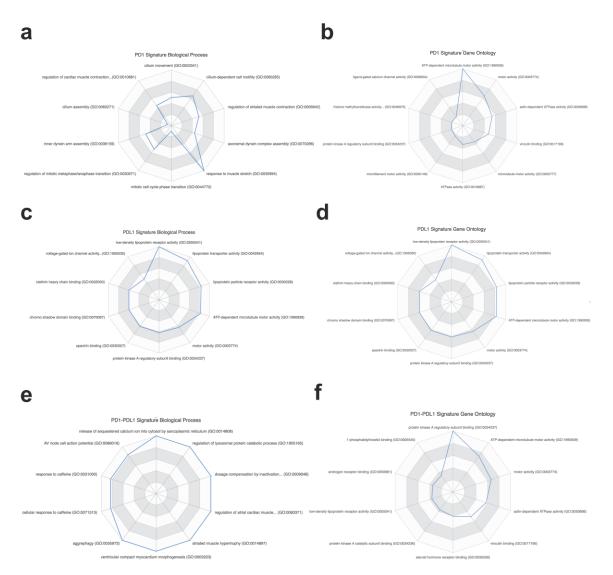
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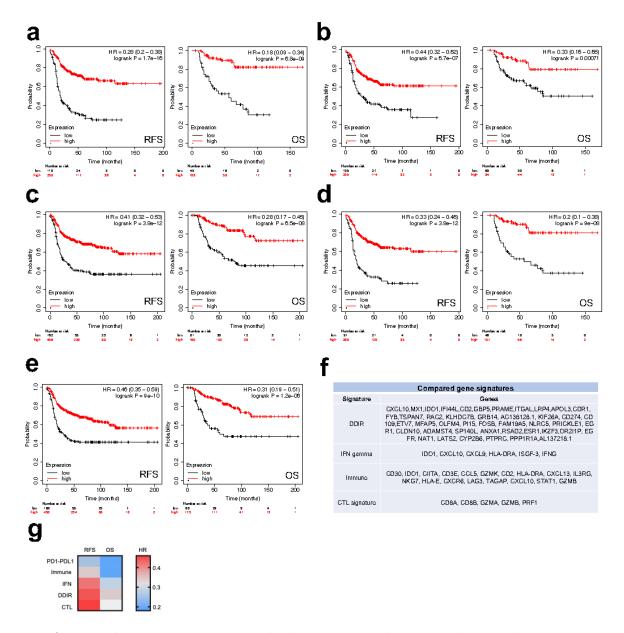
## Supplementary Materials: Genomic Mapping Identifies Mutations in RYR2 and AHNAK as Associated with Favorable Outcome in Basal-Like Breast Tumors Expressing PD-L1

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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.

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**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.



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