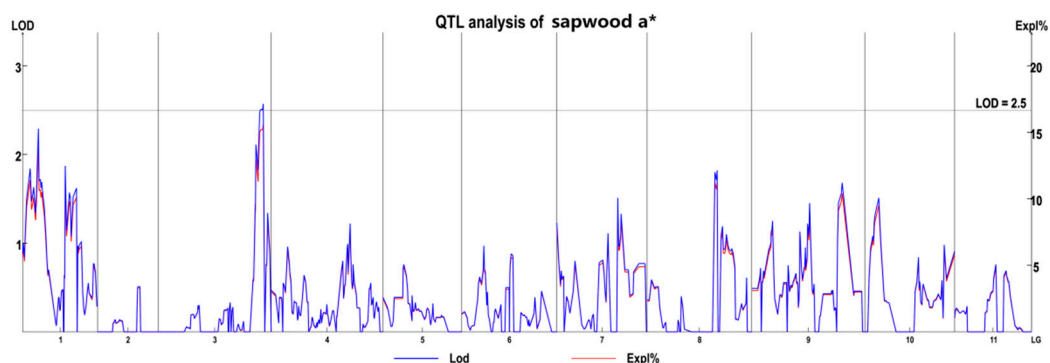


QTL analysis of growth and wood color traits in F1 family. The table indicates the position and marker numbers of each QTL, genome-wide LOD thresholds, their map position, marker number, marker name and the proportion (%) of the total phenotypic variance (PV) explained.

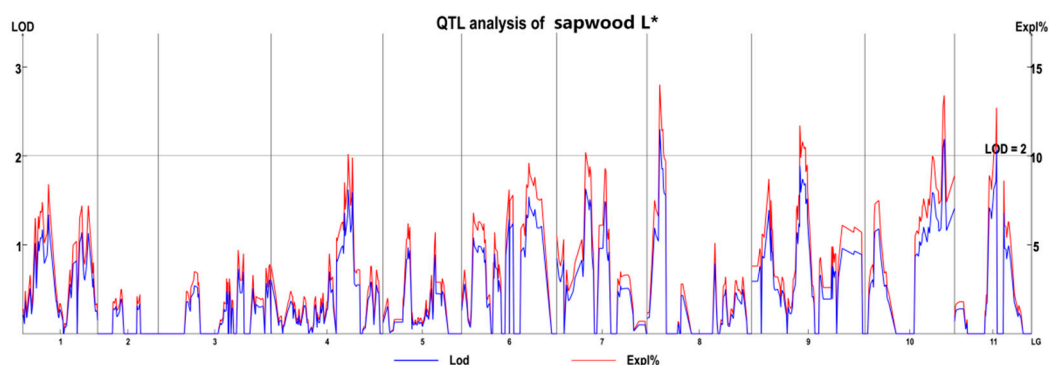
Trait	LG	Position(cM)	Marker numbers	Marker name	LOD	pv
Diameter at breast height	5	78.89	3	Marker341953,	2.11	13.30
				Marker194824,	2.11	13.30
				Marker158902	2.11	13.30
	7	12.709	14	Marker42916,	2.12	13.40
				Marker535429,	2.12	13.40
				Marker506904,	2.12	13.40
				Marker500194,	2.12	13.40
				Marker55545,	2.12	13.40
				Marker322521,	2.12	13.40
				Marker190622,	2.12	13.40
				Marker216134,	2.12	13.40
				Marker294404,	2.12	13.40
				Marker198482,	2.12	13.40
				Marker259959,	2.12	13.40
				Marker217202,	2.12	13.40
				Marker227089,	2.12	13.40
				Marker300863	2.12	13.40
heartwood diameter	1	98.823	1	Marker466118	2.02	12.80
heartwood proportion	3	127.771~129.321	11	Marker232518	2.51	15.60
				Marker297981	2.51	15.60
				Marker356559	2.51	15.60
				Marker430283	2.51	15.60
				Marker337894	2.51	15.60
				Marker354402	2.51	15.60
				Marker149004	2.51	15.60
				Marker360054	2.51	15.60
				Marker230391	2.51	15.60
				Marker211052	2.51	15.60
				Marker321676	2.51	15.60
	5	64.961	2	Marker470078	2.56	15.90
				Marker318337	2.56	15.90
heartwood a*	5	13.744	1	Marker114211	2.07	12.70
	5	43.119~ 43.53	7	Marker743514	2.06	12.70
				Marker146479	2.06	12.70
				Marker271246	2.04	12.60
				Marker496102	2.04	12.60
				Marker181901	2.04	12.60
				Marker148885	2.04	12.60
				Marker689671	2.05	12.60
	5	72.103~74.63	14	Marker78524	2.22	14.10

				Marker180177	2.22	14.10
				Marker130891	2.30	14.10
				Marker377143	2.30	14.10
				Marker163481	2.30	14.10
				Marker508121	2.30	14.10
				Marker105325	2.30	14.10
				Marker127065	2.30	14.10
				Marker367633	2.30	14.10
				Marker395316	2.30	14.10
				Marker46574	2.30	14.10
				Marker186367	2.30	14.10
				Marker71824	2.30	14.10
				Marker266066	2.30	14.10
	5	78.89	3	Marker341953	2.08	12.80
				Marker194824	2.08	12.80
				Marker158902	2.08	12.80
	8	140.072~142.751	2	Marker442260	2.22	13.60
				Marker313450	2.20	13.50
heartwood b*	11	59.907	3	Marker97557	2.66	16.00
				Marker311327	2.66	16.00
				Marker377770	2.66	16.00
heartwood L*	5	43.119~ 43.53	7	Marker743514	4.01	23.20
				Marker146479	4.01	23.20
				Marker271246	4.09	23.60
				Marker496102	4.09	23.60
				Marker181901	4.09	23.60
				Marker148885	4.09	23.60
				Marker689671	4.09	23.60
	5	46.367	7	Marker165417	4.04	23.40
				Marker163766	4.04	23.30
				Marker357435	4.04	23.30
				Marker478056	4.04	23.30
				Marker191139	4.03	23.30
				Marker68305	4.02	23.30
				Marker268186	4.02	23.30
sapwood a*	3	178.158~181.940	3	Marker288895	2.51	15.20
				Marker222650	2.50	15.20
				Marker269785	2.57	15.60
sapwood L*	10	135.802~137.718	4	Marker427491	2.09	12.08
				Marker88088	2.09	12.80
				Marker249068	2.20	13.50
				Marker57777	2.19	13.40
	11	72.570~73.820	4	Marker223975	2.07	12.70
				Marker215084	2.07	12.70

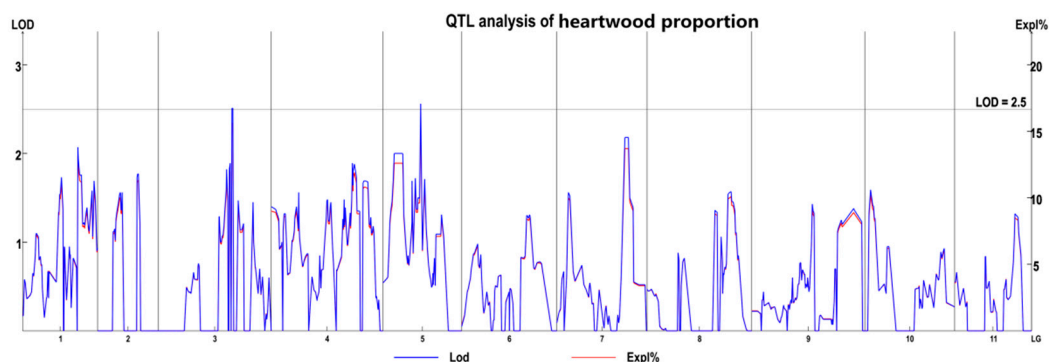
				Marker312614	2.07	12.70
				Marker370394	2.07	12.70
	8	21.831	1	Marker172270	2.30	14.00



Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for sapwood a*. The blue curve indicates LOD scores of SLAF markers against their genetic position on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position genetic map. The gray line indicates the threshold LOD score.

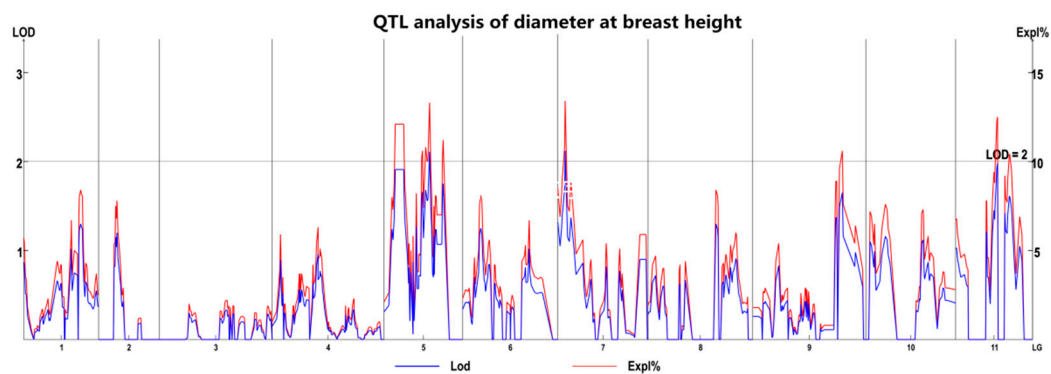


Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for sapwood L*. The blue curve indicates LOD scores of SLAF markers against their genetic position on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position genetic map. The gray line indicates the threshold LOD score.

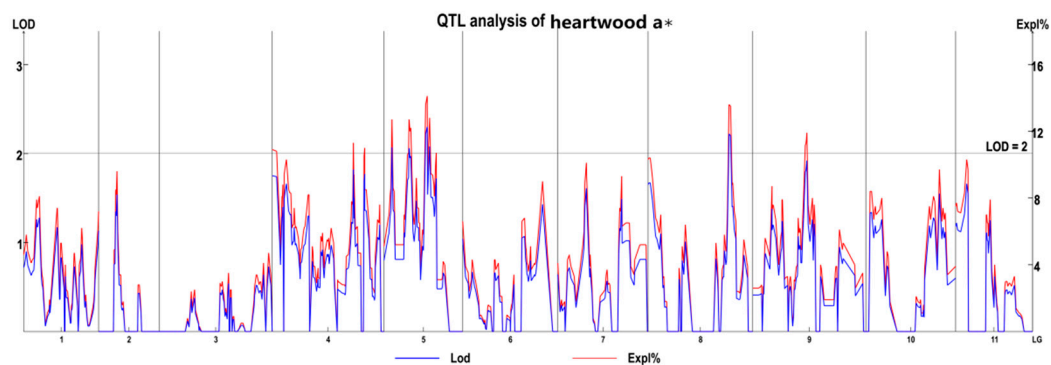


Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for heartwood proportion. The blue curve indicates LOD scores of SLAF markers against their genetic position

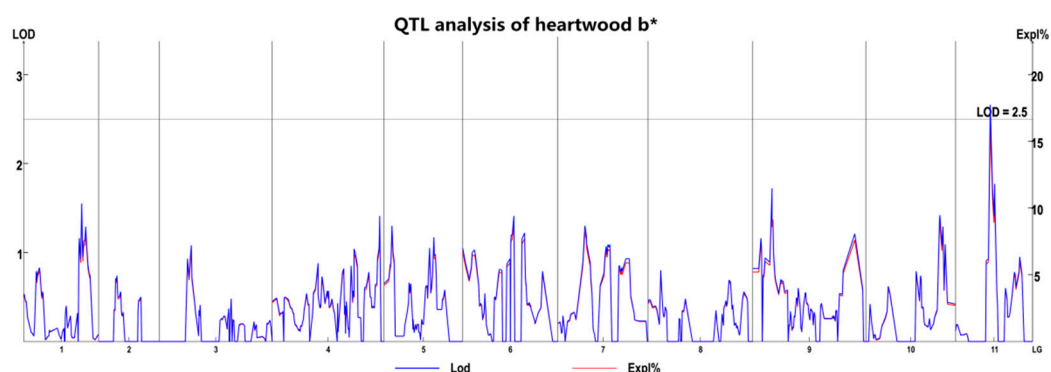
on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position on genetic map. The gray line indicates the threshold LOD score.



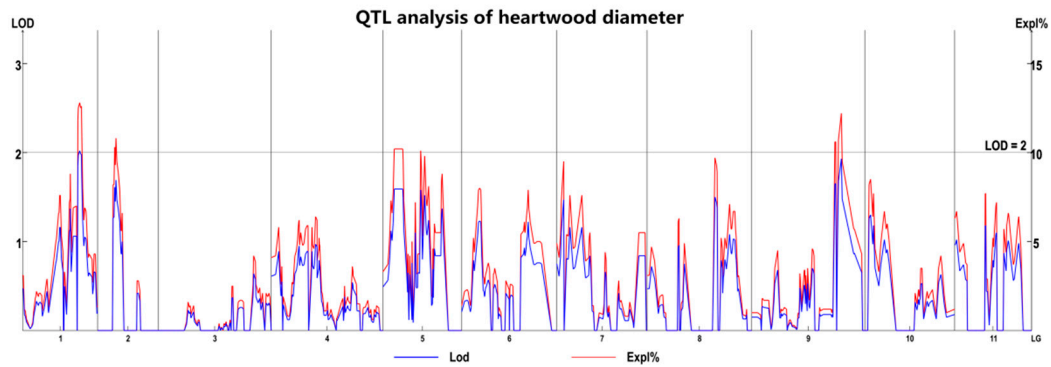
Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for diameter at breast height. The blue curve indicates LOD scores of SLAF markers against their genetic position on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position genetic map. The gray line indicates the threshold LOD score.



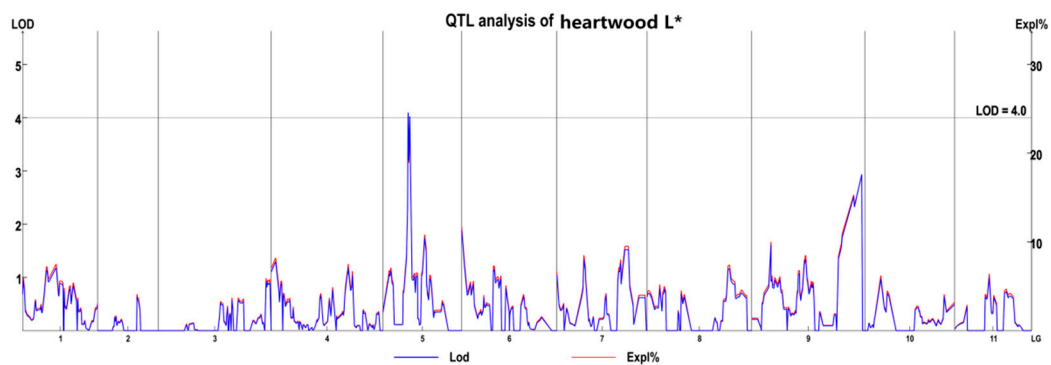
Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for heartwood a*. The blue curve indicates LOD scores of SLAF markers against their genetic position on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position genetic map. The gray line indicates the threshold LOD score.



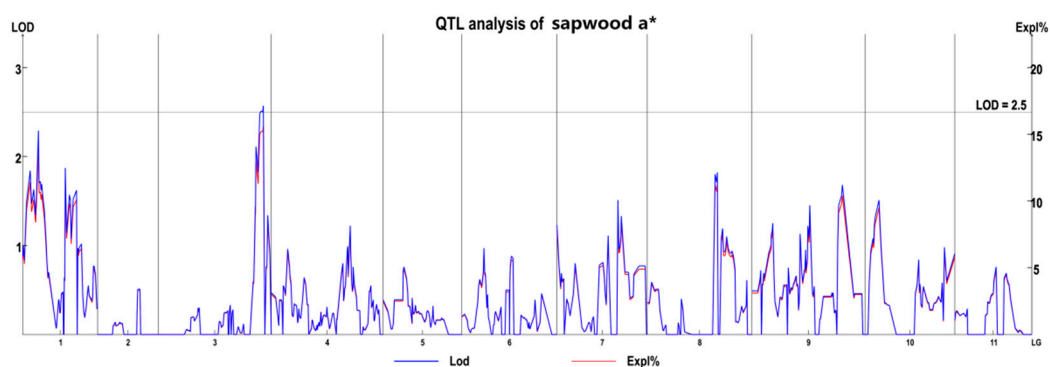
Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for heartwood b*. The blue curve indicates LOD scores of SLAF markers against their genetic position on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position genetic map. The gray line indicates the threshold LOD score.



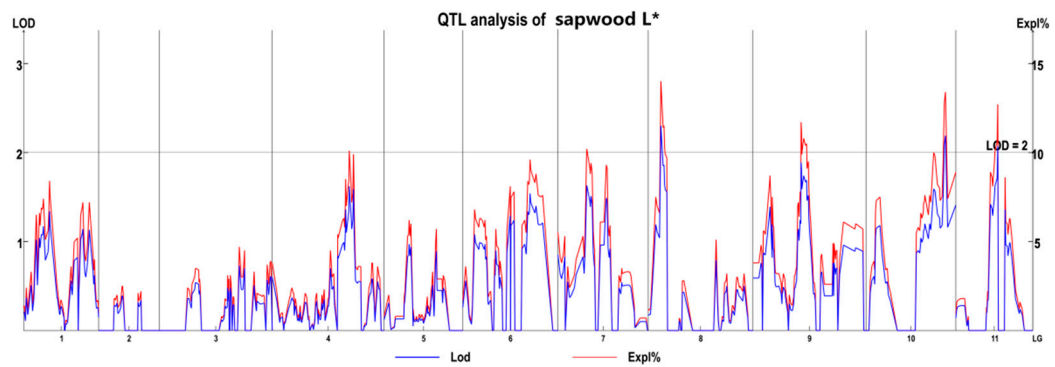
Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for heartwood diameter. The blue curve indicates LOD scores of SLAF markers against their genetic position on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position genetic map. The gray line indicates the threshold LOD score.



Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for heartwood L*. The blue curve indicates LOD scores of SLAF markers against their genetic position on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position genetic map. The gray line indicates the threshold LOD score.



Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for sapwood a*. The blue curve indicates LOD scores of SLAF markers against their genetic position on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position genetic map. The gray line indicates the threshold LOD score.



Logarithm of odds (LOD) and percent phenotypic variance explained (PVE) curves for sapwood L*. The blue curve indicates LOD scores of SLAF markers against their genetic position on genetic map. The red curve indicates the PVE of SLAF markers against their genetic position on genetic map. The gray line indicates the threshold LOD score.