Table S1. Strains ans plasmids

Strain or Plasmid	Description	Reference
Strain		
Sakai (RIMD 0509952)	Wild type EHEC O157:H7	Hayashi *et al*., 2001
SKI 1182	Sakai Δ*pchA*Δ*pchB*Δ*pchC*	Nakanishi *et al*., 2006
SKI 0855	Sakai Δ*pchA*Δ*pchB*	This study
SKI 0352	Sakai Δ*ler*	Nakanishi *et al*., 2006
SKI 1282	Sakai Δ*pchB*Δ*pchC pchA*-Strep	This study
SKI 1172	Sakai *ler*-FLAG	This study
Plasmid		
pGEM	Cloning vector	Promega
pGEM-pchA	pGEM with pchA	This study
pGEM-ler	pGEM with ler	This study

Table S2. ORFs in clusters L1

ECs#	gene/ORF	product	locus***	Bound by****
ECs0109	b0105	hypothetical protein	K12	
ECs0207	*dniR*	transcriptional regulator for nitrite reductase (cytochrome c552)	K12	P
ECs0335		putative oxidoreductase	S-loop57	P
ECs0354		putative invertase	S-loop54	P+L
ECs0355		putative invertase	S-loop54	P+L
ECs0356		hypothetical protein	S-loop54	P+L
ECs0512	*ylaD*	maltose O-acetyltransferase	K12	P+L*****
ECs0513	*hha*	haemolysin expression modulating protein	K12	P+L *****
ECs0514	*ybaJ*	hypothetical protein	K12	P+L
ECs0649	*rnk*	regulator of nucleoside diphosphate kinase	K12	
ECs0814		putative outer membrane protein	Sp3	P+L
ECs1126/2715*	*espF-M/U*	type III secretion effector EspF-U/TccP	Sp4/Sp14	P+L *****
ECs1812*	*nleA/espI*	type III secretion effector NleA/EspI	Sp9	P+L
ECs1820		hypothetical protein	Sp9	
ECs2714*	*espJ*	type III secretion effector EspJ	Sp14	P+L
ECs3500		hypothetical membrane protein	Sp17	P
ECs4550*	espF	Effector protein EspF	LEE	L *****
ECs4551	L0017	type III secretion system protein	LEE	L *****
ECs4552	*escF*	type III secretion system EscF protein	LEE	L *****
ECs4553	*cesD2*	type III secretion system chaperone CesD2	LEE	L *****
ECs4554*	*espB*	Translocator protein EspB	LEE	L *****
ECs4555*	*espD*	Translocator protein EspD	LEE	L *****
ECs4556*	*espA*	Translocator protein EspA	LEE	L *****
ECs4557	*sepL*	type III secretion system SepL protein	LEE	L
ECs4558	*escD*	type III secretion system EscD protein	LEE	P+L
ECs4559	*eae*	Gamma intimin	LEE	P+L *****
ECs4560	*cesT*	type III secretion system chaperon CesT	LEE	P+L
ECs4562*	*map*	Effector protein Map	LEE	L
ECs4563	*cesF*	type III secretion system chaperon CesF	LEE	P+L *****
ECs4564*	*espH*	Effector protein EspH	LEE	P+L *****
ECs4565	*sepQ*	type III secretion system SepQ protein	LEE	P+L *****
ECs4566	L0032	hypothetical protein	LEE	P+L *****
ECs4567	L0033	hypothetical protein	LEE	P+L *****
ECs4568	*escN*	type III secretion system protein EscN	LEE	P+L
ECs4570	L0036	hypothetical protein	LEE	P+L
ECs4571*	*sepZ*	Effector protein SepZ/ EspZ	LEE	P+L
ECs4572	L0038	hypothetical protein	LEE	P+L *****
ECs4573	*escJ*	type III secretion system EscJ protein	LEE	P+L *****
ECs4574	*sepD*	type III secretion system protein SepD	LEE	P+L *****
ECs4575	*escC*	type III secretion system EscC protein	LEE	P+L *****
ECs4576	*cesD*	type III secretion system chaperone CesD	LEE	P+L *****
ECs4577	*grlA*	Transcription regulator protein GrlA	LEE	P+L
ECs4578	*grlR*	Transcription regulator protein GrlR	LEE	P+L
ECs4579	L0045	hypothetical protein	LEE	P+L
ECs4580	*escU*	type III secretion system EscU protein	LEE	P+L
ECs4581	*escT*	type III secretion system EscT protein	LEE	P+L
ECs4582	*escS*	type III secretion system EscS protein	LEE	P+L
ECs4583	*escR*	type III secretion system EscR protein	LEE	P+L
ECs4584	L0050	hypothetical protein	LEE	P+L
ECs4585	L0051	hypothetical protein	LEE	P+L
ECs4586	L0052	hypothetical protein	LEE	P+L
ECs4587	L0053	hypothetical protein	LEE	P+L
ECs4590*	*espG*	Effector protein EspG	LEE	P+L
ECs4958		hypothetical protein	Sp18	
PO157_01	*tagA*	TagA protein	pO157 plasmid	

* gene encoding type III effector or translocator protein

** ECs4588 (ler) was not included because of artificially controlled expression

*** K12: common to K12

**** P: Pch, L: Ler, P+L: Pch and Ler.

***** bound at upstream gene

Table S3. ORFs in cluster L2

ECs#	gene/ORF	product	locus**	bound by***
ECs0119	*aceF*	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	K12	
ECs0212		hypothetical protein	S-loop13	
ECs0229		hypothetical protein	S-loop13	
ECs0235		hypothetical protein	S-loop13	
ECs0240		hypothetical membrane protein	S-loop13	P+L
ECs0241		H repeat-associated protein	S-loop13	P+L****
ECs0242		Rhs core protein	S-loop13	P+L****
ECs0243		hypothetical protein	S-loop13	P+L****
ECs0244		hypothetical protein	S-loop13	P+L ****
ECs0245		putative H repeat-associated protein	S-loop13	L
ECs0268	*phoE*	outer membrane pore protein PhoE	K12	
ECs0293		hypothetical protein	S-loop19	P+L
ECs0294		hypothetical protein	S-loop19	P+L
ECs0295		hypothetical protein	S-loop19	P+L
ECs0342	*ykgC*	putative oxidoreductase	K12	
ECs0360	*betT*	high-affinity choline transport	K12	
ECs0445	*rdgC*	recombination associated protein	K12	
ECs0451	*brnQ*	branched chain amino acid transport system II carrier protein	K12	
ECs0452	*proY*	proline permease transport protein	K12	
ECs0454		hypothetical protein	K12	
ECs0511	*ylaC*	hypothetical protein	K12	
ECs0703	b0669	putative RNA	K12	
ECs0815		antitermination protein	Sp3	P+L
ECs0816		hypothetical membrane protein	Sp3	P+L****
ECs0817		hypothetical protein	Sp3	
ECs0846	*nleB2-1'*	NleB-like protein, pseudogene	Sp3	P
ECs0848*	*nleH1-1*	Effector protein NleH1	Sp3	P
ECs0849		hypothetical protein	Sp3	P
ECs0899	b0822	hypothetical protein	K12	
ECs0949		hypothetical protein	S-loop74	P
ECs1061		hypothetical protein	Sp4	
ECs1101		hypothetical protein	Sp4	
ECs1147	*yccM*	predicted 4Fe-4S membrane protein	K12	
ECs1343		TerW protein	SpLE1	
ECs1466	*yceD*	hypothetical protein	K12	
ECs1467	*rpmF*	50S ribosomal protein L32	K12	
ECs1521		hypothetical protein	Sp6	
ECs1525		hypothetical protein	Sp6	
ECs1526		hypothetical protein	Sp6	
ECs1560*	*espX7*	Effector protein EspX7	Sp6	P
ECs1561*	*espN*	Effector protein EspN	Sp6	P
ECs1562		hypothetical protein	Sp6	P****
ECs1567*	*espO1-1*	Effector protein EspO1-1	Sp6	P
ECs1568*	*espK*	Effector protein EspK	Sp6	P
ECs1810	*nleG2-1'*	NleG pseudogene	Sp9	
ECs1811	*nleG2-1'*	NleG pseudogene	Sp9	
ECs1814*	*nleH1-2*	Effector protein NleH1-2	Sp9	P****
ECs1815*	*nleF*	Effector protein NleF	Sp9	P
ECs1821	*espO1-2*	Effector protein EspO1-2	Sp9	P+L
ECs1822		hypothetical protein	Sp9	P+L
ECs1823		hypothetical protein	Sp9	P+L
ECs1824*	*nleG*	Effector protein NleG	Sp9	P+L****
ECs1891	*ycjP*	putative transport system permease protein	K12	
ECs1903	*tpx*	thiol peroxidase	K12	
ECs1960		hypothetical protein	S-loop14	
ECs1988		hypothetical protein	S-loop14	
ECs1994/ECs2156*	*nleG2-2*/*nleG2-3*	Effector protein NleG2-2/NleG2-3	Sp10/Sp11	P ****
ECs1995/ECs2155*	*nleG6-1*/*nleG6-2*	Effector protein NleG6-1/NleG6-2	Sp10/Sp11	P ****
ECs1996/ECs2154*	*nleG5-1*/*nleG5-2*	Effector protein NleG5-1/NleG5-2	Sp10/Sp11	P
ECs2143		putative transcriptional regulator	K12	
ECs2228	*nleG3'*	NleG pseudogene	Sp12	
ECs2229	*nleG3'*	NleG pseudogene	Sp12	
ECs2263		hypothetical protein	Sp12	
ECs2264		hypothetical protein	Sp12	
ECs2365	*sodB*	superoxide dismutase	K12	
ECs2403	*ydiP*	predicted DNA-binding transcriptional regulator	K12	
ECs2460	*ynjB*	hypothetical protein	K12	
ECs2518	b1809	hypothetical protein	K12	
ECs2631		putative derepression protein	S-loop22	
ECs2637		putative transposase OrfA protein of insertion sequence IS629	S-loop22	
ECs2701	*yedR*	predicted inner membrane protein	K12	P+L
ECs2736		putative terminase small subunit	Sp14	
ECs2747		hypothetical protein	Sp14	
ECs2748		hypothetical protein	Sp14	
ECs2913	b2107	hypothetical protein	K12	
ECs2917	*yehD*	putative fimbrial-like protein	K12	P+L
ECs3140	*ais*	aluminum-inducible protein	K12	P
ECs3166	*nuoH*	NADH dehydrogenase I chain H	K12	

ECs3232		putative DNA injection protein	S-loop28	
ECs3269	*yfeO*	predicted ion channel protein	K12	
ECs3291	*yfeK*	hypothetical protein	K12	
ECs3293	*cysA*	ATP-binding component of sulfate permease A protein; chromate	K12	
ECs3314	*eutH*	ethanolamine utilization protein EutH	K12	
ECs3319	*cchA*	detox protein	K12	
ECs3367	b2505	putative outer membrane lipoprotein	K12	L
ECs3486*	*nleG8-2*	Effector protein NleG8-2	Sp17	P
ECs3487*	*espW*	Effector protein EspW	Sp17	P
ECs3488	*nleG6-3*	Effector protein NleG6-3, pseudogene	Sp17	
ECs3499		hypothetical protein	Sp17	
ECs3508		hypothetical protein	Sp17	P
ECs3509		hypothetical protein	Sp17	P
ECs3510		hypothetical protein	Sp17	P
ECs3511		hypothetical protein	Sp17	P
ECs3512		putative site specific recombinase	Sp17	P
ECs3517	*ypjC*	hypothetical protein	K12	P+L
ECs3518	*ygaQ*	hypothetical protein	K12	
ECs3535		hypothetical protein	S-loop	
ECs3616	*ybdY*	hypothetical protein	K12	P+L
ECs3703	*yqeH*	hypothetical protein	K12	P
ECs3713	b2857	hypothetical protein	K12	P
ECs3718	*eprI*	type III secretion protein EprI	ETT2	P
ECs3720		putative transcriptional regulator	ETT2	P
ECs3721	*epaS*	type III secretion protein EprS	ETT2	P
ECs3810	*tktA*	transketolase 1 isozyme	K12	
ECs3813		hypothetical lipoprotein	S-loop	
ECs3855*	*espL2*	Effector protein EspL2	SpLE3	P
ECs3857*	*nleB1*	Effector protein NleB1	SpLE3	P
ECs3858*	*nleE*	Effector protein NleE	SpLE3	P
ECs3864		hypothetical protein	SpLE3	
ECs3886	*yqhA*	hypothetical protein	K12	
ECs4000	*yhaB*	hypothetical protein	K12	P
ECs4001	*yhaC*	hypothetical protein	K12	P
ECs4145	*yrdA*	putative transferase	K12	
ECs4292		hypothetical membrane protein	S-loop87	P
ECs4324		hypothetical lipoprotein	S-loop25	
ECs4359	*yhiH*	putative ATP-binding component of a transport system	K12	
ECs4511	*rpmG*	50S ribosomal protein L33	K12	
ECs4569	*escV*	type III secretion system EscV protein	LEE	P
ECs4589		hypothetical protein	LEE	P+L
ECs4653*	*espY4*	Effector protein EspY4	S-loop39	P
ECs4656		hypothetical protein	S-loop39	P
ECs4657	*espY5'*	pseudogene	S-loop39	P
ECs4658		hypothetical protein	S-loop39	P
ECs4871	*katG*	hydroperoxidase HPI(I)	K12	
ECs4896	*trmA*	tRNA (uracil-5-)-methyltransferase	K12	
ECs4918	*yjaE*	putative transcriptional regulator	K12	
ECs5019	*lamB*	maltose high-affinity receptor LamB	K12	
ECs5095	*basR*	2-component regulatory system regulatory protein BasR	K12	
ECs5233	*yjgM*	predicted acetyltransferase	K12	
ECs5297	*yjiL*	putative enzyme	K12	
ECs5314		hypothetical protein	S-loop	P
PO157_03	*etpC*	type II secretion component	pO157_plasmid	
PO157_04	*etpD*	type II secretion component	pO157_plasmid	
PO157_05	*etpE*	type II secretion component	pO157_plasmid	
PO157_08	*etpH*	type II secretion component	pO157_plasmid	
PO157_11	*etpK*	type II secretion component	pO157_plasmid	
PO157_21	*hlyD*	hemolysin	pO157_plasmid	
PO157_22	*papX*	hypothetical protein	pO157_plasmid	
PO157_60	*toxB*	ToxB protein	pO157_plasmid	
PO157_81		hypothetical protein	pO157_plasmid	

* gene encoding type III effector protein (Tobe et al., 2006)

** K12: common to K12

*** P: Pch, L: Ler, P+L: Pch and Ler.

**** bound at upstream gene

Table S4. ORFs in cluster N

ECs#	gene/ORF	product	locus*	bound by**
ECs0017	nhaA	Na+/H antiporter	K12	
ECs0018	nhaR	transcriptional activator of nhaA	K12	
ECs0049	yabF	putative NAD(P)H oxidoreductase	K12	
ECs0079	leuL	leu operon leader peptide	K12	P+L
ECs0088	ftsI	septum formation protein FtsI	K12	
ECs0246	yafV	putative amidase-type enzyme	K12	
ECs0286		hypothetical protein	Sp1	
ECs0287		putative transcription regulator	Sp1	
ECs0324	ykgK	putative regulator	K12	L
ECs0383	yahO	hypothetical protein	K12	
ECs0439	yaiA	hypothetical protein	K12	
ECs0491	clpP	ATP-dependent proteolytic subunit of clpA-clpP serine protease ClpP	K12	
ECs0492	clpX	ATP-dependent specificity component of clpP serine protease ClpX	K12	
ECs0538	ybaS	putative glutaminase	K12	P
ECs0539	ybaT	putative amino acid/amine transport protein	K12	P
ECs0621		hypothetical protein	K12	
ECs0706	nagC	transcriptional repressor of nag (N-acetylglucosamine) operon	K12	
ECs0781	b0753	putative homeobox protein	K12	
ECs0864	ybhL	hypothetical protein	K12	
ECs0890	dps	global regulator protein Dps	K12	
ECs0912	b0833	hypothetical protein	K12	
ECs0969	infA	translation initiation factor IF-1	K12	
ECs1041	ompA	outer membrane protein 3a	K12	P
ECs1121		putative host specificity protein	Sp4	
ECs1155	cbpA	curved DNA-binding protein	K12	
ECs1159	yccJ	hypothetical protein	K12	
ECs1160		putative integrase	Sp5	
ECs1204		hypothetical protein	Sp5	
ECs1243		hypothetical protein	Sp5	
ECs1263	part	putative cytochrome	K12	
ECs1272		Rtn-like protein	S-loop	P
ECs1384		hypothetical protein	S-loop	
ECs1414	csgG	curli production assembly/transport component CsgG	K12	
ECs1429	msyB	acidic protein MsyB	K12	
ECs1506		putative phage repressor	Sp6	
ECs1510		putative replication protein	Sp6	
ECs1556		putative regulatory protein	Sp6	
ECs1566		hypothetical protein	Sp6	
ECs1662		hypothetical protein	Sp8	
ECs1672	ycgK	hypothetical protein	K12	
ECs1765		putative regulatory protein	Sp9	
ECs1813		integrase	Sp9	
ECs1829	yciE	hypothetical protein	K12	
ECs1830	yciF	putative structural proteins	K12	
ECs1831	yciG	hypothetical protein	K12	
ECs1912	b1330	hypothetical protein	K12	
ECs2032	rimL	ribosomal-protein-serine N-acetyltransferase	K12	
ECs2084	rpsV	30S ribosomal protein S22	K12	
ECs2086	osmC	osmotically inducible protein	K12	
ECs2097	xasA	acid sensitivity protein	K12	
ECs2281		hypothetical protein	K12	
ECs2291	ynfC	hypothetical protein	K12	
ECs2320	ydgA	hypothetical protein	K12	
ECs2327	hdhA	NAD-dependent 7alpha-hydroxysteroid dehydrogenase	K12	
ECs2333	blr	beta-lactam resistance protein	K12	
ECs2343	ydgR	putative proton-dependent oligopeptide transporter	K12	
ECs2370	cfa	cyclopropane fatty acyl phospholipid synthase	K12	
ECs2382	b1675	hypothetical protein	K12	
ECs2412	ydiE	hypothetical protein	K12	
ECs2414	b1701	hypothetical protein	K12	
ECs2432	b1726	hypothetical protein	K12	
ECs2464	b1758	putative cytochrome oxidase	K12	
ECs2493	yeaH	hypothetical protein	K12	
ECs2504	yeaQ	hypothetical protein	K12	
ECs2546	b1836		K12	
ECs2547	b1837	hypothetical protein	K12	
ECs2548	pphA	phosphoprotein phosphatase 1	K12	
ECs2557	yebF	hypothetical protein	K12	
ECs2579	yecN	hypothetical protein	K12	
ECs2603	yecG	putative regulator	K12	P
ECs2620		putative transcriptional regulator	Sp13	
ECs2653	uvrY	putative 2-component transcriptional regulator	K12	
ECs2691	drsB	hypothetical protein	K12	
ECs2692	b1953	hypothetical protein	K12	
ECs2695	b1957	hypothetical protein	K12	
ECs2706	yedV	putative 2-component sensor protein	K12	
ECs2712	yodB	putative cytochrome	K12	P

ECs2846	galF	putative Galf transferase	K12	P
ECs2888	b2080	hypothetical protein	K12	
ECs2909		hypothetical protein	S-loop	
ECs2910		putative outer membrane protein	S-loop	
ECs2938	yehV	putative transcriptional regulator	K12	
ECs2974	stx1A	Shiga toxin I subunit A precursor	Sp15	P
ECs3104	ompC	outer membrane protein C OmpC	K12	P+L
ECs3154	elaB	hypothetical protein	K12	
ECs3248	evgA	putative positive transcription regulator	K12	
ECs3249	evgS	putative sensor for regulator EvgA	K12	
ECs3271	b2392	high affinity manganese transport protein	K12	P+L
ECs3272	nupC	permease of transport system for 3 nucleosides	K12	P+L
ECs3284	zipA	cell division protein involved in FtsZ ring	K12	P
ECs3289	crr	glucose-specific PTS system IIA component	K12	P
ECs3394	iscA	putative iron-binding protein	K12	
ECs3466	b2603	hypothetical protein	K12	
ECs3527	b2666	hypothetical protein	K12	
ECs3530	stpA	DNA-binding protein	K12	
ECs3533	ygaM	hypothetical protein	K12	
ECs3553	csrA	carbon storage regulator	K12	
ECs3595	rpoS	sigma factor RpoS	K12	
ECs3652	b2792	hypothetical protein	K12	
ECs3690	b2833	hypothetical protein	K12	
ECs3764	recJ	ssDNA exonuclease RecJ	K12	
ECs3795	yggB	mechanosensitive channel protein	K12	
ECs3818	metK	methionine adenosyltransferase 1	K12	
ECs3920	icc	regulator of lacZ	K12	
ECs3931	glgS	glycogen biosynthesis protein GlgS	K12	
ECs3979	yqjC	hypothetical protein	K12	
ECs3980	yqjD	hypothetical protein	K12	
ECs3981	yqjE	hypothetical protein	K12	
ECs4045	pnp	polynucleotide phosphorylase	K12	P
ECs4112	yhcO	hypothetical protein	K12	L
ECs4226	trpS	tryptophan tRNA synthetase	K12	
ECs4250	feoA	ferrous iron transport protein A	K12	
ECs4294	yhhA	hypothetical protein	K12	
ECs4363	yhiM	hypothetical protein	K12	
ECs4377	slp	outer membrane protein Slp	K12	P+L
ECs4379		hypothetical protein	S-loop	P+L
ECs4380		heme utilization/transport protein	S-loop	P+L
ECs4389	hdeB	hypothetical protein	K12	P+L
ECs4390	hdeA	hypothetical protein	K12	P+L
ECs4391	hdeD	hypothetical protein	K12	P+L
ECs4392	yhiE	hypothetical protein	K12	P+L
ECs4393	yhiU	putative membrane protein	K12	P+L
ECs4395	gadW	putative ARAC-type regulatory protein	K12	P+L
ECs4396	gadX	putative ARAC-type regulatory protein	K12	P+L
ECs4418	yhjU	hypothetical protein	K12	
ECs4427		putative fimbrial protein precursor	S-loop	L
ECs4433	yhjY	putative lipase	K12	
ECs4485	cysE	serine acetyltransferase	K12	
ECs4496	htrL	involved in lipopolysaccharide biosynthesis	K12	
ECs4710	yifN	hypothetical protein	K12	
ECs4715	rhoL	rho operon leader peptide	K12	
ECs4716	rho	transcription termination factor Rho	K12	
ECs4848	yiiT	putative regulator	K12	
ECs4926	hydH	sensor kinase HydH	K12	
ECs4943		putative regulatory protein	S-loop	
ECs5006	yjbD	hypothetical protein	K12	
ECs5028	yjbJ	hypothetical protein	K12	
ECs5039	yjbR	hypothetical protein	K12	
ECs5108	yjdI	hypothetical protein	K12	
ECs5109	yjdJ	hypothetical protein	K12	
ECs5163	aidB	putative acyl coenzyme A dehydrogenase	K12	
ECs5195	ytfK	hypothetical protein	K12	
ECs5250		hypothetical protein	SpLE5	
ECs5253		putative integrase	SpLE6	
ECs5328	yjjZ	hypothetical protein	K12	
PO157_26			pO157 plasmid	

* K12: common to K12

** P: Pch, L: Ler, P+L: Pch and Ler.

Table S5. PchA binding site on chromosome

	region	genes/ORFs		Ler/Pch effect on transcription
1	Intergenic between ECs0016 and 0017	gef, nhaA	K-12	negative for nhaA
2	ECs0023-0025	ECs0023-0025	S-loop	
3	Upstream of ECs0035	carA	K-12	
4	Intergenic between ECs0079 and 0080	leuL-leuO	K-12	negative for leuL
5	Upstream of ECs0085	yabB	K-12	
6	Intergenic between ECs0116 and 0117	aroP, pdhR	K-12	
7	Upstream of ECs0207	dniR	K-12	positive for dniR
8	ECs0212-0216	ECs0212-0216	S-loop	
9	Intergenic between ECs0233 and 0234	ECs0233, 0234	S-loop	positive for ECs0235
10	ECs0237-0245	rhsI operon	rhsI/S-loop1	positive for ECs0240-0245
11	ECs0287	ECs0287	S-loop	negative for ECs0286 and 0287
12	ECs0291-0295	ECs0291-0295	S-loop	positive for ECs0293-0295
13	ECs0304	ECs0304	S-loop	
14	Upstream of ECs0324	ykgK	K-12	negative for ECs0324
15	Intergenic between ECs0333 and 0334		S-loop	
16	ECs0354-0356	ECs0354-0356	S-loop	positive for ECs0354-0356
17	Upstream of ECs0374	ECs0374	S-loop	
18	ECs0380	yahL	K-12	
19	Upstream of ECs0432	yaiB	K-12	
20	ECs0454	ECs0454	K-12	positive for ECs0454
21	ECs0472	ECs0472	K-12	
22	Upstream of ECs0486	cyoA	K-12	
23	Upstream of ECs0514	ybaJ, hha	K-12	positive for ybaJ, hha
24	ECs0548 and ECs0549	ECs0548, ECs0549	S-loop	
25	ECs0561	ybbD	K-12	
26	ECs0593	sfmC	K-12	
27	ECs0602	ECs0602	S-loop	
28	ECs5380 and ECs0603	ECs5380, ECs0603	K-12	
29	ECs0657 and 0658	citA, citC	K-12	
30	Upstream of ECs0660	dcuC	K-12	
31	ECs0662	cspE	K-12	
32	Upstream of ECs0666	lipA	K-12	
33	ECs0686	ybeU	K-12	
34	Upstream of ECs0721	speF	K-12	
35	Upstream of ECs0728	ybfA	K-12	
36	Upstream of ECs0731	yhhI	K-12	
37	ECs0744	ybgD	K-12	
38	Upstream of ECs0755	ECs0755	S-loop	
39	ECs0764 and 0765	ECs0764, 0765	S-loop	
40	Intergenic between ECs0767 and 0768		S-loop	
41	ECs0796	ybhD	K-12	
42	Intergenic between ECs0814 and 0815		S-loop12	positive for ECs0814, 0815
43	ECs0816	ECs0816	S-loop12	positive for ECs0816
44	ECs0844	ECs0844	S-loop12	
45	ECs0846 and 0847	nleC	S-loop12	positive for ECs0846
46	Upstream of ECs0848 and 0849	nleH1-1	S-loop12	positive for ECs0848 and 0849
47	Downstream of ECs0851	ybhB	K-12	
48	ECs0865	ybhM	K-12	negative for ECs0864
49	ECs0876	espX2	S-loop	
50	Intergenic between ECs0891 and 0892	ybiF, ompX	K-12	negative for ECs0890
51	ECs0912	b0833	K-12	negative for b0833
52	ECs0940	ECs0940	S-loop	
53	ECs0949 and 0950	ECs0949, 0950	S-loop	positive for ECs0949
54	Upstream of ECs0987	focA	K-12	
55	ECs1012	ompF	K-12	
56	ECs1077	ECs1077	S-loop	
57	ECs1085	ECs1085	S-loop	
58	ECs1123	ECs1123	S-loop	
59	Intergenic between ECs1125 and 1126		S-loop	positive for ECs1126
60	Upstream of ECs1143	ECs1143	S-loop	

61	ECs1157	yccE	K-12	
62	ECs1183	ECs1183	S-loop	
63	ECs1228	ECs1228	S-loop	
64	Intergenic between ECs1262 and 1263		S-loop	negative for ECs1263
65	ECs1268	ycdQ	K-12	
66	ECs1270-1274	ECs1270-1274	S-loop	negative for ECs1272
67	ECs1280-1281	ECs1280-1281	S-loop	
68	ECs1300	ECs1300	S-loop	
69	ECs1302 and 1303	ECs1302, 1303	S-loop	
70	ECs1316 and 1317	ECs1316, 1317	S-loop	
71	ECs1332 and ECs1333	ECs1332, 1333	S-loop	
72	ECs1351	ECs1351	S-loop	
73	Upstream of ECs1360 and 1361	iha	S-loop	negative for iha
74	ECs1362	ECs1362	S-loop	
75	ECs1370	ECs1370	S-loop	
76	ECs1373-1375	ECs1373-1375	S-loop	
77	Intergenic between ECs1379 and 1380		S-loop	
78	ECs1384 and 1385	ECs1384, 1385	S-loop	negative for ECs1384
79	Upstream of ECs1391	ECs1391	S-loop	
80	ECs1418 and 1419	csgB	K-12	
81	ECs1435-1436	b1057, yceO	K-12	
82	Upstream of ECs1438	yceP	K-12	
83	ECs1560 and 1561	espX7, espN	S-loop	positive for ECs1560, 1561
84	ECs1567 and 1568	espO1-1, espR1	S-loop	positive for ECs1567, 1568
85	ECs1611	ECs1611	S-loop	
86	ECs1615	ECs1615	S-loop	
87	ECs1656	ECs1656	S-loop	
88	ECs1662 and 1663	ECs1662, 1663	S-loop	negative for ECs1662
89	ECs5422	ECs5422	K-12	
90	ECs1722	chaB	K-12	
91	Upstream of ECs1729	narG	K-12	
92	Upstream of ECs1743	oppA	K-12	
93	ECs1772	ECs1772	S-loop	
94	ECs1812	nleA	S-loop	positive for ECs1812
95	Upstream of ECs1815	nleF	S-loop	positive for ECs1815
96	ECs1821-1823	spO1-2	S-loop	positive for ECs1821-1823
97	Intergenic between ECs1825 and 1826		S-loop	positive for ECs1824
98	Upstream of ECs1909	b1327	K-12	
99	ECs1910-1913	ECs1910-1913	K-12	negative for ECs1912
100	ECs1915	fnr	K-12	
101	ECs1941 and 1942	ECs1941, 1942	S-loop	
102	ECs1953-1955	ECs1953-1955	S-loop	
103	ECs1992	ECs1992	S-loop	
104	Intergenic between ECs1996 and 1997		S-loop	positive for ECs1994-1996
105	Upstream of ECs2006	ECs2006	S-loop	
106	ECs2016-2018	ECs2016-2018	S-loop	
107	Upstream of ECs2055	b1451	K-12	
108	ECs5441	ECs5441	K-12	
109	ECs5442	ECs5442	K-12	
110	ECs2073-2076	ECs2073-2076	K-12	
111	ECs2095	b1490	K-12	
112	ECs2098	gadB	K-12	negative for ECs2097
113	ECs2101	yddA	K-12	
114	ECs2104 and 2105	b1499, b1500	K-12	
115	ECs2107	b1502	K-12	
116	ECs2111		S-loop	
117	Upstream of ECs2113	ECs2113	S-loop	
118	Upstream of ECs2128	uxaB	K-12	
119	ECs214-2146	ydeH, ydeI, ydeJ	K-12	
120	ECs2158	ECs2158	S-loop	
121	Upstream of ECs2309	pntA	K-12	
122	ECs2343	ydgR	K-12	negative for ydgR

123	ECs2351	slyA	K-12	
124	ECs2364	ydhO	K-12	positive for ECs2365
125	ECs2403	b1696	K-12	positive for b1696
126	ECs2410	ydiA	K-12	
127	ECs2427	ECs2427	K-12	
128	ECs2436	b1730	K-12	
129	Intergenic between ECs2454 and 2455	cstC, xthA	K-12	
130	ECs2494 and 2495	yeaI, yeaJ	K-12	
131	Upstream of ECs2534	b1824	K-12	
132	ECs2583	yecK	K-12	
133	Intergenic between ECs2602 and 2603	flhD, yecG	K-12	negative for yecG
134	ECs2610	yecI	K-12	
135	Upstream of ECs2612	b1904	K-12	
136	ECs2620 and 2621	ECs2620, 2621	S-loop	negative for ECs2620, positive for ECs2621
137	ECs2672	yedM'	K-12	
138	ECs2674	yedM	K-12	
139	ECs2689	fliR	K-12	
140	Upstream of ECs2701	b1963	K-12	positive for ECs2701
141	ECs2714	espJ	S-loop	positive for ECs2714, 2715
142	ECs2717		S-loop	
143	ECs2780	b1983	K-12	
144	Upstream of ECs2792		S-loop	
145	Upstream of ECs2819	hisL, hisG	K-12	
146	ECs2829	ugd	K-12	
147	ECs2830-2832	ECs2830-2832	S-loop	
148	ECs2834	ECs2834	S-loop	
149	ECs2836	ECs2836	S-loop	
150	ECs2838	ECs2838	S-loop	
151	ECs2840-2845	ECs2840-2845	S-loop	
152	ECs2859	wcaF	K-12	
153	Upstream of ECs2909	ECs2909	S-loop	negative for ECs2909
154	Upstream of ECs2917	yehD	K-12	positive for yehD
155	ECs2974	sltA	S-loop	negative for ECs2974
156	ECs2995	ECs2995	S-loop	
157	ECs3104	ompC	K-12	negative for ompC
158	ECs3116	yfaL	K-12	
159	ECs3122 and 3123	ECs3122, 3123	S-loop	
160	ECs3140 and 3141	ais, b2253	K-12	positive for ais
161	ECs3157 and 3158	elaD, yfbL	K-12	
162	Upstream of ECs3172	nuoA	K-12	
163	Upstream of ECs3174	b2290	K-12	
164	Upstream of ECs3222	b2339	K-12	
165	ECs3228	b2345	K-12	
166	ECs3232	ECs3232	S-loop	positive for ECs3232
167	ECs3238	ECs3238	S-loop	
168	ECs3243	ECs3243	S-loop	
169	ECs3247 and 3248	emrK, evgA	K-12	negative for evgA
170	Intergenic between ECs3284 and 3285	zipA, cysZ	K-12	negative for zipA
171	Upstream of ECs3333	yffB	K-12	
172	ECs3485-3487	espM2, nleG8-2, espW	S-loop	positive for nleG8-2, espW
173	ECs3500	ECs3500	S-loop	positive for ECs3499, 3500
174	ECs3504	ECs3504	S-loop	
175	ECs3507-3512	ECs3507-3512	S-loop	positive for ECs3508-3512
176	ECs3517	b2650	K-12	positive for b2650
177	ECs3518 and 3519	b2654, b2657	K-12	
178	Intergenic between ECs3530 and 3531	stpA, b2670	K-12	negative for stpA
179	Intergenic between ECs3632 and 3633		K-12	
180	Ecs3639	eno	K-12	
181	Upstream of ECs3656	sdaA	K-12	
182	Intergenic between ECs3660 and 3661	fucA, fucP	K-12	
183	Intergenic between ECs3687 and 3688	ygdP, mutH	K-12	
184	ECs3703-3736	ETT2	K-12, S-loop	positive for ECs3703, 3713, 3718, 3720, 3721

185	ECs3742	ygeV	K-12	
186	ECs3750	ygfJ	K-12	
187	ECs3854 and 3855	espL2	S-loop	positive for espL2
188	ECs3856	ECs3856	S-loop	
189	ECs3857 and 3858	nleB1, nleE	S-loop	positive for nleB1 and nleE
190	ECs3859-3861	ECs3859-3861	S-loop	
191	Upstream of ECs3872	pitB'	K-12	
192	ECs3888	b3004	K-12	
193	Upstream of ECs3890	exbB	K-12	
194	ECs3955	ygjG	K-12	
195	ECs3999-3401	tdcR, yhaB, yhaC	K-12	positive for yhaB, yhaC
196	ECs4006	yhaG	K-12	
197	Upstream of ECs4051	yhbC	K-12	
198	Upstream of ECs4066	ispB	K-12	
199	Intergenic between ECs4099 and 4100	nanR, yhcL	K-12	
200	Upstream of ECs4102	sspA	K-12	
201	Upstream of ECs4111	yhcN	K-12	
202	ECs4136 and 4137	envR, acrE	K-12	
203	Intergenic between ECs4244 and 4245	yhgE, pckA	K-12	
204	Upstream of ECs4260	malT	K-12	
205	ECs4274	glgA	K-12	
206	ECs4291 and 4292	ECs4291 and 4292	S-loop	
207	ECs4361 and 4362	yhiJ, yhiK	K-12	
208	ECs4376 and 4377	yhiS, slp	K-12	negative for slp
209	Upstream of ECs4392	gadE	K-12	negative for gadE
210	ECs4395 and 4396	gadW, gadX	K-12	negative for gadX, gadW
211	ECs4400 and 4401	yhjB, yhjC	K-12	
212	Upstream of ECs4424	dppA	K-12	
213	Upstream of ECs4431	ECs4431	S-loop	
214	Downstream of ECs4441	cspA	K-12	
215	ECs4446	yiaB	K-12	
216	ECs4449	xylF	K-12	
217	ECs4466	yiaY	K-12	
218	ECs4471	yibG	K-12	
219	ECs4478-4480	yibL	K-12, S-loop	
220	ECs4496 and 4497	htrL, rfaD	K-12	negative for htrL
221	ECs4500-4504	ECs4500-4504	S-loop	
222	Intergenic between ECs4507 and 4508	kdtA	K-12	
223	Intergenic between ECs4529 and 4530	gltS, yicE	K-12	
224	ECs4530	escD	LEE	positive
225	ECs4560	tir	LEE	positive
226	ECs4563-4567	espH, sepQ	LEE	positive
227	ECs4569-4591	LEE3, LEE2, LEE1 oper	LEE	positive
228	ECs4607-4610	ECs4607-4610	S-loop	
229	ECs4643	espY4	S-loop	
230	ECs4653-4659	ECs4653-4659	S-loop	positive for ECs4653, 4656-4658
231	Upstream of ECs4670	ECs4670	S-loop	
232	Upstream of ECs4681	atpI	K-12	
233	ECs4746	corA	K-12	
234	ECs4785	yihG	K-12	
235	Intergenic between ECs4792 and 4793	glnA, yihK	K-12	
236	Upstream of ECs4812	ECs4812	S-loop	
237	Intergenic between ECs4852 and 4853	glpF, yiiU	K-12	
238	ECs4996	ECs4996	S-loop	
239	Upstream of ECs5009	yjbE	K-12	
240	ECs5021	yjbI	K-12	
241	ECs5024	plsB	K-12	
242	ECs5030	yjbL	K-12	
243	ECs5037	aphA	K-12	
244	ECs5048	yjcF	K-12	
245	Upstream of ECs5099	adiA	K-12	
246	ECs5115	cadC	K-12	

247	Upstream of ECs5168	yjfR	K-12	
248	Intergenic between ECs5180 and 5181	yjfZ	K-12	
249	ECs5230	ECs5230	K-12	
250	ECs5234	yjgN	K-12	positive for ECs5233
251	ECs5256-5259	ECs5256-5259	S-loop	
252	ECs5265	ECs5265	S-loop	
253	ECs5271 and 5272	fimB, fimE	K-12	
254	ECs5284	yjiC	K-12	
255	ECs5295	ECs5295	S-loop	
256	ECs5309 and 5310	ECs5309 and 5310	S-loop	
257	ECs5314	ECs5314	S-loop	positive for ECs5314
258	ECs5315	tsr	K-12	
259	Intergenic between ECs5324 and 5325	yjjP, yjjQ	K-12	

Table S6. Ler binding site on chromosome

	region	genes/ORFs		Ler/Pch effect on transcription
1	ECs0079-0081	leuL, leuO, ilvI	K-12	negative for leuL
2	ECs0116-0117	aroP-pdhR	K-12	
3	ECs0240	rhsI operon	S-loop	positive for ECs0240-0245
4	ECs0293-0295	ECs0293-0295	S-loop	positive for ECs0293-0295
5	Intergenic between ECs0324 and ECs0325	ykgC, ykgD	K-12	negative for ECs0324
6	ECs0354-0356	ECs0354-0356	S-loop	positive for ECs0355
7	Upstream of ECs0514	hha	K-12	positive for ECs0514
8	Upstream of ECs0755	ECs0755	S-loop	
9	Intergenic between ECs0767 and ECs0768		S-loop	
10	ECs0814	ECs0814	S-loop	positive for ECs0814 and ECs0815
11	Upstream of ECs0987	focA	K-12	
12	Intergenic between ECs1020 and ECs1021	ssuE, locus 5 fimbriae operon	locus 5	
13	Upstream of ECs1143	ymcD	K12	
14	Upstream of ECs1360 and 1361	iha	S-loop	
15	ECs1362	ECs1362	S-loop	
16	Upstream of ECs1386	ECs1386	S-loop	
17	ECs5422		K-12	
18	Upstream of ECs1812	nleA	Sp9	positive for ECs1812
19	ECs1821-1823	espO1-2	Sp9	positive for ECs1821, 1822, 1823
20	Intergenic between ECs1825 and 1826	espM1	Sp9	
21	ECs2076	nmpC	K-12	
22	Upstream of ECs2128	uxaB	K-12	
23	ECs2422-2424	pheM, rplT, rpmI	K-12	
24	Upstream of ECs2534	b1824	K-12	
25	Intergenic between ECs2701 and 2702	yedR	K-12	positive for ECs2701
26	ECs2714	espJ	Sp14	positive for ECs2714, 2715
27	ECs2840-2845	ECs2840-2845	S-loop	
28	Upstrem of ECs2917 and ECs918	locus 8 fimbriae operon	locus 8	positive for ECs2917
29	ECs3104	ompC	K-12	negative for ECs3014
30	Upstream of ECs3222	locus 10 fimbriea operon	locus 10	
31	ECs3271	mntH	K-12	negative for ECs3271
32	ECs3333	yffB	K-12	
33	ECs3366 - 3367	b2504-b2505	K-12	positive for ECs3367
34	Upstream of ECs3384		S-loop	
35	Intergenic between ECs3517 and 3518	tRNA-Ile	K-12	positive for ECs3517, 3518
36	Upstream of ECs3616	ECs3616	S-loop	positive for ECs3616
37	Intergenic between ECs3632 and ECs3633	ygcE, ygcF	K-12	
38	Upstream of ECs3652	csrB	K-12	negative for ECs3652
39	Upstream of ECs3872	pitB'	K-12	
40	ECs3985-3986	yhaH, yhaI	K-12	
41	Intergenic between ECs4099 and 4100	nanR, yhcR	K-12	
42	Upstream of ECs4111	yhcN	K-12	
43	ECs4377-ECs4398	gadW, gadB	K-12	4394, 4395
44	ECs4430-4432	locus 12 lpf operon	locus 12	
45	Downstream of ECs4441	cspA	K-12	
46	ECs4466	yiaY	K-12	
47	ECs4472	ECs4472	K-12	
48	ECs4478-4480	yibL	S-loop	
49	ECs4557-4564	espH	LEE	positive
50	Intergenic between ECs4570 and 4571	LEE3, LEE2 operon	LEE	positive
51	Upstream of ECs4573	escJ	LEE	positive
52	Upstream of ECs4577 to 4579	grlA, grlR	LEE	positive
53	ECs4583-4591	escU, escT, escS, escR, ler, espG	LEE	positive
54	ECs4601 and 4602	yicO, yicP	K-12	
55	ECs4822	yjjG	K-12	
56	Upstream of ECs4904	secE	K-12	
57	Upstream of ECs4908	rplJ	K-12	
58	ECs5091	yjdA	K-12	
59	Intergenic between ECs5324 and 5325	fhuF	K-12	

Figure S1. Binding of Ler on EHEC O157 Sakai chromosome. Vertical bars indicate the relative hybridization intensity of the precipitated DNA compared with DNA in the supernatant. Upper column shows G+C contents in gray vertical lines.

Figure S2. Binding of PchA on EHEC O157 Sakai chromosome. Vertical bars indicate the relative hybridization intensity of the precipitated DNA compared with DNA in the supernatant. Red and blue Arrowheads indicate S-loops (O157:H7 strain-specific regions) and backbone (regions conserved with *E. coli* K12) genes, respectively. Upper column shows G+C contents in gray vertical lines.

Fig. S1

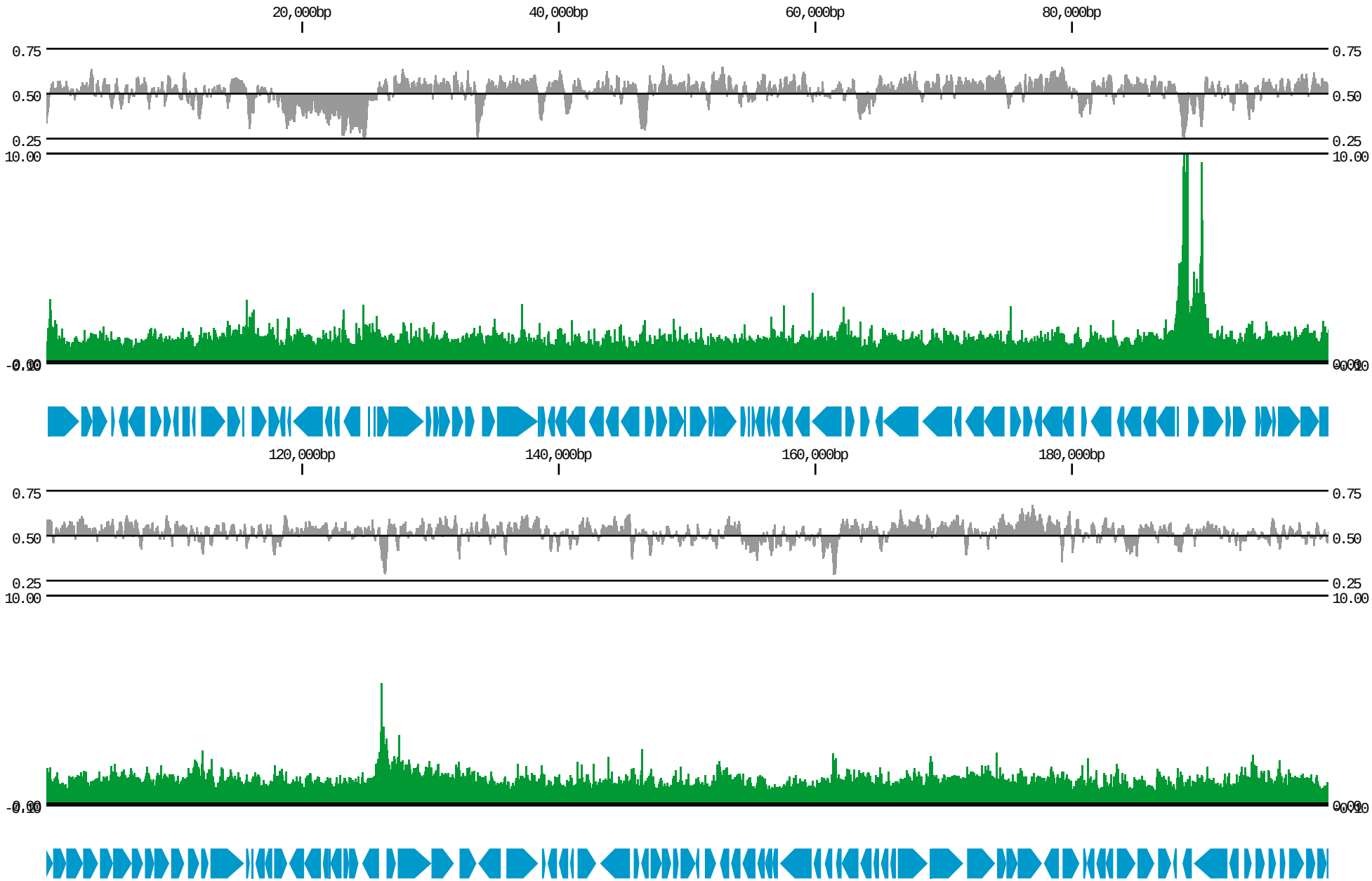
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Fig. S1 (cont.)

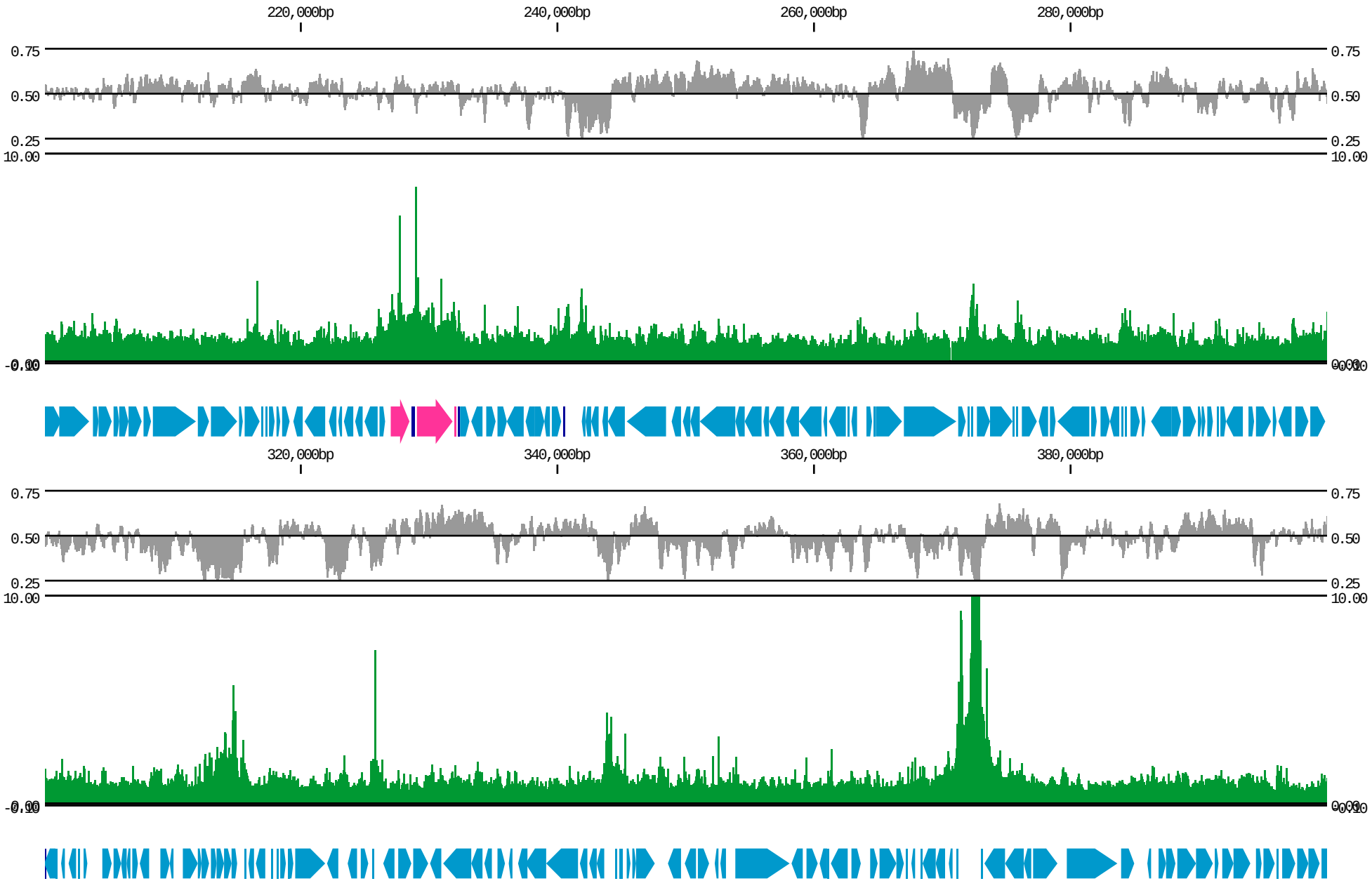
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Fig. S1 (cont.)

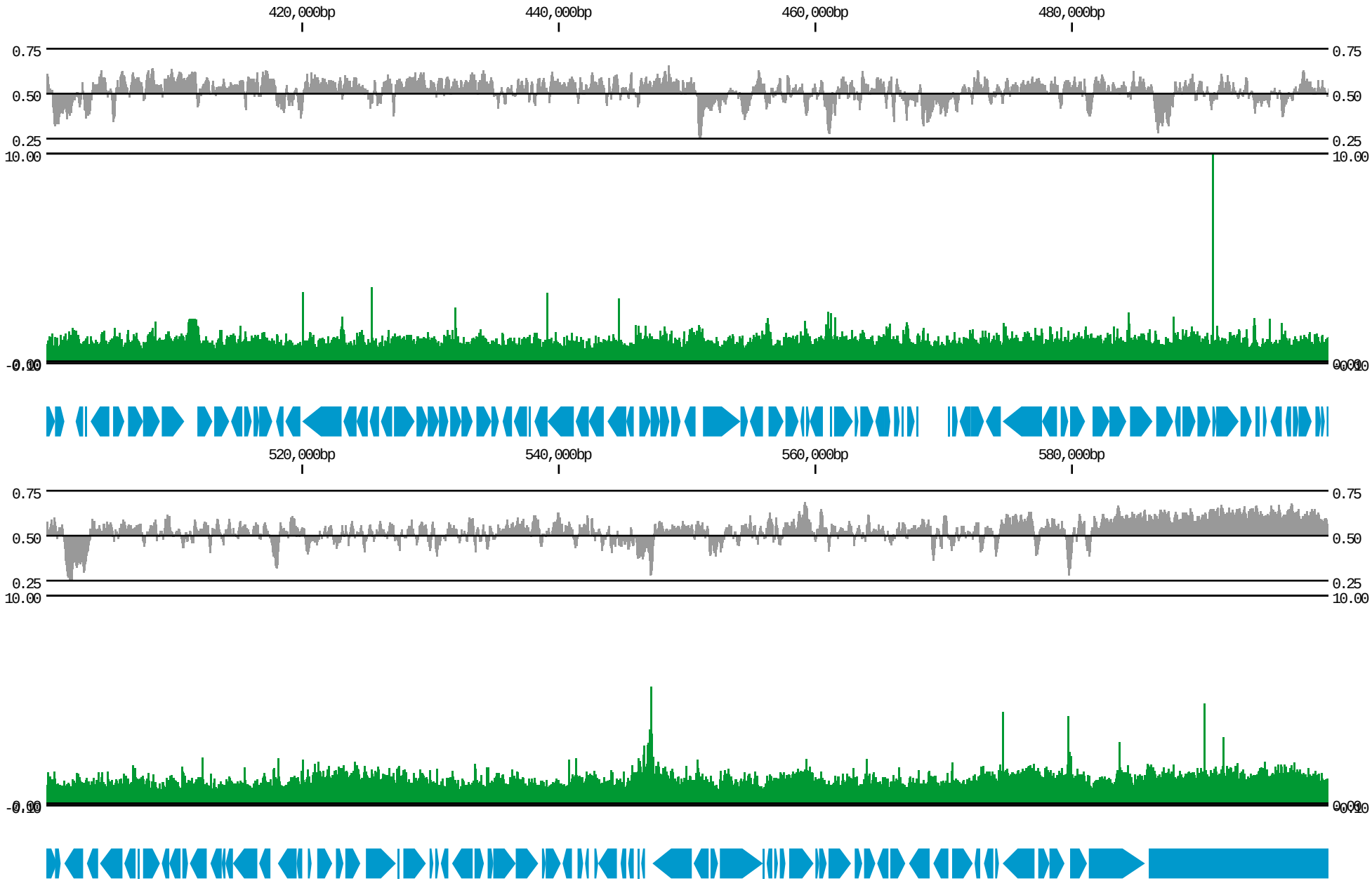
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Fig. S1 (cont.)

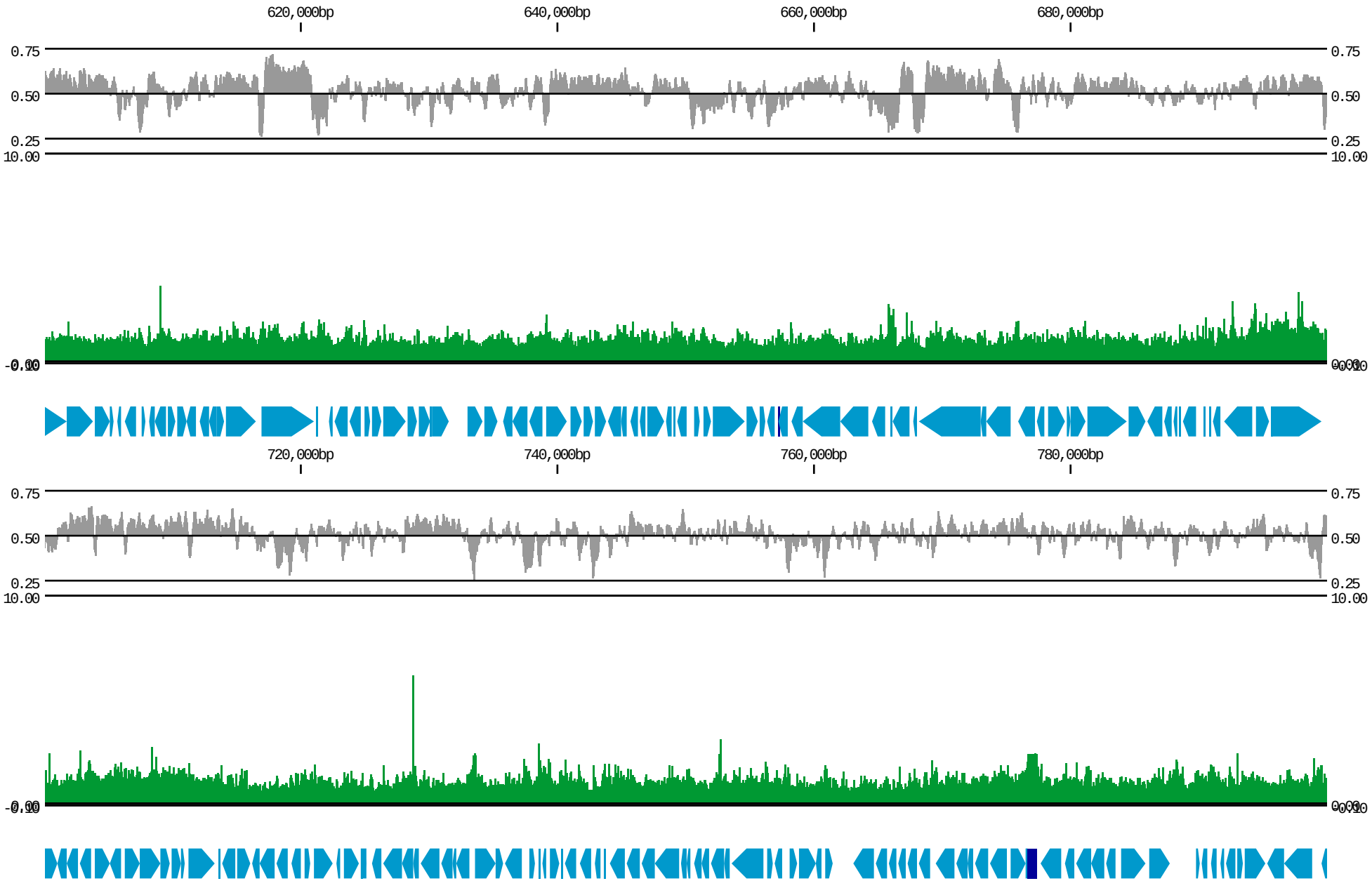
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Fig. S1 (cont.)

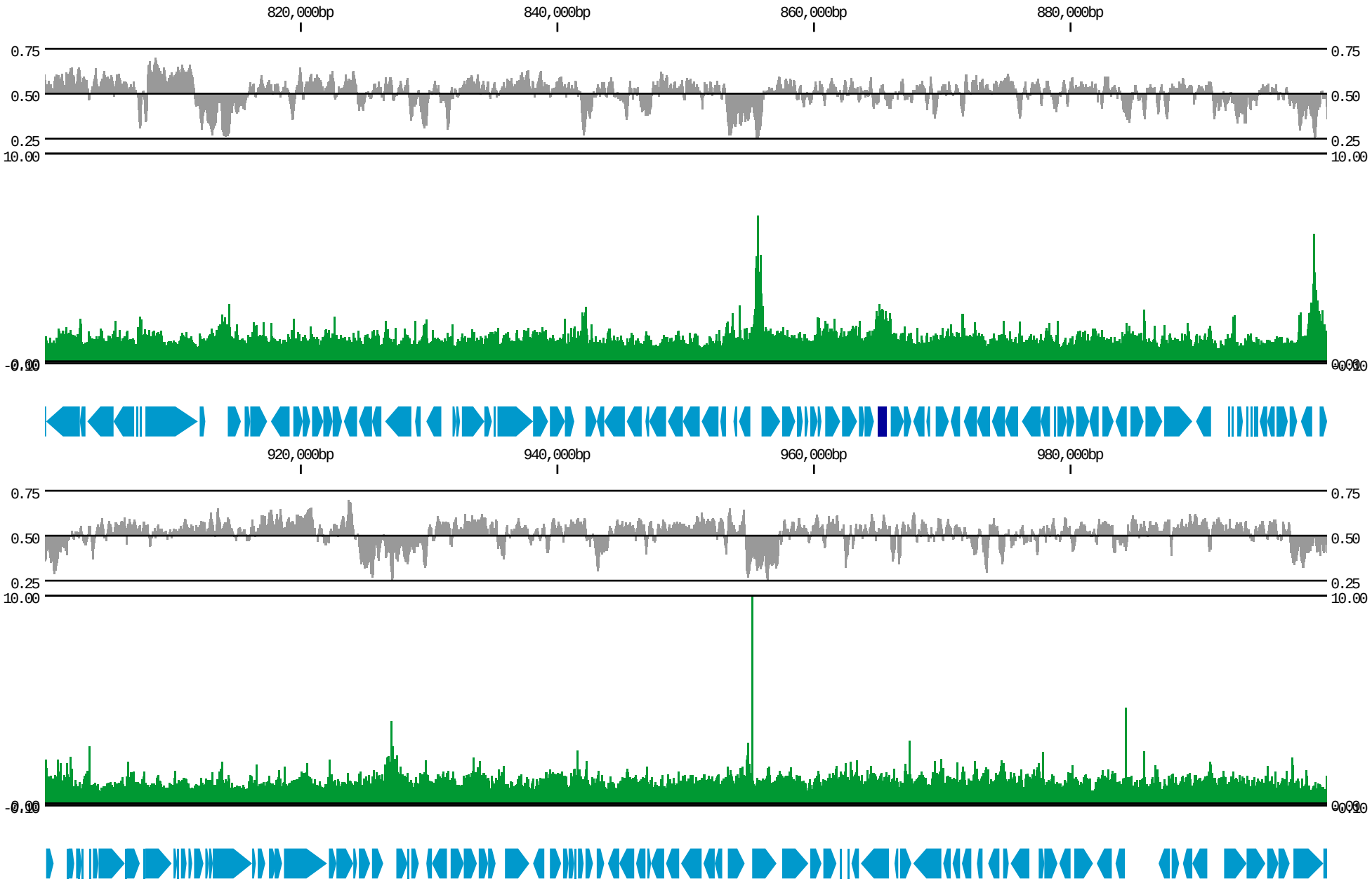
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Fig. S1 (cont.)

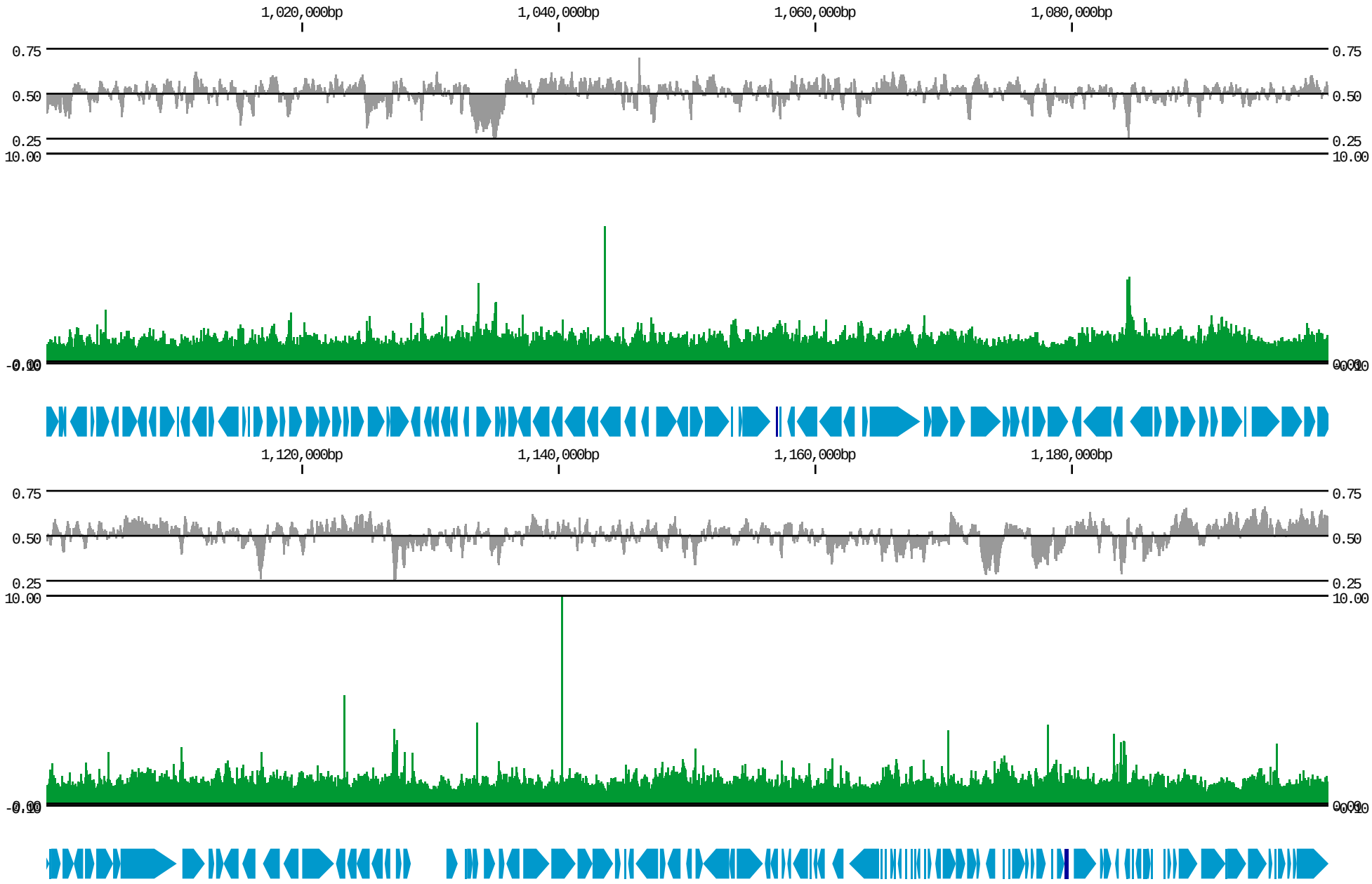
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Fig. S1 (cont.)

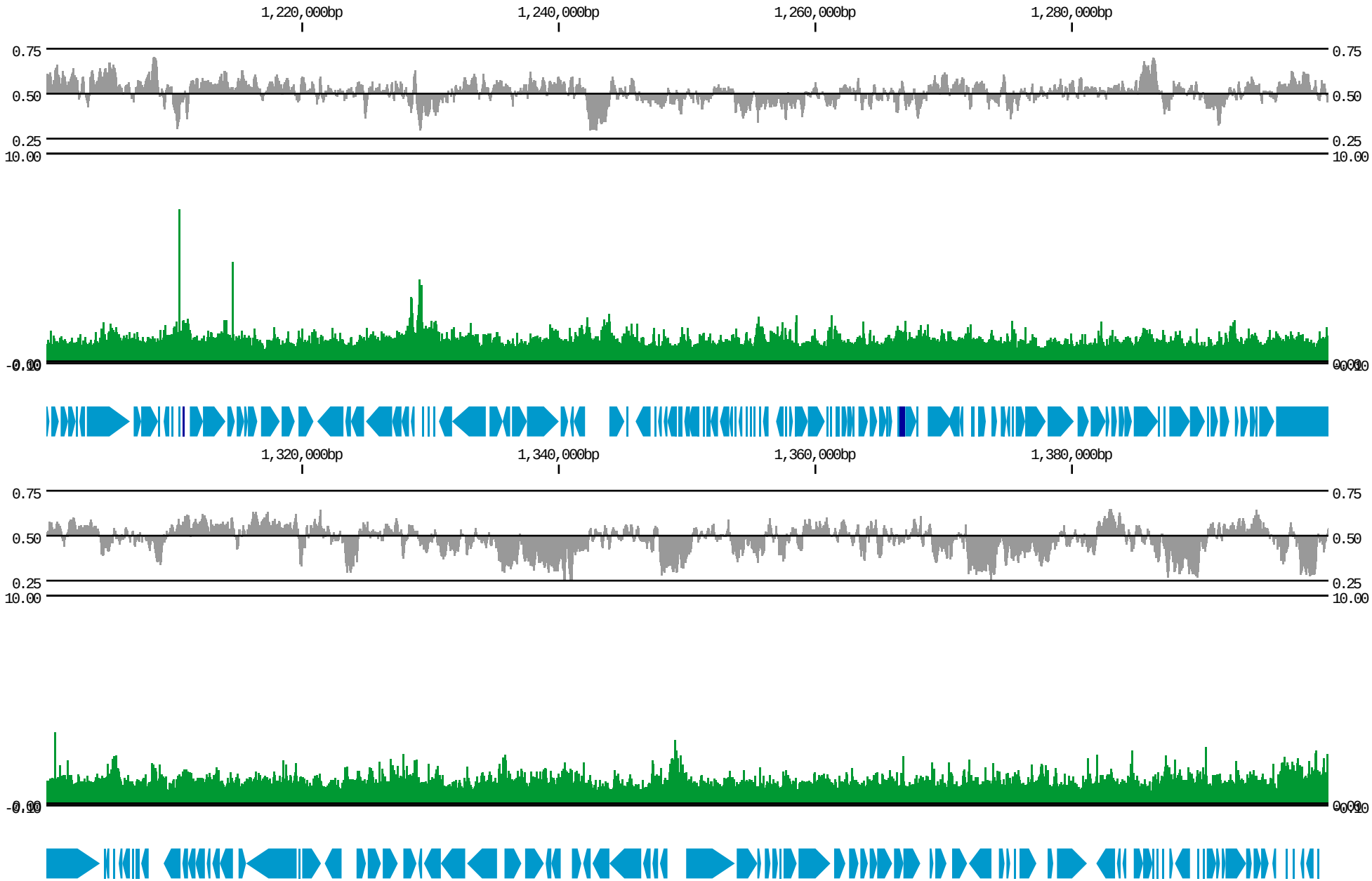
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Fig. S1 (cont.)

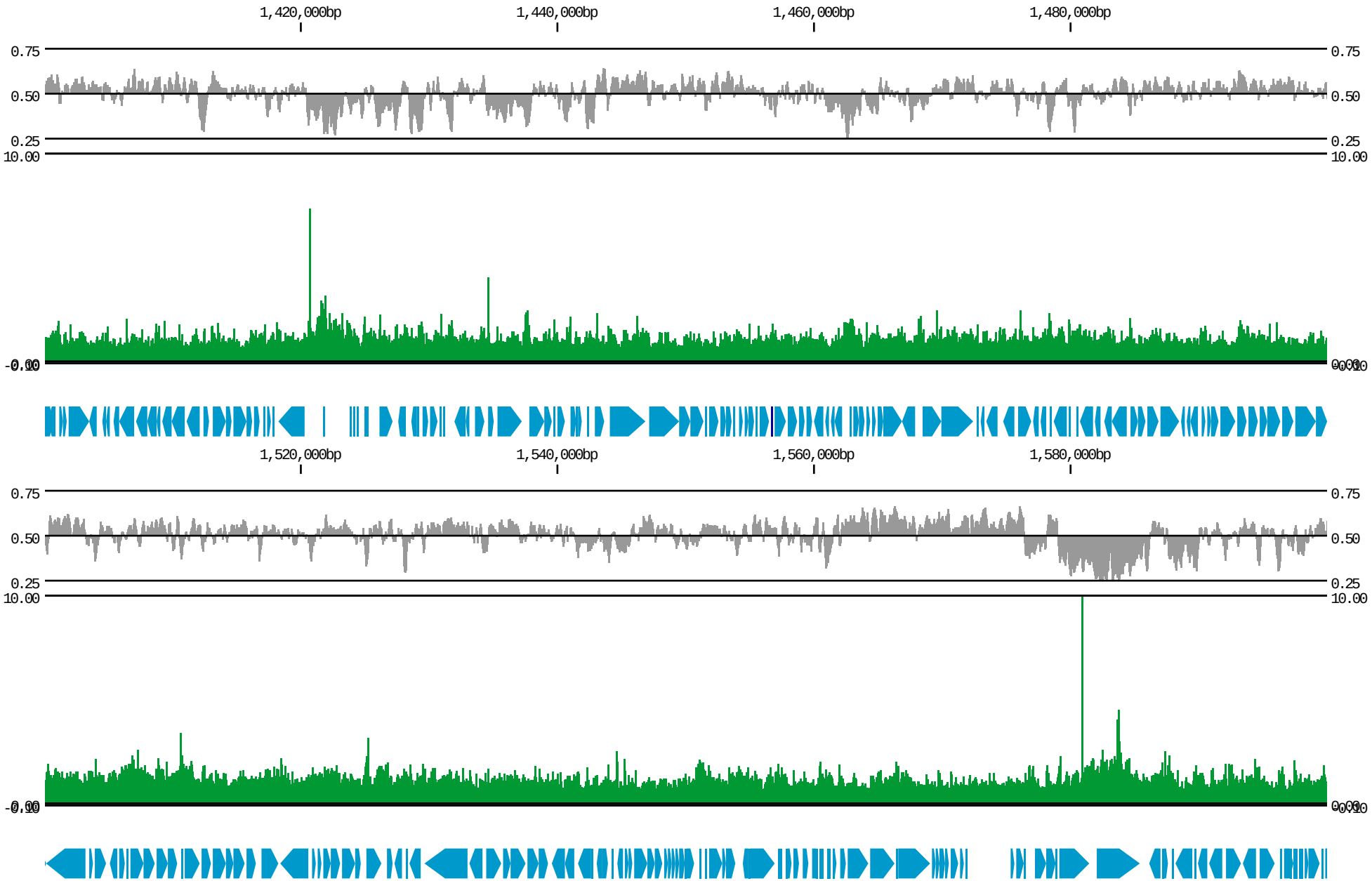
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Fig. S1 (cont.)

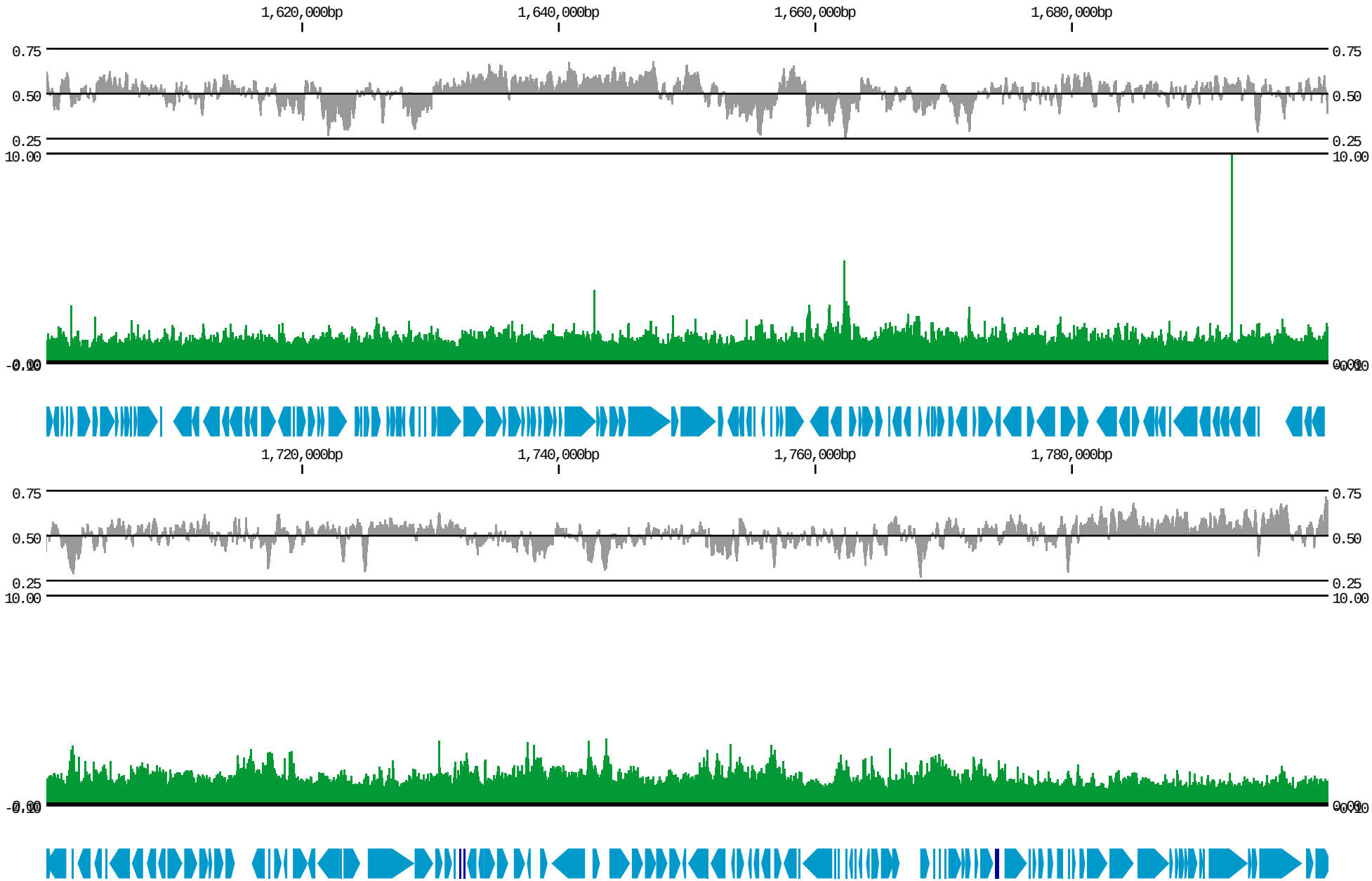
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Fig. S1 (cont.)

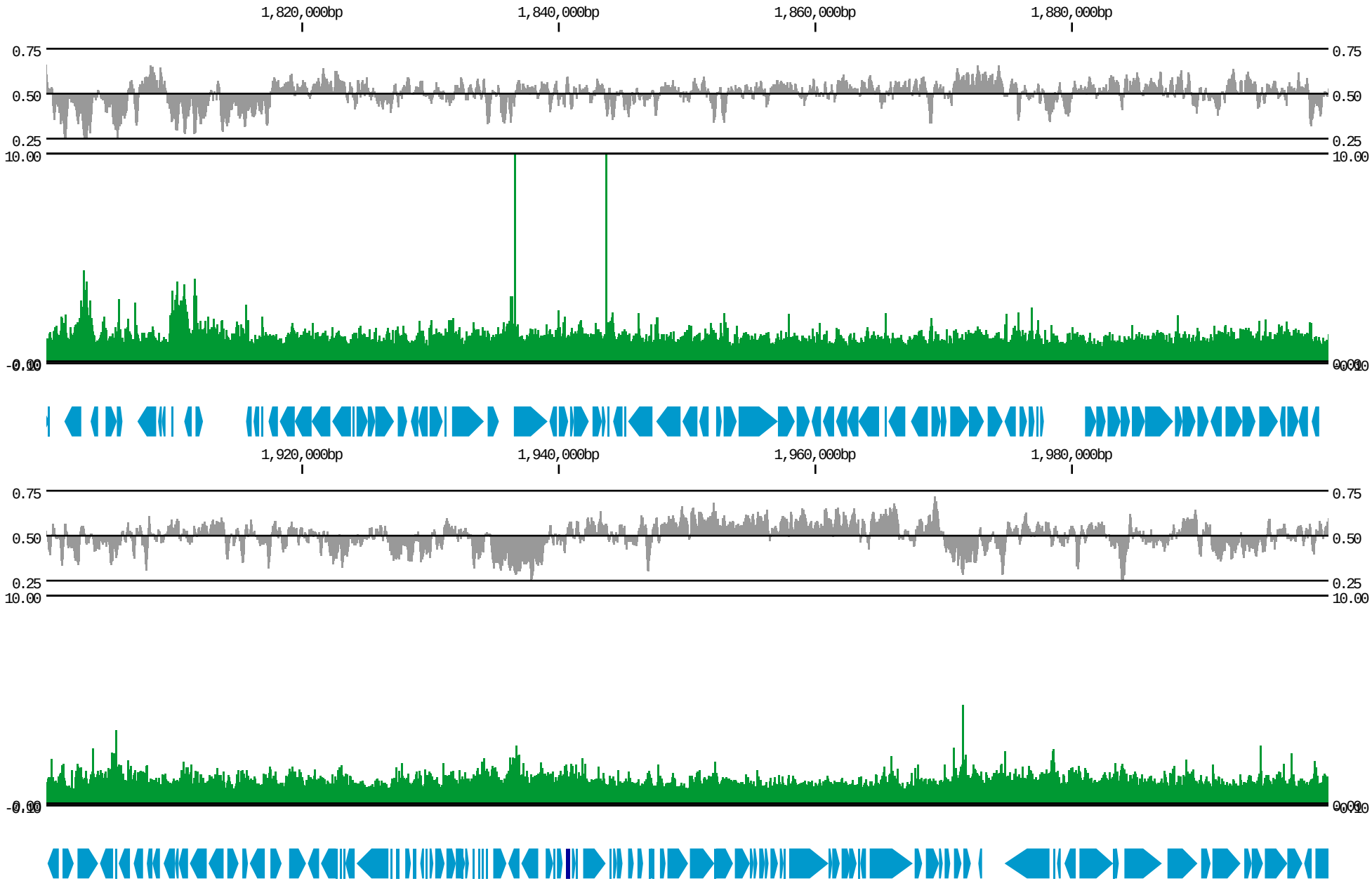
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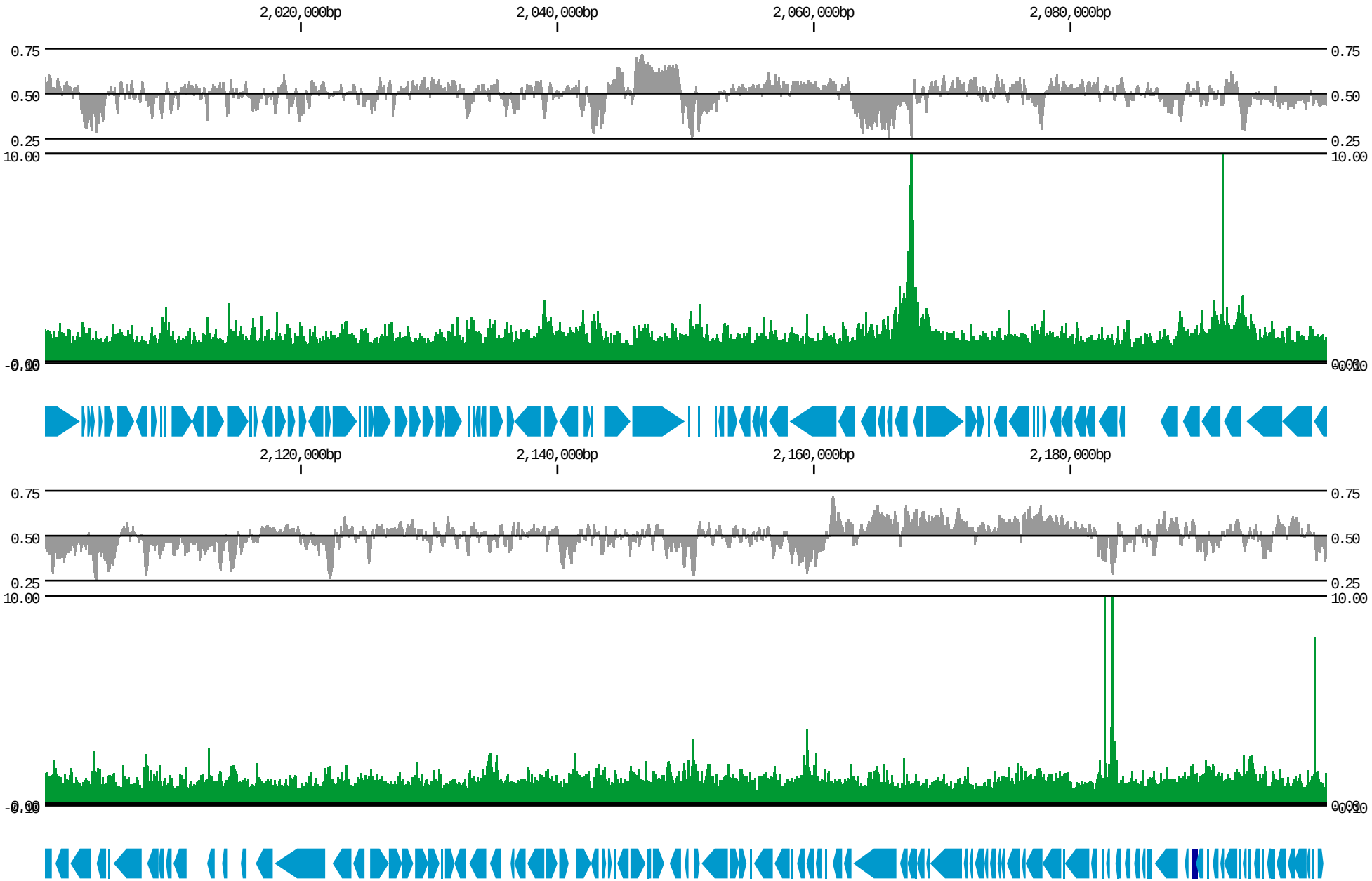
Fig. S1 (cont.)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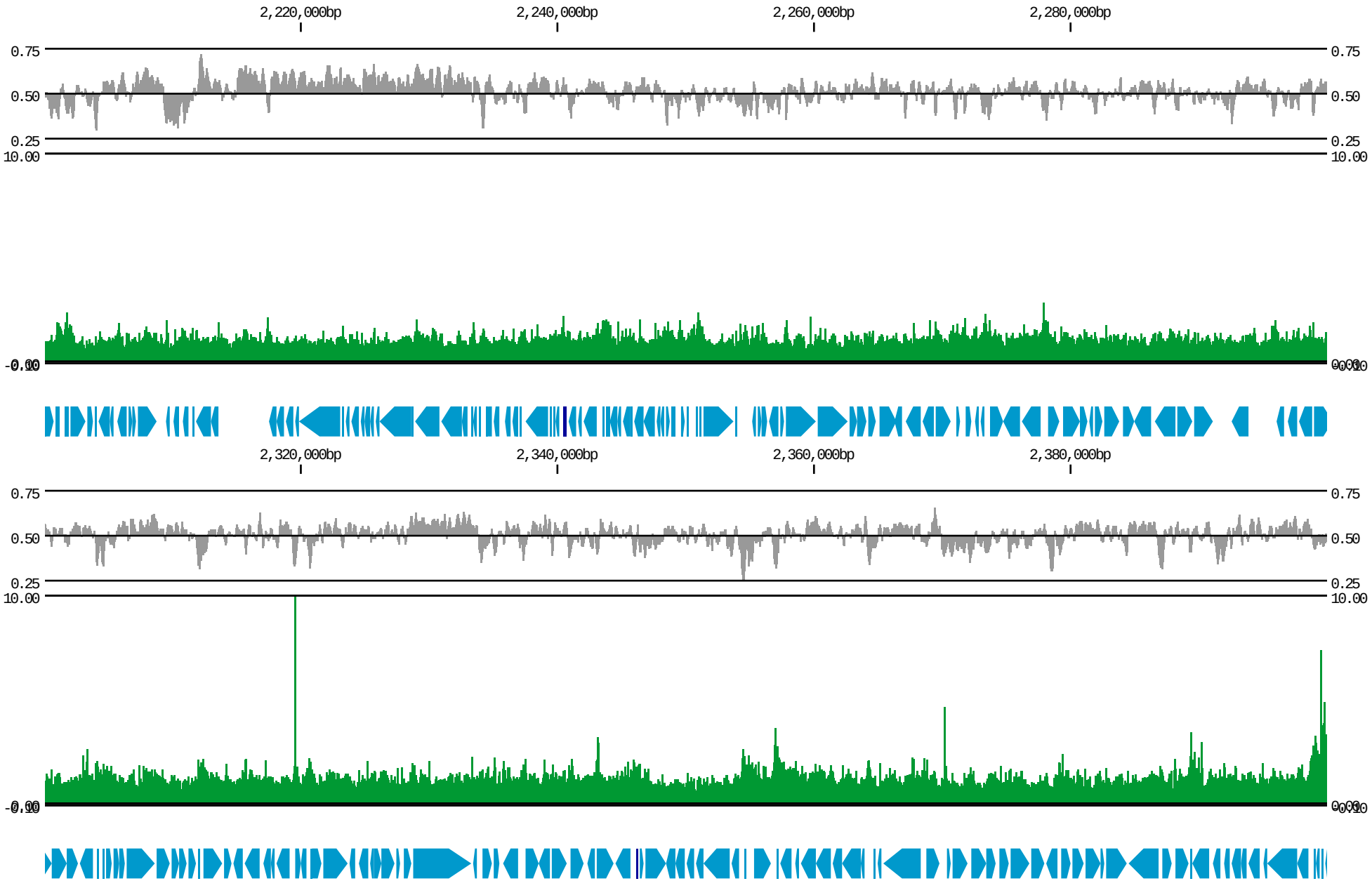
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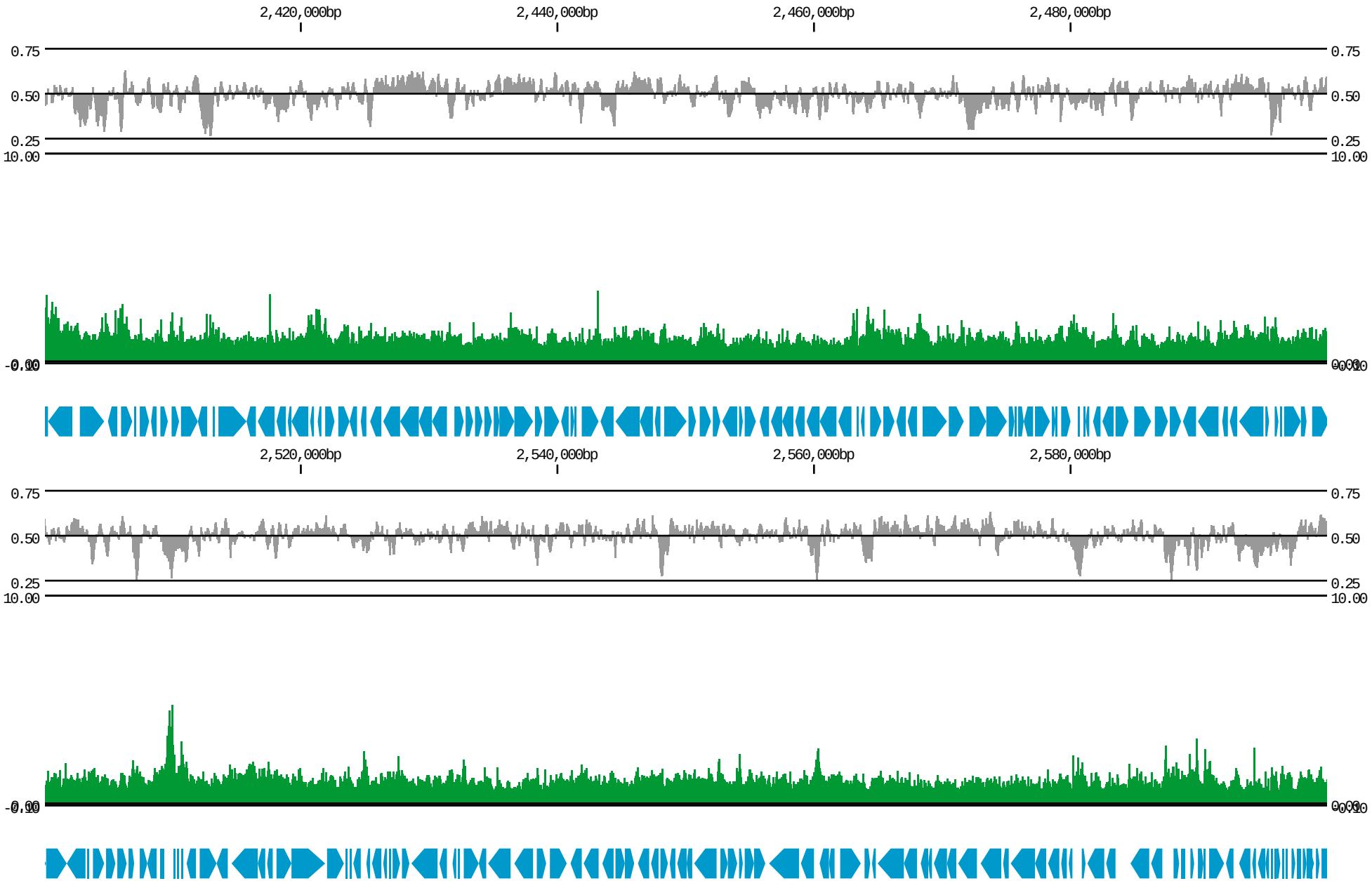
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Fig. S1 (cont.)

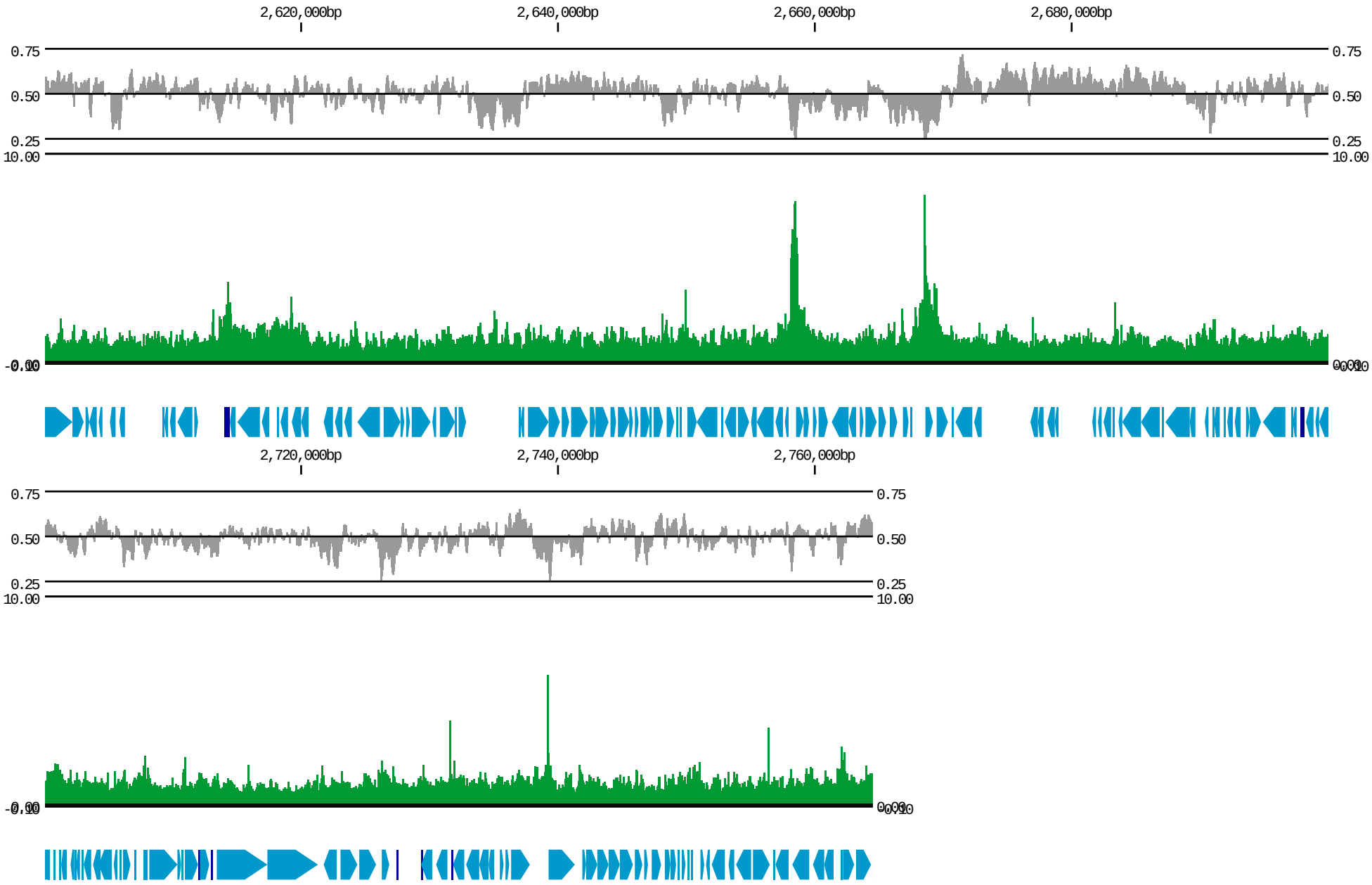
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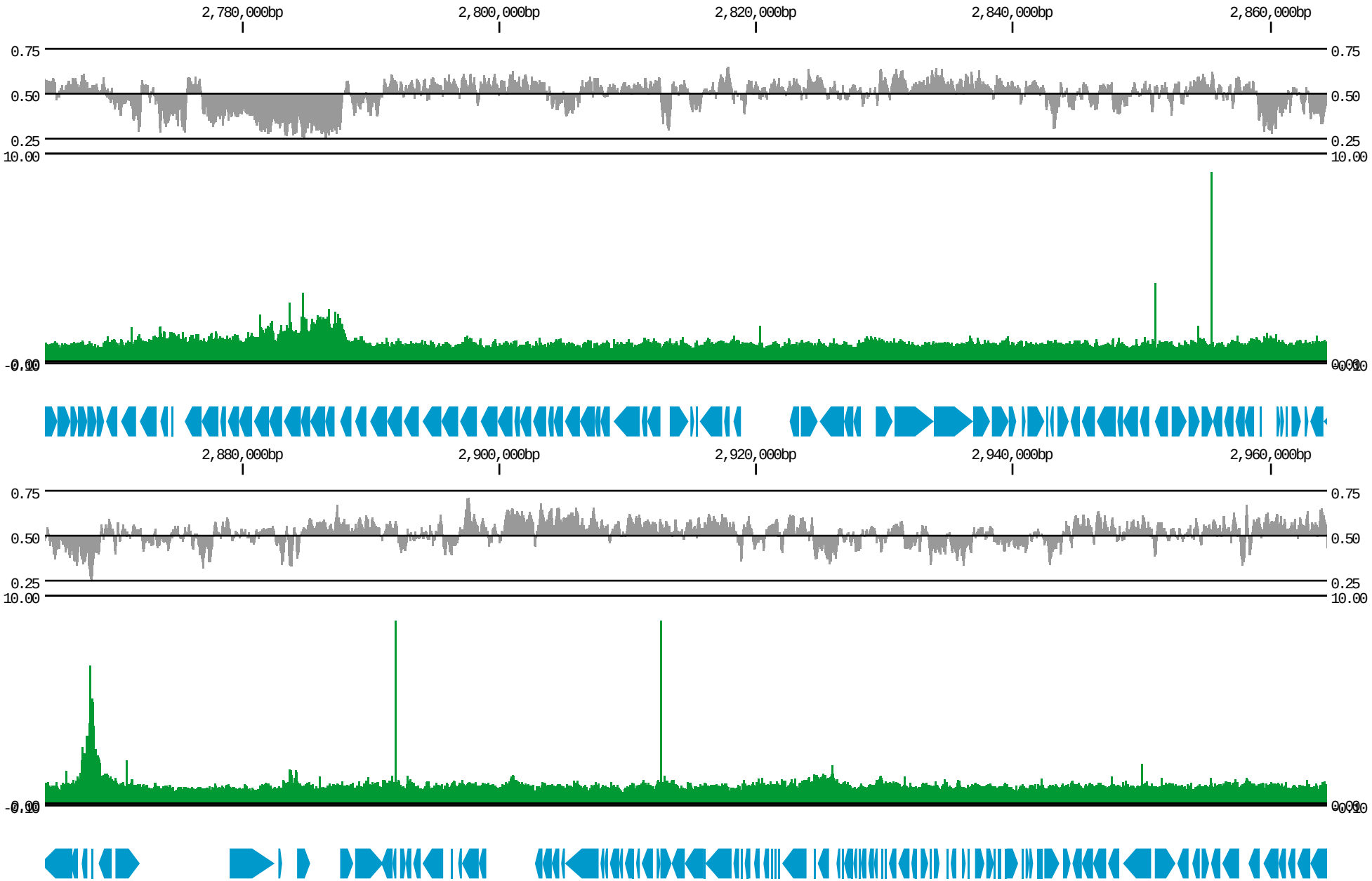
Fig. S1 (cont.)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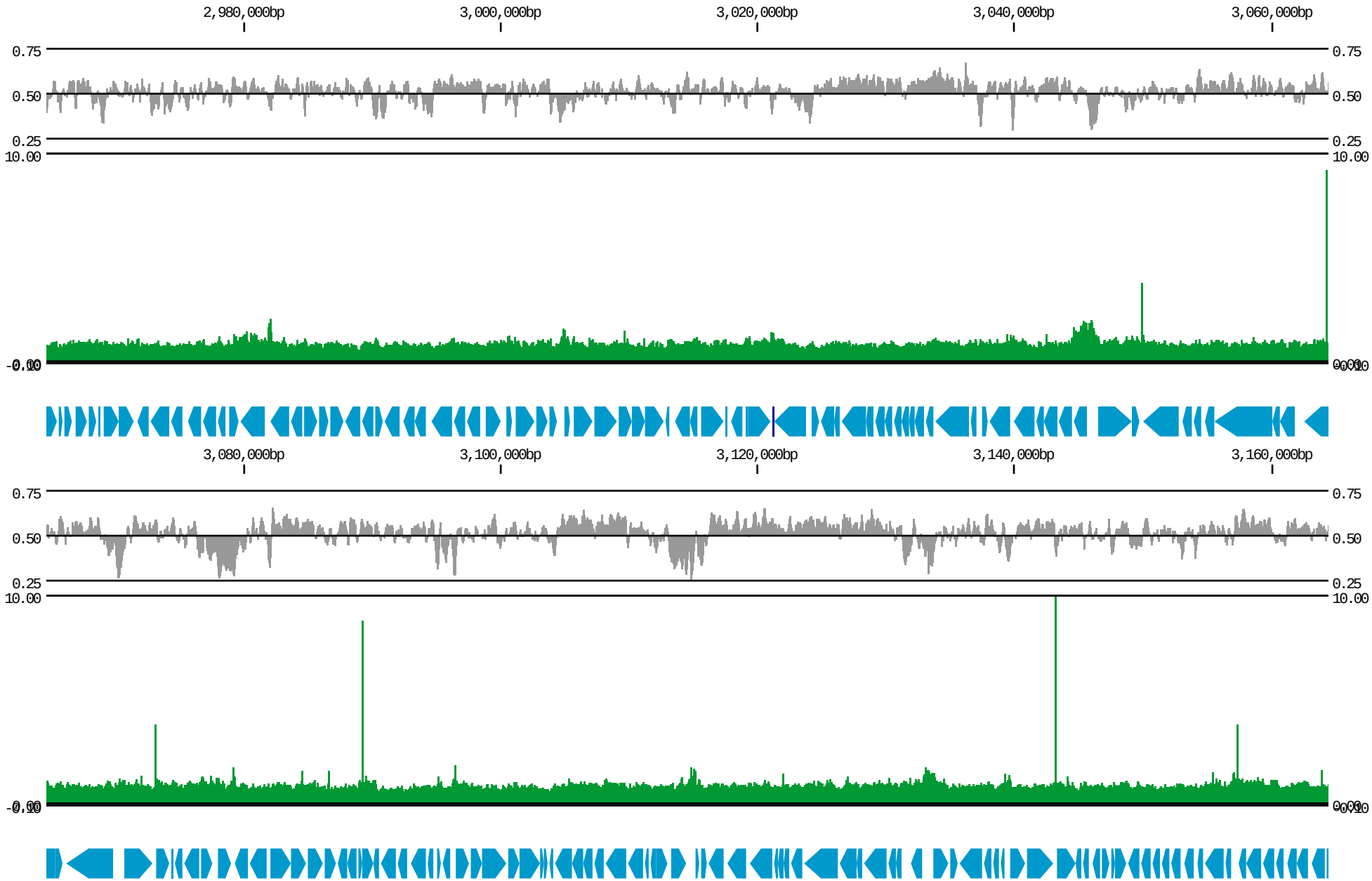
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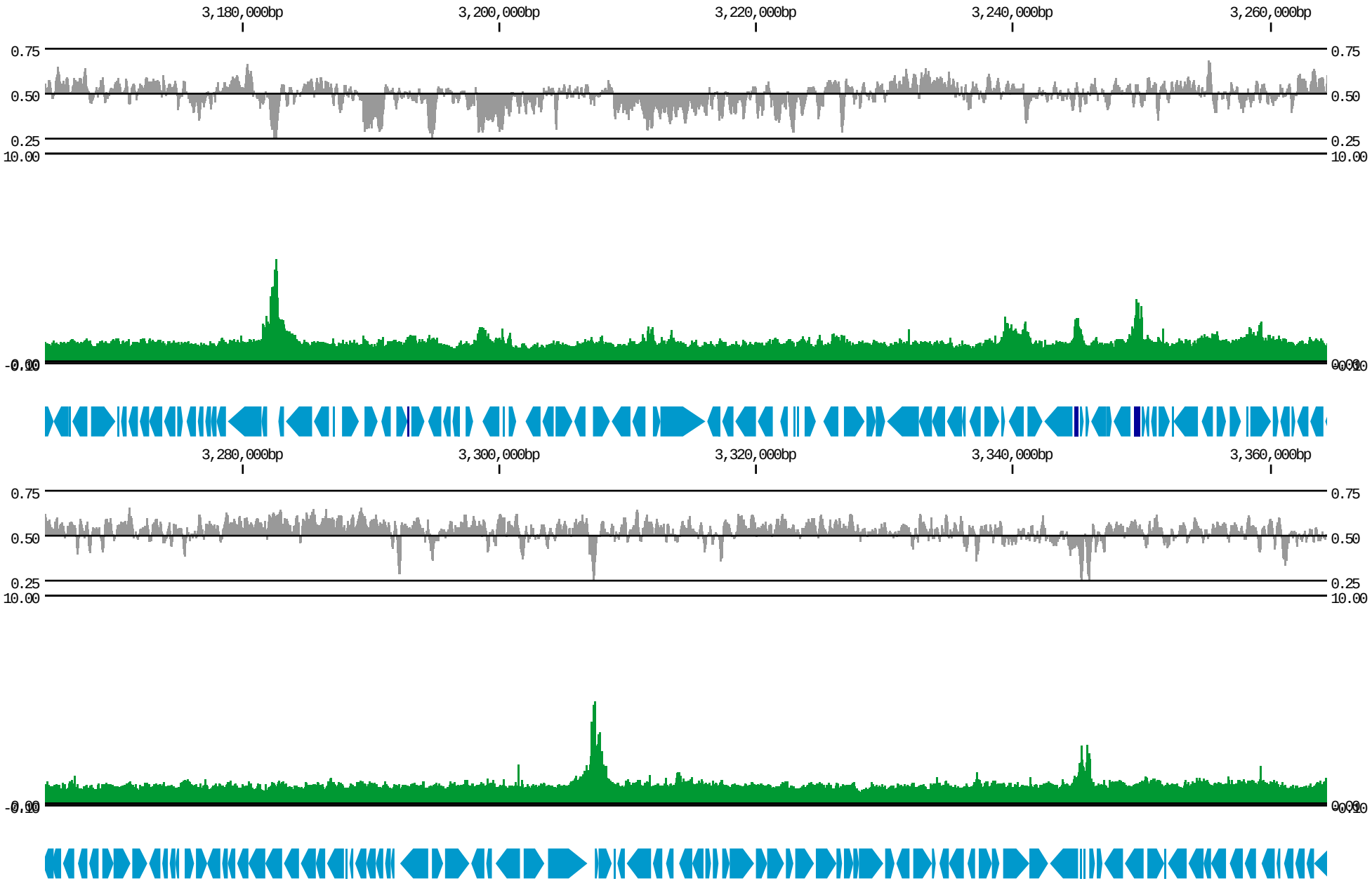
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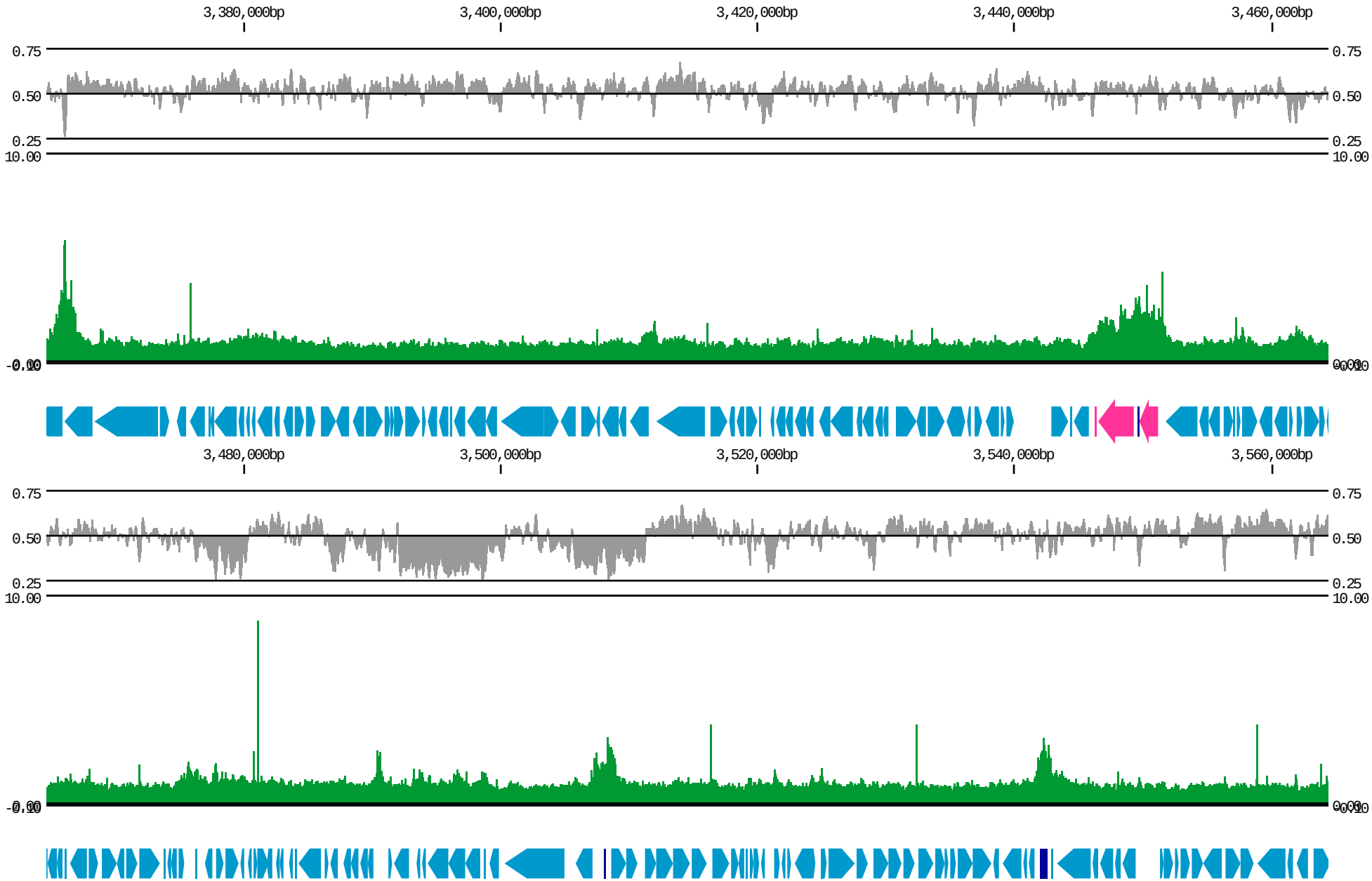
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Fig. S1 (cont.)

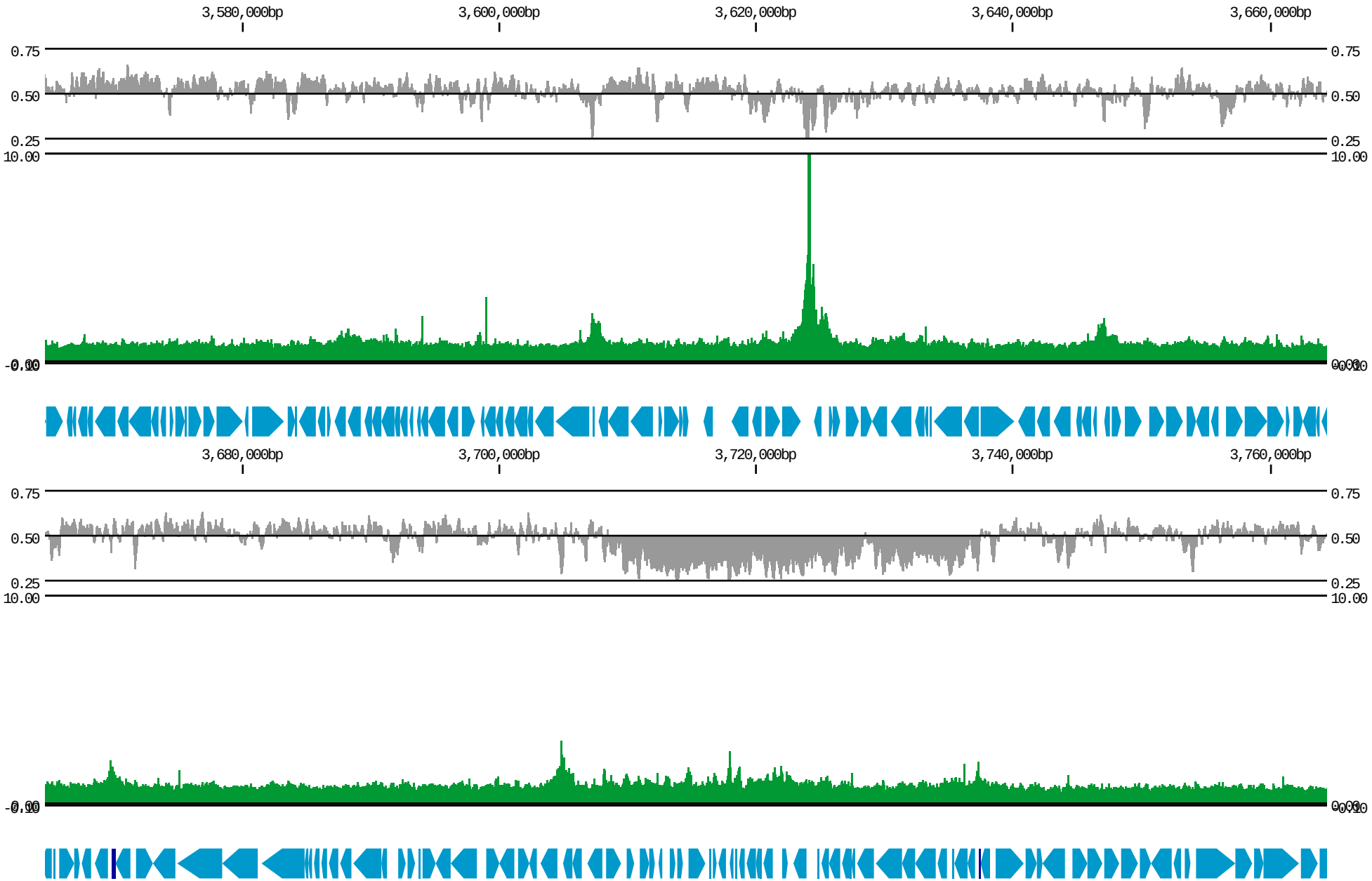
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Fig. S1 (cont.)

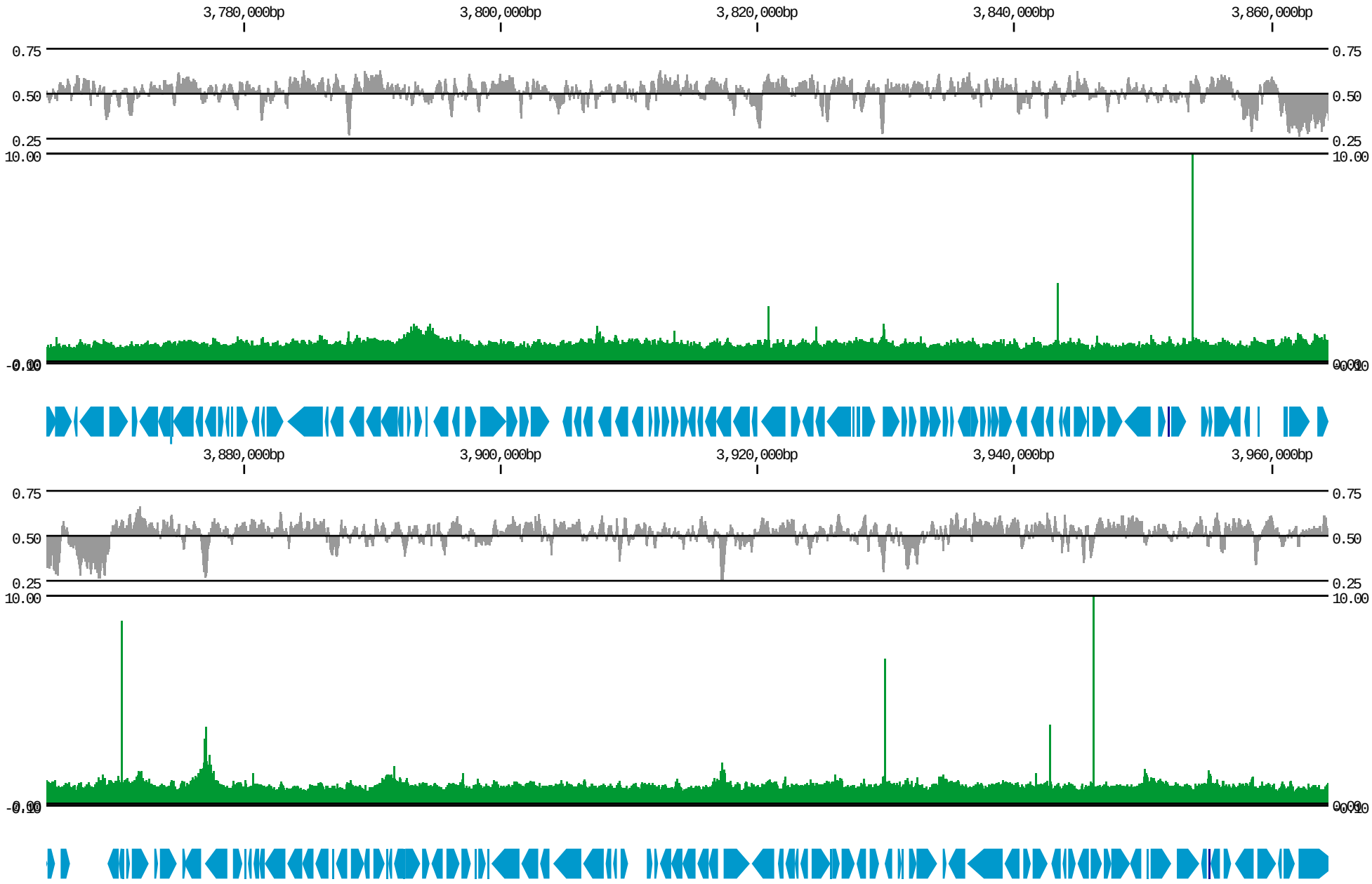
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Fig. S1 (cont.)

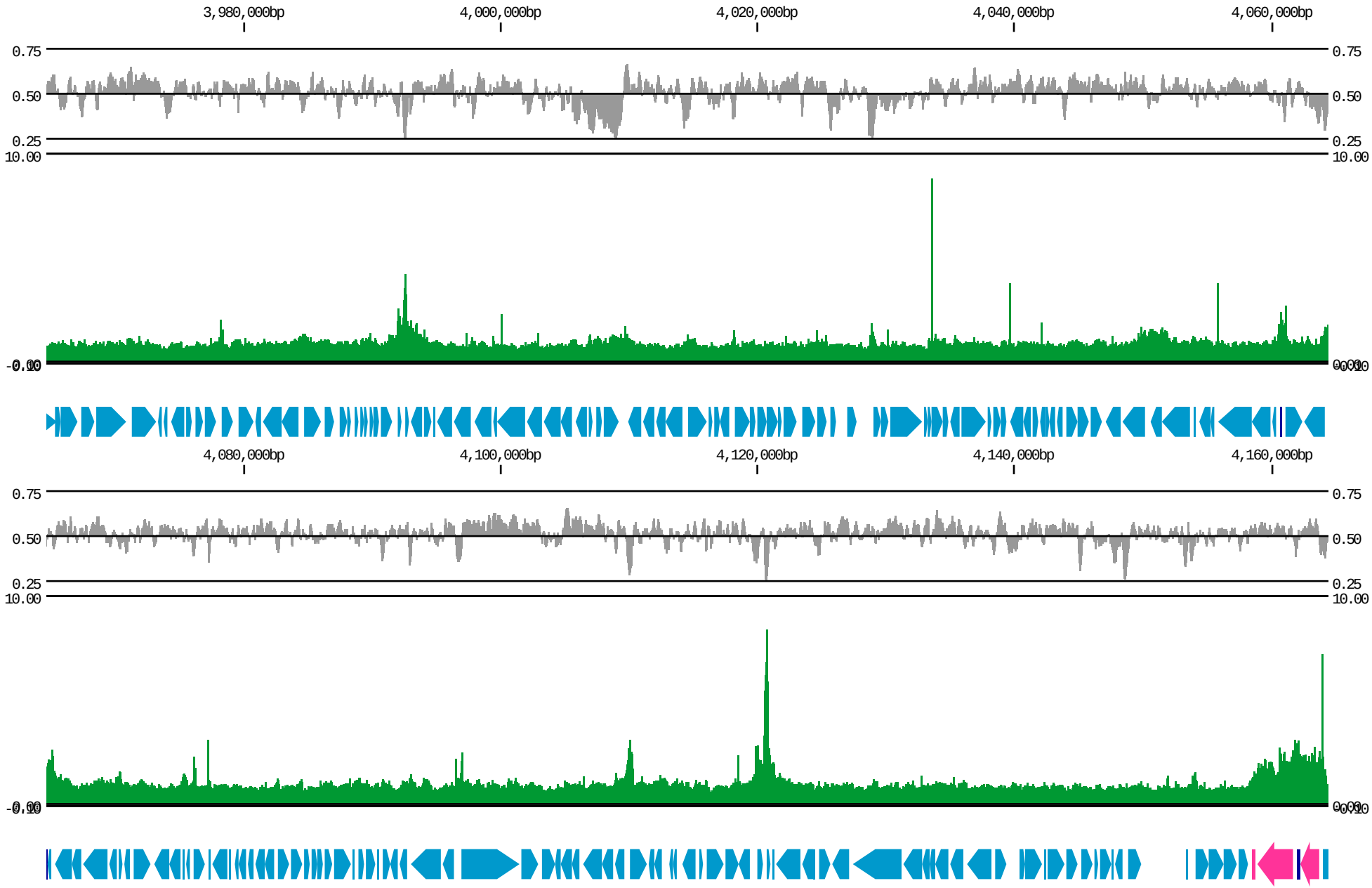
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Fig. S1 (cont.)

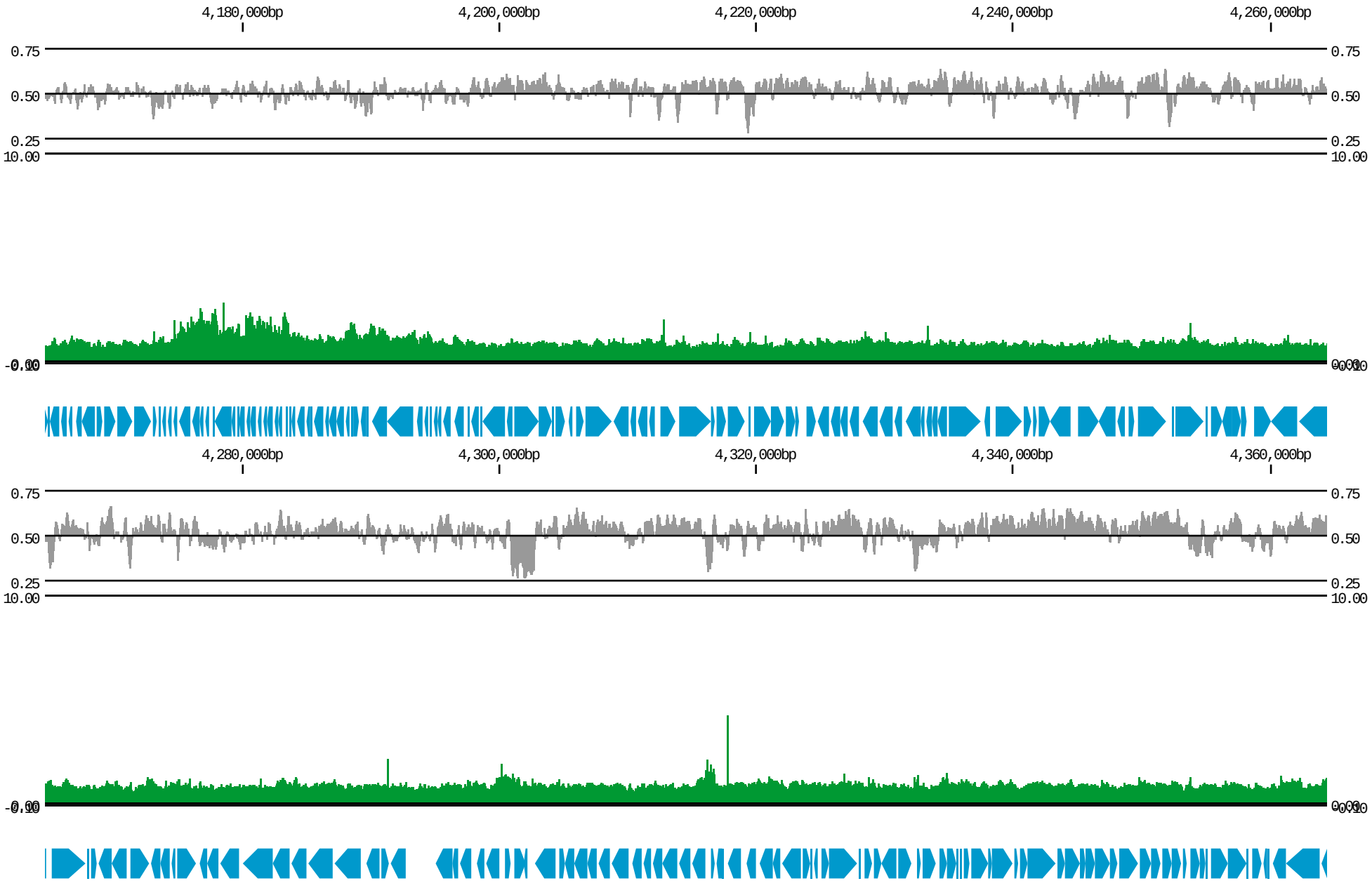
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Fig. S1 (cont.)

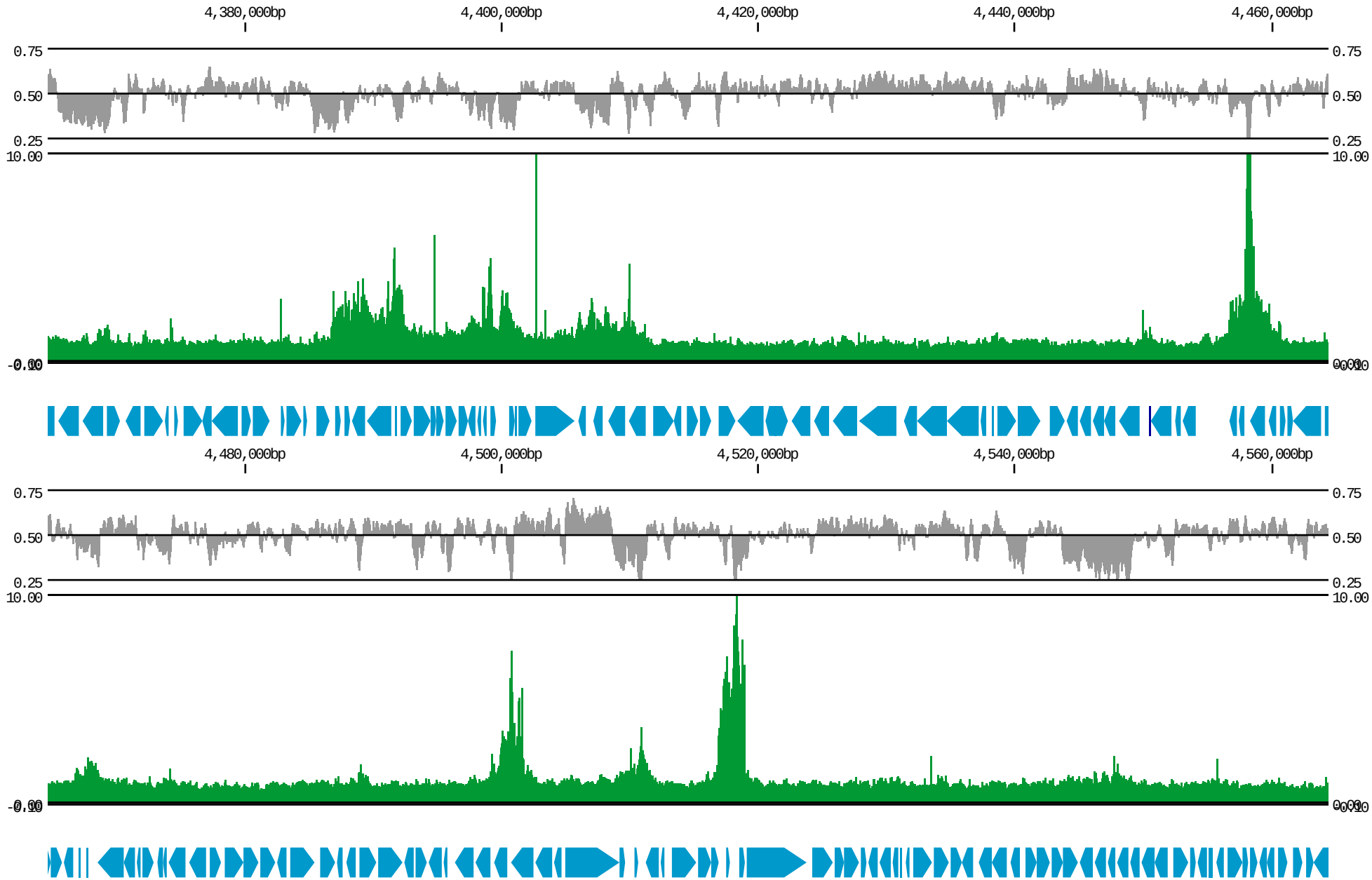
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Fig. S1 (cont.)

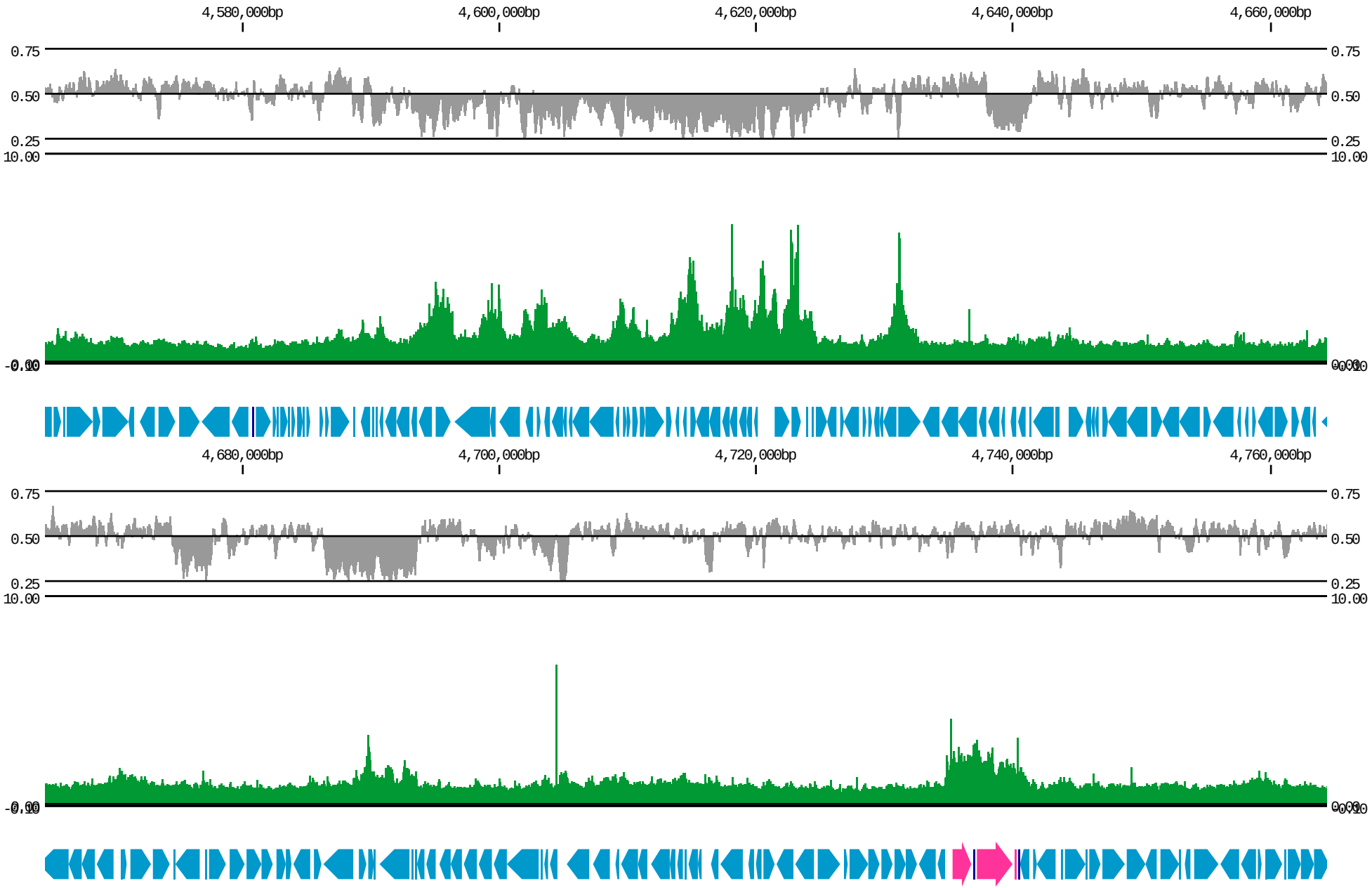
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Fig. S1 (cont.)

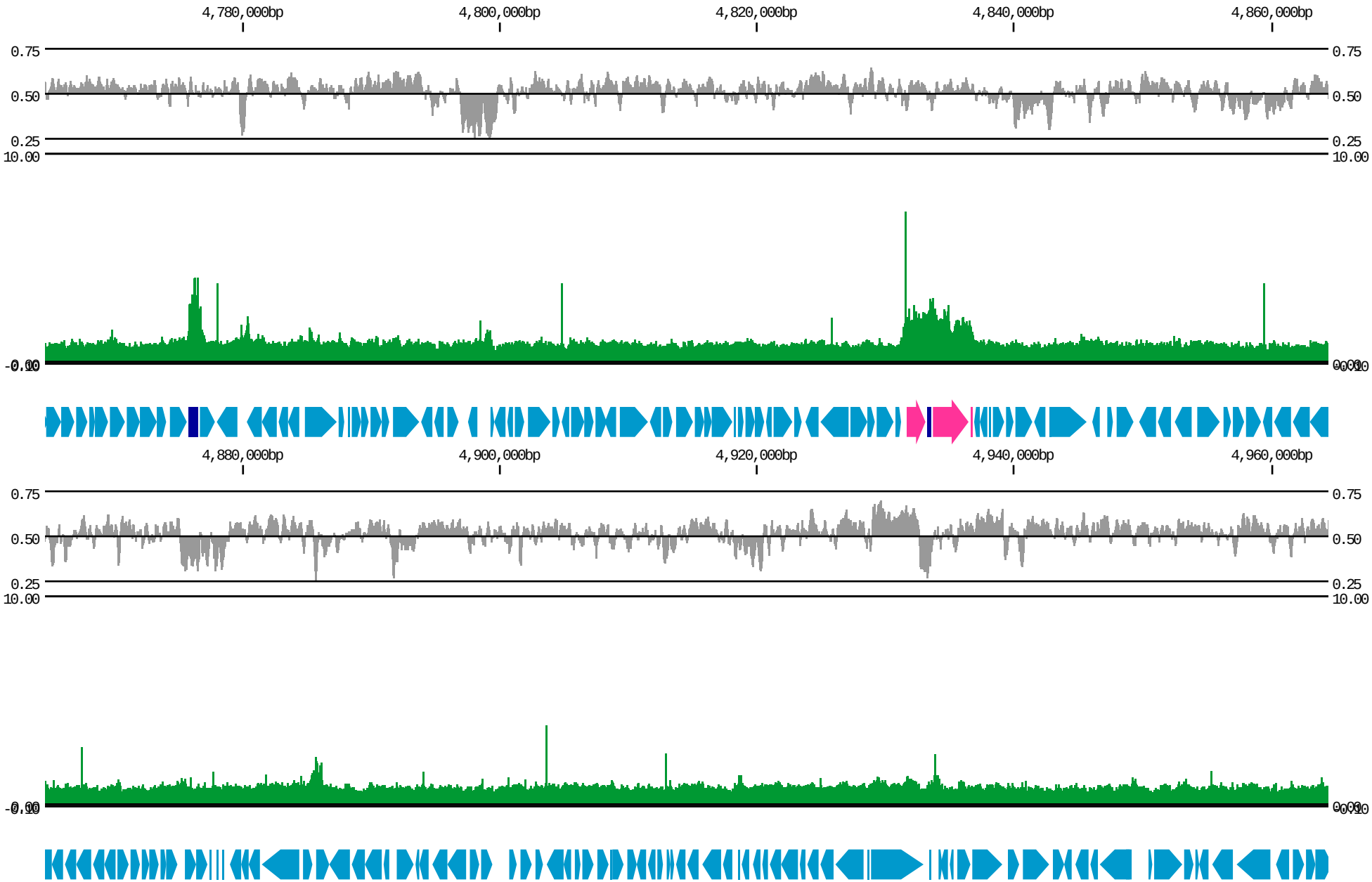
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Fig. S1 (cont.)

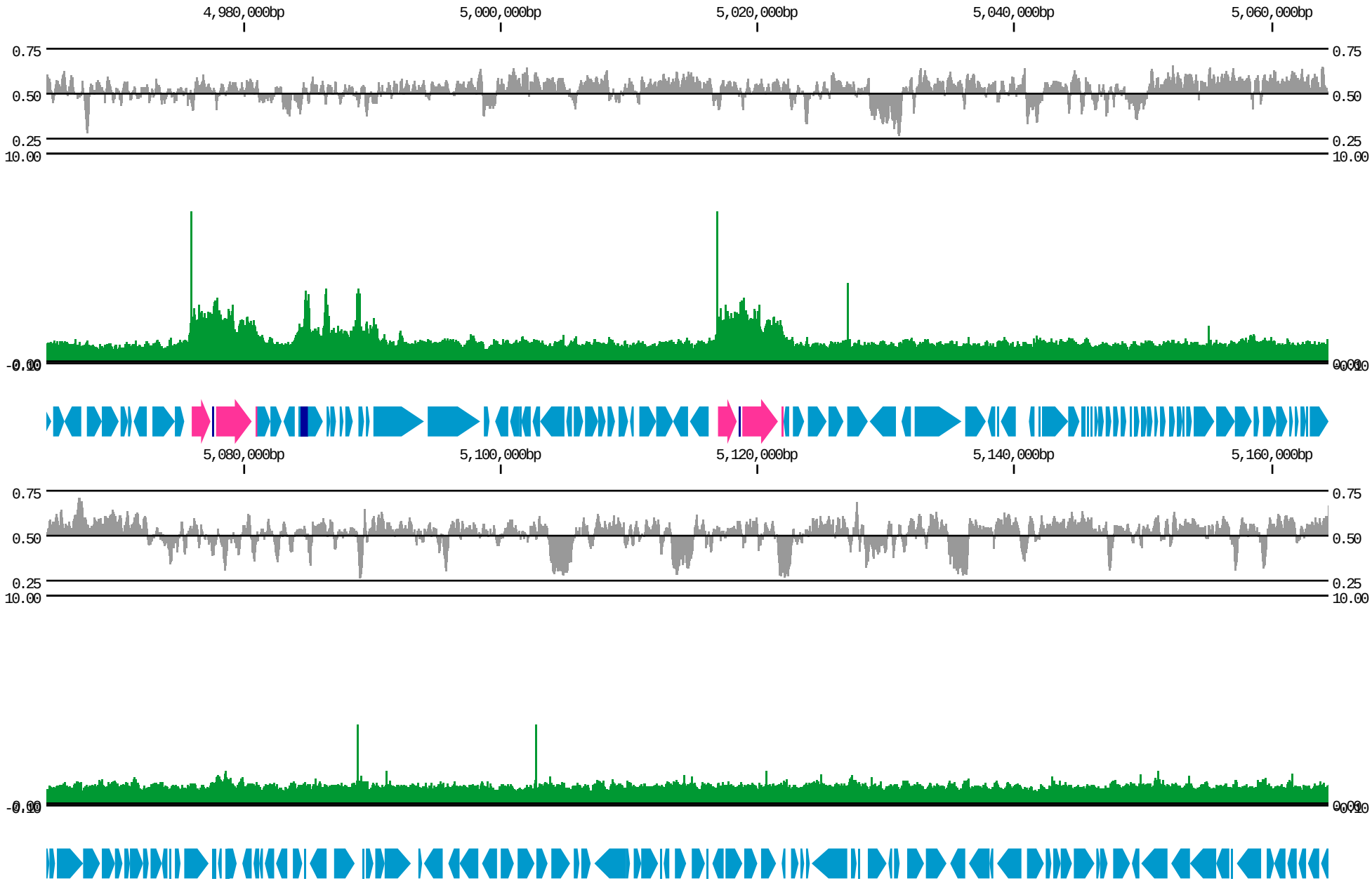
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Fig. S1 (cont.)

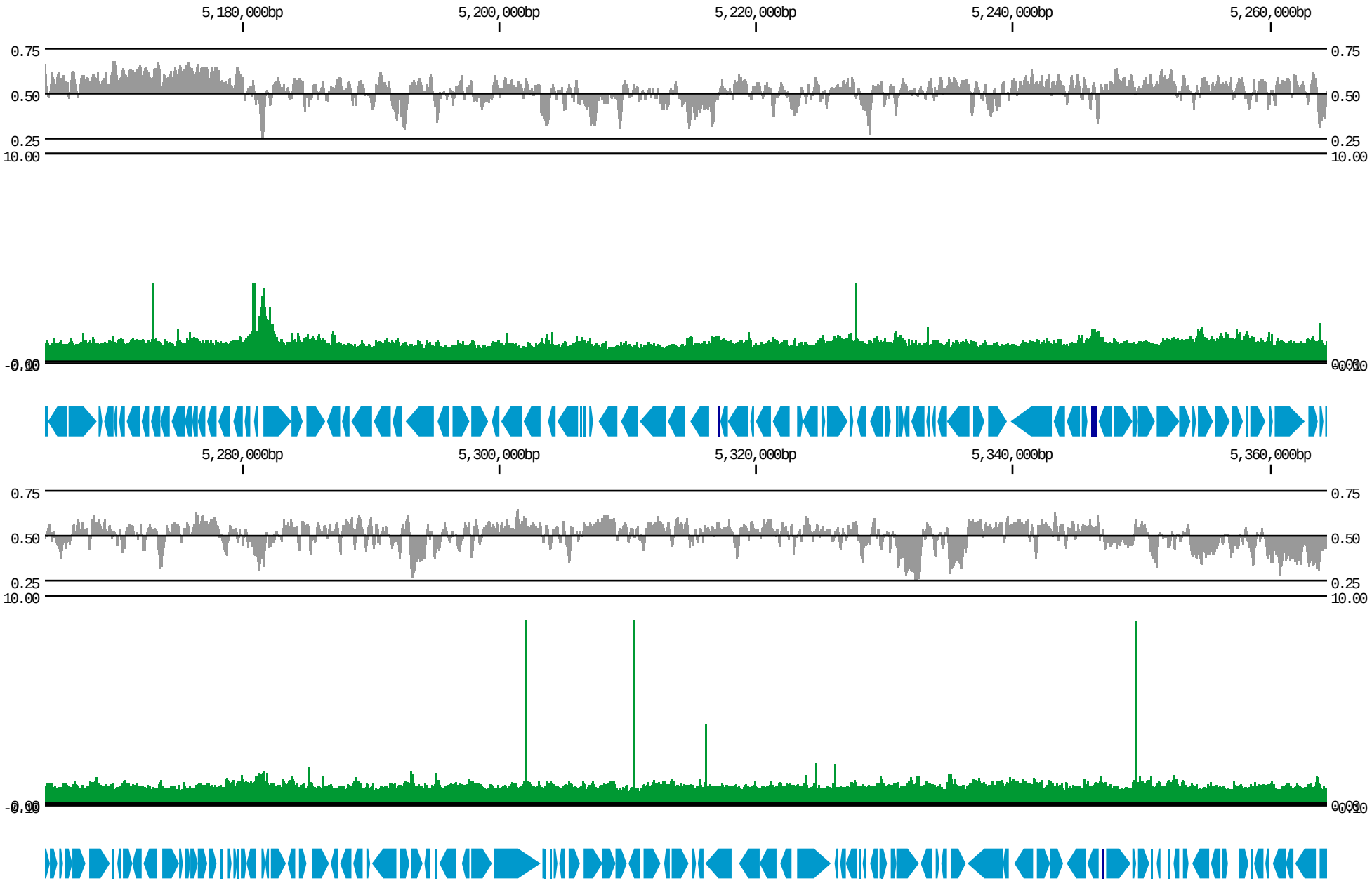
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Fig. S1 (cont.)

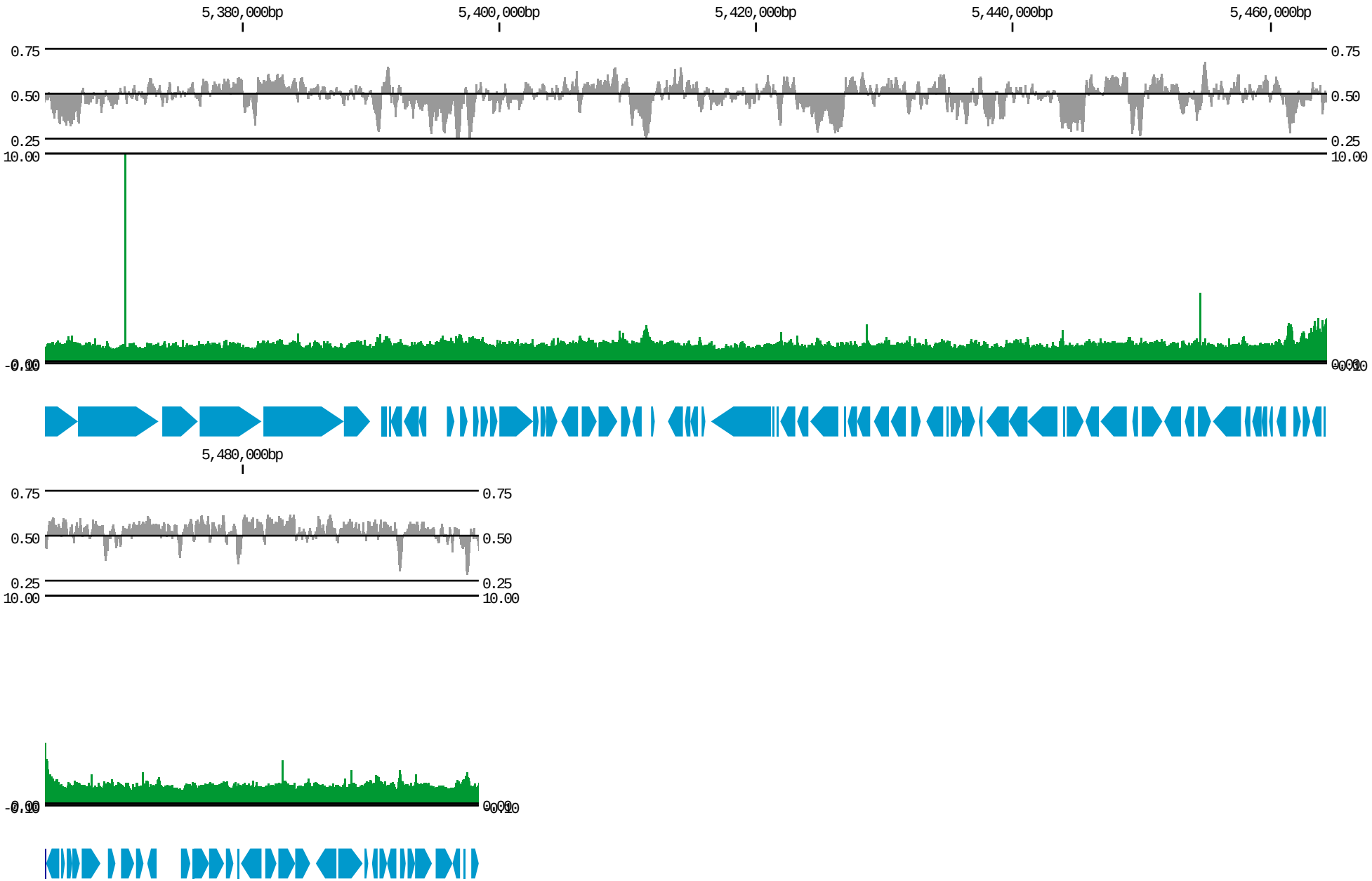
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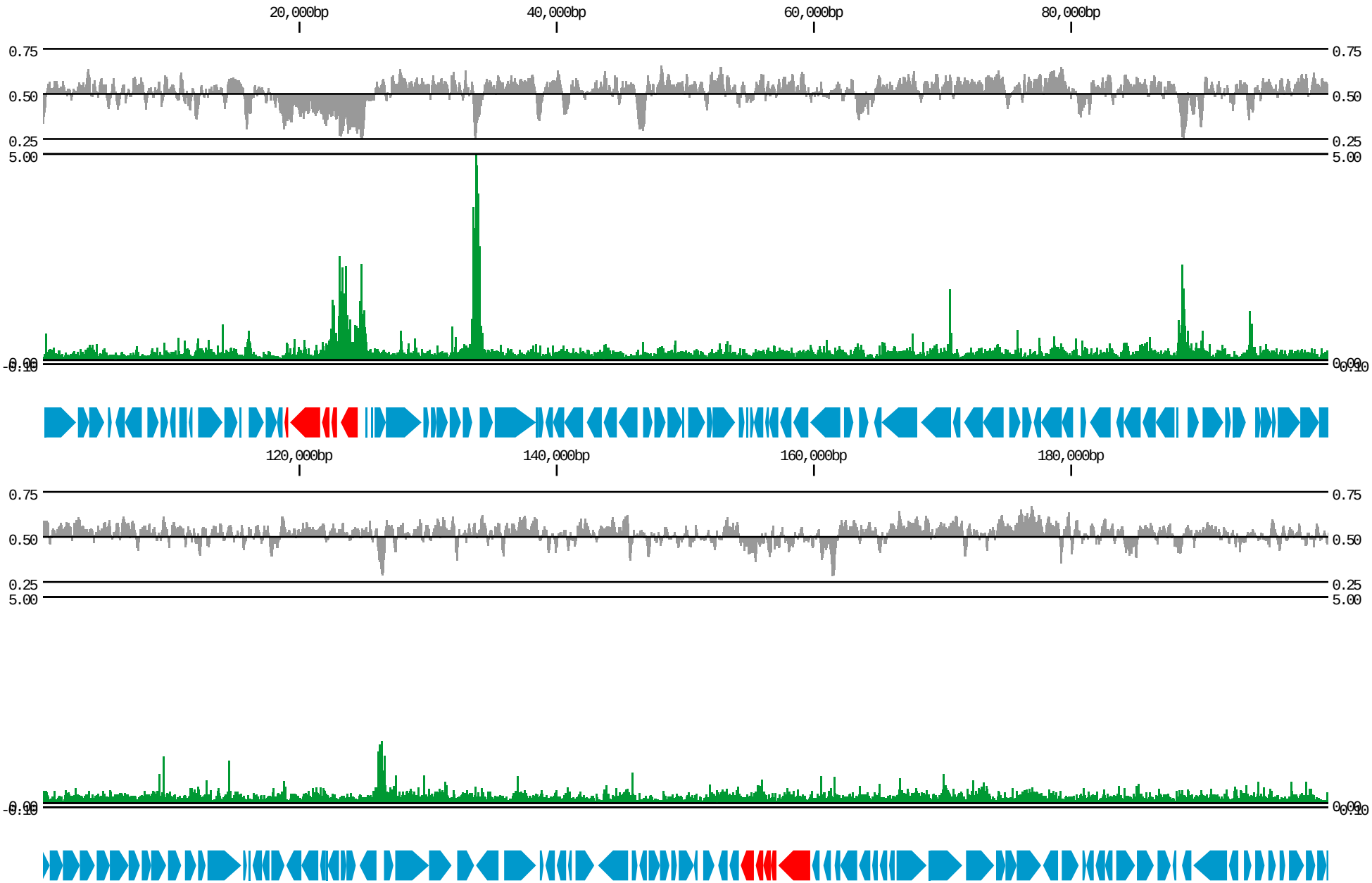
Fig. S2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60,000bp
80,000bp
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0.50
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5.00
0.00
-0.10
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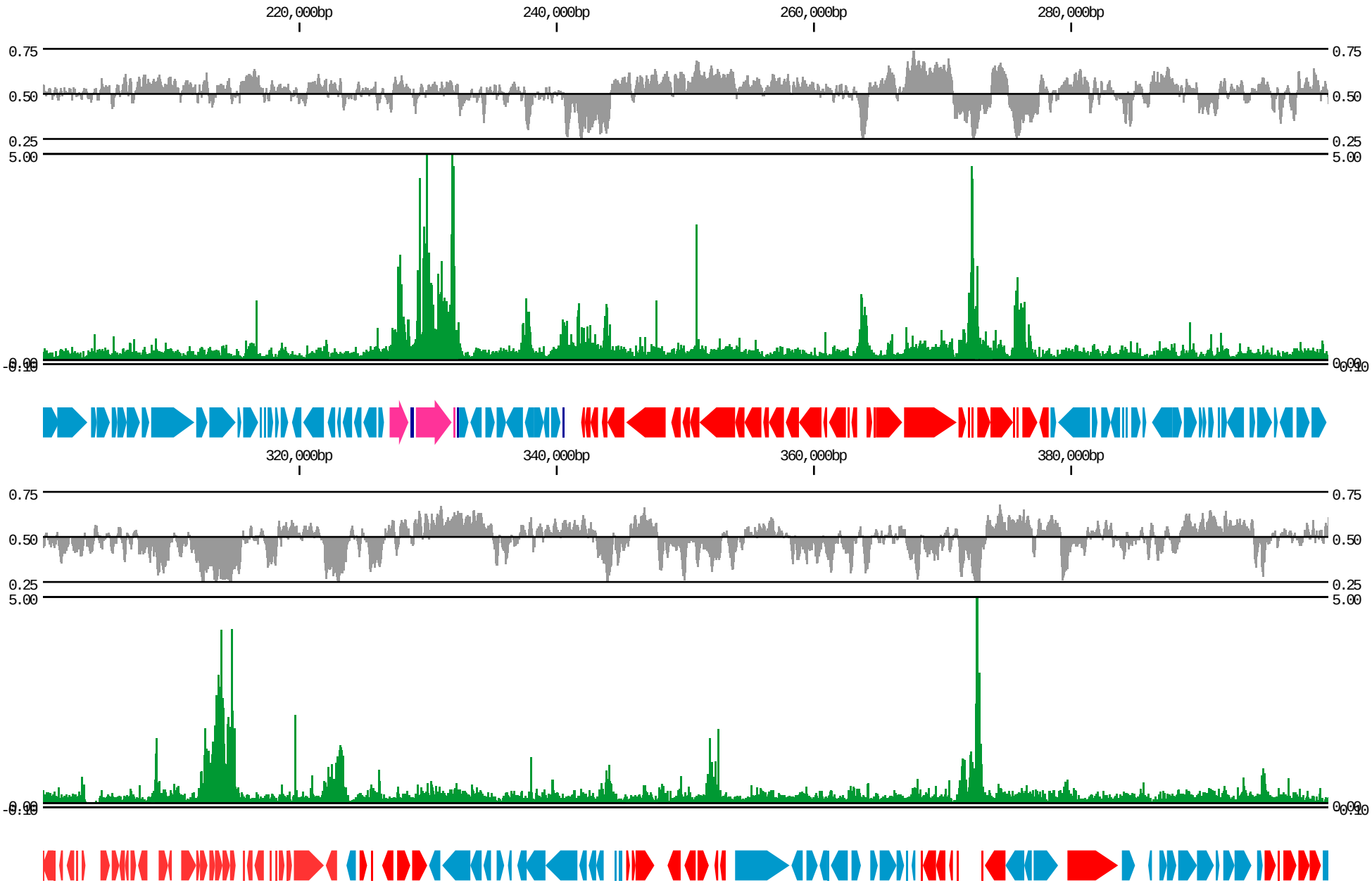
160,000bp
180,000bp

Fig. S2 (cont.)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0.25
5.00
0.00
0.10
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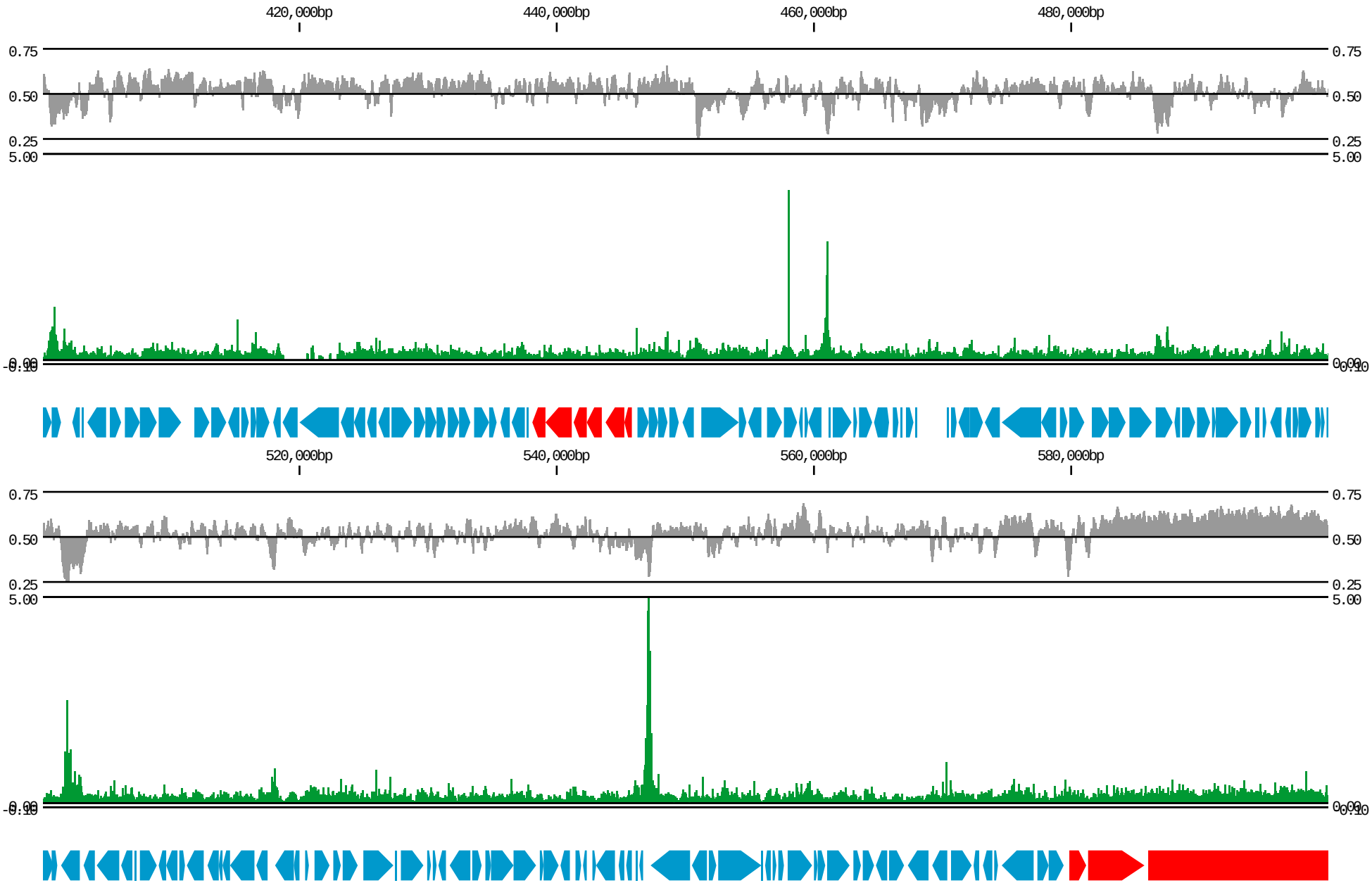
360,000bp
380,000bp

Fig. S2 (cont.)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5.00
0.00
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560,000bp
580,000bp

Fig. S2 (cont.)

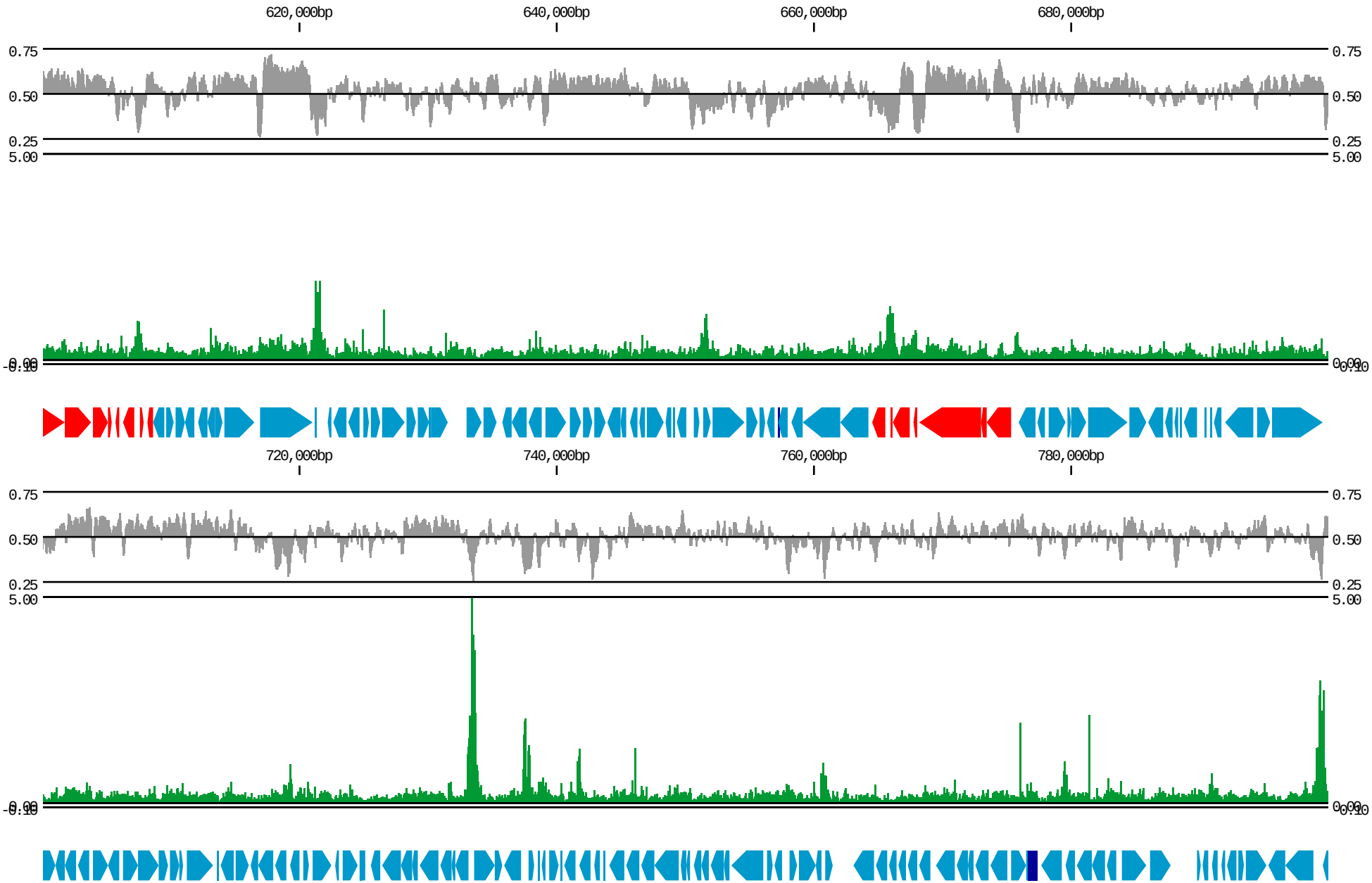
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Fig. S2 (cont.)

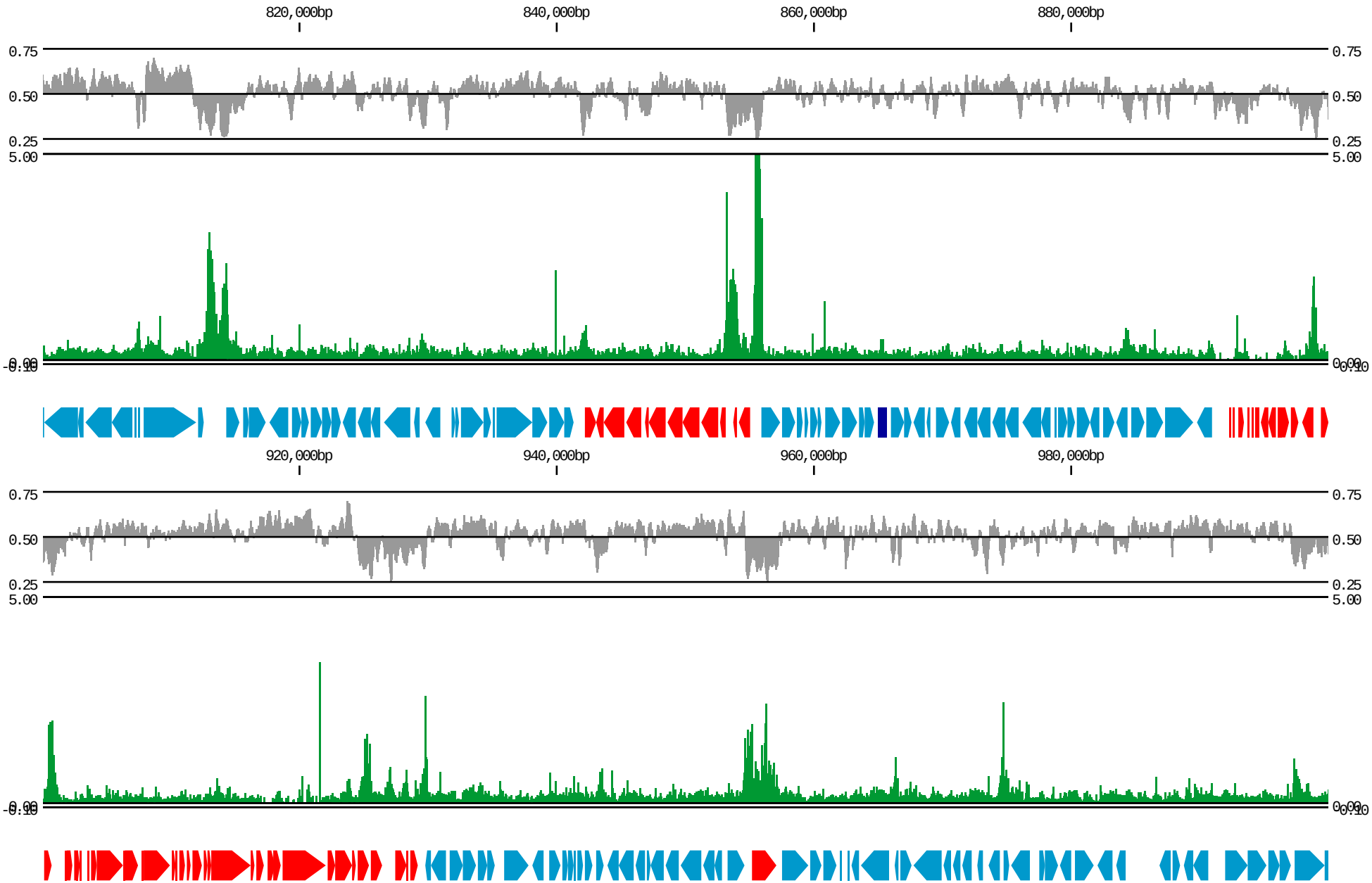
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Fig. S2 (cont.)

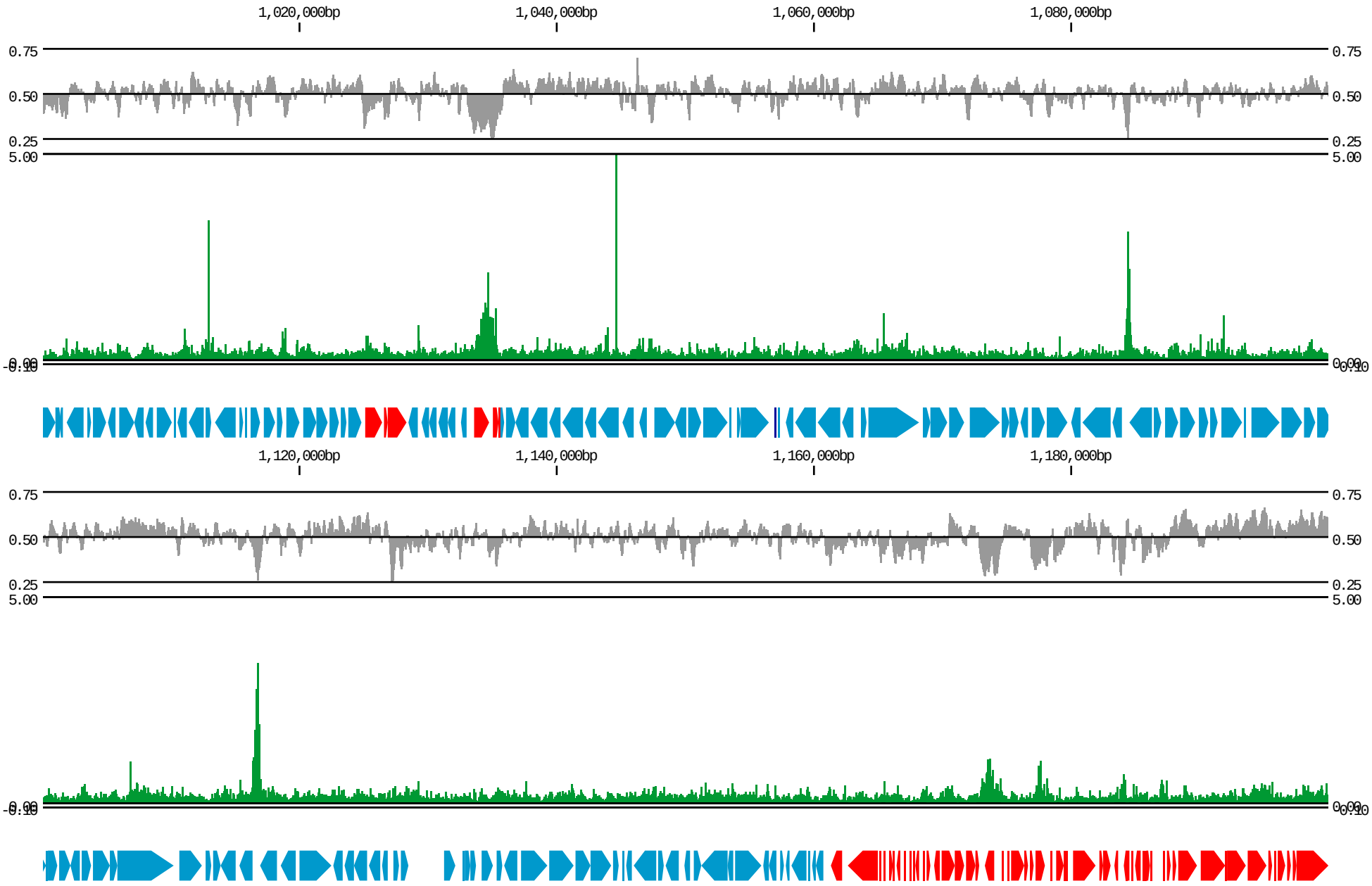
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Fig. S2 (cont.)

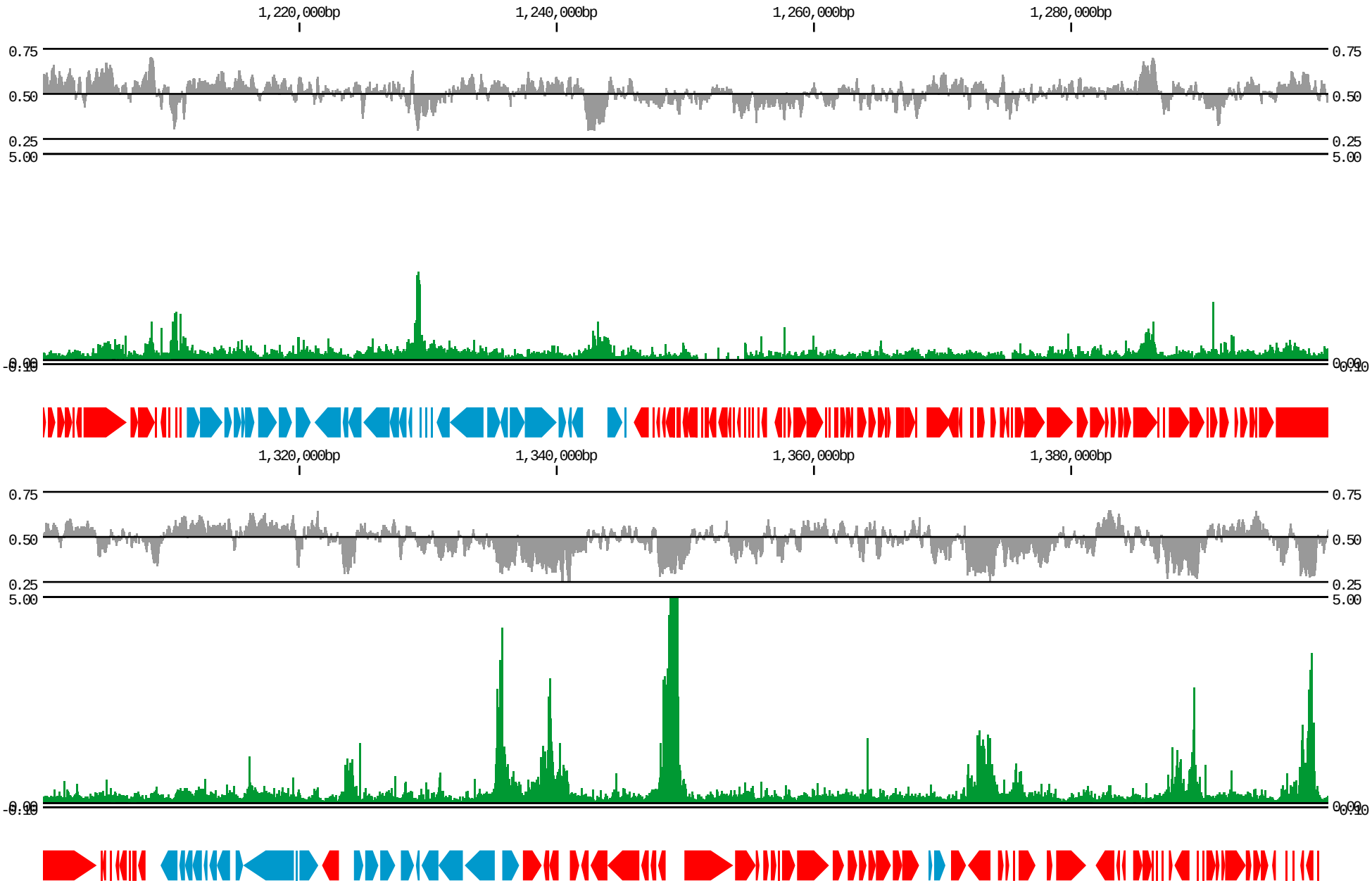
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Fig. S2 (cont.)

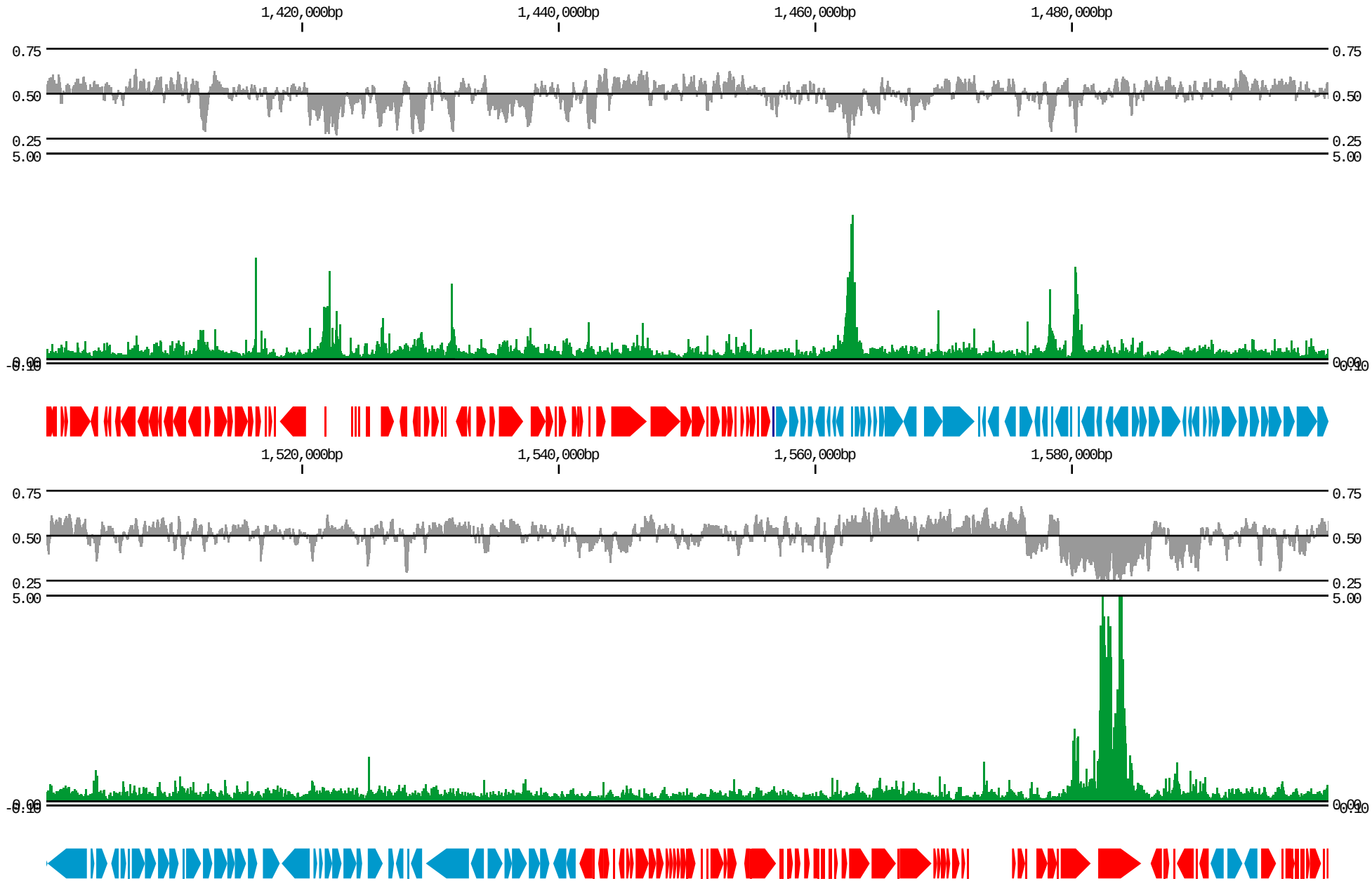
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Fig. S2 (cont.)

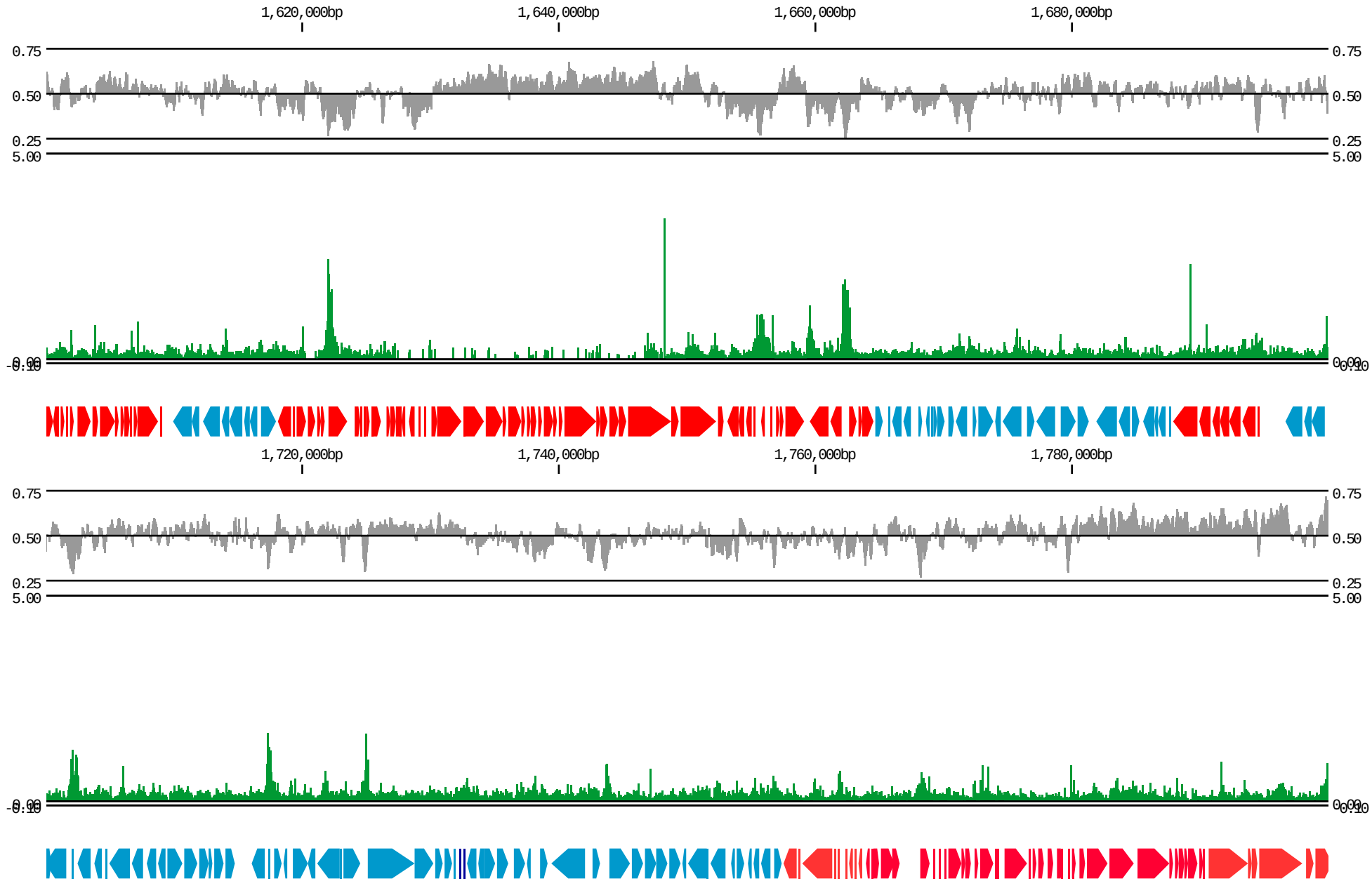
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Fig. S2 (cont.)

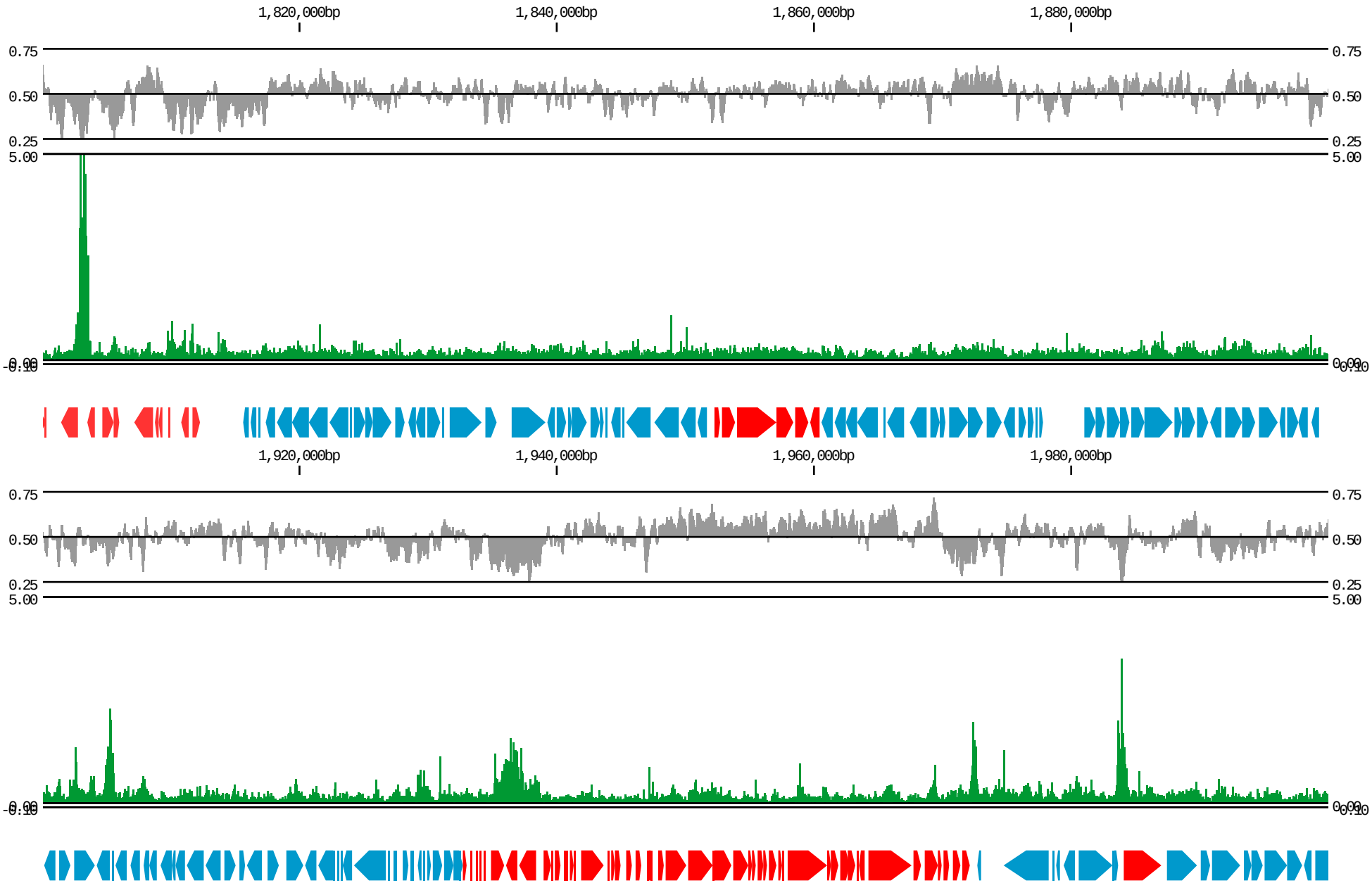
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Fig. S2 (cont.)

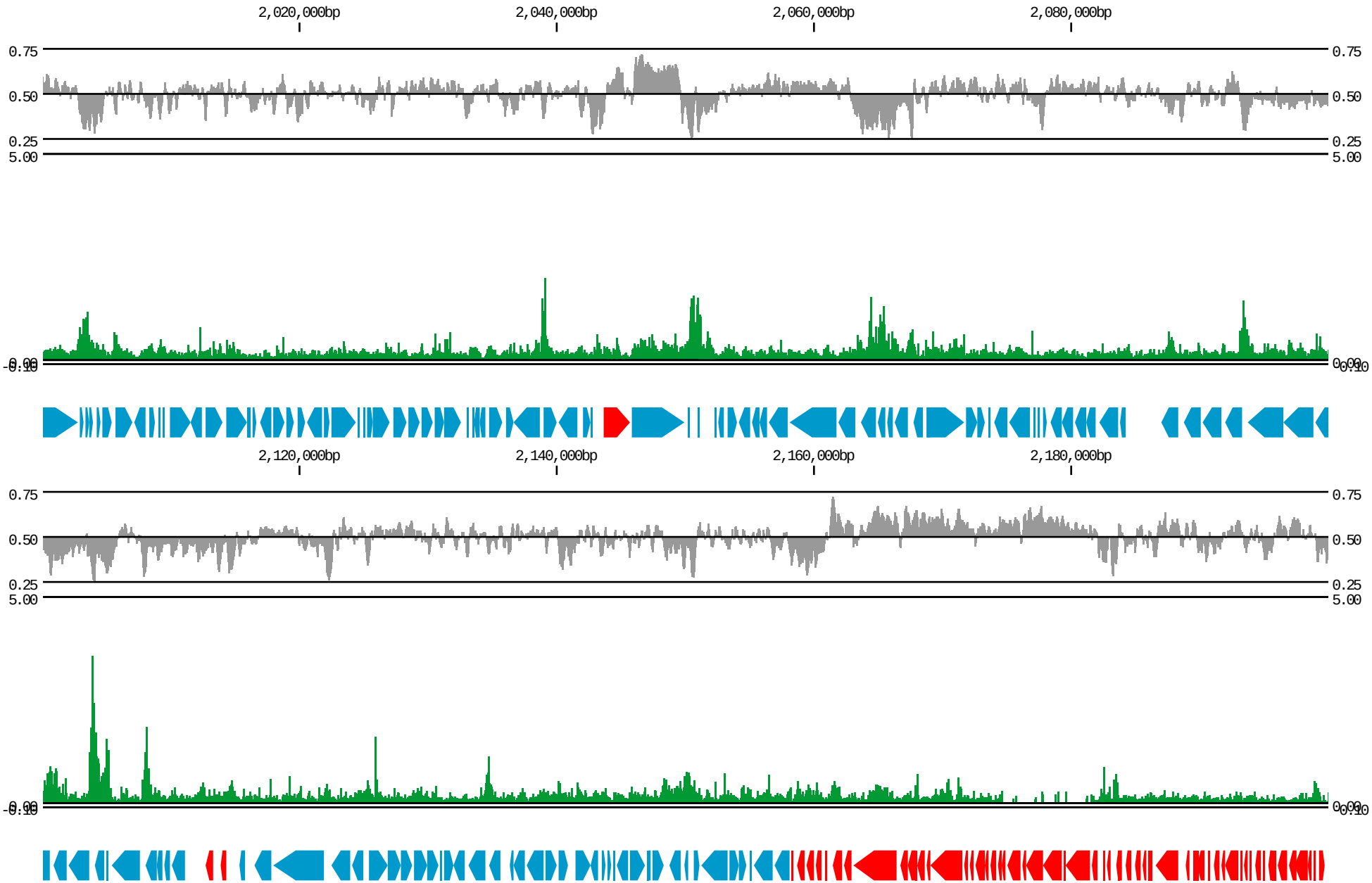
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Fig. S2 (cont.)

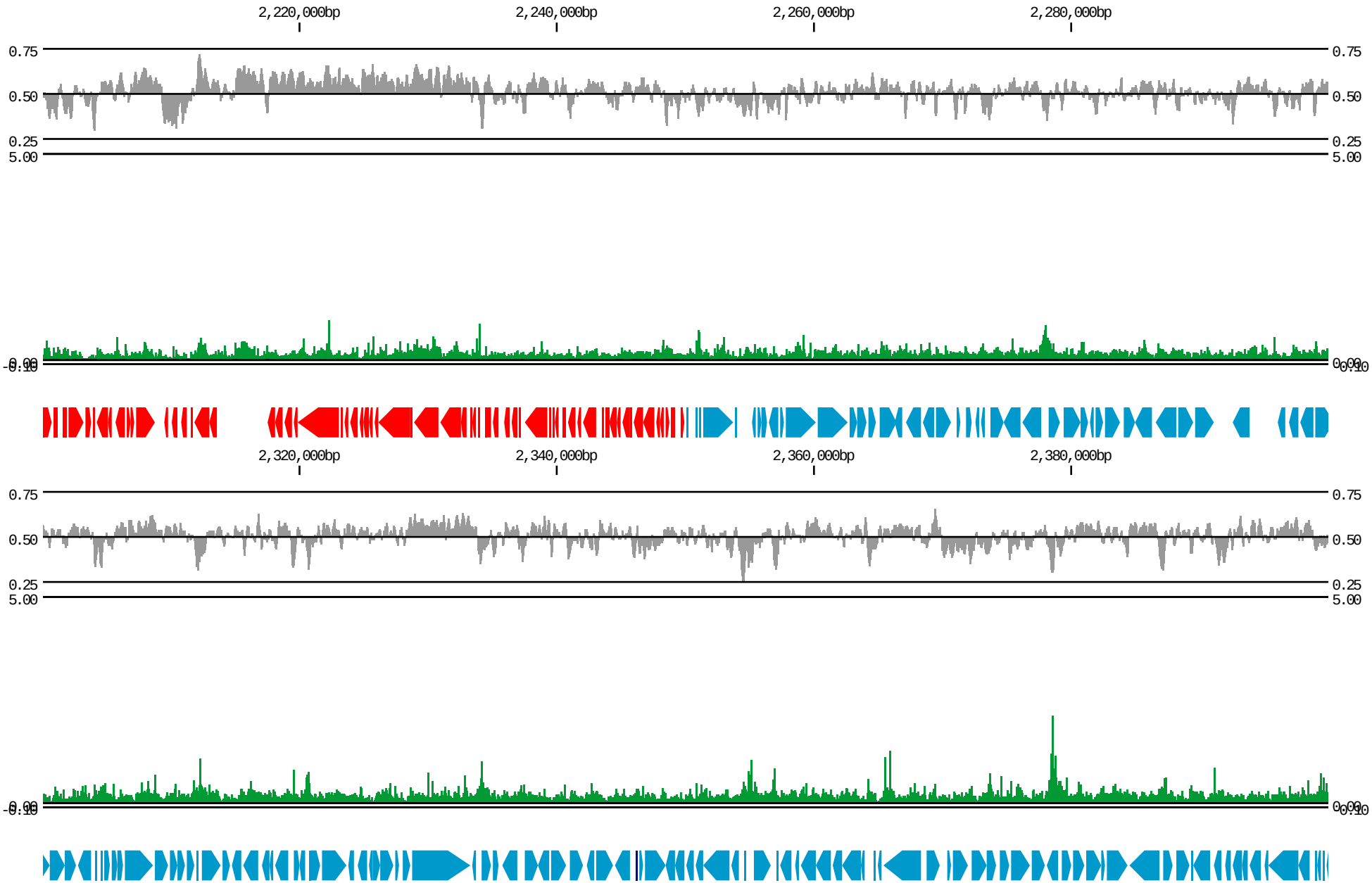
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Fig. S2 (cont.)

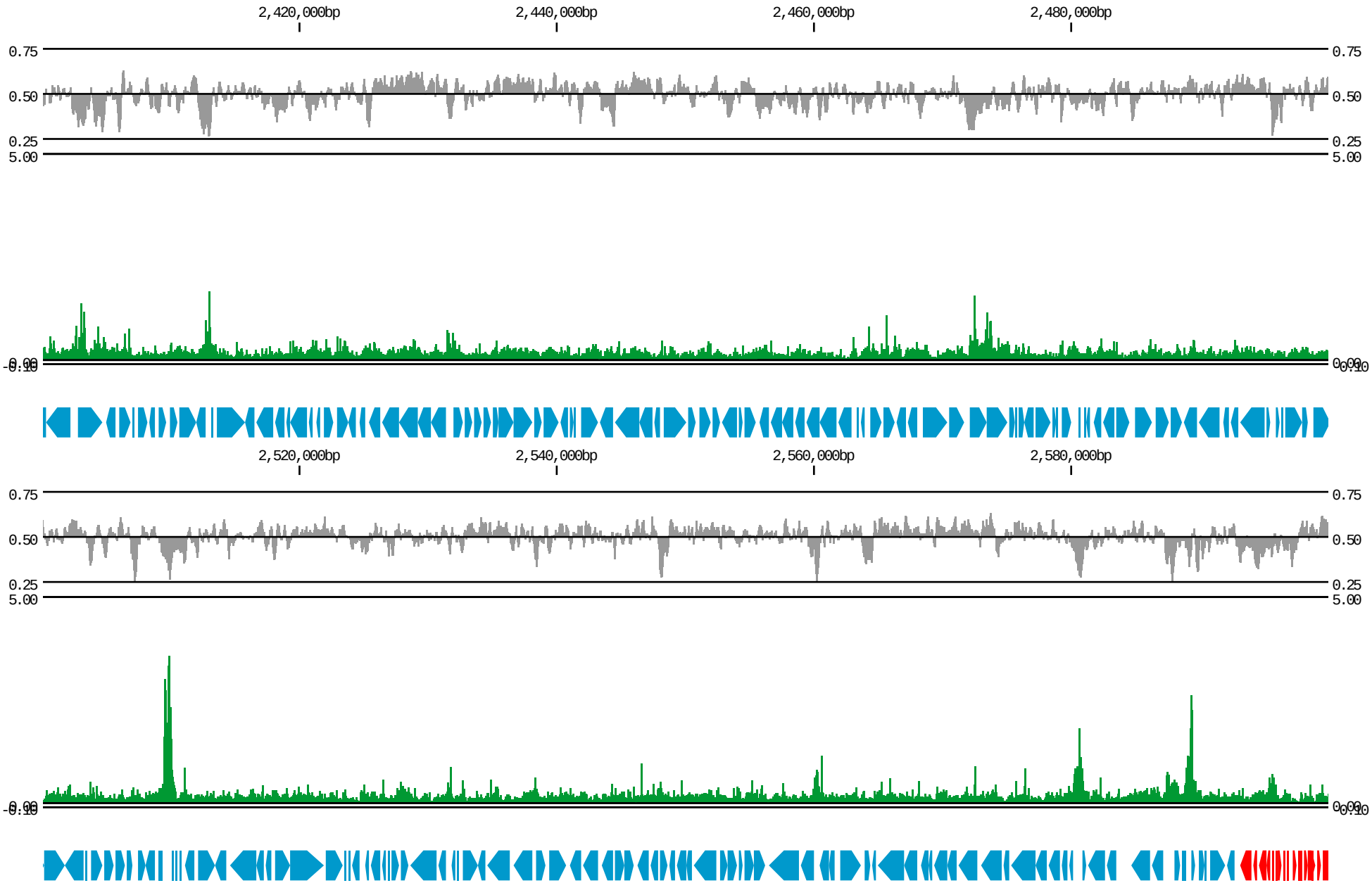
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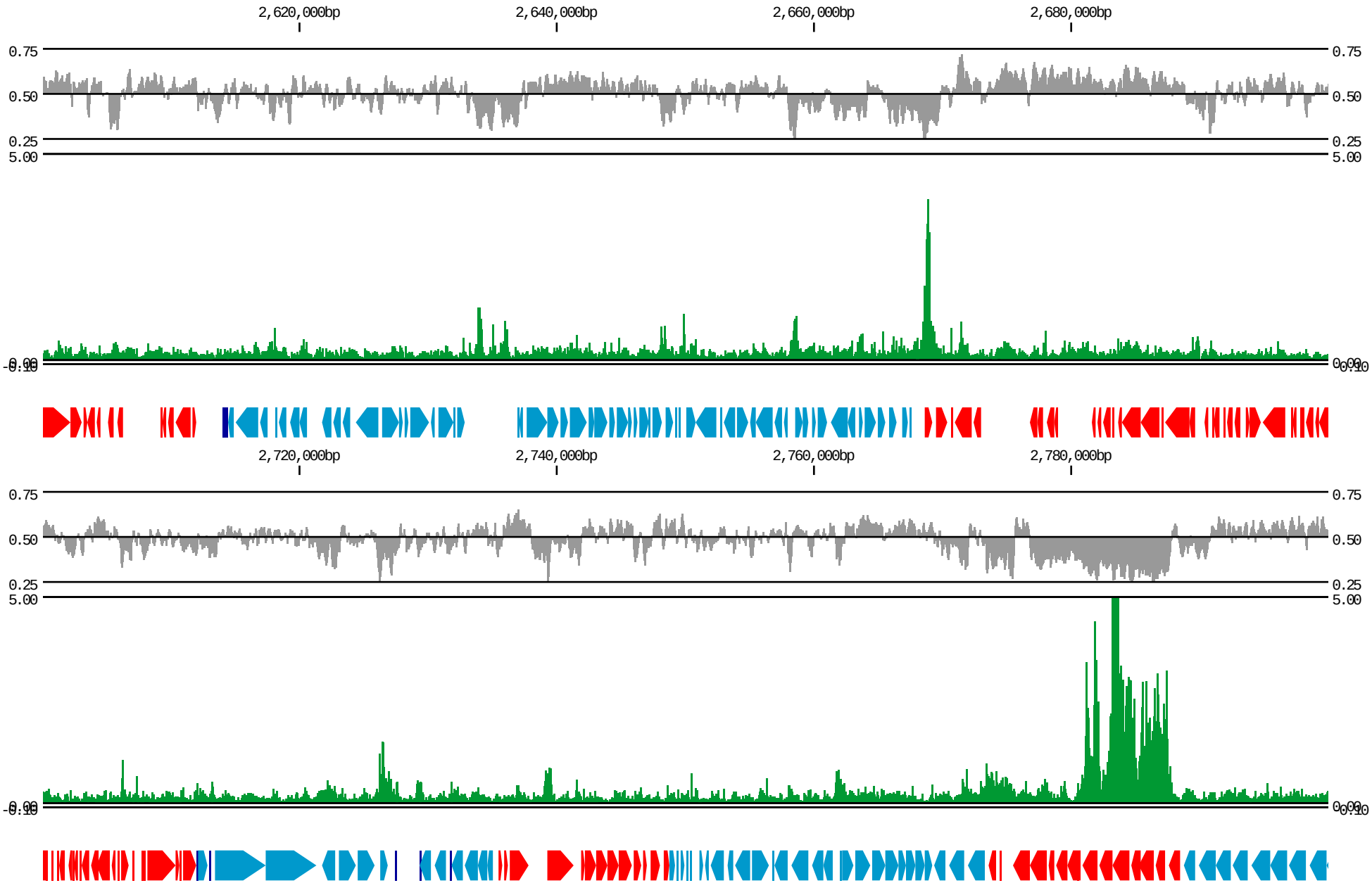
Fig. S2 (cont.)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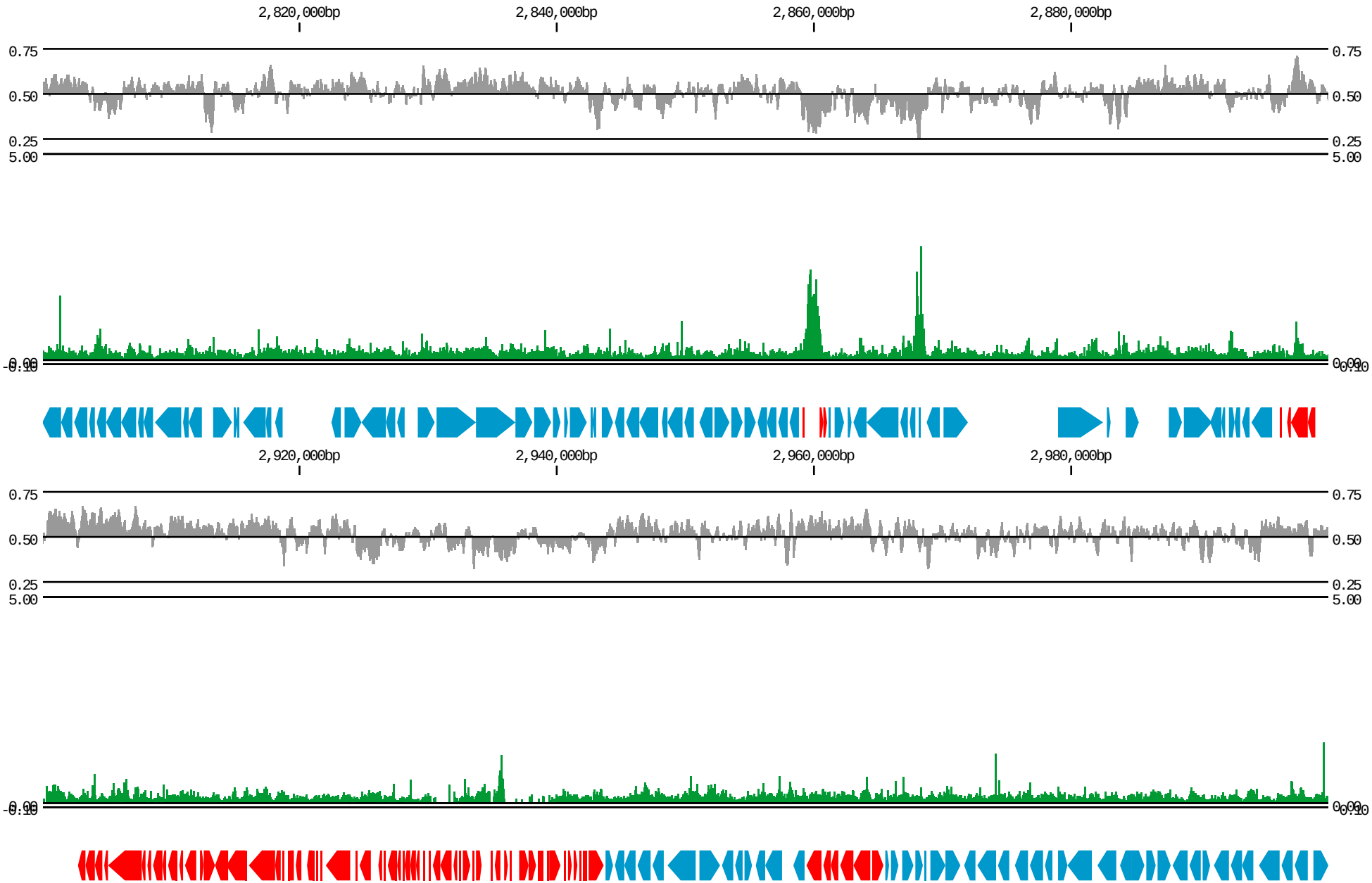
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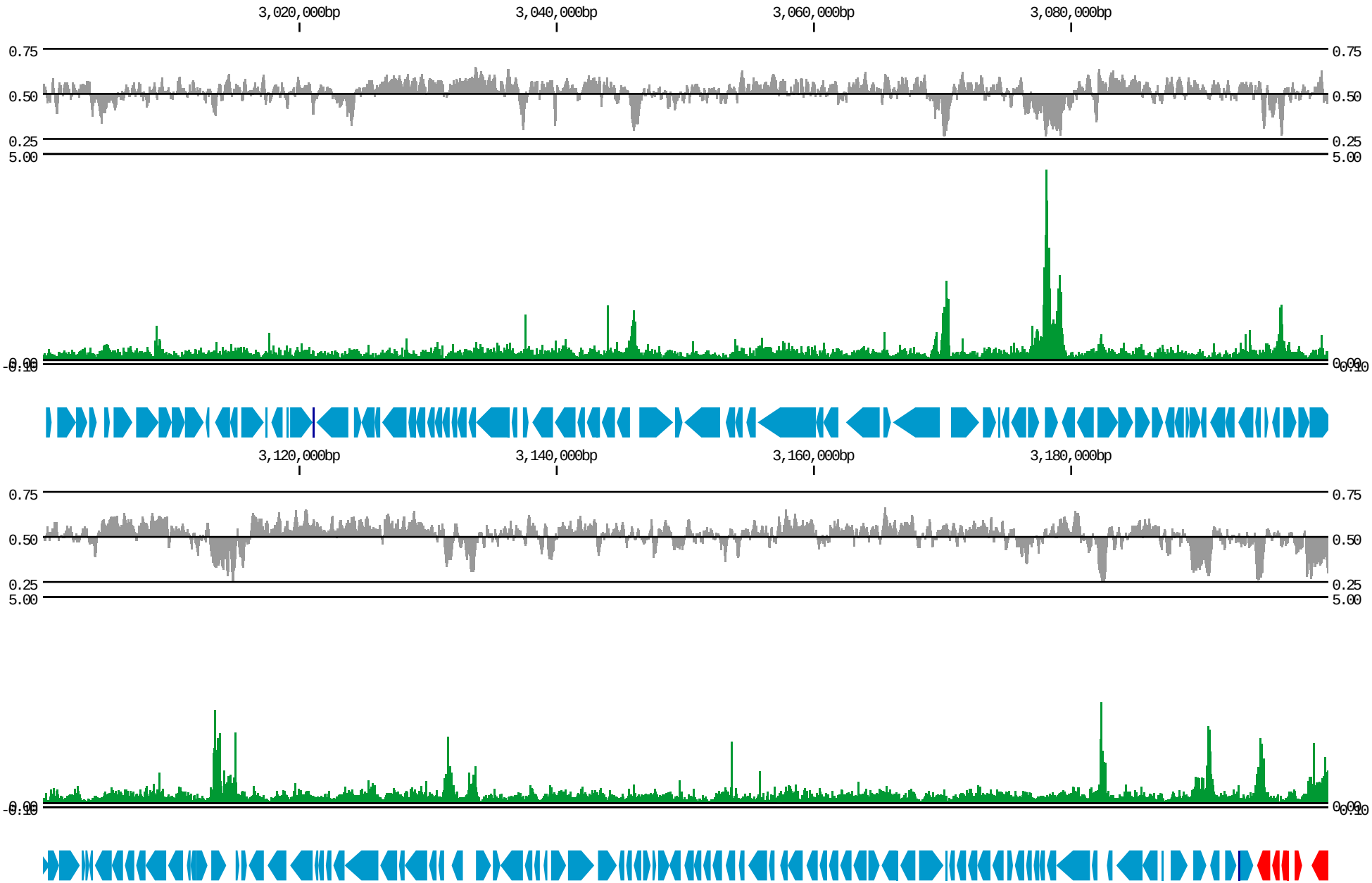
Fig. S2 (cont.)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3,040,000bp
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3,080,000bp
0.75
0.50
0.25
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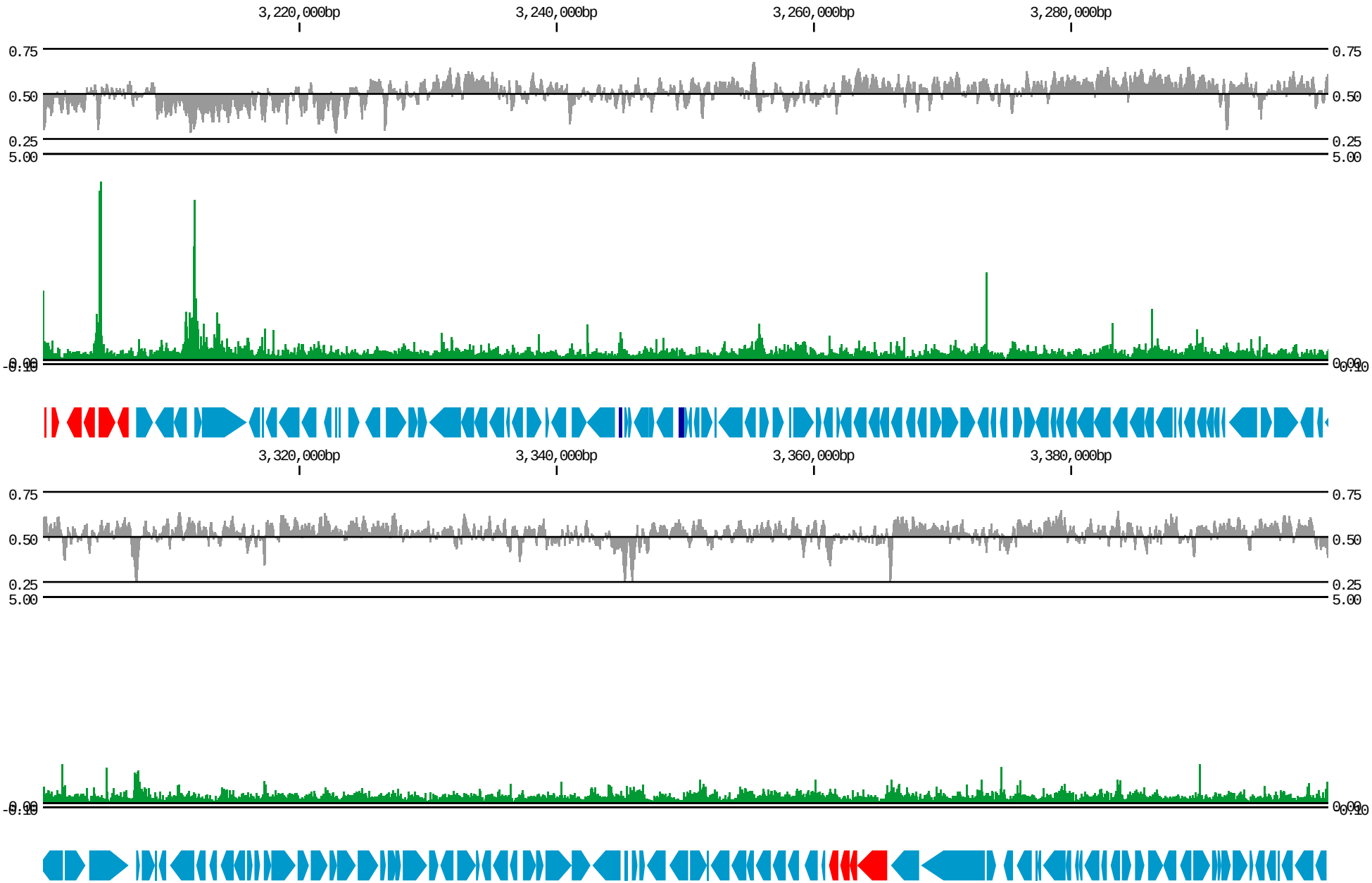
0.00
0.10
3,120,000bp
3,140,000bp
3,160,000bp
3,180,000bp

Fig. S2 (cont.)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0.75
0.50
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3,320,000bp
3,340,000bp
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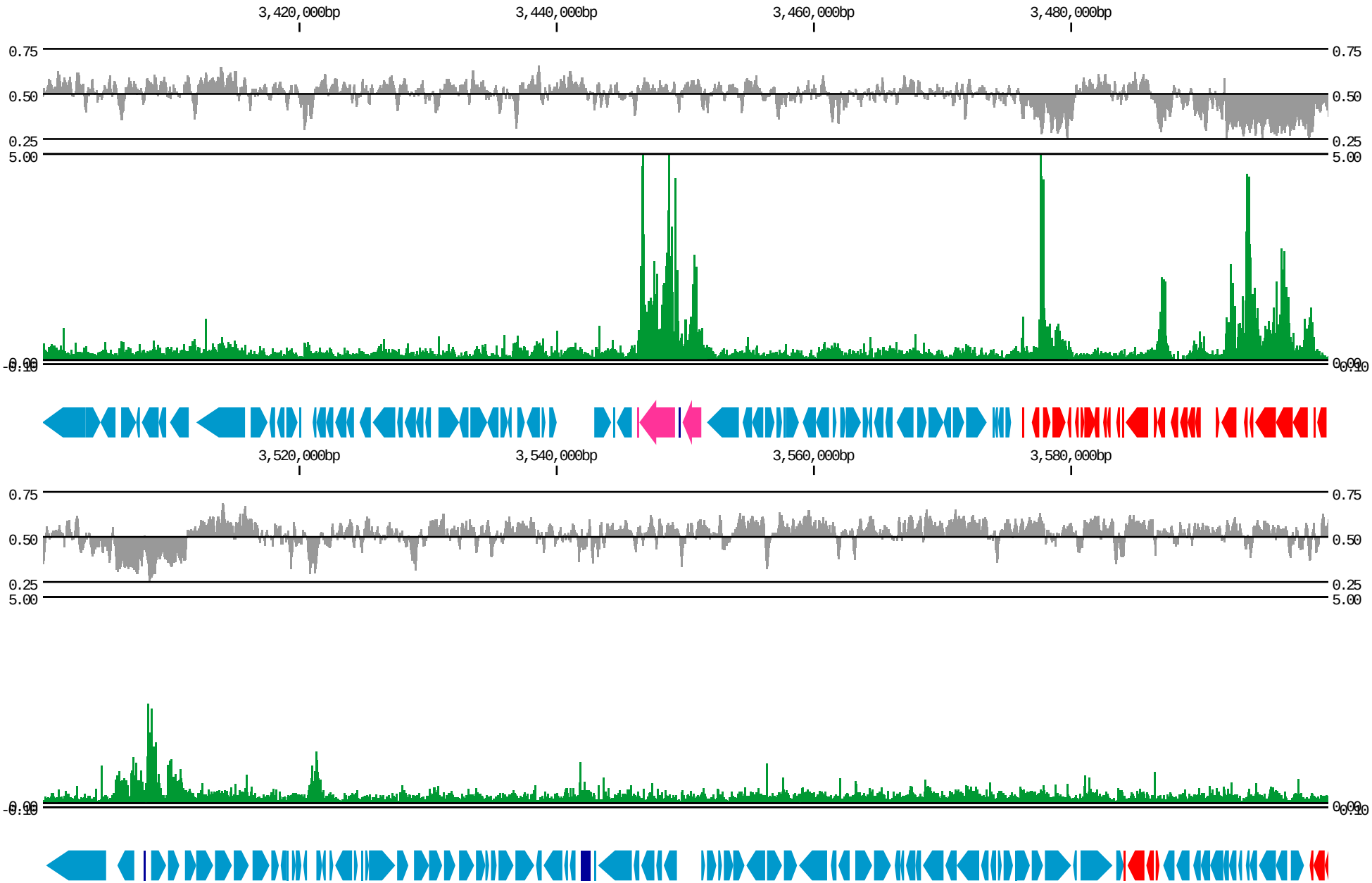
3,380,000bp

Fig. S2 (cont.)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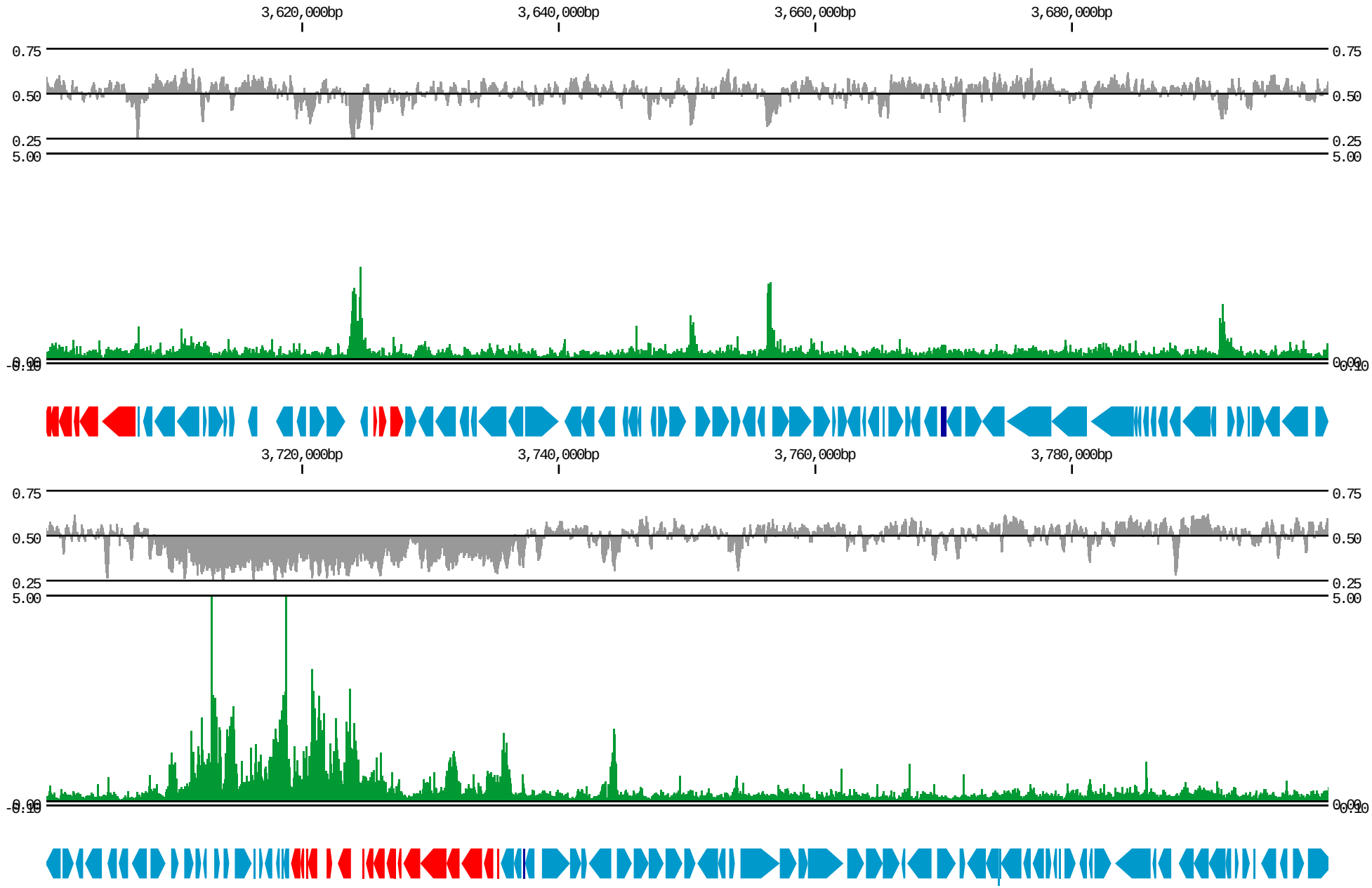
3,440,000bp
3,460,000bp
3,480,000bp
0.75
0.50
0.25
5.00
0.00
-0.10
3,520,000bp
3,540,000bp
3,560,000bp
3,580,000bp

Fig. S2 (cont.)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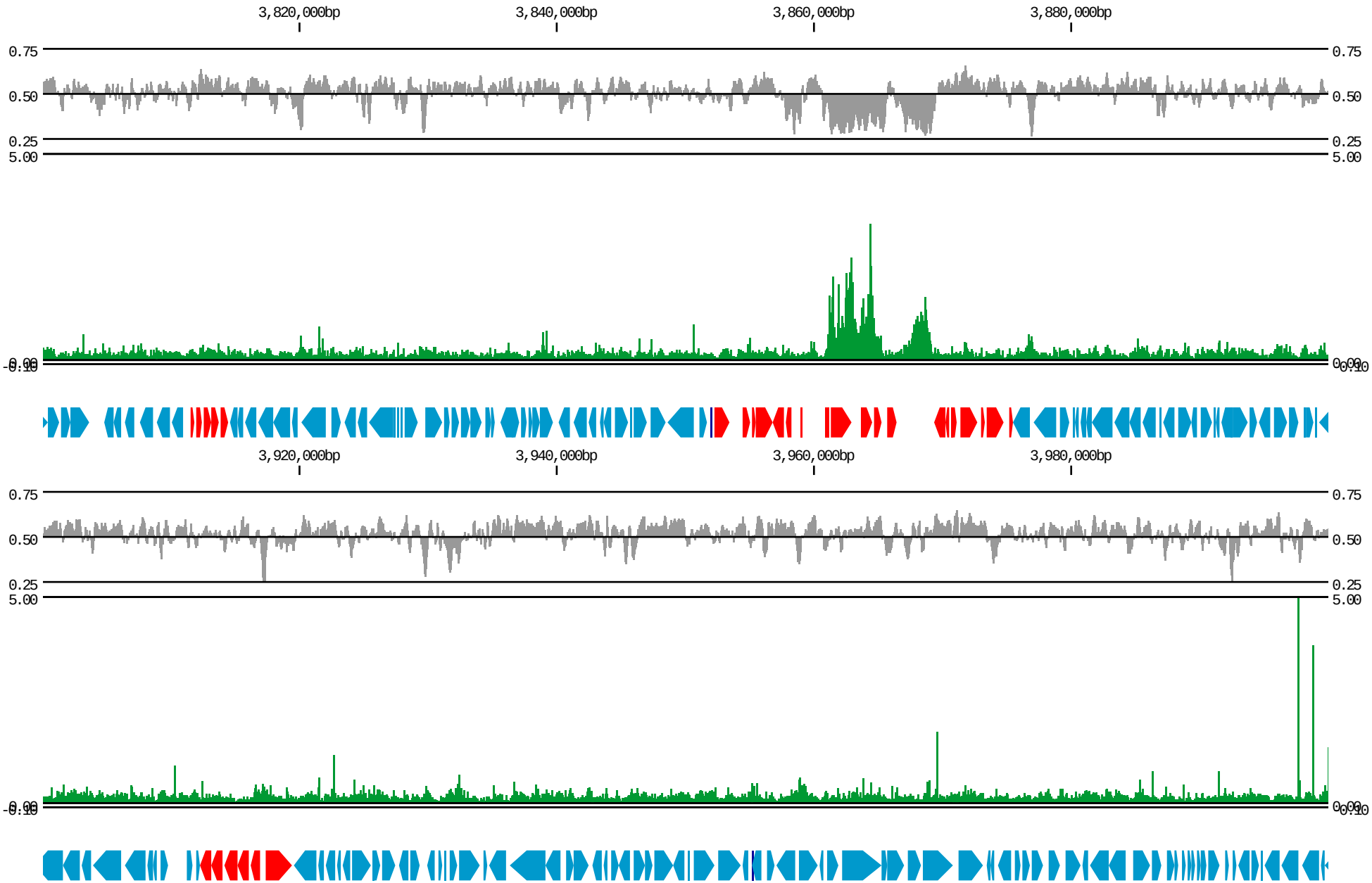
3,660,000bp
3,680,000bp
0.75
0.50
0.25
5.00
0.00
0.10
3,720,000bp
3,740,000bp
3,760,000bp
3,780,000bp

Fig. S2 (cont.)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3,860,000bp
3,880,000bp
0.75
0.50
0.25
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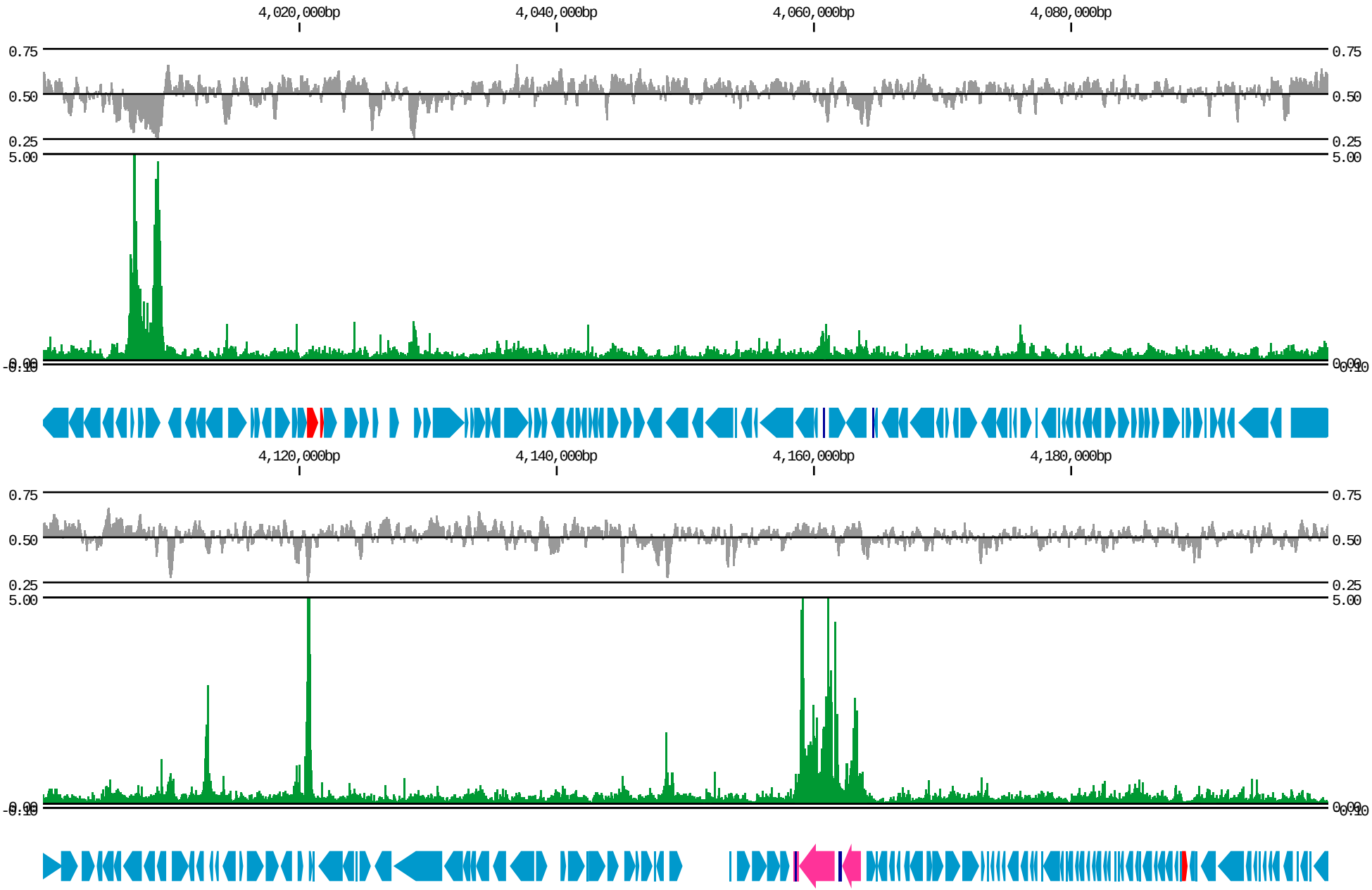
0.00
-0.10
3,920,000bp
3,940,000bp
3,960,000bp
3,980,000bp

Fig. S2 (cont.)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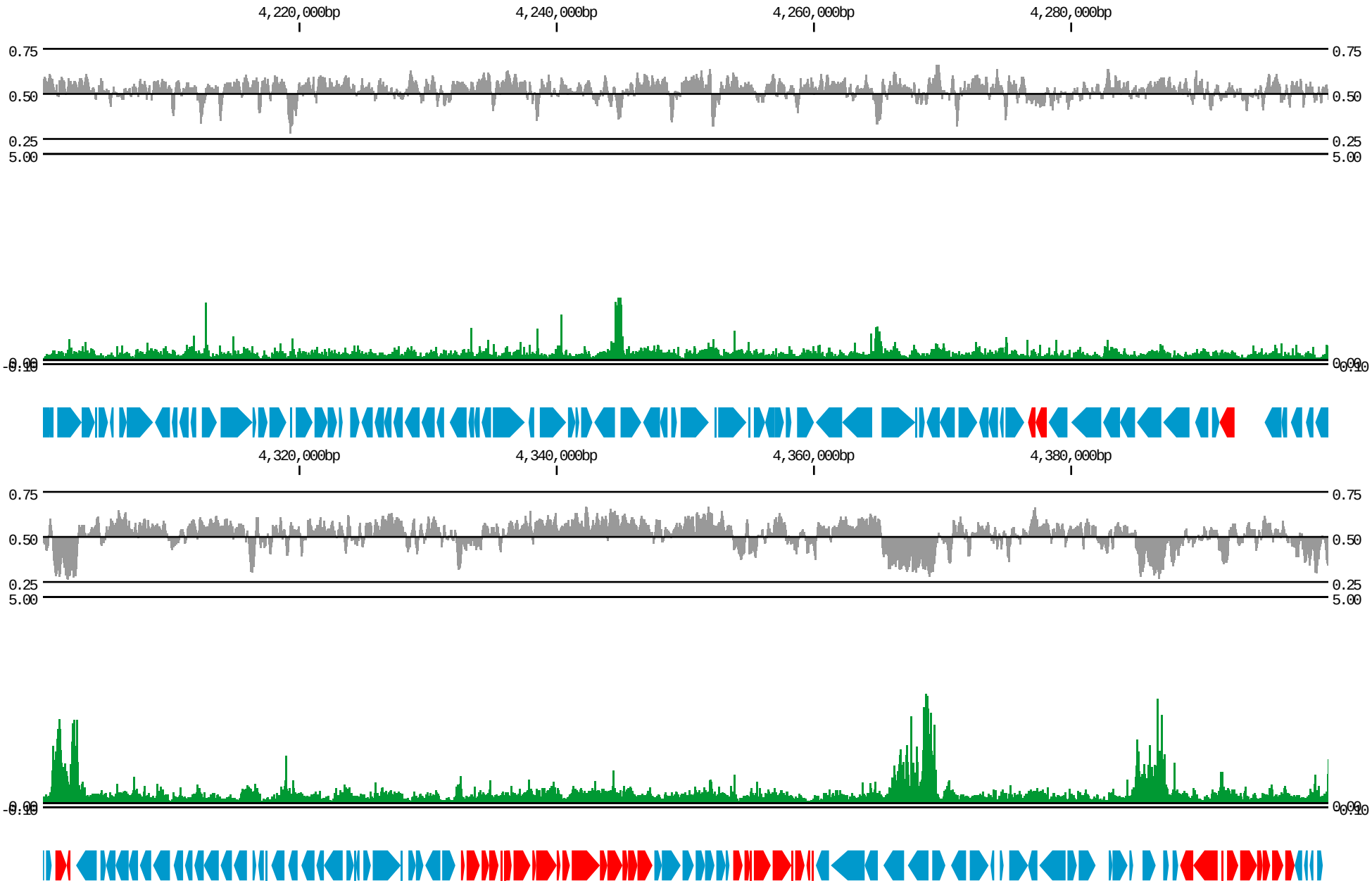
4,120,000bp
4,140,000bp
4,160,000bp
4,180,000bp

Fig. S2 (cont.)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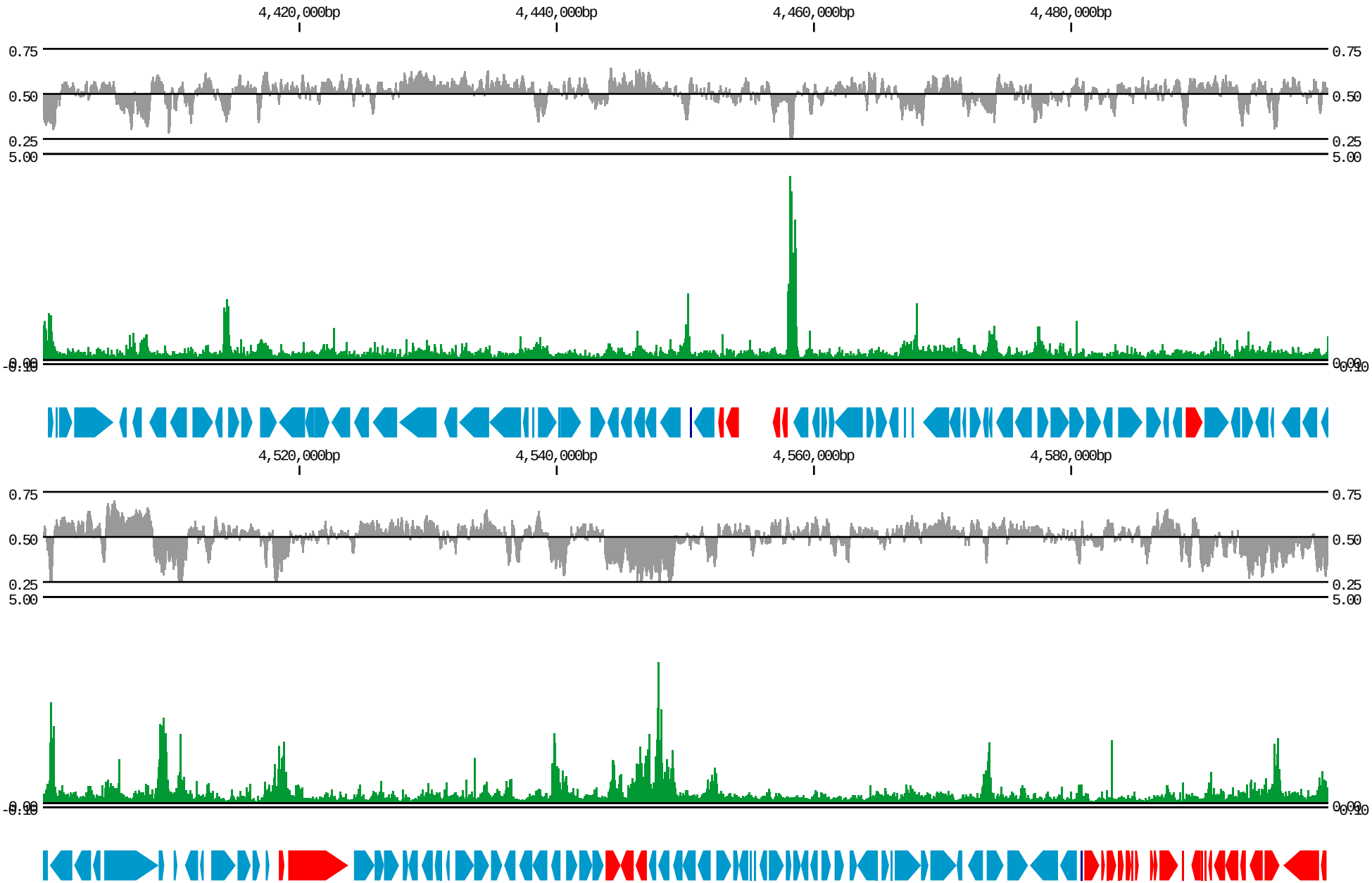
4,380,000bp
0.75
0.50
0.25
5.00
0.00
0.10

Fig. S2 (cont.)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4,480,000bp
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4,520,000bp
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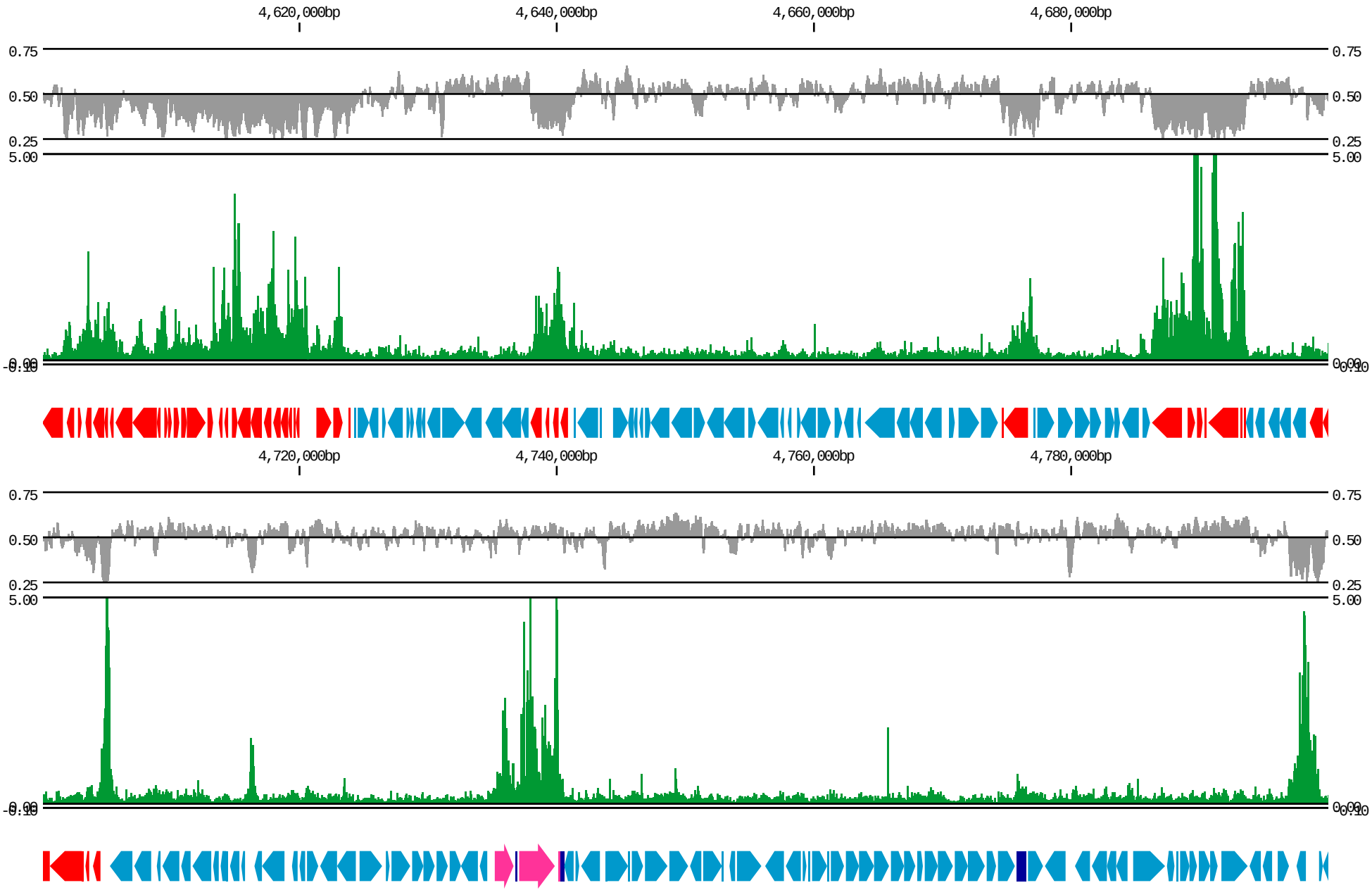
4,560,000bp
4,580,000bp

Fig. S2 (cont.)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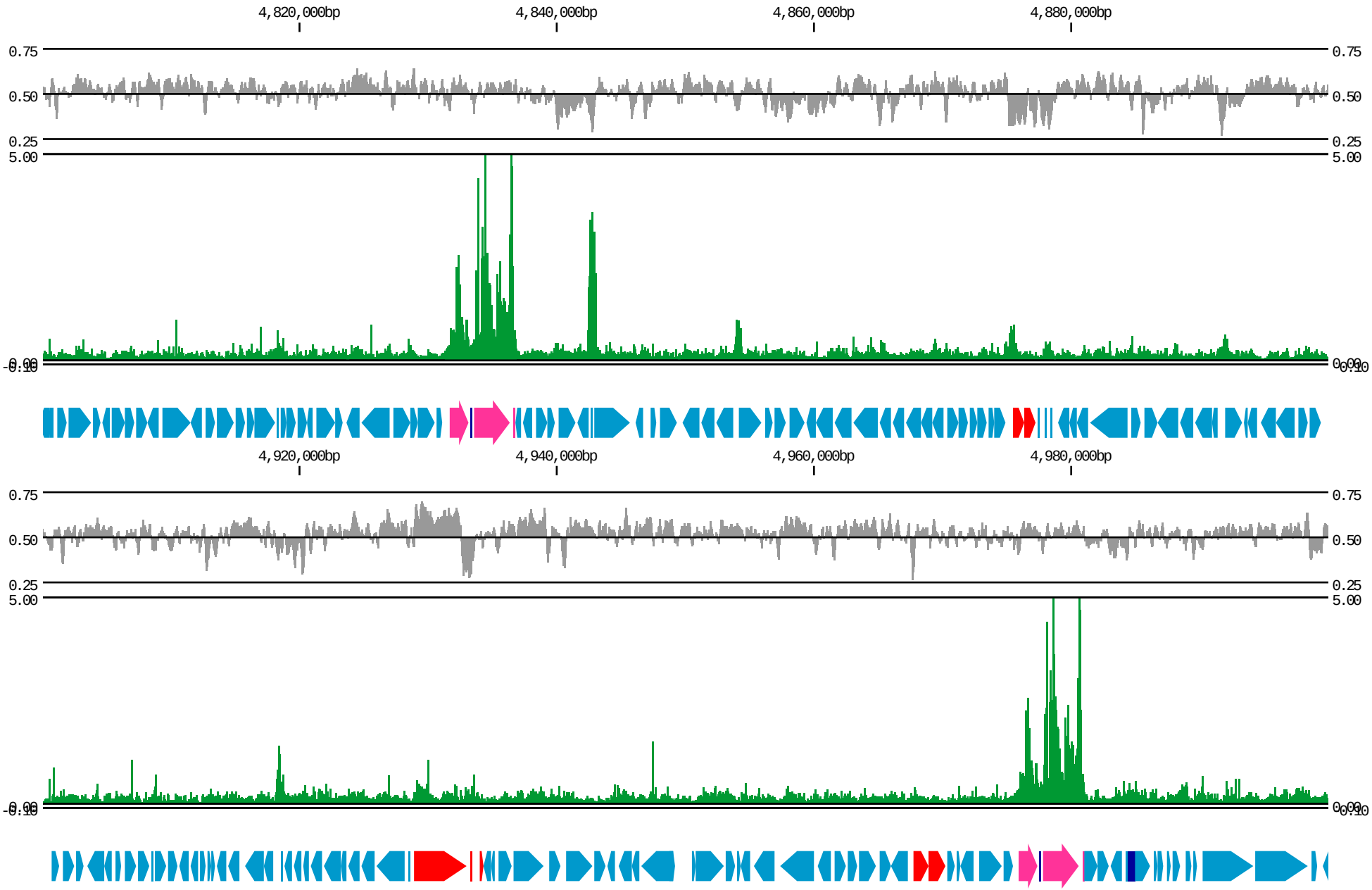
4,720,000bp
4,740,000bp
4,760,000bp
4,780,000bp

Fig. S2 (cont.)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4,840,000bp
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4,920,000bp
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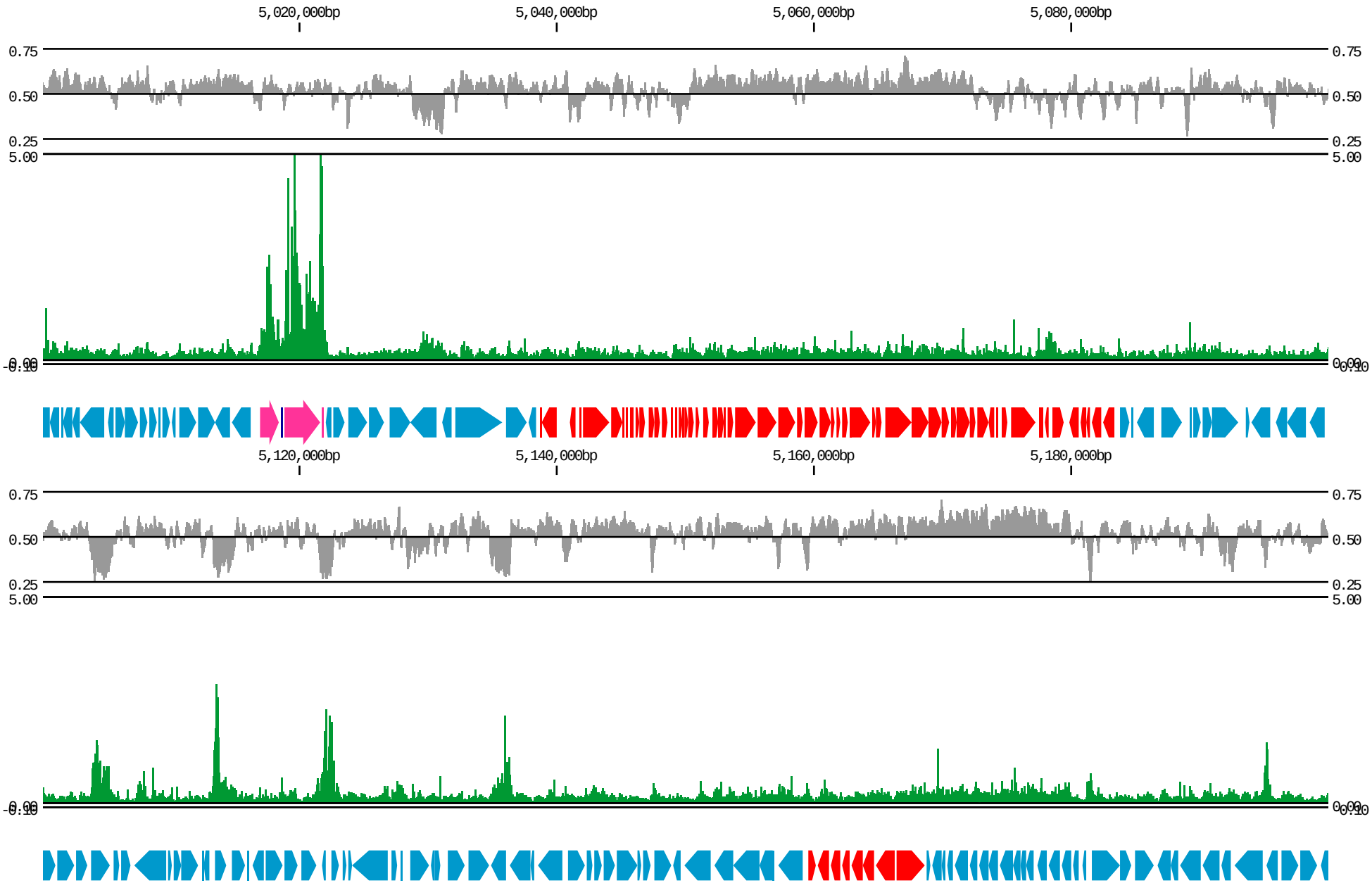
4,960,000bp
4,980,000bp

Fig. S2 (cont.)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5,160,000bp
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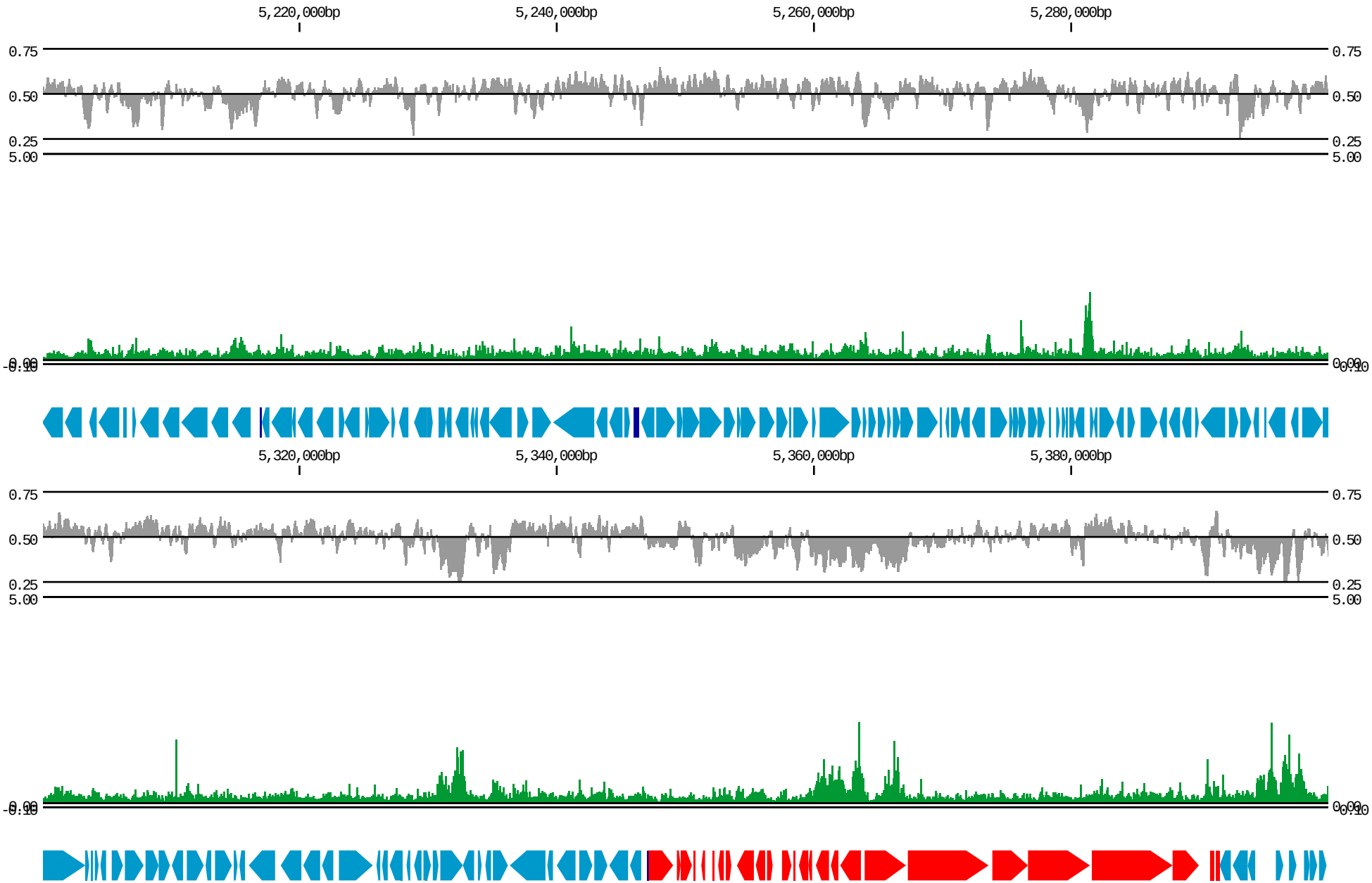
Fig. S2 (cont.)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0.10
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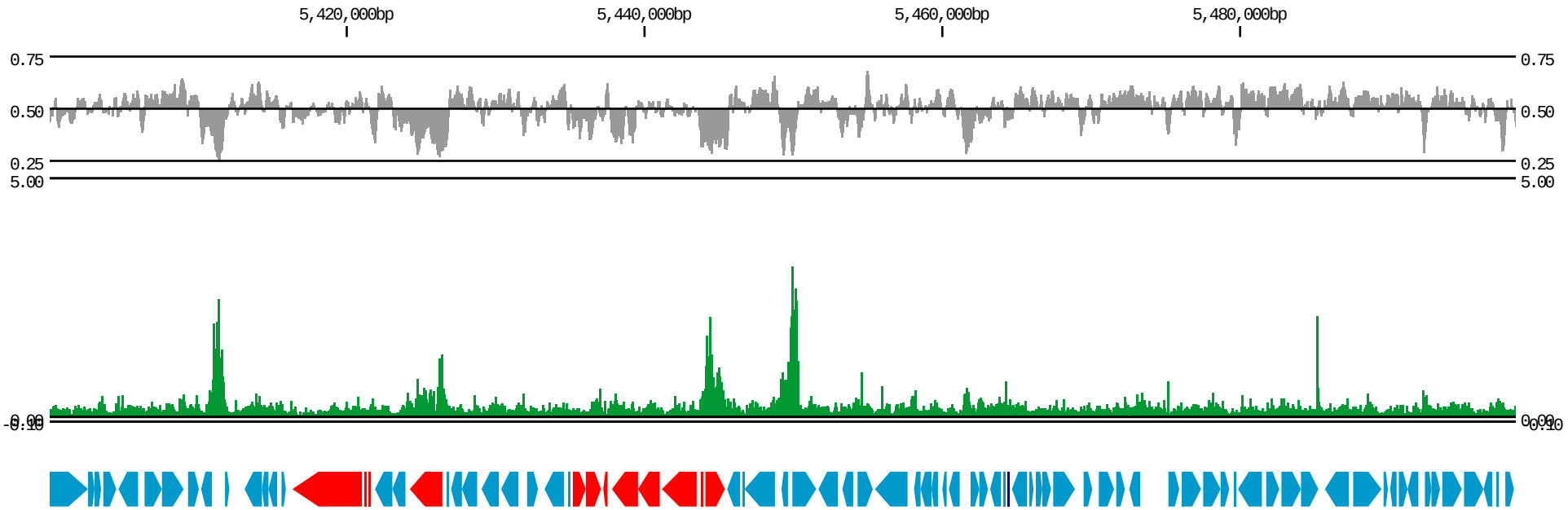
5,340,000bp
5,360,000bp
5,380,000bp

Fig. S2 (cont.)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5,460,000bp
5,480,000bp
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0.50
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