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MpLS      : MALKVFSGAMQMPIPSKLTITYLQPSHLNSSPKLLSNITKGTSRSLRVSCSSSQTTERSGNYPNPSRWDVDFIQTLH : 77
MsLS      : MALKVLSVATQMAIPSNLTTCLOPSHLKSSPKLLSSTNSSSRSLRVSCSSSQTTERSGNYPNPSRWDVDFIQSLH : 77
MlongTPS29 : MALKVFSVATQMAIPSNLTTCLOPSHLKSSPKLLSSTNSSSRSLRVSCSSSQTTERSGNYPNPSRWDVDFIQSLH : 77

MpLS      : SDYKDEKHHARRASELVTLVKMELEKETDQIRQLELIDDLQRMGLSDHFQNEFKEILSSVYLDHGYKNEPDPKEERDL : 154
MsLS      : SDYKEDKHVIRASELVTLVKMELEKETDQIRQLELIDDLQRMGLSDHFQNEFKEILSSIYLDHHYKNEPDPKEERDL : 154
MlongTPS29 : SDYKEDKHAIIRASELVTLVKMELEKETDHIRQLELIDDLQRMGLSDHFQNEFKEILSSIYLDHHYKNEPDPKEERDL : 154

MpLS      : YSTSLAFRLREHGFQVAQEVFDSFKNEEGEFKESLSDTRGLLQLYEASFLLTEGETTLESAREFATKFLEERVNE : 231
MsLS      : YSTSLAFRLREHGFQVAQEVFDSFKNEEGEFKESLSDTRGLLQLYEASFLLTEGETTLESAREFATKFLEEKVNE : 231
MlongTPS29 : YSTSLAFRLREHGFQVAQEVFDSFKNEEGEFKESLSDTRGLLQLYEASFLLTEGETTLESAREFATKFLEERVNE : 231

MpLS      : GGGDENLLTRIAYSLEIPLHWRIKRPNAPVWIDSYRKRPNMNPVVLDAILDNLIVQAHFQOELKESFRWWRTGFFV : 308
MsLS      : GGVDGDLTRIAYSLEIPLHWRIKRPNAPVWIEWYRKRPDMNPVVLDAILDNLIVQAHFQOELKESFRWWRTGFFV : 308
MlongTPS29 : GGVDGDLTRIAYSLEIPLHWRIKRPNAPVWIEWYRKRPDMNPVVLDAILDNLIVQAHFQOELKESFRWWRTGFFV : 308

MpLS      : EKLPPFARDRLVECYFWNTGIIIEPRQHASARIMMGKVNALITVIDDIYDVYGTLEELEHFTDLIRRWDIDSIDQLPDY : 385
MsLS      : EKLPPFARDRLVECYFWNTGIIIEPRQHASARIMMGKVNALITVIDDIYDVYGTLEELEHFTDLIRRWDINSIDQLPDY : 385
MlongTPS29 : EKLPPFARDRLVECYFWNTGIIIEPRQHASARIMMGKVNALITVIDDIYDVYGTLEELEHFTDLIRRWDINSIDQLPDY : 385

MpLS      : MQLCFLALNNFVDETSYDVMKEKGVNVIPLYRQSWVDLADKYMVEARWFYGGHKPSLEEYLENSWMSISGPCMLTHI : 462
MsLS      : MQLCFLALNNFVDETSYDVMKEKGVNVIPLYRQSWVDLADKYMVEARWFYGGHKPSLEEYLENSWMSISGPCMLTHI : 462
MlongTPS29 : MQLCFLALNNFVDETSYDVMKEKGVNVIPLYRQSWVDLADKYMVEARWFYGGHKPSLEEYLENSWMSISGPCMLTHI : 462

MpLS      : FFRVTDSTFKETVDSLYKYHDLVRWSSFVLRLADDLGTSVEEVSRGDVPKSLQCYMSDYNASEAEARKHVWKLIAEV : 539
MsLS      : FFRVTDSTFKETVDSLYKYHDLVRWSSFVLRLADDLGTSVEEVSRGDVPKSLQCYMSDYNASEAEARKHVWKLIAEV : 539
MlongTPS29 : FFRVTDSTFKETVDSLYKYHDLVRWSSFVLRLADDLGTSVEEVSRGDVPKSLQCYMSDYNASEAEARKHVWKLIAEV : 539

MpLS      : WKKMNAERVSKDSPFGKDFIGCAVDLGRMAQLMYHNGDGHGTQHPIIHQOMTATLFEPPFA : 599
MsLS      : WKKMNAERVSKDSPFGKDFIGCAVDLGRMAQLMYHNGDGHGTQHPIIHQOMTRTLFEPPFA : 599
MlongTPS29 : WKKMNAERVSKDSPFGKDFIGCAVDLGRMAQLMYHNGDGHGTQHPIIHQOMTRTLFEPPFA : 599

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Figure S1. Multiple sequence alignment of LS from *M. spicata*, *M. piperita*, and *M. longifolia*.