

Tables and Corresponding datasets for Teckman et al., “Baseline Analysis of a Young Alpha-1-AT Deficiency Liver Disease Cohort Reveals Frequent Portal Hypertension”, J Pediatr Gastroenterol Nutr. 2015 July ; 61(1): 94–101.

Table 1: For Native Liver Cohort vs. Post-Transplant Cohort, use categorical variable pretx

Table 2: For Mild versus Severe liver disease, use categorical variable liver_disease

Table 3: For No PHT versus PHT, use categorical variable pht

Table 4: Compare pht_us to pht

Figure 1: Use variable ihx2b02_age, by categorical variable liver_disease

Figure 2: Use variables myctxsbjid, pht, ggtp, and ast (sorted by variable pht) for a boxplot in R

Data Structure:

One observation per participant. Data are derived from two studies: LOGIC and PROBE. Thus, CRFs for both studies are provided. The column “Source Form” indicates which study (CRFs) were the source for the indicated variables. The variables are from the LOGIC study, unless denoted by dataP003. prefix which indicates that the variables are from the PROBE study.

Variable Name	Description	Source Form	Derivation	Range (continuous)/Response Options (categorical)
myctxsbjid	De-Identified Subject ID.			1 to 733
Group	Eligibility group	ELG1, ELG2, ELG3	1=all subjects in ELG1 dataset, 2=all subjects in ELG2 dataset, 3=all subjects in ELG3dataset,	1, 2, 3
Age	Age	ELG1, ELG2, ELG3	Derived from consent date – DOB : ELG1 (elg1b07dt - elg1b01dt), ELG2 (elg2b07dt - elg2b01dt), ELG3 (elg3b07dt - elg3b01dt)	0.0-24.9
ihx2b01_age	Age – 1 st symptoms noticed	ihx2, ELG1, ELG2, ELG3	Derived from myihx2b01dt – dob: ihx2 (myihx2b01dt), ELG1 (elg1b01dt), ELG2 (elg2b01dt), ELG3 (elg3b01dt)	0.0-20.2

Variable Name	Description	Source Form	Derivation	Range (continuous)/Response Options (categorical)
ihx2b02_age	Age – Liver disease diagnosed	ihx2, ELG1, ELG2, ELG3	Derived from myihx2b02dt – dob: ihx2 (myihx2b02dt), ELG1 (elg1b01dt), ELG2 (elg2b01dt), ELG3 (elg3b01dt)	0.0-20.2
dmgab02	Gender	dataP003.dma, dmg2, dmg3	Derived from: dataP003.dma (dmab02mf), DMG2A/DMG3A (dmg3ab02),	1=Male, 2=Female
dmgab03	Ethnicity	dataP003.dma, dmg2a, dmg3a	Derived from: dataP003.dma (dmab03hl), DMG2A/DMG3A (dmg2ab03) Modifications: For dataP003.dma if dmab03hl= '1' then dmgab03 = '2'; if dmab03hl = '2' then dmgab03 = '1'; if dmab03hl = '3' then dmgab03 = '66'; if dmab03hl = '9' then dmgab03 = '9'; Overall: dmgab03 in ('55','77') then dmgab03 = '66';	1 = Hispanic, 2 = Non-hispanic, 66 = Not reported
Racecat	Race Categories	dataP003.dma, dmg2a, dmg3a	Modifications: For dataP003.dma if ^missing(dmab04ai) then dmgab04a = '1'; if ^missing(dmab04ba) then dmgab04b = '1'; if ^missing(dmab04cb) then dmgab04c = '1'; if ^missing(dmab04dh) then dmgab04d = '1'; if ^missing(dmab04ew) then dmgab04e = '1'; if ^missing(dmab04gd) then dmgab04f = '66'; if ^missing(dmab04hr) then dmgab04g = '9'; For DMG2A/DMG2B dmgab04a = dmg3ab04a; dmgab04b = dmg3ab04b;	A = Native American B = Asian C = Black or African-American D = Native Hawaiian or PI E = Caucasian F = Unknown G = Refused H = Multiracial

Variable Name	Description	Source Form	Derivation	Range (continuous)/Response Options (categorical)
			dmgab04c = dmg3ab04c; dmgab04d = dmg3ab04d; dmgab04e = dmg3ab04e; dmgab04f = dmg3ab04f; dmgab04g = dmg3ab04g; Overall: If there are multiple flags for the categories below racecat='H' if compress(dmgab04a) = '1' then racecat = 'A'; if compress(dmgab04b) = '1' then racecat = 'B'; if compress(dmgab04c) = '1' then racecat = 'C'; if compress(dmgab04d) = '1' then racecat = 'D'; if compress(dmgab04e) = '1' then racecat = 'E'; if compress(dmgab04f) = '66' then racecat = 'F'; if compress(dmgab04g) = '9' then racecat = 'G';	
ZZ	ZZ Genotype/ phenotype	ELG1, ELG2, ELG3	Modifications: elge2bi = elg2e2bi; elge2biii = elg3e2biii; if elge2bi=1 or elge2biii=1 then zz=1; else zz=0;	1 = Yes 2 = No
SZ	SZ Genotype/ phenotype	ELG1, ELG2, ELG3	Modifications: elge2bii = elg2e2bii; elge2biv = elg3e2biv; if elge2bii=1 or elge2biv=1 then sz=1; else sz=0;	1 = Yes 2 = No
AST	AST (u/l)	dataP003.ilb0, lab2b	lab2b (1.0*lab2b015ul), dataP003.ilb0(max(1.0*ilba06ul, 1.0*ilbb06ul)) Modifications for incorrect values if compress(ilba06ul) = "1.61" then ilba06ul = "161";	3.6-893

Variable Name	Description	Source Form	Derivation	Range (continuous)/Response Options (categorical)
			if compress(lab2b015ul) = '6.5' then lab2b015ul = '65'; if compress(lab2b015ul) = '11.1' then lab2b016ul = '111'; if compress(lab2b015ul) = '1.56' then lab2b015ul = '156'; if compress(lab2b015ul) = '11111' then lab2b015ul = '1111';	
ALT	ALT (u/l)	dataP003.ilb0, lab2b	lab2b (1.0*lab2b016ul), dataP003.ilb0 (max(1.0*ilba07ul, 1.0*ilbb07ul)) Modifications for incorrect values if compress(ilbb07ul) = "<3" then ilbb07ul = "3"; if compress(ilbb07ul) = "LL" then ilbb07ul = "3"; if compress(lab2b016ul) = '2.5' then lab2b016ul = '25'; if compress(lab2b016ul) = '<3' then lab2b016ul = '3'; if compress(lab2b016ul) = '<6' then lab2b016ul = '6';	3.0-1054
INR	INR	dataP003.ilb1, lab2b	dataP003.ilb1(max(1.0*ilbb14in, 1.0*ilba14in)), lab2b (1.0*lab2b022inr) Modifications for incorrect values if compress(ilbb14in) = "13.1" then ilbb14in = "1.31"; if compress(ilbb14in) = "13.4" then ilbb14in = "1.34"; if compress(lab2b022inr) = '9' then lab2b022inr = '!';	0.8-130

			if compress(lab2b022inr) = '90' then lab2b022inr = '!';	
GGTP	GGTP (u/l)	dataP003.ilb1, lab2b	lab2b (1.0*lab2b110ul), dataP003.ilb1 (max(1.0*ilbb11ul, 1.0*ilba11ul) Modification for incorrect values if compress(ilbb11ul) = "9.2" then ilbb11ul = "92"; if compress(lab2b110ul) = '26.6' then lab2b110ul = '266'; if compress(lab2b110ul) = '<10' then lab2b110ul = '10'; if compress(lab2b110ul) = '96.3' then lab2b110ul = '963';	6.0-5095
ast_alt_ratio	Ratio of ALT/AST	Uses variables ALT AND AST that are defined above	ast_alt_ratio = ast / alt	0.42-6.08
pht	Portal hypertension	IHX2, dataP003.pex, phy2, dataP003.iig1, img, ith2a, dataP003.srg, dataP003.dme, ihx2, ith2b, lab2b, dataP003.ilb3	If pht3 greater than zero than pht=1, else pht=0; Modifications: if (any_ascites = 0 and any_bleeds = 0 and low_platelets = 1 and big_spleen = 0) or (any_ascites = 0 and any_bleeds = 0 and low_platelets = 0 and big_spleen = 1) then pht3 = 0.5; if any_ascites = 1 or any_bleeds = 1 or any_hps = 1 or spleen_and_platelets = 1 or srgb05dph = '1' then pht3 = 1; phy2b093 = PEXB141A; if ^missing(iiggviii) then imgb16c = '1'; Variables coded from raw data:	0= No PHT 1=PHT

			<p>if ihx2b016 = '1' or ihx2b026 = '1' or ihx2b032 = '1' or phy2b093 = '2' or phy2b094 = '1' or imgb16c = '1' or imgb37c = '1' or ith2ab01 = '1' or srgb03as = '2' or cmed02 = '1' or ^missing(cmed021) or ^missing(cmed021mg) or ^missing(cmed022) or ^missing(cmed022mg) or ^missing(cmed023ot) or ^missing(cmed023mg) then any_ascites = 1;</p> <p>if ihx2b017 = '1' or ihx2b027 = '1' or ihx2b034 = '1' or ith2bb08gb = '1' or srgb05din = '2' then any_bleeds = 1;</p> <p>if (^missing(pl) and pl < 150) or (^missing(pl_ith) and pl_ith < 150) then low_platelets = 1;</p> <p>if (^missing(nspleen) and nspleen > 2) then big_spleen = 1;</p> <p>if ith2bb10hs = '1' then any_hps = 1;</p> <p>if low_platelets = 1 and big_spleen = 1 then spleen_and_platelets = 1;</p>	
pht_us	Portal hypertension Ultrasound Finding	IHX2, dataP003.pex, phy2, dataP003.iig1, img, ith2a, dataP003.srg, dataP003.dme, ihx2, ith2b, lab2b, dataP003.ilb3	<p>If pht3_us greater than zero than pht_us =1, else pht_us =0;</p> <p>Modifications:</p> <p>if (any_ascites = 0 and any_bleeds = 0 and low_platelets = 1 and big_spleen_us = 0) or (any_ascites = 0 and any_bleeds = 0 and low_platelets = 0 and big_spleen_us = 1) then pht3_us = 0.5;</p>	0= No PHT 1=PHT

		<p>if any_ascites = 1 or any_bleeds = 1 or any_hps = 1 or spleen_and_platelets_us = 1 or srgb05dph = '1' then pht3_us = 1;</p> <p>phy2b093 = PEXB141A;</p> <p>if ^missing(iiggviii) then imgb16c = '1';</p> <p>Variables coded from raw data:</p> <p>if ihx2b016 = '1' or ihx2b026 = '1' or ihx2b032 = '1' or phy2b093 = '2' or phy2b094 = '1' or imgb16c = '1' or imgb37c = '1' or ith2ab01 = '1' or srgb03as = '2' or cmed02 = '1' or ^missing(cmed021) or ^missing(cmed021mg) or ^missing(cmed022) or ^missing(cmed022mg) or ^missing(cmed023ot) or ^missing(cmed023mg) then any_ascites = 1;</p> <p>if ihx2b017 = '1' or ihx2b027 = '1' or ihx2b034 = '1' or ith2bb08gb = '1' or srgb05din = '2' then any_bleeds = 1;</p> <p>if (^missing(pl) and pl < 150) or (^missing(pl_ith) and pl_ith < 150) then low_platelets = 1;</p> <p>if (^missing(nspleenus) and nspleenus > 7) or ^missing(imgb13a) then big_spleen_us = 1;</p> <p>if ith2bb10hs = '1' then any_hps = 1;</p> <p>if low_platelets = 1 and big_spleen_us = 1 then spleen_and_platelets_us = 1;</p>		
liver_disease	Liver disease severity: Mild vs. Severe		<p>Defaults to liver_disease=1, but liver_disease=0 if (group in (1,2) and pht = 1) or group = 3</p>	<p>0=Severe liver disease, 1=Mild liver disease</p>

pretx	Liver transplant		Defaults to pretx=1, unless group=3 then pretx=0	0=Post Transplant, 1=Native Liver
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