Electronic Supplementary Material (ESI) for Biomaterials Science.

Supporting information

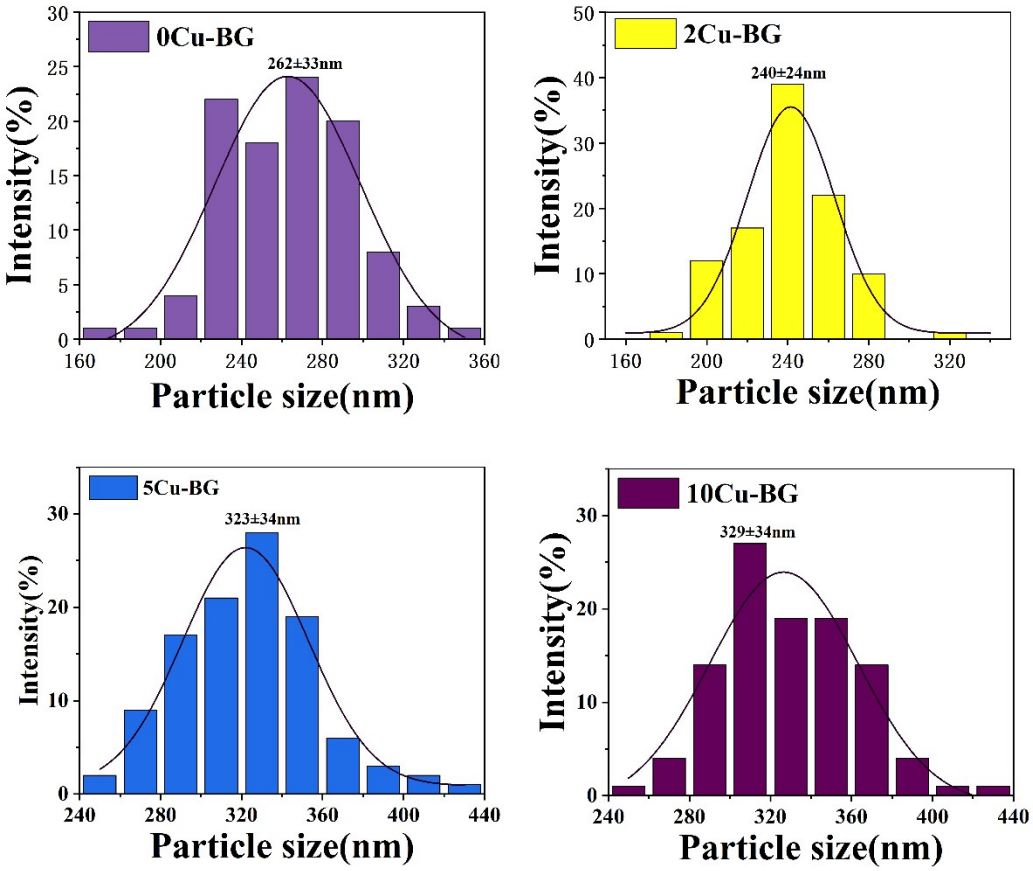

Figure S1. The particle size distribution of different Cu-BG groups.

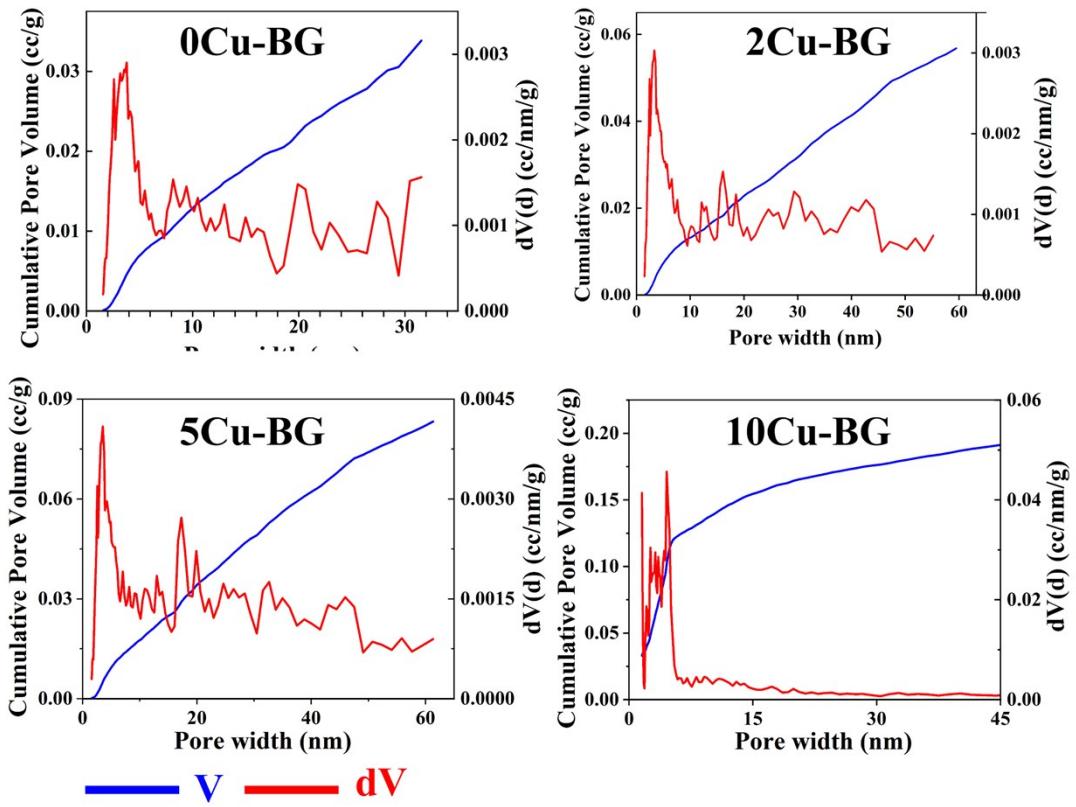

Figure S2. Pore Size Distribution of 0Cu-BG, 2Cu-BG, 5Cu-BG, 10Cu-BG calculated by DFT method.

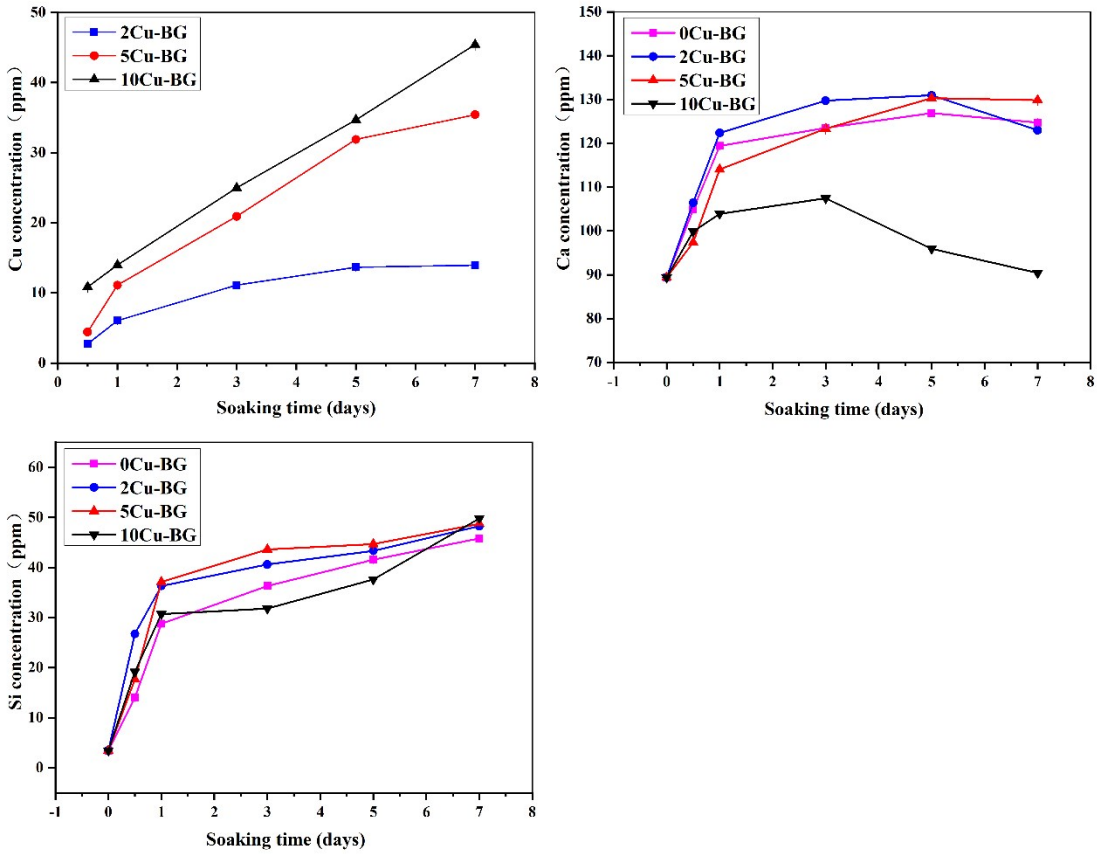

Figure S3. Cu-BG showed continuous release of Cu^{2+}, Ca^{2+} and SiO_4^{4-} ions.

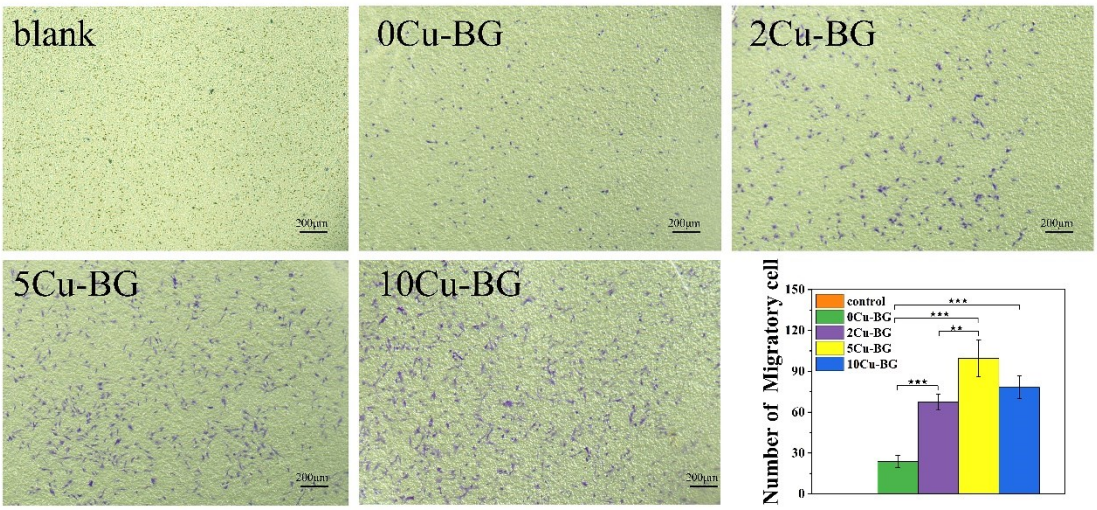

Figure S4. Cell migration and counting of hUVECs after crystal violet staining, scale bar=200 μm.

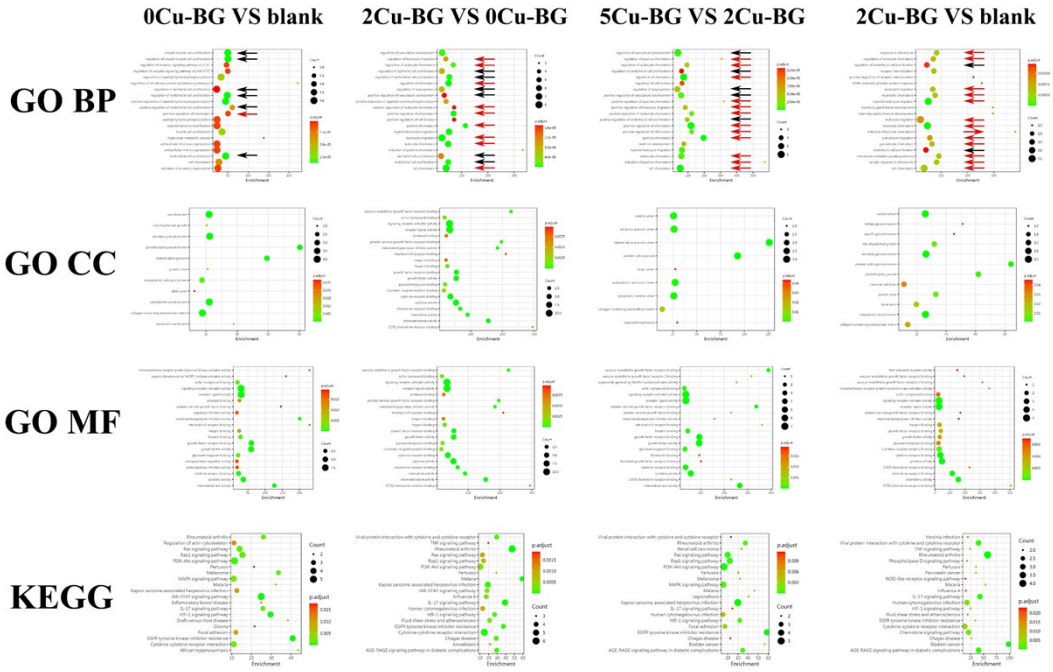

Figure S5. Cu-BG mediated the activation of hUVECs by HIF-1α and TNF-α pathways. Protein function annotation Gene Ontology (GO) and KEGG pathway were analyzed with R package "clusterProfiler". GO analysis included three subtypes: BP (biological process), MF (molecular function) and CC (cellular component). KEGG was systematic analysis of gene functions, linking genomic information with higher order functional information.

The raw data of gene enrichment analysis could be searched for free from the following URL:

file:///E:/%E6%96%87%E7%8C%AE%E5%8F%8A%E5%91%A8%E6%8A%A5/%E5%AE%9E%E9%AA%8C%E6%95%B0%E6%8D%AE/%E7%BB%86%E8%83%9E%E5%AE%9E%E9%AA%8C/%E5%86%85%E7%9A%AE%E7%BB%86%E8%83%9E%E5%88%86%E5%8C%96/wb/%E5%AE%9E%E9%AA%8C%E6%8A%A5%E5%91%8A/%E9%99%84%E4%BB%B61-4/%E9%99%84%E4%BB%B64-Data-Analysis-Report.html

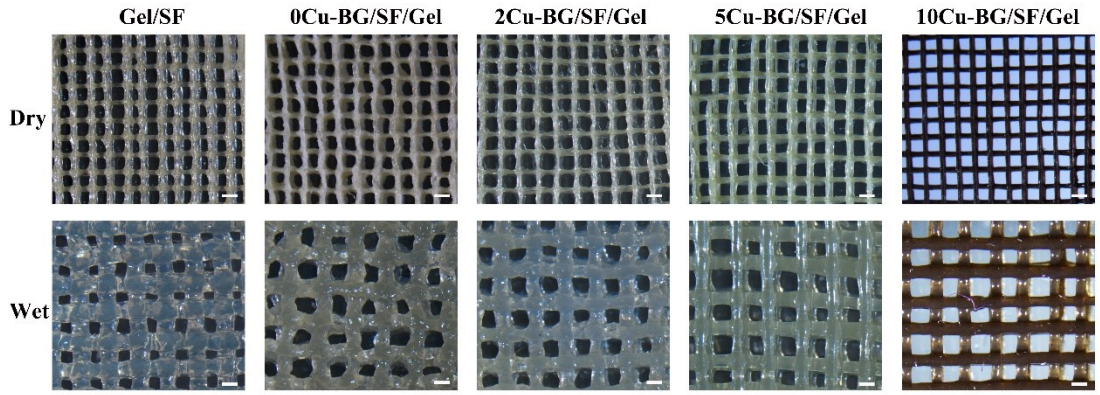

Figure S6. Gross morphology of different Gel/SF/Cu-BG scaffolds. Scale bar=500 μm.

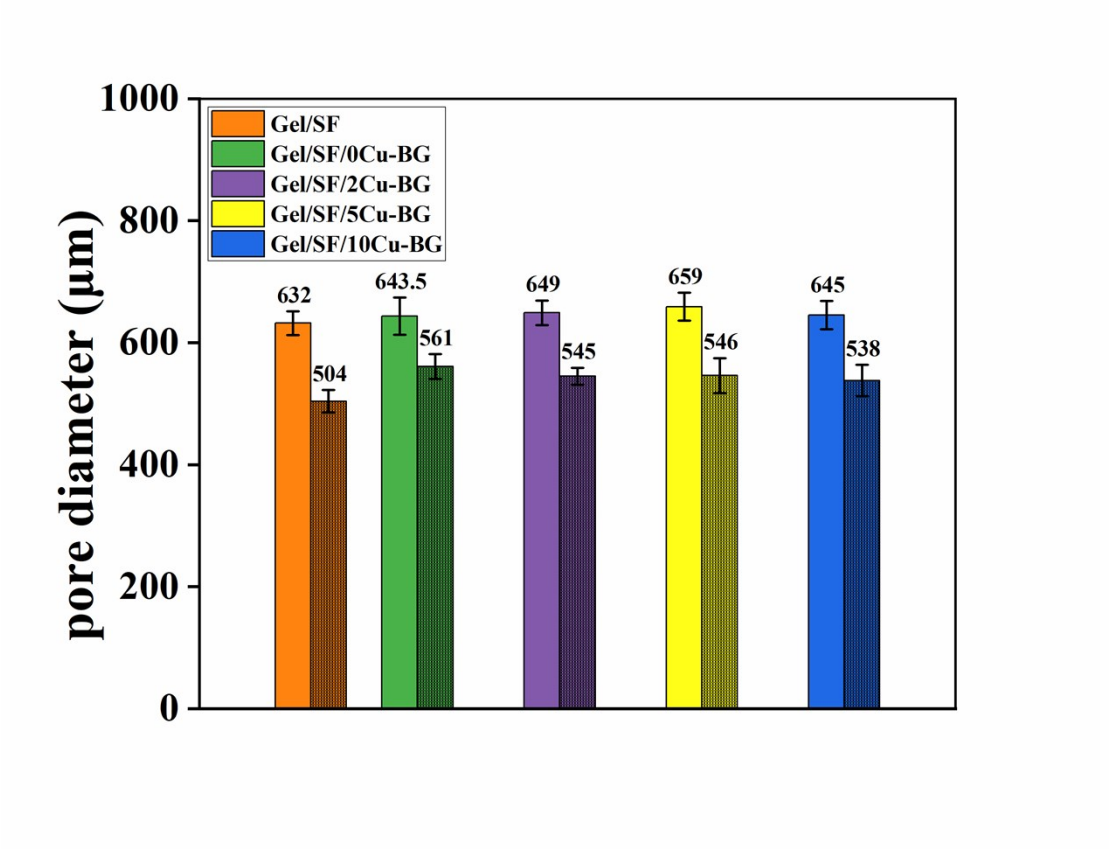

Figure S7. Gel/SF/Cu-BG scaffold of different groups showed average diameter of pore after lyophilization (light) and rehydration (dark).

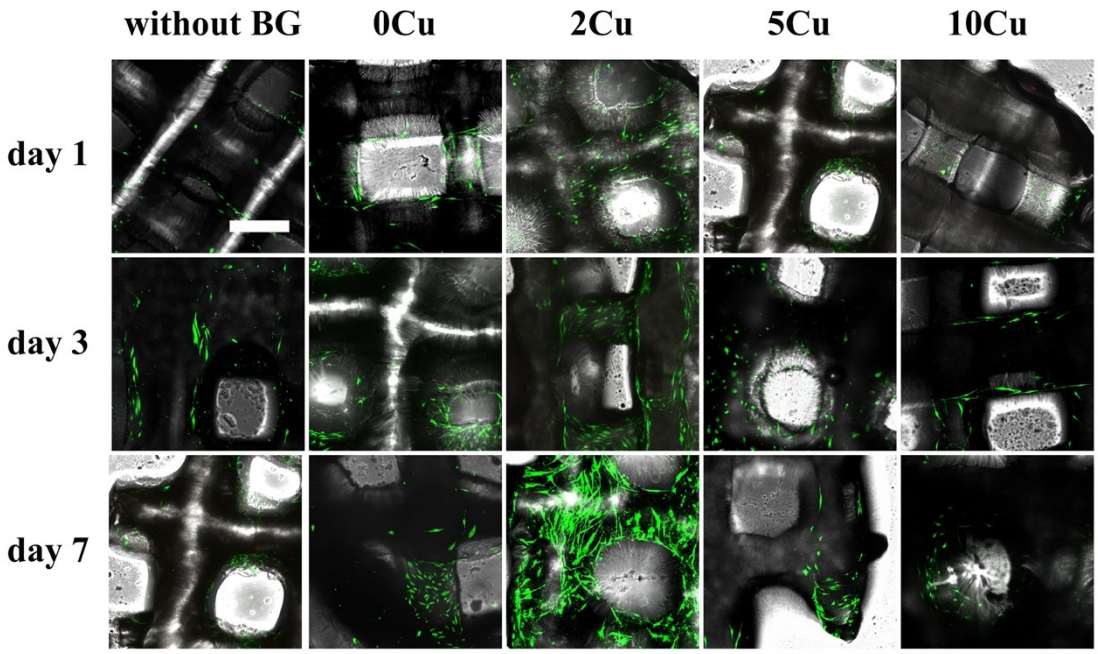

Figure S8. Proliferation and adhesion of BMSCs on Gel/SF/Cu-BG composite scaffold. Scale bar=500 μm.

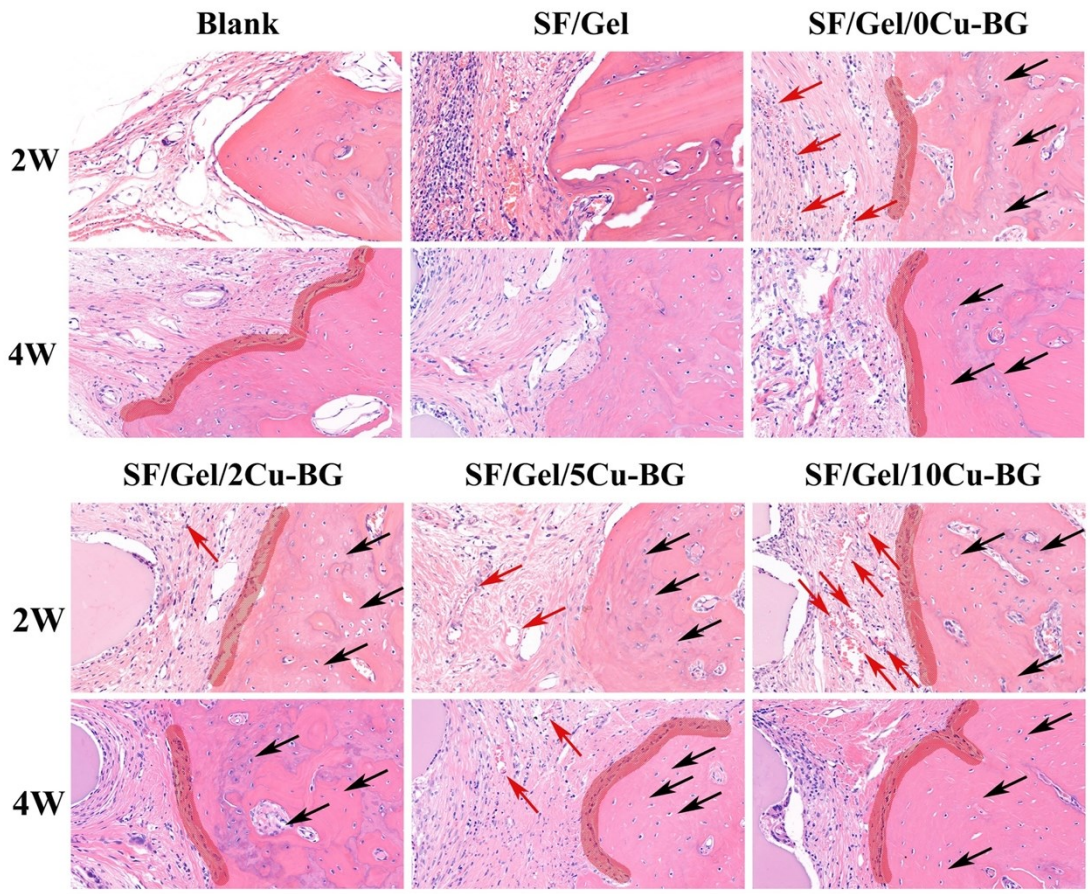

Figure S9. HE and Masson histological staining of Gel/SF/Cu-BG scaffold around tissues after implanted in the skull. Osteoblasts characterized by a monolayer arrangement were traced, blood vessels were marked with red arrows while mature bone cells were marked with black arrows. Scale bar=100 μm.

Table S1

Nucleotide sequences for real-time RT-PCR primers.

Genes	Forward primer (5'-3')	Reverse primer (5'-3')
GAPDH	GGAGTCCACTGGCGTCTTC	GCTGATGATCTTGAGGCTGTTG
HIF-1α	CAGAAGATACAAGTAGCCTC	CTGCTGGAATACTGTAACTG
VEGF	GGCAAAAACGAAAGCGCAAG	GAGGCTCCAGGGCATTAGAC
KDR	TACCTGGGGAGCTGACACTT	AGACTCAGCCCTGCAAATCC
eNOS	CTCCAGCCCCGGTACTACTC	TTAGCCACGTGGAGCAGACT
ANG	GTGCTGGGTCTGGGTCTGAC	GGCCTTGATGCTGCGCTTG
GAPDH	GTTCCTACCCCCAATGTGTCCC	TAGCCCAAGATGCCCTTCAGT
ALP	TGCCTACTTGTGTGGCGTGAA	TCACCCGAGTGGTAGTCACAATG
RUNX2	CACTGGCGGTGCAACAAGA	TTTCATAACAGCGGAGGCATTTC
OCN	AGCAGCTTGGCCCAGACCTA	TAGCGCCGGAGTCTGTTCACTAC
OPN	TGCAAACACCGTTGTAACCAAAAG C	TGCAGTGGCCGTTTGCATTTCT
Col I	ATGCCGCGACCTCAAGATG	TGAGGCACAGACGGCTGAGTA