Supplementary Material

Different modes of regulation of the expression of dextranucrase in *Leuconostoc lactis* AV1n and *Lactobacillus sakei* MN1

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Supplementary Figure S1. Analysis of the maturation of the mCherry protein in *Leuconostoc lactis* AV1n [pRCR15] strain. The bacterium was grown in MRSG medium until the middle of the exponential phase and after sedimentation and resuspension in PBS pH 7.4 the fluorescence of the cultures was measured at the indicated times. The depicted values are the average of three independent experiments.
Supplementary Figure S2. EPS production by *Leuconostoc lactis* AV1n, *Lc. lactis* AV1n[pRCR21] and *Lc. lactis* AV1n[pRCR15] in solid media. Pictures of the plates were taken after 3 days of growth on MRS agar supplemented with 2% sucrose (MRSS), glucose (MRSG), 2% maltose (MRSM) or 2% fructose (MRSF) at the indicated temperatures.
| CM70  | NRRL | Sequence Information |
|-------|------|----------------------|
| 1     | 140  | TTCAACGGATGCCCGTTGACATATTATCGTAGCGTACTGTTTAAGTATGTCAAATATGT |
| 61    | 200  | AAGGTGTGATTCTTTCAACATGTATCATGTTAACTACATTCGCCAGTAAACATAAGTCAT |
| 121   | 260  | ATGCGACTAGGAAATCTAAGTGATACAAAGTAGACAGCGACATTAAATAATAATGACGCA |
| 181   | 300  | TGAATGGGTCGCTAGGATTCTTGATTGTATCATTTTGTAATAATTGCGTTAATTGATTCA |
| 241   | 359  | AAGGTGTGATTCTTTCAACATGTATCATGTTAACTACATTCGCCAGTAAACATAAGTCAT |
| 301   | 360  | TGTTTTTTTTTTTCCAAAAGCAGCCGAAAAATATTCTTCAAATGAAATGTTTAGGGCGTC |
| 421   | 480  | AATTTTTTATATTTTATTTA |
| 481   | 540  | TGTTTTTTTTTTTCCAAAAGCAGCCGAAAAATATTCTTCAAATGAAATGTTTAGGGCGTC |
| 541   | 600  | AATTTTTTATATTTTATTTA |
| 581   | 660  | TGTTTTTTTTTTTCCAAAAGCAGCCGAAAAATATTCTTCAAATGAAATGTTTAGGGCGTC |
| 601   | 720  | TGTTTTTTTTTTTCCAAAAGCAGCCGAAAAATATTCTTCAAATGAAATGTTTAGGGCGTC |
| 661   | 840  | TGTTTTTTTTTTTCCAAAAGCAGCCGAAAAATATTCTTCAAATGAAATGTTTAGGGCGTC |
| 721   | 918  | TGTTTTTTTTTTTCCAAAAGCAGCCGAAAAATATTCTTCAAATGAAATGTTTAGGGCGTC |
| 781   | 978  | TGTTTTTTTTTTTCCAAAAGCAGCCGAAAAATATTCTTCAAATGAAATGTTTAGGGCGTC |
| 841   | 1038 | TGTTTTTTTTTTTCCAAAAGCAGCCGAAAAATATTCTTCAAATGAAATGTTTAGGGCGTC |
| 901   | 1098 | TGTTTTTTTTTTTCCAAAAGCAGCCGAAAAATATTCTTCAAATGAAATGTTTAGGGCGTC |
| CM70 2850 | GATCCGGATTTCTGATGGGCTTATCACCACACGATGGACCAATTAACAGAAGCATTTAAAATT |
| NRRL 3001 | GATCCGGATTTCTGATGGGCTTATCACCACACGATGGACCAATTAACAGAAGCATTTAAAATT |
| CM70 2910 | TATAATGCTGATCAATTGAAAACAGATAAAGAATTCACACAATTCACACAATATAACATT |
| NRRL 3061 | TATAATGCTGATCAATTGAAAACAGATAAAGAATTCACACAATTCACACAATATAACATT |
| CM70 2970 | CCAAGTACTTATGCCACAATACTAACGAATAAAGATACAGTGCCACGTGTGTACTATGGG |
| NRRL 3112 | CGTTATGGTAATGGTGCCATGACTGCTACCGATGCAGGGCAAACAATGTCTATGAAAA |
| CM70 3030 | GATATGTATACAGATGATGGTCAATACATGGCAACAAAGTCACTTTATTACGATGCAATT |
| NRRL 3172 | GATATGTATACAGATGATGGTCAATACATGGCAACAAAGTCACTTTATTACGATGCAATT |
| CM70 3090 | GATACTTTGCTGAAGTCTCGTATCAAGTATGTTTCTGGCGGGCAAACAATGTCTATGAAAA |
| NRRL 3232 | GATACTTTGCTGAAGTCTCGTATCAAGTATGTTTCTGGCGGGCAAACAATGTCTATGAAAA |
| CM70 3150 | TATAATGCTGATCAATTGAAAACAGATAAAGAATTCACACAATTCACACAATATAACATT |
| NRRL 3292 | TATAATGCTGATCAATTGAAAACAGATAAAGAATTCACACAATTCACACAATATAACATT |
| CM70 3210 | CGTTATGGTAATGGTGCCATGACTGCTACCGATGCAGGGCAAACAATGTCTATGAAAA |
| NRRL 3352 | CGTTATGGTAATGGTGCCATGACTGCTACCGATGCAGGGCAAACAATGTCTATGAAAA |
| CM70 3270 | GGTATTGCAGTAATTGAAAGTAATAACCCAGATTTGAAGTTGAGCAGTACAGATCAAGTA |
| NRRL 3412 | GGTATTGCAGTAATTGAAAGTAATAACCCAGATTTGAAGTTGAGCAGTACAGATCAAGTA |
| CM70 3330 | GTTGTAGATATGGGCATAGCGCACAAAAATCAGGCTTATCGTCCTGCTTTGTTAACAACT |
| NRRL 3472 | GTTGTAGATATGGGCATAGCGCACAAAAATCAGGCTTATCGTCCTGCTTTGTTAACAACT |
| CM70 3390 | AAAGATGGCATAGATACTTATGTATCTGATAGTGATGTCTCACAAAGCTTAATAAGATAT |
| NRRL 3532 | AAAGATGGCATAGATACTTATGTATCTGATAGTGATGTCTCACAAAGCTTAATAAGATAT |
| CM70 3450 | ACAAATAGTAATGGGCAACTTATTTTCAATAGTTCAGATATTGTTGGTACAGCAAATCCA |
| NRRL 3592 | ACAAATAGTAATGGGCAACTTATTTTCAATAGTTCAGATATTGTTGGTACAGCAAATCCA |
| CM70 3510 | CAAGTTTCTGGATACCTTGGCGGTCTGGGTACCCTTCAGATCTCAAGATGCC |
| NRRL 3652 | CAAGTTTCTGGATACCTTGGCGGTCTGGGTACCCTTCAGATCTCAAGATGCC |
| CM70 3570 | CGAACTGAAAGTATGATACACGACCAAAACATACTGATGGGAAAGACATTTGCAATCCTCAATGCGGA |
| NRRL 3712 | CGAACTGAAAGTATGATACACGACCAAAACATACTGATGGGAAAGACATTTGCAATCCTCAATGCGGA |
| CM70 3630 | CTTGATTCTCAAGTTATTTATGAAAGTTTCTCTAACTTCCAATCTACACCAACAACAGAA |
| NRRL 3772 | CTTGATTCTCAAGTTATTTATGAAAGTTTCTCTAACTTCCAATCTACACCAACAACAGAA |
| CM70 3690 | GCTGAAATGCTAATGTGCAAATTGCAAACAATACTGATTTTATACAGAGATGTTGGGAAATT |
| NRRL 3832 | GCTGAAATGCTAATGTGCAAATTGCAAACAATACTGATTTTATACAGAGATGTTGGGAAATT |
| CM70 3750 | ACGAACTTCGAGTTCCTCCACACATAATCGTTCAGATGATTGATTGTTCCCTTATAGTCA |
| NRRL 3892 | ACGAACTTCGAGTTCCTCCACACATAATCGTTCAGATGATTGATTGTTCCCTTATAGTCA |
| CM70 3810 | CAAGTTTCTGGATACCTTGGCGGTCTGGGTACCCTTCAGATCTCAAGATGCC |
| NRRL 3951 | CAAGTTTCTGGATACCTTGGCGGTCTGGGTACCCTTCAGATCTCAAGATGCC |
|     | CM70 | NRRL | CM70 | NRRL |
|-----|------|------|------|------|
| 3810| ATTATTCAAAATGGTTGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 3869 |
| 3870| AAGTATGCTCGCTGATGTTGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 3929 |
| 3930| AAGCCTATGCTCAACTAGAGATTATCTTATATATCAAGAGATTTCTGTGATCAGTTGAGTTGTTGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 3989 |
| 4050| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4011 |
| 4120| ACAACCTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4071 |
| 4190| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4119 |
| 4250| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4191 |
| 4320| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4270 |
| 4390| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4419 |
| 4460| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4559 |
| 4530| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4619 |
| 4600| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4769 |
| 4670| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4839 |
| 4740| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4909 |
| 4810| TGCTTTCAAAATCTTCTGCTGTGATGTTGTTGATTATTTCTGATGTTGATCGTTGATCTGATGTTATGATCTTTGAGTTGAATACACCAACG | 4989 |
| CM70  | 4770 | CGGAAAGCTAGCTACCTTTGACCATGATTCTGGTGATATGGAGGCGACTCGCTTTGGTG | 4829 |
|-------|------|------------------------------------------------------------|------|
| NRRL | 4912 | CGGAAAGCTAGCTACCTTTGACACTGATTCTGGTGATATGGTGACGAACCGCTTTG | 4971 |
| CM70  | 4830 | AAACACAGATGGTTCATGGTCATACTTTGGTGCTGACGGTATCGCTGTATCTGGCGCTCA | 4889 |
| NRRL | 4972 | AAACACAGATGGTACATGGTCATACTTTGGTGCTGACGGTATCGCTGTAACTGGGTCA | 5031 |
| CM70  | 4890 | GACAATTAGTGGGCAAAAATTGTTCTTTGATGCTGGCGGTCAACAGATTAAAGGTAAGGA | 4949 |
| NRRL | 5032 | GACAATTAGTGGGCAAAAATTGTTCTTTGATGCTGACGGACAACAGATTAAAGGTAAGGA | 5091 |
| CM70  | 4950 | AGCGTCTGATAAAAAGGGCAAAGTGCAATTATTATGATGCTAATTCTGGTGAAATGATCGC | 5009 |
| NRRL | 5092 | AGCGACTGATAAAAAGGGCAAAGTGCAATTATTATGATGCTAATTCTGGTGAAATGATCAC | 5151 |
| CM70  | 5010 | TAATCGTTTTGAAAAGTTATCAGATGGATCATGGGCGTACTTTAATAAAAAAGGTAACAT | 5069 |
| NRRL | 5152 | TAATCGTTTTGAAAAGTTATCAGATGGATCATGGGCGTACTTTAATAAAAAAGGTAACAT | 5111 |
| CM70  | 5070 | CTAACCGGCAGCAATCTGCAATTATCTGGCTAATTCTGGTGAAATGATCGC | 5129 |
| NRRL | 5212 | CTAACCGGCAGCAATCTGCAATTATCTGGCTAATTCTGGTGAAATGATCGC | 5271 |
| CM70  | 5130 | AGTTAAGGGTCGTGAATACACGGCTACTGATGGGAAGATGCGCTACTACGATGCAGATTC | 5189 |
| NRRL | 5272 | AGTTAAGGGTCGTGAATACACGGCTACTGATGGGAAGATGCGCTACTACGATGCAGATTC | 5331 |
| CM70  | 5190 | TGGTGATATGGTGACGGAATCTTCTGGTGATATGGTAACCA | 5249 |
| NRRL | 5332 | TGGTGATATGGTGACGGAATCTTCTGGTGATATGGTAACCA | 5391 |
| CM70  | 5250 | TGCTATTGGTTGCTGGTATCTTGGGGACAAAAATAAAAAATGAAACAACTGTATTTTG | 5309 |
| NRRL | 5392 | TGCTATTGGTTGCTGGTATCTTGGGGACAAAAATAAAAAATGAAACAACTGTATTTTG | 5451 |
| CM70  | 5310 | TGCCAATGGTCATCAGTTAAGGGGACCGCAGTAAAACAAGCTGCGGTAGCAGAAAATA | 5369 |
| NRRL | 5452 | TGCCAATGGTCATCAGTTAAGGGGACCGCAGTAAAACAAGCTGCGGTAGCAGAAAATA | 5511 |
| CM70  | 5370 | TTATGACCAAAATCTGGGGA | 5390 |
| NRRL | 5512 | TTATGACCAAAATCTGGGGA | 5532 |

**Supplementary Figure S3.** Blast alignment of the *Leuconostoc mesenteroides* CM70 *dsrLL* gene (CM70, GenBank: MK401907) and *Lc. mesenteroides* NRRL B-512F *dsrT* gene (NRRL, GenBank: AB020020.1) as well as their corresponding upstream regions.
Supplementary Figure S4. Influence of temperature and carbon source on bacterial growth. The bacterial growth of the indicated strains was represented as a function of the growth temperature (A) or the growth medium (B). Also, in (B) the ANOVA statistical analysis of the results is depicted. A $p$ value $\leq 0.05$ was considered significant. Mean pairwise comparisons were computed with a Tukey's test ($\alpha=0.05$). Means with the same letter were not significantly different.
Supplementary Figure S5. EPS production by *Lactobacillus sakei* MN1 in solid media. Pictures of the plates were taken after 4 days of growth on MRS agar supplemented with 2% sucrose (MRSS) or 2% glucose (MRSG).
| Protein   | Accession | Sequence                        | Length |
|-----------|-----------|---------------------------------|--------|
| DsrLS TMW1411 |            | MLRNYYFGETKTHYKLYKCGKNWAVMGISLFLPGMLVTSQPVSAADVATATSTSSSAVRT | 60     |
| Consensus |            | MLRNYYFGETKTHYKLYKCGKNWAVMGISLFLPGMLVTSQPVSAADVATATSTSSSAVRT |        |
| DsrLS MN1  | 1         | MLRNYYFGETKTHYKLYKCGKNWAVMGISLFLPGMLVTSQPVSAADVATATSTSSSAVRT | 60     |
| DsrLS TMW1411 | 61      | DAISESSSAKAETTSAASSSSAVKAETTTSSSAKAETIAATTGAVANADSGQTSQAV    | 120    |
| Consensus |            | DAISESSSAKAETTSAASSSSAVKAETTTSSSAKAETIAATTGAVANADSGQTSQAV    |        |
| DsrLS MN1  | 61      | DAISESSSAKAETTSAASSSSAVKAETTTSSSAKAETIAATTGAVANADSGQTSQAV    | 120    |
| DsrLS TMW1411 | 121     | TADSTSTSQVTNSQQNNTAQPSAQEAAPVSEDTSDDSDTSRTPTVTWANNKPAISDVS   | 180    |
| Consensus |            | TADSTSTSQVTNSQQNNTAQPSAQEAAPVSEDTSDDSDTSRTPTVTWANNKPAISDVS   |        |
| DsrLS MN1  | 121     | TADSTSTSQVTNSQQNNTAQPSAQEAAPVSEDTSDDSDTSRTPTVTWANNKPAISDVS   | 180    |
| DsrLS TMW1411 | 181     | TSQPATAPKADTDVSTQLVTDKTDSDSRTPTVQVAVSTTVQVTEGSKQVVT        | 240    |
| Consensus |            | TSQPATAPKADTDVSTQLVTDKTDSDSRTPTVQVAVSTTVQVTEGSKQVVT        |        |
| DsrLS MN1  | 181     | TSQPATAPKADTDVSTQLVTDKTDSDSRTPTVQVAVSTTVQVTEGSKQVVT        | 240    |
| DsrLS TMW1411 | 241     | PKEESDTDSSVQKDSQTVATATTVQKPSVSQTVGQYFDEKTYTFTGKD         | 300    |
| Consensus |            | PKEESDTDSSVQKDSQTVATATTVQKPSVSQTVGQYFDEKTYTFTGKD         |        |
| DsrLS MN1  | 241     | PKEESDTDSSVQKDSQTVATATTVQKPSVSQTVGQYFDEKTYTFTGKD         | 300    |
| DsrLS TMW1411 | 301     | HPVTGLVYANNILQYFDETGHQVKGQYVTIAGHVYVFDPASGAAGAQTVGQIDGKMKV   | 360    |
| Consensus |            | HPVTGLVYANNILQYFDETGHQVKGQYVTIAGHVYVFDPASGAAGAQTVGQIDGKMKV   |        |
| DsrLS MN1  | 301     | HPVTGLVYANNILQYFDETGHQVKGQYVTIAGHVYVFDPASGAAGAQTVGQIDGKMKV   | 360    |
| DsrLS TMW1411 | 361     | DGSQITSGFSNDAGNSQYFDESGTMQRTIAGKTYFDDKDHGLRKYGIIDNQLY  | 420    |
| Consensus |            | DGSQITSGFSNDAGNSQYFDESGTMQRTIAGKTYFDDKDHGLRKYGIIDNQLY  |        |
| DsrLS MN1  | 361     | DGSQITSGFSNDAGNSQYFDESGTMQRTIAGKTYFDDKDHGLRKYGIIDNQLY  | 420    |
| DsrLS TMW1411 | 421     | FDLDKTGVESTTSNFKGLSQTSQDDTDPPHSASAVNMSKDSFTTVDGLTAESWYVPKDIQ | 480    |
| Consensus |            | FDLDKTGVESTTSNFKGLSQTSQDDTDPPHSASAVNMSKDSFTTVDGLTAESWYVPKDIQ |        |
| DsrLS MN1  | 421     | FDLDKTGVESTTSNFKGLSQTSQDDTDPPHSASAVNMSKDSFTTVDGLTAESWYVPKDIQ | 480    |
| DsrLS TMW1411 | 481     | TSATDWRSTPDREDPRMIMTMTWPQIQAAAYLNHMSSEGLLLSDKFKSATDQRTQLNQAA | 540    |
| Consensus |            | TSATDWRSTPDREDPRMIMTMTWPQIQAAAYLNHMSSEGLLLSDKFKSATDQRTQLNQAA |        |
| DsrLS MN1  | 481     | TSATDWRSTPDREDPRMIMTMTWPQIQAAAYLNHMSSEGLLLSDKFKSATDQRTQLNQAA | 540    |
| DsrLS TMW1411 | 541     | HAVQLQIEKIQQTKEVWRLTSTMNHFIFKQSPGYNVTSETPSNDHLQGGALSINSVLT | 600    |
| Consensus |            | HAVQLQIEKIQQTKEVWRLTSTMNHFIFKQSPGYNVTSETPSNDHLQGGALSINSVLT |        |
| DsrLS MN1  | 541     | HAVQLQIEKIQQTKEVWRLTSTMNHFIFKQSPGYNVTSETPSNDHLQGGALSINSVLT | 600    |
|   | Description | Sequence | Consensus | Sequence | Consensus | Sequence |
|---|-------------|----------|-----------|----------|-----------|----------|
| DsrLS TMW1411 601 | DANSNFLMRNNPQDDGTRHYNTDTSEGYYELLANDVDNSNPVQAEQLNWLYFLTHF | DANSNFLMRNNPQDDGTRHYNTDTSEGYYELLANDVDNSNPVQAEQLNWLYFLTHF | DsrLS MN1 601 | DANSNFLMRNNPQDDGTRHYNTDTSEGYYELLANDVDNSNPVQAEQLNWLYFLTHF | DsrLS TMW1411 661 | GEIVKNDPSANFDSVRDADVNDVADLLNITAAYFRDYGVKNDLTANQLISILWGEDH | Consensus | GEIVKNDPSANFDSVRDADVNDVADLLNITAAYFRDYGVKNDLTANQLISILWGEDH | DsrLS MN1 661 | GEIVKNDPSANFDSVRDADVNDVADLLNITAAYFRDYGVKNDLTANQLISILWGEDH |
| DsrLS TMW1411 661 | GEIVKNDPSANFDSVRDADVNDVADLLNITAAYFRDYGVKNDLTANQLISILWGEDH | Consensus | GEIVKNDPSANFDSVRDADVNDVADLLNITAAYFRDYGVKNDLTANQLISILWGEDH | DsrLS MN1 661 | GEIVKNDPSANFDSVRDADVNDVADLLNITAAYFRDYGVKNDLTANQLISILWGEDH |
| DsrLS TMW1411 721 | NDPLYVKHDGSDLTMDDYMQQLWSLTKNPDNRARSAMRRFMEYLYLVDRAKDNSTSDQAI | Consensus | NDPLYVKHDGSDLTMDDYMQQLWSLTKNPDNRARSAMRRFMEYLYLVDRAKDNSTSDQAI | DsrLS MN1 721 | NDPLYVKHDGSDLTMDDYMQQLWSLTKNPDNRARSAMRRFMEYLYLVDRAKDNSTSDQAI |
| DsrLS TMW1411 721 | NDPLYVKHDGSDLTMDDYMQQLWSLTKNPDNRARSAMRRFMEYLYLVDRAKDNSTSDQAI | Consensus | NDPLYVKHDGSDLTMDDYMQQLWSLTKNPDNRARSAMRRFMEYLYLVDRAKDNSTSDQAI | DsrLS MN1 721 | NDPLYVKHDGSDLTMDDYMQQLWSLTKNPDNRARSAMRRFMEYLYLVDRAKDNSTSDQAI |
| DsrLS TMW1411 781 | NYSFVRAHSEVQTIGIVALPKVSNLAPSMEQLAAAFKVIDQRAXDSALLKARIYVAGGQTMA | Consensus | NYSFVRAHSEVQTIGIVALPKVSNLAPSMEQLAAAFKVIDQRAXDSALLKARIYVAGGQTMA | DsrLS MN1 781 | NYSFVRAHSEVQTIGIVALPKVSNLAPSMEQLAAAFKVIDQRAXDSALLKARIYVAGGQTMA |
| DsrLS TMW1411 781 | NYSFVRAHSEVQTIGIVALPKVSNLAPSMEQLAAAFKVIDQRAXDSALLKARIYVAGGQTMA | Consensus | NYSFVRAHSEVQTIGIVALPKVSNLAPSMEQLAAAFKVIDQRAXDSALLKARIYVAGGQTMA | DsrLS MN1 781 | NYSFVRAHSEVQTIGIVALPKVSNLAPSMEQLAAAFKVIDQRAXDSALLKARIYVAGGQTMA |
| DsrLS TMW1411 841 | MPAAYAMLNKTNKTIPVYGDYMDDQQYMATKSPYDIASSLARKARIYVAGGQTMA | Consensus | MPAAYAMLNKTNKTIPVYGDYMDDQQYMATKSPYDIASSLARKARIYVAGGQTMA | DsrLS MN1 841 | MPAAYAMLNKTNKTIPVYGDYMDDQQYMATKSPYDIASSLARKARIYVAGGQTMA |
| DsrLS TMW1411 841 | MPAAYAMLNKTNKTIPVYGDYMDDQQYMATKSPYDIASSLARKARIYVAGGQTMA | Consensus | MPAAYAMLNKTNKTIPVYGDYMDDQQYMATKSPYDIASSLARKARIYVAGGQTMA | DsrLS MN1 841 | MPAAYAMLNKTNKTIPVYGDYMDDQQYMATKSPYDIASSLARKARIYVAGGQTMA |
| DsrLS TMW1411 901 | DKHDILTSVRFQDGDIMNASDDKSTARTQGIVSVSNNDALAKGDTVLTMSMGHAANQA | Consensus | DKHDILTSVRFQDGDIMNASDDKSTARTQGIVSVSNNDALAKGDTVLTMSMGHAANQA | DsrLS MN1 901 | DKHDILTSVRFQDGDIMNASDDKSTARTQGIVSVSNNDALAKGDTVLTMSMGHAANQA |
| DsrLS TMW1411 901 | DKHDILTSVRFQDGDIMNASDDKSTARTQGIVSVSNNDALAKGDTVLTMSMGHAANQA | Consensus | DKHDILTSVRFQDGDIMNASDDKSTARTQGIVSVSNNDALAKGDTVLTMSMGHAANQA | DsrLS MN1 901 | DKHDILTSVRFQDGDIMNASDDKSTARTQGIVSVSNNDALAKGDTVLTMSMGHAANQA |
| DsrLS TMW1411 961 | YRALLLLTTDDGLMKYSDNGAPIYTDANGDLIFTSADIKYQNEVSGFLSVWPGAS | Consensus | YRALLLLTTDDGLMKYSDNGAPIYTDANGDLIFTSADIKYQNEVSGFLSVWPGAS | DsrLS MN1 961 | YRALLLLTTDDGLMKYSDNGAPIYTDANGDLIFTSADIKYQNEVSGFLSVWPGAS |
| DsrLS TMW1411 961 | YRALLLLTTDDGLMKYSDNGAPIYTDANGDLIFTSADIKYQNEVSGFLSVWPGAS | Consensus | YRALLLLTTDDGLMKYSDNGAPIYTDANGDLIFTSADIKYQNEVSGFLSVWPGAS | DsrLS MN1 961 | YRALLLLTTDDGLMKYSDNGAPIYTDANGDLIFTSADIKYQNEVSGFLSVWPGAS |
| DsrLS TMW1411 1021 | DTQDARATGSSAANKTGDTHSNAALDSNVIEGFSNFQEMPTTHDEFTNKIAQNDLF | Consensus | DTQDARATGSSAANKTGDTHSNAALDSNVIEGFSNFQEMPTTHDEFTNKIAQNDLF | DsrLS MN1 1021 | DTQDARATGSSAANKTGDTHSNAALDSNVIEGFSNFQEMPTTHDEFTNKIAQNDLF |
| DsrLS TMW1411 1021 | DTQDARATGSSAANKTGDTHSNAALDSNVIEGFSNFQEMPTTHDEFTNKIAQNDLF | Consensus | DTQDARATGSSAANKTGDTHSNAALDSNVIEGFSNFQEMPTTHDEFTNKIAQNDLF | DsrLS MN1 1021 | DTQDARATGSSAANKTGDTHSNAALDSNVIEGFSNFQEMPTTHDEFTNKIAQNDLF |
| DsrLS TMW1411 1141 | KSWGVTSSQLAPQYRSDTDTSFLDSLIIKNGYAFDTDRYLGFTPTKYGDVLADAILAR | Consensus | KSWGVTSSQLAPQYRSDTDTSFLDSLIIKNGYAFDTDRYLGFTPTKYGDVLADAILAR | DsrLS MN1 1141 | KSWGVTSSQLAPQYRSDTDTSFLDSLIIKNGYAFDTDRYLGFTPTKYGDVLADAILAR |
| DsrLS TMW1411 1141 | KSWGVTSSQLAPQYRSDTDTSFLDSLIIKNGYAFDTDRYLGFTPTKYGDVLADAILAR | Consensus | KSWGVTSSQLAPQYRSDTDTSFLDSLIIKNGYAFDTDRYLGFTPTKYGDVLADAILAR | DsrLS MN1 1141 | KSWGVTSSQLAPQYRSDTDTSFLDSLIIKNGYAFDTDRYLGFTPTKYGDVLADAILAR |
| DsrLS TMW1411 1141 | HSVGQVMDAFVPDPQIYNLPGQEVVAVNVRTNNNGTPQDNSDLQNYLVTSNKKGGGEYQAK | Consensus | HSVGQVMDAFVPDPQIYNLPGQEVVAVNVRTNNNGTPQDNSDLQNYLVTSNKKGGGEYQAK | DsrLS MN1 1141 | HSVGQVMDAFVPDPQIYNLPGQEVVAVNVRTNNNGTPQDNSDLQNYLVTSNKKGGGEYQAK |
| DsrLS TMW1411 1141 | HSVGQVMDAFVPDPQIYNLPGQEVVAVNVRTNNNGTPQDNSDLQNYLVTSNKKGGGEYQAK | Consensus | HSVGQVMDAFVPDPQIYNLPGQEVVAVNVRTNNNGTPQDNSDLQNYLVTSNKKGGGEYQAK | DsrLS MN1 1141 | HSVGQVMDAFVPDPQIYNLPGQEVVAVNVRTNNNGTPQDNSDLQNYLVTSNKKGGGEYQAK |
DsrLS TMW1411 1201  YGGEFLDLRLREHPDLFTTNQISTGVFIDGSTKKEWSAKYFNGSDIQGKADYVLDGA  1260
Consensus  YGGEFLDLRLREHPDLFTTNQISTGVFIDGSTKKEWSAKYFNGSDIQGKADYVLDGA  1260
DsrLS MN1  1201  YGGEFLDLRLREHPDLFTTNQISTGVFIDGSTKKEWSAKYFNGSDIQGKADYVLDGA  1260

DsrLS TMW1411 1261  SQEYFKITSNANESFLPKQMNDAMTDGFTDEKTTYYSTSGYQAKQSFQDGDDGQYY  1320
Consensus  SQEYFKITSNANESFLPKQMNDAMTDGFTDEKTTYYSTSGYQAKQSFQDGDDGQYY  1320
DsrLS MN1  1261  SQEYFKITSNANESFLPKQMNDAMTDGFTDEKTTYYSTSGYQAKQSFQDGDDGQYY  1320

DsrLS TMW1411 1321  YFDADGYMTGTSQTINGKQYYFNGVELREALFQNASGNTVYYGKTGSAVKSYVDQS  1380
Consensus  YFDADGYMTGTSQTINGKQYYFNGVELREALFQNASGNTVYYGKTGSAVKSYVDQS  1380
DsrLS MN1  1321  YFDADGYMTGTSQTINGKQYYFNGVELREALFQNASGNTVYYGKTGSAVKSYVDQS  1380

DsrLS TMW1411 1381  GVAYYFDVNGVMADRMILDGHQYFFAGGSQAKDQFLIGSCLNRLYFDQGSGMNVTNR  1440
Consensus  GVAYYFDVNGVMADRMILDGHQYFFAGGSQAKDQFLIGSCLNRLYFDQGSGMNVTNR  1440
DsrLS MN1  1381  GVAYYFDVNGVMADRMILDGHQYFFAGGSQAKDQFLIGSCLNRLYFDQGSGMNVTNR  1440

DsrLS TMW1411 1441  FAVNRGDFWFGDIALKGWQTIAGKYYFDADGRQV-----KAEEQAAAAAADA  1495
Consensus  FAVNRGDFWFGDIALKGWQTIAGKYYFDADGRQV KAAA++AAAAQAADA  1495
DsrLS MN1  1441  FAVNRGDFWFGDIALKGWQTIAGKYYFDADGRQVKAAADKAAADKAAEQAADA  1500

DsrLS TMW1411 1452  DIDNQHVPGTSVDDNQKQAEKDIDTEDIKNDPDNKTLPEAIELPNTGVDKTESITITGVVMLI  1790
Consensus  DIDNQHVPGTSVDDNQKQAEKDIDTEDIKNDPDNKTLPEAIELPNTGVDKTESITITGVVMLI  1790
DsrLS MN1  1652  DIDNQHVPGTSVDDNQKQAEKDIDTEDIKNDPDNKTLPEAIELPNTGVDKTESITITGVVMLI  1750
| Protein | Accession | Amino Acid Sequence |
|---------|-----------|---------------------|
| DsrLS TMW1.411 | 1791 | LTTIFGLLFTSKHKKD |
| Consensus | | LTTIFGLLFTSKHKKD |
| DsrLS MN1 | 1751 | LTTIFGLLFTSKHKKD |

**Supplementary Figure S6.** Blast alignment of the *Lactobacillus sakei* TMW1.411 (translation from sequence 28 of WGS project published in DDBJ/ENA/GenBank under the accession QOSE00000000) and *Lb. sakei* MN1 (translated from GenBank ATN28243) dextransucrases amino acid sequences.