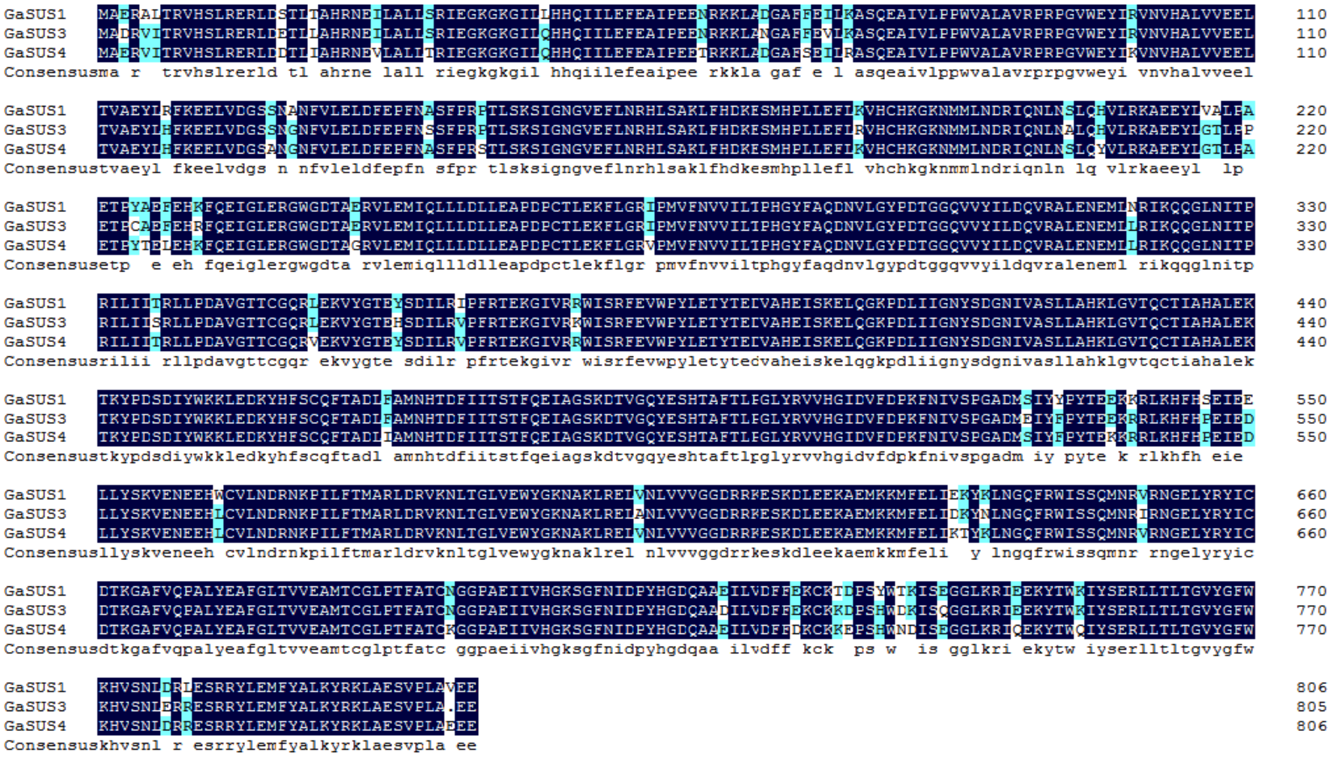
Additional file 2. Multiple alignment of the amino acid sequences between three Sus genes *GaSus1*, *GaSus3* and *GaSus4*.



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GaSUS1   MAERALTRVHSLRERLDSTLTAHRNEILALLSRIEGKGKGILLHHQIILEFEAIPEENRKKLADGAFFEILKASQEAIVLPPWVALAVRPRPGVWEYIRVNVHALVVEEL     110
GaSUS3   MADRVITRVHSLRERLDETLLAHRNEILALLSRIEGKGKGILQHHQIILEFEAIPEENRKKLANGAFFEVLKASQEAIVLPPWVALAVRPRPGVWEYIRVNVHALVVEEL     110
GaSUS4   MAERVITRVHSLRERLDDTLIAHRNEVLALLTRIEGKGKGILQHHQIILEFEAIPEETRKKLADGAFSEILRASQEAIVLPPWVALAVRPRPGVWEYIKVNVHALVVEEL     110
Consensusma r  trvhslrerld tl ahrne lall riegkgkgil hhqiilefeaipee rkkla gaf e l asqeaivlppwvalavrprpgvweyi vnvhalvveel

GaSUS1   TVAEYLRFKEELVDGSSNANFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLKVHCHKGKNMMLNDRIQNLNSLQHVLRKAEEYLVALPA     220
GaSUS3   TVAEYLHFKEELVDGSSNGNFVLELDFEPFNSSFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLRVHCHKGKNMMLNDRIQNLNALQHVLRKAEEYLGTLPP     220
GaSUS4   TVAEYLHFKEELVDGSANGNFVLELDFEPFNASFPRSTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLKVHCHKGKNMMLNDRIQNLNSLQYVLRKAEEYLGTLPA     220
Consensustvaeyl fkeelvdgs n nfvleldfepfn sfpr tlsksigngveflnrhlsaklfhdkesmhpllefl vhchkgknmmlndriqnln lq vlrkaeeyl  lp

GaSUS1   ETPYAEFEHKFQEIGLERGWGDTAERVLEMIQLLLDLLEAPDPCTLEKFLGRIPMVFNVVILTPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLNRIKQQGLNITP     330
GaSUS3   ETPCAEFEHRFQEIGLERGWGDTAERVLEMIQLLLDLLEAPDPCTLEKFLGRIPMVFNVVILTPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLNITP     330
GaSUS4   ETPYTELEHKFQEIGLERGWGDTAGRVLEMIQLLLDLLEAPDPCTLEKFLGRVPMVFNVVILTPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLNITP     330
Consensusetp  e eh fqeiglergwgdta rvlemiqllldlleapdpctlekflgr pmvfnvviltphgyfaqdnvlgypdtggqvvyildqvraleneml rikqqglnitp

GaSUS1   RILIITRLLPDAVGTTCGQRLEKVYGTEYSDILRIPFRTEKGIVRRWISRFEVWPYLETYTEDVAHEISKELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEK     440
GaSUS3   RILIISRLLPDAVGTTCGQRLEKVYGTEHSDILRVPFRTEKGIVRKWISRFEVWPYLETYTEDVAHEISKELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEK     440
GaSUS4   RILIITRLLPDAVGTTCGQRVEKVYGTEYSDILRVPFRTEKGIVRRWISRFEVWPYLETYTEDVAHEISKELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEK     440
Consensusrilii rllpdavgttcgqr ekvygte sdilr pfrtekgivr wisrfevwpyletytedvaheiskelqgkpdliignysdgnivasllahklgvtqctiahalek

GaSUS1   TKYPDSDIYWKKLEDKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYYPYTEEKKRLKHFHSEIEE     550
GaSUS3   TKYPDSDIYWKKLEDKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMEIYFPYTEEKRRLKHFHPEIED     550
GaSUS4   TKYPDSDIYWKKLEDKYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEKKRRLKHFHPEIED     550
Consensustkypdsdiywkkledkyhfscqftadl amnhtdfiitstfqeiagskdtvgqyeshtaftlpglyrvvhgidvfdpkfnivspgadm iy pyte k rlkhfh eie

GaSUS1   LLYSKVENEEHWCVLNDRNKPILFTMARLDRVKNLTGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEKAEMKKMFELIEKYKLNGQFRWISSQMNRVRNGELYRYIC     660
GaSUS3   LLYSKVENEEHLCVLNDRNKPILFTMARLDRVKNLTGLVEWYGKNAKLRELANLVVVGGDRRKESKDLEEKAEMKKMFELIDKYNLNGQFRWISSQMNRIRNGELYRYIC     660
GaSUS4   LLYSKVENEEHLCVLNDRNKPILFTMARLDRVKNLTGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEKAEMKKMFELIKTYKLNGQFRWISSQMNRVRNGELYRYIC     660
Consensusllyskveneeh cvlndrnkpilftmarldrvknltglvewygknaklrel nlvvvggdrrkeskdleekaemkkmfeli  y lngqfrwissqmnr rngelyryic

GaSUS1   DTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFNIDPYHGDQAAEILVDFFEKCKTDPSYWTKISEGGLKRIEEKYTWKIYSERLLTLTGVYGFW     770
GaSUS3   DTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFNIDPYHGDQAADILVDFFEKCKKDPSHWDKISQGGLKRIEEKYTWKIYSERLLTLTGVYGFW     770
GaSUS4   DTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVHGKSGFNIDPYHGDQAAEILVDFFDKCKKEPSHWNDISEGGLKRIQEKYTWQIYSERLLTLTGVYGFW     770
Consensusdtkgafvqpalyeafgltvveamtcglptfatc ggpaeiivhgksgfnidpyhgdqaa ilvdff kck  ps w  is gglkri ekytw iyserlltltgvygfw

GaSUS1   KHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVEE                                                                               806
GaSUS3   KHVSNLERRESRRYLEMFYALKYRKLAESVPLA.EE                                                                               805
GaSUS4   KHVSNLDRRESRRYLEMFYALKYRKLAESVPLAEEE                                                                               806
Consensuskhvsnl r esrrylemfyalkyrklaesvpla ee
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