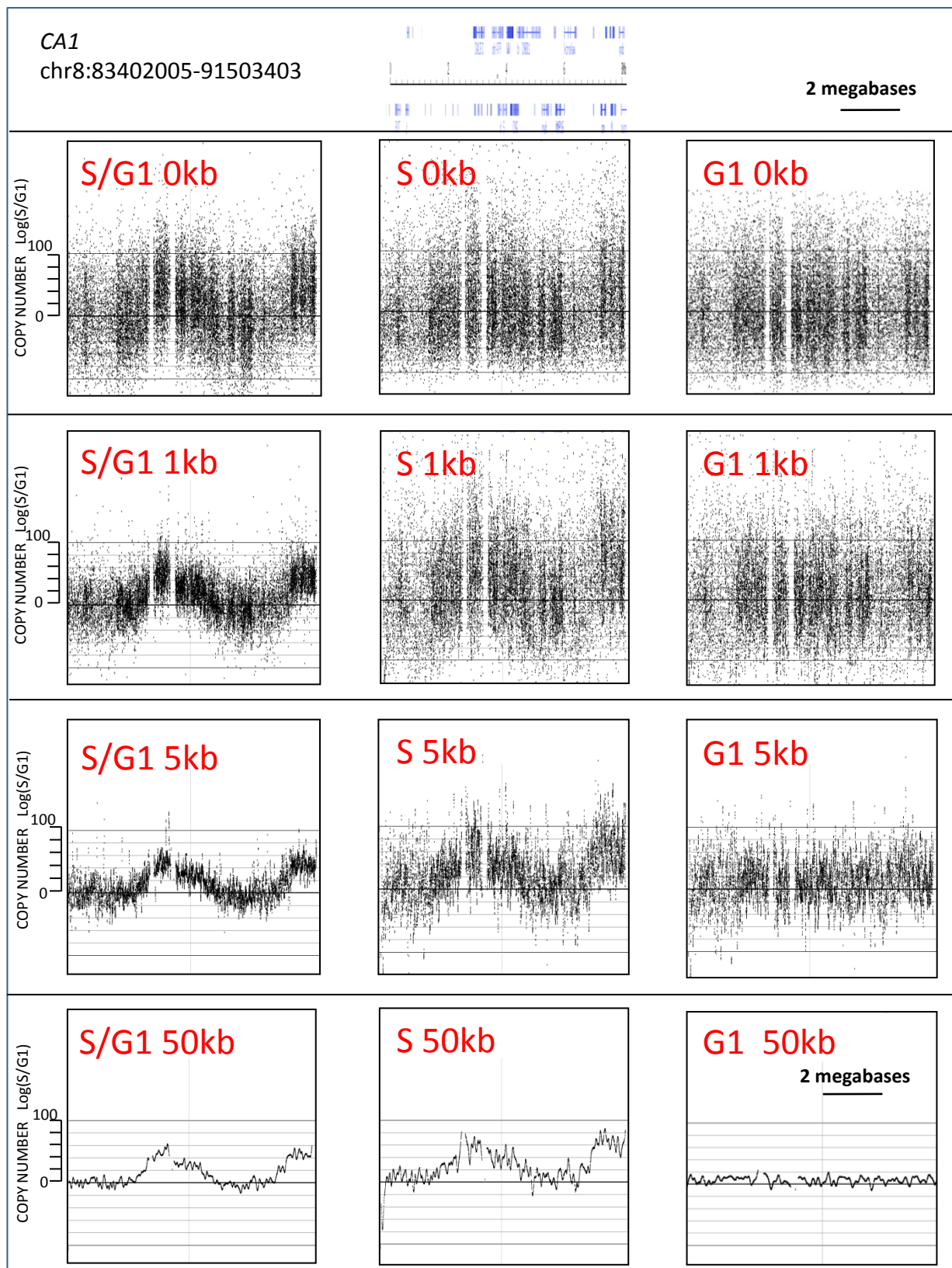
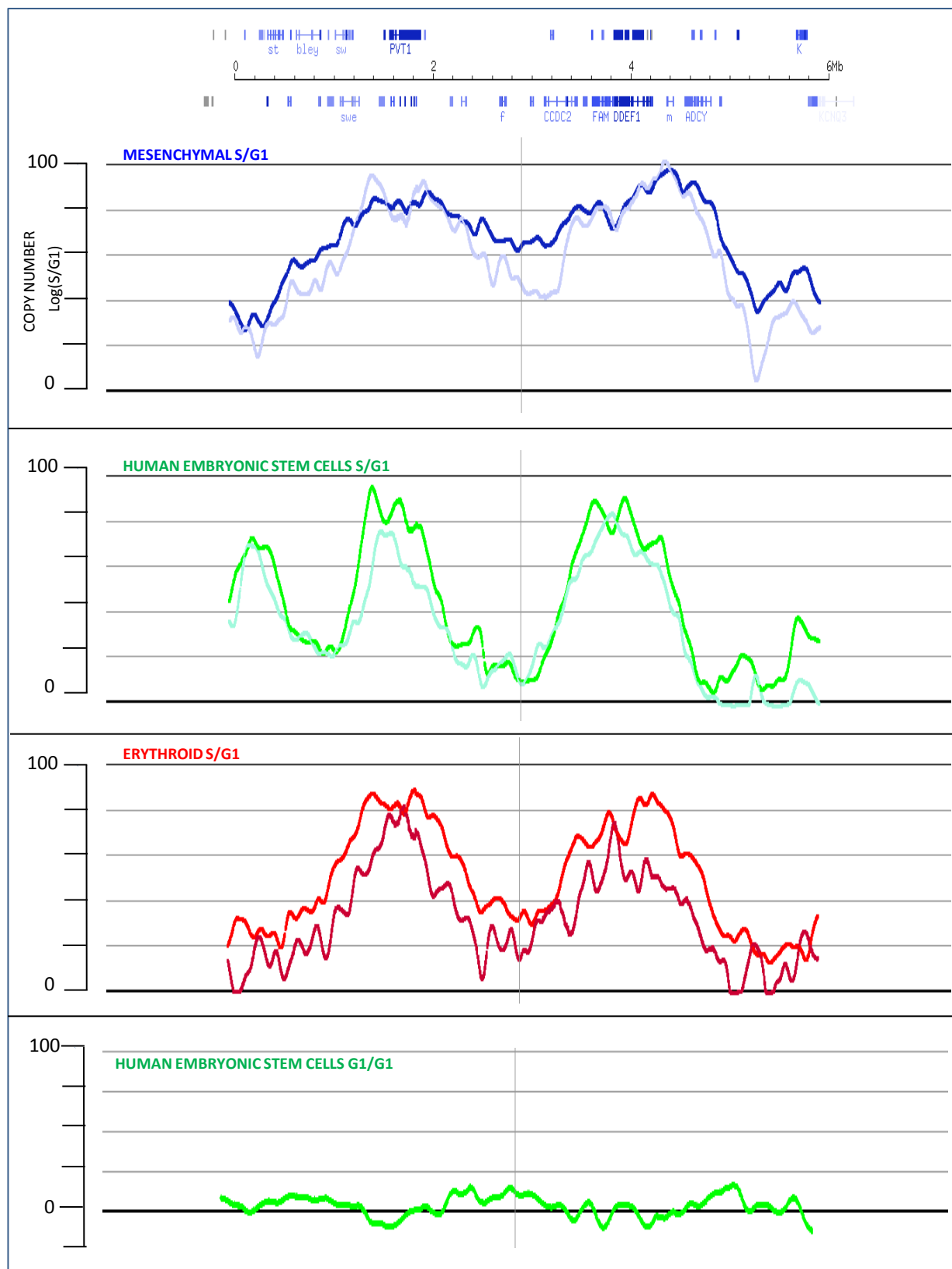


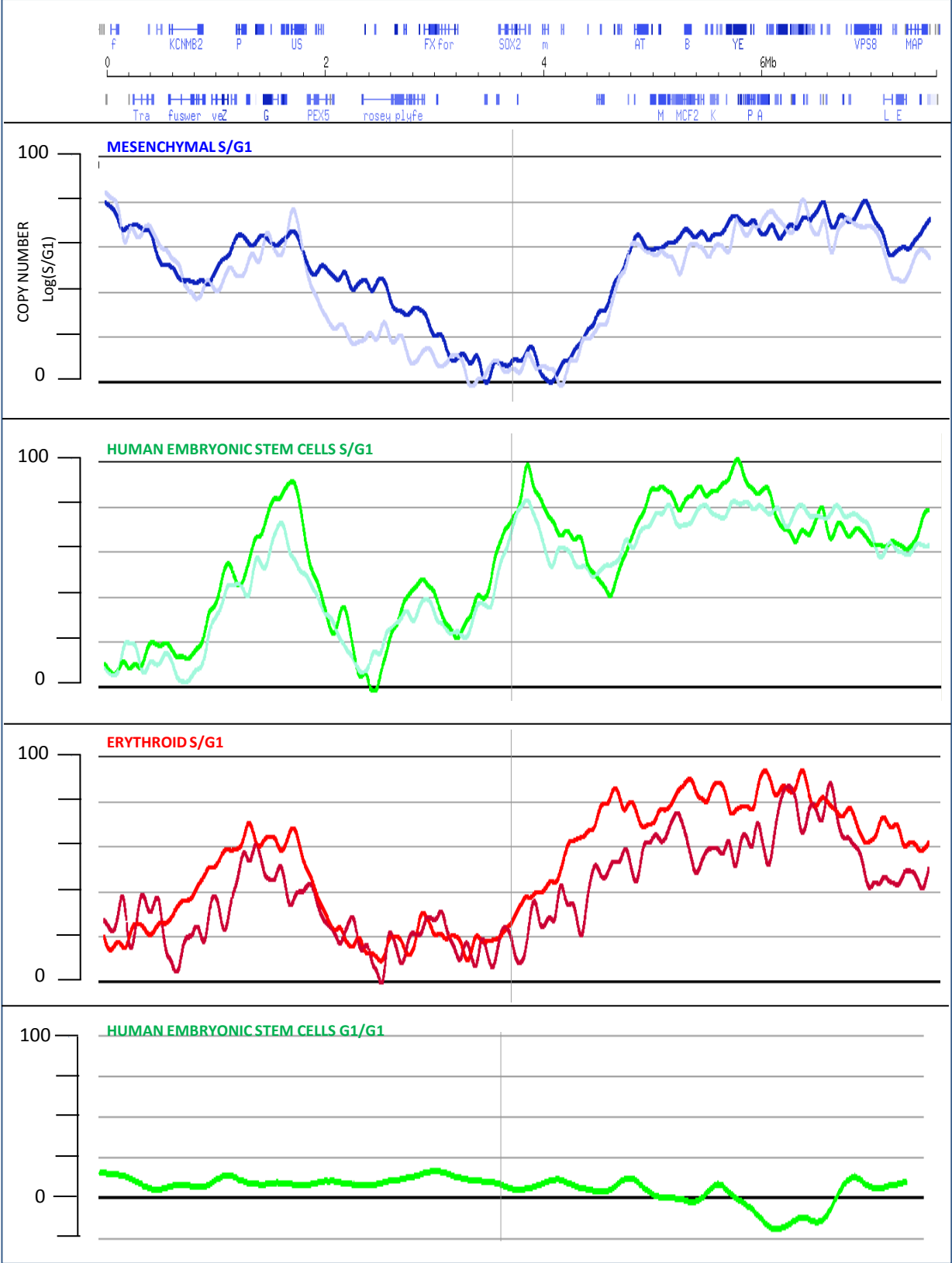
SUPPLEMENTARY TABLE S1

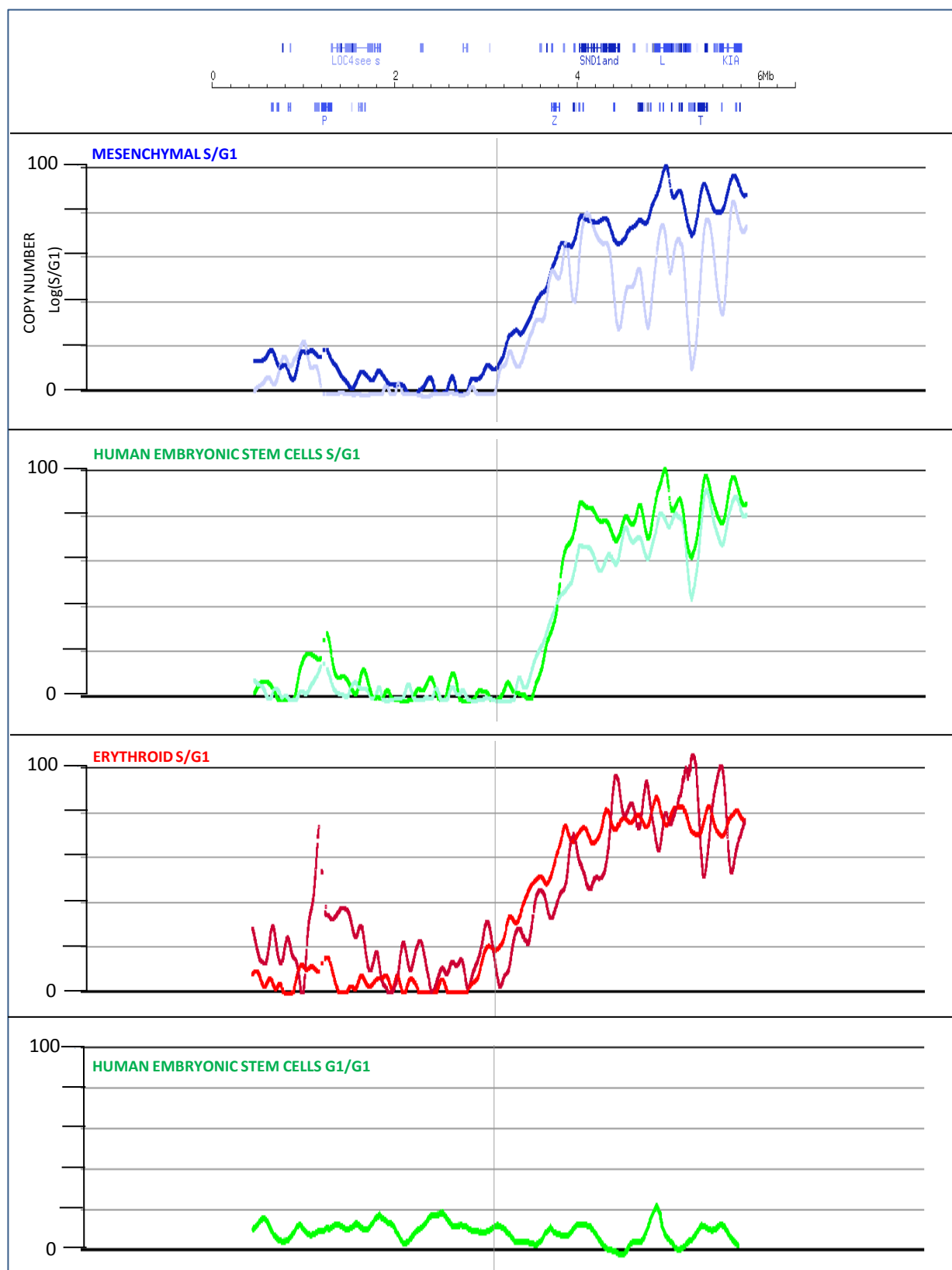
chip	Chip 1					Chip 2				
	Region nickname	chromosome	Region Start	Region End	Size	Region nickname	chromosome	Region Start	Region End	Size
1	<i>CEBPE</i>	14	21289669	21865338	575669					
1	<i>Chr19 Pick</i>	19	59023585	60024460	1000875					
1	<i>Chr21 Pick</i>	21	32666763	34362747	1695984					
1	<i>Chr22 Pick</i>	22	30128508	31828507	1699999					
1	<i>ChrX Pick</i>	X	151582202	152832201	1249999					
1	<i>Interleukin</i>	5	131332631	132332630	999999					
1	<i>Lamin B2</i>	19	1571683	3103082	1531399					
1	<i>p14ink4a(CDKN2A)</i>	9	21296602	22626401	1329799					
1	<i>p21(CDKN2B)</i>	6	36347412	37046411	698999					
1	<i>PML</i>	15	71716861	72329775	612914					
1	<i>Random 1</i>	15	40948853	42448852	1499999					
1	<i>IGF2/H19</i>	11	1388043	2900000	1511957					
1	<i>APO Cluster</i>	11	115994758	116494757	499999					
1 and 2	<i>FOXP2</i>	7	113487636	114487635	999999	<i>CFTR_FOXP2</i>	7	111398675	118561207	7162532
1 and 2	<i>CFTR</i>	7	115365024	117242449	1877425	<i>CFTR_FOXP2</i>	7	111398675	118561207	7162532
1 and 2	<i>HBB</i>	11	4237933	6241116	2003183	<i>HBB</i>	11	174472	8840227	8665755
1 and 2	<i>MYC</i>	8	127994699	129524698	1529999	<i>MYC</i>	8	127315359	133168887	5853528
1 and 2	<i>GRM8</i>	7	125633145	126796333	1163188	<i>GRM8</i>	7	123573778	128893545	5319767
1 and 2	<i>HOXA</i>	7	26199793	27699792	1499999	<i>HOXA</i>	7	25866154	28856529	2990375
1 and 2	<i>HOXB</i>	17	46587065	47577289	990224	<i>HOXB</i>	17	42647361	45417844	2770483
1 and 2	<i>IGH</i>	14	103500000	105311216	1811216	<i>IGH</i>	14	98878936	106359741	7480805
1 and 2	<i>HBA</i>	16	1	1500000	1499999	<i>HBA</i>	16	46	8309753	8309707
2				Total	28282823	<i>HOXC</i>	12	51459964	54685301	3225337
2						<i>HOXD</i>	2	175308247	178354076	3045829
2						<i>CA1</i>	8	83402005	91503403	8101398
2						<i>GATA1</i>	X	45044549	52022509	6977960
2						<i>MYH4</i>	7	7172410	12586343	5413933
2						<i>PAUVRE</i>	16	58084274	66083451	7999177
2						<i>PERI</i>	22	14441231	18439799	3998568
2						<i>POU5F1</i>	6	25490081	33491917	8001836
2						<i>SOX2</i>	3	179163983	186663501	7499518
2						<i>TAL1</i>	1	45439346	49481800	4042454
									Total	114021494

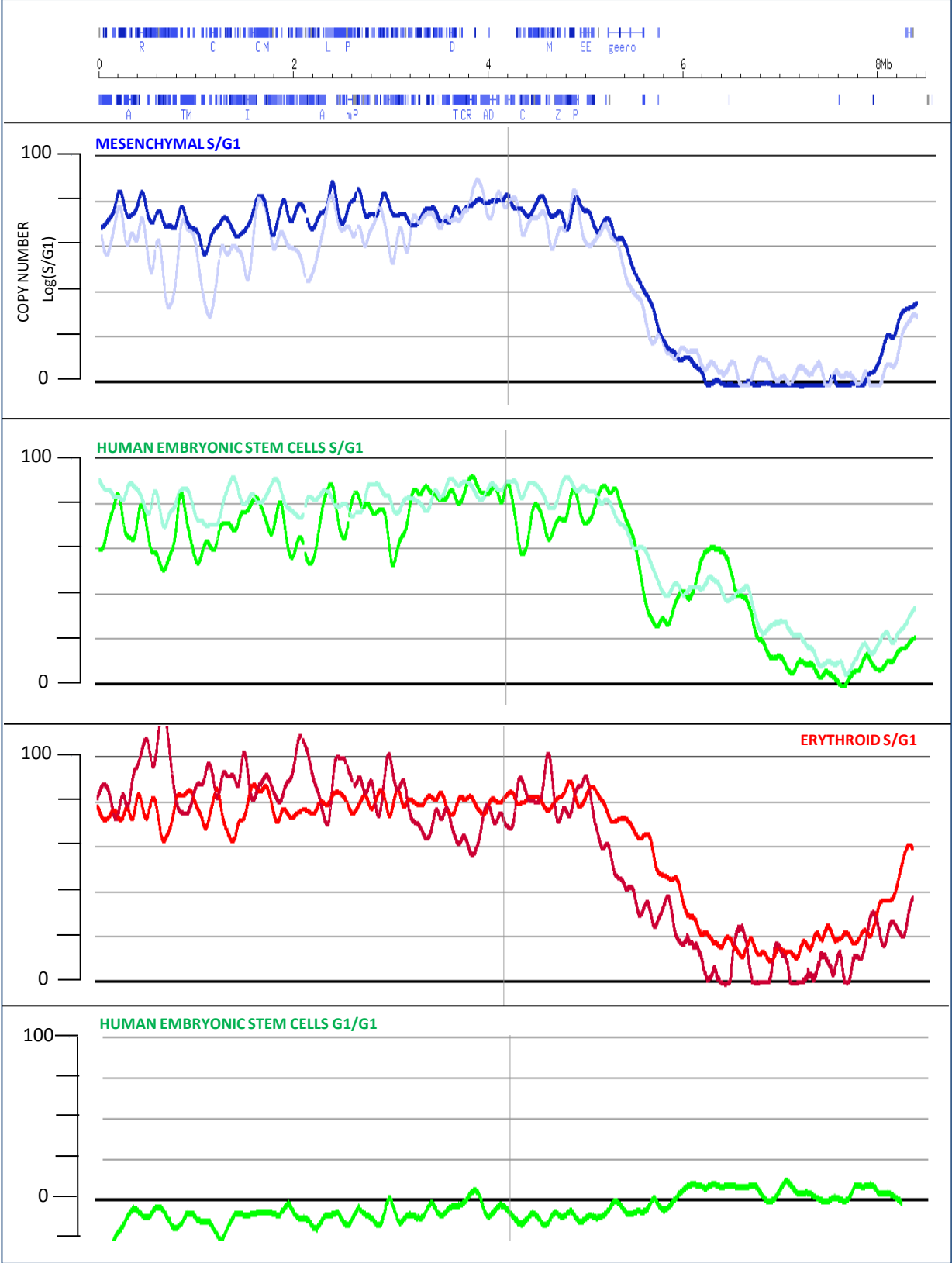
SUPPLEMENTARY FIGURE S1

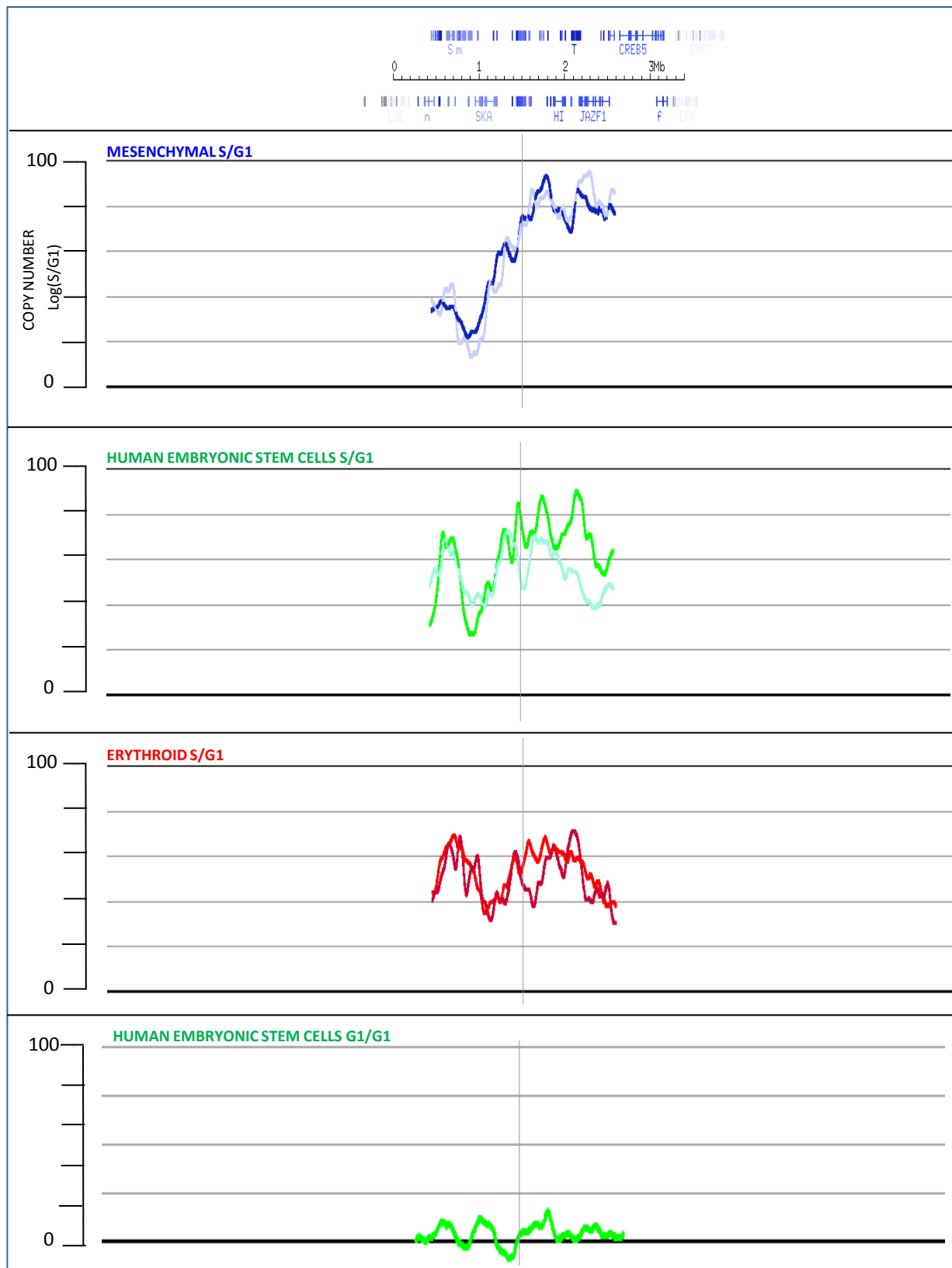


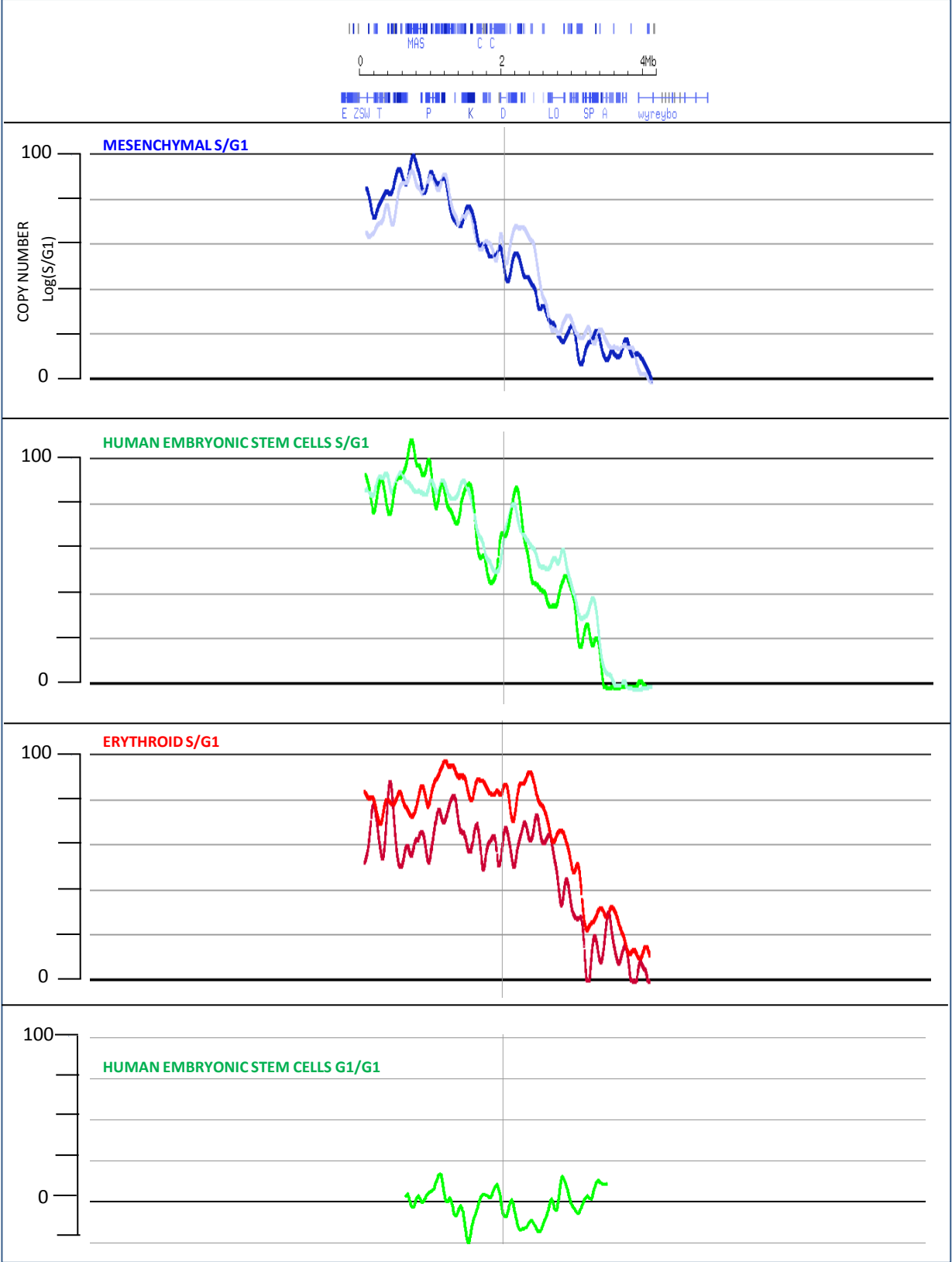


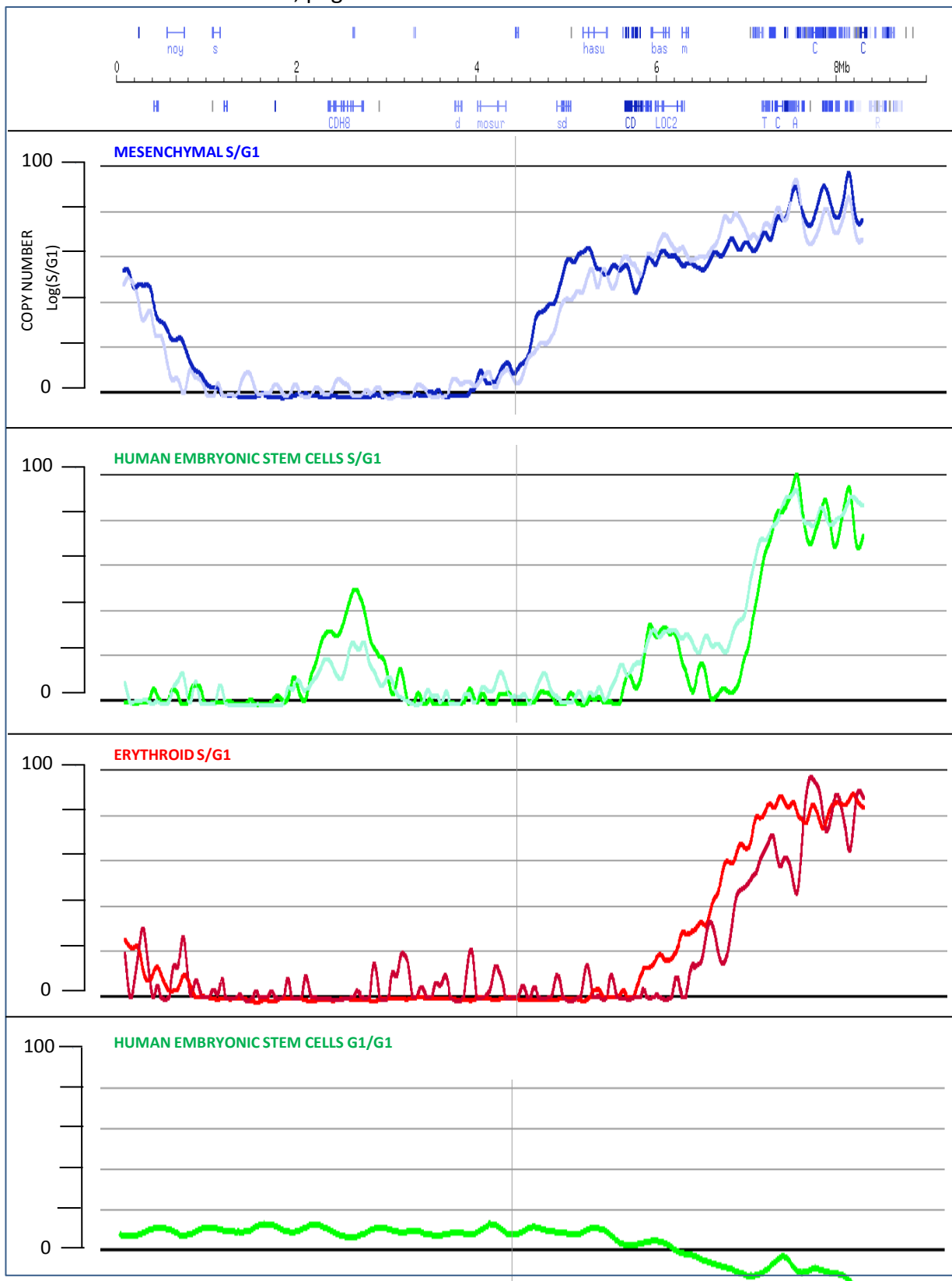


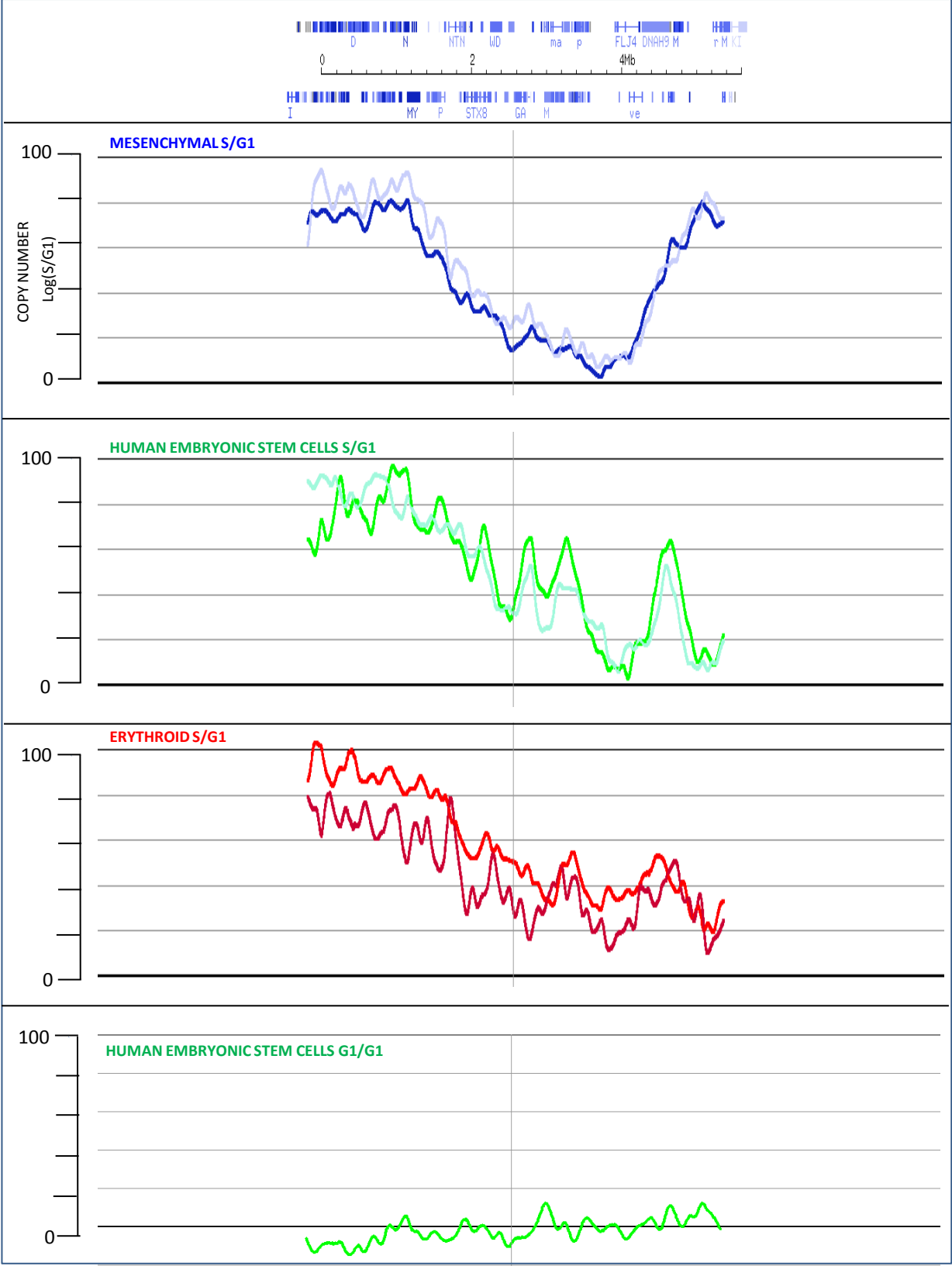


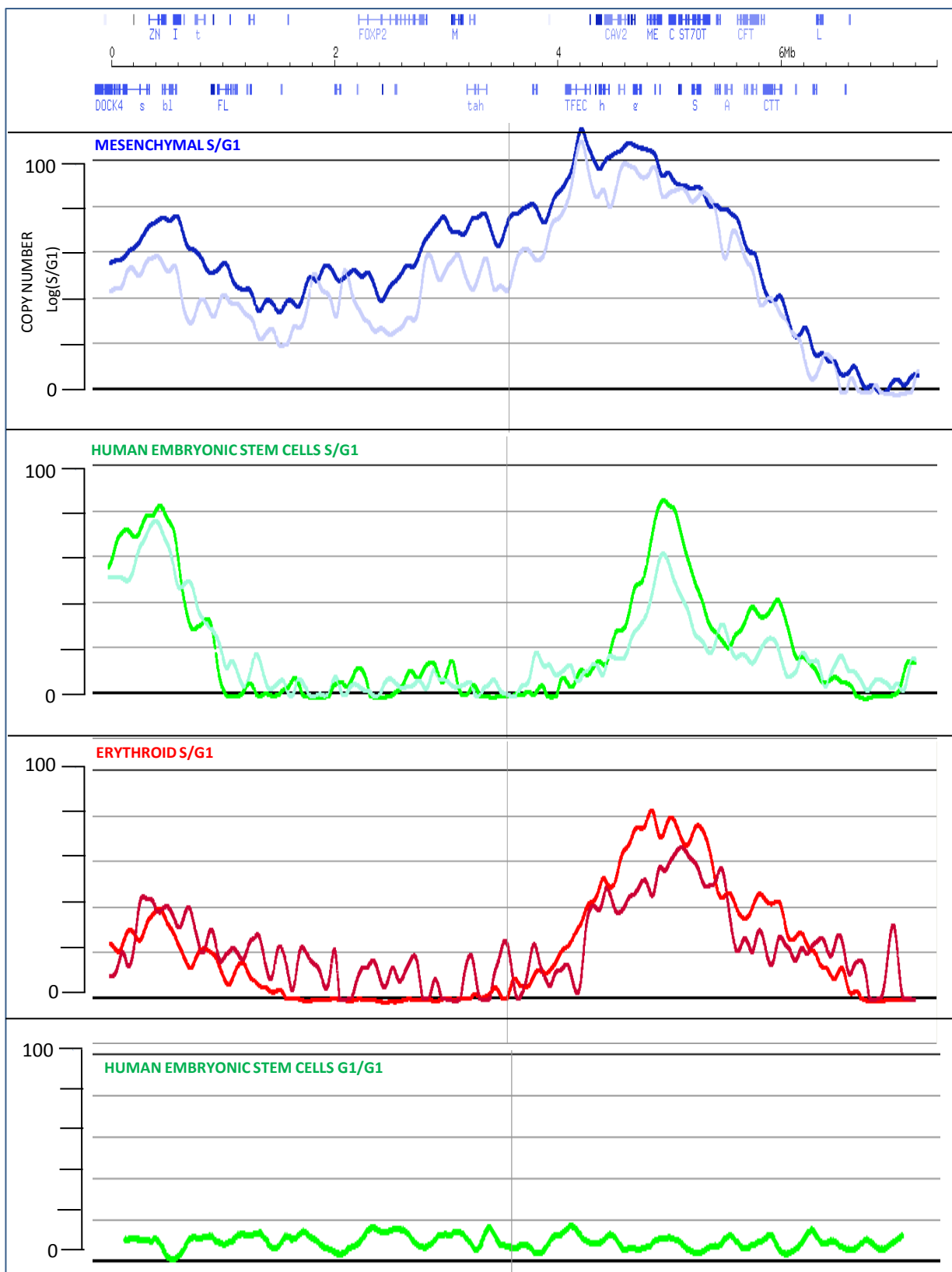


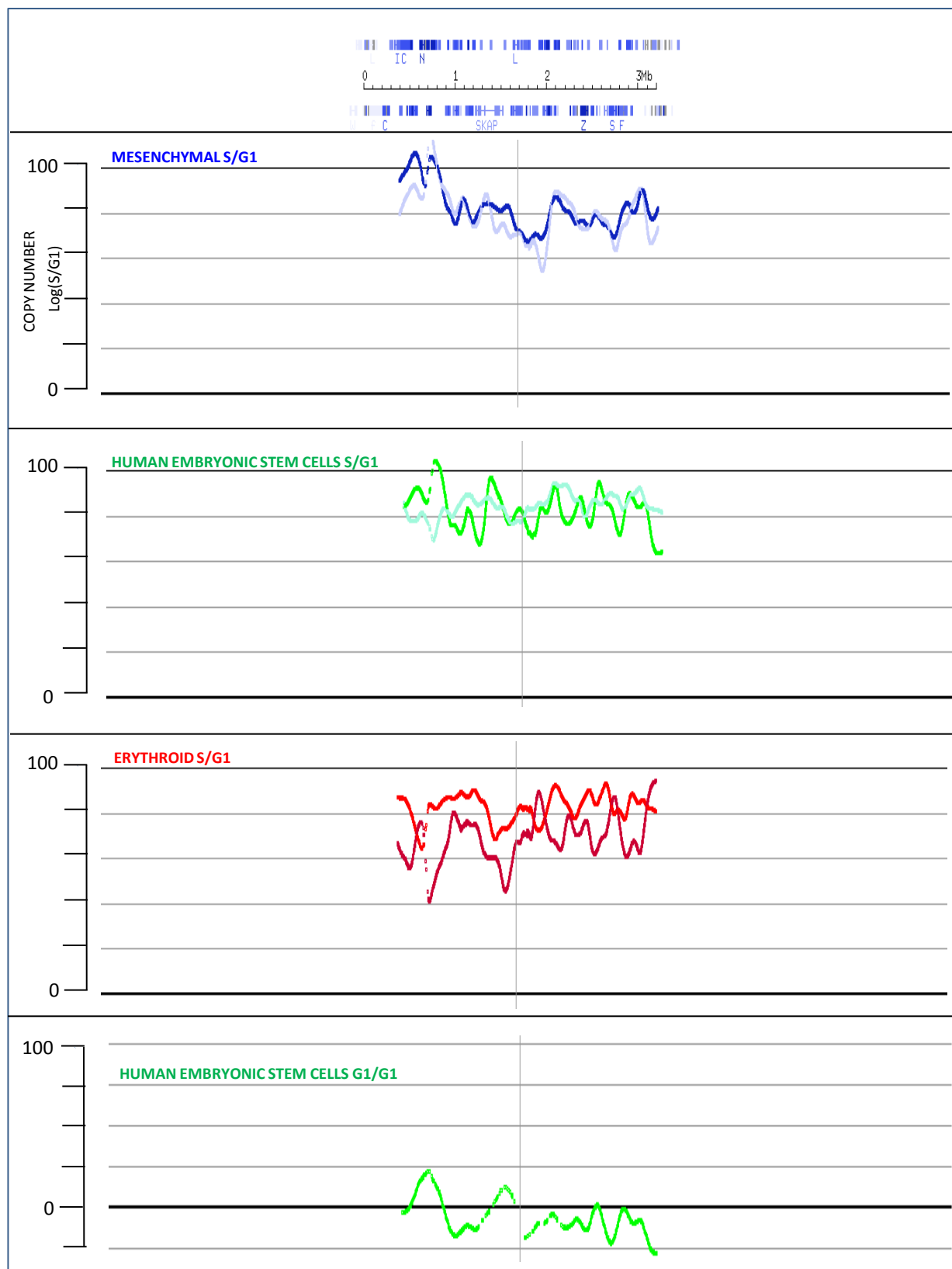


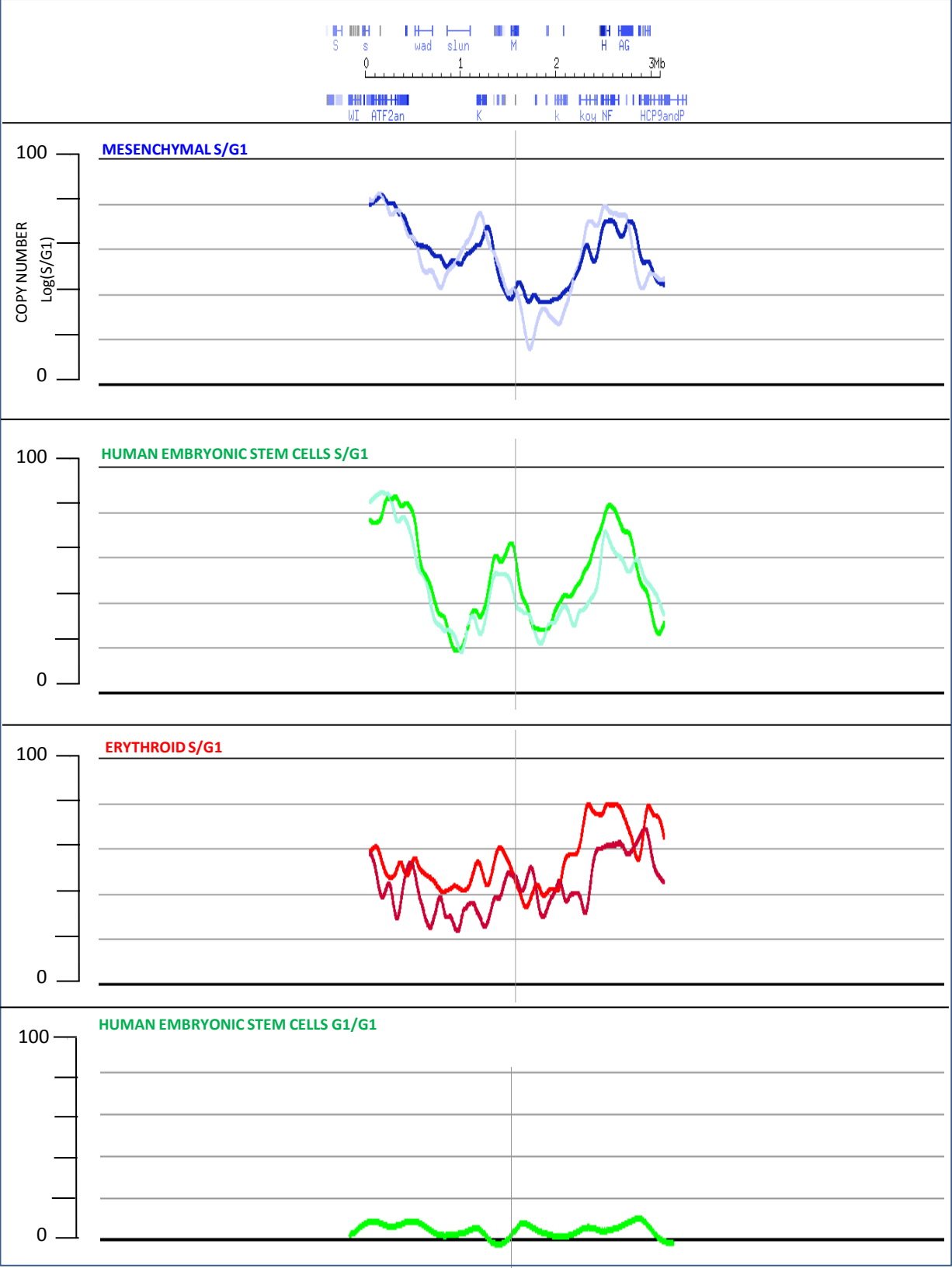


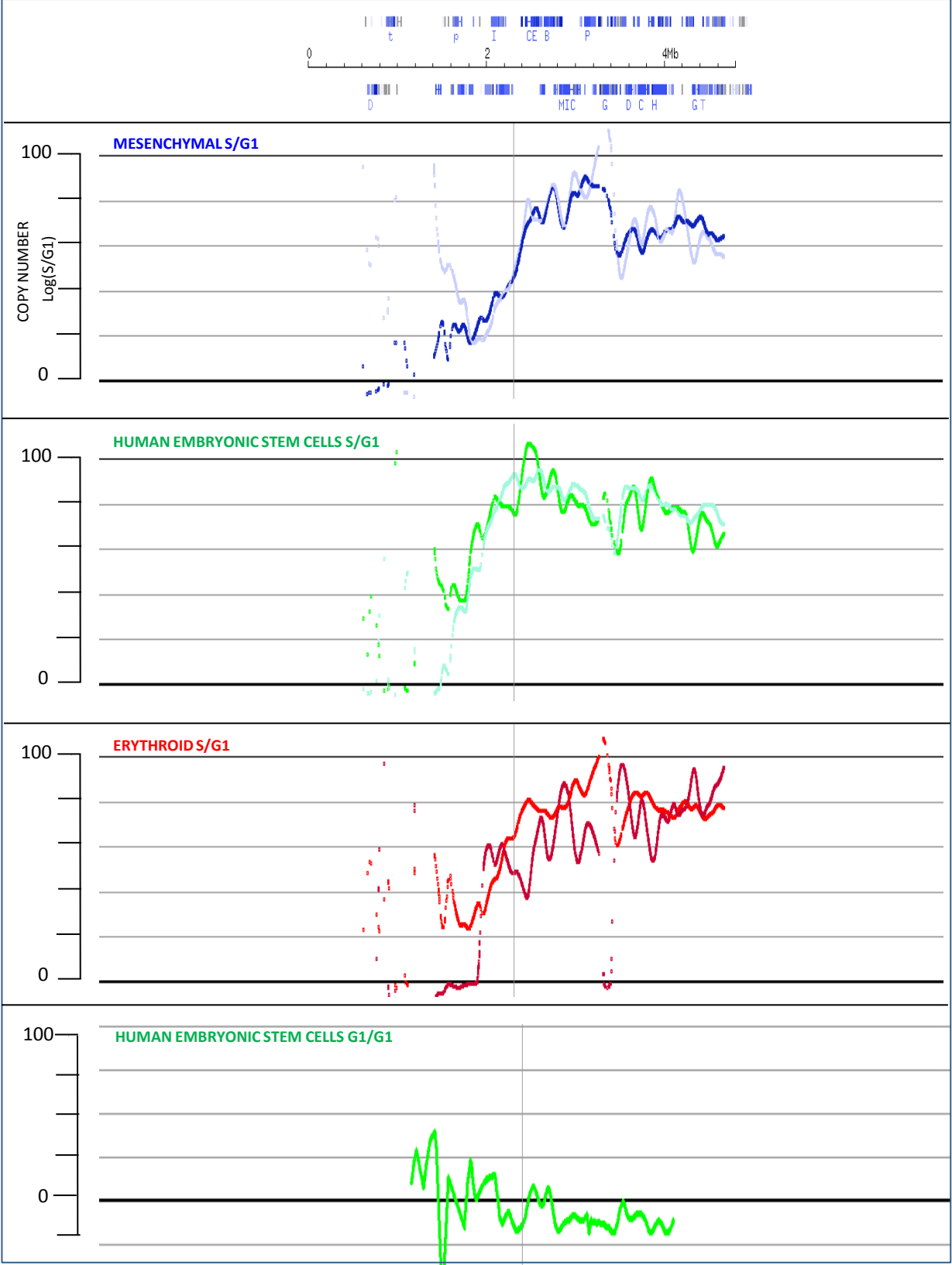


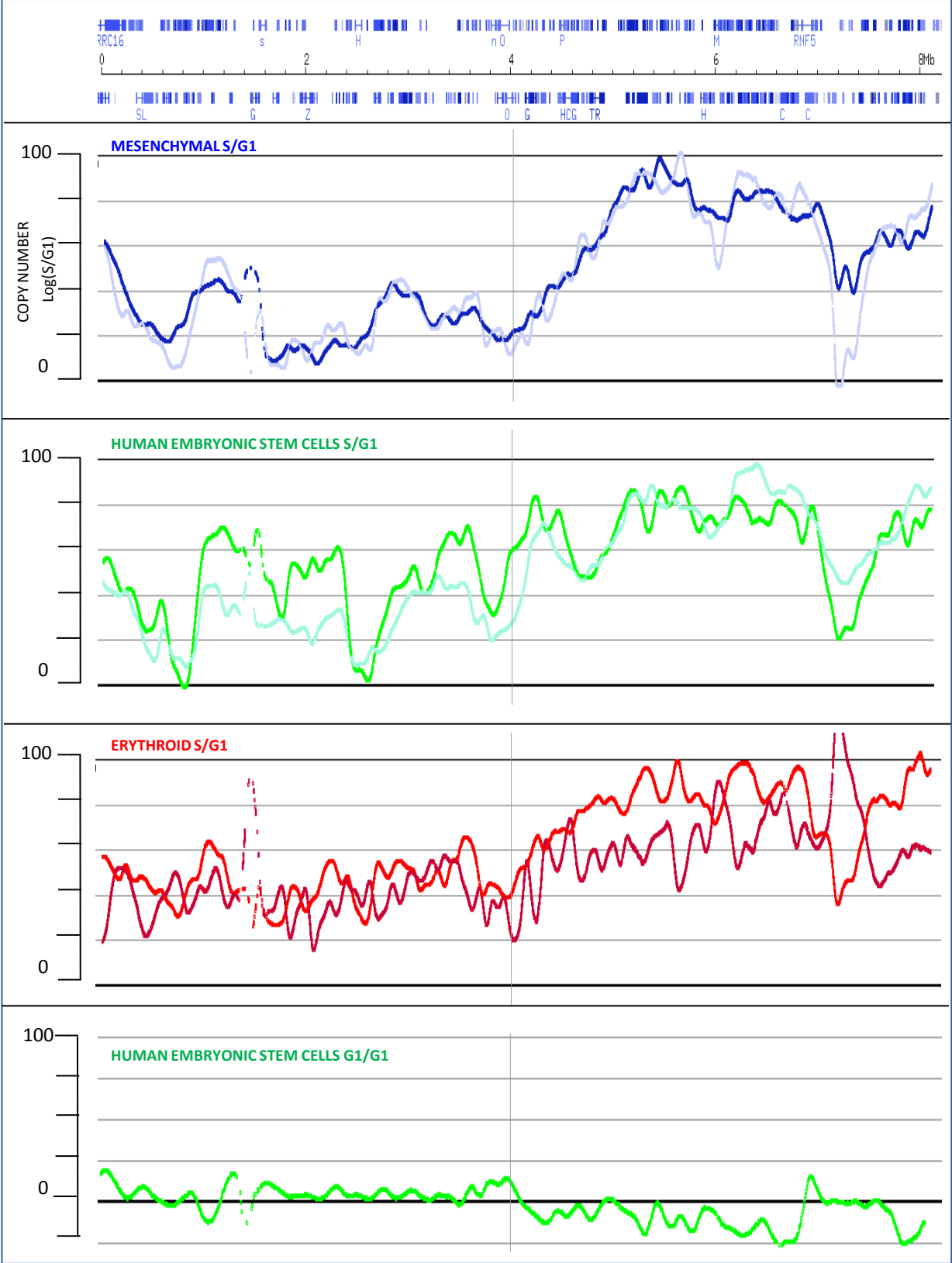


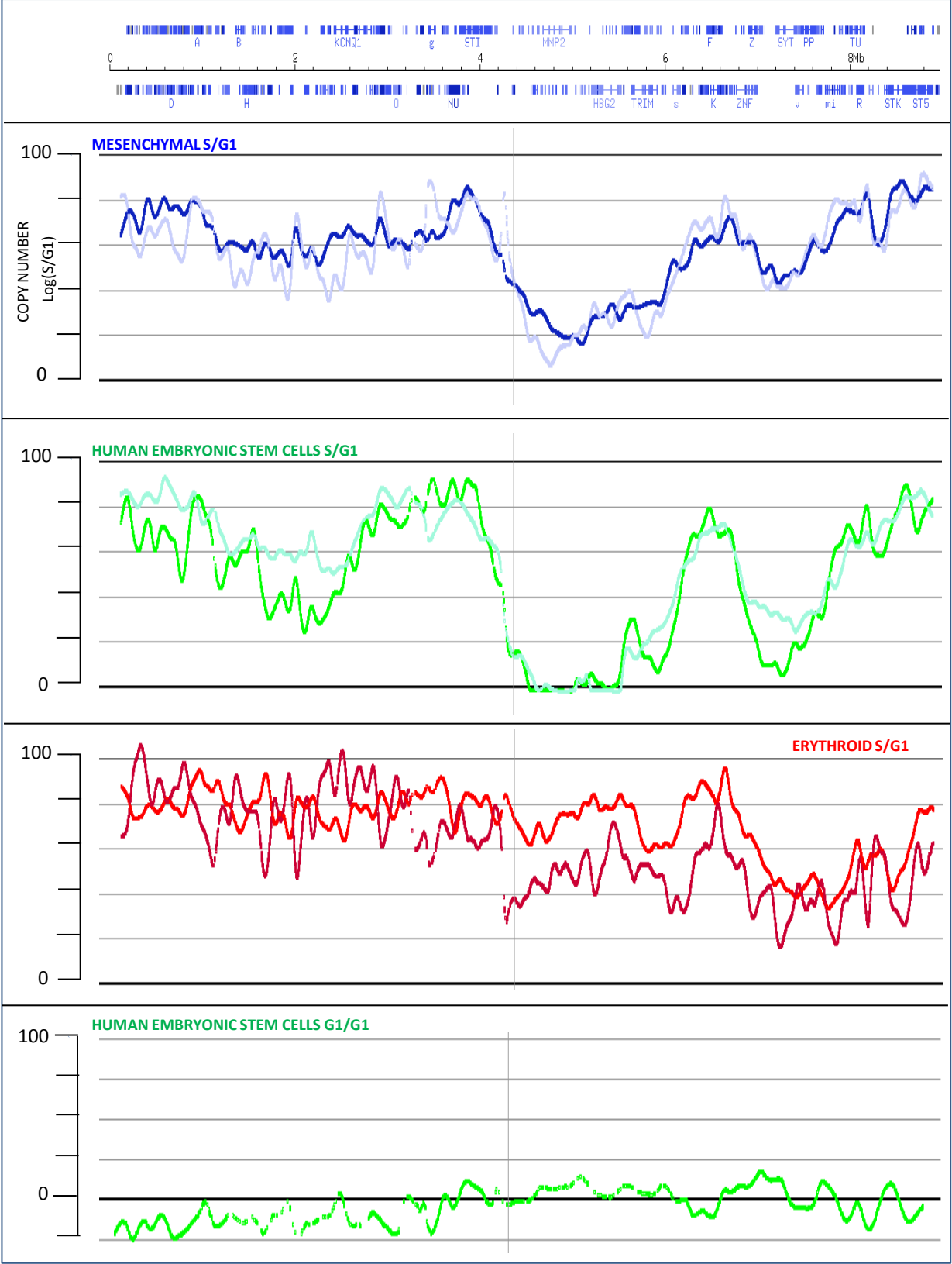


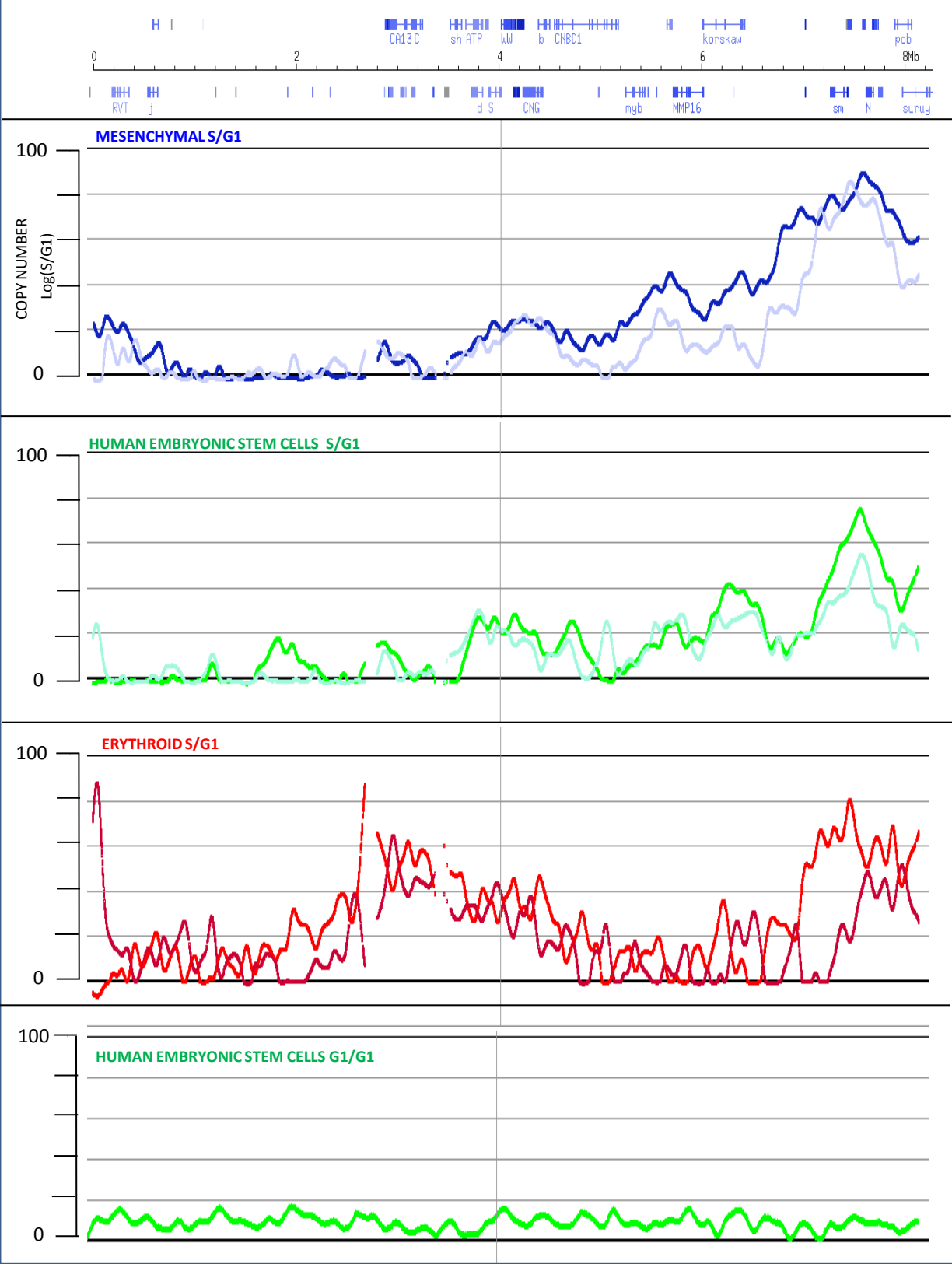


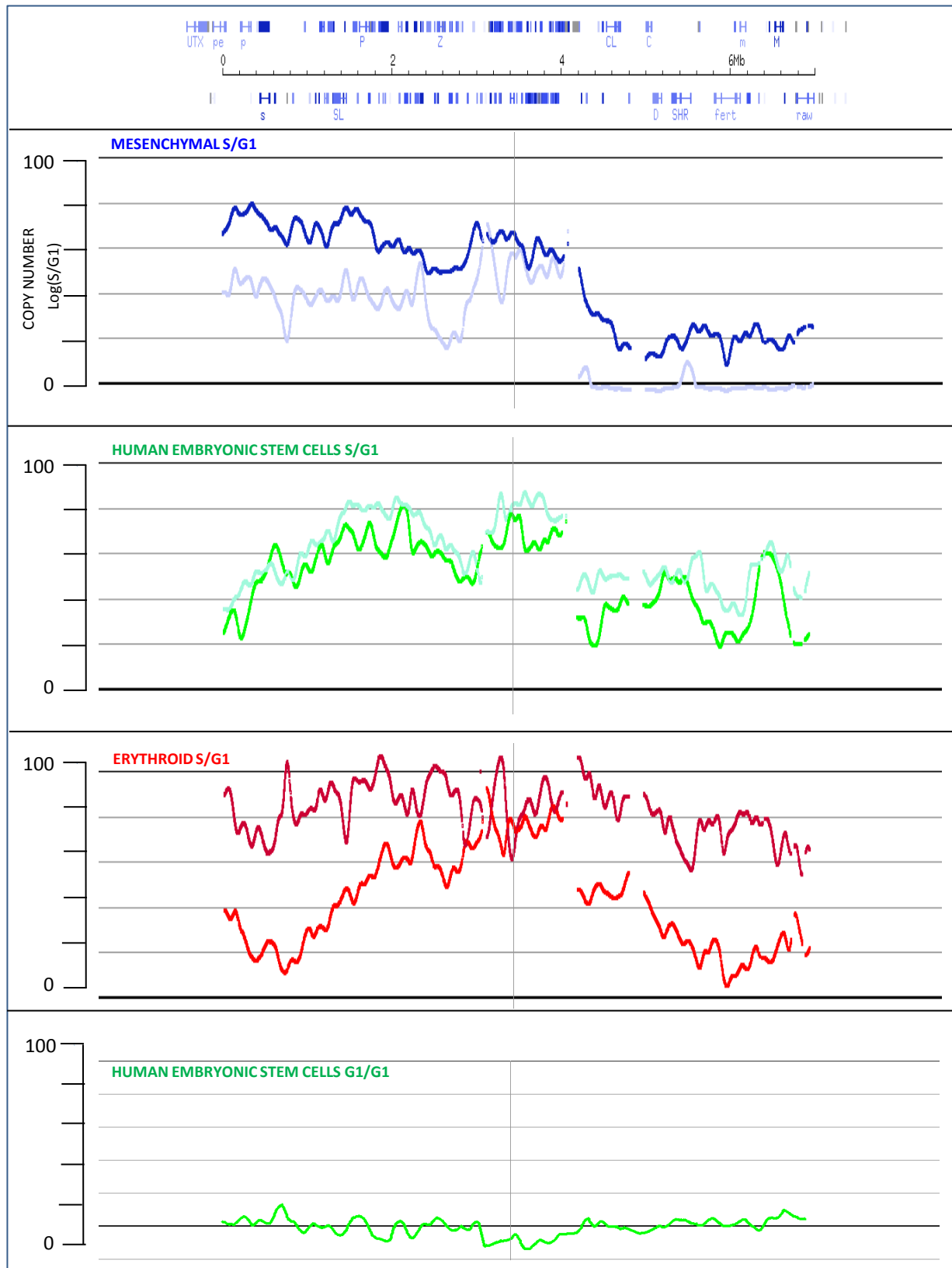


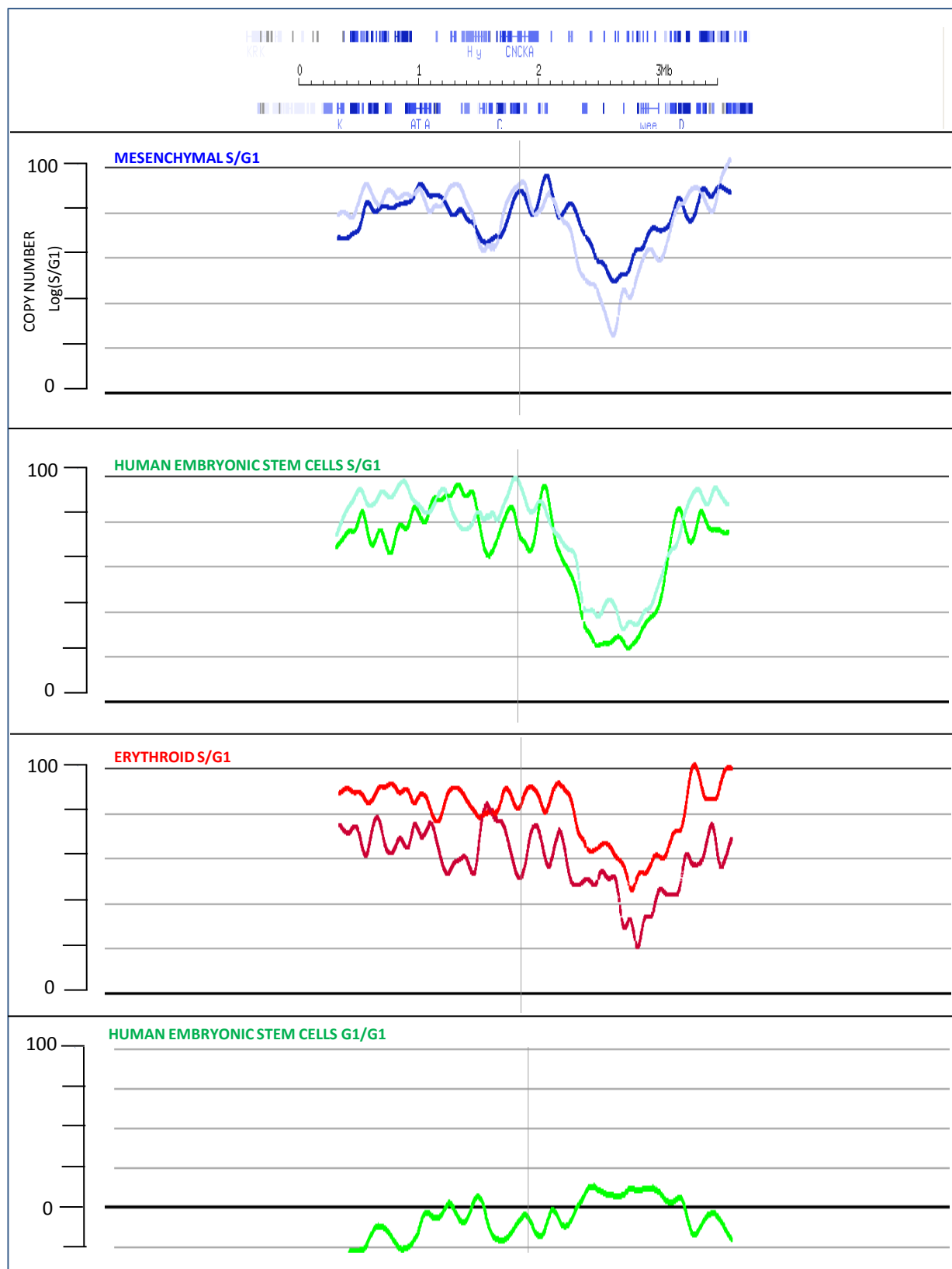


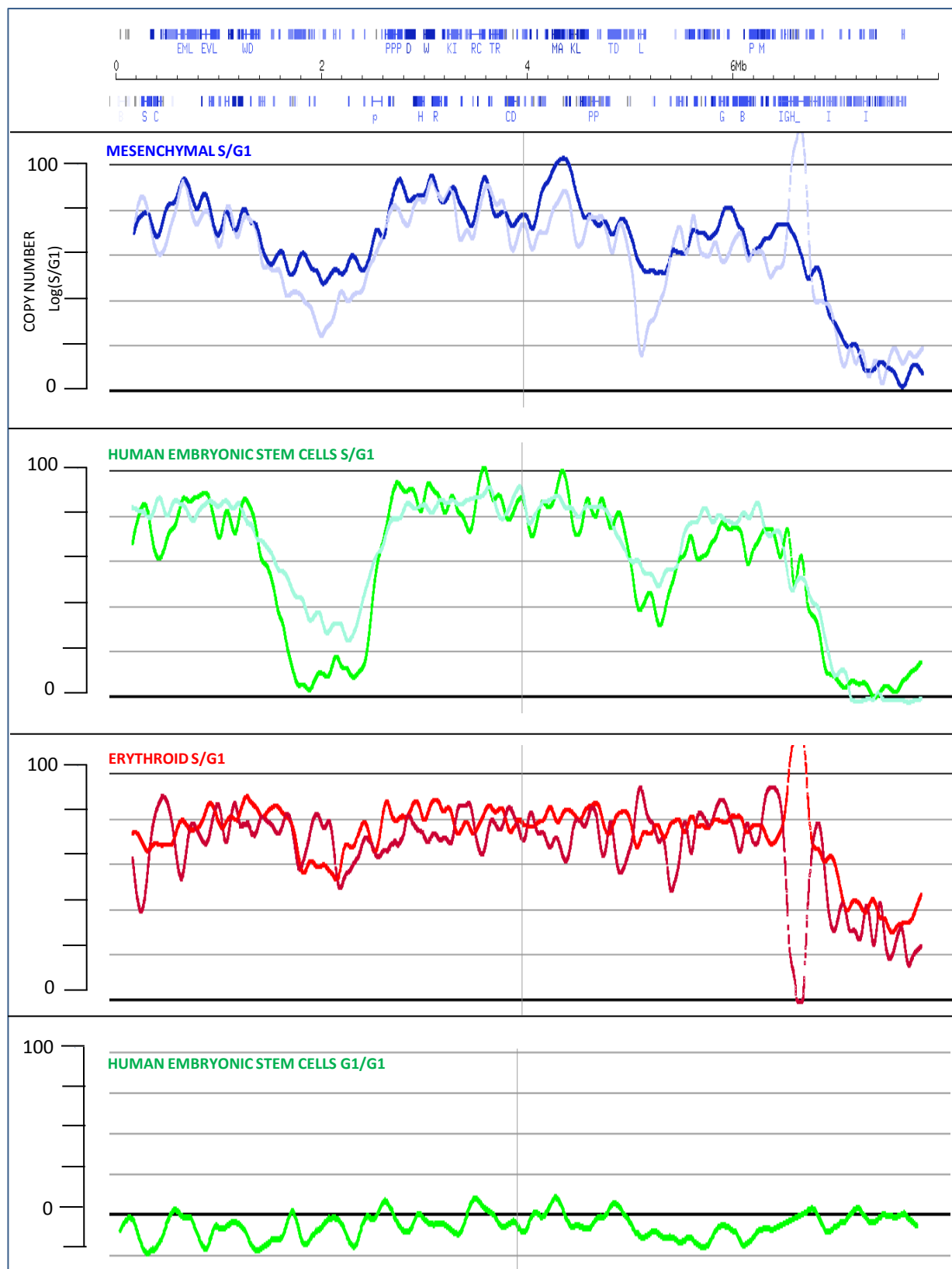




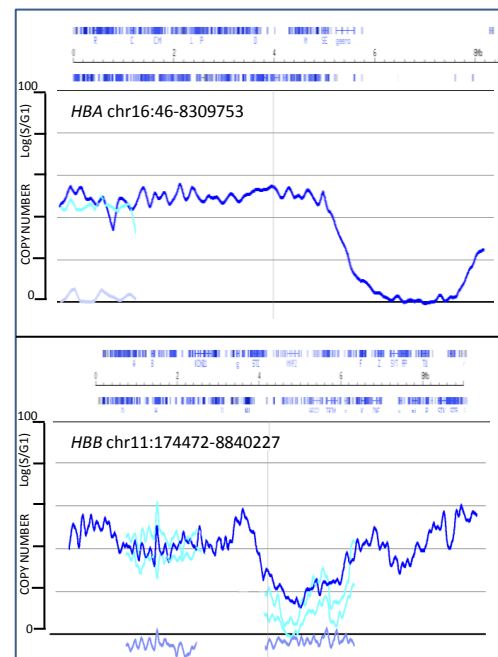
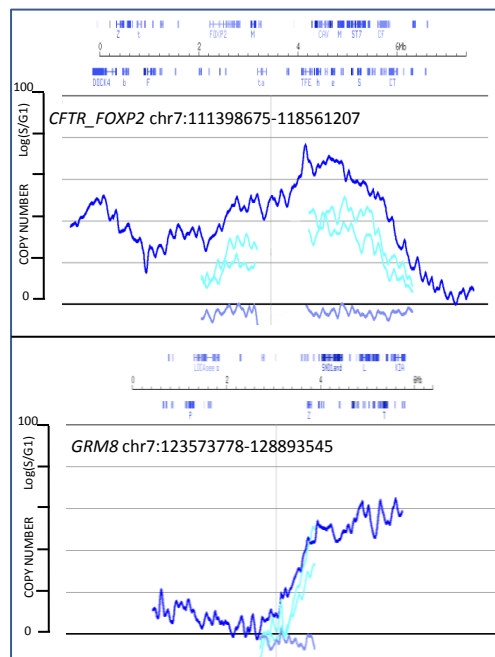
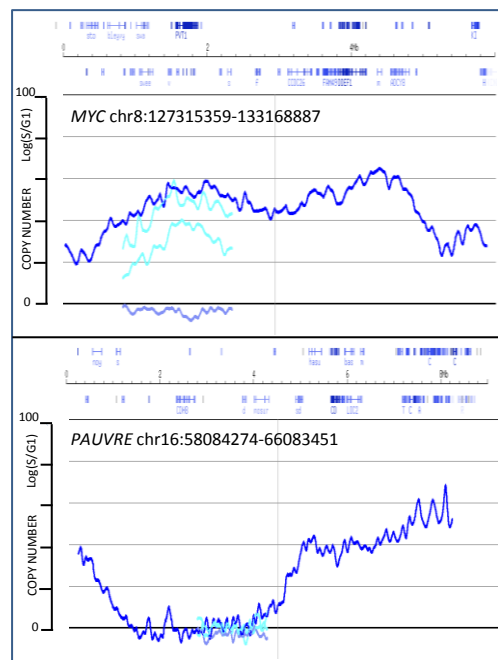
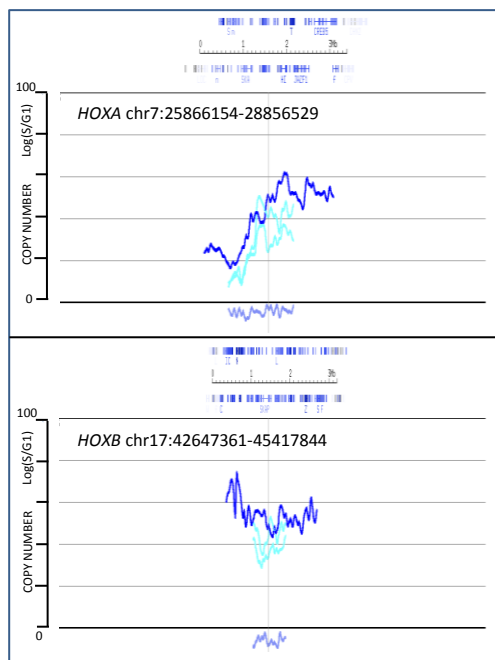








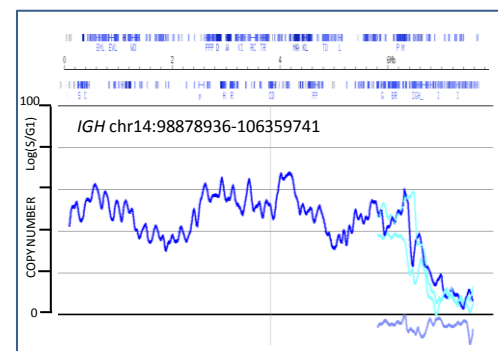
SUPPLEMENTARY FIGURE S3



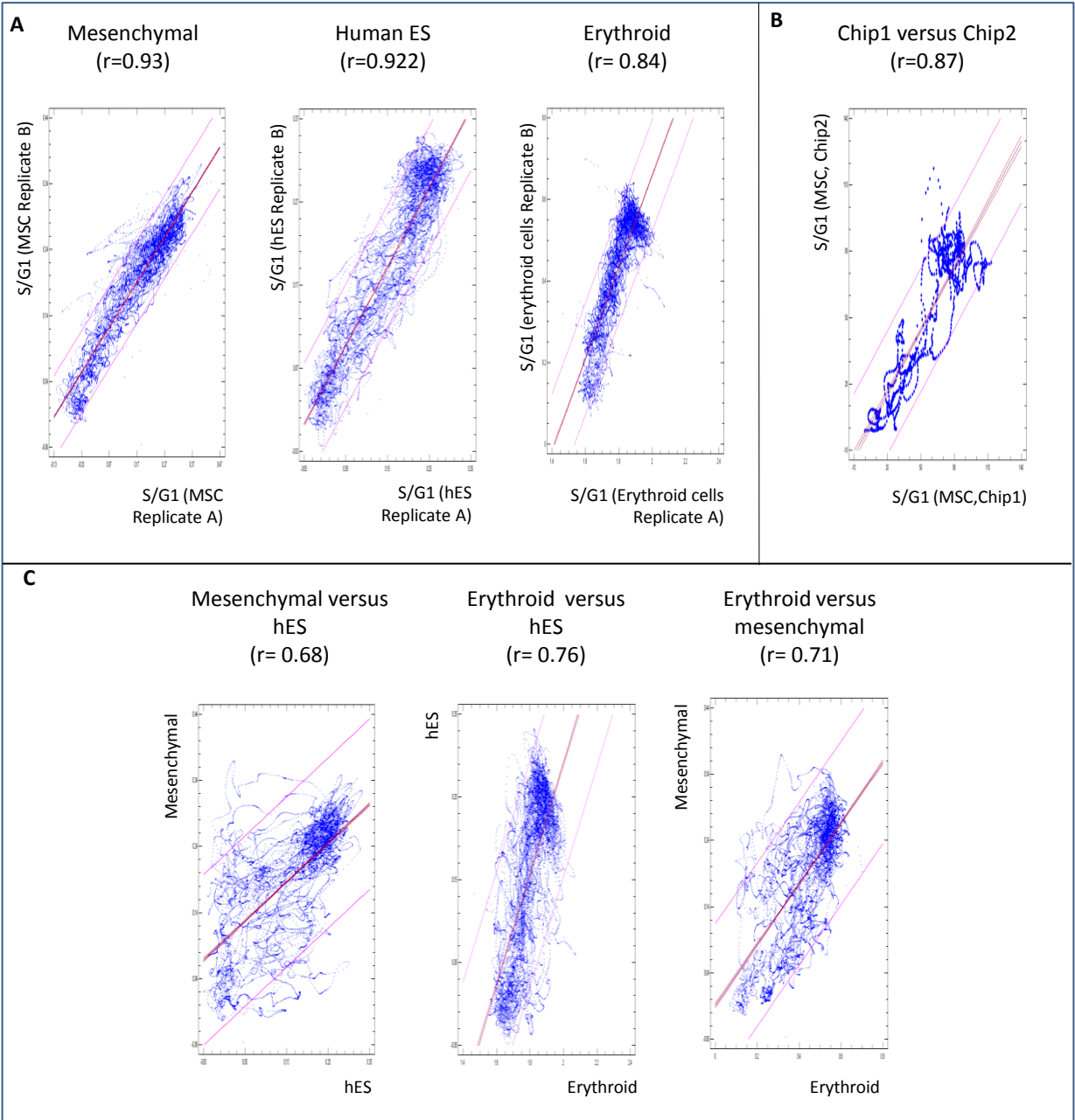
Mesenchymal S/G1 CHIP 1

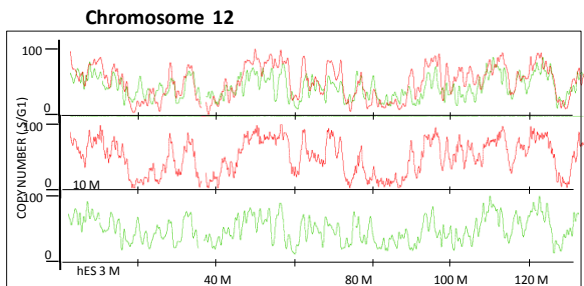
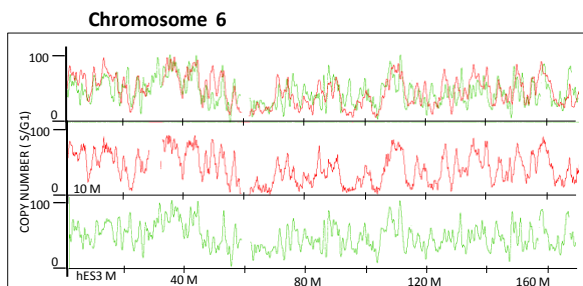
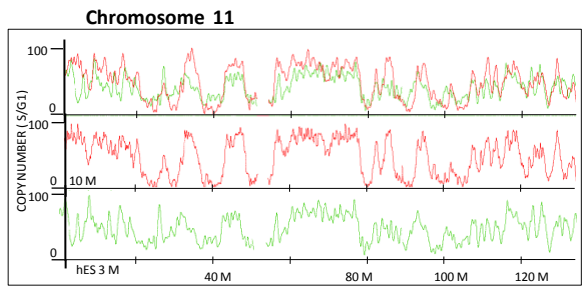
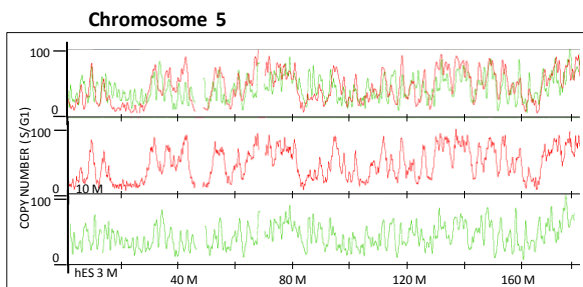
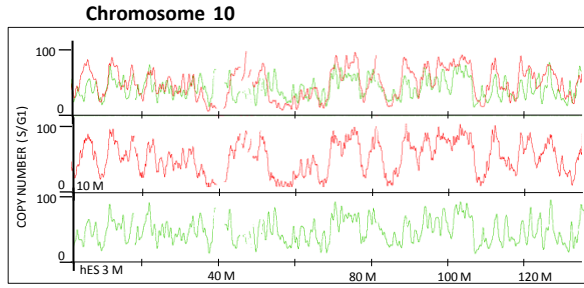
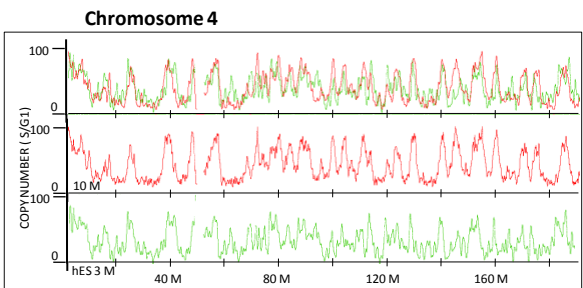
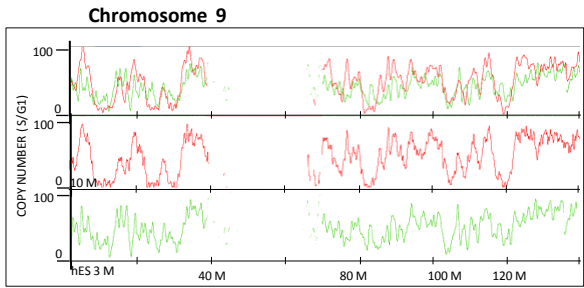
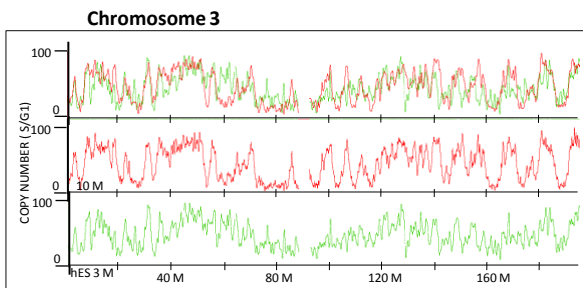
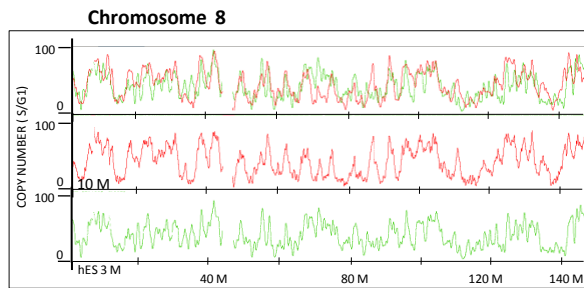
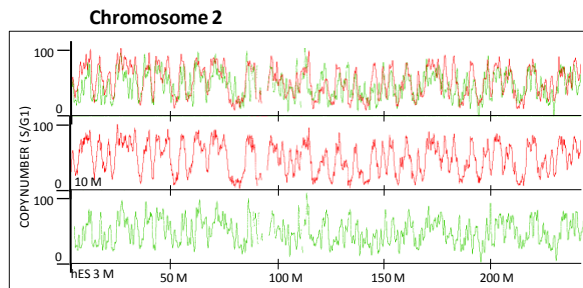
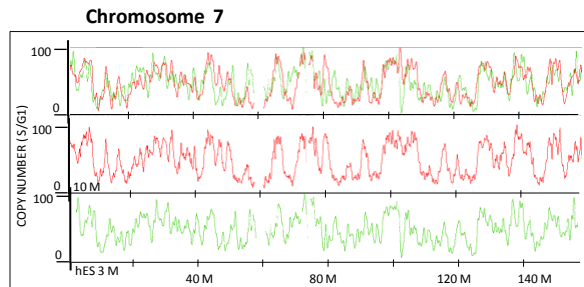
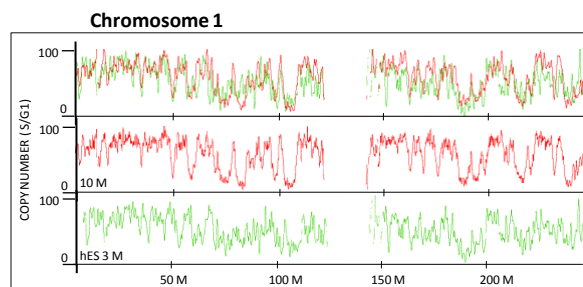
Mesenchymal S/G1 CHIP 2

Mesenchymal G1/G1 CHIP 1



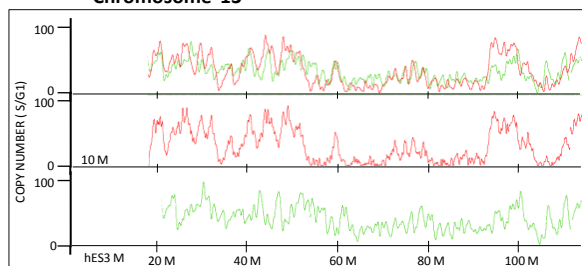
SUPPLEMENTARY FIGURE S4



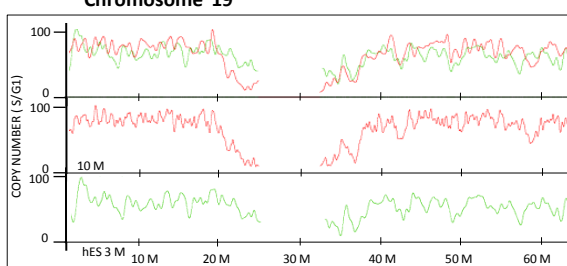


SUPPLEMENTARY FIGURE S5, page 2

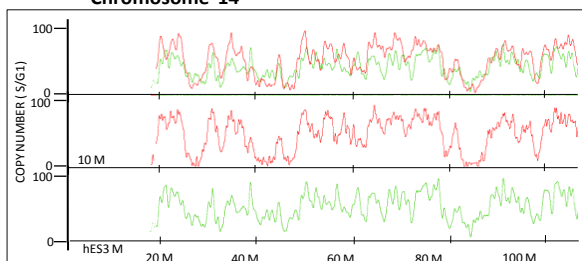
Chromosome 13



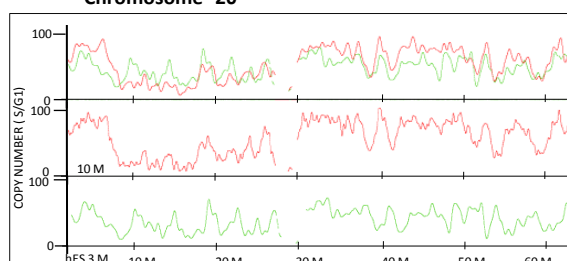
Chromosome 19



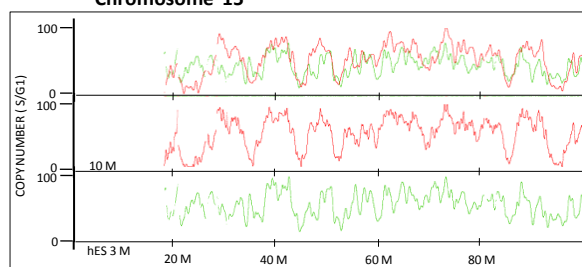
Chromosome 14



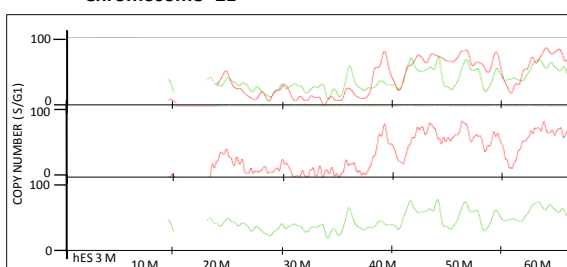
Chromosome 20



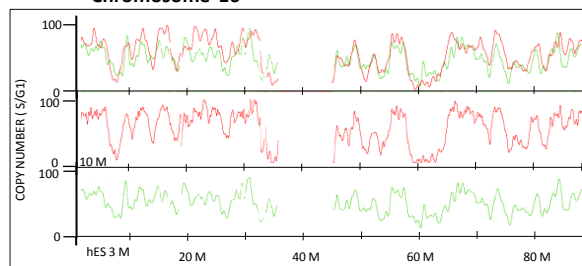
Chromosome 15



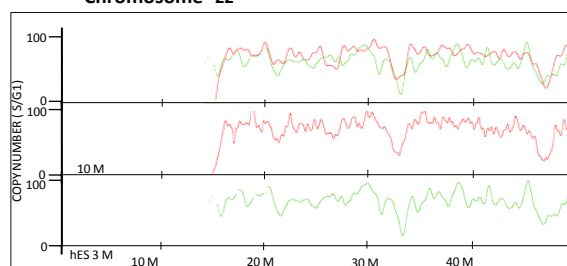
Chromosome 21



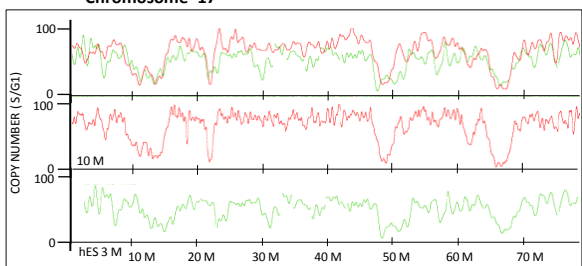
Chromosome 16



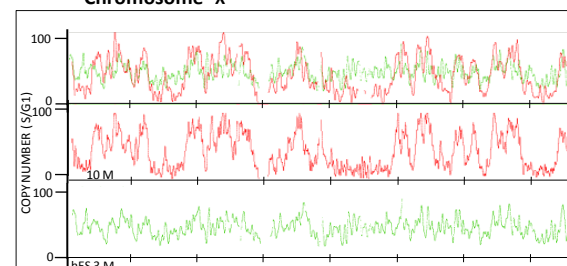
Chromosome 22



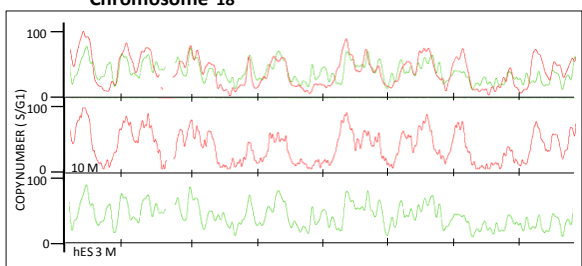
Chromosome 17



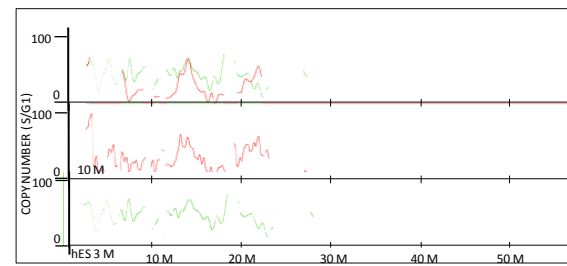
Chromosome X



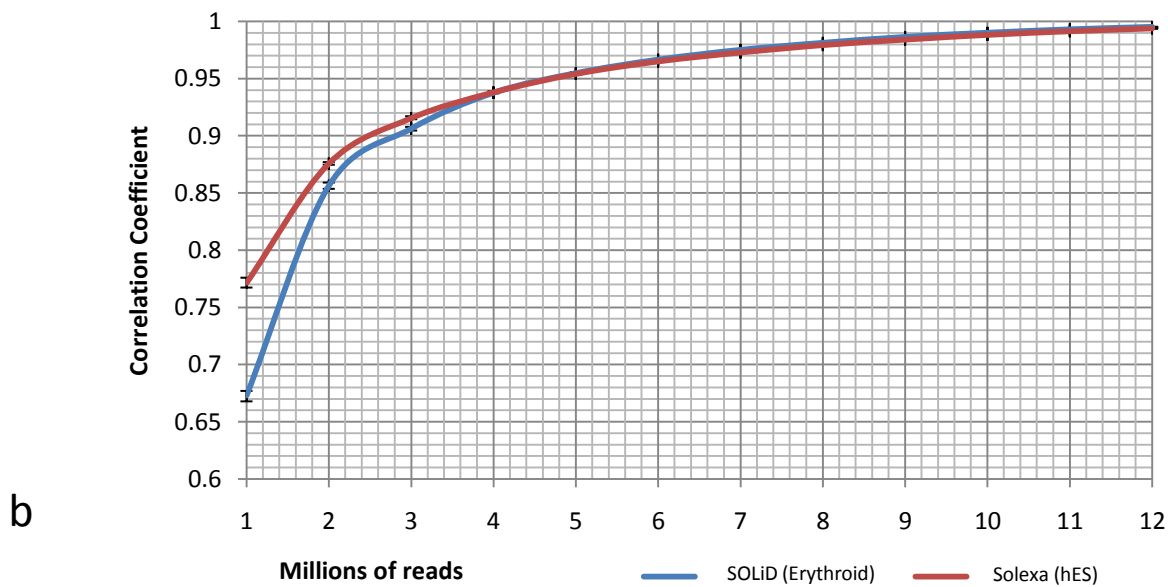
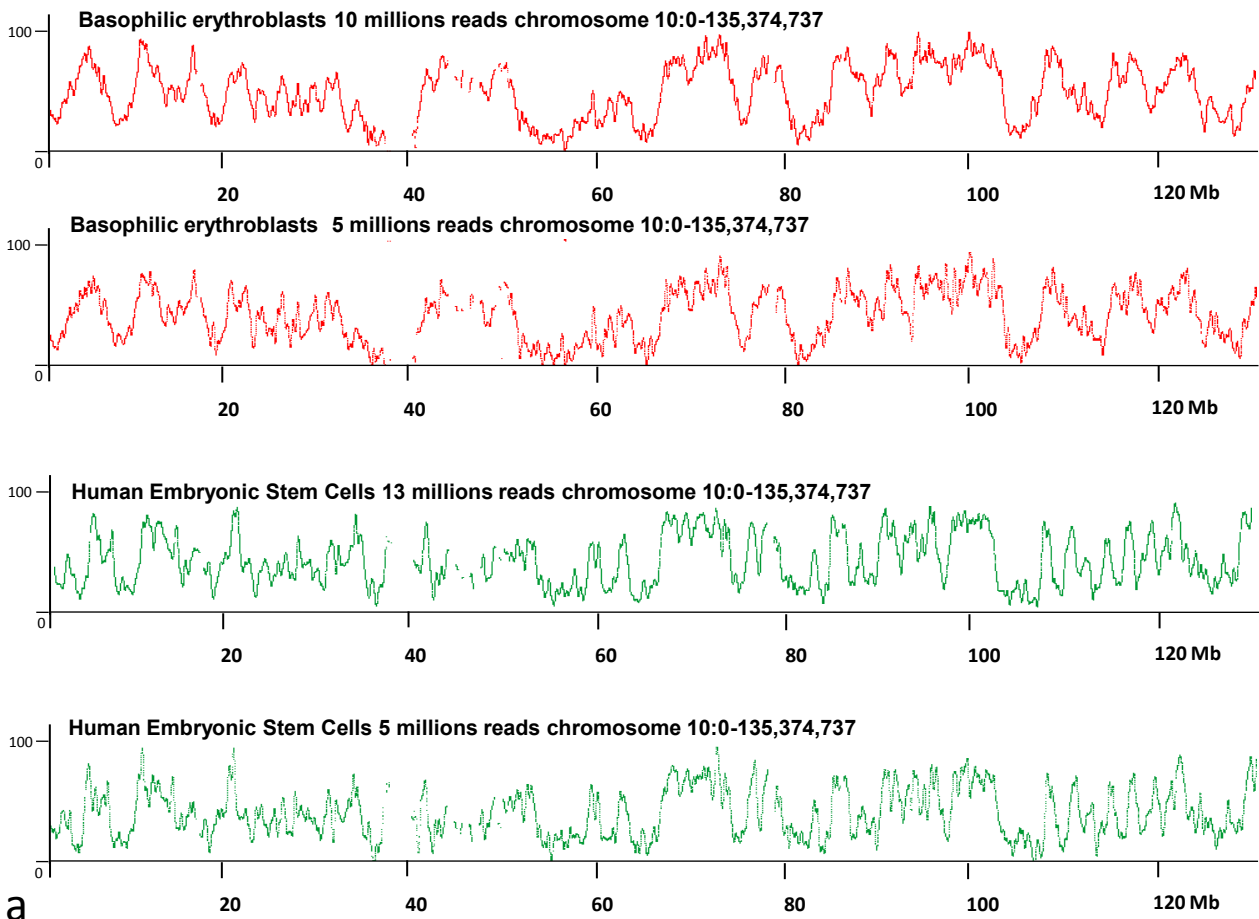
Chromosome 18



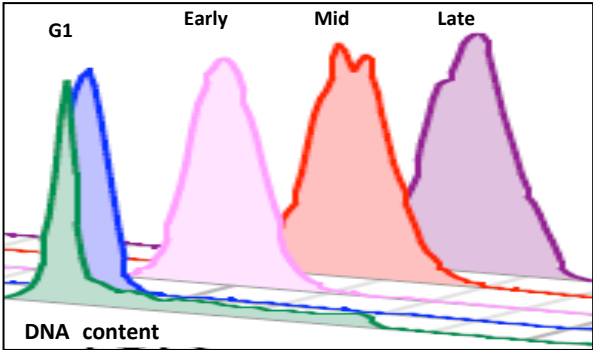
Chromosome Y

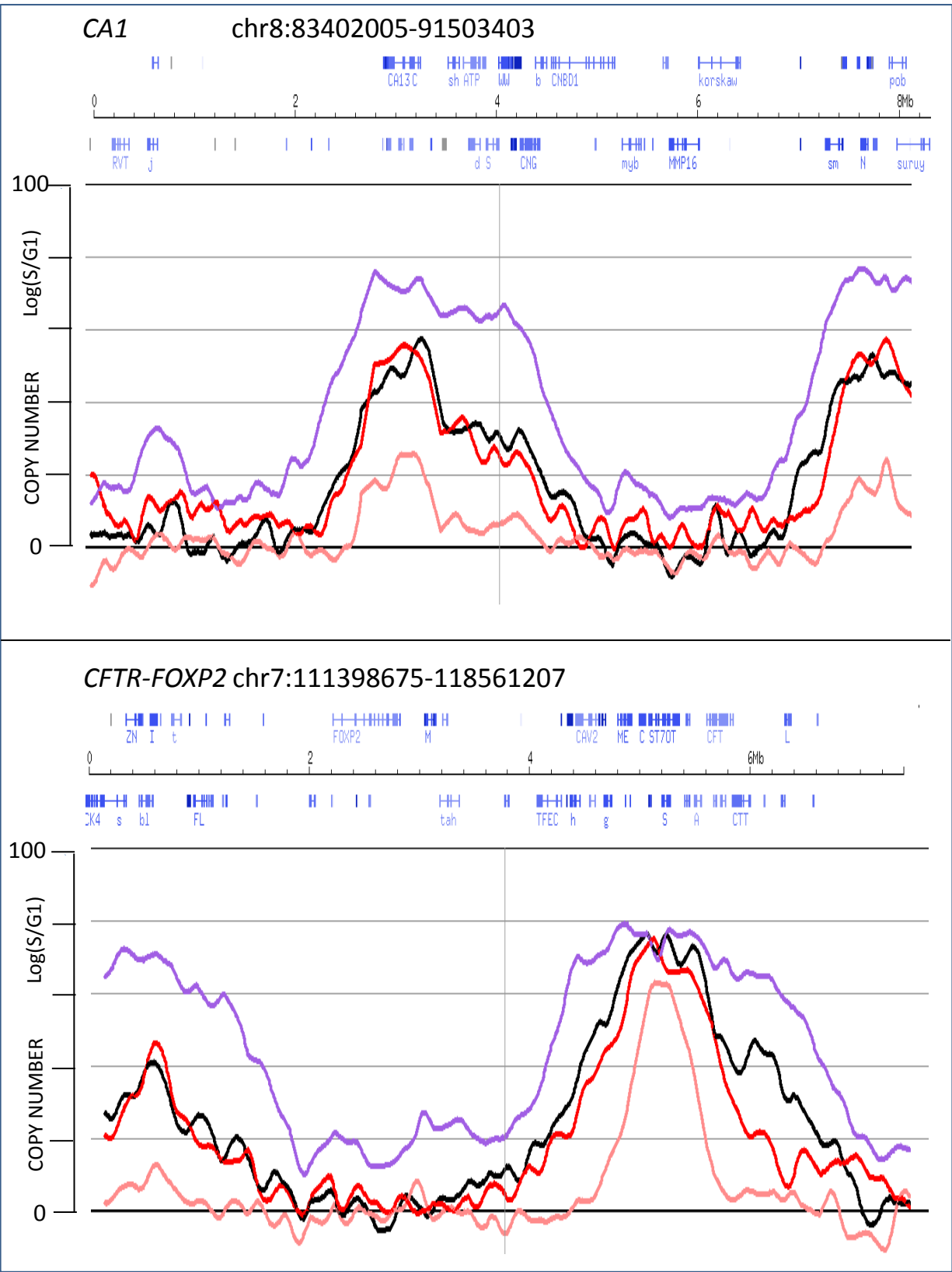


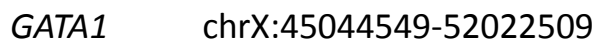
SUPPLEMENTARY FIGURE S6

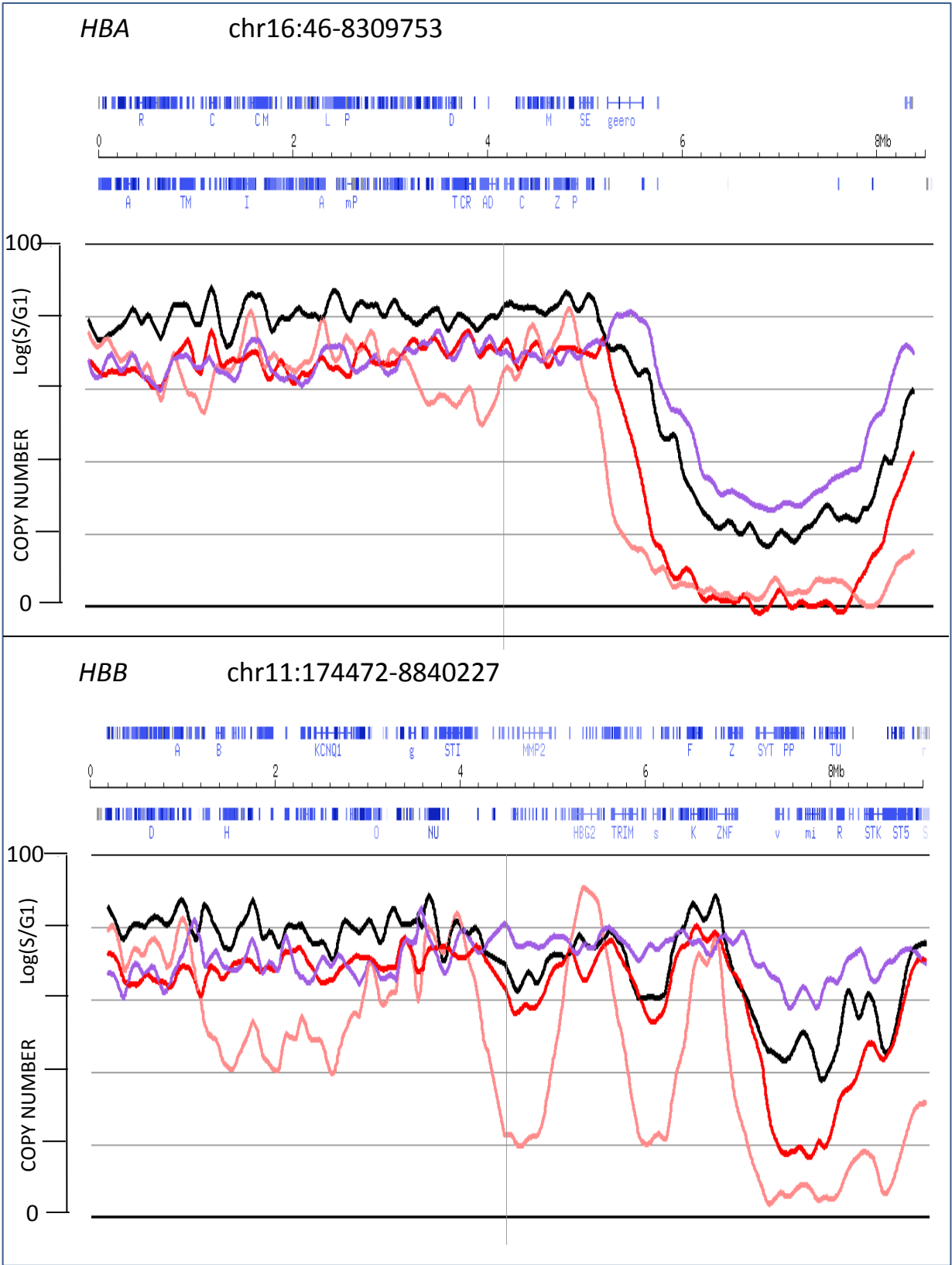


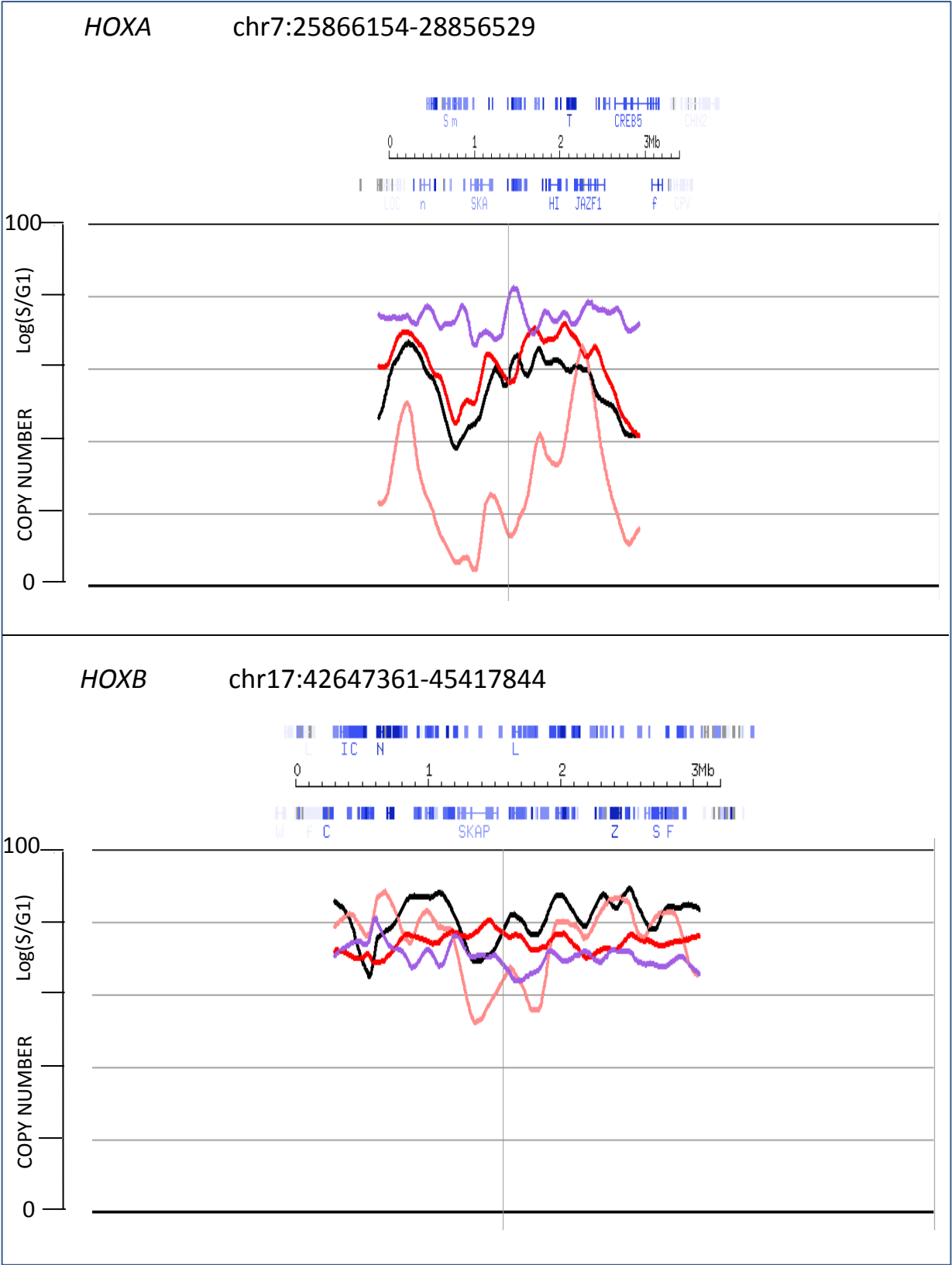
SUPPLEMENTARY FIGURE S7, page 1

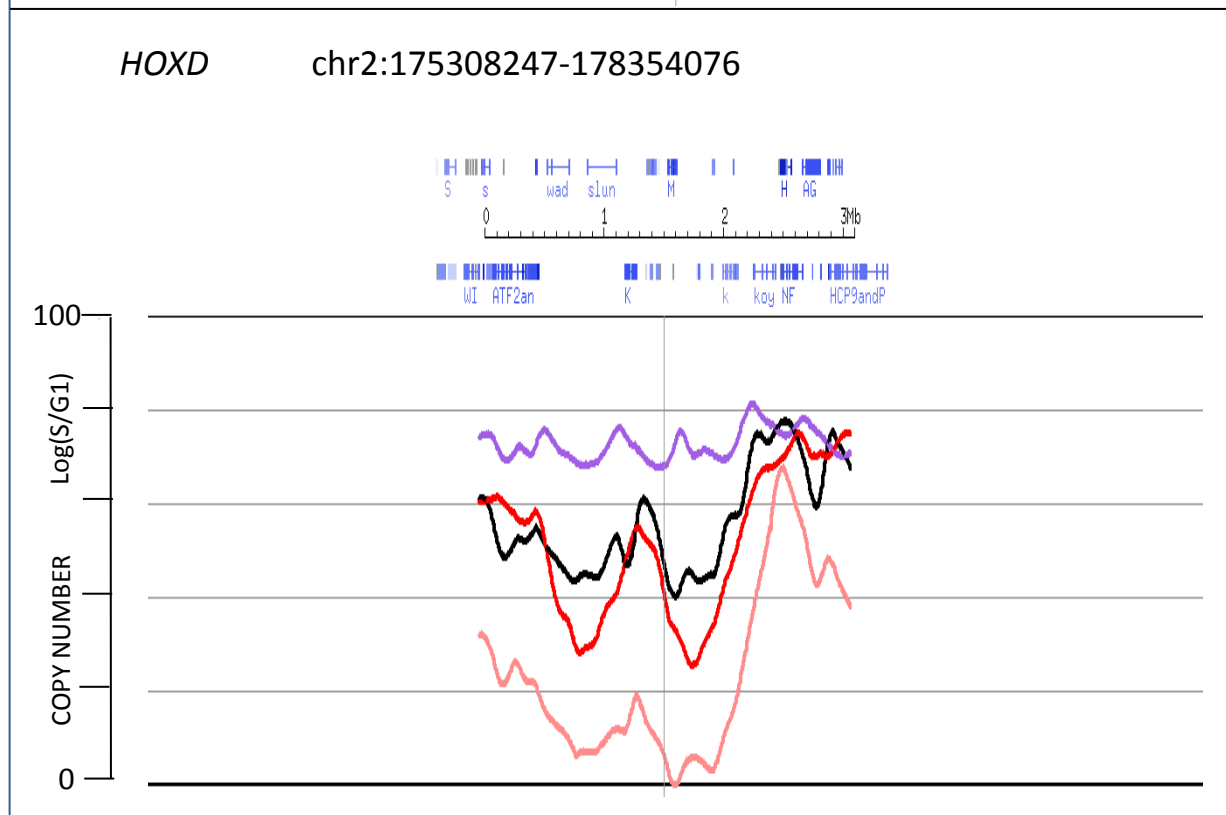


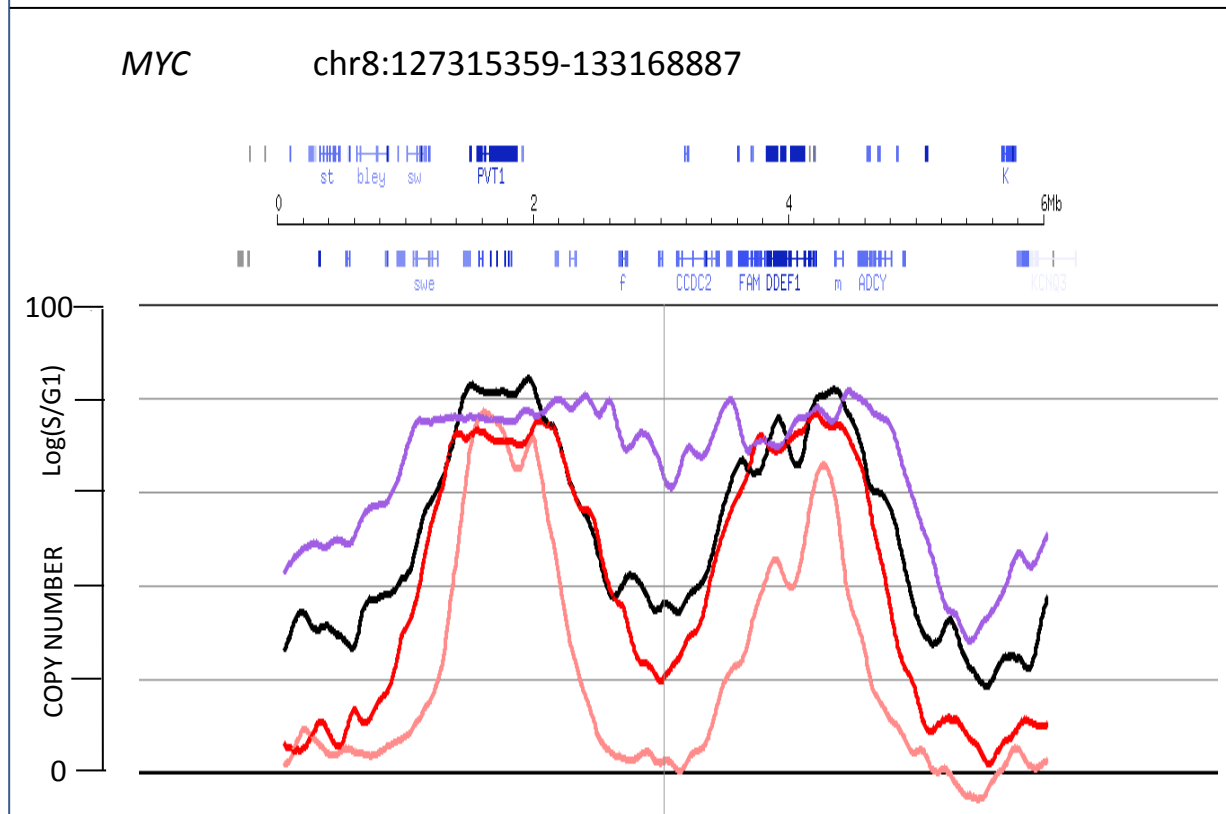
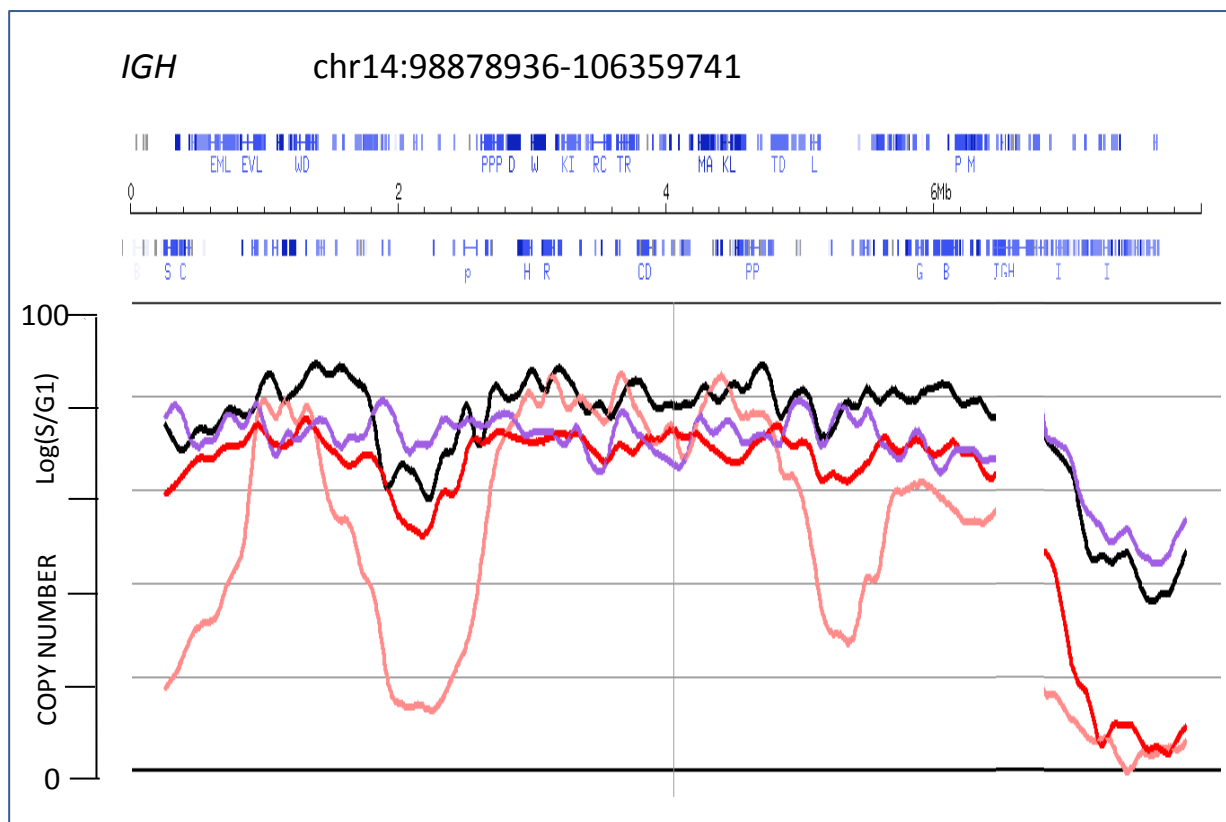


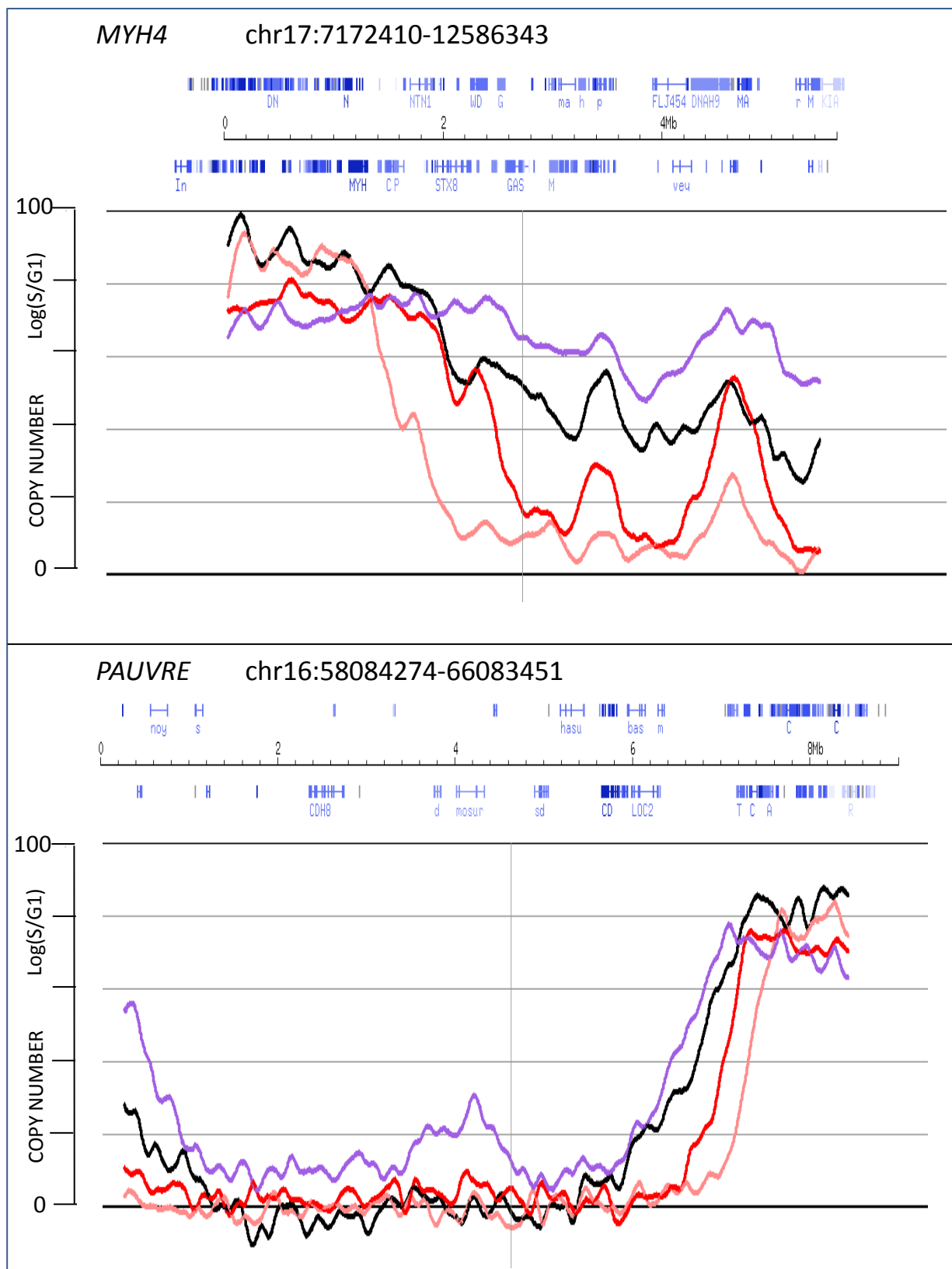


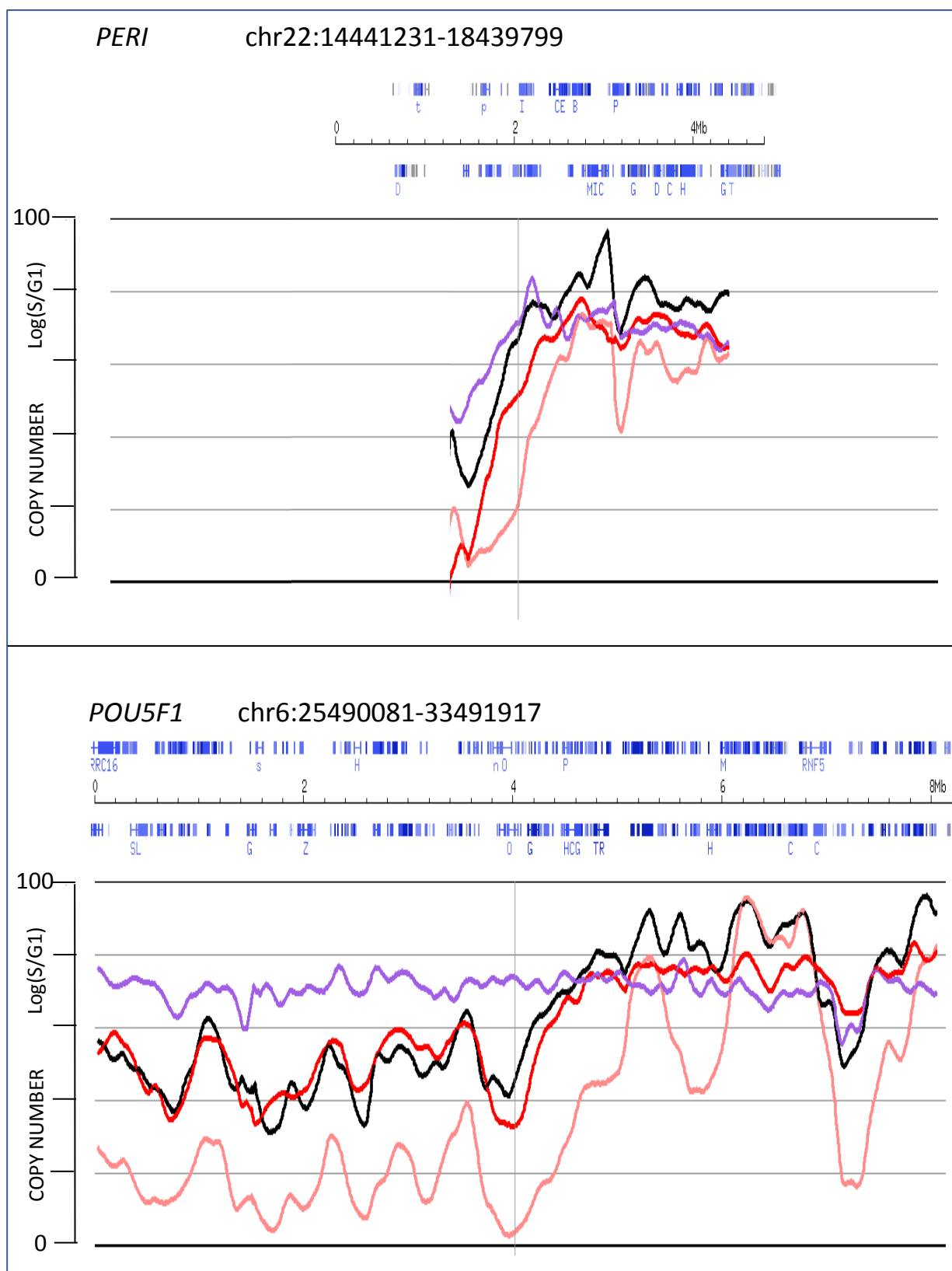


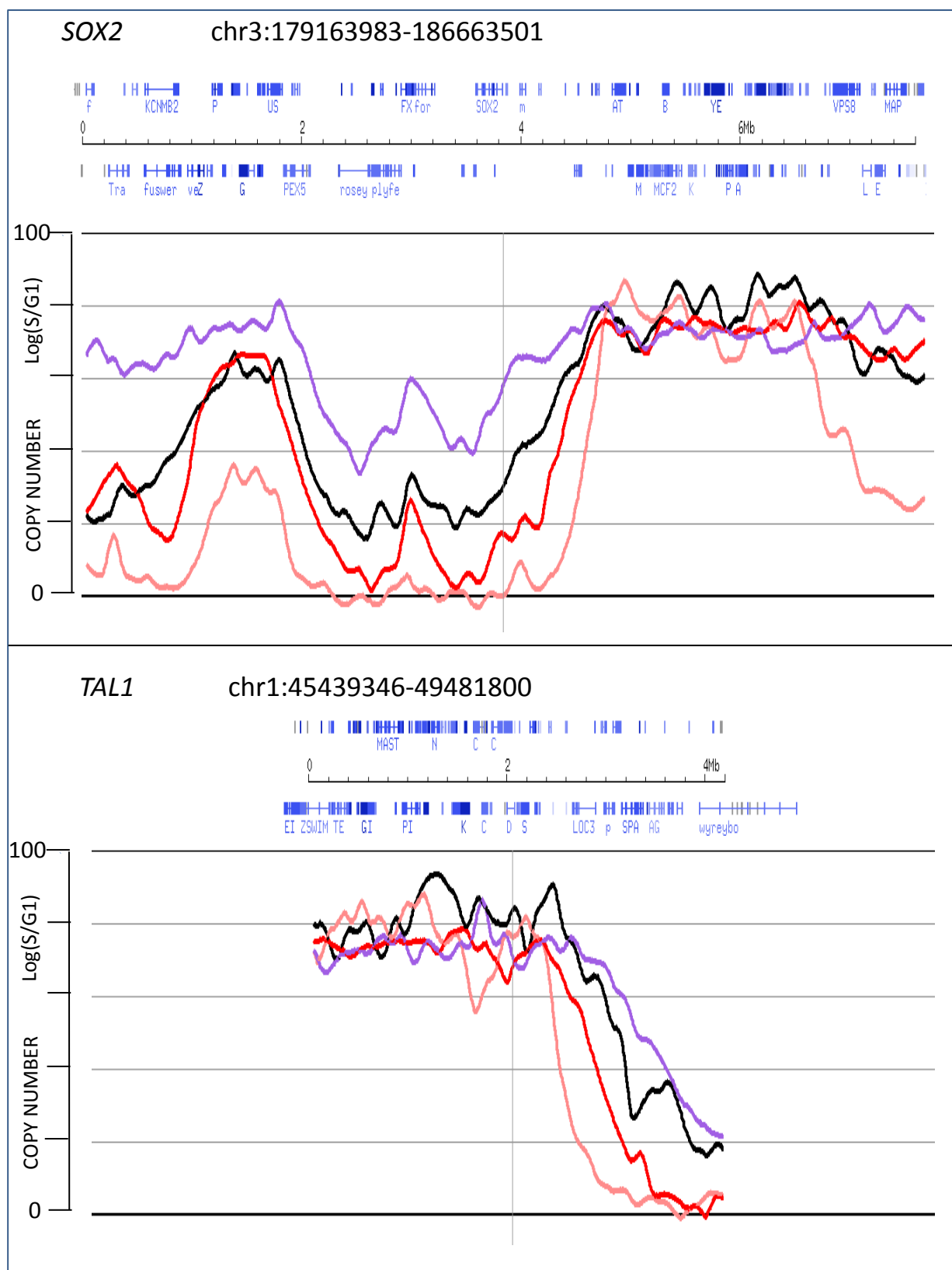




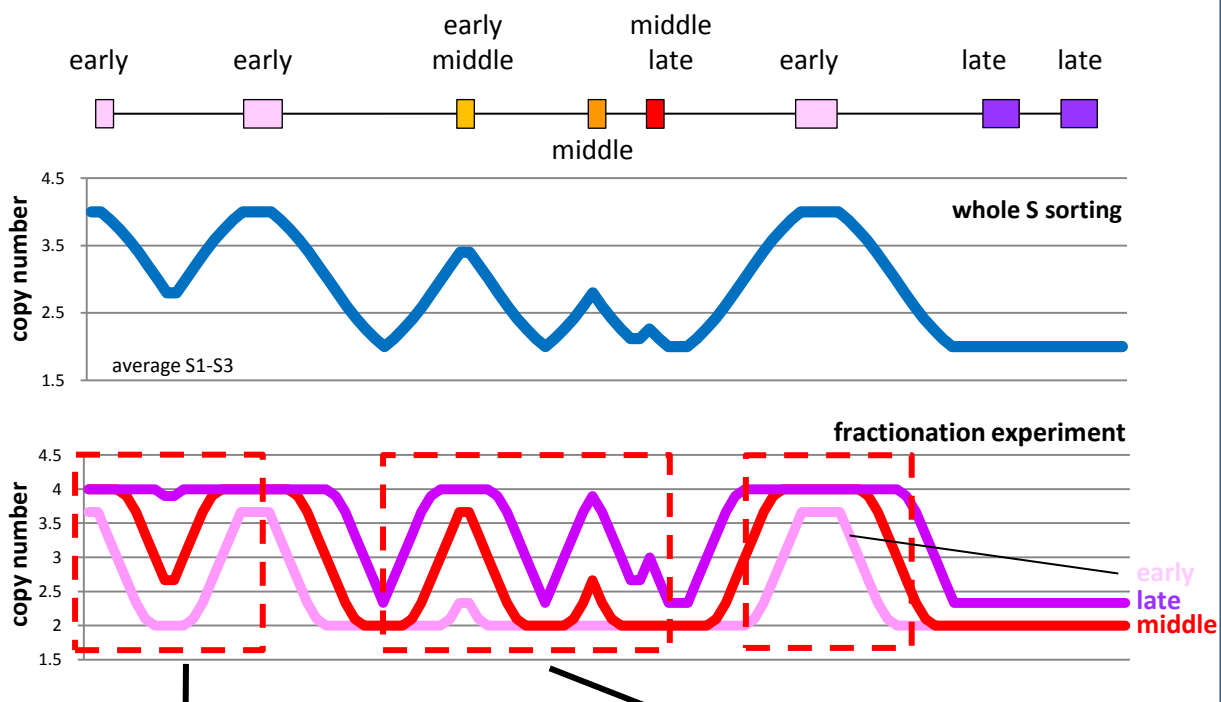






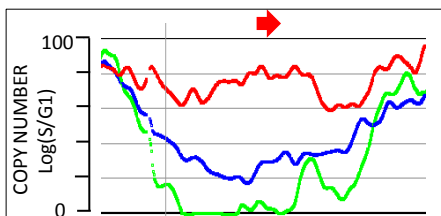
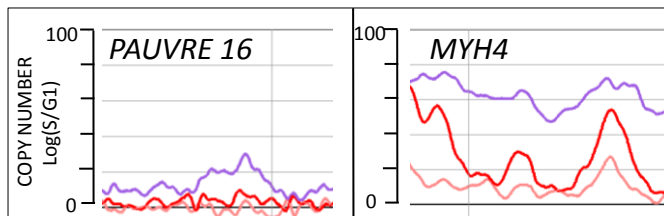
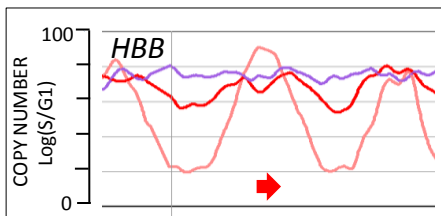
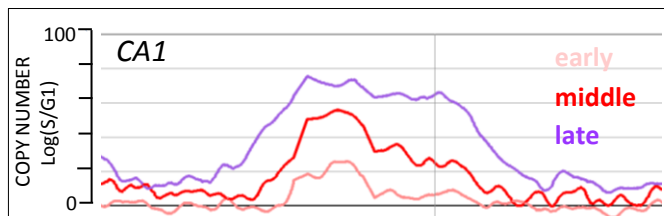
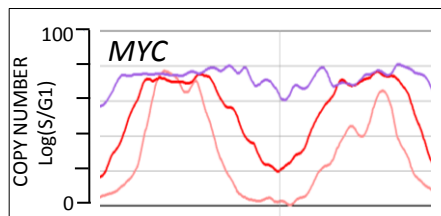


SUPPLEMENTARY FIGURE S8



Craters of decreasing depth and volcanoes with plateaux of increasing sizes induced by firing of isolated origin or found at the boundaries of origin rich and origin poor regions. These regions correspond to temporal transition regions when the whole S fraction is examined.

Peaks detected in S2 and/or S3 but not in S1, induced by temporally regulated origin firing in S2 or S3

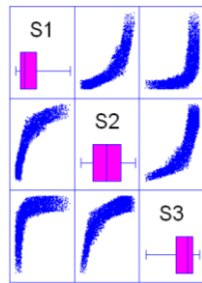


erythroid
hES
mesenchymal

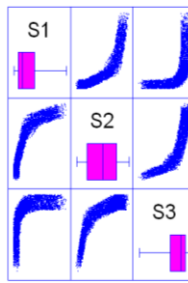
1 megabase

SUPPLEMENTARY FIGURE S9

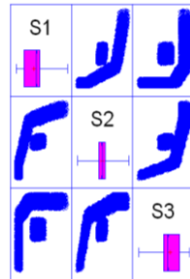
100% synchronous
2 alleles with 180 min. of
each other



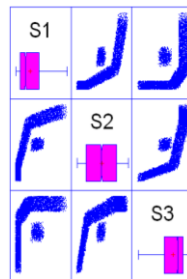
100% synchronous
2 alleles with 120 min. of
each other



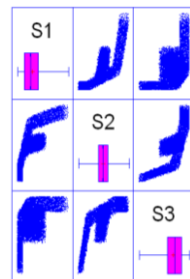
50% synchronous
50% asynchronous (0-1; 7-8)



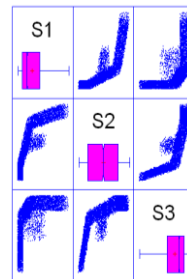
95% synchronous
5% asynchronous (0-1; 7-8)



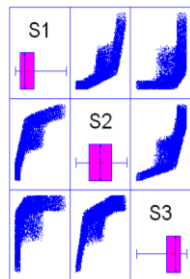
50% synchronous
50% asynchronous (0-3; 5-8)



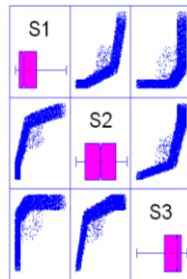
95% synchronous
5% asynchronous (0-3; 5-8)



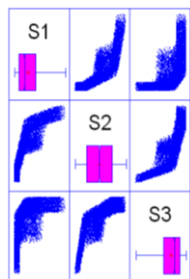
50% synchronous
50% asynchronous (0-6; 2-8)



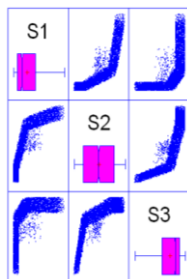
95% synchronous
5% asynchronous (0-6; 2-8)



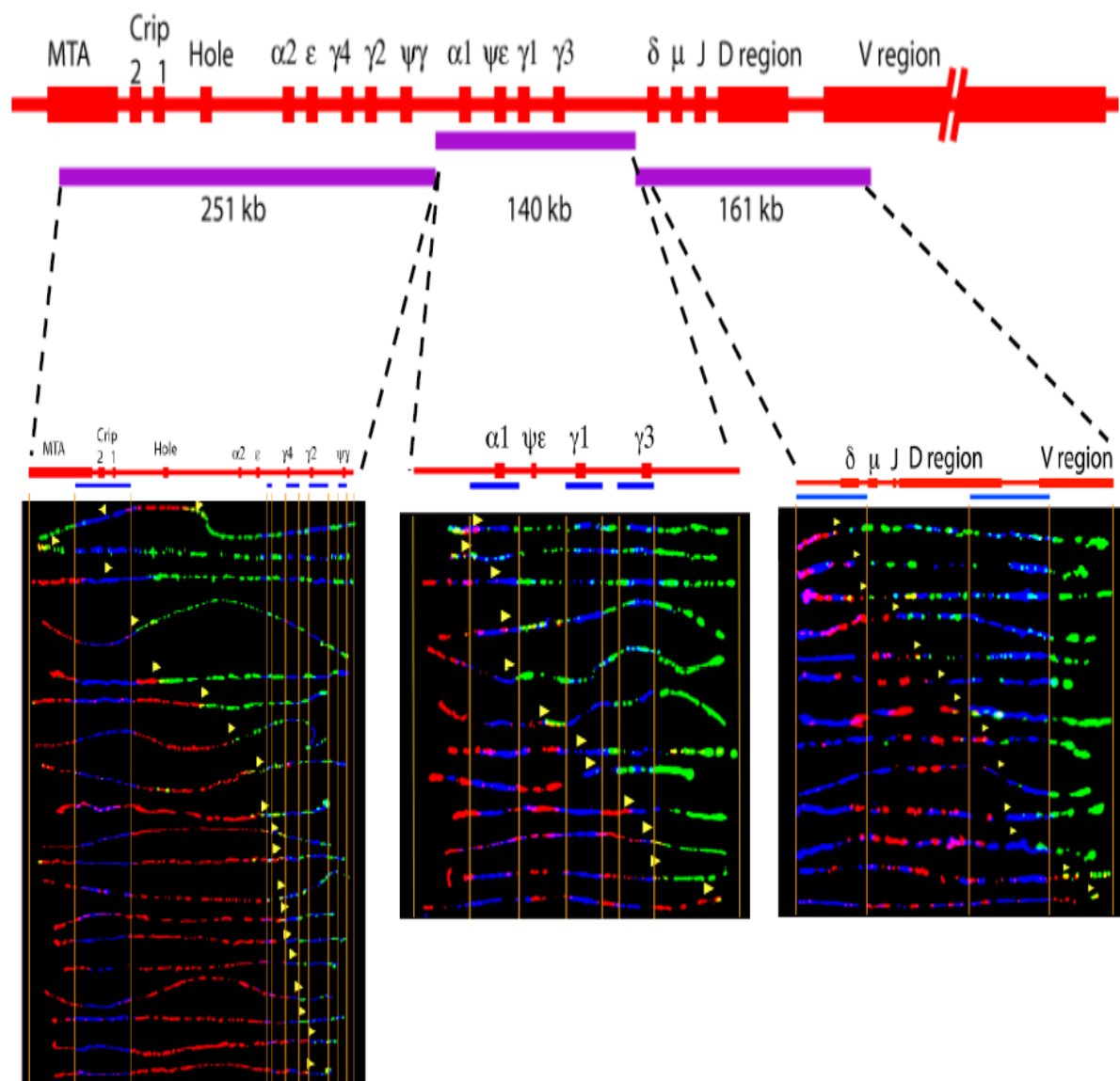
50% synchronous
50% asynchronous (0-8 0-8)

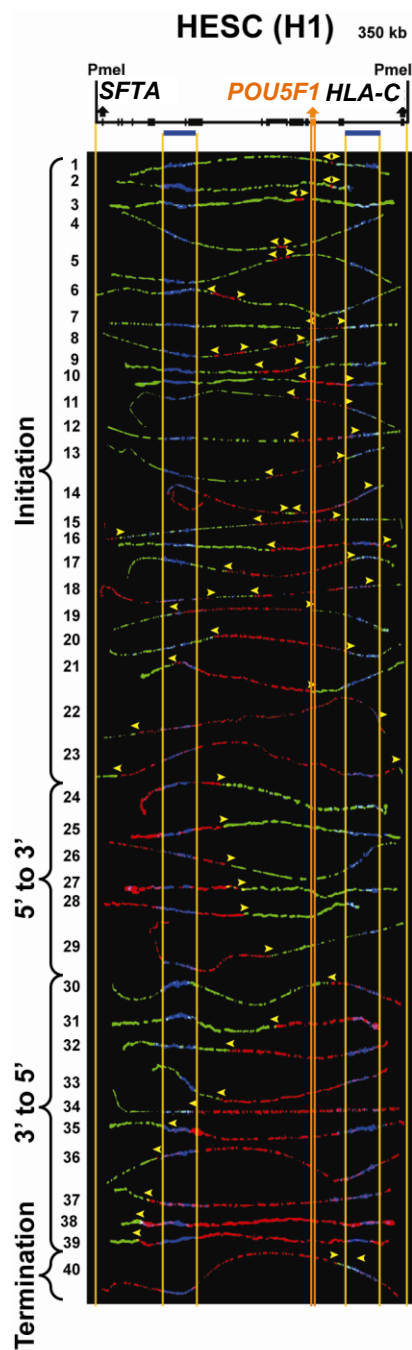


95% synchronous
5% asynchronous (0-8, 0-8)

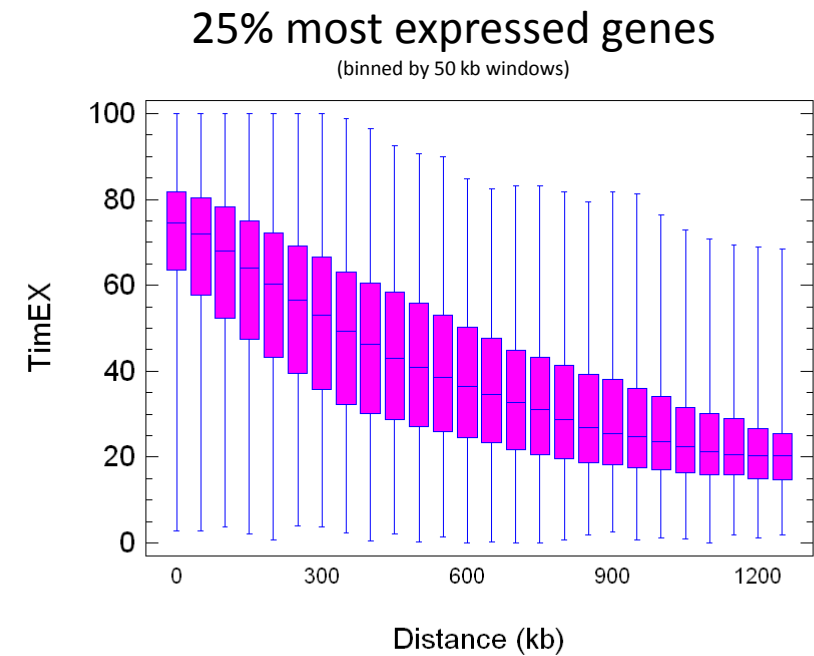


SUPPLEMENTARY FIGURE S10

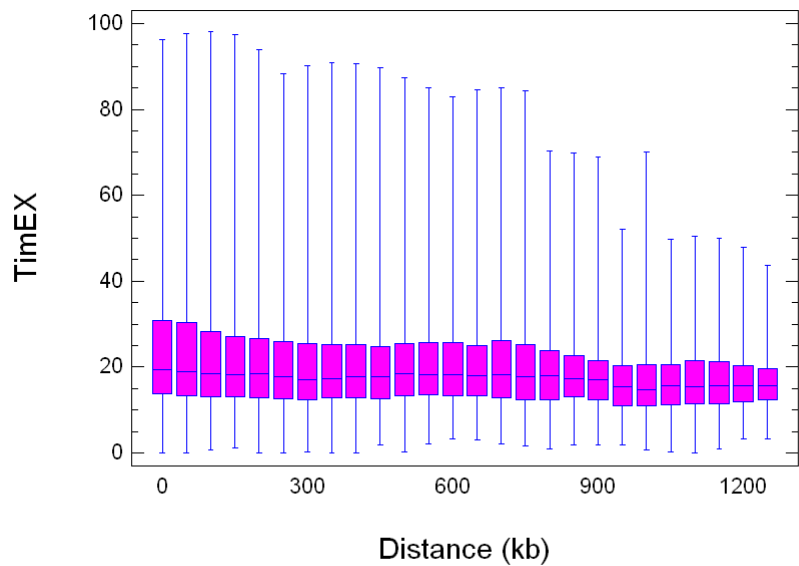




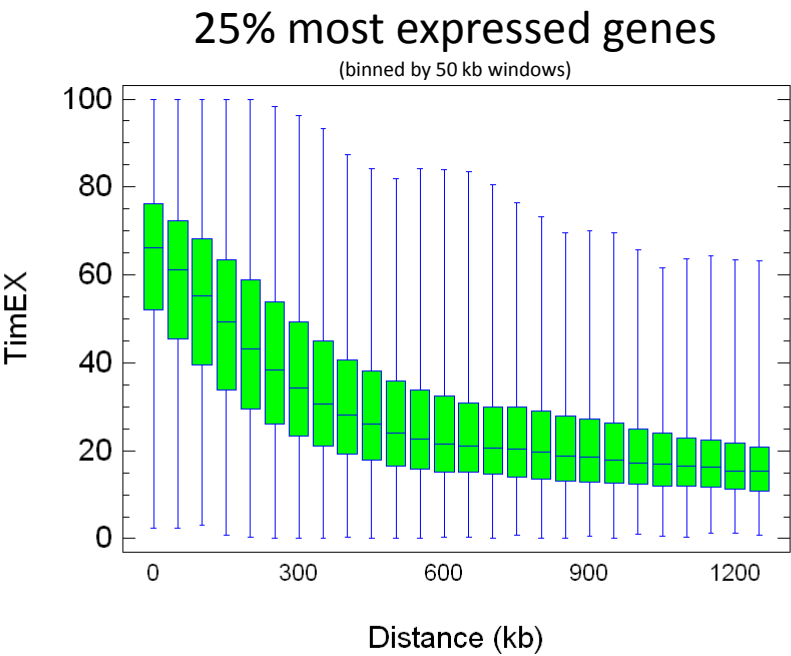
Erythroid cells
(U133 plus 2)



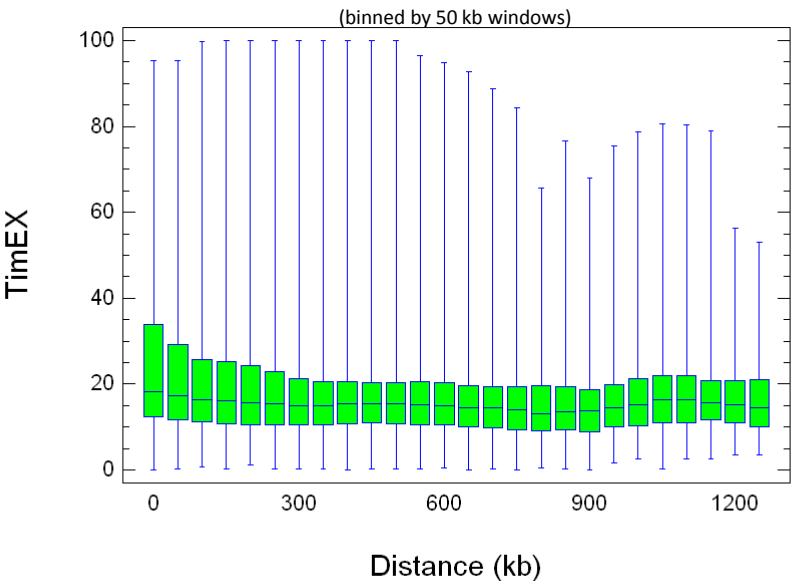
25% least expressed genes at least 500kb away
from expressed genes
(binned by 50 kb windows)



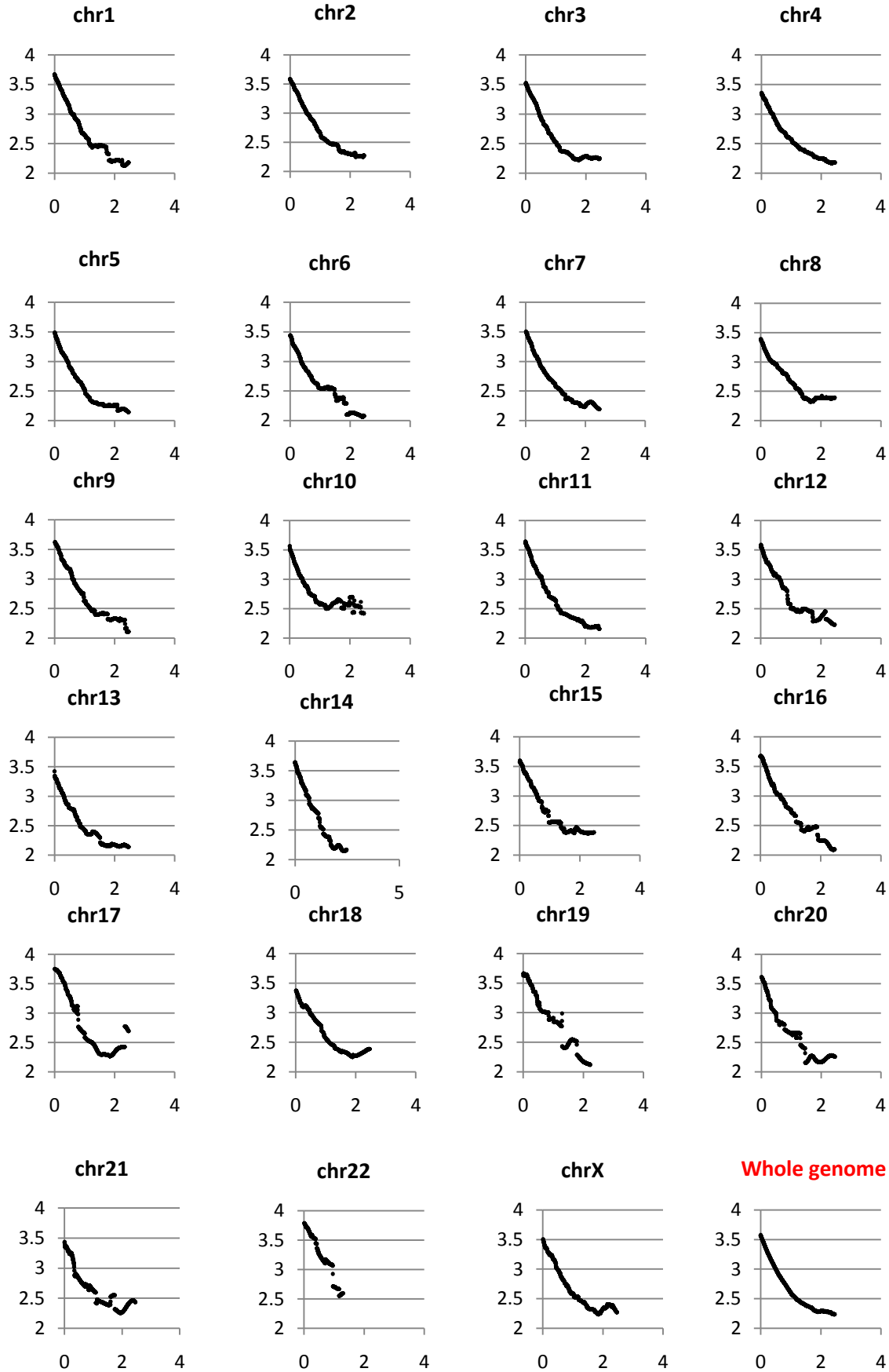
Embryonic stem cells
(U133 plus 2)

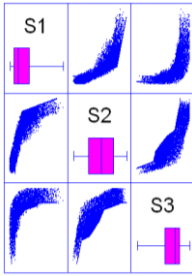


25% least expressed genes at least 500kb away
from expressed genes

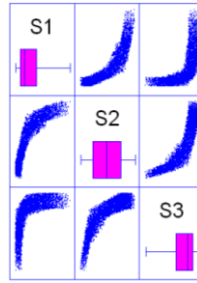


SUPPLEMENTARY FIGURE S12

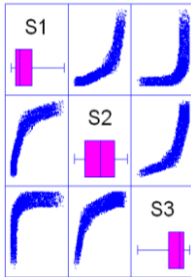




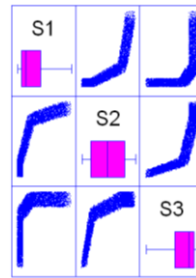
240 minutes



180 minutes



120 minutes



15minutes