



Table 3. Long runs of short chains in the top level of the net

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Breaks	Position	Aligned	Span	Break per megabase	Genes in region
759	chr19:52283288-55023011	355617	2739723	277.04	Sialic acid binding (ig-like cluster) and zinc finger cluster
307	chr19:11912709-12980044	123180	1067335	287.63	KRAB C2H2 zinc finger cluster
282	chr19:57924332-58994674	163649	1070342	263.47	KRAB C2H2 zinc finger cluster
228	chr2:129802976-130894216	284128	1091240	208.94	Ptpn18, cryptic (gene poor)
215	chr22:19036955-20094010	132206	1057055	203.4	Contains Ig l light chain locus and rhabdoid tumor deletion region
212	chr19:9294092-10142345	100712	848253	249.93	KRAB C2H2 Zinc finger cluster
209	chr8:6948129-8102614	205566	1154485	181.03	Ig region (defensin cluster)
199	chr6:28560342-29380273	99588	819931	242.7	Olfactory receptor cluster
164	chr12:11050382-11876400	124173	826018	198.54	Six taste receptors and five salivary gland genes
160	chr3:19755611-22829219	94791	3073608	52.06	HMGBl, mostly gene desert
158	chr1:153813433-154249175	48153	435742	362.6	CD1, immune response cluster
140	chr11:90897985-91367162	75731	469177	298.39	RNF18, gene poor region
124	chr17:21859306-22267186	116716	407880	304.01	TL132 protein, gene poor region
120	chr19:15050464-15453575	38600	403111	297.68	KRAB C2H2 zinc finger, olfactory cluster
115	chr18:13919892-15073531	145639	1153639	99.68	Two melocortin GPCRs

Breaks, the number of short chains in the region; Position, the location in the human genome (November 2002 freeze); Aligned, the number of aligned bases in the region; Span, the total length of the region (in human genome coordinates); Breaks per megabase, the average number of breaks between chains in each megabase in the region; Genes in region, the

properties or accessions of human RefSeq genes from the region. This table lists only the top few hot spots with the most consecutive short chains, excluding pericentromeric and telomeric regions, matches to human chromosome Y (because little sequence is available from mouse chromosome Y), and one region with extensive simple repeats of longer period than we masked. Hot spots of this type cover 5-10% of the human genome. Some are associated with clusters of mobile genes in the olfactory or zinc finger families (see text). Others are associated with immune genes. One of the largest of these regions (the fifth entry in the table) is on chromosome 22 near the Ig 1 light chain locus. This locus rearranges somatically during B cell maturation. Possibly a low level of the RAG proteins responsible for this somatic rearrangement are expressed in germ cells and occasionally cause recombination in germ cell lines in this region in mammals as well as other vertebrates. There are a number of RAG ESTs isolated from cells not in the B cell lineage, including GenBank accession no. N92955.

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