NLP _{Pva}	60 AACRDMS-KAQVYS <mark>RS</mark> GTYNGYYAIMYSWYMPKDSPSTGIGHRHDWENVVVWLDNAAS
PsojNIP	60 AGCKGSGYGTQIYGRAVKYQGVYAFMYSWYMPKDETLTGLGHRHDWEACVVWVDDIAASS
PiNPP1.1	60 AGC KGSG<mark>YGSQIYGRVAT</mark>YN<mark>GVFAIMYSWYFPK</mark>DSPLT<mark>GL</mark>GHRHDWEHVVVWVDDIKLNS
PpNPP1	60 AGC <mark>KGSGYGSQVYGRVAT</mark> YN <mark>GVYAIMYSWYFPKDSPVTGLGHRHDWEHVVVW</mark> V <mark>D</mark> DIKLDS
HaNLP3	60 SGCR <mark>GS</mark> KY <mark>GSQVYGR<mark>S</mark>T<mark>W</mark>YND<mark>VWAIMYAWYFPKD</mark>S<mark>P</mark>MLL<mark>M</mark>GHRHDWENVVVFINDPDEVE</mark>
PsNLP9	60 SSCKGSGWGSQVYGR <mark>S</mark> T <mark>W</mark> YS <mark>GRWAIMYSWYFPK</mark> DSPST <mark>GL</mark> GHRHDWEHVVVWI <mark>D</mark> NPDVEN
PsNLP37	60 AGCKGSGWGSQVYGR <mark>S</mark> T <mark>W</mark> H <mark>R</mark> DVWAIMYSWYFPKDSPST <mark>GL</mark> GHRHDWEHVIVWINNPDVPD
PsNLP54	60 SGYT <mark>GS</mark> SL <mark>GSQIYGR</mark> AVEYE <mark>GVYAFMYSWYMPKD</mark> ETLP <mark>GLGHRHDWE</mark> ACV <mark>VW</mark> L <mark>D</mark> SLDD
PsNLP58	60 SKCKGSGWGSQVYGR <mark>S</mark> T <mark>W</mark> YN <mark>GVWAIMYSWYFPKDSPS</mark> S <mark>GL</mark> GHRHDWEHVIVWI <mark>D</mark> NPDMPE
PsNLP59	60 ggcr <mark>gsg</mark> hgsqvygr <mark>s</mark> t <mark>wi</mark> ngvwaimyswyfpkd <mark>a</mark> pssk <mark>m</mark> ghrhdwehvvvfidnpdvpe
PsNLP60	60 GGCRGSG <mark>HGSQVYGR</mark> AG <mark>WF</mark> ND <mark>VWAIMYSWYFPKDSPS</mark> SR <mark>M</mark> GHRHDWEHVVVWINNPDVPE
PvNLP2	60 GMCKGSGWGSQVYGR <mark>HA<mark>lfk</mark>GVWAIMYSWYFPKD<mark>M</mark>PSTD<mark>F</mark>GHRHDWEHVIVWI<mark>EK</mark>PVVEN</mark>
PvNLP3	60 GMCKGSGWGSQVYGR <mark>HA</mark> SFR <mark>GVWAIMYVWYFPKD</mark> MPSA <mark>HF</mark> GHRHDWEHVIVWI <mark>EK</mark> PVVEN
NLP _{Pya}	121 <mark>A</mark> nivalsa <mark>sa</mark> hs <mark>gykk</mark> sfpadk <mark>syldgi</mark> takisykstwp-ldhelg <mark>ftt</mark> sagkoopliow
PsojNIP	121 <mark>PKIVALSASAHSGYNKYYPP</mark> SS <mark>SY</mark> FSGNSAKIDYSSSYVVINHALS <mark>ATS</mark> TAGETOPLI <mark>M</mark> W
PiNPP1.1	121 <mark>P</mark> SVIAVSPSAHSGYNIYHPPESN <mark>T</mark> IDGYSTKVDYSSSWLVINHALDSTTDAGETONLIMW
PpNPP1	121 <mark>P</mark> SIIAVSPSAHSGYNIYYPPESN <mark>T</mark> IDGYSAKVDYSSSWVVINHALDSTTDAGETQDLIMW
HaNLP3	121 <mark>P</mark> TILGCSTSWHSCYIKYAPCPTD <mark>S</mark> INGSSVMIKYEHSFP-LNHALN <mark>ITK</mark> DAGAYQDLIMW
PSNLP9	121 <mark>P</mark> TILSTSPSAHSGYSYYVPPSAD <mark>S</mark> IDGTSVKVNYESHWP-INHALD <mark>MTS</mark> ESGEFQDLIMW
PSNLP37	121 <mark>P</mark> IILAVTPSAHSGYSKYSPPNAD <mark>T</mark> LDGTSIKVNYESNYP-MNHATD <mark>VTT</mark> EGGDFQDLIMW
PSNLP54	121 <mark>P</mark> SIVALSASYHSTYLTYYPPDSD <mark>yl</mark> dgnsakieystswvildhsls <mark>ats</mark> tagetodlimw
PSNLP58	121 <mark>PKILAVTPSA</mark> HS <mark>GYS</mark> AQVPPDADKVDG <mark>P</mark> SVKVNYESKWP-INHALEST <mark>TKG</mark> GDYQDLIMW
PSNLP59	121 <mark>PKILGCSPSWHNGYNKYAPCPANVIDG</mark> TSVKVKYEHSWP-LNHALETT <mark>TK</mark> PGAFQDLIMW
PSNLP60	121 <mark>P</mark> KILGISASAHSGYKKYSSPPPE <mark>NL</mark> DGNSVKVNYEHAWP-INHALDTTD <mark>K</mark> AGTFQDLIMW
PvNLP2	121 <mark>V</mark> KILAVTPSAH <mark>D</mark> GYSKQVPPNPG <mark>H</mark> LNG <mark>LA</mark> AKINYESKWP-INHALE <mark>PTG</mark> LGGE <mark>K</mark> QDLILW
PvNLP3	121 <mark>V</mark> KILAVTPSFH <mark>D</mark> GYSKQVPPDPS <mark>HLNG<mark>LA</mark>AKFIYESEWP-INHALR<mark>PTRK</mark>GGK<mark>K</mark>QDLILW</mark>
NLP _{Pva}	182 EQMTQAARDALESTDFGNANVPFKS-NFQDKLVKAFFQ
PsojNIP	182 DOLTDAARRALEDTDFGDANVPFKJANFOTKLGNAFFQ
PiNPP1.1	182 DOLTDAARRALEDTDE GDAN VEERDAN FOIRLGNAITA 182 DOLTDAARTALENTDEGDAN VERKDGNELTKVGNAYYA
PDNPP1	182 DOLTDARRIALENTDE GDAN VEMEDONELTRYGNATIA 182 DOLTDAARTALENTDE GDAN VEMEDONELTRYGNATIA
HaNLP3	182 DOLLDARRALNDE ODAN VEMEDONELIN VONATIA 182 HOMPDLARRALNDTDEGKAITEMNDLNEMEKIEAAWPE
PSNLP9	182 DQLSDAARLALNTTSFGSANVPMNDGNFLTKLGKAWPF
PSNLP37	182 D QMS DLARRALNEWSFGDANVPMNDGNFVGKLDRAWPF
PSNLP54	182 D ON JELARRAHNENSE GEANVERNOONE VOREDRAWEE 182 D OL TDA <mark>ARTAL</mark> EDTD <mark>F</mark> GSANV PF KE <mark>A</mark> NFATKVAKAYYA
PSNLP58	182 TQMTDAARQALDNINFGSANVFINS <mark>G</mark> NFLGKLGKAWPF
PSNLP59	182 NQMTDFARRALNDTKFGKANTPMNDWNFLPKVEKAWPF
PSNLP60	182 EQMTEDARRALNAVHFGKANTPMNDGNFRHKLERAWPF
PVNLP2	182 EQLS <mark>SN</mark> ARHALNIVHWGDANTPFNDY <mark>V</mark> FMGKLEKAFPL
PVNLP3	182 EQMS <mark>SN</mark> ARHALNIVP <mark>W</mark> GAANTPFND <mark>FV</mark> FMGRLEKAFPF

Supplemental Figure 6: Alignment of C-termini from cytotoxic NLPs and PvNLPs

Green color indicates positions in the sequence where at least PvNLP2 or PvNLP3 shares an identical amino acid with one of the NLPs above; yellow/orange color indicates positions in the sequence where at least PvNLP2 or PvNLP3 shares an amino acid with similar chemical properties. Blue color indicates amino acids described as crucial for necrosis induction in several publications (Oome and Van den Ackerveken, 2014; Ottmann et al., 2009). Red color indicates positions of amino acids which are completely different in PvNLP2 and PvNLP3 compared to the other NLPs in the alignment.