Vysvětlení analýzy modelů

Tabulka výsledků ze summary modelu	data ze summary modelu	
Endopolyploidie (EI)	čepel	
Data transformation used	none	
Analysis type	lm	
Nr. of polyploid-diploid pairs tested	10	
Model summary*		
Intercept (Diploid standard)	0.681743	
Polyploidy effect (Polyploid standard)	-0.34876	
p-value	2.45E-13	
t-value	-8.377	
DF	1	
Among pair difference (p-value)	8.698E-11	
nr positively responding pairs	0	
nr negatively responding pairs	10	
Effect as ratio of predicted values	0.488	poměr EI polyploid/diploid za stan
Trait plasticity index	-2.047	pokud poměr záporný - otočení pc
Consistency index (%)	100	
Cold effect (Diploid treatment)	0.13298	
p-value	0.001848	
t-value	3.194	
DF	1	
Among pair difference (p-value)	2.544E-08	
nr positively responding pairs	7	
nr negatively responding pairs	3	
Effect as ratio of predicted values	1.195	poměr EI diploid za chladu/diploid
Trait plasticity index	1.195	
Consistency index (%)	70	
Polyploidy:cold interaction	0.03386	
p-value	0.560345	
t-value	0.584	
DF	1	
Among pair difference (p-value)	0.1076	
nr positively responding pairs	6	
nr negatively responding pairs	4	
Effect as ratio of predicted values	1.256	poměr (PT/DT)/(PS/DS)
Trait plasticity index	1.256	
Consistency index (%)	60	

Effect estimates for individual pairs

Pair (diploid) estimate in standard

Arabidopsis	1.6072
Brassica	0.358825
Cardamine	1.124425
Diplotaxis	0.611725
Erysimum	0.911175
Galium	0.3459
Papaver	0.1877
Raphanus	0.42452
Stellaria	1.051625
Symphytum	0.194335

Polyploidy

Arabidopsis	-0.555524
Brassica	-0.2471
Cardamine	-0.3799
Diplotaxis	-0.374274
Erysimum	-0.840924
Galium	-0.228916
Papaver	-0.133424
Raphanus	-0.17982
Stellaria	-0.418475
Symphytum	-0.075333

Cold

Arabidopsis	0.062775
Brassica	-0.2346
Cardamine	0.4395
Diplotaxis	-0.023675
Erysimum	0.58555
Galium	0.4065
Papaver	0.01995
Raphanus	0.15493
Stellaria	-0.358375
Symphytum	0.366365

Cold:polyploidy

Arabidopsis	0.31865000
Brassica	0.29420000
Cardamine	0.09670800
Diplotaxis	0.10312500
Erysimum	-0.39687500
Galium	-0.09728400
Papaver	0.01017500
Raphanus	-0.17610500
Stellaria	0.17347500
Symphytum	-0.13576900

odhad průměrné hodnoty EI (ze všech 10 dvojic) pro diploidy ve standardu
odhady pro jednotlivé dvojice (hodnoty estimate jsou odchylky od průměru (in

dardních podmínek
›měru
odhad efektu polyploidie - změny EI při změně faktoru polyploid (diploid->poly
odhad efektu chladu - změny EI při změně faktoru treat (standard->chlad) u dip
odhady pro jednotlivé dvojice (hodnoty estimate jsou odchylky od průměru (ef

za standardních podmínek

odhady pro jednotlivé dvojice (hodnoty estimate jsou odchylky od průměru (ef

odhady pro jednotlivé dvojice (hodnoty estimate jsou odchylky od průměru (ef

model: lm(ei ~ genus * polyploid * treat, data = de.cep)
summary modelu

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lm(formula = ei ~ genus * polyploid * treat, data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.48010 -0.07219 -0.00518  0.07354  0.69188

Coefficients:
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	Estimate	Std. Error	t value	Pr(>|t|)	
(Intercept)	0.67923	0.02973	22.85	< 2e-16	***
genus1	0.88999	0.08191	10.865	< 2e-16	***
genus2	-0.32041	0.08191	-3.912	0.000162	***
genus3	0.47297	0.09302	5.085	1.60E-06	***
genus4	-0.06751	0.08191	-0.824	0.411707	
genus5	0.23194	0.08191	2.831	0.005545	**
genus6	-0.33333	0.11197	-2.977	0.003606	**
genus7	-0.48988	0.08191	-5.98	3.05E-08	***
genus8	-0.25471	0.07446	-3.421	0.000888	***
genus9	0.37239	0.08191	4.546	1.46E-05	***
polyploidYES	-0.34876	0.04163	-8.377	2.45E-13	***
treatT	0.13298	0.04163	3.194	0.001848	**
genus1:polyploidYES	-0.17562	0.1157	-1.518	0.132014	
genus2:polyploidYES	0.10178	0.1157	0.88	0.381004	
genus3:polyploidYES	-0.07111	0.13142	-0.541	0.589568	
genus4:polyploidYES	-0.02552	0.13861	-0.184	0.854281	
genus5:polyploidYES	-0.49217	0.1157	-4.254	4.54E-05	***
genus6:polyploidYES	0.05978	0.13861	0.431	6.67E-01	
genus7:polyploidYES	0.21368	0.1157	1.847	0.067552	.
genus8:polyploidYES	0.16894	0.11901	1.42	0.158676	
genus9:polyploidYES	-0.06972	0.1157	-0.603	0.548066	
genus1:treatT	-0.03223	0.1157	-0.279	0.781119	
genus2:treatT	-0.36758	0.1157	-3.177	0.001949	**
genus3:treatT	0.15969	0.13142	1.215	0.227018	
genus4:treatT	-0.15665	0.1157	-1.354	0.178617	
genus5:treatT	0.45257	0.1157	3.912	0.000162	***
genus6:treatT	0.27352	0.14545	1.881	0.062776	.
genus7:treatT	-0.11468	0.1157	-0.991	0.323845	
genus8:treatT	0.02195	0.11055	0.199	0.842987	
genus9:treatT	-0.49135	0.1157	-4.247	4.67E-05	***
polyploidYES:treatT	0.03386	0.05796	0.584	0.560345	
genus1:polyploidYES:treatT	0.25364	0.16329	1.553	1.23E-01	
genus2:polyploidYES:treatT	0.26021	0.16329	1.594	1.14E-01	
genus3:polyploidYES:treatT	0.22187	0.18556	1.196	0.234493	
genus4:polyploidYES:treatT	0.06926	0.18025	0.384	0.701558	
genus5:polyploidYES:treatT	-0.43074	0.16329	-2.638	0.009601	**
genus6:polyploidYES:treatT	-0.09085	0.19072	-0.476	0.6348	
genus7:polyploidYES:treatT	-0.02204	0.16329	-0.135	0.89291	
genus8:polyploidYES:treatT	-0.20997	0.16566	-1.267	0.207761	

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genus9:polyploidYES:treatT         0.13961    0.16329     0.855    0.39449
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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.1707 on 106 degrees of freedom
Multiple R-squared:  0.9157,    Adjusted R-squared:  0.8847
F-statistic: 29.54 on 39 and 106 DF,  p-value: < 2.2e-16
Multiple R-squared:  0.9149,    Adjusted R-squared:  0.8858
F-statistic: 31.42 on 39 and 114 DF,  p-value: < 2.2e-16
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anova modelu

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Response: ei
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	Df	Sum Sq	Mean Sq	F value	Pr(>F)
genus	9	23.952	2.6613	91.3554	< 2.2e-16
polyploid	1	4.257	4.257	146.1304	< 2.2e-16
treat	1	0.641	0.641	22.0024	8.16E-06
genus:polyploid	9	2.5035	0.2782	9.5485	1.51E-10
genus:treat	9	1.7443	0.1938	6.653	1.69E-07
polyploid:treat	1	0.0122	0.0122	0.4176	5.20E-01
genus:polyploid:treat	9	0.451	0.0501	1.7203	9.32E-02
Residuals	106	3.088	0.0291		

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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
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výpočet odhadu pro jednotlivé dvojice (estimate je odchylka od interceptu)

1.56922
0.35882
1.1522
0.61172
0.91117
0.3459
0.18935
0.42452
1.05162
0.17778
-0.52438
-0.24698
-0.41987
-0.37428
-0.84093
-0.28898
-0.13508
-0.17982
-0.41848
-0.0588
0.10075
-0.2346
0.29267
-0.02367
0.58555
0.4065
0.0183
0.15493
-0.35837
0.38774
0.2875
0.29407
0.25573
0.10312
-0.39688
-0.05699
0.01182
-0.17611

0.17347
-0.15713

***
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Endopolyploidie	čepel	řapík	hlavní kořen
Data transformation used	none	none	none
Analysis type (random factor)	lm	lm	lm
Nr. of polyploid-diploid pairs tested	10	10	10
Model summary			
Intercept	0.67923	1.04712	0.57676
Polyploidy effect	-0.34876	-0.37727	-0.23248
p-value	2.45E-13	< 2e-16	< 2e-16
t-value	-8.377	-11.674	-10.097
DF	1	1	1
Among pair difference (p-value)**	1.513E-10	2.89E-15	< 2.2e-16
nr positively responding pairs***	0	0	1
nr negatively responding pairs***	10	10	9
Effect as ratio of predicted values	0.487	0.640	0.597
Trait plasticity index	-2.055	-1.563	-1.675
Consistency index (%)	100	100	90
Cold effect	0.13298	0.01729	0.1472
p-value	0.001848	0.593863	4.46E-09
t-value	3.194	0.535	6.393
DF	1	1	1
Among pair difference (p-value)**	1.686E-07	3.69E-07	0.0008549
nr positively responding pairs***	7	5	10
nr negatively responding pairs***	3	5	0
Effect as ratio of predicted values	1.196	1.017	1.255
Trait plasticity index	1.196	1.017	1.255
Consistency index (%)	70	50	100
Polyploidy:cold interaction	0.01903	0.06852	-0.06485
p-value	0.737668	0.130774	0.045594
t-value	0.336	1.523	-2.023
DF	1	1	1
Among pair difference (p-value)**	0.09318	0.02893	0.0244501
nr positively responding pairs***	6	7	4
nr negatively responding pairs***	4	3	6
Effect as ratio of predicted values	1.221	1.110	0.987
Trait plasticity index	1.221	1.110	-1.013
Consistency index (%)	60	70	60

Effect estimates for individual pairs			
Pair (diploid) estimate in standard			
Arabidopsis	1.56922	1.46312	0.6258
Brassica	0.35882	0.8209	0.47857
Cardamine	1.1522	1.47253	0.7118
Diplotaxis	0.61172	0.91017	0.41662
Erysimum	0.91117	1.08112	0.61227
Galium	0.3459	0.73825	0.825

Papaver	0.18935	1.09597	0.35475
Raphanus	0.42452	1.01634	0.65408
Stellaria	1.05162	1.32057	0.70692
Symphytum	0.17778	0.55223	0.38179
Polyploidy			
Arabidopsis	-0.52438	-0.44935	-0.33793
Brassica	-0.24698	-0.2706	-0.18938
Cardamine	-0.41987	-0.3129	-0.0684
Diplotaxis	-0.37428	-0.24832	0.01762
Erysimum	-0.84093	-0.92082	-0.5526
Galium	-0.28898	-0.54732	-0.37213
Papaver	-0.13508	-0.4603	-0.17048
Raphanus	-0.17982	-0.2086	-0.21528
Stellaria	-0.41848	-0.22857	-0.27065
Symphytum	-0.0588	-0.12592	-0.16557
Cold			
Arabidopsis	0.10075	0.04878	0.15872
Brassica	-0.2346	-0.2006	0.10345
Cardamine	0.29267	0.23274	0.2193
Diplotaxis	-0.02367	-0.19457	0.0285
Erysimum	0.58555	0.1102	0.2555
Galium	0.4065	0.16389	0.11856
Papaver	0.0183	-0.07652	0.22792
Raphanus	0.15493	-0.13981	0.12149
Stellaria	-0.35837	-0.21882	0.05512
Symphytum	0.38774	0.44761	0.18344
Cold:polyploidy			
Arabidopsis	0.28750000	0.17715000	0.07118
Brassica	0.29407000	0.10088000	-0.08262
Cardamine	0.25573000	0.09660000	0.19577
Diplotaxis	0.10312000	0.19973000	0.05393
Erysimum	-0.39688000	-0.14520000	-0.26092
Galium	-0.05699000	0.26373000	-0.27547
Papaver	0.01182000	0.12988000	-0.1649
Raphanus	-0.17611000	0.32133000	0.01961
Stellaria	0.17347000	-0.01962000	-0.01737
Symphytum	-0.15713000	-0.43928000	-0.18771

vedlejší kořen		Dry Shoot	Dry Root	Fresh Shoot	Fresh Root		
none		ln	ln	ln	ln		
lm		lm	lm	lm	lm		
10		10	10	10	10		
0.355815		-5.723719	-6.168973	-3.6448	-4.158169		
-0.180669		0.002283	-0.12345	0.06185	-0.087227		
< 2e-16		0.976253	0.177279	0.387763	0.361987		
-16.551		0.030	-1.358	0.867	-0.916		
1		1	1	1	1		
< 2.2e-16		7.016E-15	6.762E-07	< 2.2e-16	0.00000073		
1		5	4	6	3		
9		5	6	4	7		
0.492		1.002	0.884	1.064	0.916		
-2.032		1.002	-1.131	1.064	-1.091		
90		50	60	60	70		
0.025013		-0.892366	-0.913136	-1.29109	-1.07042		
0.025875		< 2e-16	< 2e-16	< 2e-16	< 2e-16		
2.26		-11.664	-10.046	-18.102	-11.235		
1		1	1	1	1		
1.87E-12		2.382E-14	< 2.2e-16	1.503E-11	5.768E-16		
5		0	2	0	0		
5		10	8	10	10		
1.070		0.410	0.401	0.275	0.343		
1.070		-2.441	-2.492	-3.637	-2.917		
50		100	80	100	100		
0.023454		0.175419	0.407581	0.13582	0.454252		
0.127215		0.102538	0.001697	0.174259	0.000877		
1.537		1.647	3.221	1.368	3.425		
1		1	1	1	1		
3.48E-05		0.0001794	0.114387	0.0002111	0.036085		
6		7	8	4	8		
4		3	2	6	2		
1.193		1.192	1.503	1.145	1.575		
1.193		1.192	1.503	1.145	1.575		
60		70	80	40	80		

0.193825	-5.470537	-6.230756	-3.38974	-4.50867		
0.222725	-5.574193	-6.096526	-3.54476	-4.162583		
0.4028	-5.213475	-5.930968	-3.38563	-3.642342		
0.227133	-6.1422	-6.844419	-3.90951	-5.164965		
0.20275	-5.976611	-6.739453	-4.11696	-4.861308		
0.56845	-6.335792	-6.805551	-4.30618	-4.704336		

0.2465	-6.054173	-6.628301	-3.8305	-4.088505		
0.38382	-5.264417	-5.213071	-3.01665	-3.129344		
0.547	-5.76411	-6.380449	-3.43357	-4.296478		
0.563147	-5.441682	-4.820236	-3.5145	-3.023159		
-0.087075	-0.207917	-0.242258	-0.0457	-0.17169		
-0.097875	0.27871	0.042977	0.27709	-0.141224		
-0.187167	0.647867	0.439235	0.73047	0.607291		
0.011766	0.294043	-0.519727	0.29067	-0.326712		
-0.19235	-0.438047	-0.292508	-0.59332	-0.105135		
-0.47145	-0.162083	-0.201947	-0.10948	-0.147476		
-0.1618	-0.058099	0.139959	0.04721	-0.02843		
-0.118387	0.078234	-0.02889	0.29992	0.184217		
-0.18235	-0.732127	-0.868046	-0.55181	-0.916226		
-0.320002	0.322249	0.296705	0.27345	0.173115		
-0.04145	-0.366422	-0.714867	-1.08664	-0.745893		
0.0708	-0.770771	-1.362707	-1.14349	-1.407651		
0.06445	-1.992992	-1.901288	-2.0692	-2.104412		
0.171717	-1.157393	-0.870425	-1.73879	-0.919389		
-0.00755	-0.396423	-0.098951	-0.79256	-0.206913		
0.074083	-0.275051	-0.077456	-0.70644	-0.357588		
-0.09175	-0.311345	0.11562	-0.64022	-0.023557		
0.173505	-1.454736	-1.945726	-1.81137	-2.135201		
-0.076575	-0.16293	0.051314	-0.82561	-0.183578		
-0.0871	-2.035597	-2.326874	-2.09658	-2.620018		
-0.005225	0.103917	0.40777	-0.09294	0.413961		
-0.05075	-0.167085	0.528302	-0.03079	0.575559		
0.09625	1.514825	1.011363	1.34147	1.19557		
-0.200916	0.0349	0.449975	-0.08767	0.221107		
0.020175	-1.021833	-0.565513	-0.95656	-0.729097		
-0.036083	0.93442	1.066083	0.80559	1.105037		
0.06695	-0.327998	-0.24535	-0.36554	-0.123321		
0.036137	0.099666	0.262845	-0.02425	0.139695		
0.083725	0.178017	0.408904	0.28548	0.6545		
0.224277	0.405361	0.751431	0.48341	1.089509		

Dry root/shoot	Fresh root/shoo	Fresh biomass	Dry biomass	WC shoot	WC root
ln	ln	ln	ln	none	none
lm	lm	lm	lm	lm	lm
10	10	10	10	10	10
-0.445255	-0.48993	-3.211356	-5.203641	0.8721785	0.8623678
-0.125733	-0.17253	0.018111	-0.034798	0.0053632	0.0066097
0.016023	0.003569	0.801026	0.66441	0.206381	0.086723
-2.448	-2.981	0.253	-0.435	1.271	1.729
1	1	1	1	1	1
4.869E-07	1.52E-05	2.247E-13	9.946E-12		
2	1	6	6	8	6
8	9	4	4	2	4
0.882	0.842	1.018	0.966	1.006	1.008
-1.134	-1.188	1.018	-1.035	1.006	1.008
80	90	60	40	80	60
-0.02077	0.19723	-1.189396	-0.902361	-0.0617993	-0.0160037
0.686788	0.000929	< 2e-16	< 2e-16	< 2e-16	0.0000587
-0.404	3.408	-16.592	-11.282	-14.650	-4.186
1	1	1	1	1	1
2.201E-11	1.29E-14	3.57E-15	6.348E-16		
6	6	0	0	0	1
4	4	10	10	10	9
0.979	1.218	0.304	0.406	0.929	0.981
-1.021	1.218	-3.285	-2.465	-1.076	-1.019
40	60	100	100	100	90
0.232162	0.34187	0.255247	0.271631	-0.0036248	0.0037145
0.001566	0.0000461	0.011956	0.016379	0.538433	0.486768
3.246	4.252	2.558	2.439	-0.617	0.698
1	1	1	1	1	1
0.0656671	0.7092	0.0004192	0.003948		
9	9	6	8	4	7
1	1	4	2	6	3
1.261	1.408	1.291	1.312	0.996	1.004
1.261	1.408	1.291	1.312	-1.004	1.004
90	90	60	80	60	70

-0.76022	-1.11893	-3.103253	-5.084499	0.874925	0.82115
-0.522334	-0.61782	-3.130918	-5.105492	0.868975	0.854325
-0.717494	-0.25672	-2.808564	-4.814724	0.839	0.8984333
-0.70222	-1.25546	-3.654188	-5.737613	0.890875	0.81235
-0.762843	-0.74435	-3.726459	-5.593386	0.843625	0.8468
-0.46976	-0.39816	-3.823484	-5.845487	0.8623	0.8771

-0.574129	-0.25801	-3.260813	-5.601208	0.892475	0.921075
0.051345	0.12173	-2.729307	-4.532011	0.89276	0.81282
-0.616341	-0.86292	-3.080135	-5.331705	0.9025	0.874725
0.621446	0.49134	-2.796439	-4.390285	0.85435	0.9048997
-0.03434	-0.126	-0.070116	-0.217348	0.0182	0.01085
-0.235733	-0.41832	0.121232	0.197371	0.002425	-0.0294
-0.208632	-0.12319	0.681472	0.585995	0.0125	0.0158334
-0.813769	-0.61739	0.179654	0.088687	0.000525	0.03285
0.145539	0.48817	-0.410205	-0.389067	-0.025825	0.026
-0.039865	-0.038	-0.138352	-0.176955	0.004775	0.006375
0.198058	-0.07565	0.015855	0.013811	0.0106	-0.0145
-0.107124	-0.35014	0.299113	0.015694	0.0222067	0.0409134
-0.135919	-0.36442	-0.643759	-0.775319	0.016175	-0.0054
-0.025545	-0.10036	0.146216	0.309151	-0.0079497	-0.0174248
-0.348445	0.34075	-1.008537	-0.463986	-0.133175	-0.005925
-0.591936	-0.26416	-1.238441	-0.953265	-0.056375	-0.0061
0.091703	-0.03521	-2.071023	-1.945377	-0.0166666	-0.0231
0.286968	0.81941	-1.490903	-1.051875	-0.08445	-0.008275
0.297471	0.58565	-0.561693	-0.287028	-0.075775	-0.017175
0.197594	0.34886	-0.52538	-0.198779	-0.0635666	-0.0398667
0.426965	0.61666	-0.328564	-0.141421	-0.0429	-0.0119
-0.490989	-0.55825	-1.680929	-1.689375	-0.04461	0.039505
0.214244	0.64204	-0.588654	-0.082002	-0.091225	-0.0323
-0.291275	-0.52345	-2.399836	-2.210502	-0.0092498	-0.0549003
0.303853	0.5069	0.054417	0.184864	-0.025775	0.002225
0.695388	0.60635	0.141718	0.046692	0.022625	0.007725
-0.503461	-0.1459	1.267375	1.36377	-0.0248333	0.0214
0.415073	0.30877	-0.160257	0.09791	-0.025925	-0.040075
0.45632	0.22746	-0.750036	-0.79912	0.00435	-0.022
0.131663	0.29945	0.970503	0.98996	-0.0211083	0.0088583
0.082648	0.24221	-0.228621	-0.258775	-0.000675	0.009875
0.163178	0.39837	-0.02918	0.192818	-0.0075566	-0.0363133
0.230887	0.36902	0.383217	0.265086	0.030225	0.033425
0.346071	0.60607	0.903334	0.633105	0.0124252	0.052025

diploid za chladu/diploid v teple

3 5

polyploid se zapoctenou interakci/polyploid bez zapocteni interakce

1.500

1.166667

22.47679
9.241803
0.721498
10.20544
4.411936
1.594479
3.605042
-1.12922
2.824303
0.168484

9 12

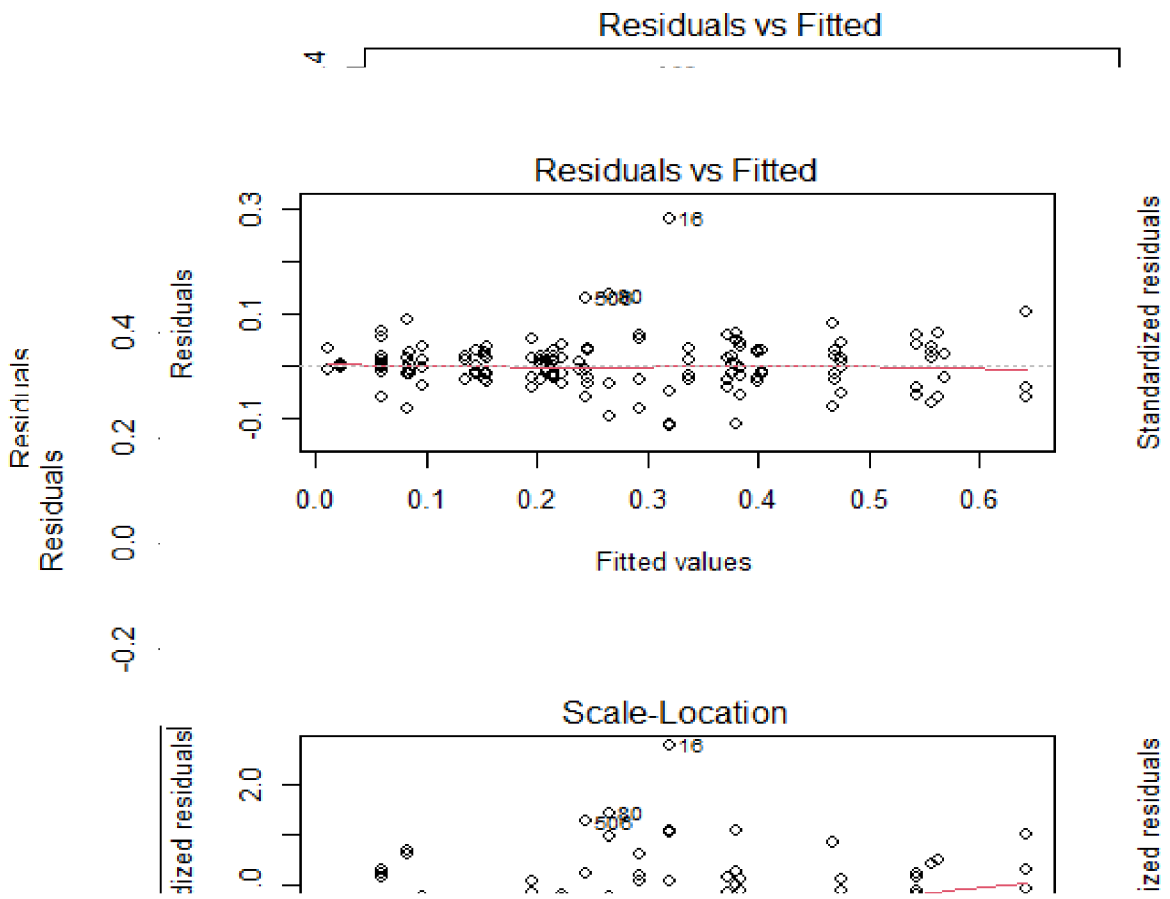
Endopolyploidie (EI)	čepel	řapík	hlavní kořen
Intercept	0.679	1.047	0.577
Efekt polyploidie	-0.349	-0.377	-0.232
p-hodnota	<0.001	<0.001	<0.001
t-hodnota	-8.377	-11.674	-10.097
Index plasticity znaku	-2.055	-1.563	-1.675
Konzistence trendu (%)	100	100	90
Efekt chladu	0.133	0.017	0.147
p-hodnota	0.002	0.594	<0.001
t-hodnota	3.194	0.535	6.393
Index plasticity znaku	1.196	1.017	1.255
Konzistence trendu (%)	70	50	100
Efekt interakce polyploidie a chladu	0.019	0.069	-0.065
p-hodnota	0.738	0.131	0.046
t-hodnota	0.336	1.523	-2.023
Index plasticity znaku	1.221	1.110	-1.013
Konzistence trendu (%)	60	70	60

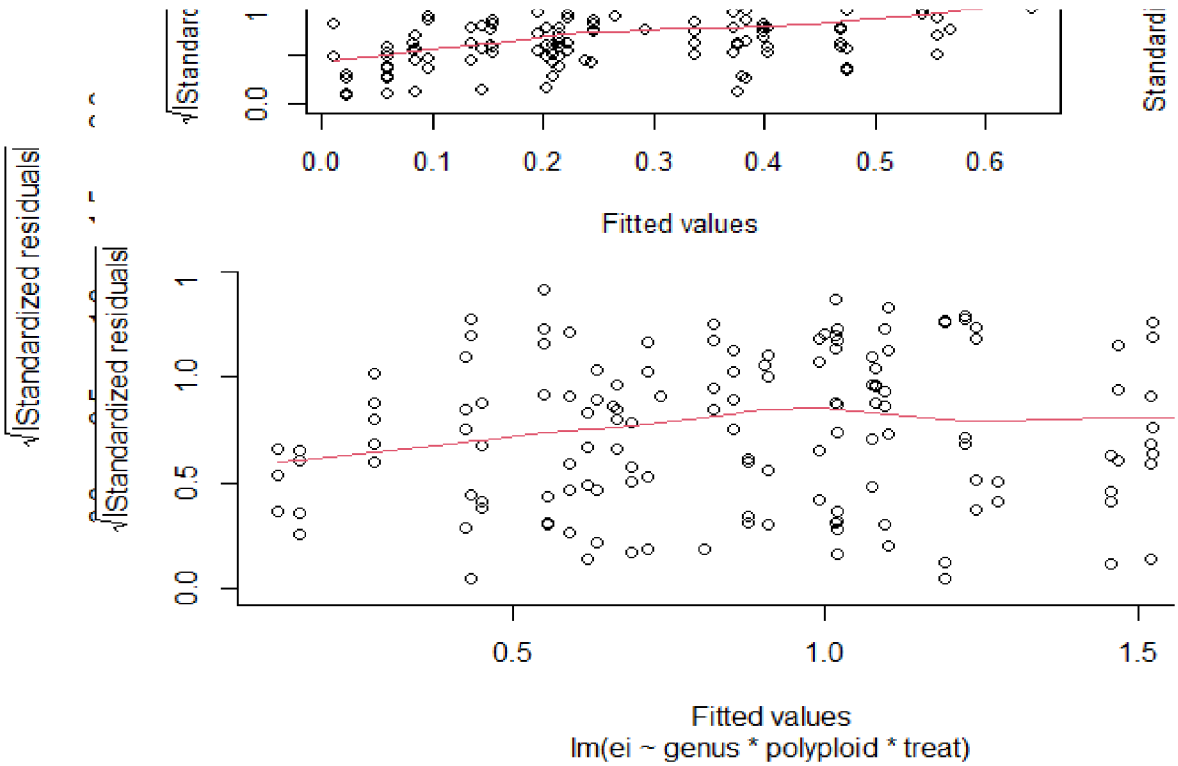
Effect estimates for individual pairs

Diploid standard	čepel	řapík	hlavní kořen
Arabidopsis	1.569	1.463	0.626
Brassica	0.359	0.821	0.479
Cardamine	1.152	1.473	0.712
Diplotaxis	0.612	0.910	0.417
Erysimum	0.911	1.081	0.612
Galium	0.346	0.738	0.825
Papaver	0.189	1.096	0.355
Raphanus	0.425	1.016	0.654
Stellaria	1.052	1.321	0.707
Symphytum	0.178	0.552	0.382
Efekt polyploidie	čepel	řapík	hlavní kořen
Arabidopsis	-0.524	-0.449	-0.338
Brassica	-0.247	-0.271	-0.189
Cardamine	-0.420	-0.313	-0.068
Diplotaxis	-0.374	-0.248	0.018
Erysimum	-0.841	-0.921	-0.553
Galium	-0.289	-0.547	-0.372
Papaver	-0.135	-0.460	-0.170
Raphanus	-0.180	-0.209	-0.215
Stellaria	-0.418	-0.229	-0.271
Symphytum	-0.059	-0.126	-0.166
Efekt chladu	čepel	řapík	hlavní kořen
Arabidopsis	0.101	0.049	0.159
Brassica	-0.235	-0.201	0.103
Cardamine	0.293	0.233	0.219
Diplotaxis	-0.024	-0.195	0.029

Erysimum	0.586	0.110	0.256
Galium	0.407	0.164	0.119
Papaver	0.018	-0.077	0.228
Raphanus	0.155	-0.140	0.121
Stellaria	-0.358	-0.219	0.055
Symphytum	0.388	0.448	0.183

Efekt interakce polyploidie a chladu	čepel	řapík	hlavní kořen
Arabidopsis	0.288	0.177	0.071
Brassica	0.294	0.101	-0.083
Cardamine	0.256	0.097	0.196
Diplotaxis	0.103	0.200	0.054
Erysimum	-0.397	-0.145	-0.261
Galium	-0.057	0.264	-0.275
Papaver	0.012	0.130	-0.165
Raphanus	-0.176	0.321	0.020
Stellaria	0.173	-0.020	-0.017
Symphytum	-0.157	-0.439	-0.188



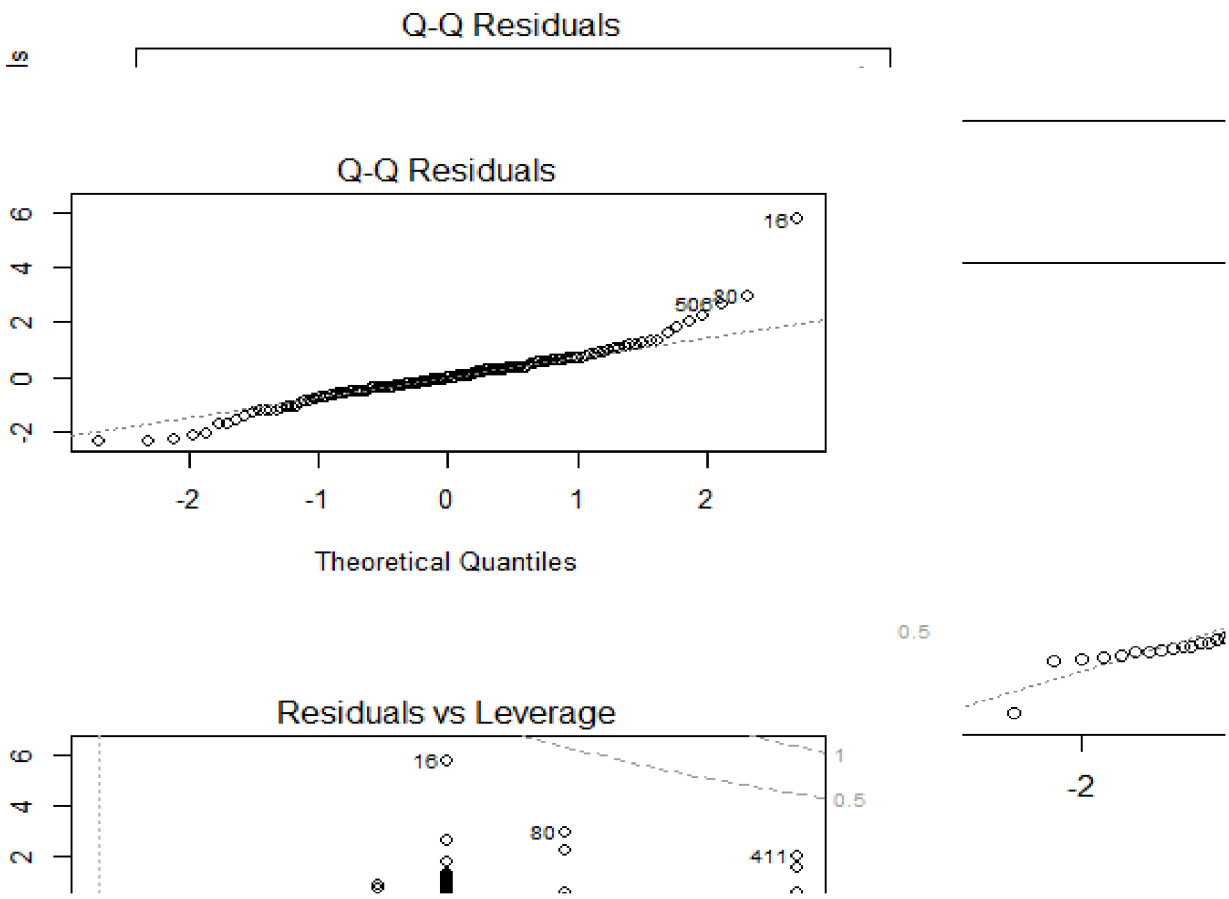

√|Standardized residuals|
0.0
0.5
1.0
1
0.5
1.0
1.5
Fitted values
lm(ei ~ genus * polyploid * treat)
√|Standarc
0.0
1
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fitted values
Standardi

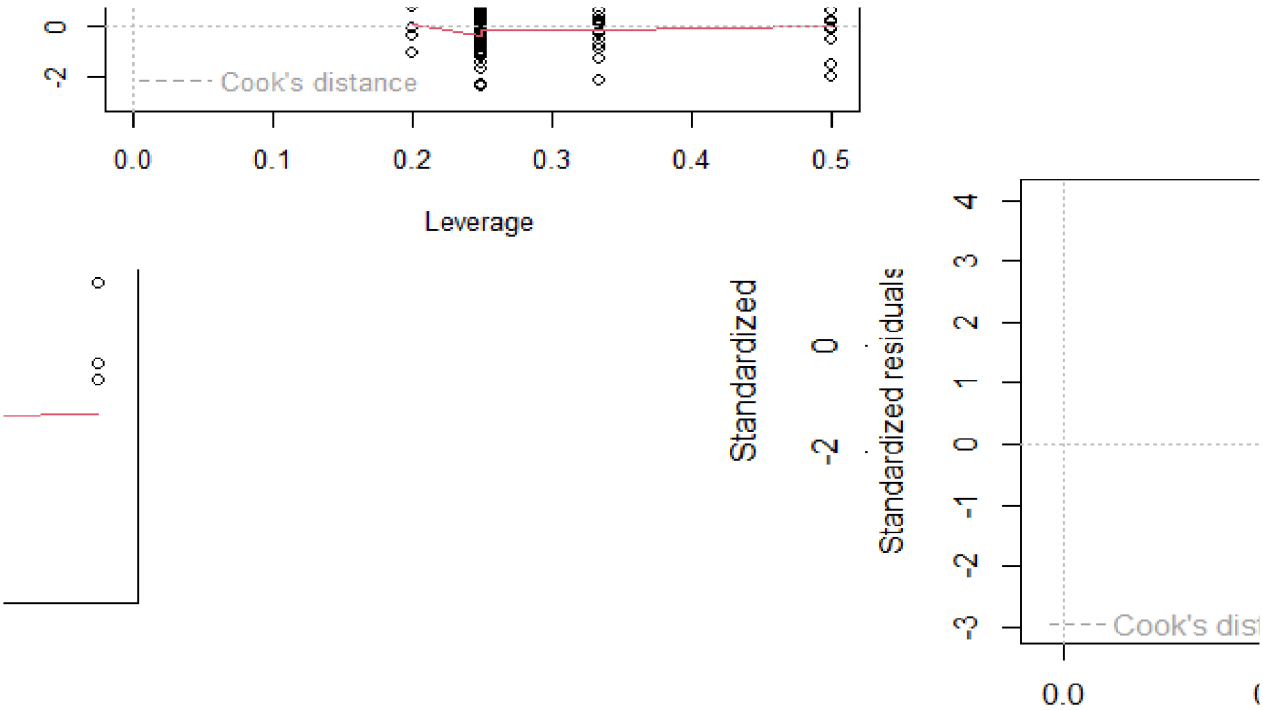
vedlejší kořen		Rychlost růstu (g/den) (log)	Suchá nadzemn	Suchá podzemn	Čerstvá nadzemı
0.356		**Intercept**	-5.724	-6.169	-3.645
-0.181		**Efekt polyploidie**	0.002	-0.123	0.062
<0.001		p-hodnota	0.976	0.177	0.388
-16.551		t-hodnota	0.030	-1.358	0.867
-2.032		Index plasticity znaku	1.002	-1.131	1.064
90		Konzistence trendu (%)	50	60	60
0.025		**Efekt chladu**	-0.892	-0.913	-1.291
0.026		p-hodnota	<0.001	<0.001	<0.001
2.260		t-hodnota	-11.664	-10.046	-18.102
1.070		Index plasticity znaku	-2.441	-2.492	-3.637
50		Konzistence trendu (%)	100	80	100
0.023		**Efekt interakce polyploidie a ch**	0.175	0.408	0.136
0.127		p-hodnota	0.103	0.002	0.174
1.537		t-hodnota	1.647	3.221	1.368
1.193		Index plasticity znaku	1.192	1.503	1.145
60		Konzistence trendu (%)	70	80	40

Effect estimates for individual

vedlejší kořen	**Diploid standard**	Suchá nadzemn	Suchá podzemn	Čerstvá nadzemı
0.194	*Arabidopsis*	-5.471	-6.231	-3.390
0.223	*Brassica*	-5.574	-6.097	-3.545
0.403	*Cardamine*	-5.213	-5.931	-3.386
0.227	*Diplotaxis*	-6.142	-6.844	-3.910
0.203	*Erysimum*	-5.977	-6.739	-4.117
0.568	*Galium*	-6.336	-6.806	-4.306
0.247	*Papaver*	-6.054	-6.628	-3.831
0.384	*Raphanus*	-5.264	-5.213	-3.017
0.547	*Stellaria*	-5.764	-6.380	-3.434
0.563	*Symphytum*	-5.442	-4.820	-3.515
vedlejší kořen	**Efekt polyploidie**			
-0.087	*Arabidopsis*	-0.208	-0.242	-0.046
-0.098	*Brassica*	0.279	0.043	0.277
-0.187	*Cardamine*	0.648	0.439	0.730
0.012	*Diplotaxis*	0.294	-0.520	0.291
-0.192	*Erysimum*	-0.438	-0.293	-0.593
-0.471	*Galium*	-0.162	-0.202	-0.109
-0.162	*Papaver*	-0.058	0.140	0.047
-0.118	*Raphanus*	0.078	-0.029	0.300
-0.182	*Stellaria*	-0.732	-0.868	-0.552
-0.320	*Symphytum*	0.322	0.297	0.273
vedlejší kořen	**Efekt chladu**			
-0.041	*Arabidopsis*	-0.366	-0.715	-1.087
0.071	*Brassica*	-0.771	-1.363	-1.143
0.064	*Cardamine*	-1.993	-1.901	-2.069
0.172	*Diplotaxis*	-1.157	-0.870	-1.739

-0.008	*Erysimum*	-0.396	-0.099	-0.793
0.074	*Galium*	-0.275	-0.077	-0.706
-0.092	*Papaver*	-0.311	0.116	-0.640
0.174	*Raphanus*	-1.455	-1.946	-1.811
-0.077	*Stellaria*	-0.163	0.051	-0.826
-0.087	*Symphytum*	-2.036	-2.327	-2.097
vedlejší kořen	**Efekt interakce polyploidie a chladu**			
-0.005	*Arabidopsis*	0.104	0.408	-0.093
-0.051	*Brassica*	-0.167	0.528	-0.031
0.096	*Cardamine*	1.515	1.011	1.341
-0.201	*Diplotaxis*	0.035	0.450	-0.088
0.020	*Erysimum*	-1.022	-0.566	-0.957
-0.036	*Galium*	0.934	1.066	0.806
0.067	*Papaver*	-0.328	-0.245	-0.366
0.036	*Raphanus*	0.100	0.263	-0.024
0.084	*Stellaria*	0.178	0.409	0.285
0.224	*Symphytum*	0.405	0.751	0.483

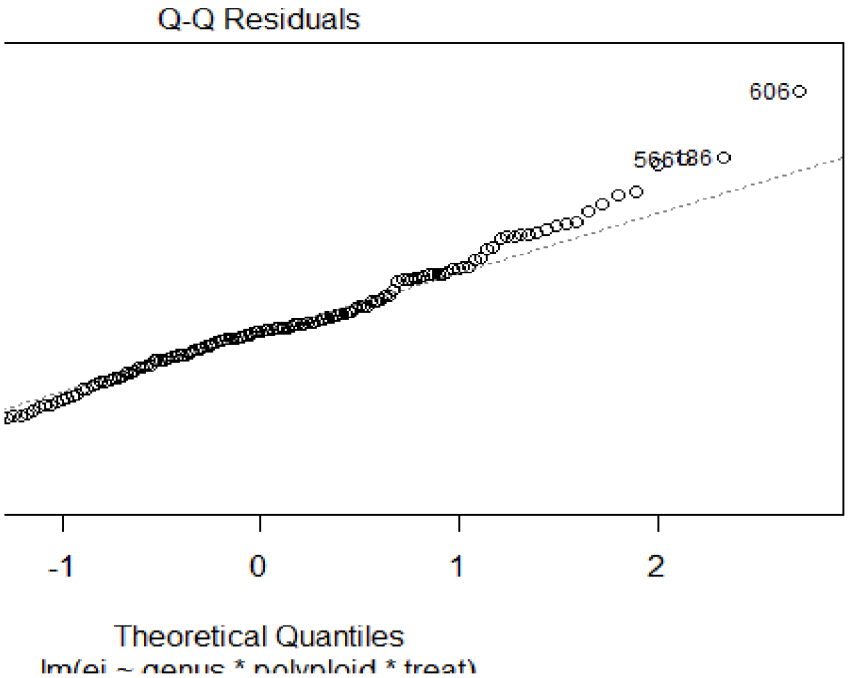



Standardized residuals
Cook's distance
Leverage
Standardized
Cook's dist

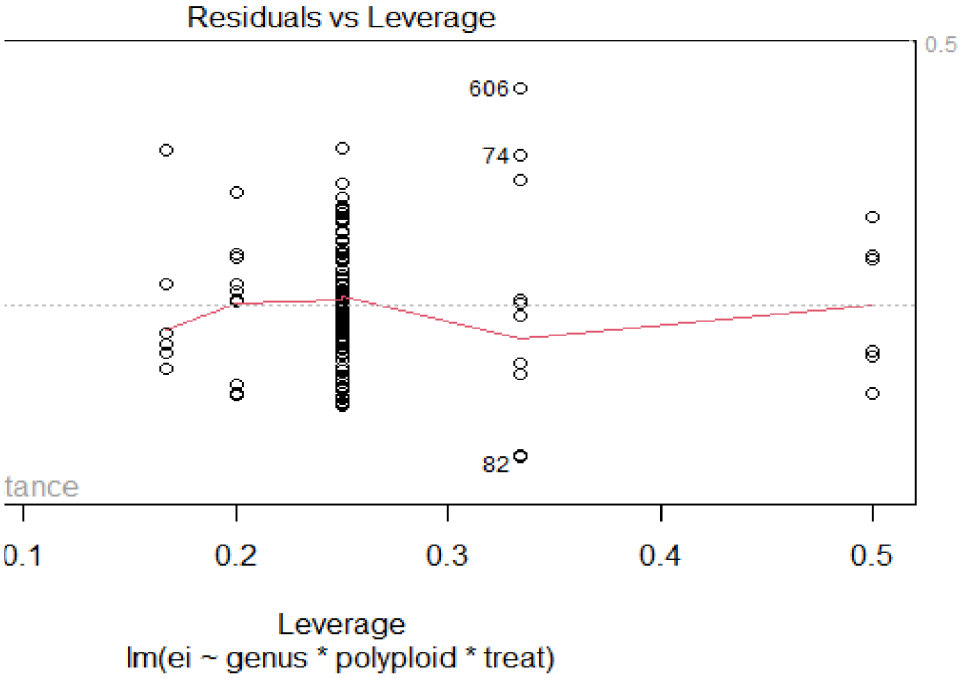
Čerstvá podzemní				Root/Shoot ratio	Dry root/shoot	Fresh root shoo
-4.158				**Intercept**	-0.445	-0.490
-0.087				**Polyploidy effect**	-0.126	-0.173
0.362				p-value	0.016	0.004
-0.916				t-value	-2.448	-2.981
-1.091				Trait plasticity index	-1.134	-1.188
70				Consistency index (%)	80	90
-1.070				**Cold effect**	-0.021	0.197
<0.001				p-value	0.687	<0.001
-11.235				t-value	-0.404	3.408
-2.917				Trait plasticity index	-1.021	1.218
100				Consistency index (%)	40	60
0.454				**Polyploidy:cold interaction**	0.232	0.342
<0.001				p-value	0.002	<0.001
3.425				t-value	3.246	4.252
1.575				Trait plasticity index	1.261	1.408
80				Consistency index (%)	90	90
				Effect estimates for individual		
Čerstvá podzemní				**Diploid standard**		
-4.509				*Arabidopsis*	-0.760	-1.11893
-4.163				*Brassica*	-0.522	-0.61782
-3.642				*Cardamine*	-0.717	-0.25672
-5.165				*Diplotaxis*	-0.702	-1.25546
-4.861				*Erysimum*	-0.763	-0.74435
-4.704				*Galium*	-0.470	-0.39816
-4.089				*Papaver*	-0.574	-0.25801
-3.129				*Raphanus*	0.051	0.12173
-4.296				*Stellaria*	-0.616	-0.86292
-3.023				*Symphytum*	0.621	0.49134
				Polyploidy		
-0.172				*Arabidopsis*	-0.034	-0.126
-0.141				*Brassica*	-0.236	-0.41832
0.607				*Cardamine*	-0.209	-0.12319
-0.327				*Diplotaxis*	-0.814	-0.61739
-0.105				*Erysimum*	0.146	0.48817
-0.147				*Galium*	-0.040	-0.038
-0.028				*Papaver*	0.198	-0.07565
0.184				*Raphanus*	-0.107	-0.35014
-0.916				*Stellaria*	-0.136	-0.36442
0.173				*Symphytum*	-0.026	-0.10036
				Cold		
-0.746				*Arabidopsis*	-0.348	0.34075
-1.408				*Brassica*	-0.592	-0.26416
-2.104				*Cardamine*	0.092	-0.03521
-0.919				*Diplotaxis*	0.287	0.81941

-0.207				*Erysimum*	0.297	0.58565
-0.358				*Galium*	0.198	0.34886
-0.024				*Papaver*	0.427	0.61666
-2.135				*Raphanus*	-0.491	-0.55825
-0.184				*Stellaria*	0.214	0.64204
-2.620				*Symphytum*	-0.291	-0.52345
				Cold:polyploidy		
0.414				*Arabidopsis*	0.304	0.5069
0.576				*Brassica*	0.695	0.60635
1.196				*Cardamine*	-0.503	-0.1459
0.221				*Diplotaxis*	0.415	0.30877
-0.729				*Erysimum*	0.456	0.22746
1.105				*Galium*	0.132	0.29945
-0.123				*Papaver*	0.083	0.24221
0.140				*Raphanus*	0.163	0.39837
0.655				*Stellaria*	0.231	0.36902
1.090				*Symphytum*	0.346	0.60607

Q-Q Residuals

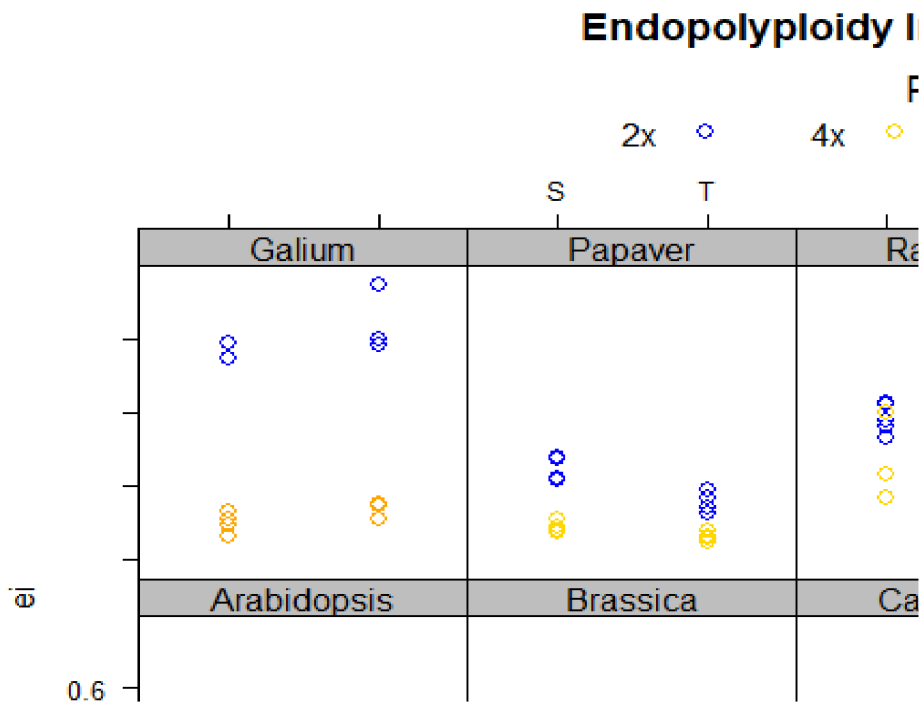


lm(ei ~ genus * polyploid * treat)
Residuals vs Leverage

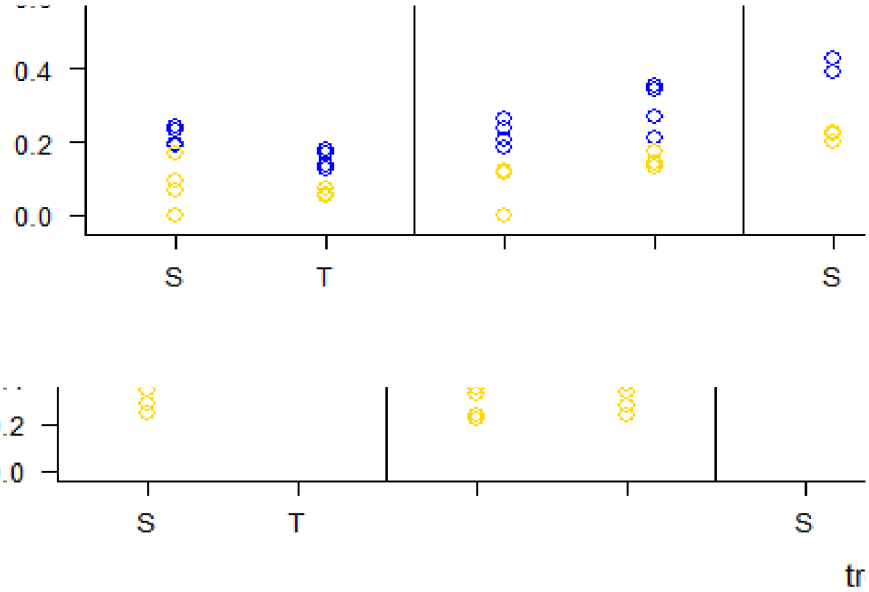


Fresh biomass	Dry biomass	WC shoot	WC root	
-3.211	-5.204	0.872	0.862	průměrný diploid v tep
0.018	-0.035	0.005	0.007	estimate ze summary (
0.801	0.664	0.206	0.087	číslo p ze summary (m)
0.253	-0.435	1.271	1.729	číslo t ze summary (m)
1.018	-1.035	1.006	1.008	jinak řečený to předch
60	40	80	60	vypočteno podle zanm
-1.189	-0.902	-0.062	-0.016	
<0.001	<0.001	< 2e-16	<0.001	
-16.592	-11.282	-14.650	-4.186	
-3.285	-2.465	-1.076	-1.019	
100	100	100	90	
0.255	0.272	-0.004	0.004	
0.012	0.016	0.538	0.487	
2.558	2.439	-0.617	0.698	
1.291	1.312	-1.004	1.004	
60	80	60	70	

-3.103	-5.084	0.875	0.821
-3.131	-5.105	0.869	0.854
-2.809	-4.815	0.839	0.898
-3.654	-5.738	0.891	0.812
-3.726	-5.593	0.844	0.847
-3.823	-5.845	0.862	0.877
-3.261	-5.601	0.892	0.921
-2.729	-4.532	0.893	0.813
-3.080	-5.332	0.903	0.875
-2.796			
-0.070			
0.121			
0.681			
0.180			
-0.410			
-0.138			
0.016			
0.299			
-0.644			
0.146			
-1.009			
-1.238			
-2.071			
-1.491			



-0.562			
-0.525			
-0.329			
-1.681			
-0.589			
-2.400			
0.054			
0.142			
1.267			
-0.160			
-0.750			
0.971			
-0.229			
-0.029			
0.383			
0.903	0.633	0.012	0.052



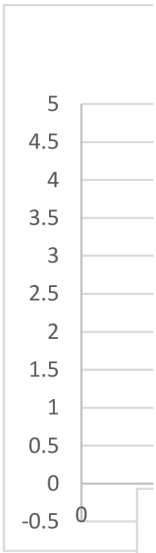
ei	biomasa	RGR	?ei efekt na biomasu nebo RGR

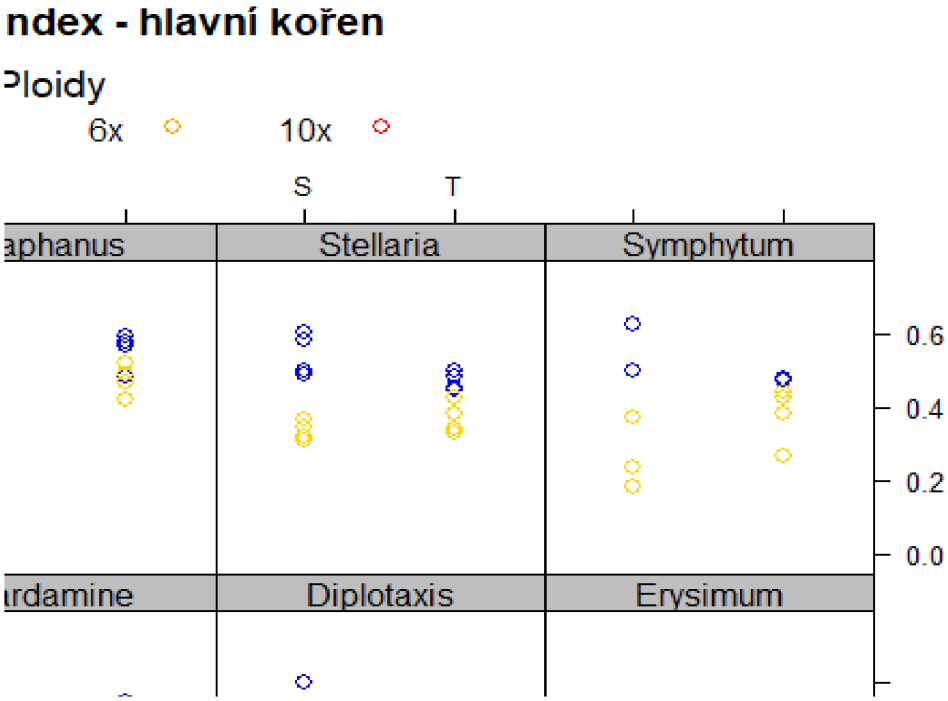
le napříč všemi 10 rody

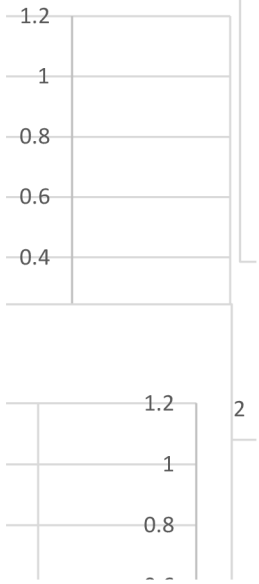
m)

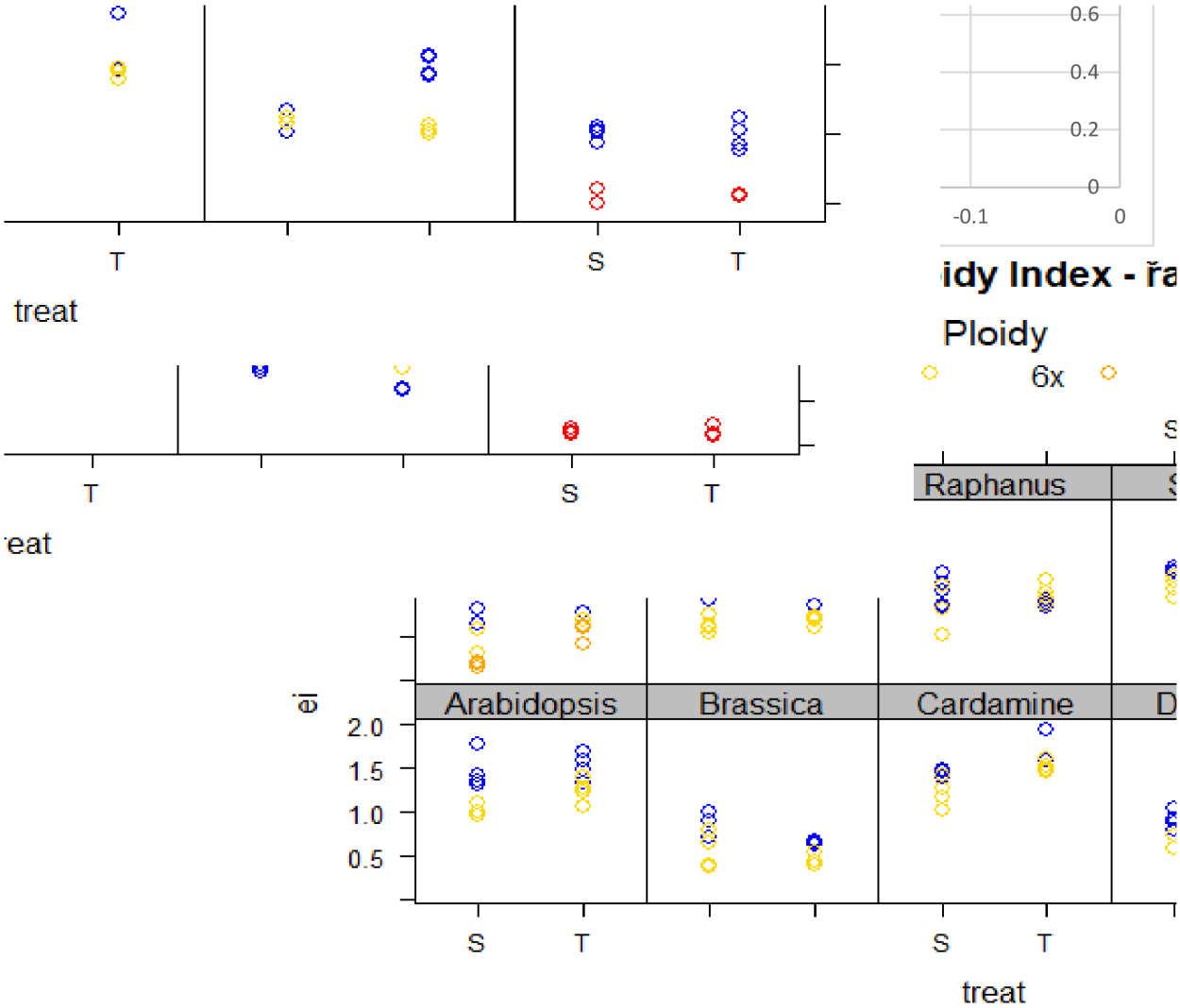
ozí + nebo - podle směru efektu a to fold ratio musí vyjít od 1 do nekonečna
énka t value a řádků 18 a 19

1.500
1.166667








0.6
0.4
0.2
0
-0.1
0
T
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treat
idy Index - ra
Ploidy
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S
T
eat
Raphanus
Arabidopsis
Brassica
Cardamine
2.0
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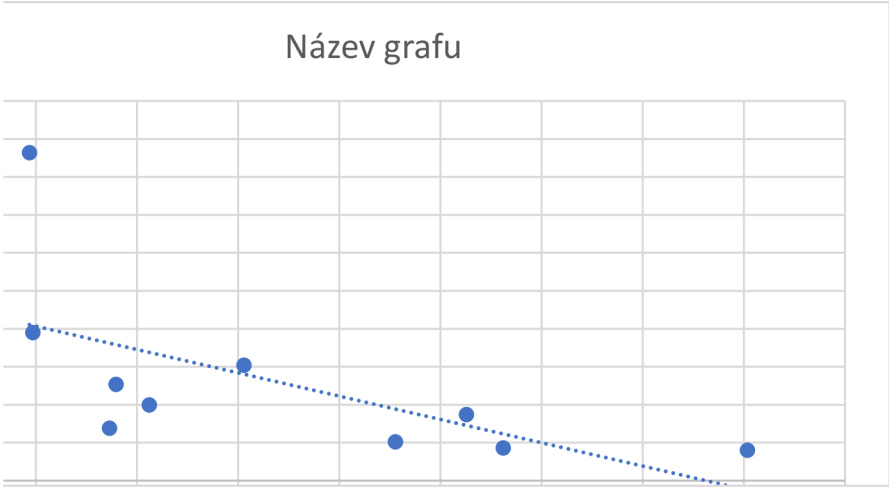
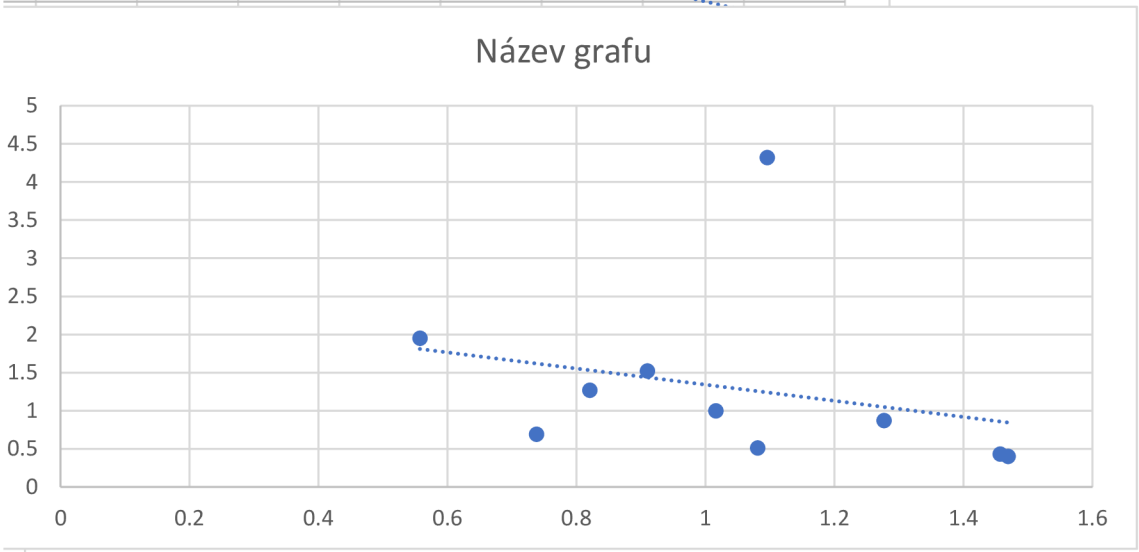
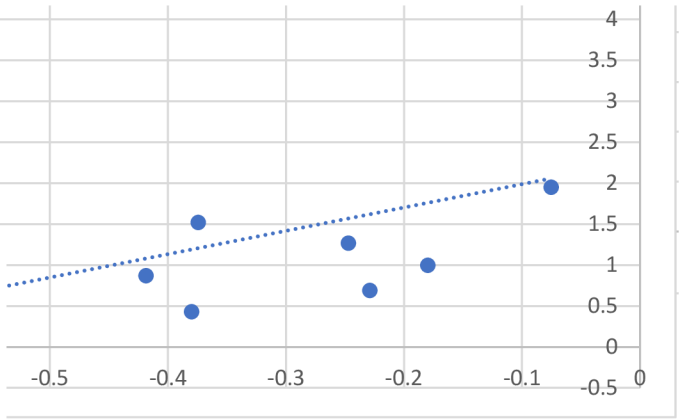
T
treat

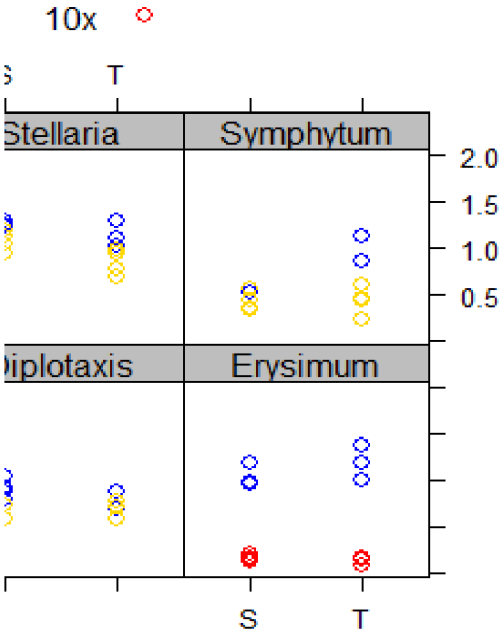

Název grafu

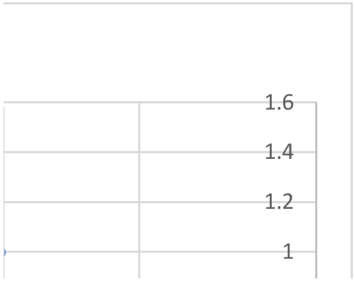

Název grafu
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6

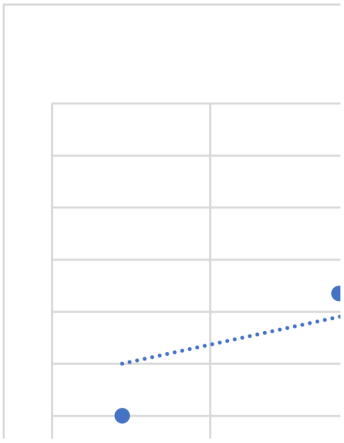
Název grafu
gsd
5
4.5

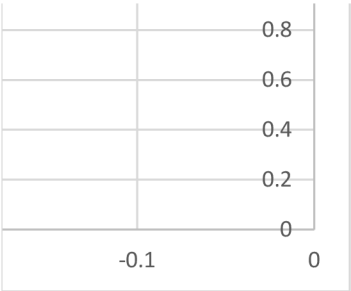

4
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
-0.5
-0.4
-0.3
-0.2
-0.1
0

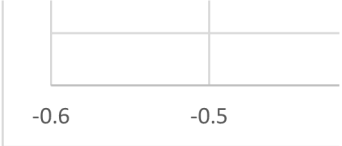
ıpík

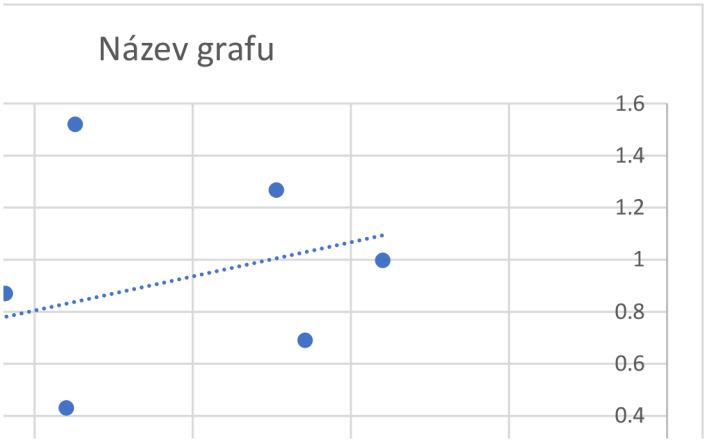

10x
T
Stellaria
Symphytum
2.0
1.5
1.0
0.5
iplotaxis
Erysimum
S
T

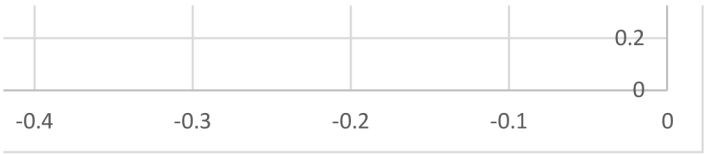

1.6
1.4
1.2
1




0.8
0.6
0.4
0.2
0
-0.1
0


-0.6
-0.5


Název grafu
1.6
1.4
1.2
1
0.8
0.6
0.4


0.2
0
-0.4
-0.3
-0.2
-0.1
0

Endopolyploidie		Dry Shoot	Dry Root	T Fresh Shoot
Data transformation used		ln	ln	ln
Analysis type (random factor)		lm	lm	lm
Nr. of polyploid-diploid pairs tested		10	10	10
Model summary*		hodnoty modelu		
Intercept		-5.723719	-6.168973	-3.6448
Polyploidy effect (i.e., model estimate at 400 ppm of C		0.002283	-0.12345	0.06185
p-value		0.976253	0.177279	0.387763
t-value		0.030	-1.358	0.867
DF		1	1	1
Among pair difference (p-value)**		7.016E-15	6.762E-07	< 2.2e-16
nr positively responding pairs***		5	4	6
nr negatively responding pairs***		5	6	4
Effect as ratio of predicted values		1.002	0.884	1.064
Trait plasticity index		1.002	-1.131	1.064
Consistency index (%)		50	60	60
Cold effect (i.e., model estimate for diploids)		-0.892366	-0.913136	-1.29109
p-value		< 2e-16	< 2e-16	< 2e-16
t-value		-11.664	-10.046	-18.102
DF		1	1	1
Among pair difference (p-value)**		2.382E-14	< 2.2e-16	1.503E-11
nr positively responding pairs***		0	2	0
nr negatively responding pairs***		10	8	10
Effect as ratio of predicted values		0.410	0.401	0.275
Trait plasticity index		-2.441	-2.492	-3.637
Consistency index (%)		100	80	100
Polyploidy:cold interaction		0.175419	0.407581	0.13582
p-value		0.102538	0.001697	0.174259
t-value		1.647	3.221	1.368
DF		1	1	1
Among pair difference (p-value)**		0.0001794	0.114387	0.0002111
nr positively responding pairs***		7	8	4
nr negatively responding pairs***		3	2	6
Effect as ratio of predicted values		1.192	1.503	1.145
Trait plasticity index		1.192	1.503	1.145
Consistency index (%)		70	80	40

** These p-values are taken from Anova model summary

*** Number of polyploid-diploid species pairs with effect estimates >0 (positiely responding) and <0 (neg

Effect estimates for individual pairs

Pair (diploid) estimate in standard (warm)

Arabidopsis		-5.470537	-6.230756	-3.38974
Brassica		-5.574193	-6.096526	-3.54476
Cardamine		-5.213475	-5.930968	-3.38563

Diplotaxis		-6.1422	-6.844419	-3.90951
Erysimum		-5.976611	-6.739453	-4.11696
Galium		-6.335792	-6.805551	-4.30618
Papaver		-6.054173	-6.628301	-3.8305
Raphanus		-5.264417	-5.213071	-3.01665
Stellaria		-5.76411	-6.380449	-3.43357
Symphytum		-5.441682	-4.820236	-3.5145
Polyploidy****				
Arabidopsis		-0.207917	-0.242258	-0.0457
Brassica		0.27871	0.042977	0.27709
Cardamine		0.647867	0.439235	0.73047
Diplotaxis		0.294043	-0.519727	0.29067
Erysimum		-0.438047	-0.292508	-0.59332
Galium		-0.162083	-0.201947	-0.10948
Papaver		-0.058099	0.139959	0.04721
Raphanus		0.078234	-0.02889	0.29992
Stellaria		-0.732127	-0.868046	-0.55181
Symphytum		0.322249	0.296705	0.27345
Cold ****				
Arabidopsis		-0.366422	-0.714867	-1.08664
Brassica		-0.770771	-1.362707	-1.14349
Cardamine		-1.992992	-1.901288	-2.0692
Diplotaxis		-1.157393	-0.870425	-1.73879
Erysimum		-0.396423	-0.098951	-0.79256
Galium		-0.275051	-0.077456	-0.70644
Papaver		-0.311345	0.11562	-0.64022
Raphanus		-1.454736	-1.945726	-1.81137
Stellaria		-0.16293	0.051314	-0.82561
Symphytum		-2.035597	-2.326874	-2.09658
Cold:polyploidy ****				
Arabidopsis		0.103917	0.40777	-0.09294
Brassica		-0.167085	0.528302	-0.03079
Cardamine		1.514825	1.011363	1.34147
Diplotaxis		0.0349	0.449975	-0.08767
Erysimum		-1.021833	-0.565513	-0.95656
Galium		0.93442	1.066083	0.80559
Papaver		-0.327998	-0.24535	-0.36554
Raphanus		0.099666	0.262845	-0.02425
Stellaria		0.178017	0.408904	0.28548
Symphytum		0.405361	0.751431	0.48341

**** Positive effects are marked yellow, negative effects are marked blue; if the difference among group

T fresh Root		Dry Shoot	Dry Root	Fresh Shoot	Fresh Root
ln		ln	ln	ln	ln
lm		lm	lm	lm	lm
10		10	10	10	10
		odlogarimtované hodnoty, převedené ma mg/den			
-4.158169		3.268	2.093	26.127	15.636
-0.087227		0.007	-0.243	1.667	-1.306
0.361987		0.976253	0.177279	0.387763	0.361987
-0.916		0.030	-1.358	0.867	-0.916
1		1	1	1	1
0.00000073		7.016E-15	6.762E-07	< 2.2e-16	0.00000073
3		5	4	6	3
7		5	6	4	7
0.916		1.002	0.884	1.064	0.916
-1.091		1.002	-1.131	1.064	-1.091
70		50	60	60	70
-1.07042		-1.929	-1.253	-18.943	-10.275
< 2e-16		< 2e-16	< 2e-16	< 2e-16	< 2e-16
-11.235		-11.664	-10.046	-18.102	-11.235
1		1	1	1	1
5.768E-16		2.382E-14	< 2.2e-16	1.503E-11	5.768E-16
0		0	2	0	0
10		10	8	10	10
0.343		0.410	0.401	0.275	0.343
-2.917		-2.441	-2.492	-3.637	-2.917
100		100	80	100	100
0.454252		0.253	0.519	-0.097	3.683
0.000877		0.102538	0.001697	0.174259	0.000877
3.425		1.647	3.221	1.368	3.425
1		1	1	1	1
0.036085		0.0001794	0.114387	0.0002111	0.036085
8		7	8	4	8
2		3	2	6	2
1.575		1.192	1.503	1.145	1.575
1.575		1.192	1.503	1.145	1.575
80		70	80	40	80

gatively responding); see below for exact effect estimates in each pair

-4.50867		4.208971333	1.967963554	33.7174423	11.01309786
-4.162583		3.794536538	2.250672992	28.87555181	15.56729562
-3.642342		5.44272731	2.655909823	33.85630615	26.19093292

-5.164965		2.150187997	1.065385046	20.05032331	5.7132628
-4.861308		2.537411023	1.183294242	16.2939729	7.740352885
-4.704336		1.771742063	1.10760971	13.48496389	9.055925356
-4.088505		2.34804315	1.32240795	21.69876354	16.76427743
-3.129344		5.172407663	5.444926616	48.96497659	43.74648554
-4.296478		3.138187108	1.694362017	32.27152553	13.61643173
-3.023159		4.332190395	8.064883602	29.76268057	48.64729856
-0.17169		-0.790131447	-0.423400157	-1.506208125	-1.737423816
-0.141224		1.219655398	0.098835794	9.219533486	-2.050293909
0.607291		4.960824614	1.464786992	36.4312856	21.88127821
-0.326712		0.735023709	-0.431818805	6.76343911	-1.592335219
-0.105135		-0.900031227	-0.300096112	-7.291716307	-0.772464098
-0.147476		-0.265104665	-0.202539466	-1.39838954	-1.241719983
-0.02843		-0.132531701	0.198660901	1.048964617	-0.469897169
0.184217		0.420908144	-0.155053399	17.12554087	8.848894242
-0.916226		-1.629079815	-0.983118011	-13.686145	-8.169506461
0.173115		1.647221866	2.785758726	9.360114016	9.194477223
-0.745893		-1.291269454	-1.005123258	-22.34292784	-5.789469341
-1.407651		-2.038970596	-1.674575123	-19.67277488	-11.75770673
-2.104412		-4.700954094	-2.259180375	-29.58070258	-22.99780403
-0.919389		-1.474374222	-0.619229986	-16.52682167	-3.435027211
-0.206913		-0.830438616	-0.111481593	-8.917944929	-1.446746372
-0.357588		-0.426044815	-0.08255265	-6.831515477	-2.722562963
-0.023557		-0.628192803	0.162086504	-10.25968679	-0.390300875
-2.135201		-3.964847078	-4.666936704	-40.96262634	-38.5747399
-0.183578		-0.471824355	0.089213878	-18.13763809	-2.28365323
-2.620018		-3.766395544	-7.277747983	-26.10556304	-45.1056997
0.413961		0.501936312	0.59670864	0.033679031	3.169426402
0.575559		-1.012334477	0.345064962	-6.649351567	4.122466449
1.19557		0.746758158	-0.169201669	-6.757689533	-5.701757075
0.221107		-0.471795154	0.401759144	-5.970395899	1.364010428
-0.729097		-0.410472694	-0.317267599	1.481423201	-2.78840922
1.105037		1.832599101	1.609896648	8.091322351	11.40888392
-0.123321		-0.418328468	-0.347151074	-4.167683398	-1.835522781
0.139695		-0.18578904	0.360121916	-14.5854905	-6.870568935
0.6545		0.494764873	0.326450882	10.38144769	5.559815744
1.089509		-1.041749471	-1.327724263	-5.22182015	-0.217642065

ɔs was not significant, i.e. xplained too little variance in the model, this is noted above the respecti

diploid za chladu/diploid v teple

3 5

polyploid se zapoctenou interakci/polyploid bez zapocteni interakce

1.500

1.166667

ve estimates as NS (if the group effect remained in the minimal model) or DEL (if the group effect was remow

9 12

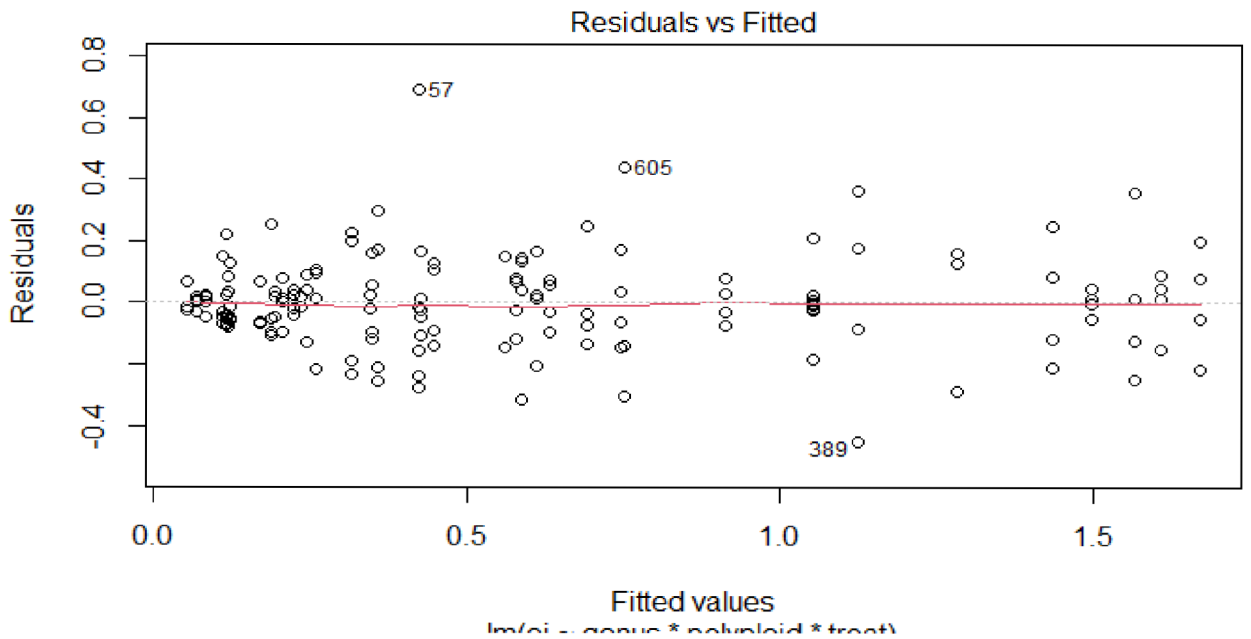
ved from the minimum model)

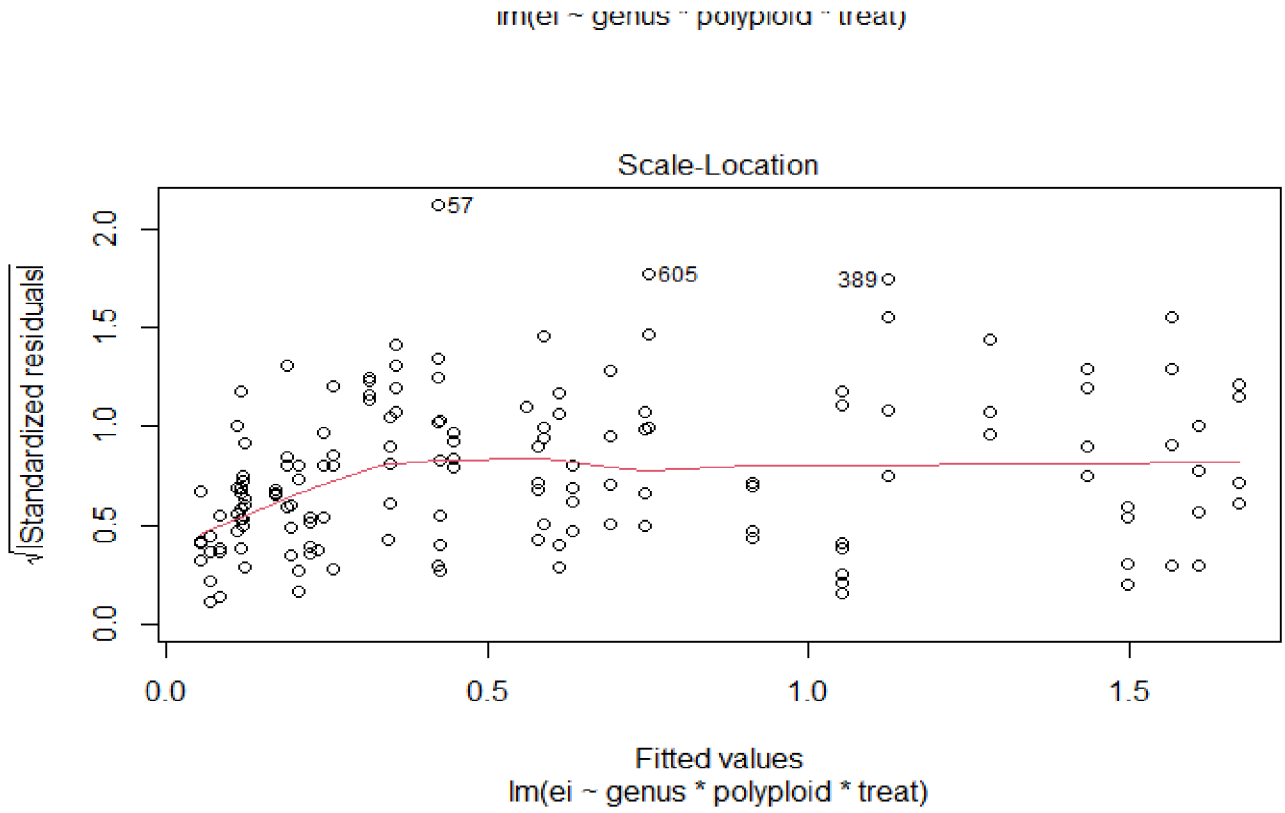
lm(ei ~ genus * polyploid * treat, data = de.cep)

```
Response: ei
                                  Df  Sum Sq  Mean Sq  F value    Pr(>F)
genus                              9  23.952   2.6613  91.3554 < 2.2e-16  ***
polyploid                          1   4.257    4.257 146.1304 < 2.2e-16  ***
treat                              1   0.641    0.641  22.0024  8.16E-06 ***
genus:polyploid                    9  2.5035   0.2782   9.5485  1.51E-10 ***
genus:treat                        9  1.7443   0.1938    6.653  1.69E-07 ***
polyploid:treat                    1  0.0122   0.0122   0.4176  5.20E-01
genus:polyploid:treat              9   0.451   0.0501   1.7203  9.32E-02 .
Residuals                        106   3.088   0.0291
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
lm(formula = ei ~ genus * polyploid * treat, data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.48010 -0.07219 -0.00518  0.07354  0.69188

Coefficients:
                                  Estimate  Std. Error  t value    Pr(>|t|)
(Intercept)                        0.67923   0.02973    22.85  < 2e-16   ***
genus1                             0.88999   0.08191   10.865  < 2e-16   ***
genus2                            -0.32041   0.08191   -3.912  0.000162  ***
genus3                             0.47297   0.09302    5.085  1.60E-06  ***
genus4                            -0.06751   0.08191   -0.824  0.411707
genus5                             0.23194   0.08191    2.831  0.005545  **
genus6                            -0.33333   0.11197   -2.977  0.003606  **
genus7                            -0.48988   0.08191    -5.98  3.05E-08  ***
genus8                            -0.25471   0.07446   -3.421  0.000888  ***
genus9                             0.37239   0.08191    4.546  1.46E-05  ***
polyploidYES                      -0.34876   0.04163   -8.377  2.45E-13  ***
treatT                             0.13298   0.04163    3.194  0.001848  **
genus1:polyploidYES               -0.17562    0.1157   -1.518  0.132014
genus2:polyploidYES                0.10178    0.1157     0.88  0.381004
genus3:polyploidYES               -0.07111   0.13142   -0.541  0.589568
genus4:polyploidYES               -0.02552   0.13861   -0.184  0.854281
genus5:polyploidYES               -0.49217    0.1157   -4.254  4.54E-05  ***
genus6:polyploidYES                0.05978   0.13861    0.431  6.67E-01
genus7:polyploidYES                0.21368    0.1157    1.847  0.067552  .
genus8:polyploidYES                0.16894   0.11901     1.42  0.158676
genus9:polyploidYES               -0.06972    0.1157   -0.603  0.548066
```

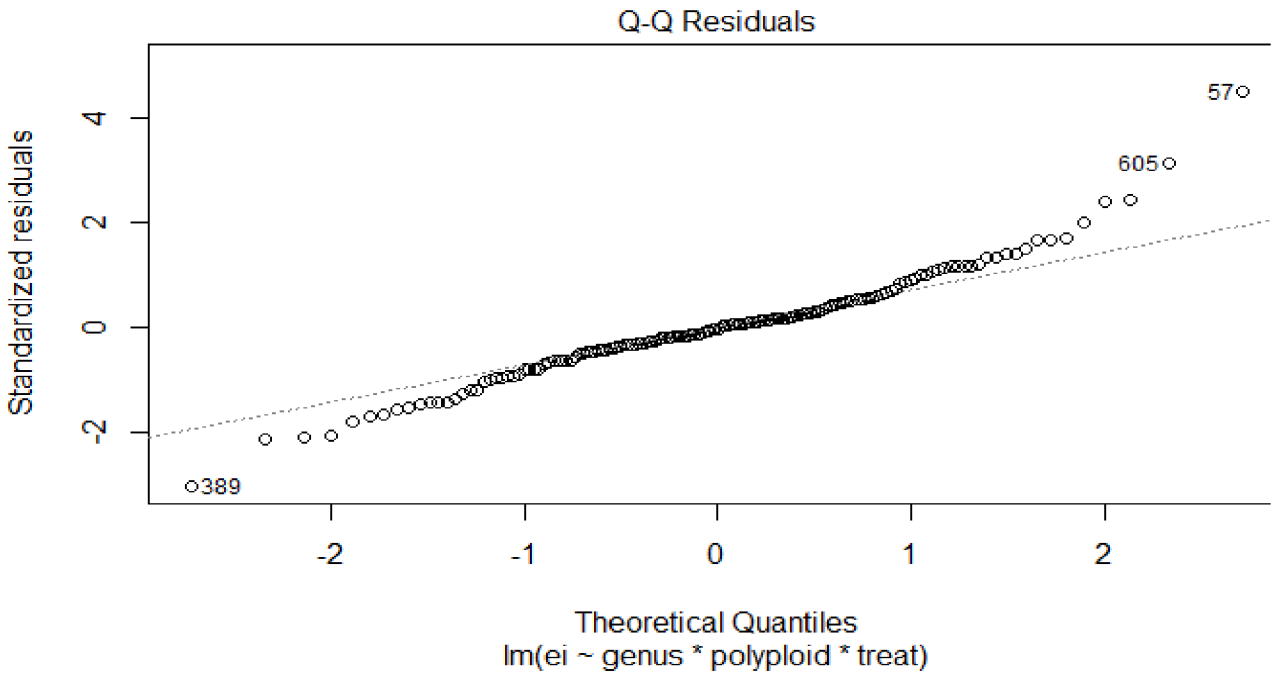
```
genus1:treatT                    -0.03223    0.1157    -0.279  0.781119
genus2:treatT                    -0.36758    0.1157    -3.177  0.001949 **
genus3:treatT                     0.15969   0.13142     1.215  0.227018
genus4:treatT                    -0.15665    0.1157    -1.354  0.178617
genus5:treatT                     0.45257    0.1157     3.912  0.000162 ***
genus6:treatT                     0.27352   0.14545     1.881  0.062776 .
genus7:treatT                    -0.11468    0.1157    -0.991  0.323845
genus8:treatT                     0.02195   0.11055     0.199  0.842987
genus9:treatT                    -0.49135    0.1157    -4.247   4.67E-05 ***
polyploidYES:treatT               0.03386   0.05796     0.584  0.560345
genus1:polyploidYES:treatT        0.25364   0.16329     1.553   1.23E-01
genus2:polyploidYES:treatT        0.26021   0.16329     1.594   1.14E-01
genus3:polyploidYES:treatT        0.22187   0.18556     1.196  0.234493
genus4:polyploidYES:treatT        0.06926   0.18025     0.384  0.701558
genus5:polyploidYES:treatT       -0.43074   0.16329    -2.638  0.009601 **
genus6:polyploidYES:treatT       -0.09085   0.19072    -0.476    0.6348
genus7:polyploidYES:treatT       -0.02204   0.16329    -0.135   0.89291
genus8:polyploidYES:treatT       -0.20997   0.16566    -1.267  0.207761
genus9:polyploidYES:treatT        0.13961   0.16329     0.855   0.39449
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.1707 on 106 degrees of freedom
Multiple R-squared:  0.9157,    Adjusted R-squared:  0.8847
F-statistic: 29.54 on 39 and 106 DF,  p-value: < 2.2e-16
```

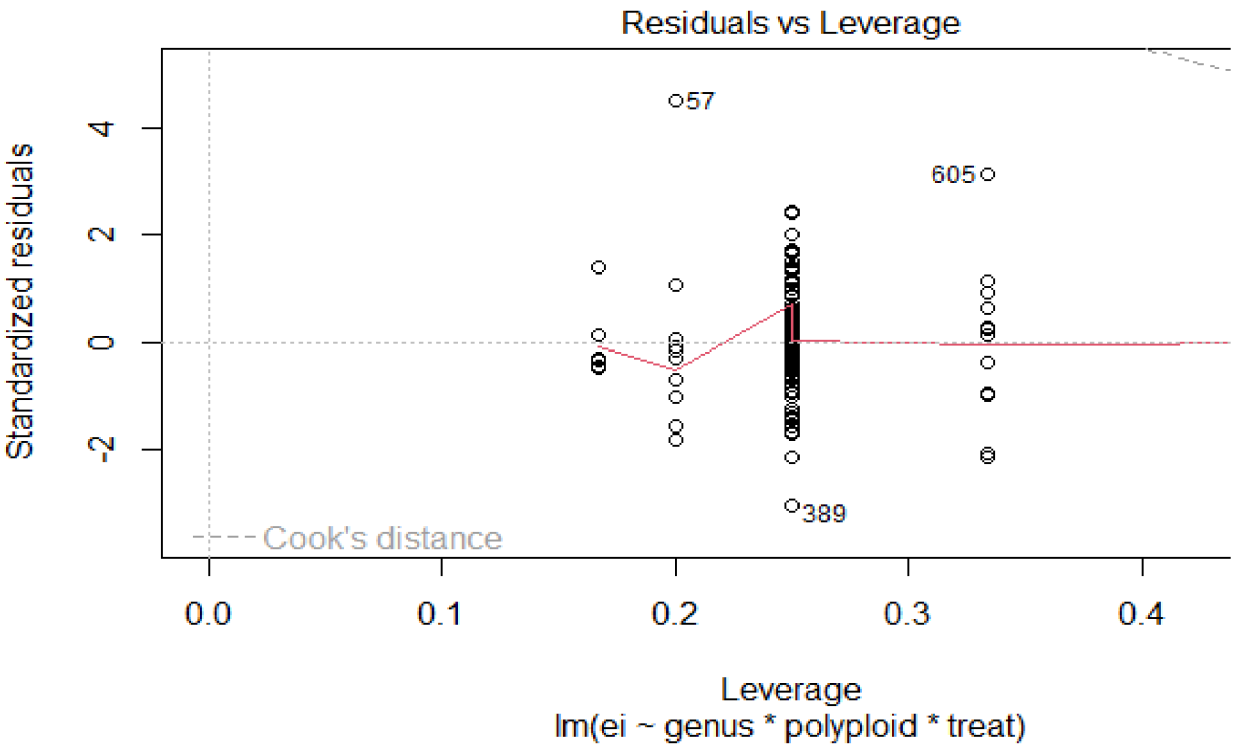


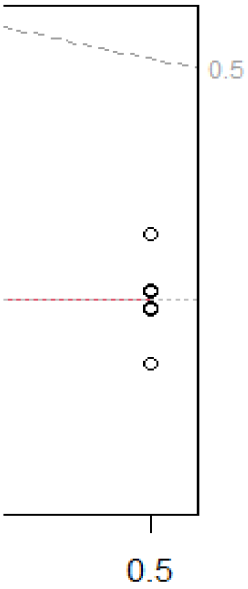

lm(ei ~ genus * polyploid * treat)
Scale-Location
57
605
389
√|Standardized residuals|
0.0
0.5
1.0
1.5
2.0
0.0
0.5
1.0
1.5
Fitted values
lm(ei ~ genus * polyploid * treat)

1.56922	
0.35882	
1.1522	
0.61172	
0.91117	
0.3459	
0.18935	
0.42452	
1.05162	
0.17778	
-0.52438	
-0.24698	
-0.41987	########
-0.37428	
-0.84093	
-0.28898	
-0.13508	
-0.17982	
-0.41848	
-0.0588	

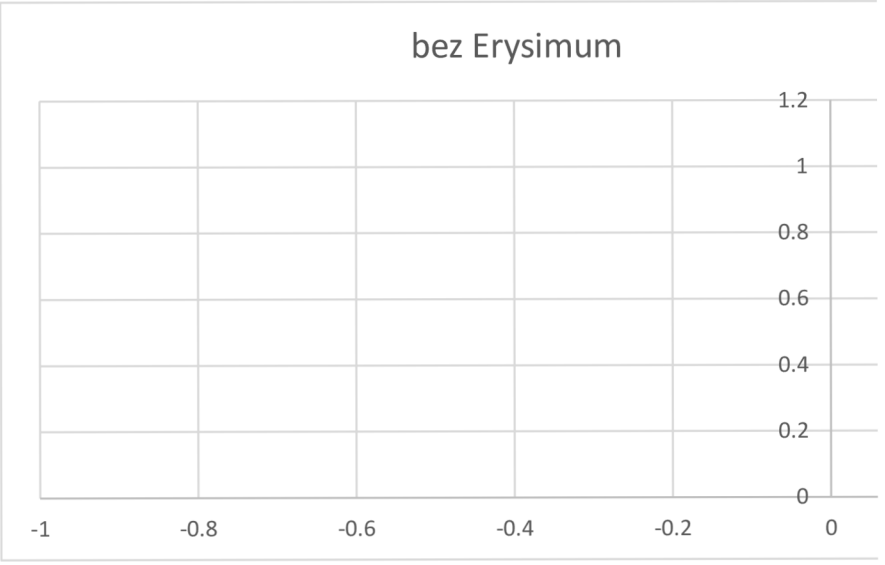
0.10075
-0.2346
0.29267
-0.02367
0.58555
0.4065
0.0183
0.15493
-0.35837
0.38774
0.2875
0.29407
0.25573
0.10312
-0.39688
-0.05699
0.01182
-0.17611
0.17347
-0.15713



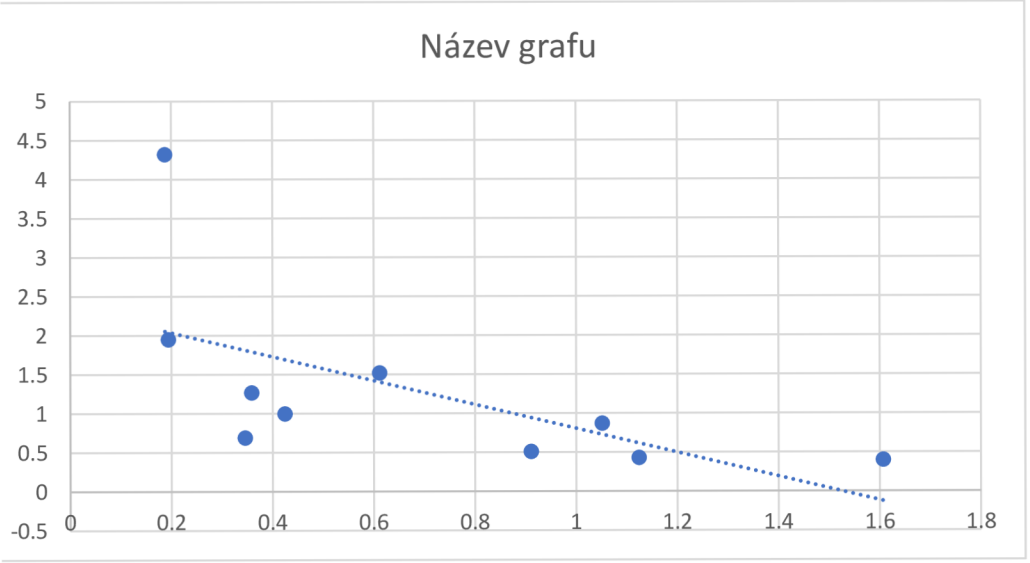

Residuals vs Leverage
Standardized residuals
4
2
0
-2
57
605
389
Cook's distance
0.0
0.1
0.2
0.3
0.4
Leverage
lm(ei ~ genus * polyploid * treat)

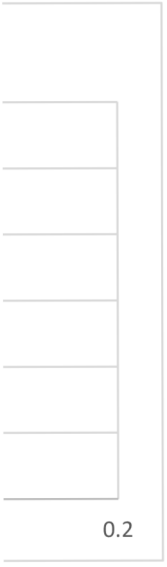

0.5
0.5

	age		gsd
1.6072	0.389335	Arabidopsis	0.4
0.358825	0.388423	Brassica	1.267418
1.124425	0.225993	Cardamine	0.43
0.611725	0.584631	Diplotaxis	1.52
0.911175	0.420392	Erysimum	0.51
0.3459	0.417784	Galium	0.69
0.1877	0.233993	Papaver	4.32
0.42452	0.381607	Raphanus	0.997
1.051625	0.430101	Stellaria	0.87
0.194335	0.346574	Symphytum	1.95



	age	
-0.55552	0.389335	Arabidopsis
-0.2471	0.388423	Brassica
-0.3799	0.225993	Cardamine
-0.37427	0.584631	Diplotaxis
-0.84092	0.420392	Erysimum
-0.22892	0.417784	Galium
-0.13342	0.233993	Papaver
-0.17982	0.381607	Raphanus
-0.41848	0.430101	Stellaria
-0.07533	0.346574	Symphytum

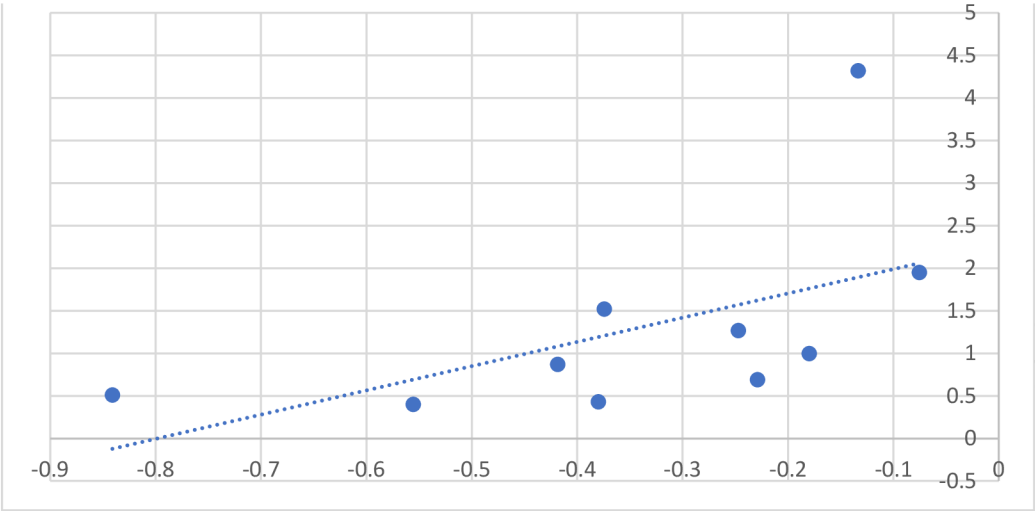




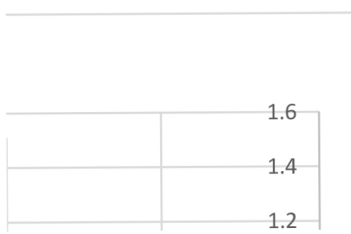
-0.55552	0.389335	Arabidopsi:	0.4
-0.2471	0.388423	Brassica	1.267418
-0.3799	0.225993	Cardamine	0.43
-0.37427	0.584631	Diplotaxis	1.52
-0.22892	0.417784	Galium	0.69
-0.17982	0.381607	Raphanus	0.997
-0.41848	0.430101	Stellaria	0.87

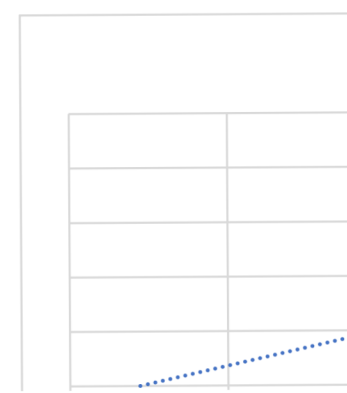
gsd

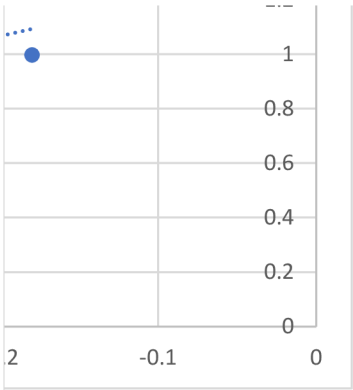
0.4
1.267418
0.43
1.52
0.51
0.69
4.32
0.997
0.87
1.95

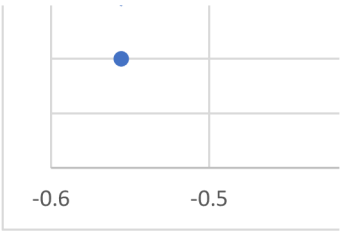


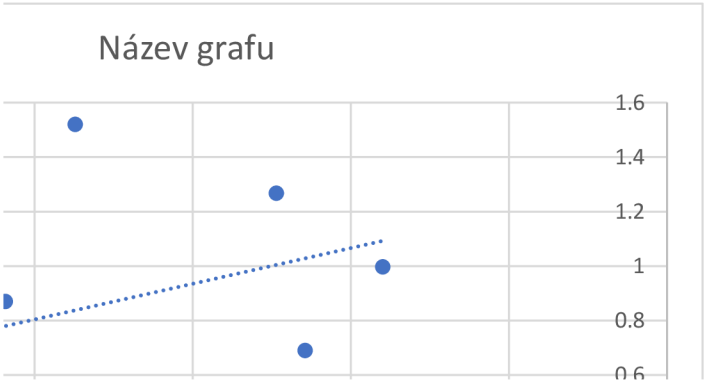
-0.55552	0.4	Arabidopsis
-0.2471	1.267418	Brassica
-0.3799	0.43	Cardamine
-0.37427	1.52	Diplotaxis
-0.22892	0.69	Galium
-0.17982	0.997	Raphanus
-0.41848	0.87	Stellaria

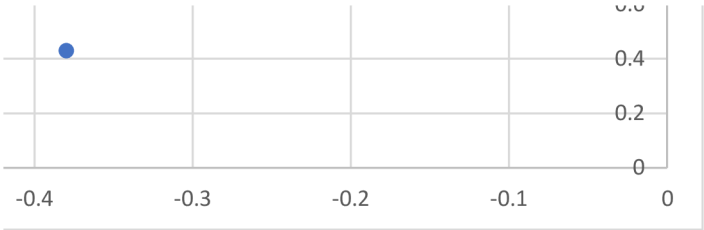





1
0.8
0.6
0.4
0.2
0
-0.1
0


-0.6
-0.5


Název grafu
1.6
1.4
1.2
1
0.8
0.6


0.4
0.2
0
-0.4
-0.3
-0.2
-0.1
0

```
m.rap<-lm(ei~genus*polyploid*treat, data=de.rap)
plot(m.rap)
anova(m.rap)

Analysis of Variance Table

Response: ei
```

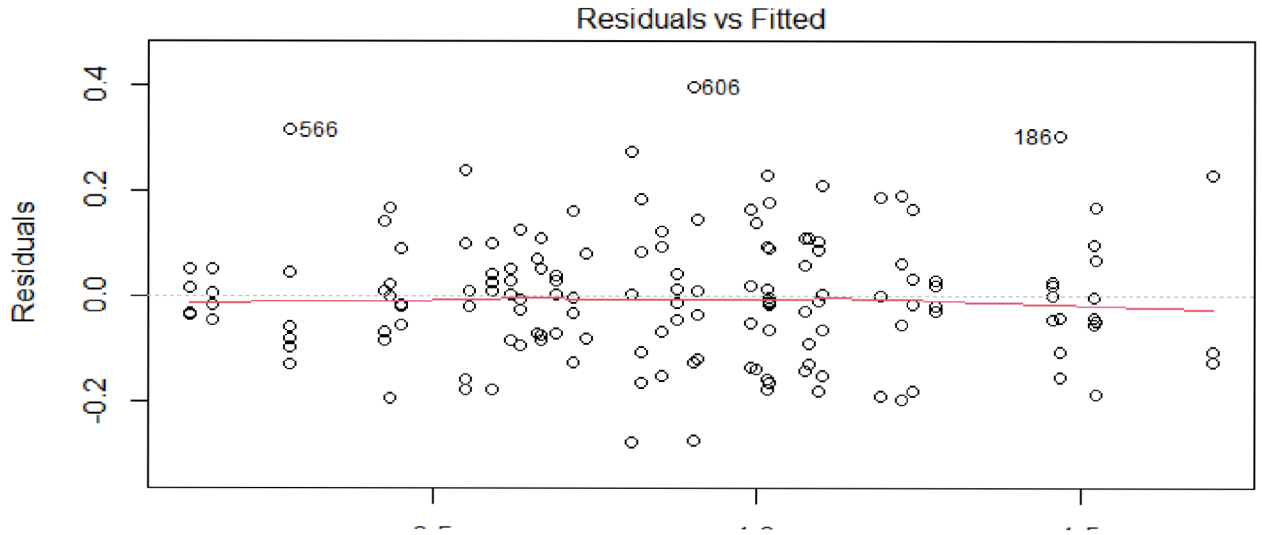
	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
genus	9	12.5264	1.3918	79.2942	< 2.2e-16	***
polyploid	1	4.3957	4.3957	250.4324	< 2.2e-16	***
treat	1	0.0478	0.0478	2.7207	0.10202	
genus:polyploid	9	2.3324	0.2592	14.7646	2.89E-15	***
genus:treat	9	1.0029	0.1114	6.3484	3.69E-07	***
polyploid:treat	1	0.0519	0.0519	2.9595	8.83E-02	.
genus:polyploid:treat	9	0.3445	0.0383	2.1808	0.02893	*
Residuals	106	1.8606	0.0176			

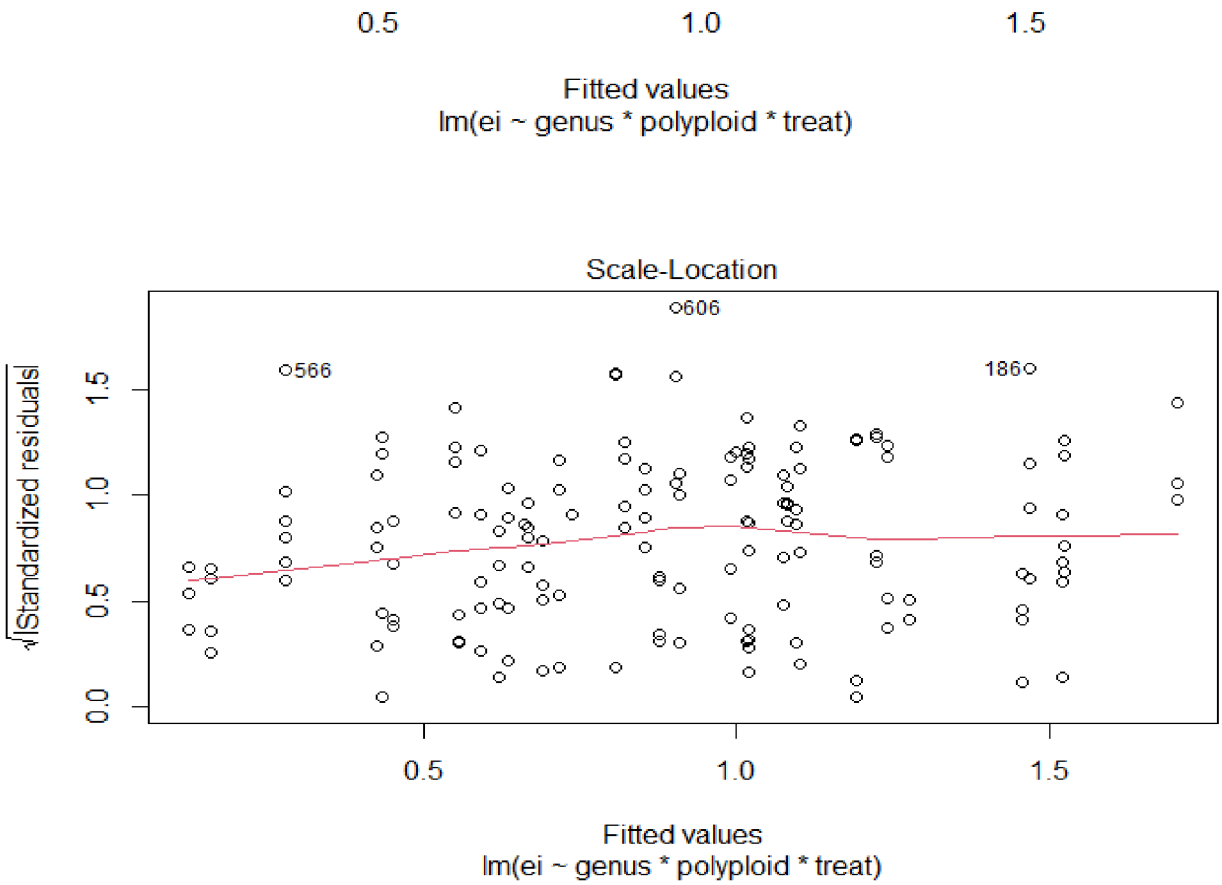
```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
summary(m.rap)

Call:
lm(formula = ei ~ genus * polyploid * treat, data = de.rap)

Residuals:
     Min       1Q   Median       3Q      Max
-0.27733 -0.07095 -0.00367  0.05210  0.39757

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)	
(Intercept)	1.04712	0.02307	45.38	< 2e-16	***
genus1	0.416	0.06358	6.543	2.20E-09	***
genus2	-0.22622	0.06358	-3.558	0.000561	***
genus3	0.42541	0.0722	5.892	4.57E-08	***
genus4	-0.13695	0.06358	-2.154	0.033519	*
genus5	0.034	0.06358	0.535	0.593959	
genus6	-0.30887	0.08691	-3.554	0.000568	***
genus7	0.04885	0.06358	0.768	0.444032	
genus8	-0.03078	0.0578	-0.533	0.595419	
genus9	0.27345	0.06358	4.301	3.80E-05	***
polyploidYES	-0.37727	0.03232	-11.674	< 2e-16	***
treatT	0.01729	0.03232	0.535	0.593863	
genus1:polyploidYES	-0.07208	0.08981	-0.803	0.42402	
genus2:polyploidYES	0.10667	0.08981	1.188	0.237569	
genus3:polyploidYES	0.06437	0.10201	0.631	0.529362	
genus4:polyploidYES	0.12895	0.10759	1.198	0.233396	
genus5:polyploidYES	-0.54355	0.08981	-6.052	2.19E-08	***

```
genus6:polyploidYES          -0.17005   0.10759    -1.581  0.116965
genus7:polyploidYES          -0.08303   0.08981    -0.924  0.357328
genus8:polyploidYES           0.16867   0.09238     1.826  0.070688 .
genus9:polyploidYES            0.1487   0.08981     1.656  0.100732

genus1:treatT                 0.03149   0.08981     0.351  0.726557
genus2:treatT                -0.21789   0.08981    -2.426  0.016949 *
genus3:treatT                 0.21545   0.10201     2.112  0.037031 *
genus4:treatT                -0.21186   0.08981    -2.359  0.020154 *
genus5:treatT                 0.09291   0.08981     1.035  0.303211
genus6:treatT                  0.1466    0.1129     1.298  0.196936
genus7:treatT                -0.09381   0.08981    -1.045  0.298599
genus8:treatT                 -0.1571   0.08581    -1.831   0.06994 .
genus9:treatT                -0.23611   0.08981    -2.629  0.009835 **

polyploidYES:treatT           0.06852   0.04499     1.523  0.130774
genus1:polyploidYES:treatT    0.10863   0.12675     0.857  0.393361
genus2:polyploidYES:treatT    0.03236   0.12675     0.255  0.799007
genus3:polyploidYES:treatT    0.02808   0.14404     0.195  0.845797
genus4:polyploidYES:treatT    0.13121   0.13992     0.938  0.350509
genus5:polyploidYES:treatT   -0.21372   0.12675    -1.686   0.09472 .
genus6:polyploidYES:treatT    0.19521   0.14805     1.319  0.190157
genus7:polyploidYES:treatT    0.06136   0.12675     0.484  0.629339
genus8:polyploidYES:treatT    0.25281   0.12859     1.966  0.051903 .
genus9:polyploidYES:treatT   -0.08814   0.12675    -0.695  0.488333
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.1325 on 106 degrees of freedom
Multiple R-squared:  0.9175,    Adjusted R-squared:  0.8872
F-statistic: 30.24 on 39 and 106 DF,  p-value: < 2.2e-16
```



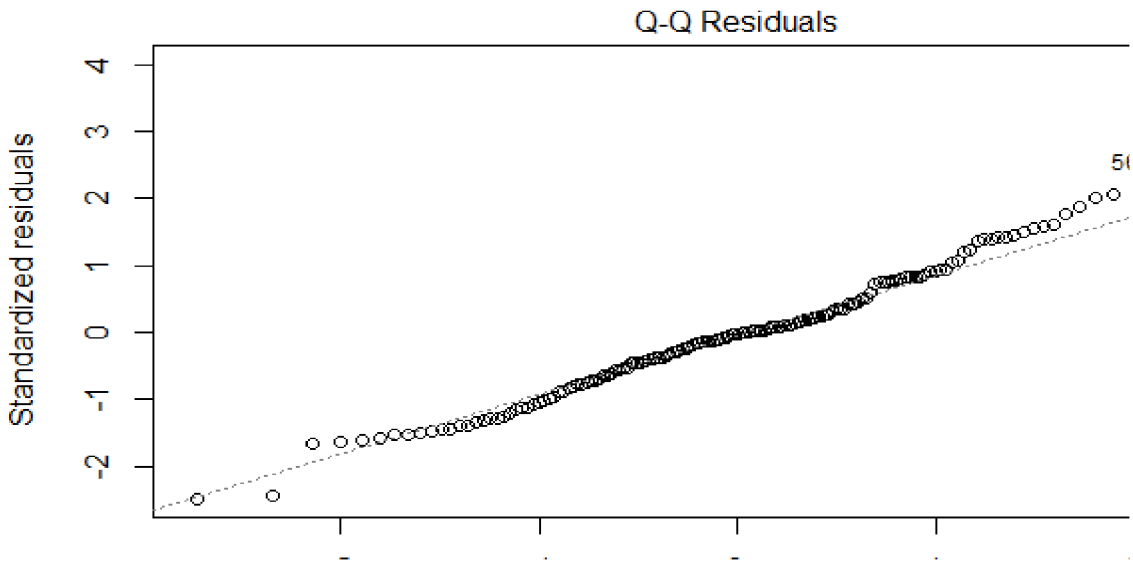

0.5
1.0
1.5
Fitted values
lm(ei ~ genus * polyploid * treat)
Scale-Location
606
566
186
√|Standardized residuals|
0.0
0.5
1.0
1.5
0.5
1.0
1.5
Fitted values
lm(ei ~ genus * polyploid * treat)

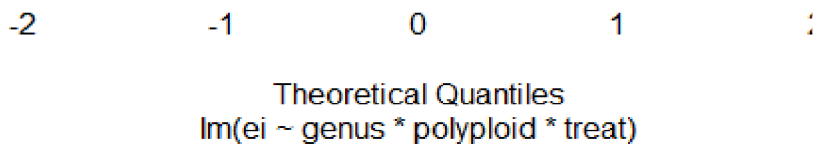
1.46312
0.8209
1.47253
0.91017
1.08112
0.73825
1.09597
1.01634
1.32057
0.55223

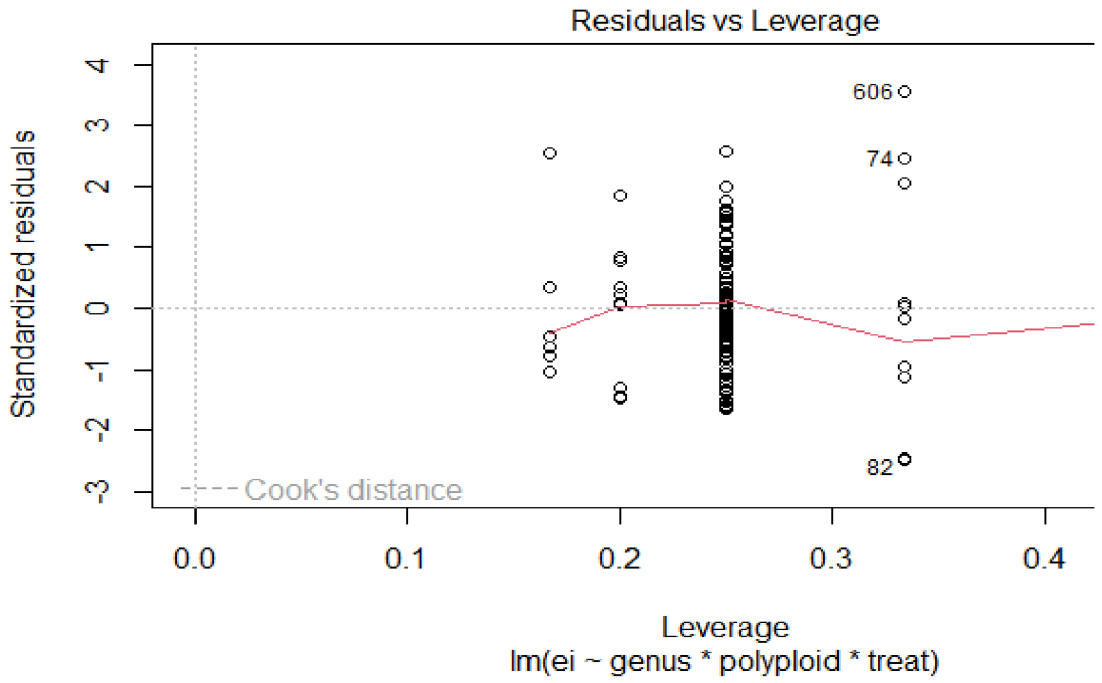
-0.44935
-0.2706
-0.3129
-0.24832
-0.92082

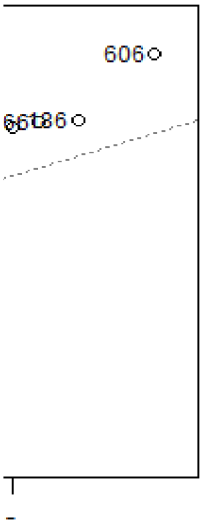
-0.54732
-0.4603
-0.2086
-0.22857
-0.12592
0.04878
-0.2006
0.23274
-0.19457
0.1102
0.16389
-0.07652
-0.13981
-0.21882
0.44761

0.17715
0.10088
0.0966
0.19973
-0.1452
0.26373
0.12988
0.32133
-0.01962
-0.43928

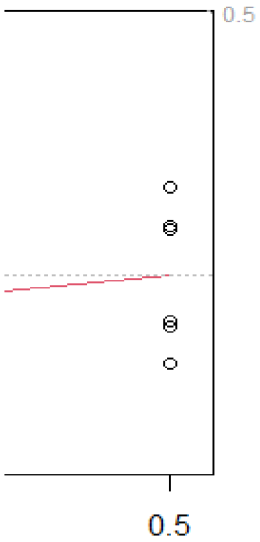



-2
-1
0
1
Theoretical Quantiles
lm(ei ~ genus * polyploid * treat)

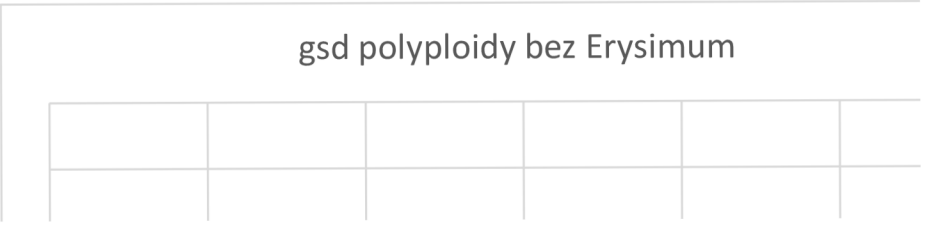

Residuals vs Leverage
Standardized residuals
4
3
2
1
0
-1
-2
-3
606
74
82
Cook's distance
0.0
0.1
0.2
0.3
0.4
Leverage
lm(ei ~ genus * polyploid * treat)

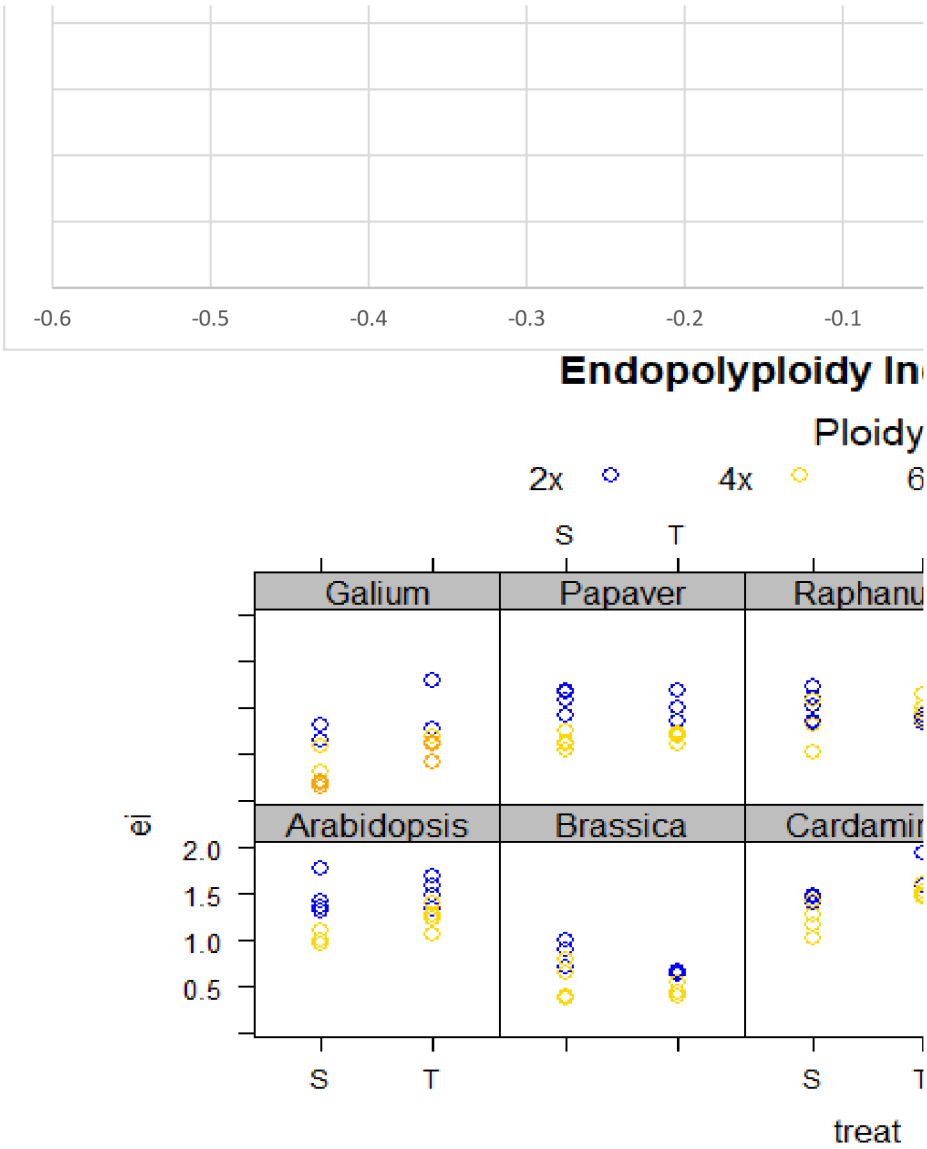

606
6186

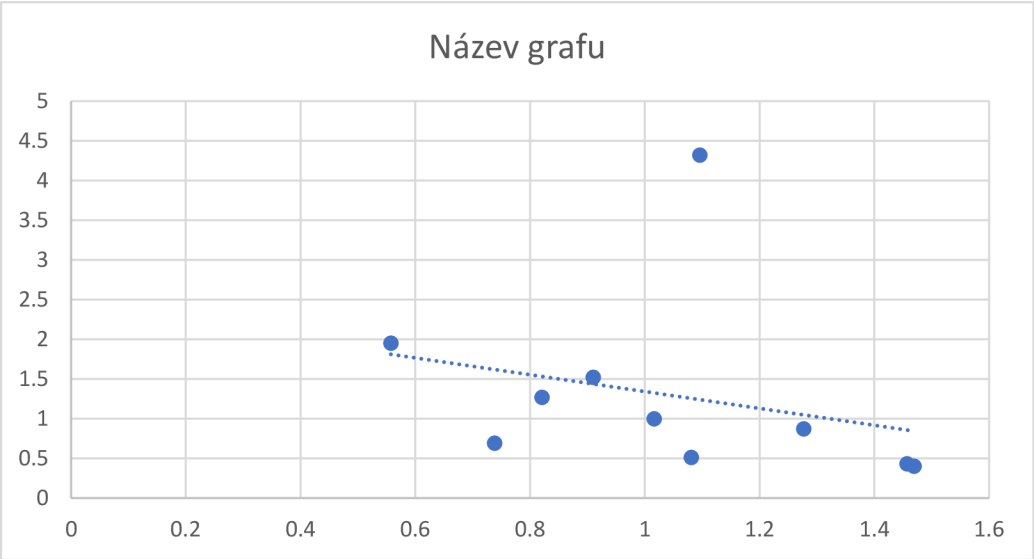
2

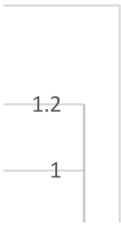


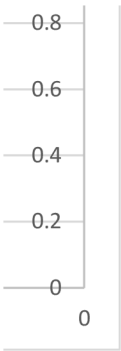
	age		gsd
1.469375	0.389335	Arabidopsis	0.4
0.8209	0.388423	Brassica	1.267418
1.4571	0.225993	Cardamine	0.43
0.910175	0.584631	Diplotaxis	1.52
1.081125	0.420392	Erysimum	0.51
0.73825	0.417784	Galium	0.69
1.095975	0.233993	Papaver	4.32
1.01634	0.381607	Raphanus	0.997
1.27705	0.430101	Stellaria	0.87
0.55763	0.346574	Symphytun	1.95



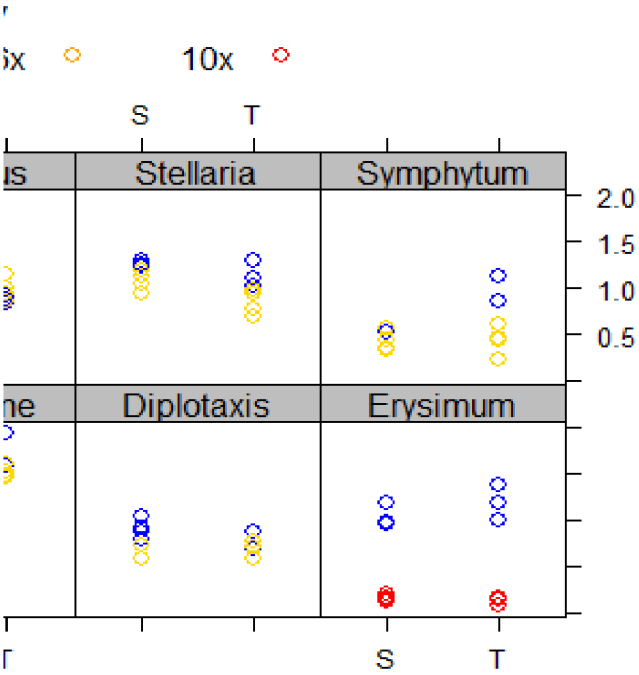

-0.6
-0.5
-0.4
-0.3
-0.2
-0.1
Endopolyploidy In
Ploidy
2x
4x
6
S
T
Galium
Papaver
Raphanu
Arabidopsis
Brassica
Cardamin
2.0
1.5
1.0
0.5
S
T
S
T
treat


Název grafu
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6


1.2
1


0.8
0.6
0.4
0.2
0
0

dex - řapík


ix
10x
S
T
Stellaria
Symphytum
2.0
1.5
1.0
0.5
Diplotaxis
Erysimum
S
T

m.hla<-lm(ei~genus*polyploid*treat, data=de.hla)

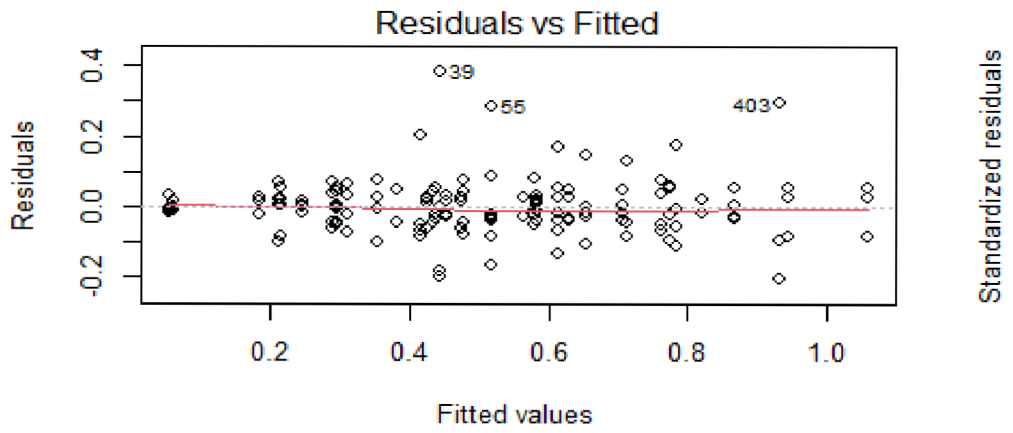
```
anova(m.hla)
Analysis of Variance Table

Response: ei
```

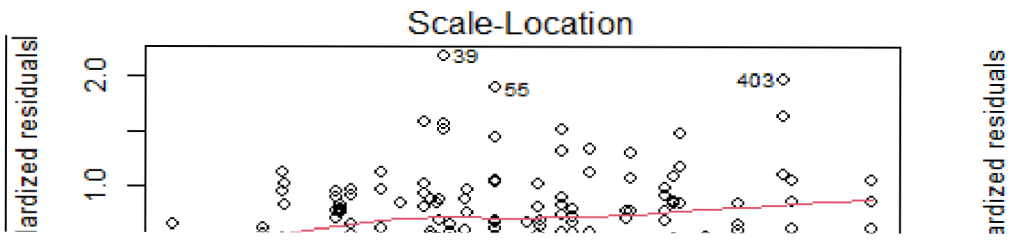
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
genus	9	3.09009	0.34334	38.5332	< 2.2e-16
polyploid	1	2.57883	2.57883	289.4208	< 2.2e-16
treat	1	0.51232	0.51232	57.4969	1.36E-11
genus:polyploid	9	1.45168	0.1613	18.1023	< 2.2e-16
genus:treat	9	0.27868	0.03096	3.4751	0.000855
polyploid:treat	1	0.03594	0.03594	4.0339	0.047139
genus:polyploid:treat	9	0.18002	0.02	2.2448	0.02445
Residuals	106	0.94449	0.00891		

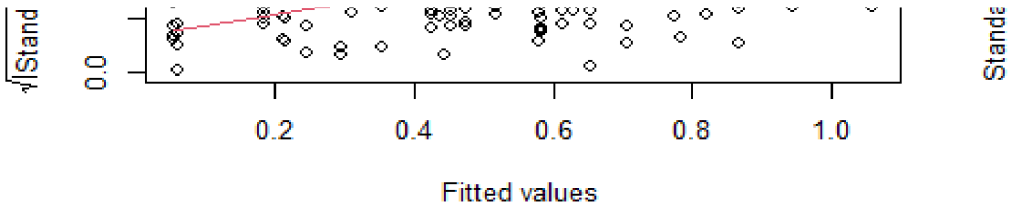
```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1


summary(m.hla)

Call:
lm(formula = ei ~ genus * polyploid * treat, data = de.hla)

Residuals:
     Min       1Q   Median       3Q      Max
-0.20280 -0.04082 -0.00476  0.03216  0.38318

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)	
(Intercept)	0.57676	0.01644	35.082	< 2e-16	***
genus1	0.04904	0.0453	1.082	0.281519	
genus2	-0.09819	0.0453	-2.167	0.032445	*
genus3	0.13504	0.05144	2.625	0.009946	**
genus4	-0.16014	0.0453	-3.535	0.000606	***
genus5	0.03551	0.0453	0.784	0.434858	
genus6	0.24824	0.06192	4.009	0.000114	***
genus7	-0.22201	0.0453	-4.901	3.45E-06	***
genus8	0.07732	0.04118	1.877	0.063204	.
genus9	0.13016	0.0453	2.873	0.00491	**
polyploidYES	-0.23248	0.02303	-10.097	< 2e-16	***
treatT	0.1472	0.02303	6.393	4.46E-09	***
genus1:polyploidYES	-0.10545	0.06399	-1.648	0.102316	
genus2:polyploidYES	0.0431	0.06399	0.674	0.502041	
genus3:polyploidYES	0.16408	0.07268	2.258	0.026026	*
genus4:polyploidYES	0.2501	0.07666	3.263	0.001486	**
genus5:polyploidYES	-0.32012	0.06399	-5.003	2.25E-06	***
genus6:polyploidYES	-0.13965	0.07666	-1.822	0.071315	.
genus7:polyploidYES	0.062	0.06399	0.969	0.334771	
genus8:polyploidYES	0.0172	0.06582	0.261	0.794398	

```
genus9:polyploidYES                    -0.03817   0.06399   -0.597  0.552046

genus1:treatT                           0.01152   0.06399    0.18   0.857451
genus2:treatT                          -0.04375   0.06399   -0.684  0.495598
genus3:treatT                           0.0721    0.07268    0.992   0.32347
genus4:treatT                          -0.1187    0.06399   -1.855  0.066356 .
genus5:treatT                           0.1083    0.06399    1.692  0.093491 .
genus6:treatT                          -0.02864   0.08044   -0.356   0.72254
genus7:treatT                           0.08072   0.06399    1.262  0.209886
genus8:treatT                          -0.02571   0.06114   -0.421  0.674971
genus9:treatT                          -0.09208   0.06399   -1.439  0.153089
polyploidYES:treatT                    -0.06485   0.03206   -2.023  0.045594 *
genus1:polyploidYES:treatT              0.13603   0.09031    1.506   0.13499
genus2:polyploidYES:treatT             -0.01777   0.09031   -0.197  0.844347
genus3:polyploidYES:treatT              0.26062   0.10263    2.539  0.012552 *
genus4:polyploidYES:treatT              0.11878   0.09969    1.191  0.236137
genus5:polyploidYES:treatT             -0.19607   0.09031   -2.171  0.032152 *
genus6:polyploidYES:treatT             -0.21062   0.10548   -1.997  0.048408 *
genus7:polyploidYES:treatT             -0.10005   0.09031   -1.108  0.270436
genus8:polyploidYES:treatT              0.08446   0.09162    0.922  0.358706
genus9:polyploidYES:treatT              0.04748   0.09031    0.526    0.6002
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.09439 on 106 degrees of freedom
Multiple R-squared:  0.8959,    Adjusted R-squared:  0.8576
F-statistic: 23.39 on 39 and 106 DF,  p-value: < 2.2e-16
```



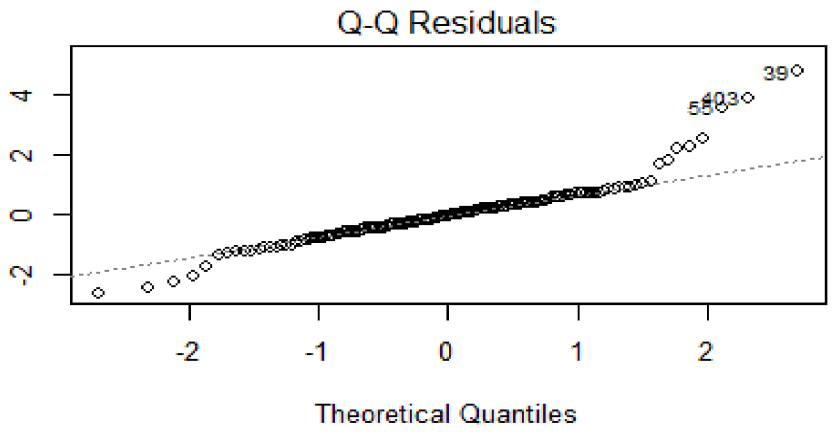


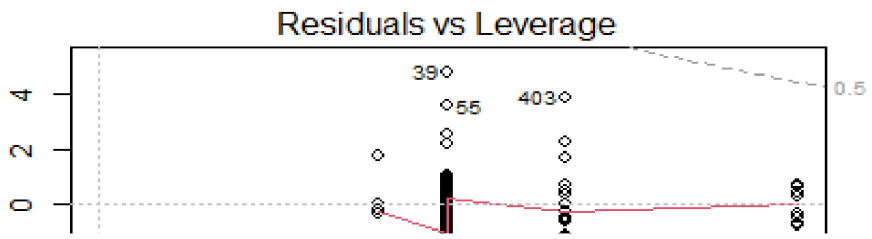

√|Stand
0.0
0.2
0.4
0.6
0.8
1.0
Fitted values
Standa

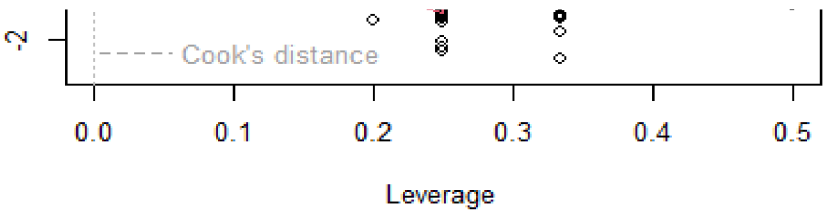
***
***
***
***
***
*
*

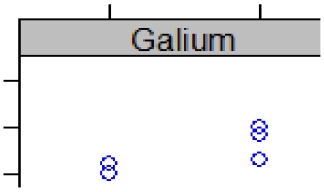
	0.6258
	0.47857
	0.7118
	0.41662
	0.61227
	0.825
	0.35475
	0.65408
	0.70692
	0.38179
	-0.33793
	-0.18938
	-0.0684
	0.01762
	-0.5526
	-0.37213
	-0.17048
	-0.21528

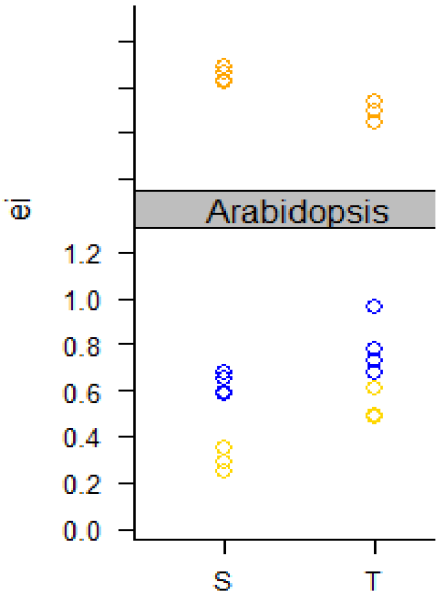
-0.27065
-0.16557
0.15872
0.10345
0.2193
0.0285
0.2555
0.11856
0.22792
0.12149
0.05512
0.18344
0.07118
-0.08262
0.19577
0.05393
-0.26092
-0.27547
-0.1649
0.01961
-0.01737
-0.18771

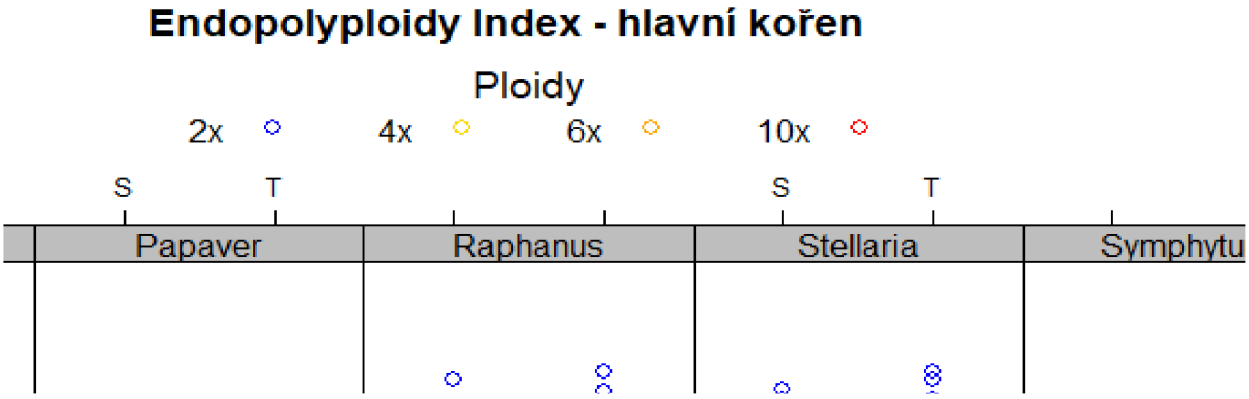


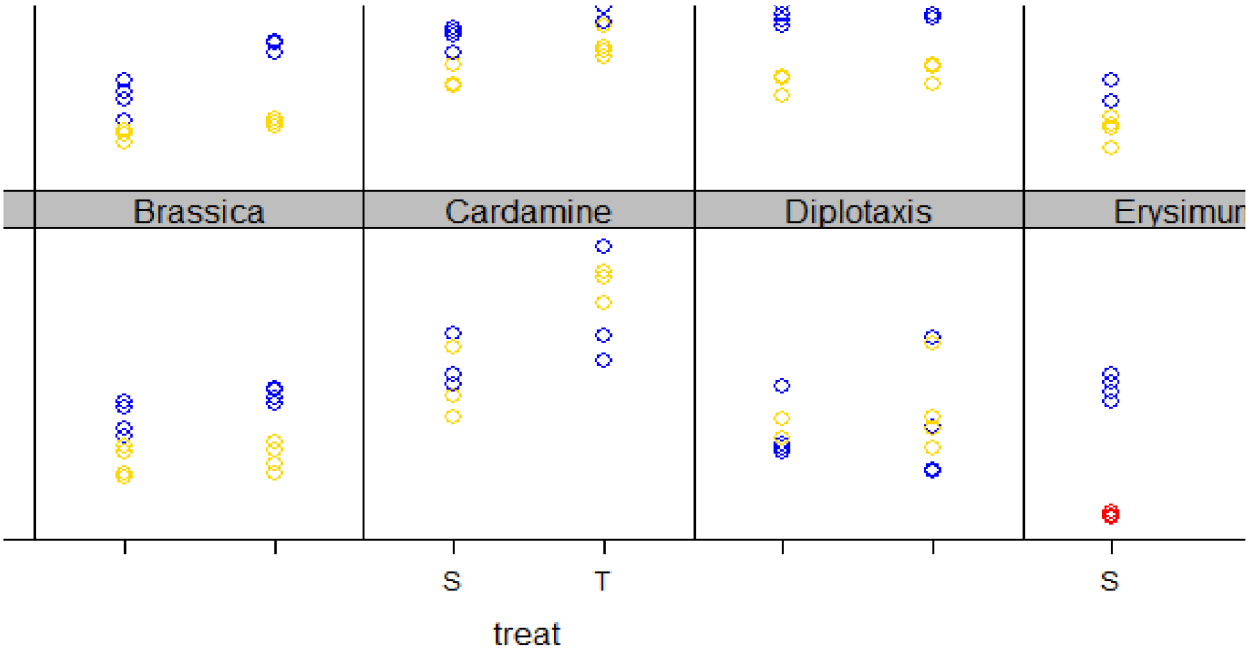


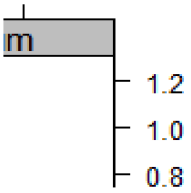

-2
Cook's distance
0.0
0.1
0.2
0.3
0.4
0.5
Leverage

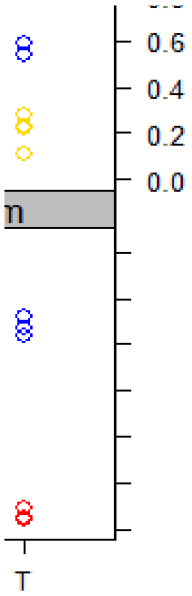

Galium


Arabidopsis
1.2
1.0
0.8
0.6
0.4
0.2
0.0
S
T


Endopolyploidy Index - hlavní kořen
Ploidy
2x
4x
6x
10x
S
T
S
T
Papaver
Raphanus
Stellaria
Symphytu


Brassica
Cardamine
Diplotaxis
Erysimur
S
T
S
treat


m
1.2
1.0
0.8


0.6
0.4
0.2
0.0
n
T

m.ved<-lm(ei~genus*polyploid*treat, data=de.ved)

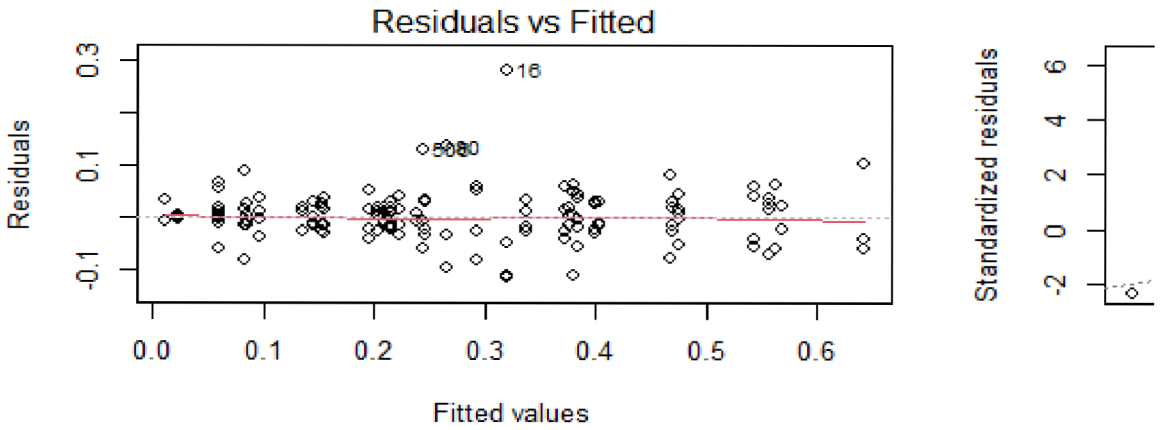
```
anova(m.ved)
Analysis of Variance Table

Response: ei
```

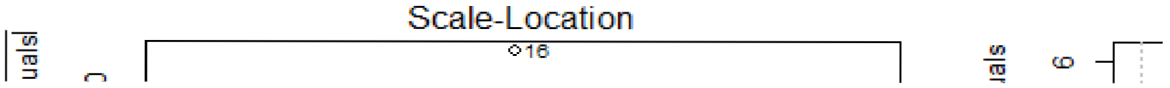
	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
genus	9	2.22857	0.24762	125.3845	< 2.2e-16	***
polyploid	1	0.90588	0.90588	458.699	< 2.2e-16	***
treat	1	0.06623	0.06623	33.5361	7.50E-08	***
genus:polyploid	9	0.39623	0.04403	22.2929	< 2.2e-16	***
genus:treat	9	0.20646	0.02294	11.6161	1.87E-12	***
polyploid:treat	1	0.00401	0.00401	2.0301	0.1572	
genus:polyploid:treat	9	0.08266	0.00918	4.6506	3.48E-05	***
Residuals	104	0.20539	0.00197			

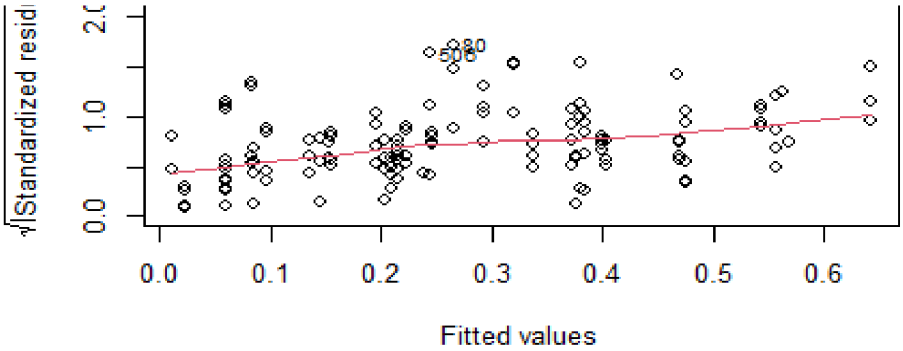
```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1


summary(m.ved)

Call:
lm(formula = ei ~ genus * polyploid * treat, data = de.ved1)

Residuals:
      Min        1Q    Median        3Q       Max
-0.114025 -0.021800 -0.000788  0.018356  0.134167

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)	
(Intercept)	0.355815	0.007845	45.353	< 2e-16	***
genus1	-0.16199	0.021366	-7.582	1.49E-11	***
genus2	-0.13309	0.021366	-6.229	1.01E-08	***
genus3	0.046985	0.024253	1.937	0.05542	.
genus4	-0.12868	0.024253	-5.306	6.37E-07	***
genus5	-0.15307	0.021366	-7.164	1.17E-10	***
genus6	0.212635	0.029181	7.287	6.38E-11	***
genus7	-0.10932	0.021366	-5.116	1.43E-06	***
genus8	0.028005	0.01943	1.441	0.152505	
genus9	0.191185	0.021366	8.948	1.50E-14	***
polyploidYES	-0.18067	0.010916	-16.551	< 2e-16	***
treatT	0.025013	0.011065	2.26	0.025875	*
genus1:polyploidYES	0.093594	0.030151	3.104	0.002459	**
genus2:polyploidYES	0.082794	0.030151	2.746	0.007111	**
genus3:polyploidYES	-0.0065	0.034241	-0.19	0.849856	
genus4:polyploidYES	0.192435	0.037891	5.079	1.68E-06	***
genus5:polyploidYES	-0.01168	0.030151	-0.387	0.699234	
genus6:polyploidYES	-0.29078	0.036112	-8.052	1.42E-12	***
genus7:polyploidYES	0.018869	0.030151	0.626	0.532818	

```
genus8:polyploidYES              0.062282  0.031012     2.008  0.047204 *
genus9:polyploidYES              -0.00168  0.030151    -0.056  0.955637

genus1:treatT                    -0.06646  0.030206      -2.2  0.029996 *
genus2:treatT                    0.045787  0.030206     1.516  0.132596
genus3:treatT                    0.039437  0.037935      1.04  0.300934
genus4:treatT                    0.146704  0.032312      4.54   1.52E-05 ***
genus5:treatT                    -0.03256  0.030206    -1.078  0.283512
genus6:treatT                     0.04907  0.037935     1.294  0.198685
genus7:treatT                    -0.11676  0.030206    -3.866  0.000193 ***
genus8:treatT                    0.148492  0.028869     5.144   1.27E-06 ***
genus9:treatT                    -0.10159  0.030206    -3.363  0.001079 **
polyploidYES:treatT              0.023454  0.015255     1.537  0.127215
genus1:polyploidYES:treatT       -0.02868  0.042575    -0.674  0.502055
genus2:polyploidYES:treatT        -0.0742  0.042575    -1.743  0.084306 .
genus3:polyploidYES:treatT       0.072796  0.051015     1.427   0.15659
genus4:polyploidYES:treatT       -0.22437  0.048366    -4.639   1.02E-05 ***
genus5:polyploidYES:treatT       -0.00328  0.042575    -0.077  0.938764
genus6:polyploidYES:treatT       -0.05954  0.049708    -1.198  0.233745
genus7:polyploidYES:treatT       0.043496  0.042575     1.022  0.309319
genus8:polyploidYES:treatT       0.012683  0.043189     0.294    0.7696
genus9:polyploidYES:treatT       0.060271  0.042575     1.416  0.159863
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.04444 on 104 degrees of freedom
Multiple R-squared:  0.9498,    Adjusted R-squared:  0.931
F-statistic: 50.51 on 39 and 104 DF,  p-value: < 2.2e-16
```






√|Standardized resid
0.0
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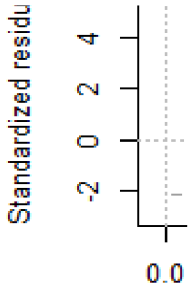
2.0
80
506
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fitted values


Standardized residu
-2
0
2
4
0.0

0.193825
0.222725
0.4028
0.227133
0.20275
0.56845
0.2465
0.38382
0.547
0.563147

-0.08708
-0.09788
-0.18717
0.011766
-0.19235
-0.47145
-0.1618

-0.11839
-0.18235
-0.32
-0.04145
0.0708
0.06445
0.171717
-0.00755
0.074083
-0.09175
0.173505
-0.07658
-0.0871
-0.00523
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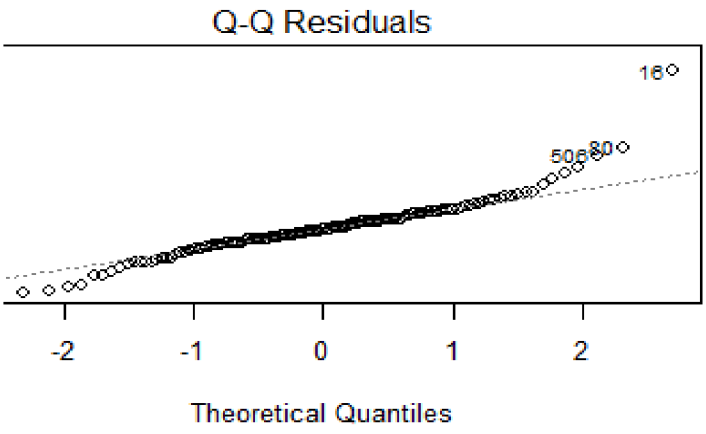
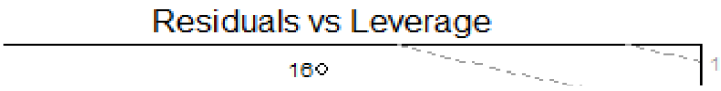
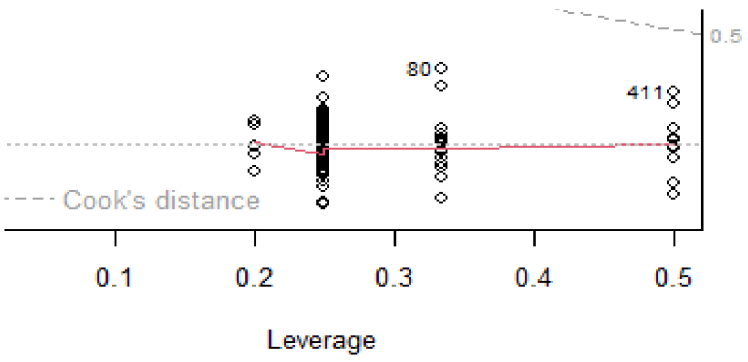
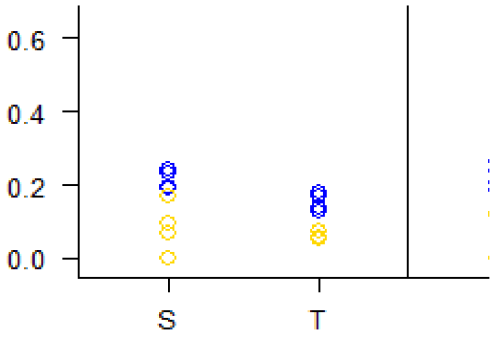
0.224277



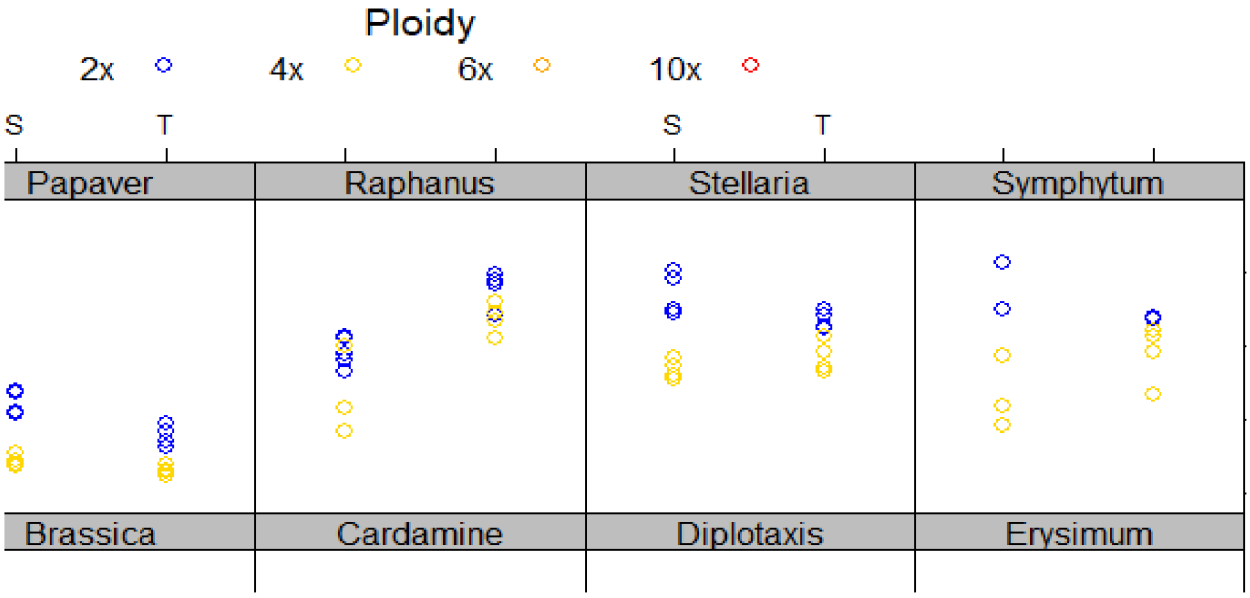


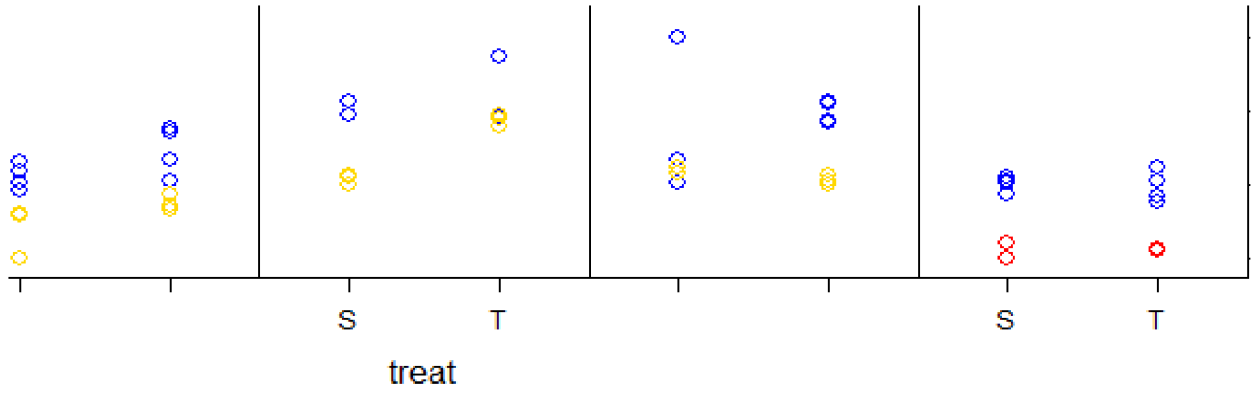

0.5
80
411
Cook's distance
0.1
0.2
0.3
0.4
0.5
Leverage

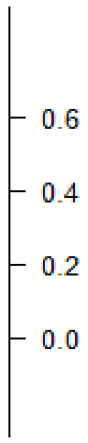
Galium
Arabidopsis


0.6
0.4
0.2
0.0
S
T

Endopolyploidy Index - hlavní kořen




S
T
S
T
treat


0.6
0.4
0.2
0.0

```
Response: log(f.shoot.day)
                       Df Sum Sq Mean Sq  F value     Pr(>F)
genus                   9  24.962   2.774  32.4409 < 2.2e-16  ***
polyploid               1   0.02    0.02   0.2378  0.626783
treat                   1  52.562  52.562   614.8 < 2.2e-16  ***
genus:polyploid         9  12.484   1.387  16.224 < 2.2e-16  ***
genus:treat             9   8.138   0.904 10.5763   1.50E-11 ***
polyploid:treat         1   0.047   0.047  0.5441  0.462348
genus:polyploid:treat   9   3.063    0.34  3.9813  0.000211 ***
Residuals             106   9.062   0.085

lm(formula = log(f.shoot.day) ~ genus * polyploid * treat,
    data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.79321 -0.16175  0.01433  0.17136  0.73805

Coefficients:
                          Estimate  Std. Error  t value    Pr(>|t|)
(Intercept)               -3.6448   0.05092    -71.572 < 2e-16    ***
genus1                    0.25506   0.14033     1.818  0.071954 .
genus2                    0.10004   0.14033     0.713  0.477488
genus3                    0.25917   0.15935     1.626  0.106821
genus4                   -0.26471   0.14033    -1.886  0.061984 .
genus5                   -0.47216   0.14033    -3.365  0.001068 **
genus6                   -0.66138   0.19181    -3.448  0.000811 ***
genus7                    -0.1857   0.14033    -1.323  0.188581
genus8                    0.62815   0.12756     4.924   3.13E-06 ***
genus9                    0.21123   0.14033     1.505  0.135229
polyploidYES              0.06185   0.07132     0.867  0.387763
treatT                   -1.29109   0.07132    -18.102 < 2e-16    ***
genus1:polyploidYES      -0.10755    0.1982    -0.543  0.588525
genus2:polyploidYES       0.21524    0.1982     1.086  0.279966
genus3:polyploidYES       0.66862   0.22513      2.97  0.003685 **
genus4:polyploidYES       0.22882   0.23745     0.964  0.337415
genus5:polyploidYES      -0.65517    0.1982    -3.306  0.001294 **
genus6:polyploidYES      -0.17133   0.23745    -0.722  0.472169
genus7:polyploidYES      -0.01464    0.1982    -0.074  0.941252
genus8:polyploidYES       0.23807   0.20387     1.168  0.245535
genus9:polyploidYES      -0.61366    0.1982    -3.096  0.002509 **
genus1:treatT             0.20445    0.1982     1.031  0.304655
genus2:treatT              0.1476    0.1982     0.745  0.458109
genus3:treatT            -0.77811   0.22513    -3.456  0.000789 ***
genus4:treatT             -0.4477    0.1982    -2.259  0.025943 *
genus5:treatT             0.49853    0.1982     2.515  0.013397 *
genus6:treatT             0.58465   0.24917     2.346  0.020814 *
genus7:treatT             0.65087    0.1982     3.284  0.001388 **
```

```
genus8:treatT                    -0.52028   0.18938   -2.747  0.007063 **        -1.81137
genus9:treatT                     0.46548    0.1982    2.348  0.020705 *         -0.82561
polyploidYES:treatT               0.13582    0.0993    1.368  0.174259           -2.09658
genus1:polyploidYES:treatT       -0.22876   0.27974   -0.818  0.415331           -0.09294
genus2:polyploidYES:treatT       -0.16661   0.27974   -0.596  0.552715           -0.03079
genus3:polyploidYES:treatT        1.20565   0.31789    3.793  0.000248 ***        1.34147
genus4:polyploidYES:treatT       -0.22349    0.3088   -0.724  0.470818           -0.08767
genus5:polyploidYES:treatT       -1.09238   0.27974   -3.905  0.000166 ***       -0.95656
genus6:polyploidYES:treatT        0.66977   0.32673    2.05  0.042844 *          0.80559
genus7:polyploidYES:treatT       -0.50136   0.27974   -1.792  0.075954 .         -0.36554
genus8:polyploidYES:treatT       -0.16007   0.28379   -0.564  0.573905           -0.02425
genus9:polyploidYES:treatT        0.14966   0.27974    0.535  0.593778            0.28548
---                                                                               0.48341
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.2924 on 106 degrees of freedom
Multiple R-squared:  0.9179,    Adjusted R-squared:  0.8876
F-statistic: 30.37 on 39 and 106 DF,  p-value: < 2.2e-16
```

```
Response: log(f.root.day)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
genus	9	43.948	4.8831	32.008	< 2.2e-16	***
polyploid	1	0.073	0.0733	0.4808	0.489591	
treat	1	23.708	23.7084	155.4058	< 2.2e-16	***
genus:polyploid	9	8.356	0.9284	6.0858	7.30E-07	***
genus:treat	9	21.457	2.3841	15.6275	5.77E-16	***
polyploid:treat	1	1.383	1.3832	9.0667	0.003254	**
genus:polyploid:treat	9	2.878	0.3198	2.0961	0.036085	*
Residuals	106	16.171	0.1526			

```
lm(formula = log(f.root.day) ~ genus * polyploid * treat, data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.88770 -0.20795 -0.01362  0.21995  0.97143

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)		
(Intercept)	-4.15817	0.068026	-61.126	< 2e-16	***	
genus1	-0.3505	0.187455	-1.87	0.064272	.	-4.50867
genus2	-0.00441	0.187455	-0.024	0.98126		-4.16258
genus3	0.515827	0.212861	2.423	0.017074	*	-3.64234
genus4	-1.0068	0.187455	-5.371	4.67E-07	***	-5.16497
genus5	-0.70314	0.187455	-3.751	0.000288	***	-4.86131
genus6	-0.54617	0.256224	-2.132	0.035351	*	-4.70434
genus7	0.069664	0.187455	0.372	0.710908		-4.08851
genus8	1.028825	0.170402	6.038	2.34E-08	***	-3.12934
genus9	-0.13831	0.187455	-0.738	0.46225		-4.29648
polyploidYES	-0.08723	0.095274	-0.916	0.361987		-3.02316
treatT	-1.07042	0.095274	-11.235	< 2e-16	***	
genus1:polyploidYES	-0.08446	0.264765	-0.319	0.750346		-0.17169
genus2:polyploidYES	-0.054	0.264765	-0.204	0.838788		-0.14122
genus3:polyploidYES	0.694518	0.300735	2.309	0.02286	*	0.607291
genus4:polyploidYES	-0.23949	0.317194	-0.755	0.451916		-0.32671
genus5:polyploidYES	-0.01791	0.264765	-0.068	0.946201		-0.10514
genus6:polyploidYES	-0.06025	0.317194	-0.19	0.849717		-0.14748
genus7:polyploidYES	0.058797	0.264765	0.222	0.824686		-0.02843
genus8:polyploidYES	0.271444	0.272339	0.997	0.321175		0.184217
genus9:polyploidYES	-0.829	0.264765	-3.131	0.002251	**	-0.91623
						0.173115
genus1:treatT	0.324527	0.264765	1.226	0.223021		-0.74589
genus2:treatT	-0.33723	0.264765	-1.274	0.205556		-1.40765
genus3:treatT	-1.03399	0.300735	-3.438	0.000838	***	-2.10441
genus4:treatT	0.151031	0.264765	0.57	0.56959		-0.91939
genus5:treatT	0.863507	0.264765	3.261	0.001492	**	-0.20691
genus6:treatT	0.712832	0.33284	2.142	0.034511	*	-0.35759
genus7:treatT	1.046863	0.264765	3.954	0.000139	***	-0.02356
genus8:treatT	-1.06478	0.252979	-4.209	5.39E-05	***	-2.1352

```
genus9:treatT                   0.886842  0.264765      3.35  0.001122 **        -0.18358
polyploidYES:treatT             0.454252  0.132646     3.425  0.000877 ***       -2.62002
genus1:polyploidYES:treatT      -0.04029  0.373687    -0.108  0.914342           0.413961
genus2:polyploidYES:treatT      0.121307  0.373687     0.325  0.746107           0.575559
genus3:polyploidYES:treatT      0.741318  0.424646     1.746  0.083755 .           1.19557
genus4:polyploidYES:treatT      -0.23315  0.412496    -0.565  0.573128           0.221107
genus5:polyploidYES:treatT      -1.18335  0.373687    -3.167  0.002014 **          -0.7291
genus6:polyploidYES:treatT      0.650785  0.436457     1.491  0.138915           1.105037
genus7:polyploidYES:treatT      -0.57757  0.373687    -1.546  0.125179           -0.12332
genus8:polyploidYES:treatT      -0.31456  0.379091     -0.83  0.408536           0.139695
genus9:polyploidYES:treatT      0.200248  0.373687     0.536   0.59317             0.6545
---                                                                              1.089509
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3906 on 106 degrees of freedom
Multiple R-squared:  0.8629,    Adjusted R-squared:  0.8125
F-statistic: 17.11 on 39 and 106 DF,  p-value: < 2.2e-16
```

m.dsd1<-lm(log(d.shoot.day)~genus*polyploid*treat, data=de.cep)

```
anova(m.dsd1)
Analysis of Variance Table

Response: log(d.shoot.day)
```

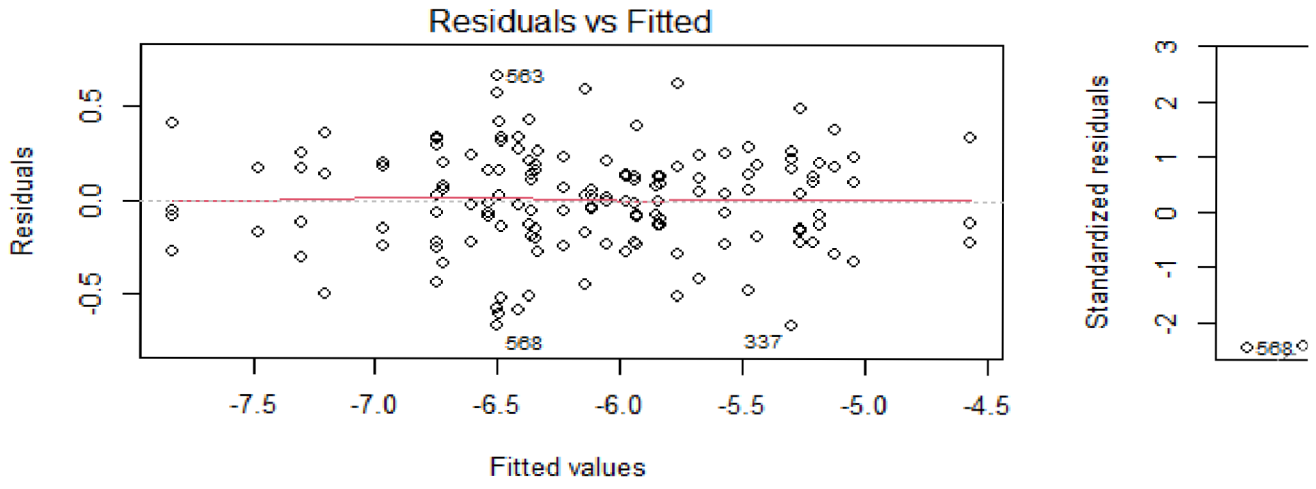
	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
genus	9	18.4334	2.0482	20.8211	< 2.2e-16	***
polyploid	1	0.0049	0.0049	0.0499	0.823714	
treat	1	21.7752	21.7752	221.362	< 2.2e-16	***
genus:polyploid	9	12.6605	1.4067	14.3004	7.02E-15	***
genus:treat	9	12.1047	1.345	13.6726	2.38E-14	***
polyploid:treat	1	0.1027	0.1027	1.0436	0.309309	
genus:polyploid:treat	9	3.577	0.3974	4.0403	0.000179	***
Residuals	106	10.4271	0.0984			

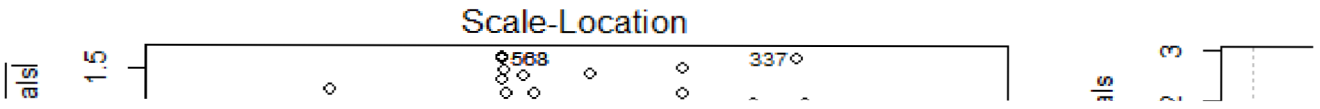
```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

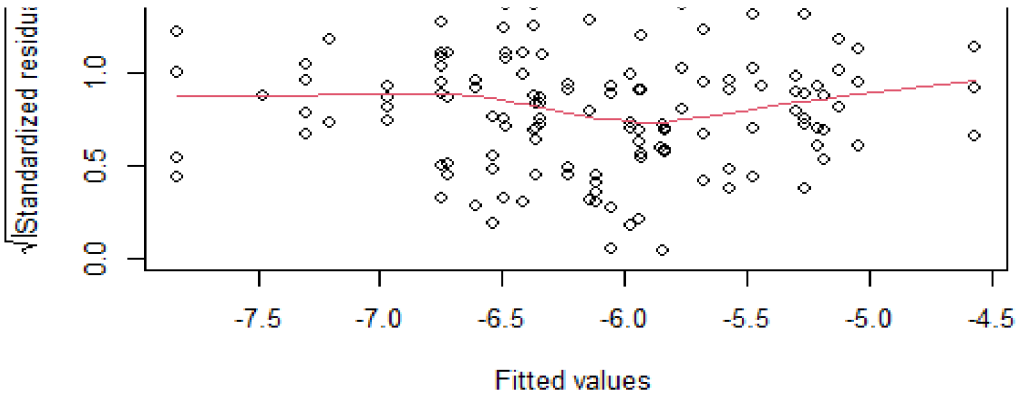
```
summary(m.dsd1)

Call:
lm(formula = log(d.shoot.day) ~ genus * polyploid * treat, data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.66434 -0.18538  0.02311  0.18203  0.66063

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)	
(Intercept)	-5.72372	0.054625	-104.783	< 2e-16	***
genus1	0.253182	0.150525	1.682	0.095513	.
genus2	0.149526	0.150525	0.993	0.322794	
genus3	0.510244	0.170926	2.985	0.003519	**
genus4	-0.41848	0.150525	-2.78	0.00643	**
genus5	-0.25289	0.150525	-1.68	0.095889	.
genus6	-0.61207	0.205746	-2.975	0.00363	**
genus7	-0.33045	0.150525	-2.195	0.030319	*
genus8	0.459302	0.136832	3.357	0.001096	**
genus9	-0.04039	0.150525	-0.268	0.788965	
polyploidYES	0.002283	0.076505	0.03	0.976253	
treatT	-0.89237	0.076505	-11.664	< 2e-16	***
genus1:polyploidYES	-0.2102	0.212604	-0.989	0.325065	
genus2:polyploidYES	0.276427	0.212604	1.3	0.196355	
genus3:polyploidYES	0.645584	0.241488	2.673	0.008698	**
genus4:polyploidYES	0.29176	0.254705	1.145	0.254589	
genus5:polyploidYES	-0.44033	0.212604	-2.071	0.040776	*
genus6:polyploidYES	-0.16437	0.254705	-0.645	0.520115	
genus7:polyploidYES	-0.06038	0.212604	-0.284	0.776957	

```
genus8:polyploidYES            0.075951  0.218686    0.347  0.729051
genus9:polyploidYES            -0.73441  0.212604   -3.454  0.000794 ***

genus1:treatT                  0.525944  0.212604    2.474  0.014955 *
genus2:treatT                  0.121595  0.212604    0.572   0.56858
genus3:treatT                  -1.10063  0.241488   -4.558  1.39E-05 ***
genus4:treatT                  -0.26503  0.212604   -1.247  0.215301
genus5:treatT                  0.495943  0.212604    2.333  0.021552 *
genus6:treatT                  0.617315  0.267268     2.31  0.022842 *
genus7:treatT                  0.581021  0.212604    2.733  0.007358 **
genus8:treatT                  -0.56237   0.20314   -2.768  0.006651 **
genus9:treatT                  0.729436  0.212604    3.431  0.000858 ***
polyploidYES:treatT            0.175419  0.106514    1.647  0.102538
genus1:polyploidYES:treatT      -0.0715  0.300067   -0.238   0.81212
genus2:polyploidYES:treatT      -0.3425  0.300067   -1.141  0.256266
genus3:polyploidYES:treatT     1.339406  0.340987    3.928  0.000153 ***
genus4:polyploidYES:treatT     -0.14052  0.331231   -0.424  0.672257
genus5:polyploidYES:treatT     -1.19725  0.300067    -3.99  0.000122 ***
genus6:polyploidYES:treatT     0.759001  0.350471    2.166  0.032579 *
genus7:polyploidYES:treatT     -0.50342  0.300067   -1.678  0.096356 .
genus8:polyploidYES:treatT     -0.07575  0.304407   -0.249  0.803956
genus9:polyploidYES:treatT     0.002598  0.300067    0.009  0.993107
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3136 on 106 degrees of freedom
Multiple R-squared:  0.8682,    Adjusted R-squared:  0.8196
F-statistic:  17.9 on 39 and 106 DF,  p-value: < 2.2e-16
```



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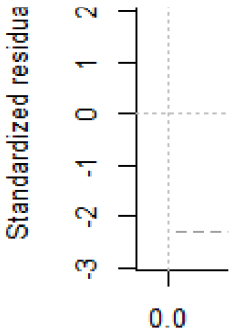
0.5
1.0
-7.5
-7.0
-6.5
-6.0
-5.5
-5.0
-4.5
Fitted values


Standardized residua
-3
-2
-1
0
1
2
0.0

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-5.21348
-6.1422
-5.97661
-6.33579
-6.05417
-5.26442
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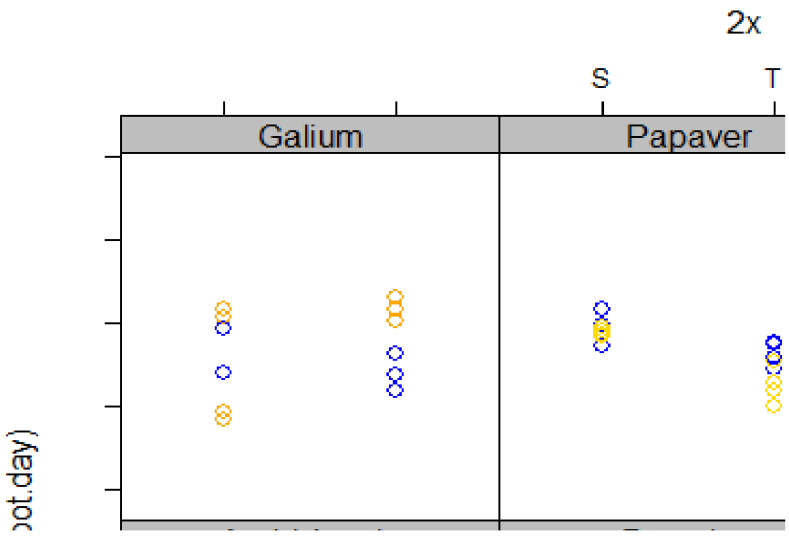

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-0.39642
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-0.31135
-1.45474
-0.16293
-2.0356
0.103917
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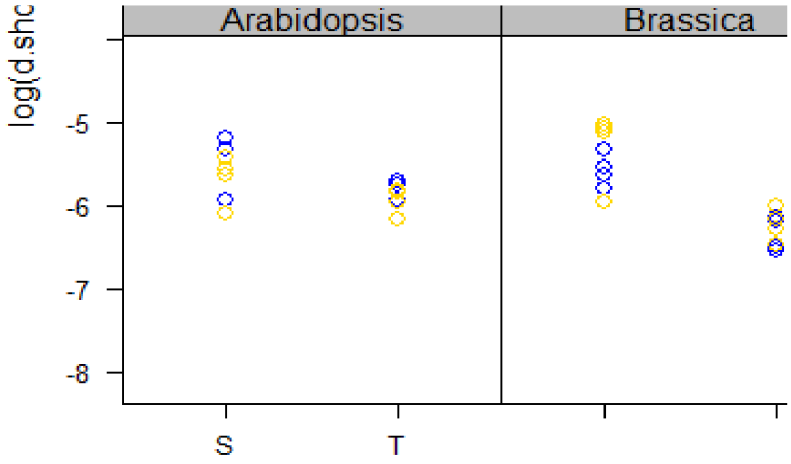
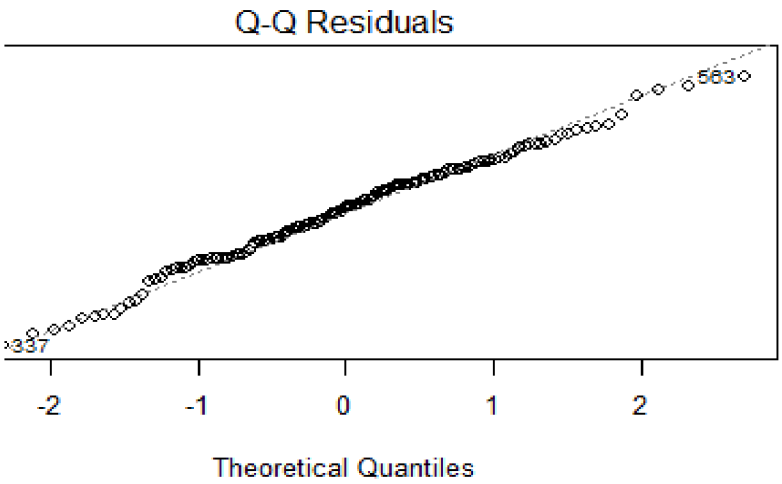
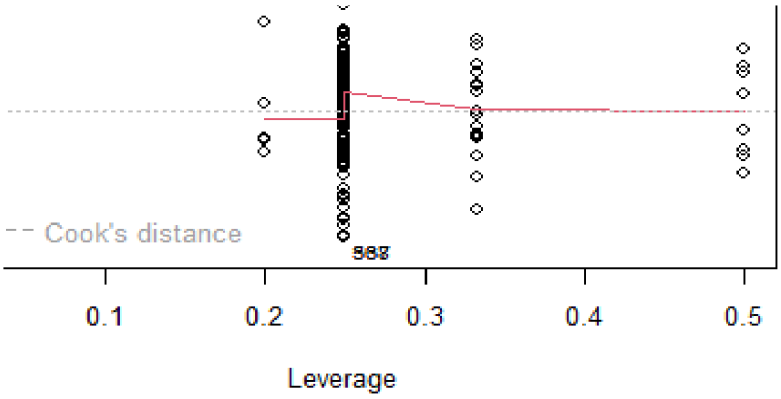
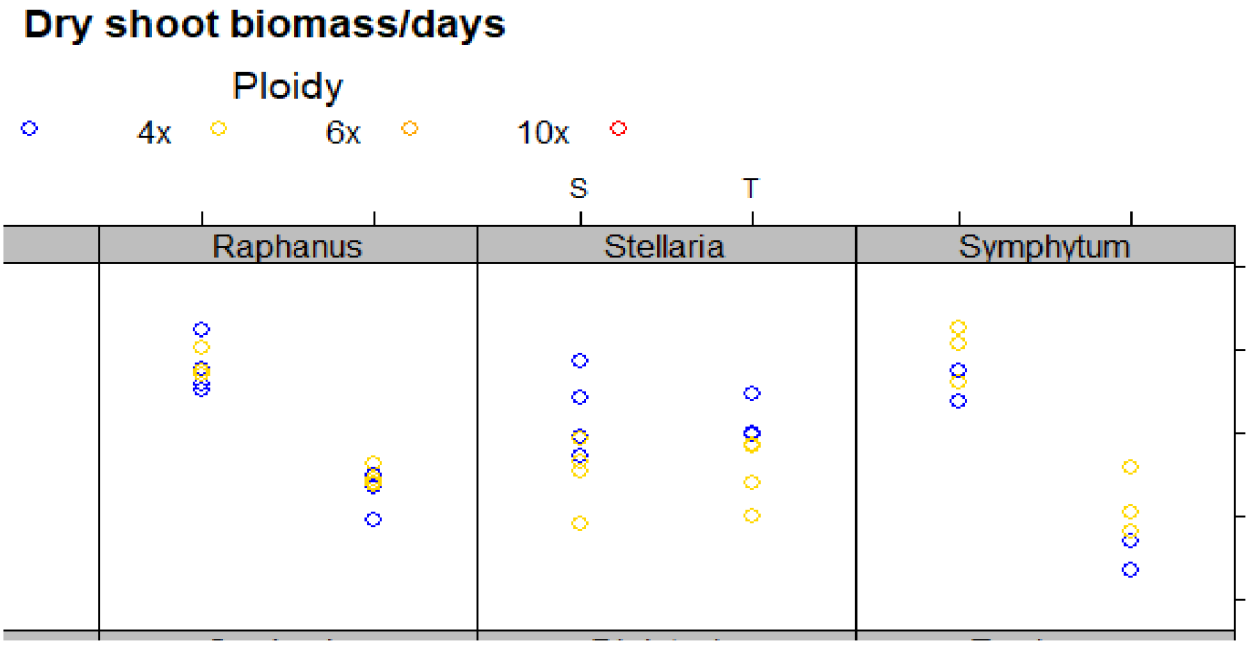
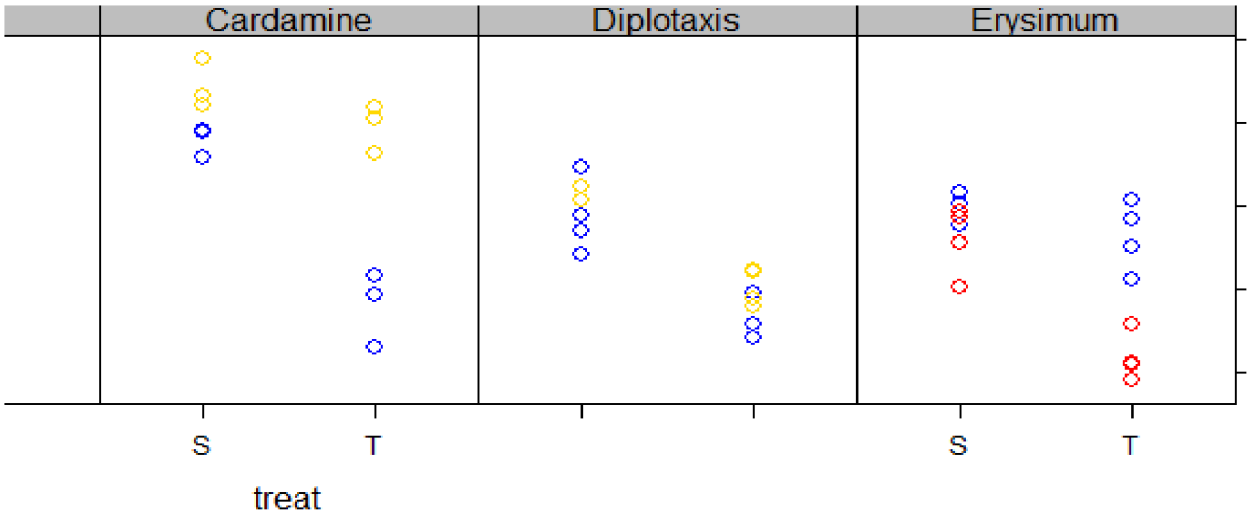
0.405361






Cook's distance
988
0.1
0.2
0.3
0.4
0.5
Leverage


Dry shoot biomass/days
Ploidy
4x
6x
10x
S
T
Raphanus
Stellaria
Symphytum


Cardamine
Diplotaxis
Erysimum
S
T
S
T
treat

-

- -5

- -6

- -7

- -8

-

-

-

-

-

m.drd1<-lm(log(d.root.day)~genus*polyploid*treat, data=de.cep)

```
anova(m.drd1)
Analysis of Variance Table

Response: log(d.root.day)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
genus	9	31.2061	3.4673	24.9729	< 2.2e-16	***
polyploid	1	0.0006	0.0006	0.0043	0.947629	
treat	1	17.0874	17.0874	123.0687	< 2.2e-16	***
genus:polyploid	9	7.6415	0.8491	6.1152	6.76E-07	***
genus:treat	9	21.5849	2.3983	17.2735	< 2.2e-16	***
polyploid:treat	1	1.1235	1.1235	8.0921	0.005337	**
genus:polyploid:treat	9	2.0437	0.2271	1.6355	0.114387	
Residuals	106	14.7175	0.1388			

```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
summary(m.drd1)

Call:
lm(formula = log(d.root.day) ~ genus * polyploid * treat, data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.90942 -0.18372 -0.00097  0.22883  0.89731

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)	
(Intercept)	-6.16897	0.064897	-95.058	< 2e-16	***
genus1	-0.06178	0.178831	-0.345	0.730415	
genus2	0.072447	0.178831	0.405	0.68621	
genus3	0.238005	0.203068	1.172	0.243806	
genus4	-0.67545	0.178831	-3.777	0.000262	***
genus5	-0.57048	0.178831	-3.19	0.001871	**
genus6	-0.63658	0.244437	-2.604	0.010528	*
genus7	-0.45933	0.178831	-2.569	0.011606	*
genus8	0.955902	0.162563	5.88	4.82E-08	***
genus9	-0.21148	0.178831	-1.183	0.239633	
polyploidYES	-0.12345	0.090891	-1.358	0.177279	
treatT	-0.91314	0.090891	-10.046	< 2e-16	***
genus1:polyploidYES	-0.11881	0.252584	-0.47	0.639058	
genus2:polyploidYES	0.166427	0.252584	0.659	0.511392	
genus3:polyploidYES	0.562685	0.2869	1.961	0.052472	.
genus4:polyploidYES	-0.39628	0.302602	-1.31	0.193174	
genus5:polyploidYES	-0.16906	0.252584	-0.669	0.504752	

```
genus6:polyploidYES              -0.0785  0.302602    -0.259  0.795823
genus7:polyploidYES             0.263409  0.252584     1.043  0.299387
genus8:polyploidYES              0.09456   0.25981     0.364  0.716616
genus9:polyploidYES              -0.7446  0.252584    -2.948  0.003936 **

genus1:treatT                   0.198269  0.252584     0.785  0.434226
genus2:treatT                   -0.44957  0.252584     -1.78  0.077961 .
genus3:treatT                   -0.98815    0.2869    -3.444  0.000821 ***
genus4:treatT                   0.042711  0.252584     0.169  0.866044
genus5:treatT                   0.814185  0.252584     3.223  0.001684 **
genus6:treatT                    0.83568  0.317528     2.632   0.00976 **
genus7:treatT                   1.028756  0.252584     4.073  8.98E-05 ***
genus8:treatT                   -1.03259   0.24134    -4.279  4.14E-05 ***
genus9:treatT                    0.96445  0.252584     3.818  0.000227 ***
polyploidYES:treatT             0.407581  0.126544     3.221  0.001697 **
genus1:polyploidYES:treatT      0.000189  0.356495     0.001  0.999578
genus2:polyploidYES:treatT      0.120721  0.356495     0.339  0.735555
genus3:polyploidYES:treatT      0.603782   0.40511      1.49  0.139084
genus4:polyploidYES:treatT      0.042394  0.393519     0.108  0.914414
genus5:polyploidYES:treatT      -0.97309  0.356495     -2.73  0.007426 **
genus6:polyploidYES:treatT      0.658502  0.416377     1.582  0.116742
genus7:polyploidYES:treatT      -0.65293  0.356495    -1.832   0.06983 .
genus8:polyploidYES:treatT      -0.14474  0.361651      -0.4  0.689807
genus9:polyploidYES:treatT      0.001323  0.356495     0.004  0.997046
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3726 on 106 degrees of freedom
Multiple R-squared:  0.8457,    Adjusted R-squared:  0.789
F-statistic:  14.9 on 39 and 106 DF,  p-value: < 2.2e-16
```

-6.23076
-6.09653
-5.93097
-6.84442
-6.73945
-6.80555
-6.6283
-5.21307
-6.38045
-4.82024

-0.24226
0.042977
0.439235
-0.51973
-0.29251

-0.20195
0.139959
-0.02889
-0.86805
0.296705
-0.71487
-1.36271
-1.90129
-0.87043
-0.09895
-0.07746
0.11562
-1.94573
0.051314
-2.32687
0.40777
0.528302
1.011363
0.449975
-0.56551
1.066083
-0.24535
0.262845
0.408904
0.751431

bez Rap DW1

```
Response: log(t.f.root.shoot)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
genus	9	24.3731	2.7081	48.5162	< 2.2e-16	***
polyploid	1	0.0047	0.0047	0.0848	0.7715	
treat	1	5.3957	5.3957	96.6644	< 2.2e-16	***
genus:polyploid	9	2.487	0.2763	4.9505	1.52E-05	***
genus:treat	9	7.0531	0.7837	14.0396	1.29E-14	***
polyploid:treat	1	1.0673	1.0673	19.1216	2.90E-05	***
genus:polyploid:treat	9	0.3507	0.039	0.6982	0.7092	
Residuals	105	5.861	0.0558			

```
lm(formula = log(t.f.root.shoot) ~ genus * polyploid * treat,
    data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.62609 -0.14098 -0.00227  0.12665  0.51192

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)		
(Intercept)	-0.48993	0.04149	-11.809	< 2e-16	***	
genus1	-0.629	0.11351	-5.541	2.24E-07	***	-1.11893
genus2	-0.12789	0.11351	-1.127	0.262435		-0.61782
genus3	0.23321	0.12886	1.81	0.073199	.	-0.25672
genus4	-0.76553	0.11351	-6.744	8.62E-10	***	-1.25546
genus5	-0.25442	0.11351	-2.241	0.027108	*	-0.74435
genus6	0.09177	0.15508	0.592	0.555282		-0.39816
genus7	0.23192	0.11351	2.043	0.043543	*	-0.25801
genus8	0.61166	0.11351	5.389	4.39E-07	***	0.12173
genus9	-0.37299	0.11351	-3.286	0.001383	**	-0.86292
polyploidYES	-0.17253	0.05787	-2.981	0.003569	**	0.49134
treatT	0.19723	0.05787	3.408	0.000929	***	
genus1:polyploidYES	0.04653	0.16024	0.29	0.772093		-0.126
genus2:polyploidYES	-0.24579	0.16024	-1.534	0.128058		-0.41832
genus3:polyploidYES	0.04934	0.18199	0.271	0.786846		-0.12319
genus4:polyploidYES	-0.44486	0.19194	-2.318	0.022403	*	-0.61739
genus5:polyploidYES	0.6607	0.16024	4.123	7.49E-05	***	0.48817
genus6:polyploidYES	0.13453	0.19194	0.701	0.484931		-0.038
genus7:polyploidYES	0.09688	0.16024	0.605	0.546748		-0.07565
genus8:polyploidYES	-0.17761	0.17146	-1.036	0.302628		-0.35014
genus9:polyploidYES	-0.19189	0.16024	-1.198	0.233796		-0.36442
						-0.10036
genus1:treatT	0.14352	0.16024	0.896	0.372475		0.34075
genus2:treatT	-0.46139	0.16024	-2.879	0.00483	**	-0.26416
genus3:treatT	-0.23244	0.18199	-1.277	0.204332		-0.03521
genus4:treatT	0.62218	0.16024	3.883	0.000181	***	0.81941
genus5:treatT	0.38842	0.16024	2.424	0.017059	*	0.58565
genus6:treatT	0.15163	0.2014	0.753	0.453216		0.34886

genus7:treatT	0.41943	0.16024	2.618	0.010164	*	0.61666
genus8:treatT	-0.75548	0.16024	-4.715	7.47E-06	***	-0.55825
genus9:treatT	0.44481	0.16024	2.776	0.006519	**	0.64204
polyploidYES:treatT	0.34187	0.08041	4.252	4.61E-05	***	-0.52345
genus1:polyploidYES:treatT	0.16503	0.2261	0.73	0.467081		0.5069
genus2:polyploidYES:treatT	0.26448	0.2261	1.17	0.244753		0.60635
genus3:polyploidYES:treatT	-0.48777	0.25692	-1.899	0.060366	.	-0.1459
genus4:polyploidYES:treatT	-0.0331	0.24957	-0.133	0.894745		0.30877
genus5:polyploidYES:treatT	-0.11441	0.2261	-0.506	0.613912		0.22746
genus6:polyploidYES:treatT	-0.04242	0.26406	-0.161	0.872667		0.29945
genus7:polyploidYES:treatT	-0.09966	0.2261	-0.441	0.660277		0.24221
genus8:polyploidYES:treatT	0.0565	0.23418	0.241	0.809807		0.39837
genus9:polyploidYES:treatT	0.02715	0.2261	0.12	0.904667		0.36902
---						0.60607

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.2363 on 105 degrees of freedom
Multiple R-squared: 0.8742, Adjusted R-squared: 0.8275
F-statistic: 18.71 on 39 and 105 DF, p-value: < 2.2e-16

m.drs1<-lm(log(d.root.shoot)~genus*polyploid*treat, data=de.cep)

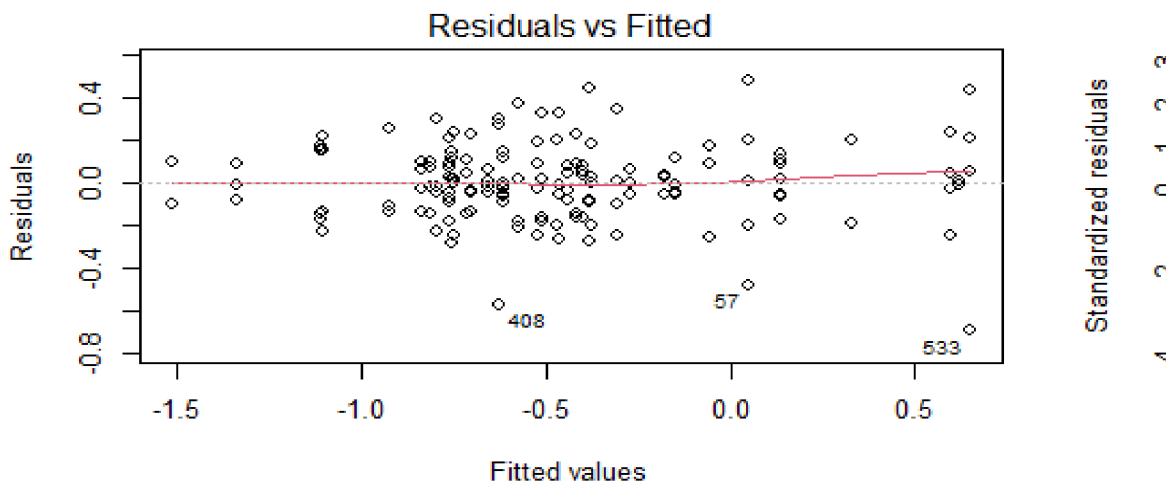
```
anova(m.drs1)
Analysis of Variance Table

Response: log(d.root.shoot)
```

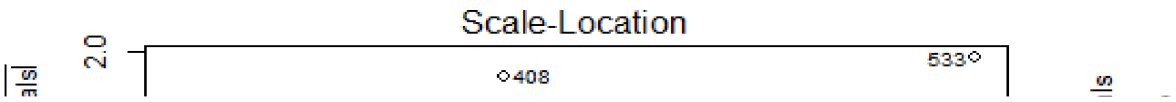
	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
genus	9	22.7714	2.53016	57.0495	< 2.2e-16	***
polyploid	1	0.0021	0.00207	0.0467	0.829325	
treat	1	0.2838	0.28377	6.3984	0.012894	*
genus:polyploid	9	2.4913	0.27681	6.2414	4.87E-07	***
genus:treat	9	4.1527	0.46141	10.4037	2.20E-11	***
polyploid:treat	1	0.547	0.54695	12.3326	0.000655	***
genus:polyploid:treat	9	0.7431	0.08257	1.8617	0.065667	.
Residuals	106	4.7011	0.04435			

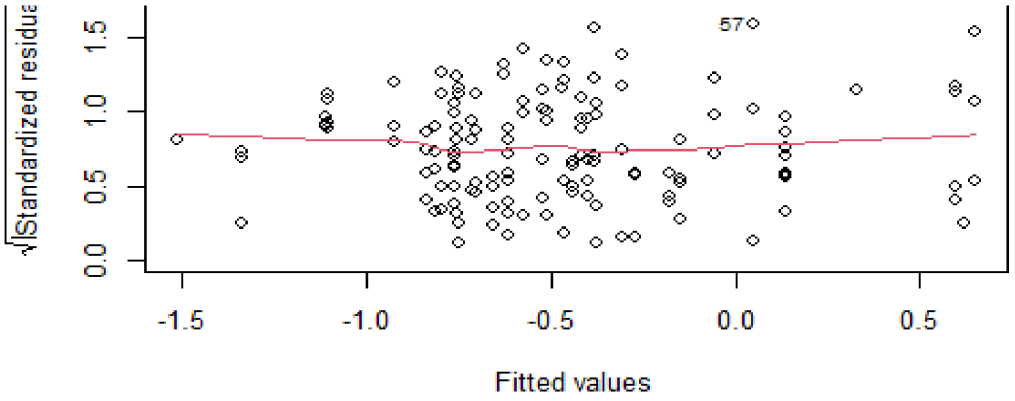
```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1


summary(m.drs1)

Call:
lm(formula = log(d.root.shoot) ~ genus * polyploid * treat, data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.69433 -0.09797 -0.00462  0.09843  0.47730

Coefficients:
```

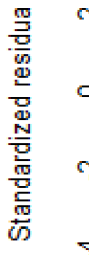
	Estimate	Std. Error	t value	Pr(>|t|)	
(Intercept)	-0.44526	0.036678	-12.139	< 2e-16	***
genus1	-0.31497	0.101071	-3.116	0.002357	**
genus2	-0.07708	0.101071	-0.763	0.44738	
genus3	-0.27224	0.114769	-2.372	0.019494	*
genus4	-0.25697	0.101071	-2.542	0.012454	*
genus5	-0.31759	0.101071	-3.142	0.002174	**
genus6	-0.02451	0.13815	-0.177	0.859547	
genus7	-0.12887	0.101071	-1.275	0.205067	
genus8	0.4966	0.091877	5.405	4.02E-07	***
genus9	-0.17109	0.101071	-1.693	0.093445	.
polyploidYES	-0.12573	0.05137	-2.448	0.016023	*
treatT	-0.02077	0.05137	-0.404	0.686788	
genus1:polyploidYES	0.091393	0.142755	0.64	0.52342	
genus2:polyploidYES	-0.11	0.142755	-0.771	0.442688	
genus3:polyploidYES	-0.0829	0.162149	-0.511	0.610239	
genus4:polyploidYES	-0.68804	0.171023	-4.023	0.000108	***
genus5:polyploidYES	0.271272	0.142755	1.9	0.060116	.
genus6:polyploidYES	0.085868	0.171023	0.502	0.616649	
genus7:polyploidYES	0.323791	0.142755	2.268	0.025346	*

```
genus8:polyploidYES            0.018609  0.146839     0.127  0.899395
genus9:polyploidYES            -0.01019  0.142755    -0.071  0.943251

genus1:treatT                  -0.32768  0.142755    -2.295  0.023681 *
genus2:treatT                  -0.57117  0.142755    -4.001  0.000117 ***
genus3:treatT                  0.112473  0.162149     0.694  0.489425
genus4:treatT                  0.307738  0.142755     2.156  0.033368 *
genus5:treatT                  0.318241  0.142755     2.229  0.027904 *
genus6:treatT                  0.218364  0.179459     1.217  0.226387
genus7:treatT                  0.447735  0.142755     3.136  0.002214 **
genus8:treatT                  -0.47022    0.1364    -3.447  0.000813 ***
genus9:treatT                  0.235014  0.142755     1.646  0.102669
polyploidYES:treatT            0.232162   0.07152     3.246  0.001566 **
genus1:polyploidYES:treatT     0.071691  0.201483     0.356  0.722685
genus2:polyploidYES:treatT     0.463226  0.201483     2.299  0.023461 *
genus3:polyploidYES:treatT     -0.73562  0.228959    -3.213  0.001741 **
genus4:polyploidYES:treatT     0.182911  0.222408     0.822  0.412688
genus5:polyploidYES:treatT     0.224158  0.201483     1.113  0.268421
genus6:polyploidYES:treatT      -0.1005  0.235327    -0.427    0.6702
genus7:polyploidYES:treatT     -0.14951  0.201483    -0.742  0.459687
genus8:polyploidYES:treatT     -0.06898  0.204397    -0.337  0.736408
genus9:polyploidYES:treatT     -0.00128  0.201483    -0.006  0.994964
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.2106 on 106 degrees of freedom
Multiple R-squared:  0.8683,    Adjusted R-squared:  0.8198
F-statistic: 17.92 on 39 and 106 DF,  p-value: < 2.2e-16
```






√|Standardized residua
0.0
0.5
1.0
1.5
57
-1.5
-1.0
-0.5
0.0
0.5
Fitted values


Standardized residua

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-0.52233
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-0.76284
-0.46976
-0.57413
0.051345
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0.621446

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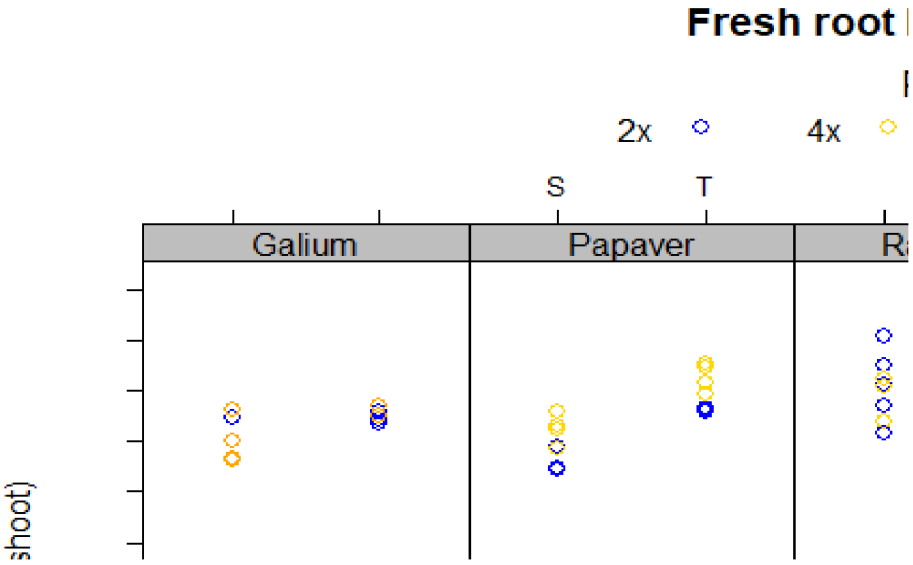
0.198058



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-0.34845
-0.59194
0.091703
0.286968
0.297471
0.197594
0.426965
-0.49099
0.214244
-0.29128
0.303853
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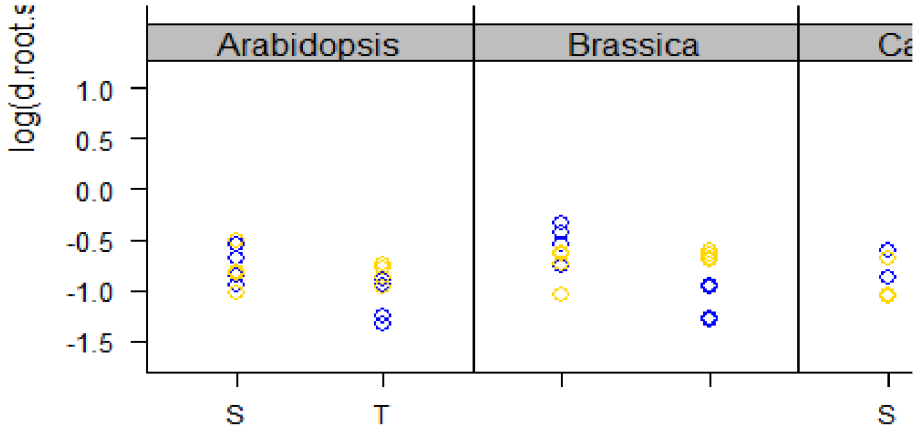
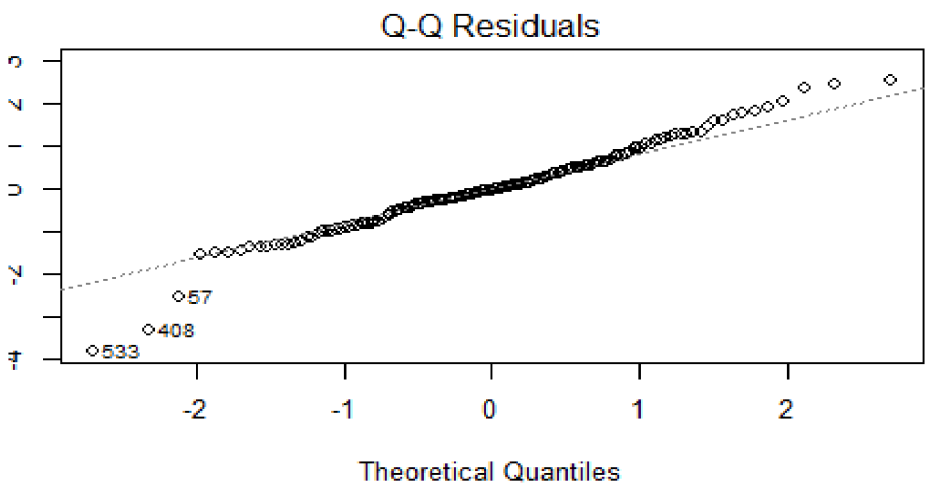
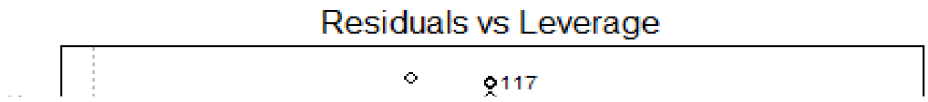
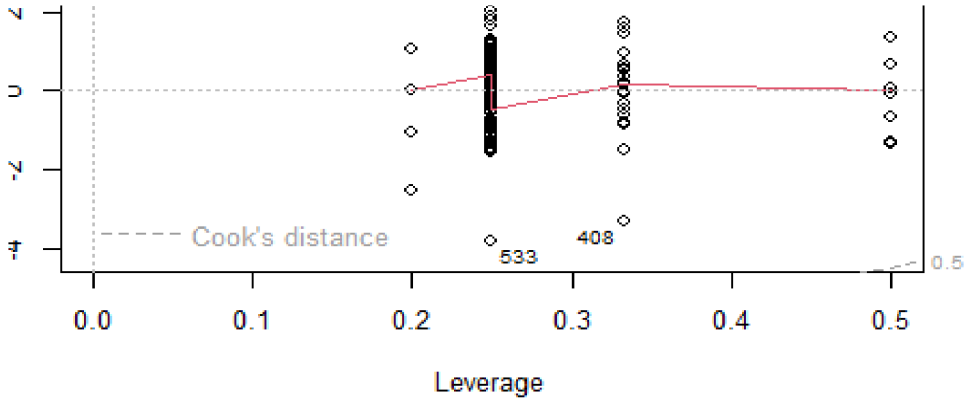
0.230887
0.346071








Cook's distance
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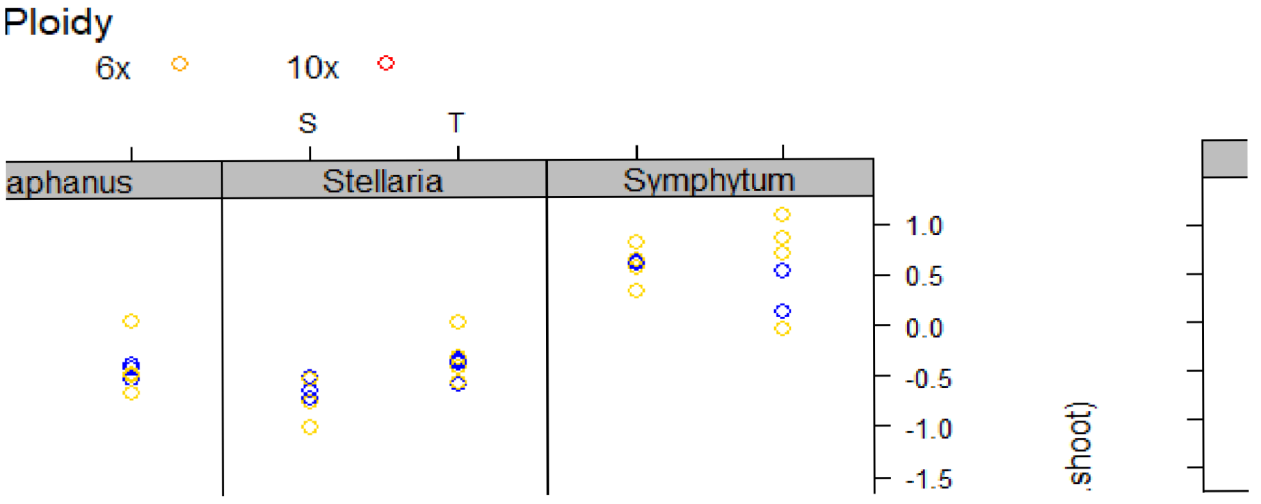
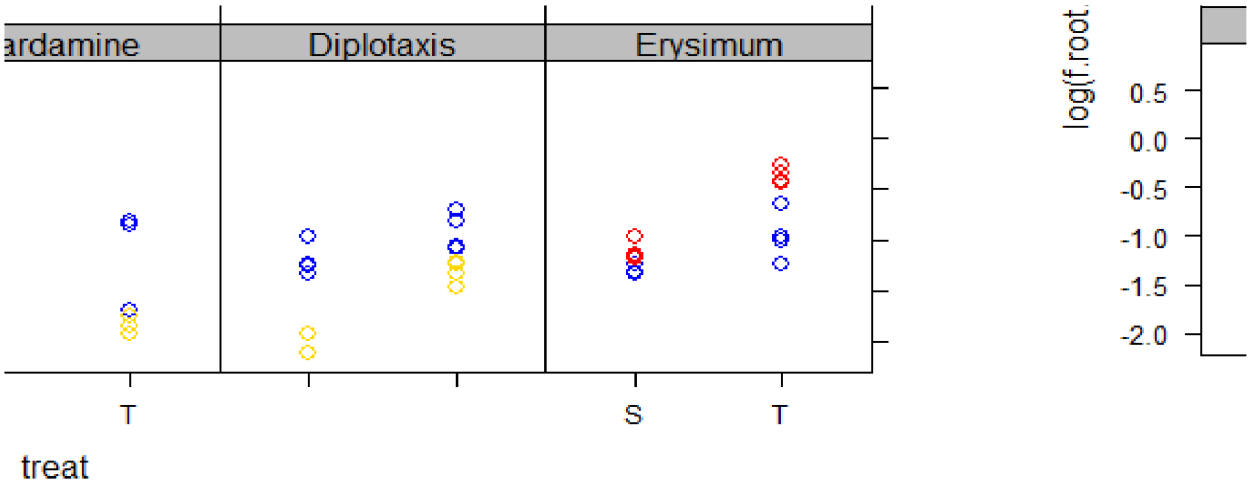
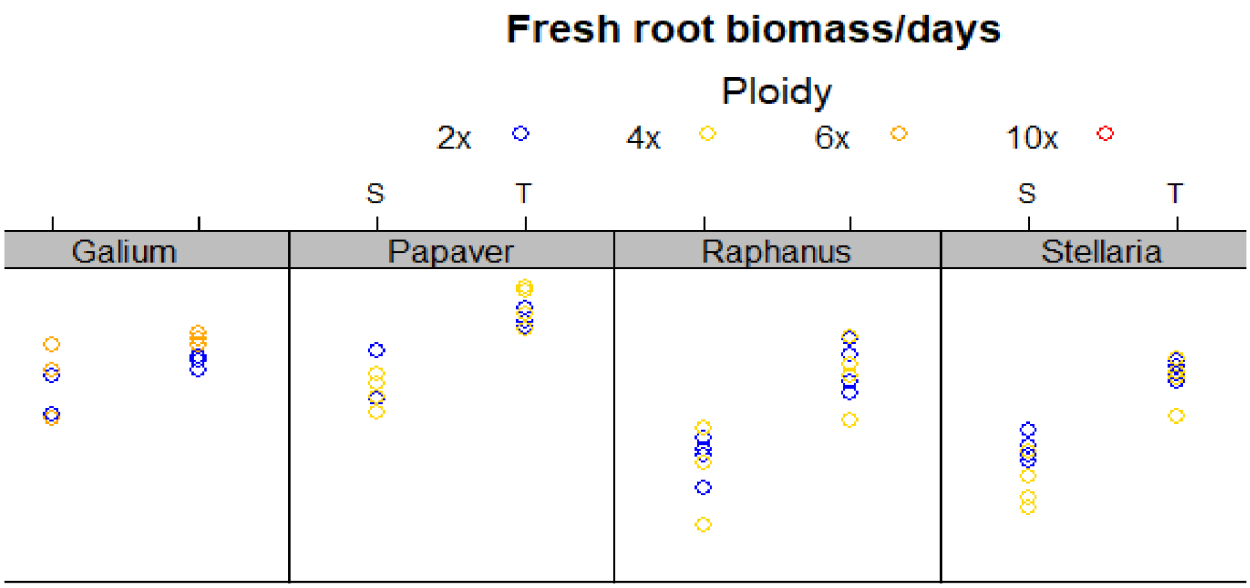
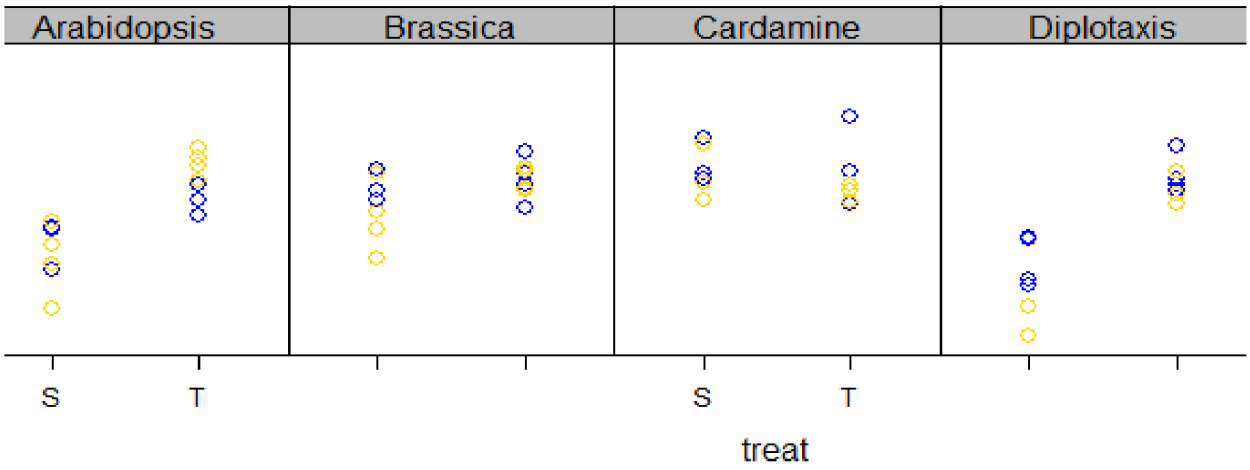
408
0.5
0.0
0.1
0.2
0.3
0.4
0.5
Leverage

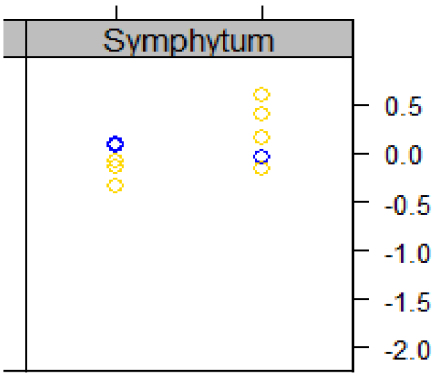
biomass/days

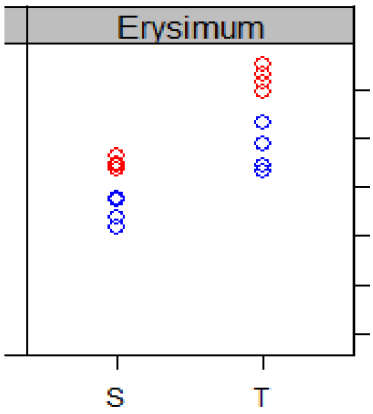



ardamine
Diplotaxis
Erysimum
log(f.root
0.5
0.0
-0.5
-1.0
-1.5
-2.0
T
S
T
treat


Fresh root biomass/days
Ploidy
2x
4x
6x
10x
S
T
S
T
Galium
Papaver
Raphanus
Stellaria


Arabidopsis
Brassica
Cardamine
Diplotaxis
S
T
S
T
treat

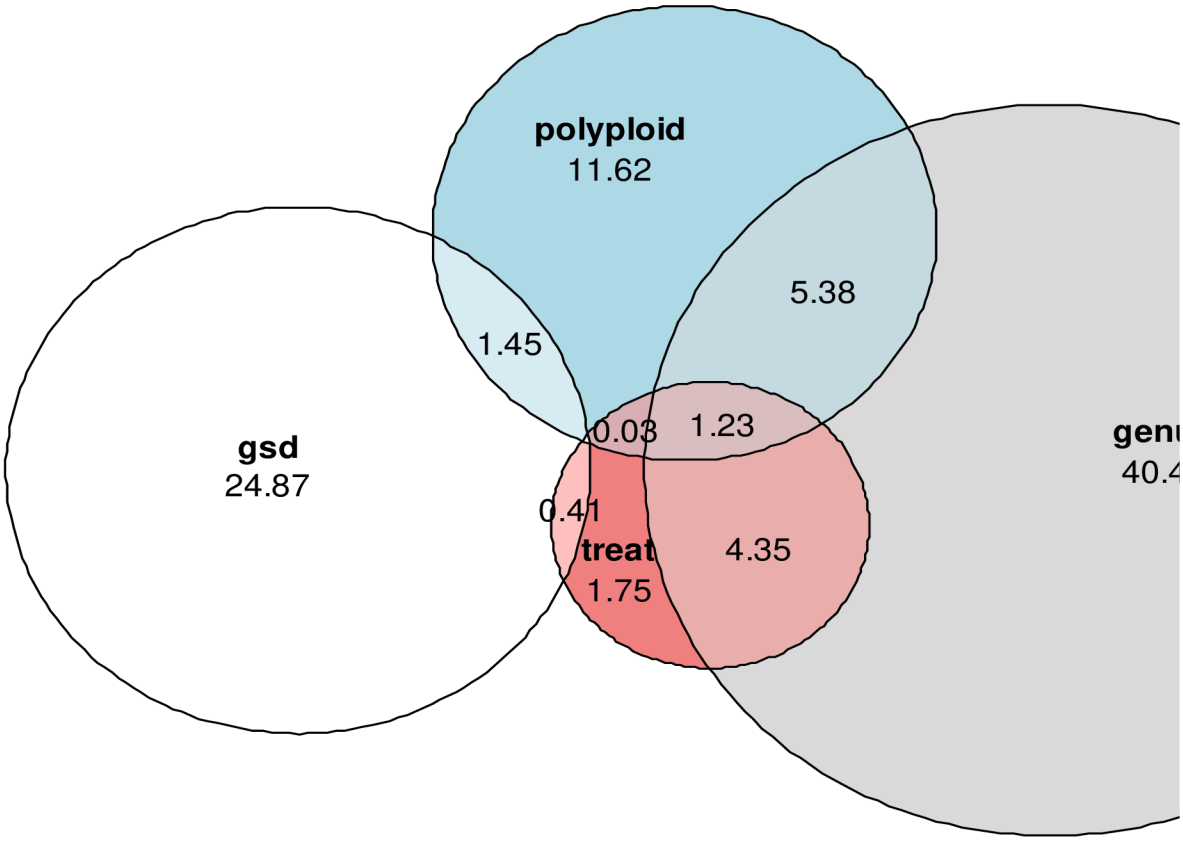

Symphytum
0.5
0.0
-0.5
-1.0
-1.5
-2.0


Erysimum
S
T

Variabilita vysvětlená velikostí genomu diploida z dané dvojice podle anovy
bez transformace
lm(ei~gsd*genus*polyploid*treat, data=de.cep)

Response: ei

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
gsd	1	9.1141	9.1141	312.8594	< 2.2e-16	***
genus	8	14.8379	1.8547	63.6674	< 2.2e-16	***
polyploid	1	4.257	4.257	146.1304	< 2.2e-16	***
treat	1	0.641	0.641	22.0024	8.16E-06	***
gsd:polyploid	1	0.5325	0.5325	18.2802	4.18E-05	***
genus:polyploid	8	1.9709	0.2464	8.4571	7.77E-09	***
gsd:treat	1	0.1512	0.1512	5.1904	0.02472	*
genus:treat	8	1.5931	0.1991	6.8359	3.24E-07	***
polyploid:treat	1	0.0122	0.0122	0.4176	0.51952	
gsd:polyploid:treat	1	0.0016	0.0016	0.0546	0.81569	
genus:polyploid:treat	8	0.4494	0.0562	1.9285	0.06308	.
Residuals	106	3.088	0.0291			

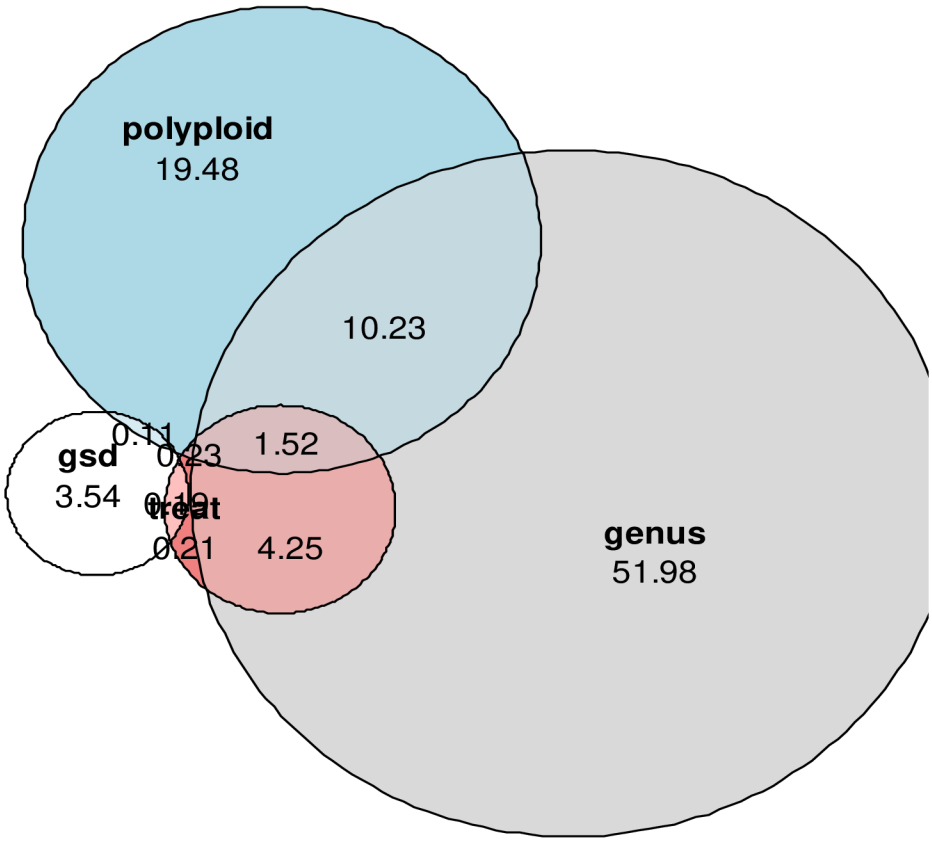


rap

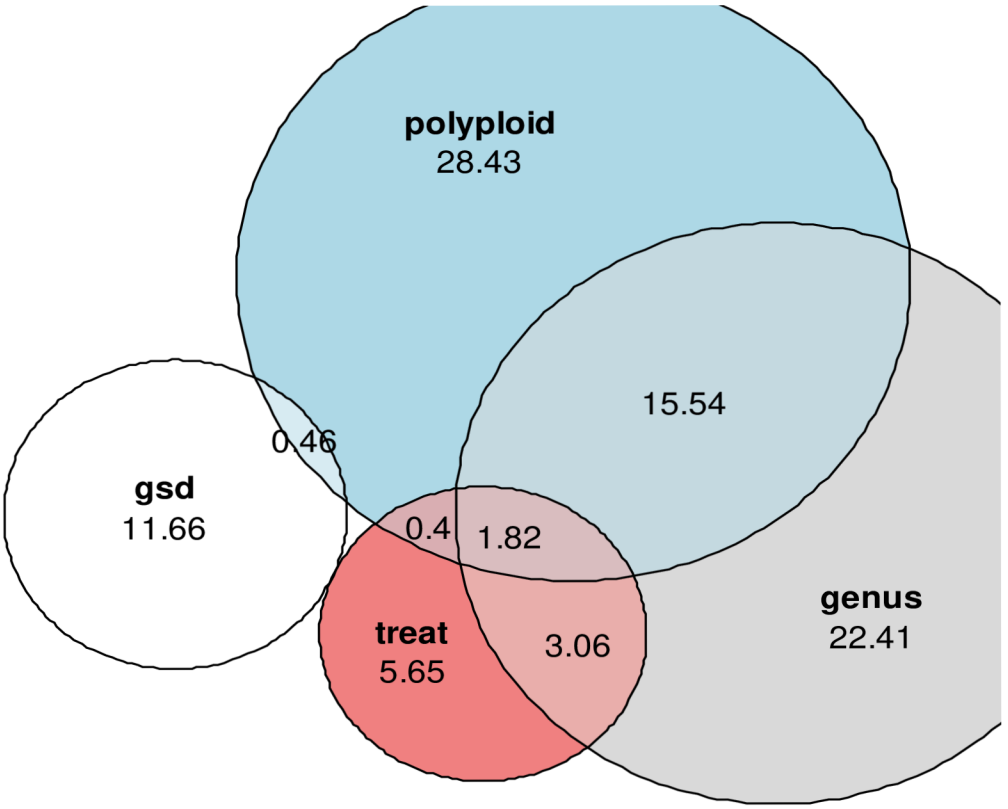
Response: ei

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
gsd	1	0.7983	0.7983	45.4783	8.380e-10	***
genus	8	11.7281	1.4660	83.5212	< 2.2e-16	***
polyploid	1	4.3957	4.3957	250.4324	< 2.2e-16	***

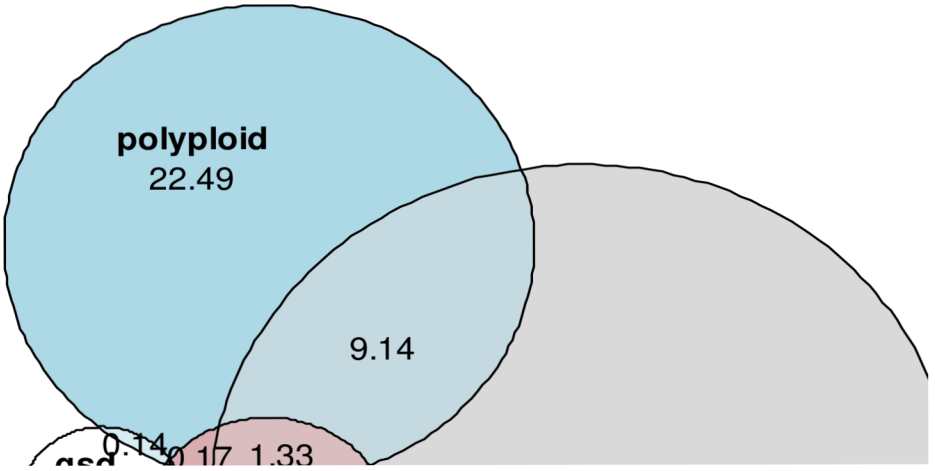
```
treat                    1  0.0478  0.0478   2.7207   0.10202
gsd:polyploid            1  0.0241  0.0241   1.3751   0.24357
genus:polyploid          8  2.3083  0.2885  16.4383 1.326e-15 ***
gsd:treat                1  0.0431  0.0431   2.4536   0.12024
genus:treat              8  0.9598  0.1200   6.8353 3.242e-07 ***
polyploid:treat          1  0.0519  0.0519   2.9595   0.08829 .
gsd:polyploid:treat      1  0.0005  0.0005   0.0312   0.86005
genus:polyploid:treat    8  0.3440  0.0430   2.4496   0.01791 *
Residuals              106  1.8606  0.0176
```

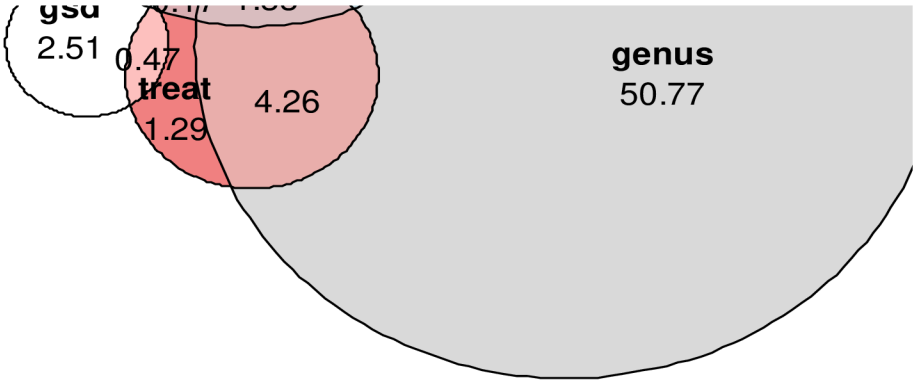



```
hla
Response: ei
                        Df  Sum Sq Mean Sq  F value    Pr(>F)
gsd                      1 1.05747 1.05747 118.6791 < 2.2e-16 ***
genus                    8 2.03262 0.25408  28.5149 < 2.2e-16 ***
polyploid                1 2.57883 2.57883 289.4208 < 2.2e-16 ***
treat                    1 0.51232 0.51232  57.4969 1.359e-11 ***
gsd:polyploid            1 0.04209 0.04209   4.7240 0.0319696 *
genus:polyploid          8 1.40958 0.17620  19.7746 < 2.2e-16 ***
gsd:treat                1 0.00123 0.00123   0.1381 0.7108798
genus:treat              8 0.27745 0.03468   3.8922 0.0004648 ***
polyploid:treat          1 0.03594 0.03594   4.0339 0.0471389 *
gsd:polyploid:treat      1 0.01516 0.01516   1.7009 0.1949983
genus:polyploid:treat    8 0.16486 0.02061   2.3128 0.0250734 *
Residuals              106 0.94449 0.00891
```




```
ved
Response: ei
                        Df  Sum Sq Mean Sq  F value    Pr(>F)
gsd                      1 0.10560 0.10560  35.8864 2.971e-08 ***
genus                    8 2.13370 0.26671  90.6335 < 2.2e-16 ***
polyploid                1 0.94530 0.94530 321.2286 < 2.2e-16 ***
treat                    1 0.05425 0.05425  18.4354 3.930e-05 ***
gsd:polyploid            1 0.00595 0.00595   2.0207   0.15813
genus:polyploid          8 0.38408 0.04801  16.3146 1.832e-15 ***
gsd:treat                1 0.01988 0.01988   6.7571   0.01068 *
genus:treat              8 0.17919 0.02240   7.6115 5.486e-08 ***
polyploid:treat          1 0.00719 0.00719   2.4437   0.12101
gsd:polyploid:treat      1 0.00269 0.00269   0.9135   0.34139
genus:polyploid:treat    8 0.05585 0.00698   2.3722   0.02174 *
Residuals              105 0.30899 0.00294
```

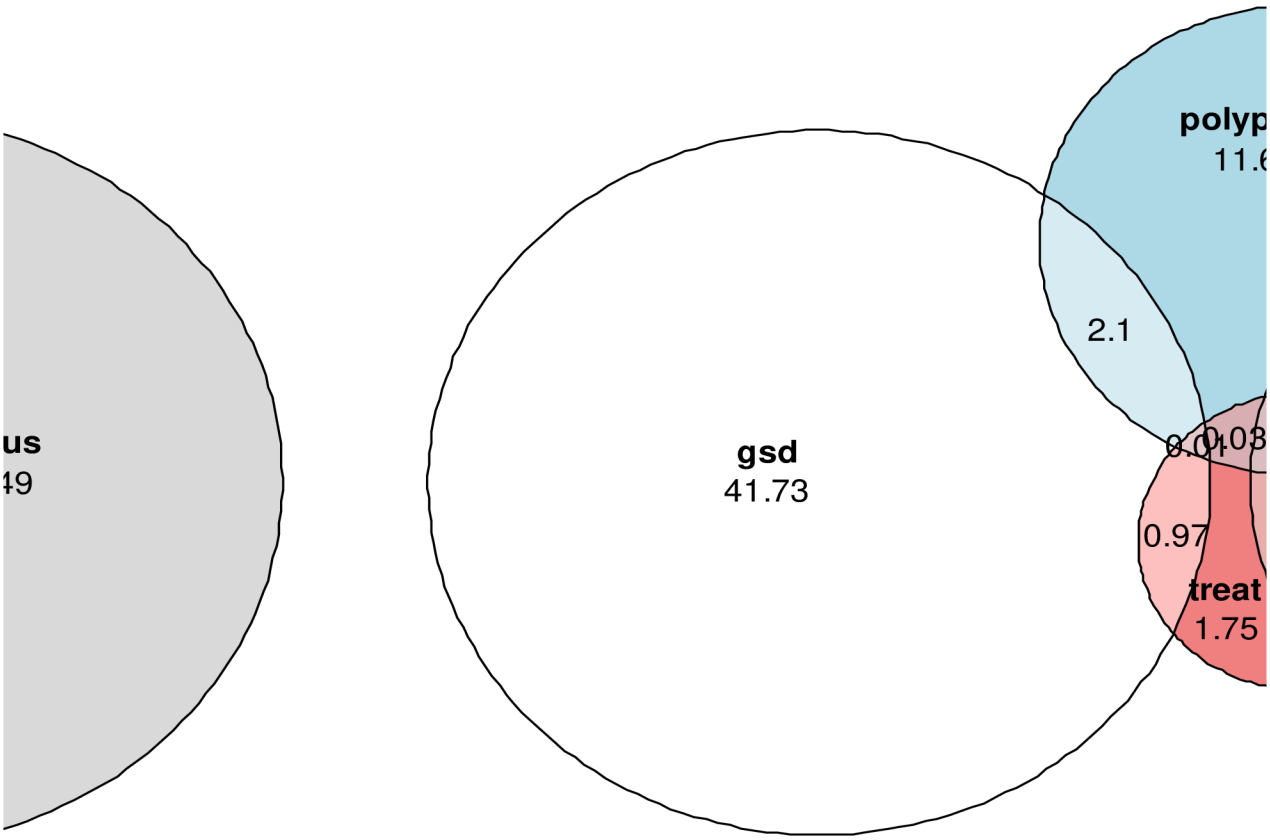



gsd
2.51
0.47
treat
1.29
4.26
genus
50.77

log
lm(ei~log(gsd)*genus*polyploid*treat, data=de.cep)

Response: ei

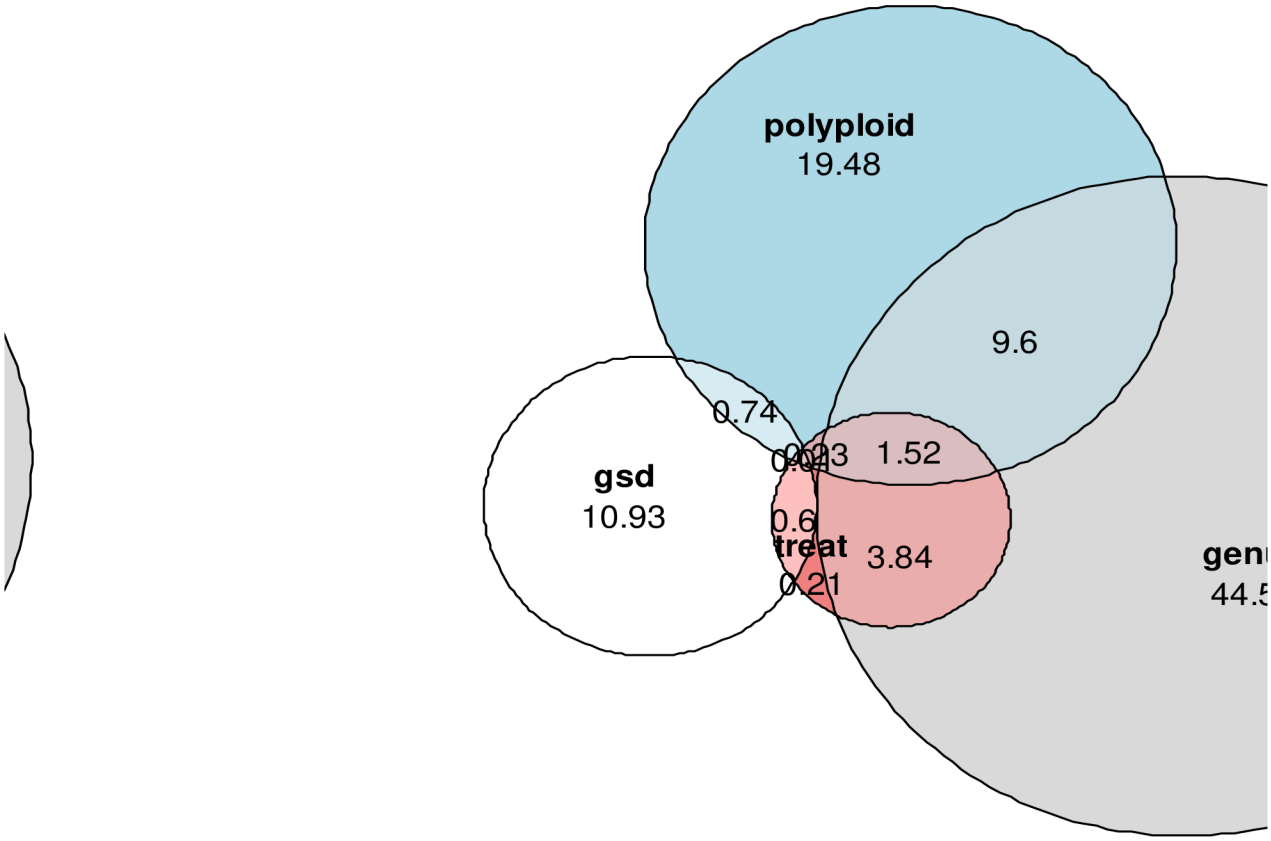
	Df	Sum Sq	Mean Sq	F value
log(gsd)	1	15.2942	15.2942	525.0022
genus	8	8.6578	1.0822	37.1496
polyploid	1	4.257	4.257	146.1304
treat	1	0.641	0.641	22.0024
log(gsd):polyploid	1	0.7698	0.7698	26.4254
genus:polyploid	8	1.7337	0.2167	7.4389
log(gsd):treat	1	0.3548	0.3548	12.1777
genus:treat	8	1.3896	0.1737	5.9625
polyploid:treat	1	0.0122	0.0122	0.4176
log(gsd):polyploid:treat	1	0.0026	0.0026	0.0905
genus:polyploid:treat	8	0.4484	0.0561	1.924
Residuals	106	3.088	0.0291	



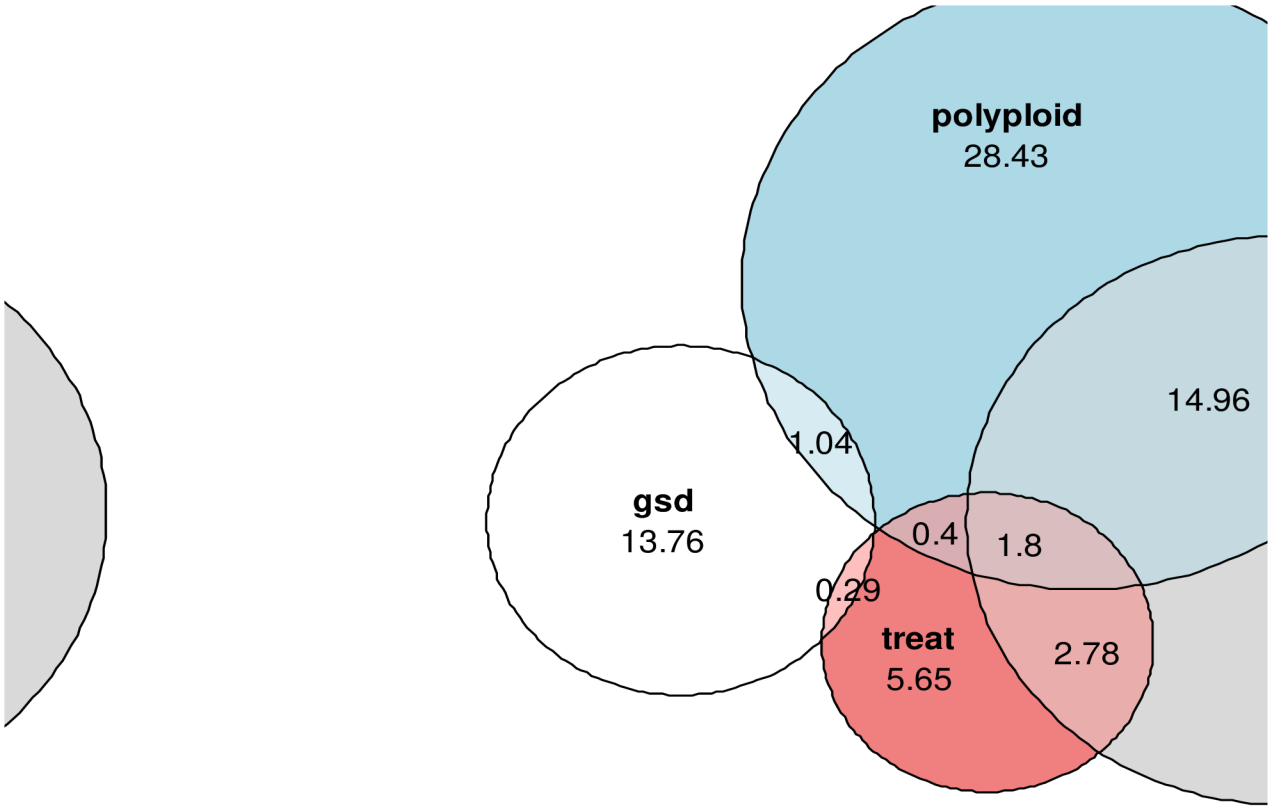
lm(ei ~ log(gsd)*genus*polyploid*treat, data = de.rap)
rap
Response: ei

	Df	Sum Sq	Mean Sq	F value	Pr(>I
log(gsd)	1	2.4667	2.4667	140.5327	< 2.2e-1
genus	8	10.0597	1.2575	71.6394	< 2.2e-1
polyploid	1	4.3957	4.3957	250.4324	< 2.2e-1

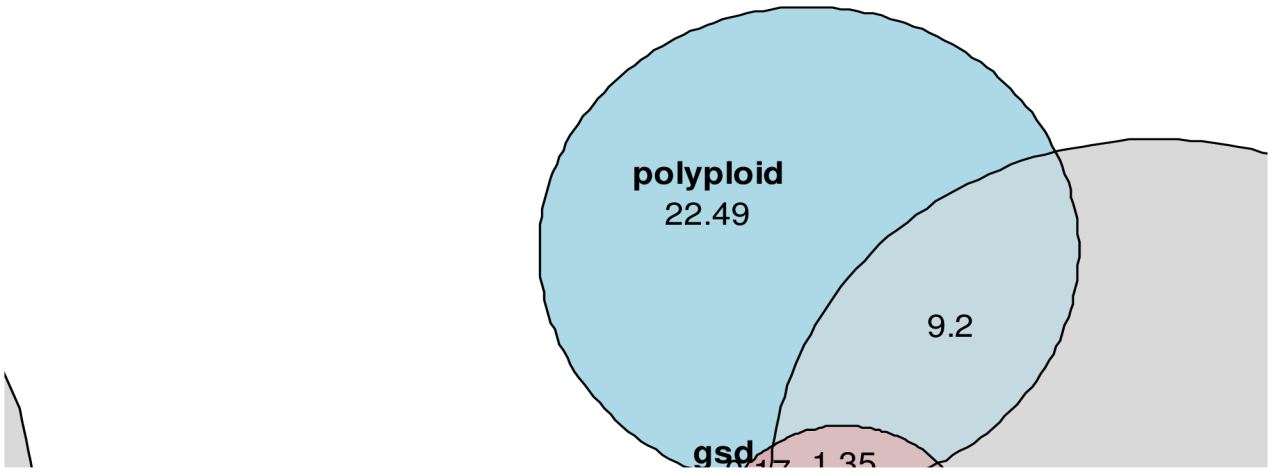
```
treat                       1  0.0478  0.0478   2.7207  0.1020
log(gsd):polyploid          1  0.1674  0.1674   9.5346  0.0025
genus:polyploid             8  2.1651  0.2706  15.4183 7.775e-
log(gsd):treat              1  0.1358  0.1358   7.7352  0.0064
genus:treat                 8  0.8671  0.1084   6.1751 1.572e-
polyploid:treat             1  0.0519  0.0519   2.9595  0.0882
log(gsd):polyploid:treat    1  0.0020  0.0020   0.1160  0.7341
genus:polyploid:treat       8  0.3425  0.0428   2.4390  0.0183
Residuals                 106  1.8606  0.0176
```

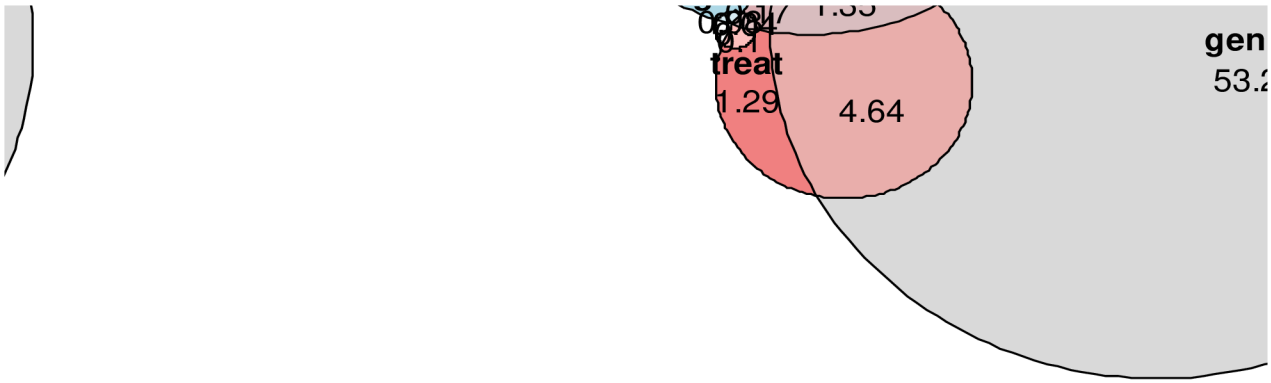



```
hla
Response: ei
                          Df  Sum Sq Mean Sq  F value    Pr(>
log(gsd)                   1 1.24843 1.24843 140.1101 < 2.2e-
genus                      8 1.84166 0.23021  25.8361 < 2.2e-
polyploid                  1 2.57883 2.57883 289.4208 < 2.2e-
treat                      1 0.51232 0.51232  57.4969 1.359e-
log(gsd):polyploid         1 0.09417 0.09417  10.5686  0.0015
genus:polyploid            8 1.35751 0.16969  19.0440 < 2.2e-
log(gsd):treat             1 0.02634 0.02634   2.9556  0.0885
genus:treat                8 0.25234 0.03154   3.5400  0.0011
polyploid:treat            1 0.03594 0.03594   4.0339  0.0471
log(gsd):polyploid:treat   1 0.01648 0.01648   1.8491  0.1767
genus:polyploid:treat      8 0.16354 0.02044   2.2942  0.0262
Residuals                106 0.94449 0.00891
```

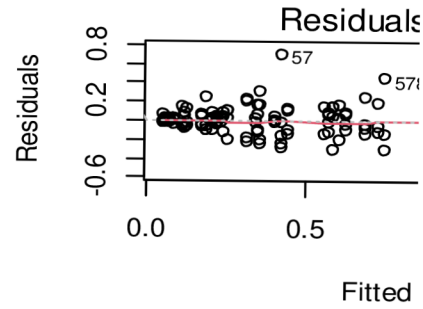


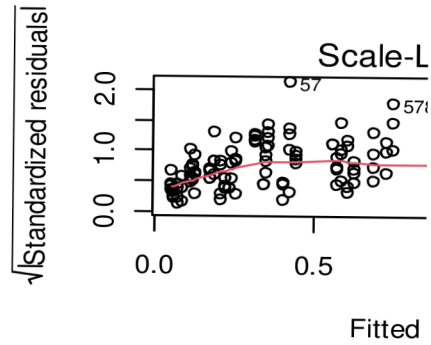

```
ved
Response: ei
                          Df  Sum Sq Mean Sq  F value    Pr(>I
log(gsd)                   1 0.00007 0.00007   0.0229   0.880(
genus                      8 2.23924 0.27990  95.1164 < 2.2e-:
polyploid                  1 0.94530 0.94530 321.2286 < 2.2e-:
treat                      1 0.05425 0.05425  18.4354 3.930e-(
log(gsd):polyploid         1 0.00344 0.00344   1.1687   0.282:
genus:polyploid            8 0.38659 0.04832  16.4211 1.528e-:
log(gsd):treat             1 0.00412 0.00412   1.4009   0.239:
genus:treat                8 0.19495 0.02437   8.2811 1.201e-(
polyploid:treat            1 0.00719 0.00719   2.4437   0.121(
log(gsd):polyploid:treat   1 0.00166 0.00166   0.5629   0.454:
genus:polyploid:treat      8 0.05688 0.00711   2.4160   0.019!
Residuals                105 0.30899 0.00294
```

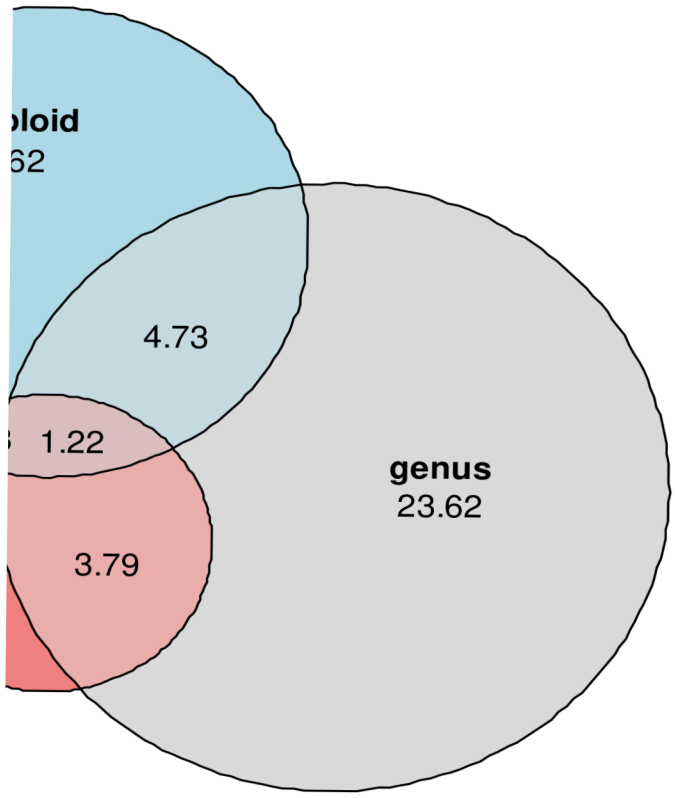



treat
1.29
4.64
gen

Pr(>F)	
< 2.2e-16	***
< 2.2e-16	***
< 2.2e-16	***
8.16E-06	***
1.26E-06	***
7.89E-08	***
0.000706	***
2.63E-06	***
0.519518	
0.764195	
0.063744	.

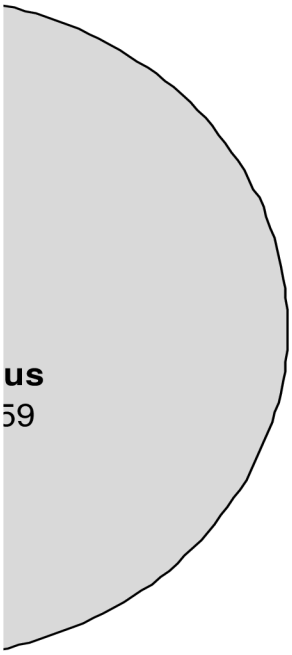




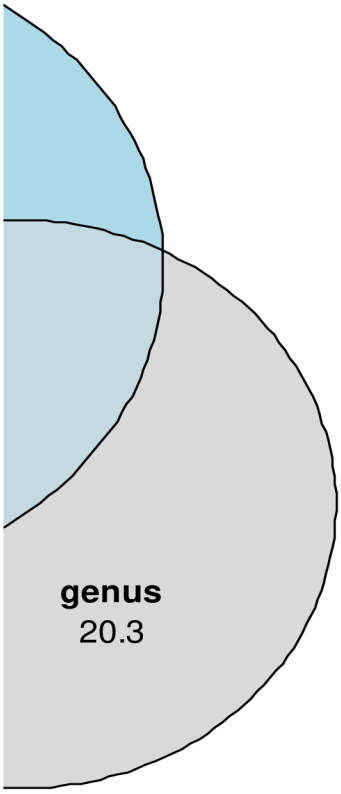


F)
16 ***
16 ***
16 ***

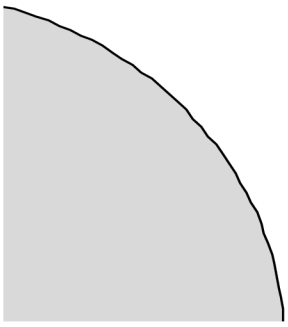
17
74 **
15 ***
11 **
06 ***
91 .
12
83 *

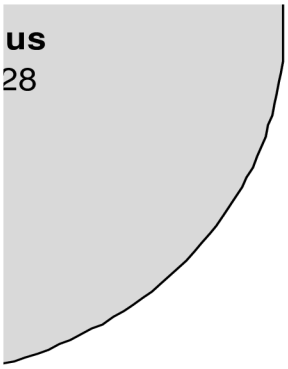


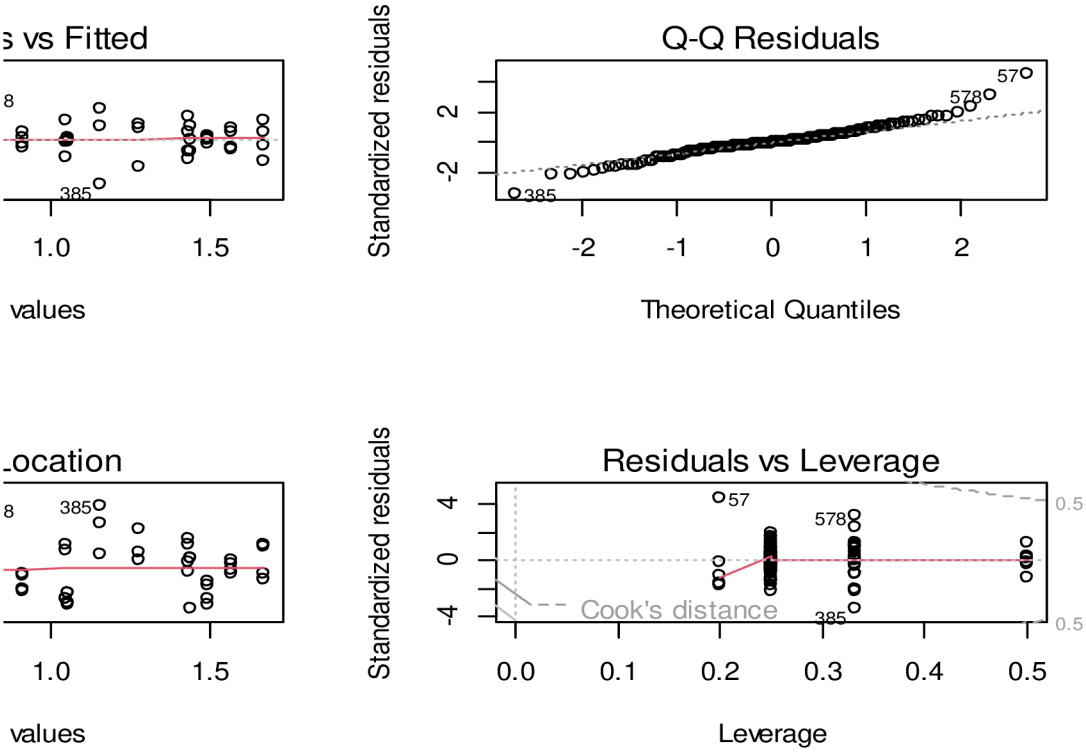
F)
16 ***
16 ***
16 ***
11 ***
42 **
16 ***
01 .
41 **
39 *
71
36 *



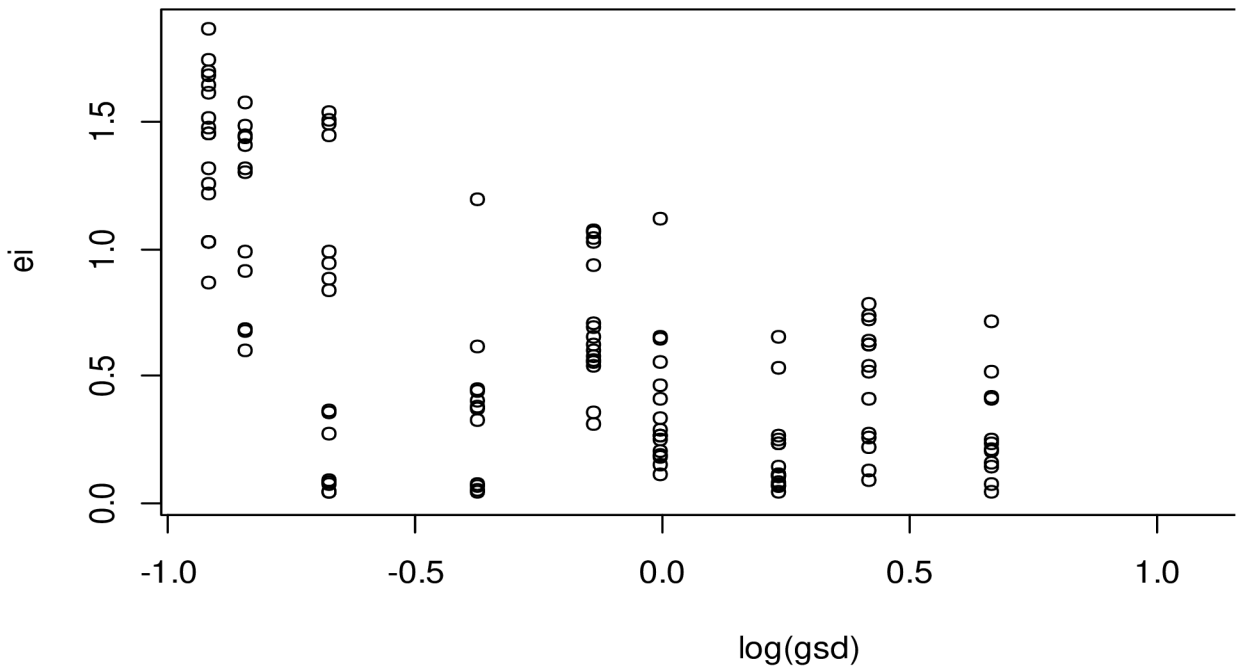

```
F)
01
16  ***
16  ***
05  ***
14
15  ***
24
08  ***
01
76
52  *
```



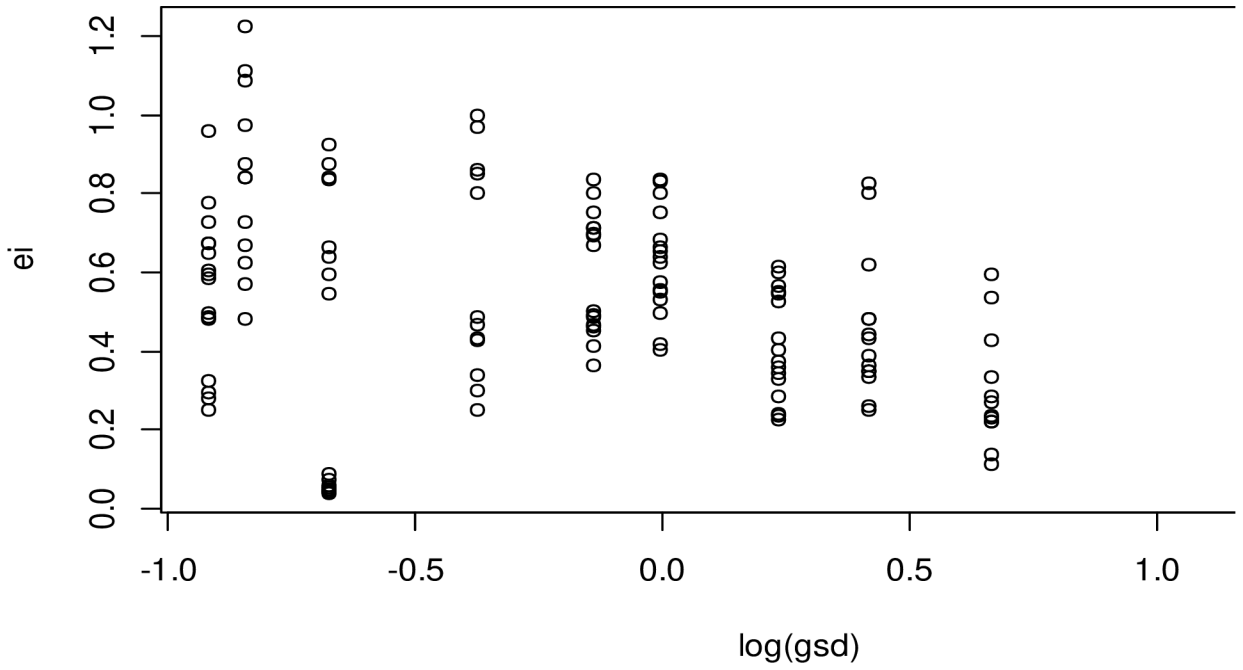

us
28


s vs Fitted
8
385
1.0
1.5
values
Q-Q Residuals
Standardized residuals
57
578
385
-2
2
-2
-1
0
1
2
Theoretical Quantiles
Location
8
385
1.0
1.5
values
Residuals vs Leverage
Standardized residuals
57
578
385
Cook's distance
0.5
0.5
-4
0
4
0.0
0.1
0.2
0.3
0.4
0.5
Leverage

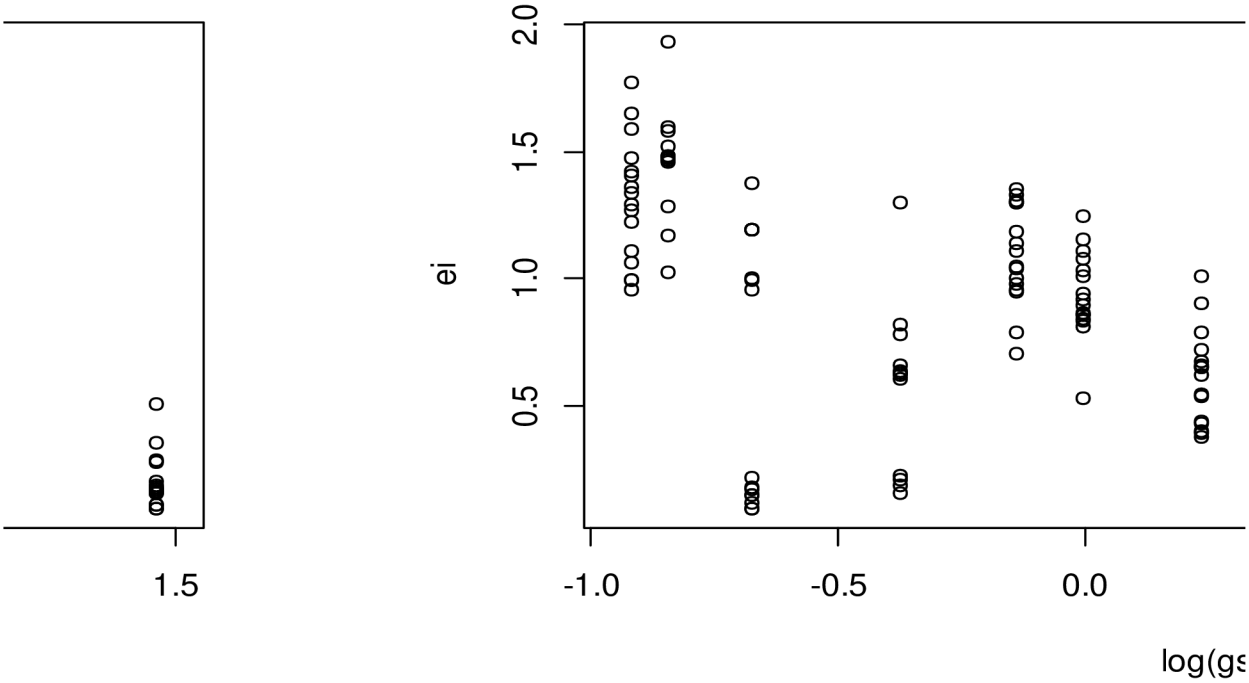
ei~log(velikost genomu diploida)
čepel



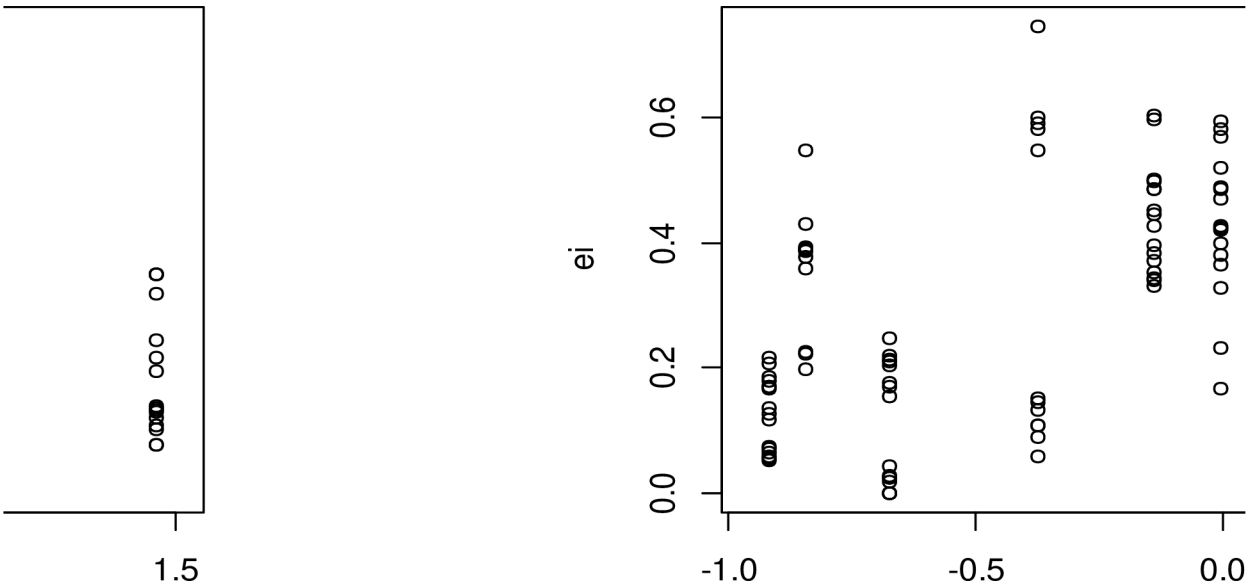
hlavní kořen

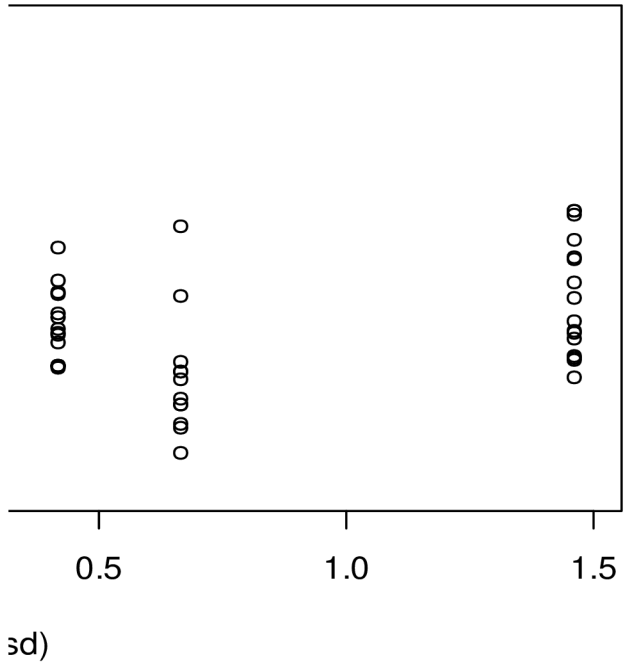


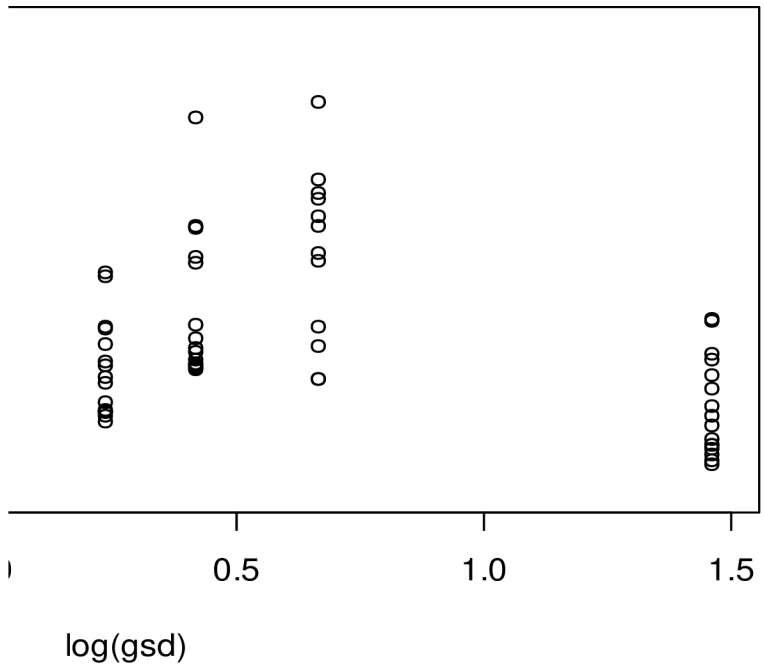
řapík



vedlejší kořen




0.5
1.0
1.5
sd)


0.5
1.0
1.5
log(gsd)

```
lm(formula = wc.shoot ~ genus * polyploid * treat, data = de.cep)

Residuals:
      Min        1Q    Median        3Q       Max
-0.042075 -0.008600  0.000338  0.008394  0.051467

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)		
(Intercept)	0.872179	0.003012	289.57	< 2e-16	***	
genus1	0.002747	0.0083	0.331	0.741366		0.874925
genus2	-0.0032	0.0083	-0.386	0.700292		0.868975
genus3	-0.03318	0.009425	-3.52	0.000637	***	0.839
genus4	0.018697	0.0083	2.253	0.026342	*	0.890875
genus5	-0.02855	0.0083	-3.44	0.000832	***	0.843625
genus6	-0.00988	0.011345	-0.871	0.385855		0.8623
genus7	0.020297	0.0083	2.445	0.016116	*	0.892475
genus8	0.020582	0.007545	2.728	0.007462	**	0.89276
genus9	0.030322	0.0083	3.653	0.000404	***	0.9025
polyploidYES	0.005363	0.004218	1.271	0.206381		0.85435
treatT	-0.0618	0.004218	-14.65	< 2e-16	***	
genus1:polyploidYES	0.012837	0.011723	1.095	0.275988		0.0182
genus2:polyploidYES	-0.00294	0.011723	-0.251	0.802581		0.002425
genus3:polyploidYES	0.007137	0.013316	0.536	0.593096		0.0125
genus4:polyploidYES	-0.00484	0.014044	-0.344	0.731157		0.000525
genus5:polyploidYES	-0.03119	0.011723	-2.66	0.009016	**	-0.02583
genus6:polyploidYES	-0.00059	0.014044	-0.042	0.966674		0.004775
genus7:polyploidYES	0.005237	0.011723	0.447	0.655989		0.0106
genus8:polyploidYES	0.016844	0.012058	1.397	0.165378		0.022207
genus9:polyploidYES	0.010812	0.011723	0.922	0.358475		0.016175
						-0.00795
genus1:treatT	-0.07138	0.011723	-6.089	1.85E-08	***	-0.13318
genus2:treatT	0.005424	0.011723	0.463	0.644518		-0.05638
genus3:treatT	0.045133	0.013316	3.389	0.000984	***	-0.01667
genus4:treatT	-0.02265	0.011723	-1.932	0.056007	.	-0.08445
genus5:treatT	-0.01398	0.011723	-1.192	0.235857		-0.07578
genus6:treatT	-0.00177	0.014737	-0.12	0.90477		-0.06357
genus7:treatT	0.018899	0.011723	1.612	0.109898		-0.0429
genus8:treatT	0.017189	0.011201	1.535	0.127856		-0.04461
genus9:treatT	-0.02943	0.011723	-2.51	0.013581	*	-0.09123
polyploidYES:treatT	-0.00362	0.005873	-0.617	0.538433		-0.00925
genus1:polyploidYES:treatT	-0.02215	0.016546	-1.339	0.18352		-0.02578
genus2:polyploidYES:treatT	0.02625	0.016546	1.587	0.1156		0.022625
genus3:polyploidYES:treatT	-0.02121	0.018802	-1.128	0.261866		-0.02483
genus4:polyploidYES:treatT	-0.0223	0.018264	-1.221	0.224797		-0.02593
genus5:polyploidYES:treatT	0.007975	0.016546	0.482	0.630805		0.00435
genus6:polyploidYES:treatT	-0.01748	0.019325	-0.905	0.367666		-0.02111
genus7:polyploidYES:treatT	0.00295	0.016546	0.178	0.858839		-0.00068
genus8:polyploidYES:treatT	-0.00393	0.016785	-0.234	0.815243		-0.00756
genus9:polyploidYES:treatT	0.03385	0.016546	2.046	0.043246	*	0.030225
---						0.012425

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.01729 on 106 degrees of freedom
Multiple R-squared:  0.9127,	Adjusted R-squared:  0.8806 
F-statistic: 28.43 on 39 and 106 DF,  p-value: < 2.2e-16
```

```
m <- lm(wc.root~genus*polyploid*treat, data=de.cep)
Response: wc.root
                        Df    Sum Sq    Mean Sq F value     Pr(>F)
genus                    9  0.136622    0.01518   61.8041 < 2.2e-16   ***
polyploid                1  0.002185   0.002185    8.8945    0.00355 **
treat                    1  0.004737   0.004737   19.2861   2.67E-05 ***
genus:polyploid          9  0.008585   0.000954    3.8836   0.000276 ***
genus:treat              9  0.008998      0.001    4.0705   0.000165 ***
polyploid:treat          1   0.00005   4.98E-05    0.2026   0.653534
genus:polyploid:treat    9  0.006478    0.00072    2.9304   0.003839 **
Residuals              106  0.026036   0.000246

lm(formula = wc.root ~ genus * polyploid * treat, data = de.cep)

Residuals:
      Min        1Q    Median        3Q       Max
-0.055020 -0.007121  0.000338  0.007708  0.036680

Coefficients:
                          Estimate   Std. Error  t value     Pr(>|t|)
(Intercept)               0.862368     0.00273   315.938  < 2e-16    ***
genus1                   -0.04122    0.007522     -5.48   2.90E-07 ***        0.82115
genus2                   -0.00804    0.007522    -1.069   0.287362            0.854325
genus3                   0.036066    0.008541     4.223   5.12E-05 ***        0.898433
genus4                   -0.05002    0.007522     -6.65   1.32E-09 ***        0.81235
genus5                   -0.01557    0.007522     -2.07   0.040906 *           0.8468
genus6                   0.014732    0.010281     1.433   0.154812             0.8771
genus7                   0.058707    0.007522     7.805   4.45E-12 ***        0.921075
genus8                   -0.04955    0.006837    -7.247   7.21E-11 ***        0.81282
genus9                   0.012357    0.007522     1.643   0.103367            0.874725
polyploidYES              0.00661    0.003823     1.729   0.086723 .           0.9049
treatT                     -0.016    0.003823    -4.186   5.87E-05 ***
genus1:polyploidYES       0.00424    0.010624     0.399   0.690592            0.01085
genus2:polyploidYES      -0.03601    0.010624     -3.39   0.000984 ***        -0.0294
genus3:polyploidYES      0.009224    0.012067     0.764   0.446341            0.015833
genus4:polyploidYES       0.02624    0.012727     2.062    0.04168 *           0.03285
genus5:polyploidYES       0.01939    0.010624     1.825   0.070785 .            0.026
genus6:polyploidYES      -0.00023    0.012727    -0.018   0.985324            0.006375
genus7:polyploidYES      -0.02111    0.010624    -1.987   0.049497 *           -0.0145
genus8:polyploidYES      0.034304    0.010928     3.139   0.002195 **         0.040913
genus9:polyploidYES      -0.01201    0.010624     -1.13   0.260831             -0.0054
                                                                             -0.01742
genus1:treatT            0.010079    0.010624     0.949    0.34493            -0.00593
genus2:treatT            0.009904    0.010624     0.932   0.353336             -0.0061
genus3:treatT              -0.0071    0.012067    -0.588   0.557728             -0.0231
genus4:treatT            0.007729    0.010624     0.727   0.468525            -0.00828
genus5:treatT            -0.00117    0.010624     -0.11   0.912414            -0.01718
genus6:treatT            -0.02386    0.013355    -1.787   0.076828 .          -0.03987
genus7:treatT            0.004104    0.010624     0.386   0.700066             -0.0119
genus8:treatT            0.055509    0.010151     5.468   3.05E-07 ***        0.039505
```

```
genus9:treatT                    -0.0163  0.010624    -1.534  0.128016            -0.0323
polyploidYES:treatT             0.003715  0.005322     0.698  0.486768            -0.0549
genus1:polyploidYES:treatT      -0.00149  0.014994    -0.099  0.921057           0.002225
genus2:polyploidYES:treatT      0.004011  0.014994     0.267  0.789625           0.007725
genus3:polyploidYES:treatT      0.017686  0.017039     1.038  0.301653             0.0214
genus4:polyploidYES:treatT      -0.04379  0.016551    -2.646  0.009393 **        -0.04008
genus5:polyploidYES:treatT      -0.02571  0.014994    -1.715  0.089271 .           -0.022
genus6:polyploidYES:treatT      0.005144  0.017513     0.294  0.769546           0.008858
genus7:polyploidYES:treatT      0.006161  0.014994     0.411  0.682003           0.009875
genus8:polyploidYES:treatT      -0.04003  0.015211    -2.632  0.009768 **        -0.03631
genus9:polyploidYES:treatT      0.029711  0.014994     1.981  0.050127 .         0.033425
---                                                                              0.052025
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.01567 on 106 degrees of freedom
Multiple R-squared:  0.8656,    Adjusted R-squared:  0.8161
F-statistic:  17.5 on 39 and 106 DF,  p-value: < 2.2e-16
```

celková fresh biomasa

m <- lm(log(fb)~genus*polyploid*treat, data=de.cep)

```
Response: log(fb)
                       Df Sum Sq Mean Sq  F value    Pr(>F)
genus                   9 21.992   2.444  28.2939 < 2.2e-16 ***
polyploid               1  0.066   0.066   0.7588 0.3856652
treat                   1 38.405  38.405 444.6873 < 2.2e-16 ***
genus:polyploid         9  9.758   1.084  12.5548 2.247e-13 ***
genus:treat             9 11.390   1.266  14.6535 3.570e-15 ***
polyploid:treat         1  0.318   0.318   3.6850 0.0575910 .
genus:polyploid:treat   9  2.901   0.322   3.7328 0.0004192 ***
Residuals             106  9.154   0.086

lm(formula = log(fb) ~ genus * polyploid * treat, data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.75855 -0.15835  0.01638  0.16365  0.68712

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)		
(Intercept)	-3.21136	0.051183	-62.743	< 2e-16	***	
genus1	0.108103	0.14104	0.766	0.445101		-3.10325
genus2	0.080438	0.14104	0.57	0.569666		-3.13092
genus3	0.402792	0.160156	2.515	0.013405	*	-2.80856
genus4	-0.44283	0.14104	-3.14	0.002191	**	-3.65419
genus5	-0.5151	0.14104	-3.652	0.000406	***	-3.72646
genus6	-0.61213	0.192782	-3.175	0.001961	**	-3.82348
genus7	-0.04946	0.14104	-0.351	0.726542		-3.26081
genus8	0.482049	0.12821	3.76	0.000279	***	-2.72931
genus9	0.131221	0.14104	0.93	0.354288		-3.08014
polyploidYES	0.018111	0.071684	0.253	0.801026		-2.79644
treatT	-1.1894	0.071684	-16.592	< 2e-16	***	
genus1:polyploidYES	-0.08823	0.199208	-0.443	0.658749		-0.07012
genus2:polyploidYES	0.103121	0.199208	0.518	0.60578		0.121232
genus3:polyploidYES	0.663361	0.226272	2.932	0.004131	**	0.681472
genus4:polyploidYES	0.161543	0.238656	0.677	0.499952		0.179654
genus5:polyploidYES	-0.42832	0.199208	-2.15	0.033821	*	-0.41021
genus6:polyploidYES	-0.15646	0.238656	-0.656	0.5135		-0.13835
genus7:polyploidYES	-0.00226	0.199208	-0.011	0.990987		0.015855
genus8:polyploidYES	0.281002	0.204907	1.371	0.173157		0.299113
genus9:polyploidYES	-0.66187	0.199208	-3.323	0.001225	**	-0.64376
						0.146216
genus1:treatT	0.180859	0.199208	0.908	0.365996		-1.00854
genus2:treatT	-0.04905	0.199208	-0.246	0.806004		-1.23844
genus3:treatT	-0.88163	0.226272	-3.896	0.000171	***	-2.07102
genus4:treatT	-0.30151	0.199208	-1.514	0.133122		-1.4909
genus5:treatT	0.627703	0.199208	3.151	0.002115	**	-0.56169
genus6:treatT	0.664016	0.250428	2.652	0.009242	**	-0.52538

genus7:treatT	0.860832	0.199208	4.321	3.51E-05	***	-0.32856
genus8:treatT	-0.49153	0.19034	-2.582	0.011176	*	-1.68093
genus9:treatT	0.600742	0.199208	3.016	0.00321	**	-0.58865
polyploidYES:treatT	0.255247	0.099803	2.558	0.011956	*	-2.39984
genus1:polyploidYES:treatT	-0.20083	0.28116	-0.714	0.476617		0.054417
genus2:polyploidYES:treatT	-0.11353	0.28116	-0.404	0.687181		0.141718
genus3:polyploidYES:treatT	1.012128	0.319502	3.168	0.002007	**	1.267375
genus4:polyploidYES:treatT	-0.4155	0.310361	-1.339	0.183507		-0.16026
genus5:polyploidYES:treatT	-1.00528	0.28116	-3.575	0.000528	***	-0.75004
genus6:polyploidYES:treatT	0.715256	0.328388	2.178	0.031616	*	0.970503
genus7:polyploidYES:treatT	-0.48387	0.28116	-1.721	0.088174	.	-0.22862
genus8:polyploidYES:treatT	-0.28443	0.285226	-0.997	0.32094		-0.02918
genus9:polyploidYES:treatT	0.12797	0.28116	0.455	0.649932		0.383217
---						0.903334

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.2939 on 106 degrees of freedom
Multiple R-squared: 0.9026, Adjusted R-squared: 0.8668
F-statistic: 25.19 on 39 and 106 DF, p-value: < 2.2e-16

celková dry biomasa

m <- lm(log(db)~genus*polyploid*treat, data=de.cep)

```
Response: log(db)
                       Df  Sum Sq Mean Sq  F value    Pr(>F)
genus                   9 19.6519  2.1835  20.3076 < 2.2e-16 ***
polyploid               1  0.0001  0.0001   0.0011  0.973308
treat                   1 19.6698 19.6698 182.9356 < 2.2e-16 ***
genus:polyploid         9 10.4167  1.1574  10.7643 9.946e-12 ***
genus:treat             9 15.0726  1.6747  15.5755 6.348e-16 ***
polyploid:treat         1  0.3839  0.3839   3.5701  0.061559 .
genus:polyploid:treat   9  2.8259  0.3140   2.9201  0.003948 **
Residuals             106 11.3975  0.1075

lm(formula = log(db) ~ genus * polyploid * treat, data = de.cep)

Residuals:
     Min       1Q   Median       3Q      Max
-0.66285 -0.18955  0.00634  0.18611  0.70001

Coefficients:
```

	Estimate	Std. Error	t value	Pr(>|t|)		
(Intercept)	-5.20364	0.05711	-91.116	< 2e-16	***	
genus1	0.119142	0.157373	0.757	0.450688		-5.0845
genus2	0.098149	0.157373	0.624	0.534183		-5.10549
genus3	0.388917	0.178702	2.176	0.031749	*	-4.81472
genus4	-0.53397	0.157373	-3.393	0.000973	***	-5.73761
genus5	-0.38975	0.157373	-2.477	0.014846	*	-5.59339
genus6	-0.64185	0.215107	-2.984	0.003534	**	-5.84549
genus7	-0.39757	0.157373	-2.526	0.013006	*	-5.60121
genus8	0.67163	0.143057	4.695	8.02E-06	***	-4.53201
genus9	-0.12806	0.157373	-0.814	0.417604		-5.33171
polyploidYES	-0.0348	0.079985	-0.435	0.66441		-4.39029
treatT	-0.90236	0.079985	-11.282	< 2e-16	***	
genus1:polyploidYES	-0.18255	0.222277	-0.821	0.413333		-0.21735
genus2:polyploidYES	0.232169	0.222277	1.045	0.298628		0.197371
genus3:polyploidYES	0.620793	0.252474	2.459	0.015558	*	0.585995
genus4:polyploidYES	0.123485	0.266292	0.464	0.643799		0.088687
genus5:polyploidYES	-0.35427	0.222277	-1.594	0.113954		-0.38907
genus6:polyploidYES	-0.14216	0.266292	-0.534	0.594571		-0.17696
genus7:polyploidYES	0.048609	0.222277	0.219	0.827314		0.013811
genus8:polyploidYES	0.050492	0.228636	0.221	0.825641		0.015694
genus9:polyploidYES	-0.74052	0.222277	-3.332	0.00119	**	-0.77532
						0.309151
genus1:treatT	0.438375	0.222277	1.972	0.051191	.	-0.46399
genus2:treatT	-0.0509	0.222277	-0.229	0.819302		-0.95327
genus3:treatT	-1.04302	0.252474	-4.131	7.23E-05	***	-1.94538
genus4:treatT	-0.14951	0.222277	-0.673	0.502634		-1.05188
genus5:treatT	0.615333	0.222277	2.768	0.006652	**	-0.28703
genus6:treatT	0.703582	0.279428	2.518	0.0133	*	-0.19878

```
genus7:treatT                    0.76094  0.222277     3.423   0.00088 ***        -0.14142
genus8:treatT                   -0.78701  0.212382    -3.706  0.000337 ***        -1.68938
genus9:treatT                   0.820359  0.222277     3.691  0.000355 ***          -0.082
polyploidYES:treatT             0.271631   0.11136     2.439  0.016379 *           -2.2105
genus1:polyploidYES:treatT      -0.08677  0.313719    -0.277  0.782645            0.184864
genus2:polyploidYES:treatT      -0.22494  0.313719    -0.717  0.474946            0.046692
genus3:polyploidYES:treatT      1.092139    0.3565     3.064  0.002774 **          1.36377
genus4:polyploidYES:treatT      -0.17372  0.346301    -0.502  0.616956             0.09791
genus5:polyploidYES:treatT      -1.07075  0.313719    -3.413  0.000911 ***        -0.79912
genus6:polyploidYES:treatT      0.718329  0.366416      1.96  0.052571 .           0.98996
genus7:polyploidYES:treatT      -0.53041  0.313719    -1.691  0.093832 .          -0.25878
genus8:polyploidYES:treatT      -0.07881  0.318256    -0.248  0.804893            0.192818
genus9:polyploidYES:treatT      -0.00655  0.313719    -0.021  0.983395            0.265086
---                                                                               0.633105
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3279 on 106 degrees of freedom
Multiple R-squared:  0.8565,    Adjusted R-squared:  0.8037
F-statistic: 16.22 on 39 and 106 DF,  p-value: < 2.2e-16
```