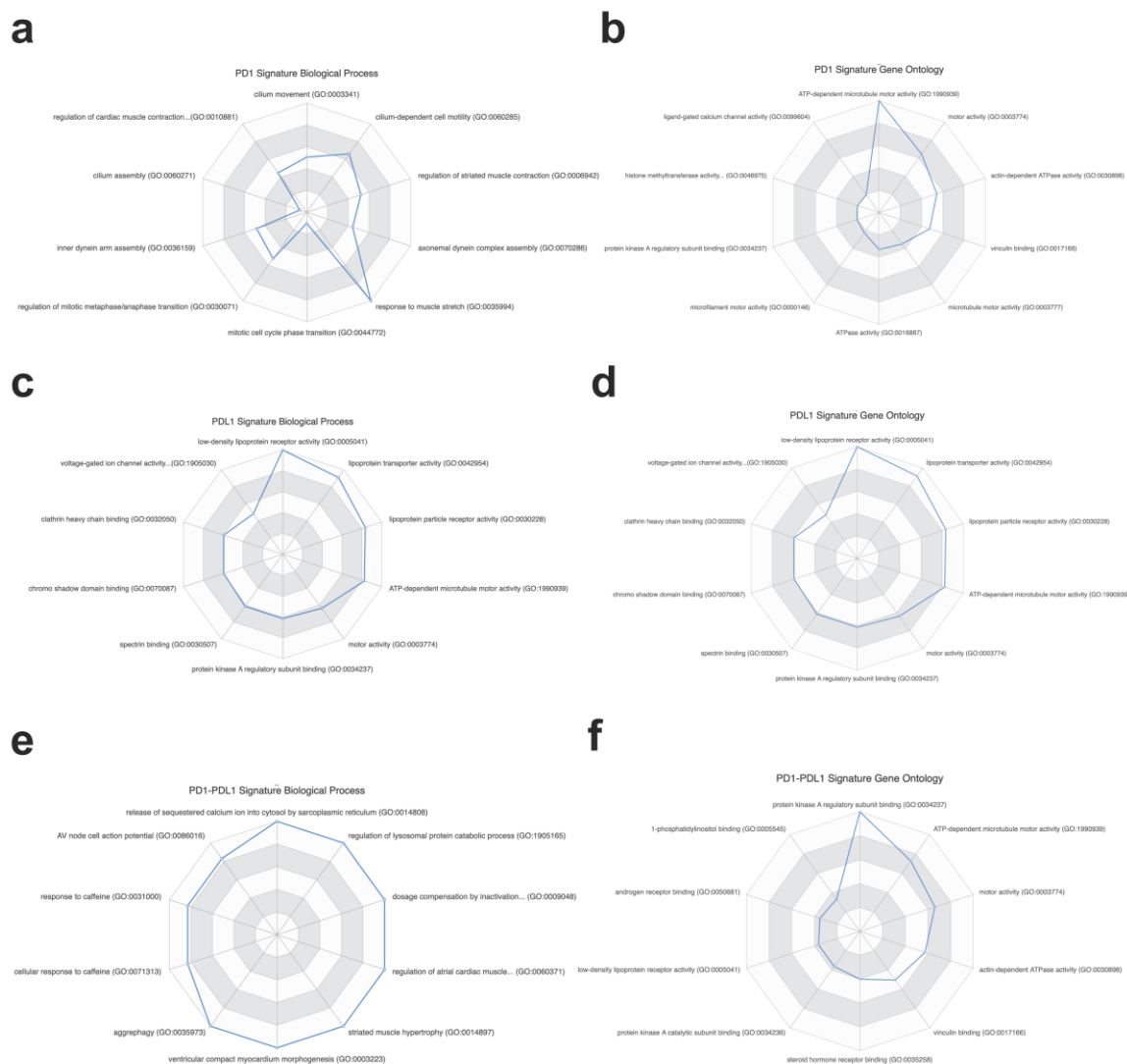
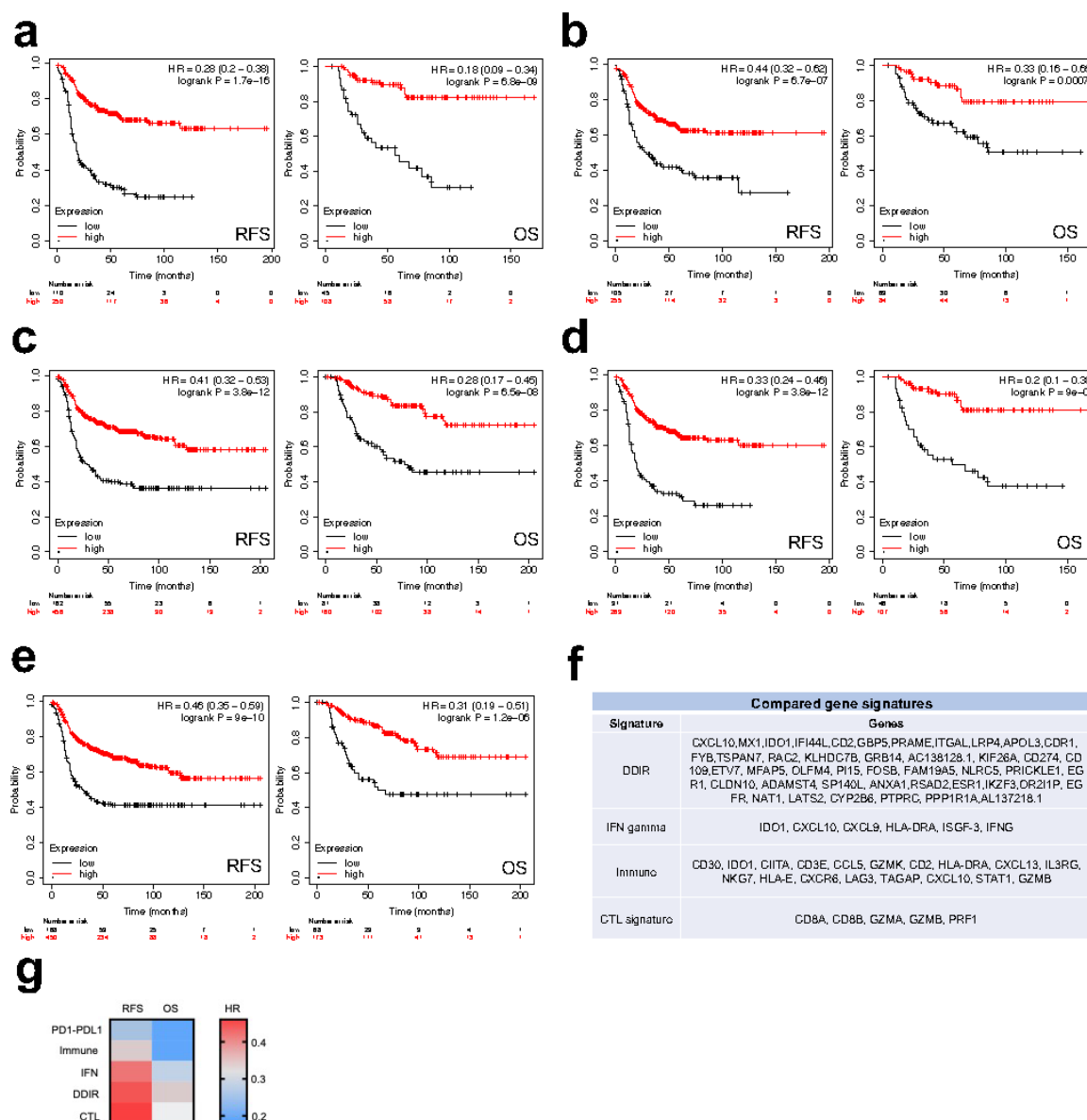


# Supplementary Materials: Genomic Mapping Identifies Mutations in RYR2 and AHNAK as Associated with Favorable Outcome in Basal-Like Breast Tumors Expressing PD-L1

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**Figure S1.** Molecular functions of the identified gene signatures. (A) Main biological processes regulated by the PD1 high-expressing tumors, ranked by combination score. (B) Main molecular functions regulated by the PD1 high-expressing tumors, ranked by combination score. (C) Main biological processes regulated by the PD-L1 high-expressing tumors, ranked by combination score. (D) Main molecular functions regulated by the PD-L1 high-expressing tumors, ranked by combination score. (E) Main biological processes regulated by the PD1-PD-L1 high-expressing mutation joint signature, ranked by combination score. (F) Main molecular functions regulated by the PD1-PD-L1 high-expressing mutation joint signature, ranked by combination score.



**Figure S2.** The PD1-PD-L1 signature predicts better prognosis than previously proposed signatures. The new gene signature predicts better prognosis in terms of RFS (left panels) and OS (right panels) (A) than previously proposed immune gene expression signatures reported in the literature, as the DDIR (B), IFN (C), Immune (D) and CTL (E) signatures. (F) Components of the previously proposed gene signatures. (G) Heatmap comparing HR conferred by several gene signatures in terms of RFS and OS including the DDIR, IFN, Immune and CTL signature.

