

## 1 Supplemental Material

2 **Suppl. Table 1.** Sampled *Fagus sylvatica* individuals. Given are the phenotype, sampling location,  
3 sampling date, geographical coordinates in decimal degrees, the pool to which the individual  
4 contributed to (h=healthy, d=damaged), whether it was individually re-sequenced (x) and whether it  
5 was used in the SNP assay to validate the results (x).

TreelD	Phenotype	Location	Sampling date	Latitude	Longitude	Pool (set 1)	individually re-sequenced	Validation (set 2)
PF_001	damaged	Königstein	29.08.2019	50.1957342	8.4648591	dNorth		
PF_002	healthy	Königstein	29.08.2019	50.1957187	8.4648341	hNorth	x	
PF_003	damaged	Königstein	29.08.2019	50.1964726	8.4664262	dNorth	x	
PF_004	healthy	Königstein	29.08.2019	50.1964232	8.4664275	hNorth	x	
PF_005	damaged	Königstein	29.08.2019	50.1929421	8.456941	dNorth	x	
PF_006	healthy	Königstein	29.08.2019	50.1928331	8.4568086	hNorth	x	
PF_007	damaged	Königstein	29.08.2019	50.1925453	8.457816	dNorth	x	
PF_008	healthy	Königstein	29.08.2019	50.1925741	8.4578839	hNorth	x	
PF_009	damaged	Königstein	29.08.2019	50.1926029	8.4579518	dNorth	x	
PF_010	healthy	Königstein	29.08.2019	50.1926317	8.4580197	hNorth	x	
PF_011	damaged	Obernhein	03.09.2019	50.2825898	8.5712681	dNorth		
PF_012	healthy	Obernhein	03.09.2019	50.2827911	8.5711075	hNorth		
PF_013	damaged	Obernhein	03.09.2019	50.2820637	8.5734056	dNorth		
PF_014	healthy	Obernhein	03.09.2019	50.282214	8.5734601	hNorth		
PF_015	damaged	Obernhein	03.09.2019	50.2817116	8.5761923	dNorth		
PF_016	healthy	Obernhein	03.09.2019	50.2816381	8.5761487	hNorth	x	
PF_017	damaged	Obernhein	03.09.2019	50.2821782	8.5704083	dNorth	x	
PF_018	healthy	Obernhein	03.09.2019	50.2821327	8.5704883	hNorth	x	
PF_019	damaged	Obernhein	03.09.2019	50.2816941	8.5700475	dNorth	x	
PF_020	healthy	Obernhein	03.09.2019	50.2817058	8.570133	hNorth	x	
PF_021	damaged	Usingen	04.09.2019	50.3392732	8.4913495	dNorth	x	
PF_022	healthy	Usingen	04.09.2019	50.3391762	8.491312	hNorth	x	
PF_023	damaged	Usingen	04.09.2019	50.3397337	8.4924001	dNorth	x	
PF_024	healthy	Usingen	04.09.2019	50.3396942	8.4924593	hNorth	x	
PF_025	damaged	Usingen	04.09.2019	50.344079	8.4932305	dNorth	x	
PF_026	healthy	Usingen	04.09.2019	50.3440912	8.4933098	hNorth	x	
PF_027	damaged	Usingen	04.09.2019	50.3452681	8.4959808	dNorth	x	
PF_028	healthy	Usingen	04.09.2019	50.3451246	8.4962431	hNorth	x	
PF_029	damaged	Usingen	04.09.2019	50.3416761	8.4918323	dNorth	x	
PF_030	healthy	Usingen	04.09.2019	50.3417203	8.4917173	hNorth	x	
PF_031	damaged	Eppenhain	05.09.2019	50.1736813	8.3908577	dNorth	x	

PF_032	healthy	Eppenhain	05.09.2019	50.1736578	8.39113553	hNorth	x
PF_033	damaged	Eppenhain	05.09.2019	50.1750866	8.3891472	dNorth	x
PF_034	healthy	Eppenhain	05.09.2019	50.175069	8.3892187	hNorth	x
PF_035	damaged	Eppenhain	05.09.2019	50.1754443	8.3876407	dNorth	x
PF_036	healthy	Eppenhain	05.09.2019	50.1754007	8.3875849	hNorth	x
PF_037	damaged	Eppenhain	05.09.2019	50.1746449	8.3872509	dNorth	x
PF_038	healthy	Eppenhain	05.09.2019	50.1746095	8.3874874	hNorth	x
PF_039	damaged	Eppenhain	05.09.2019	50.1734334	8.3904983	dNorth	x
PF_040	healthy	Eppenhain	05.09.2019	50.1733173	8.390211	hNorth	x
PF_041	damaged	Eppenhain	05.09.2019	50.1745915	8.3907433	dNorth	x
PF_042	healthy	Eppenhain	05.09.2019	50.1745128	8.3908124	hNorth	x
PF_050	damaged	Bad Camberg	06.09.2019	50.2976336	8.2980473	dNorth	
PF_051	healthy	Bad Camberg	06.09.2019	50.2975811	8.298169	hNorth	
PF_052	damaged	Daubringen	07.09.2019	50.6483759	8.7419719	dNorth	x
PF_053	healthy	Daubringen	07.09.2019	50.6482664	8.7421457	hNorth	x
PF_054	damaged	Daubringen	07.09.2019	50.6480228	8.7428739	dNorth	x
PF_055	healthy	Daubringen	07.09.2019	50.6478157	8.742954	hNorth	x
PF_056	damaged	Daubringen	07.09.2019	50.648846	8.7426283	dNorth	x
PF_057	healthy	Daubringen	07.09.2019	50.6489798	8.7423211	hNorth	x
PF_058	damaged	Schwabendorf	07.09.2019	50.8927904	8.8879419	dNorth	x
PF_059	healthy	Schwabendorf	07.09.2019	50.8929008	8.8881284	hNorth	x
PF_060	damaged	Schwabendorf	07.09.2019	50.8951542	8.8822243	dNorth	x
PF_061	healthy	Schwabendorf	07.09.2019	50.8952005	8.882144	hNorth	x
PF_062	damaged	Oberurff	07.09.2019	51.0458016	9.1505195	dNorth	x
PF_063	healthy	Oberurff	07.09.2019	51.0457499	9.1505234	hNorth	x
PF_064	damaged	Oberurff	07.09.2019	51.0461483	9.1478112	dNorth	x
PF_065	healthy	Oberurff	07.09.2019	51.0461706	9.1474544	hNorth	x
PF_066	damaged	Oberurff	07.09.2019	51.0453396	9.1466057	dNorth	x
PF_067	healthy	Oberurff	07.09.2019	51.0453396	9.146057	hNorth	x
PF_068	damaged	Oberurff	07.09.2019	51.0463978	9.1432389	dNorth	x
PF_069	healthy	Oberurff	07.09.2019	51.0464672	9.1435546	hNorth	x
PF_070	damaged	Neukirchen	08.09.2019	50.8848091	9.3557289	dNorth	x
PF_071	healthy	Neukirchen	08.09.2019	50.88496	9.3560291	hNorth	x
PF_072	damaged	Langenhain	09.09.2019	50.0955818	8.4101217	dNorth	x
PF_073	healthy	Langenhain	09.09.2019	50.0956666	8.4105235	hNorth	x
PF_074	damaged	Langenhain	09.09.2019	50.0959896	8.4104922	dNorth	x
PF_075	healthy	Langenhain	09.09.2019	50.0960509	8.4105981	hNorth	x
PF_076	damaged	Langenhain	09.09.2019	50.0947953	8.4151317	dNorth	x

PF_077	healthy	Langenhain	09.09.2019	50.0947434	8.4150994	hNorth	x
PF_078	damaged	Langenhain	09.09.2019	50.0911467	8.41578726	dNorth	x
PF_079	healthy	Langenhain	09.09.2019	50.0912627	8.415817	hNorth	
PF_080	damaged	Langenhain	09.09.2019	50.0901299	8.4166724	dNorth	x
PF_081	healthy	Langenhain	09.09.2019	50.090096	8.4166748	hNorth	x
PF_082	damaged	Langenhain	09.09.2019	50.0940815	8.4100466	dNorth	x
PF_083	healthy	Langenhain	09.09.2019	50.0939183	8.4099548	hNorth	x
PF_085	damaged	Theistal	11.09.2019	50.1480865	8.2445088	dNorth	x
PF_086	healthy	Theistal	11.09.2019	50.1480164	8.2447881	hNorth	x
PF_087	damaged	Theistal	11.09.2019	50.1517267	8.2464193	dNorth	x
PF_088	healthy	Theistal	11.09.2019	50.151875	8.2461256	hNorth	x
PF_089	damaged	Theistal	11.09.2019	50.1532534	8.2456221	dNorth	x
PF_090	healthy	Theistal	11.09.2019	50.1528409	8.2455616	hNorth	x
PF_091	damaged	Theistal	11.09.2019	50.1539513	8.2466804	dNorth	x
PF_092	healthy	Theistal	11.09.2019	50.1540134	8.2462949	hNorth	x
PF_093	damaged	Schlangenbad	11.09.2019	50.1027276	8.1136673	dNorth	x
PF_094	healthy	Schlangenbad	11.09.2019	50.1025753	8.1136931	hNorth	x
PF_095	damaged	Schlangenbad	11.09.2019	50.0997272	8.1101568	dNorth	x
PF_096	healthy	Schlangenbad	11.09.2019	50.099823	8.1103387	hNorth	x
PF_100	damaged	Wehrheim	12.09.2019	50.3153263	8.5819508	dNorth	x
PF_101	healthy	Wehrheim	12.09.2019	50.315372	8.5820711	hNorth	x
PF_102	damaged	Wehrheim	12.09.2019	50.3145513	8.5854558	dNorth	x
PF_103	healthy	Wehrheim	12.09.2019	50.3145748	8.585572	hNorth	x
PF_104	damaged	Wehrheim	12.09.2019	50.3147404	8.585804	dNorth	x
PF_105	healthy	Wehrheim	12.09.2019	50.3146745	8.5858773	hNorth	x
PF_106	damaged	Wehrheim	12.09.2019	50.3149149	8.5859893	dNorth	x
PF_107	healthy	Wehrheim	12.09.2019	50.31472242	8.5861579	hNorth	x
PF_108	damaged	Wehrheim	12.09.2019	50.3149559	8.5866045	dNorth	x
PF_109	healthy	Wehrheim	12.09.2019	50.3150733	8.5866527	hNorth	x
PF_110	damaged	Wehrheim	12.09.2019	50.3155392	8.587186	dNorth	x
PF_111	healthy	Wehrheim	12.09.2019	50.3154613	8.5872255	hNorth	x
PF_112	damaged	Wehrheim	12.09.2019	50.3130127	8.580265	dNorth	x
PF_113	healthy	Wehrheim	12.09.2019	50.3130103	8.5800785	hNorth	x
PF_114	damaged	Wehrheim	12.09.2019	50.3141899	8.581059	dNorth	x
PF_115	healthy	Wehrheim	12.09.2019	50.314164	8.5809636	hNorth	x
S_001	damaged	Bot. Garten	26.08.2019	49.79971	8.95682	dSouth	
S_002	healthy	Bot. Garten	26.08.2019	49.86852	8.67999	hSouth	
S_003	damaged	Bot. Garten	26.08.2019	49.86856	8.68018	dSouth	

S_004	healthy	Bot. Garten	26.08.2019	49.86856	8.68018	hSouth
S_005	damaged	Vivarium	26.08.2019	49.86855	8.68017	dSouth
S_006	healthy	Vivarium	26.08.2019	49.86436	8.6842	hSouth
S_007	damaged	Vivarium	26.08.2019	49.8644	8.68418	dSouth
S_008	healthy	Vivarium	26.08.2019	49.8644	8.68418	hSouth
S_009	damaged	Vivarium	26.08.2019	49.8644	8.68418	dSouth
S_010	healthy	Vivarium	26.08.2019	49.8644	8.68418	hSouth
S_011	damaged	Vivarium	26.08.2019	49.8644	8.68418	dSouth
S_012	healthy	Vivarium	26.08.2019	49.8644	8.68418	hSouth
S_013	damaged	VivariumII	26.08.2019	49.8644	8.68418	dSouth
S_014	healthy	VivariumII	26.08.2019	49.8644	8.68418	hSouth
S_015	damaged	VivariumII	26.08.2019	49.86227	8.68876	dSouth
S_016	healthy	VivariumII	26.08.2019	49.86241	8.68874	hSouth
S_017	damaged	VivariumII	26.08.2019	49.86199	8.68894	dSouth
S_018	healthy	VivariumII	26.08.2019	49.86196	8.68885	hSouth
S_019	damaged	VivariumII	26.08.2019	49.86092	8.69278	dSouth
S_020	healthy	VivariumII	26.08.2019	49.86031	8.69225	hSouth
S_021	damaged	VivariumIII	27.08.2019	49.85883	8.69445	dSouth
S_022	healthy	VivariumIII	27.08.2019	49.85883	8.69445	hSouth
S_023	damaged	VivariumIII	27.08.2019	49.85882	8.69446	dSouth
S_024	healthy	VivariumIII	27.08.2019	49.85882	8.69446	hSouth
S_025	damaged	VivariumIII	27.08.2019	49.85862	8.6944	dSouth
S_026	healthy	VivariumIII	27.08.2019	49.85862	8.6944	hSouth
S_027	damaged	VivariumIII	27.08.2019	49.85637	8.69584	dSouth
S_028	healthy	VivariumIII	27.08.2019	49.85637	8.69584	hSouth
S_029	damaged	VivariumIII	27.08.2019	49.8565	8.69616	dSouth
S_030	healthy	VivariumIII	27.08.2019	49.8565	8.69616	hSouth
S_031	damaged	VivariumIII	27.08.2019	49.8565	8.69616	dSouth
S_032	healthy	VivariumIII	27.08.2019	49.8565	8.69616	hSouth
S_033	damaged	VivariumIII	27.08.2019	49.85576	8.69886	dSouth
S_034	healthy	VivariumIII	27.08.2019	49.85576	8.69886	hSouth
S_035	damaged	VivariumIII	27.08.2019	49.85576	8.69886	dSouth
S_036	healthy	VivariumIII	27.08.2019	49.85576	8.69886	hSouth
S_037	damaged	VivariumIII	27.08.2019	49.85329	8.6938	dSouth
S_038	healthy	VivariumIII	27.08.2019	49.85329	8.6938	hSouth
S_039	damaged	VivariumIII	27.08.2019	49.85329	8.6938	dSouth
S_040	healthy	VivariumIII	27.08.2019	49.85329	8.6938	hSouth
S_041	damaged	VivariumIII	27.08.2019	49.85021	8.9391	dSouth

S_042	healthy	VivariumIII	27.08.2019	49.85021	8.9391	hSouth	
S_043	damaged	Neu-Isenburg	28.08.2019	49.85585	8.69554	dSouth	
S_044	healthy	Neu-Isenburg	28.08.2019	49.85585	8.69554	hSouth	
S_045	damaged	Neu-Isenburg	28.08.2019	49.85585	8.69554	dSouth	
S_046	healthy	Neu-Isenburg	28.08.2019	49.85585	8.69554	hSouth	
S_047	damaged	Neu-Isenburg	28.08.2019	49.85585	8.69554	dSouth	
S_048	healthy	Neu-Isenburg	28.08.2019	49.85585	8.69554	hSouth	
S_049	damaged	Neu-Isenburg	28.08.2019	49.85585	8.69554	dSouth	
S_050	healthy	Neu-Isenburg	28.08.2019	49.85585	8.69554	hSouth	
S_051	damaged	Neu-Isenburg	28.08.2019	49.85585	8.69554	dSouth	
S_052	healthy	Neu-Isenburg	28.08.2019	49.85585	8.69554	hSouth	
S_053	damaged	Neu-Isenburg	28.08.2019	49.85585	8.69554	dSouth	
S_054	healthy	Neu-Isenburg	28.08.2019	49.85585	8.69554	hSouth	
S_055	damaged	Neu-Isenburg	28.08.2019	49.85585	8.69554	dSouth	
S_056	healthy	Neu-Isenburg	28.08.2019	49.85585	8.69554	hSouth	
S_057	damaged	Neu-Isenburg	28.08.2019	49.85585	8.69554	dSouth	
S_058	healthy	Neu-Isenburg	28.08.2019	49.85585	8.69554	hSouth	
S_059	damaged	Neu-Isenburg	28.08.2019	49.85585	8.69554	dSouth	
S_060	healthy	Neu-Isenburg	28.08.2019	49.85585	8.69554	hSouth	
S_061	damaged	Westwald	29.09.2019	49.855069	8.617017	dSouth	
S_062	healthy	Westwald	29.09.2019	49.855069	8.617017	hSouth	
S_063	damaged	Westwald	29.09.2019	49.85495	8.61703	dSouth	x
S_064	healthy	Westwald	29.09.2019	49.85495	8.61703	hSouth	
S_065	damaged	Westwald	29.09.2019	49.85495	8.61703	dSouth	
S_066	healthy	Westwald	29.09.2019	49.85495	8.61703	hSouth	x
S_067	damaged	Westwald	29.09.2019	49.85494	8.61702	dSouth	
S_068	healthy	Westwald	29.09.2019	49.85494	8.61702	hSouth	
S_069	damaged	Westwald	29.09.2019	49.854909	8.618146	dSouth	
S_070	healthy	Westwald	29.09.2019	49.854909	8.618146	hSouth	
S_071	damaged	Westwald	29.09.2019	49.85494	8.61702	dSouth	x
S_072	healthy	Westwald	29.09.2019	49.85494	8.61702	hSouth	x
S_073	damaged	Westwald	29.09.2019	49.85494	8.61702	dSouth	
S_074	healthy	Westwald	29.09.2019	49.85494	8.61702	hSouth	
S_075	damaged	Westwald	29.09.2019	49.85494	8.61702	dSouth	
S_076	healthy	Westwald	29.09.2019	49.85494	8.61702	hSouth	
S_077	damaged	Westwald	29.09.2019	49.85494	8.61702	dSouth	x
S_078	healthy	Westwald	29.09.2019	49.85494	8.61702	hSouth	x
S_079	damaged	Westwald	29.09.2019	49.85494	8.61702	dSouth	

S_080	healthy	Westwald	29.09.2019	49.85494	8.61702	hSouth	
S_081	damaged	Westwald	29.09.2019	49.85494	8.61702	dSouth	X
S_082	healthy	Westwald	29.09.2019	49.85494	8.61702	hSouth	X
S_083	damaged	Westwald	29.09.2019	49.85494	8.61702	dSouth	
S_084	healthy	Westwald	29.09.2019	49.85494	8.61702	hSouth	
S_085	damaged	Roßdorf	02.09.2019	49.85494	8.61702	dSouth	
S_086	healthy	Roßdorf	02.09.2019	49.85494	8.61702	hSouth	
S_087	damaged	Roßdorf	02.09.2019	49.85943	8.70791	dSouth	X
S_088	healthy	Roßdorf	02.09.2019	49.85943	8.70791	hSouth	X
S_089	damaged	Roßdorf	02.09.2019	49.85943	8.70786	dSouth	
S_090	healthy	Roßdorf	02.09.2019	49.85943	8.70786	hSouth	
S_091	damaged	Roßdorf	02.09.2019	49.85977	8.70795	dSouth	
S_092	healthy	Roßdorf	02.09.2019	49.85977	8.70795	hSouth	
S_093	damaged	Roßdorf	02.09.2019	49.86221	8.718	dSouth	X
S_094	healthy	Roßdorf	02.09.2019	49.86221	8.718	hSouth	X
S_095	damaged	Roßdorf	02.09.2019	49.86211	8.71801	dSouth	
S_096	healthy	Roßdorf	02.09.2019	49.86211	8.71801	hSouth	
S_097	damaged	Roßdorf	02.09.2019	49.86211	8.71801	dSouth	
S_098	healthy	Roßdorf	02.09.2019	49.86211	8.71801	hSouth	
S_099	damaged	Roßdorf	02.09.2019	49.86089	8.70835	dSouth	
S_100	healthy	Roßdorf	02.09.2019	49.86089	8.70835	hSouth	
S_101	damaged	Roßdorf	02.09.2019	49.86095	8.70771	dSouth	
S_102	healthy	Roßdorf	02.09.2019	49.86095	8.70771	hSouth	
S_103	damaged	Roßdorf	02.09.2019	49.86103	8.70769		x
S_104	healthy	Roßdorf	02.09.2019	49.86103	8.70769		x
S_105	damaged	Burg Breuberg	03.09.2019	49.8259	9.0341	dSouth	
S_106	healthy	Burg Breuberg	03.09.2019	49.8259	9.0341	hSouth	
S_107	damaged	Burg Breuberg	03.09.2019	49.82447	9.03196	dSouth	
S_108	healthy	Burg Breuberg	03.09.2019	49.82447	9.03196	hSouth	
S_109	damaged	Burg Breuberg	03.09.2019	49.82457	9.03155	dSouth	
S_110	healthy	Burg Breuberg	03.09.2019	49.82457	9.03155	hSouth	
S_111	damaged	Burg Breuberg	03.09.2019	49.82736	9.0267	dSouth	
S_112	healthy	Burg Breuberg	03.09.2019	49.82736	9.0267	hSouth	
S_113	damaged	Burg Breuberg	03.09.2019	49.827	9.02706	dSouth	
S_114	healthy	Burg Breuberg	03.09.2019	49.827	9.02706	hSouth	
S_115	damaged	Burg Breuberg	03.09.2019	49.82689	9.02076	dSouth	
S_116	healthy	Burg Breuberg	03.09.2019	49.82689	9.02076	hSouth	
S_117	damaged	Burg Breuberg	03.09.2019	49.82692	9.02038		x

S_118	healthy	Burg Breuberg	03.09.2019	49.82692	9.02038		x
S_119	damaged	Burg Breuberg	03.09.2019	49.82322	9.02107	dSouth	
S_120	healthy	Burg Breuberg	03.09.2019	49.82322	9.02107	hSouth	
S_121	damaged	Burg Breuberg	03.09.2019	49.82305	9.02048	dSouth	
S_122	healthy	Burg Breuberg	03.09.2019	49.82305	9.02048	hSouth	
S_123	damaged	Burg Breuberg	03.09.2019	49.82301	9.02096	dSouth	
S_124	healthy	Burg Breuberg	03.09.2019	49.82301	9.02096	hSouth	
S_125	damaged	Heusenstamm	04.09.2019	50.04919	8.69445	dSouth	
S_126	healthy	Heusenstamm	04.09.2019	50.04919	8.69445	hSouth	
S_127	damaged	Heusenstamm	04.09.2019	50.04919	8.69445	dSouth	
S_128	healthy	Heusenstamm	04.09.2019	50.04919	8.69445	hSouth	
S_129	damaged	Heusenstamm	04.09.2019	50.0577	8.7788		x
S_130	healthy	Heusenstamm	04.09.2019	50.0577	8.7788		x
S_131	damaged	Heusenstamm	04.09.2019	50.0575	8.7787	dSouth	
S_132	healthy	Heusenstamm	04.09.2019	50.0575	8.7787	hSouth	
S_133	damaged	Heusenstamm	04.09.2019	50.05774	8.7796	dSouth	
S_134	healthy	Heusenstamm	04.09.2019	50.05774	8.7796	hSouth	
S_135	damaged	Heusenstamm	04.09.2019	50.05574	8.7795	dSouth	
S_136	healthy	Heusenstamm	04.09.2019	50.05574	8.7795	hSouth	
S_137	damaged	Heusenstamm	04.09.2019	50.0562	8.7787	dSouth	
S_138	healthy	Heusenstamm	04.09.2019	50.0562	8.7787	hSouth	
S_139	damaged	Heusenstamm	04.09.2019	50.0562	8.7787	dSouth	
S_140	healthy	Heusenstamm	04.09.2019	50.0562	8.7787	hSouth	
S_141	damaged	Heusenstamm	04.09.2019	50.0562	8.7787	dSouth	
S_142	healthy	Heusenstamm	04.09.2019	50.0562	8.7787	hSouth	
S_143	damaged	Heusenstamm	04.09.2019	50.0562	8.7787		x
S_144	healthy	Heusenstamm	04.09.2019	50.0562	8.7787		x
S_145	damaged	Heusenstamm	04.09.2019	50.0556	8.7788		x
S_146	healthy	Heusenstamm	04.09.2019	50.0556	8.7788		x
S_147	damaged	Heusenstamm	04.09.2019	50.056	8.78	dSouth	
S_148	healthy	Heusenstamm	04.09.2019	50.056	8.78	hSouth	
S_149	damaged	Heusenstamm	04.09.2019	50.0557	8.779	dSouth	
S_150	healthy	Heusenstamm	04.09.2019	50.0557	8.779	hSouth	
S_151	damaged	Heusenstamm	04.09.2019	50.0557	8.779	dSouth	
S_152	healthy	Heusenstamm	04.09.2019	50.0557	8.779	hSouth	
S_153	damaged	Heusenstamm	04.09.2019	50.0552	8.7797	dSouth	
S_154	healthy	Heusenstamm	04.09.2019	50.0552	8.7797	hSouth	
S_155	damaged	Eschollbrücken	06.09.2019	49.844862	8.6033987	dSouth	

S_156	healthy	Eschollbrücken	06.09.2019	49.844862	8.6033987	hSouth	
S_157	damaged	Eschollbrücken	06.09.2019	49.8451033	8.6033906	dSouth	
S_158	healthy	Eschollbrücken	06.09.2019	49.8451033	8.6033906	hSouth	
S_159	damaged	Eschollbrücken	06.09.2019	49.8452741	8.6933477	dSouth	
S_160	healthy	Eschollbrücken	06.09.2019	49.8452741	8.6933477	hSouth	
S_161	damaged	Eschollbrücken	06.09.2019	49.8464188	8.6058807	dSouth	
S_162	healthy	Eschollbrücken	06.09.2019	49.8464188	8.6058807	hSouth	
S_163	damaged	Eschollbrücken	06.09.2019	49.8461255	8.6064631		x
S_164	healthy	Eschollbrücken	06.09.2019	49.8461255	8.6064631		x
S_165	damaged	Eschollbrücken	06.09.2019	49.8381468	8.613406	dSouth	
S_166	healthy	Eschollbrücken	06.09.2019	49.8381468	8.613406	hSouth	
S_167	damaged	Eschollbrücken	06.09.2019	49.8371837	8.6154874	dSouth	
S_168	healthy	Eschollbrücken	06.09.2019	49.8371837	8.6154874	hSouth	
S_169	damaged	Eschollbrücken	06.09.2019	49.8368364	8.6172492		x
S_170	healthy	Eschollbrücken	06.09.2019	49.8368364	8.6172492		x
S_171	damaged	Eschollbrücken	06.09.2019	49.8364971	8.6193427	dSouth	
S_172	healthy	Eschollbrücken	06.09.2019	49.8364971	8.6193427	hSouth	
S_173	damaged	Eschollbrücken	06.09.2019	49.8366439	8.617927	dSouth	
S_174	healthy	Eschollbrücken	06.09.2019	49.8366439	8.617927	hSouth	
S_175	damaged	Eschollbrücken	06.09.2019	49.83549	8.6063276		x
S_176	healthy	Eschollbrücken	06.09.2019	49.83549	8.6063276		x
S_177	damaged	Eschollbrücken	06.09.2019	49.836002	8.6057516	dSouth	
S_178	healthy	Eschollbrücken	06.09.2019	49.836002	8.6057516	hSouth	
S_179	damaged	Eschollbrücken	06.09.2019	49.8364465	8.6051897		x
S_180	healthy	Eschollbrücken	06.09.2019	49.8364465	8.6051897		x
S_181	damaged	Neu Isenburg	09.09.2019	50.0643187	8.7090884	dSouth	
S_182	healthy	Neu Isenburg	09.09.2019	50.0643187	8.7090884	hSouth	
S_183	damaged	Neu Isenburg	09.09.2019	50.0650797	8.7098096	dSouth	
S_184	healthy	Neu Isenburg	09.09.2019	50.0650797	8.7098096	hSouth	
S_185	damaged	Neu Isenburg	09.09.2019	50.0659154	8.7102773	dSouth	
S_186	healthy	Neu Isenburg	09.09.2019	50.0659154	8.7102773	hSouth	
S_187	damaged	Neu Isenburg	09.09.2019	50.0659301	8.7100359	dSouth	
S_188	healthy	Neu Isenburg	09.09.2019	50.0659301	8.7100359	hSouth	
S_189	damaged	Neu Isenburg	09.09.2019	50.0686111	8.7121451	dSouth	
S_190	healthy	Neu Isenburg	09.09.2019	50.0686111	8.7121451	hSouth	
S_191	damaged	Neu Isenburg	09.09.2019	50.0691756	8.7123064	dSouth	
S_192	healthy	Neu Isenburg	09.09.2019	50.0691756	8.7123064	hSouth	
S_193	damaged	Neu Isenburg	09.09.2019	50.0710306	8.7127781	dSouth	



S_194	healthy	Neu Isenburg	09.09.2019	50.0710306	8.7127781	hSouth	
S_195	damaged	Neu Isenburg	09.09.2019	50.0716691	8.7111252	dSouth	
S_196	healthy	Neu Isenburg	09.09.2019	50.0716691	8.7111252	hSouth	
S_197	damaged	Neu Isenburg	09.09.2019	50.0715402	8.7110297	dSouth	
S_198	healthy	Neu Isenburg	09.09.2019	50.0715402	8.7110297	hSouth	
S_199	damaged	Neu Isenburg	09.09.2019	50.0710603	8.7121176	dSouth	
S_200	healthy	Neu Isenburg	09.09.2019	50.0710603	8.7121176	hSouth	
S_201	damaged	Neu Isenburg	09.09.2019	50.0681943	8.7052592	dSouth	
S_202	healthy	Neu Isenburg	09.09.2019	50.0681943	8.7052592	hSouth	
S_203	damaged	Neu Isenburg	09.09.2019	50.0671452	8.7042427	dSouth	
S_204	healthy	Neu Isenburg	09.09.2019	50.0671452	8.7042427	hSouth	
S_205	damaged	Wegscheide	10.09.2019	50.2076	9.4126		x
S_206	healthy	Wegscheide	10.09.2019	50.2076	9.4126		x
S_207	damaged	Wegscheide	10.09.2019	50.2076	9.4126	dSouth	
S_208	healthy	Wegscheide	10.09.2019	50.2076	9.4126	hSouth	
S_209	damaged	Wegscheide	10.09.2019	50.2149354	9.419513	dSouth	
S_210	healthy	Wegscheide	10.09.2019	50.2149354	9.419513	hSouth	
S_211	damaged	Wegscheide	10.09.2019	50.2114485	9.409662	dSouth	
S_212	healthy	Wegscheide	10.09.2019	50.2114485	9.409662	hSouth	
S_213	damaged	Wegscheide	10.09.2019	50.2114485	9.409662	dSouth	
S_214	healthy	Wegscheide	10.09.2019	50.2114485	9.409662	hSouth	
S_215	damaged	Wegscheide	10.09.2019	50.2109	9.4086	dSouth	
S_216	healthy	Wegscheide	10.09.2019	50.2109	9.4086	hSouth	
S_217	damaged	Waldstadion	10.09.2019	50.0546504	8.6626215	dSouth	
S_218	healthy	Waldstadion	10.09.2019	50.0546504	8.6626215	hSouth	
S_219	damaged	Waldstadion	10.09.2019	50.0555269	8.6618698	dSouth	
S_220	healthy	Waldstadion	10.09.2019	50.0555269	8.6618698	hSouth	
S_221	damaged	Waldstadion	10.09.2019	50.0568445	8.6610993	dSouth	
S_222	healthy	Waldstadion	10.09.2019	50.0568445	8.6610993	hSouth	
S_223	damaged	Waldstadion	10.09.2019	50.0572346	8.6619006	dSouth	
S_224	healthy	Waldstadion	10.09.2019	50.0572346	8.6619006	hSouth	
S_225	damaged	Waldstadion	10.09.2019	50.0573499	8.661843	dSouth	
S_226	healthy	Waldstadion	10.09.2019	50.0573499	8.661843	hSouth	
S_227	damaged	Waldstadion	10.09.2019	50.0589663	8.6609092	dSouth	
S_228	healthy	Waldstadion	10.09.2019	50.0589663	8.6609092	hSouth	
S_229	damaged	Waldstadion	10.09.2019	50.0587827	8.6609424	dSouth	
S_230	healthy	Waldstadion	10.09.2019	50.0587827	8.6609424	hSouth	
S_231	damaged	Messel	11.09.2019	49.9648055	8.7305273	dSouth	

S_232	healthy	Messel	11.09.2019	49.9648055	8.7305273	hSouth	
S_233	damaged	Messel	11.09.2019	49.9653231	8.7286833	dSouth	
S_234	healthy	Messel	11.09.2019	49.9653231	8.7286833	hSouth	
S_235	damaged	Messel	11.09.2019	49.9672891	8.7267089	dSouth	
S_236	healthy	Messel	11.09.2019	49.9672891	8.7267089	hSouth	
S_237	damaged	Messel	11.09.2019	49.9673648	8.726613	dSouth	
S_238	healthy	Messel	11.09.2019	49.9673648	8.726613	hSouth	
S_239	damaged	Messel	11.09.2019	49.9685641	8.7259826	dSouth	
S_240	healthy	Messel	11.09.2019	49.9685641	8.7259826	hSouth	
S_241	damaged	Messel	11.09.2019	49.9702459	8.7244602	dSouth	
S_242	healthy	Messel	11.09.2019	49.9702459	8.7244602	hSouth	
S_243	damaged	Messel	11.09.2019	49.9722449	8.7156846	dSouth	
S_244	healthy	Messel	11.09.2019	49.9722449	8.7156846	hSouth	
S_245	damaged	Messel	11.09.2019	49.9722449	8.7156806		x
S_246	healthy	Messel	11.09.2019	49.9722449	8.7156806		x
S_247	damaged	Messel	11.09.2019	49.9724476	8.7142302	dSouth	
S_248	healthy	Messel	11.09.2019	49.9724476	8.7142302	hSouth	
S_249	damaged	Messel	11.09.2019	49.9718971	8.7119104	dSouth	
S_250	healthy	Messel	11.09.2019	49.9718971	8.7119104	hSouth	
S_251	damaged	Messel	11.09.2019	49.9719081	8.7114799	dSouth	
S_252	healthy	Messel	11.09.2019	49.9719081	8.7114799	hSouth	
S_253	damaged	Lorsch	12.09.2019	49.6491886	8.5376088	dSouth	
S_254	healthy	Lorsch	12.09.2019	49.6491886	8.5376088	hSouth	
S_255	damaged	Lorsch	12.09.2019	49.6493532	8.5369721	dSouth	
S_256	healthy	Lorsch	12.09.2019	49.6493532	8.5369721	hSouth	
S_257	damaged	Lorsch	12.09.2019	49.6488428	8.5381241	dSouth	
S_258	healthy	Lorsch	12.09.2019	49.6488428	8.5381241	hSouth	
S_259	damaged	Lorsch	12.09.2019	49.6485083	8.5392349	dSouth	
S_260	healthy	Lorsch	12.09.2019	49.6485083	8.5392349	hSouth	
S_261	damaged	Lorsch	12.09.2019	49.6481419	8.5395785	dSouth	
S_262	healthy	Lorsch	12.09.2019	49.6481419	8.5395785	hSouth	
S_263	damaged	Lorsch	12.09.2019	49.6462656	8.5421035	dSouth	
S_264	healthy	Lorsch	12.09.2019	49.6462656	8.5421035	hSouth	
S_265	damaged	Lorsch	12.09.2019	49.6464364	8.5415305		x
S_266	healthy	Lorsch	12.09.2019	49.6464364	8.5415305		x
S_267	damaged	Lorsch	12.09.2019	49.6463205	8.5410504	dSouth	
S_268	healthy	Lorsch	12.09.2019	49.6463205	8.5410504	hSouth	
S_269	damaged	Lorsch	12.09.2019	49.6452786	8.5358174	dSouth	

S_270	healthy	Lorsch	12.09.2019	49.6452786	8.5358174	hSouth	
S_271	damaged	Lorsch	12.09.2019	49.6451675	8.5351421	dSouth	
S_272	healthy	Lorsch	12.09.2019	49.6451675	8.5351421	hSouth	
S_273	damaged	Lorsch	12.09.2019	49.649297	8.5362281		x
S_274	healthy	Lorsch	12.09.2019	49.649297	8.5362281		x
S_275	damaged	Lorsch	12.09.2019	49.6494678	8.5366794	dSouth	
S_276	healthy	Lorsch	12.09.2019	49.6494678	8.5366794	hSouth	
S_277	damaged	Heusenstamm	13.09.2019	50.0580508	8.7747529	dSouth	
S_278	healthy	Heusenstamm	13.09.2019	50.0580508	8.7747529	hSouth	
S_279	damaged	Heusenstamm	13.09.2019	50.0580635	8.7746208		x
S_280	healthy	Heusenstamm	13.09.2019	50.0580635	8.7746208		x
S_281	damaged	Heusenstamm	13.09.2019	50.057182	8.773846	dSouth	
S_282	healthy	Heusenstamm	13.09.2019	50.057182	8.773846	hSouth	
S_283	damaged	Heusenstamm	13.09.2019	50.0571046	8.7740264	dSouth	
S_284	healthy	Heusenstamm	13.09.2019	50.0571046	8.7740264	hSouth	
S_285	damaged	Heusenstamm	13.09.2019	50.0566422	8.7736616	dSouth	
S_286	healthy	Heusenstamm	13.09.2019	50.0566422	8.7736616	hSouth	
S_287	damaged	Heusenstamm	13.09.2019	50.0561296	8.7732438	dSouth	
S_288	healthy	Heusenstamm	13.09.2019	50.0561296	8.7732438	hSouth	
S_289	damaged	Heusenstamm	13.09.2019	50.0559955	8.7728465	dSouth	
S_290	healthy	Heusenstamm	13.09.2019	50.0559955	8.7728465	hSouth	
S_291	damaged	Heusenstamm	13.09.2019	50.055472	8.7729314	dSouth	
S_292	healthy	Heusenstamm	13.09.2019	50.055472	8.7729314	hSouth	
S_293	damaged	Heusenstamm	13.09.2019	50.055181	8.772228	dSouth	
S_294	healthy	Heusenstamm	13.09.2019	50.055181	8.772228	hSouth	
S_295	damaged	Heusenstamm	13.09.2019	50.0551293	8.7723349	dSouth	
S_296	healthy	Heusenstamm	13.09.2019	50.0551293	8.7723349	hSouth	
S_297	damaged	Heusenstamm	13.09.2019	50.0549188	8.7721502	dSouth	
S_298	healthy	Heusenstamm	13.09.2019	50.0549188	8.7721502	hSouth	
S_299	damaged	Heusenstamm	13.09.2019	50.0548086	8.7726598		X
S_300	healthy	Heusenstamm	13.09.2019	50.0548086	8.7726598		X
conf_001	damaged	Schloßborn	03.08.2020	50.1904623	8.373935		x
conf_002	healthy	Schloßborn	03.08.2020	50.1902617	8.3738026		X
conf_003	damaged	Schloßborn	03.08.2020	50.1887401	8.372701		
conf_004	healthy	Schloßborn	03.08.2020	50.1879031	8.3716613		X
conf_005	damaged	Schloßborn	03.08.2020	50.1865722	8.3710684		X
conf_006	healthy	Schloßborn	03.08.2020	50.18656127	8.3711265		X
conf_007	damaged	Schloßborn	03.08.2020	50.1857023	8.3708097		X

conf_008	healthy	Schloßborn	03.08.2020	50.1851555	8.3712359	X
conf_009	damaged	Schloßborn	03.08.2020	50.1852938	8.371852	X
conf_010	healthy	Schloßborn	03.08.2020	50.1851807	8.3722412	X
conf_011	healthy	Schloßborn	03.08.2020	50.1864421	8.3767229	X
conf_012	damaged	Schloßborn	03.08.2020	50.1864287	8.3764222	X
conf_013	damaged	Ruppertshain	04.08.2020	50.181629	8.4018675	X
conf_014	healthy	Ruppertshain	04.08.2020	50.1815555	8.4018799	X
conf_016	healthy	Ruppertshain	04.08.2020	50.1818417	8.4023975	X
conf_017	damaged	Ruppertshain	04.08.2020	50.1846569	8.4022888	X
conf_018	healthy	Ruppertshain	04.08.2020	50.1847183	8.40225810	X
conf_019	damaged	Ruppertshain	04.08.2020	50.1867665	8.4029614	X
conf_020	healthy	Ruppertshain	04.08.2020	50.1868466	8.4029997	X
conf_021	damaged	Ruppertshain	04.08.2020	50.1868411	8.4040772	X
conf_022	healthy	Ruppertshain	04.08.2020	50.1877796	8.4046797	X
conf_023	damaged	Ruppertshain	04.08.2020	50.1829212	8.3987642	X
conf_024	healthy	Ruppertshain	04.08.2020	50.182956	8.3987399	X
conf_025	damaged	Ruppertshain	04.08.2020	50.1808246	8.3990728	X
conf_026	healthy	Ruppertshain	04.08.2020	50.1806971	8.39899759	X
conf_027	damaged	Ruppertshain	04.08.2020	50.179967	8.3994577	X
conf_028	healthy	Ruppertshain	04.08.2020	50.1798082	8.399525	X
conf_029	damaged	Ruppertshain	04.08.2020	50.1782612	8.3999872	X
conf_030	healthy	Ruppertshain	04.08.2020	50.1782916	8.4002846	X
conf_032	healthy	Falkenstein	05.08.2020	50.201454	8.4872785	X
conf_033	damaged	Falkenstein	05.08.2020	50.2015038	8.4874409	X
conf_034	damaged	Falkenstein	05.08.2020	50.201115	8.4876516	X
conf_036	healthy	Falkenstein	05.08.2020	50.2018627	8.4875841	X
conf_037	damaged	Falkenstein	05.08.2020	50.2011419	8.4892266	x
conf_038	healthy	Falkenstein	05.08.2020	50.2012289	8.489425	x
conf_039	healthy	Falkenstein	05.08.2020	50.2013307	8.4905266	
conf_040	damaged	Falkenstein	05.08.2020	50.2004517	8.4905881	x
conf_041	healthy	Falkenstein	05.08.2020	50.2008376	8.4909408	x
conf_042	damaged	Falkenstein	05.08.2020	50.20009229	8.4909295	x
conf_043	damaged	Falkenstein	05.08.2020	50.1997086	8.4828883	x
conf_045	healthy	Falkenstein	05.08.2020	50.1992717	8.480502	x
conf_046	damaged	Falkenstein	05.08.2020	50.1995271	8.4806157	x
conf_047	healthy	Falkenstein	05.08.2020	50.1995032	8.4806215	x
conf_050	damaged	Rote Mühle	07.08.2020	50.1612598	8.452304	x
conf_051	healthy	Rote Mühle	07.08.2020	50.1610649	8.4526065	x

conf_052	damaged	Rote Mühle	07.08.2020	50.1611651	8.4520887	x
conf_053	healthy	Rote Mühle	07.08.2020	50.1611113	8.4520672	x
conf_054	damaged	Rote Mühle	07.08.2020	50.1611776	8.4511498	x
conf_055	healthy	Rote Mühle	07.08.2020	50.1611331	8.450964	x
conf_056	damaged	Rote Mühle	07.08.2020	50.1612598	8.4508452	x
conf_057	healthy	Rote Mühle	07.08.2020	50.1614085	8.4509926	x
conf_058	damaged	Rote Mühle	07.08.2020	50.1617899	8.4504762	x
conf_059	healthy	Rote Mühle	07.08.2020	50.1617076	8.4505298	x

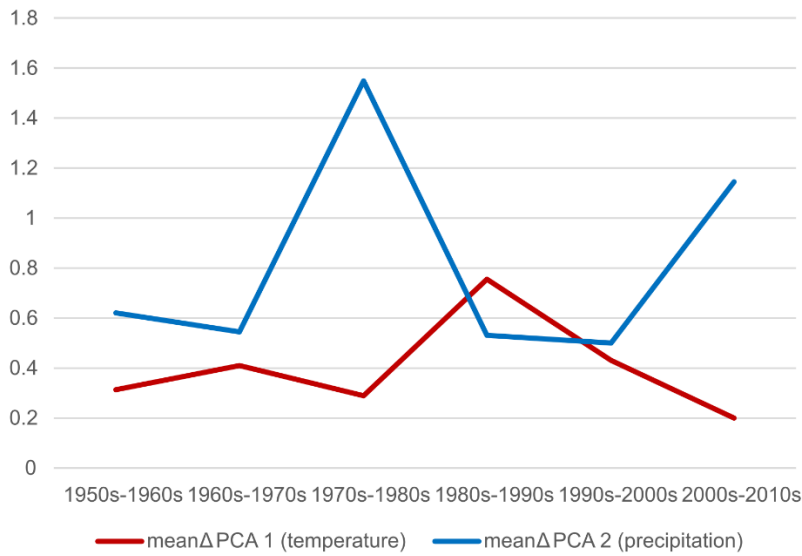
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8 **Suppl. Table 2.** Results from Mann-Whitney U-test on difference between damaged and healthy  
9 trees for various parameters.

Parameter	Mann-Whitney U	p
trunk circumference	10718	0.48
tree height	9874	0.27
canopy closure	10820	0.56
competition index	10809	0.57
dried leaves	202	<b>&lt;0.001</b>
leaf loss	352	<b>&lt;0.001</b>

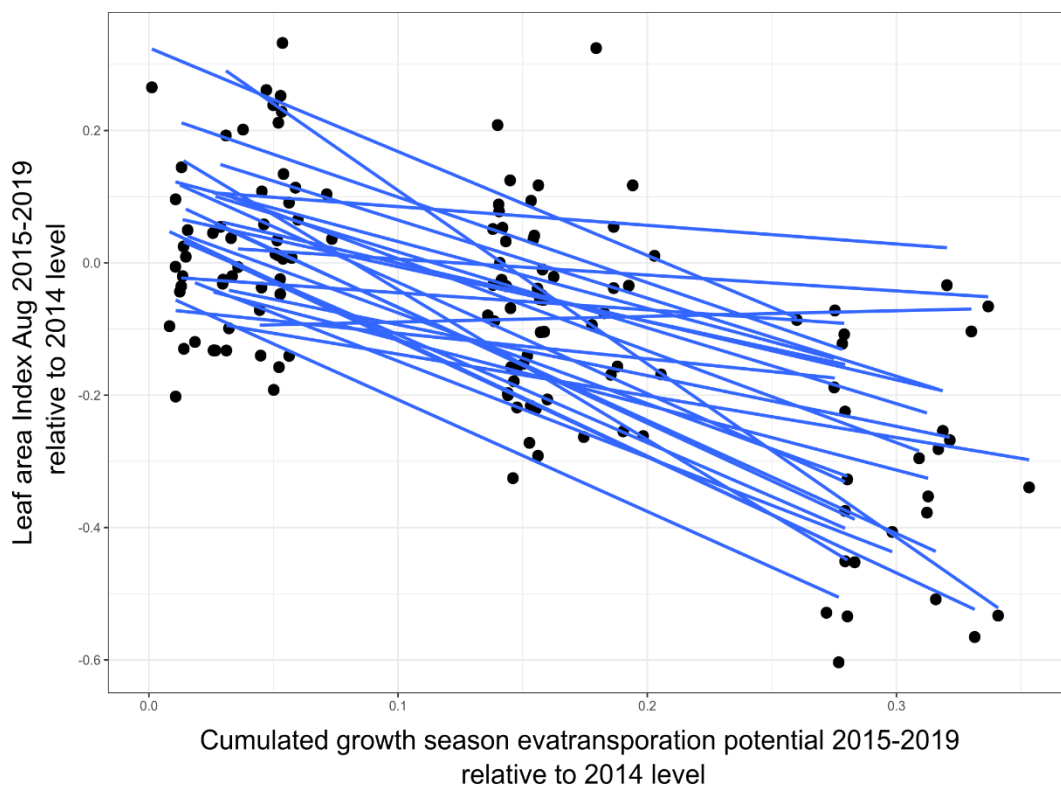
11 **Suppl. Fig.1.** Climate change dynamics. Mean change of sampling site values along PCA axis 1  
12 (temperature, red) and PCA axis 2 (precipitation, blue) among decades.



13

14

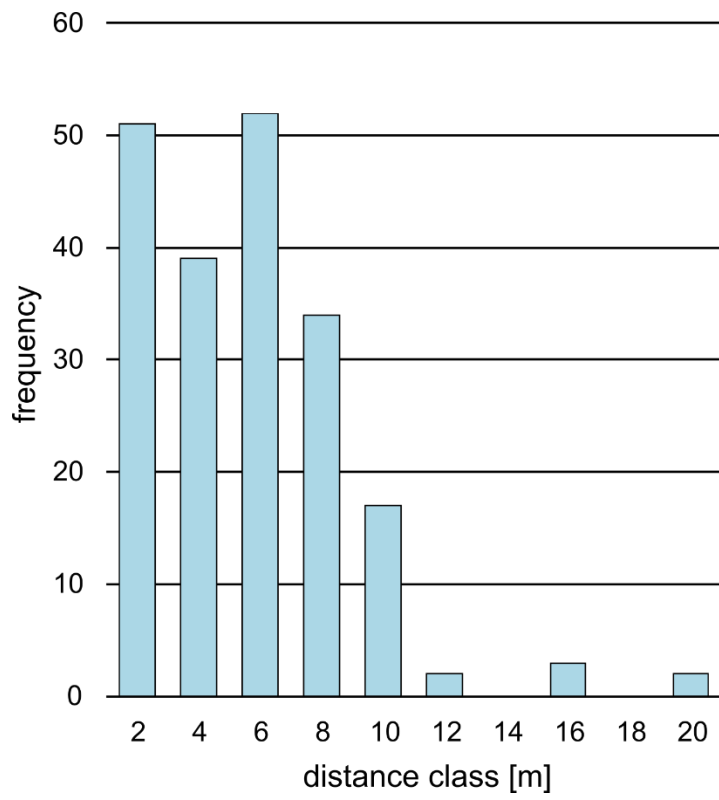
15 **Suppl. Fig. 2.** Plot of “relative Leaf Area Index” change relative to 2014 values against “cumulated  
16 evatranspiration potential” change during the growth season relative to 2014 values for all 1 x 1 km  
17 plots encompassing the 27 sampling sites. The overall correlation is  $r = 0.695$ .



18

19

20 **Suppl. Fig. 3.** Distribution of pairwise distances between the paired trees.



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24 **Suppl. Fig. 4.** Exemplary pictures of damaged and healthy beech tree pairs from several sampling  
25 sites.



USI PF\_029



USI PF\_030



EPP PF\_039



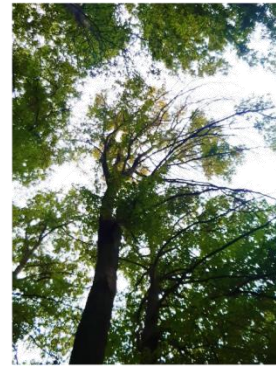
EPP PF\_040



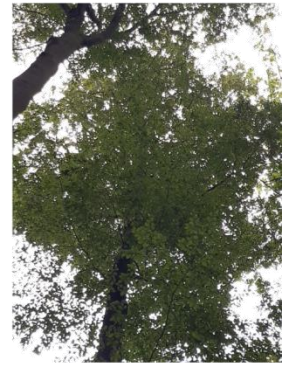
BCA PF\_050



BCA PF\_051



DAU PF\_054



DAU PF\_055



OUR PF\_068



OUR PF\_069



SWD PF\_060



SWD PF\_061



NEK PF\_070



NEK PF\_071



LAH PF\_076



LAH PF\_077

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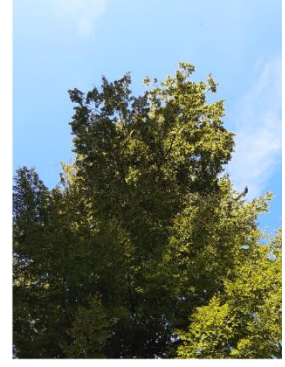
SLB PF\_095



SLB PF\_096



THT PF\_089



THT PF\_090



WEH PF\_110



WEH PF\_111



OBH PF\_019

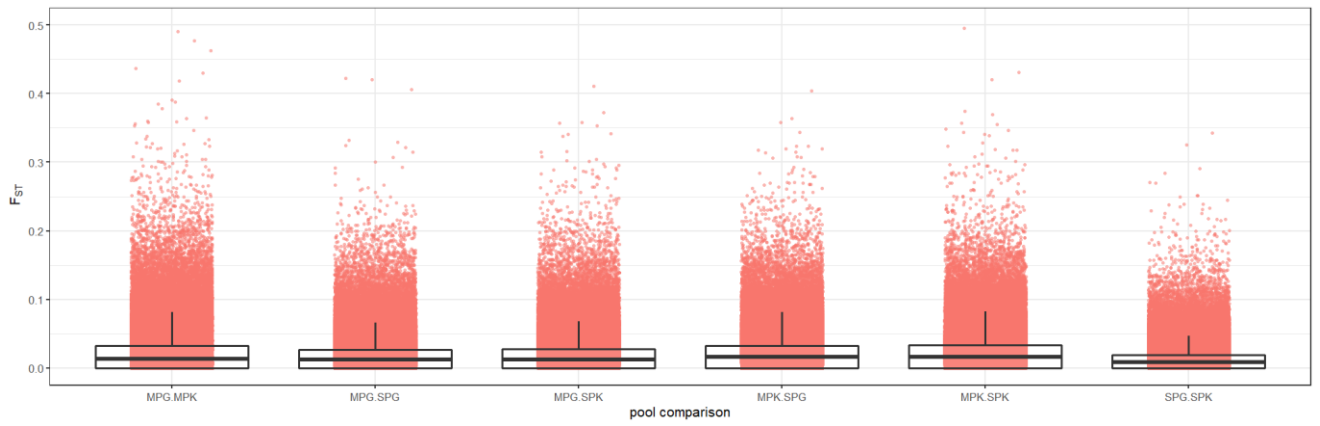


OBH PF\_020

28

29

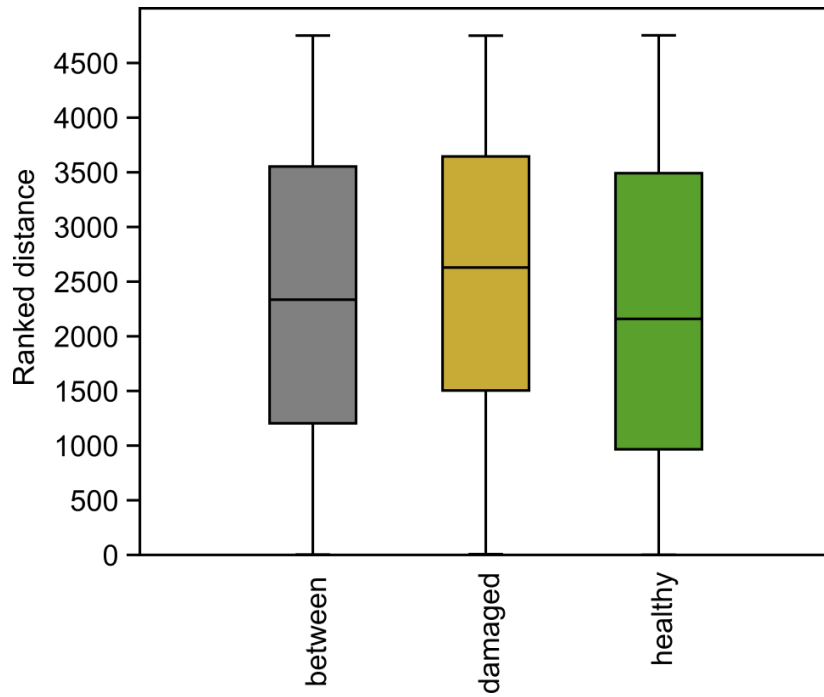
30 **Suppl. Fig. 5.** Genome-wide  $F_{ST}$  distributions in 1 kb windows. Comparisons between all pools. Please  
31 note that the standard deviation included zero in all cases.



32

33

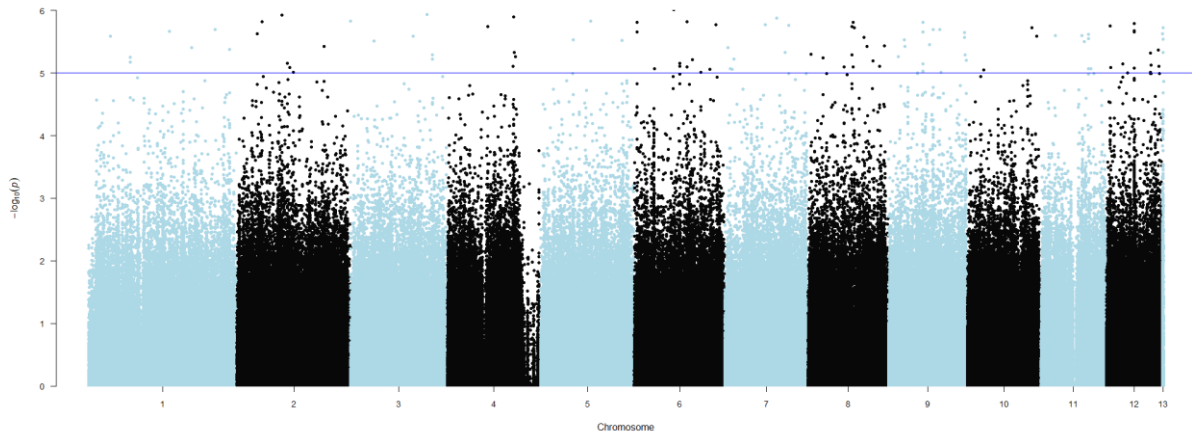
34 **Suppl. Fig. 6.** Genomic similarity among individuals within and among phenotypic classes.  
35 Permutation ANOSIM shows that the differences are not significant ( $p = 0.76$ ).



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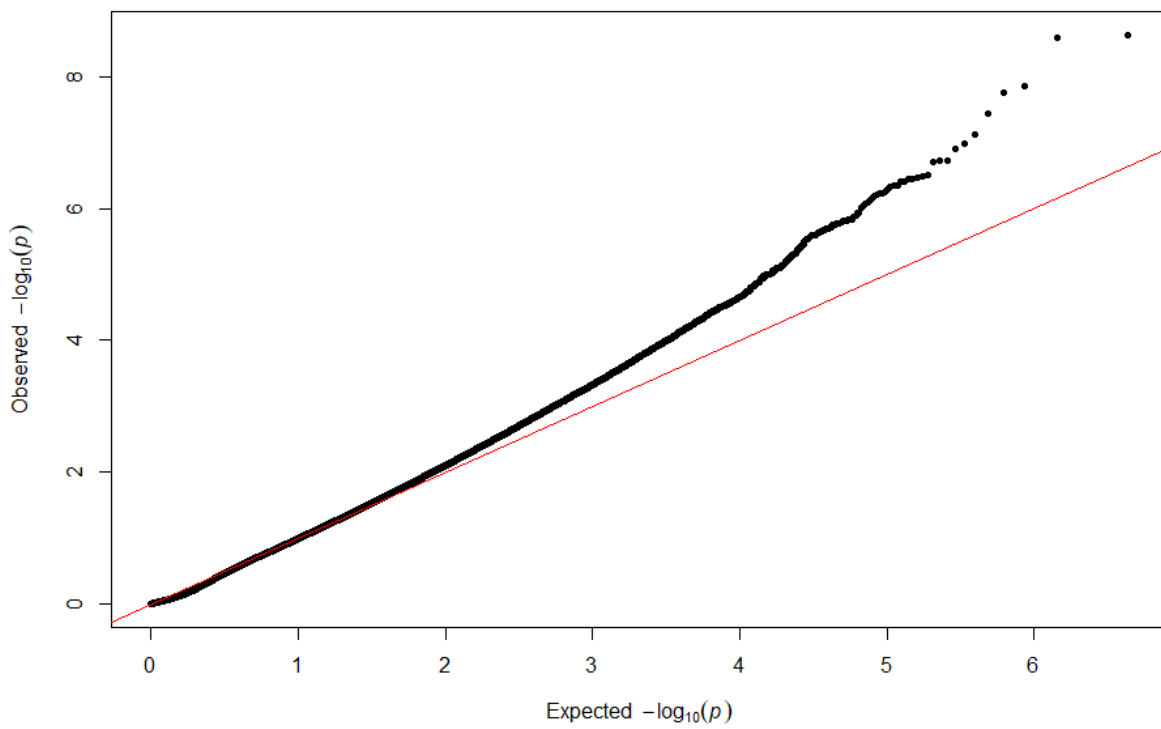
39 **Suppl. Fig. 7.** A) Manhattan plot of uncorrected p values from CMH test and B) corresponding QQ-  
40 plot. SNPs on different chromosomes are alternatingly coloured blue and black.

41 A)



42

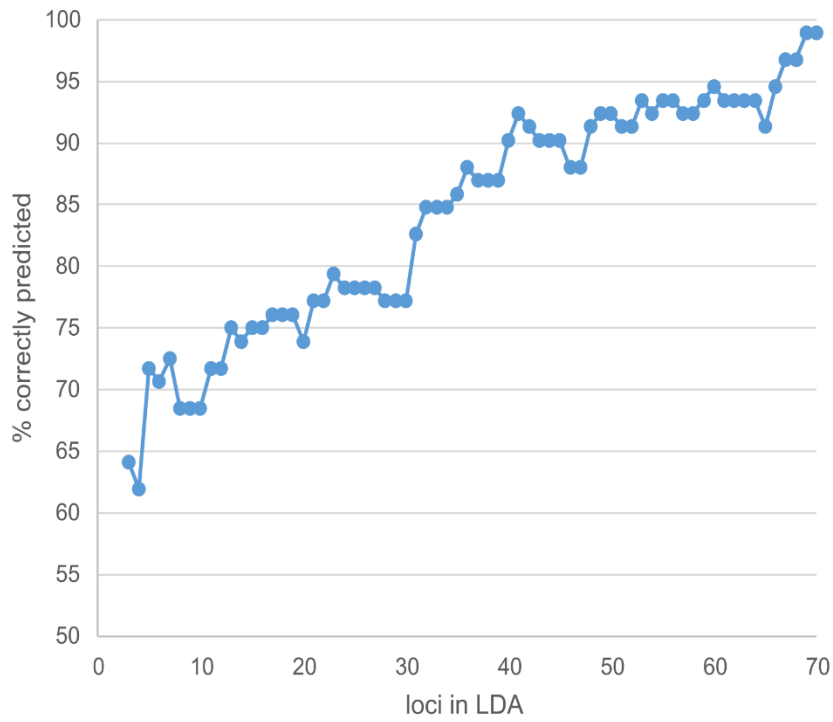
43 B)



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46 **Suppl. Fig. 8.** Increase of LDA prediction success with the number of loci involved. Loci were added  
47 according to their decreasing contribution in the final analysis.

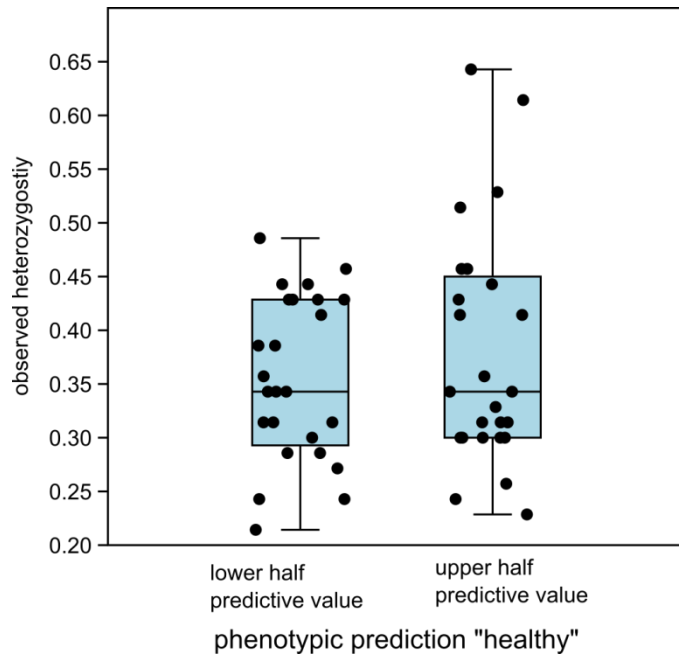


48

49

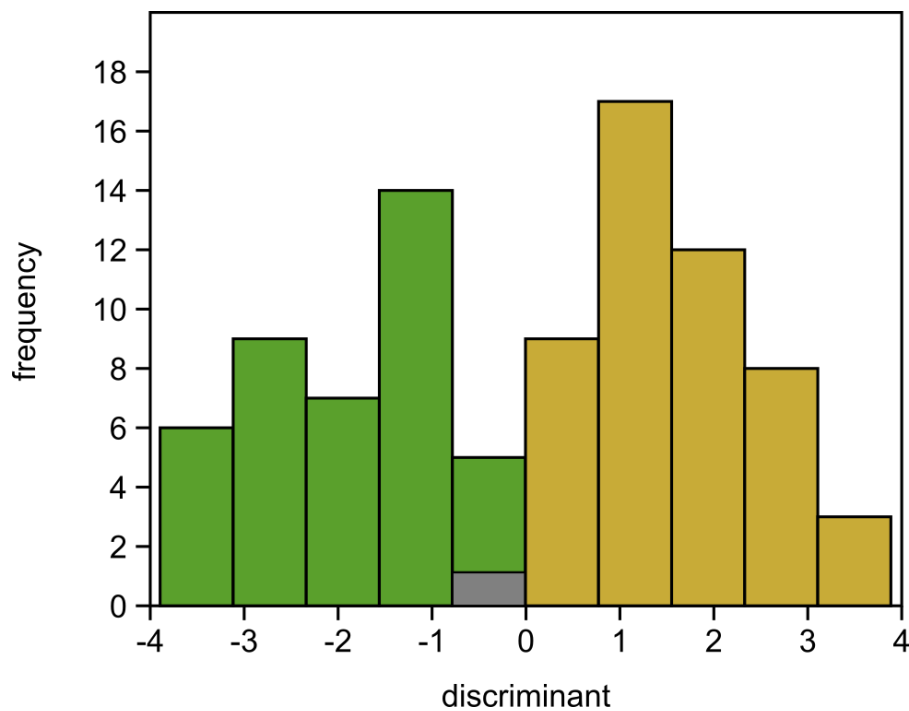
50 **Suppl. Fig. 9.** Comparison of observed heterozygosity between lower and upper half of predictive  
51 values "healthy" in DA. The medians are not significantly different (Mann-Whitney U = 293.5, p same  
52 median = 0.72).

53



54

55 **Suppl. Fig.10.** Histogram of LDA results. Individuals, where the predicted phenotype did not match  
56 the observed phenotype are shown in grey, individuals with matching observed/predicted phenotype  
57 in green (healthy) or in ochre (damaged).



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**Suppl. Table 3.** List of genes with significant SNPs. Functional annotations and relation to drought phenotype are given whenever available.

<i>F. sylvatica</i> gene ID	Best BLAST hit ID	BLAST hit protein name	taxon	UniProt ID	UniProt protein name	function (UniProt)	citation function	relation to drought phenotype	citation
1.g3851.t1	KUM50718.1	hypothetical protein ABT39_MTgene562	<i>Picea glauca</i>	none	-	-	-	-	-
10.g3914.t1	XP_023883481.1	uncharacterized protein LOC111995782 isoform X1	<i>Quercus suber</i>	none	-	-	-	-	-
11.g2467.t1	XP_023923514.1	exosome complex exonuclease RRP46 homolog isoform X1	<i>Quercus suber</i>	EXOS5_ORYSJ	Exosome complex exonuclease RRP46 homolog	mRNA degradation	Xiang, D., Yang, H., Venglat, P., Cao, Y., Wen, R., Ren, M., ... & Weijers, D. (2011). POPCORN functions in the auxin pathway to regulate embryonic body plan and meristem organization in Arabidopsis. <i>The Plant Cell</i> , 23(12), 4348-4367.	-	-
11.g2832.t1	XP_030949821.1	WD repeat-containing protein PCN-like	<i>Quercus lobata</i>	PCN_ARATH	WD repeat-containing protein PCN	Involved in auxin signalling pathway. Required for embryo development and meristem organization. Functions in the auxin pathway, integrating auxin signalling in the organization	-	drought stress response	Park, S. R., Hwang, J., & Kim, M. (2020). The Arabidopsis WDR55 is positively involved in ABA-mediated



						and maintenance of the shoot apical meristem (SAM) and root apical meristem (RAM).			drought tolerance response. Plant Biotechnology Reports, 1-12.
12.g1695.t1	XP_030973623.1	uncharacterized protein LOC115993791	<i>Quercus lobata</i>	F4I5S1_ARATH	PB1 domain-containing protein tyrosine kinase	not well characterised	-	-	-
2.g4736.t1	KAF3975221.1	hypothetical protein CMV_001513	<i>Castanea mollissima</i>	none	-	-	-	-	-
3.g3590.t1	XP_030942104.1	uncharacterized protein LOC115967180	<i>Quercus lobata</i>	none	-	-	-	-	-
4.g3980.t1	XP_030950630.1	cytokinin dehydrogenase 5	<i>Quercus lobata</i>	CKX1_ARATH	Cytokinin dehydrogenase 1	Catalyzes the oxidation of cytokinins, a family of N6-substituted adenine derivatives that are plant hormones, where the substituent is an isopentenyl group.	Werner, T., Motyka, V., Laucou, V., Smets, R., Van Onckelen, H., & Schmülling, T. (2003). Cytokinin-deficient transgenic Arabidopsis plants show multiple developmental alterations indicating opposite functions of cytokinins in the regulation of shoot and root meristem activity. The Plant Cell, 15(11), 2532-	drought stress response	Emery, R. J., & Kisiala, A. (2020). The Roles of Cytokinins in Plants and Their Response to Environmental Stimuli. Li, W., Herrera-Estrella, L., & Tran, L. S. P. (2016). The Yin-Yang of cytokinin homeostasis and drought acclimation/adaptation. Trends in Plant Science,

							2550.		21(7), 548-550.
5.g1807.t1	XP_030939294.1	guanosine nucleotide diphosphate dissociation inhibitor 2	<i>Quercus lobata</i>	GDI2_ARATH	Guanosine nucleotide diphosphate dissociation inhibitor 2	Regulates the GDP/GTP exchange reaction of most RAB proteins by inhibiting the dissociation of GDP from them, and the subsequent binding of GTP.	Ueda, T., Yoshizumi, T., Anai, T., Matsui, M., Uchimiya, H., & Nakano, A. (1998). AtGDI2, a novel Arabidopsis gene encoding a Rab GDP dissociation inhibitor. <i>Gene</i> , 206(1), 137-143.	environmental stress response	Carvalho, B. M., Viana, A. P., dos Santos, P. H. D., Generoso, A. L., Corrêa, C. C. G., Silveira, V., ... & Santos, E. A. (2019). Proteome of resistant and susceptible <i>Passiflora</i> species in the interaction with cowpea aphid-borne mosaic virus reveals distinct responses to pathogenesis. <i>Euphytica</i> , 215(10), 167.
6.g2227.t1	THG21676.1	hypothetical protein TEA_000305	<i>Camellia sinensis</i> var. <i>sinensis</i>	NDUS7_ARATH	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	Core subunit of the mitochondrial membrane respiratory chain NADH dehydrogenase (Complex I) that is believed to belong to the minimal assembly required for catalysis. Complex I functions in the transfer of electrons from NADH to the respiratory chain. The immediate electron acceptor for the enzyme is believed to be ubiquinone		drought stress response	Zhang, S., Zhang, L., Zhou, K., Li, Y., & Zhao, Z. (2017). Changes in protein profile of <i>Platycladus orientalis</i> (L.) roots and leaves in response to drought stress. <i>Tree Genetics &amp; Genomes</i> , 13(4), 76.

6.g2921.t1	KAB1222126.1	Ribonuclease H2 subunit C	<i>Morella rubra</i>	RNH2A_ARATH	Ribonuclease H2 subunit A	Catalytic subunit of RNase HII, an endonuclease that specifically degrades the RNA of RNA:DNA hybrids. Participates in DNA replication, possibly by mediating the removal of lagging-strand Okazaki fragment RNA primers during DNA replication. Mediates the excision of single ribonucleotides from DNA:RNA duplexes	-	-	-
7.g177.t1	XP_018842121.1	PREDICTED: tubby-like F-box protein 8 isoform X1	<i>Juglans regia</i>	TLP10_ARATH	Tubby-like F-box protein 10	Component of SCF(ASK-cullin-F-box) E3 ubiquitin ligase complexes, which may mediate the ubiquitination and subsequent proteasomal degradation of target proteins	-	drought stress response	Xu, J., Xing, S., Sun, Q., Zhan, C., Liu, X., Zhang, S., & Wang, X. (2019). The expression of a tubby-like protein from <i>Malus domestica</i> (Md TLP7) enhances abiotic stress tolerance in <i>Arabidopsis</i> . <i>BMC plant biology</i> , 19(1), 1-8.
7.g1655.t1	XP_023909357.1	histone deacetylase 6	<i>Quercus suber</i>	HDA6	Histone deacetylase 6	Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell	"Identification of <i>Arabidopsis</i> histone deacetylase HDA6 mutants that affect transgene expression." Murfett J., Wang X.-J., Hagen G.,	drought stress	Zheng, Y., Ding, Y., Sun, X., Xie, S., Wang, D., Liu, X., ... & Zhou, D. X. (2016). Histone deacetylase HDA9 negatively regulates salt and drought stress

						cycle progression and developmental events.	Guilfoyle T.J. Plant Cell 13:1047-1061(2001)		responsiveness in Arabidopsis. Journal of experimental botany, 67(6), 1703-1713.
7.g2350.t1	KAF3966828.1	hypothetical protein CMV_009102	<i>Castanea mollissima</i>	PRK4_ARATH	Pollen receptor-like kinase 4	Receptor-like kinase involved in the control of pollen germination and pollen tube polar growth. Can phosphorylate ROPGEF1 in vitro	Chang, F., Gu, Y., Ma, H., & Yang, Z. (2013). AtPRK2 promotes ROP1 activation via RopGEFs in the control of polarized pollen tube growth. Molecular plant, 6(4), 1187-1201.	environmental stress response	Guo, J., Dong, X., Li, Y., & Wang, B. (2020). NaCl treatment markedly enhanced pollen viability and pollen preservation time of euhalophyte Suaeda salsa via up regulation of pollen development-related genes. Journal of plant research, 133(1), 57-71.
7.g3617.t1	XP_023924613.1	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 10-like isoform X1	<i>Quercus suber</i>	LSH4_ARATH	Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 4	Probable transcription regulator that acts as a developmental regulator by promoting cell growth in response to light. May suppress organ differentiation in the boundary region	Takeda, S., Hanano, K., Kariya, A., Shimizu, S., Zhao, L., Matsui, M., ... & Aida, M. (2011). CUP-SHAPED COTYLEDON1 transcription factor activates the expression of LSH4 and LSH3, two members of the ALOG gene family, in	-	

							shoot organ boundary cells. The Plant Journal, 66(6), 1066-1077.		
7.g3816.t1	XP_018811587.1	ethylene-responsive transcription factor 12-like	<i>Juglans regia</i>	TAFCL_ARATH	Transcription initiation factor TFIID subunit 12b	TAFs are components of the transcription factor IID (TFIID) complex that is essential for mediating regulation of RNA polymerase transcription. Required for the expression of a subset of ethylene-responsive genes (By similarity). Involved in the negative regulation of cytokinin sensitivity	-	-	-
7.g552.t1	No hits found		-	-	-	-	-	-	-
8.g3494.t1	XP_022750437.1	V-type proton ATPase subunit C	<i>Durio zibethinus</i>	VATC_ARATH	V-type proton ATPase subunit C	Subunit of the peripheral V1 complex of vacuolar ATPase. Subunit C is necessary for the assembly of the catalytic sector of the enzyme and is likely to have a specific function in its catalytic activity. V-ATPase is responsible for acidifying a variety of intracellular compartments in eukaryotic cells	-	drought stress response	Kausar, R., Arshad, M., Shahzad, A., & Komatsu, S. (2013). Proteomics analysis of sensitive and tolerant barley genotypes under drought stress. Amino Acids, 44(2), 345-359. Li, J., Jia, H., Han, X., Zhang, J., Sun, P., Lu, M., & Hu, J. (2016). Selection of reliable reference genes for gene expression analysis under abiotic

									stresses in the desert biomass willow, <i>Salix psammophila</i> . <i>Frontiers in plant science</i> , 7, 1505.
9.g3080.t1	XP_030929046.1	probable inactive purple acid phosphatase 29	<i>Quercus lobata</i>	PPA14_ARATH	Probable inactive purple acid phosphatase 14	-	-	drought stress response	Street, N. R., Skogström, O., Sjödin, A., Tucker, J., Rodríguez-Acosta, M., Nilsson, P., ... & Taylor, G. (2006). The genetics and genomics of the drought response in <i>Populus</i> . <i>The Plant Journal</i> , 48(3), 321-341. Prinsi, B., Negri, A. S., Failla, O., Scienza, A., & Espen, L. (2018). Root proteomic and metabolic analyses reveal specific responses to drought stress in differently tolerant grapevine rootstocks. <i>BMC plant biology</i> , 18(1), 126.
9.g4504.t1	KAF3976808.1	hypothetical protein CMV_000062	<i>Castanea mollissi</i>	TBL33_ARATH	Protein trichome birefring	Probable xylan acetyltransferase that plays a role in xylan acetylation and	Yuan, Y., Teng, Q., Zhong, R., Haghghat, M.,	drought stress response	Shuai, P., Liang, D., Zhang, Z., Yin, W., & Xia, X. (2013).

			<i>ma</i>		ence-like 33	normal deposition of secondary cell walls	Richardson, E. A., & Ye, Z. H. (2016). Mutations of Arabidopsis TBL32 and TBL33 affect xylan acetylation and secondary wall deposition. PLoS One, 11(1), e0146460.		Identification of drought- responsive and novel Populus trichocarpamicroR NAs by high- throughput sequencing and their targets using degradome analysis. BMC Genomics, 14(1), 233.
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**Suppl. Table 4.** List of genes closest to significant SNPs. Functional annotations and relation to drought phenotype are given whenever available.

<i>F. sylvatica</i> gene ID	Best BLAST hit ID	BLAST hit protein name	taxon	UniProt ID	UniProt protein name	function (UniProt)	citation function	relation to drought phenotype	citation
Backbone_621.g33	KAF3957547	hypothetical protein CMV_017449	<i>Castanea mollissima</i>						
Backbone_621.g49	XP_030932040	pathogen-related protein	<i>Quercus lobata</i>						
1.g1111	KAF3976566	hypothetical protein CMV_000247	<i>Castanea mollissima</i>	ACBP4_ARATH	Acyl-CoA-binding domain-containing protein 4	Binds medium- and long-chain acyl-CoA esters with very high affinity. Can interact in vitro with oleoyl-CoA, barely with palmitoyl-CoA, but not with arachidonyl-CoA.	Leung, K. C., Li, H. Y., Mishra, G., & Chye, M. L. (2005). ACBP4 and ACBP5, novel Arabidopsis acyl-CoA-binding proteins with kelch motifs that bind oleoyl-CoA. <i>Plant molecular biology</i> , 55(2), 297-309.	environmental stress response	Du, Z. Y., Arias, T., Meng, W., & Chye, M. L. (2016). Plant acyl-CoA-binding proteins: an emerging family involved in plant development and stress responses. <i>Progress in Lipid Research</i> , 63, 165-181.
1.g2051	XP_031256586	aspartic proteinase nepenthesin-1-like	<i>Pistacia vera</i>					drought stress response	Prinsi, B., Negri, A. S., Failla, O., Scienza, A., & Espen, L. (2018). Root proteomic and metabolic analyses reveal specific responses to drought stress in differently



									tolerant grapevine rootstocks. BMC plant biology, 18(1), 126.
1.g5025	No hits found								
1.g6250	XP_030925267	BTB/POZ domain and ankyrin repeat-containing protein NOOT2	<i>Quercus lobata</i>	NPR5_ARATH	Regulatory protein NPR5	May act as a substrate-specific adapter of an E3 ubiquitin-protein ligase complex (CUL3-RBX1-BTB) which mediates the ubiquitination and subsequent proteasomal degradation of target proteins	Hepworth, S. R., Zhang, Y., McKim, S., Li, X., & Haughn, G. W. (2005). BLADE-ON-PETIOLE-dependent signaling controls leaf and floral patterning in Arabidopsis. The Plant Cell, 17(5), 1434-1448.		
1.g7050	PQQ17864	insulin-degrading enzyme-like 1 peroxisomal	<i>Prunus yedoensis</i>	IDE1_ARATH	insulin-degrading enzyme-like 1 peroxisomal	Peptidase that might be involved in pathogen or wound response.	Lingard, M. J., & Bartel, B. (2009). Arabidopsis LON2 is necessary for peroxisomal function and sustained matrix protein import. Plant physiology, 151(3), 1354-1365.		

2.g1138	XP_01881850 2	PREDICTED: uncharacterized protein LOC108989373 isoform X3	<i>Juglans regia</i>						
2.g1372	KAF3967401	hypothetical protein CMV_008608	<i>Castanea mollissima</i>						
2.g1982	No hits found								
2.g4924	TKY55186	Spermine synthase	<i>Spatholobus suberectus</i>	SPSY_ARATH	Spermine synthase			drought stress response	Yamaguchi, K., Takahashi, Y., Berberich, T., Imai, A., Takahashi, T., Michael, A. J., & Kusano, T. (2007). A protective role for the polyamine spermine against drought stress in Arabidopsis. Biochemical and biophysical research communications, 352(2), 486-490.
3.g1427	XP_03094022 3	uncharacterized protein LOC115965177	<i>Quercus lobata</i>						
3.g4686	KAF3964003	hypothetical protein CMV_011671	<i>Castanea mollissima</i>						
4.g1310	KAF3954505	hypothetical protein CMV_020159	<i>Castanea mollissima</i>	Q9C6S8_ARATH	Pre-mRNA- splicing factor of RES complex protein			drought stress response	Qi, Y., Yao, X., Zhao, D., & Lu, L. (2018). Overexpression of SbSKIP, a pre-mRNA splicing factor from

									Sorghum bicolor, enhances root growth and drought tolerance in Petunia hybrida. Scientia Horticulturae, 240, 281-287.
4.g3868	KAF3971069	hypothetical protein CMV_005309	<i>Castanea mollissima</i>						
4.g3915	KAF3976838	hypothetical protein CMV_000012	<i>Castanea mollissima</i>						
5.g2789	XP_023898567	uncharacterized protein LOC112010459 isoform X2	<i>Quercus suber</i>	Q9M089_ARATH	Keratin-associated protein (DUF1218)			drought stress response	Xu, J., Yuan, Y., Xu, Y., Zhang, G., Guo, X., Wu, F., ... & Tang, Q. (2014). Identification of candidate genes for drought tolerance by whole-genome resequencing in maize. BMC Plant Biology, 14(1), 83.
5.g3716	XP_023870312	dynammin-related protein 5A	<i>Quercus suber</i>	DRP5A_ARATH	Dynammin-related protein 5A	Probable microtubule-associated force-producing protein that is targeted to the forming cell plate during cytokinesis. May play a role in cell division	Miyagishima, S. Y., Kuwayama, H., Urushihara, H., & Nakanishi, H. (2008). Evolutionary linkage between eukaryotic cytokinesis and	drought stress response	Ren, Z., Zhang, D., Cao, L., Zhang, W., Zheng, H., Liu, Z., ... & Su, H. (2020). Functions and regulatory framework of ZmNST3 in maize under lodging and drought stress. Plant, Cell & Environment, 43(9), 2272-2286.

							chloroplast division by dynamin proteins. Proceedings of the National Academy of Sciences, 105(39), 15202-15207.		
5.g4697	XP_023901205	cytochrome b561 and DOMON domain-containing protein At4g12980-like	<i>Quercus suber</i>						
6.g180	KNA23105	hypothetical protein SOVF_026910	<i>Spinacia oleracea</i>						
6.g3229	XP_015867595	transcription initiation factor TFIID subunit 11	<i>Ziziphus jujuba</i>	TA14B_ARATH	Transcription initiation factor TFIID	Negative regulator of flowering controlling the H4K5 acetylation levels in the FLC and FT chromatin. Positively regulates FLC expression.	Zacharaki, V., Benhamed, M., Poullos, S., Latrasse, D., Papoutsoglou, P., Delarue, M., & Vlachonasios, K. E. (2012). The Arabidopsis ortholog of the YEATS domain containing protein YAF9a regulates flowering by	drought stress response	Parvathi, M. S., Nataraja, K. N., Reddy, Y. N., Naika, M. B., & Gowda, M. C. (2019). Transcriptome analysis of finger millet ( <i>Eleusine coracana</i> (L.) Gaertn.) reveals unique drought responsive genes. <i>Journal of genetics</i> , 98(2), 46.

							controlling H4 acetylation levels at the FLC locus. Plant science, 196, 44-52.		
6.g823	No hits found								
7.g1655	XP_023909357	histone deacetylase 6	<i>Quercus suber</i>	HDA6_ARATH	Histone deacetylase 6	Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4).		drought stress response	Kim, J. M., Sasaki, T., Ueda, M., Sako, K., & Seki, M. (2015). Chromatin changes in response to drought, salinity, heat, and cold stresses in plants. <i>Frontiers in plant science</i> , 6, 114.
7.g2958	KAF3966011	hypothetical protein CMV_009858	<i>Castanea mollissima</i>	F4I6B2_ARATH	SIT4 phosphatase-associated family protein				
7.g3483	XP_023874962	uncharacterized protein LOC111987473	<i>Quercus suber</i>						
7.g3669	XP_023883887	protein trichome birefringence-like 38	<i>Quercus suber</i>	TBL38_ARATH	protein trichome birefringence-like 38	May act as a bridging protein that binds pectin and other cell wall polysaccharides. Probably involved in maintaining		drought stress response	Shuai, P., Liang, D., Zhang, Z., Yin, W., & Xia, X. (2013). Identification of drought-responsive and novel <i>Populus trichocarpa</i> microRNAs by high-throughput sequencing and their

						esterification of pectins			targets using degradome analysis. BMC Genomics, 14(1), 233.
8.g199	KAF3962723	hypothetical protein CMV_012798	<i>Castanea mollissima</i>						
8.g2624	No hits found								
8.g2764	RUS78569	hypothetical protein EGW08_013676, partial	<i>Elysia chlorotica</i>						
8.g2926	RUS32681	hypothetical protein BC938DRAFT_474617	<i>Jimgerdemanni a flammicorona</i>						
8.g3326	XP_030953364	sister chromatid cohesion protein SCC2	<i>Quercus lobata</i>	SCC2_ARATH	sister chromatid cohesion protein SCC2	Essential protein required for cell fate determination during embryogenesis	Sebastian, J., Ravi, M., Andreuzza, S., Panoli, A. P., Marimuthu, M. P., & Siddiqi, I. (2009). The plant adherin AtSCC2 is required for embryogenesis and sister-chromatid cohesion during meiosis in Arabidopsis. The Plant Journal, 59(1), 1-13.		

8.g3872	XP_030953755	surfeit locus protein 2	<i>Quercus lobata</i>	SURF1_ARATH	Surfeit locus protein 1	Probably involved in the biogenesis of the COX complex			
8.g4454	KAF3955069	hypothetical protein CMV_019673	<i>Castanea mollissima</i>						
8.g4554	KAF3975054	hypothetical protein CMV_001659	<i>Castanea mollissima</i>						
8.g935	KAF3972759	hypothetical protein CMV_003766	<i>Castanea mollissima</i>						
9.g1013	KAF3963767	hypothetical protein CMV_011877	<i>Castanea mollissima</i>						
9.g1025	XP_023873320	cytosolic sulfotransferase 5-like	<i>Quercus suber</i>						
9.g2127	No hits found								
9.g4398	KAB5561320	hypothetical protein DKX38_006277	<i>Salix brachista</i>						
9.g4504	KAF3976808	hypothetical protein CMV_000062	<i>Castanea mollissima</i>	TBL33_ARATH	Protein trichome birefringence-like 33	Probable xylan acetyltransferase that plays a role in xylan acetylation and normal deposition of secondary cell walls	Yuan, Y., Teng, Q., Zhong, R., Haghghat, M., Richardson, E. A., & Ye, Z. H. (2016). Mutations of Arabidopsis TBL32 and TBL33 affect xylan acetylation and secondary	drought stress response	Shuai, P., Liang, D., Zhang, Z., Yin, W., & Xia, X. (2013). Identification of drought-responsive and novel Populus trichocarpamicroRNAs by high-throughput sequencing and their targets using degradome analysis. <i>Bmc Genomics</i> , 14(1),

							wall deposition. PLoS One, 11(1), e0146460.		233.
9.g4548	XP_023928861	uncharacterized protein LOC112040195	<i>Quercus suber</i>						
9.g4606	XP_030928366	LOW QUALITY PROTEIN: E3 ubiquitin-protein ligase SHPRH	<i>Quercus lobata</i>						
9.g653	KAF3952878	hypothetical protein CMV_021616	<i>Castanea mollissima</i>						
10.g4171	ONI05229	hypothetical protein PRUPE_6G363600	<i>Prunus persica</i>						
11.g2603	XP_023892377	amino acid permease 6-like	<i>Quercus suber</i>	AAP6_ARATH	Amino acid permease 6	Amino acid-proton symporter. Stereospecific transporter with a broad specificity for tryptophan, proline, and neutral and acidic amino acids.	Rentsch, D., Hirner, B., Schmelzer, E., & Frommer, W. B. (1996). Salt stress-induced proline transporters and salt stress-repressed broad specificity amino acid permeases identified by suppression of	environmental stress response	Rentsch, D., Hirner, B., Schmelzer, E., & Frommer, W. B. (1996). Salt stress-induced proline transporters and salt stress-repressed broad specificity amino acid permeases identified by suppression of a yeast amino acid permease-targeting mutant. The Plant Cell, 8(8), 1437-1446.



							a yeast amino acid permease-targeting mutant. The Plant Cell, 8(8), 1437-1446.		
11.g787	No hits found								
12.g1692	KAF3972258	hypothetical protein CMV_004214	<i>Castanea mollissima</i>						
12.g2592	No hits found								
12.g3049	XP_023886583	transcription factor TCP15	<i>Quercus suber</i>	TCP15_ARATH	transcription factor TCP15	Transcription factor involved the regulation of plant development. Together with TCP14, modulates plant stature by promoting cell division in young internodes.	Kieffer, M., Master, V., Waites, R., & Davies, B. (2011). TCP14 and TCP15 affect internode length and leaf shape in Arabidopsis. The Plant Journal, 68(1), 147-158.	environmental stress response	Viola, I. L., Camoirano, A., & Gonzalez, D. H. (2016). Redox-dependent modulation of anthocyanin biosynthesis by the TCP transcription factor TCP15 during exposure to high light intensity conditions in Arabidopsis. Plant Physiology, 170(1), 74-85.
12.g922	KAF3957893	hypothetical protein CMV_017140	<i>Castanea mollissima</i>						

Suppl. Table 5. List of 20 most informative SNPs as selected by the eSPA Analysis allowing for 85% correct classification.

	scaffold	position	gene	swiss_prot_id_(arabidopsis_thaliana)
41	Fsyl.bwa_aln.clean.counts_GATC.12g6	1385435	/	/
56	Fsyl.bwa_aln.clean.counts_GATC.12g7	31456694	Fsyl.bwa_aln.clean.counts_GATC.12g7.g3617.t1	Q9S7R3
14	Fsyl.bwa_aln.clean.counts_GATC.12g12	7252002	/	/
9	Fsyl.bwa_aln.clean.counts_GATC.12g11	21712586	/	/
42	Fsyl.bwa_aln.clean.counts_GATC.12g6	1559115	/	/
43	Fsyl.bwa_aln.clean.counts_GATC.12g6	1559277	/	/
44	Fsyl.bwa_aln.clean.counts_GATC.12g6	1559370	/	/
27	Fsyl.bwa_aln.clean.counts_GATC.12g2	22433752	/	/
58	Fsyl.bwa_aln.clean.counts_GATC.12g7	33110000	Fsyl.bwa_aln.clean.counts_GATC.12g7.g3816.t1	Q94ID6
36	Fsyl.bwa_aln.clean.counts_GATC.12g4	34077017	Fsyl.bwa_aln.clean.counts_GATC.12g4.g3980.t1	Q67YUo
84	Fsyl.bwa_aln.clean.counts_GATC.12g9	38251152	/	/
85	Fsyl.bwa_aln.clean.counts_GATC.12g9	38652380	/	/
59	Fsyl.bwa_aln.clean.counts_GATC.12g8	1582675	/	/
1	Fsyl.bwa_aln.clean.counts_GATC.12g1	10993370	/	/
78	Fsyl.bwa_aln.clean.counts_GATC.12g9	20434572	/	/
82	Fsyl.bwa_aln.clean.counts_GATC.12g9	37955715	Fsyl.bwa_aln.clean.counts_GATC.12g9.g4504.t1	F4IH21
80	Fsyl.bwa_aln.clean.counts_GATC.12g9	25538827	Fsyl.bwa_aln.clean.counts_GATC.12g9.g3080.t1	Q9FMK9
34	Fsyl.bwa_aln.clean.counts_GATC.12g4	33216309	/	/
70	Fsyl.bwa_aln.clean.counts_GATC.12g9	5021966	/	/
69	Fsyl.bwa_aln.clean.counts_GATC.12g8	38060740	/	/

**Suppl. Info 1.** Software pipeline and commands used for PoolSeq analysis.

#AUTOTRIM

```
perl ../autotrim-master/autotrim.pl -fofn files.txt -trim ../trimmomatic_options -tt 12 -log /data/FagusPools -tp /home/mpfenninger/Trimmomatic-0.39/trimmomatic-0.39.jar -fqcp /home/mpfenninger/FastQC/fastqc
```

#Mapping with BWA

```
bwa index Beech_12Chr.masked.fas
```

```
bwa mem -t 12 -k 30 /Genome/Fagus_sylvatica_genome.fasta XXX_R1.autotrim.paired.fq XXX_R2_autotrim.paired.fq > XXX_bwamem.sam
```

```
while read poollist
do samtools view -b $poollist"_bwamem.sam" > $poollist".bam"
done < poollist
wait
```

```
samtools sort XX.bam > XX.sort.bam
```

#Remove Duplicates with Picard

```
java -jar /home/mpfenninger/Picard/picard.jar MarkDuplicates I=MPG.sort.bam O=MPG.sort.rmd.bam M=PoolMPG.dupstat.txt
VALIDATION_STRINGENCY=SILENT REMOVE_DUPLICATES=TRUE
```

#Remove low quality mappings with SAMtools

```
samtools view -q 20 -@ 14 -f 0x0002 -F 0x0004 -F 0x0008 -b MPG.sort.rmd.bam > MPG.sort.rmd.q20.bam
```

```
samtools index MPG.sort.rmd.q20.bam
```

#Create pileup with mpileup

```
samtools mpileup -f /data/FagusPools/Genome/Fagus_sylvatica_genome.fasta -B -Q 0 MPG.sort.rmd.q20.bam MPK.sort.rmd.q20.bam
```

```
SPG.sort.rmd.q20.bam SPK.sort.rmd.q20.bam > FagusPool.mpileup
```

```
#Convert mpileup to sync with Popoolation 2_1201
```

```
java -jar ~/popoolation2_1201/mpileup2sync.jar --input FagusPool.mpileup --output FagusPool.sync --fastq-type sanger --min-qual 20 --threads 14
```

```
#Filtering for indels
```

```
#get indels
```

```
perl ~/popoolation2_1201/indel_filtering/identify-indel-regions.pl --indel-window 5 --input FagusPool.mpileup --output FagusPool.indels.gtf
```

```
#remove indels from sync
```

```
perl ~/popoolation2_1201/indel_filtering/filter-sync-by-gtf.pl --input FagusPool.sync --gtf FagusPool.indels.gtf --output FagusPool.idf.sync
```

```
#Fst calculation
```

```
perl ~/popoolation2_1201/fst-sliding.pl --input FagusPool.idf.sync --output Fagus.fst --min-count 2 --min-coverage 15 --max-coverage 2% --pool-size 100 --window-size 1000 --step-size 1000
```

```
#Fisher's exact test with PoolSeq 0.35 in R
```

```
library("poolSeq")
```

```
Fagus <- read.sync(file="/data/FagusPools/FagusPool.idf.sync", gen=c(0,1,0,1), repl=c(1,1,2,2), keepOnlyBiallelic=TRUE)
```

```
afMPG <- af(sync=Fagus, repl=1, gen=0)
```

```
afMPK <- af(sync=Fagus, repl=1, gen=1)
```

```
afSPG <- af(sync=Fagus, repl=2, gen=0)
```

```
afSPK <- af(sync=Fagus, repl=2, gen=1)
```

```
write.table(afMPG, "afMPG.txt", sep="\t")
```

```
write.table(afMPK, "afMPK.txt", sep="\t")
```

```
write.table(afSPG, "afSPG.txt", sep="\t")
```

```
write.table(afSPK, "afSPK.txt", sep="\t")
```

```
covMPG <- coverage(sync=Fagus, repl=1, gen=0)
```

```
covMPK <- coverage(sync=Fagus, repl=1, gen=1)
covSPG <- coverage(sync=Fagus, repl=2, gen=0)
covSPK <- coverage(sync=Fagus, repl=2, gen=1)
```

```
AFC_MP <- afMPG - afMPK
write.table(AFC_MP, "AFC_MP.txt", sep="\t")
AFC_SP <- afSPG - afSPK
write.table(AFC_SP, "AFC_SP.txt", sep="\t")
```

```
NA_MPG <- t(covMPG * afMPG)
Na_MPG <- covMPG - NA_MPG
NA_MPK <- t(covMPK * afMPK)
Na_MPK <- covMPK - NA_MPK
```

```
NA_SPG <- t(covSPG * afSPG)
Na_SPG <- covSPG - NA_SPG
NA_SPK <- t(covSPK * afSPK)
Na_SPK <- covSPK - NA_SPK
```

```
p.valuesMPmaxcov120 <- chi.sq.test(A0 = NA_MPG, a0 = Na_MPG, At = NA_MPK, at = Na_MPK, min.cov=15, min.cnt = 3, max.cov=120, log = TRUE)
quantile(p.valuesMPmaxcov120, probs = c(0.999, 0.9999, 0.99999), na.rm = TRUE, names = TRUE)
p.valuesSPmaxcov120 <- chi.sq.test(A0 = NA_SPG, a0 = Na_SPG, At = NA_SPK, at = Na_SPK, min.cov=15, min.cnt = 3, max.cov=120, log = TRUE)
quantile(p.valuesSPmaxcov120, probs = c(0.999, 0.9999, 0.99999), na.rm = TRUE, names = TRUE)
```

```
pdf("MPmaxcov120.pdf")
plot(p.valuesMPmaxcov120, main=paste0("MP"), ylim=c(0, max(p.valuesMPmaxcov120, na.rm=TRUE)), xlab="position", ylab="-log10(p)", pch=".")
dev.off()
pdf("SPmaxcov120.pdf")
plot(p.valuesSPmaxcov120, main=paste0("SP"), ylim=c(0, max(p.valuesMPmaxcov120, na.rm=TRUE)), xlab="position", ylab="-log10(p)", pch=".")
dev.off()
```

```
write.table(p.valuesMPmaxcov120, "p.valuestotmaxcov120.txt", sep="\t")
write.table(p.valuestotmaxcov120, "p.valuestotmaxcov120.txt", sep="\t")
```

```
#cmh-Test
```

```
covG <- t(coverage(sync=Fagus, repl=1:2, gen=0))
covK <- t(coverage(sync=Fagus, repl=1:2, gen=1))
A_G <- t(af(sync=Fagus, repl=1:2, gen=0)) * covG
a_G <- covG - A_G
write.table(A_G, "afG.txt", sep="/t")
A_K <- t(af(sync=Fagus, repl=1:2, gen=1)) * covK
a_K <- covK - A_K
write.table(A_K, "afK.txt", sep="/t")
p.valuestot <- cmh.test(A0 = A_G, a0=a_G, At=A_K, at=a_K, min.cov=15, max.cov=100, min.cnt=3, log=TRUE)
write.table(p.valuestot, "p.valuestot.txt", sep="\t")
```

```
p.valuestot <- cmh.test(A0 = A_G, a0=a_G, At=A_K, at=a_K, min.cov=15, max.cov=100, min.cnt=3, log=TRUE)
pdf("cmh.pdf")
plot(p.valuestot, main=paste0("cmh_fdr"), ylim=c(0, max(p.valuestot, na.rm=TRUE)), xlab="position", ylab="-log10(p)", pch=".")
dev.off()
quantile(p.valuestot, probs = c(0.999, 0.9999, 0.99999), na.rm = TRUE, names = TRUE)
write.table(p.valuestot, "p.valuestot.txt", sep="\t")
write.table(A_G, "afG.txt", sep="/t")
write.table(A_K, "afK.txt", sep="/t")
length(p.fdr[p.fdr > 4])
```

**Suppl. Info 2.** Workflow individual reseq GWAS

####workflow beech GWAS individual reseq data#####

####May 2020 Barbara Feldmeyer#####

autotrim v.0.6.1

bcftools v.1.9

gatk v.4.1.7.0

picard v.2.20.8

plink v.1.90b6.13

samtools v.1.10

1) trim reads with autotrim (<https://github.com/schell/autotrim>)

2) index genome file

bwa index Fagus\_sylvatica\_genome\_v2\_masked.fasta

samtools faidx Fagus\_sylvatica\_genome\_v2\_masked.fasta

AND create dictionary

picard CreateSequenceDictionary.jar R=Fagus\_sylvatica\_genome\_v2\_masked.fasta

Step3a map reads to genome Fagus\_sylvatica\_genome\_v2\_masked.fasta

```
bwa mem -M -t 10 Fagus_sylvatica_genome_v2_masked.fasta $i_1_autotrim.paired.fq $i_2_autotrim.paired.fq | samtools sort -l 9 -O BAM -o  
${FILES[$SLURM_ARRAY_TASK_ID]}.sort.bam"#
```

3b)MarkDuplicates

```
picard MarkDuplicates I=$i.sort.bam O=$i.sort.bam_marked_dup.bam M=$i.sort.bam_marked_dup_metrics.txt VALIDATION_STRINGENCY=SILENT
```

```
REMOVE_DUPLICATES=true
```

3c) SortSAM

```
picard SortSam I=$i.sort.bam_marked_dup.bam O=$i.sort.bam_marked_dup.bam_sorted.bam VALIDATION_STRINGENCY=SILENT
```

```
SORT_ORDER=coordinate
```

3d) index bam

```
picard BuildBamIndex INPUT=$i.sort.bam_marked_duplicates.bam_sorted.bam
```

3e) check mapping quality with qualimap

```
qualimap multi-bamqc -r -d qualimap_commands
```

==>> PF\_001 very bad mapping quality (<1%!!!!) and skewed GC ratio in PF\_050 => remove these two samples from further analyses

3f) create file with sample.bam specific read groups

```
sed 's/.*data\\/' checkSize.xls | sed 's/\\/\\/tRGSM=/' | sed 's/_BD.*HW/ RGID=HW/' | sed 's/_L/./' | sed 's/_[0-9].fq.gz/ RGLB=SOME RGPL=illumina  
RGPU=2/' > readgroups_beech.txt
```

3g) create batch file to run picard to modify and add readgroups to .bam file header

```
picard AddOrReplaceReadGroups I="$i.sort.bam_marked_duplicates.bam_sorted.bam" O="$i.sort.bam_marked_duplicates_sorted_rehead.bam"  
RGSM=$i RGID=HWTH2DSXX.4 RGLB=SOME RGPL=illumina RGPU=2" &
```

3h) index renamed bams

```
#####
```

```
#Round1
```

```
#####
```

4a)run HaplotypeCaller in GVCF mode

```
gatk HaplotypeCaller -I $i -O $i_haploCall.gvcf -R Fagus_sylvatica_genome.fasta -ERC GVCF
```

4b) combine using combineGVCF

```
gatk CombineGVCFs -R Fagus_sylvatica_genome_v2_masked.fasta --variant PF_002.sort.bam_marked_duplicates_sorted_rehead.bam_haploCall.gvcf --  
variant PF_003.sort.bam_marked_duplicates_sorted_rehead.bam_haploCall.gvcf ... -O beech_cohort98indivs_R1.gvcf" &
```

4c) GenotypeGVCFs to jointly call Haplotypes

```
GenotypeGVCFs -R Fagus_sylvatica_genome_v2_masked.fasta -V beech_cohort98indivs_R1.gvcf -O beech_cohort98indivs_R1_genotyped.gvcf
```

4d) call and subset SNPs



```
gatk SelectVariants -V beech_cohort98indivs_R1_genotyped.gvcf --select-type-to-include SNP -O beech_cohort98indivs_R1_genotyped_SNPs.vcf
```

4e) create summary stats

```
bcftools stats beech_cohort98indivs_R1_genotyped_SNPs.vcf > beech_cohort98indivs_R1_genotyped_SNPs_summaryStats.txt
```

4f) hard-filter SNPs (we conduct this conservative hard filtration step since we don't have any pre-existing SNP set available to recalibrate SNPs)

```
gatk VariantFiltration -R Fagus_sylvatica_genome_v2_masked.fasta -V beech_cohort98indivs_R1_genotyped_SNPs.vcf -O  
beech_cohort98indivs_R1_genotyped_SNPs_hardfiltration.vcf --filter-expression 'QD < 2.0' --filter-name 'QD2' --filter-expression 'MQ < 50.0' --filter-name  
'MQ50' --filter-expression 'MQRankSum < -12.5' --filter-name 'MQRankSum-12.5' --filter-expression 'ReadPosRankSum < -8.0' --filter-name 'ReadPosRankSum-  
8' --filter-expression 'FS > 80.0' --filter-name 'FS' --filter-expression 'SOR > 4.00' --filter-name 'SOR_4' --filter-expression 'QUAL < 10.0' --filter-name 'QUAL_10'
```

-grep and save passed variants

```
grep -E '^#|PASS' beech_cohort98indivs_R1_genotyped_SNPs_hardfiltration.vcf > beech_cohort98indivs_R1_genotyped_SNPs_hardfiltrationPASS.vcf
```

4g) Baserecalibration

```
gatk --java-options "-Xmx4g" BaseRecalibrator -I $i -O fagus_recalR1_data.table -R Fagus_sylvatica_genome_v2_masked.fasta --known-sites  
beech_cohort98indivs_R1_genotyped_indels_hardfiltration.vcf --known-sites beech_cohort98indivs_R1_genotyped_SNPs_hardfiltration.vcf
```

4h) apply BQSR

```
gatk --java-options "-Xmx4g" ApplyBQSR -I $i -O $i_abqsr_R1.bam -R Fagus_sylvatica_genome_v2_masked.fasta --bqsr-recal-file  
fagus_recalR1_data.table
```

```
#####
```

```
#Round 2
```

```
#####
```

5a) R2\_haplocaller

```
gatk --java-options "-Xmx4g" HaplotypeCaller -I $i -O $i_haploCall_R2.gvcf -R Fagus_sylvatica_genome_v2_masked.fasta -ERC GVCF
```

5b) R2\_combine GVCF

```
gatk CombineGVCFs -R Fagus_sylvatica_genome_v2_masked.fasta --variant .... -O beech_cohort98indivs_R2.gvcf" &
```

5c) R2\_GenotypeGVCFs

```
gatk --java-options "-Xmx250G" GenotypeGVCFs -R Fagus_sylvatica_genome_v2_masked.fasta -V beech_cohort98indivs_R2.gvcf -O beech_cohort98indivs_R2_genotyped.gvcf
```

5d) R2\_call, select and subset SNPs

```
gatk SelectVariants -V beech_cohort98indivs_R2_genotyped.gvcf --select-type-to-include SNP -O beech_cohort98indivs_R2_genotyped_SNPs.vcf
```

create summary stats

```
bcftools stats beech_cohort98indivs_R2_genotyped_SNPs.vcf > beech_cohort98indivs_R2_genotyped_SNPs_summaryStats.txt
```

6) variant filtration

6a) Variants to table (Extract Variant Quality Score)

```
gatk --java-options "-Xmx250G" VariantsToTable R Fagus_sylvatica_genome_v2_masked.fasta -V beech_cohort98indivs_R2_genotyped_SNPs.vcf -F CHROM -F POS -F QUAL -F QD -F DP -F MQ -F MQRankSum -F FS -F ReadPosRankSum -F SOR -O cohort_all98beechSamples_genotyped_snp.table" &
```

6b) create diagnostic plots for Variants run skript in R following (<https://evodify.com/gatk-in-non-model-organism/>)

```
#####
```

```
library('gridExtra')
```

```
library('ggplot2')
```

```
VCFsnps <- read.csv('cohort_all98beechSamples_genotyped_snp.table', header = T, na.strings=c("", "NA"), sep = "\t")
```

```
VCFindel <- read.csv('cohort_all98beechSamples_genotyped_indel.table', header = T, na.strings=c("", "NA"), sep = "\t")
```

```
dim(VCFsnps)
```

```
dim(VCFindel)
```

```
VCF <- rbind(VCFsnps, VCFindel)
```

```
VCF$Variant <- factor(c(rep("SNPs", dim(VCFsnps)[1]), rep("Indels", dim(VCFindel)[1])))
```

```
snps <- '#A9E2E4'
```

```
indels <- '#F4CCCA'
```

```
DP <- ggplot(VCF, aes(x=DP, fill=Variant)) + geom_density(alpha=0.3) +  
geom_vline(xintercept=c(10,6200))
```

```
QD <- ggplot(VCF, aes(x=QD, fill=Variant)) + geom_density(alpha=.3) +
```

```
geom_vline(xintercept=2, size=0.7)
```

```
FS <- ggplot(VCF, aes(x=FS, fill=Variant)) + geom_density(alpha=.3) +  
geom_vline(xintercept=c(60, 200), size=0.7) + ylim(0,0.1)
```

```
MQ <- ggplot(VCF, aes(x=MQ, fill=Variant)) + geom_density(alpha=.3) +  
geom_vline(xintercept=40, size=0.7)
```

```
MQRankSum <- ggplot(VCF, aes(x=MQRankSum, fill=Variant)) + geom_density(alpha=.3) +  
geom_vline(xintercept=-20, size=0.7)
```

```
SOR <- ggplot(VCF, aes(x=SOR, fill=Variant)) + geom_density(alpha=.3) +  
geom_vline(xintercept=c(4, 10), size=1, colour = c(snps,indels))
```

```
ReadPosRankSum <- ggplot(VCF, aes(x=ReadPosRankSum, fill=Variant)) + geom_density(alpha=.3) +  
geom_vline(xintercept=c(-10,10,-20,20), size=1, colour = c(snps,snps,indels,indels)) + xlim(-30, 30)
```

```
svg("cohort_98individuals_R2_beech20200609.svg", height=20, width=15)  
theme_set(theme_gray(base_size = 18))  
grid.arrange(QD, DP, FS, MQ, MQRankSum, SOR, ReadPosRankSum, nrow=4)  
dev.off()  
#####
```

#### 6c) VariantFiltration

```
gatk VariantFiltration -R Fagus_sylvatica_genome_v2_masked.fasta -V beech_cohort98indivs_R2_genotyped_SNPs.vcf -O  
beech_cohort98indivs_R2_genotyped_SNPs.vcf_filtered.vcf --filter-expression 'QD < 2.0' --filter-name 'QD2' --filter-expression 'MQ < 40.0' --filter-name  
'MQ_40' --filter-expression 'SOR > 4.00' --filter-name 'SOR_4' --filter-expression 'QUAL < 10.0' --filter-name 'QUAL_10' --filter-expression 'FS > 60.0' --filter-name  
'FS_60'
```

-grep and save passed variants

```
grep -E '^#|PASS' beech_cohort98indivs_R2_genotyped_SNPs.vcf_filtered.vcf > beech_cohort98indivs_R2_genotyped_SNPs.vcf_filteredPASSED.vcf  
-stats  
bcftools stats beech_cohort98indivs_R2_genotyped_SNPs.vcf_filteredPASSED.vcf
```

## 7) Plink association analysis

### 7.1. create phenotype file containing relevant phenotype information

beech\_phenotype.phe

### 7.2. convert .vcf file to plink .ped format and keep biallic only

```
plink --vcf beech_cohort98indivs_R2_genotyped_SNPs.vcf_filteredPASSED_genotypeFiltered.vcf --biallelic-only strict --double-id --allow-extra-chr --set-missing-var-ids @:# --indep-pairwise 50 10 0.1 --out beech_cohort98indivs_SNPs
```

### 7.2b. additionally create a file with all sites, i.e. do not remove linked loci

```
plink --vcf beech_cohort98indivs_R2_genotyped_SNPs.vcf_filteredPASSED_genotypeFiltered.vcf --biallelic-only strict --double-id --allow-extra-chr --set-missing-var-ids @:# --make-bed --out beech_cohort98indivs_linkedSNPs
```

### 7.3. create PCA from linkage-pruned sites

-run plink to create PCA values

```
plink --vcf beech_cohort98indivs_R2_genotyped_SNPs.vcf_filteredPASSED_genotypeFiltered.vcf --double-id --allow-extra-chr --set-missing-var-ids @:# --extract beech_cohort98indivs_SNPs.prune.in --make-bed --pca --out beech_cohort98indivs_SNPs
```

-run R to plot the PCA

```
library(tidyverse)
pca<-read_table2("beech_cohort98indivs_SNPs.eigenvec", col_names=FALSE)
eigenval<-scan("beech_cohort98indivs_SNPs.eigenval")
pca <- pca[,-1]
names(pca)[1] <- "ind"
names(pca)[2:ncol(pca)] <- paste0("PC", 1:(ncol(pca)-1))
```

### 7.4. create missing stats

```
plink -bfile beech_cohort98indivs_SNPs --missing --out miss_stat_SNPs --allow-extra-chr
```

### 7.5. summary stats allele frequency

```
plink -bfile beech_cohort98indivs_SNPs --freq --out freq_stat_SNPs --allow-extra-chr
```

7.6. association analysis with automatic correction for multiple testing

```
plink --assoc --bfile beech_cohort98indivs_SNPs --allow-no-sex --adjust --allow-extra-chr
```