

## Product datasheet for **KN302248**

### Brca1 Mouse Gene Knockout Kit (CRISPR)

#### Product data:

Product Type:	Knockout Kits (CRISPR)
Format:	2 gRNA vectors, 1 GFP-puro donor, 1 scramble control
Donor DNA:	GFP-puro
Symbol:	Brca1
Locus ID:	12189
Components:	<p><b>KN302248G1</b>, Brca1 gRNA vector 1 in pCas-Guide CRISPR vector (GE100002), Target Sequence: AAATCTTAGAGTGTCCGATC</p> <p><b>KN302248G2</b>, Brca1 gRNA vector 2 in pCas-Guide CRISPR vector (GE100002), Target Sequence: CTTCTGTTGACTTACCAGAT</p> <p><b>KN302248D</b>, donor DNA containing left and right homologous arms and GFP-puro functional cassette.</p>

#### Homologous arm and GFP-puro sequences:

pUC vector backbone in gray; **Left arm sequence in blue**; **GFP-puro in green**; **Right arm in violet**

```

AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAGCG GTTAGCTCCT TCGGTCCTCC GATCGTTGTC
AGAAGTAAGT TGGCCGAGT GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT ACTGTCATGC
CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC CAAGTCATTC TGAGAATAGT GTATGCCGGC
ACCGAGTTGC TCTTGCCCGG CGTCAATACG GGATAATACC GCGCCACATA GCAGAATTTT AAAAGTGCTC
ATCATTTGAA AACGTTCTTC GGGCGAAAA CTCTCAAGGA TCTTACCCTG GTTGAGATCC AGTTCGATGT
AACCCACTCG TGCACCCAAC TGATCTTCAG CATCTTTTAC TTTACCAGC GTTTCTGGGT GAGCAAAAAC
AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT GAATACTCAT ACTCTTCCTT
TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA TGAGCGGATA CATATTTGAA TGTATTTAGA
AAAATAAACA AATAGGGGTT CCGCGCACAT TTCCCGAAA AGTGCCACCT GACGTCTAAG AAACCATTAT
TATCATGACA TTAACCTATA AAAATAGGCG TATCACGAGG CCCTTTCGGG TCGCGGTTT CGGTGATGAC
GGTAAAACC TCTGACACAT GCAGCTCCCG TTGACGGTCA CAGCTTGCT GTAAAGCGGAT GCCGGGAGCA
GACAAGCCCG TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA
GCAGATTGTA CTGAGAGTGC ACCATAAAAT TGTAACGTT AATATTTTGT TAAAATTCGC GTTAAATTTT
TGTTAAATCA GCTCATTTTT TAACCAATAG GCCGAAATCG GCAAAAATCCC TTATAAATCA AAAGAATAGC
CCGAGATAGG GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG ACTCCAACGT
CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA CGTGAACCAT CACCAAATC AAGTTTTTTG
GGGTCGAGGT GCCGTAAAGC ACTAAATCGG AACCCATAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
AGCCGGCGAA CGTGCGGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC GCTAGGGCGC TGGCAAGTGT
AGCGGTACG CTGCGGTAA CCACCACACC CGCCGCGCTT AATGCGCCGC TACAGGGCGC GACTATGGT
TGCTTTGACG TATGCGGTGT GAAATACCGC ACAGATCGCT AAGGAGAAAA TACCGCATCA GGCGCCATTC
GCCATTCAGG CTGCGCAACT GTTGGGAAGG GCGATCGGTG CGGGCCTCTT CGCTATTACG CCAGCTGGCG
AAAGGGGAT GTGCTGCAAG GCGATTAAGT TGGTAACGC CAGGGTTTTC CCAGTACGA CGTTGTAATA
CGACGGCCAG TGAATTGGAG GCTACAGTCA GTGGAGAGGA CTTTCACAGG CTGTCGCCGT GCTCATTTGA

```



[View online »](#)

TAACTGCCCG TTATTCATGC GACACTGTCT TCAGACATGC TAGAAAAGGG CATTGGATCC CATTACAGAT  
 GGTGTGAGC CACCGTGTGG ATGCTGGGAA TTGAACCTTT GGAAGAGCAG TGAGTTTACT TAACTGCTGA  
 GCCATCTTAT TAGTCCCTTG TTTTGTTTT TTAGTGAAGT TTTTTCATCA ACTGTTGGTA TAATTTAAA  
 GCACTCCAAA TTTAAATTTT TCTTATTTAG AAATGACAAG CCTGGTGCAG TAGCTTAAAC ACCTGTACTC  
 AGTAGGCTGA GGCAGGGCGA TTGCTTCAAG TTGGAGGCTA ATCTGGGCTG CATAATTATT TCCAGATGTG  
 TGTGGGCTTC AGCGTGAGAA CTCCTCCAAA AAGCATGGAT GGGGGTGACT TACCTTCAGT AATCCAGCA  
 CTAAGTGGGT GGAGGCAGGA GGATCAGAGG TTTAAGACTA GCCTTGAGTA CATAAGGTAC AAAGCCAGTG  
 TGGGTTACAT GACATCTTGT CTCAAAAAGG GAAAGAAAGT TGGCAAGGTA AGCTACTGTA TTTAAAAGCC  
 CTTTAATGTA GTTTAATTGC ATGTGTTTTT AAATTTGTGT TAAAAGTTCA CTGGAAGTGG AAGAACTAG  
 CATGGAGAGC GACGAGAGCG GCCTGCCCGC CATGGAGATC GAGTGCCGCA TCACCGGCAC CCTGAACGGC  
 GTGGAGTTCG AGCTGGTGGG CGGCGGAGAG GGCACCCCGC AGCAGGGCCG CATGACCAAC AAGATGAAGA  
 GCACCAAAGG CGCCCTGACC TTCAGCCCTT ACCTGCTGAG CCACGTGATG GGCTACGGCT TCTACCACTT  
 CGGCACCTAC CCCAGCGGCT ACGAGAACC CTTCCTGCAC GCCATCAACA ACGGCGGCTA CACCAACACC  
 CGCATCGAGA AGTACGAGGA CGGCGGCGTG CTGCACGTGA GCTTCAGCTA CCGCTACGAG GCCGGCCGCG  
 TGATCGGCGA CTTCAAGGTG ATGGGCACCG GCTTCCCGA GGACAGCGTG ATCTTACCAG ACAAGATCAT  
 CCGCAGCAAC GCCACCGTGG AGCACCTGCA CCCCATGGGC GATAACGATC TGGATGGCAG CTTACCCCGC  
 ACCTTCAGCC TGC GCGACGG CGGCTACTAC AGCTCCGTGG TGGACAGCCA CATGCACCTT AAGAGCGCCA  
 TCCACCCAG CATCCTGCAG AACGGGGGCC CCATGTTTCG CTTCCGCGC GTGGAGGAGG ATCACAGCAA  
 CACCGAGCTG GGCATCGTGG AGTACCAGCA CGCCTTCAAG ACCCCGGATG CAGATGCCGG TGAAGAAAGA  
 GTTTAAGAAT TCCGATCATA TTCAATAACC CTTAATATAA CTTCTGATAA TGTATGCTAT ACGAAGTTAT  
 TAGGTCTGAA GAGGAGTTTA CGTCCAGCCA AGCTTAGGAT CTCGACCTCG AAATTCTACC GGGTAGGGGA  
 GGCCTTTTC CCAAGGCAGT CTGGAGCATG CGCTTTAGCA GCCCGCTGG GCACCTGGCG CTACACAAGT  
 GGCCTCTGGC CTCGCACACA TTCCACATCC ACCGGTAGGC GCCAACCGAC TCCGTTCTTT GTTGGCCCTT  
 TCGCGCCACC TTCTACTCCT CCCCTAGTCA GGAAGTTCCC CCCC GCCCGCAGCTCGCGT CGTGCAGGAC  
 GTGACAAATG GAAGTAGCAC GTCTACTAG TCTCGTGAG ATGGACAGCA CCGCTGAGCA ATGGAAGCGG  
 GTAGGCCTTT GGGGAGCGG CCAATAGCAG CTTTGTCTCT TCGCTTCTG GGCTCAGAGG CTGGGAAGGG  
 GTGGGTCCGG GGGCGGGCTC AGGGGCGGGC TCAGGGGCGG GCGGGGCGCC CGAAGGTCTT CCGGAGGCC  
 GGCATTCTGC ACGCTTCAA AGCGCACGTC TGCCGCGCTG TTCTCCTCTT CCTCATCTCC GGGCCTTTTCG  
 ACCTGCATCC ATCTAGATCT CGAGCAGCTG AAGCTTACCA TGACCGAGTA CAAGCCACG GTGCGCCTCG  
 CCACCCGCGA CGACGTCCC AGGGCCGTAC GCACCCTCGC CGCCGCGTTC GCCGACTACC CCGCCACGCG  
 CCACACCGTC GATCCGGACC GCCACATCGA GCGGGTCACC GAGCTGCAAG AACTCTTCT CACGCGCGTC  
 GGGCTCGACA TCGGCAAGGT GTGGGTGCGG GACGACGGCG CCGCGGTGGC GGTCTGACC ACGCCGAGA  
 GCGTCAAGC GGGGCGGGT TCGCCGAGA TCGGCCGCG CATGGCCGAG TTGAGCGGTT CCCGGCTGGC  
 CGCGCAGCAA CAGATGGAAG GCCTCCTGGC GCCGACCGG CCAAGGAGC CCGCGTGGTT CCTGGCCACC  
 GTCGGCGTCT CGCCGACCA CCAGGGCAAG GGTCTGGGCA GCGCCGTCGT GCTCCCCGA GTGGAGGCGG  
 CCGAGCGCGC CGGGGTGCC GCCTTCTTGG AGACCTCCG GCCCACAACT CCCCCCTTCT ACGAGCGGCT  
 CGGCTTACC GTCACCGCCG ACGTCGAGGT GCCCGAAGGA CCGCGCACCT GGTGCATGAC CCGCAAGCCC  
 GGTGCCTGAC GCCCGCCCA CGACCCGACG CGCCGACCG AAAGGAGCGC ACGACCCAT GCATCGATGA  
 TATCAGATCC CCGGATGCA GAAATTGATG ATCTATTAAA CAATAAAGAT GTCCACTAAA ATGGAAGTTT  
 TTCTGTCTAT ACTTTGTTAA GAAGGGTGAG AACAGAGTAC CTACATTTT AATGGAAGGA TTGGAGCTAC  
 GGGGTGGGG GTGGGTGGG ATTAGATAAA TGCTGTCTT TTAAGTGAAG CTCTTTACTA TTGCTTTATG  
 ATAATGTTT ATAGTTGGAT ATCATAATTT AAACAAGCAA AACCAAATTA AGGGCCAGCT CATTCTCTCC  
 ACTCATGATC TATAGATCTA TAGATCTCTC GTGGGATCAT TGTTTTTCTT TTGATTCCCA CTTTGTGGTT  
 CTAAGTACTG TGGTTTCAA ATGTGTCACT TTCATAGCCT GAAGAACGAG ATCAGCAGCC TCTGTTCCAC  
 ATACACTTCA TTCTCAGTAT TGTTTTGCCA AGTTCTAATT CCATCAGAAG CTGGTCGAGA TCCGGAACCC  
 TTAATATAAC TTCGTATAAT GTATGCTATA CGAAGTTATT AGGTCCCTCG AAGAGGTTCA CTAGGCGCGC  
 CATGTGGTTA CTGTTTCATG AAATGAGTAG CAGAGGCTTA AGATAGTAGA GAAAAACT CTGTATTTAA  
 AGGACTTTGT ATTTTTCATC CCTGAAGAGT TTTAAAATA CAGAAAGGTG GTCTTCACTC TGCCATCCCT  
 CCTCCCTGTC CAGGCAAAGC CTGACTTGAT GTGTTCTTCC TCATGGCAGG ATTCTGGCTT TTTCTCCAGG  
 GGTGGGACAG CCTGATCTCT TAGAATGACT CTCATAAATA GCATCAGAAT AACAAATGAA TGCTTGGGGT  
 TTGTGAGGGC CTCTGTCTAC CTTTGACTT AGGGTGGAAA CTGGTCTCTG AAATTTACAT GAGAGTGCCC  
 CTGTCTCAG CTTTTCAGCA GTCCAGTGTG GGATGAGGTT TTAATTTCT CTTTCTATAA AATTAATTGA

```

GGCCTGACCT TTTGGTCTAT TCAGGCCTTT CCACTTTCTT GCTTTTTTGT TTTGTTTTTG GTTGGGGGTT
ATACTAGATT TGGTTAGACC AACTCAATCT CAAACTCACC ATCTTGCCCA GGCTGGCTTT GAACTCAGAT
CCTCCTGCCA AGGATTCTAG GCATACACTA CCATACCTGG CTCACTCTCG CCGGTTGGAC TTTAGATCAG
AAGGGATCTT GCTGCCGCC GAAAGAGGAA GGGCTGGAAG AGGAAGGAGC TTGGCGTAAT CATGGTCATA
GCTGTTTTCT GTGTGAAATT GTTATCCGCT CACAATTCCA CACAACATAC GAGCCGGAAG CATAAAGTGT
AAAGCCTGGG GTGCCTAATG AGTGAGCTAA CTCACATTAA TTGCGTTGCG CTCACTGCCC GCTTTCCAGT
CGGAAACCT GTCGTGCCAG CTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT TGCATATTGG
GCGCTCTTCC GCTTCTCGC TCACTGACTC GCTGCGCTCG GTCGTTTCGG TCGGGCGAGC GGTATCAGCT
CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAAG
GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC GCCCCCCTGA
CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG
TTTCCCCTG GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCT
TTCTCCCTC GGAAGCGTG GCGCTTTCTC ATAGCTCAG CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT
TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCCCTCAG CCCGACCCT GCGCCTTATC CGGTAACTAT
CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA
GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGAAC
AGTATTTGGT ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC
AAACAAACCA CCGCTGGTAG CCGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA AAAAAAGGAT
CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACCTAC GTTAAGGGAT
TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG TTTTAAATCA
ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG
CGATCTGTCT ATTTCTGTTCA TCCATAGTTG CCTGACTCCC CGTCGTGTAG ATAACCTACGA TACGGGAGGG
CTTACCATCT GGCCCCAGTG CTGCAATGAT ACCGCGAGAA CCACGCTCAC CGGCTCCAGA TTTATCAGCA
ATAAACCAGC CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCCTCC ATCCAGTCTA
TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC
TACAGGCATC GTGGTGTAC GCTCGTCGTT TGGTATGGCT TCATTCAGCT CCGGTTCCCA ACGATC

```

**GE100003**, scramble sequence in pCas-Guide vector

**Disclaimer:**

These products are manufactured and supplied by OriGene under license from ERS. The kit is designed based on the best knowledge of CRISPR technology. The system has been functionally validated for knocking-in the cassette downstream the native promoter. The efficiency of the knock-out varies due to the nature of the biology and the complexity of the experimental process.

**RefSeq:**

[NM\\_009764](#)

**UniProt ID:**

[P48754](#)

**Summary:**

E3 ubiquitin-protein ligase that specifically mediates the formation of 'Lys-6'-linked polyubiquitin chains and plays a central role in DNA repair by facilitating cellular responses to DNA damage. It is unclear whether it also mediates the formation of other types of polyubiquitin chains. The E3 ubiquitin-protein ligase activity is required for its tumor suppressor function. The BRCA1-BARD1 heterodimer coordinates a diverse range of cellular pathways such as DNA damage repair, ubiquitination and transcriptional regulation to maintain genomic stability. Regulates centrosomal microtubule nucleation. Required for normal cell cycle progression from G2 to mitosis. Required for appropriate cell cycle arrests after ionizing irradiation in both the S-phase and the G2 phase of the cell cycle. Involved in transcriptional regulation of P21 in response to DNA damage. Required for FANCD2 targeting to sites of DNA damage. May function as a transcriptional regulator. Contributes to homologous recombination repair (HRR) via its direct interaction with PALB2, fine-tunes recombinational repair partly through its modulatory role in the PALB2-dependent loading of BRCA2-RAD51 repair machinery at DNA breaks. Component of the BRCA1-RBBP8 complex which regulates CHEK1 activation and controls cell cycle G2/M checkpoints on DNA damage via BRCA1-mediated ubiquitination of RBBP8. Acts as a transcriptional activator (By similarity). Inhibits lipid synthesis by binding to inactive phosphorylated ACACA and preventing its dephosphorylation.[UniProtKB/Swiss-Prot Function]

**Product images:**
