

Table S1 Hub gene in the black module

Gene	GS	MM	Spearman correlation coefficient	P.val	P.adj
<i>ARRB2</i>	-0.58442	0.888651	-0.365	0.006	0.222
<i>CD68</i>	-0.35426	0.872196	-0.297	0.026	0.369
<i>CTSB</i>	-0.43065	0.862218	-0.29	0.03	0.369
<i>FCER1G</i>	-0.47179	0.855662	-0.274	0.041	0.369
<i>G6PD</i>	-0.58611	0.864425	-0.239	0.076	0.369
<i>LAIR1</i>	-0.38299	0.85962	-0.264	0.049	0.369
<i>TKT</i>	-0.50982	0.833433	-0.255	0.058	0.369
<i>TRPC1</i>	0.537579	-0.80247	0.245	0.069	0.369
<i>ADAP2</i>	-0.52754	0.826758	-0.201	0.138	0.475
<i>GBGT1</i>	-0.45369	0.806934	-0.181	0.183	0.475
<i>ITGAX</i>	-0.39333	0.805234	-0.208	0.124	0.475
<i>PGD</i>	-0.62815	0.869171	-0.203	0.134	0.475
<i>PIK3AP1</i>	-0.46572	0.810135	-0.185	0.173	0.475
<i>PKM</i>	-0.43334	0.840774	-0.196	0.149	0.475
<i>STXBP2</i>	-0.53182	0.848441	-0.185	0.172	0.475
<i>IFI30</i>	-0.2682	0.823608	-0.157	0.248	0.57
<i>LIMK1</i>	-0.25766	0.810733	-0.152	0.263	0.57
<i>SPI1</i>	-0.48211	0.843326	-0.154	0.256	0.57
<i>COLGALT1</i>	-0.33104	0.873574	-0.146	0.282	0.579
<i>NCKAP1L</i>	-0.31435	0.864211	-0.126	0.354	0.658
<i>NLRC4</i>	-0.63074	0.803129	-0.13	0.339	0.658
<i>CD53</i>	-0.49556	0.826321	-0.108	0.427	0.758
<i>APBB1IP</i>	-0.63169	0.839587	-0.089	0.515	0.769
<i>DOCK2</i>	-0.2554	0.804507	-0.085	0.532	0.769
<i>FKBP15</i>	-0.50056	0.845252	-0.099	0.47	0.769
<i>NCF2</i>	-0.46581	0.809243	-0.092	0.5	0.769
<i>PTPN6</i>	-0.38979	0.849464	-0.093	0.497	0.769
<i>CTSD</i>	-0.28275	0.807227	-0.076	0.576	0.775
<i>ITGAM</i>	-0.62322	0.815394	-0.079	0.56	0.775
<i>NCF4</i>	-0.59108	0.803119	0.066	0.627	0.788
<i>TWF2</i>	-0.34806	0.826502	-0.069	0.613	0.788
<i>CYBB</i>	-0.39194	0.800834	0.058	0.673	0.795
<i>SHKBP1</i>	-0.57217	0.834223	-0.06	0.662	0.795
<i>MYO1F</i>	-0.55671	0.832104	-0.051	0.709	0.813
<i>ATP6V0D1</i>	-0.35684	0.82852	-0.032	0.816	0.896
<i>SIGLEC9</i>	-0.57612	0.810031	-0.03	0.827	0.896
<i>ACP2</i>	-0.48028	0.828447	-0.004	0.979	0.979
<i>ITGB2</i>	-0.44128	0.848766	0.011	0.938	0.979
<i>SYK</i>	-0.45454	0.874867	-0.005	0.972	0.979

Genes in black module with MM >0.8, GS >0.2. Spearman correlation calculated the correlation coefficient between gene expression and mPAP. FDR was used for multiple testing correction. MM, module membership; GS, gene significance; mPAP, mean pulmonary artery pressure; FDR, false discovery rate.