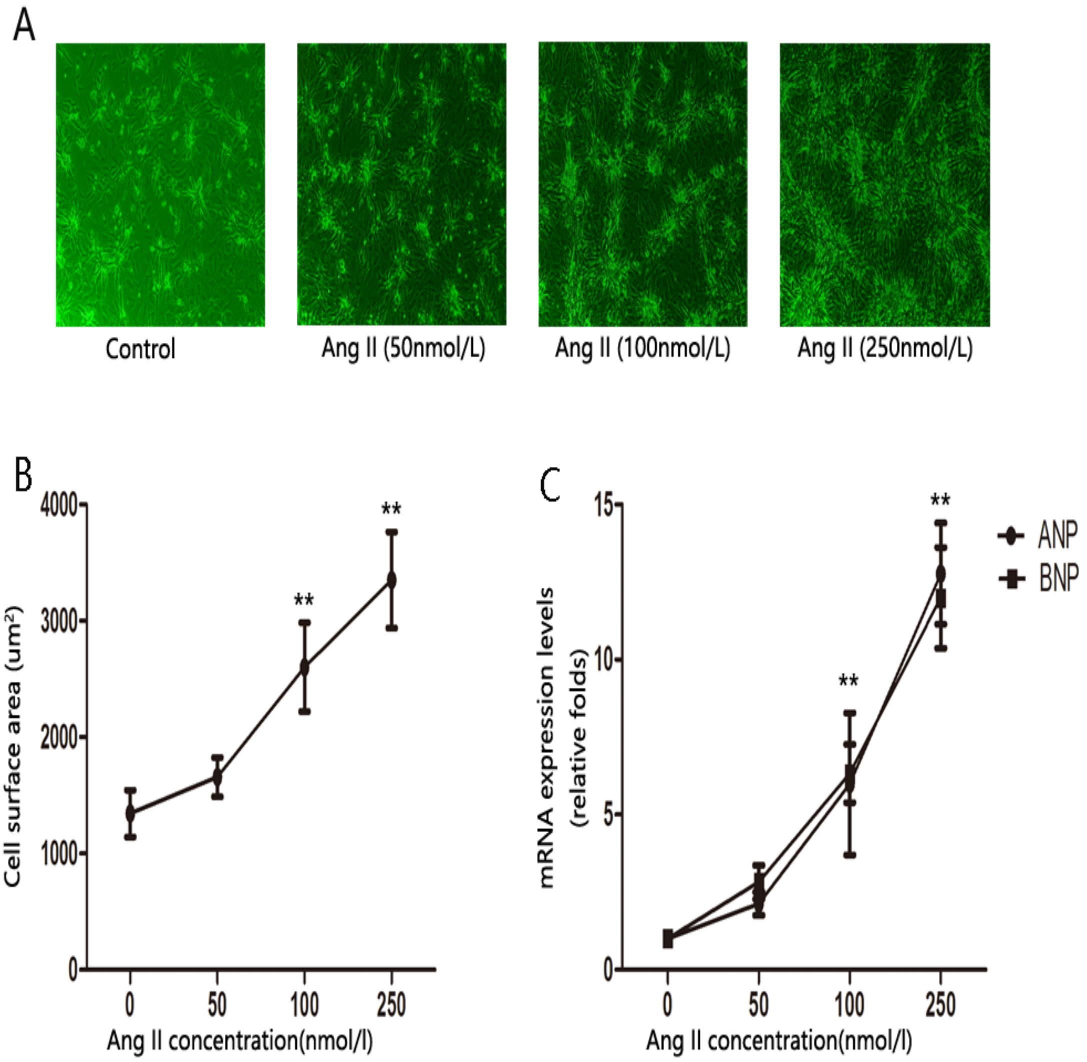

Fig.S1. Ang II-induced cardiomyocyte hypertrophy in a concentration-dependent manner. (A) Microscope picture of myocardial cells. (B) Quantification of cell surface area**.** (C) ANF and BNP mRNA expression levels. Data are expressed as the mean ± SEM (n=3). $^{**}P<0.01$ versus control. ANF: atrial natriuretic factor, BNP: brain natriuretic peptide, Ang II: angiotensin II.

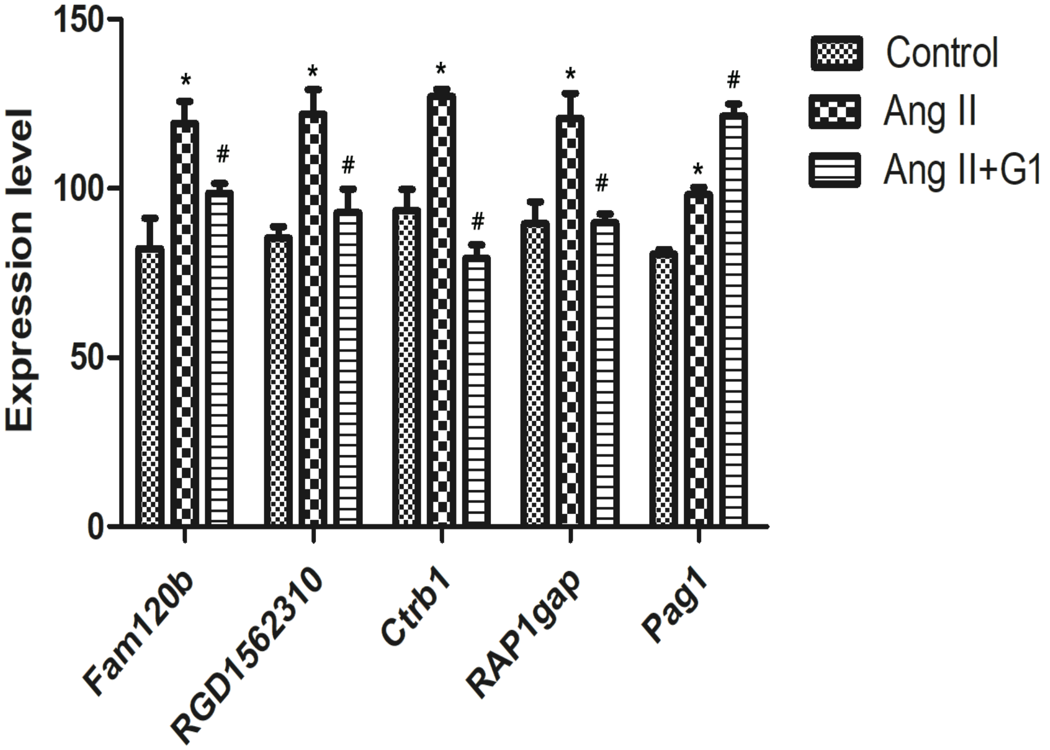

Fig.S2. The expression level of Fam120B, RGD1562310, Ctrb1, RAP1gap, and Pag1 in each group. Data are expressed as the mean±SEM (n=3). **P<0.01* versus control. $^{\#}$*P<0.01* versus Ang II. Ang II: angiotensin II.

Table S1. Summary results from GO analysis in G1 vs. vehicle treated cardiomyocytes

GO-ID	Term	Category	P-Value	%Diff	%Ref	Over/Under
GO:0009987	cellular process	P	0.118	97.222	87.343	OVER
GO:0044699	single-organism process	P	0.214	88.889	78.942	OVER
GO:0044464	cell part	C	0.096	86.111	92.390	UNDER
GO:0005623	cell	C	0.096	86.111	92.390	UNDER
GO:0005488	binding	F	0.796	86.111	87.193	UNDER
GO:0044763	single-organism cellular process	P	0.140	83.333	71.236	OVER
GO:0005622	intracellular	C	0.082	80.556	89.416	UNDER
GO:0044424	intracellular part	C	0.094	80.556	88.803	UNDER
GO:0005515	protein binding	F	0.842	80.556	76.650	OVER
GO:0043226	organelle	C	0.026	72.222	85.447	UNDER
GO:0065007	biological regulation	P	0.603	69.444	63.693	OVER
GO:0071704	organic substance metabolic process	P	0.860	69.444	66.735	OVER
GO:0005737	cytoplasm	C	0.344	66.667	73.118	UNDER
GO:0050794	regulation of cellular process	P	0.397	66.667	57.733	OVER
GO:0050789	regulation of biological process	P	0.608	66.667	60.597	OVER
GO:0043227	membrane-bounded organelle	C	0.018	63.889	80.005	UNDER
GO:0044238	primary metabolic process	P	0.863	63.889	64.416	UNDER
GO:0043229	intracellular organelle	C	0.005	61.111	80.346	UNDER
GO:0050896	response to stimulus	P	0.094	61.111	46.222	OVER
GO:0044237	cellular metabolic process	P	0.289	58.333	66.312	UNDER
GO:0044444	cytoplasmic part	C	0.732	58.333	61.320	UNDER
GO:0043170	macromolecule metabolic process	P	1.000	58.333	56.847	OVER
GO:0016020	membrane	C	0.617	55.556	49.973	OVER
GO:0044707	single-multicellular organism process	P	0.010	52.778	31.247	OVER
GO:0032501	multicellular organismal process	P	0.020	52.778	33.170	OVER
GO:0043231	intracellular membrane-bounded organelle	C	0.004	50.000	72.613	UNDER
GO:0007154	cell communication	P	0.050	50.000	33.306	OVER
GO:0051716	cellular response to stimulus	P	0.239	50.000	40.030	OVER
GO:0048583	regulation of response to stimulus	P	0.002	47.222	22.913	OVER
GO:0048519	negative regulation of biological process	P	0.026	47.222	29.105	OVER
GO:0007165	signal transduction	P	0.029	47.222	29.801	OVER
GO:0044767	single-organism developmental process	P	0.043	47.222	30.115	OVER
GO:0032502	developmental process	P	0.046	47.222	30.878	OVER
GO:0044700	single organism signaling	P	0.049	47.222	31.383	OVER

GO:0023052	signaling	P	0.071	47.222	31.547	OVER
GO:0048518	positive regulation of biological process	P	0.160	47.222	34.656	OVER
GO:0016043	cellular component organization	P	0.738	47.222	43.603	OVER
GO:0071840	cellular component organization or biogenesis	P	0.869	47.222	45.486	OVER
GO:0006807	nitrogen compound metabolic process	P	1.000	47.222	47.572	UNDER
GO:0048856	anatomical structure development	P	0.022	44.444	26.378	OVER
GO:0044260	cellular macromolecule metabolic process	P	0.315	44.444	53.410	UNDER
GO:1901576	organic substance biosynthetic process	P	0.499	44.444	38.734	OVER
GO:0009058	biosynthetic process	P	0.609	44.444	39.280	OVER
GO:0019222	regulation of metabolic process	P	0.734	44.444	40.194	OVER
GO:0044422	organelle part	C	0.004	41.667	64.785	UNDER
GO:0048731	system development	P	0.007	41.667	21.345	OVER
GO:0044446	intracellular organelle part	C	0.008	41.667	63.830	UNDER
GO:0007275	multicellular organismal development	P	0.019	41.667	24.004	OVER
GO:0048523	negative regulation of cellular process	P	0.059	41.667	26.773	OVER
GO:0019538	protein metabolic process	P	0.606	41.667	36.948	OVER

GO-ID: ID of GO term; Term: name of GO term; Category: categories of GO term; P: Biology Process; F: Molecular Function; C: Cellular Component; % Diff: the proportion of differential protein sets related to this pathway ; %Ref: the proportion of proteins associated with this pathway in all qualitative protein sets ; Over/Under: relative to the proportion of background proteins associated with the GO term.

Table S2. KEEG analysis results in G1 vs. vehicle treated cardiomyocytes

MapID	**MapName**	**%Diff**	**%Ref**	**P Value**	**Over/Under**
ko05200	Pathways in cancer	2.778	2.674	0.624	OVER
ko04151	PI3K-Akt signaling pathway	5.556	1.910	0.150	OVER
ko05010	Alzheimer's disease	5.556	1.883	0.147	OVER
ko05016	Huntington's disease	2.778	1.869	0.494	OVER
ko04510	Focal adhesion	5.556	1.596	0.112	OVER
ko05205	Proteoglycans in cancer	5.556	1.555	0.107	OVER
ko01200	Carbon metabolism	2.778	1.446	0.409	OVER
ko05012	Parkinson's disease	2.778	1.446	0.409	OVER
ko04932	Non-alcoholic fatty liver disease (NAFLD)	5.556	1.364	0.086	OVER
ko00190	Oxidative phosphorylation	2.778	1.364	0.391	OVER
ko04217	Necroptosis	2.778	1.214	0.357	OVER
ko04015	Rap1 signaling pathway	5.556	1.214	0.070	OVER
ko05206	MicroRNAs in cancer	2.778	1.187	0.350	OVER
ko05164	Influenza A	2.778	1.173	0.347	OVER
ko05418	Fluid shear stress and atherosclerosis	2.778	1.050	0.317	OVER
ko04145	Phagosome	2.778	1.010	0.307	OVER
ko04371	Apelin signaling pathway	5.556	0.969	0.047	OVER
ko01230	Biosynthesis of amino acids	2.778	0.955	0.293	OVER
ko04390	Hippo signaling pathway	2.778	0.955	0.293	OVER
ko04152	AMPK signaling pathway	2.778	0.941	0.289	OVER
ko04066	HIF-1 signaling pathway	2.778	0.928	0.286	OVER
ko05202	Transcriptional misregulation in cancer	2.778	0.900	0.278	OVER
ko04310	Wnt signaling pathway	2.778	0.832	0.260	OVER
ko00010	Glycolysis / Gluconeogenesis	2.778	0.819	0.257	OVER
ko05034	Alcoholism	2.778	0.778	0.246	OVER
ko04211	Longevity regulating pathway	2.778	0.696	0.223	OVER
ko04620	Toll-like receptor signaling pathway	2.778	0.587	0.191	OVER
ko04350	TGF-beta signaling pathway	2.778	0.573	0.187	OVER
ko04214	Apoptosis - fly	2.778	0.573	0.187	OVER
ko05414	Dilated cardiomyopathy	2.778	0.546	0.179	OVER
ko00520	Amino sugar and nucleotide sugar metabolism	2.778	0.546	0.179	OVER
ko04115	p53 signaling pathway	2.778	0.518	0.171	OVER
ko04260	Cardiac muscle contraction	2.778	0.505	0.167	OVER
ko05221	Acute myeloid leukemia	2.778	0.491	0.163	OVER
ko04512	ECM-receptor interaction	8.333	0.491	0.001	OVER
ko05410	Hypertrophic cardiomyopathy (HCM)	2.778	0.491	0.163	OVER
ko04920	Adipocytokine signaling pathway	2.778	0.464	0.154	OVER
ko04514	Cell adhesion molecules (CAMs)	5.556	0.437	0.011	OVER
ko03320	PPAR signaling pathway	5.556	0.423	0.010	OVER
ko05416	Viral myocarditis	2.778	0.409	0.138	OVER
ko00710	Carbon fixation in photosynthetic organisms	2.778	0.396	0.133	OVER

ko04623	Cytosolic DNA-sensing pathway	2.778	0.396	0.133	OVER
ko05322	Systemic lupus erythematosus	2.778	0.341	0.116	OVER
ko05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	2.778	0.341	0.116	OVER
ko04930	Type II diabetes mellitus	2.778	0.286	0.098	OVER
ko05219	Bladder cancer	2.778	0.259	0.089	OVER
ko05144	Malaria	5.556	0.246	0.003	OVER

Map ID: ID of KEGG pathway; %Diff: the proportion of differential protein sets related to this pathway; %Ref: the proportion of proteins associated with this pathway in all qualitative protein sets; Over/Under: relative to the proportion of background proteins associated with the GO term.