The structural origin of metabolic quantitative diversity

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Supplementary Materials

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Metabolite	mean \pm s.d. (μ M)	Metabolite	mean \pm s.d. (μ M)	
2-Aminobutyrate	16.7 ± 5.7	Glycerol	78.4 ± 29.0	
2-Hydroxybutyrate	34.7 ± 15.8	Glycine	220.2 ± 68.4	
2-Oxoisocaproate	24.4 ± 6.2	Histidine	79.1 ± 10.6	
3-Hydroxybutyrate	95.2 ± 125.0	Isoleucine	57.9 ± 17.7	
3-Hydroxyisobutyrate	12.1 ± 3.8	Lactate	2222.7 ± 605.6	
3-Methyl-2-oxovalerate	18.4 ± 4.3	Leucine	109.3 ± 25.8	
Acetate	37.3 ± 9.0	Lysine	119.9 ± 23.7	
Acetone	7.9 ± 7.0	Methionine	23.5 ± 6.1	
Alanine	331.8 ± 80.7	Ornithine	63.2 ± 15.8	
Arginine	62.2 ± 15.6	Phenylalanine	58.2 ± 10.5	
Asparagine	56.5 ± 11.5	Proline	158.5 ± 48.4	
Carnitine	49.6 ± 10.3	Pyruvate	73.8 ± 17.1	
Creatine	33.3 ± 17.3	Serine	114.7 ± 21.5	
Creatinine	55.1 ± 19.6	Succinate	6.9 ± 1.3	
Cysteine	52.2 ± 17.3	Threonine	132.3 ± 29.3	
Formate	16.6 ± 3.3	Tryptophan	49.0 ± 9.1	
Glucose	4844.2 ± 994.2	Tyrosine	64.8 ± 14.9	
Glutamate	53.6 ± 16.6	Valine	209.2 ± 43.5	
Glutamine	528.6 ± 65.4			

Supplementary Table S1: Plasma metabolites identified and quantified in this study

					Average		Fold c	hange
Meabolite	SNP	gene	sex	wt	hetero	homo	hetero/wt	homo/wt
asparagine	rs8012505	ASPG	all	54.6	61.8	80.8	1.13	1.48
			male	56.1	59.8	84.7	1.07	1.51
			female	53.8	63.1	78.9	1.17	1.47
phenylalanine	rs118092776	PAH	all	57.2	68.2	N.A.	1.19	N.A.
			male	59.9	70.9	N.A.	1.18	N.A.
			female	55.6	66.6	N.A.	1.2	N.A.
proline	rs5747933	PRODH	all	149.5	179.0	231.1	1.2	1.55
			male	165.3	199.0	271.4	1.2	1.64
			female	139.9	168.2	210.9	1.2	1.51
Glycine	rs1047891	CPS1	all	194.8	280.4	313.6	1.44	1.61
			male	187.8	217.5	213.5	1.16	1.14
			female	199.4	312.2	333.6	1.57	1.67
formate	rs1801133	MTHFR	all	17.6	16.4	15.0	0.93	0.85
			male	18.1	16.6	15.5	0.92	0.86
			female	17.2	16.3	14.7	0.95	0.85
creatinine	rs820336	MYLK	all	54.9	61.5	N.A.	1.12	N.A.
			male	66.9	63.2	N.A.	0.94	N.A.
			female	47.6	60.3	N.A.	1.27	N.A.

Supplementary Table S2: average values of metabolites

Metabolite	sex	–log P	n	SNP	Chr.	Gene	Allele	MAF	Residue change
asparagine	all	14.19	505	rs8012505	14	ASPG	C>G	0.127	S344R
proline	all	14.88	467	rs5747933	22	PRODH	G>T	0.148	T275N
phenylalanine	all	12.54	511	rs118092776	12	PAH	C>T	0.047	R53H
glycine	all	50.66	509	rs1047891	2	CPS1	C>A	0.152	T1406N
formate	all	8.34	498	rs1801133	1	MTHFR	C>T	0.397	A222V

Supplementary Table S3a: Genome-wide significant loci associated with metabolites

Supplementary Table S3b: Loci associated with metabolites (sex specific)

Metabolite	sex	-log P	n	SNP	Chr.	Gene	Allele	MAF	Residue change
asparagine	female	11.23	314	rs8012505	14	ASPG	C>G		S344R
glycine	female	44.64	317	rs1047891	2	CPS1	C>A		T1406N
creatinine	female	6.90	316	rs820336	3	MYLK	G>A	(0.020	intron
								for all)	













Supplementary Figure S1: Regional association plots for loci reported in this study. Statistical Significance of associated SNPs are plotted on the $-\log_{10}(P$ -value) scale as a function of chromosomal position (NCBI 37). The identified causal SNP at each locus is shown in purple. Correlation of the causal SNP to other SNPs at each locus is shown on a scale from minimal (blue) to maximal (red). Estimate recombination rate are also shown.

Rat phenylalanine hydroxylase (PAH) (PDB ID: 2PHM)



Human CPS1 C-terminal regulatory domain (PDB ID:2YVQ)

b



Supplementary Figure S2: (a) Structural characteristics of the non-synonymous variants in PAH. (b) Orientation of the regulatory domain relative to the catalytic domain in *E coli* CPS structure (PDB ID: 2BXR). All figures were made using the PyMOL Software Package (https://www.pymol.org/).



Supplementary Figure S3: Schematic representation of metabolite pathway involving glycine. CPS1 was shown in red. Glycine was shown in green.



Supplementary Figure S4: Distribution of the plasma creatinine concentration across the genotype of a locus summarized in Supplementary Table S3b. The distribution was shown using a violin plot. This figure was made using R package.