

Figure S1. Scatter plots of global gene expression values for the trichomes of each cultivar versus those of stem tissue (left) and their corresponding D-values – M-values plots (right).

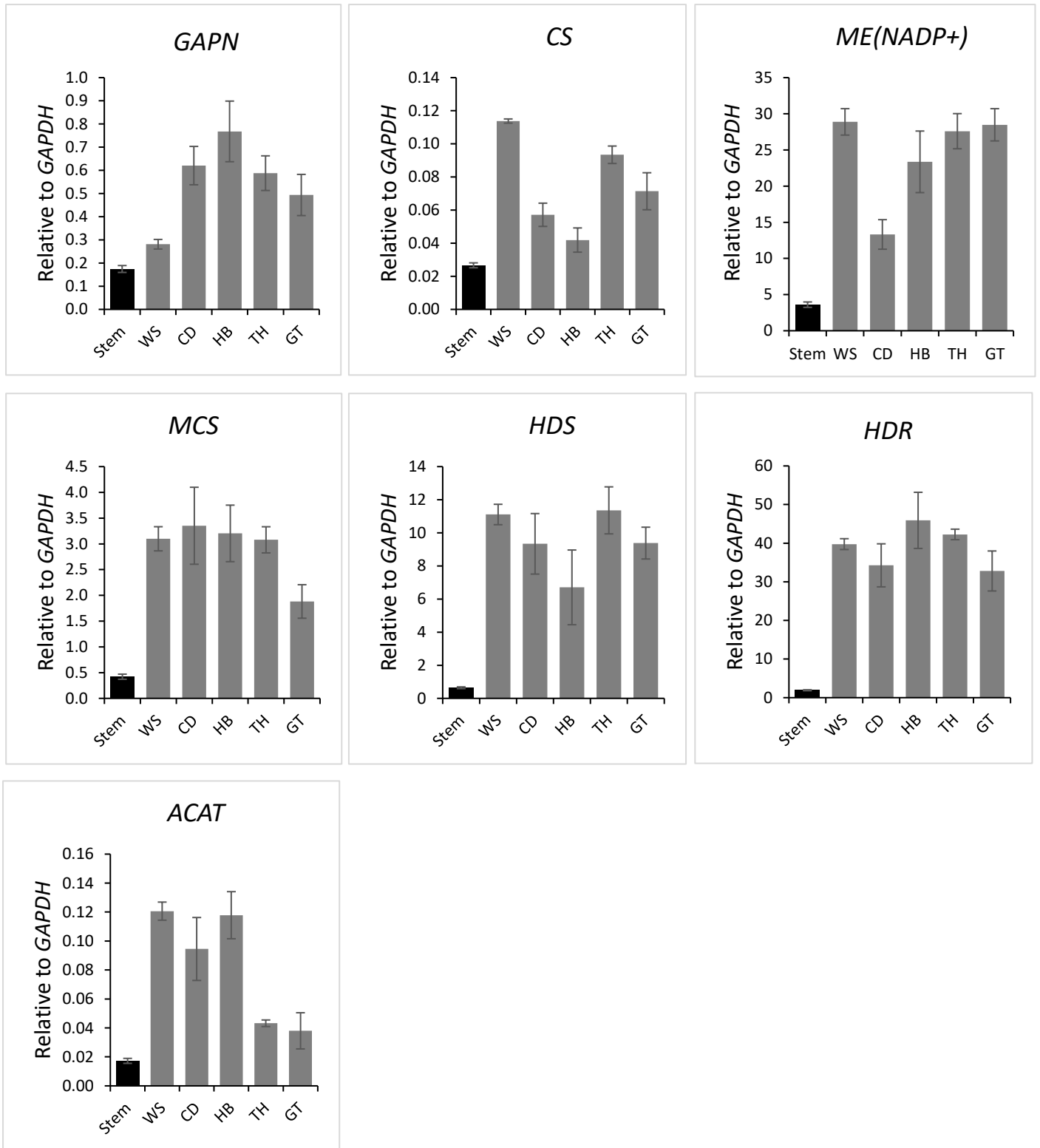
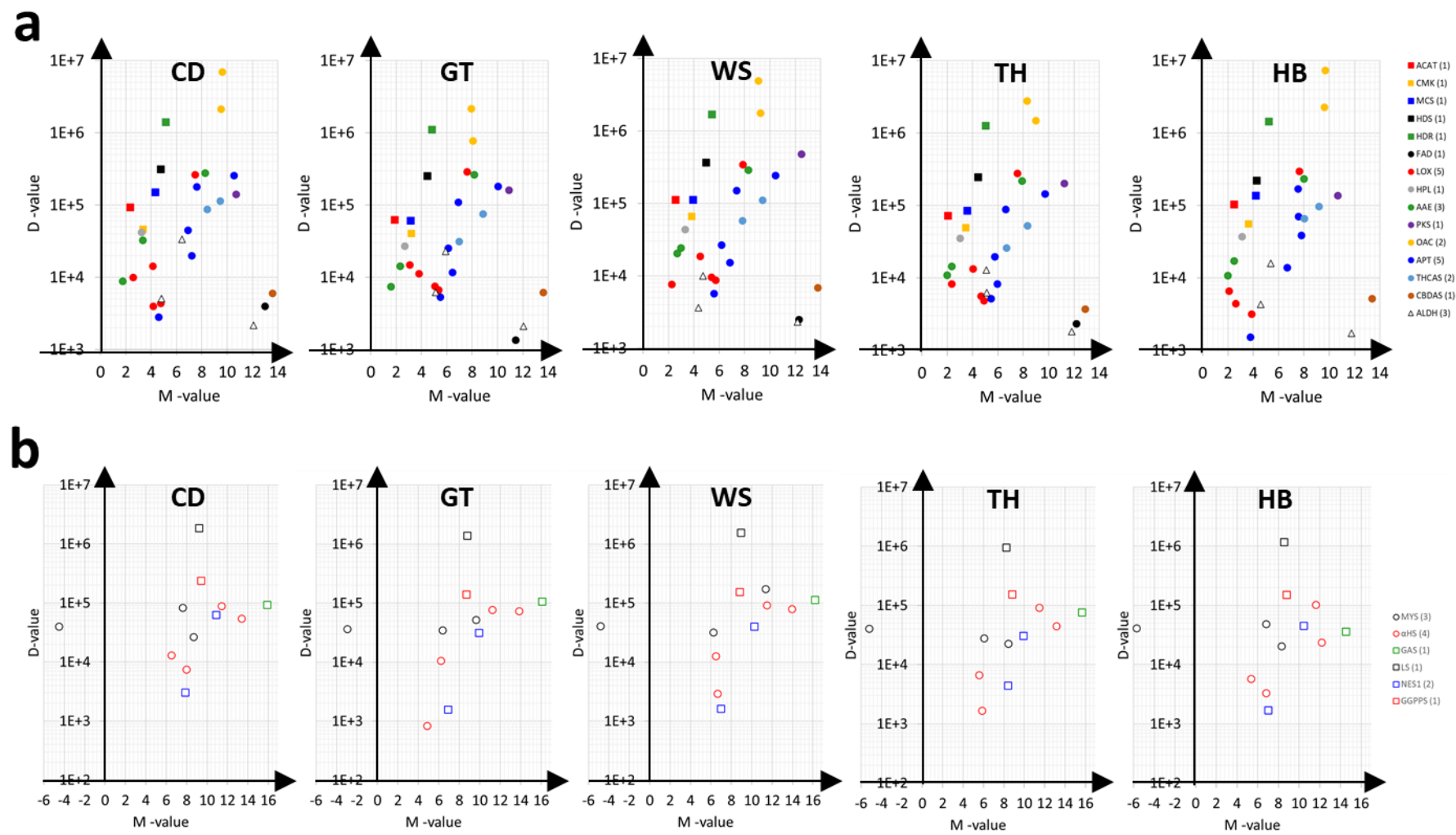


Figure S3. Expression of *GAPN*, *CS*, *ME(NADP+)*, *MCS*, *HDS*, *HDR* and *ACAT* in the trichomes of five cultivars and stem of HB cultivar.



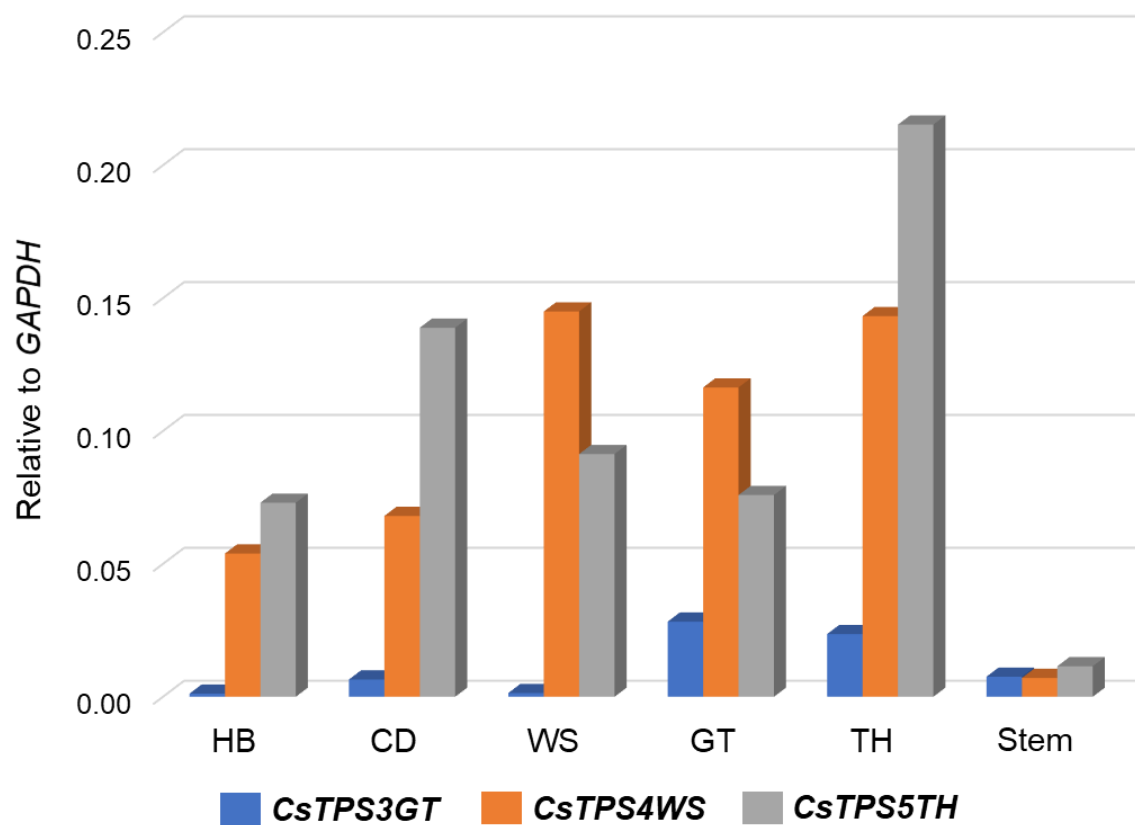


Figure S5. Expression of *CsTPS3GT*, *CsTPS4WS*, and *CsTPS5TH* in the trichomes of five cultivars and stem of HB cultivar.

RR(X₈)W

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CsTPS3GT  -----MTQLGVSSSTP-----IFKDQPAATVR---RSNYKPTLWDAHFFQSLQVIY  45
CsTPS4WS  MSSIIYSPFTSLLPLKPISSASSTATINTRLKSRFRSSILVLRPQQRRSAKYHPTVWENKHIDSFFTPY  70
CsTPS5TH  -----MASPFLYVPS---KHGNGLQSFTDPFYMEYTRNIR  32

CsTPS3GT  TEESYGKRINELKEDVRRILEKEAENPLVKLEQINDLSRLGISYHFEDQIKTILN-----LTFNNNN  107
CsTPS4WS  NYELHSERLQELKQITSTSLR-TTKDPCILLKLDSIQRLGLEHYHFENEIEDAVS-----FIYAHND  131
CsTPS5TH  EMKNVMNSILADDDYR-----ERSIEALNLVNAVLRVGDYHVQDEIKSILEREHIIFSDHISNQYF  95

CsTPS3GT  ALWKKDNLMTATALHFKLLRQYGFSPVSSEVFNAFNEKKEFKESLSKDVKGMVCLLYEASFYSFRGEPTLD  177
CsTPS4WS  QTTSN-DLEMTALRFRIILRQHGLF-VGSDVFDRFRGRDGKFLDSISSNKHGILSLYEASHLGMPEENVLE  199
CsTPS5TH  NNINQDHLMEVSLRFRILLRQGGYDVSPDVFNELMDKKGNFNVLVEEDREGLRELFEASQVRIEGEEVLE  165

CsTPS3GT  EARDFTTKHLKQYLMTRQSQFTRVDHDDDDHDLVKLVEHALDDLPLHWRLPRLEARWFIDMYAERNYDMN  247
CsTPS4WS  EAKSFTTKRLRYFSAG-----KMDTTLFGKQVKQSLEVPLYWRMPRSEARNFIDLYQMDETKS-  257
CsTPS5TH  EAEVFSGGHLKEWANLHR-----HTSEARSIQLTLDQPCCHKSLARVTSPNFLDSSESANTTTID  223

CsTPS3GT  -----PTFLDFAKLDVNFVQSAYQRELKYISRWWSSGSRLTERLPFARDRVVEIFYSAVALKYEAEAFGFV  311
CsTPS4WS  -----VTLELAKLDVNLVQSVHQNELKELGRWWDDLGFKKNLPFARDRVVENYLWAMGIVSEPQFSKC  321
CsTPS5TH  QGWTWMTLLNKLVTMDKKIVQSIHQREIVLVSKWWKELGLAEBLKFARDQPPKWYLWTVASLPDPSLSEE  293

CsTPS3GT  RTVMTKIGILLTLMDDIYDVYGTLDELQLFLEATERWNINEL-DQLPDYMKILFVAFYNNVNEISYVVLK  380
CsTPS4WS  RIGLTKFVCILTAIDDVYDIYGSLDELELFTNAVESWDIRAIRDEFPLYLKTCYLGMLNFGNEVIDDVLQ  391
CsTPS5TH  RIELTKPISLVYIDDIFDVYGTLDELTLFTDAVNWEIKEQ---LPDYLKICFKALDDITNKISYVYR  360

CsTPS3GT  ENGIHTIKYLKKALGDLCKCYMEEAKWFHSGHIPSLEEFIENGWKSITIPLCLIYHYCLITT---SITEQ  447
CsTPS4WS  NHGLNISSYIKEEWLNCKSYLVEARWFYNDYTPSLNEYLENSSTSVGGHAAIVHACILLDGSIPETLL  461
CsTPS5TH  KHGWNPIDSLRKSWGKLCNAFLLEAEWFGCGKLPNEEYLKNAIVSGVHVVLVHMFFLLEG---ISME  427

CsTPS3GT  DMEHLLQYPTILRVSGTVERFIDDLGTSSDELERGDNPSSIQCYMREKGVSENE-SREHWNLISEGWKE  516
CsTPS4WS  DYNFNHFHSKLIYWSSLITRLSDDLGTSKDELKRGDVKKSVECYMAEKGIWEEEAINHIKELRRNSWKM  531
CsTPS5TH  AVNLLDNIPGLVSSTAAILRLWDDLGSKDENQNGHDGSYVECYMKRHKECSMGEAREQWIRMIKNEWER  497

CsTPS3GT  IN-EVKASTSPYSQVFIESAIDFVRGAMEMYHKGDGFGTNQDRYLKTKVVNMFFDPIPI-----  574
CsTPS4WS  VNKEIIIGNNCLPKIMVKMCLNMARTAQFIFQHGDGIGTSTG-ATKHRLASLIVKPVPIIDPCSKPINGL  600
CsTPS5TH  LNKECFS-SKHFPMCFRKGCLNAARMVPVMYDYDD---HHRLPGLQNYINSLLSHQTI-----  551

CsTPS3GT  -----  574
CsTPS4WS  GDSHTTIKIKK  613
CsTPS5TH  -----  551

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DDXXD

NSE/DTE

Figure S6. Amino acid sequence alignment of CsTPS3GT, CsTPS4WS, and CsTPS5TH. Conserved regions are highlighted in black, while similar regions are in gray. Amino acids that are usually conserved in CsTPSs, are shown in red boxes. ‘WW’: conserved tandem tryptophan motif; ‘RR(X₈)W’: tandem arginine motif of mono-TPS; ‘DDXXD’: divalent metal ion-assisted binding and ionization motif. The plastid-targeting transit peptide is underlined.

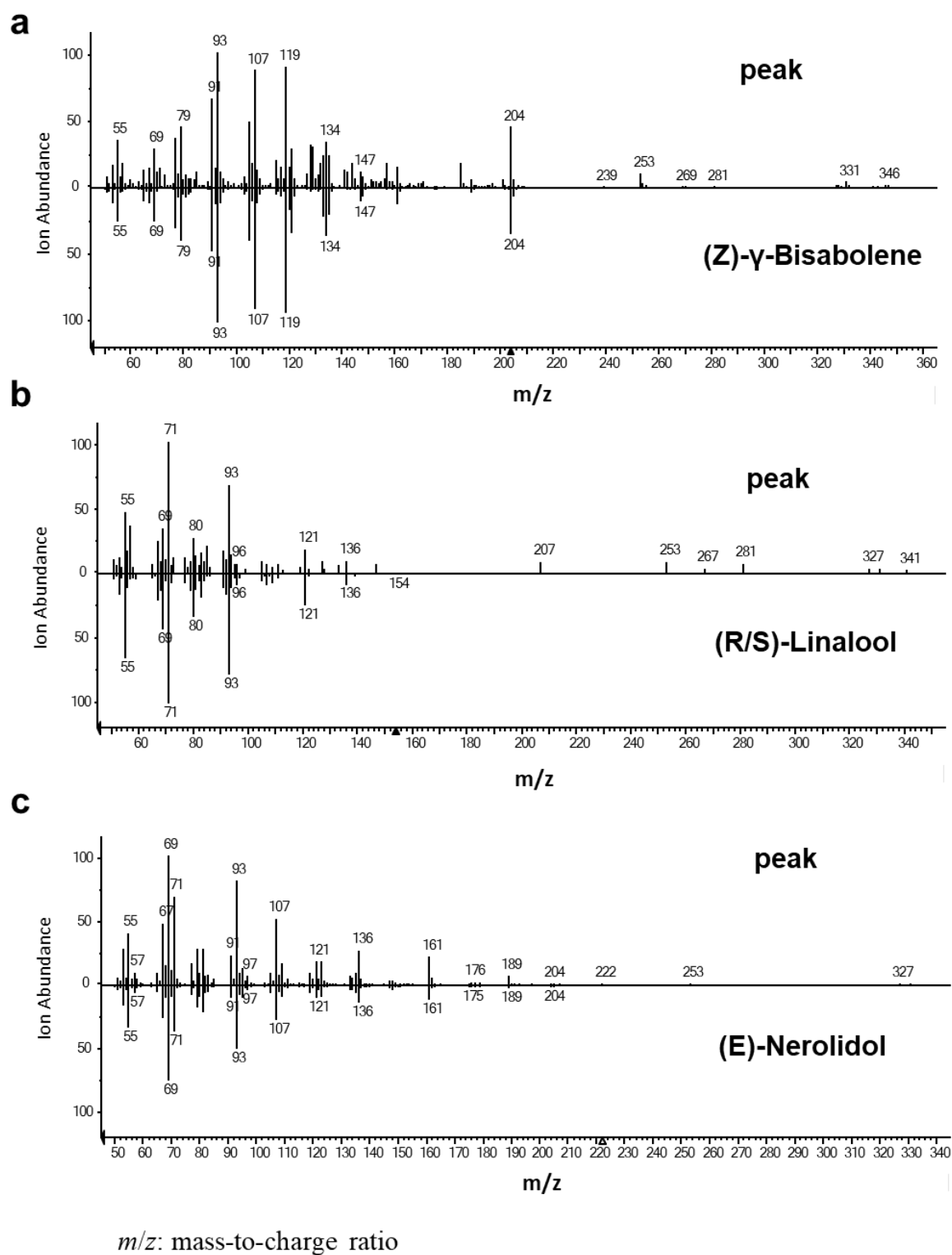


Figure S7. Mass spectra of the products produced by CsTPS3GT (a), CsTPS4WS (b), and CsTPS5TH (c).