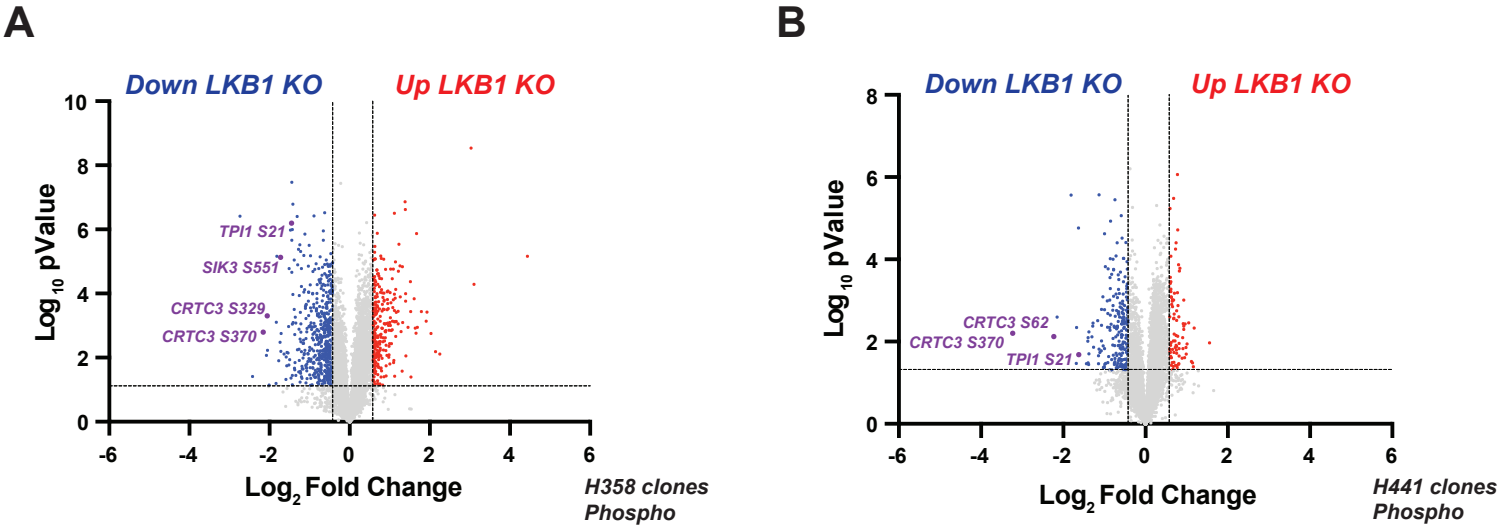
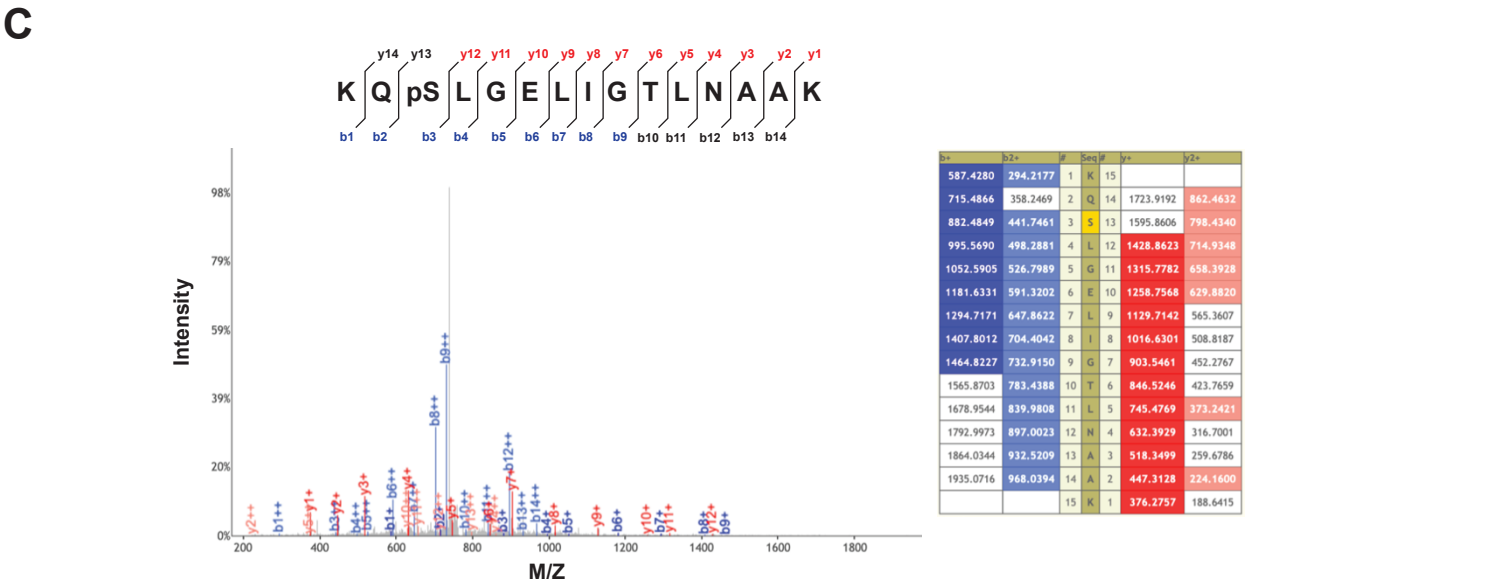
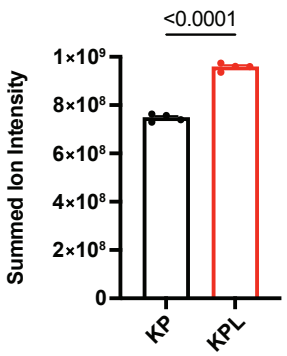




b+	b2+	#	Seq	#	y+	y2+
587.4280	294.2177	1	K	15		
715.4866	358.2469	2	Q	14	1723.9192	862.4632
882.4849	441.7461	3	S	13	1595.8606	798.4340
995.5690	498.2881	4	L	12	1428.8623	714.9348
1052.5905	526.7989	5	G	11	1315.7782	658.3928
1181.6331	591.3202	6	E	10	1258.7568	629.8820
1294.7171	647.8622	7	L	9	1129.7142	565.3607
1407.8012	704.4042	8	I	8	1016.6301	508.8187
1464.8227	732.9150	9	G	7	903.5461	452.2767
1565.8703	783.4388	10	T	6	846.5246	423.7659
1678.9544	839.9808	11	L	5	745.4769	373.2421
1792.9973	897.0023	12	N	4	632.3929	316.7001
1864.0344	932.5209	13	A	3	518.3499	259.6786
1935.0716	968.0394	14	A	2	447.3128	224.1600
		15	K	1	376.2757	188.6415



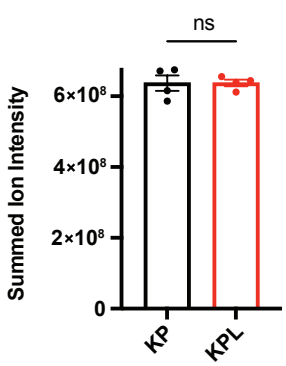


Figure S2

Figure S2. Phosphorylation of human TPI1 is LKB1-dependent.
(A and **B)** Volcano plots for comparison of phospho-peptides enriched from lysates of H358 and H441 isogenic cells respectively with and without LKB1 [2 KP clones (H358: sgNT1.4 and sgNT1.6; H441: sgNT1.2 and sgNT1.4) and 2 KPL clones (H358: sgLKB1-2.1 and sgLKB1-3.2. H441: sgLKB1-2.2 and sgLKB1-3.3) with 2 biological replicates for each cell line, N=4 per genotype]. Cells were grown in 0.5 mM glucose for 6 hours before lysis. Phospho-peptides that pass statistical criteria (p-value <0.05) are highlighted in black, red, and blue, peptides that do not satisfy this criterion are colored grey. Phospho-peptides highlighted in red satisfy a fold-change threshold (>1.5) upon LKB1 deletion; those highlighted in blue satisfy the fold change threshold (<-1.5) upon LKB1 deletion. **(C)** Representative MS/MS spectrum for phospho-peptide of TPI1 containing Ser21. Mapped b+ and y+ ions labeled with blue and red respectively in the spectrum and corresponding mass/charge peeks listed in table format. Cartoon above shows predicted peptide fragmentation with identified b+ and y+ colored blue and red, respectively. **(D** and **E)** Bar graphs for TPI1 protein expression of summed ion intensities for TPI1 protein expression from companion unenriched total proteomic analyses. Cell-lines treated with 0.5 mM glucose for 6 hr prior to collection. Data presented are representative of 4 independent biological experiments and reported as the mean (-/+s.e.m.). Statistical significance determined by two-tailed paired t-test.