Supplementary Materials

Table S1. Proteins including each node in Fig. 1(C) and Fig. 1(D).

#	GO Term	% Associated	# of Copos	Associated Genes Found
1	alpha-beta T cell activation involved in	4.347826	3	[IFNG, IL2, IL6]
2	alpha-beta T cell differentiation involved	4.347826	3	[IFNG, IL2, IL6]
3	CD4-positive, alpha-beta T cell differentiation involved in immune	4.411765	3	[IFNG, IL2, IL6]
4	negative regulation of cytokine biosynthetic process	8.333333	3	[IL10, IL6, INHBB]
5	negative regulation of response to drug	6	3	[IL10, IL6, MET]
6	cell death in response to hydrogen peroxide	5.555555	3	[IL10, IL6, MET]
7	regulation of hydrogen peroxide-induced cell death	6	3	[IL10, IL6, MET]
8	regulation of response to reactive oxygen species	4.918033	3	[IL10, IL6, MET]
9	negative regulation of hydrogen peroxide- induced cell death	8.333333	3	[IL10, IL6, MET]
10	negative regulation of cellular response to drug	8.333333	3	[IL10, IL6, MET]
11	regulation of cellular response to drug	5.454545	3	[IL10, IL6, MET]
12	negative regulation of cellular response to oxidative stress	4	3	[IL10, IL6, MET]
13	negative regulation of response to reactive oxygen species	8.333333	3	[IL10, IL6, MET]
14	negative regulation of oxidative stress- induced cell death	4	3	[IL10, IL6, MET]
15	cytokine activity	4.642857	13	[BMP2, CXCL1, CXCL8, EML2, GDF1, GDF3, IFNG, IL10, IL2, IL6, INHBB, MSTN, TNFSF8]
16	growth factor activity	4.878049	10	[BMP2, CXCL1, FGF19, GDF1, GDF3, IL10, IL2, IL6, INHBB, MSTN]
17	regulation of pathway-restricted SMAD protein phosphorylation	9.459459	7	[ACVR1, ACVR2A, BMP2, GDF1, GDF3, INHBB, MSTN]
18	positive regulation of osteoblast differentiation	6.756757	5	[ACVR1, ACVR2A, ACVR2B, BMP2, IL6]
19	positive regulation of pathway-restricted SMAD protein phosphorylation	12.5	7	[ACVR1, ACVR2A, BMP2, GDF1, GDF3, INHBB, MSTN]
20	pathway-restricted SMAD protein phosphorylation	9.090909	7	[ACVR1, ACVR2A, BMP2, GDF1, GDF3, INHBB, MSTN]
21	SMAD protein signal transduction	4.854369	5	[BMP2, GDF1, GDF3, INHBB, MSTN]
22	positive regulation of epithelial to mesenchymal transition	5.357143	3	[ACVR1, BMP2, IL6]
23	activin receptor signaling pathway	6.060606	4	[ACVR1, ACVR2A, ACVR2B, INHBB]

24	positive regulation of bone mineralization	8	4	[ACVR1, ACVR2A,
				ACVR2B, BMP2]
25	positive regulation of transmembrane	5.797101	8	[ACVR1, ACVR2A,
	receptor protein serine/threonine kinase			ACVR2B, BMP2, GDF1,
	signaling pathway			GDF3, INHBB, MSTN]
26	positive regulation of ossification	4.716981	5	[ACVR1, ACVR2A,
				ACVR2B, BMP2, IL6]
27	activin-activated receptor activity	33.33333	3	[ACVR1, ACVR2A,
				ACVR2B]
28	regulation of activin receptor signaling	6.976744	3	[ACVR1, ACVR2A,
	pathway			ACVR2B]
29	regulation of bone mineralization	4.210526	4	[ACVR1, ACVR2A,
				ACVR2B, BMP2]
30	positive regulation of biomineral tissue	6.666667	4	[ACVR1, ACVR2A,
	development			ACVR2B, BMP2]
31	gastrulation with mouth forming second	12.12121	4	[ACVR1, ACVR2A,
				ACVR2B, GDF3]
32	transforming growth factor beta-activated	18.75	3	[ACVR1, ACVR2A,
	receptor activity			ACVR2B]
33	transmembrane receptor protein	15.78947	3	[ACVR1, ACVR2A,
	serine/threonine kinase activity			ACVR2B]