

Supplemental Table S2: Interactions between testosterone replacement therapy (TRT), body mass index (BMI), and day 42 hemolysis in 18 blood donors from Vitalant’s cohort.

Hemolysis ~ BMI + TRT + BMI*TRT				
	β TRT	p value TRT	β interaction	p value interaction
Storage hemolysis	-0.51	0.37	0.02	0.30
Osmotic hemolysis	-7.56	0.84	-0.06	0.96
Oxidative hemolysis	8.51	0.81	-0.36	0.77

Supplemental Table S3: RBC posttransfusion recovery (percentage and standard deviation, SD) stratified by blood donor body mass index (BMI). Human leukocyte-reduced RBCs from 14 blood donors were stored for 42 days and later transfused into NSG mice as described under Supplemental Methods.

BMI (kg/m²)	<25			25-29.9			≥30		
Time after transfusion	Mean (%)	SD	n	Mean (%)	SD	n	Mean (%)	SD	n
10 min	44.8	10.5	3	47.2	11.5	6	34.7	7.3	5
2-h	29.5	10.6	3	30.5	8.2	6	22.0	5.2	5
4-h	35.0	11.9	3	25.1	8.7	6	24.1	7.8	5
8-h	22.1	7.0	3	18.1	5.4	6	15.3	4.9	5
24-h	7.3	7.6	3	4.4	4.1	6	3.8	2.9	5

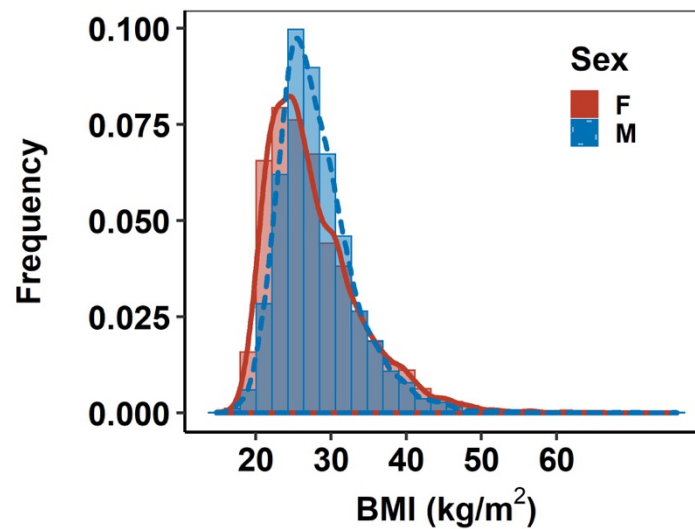
Supplemental Table S4 for Figure 2: Linear regression analysis of blood donor body mass index (BMI) with each of the three day-42 hemolysis measures and ferritin. Data derived from 13,317 blood donors who participated in the National Heart, Lung, and Blood Institute Red Blood Cell Omics (RBC-Omics) study between 2013-2015. Parameter estimates represent the change in each variable per each BMI unit in male and female donors. p values obtained by multivariable linear regression.

Measure	Males		Females		
	Parameter estimate	P	Parameter estimate	P	
All donors	Storage hemolysis	0.0026	<0.001	0.00095	0.13
	Osmotic hemolysis	0.27	<0.001	0.25	<0.001
	Oxidative hemolysis	0.36	<0.001	0.30	<0.001
	Ferritin	1.43	<0.001	0.60	<0.001
First-time donors	Oxidative hemolysis	0.34	<0.001	0.26	<0.001
	Ferritin	3.67	<0.001	1.17	<0.001

Supplemental Table S5 for Figure 3: Demographic and hemolysis data for the 15 blood donors with low and high BMI groups ($20.5 \pm 1.0 \text{ kg/m}^2$ defined as low BMI versus $44.1 \pm 5.1 \text{ kg/m}^2$ defined as high BMI). p-values were calculated for continuous variables using rank test.

	BMI low group	BMI high group	p-value
Sex (Males/Females)	6/9	8/7	
Age (Mean\pmSD)	50.7 \pm 15.2	52.2 \pm 14.4	0.42
Race (White/African American/Asian/Hispanic)	12/0/2/1	8/3/2/2	
Storage hemolysis (Mean\pmSD)	0.40 \pm 0.61	0.42 \pm 0.31	0.13
Osmotic hemolysis (Mean\pmSD)	27.6 \pm 14.5	34.4 \pm 12.5	0.22
Oxidative hemolysis (Mean\pmSD)	18.2 \pm 9.3	37.1 \pm 9.7	<0.001
Ferritin hemolysis (Mean\pmSD)	18.9 \pm 10.2	92.5 \pm 103.5	<0.001

Supplemental Figure S1 for Figure 2: Distribution of blood donor body mass index (BMI) by sex in the RBC-Omics cohort.



SUPPLEMENTAL METHODS:

Hemolysis assays:

Hemolysis was determined on a weekly basis in Vitalant's cohort and on day 39-42 in RBC-Omics. In each testing day, two aliquots (1mL each) were collected from each bag. One aliquot was used for spontaneous storage hemolysis and the other for the stress hemolysis assays. Hemoglobin levels were determined using the Drabkin's method.¹ Spontaneous storage hemolysis was determined by $\frac{(100-HCT) \times Hb_{supernatant}}{Hb_{total}}$. HCT is the sample hematocrit, $Hb_{supernatant}$ corresponds to the levels of free hemoglobin obtained after centrifugation (1500G, 10 minutes, 18°C) measured in the supernatant, and Hb_{total} refers to the total amount of sample hemoglobin before centrifugation. The other aliquot was washed three times with phosphate-buffered saline and packed RBCs were subjected to osmotic and oxidative hemolysis as described before.^{2,3} In brief, osmotic stress was induced by incubating RBCs in pink test buffer (a hypotonic solution containing 70mM Bis-Tris, 25mM sodium chloride, and 135mM glycerol; pH 6.6) at room temperature for four hours and hemolysis was calculated using $\frac{Hb_{osmotic}}{Hb_{total}} \times 100$, where $Hb_{osmotic}$ equals the level of free hemoglobin in the supernatant after centrifugation (1500G, 10 minutes, 18°C) and Hb_{total} is the total level of hemoglobin in the sample. Oxidative hemolysis was determined by incubating a suspension of washed RBCs with 150mM AAPH at 37°C for three hours. Percent hemolysis was calculated using $\frac{Hb_{AAPH} - Hb_{control}}{Hb_{total}} \times 100$, where Hb_{AAPH} corresponds to the free hemoglobin in treated samples after centrifugation (1500G, 10 minutes, 18°C), $Hb_{control}$ refers to the free hemoglobin in untreated samples, and Hb_{total} corresponds to the total amount of hemoglobin in each sample.

Quantification of RBC posttransfusion recovery in NSG mice:

Male and female (5-12 weeks old) immunodeficient NOD.Cg-*Prkdc*^{scid} *Il2rg*^{tm1Wjl}/SzJ (NSG) mice⁴ (The Jackson Laboratory) were bred, housed and maintained in a specific pathogen free vivarium under barrier conditions at Vitalant Research Institute (San Francisco, CA). These mice have been used for engraftment of human hematopoietic tissues as they lack murine lymphoid cells.⁴ The data reported in this study were from 14 blood donors (Vitalant cohort), for whom we quantified RBC posttransfusion recovery over time after infusion into 8-10 NSG mice per donor sample. In all cases, LR-RBCs stored for 39-42 days were acclimated to room temperature for a minimum of 30 minutes and each sample hematocrit was adjusted to 60±6% with sterile PBS prior to transfusion. NSG mice were gently warmed under heat lamps prior to intravenous lateral tail vein injection of 200 µL of human RBCs. Blood was collected from mice pre-injection and at 10 minutes, 2, 4, 8, and 24 hours post infusion by tail tip excision and collection into Sarstedt Minivette tubes coated with anticoagulant ethylenediaminetetraacetic acid. A 5 µL aliquot of this collection was promptly aliquoted and resuspended in sterile filtered PBS with 5% mouse serum, 0.01% sodium azide and 14% citrate phosphate dextrose adenine-1 solution for staining and flow cytometry. Quantification of RBC posttransfusion recovery was determined by

flow cytometric analysis using the human-specific marker for erythrocyte membrane glycoprotein A (CD235a-phycoerythrin; Biolegend, HI264).

RBC posttransfusion recovery was determined by staining murine whole blood samples with a human-specific marker for erythrocyte membrane glycoprotein A (CD235A-phycoerythrin; Biolegend, HI264). Samples were incubated for 30 minutes at 4°C, washed in PBS, resuspended in a 1:500 dilution of propidium iodide and run on a BD FACS LSR II (BD Biosciences) with acquisition by BD FACSDiva software. Analysis of cytometry data was performed on FlowJo software version 10 (FlowJo, LLC). Data normalization was generated according to the National Centre for the Replacement, Refinement and Reduction of Animals in Research (NC3Rs).⁵ Baseline mouse total blood volume was estimated by multiplying mouse weight by the practical blood sample volume value of 58.5 mL/kg. Total mouse recipient RBCs prior to transfusion was estimated by multiplying the estimated total blood volume by the mouse pre-transfusion RBC count. The estimated expected total recovery of human RBCs from mouse recipients after transfusion was calculated by dividing the total number of human RBCs used for transfusion by the estimated total mouse recipient RBCs. This was set as the maximum human RBC recovery value and the flow cytometry readings of human RBC recovery at the subsequent timepoints was a fraction thereof. Analysis and plots were generated on Prism version 7 (GraphPad Software, San Diego, CA) using matched two-way analysis of variance (ANOVA) followed by Tukey's multiple comparison post-test to compare each group to every other group. Additional information is referenced below.⁶

REFERENCES:

1. Zwart A, van Assendelft OW, Bull BS, England JM, Lewis SM, Zijlstra WG. Recommendations for reference method for haemoglobinometry in human blood (ICSH standard 1995) and specifications for international haemoglobinocyanide standard (4th edition). *J Clin Pathol* 1996;**49**: 271-4.
2. Kanas T, Lanteri MC, Page GP, Guo Y, Endres SM, Stone M, Keating S, Mast AE, Cable RG, Triulzi DJ, Kiss JE, Murphy EL, Kleinman S, Busch MP, Gladwin MT. Ethnicity, sex, and age are determinants of red blood cell storage and stress hemolysis: results of the REDS-III RBC-Omics study. *Blood Adv* 2017;**1**: 1132-41.
3. Kanas T, Sinchar D, Osei-Hwedieh D, Baust JJ, Jordan A, Zimring JC, Waterman HR, de Wolski KS, Acker JP, Gladwin MT. Testosterone-dependent sex differences in red blood cell hemolysis in storage, stress, and disease. *Transfusion* 2016;**56**: 2571-83.
4. Shultz LD, Ishikawa F, Greiner DL. Humanized mice in translational biomedical research. *Nat Rev Immunol* 2007;**7**: 118-30.
5. *The NC3Rs: Pioneering better science [monograph on the internet]*. National Centre for the Replacement, Refinement and Reduction of Animals in Research 2020. Available from: ; <https://www.nc3rs.org.uk>
6. Blessinger SA, Tran JQ, Jackman RP, Gilfanova R, Rittenhouse J, Gutierrez AG, Heitman JW, Hazegh K, Kanas T, Muench MO. Immunodeficient mice are better for modeling the transfusion of human blood components than wild-type mice. *PLoS One* 2020;**15**: e0237106.