A

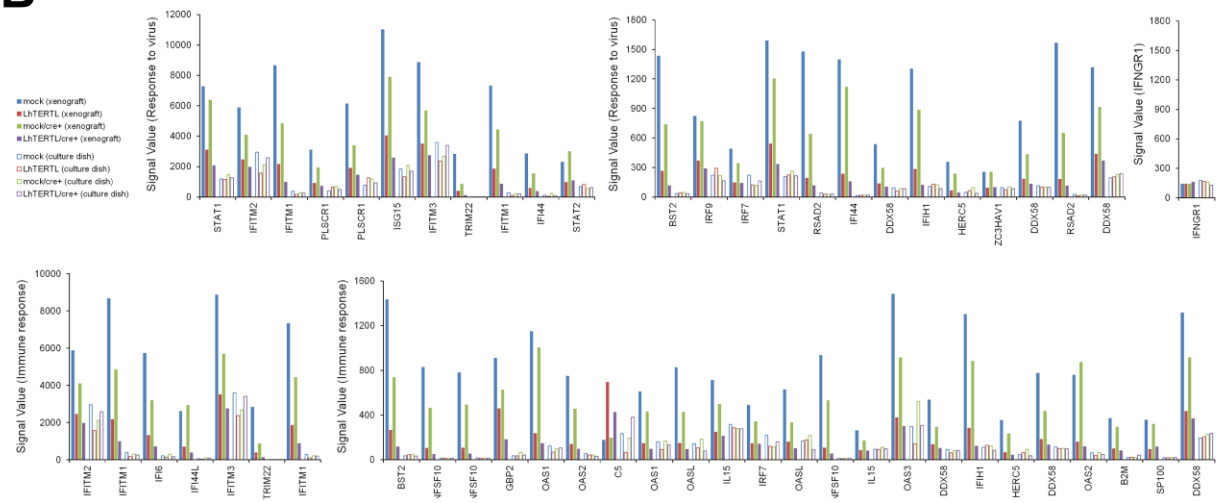
Enrichment of Gene Ontology categories from up- and down-regulated genes by telomere elongation (xenograft)

GO Accession	GO Term	Count in Telomere elongation	%	Count in Total	%	p-value
GO:0009615	response to virus	17	13.82	158	0.92	1.30E-15
GO:0051707	response to other organism	20	16.26	401	2.33	8.04E-12
GO:0009607	response to biotic stimulus	20	16.26	427	2.49	2.50E-11
GO:0051704	multi-organism process	27	21.95	861	5.01	6.04E-11
GO:0002376	immune system process	27	21.95	1082	6.30	8.97E-09
GO:0006955	immune response	20	16.26	656	3.82	4.12E-08
GO:0044419	interspecies interaction between organisms	13	10.57	355	2.07	1.60E-06
GO:0006952	defense response	18	14.63	715	4.16	3.31E-06

Enrichment of Gene Ontology categories from up- and down-regulated genes by telomere elongation (culture dish)

GO Accession	GO Term	Count in Telomere elongation	%	Count in Total	%	p-value
GO:0006259	DNA metabolic process	17	24.64	715	4.16	2.20E-09
GO:0006260	DNA replication	10	14.49	192	1.12	4.62E-09

B



C

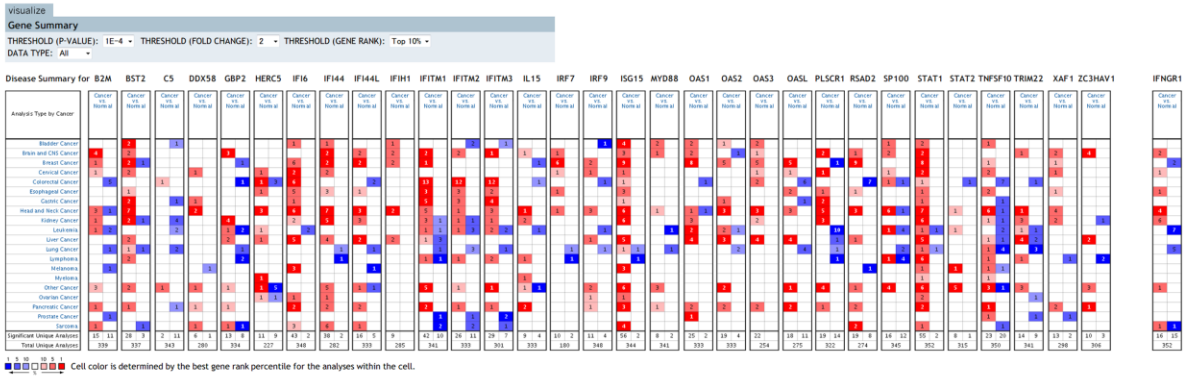


FIG S5 The intrinsic transcriptional response to tumor formation is abolished by telomere elongation. (**A**) GO categories affected by telomere elongation in xenograft (left panel) or culture dishes (right panel). GeneChip probes with fold change values greater than 2.0 (xenograft) or 1.5 (culture dishes) due to telomere elongation (190 probes) were subjected to GO analysis. Enriched GO categories were sorted by

increasing P value. Each category has more than 10 probes that were affected by telomere elongation (a total of 54,675 probe sets, $P < 0.01$ Fisher's exact test). In a xenograft setting, all enriched categories were related to the innate immune system. (**B**) Representative probe sets in response to virus (upper) and immune response (lower) categories. Most probes were downregulated in telomere-elongated tumors. The graphs were divided into two parts by high or low signal values. IFNGR1 expressions exhibited no differences in each sample (see Discussion section). (**C**) Disease summary of "Immune response" or "Response to virus" categories analyzed using the Oncomine database. Expression of most genes listed are upregulated in cancer as compared to the normal tissues. In accordance with upregulation in telomere-elongated xenografts, only the C5 (complement component 5) gene is under-expressed in cancer. Expression of IFNGR1 is similar in cancer and normal tissues, unlike differentiated normal cells (see Discussion section).