chr	start position	end position	chr region	p-value	adjusted p-value	# input genes in the region	# genes in the region	% enrichment
12	6727434	6750379	p13.31	0.00790	0.03962	2	2	100.00%
12	14818672	15026066	p12.3	0.00209	0.03434	4	8	50.00%
12	14818672	14847668	p12.3	0.00790	0.03962	2	2	100.00%
12	14986232	15026066	p12.3	0.00790	0.03962	2	2	100.00%
12	32003620	32789750	p11.21	0.00129	0.02848	4	7	57.14%
12	32723491	32789750	p11.21	0.00790	0.03962	2	2	100.00%
12	54396088	54501736	q13.2	0.00012	0.01349	5	7	71.43%
12	54832471	54841627	q13.2	0.00790	0.03962	2	2	100.00%
12	55443375	55791428	q13.3	0.00639	0.03962	4	11	36.36%
12	56303460	56401605	q14.1	0.00790	0.03962	2	2	100.00%
12	67919663	68281624	q15	0.00760	0.03962	3	6	50.00%
12	67919663	68034280	q15	0.00790	0.03962	2	2	100.00%
12	92326221	93377851	q22	0.00002	0.01164	6	8	75.00%
12	94891273	94953496	q23.1	0.00790	0.03962	2	2	100.00%
12	108851992	109273278	q24.11	0.00760	0.03962	3	6	50.00%
12	109046687	109273278	q24.11	0.00790	0.03962	2	2	100.00%
12	119263516	119391941	q24.31	0.00461	0.03962	3	5	60.00%