

Metabolic pathways that correlate with post-transfusion circulation of stored murine red blood cells

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Supplemental Table 1

Tukey's multiple comp	Fresh RBC recovery				Stored RBC recovery			
	Mean Diff.	95% CI of diff.	Result	Adj P Value	Mean Diff.	95% CI of diff.	Result	Adj P Value
C57Bl/6J vs. FVB/NJ	-0.05167	-0.7702 to 0.6668	ns	> 0.9999	0.6696	0.1391 to 1.200	**	0.0053
C57Bl/6J vs. Balb/cByJ	-0.01967	-0.7382 to 0.6988	ns	> 0.9999	0.05882	-0.4716 to 0.5892	ns	> 0.9999
C57Bl/6J vs. BTBR T+Ipr3tf/J	-0.07567	-0.7942 to 0.6428	ns	> 0.9999	0.01742	-0.5130 to 0.5478	ns	> 0.9999
C57Bl/6J vs. 129S1/SvmJ	0.01733	-0.7012 to 0.7358	ns	> 0.9999	0.2859	-0.2446 to 0.8163	ns	0.7483
C57Bl/6J vs. 129X1/SvJ	-0.04333	-0.7618 to 0.6752	ns	> 0.9999	0.2967	-0.2338 to 0.8271	ns	0.7045
C57Bl/6J vs. A/J	-0.024	-0.7425 to 0.6945	ns	> 0.9999	0.2176	-0.3128 to 0.7480	ns	0.9457
C57Bl/6J vs. AKR/J	0.05933	-0.6592 to 0.7778	ns	> 0.9999	0.7143	0.1839 to 1.245	**	0.0025
C57Bl/6J vs. C3H/HeJ	-0.03717	-0.8405 to 0.7661	ns	> 0.9999	0.5136	-0.01678 to 1.044	ns	0.0643
C57Bl/6J vs. DBA/2j	0.03867	-0.6798 to 0.7572	ns	> 0.9999	0.4519	-0.07854 to 0.9823	ns	0.1525
C57Bl/6J vs. NOD/ShiLtJ	0.03	-0.6885 to 0.7485	ns	> 0.9999	0.3601	-0.1704 to 0.8905	ns	0.4332
C57Bl/6J vs. KK/HIJ	0.3937	-0.3248 to 1.112	ns	0.7247	1.281	0.7502 to 1.811	****	< 0.0001
C57Bl/6J vs. LG/J	0.1167	-0.6018 to 0.8352	ns	> 0.9999	0.9553	0.4249 to 1.486	****	< 0.0001
FVB/NJ vs. Balb/cByJ	0.032	-0.6865 to 0.7505	ns	> 0.9999	-0.6107	-1.141 to -0.08032	*	0.014
FVB/NJ vs. BTBR T+Ipr3tf/J	-0.024	-0.7425 to 0.6945	ns	> 0.9999	-0.6521	-1.183 to -0.1217	**	0.0071
FVB/NJ vs. 129S1/SvmJ	0.069	-0.6495 to 0.7875	ns	> 0.9999	-0.3837	-0.9141 to 0.1467	ns	0.3426
FVB/NJ vs. 129X1/SvJ	0.008333	-0.7102 to 0.7268	ns	> 0.9999	-0.3729	-0.9033 to 0.1575	ns	0.3826
FVB/NJ vs. A/J	0.02767	-0.6908 to 0.7462	ns	> 0.9999	-0.452	-0.9824 to 0.07844	ns	0.1524
FVB/NJ vs. AKR/J	0.111	-0.6075 to 0.8295	ns	> 0.9999	0.04473	-0.4857 to 0.5752	ns	> 0.9999
FVB/NJ vs. C3H/HeJ	0.0145	-0.7888 to 0.8178	ns	> 0.9999	-0.1559	-0.6863 to 0.3745	ns	0.996
FVB/NJ vs. DBA/2j	0.09033	-0.6282 to 0.8088	ns	> 0.9999	-0.2177	-0.7481 to 0.3127	ns	0.9455
FVB/NJ vs. NOD/ShiLtJ	0.08167	-0.6368 to 0.8002	ns	> 0.9999	-0.3095	-0.8399 to 0.2209	ns	0.65
FVB/NJ vs. KK/HIJ	0.4453	-0.2732 to 1.164	ns	0.5613	0.6111	0.08067 to 1.142	*	0.014
FVB/NJ vs. LG/J	0.1683	-0.5502 to 0.8868	ns	0.9995	0.2858	-0.2447 to 0.8162	ns	0.7487
Balb/cByJ vs. BTBR T+Ipr3tf/J	-0.056	-0.7745 to 0.6625	ns	> 0.9999	-0.04139	-0.5718 to 0.4890	ns	> 0.9999
Balb/cByJ vs. 129S1/SvmJ	0.037	-0.6815 to 0.7555	ns	> 0.9999	0.227	-0.3034 to 0.7575	ns	0.9282
Balb/cByJ vs. 129X1/SvJ	-0.02367	-0.7422 to 0.6948	ns	> 0.9999	0.2378	-0.2926 to 0.7683	ns	0.9043
Balb/cByJ vs. A/J	-0.004333	-0.7228 to 0.7142	ns	> 0.9999	0.1588	-0.3717 to 0.6892	ns	0.9953
Balb/cByJ vs. AKR/J	0.079	-0.6395 to 0.7975	ns	> 0.9999	0.6555	0.1250 to 1.186	**	0.0067
Balb/cByJ vs. C3H/HeJ	-0.0175	-0.8208 to 0.7858	ns	> 0.9999	0.4548	-0.07560 to 0.9853	ns	0.1468
Balb/cByJ vs. DBA/2j	0.05833	-0.6602 to 0.7768	ns	> 0.9999	0.3931	-0.1374 to 0.9235	ns	0.31
Balb/cByJ vs. NOD/ShiLtJ	0.04967	-0.6688 to 0.7682	ns	> 0.9999	0.3012	-0.2292 to 0.8317	ns	0.6853
Balb/cByJ vs. KK/HIJ	0.4133	-0.3052 to 1.132	ns	0.6639	1.222	0.6914 to 1.752	****	< 0.0001
Balb/cByJ vs. LG/J	0.1363	-0.5822 to 0.8548	ns	> 0.9999	0.8965	0.3661 to 1.427	***	0.0001
BTBR T+Ipr3tf/J vs. 129S1/SvmJ	0.093	-0.6255 to 0.8115	ns	> 0.9999	0.2684	-0.2620 to 0.7989	ns	0.8134
BTBR T+Ipr3tf/J vs. 129X1/SvJ	0.03233	-0.6862 to 0.7508	ns	> 0.9999	0.2792	-0.2512 to 0.8097	ns	0.774
BTBR T+Ipr3tf/J vs. A/J	0.05167	-0.6668 to 0.7702	ns	> 0.9999	0.2002	-0.3303 to 0.7306	ns	0.9697
BTBR T+Ipr3tf/J vs. AKR/J	0.135	-0.5835 to 0.8535	ns	> 0.9999	0.6969	0.1664 to 1.227	**	0.0033
BTBR T+Ipr3tf/J vs. C3H/HeJ	0.0385	-0.7648 to 0.8418	ns	> 0.9999	0.4962	-0.03420 to 1.027	ns	0.0829
BTBR T+Ipr3tf/J vs. DBA/2j	0.1143	-0.6042 to 0.8328	ns	> 0.9999	0.4345	-0.09596 to 0.9649	ns	0.1907
BTBR T+Ipr3tf/J vs. NOD/ShiLtJ	0.1057	-0.6128 to 0.8242	ns	> 0.9999	0.3426	-0.1878 to 0.8731	ns	0.506
BTBR T+Ipr3tf/J vs. KK/HIJ	0.4693	-0.2492 to 1.188	ns	0.4852	1.263	0.7328 to 1.794	****	< 0.0001
BTBR T+Ipr3tf/J vs. LG/J	0.1923	-0.5262 to 0.9108	ns	0.9982	0.9379	0.4075 to 1.468	****	< 0.0001
129S1/SvmJ vs. 129X1/SvJ	-0.06067	-0.7792 to 0.6578	ns	> 0.9999	0.01079	-0.5196 to 0.5412	ns	> 0.9999
129S1/SvmJ vs. A/J	-0.04133	-0.7598 to 0.6772	ns	> 0.9999	-0.06828	-0.5987 to 0.4621	ns	> 0.9999
129S1/SvmJ vs. AKR/J	0.042	-0.6765 to 0.7605	ns	> 0.9999	0.4284	-0.1020 to 0.9589	ns	0.2056
129S1/SvmJ vs. C3H/HeJ	-0.0545	-0.8578 to 0.7488	ns	> 0.9999	0.2278	-0.3026 to 0.7582	ns	0.9268
129S1/SvmJ vs. DBA/2j	0.02133	-0.6972 to 0.7398	ns	> 0.9999	0.166	-0.3644 to 0.6964	ns	0.9931
129S1/SvmJ vs. NOD/ShiLtJ	0.01267	-0.7058 to 0.7312	ns	> 0.9999	0.0742	-0.4562 to 0.6046	ns	> 0.9999
129S1/SvmJ vs. KK/HIJ	0.3763	-0.3422 to 1.095	ns	0.7751	0.9948	0.4644 to 1.525	****	< 0.0001
129S1/SvmJ vs. LG/J	0.09933	-0.6192 to 0.8178	ns	> 0.9999	0.6695	0.1390 to 1.200	**	0.0053
129X1/SvJ vs. A/J	0.01933	-0.6992 to 0.7378	ns	> 0.9999	-0.07907	-0.6095 to 0.4514	ns	> 0.9999
129X1/SvJ vs. AKR/J	0.1027	-0.6158 to 0.8212	ns	> 0.9999	0.4176	-0.1128 to 0.9481	ns	0.2343
129X1/SvJ vs. C3H/HeJ	0.006167	-0.7971 to 0.8095	ns	> 0.9999	0.217	-0.3134 to 0.7474	ns	0.9467
129X1/SvJ vs. DBA/2j	0.082	-0.6365 to 0.8005	ns	> 0.9999	0.1552	-0.3752 to 0.6857	ns	0.9961
129X1/SvJ vs. NOD/ShiLtJ	0.07333	-0.6452 to 0.7918	ns	> 0.9999	0.06341	-0.4670 to 0.5938	ns	> 0.9999
129X1/SvJ vs. KK/HIJ	0.437	-0.2815 to 1.156	ns	0.5882	0.984	0.4536 to 1.514	****	< 0.0001
129X1/SvJ vs. LG/J	0.16	-0.5585 to 0.8785	ns	0.9997	0.6587	0.1283 to 1.189	**	0.0063
A/J vs. AKR/J	0.08333	-0.6352 to 0.8018	ns	> 0.9999	0.4967	-0.03372 to 1.027	ns	0.0823
A/J vs. C3H/HeJ	-0.01317	-0.8165 to 0.7901	ns	> 0.9999	0.2961	-0.2344 to 0.8265	ns	0.707
A/J vs. DBA/2j	0.06267	-0.6558 to 0.7812	ns	> 0.9999	0.2343	-0.2961 to 0.7647	ns	0.9126
A/J vs. NOD/ShiLtJ	0.054	-0.6645 to 0.7725	ns	> 0.9999	0.1425	-0.3879 to 0.6729	ns	0.9982
A/J vs. KK/HIJ	0.4177	-0.3008 to 1.136	ns	0.6502	1.063	0.5327 to 1.594	****	< 0.0001
A/J vs. LG/J	0.1407	-0.5778 to 0.8592	ns	> 0.9999	0.7378	0.2073 to 1.268	**	0.0016
AKR/J vs. C3H/HeJ	-0.0965	-0.8998 to 0.7068	ns	> 0.9999	-0.2006	-0.7311 to 0.3298	ns	0.9692
AKR/J vs. DBA/2j	-0.02067	-0.7392 to 0.6978	ns	> 0.9999	-0.2624	-0.7928 to 0.2680	ns	0.8339
AKR/J vs. NOD/ShiLtJ	-0.02933	-0.7478 to 0.6892	ns	> 0.9999	-0.3542	-0.8846 to 0.1762	ns	0.4572
AKR/J vs. KK/HIJ	0.3343	-0.3842 to 1.053	ns	0.878	0.5664	0.03595 to 1.097	*	0.0287
AKR/J vs. LG/J	0.05733	-0.6612 to 0.7758	ns	> 0.9999	0.241	-0.2894 to 0.7715	ns	0.8964
C3H/HeJ vs. DBA/2j	0.07583	-0.7275 to 0.8791	ns	> 0.9999	-0.06176	-0.5922 to 0.4687	ns	> 0.9999
C3H/HeJ vs. NOD/ShiLtJ	0.06717	-0.7361 to 0.8705	ns	> 0.9999	-0.1536	-0.6840 to 0.3768	ns	0.9965
C3H/HeJ vs. KK/HIJ	0.4308	-0.3725 to 1.234	ns	0.7493	0.767	0.2366 to 1.297	***	0.001
C3H/HeJ vs. LG/J	0.1538	-0.6495 to 0.9571	ns	> 0.9999	0.4417	-0.08874 to 0.9721	ns	0.1741
DBA/2j vs. NOD/ShiLtJ	-0.008667	-0.7272 to 0.7098	ns	> 0.9999	-0.09182	-0.6222 to 0.4386	ns	> 0.9999
DBA/2j vs. KK/HIJ	0.355	-0.3635 to 1.074	ns	0.8312	0.8288	0.2984 to 1.359	***	0.0003
DBA/2j vs. LG/J	0.078	-0.6405 to 0.7965	ns	> 0.9999	0.5034	-0.02698 to 1.034	ns	0.0746
NOD/ShiLtJ vs. KK/HIJ	0.3637	-0.3548 to 1.082	ns	0.8093	0.9206	0.3902 to 1.451	****	< 0.0001
NOD/ShiLtJ vs. LG/J	0.08667	-0.6318 to 0.8052	ns	> 0.9999	0.5953	0.06484 to 1.126	*	0.0181
KK/HIJ vs. LG/J	-0.277	-0.9955 to 0.4415	ns	0.9633	-0.3253	-0.8558 to 0.2051	ns	0.5811

Supplemental Table 2

Stored RBCs	p-value	q-value	CORRELATION	Super Pathway	Sub Pathway
Positive Correlation					
docosapentaenoate (n6 DPA; 22:5n6)	2.87E-06	2.83E-05	6.52E-01	Lipid	Polyunsaturated Fatty Acid (n3 and n6)
cis-4-decenoyl carnitine	6.41E-06	6.08E-05	6.35E-01	Lipid	Fatty Acid Metabolism(Acyl Carnitine)
1-arachidonoyl-GPI (20:4)*	2.75E-05	2.00E-04	5.99E-01	Lipid	Lysolipid
docosahexaenoate (DHA; 22:6n3)	4.08E-05	3.00E-04	5.89E-01	Lipid	Polyunsaturated Fatty Acid (n3 and n6)
palmitoyl-oleoyl-glycerophosphoglycerol (2)	4.19E-05	3.00E-04	5.88E-01	Lipid	Phosphatidylglycerol
1-arachidonoyl-GPE (20:4)*	1.00E-04	6.00E-04	5.62E-01	Lipid	Lysolipid
17-HDoHe	1.00E-04	6.00E-04	5.55E-01	Lipid	Fatty Acid, Monohydroxy
1-linoleoylglycerol (18:2)	1.00E-04	6.00E-04	5.53E-01	Lipid	Monoacylglycerol
alpha-tocopherol	2.00E-04	1.10E-03	5.39E-01	Cofactors and Vitamins	Tocopherol Metabolism
12-HETE	3.00E-04	1.50E-03	5.35E-01	Lipid	Eicosanoid
tryptophan	5.00E-04	2.30E-03	5.12E-01	Amino Acid	Tryptophan Metabolism
Negative Correlation					
dodecanedioate	1.80E-14	4.72E-12	-8.79E-01	Lipid	Fatty Acid, Dicarboxylate
16-hydroxypalmitate	8.40E-14	9.99E-12	-8.69E-01	Lipid	Fatty Acid, Monohydroxy
5-hydroxyhexanoate	1.17E-13	9.99E-12	-8.67E-01	Lipid	Fatty Acid, Monohydroxy
sebacate (decanedioate)	1.71E-12	1.10E-10	-8.46E-01	Lipid	Fatty Acid, Dicarboxylate
2-hydroxydecanoate	2.39E-12	1.22E-10	-8.43E-01	Lipid	Fatty Acid, Monohydroxy
2-aminoheptanoate	5.55E-12	2.37E-10	-8.36E-01	Lipid	Fatty Acid, Amino
caproate (6:0)	1.01E-10	3.64E-09	-8.08E-01	Lipid	Medium Chain Fatty Acid
heptanoate (7:0)	1.18E-10	3.64E-09	-8.06E-01	Lipid	Medium Chain Fatty Acid
caprylate (8:0)	1.28E-10	3.64E-09	-8.05E-01	Lipid	Medium Chain Fatty Acid
2-hydroxyoctanoate	1.89E-10	4.64E-09	-8.01E-01	Lipid	Fatty Acid, Monohydroxy
undecanedioate	1.99E-10	4.64E-09	-8.01E-01	Lipid	Fatty Acid, Dicarboxylate
pelargonate (9:0)	5.51E-10	1.18E-08	-7.89E-01	Lipid	Medium Chain Fatty Acid
13-HODE + 9-HODE	1.65E-09	3.25E-08	-7.75E-01	Lipid	Fatty Acid, Monohydroxy
9,10-DiHOME	4.60E-09	8.42E-08	-7.62E-01	Lipid	Fatty Acid, Dihydroxy
8-hydroxyoctanoate	1.33E-08	2.27E-07	-7.47E-01	Lipid	Fatty Acid, Monohydroxy
pentadecanoate (15:0)	6.51E-08	1.04E-06	-7.23E-01	Lipid	Long Chain Fatty Acid
azelate (nonanedioate)	7.31E-08	1.10E-06	-7.21E-01	Lipid	Fatty Acid, Dicarboxylate
alpha-hydroxycaproate	9.40E-08	1.34E-06	-7.17E-01	Lipid	Fatty Acid, Monohydroxy
hexadecanedioate	1.18E-07	1.59E-06	-7.13E-01	Lipid	Fatty Acid, Dicarboxylate
suberate (octanedioate)	1.58E-07	1.99E-06	-7.08E-01	Lipid	Fatty Acid, Dicarboxylate
3-hydroxysebacate	1.63E-07	1.99E-06	-7.07E-01	Lipid	Fatty Acid, Monohydroxy
2-hydroxypalmitate	5.99E-07	6.98E-06	-6.84E-01	Lipid	Fatty Acid, Monohydroxy
4-hydroxy-nonenal-glutathione	6.64E-07	7.40E-06	-6.82E-01	Amino Acid	Glutathione Metabolism
indole-3-carboxylic acid	8.70E-07	9.29E-06	-6.77E-01	Amino Acid	Tryptophan Metabolism
pimelate (heptanedioate)	9.77E-07	1.00E-05	-6.74E-01	Lipid	Fatty Acid, Dicarboxylate
4-hydroxybutyrate (GHB)	8.34E-06	7.63E-05	-6.28E-01	Lipid	Fatty Acid, Monohydroxy
glutarate (pentanedioate)	1.23E-05	1.00E-04	-6.19E-01	Amino Acid	Lysine Metabolism
5-HETE	1.60E-05	1.00E-04	-6.13E-01	Lipid	Eicosanoid
palmitoleate (16:1n7)	1.89E-05	2.00E-04	-6.09E-01	Lipid	Long Chain Fatty Acid
phenylalanyl-glycine	2.05E-05	2.00E-04	-6.07E-01	Peptide	Dipeptide
2-oxoadipate	4.15E-05	3.00E-04	-5.89E-01	Amino Acid	Lysine Metabolism
2-hydroxyadipate	4.18E-05	3.00E-04	-5.88E-01	Lipid	Fatty Acid, Dicarboxylate
4-methyl-2-oxopentanoate	1.00E-04	6.00E-04	-5.63E-01	Amino Acid	Leucine, Isoleucine and Valine Metabolism
tetradecanedioate	1.00E-04	6.00E-04	-5.55E-01	Lipid	Fatty Acid, Dicarboxylate
1-palmitoylglycerol (16:0)	2.00E-04	1.10E-03	-5.51E-01	Lipid	Monoacylglycerol
xanthine	2.00E-04	1.10E-03	-5.50E-01	Nucleotide	Purine Metabolism, (Hypo)Xanthine/Inosine containing
cis-vaccenate (18:1n7)	2.00E-04	1.10E-03	-5.39E-01	Lipid	Long Chain Fatty Acid
caprate (10:0)	2.00E-04	1.10E-03	-5.39E-01	Lipid	Medium Chain Fatty Acid
arachidate (20:0)	3.00E-04	1.50E-03	-5.32E-01	Lipid	Long Chain Fatty Acid
myristate (14:0)	3.00E-04	1.50E-03	-5.29E-01	Lipid	Long Chain Fatty Acid
methionine sulfoxide	4.00E-04	2.00E-03	-5.24E-01	Amino Acid	Methionine, Cysteine, SAM and Taurine Metabolism
palmitate (16:0)	4.00E-04	2.00E-03	-5.18E-01	Lipid	Long Chain Fatty Acid
glycerol 3-phosphate	5.00E-04	2.30E-03	-5.16E-01	Lipid	Glycerolipid Metabolism
1-oleoyl-GPI (18:1)*	5.00E-04	2.30E-03	-5.16E-01	Lipid	Lysolipid
1-palmitoyl-GPI (16:0)*	5.00E-04	2.30E-03	-5.16E-01	Lipid	Lysolipid
6-oxopiperidine-2-carboxylic acid	6.00E-04	2.70E-03	-5.09E-01	Amino Acid	Lysine Metabolism
10-heptadecenoate (17:1n7)	6.00E-04	2.70E-03	-5.08E-01	Lipid	Long Chain Fatty Acid
3-methyl-2-oxobutyrate	7.00E-04	3.00E-03	-5.02E-01	Amino Acid	Leucine, Isoleucine and Valine Metabolism
4-hydroxy-2-nonenal	7.00E-04	3.00E-03	-5.02E-01	Lipid	Fatty Acid, Oxidized
Fresh RBCs					
Positive Correlation					
aspartate	1.11E-06	3.00E-04	7.12E-01	Amino Acid	Alanine and Aspartate Metabolism
2'-deoxyuridine	9.78E-06	9.00E-04	6.65E-01	Nucleotide	Pyrimidine Metabolism, Uracil Containing
deoxycarnitine	2.00E-04	4.00E-03	5.81E-01	Lipid	Carnitine Metabolism
glycylleucine	3.00E-04	4.90E-03	5.67E-01	Peptide	Dipeptide
trans-4-hydroxyproline	4.00E-04	5.30E-03	5.59E-01	Amino Acid	Urea cycle; Arginine and Proline Metabolism
thymidine	4.00E-04	5.30E-03	5.56E-01	Nucleotide	Pyrimidine Metabolism, Thymine containing
isoleucylglycine	5.00E-04	5.80E-03	5.51E-01	Peptide	Dipeptide
gamma-glutamyltyrosine	6.00E-04	6.40E-03	5.44E-01	Peptide	Gamma-glutamyl Amino Acid
valylglycine	7.00E-04	7.20E-03	5.41E-01	Peptide	Dipeptide
N6-acetyllysine	9.00E-04	7.60E-03	5.31E-01	Amino Acid	Lysine Metabolism
glutamine	9.00E-04	7.60E-03	5.31E-01	Amino Acid	Glutamate Metabolism
N-acetyltaurine	9.00E-04	7.60E-03	5.29E-01	Amino Acid	Methionine, Cysteine, SAM and Taurine Metabolism
N-acetyl-glycine	1.20E-03	9.30E-03	5.19E-01	Amino Acid	Glycine, Serine and Threonine Metabolism
5,6-dihydrothymine	1.30E-03	9.50E-03	5.15E-01	Nucleotide	Pyrimidine Metabolism, Thymine containing
Negative Correlation					
palmitate (16:0)	7.22E-06	9.00E-04	-0.67	Lipid	Long Chain Fatty Acid

Supplemental Table 2

glycerol 3-phosphate	1.40E-05	1.00E-03	-0.66	Lipid	Glycerolipid Metabolism
alpha-ketoglutarate	2.47E-05	1.40E-03	-0.64	Energy	TCA Cycle
palmitoleate (16:1n7)	7.92E-05	2.80E-03	-0.61	Lipid	Long Chain Fatty Acid
stearate (18:0)	9.83E-05	2.80E-03	-0.60	Lipid	Long Chain Fatty Acid
1-oleoylglycerol (18:1)	1.00E-04	2.80E-03	-0.60	Lipid	Monoacylglycerol
linoleate (18:2n6)	1.00E-04	2.80E-03	-0.60	Lipid	Polyunsaturated Fatty Acid (n3 and n6)
eicosenoate (20:1)	1.00E-04	2.80E-03	-0.59	Lipid	Long Chain Fatty Acid
10-heptadecenoate (17:1n7)	2.00E-04	4.00E-03	-0.59	Lipid	Long Chain Fatty Acid
dihomo-linoleate (20:2n6)	2.00E-04	4.00E-03	-0.58	Lipid	Polyunsaturated Fatty Acid (n3 and n6)
alpha-tocopherol	2.00E-04	4.00E-03	-0.58	Vitamin	Tocopherol
4-hydroxy-nonenal-glutathione	3.00E-04	4.90E-03	-0.57	Amino Acid	Glutathione Metabolism
20a-dihydroprogesterone	3.00E-04	4.90E-03	-0.56	Lipid	Steroid
margarate (17:0)	4.00E-04	5.30E-03	-0.56	Lipid	Long Chain Fatty Acid
4-methyl-2-oxopentanoate	4.00E-04	5.30E-03	-0.56	Amino Acid	Leucine, Isoleucine and Valine Metabolism
2-phosphoglycerate	5.00E-04	5.80E-03	-0.55	Carbohydrate	Glycolysis, Gluconeogenesis, and Pyruvate Metabolism
oleate (18:1n9)	5.00E-04	5.80E-03	-0.55	Lipid	Long Chain Fatty Acid
linolenate [alpha or gamma; (18:3n3 or 6)]	6.00E-04	6.40E-03	-0.55	Lipid	Polyunsaturated Fatty Acid (n3 and n6)
3-methyl-2-oxobutyrate	8.00E-04	7.60E-03	-0.53	Amino Acid	Leucine, Isoleucine and Valine Metabolism
cis-vaccenate (18:1n7)	8.00E-04	7.60E-03	-0.53	Lipid	Long Chain Fatty Acid
10-nonadecenoate (19:1n9)	9.00E-04	7.60E-03	-0.53	Lipid	Long Chain Fatty Acid
succinylcarnitine	1.10E-03	8.80E-03	-0.52	Energy	TCA Cycle
3-methyl-2-oxovalerate	1.10E-03	8.80E-03	-0.52	Amino Acid	Leucine, Isoleucine and Valine Metabolism
2-oleoylglycerol (18:1)	1.30E-03	9.50E-03	-0.52	Lipid	Monoacylglycerol

Ratio of Stored to Fresh	p-value	q-value	CORRELATION	Super Pathway	Sub Pathway
Positive Correlation					
1-arachidonoyl-GPI (20:4)*	4.17E-06	5.35E-05	6.77E-01	lipid	Lysolipid
dihomo-linolenate (20:3n3 or n6)	5.49E-06	6.52E-05	6.71E-01	lipid	Polyunsaturated Fatty Acid (n3 and n6)
1-linoleoylglycerol (18:2)	6.43E-06	6.95E-05	6.67E-01	lipid	Lysolipid
12-HETE	1.41E-05	1.00E-04	6.49E-01	lipid	Eicosanoid
alpha-tocopherol	1.41E-05	1.00E-04	6.49E-01	Vitamin	Tocopherol
1-arachidonoyl-GPE (20:4)*	1.83E-05	2.00E-04	6.42E-01	lipid	Lysolipid
docosahexaenoate (DHA; 22:6n3)	3.34E-05	3.00E-04	6.27E-01	lipid	Polyunsaturated Fatty Acid (n3 and n6)
glutathione, reduced (GSH)	6.88E-05	5.00E-04	6.07E-01	Amino Acid	glutathione metabolism
adrenate (22:4n6)	7.83E-05	6.00E-04	6.03E-01	lipid	Polyunsaturated Fatty Acid (n3 and n6)
1-linoleoyl-GPE (18:2)*	2.00E-04	1.30E-03	5.79E-01	lipid	Lysolipid
docosapentaenoate (n6 DPA; 22:5n6)	3.00E-04	1.90E-03	5.65E-01	lipid	Polyunsaturated Fatty Acid (n3 and n6)
docosapentaenoate (n3 DPA; 22:5n3)	5.00E-04	2.90E-03	5.48E-01	lipid	Polyunsaturated Fatty Acid (n3 and n6)
17-HDoHe	5.00E-04	2.90E-03	5.47E-01	lipid	Fatty Acid, Monohydroxy
1-linoleoyl-GPI (18:2)*	6.00E-04	3.20E-03	5.36E-01	lipid	Lysolipid
cis-4-decenoyl carnitine	8.00E-04	4.20E-03	5.28E-01	lipid	Fatty Acid Metabolism (Acyl Carnitines)
stearoyl-arachidonoyl-glycerophosphocholine(2)	1.20E-03	5.70E-03	5.13E-01	lipid	Phosphatidylcholine Metabolism
2-oleoylglycerol (18:1)	1.20E-03	5.70E-03	5.11E-01	lipid	monoacylglycerol
Negative Correlation					
undecanedioate	1.15E-10	2.73E-08	-8.36E-01	lipid	Fatty Acid, Dicarboxylate
sebacate (decanedioate)	5.01E-10	5.95E-08	-8.21E-01	lipid	Fatty Acid, Dicarboxylate
5-hydroxyhexanoate	1.90E-09	1.51E-07	-8.05E-01	lipid	Fatty Acid, Monohydroxy
2-aminoheptanoate	2.67E-09	1.51E-07	-8.01E-01	lipid	Fatty Acid, Amino
2-hydroxydecanoate	3.18E-09	1.51E-07	-7.99E-01	lipid	Fatty Acid, Monohydroxy
azelate (nonanedioate)	1.96E-08	7.76E-07	-7.74E-01	lipid	Fatty Acid, Dicarboxylate
suberate (octanedioate)	2.48E-08	8.20E-07	-7.70E-01	lipid	Fatty Acid, Dicarboxylate
2-hydroxyoctanoate	2.76E-08	8.20E-07	-7.69E-01	lipid	Fatty Acid, Monohydroxy
caprylate (8:0)	4.19E-08	1.11E-06	-7.62E-01	lipid	Medium Chain Fatty Acid
heptanoate (7:0)	9.66E-08	2.30E-06	-7.49E-01	lipid	Medium Chain Fatty Acid
8-hydroxyoctanoate	2.23E-07	4.82E-06	-7.35E-01	lipid	Fatty Acid, Monohydroxy
16-hydroxypalmitate	2.98E-07	5.90E-06	-7.30E-01	lipid	Fatty Acid, Monohydroxy
kynurenine	3.71E-07	6.78E-06	-7.26E-01	amino acid	Tryptophan Metabolism
indole-3-carboxylic acid	1.05E-06	1.78E-05	-7.06E-01	amino acid	Tryptophan Metabolism
2-hydroxypalmitate	1.29E-06	2.04E-05	-7.02E-01	lipid	Fatty Acid, Monohydroxy
N6-succinyladenosine	1.87E-06	2.78E-05	-6.94E-01	nucleotide	Purine Metabolism
glutarate (pentanedioate)	2.82E-06	3.94E-05	-6.86E-01	amino acid	Lysine Metabolism
pelargonate (9:0)	4.28E-06	5.35E-05	-6.77E-01	lipid	Medium Chain Fatty Acid
pimelate (heptanedioate)	6.29E-06	6.95E-05	-6.68E-01	lipid	Fatty Acid, Dicarboxylate
hexadecanedioate	2.23E-05	2.00E-04	-6.37E-01	lipid	Fatty Acid, Dicarboxylate
dodecanedioate	2.45E-05	2.00E-04	-6.35E-01	lipid	Fatty Acid, Dicarboxylate
3-hydroxysebacate	4.49E-05	4.00E-04	-6.19E-01	lipid	Fatty Acid, Monohydroxy
caproate (6:0)	6.96E-05	5.00E-04	-6.06E-01	lipid	Medium Chain Fatty Acid
glycolate (hydroxyacetate)	7.31E-05	5.00E-04	-6.05E-01	Xenobiotic	Chemical
4-hydroxy-nonenal-glutathione	1.00E-04	7.00E-04	-5.93E-01	amino acid	Glutathione Metabolism
N6-acetyllysine	1.00E-04	7.00E-04	-5.87E-01	amino acid	Lysine Metabolism
2-hydroxystearate	3.00E-04	1.90E-03	-5.58E-01	lipid	Fatty Acid, Monohydroxy
9,10-DiHOME	5.00E-04	2.90E-03	-5.44E-01	lipid	Fatty Acid, Dihydroxy
alpha-hydroxycaproate	6.00E-04	3.20E-03	-5.39E-01	lipid	Fatty Acid, Monohydroxy
glycylvaline	6.00E-04	3.20E-03	-5.36E-01	peptide	dipeptide
2-hydroxybutyrate (AHB)	1.00E-03	5.00E-03	-5.21E-01	amino acid	Methionine, Cysteine, SAM and Taurine Metabolism
aspartate	1.00E-03	5.00E-03	-5.20E-01	amino acid	Alanine and Aspartate Metabolism
uracil	1.00E-03	5.00E-03	-5.17E-01	nucleotide	Pyrimidine Metabolism, Uracil containing

Supplemental Table 1: ANOVA analysis of statistical significance in differences of 24 hr RBC recoveries between strains for fresh or stored RBCs. Recoveries of stored RBCs were compared for differences in mean of \log_{10} -transformed data. No significant differences were observed for any fresh RBCs. Significant differences for stored RBCs are indicated by shading. All values show combined data of all three experiments shown in figure 1.

Supplemental Table 2: All analytes that correlated with 24 hr RBC recoveries of stored RBCs that have a Pearson's coefficient of greater than 0.5 or lesser than -0.5, and also had p values of less than 0.05 and q values of less than 0.01 are shown. Lists are broken down as to "positive correlations" and "negative correlations" of the indicated analytes with 24-hour recoveries of transfused stored RBCs with regards to analytes measured in (Stored RBCs), (Fresh RBCs), or the (Ratio of Stored to Fresh RBCs). All correlations were performed with 24-hour recoveries of stored RBCs. Thus, the correlations for (Fresh RBCs) are the levels of measured analytes at time of collection correlated to the 24 hour recoveries obtained 7 days later after storage. All values show combined data of all three experiments shown in figure 1.

Supplemental Methods

Ultrahigh Performance Liquid Chromatography-Tandem Mass Spectroscopy (UPLC-MS/MS):

The LC/MS platform was based on a Waters ACQUITY ultra-performance liquid chromatography (UPLC) and a Thermo Scientific Q-Exactive high resolution/accurate mass spectrometer interfaced with a heated electrospray ionization (HESI-II) source and Orbitrap mass analyzer operated at 35,000 mass resolution. The sample extract was dried then reconstituted in acidic or basic LC-compatible solvents, each of which contained 8 or more injection standards at fixed concentrations to ensure injection and chromatographic consistency. One aliquot was analyzed using acidic positive ion optimized conditions and the other using basic negative ion optimized conditions in two independent injections using separate dedicated columns (Waters UPLC BEH C18-2.1x100 mm, 1.7 μ m). Extracts reconstituted in acidic conditions were gradient eluted from a C18 column using water and methanol containing 0.1% formic acid. The basic extracts were similarly eluted from C18 using methanol and water, however with 6.5mM Ammonium Bicarbonate. The third aliquot was analyzed via negative ionization following elution from a HILIC column (Waters UPLC BEH Amide 2.1x150 mm, 1.7 μ m) using a gradient consisting of water and acetonitrile with 10mM Ammonium Formate. The MS analysis alternated between MS and data-dependent MS2 scans using dynamic exclusion, and the scan range was from 80-1000 m/z.

Gas Chromatography-Mass Spectroscopy (GC-MS):

The samples destined for analysis by GC-MS were dried under vacuum for a minimum of 18 h prior to being derivatized under dried nitrogen using bistrimethyl-silyltrifluoroacetamide. Derivatized samples were separated on a 5% diphenyl / 95% dimethyl polysiloxane fused silica column (20 m x 0.18 mm ID; 0.18 μ m film thickness) with helium as carrier gas and a temperature ramp from 60° to 340°C in a 17.5 min period. Samples were analyzed on a Thermo-Finnigan Trace DSQ fast-scanning single-

quadrupole mass spectrometer using electron impact ionization (EI) and operated at unit mass resolving power. The scan range was from 50–750 m/z.