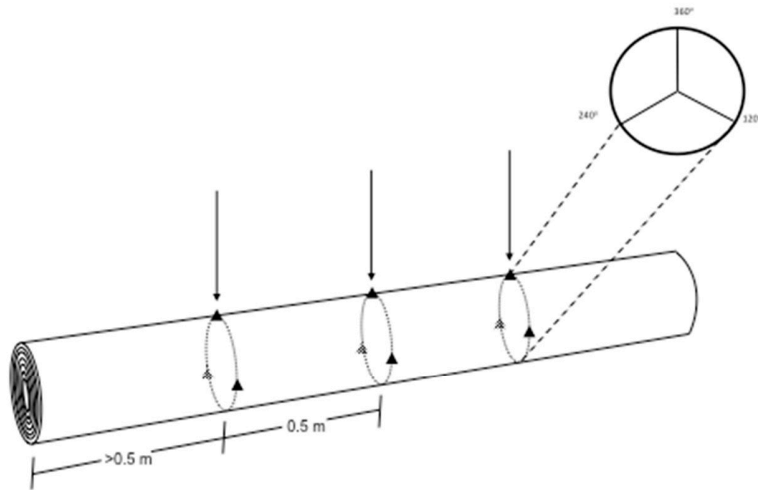
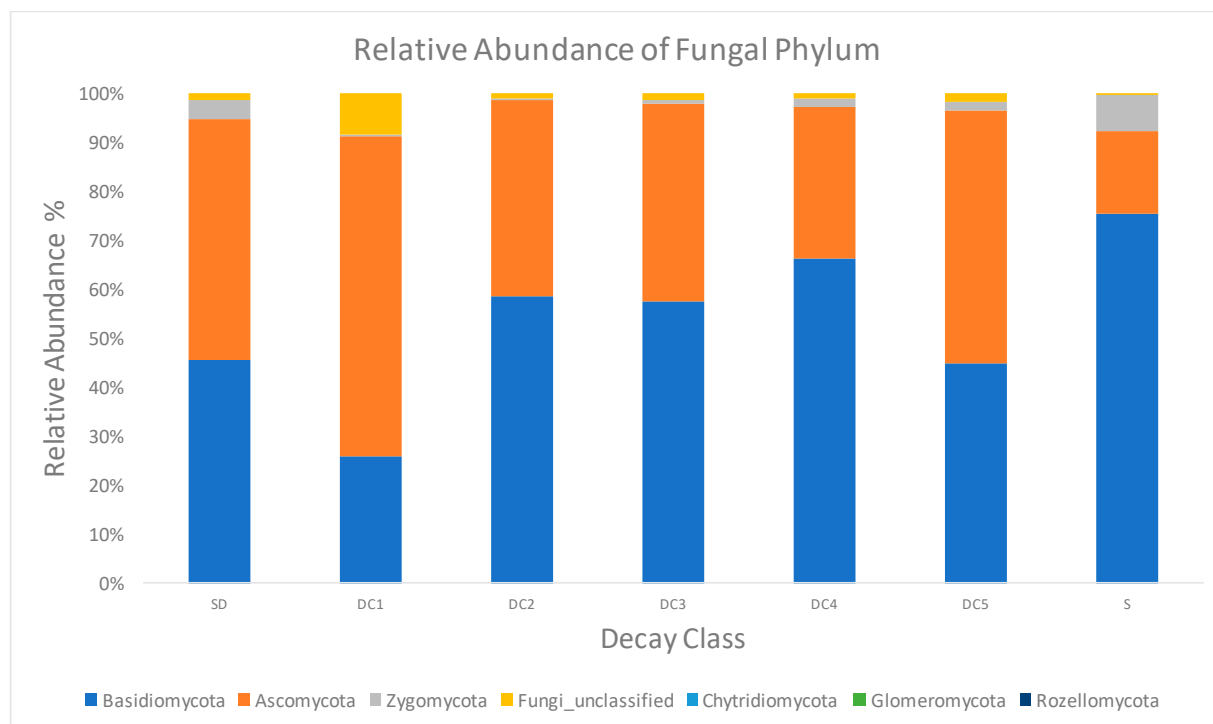


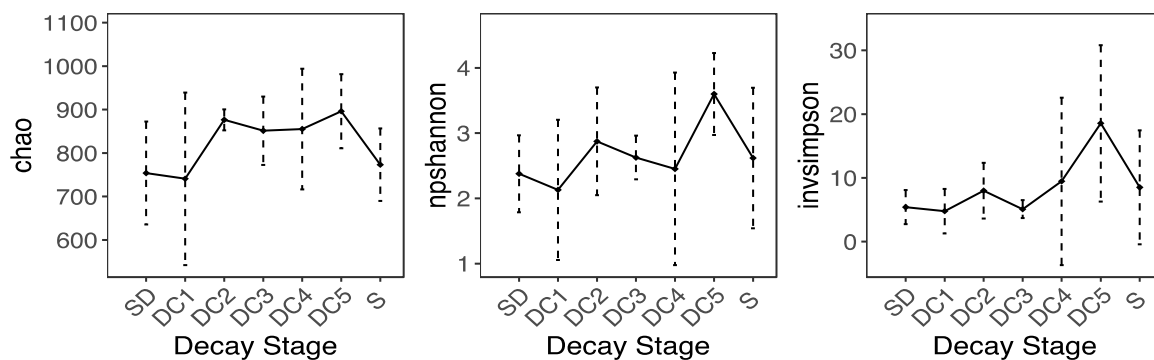
Supplemental Figures & Tables



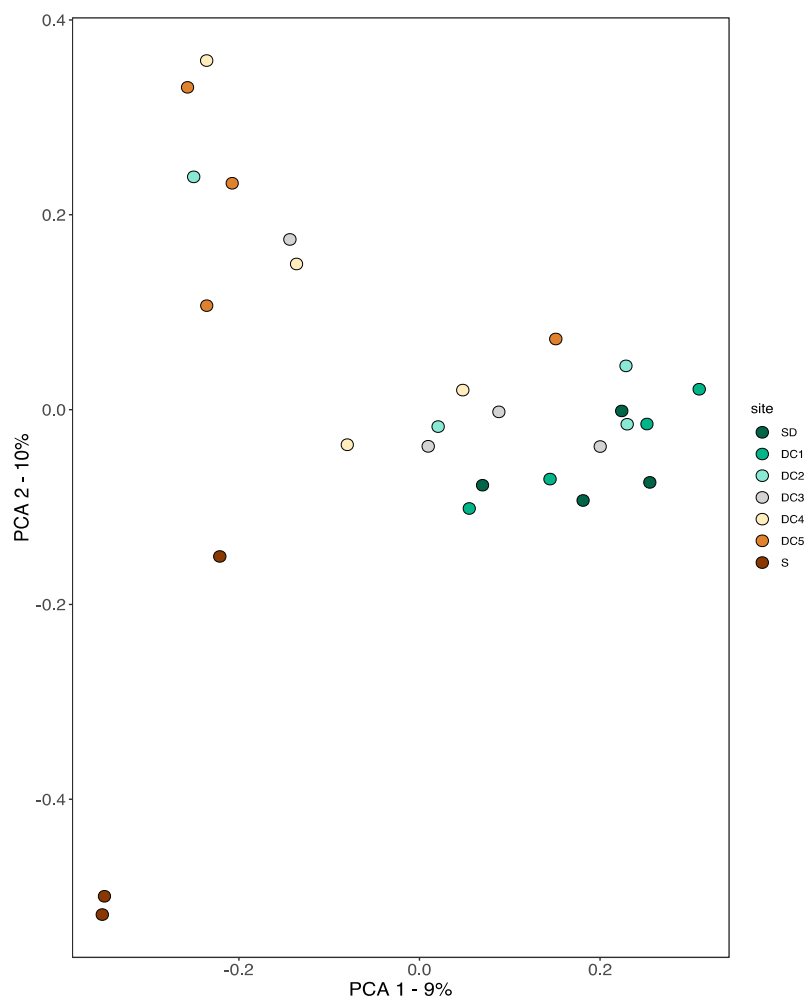
Supplemental Figure S1. Logs were sampled in boles of *Populus grandidentata* at 9 points. First, 3 transects running perpendicular to the length of the log were found, each $\sim 0.5\text{ m}$ from each other or from the end of the log. Then 3 drilling points were identified along each transect (at 360 (top of the log), 120 , and 240 degrees) from which to collect samples. The 9 samples were composited for community and chemistry analyses.



Supplemental Figure S2. The average abundances (as % of classified sequences) of the dominant fungal phyla across standing dead (SD) wood, the various wood decay stages (DC1-DC5), and soil (S). (SD=standing dead, DC1=decay class 1, DC2=decay class 2, DC3=decay class 3, DC4=decay class 4, DC5=decay class 5). N=27 (4 per decay stage of log, 3 soil).



Supplemental Figure S3. Diversity indices across CWD decay stages from standing dead to soil. No differences (n.s.) were found in richness based on abundances (chao) or evenness + richness (npshannon & invsimpson) indices within wood or between wood and soil. Hashed whiskers represent standard deviation. (SD=standing dead, DC1=decay class 1, DC2=decay class 2, DC3=decay class 3, DC4=decay class 4, DC5=decay class 5). N=27 (4 per decay stage of log, 3 soil).



Supplemental Figure S4. Principal coordinates analysis (PCoA) of fungal communities in soil and wood decay stage samples based on Bray-curtis abundance using ThetaYC calculator of dissimilarity. The PCoA explains 19% of the total variation in fungal community dissimilarity. (SD=standing dead, DC1=decay class 1, DC2=decay class 2, DC3=decay class 3, DC4=decay class 4, DC5=decay class 5). N=27 (4 per decay stage of log, 3 soil).

Supplemental Table S1. Coarse woody debris classification guide adapted from the Forest Inventory and Analysis National Core Field Guide. Note: Decay class 5 logs are difficult to identify as they blend into the duff, litter, and soil layers. The decay class 5 logs in our study were identified using samples from an older study. Estimates of log ages were based on decay rates in other published studies (Harmon et al., 2020; Kahl et al., 2017).

Coarse Woody Debris Decay Classification			
Decay Class	Structural Integrity	Texture of Rotten Portions	Estimated Ages of Logs in Each Category (years)
Standing Dead	Sound, bark intact, branches present, standing of own volition and not leaning	Intact with no visible rot	2-5
Decay Class 1	Sound, freshly fallen, Intact logs, bark still intact	Intact, no rot; no conks on stem; decay absent	5-15
Decay Class 2	Sound, log holds its shape, bark mostly intact	Mostly intact; sapwood partly soft (starting to decay) but can't be pulled apart by hand	15-25
Decay Class 3	Log becoming soft, Heartwood sound; Bark beginning to sluff off,	Sapwood can be pulled apart by hand or sapwood absent, large pieces	25-35
Decay Class 4	Heartwood rotten; Bark gone, log no longer holds shape, establishment of mosses and herbaceous plants	Soft, sapwood mostly absent, can be pulled apart easily by hand, small pieces; A metal pin can be pushed into heartwood	35-45
Decay Class 5	None, Piece no longer maintains its shape, log spreads out on ground, substrate for plants	Soft, very small pieces, can crumble when dry	45-60

Supplemental Table S2. The six enzymes measured, their abbreviations, target molecules, and enzyme commission numbers (E.C. Number).

Enzyme	Abbreviation	Target molecule	E.C. Number
β -1,4-glucosidase	BG	Cellulose	3.2.1.21
1,4- β -cellobiosidase	CHB	Cellulose	3.2.1.91
β -D-xylosidase	XYLO	Hemicellulose	3.2.1.37
Leucyl aminopeptidase	LAP	Polypeptides	3.4.11.1
Phenol oxidase	PHEN_OX	Lignin	1.10.3.2
Peroxidase	PER	Hydrogen Peroxide	1.11.1.7

Supplemental Table S3. Total number of observed OTUs and calculations of coverage by sample. (SD=standing dead, DC1=decay class 1, DC2=decay class 2, DC3=decay class 3, DC4=decay class 4, DC5=decay class 5). N=27 (4 per decay stage of log, 3 soil).

Sample	Sequence coverage (%)	OTU observations	Treatment	Accession #
SD	0.997204	511	Standing Dead	SRR26222475
SD	0.996953	552	Standing Dead	SRR26222474
SD	0.997126	630	Standing Dead	SRR26222463
SD	0.997719	454	Standing Dead	SRR26222465
DC1	0.99641	741	Decay Class 1	SRR26222455
DC1	0.997523	371	Decay Class 1	SRR26222454
DC1	0.998032	457	Decay Class 1	SRR26222457
DC1	0.997506	456	Decay Class 1	SRR26222453
DC2	0.997026	530	Decay Class 2	SRR26222451
DC2	0.997135	628	Decay Class 2	SRR26222468
DC2	0.996894	604	Decay Class 2	SRR26222464
DC2	0.996856	659	Decay Class 2	SRR26222452
DC3	0.997026	579	Decay Class 3	SRR26222450
DC3	0.996745	667	Decay Class 3	SRR26222449
DC3	0.996981	632	Decay Class 3	SRR26222473
DC3	0.997144	545	Decay Class 3	SRR26222462
DC4	0.996717	583	Decay Class 4	SRR26222472
DC4	0.997406	435	Decay Class 4	SRR26222471
DC4	0.996681	700	Decay Class 4	SRR26222461
DC4	0.996697	662	Decay Class 4	SRR26222458
DC5	0.996856	730	Decay Class 5	SRR26222467
DC5	0.996826	809	Decay Class 5	SRR26222460
DC5	0.996636	654	Decay Class 5	SRR26222459
DC5	0.997405	559	Decay Class 5	SRR26222456
S	0.997544	520	Soil	SRR26222470
S	0.997547	513	Soil	SRR26222469
S	0.996994	710	Soil	SRR26222466

Supplemental Table S4. Twenty most abundant fungal OTUs identified by matching sequences to the UNITE fungal database.

OTU	# of sequences		taxon
OTU	Size	Guild	Taxon
Otu00001	148821	Wood Saprotroph	<i>Rigidoporus corticola</i>
Otu00002	142937	Undefined Saprotroph	<i>Saccharomycetales unclassified</i>
Otu00003	138975	Undefined Saprotroph	<i>Scheffersomyces shehatae</i>
Otu00004	118428	Undefined Saprotroph	<i>Rhodotorula lignophila</i>
Otu00005	116735	Undefined Saprotroph	<i>Pichia</i> sp
Otu00006	109789	Wood Saprotroph	<i>Trichaptum biforme</i>
Otu00007	84795	Undefined Saprotroph	<i>Basidiodendron</i> sp
Otu00008	84265	Ectomycorrhizal	<i>Russula</i> sp
Otu00009	73083	Wood Saprotroph	<i>Phlebia centrifuga</i>
Otu00010	69490	Wood Saprotroph	<i>Trechispora</i> sp
Otu00011	68481	Undefined Saprotroph	<i>Candida boleticola</i>
Otu00012	68229	Wood Saprotroph	<i>Perenniporia</i>
Otu00013	59905	Wood Saprotroph	<i>Phlebia fuscoatra</i>
Otu00014	58969	Undefined Saprotroph	<i>Saccharomycete</i>
Otu00015	54601	Endophyte	<i>Leptodontidium</i>
Otu00016	53112	Wood Saprotroph	<i>Bjerkandera</i>
Otu00017	50915	Wood Saprotroph	<i>Aporpium macroporum</i>
Otu00018	48536	Undefined Saprotroph	<i>Candida ergatensis</i>
Otu00019	47133	Wood Saprotroph	<i>Phanochaete sordida</i>
Otu00020	46914	Ectomycorrhizal	<i>Piloderma sphaerosporum</i>

Supplemental Table S5. pH values determined for each composite sample derived from all standing dead trees and downed logs, and combined soil and leaf litter samples. (SD=standing dead, DC1=decay class 1, DC2=decay class 2, DC3=decay class 3, DC4=decay class 4, DC5=decay class 5, S=combined soil samples, LL=leaf litter). N=26 (4 per decay stage of log, 1 soil, 1 leaf litter).

Sample	pH
SD	4.61
SD	5.11
SD	5.02
SD	4.77
DC1	4.79
DC1	5.86
DC1	6
DC1	5.46
DC2	4.43
DC2	5.73
DC2	5.50
DC2	5.06
DC3	4.13
DC3	4.57
DC3	4.75
DC3	6.00
DC4	4.90
DC4	6.01
DC4	5.14
DC4	4.03
DC5	5.18
DC5	4.51
DC5	4.69
DC5	4.17
S	4.84
LL	4.79

Supplemental Table S6. Correlations comparing activity of individual enzymes versus %N indicates a significant increase for all enzymes except phenol oxidase.

Enzyme	r	P value
β -1,4-glucosidase (BG)	0.58	0.002
1,4- β -cellobiosidase (CHB)	0.52	0.01
β -D-xylosidase (XYLO)	0.73	<0.0001
Leucyl aminopeptidase (LAP)	0.69	<0.0001
Phenol oxidase (PHEN OX)	-0.21	0.29
Peroxidase (PER)	0.52	0.01