

Table S1 – Essential amino acid (EAA) and non-essential amino acid (NEAA) composition of the casein and soy proteins used to formulate the experimental diets

		Casein, gm%	Soy, gm%
EAA	His ¹	2.6	2.6
	Ile	4.3	4.9
	Leu	9.0	8.2
	Lys	7.5	6.3
	Met	2.9	1.3
	Phe	4.8	5.2
	Thr	4.1	3.7
	Trp	1.2	1.4
	Val	5.3	5
NEAA	Ala	2.9	4.3
	Arg	3.4	7.6
	Asn	4	NA
	Asp	2.9	11.6
	Cys	0.7	1.3
	Gln	9.8	NA
	Glu	11.9	19.1
	Gly	1.7	4.2
	Pro	10.1	5.1
	Ser	5.7	5.2
	Tyr	5.2	3.8
Total %		100	100.8

¹Three letter abbreviations of amino acids. Sulfur amino acids, methionine and cysteine highlighted in yellow.

Table S2 – Primers used for real time PCR analysis.

<i>Gene</i>	Forward	Reverse
<i>Scd1</i>	GTGCCGTGGGCGAGGGCTTC	AGCCCAAAGCTCAGCTACTCTT
<i>Fasn</i>	TCCTGGAACGAGAACACGATCT	GAGACGTGTCACTCCTGGACTTG
<i>Fgf21</i>	TGACACCCAGGATTTGAATGAC	GCAGCCAATGATGTGTGCTTAC
<i>Asns</i>	GGGGGCCTGGACTCGAGCTT	TTGCCACCTTTCTAGCGGCCA
<i>Psat1</i>	CAGTGGAGCGCCAGAATAGAA	CCTGTGCCCCCTTCAAGGAG
<i>Mgst3</i>	ATGGCTGTCCTCTCTAAGGAG	CTCTACCTTGACTTCTTGCGG
<i>Ucp1</i>	GATCCAAGGTGAAGGCCAGG	GTTGACAAGCTTTCTGTGGTGG
<i>Cox7a1</i>	CAGCGTCATGGTCAGTCTGT	AGAAAACCGTGTGGCAGAGA
<i>Cox8b</i>	AGTTCACAGTGGTTCCCAAAG	ACCATGAAGCCAACGACTATG
<i>Cidea</i>	ATCACAACTGGCCTGGTTACG	TACTACCCGGTGTCCATTCT
<i>Cyclophilin</i>	CTTCGAGCTGTTTGCAGACAAAGT	AGATGCCAGGACCTGTATGCT

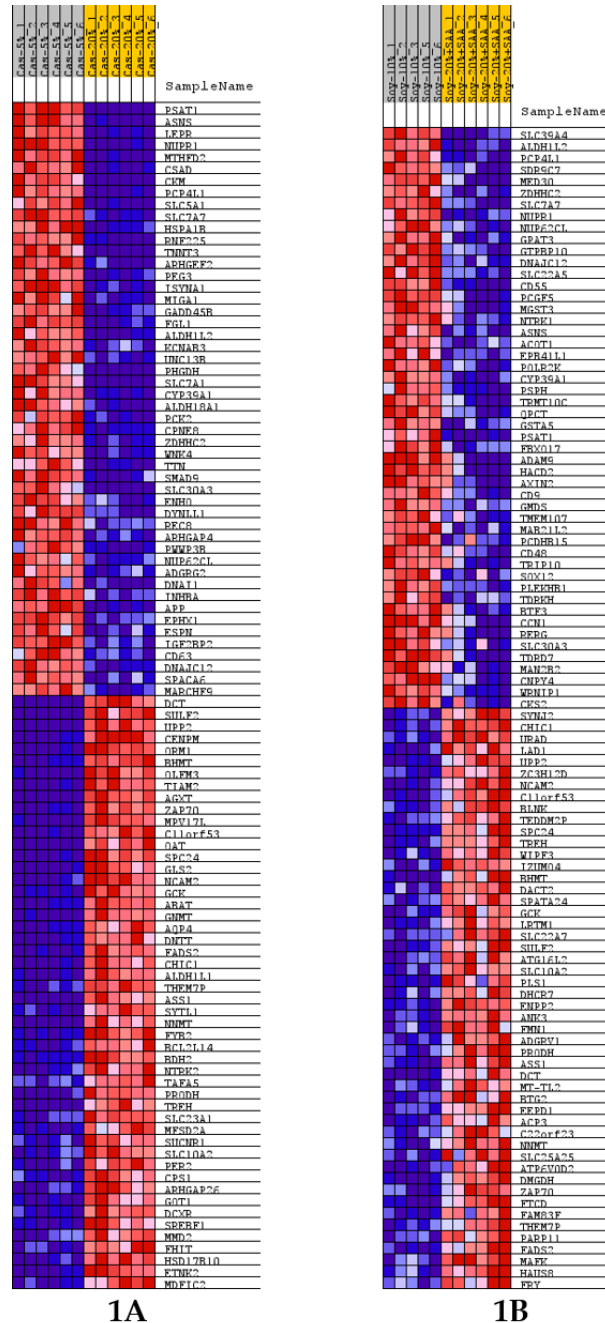


Figure S1: Gene Set Enrichment Analysis (GSEA) of hepatic gene expression in mice fed sulfur amino acid-matched control diets formulated from casein (Cas-20%) or soy (Soy-20%+SAA), and sulfur amino acid-matched protein restricted diets formulated from casein (Cas-5%) or soy (Soy-10%). The heat maps are shown for the top 50 up-regulated and down-regulated genes for the Cas-5% to Cas-20% (**1A**) and Soy-10% to Soy-20%+SAA comparisons (**1B**). The heat maps present the normalized enrichment scores for each mouse and the corresponding individual genes within the gene set [blue = downregulation, red = upregulation, (FDR > 0.1)].

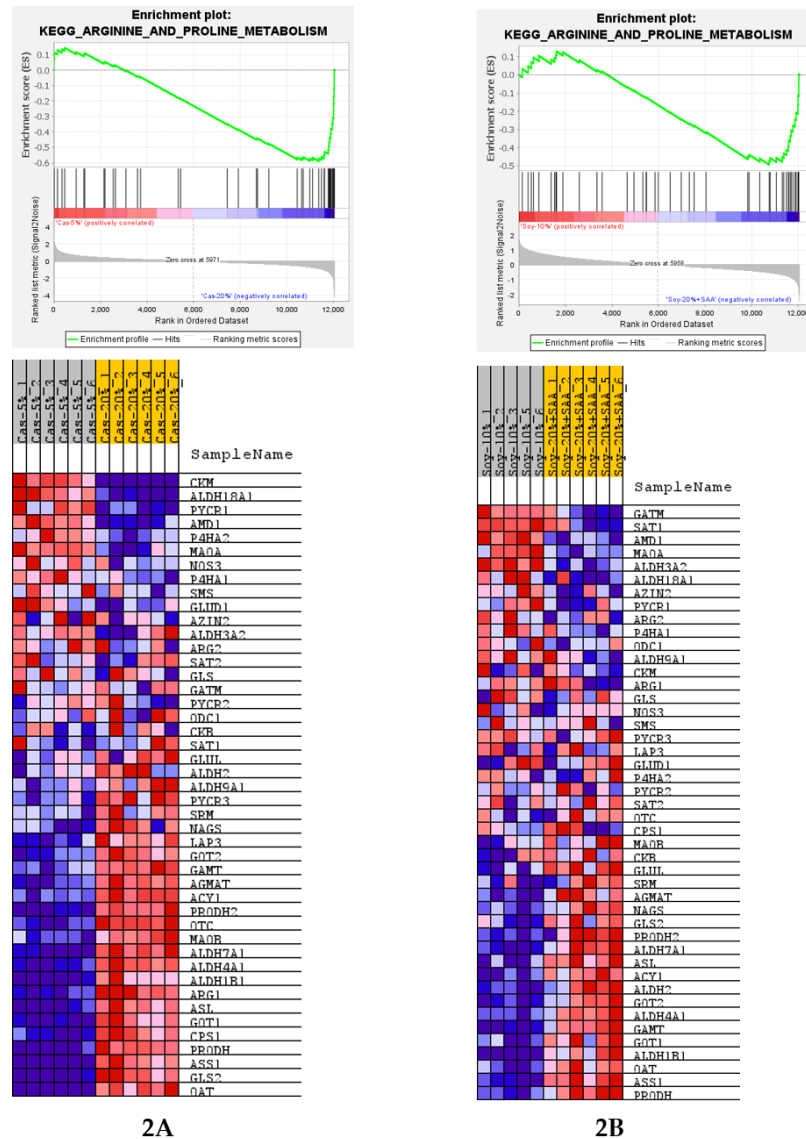


Figure S2: Gene set enrichment analysis (GSEA) of hepatic gene expression in mice fed sulfur amino acid-matched control diets formulated from casein (Cas-20%) or soy (Soy-20%+SAA), and sulfur amino acid-matched protein restricted diets formulated from casein (Cas-5%) or soy (Soy-10%). The enrichment plots and corresponding heat maps are shown for the top-scoring KEGG Arginine-Proline Metabolism gene set for the Cas-5% to Cas-20% (**2A**) and Soy-10% to Soy-20%+SAA comparisons (**2B**). Enrichment was computed as described in the Material and Methods and the individual contributions of pathway genes to the pathway enrichment signal were visualized via enrichment plots depicting the trajectory of a normalized pathway enrichment score against the rank of the pathway genes in the context of the full gene list. Accompanying heat maps present the normalized enrichment scores for individual genes within the gene set [blue = downregulation, red = upregulation, gray = not significant (FDR > 0.1)].

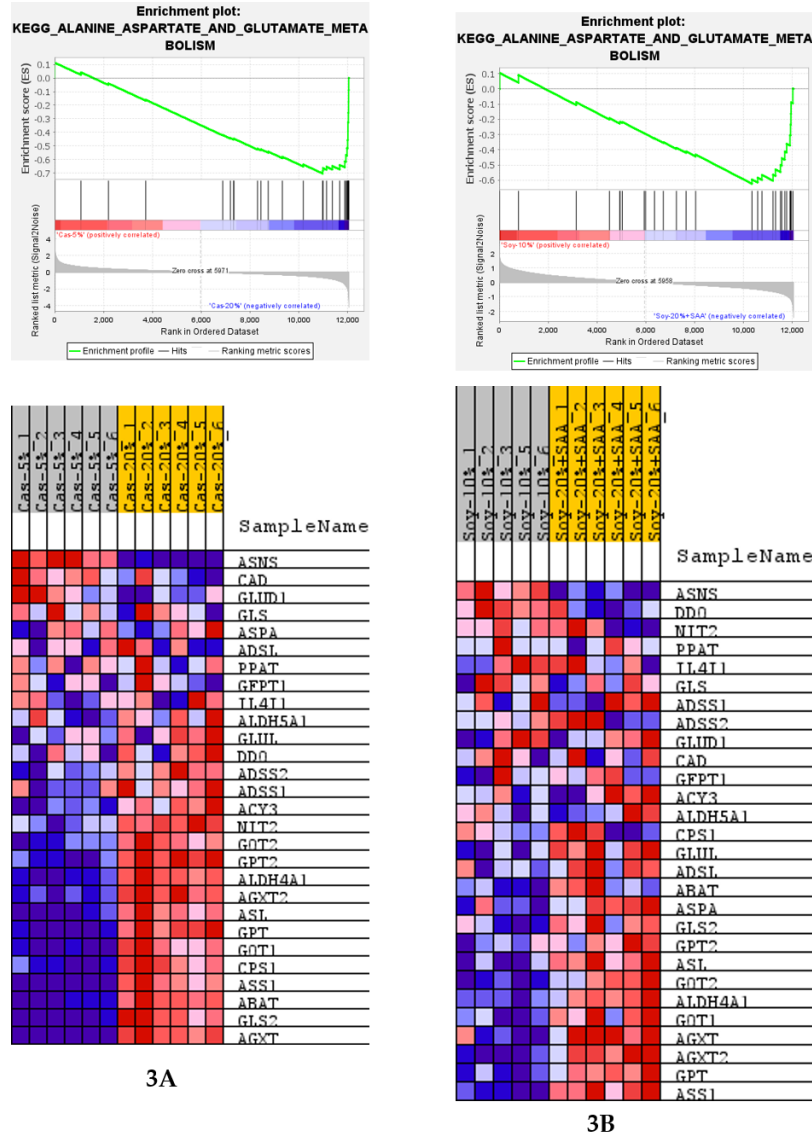
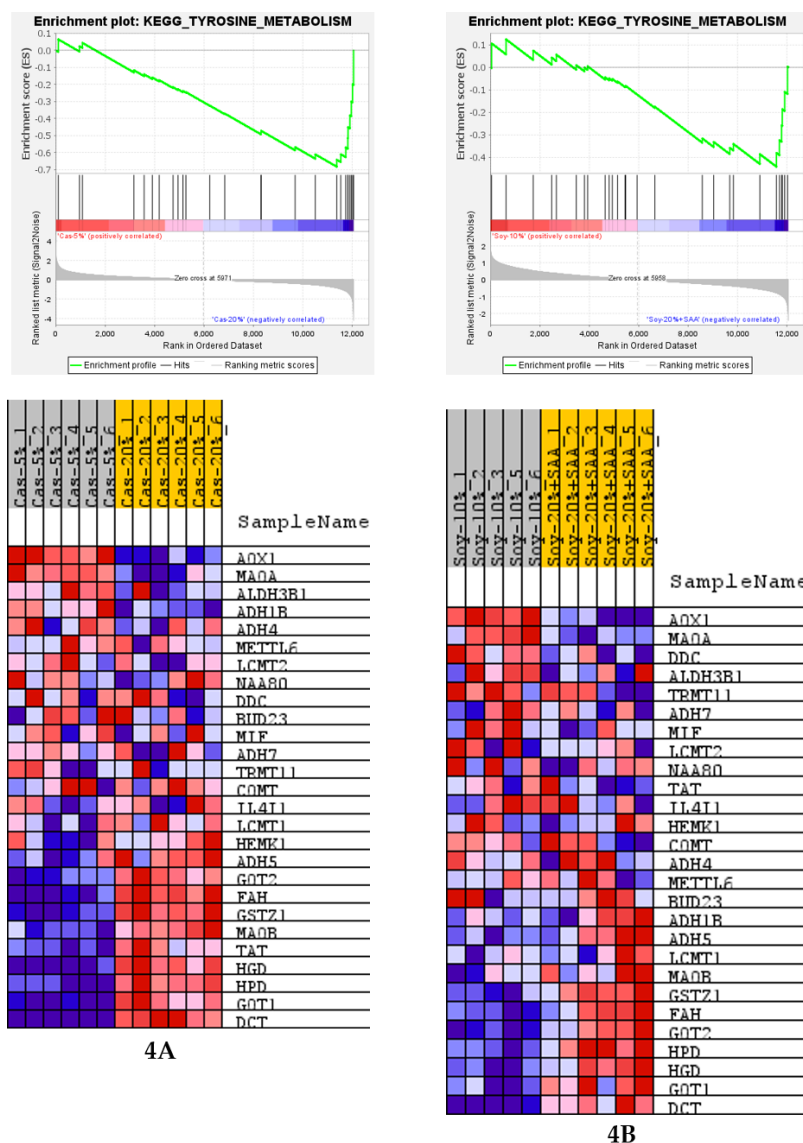


Figure S3: Gene set enrichment analysis (GSEA) of hepatic gene expression in mice fed sulfur amino acid-matched control diets formulated from casein (Cas-20%) or soy (Soy-20%+SAA), and sulfur amino acid-matched protein restricted diets formulated from casein (Cas-5%) or soy (Soy-10%). The enrichment plots and corresponding heat maps are shown for the top-scoring KEGG Alanine-Aspartate-Glutamate Metabolism gene set for the Cas-5% to Cas-20% (**3A**) and Soy-10% to Soy-20%+SAA comparisons (**3B**). Enrichment was computed as described in the Material and Methods and the individual contributions of pathway genes to the pathway enrichment signal were visualized via enrichment plots depicting the trajectory of a normalized pathway enrichment score against the rank of the pathway genes in the context of the full gene list. Accompanying heat maps present the normalized enrichment scores for individual genes within the gene set [blue = downregulation, red = upregulation, gray = not significant (FDR > 0.1)].



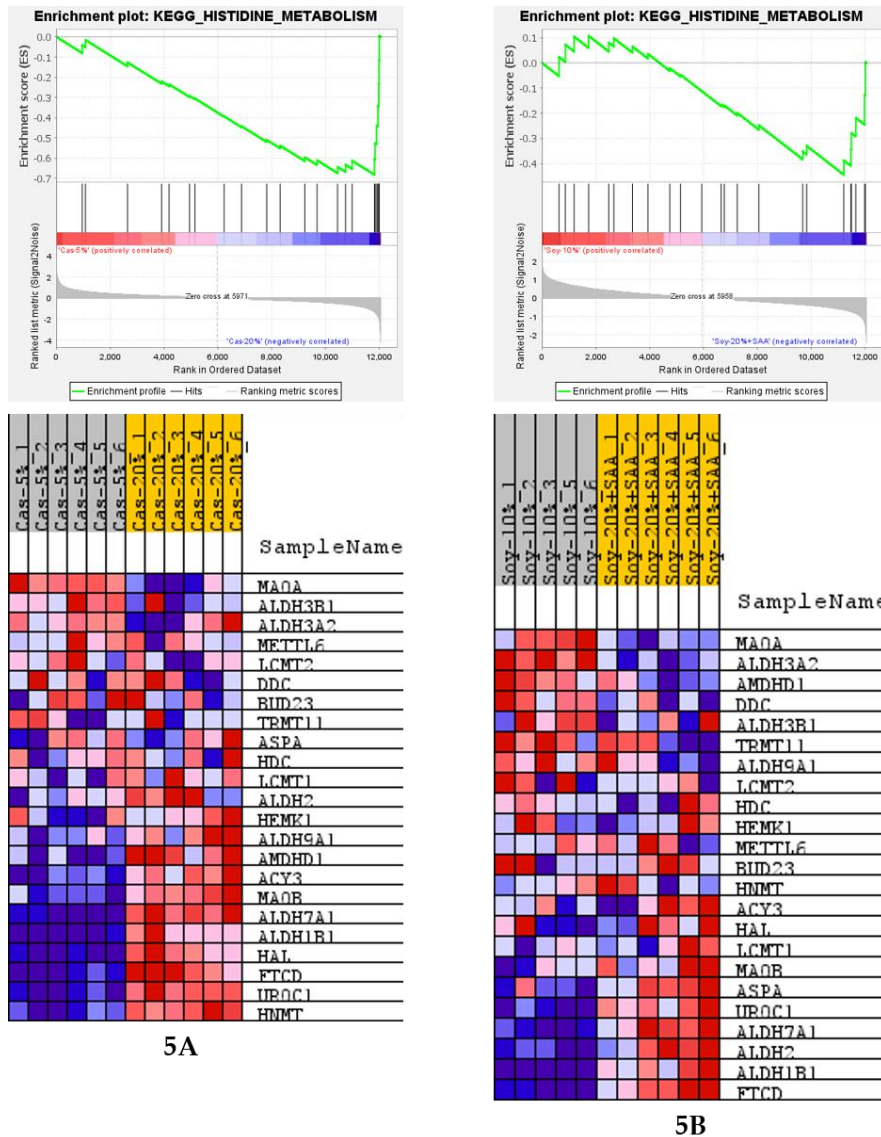


Figure S5: Gene set enrichment analysis (GSEA) of hepatic gene expression in mice fed sulfur amino acid-matched control diets formulated from casein (Cas-20%) or soy (Soy-20%+SAA), and sulfur amino acid-matched protein restricted diets formulated from casein (Cas-5%) or soy (Soy-10%). The enrichment plots and corresponding heat maps are shown for the top-scoring KEGG Histidine Metabolism gene set for the Cas-5% to Cas-20% (**5A**) and Soy-10% to Soy-20%+SAA comparisons (**5B**). Enrichment was computed as described in the Material and Methods and the individual contributions of pathway genes to the pathway enrichment signal were visualized via enrichment plots depicting the trajectory of a normalized pathway enrichment score against the rank of the pathway genes in the context of the full gene list. Accompanying heat maps present the normalized enrichment scores for individual genes within the gene set [blue = downregulation, red = upregulation, gray = not significant (FDR > 0.1)].

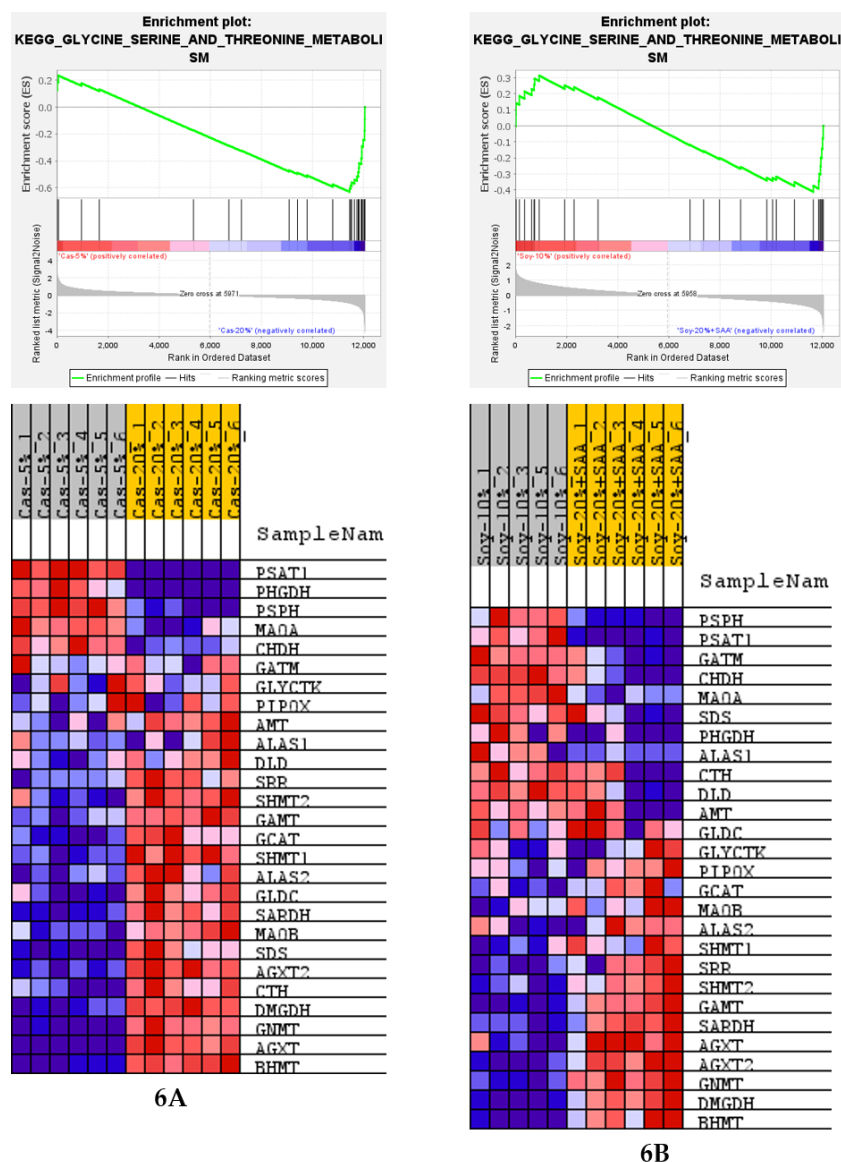


Figure S6: Gene set enrichment analysis (GSEA) of hepatic gene expression in mice fed sulfur amino acid-matched control diets formulated from casein (Cas-20%) or soy (Soy-20%+SAA), and sulfur amino acid-matched protein restricted diets formulated from casein (Cas-5%) or soy (Soy-10%). The enrichment plots and corresponding heat maps are shown for the top-scoring KEGG Glycine-Serine-Threonine Metabolism gene set for the Cas-5% to Cas-20% (**6A**) and Soy-10% to Soy-20%+SAA comparisons (**6B**). Enrichment was computed as described in the Material and Methods and the individual contributions of pathway genes to the pathway enrichment signal were visualized via enrichment plots depicting the trajectory of a normalized pathway enrichment score against the rank of the pathway genes in the context of the full gene list. Accompanying heat maps present the normalized enrichment scores for individual genes within the gene set [blue = downregulation, red = upregulation, gray = not significant (FDR > 0.1)].

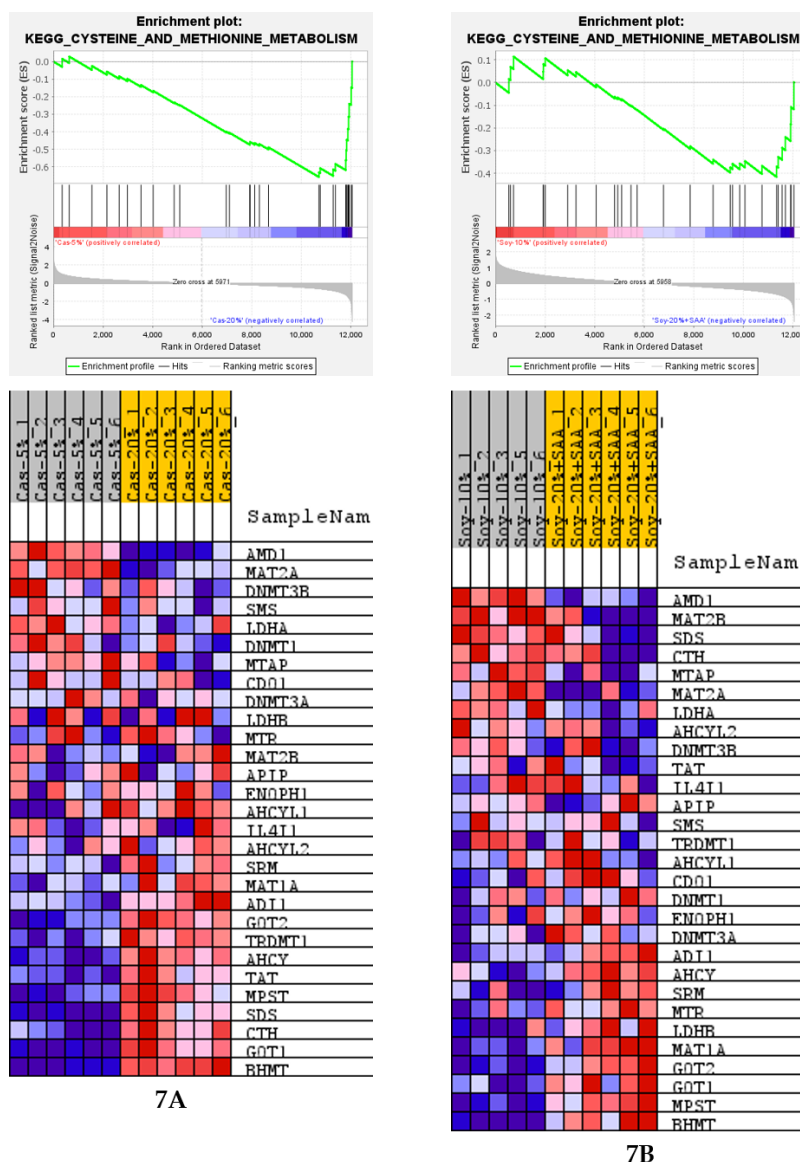


Figure S7: Gene set enrichment analysis (GSEA) of hepatic gene expression in mice fed sulfur amino acid-matched control diets formulated from casein (Cas-20%) or soy (Soy-20%+SAA), and sulfur amino acid-matched protein restricted diets formulated from casein (Cas-5%) or soy (Soy-10%). The enrichment plots and corresponding heat maps are shown for the top-scoring KEGG Cysteine-Methionine Metabolism gene set for the Cas-5% to Cas-20% (7A) and Soy-10% to Soy-20%+SAA comparisons (7B). Enrichment was computed as described in the Material and Methods and the individual contributions of pathway genes to the pathway enrichment signal were visualized via enrichment plots depicting the trajectory of a normalized pathway enrichment score against the rank of the pathway genes in the context of the full gene list. Accompanying heat maps present the normalized enrichment scores for individual genes within the gene set [blue = downregulation, red = upregulation, gray = not significant (FDR > 0.1)].

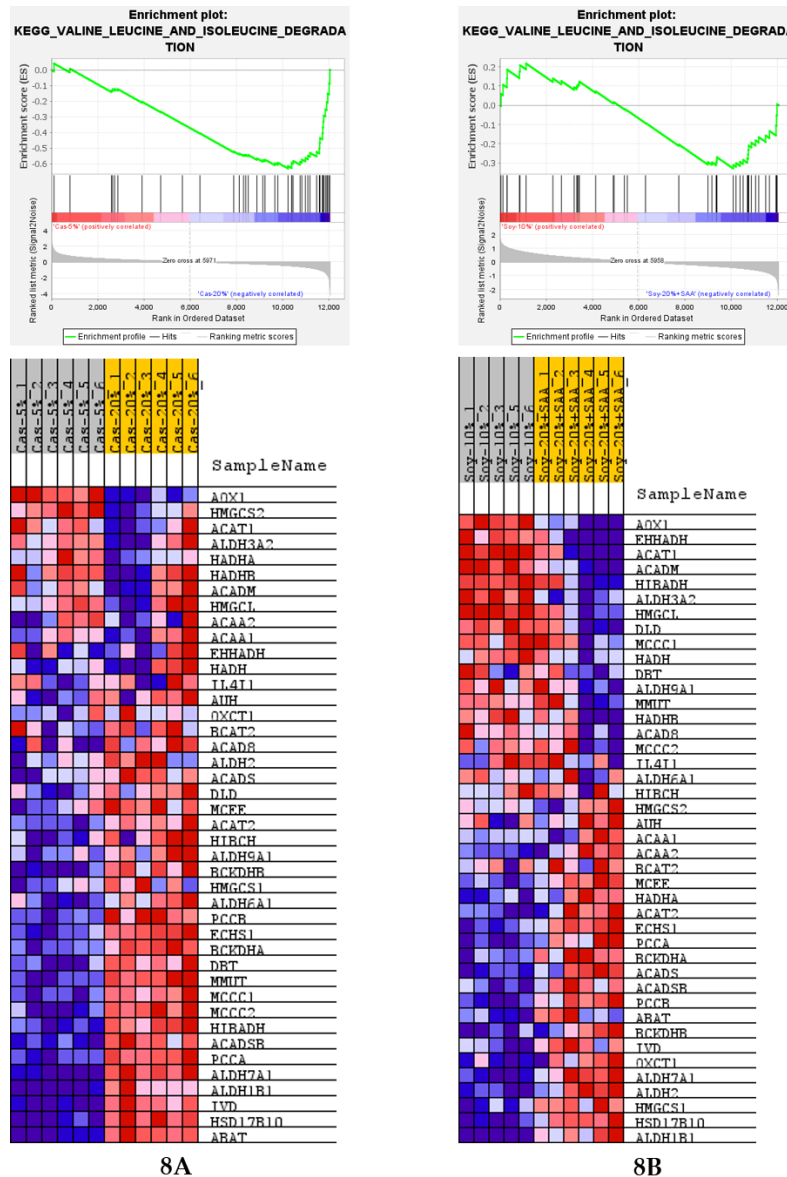


Figure S8: Gene set enrichment analysis (GSEA) of hepatic gene expression in mice fed sulfur amino acid-matched control diets formulated from casein (Cas-20%) or soy (Soy-20%+SAA), and sulfur amino acid-matched protein restricted diets formulated from casein (Cas-5%) or soy (Soy-10%). The enrichment plots and corresponding heat maps are shown for the top-scoring KEGG Valine-Isoleucine-Leucine Degradation gene set for the Cas-5% to Cas-20% (**8A**) and Soy-10% to Soy-20%+SAA comparisons (**8B**). Enrichment was computed as described in the Material and Methods and the individual contributions of pathway genes to the pathway enrichment signal were visualized via enrichment plots depicting the trajectory of a normalized pathway enrichment score against the rank of the pathway genes in the context of the full gene list. Accompanying heat maps present the normalized enrichment scores for individual genes within the gene set [blue = downregulation, red = upregulation, gray = not significant (FDR > 0.1)].

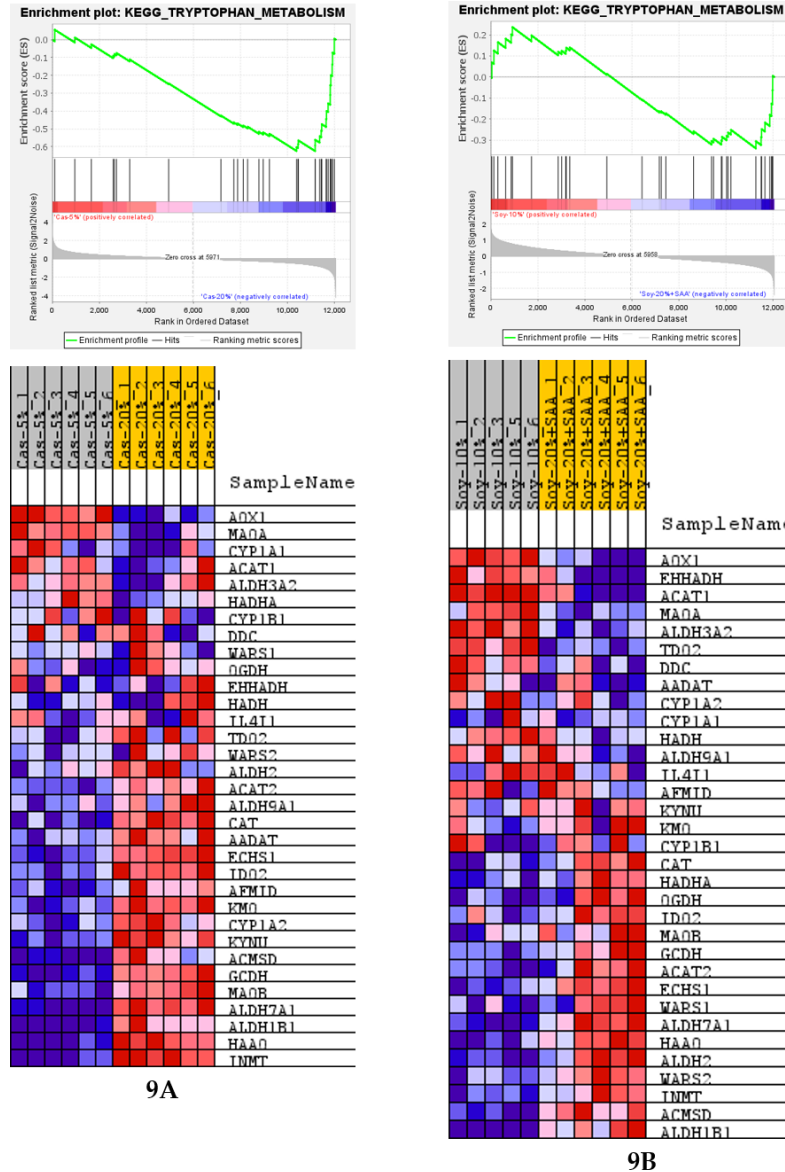


Figure S9: Gene set enrichment analysis (GSEA) of hepatic gene expression in mice fed sulfur amino acid-matched control diets formulated from casein (Cas-20%) or soy (Soy-20%+SAA), and sulfur amino acid-matched protein restricted diets formulated from casein (Cas-5%) or soy (Soy-10%). The enrichment plots and corresponding heat maps are shown for the top-scoring KEGG Tryptophan Metabolism gene set for the Cas-5% to Cas-20% (9A) and Soy-10% to Soy-20%+SAA comparisons (9B). Enrichment was computed as described in the Material and Methods and the individual contributions of pathway genes to the pathway enrichment signal were visualized via enrichment plots depicting the trajectory of a normalized pathway enrichment score against the rank of the pathway genes in the context of the full gene list. Accompanying heat maps present the normalized enrichment scores for individual genes within the gene set [blue = downregulation, red = upregulation, gray = not significant (FDR > 0.1)].