

Figure S1

>LaSCL6 MNGMLRSTSGNSLPPAQLKHQILQSKTSPVQAQKRHKCSLSRSGGEIEPTSVLDIRSPSTSTLSSSLGGSSSAGAAVAVSGGLLCEAVSDGGGGGSGSGGAETLLLESSGKEAFNNGGGSTNSPARWYPNRRSSGGSGRE
GFGWRLNNGEQPGGGGMLGKSEVKKEEPQQQQQQSRAEEWGPCCGGGAGVMEDESMLLESAGAPDQSLMRWLLGEIEDPKDLPPQIKANTSGGSASAAHFEDPSIEPNFGDPVAFSFSNNISDV IAPPQAPPPSSFRAPYPTLSNQ
PQQQFISPPAPPPPPPPPPFAYNAPIPTPFVNAYHPEVLFSAPAVYGSNPAQHFGPDFPRFNMA SDPTRNNNNLLFDMPLPAPKRFGLHQLWQQTFRKQQYMNMMKPQHQQELLQSLQRRQQFLHQPPPPPHHQLRQKAI VNNTLKVES
SGAAAEVQVIVEQLKAAAEAVELGNLDHAQAILARLNQHL SPLGKPLHRAAFYFKEALASRLNATASTTGGDNRNATGSGTGTNSISPLDMVHKISAYKSFSEASPLAQFAHFTANQALLEALDGAEA IHI IDFEI GLGGQWASFLQELAVKL
GGAPPVRLTALGTSASSSLEHLTRDNL CNFAKQLNVPEFELLHLDRIESLTLREREAVAVNLSLLPSTFTSLDSISRLLNLIKNSPRAVVAVDAETTASAAATSPAASFVHHFLEALQFYSFMFDSLDAVINIMDAVHKIEKFLAPKIDAT
ISSAAKPPWKTLFASAGFSVAFSNTFTQAEYLIQRLHGRGFEVLKAHTALLLGWQGRPLVSATAWRCGPPP*

>AtU6-26-52 MNGMLRSTSGNSLPPAQLKHQILQSKTSPVQAQKRHKCSLSRSGGEIEPTSVLDIRSPSTSTLSSSLGGSSSAGAAVAVSGGLLCEAVSDGGGGGSGSGGAETLLLESSGKEAFNNGGGSTNSPARWYPNRRSSGGSGRE
GFGWRLNNGEQPGGGGMLGKSEVKKEEPQQQQQQSRAEEWGPCCGGGAGVMEDESMLLESAGAPDQSLMRWLLGEIEDPKDLPPQIKANTSGGSASAAHFEDPSIEPNFGDPVAFSFSNNISDV IAPPQAPPPSSFRAPYPTLSNQ
PQQQFISPPAPPPPPPPPPFAYNAPIPTPFVNAYHPEVLFSAPAVYGSNPAQHFGPDFPRFNMA SDPTRNNNNLLFDMPLPAPKRFGLHQLWQQTFRKQQYMNMMKPQHQQELLQSLQRRQQFLHQPPPPPHHQLRQKAI VNNTLKVES
SGAAAEVQVIVEQLKAAAEAVELGNLDHAQAILARLNQHL SPLGKPLHRAAFYFKEALASRLNATASTTGGDNRNATGSGTGTNSISPLDMVHKISAYKSFSEASPLAQFAHFTANQALLEALDGAEA IHI IDFEI GLGGQWASFLQELAVKL
GGAPPVRLTALGTSASSSLEHLTRDNL CNFAKQLNVPEFELLHLDRIESLTLREREAVAVNLSLLPSTFTSLDSISRLLNLIKNSPRAVVAVDAETTASAAATSPAASFVHHFLEALQFYSFMFDSLDAVINIMDAVHKIEKFLAPKIDAT
ISSAAKPPWKTLFASAGFSVAFSNTFTQAEYLIQRLHGRGFEVLKAHTALLLGWQGRPLVSATAWRCGPPP*

>AtU6-26-59 MNGMLRSTSGNSLPPAQLKHQILQSKTSPVQAQKRHKCSLSRSGGEIEPTSVLDIRSPSTSTLSSSLGGSSSAGAAVAVSGGLLCEAVSDGGGGGSGSGGAETLLLESSGKEAFNNGGGSTNSPARWYPNRRSSGGSGRE
GFGWRLNNGEQPGGGGMLGKSEVKKEEPQQQQQQSRAEEWGPCCGGGAGVMEDESMLLESAGAPDQSLMRWLLGEIEDPKDLPPQIKANTSGGSASAAHFEDPSIEPNFGDPVAFSFSNNISDV IAPPQAPPPSSFRAPYPTLSNQ
PQQQFISPPAPPPPPPPPPFAYNAPIPTPFVNAYHPEVLFSAPAVYGSNPAQHFGPDFPRFNMA SDPTRNNNNLLFDMPLPAPKRFGLHQLWQQTFRKQQYMNMMKPQHQQELLQSLQRRQQFLHQPPPPPHHQLRQKAI VNNTLKVES
SGAAAEVQVIVEQLKAAAEAVELGNLDHAQAILARLNQHL SPLGKPLHRAAFYFKEALASRLNATASTTGGDNRNATGSGTGTNSISPLDMVHKISAYKSFSEASPLAQFAHFTANQALLEALDGAEA IHI IDFEI GLGGQWASFLQELAVKL
GGAPPVRLTALGTSASSSLEHLTRDNL CNFAKQLNVPEFELLHLDRIESLTLREREAVAVNLSLLPSTFTSLDSISRLLNLIKNSPRAVVAVDAETTASAAATSPAASFVHHFLEALQFYSFMFDSLDAVINIMDAVHKIEKFLAPKIDAT
ISSAAKPPWKTLFASAGFSVAFSNTFTQAEYLIQRLHGRGFEVLKAHTALLLGWQGRPLVSATAWRCGPPP*

>AtU6-26-60 MNGMLRSTSGNSLPPAQLKHQILQSKTSPVQAQKRHKCSLSRSGGEIEPTSVLDIRSPSTSTLSSSLGGSSSAGAAVAVSGGLLCEAVSDGGGGGSGSGGAETLLLESSGKEAFNNGGGSTNSPARWYPNRRSSGGSGRE
GFGWRLNNGEQPGGGGMLGKSEVKKEEPQQQQQQSRAEEWGPCCGGGAGVMEDESMLLESAGAPDQSLMRWLLGEIEDPKDLPPQIKANTSGGSASAAHFEDPSIEPNFGDPVAFSFSNNISDV IAPPQAPPPSSFRAPYPTLSNQ
PQQQFISPPAPPPPPPPPPFAYNAPIPTPFVNAYHPEVLFSAPAVYGSNPAQHFGPDFPRFNMA SDPTRNNNNLLFDMPLPAPKRFGLHQLWQQTFRKQQYMNMMKPQHQQELLQSLQRRQQFLHQPPPPPHHQLRQKAI VNNTLKVES
SGAAAEVQVIVEQLKAAAEAVELGNLDHAQAILARLNQHL SPLGKPLHRAAFYFKEALASRLNATASTTGGDNRNATGSGTGTNSISPLDMVHKISAYKSFSEASPLAQFAHFTANQALLEALDGAEA IHI IDFEI GLGGQWASFLQELAVKL
GGAPPVRLTALGTSASSSLEHLTRDNL CNFAKQLNVPEFELLHLDRIESLTLREREAVAVNLSLLPSTFTSLDSISRLLNLIKNSPRAVVAVDAETTASAAATSPAASFVHHFLEALQFYSFMFDSLDAVINIMDAVHKIEKFLAPKIDAT
ISSAAKPPWKTLFASAGFSVAFSNTFTQAEYLIQRLHGRGFEVLKAHTALLLGWQGRPLVSATAWRCGPPP*

>LaU6-1-16 MNGMLRSTSGNSLPPAQLKHQILQSKTSPVQAQKRHKCSLSRSGGEIEPTSVLDIRSPSTSTLSSSLGGSSSAGAAVAVSGGLLCEAVSDGGGGGSGSGGAETLLLESSGKEAFNNGGGSTNSPARWYPNRRSSGGSGRE
GFGWRLNNGEQPGGGGMLGKSEVKKEEPQQQQQQSRAEEWGPCCGGGAGVMEDESMLLESAGAPDQSLMRWLLGEIEDPKDLPPQIKANTSGGSASAAHFEDPSIEPNFGDPVAFSFSNNISDV IAPPQAPPPSSFRAPYPTLSNQ
PQQQFISPPAPPPPPPPPPFAYNAPIPTPFVNAYHPEVLFSAPAVYGSNPAQHFGPDFPRFNMA SDPTRNNNNLLFDMPLPAPKRFGLHQLWQQTFRKQQYMNMMKPQHQQELLQSLQRRQQFLHQPPPPPHHQLRQKAI VNNTLKVES
SGAAAEVQVIVEQLKAAAEAVELGNLDHAQAILARLNQHL SPLGKPLHRAAFYFKEALASRLNATASTTGGDNRNATGSGTGTNSISPLDMVHKISAYKSFSEASPLAQFAHFTANQALLEALDGAEA IHI IDFEI GLGGQWASFLQELAVKL
GGAPPVRLTALGTSASSSLEHLTRDNL CNFAKQLNVPEFELLHLDRIESLTLREREAVAVNLSLLPSTFTSLDSISRLLNLIKNSPRAVVAVDAETTASAAATSPAASFVHHFLEALQFYSFMFDSLDAVINIMDAVHKIEKFLAPKIDAT
ISSAAKPPWKTLFASAGFSVAFSNTFTQAEYLIQRLHGRGFEVLKAHTALLLGWQGRPLVSATAWRCGPPP*

>LaU6-7-6 MNGMLRSTSGNSLPPAQLKHQILQSKTSPVQAQKRHKCSLSRSGGEIEPTSVLDIRSPSTSTLSSSLGGSSSAGAAVAVSGGLLCEAVSDGGGGGSGSGGAETLLLESSGKEAFNNGGGSTNSPARWYPNRRSSGGSGRE
GFGWRLNNGEQPGGGGMLGKSEVKKEEPQQQQQQSRAEEWGPCCGGGAGVMEDESMLLESAGAPDQSLMRWLLGEIEDPKDLPPQIKANTSGGSASAAHFEDPSIEPNFGDPVAFSFSNNISDV IAPPQAPPPSSFRAPYPTLSNQ
PQQQFISPPAPPPPPPPPPFAYNAPIPTPFVNAYHPEVLFSAPAVYGSNPAQHFGPDFPRFNMA SDPTRNNNNLLFDMPLPAPKRFGLHQLWQQTFRKQQYMNMMKPQHQQELLQSLQRRQQFLHQPPPPPHHQLRQKAI VNNTLKVES
SGAAAEVQVIVEQLKAAAEAVELGNLDHAQAILARLNQHL SPLGKPLHRAAFYFKEALASRLNATASTTGGDNRNATGSGTGTNSISPLDMVHKISAYKSFSEASPLAQFAHFTANQALLEALDGAEA IHI IDFEI GLGGQWASFLQELAVKL
GGAPPVRLTALGTSASSSLEHLTRDNL CNFAKQLNVPEFELLHLDRIESLTLREREAVAVNLSLLPSTFTSLDSISRLLNLIKNSPRAVVAVDAETTASAAATSPAASFVHHFLEALQFYSFMFDSLDAVINIMDAVHKIEKFLAPKIDAT
ISSAAKPPWKTLFASAGFSVAFSNTFTQAEYLIQRLHGRGFEVLKAHTALLLGWQGRPLVSATAWRCGPPP*

Figure S1. Protein sequence after gene editing in *LaSCL6*. The red background in the figure indicates an amino acid substitution, and the red dashed lines indicate deletion segments of amino acid.