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# Product datasheet for SC201518

## RAD51C (NM_002876) Human 3' UTR Clone

### Product data:

| | |
|---|---|
| **Product Type:** | 3' UTR Clones |
| **Product Name:** | RAD51C (NM_002876) Human 3' UTR Clone |
| **Vector:** | pMirTarget (PS100062) |
| **Symbol:** | RAD51C |
| **Synonyms:** | BROVCA3; FANCO; R51H3; RAD51L2 |
| **ACCN:** | NM_002876 |
| **Insert Size:** | 171 bp |
| **Insert Sequence:** | >SC201518 3'UTR clone of NM_002876<br>The sequence shown below is from the reference sequence of NM_002876. The complete sequence of this clone may contain minor differences, such as SNPs.<br>Blue=Stop Codon Red=Cloning site<br><br>GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG<br>TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC<br>CCAGGTGTTGGAAAAACACAATTATGGTAAATAAAGTGTTCTCCTTTTAAGGGTGGGTTTAATAACAT<br>ATTATGAAAGTAGTATTTTGTACTATCGTCAGGAAACCAAATAAGATATATATGTGCTCTTAATTTTAA<br>GTGTGTATGTGCATTAAACAAAAATTAGCTTAC<br>ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA<br>CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG |
| **Restriction Sites:** | SgfI-MluI |
| **OTI Disclaimer:** | Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs). |
| **Components:** | The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials. |
| **RefSeq:** | NM_002876.4 |

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**Summary:** This gene is a member of the RAD51 family. RAD51 family members are highly similar to bacterial RecA and Saccharomyces cerevisiae Rad51 and are known to be involved in the homologous recombination and repair of DNA. This protein can interact with other RAD51 paralogs and is reported to be important for Holliday junction resolution. Mutations in this gene are associated with Fanconi anemia-like syndrome. This gene is one of four localized to a region of chromosome 17q23 where amplification occurs frequently in breast tumors. Overexpression of the four genes during amplification has been observed and suggests a possible role in tumor progression. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jul 2013]

**Locus ID:** 5889

**MW:** 6.7