Table S1. Genes identified by GSEA analysis contributing to the upregulated oxidative

phosphorylation pathway in both PRA transgenics and LumB breast cancer subtype. Genes that

were also in our original list and are highlighted.

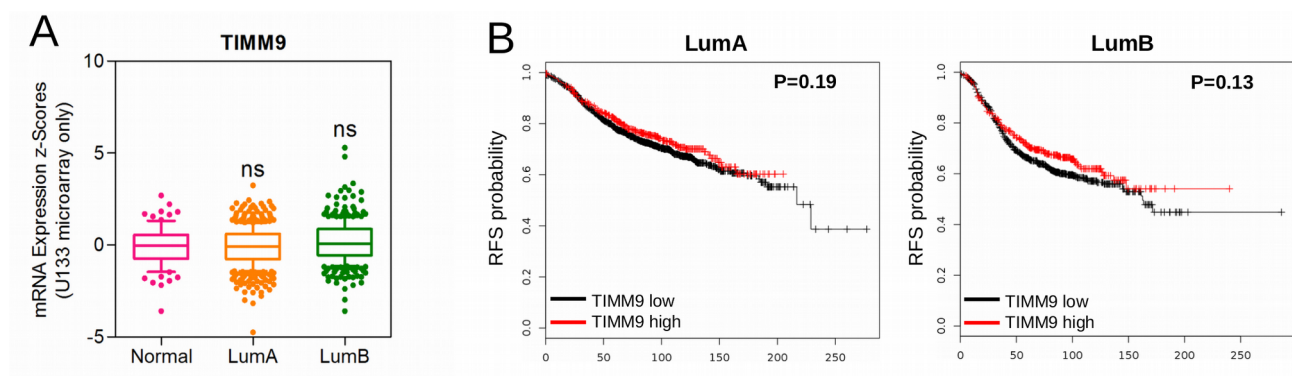| **Oxidative phosphorylation pathway genes (GSEA analysis)** |
|---|
| ATP5B \| ATP5G3 \| ATP5J \| ATP6AP1 \| ATP6V0C \| ATP6V1C1 \| DLAT \| GRPEL1 \| HSD17B10 \| ISCA1 LDHA \| LRPPRC \| MDH1 \| MRPL15 \| MRPL35 \| MRPS11 \| MTRR \| NDUFB2 \| NDUFS2 \| NDUFS8 \| NDUFV2 \| NNT \| OPA1 \| **PDHB** \| PDHX \| SDHB \| **TIMM9** \| UQCRB \| UQCRH |

Figure S1. A) TIMM9 expression, from the oxidative phosphorylation pathway, in samples from

the METABRIC study, classified by subtype. ns=not significant, One-way ANOVA Tukey's

multiple comparison test. B) Relapse-free survival curves according to TIMM9 expression for the

luminal breast cancer subtypes.

Table S2. Genes identified by GSEA analysis contributing to the downregulated TNFA signaling

via NFKB pathway in PRA transgenics, LumA and LumB breast cancer subtypes (with few

exceptions). Genes that were also in our original list and are highlighted.

TNFA signaling via NFKB pathway genes (GSEA analysis) identified in PRA transgenics, LumA and Lumb breast cancer subtypes
ATF3 | B4GALT5 | **BMP2** | BTG1 | **CCL2** | CCL5 | CD69 | CEBPB | CEBPD | CXCL1 | CXCL2 | CYR61 | DUSP1 | **EGR1** | EGR2 | **EGR3** | EHD1 | F3 | FOS | **FOSB** | GEM | HBEGF | **IER2** | IER5 | **IL7R** | IRS2 | JAG1 | JUN | **JUNB** | KLF10 | **KLF2** | KLF4 | **LAMB3** | MAP3K8 | NFKBIA | **NR4A1** | **PDE4B** | PPAP2B | PPP1R15A | PTGER4 | PTGS2 | PTPRE | RCAN1 | SERPINE1 | SIK1 | SLC2A3 | TGIF1 | TNFAIP3 | TNFAIP8 | TRAF1 | **ZFP36**

Genes identified in PRA trasgenics and LumA breast cancer subtype exclusively
DUSP2 | **KYNU** | SMAD3

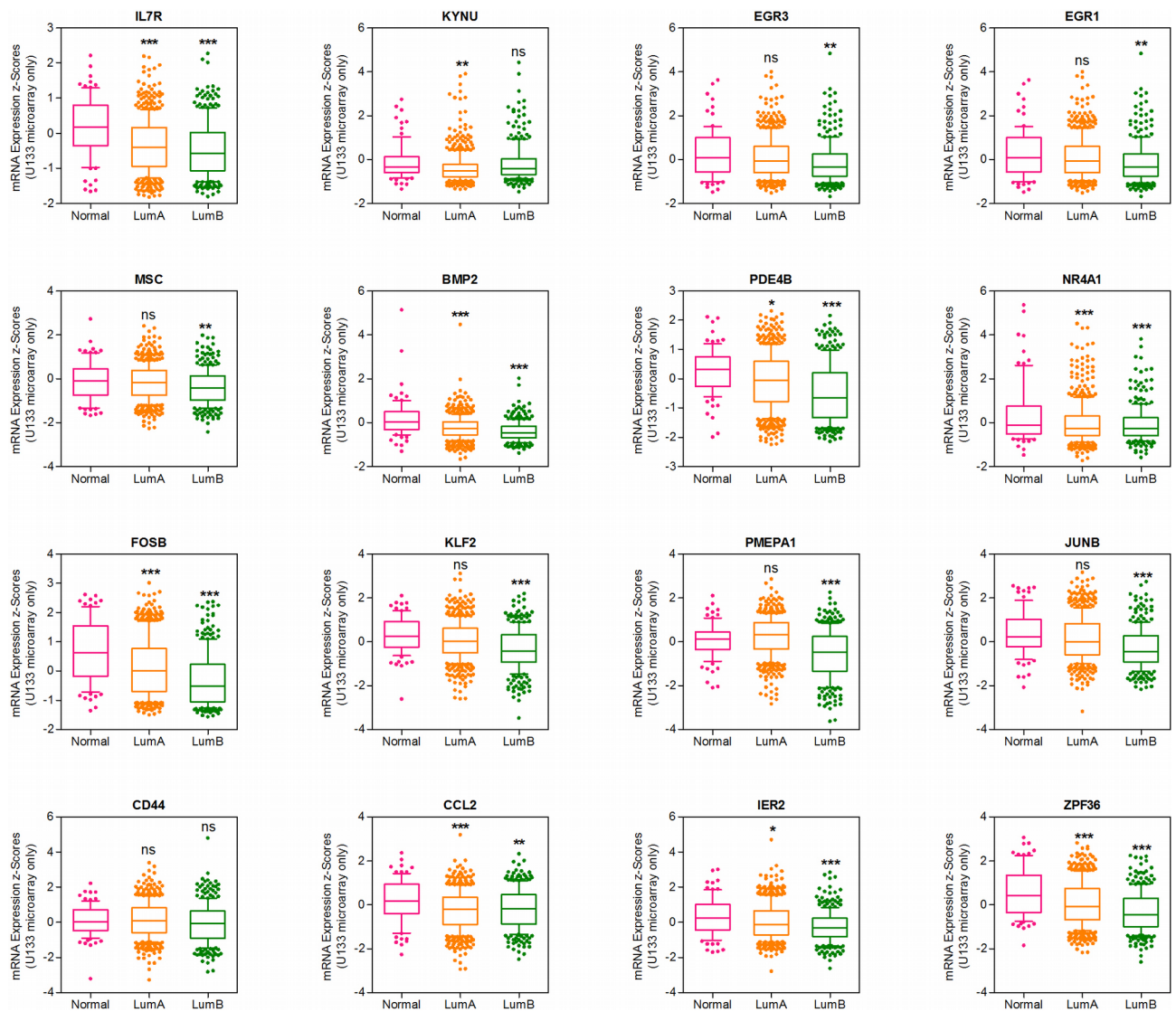| **Genes identified in PRA trasgenics and LumB breast cancer subtype exclusively** |
|---|
| BTG2 \| **CD44** \| GADD45B \| GFPT2 \| HES1 \| KDM6B \| **MSC** \| **PMEPA1** |

Figure S2. Expression of genes from the TNFA signaling through NFKB pathway (Table 4) in samples from the METABRIC study, classified by subtype. ***P<0.001, **P<0.01, *P<0.05, ns=not significant, One-way ANOVA Tukey's multiple comparison test.
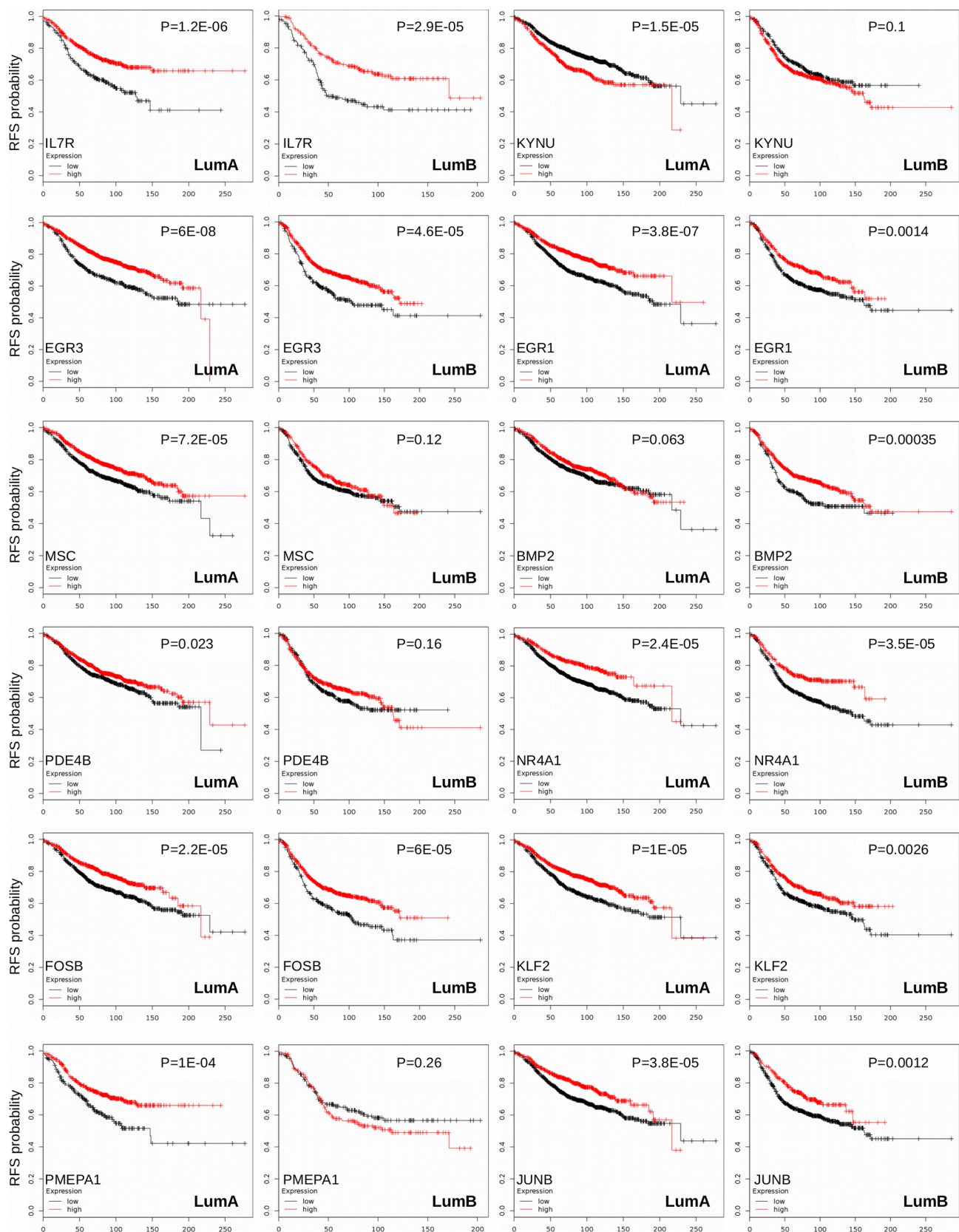
Figure S3. Relapse-free survival curves according to expression of the genes presented in Figure S2 for the luminal breast cancer subtypes.
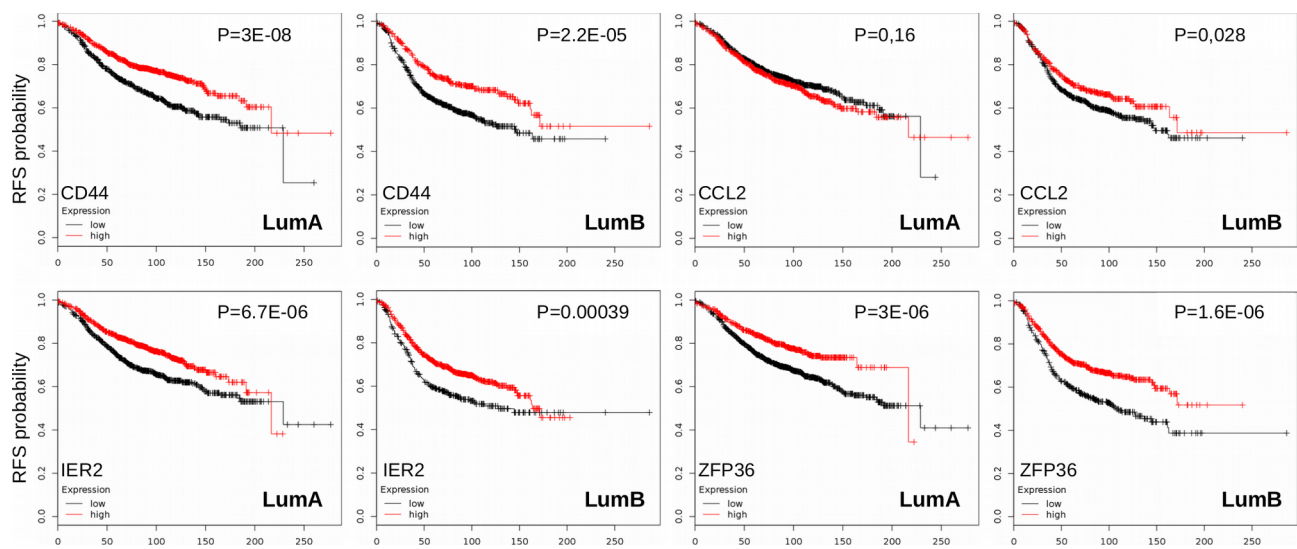
Figure S3 continued.