Gene ontology analyses summary

1. High mountain / Cold conditions

a. Progenitors G4 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	0	0	0
Total genes	0	0	0
Athal ID matches	0 (0%)	0 (0%)	0 (0%)
Gene Enrichment	No genes	No genes	No genes
Gene Enrichment all	No genes		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	100	65	10
Total genes	32	32	3
Athal ID matches	14 (43.8%)	17 (53.1%)	2 (66.7%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		

b. *A. kamchatica* synthetic G1 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	1'602	2'063	1'046
Total genes	861	1164	464
Athal ID matches	334 (38.8%)	321 (27.6%)	124 (26.7%)
Gene Enrichment	Yes, cellular process	No	No
Gene Enrichment all	Yes, cellular process		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	2'425	2'550	2'362
Total genes	1'208	1'280	1'005
Athal ID matches	429 (35.5%)	340 (26.6%)	289 (28.8%)
Gene Enrichment	Yes, organic substance metabolic process	Yes, organic substance, primary, nitrogen compound and cellular metabolic process	No
Gene Enrichment all	Yes, small molecule, organic, primary and cellular metabolic process		

c. A. kamchatica synthetic G4 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	3'224	2'748	1'253
Total genes	1'590	1'474	495
Athal ID matches	650 (40.9%)	385 (26.1%)	123 (24.8%)
Gene Enrichment	Yes, cellular response to oxygen-containing compound, organic substance and cellular metabolic process	No	No
Gene Enrichment all	Yes, cellular response to oxygen-containing compound, organic substance and cellular metabolic process		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	4'063	3'371	6'771
Total genes	1'981	1'538	2'667
Athal ID matches	823 (41.5%)	438 (28.5%)	717 (26.9%)
Gene Enrichment	Yes, ion transport, response to stimulus, organic substance, primary and cellular metabolic process	Yes, cellular process	Yes, transmembrane transport
Gene Enrichment all	-		

d. *A. kamchatica* synthetic G4 vs *A. kamchatica* synthetic G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	351	342	2'394
Total genes	198	206	712
Athal ID matches	72 (36.4%)	55 (26.7%)	172 (24.2%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	311	319	2'074
Total genes	158	180	681
Athal ID matches	48 (30.4%)	59 (32.8%)	195 (28.6%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		

e. *A. kamchatica* natural (ALK) G1 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	31’477	13’420	8’719
Total genes	17’665	6’586	4’159
Athal ID matches	11’407 (64.6%)	1’567 (23.8%)	988 (23.8%)
Gene Enrichment			
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	30’193	11’158	8’704
Total genes	16’865	5’182	3’855
Athal ID matches	11’796 (69.9%)	1’349 (26%)	1’093 (28.4%)
Gene Enrichment			
Gene Enrichment all			

f. *A. kamchatica* natural (ALK) G4 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	27’485	10’483	8’050
Total genes	15'891	5'508	3'949
Athal ID matches	10’253 (64.5%)	1’341 (24.3%)	870 (22%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	26’239	9’099	7’142
Total genes	15'034	4'392	3'251
Athal ID matches	10’589 (70.4%)	1’182 (26.9%)	893 (27.5%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

g. *A. kamchatica* natural (ALK) G4 vs synthetic G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	27’789	9’316	6’296
Total genes	16'261	4'973	3'307
Athal ID matches	10'597 (65.2%)	1'206 (24.3%)	755 (22.8%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	23’719	6’869	4’646
Total genes	13'853	3'748	2'382
Athal ID matches	9'775 (70.6%)	997 (26.6%)	580 (24.3%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

h. *A. kamchatica* natural (ALK) G4 vs synthetic G4

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	23’863	8’288	9’109
Total genes	13923	4262	4104
Athal ID matches	8961 (64.4%)	1046 (24.5%)	873 (21.3%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	16’656	5’155	5’448
Total genes	9753	2723	2555
Athal ID matches	6543 (67.1%)	699 (25.7%)	556 (21.8%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

i. *A. kamchatica* natural (ALK) G4 vs *A. kamchatica* natural (ALK) G1

iii. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	0	13	0
Total genes	0	7	0
Athal ID matches	0 (0%)	1 (14.3%)	0 (0%)
Gene Enrichment	No genes	No	No genes
Gene Enrichment all	No		

iv. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	0	6	0
Total genes	0	4	0
Athal ID matches	0 (0%)	0 (0%)	0 (0%)
Gene Enrichment	No genes	No	No genes
Gene Enrichment all	No		

j. *A. kamchatica* natural (TKS) G1 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	33’049	15’079	8’175
Total genes	18’400	7’557	3’928
Athal ID matches	11’959 (65%)	1’712 (22.7%)	917 (23.3%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	32’110	11’940	9’567
Total genes	18’470	5773	4117
Athal ID matches	13’045 (70.6%)	1517 (26.3%)	1129 (27.4%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

k. *A. kamchatica* natural (TKS) G1 vs synthetic G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	33’038	12’849	8’281
Total genes	18’433	6579	3779
Athal ID matches	12’067 (65.5%)	1512 (23%)	887 (23.5%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	29’722	10’407	7’171
Total genes	17399	5394	3182
Athal ID matches	12367 (71.1%)	1349 (25%)	822 (25.8%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

I. *A. kamchatica* natural (TKS) G1 vs synthetic G4

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	28’704	10’478	8’151
Total genes	16’167	5’471	3’920
Athal ID matches	10’392 (64.3%)	1’341 (24.5%)	840 (21.4%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	21’341	7’084	5’811
Total genes	12’447	3’830	2’786
Athal ID matches	8’480 (68.1%)	982 (25.6%)	613 (22%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

m. *A. kamchatica* natural (TKS) G1 vs *A. kamchatica* natural (TKS) G5

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	0	0	568
Total genes	0	0	89
Athal ID matches	0 (0%)	0 (0%)	32 (36%)
Gene Enrichment	No genes	No genes	
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	0	3	300
Total genes	0	2	58
Athal ID matches	0 (0%)	1 (50%)	22 (37.9%)
Gene Enrichment	No genes	No genes	
Gene Enrichment all			

2. Low land / Hot conditions

a. Progenitors G4 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	13	213	116
Total genes	7	132	50
Athal ID matches	2 (28.6%)	20 (15.2%)	13 (26%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	0	217	1'236
Total genes	0	167	373
Athal ID matches	0 (0%)	22 (13.2%)	78 (20.9%)
Gene Enrichment	No genes	No	No
Gene Enrichment all	No		

b. *A. kamchatica* synthetic G1 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	1'990	6'115	2'118
Total genes	1'118	4'144	944
Athal ID matches	462 (41.3%)	642 (15.5%)	229 (24.3%)
Gene Enrichment	Yes, response to chemical and cellular process	No	No
Gene Enrichment all	No		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	2'611	2'421	4'136
Total genes	1'391	1'248	1'287
Athal ID matches	535 (38.5%)	304 (24.4%)	370 (28.7%)
Gene Enrichment	Yes, metabolic and cellular process	No	No
Gene Enrichment all	No		

c. *A. kamchatica* synthetic G4 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	3'447	8'746	8'538
Total genes	1’721	3'710	2'673
Athal ID matches	705 (41%)	911 (24.6%)	669 (25%)
Gene Enrichment	Yes, cellular process and response to chemical	Yes, cellular process	Yes, nitrogen compound, organic substance, primary and cellular metabolic process
Gene Enrichment all	Yes, cellular process		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	3’874	5’848	3’011
Total genes	1’907	3’640	1’247
Athal ID matches	744 (39%)	554 (15.2%)	374 (30%)
Gene Enrichment	Yes, mitotic cytokinesis, organic substance, cellular and primary metabolic process	Yes, organic substance, primary and cellular metabolic process	No
Gene Enrichment all	No		

d. *A. kamchatica* synthetic G4 vs *A. kamchatica* synthetic G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	313	93	1'373
Total genes	181	70	287
Athal ID matches	53 (29.3%)	20 (28.6%)	95 (33.1%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	323	80	1'241
Total genes	182	73	328
Athal ID matches	56 (30.8%)	19 (26%)	106 (32.3%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		

e. *A. kamchatica* natural (ALK) G1 vs progenitors G1

iii. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	34’040	14’573	10’222
Total genes	18’917	7’118	4’779
Athal ID matches	12’124 (64.1%)	1’653 (23.2%)	1’096 (22.9%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

iv. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	31’693	14’486	11’795
Total genes	17’416	6’839	4’616
Athal ID matches	12’069 (69.3%)	1’489 (21.8%)	1’111 (24.1%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

f. *A. kamchatica* natural (ALK) G1 vs synthetic G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	33’709	12’315	8’932
Total genes	19’044	6’701	4’292
Athal ID matches	12’345 (64.8%)	1’371 (20.5%)	920 (21.4%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	30’401	8’951	7’235
Total genes	16’953	4’964	3’487
Athal ID matches	11’705 (69%)	1’190 (24%)	799 (22.9%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

g. *A. kamchatica* natural (ALK) G1 vs synthetic G4

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	29’668	12’224	13’259
Total genes	17’197	5’728	5’120
Athal ID matches	11’142 (64.8%)	1’371 (23.9%)	1’110 (21.7%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	23’328	8’233	9’378
Total genes	13’436	4’115	3’787
Athal ID matches	9’129 (67.9%)	1’045 (25.4%)	853 (22.5%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

n. *A. kamchatica* natural (ALK) G4 vs *A. kamchatica* natural (ALK) G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	6	3	8
Total genes	7	3	7
Athal ID matches	3 (42.9%)	1 (33.3%)	5 (71.4%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	8	2	7
Total genes	7	3	7
Athal ID matches	2 (28.6%)	2 (66.7%)	1 (14.3%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		

o. *A. kamchatica* natural (TKS) G1 vs progenitors G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	34’308	16’181	10’167
Total genes	19’002	8’100	4’707
Athal ID matches	12’308 (64.8%)	1’800 (22.2%)	1’132 (24%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	32’821	11’492	10’102
Total genes	18’775	5’707	4’284
Athal ID matches	13’277 (70.7%)	1’436 (25.2%)	1’038 (24.2%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

p. *A. kamchatica* natural (TKS) G1 vs synthetic G1

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	33156	10215	7952
Total genes	18680	5557	3947
Athal ID matches	12190 (65.3%)	1314 (23.6%)	833 (21.1%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	31’101	7’612	6’834
Total genes	18’155	4’276	3’342
Athal ID matches	12’933 (71.2%)	1’186 (27.7%)	793 (23.7%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

q. *A. kamchatica* natural (TKS) G1 vs synthetic G4

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	30'069	11'608	10'749
Total genes	17'049	5'909	4'515
Athal ID matches	11'104 (65.1%)	1'363 (23.1%)	977 (21.6%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	24'451	7'559	7'613
Total genes	14'446	4'103	3'378
Athal ID matches	10'125 (70.1%)	1'006 (24.5%)	769 (22.8%)
Gene Enrichment	Too many genes		
Gene Enrichment all			

r. *A. kamchatica* natural (TKS) G1 vs *A. kamchatica* natural (TKS) G5

i. *halleri*-side

Context	CG	CHG	CHH
Total DMRs	24	155	442
Total genes	12	86	70
Athal ID matches	5 (41.7%)	46 (53.5%)	25 (35.7%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		

ii. *lyrata*-side

Context	CG	CHG	CHH
Total DMRs	12	91	327
Total genes	4	61	75
Athal ID matches	1 (25%)	38 (62.3%)	21 (28%)
Gene Enrichment	No	No	No
Gene Enrichment all	No		