

## Supplementary Data

SUPPLEMENTARY TABLE 1. GENES WITH  $\geq 2$ -FOLD CHANGE FROM BASELINE TO 6 H POST -SRC

<i>Gene Symbol</i>	<i>Gene title</i>	<i>Fold change</i>	<i>FDR-corrected p value</i>
<i>PDK4</i>	Pyruvate dehydrogenase kinase, isozyme 4	3.12	0.0001
<i>MIR21</i>	MicroRNA 21	2.68	0.0003
<i>FAM198B</i>	Family with sequence similarity 198, member B	2.22	0.0007
<i>PTPRO</i>	Protein tyrosine phosphatase, receptor type, O	2.21	0.0003
<i>ADAMTS5</i>	ADAM metallopeptidase with thrombospondin type 1 motif, 5	2.18	0.0002
<i>SLITRK4</i>	SLIT and NTRK-like family, member 4	2.17	<0.0001
<i>FOLR3</i>	Folate receptor 3 (gamma)	2.06	0.0002
<i>STEAP4</i>	STEAP family member 4	2.01	0.0002
<i>MBNL2</i>	Muscleblind-like 2 (Drosophila)	-2.06	0.0001
<i>SPON2</i>	Spondin 2, extracellular matrix protein	-2.06	0.0006
<i>GZMB</i>	Granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	-2.07	0.0001
<i>KLF12</i>	Kruppel-like factor 12	-2.07	0.0005
<i>SYNE2</i>	Spectrin repeat containing, nuclear envelope 2	-2.08	0.0004
<i>GZMH</i>	Granzyme H (cathepsin G-like 2, protein h-CCPX)	-2.10	0.0004
<i>MYBL1</i>	V-myb myeloblastosis viral oncogene homolog (avian)-like 1	-2.15	0.0002
<i>ZNF831</i>	Zinc finger protein 831	-2.21	0.0009
<i>CDC14A</i>	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-2.22	0.0006
<i>TARP</i>	TCR gamma alternate reading frame protein	-2.24	0.0012
<i>GATA3</i>	GATA binding protein 3	-2.29	0.0009
<i>TARP /TRGC2</i>	TCR gamma alternate reading frame protein /T cell receptor gamma constant 2	-2.31	0.0009
<i>CD96</i>	CD96 molecule	-2.32	0.0006
<i>PER1</i>	Period homolog 1 (Drosophila)	-2.35	0.0002
<i>MGAT4A</i>	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	-2.54	0.0005
<i>RORA</i>	RAR-related orphan receptor A	-2.69	0.0002
<i>CCL4</i>	Chemokine (C-C motif) ligand 4	-3.39	0.0004

SRC, sports-related concussion; FDR, false discovery rate.