



Saccharomyces cerevisiae as a host for chondroitin production

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Table S1. Primers used in this study.

Purpose	Name	Template	Sequence (5' → 3')	Restriction enzyme
Cloning of <i>Giuae</i> in pSP-GM1 (PGK1)	Gi_uae_Fw1	pUC57_Giuae	AAAGGATCCAAAAAATGCATCACCATCAC CATCACCAGAATCATTCCTTCTTGG	<i>Bam</i> HI
	Gi_uae_Rv1		AAAAC TCGAGCTATAATCCAATACCTTTTAC ATC	<i>Xho</i> I
Cloning of <i>Btchsy</i> in pSP-GM1 (PGK1)	Bt_chsy1_Fw	pUC57_Btchsy1	AAAGGATCCAAAAAATGCATCACCATCAC CATCACGCTGTCCGAGGTCTGAAGAGC	<i>Bam</i> HI
	Bt_chsy1_Rv		AAAAC TCGAGTTAAGCCGTGCGGACTGAGC	<i>Xho</i> I
Cloning of <i>Giuae</i> in pSP-GM1_(PTEF)	Giuae_tefp_Fw	pSP-GM1_Giuae	ATTTGCGGCCGCAAAACAATGCATCACCAT CACCAT	<i>Not</i> I
	Giuae_tefp_Rv		AACGAGCTCCTATAATCCAATACCTTTTACA TC	<i>Sac</i> I
<i>Zmugd</i> cloning in pSP-GM1_tefp_Giuae	Zm_psp_Fw	pSP-GM1_Zmugd	AAAGGATCCAAAAAATGCATCACCATCAC CATCACC GCATTACCATGATCGGTTCC	<i>Bam</i> HI
	Zm_psp_Rv		AAAGCTAGCTTACCCTGCATTGGGTCGAC	<i>Nhe</i> I
<i>Btchsy</i> cloning in pBEVY	Btchsy_pBEV_Y_Fw	pSP-GM1_Btchsy	AACGCGGATCCAAAACAATGCATCACCATC AC	<i>Bam</i> HI
	Btchsy_pBEV_Y_Rv		AACGCCGTCGACTTAAGCCGTGCGGACTGA GC	<i>Sal</i> I
<i>kfoA</i> cloning in pSP-GM1_Zmugd	kfoA_psp_Fw	pETM6_kfoCA	ATTTGCGGCCGCAAAACAATGAATATATTA GTTACAGGTG	<i>Not</i> I
	kfoA_psp_Rv		AACGAGCTCTTAAATATAACCATTTGGGTTT	<i>Sac</i> I
<i>kfoC</i> cloning in pBEVY-L	kfoC_pBEVY_Fw	pETM6_kfoCA	AACGCGGATCCAAAACAATGAGTATTCTTA ATCAAGC	<i>Bam</i> HI
	kfoC_pBEVY_Rv		AACGCCGTCGACTTATAAATCATTCTCTATT TTTTCCC	<i>Sal</i> I
Colony PCR and sequencing				
	tADH1_Fw	pSP-GM1_tefp_Giuae / pSP-GM1_Zmugd_kfoA	CCTAAGAGTCACTTTAAAATTTGT	
	TEF1p_Rv		CGTACCACTTCAAAACACC	
	PGK1p_FW	pSP-GM1_Zmugd / pSP-GM1_Giuae_Zmugd	GTGATCTCCAGAGCAAAGT	
	CYCt_REV		CTTCGAGCGTCCCAAAC	
	tADH1_Fw	pBEVY_Btchsy / pBEVY_kfoC	CCTAAGAGTCACTTTAAAATTTGT	
	pGAL_middle_Rv		ATTATTCCCCTACTTGACTAATAAG	
	Bt_chsy1_midle	pBEVY_Btchsy	CGGTAAATGTTTAAGAGAGATG	
	kfoC_pBEVY_Rv	pBEVY_kfoC	AACGCCGTCGACTTATAAATCATTCTCTATT TTTTCCC	



Table S2. Codon-optimized gene sequences (5' → 3') for *Saccharomyces cerevisiae*.

>Chondroitin synthase (chsy1) (2412 bp GC%: 41,54; CAI: 0,74)

ATGGCTGTCCGAGGTCGAAGAGCATGGTTAAGCGTTTTGCTGGGTTAGTTCTTGTTT
TGTCTTAGCCTCTAGACTCGTTTTGCCGAGGGCTTCTGAGTTAAAAAGAGCAGGCCCA
CGGAGAAGAGCTAGTCCAGAGGCTTGTAGGCCGGGTCAGGCAGCAGCCGTACCATT
AGCTGGAGGTGCTAGAGGAGATGCGAGAGGCCAAAGATTATGGCCCCACGGGGAAG
CTCAAGACGGTGTTCCTCCCGCGACCGCAATTTCTTATTCGTAGGAGTCATGACCGCTCA
AAAGTATCTACAAACGAGAGCTGTGGCTGCTTTCAGAACTTGGTCAAAAACCTATCCC
AGGCAAGGTGCAATTTTTCTCATCTGAAGGTTCTGATACCAGTATTAGTATTCCTGTG
GTCCCATTTGCGAGGTGTTGATGATTCATATCCGCCTCAGAAAAAATCATTATGATGT
TAAAATATATGCATGATCATTACTTGGATAAGTACGAATGGTTCATGAGAGCTGACG
ATGATGTTTATATTAAGGTGACAGATTGGAATCATTCTTAAGATCGCTCAACAGCAG
CGAGCCTTTGTTCTTGGGACAGACCGGCTTAGGAACCACTGAAGAAATGGGAAAAC
TGCTCTAGAACCCGGTGAAAACTTTTGCATGGGAGGCCCGGGCGTTATTATGAGCAG
AGAAGTATTGAGAAGAATGGTACCTCACATCGGTAAATGTTTAAGAGAGATGTACAC
TACTCACGAGGATGTAGAGGTGGGTCGCTGCGTTAGAAGATTTGCTGGTGTACAATG
CGTCTGGTCGTACGAAATGCAACAACCTCTTTTATGAAAATTATGAACAAAATAAAAA
AGGTTACATACGTGATTTACACAATTCCAAGATACATAGAGCCATCACCTTACATCCT
AACAAAAATCCTCCATATCAATATCGTTTGACAGCTATATGCTTTCTAGAAAAATCG
CTGAACCTGAGACATCGTACTATCCAACCTGCATCGCGAGATTGTCCTTATGTCCAAGTA
CAGTAATACGGAAGTTCATAAAGAGGATTTGCAATTAGGTATTCCACCGTCTTTCATG
AGATTTCAACCAAGACAAAGAGAAGAAATTTTGGAATGGGAATTTCTAACCGGTAA
GTATTTATATAGTGCAGCCGATAGCCAGCCCCACGTAGAGGTATGGACAGCGCCCA
AAGAGAAGCATTGGATGATATTGTTATGCAAGTTATGGAAATGATAAATGCCAATGC
CAAACTAGAGGGAGAATTATAGATTTCAAAGAAATTCAATACGGTTATCGCCGTGT
TAATCCGATGTACGGGGCTGAATATATACTGGATTTGTTGTTGCTTTACAAGAAACAT
AAAGGTAAGAAAATGACAGTTCAGTTAGAAGACATGCCTATTTGCAACAACTTTTT
TCAAAAATTCAGTTTGTGTAACATGAAGAACTTGATGCAAAGGAATTGGCGAATAAA
ATTAATCAAGAATCCGGCTCCCTGTCTTCTGTCCAATTCATTGAAAAAGTTGGTGC
CATTTCAACTTCCCGGGAGTAAAAACGAACACAAAGAACCTAAGGAGAAAAAGATT
AATATTTTAATCCCCCTGAGCGGAAGATTTGACATGTTTGTCCGTTTCATGGGAACT
TTGAAAAGACATGTTTAATTCCGAATCAAAACGTGAAACTGGTTGTCTTATTGTTTAA
TTCTGATTGCAACCCTGACAAAGCCAAGCAAGTGGAACCTATGCGTGATTACAGAAT
TAAATATCCCAAGGCCGATATGCAAATTTTGCCGGTGTGAGGTGAGTTTTCCAGAGCC
TTGGCATTGGAGGTGGGCAGTTCTCAATTTAACAATGAGAGTCTTTTGTTTTTCTGTGA
TGTTGACTTAGTCTTCACGGCCGAGTTTTTGCAACGTTGTAGAGCTAACACTGTCTTAG
GCCAACAAATTTACTTCCCTATTATCTTCTCACAATATGATCCTAAAATTGTCTACTCC
GGCAAAGTTCCAAGTGATAATCACTTTGCTTTTACTCAGAAAACTGGTTTTTGGAGGA
ATTATGGATTTGGAATTACGTGTATATACAAAGGGGATTTAGTGAGGGTGGGTGGCTT
TGATGTGTCCATCCAGGGTTGGGGTCTGGAAGATGTTCGATTTATTCAACAAAGTCGTT
CAAGCAGGGCTTAAACTTTTCAGGAGCCAGGAAGTTGGCGTGGTCCACGTACACCAT
CCTGTTTTTTGTGATCCGAACCTTAGATCCTAAGCAATACAAAATGTGTTTGGGCAGTA
AAGCCTCCACTTATGGTAGCACTCATCAATTGGCAGAAATGTGGTTAGAAAAAACG
ATCCCAATTACTCTAAGTCGAGTAACAACAACGGCTCAGTCCGCACGGCTTAA



>UDP-N-acetylglucosamine 4-epimerase (UAE) (1158 bp GC%: 42,31; CAI: 0,77)

ATGCAGAATCATTCTTCTTGGGTAAAACGGTCTTGATCACAGGCGGTTGTGGTTTCA
TTGGATCTCATTGTTAGAGGCTTGTCATGTTCTCGGTATGACCGTCTATGTTTTAGAT
AACCTCAGTTCTGGTAAGAATGTATTTAAGACAACATCTGATTGTTCTTCATCATTGGT
TTAACTATCGGTGACATTAGAGACAAGGCTATCTTCTCTAGACTTCCGCAGAAAATT
GACTTCGTCATTCATTTGGCCGCAGCTGTTTCTGTTGCCGAATCAGTAACAAATCCGC
AGAAATATATGTTAACCAATGTTGAGGGTAGTAGAAACGTTTTCCAGTATGCTGTTGA
CGCAAAGGCTTCAGCCGTCTTAAGTGCTTCTACTGCTGCATATTACGGCGATTGTGGT
AAGTCAGCTATTACCGAGGCTTTCCCCTATGGTGGCATTCTCCATACGCTGAAAGTA
AGATGGAGATGGAGAGATTAGGAGCCGAATTTCAAAAGACATCTCGTTGCAGATTCA
TTTTCTGCAGATTTTTCAATGTCTACGGCCCTAGACAGGACCCCTCCTCGCCCTACACT
GGAGTTATGAGTATTTTTATGGACAGGTGCGCCGCTAGAAAACCGATTACAATCTTTG
GTACCGGCGAGCAAACAAGAGATTTTGTTCATCAAGGACTTAATTGTCGCTGCCAT
TAACTTATTAGGTCAATTGGATAAGTTTCCTATTGGAGCAGATGCCGTGCAACAGAAC
GATCCAGAAGAAGTCCAAAGGTCCGCATATACCGGTGAAGGTGTGTACCCAACTGTT
TTCAACATCGGATCGGGAATTTGATCAGTGTCAATGAGCTTGCTGAATTAGCCAAA
ATTGTTTCTGGTAGACATGAAGTGGAATTTGTTTCATGGAGAACCACGTAGTGGAGAC
ATATTGCATTATTATCCGATTGCACTAGGATTAGAAACGCTACTGGATGGAGCGCAT
CTACTACTCTTAGAGTTGGTATGTCTGAACTTGGGGATGGGCTGCTGGCGAAATTAG
TTACTTGTCTGGTGACTTGGTAAAGAGTGTGGAAAACGAATTAAAGATTGATGGGGTT
TCAGTAGCAAAATCTCTATGTGGTAAAGATGCAGATGTAAAAGGTATTGGATTATAG