

## SUPPLEMENTAL FIGURES

**guide #1**    quality score: **96**

**guide sequence:** GGTGCTAGCCTTGCGTTCCG    **AGG**

**on-target locus:** unknown

**number of offtarget sites:** 40 (8 are in genes)

top 20 genome-wide off-target sites

show all exonic

| sequence                 | score | mismatches        | UCSC gene    | locus            |
|--------------------------|-------|-------------------|--------------|------------------|
| AGTGCTGCCCGTGCCTTCCGAGG  | 0.6   | 4MMs [1:7:8:11]   | NM_001195545 | chr17:+38100934  |
| AGGGCTAGCCTGGCGTTCCCCAG  | 0.3   | 4MMs [1:3:12:20]  |              | chr13:-30497928  |
| GTTGCTGGCATTGCCTTCCGCAG  | 0.3   | 4MMs [2:7:10:15]  | NM_024344    | chr15:+42694244  |
| GCTGCAAGCTTTGCTTTCCGAAG  | 0.2   | 4MMs [2:6:10:15]  |              | chr10:-118563890 |
| TATTCTAGCCTTGGGTTCCGGGG  | 0.2   | 4MMs [1:2:4:14]   |              | chr5:+57389224   |
| GAGGCTAACCTTGTAGTTCCGAGG | 0.2   | 4MMs [2:3:8:14]   |              | chr8:-123891316  |
| AGGGCTAGCCTCGCATTCCGGAG  | 0.2   | 4MMs [1:3:12:15]  |              | chr12:+124874211 |
| ATTGCTAGCCTTGCTTTCCAGAG  | 0.2   | 4MMs [1:2:15:20]  |              | chr13:-74478243  |
| GATGCTAGCTTTACTTTCCGGAG  | 0.1   | 4MMs [2:10:13:15] |              | chr11:+56945800  |
| GGGGCAAGCCTTGCGTTCTTTAG  | 0.1   | 4MMs [3:6:19:20]  |              | chr5:-5189109    |
| GATGCTAGCTTTGCCTTCTGCAG  | 0.1   | 4MMs [2:10:15:19] |              | chr21:+32187762  |
| GGTGCTCTCCTTGCTTGCCGTGG  | 0.1   | 4MMs [7:8:15:17]  |              | chr4:-99552388   |
| GAAGCTAGCCTTGCGTTTTGCGG  | 0.1   | 4MMs [2:3:18:19]  | NM_001102401 | chr8:-33370653   |
| GGGCTGGCCTTGCCCTCAGTAG   | 0.1   | 4MMs [3:7:15:19]  |              | chr3:+140056521  |
| GATGCTAGCCATCCTTTCCGCAG  | 0.1   | 4MMs [2:11:13:15] |              | chr9:-87343660   |
| GGTACTGGCCTCGCGATCCGCAG  | 0.1   | 4MMs [4:7:12:16]  | NM_006861    | chr12:+120554489 |
| GGTGCAGGCGTGCCTTCCGGGG   | 0.1   | 4MMs [6:9:11:15]  |              | chr1:-2029025    |
| GGTGCAGGCGTGCCTTCCGGGG   | 0.1   | 4MMs [6:9:11:15]  |              | chr1:-2029090    |
| GGGGCTAGTCATGAGTTCCGGGG  | 0.1   | 4MMs [3:9:11:14]  |              | chr19:+5966254   |
| GATGCTAGACTTGTGTTCCACAG  | 0.1   | 4MMs [2:9:14:20]  |              | chr9:-133279454  |

**Supplemental Figure I.** Output from CRISPR Design server.

Processing input tag: GGTGCTAGCCTTGCCTTCCGNGG  
 Search in target database: hg38  
 Length: 23  
 searching for no indel hits allowing up to 2 mismatch(es) ... Done  
 searching for 1b-deletion hits allowing up to 1 mismatch(es) ..... Done  
 searching for 1b-insertion hits allowing up to 1 mismatch(es) ..... Done

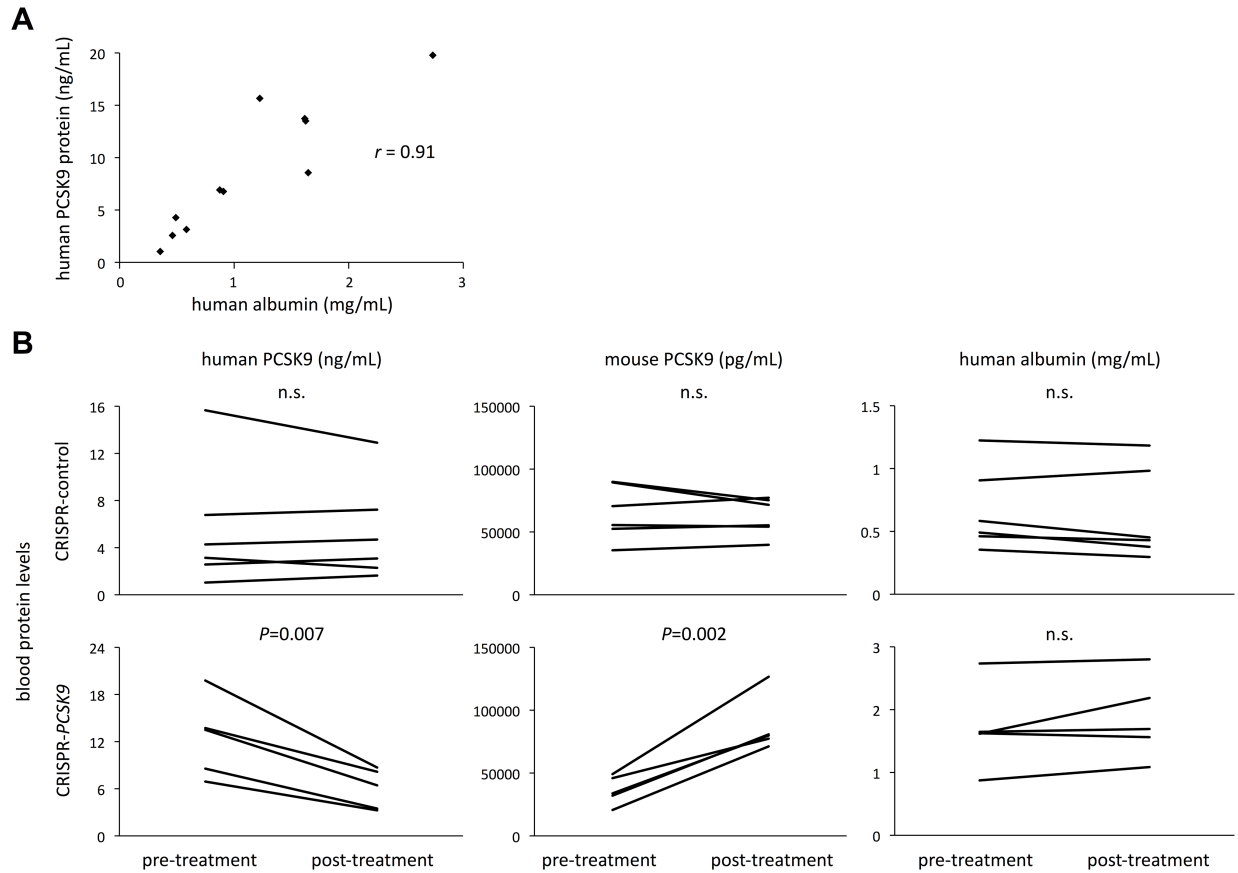
[View raw search results in txt file](#)

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| Result   | Query type              | Mismatch | Hit ends in RG | chr position                             | Strand | Cut site  | Score |
|--|-------------------------|----------|----------------|--|--------|-----------|-------|
| GGTGCTAGCCTTGCCTTCCGAGG -- hit<br>GGTGCTAGCCTTGCCTTCCGNGG -- query   | No indel                | 0        | Yes            | <a href="#">Chr1:55039960-55039982</a>   | +      | 55039976  | 0     |
| ^GTGCTAGCCTTGCCTTCCGAGG -- hit<br>GGTGCTAGCCTTGCCTTCCGNGG -- query   | Del 19, or Del 20       | 0        | Yes            | <a href="#">Chr1:55039961-55039982</a>   | +      | 55039976  | 0.63  |
| GT^GCTAGCCTTGCCTTCCGAGG -- hit<br>GGTGCTAGCCTTGCCTTCCGNGG -- query   | Del 18                  | 1        | Yes            | <a href="#">Chr1:55039961-55039982</a>   | +      | 55039976  | 0.79  |
| GGTGC^AGCCTTGCCTTCCGAGG -- hit<br>GGTGCTAGCCTTGCCTTCCGNGG -- query   | Del 15                  | 1        | Yes            | <a href="#">Chr5:168269438-168269459</a> | -      | 168269444 | 2.62  |
| GGTGCTAGCCTTGCCTTCC^GAG -- hit<br>GGTGCTAGCCTTGCCTTCCGNGG -- query   | Del 1                   | 1        | Yes            | <a href="#">Chr1:55039960-55039981</a>   | +      | 55039975  | 26.51 |
| GGTGCTAGCCTTGCCTTCCG^AG -- hit<br>GGTGCTAGCCTTGCCTTCCGNGG -- query   | Del PAM 3               | 1        | Yes            | <a href="#">Chr1:55039960-55039981</a>   | +      | 55039975  | 40.51 |
| GGTGCTAGCCTTGCCTTCCGA^G -- hit<br>GGTGCTAGCCTTGCCTTCCGNGG -- query   | Del PAM 1, or Del PAM 2 | 0        | Yes            | <a href="#">Chr1:55039960-55039981</a>   | +      | 55039975  | 20.51 |
| TGGTGCTAGCCTTGCCTTCCGAGG -- hit<br>GNGTGCTAGCCTTGCCTTCCGNGG -- query | Ins 19                  | 1        | Yes            | <a href="#">Chr1:55039959-55039982</a>   | +      | 55039976  | 0.95  |
| TGGTGCTAGCCTTGCCTTCCGAGG -- hit<br>GNGTGCTAGCCTTGCCTTCCGNGG -- query | Ins 18                  | 1        | Yes            | <a href="#">Chr1:55039959-55039982</a>   | +      | 55039976  | 0.97  |
| GGTGCTAGCCTTGCCTTCCGAGGA -- hit<br>GGTGCTAGCCTTGCCTTCCGNGG -- query  | Ins PAM 2, or Ins PAM 3 | 1        | No             | <a href="#">Chr1:55039960-55039983</a>   | +      | 55039977  | 40.7  |
| GGTGCTAGCCTTGCCTTCCGAGGA -- hit<br>GGTGCTAGCCTTGCCTTCCGNGG -- query  | Ins PAM 1               | 1        | No             | <a href="#">Chr1:55039960-55039983</a>   | +      | 55039977  | 40.7  |

**Supplemental Figure II.** Output from COSMID server.



**Supplemental Figure III.** Pre-treatment and post-treatment human PCSK9 protein, mouse PCSK9 protein, and human albumin levels in the blood. **A**, Pre-treatment human PCSK9 and albumin levels in individual mice are highly correlated.  $r$  is the Pearson correlation coefficient. **B**, Pre-treatment and post-treatment levels in individual mice in the two treatment groups.  $P$  values were calculated with the paired t-test.