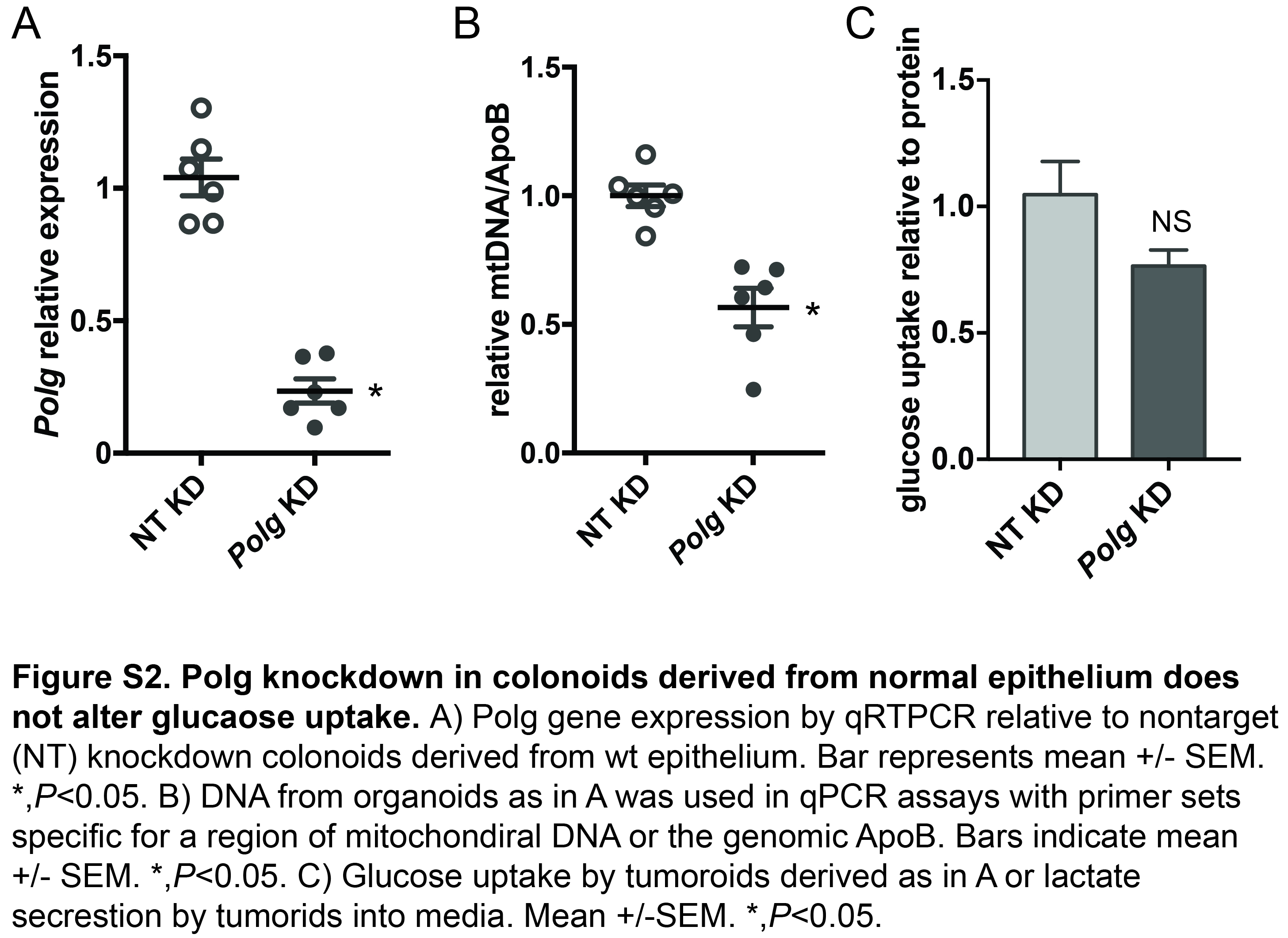


**Additinal file 1 Figure S1. Additional gene and protein expression in mock and ETBF-induced tumors.** A) Gene expression by qPCR relative to mock epithelium from indicated tissue 8 weeks post-infection. Mean +/- SEM. N=6. \**P* < 0.05 compared with mock Min epithelium. #*P* < 0.05 compared to *Msh2l/lVC*Min ETBF tumors. B) Western blots were run using protein isolated from indicated tissue 8 weeks post-infection. Blots are representative of two independent sets of biological replicates.



**Additional file 1 Figure S2. *Polg* knockdown in colonoids derived from normal epithelium does not alter glucose uptake.** A) *Polg* gene expression by qRTPCR relative to nontarget (NT) knockdown colonoids derived from wt epithelium. Bar represents mean +/- SEM. \**P* < 0.05. B) DNA from organoids as in A was used in qPCR assays with primer sets specific for a region of mitochondiral DNA or the genomic ApoB. Bars indicate mean +/- SEM. \**P* < 0.05. C) Glucose uptake by tumoroids derived as in A. Mean +/-SEM. NS – not significant.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Additional file 1 Table S1. Primer sequences for qMSP and mtDNA content and assays used for TaqMan gene expression.** | | | | | | | | | | |
|  |  | |  | |  | | |  | | |
| **qMSP Primer Sequences** | | | |  | | |  | | |
| *Polg* | Left M | GTTCGTGTTTTTGTAGGTGTTTTAC | | Right M | | | CCCTCTACTCATCCAAATATTATCG | | |
|  | Left U | TTGTGTTTTTGTAGGTGTTTTATGT | | Right U | | | CCCTCTACTCATCCAAATATTATCAA | | |
| *Gapdh* | Left M | GTATTGTATAAGAAGATGCGGTCGT | | Right M | | | TACACGTAACTCAAACCTCTACGC | | |
|  | Left U | GGTATTGTATAAGAAGATGTGGTTGT | | Right U | | | TACACATAACTCAAACCTCTACACC | | |
|  |  |  | |  | | |  | | |
| **Applied Biosystems Taqman Gene Expression Assays** | | | |  | | |  | | |
| *Polg* | mm00450527\_m1 | | |  | | |  | | |
| *PPIA* | Mm02342430\_g1 | | |  | | |  | | |
|  |  |  | |  | | |  | | |
| **mtDNA content** | | | |  | | |  | | |
| mtDNA set1 | Fwd | AATCAATGGTTCAGGTCA | | Rev | | ACGGAGGATGGTAGATTA | | |
| mtDNA set2 | Fwd | CTCCGTGCTACCTAAACACCTTATC | | Rev | | GACCTAAGAAGATTGTGAAGTAGATGATG | | |
| ApoB | Fwd | CACGTGGGCTCCAGCATT | | Rev | | TCACCAGTCATTTCTGCCTTTG | | |

|  |  |
| --- | --- |
| **Additional file 1 Table S2. Fold change in expression by RT2 Profiler Glucose Metabolism PCR Array.** | |
|  | Fold change ETBF Min tumor relative to mock epithelium |
| **Prps1l1** | 20.39 |
| **Hk3** | 6.23 |
| Pygm | 2.6 |
| Rpia | 2.27 |
| **Gck** | -102.54 |
| **Aldob** | -19.16 |
| Phkg1 | -11.24 |
| Pck1 | -6.5 |
| Cs | -3.46 |
| Galm | -2.97 |
| Pdp2 | -2.93 |
| Suclg1 | -2.85 |
| Eno3 | -2.85 |
| Eno2 | -2.73 |
| Gapdh | -2.68 |
| Pdk1 | -2.48 |
| Idh3a | -2.46 |
| Suclg2 | -2.46 |
| Sdha | -2.33 |
| Pdpr | -2.31 |
| Aco1 | -2.28 |
| Gsk3a | -2.23 |
| Ogdh | -2.19 |
| Ugp2 | -2.11 |
| Idh3b | -2.07 |
| Prps1 | -2.04 |
|  |  |
| Changes in bold gene names were verified by qRTPCR. | |