

Data File Download



Search by Gene

Search by Disease Search Proteome Database

Data File Download

HOME SITE MAP

The application procedure is necessary for downloading JSNP, Illumina 110K and Illumina 550K/610K genome scan data. Please click here for detail.

JSNP Genome Scan

Disease	ReadMe	SNP Frequency Data
5 Disease Combined (1st screening)	<u>html</u>	<u>zip</u> (2,262.4 kb)
Alzheimer's disease (1st screening)	<u>html</u>	<u>zip</u> (1,919.4 kb)
Gastric cancer (1st screening)	<u>html</u>	<u>zip</u> (1,961.5 kb)
Diabetes mellitus (1st screening)	<u>html</u>	<u>zip</u> (1,854.4 kb)
Hypertension (1st screening)	<u>html</u>	<u>zip</u> (1,823.1 kb)
Bronchial asthma (1st screening)	<u>html</u>	<u>zip</u> (1,827 kb)
Alzheimer's disease (2nd screening)	<u>html</u>	<u>zip</u> (112 kb)
Gastric cancer (2nd screening)	<u>html</u>	<u>zip</u> (113 kb)
Diabetes mellitus (2nd screening)	<u>html</u>	<u>zip</u> (117 kb)
Hypertension (2nd screening)	<u>html</u>	<u>zip</u> (113.7 kb)
Bronchial asthma (2nd screening)	<u>html</u>	<u>zip</u> (100.5 kb)

Description 5 Disease Combined (1st screening	SNP/Gene symbol list
5 Disease Combined (1st screening)	<u>zip</u> (899 kb)

Description	ID list
Correspondence table of JSNP ID and dbSNPrs ID	<u>zip</u> (1,060 kb)

Illumina 110K Genome Scan

Disease	SNP Frequency Data
All group combined	<u>zip</u> (2,846 kb)
Japanese population control (female)	<u>zip</u> (2,664.3 kb)
Japanese population control (male)	<u>zip</u> (2,263.6 kb)
Patients with various types of cancers	<u>zip</u> (2,784.5 kb)

Pharmacogenomic analyses	ReadMe	SNP Data
Pharmacokinetic parameters of gemcitabine (AUC)	<u>html</u>	<u>zip</u> (2,667.4 kb)
Pharmacokinetic parameters of gemcitabine (Kel)	<u>html</u>	<u>zip</u> (2,667.9 kb)
Pharmacokinetic parameters of gemcitabine (Volume)	<u>html</u>	zip (2,620.1 kb)
Pharmacokinetic parameters of gemcitabine (Cmax)	<u>html</u>	<u>zip</u> (3,127.9 kb)
Pharmacokinetic parameters of gemcitabine (MRT)	<u>html</u>	<u>zip</u> (3,127.8 kb)

Illumina 550K/610K Genome Scan

Disease		SNP Frequency Data
	Tokyo	<u>zip</u> (16,412.6 kb)
Japanese population control	Osaka	<u>zip</u> (16,257.7 kb)
	Ibaraki	<u>zip</u> (16,587.8 kb)

	Tokyo+Osaka+Ibaraki zip (18,435.5 kb)
Alzheimer's disease	<u>zip</u> (93,092.8 kb)
Pancreatic cancer	<u>zip</u> (92,506.0 kb)
Bronchial asthma	<u>zip</u> (106,148.4 kb)

Candidate Gene Approach

Project ID	Description	SNP/Gene symbol list	Frequency data
CGA01	Allele frequencies of single nucleotide polymorphisms (SNPs) in 40 candidate genes for gene-environment studies on cancer: data from population-based Japanese random samples.	<u>zip</u> (4.2 kb)	-
CGA02	Polymorphisms in cancer-related genes.	<u>zip</u> (37.3 kb)	<u>zip</u> (13.6 kb)
CGA03	Polymorphisms in genes coding for Drug-Responsive Molecules.	<u>zip</u> (2.6 kb)	-
CGA04	Case-control study on 198 patients with pancreatic cancer and 182 controls.	<u>zip</u> (5.5 kb)	<u>zip</u> (3.8 kb)
CGA05	Allele frequencies of SNPs in the prion protein gene on Alzheimer's disease patients: data from population-based Japanese random samples.	<u>zip</u> (0.4 kb)	<u>zip</u> (0.4 kb)
CGA06	Genotype and allele frequencies of the TrkA gene SNPs in patients with sporadic Alzheimer's disease and control subjects	<u>zip</u> (0.5 kb)	<u>zip</u> (0.4 kb)
CGA07	Genotype and allele frequencies of the TrkA gene SNPs in patients with sporadic Alzheimer's disease and control subjects.	<u>zip</u> (2 kb)	<u>zip</u> (1.6 kb)
CGA08	Association between a missense polymorphism of the P75NTR gene and Alzheimer's disease, Association study between plasminogen activator urokinase gene and Alzheimer's disease, Association study between insulin-like growth factors (IGFs) and Alzheimer's disease.	<u>zip</u> (0.5 kb)	<u>zip</u> (0.6 kb)
CGA09	Allele frequencies of SNP in cystathionine-beta-synthase gene on senile dementia of Alzheimer type: data from population-based Japanese random samples.	<u>zip</u> (0.3 kb)	<u>zip</u> (0.3 kb)
<u>CGA10</u>	Allele frequencies of SNPs in ORMDL2 gene for gene-environment studies on Alzheimer's disease: data from population-based Japanese random samples.	<u>zip</u> (0.3 kb)	-
<u>CGA11</u>	Allele frequencies of SNPs in UCH-L1 gene for gene-environment studies on Alzheimer's disease: data from population-based Japanese random samples and patients of Alzheimer's disease.	<u>zip</u> (0.4 kb)	<u>zip</u> (0.3 kb)
CGA12	Genotype and allele frequencies of 5,438 SNPs in 222 candidate genes coding for drug metabolizing enzymes or transporters analyzed by RIKEN: data on 1,518 Japanese people including cancer patients and healthy volunteers.	<u>zip</u> (94.4 kb)	<u>zip</u> (89.4 kb)
CGA13	A case-control study on 570 patients with breast cancer and 497 controls in Thailand.	<u>zip</u> (2.5 kb)	<u>zip</u> (3.1 kb)

JPHC Study (a genome cohort in Japan)

Description	.vcf file
Whole exome sequencing using Agilent SureSelect Human All Exon V4+UTRs+lincRNAotal was performed on germline DNA of the total 192 participants of JPHC Study from different regions in Japan (17 from Iwate, 15 from Akita, 35 from Ibaraki, 13 from Niigata, 19 from Nagano, 21 from Kochi, 28 from Nagasaki, 10 from Okinawa (Chubu) and 34 from Okinawa (Miyako)). The non-reference allele call results, including false positives, were aggregated in a VCF file of the Japanese people with average health conditions, so that the file can be used as a Panel Of Normal samples (PON, see below). About PON	<u>zip</u> (31.6 mb)

MuTect, which is a method developed at the Broad Institute, identifies somatic point mutations in next generation sequencing data of cancer genomes. MuTect can use a Panel Of Normal samples (PON) filter to screen out false positives by rare error models. This VCF file was assembled as one of the standard PONs of Japanese people and is ready for the use by the MuTect pipeline. The file has the aggregated inforrmation of the non-reference allele calls by MuTect and includes false positive results.

Whole exome sequencing using Agilent SureSelect Human All Exon V4+UTRs+lincRNAotal was performed on germline DNA of the total 192 participants of JPHC Study from different regions in Japan (17 from Iwate, 15 from Akita, 35 from Ibaraki, 13 from Niigata, 19 from Nagano, 21 from Kochi, 28 from Nagasaki, 10 from Okinawa (Chubu) and 34 from Okinawa (Miyako)). The base-call results by the UnifiedGenotyper of GATK 2.2 were aggregated in a VCF file without individual genotype data.

Expression Analysis

Experiment ID	Experiment Name	GeMDBJ format	MAGE-ML format	.cel file(s)
EXPR001	Normal tissue series.	<u>zip</u> (6,397.2 kb)	<u>zip</u> (3,572.7 kb)	zip (204.5 mb) [*]
EXPR002	Kidney (Non-cancerous, Adenocarcinoma)	<u>zip</u> (3,696.8 kb)	<u>zip</u> (2,037 kb)	zip (158.8 mb) [*]
EXPR003	Kidney (Cell line)	<u>zip</u> (406.4 kb)	<u>zip</u> (264.3 kb)	zip (17.6 mb) [*]
EXPR004	Stomach (Cell line)	<u>zip</u> (1,206 kb)	<u>zip</u> (687.3 kb)	zip (49.3 mb) [*]
EXPR005	Blood, Leukocyte (Normal, Acute myeloid leukemia)	<u>zip</u> (3,945.5 kb)	<u>zip</u> (2,159.8 kb)	zip (159.2 mb) [*]
EXPR006	Blood, Cells Panel (Asthma)	<u>zip</u> (1,208.6 kb)	<u>zip</u> (703.3 kb)	zip (37.2 mb) [*]
EXPR007	Blood, PBMC (LPS/CpG stimulation time course)	<u>zip</u> (1,277.5 kb)	<u>zip</u> (726 kb)	zip (58 mb) [*]
EXPR008	Blood vessel, Cell line, Umbilical vein endothelial cell, HUVEC	<u>zip</u> (68.4 kb)	<u>zip</u> (83.7 kb)	zip (3.1 mb) [*]
EXPR009	Brain, Brain cortex (Amyotrophic lateral sclerosis as control , Alzheimer's disease)	<u>zip</u> (4,378.6 kb)	<u>zip</u> (2,537.6 kb)	zip (169.1 mb)-*
EXPR010	Blood, PBMC (LPS stimulation time course)	<u>zip</u> (1,230.5 kb)	<u>zip</u> (712.5 kb)	zip (40.8 mb)-*
EXPR011	Stomach (Cell line/spontaneous, 5Aza-dC+TSA)	<u>zip</u> (17,916.7 kb)	<u>zip</u> (9,658.8 kb)	zip (143.9 mb) ⁺ zip (212.9 mb) ⁺ zip (208.2 mb) ⁺ zip (170.5 mb) ⁺
EXPR012	Stomach (Non-cancerous, Cancerous)	<u>zip</u> (4,869.0 kb)	<u>zip</u> (2,661.9 kb)	zip (208.4 mb)-
EXPR013	B cell (Control vs. Teatment)	<u>zip</u> (362.6 kb)	<u>zip</u> (264.8 kb)	zip (11.3 mb)-
EXPR014	Eosinophil (Control vs. Teatment)	<u>zip</u> (484.1 kb)	<u>zip</u> (328.1 kb)	<u>zip</u> (14.8

EXPR015	NK cell (Spontaneous)	<u>zip</u> (122 kb)	zip (139.7 kb)	mb) * zip (3.
<u>LXI IX013</u>	Two cen (opontaneous)	<u>ZID</u> (122 NJ)	21b (100.7 kb)	mb) [*]
EXPR016	CBMC (Spontaneous)	<u>zip</u> (122.4 kb)	<u>zip</u> (140 kb)	mb)-
EXPR017	CBMC (Spontaneous)	<u>zip</u> (122.9 kb)	<u>zip</u> (140.7 kb)	<u>zip</u> (3. mb) [*]
EXPR018	РВМС	<u>zip</u> (122 kb)	<u>zip</u> (139.6 kb)	<u>zip</u> (3. mb) [*]
EXPR019	PBMC (Control vs. Teatment)	<u>zip</u> (484 kb)	zip (328.4 kb)	<u>zip</u> (1: mb) *
EXPR020	PBMC (Control vs. Teatment)	<u>zip</u> (607 kb)	zip (393.3 kb)	<u>zip</u> (18 mb) *
EXPR021	PBMC (Control vs. Teatment)	<u>zip</u> (845.4 kb)	<u>zip</u> (515.4 kb)	zip (26 mb)-
EXPR022	PBMC (Control vs. Teatment)	<u>zip</u> (848.2 kb)	<u>zip</u> (518.6 kb)	zip (26 mb)-
EXPR023	PBMC (Control vs. Teatment)	<u>zip</u> (725.3 kb)	zip (453.7 kb)	<u>zip</u> (22 mb) *
EXPR024	PBMC (Control vs. Teatment)	<u>zip</u> (484.2 kb)	zip (328.7 kb)	<u>zip</u> (14 mb)-
EXPR025	PBMC (Control vs. Teatment)	<u>zip</u> (363.7 kb)	<u>zip</u> (266 kb)	<u>zip</u> (11 mb)-
EXPR026	PBMC (Control vs. Teatment)	<u>zip</u> (844.2 kb)	<u>zip</u> (514.7 kb)	<u>zip</u> (20 mb)-
EXPR027	PBMC (GeneChip protocol comparison)	<u>zip</u> (967.5 kb)	<u>zip</u> (580.2 kb)	<u>zip</u> (3 ⁻ mb) [*]
EXPR028	PBMC (Spontaneous)	<u>zip</u> (970.3 kb)	<u>zip</u> (582.1 kb)	zip (29 mb)-
EXPR029	RPMI8226 (Control vs. Teatment)	<u>zip</u> (481.7 kb)	<u>zip</u> (326 kb)	<u>zip</u> (1: mb)-
EXPR030	RPMI8226 (Control vs. Teatment)	<u>zip</u> (840.6 kb)	<u>zip</u> (512.5 kb)	<u>zip</u> (26 mb)-
EXPR031	THP-1 (Control vs. Teatment)	<u>zip</u> (605.3 kb)	<u>zip</u> (392.1 kb)	<u>zip</u> (18 mb) *
EXPR032	Whole Blood (RNA extraction protocol comparison)	<u>zip</u> (730 kb)	<u>zip</u> (457.8 kb)	<u>zip</u> (22 mb) *
EXPR033	Whole Blood (Spontaneous)	<u>zip</u> (123.2 kb)	<u>zip</u> (140.7 kb)	<u>zip</u> (3. mb)-*
EXPR034	A549 (Control vs. Teatment)	<u>zip</u> (2,278.6 kb)	zip (1,259.2 kb)	<u>zip</u> (7′ mb)-
EXPR035	A549 (Control vs. Teatment)	<u>zip</u> (361.8 kb)	zip (264.5 kb)	<u>zip</u> (11 mb)-
EXPR036	A549 (Control vs. Teatment)	<u>zip</u> (1,078.7 kb)	zip (635.3 kb)	zip (34 mb)-
EXPR037	BEAS-2B (Control vs. Teatment)	<u>zip</u> (961 kb)	<u>zip</u> (576 kb)	zip (30 mb)-
EXPR038	BEAS-2B (Teatment)	<u>zip</u> (959.9 kb)	<u>zip</u> (574.8 kb)	<u>zip</u> (30 mb) *
EXPR039	NHBE (Control vs. Teatment)	zip (481.9 kb)	<u>zip</u> (327 kb)	<u>zip</u> (18

EXPR040	NHBE (Spontaneous)	<u>zip</u> (121.5 kb)	<u>zip</u> (139.6 kb)	<u>zip</u> (3.8 mb) *
EXPR041	NHEK-Neo (Control vs. Teatment)	<u>zip</u> (961.2 kb)	<u>zip</u> (575.9 kb)	<u>zip</u> (30 mb)-
EXPR042	Reference Total RNA (GeneChip protocol comparison)	<u>zip</u> (491.4 kb)	zip (334.4 kb)	<u>zip</u> (15 mb) *
EXPR043	Lung, (Non-cancerous, NSCLC:non-small-cell lung cancer)	<u>zip</u> (16,921 kb)	<u>zip</u> (9,135.4 kb)	zip (138.7 mb)- zip (147.2 mb)- zip (12 mb)- zip (114.3 mb)- zip (108.5 mb)-
EXPR044	Liver, (Non-cancerous, Nodule-in-nodule type HCC early and progressed components)	<u>zip</u> (1,425.9 kb)	<u>zip</u> (810.3 kb)	<u>zip</u> (61 mb) *
EXPR045	Liver, (Non-cancerous, HCCs with and without intrahepatic metastasis)	<u>zip</u> (5,431.6 kb)	zip (2,958 kb)	<u>zip</u> (64 mb) *
EXPR046	Head and Neck (carcinoma)	<u>zip</u> (7,605.3 kb)	<u>zip</u> (4,028.5 kb)	zip (347.6 mb)-*
EXPR047	Esophagus (Non-cancerous/Neoplasm)	<u>zip</u> (22,561.5 kb)	<u>zip</u> (12,094.3 kb)	zip (127.9 mb) ⁻ zip (151.3 mb) ⁻ zip (129.8 mb) ⁻ zip (147.9 mb) ⁻ zip (140.6 mb) ⁻ zip (135.9 mb) ⁻ zip (13 mb) ⁻
EXPR048	Esophagus (Neoplasm)	<u>zip</u> (7,903 kb)	<u>zip</u> (4,200 kb)	zip (336.7 mb)-
EXPR050	Liver (Cell line)	<u>zip</u> (339.5 kb)	zip (229.2 kb)	<u>zip</u> (14 mb)-
EXPR051	Pancreas (Cell line)	<u>zip</u> (1,928.5 kb)	<u>zip</u> (1,158.3 kb)	<u>zip</u> (54 mb)-
EXPR052	Ovary (Cell line)	<u>zip</u> (750.1 kb)	<u>zip</u> (451.1 kb)	zip (31 mb)-*

EXPR053	Pancreas (Xenografts of primary tumors)	zip (3,376.1 kb)	<u>zip</u> (1,917.6 kb)	zip (54.5 mb)-
EXPR054P	Soft tissue (Pleomorphic malignant fibrous histiocytoma, Myxofibrosarcoma)	zip (4,230.2 kb)	<u>zip</u> (2,282.8 kb)	<u>zip</u> (75.3 mb)-
EXPR055P	EPCs, HUVEC, LMEC, AoEC (using PCR amplified cDNA)	zip (333.4 kb)	zip (221.3 kb)	<u>zip</u> (14.9 mb)-
EXPR056	Pancreatic carcinoma (Cell line)	zip (2,597.1 kb)	zip (1,488.6 kb)	<u>zip</u> (43.3 mb)-
EXPR058P	Soft tissue (Pleomorphic malignant fibrous histiocytoma, Myxofibrosarcoma, Myxoid liposarcoma, Synovial sarcoma, Leiomyosarcoma, Fibrosarcoma, and Malignant peripheral nerve sheath tumor)	<u>zip</u> (10,648.4 kb)	<u>zip</u> (5,445.2 kb)	

^{*}Zip files will be about three times larger after the decompression. Please check your free space of HDD.

Proteome

Project Name	Description	Expression Analysis	Protein Information
Pancreatic cancer cell line	9 cancer cell lines and 2 normal cell lines.	<u>zip</u> (198 kb)	<u>zip</u> (328 kb)
Esophageal cancer	53 tumor tissues and 58 normal epithelial tissues.	<u>zip</u> (3,267 kb)	<u>zip</u> (565 kb)
Ewing's sarcoma	3 cases with good prognosis and 5 cases with poor prognosis	<u>zip</u> (166 kb)	<u>zip</u> (130 kb)
Lung Adenocarcinoma	262 tumor tissues from patients with resected stage IA-IIIA lung adenocarcinoma.	zip (6,728 kb)	<u>zip</u> (316 kb)
Malignant Pleural Mesothelioma	11 malignant pleural mesothelioma tissues, 11 lung adenocarcinoma tissues, 13 lung squamous cell carcinoma tissues, 3 pleomorphic carcinoma tissues, and 6 synovial sarcoma tissues	<u>zip</u> (1,388 kb)	<u>zip</u> (447 kb)
Colorectal cancer	66 colorectal cancer tissues and 67 normal colon mucosal tissues.	<u>zip</u> (3,377 kb)	<u>zip</u> (366 kb)
Cholangiocarcinoma	10 cancer cell lines, 9 xenograft tissues and 13 primary tumor tissues.	<u>zip</u> (1,286 kb)	<u>zip</u> (378 kb)
Liver cancer cell line	21 cancer cell lines.	<u>zip</u> (604 kb)	<u>zip</u> (590 kb)

DIGE QuickViewer Installer, Manual (Japanese Only) zip (2,035 kb)

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