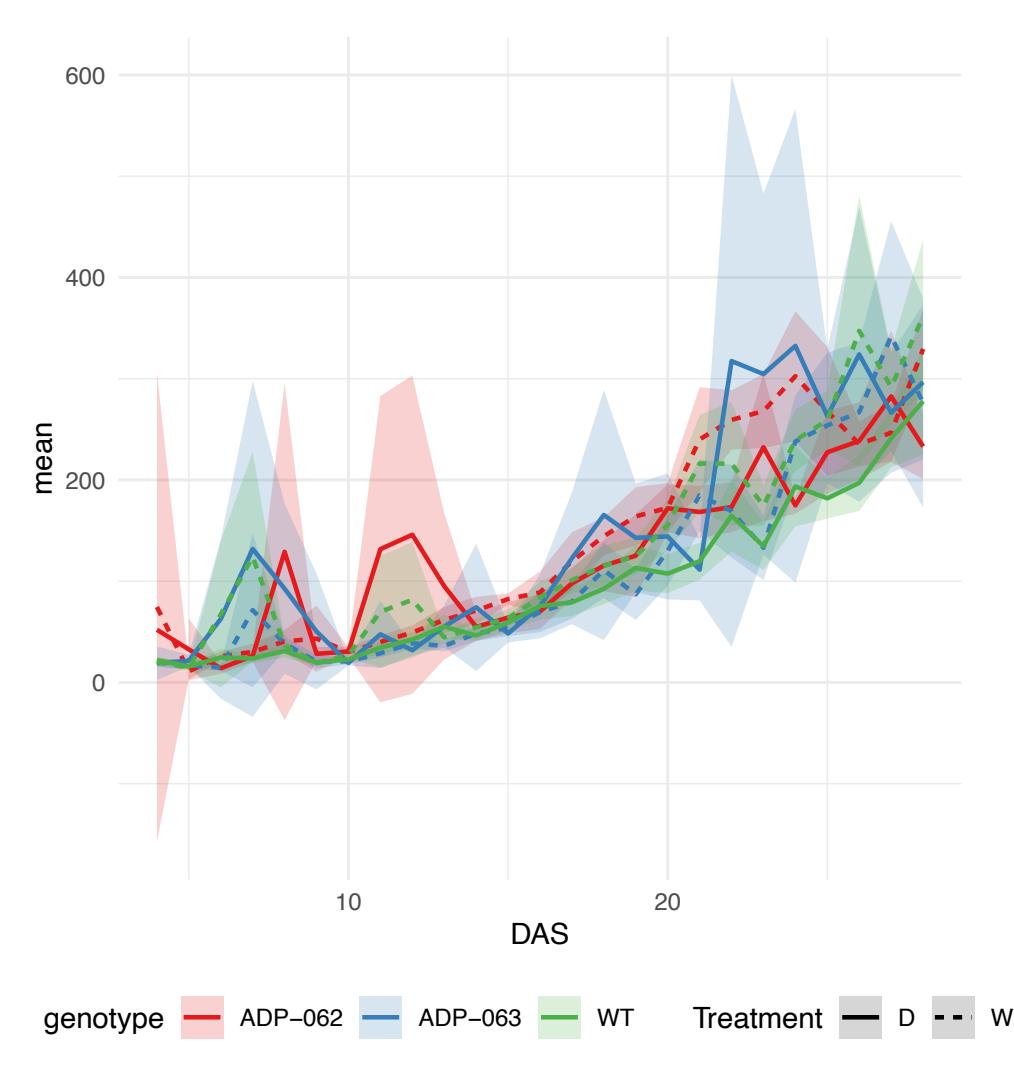
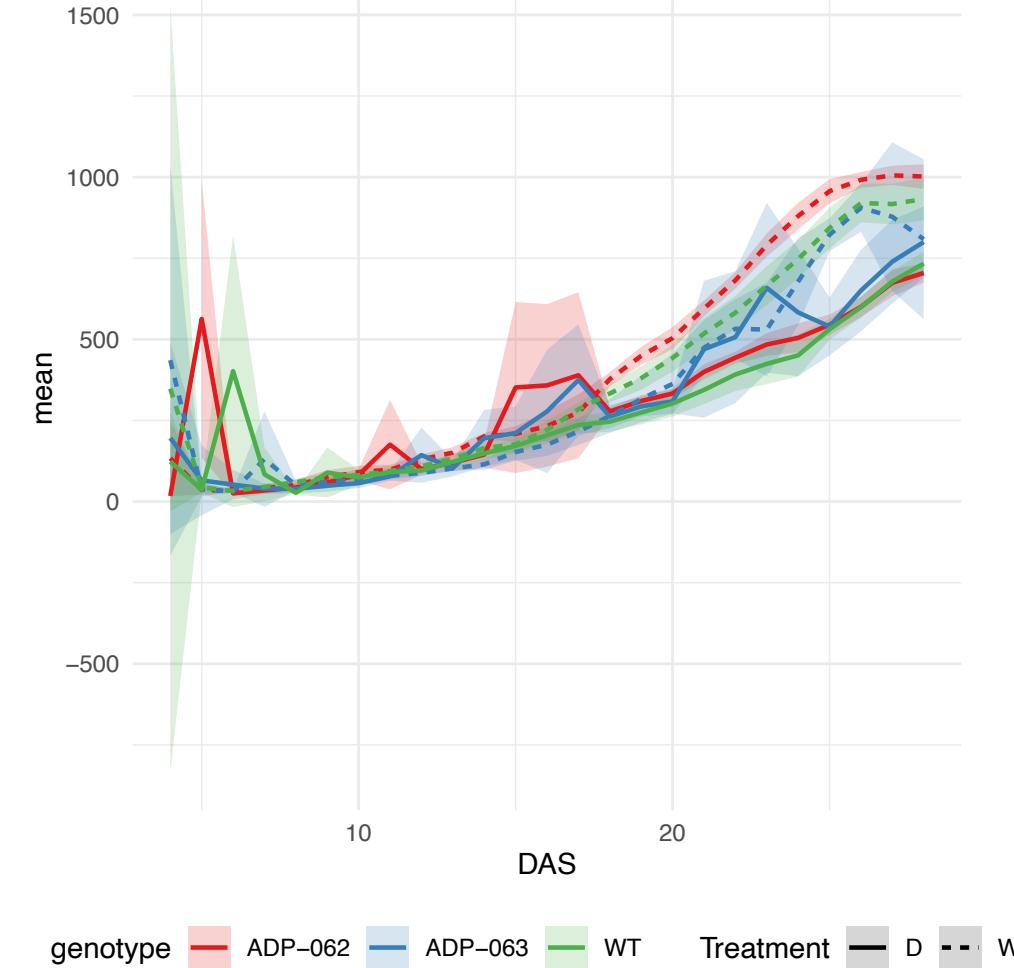


Trait / Gene AT3G51895 AT5G03260 AT3G05630 AT5G54610 AT3G06035 AT3G45600 AT3G16460 AT2G39350 AT2G44450 AT2G18450 AT4G11070

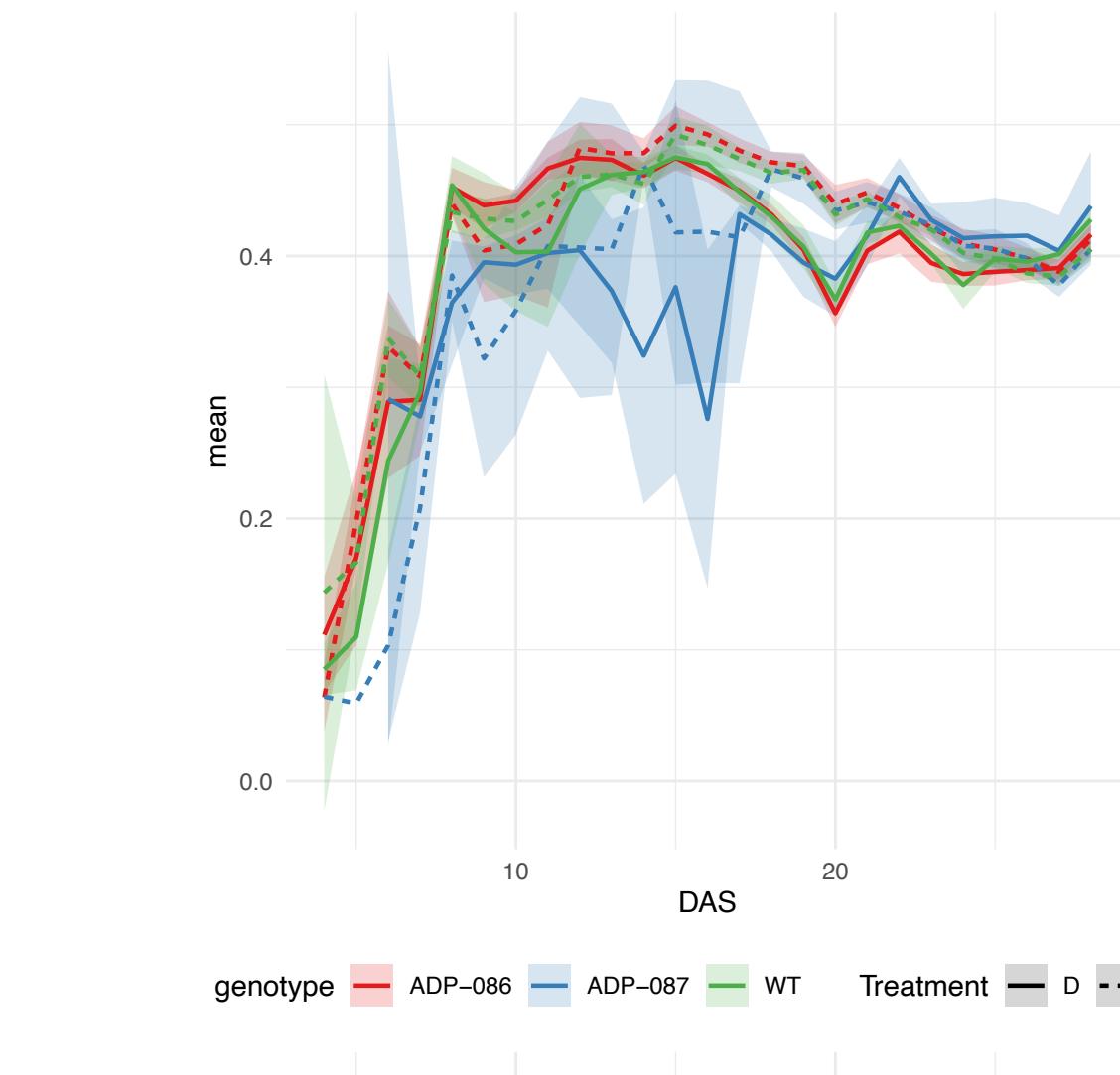
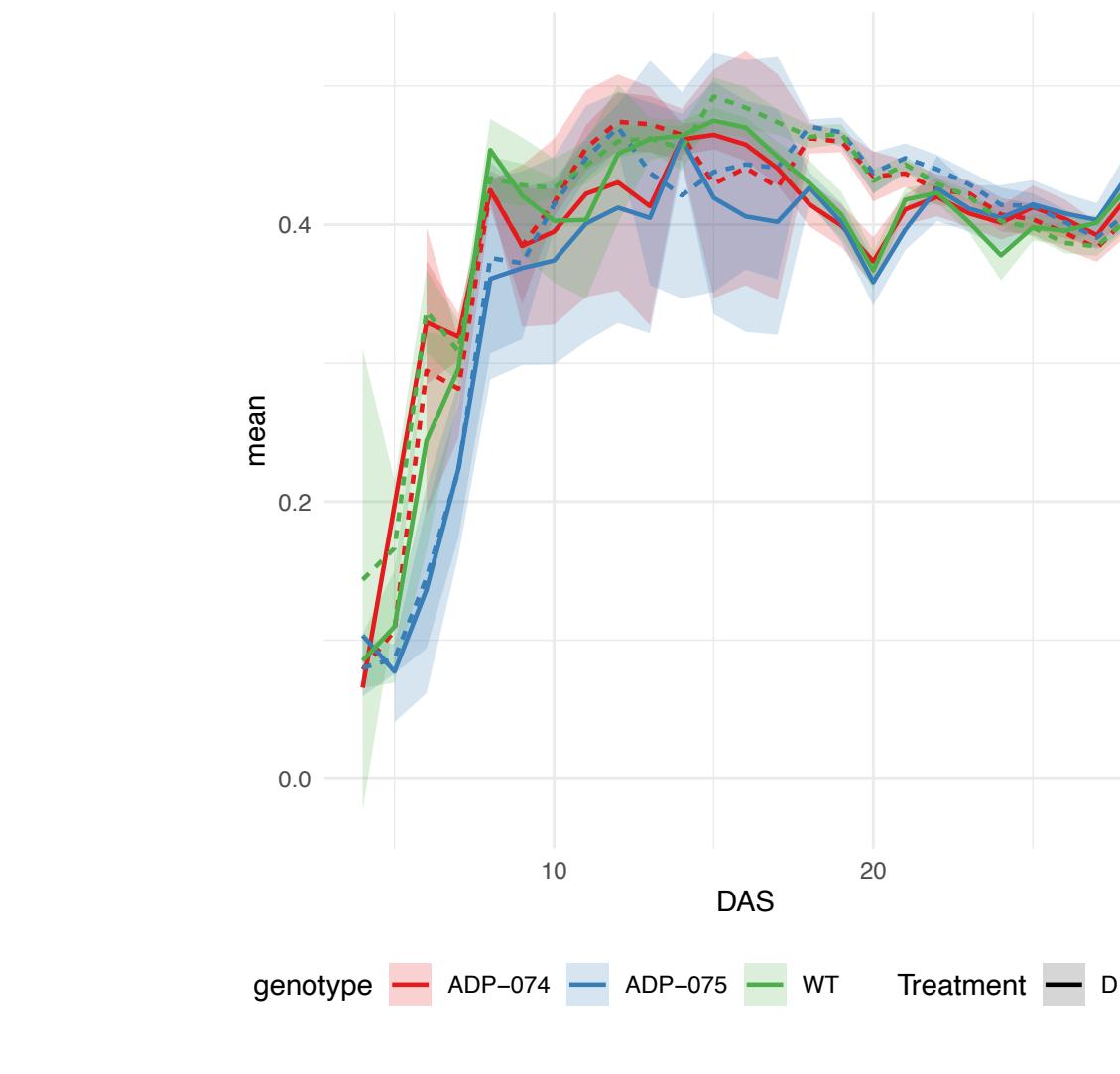
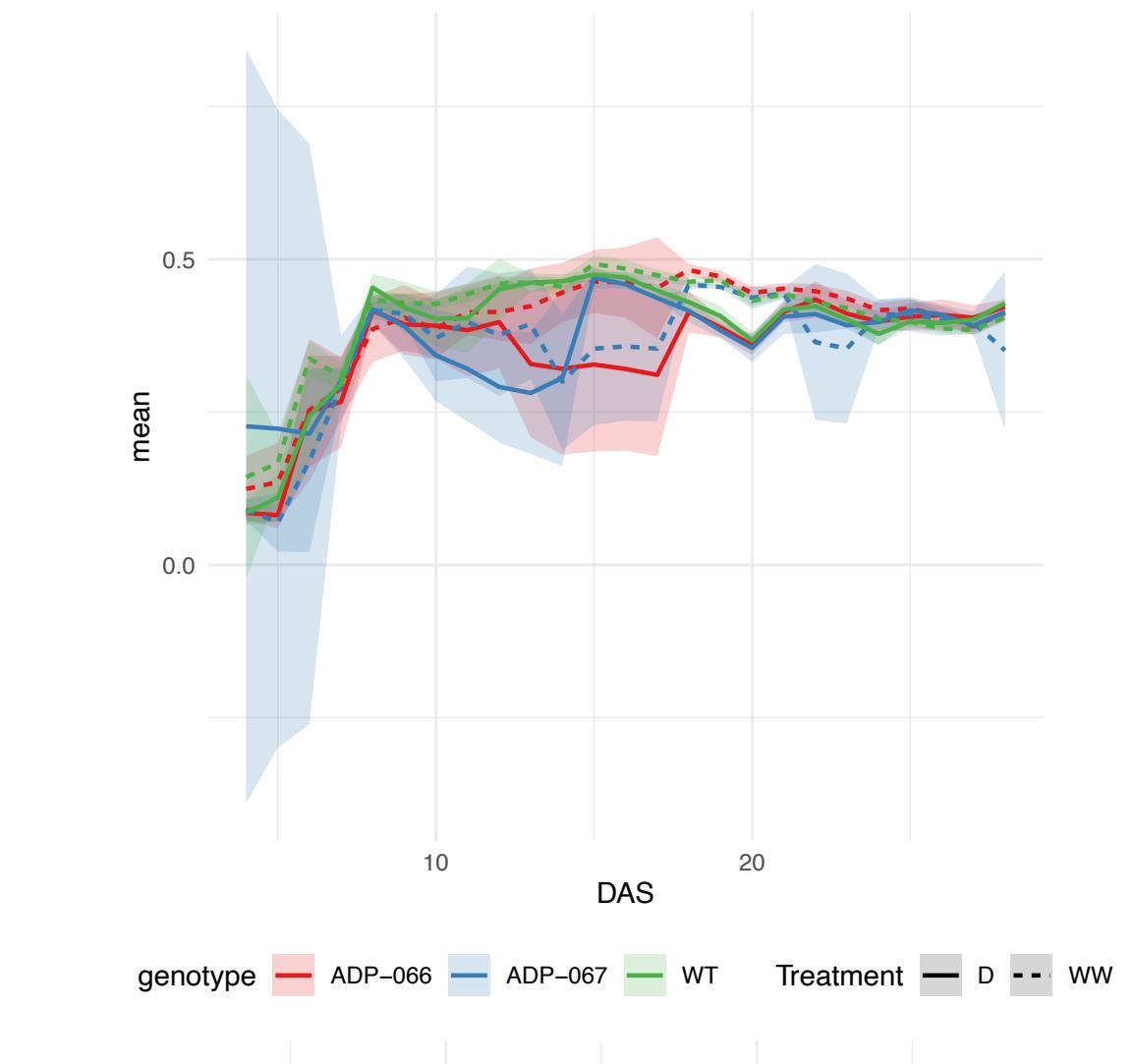
top.geometry.fluo
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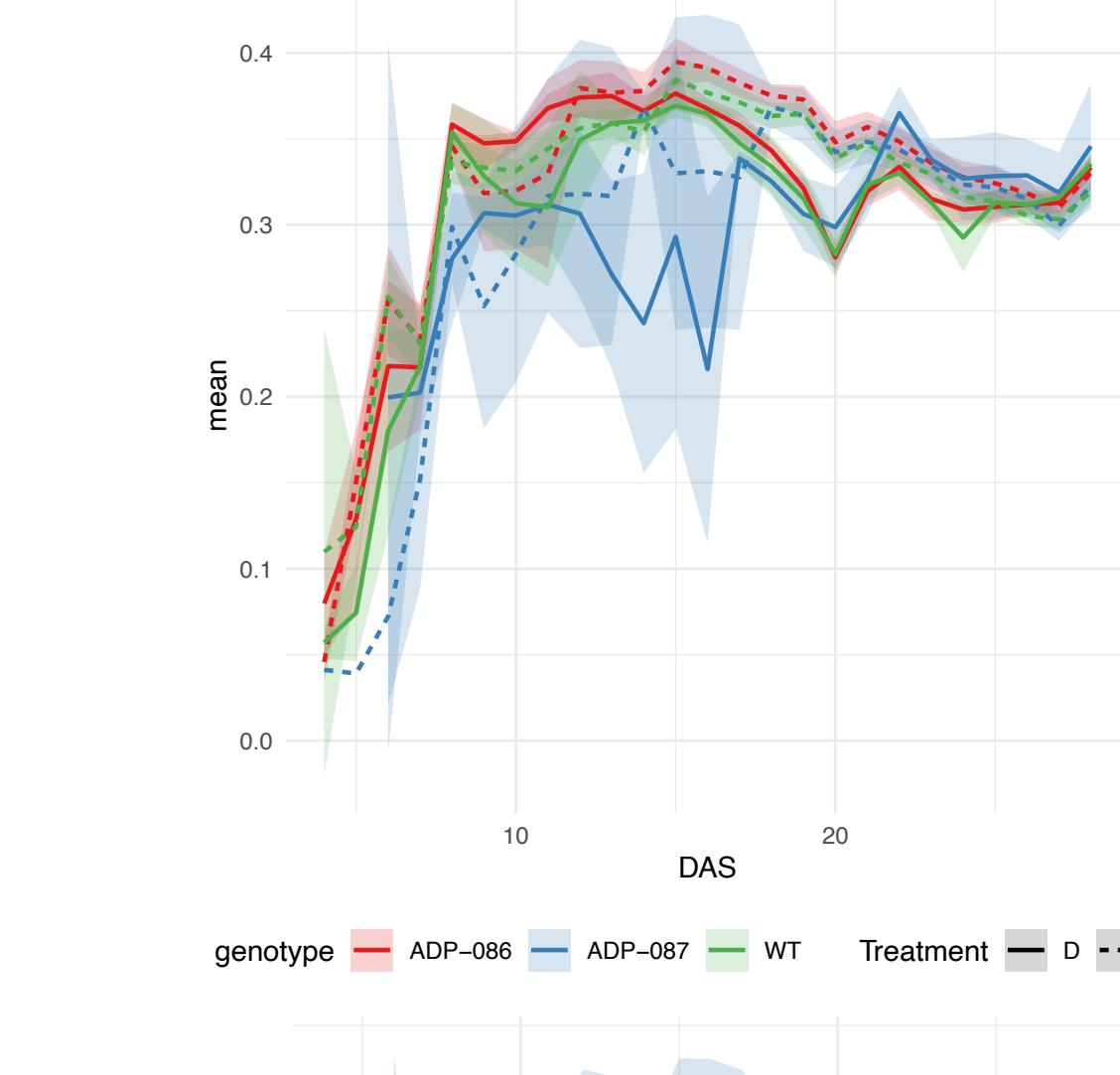
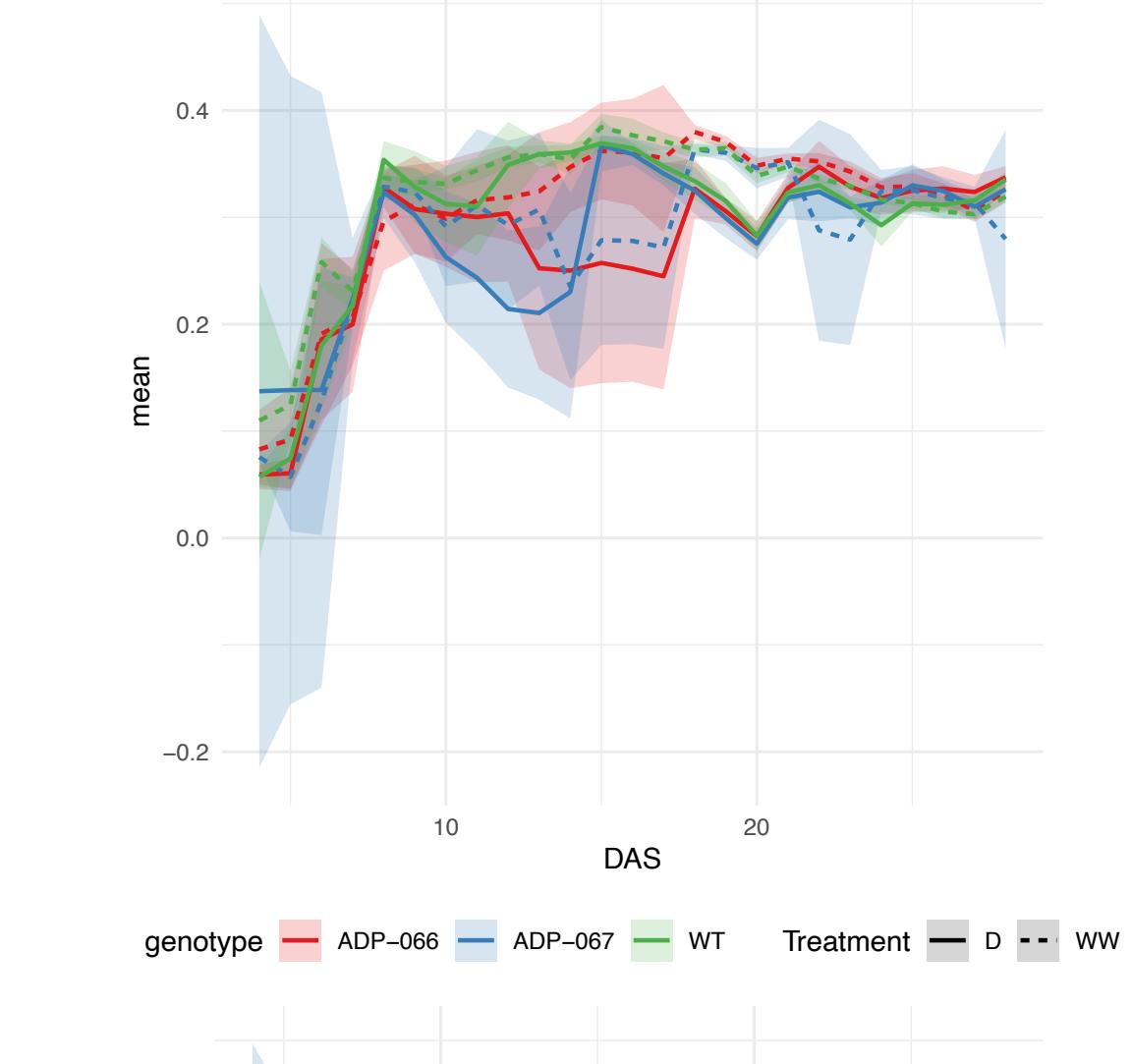
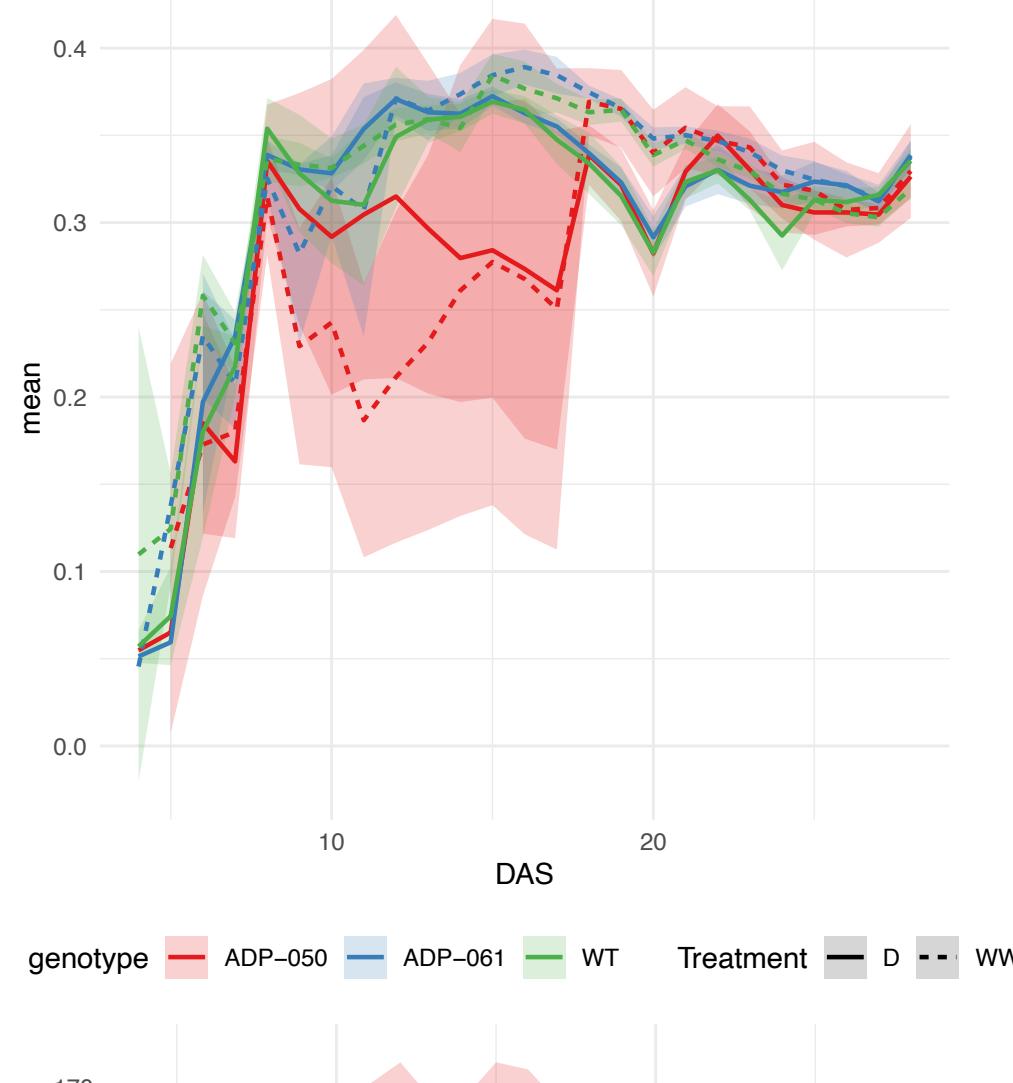
top.geometry.fluo
minrectangle.length
b.px



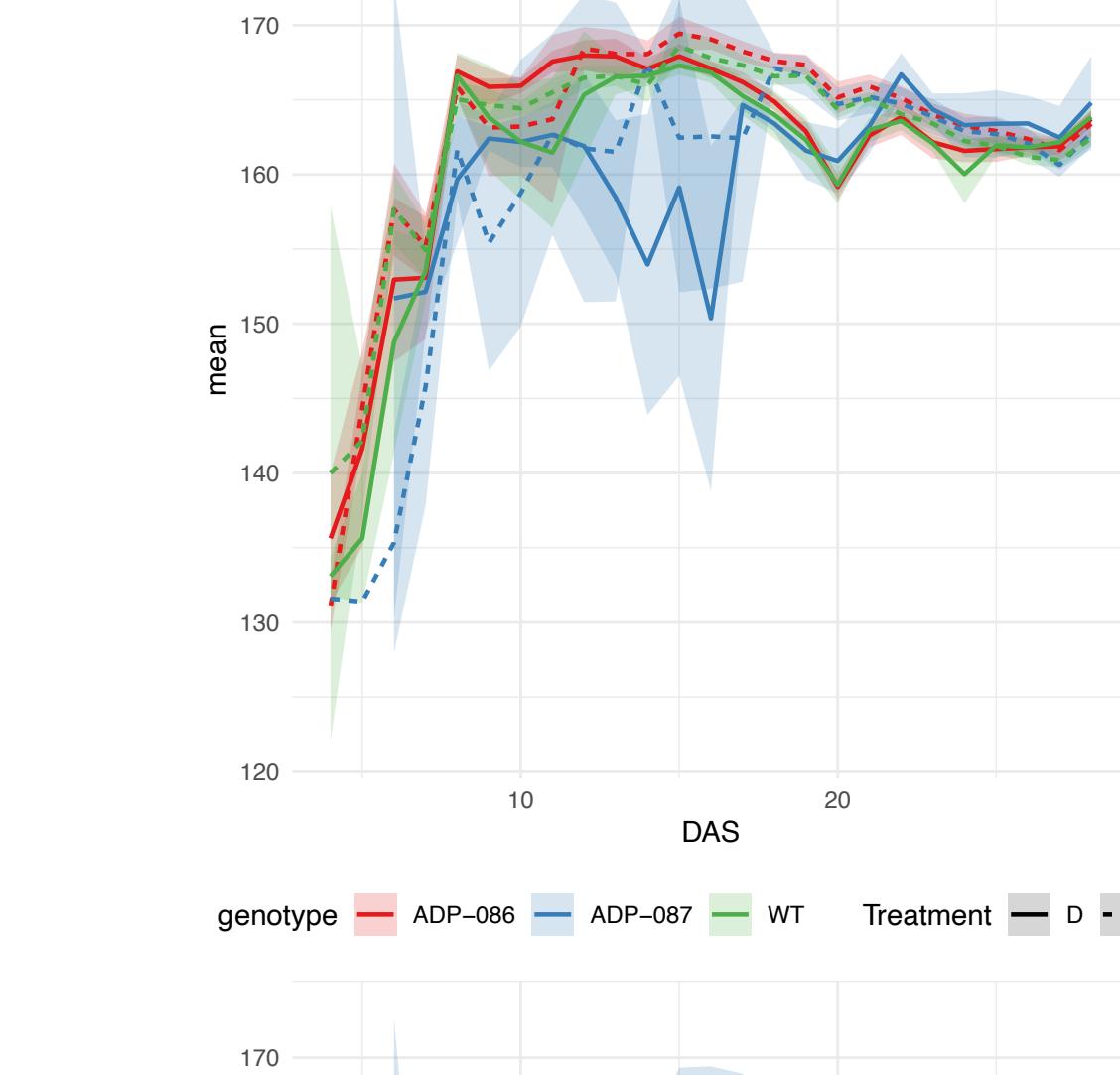
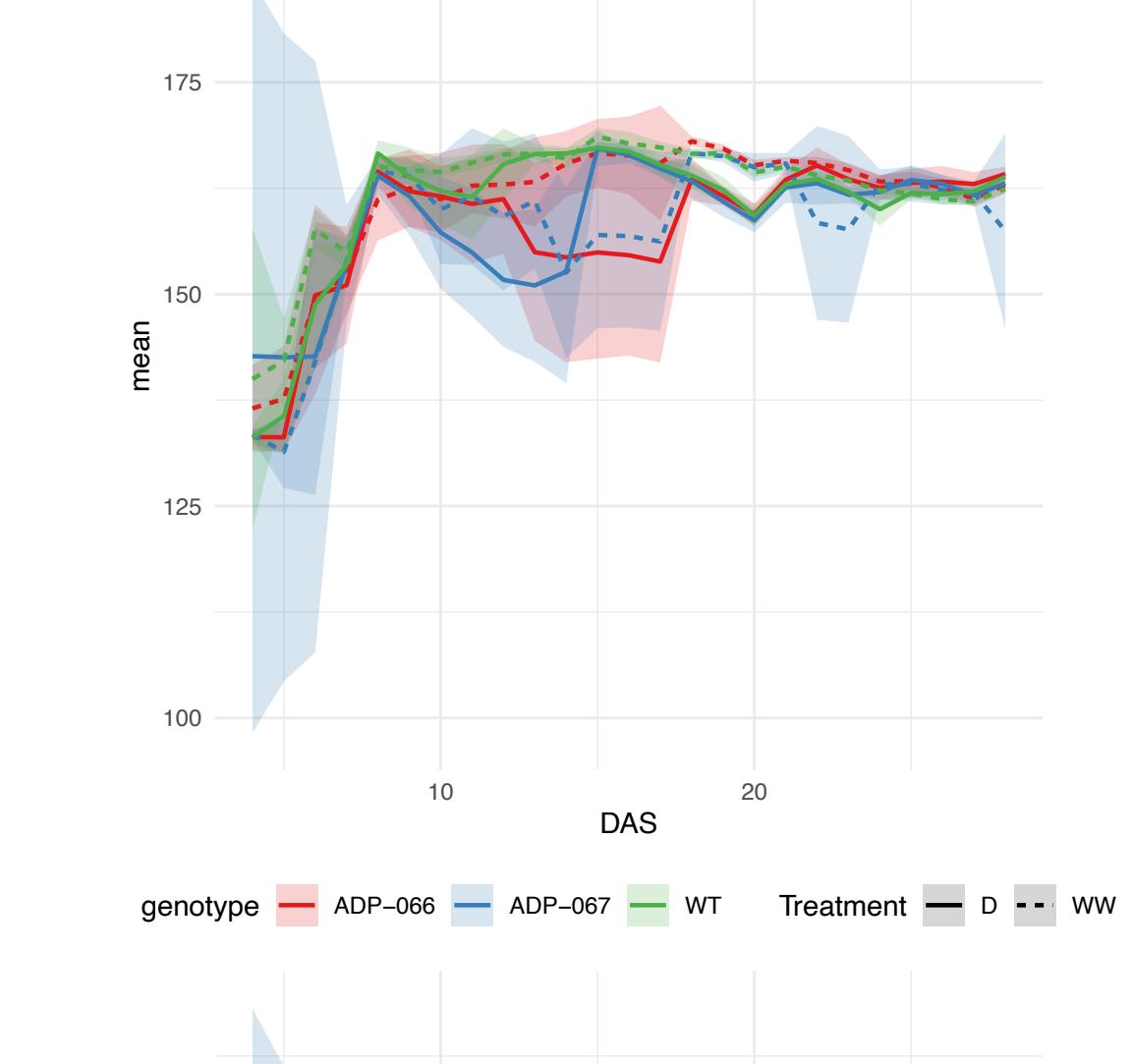
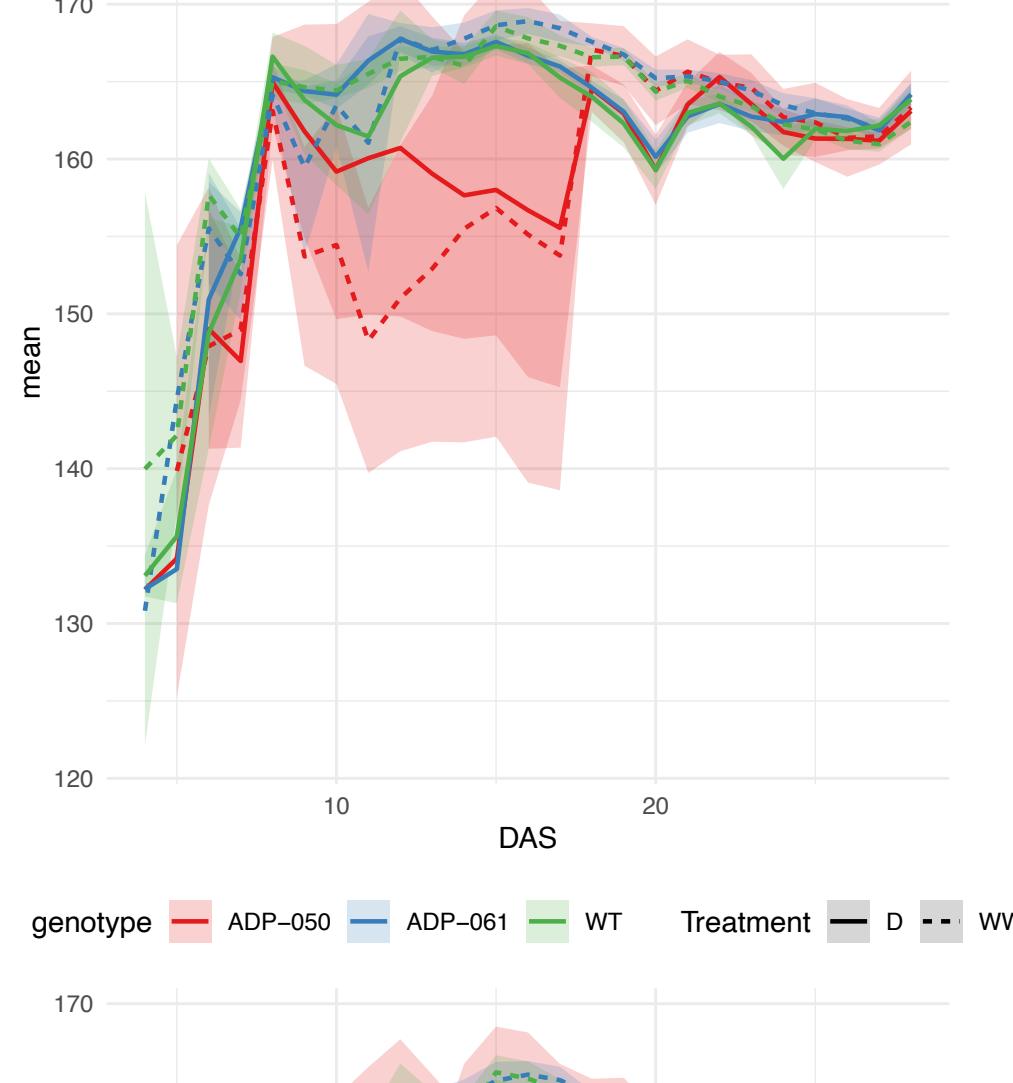
top.intensity.fluo
hsv.v.mean



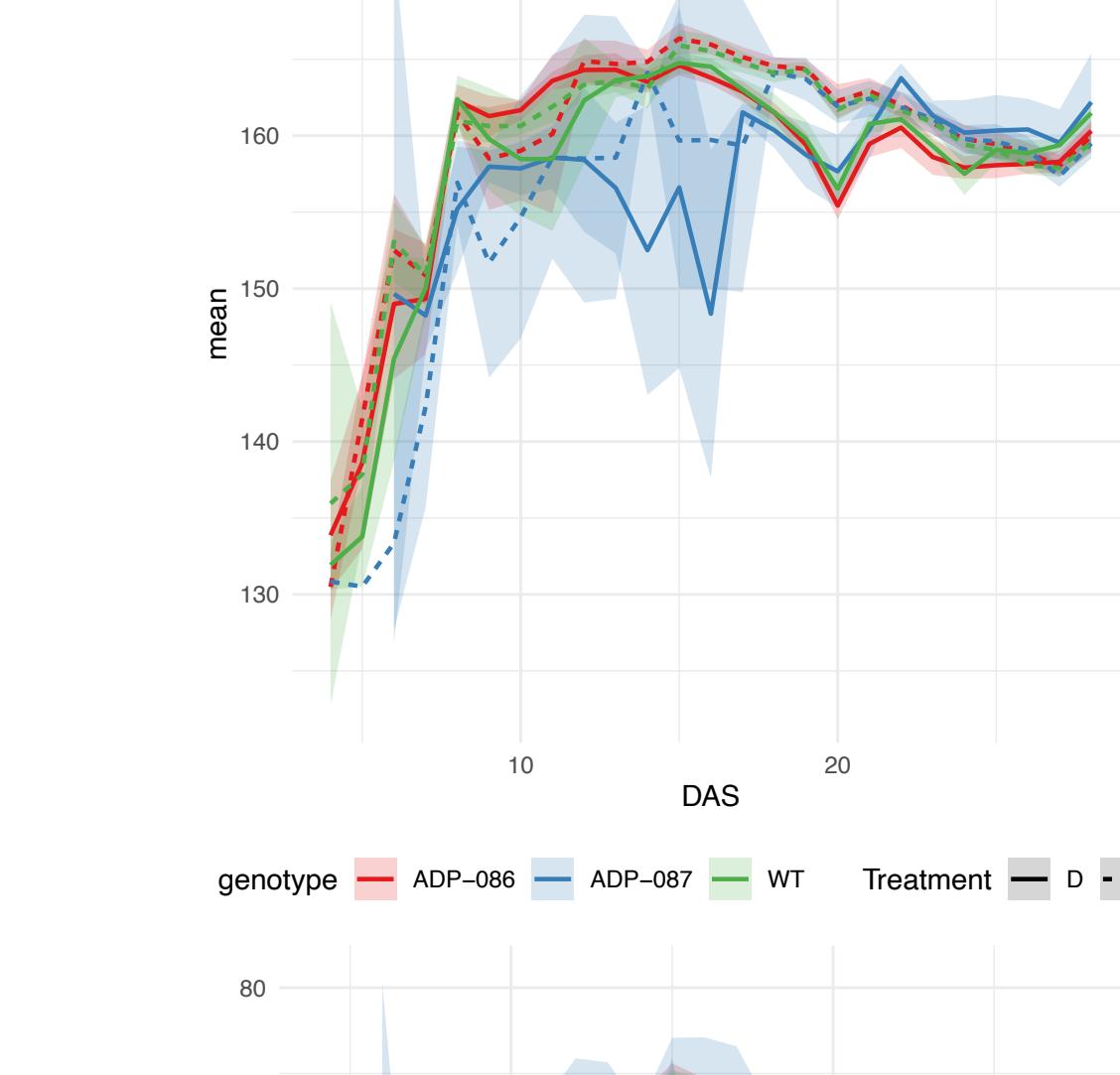
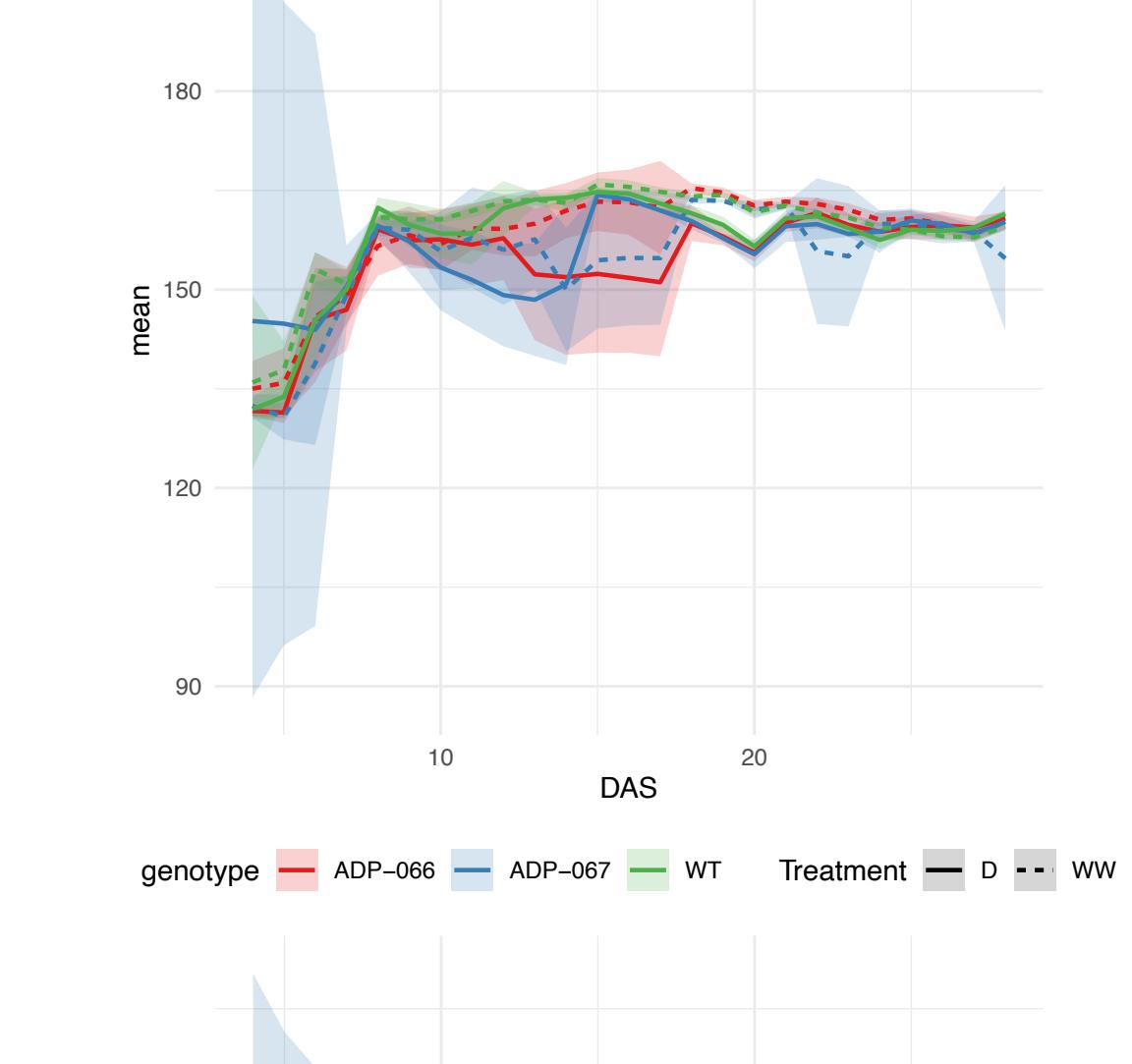
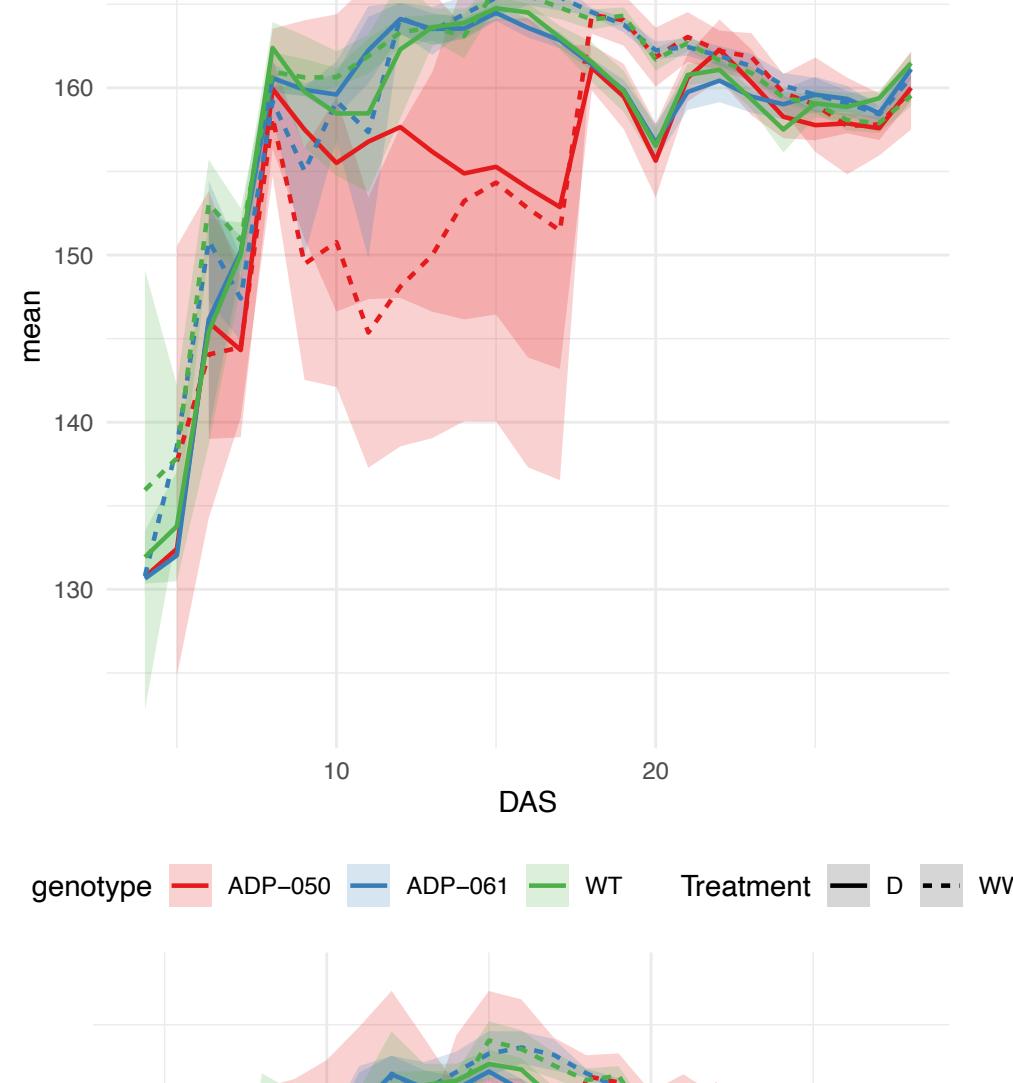
top.intensity.fluo
intensity.mean



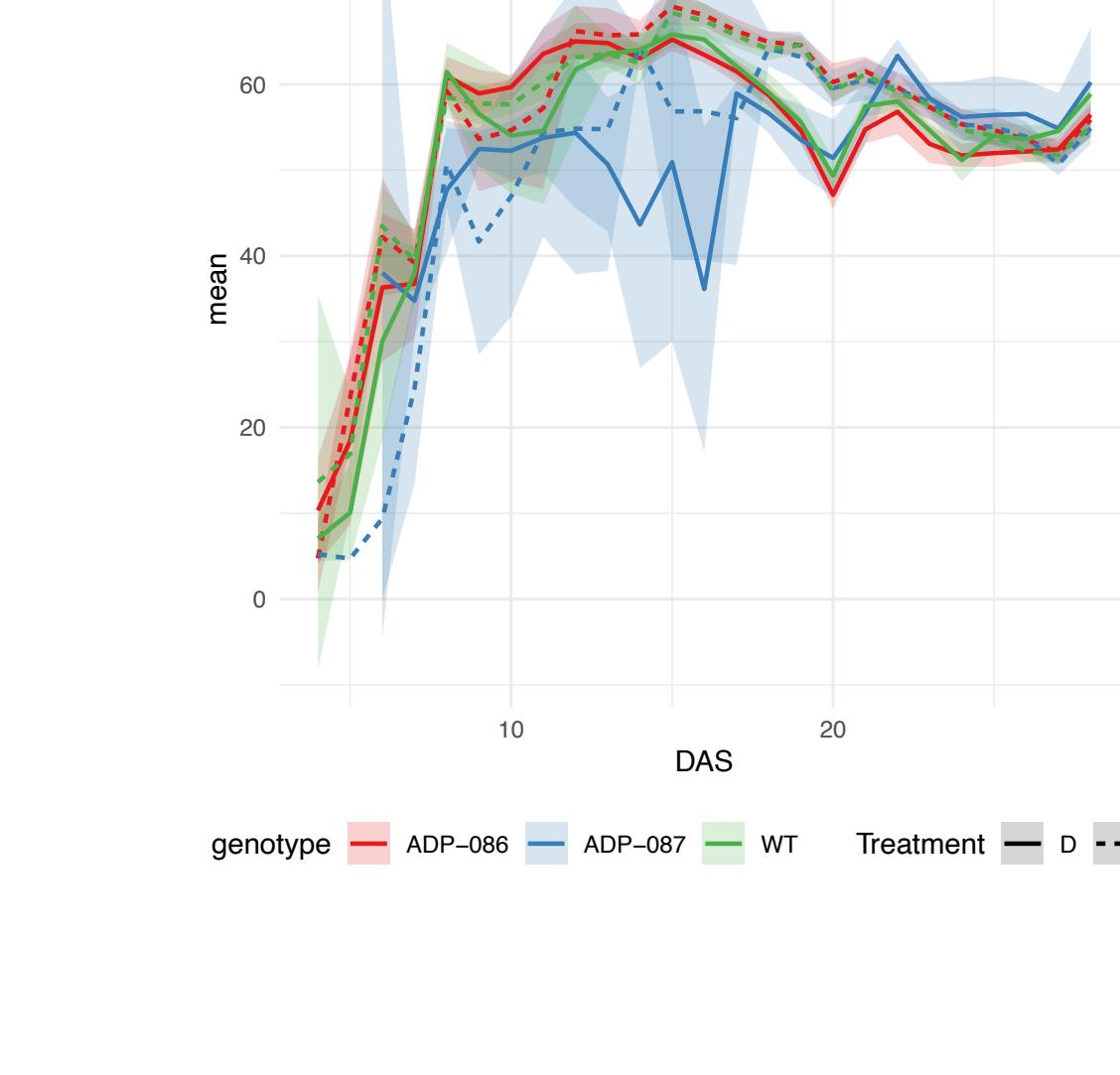
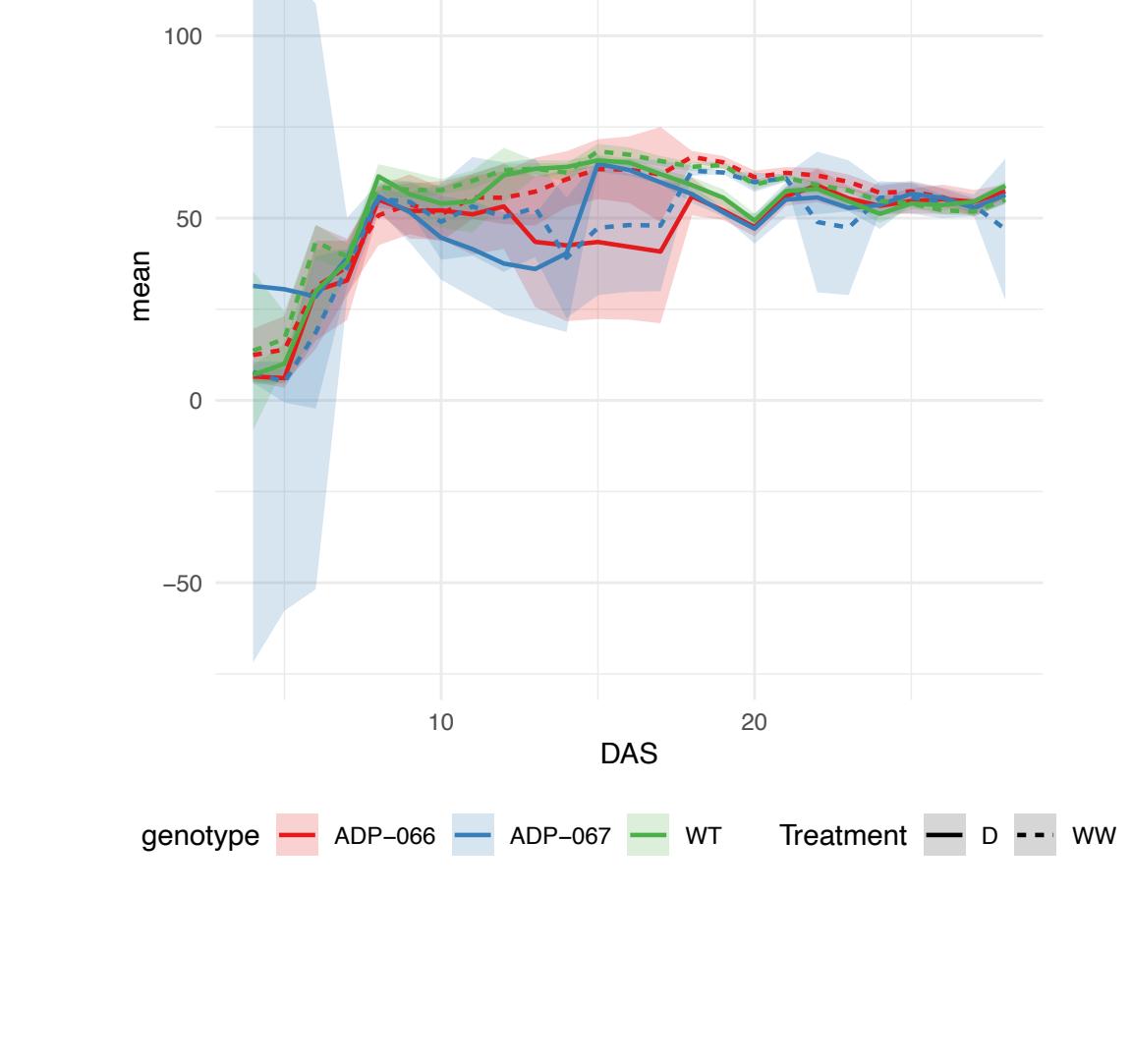
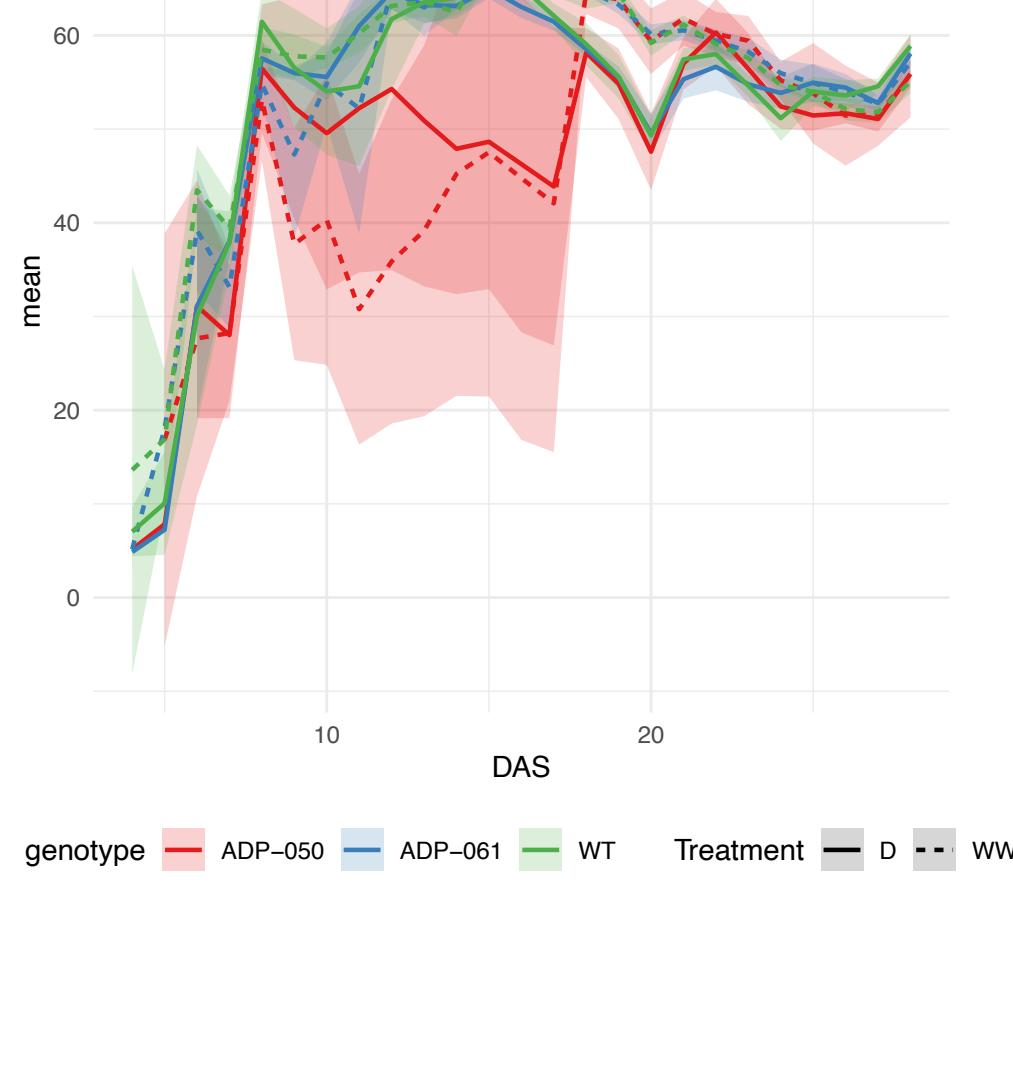
top.intensity.fluo
lab.a.mean



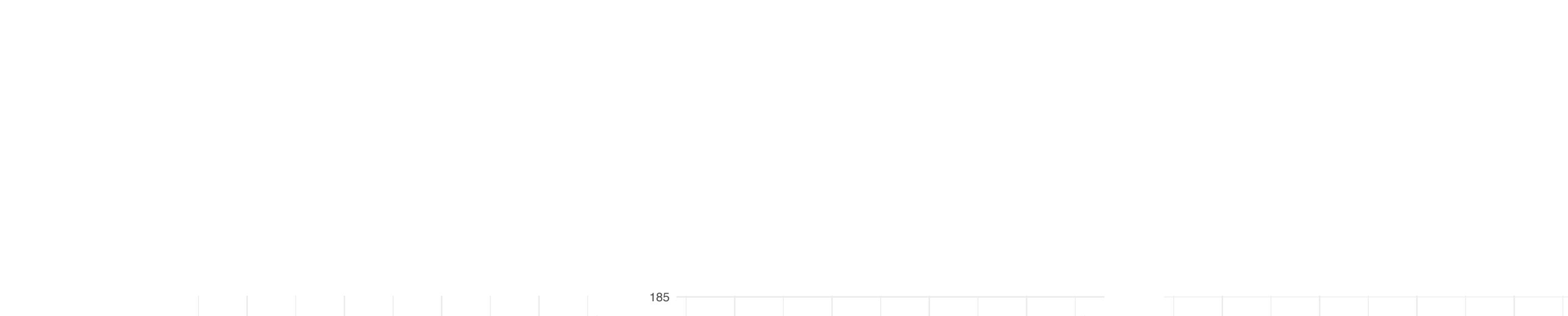
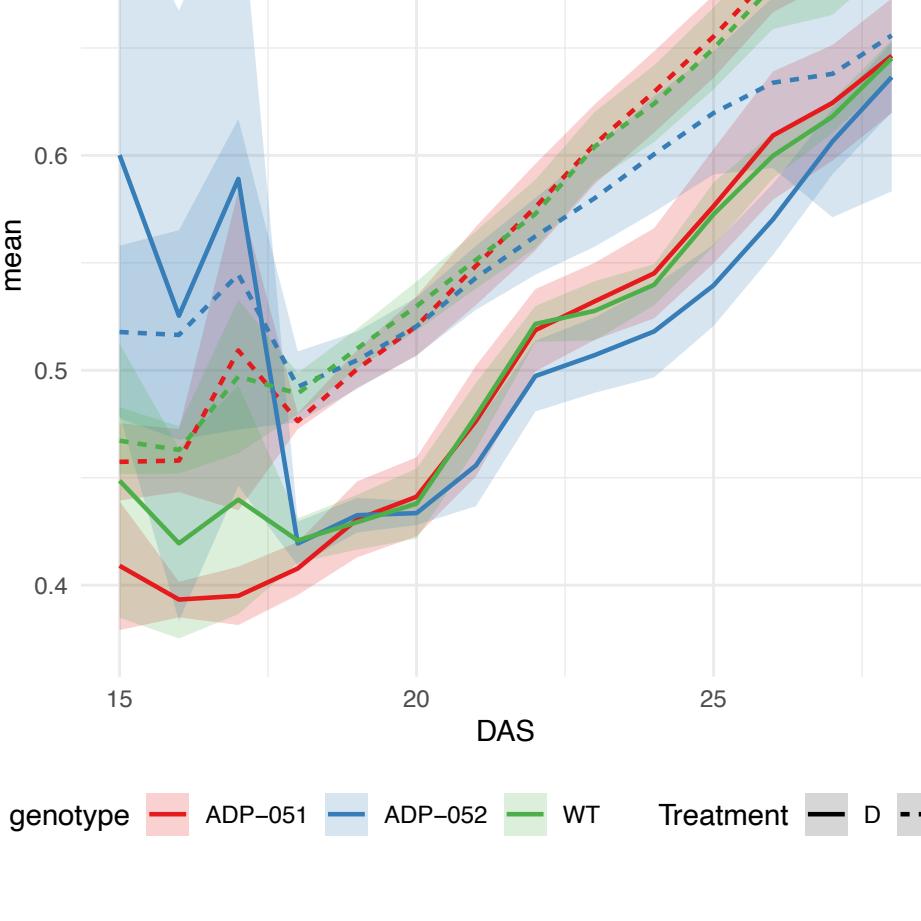
top.intensity.fluo
lab.b.mean



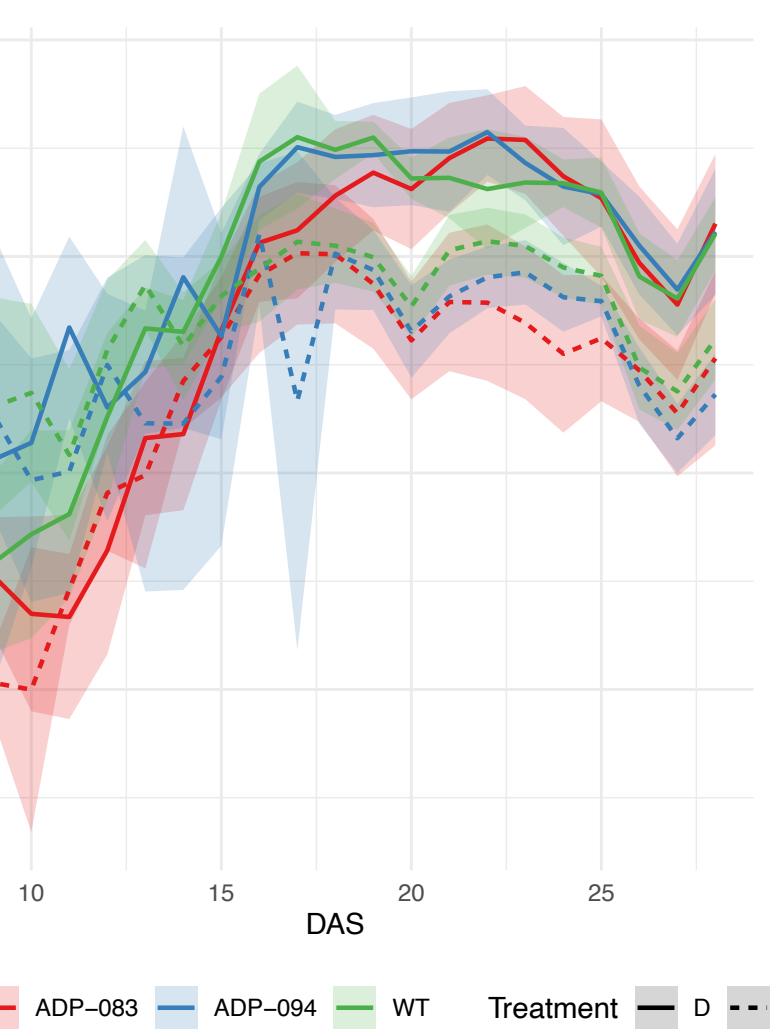
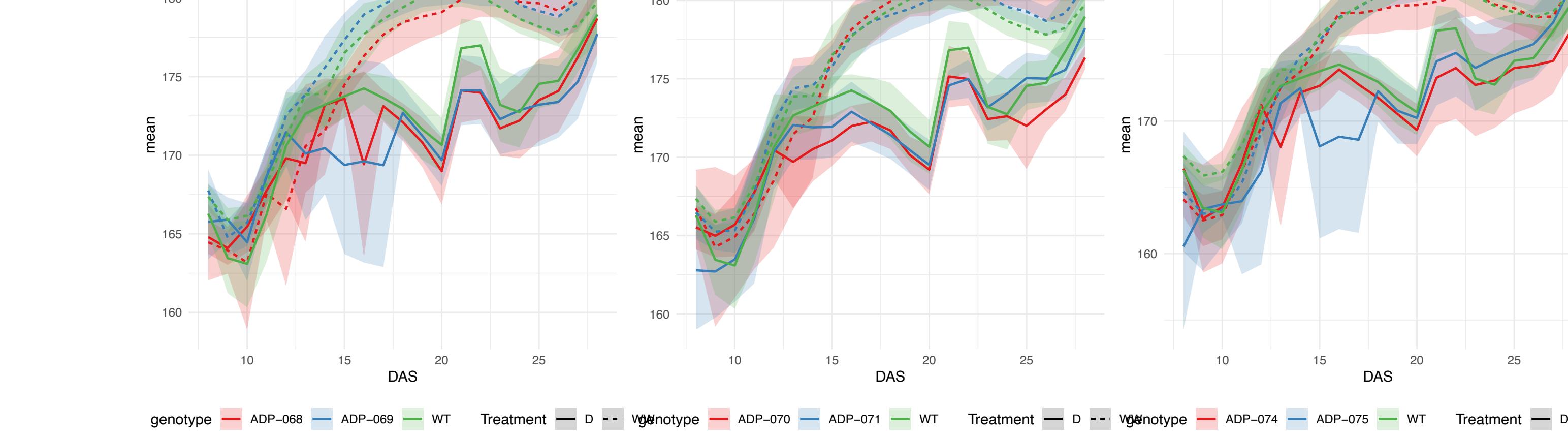
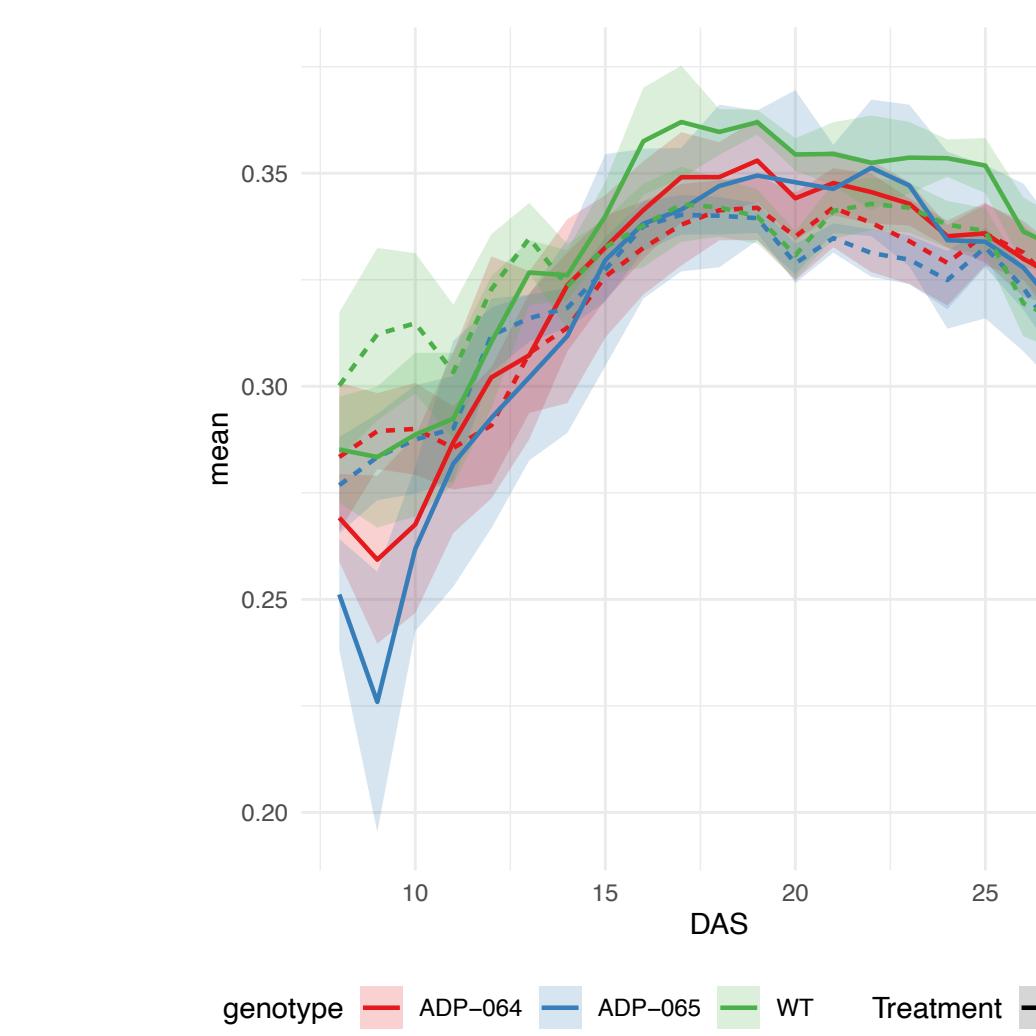
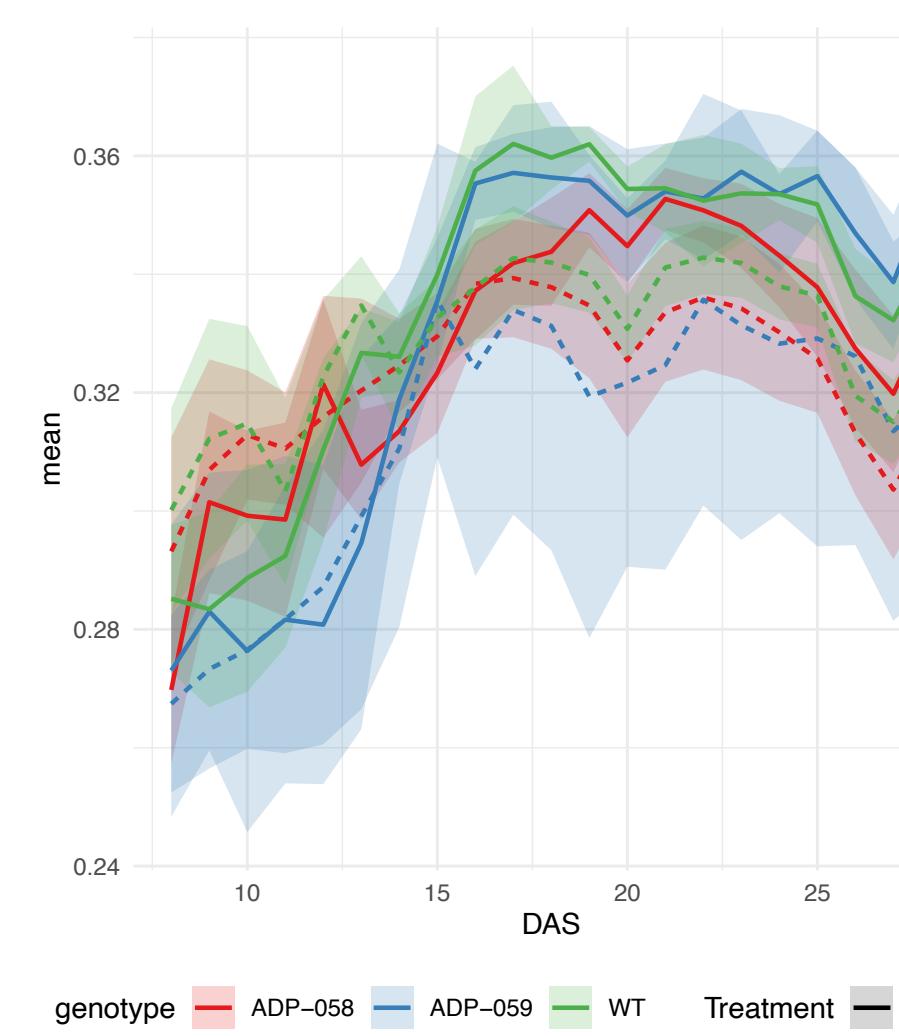
top.intensity.fluo
lab.l.mean



top.intensity.nir
mean



top.intensity.vis
lab.b.mean



top.intensity.vis
rgb.blue.mean

Genotype	Knockout.Line	Targeted.Gene	Primer.R	Primer.L
ADP-050	SALK_023190C	AT3G51895	AATTCCAAGAGAGGGCTTCGAG	CTGGCTTTGTGTCCTCTCTG
ADP-051	GABI-KAT_571C05	AT5G03260	TAGGTACTCCAACGGTGTCTCT	GACC GTGGTGGAAATCGATG
ADP-052	GABI-KAT_782F01	AT5G03260	TAGGTACTCCAACGGTGTCTCT	GTTTAGTCAAAACCGACCGG
ADP-058	GABI-KAT_760A01	AT3G05630	TCAGTATAGTGCAGAGGAAGAGCA	TCTTACACCTGGAGCTTCAGT
ADP-059	GABI-KAT_123E01	AT3G05630	TCCAAATGCAACACTAAAAACTG	ACAGCAAGAACCGGCTCAA
ADP-061	SALK_060617C	AT3G51895	AATGTT CCTATCCTGATGGGC	TGATGCTCCC ATCTACTTTGC
ADP-062	GABI-KAT_883C03	AT5G54610	TGTCCTGAAAGCATTAAAGATGTG	ATGTGAGATCTCTGGCTCG
ADP-063	GABI-KAT_537B07	AT5G54610	GT TAAATGGTTGATCCGTGTTCT	TCAGGTCGCTTTGGGTTTG
ADP-064	SALK_118837C	AT3G06035	TTCAGGATCTTAGATCTGGTCTG	TCCGAGAATATCCTGCATTG
ADP-065	SALK_000844C	AT3G06035	CTAGCTGACGAAATCGCAGAC	AGAGCCCCAATTGAGAGCTAC
ADP-066	GABI-KAT_154B05	AT3G45600	ACAATTTAGGTCCCTCATGTGTT	AGAAAATAAACAAAACAGAGCATTCT
ADP-067	GABI-KAT_026G04	AT3G45600	ACAATTTAGGTCCCTCATGTGTT	GCAACAACCGGACTGCAAAT
ADP-068	GABI-KAT_164E10	AT3G16460	TTTGACTTTGATCGTTAAGGCT	TGGTTGTGAAAGTCACGCC
ADP-069	GABI-KAT_146E08	AT3G16460	TTTGACTTTGATCGTTAAGGCT	GGTACCAAGGAAACCGGAGA
ADP-070	GABI-KAT_306E08	AT2G39350	GAGATCCACTATAACCGGTGTGG	ATCGGATTGCAAAAGGAAGC
ADP-071	GABI-KAT_850E07	AT2G39350	CATGAAGATATAACGTTCTGGAGA	CGTGTCTCGGTTGCTGA
ADP-074	GABI-KAT_161E04	AT2G44450	AATACTGGTAGGTGAGAGGAGGT	AGCCTGGTTGATTCCCTCTT
ADP-075	GABI-KAT_365C01	AT2G44450	TGAAAACCATGAGATTCTTCAAAA	GCAAATGTAGTTGGAGCCA
ADP-083	GABI-KAT_920B04	AT2G18450	CGAGTTCCTAAAATGCAAAGTTTC	AGGTGATGATCCAGATGCTGT
ADP-086	SALK_068648C	AT4G11070	GGGGAAGCCTGTGTTAATCTC	GAAAGGTTCCAGGATCTCCAG
ADP-087	SALK_105785C	AT4G11070	GGGGAAGCCTGTGTTAATCTC	CAGGAAGATGTTGCCAAAGTG
ADP-094	GABI-KAT_254B04	AT2G18450	CTTCTAAAATCCGCTTAAACATGC	TGGCCTATATTACCCCAATGTG