

**TableS1. Primers used in this study.**

Name	Sequences (5'→3')
<b>Primers for retinoid biosynthesis pathway construction</b>	
<i>blh<sub>SR</sub></i> -F-XbaI	GCTCTAGAAGGAGGATTACAAAATGCACAACCCGGTTACCC
<i>blh<sub>SR</sub></i> -R-EcoRI	GGAATTCTCAGGAGACGGCCTGGG
<i>ALDH1A2</i> -F-XbaI	GCTCTAGAATGACTTCCAGCAAGATAGAGAT
<i>ALDH1A2</i> -R-EcoRI	GGAATTCTTAGGAGTTCTTCTGGGGGAT
pUCM-F	TCTAGAGCGCCCGGGGA
mRS12-pUCM-R	<u>GTTTAAACTGACTGACGCACCAAAAGCGCTCACAATTCCACACAACA</u>
mRS37-pUCM-R	<u>GTTTAAACAATAAATTACGAGCCAGTCGCTCACAATTCCACACAACA</u>
mRS46-pUCM-R	<u>GTTTAAACCGAATTGGTGGGGCGAGACGCTCACAATTCCACACAACA</u>
mRS-H-pUCM-F-BamHI	CGCGGATCCTTTTTGTAGTAAAGGAGCATCGCTAAGGAGGATTACAAATCTAGA ATG
mRS-M-pUCM-F BamHI	CGCGGATCCTTTTTGTAGTAAAGAAGCAGGAGGATTACAAATCTAGAATG
mRS-R-BamHI	CGCGGATCCCGCTCACAATTCCACACAAC
pET- <i>blh<sub>SR</sub></i> -F-XbaI	GCTCTAGAATGCACAACCCGGTTACCC
pET- <i>blh<sub>SR</sub></i> -R-HindIII	CCCAAGCTTGGAGACGGCCTGGGGG
pET- <i>ALDH1A2</i> -F-BamHI	CGCGGATCCATGACTTCCAGCAAGATAGAGAT
pET- <i>ALDH1A2</i> -R-EcoRI	CGGAATTCCGGAGTTCTTCTGGGGGATC
pSTVM2-sub-USER-3-F	AGACAGUCATAAGTGCGG
pSTVM2-sub-USER-1-R	ATGCAACUCGTAGGACAG
pUC- sub-USER-3-F	AGACAGUCAATCTGCTCTGATGCC
pUC- sub-USER-1-R	ATGCAACUCATAATGAATCGGCCAAC
pUC-sub-USER-1-F	AGTTGCAUCCCGACTGGAAAGCG
pUC-sub-USER-2-F	ATCCATGUCCCGACTGGAAAGCG
pUC-sub-USER-5-F	ATATGCGAUCCCGACTGGAAAGCG
pUC-sub-USER-2-R	ACATGGAUATGCGGTGTGAAATACC
pUC-sub-USER-5-R	ATCGCATAUATGCGGTGTGAAATACCG
pUC-sub-USER-3-R	ACTGTCUATGCGGTGTGAAATACCG
Gibson-pSTVM2-F	AGACAGTCATAAGTGCGGC
Gibson- <i>blh<sub>SR</sub></i> -F	CCCCCAGAAGAACTCCTAATTCCTCCGACTGGAAAGCG
Gibson- <i>blh<sub>SR</sub></i> -R	GCCGCACTTATGACTGTCTTATGCGGTGTGAAATACCG
Gibson- <i>ALDH1A2</i> -R	TTAGGAGTTCTTCTGGGGG

### Primers for genome editing

<i>ybbO</i> -FRT-KO-F	GTTTATTGCCGACTGGATGGCGAAGCAGTTGCAGCCTTTAGTAAATCATGAAATT AACCCTCACTAAAGGGC
<i>ybbO</i> -FRT-KO-R	GACATGGGGGCTTAAGCGCGCGCTTCAACTCACCCCTGCAATATTTTGTACGAC TCACTATAGGGCTC
<i>ybbO</i> -Confirm-F	TCTGCTGAAACAGCATCAG
<i>ybbO</i> -Confirm-R	GTTCTGATTGACAACTGC
malT-UP-F	AGTCGCTTAAGGCCCTGC
malT-UP-R	TCTTCCAGTGCCAGTTTTGC
malT-Down-F	AGCAAACCGAACAGATGGCA
malT-Down-R	AAGACTTCAATCCCGCTACG
malT- <i>blh<sub>SR</sub></i> -F	GCAAAACTGGCACTGGAAGAAGGTTTCCCGACTGGAAAG
malT- <i>blh<sub>SR</sub></i> -R	TGCCATCTGTTTCGGTTTGCTACTATCGTCGCCGCACTTAT
malT- <i>ALDH1A2</i> -F	GCAAAACTGGCACTGGAAGACCCTGTCCTACGAGTTGCAT
malT- <i>ALDH1A2</i> -R	TGCCATCTGTTTCGGTTTGCTTTAGGAGTTCTTCTGGGGGAT

### Quantitative analysis of gene transcription levels

<i>blh<sub>SR</sub></i> -RT-F	ATGTCGATGGCCCAGTTC
<i>blh<sub>SR</sub></i> -RT-R	GGGTCATGATGGCGATCA
<i>ALDH1A2</i> -RT-F	TATGTGGATTTGCAGGGCGT
<i>ALDH1A2</i> -RT-R	ATTGCCACAGCACAAAGCTG

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\*Bold letters indicate restriction enzyme sites.

\*Underline indicates 5'UTR sequence.