Supplementary Figures

Molecular, physiological and phylogenetic traits of *Lactococcus* 936-type phages from distinct dairy environments

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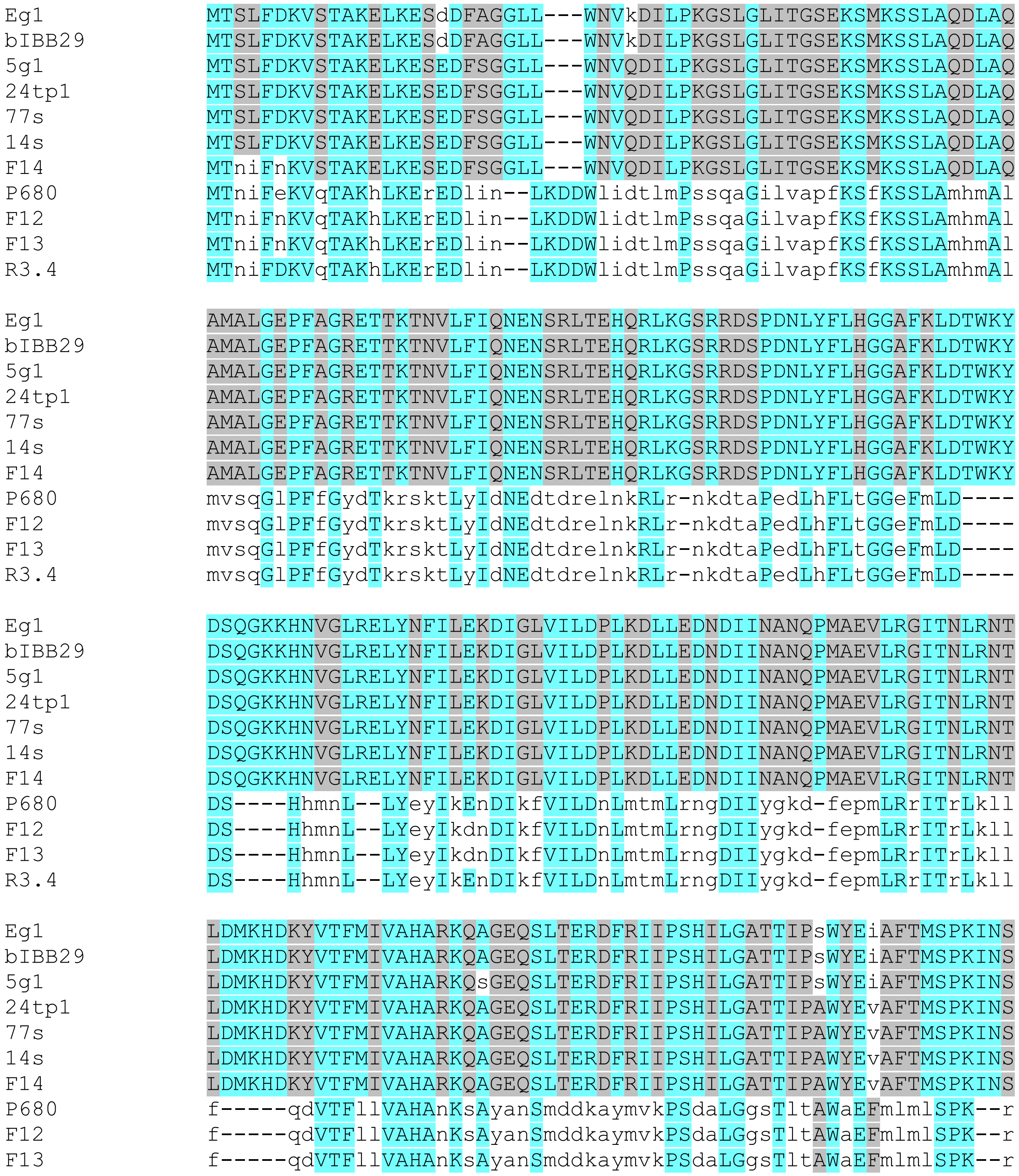
Supplementary Figure S1. Multiple sequence alignment of putative DNA polymerase subunits of *Lactococcus* phages sequenced in this study and phages bIBB29, R3.4 and P680 as the nearest homologues. Similar residues are coloured according to their conservation based on BLOSUM62 scoring (max: 3.0, light blue; low: 0.5, grey).



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Eg1              MTSLFDKVSTAKELKESdDFAGGLL---WNVkDILPKGSLGLITGSEKSMKSSLAQDLAQ
bIBB29           MTSLFDKVSTAKELKESdDFAGGLL---WNVkDILPKGSLGLITGSEKSMKSSLAQDLAQ
5g1              MTSLFDKVSTAKELKESEDFSGGLL---WNVQDILPKGSLGLITGSEKSMKSSLAQDLAQ
24tp1            MTSLFDKVSTAKELKESEDFSGGLL---WNVQDILPKGSLGLITGSEKSMKSSLAQDLAQ
77s              MTSLFDKVSTAKELKESEDFSGGLL---WNVQDILPKGSLGLITGSEKSMKSSLAQDLAQ
14s              MTSLFDKVSTAKELKESEDFSGGLL---WNVQDILPKGSLGLITGSEKSMKSSLAQDLAQ
F14              MTniFnKVSTAKELKESEDFSGGLL---WNVQDILPKGSLGLITGSEKSMKSSLAQDLAQ
P680             MTniFeKVqTAKhLKErEDlin--LKDDWlidtlmPssqaGilvapfKSfKSSLAmhmAl
F12              MTniFnKVqTAKhLKErEDlin--LKDDWlidtlmPssqaGilvapfKSfKSSLAmhmAl
F13              MTniFnKVqTAKhLKErEDlin--LKDDWlidtlmPssqaGilvapfKSfKSSLAmhmAl
R3.4             MTniFDKVqTAKhLKErEDlin--LKDDWlidtlmPssqaGilvapfKSfKSSLAmhmAl

Eg1              AMALGEPFAGRETTKTNVLFIQNENSRLTEHQRLKGSRRDSPDNLYFLHGGAFKLDTWKY
bIBB29           AMALGEPFAGRETTKTNVLFIQNENSRLTEHQRLKGSRRDSPDNLYFLHGGAFKLDTWKY
5g1              AMALGEPFAGRETTKTNVLFIQNENSRLTEHQRLKGSRRDSPDNLYFLHGGAFKLDTWKY
24tp1            AMALGEPFAGRETTKTNVLFIQNENSRLTEHQRLKGSRRDSPDNLYFLHGGAFKLDTWKY
77s              AMALGEPFAGRETTKTNVLFIQNENSRLTEHQRLKGSRRDSPDNLYFLHGGAFKLDTWKY
14s              AMALGEPFAGRETTKTNVLFIQNENSRLTEHQRLKGSRRDSPDNLYFLHGGAFKLDTWKY
F14              AMALGEPFAGRETTKTNVLFIQNENSRLTEHQRLKGSRRDSPDNLYFLHGGAFKLDTWKY
P680             mvsqGlPFfGydTkrsktLyIdNEdtdrelnkRLr-nkdtaPedLhFLtGGeFmLD----
F12              mvsqGlPFfGydTkrsktLyIdNEdtdrelnkRLr-nkdtaPedLhFLtGGeFmLD----
F13              mvsqGlPFfGydTkrsktLyIdNEdtdrelnkRLr-nkdtaPedLhFLtGGeFmLD----
R3.4             mvsqGlPFfGydTkrsktLyIdNEdtdrelnkRLr-nkdtaPedLhFLtGGeFmLD----

Eg1              DSQGKKHNVGLRELYNFILEKDIGLVILDPLKDLLEDNDIINANQPMAEVLRGITNLRNT
bIBB29           DSQGKKHNVGLRELYNFILEKDIGLVILDPLKDLLEDNDIINANQPMAEVLRGITNLRNT
5g1              DSQGKKHNVGLRELYNFILEKDIGLVILDPLKDLLEDNDIINANQPMAEVLRGITNLRNT
24tp1            DSQGKKHNVGLRELYNFILEKDIGLVILDPLKDLLEDNDIINANQPMAEVLRGITNLRNT
77s              DSQGKKHNVGLRELYNFILEKDIGLVILDPLKDLLEDNDIINANQPMAEVLRGITNLRNT
14s              DSQGKKHNVGLRELYNFILEKDIGLVILDPLKDLLEDNDIINANQPMAEVLRGITNLRNT
F14              DSQGKKHNVGLRELYNFILEKDIGLVILDPLKDLLEDNDIINANQPMAEVLRGITNLRNT
P680             DS----HhmnL--LYeyIkEnDIkfVILDnLmtmLrngDIIygkd-fepmLRrITrLkll
F12              DS----HhmnL--LYeyIkdnDIkfVILDnLmtmLrngDIIygkd-fepmLRrITrLkll
F13              DS----HhmnL--LYeyIkdnDIkfVILDnLmtmLrngDIIygkd-fepmLRrITrLkll
R3.4             DS----HhmnL--LYeyIkEnDIkfVILDnLmtmLrngDIIygkd-fepmLRrITrLkll

Eg1              LDMKHDKYVTFMIVAHARKQAGEQSLTERDFRIIPSHILGATTIPsWYEiAFTMSPKINS
bIBB29           LDMKHDKYVTFMIVAHARKQAGEQSLTERDFRIIPSHILGATTIPsWYEiAFTMSPKINS
5g1              LDMKHDKYVTFMIVAHARKQsGEQSLTERDFRIIPSHILGATTIPsWYEiAFTMSPKINS
24tp1            LDMKHDKYVTFMIVAHARKQAGEQSLTERDFRIIPSHILGATTIPAWYEvAFTMSPKINS
77s              LDMKHDKYVTFMIVAHARKQAGEQSLTERDFRIIPSHILGATTIPAWYEvAFTMSPKINS
14s              LDMKHDKYVTFMIVAHARKQAGEQSLTERDFRIIPSHILGATTIPAWYEvAFTMSPKINS
F14              LDMKHDKYVTFMIVAHARKQAGEQSLTERDFRIIPSHILGATTIPAWYEvAFTMSPKINS
P680             f-----qdVTFllVAHAnKsAyanSmddkaymvkPSdaLGgsTltAWaEFmlmlSPK--r
F12              f-----qdVTFllVAHAnKsAyanSmddkaymvkPSdaLGgsTltAWaEFmlmlSPK--r
F13              f-----qdVTFllVAHAnKsAyanSmddkaymvkPSdaLGgsTltAWaEFmlmlSPK--r
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R3.4            f-----qdVTFllVAHAnKsAyanSmddkaymvkPSdaLGgsTltAWaEFmlmlSPK--r

Eg1             KTKNrYSIMKVFARNFAFNDEILWGYVGSAFTSIEQDKKEPDSELVEKVKRETPIETTKE
bIBB29          KTKNrYSIMKVFARNFAFNDEILWGYVGSAFTSIEQDKKEPDSELVEKVKRETPIETTKE
5g1             KTKNrYSIMKVFARNFAFNnEILWGYVGSAFTSIEQDKKEPDSELVEKVKRETPIETTKE
24tp1           KTKNgYSIMKVFARNFAFNnEILWGYVGSvFTSIEQDKKEPDSELiEeVKqETPIETTKE
77s             KTKNgYSIMKVFARNFAFNnEILWGYVGSAFTSIEQDKKEPDSELVEKVKRETPIETTKE
14s             KTKNgYSIMKVFARNFAFNnEILWGYVGSAFTSIEQDKKEPDSELVEKVKRETPIETTKE
F14             KTKNgYSIMKVFARNFAFNnEILWGYVGSAFTSIEQDKKEPDSELVEKVKRETPIETTKE
P680            gkhNDfSklsVkARgyqFdDdlnfsYVdSvFTcvnksKKEPDSELiEeVKqETPIETTKE
F12             gkyNDfSklsVkARgyqFdDdlnfsYVdSvFTcvnksKKEPDSELVEKVKRETPIETTKE
F13             gkyNDfSklsVkARgyqFdDdlnfsYVdSvFTcvnksKKEPDSELVEKVKRETPIETTKE
R3.4            gkhNDfSklsVkARgyqFdDdlnfsYVdSvFTcvnksKKEPDnELVEKVKaETPIETTKE

Eg1             SAQAFLDLAKEQGKVIEND
bIBB29          SAQAFLDLAKEQGKVIEND
5g1             SAQAFLDLAKEQGKVIEND
24tp1           SAQAFLDLAKEQGKVIEND
77s             SAQAFLDLAKEQGKVIEND
14s             SAQAFLDLAKEQGKVIEND
F14             SAQAFLDLAKEQGKVIEND
P680            SAQAFLDLAKEQGKVtEND
F12             SAQAFLDLAKEQGKVIEND
F13             SAQAFLDLAKEQGKVIEND
R3.4            SAQAFLDLAKEQGKVIEND
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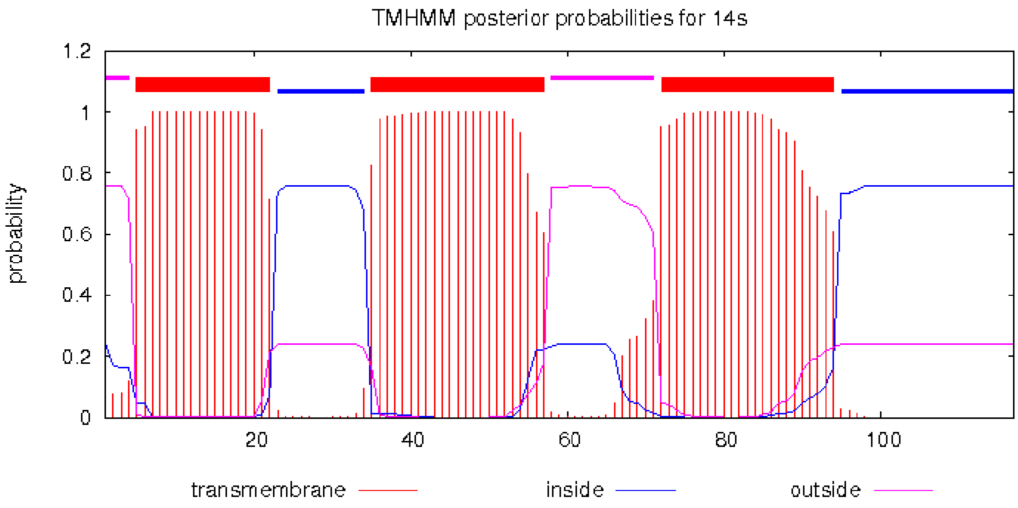
Supplementary Figure S2. Identification of transmembrane domains of the putative holins of *Lactococcus* phages sequenced in this study. Prediction of transmembrane domains was performed using the TMHMM tool (Krogh et al., 2001).



Supplementary Figure S3. Multiple sequence alignment of receptor binding proteins (RBPs) of *Lactococcus* phages sequenced in this study with protein representative of 936-type RBP subgroups recognized by Murphy et al. (2016). Similar residues are coloured according to their conservation based on BLOSUM62 scoring (max: 3.0, light blue; min: 0.5, grey).

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645             MTIKkFTFFSPNGTEFPVsANaDAKLYMLLSEKDYSQFliRHWETPINTALNRIYTNTSL
340             MTIKkFTFFSPNGTEFPVsANaDAKLYMLLSEKDYSQFliRHWETPINTALNRIYTNTSL
P475            MTIKkFTFFSPNGTEFPVsANaDAKLYMLLSEKDYSQFslRHWETPINTALNRIYkNTSL
77s             MTIKNFTFFSPNGTEFPVGANNDAKLYMLLSEKDYSQFslRHWETPINTdLNRIYkNTSL
bIBB29          MTIKNFTFFSPNGTEFPVGANNDAKLYMLLSEKDYSQFslRHWETPINTALNRIYkNTSL
24tp1           MTIKNFTFFSPNGTEFPVGANNDAKLYMLLSEKDYSQFslRHWETPINTALNRIYkNTSL
5g1             MTIKNFTFFSPNGTEFPVGANNDAKLYMLLSEKDYSQFslRHWETPINTALNRIYkNTSL
F12             MTIKNFTFFSPNGTEFPVGANNDAKLYMLLSEKDYSQFslRHWETPINTALNRIYkNTSL
F13             MTIKNFTFFSPNGTEFPVGANNDAKLYMLLSEKDYSQFslRHWETPINTALNRIYkNTSL
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Eg1             MTIKNFTFFSPNGTEFPVGANNDAKLYMLLSEKDYSQFslRHWETPINTALNRIYkNTSL
14s             MTIKNFTFFSPNGTEFPVGANNDAKLYMLLSEKDYSQFslRHWETPINTALNRIYkNTSL
936             MTIKNFTFFSPNGTEFPVGsNNDAKLYMmLtgmDYktiRRkdWlTPtNsgLNvIYnNTSi
sk1             MTIKNFTFFSPNsTEFPVGsNNDgKLYMmLtgmDYrtiRRkdWssPlNTALNvqYTNTSi
p2              MTIKNFTFFSPNsTEFPVGsNNDgKLYMmLtgmDYrtiRRkdWssPlNTALNvqYTNTSi
712             MTIKNFTFFSPNGTEFPVGsNNDAKLYMmLtgmDYktiRRkdWvePlNTsLNvMYpNTSi
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ASCC281         MTIKNFTFFSPNGTEFPVGsNNDgKLYMmLtgmDYgtiRRkdWssPlNiALNvqYTNTSi
P008            MTIKNFTFFSPNGTEFPVGsNNDgKLYMmLtgmDYgtiRRkdWtsPlNTALNvqYTNTSi
P113g           MTIKNFTFFSPNGTEFPVGsNNDgKLYMmLagmDYgtiRRkdWtsPlNTALNvqYTNTSi
bIL170          MTIKNFTFFSPNGTEFPVGsNNDgKLYMmLagmDYgtiRRkdWtsPlNTALNvqYTNTSi
PhiL.6          MTIKNFTFFSPNGTEFPVGsNNDgKLYMmLtgmDYgtiRRkdWtsPlNTALNvqYTNTSi
Phi155          MTIKyFTFFSPNnTEFPVGsNNDAKLYMmLtgmDYgtiRRkdWsaPVNTALNvqYTNTSi

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340             LVGGRYFELYNEAVALNSNATNFVHANIDISNvTNPVTiSVETSnNSNkVDINTGVGVLK
P475            LVGGRYFELYdEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
77s             LVGGRYFELYNEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
bIBB29          LVGGRYFELYNEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
24tp1           LVGGRYFELYNEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
5g1             LVGGRYFELYNEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
F12             LVGGRYFELYNEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
F13             LVGGRYFELYNEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
F14             LVGGRYFELYNEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
Eg1             LVGGRYFELYNEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
14s             LVGGRYFELYNEAVALNSNATNFVHANIDISNaTNPVTmSVETSDNSNQVDINTGVGVLK
936             iaGGRYFELsfEtVALNaNsvNyiHANIDltqTTrPVsLSaEkSDNSNsVDlNnaLGVLK
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712             iaGGRYFELlsEtVALkaNsvNyiHANIDltkTaNPVsLSaEnvDNSNnVDfNnrsGVLK
PhiC0139        iaGGRYFELsNEtVALkpNsvNyiHANIDltqTThPVsLSaEnSnNSNnVDlNnnsGVLK
ASCC281         iaGGRYFELsNEtVALkpNsvNyiHANIDlSqTThPVsLSaETaDdSNnVDlNnnsGVLK
P008            iaGGRYFELsNEtVALkaNsvNyiHANIDltqTahPVTLSaETSnNSNnVDlNnnsGVLK
P113g           iaGGRYFELlNEtVALkgNAvNyiHANIDltqTahPVTLSaETSDNSNnVDlNnnsGVLK
bIL170          iaGGRYFELlNEtVALkgNAvNyiHANIDltqTahPVTLSaETSnNSNnVDlNnnsGVLK
PhiL.6          iaGGRYFELsNEtVALkgNsvNyiHANIDltqTahPVsLSaETinNSNhVDlNnssGVLK
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340            KCIEVVETNAiGVSAVTKPSGSSILEKIYP----VGAYYfSSQPTEPATLF-----GFGT
P475           KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
77s            KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
bIBB29         KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
24tp1          KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
5g1            KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
F12            KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
F13            KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
F14            KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
Eg1            KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
14s            KCIEVVETNAMGVSAVTKPSGSSIiEKIYP----VGAYYLSSQPTEPATLF-----GFGT
936            vlIdirtTNgtdVTlqkaPdnvtyLdKav-----InsiisSStvdsgqvktAtinTGhGr
sk1            vCfdiVtTsgtGVTstkptvqTStLdsIs-----VndmtvSgsidvPvqtl-tveAGnGl
p2             vCfdiVtTsgtGVTstkpivqTStLdsIs-----VndmtvSgsidvPvqtl-tveAGnGl
712            vlIdirtTdgMGVisekaPdnityLdKVv-----InsisttSgvlDi---------GnGv
PhiC0139       vvIdirtTNgiGVisdktPdnvtyLdKVi-----tnsleMkgfadsyisIF----StaGd
ASCC281        vvIdirtTNgtGVintktPdnvtyLdKVi-----tnsleMkgfadsyvafFANk--GgGn
P008           vvIdirtTNgtGVinaksPtehtLLddVi-----Ins--LvnkkdiPwTdl-NrASGvGs
P113g          vvIdirtTNgtGVinakQPtehtLLddVi-----Ins--LvnQkdvPwTdl-NrAgGvGs
bIL170         vvIdirtTNgtGVisaeQPtehtLLddVi-----Ins--LvnkkdiPwTdl-NrASGvGs
PhiL.6         vlIdirtTNgLGVisseiPkqittLdelatKTAkIedltvkgdikgwtsVs----mqnva
Phi155         vlIdirtTNgLGVisseiPkqittLdelatKTAnIedltvkgdikgwtsVs----mqnva

645            WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
340            WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
P475           WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
77s            WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
bIBB29         WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
24tp1          WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
5g1            WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
F12            WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
F13            WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
F14            WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
Eg1            WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
14s            WSRVKGRGLvGVD-ESDSAlSsGGKQG-----GS-----TNPLSQHTITPSSGQFVVARG
936            sAvItriGntvti-tSqSqySsepanG-----sw-----ergvStlpVg-----FrpAte
sk1            dlQltkknndlVi--vrffgSvsniQk-----GwNM---sgtwvdrpfrPavvQsLV---
p2             qlQltkknndlVi--vrffgSvsniQk-----GwNM---sgtwvdrpfrPaAvQsLV---
712            tfswq-kkadiVE------fhwGGRltsins-GAsfpvkapfqlipdkvkelv-------
PhiC0139       titItapwdctaE--vElfyhgwGygGGeWEIG--------------IngSNGvtktyei
ASCC281        tvtftapwdctaE-velfyhgwG-ygGGeWEIGi-----TtPsgltqIyeaT--------
P008           tgilqaRiInsViYvrgNsipvpnvap-----nf-----ivPvg--TfpPafGtnLpqfd
P113g          tgtlqaRiInGViYvrgNsipvpnvap-----nf-----ivPvg--TfpPafGtnLpqfd
bIL170         tgilqaRiInGViYvrgNsipvpnvap-----nf-----ivPvg--TfpPafGtnLpqfd
PhiL.6         sAtlqykkInGVi-clrgsgnwGafka-----nS-----Tkvvg--sLpPevrptdntqf
Phi155         sAtlqykkInGai-clrgsgnwGafka-----nS-----Tkvvg--sLpPevrptdntqf

645            AGnrHWSSGGAPSNSYAMDTENGGV--TVGDNTNHNNWQPFEAAYIWKRIN----------
340            AGnrHWSSGGAPSNSYAMDTENGGV--TVGDNTNHNNWQPFEAAYIWKRIN----------
P475           AGnrHWSSGGAPSNSYAMDTENGGV--iVGDNTNHNNWQPFEAAYIWKRIN----------
77s            AGKWHWSSGGAPSNSYAMDTENGGI--TVGDNTNHNNWQPFEAAYIWKRIN----------
bIBB29         AGKWHWSSGGAPSNSYAMDTENGGV--TVGDNTNHNNWQPFEAAYIWKRIN----------
24tp1          AGKWHWSSGGAPSNSYAMDTENGGV--TVGDNTNHNNWQPFEAAYIWKRIN----------
5g1            AGKWHWSSGGAPSNSYAMDTENGGV--TVGDNTNHNNWQPFEAAYIWKRIN----------
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F12          AGKWHWSSGGAPSNSYAMDTENGGI--TVGDNTNHNNWQPFEAAYIWKRIN----------
F13          AGKWHWSSGGAPSNSYAMDTENGGI--TVGDNTNHNNWQPFEAAYIWKRIN----------
F14          AGKWHWSSGGAPSNSYAMDTENGGI--TVGDNTNHNNWQPFEAAYIWKRIN----------
Eg1          AGKWHWSSGGAPSNSYAMDTENGGI--TVGDNTNHNNWQPFEAAYIWKRIN----------
14s          AGKWHWSSGGAPSNSYAMDTENGGI--TVGDNTNHNNWQPFEAAYIWKRIN----------
936          tliYnhdltipskfSwnllhtNGlI-----DlfsngN--ikttdYIltsgqFwiTkdkLpe
sk1          ---gHfAg---rdtSFhiDinpnGsitwwGEsidntp--iatrgngsyfIk----------
p2           ---gHfAg---rdtSFhiDinpnGsitwwGaNidktp--iatrgngsyfIk----------
712          ---gHfpt---tSNSFhiDlEhdGtfrwwGEdkas----gsvrgtamyfIk----------
PhiC0139     t--gy--tkGhdSqaiAMpTsaGftglkkGqqytfNk--rdvsgraggatrvkiiVkLyrN
ASCC281      ---gytNghnSqalampakaiysGL--kkGqqytfdk--rdasglaggskhemmiVkLykN
P008         ta-gtfyShGnlSlSl-inmspsGI--aVGn--------PnntsmngKtIsFvLSVPLL--
P113g        ta-gtfySpGhlSlSl-inmspsGI--aVGn--------PnntsmngKtIsFaLSaPLL--
bIL170       ss-gtfyShGnlSlSl-inmspsGI--aVGn--------PnntsmngKtIsFaLSaPLL--
PhiL.6       emttqrAnnnnkpmelliDTngtis--vwsysags----gnyggvVgtyfq----------
Phi155       emttqrAnnnnkpmelqiDTngtis--vwsysags----gnyggvVgtyfq----------
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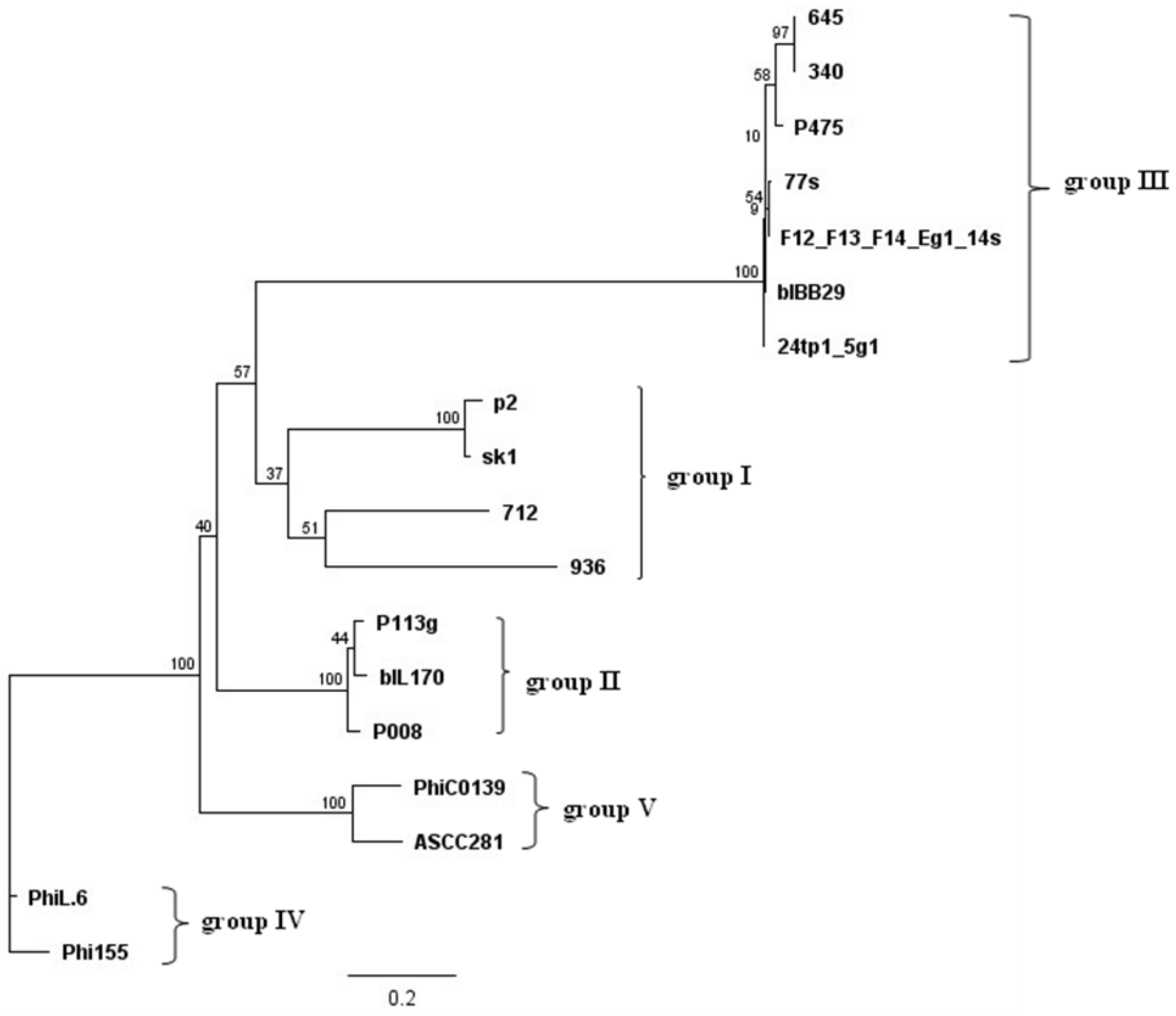
Supplementary Figure S4. Maximum-likelihood phylogenetic tree of receptor binding proteins (RBPs) of *Lactococcus* phages sequenced in this study. RBP phylogenies were reconstructed from multiple alignment of complete protein sequences, which were generated using MUSCLE with 8 iterations (default settings). A maximum-likelihood tree was constructed using PHYML and the Junker-Castor substitution model with 100 bootstrap resamplings. The scale bar represents evolutionary distance. Consensus support (%) is marked at each node.



Supplementary Figure S5. Multiple sequence alignment of putative TpeX proteins of *Lactococcus* phages sequenced in this study with the TpeX identified in other 936-type phages (Murphy et al., 2016). Similar residues are coloured according to their conservation based on BLOSUM62 scoring (max: 3.0, light blue; min: 0.5, grey).

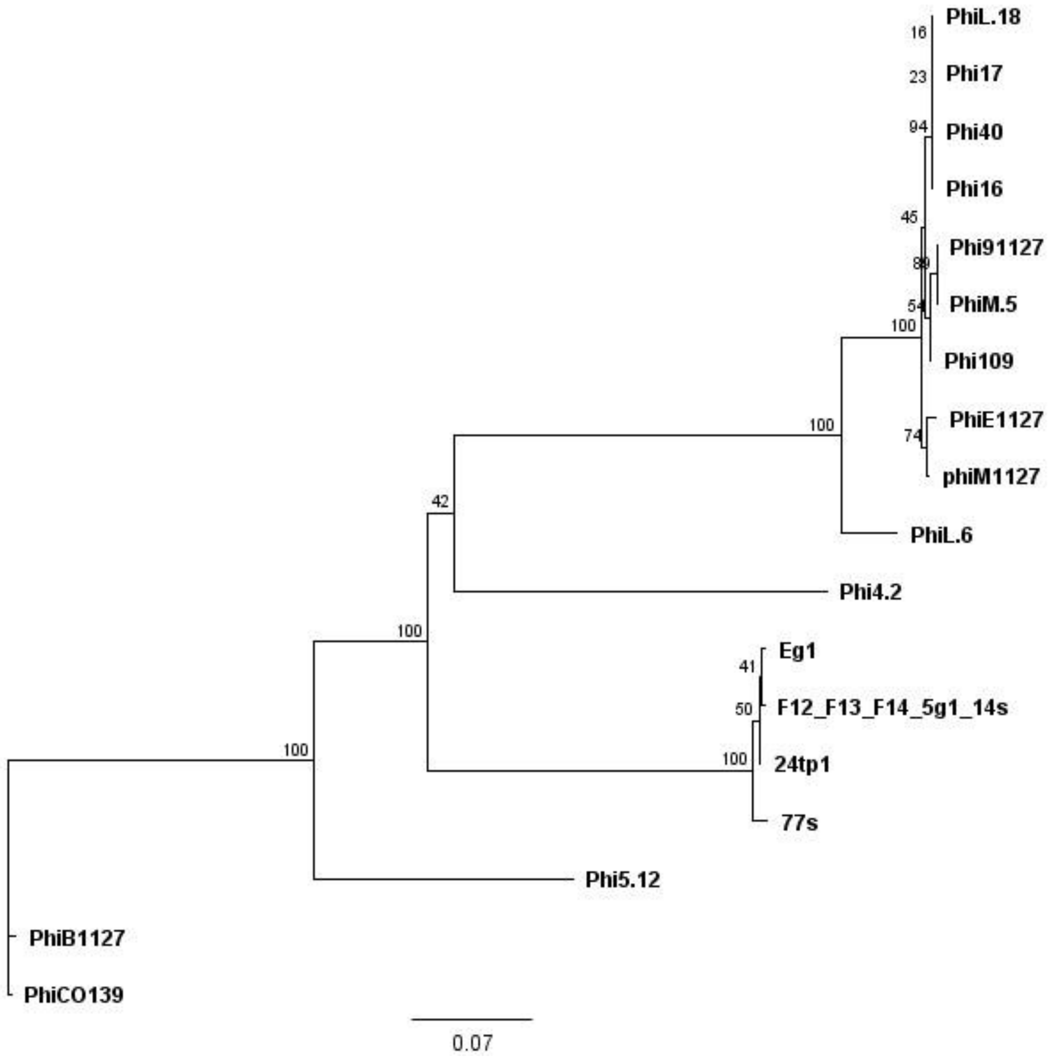
```
Phi145          -----mLNf----------SsgvtfGkhygwpagtatpsKnraysqkvkvtpndqytisA
Phi93           -----mLNf----------SsgvtfGkhygwpagtatpsKnraysqkvkvtpndqytisA
Eg1             MTVYPNLNLLKNTRTTSATSTSSAWGTLFSSEQIYDSAIKSKTGVSAMTLGFDVSVPLNA
24tp1           MTVYPNLNLLKNTRTTSATSTSSAWGTLFSSEQIYDSAIKSKTGVSAMTLaFDVSVPLNA
F14             MTVYPNLNLLKNTRTTSATSTSSAWGTLFSSEQIYDSAIKSKTGVSAMTLGFDVSVPLNA
5g1             MTVYPNLNLLKNTRTTSATSTSSAWGTLFSSEQIYDSAIKSKTGVSAMTLGFDVSVPLNA
F12             MTVYPNLNLLKNTRTTSATSTSSAWGTLFSSEQIYDSAIKSKTGVSAMTLGFDVSVPLNA
F13             MTVYPNLNLLKNTRTTSATSTSSAWGTLFSSEQIYDSAIKSKTGVSAMTLGFDVSVPLNA
77s             -------NLLKNTRTTSATSTSSAWGTLFSSEQIYDSAIKSKTGVSAMTLGFDVSVPLNA
14s             MTVYPNLNLLKNTRTTSATSTSSAWGTLFSSEQIYDSAIKSKTGVSAMTLGFDVSVPLNA

Phi145          dwkNanwlsiyGftnegdttavAr-ygsanGtGTGsWdsnfvggytaandmtftVpdnvn
Phi93           dwkNanwlsiyGftnegdttavAr-ygsanGtGTGsWdsnfvggytaandmtftVpdnvn
Eg1             KVGNNISVQLKGQNSQAHGNVGANDFNTIVGE---KWHNIEQSDLGKkIRLSTSVELDPK
24tp1           KVGNNISVQLKGQNSQAHGNVGANDFNTIVGE---KWHNIEQSDLGKTIRLSTSVELDPK
F14             KVGNNISVQLKGQNSQAHGNVGANDFNTIVGE---KWHNIEQSDLGKTIRLSTSVELDPK
5g1             KVGNNISVQLKGQNSQAHGNVGANDFNTIVGE---KWHNIEQSDLGKTIRLSTSVELDPK
F12             KVGNNISVQLKGQNSQAHGNVGANDFNTIVGE---KWHNIEQSDLGKTIRLSTSVELDPK
F13             KVGNNISVQLKGQNSQAHGNVGANDFNTIVGE---KWHNIEQSDLGKTIRLSTSVELDPK
77s             KVGNNISVQLKGQNSQAHGNVGANDFNTIVGE---KWHNIEQSDLGKTIRLSTSVELDPK
14s             KVGNNISVQLKGQNSQAHGNVGANDFNTIVGE---KWHNIEQSDLGKTIRLSTSVELDPK

Phi145          YivasyAskspDtlTlq------GLlngKpKLEqGSkvTPWmrSSSEtiesDYPSYIGnY
Phi93           YivasyAskspDtlTlq------GLlngKpKLEqGSkvTPWmrSSSEtiesDYPSYIGnY
Eg1             YqSFDTALADTDSITIRQVEGTPGLVYSKLKLEPGSTDTPWIPSSSEVTAEDYPSYIGTY
24tp1           YqSFDTALADTDSITIRQVEGTPGLVYSKLKLEPGSTDTPWIPSSSEVTAEDYPSYIGTY
F14             YHSFDTALADTDSITIRQVEGTPGLVYSKLKLEPGSTDTPWIPSSSEVTAEDYPSYIGTY
5g1             YHSFDTALADTDSITIRQVEGTPGLVYSKLKLEPGSTDTPWIPSSSEVTAEDYPSYIGTY
F12             YHSFDTALADTDSITIRQVEGTPGLVYSKLKLEPGSTDTPWIPSSSEVTAEDYPSYIGTY
F13             YHSFDTALADTDSITIRQVEGTPGLVYSKLKLEPGSTDTPWIPSSSEVTAEDYPSYIGTY
77s             YHSFDTALADTDSITIRQVEGTPGLVYSKLKLEPGSTDTPWIPSSSEVTAEDYPSYIGTY
14s             YHSFDTALADTDSITIRQVEGTPGLVYSKLKLEPGSTDTPWIPSSSEVTAEDYPSYIGTY

Phi145          TgKivdgQSTDPvrYnWKKIE
Phi93           TgKivdgQSTDPvrYnWKKIE
Eg1             TDKNSNEQSTDPEKYTWKKIE
24tp1           TDKNSNEQSTDPEKYTWKKIE
F14             TDKNSNEQSTDPEKYTWKKIE
5g1             TDKNSNEQSTDPEKYTWKKIE
F12             TDKNSNEQSTDPEKYTWKKIE
F13             TDKNSNEQSTDPEKYTWKKIE
77s             TDKNSNEQSTDPEKYTWKKIE
14s             TDKNSNEQSTDPEKYTWKKIE
```

Supplementary Figure S6. Maximum-likelihood phylogenetic tree of MTP extension of *Lactococcus* phages sequenced in this study with the MTP extensions identified in other 936-type phages (Murphy et al., 2016). MTP extension phylogenies were reconstructed from multiple alignment of major tail protein extension sequences generated using MUSCLE with 8 iterations (default settings). A maximum-likelihood tree was built using PHYML and the Junker-Castor substitution model with 100 bootstrap resamplings. The scale bar represents evolutionary distance. Consensus support (%) is marked at each node.



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Supplementary Tables.

Supplementary Table S1. Host range studies of *Lactococcus* phages sequenced in this study tested on industrial, laboratory and environmental *L. lactis* strains. Grey-shaded boxes indicate clear plaques; light grey boxes indicate turbid plaques formed on the specified strains.

	Bacteriophages							
	Eg1	F12	F13	F14	5g1	14s	77s	24tp1
Industrial strains								
L. lactis subsp. *cremoris*								
IBB694								
IBB695								
IBB696								
IBB697								
IBB698								
IBB699								
IBB700								
IBB1788								
IBB1789								
IBB1790								
IBB1791								
IBB1792								
L. lactis subsp. *lactis*								
IBB743								
IBB749[*]								
IBB750[*]								
IBB752								
IBB753								
IBB754								
IBB757								
IBB758								
IBB759								
IBB761								
IBB763								
IBB764								
IBB1784								
IBB1796								
L. lactis subsp. *lactis* biovar. *diacetylactis*								

IBB734[*]	▓	▓	▓	▓
IBB735[*]	▓	▓	▓	▓
IBB736[*]		░	▓	
IBB737[*]		░	░	
IBB738[*]		░	░	
IBB742		░	░	
IBB744	▓	▓	▓	▓
IBB745	▓	▓	▓	▓
IBB746	▓	▓	▓	▓
IBB747	▓	▓	▓	▓
IBB748[*]	▓	▓	▓	▓
IBB751[*]	▓	▓	▓	▓
IBB755				
IBB756				
IBB760				
IBB762				
IBB1286[*]	▓	▓	▓	▓
Natural isolates				
L. lactis subsp. *cremoris*				
IBB338				
IBB339				
IBB340				
IBB341				
IBB342				
IBB704				
L. lactis subsp. *lactis*				
10LC				
other *Lactococcus* species				
L. garvieae 3LC				
L. plantarum 76B				
L. laudensis 115				
L. raffinolactis 87B				
Laboratory strains				
L. lactis subsp. *cremoris*				
LM0230				
MG1363				
IBB477				
NZ9000				
L. lactis subsp. *lactis* biovar. *diacetylactis*				
IL1403	▓	▓	▓	▓

F7/2	▓	░	▓

*The industrial starter strains used at the time of whey sample collection.