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S1 Fig. Increased levels of genes in pathways associated with T and NK cell activity, categorized by fatigue severity, measured using the nCounter.

(A-C) Mean log2 signal of all genes in the top enriched pathways, (A) enriched in T cells, (B) enriched in NK cells, and (C) T cell activation at pre-dose 1.

(D-F) Mean log2 signal of all genes in the top enriched pathways, (D) enriched in T cells, (E) enriched in NK cells, and (F) T cell activation at pre-dose 2.

(G) Gene expression of the top leading edge genes in the top enriched pathways at pre-dose 1 and 2. Z scores of raw log2 counts are displayed.

Data presented as means ± SD. Unpaired student's T test were used for experiments comparing 2 groups. *P < 0.05, **P < 0.01, ****P<0.0001.

Data underlying this Figure can be found in S2_Data.

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