_la 147-150   /*
*/     10:                                     /*
```

```
*/     Q30rleg_fat 1-4 Q30rleg_fmass 5-8 Q30rleg_ffm 9-12 Q30rleg_pmmass 13-16 Q30lleg_fat 17-20 Q30lleg_fmass 21-24 Q30lleg_ffm 25-28
Q30lleg_pmmass 29-32       /*
*/     Q30rarm_fat 33-36 Q30rarm_fmass 37-40 Q30rarm_ffm 41-44 Q30rarm_pmmass 45-48 Q30larm_fat 49-52 Q30larm_fmass 53-56 Q30larm_ffm 57-60
Q30larm_pmmass 61-64       /*
*/     Q30trunk_fat 65-68 Q30trunk_fmass 69-72 Q30trunk_ffm 73-76 Q30trunk_pmmass 77-80       /*
*/     Q30BT_SUCC 81 Q30BT_PR 82 Q30BT_TIMEH 83-84 Q30BT_TIMEM 85-86 Q30BT_FAST_INSTR 87 Q30BT_FAST_TLEH 88-89 Q30BT_FAST_TLEM 90-91
Q30BT_FAST_DLE 92   /*
*/     Q30BT_id_batch 93-95 Q30BT_id_serial 96-103 Q30BT_IncS_A 104 Q30BT_IncS_B 105 Q30BT_IncS_C 106 Q30BT_IncS_DE 107 Q30BT_IncS_FJ 108   /*
*/     Q30BT_IncS_K 109 Q30BT_IncS_LN 110 Q30BT_IncS_PS 111 Q30BT_IncS_T 112 Q30ecg  113 Q30ankle_oed_l 114 Q30ankle_oed_r 115 Q30actigraph
116    /*
*/     Q30actigraph_id_batch 117-119 Q30actigraph_id_serial 120-127 Q30bstat_dob_d 128-129 Q30bstat_dob_m 130-131 Q30bstat_dob_y 132-135     /*
*/     Q30bstat_RoomTemp 136-139 Q30bstat_SkinTemp 140-143 Q30bstat_Pacemaker 144 Q30bstat_Instrument 145 Q30bodystat 146-148 Q30cons_q1 149
Q30cons_q2 150      /*
*/     Q30cons_q3 151 Q30cons_signed 152  str Q30cons_date 153-160 Q30xd 161-162 Q30xm 163-164 Q30xy 165-168 Q30ExamTown 169-170      /*
*/     11:                                   /*
*/     Q30bioch_day 1-2 Q30bioch_month 3-4 Q30bioch_year 5-8 Q30sodium 9-11 Q30potass 12-14 Q30creat 15-17 Q30urea 18-21 Q30alb 22-23 Q30tbili
24-25 Q30aphos 26-28/*
*/     Q30ast 29-31 Q30alt 32-34 Q30phosph 35-38 Q30calc 39-42 Q30ccalc 43-46 Q30chol 47-49 Q30chdr 50-52 Q30hdlc 53-55 Q30ldlc 56-58 Q30trig
59-61 Q30ggt 62-64  /*
*/     Q30magn 65-68 Q30tprot 69-70 Q30urat 71-74 Q30gluc 75-78 Q30hba1c 79-82 Q30hba1c_note 83-83 Q30Bioch_note 84-84 q30Haem_day 85-86
q30Haem_month 87-88 /*
*/     q30Haem_year 89-92 q30Hb 93-96 q30WBC 97-101 q30PLAT 102-104 q30RBC 105-108 q30RDW 109-112 q30HCT 113-117 q30MCV 118-122 q30MCH 123-126
q30MCHC 127-130     /*
*/     q30Neutro_Abs 131-135 q30Lymph_abs 136-140 q30Monocy_abs 141-144 q30Eosin_Abs 145-148 q30Baso_abs 149-152 q30MPV 153-156 q30Haem_note
157    /*
*/     12:          /*
*/     serial_ecg  1-8 Q30ECG_Count  9-9 Q30ECG_Age  10-11  /*
*/     Q30ECG_Heart_Rate_bpm  12-14 Q30ECG_P_axis_degree  15-20 Q30ECG_QRS_axis_degree  21-26       /*
*/     Q30ECG_T_axis_degree  27-32 Q30ECG_P_duration_ms  33-35 Q30ECG_QRS_duration_ms  36-38 /*
*/     Q30ECG_PR_interval_ms  39-44 Q30ECG_QT_interval_ms  45-47 Q30ECG_QTC_interval_ms  48-51      /*
*/     Q30ECG_Minnesota_group1_L  52-54 Q30ECG_Serial_type1_1  55-55 Q30ECG_Minnesota_group1_P  56-58      /*
*/     Q30ECG_Srial_type1_2  59-59 Q30ECG_Minnesota_group1_A  60-62 Q30ECG_Serial_type1_3  63-63    /*
*/     Q30ECG_Minnesota_group2_1  64-66 Q30ECG_No_serial_comparison1 67-67 Q30ECG_Minnesota_group2_2  68-68       /*
*/     Q30ECG_No_serial_comparison2  69-69 Q30ECG_Snnesota_group3  70-72 Q30ECG_No_serial_comparison3  73-73      /*
*/     Q30ECG_Minnesota_group4_L  74-76 Q30ECG_Serial_type1_4  77-77 Q30ECG_Minnesota_group4_P  78-80      /*
*/     Q30ECG_Serial_type1_5  81-81 Q30ECG_Minnesota_group4_A  82-84 Q30ECG_Serial_type1_6  85-85   /*
*/     Q30ECG_Minnesota_group5_L  86-88 Q30ECG_Serial_type1_7  89-89 Q30ECG_Minnesota_group5_P  90-92      /*
*/     Q30ECG_Serial_type1_8  93-93 Q30ECG_Minnesota_group5_A  94-96 Q30ECG_Serial_type1_9  97-97   /*
*/     Q30ECG_Minnesota_group6  98-100 Q30ECG_No_serial_comparison4  101-101 Q30ECG_Minnesota_group7_1  102-104   /*
*/     Q30ECG_Serial_type1_10  105-105 Q30ECG_Minnesota_group7_2  106-108 Q30ECG_No_serial_comparison5  109-109   /*
*/     Q30ECG_Minnesota_group8_1  110-112 Q30ECG_No_serial_comparison6  113-113 Q30ECG_Minnesota_group8_2  114-116      /*
*/     Q30ECG_No_serial_comparison7  117-117 Q30ECG_Minnesota_group8_3  118-120 Q30ECG_No_serial_comparison8  121-121    /*
*/     Q30ECG_Minnesota_group8_4  122-124 Q30ECG_No_serial_comparison9  125-125 Q30ECG_Minnesota_group9_L  126-128      /*
*/     Q30ECG_Serial_type1_11  129-129 Q30ECG_Minnesota_group9_P  130-132  Q30ECG_Serial_type1_12  133-133       /*
*/     Q30ECG_Minnesota_group9_A  134-136 Q30ECG_Serial_type1_13  137-137 Q30ECG_Minnesota_group9m_1  138-140     /*
*/     Q30ECG_No_serial_comparison10  141-141 Q30ECG_Minnesota_group9m_2  142-142 Q30ECG_No_serial_comparison11 143-143  /*
*/     Q30ECG_LVMI_Rautaharju_  144-149  Q30ECG_LVMI_F_Huwez  150-156 Q30ECG_Summary_1  157-162     /*
*/     Q30ECG_Cornell_Index_V  163-166 Q30ECG_Cornell_Product_VS  167-173 Q30ECG_Sokolow_Lyon_V  174-177   /*
*/     Q30ECG_QRS_voltage_sum_V  178-182 Q30ECG_QRS_voltage_prod_VS  183-190 Q30ECG_SYS_DATE_D  191-192    /*
*/     Q30ECG_SYS_DATE_M  193-194 Q30ECG_SYS_DATE_Y  195-198 Q30ECG_RECEIVED_D  199-200 Q30ECG_RECEIVED_M  201-202       /*
```

```
*/     Q30ECG_RECEIVED_Y  203-206       /*
*/     13:          /*
*/     Serial_tym 1-8 Q30TYM_score1_Full_name  9 Q30TYM_score2_Today_Day 10  Q30TYM_score3_Today_Date 11 Q30TYM_score4_How_old 12     /*
*/     Q30TYM_score5_Date_born 13 Q30TYM_score6_Copy_sentence 14  Q30TYM_score7_PM 15  Q30TYM_score8_WWI 16 Q30TYM_score9_Sums 17     /*
*/     Q30TYM_score10_Creatures_S 18  Q30TYM_score11_Carrot 19 Q30TYM_score12_Lion  20 Q30TYM_score13_Name_items 21                 /*
*/     Q30TYM_score14_Join_circles  22 Q30TYM_score15_Clock  23 Q30TYM_score16_Rewrite_sentence 24                                 /*
*/  with_q30qr 31 with_q30ds 32 with_Q30bioch 33 with_q30Haem 34 with_q30ecg 35 with_q30tym 36                                   /*
*/ using "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file/Q30_5DEC13.dat"


/*PAGE 2*/
sum coder q3010d q3010m    q3010y q3011d q3011m q3011y q3020a q3020ay q3020b q3020by q3020c    q3020cy      q3020d q3020dy      q3020e q3020ey
      q3020f /*
*/ q3020fy   q3020g q3020gy      q3020h q3020hy      q3020i q3020iy      q3020j q3020jy      q3020k q3020ky      q3021  q3021y q3021a q3030
q3030y q3030a q3030b q3030c

/*page 3 */
sum q3040a   q3040ay      q3040b q3040by      q3040c q3040cy      q3040d q3040dy q3040e q3040ey q3040f q3040fy q3040g  q3040gy      q3040h
q3050 q3050y  /*
*/ q3051feet q3051kidney q3051eyes      q3051nerves  q3060 q3060y q3061site1   q3061site2

/*page 4 */
sum q3070a  q3070b  q3070c  q3070d q3070e q3070f q3070g q3070h q3070i q3070j q3070k q3070l q3070m q3070n q3070o q3070p q3070q q3070r q3070s
q3070t /*
*/ q3070u1 q3070u2 q3080 q3080y q3081 q3081o q3082knees q3082hips q3082feet q3082wrist q3082back q3082neck q3082shoulder q3082oth q3082ou

/*page 5 */
sum q3090knees  q3090hips q3090feet q3090wrist q3090back q3090neck q3090shoulder q3090other q30100 q30101 q30110 q30111 q30111y q30112 q30112y
/*
*/ q30113 q30114 q30115 q30120 q30121 q30130 q30131 q30132

/*page 6 */
sum  q30140  q30141  q30142  q30143  q30150  q30151  q30152  q30153  q30154  q30155  q30160  q30161  q30162

/*page 7 */
sum q30170  q30171  q30172  q30173  q30180  q30180a  q30180b  q30182  q30183  q30184 q30185  q30186l  q30186r

/*page 8 */
sum q30190st  q30190lb  q30190kg  q30191  q30192  q30193ydiet  q30193yexer  q30194  q30195  q30196pc  q30196ma  q30196ih /*
*/ q30200  q30201  q30202  q30203  q30204

/*page 9 */
sum q30210  q30211  q30212 q30213beer q30213wine q30213spirits q30213combi q30213lowalc  q30214ww q30214wwgl q30215rw  q30215rwgl /*
*/q30216bmeal  q30216wmeal  q30216ameal  q30216smeal  q30217  q30218pc  q30218da  q30218ih  q30218or  q30219  q302110  q302111  q302112

/*page 10 */
sum q30220  q30221  q30222  q30223  q30224  q30225  q30226  q30227  q30228  q30229  q302210

/*page 11 */
sum q30230  q30231 q30232 q30233 q30234 q30235 q30240 q30240a q30240b q30241a q30241b q30241c q30241d q30241e q30241f /*
```

```
*/ q30242a  q30242b  q30242c  q30242d  q30242e

/*page 12 */
sum q30250  q30251  q30252  q30260a  q30260b  q30260c  q30260d  q30260e  q30260f  q30260g  q30260h  q30260i  q30260j  q30260k  /*
*/ q30260l  q30260m  q30260n  q30260o  q30260p  q30260q  q30260r  q30260s

/*page 13 */
sum q30270  q30271 q30272 q30273 q30274 q30275 q30280 q30280ws  q30280wf q30280wch q30290 q30291 q30292 q30293 q30294  /*
*/ q30295bath  q30295cou  q30295arth  q30295leg  q30295thir  q30295wor  q30295oth  q30295ou

/*page 14 */
sum q30296  q30297  q30298  q30299  q30300  q30301  q30302  q30302dk  q30303  q30303dk  q30304  q30305  q30306a  q30306b  q30306c /*
*/ q30306d  q30306e  q30306f

/*page 15 */
sum q30307a  q30307b  q30307c  q30307d  q30307e  q30307f  q30307g  q30307h  q30310a  q30310b  q30310c  q30310d  q30310e  q30310f  /*
*/ q30310g  q30310h  q30310i  q30310j  q30310k  q30320  q30321

/*page 16 */
sum q30330 q30331 q30332 q30333 q30334 q30335 q30340a q30340ah q30340b q30340bh  q30340c  q30340ch  q30340d  q30340dh  q30340e  /*
*/q30340eh  q30340f  q30340fh  q30340g  q30340gh  q30340h  q30340hh  q30340i  q30340ih  q30340j  q30340jh

/*page 17 */
sum q30340k  q30340kh  q30340l  q30340lh  q30340m  q30340mh  q30340n  q30340nh  q30340o  q30340oh  q30340p  q30340ph  q30340q  /*
*/ q30340qh  q30340r q30340rh q30340s q30340sh  q30350  q30351  q30360  q30370  q30371  q30372  q30373  q30374  q30375 q30376  q30377 q30378

/*page 18 */
sum q30380a  q30380b  q30380c  q30380d  q30380e  q30380f q30380g q30380h q30380i q30380j q30380k q30390 q30390a q30390b q30390c  /*
*/ q30390d  q30390e  q30390f  q30400a  q30400b  q30410

/*page 19 */
sum q30420a  q30420b  q30420c  q30420d  q30420e  q30420f  q30420g  q30420h  q30430  q30431  q30432  q30433  q30440  /*
*/ q30441  q30441yr  q30442  q30442yr  q30443  q30444  q30444yr  q30445  q30446  q30447  q30448  q30449

/*page 20 */
sum q3045medyr1  q3045medpr1  q3045bnf12_1  q3045bnf34_1  q3045bnf5_1  q3045bnf6_1 q3045icd1 /*
*/  q3045medyr2  q3045medpr2  q3045bnf12_2  q3045bnf34_2  q3045bnf5_2  q3045bnf6_2 q3045icd2 /*
*/  q3045medyr3  q3045medpr3  q3045bnf12_3  q3045bnf34_3  q3045bnf5_3  q3045bnf6_3 q3045icd3 /*
*/  q3045medyr4  q3045medpr4  q3045bnf12_4  q3045bnf34_4  q3045bnf5_4  q3045bnf6_4 q3045icd4 /*
*/  q3045medyr5  q3045medpr5  q3045bnf12_5  q3045bnf34_5  q3045bnf5_5  q3045bnf6_5 q3045icd5 /*
*/  q3045medyr6  q3045medpr6  q3045bnf12_6  q3045bnf34_6  q3045bnf5_6  q3045bnf6_6 q3045icd6 /*
*/  q3045medyr7  q3045medpr7  q3045bnf12_7  q3045bnf34_7  q3045bnf5_7  q3045bnf6_7 q3045icd7 /*
*/  q3045medyr8  q3045medpr8  q3045bnf12_8  q3045bnf34_8  q3045bnf5_8  q3045bnf6_8 q3045icd8 /*
*/  q3045medyr9  q3045medpr9  q3045bnf12_9  q3045bnf34_9  q3045bnf5_9  q3045bnf6_9 q3045icd9 /*
*/  q3045medyr10  q3045medpr10  q3045bnf12_10  q3045bnf34_10  q3045bnf5_10  q3045bnf6_10 q3045icd10


/*page 21 */
sum  q30460  q30461  q30462  q30463  q30464  /*
*/ q30465a_name  q30465a_often  q30465a_long  q30465b_name  q30465b_often  q30465b_long /*
```

```
*/ q30465c_name  q30465c_often  q30465c_long  q30465d_name  q30465d_often  q30465d_long /*
*/ q30465e_name  q30465e_often  q30465e_long  q30465f_name  q30465f_often  q30465f_long /*
*/ q30465g_name  q30465g_often  q30465g_long  q30465h_name  q30465h_often  q30465h_long /*
*/ q30465i_name  q30465i_often  q30465i_long  q30465j_name  q30465j_often  q30465j_long /*
*/ q30465k_name  q30465k_often  q30465k_long  q30465l_name  q30465l_often  q30465l_long /*
*/ q30466a_name  q30466a_often  q30466a_long  q30466b_name  q30466b_often  q30466b_long /*
*/ q30466c_name  q30466c_often  q30466c_long  q30466d_name  q30466d_often  q30466d_long /*
*/ q30466e_name  q30466e_often  q30466e_long

/*page 22 */
sum  d3010  d3011  d3020  d3021  d3022  d3023  d3024  d3025  d3026  d3027  d3028  d3030  d3031  d3032

/*page 23 */
sum  d3040  d3041  d3042  d3043  d3044  d3045  d3046  d3047  d3048  d3049  d30410  d30411  d30412  d30413  d30414 /*
*/d3050  d3051  d3052  d3053  d3054  d3055  d3056ou1  d3056ou2  d3056ou3  d3056ou4  d3056ou5

sum d3060  d3061  d3070  d3071  d3073  d3074  d3075  d3077slices  d3077thick  d3078slices  d3078thick  d3079slices  d3079thick  d30710slices
/*
*/ d30710thick  d3080  d3081  d3082  d3083  d3084  d3090  d3091  d3092  d3093  d3094  d3095  d3096  d3097  d3098

/*page 24 */
sum  d30100  d30101  d30110  d30111  d30112  d30113  d30114    d30120  d30121  d30122  d30130  d30130o  d30131  d30132  d30140  d30141  /*
*/ d30150but  d30150ffmarg  d30150ffmarg_ou  d30150lfmarg  d30150lfmarg_ou  d30150hmarg  d30151  d30152  d30152_br  d30153  d30153_br  /*
*/ d30160nadul  d30160nch1to4  d30160nch5to16  d30160nch_u1yr  d30161lbs  d30161ozs  d30161gr  d30162lbs  d30162ozs  d30162gr  d30163lbs  /*
*/ d30163ozs  d30163gr  d30164ozs  d30164ml  d30165ozs  d30165ml  d30166ozs  d30166ml  d30167lbs  d30167ozs  d30167gr  d30168lbs  d30168ozs /*
*/ d30168gr  d30169lbs  d30169ozs  d30169gr

/*page 25 */
sum  d30170  d30171  d30172  d30173  d30174  d30175  d30177  d30180  d30181  /*
*/ d30181mon_i  d30181mon_ii  d30181mon_iii  d30181mon_iv  d30181mon_v  d30181tue_i   d30181tue_ii   d30181tue_iii  d30181tue_iv  d30181tue_v
/*
*/ d30181wed_i  d30181wed_ii  d30181wed_iii  d30181wed_iv  d30181wed_v  d30181thu_i  d30181thu_ii  d30181thu_iii  d30181thu_iv  d30181thu_v /*
*/ d30181fri_i  d30181fri_ii  d30181fri_iii  d30181fri_iv  d30181fri_v  d30181sat_i  d30181sat_ii  d30181sat_iii  d30181sat_iv  d30181sat_v /*
*/ d30181sun_i  d30181sun_ii  d30181sun_iii  d30181sun_iv  d30181sun_v  d30182  d30183

/*DATA SHEET*/
sum    Q30time_hour  /*
*/     Q30time_min   /*
*/     Q30sitstand5  /*
*/     Q30sitstand5_secs    /*
*/     Q30sitstand5t_n      /*
*/     Q30walk3m     /*
*/     Q30walk3m_secs       /*
*/     Q30walk3m_inc /*
*/     Q30height     /*
*/     Q30weight     /*
*/     Q30weight2    /*
*/     Q30waistc1    /*
*/     Q30waistc2    /*
*/     Q30hip1       /*
```

```
*/     Q30hip2      /*
*/     Q30armc      /*
*/     Q30tricep1   /*
*/     Q30tricep2   /*
*/     Q30subscap1  /*
*/     Q30subscap2  /*
*/     Q30sbpsit1   /*
*/     Q30sbpsit2   /*
*/     Q30sbpstand1 /*
*/     Q30sbpstand2 /*
*/     Q30dbpsit1   /*
*/     Q30dbpsit2   /*
*/     Q30dbpstand1 /*
*/     Q30dbpstand2 /*
*/     Q30hratesit1 /*
*/     Q30hratesit2 /*
*/     Q30hratestand1     /*
*/     Q30hratestand2     /*
*/     Q30bp_cuff   /*
*/     Q30bp_instr  /*
*/     Q30faintness /*
*/     Q30breathless/*
*/     Q30room_temp /*
*/     Q30ethnicity /*
*/     Q30spir_instr/*
*/     Q30inh24h    /*
*/     Q30time_inh_h/*
*/     Q30time_inh_m/*
*/     Q30btv_dsheet/*
*/     Q30ci  /*
*/     Q30grip_instr/*
*/     Q30grip_r1   /*
*/     Q30grip_r2   /*
*/     Q30grip_r3   /*
*/     Q30grip_dom_r/*
*/     Q30grip_l1   /*
*/     Q30grip_l2   /*
*/     Q30grip_l3   /*
*/     Q30grip_dom_l/*
*/     Q30spir_ref  /*
*/     Q30spir_nblows     /*
*/     Q30spir_btv  /*
*/     Q30fvc /*
*/     Q30fev05     /*
*/     Q30fev1      /*
*/     Q30pef /*
*/     Q30fef2575   /*
*/     Q30fef7585   /*
*/     Q30fef25     /*
*/     Q30fef50     /*
```

```
*/	Q30fef75	/*
*/	Q30bc_dated	/*
*/	Q30bc_datem	/*
*/	Q30bc_datey	/*
*/	Q30bc_timeh	/*
*/	Q30bc_timem	/*
*/	Q30bc_bodytype		/*
*/	Q30bc_gender	/*
*/	Q30bc_age	/*
*/	Q30bc_height	/*
*/	Q30bc_weight	/*
*/	Q30bc_bmi	/*
*/	Q30bc_BMR_kj	/*
*/	Q30bc_bmr_kcal		/*
*/	Q30bc_fat_pc	/*
*/	Q30bc_fatmass	/*
*/	Q30bc_ffm	/*
*/	Q30bc_tbw	/*
*/	Q30bc_VFR	/*
*/	Q30bc_drange_fatpc_min	/*
*/	Q30bc_drange_fatpc_max	/*
*/	Q30bc_drange_fmass_min	/*
*/	Q30bc_drange_fmass_max	/*
*/	Q30imp_wb	/*
*/	Q30imp_rl	/*
*/	Q30imp_ll	/*
*/	Q30imp_ra	/*
*/	Q30imp_la	/*
*/	Q30rleg_fat	/*
*/	Q30rleg_fmass	/*
*/	Q30rleg_ffm	/*
*/	Q30rleg_pmmass		/*
*/	Q30lleg_fat	/*
*/	Q30lleg_fmass	/*
*/	Q30lleg_ffm	/*
*/	Q30lleg_pmmass		/*
*/	Q30rarm_fat	/*
*/	Q30rarm_fmass	/*
*/	Q30rarm_ffm	/*
*/	Q30rarm_pmmass		/*
*/	Q30larm_fat	/*
*/	Q30larm_fmass	/*
*/	Q30larm_ffm	/*
*/	Q30larm_pmmass		/*
*/	Q30trunk_fat	/*
*/	Q30trunk_fmass		/*
*/	Q30trunk_ffm	/*
*/	Q30trunk_pmmass		/*
*/	Q30BT_SUCC	/*
*/	Q30BT_PR	/*
```

```
*/     Q30BT_TIMEH  /*
*/     Q30BT_TIMEM  /*
*/     Q30BT_FAST_INSTR    /*
*/     Q30BT_FAST_TLEH     /*
*/     Q30BT_FAST_TLEM     /*
*/     Q30BT_FAST_DLE      /*
*/     Q30BT_id_batch      /*
*/     Q30BT_id_serial     /*
*/     Q30BT_IncS_A /*
*/     Q30BT_IncS_B /*
*/     Q30BT_IncS_C /*
*/     Q30BT_IncS_DE/*
*/     Q30BT_IncS_FJ/*
*/     Q30BT_IncS_K /*
*/     Q30BT_IncS_LN/*
*/     Q30BT_IncS_PS/*
*/     Q30BT_IncS_T /*
*/     Q30ecg /*
*/     Q30ankle_oed_l      /*
*/     Q30ankle_oed_r      /*
*/     Q30actigraph /*
*/     Q30actigraph_id_batch      /*
*/     Q30actigraph_id_serial     /*
*/     Q30bstat_dob_d      /*
*/     Q30bstat_dob_m      /*
*/     Q30bstat_dob_y      /*
*/     Q30bstat_RoomTemp   /*
*/     Q30bstat_SkinTemp   /*
*/     Q30bstat_Pacemaker  /*
*/     Q30bstat_Instrument /*
*/     Q30bodystat  /*
*/     Q30cons_q1   /*
*/     Q30cons_q2   /*
*/     Q30cons_q3   /*
*/     Q30cons_signed      /*
*/     Q30xd  /*
*/     Q30xm  /*
*/     Q30xy  /*
*/     Q30ExamTown  /*
/*BIOCHEMISTRY*/
*/     Q30bioch_day /*
*/     Q30bioch_month      /*
*/     Q30bioch_year/*
*/     Q30sodium    /*
*/     Q30potass    /*
*/     Q30creat     /*
*/     Q30urea      /*
*/     Q30alb /*
*/     Q30tbili     /*
*/     Q30aphos     /*
```

```
*/	Q30ast	/*
*/	Q30alt	/*
*/	Q30phosph	/*
*/	Q30calc	/*
*/	Q30ccalc	/*
*/	Q30chol	/*
*/	Q30chdr	/*
*/	Q30hdlc	/*
*/	Q30ldlc	/*
*/	Q30trig	/*
*/	Q30ggt	/*
*/	Q30magn	/*
*/	Q30tprot	/*
*/	Q30urat	/*
*/	Q30gluc	/*
*/	Q30hba1c	/*
*/	Q30hba1c_note	/*
*/	Q30Bioch_note	/*
/* HAEMATOLOGY*/
*/	q30Haem_day	/*
*/	q30Haem_month	/*
*/	q30Haem_year	/*
*/	q30Hb	/*
*/	q30WBC	/*
*/	q30PLAT	/*
*/	q30RBC	/*
*/	q30RDW	/*
*/	q30HCT	/*
*/	q30MCV	/*
*/	q30MCH	/*
*/	q30MCHC	/*
*/	q30Neutro_Abs	/*
*/	q30Lymph_abs	/*
*/	q30Monocy_abs	/*
*/	q30Eosin_Abs	/*
*/	q30Baso_abs	/*
*/	q30MPV	/*
*/	q30Haem_note	/*
/*ECG */
*/	serial_ecg	/*
*/	Q30ECG_Count	/*
*/	Q30ECG_Age	/*
*/	Q30ECG_Heart_Rate_bpm	/*
*/	Q30ECG_P_axis_degree	/*
*/	Q30ECG_QRS_axis_degree	/*
*/	Q30ECG_T_axis_degree	/*
*/	Q30ECG_P_duration_ms	/*
*/	Q30ECG_QRS_duration_ms	/*
*/	Q30ECG_PR_interval_ms	/*
*/	Q30ECG_QT_interval_ms	/*
```

```
*/     Q30ECG_QTC_interval_ms     /*
*/     Q30ECG_Minnesota_group1_L  /*
*/     Q30ECG_Serial_type1_1      /*
*/     Q30ECG_Minnesota_group1_P  /*
*/     Q30ECG_Srial_type1_2       /*
*/     Q30ECG_Minnesota_group1_A  /*
*/     Q30ECG_Serial_type1_3      /*
*/     Q30ECG_Minnesota_group2_1  /*
*/     Q30ECG_No_serial_comparison1      /*
*/     Q30ECG_Minnesota_group2_2  /*
*/     Q30ECG_No_serial_comparison2      /*
*/     Q30ECG_Snnesota_group3     /*
*/     Q30ECG_No_serial_comparison3      /*
*/     Q30ECG_Minnesota_group4_L  /*
*/     Q30ECG_Serial_type1_4      /*
*/     Q30ECG_Minnesota_group4_P  /*
*/     Q30ECG_Serial_type1_5      /*
*/     Q30ECG_Minnesota_group4_A  /*
*/     Q30ECG_Serial_type1_6      /*
*/     Q30ECG_Minnesota_group5_L  /*
*/     Q30ECG_Serial_type1_7      /*
*/     Q30ECG_Minnesota_group5_P  /*
*/     Q30ECG_Serial_type1_8      /*
*/     Q30ECG_Minnesota_group5_A  /*
*/     Q30ECG_Serial_type1_9      /*
*/     Q30ECG_Minnesota_group6    /*
*/     Q30ECG_No_serial_comparison4      /*
*/     Q30ECG_Minnesota_group7_1  /*
*/     Q30ECG_Serial_type1_10     /*
*/     Q30ECG_Minnesota_group7_2  /*
*/     Q30ECG_No_serial_comparison5      /*
*/     Q30ECG_Minnesota_group8_1  /*
*/     Q30ECG_No_serial_comparison6      /*
*/     Q30ECG_Minnesota_group8_2  /*
*/     Q30ECG_No_serial_comparison7      /*
*/     Q30ECG_Minnesota_group8_3  /*
*/     Q30ECG_No_serial_comparison8      /*
*/     Q30ECG_Minnesota_group8_4  /*
*/     Q30ECG_No_serial_comparison9      /*
*/     Q30ECG_Minnesota_group9_L  /*
*/     Q30ECG_Serial_type1_11     /*
*/     Q30ECG_Minnesota_group9_P  /*
*/     Q30ECG_Serial_type1_12     /*
*/     Q30ECG_Minnesota_group9_A  /*
*/     Q30ECG_Serial_type1_13     /*
*/     Q30ECG_Minnesota_group9m_1 /*
*/     Q30ECG_No_serial_comparison10     /*
*/     Q30ECG_Minnesota_group9m_2 /*
*/     Q30ECG_No_serial_comparison11     /*
*/     Q30ECG_LVMI_Rautaharju_    /*
```

```
*/     Q30ECG_LVMI_F_Huwez /*
*/     Q30ECG_Summary_1    /*
*/     Q30ECG_Cornell_Index_V     /*
*/     Q30ECG_Cornell_Product_VS  /*
*/     Q30ECG_Sokolow_Lyon_V      /*
*/     Q30ECG_QRS_voltage_sum_V   /*
*/     Q30ECG_QRS_voltage_prod_VS /*
*/     Q30ECG_SYS_DATE_D   /*
*/     Q30ECG_SYS_DATE_M   /*
*/     Q30ECG_SYS_DATE_Y   /*
*/     Q30ECG_RECEIVED_D   /*
*/     Q30ECG_RECEIVED_M   /*
*/     Q30ECG_RECEIVED_Y   /*
/*TEST YOUR MEMORY*/
*/     Serial_tym   /*
*/     Q30TYM_score1_Full_name    /*
*/     Q30TYM_score2_Today_Day    /*
*/     Q30TYM_score3_Today_Date   /*
*/     Q30TYM_score4_How_old      /*
*/     Q30TYM_score5_Date_born    /*
*/     Q30TYM_score6_Copy_sentence      /*
*/     Q30TYM_score7_PM    /*
*/     Q30TYM_score8_WWI   /*
*/     Q30TYM_score9_Sums  /*
*/     Q30TYM_score10_Creatures_S /*
*/     Q30TYM_score11_Carrot      /*
*/     Q30TYM_score12_Lion /*
*/     Q30TYM_score13_Name_items  /*
*/     Q30TYM_score14_Join_circles      /*
*/     Q30TYM_score15_Clock       /*
*/     Q30TYM_score16_Rewrite_sentence  /*
/* INDICATOR VARIABLES*/
*/     with_q30qr   /*
*/     with_q30ds   /*
*/     with_q30ecg  /*
*/     with_q30tym  /*
*/     with_q30ecg         /*
*/     with_q30tym

ren with_Q30bioch with_q30bioch

label var     serial "BRHS STUDY NUMBER  "

label var     q30batch "Q30 EXAMINATION BATCH NUMBER  "
label var     Q30obs   "Observer  "
label var     Q30time_hour  "Time of screening: HOUR  "
label var     Q30time_min  "Time of screening: MINUTES       "
label var     Q30sitstand5  "Unable to do Sit/Stand test  -reason:  "
label var     Q30sitstand5_secs  "Time taken to do Sit/Stand 5 times : Seconds   "
label var     Q30sitstand5t_n   "Number of times able to Sit/stand in 30sec      "
```

```
label var    Q30sitstand5t_h   "Used hands to do sit/stand test    "
label var    Q30walk3m  "Unable to do the Walk 3meters  test  - reason:  "
label var    Q30walk3m_secs  "Time taken to Walk 3m: Seconds       "
label var    Q30walk3m_inc  "Unable to complete Walk 3m test in 30sec     "
label var    Q30height  "Height (cm)    "
label var    Q30ht_p   "Height measurement Problem   "
label var    Q30weight  "Weight (using Tanita scales OR digital scales) (kg)    "
label var    Q30wt_p   "Weight measurement Problem   "
label var    Q30weight2  "Weight (for those with pacemaker - using digital scales) (kg)      "
label var    Q30waistc1  "Waist circumference - measurement 1 - (cm)      "
label var    Q30waistc2  "Waist circumference - measurement 2 - (cm)      "
label var    Q30waist_p  "Waist circumference - measurement Problem       "
label var    Q30hip1  "Hip circumference measurement 1 (cm) "
label var    Q30hip2  "Hip circumference measurement 2 (cm) "
label var    Q30hip_p    "Hip circumference measurement Problem    "
label var    Q30armc  "Arm circumference (cm)  "
label var    Q30armc_p   "Arm circumference problem  "
label var    Q30tricep1  "Triceps measurement 1 (mm) "
label var    Q30tricep2  "Triceps measurement 2 (mm) "
label var    Q30tricep_p   "Triceps measurement Problem     "
label var    Q30subscap1  "Subscap measurement  1 (mm)      "
label var    Q30subscap2  "Subscap measurement  2 (mm)      "
label var    Q30subscap_p  "Subscap measurement Problem     "
label var    Q30sbpsit1  "SBP sitting - measurement 1       "
label var    Q30sbpsit2  "SBP sitting - measurement 2       "
label var    Q30sbpstand1  "SBP standing - measurement 1    "
label var    Q30sbpstand2  "SBP standing - measurement 2    "
label var    Q30dbpsit1  "DBP sitting - measurement 1       "
label var    Q30dbpsit2  "DBP sitting - measurement 2       "
label var    Q30dbpstand1  "DBP  standing - measurement 1   "
label var    Q30dbpstand2  "DBP  standing - measurement 2   "
label var    Q30hratesit1  "Heart Rate  sitting - measurement 1    "
label var    Q30hratesit2  "Heart Rate  sitting - measurement 2    "
label var    Q30hratestand1  "Heart Rate  standing - measurement 1"
label var    Q30hratestand2  "Heart Rate  standing - measurement 2"
label var    Q30bp_cuff  "BP cuff size (based on Arm circ(cm)      "
label var    Q30bp_instr   "BP instrument     "
label var    Q30bp_instr_p   "BP instrument problem  "
label var    Q30faintness  "Subject felt Faint"
label var    Q30breathless  "Subject felt Breathless "
label var    Q30room_temp  "Room temperature(oC)     "
label var    Q30ethnicity  "Ethnicity   "
label var    Q30spir_instr  "Spirometry instrument number   "
label var    Q30inh24h  "Subject used Inhaler in last 24hours      "
label var    Q30time_inh_h  "Subject used Inhaler: TIME inhaler used HOUR       "
label var    Q30time_inh_m  "Subject used Inhaler: TIME inhaler used MINUTES    "
label var    Q30btv_dsheet  "BTV from lung function output - recorded on datasheet    "
label var    Q30ci  "Contraindications to the lung function test  "
label var    Q30ci_p  "Problem with performing Lung Function test  "
label var    Q30grip_instr  "Grip instrument - number       "
```

```
label var    Q30grip_r1  "Grip strength RIGHT HAND measurement 1   "
label var    Q30grip_r2  "Grip strength RIGHT HAND measurement 2   "
label var    Q30grip_r3  "Grip strength RIGHT HAND measurement 3   "
label var    Q30grip_dom_r  "Grip strength RIGHT HAND Dominant     "
label var    Q30grip_rp  "Grip strength RIGHT HAND Problem  "
label var    Q30grip_l1  "Grip strength LEFT HAND measurement 1    "
label var    Q30grip_l2  "Grip strength LEFT HAND measurement 2    "
label var    Q30grip_l3  "Grip strength LEFT HAND measurement 3    "
label var    Q30grip_dom_l  "Grip strength LEFT HAND Dominant      "
label var    Q30grip_lp  "Grip strength LEFT HAND Problem   "
label var    Q30spir_ref  "Spirometry batch number   "
label var    Q30spir_nblows  "Spirometry Number of Blows    "
label var    Q30spir_btv  "Spirometry BTV     "
label var    Q30fvc "Spirometry FVC     "
label var    Q30fev05 "Spirometry FEV0.5       "
label var    Q30fev1 "Spirometry FEV1   "
label var    Q30pef "Spirometry PEF     "
label var    Q30fef2575 "Spirometry FEF 25-75%"
label var    Q30fef7585 "Spirometry FEF 75-85%"
label var    Q30fef25 "Spirometry FEF 25%     "
label var    Q30fef50 "Spirometry FEF 50%     "
label var    Q30fef75 "Spirometry FEF 75%     "
label var    Q30bc_dated  "Body Composition date - day      "
label var    Q30bc_datem  "Body Composition date - month    "
label var    Q30bc_datey  "Body Composition date - year     "
label var    Q30bc_timeh  "Body Composition time - hour     "
label var    Q30bc_timem  "Body Composition time - mins     "
label var    Q30bc_bodytype  "Body Composition - Body type  "
label var    Q30bc_gender  "Body Composition - Gender       "
label var    Q30bc_age  "Body Composition - Age      "
label var    Q30bc_height  "Body Composition - height       "
label var    Q30bc_weight  "Body Composition - weight       "
label var    Q30bc_bmi  "Body Composition - bmi      "
label var    Q30bc_BMR_kj  "Body Composition - Basal Metabolic Rate (kj -kilojoules)  "
label var    Q30bc_bmr_kcal  "Body Composition -  Basal Metabolic Rate (kcal- kilocalories)  "
label var    Q30bc_fat_pc "Body Composition - %Fat   "
label var    Q30bc_fatmass  "Body Composition - Fat Mass    "
label var    Q30bc_ffm  "Body Composition - Fat Free Mass   "
label var    Q30bc_tbw  "Body Composition - Total Body Water      "
label var    Q30bc_VFR  "Body Composition - Visceral Fat Rating   "
label var    Q30bc_drange_fatpc_min  "Body Composition - %Fat Desirable range Min     "
label var    Q30bc_drange_fatpc_max "Body Composition - %Fat Desirable range Max      "
label var    Q30bc_drange_fmass_min  "Body Composition - Fat Mass Desirable range Min  "
label var    Q30bc_drange_fmass_max  "Body Composition - Fat Mass Desirable range Max  "
label var    Q30imp_wb  "Impedance Whole Body  "
label var    Q30imp_rl  "Impedance Right Leg   "
label var    Q30imp_ll  "Impedance Left Leg    "
label var    Q30imp_ra  "Impedance Right Arm   "
label var    Q30imp_la  "Impedance Left Arm    "
label var    Q30rleg_fat  "Right Leg FAT%     "
```

```
label var    Q30rleg_fmass  "Right Leg FAT MASS      "
label var    Q30rleg_ffm  "Right Leg Fat Free Mass   "
label var    Q30rleg_pmmass  "Right Leg Predicted Muscle Mass      "
label var    Q30lleg_fat  "Left Leg FAT%      "
label var    Q30lleg_fmass  "Left Leg FAT MASS"
label var    Q30lleg_ffm  "Left Leg Fat Free Mass    "
label var    Q30lleg_pmmass  "Left Leg Predicted Muscle Mass       "
label var    Q30rarm_fat  "Right Arm FAT%     "
label var    Q30rarm_fmass  "Right Arm FAT MASS      "
label var    Q30rarm_ffm  "Right Arm Fat Free Mass   "
label var    Q30rarm_pmmass  "Right Arm Predicted Muscle Mass      "
label var    Q30larm_fat  "Left Arm FAT%      "
label var    Q30larm_fmass  "Left Arm FAT MASS"
label var    Q30larm_ffm  "Left Arm Fat Free Mass    "
label var    Q30larm_pmmass  "Left Arm Predicted Muscle Mass       "
label var    Q30trunk_fat  "Trunk Fat%  "
label var    Q30trunk_fmass  "Trunk Fat Mass  "
label var    Q30trunk_ffm  "Trunk Fat Free Mass      "
label var    Q30trunk_pmmass  "Trunk Predicted Muscle Mass  "
label var    Q30BT_SUCC  "Blood Test performed successfully       "
label var    Q30BT_PR  "Blood Test problem    "
label var    Q30BT_TIMEH  "Blood Test Time - Hour    "
label var    Q30BT_TIMEM  "Blood Test Time - Min     "
label var    Q30BT_FAST_INSTR  "Blood Test Fasting instructions    "
label var    Q30BT_FAST_TLEH  "Blood Test - Time last eaten Hour   "
label var    Q30BT_FAST_TLEM  "Blood Test - Time last eaten Min    "
label var    Q30BT_FAST_DLE  "Blood Test - DAY last eaten   "
label var    Q30BT_id_batch  "Blood Test - batch number     "
label var    Q30BT_id_serial "Blood Test - serial number    "
label var    Q30BT_IncS_A  "Citrate- Green tube      "
label var    Q30BT_IncS_B  "Citrate- Green tube      "
label var    Q30BT_IncS_C  "Serum gel - Yellow Tube  "
label var    Q30BT_IncS_DE  "Serum gel - Yellow Tube "
label var    Q30BT_IncS_FJ  "Serum gel - Yellow Tube "
label var    Q30BT_IncS_K  "EDTA       "
label var    Q30BT_IncS_LN  "EDTA - Red Tube  "
label var    Q30BT_IncS_PS  "EDTA - Red Tube  "
label var    Q30BT_IncS_T  "Fluroride oxalate "
label var    Q30ecg  "ECG performed    "
label var    Q30ankle_oed_l  "Ankle oedema Left leg  "
label var    Q30ankle_oed_r  "Ankle oedema Right leg "
label var    Q30actigraph  "Agreed to take part in Atcigraph study/wear actigraph     "
label var    Q30actigraph_id_batch  "recorded batch  "
label var    Q30actigraph_id_serial  "recorded serial      "
label var    Q30bstat_dob_d  "BODYSTAT - DOB day     "
label var    Q30bstat_dob_m  "BODYSTAT - DOB month   "
label var    Q30bstat_dob_y  "BODYSTAT - DOB year    "
label var    Q30bstat_RoomTemp  "BODYSTAT - Room Temperature      "
label var    Q30bstat_SkinTemp  "BODYSTAT - Skin Temperature      "
label var    Q30bstat_Pacemaker  "BODYSTAT - Pacemaker is worn     "
```

```
label var    Q30bstat_Instrument "BODYSTAT - Instrument     "
label var    Q30bodystat "BODYSTAT - reading   "
label var    Q30cons_q1  "Q1 Consent form      "
label var    Q30cons_q2  "Q2 Consent form      "
label var    Q30cons_q3  "Q3 Consent form      "
label var    Q30cons_signed  "Consent was signed      "
label var    Q30cons_date   "Date consent was signed "
label var    Q30xd  "Q30 screening Examination DAY   "
label var    Q30xm  "Q30 screening Examination MONTH "
label var    Q30xy  "Q30 screening Examination YEAR  "
label var    Q30ExamTown   "Town where participant was examined    "
label var    Q30bioch_day "Bioch Laboratory date(day)       "
label var    Q30bioch_month "Bioch Laboratory date(month)   "
label var    Q30bioch_year "Bioch Laboratory date(year)     "
label var    Q30sodium "Sodium   mmol/l "
label var    Q30potass "potassium   mmol/l     "
label var    Q30creat "Creatinine   µ mol/l    "
label var    Q30urea "Urea  mmol/l      "
label var    Q30alb "Albumin   g/l      "
label var    Q30tbili "Total Bilirubin  µ mol/l       "
label var    Q30aphos "Alk Phosphate  mmol/l   "
label var    Q30ast "Aspartame Transaminase   u/l     "
label var    Q30alt "Alanine Transaminase u/l  "
label var    Q30phosph "Phosphate  mmol/l      "
label var    Q30calc "Calcium           "
label var    Q30ccalc "Corrected Calcium             "
label var    Q30chol "Cholesterol    mmol/l    "
label var    Q30chdr "CHDR             "
label var    Q30hdlc "HDL  mmol/l       "
label var    Q30ldlc "LDL   mmol/l      "
label var    Q30trig "Triglycerides  mmol/l    "
label var    Q30ggt "Gamma GT u/l       "
label var    Q30magn "magnesium                "
label var    Q30tprot "Total Protein g/l       "
label var    Q30urat "Urate             "
label var    Q30gluc "Blood Glucose mmol/l     "
label var    Q30hba1c "Glycated Haemoglobin  %"
label var    Q30hba1c_note "Biochemistry Laboratory comment ON HBA1C     "
label var    Q30Bioch_note "Biochemistry Laboratory comment "
label var    q30Haem_day "Haem Laboratory date(day)  "
label var    q30Haem_month  "Haem Laboratory date(month)    "
label var    q30Haem_year "Haem Laboratory date(year)       "
label var    q30Hb "Haemoglobin  g/l    "
label var    q30WBC "White Blood Cell Count  109 /l  "
label var    q30PLAT "Platelets 109 /l  "
label var    q30RBC "Red Blood Cell Count  1012 /l   "
label var    q30RDW "Red Blood Cell Distribution Width            "
label var    q30HCT "Hematocrit l/l     "
label var    q30MCV "Mean Cell Volume  fl      "
label var    q30MCH "Mean Cell Hemoglobin  pg  "
```

```
label var    q30MCHC "Mean Cell Hemoglobin Concentration  g/dl    "
label var    q30Neutro_Abs "Neutrophils Absolue Value       "
label var    q30Lymph_abs "Lymphocytes Absolute Value "
label var    q30Monocy_abs "Monocytes Absolute Value  "
label var    q30Eosin_Abs "Eosinophils Absolute Value "
label var    q30Baso_abs "Basophils Absolute Value    "
label var    q30MPV "Mean Platelet Volume      "
label var    q30Haem_note "Haematology Laboratory comment   "

label var    serial_ecg "ECG ID  "

label var    Q30ECG_Count "ECG Count    "
label var    Q30ECG_Age "Age     "
label var    Q30ECG_Heart_Rate_bpm "Heart Rate (bpm) "
label var    Q30ECG_P_axis_degree "P axis (degree)   "
label var    Q30ECG_QRS_axis_degree "QRS axis (degree)      "
label var    Q30ECG_T_axis_degree "T axis (degree)   "
label var    Q30ECG_P_duration_ms "P duration (ms)   "
label var    Q30ECG_QRS_duration_ms "QRS duration (ms)      "
label var    Q30ECG_PR_interval_ms "PR interval (ms) "
label var    Q30ECG_QT_interval_ms "QT interval (ms) "
label var    Q30ECG_QTC_interval_ms "QTC interval (ms)      "
label var    Q30ECG_Minnesota_group1_L "Minnesota group1_L  "
label var    Q30ECG_Serial_type1_1 "Serial type1_1   "
label var    Q30ECG_Minnesota_group1_P "Minnesota group1_P  "
label var    Q30ECG_Srial_type1_2 "Srial type1_2     "
label var    Q30ECG_Minnesota_group1_A "Minnesota group1_A  "
label var    Q30ECG_Serial_type1_3 "Serial type1_3   "
label var    Q30ECG_Minnesota_group2_1 "Minnesota group2_1  "
label var    Q30ECG_No_serial_comparison1 "No serial comparison    "
label var    Q30ECG_Minnesota_group2_2 "Minnesota group2_2  "
label var    Q30ECG_No_serial_comparison2 "No serial comparison    "
label var    Q30ECG_Snnesota_group3 "Snnesota group3 "
label var    Q30ECG_No_serial_comparison3 "No serial comparison    "
label var    Q30ECG_Minnesota_group4_L "Minnesota group4_L  "
label var    Q30ECG_Serial_type1_4 "Serial type1_4   "
label var    Q30ECG_Minnesota_group4_P "Minnesota group4_P  "
label var    Q30ECG_Serial_type1_5 "Serial type1_5   "
label var    Q30ECG_Minnesota_group4_A "Minnesota group4_A  "
label var    Q30ECG_Serial_type1_6 "Serial type1_6   "
label var    Q30ECG_Minnesota_group5_L "Minnesota group5_L  "
label var    Q30ECG_Serial_type1_7 "Serial type1_7   "
label var    Q30ECG_Minnesota_group5_P "Minnesota group5_P  "
label var    Q30ECG_Serial_type1_8 "Serial type1_8   "
label var    Q30ECG_Minnesota_group5_A "Minnesota group5_A  "
label var    Q30ECG_Serial_type1_9 "Serial type1_9   "
label var    Q30ECG_Minnesota_group6 "Minnesota group6      "
label var    Q30ECG_No_serial_comparison4 "No serial comparison    "
label var    Q30ECG_Minnesota_group7_1 "Minnesota group7_1  "
label var    Q30ECG_Serial_type1_10 "Serial type1_10 "
```

```
label var    Q30ECG_Minnesota_group7_2 "Minnesota group7_2  "
label var    Q30ECG_No_serial_comparison5 "No serial comparison   "
label var    Q30ECG_Minnesota_group8_1 "Minnesota group8_1  "
label var    Q30ECG_No_serial_comparison6 "No serial comparison   "
label var    Q30ECG_Minnesota_group8_2 "Minnesota group8_2  "
label var    Q30ECG_No_serial_comparison7 "No serial comparison   "
label var    Q30ECG_Minnesota_group8_3 "Minnesota group8_3  "
label var    Q30ECG_No_serial_comparison8 "No serial comparison   "
label var    Q30ECG_Minnesota_group8_4 "Minnesota group8_4  "
label var    Q30ECG_No_serial_comparison9 "No serial comparison   "
label var    Q30ECG_Minnesota_group9_L "Minnesota group9_L  "
label var    Q30ECG_Serial_type1_11 "Serial type1_11 "
label var    Q30ECG_Minnesota_group9_P "Minnesota group9_P  "
label var    Q30ECG_Serial_type1_12 "Serial type1_12 "
label var    Q30ECG_Minnesota_group9_A "Minnesota group9_A  "
label var    Q30ECG_Serial_type1_13 "Serial type1_13 "
label var    Q30ECG_Minnesota_group9m_1 "Minnesota group9m_1      "
label var    Q30ECG_No_serial_comparison10 "No serial comparison  "
label var    Q30ECG_Minnesota_group9m_2 "Minnesota group9m_2      "
label var    Q30ECG_No_serial_comparison11 "No serial comparison  "
label var    Q30ECG_LVMI_Rautaharju_ "LVMI Rautaharju      "
label var    Q30ECG_LVMI_F_Huwez "LVMI F. Huwez      "
label var    Q30ECG_Summary_1 "Summary_1      "
label var    Q30ECG_Cornell_Index_V "Cornell Index (µV)     "
label var    Q30ECG_Cornell_Product_VS "Cornell Product (µV.S)     "
label var    Q30ECG_Sokolow_Lyon_V "Sokolow-Lyon (µV)      "
label var    Q30ECG_QRS_voltage_sum_V "QRS voltage sum (µV) "
label var    Q30ECG_QRS_voltage_prod_VS "QRS voltage prod (µV.S)  "
label var    Q30ECG_SYS_DATE_D "System date- day     "
label var    Q30ECG_SYS_DATE_M "System date -month   "
label var    Q30ECG_SYS_DATE_Y "Systen date - year   "
label var    Q30ECG_RECEIVED_D "Received date - day  "
label var    Q30ECG_RECEIVED_M "Received date - month      "
label var    Q30ECG_RECEIVED_Y "Received date - year "

label var    Q30TYM_score1_Full_name "Please write your full name  "
label var    Q30TYM_score2_Today_Day "Today is …… DAY      "
label var    Q30TYM_score3_Today_Date "Today's date is the …      "
label var    Q30TYM_score4_How_old "How old are you … years "
label var    Q30TYM_score5_Date_born "On what date where you born  "
label var    Q30TYM_score6_Copy_sentence "Please copy the following sentence    "
label var    Q30TYM_score7_PM "Who is the Prime Minister(PM)      "
label var    Q30TYM_score8_WWI "In what year the World War I start?      "
label var    Q30TYM_score9_Sums "Sums - score for correct calculations   "
label var    Q30TYM_score10_Creatures_S "List four Creatures beginning with S   "
label var    Q30TYM_score11_Carrot "Why is a carrot like a potato  "
label var    Q30TYM_score12_Lion "Why is a lion like a wolf "
label var    Q30TYM_score13_Name_items "Please Name these items on drawing      "
label var    Q30TYM_score14_Join_circles "Join circles together to form a letter      "
label var    Q30TYM_score15_Clock "Dray a clock face "
```

```
label var    Q30TYM_score16_Rewrite_sentence "Write down sentence copied earlier       "
label var    with_q30qr  "Participant returned a Q30 Qr     "
label var    with_q30ds  "Participant has a Data Sheet      "
label var    with_q30bioch "with Biochemistry result "
label var    with_q30Haem "with Haematology result   "
label var    with_q30ecg  "Participant has ECG data  "
label var    with_q30tym "Participant has Test Your Memory data   "


saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file/Q30_5DEC13", replace


******************************************************
**************************  recoding of age
******************************************************



*** impute missing value for date of questionnaire if we have year

replace q3010d=1 if serial==140453
replace q3010d=15 if serial==114151 | serial==2064445 | serial==2094706 | serial==2188561 | serial==3126784 | serial==3300762
replace q3010m=8 if serial==114151 | serial==2064445 | serial==2094706 | serial==2188561 | serial==3126784 | serial==3300762


/* date q30 */
gen Q30date_quest=mdy(q3010m,q3010d,q3010y)
/* date examination */
gen Q30date_exam=mdy(Q30xm,Q30xd,Q30xy)
/* date bioch laboratory */
gen Q30date_lab=mdy(Q30bioch_month, Q30bioch_day, Q30bioch_year)

gen diff=Q30date_lab-Q30date_exam


******************************************************
**************************  insert date of birth
******************************************************

mmerge serial using "S:\Pop_Health\BRHS_Winter_Deaths\data\post codes\Olia_Q1_town_dob", ukeep(day month year)
keep if _merge==3


renvars day month year, prefix(dob_)
replace dob_year=1900+dob_year

gen dob=mdy(dob_month,dob_day,dob_year)
tabmiss dob

gen Q30age=(Q30date_exam-dob)/365.25
replace Q30age=(Q30date_quest-dob)/365.25 if Q30age==.
```

```
tabmiss Q30age


******************************************************
**************************  impute age using actigraph date
******************************************************

* use age from RS questionaire, more or less contemporary

mmerge serial using "S:\Pop_Health\PCPH_BRHS_ActiGraph\BRHS data\not validated data\after
Choi\Actigraph_A1_A2_with_greendiary_RSonly_with_derived_vars_and_Q20.dta", ukeep(*age* *start*)
drop if _merge==2

replace Q30age=a1age if Q30age==.
drop a1* age20 _merge
tabmiss Q30age

drop choi_startdate

mmerge serial using "S:\Pop_Health\PCPH_BRHS_ActiGraph\BRHS data\not validated data\after
Choi\Actigraph_A1_with_greendiary_RS_POSTAL_with_derived_vars_and_Q20.dta", ukeep(*age* *start*)
drop if _merge==2

replace Q30age=A1_a1age if Q30age==.

drop A1_choi_startdate-_merge

gen Q30age3cat=1 if Q30age<75
replace Q30age3cat=2 if Q30age>=75 & Q30age<80
replace Q30age3cat=3 if Q30age>=80 & Q30age!=.

label define Q30age3cat 1 "Age<75" 2 "Age 75-79" 3 "Age 80+"
label values Q30age3cat Q30age3cat
label var Q30age3cat "Age"


/*
preserve
keep serial Q30date_exam q30date_quest dob Q30age a1age *start*
keep if Q30age==.
keep serial
restore
*/

/*
* median of questionnaire date
sum q30date_quest, d
* median=18737
replace Q30age=(18737-dob)/365.25 if Q30age==.
sum Q30age
```

```
*/



******************************************************
**************************  OBSERVER RECODE
******************************************************

encode Q30obs, generate(Q30obs_num)



tabmiss Q30age

******************************************************
**************************  time of the day recoding
******************************************************




tab Q30time_hour Q30time_min
recode Q30time_hour (8 9 10  = 1) (11 12 = 2) (13 14 15 = 3) (16 17 18 = 4), gen(hh_cat)
label define hh_cat 1 "8h-9h-10h" 2 "11h-12h" 3 "13h-14h-15h" 4 "16h-17h-18h", modify
label values hh_cat hh_cat
label var hh_cat "Hour of the day"

gen time_hour_mm=((Q30time_hour*60)+Q30time_min)/60

******************************************************
**************************  time of the day recoding
******************************************************

recode Q30time_hour (8 9 10  = 1) (11 12 = 1) (13 14 15 = 2) (16 17 18 = 2), gen(hh_cat2)
label define hh_cat2 1 "Morning" 2 "Afternoon", modify
label values hh_cat2 hh_cat2
label var hh_cat2 "Part of the day"

******************************************************
**************************  recoding follow the instructions
******************************************************

label define fasting 1 "1.YES" 2 "2.NO" 3 "3.Diabetes", modify
label values Q30BT_FAST_INSTR fasting



recode  Q30BT_FAST_INSTR (1 2 =1) (3=2), gen(Q30BT_FAST_INSTR2)
tab Q30BT_FAST_INSTR2 Q30BT_FAST_INSTR
```

```
label define Q30BT_FAST_INSTR2 1 "1.Non diabetics" 2 "2.Diabetics", modify
label values Q30BT_FAST_INSTR2 Q30BT_FAST_INSTR2
label var Q30BT_FAST_INSTR2 "Diabetic status"

******************************************************
**************************  fasting recoding
******************************************************

tab1 Q30BT_FAST_INSTR Q30BT_FAST_TLEH Q30BT_FAST_TLEM

recode Q30BT_FAST_DLE 0=1 3=2


sort Q30obs Q30time_hour Q30BT_FAST_TLEH
gen fasting_same_day=Q30time_hour-Q30BT_FAST_TLEH if Q30BT_FAST_DLE==1

browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30BT_FAST_DLE==1

sort Q30obs Q30BT_FAST_DLE Q30time_hour Q30BT_FAST_TLEH
browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30obs=="GR"
browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30obs=="IB"
browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30obs=="NG"
browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30obs=="RW"
browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30obs=="SA"


***************** cleaning RW

replace Q30BT_FAST_DLE=2 if serial==    139121 /*
*/ | serial== 141663 /*
*/ | serial== 143762 /*
*/ | serial== 119868 /*
*/ | serial== 245169 /*
*/ | serial== 225721 /*
*/ | serial== 241323 /*
*/ | serial== 142077 /*
*/ | serial== 246236 /*
*/ | serial== 118669 /*
*/ | serial== 118891 /*
*/ | serial== 134158 /*
*/ | serial== 119771 /*
*/ | serial== 209421 /*
*/ | serial== 246084 /*
*/ | serial== 203776 /*
*/ | serial== 134993 /*
*/ | serial== 122992 /*
*/ | serial== 136016 /*
*/ | serial== 233181 /*
*/ | serial== 138546
```

```
replace Q30BT_FAST_INSTR=1 if serial==  139121 /*
*/ | serial== 141663 /*
*/ | serial== 143762 /*
*/ | serial== 119868 /*
*/ | serial== 245169 /*
*/ | serial== 225721 /*
*/ | serial== 241323 /*
*/ | serial== 142077 /*
*/ | serial== 246236 /*
*/ | serial== 118669 /*
*/ | serial== 118891 /*
*/ | serial== 134158 /*
*/ | serial== 119771 /*
*/ | serial== 209421 /*
*/ | serial== 246084 /*
*/ | serial== 203776 /*
*/ | serial== 134993 /*
*/ | serial== 122992 /*
*/ | serial== 136016 /*
*/ | serial== 233181 /*
*/ | serial== 138546

replace Q30BT_FAST_TLEH=20 if serial==118891
replace Q30BT_FAST_TLEH=22 if serial==134158
replace Q30BT_FAST_TLEH=19 if serial==119771
replace Q30BT_FAST_TLEH=22 if serial==209421
replace Q30BT_FAST_TLEH=22 if serial==246084
replace Q30BT_FAST_TLEH=20 if serial==203776
replace Q30BT_FAST_TLEH=21 if serial==134993
replace Q30BT_FAST_TLEH=22 if serial==122992
replace Q30BT_FAST_TLEH=19 if serial==136016
replace Q30BT_FAST_TLEH=20 if serial==233181
replace Q30BT_FAST_TLEH=19 if serial==138546

***************** cleaning RW

*** check with lucy
*** 118781
*** 121485

browse serial Q30obs      Q30BT_FAST_INSTR    Q30time_hour Q30BT_FAST_TLEH     Q30BT_FAST_TLEM Q30BT_FAST_DLE    fasting_same_day
       Q30time_inh_h Q30time_inh_m Q30BT_TIMEH   Q30BT_TIMEM /*
*/ if serial==118781 | serial==121485

replace Q30BT_FAST_INSTR=2 if serial==121485

*** 118781 messy one
replace Q30BT_FAST_DLE=1 if serial==118781
```

```
/*
serial Q30obs Q30BT_FAST_INSTR    Q30time_hour  Q30BT_FAST_TLEH     Q30BT_FAST_DLE
118781 RW     2.NO   10     10     2
*/

replace Q30BT_FAST_DLE=1 if serial==118781 | serial==136643 | serial==137534 | serial==240773
replace Q30BT_FAST_INSTR=1 if serial==247703
replace Q30BT_FAST_INSTR=1 if serial==220144
replace Q30BT_FAST_INSTR=1 if serial==208715
replace Q30BT_FAST_DLE=2 if serial==220144

replace Q30time_min=29 if serial==124356
/*
serial Q30obs Q30BT_FAST_INSTR    Q30time_hour  Q30BT_FAST_TLEH     Q30BT_FAST_DLE      fasting_same_day    Q30time_inh_h Q30time_inh_m
       Q30BT_TIMEH   Q30BT_TIMEM
124356 RW     3.Diabetes   17     8      1
*/


***************** cleaning NG

replace Q30BT_FAST_DLE=2 if serial==    236534 /*
*/ | serial== 237031 /*
*/ | serial== 215097

replace Q30BT_FAST_TLEH=22 if serial==244355

***************** cleaning NG
*** check with Lucy
*** 234356
*** 244355
*** 236006
*** 121661
*** 123289


browse serial Q30obs Q30BT_FAST_INSTR   Q30time_hour Q30time_min   Q30BT_FAST_TLEH     Q30BT_FAST_TLEM Q30BT_FAST_DLE    fasting_same_day
       Q30time_inh_h Q30time_inh_m Q30BT_TIMEH   Q30BT_TIMEM /*
*/ if serial==234356 | serial==244355 | serial==236006 | serial==121661 | serial==123289

* serial 234356
replace Q30BT_FAST_TLEH=8 if serial==234356
replace Q30BT_FAST_TLEM=30 if serial==234356
replace Q30BT_TIMEH=14 if serial==234356
replace Q30BT_TIMEM=12 if serial==234356
replace Q30BT_FAST_DLE=1 if serial==234356
```

```
* serial 244355
replace Q30BT_FAST_TLEH=19 if serial==244355
replace Q30BT_FAST_TLEM=0 if serial==244355
replace Q30BT_TIMEH=10 if serial==244355
replace Q30BT_TIMEM=45 if serial==244355
replace Q30BT_FAST_DLE=2 if serial==244355


replace Q30BT_FAST_DLE=1 if serial==236006
replace Q30BT_FAST_DLE=2 if serial==237502
replace Q30time_hour=13 if serial==137314

/*
serial Q30obs Q30BT_FAST_INSTR    Q30time_hour  Q30BT_FAST_TLEH     Q30BT_FAST_DLE      fasting_same_day    Q30time_inh_h Q30time_inh_m
       Q30BT_TIMEH   Q30BT_TIMEM
124356 RW     3.Diabetes   17     8      1
137314 NG     1.YES  18     18     2                          13     5
*/


***************** cleaning IB
*** check with Lucy
*** 3315225
*** 3190636
*** 3290561
*** 33827


browse serial Q30obs       Q30BT_FAST_INSTR    Q30time_hour  Q30BT_FAST_TLEH     Q30BT_FAST_TLEM Q30BT_FAST_DLE   fasting_same_day
       Q30time_inh_h Q30time_inh_m Q30BT_TIMEH   Q30BT_TIMEM /*
*/ if serial==3315225 | serial==3190636 | serial==3290561 | serial==33827

replace Q30BT_FAST_INSTR=2 if serial==3315225

***************** cleaning GR
*** check with Lucy
*** 3168515
*** 3211635
*** 3318756
*** 3263243


browse serial Q30obs       Q30BT_FAST_INSTR    Q30time_hour  Q30BT_FAST_TLEH     Q30BT_FAST_TLEM Q30BT_FAST_DLE   fasting_same_day
       Q30time_inh_h Q30time_inh_m Q30BT_TIMEH   Q30BT_TIMEM /*
*/ if serial==3168515 | serial==3211635 | serial==3318756 | serial==3263243

replace Q30BT_FAST_INSTR=2 if serial==3168515
replace Q30BT_FAST_INSTR=2 if serial==3211635

replace Q30BT_FAST_INSTR=1 if serial==3132581
```

```
replace Q30BT_FAST_INSTR=1 if serial==2167243



tab Q30BT_FAST_TLEH if Q30BT_FAST_DLE==2

tab Q30BT_FAST_TLEH if Q30BT_FAST_DLE==1



browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30BT_FAST_DLE==1 & Q30BT_FAST_TLEH>=14



*******************************************************************************
*******************************************************************************
*******************************************************************************
*******************************************************************************

****
**** IMPUTATION WITH MEDIAN
****


*******************************************************************************
*******************************************************************************
*******************************************************************************
*******************************************************************************

sum Q30BT_FAST_TLEH if Q30BT_FAST_DLE==2, d
browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30BT_FAST_DLE==2

**** replace with median if Q30BT_FAST_DLE==2 & Q30BT_FAST_TLEH==.
replace Q30BT_FAST_TLEH=20 if Q30BT_FAST_DLE==2 & Q30BT_FAST_TLEH==.
replace Q30BT_FAST_INSTR=1 if Q30BT_FAST_DLE==2 & Q30BT_FAST_INSTR==.

tabmiss  Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE if Q30BT_FAST_DLE==2

browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30BT_FAST_DLE==1

sum Q30BT_FAST_TLEH if Q30BT_FAST_DLE==1 & Q30time_hour==14, d
* 8
sum Q30BT_FAST_TLEH if Q30BT_FAST_DLE==1 & Q30time_hour==16, d
* 9

replace Q30BT_FAST_TLEH=8 if serial==3200709
replace Q30BT_FAST_TLEH=9 if serial==131188


****************************************************************************
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****
****                  REDEFINE DIABETES
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************

/*
1. Redefine diabetes status by using
A) information from Q30 questionnaire and
B) information from the datasheet. Further to this
C) using insulin, but for the time being it’s not necessary
*/


gen diabetes_q30_ds=1 if q3050==1 | Q30BT_FAST_INSTR==3
replace diabetes_q30_ds=0 if diabetes_q30_ds==.
tab diabetes_q30_ds


label define diabetes_q30_ds 0 "0.Non Diabetics" 1 "1.Diabetics", modify
label values diabetes_q30_ds diabetes_q30_ds

tab Q30BT_FAST_INSTR diabetes_q30_ds
replace Q30BT_FAST_INSTR=3 if diabetes_q30_ds==1 & q30batch!=.

tab Q30BT_FAST_INSTR diabetes_q30_ds

tab Q30BT_FAST_INSTR

browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE fasting_same_day if Q30BT_FAST_INSTR==3

tabmiss Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE  if q30batch!=.

browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE if q30batch!=.

replace Q30BT_FAST_DLE=2 if serial==    142011 /*
*/ | serial== 135785 /*
*/ | serial== 2113343      /*
*/ | serial== 133743 /*
*/ | serial== 142022 /*
*/ | serial== 139921 /*
*/ | serial== 3120445      /*
*/ | serial== 121397 /*
*/ | serial== 135741 /*
*/ | serial== 3281595
```

```
replace Q30BT_FAST_DLE=1 if Q30BT_FAST_DLE==. & Q30BT_FAST_TLEH!=.


*******************************************************************************
*******************************************************************************
*******************************************************************************
*******************************************************************************

****
**** IMPUTATION WITH MEDIAN
****


*******************************************************************************
*******************************************************************************
*******************************************************************************
*******************************************************************************

sum Q30BT_FAST_TLEH if Q30BT_FAST_INSTR==3  & Q30time_hour==10, d
* 8
sum Q30BT_FAST_TLEH if Q30BT_FAST_INSTR==3  & Q30time_hour==12, d
* 9
sum Q30BT_FAST_TLEH if Q30BT_FAST_INSTR==3  & Q30time_hour==17, d
* 12

replace Q30BT_FAST_TLEH=8 if serial==124356
replace Q30BT_FAST_TLEH=9 if serial==2209551
replace Q30BT_FAST_TLEH=12 if serial==127702 | serial==111244


replace Q30BT_FAST_DLE=1 if serial==124356
replace Q30BT_FAST_DLE=1 if serial==2209551

replace Q30BT_FAST_DLE=2 if serial==127702 | serial==111244

tabmiss Q30BT_FAST_INSTR Q30time_hour Q30BT_FAST_TLEH Q30BT_FAST_DLE  if q30batch!=.


browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30time_min Q30BT_FAST_TLEH Q30BT_FAST_TLEM  Q30BT_FAST_DLE if q30batch!=.

********** replace minutes
recode Q30time_min .=0 if q30batch!=.
recode Q30BT_FAST_TLEM .=0  if q30batch!=.


*********  replace midnight
replace Q30BT_FAST_TLEH=23 if serial==219431 | serial==123773
replace Q30BT_FAST_TLEM=59 if serial==219431 | serial==123773
```

```
*******************************************************************************
*******************************************************************************
*******************************************************************************
*******************************************************************************

****
**** EXACT FASTING TIME
****


*******************************************************************************
*******************************************************************************
*******************************************************************************
*******************************************************************************



*******************************************************************************
*******************************************************************************
*******************************************************************************
*******************************************************************************

****
**** FASTING THE SAME DAY OF EXAMINATION
****


*******************************************************************************
*******************************************************************************
*******************************************************************************
*******************************************************************************

gen diff_same_day=(((Q30time_hour*60)+Q30time_min)-((Q30BT_FAST_TLEH*60)+Q30BT_FAST_TLEM))/60 if Q30BT_FAST_DLE==1 & q30batch!=.

sum diff_same_day
sum diff_same_day if Q30BT_FAST_INSTR==3
sum diff_same_day if Q30BT_FAST_INSTR!=3

gen diff_over_night=( ( (24*60)-  ((Q30BT_FAST_TLEH*60)+Q30BT_FAST_TLEM)  ) +  ((Q30time_hour*60)+Q30time_min) ) /60   if Q30BT_FAST_DLE==2 &
q30batch!=.

sum diff_over_night, d


browse serial Q30obs Q30BT_FAST_INSTR Q30time_hour Q30time_min Q30BT_FAST_TLEH Q30BT_FAST_TLEM  Q30BT_FAST_DLE  diff_over_night if
Q30BT_FAST_DLE==2
```

```
gen exact_fasting=diff_same_day if Q30BT_FAST_DLE==1 & q30batch!=.
replace exact_fasting=diff_over_night if Q30BT_FAST_DLE==2 & q30batch!=.

tabmiss exact_fasting if q30batch!=.
sum exact_fasting if q30batch!=.

sum exact_fasting if q30batch!=. & diabetes_q30_ds==1
sum exact_fasting if q30batch!=. & Q30BT_FAST_INSTR==3
sum exact_fasting if q30batch!=. & diabetes_q30_ds==0


********************************************************************************
********************************************************************************
********************************************************************************
********************************************************************************

****
**** FASTING TIME ROUNDED
****


********************************************************************************
********************************************************************************
********************************************************************************
********************************************************************************

gen round_fasting=exact_fasting if q30batch!=.
replace round_fasting=exact_fasting+1 if Q30time_min>30 & Q30time_min!=.  & q30batch!=.

gen round_fasting_trunc=trunc(round_fasting)
browse exact_fasting round_fasting round_fasting_trunc

tab round_fasting_trunc
label var round_fasting_trunc "Fasting time calculated"
drop round_fasting
label var exact_fasting "Exact fasting time"

recode round_fasting_trunc (5 4 3 2 1 0 = 1) (6 7 8 9 10 11 12= 2) (13 14 15 16 17 18 = 3) (19 20 21 22 23 24 25 = 4), gen(fasting_status)
label define fasting_status 1 "<6h" 2 "6-12h" 3 "13-18" 4 "18-24", modify
label values fasting_status fasting_status

**** approx fasting when I have few cases on the extreme
replace round_fasting_trunc=1 if round_fasting_trunc==0
replace round_fasting_trunc=23 if round_fasting_trunc>23 & round_fasting_trunc!=.

**** recode fasting rounded: if >20 then =20

replace round_fasting_trunc=20 if round_fasting_trunc>20 & round_fasting_trunc!=.
```

```
******************************************************
**************************  fasting recoding 2
******************************************************

recode round_fasting_trunc (5 4 3 2 1 0 = 1) (6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 = 2), gen(fasting_status2)
label define fasting_status2 1 "<6h" 2 ">=6h", modify
label values fasting_status2 fasting_status2

tab fasting_status2



******************************************************
**************************  rounded hour of examination
******************************************************


gen Q30time_hour_round=Q30time_hour
replace Q30time_hour_round=Q30time_hour_round+1 if Q30time_min>30 & Q30time_min!=.




******************************************************
**************************  BMI
******************************************************

gen Q30height2=Q30height*Q30height
gen Q30height100=Q30height/100
gen Q30height100_2=Q30height100*Q30height100
gen Q30bmi=Q30weight/Q30height100_2
sum Q30bmi
drop Q30height100 Q30height100_2
label var Q30bmi "BMI"

gen Q30bmi_4cat=0 if Q30bmi>=18.5 & Q30bmi<25
replace Q30bmi_4cat=1 if Q30bmi<18.5
replace Q30bmi_4cat=2 if Q30bmi>=25 & Q30bmi<30
replace Q30bmi_4cat=3 if Q30bmi>=30 & Q30bmi!=.
label define Q30bmi_4cat 0 "BMI >=18.5-25" 1 "BMI <18.5" 2 "BMI >=25-30" 3 "BMI >=30"
label values Q30bmi_4cat Q30bmi_4cat


******************************************************
**************************  BLOOD PRESSURE
******************************************************

**** data entry error
```

```
replace Q30sbpsit1=141 if serial==2076493 & Q30sbpsit1==191


******************************************************
**************************  DIFFERENCE BETWEEN 1ST AND 2ND BP MEASURE
******************************************************

gen diff_Q30sbpsit12=Q30sbpsit1-Q30sbpsit2
gen diff_Q30dbpsit12=Q30dbpsit1-Q30dbpsit2
sum diff_Q30sbpsit12 diff_Q30dbpsit12,d

fsum diff_Q30sbpsit12 diff_Q30dbpsit12, s(min p5 p25 mean median p75 p95 max)

******************************************************
**************************  DIFFERENCE BETWEEN SYSTOLIC AND DIASTOLIC 1ST MEASURE
******************************************************

gen diff_sys_dia_BP1=Q30sbpsit1-Q30dbpsit1
gen diff_sys_dia_BP2=Q30sbpsit2-Q30dbpsit2
fsum diff_sys_dia_BP1 diff_sys_dia_BP2, s(min p5 p25 mean median p75 p95 max)

fsum diff_Q30sbpsit12 diff_Q30dbpsit12, s(min p1 p5 p25 mean median p75 p95 p99 max)



******************************************************
**************************  systolic blood pressure sitting avg 2 measures
******************************************************

gen Q30sbpsit12=(Q30sbpsit1+Q30sbpsit2)/2
misstable pattern  Q30sbpsit1 Q30sbpsit2 Q30sbpsit12

/*

   Missing-value patterns
     (1 means complete)

              |   Pattern
    Percent   |  1  2  3
  ------------+-------------
       80%    |  1  1  1
              |
       20     |  0  0  0
       <1     |  1  0  0
  ------------+-------------
      100%    |

  Variables are  (1) Q30sbpsit1  (2) Q30sbpsit12  (3) Q30sbpsit2

*/
```

```
sum diff_Q30sbpsit12, d
replace Q30sbpsit12=Q30sbpsit1-(`r(mean)'/2) if Q30sbpsit2==.

misstable pattern  Q30sbpsit1 Q30sbpsit2 Q30sbpsit12
tabmiss Q30sbpsit12



******************************************************
**************************  diastolic blood pressure sitting avg 2 measures
******************************************************

gen Q30dbpsit12=(Q30dbpsit1+Q30dbpsit2)/2
misstable pattern  Q30dbpsit1 Q30dbpsit2 Q30dbpsit12

/*

   Missing-value patterns
     (1 means complete)

              |   Pattern
    Percent   |  1  2  3
  ------------+-------------
       80%    |  1  1  1
              |
       20     |  0  0  0
       <1     |  1  0  0
  ------------+-------------
      100%    |

  Variables are  (1) Q30sbpsit1  (2) Q30sbpsit12  (3) Q30sbpsit2

*/

sum diff_Q30dbpsit12, d
replace Q30dbpsit12=Q30dbpsit1-(`r(mean)'/2) if Q30dbpsit2==.

misstable pattern  Q30dbpsit1 Q30dbpsit2 Q30dbpsit12
tabmiss Q30dbpsit12



******************************************************
**************************  recode of BP problem
******************************************************

encode Q30bp_instr_p, gen(Q30bp_instr_p_num)
recode Q30bp_instr_p_num (1 = 1) ( 2 3 4 = 2) , gen (Q30bp_instr_p_yn)
label define Q30bp_instr_p_yn 1 "No BP instr prob" 2 "Yes BP instr prob", modify
```

```
tab Q30bp_instr_p_num Q30bp_instr_p_yn
label var Q30bp_instr_p_yn "BP Instrument problems"


******************************************************
**************************  sitting heart rate avg 2 measures
******************************************************

gen Q30hratesit12=(Q30hratesit1+Q30hratesit2)/2
misstable pattern  Q30hratesit1 Q30hratesit2 Q30hratesit12
replace Q30hratesit12=Q30hratesit1 if Q30hratesit2==.
replace Q30hratesit12=Q30hratesit2 if Q30hratesit1==.
misstable pattern  Q30hratesit1 Q30hratesit2 Q30hratesit12
tabmiss Q30hratesit12


******************************************************
**************************  standing heart rate avg 2 measures
******************************************************

gen Q30hratestand12=(Q30hratestand1+Q30hratestand2)/2
misstable pattern  Q30hratestand1 Q30hratestand2 Q30hratestand12
replace Q30hratestand12=Q30hratestand1 if Q30hratestand2==.
replace Q30hratestand12=Q30hratestand2 if Q30hratestand1==.
misstable pattern  Q30hratestand1 Q30hratestand2 Q30hratestand12
tabmiss Q30hratestand12

*********************************************
*********************************************
**************
**************    RECODE VARIABLES FOR FEV1
**************
*********************************************
*********************************************



sum Q30spir_btv
recode Q30spir_btv (-20/-3.01 = 0) (-3/3 = 1) (3.01/99 = 0) (.=.), gen(Q30spir_btv_cat)
label define Q30spir_btv_cat 1 "<=|3%|" 0 ">|3%|" , modify
label values Q30spir_btv_cat Q30spir_btv_cat
label var Q30spir_btv_cat "FEV1 test variation"


tab Q30ci_p
replace Q30ci_p="2" if Q30ci_p=="P"
tab Q30ci_p
* browse serial Q30fev1 Q30spir_nblows Q30spir_btv Q30ci_p if Q30fev1!=. & serial==231067

bys Q30ci_p: sum Q30fev1
```

```
* browse serial Q30fev1 Q30spir_nblows Q30spir_btv Q30ci_p if Q30fev1!=.

destring Q30ci_p, replace
label define Q30ci_p 2 "Participant problem" 1 "Machine problem" 0 "Normal blow" , modify
label values Q30ci_p Q30ci_p
label var Q30ci_p "FEV1 blow indication"

replace Q30ci_p=. if Q30fvc==. & Q30fev05==. & Q30fev1==. & Q30pef==. & Q30fef2575==. & Q30fef7585==. & Q30fef25==. & Q30fef50==. & Q30fef75==.


* remember
* q30100-q30115 fractures and falls
* q30210-q302112 alchool
* q30220-q302210 PA
* q30270-q30275 Fitness
* q30240-q30241




******************************************************************************
******************************************************************************
******************************************************************************
******************************************************************************
****
****                  MARKERS AND NORMALITY ????
****
******************************************************************************
******************************************************************************
******************************************************************************
******************************************************************************

cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\normality"

* gladder Q30hdlc

* gladder Q30ldlc


/*
foreach marker in   Q30hdlc Q30ldlc   {

            gen `marker'_sqrt=sqrt(`marker')

}

hist Q30hdlc
hist Q30hdlc_sqrt
```

```
hist Q30ldlc
hist Q30ldlc_sqrt

*/


/*
foreach marker in  Q30chol Q30hdlc Q30ldlc Q30trig  Q30hba1c Q30gluc  Q30hdlc Q30ldlc {

            gladder `marker'
                    graph export `marker'.png, replace
}


*/

foreach marker in  Q30chol Q30hdlc Q30ldlc Q30trig  Q30hba1c Q30gluc  {

            gen `marker'_log=log(`marker')

}







/* chronic desease */
foreach name in   q3020a q3020e q3020f q3020i q3030 q3050 q3060 q3070e q3070o q3070p {

     recode `name' .=2

        }


egen q30nchronic=anycount(q3020a q3020e q3020f q3020i q3030 q3050 q3060 q3070e q3070o q3070p) , values(1)

tab q30nchronic

label variable q30nchronic "Q30 Number of Chronic conditions, %(n)"
tab q30nchronic, m
gen q30nchronic3=q30nchronic
recode q30nchronic3 (4 5 6 7 8 9 =3)
label variable q30nchronic3 "Q30 Number of Chronic conditions, %(n)"
label define q30nchronic3  0 "None" 1 " 1" 2 " 2" 3 " >=3", modify
label value q30nchronic3 q30nchronic3

tab q30nchronic3
```

```
summ q3020a q3020e q3020f q3020i q3030 q3050 q3060 q3070e q3070o q3070p  q30nchronic


gen q30nchronic1=q30nchronic
recode q30nchronic1 (0 =0)
recode q30nchronic1 (1 2 3 4 5 6 7 8 9 =1)
label variable q30nchronic1 "Q30 Number of Chronic conditions, %(n)"
label define q30nchronic1  0 "None" 1 "1+"
label value q30nchronic1 q30nchronic1

tab q30nchronic1


/* vision problems */

foreach name in  q3070d q3070k q3070n {

     recode `name' .=2

        }


egen vision=anycount(q3070d q3070k q3070n) , values(1)

tab vision

label variable vision "Q30 Vision problems"
label define vision  0 "None" 1 " 1" 2 " 2" 3 "3", modify
label value vision vision

tab vision

gen vision2=vision
recode vision2 3=2

label variable vision2 "Q30 Vision problems"
label define vision2  0 "None" 1 " 1" 2 ">=2", modify
label value vision2 vision2

tab vision2

ren vision q30vision
ren vision2 q30vision2




/* EQ5D quality of life score*/
gen eq5d1=q30233
gen eq5d2=q30260g
```

```
gen eq5d3=q30232
gen eq5d4=q30231
gen eq5d5=q30235
gen eq5dtherm=q30235
// Use the EQ5D UK scoring function (Luo et al. 2007, Dolan et al. 1996,1997 )
// Scoring developped Dolan 1997 (Modeling Valuations for EuroQol Health States ), score clearer in Luo 2007.
// Range=  -0.594 to 1.0


gen eq5nomiss=1 if (eq5d1!=. & eq5d2!=. & eq5d3!=. & eq5d4!=. & eq5d5!=. )
gen items = 0.069*(eq5d1==2) + 0.314*(eq5d1==3) + ///
   0.104*(eq5d2==2) + 0.214*(eq5d2==3) + ///
   0.036*(eq5d3==2) + 0.094*(eq5d3==3) + ///
   0.123*(eq5d4==2) + 0.386*(eq5d4==3) + ///
   0.071*(eq5d5==2) + 0.236*(eq5d5==3) if eq5nomiss==1
gen n3=0 if eq5nomiss==1
replace n3= 0.269 if max(eq5d1,eq5d2,eq5d3,eq5d4,eq5d5)>=3 & eq5nomiss==1
gen c = 0.081 if max(eq5d1,eq5d2,eq5d3,eq5d4,eq5d5)>=2  & eq5nomiss==1
replace c = 0 if max(eq5d1,eq5d2,eq5d3,eq5d4,eq5d5)==1 & eq5nomiss==1
gen eq5sco=1 - (c + items + n3 ) if eq5nomiss==1
label var eq5sco "Q30 EQ5D score"
order eq5sco, before(eq5dtherm)
drop eq5nomiss items c n3
sum eq5sco,det



/* falls */

tab q30113

replace q30113=2 if q30114==0
replace q30113=1 if q30114>0 & q30113==2 & q30114!=. & q30113!=.
replace q30113=1 if q30114>0 & q30113==. & q30114!=.


tab q30114 q30113, m

gen q30fall=q30113
recode q30fall (2=0)
replace q30fall=1 if q30114>=1 & q30114<=50
label var q30fall "Q30 Falls in the past 12 months, %(n)"
label define q30fall   0"no fall" 1 "fall"
label value  q30fall  q30fall

tab q30fall q30113,mi col nolab


/*drop q30fall */
```

```
gen q30recfall=q30fall
replace q30recfall=0 if q30114==1
label var q30recfall "Q30 Falls in the past 12 months, %(n)"
label define q30recfall   0 "no/ 1 fall" 1 "2+falls"
label value  q30recfall  q30recfall
tab q30114 q30recfall
tab q30recfall

tab q30114 q30fall
tab q30recfall q30fall
tab q30recfall q30fall
gen q30fall3=q30fall
replace q30fall3=1 if (q30recfall==1 & q30fall==0)
replace q30fall3=2 if (q30recfall==1 & q30fall==1)
label var q30fall3 "Q30 Falls in the past 12 months, %(n)"
label define q30fall3  0"no fall" 1 "1 fall" 2 "2+falls"
label value q30fall3 q30fall3
tab q30fall3
tab q30114 q30fall3

tab q30fall q30115
/*drop A1hospfall*/




/* Long standing illness */

tab q30240 q30240a, m
tab q30240 q30240b, m


replace q30240=1 if q30240a==1 & q30240==.
replace q30240=1 if q30240b==1 & q30240==.

replace q30240=2 if q30240a==2 & q30240==.
* replace q30240=2 if q30240a==. & q30240b==. & q30240==.
* replace q30240a=2 if q30240a==. & q30240==1

tab q30240 q30240a, m

gen q30disability=0 if q30240==2
* replace q30disability=0 if q30240==1 & q30240a==2
replace q30disability=1 if q30240==1

* & q30240a==1


label define q30disability 0 "No" 1 "Yes", replace
label value q30disability q30disability
```

```
label variable q30disability "Q30 Long standing disability"

tab q30disability
tabmiss q30disability



/* life circumstances */


* single status
gen q30single_status=1 if q30330==1
replace q30single_status=0 if q30330==2
replace q30single_status=2 if q30330==3 | q30330==4 | q30330==5

label define q30single_status 1 "Single" 0 "Married" 2 "Widowed/Divorced/Separated/Other", modify
label value q30single_status q30single_status
label var q30single_status "Q30 Present Circumstances"

tab q30single_status,m



* Living with

tab q30332, m
tab q30333 q30332, m

* NOOOO  replace q30332=1 if q30333==1 & q30332==.
* NOOOO  replace q30332=1 if q30333==4 & q30332==.

label define q30living 1 "At home, with family/people" 2 "At home, alone" 3 "Residential home" 4 "Nursing home", modify

gen q30living=2 if q30332==1
replace q30living=1 if (q30332>=2 & q30332<=4)
replace q30living=3 if q30333==4
replace q30living=4 if q30333==5

label value q30living q30living
label var q30living "Q30 At present are you living"

tab q30living, m

tab q30single_status q30330

tab q30living q30single_status, m


/* number of medication */
```

```
foreach num of numlist 1 2 3 4 5 6 7 8 9 10 {

gen pr_medicine`num'=1 if  q3045bnf12_`num'!=.

}

tabmiss pr_medicine*

egen q30n_pr_medicine=rowtotal(pr_medicine1-pr_medicine10)
tab q30n_pr_medicine

label var q30n_pr_medicine "Q30 prescribed medicine"




*******************************************************
****************  BLOOD PRESSURE ARM CINCUMFERNCE BY BP CUFF SIZE
*******************************************************

* BP cuff size (based on Arm circ(cm)   Arm circ <22cm =1,    22-32cm=2,   3= >32cm=3

label define Q30bp_cuff 1 "1=<22cm" 2 "2=22-32cm" 3 "3=>32cm", modify
label values Q30bp_cuff Q30bp_cuff

*******************************************************
****************  BLOOD PRESSURE MEDICATIONS
*******************************************************

* beta blocker data (BNF code 2.4 from Q45 in the q30 questionnaire)

/* Peter Whincuop list

Blood pressure lowering medications
2.2.1   2.2.3   2.2.4  2.2.8
2.4
2.5.1 to 2.5.5 inclusive
2.6.2


Blood pressure lowering medications label

BNF code: 2.2.1 Thiazides and related diuretics
BNF code: 2.2.3 Potassium sparing diuretics and aldosterone antagonists
BNF code: 2.2.4 Potassium-sparing diuretics with other diuretcis
BNF code: 2.2.8 Diuretic with potrassium
BNF code: 2.4   Beta-adrenoceptor blocking drugs
BNF code: 2.5.1 Vasodilator antihypertensive drugs
BNF code: 2.5.2 Centrally acting antihypertensive drugs
```

```
BNF code: 2.5.3 Adrenergic neuron blocking
BNF code: 2.5.4 Alpha adrenoceptor blocking drugs
BNF code: 2.5.5 Drugs affecting the renin-angiotensin system
BNF code: 2.6.2 Calcium channel blockers

*/

* BNF code: Blood pressure


******************************** error in the questionnaire I checked

replace q3045bnf12_10=.    if serial==221413
replace q3045bnf34_10=.     if serial==221413
replace q3045bnf5_10=.      if serial==221413
replace q3045bnf6_10=. if serial==221413

********************************

replace q3045bnf12_8=9     if serial==1835
replace q3045bnf34_8=9      if serial==1835
replace q3045bnf5_8=9       if serial==1835
replace q3045bnf6_8=9 if serial==1835




foreach num of numlist 1 2 3 4 5 6 7 8 9 10 {

gen BNF221_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==2 & q3045bnf5_`num'==1
gen BNF223_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==2 & q3045bnf5_`num'==3
gen BNF224_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==2 & q3045bnf5_`num'==4
gen BNF228_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==2 & q3045bnf5_`num'==8
gen BNF24_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==4
gen BNF251_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==5 & q3045bnf5_`num'==1
gen BNF252_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==5 & q3045bnf5_`num'==2
gen BNF253_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==5 & q3045bnf5_`num'==3
gen BNF254_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==5 & q3045bnf5_`num'==4
gen BNF255_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==5 & q3045bnf5_`num'==5
gen BNF262_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==6 & q3045bnf5_`num'==2

}

foreach name in 221 223 224 228 24 251 252 253 254 255 262 {

egen q30n_BNF`name'=rowtotal(BNF`name'_1 BNF`name'_2 BNF`name'_3 BNF`name'_4 BNF`name'_5 BNF`name'_6 BNF`name'_7 BNF`name'_8 BNF`name'_9
BNF`name'_10)

}
```

```
tab1 q30n_BNF221-q30n_BNF262

egen bp_drugs_use_n=rowtotal(q30n_BNF221-q30n_BNF262)
tab bp_drugs_use_n

gen bp_drugs_use=0 if q30n_BNF221 ==0    & /*
*/     q30n_BNF223  ==0    & /*
*/     q30n_BNF224  ==0    & /*
*/     q30n_BNF228  ==0    & /*
*/     q30n_BNF24   ==0    & /*
*/     q30n_BNF251  ==0    & /*
*/     q30n_BNF252  ==0    & /*
*/     q30n_BNF253  ==0    & /*
*/     q30n_BNF254  ==0    & /*
*/     q30n_BNF255  ==0    & /*
*/     q30n_BNF262  ==0

recode bp_drugs_use .=1
tab bp_drugs_use


recode bp_drugs_use_n (0=0) (1=1) (2=2) (3 4 5 6 7 8 9 10 =3), gen(bp_drugs_use_n4cat)
label define bp_drugs_use_n4cat 0 "None" 1 "1" 2 "2" 3 "3+", modify
label values bp_drugs_use_n4cat bp_drugs_use_n4cat
label var bp_drugs_use_n4cat "Blood pressure drugs use"


* BNF code: just beta blockers
foreach num of numlist 1 2 3 4 5 6 7 8 9 10 {

gen beta_blocker`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==4

}

tabmiss beta_blocker*
egen q30n_beta_blocker=rowtotal(beta_blocker1-beta_blocker10)
tab q30n_beta_blocker
gen q30_beta_blocker1=q30n_beta_blocker
recode q30_beta_blocker1 2=1




/* thisis the 4 item scale defined by vanMarwijk in BJGP 1995, 45: 195-199*/
*drop gds*
gen gdstemp1=q30380a-1
gen gdstemp2=q30380d-1
gen gdstemp3=1 if q30380f==1
replace gdstemp3=0 if q30380f==2
```

```
gen gdstemp4=1 if q30380e==1
replace gdstemp4=0 if q30380e==2
*drop gdstemp5

summ gdstemp1 gdstemp2 gdstemp3 gdstemp4
egen gdstemp5=rowtotal(gdstemp1 gdstemp2 gdstemp3 gdstemp4) if (gdstemp1!=. |  gdstemp2!=. | gdstemp3 !=. |gdstemp4 !=. )
summ gdstemp5
tab gdstemp5
gen gds=0 if gdstemp5<=2
replace gds=1 if gdstemp5>=2 & gdstemp5!=.
label var gds "GDS 4 van Marwijk"
tab gds gdstemp5, col
label define gds 0 "score <2" 1 "score >=2"
label value gds gds


gen gds1=gds
recode gds1 (1=0) (0=1)
label var gds1 "Q30 Geriatric Depression Scale"
label define gds1 1 "<2" 0 ">2 (depressed)", modify
label value gds1 gds1
tab gds gds1

ren gds1 q30gds1


****************  smoking habits


tab q30200, m
gen q30smo=q30200
label var q30smo "Q30 Smoking cigarettes"
label define q30smo 1 "Yes" 2 "No" 3 "Ex-smoker", modify
label value q30smo q30smo
tab q30smo

tab1 q30203 q30204
destring q30203 q30204, replace
replace q30smo=3 if  q30202==4

tab q30smo


gen q30smoke_all=1 if q30smo==1 | q30203==1 | q30204==1
recode q30smoke_all .=0
tab q30smoke_all, m
label var q30smoke_all "Q30 Smoking cigarettes/pipe/cigars"
label define q30smoke_all 1 "Yes" 0 "No" , modify
label value q30smoke_all q30smoke_all
```

```
tab q30smoke_all q30204

egen q30chd=anycount(q3020a q3020e q3020f q3020i) , values(1)

gen q30chd1=q30chd
recode q30chd1 (0 =0)
recode q30chd1 (1 2 3 4 =1)
label variable q30chd1 "CHD (Q30 A-E-F-I), %(n)"
label define q30chd1  0 "None" 1 "1+"
label value q30chd1 q30chd1

preserve
use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\calendar_days_2010_2011_2012.dta", clear
ren date_day Q30date_exam
ren day_of_the_year doy
saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\calendar_days_2010_2011_2012_date_exam.dta", replace
restore

mmerge Q30date_exam using "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\calendar_days_2010_2011_2012_date_exam.dta"
drop if _merge==2






******************************************************
****************  TOWN ORDER
******************************************************


tab Q30ExamTown Q30xm if Q30xy==2010

/*


Town where |
participan |
     t was |            Q30 screening Examination MONTH
  examined |         7          9         10         11         12 |     Total
-----------+-------------------------------------------------------+----------
         1 |        69          0          0          0          0 |        69 
         2 |         0         96          0          0          0 |        96 
         3 |         0         44         55          0          0 |        99 
         4 |         0          0         91          0          0 |        91 
         5 |         0          0          0         92          0 |        92 
         6 |         0          0          0         11         15 |        26 
-----------+-------------------------------------------------------+----------
     Total |        69        140        146        103         15 |       473
```

```
*/

gen Q30ExamTown_order=1 if Q30ExamTown==1
replace Q30ExamTown_order=2 if Q30ExamTown==2
replace Q30ExamTown_order=3 if Q30ExamTown==3
replace Q30ExamTown_order=4 if Q30ExamTown==4
replace Q30ExamTown_order=5 if Q30ExamTown==5
replace Q30ExamTown_order=6 if Q30ExamTown==6

tab Q30ExamTown Q30xm if Q30xy==2011

/*
Town where |
participan |
     t was |                                             Q30 screening Examination MONTH
  examined |         1          2          3          4          5          6          7          8          9         10         11 |
Total
-----------+-------------------------------------------------------------------------------------------------------------------------+--------
--
         7 |         0          0          0          0          0         83          0          0          0          0          0 |
83
         8 |         0         39          0          0          0          0          0          0          0          0          0 |
39
         9 |         0         39          0          0          0          0          0          0          0          0          0 |
39
        10 |         0          0         91          0          0          0          0          0          0          0          0 |
91
        12 |         0          0         28         25          0          0          0          0          0          0          0 |
53
        13 |         0          0          0          0        105          0          0          0          0          0          0 |
105
        14 |        63          0          0          0          0          0          0          0          0          0          0 |
63
        15 |         0          0          0          0          0         36          0          0          0          0          0 |
36
        16 |         0          0          0          0          0          0         82          0          0          0          0 |
82
        17 |         0          0          0          0          0          0         40         42          0          0          0 |
82
        18 |         0          0          0          0          0          0          0          0         70          0          0 |
70
        20 |         0          0          0          0          0          0          0          0          0         52          0 |
52
        21 |         0          0          0          0          0          0          0          0          0          0         73 |
73
        22 |         0          0          0          0          0          0          0          0          0          0         41 |
41
        31 |         0          0          0          0         10          0          0          0          0          0          0 |
10
```

```
        32 |          0          0          0          0          0          0          0          0         10          0          0 |
10
-----------+-----------------------------------------------------------------------------------------------------------------------+--------
--
     Total |         63         78        119         25        115        119        122         42         80         52        114 |
929

*/

replace Q30ExamTown_order=7 if Q30ExamTown==14
replace Q30ExamTown_order=8 if Q30ExamTown==8
replace Q30ExamTown_order=9 if Q30ExamTown==9
replace Q30ExamTown_order=10 if Q30ExamTown==10
replace Q30ExamTown_order=11 if Q30ExamTown==12
replace Q30ExamTown_order=12 if Q30ExamTown==13
replace Q30ExamTown_order=13 if Q30ExamTown==31
replace Q30ExamTown_order=14 if Q30ExamTown==7
replace Q30ExamTown_order=15 if Q30ExamTown==15
replace Q30ExamTown_order=16 if Q30ExamTown==16
replace Q30ExamTown_order=17 if Q30ExamTown==17
replace Q30ExamTown_order=18 if Q30ExamTown==18
replace Q30ExamTown_order=19 if Q30ExamTown==32
replace Q30ExamTown_order=20 if Q30ExamTown==20
replace Q30ExamTown_order=21 if Q30ExamTown==21
replace Q30ExamTown_order=22 if Q30ExamTown==22

tab Q30ExamTown Q30xm if Q30xy==2012

/*
Town where |
participan |
     t was |            Q30 screening Examination MONTH
  examined |          1          2          3          5          6 |     Total
-----------+-------------------------------------------------------+----------
        11 |          0         55          0          0          0 |        55
        19 |          0          0         75          0          0 |        75
        23 |         51          0          0          0          0 |        51
        24 |          7         44          0          0          0 |        51
        41 |          0          0          0         39         49 |        88
-----------+-------------------------------------------------------+----------
     Total |         58         99         75         39         49 |       320

*/

replace Q30ExamTown_order=23 if Q30ExamTown==23
replace Q30ExamTown_order=24 if Q30ExamTown==24
replace Q30ExamTown_order=25 if Q30ExamTown==11
replace Q30ExamTown_order=26 if Q30ExamTown==19
replace Q30ExamTown_order=27 if Q30ExamTown==41
```

```
tab Q30ExamTown_order Q30ExamTown


label define Q30ExamTown_order    1      "n_1_month_7_year_2010_town_ex_1" /*
*/     2      "n_2_month_9_year_2010_town_ex_2" /*
*/     3      "n_3_month_9_year_2010_town_ex_3" /*
*/     4      "n_4_month_10_year_2010_town_ex_4" /*
*/     5      "n_5_month_11_year_2010_town_ex_5" /*
*/     6      "n_6_month_11_year_2010_town_ex_6" /*
*/     7      "n_7_month_1_year_2011_town_ex_14" /*
*/     8      "n_8_month_2_year_2011_town_ex_8" /*
*/     9      "n_9_month_2_year_2011_town_ex_9" /*
*/     10     "n_10_month_3_year_2011_town_ex_10" /*
*/     11     "n_11_month_3_year_2011_town_ex_12" /*
*/     12     "n_12_month_5_year_2011_town_ex_13" /*
*/     13     "n_13_month_5_year_2011_town_ex_31" /*
*/     14     "n_14_month_6_year_2011_town_ex_7" /*
*/     15     "n_15_month_6_year_2011_town_ex_15" /*
*/     16     "n_16_month_7_year_2011_town_ex_16" /*
*/     17     "n_17_month_7_year_2011_town_ex_17" /*
*/     19     "n_19_month_9_year_2011_town_ex_32" /*
*/     18     "n_18_month_9_year_2011_town_ex_18" /*
*/     20     "n_20_month_10_year_2011_town_ex_20" /*
*/     21     "n_21_month_11_year_2011_town_ex_21" /*
*/     22     "n_22_month_11_year_2011_town_ex_22" /*
*/     23     "n_23_month_1_year_2012_town_ex_23" /*
*/     24     "n_24_month_1_year_2012_town_ex_24" /*
*/     25     "n_25_month_2_year_2012_town_ex_11" /*
*/     26     "n_26_month_3_year_2012_town_ex_19" /*
*/     27     "n_27_month_5_year_2012_town_ex_41", modify

label values Q30ExamTown_order Q30ExamTown_order
label var Q30ExamTown_order "Order for Town of examination"

recode Q30xm (12 1 2 = 1) (3 4 5 = 2) (6 7 8 = 3) (9 10 11 = 4), gen(Q30Season)
label define Q30Season 1 "Winter (Dec-Feb)" 2 "Spring (March-May)" 3 "Summer (Jun-Aug)" 4 "Autumn (Sept-Nov)", modify
label values Q30Season Q30Season
label var Q30Season "Season"




********************   *************************
*********************************************
**************
**************    Generate variables Atrial Fibrillation, Atrial flutter and Tachycardia
**************
*********************************************
*********************************************
```

```
ren Q30ECG_Snnesota_group3 Q30ECG_Minnesota_group3

* keep serial *Minnesota*


gen atrial_fibr=1 if (     Q30ECG_Minnesota_group1_L  ==831 |                           Q30ECG_Minnesota_group1_L  ==833) | /*
*/ (   Q30ECG_Minnesota_group1_P  ==831 |                           Q30ECG_Minnesota_group1_P  ==833) | /*
*/ (   Q30ECG_Minnesota_group1_A  ==831 |                           Q30ECG_Minnesota_group1_A  ==833) | /*
*/ (   Q30ECG_Minnesota_group2_1  ==831 |                           Q30ECG_Minnesota_group2_1  ==833) | /*
*/ (   Q30ECG_Minnesota_group2_2  ==831 |                           Q30ECG_Minnesota_group2_2  ==833) | /*
*/ (   Q30ECG_Minnesota_group3        ==831 |                       Q30ECG_Minnesota_group3        ==833) | /*
*/ (   Q30ECG_Minnesota_group4_L  ==831 |                           Q30ECG_Minnesota_group4_L  ==833) | /*
*/ (   Q30ECG_Minnesota_group4_P  ==831 |                           Q30ECG_Minnesota_group4_P  ==833) | /*
*/ (   Q30ECG_Minnesota_group4_A  ==831 |                           Q30ECG_Minnesota_group4_A  ==833) | /*
*/ (   Q30ECG_Minnesota_group5_L  ==831 |                           Q30ECG_Minnesota_group5_L  ==833) | /*
*/ (   Q30ECG_Minnesota_group5_P  ==831 |                           Q30ECG_Minnesota_group5_P  ==833) | /*
*/ (   Q30ECG_Minnesota_group5_A  ==831 |                           Q30ECG_Minnesota_group5_A  ==833) | /*
*/ (   Q30ECG_Minnesota_group6        ==831 |                       Q30ECG_Minnesota_group6        ==833) | /*
*/ (   Q30ECG_Minnesota_group7_1  ==831 |                           Q30ECG_Minnesota_group7_1  ==833) | /*
*/ (   Q30ECG_Minnesota_group7_2  ==831 |                           Q30ECG_Minnesota_group7_2  ==833) | /*
*/ (   Q30ECG_Minnesota_group8_1  ==831 |                           Q30ECG_Minnesota_group8_1  ==833) | /*
*/ (   Q30ECG_Minnesota_group8_2  ==831 |                           Q30ECG_Minnesota_group8_2  ==833) | /*
*/ (   Q30ECG_Minnesota_group8_3  ==831 |                           Q30ECG_Minnesota_group8_3  ==833) | /*
*/ (   Q30ECG_Minnesota_group8_4  ==831 |                           Q30ECG_Minnesota_group8_4  ==833) | /*
*/ (   Q30ECG_Minnesota_group9_L  ==831 |                           Q30ECG_Minnesota_group9_L  ==833) | /*
*/ (   Q30ECG_Minnesota_group9_P  ==831 |                           Q30ECG_Minnesota_group9_P  ==833) | /*
*/ (   Q30ECG_Minnesota_group9_A  ==831 |                           Q30ECG_Minnesota_group9_A  ==833) | /*
*/ (   Q30ECG_Minnesota_group9m_1 ==831 |                           Q30ECG_Minnesota_group9m_1 ==833) | /*
*/ (   Q30ECG_Minnesota_group9m_2 ==831 |                           Q30ECG_Minnesota_group9m_2 ==833)

replace atrial_fibr=0 if atrial_fibr!=1 & q30batch!=.
tab atrial_fibr, m
label var atrial_fibr "Atrial Fibrillation"
label define atrial_fibr 0 "No AT" 1 "Yes AT"
label values atrial_fibr atrial_fibr


gen atrial_flutter=1 if (  Q30ECG_Minnesota_group1_L  ==832 |                           Q30ECG_Minnesota_group1_L  ==834) | /*
*/ (   Q30ECG_Minnesota_group1_P  ==832 |                           Q30ECG_Minnesota_group1_P  ==834) | /*
*/ (   Q30ECG_Minnesota_group1_A  ==832 |                           Q30ECG_Minnesota_group1_A  ==834) | /*
*/ (   Q30ECG_Minnesota_group2_1  ==832 |                           Q30ECG_Minnesota_group2_1  ==834) | /*
*/ (   Q30ECG_Minnesota_group2_2  ==832 |                           Q30ECG_Minnesota_group2_2  ==834) | /*
*/ (   Q30ECG_Minnesota_group3        ==832 |                       Q30ECG_Minnesota_group3        ==834) | /*
*/ (   Q30ECG_Minnesota_group4_L  ==832 |                           Q30ECG_Minnesota_group4_L  ==834) | /*
*/ (   Q30ECG_Minnesota_group4_P  ==832 |                           Q30ECG_Minnesota_group4_P  ==834) | /*
*/ (   Q30ECG_Minnesota_group4_A  ==832 |                           Q30ECG_Minnesota_group4_A  ==834) | /*
*/ (   Q30ECG_Minnesota_group5_L  ==832 |                           Q30ECG_Minnesota_group5_L  ==834) | /*
*/ (   Q30ECG_Minnesota_group5_P  ==832 |                           Q30ECG_Minnesota_group5_P  ==834) | /*
*/ (   Q30ECG_Minnesota_group5_A  ==832 |                           Q30ECG_Minnesota_group5_A  ==834) | /*
```

```
*/ (   Q30ECG_Minnesota_group6          ==832 |                       Q30ECG_Minnesota_group6          ==834) | /*
*/ (   Q30ECG_Minnesota_group7_1  ==832 |                          Q30ECG_Minnesota_group7_1  ==834) | /*
*/ (   Q30ECG_Minnesota_group7_2  ==832 |                          Q30ECG_Minnesota_group7_2  ==834) | /*
*/ (   Q30ECG_Minnesota_group8_1  ==832 |                          Q30ECG_Minnesota_group8_1  ==834) | /*
*/ (   Q30ECG_Minnesota_group8_2  ==832 |                          Q30ECG_Minnesota_group8_2  ==834) | /*
*/ (   Q30ECG_Minnesota_group8_3  ==832 |                          Q30ECG_Minnesota_group8_3  ==834) | /*
*/ (   Q30ECG_Minnesota_group8_4  ==832 |                          Q30ECG_Minnesota_group8_4  ==834) | /*
*/ (   Q30ECG_Minnesota_group9_L  ==832 |                          Q30ECG_Minnesota_group9_L  ==834) | /*
*/ (   Q30ECG_Minnesota_group9_P  ==832 |                          Q30ECG_Minnesota_group9_P  ==834) | /*
*/ (   Q30ECG_Minnesota_group9_A  ==832 |                          Q30ECG_Minnesota_group9_A  ==834) | /*
*/ (   Q30ECG_Minnesota_group9m_1 ==832 |                          Q30ECG_Minnesota_group9m_1 ==834) | /*
*/ (   Q30ECG_Minnesota_group9m_2 ==832 |                          Q30ECG_Minnesota_group9m_2 ==834)


tab atrial_flutter, m
replace atrial_flutter=0 if atrial_flutter!=1 & q30batch!=.
label var atrial_flutter "Atrial Flutter"
label define atrial_flutter 0 "No AF" 1 "Yes AF"
label values atrial_flutter atrial_flutter



gen tachycardias=1 if (    Q30ECG_Minnesota_group1_L  ==841 |                          Q30ECG_Minnesota_group1_L  ==842) | /*
*/ (   Q30ECG_Minnesota_group1_P  ==841 |                          Q30ECG_Minnesota_group1_P  ==842) | /*
*/ (   Q30ECG_Minnesota_group1_A  ==841 |                          Q30ECG_Minnesota_group1_A  ==842) | /*
*/ (   Q30ECG_Minnesota_group2_1  ==841 |                          Q30ECG_Minnesota_group2_1  ==842) | /*
*/ (   Q30ECG_Minnesota_group2_2  ==841 |                          Q30ECG_Minnesota_group2_2  ==842) | /*
*/ (   Q30ECG_Minnesota_group3          ==841 |                       Q30ECG_Minnesota_group3          ==842) | /*
*/ (   Q30ECG_Minnesota_group4_L  ==841 |                          Q30ECG_Minnesota_group4_L  ==842) | /*
*/ (   Q30ECG_Minnesota_group4_P  ==841 |                          Q30ECG_Minnesota_group4_P  ==842) | /*
*/ (   Q30ECG_Minnesota_group4_A  ==841 |                          Q30ECG_Minnesota_group4_A  ==842) | /*
*/ (   Q30ECG_Minnesota_group5_L  ==841 |                          Q30ECG_Minnesota_group5_L  ==842) | /*
*/ (   Q30ECG_Minnesota_group5_P  ==841 |                          Q30ECG_Minnesota_group5_P  ==842) | /*
*/ (   Q30ECG_Minnesota_group5_A  ==841 |                          Q30ECG_Minnesota_group5_A  ==842) | /*
*/ (   Q30ECG_Minnesota_group6          ==841 |                       Q30ECG_Minnesota_group6          ==842) | /*
*/ (   Q30ECG_Minnesota_group7_1  ==841 |                          Q30ECG_Minnesota_group7_1  ==842) | /*
*/ (   Q30ECG_Minnesota_group7_2  ==841 |                          Q30ECG_Minnesota_group7_2  ==842) | /*
*/ (   Q30ECG_Minnesota_group8_1  ==841 |                          Q30ECG_Minnesota_group8_1  ==842) | /*
*/ (   Q30ECG_Minnesota_group8_2  ==841 |                          Q30ECG_Minnesota_group8_2  ==842) | /*
*/ (   Q30ECG_Minnesota_group8_3  ==841 |                          Q30ECG_Minnesota_group8_3  ==842) | /*
*/ (   Q30ECG_Minnesota_group8_4  ==841 |                          Q30ECG_Minnesota_group8_4  ==842) | /*
*/ (   Q30ECG_Minnesota_group9_L  ==841 |                          Q30ECG_Minnesota_group9_L  ==842) | /*
*/ (   Q30ECG_Minnesota_group9_P  ==841 |                          Q30ECG_Minnesota_group9_P  ==842) | /*
*/ (   Q30ECG_Minnesota_group9_A  ==841 |                          Q30ECG_Minnesota_group9_A  ==842) | /*
*/ (   Q30ECG_Minnesota_group9m_1 ==841 |                          Q30ECG_Minnesota_group9m_1 ==842) | /*
*/ (   Q30ECG_Minnesota_group9m_2 ==841 |                          Q30ECG_Minnesota_group9m_2 ==842)

replace tachycardias=0 if tachycardias!=1 & q30batch!=.
label var tachycardias "Tachycardias"
label define tachycardias 0 "No Tachycardias" 1 "Yes Tachycardias", modify
```

```
label values tachycardias tachycardias


gen atrial_fib_flu=1 if atrial_fibr==1 | atrial_flutter==1
replace atrial_fib_flu=0 if atrial_fibr!=1 & atrial_flutter!=1 & q30batch!=.
label var atrial_fib_flu "Atrial Fibr+Flutter"
label define atrial_fib_flu 0 "No" 1 "Yes"
label values atrial_fib_flu atrial_flutter

gen atrial_fib_flu_tac=1 if atrial_fib_flu==1 | tachycardias==1
replace atrial_fib_flu_tac=0 if atrial_fib_flu!=1 & tachycardias!=1 & q30batch!=.
label var atrial_fib_flu_tac "Atrial Fibr+Flutter and Tachy"
label define atrial_fib_flu_tac 0 "No" 1 "Yes"
label values atrial_fib_flu_tac atrial_fib_flu_tac

**************    RECODE PEOPLE WITHOUT ECG FROM "NO" TO "MISSING"

tab with_q30ecg

foreach name in atrial_fibr atrial_flutter tachycardias atrial_fib_flu atrial_fib_flu_tac {

    replace `name'=. if with_q30ecg==0

}

tabmiss atrial_fibr atrial_flutter tachycardias atrial_fib_flu atrial_fib_flu_tac


preserve
keep if  q30batch!=.
saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", replace
restore


********************   *************************
*********************************************
**************
**************    VERY IMPORTANT KEEP
**************
*********************************************
*********************************************


* saveold "S:\Pop_Health\PCPH_BRHS\Claudio\Claudio PhD documents\Papers\Paper 2 season weather PA\Q30_adapted_paper2_PhD.dta", replace


/*
* 2. A1+A2 RS in wide form with average weekly measures of PA and SB
* open the data base
```

```
mmerge serial using "S:\Pop_Health\PCPH_BRHS_ActiGraph\BRHS data\not validated data\after
Choi\Actigraph_A1_A2_with_greendiary_RSonly_with_derived_vars_and_Q20.dta", ukeep(green_diary-sed_breaks_h_day9 )
keep if _merge!=2


**** get the derived variables for % of time in SED LIPA MVPA
**** step1 % of each day
**** Note

foreach day in 1 2 3 4 5 6 7 8 9 {

        foreach name in choi_sed_day  /*
  */ choi_light_100_1040_day choi_copeland_mvpa_day choi_freedson_mvpa_day /*
  */  mvpa_1041_min_bt10_day   {

            gen perc_`name'`day'=(`name'`day'/choi_wear_time_day`day')*100

 }
 }

*** check if results are reasonable and consistent

sum perc_choi_sed_day*
sum perc_choi_copeland_mvpa_day*

**** step2 % of the week

foreach var in  perc_choi_sed_day  perc_choi_light_100_1040_day /*
*/  perc_choi_copeland_mvpa_day perc_choi_freedson_mvpa_day  /*
*/  perc_mvpa_1041_min_bt10_day  {


    egen `var'=rowmean(`var'1 `var'2 `var'3 `var'4 `var'5 `var'6 `var'7 `var'8 `var'9)


 }


*** check if results are reasonable and consistent

sum perc_choi_sed_day perc_choi_light_100_1040_day perc_choi_copeland_mvpa_day perc_choi_freedson_mvpa_day perc_mvpa_1041_min_bt10_day


**** step3 avg of minutes in each PA level over a week

foreach var in VT_day steps_day choi_sed_day choi_ll_100_759_day choi_hl_760_1040_day choi_hl_760_1950_day /*
  */ choi_light_100_1040_day choi_light_100_1950_day choi_copeland_mvpa_day choi_freedson_mvpa_day choi_vigor_day /*
  */ choi_wear_time_day mvpa_1041_min_bt10_day  sed_n_bt60_day sed_n_bt30_day /*
  */ sed_n_bt_0_15_day sed_n_bt_15_30_day sed_n_bt_30_60_day sed_n_bt_60_120_day sed_n_bt_0_30_day /*
  */ sed_breaks_h_day {
```

```
  egen `var'_avg=rowmean(`var'1 `var'2 `var'3 `var'4 `var'5 `var'6 `var'7 `var'8 `var'9)

  }


 **** step4 do the same but for VT per minutes, and not just for VT (total)

 foreach day in 1 2 3 4 5 6 7 8 9 {

             gen VT_min`day'=(VT_day`day'/choi_wear_time_day`day')

 }

  foreach var in VT_min {

  egen `var'_avg=rowmean(`var'1 `var'2 `var'3 `var'4 `var'5 `var'6 `var'7 `var'8 `var'9)

  }


*** check if results are reasonable and consistent

drop green_diary-sed_breaks_h_day9
drop perc_choi_sed_day1-perc_mvpa_1041_min_bt10_day9 VT_min1-VT_min9

sum VT_min_avg steps_day_avg choi_sed_day_avg choi_wear_time_day_avg sed_n_bt_0_30_day_avg sed_breaks_h_day_avg



mmerge serial using "S:\Pop_Health\PCPH_BRHS_ActiGraph\BRHS data\Q30\self_reported_PA_score_Q30.dta", ukeep(PA_index PA_sum q30224)
keep if _merge!=2
ren PA_index PA_index_Q30
ren PA_sum PA_sum_Q30

*/


* saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_PA_obj", replace

mmerge serial using "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30BRHS_CRP_TPA_VWF_DDIMER_IL6"

mmerge serial using  "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30NTproBNP hsTNT.csv"


mmerge serial using "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Summary documentation for Olia\Q30_block_of_variables_Olia",
ukeep(dQ30hour-dQ30fvc_adj_h3)
```

```
******************************************************
****************  FROM BARBARA JEFFERIS
******************************************************



******************************************************
****************  LIPID LOWERING MEDICATIONS
******************************************************

* STATIN data (BNF code 2.12 from Q45 in the q30 questionnaire)

/* Peter Whincup list

LIPID REGULATING DRUGS
2.12

lipid lowering medications label

BNF code: 2.12 Statins*/

foreach num of numlist 1 2 3 4 5 6 7 8 9 10 {

gen BNF212_`num'=1 if  q3045bnf12_`num'==2 & q3045bnf34_`num'==12
}

foreach name in 212 {

egen q30n_BNF`name'=rowtotal(BNF`name'_1 BNF`name'_2 BNF`name'_3 BNF`name'_4 BNF`name'_5 BNF`name'_6 BNF`name'_7 BNF`name'_8 BNF`name'_9 BNF`name'_10)
}

tab1 BNF212_1-q30n_BNF212

egen q30statins_use_n=rowtotal(q30n_BNF212)
tab q30statins_use_n

gen q30statins_use=q30n_BNF212
recode q30statins_use (2=1)  (3=1) ( 4=1)
tab q30statins_use

/* crosstabs to check the variable looks ok */
foreach num of numlist 1 2 3 4 5 6 7 8 9 10 {

tab q30statins_use_n BNF212_`num'
}
```

```
*****************************************************
******************** BETA BLOCKERS ******************
*****************************************************

************ Beta Blockers BNF code 2.4 from Q45 in the q30 questionnaire*

/* same categories as from Q20 medications list*/

gen q30_bbl_use=0
forvalues i=1/10 {
replace q30_bbl_use=1 if q3045bnf12_`i'==2 &  q3045bnf34_`i'==4
}
label var q30_bbl_use "Q30 Beta Blockers BNF 2.4"
tab q30_bbl_use

*****************************************************
******************** ACE INHIBITORS ******************
*****************************************************

/*** ace inhibitors  BNF code 2.5.5.1 from Q45 in the q30 questionnaire*************/



gen q30_ace_use=0
forvalues i=1/10 {
replace q30_ace_use=1 if q3045bnf12_`i'==2 &  q3045bnf34_`i'==5  &  q3045bnf5_`i'==5 &  q3045bnf6_`i'==1
}
label var q30_ace_use "Q30 Ace inhibitors BNF 2.5.5.1"
tab q30_ace_use


*****************************************************
******************** ALL RENIN ANGIOTENSIN DRUGS******************
*****************************************************


/*** all drugs acting on renin angiotensin system BNF code 2.5.5 from Q45 in the q30 questionnaire***/

gen q30_renin_use=0
forvalues i=1/10 {
replace q30_renin_use=1 if q3045bnf12_`i'==2 &  q3045bnf34_`i'==5  &  q3045bnf5_`i'==5
}
label var q30_renin_use "Q30 renin angiotensin BNF 2.5.5"
tab q30_renin_use

*****************************************************
************* CALCIUM CHANNEL BLOCKERS **************
*****************************************************
```

```
************ BNF code 2.6.2 from Q45 in the q30 questionnaire*

/*** calcium channel blockers BNF code 2.6.2 ***/
gen q30_cal_ch_use=0
forvalues i=1/10 {
replace q30_cal_ch_use=1 if q3045bnf12_`i'==2 &  q3045bnf34_`i'==6  &  q3045bnf5_`i'==2
}
label var q30_cal_ch_use "Q30 Calcium Channel blockers BNF 2.6.2"
tab q30_cal_ch_use




*****************************************************
*************** Thiazide diuretics ******************
*****************************************************

*********BNF code 2.2.1 from Q45 in the q30 questionnaire*

/* same categories as from Q20 medications list*/

gene q30_thi_use=0
forvalues i=1/10 {
replace q30_thi_use=1 if q3045bnf12_`i'==2 & q3045bnf34_`i'==2 & q3045bnf5_`i'==1
}
label var q30_thi_use "Q30 thiazide diuretics BNF 2.2.1"
tab q30_thi_use

*****************************************************
************ diuretics with potassium ***************
*****************************************************

*********BNF code 2.2.8 from Q45 in the q30 questionnaire*

/* same categories as from Q20 medications list*/

gene q30_diur_use=0
forvalues i=1/10 {
replace q30_diur_use=1 if q3045bnf12_`i'==2 & q3045bnf34_`i'==2 & q3045bnf5_`i'==8
}
label var q30_diur_use "Q30 diuretics with potassium BNF 2.2.8"
tab q30_diur_use

*****************************************************
************ total antihypertensives ***************
*****************************************************

********* from Q45 in the q30 questionnaire*
/*
```

```
Thiazides 2.2.1, diuretics with potassium 2.2.8, beta-blockers 2.4, drugs affecting the renin-angiotensin system 2.5.5  and other
antihypertensives (? check with PW what this might include?) and calcium channel blockers 2.6.2.*/

/* same categories as from Q20 medications list*/

gene q30_antihyp_use=0
replace q30_antihyp_use=1 if q30_bbl_use==1 | q30_renin_use==1 | q30_cal_ch_use==1 | q30_thi_use==1 | q30_diur_use==1
label var q30_antihyp_use "Q30 antihypertensives"
tab q30_antihyp_use

*****************************************************
**************** Non opioid analgesics **************
*****************************************************

*********BNF code 4.7.1 from Q45 in the q30 questionnaire*

/* same categories as from Q20 medications list*/


gene q30_nonop_use=0
forvalues i=1/10 {
replace q30_nonop_use=1 if q3045bnf12_`i'==4 & q3045bnf34_`i'==7 & q3045bnf5_`i'==1
}
label var q30_nonop_use "Q30 Non opioid analgesics BNF 4.7.1"
tab q30_nonop_use


*****************************************************
******************** Pain killers *******************
*****************************************************

********* BNF code 4.7 from Q45 in the q30 questionnaire*

/* same categories as from Q20 medications list*/

gene q30_paink_use=0
forvalues i=1/10 {
replace q30_paink_use=1 if q3045bnf12_`i'==4 & q3045bnf34_`i'==7
}
label var q30_paink_use "Q30 Painkillers BNF 4.7"
tab q30_paink_use

*****************************************************
***********Musculoskeletal medications **************
*****************************************************

********* BNF code 10.1, 10.2, 10.3 from Q45 in the q30 questionnaire*

/* same categories as from Q20 medications list*/
```

```
gene q30_musc_use=0
forvalues i=1/10 {
replace q30_musc_use=1 if q3045bnf12_`i'==10 & q3045bnf34_`i'==1
replace q30_musc_use=2 if q3045bnf12_`i'==10 & q3045bnf34_`i'==2
replace q30_musc_use=3 if q3045bnf12_`i'==10 & q3045bnf34_`i'==3
}
recode q30_musc_use  (2 3=1)
label var q30_musc_use "Q30 musculoskeletal BNF 10.1,10.2,10.3"
tab q30_musc_use


*****************************************************
************************ NSAID **********************
*****************************************************

********* BNF code 10.1.1 from Q45 in the q30 questionnaire*

/* same categories as from Q20 medications list*/

gene q30_nsaid_use=0
forvalues i=1/10 {
replace q30_nsaid_use=1 if q3045bnf12_`i'==10 & q3045bnf34_`i'==1 & q3045bnf5_`i'==1
}
label var q30_nsaid_use "Q30 NSAID BNF 10.1.1"
tab q30_nsaid_use


*****************************************************
****************** anti-depressants ****************
*****************************************************

********* BNF code 4.3 from Q45 in the q30 questionnaire*

/* same categories as from Q20 medications list*/

gene q30_adepr_use=0
forvalues i=1/10 {
replace q30_adepr_use=1 if q3045bnf12_`i'==4 & q3045bnf34_`i'==3
}
label var q30_adepr_use "Q30 antidepressant BNF 4.3"
tab q30_adepr_use


*****************************************************
********* Anti coagulant, Warfarin ******************
*****************************************************

********* BNF code 2.8.2 from Q45 in the q30 questionnaire*
```

```
/* same categories as from Q20 medications list*/

gene q30_anticoag_use=0
forvalues i=1/10 {
replace q30_anticoag_use=1 if q3045bnf12_`i'==2 & q3045bnf34_`i'==8& q3045bnf5_`i'==2
}
label var q30_anticoag_use "Q30 anticoagulants BNF 2.8.2"
tab q30_anticoag_use






saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables_2147_men", replace

keep if  q30batch!=.

saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables_1722_men", replace


use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables_1722_men", clear


mmerge serial using "S:\Pop_Health\BRHS_Winter_Deaths\data\RAW DATA EVENTS FROM OLIA\FIRST_HF_EVER_UPTO2012.dta"


/*
use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear


keep serial atrial_fibr atrial_flutter tachycardias atrial_fib_flu atrial_fib_flu_tac /*
*/ bp_drugs_use_n bp_drugs_use bp_drugs_use_n4cat q30n_beta_blocker q30_beta_blocker1 q30n_pr_medicine with_q30ecg


saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adjusted variables for Olia\Q30_mix_of_variables.dta", replace

drop q30n_pr_medicine bp_drugs_use_n bp_drugs_use bp_drugs_use_n4cat q30n_beta_blocker q30_beta_blocker1

export delimited using "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adjusted variables for Olia\atrial_fibr_flutter_and_tachy.csv",
nolabel replace


 */
```

APPENDIX 2: 22. Non Diabetics - Total Cholesterol, LDL, HDL, triglycerides, insulin, glucose, HBA.do

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****     Here I generate the data base I need to use in R to produce the GAMS
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear

tab fasting_status2, nolab
tab fasting_status2, nolab m
tab Q30BT_FAST_INSTR, nolab


gen sin_tod=sin((2*3.14159/24)*time_hour_mm)
gen cosin_tod=cos((2*3.14159/24)*time_hour_mm )

gen time_hour_mm2=time_hour_mm*time_hour_mm


keep if fasting_status2==2 & diabetes_q30_ds==0

saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\non_diabetics_fastin_more_than_6", replace




****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
*  EXPLORE Total Cholesterol, LDL, HDL, triglycerides, insulin, glucose, HBA
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear
```

```
keep if q30batch!=.
count

tab1 fasting_status fasting_status2


sum Q30time_hour Q30time_min time_hour_mm


tab diabetes_q30_ds

tab Q30age3cat diabetes_q30_ds, row

/*
diabetes_q3 |
       0_ds |      Freq.     Percent        Cum.
------------+-----------------------------------
          0 |      1,458       84.67       84.67
          1 |        264       15.33      100.00
------------+-----------------------------------
      Total |      1,722      100.00
*/


/*

           |    diabetes_q30_ds
       Age | 0.Non Dia  1.Diabeti |     Total
-----------+----------------------+----------
    Age<75 |       398         73 |       471
           |     84.50      15.50 |    100.00
-----------+----------------------+----------
 Age 75-79 |       550        117 |       667
           |     82.46      17.54 |    100.00
-----------+----------------------+----------
   Age 80+ |       510         74 |       584
           |     87.33      12.67 |    100.00
-----------+----------------------+----------
     Total |     1,458        264 |     1,722
           |     84.67      15.33 |    100.00

*/

browse Q30obs Q30time_hour Q30time_min  Q30BT_FAST_INSTR  round_fasting_trunc  Q30BT_FAST_TLEM  Q30BT_FAST_DLE
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****                  NORMALITY ASSUMPTION LIST
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************

* use total cholesterol original
* use LDL cholesterol sqrt
* use HDL cholesterol sqrt
* use glucose log
* use gligatec haemoglobin log
* use insuline adjusted log
* use tryglicerid log



****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****                  FASTING DURATION TRANSFORMATION ??????
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************

/*

gen round_fasting_trunc_13H=1 if round_fasting_trunc>=13 & round_fasting_trunc!=.
replace round_fasting_trunc_13H=0 if round_fasting_trunc<13

*/



tab Q30BT_FAST_INSTR, m

/*

 Blood Test |
```

```
    Fasting |
instruction |
    s       |      Freq.     Percent        Cum.
------------+-----------------------------------
      1.YES |      1,296       75.26       75.26
       2.NO |        135        7.84       83.10
 3.Diabetes |        264       15.33       98.43
          . |         27        1.57      100.00
------------+-----------------------------------
      Total |      1,722      100.00


*/

tab diabetes_q30_ds

/*

diabetes_q30_ds |      Freq.     Percent        Cum.
----------------+-----------------------------------
0.Non Diabetics |      1,458       84.67       84.67
    1.Diabetics |        264       15.33      100.00
----------------+-----------------------------------
          Total |      1,722      100.00
*/

tab round_fasting_trunc

/*

    Fasting |
       time |
 calculated |      Freq.     Percent        Cum.
------------+-----------------------------------
          1 |         30        1.77        1.77
          2 |         53        3.13        4.90
          3 |         78        4.60        9.50
          4 |         54        3.19       12.68
          5 |         57        3.36       16.05
          6 |        133        7.85       23.89
          7 |        149        8.79       32.68
          8 |         98        5.78       38.47
          9 |         37        2.18       40.65
         10 |         14        0.83       41.47
         11 |         41        2.42       43.89
         12 |         94        5.55       49.44
         13 |        122        7.20       56.64
         14 |        134        7.91       64.54
         15 |        170       10.03       74.57
```

```
         16 |        123        7.26       81.83
         17 |        120        7.08       88.91
         18 |         89        5.25       94.16
         19 |         42        2.48       96.64
         20 |         57        3.36      100.00
------------+-----------------------------------
      Total |      1,695      100.00




*/

sum round_fasting_trunc, d
bys diabetes_q30_ds: sum round_fasting_trunc, d
bys diabetes_q30_ds: sum round_fasting_trunc

fsum round_fasting_trunc if diabetes_q30_ds==0

/*

            Variable |        N     Mean       SD      Min      Max
---------------------+---------------------------------------------
 round_fasting_trunc |     1431    12.16     4.86     0.00    24.00



 */

fsum round_fasting_trunc if diabetes_q30_ds==1

/*


            Variable |        N     Mean       SD      Min      Max
---------------------+---------------------------------------------
 round_fasting_trunc |      264     6.67     5.46     1.00    24.00


*/


count if diabetes_q30_ds==1 & round_fasting_trunc<6
count if diabetes_q30_ds==0 & round_fasting_trunc<6


tab round_fasting_trunc if diabetes_q30_ds==0
tab round_fasting_trunc if diabetes_q30_ds==1
```

```
* 126:7=110:X
* x=7*110/126
* be careful with glucose values between 6 an 7

scatter Q30gluc q30insulin_adj if diabetes_q30_ds==0


hist Q30gluc_log
hist Q30gluc





****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****   EXPLORE LIPIDS
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


tab fasting_status2, nolab
tab fasting_status
tab fasting_status, nolab






****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****   DESCRIPTIVE STATISTICS TABLES BY DIABETIC STATUS
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
```

```
cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\csv"


foreach name in Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj {

svyset [pw=serial]
tabout diabetes_q30_ds using table_`name'.csv, c(mean `name' sd `name') f(1m 1m) sum npos(lab) nlab((N=#)) style(csv) replace

}




foreach name in Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj {

       graph box `name', over(diabetes_q30_ds) xsize(2) ysize(3)
          graph save `name'_box_plot, replace
}

graph combine Q30chol_box_plot.gph Q30hdlc_box_plot.gph /*
   */ Q30ldlc_box_plot.gph Q30trig_log_box_plot.gph Q30hba1c_log_box_plot.gph /*
   */ Q30gluc_log_box_plot.gph q30insulin_log_adj_box_plot.gph, graphregion(color(white))
graph export all_box_plot.png, replace



clear
cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\csv"
! dir *.csv /a-d /b >"S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\csv\filelist\filelist.txt"

******* open the txt file and read the first line
file open myfile using "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\csv\filelist\filelist.txt", read
file read myfile line


while r(eof)==0 { /* while you're not at the end of the file */

import delimited "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\csv\\\`line'", delimiter("$,") rowrange(3)
clear

drop mean
ren sd mean
drop v4
ren v5 sd

gen variable="`line'"
split variable, p("table_", ".csv")
```

```
drop variable variable1
order variable2
ren variable2 variable

saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\dta\\\`line'.dta", replace

file read myfile line


}


file close myfile



clear
cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\dta"
! dir *.dta /a-d /b >"S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\dta\filelist\filelist.txt"


file open myfile using "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\dta\filelist\filelist.txt", read
file read myfile line


drop _all
use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\dta\\\`line'"
cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\dta\master"
saveold master_data, replace
file read myfile line

***** append all files together

while r(eof)==0 { /* while you're not at the end of the file */
	drop _all
	use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\dta\\\`line'"
	append using master_data.dta
	cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\dta\master"
	saveold master_data.dta, replace
	drop _all
	file read myfile line
}

file close myfile


use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\dta\master\master_data.dta", clear
```

```
cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis"


use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear

cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\graphs"


hist Q30time_hour_round, freq discrete xlabel(9 10 11 12 13 14 15 16 17) xtitle(hour of examination) graphregion(color(white))
graph export hour_of_examination_line.png, replace


hist round_fasting_trunc, freq discrete xlabel(1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20) xtitle(Fasting time)
graphregion(color(white))
graph export fasting_time.png, replace


hist round_fasting_trunc if Q30time_hour_round>=14 & Q30time_hour_round!=., freq title(Examined in the afternoon (14-18)) discrete xlabel(1 2
3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20) xtitle(Fasting time) graphregion(color(white))
graph export fasting_time_invited_afternoon.png, replace


hist round_fasting_trunc if Q30time_hour_round<=13, freq discrete title(Examined in the morning (9-13)) xlabel(1 2 3 4 5 6 7 8 9 10 11 12 13
14 15 16 17 18 19 20) xtitle(Fasting time) graphregion(color(white))
graph export fasting_time_invited_morning.png, replace
```

```
collapse (mean)   Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */    (semean) se_Q30chol=Q30chol se_Q30hdlc=Q30hdlc se_Q30ldlc=Q30ldlc se_Q30trig_log=Q30trig_log /*
   */    se_Q30hba1c_log=Q30hba1c_log se_Q30gluc_log=Q30gluc_log se_q30insulin_log_adj=q30insulin_log_adj, by(diabetes_q30_ds)


foreach name in Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj {

gen `name'_u = `name' + 1.96*se_`name'
gen `name'_l = `name' - 1.96*se_`name'

}


label var diabetes_q30_ds "Diabetes status"


label define diabetes_q30_ds 0 "0.Non Diabetics" 1 "1.Diabetics", modify
label values diabetes_q30_ds diabetes_q30_ds


foreach marker in Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj  {

/*
graph box `marker', over(w_month)
graph export `marker'_graphbox.png, replace
*/

label var diabetes_q30_ds "Diabetes status"
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
twoway (scatter `marker' diabetes_q30_ds, msymbol(S) msize(small) ) (rcap `marker'_u `marker'_l diabetes_q30_ds, lcolor(black) lwidth(thick))
, /*
*/ xlabel(0 "Non-diabetics" 1 "Diabetics", angle(45)) graphregion(color(white)) ylabel(, angle(horizontal) labsize(large)) title(`marker',
size(vlarge)) ytitle(mean, size(large))  legend(row(3)) legend(off)
graph save `marker'_line_diabetes_vs_not, replace

}



graph combine Q30chol_line_diabetes_vs_not.gph  Q30ldlc_line_diabetes_vs_not.gph Q30hdlc_line_diabetes_vs_not.gph
Q30trig_log_line_diabetes_vs_not.gph, row(1) ysize(1) xsize(1.5) title(Total population)
graph export cholesterol_line_diabetes_vs_not.png, replace

graph combine Q30hba1c_log_line_diabetes_vs_not.gph Q30gluc_log_line_diabetes_vs_not.gph q30insulin_log_adj_line_diabetes_vs_not.gph, row(1)
ysize(1) xsize(1.5) title(Total population)
graph export hba_insuline_glucose_line_diabetes_vs_not.png, replace
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****       GRAPHS DIRECTORY
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************




****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****      NON DIABETICS   PLOT MEAN  HOUR OF THE DAY
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************

use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear


sum *Q30time*



keep if diabetes_q30_ds==0

collapse (mean)   Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */    (semean) se_Q30chol=Q30chol se_Q30hdlc=Q30hdlc se_Q30ldlc=Q30ldlc se_Q30trig_log=Q30trig_log /*
   */    se_Q30hba1c_log=Q30hba1c_log se_Q30gluc_log=Q30gluc_log se_q30insulin_log_adj=q30insulin_log_adj, by(Q30time_hour_round)


foreach name in Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj {

gen `name'_u = `name' + 1.96*se_`name'
gen `name'_l = `name' - 1.96*se_`name'

}
```

```
label var Q30time_hour_round "Hour of examination"

drop if Q30time_hour_round==18 | Q30time_hour_round==19


foreach marker in Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj  {

/*
graph box `marker', over(w_month)
graph export `marker'_graphbox.png, replace
*/

label var Q30time_hour_round "Hour of examination"
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
twoway (scatter `marker' Q30time_hour_round, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l Q30time_hour_round,
lcolor(black) lwidth(thick) legend(on)) (line `marker' Q30time_hour_round, lcolor(black) lpattern(dash)), /*
*/ xlabel(9 10 11 12 13 14 15 16 17, labsize(large)) graphregion(color(white)) ylabel(, angle(horizontal) labsize(large)) title(`marker',
size(vlarge)) ytitle(mean, size(large)) xtitle(Hour of examination, size(large)) legend(row(3)) legend(off)
graph save `marker'_line_non_diabetics, replace
graph export `marker'_linenon_diabetics.png, replace

}



graph combine Q30chol_line_non_diabetics.gph  Q30ldlc_line_non_diabetics.gph Q30hdlc_line_non_diabetics.gph
Q30trig_log_line_non_diabetics.gph, row(1) ysize(5) xsize(16) title(Non-Diabetics)
graph export cholesterol_line_non_diabetics.png, replace

graph combine Q30hba1c_log_line_non_diabetics.gph Q30gluc_log_line_non_diabetics.gph q30insulin_log_adj_line_non_diabetics.gph, row(1)
ysize(5) xsize(16) title(Non-Diabetics)
graph export hba_insuline_glucose_line_non_diabetics.png, replace









****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
```

```
****          PLOT MEAN BY FASTING TIME  NON DIABETICS
****
***************************************************************************
***************************************************************************
***************************************************************************
***************************************************************************

use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear


tab round_fasting_trunc, m


replace round_fasting_trunc=1 if round_fasting_trunc==0
replace round_fasting_trunc=23 if round_fasting_trunc>23 & round_fasting_trunc!=.


keep if diabetes_q30_ds==0



collapse (mean)   Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */    (semean) se_Q30chol=Q30chol se_Q30hdlc=Q30hdlc se_Q30ldlc=Q30ldlc se_Q30trig_log=Q30trig_log /*
   */    se_Q30hba1c_log=Q30hba1c_log se_Q30gluc_log=Q30gluc_log se_q30insulin_log_adj=q30insulin_log_adj, by(round_fasting_trunc)


foreach name in Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj {

gen `name'_u = `name' + 1.96*se_`name'
gen `name'_l = `name' - 1.96*se_`name'

}


label var round_fasting_trunc "Fasting time"


foreach marker in Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj  {

/*
graph box `marker', over(w_month)
graph export `marker'_graphbox.png, replace
*/

label var round_fasting_trunc "Fasting time"
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
twoway (scatter `marker' round_fasting_trunc, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l round_fasting_trunc,
lcolor(black) lwidth(thick) legend(on)) (line `marker' round_fasting_trunc, lcolor(black) lpattern(dash)), /*
```

```
*/ xlabel(1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20, alternate labsize(large)) graphregion(color(white)) ylabel(, angle(horizontal)
labsize(large)) title(`marker', size(vlarge)) ytitle(mean, size(large)) xtitle(Fasting time, size(large)) legend(row(3)) legend(off)
graph save `marker'_line_fasting_non_diabetics, replace
graph export `marker'_line_fasting_non_diabetics.png, replace

}



graph combine Q30chol_line_fasting_non_diabetics.gph  Q30ldlc_line_fasting_non_diabetics.gph Q30hdlc_line_fasting_non_diabetics.gph
Q30trig_log_line_fasting_non_diabetics.gph, row(1) ysize(5) xsize(16) title(Non Diabetics)
graph export cholesterol_line_fasting_non_diabetics.png, replace

graph combine Q30hba1c_log_line_fasting_non_diabetics.gph Q30gluc_log_line_fasting_non_diabetics.gph
q30insulin_log_adj_line_fasting_non_diabetics.gph, row(1) ysize(5) xsize(16) title(Non Diabetics)
graph export hba_insuline_glucose_line_fasting_non_diabetics.png, replace
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        MODELS
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
```

```
use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear


gen sin_tod=sin((2*3.14159/24)*time_hour_mm)
gen cosin_tod=cos((2*3.14159/24)*time_hour_mm )

hist time_hour_mm

tab Q30BT_FAST_INSTR2
tab Q30BT_FAST_INSTR2, nolab


recode fasting_status2 1=2 2=1
label define fasting_status2 2 "<6h" 1 ">=6h", modify
label values fasting_status2 fasting_status2

tab  fasting_status2


keep if q30batch!=.
count
*1722

tab1 fasting_status fasting_status2







****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****   sensitivity analysis
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


gen time_hour_mm2=time_hour_mm^2
label var time_hour_mm2 "time_hour_mm_quad"

label var round_fasting_trunc "Fasting time"
```

```
bys fasting_status2: sum round_fasting_trunc

count if diabetes_q30_ds==0 & fasting_status2==1



foreach marker in  Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj {

* NON DIABETICS AND FASTERS > 6 HOURS

* model 1
regress `marker' round_fasting_trunc if diabetes_q30_ds==0 & fasting_status2==1
est store m1`marker'

* model 2
regress `marker' time_hour_mm if diabetes_q30_ds==0 & fasting_status2==1
est store m2`marker'

* model 2.2
regress `marker' time_hour_mm time_hour_mm2 if diabetes_q30_ds==0 & fasting_status2==1
est store m22`marker'

* model 2.3
regress `marker' sin_tod cosin_tod if diabetes_q30_ds==0 & fasting_status2==1
est store m23`marker'

* model 3
regress `marker' round_fasting_trunc time_hour_mm if diabetes_q30_ds==0 & fasting_status2==1
est store m3`marker'

* model 3.2
regress `marker' round_fasting_trunc time_hour_mm time_hour_mm2 if diabetes_q30_ds==0 & fasting_status2==1
est store m32`marker'

* model 3.3
regress `marker' round_fasting_trunc sin_tod cosin_tod if diabetes_q30_ds==0 & fasting_status2==1
est store m33`marker'

}




cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis"


 foreach marker in Q30chol  {
```

```
 estout m1`marker'  m2`marker' m22`marker' m23`marker' m3`marker' m32`marker' m33`marker'  using non_diabetic_fasters.xls, cells ("b(fmt(4))
ci_l(fmt(4)) ci_u(fmt(4))") label  legend collabels("Coeff" "LB" "UB")  stats(r2)  replace

 }

  foreach marker in  Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj  {



 estout m1`marker'  m2`marker' m22`marker' m23`marker' m3`marker' m32`marker' m33`marker'  using non_diabetic_fasters.xls, cells ("b(fmt(4))
ci_l(fmt(4)) ci_u(fmt(4))") label  legend collabels("Coeff" "LB" "UB")  stats(r2)    append



 }




foreach marker in  Q30trig_log  {


* model 4
regress `marker' i.fasting_status2 if diabetes_q30_ds==0
est store m4`marker'

* model 5
regress `marker' i.fasting_status2 time_hour_mm if diabetes_q30_ds==0
est store m5`marker'

* model 6
regress `marker' i.fasting_status2 time_hour_mm time_hour_mm2 if diabetes_q30_ds==0
est store m5`marker'

}










insheet using non_diabetic_fasters.xls, clear
```

```
keep if v1=="round_fasting_trunc" /*
*/ | v1=="Fasting time" /*
*/ | v1=="sin_tod" | v1=="cosin_tod" /*
*/ | v1=="sin_tod" | v1=="cosin_tod" /*
*/ | v1=="time_hour_mm" /*
*/ | v1=="time_hour_mm2" /*
*/ | v1=="time_hour_mm_quad" /*
*/ | v1=="r2" /*
*/ | v1==""


gen Model1=v2+"("+v3+","+v4+")"
gen Model2=v5+"("+v6+","+v7+")"
gen Model22=v8+"("+v9+","+v10+")"
gen Model23=v11+"("+v12+","+v13+")"
gen Model3=v14+"("+v15+","+v16+")"
gen Model32=v17+"("+v18+","+v19+")"
gen Model33=v20+"("+v21+","+v22+")"


keep v1 Model*

replace v1="Fasting time (hours, continuous)" if v1=="Fasting time"
replace v1="Sine term for hour of the day" if v1=="sin_tod"
replace v1="Cosine term for hour of the day" if v1=="cosin_tod"
replace v1="Hour of the day (linear term)" if v1=="time_hour_mm"
replace v1="Hour of the day (quadratic term)" if v1=="time_hour_mm2"


foreach model in Model1 Model2 Model22 Model23 Model3 Model32 Model33 {

    replace `model'="" if `model'=="(,)"

}










****************************************************************************
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****
****        FASTING TIME AND HOUR OF THE DAY TRANSFORMATION
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        BASED ON JON EMBERSON WORK
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear

* replace round_fasting_trunc=19.99 if round_fasting_trunc>=20 & round_fasting_trunc!=.

tab round_fasting_trunc

gen fasting_interval=0 if round_fasting_trunc<6
replace fasting_interval=1 if round_fasting_trunc>=6 & round_fasting_trunc!=.

gen fasting_interval_mod=0       if round_fasting_trunc==0
replace fasting_interval_mod=1   if round_fasting_trunc==1
replace fasting_interval_mod=2   if round_fasting_trunc==2
replace fasting_interval_mod=3   if round_fasting_trunc==3
replace fasting_interval_mod=4   if round_fasting_trunc==4
replace fasting_interval_mod=5   if round_fasting_trunc==5


replace fasting_interval_mod=0   if round_fasting_trunc==6
replace fasting_interval_mod=1   if round_fasting_trunc==7
replace fasting_interval_mod=2   if round_fasting_trunc==8
replace fasting_interval_mod=3   if round_fasting_trunc==9
replace fasting_interval_mod=4   if round_fasting_trunc==10
replace fasting_interval_mod=5   if round_fasting_trunc==11
replace fasting_interval_mod=6   if round_fasting_trunc==12
```

```
replace fasting_interval_mod=7   if round_fasting_trunc==13
replace fasting_interval_mod=8   if round_fasting_trunc==14
replace fasting_interval_mod=9   if round_fasting_trunc==15
replace fasting_interval_mod=10  if round_fasting_trunc==16
replace fasting_interval_mod=11  if round_fasting_trunc==17
replace fasting_interval_mod=12  if round_fasting_trunc==18
replace fasting_interval_mod=13  if round_fasting_trunc==19
replace fasting_interval_mod=14  if round_fasting_trunc==20
replace fasting_interval_mod=15  if round_fasting_trunc==21
replace fasting_interval_mod=16  if round_fasting_trunc==22
replace fasting_interval_mod=17  if round_fasting_trunc==23
replace fasting_interval_mod=18  if round_fasting_trunc==24


browse round_fasting_trunc fasting_interval fasting_interval_mod


tab Q30time_hour_round

gen hour_interval=0 if Q30time_hour_round<=13
replace hour_interval=1 if Q30time_hour_round>13 & Q30time_hour_round!=.

gen hour_interval_mod=1 if Q30time_hour_round==9
replace hour_interval_mod=2 if Q30time_hour_round==10
replace hour_interval_mod=3 if Q30time_hour_round==11
replace hour_interval_mod=4 if Q30time_hour_round==12
replace hour_interval_mod=5 if Q30time_hour_round==13
replace hour_interval_mod=0 if Q30time_hour_round==14
replace hour_interval_mod=1 if Q30time_hour_round==15
replace hour_interval_mod=2 if Q30time_hour_round==16
replace hour_interval_mod=3 if Q30time_hour_round==17

browse Q30time_hour_round hour_interval hour_interval_mod


tab fasting_interval

foreach marker in  Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj {

* NON DIABETICS

* model 1
xi:regress `marker' i.fasting_interval fasting_interval_mod if diabetes_q30_ds==0
est store m1`marker'

* model 2
xi:regress `marker' i.hour_interval  hour_interval_mod if diabetes_q30_ds==0
est store m2`marker'
```

```
* model 3
xi:regress `marker' i.fasting_interval fasting_interval_mod i.hour_interval  hour_interval_mod  if diabetes_q30_ds==0
est store m3`marker'

* model 4
xi:regress `marker' i.fasting_interval*fasting_interval_mod i.hour_interval*hour_interval_mod  if diabetes_q30_ds==0
est store m4`marker'

}





cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis"


 foreach marker in Q30chol  {

 estout m1`marker'  m2`marker'  m3`marker' m4`marker' using non_diabetic_jon_emb_transform.xls, cells ("b(fmt(4)) ci_l(fmt(4)) ci_u(fmt(4))")
label  legend collabels("Coeff" "LB" "UB")  stats(r2 r2_a, labels("R-Square" "Adj. R-Square"))  replace

 }

  foreach marker in  Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj  {



 estout m1`marker'  m2`marker'  m3`marker' m4`marker'  using non_diabetic_jon_emb_transform.xls, cells ("b(fmt(4)) ci_l(fmt(4)) ci_u(fmt(4))")
label  legend collabels("Coeff" "LB" "UB")  stats(r2 r2_a, labels("R-Square" "Adj. R-Square"))    append



 }






insheet using non_diabetic_jon_emb_transform.xls, clear


keep if v1=="o.fasting_interval==1" /*
*/ | v1=="fasting_interval==1" /*
*/ | v1=="fasting_interval_mod" /*
*/ | v1=="hour_interval==1" /*
*/ | v1=="hour_interval_mod" /*
```

```
*/ | v1=="R-Square" /*
*/ | v1=="Adj. R-Square" /*
*/ | v1=="" /*
*/ | v1=="(fasting_interval==1)*fasting_interval_mod" /*
*/ | v1=="(hour_interval==1)*hour_interval_mod"


gen Model1=v2+"("+v3+","+v4+")"
gen Model2=v5+"("+v6+","+v7+")"
gen Model3=v8+"("+v9+","+v10+")"
gen Model4=v11+"("+v12+","+v13+")"



keep v1 Model*

replace v1="Fasting time (>=6h vs <6)" if v1=="o.fasting_interval==1"
replace v1="Fasting time (>=6h vs <6)" if v1=="fasting_interval==1"
replace v1="Fasting time continuous (transformed)" if v1=="fasting_interval_mod"
replace v1="Hour of the day (>13 vs <=13)" if v1=="hour_interval==1"
replace v1="Hour of the day continuous (transformed)" if v1=="hour_interval_mod"
replace v1="(fasting_interval==1)*Fasting time continuous (transformed)" if v1=="(fasting_interval==1)*fasting_interval_mod"
replace v1="(hour_interval==1)*Hour of the day continuous (transformed)" if v1=="(hour_interval==1)*hour_interval_mod"


foreach model in Model1 Model2 Model3 Model4{

    replace `model'="" if `model'=="(,)"

}







*****************************************************************************
*****************************************************************************
*****************************************************************************
*****************************************************************************
****
****        FASTING TIME AND HOUR OF THE DAY TRANSFORMATION
****
*****************************************************************************
*****************************************************************************
*****************************************************************************
*****************************************************************************
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        BASED ON JON EMBERSON WORK - NON DIABETICS AND FASTERS
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear

* replace round_fasting_trunc=19.99 if round_fasting_trunc>=20 & round_fasting_trunc!=.

tab round_fasting_trunc

gen fasting_interval=0 if round_fasting_trunc<6
replace fasting_interval=1 if round_fasting_trunc>=6 & round_fasting_trunc!=.

gen fasting_interval_mod=0       if round_fasting_trunc==0
replace fasting_interval_mod=1   if round_fasting_trunc==1
replace fasting_interval_mod=2   if round_fasting_trunc==2
replace fasting_interval_mod=3   if round_fasting_trunc==3
replace fasting_interval_mod=4   if round_fasting_trunc==4
replace fasting_interval_mod=5   if round_fasting_trunc==5


replace fasting_interval_mod=0   if round_fasting_trunc==6
replace fasting_interval_mod=1   if round_fasting_trunc==7
replace fasting_interval_mod=2   if round_fasting_trunc==8
replace fasting_interval_mod=3   if round_fasting_trunc==9
replace fasting_interval_mod=4   if round_fasting_trunc==10
replace fasting_interval_mod=5   if round_fasting_trunc==11
replace fasting_interval_mod=6   if round_fasting_trunc==12
replace fasting_interval_mod=7   if round_fasting_trunc==13
replace fasting_interval_mod=8   if round_fasting_trunc==14
replace fasting_interval_mod=9   if round_fasting_trunc==15
replace fasting_interval_mod=10  if round_fasting_trunc==16
replace fasting_interval_mod=11  if round_fasting_trunc==17
replace fasting_interval_mod=12  if round_fasting_trunc==18
replace fasting_interval_mod=13  if round_fasting_trunc==19
replace fasting_interval_mod=14  if round_fasting_trunc==20
replace fasting_interval_mod=15  if round_fasting_trunc==21
replace fasting_interval_mod=16  if round_fasting_trunc==22
```

```
replace fasting_interval_mod=17  if round_fasting_trunc==23
replace fasting_interval_mod=18  if round_fasting_trunc==24


browse round_fasting_trunc fasting_interval fasting_interval_mod


tab Q30time_hour_round

gen hour_interval=0 if Q30time_hour_round<=13
replace hour_interval=1 if Q30time_hour_round>13 & Q30time_hour_round!=.

gen hour_interval_mod=1 if Q30time_hour_round==9
replace hour_interval_mod=2 if Q30time_hour_round==10
replace hour_interval_mod=3 if Q30time_hour_round==11
replace hour_interval_mod=4 if Q30time_hour_round==12
replace hour_interval_mod=5 if Q30time_hour_round==13
replace hour_interval_mod=0 if Q30time_hour_round==14
replace hour_interval_mod=1 if Q30time_hour_round==15
replace hour_interval_mod=2 if Q30time_hour_round==16
replace hour_interval_mod=3 if Q30time_hour_round==17

browse Q30time_hour_round hour_interval hour_interval_mod


tab fasting_interval

foreach marker in  Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj {

* NON DIABETICS AND FASTERS

* model 1
xi:regress `marker'  fasting_interval_mod if diabetes_q30_ds==0 & fasting_interval==1
est store m1`marker'

* model 2
xi:regress `marker'  i.hour_interval  hour_interval_mod if diabetes_q30_ds==0 & fasting_interval==1
est store m2`marker'

* model 3
xi:regress `marker'  fasting_interval_mod i.hour_interval  hour_interval_mod  if diabetes_q30_ds==0 & fasting_interval==1
est store m3`marker'

* model 4
xi:regress `marker'  fasting_interval_mod i.hour_interval*hour_interval_mod  if diabetes_q30_ds==0 & fasting_interval==1
est store m4`marker'

}
```

```
cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis"


 foreach marker in Q30chol  {

 estout m1`marker'  m2`marker'  m3`marker' m4`marker' using non_diabetic_fasters_jon_emb_transform.xls, cells ("b(fmt(4)) ci_l(fmt(4))
ci_u(fmt(4))") label  legend collabels("Coeff" "LB" "UB")  stats(r2 r2_a, labels("R-Square" "Adj. R-Square"))  replace

 }

  foreach marker in  Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj  {



 estout m1`marker'  m2`marker'  m3`marker' m4`marker'  using non_diabetic_fasters_jon_emb_transform.xls, cells ("b(fmt(4)) ci_l(fmt(4))
ci_u(fmt(4))") label  legend collabels("Coeff" "LB" "UB")  stats(r2 r2_a, labels("R-Square" "Adj. R-Square"))    append



 }






insheet using non_diabetic_fasters_jon_emb_transform.xls, clear


keep if v1=="o.fasting_interval==1" /*
*/ | v1=="fasting_interval==1" /*
*/ | v1=="fasting_interval_mod" /*
*/ | v1=="hour_interval==1" /*
*/ | v1=="hour_interval_mod" /*
*/ | v1=="R-Square" /*
*/ | v1=="Adj. R-Square" /*
*/ | v1=="" /*
*/ | v1=="(fasting_interval==1)*fasting_interval_mod" /*
*/ | v1=="(hour_interval==1)*hour_interval_mod"


gen Model1=v2+"("+v3+","+v4+")"
gen Model2=v5+"("+v6+","+v7+")"
gen Model3=v8+"("+v9+","+v10+")"
```

```
gen Model4=v11+"("+v12+","+v13+")"



keep v1 Model*

replace v1="Fasting time (>=6h vs <6)" if v1=="o.fasting_interval==1"
replace v1="Fasting time (>=6h vs <6)" if v1=="fasting_interval==1"
replace v1="Fasting time continuous (transformed)" if v1=="fasting_interval_mod"
replace v1="Hour of the day (>13 vs <=13)" if v1=="hour_interval==1"
replace v1="Hour of the day continuous (transformed)" if v1=="hour_interval_mod"
replace v1="(fasting_interval==1)*Fasting time continuous (transformed)" if v1=="(fasting_interval==1)*fasting_interval_mod"
replace v1="(hour_interval==1)*Hour of the day continuous (transformed)" if v1=="(hour_interval==1)*hour_interval_mod"


foreach model in Model1 Model2 Model3 Model4{

    replace `model'="" if `model'=="(,)"

}
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
```

```
****        FINAL ADJUSTEMENT
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        BASED ON JON EMBERSON WORK
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************



use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear

* replace round_fasting_trunc=19.99 if round_fasting_trunc>=20 & round_fasting_trunc!=.

tab round_fasting_trunc

gen fasting_interval=0 if round_fasting_trunc<6
replace fasting_interval=1 if round_fasting_trunc>=6 & round_fasting_trunc!=.

gen fasting_interval_mod=0       if round_fasting_trunc==0
replace fasting_interval_mod=1   if round_fasting_trunc==1
replace fasting_interval_mod=2   if round_fasting_trunc==2
replace fasting_interval_mod=3   if round_fasting_trunc==3
replace fasting_interval_mod=4   if round_fasting_trunc==4
replace fasting_interval_mod=5   if round_fasting_trunc==5


replace fasting_interval_mod=0   if round_fasting_trunc==6
replace fasting_interval_mod=1   if round_fasting_trunc==7
replace fasting_interval_mod=2   if round_fasting_trunc==8
replace fasting_interval_mod=3   if round_fasting_trunc==9
replace fasting_interval_mod=4   if round_fasting_trunc==10
replace fasting_interval_mod=5   if round_fasting_trunc==11
replace fasting_interval_mod=6   if round_fasting_trunc==12
replace fasting_interval_mod=7   if round_fasting_trunc==13
replace fasting_interval_mod=8   if round_fasting_trunc==14
replace fasting_interval_mod=9   if round_fasting_trunc==15
```

```
replace fasting_interval_mod=10  if round_fasting_trunc==16
replace fasting_interval_mod=11  if round_fasting_trunc==17
replace fasting_interval_mod=12  if round_fasting_trunc==18
replace fasting_interval_mod=13  if round_fasting_trunc==19
replace fasting_interval_mod=14  if round_fasting_trunc==20
replace fasting_interval_mod=15  if round_fasting_trunc==21
replace fasting_interval_mod=16  if round_fasting_trunc==22
replace fasting_interval_mod=17  if round_fasting_trunc==23
replace fasting_interval_mod=18  if round_fasting_trunc==24


browse round_fasting_trunc fasting_interval fasting_interval_mod


tab Q30time_hour_round

gen hour_interval=0 if Q30time_hour_round<=13
replace hour_interval=1 if Q30time_hour_round>13 & Q30time_hour_round!=.

gen hour_interval_mod=1 if Q30time_hour_round==9
replace hour_interval_mod=2 if Q30time_hour_round==10
replace hour_interval_mod=3 if Q30time_hour_round==11
replace hour_interval_mod=4 if Q30time_hour_round==12
replace hour_interval_mod=5 if Q30time_hour_round==13
replace hour_interval_mod=0 if Q30time_hour_round==14
replace hour_interval_mod=1 if Q30time_hour_round==15
replace hour_interval_mod=2 if Q30time_hour_round==16
replace hour_interval_mod=3 if Q30time_hour_round==17

browse Q30time_hour_round hour_interval hour_interval_mod






****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        MODEL 3
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        NON DIABETICS MODEL 3 FOR Q30hdlc Q30ldlc Q30trig_log  q30insulin_log_adj
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************



foreach marker in Q30hdlc Q30ldlc Q30trig_log  q30insulin_log_adj {

xi:regress `marker' i.fasting_interval fasting_interval_mod i.hour_interval  hour_interval_mod if diabetes_q30_ds==0
predict `marker'_pred if e(sample), xb
predict `marker'_res if e(sample), residuals


sum `marker' if diabetes_q30_ds==0, d
gen `marker'_adj=`r(mean)'+(`marker'-`marker'_pred) if diabetes_q30_ds==0


}



****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        MODEL 2
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        NON DIABETICS MODEL 2 FOR Q30hba1c_log Q30gluc_log
****
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************



foreach marker in  Q30hba1c_log Q30gluc_log  {

xi:regress `marker'  i.hour_interval  hour_interval_mod if diabetes_q30_ds==0
predict `marker'_pred if e(sample), xb
predict `marker'_res if e(sample), residuals


sum `marker' if diabetes_q30_ds==0, d
gen `marker'_adj=`r(mean)'+(`marker'-`marker'_pred) if diabetes_q30_ds==0


}



****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        report values to original format
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************




foreach marker in Q30hba1c Q30gluc Q30trig {

gen d`marker'_adj=exp(`marker'_log_adj) if diabetes_q30_ds==0


}


foreach marker in  q30insulin {

gen d`marker'_adj_adj=exp(`marker'_log_adj_adj) if diabetes_q30_ds==0
```

```
}



browse serial diabetes_q30_ds Q30hdlc Q30hdlc_adj Q30ldlc Q30ldlc_adj Q30hba1c dQ30hba1c_adj Q30gluc dQ30gluc_adj q30insulin_adj
dq30insulin_adj_adj Q30trig dQ30trig_adj



keep if diabetes_q30_ds==0


scatter dq30insulin_adj_adj q30insulin_adj
scatter Q30gluc dQ30gluc_adj
sum Q30gluc dQ30gluc_adj

keep serial fasting_interval Q30time_hour_round *_adj diabetes_q30_ds

* Q30chol Q30hdlc Q30ldlc Q30trig Q30hba1c Q30gluc q30insulin_adj

drop *log*
ren q30insulin_adj Q30insulin_batch

renpfix Q30 dQ30

ren dq30insulin_adj_adj dQ30insulin_adj
ren fasting_interval dQ30fasting

tabmiss dQ30ldlc_adj dQ30hba1c_adj dQ30gluc_adj dQ30insulin_adj
tab dQ30fasting

ren dQ30time_hour_round dQ30hour

order serial dQ30hour dQ30fasting

ren dQ30insulin_batch Q30insulin_batch

ren diabetes_q30_ds dQ30diabetes


saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_adjustment_non_diabetics", replace
```

```
/*



****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****       GRAPHS NOT ADJUSTED VS ADJUSTED
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************

****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****      NON DIABETICS   PLOT MEAN  HOUR OF THE DAY
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************

cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\graphs"

keep if diabetes_q30_ds==0


preserve


collapse (mean)    Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
```

```
   */              Q30hdlc_adj Q30ldlc_adj Q30trig_log_adj Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj /*

   */    (semean)  se_Q30hdlc=Q30hdlc se_Q30ldlc=Q30ldlc se_Q30trig_log=Q30trig_log /*
   */    se_Q30hba1c_log=Q30hba1c_log se_Q30gluc_log=Q30gluc_log se_q30insulin_log_adj=q30insulin_log_adj  /*

   */    (semean)  se_Q30hdlc_adj=Q30hdlc_adj se_Q30ldlc_adj=Q30ldlc_adj se_Q30trig_log_adj=Q30trig_log_adj /*
   */    se_Q30hba1c_log_adj=Q30hba1c_log_adj se_Q30gluc_log_adj=Q30gluc_log_adj se_q30insulin_log_adj_adj=q30insulin_log_adj_adj,
by(Q30time_hour_round)


foreach name in Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */              Q30hdlc_adj Q30ldlc_adj Q30trig_log_adj Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj  {

gen `name'_u = `name' + 1.96*se_`name'
gen `name'_l = `name' - 1.96*se_`name'

}


label var Q30time_hour_round "Hour of examination"

drop if Q30time_hour_round==18 | Q30time_hour_round==19


foreach name in    Q30trig_log     Q30hba1c_log     Q30gluc_log     q30insulin_log_adj /*
   */              Q30trig_log_adj Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj  {

replace `name'=exp(`name')
replace `name'_u =exp(`name'_u)
replace `name'_l =exp(`name'_l)

}

rensfix _log
rensfix _log_adj _adj
rensfix _log_adj_adj _adj_adj
rensfix _log_u _u
rensfix _log_l _l
rensfix _log_adj_u _adj_u
rensfix _log_adj_l _adj_l
rensfix _log_adj_adj_u _adj_adj_u
rensfix _log_adj_adj_l _adj_adj_l



/*
foreach marker in Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */              Q30hdlc_adj Q30ldlc_adj Q30trig_log_adj Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj  {
```

```
label var Q30time_hour_round "Hour of examination"
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
twoway (scatter `marker' Q30time_hour_round, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l Q30time_hour_round,
lcolor(black) lwidth(thick) legend(on)) (line `marker' Q30time_hour_round, lcolor(black) lpattern(dash)), /*
*/ xlabel(9 10 11 12 13 14 15 16 17, labsize(large)) graphregion(color(white)) ylabel(, angle(horizontal) labsize(large)) title(`marker',
size(vlarge)) ytitle(mean, size(large)) xtitle(Hour of examination, size(large)) legend(row(3)) legend(off)
graph save `marker'_line_non_diabetics, replace
graph export `marker'_line_non_diabetics.png, replace

}






graph combine Q30hdlc_line_non_diabetics.gph Q30hdlc_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics) ycommon

graph combine Q30ldlc_line_non_diabetics.gph Q30ldlc_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics) ycommon

graph combine Q30trig_log_line_non_diabetics.gph Q30trig_log_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics) ycommon

graph combine  q30insulin_log_adj_line_non_diabetics.gph  q30insulin_log_adj_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-
Diabetics) ycommon

graph combine  Q30gluc_log_line_non_diabetics.gph  Q30gluc_log_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics)
ycommon

graph export cholesterol_line_non_diabetics.png, replace

graph combine Q30hba1c_log_line_non_diabetics.gph Q30gluc_log_line_non_diabetics.gph q30insulin_log_adj_line_non_diabetics.gph, row(1)
ysize(5) xsize(16) title(Non-Diabetics)
graph export hba_insuline_glucose_line_non_diabetics.png, replace


*/


foreach marker in Q30hdlc Q30ldlc Q30trig Q30hba1c Q30gluc q30insulin_adj /*
   */               {


label var Q30time_hour_round "Hour of examination"
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
twoway (scatter `marker' Q30time_hour_round, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l Q30time_hour_round,
lcolor(black) lwidth(thick) legend(on)) (line `marker' Q30time_hour_round, lcolor(black) lpattern(dash)), /*
```

```
*/ xlabel(9 10 11 12 13 14 15 16 17, labsize(large)) graphregion(color(white)) ylabel(, angle(horizontal) labsize(large)) title(`marker',
size(vlarge)) subtitle(Not adjusted) ytitle(mean, size(large)) xtitle(Hour of examination, size(large)) legend(row(3)) legend(off)
graph save `marker'_line_non_diabetics, replace
graph export `marker'_line_non_diabetics.png, replace

}



foreach marker in  /*
   */              Q30hdlc_adj Q30ldlc_adj Q30trig_adj Q30hba1c_adj Q30gluc_adj q30insulin_adj_adj  {


label var Q30time_hour_round "Hour of examination"
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
twoway (scatter `marker' Q30time_hour_round, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l Q30time_hour_round,
lcolor(black) lwidth(thick) legend(on)) (line `marker' Q30time_hour_round, lcolor(black) lpattern(dash)), /*
*/ xlabel(9 10 11 12 13 14 15 16 17, labsize(large)) graphregion(color(white)) ylabel(, angle(horizontal) labsize(large)) title(`marker',
size(vlarge)) subtitle(Adjusted) ytitle(mean, size(large)) xtitle(Hour of examination, size(large)) legend(row(3)) legend(off)
graph save `marker'_line_non_diabetics, replace
graph export `marker'_line_non_diabetics.png, replace

}





graph combine Q30hdlc_line_non_diabetics.gph Q30hdlc_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics) ycommon
graph export Q30hdlc_original_vs_adj.png, replace

graph combine Q30ldlc_line_non_diabetics.gph Q30ldlc_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics) ycommon
graph export Q30ldlc_original_vs_adj.png, replace

graph combine Q30trig_line_non_diabetics.gph Q30trig_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics) ycommon
graph export Q30trig_original_vs_adj.png, replace

graph combine  q30insulin_adj_line_non_diabetics.gph  q30insulin_adj_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics)
ycommon
graph export Q30insulin_original_vs_adj.png, replace

graph combine  Q30gluc_line_non_diabetics.gph  Q30gluc_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics) ycommon
graph export Q30gluc_original_vs_adj.png, replace

graph combine  Q30hba1c_line_non_diabetics.gph  Q30hba1c_adj_line_non_diabetics.gph, row(1) ysize(1) xsize(2) title(Non-Diabetics) ycommon
graph export Q30hba1c_original_vs_adj.png, replace
```

```
restore



****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****      NON DIABETICS   PLOT MEAN  FASTING TIME
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************



collapse (mean)    Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */              Q30hdlc_adj Q30ldlc_adj Q30trig_log_adj Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj /*

   */    (semean)  se_Q30hdlc=Q30hdlc se_Q30ldlc=Q30ldlc se_Q30trig_log=Q30trig_log /*
   */    se_Q30hba1c_log=Q30hba1c_log se_Q30gluc_log=Q30gluc_log se_q30insulin_log_adj=q30insulin_log_adj  /*

   */    (semean)  se_Q30hdlc_adj=Q30hdlc_adj se_Q30ldlc_adj=Q30ldlc_adj se_Q30trig_log_adj=Q30trig_log_adj /*
   */    se_Q30hba1c_log_adj=Q30hba1c_log_adj se_Q30gluc_log_adj=Q30gluc_log_adj se_q30insulin_log_adj_adj=q30insulin_log_adj_adj,
by(round_fasting_trunc)


foreach name in Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */              Q30hdlc_adj Q30ldlc_adj Q30trig_log_adj Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj  {

gen `name'_u = `name' + 1.96*se_`name'
gen `name'_l = `name' - 1.96*se_`name'

}


label var round_fasting_trunc "Fasting time"



cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\graphs"
```

```
foreach name in    Q30trig_log     Q30hba1c_log     Q30gluc_log     q30insulin_log_adj /*
   */              Q30trig_log_adj Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj  {

replace `name'=exp(`name')
replace `name'_u =exp(`name'_u)
replace `name'_l =exp(`name'_l)

}

rensfix _log
rensfix _log_adj _adj
rensfix _log_adj_adj _adj_adj
rensfix _log_u _u
rensfix _log_l _l
rensfix _log_adj_u _adj_u
rensfix _log_adj_l _adj_l
rensfix _log_adj_adj_u _adj_adj_u
rensfix _log_adj_adj_l _adj_adj_l




foreach marker in Q30hdlc Q30ldlc Q30trig Q30hba1c Q30gluc q30insulin_adj /*
   */               {


label var round_fasting_trunc "Hour of examination"
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
twoway (scatter `marker' round_fasting_trunc, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l round_fasting_trunc,
lcolor(black) lwidth(thick) legend(on)) (line `marker' round_fasting_trunc, lcolor(black) lpattern(dash)), /*
*/ xlabel(1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20, labsize(med)) graphregion(color(white)) ylabel(, angle(horizontal)
labsize(large)) title(`marker', size(vlarge)) subtitle(Not adjusted) ytitle(mean, size(large)) xtitle(Fasting time, size(large))
legend(row(3)) legend(off)
graph save `marker'_line_non_diabetics_fasting, replace
graph export `marker'_line_non_diabetics_fasting.png, replace

}



foreach marker in  /*
   */              Q30hdlc_adj Q30ldlc_adj Q30trig_adj Q30hba1c_adj Q30gluc_adj q30insulin_adj_adj  {


label var round_fasting_trunc "Hour of examination"
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
```

```
twoway (scatter `marker' round_fasting_trunc, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l round_fasting_trunc,
lcolor(black) lwidth(thick) legend(on)) (line `marker' round_fasting_trunc, lcolor(black) lpattern(dash)), /*
*/ xlabel(1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20, labsize(med) ) graphregion(color(white)) ylabel(, angle(horizontal)
labsize(large)) title(`marker', size(vlarge)) subtitle(Adjusted) ytitle(mean, size(large)) xtitle(Fasting time, size(large)) legend(row(3))
legend(off)
graph save `marker'_line_non_diabetics_fasting, replace
graph export `marker'_line_non_diabetics_fasting.png, replace

}









graph combine  Q30hdlc_line_non_diabetics_fasting.gph Q30hdlc_adj_line_non_diabetics_fasting.gph, row(1) ysize(1) xsize(2) title(Non-
Diabetics) ycommon
graph export   Q30hdlc_original_vs_adj_fasting.png, replace

graph combine  Q30ldlc_line_non_diabetics_fasting.gph Q30ldlc_adj_line_non_diabetics_fasting.gph, row(1) ysize(1) xsize(2) title(Non-
Diabetics) ycommon
graph export   Q30ldlc_original_vs_adj_fasting.png, replace

graph combine  Q30trig_line_non_diabetics_fasting.gph Q30trig_adj_line_non_diabetics_fasting.gph, row(1) ysize(1) xsize(2) title(Non-
Diabetics) ycommon
graph export   Q30trig_original_vs_adj_fasting.png, replace

graph combine  q30insulin_adj_line_non_diabetics_fasting.gph  q30insulin_adj_adj_line_non_diabetics_fasting.gph, row(1) ysize(1) xsize(2)
title(Non-Diabetics) ycommon
graph export   Q30insulin_original_vs_adj_fasting.png, replace

graph combine  Q30gluc_line_non_diabetics_fasting.gph  Q30gluc_adj_line_non_diabetics_fasting.gph, row(1) ysize(1) xsize(2) title(Non-
Diabetics) ycommon
graph export   Q30gluc_original_vs_adj_fasting.png, replace

graph combine  Q30hba1c_line_non_diabetics_fasting.gph  Q30hba1c_adj_line_non_diabetics_fasting.gph, row(1) ysize(1) xsize(2) title(Non-
Diabetics) ycommon
graph export   Q30hba1c_original_vs_adj_fasting.png, replace




*/
```

APPENDIX 3: 23. Diabetics - Total Cholesterol, LDL, HDL, triglycerides, insulin, glucose, HBA.do

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        DIABETICS
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        FASTING TIME TRANSFORMATION
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        BASED ON JON EMBERSON WORK
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear


tab round_fasting_trunc

gen fasting_interval=0 if round_fasting_trunc<6
replace fasting_interval=1 if round_fasting_trunc>=6 & round_fasting_trunc!=.

gen fasting_interval_mod=0       if round_fasting_trunc==0
```

```
replace fasting_interval_mod=1   if round_fasting_trunc==1
replace fasting_interval_mod=2   if round_fasting_trunc==2
replace fasting_interval_mod=3   if round_fasting_trunc==3
replace fasting_interval_mod=4   if round_fasting_trunc==4
replace fasting_interval_mod=5   if round_fasting_trunc==5


replace fasting_interval_mod=0   if round_fasting_trunc==6
replace fasting_interval_mod=1   if round_fasting_trunc==7
replace fasting_interval_mod=2   if round_fasting_trunc==8
replace fasting_interval_mod=3   if round_fasting_trunc==9
replace fasting_interval_mod=4   if round_fasting_trunc==10
replace fasting_interval_mod=5   if round_fasting_trunc==11
replace fasting_interval_mod=6   if round_fasting_trunc==12
replace fasting_interval_mod=7   if round_fasting_trunc==13
replace fasting_interval_mod=8   if round_fasting_trunc==14
replace fasting_interval_mod=9   if round_fasting_trunc==15
replace fasting_interval_mod=10  if round_fasting_trunc==16
replace fasting_interval_mod=11  if round_fasting_trunc==17
replace fasting_interval_mod=12  if round_fasting_trunc==18
replace fasting_interval_mod=13  if round_fasting_trunc==19
replace fasting_interval_mod=14  if round_fasting_trunc==20
replace fasting_interval_mod=15  if round_fasting_trunc==21
replace fasting_interval_mod=16  if round_fasting_trunc==22
replace fasting_interval_mod=17  if round_fasting_trunc==23
replace fasting_interval_mod=18  if round_fasting_trunc==24


browse round_fasting_trunc fasting_interval fasting_interval_mod


tab Q30time_hour_round

gen hour_interval=0 if Q30time_hour_round<=13
replace hour_interval=1 if Q30time_hour_round>13 & Q30time_hour_round!=.

gen hour_interval_mod=1 if Q30time_hour_round==9
replace hour_interval_mod=2 if Q30time_hour_round==10
replace hour_interval_mod=3 if Q30time_hour_round==11
replace hour_interval_mod=4 if Q30time_hour_round==12
replace hour_interval_mod=5 if Q30time_hour_round==13
replace hour_interval_mod=0 if Q30time_hour_round==14
replace hour_interval_mod=1 if Q30time_hour_round==15
replace hour_interval_mod=2 if Q30time_hour_round==16
replace hour_interval_mod=3 if Q30time_hour_round==17

browse Q30time_hour_round hour_interval hour_interval_mod


tab fasting_interval
```

```
foreach marker in  Q30chol Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj {

*  DIABETICS

* model 1
xi:regress `marker' i.fasting_interval fasting_interval_mod if diabetes_q30_ds==1
est store m1`marker'

* model 2
xi:regress `marker' i.hour_interval  hour_interval_mod if diabetes_q30_ds==1
est store m2`marker'

* model 3
xi:regress `marker' i.fasting_interval fasting_interval_mod i.hour_interval  hour_interval_mod  if diabetes_q30_ds==1
est store m3`marker'

* model 4
xi:regress `marker' i.fasting_interval*fasting_interval_mod i.hour_interval*hour_interval_mod  if diabetes_q30_ds==1
est store m4`marker'

}




cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis"


 foreach marker in Q30chol  {

 estout m1`marker'  m2`marker'  m3`marker' m4`marker' using diabetic_fasters_jon_emb_transform.xls, cells ("b(fmt(4)) ci_l(fmt(4))
ci_u(fmt(4))") label  legend collabels("Coeff" "LB" "UB")   stats(r2 r2_a, labels("R-Square" "Adj. R-Square"))  replace

 }

  foreach marker in  Q30hdlc Q30ldlc Q30trig_log Q30hba1c_log Q30gluc_log q30insulin_log_adj  {



 estout m1`marker'  m2`marker'  m3`marker' m4`marker'  using diabetic_fasters_jon_emb_transform.xls, cells ("b(fmt(4)) ci_l(fmt(4))
ci_u(fmt(4))") label  legend collabels("Coeff" "LB" "UB")  stats(r2 r2_a, labels("R-Square" "Adj. R-Square"))   append



 }
```

```
insheet using diabetic_fasters_jon_emb_transform.xls, clear


keep if v1=="o.fasting_interval==1" /*
*/ | v1=="fasting_interval==1" /*
*/ | v1=="fasting_interval_mod" /*
*/ | v1=="hour_interval==1" /*
*/ | v1=="hour_interval_mod" /*
*/ | v1=="R-Square" /*
*/ | v1=="Adj. R-Square" /*
*/ | v1=="" /*
*/ | v1=="(fasting_interval==1)*fasting_interval_mod" /*
*/ | v1=="(hour_interval==1)*hour_interval_mod"


gen Model1=v2+"("+v3+","+v4+")"
gen Model2=v5+"("+v6+","+v7+")"
gen Model3=v8+"("+v9+","+v10+")"
gen Model4=v11+"("+v12+","+v13+")"



keep v1 Model*

replace v1="Fasting time (>=6h vs <6)" if v1=="o.fasting_interval==1"
replace v1="Fasting time (>=6h vs <6)" if v1=="fasting_interval==1"
replace v1="Fasting time continuous (transformed)" if v1=="fasting_interval_mod"
replace v1="Hour of the day (>13 vs <=13)" if v1=="hour_interval==1"
replace v1="Hour of the day continuous (transformed)" if v1=="hour_interval_mod"
replace v1="(fasting_interval==1)*Fasting time continuous (transformed)" if v1=="(fasting_interval==1)*fasting_interval_mod"
replace v1="(hour_interval==1)*Hour of the day continuous (transformed)" if v1=="(hour_interval==1)*hour_interval_mod"


foreach model in Model1 Model2 Model3 Model4{

    replace `model'="" if `model'=="(,)"

}
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        FINAL ADJUSTEMENT
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************


****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        BASED ON JON EMBERSON WORK
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************



use "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_5DEC13_with_derived_variables", clear

* replace round_fasting_trunc=19.99 if round_fasting_trunc>=20 & round_fasting_trunc!=.

tab round_fasting_trunc

gen fasting_interval=0 if round_fasting_trunc<6
replace fasting_interval=1 if round_fasting_trunc>=6 & round_fasting_trunc!=.

gen fasting_interval_mod=0       if round_fasting_trunc==0
replace fasting_interval_mod=1   if round_fasting_trunc==1
replace fasting_interval_mod=2   if round_fasting_trunc==2
replace fasting_interval_mod=3   if round_fasting_trunc==3
replace fasting_interval_mod=4   if round_fasting_trunc==4
replace fasting_interval_mod=5   if round_fasting_trunc==5


replace fasting_interval_mod=0   if round_fasting_trunc==6
replace fasting_interval_mod=1   if round_fasting_trunc==7
replace fasting_interval_mod=2   if round_fasting_trunc==8
replace fasting_interval_mod=3   if round_fasting_trunc==9
replace fasting_interval_mod=4   if round_fasting_trunc==10
replace fasting_interval_mod=5   if round_fasting_trunc==11
```

```
replace fasting_interval_mod=6   if round_fasting_trunc==12
replace fasting_interval_mod=7   if round_fasting_trunc==13
replace fasting_interval_mod=8   if round_fasting_trunc==14
replace fasting_interval_mod=9   if round_fasting_trunc==15
replace fasting_interval_mod=10  if round_fasting_trunc==16
replace fasting_interval_mod=11  if round_fasting_trunc==17
replace fasting_interval_mod=12  if round_fasting_trunc==18
replace fasting_interval_mod=13  if round_fasting_trunc==19
replace fasting_interval_mod=14  if round_fasting_trunc==20
replace fasting_interval_mod=15  if round_fasting_trunc==21
replace fasting_interval_mod=16  if round_fasting_trunc==22
replace fasting_interval_mod=17  if round_fasting_trunc==23
replace fasting_interval_mod=18  if round_fasting_trunc==24


browse round_fasting_trunc fasting_interval fasting_interval_mod


tab Q30time_hour_round

gen hour_interval=0 if Q30time_hour_round<=13
replace hour_interval=1 if Q30time_hour_round>13 & Q30time_hour_round!=.

gen hour_interval_mod=1 if Q30time_hour_round==9
replace hour_interval_mod=2 if Q30time_hour_round==10
replace hour_interval_mod=3 if Q30time_hour_round==11
replace hour_interval_mod=4 if Q30time_hour_round==12
replace hour_interval_mod=5 if Q30time_hour_round==13
replace hour_interval_mod=0 if Q30time_hour_round==14
replace hour_interval_mod=1 if Q30time_hour_round==15
replace hour_interval_mod=2 if Q30time_hour_round==16
replace hour_interval_mod=3 if Q30time_hour_round==17

browse Q30time_hour_round hour_interval hour_interval_mod




****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        MODEL 3
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****     DIABETICS MODEL 3 FOR Q30hdlc  Q30hba1c_log q30insulin_log_adj
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************



foreach marker in  Q30hdlc Q30gluc_log  {

xi:regress `marker' i.fasting_interval fasting_interval_mod i.hour_interval  hour_interval_mod if diabetes_q30_ds==1
predict `marker'_pred if e(sample), xb
predict `marker'_res if e(sample), residuals


sum `marker' if diabetes_q30_ds==1, d
gen `marker'_adj=`r(mean)'+(`marker'-`marker'_pred) if diabetes_q30_ds==1


}


****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****     DIABETICS MODEL 1 FOR Q30chol, Q30ldlc,  Q30hba1c_log,  q30insulin_log_adj
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************



foreach marker in  Q30chol Q30ldlc  Q30hba1c_log  q30insulin_log_adj  {

xi:regress `marker' i.fasting_interval fasting_interval_mod  if diabetes_q30_ds==1
predict `marker'_pred if e(sample), xb
predict `marker'_res if e(sample), residuals


sum `marker' if diabetes_q30_ds==1, d
```

```
gen `marker'_adj=`r(mean)'+(`marker'-`marker'_pred) if diabetes_q30_ds==1


}



foreach marker in Q30hba1c Q30gluc {

gen d`marker'_adj=exp(`marker'_log_adj) if diabetes_q30_ds==1


}


foreach marker in  q30insulin {

gen d`marker'_adj_adj=exp(`marker'_log_adj_adj) if diabetes_q30_ds==1


}


keep if diabetes_q30_ds==1


scatter dq30insulin_adj_adj q30insulin_adj
scatter Q30gluc dQ30gluc_adj
sum Q30gluc dQ30gluc_adj

keep serial fasting_interval Q30time_hour_round *_adj diabetes_q30_ds

* Q30chol Q30hdlc Q30ldlc Q30trig Q30hba1c Q30gluc q30insulin_adj

drop *log*
ren q30insulin_adj Q30insulin_batch

renpfix Q30 dQ30

ren dq30insulin_adj_adj dQ30insulin_adj
ren fasting_interval dQ30fasting

tabmiss dQ30ldlc_adj dQ30hba1c_adj dQ30gluc_adj dQ30insulin_adj
tab dQ30fasting

ren dQ30time_hour_round dQ30hour

order serial dQ30hour dQ30fasting

ren dQ30insulin_batch Q30insulin_batch
```

```
ren diabetes_q30_ds dQ30diabetes


saveold "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\Q30_adjustment_diabetics", replace



/*

****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****       GRAPHS NOT ADJUSTED VS ADJUSTED
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************



****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        DIABETICS  PLOT MEAN BY HOUR OF THE DAY
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************

preserve

cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\graphs"

keep if diabetes_q30_ds==1



collapse (mean)    Q30hdlc Q30chol Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
```

```
   */              Q30hdlc_adj Q30chol_adj  Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj /*

   */    (semean)  se_Q30hdlc=Q30hdlc se_Q30chol=Q30chol  /*
   */    se_Q30hba1c_log=Q30hba1c_log se_Q30gluc_log=Q30gluc_log se_q30insulin_log_adj=q30insulin_log_adj  /*

   */    (semean)  se_Q30hdlc_adj=Q30hdlc_adj se_Q30chol_adj=Q30chol_adj  /*
   */    se_Q30hba1c_log_adj=Q30hba1c_log_adj se_Q30gluc_log_adj=Q30gluc_log_adj se_q30insulin_log_adj_adj=q30insulin_log_adj_adj,
by(Q30time_hour_round)


foreach name in Q30hdlc Q30chol Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */              Q30hdlc_adj Q30chol_adj Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj  {

gen `name'_u = `name' + 1.96*se_`name'
gen `name'_l = `name' - 1.96*se_`name'

}


label var Q30time_hour_round "Hour of examination"

drop if Q30time_hour_round==18 | Q30time_hour_round==19


foreach name in         Q30hba1c_log     Q30gluc_log     q30insulin_log_adj /*
   */                   Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj  {

replace `name'=exp(`name')
replace `name'_u =exp(`name'_u)
replace `name'_l =exp(`name'_l)

}

rensfix _log
rensfix _log_adj _adj
rensfix _log_adj_adj _adj_adj
rensfix _log_u _u
rensfix _log_l _l
rensfix _log_adj_u _adj_u
rensfix _log_adj_l _adj_l
rensfix _log_adj_adj_u _adj_adj_u
rensfix _log_adj_adj_l _adj_adj_l




foreach marker in Q30chol Q30hdlc Q30hba1c Q30gluc q30insulin_adj /*
   */               {


label var Q30time_hour_round "Hour of examination"
```

```
twoway (scatter `marker' Q30time_hour_round, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l Q30time_hour_round,
lcolor(black) lwidth(thick) legend(on)) (line `marker' Q30time_hour_round, lcolor(black) lpattern(dash)), /*
*/ xlabel(9 10 11 12 13 14 15 16 17, labsize(med)) graphregion(color(white)) ylabel(, angle(horizontal) labsize(large)) title(`marker',
size(vlarge)) subtitle(Not adjusted) ytitle(mean, size(large)) xtitle(Hour of the day, size(large)) legend(row(3)) legend(off)
graph save `marker'_line_diabetics_hour_of_day, replace

}



foreach marker in  Q30chol_adj  Q30hdlc_adj  Q30hba1c_adj Q30gluc_adj q30insulin_adj_adj  {


label var Q30time_hour_round "Hour of examination"
twoway (scatter `marker' Q30time_hour_round, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l Q30time_hour_round,
lcolor(black) lwidth(thick) legend(on)) (line `marker' Q30time_hour_round, lcolor(black) lpattern(dash)), /*
*/ xlabel(9 10 11 12 13 14 15 16 17, labsize(med) ) graphregion(color(white)) ylabel(, angle(horizontal) labsize(large)) title(`marker',
size(vlarge)) subtitle(Adjusted) ytitle(mean, size(large)) xtitle(Hour of the day, size(large)) legend(row(3)) legend(off)
graph save `marker'_line_diabetics_hour_of_day, replace

}



graph combine  Q30chol_line_diabetics_hour_of_day.gph Q30chol_adj_line_diabetics_hour_of_day.gph, row(1) ysize(1) xsize(2) title(Diabetics)
ycommon
graph export   Q30chol_original_vs_adj_hour_of_day.png, replace

graph combine  Q30hdlc_line_diabetics_hour_of_day.gph Q30hdlc_adj_line_diabetics_hour_of_day.gph, row(1) ysize(1) xsize(2) title(Diabetics)
ycommon
graph export   Q30hdlc_original_vs_adj_hour_of_day_diabetics.png, replace

graph combine  q30insulin_adj_line_diabetics_hour_of_day.gph  q30insulin_adj_adj_line_diabetics_hour_of_day.gph, row(1) ysize(1) xsize(2)
title(Diabetics) ycommon
graph export   Q30insulin_original_vs_adj_hour_of_day.png, replace

graph combine  Q30gluc_line_diabetics_hour_of_day.gph  Q30gluc_adj_line_diabetics_hour_of_day.gph, row(1) ysize(1) xsize(2) title(Diabetics)
ycommon
graph export   Q30gluc_original_vs_adj_hour_of_day.png, replace

graph combine  Q30hba1c_line_diabetics_hour_of_day.gph  Q30hba1c_adj_line_diabetics_hour_of_day.gph, row(1) ysize(1) xsize(2) title(Diabetics)
ycommon
graph export   Q30hba1c_original_vs_adj_hour_of_day.png, replace


restore
```

```
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************
****
****        DIABETICS  PLOT MEAN BY FASTING TIME
****
****************************************************************************
****************************************************************************
****************************************************************************
****************************************************************************



keep if diabetes_q30_ds==1

***** NB important recode fasting time >18

replace round_fasting_trunc=14 if round_fasting_trunc>14 & round_fasting_trunc!=.
replace round_fasting_trunc=9 if round_fasting_trunc==10
replace round_fasting_trunc=12 if round_fasting_trunc==11 | round_fasting_trunc==13


tab round_fasting_trunc

collapse (mean)    Q30hdlc Q30chol Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */              Q30hdlc_adj Q30chol_adj  Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj /*

   */    (semean)  se_Q30hdlc=Q30hdlc se_Q30chol=Q30chol  /*
   */    se_Q30hba1c_log=Q30hba1c_log se_Q30gluc_log=Q30gluc_log se_q30insulin_log_adj=q30insulin_log_adj  /*

   */    (semean)  se_Q30hdlc_adj=Q30hdlc_adj se_Q30chol_adj=Q30chol_adj  /*
   */    se_Q30hba1c_log_adj=Q30hba1c_log_adj se_Q30gluc_log_adj=Q30gluc_log_adj se_q30insulin_log_adj_adj=q30insulin_log_adj_adj ,
by(round_fasting_trunc)


foreach name in Q30hdlc Q30chol Q30hba1c_log Q30gluc_log q30insulin_log_adj /*
   */              Q30hdlc_adj Q30chol_adj Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj  {

gen `name'_u = `name' + 1.96*se_`name'
gen `name'_l = `name' - 1.96*se_`name'

}
```

```
label var round_fasting_trunc "Fasting time"



cd "S:\Pop_Health\BRHS_Winter_Deaths\Q30 master file\adj fasting sensitivity analysis\graphs"


foreach name in         Q30hba1c_log     Q30gluc_log     q30insulin_log_adj /*
   */                   Q30hba1c_log_adj Q30gluc_log_adj q30insulin_log_adj_adj  {

replace `name'=exp(`name')
replace `name'_u =exp(`name'_u)
replace `name'_l =exp(`name'_l)

}

rensfix _log
rensfix _log_adj _adj
rensfix _log_adj_adj _adj_adj
rensfix _log_u _u
rensfix _log_l _l
rensfix _log_adj_u _adj_u
rensfix _log_adj_l _adj_l
rensfix _log_adj_adj_u _adj_adj_u
rensfix _log_adj_adj_l _adj_adj_l


* 11 12 13 14 15 16 17 18 19 20

foreach marker in Q30chol Q30hdlc Q30hba1c Q30gluc q30insulin_adj {


label var round_fasting_trunc "Hour of examination"
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
twoway (scatter `marker' round_fasting_trunc, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l round_fasting_trunc,
lcolor(black) lwidth(thick) legend(on)) (line `marker' round_fasting_trunc, lcolor(black) lpattern(dash)), /*
*/ xlabel(1 2 3 4 5 6 7 8 9 10 11 12 13 14 , labsize(med)) graphregion(color(white)) ylabel(, angle(horizontal) labsize(large))
title(`marker', size(vlarge)) subtitle(Not adjusted) ytitle(mean, size(large)) xtitle(Fasting time, size(large)) legend(row(3)) legend(off)
graph save `marker'_line_diabetics_fasting, replace
* graph export `marker'_line_diabetics_fasting.png, replace

}



foreach marker in  /*
   */              Q30chol_adj Q30hdlc_adj  Q30hba1c_adj Q30gluc_adj q30insulin_adj_adj  {


label var round_fasting_trunc "Hour of examination"
```

```
* twoway line `marker' w_month, xlabel(1 2 3 4 5 6 7 8 9 10 11 12) lwidth(thick) graphregion(color(white)) ylabel(, angle(horizontal))
title(`marker')
twoway (scatter `marker' round_fasting_trunc, msymbol(S) msize(small) legend(off)) (rcap `marker'_u `marker'_l round_fasting_trunc,
lcolor(black) lwidth(thick) legend(on)) (line `marker' round_fasting_trunc, lcolor(black) lpattern(dash)), /*
*/ xlabel(1 2 3 4 5 6 7 8 9 10 11 12 13 14 , labsize(med) ) graphregion(color(white)) ylabel(, angle(horizontal) labsize(large))
title(`marker', size(vlarge)) subtitle(Adjusted) ytitle(mean, size(large)) xtitle(Fasting time, size(large)) legend(row(3)) legend(off)
graph save `marker'_line_diabetics_fasting, replace
* graph export `marker'_line_diabetics_fasting_adj.png, replace

}






graph combine  Q30chol_line_diabetics_fasting.gph Q30chol_adj_line_diabetics_fasting.gph, row(1) ysize(1) xsize(2) title(Diabetics) ycommon
graph export   Q30chol_original_vs_adj_fasting.png, replace

graph combine  Q30hdlc_line_diabetics_fasting.gph Q30hdlc_adj_line_diabetics_fasting.gph, row(1) ysize(1) xsize(2) title(Diabetics) ycommon
graph export   Q30hdlc_original_vs_adj_fasting.png, replace

graph combine  q30insulin_adj_line_diabetics_fasting.gph  q30insulin_adj_adj_line_diabetics_fasting.gph, row(1) ysize(1) xsize(2)
title(Diabetics) ycommon
graph export   Q30insulin_original_vs_adj_fasting.png, replace

graph combine  Q30gluc_line_diabetics_fasting.gph  Q30gluc_adj_line_diabetics_fasting.gph, row(1) ysize(1) xsize(2) title(Diabetics) ycommon
graph export   Q30gluc_original_vs_adj_fasting.png, replace

graph combine  Q30hba1c_line_diabetics_fasting.gph  Q30hba1c_adj_line_diabetics_fasting.gph, row(1) ysize(1) xsize(2) title(Diabetics) ycommon
graph export   Q30hba1c_original_vs_adj_fasting.png, replace




*/
```