

# Molecular Biology Project Draft

Gene Product Targeting for Breast Cancer

~~Name~~

Worcester Polytechnic Institute

### Background

This paper explores product targeting methods for breast cancer that have spread to lymph nodes. Through these methodologies it is theoretically possible to pause the extension of Telomeres, whose existence allows the rapid continuous growth of cancer cells. The methods of Telomere length maintenance to be discussed are C-Circles and Telomerase. “C-Circles are a self-overlapping structure at the end of DNA, and Telomerase is a protein product of the hTERT gene, whose over-expression can be a sign of Cancer”<sup>2</sup>. Once the type of Telomere length maintenance is determined (or mix of both), dCas9 can be used to block transcription and thereby halting or slowing down the replication process of cancer cells. Stopping these mechanisms would prevent the extension of Telomeres in the DNA, causing possibly leading cell death upon continuous replication. The strength of this method can then be determined by Spectral Analysis for the absence of Telomerase expression, and a C-Circle Assay (CCA) for the removal of C-Circles.

### Experimental Design

Initially through a Sentinel lymph node dissection (SLND), sample tissue is collected from the patients arm pit to remove the tumor and lymph nodes. Once the tumor DNA is cloned, the sample cells can then be tested to determine their Telomere length maintenance system. To do so, RNAseq will be used due to the small amount of required starting material and little to be known about the sequence. Paired with a reference genome of a healthy lymph node, the expression levels of the hTERT gene can be compared to determine the expression level of the hTERT gene. If an over expression is determined, then Telomerase is known to be used to as a Telomere length maintenance system. Normally, one may use Illumina Deep Sequencing to obtain the sequence of hTERT to be used as the sgRNA in dCas9, but because it is commonly known (5' TGGTTTCTGTGTGGTGTCA 3') and one can simply purchase the sequence or make one their own (not recommended). To test for ALT+ sequences, CCA is to be conducted using the original tumor sample. If a relatively large product remains, then the sequence is ALT+. Similarly to the hTERT gene, the sequence of C-Circles is also commonly known (5' TTAGGG 3' repeat) and can be purchased as a sgRNA sequence via a third party company, if the tested sequences are ALT+. With vital sgRNA acquired it is imperative to store it as a vector with dCas9 by induced homologous recombination for mass production and ease of access. The dCas9 and sgRNA plasmids can then be inserted into stem cells via hydrodynamic injection which in turn are inserted into the tumorous area ex vivo.

### Analysis

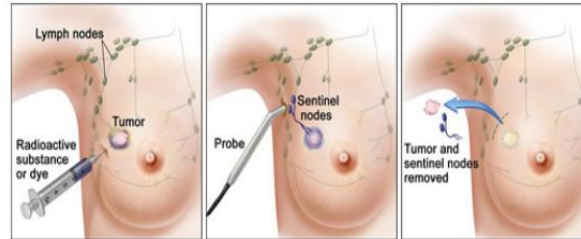
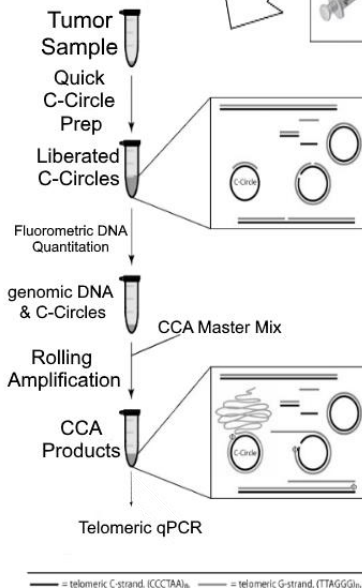
Given a period of healing time from the SLND and hydrodynamic injection, it is then possible to analyze the results. To do so, another SLND is to take place on the same arm as the first time. Similarly as before, tests must be conducted to determine if the cell's hTERT gene is expressed and if the C-Circles have been removed, which can be done via RNAseq and qPCR respectively. During RNAseq the cell's RNA is reverse-transcribed, sheared and incorporated into a flow-cell where images are processed by a machine and software as multidimensional matrix. The matrix is then manipulated through a Principal Component Analysis (PCA) to reduce dimensionality, and ran against a series of feature based eigenvectors of similar cDNA sequences. The result is a list of values in order of feature correlation, the first result is the cDNA sequence most similar to the input cDNA. Based on the eigenvalue of the output you can then determine the corresponding features that are absent or present in the sequence. If the eigenvalue is low in the vector for hTERT expression, it is definitive that hTERT has been inhibited. To detect C-Circles, a CCA is to be conducted using the original tumor sample (at least 100 cells)<sup>6</sup>. CCA, similar to PCR, is a process in which the DNA is replicated in a test tube. CCA however, does not use a primer which allows only self-replicating sequences to have products, such as C-Circles. Thereby the amount of product visualized would be a direct correlation to the existence of C-Circles in the genomic sequence.

### Cautions & Limitations

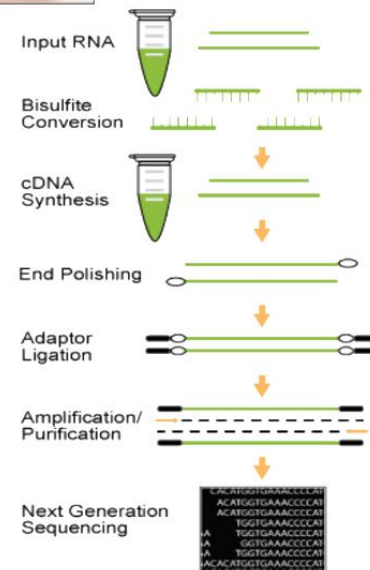
It is imperative to note that dCas9 requires the existence of a PAM sequence near the location of the desired inhibited sequence. Without one, dCas9 will not function properly and the tumorous cells will continue to spread. SLND alone can cause a lot of damage to the patient's nervous system especially when regarding the removal of high level axilla, and has many side-effects such as swelling, infection and axillary web syndrome<sup>22</sup>. It is also possible that due to the lack of Telomerase, tumorous and surrounding cells may encounter mutations or commit mass cell death leading to increasing problems. Due to human cells having another copy of their chromosomes, this method may not fully override mutations in the cancerous cells.

## Sentinel lymph node dissection

### C-Circle Assay



### RNAseq



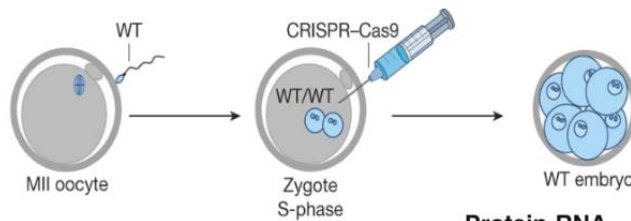
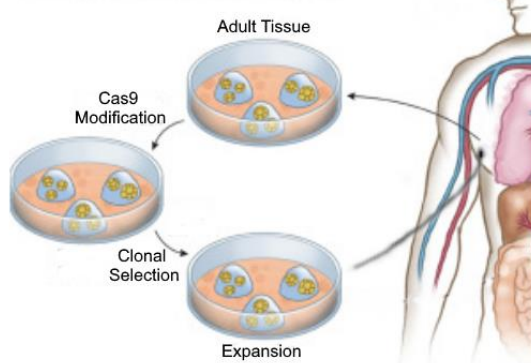
### Cas9 & sgRNA From 3rd party

Cas9/guide RNA transfected cells (mixed population)

### Hydrodynamic Injection of Cas9 & sgRNA

### Stem cells inserted into host

#### Cell culture-based ex vivo editing

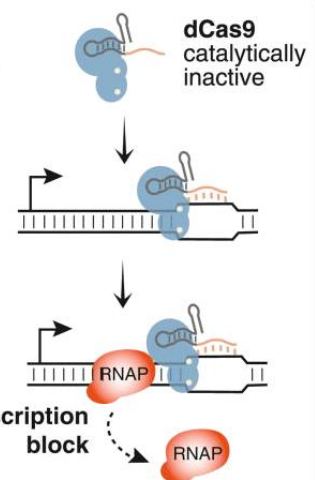


#### Protein-RNA complex assembly

### dCas9 blocks hTERT

#### RNA-guided targeting

#### Transcription block



## References

- 1) Cheung, I., Schertzer, M., Baross, A., Rose, A. M., Lansdorp, P. M., & Baird, D. M. (2004). Strain-specific telomere length revealed by single telomere length analysis in *Caenorhabditis elegans*. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC443537/>
- 2) Muntoni, A., & Reddel, R. R. (2005, October 15). First molecular details of ALT in human tumor cells | Human Molecular Genetics | Oxford Academic. Retrieved December 06, 2017, from [https://academic.oup.com/hmg/article/14/suppl\\_2/R191/663270](https://academic.oup.com/hmg/article/14/suppl_2/R191/663270)
- 3) Telomerase reverse transcriptase. (2017, December 05). Retrieved December 06, 2017, from [https://en.wikipedia.org/wiki/Telomerase\\_reverse\\_transcriptase](https://en.wikipedia.org/wiki/Telomerase_reverse_transcriptase)
- 4) Wang, H., Chen, S., Jiang, J., Zhang, F., & Chen, F. (2015). Reference gene selection for cross-species and cross-ploidy level comparisons in *Chrysanthemum* spp. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4308696/>
- 5) What is Real-Time PCR (qPCR)? (n.d.). Retrieved December 06, 2017, from <http://www.bio-rad.com/en-ca/applications-technologies/what-real-time-pcr-qpcr>
- 6) Henson, J. D., Lau, L. M., Koch, S., Martin, N., Dagg, R. A., & Reddel, R. R. (2017, February 01). The C-Circle Assay for alternative-lengthening-of-telomeres activity. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pubmed/27595911>
- 7) Skvortsov, D., Zvereva, M., Shpanchenko, O., & Dontsova, O. (2011). Assays for Detection of Telomerase Activity. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3347595/>
- 8) Ludlow, A. T., Robin, J. D., Sayed, M., Litterst, C. M., Shelton, D. N., Shay, J. W., & Wright, W. E. (2014, July). Quantitative telomerase enzyme activity determination using droplet digital PCR with single cell resolution. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pubmed/24861623>
- 9) Liu, J., Ge, L., & Zhang, G. (2006, January 21). Telomerase activity and human telomerase reverse transcriptase expression in colorectal carcinoma. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4066070/>

- 10) Hartig, J. S., & Kool, E. T. (2004, November 01). Small circular DNAs for synthesis of the human telomere repeat: varied sizes, structures and telomere-encoding activities. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pubmed/15520461>
- 11) Lau, L. M., Dagg, R. A., Henson, J. D., Au, A. Y., Royds, J. A., & Reddel, R. R. (2013, January). Detection of alternative lengthening of telomeres by telomere quantitative PCR. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3553966/>
- 12) Kargar, P. K., Yasaei, H., Anjomani-Virmouni, S., Mangiapane, G., & Slijepcevic, P. (2016, July 26). Analysis of alternative lengthening of telomere markers in BRCA1 defective cells. Retrieved December 06, 2017, from <http://onlinelibrary.wiley.com/doi/10.1002/gcc.22386/full>
- 13) De, A. D., Campbell, F. C., Dokal, I., Fairbairn, L. J., Graham, G. J., Jahoda, C. A., & Porterg, A. C. (2004, June). Total deletion of in vivo telomere elongation capacity: an ambitious but possibly ultimate cure for all age-related human cancers. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pubmed/15247008>
- 14) OncoSENS: Making cancerous mutations harmless. (2016, September 03). Retrieved December 06, 2017, from <http://www.sens.org/research/introduction-to-sens-research/cancerous-cells>
- 15) Telomerase has an Off Switch. (2014, September 22). Retrieved December 06, 2017, from <https://www.fightaging.org/archives/2014/09/telomerase-has-an-off-switch/>
- 16) Han, X., Zhang, H., Jia, M., Han, G., & Jiang, W. (2004, August). Expression of TIMP-3 gene by construction of a eukaryotic cell expression vector and its role in reduction of metastasis in a human breast cancer cell line. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pubmed/16225775>
- 17) Oganessian, L., & Karlseder, J. (2011, April 22). Mammalian 5' C-rich telomeric overhangs are a mark of recombination-dependent telomere maintenance. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3082866/>
- 18) Qi, L. S., Larson, M. H., Gilbert, L. A., Doudna, J. A., Weissman, J. S., Arkin, A. P., & Lim, W. A. (2013, February 28). Repurposing CRISPR as an RNA-Guided Platform for Sequence-Specific Control of Gene Expression. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3664290/>
- 19) Jessing, C., Langhans, L., Jensen, M. B., Talman, M. L., Tvedskov, T. F., & Kroman, N. (n.d.). Axillary lymph node dissection in breast cancer patients after sentinel node biopsy. Retrieved December 06, 2017, from <https://www.ncbi.nlm.nih.gov/pubmed/29168429>
- 20) Inc., A. B. (n.d.). HTERT Cell Immortalization Reagents. Retrieved December 06, 2017, from <https://www.abmgood.com/hTERT-Cell-Immortalization.html#>
- 21) Synthetic sgRNA. (n.d.). Retrieved December 06, 2017, from <https://www.synthego.com/products/synthetic-sgrna-kit-for-crispr/>
- 22) How Many Lymph Nodes Are Removed? (n.d.). Retrieved December 06, 2017, from [http://www.breastcancer.org/treatment/surgery/lymph\\_node\\_removal/number\\_removed](http://www.breastcancer.org/treatment/surgery/lymph_node_removal/number_removed)
- 23) He, F. (2011). Standard DNA Cloning. *Bio-protocol* Bio101: e52. DOI: [10.21769/BioProtoc.52](https://doi.org/10.21769/BioProtoc.52).

- 24) Advances in Therapeutic CRISPR/Cas9 Genome Editing.” Translational Research, Mosby, 26 Sept. 2015, [www.sciencedirect.com/science/article/pii/S1931524415003321](http://www.sciencedirect.com/science/article/pii/S1931524415003321)