Supplementary Figure Legends

<u>Supplementary Figure 1: Immunophenotyping of BMT and tumor cells reveals</u> <u>mesenchymal/osteoblastic identity.</u>

(A) Flow cytometry analysis (histogram) of directly collected and/or cultured BM from a Cre- mouse (Cre-Direct BM), tumor (Direct DKOT/Cult DKOT) and paired BM cells (Direct DKO BMT/Cult DKO BMT) collected from DKO mouse demonstrating the expression of mesenchymal (Sca-1 and CD29) vs. hematopoietic (CD45.2) markers in tdTomato positive cells; representative experiment. (**Bi, Bii**) A bar graph demonstrating the percentage of hematopoietic and mesenchymal population in direct and cultured BMT and tumor cells respectively (n=3). (**C**) mRNA levels of osteoblast markers in DKO BMT and tumor (DKOT) cells vs WT BM (Cre+ WT BM) cells (n=3) (**p-value<0.01, ***p-value <0.001, ****p-value<0.0001, ns: not significant). (**D**) Alizarin Red Staining demonstrating calcium deposition during osteoblast differentiation of tumor, BMT and yBM cells. (**E**) mRNA levels of osteoblast differentiation markers of tumor, BMT and yBM cells. US: Unstained, S: Stained, **Direct**: Directly collected BM before culturing, **Cult**: Cultured.

<u>Supplementary Figure 2: young BM (yBM)-derived cells are of</u> mesenchymal/osteoblastic identity and exhibit metastatic ability.

(A) Flow cytometry analysis (histogram) of directly collected and/or cultured BM from a Cre negative mouse (Cre-BM-2m), young BM (DKO-Direct BM-2m) demonstrating the expression of mesenchymal (Sca-1 and CD29) vs. hematopoietic (CD45.2) markers in tdTomato positive cells; representative experiment. (B) A bar graph demonstrating the percentage of hematopoietic and mesenchymal population in direct and cultured yBM cells (n=3). (C) mRNA levels of osteoblast markers in yBM and WT BM cells (Cre+WT BM). (** p-value< 0.01, ****p-value<0.0001). (D) Wound healing assay-migration. Time plot representing the Relative Wound Density of yBM, BMT and tumor cells (n=3). (F) Wound healing assay-invasion. Time plot representing the Relative Wound Density of yBM, BMT and tumor cells (n=3). US: Unstained, S: Stained, Direct: Directly collected BM before culturing, Cult: Cultured.

Supplementary Figure 3: Early Genes Contributing to Osteosarcomagenesis.

(A) Heat map of the 303 mutual genes between vBM and tumor cells represented in the venn diagram in Fig 5B. (B) Heat map of the DE genes between yBM (n=6) and BMT (n=3) compared to the control BM cells (n=4). (C) Venn diagram analysis of yBM SKO and Tumor DKO (Tum-DKO) representing the common and unique genes between them-upper panel, Bar graph representing the significant pathways (Myc Targets) unique for DKO tumor cells compared to SKO yBM cells-lower panel. (D) Venn diagram analysis of yBM SKO and BMT DKO, representing the common and unique genes between them-upper panel, Bar graph representing the significant pathways (Myc Targets) unique for DKO BMT cells compared to SKO yBM cells-lower panel. (E) Venn diagram analysis of SKO yBM and SKO tumor cells representing the common and unique genes between them-upper panel. Bar graph representing the significant pathways (Myc Targets) unique for SKO tumor cells compared to SKO yBM cells-lower panel. (F) Venn diagram analysis of SKO and DKO tumor cells representing the common and unique genes between them-upper panel, Bar graph representing the significant pathways (Myc Targets) mutual between DKO and SKO tumor cells-lower panel. (G) Heat map of the 40 Myc target genes that are upregulated in yBM, and tumor cells compared to control cells. (H) Heat map of the 39 Myc target genes that are upregulated in yBM and BMT cells compared to control cells.

Supplementary Figure 4: Generation of a traceable mouse model of SKO-p53 osteosarcoma cell.

(A) Schematic illustration of the experimental SKO-p53 OS mouse model. (B) Genomic PCR of Cre negative (Cre-), Cre positive (Cre+ WT) and Single knock out (SKO^{TOM}) and Double knock out (DKO^{TOM}) mice. Labels in the left panel represent the primer pairs and in the right panel represent the expected band size. (C) Immunoblotting of WWOX, p53 and tdTomato in the SKO BM, DKO BM cells before (0 min) and after (30, 120 min) of ionizing radiation exposure (IR-10Gy). PC-(positive control)-HEPG2 cells treated with nutlin (MDM2-inhibitor). (D) Summary graph of flow cytometry analysis of the percentage of tdTomato positive cells in DKO BM, SKO BM and wild type BM cells (Cre+WT BM) at different ages. (E) A bar graph demonstrating the percentage of hematopoietic and mesenchymal population in direct and cultured

yBM SKO cells (n=3). **(F)** Flow cytometry analysis (histogram) of directly collected and cultured BM from a yBM-SKO demonstrating the expression of mesenchymal (Sca-1 and CD29) vs. hematopoietic (CD45.2) markers in tdTomato positive cells; representative experiment. **WT**: Wildtype, **SKO**: Single Knock Out, **DKO**: Double Knock Out, **BM**: Bone Marrow.

<u>Supplementary Figure 5: MCM7 upregulation in DKO yBM cells promotes their</u> <u>tumorigenicity.</u>

(A) Representative images of the OS tumors developed in NOD/SCID mice after intratibial (IT) injection of DKO-yBM cells compared to SKO-yBM-upper panel, H&E of the developed tumors-lower panel. Histological validation indicates OS characteristics. (B) Bar graph representing the percentage of immunocompromised mice that developed OS after IT injection of SKO and DKO yBM cells. (C) Color coded heatmap of normalized expression (TPM) of top 100 genes harbouring the highest Myc enrichment at promoters. (D) Color coded heatmap of normalized expression (TPM) of top 100 genes state expression (TPM) of 100 genes depleted in Myc at promoters. (E) Gene snapshots of examples of the MYC-enriched promoters. (F) Immunoblotting of MCM7 and c-Myc in SKO-yBM and DKO-yBM cells (the numbers indicate biological repeats), quantification of MCM7 and Myc protein levels relative to SKO yBM cells are shown. (G) Quantification of colony formation of SKO-yBM and DKO-yBM (n=3). ****p-value<0.0001.

<u>Supplemental Tabel 1: qPCR primers list and their sequences along with the predicted sizes.</u>











Pes1

yBM Tumor CTRL



Mutual genes between Tum-SKO and Tum-DKO (324 genes)



Н

В



Figure 3S



Figure 4S

Α

В



Gene		Sequence	Product size
Osterix	Osx	F:CCCTTCTCAAGCACCAATGG	
		R:AGGGTGGGTAGTCATTTGCATAG	85 bp
RUNX2	RUNX2	F:CGGCCCTCCCTGAACTCT	
		R:TGCCTGCCTGGGATCTGTA	75 bp
Colagen1A1	Col1A1	F:CTTGGTGGTTTTGTATTCGATGAC	
		R:GCGAAGGCAACAGTCGCT	101 bp
Osteocalcin	OC	F:CTGACAAAGCCTTCATGTCCAA	
		R:GCGCCGGAGTCTGTTCACTA	59 bp
MCM7	MCM7	F:AGTATGGGACCCAGTTGGTTC	
		R:GCATTCTCGCAAATTGAGTCG	115 bp
с-Мус	c-Myc	F:ATGCCCCTCAACGTGAACTTC	
		R:CGCAACATAGGATGGAGAGCA	228 bp
HPRT	HPRT	F:TCAGTCAACGGGGGACATAAA	
		R:GGGGCTGTACTGCTTAACCAG	142 bp
Supv3l1	Supv3l1	F:CTGGCAGATTCAGCTCACAC	
		R:TGCCCATCAACTTGTGCAAA	223 bp
Cad	Cad	F:GCAAGTGGTTTGAATCCTCGG	
		R:CATTGGGGTCCACGAATGG	246 bp
Mrto4	Mrto4	F:GCCAACATGAGGAACAGCAA	
		R:AGCCCAACTTCACCTCTCAA	170 bp