

GpFUS1	1	MWTEFGIVLYLICIQVFA--ODCSIVNIDNTVVLEPEGPVVAGRPYNFSSII	48
CrFUS1	1	MPIDF--ILVLL--AAV-AKSDCSVV--AD-FKIDFQTSIFTAGNAYNITLT	45
GpFUS1	49	LRDNDLQPVONLYDPLLAVGCPN-SEENENLCTTYSLRPLGDGVYVVSIVL	97
CrFUS1	46	LLDSYGDEPTCVLYDPLLSVSCPSSSSNGRDFCSLQLSPLVNGVYNIKVIP	95
GpFUS1	98	LTFKCAHEPWPPQYNPSARLEPDEYFTGGVTFVSVVYDEVHVPSPFFPIAVS	147
CrFUS1	96	QTLWCGHTVWPEPYSVAELPDVYFACDTAIRITYNGRDIQGSPPFVTVO	145
GpFUS1	148	PAEELSAALSVMVDPVSGSSGRMELVARLYQVTDYSNWIWIRNPDLINA	197
CrFUS1	146	AEPHISTALSIVNVAVPAKCVASSREAIAYFYQISDRFTNWIREKSIATQ	195
GpFUS1	198	ISVKSASTGVSFALQWQWQWIEILARSEQSCNYSLEVLVQYPDGRAEPL	247
CrFUS1	196	LRVS--AYPDADISVQWQWQWIVLYANSTAGMYRFOVYFIDDDGSEVEI	244
GpFUS1	248	RIQS-AKGISFSGSFEVRPGVLEISNFDVKVSNTOIVAGSLYHVTVQSRD	296
CrFUS1	245	RILSPGLGLSYDGSFEVLELALDEAKITASGLPQEVVACIPVSLTLOAMD	294
GpFUS1	297	RESNPTPLSDPAQYTTWLEOVQNSSIVTMSISSSG-HVQLEE-IVNATISP	344
CrFUS1	295	IYSNPTRLVDEPSYQPFQOPDNKTLQVRLVTVDSGALQENVVAIPTNT	344
GpFUS1	345	GGLAQWHIREREATSYRMVITYHGSVMAVLFSAVDVVPGPPSFSKSTFD	394
CrFUS1	345	TGACSWSITEFTSMDYSVSVTYKESVLMHFS---ITVRNAQASPSNSTAL	391
GpFUS1	395	IKDTFEAGPLLIVARFADWGNPTLGSANVVVSELKNGAQLLPSERAVN-	443
CrFUS1	392	LPEIQAGTTHLYVTPTWGN-IAPLANNDLSIGLTGSTFFHSTFVPEP	440
GpFUS1	443	----QEVVYSVNIIFRAGAMAVRISIGADALVRNITVPIPLRTISLHDSWVS	489
CrFUS1	441	VRKGDYSVYSLTTEAGLVVVSLOLHNSWLEKNITTEASYPSLQRSYVL	490
GpFUS1	490	GYGAGSLSAFGPTFVTAGVOYSVWVHAYDIYGNQLHKDSNCCGLOIGGAG	539
CrFUS1	491	GFGAGDPYGFAPTPLVAGEQYVLRVFIKDLVGNLTIQAD-KVVDLNIIVCPG	539
GpFUS1	540	PTAVMTDIEEDTGKLGFSYNIITVSGNYTVSLATTEGFLHGGFIOVRSQAQ	589
CrFUS1	540	QVLMNMSMLPSGAFEVIYQPIVVGVIYAVIANLITGLLLHRCAVYVQPGTF	589
GpFUS1	590	QYQRTKMYFPSTAVAGMSFYATVEFTDSEGNPAPVTGVLSVLIITG-CVQT	638
CrFUS1	590	NPNAITLQVPDYIVAGEASSFKLAFHDSYGNAAASSGEASVVVFKYCGES	639
GpFUS1	639	HTTEVAMNGDCNATISLOLOVASTYAYGYMNGIILGSTASAVVILPATP	688
CrFUS1	640	LSFPLNLSCKFIEELPFRIMHSGLYAFSISVNSVIVKSNNGYLHVVEGSA	689
GpFUS1	689	AKAAEAAILGAGVDTVRLAYSFYDAYDNMIYVKDLEDGLGIALEPVRPWEA	738
CrFUS1	690	YALNITELKMTDRLLLEVYAYVVDEMLNSLNAAAMTA-FAVALDEPILFHG	738
GpFUS1	739	NVTFERSNSMSISLWYEPSSPOOITVIFRGVALHTYVWTSVVPMQEDIL	788
CrFUS1	739	NVTLIS-STGITLQDKDE-AIENTLOVOLKISNTIFENCQWKPAAHATI	786
GpFUS1	789	RKRWRG-IVASACGALLGCSLLICVVTQVSRHTP	824
CrFUS1	787	RRVRSIGPLIATITAVCVILFASIALVWSFRMDRHKP	823

Figure S6. Alignment of the amino acid sequences of the GpFUS1 and CrFUS1 proteins.

Identical or similar residues have solid or shaded backgrounds, respectively.

Underlined residues are aligned in Figure S7. The GC content of *GpFUS1* CDS and introns are moderate (~50%), showing a common feature found in most of the previously identified mating type-specific genes (*CrFUS1*: 47.7%; *CrMID*: 50.5%; *GpMID*: 52.9%; *GpMTD1*: 55.5%).