Table S1. Age-matching of bone marrow donor cohorts

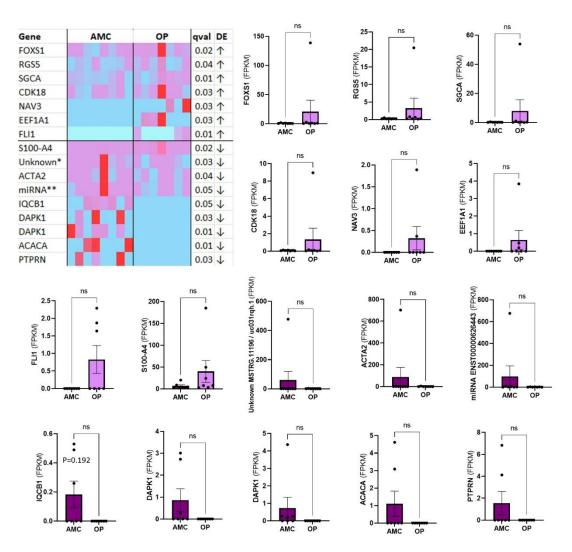| Parameter	RNAseq		Proliferation		CFU-F		CFU-O		Alizarin		OilRedO	
	AMC	OP	AMC	OP	AMC	OP	AMC	OP	AMC	OP	AMC	OP
Mean	66	79	70	80	75	80	75	80	71	78	70	74
n	7	7	7	6	18	6	12	5	6	4	8	9
SD	5.0	4.8	1.7	3.9	6	7	4	7	8	10	5	8
SEM	1.9	1.8	0.6	1.6	1.4	2.7	1.2	3.3	3	5	1.8	2.6
t test	$P = 0.001$		$P = 0.001$ (Welch's)		$P = 0.125$		$P = 0.105$		$P = 0.492$		$P = 0.172$	

Figure S1. Genes with high fold change but lack of statistical significance between people with and without osteoporosis. Heatmap and corresponding scatter plots of the 16 genes originally defined as differentially expressed (based on analysis of fold change $q < 0.05$), but that were subsequently identified as having no significant difference ($P > 0.05$) using individual t test/Mann-Whitney of fragments per kilobase of transcript per million reads. Statistical tests were performed with and without outliers where appropriate (ROUT, $Q = 1\%$) and no statistically significant inter-group difference in expression was observed. Differential expression was assessed between MSCs from

people living with osteoporosis and AMC donors without osteoporosis. The inappropriate categorisation of differentially expressed genes in the initial analysis was resultant from the disproportionate contribution of outliers to the intergroup fold-change values. * Unknown protein MSTRG.11196/uc031rqh.1; ** miRNA ENST00000626443/uc062hej.1/ENSG00000281814/AC090950.1-201