

Target position file

start	end	targetID@subID
2	82	GeneX@Exon1
120	200	GeneX@Exon2
320	500	GeneY@Exon1
620	750	GeneY@Exon2
650	900	GeneZ@Exon1
1300	1350	GeneZ@Exon2
1600	1800	GeneZ@Exon3

Tag position file

start	end	tagID
7	41	tag1
30	64	tag2
75	109	tag3
90	124	tag4
675	701	tag5
1710	1744	tag6

SNP position file

start	end	snpID
23	24	snp1
38	39	snp2
66	67	snp3
115	116	snp4
702	703	snp5
1800	1801	snp6



MATCH

MATCH

Tag2Target match file

tagID	targetID@subID
tag1	GeneX@Exon1
tag2	GeneX@Exon1
tag5	GeneY@Exon2
tag5	GeneZ@Exon1
tag6	GeneZ@Exon3

Tag2SNP match file

tagID	snpID
tag1	Snp1
tag1	snp2
tag4	snp4



ANNOTATE



Tag annotation file

tagID	targetID	hasSNP
tag1	GeneX	yes
tag2	GeneX	no
tag5	GeneY	yes
tag5	GeneY	no
tag6	GeneZ	no