

**Table S1: Summary of gene functional annotation by chromosome in AB32**

Gene ontology term enrichment was determined for the subset of PR binding region-associated genes in AB32 cells on chromosomes 2, 8 and 11.

<b>Chr 2 (58 IDs)</b>		
<b>Annotation Cluster</b>	<b>Enrichment Score</b>	<b>Function</b>
1	2.75	Metabolism
2	1.61	GTPase activity
3	0.91	Metabolism

  

<b>Chr 8 (25 IDs)</b>		
<b>Annotation Cluster</b>	<b>Enrichment Score</b>	<b>Function</b>
1	1.62	Apoptosis
4	0.72	Catabolism
6	0.55	Transcriptional regulation
7	0.52	Apoptosis
8	0.39	Nucleotide binding
11	0.11	Metal ion binding

  

<b>Chr 11 (39 IDs)</b>		
<b>Annotation Cluster</b>	<b>Enrichment Score</b>	<b>Function</b>
1	1.57	Metabolism
3	0.73	DNA repair
4	0.72	Protein complex assembly
5	0.70	Transcriptional regulation
6	0.63	Phosphorylation
7	0.51	Transcriptional regulation
8	0.37	Apoptosis