Journal Club (30mins+30minsQA) (Thu)1400-1500	**Presentor**	**Topic**	**Progress report (15mins+5minQA) (Fri)1300-1400**	**Presentor**		
2/16	PX	High-coverage whole-genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios	2/17	Calvin	HW	Pinfei
2/23	Daphne	Major sex differences in allele frequencies for X chromosomal variants in both the 1000 Genomes Project and gnomAD	2/24	郁書	PX	PM
3/2	Pinfei	Myelodysplastic Syndrome associated TET2 mutations affect NK cell function and genome methylation	3/3	庭暄	YT	
3/9	YT	Comprehensive SMN1 and SMN2 profiling for spinal muscular atrophy analysis using long-read PacBio HiFi sequencing	3/10	俐伶	俐伶	Calvin

Journal Club (30mins+30minsQA) (Thu)1400-1500	Presentor	Topic	Progress report (15mins+5minQA) (Fri)1300-1400	Presentor		
3/16	PM	Structural variant detection in cancer genomes: computational challenges and perspectives for precision oncology	3/17	HW	Pinfei	郁書
3/23	俐伶	Spinal muscular atrophy diagnosis and carrier screening from genome sequencing data	3/24	PX	PM	
3/30	PX	預口試	3/31	YT	庭暄	
4/6	HW	Analysis of KIR gene variants in The Cancer Genome Atlas and UK Biobank using KIRCLE - BMC Biology	4/7	Calvin	HW	Pinfei
4/13	庭暄		4/14	郁書	PM	
4/20		Clara	4/21	庭暄	YT	PX
4/27	Pinfei	A cross-disorder dosage sensitivity map of the human genome	4/28	俐伶	俐伶	HW
5/4	YT	Mono- and biallelic variant effects on disease at biobank scale	5/5	Calvin	Pinfei	郁書

Journal Club (30mins+30minsQA) (Thu)1400-1500	**Presentor**	**Topic**	**Progress report (15mins+5minQA) (Fri)1300-1400**	**Presentor**		
5/11	俐伶	Taiwan Biobank: A rich biomedical research database of the Taiwanese population	5/12	PX	PM	庭暄
5/18	PM	Structural variant detection in cancer genomes: computational challenges and perspectives for precision oncology	5/19	YT	自航	自航
5/25	PX	Structural variation across 138,134 samples in the TOPMed consortium	5/26	Calvin	HW	Pinfei
6/1	暫停一次		6/2	郁書	PX	PM
6/8			6/9	庭暄	YT	
6/15	HW	Analysis of KIR gene variants in The Cancer Genome Atlas and UK Biobank using KIRCLE - BMC Biology	6/16	俐伶	俐伶	Calvin
6/22	端午		6/23	端午	端午	端午
6/29	Pinfei		6/30	HW	Pinfei	郁書

Journal Club (30mins+30minsQA) (Thu)1400-1500	**Presentor**	**Topic**	**Progress report (15mins+5minQA) (Fri)1300-1400**	**Presentor**		
7/6	YT	Whole genome sequencing identifies structural variants contributing to hematologic traits in the NHLBI TOPMed program - PubMed	7/7	PX	PM	庭暄
7/13	俐伶		7/14	YT	自航	自航
7/20	PM	Structural variant detection in cancer genomes: computational challenges and perspectives for precision oncology	7/21	Calvin	HW	Pinfei
7/27	HW	Analysis of HLA Variants and Graves' Disease and Its Comorbidities Using a High Resolution Imputation System to Examine Electronic Medical Health Records	7/28	郁書	PX	PM
8/3	庭暄		8/4	庭暄	YT	
8/10	PX		8/11	俐伶	俐伶	Calvin
8/17			8/18	HW	Pinfei	郁書
8/24	Pinfei		8/25	PX	PM	庭暄

Journal Club (30mins+30minsQA) (Thu)1400-1500	**Presentor**	**Topic**	**Progress report (15mins+5minQA) (Fri)1300-1400**	**Presentor**		
8/31	YT		9/1	YT	自航	自航

Updated paper:

- Truvari: refined structural variant comparison preserves allelic diversity
- Scaling national and international improvement in virtual gene panel curation via a collaborative approach to discordance resolution
- Pinfei A cross-disorder dosage sensitivity map of the human genome
- Profiling variable-number tandem repeat variation across populations using repeat-pangenome graphs
- Points to consider in the detection of germline structural variants using next-generation sequencing: A statement of the American College of Medical Genetics and Genomics (ACMG)
- A joint NCBI and EMBL-EBI transcript set for clinical genomics and research
- Genomic analyses of 10,376 individuals in the Westlake BioBank for Chinese (WBBC) pilot project
- Personalized genome assembly for accurate cancer somatic mutation discovery using tumor-normal paired reference samples (Genome Biology 2022)
- Structural variant analysis of a cancer reference cell line sample using multiple sequencing technologies (Genome Biology 2022)
- Variant calling and benchmarking in an era of complete human genome sequences (Nature Reviews Genetics 2023)