

```
Last login: Fri Apr 12 17:26:52 on ttys000
source ~/.zprofile
mariapalafox@x86_64-apple-darwin13 ~ % source ~/.zprofile
(base) mariapalafox@ 7:36PM ~ % cd Desktop
(base) mariapalafox@ 7:46PM Desktop % ssh palafm01@minerva.hpc.mssm.edu
#####
```

From April 30st, 2020, Minerva is accessbile only via VPN.

To request VPN:

<https://labs.icahn.mssm.edu/minervalab/internal-users-minerva-action-required-external-login-nodes-being-removed-on-april-15/>

New Minerva website:

<https://labs.icahn.mssm.edu/minervalab/>

#####

Please input your password and two factor token:

(palafm01@minerva.hpc.mssm.edu) Password:

Last failed login: Fri Apr 12 18:37:09 EDT 2024 from 10.125.146.225 on ssh:notty

There were 13 failed login attempts since the last successful login.

=====

Run "Minerva_help" for useful Minerva commands and websites

Minerva Documentation at <https://labs.icahn.mssm.edu/minervalab/documentation/>

Globus guide at <https://labs.icahn.mssm.edu/minervalab/documentation/file-transfer-globus/>

Minerva training slides at <https://labs.icahn.mssm.edu/minervalab/resources/the-minerva-user-group-and-training-classes/>

Data Ark Data Sets available on Minerva at <https://labs.icahn.mssm.edu/minervalab/resources/data-ark/>

GPU guide at <https://labs.icahn.mssm.edu/minervalab/documentation/gpgpu/>

====*****If you have NIH-funded projects, you MUST include the following acknowledgement in all your publications*****====

This work was supported in part through the computational and data resources and staff expertise provided by Scientific Computing and Data at the Icahn School of Medicine at Mount Sinai and supported by the Clinical and Translational Science Awards (CTSA) grant UL1TR004419 from the National Center for Advancing Translational Sciences. Research reported in this publication was also supported by the Office of Research Infrastructure of the National Institutes of Health under award number S100D026880 and S100D030463. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

====*****If you DONOT have NIH-funded projects, you MUST include the following acknowledgement in all your publications*****====

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=====!!!!!!SEVEN Minerva SPRING TRAINING SESSIONS!!!!!!=====

FULL details at <https://labs.icahn.mssm.edu/minervalab/minerva-hpc-information-and-training-sessions-2/>

Session 2: Load Sharing Facility (LSF) Job Scheduler – Wednesday, April 3, 1 pm-2 pm

Location: Icahn School of Medicine building (1425 Madison Ave) Room 14-84 (14th FL)

Zoom Registration at https://mssm.zoom.us/webinar/register/WN_lVp2A5SvRV6iL_1u4PeCTA

GPU/AI

Session 3. Introduction to GPU/AI resources on Minerva – Wednesday, April 10, 1 pm -2 pm

Session 4. 5 Ways to Get Started with GPUs – Friday, April 12, 1 pm-2 pm

Session 5: Accelerated General Data Science in Medicine with RAPIDS, CuPy and Numba – Wednesday, April 17, 1 pm-2 pm

Session 7: How to Accelerate Genome Analysis Toolkit (GATK) by using Parabricks – Wednesday, May 1, 1 pm-2 pm

Data Ark

Session 6: Introduction to Data Ark - Mount Sinai Data Commons – Wednesday, April 24, 1 pm-2 pm

Location: Icahn School of Medicine building (1425 Madison Ave) Room L3-36 (3rd FL)

Zoom Registration at https://mssm.zoom.us/webinar/register/WN_MblDa2FySuKpVbvHig7ArQ

=== Send tickets to hpchelp@hpc.mssm.edu ===

!!!!!!WE DO NOT BACKUP USER FILES

!!!!!!PLEASE ARCHIVE/BACKUP YOUR IMPORTANT FILES

=====

Disk quotas for user palafm01 (uid 26222):

Filesystem	space	quota	limit	grace	files	quota	limit	grace
nfs01-ib0:/hpc	40K	19456M	20480M		15	0	0	

Last report update 2024-04-15-13:34

Project(arion)	User	Usage	Files
arion_projects_vascbrain	palafm01	0	1
root	palafm01	0	24

[palafm01@li03c03 ~]\$ pwd

-bash: pwd: command not found

[palafm01@li03c03 ~]\$ pwd

```
/hpc/users/palafm01
[palafm01@li03c03 ~]$ ls
[palafm01@li03c03 ~]$ ls
[palafm01@li03c03 ~]$ cd ..
[palafm01@li03c03 users]$ ls
```

abbote02	choi01	gillr10	kollis05	moik01	rezazs01	torrem67
abida02	choik06	giottb01	konerk01	molzaa01	rhoads01	torrem68
abraham12	choiy07	girdhk01	kongy02	monach01	richaa21	tostag01
adamsa23	chos14	gleasa01	konovk01	moncam01	richtf01	townsk05
adlerm14	chowda26	gleasc04	kornbi01	mongai01	riinan01	trann05
admodifiers	chowed01	glennm10	koromm03	montek06	riraks01	tristm01
adsp	chrisa21	gnjats01	kosowj01	moohlh01	rissop01	troncl03
afzalr01	chrisb05	goateomics	kosoyr01	morgap04	riverm99	tsanka01
agarwa18	chuk15	gobbut01	koutrm02	morges01	rna	tsankova_admin
agarwp02	chul08	gohels01	kowalr03	morril11	rocann03	tssetsf01
agawua01	chunga08	golesn01	kozike01	mosaic	rocheg01	turhab01
aggarar01	chuny02	gomesp04	kozlea01	moskeo01	rodrij188	turnej11
aggarv01	churnc01	gonzaa51	kreka01	mscicadmin	rodri171	turnoe01
aggarv02	cillea01	gonzae34	krishr12	msm_admin	rodri15	tuz01
aguirk04	cimenc01	gorinn01	kritze01	muenzk01	rodriy04	tylers01
ahmadr02	civlja01	gottas01	kroneb01	mukhek03	rosemf01	tzavan01
ahmedn29	clarkj25	gownip01	kruga01	mukhek05	rosenb16	ukbiobankadmin
aikom01	clarku01	gp-cryoadmin	ksiezm01	mukunp01	rosene22	ulukag01
ajanab03	clemej05	greaty01	kubler01	muldel01	rosenj57	vaida02
akaluy01	coccie01	greend41	kudrid01	mulleb01	rosenn36	valdeb02
akinka05	cogaadmin	greenk27	kulkak01	mullin04	rothsj06	valena17
alabbs01	cohene20	greenr49	kumara82	muncha01	roudqv01	valend08
alburb02	cohenl07	grimee01	kunoa01	nadkag01	roussoslab	vanbah01
alcalc01	cohenp05	grosse08	kurowa01	nadkarnilab-admin	roussp01	vandea10
alcane07	colbes01	guckhp01	kwasia01	nadukr01	rowanb01	vanooj01
alleve01	colemc07	guindm01	kyriad02	naira12	rsheu01	vanvlt02
altaiz01	colemc08	guisad01	lagana01	naitot01	ruand01	vanvok01
althok01	colonj34	gulamf01	lahoty01	narasa01	rubena05	vargac10
altmag01	comelp01	gumus01	lakhac01	nashij01	ruchnd01	vartan01
alzaha01	congxo1	guor01	lallim01	naskat01	ruff01	vasudv02
aminih01	cookea02	guow03	lamare01	nativm02	ruizom01	vazar01
amreeb01	correj08	guptam18	lambel02	neala03	ruthek04	vemurk01
andres12	cotea02	gurums01	lambet02	neffr01	ryderj03	venkas08
ankerj01	craryj01	gutiei03	lamm05	neue01	rykund01	ventun01
anyfam01	crokem02	gutien07	landii03	neukap01	sachsd01	verbam01
arakea01	cryosparctest-admin	gux01	larosf01	nga14	saddih01	veremb01
archiving_bings	cryosparc-user	gyasia01	lashbn01	ngaik01	saffem03	vhatkt01
argmac01	cullis01	haass02	laube02	ngj05	sakhua01	viegac01
arista03	cummid06	habibj02	layerd01	nguyec05	salasl04	villaa06
arivan01	cunni06	hackmn01	laynet03	nguyed06	salsan01	vinsod01
arooja01	daidd02	hadasy01	lazarm11	nguyeh16	sanchm63	virant01
arrasj01	daij06	haghi01	lazarus_cryo-admin	nguyep07	sanchoc03	voloug01
asgars03	daiy07	haghighi_admin	leea63	nguyet47	sangz01	vornhe01
asline01	damarn02	hahna03	leed28	nguyet50	sanies01	vpnh02
assadn01	damleg01	haidef02	leed62	nguyet57	sariys01	vyt01
athanr01	daniem14	halasl01	leed77	nicolp01	sartof01	wacked01
ayalaj19	danzet01	halvom01	leej111	nim01	sawana02	wackerlab_cryoadmin
ayvasv01	danzio01	hamonp01	leej167	nirens01	sazeic01	wackerlab-cryoadmin.tbd
babrob01	danzn01	hanh09	leel23	novikg01	sc	walker05
babupk01	dasa06	hankss01	leel26	nudelg01	schade01	wange13
baggea01	dasild04	hanw07	leer50	nukavn01	schafm03	wangh35
bairam01	daskeb01	haoc03	lees111	nwanec01	schmig04	wangh36
bajicg01	dealms01	haok01	lees117	oconnp06	schnej22	wang12
balasu01	defeln01	harern01	leew13	oconns05	schron01	wangm05
balbon01	defrej02	harnea01	leew14	oconns06	schuml01	wangm08
bangs02	degrae01	hassod01	leew17	odonnt02	scottm24	wangw32
bankes02	degtya01	haurej01	leforr01	oeltef01	seahc01	wangx38
banuec01	delgaa07	hec10	lehres01	ohw02	seaveradmin	wangx40
baptia05	demird01	heddej01	leonep03	olumue01	sebrar01	wangx44
baptii01	dengc02	heflim01	lepowl01	oreilp01	seeles01	wangy27
barrae02	dengg02	hegdes02	lessec02	oria01	selvam01	wangy33
bartul01	depina02	heisis01	levene03	ortegr01	seoh02	wangz18
barupd01	derear02	hemmeb01	levene04	osmanr01	service_xltech	wangz19
barvij01	derese01	henaoj02	levys17	oterol04	sevimc01	wangz21
bazilm05	derosc01	hendee03	levyt03	ozbeys01	shadrm01	warbup01
becheo01	desmaj01	hernad36	lewisd36	padhia01	shafrk01	warrea08
becke01	desoui01	herrin01	lewise11	paib01	shahh06	warriro01
becker03	devara02	heyern01	liharl02	palafm01	shahr24	watanh02
becklab_admin	dibelh01	hirscl07	lij61	palm01	shakyd01	watanr01
beckmn01	dicksj02	hoangd02	lik17	pandeg01	shangj01	webbb02
bedirk01	diezov01	hoffmd09	lik26	pankoa01	shaon01	weeklb01

beganp01	dilips01	hoffmg01	lim39	panti01	sharma45	weia03
bekris02	dillac01	hoganc04	linge01	pareka02	sharmh15	weic04
beltrj11	dinizm01	hoggac01	lingik01	parke15	sharmr06	weilep01
benazm01	disalg01	holtb01	lint07	parkis01	shemir03	weismj01
bendlj01	ditulF02	hoppem02	linx19	parkk14	shenl03	weitzs01
benmek01	divagt01	hos09	lioul01	parkm17	shermj09	wengeb01
bennej21	dogran01	hossar07	LiShen_admin	parkr02	sheuc01	wenglk01
bercor01	domidata	houldj01	liuc06	parpoa01	shevlb01	wenq01
bergea18	domind07	housea03	liuc10	parsonsadmin	shibar02	whitek04
bergqt01	dongp01	houveg01	liuh20	parvam01	shins21	wickrs01
bermaj08	dor01	hradif01	liun05	patela110	shirss01	wiener02
bernel01	dossaj01	hsrdata_admin	lius18	patelf06	siad01	wilsoa28
bernhl03	doughm04	hsuanc01	liux07	pateln127	siehw01	wilsoe22
beykma01	downeh02	huangk06	liuy22	patels115	sigelk01	windae01
bhagwa01	drachs01	humble01	liuy35	patelt16	signam01	winstk01
bhall02	drfroa01	humphj04	liuy39	pathologywsi_web	signer01	wojcim01
bhattm11	dsouzd04	hur03	livana02	patila06	simonn26	wongh04
bhedas01	dsouzs04	hutchk02	liy40	patinj01	simonn10	woodr04
bicakm01	duboi01	huw06	liy42	paulf03	sims01	wuh13
bihem01	duffya02	ibesw01	liy54	pavlya01	singhb22	wur10
bijia01	duongs02	ibings01	loadadmin	pawlip01	singhm14	wuy21
birnbr02	duplek01	ilkovm01	loboi01	pedicc01	singhs100	wuz07
bobrot01	durenm02	illins01	loherp01	pedrov01	singhs83	wuz08
boixa01	duttas04	imtia03	lohy01	pejavv01	singhs96	wylerb01
bonavb01	ebnerj01	indias01	lol01	pengs03	siskr02	xgail01
borrej02	ebraht01	invera03	loosr01	peream01	sistia01	xiad01
bouhae01	edwart10	ioanng02	lounsw01	perezp12	slauga01	xiaoy04
boukes01	eggess01	ioniti03	lozanr01	peris01	slesinger-cryoadmin	xiez01
bowlek01	egglel01	ipm	lubitg01	perkd01	slesip02	xiongy01
brat	elahif01	iriki01	luffs01	perkim01	sloofl01	xnat_irw
breene02	elhaim01	irizaa03	luj12	peteri02	slosat03	xuc04
breenm01	ellisr05	iyegbc01	lujama01	peterl02	smitha55	xuj24
brewek04	elmasa02	jacobc05	lukato01	petrab01	smithg17	xuk07
brophe01	elyb01	jacobm07	lukinj01	petraf01	smitr01	xum04
brownm82	emhsr-admin	jacoby02	lukszm01	petris05	socraa01	xup04
buckld05	ensari01	jadhab01	lunda02	petrok01	songh05	xuz07
buckum01	eolia01	jainp08	lundse01	phadna01	songl05	yadavv03
buk02	epibrowser	jalads01	luy12	philis12	songq01	yanga27
bunyas02	epstem06	janecm01	macdok02	phuay01	songw01	yangh17
burgee02	erekaa02	jangb03	macdol02	piaoz03	songx04	yangj27
burstd02	erjavl01	jangdm02	magenta01	picard03	songy12	yangj31
busson02	esposs02	jangj06	maherc01	pierap01	sonim01	yangn07
butas01	esteb02	janusm01	mahjab01	pillas03	sooj02	yangs17
butleg04	estilm01	jardis02	mahonr02	pinniu01	soongb02	yaoh01
buxbaa02	evansv03	jayarp02	mal06	pintod02	sorgs01	yaom03
buxbaj01	evardr01	jethav01	malikr02	piquem01	soroke02	yashac01
byunm01	faithj02	jia02	man02	piquem02	soroua01	yeturs08
cabalm04	falcoc04	jiangb02	mandaa05	pjanim03	souait02	yingz01
cabalr04	fangg03	jiangj07	mangoj02	planua01	spehak01	yitshm01
caggic02	fans03	jiangp06	manigc02	plazaa01	spencc13	yiz01
cahann01	fany03	jiangt04	marcoe02	poddan01	spindm02	yoonj17
callej03	fariag01	jiangw02	margom04	podlea01	spiven01	yoony09
campag01	farrek04	johnsj64	marina10	polide01	sridhs01	yoos06
canalp02	fenneb02	johnsk86	marina16	porrac01	srisua01	youngh02
cantoa03	fentos02	johnsm50	markek03	pradha04	stalbl01	yousm03
caox01	ferlaj01	jordad05	marketscan	prashf01	stanea02	yua27
cappic01	ferrea06	joshia13	marquc08	preusm01	stapym01	yuang01
carcas01	ferrec14	joshih02	marquc11	priggk01	stechy01	yug03
carroe09	filipd02	joshit02	marros02	printa04	steind16	yuh04
castre11	filizolalab	jostes01	marsae01	provad01	stewao02	yuh08
cattoa01	finka03	juh01	marshd13	prytki01	stocka01	yuj25
celebjadmin	fiorev01	jungs10	martia68	psychgenadmin	strasaa01	zafers02
cerinb01	fiorib01	justa01	martij172	pullit02	suarem08	zaidz01
chaz01	fischj04	kaintk01	martim78	pulsij01	sullim11	zakiy01
chaj03	fleysl01	kajid02	martit26	qasims01	sumowj01	zamard03
chamin01	flodad01	kalagp01	marxg01	qij01	sunc04	zamojm01
chanc36	fludee01	kandos01	maryas01	quidwm02	sunh14	zatorn01
chandp05	fludee02	kannah01	mas07	rabbaa02	sunr02	zbareg01
changa20	fontas06	karaa01	massen06	radkee01	suns09	zebroa01
changh14	forrei01	karabm01	mathud03	rafatf01	suny04	zeibed01
changj33	forstc01	karake01	may08	rahmas14	sunz04	zengb02
chanj24	foxb02	karlom01	maz07	rahmat03	susmaa01	zengq02
charna02	frasem04	karsm02	mccanj06	rajaup01	sutkoj01	zhangb03
chatzc02	freedg02	karven01	mccuss01	rajt01	swansm02	zhangd14
chatzc03	freudy02	kaszet01	mcdona09	ramaka02	syedb01	zhangj62
chavej12	fribom01	kathij01	mckina04	rambam01	syedm13	zhangl26

chdi	fridrm01	katss02	mclaic01	ramira22	szesko_admin	zhangw09
chenc51	friedb08	kauffj01	mclenk02	ramirj30	szeszp01	zhangx24
chengc12	friedr05	kaufmo01	meadoa02	ramm02	taglim02	zhangx32
chengh04	fuchst04	kellyg03	medinc13	ramosn13	takkak01	zhangy40
chengw06	fultob01	kenny02	meic07	ramoss18	talwas01	zhangz05
chengy10	fuq01	kepina01	melned01	ramses01	tandop03	zhangz19
chenj02admin	fushia01	keraii01	menonk02	randoh01	tangy08	zhangz20
chenl54	fuw01	khaliz03	meranr01	ranglm01	tangy11	zhaoh02
chenla01	gai101	kimc46	merzoe01	ranti01	tasakr01	zhaow05
chenm37	ganesg01	king20	mesroa02	raov04	tastac01	zhaoy14
chenns01	gaox08	kimm61	mestrg01	rashea05	techdev	zhaoz03
chenr07	garci062	kimm62	mevery05	ratcsg01	techdev6	zhengs07
chenr11	garcim54	kimt15	mezeim01	ravia04	tengs07	zhoub04
chens61	gardng03	kimurh01	miam01	rawalo01	teppea02	zhour02
chent12	gargp01	kimy56	mice1r03	reala02	theodd05	zhoux05
cheny60	gelbb01	kinros01	micar13	rebelv01	therrk01	zhua06
chenz09	gellej01	kirchm05	midyav01	rechko01	thomaa68	zhuj05
chessa01	generb01	kittrh01	mina03	rechte01	thomaa74	zhux02
chestm01	gergut01	kittss01	minerg01	reddam02	thomam32	zilibeg01
cheunk02	gettlk01	klange01	mizet01	reinfe01	thompr21	
chinc18	gey01	kleinr08	mmedsadmin	rentoa01	thorpa03	
chisha02	ghelie01	kodysy02	moeins01	rentzf01	tichks01	
chob04	ghoshr05	koenid03	mognoi01	restrp01	tomall01	
choh07	gibsok04	kohlis03	mohamk08	revab01	torred23	

[palafm01@li03c03 users]\$ cd ..

[palafm01@li03c03 hpc]\$ ls

admin-scripts backups benchmark config data home logs lsf packages slurm stats tsm users web

[palafm01@li03c03 hpc]\$ cd data

-bash: cd: data: Permission denied

[palafm01@li03c03 hpc]\$ cd slurm

-bash: cd: slurm: Permission denied

[palafm01@li03c03 hpc]\$ cd lsf

[palafm01@li03c03 lsf]\$ ls

10.1 allocation conf conf.backup08152022 log lsf-10.1-tar lsf-perl-api LSF_redist.txt pam_lsf patch patch.conf properties work

[palafm01@li03c03 lsf]\$ cd work

[palafm01@li03c03 work]\$ ls

chimera

[palafm01@li03c03 work]\$ ls

chimera

[palafm01@li03c03 work]\$ cd

[palafm01@li03c03 ~]\$ ls

[palafm01@li03c03 ~]\$ ls

[palafm01@li03c03 ~]\$ cd ..

[palafm01@li03c03 users]\$ ls

abbote02	choi01	gillr10	kollis05	moik01	rezazs01	torrem67
abida02	choik06	giottb01	konerk01	molzaa01	rhoads01	torrem68
abrah12	choiy07	girdhk01	kongy02	monach01	richaa21	tostag01
adamsa23	chos14	gleasa01	konovk01	moncam01	richtf01	townsk05
adlerm14	chowda26	gleasc04	kornbi01	mongai01	riinan01	tranm05
admodifiers	chowed01	glenm10	koromm03	montek06	riraks01	tristm01
adsp	chrisa21	gnjats01	kosowj01	moohl01	rissop01	troncl03
afzalr01	chrisb05	goateomics	kosoyr01	morgap04	riverm99	tsanka01
agarwa18	chuk15	gobbut01	koutrm02	morges01	rna	tsankova_admin
agarwp02	chul08	gohe1s01	kowalr03	morril11	rocann03	tsetsf01
agawua01	chunga08	golesn01	kozike01	mosaic	rocheg01	turhab01
aggara01	chuny02	gomesp04	kozlea01	moskeo01	rodrij188	turnej11
aggarrv01	churcn01	gonzaa51	kreka01	mscicadmin	rodri171	turroe01
aggarrv02	cillea01	gonzae34	krishr12	msm_admin	rodri15	tuz01
aguirk04	cimenc01	gorinn01	kritze01	muenzk01	rodriy04	tylers01
ahmadr02	civlja01	gottas01	kroneb01	mukhek03	rosemf01	tzavan01
ahmedn29	clarkj25	gownip01	krugea01	mukhek05	rosenb16	ukbiobankadmin
aiskom01	clarku01	gp-cryoadmin	ksiezm01	mukunp01	rosene22	ulukag01
ajanab03	clemej05	greaty01	kubler01	muldel01	rosenj57	vaida02
akaluy01	coccie01	greend41	kudrid01	mulleb01	rosenm36	valdeb02
akinka05	cogaadmin	greenk27	kulkak01	mullin04	rothsj06	valena17
alabbs01	cohene20	greenr49	kumara82	muncha01	roudqv01	valend08
alburb02	cohenl07	grimee01	kunoa01	nadkag01	roussoslab	vanbah01
alcalc01	cohenp05	grosse08	kurowa01	nadkarnilab-admin	roussp01	vandea10
alcane07	colbes01	guckhp01	kwasia01	nadukr01	rowanb01	vanooj01
alleve01	colemc07	guindm01	kyriad02	naira12	rsheu01	vanvlt02
altaiz01	colemc08	guisad01	lagana01	naitot01	ruand01	vanvok01
althok01	colonj34	gulamf01	lahoty01	narasa01	rubena05	vargac10
altmag01	comelp01	gumus01	lakhac01	nashij01	ruchnd01	vartan01
alzaha01	congxx01	guor01	lallim01	naskat01	ruff01	vasudv02
aminih01	cookea02	guow03	lamare01	nativm02	ruizom01	vazar01
amreeb01	correj08	guptam18	lambel02	neala03	ruthek04	vemurk01

andres12	cotea02	gurums01	lambet02	neffr01	ryderj03	venkas08
ankerj01	craryj01	gutiei03	lamw05	neue01	rykund01	ventun01
anyfam01	crokem02	gutien07	landii03	neukap01	sachsd01	verbam01
arakea01	cryosparctest-admin	gux01	larosf01	nga14	saddih01	veremb01
archiving_bings	cryosparc-user	gyasia01	lashbn01	ngaik01	saffem03	vhatkt01
argmac01	cullis01	haass02	laube02	ngj05	sakhua01	viegac01
arista03	cummi006	habibj02	layerd01	nguyec05	salasl04	villaa06
arivan01	cunni006	hackmn01	laynet03	nguyed06	salsan01	vinsod01
arobja01	dai002	hadasy01	lazarm11	nguyeh16	sanchm63	virant01
arrasj01	daij06	haghi01	lazarus_cryo-admin	nguyep07	sancho03	voloug01
asgars03	daiy07	haghighi_admin	leea63	nguyet47	sangz01	vornhe01
asline01	damarn02	hahna03	leed28	nguyet50	sanies01	vpnh02
assadn01	damleg01	haidef02	leed62	nguyet57	sariys01	vyt01
athanr01	daniem14	halasl01	leed77	nicolp01	sartof01	wacked01
ayalaj19	danzet01	halvom01	leej111	nim01	sawana02	wackerlab_cryoadmin
ayvasv01	danzio01	hamonp01	leej167	nirens01	sazeic01	wackerlab-cryoadmin.tbd
babrob01	danzn01	hanh09	leel23	novikg01	sc	walker05
babupk01	dasa006	hankss01	leel26	nudelg01	schade01	wange13
baggea01	dasil004	hanw07	leer50	nukavn01	schafm03	wangh35
bairam01	daskeb01	haoc03	lees111	nwanec01	schmig04	wangh36
bajicg01	dealms01	haok01	lees117	oconnp06	schnej22	wangl22
balasu01	defeln01	harern01	leew13	oconns05	schron01	wangm05
balbon01	defrej02	harnea01	leew14	oconns06	schuml01	wangm08
bangs02	degrae01	hassod01	leew17	odonnt02	scottm24	wangw32
bankes02	degtya01	haurej01	leforr01	oeltef01	seahc01	wangx38
banuec01	delgaa07	hec10	lehres01	ohw02	seaveradmin	wangx40
baptia05	demird01	heddej01	leonep03	olumue01	sebrar01	wangx44
baptii01	dengc02	heflim01	lepowl01	oreilp01	seeles01	wangy27
barrae02	dengg02	hegdes02	lessec02	oria01	selvam01	wangy33
bartul01	depina02	heisis01	levene03	ortegr01	seoh02	wangz18
barupd01	derear02	hemmeb01	levene04	osmanr01	service_xltech	wangz19
barvi01	derese01	henaaj02	levys17	oterol04	sevimc01	wangz21
bazilm05	derosc01	hendee03	levyt03	ozbeys01	shadrm01	warbup01
becheo01	desmaj01	hernad36	lewisd36	padhia01	shafkr01	warrea08
becke01	desoui01	herrin01	lewise11	paib01	shahh06	warrir01
beckec03	devara02	heyerm01	liharl02	palafm01	shahr24	watanh02
becklab_admin	dibelh01	hirscl07	lij61	palm01	shakyd01	watanr01
beckmn01	dicksj02	hoangd02	lik17	pandeg01	shangj01	webbb02
bedirk01	diezov01	hoffmd09	lik26	pankoa01	shaon01	weeklb01
beganp01	dilips01	hoffmg01	lim39	panti01	sharma45	weia03
bekris02	dillac01	hoganc04	linge01	pareka02	sharmh15	weic04
beltrj11	dinizm01	hoggac01	lingik01	parke15	sharmr06	weilep01
benazm01	disalg01	holtb01	lint07	parkis01	shemir03	weismj01
bendlj01	ditulf02	hoppem02	linx19	parkk14	shenl03	weitzs01
benmek01	divagt01	hos09	lioul01	parkm17	shermj09	wengeb01
bennej21	dogran01	hossar07	LiShen_admin	parkr02	sheuc01	wenglk01
bercor01	domidata	houldj01	liuc06	parpoa01	shevlb01	wenq01
bergea18	domind07	housea03	liuc10	parsonsadmin	shibar02	whitek04
bergqt01	dongp01	houveg01	liuh20	parvam01	shins21	wickrs01
bermaj08	dor01	hradif01	liun05	patela110	shirss01	wiener02
bernel01	dossaj01	hsrdata_admin	lius18	patelf06	siad01	wilsoa28
bernhl03	doughm04	hsuanc01	liux07	pateln127	siehw01	wilsoe22
beykma01	downeh02	huangk06	liuy22	patels115	sigelk01	windae01
bhagwa01	drachs01	humble01	liuy35	patelt16	signam01	winstk01
bhalls02	drfrod01	humphj04	liuy39	pathologywsi_web	signer01	wojcim01
bhattm11	dsouz004	hur03	livana02	patila06	simonn26	wongh04
bhedas01	dsouzs04	hutchk02	liy40	patinj01	simonn10	woodr04
bicakm01	duboib01	huw06	liy42	paulf03	sims01	wuh13
bihiem01	duffya02	ibesw01	liy54	pavlya01	singhb22	wur10
bijia01	duongs02	ibings01	loadadmin	pawlip01	singhm14	wuy21
birnbr02	duplek01	ilkovm01	loboi01	pedicc01	singhs100	wuz07
bobrot01	durenm02	illins01	loherp01	pedrov01	singhs83	wuz08
boixa01	duttas04	imtia03	lohy01	pejavv01	singhs96	wylerb01
bonavb01	ebnerj01	indias01	lol01	pengs03	siskr02	xgail01
borrej02	ebraht01	invera03	loosr01	peream01	sistia01	xiad01
bouhae01	edwart10	ioanng02	lounsw01	perezp12	slauga01	xiaoy04
boukes01	eggert01	ioniti03	lozanr01	peris01	slesinger-cryoadmin	xiez01
bowlek01	egglet01	ipm	lubitg01	perkd01	slesip02	xiongy01
brat	elahif01	iriki01	luffs01	perkim01	sloofl01	xnat_irw
breene02	elhaim01	irizaa03	luj12	peteri02	slosat03	xuc04
breenm01	ellisr05	iyegbc01	lujama01	peterl02	smitha55	xuj24
brewek04	elmasa02	jacobc05	lukato01	petrab01	smithg17	xuk07
brophe01	elyb01	jacobm07	lukinj01	petraf01	smitr01	xum04
brownm82	emhsr-admin	jacoby02	lukszm01	petris05	socraa01	xup04
buckld05	ensari01	jadhab01	lunda02	petrok01	songh05	xuz07
buckum01	eolia01	jainp08	lundse01	phadna01	songl05	yadavv03

buk02	epibrowser	jalads01	luy12	philis12	songq01	yanga27
bunyas02	epstem06	janecm01	macdok02	phuay01	songw01	yangh17
burgee02	erekaa02	jangb03	macdol02	piaoz03	songx04	yangj27
burstd02	erjavl01	jangdm02	magna01	picard03	songy12	yangj31
bussan02	espass02	jangj06	maherc02	pierap01	sonim01	yangn07
butas01	estebr02	janusm01	mahjab01	pillas03	sooj02	yangs17
butleg04	estilm01	jardis02	mahonr02	pinniu01	soongb02	yaoh01
buxbaa02	evansv03	jayarp02	mal06	pintod02	sorgs01	yaom03
buxbaj01	evardr01	jethav01	malikr02	piquem01	soroke02	yashac01
byunm01	faithj02	jia02	man02	piquem02	soroua01	yeturs08
cabalr04	falcoc04	jiangb02	mandaa05	pjanim03	souait02	yingz01
caggic02	fangg03	jiangj07	mangoj02	planua01	spehak01	yitshm01
cahann01	fans03	jiangp06	manigc02	plazaa01	spenc13	yiz01
callej03	fany03	jiangt04	marcoe02	poddan01	spindm02	yoonj17
campag01	fariag01	jiangw02	margom04	podlea01	spiven01	yoony09
canalp02	farrek04	johnsj64	marina10	polide01	sridhs01	yoos06
cantaa03	fenneb02	johnsk86	marina16	porrac01	srisua01	youngh02
caox01	fentos02	johnsm50	markek03	pradha04	stalbl01	yousm03
cappic01	ferlaj01	jordad05	marketcan	prashf01	stanea02	yua27
carcas01	ferrea06	joshia13	marquc08	preusm01	stapym01	yuang01
carroe09	ferrec14	joshih02	marquc11	priggk01	stechy01	yug03
castre11	filipd02	joshit02	marros02	printa04	steind16	yuh04
catto01	filizolalab	jostes01	marsae01	provad01	stewao02	yuh08
celebjadmin	finka03	juh01	marshd13	prytki01	stocka01	yuj25
cetib01	fiorev01	jungs10	martia68	psychgenadmin	strasa01	zafers02
chaiz01	fiorb01	justa01	martij172	pullit02	suare08	zaidz01
chaj03	fischj04	kaintk01	martim78	pulsij01	sullim11	zakiy01
chamin01	fleysl01	kajid02	martit26	qasims01	sumowj01	zamard03
chanc36	flodad01	kalagp01	marxg01	qij01	sunc04	zamojm01
chandp05	fludee01	kandos01	maryas01	quidwm02	sunh14	zatorn01
changa20	fludee02	kannah01	mas07	rabbaa02	sunr02	zbareg01
changh14	fontas06	karaa01	massen06	radkee01	suns09	zebroa01
changj33	forrei01	karabm01	mathud03	rafatf01	suny04	zeibed01
chanj24	forstc01	karake01	may08	rahmas14	sunz04	zengb02
charna02	foxb02	karlom01	maz07	rahmat03	susmaa01	zengq02
chatzc02	frases04	karsm02	mccanj06	rajaup01	sutkoj01	zhangb03
chatzc03	freedg02	karven01	mccuss01	rajt01	swansm02	zhangd14
chatzc03	freudy02	kaszet01	mcdona09	ramaka02	syedb01	zhangj62
chavej12	fribom01	kathij01	mckina04	rambam01	syedm13	zhangl26
chdi	fridrm01	katss02	mclaic01	ramira22	szeszk0_admin	zhangw09
chenc51	friedb08	kauffj01	mclenk02	ramirj30	szeszp01	zhangx24
chengc12	friedr05	kaufmo01	meadoa02	ramm02	taglim02	zhangx32
chengh04	fuchst04	kellyg03	medinc13	ramosn13	takkak01	zhangy40
chengw06	fultob01	kennye02	meic07	ramoss18	talwas01	zhangz05
chengy10	fuq01	kepina01	melned01	ramses01	tandop03	zhangz19
chenj02admin	fushia01	keraii01	menonk02	randoh01	tangy08	zhangz20
chenl54	fuw01	khaliz03	meranr01	ranglm01	tangy11	zhaoh02
chenla01	gail01	kimc46	merzoe01	rantid01	tasakr01	zhaow05
chenm37	ganesg01	king20	mesroa02	raov04	tastac01	zhaoy14
chenns01	gaox08	kimm61	mestrg01	rashea05	techdev	zhaoz03
chenr07	garciy62	kimm62	meyery05	ratscg01	techdev6	zhengs07
chenr11	garcim54	kimt15	mezeim01	ravia04	tengs07	zhoub04
chens61	gardng03	kimurh01	miam01	rawalo01	teppea02	zhour02
chent12	gargp01	kimy56	micelr03	reala02	theodd05	zhoux05
cheny60	gelbb01	kinros01	midyav01	rebelv01	therrk01	zhua06
chenz09	gellej01	kirchm05	michar13	rechko01	thomaa68	zhuj05
chessa01	generb01	kittrh01	mina03	rechte01	thomaa74	zhux02
chestm01	gergut01	kittss01	minerg01	reddam02	thomam32	zilibeg01
cheunk02	gettlk01	klange01	mizet01	reinfe01	thompr21	
chinc18	gey01	kleinr08	mmedsadmin	rentoa01	thorpa03	
chisha02	ghelie01	kodysy02	moeins01	rentzf01	tichks01	
chob04	ghoshr05	koenid03	mognoi01	restrp01	tomall01	
choh07	gibsok04	kohlis03	mohamk08	revab01	torred23	

```

[palafm01@li03c03 users]$ cd sc
[palafm01@li03c03 sc]$ ls
ls: cannot open directory .: Permission denied
[palafm01@li03c03 sc]$ ls
ls: cannot open directory .: Permission denied
[palafm01@li03c03 sc]$
[palafm01@li03c03 sc]$
[palafm01@li03c03 sc]$ ls
ls: cannot open directory .: Permission denied
[palafm01@li03c03 sc]$ cd arion
-bash: cd: arion: No such file or directory
[palafm01@li03c03 sc]$ cd
[palafm01@li03c03 ~]$

```

```
[palafm01@li03c03 ~]$ ls
[palafm01@li03c03 ~]$ ls
[palafm01@li03c03 ~]$ cd ..
[palafm01@li03c03 users]$ ls
```

abbote02	choi01	gillr10	kollis05	moik01	rezazs01	torrem67
abida02	choik06	giottb01	konerk01	molzaa01	rhoads01	torrem68
abraham12	choiy07	girrdhk01	kongy02	monach01	richaa21	tostag01
adamsa23	chos14	gleasa01	konovk01	moncam01	richtf01	townsk05
adlerm14	chowda26	gleasc04	kornbi01	mongai01	rianan01	tranm05
admodifiers	chowed01	glenm10	koromm03	montek06	riraks01	tristm01
adsp	chrisa21	gnjats01	kosowj01	moohlh01	rissop01	troncl03
afzalr01	chrisb05	goateomics	kosoyr01	morgap04	riverm99	tsanka01
agarwa18	chuk15	gobbut01	koutrm02	morges01	rna	tsankova_admin
agarwp02	chul08	gohels01	kowalr03	morril11	rocannm03	tssetsf01
agawua01	chunga08	golesn01	kozike01	mosaic	rocheg01	turhab01
aggara01	chuny02	gomesp04	kozlea01	moskeo01	rodriji188	turnej11
aggarrv01	churcn01	gonzaa51	kreka01	mscicadmin	rodri171	turnroe01
aggarrv02	cillea01	gonzae34	krishr12	msm_admin	rodri15	tuz01
aguirk04	cimenc01	gorinnm01	kritze01	muenzk01	rodriy04	tylers01
ahmadr02	civlja01	gottas01	kroneb01	mukhek03	rosemf01	tzavan01
ahmedn29	clarkj25	gownip01	krugea05	mukhek05	rosenb16	ukbiobankadmin
aiskom01	clarku01	gp-cryoadmin	ksiezm01	mukunp01	rosene22	ulukag01
ajanab03	clemej05	greaty01	kubler01	muldel01	rosenj57	vaida02
akaluy01	coccie01	greend41	kudrid01	mulleb01	rosenm36	valdeb02
akinka05	cogaadmin	greenk27	kulkak01	mullin04	rothsj06	valena17
alabbs01	cohene20	greenr49	kumara82	muncha01	roudqv01	valend08
alburb02	cohenl07	grimee01	kunoa01	nadkag01	roussoslab	vanbah01
alcal01	cohenp05	grosse08	kurowa01	nadkarnilab-admin	roussp01	vandea10
alcane07	colbes01	guckhp01	kwasia01	nadukr01	rowanb01	vanooj01
alleve01	colemc07	guindm01	kyriad02	naira12	rsheu01	vanvlt02
altaiz01	colemc08	guisad01	lagana01	naitot01	ruand01	vanvok01
althok01	colonj34	gulamf01	lahoty01	narasa01	rubena05	vargac10
altmag01	comelp01	gumus701	lakhac01	nashij01	ruchnd01	vartan01
alzaha01	congx01	guor01	lallim01	naskat01	ruff01	vasudv02
aminih01	cookea02	guow03	lamare01	nativm02	ruizom01	vazar01
amreeb01	correj08	guptam18	lambel02	neala03	ruthek04	vemurk01
andres12	cotea02	gurums01	lambet02	neffr01	ryderj03	venkas08
ankerj01	craryj01	gutiei03	lamw05	neue01	rykund01	ventun01
anyfam01	crokem02	gutien07	landii03	neukap01	sachsd01	verbam01
arakea01	cryosparctest-admin	gux01	larosf01	nga14	saddih01	veremb01
archiving_bings	cryosparc-user	gyasia01	lashbn01	ngaik01	saffem03	vhatkt01
argmac01	cullis01	haass02	laube02	ngj05	sakhua01	viegac01
arista03	cummi06	habibj02	layerd01	nguyec05	salas104	villaa06
arivan01	cunnia06	hackmn01	laynet03	nguyed06	salsan01	vinsod01
arooja01	daidd02	hadasy01	lazarm11	nguyeh16	sanchm63	virant01
arrasj01	daij06	haghif01	lazarus_cryo-admin	nguyep07	sancho03	voloug01
asgars03	daiy07	haghighi_admin	lea63	nguyet47	sangz01	vornhe01
asline01	damarn02	hahna03	leed28	nguyet50	sanies01	vpn02
assadn01	damleg01	haidef02	leed62	nguyet57	sariys01	vyt01
athanr01	daniem14	halasl01	leed77	nicolp01	sartof01	wacked01
ayalaj19	danzet01	halvom01	leej111	nim01	sawana02	wackerlab_cryoadmin
ayvasv01	danzio01	hamonp01	leej167	nirens01	sazeic01	wackerlab_cryoadmin.tbd
babrob01	danzn01	hanh09	leel23	novikg01	sc	walker05
babupk01	dasa06	hankss01	leel26	nudelg01	schade01	wange13
baggea01	dasild04	hanw07	leer50	nukavn01	schafm03	wangh35
bairam01	daskeb01	haoc03	lees111	nwanec01	schmig04	wangh36
bajicg01	dealms01	haok01	lees117	oconnp06	schnej22	wangl2a
balasu01	defeln01	harern01	leew13	oconns05	schron01	wangm05
balbon01	defrej02	harnea01	leew14	oconns06	schuml01	wangm08
bangs02	degrae01	hassod01	leew17	odonnt02	scottm24	wangw32
bankes02	degtya01	haurej01	leforr01	oeltef01	seahc01	wangx38
banuec01	delgaa07	hec10	lehres01	ohw02	seaveradmin	wangx40
baptia05	demird01	heddej01	leonep03	olumue01	sebrar01	wangx44
baptii01	dengc02	heflim01	lepowl01	oreilp01	seeles01	wangy27
barrae02	dengg02	hegdes02	lessec02	oria01	selvam01	wangy33
bartul01	depina02	heisis01	levene03	ortegr01	seoh02	wangz18
barupd01	derear02	hemmeb01	levene04	osmanr01	service_xltech	wangz19
barvij01	derese01	henaoj02	levys17	oterol04	sevime01	wangz21
bazilm05	derosc01	hendee03	levyt03	ozbeyes01	shadrm01	warbup01
becheo01	desmaj01	hernad36	lewisd36	padhia01	shafkr01	warrea08
becke01	desoui01	herrin01	lewisle11	paib01	shahh06	warri01
beckec03	devara02	heyerm01	liharl02	palafm01	shahr24	watanh02
becklab_admin	dibelh01	hirschl07	lij61	palm01	shakyd01	watanr01
beckmn01	dicksj02	hoangd02	lik17	pandeg01	shangj01	webbb02
bedirk01	diezov01	hoffmd09	lik26	pankoa01	shaon01	weeklb01
beganp01	dilips01	hoffmg01	lim39	panti01	sharma45	weia03

bekris02	dillac01	hoganc04	linge01	pareka02	sharmh15	weic04
beltrj11	dinizm01	hoggac01	lingik01	parke15	sharmr06	weilep01
benazm01	disalg01	holtb01	lint07	parkis01	shemir03	weismj01
bendlj01	ditulf02	hoppem02	linx19	parkk14	shenl03	weitzs01
benmek01	divagt01	hos09	lioul01	parkm17	shermj09	wengeb01
bennej21	dogran01	hossar07	LiShen_admin	parkr02	sheuc01	wenglk01
bercor01	domidata	houldj01	liuc06	parpoa01	shevlb01	wenq01
bergea18	domind07	housea03	liuc10	parsonsadmin	shibar02	whitek04
bergqt01	dongp01	houveg01	liuh20	parvam01	shins21	wickrs01
bermaj08	dor01	hradif01	liun05	patela110	shirss01	wiener02
bernel01	dossaj01	hsrdata_admin	lius18	patelf06	siad01	wilsoa28
bernhl03	doughm04	hsuanc01	liux07	pateln127	siehw01	wilsoe22
beykma01	downeh02	huangk06	liuy22	patels115	sigelk01	windae01
bhagwa01	drachs01	humble01	liuy35	patelt16	signam01	winstk01
bhalls02	drfroa01	humphj04	liuy39	pathologywsi_web	signer01	wojcim01
bhattm11	dsouz04	hur03	livana02	patila06	simonm26	wongh04
bhedas01	dsouzs04	hutchk02	liy40	patinj01	simonn10	woodr04
bicakm01	duboib01	huw06	liy42	paulf03	sims01	wuh13
bihiem01	duffya02	ibesw01	liy54	pavlya01	singhb22	wur10
bijia01	duongs02	ibings01	loadadmin	pawlip01	singhm14	wuy21
birnbr02	duplek01	ilkovm01	loboi01	pedicc01	singhs100	wuz07
bobrot01	durenm02	illins01	loherp01	pedrov01	singhs83	wuz08
boixa01	duttas04	imtiaz03	lohy01	pejavv01	singhs96	wylerb01
bonavb01	ebnerj01	indias01	lol01	pengs03	siskr02	xgail01
borrej02	ebraht01	invera03	loosr01	peream01	sistia01	xiad01
bouhae01	edwart10	ioang02	lounsw01	perezp12	slauga01	xiaoy04
boukes01	eggess01	ioniti03	lozanr01	peris01	slesinger-cryoadmin	xiez01
bowlek01	egglet01	ipm	lubitg01	perkd01	slesip02	xiongy01
brat	elahif01	iriki01	luffs01	perkim01	sloofl01	xnat_irw
breene02	elhaim01	irizaa03	luj12	peteri02	slosat03	xuc04
breenm01	ellisr05	iyegbc01	lujama01	peterl02	smitha55	xuj24
brewek04	elmasa02	jacobc05	lukato01	petrab01	smithg17	xuk07
brophe01	elyb01	jacobm07	lukinj01	petraf01	smitr01	xum04
brownm82	emhsr-admin	jacoby02	lukszm01	petris05	socraa01	xup04
buckld05	ensari01	jadhab01	lunda02	petrok01	songh05	xuz07
buckum01	eolia01	jainp08	lundse01	phadna01	songl05	yadavv03
buk02	epibrowser	jalads01	luy12	philis12	songq01	yanga27
bunyas02	epstem06	janecm01	macdok02	phuay01	songw01	yangh17
burgee02	erekaa03	jangb03	macdol02	piaoz03	songx04	yangj27
burstd02	erjavl01	jangdm02	magenta01	picard03	songy12	yangj31
busson02	espess02	jangj06	maherc02	pierap01	sonim01	yangn07
butas01	estebr02	janusm01	mahjab01	pillas03	sooj02	yangs17
butleg04	estilm01	jardis02	mahonr02	pinniu01	soongb02	yaoh01
buxbaa02	evansv03	jayarp02	mal06	pintod02	sorgs01	yaom03
buxbaj01	evardr01	jethav01	malikr02	piquem01	soroke02	yashac01
byunm01	faithj02	jia02	man02	piquem02	soroua01	yeturs08
cabalm04	falcoc04	jiangb02	mandaa05	pjanim03	souait02	yingz01
cabalr04	fangg03	jiangj07	mangoj02	planua01	spehak01	yitshm01
caggic02	fans03	jiangp06	manigc02	plazaa01	spencc13	yiz01
cahann01	fany03	jiangt04	marcoe02	poddan01	spindm02	yoony17
callej03	fariag01	jiangw02	margom04	podlea01	spiven01	yoony09
campag01	farrek04	johnsj64	marina10	polide01	sridhs01	yoo06
canalp02	fenneb02	johnsk86	marina16	porrac01	srisua01	youngh02
cantoa03	fentos02	johnsm50	markek03	pradha04	stalbl01	youssm03
caox01	ferlaj01	jordad05	marketscan	prashf01	stanea02	yua27
cappic01	ferrea06	joshia13	marquc08	preusm01	stapym01	yuang01
carcas01	ferrec14	joshih02	marquc11	priggk01	stechy01	yug03
carroe09	filipd02	joshit02	marros02	printa04	steind16	yuh04
castre11	filizolalab	jostes01	marsae01	provad01	stewao02	yuh08
cattoa01	finka03	juh01	marshd13	prytki01	stocka01	yuj25
celebjadmin	fiorev01	jungs10	martia68	psychgenadmin	strasa01	zafers02
cetinb01	fiorib01	justa01	martij172	pullit02	suarem08	zaidz01
chaiz01	fischj04	kaintk01	martim78	pulsij01	sullim11	zakiy01
chaj03	fleysl01	kajid02	martit26	qasims01	sumowj01	zamard03
chamin01	flodad01	kalagp01	marxg01	qij01	sunc04	zamojm01
chanc36	fludee01	kandos01	maryas01	quidwm02	sunh14	zatorn01
chandp05	fludee02	kannah01	mas07	rabbaa02	sunr02	zbareg01
changa20	fontas06	karaa01	massen06	radkee01	suns09	zebroa01
changh14	forrei01	karabm01	mathud03	rafatf01	suny04	zeibed01
changj33	forstc01	karake01	may08	rahmas14	sunz04	zengb02
chanj24	foxb02	karlom01	maz07	rahmat03	susmaa01	zengq02
charna02	frasem04	karsm02	mccanj06	rajaup01	sutkoj01	zhangb03
chatzc02	freedg02	karven01	mccuss01	rajt01	swansm02	zhangd14
chatzc03	freudy02	kaszet01	mcdona09	ramaka02	syedb01	zhangj62
chavej12	fribom01	kathij01	mckina04	rambam01	syedm13	zhangl26
chdi	fridrm01	katss02	mclaic01	ramira22	szeszko_admin	zhangw09

chenc51	friedb08	kauffj01	mclenk02	ramirj30	szeszp01	zhangx24
chengc12	friedr05	kaufmo01	meadoa02	ramm02	taglim02	zhangx32
chengh04	fuchst04	kellyg03	medinc13	ramosn13	takkak01	zhangy40
chengw06	fultob01	kennye02	meic07	ramoss18	talwas01	zhangz05
chengy10	fuq01	kepin01	melned01	ramses01	tandop03	zhangz19
chenj02admin	fushia01	keraii01	menonk02	randoh01	tangy08	zhangz20
chenl54	fuw01	khaliz03	meranr01	ranglm01	tangy11	zhaoh02
chenla01	gail01	kimc46	merzoe01	rantid01	tasakr01	zhaow05
chenm37	ganesg01	king20	mesroa02	raov04	tastac01	zhaoy14
chenns01	gaox08	kimm61	mestrgr01	rashea05	techdev	zhaoz03
chenr07	garci j62	kimm62	mevery05	ratscg01	techdev6	zhengs07
chenr11	garcim54	kimt15	mezeim01	ravia04	tengs07	zhoub04
chens61	gardng03	kimurh01	miam01	rawalo01	teppea02	zhour02
chent12	gargp01	kimy56	micelr03	reala02	theodd05	zhoux05
cheny60	gelbb01	kinros01	miclar13	rebelv01	therrk01	zhua06
chenz09	gellej01	kirchm05	midyav01	rechko01	thomaa68	zhuj05
chessa01	generb01	kittrh01	mina03	rechte01	thomaa74	zhux02
chestm01	gergut01	kittss01	minerg01	reddam02	thomam32	zilibeg01
cheunk02	gettlk01	klange01	mizet01	reinfe01	thompr21	
chinc18	gey01	kleinr08	mmedsadmin	rentoa01	thorpa03	
chisha02	ghelie01	kodysy03	moeins01	rentzf01	tichks01	
chob04	ghoshr05	koenid03	mognoi01	restrp01	tollall01	
choh07	gibsok04	kohlis03	mohamk08	revab01	torred23	
[palafm01@li03c03 users]\$ cd sc						
[palafm01@li03c03 sc]\$ ls						
ls: cannot open directory .: Permission denied						
[palafm01@li03c03 sc]\$ cd ..						
[palafm01@li03c03 users]\$ ls						
abbote02	choi01	gillr10	kollis05	moik01	rezazs01	torrem67
abida02	choik06	giottb01	konerk01	molzaa01	rhoads01	torrem68
abraha12	choiy07	girdhk01	kongy02	monach01	richaa21	tostag01
adamsa23	chos14	gleasa01	konovk01	moncam01	richtf01	townsk05
adlerm14	chowda26	gleasc04	kornbi01	mongai01	riinan01	tranm05
admodifiers	chowed01	glenm10	koromm03	montek06	riraks01	tristm01
adsp	chrisa21	gnjats01	kosowj01	moolhl01	rissop01	troncl03
afzalr01	chrisb05	goateomics	kosoyr01	morgap04	riverm99	tsanka01
agarwa18	chuk15	gobbut01	koutrm02	morges01	rna	tsankova_admin
agarwp02	chul08	gohels01	kowalr03	morrl11	rocann03	tssetsf01
agawua01	chunga08	golesn01	koziike01	mosaic	rocheg01	turhab01
aggara01	chuny02	gomesp04	kozlea01	moskeo01	rodrij188	turnej11
aggary01	churcn01	gonzaa51	kreka01	mscicadmin	rodri171	turroe01
aggary02	cillea01	gonzae34	krishr12	msm_admin	rodriin15	tuz01
agurk04	cimenc01	gorinn01	kritze01	muenzk01	rodriy04	tylers01
ahmadr02	civlja01	gottas01	kroneb01	mukhek03	rosemf01	tzavan01
ahmedn29	clarkj25	gownip01	krugea01	mukhek05	rosenb16	ukbiobankadmin
aiskom01	clarku01	gp-cryoadmin	ksiezm01	mukunp01	rosene22	ulukag01
ajanab03	clamej05	greaty01	kubler01	muldel01	rosenj57	vaide02
akaluy01	coccie01	greend41	kudrid01	mulleb01	rosenm36	valdeb02
akinka05	cogaadmin	greenk27	kulkak01	mullin04	rothsj06	valena17
alabbs01	cohene20	greenr49	kumara82	muncha01	roudqv01	valend08
alburb02	cohenl07	grimee01	kunoa01	nadkag01	roussoslab	vanbah01
alcalc01	cohenp05	grosse08	kurowa01	nadkarnilab-admin	roussp01	vandea10
alcane07	colbes01	guckhp01	kwasia01	nadukr01	rowanb01	vanooj01
allege01	colemc07	guindm01	kyriad02	naira12	rsheu01	vanvlt02
altaiz01	colemc08	guisad01	lagana01	naitot01	ruand01	vanvok01
althok01	colonj34	gulamf01	lahoty01	narasa01	rubena05	vargac10
altmag01	comelp01	gumus01	lakhac01	nashij01	ruchnd01	vartan01
alzaha01	congxo1	guor01	lallim01	naskat01	ruff01	vasudv02
aminih01	cookea02	guow03	lamare01	nativm02	ruizom01	vazar01
amreeb01	correj08	guptam18	lambel02	neala03	ruthek04	vemurk01
andres12	cotea02	gurums01	lambet02	neffr01	ryderj03	venkas08
ankerj01	craryj01	gutiei03	lamw05	neue01	rykund01	ventun01
anyfam01	crokem02	gutien07	landii03	neukap01	sachsd01	verbam01
arakea01	cryosparctest-admin	gux01	larosf01	nga14	saddih01	veremb01
archiving_bings	cryosparc-user	gyasia01	lashbn01	ngaik01	saffem03	vhatkt01
argmac01	cullis01	haass02	laube02	ngj05	sakhua01	viegac01
arista03	cummid06	habibj02	layerd01	nguyec05	salasl04	villaa06
arivan01	cunniad06	hackmn01	laynet03	nguyed06	salsan01	vinsod01
arooja01	dai02	hadasy01	lazarm11	nguyeh16	sanchm63	virant01
arrasj01	daij06	haghi01	lazarus_cryo-admin	nguyep07	sancho03	voloug01
asgars03	daiy07	haghighi_admin	leea63	nguyet47	sangz01	vornhe01
asline01	damarn02	hahna03	leed28	nguyet50	sanies01	vpnh02
assadr01	damleg01	haidef02	leed62	nguyet57	sariys01	vyt01
athanr01	daniem14	halasl01	leed77	nicolp01	sartof01	wacked01
ayalaj19	danzet01	halvom01	leej111	nim01	sawana02	wackerlab_cryoadmin
ayvasv01	danzio01	hamonp01	leej167	nirens01	sazeic01	wackerlab-cryoadmin.tbd

babrob01	danzn01	hanh09	leel23	novikg01	sc	walker05
babupk01	dasao6	hankss01	leel26	nudelg01	schade01	wange13
baggea01	dasild04	hanw07	leer50	nukavn01	schafm03	wangh35
bairam01	daskeb01	haoc03	lees111	nwanec01	schmig04	wangh36
bajicg01	dealms01	haok01	lees117	oconnp06	schnej22	wangl28
balasu01	defeln01	harern01	leew13	oconns05	schron01	wangm05
balbon01	defrej02	harnea01	leew14	oconns06	schuml01	wangm08
bangs02	degrae01	hassod01	leew17	odonnt02	scottm24	wangw32
bankes02	degtya01	haurej01	leforr01	oeltef01	seahc01	wangx38
banuec01	delgaa07	hec10	lehres01	ohw02	seaveradmin	wangx40
baptia05	demird01	heddej01	leonep03	olumue01	sebrar01	wangx44
baptii01	dengc02	heflim01	lepowl01	oreilp01	seeles01	wangy27
barrae02	dengg02	hegdse02	lessec02	oria01	selvam01	wangy33
bartul01	depina02	heisis01	levene03	ortegr01	seoh02	wangz18
barupd01	derear02	hemmeb01	levene04	osmanr01	service_xltech	wangz19
barvij01	derese01	henaoj02	levys17	oterol04	sevimc01	wangz21
bazilm05	derosc01	hender03	levyt03	ozbays01	shadrm01	warbup01
becheo01	desmaj01	hernad36	lewisd36	padhia01	shafrk01	warrea08
becke01	desoui01	herrin01	lewise11	paib01	shahh06	warrir01
beckec03	devara02	heyerm01	liharl02	palafm01	shahr24	watanh02
becklab_admin	dibelh01	hirscl07	lij61	palm01	shakyd01	watanr01
beckmn01	dicksj02	hoangd02	lik17	pandeg01	shangj01	webbbb02
bedirk01	diezov01	hoffmd09	lik26	pankoa01	shaon01	weeklb01
beganp01	dilips01	hoffmg01	lim39	panti01	sharma45	weia03
bekris02	dillac01	hoganc04	linge01	pareka02	sharmh15	weic04
beltrj11	dinizm01	hoggac01	lingik01	parke15	sharmr06	weilep01
benazm01	disalg01	holtb01	lint07	parkis01	shemir03	weismj01
bendlj01	ditulf02	hoppem02	linx19	parkk14	shenl03	weitzs01
benmek01	divagt01	hos09	lioul01	parkm17	shermj09	wengeb01
bennej21	dogran01	hossar07	LiShen_admin	parkr02	sheuc01	wenglk01
bercor01	domidata	houldj01	liuc06	parpoa01	shevlb01	wenq01
bergea18	domind07	housea03	liuc10	parsonsadmin	shibar02	whitek04
bergqt01	dongp01	houveg01	liuh20	parvam01	shins21	wickrs01
bermaj08	dor01	hradi01	liun05	patela110	shirss01	wiener02
bernel01	dossaj01	hsrdata_admin	lius18	patelf06	siad01	wilsoa28
bernhl03	doughm04	hsuanc01	liux07	pateln127	siehw01	wilsoe22
beykma01	downeh02	huangk06	liuy22	patels115	sigelk01	windae01
bhagwa01	drachs01	humble01	liuy35	patelt16	signam01	winstk01
bhalls02	drfroa01	humphj04	liuy39	pathologywsi_web	signer01	wojcim01
bhattm11	dsouz04	hur03	livana02	patila06	simonm26	wongh04
bhedas01	dsouzs04	hutchk02	liy40	patinj01	simonn10	woodr04
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brat	elahif01	irikih01	luffs01	perkim01	sloofl01	xnat_irw
breene02	elhaim01	irizaa03	luj12	peteri02	slosat03	xuc04
breenn01	ellisr05	iyegbc01	lujama01	peterl02	smitha55	xuj24
brewek04	elmasa02	jacabc05	lukato01	petrab01	smithg17	xuk07
brophe01	elyb01	jacobm07	lukinj01	petraf01	smitr01	xum04
brownm82	emhsr-admin	jacoby02	lukszm01	petris05	socraa01	xup04
buckld05	ensari01	jadhab01	lunda02	petrok01	songh05	xuz07
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burgee02	erekaa02	jangb03	macdol02	piao03	songx04	yangj27
burstd02	erjavl01	jangdm02	magenta01	picard03	songy12	yangj31
busson02	esposs02	jangj06	maherc02	pierap01	sonim01	yangn07
butas01	estebr02	janusm01	mahjab01	pillas03	sooj02	yangs17
butleg04	estilm01	jardis02	mahonr02	pinniu01	soongb02	yaoh01
buxbaa02	evansv03	jayarp02	mal06	pintod02	sorgs01	yaom03
buxbaj01	evardr01	jethav01	malikr02	piquem01	soroke02	yashac01
byunm01	faithj02	jia02	man02	piquem02	soroua01	yeturs08
cabalr04	falcoc04	jiangb02	mandaa05	pjanim03	souait02	yingz01
caggic02	fangg03	jiangj07	mangoj02	planua01	spehak01	yitshm01
cahann01	fans03	jiangp06	manigc02	plazaa01	spence13	yiz01
callej03	fany03	jiangt04	marcoe02	poddan01	spindm02	yoonj17
campag01	fariag01	jiangw02	margom04	podlea01	spiven01	yoony09
	farrek04	johnsj64	marina10	polide01	sridhs01	yoos06

canalp02	fenneb02	johnsk86	marina16	porrac01	srisua01	youngh02
cantoa03	fentos02	johnsm50	markek03	pradha04	stalbl01	youssm03
caox01	ferlaj01	jordad05	marketscan	prashf01	stanea02	yua27
cappic01	ferrea06	joshia13	marquc08	preusm01	stapym01	yuang01
carcas01	ferrec14	joshih02	marquc11	priggk01	stechy01	yug03
carroe09	filipd02	joshit02	marros02	printa04	steind16	yuh04
castre11	filizolalab	jostes01	marsae01	provad01	stewao02	yuh08
cattoa01	finka03	juh01	marshd13	prytki01	stocka01	yuj25
celebjadmin	fiorev01	jungs10	martia68	psychgenadmin	strasa01	zafers02
cetib01	fiorib01	justa01	martij172	pullit02	suarem08	zaidz01
chaiz01	fischj04	kaintk01	martim78	pulsij01	sullim11	zakiy01
chaj03	fleysl01	kajid02	martit26	qasims01	sumowj01	zamard03
chamin01	flodad01	kalagp01	marxg01	qij01	sunc04	zamojm01
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chandp05	fludee02	kannah01	mas07	rabbaa02	sunr02	zbareg01
changa20	fontas06	karaa01	massen06	radkee01	suns09	zebroa01
changh14	forrei01	karabm01	mathud03	rafatf01	suny04	zeibed02
changj33	forstc01	karake01	may08	rahmas14	sunz04	zengb02
chanj24	foxb02	karlom01	maz07	rahmat03	susmaa01	zengq02
charna02	frasesm04	karasm02	mccanj06	rajaup01	sutkoj01	zhangb03
chatzc02	freedg02	karven01	mccuss01	rajt01	swansm02	zhangd14
chatzc03	freudy02	kaszet01	mcdona09	ramaka02	syedb01	zhangj62
chavej12	fribom01	kathij01	mckina04	rambam01	syedm13	zhangl26
chdi	fridrm01	katss02	mclaic01	ramira22	szeszko_admin	zhangw09
chenc51	friedb08	kauffj01	mclenk02	ramirj30	szeszp01	zhangx24
chengc12	friedr05	kaufmo01	meadoa02	ramm02	taglim02	zhangx32
chengh04	fuchst04	kellyg03	medinc13	ramosn13	takkak01	zhangy40
chengw06	fultab01	kennye02	meic07	ramoss18	talwas01	zhangz05
chengy10	fuq01	kepina01	melned01	ramses01	tandop03	zhangz19
chenj02admin	fushia01	keraii01	menonk02	randoh01	tangy08	zhangz20
chenl54	fuw01	khaliz03	meranr01	ranglm01	tangy11	zhaoh02
chenla01	gail01	kimc46	merzoe01	rantid01	tasakr01	zhaow05
chern37	ganesg01	king20	mesroa02	raov04	tastac01	zhaoy14
chenns01	gaox08	kimm61	mestrg01	rashea05	techdev	zhaoz03
chenr07	garciy62	kimm62	meyery05	ratscg01	techdev6	zhengs07
chenr11	garcim54	kimt15	mezeim01	ravia04	tengs07	zhoub04
chens61	gardng03	kimurh01	miam01	rawalo01	teppea02	zhour02
chent12	gargp01	kimy56	micelr03	reala02	theodd05	zhoux05
cheny60	gelbb01	kinros01	miclar13	rebelv01	therrk01	zhua06
chenz09	gellej01	kirchm05	midyav01	rechko01	thomaa68	zhuj05
chessa01	generb01	kittrh01	mina03	rechte01	thomaa74	zhux02
chestm01	gergut01	kittss01	minerg01	reddam02	thomam32	zilbeg01
cheunk02	gettlk01	klange01	mizet01	reinfe01	thompr21	
chinc18	gey01	kleinr08	mmedsadmin	rentoa01	thorpa03	
chisha02	ghelie01	kodysy02	moeins01	rentzf01	tichks01	
chob04	ghoshr05	koenid03	mognoi01	restrp01	tomall01	
choh07	gibsok04	kohlis03	mohamk08	revab01	torred23	

```

[palafm01@li03c03 users]$ cd ..
[palafm01@li03c03 hpc]$ ls
admin-scripts backups benchmark config data home logs lsf packages slurm stats tsm users web
[palafm01@li03c03 hpc]$ cd ..
[palafm01@li03c03 /]$ ls
bin dev gpfs hpc lib local misc net proc run sc sys usr xcat-inventory_build
boot etc home install lib64 media mnt opt root sbin srv tmp var xcatpost
[palafm01@li03c03 /]$ cd sc
[palafm01@li03c03 sc]$ ls
arion cmsdata orga
[palafm01@li03c03 sc]$ cd arion
[palafm01@li03c03 arion]$ ls
disabled_users_home gpfs oldHPCBackup packages projects scratch trash trashadineto tsm work
[palafm01@li03c03 arion]$ cd projects/
[palafm01@li03c03 projects]$ ls

```

abcd	ChowellLab	GCF_OUTPUT	KennyComputational	osmanr01c	sbsuser
abcd_indices	ChromoZoom	GENECAD	kennylab	pacbio	scec_editing
adineto	CISNET	Gene-PARE	KET-MCI	PacbioGenomes	SCENT
adolpvs	clamej05a	GenomicsProstate	KETMR_K23	packages	schade01a
ad-omics	CL_RNAseq	geospatial_ctsa	kiralyLab	PAGES	schaeferLab
ADsystems	COGA	glycoprotein	kleinr08a	pandeg01a	SchizophreniaSVs
AD-TS	CogNeuro	gnbr	kleinr08b	Pan-Squamous	schlea02a
aggara01a	CommonMind	GnjaticLab	Konigorski_lab	pareks02a	schzrnas
aggara01c	COMP201	GOCAR	kraft_lab	parsonslab	scMultiscale
aggara01d	comppath_500k	GPCRSLC	KRAS	parvam01a	scNetwork
AGS_COVID19	comppath_detectors	GriceWES	Labprojects	pathologywsi	scRNA-limbal_stem_
cells					
AHASTratNet	comppath_dev	GTEX	LAG	paul_oreilly	scRNATools
ai	comppath_HNSCC_TMA	GuccioneLab	Lazarus_Cryo	PBG	sealfs01a

AIGH	comppath_liver	guLab	LCNE	PBGTCGA	sealfs01a1
AINO	comppath_lungEGFR	gumus-hipc	LEAP	PCa-Genomics	Seq
airms	comppath_prostateCIN	gumus01a	lessec02p1	PCOSgenetic	SeqLiver
airms_workspace	comppath_viewer	guptay01	LevinsonMDD	PD1signal	sezen-erk
AirUS	ConAD	gutbiome	LINCS	pd-omics	SGG
akbars02a	cordoc02a	H_ad-omics	lin_lab	pejaverlab	sharpa01a
AllSample_VCFFILE_woW0112	COVID	H_aggara01d	Lippert_lab	Perturb-map	shenl03_ml
als-omics	CRAMP_Study	haghif01a	load	peteri02a	Signatures
AMPADWGS	craniofacial	H_AHASTratNet	LOAD	PetraliaLab	sinai-biodesign
AndyIslet	CranioNet	hansor03a	loosr01a	PGDAC	SITAMCOF
ANRP	CranioProject	haok01a	losicb01a	PGV	sleeplab
AQP4	creeds	haok01b	lothar_lab	PHIME-3	SlesingerLab
AREP	CRIPT	HAPmodel	lujama01a	pid_detection	songlab
argmac01a	cross_prime	H_ASChub	lukszaLab	pintod02a	span
ASColumbia	croxsp01a	hATTR	lungwgs	pintod02b	SPARK
ASChub	cryosparc	H_bicsharing	LymeMind	pintod02c	SpikeID
AsgariLab	cryosparcTest	H_bsr2401	LymeMIND2	PLK2	SRB_DG
asthma-allergy	ctcl	H_buxbaj01a	mabc	pMorpheus	STARNET
AtopicDerm	CVDlung	HCC	MACRO	polyg	statgen
bakellab	CV_NSGY	H_clemej05a	mahajm02a	PostopOutcomes	StatHighD
bashia02a	DAC_Murrough	hcup-study	mahjani	prcasurv	sterne04a
bashia02b	DADIsorders	HDPMM	MASCTCD	precisemd	stolog01a
bashia02c	DARPA	H_dudlej01d	mc_dp2	preproc	strive
bashia02d	data-ark	HERVP	MCSimu	primavo	StrokeCode
BAT-NATIVE	dbGAP_CVD	HetLiverCancer	MDMA	prism-mtDNA	subtilis
bcisrf	dcalab	Heyne_lab	MECONIUM	PROGRESS-MRI	sumo
BC_Reservoir	ddp	H_filizm02a	Merad_Lab	project1000	sumo2
BCWG	deep_phenotype	H_gulab	meradm01a	ProteinDesign	SuperHairGEL
BD2K	DeepPROTAC	H_hypatia_shortclinicaltrials	MetaDope	PsoriasisMulti	Szeszko_Biobank
BDS1005	DHasthma	H_TcahnInstitute	mezeim01a	psychAD	taumomics
BeckerLab	DHIPC	HIMC	mezeim01b	psychgen	TCGA
becklab	DigiIBD	HIIVAN	Microglia	psychgen2	tenoeb01a
Bedmaster	Digital	hmDNAm	midbrain_cross_disorder	psychres	test
BernerLab	dincea01a	H_MMEDS	mincej01a	PVI	Tmuris
bernse03a	DiseaseGeneCell	H_onellab	MLCM	PVR	tochea01a
bhardwajLab	dleseq	hoshiy01a	MLCxCancer	R61_Ezogabine	TRD
bicbot	DLP	Houton_Sander	ML_DTC_Recurrence_Risk	RADIEMS	Tsankov_Normal_Lun
g					
bicsharing	DOCM	H_pacbio	ML_in_Heme	radonc_headneck	TSM_TEMP
bigbrain	DRISM	H_PBG	MLlabAllergy	RandR	tuz01a2
BiNGS	DrugSensitivity	hpcadmins	ml_liver_nmp	RAPPS	tuz01b
Biofeedback_VTA	DTR-EFGR	hpcstaff	MMAAAS	rareADRs	ubarri01a
BK_Lab	duboin02a	H_pd-omics	MMEDS	regeneron	ubarri01b
bladder-seq	DYRKNFAT	H_PGDAC	mm-kinase	Resilience	ubarri01c
BMEII_DT	dysphonia	hpims-hpi	MML	rg_bowcoa01	ukb18177_oreilly
BMI1007	EASI-COG	H_rg_psychgen	MNMcohort	rg_buxbaj01a	UKBGWAS
BrainVar	ECHO_ML	HSC_and_Leukemia	moebius	rg_byunm01	UKBIOBANK
BRD4	ECHOpm	H_schlea02a	motor	rg_choj07	untreatedIBD
breast_nlp	ehrlich00	H_Seqliver	MouseDIPGscRNAseq	rg_cunnic02	urology_llms
breen_lab	EHR_ML	H_Signatures	MPN-seq	rg_dunaia01	va-biobank
BRNAFXTAS	elahiomics	HSRData	mscic1	rg_gelbb01	VandECMS
brbrtseq	eMERGE	HTS	mscic2	rg_goatea01	vascbrain
brccs	emhsr	H_tuz01a	msdw_covid	rg_gumus01	VIMS
brrCD8TscmIFN	endocare	Huygens	MSIH-seq	rg_HPIMS	VIVA
brrdnt3a	ensari_lab	H_webbb02a	MSM	rg_huangk06	walkerlab
brriaavgrn	envepi	hyapatia_shortclinicaltrials	MTC	rg_kennye02	walshm02a
brrifnmemory	EPIASD	ibdgc	MUBCD	rg_kleinr08	wanglab
brrmpia	epiAUD	IcahnInstitute	myeloidiPSC	rg_kontoa02	watanabe
brrnrhv	epigenAD	IFNbeta	NARC	rg_lagana01	watanh02a
brrrnvc	epigenBD	igh	NASAWES	rg_nicolp01	webbb02a
brryfvax	epilepsy_prediction_project	Ignaz	ncRNAs	rg_parsons	weijiaTemp
BSR3101	epimark	immunotherapy	Nestlerlab	rg_peterl02	WL
bsr6402	ESCAPE1	INC	Neurofeedback_connectome	rg_psychgen	wnv_forecast
BTCseq	ExoRNA	InfectiousDisease	ngs	rg_sharpa01	WTC_Cancer
buxbaj01a	faithj02a	ipm	NGSCRC	rg_turroe01	XEN1101
buxbaum_data	Fanconi	ipm_Sema4	NGS-MiSeq	rg_turroe01-snap	XLTEK
CABGvsPCI	fangg03a	IRW-BMEII	nicu_ai	rg_voloug01	xuj09a
Cai_ApoE	fangg03b	ISDandHC	nicunet	rg_zhangw09	YangLab_NGS
CALCIUM	Faroese	ISDS	NLPSDOH	RMsystems	yangy13a
canan	fibro-mann	Itan_lab	NMAGM	robot	YEATS
cbd_neuroimaging	filizm02a	jacobm07a	nmibc_bcg	rosenb16a	Yong_Lab_SCS
CCG	FioreLab	JanssenIBD	ochanj01a	roussp01a	YuanLab
celebj01a	FLAI	JanssenIBD-Prospective	01fMem	roussp01b	zeynep_chip
cellPlasticity	FluVac	jianglab	OneBatch	RTP	zeynep_signatures
chdiTrios	FMD	ji_lab	onellab	SAA	zeynep_virus
CHEAR_Untargeted	friedmanlab	Johnsonlab	ophth_glaucoma	sachsd01a	zhangb03a

chenj02a	friedr05-bioinf	K01_connectome	OrACLE_AIWG	Sahoolab	zhangb03b
chessa01a	fuchs_lab	K01_VTA	Organoid_formation	SALUD	zhangw09a
chessa01b	funEpi	k23	OSHAL	sam_bryn	zhoum01a
chessa01c	GCF_MicroArray	karrj02a	osmanr01a	samstr01a	zhuj05a
Chipuk_Laboratory	GCF_MiSeq	kellnc01a	osmanr01b	sbdd	zwakat01a

```

[palafm01@li03c03 projects]$ cd vascbrain/
[palafm01@li03c03 vascbrain]$ ls
A5002 A5009 C7001 C7006          create_rapid_structure.py      N2001 N2006 P6003 P6009      pipeline_trace.txt      sample_fastq_table.
tsv
A5004 A5010 C7002 C7007          FileZilla_3.66.5_win64-setup.exe N2002 N2007 P6004 P6011      pipeline_trace.txt.1    WGS-iPSC
A5006 A5012 C7003 C7009          multiqc_general_stats.txt      N2003 N2008 P6006 pilot      pipeline_trace.txt.2    work
A5007 BioMe C7004 create_fastq_key.R multiqc_report.html           N2004 P6002 P6008 pilot_data report.html
[palafm01@li03c03 vascbrain]$ pwd
/sc/arion/projects/vascbrain
[palafm01@li03c03 vascbrain]$ client_loop: send disconnect: Broken pipe
(base) mariapalafm@11:56PM Desktop % ssh palafm01@minerva.hpc.mssm.edu
#####

```

From April 30st, 2020, Minerva is accessbile only via VPN.

To request VPN:
<https://labs.icaohn.mssm.edu/minervalab/internal-users-minerva-action-required-external-login-nodes-being-removed-on-april-15/>

New Minerva website:
<https://labs.icaohn.mssm.edu/minervalab/>

Please input your password and two factor token:

(palafm01@minerva.hpc.mssm.edu) Password:
Last login: Mon Apr 15 19:47:53 2024 from 10.125.146.225
=====

Run "Minerva_help" for useful Minerva commands and websites

Minerva Documentation at <https://labs.icaohn.mssm.edu/minervalab/documentation/>
Globus guide at <https://labs.icaohn.mssm.edu/minervalab/documentation/file-transfer-globus/>
Minerva training slides at <https://labs.icaohn.mssm.edu/minervalab/resources/the-minerva-user-group-and-training-classes/>
Data Ark Data Sets available on Minerva at <https://labs.icaohn.mssm.edu/minervalab/resources/data-ark/>
GPU guide at <https://labs.icaohn.mssm.edu/minervalab/documentation/gpgpu/>

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=====!!!!!!SEVEN Minerva SPRING TRAINING SESSIONS!!!!!!=====

FULL details at <https://labs.icaohn.mssm.edu/minervalab/minerva-hpc-information-and-training-sessions-2/>

Session 2: Load Sharing Facility (LSF) Job Scheduler – Wednesday, April 3, 1 pm-2 pm
Location: Icahn School of Medicine building (1425 Madison Ave) Room 14-84 (14th FL)
Zoom Registration at https://mssm.zoom.us/webinar/register/WN_lVp2A5SvRV6iL1u4PeCTA

GPU/AI

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Session 4: 5 Ways to Get Started with GPUs – Friday, April 12, 1 pm-2 pm
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Session 7: How to Accelerate Genome Analysis Toolkit (GATK) by using Parabricks – Wednesday, May 1, 1 pm-2 pm

Data Ark

Session 6: Introduction to Data Ark - Mount Sinai Data Commons – Wednesday, April 24, 1 pm-2 pm
Location: Icahn School of Medicine building (1425 Madison Ave) Room L3-36 (3rd FL)
Zoom Registration at https://mssm.zoom.us/webinar/register/WN_Mblda2FySuKpVbvHg7ArQ

=== Send tickets to hpchelp@hpc.mssm.edu ===

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!!!!!!PLEASE ARCHIVE/BACKUP YOUR IMPORTANT FILES
=====

Disk quotas for user palafm01 (uid 26222):

Filesystem	space	quota	limit	grace	files	quota	limit	grace
nfs01-ib0:/hpc	40K	19456M	20480M		15	0	0	

Last report update 2024-04-16-13:40

Project(arion)	User	Usage	Files
arion_projects_vascbrain	palafm01	0	1
root	palafm01	0	24

[palafm01@li03c03 ~]\$ cd /sc/arion/projects/vascbrain

[palafm01@li03c03 ~]\$ cd /sc/arion/projects/vascbrain

```
A5002 A5010 C7003 create_fastq_key.R N2001 N2007 P6006 pilot_data sample_fastq_table.tsv
A5004 A5012 C7004 create_rapid_structure.py N2002 N2008 P6008 pipeline_trace.txt WGS-iPSC
A5006 BioMe C7006 FileZilla_3.66.5_win64-setup.exe N2003 P6002 P6009 pipeline_trace.txt.1 work
A5007 C7001 C7007 multiqc_general_stats.txt N2004 P6003 P6011 pipeline_trace.txt.2
A5009 C7002 C7009 multiqc_report.html N2006 P6004 pilot report.html
```

[palafm01@li03c03 ~]\$ cd WGS-iPSC/

[palafm01@li03c03 WGS-iPSC]\$ ls

[palafm01@li03c03 WGS-iPSC]\$ ls

[palafm01@li03c03 WGS-iPSC]\$ ls

FastQC_output MD5 Novogene report raw_data raw_data.zip Readme.html

[palafm01@li03c03 WGS-iPSC]\$ cd

[palafm01@li03c03 ~]\$ ls

Lingo Reminder.rtf

[palafm01@li03c03 ~]\$ rm Lingo\ Reminder.rtf

[palafm01@li03c03 ~]\$ ls

[palafm01@li03c03 ~]\$ vim .bash

.bash_history .bash_logout .bash_profile .bashrc

[palafm01@li03c03 ~]\$ vim .bash_profile

[palafm01@li03c03 ~]\$ vim .bashrc

[palafm01@li03c03 ~]\$ source .bashrc

[palafm01@li03c03 ~]\$ data

[palafm01@li03c03 ~]\$ cd

[palafm01@li03c03 ~]\$ client_loop: send disconnect: Broken pipe

(base) mariapalafm01@11:57PM Desktop % ssh palafm01@minerva.hpc.mssm.edu

#####

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New Minerva website:

<https://labs.icahn.mssm.edu/minervalab/>

#####

Please input your password and two factor token:

(palafm01@minerva.hpc.mssm.edu) Password:

Last failed login: Tue Apr 16 15:41:10 EDT 2024 from 10.125.143.75 on ssh:notty

There were 12 failed login attempts since the last successful login.

Last login: Tue Apr 16 15:00:01 2024 from 10.125.143.75

=====

Run "Minerva_help" for useful Minerva commands and websites

Minerva Documentation at <https://labs.icahn.mssm.edu/minervalab/documentation/>

Globus guide at <https://labs.icahn.mssm.edu/minervalab/documentation/file-transfer-globus/>

Minerva training slides at <https://labs.icahn.mssm.edu/minervalab/resources/the-minerva-user-group-and-training-classes/>

Data Ark Data Sets available on Minerva at <https://labs.icahn.mssm.edu/minervalab/resources/data-ark/>

GPU guide at <https://labs.icahn.mssm.edu/minervalab/documentation/gpgpu/>

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!!!!PLEASE ARCHIVE/BACKUP YOUR IMPORTANT FILES

```
=====
Disk quotas for user palafm01 (uid 26222):
  Filesystem  space  quota  limit  grace  files  quota  limit  grace
nfs01-ib0:/hpc 44K  19456M  20480M          16          0          0
Last report update 2024-04-17-03:42
Project(arion)      User      Usage      Files
arion_scratch       palafm01    0           1
root                palafm01    0          24
arion_projects_vascbrain palafm01 186.7G     83
[palafm01@li03c03 ~]$ data
[palafm01@li03c03 vascbrain]$ ls
A5002 C7004      N2003 P6011
A5004 C7006      N2004 pilot
A5006 C7007      N2006 pilot_data
A5007 C7009      N2007 pipeline_trace.txt
A5009 create_fastq_key.R      N2008 pipeline_trace.txt.1
A5010 create_rapid_structure.py P6002 pipeline_trace.txt.2
A5012 FileZilla_3.66.5_win64-setup.exe P6003 report.html
BioMe multiqc_general_stats.txt P6004 sample_fastq_table.tsv
C7001 multiqc_report.html    P6006 WGS-iPSC
C7002 N2001      P6008 work
C7003 N2002      P6009
[palafm01@li03c03 vascbrain]$ cd WGS-iPSC/
[palafm01@li03c03 WGS-iPSC]$ ls
FastQC_output MD5 Novogene report raw_data raw_data.zip Readme.html
[palafm01@li03c03 WGS-iPSC]$ mkdir aligned_reads reads scripts results data
[palafm01@li03c03 WGS-iPSC]$ ls
aligned_reads FastQC_output Novogene report raw_data.zip reads scripts
data          MD5          raw_data      Readme.html  results
[palafm01@li03c03 WGS-iPSC]$ ls
aligned_reads FastQC_output Novogene report raw_data.zip reads scripts
data          MD5          raw_data      Readme.html  results
[palafm01@li03c03 WGS-iPSC]$ unzip -l raw_data.zip
Archive: raw_data.zip
  Length      Date    Time    Name
-----
185370  05-25-2022 18:06 raw_data/Rawdata_Readme.pdf
162    05-26-2022 17:54 raw_data/P732912/MD5.txt
23948553718 05-25-2022 23:03 raw_data/P732912/P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz
24432028934 05-25-2022 22:56 raw_data/P732912/P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
25530322114 05-26-2022 04:13 raw_data/P931263/P931263_FDSW220142848-1r_HYMM2DSX2_L1_1.fq.gz
26308842234 05-26-2022 04:15 raw_data/P931263/P931263_FDSW220142848-1r_HYMM2DSX2_L1_2.fq.gz
162    05-26-2022 17:54 raw_data/P931263/MD5.txt
-----
100219932694 7 files
[palafm01@li03c03 WGS-iPSC]$ bsub
bsub> ^C
[palafm01@li03c03 WGS-iPSC]$ bsub -q interactive -n 1 -R 4
bsub> ^C
[palafm01@li03c03 WGS-iPSC]$ bsub -P vascbrain -q interactive -n 8 -W 15 -R span[hosts=1]
bsub>
bsub> ^C
[palafm01@li03c03 WGS-iPSC]$ bsub -P vascbrain
bsub> ^C
[palafm01@li03c03 WGS-iPSC]$ mybalance
User_ID      Project_name  BODE/CATS
-----
palafm01     acc_vascbrain No
```



```

[palafm01@li03c03 WGS-iPSC]$ bsub -P acc_vascbrain -q interactive -n 8 -W 15 -R span[hosts=1]
bsub> bjobs
bsub> ^C
[palafm01@li03c03 WGS-iPSC]$ bsub -P acc_vascbrain -q interactive -W 6:00 -J WGS1 -n 8 -R span[hosts=1]
bsub> ^C
[palafm01@li03c03 WGS-iPSC]$ bjobs -l
No unfinished job found
[palafm01@li03c03 WGS-iPSC]$ cd
[palafm01@li03c03 ~]$ ls
[palafm01@li03c03 ~]$ bsub -P acc_vascbrain -q interactive -W 6:00 -J WGS1 -n 8 -R span[hosts=1]
bsub> ^C
[palafm01@li03c03 ~]$ data
[palafm01@li03c03 vascbrain]$ cd WGS-iPSC/
[palafm01@li03c03 WGS-iPSC]$ ls
aligned_reads  FastQC_output  Novogene report  raw_data.zip  reads  scripts
data           MD5             raw_data         Readme.html   results
[palafm01@li03c03 WGS-iPSC]$ unzip raw_data.zip
Archive:  raw_data.zip
replace raw_data/Rawdata_Readme.pdf? [y]es, [n]o, [A]ll, [N]one, [r]ename: y
  inflating: raw_data/Rawdata_Readme.pdf
replace raw_data/P732912/MD5.txt? [y]es, [n]o, [A]ll, [N]one, [r]ename: y
  inflating: raw_data/P732912/MD5.txt
replace raw_data/P732912/P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz? [y]es, [n]o, [A]ll, [N]one, [r]ename: y
  inflating: raw_data/P732912/P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz  y

replace raw_data/P732912/P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz? [y]es, [n]o, [A]ll, [N]one, [r]ename:  inflating: raw_data/P732912/P732912_F
DSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
replace raw_data/P931263/P931263_FDSW220142848-1r_HYMM2DSX2_L1_1.fq.gz? [y]es, [n]o, [A]ll, [N]one, [r]ename: y
  inflating: raw_data/P931263/P931263_FDSW220142848-1r_HYMM2DSX2_L1_1.fq.gz  y

replace raw_data/P931263/P931263_FDSW220142848-1r_HYMM2DSX2_L1_2.fq.gz? [y]es, [n]o, [A]ll, [N]one, [r]ename:  inflating: raw_data/P931263/P931263_F
DSW220142848-1r_HYMM2DSX2_L1_2.fq.gz  y

replace raw_data/P931263/MD5.txt? [y]es, [n]o, [A]ll, [N]one, [r]ename:  inflating: raw_data/P931263/MD5.txt
error: invalid zip file with overlapped components (possible zip bomb)
To unzip the file anyway, rerun the command with UNZIP_DISABLE_ZIPBOMB_DETECTION=TRUE environment variable
[palafm01@li03c03 WGS-iPSC]$ bsub -P acc_vascbrain -q interactive -n 4 -W 2:00 -R rusage[mem=4000] -R span[hosts=1] -Is /bin/bash
Job <124353955> is submitted to queue <interactive>.
<<Waiting for dispatch ...>>
<<Starting on lc02a28.chimera.hpc.mssm.edu>>
[palafm01@lc02a28 WGS-iPSC]$ ls
aligned_reads  FastQC_output  Novogene report  raw_data.zip  reads  scripts
data           MD5             raw_data         Readme.html   results
[palafm01@lc02a28 WGS-iPSC]$ cd raw_data
[palafm01@lc02a28 raw_data]$ ls
P732912  P931263  Rawdata_Readme.pdf
[palafm01@lc02a28 raw_data]$ cd P732912/
[palafm01@lc02a28 P732912]$ ls
MD5.txt  P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz  P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@lc02a28 P732912]$ cd ..
[palafm01@lc02a28 raw_data]$ ls
P732912  P931263  Rawdata_Readme.pdf
[palafm01@lc02a28 raw_data]$ cd ..
[palafm01@lc02a28 WGS-iPSC]$ ls
aligned_reads  FastQC_output  Novogene report  raw_data.zip  reads  scripts
data           MD5             raw_data         Readme.html   results
[palafm01@lc02a28 WGS-iPSC]$ cd raw_data
[palafm01@lc02a28 raw_data]$ ls
P732912  P931263  Rawdata_Readme.pdf
[palafm01@lc02a28 raw_data]$ ls
P732912  P931263  Rawdata_Readme.pdf
[palafm01@lc02a28 raw_data]$ cd ..
[palafm01@lc02a28 WGS-iPSC]$ pwd
/sc/arion/projects/vascbrain/WGS-iPSC
[palafm01@lc02a28 WGS-iPSC]$ pwd
/sc/arion/projects/vascbrain/WGS-iPSC
[palafm01@lc02a28 WGS-iPSC]$ mkdir hg38
[palafm01@lc02a28 WGS-iPSC]$ wget -P /sc/arion/projects/vascbrain/WGS-iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
--2024-04-17 07:46:45-- https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
Resolving hgdownload.soe.ucsc.edu (hgdownload.soe.ucsc.edu)... 128.114.119.163
Connecting to hgdownload.soe.ucsc.edu (hgdownload.soe.ucsc.edu)128.114.119.163:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 983659424 (938M) [application/x-gzip]
Saving to: '/sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.fa.gz'

```

```

100%[=====>] 983,659,424 39.0MB/s in 25s

```

2024-04-17 07:47:10 (38.2 MB/s) - '/sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.fa.gz' saved [983659424/983659424]

[palafm01@lc02a28 WGS-iPSC]\$ gunzip /sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.fa.gz

```
[palafm01@lc02a28 WGS-iPSC]$
[palafm01@lc02a28 WGS-iPSC]$
[palafm01@lc02a28 WGS-iPSC]$ ls
aligned_reads  FastQC_output  MD5          raw_data      Readme.html  results
data          hg38           Novogene report  raw_data.zip  reads        scripts
[palafm01@lc02a28 WGS-iPSC]$ cd hg38
[palafm01@lc02a28 hg38]$ ls
hg38.fa
[palafm01@lc02a28 hg38]$ cd ..
[palafm01@lc02a28 WGS-iPSC]$ ls
aligned_reads  FastQC_output  MD5          raw_data      Readme.html  results
data          hg38           Novogene report  raw_data.zip  reads        scripts
[palafm01@lc02a28 WGS-iPSC]$ samtools faidx /sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.fa
bash: samtools: command not found
[palafm01@lc02a28 WGS-iPSC]$ module avail
```

```
----- /usr/share/lmod/lmod/modulefiles/Core -----
lmod      settarg
```

```
----- /opt/hpc/packages/minerva-centos7/modulefiles -----
1.79.1                                libbsd/0.11.6                (D)
ANTs/1.9                              libcap/v2
ANTs/2.4.2                            (D)  libcares/1.16.1
BGW-TWAS/07192023                     libdrm/2.4.102
BN/2012                                (D)  libdrm/2.4.107
BaseSpaceCLI/1.1.0                     libdrm/2.4.112
BaseSpaceCLI/1.5.3                     (D)  libdrm/2.4.115-gcc-11.2.0  (D)
BrainNetViewer/1.7                     libedit/3.1
CPAN/5.16.3                            (D)  libelf/0.8.2-gcc-11.2.0
CPAN/5.36.0                            libepoxy/1.5.4
CTPL/0.0.2                             libevent/2.1.12-gcc-11.2.0  (D)
CTPL/0.3.3                             (D)  libexif/0.6.24
EDirect/15.5                           libfabric/1.11.1
FastSMC/18Sep2020                       libffi/3.0.9
FoxitReader/2.4.5                       libffi/3.3
G-PhoCS/1.3                             libffi/3.4.2
GWAMA/2.2.2                             libffi/3.4.4-gcc-11.2.0  (D)
GenomeAlignmentTools/1.0                 libgd/2.3.0
GraphicsMagick/1.3.36                    libgflags/2.2.2
HiC-Pro/3.1.0                             libgit2/1.1.0
ICU/73.2-gcc-11.2.0                     libglew/2.1.0
Imath/3.1.5                             libglm/0.9.9.8
JasPer/4.0.0-gcc-11.2.0                  libglu/9.0.1
LSFqueue/1.0                             libglvnd/1.6.0-gcc-11.2.0
LeTRS/2.2.1                             libgsf/1.14.17
LibreOffice/6.4.6                       libgsf/1.14.49            (D)
LibreOffice/7.4.3.2                     (D)  libidn/1.9
MAESTRO/1.3.1                           libimagequant/4.0.0
MCR/R2017a                               libjpeg-turbo/3.0.0-nasm-2.15.05
MCR/R2017b                               libjpeg/v9
MCR/R2018a                               libmd/1.0.4
MCR/R2019b                               libmng/2.0.3
MCR/R2020b                               (D)  libmnl/1.0.5
MsCAVIAR/6May2021                       libnet/0.10.11
NBIA/4.2.1                              libnet/1.3                (D)
NVFlare/2.4.0                           libnftables/1.0.4
NiftyFit/29Jun17                         libnftnl/1.2.2
PRScs/4Jun2021                           libnl/3.5.0
PTRC/1.1                                libnvidia-container/1.13.4
ParseBio/1.0.4                           libpciaccess/0.16         (D)
R/3.5.1t                                libpng/1.6.40-gcc-11.2.0
R/3.5.3                                  libpsm-infinipath/3.3.26
R/3.6.0dev                               librsvg/2.50.2
R/3.6.0                                  libsigc++/2.0.18
R/3.6.2                                  libsigc++/2.10.2
R/3.6.3                                  libsigc++/3.0.2          (D)
R/4.0.2                                  libsodium/1.0.18
R/4.0.3                                  libspng/0.7.2
R/4.0.4-llvm                             libtiff/test
R/4.1.0-cairo                             libtiff/3.9.7
```

R/4.1.0		libtiff/4.6.0t	(D)
R/4.2.0	(D)	libunwind/1.6.2-gcc-11.2.0	
R/4.2.1		liburcu/v0.14.0-67	
R/4.2.2		liburcu/0.12	
R/4.3.0		liburcu/0.14	(D)
R/4.3.3-intel-mkl		libvips/8.10.6	
R/4.3.3		libvips/8.12.2	(D)
ReadZS/1.0.0		libwebp/1.2.3	
Rmath/3.5.3		libxcb-iccm/0.4.1-5	
Rmath/3.6.3	(D)	libxcb-image/0.4.0-2	
Seurat/3.0		libxcb-keysyms/0.4.0	
abc/0.2.2		libxcb-render-util/0.3.9	
adam/0.27.0		libxcb/1.15	(D)
adapterremoval/2.3.1		libxinerama/190ct2021	
adfr/1.0		libxkbcommon/1.4.0	
admixtools/7.0.2		libxkbcommon/1.5.0	(D)
admixture/1.3.0		libxml2/2.9.10	(D)
advntr/1.3.3		libxmlsec1/1.2.31	
afni/22.3.03		libxshmfence/1.3.2-gcc-11.2.0	
afni/24.0.05		libxslt/1.1.34	
alphafold/2.2.0		libxtend/0.1.6	
alphafold/2.3.2.singularity		liftover/09-Jul-2019	
alphafold/2.3.2.singularity		linuxbrew/2.2.5	(D)
alphafold/2.3.2	(D)	llvm-project/8.0.1	
alphamissense/0.0.1		llvm/10.0.1	
amazon-genomics-cli/1.6.0		llvm/11.1.0	
amazon-genomics-cli/1.6.0		llvm/13.0.1	
amber/18-tools-18-v100		llvm/14.0.6	
amber/18-tools-18		llvm/16.0.6	(D)
amber/20-tools-20-a100		lofreq/2.1.5	(D)
amber/20-tools-20-v100		longtr/2023-12-01	
amber/20-tools-20		lopass/2021-07-19	
amber/20-tools-21-a100		lortia/0.9.9	
amber/20-tools-21-v100		lpsolve/5.5.2.11	
amber/20-tools-21		lsf/10.1	(D)
amber/22-tools-23-a100		lsf_drmaa/1.11re	
amber/22-tools-23-v100	(D)	lsf_drmaa/1.11	(D)
anaconda2/latest		lsgkm/2020-09-09	
anaconda2/2019.03		lz4/1.9.3	
anaconda2/2019.10dev		lz4/1.9.4-gcc-11.2.0	(D)
anaconda2/2019.10	(D)	lz4/1.9.4-gcc-11.2.0	
anaconda3/junk		lzip/1.22	
anaconda3/latest		macs/3.0.0b1	(D)
anaconda3/2018.12	(D)	mafft/7.505	(D)
anaconda3/2019.10		magnum/2.5.4-ampere	
anaconda3/2020.11		magnum/2.5.4-volta	
anaconda3/2021.5		magnum/2.5.4	(D)
anaconda3/2022.10		magnum_gwas/1.0.7b	
anaconda3/2023.09		magnum_gwas/1.0.8	
anaconda3/2024.02		magnum_gwas/1.10	(D)
annotsv/2.2		make/4.2	(D)
annotsv/3.0.7	(D)	makehub/1.0.5	
ant/1.10.9		mallet/202108	
apache-maven/3.6.1		manta/1.6.0	
apptainer/1.2.5		mantra/1.0	
arcashla/0.2.0		marketscan/9.4	
aria2/1.35.0		matlab/R2012b	
arpack-ng/3.8.0		matlab/R2017a	
arrow/0.16.0		matlab/R2018b	
arvados-cli/2.0.3.1		matlab/R2019a	
aselux/1.0.2-beta		matlab/R2020b	
aspera-connect/3.9.6		matlab/R2021a	
aspera-connect/4.2.4	(D)	matlab/R2021b	
at-spi2-atk/2.38.0		matlab/R2022a	(D)
at-spi2-core/2.40.3		matlab_runtime/R2019b	(D)
atacprimertool/1.0		megan/6.18.10	(D)
ataqv/1.2.1		meme/5.1.0	
athr/2.0.0		meme/5.4.1	
atk/2.34.1		meme/5.5.1	(D)
atk/2.36.0		mesa/20.1.6	
atlas/3.10.3		mesa/22.1.4	(D)
atool/0.39.0		mesc/24jun2022	
augustus/f748db4		metabat/2.12.1	
autoconf/2.71	(D)	metal/2018-08-28	(D)
autodock/4.2.6		metamaps/2020-12-07	
autodock_vina/1.1.2		metaphlan/097a52362c79	(D)
		metasoft/2.0.1	

aws-cdk/2.75.1		methpipe/4.1.1	
awscli/latest		methyldackel/0.4.0	
awscli/1.18.195		micromamba/1.5.3-0	
awscli/2.2.14		migec/1.2.9	
awscli/2.4.0		miniforge3/23.3.1-1	
awscli/2.15.15	(D)	minimac4/1.0.2	
axel/2.17.6		minimac4/1.6	(D)
azcopy/10.15.0		minimap2/2.24	(D)
bam2fastx/1.3.1		miso/0.5.4	
bambamc/0.0.50		mixcr/3.0.13	(D)
bamscale/1.0		mmseqs2/13-45111	(D)
bamsurgeon/2019-10		mmvec/1.0.6	
bamtofastq/1.4.1		model-angelo/0.2.4	
bamtools/2.5.1	(D)	modeller/10.4	(D)
basset/0.1.0		monai/1.3.0	
bayestyper/1.5		mosdepth/0.3.1	(D)
bazam/1.0.2		mothur/1.43.0	(D)
bazel/0.24.1	(D)	motioncor2/1.4.2	(D)
bazel/0.29.1		mpfr/4.0.2	(D)
bazel/2.0.0		mpibzip2/0.6	
bbmap/39.06		mplayer/1.5	
bcel/6.4.1		mpxstreveal/2022-10-19	
bcftools/1.9		mr-mega/0.1.5	
bcftools/1.10.2		mr-mega/0.2	(D)
bcftools/1.12		mricon/1.0.20190902	
bcftools/1.15.1		mrtrix3/3.0_RC4	
bcftools/1.16		mrtrix3/3.0.3	
bcftools/1.17	(D)	mrtrix3/3.0.4	(D)
bcl2fastq/2.20.0p3	(D)	msgsteiner/1.3	
beagle/5.1		msisensor-pro/1.0.a	
bedops/2.4.36	(D)	msisensor/0.6	
bedtools/2.29.2		msodbcsql17/17.6.1.1	
bedtools/2.31.0	(D)	mtag/2017-April	
bfg/1.13.2		mtoolbox/1.2.1	
bgen/1.1.7		mutect/1.1.6	
bgen/2020-03-13	(D)	mutserve/2.0.0-rc12	
binutils/2.38		mutsig/1.41	
binutils/2.40-gcc-11.2.0	(D)	mysql++/3.3.0	
biogrinder/0.5.3		mysql/8.0.20	
biolibc/0.2.3		namd/2.13-smp-cuda	
bionemo/1.3		namd/2.13	
bismark/0.22.3	(D)	namd/2.14-smp-cuda	(D)
bison/3.5		namd/2.14	
blast/2.9.0+		namd/3.0a13-multicore-cuda-A100	
blast/2.13.0+		namd/3.0a13-multicore-cuda-H100	
bolotie/3May2021		namd/3.0a13-multicore-cuda-V100	
bolt/2.3.6		namd/3.0a13-multicore-cuda	
boost/1.60.0c		namd/3.0b3-multicore-cuda-A100	
boost/1.60.0.test		namd/3.0b3-multicore-cuda-V100	
boost/1.69.0.intel		nano/4.2	
boost/1.69.0		nasm/2.15.05	
boost/1.78.0-gcc-11.2.0		nbc/1.1	
boost/1.82.0-gcc-11.2.0		ncboost/1.0.0	
bowtie/1.3.0	(D)	nccl/2.19.4	
bowtie2/2.4.1	(D)	ncdu/1.15.1	
bowtie2/2.4.4		ncurses/6.4-gcc-11.2.0	
boxcli/3.0.0		netcat/1.10	
brainiak/0.11		netpbm/10.79.00	
braker/2.1.6		netsurf/3.0	(D)
brotli/1.0.9-gcc-11.2.0		nextflow/20.10.0	
bs-cli/1.1.0		nextflow/21.10.6	
bustools/0.40.0		nextflow/22.02.1	
bwtool/2019.09.21		nextflow/22.10.6	(D)
bx_python/0.7.3		ngmerge/0.3	
byacc/23May2021		ngs-bits/2020_03	(D)
bzip2/1.0.8-gcc-11.2.0	(D)	ngs-sdk/2.11.0	
c3d/1.4.0		ninja/1.11.0	(D)
cDNA_Cupcake/19.0.0		nlopt/2.7.1	
cadd/1.6		noddi/1.05	(D)
cairo/1.17.4		nodejs/10.16.3	
cairo/1.17.6-gcc-11.2.0	(D)	nodejs/14.15.1	
capnp/0.8.0		nodejs/14.17.5	
cargs/1.0.3		nodejs/18.16.1-gcc-11.2.0	(D)
ccmpred/0.3.2		nsight-systems/2019.4.2	
ccp4/8.0	(D)	nvtap/1.2.2	
ccpem/1.6.0		ocaml/4.11.1	(D)

cdbfasta/2018.10.05		octave/5.2.0	
cdna_cupcake/7.0		octave/6.2.0	(D)
cdna_cupcake/7.6		oligoarrayaux/3.8	
cdna_cupcake/8.1		oneAPI/p_2024.1.0.560	
cdna_cupcake/9.0.1		oneapi/p_2024.1.0.560	
cdna_cupcake/9.1.1	(D)	onedrive-cli/1.0.6	
cdna_cupcake/10.0.1		ontad/1.2	
cdna_cupcake/11.0.0		openBLAS/0.3.13	
cdna_cupcake/19.0.0		openBLAS/0.3.21	(D)
cdna_cupcake/21.0.0		openEXR/3.1.5	
cdna_cupcake/28.0.0		openbabel/3.1.1	
cellbender/0.2.1-cpu		opencv/3.4.6	
cellbender/0.2.1-gpu	(D)	opencv/4.1.0	
cellranger-arc/1.0.0		opencv/4.5.1	(D)
cellranger-arc/1.0.1		openeye/2020.2.0	(D)
cellranger-arc/2.0.0		openjpeg/2.3.1	
cellranger-arc/2.0.2	(D)	openjpeg/2.4.0	(D)
cellranger-atac/1.1.0		openmpi/4.0.1	(D)
cellranger-atac/1.2.0		openmpi/4.0.5	
cellranger-atac/2.0.0		openslide/3.4.1	
cellranger-atac/2.1.0	(D)	openssl/1.1.1w-GCC-4.8.5	
cellranger-dna/1.1.0		optitype/1.3.3	(D)
cellranger/3.1.0		orca/1.3.1	
cellranger/4.0.0		orqas/9May2019	
cellranger/5.0.0		p7zip/16.02	
cellranger/5.0.1		p7zip/23.01	(D)
cellranger/6.0.0		pairadise/1.0.0	
cellranger/6.0.0-p3		pandaseq/2.11	
cellranger/6.1.0		pango/1.40.1	
cellranger/6.1.2		pango/1.44.7	(D)
cellranger/7.0.0		panphlan/3.0	
cellranger/7.0.1		parabricks/4.3.0-1	
cellranger/7.1.0		paraclu/2021-02-04	
cellranger/7.2.0		paragraph/2.4a	(D)
cellranger/8.0.0	(D)	paralyzer/1.5	
cellsnr-lite/1.2.2		paraview/5.11.0	(D)
centrifuge/1.0.4		pcr/8.44	
cgif/0.3.0		pcr/8.45	(D)
chiapipe/13Aug2020		pcr2/10.35	
chrom3d/1.0.2		pcr2/10.40-gcc-11.2.0	(D)
chrompainter/0.0.4		pdf2svg/0.2.3	
cipher/1.0.0		peakachu/0.2.0	
circos/0.69-6	(D)	peakhood/0.3	
clark/1.2.6.1		pear/0.9.11	
clipper/2.1.0		pennncnv/1.0.5	
clomics/1.0		peregrine/1.6.3	
cmake/3.14.1		perf/3.10.0	
cmake/3.19.3		periscope/0.1.2	
cmake/3.22.0	(D)	perl5/5.36.0.p	
cmake/3.25.2-gcc-11.2.0		perl5/5.36.0	(D)
cns/1.3		petsc/3.18.5-cuda	
cnvision/2015-10-27		petsc/3.18.5	(D)
cnvator/0.2.7		phantomjs/2.1.1	
cnvator/0.4.1	(D)	phenix/2.1.0	
cnvator/0.4.1p3		phenix/1.15.2	(D)
comet/0.1.13		phenix/1.19.2	
conga/0.1.1		phonon/4.8	
coverm/0.6.0		php/8.1.6	
cppunit/1.13.2		phylosift/1.0.0_01	
cppunit/1.15.1	(D)	phylowgs/1.0-rc2	
cramtools/3.0		picard/2.20.0	
crmapper/2020-04-10	(D)	picard/2.20.5	
cread/0.84		picard/2.22.3	
cryosparc/2.9.0		picard/2.26.10	
cscoretol/1.1		picard/3.1.1	
ctffind/4.1.13		picrust/1.1.4-anaconda2	
ctffind/4.1.14		picrust2/2.3.0b	
cuFFTAdvisor/100ct2019		pileup_region/2022	
cuda-compat/11.7.0		piper/2.0.0	
cuda-compat/12.1.1	(D)	piranha/1.1.3	
cuda/10.1.105		pixmap/0.40.0	
cuda/10.2.89		pixmap/0.42.2-gcc-11.2.0	(D)
cuda/11.0.2		plink/1.90b6.10	
cuda/11.1	(D)	plink/1.90b6.18	
cuda/11.3		plink/1.90b6.21	(D)
cuda/11.3.1		plink/2.0dev060421	

cuda/11.7.0		plink2/dev.3May22	
cuda/11.8.0		plink2/dev.15Apr22	
cuda/12.0.1		plink2/dev.26Jun	
cuda/12.1.1		plink2/v2.00a3.3.cuda	
cudf/cuda100		plink2/v2.00a3.3	
cuda/7.6.5		plink2/2.3	
cuda/8.0.5	(D)	plumed/isdb-intel	
cuda/8.2.0		plumed/2.6.2	(D)
cuda/8.9.5-11		polyfun/2022-02-04	
cuda/8.9.5-12		poppler/22.07.0	(D)
curl/7.64.1	(D)	popscle/0.1b	
curl/7.74.0		proj/6.3.1	
cutadapt/4.2		proj/8.1.0	(D)
cutruntools/2020-01-04		prothint/2.6.0	
d4tools/0.3.0		protobuf-c/1.3.3	
dap/1.0.0		protobuf-c/1.4.0	(D)
dataark/1.0		protobuf/3.11.4	
datamash/1.4		protobuf/3.21.1	(D)
dbeaver/22.3.4		protoc-c/1.3.3	
dbus/1.12.20	(D)	proxies/1	
dcm2nix/1.0.20201102		prsize/2.2.6	
dcm2nix/1.0.20230411	(D)	prsize/4Nov2021	(D)
dcm2k/3.6.7		pugixml/1.14	
deepEMhancer/2Dec2020		purge_dups/1.2.5	
deepabcut/2.3		pv/1.6.20	
deepabcut/2.3.1	(D)	pycharm/2019-03-01	(D)
deepvariant/0.8.0		pyem/0.5	(D)
deepvariant/1.1.0		pyqt/4.12.3	
deepvariant/1.2.0		pyqt4/4.12.3	
deepvariant/1.3.0		pyscenic/0.10.0	
deepvariant/1.4.0		pyscenic/0.11.2	(D)
deepvariant/1.5.0		python/2.7.16	
deepvariant/1.6.0	(D)	python/2.7.17-UCS4	
dejagru/1.6.3		python/2.7.17	
delly/1.1.6	(D)	python/3.7.3	(D)
demuxlet/20190325		python/3.8.2	
dggm/10Mar2019		python/3.10.4	
diamond/0.8.38		python/3.10.14-GCC-4.8.5	
diamond/0.9.31	(D)	python/3.10.14	
dipy/1.7.0		pytorch/1.2.2	
dlang/2.099.0		pytorch/2.2.2-cuda11.8-py3.12	
dmtcp/2.6.0		pytorch/2.2.2-cuda12.1-py3.12	(D)
docbook/4.3		qctool/2.0.6	(D)
dock/6.9	(D)	qhull/7.3.2	
double-conversion/3.3.0-gcc-11.2.0		qhull/8.0.2	(D)
drop2/2019-Nov		qiime/2022.11	
dropest/0.8.6		grupdate/1.1.2	
dx-toolkit/0.314.0		qt/5.12.12	
dx-toolkit/0.325.1	(D)	qtltools/1.2	
ea-utils/1.04.807		qtltools/1.3	(D)
echoR/0.2.3		qualimap/2.2.1	
eclipse/cpp-2019-06		qupath/0.3.2	
eclipse/java-2019-06		qupath/0.4.3	(D)
edirect/20.1.20230731		rail-rna/0.2.4b	(D)
eigen/3.3.9		ramble/2020-08-25	
eigen/3.4.0	(D)	rapids/24.02-cuda12	
elastix/5.0.0		rapids/24.02-cuda118	
elfutils/0.187		rapids/24.02	(D)
emacs/26.1		raremetal/4.15.1	(D)
emacs/26.3		raremetal2/21Mar2018	
emacs/27.1	(D)	rasqual/2019-11-04	(D)
enformer/jan2023		rasterio/1.0.22	
ensemble/0.1.0		raven/1.8.1	
ensemble/0.2.0		re2c/3.0	
ensemble/0.4.0	(D)	reditools/2.0	
epa-ng/0.3.8		redstone/2.1.0	
ess/18.10.2	(D)	regenie/1.0.5.6	
exa/10.2		regenie/1.0.6.9	
expansionhunter/v3.2.0		regenie/1.0.7	
expansionhunter/v3.2.2		regenie/2.0.1	
expansionhunter/v5.0.0	(D)	regenie/2.0.2	
expansionhunterdenovo/0.8.7		regenie/2.2.1	
expansionhunterdenovo/0.9.1		regenie/2.2.4	
expansionhunterdenovo/2019-Sep	(D)	regenie/3.0	
expat/2.5.0-gcc-11.2.0	(D)	regenie/3.1.3	
expect/5.45.4		regenie/3.2.2	(D)

fastenloc/1.0		regenie/3.4.1	
fastenloc/2.0	(D)	regenie/2020-06-24	
fastp/0.20.0		regtools/0.5.1	
fastp/0.23.2	(D)	relion/3.0.8gcc	
fastq-tools/0.8		relion/3.0.8gpu	
fastqc/0.11.9	(D)	relion/3.0.8	
fastqtl/gtex_v6p		relion/3.1.2gpu-dev	
fastqvalidator/0.1.1		relion/3.1.2gpu	
fasttree/2.1.11	(D)	relion/3.1.2	
fastx_toolkit/0.0.13		relion/3.1.3gpu_v	
fbat/V204		relion/3.1.3gpu	
fcgene/1.0.7		relion/4.0.1	
fdupes/2.0.0		relion/5.0-beta-gpu	
feh/3.4		repeatmasker/4.1.1	(D)
ffmpeg/4.4	(D)	reviewer/0.1.1	
fftw/3.3.9	(D)	reviewer/0.2.7	(D)
fgbio/0.8.1		rgt/0.12.1	
fgbio/2.2.1	(D)	ribomap/1.2	
file/5.40		rmats/4.0.2	
finemap/1.3.1		rmats/4.1.0	
finemap/1.4	(D)	rmats/4.1.2	(D)
finestructure/4.1.1		rmblast/2.9.0	
firefox/69.0		rnaeditingindexer/2019-11-19	
firefox/124.0.1	(D)	roary/3.13.0	
fithichip/9.0		root/6.18.02	
fix/1.06.15		root/6.22.2	
flair/1.4		root/6.24.0	
flashpca/2.0		rose/1.2.0	
flex/2.6.4-gcc-11.2.0		rsem/1.3.1	
flex/2.6.4	(D)	rsem/1.3.3	(D)
flexbar/3.5.0	(D)	rserver/2023.03.0	
fltk/1.3.3c		rstudio/1.1.463	(D)
flye/2.9.1		rstudio/2022.02.1-461	
fmrprep/20.2.7		rstudio_singularity/3.6.2	
fmrprep/23.1.4	(D)	rstudio_singularity/2023.06.0-421	(D)
fontconfig/2.13.94		ruby/2.6.3	(D)
fontconfig/2.14.2-gcc-11.2.0	(D)	rust/1.49.0	
forestplot/1.0.3		rust/1.57.0	
freebayes/1.3.2	(D)	rust/1.61.0	(D)
freesurfer/dev-2024-03-12		ruth/2019-08-09	
freesurfer/6.0.0		rv-tdt/2.0	
freesurfer/7.1.0		saige/0.39.2	
freesurfer/7.1.1x		saige/1.1.6	
freesurfer/7.1.1	(D)	saige/1.1.9	
freesurfer/7.2.0		saige/1.3.1	(D)
freesurfer/7.3.2		salmon/0.13.1	
freesurfer/7.4.1		salmon/1.0.0	
freetds/1.2.18		salmon/1.1.0	
freetds/1.4.3	(D)	salmon/1.2.1	
freetype/2.10.0		salmon/1.4.0	(D)
freetype/2.13.0-gcc-11.2.0	(D)	salmonTE/0.4	
fribidi/1.0.5		samblaster/0.1.24	(D)
fsl/6.0.1		samtools/1.6	
fsl/6.0.3		samtools/1.9re	
fsl/6.0.5.2x		samtools/1.9	
fsl/6.0.5.2		samtools/1.11	
fsl/6.0.7.8		samtools/1.12	
fsl/6.0.7.9	(D)	samtools/1.13	
funpack/2.3.2		samtools/1.15.1	
fuse/3.16.2		samtools/1.16	
fusera/0.0.18		samtools/1.17	(D)
fusioncatcher/1.3.3	(D)	sas/9.4	
fusorsv/Jun-27-2019		savvy/1.3.0	
gangstr/2.4.3	(D)	savvy/2.1.0	(D)

[palafm01@lc02a28 WGS-iPSC]\$ module load samtools/1.17

[palafm01@lc02a28 WGS-iPSC]\$ samtools faidx /sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.fa

[palafm01@lc02a28 WGS-iPSC]\$

[palafm01@lc02a28 WGS-iPSC]\$ module load gatk

[palafm01@lc02a28 WGS-iPSC]\$ gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.dict

Using GATK jar /hpc/packages/minerva-centos7/gatk/4.3.0.0/gatk-4.3.0.0/gatk-package-4.3.0.0-local.jar

Running:

java -Dsamjdk.use_async_io_read_samtools=false -Dsamjdk.use_async_io_write_samtools=true -Dsamjdk.use_async_io_write_tribble=false -Dsamjdk.compression_level=2 -jar /hpc/packages/minerva-centos7/gatk/4.3.0.0/gatk-4.3.0.0/gatk-package-4.3.0.0-local.jar CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.dict

INFO 2024-04-17 07:59:08 CreateSequenceDictionary

***** NOTE: Picard's command line syntax is changing.

***** For more information, please see:

[https://github.com/broadinstitute/picard/wiki/Command-Line-Syntax-Transition-For-Users-\(Pre-Transition\)](https://github.com/broadinstitute/picard/wiki/Command-Line-Syntax-Transition-For-Users-(Pre-Transition))

***** The command line looks like this in the new syntax:

***** CreateSequenceDictionary -R /sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.fa -O /sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.dict

07:59:08.438 INFO NativeLibraryLoader - Loading libgkl_compression.so from jar:file:/hpc/packages/minerva-centos7/gatk/4.3.0.0/gatk-4.3.0.0/gatk-pac
kage-4.3.0.0-local.jar!/com/intel/gkl/native/libgkl_compression.so

[Wed Apr 17 07:59:08 EDT 2024] CreateSequenceDictionary OUTPUT=/sc/arion/projects/vascbrain/WGS-iPSC/hg38/hg38.dict REFERENCE=/sc/arion/projects/vasc
brain/WGS-iPSC/hg38/hg38.fa TRUNCATE_NAMES_AT_WHITESPACE=true NUM_SEQUENCES=2147483647 VERBOSITY=INFO QUIET=false VALIDATION_STRINGENCY=STRICT COM
PRESSION_LEVEL=2 MAX_RECORDS_IN_RAM=500000 CREATE_INDEX=false CREATE_MD5_FILE=false GA4GH_CLIENT_SECRETS=client_secrets.json USE_JDK_DEFLATER=false U
SE_JDK_INFLATER=false

[Wed Apr 17 07:59:18 EDT 2024] Executing as palafm01@lc02a28 on Linux 3.10.0-1160.el7.x86_64 amd64; Java HotSpot(TM) 64-Bit Server VM 1.8.0_211-b12;
Deflater: Intel; Inflater: Intel; Provider GCS is available; Picard version: 4.3.0.0

[Wed Apr 17 07:59:31 EDT 2024] picard.sam.CreateSequenceDictionary done. Elapsed time: 0.38 minutes.

Runtime.totalMemory()=902823936

Tool returned:

0

[palafm01@lc02a28 WGS-iPSC]\$

[palafm01@lc02a28 WGS-iPSC]\$ wget -P /sc/arion/projects/vascbrain/WGS-iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/
hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf

--2024-04-17 08:00:13-- https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf

Resolving storage.googleapis.com (storage.googleapis.com)... 142.250.81.251, 142.250.65.219, 142.250.65.187, ...

Connecting to storage.googleapis.com (storage.googleapis.com)|142.250.81.251|:443... connected.

HTTP request sent, awaiting response... 200 OK

Length: 10950827213 (10G) [text/x-vcard]

Saving to: '/sc/arion/projects/vascbrain/WGS-iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf'

100%[=====>] 10,950,827,213 102MB/s in 1m 40s

2024-04-17 08:01:53 (104 MB/s) - '/sc/arion/projects/vascbrain/WGS-iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf' saved [10950827213/10950827213]

[palafm01@lc02a28 WGS-iPSC]\$ wget -P /sc/arion/projects/vascbrain/WGS-iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/
hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx

--2024-04-17 08:02:30-- https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx

Resolving storage.googleapis.com (storage.googleapis.com)... 142.250.176.219, 142.250.80.27, 142.250.80.123, ...

Connecting to storage.googleapis.com (storage.googleapis.com)|142.250.176.219|:443... connected.

HTTP request sent, awaiting response... 200 OK

Length: 12480412 (12M) [application/octet-stream]

Saving to: '/sc/arion/projects/vascbrain/WGS-iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf.idx'

100%[=====>] 12,480,412 65.0MB/s in 0.2s

2024-04-17 08:02:30 (65.0 MB/s) - '/sc/arion/projects/vascbrain/WGS-iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf.idx' saved [12480412/12480412]

[palafm01@lc02a28 WGS-iPSC]\$ ls

aligned_reads FastQC_output MD5 raw_data Readme.html results
data hg38 Novogene report raw_data.zip reads scripts

[palafm01@lc02a28 WGS-iPSC]\$ cd hg38/

[palafm01@lc02a28 hg38]\$ ls

hg38.dict hg38.fa.fai Homo_sapiens_assembly38.dbsnp138.vcf.idx

hg38.fa Homo_sapiens_assembly38.dbsnp138.vcf

[palafm01@lc02a28 hg38]\$ cd

[palafm01@lc02a28 ~]\$

[palafm01@lc02a28 ~]\$ data

[palafm01@lc02a28 vascbrain]\$ cd WGS-iPSC/

[palafm01@lc02a28 WGS-iPSC]\$ pwd

/sc/arion/projects/vascbrain/WGS-iPSC

[palafm01@lc02a28 WGS-iPSC]\$ cd

[palafm01@lc02a28 ~]\$ vim .bashrc

[palafm01@lc02a28 ~]\$ source .bashrc

[palafm01@lc02a28 ~]\$ wgs

[palafm01@lc02a28 WGS-iPSC]\$ ls

aligned_reads FastQC_output MD5 raw_data Readme.html results
data hg38 Novogene report raw_data.zip reads scripts

[palafm01@lc02a28 WGS-iPSC]\$ mkdir results12

[palafm01@lc02a28 WGS-iPSC]\$ ls

```

aligned_reads FastQC_output MD5      raw_data      Readme.html  results  scripts
data          hg38          Novogene report raw_data.zip  reads     results12

[palafm01@lc02a28 WGS-iPSC]$ rm results
rm: cannot remove 'results': Is a directory
[palafm01@lc02a28 WGS-iPSC]$ rm -r results
[palafm01@lc02a28 WGS-iPSC]$ ls
aligned_reads FastQC_output MD5      raw_data      Readme.html  results12
data          hg38          Novogene report raw_data.zip  reads     scripts
[palafm01@lc02a28 WGS-iPSC]$ mkdir data12
[palafm01@lc02a28 WGS-iPSC]$ mkdir aligned_reads12
[palafm01@lc02a28 WGS-iPSC]$ rm -r reads
[palafm01@lc02a28 WGS-iPSC]$ rm -r aligned_reads
[palafm01@lc02a28 WGS-iPSC]$ rm -r data
[palafm01@lc02a28 WGS-iPSC]$ ls
aligned_reads12 FastQC_output MD5      raw_data      Readme.html  scripts
data12          hg38          Novogene report raw_data.zip  results12
[palafm01@lc02a28 WGS-iPSC]$ module avail

```

```

----- /usr/share/lmod/lmod/modulefiles/Core -----
lmod      settarg

----- /opt/hpc/packages/minerva-centos7/modulefiles -----
1.79.1                                libbsd/0.11.6                                (D)
ANTs/1.9                              libcap/v2
ANTs/2.4.2                            (D)      libcares/1.16.1
BGW-TWAS/07192023                    libdrm/2.4.102
BN/2012                               (D)      libdrm/2.4.107
BaseSpaceCLI/1.1.0                   libdrm/2.4.112
BaseSpaceCLI/1.5.3                   (D)      libdrm/2.4.115-gcc-11.2.0      (D)
BrainNetViewer/1.7                   libedit/3.1
CPAN/5.16.3                          (D)      libelf/0.8.2-gcc-11.2.0
CPAN/5.36.0                          libepoxy/1.5.4
CTPL/0.0.2                           libevent/2.1.12-gcc-11.2.0      (D)
CTPL/0.3.3                           (D)      libexif/0.6.24
EDirect/15.5                         libfabric/1.11.1
FastSMC/18Sep2020                    libffi/3.0.9
FoxitReader/2.4.5                   libffi/3.3
G-PhoCS/1.3                         libffi/3.4.2
GWAMA/2.2.2                         libffi/3.4.4-gcc-11.2.0      (D)
GenomeAlignmentTools/1.0             libgd/2.3.0
GraphicsMagick/1.3.36               libgflags/2.2.2
HiC-Pro/3.1.0                       libgit2/1.1.0
ICU/73.2-gcc-11.2.0                 libglew/2.1.0
Imath/3.1.5                         libglm/0.9.9.8
JasPer/4.0.0-gcc-11.2.0             libglu/9.0.1
LSFqueue/1.0                        libglvnd/1.6.0-gcc-11.2.0
LeTRS/2.2.1                         libgsf/1.14.17
LibreOffice/6.4.6                   libgsf/1.14.49                (D)
LibreOffice/7.4.3.2                 (D)      libidn/1.9
MAESTRO/1.3.1                      libimagequant/4.0.0
MCR/R2017a                          libjpeg-turbo/3.0.0-nasm-2.15.05
MCR/R2017b                          libjpeg/v9
MCR/R2018a                          libmd/1.0.4
MCR/R2019b                          libmng/2.0.3
MCR/R2020b                          (D)      libmnl/1.0.5
MsCAVIAR/6May2021                  libnet/0.10.11
NBIA/4.2.1                          libnet/1.3                    (D)
NVFlare/2.4.0                      libnftables/1.0.4
NiftyFit/29Jun17                   libnftnl/1.2.2
PRScs/4Jun2021                     libnl/3.5.0
PTRC/1.1                           libnvidia-container/1.13.4
ParseBio/1.0.4                     libpciaccess/0.16             (D)
R/3.5.1t                           libpng/1.6.40-gcc-11.2.0
R/3.5.3                             libpsm-infinipath/3.3.26
R/3.6.0dev                          librsvg/2.50.2
R/3.6.0                             libsigc++/2.0.18
R/3.6.2                             libsigc++/2.10.2
R/3.6.3                             libsigc++/3.0.2              (D)
R/4.0.2                             libsodium/1.0.18
R/4.0.3                             libspng/0.7.2
R/4.0.4-llvm                       libtiff/test
R/4.1.0-cairo                      libtiff/3.9.7
R/4.1.0                             libtiff/4.6.0t              (D)
R/4.2.0                             (D)      libunwind/1.6.2-gcc-11.2.0
R/4.2.1                             liburcu/v0.14.0-67
R/4.2.2                             liburcu/0.12

```

R/4.3.0		liburcu/0.14	(D)
R/4.3.3-intel-mkl		libvips/8.10.6	
R/4.3.3		libvips/8.12.2	(D)
ReadZS/1.0.0		libwebp/1.2.3	
Rmath/3.5.3		libxcb-icc/0.4.1-5	
Rmath/3.6.3	(D)	libxcb-image/0.4.0-2	
Seurat/3.0		libxcb-keysyms/0.4.0	
abc/0.2.2		libxcb-render-util/0.3.9	
adam/0.27.0		libxcb/1.15	(D)
adapterremoval/2.3.1		libxinerama/190ct2021	
adfr/1.0		libxkbcommon/1.4.0	
admixtools/7.0.2		libxkbcommon/1.5.0	(D)
admixture/1.3.0		libxml2/2.9.10	(D)
advntr/1.3.3		libxmlsec1/1.2.31	
afni/22.3.03		libxshmfence/1.3.2-gcc-11.2.0	
afni/24.0.05		libxslt/1.1.34	
alphafold/2.2.0		libxtend/0.1.6	
alphafold/2.3.2-singularity		liftover/09-Jul-2019	
alphafold/2.3.2.singularity		linuxbrew/2.2.5	(D)
alphafold/2.3.2	(D)	llvm-project/8.0.1	
alphamissense/0.0.1		llvm/10.0.1	
amazon-genomics-cli/1.6.0		llvm/11.1.0	
amazon-genomics-cli/1.6.0		llvm/13.0.1	
amber/18-tools-18-v100		llvm/14.0.6	
amber/18-tools-18		llvm/16.0.6	(D)
amber/20-tools-20-a100		lofreq/2.1.5	(D)
amber/20-tools-20-v100		longtr/2023-12-01	
amber/20-tools-20		lopass/2021-07-19	
amber/20-tools-21-a100		lortia/0.9.9	
amber/20-tools-21-v100		lpsolve/5.5.2.11	
amber/20-tools-21		lsf/10.1	(D)
amber/22-tools-23-a100		lsf_drmaa/1.11re	
amber/22-tools-23-v100	(D)	lsf_drmaa/1.11	(D)
anaconda2/latest		lsgkm/2020-09-09	
anaconda2/2019.03		lz4/1.9.3	
anaconda2/2019.10dev		lz4/1.9.4-gcc-11.2.0	(D)
anaconda2/2019.10	(D)	lzip/1.22	
anaconda3/junk		macs/3.0.0b1	(D)
anaconda3/latest		mafft/7.505	(D)
anaconda3/2018.12	(D)	magma/2.5.4-ampere	
anaconda3/2019.10		magma/2.5.4-volta	
anaconda3/2020.11		magma/2.5.4	(D)
anaconda3/2021.5		magma_gwas/1.0.7b	
anaconda3/2022.10		magma_gwas/1.0.8	
anaconda3/2023.09		magma_gwas/1.10	(D)
anaconda3/2024.02		make/4.2	(D)
annotsv/2.2		makehub/1.0.5	
annotsv/3.0.7	(D)	mallet/202108	
ant/1.10.9		manta/1.6.0	
apache-maven/3.6.1		mantra/1.0	
apptainer/1.2.5		marketscan/9.4	
arcashla/0.2.0		matlab/R2012b	
aria/2.1.35.0		matlab/R2017a	
arpack-ng/3.8.0		matlab/R2018b	
arrow/0.16.0		matlab/R2019a	
arvados-cli/2.0.3.1		matlab/R2020b	
aselux/1.0.2-beta		matlab/R2021a	
aspera-connect/3.9.6		matlab/R2021b	
aspera-connect/4.2.4	(D)	matlab/R2022a	(D)
at-spi2-atk/2.38.0		matlab_runtime/R2019b	(D)
at-spi2-core/2.40.3		megan/6.18.10	(D)
atacprimertool/1.0		meme/5.1.0	
ataqv/1.2.1		meme/5.4.1	
athr/2.0.0		meme/5.5.1	(D)
atk/2.34.1		mesa/20.1.6	
atk/2.36.0		mesa/22.1.4	(D)
atlas/3.10.3		mesc/24jun2022	
atool/0.39.0		metabat/2.12.1	
augustus/f748db4		metal/2018-08-28	(D)
autoconf/2.71	(D)	metamaps/2020-12-07	
autodock/4.2.6		metaphlan/097a52362c79	(D)
autodock_vina/1.1.2		metasoft/2.0.1	
aws-cdk/2.75.1		methpipe/4.1.1	
awscli/latest		methyldackel/0.4.0	
awscli/1.18.195		micromamba/1.5.3-0	
awscli/2.2.14		migec/1.2.9	

awscli/2.4.0		miniforge3/23.3.1-1	
awscli/2.15.15	(D)	minimac4/1.0.2	
axel/2.17.6		minimac4/1.6	(D)
azcopy/10.15.0		minimap2/2.24	(D)
bam2fastx/1.3.1		miso/0.5.4	
bambamc/0.0.50		mixcr/3.0.13	(D)
bamscale/1.0		mmseqs2/13-45111	(D)
bamsurgeon/2019-10		mmvec/1.0.6	
bamtofastq/1.4.1		model-angelo/0.2.4	
bamtools/2.5.1	(D)	modeller/10.4	(D)
basset/0.1.0		monai/1.3.0	
bayestyper/1.5		mosdepth/0.3.1	(D)
bazam/1.0.2		mothur/1.43.0	(D)
bazel/0.24.1	(D)	motioncor2/1.4.2	(D)
bazel/0.29.1		mpfr/4.0.2	(D)
bazel/2.0.0		mpibzip2/0.6	
bbmap/39.06		mplayer/1.5	
bcel/6.4.1		mpxstreveal/2022-10-19	
bcftools/1.9		mr-mega/0.1.5	
bcftools/1.10.2		mr-mega/0.2	(D)
bcftools/1.12		mricon/1.0.20190902	
bcftools/1.15.1		mrtrix3/3.0_RC4	
bcftools/1.16		mrtrix3/3.0.3	
bcftools/1.17	(D)	mrtrix3/3.0.4	(D)
bcl2fastq/2.20.0p3	(D)	msgsteiner/1.3	
beagle/5.1		msisensor-pro/1.0.a	
bedops/2.4.36	(D)	msisensor/0.6	
bedtools/2.29.2		msodbcsql17/17.6.1.1	
bedtools/2.31.0	(D)	mtag/2017-April	
bfg/1.13.2		mttoolbox/1.2.1	
bgen/1.1.7		mutect/1.1.6	
bgen/2020-03-13	(D)	mutserve/2.0.0-rc12	
binutils/2.38		mutsig/1.41	
binutils/2.40-gcc-11.2.0	(D)	mysql+/3.3.0	
biogrinder/0.5.3		mysql/8.0.20	
biolibc/0.2.3		namd/2.13-smp-cuda	
bionemo/1.3		namd/2.13	
bismark/0.22.3	(D)	namd/2.14-smp-cuda	(D)
bison/3.5		namd/2.14	
blast/2.9.0+		namd/3.0a13-multicore-cuda-A100	
blast/2.13.0+		namd/3.0a13-multicore-cuda-H100	
bolotie/3May2021		namd/3.0a13-multicore-cuda-V100	
bolt/2.3.6		namd/3.0a13-multicore-cuda	
boost/1.60.0c		namd/3.0b3-multicore-cuda-A100	
boost/1.60.0.test		namd/3.0b3-multicore-cuda-V100	
boost/1.69.0.intel		nano/4.2	
boost/1.69.0		nasm/2.15.05	
boost/1.78.0-gcc-11.2.0		nbcl/1.1	
boost/1.82.0-gcc-11.2.0		ncboost/1.0.0	
bowtie/1.3.0	(D)	nccl/2.19.4	
bowtie2/2.4.1	(D)	ncdu/1.15.1	
bowtie2/2.4.4		ncurses/6.4-gcc-11.2.0	
boxcli/3.0.0		netcat/1.10	
brainiak/0.11		netpbm/10.79.00	
braker/2.1.6		netsurfp/3.0	(D)
brotli/1.0.9-gcc-11.2.0		nextflow/20.10.0	
bs-cli/1.1.0		nextflow/21.10.6	
bustools/0.40.0		nextflow/22.02.1	
bwtool/2019.09.21		nextflow/22.10.6	(D)
bx_python/0.7.3		ngmerge/0.3	
byacc/23May2021		ngs-bits/2020_03	(D)
bzip2/1.0.8-gcc-11.2.0	(D)	ngs-sdk/2.11.0	
c3d/1.4.0		ninja/1.11.0	(D)
cDNA_Cupcake/19.0.0		nlopt/2.7.1	
cadd/1.6		noddi/1.05	(D)
cairo/1.17.4		nodejs/10.16.3	
cairo/1.17.6-gcc-11.2.0	(D)	nodejs/14.15.1	
capnp/0.8.0		nodejs/14.17.5	
cargs/1.0.3		nodejs/18.16.1-gcc-11.2.0	(D)
ccmpred/0.3.2		nsight-systems/2019.4.2	
ccp4/8.0	(D)	nvtop/1.2.2	
ccpem/1.6.0		ocaml/4.11.1	(D)
cdbfasta/2018.10.05		octave/5.2.0	

[palafm01@lc02a28 WGS-iPSC]\$ module load bwa

[palafm01@lc02a28 WGS-iPSC]\$ bwa -v

[main] unrecognized command '-v'

```
[palafm01@lc02a28 WGS-iPSC]$ bwa --help
[main] unrecognized command '--help'
[palafm01@lc02a28 WGS-iPSC]$ bwa
```

Program: bwa (alignment via Burrows-Wheeler transformation)
Version: 0.7.15-r1140
Contact: Heng Li <lh3@sanger.ac.uk>

Usage: bwa <command> [options]

Command: index index sequences in the FASTA format
mem BWA-MEM algorithm
fastmap identify super-maximal exact matches
pemerger merge overlapping paired ends (EXPERIMENTAL)
aln gapped/ungapped alignment
samse generate alignment (single ended)
sampe generate alignment (paired ended)
bwasw BWA-SW for long queries

shm manage indices in shared memory
fa2pac convert FASTA to PAC format
pac2bwt generate BWT from PAC
pac2bwtgen alternative algorithm for generating BWT
bwtupdate update .bwt to the new format
bwt2sa generate SA from BWT and Occ

Note: To use BWA, you need to first index the genome with 'bwa index'.
There are three alignment algorithms in BWA: 'mem', 'bwasw', and
'aln/samse/sampe'. If you are not sure which to use, try 'bwa mem'
first. Please 'man ./bwa.1' for the manual.

```
[palafm01@lc02a28 WGS-iPSC]$ cd scripts/
[palafm01@lc02a28 scripts]$ ls
[palafm01@lc02a28 scripts]$ touch variant_calling.sh
[palafm01@lc02a28 scripts]$ vim variant_calling.sh
[palafm01@lc02a28 scripts]$ bsub < variant_calling.sh
Job <124354105> is submitted to queue <premium>.
[palafm01@lc02a28 scripts]$ myjobs
bash: myjobs: command not found
[palafm01@lc02a28 scripts]$ jobs
[palafm01@lc02a28 scripts]$ bjobs
      JOBID      USER      JOB_NAME      STAT      QUEUE      FROM_HOST      EXEC_HOST      SUBMIT_TIME      START_TIME      TIME_LEFT
124354105 palafm01 CAD12      RUN      premium lc02a28.ch lc02e16 Apr 17 08:21 Apr 17 08:21 5:33 L
124353955 palafm01 /bin/bash    RUN      interactiv li03c03.ch 4*lc02a28 Apr 17 07:17 Apr 17 07:17 0:29 L
[palafm01@lc02a28 scripts]$ User defined signal 2
[palafm01@li03c03 WGS-iPSC]$ bjobs
No unfinished job found
[palafm01@li03c03 WGS-iPSC]$ ls
aligned_reads12 data12 FastQC_output hg38 MD5 Novogene report raw_data raw_data.zip Readme.html results12 scripts
[palafm01@li03c03 WGS-iPSC]$ cd results12/
[palafm01@li03c03 results12]$ ls
[palafm01@li03c03 results12]$ ls
[palafm01@li03c03 results12]$ cd ..
[palafm01@li03c03 WGS-iPSC]$ ls
aligned_reads12 data12 FastQC_output hg38 MD5 Novogene report raw_data raw_data.zip Readme.html results12 scripts
[palafm01@li03c03 WGS-iPSC]$ cd aligned_reads12/
[palafm01@li03c03 aligned_reads12]$ ls
[palafm01@li03c03 aligned_reads12]$ cd
[palafm01@li03c03 ~]$ ls
[palafm01@li03c03 ~]$ ls
[palafm01@li03c03 ~]$ ls
[palafm01@li03c03 ~]$ wgs
-bash: wgs: command not found
[palafm01@li03c03 ~]$ wgs
-bash: wgs: command not found
[palafm01@li03c03 ~]$ vim .bash
.bash_history .bash_logout .bash_profile .bashrc
[palafm01@li03c03 ~]$ vim .bashrc
[palafm01@li03c03 ~]$ wgs
-bash: wgs: command not found
[palafm01@li03c03 ~]$ data
[palafm01@li03c03 vascbrain]$ ls
A5002 A5007 A5012 C7002 C7006 create_fastq_key.R multiqc_general_stats.txt N2002 N2006 P6002 P6006 P6011 pipeline_trac
e.txt report.html work
A5004 A5009 BioMe C7003 C7007 create_rapid_structure.py multiqc_report.html N2003 N2007 P6003 P6008 pilot pipeline_trac
e.txt.1 sample_fastq_table.tsv
```

```

A5006 A5010 C7001 C7004 C7009 FileZilla_3.66.5_win64-setup.exe N2001 N2004 N2008 P6004 P6009 pilot_data pipeline_trac
e.txt.2 WGS-iPSC
[palafm01@li03c03 vascbrain]$ cd
[palafm01@li03c03 ~]$ ls
[palafm01@li03c03 ~]$ vim .bashrc
[palafm01@li03c03 ~]$ data
[palafm01@li03c03 vascbrain]$ ls
A5002 A5007 A5012 C7002 C7006 create_fastq_key.R multiqc_general_stats.txt N2002 N2006 P6002 P6006 P6011 pipeline_trac
e.txt report.html work
A5004 A5009 BioMe C7003 C7007 create_rapid_structure.py multiqc_report.html N2003 N2007 P6003 P6008 pilot pipeline_trac
e.txt.1 sample_fastq_table.tsv
A5006 A5010 C7001 C7004 C7009 FileZilla_3.66.5_win64-setup.exe N2001 N2004 N2008 P6004 P6009 pilot_data pipeline_trac
e.txt.2 WGS-iPSC
[palafm01@li03c03 vascbrain]$ mv WGS-iPSC WGS_iPSC
[palafm01@li03c03 vascbrain]$ ls
A5002 A5007 A5012 C7002 C7006 create_fastq_key.R multiqc_general_stats.txt N2002 N2006 P6002 P6006 P6011 pipeline_trac
e.txt report.html work
A5004 A5009 BioMe C7003 C7007 create_rapid_structure.py multiqc_report.html N2003 N2007 P6003 P6008 pilot pipeline_trac
e.txt.1 sample_fastq_table.tsv
A5006 A5010 C7001 C7004 C7009 FileZilla_3.66.5_win64-setup.exe N2001 N2004 N2008 P6004 P6009 pilot_data pipeline_trac
e.txt.2 WGS-iPSC
[palafm01@li03c03 vascbrain]$ wgs
-bash: wgs: command not found
[palafm01@li03c03 vascbrain]$ cd
[palafm01@li03c03 ~]$ source .bashrc
[palafm01@li03c03 ~]$ wgs
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads12 data12 FastQC_output hg38 MD5 Novogene report raw_data raw_data.zip Readme.html results12 scripts
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ cat *.stderr
/local/JOBS/1713356512.124354105.shell: line 12: call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices work
flow: command not found
Skipping '/sc/arion/projects/vascbrain/WGS-iPSC/raw_data/P732912/SRR062634_1.filt.fastq.gz' which didn't exist, or couldn't be read
Skipping '/sc/arion/projects/vascbrain/WGS-iPSC/raw_data/P732912/SRR062634_2.filt.fastq.gz' which didn't exist, or couldn't be read
[bwa_index] Pack FASTA... 20.44 sec
[bwa_index] Construct BWT for the packed sequence...
[BWTIncCreate] textLength=6418572210, availableWord=463634060
[BWTIncConstructFromPacked] 10 iterations done. 999999986 characters processed.
[BWTIncConstructFromPacked] 20 iterations done. 1999999986 characters processed.
[BWTIncConstructFromPacked] 30 iterations done. 2999999986 characters processed.
[BWTIncConstructFromPacked] 40 iterations done. 3999999986 characters processed.
[BWTIncConstructFromPacked] 50 iterations done. 4999999986 characters processed.
[BWTIncConstructFromPacked] 60 iterations done. 5999999986 characters processed.
[BWTIncConstructFromPacked] 70 iterations done. 6999999986 characters processed.
[BWTIncConstructFromPacked] 80 iterations done. 7999999986 characters processed.
[BWTIncConstructFromPacked] 90 iterations done. 8999999986 characters processed.
[BWTIncConstructFromPacked] 100 iterations done. 9999999986 characters processed.
[BWTIncConstructFromPacked] 110 iterations done. 10999999986 characters processed.
[BWTIncConstructFromPacked] 120 iterations done. 11999999986 characters processed.
[BWTIncConstructFromPacked] 130 iterations done. 12999999986 characters processed.
[BWTIncConstructFromPacked] 140 iterations done. 13999999986 characters processed.
[BWTIncConstructFromPacked] 150 iterations done. 14999999986 characters processed.
[BWTIncConstructFromPacked] 160 iterations done. 15999999986 characters processed.
[BWTIncConstructFromPacked] 170 iterations done. 16999999986 characters processed.
[BWTIncConstructFromPacked] 180 iterations done. 17999999986 characters processed.
[BWTIncConstructFromPacked] 190 iterations done. 18999999986 characters processed.
[BWTIncConstructFromPacked] 200 iterations done. 19999999986 characters processed.
[BWTIncConstructFromPacked] 210 iterations done. 20999999986 characters processed.
[BWTIncConstructFromPacked] 220 iterations done. 21999999986 characters processed.
[BWTIncConstructFromPacked] 230 iterations done. 22999999986 characters processed.
[BWTIncConstructFromPacked] 240 iterations done. 23999999986 characters processed.
[BWTIncConstructFromPacked] 250 iterations done. 24999999986 characters processed.
[BWTIncConstructFromPacked] 260 iterations done. 25999999986 characters processed.
[BWTIncConstructFromPacked] 270 iterations done. 26999999986 characters processed.
[BWTIncConstructFromPacked] 280 iterations done. 27999999986 characters processed.
[BWTIncConstructFromPacked] 290 iterations done. 28999999986 characters processed.
[BWTIncConstructFromPacked] 300 iterations done. 29999999986 characters processed.
[BWTIncConstructFromPacked] 310 iterations done. 30999999986 characters processed.
[BWTIncConstructFromPacked] 320 iterations done. 31999999986 characters processed.
[BWTIncConstructFromPacked] 330 iterations done. 32999999986 characters processed.
[BWTIncConstructFromPacked] 340 iterations done. 33999999986 characters processed.
[BWTIncConstructFromPacked] 350 iterations done. 34999999986 characters processed.
[BWTIncConstructFromPacked] 360 iterations done. 35999999986 characters processed.
[BWTIncConstructFromPacked] 370 iterations done. 36999999986 characters processed.

```

```

[BWTIncConstructFromPacked] 380 iterations done. 3799999986 characters processed.
[BWTIncConstructFromPacked] 390 iterations done. 3899999986 characters processed.
[BWTIncConstructFromPacked] 400 iterations done. 3999999986 characters processed.
[BWTIncConstructFromPacked] 410 iterations done. 4099999986 characters processed.
[BWTIncConstructFromPacked] 420 iterations done. 4199999986 characters processed.
[BWTIncConstructFromPacked] 430 iterations done. 4299999986 characters processed.
[BWTIncConstructFromPacked] 440 iterations done. 4399999986 characters processed.
[BWTIncConstructFromPacked] 450 iterations done. 4499999986 characters processed.
[BWTIncConstructFromPacked] 460 iterations done. 4599999986 characters processed.
[BWTIncConstructFromPacked] 470 iterations done. 4699999986 characters processed.
[BWTIncConstructFromPacked] 480 iterations done. 4799999986 characters processed.
[BWTIncConstructFromPacked] 490 iterations done. 4899999986 characters processed.
[BWTIncConstructFromPacked] 500 iterations done. 4999999986 characters processed.
[BWTIncConstructFromPacked] 510 iterations done. 5099999986 characters processed.
[BWTIncConstructFromPacked] 520 iterations done. 5199999986 characters processed.
[BWTIncConstructFromPacked] 530 iterations done. 5299999986 characters processed.
[BWTIncConstructFromPacked] 540 iterations done. 5399999986 characters processed.
[BWTIncConstructFromPacked] 550 iterations done. 5499999986 characters processed.
[BWTIncConstructFromPacked] 560 iterations done. 5599999986 characters processed.
[BWTIncConstructFromPacked] 570 iterations done. 5699999986 characters processed.
[BWTIncConstructFromPacked] 580 iterations done. 5798165394 characters processed.
[BWTIncConstructFromPacked] 590 iterations done. 5886412978 characters processed.
[BWTIncConstructFromPacked] 600 iterations done. 5964843650 characters processed.
[BWTIncConstructFromPacked] 610 iterations done. 6034549010 characters processed.
[BWTIncConstructFromPacked] 620 iterations done. 6096499330 characters processed.
[BWTIncConstructFromPacked] 630 iterations done. 6151556914 characters processed.
[BWTIncConstructFromPacked] 640 iterations done. 6200488210 characters processed.
[BWTIncConstructFromPacked] 650 iterations done. 6243974434 characters processed.
[BWTIncConstructFromPacked] 660 iterations done. 6282621122 characters processed.
[BWTIncConstructFromPacked] 670 iterations done. 6316966322 characters processed.
[BWTIncConstructFromPacked] 680 iterations done. 6347488418 characters processed.
[BWTIncConstructFromPacked] 690 iterations done. 6374612482 characters processed.
[BWTIncConstructFromPacked] 700 iterations done. 6398716386 characters processed.
[BWTIncConstructFromPacked] 710 iterations done. 6418572210 characters processed.
[bwa_index] 2644.70 seconds elapse.
[bwa_index] Update BWT... [palafm01@li03c03 scripts]$ less 124354105.stdout
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ vim variant_calling.sh
[palafm01@li03c03 scripts]$ rm variant_calling.sh
[palafm01@li03c03 scripts]$ touch variant_calling_v2.sh
[palafm01@li03c03 scripts]$ vim variant_calling_v2.sh
[palafm01@li03c03 scripts]$ mv variant_calling_v2.sh variant_calling.sh
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads12 data12 FastQC_output hg38 MD5 Novogene report raw_data raw_data.zip Readme.html results12 scripts
[palafm01@li03c03 WGS_iPSC]$ cd data12/
[palafm01@li03c03 data12]$ ls
[palafm01@li03c03 data12]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ mkdir data aligned_reads results
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads aligned_reads12 data data12 FastQC_output hg38 MD5 Novogene report raw_data raw_data.zip Readme.html results results12 scr
ipts
[palafm01@li03c03 WGS_iPSC]$ rm -r data12/
[palafm01@li03c03 WGS_iPSC]$ rm -r results12/
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads aligned_reads12 data FastQC_output hg38 MD5 Novogene report raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ rm -r Novogene\ report/
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads aligned_reads12 data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ rm -r aligned_reads12/
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd data
[palafm01@li03c03 data]$ ls
[palafm01@li03c03 data]$ cd
[palafm01@li03c03 ~]$ wgs
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd FastQC_output/
[palafm01@li03c03 FastQC_output]$ ls
P732912_FDSW220142847-1r_HYMM2DSX2_L1_1_fastqc.html P732912_FDSW220142847-1r_HYMM2DSX2_L1_2_fastqc.zip P931263_FDSW220142848-1r_HYMM2DSX2_L1_2_fas
tc.html
P732912_FDSW220142847-1r_HYMM2DSX2_L1_1_fastqc.zip P931263_FDSW220142848-1r_HYMM2DSX2_L1_1_fastqc.html P931263_FDSW220142848-1r_HYMM2DSX2_L1_2_fas

```



```

tqc.zip
P732912_FDSW220142847-1r_HYMM2DSX2_L1_2_fastqc.html P931263_FDSW220142848-1r_HYMM2DSX2_L1_1_fastqc.zip
[palafm01@li03c03 FastQC_output]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd raw_data
[palafm01@li03c03 raw_data]$ ls
P732912 P931263 Rawdata_Readme.pdf
[palafm01@li03c03 raw_data]$ cd P732912/
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ lss
-bash: lss: command not found
[palafm01@li03c03 P732912]$ ls -l
total 47246689
-rw-r----- 1 palafm01 vascbrain 162 May 26 2022 MD5.txt
-rw-r----- 1 palafm01 vascbrain 23948553718 May 25 2022 P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz
-rw-r----- 1 palafm01 vascbrain 24432028934 May 25 2022 P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ ls -s
total 47246689
1 MD5.txt 23387264 P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz 23859424 P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ ls -sh
total 46G
512 MD5.txt 23G P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz 23G P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ mv P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ mv P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ cd ..
[palafm01@li03c03 raw_data]$ ls
P732912 P931263 Rawdata_Readme.pdf
[palafm01@li03c03 raw_data]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ vim variant_calling.sh
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ bsub < variant_calling.sh
Job <124439081> is submitted to queue <premium>.
[palafm01@li03c03 scripts]$ bjobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT
124439081 palafm01 * looks okay PEND premium li03c03.ch - Apr 17 17:35 - -
[palafm01@li03c03 scripts]$ bjobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT
124439081 palafm01 * looks okay RUN premium li03c03.ch lc02g08 Apr 17 17:35 Apr 17 17:35 5:52 L
[palafm01@li03c03 scripts]$ bjobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT
124439081 palafm01 * looks okay RUN premium li03c03.ch lc02g08 Apr 17 17:35 Apr 17 17:35 5:47 L
[palafm01@li03c03 scripts]$ bjobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT
124439081 palafm01 * looks okay RUN premium li03c03.ch lc02g08 Apr 17 17:35 Apr 17 17:35 5:45 L
[palafm01@li03c03 scripts]$ bjobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT
124439081 palafm01 * looks okay RUN premium li03c03.ch lc02g08 Apr 17 17:35 Apr 17 17:35 5:30 L
[palafm01@li03c03 scripts]$ bjobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT
124439081 palafm01 * looks okay RUN premium li03c03.ch lc02g08 Apr 17 17:35 Apr 17 17:35 5:17 L
[palafm01@li03c03 scripts]$ bjobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT
124439081 palafm01 * looks okay RUN premium li03c03.ch lc02g08 Apr 17 17:35 Apr 17 17:35 4:43 L
[palafm01@li03c03 scripts]$ bjobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT
124439081 palafm01 * looks okay RUN premium li03c03.ch lc02g08 Apr 17 17:35 Apr 17 17:35 4:43 L
[palafm01@li03c03 scripts]$ bjobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT

```

124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:43 L
[palafm01@li03c03 scripts]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:20 L
[palafm01@li03c03 scripts]\$ ls									
124354105.stderr 124354105.stdout variant_calling.sh									
[palafm01@li03c03 scripts]\$ ls-l									
-bash: ls-l: command not found									
[palafm01@li03c03 scripts]\$ cd									
[palafm01@li03c03 ~]\$ ls									
[palafm01@li03c03 ~]\$ vim .bashrc									
[palafm01@li03c03 ~]\$ source .bashrc									
[palafm01@li03c03 ~]\$ bjobs									
JOBDID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124439081	palafm01	* looks okay	RUN	premium	li03c03.ch	lc02g08	Apr 17 17:35	Apr 17 17:35	4:14 L
[palafm01@li03c03 ~]\$ ls									
[palafm01@li03c03 ~]\$ wgs									
[palafm01@li03c03 WGS_iPSC]\$ ls									
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts									
[palafm01@li03c03 WGS_iPSC]\$ cd aligned_reads/									
[palafm01@li03c03 aligned_reads]\$ ls									
[palafm01@li03c03 aligned_reads]\$ cd ..									
[palafm01@li03c03 WGS_iPSC]\$ cd data									
[palafm01@li03c03 data]\$ ls									
[palafm01@li03c03 data]\$ cd ..									
[palafm01@li03c03 WGS_iPSC]\$ cd results/									
[palafm01@li03c03 results]\$ ls									
[palafm01@li03c03 results]\$ cd ..									
[palafm01@li03c03 WGS_iPSC]\$ cd scripts/									
[palafm01@li03c03 scripts]\$ ls									
124354105.stderr 124354105.stdout variant_calling.sh									
[palafm01@li03c03 scripts]\$ lss									
total 34K									
-rw-r-----	1	palafm01	vascbrain	6.4K	Apr 17 09:06	124354105.stderr			
drwxr-s---	2	palafm01	vascbrain	4.0K	Apr 17 17:35	.			
drwxr-s---	10	palafm01	vascbrain	4.0K	Apr 17 17:23	..			
-rw-r-----	1	palafm01	vascbrain	3.5K	Apr 17 09:06	124354105.stdout			
-rw-r-----	1	palafm01	vascbrain	3.5K	Apr 17 17:35	variant_calling.sh			
[palafm01@li03c03 scripts]\$ cd ..									
[palafm01@li03c03 WGS_iPSC]\$ cd hg38/									

```

[palafm01@li03c03 hg38]$ ls
hg38.dict hg38.fa hg38.fa.amb hg38.fa.ann hg38.fa.bwt hg38.fa.fai hg38.fa.pac Homo_sapiens_assembly38.dbsnp138.vcf Homo_sapiens_assembly38.db
snp138.vcf.idx
[palafm01@li03c03 hg38]$ lss
total 17G
-rw-r----- 1 palafm01 vascbrain 11G Jul 21 2016 Homo_sapiens_assembly38.dbsnp138.vcf
-rw-r----- 1 palafm01 vascbrain 3.1G Jan 16 2014 hg38.fa
-rw-r----- 1 palafm01 vascbrain 1.5G Apr 17 09:06 hg38.fa.bwt
-rw-r----- 1 palafm01 vascbrain 1.5G Apr 17 08:22 hg38.fa.pac
-rw-r----- 1 palafm01 vascbrain 12M Jul 21 2016 Homo_sapiens_assembly38.dbsnp138.vcf.idx
-rw-r----- 1 palafm01 vascbrain 59K Apr 17 07:59 hg38.dict
-rw-r----- 1 palafm01 vascbrain 22K Apr 17 08:22 hg38.fa.ann
-rw-r----- 1 palafm01 vascbrain 21K Apr 17 08:22 hg38.fa.amb
-rw-r----- 1 palafm01 vascbrain 19K Apr 17 07:57 hg38.fa.fai
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 17 09:06 .
drwxr-s--- 10 palafm01 vascbrain 4.0K Apr 17 17:23 ..
[palafm01@li03c03 hg38]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ cat variant_calling.sh
UB -J CAD12step1
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R usage[mem=4000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# # # call germline variants in a human WGS paired end reads # # #
# # # 2 X 100bp following GATK4 best practices workflow # # #

# v2 code updates: #####

# [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script
# [done] bashrc alias did not work with WGS-iPSC, so - must be a problem

# [1] update raw data file name by replacing - for _
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz

# ☐ rename script from .sh to .lsf?
# going to test without making this change

# ☐ express instead of premium queue?
# for fast turnaround, premium is default

# lsf parameter considerations: #####

# error and output
# BSUB -oo %J.stdout
# BSUB -eo %J.stderr
# or
#BSUB -o %J.stdout
#BSUB -e %J.stderr

# requirements: #####

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # directories
# /sc/arion/projects/vascbrain/WGS_iPSC/

# # update reads value for each sample
# # CAD12:
# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912

```

```

## # CAD63:
## # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263

ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"

known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"

aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"

reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"

results="/sc/arion/projects/vascbrain/WGS_iPSC/results"

data="/sc/arion/projects/vascbrain/WGS_iPSC/data"

##### Prep files (RUN ONLY ONCE) #####

## # make ref folder
## # mkdir hg38

## # download reference files to folder and unzip #####
## # wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
## # gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz

## # index ref - .fai file before running haplotype caller #####
## # samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa

## # create ref dict file before running haplotype caller #####
## # gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict

## # download known sites files for BQSR from GATK resource bundle #####
## # wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf
## # wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx

##### VARIANT CALLING STEPS #####

# -----
# STEP 1: QC - Run fastqc
# -----

echo "STEP 1: QC - Run fastqc"

fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz -o ${reads}/
fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}/

echo "STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?"

# No trimming required if quality looks okay

[palafm01@li03c03 scripts]$ cd ../raw_data
[palafm01@li03c03 raw_data]$ ls
P732912 P931263 Rawdata_Readme.pdf
[palafm01@li03c03 raw_data]$ cd P732912/
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.zip P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.zip P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.zip
[palafm01@li03c03 P732912]$ bjobs
No unfinished job found
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.zip P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.zip
[palafm01@li03c03 P732912]$ cd ../../scripts/
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout 124439081.stderr 124439081.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ lss

```

```

total 67K
-rw-r----- 1 palafm01 vascbrain 9.9K Apr 17 19:25 124439081.stdout
-rw-r----- 1 palafm01 vascbrain 6.4K Apr 17 09:06 124354105.stderr
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 17 19:25 .
drwxr-s--- 10 palafm01 vascbrain 4.0K Apr 17 17:23 ..
-rw-r----- 1 palafm01 vascbrain 3.5K Apr 17 09:06 124354105.stdout
-rw-r----- 1 palafm01 vascbrain 3.5K Apr 17 17:35 variant_calling.sh
-rw-r----- 1 palafm01 vascbrain 2.8K Apr 17 19:25 124439081.stderr
[palafm01@li03c03 scripts]$ cat 124439081.stdout
Sender: LSF System <lsfadmin@lc02g08>
Subject: Job 124439081: <UB -J CAD12step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.stderr;#BSUB -L /bin/bash; # # # call germline variants in a human WGS paired end reads # # #; # # # 2 X 100bp following GATK4 best practices workflow # # #; # v2 code updates: #####; # [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script; # [done] bashrc alias did not work with WGS-iPSC, so - must be a problem; # [1] update raw data file name by replacing - for _; # [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz; # [ ] rename script from .sh to .lsf?; # going to test without making this change; # [ ] express instead of premium queue?; # for fast turnaround, premium is default; # lsf parameter considerations: #####; #####; # error and output; # BSUB -oo %J.stdout; # BSUB -eo %J.stderr; # or; #BSUB -o %J.stdout; #BSUB -e %J.stderr; # requirements: #####; module load samtools/1.17;module load gatk;module load fastqc;module load bwa; # # directories; # /sc/arion/projects/vascbrain/WGS_iPSC; # # update reads value for each sample;# # CAD12;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912;# # CAD63;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"; known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"; aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"; reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"; results="/sc/arion/projects/vascbrain/WGS_iPSC/results"; data="/sc/arion/projects/vascbrain/WGS_iPSC/data"; ##### Prep files (RUN ONLY ONCE) #####; # # make ref folder;# mkdir hg38; # # download reference files to folder and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz;# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz; # # index ref - .fai file before running haplotype caller #####;# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa; # # create ref dict file before running haplotype caller #####;# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict; # # download known sites files for BQSR from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS #####; # -----;# STEP 1: QC - Run fastqc;# -----; echo "STEP 1: QC - Run fastqc"; fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz -o ${reads}/;fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}/; echo "STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?"; # No trimming required if quality looks okay> in cluster <chimera> Done

Job <UB -J CAD12step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.stderr;#BSUB -L /bin/bash; # # # call germline variants in a human WGS paired end reads # # #; # # # 2 X 100bp following GATK4 best practices workflow # # #; # v2 code updates: #####; # [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script; # [done] bashrc alias did not work with WGS-iPSC, so - must be a problem; # [1] update raw data file name by replacing - for _; # [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz; # [ ] rename script from .sh to .lsf?; # going to test without making this change; # [ ] express instead of premium queue?; # for fast turnaround, premium is default; # lsf parameter considerations: #####; #####; # error and output; # BSUB -oo %J.stdout; # BSUB -eo %J.stderr; # or; #BSUB -o %J.stdout; #BSUB -e %J.stderr; # requirements: #####; module load samtools/1.17;module load gatk;module load fastqc;module load bwa; # # directories;# /sc/arion/projects/vascbrain/WGS_iPSC; # # update reads value for each sample;# # CAD12;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912;# # CAD63;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"; known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"; aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"; reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"; results="/sc/arion/projects/vascbrain/WGS_iPSC/results"; data="/sc/arion/projects/vascbrain/WGS_iPSC/data"; ##### Prep files (RUN ONLY ONCE) #####; # # make ref folder;# mkdir hg38; # # download reference files to folder and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz;# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz; # # index ref - .fai file before running haplotype caller #####;# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa; # # create ref dict file before running haplotype caller #####;# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict; # # download known sites files for BQSR from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS #####; # -----;# STEP 1: QC - Run fastqc;# -----; echo "STEP 1: QC - Run fastqc"; fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz -o ${reads}/;fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}/; echo "STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?"; # No trimming required if quality looks okay> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Wed Apr 17 17:35:30 2024
Job was executed on host(s) <lc02g08>, in queue <premium>, as user <palafm01> in cluster <chimera> at Wed Apr 17 17:35:37 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
Started at Wed Apr 17 17:35:37 2024
Terminated at Wed Apr 17 19:25:55 2024
Results reported at Wed Apr 17 19:25:55 2024

```

Your job looked like:

```

-----
# LSBATCH: User input
UB -J CAD12step1
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00

```

```

#BSUB -R rusage[mem=4000]
#BSUB -oo %J.stdout
#BSUB -eo %J.st derr
#BSUB -L /bin/bash

# # # call germline variants in a human WGS paired end reads # # #
# # # 2 X 100bp following GATK4 best practices workflow # # #

# v2 code updates: #####

# [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script
# [done] bashrc alias did not work with WGS-iPSC, so - must be a problem

# [1] update raw data file name by replacing - for _
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz

# ☐ rename script from .sh to .lsf?
# going to test without making this change

# ☐ express instead of premium queue?
# for fast turnaround, premium is default

# lsf parameter considerations: #####

# error and output
# BSUB -oo %J.stdout
# BSUB -eo %J.st derr
# or
#BSUB -o %J.stdout
#BSUB -e %J.st derr

# requirements: #####

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # directories
# /sc/arion/projects/vascbrain/WGS_iPSC/

(... more ...)
-----

Successfully completed.

Resource usage summary:

CPU time : 6594.62 sec.
Max Memory : 306 MB
Average Memory : 217.97 MB
Total Requested Memory : 4000.00 MB
Delta Memory : 3694.00 MB
Max Swap : -
Max Processes : 6
Max Threads : 17
Run time : 6618 sec.
Turnaround time : 6625 sec.

The output (if any) follows:

STEP 1: QC - Run fastqc
Analysis complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Analysis complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?

PS:

Read file <124439081.st derr> for st derr output of this job.

```

```

[palafm01@li03c03 scripts]$ cat 124439081.std
124439081.stderr 124439081.stdout
[palafm01@li03c03 scripts]$ cat 124439081.stderr
/local/JOBS/1713389730.124439081.shell: line 1: UB: command not found
Started analysis of P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 5% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 10% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 15% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 20% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 25% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 30% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 35% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 40% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 45% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 50% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 55% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 60% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 65% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 70% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 75% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 80% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 85% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 90% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Approx 95% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Started analysis of P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 5% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 10% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 15% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 20% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 25% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 30% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 35% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 40% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 45% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 50% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 55% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 60% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 65% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 70% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 75% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 80% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 85% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 90% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
Approx 95% complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout 124439081.stderr 124439081.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ cat 124439081.stdout
Sender: LSF System <lsfadmin@lc02g08>
Subject: Job 124439081: <UB -J CAD12step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.stderr;#BSUB -L /bin/bash; # # # call germline variants in a human WGS paired end reads # # #; # # # 2 X 100bp following GATK4 best practices workflow # # #; # v2 code updates: #####; # [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script; # [done] bashrc alias did not work with WGS-iPSC, so - must be a problem; # [1] update raw data file name by replacing - for _; # [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz; # [] rename script from .sh to .lsf?; # going to test without making this change; # [] express instead of premium queue?; # for fast turnaround, premium is default; # lsf parameter considerations: #####; #####; # error and output; # BSUB -oo %J.stdout; # BSUB -eo %J.stderr; # or; #BSUB -o %J.stdout; #BSUB -e %J.stderr; # requirements: #####; module load samtools/1.17;module load gatk;module load fastqc;module load bwa; # # director ies;# /sc/arion/projects/vascbrain/WGS_iPSC; # # update reads value for each sample;# # CAD12;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912;# # CAD63;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"; known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"; aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"; reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"; results="/sc/arion/projects/vascbrain/WGS_iPSC/results"; data="/sc/arion/projects/vascbrain/WGS_iPSC/data"; ##### Prep files (RUN ONLY ONCE) #####; # # make ref folder;# mkdir hg38; # # download refere nce files to folder and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz;# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz; # # index ref - .fai file before running haplotype caller #####;# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa; # # create ref dict file before running haplotype caller #####;# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict; # # download known sites files for BQSR from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS #####; # -----;# STEP 1: QC - Run fastqc;# -----; echo "STEP 1: QC - Run fastqc"; fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz -o ${reads}/;fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}/; echo "STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?"; # No trimming required if quality looks okay> in cluster <chimera> Done

Job <UB -J CAD12step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.stderr;#BSUB -L /bin/bash; # # # call germline variants in a human WGS paired end reads # # #; # # # 2 X 100bp following GATK4 best practices workflow # # #; # v2 code updates: #####; # [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this scr

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732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.f
q.gz now P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz; # [] rename script from .sh to .lsf? ; # going to test without making this change; # [] ex
press instead of premium queue? ; # for fast turnaround, premium is default; # lsf parameter considerations: #####
; # error and output ; # BSUB -oo %J.stdout; # BSUB -eo %J.stderr; # or; #BSUB -o %J.stdout; #BSUB -e %J.stderr; # requirements:
#####; module load samtools/1.17;module load gatk;module load fastqc;module load bwa; # # directories;# /sc/arion/proj
ects/vascbrain/WGS_iPSC/; # # update reads value for each sample;# # CAD12;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912;# # CAD63;# #
/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"; known_sites="/sc/arion/projects/va
scbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"; aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"; reads="/sc/arion/pr
jects/vascbrain/WGS_iPSC/raw_data/P732912"; results="/sc/arion/projects/vascbrain/WGS_iPSC/results"; data="/sc/arion/projects/vascbrain/WGS_iPSC/dat
a"; ##### Prep files (RUN ONLY ONCE) #####; # # make ref folder;# mkdir hg38; # # download reference files to folder
and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz;# gunz
ip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz; # # index ref - .fai file before running haplotype caller #####;# samtools faidx /sc/
arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa; # # create ref dict file before running haplotype caller #####;# gatk CreateSequenceDictionary
R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa D=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict; # # download known sites files for BQSR
from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resou
rces/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics
-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS #####;
# -----;# STEP 1: QC - Run fastqc ;# -----; echo "STEP 1: QC - Run fastqc"; fastqc ${reads}/P732912_FDSW220142847-1r_HYM
M2DSX2_L1_1.fq.gz -o ${reads}/fastqc ${reads}/P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}/; echo "STEP 1: fastqc RESULT - No trimming
required if quality looks okay. is it ok?"; # No trimming required if quality looks okay> was submitted from host <li03c03.chimera.hpc.mssm.edu> by u
ser <palafm01> in cluster <chimera> at Wed Apr 17 17:35:30 2024
Job was executed on host(s) <lc02g08>, in queue <premium>, as user <palafm01> in cluster <chimera> at Wed Apr 17 17:35:37 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
Started at Wed Apr 17 17:35:37 2024
Terminated at Wed Apr 17 19:25:55 2024
Results reported at Wed Apr 17 19:25:55 2024

```

Your job looked like:

```

-----
# LSBATCH: User input
UB -J CAD12step1
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=4000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# # # call germline variants in a human WGS paired end reads # # #
# # # 2 X 100bp following GATK4 best practices workflow # # #

# v2 code updates: #####

# [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script
# [done] bashrc alias did not work with WGS-iPSC, so - must be a problem

# [1] update raw data file name by replacing - for _
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz

# [] rename script from .sh to .lsf?
# going to test without making this change

# [] express instead of premium queue?
# for fast turnaround, premium is default

# lsf parameter considerations: #####

# error and output
# BSUB -oo %J.stdout
# BSUB -eo %J.stderr
# or
#BSUB -o %J.stdout
#BSUB -e %J.stderr

# requirements: #####

module load samtools/1.17

```

```
module load gatk
module load fastqc
module load bwa
```

```
# # directories
# /sc/arion/projects/vascbrain/WGS_iPSC/
```

```
(... more ...)
```

Successfully completed.

Resource usage summary:

```
CPU time : 6594.62 sec.
Max Memory : 306 MB
Average Memory : 217.97 MB
Total Requested Memory : 4000.00 MB
Delta Memory : 3694.00 MB
Max Swap : -
Max Processes : 6
Max Threads : 17
Run time : 6618 sec.
Turnaround time : 6625 sec.
```

The output (if any) follows:

STEP 1: QC - Run fastqc

Analysis complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz

Analysis complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz

STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?

PS:

Read file <124439081.stderr> for stderr output of this job.

```
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout 124439081.stderr 124439081.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ lss
total 67K
-rw-r----- 1 palafm01 vascbrain 9.9K Apr 17 19:25 124439081.stdout
-rw-r----- 1 palafm01 vascbrain 6.4K Apr 17 09:06 124354105.stderr
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 17 19:25 .
drwxr-s--- 10 palafm01 vascbrain 4.0K Apr 17 17:23 ..
-rw-r----- 1 palafm01 vascbrain 3.5K Apr 17 09:06 124354105.stdout
-rw-r----- 1 palafm01 vascbrain 3.5K Apr 17 17:35 variant_calling.sh
-rw-r----- 1 palafm01 vascbrain 2.8K Apr 17 19:25 124439081.stderr
[palafm01@li03c03 scripts]$ cd ../raw_data
[palafm01@li03c03 raw_data]$ ls
P732912 P931263 Rawdata_Readme.pdf
[palafm01@li03c03 raw_data]$ cd P732912/
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.zip P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fast
qc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fast
qc.zip
[palafm01@li03c03 P732912]$ lss
total 46G
-rw-r----- 1 palafm01 vascbrain 23G May 25 2022 P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
-rw-r----- 1 palafm01 vascbrain 23G May 25 2022 P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
-rw-r----- 1 palafm01 vascbrain 677K Apr 17 19:25 P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.zip
-rw-r----- 1 palafm01 vascbrain 675K Apr 17 18:30 P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.zip
-rw-r----- 1 palafm01 vascbrain 239K Apr 17 19:25 P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.html
-rw-r----- 1 palafm01 vascbrain 237K Apr 17 18:30 P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.html
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 17 19:25 .
drwxr-s--- 4 palafm01 vascbrain 4.0K Apr 17 06:47 ..
-rw-r----- 1 palafm01 vascbrain 162 May 26 2022 MD5.txt
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.html
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.zip
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.zip P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
[palafm01@li03c03 P732912]$ pwd
/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912
```

```

[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.html
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.zip
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.zip P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fq.gz
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fq.gz
[palafm01@li03c03 P732912]$ wgs
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd raw_data
[palafm01@li03c03 raw_data]$ ls
P732912 P931263 Rawdata_Readme.pdf
[palafm01@li03c03 raw_data]$ cd P931263/
[palafm01@li03c03 P931263]$ ls
MD5.txt P931263_FDSW220142848-1r_HYMM2DSX2_L1_1_fq.gz P931263_FDSW220142848-1r_HYMM2DSX2_L1_2_fq.gz
[palafm01@li03c03 P931263]$ mv P931263_FDSW220142848-1r_HYMM2DSX2_L1_1_fq.gz P931263_FDSW220142848_1r_HYMM2DSX2_L1_1_fq.gz
[palafm01@li03c03 P931263]$ mv P931263_FDSW220142848-1r_HYMM2DSX2_L1_2_fq.gz P931263_FDSW220142848_1r_HYMM2DSX2_L1_2_fq.gz
[palafm01@li03c03 P931263]$ ls
MD5.txt P931263_FDSW220142848_1r_HYMM2DSX2_L1_1_fq.gz P931263_FDSW220142848_1r_HYMM2DSX2_L1_2_fq.gz
[palafm01@li03c03 P931263]$ cd ..
[palafm01@li03c03 raw_data]$ ls
P732912 P931263 Rawdata_Readme.pdf
[palafm01@li03c03 raw_data]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout 124439081.stderr 124439081.stdout variant_calling.sh
[palafm01@li03c03 scripts]$ vim variant_calling.sh
[palafm01@li03c03 scripts]$ bsub < variant_calling.sh
Job <124669344> is submitted to queue <premium>.
[palafm01@li03c03 scripts]$ mkdir CAD12_std
[palafm01@li03c03 scripts]$ ls
124354105.stderr 124354105.stdout 124439081.stderr 124439081.stdout CAD12_std variant_calling.sh
[palafm01@li03c03 scripts]$ mv *.stderr CAD12_std/
[palafm01@li03c03 scripts]$ ls
124354105.stdout 124439081.stdout CAD12_std variant_calling.sh
[palafm01@li03c03 scripts]$ mv *.stdout CAD12_std/
[palafm01@li03c03 scripts]$ ls
CAD12_std variant_calling.sh
[palafm01@li03c03 scripts]$ mkdir CAD63_std
[palafm01@li03c03 scripts]$ ls
CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ chmod 750 variant_calling.sh
[palafm01@li03c03 scripts]$ ls
CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cd
[palafm01@li03c03 ~]$ wgs
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd raw_data
[palafm01@li03c03 raw_data]$ ls
P732912 P931263 Rawdata_Readme.pdf
[palafm01@li03c03 raw_data]$ cd P732912/
[palafm01@li03c03 P732912]$ ls
MD5.txt P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.html
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.html P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fastqc.zip
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fastqc.zip P732912_FDSW220142847_1r_HYMM2DSX2_L1_2_fq.gz
P732912_FDSW220142847_1r_HYMM2DSX2_L1_1_fq.gz
[palafm01@li03c03 P732912]$ cd ..
[palafm01@li03c03 raw_data]$ ls
P732912 P931263 Rawdata_Readme.pdf
[palafm01@li03c03 raw_data]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ vim variant_calling.sh
[palafm01@li03c03 scripts]$ bsub < variant_calling.sh
Job <124675700> is submitted to queue <premium>.
[palafm01@li03c03 scripts]$ myjobs
-bash: myjobs: command not found
[palafm01@li03c03 scripts]$ bjobs

```

JOBID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124669344	palafm01	variant_calling.sh	COMPLETED	premium	li03c03	li03c03	2023-10-27 10:10:10	2023-10-27 10:10:10	00:00:00
124675700	palafm01	variant_calling.sh	COMPLETED	premium	li03c03	li03c03	2023-10-27 10:10:10	2023-10-27 10:10:10	00:00:00

```
124675700 palafm01 CAD12step2 RUN premium li03c03.ch lc02c15 Apr 18 06:05 Apr 18 06:05 6:0 L
124669344 palafm01 * looks okay RUN premium li03c03.ch lc01e30 Apr 18 05:41 Apr 18 05:41 5:36 L
[palafm01@li03c03 scripts]$ jobs
JOBID USER JOB_NAME STAT QUEUE FROM_HOST EXEC_HOST SUBMIT_TIME START_TIME TIME_LEFT
124675700 palafm01 CAD12step2 RUN premium li03c03.ch lc02c15 Apr 18 06:05 Apr 18 06:05 5:45 L
124669344 palafm01 * looks okay RUN premium li03c03.ch lc01e30 Apr 18 05:41 Apr 18 05:41 5:22 L
```

```
[palafm01@li03c03 scripts]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ cd CAD12_std/
[palafm01@li03c03 CAD12_std]$ ls
124354105.stderr 124354105.stdout 124439081.stderr 124439081.stdout
[palafm01@li03c03 CAD12_std]$ ls
total 66K
```

```
-rw-r----- 1 palafm01 vascbrain 9.9K Apr 17 19:25 124439081.stdout
-rw-r----- 1 palafm01 vascbrain 6.4K Apr 17 09:06 124354105.stderr
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 05:42 .
drwxr-s--- 4 palafm01 vascbrain 4.0K Apr 18 06:05 ..
-rw-r----- 1 palafm01 vascbrain 3.5K Apr 17 09:06 124354105.stdout
-rw-r----- 1 palafm01 vascbrain 2.8K Apr 17 19:25 124439081.stderr
[palafm01@li03c03 CAD12_std]$ cat 124439081.stdout
```

Sender: LSF System <lsfadmin@lc02g08>

Subject: Job 124439081: <UB -J CAD12step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.stderr;#BSUB -L /bin/bash; # # # call germline variants in a human WGS paired end reads # # #; # # 2 X 100bp following GATK4 best practices workflow # # #; # v2 code updates: #####; # [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script; # [done] bashrc alias did not work with WGS-iPSC, so - must be a problem; # [1] update raw data file name by replacing - for _; # [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz; # [] rename script from .sh to .lsf?; # going to test without making this change; # [] express instead of premium queue?; # for fast turnaround, premium is default; # lsf parameter considerations: #####; # error and output; # BSUB -oo %J.stdout; # BSUB -eo %J.stderr; # or; #BSUB -o %J.stdout; #BSUB -e %J.stderr; # requirements: #####; module load samtools/1.17;module load gatk;module load fastq;module load bwa; # # directories;# /sc/arion/projects/vascbrain/WGS_iPSC/; # # update reads value for each sample;# # CAD12;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912;# # CAD63;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"; known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"; aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"; reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"; results="/sc/arion/projects/vascbrain/WGS_iPSC/results"; data="/sc/arion/projects/vascbrain/WGS_iPSC/data"; ##### Prep files (RUN ONLY ONCE) #####; # make ref folder;# mkdir hg38; # # download reference files to folder and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz;# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz; # # index ref - .fai file before running haplotype caller #####;# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa; # # create ref dict file before running haplotype caller #####;# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict; # # download known sites files for BQSR from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS #####; # STEP 1: QC - Run fastq;# -----; echo "STEP 1: QC - Run fastq"; fastq \${reads}/P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz -o \${reads}/; fastq \${reads}/P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz -o \${reads}/; echo "STEP 1: fastq RESULT - No trimming required if quality looks okay. is it ok?"; # No trimming required if quality looks okay> in cluster <chimera> Done

Job <UB -J CAD12step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.stderr;#BSUB -L /bin/bash; # # # call germline variants in a human WGS paired end reads # # #; # # 2 X 100bp following GATK4 best practices workflow # # #; # v2 code updates: #####; # [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script; # [done] bashrc alias did not work with WGS-iPSC, so - must be a problem; # [1] update raw data file name by replacing - for _; # [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz; # [] rename script from .sh to .lsf?; # going to test without making this change; # [] express instead of premium queue?; # for fast turnaround, premium is default; # lsf parameter considerations: #####; # error and output; # BSUB -oo %J.stdout; # BSUB -eo %J.stderr; # or; #BSUB -o %J.stdout; #BSUB -e %J.stderr; # requirements: #####; module load samtools/1.17;module load gatk;module load fastq;module load bwa; # # directories;# /sc/arion/projects/vascbrain/WGS_iPSC/; # # update reads value for each sample;# # CAD12;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912;# # CAD63;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"; known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"; aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"; reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"; results="/sc/arion/projects/vascbrain/WGS_iPSC/results"; data="/sc/arion/projects/vascbrain/WGS_iPSC/data"; ##### Prep files (RUN ONLY ONCE) #####; # make ref folder;# mkdir hg38; # # download reference files to folder and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz;# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz; # # index ref - .fai file before running haplotype caller #####;# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa; # # create ref dict file before running haplotype caller #####;# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict; # # download known sites files for BQSR from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS #####; # STEP 1: QC - Run fastq;# -----; echo "STEP 1: QC - Run fastq"; fastq \${reads}/P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz -o \${reads}/; fastq \${reads}/P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz -o \${reads}/; echo "STEP 1: fastq RESULT - No trimming required if quality looks okay. is it ok?"; # No trimming required if quality looks okay> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Wed Apr 17 17:35:30 2024

Job was executed on host(s) <lc02g08>, in queue <premium>, as user <palafm01> in cluster <chimera> at Wed Apr 17 17:35:37 2024

</hpc/users/palafm01> was used as the home directory.

</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.

Started at Wed Apr 17 17:35:37 2024

Terminated at Wed Apr 17 19:25:55 2024

Results reported at Wed Apr 17 19:25:55 2024

Your job looked like:

```
-----
# LSBATCH: User input
UB -J CAD12step1
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=4000]
#BSUB -oo %J.stdout
#BSUB -eo %J.st derr
#BSUB -L /bin/bash

# # # call germline variants in a human WGS paired end reads # # #
# # # 2 X 100bp following GATK4 best practices workflow # # #

# v2 code updates: #####

# [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script
# [done] bashrc alias did not work with WGS-iPSC, so - must be a problem

# [1] update raw data file name by replacing - for _
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz

# ☐ rename script from .sh to .lsf?
# going to test without making this change

# ☐ express instead of premium queue?
# for fast turnaround, premium is default

# lsf parameter considerations: #####

# error and output
# BSUB -oo %J.stdout
# BSUB -eo %J.st derr
# or
#BSUB -o %J.stdout
#BSUB -e %J.st derr

# requirements: #####

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # directories
# /sc/arion/projects/vascbrain/WGS_iPSC/

(... more ...)
```

Successfully completed.

Resource usage summary:

CPU time :	6594.62 sec.
Max Memory :	306 MB
Average Memory :	217.97 MB
Total Requested Memory :	4000.00 MB
Delta Memory :	3694.00 MB
Max Swap :	-
Max Processes :	6
Max Threads :	17
Run time :	6618 sec.
Turnaround time :	6625 sec.

The output (if any) follows:

STEP 1: QC - Run fastqc
Analysis complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Analysis complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?

PS:

Read file <124439081.stderr> for stderr output of this job.

```
[palafm01@li03c03 CAD12_std]$ myjobs
-bash: myjobs: command not found
[palafm01@li03c03 CAD12_std]$ bjobs
      JOBID      USER      JOB_NAME      STAT      QUEUE      FROM_HOST      EXEC_HOST      SUBMIT_TIME      START_TIME      TIME_LEFT
    124675700    palafm01    CAD12step2    RUN      premium    li03c03.ch      lc02c15    Apr 18 06:05    Apr 18 06:05      5:42 L
    124669344    palafm01    * looks okay    RUN      premium    li03c03.ch      lc01e30    Apr 18 05:41    Apr 18 05:41      5:19 L
[palafm01@li03c03 CAD12_std]$ bjobs
No unfinished job found
[palafm01@li03c03 CAD12_std]$ ls
124354105.stderr 124354105.stdout 124439081.stderr 124439081.stdout
[palafm01@li03c03 CAD12_std]$ lss
total 66K
-rw-r----- 1 palafm01 vascbrain 9.9K Apr 17 19:25 124439081.stdout
-rw-r----- 1 palafm01 vascbrain 6.4K Apr 17 09:06 124354105.stderr
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 05:42 .
drwxr-s--- 4 palafm01 vascbrain 4.0K Apr 18 07:31 ..
-rw-r----- 1 palafm01 vascbrain 3.5K Apr 17 09:06 124354105.stdout
-rw-r----- 1 palafm01 vascbrain 2.8K Apr 17 19:25 124439081.stderr
[palafm01@li03c03 CAD12_std]$ cat 124439081.stdout
Sender: LSF System <lsfadmin@lc02g08>
Subject: Job 124439081: <UB -J CAD12step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.stderr;#BSUB -L /bin/bash; # # # call germline variants in a human WGS paired end reads # # #; # # 2 X 100bp following GATK4 best practices workflow # # #; # v2 code updates: #####; # [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script; # [done] bashrc alias did not work with WGS-iPSC, so - must be a problem; # [1] update raw data file name by replacing - for _; # [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz; # [] rename script from .sh to .lsf? ; # going to test without making this change; # [] express instead of premium queue? ; # for fast turnaround, premium is default; # lsf parameter considerations: #####; #####; # error and output ; # BSUB -oo %J.stdout; # BSUB -eo %J.stderr; # or; #BSUB -o %J.stdout; #BSUB -e %J.stderr; # requirements: #####; module load samtools/1.17;module load gatk;module load fastqc;module load bwa; # # directories;# /sc/arion/projects/vascbrain/WGS_iPSC/; # # update reads value for each sample;# # CAD12;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912;# # CAD63;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"; known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"; aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"; reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"; results="/sc/arion/projects/vascbrain/WGS_iPSC/results"; data="/sc/arion/projects/vascbrain/WGS_iPSC/data"; ##### Prep files (RUN ONLY ONCE) #####; # # make ref folder;# mkdir hg38; # # download reference files to folder and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz;# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz; # # index ref - .fai file before running haplotype caller #####;# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa; # # create ref dict file before running haplotype caller #####;# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict; # # download known sites files for BQSR from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS #####; #####; # -----; STEP 1: QC - Run fastqc ;# -----; echo "STEP 1: QC - Run fastqc"; fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz -o ${reads}/fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}/; echo "STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?"; # No trimming required if quality looks okay> in cluster <chimera> Done
```

```
Job <UB -J CAD12step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.stderr;#BSUB -L /bin/bash; # # # call germline variants in a human WGS paired end reads # # #; # # 2 X 100bp following GATK4 best practices workflow # # #; # v2 code updates: #####; # [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script; # [done] bashrc alias did not work with WGS-iPSC, so - must be a problem; # [1] update raw data file name by replacing - for _; # [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz; # [] rename script from .sh to .lsf? ; # going to test without making this change; # [] express instead of premium queue? ; # for fast turnaround, premium is default; # lsf parameter considerations: #####; #####; # error and output ; # BSUB -oo %J.stdout; # BSUB -eo %J.stderr; # or; #BSUB -o %J.stdout; #BSUB -e %J.stderr; # requirements: #####; module load samtools/1.17;module load gatk;module load fastqc;module load bwa; # # directories;# /sc/arion/projects/vascbrain/WGS_iPSC/; # # update reads value for each sample;# # CAD12;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912;# # CAD63;# # /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"; known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"; aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"; reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"; results="/sc/arion/projects/vascbrain/WGS_iPSC/results"; data="/sc/arion/projects/vascbrain/WGS_iPSC/data"; ##### Prep files (RUN ONLY ONCE) #####; # # make ref folder;# mkdir hg38; # # download reference files to folder and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz;# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz; # # index ref - .fai file before running haplotype caller #####;# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa; # # create ref dict file before running haplotype caller #####;# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict; # # download known sites files for BQSR from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics
```

```
-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS #####;
# -----;# STEP 1: QC - Run fastqc ;# -----; echo "STEP 1: QC - Run fastqc"; fastqc ${reads}/P732912_FDSW220142847_1r_HYM
M2DSX2_L1_1.fq.gz -o ${reads}/;fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}/; echo "STEP 1: fastqc RESULT - No trimming
required if quality looks okay. is it ok?"; # No trimming required if quality looks okay> was submitted from host <li03c03.chimera.hpc.mssm.edu> by u
ser <palafm01> in cluster <chimera> at Wed Apr 17 17:35:30 2024
Job was executed on host(s) <lc02g08>, in queue <premium>, as user <palafm01> in cluster <chimera> at Wed Apr 17 17:35:37 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
Started at Wed Apr 17 17:35:37 2024
Terminated at Wed Apr 17 19:25:55 2024
Results reported at Wed Apr 17 19:25:55 2024
```

Your job looked like:

```
-----
# LSBATCH: User input
UB -J CAD12step1
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=4000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# # # call germline variants in a human WGS paired end reads # # #
# # # 2 X 100bp following GATK4 best practices workflow # # #

# v2 code updates: #####

# [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script
# [done] bashrc alias did not work with WGS-iPSC, so - must be a problem

# [1] update raw data file name by replacing - for _
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_1.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P732912_FDSW220142847-1r_HYMM2DSX2_L1_2.fq.gz now P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz

# ☐ rename script from .sh to .lsf?
# going to test without making this change

# ☐ express instead of premium queue?
# for fast turnaround, premium is default

# lsf parameter considerations: #####

# error and output
# BSUB -oo %J.stdout
# BSUB -eo %J.stderr
# or
#BSUB -o %J.stdout
#BSUB -e %J.stderr

# requirements: #####

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # directories
# /sc/arion/projects/vascbrain/WGS_iPSC/

(... more ...)
```

Successfully completed.

Resource usage summary:

CPU time :	6594.62 sec.
Max Memory :	306 MB

```
Average Memory :          217.97 MB
Total Requested Memory :    4000.00 MB
Delta Memory :              3694.00 MB
Max Swap :                  -
Max Processes :              6
Max Threads :               17
Run time :                  6618 sec.
Turnaround time :           6625 sec.
```

The output (if any) follows:

```
STEP 1: QC - Run fastqc
Analysis complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
Analysis complete for P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?
```

PS:

Read file <124439081.stderr> for stderr output of this job.

```
[palafm01@li03c03 CAD12_std]$ cd ..
[palafm01@li03c03 scripts]$ ls
124669344.stderr 124669344.stdout 124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ lss
total 68K
-rw-r----- 1 palafm01 vascbrain 9.7K Apr 18 07:31 124669344.stdout
-rw-r----- 1 palafm01 vascbrain 6.0K Apr 18 06:44 124675700.stderr
drwxr-s--- 4 palafm01 vascbrain 4.0K Apr 18 07:31 .
drwxr-s--- 10 palafm01 vascbrain 4.0K Apr 17 17:23 ..
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 05:42 CAD12_std
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 05:42 CAD63_std
-rwxr-x--- 1 palafm01 vascbrain 3.7K Apr 18 06:05 variant_calling.sh
-rw-r----- 1 palafm01 vascbrain 3.5K Apr 18 06:44 124675700.stdout
-rw-r----- 1 palafm01 vascbrain 2.8K Apr 18 07:31 124669344.stderr
[palafm01@li03c03 scripts]$ cat
^C
[palafm01@li03c03 scripts]$ 124675700.stdout
-bash: 124675700.stdout: command not found
[palafm01@li03c03 scripts]$ cat 124675700.stdout
Sender: LSF System <lsfadmin@lc02c15>
Subject: Job 124675700: <CAD12step2> in cluster <chimera> Exited
```

Job <CAD12step2> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 06:05:13 2024
Job was executed on host(s) <lc02c15>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 06:05:16 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_ipSC/scripts> was used as the working directory.
Started at Thu Apr 18 06:05:16 2024
Terminated at Thu Apr 18 06:44:00 2024
Results reported at Thu Apr 18 06:44:00 2024

Your job looked like:

```
-----
# LSBATCH: User input
#!/bin/bash
#BSUB -J CAD12step2
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=4000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices workflow

# code updates:
# [1] change minerva dir name from WGS-ipSC to WGS_ipSC and update this script [done] bashrc alias did not work with WGS-ipSC, so - must be a problem
# [1] update raw data file name by replacing - for _
# [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
# [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_2.fq.gz
```



```
# requirements:
module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # update reads dir for specific sample
#CAD12: /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912
#CAD63: /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263

reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"
#reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"

ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"
known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"
aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"
results="/sc/arion/projects/vascbrain/WGS_iPSC/results"
data="/sc/arion/projects/vascbrain/WGS_iPSC/data"

##### Prep files (RUN ONLY ONCE) #####

# # make ref folder
# mkdir hg38

# # download reference files to folder and unzip #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz

# # index ref - .fai file before running haplotype caller #####

(... more ...)
```

TERM_MEMLIMIT: job killed after reaching LSF memory usage limit.
Exited with exit code 130.

Resource usage summary:

CPU time :	2312.83 sec.
Max Memory :	4000 MB
Average Memory :	1135.49 MB
Total Requested Memory :	4000.00 MB
Delta Memory :	0.00 MB
Max Swap :	2 MB
Max Processes :	6
Max Threads :	8
Run time :	2323 sec.
Turnaround time :	2327 sec.

The output (if any) follows:

STEP 2: Map to reference using BWA-MEM

PS:

Read file <124675700.stderr> for stderr output of this job.

```
[palafm01@li03c03 scripts]$ ls
124669344.stderr 124669344.stdout 124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cat 124669344.stdout
Sender: LSF System <lsfadmin@lc01e30>
Subject: Job 124669344: <UB -J CAD63step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.stderr;#BSUB -L /bin/bash; # # # call germline variants in a human WGS paired end reads # # #;# # # 2 X 100bp following GATK4 best practices workflow # # #; # v2 code updates: #####; # [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script [done] bashrc alias did not work with WGS-iPSC, so - must be a problem; # [1] update raw data file name by replacing - for _; # [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz; # [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_1.fq.gz; # [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_2.fq.gz; # requirements: #####; module load samtools/1.17;module load gatk;module load fastqc;module load bwa; # # update reads dir for specific sample;# # CAD12: /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912;# # CAD63: /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"; ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa";known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf";aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads";results="/sc/arion/projects/vascbrain/WGS_iPSC/results";data="/sc/arion/projects/vascbrain/WGS_iPSC/data"; ##### Prep files (RUN ONLY ONCE) #####; # # make ref folder;# mkdir hg38; # # download reference files to folder and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz;# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz; # # index ref - .fai file before running haplotype caller #####;# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa; # # create ref dict file before running haplotype caller ##
```

```
#####;# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict;
# # download known sites files for BQSR from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.
googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38
/ https://storage.googleapis.com/genomics-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS
#####;# # -----;# STEP 1: QC - Run fastqc ;# -----; echo "STEP 1: QC - Run fastqc"; # f
astqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz -o ${reads}/;# fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}
/; fastqc ${reads}/P931263_FDSW220142848_1r_HYMM2DSX2_L1_1.fq.gz -o ${reads}/;fastqc ${reads}/P931263_FDSW220142848_1r_HYMM2DSX2_L1_2.fq.gz -o ${read
s}/; echo "STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?";# No trimming required if quality looks okay> in cluster <c
himera> Done
```

```
Job <UB -J CAD63step1;#BSUB -P acc_vascbrain;#BSUB -q premium;#BSUB -n 1;#BSUB -W 6:00;#BSUB -R rusage[mem=4000];#BSUB -oo %J.stdout;#BSUB -eo %J.std
err;#BSUB -L /bin/bash;# # # call germline variants in a human WGS paired end reads # # #;# # # 2 X 100bp following GATK4 best practices workflow # # #
# #; # v2 code updates: #####;# [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this scr
ipt [done] bashrc alias did not work with WGS-iPSC, so - must be a problem;# [1] update raw data file name by replacing - for _; # [done] P73291
2_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz; # [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz; # [done] P931263_FDSW220142848_1r_HYMM2DSX2_L
1_1.fq.gz ; # [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_2.fq.gz; # requirements: #####; module load samtools/1
.17;module load gatk;module load fastqc;module load bwa;# # update reads dir for specific sample;# # CAD12: /sc/arion/projects/vascbrain/WGS_iPSC/ra
w_data/P732912;# # CAD63: /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263; reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"; ref
="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa";known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf";a
ligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads";results="/sc/arion/projects/vascbrain/WGS_iPSC/results";data="/sc/arion/projects/v
ascbrain/WGS_iPSC/data"; ##### Prep files (RUN ONLY ONCE) #####;# # make ref folder;# mkdir hg38;# # download refer
ence files to folder and unzip #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZ
ips/hg38.fa.gz;# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz;# # index ref - .fai file before running haplotype caller #####;
# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa;# # create ref dict file before running haplotype caller #####;# gatk Crea
teSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict;# # download known
sites files for BQSR from GATK resource bundle #####;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genom
ics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf;# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.go
ogleapis.com/genomics-public-data/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf.idx; ##### VARIANT CALLING STEPS #####
#####;# # -----;# STEP 1: QC - Run fastqc ;# -----; echo "STEP 1: QC - Run fastqc"; # fastqc ${reads}/P7329
12_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz -o ${reads}/;# fastqc ${reads}/P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}/; fastqc ${reads}/P
931263_FDSW220142848_1r_HYMM2DSX2_L1_1.fq.gz -o ${reads}/;fastqc ${reads}/P931263_FDSW220142848_1r_HYMM2DSX2_L1_2.fq.gz -o ${reads}/; echo "STEP 1: f
astqc RESULT - No trimming required if quality looks okay. is it ok?";# No trimming required if quality looks okay> was submitted from host <li03c03.
chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 05:41:43 2024
Job was executed on host(s) <lc01e30>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 05:41:46 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
Started at Thu Apr 18 05:41:46 2024
Terminated at Thu Apr 18 07:31:03 2024
Results reported at Thu Apr 18 07:31:03 2024
```

Your job looked like:

```
-----
# LSBATCH: User input
UB -J CAD63step1
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=4000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# # # call germline variants in a human WGS paired end reads # # #
# # # 2 X 100bp following GATK4 best practices workflow # # #
```

```
# v2 code updates: #####
```

```
# [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script [done] bashrc alias did not work with WGS-iPSC, so - must be a problem
```

```
# [1] update raw data file name by replacing - for _
```

```
# [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
```

```
# [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_2.fq.gz
```

```
# requirements: #####
```

```
module load samtools/1.17
module load gatk
module load fastqc
```

module load bwa

```
# # update reads dir for specific sample
# # CAD12: /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912
# # CAD63: /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263
```

reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"

```
ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"
known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"
aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"
results="/sc/arion/projects/vascbrain/WGS_iPSC/results"
data="/sc/arion/projects/vascbrain/WGS_iPSC/data"
```

Prep files (RUN ONLY ONCE)

```
# # make ref folder
# mkdir hg38
```

(... more ...)

Successfully completed.

Resource usage summary:

CPU time :	6536.46 sec.
Max Memory :	299 MB
Average Memory :	215.74 MB
Total Requested Memory :	4000.00 MB
Delta Memory :	3701.00 MB
Max Swap :	-
Max Processes :	6
Max Threads :	17
Run time :	6557 sec.
Turnaround time :	6560 sec.

The output (if any) follows:

STEP 1: QC - Run fastqc
Analysis complete for P931263_FDSW220142848_1r_HYMM2DSX2_L1_1.fq.gz
Analysis complete for P931263_FDSW220142848_1r_HYMM2DSX2_L1_2.fq.gz
STEP 1: fastqc RESULT - No trimming required if quality looks okay. is it ok?

PS:

Read file <124669344.stderr> for stderr output of this job.

```
[palafm01@li03c03 scripts]$ touch variant_calling.sh
[palafm01@li03c03 scripts]$ ls
124669344.stderr 124669344.stdout 124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ vim variant_calling.sh
[palafm01@li03c03 scripts]$ bsub < variant_calling.sh
Job <124703558> is submitted to queue <premium>.
[palafm01@li03c03 scripts]$ less 124669344.stdout
[palafm01@li03c03 scripts]$ mv 124669344.stdout CAD63_std/
[palafm01@li03c03 scripts]$ ls
124669344.stderr 124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cd CAD63_std/
[palafm01@li03c03 CAD63_std]$ ls
124669344.stdout
[palafm01@li03c03 CAD63_std]$ cd ..
[palafm01@li03c03 scripts]$ ls
124669344.stderr 124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ mv 124669344.stderr CAD63_std/
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cat 124675700.stdout
Sender: LSF System <lsfadmin@lc02c15>
Subject: Job 124675700: <CAD12step2> in cluster <chimera> Exited
```

Job <CAD12step2> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 06:05:13 2024
Job was executed on host(s) <lc02c15>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 06:05:16 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.

Started at Thu Apr 18 06:05:16 2024
Terminated at Thu Apr 18 06:44:00 2024
Results reported at Thu Apr 18 06:44:00 2024

Your job looked like:

```
-----  
# LSBATCH: User input  
#!/bin/bash  
#BSUB -J CAD12step2  
#BSUB -P acc_vascbrain  
#BSUB -q premium  
#BSUB -n 1  
#BSUB -W 6:00  
#BSUB -R rusage[mem=4000]  
#BSUB -oo %J.stdout  
#BSUB -eo %J.stderr  
#BSUB -L /bin/bash  
  
# call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices workflow  
  
# code updates:  
# [1] change minerva dir name from WGS-iPSC to WGS_iPSC and update this script [done] bashrc alias did not work with WGS-iPSC, so - must be a problem  
# [1] update raw data file name by replacing - for _  
# [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz  
# [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz  
# [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_1.fq.gz  
# [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_2.fq.gz  
  
# requirements:  
module load samtools/1.17  
module load gatk  
module load fastqc  
module load bwa  
  
## update reads dir for specific sample  
#CAD12: /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912  
#CAD63: /sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263  
  
reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"  
#reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"  
  
ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"  
known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"  
aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"  
results="/sc/arion/projects/vascbrain/WGS_iPSC/results"  
data="/sc/arion/projects/vascbrain/WGS_iPSC/data"  
  
##### Prep files (RUN ONLY ONCE) #####  
  
## make ref folder  
# mkdir hg38  
  
## download reference files to folder and unzip #####  
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz  
# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz  
  
## index ref - .fai file before running haplotype caller #####  
  
(... more ...)
```

TERM_MEMLIMIT: job killed after reaching LSF memory usage limit.
Exited with exit code 130.

Resource usage summary:

CPU time :	2312.83 sec.
Max Memory :	4000 MB
Average Memory :	1135.49 MB
Total Requested Memory :	4000.00 MB
Delta Memory :	0.00 MB
Max Swap :	2 MB
Max Processes :	6
Max Threads :	8
Run time :	2323 sec.

Turnaround time : 2327 sec.

The output (if any) follows:

STEP 2: Map to reference using BWA-MEM

PS:

Read file <124675700.stderr> for stderr output of this job.

```
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ vim variant_calling.sh
[palafm01@li03c03 scripts]$ bsub < variant_calling.sh
Job <124704501> is submitted to queue <premium>.
[palafm01@li03c03 scripts]$ bjobs
  JOBID      USER      JOB_NAME  STAT      QUEUE  FROM_HOST  EXEC_HOST  SUBMIT_TIME  START_TIME  TIME_LEFT
    124704501 palafm01  CAD63step2  RUN      premium li03c03.ch    lc02c11  Apr 18 07:52  Apr 18 07:52    5:56 L
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout 124703558.stderr 124703558.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ lss
total 68K
-rw-r----- 1 palafm01 vascbrain 6.0K Apr 18 06:44 124675700.stderr
-rwxr-x--- 1 palafm01 vascbrain 4.2K Apr 18 07:52 variant_calling.sh
drwxr-s--- 4 palafm01 vascbrain 4.0K Apr 18 07:52 .
drwxr-s--- 10 palafm01 vascbrain 4.0K Apr 17 17:23 ..
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 05:42 CAD12_std
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 07:50 CAD63_std
-rw-r----- 1 palafm01 vascbrain 3.6K Apr 18 07:52 124703558.stdout
-rw-r----- 1 palafm01 vascbrain 3.5K Apr 18 06:44 124675700.stdout
-rw-r----- 1 palafm01 vascbrain 875 Apr 18 07:52 124703558.stderr
[palafm01@li03c03 scripts]$ less 124703558.stdout
[palafm01@li03c03 scripts]$ mv 124703558.stdout CAD12_std/
[palafm01@li03c03 scripts]$ cat 124703558.stderr
[bwa_index] Pack FASTA... 19.38 sec
[bwa_index] Construct BWT for the packed sequence...
[BWTIncCreate] textLength=6418572210, availableWord=463634060
[BWTIncConstructFromPacked] 10 iterations done. 99999986 characters processed.
[BWTIncConstructFromPacked] 20 iterations done. 199999986 characters processed.
[BWTIncConstructFromPacked] 30 iterations done. 299999986 characters processed.
[BWTIncConstructFromPacked] 40 iterations done. 399999986 characters processed.
[BWTIncConstructFromPacked] 50 iterations done. 499999986 characters processed.
[BWTIncConstructFromPacked] 60 iterations done. 599999986 characters processed.
BWTIncConstructFromPacked() : Can't read from /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.pac : Unexpected end of file
[bwt_restore_sa] fail to open file '/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.sa' : No such file or directory
[palafm01@li03c03 scripts]$ bjobs
  JOBID      USER      JOB_NAME  STAT      QUEUE  FROM_HOST  EXEC_HOST  SUBMIT_TIME  START_TIME  TIME_LEFT
    124704501 palafm01  CAD63step2  RUN      premium li03c03.ch    lc02c11  Apr 18 07:52  Apr 18 07:52    5:54 L
[palafm01@li03c03 scripts]$ bjobs
  JOBID      USER      JOB_NAME  STAT      QUEUE  FROM_HOST  EXEC_HOST  SUBMIT_TIME  START_TIME  TIME_LEFT
    124704501 palafm01  CAD63step2  RUN      premium li03c03.ch    lc02c11  Apr 18 07:52  Apr 18 07:52    5:50 L
[palafm01@li03c03 scripts]$ cd
[palafm01@li03c03 ~]$ wgs
[palafm01@li03c03 WGS_iPSC]$ cd aligned_reads/
[palafm01@li03c03 aligned_reads]$ ls
P732912.paired.sam
[palafm01@li03c03 aligned_reads]$ rm P732912.paired.sam
[palafm01@li03c03 aligned_reads]$ ls
[palafm01@li03c03 aligned_reads]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout 124703558.stderr CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cat
^C
[palafm01@li03c03 scripts]$ cat 124703558.stderr
[bwa_index] Pack FASTA... 19.38 sec
[bwa_index] Construct BWT for the packed sequence...
[BWTIncCreate] textLength=6418572210, availableWord=463634060
[BWTIncConstructFromPacked] 10 iterations done. 99999986 characters processed.
[BWTIncConstructFromPacked] 20 iterations done. 199999986 characters processed.
[BWTIncConstructFromPacked] 30 iterations done. 299999986 characters processed.
[BWTIncConstructFromPacked] 40 iterations done. 399999986 characters processed.
[BWTIncConstructFromPacked] 50 iterations done. 499999986 characters processed.
```

```

[BWTIncConstructFromPacked] 60 iterations done. 599999986 characters processed.
BWTIncConstructFromPacked() : Can't read from /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.pac : Unexpected end of file
[bwt_restore_sa] fail to open file '/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.sa' : No such file or directory
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout 124703558.stderr CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cd CAD12_std/
[palafm01@li03c03 CAD12_std]$ ls
124354105.stderr 124354105.stdout 124439081.stderr 124439081.stdout 124703558.stdout
[palafm01@li03c03 CAD12_std]$ cd ..
[palafm01@li03c03 scripts]$ mv *588.stderr CAD12_std/
mv: cannot stat '*588.stderr': No such file or directory
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout 124703558.stderr CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ mv 124703558.stderr CAD12_std/
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ vim variant_calling.sh
[palafm01@li03c03 scripts]$ bsub < variant_calling.sh
Job <124712019> is submitted to queue <premium>.
[palafm01@li03c03 scripts]$ myjobs
-bash: myjobs: command not found
[palafm01@li03c03 scripts]$ myjobs
-bash: myjobs: command not found
[palafm01@li03c03 scripts]$ bjobs
      JOBID      USER      JOB_NAME      STAT      QUEUE      FROM_HOST      EXEC_HOST      SUBMIT_TIME      START_TIME      TIME_LEFT
      124704501   palafm01   CAD63step2   RUN       premium   li03c03.ch      lc02c11      Apr 18 07:52   Apr 18 07:52   5:32 L
      124712019   palafm01   CAD12step2   PEND       premium   li03c03.ch      -            Apr 18 08:20   -             -
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout 124704501.stderr 124704501.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ bjobs
      JOBID      USER      JOB_NAME      STAT      QUEUE      FROM_HOST      EXEC_HOST      SUBMIT_TIME      START_TIME      TIME_LEFT
      124712019   palafm01   CAD12step2   RUN       premium   li03c03.ch      lc02c11      Apr 18 08:20   Apr 18 08:20   5:59 L
[palafm01@li03c03 scripts]$ cat 124704501.stdout
Sender: LSF System <lsfadmin@lc02c11>
Subject: Job 124704501: <CAD63step2> in cluster <chimera> Done

Job <CAD63step2> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 07:52:38 2024
Job was executed on host(s) <lc02c11>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 07:52:42 2024
~/hpc/users/palafm01> was used as the home directory.
~/sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
Started at Thu Apr 18 07:52:42 2024
Terminated at Thu Apr 18 08:20:33 2024
Results reported at Thu Apr 18 08:20:33 2024

Your job looked like:

-----
# LSBATCH: User input
#!/bin/bash
#BSUB -J CAD63step2
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=16000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# # call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices workflow

# code updates:
# [1] changed minerva dir name from WGS-iPSC to WGS_iPSC because alias did not work
# [2] updated raw data filenames by replacing - with _ chr

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # update reads dir for specific sample
#reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"
reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"

# consistent dir's between samples
ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"

```

```
known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"
aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"
results="/sc/arion/projects/vascbrain/WGS_iPSC/results"
data="/sc/arion/projects/vascbrain/WGS_iPSC/data"

##### Prep files (RUN ONLY ONCE) #####

# # make ref folder
# mkdir hg38

# # download reference files to folder and unzip #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz

# # index ref - .fai file before running haplotype caller #####
# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa

# # create ref dict file before running haplotype caller #####
# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict

# # download known sites files for BQSR from GATK resource bundle #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf
```

(... more ...)

Successfully completed.

Resource usage summary:

CPU time :	1664.58 sec.
Max Memory :	1772 MB
Average Memory :	947.84 MB
Total Requested Memory :	16000.00 MB
Delta Memory :	14228.00 MB
Max Swap :	-
Max Processes :	6
Max Threads :	7
Run time :	1670 sec.
Turnaround time :	1675 sec.

The output (if any) follows:

STEP 2: Map to reference using BWA-MEM
STEP 2: read alignment to ref genome hg38 complete!

PS:

Read file <124704501.stderr> for stderr output of this job.

```
[palafm01@li03c03 scripts]$ cat 124704501.stderr
[bwa_index] Pack FASTA... 19.60 sec
[bwa_index] Construct BWT for the packed sequence...
[BWTIncCreate] textLength=6418572210, availableWord=463634060
[BWTIncConstructFromPacked] 10 iterations done. 99999986 characters processed.
[BWTIncConstructFromPacked] 20 iterations done. 199999986 characters processed.
[BWTIncConstructFromPacked] 30 iterations done. 299999986 characters processed.
[BWTIncConstructFromPacked] 40 iterations done. 399999986 characters processed.
[BWTIncConstructFromPacked] 50 iterations done. 499999986 characters processed.
[BWTIncConstructFromPacked] 60 iterations done. 599999986 characters processed.
[BWTIncConstructFromPacked] 70 iterations done. 699999986 characters processed.
[BWTIncConstructFromPacked] 80 iterations done. 799999986 characters processed.
[BWTIncConstructFromPacked] 90 iterations done. 899999986 characters processed.
[BWTIncConstructFromPacked] 100 iterations done. 999999986 characters processed.
[BWTIncConstructFromPacked] 110 iterations done. 1099999986 characters processed.
[BWTIncConstructFromPacked] 120 iterations done. 1199999986 characters processed.
[BWTIncConstructFromPacked] 130 iterations done. 1299999986 characters processed.
[BWTIncConstructFromPacked] 140 iterations done. 1399999986 characters processed.
[BWTIncConstructFromPacked] 150 iterations done. 1499999986 characters processed.
[BWTIncConstructFromPacked] 160 iterations done. 1599999986 characters processed.
[BWTIncConstructFromPacked] 170 iterations done. 1699999986 characters processed.
[BWTIncConstructFromPacked] 180 iterations done. 1799999986 characters processed.
[BWTIncConstructFromPacked] 190 iterations done. 1899999986 characters processed.
[BWTIncConstructFromPacked] 200 iterations done. 1999999986 characters processed.
```

```
[BWTIncConstructFromPacked] 210 iterations done. 2099999986 characters processed.
[BWTIncConstructFromPacked] 220 iterations done. 2199999986 characters processed.
[BWTIncConstructFromPacked] 230 iterations done. 2299999986 characters processed.
[BWTIncConstructFromPacked] 240 iterations done. 2399999986 characters processed.
[BWTIncConstructFromPacked] 250 iterations done. 2499999986 characters processed.
[BWTIncConstructFromPacked] 260 iterations done. 2599999986 characters processed.
[BWTIncConstructFromPacked] 270 iterations done. 2699999986 characters processed.
[BWTIncConstructFromPacked] 280 iterations done. 2799999986 characters processed.
[BWTIncConstructFromPacked] 290 iterations done. 2899999986 characters processed.
[BWTIncConstructFromPacked] 300 iterations done. 2999999986 characters processed.
[BWTIncConstructFromPacked] 310 iterations done. 3099999986 characters processed.
[BWTIncConstructFromPacked] 320 iterations done. 3199999986 characters processed.
[BWTIncConstructFromPacked] 330 iterations done. 3299999986 characters processed.
[BWTIncConstructFromPacked] 340 iterations done. 3399999986 characters processed.
[BWTIncConstructFromPacked] 350 iterations done. 3499999986 characters processed.
[BWTIncConstructFromPacked] 360 iterations done. 3599999986 characters processed.
[BWTIncConstructFromPacked] 370 iterations done. 3699999986 characters processed.
[BWTIncConstructFromPacked] 380 iterations done. 3799999986 characters processed.
[BWTIncConstructFromPacked] 390 iterations done. 3899999986 characters processed.
[BWTIncConstructFromPacked] 400 iterations done. 3999999986 characters processed.
[BWTIncConstructFromPacked] 410 iterations done. 4099999986 characters processed.
[BWTIncConstructFromPacked] 420 iterations done. 4199999986 characters processed.
[BWTIncConstructFromPacked] 430 iterations done. 4299999986 characters processed.
[BWTIncConstructFromPacked] 440 iterations done. 4399999986 characters processed.
[BWTIncConstructFromPacked] 450 iterations done. 4499999986 characters processed.
[BWTIncConstructFromPacked] 460 iterations done. 4599999986 characters processed.
[BWTIncConstructFromPacked] 470 iterations done. 4699999986 characters processed.
[BWTIncConstructFromPacked] 480 iterations done. 4799999986 characters processed.
[BWTIncConstructFromPacked] 490 iterations done. 4899999986 characters processed.
[BWTIncConstructFromPacked] 500 iterations done. 4999999986 characters processed.
BWTIncConstructFromPacked() : Can't read from /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.pac : Unexpected end of file
[bwt_restore_sa] fail to open file '/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.sa' : No such file or directory
[palafm01@li03c03 scripts]$ bjobs
```

JOBID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124712019	palafm01	CAD12step2	RUN	premium	li03c03.ch	lc02c11	Apr 18 08:20	Apr 18 08:20	5:58 L

```
[palafm01@li03c03 scripts]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd aligned_reads/
[palafm01@li03c03 aligned_reads]$ ls
P931263.paired.sam
```

```
[palafm01@li03c03 aligned_reads]$ rm P931263.paired.sam
[palafm01@li03c03 aligned_reads]$ bjobs
```

JOBID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124712019	palafm01	CAD12step2	RUN	premium	li03c03.ch	lc02c11	Apr 18 08:20	Apr 18 08:20	5:55 L

```
[palafm01@li03c03 aligned_reads]$ ls
[palafm01@li03c03 aligned_reads]$ ls
[palafm01@li03c03 aligned_reads]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout 124704501.stderr 124704501.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cat 124704501.stdout
Sender: LSF System <lsfadmin@lc02c11>
Subject: Job 124704501: <CAD63step2> in cluster <chimera> Done
```

Job <CAD63step2> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 07:52:38 2024
Job was executed on host(s) <lc02c11>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 07:52:42 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
Started at Thu Apr 18 07:52:42 2024
Terminated at Thu Apr 18 08:20:33 2024
Results reported at Thu Apr 18 08:20:33 2024

Your job looked like:

```
-----
# LSBATCH: User input
#!/bin/bash
#BSUB -J CAD63step2
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=16000]
```



```

#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

## call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices workflow

# code updates:
# [1] changed minerva dir name from WGS-iPSC to WGS_iPSC because alias did not work
# [2] updated raw data filenames by replacing - with _ chr

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

## update reads dir for specific sample
#reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"
reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"

# consistent dir's between samples
ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"
known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"
aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"
results="/sc/arion/projects/vascbrain/WGS_iPSC/results"
data="/sc/arion/projects/vascbrain/WGS_iPSC/data"

##### Prep files (RUN ONLY ONCE) #####

## make ref folder
# mkdir hg38

## download reference files to folder and unzip #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz

## index ref - .fai file before running haplotype caller #####
# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa

## create ref dict file before running haplotype caller #####
# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict

## download known sites files for BQSR from GATK resource bundle #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf

```

(... more ...)

Successfully completed.

Resource usage summary:

CPU time :	1664.58 sec.
Max Memory :	1772 MB
Average Memory :	947.84 MB
Total Requested Memory :	16000.00 MB
Delta Memory :	14228.00 MB
Max Swap :	-
Max Processes :	6
Max Threads :	7
Run time :	1670 sec.
Turnaround time :	1675 sec.

The output (if any) follows:

STEP 2: Map to reference using BWA-MEM
 STEP 2: read alignment to ref genome hg38 complete!

PS:

Read file <124704501.stderr> for stderr output of this job.

```

[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout 124704501.stderr 124704501.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ mv 124704501.stdout CAD63_std/

```

```
[palafm01@li03c03 scripts]$ mv 124704501.stderr CAD63_std/
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cat *700.stderr
[bwa_index] Pack FASTA... 19.51 sec
[bwa_index] Construct BWT for the packed sequence...
[BWTIncCreate] textLength=6418572210, availableWord=463634060
[BWTIncConstructFromPacked] 10 iterations done. 999999986 characters processed.
[BWTIncConstructFromPacked] 20 iterations done. 1999999986 characters processed.
[BWTIncConstructFromPacked] 30 iterations done. 2999999986 characters processed.
[BWTIncConstructFromPacked] 40 iterations done. 3999999986 characters processed.
[BWTIncConstructFromPacked] 50 iterations done. 4999999986 characters processed.
[BWTIncConstructFromPacked] 60 iterations done. 5999999986 characters processed.
[BWTIncConstructFromPacked] 70 iterations done. 6999999986 characters processed.
[BWTIncConstructFromPacked] 80 iterations done. 7999999986 characters processed.
[BWTIncConstructFromPacked] 90 iterations done. 8999999986 characters processed.
[BWTIncConstructFromPacked] 100 iterations done. 9999999986 characters processed.
[BWTIncConstructFromPacked] 110 iterations done. 10999999986 characters processed.
[BWTIncConstructFromPacked] 120 iterations done. 11999999986 characters processed.
[BWTIncConstructFromPacked] 130 iterations done. 12999999986 characters processed.
[BWTIncConstructFromPacked] 140 iterations done. 13999999986 characters processed.
[BWTIncConstructFromPacked] 150 iterations done. 14999999986 characters processed.
[BWTIncConstructFromPacked] 160 iterations done. 15999999986 characters processed.
[BWTIncConstructFromPacked] 170 iterations done. 16999999986 characters processed.
[BWTIncConstructFromPacked] 180 iterations done. 17999999986 characters processed.
[BWTIncConstructFromPacked] 190 iterations done. 18999999986 characters processed.
[BWTIncConstructFromPacked] 200 iterations done. 19999999986 characters processed.
[BWTIncConstructFromPacked] 210 iterations done. 20999999986 characters processed.
[BWTIncConstructFromPacked] 220 iterations done. 21999999986 characters processed.
[BWTIncConstructFromPacked] 230 iterations done. 22999999986 characters processed.
[BWTIncConstructFromPacked] 240 iterations done. 23999999986 characters processed.
[BWTIncConstructFromPacked] 250 iterations done. 24999999986 characters processed.
[BWTIncConstructFromPacked] 260 iterations done. 25999999986 characters processed.
[BWTIncConstructFromPacked] 270 iterations done. 26999999986 characters processed.
[BWTIncConstructFromPacked] 280 iterations done. 27999999986 characters processed.
[BWTIncConstructFromPacked] 290 iterations done. 28999999986 characters processed.
[BWTIncConstructFromPacked] 300 iterations done. 29999999986 characters processed.
[BWTIncConstructFromPacked] 310 iterations done. 30999999986 characters processed.
[BWTIncConstructFromPacked] 320 iterations done. 31999999986 characters processed.
[BWTIncConstructFromPacked] 330 iterations done. 32999999986 characters processed.
[BWTIncConstructFromPacked] 340 iterations done. 33999999986 characters processed.
[BWTIncConstructFromPacked] 350 iterations done. 34999999986 characters processed.
[BWTIncConstructFromPacked] 360 iterations done. 35999999986 characters processed.
[BWTIncConstructFromPacked] 370 iterations done. 36999999986 characters processed.
[BWTIncConstructFromPacked] 380 iterations done. 37999999986 characters processed.
[BWTIncConstructFromPacked] 390 iterations done. 38999999986 characters processed.
[BWTIncConstructFromPacked] 400 iterations done. 39999999986 characters processed.
[BWTIncConstructFromPacked] 410 iterations done. 40999999986 characters processed.
[BWTIncConstructFromPacked] 420 iterations done. 41999999986 characters processed.
[BWTIncConstructFromPacked] 430 iterations done. 42999999986 characters processed.
[BWTIncConstructFromPacked] 440 iterations done. 43999999986 characters processed.
[BWTIncConstructFromPacked] 450 iterations done. 44999999986 characters processed.
[BWTIncConstructFromPacked] 460 iterations done. 45999999986 characters processed.
[BWTIncConstructFromPacked] 470 iterations done. 46999999986 characters processed.
[BWTIncConstructFromPacked] 480 iterations done. 47999999986 characters processed.
[BWTIncConstructFromPacked] 490 iterations done. 48999999986 characters processed.
[BWTIncConstructFromPacked] 500 iterations done. 49999999986 characters processed.
[BWTIncConstructFromPacked] 510 iterations done. 50999999986 characters processed.
[BWTIncConstructFromPacked] 520 iterations done. 51999999986 characters processed.
[BWTIncConstructFromPacked] 530 iterations done. 52999999986 characters processed.
[BWTIncConstructFromPacked] 540 iterations done. 53999999986 characters processed.
[BWTIncConstructFromPacked] 550 iterations done. 54999999986 characters processed.
[BWTIncConstructFromPacked] 560 iterations done. 55999999986 characters processed.
[BWTIncConstructFromPacked] 570 iterations done. 56999999986 characters processed.
[BWTIncConstructFromPacked] 580 iterations done. 5798165394 characters processed.
[BWTIncConstructFromPacked] 590 iterations done. 5886412978 characters processed.
[BWTIncConstructFromPacked] 600 iterations done. 5964843650 characters processed.
[BWTIncConstructFromPacked] 610 iterations done. 6034549010 characters processed.
[BWTIncConstructFromPacked] 620 iterations done. 6096499330 characters processed.
[BWTIncConstructFromPacked] 630 iterations done. 6151556914 characters processed.
[BWTIncConstructFromPacked] 640 iterations done. 6200488210 characters processed.
[BWTIncConstructFromPacked] 650 iterations done. 6243974434 characters processed.
[BWTIncConstructFromPacked] 660 iterations done. 6282621122 characters processed.
[BWTIncConstructFromPacked] 670 iterations done. 6316966322 characters processed.
[BWTIncConstructFromPacked] 680 iterations done. 6347488418 characters processed.
[BWTIncConstructFromPacked] 690 iterations done. 6374612482 characters processed.
```

```
[BWTIncConstructFromPacked] 700 iterations done. 6398716386 characters processed.
[BWTIncConstructFromPacked] 710 iterations done. 6418572210 characters processed.
[bwa_index] 2277.74 seconds elapse.
[bwa_index] Update BWT... /local/JOBS/1713434713.124675700.shell: line 87: 254274 Killed          bwa index ${ref}
[palafm01@li03c03 scripts]$ ls
124675700.stderr 124675700.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ lss
total 67K
-rw-r----- 1 palafm01 vascbrain 6.0K Apr 18 06:44 124675700.stderr
-rwxr-x--- 1 palafm01 vascbrain 4.2K Apr 18 08:20 variant_calling.sh
drwxr-s--- 4 palafm01 vascbrain 4.0K Apr 18 08:25 .
drwxr-s--- 10 palafm01 vascbrain 4.0K Apr 17 17:23 ..
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 08:19 CAD12_std
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 08:25 CAD63_std
-rw-r----- 1 palafm01 vascbrain 3.5K Apr 18 06:44 124675700.stdout
[palafm01@li03c03 scripts]$ cat *700.stdout
Sender: LSF System <lsfadmin@lc02c15>
Subject: Job 124675700: <CAD12step2> in cluster <chimera> Exited
```

Job <CAD12step2> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 06:05:13 2024
Job was executed on host(s) <lc02c15>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 06:05:16 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_ipSC/scripts> was used as the working directory.
Started at Thu Apr 18 06:05:16 2024
Terminated at Thu Apr 18 06:44:00 2024
Results reported at Thu Apr 18 06:44:00 2024

Your job looked like:

```
-----
# LSBATCH: User input
#!/bin/bash
#BSUB -J CAD12step2
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=4000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices workflow

# code updates:
# [1] change minerva dir name from WGS-ipSC to WGS_ipSC and update this script [done] bashrc alias did not work with WGS-ipSC, so - must be a problem
# [1] update raw data file name by replacing - for _
# [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P732912_FDSW220142847_1r_HYMM2DSX2_L1_2.fq.gz
# [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_1.fq.gz
# [done] P931263_FDSW220142848_1r_HYMM2DSX2_L1_2.fq.gz

# requirements:
module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # update reads dir for specific sample
#CAD12: /sc/arion/projects/vascbrain/WGS_ipSC/raw_data/P732912
#CAD63: /sc/arion/projects/vascbrain/WGS_ipSC/raw_data/P931263

reads="/sc/arion/projects/vascbrain/WGS_ipSC/raw_data/P732912"
#reads="/sc/arion/projects/vascbrain/WGS_ipSC/raw_data/P931263"

ref="/sc/arion/projects/vascbrain/WGS_ipSC/hg38/hg38.fa"
known_sites="/sc/arion/projects/vascbrain/WGS_ipSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"
aligned_reads="/sc/arion/projects/vascbrain/WGS_ipSC/aligned_reads"
results="/sc/arion/projects/vascbrain/WGS_ipSC/results"
data="/sc/arion/projects/vascbrain/WGS_ipSC/data"

##### Prep files (RUN ONLY ONCE) #####

# # make ref folder
# mkdir hg38
```


JOBID	USER	JOB_NAME	STAT	QUEUE	FROM_HOST	EXEC_HOST	SUBMIT_TIME	START_TIME	TIME_LEFT
124712019	palafm01	CAD12step2	RUN	premium	li03c03.ch	lc02c11	Apr 18 08:20	Apr 18 08:20	5:39 L

```

[palafm01@li03c03 aligned_reads]$ bjobs
No unfinished job found
[palafm01@li03c03 aligned_reads]$ ls
P732912.paired.sam
[palafm01@li03c03 aligned_reads]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads  data  FastQC_output  hg38  MD5  raw_data  raw_data.zip  Readme.html  results  scripts
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
124712019.stderr  124712019.stdout  CAD12_std  CAD63_std  variant_calling.sh
[palafm01@li03c03 scripts]$ cat *out
Sender: LSF System <lsfadmin@lc02c11>
Subject: Job 124712019: <CAD12step2> in cluster <chimera> Done

```

Job <CAD12step2> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 08:20:21 2024
Job was executed on host(s) <lc02c11>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 08:20:27 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
Started at Thu Apr 18 08:20:27 2024
Terminated at Thu Apr 18 09:10:30 2024
Results reported at Thu Apr 18 09:10:30 2024

Your job looked like:

```

-----
# LSBATCH: User input
#!/bin/bash
#BSUB -J CAD12step2
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=16000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# # call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices workflow

# code updates:
# [1] changed minerva dir name from WGS-iPSC to WGS_iPSC because alias did not work
# [2] updated raw data filenames by replacing - with _ chr

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # update reads dir for specific sample
reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"
#reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"

# consistent dir's between samples
ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"
known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"
aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"
results="/sc/arion/projects/vascbrain/WGS_iPSC/results"
data="/sc/arion/projects/vascbrain/WGS_iPSC/data"

##### Prep files (RUN ONLY ONCE) #####

# # make ref folder
# mkdir hg38

# # download reference files to folder and unzip #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz

# # index ref - .fai file before running haplotype caller #####
# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa

# # create ref dict file before running haplotype caller #####
# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict

```

```
## download known sites files for BQSR from GATK resource bundle #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assemb
ly38.dbsnp138.vcf
```

(... more ...)

Successfully completed.

Resource usage summary:

CPU time :	2994.12 sec.
Max Memory :	4597 MB
Average Memory :	2041.25 MB
Total Requested Memory :	16000.00 MB
Delta Memory :	11403.00 MB
Max Swap :	2 MB
Max Processes :	4
Max Threads :	5
Run time :	3003 sec.
Turnaround time :	3009 sec.

The output (if any) follows:

```
STEP 2: Map to reference using BWA-MEM
[bwt_gen] Finished constructing BWT in 710 iterations.
STEP 2: read alignment to ref genome hg38 complete!
```

PS:

Read file <124712019.stderr> for stderr output of this job.

```
[palafm01@li03c03 scripts]$ ls
124712019.stderr 124712019.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cd *err
-bash: cd: 124712019.stderr: Not a directory
[palafm01@li03c03 scripts]$ cat *eff
cat: *eff: No such file or directory
[palafm01@li03c03 scripts]$ cat *err
[bwa_index] Pack FASTA... 19.40 sec
[bwa_index] Construct BWT for the packed sequence...
[BWTIncCreate] textLength=6418572210, availableWord=463634060
[BWTIncConstructFromPacked] 10 iterations done. 99999986 characters processed.
[BWTIncConstructFromPacked] 20 iterations done. 199999986 characters processed.
[BWTIncConstructFromPacked] 30 iterations done. 299999986 characters processed.
[BWTIncConstructFromPacked] 40 iterations done. 399999986 characters processed.
[BWTIncConstructFromPacked] 50 iterations done. 499999986 characters processed.
[BWTIncConstructFromPacked] 60 iterations done. 599999986 characters processed.
[BWTIncConstructFromPacked] 70 iterations done. 699999986 characters processed.
[BWTIncConstructFromPacked] 80 iterations done. 799999986 characters processed.
[BWTIncConstructFromPacked] 90 iterations done. 899999986 characters processed.
[BWTIncConstructFromPacked] 100 iterations done. 999999986 characters processed.
[BWTIncConstructFromPacked] 110 iterations done. 1099999986 characters processed.
[BWTIncConstructFromPacked] 120 iterations done. 1199999986 characters processed.
[BWTIncConstructFromPacked] 130 iterations done. 1299999986 characters processed.
[BWTIncConstructFromPacked] 140 iterations done. 1399999986 characters processed.
[BWTIncConstructFromPacked] 150 iterations done. 1499999986 characters processed.
[BWTIncConstructFromPacked] 160 iterations done. 1599999986 characters processed.
[BWTIncConstructFromPacked] 170 iterations done. 1699999986 characters processed.
[BWTIncConstructFromPacked] 180 iterations done. 1799999986 characters processed.
[BWTIncConstructFromPacked] 190 iterations done. 1899999986 characters processed.
[BWTIncConstructFromPacked] 200 iterations done. 1999999986 characters processed.
[BWTIncConstructFromPacked] 210 iterations done. 2099999986 characters processed.
[BWTIncConstructFromPacked] 220 iterations done. 2199999986 characters processed.
[BWTIncConstructFromPacked] 230 iterations done. 2299999986 characters processed.
[BWTIncConstructFromPacked] 240 iterations done. 2399999986 characters processed.
[BWTIncConstructFromPacked] 250 iterations done. 2499999986 characters processed.
[BWTIncConstructFromPacked] 260 iterations done. 2599999986 characters processed.
[BWTIncConstructFromPacked] 270 iterations done. 2699999986 characters processed.
[BWTIncConstructFromPacked] 280 iterations done. 2799999986 characters processed.
[BWTIncConstructFromPacked] 290 iterations done. 2899999986 characters processed.
[BWTIncConstructFromPacked] 300 iterations done. 2999999986 characters processed.
[BWTIncConstructFromPacked] 310 iterations done. 3099999986 characters processed.
[BWTIncConstructFromPacked] 320 iterations done. 3199999986 characters processed.
[BWTIncConstructFromPacked] 330 iterations done. 3299999986 characters processed.
```

```

[BWTIncConstructFromPacked] 340 iterations done. 3399999986 characters processed.
[BWTIncConstructFromPacked] 350 iterations done. 3499999986 characters processed.
[BWTIncConstructFromPacked] 360 iterations done. 3599999986 characters processed.
[BWTIncConstructFromPacked] 370 iterations done. 3699999986 characters processed.
[BWTIncConstructFromPacked] 380 iterations done. 3799999986 characters processed.
[BWTIncConstructFromPacked] 390 iterations done. 3899999986 characters processed.
[BWTIncConstructFromPacked] 400 iterations done. 3999999986 characters processed.
[BWTIncConstructFromPacked] 410 iterations done. 4099999986 characters processed.
[BWTIncConstructFromPacked] 420 iterations done. 4199999986 characters processed.
[BWTIncConstructFromPacked] 430 iterations done. 4299999986 characters processed.
[BWTIncConstructFromPacked] 440 iterations done. 4399999986 characters processed.
[BWTIncConstructFromPacked] 450 iterations done. 4499999986 characters processed.
[BWTIncConstructFromPacked] 460 iterations done. 4599999986 characters processed.
[BWTIncConstructFromPacked] 470 iterations done. 4699999986 characters processed.
[BWTIncConstructFromPacked] 480 iterations done. 4799999986 characters processed.
[BWTIncConstructFromPacked] 490 iterations done. 4899999986 characters processed.
[BWTIncConstructFromPacked] 500 iterations done. 4999999986 characters processed.
[BWTIncConstructFromPacked] 510 iterations done. 5099999986 characters processed.
[BWTIncConstructFromPacked] 520 iterations done. 5199999986 characters processed.
[BWTIncConstructFromPacked] 530 iterations done. 5299999986 characters processed.
[BWTIncConstructFromPacked] 540 iterations done. 5399999986 characters processed.
[BWTIncConstructFromPacked] 550 iterations done. 5499999986 characters processed.
[BWTIncConstructFromPacked] 560 iterations done. 5599999986 characters processed.
[BWTIncConstructFromPacked] 570 iterations done. 5699999986 characters processed.
[BWTIncConstructFromPacked] 580 iterations done. 5798165394 characters processed.
[BWTIncConstructFromPacked] 590 iterations done. 5886412978 characters processed.
[BWTIncConstructFromPacked] 600 iterations done. 5964843650 characters processed.
[BWTIncConstructFromPacked] 610 iterations done. 6034549010 characters processed.
[BWTIncConstructFromPacked] 620 iterations done. 6096499330 characters processed.
[BWTIncConstructFromPacked] 630 iterations done. 6151556914 characters processed.
[BWTIncConstructFromPacked] 640 iterations done. 6200488210 characters processed.
[BWTIncConstructFromPacked] 650 iterations done. 6243974434 characters processed.
[BWTIncConstructFromPacked] 660 iterations done. 6282621122 characters processed.
[BWTIncConstructFromPacked] 670 iterations done. 6316966322 characters processed.
[BWTIncConstructFromPacked] 680 iterations done. 6347488418 characters processed.
[BWTIncConstructFromPacked] 690 iterations done. 6374612482 characters processed.
[BWTIncConstructFromPacked] 700 iterations done. 6398716386 characters processed.
[BWTIncConstructFromPacked] 710 iterations done. 6418572210 characters processed.
[bwa_index] 2166.76 seconds elapse.
[bwa_index] Update BWT... 12.84 sec
[bwa_index] Pack forward-only FASTA... 11.77 sec
[bwa_index] Construct SA from BWT and Occ... 776.19 sec
[main] Version: 0.7.15-r1140
[main] CMD: bwa index /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa
[main] Real time: 2997.501 sec; CPU: 2986.970 sec
[M:bwa_idx_load_from_disk] read 0 ALT contigs
[W:bseq_read] the 2nd file has fewer sequences.
[W:bseq_read] the 2nd file has fewer sequences.
[M:process] read 4 sequences (707 bp)...
[M:mem_pestat] # candidate unique pairs for (FF, FR, RF, RR): (0, 0, 0, 0)
[M:mem_pestat] skip orientation FF as there are not enough pairs
[M:mem_pestat] skip orientation FR as there are not enough pairs
[M:mem_pestat] skip orientation RF as there are not enough pairs
[M:mem_pestat] skip orientation RR as there are not enough pairs
[mem_sam_pe] paired reads have different names: "ANwIz?Sloam?<?nX???<?I??+ "M", "?d"

```

```

[palafm01@li03c03 scripts]$ ls
124712019.stderr 124712019.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ vim variant_calling.sh
[palafm01@li03c03 scripts]$ bsub < variant_calling.sh
Job <124745367> is submitted to queue <premium>.
[palafm01@li03c03 scripts]$ bjobs
      JOBID      USER      JOB_NAME      STAT      QUEUE      FROM_HOST      EXEC_HOST      SUBMIT_TIME      START_TIME      TIME_LEFT
124745367 palafm01 CAD63step2  PEND      premium li03c03.ch      -      Apr 18 10:22      -      -
[palafm01@li03c03 scripts]$ ls
124712019.stderr 124712019.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ wgs
[palafm01@li03c03 WGS_iPSC]$ ls
aligned_reads data FastQC_output hg38 MD5 raw_data raw_data.zip Readme.html results scripts
[palafm01@li03c03 WGS_iPSC]$ cd aligned_reads/
[palafm01@li03c03 aligned_reads]$ lss
total 33K
-rw-r----- 1 palafm01 vascbrain 17K Apr 18 09:10 P732912.paired.sam
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 09:10 .
drwxr-s--- 10 palafm01 vascbrain 4.0K Apr 17 17:23 ..
[palafm01@li03c03 aligned_reads]$ samtools view P732912.paired.sam | less

```



```

-bash: samtools: command not found
[palafm01@li03c03 aligned_reads]$ samtools view P732912.paired.sam | less
-bash: samtools: command not found
[palafm01@li03c03 aligned_reads]$
[palafm01@li03c03 aligned_reads]$ lss
total 33K
-rw-r----- 1 palafm01 vascbrain 17K Apr 18 09:10 P732912.paired.sam
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 09:10 .
drwxr-s--- 10 palafm01 vascbrain 4.0K Apr 17 17:23 ..
[palafm01@li03c03 aligned_reads]$ less P732912.paired.sam
[palafm01@li03c03 aligned_reads]$ samtools view P732912.paired.sam | less
-bash: samtools: command not found
[palafm01@li03c03 aligned_reads]$ less P732912.paired.sam
[palafm01@li03c03 aligned_reads]$ samtools flagstat P732912.paired.sam
-bash: samtools: command not found
[palafm01@li03c03 aligned_reads]$ module load samtools
[palafm01@li03c03 aligned_reads]$ samtools --version
samtools 1.17
Using htslib 1.17
Copyright (C) 2023 Genome Research Ltd.

```

Samtools compilation details:

```

Features:      build=configure curses=yes
CC:           gcc
CPPFLAGS:
CFLAGS:       -Wall -g -O2
LDFLAGS:
HTSDIR:       htslib-1.17
LIBS:
CURSES_LIB:   -lnursesw

```

HTSlib compilation details:

```

Features:      build=configure libcurl=yes S3=yes GCS=yes libdeflate=no lzma=yes bzip2=yes plugins=no htscodcs=1.4.0
CC:           gcc
CPPFLAGS:
CFLAGS:       -Wall -g -O2 -fvisibility=hidden
LDFLAGS:      -fvisibility=hidden

```

HTSlib URL scheme handlers present:

```

built-in:      preload, data, file
S3 Multipart Upload:      s3w, s3w+https, s3w+http
Amazon S3:      s3+https, s3+http, s3
Google Cloud Storage:     gs+http, gs+https, gs
libcurl:        imaps, pop3, http, gopher, sftp, ftps, imap, smtp, smtps, rtsp, scp, ftp, telnet, ldap, https, ldaps, tftp, pop3s, dict
crypt4gh-needed: crypt4gh
mem:            mem

```

```

[palafm01@li03c03 aligned_reads]$ ls
P732912.paired.sam
[palafm01@li03c03 aligned_reads]$ samtools flagstat P732912.paired.sam
0 + 0 in total (QC-passed reads + QC-failed reads)
0 + 0 primary
0 + 0 secondary
0 + 0 supplementary
0 + 0 duplicates
0 + 0 primary duplicates
0 + 0 mapped (N/A : N/A)
0 + 0 primary mapped (N/A : N/A)
0 + 0 paired in sequencing
0 + 0 read1
0 + 0 read2
0 + 0 properly paired (N/A : N/A)
0 + 0 with itself and mate mapped
0 + 0 singletons (N/A : N/A)
0 + 0 with mate mapped to a different chr
0 + 0 with mate mapped to a different chr (mapQ>=5)
[palafm01@li03c03 aligned_reads]$ samtools view P732912.paired.sam | less
[palafm01@li03c03 aligned_reads]$ ls
P732912.paired.sam P931263.paired.sam
[palafm01@li03c03 aligned_reads]$ bjobs
No unfinished job found
[palafm01@li03c03 aligned_reads]$ ls
P732912.paired.sam P931263.paired.sam
[palafm01@li03c03 aligned_reads]$ lss
total 65K
-rw-r----- 1 palafm01 vascbrain 17K Apr 18 11:13 P931263.paired.sam
-rw-r----- 1 palafm01 vascbrain 17K Apr 18 09:10 P732912.paired.sam

```



```
drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 11:13 .
drwxr-s--- 10 palafm01 vascbrain 4.0K Apr 17 17:23 ..
[palafm01@li03c03 aligned_reads]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ cd
[palafm01@li03c03 ~]$ wgs
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
124712019.stderr 124712019.stdout 124745367.stderr 124745367.stdout CAD12_std CAD63_std variant_calling.sh
[palafm01@li03c03 scripts]$ cat *.stdout
cat: *.stdout: No such file or directory
[palafm01@li03c03 scripts]$ cat *.stderr
Sender: LSF System <lsfadmin@lc02c11>
Subject: Job 124712019: <CAD12step2> in cluster <chimera> Done
```

Job <CAD12step2> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 08:20:21 2024
Job was executed on host(s) <lc02c11>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 08:20:27 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
Started at Thu Apr 18 08:20:27 2024
Terminated at Thu Apr 18 09:10:30 2024
Results reported at Thu Apr 18 09:10:30 2024

Your job looked like:

```
-----
# LSBATCH: User input
#!/bin/bash
#BSUB -J CAD12step2
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=16000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# # call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices workflow

# code updates:
# [1] changed minerva dir name from WGS-iPSC to WGS_iPSC because alias did not work
# [2] updated raw data filenames by replacing - with _ chr

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # update reads dir for specific sample
reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"
#reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"

# consistent dir's between samples
ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"
known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"
aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"
results="/sc/arion/projects/vascbrain/WGS_iPSC/results"
data="/sc/arion/projects/vascbrain/WGS_iPSC/data"

##### Prep files (RUN ONLY ONCE) #####

# # make ref folder
# mkdir hg38

# # download reference files to folder and unzip #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz

# # index ref - .fai file before running haplotype caller #####
# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa

# # create ref dict file before running haplotype caller #####
# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict

# # download known sites files for BQSR from GATK resource bundle #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assemb
```

ly38.dbsnp138.vcf

(... more ...)

Successfully completed.

Resource usage summary:

CPU time :	2994.12 sec.
Max Memory :	4597 MB
Average Memory :	2041.25 MB
Total Requested Memory :	16000.00 MB
Delta Memory :	11403.00 MB
Max Swap :	2 MB
Max Processes :	4
Max Threads :	5
Run time :	3003 sec.
Turnaround time :	3009 sec.

The output (if any) follows:

STEP 2: Map to reference using BWA-MEM
[bwt_gen] Finished constructing BWT in 710 iterations.
STEP 2: read alignment to ref genome hg38 complete!

PS:

Read file <124712019.stderr> for stderr output of this job.

Sender: LSF System <lsfadmin@lc02c11>
Subject: Job 124745367: <CAD63step2> in cluster <chimera> Done

Job <CAD63step2> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 10:22:56 2024
Job was executed on host(s) <lc02c11>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 10:23:01 2024
</hpc/users/palafm01> was used as the home directory.
</sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
Started at Thu Apr 18 10:23:01 2024
Terminated at Thu Apr 18 11:13:35 2024
Results reported at Thu Apr 18 11:13:35 2024

Your job looked like:

LSBATCH: User input
#!/bin/bash
#BSUB -J CAD63step2
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=16000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices workflow

code updates:
[1] changed minerva dir name from WGS-iPSC to WGS_iPSC because alias did not work
[2] updated raw data filenames by replacing - with _ chr

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

update reads dir for specific sample
#reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"
reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"

consistent dir's between samples
ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"
known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"
aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"

```

results="/sc/arion/projects/vascbrain/WGS_iPSC/results"
data="/sc/arion/projects/vascbrain/WGS_iPSC/data"

##### Prep files (RUN ONLY ONCE) #####

# # make ref folder
# mkdir hg38

# # download reference files to folder and unzip #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz

# # index ref - .fai file before running haplotype caller #####
# samtools faidx /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa

# # create ref dict file before running haplotype caller #####
# gatk CreateSequenceDictionary R=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa O=/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.dict

# # download known sites files for BQSR from GATK resource bundle #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://storage.googleapis.com/genomics-public-data/resources/broad/hg38/v0/Homo_sapiens_assembly38.dbsnp138.vcf

(... more ...)

```

Successfully completed.

Resource usage summary:

CPU time :	3017.70 sec.
Max Memory :	4597 MB
Average Memory :	2037.33 MB
Total Requested Memory :	16000.00 MB
Delta Memory :	11403.00 MB
Max Swap :	-
Max Processes :	5
Max Threads :	6
Run time :	3033 sec.
Turnaround time :	3039 sec.

The output (if any) follows:

```

STEP 2: Map to reference using BWA-MEM
[bwt_gen] Finished constructing BWT in 710 iterations.
STEP 2: read alignment to ref genome hg38 complete!

```

PS:

Read file <124745367.stderr> for stderr output of this job.

```

[palafm01@li03c03 scripts]$ cd hg38
-bash: cd: hg38: No such file or directory
[palafm01@li03c03 scripts]$ cd ..
[palafm01@li03c03 WGS_iPSC]$ cd hg38
[palafm01@li03c03 hg38]$ ls
hg38.dict  hg38.fa.amb  hg38.fa.bwt  hg38.fa.pac  Homo_sapiens_assembly38.dbsnp138.vcf
hg38.fa    hg38.fa.ann  hg38.fa.fai  hg38.fa.sa   Homo_sapiens_assembly38.dbsnp138.vcf.idx
[palafm01@li03c03 hg38]$ ls -lh
total 19G
-rw-r----- 1 palafm01 vascbra 59K Apr 17 07:59 hg38.dict
-rw-r----- 1 palafm01 vascbra 3.1G Jan 16 2014 hg38.fa
-rw-r----- 1 palafm01 vascbra 21K Apr 18 11:00 hg38.fa.amb
-rw-r----- 1 palafm01 vascbra 22K Apr 18 11:00 hg38.fa.ann
-rw-r----- 1 palafm01 vascbra 3.0G Apr 18 11:00 hg38.fa.bwt
-rw-r----- 1 palafm01 vascbra 19K Apr 17 07:57 hg38.fa.fai
-rw-r----- 1 palafm01 vascbra 766M Apr 18 11:00 hg38.fa.pac
-rw-r----- 1 palafm01 vascbra 1.5G Apr 18 11:13 hg38.fa.sa
-rw-r----- 1 palafm01 vascbra 11G Jul 21 2016 Homo_sapiens_assembly38.dbsnp138.vcf
-rw-r----- 1 palafm01 vascbra 12M Jul 21 2016 Homo_sapiens_assembly38.dbsnp138.vcf.idx
[palafm01@li03c03 hg38]$ man ls
[palafm01@li03c03 hg38]$ ls -c
hg38.fa.sa  hg38.fa.bwt  hg38.fa.fai
hg38.fa.amb  Homo_sapiens_assembly38.dbsnp138.vcf.idx  hg38.fa
hg38.fa.ann  Homo_sapiens_assembly38.dbsnp138.vcf
hg38.fa.pac  hg38.dict

```

```

[palafm01@li03c03 hg38]$ ls -lch
total 19G
-rw-r----- 1 palafm01 vascbrain 59K Apr 17 07:59 hg38.dict
-rw-r----- 1 palafm01 vascbrain 3.1G Apr 17 07:47 hg38.fa
-rw-r----- 1 palafm01 vascbrain 21K Apr 18 11:00 hg38.fa.amb
-rw-r----- 1 palafm01 vascbrain 22K Apr 18 11:00 hg38.fa.ann
-rw-r----- 1 palafm01 vascbrain 3.0G Apr 18 11:00 hg38.fa.bwt
-rw-r----- 1 palafm01 vascbrain 19K Apr 17 07:57 hg38.fa.fai
-rw-r----- 1 palafm01 vascbrain 766M Apr 18 11:00 hg38.fa.pac
-rw-r----- 1 palafm01 vascbrain 1.5G Apr 18 11:13 hg38.fa.sa
-rw-r----- 1 palafm01 vascbrain 11G Apr 17 08:01 Homo_sapiens_assembly38.dbsnp138.vcf
-rw-r----- 1 palafm01 vascbrain 12M Apr 17 08:02 Homo_sapiens_assembly38.dbsnp138.vcf.idx
[palafm01@li03c03 hg38]$ man ls
[palafm01@li03c03 hg38]$ ls -ht
hg38.fa.sa hg38.fa.pac hg38.fa.fai hg38.fa
hg38.fa.amb hg38.fa.bwt Homo_sapiens_assembly38.dbsnp138.vcf.idx
hg38.fa.ann hg38.dict Homo_sapiens_assembly38.dbsnp138.vcf
[palafm01@li03c03 hg38]$ ls -lsht
total 19G
1.5G -rw-r----- 1 palafm01 vascbrain 1.5G Apr 18 11:13 hg38.fa.sa
32K -rw-r----- 1 palafm01 vascbrain 21K Apr 18 11:00 hg38.fa.amb
32K -rw-r----- 1 palafm01 vascbrain 22K Apr 18 11:00 hg38.fa.ann
766M -rw-r----- 1 palafm01 vascbrain 766M Apr 18 11:00 hg38.fa.pac
3.0G -rw-r----- 1 palafm01 vascbrain 3.0G Apr 18 11:00 hg38.fa.bwt
64K -rw-r----- 1 palafm01 vascbrain 59K Apr 17 07:59 hg38.dict
32K -rw-r----- 1 palafm01 vascbrain 19K Apr 17 07:57 hg38.fa.fai
12M -rw-r----- 1 palafm01 vascbrain 12M Jul 21 2016 Homo_sapiens_assembly38.dbsnp138.vcf.idx
11G -rw-r----- 1 palafm01 vascbrain 11G Jul 21 2016 Homo_sapiens_assembly38.dbsnp138.vcf
3.1G -rw-r----- 1 palafm01 vascbrain 3.1G Jan 16 2014 hg38.fa
[palafm01@li03c03 hg38]$
[palafm01@li03c03 hg38]$ cd
[palafm01@li03c03 ~]$ vim .bashrc
[palafm01@li03c03 ~]$ source .bashrc
[palafm01@li03c03 ~]$ wgs
[palafm01@li03c03 WGS_iPSC]$ cd scripts/
[palafm01@li03c03 scripts]$ ls
124712019.stderr 124745367.stderr CAD12_std variant_calling.sh
124712019.stdout 124745367.stdout CAD63_std
[palafm01@li03c03 scripts]$ sh
sh-4.2$ ^C
sh-4.2$ ^C
sh-4.2$ ^C
sh-4.2$ :q
sh: :q: command not found
sh-4.2$ quit
sh: quit: command not found
sh-4.2$ quit()
>
> ^C
sh-4.2$ ^C
sh-4.2$ ^C
sh-4.2$ exit
exit
[palafm01@li03c03 scripts]$ ls
124712019.stderr 124745367.stderr CAD12_std variant_calling.sh
124712019.stdout 124745367.stdout CAD63_std
[palafm01@li03c03 scripts]$ pwd
/sc/arion/projects/vascbrain/WGS_iPSC/scripts
[palafm01@li03c03 scripts]$ out
-bash: out: command not found
[palafm01@li03c03 scripts]$ cd
[palafm01@li03c03 ~]$ vim .bashrc
[palafm01@li03c03 ~]$ source .bashrc
[palafm01@li03c03 ~]$ out
[palafm01@li03c03 scripts]$ ls
124712019.stderr 124745367.stderr CAD12_std variant_calling.sh
124712019.stdout 124745367.stdout CAD63_std
[palafm01@li03c03 scripts]$ wgs
[palafm01@li03c03 WGS_iPSC]$ cd hg38
[palafm01@li03c03 hg38]$ ls
hg38.dict hg38.fa.amb hg38.fa.bwt hg38.fa.pac Homo_sapiens_assembly38.dbsnp138.vcf
hg38.fa hg38.fa.ann hg38.fa.fai hg38.fa.sa Homo_sapiens_assembly38.dbsnp138.vcf.idx
[palafm01@li03c03 hg38]$ lst
total 19G
1.5G -rw-r----- 1 palafm01 vascbrain 1.5G Apr 18 11:13 hg38.fa.sa
32K -rw-r----- 1 palafm01 vascbrain 21K Apr 18 11:00 hg38.fa.amb

```

```

32K -rw-r----- 1 palafm01 vascbrain 22K Apr 18 11:00 hg38.fa.ann
766M -rw-r----- 1 palafm01 vascbrain 766M Apr 18 11:00 hg38.fa.pac
3.0G -rw-r----- 1 palafm01 vascbrain 3.0G Apr 18 11:00 hg38.fa.bwt
64K -rw-r----- 1 palafm01 vascbrain 59K Apr 17 07:59 hg38.dict
32K -rw-r----- 1 palafm01 vascbrain 19K Apr 17 07:57 hg38.fa.fai
12M -rw-r----- 1 palafm01 vascbrain 12M Jul 21 2016 Homo_sapiens_assembly38.dbsnp138.vcf.idx
11G -rw-r----- 1 palafm01 vascbrain 11G Jul 21 2016 Homo_sapiens_assembly38.dbsnp138.vcf
3.1G -rw-r----- 1 palafm01 vascbrain 3.1G Jan 16 2014 hg38.fa
[palafm01@li03c03 hg38]$ out
[palafm01@li03c03 scripts]$ lst
total 98K
512 -rw-r----- 1 palafm01 vascbrain 3.7K Apr 18 11:13 124745367.stdout
32K -rw-r----- 1 palafm01 vascbrain 7.4K Apr 18 11:13 124745367.stderr
32K -rwxr-x--- 1 palafm01 vascbrain 4.2K Apr 18 10:22 variant_calling.sh
512 -rw-r----- 1 palafm01 vascbrain 3.7K Apr 18 09:10 124712019.stdout
32K -rw-r----- 1 palafm01 vascbrain 6.8K Apr 18 09:10 124712019.stderr
512 drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 08:26 CAD12_std
512 drwxr-s--- 2 palafm01 vascbrain 4.0K Apr 18 08:25 CAD63_std
[palafm01@li03c03 scripts]$ cat 124745367.stdout
Sender: LSF System <lsfadmin@lc02c11>
Subject: Job 124745367: <CAD63step2> in cluster <chimera> Done

```

Job <CAD63step2> was submitted from host <li03c03.chimera.hpc.mssm.edu> by user <palafm01> in cluster <chimera> at Thu Apr 18 10:22:56 2024
 Job was executed on host(s) <lc02c11>, in queue <premium>, as user <palafm01> in cluster <chimera> at Thu Apr 18 10:23:01 2024
 </hpc/users/palafm01> was used as the home directory.
 </sc/arion/projects/vascbrain/WGS_iPSC/scripts> was used as the working directory.
 Started at Thu Apr 18 10:23:01 2024
 Terminated at Thu Apr 18 11:13:35 2024
 Results reported at Thu Apr 18 11:13:35 2024

Your job looked like:

```

-----
# LSBATCH: User input
#!/bin/bash
#BSUB -J CAD63step2
#BSUB -P acc_vascbrain
#BSUB -q premium
#BSUB -n 1
#BSUB -W 6:00
#BSUB -R rusage[mem=16000]
#BSUB -oo %J.stdout
#BSUB -eo %J.stderr
#BSUB -L /bin/bash

# # call germline variants in a human WGS paired end reads 2 X 100bp following GATK4 best practices workflow

# code updates:
# [1] changed minerva dir name from WGS-iPSC to WGS_iPSC because alias did not work
# [2] updated raw data filenames by replacing - with _ chr

module load samtools/1.17
module load gatk
module load fastqc
module load bwa

# # update reads dir for specific sample
#reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P732912"
reads="/sc/arion/projects/vascbrain/WGS_iPSC/raw_data/P931263"

# consistent dir's between samples
ref="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa"
known_sites="/sc/arion/projects/vascbrain/WGS_iPSC/hg38/Homo_sapiens_assembly38.dbsnp138.vcf"
aligned_reads="/sc/arion/projects/vascbrain/WGS_iPSC/aligned_reads"
results="/sc/arion/projects/vascbrain/WGS_iPSC/results"
data="/sc/arion/projects/vascbrain/WGS_iPSC/data"

##### Prep files (RUN ONLY ONCE) #####

# # make ref folder
# mkdir hg38

# # download reference files to folder and unzip #####
# wget -P /sc/arion/projects/vascbrain/WGS_iPSC/hg38/ https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.gz
# gunzip /sc/arion/projects/vascbrain/WGS_iPSC/hg38/hg38.fa.gz

```