Table S2. Transcriptional Regulators, Kinases and Phosphatases that Affect Amino Acid Metabolism. Related to Figure 3 B-C.

amino acid	transcriptional regulator (number)	kinase (number)	phosphatase (number)	total No
alanine	*ADA2 GAT1 GCR2 HAP5 HMO1 HOT1 LEU3 MOT2 RGT1 SPT10 USV1 YRR1* **(12)**	*ADK1 BUB1 CLB2 DBF2 ELM1 FAB1 GIN4 MCK1 PCL7 PHO80 PHO85 SKY1 TCO89 VIP1* **(14)**	*OCA1 PTC6 SAP155* **(3)**	29
aspartate	*HAP5 HIR2 IXR1 MOT2 SIR3 SPT10 UME6 XBP1* **(8)**	*MCK1 PHO80 SCH9 SLT2 SPS1 VIP1* **(6)**	*OCA1 PTC1 SIT4* **(3)**	17
glutamate	*GCR2 GLN3 NRG1 RGT1 SPT10 YRR1* **(6)**	*ADK1 DBF2 ELM1 FAB1 KIN4 MRK1 NPR1 SKM1* **(8)**	*OCA1 SAP155 SIT4* **(3)**	17
phenylalanine	*SPT10 YRR1* **(2)**	*CTK3 PHO85 VIP1* **(3)**	*SIT4* **(1)**	6
glycine	*SKO1 SNF2 SOK2 TYE7 YRR1* **(5)**	*FRK1 PHO80 SSN3* **(3)**	*OCA1* **(1)**	9
histidine	*PHO2 YRR1* **(2)**	*CGI121 FAB1 SSN8 TCO89* **(4)**	*SIT4* **(1)**	7
isoleucine	*AFT1 SFL1 SPT10 SWI6 YRR1* **(5)**	*YGK3* **(1)**	*OCA1 PTC6* **(2)**	8
lysine	*ADA2 CIN5 HIR2 LYS14 PHO2 SFL1 SFP1 SIR2 SNF2 ZAP1* **(10)**	*ADK1 MRK1 PHO85 SSN8* **(4)**	*OCA1 SIT4* **(2)**	16
leucine	*YRR1* **(1)**			1
methionine	*AFT1 MIG1 MOT2 SFP1 SPT10 YRR1* **(6)**	*ADK1* **(1)**	*SIT4* **(1)**	8
asparagine	*CIN5 GLN3 HAP2 HAP5 LYS14 SFP1 UME6 YRR1* **(8)**	*ADK1 CKA2 FAB1 SCH9 TCO89 YCK3* **(6)**		14
proline	*AFT1 GCR2 GLN3 HMO1 LEU3 LYS14 SPT10 SWI6* **(8)**	*ADK1 CKA2 CTK3 FAB1 NPR1 PHO85 SCH9* **(7)**	*OCA1 SAP155* **(2)**	17
glutamine	*ADA2 GLN3 HAP2 HAP5 LEU3 SWI6 YRR1* **(7)**	*CKA2 PHO85 SCH9* **(3)**	*OCA1 PTC1* **(2)**	12
arginine	*AFT1 ARG81 DOT6 LEU3 LYS14 PHO2 SWI6* **(7)**	*CGI121 MCK1 NPR1 PBS2 SCH9* **(5)**	*SIT4* **(1)**	13
serine	*CHA4 HMO1 IXR1 LEU3 LYS14 RPH1 SKO1 SNF2 SPT2 USV1 YRR1* **(11)**	*ADK1 ELM1 FAB1 PCL1 PCL5 PHO80 PRO1 SKY1 SSN3 TCO89* **(10)**	*OCA1 PTC1* **(2)**	23
threonine	*ADR1 DAL81 GZF3 HOT1 SIR2 SNF2 SPT10 UME6 YRR1* **(9)**	*ADK1 CKA2 CTK3 FAB1 PHO80 YGK3* **(6)**	*PTC1 SAP4* **(2)**	17
valine	*AFT1 AFT2 DAL81 LEU3 SNF2 SPT10* **(6)**	*FAB1 FRK1 PKH2 PRO1 TCO89* **(5)**	*OCA1 PTC1 PTC6* **(3)**	14
tryptophan	*GCN4 LYS14 SUM1 YRR1* **(4)**	*VIP1* **(1)**		5
tyrosine	*AFT1 ASH1 LEU3 LYS14 MAC1 MOT2 PHO2 SNF2 SPT10 SUM1 ZAP1* **(11)**	*ADK1 PBS2 PHO85 PRO1 SSN8 TCO89 VIP1* **(7)**	*OCA1 PTC1 SIT4* **(3)**	21

Table S4. Assignment of strains to batches. Related to STAR Methods.

batch 1	batch 2	batch 3	batch 4	batch 5	batch 6	batch 7	batch 8	batch 9	batch 10	batch 11
43	23	16	38	25	13	21	27	17	32	26
28	7	31	20	5	9	36	8	14	42	4
41	1	37	11	12	29	19	10	18	34	30
15	44	24	22	6	40	3	35	2	33	39
		B	C	47	45	G	E	D	A	46
		49	74	71&F	70	72	48	50	51&73	75

Table S5. Details for the analytical method to determine amino acids levels by LC-MS/MS; SRM transitions. Related to STAR Methods.

amino acid	compound abbreviation	SRM transition	fragmentor (V)	collision energy (V)	retention time (min)	external calibration
alanine	A	90 > 44.1	50	8	1.87	linear
arginine	R	175.1 > 70	100	15	2.37	power
asparagine	N	133.1 > 74	80	9	2.12	linear
aspartate	D	134.1 > 74	80	10	2.24	linear
glutamate	E	148.1 > 84.1	75	10	2.09	power
glutamine	Q	147.1 > 84	50	16	2.07	power
glycine	G	76 > 30.1	50	5	1.98	linear
histidine	H	156.1 > 110.2	80	12	2.36	power
isoleucine	I	132.1 > 86	80	8	1.33	power
leucine	L	132.1 > 86	80	8	1.24	power
lysine	K	147.1 > 84	50	16	2.41	power
methionine	M	150.1 > 104	40	8	1.47	linear
phenylalanine	F	166.1 > 120	100	9	1.23	power
proline	P	116.1 > 70.1	100	13	1.60	power
serine	S	106 > 60	40	9	2.10	power
threonine	T	120.1 > 74	80	9	1.96	power
tryptophane	W	205.1 > 188	85	5	1.29	linear
tyrosine	Y	182 > 165	90	5	1.64	power
valine	V	118.1 > 71.9	100	10	1.57	power