

The image shows a web browser window with the URL <http://www.outknocker.org/>. The page title is "OutKnocker" and there is a "RESTART" button in the top right corner. The interface contains several input fields and a "START" button, each with a red box highlighting it and a text instruction:

- Gene Name (optional):** Input field contains "hsBIRC3". Instruction: "Enter gene name here."
- Reference Sequence:** Input field contains "CACAGTGGTAGGAACTTCTCATCAAGGCAGAAAAATCTTGATTTGCTCTGGAGTTTACAGGATTTGATGGAGAGTTTGAATAAGAGCCACGG". Instruction: "Enter reference sequence here (same orientation as sequencing read)."
- Nuclease Target Site:** Input field contains "CCACGGAAATATCCACTGTTTTTC". Instruction: "Enter nuclease target site here (same orientation as sequencing read)."
- Indel Threshold [%]:** Input field contains "2". Instruction: "Set a threshold for calling an individual indel event."
- Phred Score Threshold (optional):** Input field contains "60". Instruction: "Enter Phred score threshold here."
- Targeting mutagenesis oligonucleotide (optional), [highlighted region] (optional):** Empty input field. Instruction: "Optionally enter donor oligonucleotide sequence"
- Checkboxes:** "Show basewise alignments (disable to use less memory)" is checked. Instruction: "Choose if alignment of raw reads shall be visualized"
- FASTQ Files (MiSeq):** Input area with "Durchsuchen..." and "Keine Dateien ausgewählt.". Instruction: "Upload FASTQ sequencing files here (multiple files can be uploaded at once)"
- START** button. Instruction: "Press 'START' to run OutKnocker."

At the bottom left, there is a link for [Frequently Asked Questions](#).